External validation of serum biomarkers predicting short-term and mid/long-term relapse in Crohn's disease patients stopping infliximab

Nicolas Pierre[1], Vân Anh Huynh-Thu[2], Dominique Baiwir[3], Gabriel Mazzucchelli[4], Maximilien Fléron[3], Lisette Trzpiot[4], Gauthier Eppe[4], Edwin De Pauw[4], David Laharie[5], Jack Satsangi[6], Peter Bossuyt[7], Lucine Vuitton[8,9], Sophie Vieujean[1,10], Jean-Frédéric Colombel[11], Marie-Alice Meuwis[1,10,#], Edouard Louis[1,10,#], GETAID and the SPARE-Biocycle research group

[1]Laboratory of Translational Gastroenterology, GIGA-institute, University of Liege, Liege, Belgium; [2]Department of Electrical Engineering and Computer Science, University of Liege, Liege, Belgium; [3]GIGA Proteomics Facility, University of Liege, Liege, Belgium; [4]Laboratory of Mass Spectrometry, MolSys Research Unit, University of Liege, Liege, Belgium; [5]Service d'Hépato-gastroentérologie et oncologie digestive, Centre Hospitalier Universitaire de Bordeaux, Bordeaux, France; [6]Translational Gastroenterology Unit, John Radcliffe Hospital, Oxford, United Kingdom; [7]Imelda GI Clinical Research Center, Imelda General Hospital, Bonheiden, Belgium; [8]Department of Gastroenterology, Besançon Univeristy Hospital, Besançon, France; [9]UMR 1098, Franche-Comté University, Besançon, France; [10]Hepato-Gastroenterology and Digestive Oncology Department, Liege University Hospital, Liege, Belgium; [11]Division of Gastroenterology, Icahn School of Medicine at Mount Sina, New York, USA. [#]*Equally contributed to this work.*

Corresponding author:

Nicolas Pierre; Address: Laboratory of Translational Gastroenterology, GIGA institute, Bât. B34 Quartier Hôpital, avenue de l'Hôpital 11, 4000 Liege, Belgium; Tel: +32 4 3662538; Email: nicolas.pierre@uliege.be

Word count: 3402

Abstract

Objective: In Crohn's disease (CD) patients on combination therapy (infliximab and immunosuppressant) and stopping infliximab (STORI cohort), the risk of short-term (≤6 months) and mid/long-term relapse (>6 months) was associated with distinct blood protein profiles. Our aim was to test the external validity of this finding in the SPARE cohort.

Design: In SPARE, patients with CD in sustained steroid-free clinical remission and on combination therapy were randomly allocated to three arms: continuing combination therapy, stopping infliximab or stopping immunosuppressant. In the baseline serum of the STORI and SPARE (arm stopping infliximab) cohorts, we studied 202 immune-related proteins. The proteins associated with time to relapse (univariable Cox model) were compared between STORI and SPARE. The discriminative ability of biomarkers (individually and combined in pairs) was evaluated by the c-statistic (concordance analysis) which was compared to CRP, faecal calprotectin and a previously validated model (CEASE).

Results: In STORI and SPARE, distinct blood protein profiles were associated with the risk of short-term (eg, high level: CRP, HP, IL6, CLEC4C) and mid/long-term relapse (eg, low level: FLT3LG, SERPINA4, FGF2). At external validation, the top 10 biomarker pairs showed a higher c-statistic than the CEASE model, CRP and faecal calprotectin in predicting short-term (0.76-0.80 vs 0.74 vs 0.71 vs 0.69, respectively) and mid/long-term relapse (0.66-0.68 vs 0.61 vs 0.52 vs 0.59, respectively).

Conclusion: In CD patients stopping infliximab, we confirm that the risk of short-term and mid/long-term relapse is associated with distinct blood protein profiles showing the potential to guide infliximab withdrawal.

Keywords: Crohn's disease; infliximab withdrawal; relapse prediction; biomarkers

What is already known on this topic

In Crohn's disease patients in infliximab-induced remission, infliximab withdrawal may be contemplated for different reasons (safety concerns, healthcare costs and patient preference) but this decision remains difficult since relapse is largely unpredictable. Previously, we reported that, in Crohn's disease patients stopping infliximab (STORI cohort), the risk of short-term (≤6 months) and mid/long-term (>6 months) relapse was associated with distinct blood protein profiles. The validation of this result in an independent cohort is expected.

What this study adds

Validation in an independent cohort (SPARE) of distinct serum biomarkers predicting short-term and mid/long-term relapse in Crohn's disease patients stopping infliximab.

How this study might affect research, practice or policy

The biological condition characterising mid/long-term relapsers is of interest for basic research, as it represents early phase of Crohn's disease reactivation, i.e, the one preceding the inflammatory flare (short-term relapsers). In this setting, our data suggest that the inflammatory flare is preceded by a reduced anti-inflammatory and wound healing capacities. By showing a relation between biological profiles and prediction time-windows, our results also invite us to rethink the way that predictive biomarkers are searched. The validated biomarkers might pave the way for detecting early phase of Crohn's disease reactivation and, by doing so, they could support or discourage the decision of infliximab withdrawal.

Introduction

In Crohn's disease (CD), anti-tumour necrosis factor-α (TNFα) treatment can induce long term sustained steroid-free remission. Once remission is achieved, anti-TNFα withdrawal may be contemplated for different reasons: safety concerns, healthcare costs and patient preference[1–3]. A meta-analysis demonstrated that, in a homogenous manner across studies, ~50% of CD patients in remission and stopping anti-TNFα do not relapse over a two years period[4]. Thus, a non-negligible part of CD patients could benefit from a drug holiday. However, relapse remains largely unpredictable, thus making anti-TNFα withdrawal a difficult decision[5]. In this context, biomarkers predicting relapse are expected[5].

Previously, we reported that, in CD patients stopping infliximab (STORI cohort)[6], the risk of short-term (≤6 months) and mid/long-term relapse (>6 months) was associated with distinct blood protein profiles[7,8]. This result needs to be validated in an independent cohort. To this end, the SPARE cohort appears as an ideal and expected validation dataset[9,10]. The SPARE study is an open-label, randomised controlled trial where patients with CD in sustained steroid-free clinical remission, receiving combination therapy (infliximab and immunosuppressant), were allocated to three arms: continuing combination therapy, stopping infliximab or stopping immunosuppressant[11]. Thus, in the SPARE cohort, the arm stopping infliximab is equivalent to the STORI trial.

By using the SPARE cohort to validate the biomarkers highlighted in the STORI cohort, the present study aims were: 1) to confirm the distinct blood protein profiles associated with the risk of short-term and mid/long-term relapse; 2) to test the external validity of biomarkers predicting relapse and to compare their performance against the reference biomarkers used in clinical routine practice (C-reactive protein (CRP); faecal calprotectin (FC)) and a validated model including clinical parameters for predicting relapse after anti-TNFα withdrawal (CEASE model)[12].

Methods

Patients and protocol

The STORI (n=115) and SPARE (n=211) cohorts have been described previously[6,11]. Briefly, the CD patients in STORI (from 20 centres in Belgium and France) and SPARE (from 64 centres in Europe and Australia) were in clinical remission (CD activity index (CDAI) <150 and corticosteroid-free >6 months) and had been treated with combination therapy (infliximab and immunosuppressant >12 months in STORI and >8 months in SPARE). In the STORI study, infliximab was withdrawn, while in the SPARE study, patients were randomised to three arms: continuing combination therapy, stopping infliximab or stopping immunosuppressant. Proteins were measured in the baseline samples (sera and faeces) of the STORI and SPARE cohorts. In the STORI study, relapse was defined by a CDAI >250 or between 150 and 250 with an increase of ≥70 points from baseline over two consecutive weeks. In the SPARE study, relapse was defined by either: 1) CDAI ≥250 or between 150 and 250 with an increase of ≥70 points over two consecutive visits (1 week apart) and an objective sign of inflammation (CRP >5 $mg.L^{-1}$ or FC >250 $\mu g.g^{-1}$); 2) new or reopened perianal or entero-cutaneous fistula; 3) intra-abdominal abscess (size ≥3 cm) or a perianal abscess (size ≥2 cm); 4) intestinal obstruction confirmed by imaging and requiring hospital admission. The STORI study was registered with ClinicalTrials.gov (NCT00571337), and approved by the Ethics Committee of the Saint-Louis Hospital (CPP 2005/2014) and the AFSSAPS (0809/ALV/EG05). The SPARE study was registered with ClinicalTrials.gov (NCT02177071) and with EU Clinical Trials Register (EUDRACT 2014-002311-41), and approved by the appropriate institutional review boards or ethics committees of each country. The STORI and SPARE studies were executed in accordance with the Declaration of Helsinki, Good Clinical Practice guidelines, and applicable local regulations. All patients gave their written informed consent.

Patient and public involvement

Patients or the public were not involved in the design, or conduct, or reporting, or dissemination plans of our research.

Study design

In the baseline samples of the STORI cohort, we had previously measured 163 proteins[7,8]: 1) 69 in the serum using selected reaction monitoring (SRM); 2) 92 in the serum using proximity extension assay (PEA, immune response panel, Olink); 3) CRP (clinical measurement); 4) FC. In the present study, these measurements were carried out in baseline samples from patients of SPARE who were randomised to the arm stopping infliximab. In addition to test the external validity of our previously published results (STORI cohort), we generated a new dataset (PEA cytokine panel, 45 serum proteins) in the STORI cohort and validated it in the SPARE cohort (arm stopping infliximab).

Proteins measured by SRM were selected from our biomarker discovery pipeline performed in the STORI cohort to find predictors of relapse[8]. Those proteins are mainly related to the inflammatory response (eg, acute-phase response, blood coagulation, complement pathway) (Supplementary Table 1). The proteins measured by the PEA immune response and cytokines panels are notably involved in inflammation, adaptive immune response, cytokine-mediated signalling pathways, lymphocyte activation and defence response to virus (Supplementary Table 1).

Five proteins were measured two times (replicates of measurement), as they were included in the two PEA panels (CCL11, CXCL12, IL6, IL10) or measured by SRM and in routine clinical practice (CRP). The replicates of measurement were correlated (Spearman) to evaluate their reproducibility (Supplementary Tables 2 and 3). CXCL12 was excluded from analysis due

to the low correlation between replicates of measurement (0.52 in STORI and 0.62 in SPARE, Supplementary Tables 2 and 3). Thus, the comparison between the STORI and SPARE (arm stopping infliximab) cohorts involved 202 immune-related proteins (Supplementary Table 1).

To investigate biomarkers of relapse in a broader context than infliximab withdrawal, we also measured the SRM markers, together with CRP and FC in baseline samples of patients randomised to the other arms of the SPARE study (n=130). Due to sample availability, the proteomic experiments were performed on subsets of the STORI and SPARE cohorts (Figure 1).

Selected reaction monitoring

The SRM method was developed in-house as described in Supplementary methods and Supplementary Table 4. In SPARE (all arms), the CRP measured in clinical routine (hsCRP) and in SRM showed an excellent correlation (r=0.99) (Supplementary Figure 1). A similar result (r=0.96) was obtained in STORI[8], thus supporting the quality of our technological development. The analytical performance of our SRM method is further shown by our quality controls: intra-day precision, inter-day precision, stability of the instrumental set-up over time, guaranties on target identity and quantotypic properties of the selected peptides (Supplementary methods).

Proximity extension assay

The methods related to the PEA technology has been fully described elsewhere[13]. The analytical performances of each PEA assay are shown on Olink's website (https://www.olink.com/): intra-assay precision, inter-assay precision, limit of detection, lower limit of quantification, upper limit of quantification, hook effect and dynamic range.

176 **Measurement of faecal calprotectin and CRP**

177 FC was measured by ELISA (PhiCal test, Lysaker, Norway) in STORI and by turbidimetric
178 immunoassay (Bühlmann fCAL turbo test, Bühlmann, Switzerland) in SPARE. CRP was
179 measured by SRM and by high-sensitivity turbidimetric immunoassay (hsCRP) in STORI and
180 SPARE.

181

182 **Statistical analysis**

183 Results are reported according to the TRIPOD statements[14]. For the follow-up data, days were
184 converted to months using the following formula: 1 day = 0.0328767 month. As previously
185 described[7,8], proteins associated with the risk of short-term (≤6 months) and mid/long-term
186 relapse (>6 months) were investigated by using time to relapse and time of follow-up to
187 generate two datasets from the original one: 1) short-term relapse dataset in which mid/long-
188 term relapsers were classified as non-relapsers and the follow-up of non-relapsers was censored
189 at 6 months; 2) mid/long-term relapse dataset in which short-term relapsers and non-relapsers
190 with a follow-up ≤6 months were excluded.

191 To characterise the blood protein profiles associated with the different times to relapse, the
192 univariable Cox model was applied as previously described[7,8]. The reproduction of this analysis
193 intended to generate results comparable to our previous studies[7,8]. Briefly, the univariable Cox
194 model was used to associate the time to relapse with the dichotomised level of each protein.
195 The cut-offs for each protein level were optimised separately in STORI and in SPARE using
196 the maximum of the Youden's index. The Cox model generated the hazard ratio (HR) and its
197 associated statistics. The Cox proportional hazard assumption was checked graphically
198 (crossing of the Kaplan Meier curves) and using the Schoenfeld residuals test. The variables
199 violating this assumption were excluded. The biological convergences between STORI and
200 SPARE were investigated by selecting proteins respecting the following criteria: 1) HR with p-

value<0.1 in the short-term relapse dataset or mid/long-term relapse dataset of STORI and SPARE; 2) HR having the same direction (<1 or >1) in the short-term relapse dataset or mid/long-term relapse dataset of STORI and SPARE.

The external validation of biomarkers was restricted to proteins showing biological convergences between the two cohorts (see above) and this was performed with the following procedure. The level of each protein was first standardised to zero mean and unit variance. By using the continuous and standardised levels of proteins (individually and systematically combined in pairs), the coefficients of the Cox models were fitted to the STORI cohort (development dataset) and they were then applied to the SPARE cohort (validation dataset). Similarly, the Cox models were fitted to the SPARE cohort (development dataset) and applied to the STORI cohort (validation dataset). The discriminative ability of biomarkers was evaluated using the mean of the Harrel's c-statistic[15] obtained in the validation datasets (STORI and SPARE). As previously defined[15]: "Discrimination measures a predictor's ability to separate patients with different responses.". The c-statistic provides values between 0 and 1, where 0.5 and 1 correspond to a random and perfect discrimination, respectively. The 95% confidence interval of the c-statistic was obtained with a stratified bootstrap procedure (n=500) performed on the development datasets. The discriminative ability of biomarkers was compared to the one obtained with CRP, FC and the CEASE model including nine clinical variables[12]: age (per 10 years); smoking (yes vs no); age at diagnosis (per 5 years); L4 upper GI (yes vs no); immunosuppressant (yes vs no); type of anti-TNF used (infliximab vs adalimumab); second-line anti-TNF (yes vs no); CRP (per doubling) and FC (per doubling).

The correlations were determined by the Spearman's rank test. All statistical tests were two-sided. The statistical analyses were conducted using Python 3.9, R 3.3.1 and GraphPad Prism 9.4.1. The Cox survival analysis was performed using the Python library lifelines 0.27[16]. The heat maps and volcano plots were generate using the ggplot2 R package[17].

Results

Study population and follow-up in STORI and SPARE (arm stopping infliximab)

The clinical characteristics and the follow-up data of the STORI and SPARE cohorts are presented in Table 1. In STORI and SPARE (arm stopping infliximab), the relapse rate was 45% (52/115) and 35% (25/71) over a median follow-up of 20.9 and 24.1 months, respectively. As shown by the IQR, the follow-up showed a higher variability in STORI than SPARE (arm stopping infliximab) (7.0-30.0 vs 23.8-24.8, respectively). This difference is due to the fact that the SPARE protocol included a follow-up duration of two years while, in STORI, the end of follow-up was the date of the closure of the study. In STORI and SPARE (arm stopping infliximab), the majority of relapses occurred more than 6 months after stopping infliximab (STORI: 60% (31/52); SPARE: 60% (15/25)). The patients from STORI and SPARE (arm stopping infliximab) had close median times of short-term relapse (3.8 vs 3.5 months, respectively) and mid/long-term relapse (8.2 vs 10.3 months, respectively).

Proteins associated with the risk of short-term and mid/long-term relapse in the STORI and SPARE cohorts

The results from the STORI and SPARE (arm stopping infliximab) cohorts converged to show distinct blood protein profiles associated with the risk of short-term and mid/long-term relapse (Figures 2-3-4). Similar results were obtained when STORI was compared to all arms of SPARE (analysis restricted to SRM markers) (Supplementary Figures 2-3-4). Five proteins (CFB, CLU, IFNG, IL15, ORM1) were associated with both the risk of short-term and mid/long-term relapse in STORI and SPARE (arm stopping infliximab) (Figure 2). Of note, CLU presented an opposite association (HR>1 vs HR<1) for the risk of short-term and mid/long-term relapse (Figure 2). The convergent results between STORI and SPARE (arm

stopping infliximab) were more numerous for proteins associated with the risk of short-term relapse than for those associated with the risk of mid/long-term relapse (45 vs 23) (Figure 2). Similar results were obtained when STORI was compared to all arms of SPARE (analysis restricted to SRM markers) (Supplementary Figures 2-3-4).

In STORI and SPARE (arm stopping infliximab), a high level of inflammatory response proteins was strongly associated with the risk of short-term relapse (27 markers, among which 14 had HR with p-value<0.05 in the two cohorts) and weakly associated with the risk of mid/long-term relapse (8 markers, among which 1 (CFB) had HR with p-value<0.05 in the two cohorts) (Figure 2). The risk of mid/long-term relapse was specifically associated with a low level of proteins having anti-inflammatory properties (APOA1, HSD11B1, SERPINA4, IL10, FLT3LG) (Figure 2). Of note, the result for IL10 was obtained with the PEA immune response panel. When IL10 was measured with the PEA cytokine panel, this led to the same conclusion in STORI but not in SPARE (arm stopping infliximab) (Figure 4).

External validation of biomarkers

The selected serum proteins (Figure 2) along with the CEASE model, CRP and FC were submitted to external validation (see methods). All these results are presented in Supplementary Tables 5-10. The top 10 pairs of biomarkers showed a higher c-statistic (discriminative ability) than the CEASE model, CRP and FC to predict short-term (0.76-0.80 vs 0.74 vs 0.71 vs 0.69, respectively) and mid/long-term relapse (0.66-0.68 vs 0.61 vs 0.52 vs 0.59, respectively) (Table 2). The combination of SIT1 and HP showed a higher c-statistic than the CEASE model, CRP and FC in predicting relapse during the whole follow-up period (0.67 vs 0.66 vs 0.62 vs 0.64, respectively) (Table 2). Of note, HP and FLT3LG were overrepresented in the best pairs of biomarkers (Table 2) and, when taken individually, these proteins showed the highest c-statistic for predicting short-term (0.74) and mid/long-term relapse (0.66), respectively (Supplementary

Tables 8 and 9, respectively). Finally, the c-statistic of the top 10 pairs of biomarkers, CEASE model, CRP and FC were higher for predicting short-term than mid/long-term relapse (Table 2).

Discussion

By studying 202 serum proteins and FC in two independent cohorts (STORI and SPARE), we confirmed that, in CD patients stopping infliximab, the risk of short-term and mid/long-term relapse is associated with distinct biological profiles. We also highlighted the potential of novel serum biomarkers over clinical parameters to guide the decision of anti-TNFα withdrawal.

Overall, our study showed that predicting short-term and mid/long-term relapse require to target proteins involved in different functions. The risk of short-term relapse is mainly predicted by inflammatory proteins such as those used in clinical routine (CRP and FC), while predicting mid/long-term relapse would require targeting proteins involved in different functions (eg, anti-inflammatory and wound healing). The prediction of mid/long-term relapse has a practical interest since, after stopping infliximab, the majority of relapsers showed a time to relapse superior to 6 months (60% in STORI and SPARE). Finally, from a conceptual point of view, predicting short-term and mid/long-term relapse could make clinical decision-making more granular by guiding different therapeutic strategies.

Inflammation-related proteins were strongly associated with the risk of short-term relapse and weakly associated with the risk of mid/long-term relapse. This observation highlights the continuous progression of inflammation before relapse and, by doing so, it supports that our methodological approach (stratification based on survival data) can capture a dynamic information from cross-sectional samples (baseline).

The converging results between the two cohorts were more numerous and marked for proteins associated with risk of short-term relapse than for those associated with risk of

mid/long-term relapse. This observation appears logical and intuitive when considering the disease dynamics. It is very likely that biological dysfunctions become more prominent and homogenous as relapse approaches. Indeed, whatever the initial cause of relapse, it ends with an inflammatory flare, making the biological profile associated with the risk of short-term relapse robust. On the other hand, biological dysfunctions preceding the inflammatory flare could be more discreet and heterogeneous, making the biological profile associated with the risk of mid/long-term relapse more difficult to capture. Indeed, this state being closer to relapse triggers, it could strongly depend on individual interactions between genetics and environmental factors.

The biological condition of mid/long-term relapsers is of interest, as it represents early phase of CD reactivation, i.e, the one preceding the inflammatory flare (short-term relapsers). We reported associations between the risk of mid/long-term relapse and the low serum level of FLT3LG, FGF2, IL10 and SERPINA4. FLT3LG is a cytokine that promotes the proliferation of hematopoietic stem cells, along with the expansion and function of conventional dendritic cells (cDC) and plasmacytoid DC (pDC)[18]. Of note, we observed that CLEC4C, a specific marker of pDC[19], was associated with the risk of short-term relapse in STORI and SPARE. In a mice model of ileitis, administration of FLT3LG reduced the disease severity, and led to an expansion of the pro-regulatory dendritic cells ($CD103^+$ DC) and Tregs ($CD4^+/CD25^+/FoxP3^+$) in the lamina propria[20]. Thus, FLT3LG seems to exert potent anti-inflammatory effects in the gut[20]. FGF2 is a growth factor that promotes wound healing of the intestinal epithelium via its action on stem cell survival, epithelial cell proliferation and restitution[21]. Remarkably, FGF2 administration (recombinant) and FGF2 genetic ablation alleviated and worsened DSS-induced colitis, respectively[21,22]. Mechanistically, it has been shown that TGFβ1 stimulates the production of FGF2 by lamina propria Treg during DSS-induced colitis[22]. Then, cooperation between the FGF2 and IL17 signalling promotes epithelium wound healing[22]. IL10 has potent

and broad anti-inflammatory actions which are indispensable to maintain intestinal immune tolerance[23]. SERPINA4 is mainly produced by the liver, it has anti-inflammatory, anti-oxidative and anti-apoptotic effects[24]. Although the role of SERPINA4 in the mucosal homeostasis is unknown, its low serum level has been associated with the preclinical phase of CD (complication at diagnosis)[25]. Considering the available evidence, we hypothesise that a defect of wound healing mechanisms and a reduction of anti-inflammatory capacities precede the inflammatory flare.

Our markers converged with those highlighted in the preclinical phase of CD (PREDICT and GEM projects). Sixteen proteins predicting CD (up to 5 years before diagnosis)[26,27] and/or complication at diagnosis (B2, B3 phenotypes or surgery)[25] were also associated with the risk of relapse in STORI and SPARE (CRP, APCS, SAA1, SERPINA3, SERPIND1, SERPINA4, C5, C6, C9, CFH, CFB, CFI, HGF, CXCL9, IL10, IL7). This observation could suggest that disease reactivation after a sustained remission at least partly follows the same pathways as during preclinical phase of disease occurrence.

The generalisability of the highlighted biomarkers needs to be further evaluated. This perspective provides an opportunity to perform a "strong external validation"[28], i.e, validation in various clinical settings such as: 1) relapse after withdrawal of other anti-TNFα therapies than infliximab (eg, adalimumab, certolizumab pegol); 2) relapse after withdrawal of biologics others than anti-TNFα (anti-α4β7 integrin, anti-IL12/IL23 and anti-IL23; 3) relapse in ulcerative colitis.

Our study has several strengths. Our datasets[29,30] can be verified, reused and our work meets the need for validation studies in biomarker research[31]. Furthermore, we studied well-characterised and comparable prospective cohorts with robust technologies (SRM and PEA)[13,32]. The SRM method was developed in-house and we provide evidence of its specificity and precision (mean intra-day variation=5%, mean inter-day variation=15%). PEA is a proven

technology with high specificity[13] and precision (PEA immune response panel: mean intra-day variation=9%, mean inter-day variation=17%; PEA cytokine panel: mean intra-day variation=4%, mean inter-day variation=6%). PEA and mass spectrometry-based proteomics are complementary technologies. In blood, their combination allows to study various biological processes by increasing proteome coverage[33]. Indeed, SRM mainly targets high-abundant proteins (down to ~1 $\mu g.mL^{-1}$)[32] while PEA allows to investigate low-abundant proteins (down to ~1 $pg.mL^{-1}$)[33].

Our work has some limitations. The proportion of missing data was relatively high for FC. Secondly, the lack of replication of the IL10 finding in the SPARE cohort. This result being particularly important, its validity needs to be clarified in independents studies. Thirdly, we did not collect data on ethnicity. Given the centres involved in patient recruitment, it is very likely that our results were mainly collected from European populations. The generalisation of our findings to other populations needs to be investigated.

In summary, we confirm that the risk of short-term and mid/long-term relapse is associated with distinct blood protein profiles in CD patients stopping infliximab. The risk of short-term relapse is mainly associated with a high level of inflammatory proteins while the risk of mid/long-term relapse is notably associated with a low level of anti-inflammatory proteins. We also externally validated serum biomarkers predicting relapse and showed potential for clinical translation and guidance in treatment de-escalation.

Acknowledgments

The following GETAID Centers (investigators) participated in the STORI trial: Amiens (Jean-Louis Dupas), Bordeaux (David Laharie), Caen (Jean-Marie Reimund), Clichy-Beaujon (Yoram Bouhnik), Colombes-L Mourier (Pauline Jouet), Gent (Martine De Vos), Liège (Jacques Belaiche, Edouard Louis), Lille (Jean-Frédéric Colombel, Gwenola Vernier-

Massouille), Lyon (Stéphane Nancey), Marseille (Jean Charles Grimaud), Montpellier (Michel Veyrac), Nantes (Arnaud Boureille, Mathurin Flamant), Paris-HEGP (Raymond Jian), Paris-Lariboisière (Philippe Marteau), Paris-St Louis (Marc Lemann, Matthieu Allez), Rouen (Guillaume Savoye), Strasbourg (Bernard Duclos) and Tours (Laurence Picon).

SPARE trial was funded by the European Union's Horizon 2020 research and innovation programme, under the grant agreement number 633168— BIOCYCLE (PHC-13-2014). The members of SPARE Biocycle research group collaborative authorship can be found in the appendix. Sylvie Chevret wrote the statistical plan. GETAID was the main promotor of the SPARE clinical trial and was the promotor of the trial in France. GETAID gave delegation for specific national tasks (including, local submission to ethics committee and national health authorities, national insurances, and centres monitoring) to national co-promotors. CHU Liège (Liège, Belgium), The Skane University Hospital (Lund, Sweden), The AMC Medical Research (Amsterdam, Netherlands), The CDE Service GMBH (Kiel, Germany), the University of Edinburgh (Edinburgh, UK), and St-Vincent Hospital (Melbourne, VIC, Australia) were the national co-promotors. The GETAID, the Swedish Organization for the study of IBD (SOIBD), and the Belgian IBD research and development (BIRD) actively participated in the study (trial protocol reviewing and centres selection in France, Sweden, and Belgium).

Contributors

EL and J-FC conceived the STORI and SPARE trials. EL, DL, J-FC, PB, LV and JS were involved in the recruitment of patients and their follow-up. NP developed the SRM method with the help of M-AM and DB. NP and LT performed the sample preparation for the SRM analysis. DB, GM, MF, LT, GE and ED-P managed the instrumental set-up for the SRM analysis. NP, SV and VAH-T verified and curated the data. VAH-T and NP performed the

statistical analysis. NP created the figures. NP wrote the manuscript. EL, M-AM, SV, VAH-T, PB, JS and J-FC critically reviewed the manuscript. NP is the guarantor.

Funding

This work was supported by the European Union's Horizon 2020 under the grant agreement N° 633168 — BIOCYCLE (PHC-13-2014), the Walloon Region and the Fond Européen de Développement Régional (FEDER) [Grant portfolio 246099-510388] and internal funding from the Liege University Hospital.

Competing interests

PB has received research grants from AbbVie, Amgen, Celltrion, Mylan, Pfizer, and Takeda; lecture fees from AbbVie, Celltrion, Janssen, Lilly, and Takeda; and consulting fees from AbbVie, Arena Pharmaceuticals, Bristol Myers Squibb, Celltrion, Dr Falk Pharma, Galapagos, Janssen, Lilly, Pentax, PSI-CRO, Roche, Takeda, and Tetrameros. LV has received fees from AbbVie, Amgen, Biogen, Mylan, Takeda, MSD, Janssen, Pfizer, Ferring, and Galapagos. SV has received speaker's fees from Abbvie, Ferring, Janssen and Takeda. J-FC has received grants from AbbVie, Janssen Pharmaceuticals, Prometheus, Takeda and Bristol Myers Squibb; receiving payment for lectures from AbbVie, and Takeda; receiving consulting fees from AbbVie, Amgen, AnaptysBio, Allergan, Arena Pharmaceuticals, Boehringer Ingelheim, Bristol Myers Squibb, Celgene Corporation, Celltrion, Eli Lilly, Ferring Pharmaceuticals, Galmed Research, Glaxo Smith Kline, Genentech (Roche), Janssen Pharmaceuticals, Kaleido Biosciences, Immunic, Invea, Iterative Scopes, Merck, Landos, Microba Life Science, Novartis, Otsuka Pharmaceutical, Pfizer, Protagonist Therapeutics, Prometheus, Sanofi, Seres, Takeda, Teva, TiGenix, Vifor; and hold stock options in Intestinal Biotech Development. EL has received educational and research grants from Janssen, Pfizer, AbbVie, and Takeda,

Fresenius-Kabi; speaker fees from AbbVie, Dr Falk Pharma, Ferring, Janssen, Pfizer, Celgene, Bristol Myers Squibb (BMS), Galapagos, and Takeda; advisory board fees for AbbVie, Celgene, Ferring, Janssen, BMS, Pfizer, Takeda, Gilead-Galapagos, Arena, and Elli Lilly; and consultancy fees from AbbVie. All other authors declare no competing interests.

Data availability statement

All the data (clinical, SRM and PEA) supporting our findings are available at https://panoramaweb.org/7PNxFY.url (username: panorama+reviewer252@proteinms.net; password: ^+wW%q@f18Nc#C). For the STORI study, SRM raw data are available at https://panoramaweb.org/atQBcH.url (dataset identifier: PXD019434). For the SPARE study, SRM raw data are available at https://panoramaweb.org/7PNxFY.url (username: panorama+reviewer252@proteinms.net; password: ^+wW%q@f18Nc#C, dataset identifier: PXD051233). The Python codes used for data analysis are available at https://github.com/vahuynh/STORI_SPARE.

References

1. Louis E. Tailoring Biologic or Immunomodulator Treatment Withdrawal in Inflammatory Bowel Disease. Front Med. 2020;6:302.

2. Noor NM, Sousa P, Bettenworth D, Gomollón F, Lobaton T, Bossuyt P, et al. ECCO Topical Review on Biological Treatment Cycles in Crohn's Disease. J Crohns Colitis. 2023 Jul;17(7):1031–45.

3. Torres J, Boyapati RK, Kennedy NA, Louis E, Colombel J-F, Satsangi J. Systematic Review of Effects of Withdrawal of Immunomodulators or Biologic Agents From Patients With Inflammatory Bowel Disease. Gastroenterology. 2015 Dec;149(7):1716–30.

4. Kennedy NA, Warner B, Johnston EL, Flanders L, Hendy P, Ding NS, et al. Relapse after withdrawal from anti-TNF therapy for inflammatory bowel disease: an observational study, plus systematic review and meta-analysis. Aliment Pharmacol Ther. 2016 Apr;43(8):910–23.

5. Chapman TP, Gomes CF, Louis E, Colombel J-F, Satsangi J. De-escalation of immunomodulator and biological therapy in inflammatory bowel disease. Lancet Gastroenterol Hepatol. 2020 Jan 1;5(1):63–79.

6. Louis E, Mary J, Vernier–Massouille G, Grimaud J, Bouhnik Y, Laharie D, et al. Maintenance of Remission Among Patients With Crohn's Disease on Antimetabolite Therapy After Infliximab Therapy Is Stopped. Gastroenterology. 2012 Jan 1;142(1):63-70.e5.

7. Pierre N, Huynh-Thu VA, Marichal T, Allez M, Bouhnik Y, Laharie D, et al. Distinct blood protein profiles associated with the risk of short-term and mid/long-term clinical relapse in patients with Crohn's disease stopping infliximab: when the remission state hides different types of residual disease activity. Gut. 2023 Mar;72(3):443–50.

8. Pierre N, Baiwir D, Huynh-Thu VA, Mazzucchelli G, Smargiasso N, De Pauw E, et al. Discovery of biomarker candidates associated with the risk of short-term and mid/long-term relapse after infliximab withdrawal in Crohn's patients: a proteomics-based study. Gut. 2021 Aug 1;70(8):1450 LP – 1457.

9. Alsoud D, Vermeire S, Verstockt B. Biomarker discovery for personalized therapy selection in inflammatory bowel diseases: Challenges and promises. Curr Res Pharmacol drug Discov. 2022;3:100089.

10. Verstockt B, Abreu N, Torres J. Selecting the Ideal Candidate for Anti-TNF Discontinuation in Crohn's Disease, Dream or Reality? Gastroenterology. 2021

Jul;161(1):353–5.

11. Louis E, Resche-Rigon M, Laharie D, Satsangi J, Ding N, Siegmund B, et al. Withdrawal of infliximab or concomitant immunosuppressant therapy in patients with Crohn's disease on combination therapy (SPARE): a multicentre, open-label, randomised controlled trial. Lancet Gastroenterol Hepatol. 2023;8(3):215–27.

12. Ten Bokkel Huinink S, de Jong DC, Nieboer D, Thomassen D, Steyerberg EW, Dijkgraaf MGW, et al. Validation and update of a prediction model for risk of relapse after cessation of anti-TNF treatment in Crohn's disease. Eur J Gastroenterol Hepatol. 2022 Oct;34(10):983–92.

13. Assarsson E, Lundberg M, Holmquist G, Björkesten J, Thorsen SB, Ekman D, et al. Homogenous 96-plex PEA immunoassay exhibiting high sensitivity, specificity, and excellent scalability. PLoS One. 2014;9(4):e95192.

14. Moons KGM, Altman DG, Reitsma JB, Ioannidis JPA, Macaskill P, Steyerberg EW, et al. Transparent Reporting of a multivariable prediction model for Individual Prognosis or Diagnosis (TRIPOD): explanation and elaboration. Ann Intern Med. 2015 Jan;162(1):W1-73.

15. Harrell FEJ, Lee KL, Mark DB. Multivariable prognostic models: issues in developing models, evaluating assumptions and adequacy, and measuring and reducing errors. Stat Med. 1996 Feb;15(4):361–87.

16. Davidson-Pilon C. lifelines: survival analysis in Python. J Open Source Softw. 2019;4(40):1317.

17. Wickham H. Ggplot2: Elegant Graphics for Data Analysis. 2nd ed. Springer Publishing Company, Incorporated; 2009.

18. Cueto FJ, Sancho D. The Flt3L/Flt3 Axis in Dendritic Cell Biology and Cancer Immunotherapy. Cancers (Basel). 2021 Mar;13(7).

19. Chiffoleau E. C-Type Lectin-Like Receptors As Emerging Orchestrators of Sterile Inflammation Represent Potential Therapeutic Targets. Front Immunol. 2018;9:227.

20. Collins CB, Aherne CM, McNamee EN, Lebsack MDP, Eltzschig H, Jedlicka P, et al. Flt3 ligand expands $CD103^+$ dendritic cells and $FoxP3^+$ T regulatory cells, and attenuates Crohn's-like murine ileitis. Gut. 2012 Aug;61(8):1154–62.

21. Matsuura M, Okazaki K, Nishio A, Nakase H, Tamaki H, Uchida K, et al. Therapeutic effects of rectal administration of basic fibroblast growth factor on experimental murine colitis. Gastroenterology. 2005 Apr;128(4):975–86.

22. Song X, Dai D, He X, Zhu S, Yao Y, Gao H, et al. Growth Factor FGF2 Cooperates with Interleukin-17 to Repair Intestinal Epithelial Damage. Immunity. 2015 Sep;43(3):488–501.

23. Wei H-X, Wang B, Li B. IL-10 and IL-22 in Mucosal Immunity: Driving Protection and Pathology. Front Immunol. 2020;11:1315.

24. Li P, Bledsoe G, Yang Z-R, Fan H, Chao L, Chao J. Human kallistatin administration reduces organ injury and improves survival in a mouse model of polymicrobial sepsis. Immunology. 2014 Jun;142(2):216–26.

25. Choung RS, Petralia F, Torres J, Ungaro RC, Porter C, Sato T, et al. Preclinical Serological Signatures are Associated With Complicated Crohn's Disease Phenotype at Diagnosis. Clin Gastroenterol Hepatol. 2023 Feb;21(11):2928-2937.e12.

26. Leibovitzh H, Lee SH, Raygoza Garay JA, Espin-Garcia O, Xue M, Neustaeter A, et al. Immune response and barrier dysfunction-related proteomic signatures in preclinical

phase of Crohn's disease highlight earliest events of pathogenesis. Gut. 2023 Feb;72(8):1462–71.

27. Torres J, Petralia F, Sato T, Wang P, Telesco SE, Choung RS, et al. Serum Biomarkers Identify Patients Who Will Develop Inflammatory Bowel Diseases Up to 5 Years Before Diagnosis. Gastroenterology. 2020 Jul;159(1):96–104.

28. Steyerberg EW, Vergouwe Y. Towards better clinical prediction models: seven steps for development and an ABCD for validation. Eur Heart J. 2014 Aug;35(29):1925–31.

29. [dataset] Pierre N, Huynh-Thu VA, Baiwir D, Mazzucchelli G, Fléron M, Trzpiot L, et al. Data from: External validation of serum biomarkers predicting short-term and mid/long-term relapse in Crohn's disease patients stopping infliximab. Panorama. 2024. https://panoramaweb.org/7PNxFY.url

30. [dataset] Pierre N, Baiwir D, Huynh-Thu VA, Mazzucchelli G, Smargiasso N, De Pauw E, et al. Data from: Discovery of biomarker candidates associated with the risk of short-term and mid/long-term relapse after infliximab withdrawal in Crohn's patients: a proteomics-based study. Panorama. 2020. https://panoramaweb.org/atQBcH.url

31. Gisbert JP, Chaparro M. Clinical Usefulness of Proteomics in Inflammatory Bowel Disease: A Comprehensive Review. J Crohns Colitis. 2019 Mar;13(3):374–84.

32. Picotti P, Aebersold R. Selected reaction monitoring-based proteomics: workflows, potential, pitfalls and future directions. Nat Methods. 2012 May;9(6):555–66.

33. Petrera A, von Toerne C, Behler J, Huth C, Thorand B, Hilgendorff A, et al. Multiplatform Approach for Plasma Proteomics: Complementarity of Olink Proximity Extension Assay Technology to Mass Spectrometry-Based Protein Profiling. J Proteome Res. 2021 Jan;20(1):751–62.

Table 1. Patients' characteristics and follow-up	STORI (n=115)	SPARE, infliximab withdrawal (n=71)	SPARE, immunosuppressant withdrawal (n=69)	SPARE, combination therapy (n=71)
Age (years), median (IQR)	32 (26-39)	32 (25-42.5)	31 (26–44)	37 (27-45.5)
Gender				
Female	66 (57%)	28 (39%)	31 (45%)	33 (46%)
Male	49 (43%)	43 (61%)	38 (55%)	38 (54%)
Disease duration (years), median (IQR)	7.8 (4.5-11.8)	6.7 (3.3-10.7)	6.8 (2.9–12.6)	6.4 (3.2-12.7)
Active smoker	45 (39%)	14 (20%)	17 (25%), n=68	17 (24%)
Disease location				
Ileal (L1)	14 (12%)	10 (14%)	13 (19%)	15 (21%)
Colonic (L2)	36 (31%)	20 (28%)	21 (30%)	24 (34%)
Ileocolonic (L3)	64 (56%)	41 (58%)	35 (51%)	32 (45%)
Upper gastrointestinal tract (L4)	9 (8%)	8 (11%)	5 (7%)	10 (14%)
Previous intestinal resection	25 (22%)	13 (18%)	17 (25%)	13 (18%)
Steroid treatment between 12 and 6 months before screening	8 (7%)	1 (1%)	3 (4%)	6 (8%), n=69
CDAI, median (IQR)	37 (20-61)	38 (18–57.5)	42 (25–83)	53 (25-77.5)
Treatment history				
Methotrexate	19 (17%)	2 (3%)	6 (9%)	5 (7%)
Azathioprine/mercaptopurine	96 (83%)	69 (97%)	63 (91%)	66 (93%)
Duration of infliximab treatment (years), median (IQR)	2.2 (1.5-3.1)	2.5 (1.4–4.5)	2.6 (1.6–4.0)	2.3 (1.5-3.6)
Endoscopy				
CDEIS, median (IQR)	0.7 (0.0-2.9)	0 (0-0)	0 (0-0)	0 (0-0)
CDEIS=0	40 (35%)	63 (89%)	57 (83%)	58 (82%)
Remaining ulcers	39 (34%)	8 (11%)	6 (9%)	8 (11%)
Biologic variables				
Haemoglobin level, $g.L^{-1}$, median (IQR)	135 (128-144)	142 (137-151)	140 (133–149)	140 (132-145)
Haematocrit, %, median (IQR)	40 (37-43)	41 (40-44)	41 (39-44)	41 (39-43.5)
Leukocyte count, $10^9.L^{-1}$, median (IQR)	6.1 (5.0-7.5)	5.3 (4.5-7.0)	6.3 (5.3–7.6)	5.5 (4.9-6.8)
Platelet count, $10^9.L^{-1}$, median (IQR)	272 (233-313)	256 (216–299), n=69	254 (215-302)	244 (217-307)
hsCRP level, $mg.L^{-1}$, median (IQR)	2.0 (0.9-4.8), n=109	1.2 (0.6-2.3), n=69	1.2 (0.5-2.6), n=66	1.2 (0.5-2.8), n=69
Faecal calprotectin, $\mu g.g^{-1}$, median (IQR)	51 (30-318), n=85	95 (22-289), n=47	61 (22-195), n=53	77 (25-315), n=44
Infliximab trough level, $mg.L^{-1}$, median (IQR)	3.7 (1.7-8.0)	4.1 (2.5-6.3), n=69	4.1 (2.4-5.7), n=66	3.6 (2.6-5.9), n=69
Follow-up				
Number of relapsers	52 (45%)	25 (35%)	6 (9%)	8 (11%)
Number of short-term relapsers (< 6 months)	21 (40%)	10 (40%)	2 (33%)	2 (25%)
Number of mid/long-term relapsers (> 6 months)	31 (60%)	15 (60%)	4 (67%)	6 (75%)

Number of non-relapsers	63 (55%)	46 (65%)	63 (91%)	63 (89%)
Time to relapse of short-term relapsers (months), median (IQR)	3.8 (2.8-4.4)	3.5 (3.3-3.9)	4.6 (4.2-5.1)	3.7 (2.8-4.6)
Time to relapse of mid/long-term relapsers (months), median (IQR)	8.2 (6.8-12.1)	10.3 (7.9-12.6)	19.1 (18.2-20.4)	19.0 (16.9-20.7)
Time of follow-up of non-relapsers (months), median (IQR)	20.9 (7.0-30.0)	24.1 (23.8-24.8)	23.9 (21.6-24.3)	23.9 (17.6-24.2)

Table 2. Discriminative ability of the top 10 biomarker pairs, FC, CRP and CEASE model for predicting relapse

	Gene names 1	Gene names 2	Mean c-statistic (CI) validation datasets (STORI and SPARE), n=SPARE-STORI
Short-term relapse (< 6 months)	CLEC4C	ITGA11	0.80 (0.76-0.81), n=63-101
	FC	HP	0.79 (0.70-0.81), n=44-77
	FC	F9	0.78 (0.67-0.79), n=44-77
	CLEC4C	SAA1	0.77 (0.53-0.79), n=63-101
	IL6_PEA_IR	HP	0.77 (0.66-0.78), n=63-101
	KLRD1	HP	0.77 (0.74-0.78), n=63-101
	ITGA11	HP	0.77 (0.74-0.78), n=63-101
	CLEC4C	HP	0.77 (0.73-0.78), n=63-101
	CLEC4C	CRP_SRM	0.77 (0.66-0.78), n=63-101
	IL6_PEA_cytokine	HP	0.76 (0.71-0.79), n=63-102
	CEASE model	NA	0.74, n=46-83
	hsCRP	NA	0.71, n=69-109
	FC	NA	0.69, n=47-85
Mid/long-term relapse (> 6 months)	FLT3LG	TNF	0.68 (0.65-0.69), n=53-73
	SIT1	FLT3LG	0.67 (0.60-0.68), n=53-73
	FLT3LG	SERPINA4	0.67 (0.57-0.69), n=53-73
	CXCL9	FLT3LG	0.67 (0.55-0.69, n=53-73
	FLT3LG	IFNG	0.67 (0.55-0.70), n=53-73
	FLT3LG	IL17C	0.66 (0.53-0.67), n=53-73
	FGF2	FLT3LG	0.66 (0.58-0.71), n=53-73
	FLT3LG	C8A	0.66 (0.55-0.67), n=53-73
	FGF2	ORM1	0.66 (0.49-0.67), n=53-73
	IL10_PEA_IR	FLT3LG	0.66 (0.61-0.68), n=53-73
	CEASE model	NA	0.61, n=40-56
	FC	NA	0.59, n=41-57
	hsCRP	NA	0.52, n=57-76
Relapse in the non-stratified dataset	SIT1	HP	0.67 (0.61-0.68) n=63-101
	CEASE model	NA	0.66, n=46-83
	HP	APOA1	0.66 (0.62-0.68), n=67-102
	FLT3LG	HP	0.66 (0.63-0.67), n=63-101
	hsCRP	HP	0.66 (0.59-0.67), n=67-98
	CRP_SRM	HP	0.66 (0.58-0.67), n=67-102
	MILR1	HP	0.65 (0.55-0.67), n=63-101
	HP	SAA1	0.65 (0.58-0.66), n=67-102
	HP	C2	0.65 (0.60-0.66), n=67-102
	FC	HP	0.65 (0.44-0.69), n=44-77
	hsCRP	SIT1	0.65 (0.58-0.67), n=63-98
	FC	NA	0.64, n=47-85
	hsCRP	NA	0.62, n=69-109

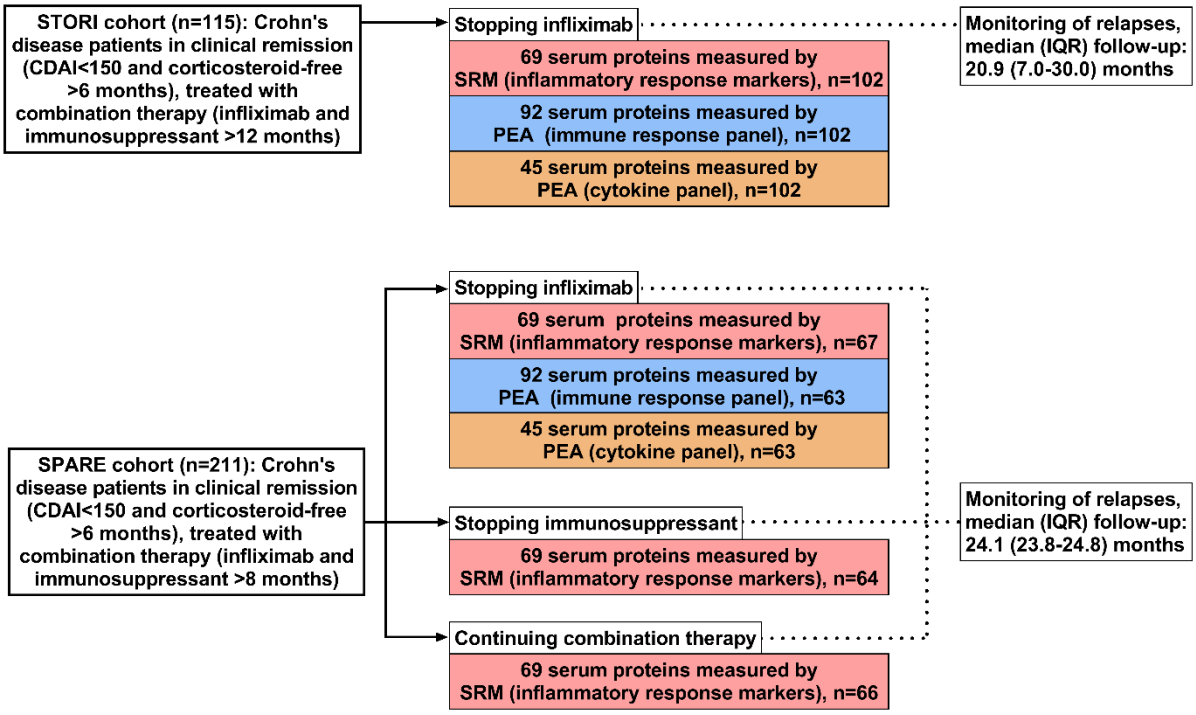


Figure 1. Experimental design. CDAI, Crohn's Disease Activity Index; IQR, interquartile range; PEA, proximity extension assay; SRM, selected reaction monitoring.

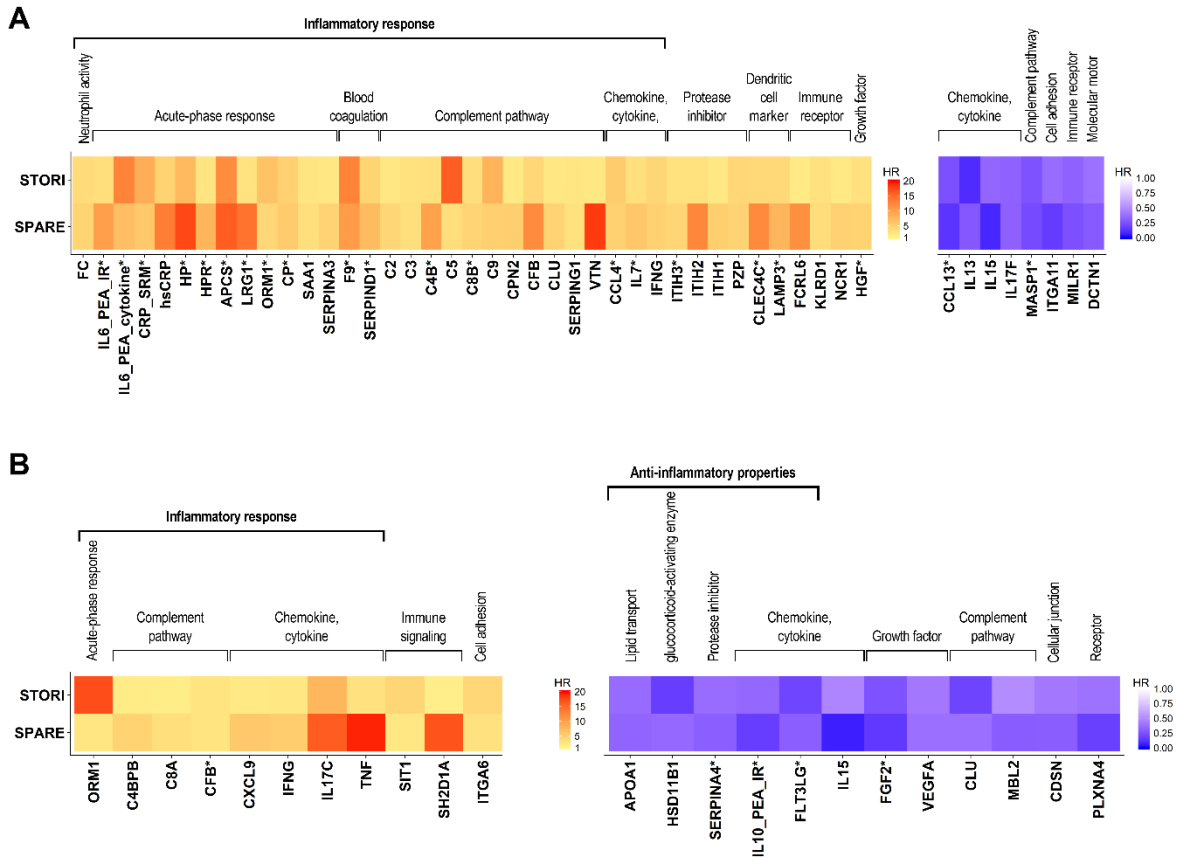


Figure 2. Proteins associated with the risk of short-term and mid/long-term relapse in the STORI and SPARE (arm stopping infliximab) cohorts. (A) risk of short-term relapse (≤6 months). (B) risk of mid/long-term relapse (>6 months). p-value<0.1 in STORI and SPARE; *p-value<0.05 in STORI and SPARE. CRP_SRM: CRP measured by SRM; hsCRP: CRP measured by high-sensitivity turbidimetric immunoassay; IL6_PEA_IR: IL6 measured by the PEA immune response panel; IL6_PEA_cytokine: IL6 measured by the PEA cytokine panel; IL10_PEA_IR: IL10 measured by the PEA immune response panel; IL10_PEA_cytokine: IL10 measured by the PEA cytokine panel.

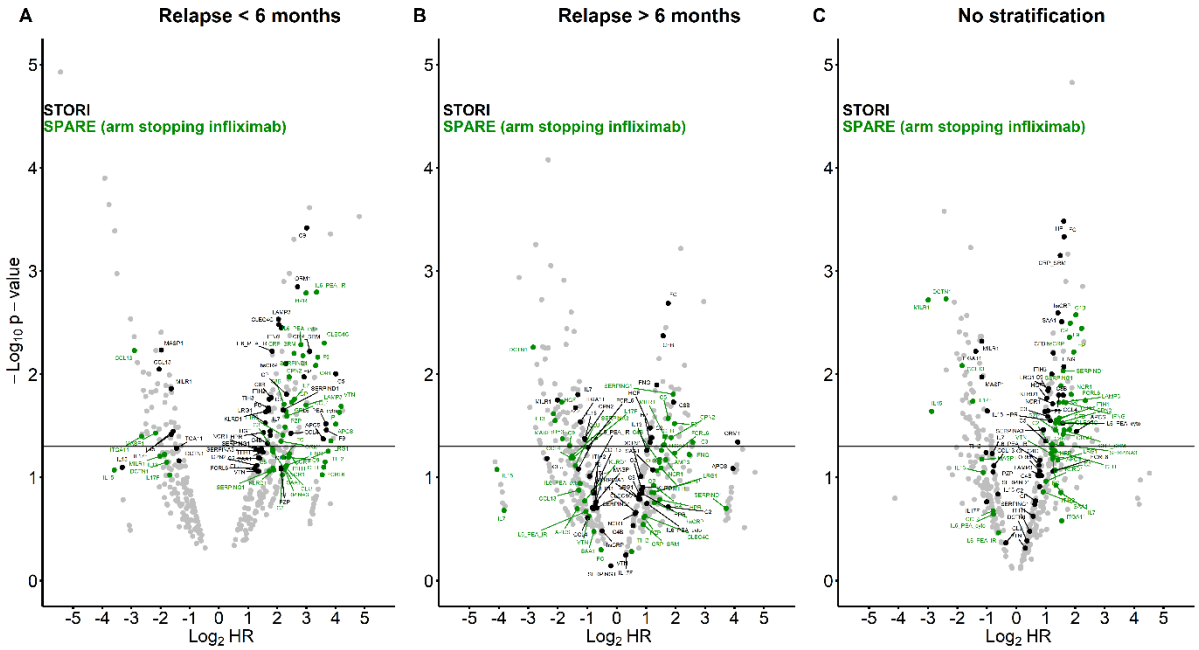


Figure 3. Proteins associated with the risk of short-term relapse in STORI and SPARE (arm stopping infliximab). In STORI and SPARE (arm stopping infliximab), the association between the level of each protein and the time to relapse was depicted in volcano plots (A: short-term relapse dataset; B: mid/long-term relapse dataset; C: non-stratified dataset) with the x-axis representing the magnitude of the risk (Log_2 HR) and the y-axis its degree of significance ($-Log_{10}$ p-value). The horizontal lines correspond to p-value=0.05. CRP_SRM: CRP measured by SRM; hsCRP: CRP measured by high-sensitivity turbidimetric immunoassay; IL6_PEA_IR: IL6 measured by the PEA immune response panel; IL6_PEA_cytokine: IL6 measured by the PEA cytokine panel.

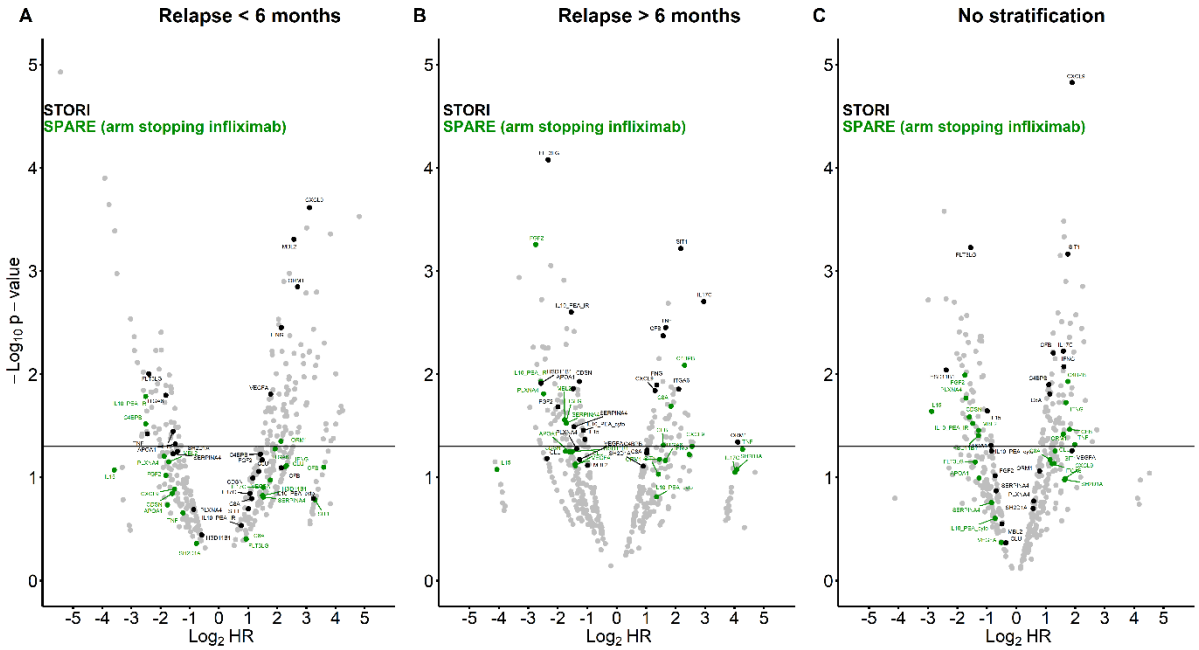
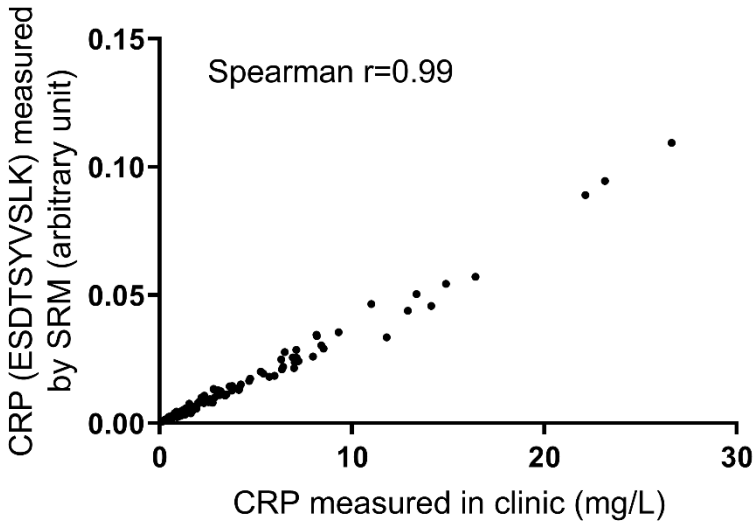
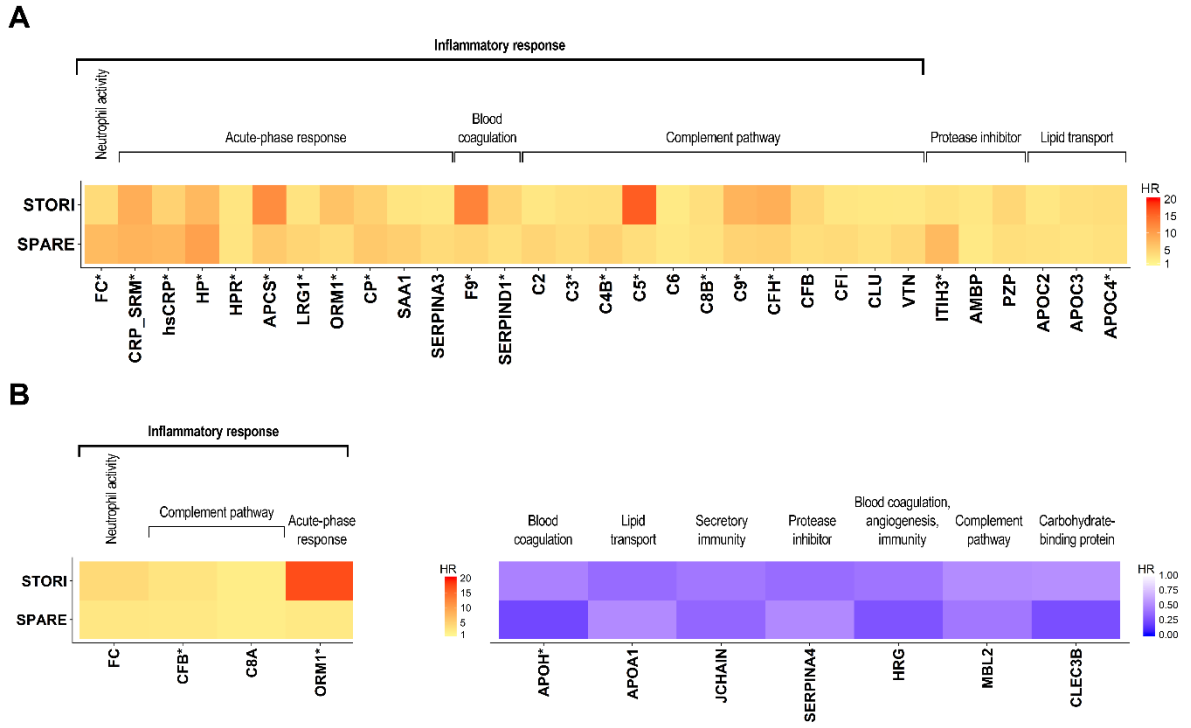


Figure 4. Proteins associated with the risk of mid/long-term relapse in STORI and SPARE (arm stopping infliximab). In STORI and SPARE (arm stopping infliximab), the association between the level of each protein and the time to relapse was depicted in volcano plots (A: short-term relapse dataset; B: mid/long-term relapse dataset; C: non-stratified dataset) with the x-axis representing the magnitude of the risk (Log_2 HR) and the y-axis its degree of significance ($-Log_{10}$ p-value). The horizontal lines correspond to p-value=0.05. IL10_PEA_IR: IL10 measured by the PEA immune response panel; IL10_PEA_cytokine: IL10 measured by the PEA cytokine panel.

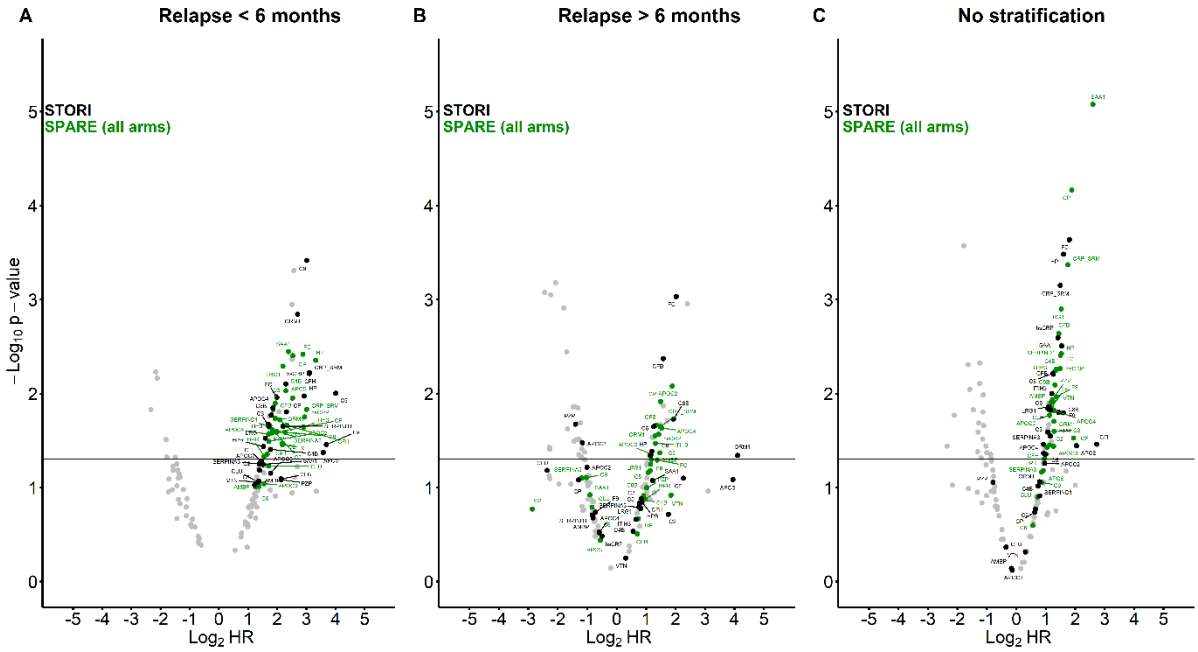


Supplementary Figure 1. Correlation between CRP measured in routine clinical practice and in SRM. Correlation obtained in the SPARE cohort (n=196). CRP, C-reactive protein; SRM, selected reaction monitoring.

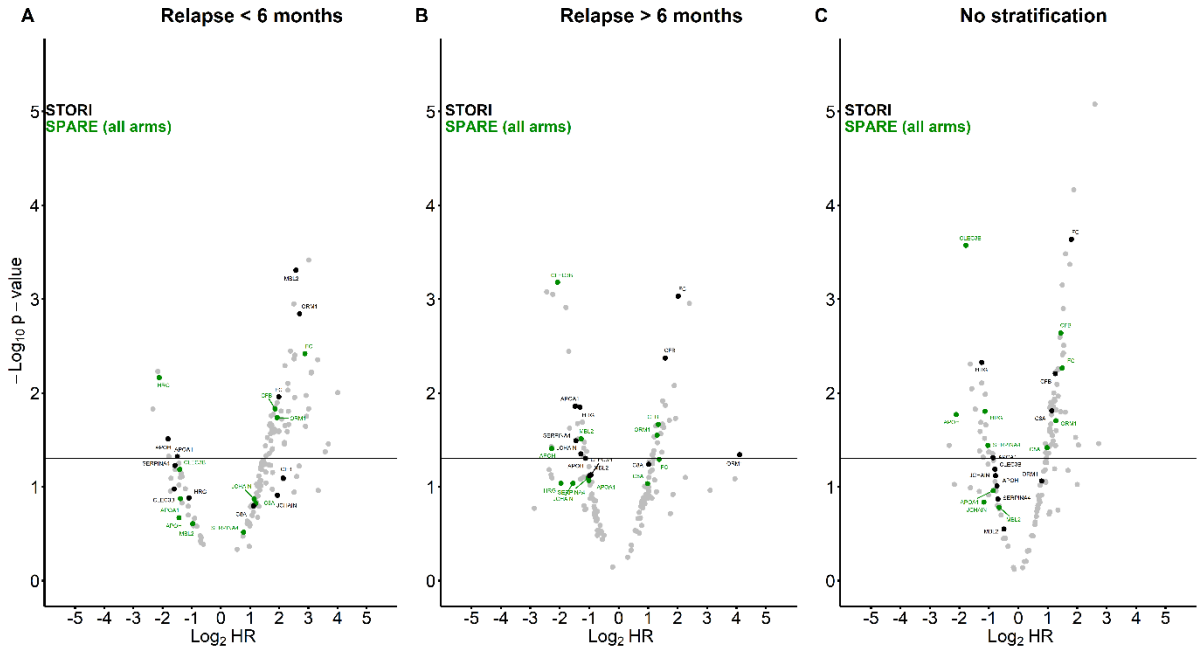


Supplementary Figure 2. Proteins associated with the risk of short-term and mid/long-term relapse in the STORI and SPARE (all arms) cohorts. (A) risk of short-term relapse

(≤6 months). (B) risk of mid/long-term relapse (>6 months). p-value<0.1 in STORI and SPARE; *p-value<0.05 in STORI and SPARE. CRP_SRM: CRP measured by SRM; hsCRP: CRP measured by high-sensitivity turbidimetric immunoassay.



Supplementary Figure 3. Proteins associated with the risk of short-term relapse in STORI and SPARE (all arms). In STORI and SPARE (all arms), the association between the level of each protein and the time to relapse was depicted in volcano plots (A: short-term relapse dataset; B: mid/long-term relapse dataset; C: non-stratified dataset) with the x-axis representing the magnitude of the risk (Log_2 HR) and the y-axis its degree of significance ($-Log_{10}$ p-value). The horizontal lines correspond to p-value=0.05. CRP_SRM: CRP measured by SRM; hsCRP: CRP measured by high-sensitivity turbidimetric immunoassay.



Supplementary Figure 4. Proteins associated with the risk of mid/long-term relapse in STORI and SPARE (all arms). In STORI and SPARE (all arms), the association between the level of each protein and the time to relapse was depicted in volcano plots (A: short-term relapse dataset; B: mid/long-term relapse dataset; C: non-stratified dataset) with the x-axis representing the magnitude of the risk (Log_2 HR) and the y-axis its degree of significance ($-Log_{10}$ p-value). The horizontal lines correspond to p-value=0.05.

SRM is a targeted mass spectrometry technique that can be used to perform bottom-up proteomics and known to generate robust quantitative information[1]. The SRM method used in the present study is an upgrade of the one we developed previously[2]. The main improvement concerns the use of synthetic peptides with stable isotope-labelling to normalise the signal of every endogenous targeted peptide. The present SRM method targets 70 proteins, 196 peptides, 392 precursors and 1246 fragments (Supplementary Table 5). The Supplementary method 1 describes the technical development of our SRM method. The Supplementary method 2 presents an evaluation of our SRM method with a series of quality controls (intra-day precision, inter-day precision, stability of the instrumental set-up over time, guaranties on target identity and quantotypic properties of the selected peptides).

Supplementary method 1: SRM method

SRM method development

MS/MS experiments were conducted as previously described[2] to generate SRM coordinates (m/z of precursors, m/z of fragments, retention times) from synthetic peptides. The final selection of peptides and fragments result from steps of refinements which were guided by intra-day precision (CV<30%), signal quality, signal intensity (3-5 most intense fragments, 2-4 most intense precursors) and the evaluation of quantotypic properties of peptides (see below).

Sample preparation

Serum protein concentration was obtained using the BCA Protein Assay Kit (Thermo Fisher Scientific) according to the manufacturer's instructions. Then, 20 µg of total proteins and 70 ng of the internal standard protein (Enolase 1, ENO1) were digested with the Trypsin/Lys-C Mix Mass Spec Grade (Promega, USA) according to the manufacturer's instructions. The peptide mixture (3.5 µg) was purified on ZipTip C18 (Thermo Fisher Scientific), vacuum-dried and

stored at –20 °C. Prior to injection on the LC-MS system, the peptide mixture was solubilised in 46.7 µL of a solution containing: 1) 31.5 µL of 0.1% formic acid; 2) crude synthetic peptides with stable isotope-labelling (^{13}C, ^{15}N on the C-terminal R/K or internal L) (SpikeTides L, JPT Peptide Technologies, DE) which are analogues of the endogenous targeted peptides: 10 µL of the peptide solution concentrated at 52 fmol.µL^{-1} (each peptide) in 11.3% acetonitrile and 80% ammonium bicarbonate 0.1 M; 3) a synthetic peptide (VNQIGTLSESIK, ENO1) with stable isotope-labelling (^{13}C, ^{15}N on the C-terminal K) (HeavyPeptide AQUA Ultimate, Thermo Fisher Scientific, USA): 5.2 µL of the peptide solution concentrated at 50 fmol.µL^{-1} in 5% acetonitrile. Finally, 9 µL of this mix was injected on the instrumental set-up thus corresponding to 0.675 µg of proteins digest (without considering losses during sample preparation), 100 fmol of each SpikeTides L heavy peptide and 50 fmol of the VNQIGTLSESIK synthetic peptide.

Instrumental set-up

SRM was performed on a triple quadrupole (QQQ) mass spectrometer Xevo^{TM} TQ-S equipped with a nano-electrospray source operated in positive ion mode. The capillary voltage, the temperature of the source and the gas pressure were set to respectively 2.9 kV, 100 °C and 3.5e-3 (argon gas flow set at 0.15). A mass window of 0.75 Da was used to select precursors and fragments in Q1 and Q3, respectively. In Q2, precursors were fragmented with a predicted collision energy[3]. The measurements were performed with the following settings: scheduled mode, a retention time window of 4 min, at least 12 points per peak (considering a peak width of 25 s). These parameters resulted in dwell times ranging from 11 to 257 ms, cycle times ranging from 1.03 to 2.11 s and a number of points per peak ranging from 14 to 29 (considering a peak width of 30 s).

Raw data processing

The raw data were imported and processed in Skyline (version 21.2.0.369). The automatic integration of each SRM trace was manually controlled and corrected if necessary. The quantification was based on the intensity of the 2 most intense fragments of each peptide (total area). The protein quantification was obtained with the following formula:

$$\frac{\text{((total area peptide 1 +…+ total area peptide n)/ (total area peptide heavy 1 +…+ total area peptide heavy n))}}{\text{(total area VNQIGTLSESIK/ total area VNQIGTLSESIK heavy)}}$$

Supplementary method 2: quality controls of the SRM method

Intra-day precision

The intra-day precision was determined by the coefficient of variation (CV) calculated from 3 digestion replicates (technical replicates) of 2 serum pools representative of the study: non-relapsers patients (n=7) and relapsers patients (n=7) of the STORI study. Based on this repeatability test, the 69 proteins of the SRM method were measured with a mean CV (±SD) of 5.1% (2.3) and 4.5% (3.0) in the serum pool of non-relapsers and relapsers, respectively (Supplementary Table 5). The maximum intra-day CV was 18.8% (C-reactive protein (CRP) in the serum pool of non-relapsers) (Supplementary Table 5).

Inter-day precision

The samples were prepared in 9 days and by groups of 19-24. They were injected on the instrumental set-up over a period of ~2 months. To control the inter-day variation of this procedure, an external standard (serum pool) was digested each day of the sample processing. These external standards were injected every 25 samples (9 in all) and allowed to calculate a mean inter-day CV (±SD) of 14.6% (1.9) for the 69 targeted proteins. The maximum inter-day CV was 19.3% (Apolipoprotein A-II (APOA2)).

Stability of the instrumental set-up over time

The samples of the SPARE cohort were injected on the LC-MS system over a period of ~2 months. To evaluate the stability of the instrumental set-up during this period, purification (zip-tip) replicates of a digested sample (serum pool) were injected every 24 samples (10 in all). For this quality control, the mean CV (±SD) of the 69 targeted proteins was 6.4% (2.2) and the maximum CV was 14.2% (APOA2).

Guaranties on target identity

In the initial SRM method, endogenous peptides were identified through MS/MS data as previously described[2]. In this upgraded SRM method, identification of endogenous peptides was further supported by the systematic co-elution of their heavy counterpart whose sequence was confirmed by MS/MS data. As recommended[4], the identity of peptides was also supported by the co-elution of their fragments which was systematically observed in our experiment.

Quantotypic properties of peptides

In bottom-up proteomics, quantitative information relies on the assumption that the abundance of a given protein is stoichiometrically equivalent to abundance of its peptides (quantotypic). Currently, there is no way to predict and guaranty the quantotypic properties of peptides[5]. Intuitively, if they have quantotypic properties, peptides of the same protein should have highly correlated signals[5]. Thus, controlling these correlations is way to evaluate the quantotypic properties of peptides[5]. In our experiment, the signal of peptides of the same protein were compared using correlation matrices (202 correlations) performed on the 219 injected samples. Based on this analysis, the mean (± SD) coefficient of correlation was 0.95 (0.06) and its minimum was 0.69 (LTLTPWVGLR vs CTWLIEGQPNR, attractin (ATRN)). For the 5 proteins measured with 1 peptide (CRP, APOA2, Immunoglobulin heavy variable 3-23

(IGHV3-23), Mannan-binding lectin serine protease 2 (MASP2), ENO1), the correlation matrices abovementioned could not be made. The quantotypic properties of the peptide measuring CRP (ESDTSYVSLK) is well supported by its correlation with the clinical measurement of CRP which was obtained in the SPARE (Spearman r=0.99, Figure 1) and STORI cohorts (Spearman r=0.96)[2].

References

1. Picotti P, Aebersold R Selected reaction monitoring-based proteomics: workflows, potential, pitfalls and future directions. *Nat Methods* 2012;**9**(6):555–66.

2. Pierre N, Baiwir D, Huynh-Thu VA, Mazzucchelli G, Smargiasso N, De Pauw E, et al. Discovery of biomarker candidates associated with the risk of short-term and mid/long-term relapse after infliximab withdrawal in Crohn's patients: a proteomics-based study. *Gut* 2021;**70**(8):1450 LP – 1457.

3. Maclean B, Tomazela DM, Abbatiello SE, Zhang S, Whiteaker JR, Paulovich AG, et al. Effect of collision energy optimization on the measurement of peptides by selected reaction monitoring (SRM) mass spectrometry. *Anal Chem* 2010;**82**(24):10116–24.

4. Carr SA, Abbatiello SE, Ackermann BL, Borchers C, Domon B, Deutsch EW, et al. Targeted peptide measurements in biology and medicine: best practices for mass spectrometry-based assay development using a fit-for-purpose approach. *Mol Cell Proteomics* 2014:907–17.

5. Worboys JD, Sinclair J, Yuan Y, Jorgensen C Systematic evaluation of quantotypic peptides for targeted analysis of the human kinome. *Nat Methods* 2014;**11**(10):1041–4.

Supplementary Table 1. Proteins investigated

Technology	Protein names	Gene names	Uniprot accession numbers
PEA (immune response)	Neurabin-2	PPP1R9B	Q96SB3
PEA (immune response)	Beta-galactosidase	GLB1	P16278
PEA (immune response)	PC4 and SFRS1-interacting protein	PSIP1	O75475
PEA (immune response)	Zinc finger and BTB domain-containing protein 16	ZBTB16	Q05516
PEA (immune response)	Interleukin-1 receptor-associated kinase 4	IRAK4	Q9NWZ3
PEA (immune response)	Tryptase alpha/beta-1	TPSAB1	Q15661
PEA (immune response)	Hematopoietic lineage cell-specific protein	HCLS1	P14317
PEA (immune response)	Contactin-associated protein-like 2	CNTNAP2	Q9UHC6
PEA (immune response)	C-type lectin domain family 4 member G	CLEC4G	Q6UXB4
PEA (immune response)	Interferon regulatory factor 9	IRF9	Q00978
PEA (immune response)	Tumor necrosis factor receptor superfamily member EDAR	EDAR	Q9UNE0
PEA (immune response)	Interleukin-6	IL6	P05231
PEA (immune response)	Diacylglycerol kinase zeta	DGKZ	Q13574
PEA (immune response)	C-type lectin domain family 4 member C	CLEC4C	Q8WTT0
PEA (immune response)	Interleukin-1 receptor-associated kinase 1	IRAK1	P51617
PEA (immune response)	C-type lectin domain family 4 member A	CLEC4A	Q9UMR7
PEA (immune response)	Peroxiredoxin-1	PRDX1	Q06830
PEA (immune response)	Thioredoxin-dependent peroxide reductase, mitochondrial	PRDX3	P30048
PEA (immune response)	Fibroblast growth factor 2	FGF2	P09038
PEA (immune response)	Peroxiredoxin-5, mitochondrial	PRDX5	P30044
PEA (immune response)	Inactive dipeptidyl peptidase 10	DPP10	Q8N608
PEA (immune response)	Tripartite motif-containing protein 5	TRIM5	Q9C035
PEA (immune response)	Dynactin subunit 1	DCTN1	Q14203
PEA (immune response)	Integrin alpha-6	ITGA6	P23229
PEA (immune response)	Corneodesmosin	CDSN	Q15517
PEA (immune response)	Polypeptide N-acetylgalactosaminyltransferase 3	GALNT3	Q14435
PEA (immune response)	FXYD domain-containing ion transport regulator 5	FXYD5	Q96DB9
PEA (immune response)	TNF receptor-associated factor 2	TRAF2	Q12933
PEA (immune response)	E3 ubiquitin-protein ligase TRIM21	TRIM21	P19474
PEA (immune response)	Leukocyte immunoglobulin-like receptor subfamily B member 4	LILRB4	Q8NHJ6
PEA (immune response)	Neurotrophin-4	NTF4	P34130
PEA (immune response)	Keratin, type I cytoskeletal 19	KRT19	P08727
PEA (immune response)	Integral membrane protein 2A	ITM2A	O43736
PEA (immune response)	Histamine N-methyltransferase	HNMT	P50135
PEA (immune response)	Eotaxin	CCL11	P51671

PEA (immune response)	Allergin-1	MILR1	Q7Z6M3
PEA (immune response)	Egl nine homolog 1	EGLN1	Q9GZT9
PEA (immune response)	Nuclear factor of activated T-cells, cytoplasmic 3	NFATC3	Q12968
PEA (immune response)	Lymphocyte antigen 75	LY75	O60449
PEA (immune response)	Eukaryotic translation initiation factor 5A-1	EIF5A	P63241
PEA (immune response)	Eukaryotic translation initiation factor 4 gamma 1	EIF4G1	Q04637
PEA (immune response)	T-cell-specific surface glycoprotein CD28	CD28	P10747
PEA (immune response)	Parathyroid hormone/parathyroid hormone-related peptide receptor	PTH1R	Q03431
PEA (immune response)	Baculoviral IAP repeat-containing protein 2	BIRC2	Q13490
PEA (immune response)	11-beta-hydroxysteroid dehydrogenase 1	HSD11B1	P28845
PEA (immune response)	Merlin	NF2	P35240
PEA (immune response)	Plexin-A4	PLXNA4	Q9HCM2
PEA (immune response)	SH2B adapter protein 3	SH2B3	Q9UQQ2
PEA (immune response)	Fc receptor-like protein 3	FCRL3	Q96P31
PEA (immune response)	Cytoskeleton-associated protein 4	CKAP4	Q07065
PEA (immune response)	Transcription factor Jun	JUN	P05412
PEA (immune response)	Protein HEXIM1	HEXIM1	O94992
PEA (immune response)	C-type lectin domain family 4 member D	CLEC4D	Q8WXI8
PEA (immune response)	Protein kinase C theta type	PRKCQ	Q04759
PEA (immune response)	Methylated-DNA--protein-cysteine methyltransferase	MGMT	P16455
PEA (immune response)	Triggering receptor expressed on myeloid cells 1	TREM1	Q9NP99
PEA (immune response)	Coxsackievirus and adenovirus receptor	CXADR	P78310
PEA (immune response)	Interleukin-10	IL10	P22301
PEA (immune response)	SRSF protein kinase 2	SRPK2	P78362
PEA (immune response)	Natural killer cells antigen CD94	KLRD1	Q13241
PEA (immune response)	Transcription regulator protein BACH1	BACH1	O14867
PEA (immune response)	Phosphoinositide 3-kinase adapter protein 1	PIK3AP1	Q6ZUJ8
PEA (immune response)	Protein sprouty homolog 2	SPRY2	O43597
PEA (immune response)	Stanniocalcin-1	STC1	P52823
PEA (immune response)	Aryl hydrocarbon receptor nuclear translocator	ARNT	P27540
PEA (immune response)	Protein FAM3B	FAM3B	P58499
PEA (immune response)	SH2 domain-containing protein 1A	SH2D1A	O60880
PEA (immune response)	Islet cell autoantigen 1	ICA1	Q05084
PEA (immune response)	DNA fragmentation factor subunit alpha	DFFA	O00273
PEA (immune response)	Discoidin, CUB and LCCL domain-containing protein 2	DCBLD2	Q96PD2
PEA (immune response)	Fc receptor-like protein 6	FCRL6	Q6DN72
PEA (immune response)	Natural cytotoxicity triggering receptor 1	NCR1	O76036
PEA (immune response)	Stromal cell-derived factor 1	CXCL12	P48061
PEA (immune response)	Amphiregulin	AREG	P15514

PEA (immune response)	Interferon lambda receptor 1	IFNLR1	Q8IU57
PEA (immune response)	Dual adapter for phosphotyrosine and 3-phosphotyrosine and 3-phosphoinositide	DAPP1	Q9UN19
PEA (immune response)	Protein-arginine deiminase type-2	PADI2	Q9Y2J8
PEA (immune response)	Signaling threshold-regulating transmembrane adapter 1	SIT1	Q9Y3P8
PEA (immune response)	Mannan-binding lectin serine protease 1	MASP1	P48740
PEA (immune response)	Lysosome-associated membrane glycoprotein 3	LAMP3	Q9UQV4
PEA (immune response)	C-type lectin domain family 7 member A	CLEC7A	Q9BXN2
PEA (immune response)	C-type lectin domain family 6 member A	CLEC6A	Q6EIG7
PEA (immune response)	Antiviral innate immune response receptor RIG-I	RIGI	O95786
PEA (immune response)	Interleukin-12 receptor subunit beta-1	IL12RB1	P42701
PEA (immune response)	TRAF family member-associated NF-kappa-B activator	TANK	Q92844
PEA (immune response)	Integrin alpha-11	ITGA11	Q9UKX5
PEA (immune response)	Importin subunit alpha-5	KPNA1	P52294
PEA (immune response)	Lymphocyte activation gene 3 protein	LAG3	P18627
PEA (immune response)	Interleukin-5	IL5	P05113
PEA (immune response)	CD83 antigen	CD83	Q01151
PEA (immune response)	Integrin beta-6	ITGB6	P18564
PEA (immune response)	Butyrophilin subfamily 3 member A2	BTN3A2	P78410
PEA (cytokine)	C-C motif chemokine 8	CCL8	P80075
PEA (cytokine)	Interleukin-33	IL33	O95760
PEA (cytokine)	Stromal cell-derived factor 1	CXCL12	P48061
PEA (cytokine)	Oxidized low-density lipoprotein receptor 1	OLR1	P78380
PEA (cytokine)	Interleukin-2	IL2	P60568
PEA (cytokine)	C-X-C motif chemokine 9	CXCL9	Q07325
PEA (cytokine)	Protransforming growth factor alpha	TGFA	P01135
PEA (cytokine)	Interleukin-1 beta	IL1B	P01584
PEA (cytokine)	Interleukin-6	IL6	P05231
PEA (cytokine)	Interleukin-4	IL4	P05112
PEA (cytokine)	Tumor necrosis factor ligand superfamily member 12	TNFSF12	O43508
PEA (cytokine)	Thymic stromal lymphopoietin	TSLP	Q969D9
PEA (cytokine)	Eotaxin	CCL11	P51671
PEA (cytokine)	Hepatocyte growth factor	HGF	P14210
PEA (cytokine)	Fms-related tyrosine kinase 3 ligand	FLT3LG	P49771
PEA (cytokine)	Interleukin-17F	IL17F	Q96PD4
PEA (cytokine)	Interleukin-7	IL7	P13232
PEA (cytokine)	Interleukin-13	IL13	P35225
PEA (cytokine)	Interleukin-18	IL18	Q14116
PEA (cytokine)	C-C motif chemokine 13	CCL13	Q99616
PEA (cytokine)	Tumor necrosis factor ligand superfamily member 10	TNFSF10	P50591

PEA (cytokine)	C-X-C motif chemokine 10	CXCL10	P02778
PEA (cytokine)	Interferon gamma	IFNG	P01579
PEA (cytokine)	Interleukin-10	IL10	P22301
PEA (cytokine)	C-C motif chemokine 19	CCL19	Q99731
PEA (cytokine)	Tumor necrosis factor	TNF	P01375
PEA (cytokine)	Interleukin-15	IL15	P40933
PEA (cytokine)	C-C motif chemokine 3	CCL3	P10147
PEA (cytokine)	Interleukin-8	CXCL8	P10145
PEA (cytokine)	Macrophage metalloelastase	MMP12	P39900
PEA (cytokine)	Granulocyte-macrophage colony-stimulating factor	CSF2	P04141
PEA (cytokine)	Granulocyte colony-stimulating factor	CSF3	P09919
PEA (cytokine)	Vascular endothelial growth factor A	VEGFA	P15692
PEA (cytokine)	Interleukin-17C	IL17C	Q9P0M4
PEA (cytokine)	Pro-epidermal growth factor	EGF	P01133
PEA (cytokine)	C-C motif chemokine 2	CCL2	P13500
PEA (cytokine)	Interleukin-17A	IL17A	Q16552
PEA (cytokine)	Oncostatin-M	OSM	P13725
PEA (cytokine)	Macrophage colony-stimulating factor 1	CSF1	P09603
PEA (cytokine)	C-C motif chemokine 4	CCL4	P13236
PEA (cytokine)	C-X-C motif chemokine 11	CXCL11	O14625
PEA (cytokine)	Lymphotoxin-alpha	LTA	P01374
PEA (cytokine)	C-C motif chemokine 7	CCL7	P80098
PEA (cytokine)	Interstitial collagenase	MMP1	P03956
PEA (cytokine)	Interleukin-27	IL27	Q8NEV9_Q14213
SRM	Thrombospondin-1	THBS1	P07996
SRM	Neutrophil defensin 1	DEFA1	P59665
SRM	C-reactive protein	CRP	P02741
SRM	Haptoglobin	HP	P00738
SRM	Alpha-1-acid glycoprotein 1	ORM1	P02763
SRM	Protein AMBP	AMBP	P02760
SRM	Serum amyloid A-1 protein	SAA1	P0DJI8
SRM	Beta-Ala-His dipeptidase	CNDP1	Q96KN2
SRM	Leucine-rich alpha-2-glycoprotein	LRG1	P02750
SRM	Kallistatin	SERPINA4	P29622
SRM	Alpha-2-HS-glycoprotein	AHSG	P02765
SRM	Immunoglobulin kappa variable 4-1	IGKV4-1	P06312
SRM	Immunoglobulin lambda constant 6	IGLC6	P0CF74
SRM	Sex hormone-binding globulin	SHBG	P04278
SRM	Immunoglobulin J chain	JCHAIN	P01591

SRM	Inter-alpha-trypsin inhibitor heavy chain H3	ITIH3	Q06033
SRM	Apolipoprotein A-I	APOA1	P02647
SRM	Complement component C9	C9	P02748
SRM	Complement C5	C5	P01031
SRM	Alpha-1-antichymotrypsin	SERPINA3	P01011
SRM	Mannose-binding protein C	MBL2	P11226
SRM	Complement component C7	C7	P10643
SRM	Complement C3	C3	P01024
SRM	Apolipoprotein A-II	APOA2	P02652
SRM	Apolipoprotein C-II	APOC2	P02655
SRM	Apolipoprotein C-III	APOC3	P02656
SRM	Apolipoprotein C-IV	APOC4	P55056
SRM	Apolipoprotein L1	APOL1	O14791
SRM	Attractin	ATRN	O75882
SRM	Beta-2-glycoprotein 1	APOH	P02749
SRM	C4b-binding protein beta chain	C4BPB	P20851
SRM	Carboxypeptidase N subunit 2	CPN2	P22792
SRM	Ceruloplasmin	CP	P00450
SRM	Clusterin	CLU	P10909
SRM	Coagulation factor IX	F9	P00740
SRM	Coagulation factor X	F10	P00742
SRM	Complement C2	C2	P06681
SRM	Complement C4-B	C4B	P0C0L5
SRM	Complement component C6	C6	P13671
SRM	Complement component C8 alpha chain	C8A	P07357
SRM	Complement component C8 beta chain	C8B	P07358
SRM	Complement component C8 gamma chain	C8G	P07360
SRM	Complement factor B	CFB	P00751
SRM	Complement factor H	CFH	P08603
SRM	Complement factor H-related protein 2	CFHR2	P36980
SRM	Complement factor I	CFI	P05156
SRM	Ficolin-3	FCN3	O75636
SRM	Gelsolin	GSN	P06396
SRM	Haptoglobin-related protein	HPR	P00739
SRM	Heparin cofactor 2	SERPIND1	P05546
SRM	Histidine-rich glycoprotein	HRG	P04196
SRM	Immunoglobulin heavy constant alpha 1	IGHA1	P01876
SRM	Immunoglobulin heavy variable 3-23	IGHV3-23	P01764
SRM	Insulin-like growth factor-binding protein complex acid labile subunit	IGFALS	P35858

SRM	Inter-alpha-trypsin inhibitor heavy chain H1	ITIH1	P19827
SRM	Inter-alpha-trypsin inhibitor heavy chain H2	ITIH2	P19823
SRM	L-selectin	SELL	P14151
SRM	Lumican	LUM	P51884
SRM	Mannan-binding lectin serine protease 2	MASP2	O00187
SRM	Pigment epithelium-derived factor	SERPINF1	P36955
SRM	Plasma protease C1 inhibitor	SERPING1	P05155
SRM	Plasminogen	PLG	P00747
SRM	Pregnancy zone protein	PZP	P20742
SRM	Serotransferrin	TF	P02787
SRM	Serum amyloid A-4 protein	SAA4	P35542
SRM	Serum amyloid P-component	APCS	P02743
SRM	Tetranectin	CLEC3B	P05452
SRM	Thyroxine-binding globulin	SERPINA7	P05543
SRM	Vitronectin	VTN	P04004
hsCRP	C-reactive protein	CRP	P02741
ELISA (STORI) and turbidimetric immunoassay (SPARE)	Calprotectin	S100A8/A9	P05109/P06702

Supplementary Table 2. Correlation between the measurement replicates in STORI

	CXCL12 PEA_cytokine	CCL11 PEA_cytokine	IL6 PEA_cytokine	IL10 PEA_cytokine	hsCRP
CXCL12 PEA_IR	0.52 (p<0.0001)				
CCL11 PEA_IR		0.84 (p<0.0001)			
IL6 PEA_IR			0.93 (p<0.0001)		
IL10 PEA_IR				0.80 (p<0.0001)	
CRP_SRM					0.96 (p<0.0001)

Spearman's rank test. PEA: proximity extension assay; IR: immune response; SRM: selected reaction monitoring

Supplementary Table 3. Correlation between the measurement replicates in SPARE

	CXCL12 PEA_cytokine	CCL11 PEA_cytokine	IL6 PEA_cytokine	IL10 PEA_cytokine	hsCRP
CXCL12 PEA_IR	0.62 (p<0.0001)				
CCL11 PEA_IR		0.88 (p<0.0001)			
IL6 PEA_IR			0.95 (p<0.0001)		
IL10 PEA_IR				0.70 (p<0.0001)	
CRP_SRM					0.99 (p<0.0001)

Spearman's rank test. PEA: proximity extension assay; IR: immune response; SRM: selected reaction monitoring

Supplementary Table 4. SRM method

Protein Description	Gene name	Protein Accession	Peptide	Modified sequence monoisoptopic masses	Precursor	Precursor m/z	Precursor Charge	Collision Energy	Product m/z	Fragment Ion	Product Charge	Predicted Retention Time	Average Measured Retention Time	CV in the non-relapsers pool (%)	CV in the relapsers pool (%)
Thrombospondin-1	THBS1	P07996	GGVNDNFQGVLQNVR	GGVNDNFQGVLQNVR	808.9106++	808.91061	2	28.9	913.52139	y8	1	64.06	70.71	3.1	6.4
Thrombospondin-1	THBS1	P07996	GGVNDNFQGVLQNVR	GGVNDNFQGVLQNVR	808.9106++	808.91061	2	28.9	785.462812	y7	1	64.06	70.71		
Thrombospondin-1	THBS1	P07996	GGVNDNFQGVLQNVR	GGVNDNFQGVLQNVR	808.9106++	808.91061	2	28.9	629.372935	y5	1	64.06	70.71		
Thrombospondin-1	THBS1	P07996	GGVNDNFQGVLQNVR	GGVNDNFQGVLQNVR[+10.008269]	813.9147++ (heavy)	813.914744	2	28.9	923.529659	y8	1	64.06	70.71		
Thrombospondin-1	THBS1	P07996	GGVNDNFQGVLQNVR	GGVNDNFQGVLQNVR[+10.008269]	813.9147++ (heavy)	813.914744	2	28.9	795.471081	y7	1	64.06	70.71		
Thrombospondin-1	THBS1	P07996	GGVNDNFQGVLQNVR	GGVNDNFQGVLQNVR[+10.008269]	813.9147++ (heavy)	813.914744	2	28.9	639.381204	y5	1	64.06	70.71		
Thrombospondin-1	THBS1	P07996	FVFGTTPEDILR	FVFGTTPEDILR	697.8694++	697.869359	2	24.8	1148.594615	y10	1	89.28	95.73		
Thrombospondin-1	THBS1	P07996	FVFGTTPEDILR	FVFGTTPEDILR	697.8694++	697.869359	2	24.8	1001.526201	y9	1	89.28	95.73		
Thrombospondin-1	THBS1	P07996	FVFGTTPEDILR	FVFGTTPEDILR	697.8694++	697.869359	2	24.8	247.144104	b2	1	89.28	95.73		
Thrombospondin-1	THBS1	P07996	FVFGTTPEDILR	FVFGTTPEDILR[+10.008269]	702.8735++ (heavy)	702.873494	2	24.8	1158.602884	y10	1	89.28	95.73		
Thrombospondin-1	THBS1	P07996	FVFGTTPEDILR	FVFGTTPEDILR[+10.008269]	702.8735++ (heavy)	702.873494	2	24.8	1011.53447	y9	1	89.28	95.73		
Thrombospondin-1	THBS1	P07996	FVFGTTPEDILR	FVFGTTPEDILR[+10.008269]	702.8735++ (heavy)	702.873494	2	24.8	247.144104	b2	1	89.28	95.73		
Neutrophil defensin 1	DEFA1	P59665	IPACIAGER	IPAC[+57.021464]IAGER	493.7580++	493.758026	2	17.2	873.424713	y8	1	22.31	24.93	2.9	1.7
Neutrophil defensin 1	DEFA1	P59665	IPACIAGER	IPAC[+57.021464]IAGER	493.7580++	493.758026	2	17.2	776.371949	y7	1	22.31	24.93		
Neutrophil defensin 1	DEFA1	P59665	IPACIAGER	IPAC[+57.021464]IAGER	493.7580++	493.758026	2	17.2	705.334835	y6	1	22.31	24.93		
Neutrophil defensin 1	DEFA1	P59665	IPACIAGER	IPAC[+57.021464]IAGER	493.7580++	493.758026	2	17.2	432.220122	y4	1	22.31	24.93		
Neutrophil defensin 1	DEFA1	P59665	IPACIAGER	IPAC[+57.021464]IAGER[+10.008269]	498.7622++ (heavy)	498.762161	2	17.2	883.432982	y8	1	22.31	24.93		
Neutrophil defensin 1	DEFA1	P59665	IPACIAGER	IPAC[+57.021464]IAGER[+10.008269]	498.7622++ (heavy)	498.762161	2	17.2	786.380218	y7	1	22.31	24.93		
Neutrophil defensin 1	DEFA1	P59665	IPACIAGER	IPAC[+57.021464]IAGER[+10.008269]	498.7622++ (heavy)	498.762161	2	17.2	715.343104	y6	1	22.31	24.93		
Neutrophil defensin 1	DEFA1	P59665	IPACIAGER	IPAC[+57.021464]IAGER[+10.008269]	498.7622++ (heavy)	498.762161	2	17.2	442.228391	y4	1	22.31	24.93		
Neutrophil defensin 1	DEFA1	P59665	YGTCIYQGR	YGTC[+57.021464]IYQGR	559.2584++	559.25839	2	19.6	796.377034	y6	1	29.57	25.22		
Neutrophil defensin 1	DEFA1	P59665	YGTCIYQGR	YGTC[+57.021464]IYQGR	559.2584++	559.25839	2	19.6	636.346386	y5	1	29.57	25.22		
Neutrophil defensin 1	DEFA1	P59665	YGTCIYQGR	YGTC[+57.021464]IYQGR	559.2584++	559.25839	2	19.6	523.262322	y4	1	29.57	25.22		
Neutrophil defensin 1	DEFA1	P59665	YGTCIYQGR	YGTC[+57.021464]IYQGR[+10.008269]	564.2625++ (heavy)	564.262525	2	19.6	806.385303	y6	1	29.57	25.22		
Neutrophil defensin 1	DEFA1	P59665	YGTCIYQGR	YGTC[+57.021464]IYQGR[+10.008269]	564.2625++ (heavy)	564.262525	2	19.6	646.354655	y5	1	29.57	25.22		
Neutrophil defensin 1	DEFA1	P59665	YGTCIYQGR	YGTC[+57.021464]IYQGR[+10.008269]	564.2625++ (heavy)	564.262525	2	19.6	533.270591	y4	1	29.57	25.22		
C-reactive protein	CRP	P02741	ESDTSYVSLK	ESDTSYVSLK	564.7746++	564.774593	2	19.8	696.392667	y6	1	35.55	31.25	18.8	2.4
C-reactive protein	CRP	P02741	ESDTSYVSLK	ESDTSYVSLK	564.7746++	564.774593	2	19.8	609.360639	y5	1	35.55	31.25		
C-reactive protein	CRP	P02741	ESDTSYVSLK	ESDTSYVSLK	564.7746++	564.774593	2	19.8	446.29731	y4	1	35.55	31.25		
C-reactive protein	CRP	P02741	ESDTSYVSLK	ESDTSYVSLK	564.7746++	564.774593	2	19.8	347.228896	y3	1	35.55	31.25		
C-reactive protein	CRP	P02741	ESDTSYVSLK	ESDTSYVSLK[+8.014199]	568.7817++ (heavy)	568.781693	2	19.8	704.406866	y6	1	35.55	31.25		
C-reactive protein	CRP	P02741	ESDTSYVSLK	ESDTSYVSLK[+8.014199]	568.7817++ (heavy)	568.781693	2	19.8	617.374838	y5	1	35.55	31.25		
C-reactive protein	CRP	P02741	ESDTSYVSLK	ESDTSYVSLK[+8.014199]	568.7817++ (heavy)	568.781693	2	19.8	454.311509	y4	1	35.55	31.25		
C-reactive protein	CRP	P02741	ESDTSYVSLK	ESDTSYVSLK[+8.014199]	568.7817++ (heavy)	568.781693	2	19.8	355.243095	y3	1	35.55	31.25		
Haptoglobin	HP	P00738	QLVEIEK	QLVEIEK	429.7502++	429.750193	2	14.8	730.434532	y6	1	31.64	28.03	7.1	5.1
Haptoglobin	HP	P00738	QLVEIEK	QLVEIEK	429.7502++	429.750193	2	14.8	617.350468	y5	1	31.64	28.03		
Haptoglobin	HP	P00738	QLVEIEK	QLVEIEK	429.7502++	429.750193	2	14.8	518.282054	y4	1	31.64	28.03		
Haptoglobin	HP	P00738	QLVEIEK	QLVEIEK	429.7502++	429.750193	2	14.8	389.239461	y3	1	31.64	28.03		
Haptoglobin	HP	P00738	QLVEIEK	QLVEIEK[+8.014199]	433.7573++ (heavy)	433.757292	2	14.8	738.448731	y6	1	31.64	28.03		
Haptoglobin	HP	P00738	QLVEIEK	QLVEIEK[+8.014199]	433.7573++ (heavy)	433.757292	2	14.8	625.364667	y5	1	31.64	28.03		
Haptoglobin	HP	P00738	QLVEIEK	QLVEIEK[+8.014199]	433.7573++ (heavy)	433.757292	2	14.8	526.296253	y4	1	31.64	28.03		
Haptoglobin	HP	P00738	QLVEIEK	QLVEIEK[+8.014199]	433.7573++ (heavy)	433.757292	2	14.8	397.25366	y3	1	31.64	28.03		
Haptoglobin	HP	P00738	VGYVSGWGR	VGYVSGWGR	490.7511++	490.751058	2	17.1	661.341635	y6	1	49.19	41.8		
Haptoglobin	HP	P00738	VGYVSGWGR	VGYVSGWGR	490.7511++	490.751058	2	17.1	562.273221	y5	1	49.19	41.8		
Haptoglobin	HP	P00738	VGYVSGWGR	VGYVSGWGR	490.7511++	490.751058	2	17.1	320.160482	b3	1	49.19	41.8		
Haptoglobin	HP	P00738	VGYVSGWGR	VGYVSGWGR[+10.008269]	495.7552++ (heavy)	495.755193	2	17.1	671.349904	y6	1	49.19	41.8		

Haptoglobin	HP	P00738	VGYVSGWGR	VGYVSGWGR[+10.008269]	495.7552++ (heavy)	495.755193	2	17.1	572.28149	y5	1	49.19	41.8		
Haptoglobin	HP	P00738	VGYVSGWGR	VGYVSGWGR[+10.008269]	495.7552++ (heavy)	495.755193	2	17.1	320.160482	b3	1	49.19	41.8		
Haptoglobin	HP	P00738	VTSIQDWVQK	VTSIQDWVQK	602.3220++	602.322045	2	21.2	1003.520721	y8	1	55.16	55.67		
Haptoglobin	HP	P00738	VTSIQDWVQK	VTSIQDWVQK	602.3220++	602.322045	2	21.2	803.404629	y6	1	55.16	55.67		
Haptoglobin	HP	P00738	VTSIQDWVQK	VTSIQDWVQK	602.3220++	602.322045	2	21.2	675.346051	y5	1	55.16	55.67		
Haptoglobin	HP	P00738	VTSIQDWVQK	VTSIQDWVQK[+8.014199]	606.3291++ (heavy)	606.329144	2	21.2	1011.53492	y8	1	55.16	55.67		
Haptoglobin	HP	P00738	VTSIQDWVQK	VTSIQDWVQK[+8.014199]	606.3291++ (heavy)	606.329144	2	21.2	811.418828	y6	1	55.16	55.67		
Haptoglobin	HP	P00738	VTSIQDWVQK	VTSIQDWVQK[+8.014199]	606.3291++ (heavy)	606.329144	2	21.2	683.36025	y5	1	55.16	55.67		
Alpha-1-acid glycoprotein 1	ORM1	P02763	WFYIASAFR	WFYIASAFR	580.7980++	580.798009	2	20.4	827.441014	y7	1	93.38	98.11	6.1	10.5
Alpha-1-acid glycoprotein 1	ORM1	P02763	WFYIASAFR	WFYIASAFR	580.7980++	580.798009	2	20.4	664.377686	y6	1	93.38	98.11		
Alpha-1-acid glycoprotein 1	ORM1	P02763	WFYIASAFR	WFYIASAFR	580.7980++	580.798009	2	20.4	551.293622	y5	1	93.38	98.11		
Alpha-1-acid glycoprotein 1	ORM1	P02763	WFYIASAFR	WFYIASAFR[+10.008269]	585.8021++ (heavy)	585.802143	2	20.4	837.449283	y7	1	93.38	98.11		
Alpha-1-acid glycoprotein 1	ORM1	P02763	WFYIASAFR	WFYIASAFR[+10.008269]	585.8021++ (heavy)	585.802143	2	20.4	674.385955	y6	1	93.38	98.11		
Alpha-1-acid glycoprotein 1	ORM1	P02763	WFYIASAFR	WFYIASAFR[+10.008269]	585.8021++ (heavy)	585.802143	2	20.4	561.301891	y5	1	93.38	98.11		
Alpha-1-acid glycoprotein 1	ORM1	P02763	TEDTIFLR	TEDTIFLR	497.7638++	497.763831	2	17.4	764.430115	y6	1	60.76	49.92		
Alpha-1-acid glycoprotein 1	ORM1	P02763	TEDTIFLR	TEDTIFLR	497.7638++	497.763831	2	17.4	649.403172	y5	1	60.76	49.92		
Alpha-1-acid glycoprotein 1	ORM1	P02763	TEDTIFLR	TEDTIFLR	497.7638++	497.763831	2	17.4	435.27143	y3	1	60.76	49.92		
Alpha-1-acid glycoprotein 1	ORM1	P02763	TEDTIFLR	TEDTIFLR[+10.008269]	502.7680++ (heavy)	502.767966	2	17.4	774.438384	y6	1	60.76	49.92		
Alpha-1-acid glycoprotein 1	ORM1	P02763	TEDTIFLR	TEDTIFLR[+10.008269]	502.7680++ (heavy)	502.767966	2	17.4	659.411441	y5	1	60.76	49.92		
Alpha-1-acid glycoprotein 1	ORM1	P02763	TEDTIFLR	TEDTIFLR[+10.008269]	502.7680++ (heavy)	502.767966	2	17.4	445.279699	y3	1	60.76	49.92		
Alpha-1-acid glycoprotein 1	ORM1	P02763	EQLGEFYEALDCLR	EQLGEFYEALDC[+57.021464]LR	871.9063++	871.906344	2	31.2	1186.556121	y9	1	125.52	105.27		
Alpha-1-acid glycoprotein 1	ORM1	P02763	EQLGEFYEALDCLR	EQLGEFYEALDC[+57.021464]LR	871.9063++	871.906344	2	31.2	1039.487707	y8	1	125.52	105.27		
Alpha-1-acid glycoprotein 1	ORM1	P02763	EQLGEFYEALDCLR	EQLGEFYEALDC[+57.021464]LR	871.9063++	871.906344	2	31.2	747.381785	y6	1	125.52	105.27		
Alpha-1-acid glycoprotein 1	ORM1	P02763	EQLGEFYEALDCLR	EQLGEFYEALDC[+57.021464]LR[+10.00826	876.9105++ (heavy)	876.910479	2	31.2	1196.56439	y9	1	125.52	105.27		
Alpha-1-acid glycoprotein 1	ORM1	P02763	EQLGEFYEALDCLR	EQLGEFYEALDC[+57.021464]LR[+10.00826	876.9105++ (heavy)	876.910479	2	31.2	1049.495976	y8	1	125.52	105.27		
Alpha-1-acid glycoprotein 1	ORM1	P02763	EQLGEFYEALDCLR	EQLGEFYEALDC[+57.021464]LR[+10.00826	876.9105++ (heavy)	876.910479	2	31.2	757.390054	y6	1	125.52	105.27		
Protein AMBP	AMBP	P02760	GVCEETSGAYEK	GVC[+57.021464]EETSGAYEK	665.2850++	665.284999	2	23.5	1013.442196	y9	1	7.09	15.93	8.0	5.7
Protein AMBP	AMBP	P02760	GVCEETSGAYEK	GVC[+57.021464]EETSGAYEK	665.2850++	665.284999	2	23.5	884.399603	y8	1	7.09	15.93		
Protein AMBP	AMBP	P02760	GVCEETSGAYEK	GVC[+57.021464]EETSGAYEK	665.2850++	665.284999	2	23.5	755.35701	y7	1	7.09	15.93		
Protein AMBP	AMBP	P02760	GVCEETSGAYEK	GVC[+57.021464]EETSGAYEK[+8.014199]	669.2921++ (heavy)	669.292099	2	23.5	1021.456395	y9	1	7.09	15.93		
Protein AMBP	AMBP	P02760	GVCEETSGAYEK	GVC[+57.021464]EETSGAYEK[+8.014199]	669.2921++ (heavy)	669.292099	2	23.5	892.413802	y8	1	7.09	15.93		
Protein AMBP	AMBP	P02760	GVCEETSGAYEK	GVC[+57.021464]EETSGAYEK[+8.014199]	669.2921++ (heavy)	669.292099	2	23.5	763.371209	y7	1	7.09	15.93		
Protein AMBP	AMBP	P02760	ETLLQDFR	ETLLQDFR	511.2693++	511.269281	2	17.9	678.35695	y5	1	65.44	64.18		
Protein AMBP	AMBP	P02760	ETLLQDFR	ETLLQDFR	511.2693++	511.269281	2	17.9	565.272886	y4	1	65.44	64.18		
Protein AMBP	AMBP	P02760	ETLLQDFR	ETLLQDFR	511.2693++	511.269281	2	17.9	322.187366	y2	1	65.44	64.18		
Protein AMBP	AMBP	P02760	ETLLQDFR	ETLLQDFR[+10.008269]	516.2734++ (heavy)	516.273415	2	17.9	688.365219	y5	1	65.44	64.18		
Protein AMBP	AMBP	P02760	ETLLQDFR	ETLLQDFR[+10.008269]	516.2734++ (heavy)	516.273415	2	17.9	575.281155	y4	1	65.44	64.18		
Protein AMBP	AMBP	P02760	ETLLQDFR	ETLLQDFR[+10.008269]	516.2734++ (heavy)	516.273415	2	17.9	332.195635	y2	1	65.44	64.18		
Serum amyloid A-1 protein	SAA1	P0DJI8	SFFSFLGEAFDGAR	SFFSFLGEAFDGAR	775.8673++	775.867348	2	27.6	935.458121	y9	1	127.08	133.82	5.7	15.4
Serum amyloid A-1 protein	SAA1	P0DJI8	SFFSFLGEAFDGAR	SFFSFLGEAFDGAR	775.8673++	775.867348	2	27.6	636.31	y6	1	127.08	133.82		
Serum amyloid A-1 protein	SAA1	P0DJI8	SFFSFLGEAFDGAR	SFFSFLGEAFDGAR	775.8673++	775.867348	2	27.6	303.177529	y3	1	127.08	133.82		
Serum amyloid A-1 protein	SAA1	P0DJI8	SFFSFLGEAFDGAR	SFFSFLGEAFDGAR	775.8673++	775.867348	2	27.6	235.107718	b2	1	127.08	133.82		
Serum amyloid A-1 protein	SAA1	P0DJI8	SFFSFLGEAFDGAR	SFFSFLGEAFDGAR[+10.008269]	780.8715++ (heavy)	780.871482	2	27.6	945.46639	y9	1	127.08	133.82		
Serum amyloid A-1 protein	SAA1	P0DJI8	SFFSFLGEAFDGAR	SFFSFLGEAFDGAR[+10.008269]	780.8715++ (heavy)	780.871482	2	27.6	646.318269	y6	1	127.08	133.82		
Serum amyloid A-1 protein	SAA1	P0DJI8	SFFSFLGEAFDGAR	SFFSFLGEAFDGAR[+10.008269]	780.8715++ (heavy)	780.871482	2	27.6	313.185798	y3	1	127.08	133.82		
Serum amyloid A-1 protein	SAA1	P0DJI8	SFFSFLGEAFDGAR	SFFSFLGEAFDGAR[+10.008269]	780.8715++ (heavy)	780.871482	2	27.6	235.107718	b2	1	127.08	133.82		
Serum amyloid A-1 protein	SAA1	P0DJI8	FFGHGAEDSLADQAANEWGR	FFGHGAEDSLADQAANEWGR	726.6594+++	726.659358	3	24.8	803.379477	y7	1	87.59	73.54		
Serum amyloid A-1 protein	SAA1	P0DJI8	FFGHGAEDSLADQAANEWGR	FFGHGAEDSLADQAANEWGR	726.6594+++	726.659358	3	24.8	732.342363	y6	1	87.59	73.54		
Serum amyloid A-1 protein	SAA1	P0DJI8	FFGHGAEDSLADQAANEWGR	FFGHGAEDSLADQAANEWGR	726.6594+++	726.659358	3	24.8	661.305249	y5	1	87.59	73.54		
Serum amyloid A-1 protein	SAA1	P0DJI8	FFGHGAEDSLADQAANEWGR	FFGHGAEDSLADQAANEWGR[+10.008269]	729.9954+++ (heavy)	729.995447	3	24.8	813.387746	y7	1	87.59	73.54		

Serum amyloid A-1 protein	SAA1	P0DJI8	FFGHGAEDSLADQAANEWGR	FFGHGAEDSLADQAANEWGR[+10.008269]	729.9954+++ (heavy)	729.995447	3	24.8	742.350632	y6	1	87.59	73.54		
Serum amyloid A-1 protein	SAA1	P0DJI8	FFGHGAEDSLADQAANEWGR	FFGHGAEDSLADQAANEWGR[+10.008269]	729.9954+++ (heavy)	729.995447	3	24.8	671.313518	y5	1	87.59	73.54		
Beta-Ala-His dipeptidase	CNDP1	Q96KN2	ALEQDLPVNIK	ALEQDLPVNIK	620.3508++	620.350802	2	21.9	798.47198	y7	1	54.42	61.97	7.6	4.5
Beta-Ala-His dipeptidase	CNDP1	Q96KN2	ALEQDLPVNIK	ALEQDLPVNIK	620.3508++	620.350802	2	21.9	683.445037	y6	1	54.42	61.97		
Beta-Ala-His dipeptidase	CNDP1	Q96KN2	ALEQDLPVNIK	ALEQDLPVNIK	620.3508++	620.350802	2	21.9	570.360973	y5	1	54.42	61.97		
Beta-Ala-His dipeptidase	CNDP1	Q96KN2	ALEQDLPVNIK	ALEQDLPVNIK[+8.014199]	624.3579++ (heavy)	624.357902	2	21.9	806.486179	y7	1	54.42	61.97		
Beta-Ala-His dipeptidase	CNDP1	Q96KN2	ALEQDLPVNIK	ALEQDLPVNIK[+8.014199]	624.3579++ (heavy)	624.357902	2	21.9	691.459236	y6	1	54.42	61.97		
Beta-Ala-His dipeptidase	CNDP1	Q96KN2	ALEQDLPVNIK	ALEQDLPVNIK[+8.014199]	624.3579++ (heavy)	624.357902	2	21.9	578.375172	y5	1	54.42	61.97		
Beta-Ala-His dipeptidase	CNDP1	Q96KN2	AIHLDLEEYR	AIHLDLEEYR	420.2191+++	420.21906	3	13.8	596.267467	y4	1	55.58	59.02		
Beta-Ala-His dipeptidase	CNDP1	Q96KN2	AIHLDLEEYR	AIHLDLEEYR	420.2191+++	420.21906	3	13.8	467.224873	y3	1	55.58	59.02		
Beta-Ala-His dipeptidase	CNDP1	Q96KN2	AIHLDLEEYR	AIHLDLEEYR	420.2191+++	420.21906	3	13.8	338.18228	y2	1	55.58	59.02		
Beta-Ala-His dipeptidase	CNDP1	Q96KN2	AIHLDLEEYR	AIHLDLEEYR	420.2191+++	420.21906	3	13.8	550.298373	b5	1	55.58	59.02		
Beta-Ala-His dipeptidase	CNDP1	Q96KN2	AIHLDLEEYR	AIHLDLEEYR[+10.008269]	423.5551+++ (heavy)	423.555149	3	13.8	606.275736	y4	1	55.58	59.02		
Beta-Ala-His dipeptidase	CNDP1	Q96KN2	AIHLDLEEYR	AIHLDLEEYR[+10.008269]	423.5551+++ (heavy)	423.555149	3	13.8	477.233142	y3	1	55.58	59.02		
Beta-Ala-His dipeptidase	CNDP1	Q96KN2	AIHLDLEEYR	AIHLDLEEYR[+10.008269]	423.5551+++ (heavy)	423.555149	3	13.8	348.190549	y2	1	55.58	59.02		
Beta-Ala-His dipeptidase	CNDP1	Q96KN2	AIHLDLEEYR	AIHLDLEEYR[+10.008269]	423.5551+++ (heavy)	423.555149	3	13.8	550.298373	b5	1	55.58	59.02		
Leucine-rich alpha-2-glycoprote	LRG1	P02750	ALGHLDLSGNR	ALGHLDLSGNR	576.8096++	576.809636	2	20.3	774.410442	y7	1	37.43	32.82	5.2	2.4
Leucine-rich alpha-2-glycoprote	LRG1	P02750	ALGHLDLSGNR	ALGHLDLSGNR	576.8096++	576.809636	2	20.3	661.326378	y6	1	37.43	32.82		
Leucine-rich alpha-2-glycoprote	LRG1	P02750	ALGHLDLSGNR	ALGHLDLSGNR	576.8096++	576.809636	2	20.3	546.299435	y5	1	37.43	32.82		
Leucine-rich alpha-2-glycoprote	LRG1	P02750	ALGHLDLSGNR	ALGHLDLSGNR	576.8096++	576.809636	2	20.3	379.208829	b4	1	37.43	32.82		
Leucine-rich alpha-2-glycoprote	LRG1	P02750	ALGHLDLSGNR	ALGHLDLSGNR[+10.008269]	581.8138++ (heavy)	581.81377	2	20.3	784.418711	y7	1	37.43	32.82		
Leucine-rich alpha-2-glycoprote	LRG1	P02750	ALGHLDLSGNR	ALGHLDLSGNR[+10.008269]	581.8138++ (heavy)	581.81377	2	20.3	671.334647	y6	1	37.43	32.82		
Leucine-rich alpha-2-glycoprote	LRG1	P02750	ALGHLDLSGNR	ALGHLDLSGNR[+10.008269]	581.8138++ (heavy)	581.81377	2	20.3	556.307704	y5	1	37.43	32.82		
Leucine-rich alpha-2-glycoprote	LRG1	P02750	ALGHLDLSGNR	ALGHLDLSGNR[+10.008269]	581.8138++ (heavy)	581.81377	2	20.3	379.208829	b4	1	37.43	32.82		
Leucine-rich alpha-2-glycoprote	LRG1	P02750	DLLLPQPDLR	DLLLPQPDLR	590.3402++	590.340238	2	20.8	725.394064	y6	1	78.07	78.35		
Leucine-rich alpha-2-glycoprote	LRG1	P02750	DLLLPQPDLR	DLLLPQPDLR	590.3402++	590.340238	2	20.8	229.118283	b2	1	78.07	78.35		
Leucine-rich alpha-2-glycoprote	LRG1	P02750	DLLLPQPDLR	DLLLPQPDLR	590.3402++	590.340238	2	20.8	342.202347	b3	1	78.07	78.35		
Leucine-rich alpha-2-glycoprote	LRG1	P02750	DLLLPQPDLR	DLLLPQPDLR[+10.008269]	595.3444++ (heavy)	595.344372	2	20.8	735.402333	y6	1	78.07	78.35		
Leucine-rich alpha-2-glycoprote	LRG1	P02750	DLLLPQPDLR	DLLLPQPDLR[+10.008269]	595.3444++ (heavy)	595.344372	2	20.8	229.118283	b2	1	78.07	78.35		
Leucine-rich alpha-2-glycoprote	LRG1	P02750	DLLLPQPDLR	DLLLPQPDLR[+10.008269]	595.3444++ (heavy)	595.344372	2	20.8	342.202347	b3	1	78.07	78.35		
Leucine-rich alpha-2-glycoprote	LRG1	P02750	GQTLLAVAK	GQTLLAVAK	450.7793++	450.779285	2	15.6	715.471252	y7	1	35.33	35.51		
Leucine-rich alpha-2-glycoprote	LRG1	P02750	GQTLLAVAK	GQTLLAVAK	450.7793++	450.779285	2	15.6	501.339509	y5	1	35.33	35.51		
Leucine-rich alpha-2-glycoprote	LRG1	P02750	GQTLLAVAK	GQTLLAVAK	450.7793++	450.779285	2	15.6	388.255445	y4	1	35.33	35.51		
Leucine-rich alpha-2-glycoprote	LRG1	P02750	GQTLLAVAK	GQTLLAVAK[+8.014199]	454.7864++ (heavy)	454.786384	2	15.6	723.485451	y7	1	35.33	35.51		
Leucine-rich alpha-2-glycoprote	LRG1	P02750	GQTLLAVAK	GQTLLAVAK[+8.014199]	454.7864++ (heavy)	454.786384	2	15.6	509.353708	y5	1	35.33	35.51		
Leucine-rich alpha-2-glycoprote	LRG1	P02750	GQTLLAVAK	GQTLLAVAK[+8.014199]	454.7864++ (heavy)	454.786384	2	15.6	396.269644	y4	1	35.33	35.51		
Kallistatin	SERPINA4	P29622	IAPANADFAFR	IAPANADFAFR	596.8091++	596.809105	2	21	911.436992	y8	1	62.95	58.97	5.6	3.6
Kallistatin	SERPINA4	P29622	IAPANADFAFR	IAPANADFAFR	596.8091++	596.809105	2	21	840.399878	y7	1	62.95	58.97		
Kallistatin	SERPINA4	P29622	IAPANADFAFR	IAPANADFAFR	596.8091++	596.809105	2	21	655.319837	y5	1	62.95	58.97		
Kallistatin	SERPINA4	P29622	IAPANADFAFR	IAPANADFAFR[+10.008269]	601.8132++ (heavy)	601.813239	2	21	921.445261	y8	1	62.95	58.97		
Kallistatin	SERPINA4	P29622	IAPANADFAFR	IAPANADFAFR[+10.008269]	601.8132++ (heavy)	601.813239	2	21	850.408147	y7	1	62.95	58.97		
Kallistatin	SERPINA4	P29622	IAPANADFAFR	IAPANADFAFR[+10.008269]	601.8132++ (heavy)	601.813239	2	21	665.328106	y5	1	62.95	58.97		
Kallistatin	SERPINA4	P29622	LGFTDLFSK	LGFTDLFSK	514.2766++	514.276575	2	18	914.461809	y8	1	80.56	92.29		
Kallistatin	SERPINA4	P29622	LGFTDLFSK	LGFTDLFSK	514.2766++	514.276575	2	18	710.371932	y6	1	80.56	92.29		
Kallistatin	SERPINA4	P29622	LGFTDLFSK	LGFTDLFSK	514.2766++	514.276575	2	18	381.213246	y3	1	80.56	92.29		
Kallistatin	SERPINA4	P29622	LGFTDLFSK	LGFTDLFSK[+8.014199]	518.2837++ (heavy)	518.283674	2	18	922.476008	y8	1	80.56	92.29		
Kallistatin	SERPINA4	P29622	LGFTDLFSK	LGFTDLFSK[+8.014199]	518.2837++ (heavy)	518.283674	2	18	718.386131	y6	1	80.56	92.29		
Kallistatin	SERPINA4	P29622	LGFTDLFSK	LGFTDLFSK[+8.014199]	518.2837++ (heavy)	518.283674	2	18	389.227445	y3	1	80.56	92.29		
Kallistatin	SERPINA4	P29622	WADLSGITK	WADLSGITK	495.7664++	495.766374	2	17.3	804.446159	y8	1	50.82	53.8		
Kallistatin	SERPINA4	P29622	WADLSGITK	WADLSGITK	495.7664++	495.766374	2	17.3	733.409046	y7	1	50.82	53.8		

Kallistatin	SERPINA4	P29622	WADLSGITK	WADLSGITK	495.7664++	495.766374	2	17.3	505.298038	y5	1	50.82	53.8		
Kallistatin	SERPINA4	P29622	WADLSGITK	WADLSGITK[+8.014199]	499.7735++ (heavy)	499.773474	2	17.3	812.460358	y8	1	50.82	53.8		
Kallistatin	SERPINA4	P29622	WADLSGITK	WADLSGITK[+8.014199]	499.7735++ (heavy)	499.773474	2	17.3	741.423245	y7	1	50.82	53.8		
Kallistatin	SERPINA4	P29622	WADLSGITK	WADLSGITK[+8.014199]	499.7735++ (heavy)	499.773474	2	17.3	513.312237	y5	1	50.82	53.8		
Alpha-2-HS-glycoprotein	AHSG	P02765	EHAVEGDCDFQLLK	EHAVEGDC[+57.021464]DFQLLK	554.2594+++	554.259367	3	18.6	763.434866	y6	1	69.93	54.83	5.9	2.2
Alpha-2-HS-glycoprotein	AHSG	P02765	EHAVEGDCDFQLLK	EHAVEGDC[+57.021464]DFQLLK	554.2594+++	554.259367	3	18.6	648.407923	y5	1	69.93	54.83		
Alpha-2-HS-glycoprotein	AHSG	P02765	EHAVEGDCDFQLLK	EHAVEGDC[+57.021464]DFQLLK	554.2594+++	554.259367	3	18.6	338.145895	b3	1	69.93	54.83		
Alpha-2-HS-glycoprotein	AHSG	P02765	EHAVEGDCDFQLLK	EHAVEGDC[+57.021464]DFQLLK[+8.014199	556.9308+++ (heavy)	556.930766	3	18.6	771.449065	y6	1	69.93	54.83		
Alpha-2-HS-glycoprotein	AHSG	P02765	EHAVEGDCDFQLLK	EHAVEGDC[+57.021464]DFQLLK[+8.014199	556.9308+++ (heavy)	556.930766	3	18.6	656.422122	y5	1	69.93	54.83		
Alpha-2-HS-glycoprotein	AHSG	P02765	EHAVEGDCDFQLLK	EHAVEGDC[+57.021464]DFQLLK[+8.014199	556.9308+++ (heavy)	556.930766	3	18.6	338.145895	b3	1	69.93	54.83		
Alpha-2-HS-glycoprotein	AHSG	P02765	FSVVYAK	FSVVYAK	407.2289++	407.228896	2	14	666.382102	y6	1	35.99	35.04		
Alpha-2-HS-glycoprotein	AHSG	P02765	FSVVYAK	FSVVYAK	407.2289++	407.228896	2	14	480.28166	y4	1	35.99	35.04		
Alpha-2-HS-glycoprotein	AHSG	P02765	FSVVYAK	FSVVYAK	407.2289++	407.228896	2	14	235.107718	b2	1	35.99	35.04		
Alpha-2-HS-glycoprotein	AHSG	P02765	FSVVYAK	FSVVYAK[+8.014199]	411.2360++ (heavy)	411.235996	2	14	674.396301	y6	1	35.99	35.04		
Alpha-2-HS-glycoprotein	AHSG	P02765	FSVVYAK	FSVVYAK[+8.014199]	411.2360++ (heavy)	411.235996	2	14	488.295859	y4	1	35.99	35.04		
Alpha-2-HS-glycoprotein	AHSG	P02765	FSVVYAK	FSVVYAK[+8.014199]	411.2360++ (heavy)	411.235996	2	14	235.107718	b2	1	35.99	35.04		
Immunoglobulin kappa variable	IGKV4-1	P06312	DIVMTQSPDSLAVSLGER	DIVMTQSPDSLAVSLGER	959.4829++	959.482947	2	34.4	1143.600428	y11	1	82.5	85.66	4.4	8.7
Immunoglobulin kappa variable	IGKV4-1	P06312	DIVMTQSPDSLAVSLGER	DIVMTQSPDSLAVSLGER	959.4829++	959.482947	2	34.4	229.118283	b2	1	82.5	85.66		
Immunoglobulin kappa variable	IGKV4-1	P06312	DIVMTQSPDSLAVSLGER	DIVMTQSPDSLAVSLGER	959.4829++	959.482947	2	34.4	328.186697	b3	1	82.5	85.66		
Immunoglobulin kappa variable	IGKV4-1	P06312	DIVMTQSPDSLAVSLGER	DIVMTQSPDSLAVSLGER[+10.008269]	964.4871++ (heavy)	964.487082	2	34.4	1153.608697	y11	1	82.5	85.66		
Immunoglobulin kappa variable	IGKV4-1	P06312	DIVMTQSPDSLAVSLGER	DIVMTQSPDSLAVSLGER[+10.008269]	964.4871++ (heavy)	964.487082	2	34.4	229.118283	b2	1	82.5	85.66		
Immunoglobulin kappa variable	IGKV4-1	P06312	DIVMTQSPDSLAVSLGER	DIVMTQSPDSLAVSLGER[+10.008269]	964.4871++ (heavy)	964.487082	2	34.4	328.186697	b3	1	82.5	85.66		
Immunoglobulin kappa variable	IGKV4-1	P06312	NYLAWYQQKPGQPPK	NYLAWYQQKPGQPPK	606.6493+++	606.649294	3	20.5	623.351137	y6	1	59.71	54.87		
Immunoglobulin kappa variable	IGKV4-1	P06312	NYLAWYQQKPGQPPK	NYLAWYQQKPGQPPK	606.6493+++	606.649294	3	20.5	341.218332	y3	1	59.71	54.87		
Immunoglobulin kappa variable	IGKV4-1	P06312	NYLAWYQQKPGQPPK	NYLAWYQQKPGQPPK	606.6493+++	606.649294	3	20.5	391.197596	b3	1	59.71	54.87		
Immunoglobulin kappa variable	IGKV4-1	P06312	NYLAWYQQKPGQPPK	NYLAWYQQKPGQPPK[+8.014199]	609.3207+++ (heavy)	609.320694	3	20.5	631.365336	y6	1	59.71	54.87		
Immunoglobulin kappa variable	IGKV4-1	P06312	NYLAWYQQKPGQPPK	NYLAWYQQKPGQPPK[+8.014199]	609.3207+++ (heavy)	609.320694	3	20.5	349.23253	y3	1	59.71	54.87		
Immunoglobulin kappa variable	IGKV4-1	P06312	NYLAWYQQKPGQPPK	NYLAWYQQKPGQPPK[+8.014199]	609.3207+++ (heavy)	609.320694	3	20.5	391.197596	b3	1	59.71	54.87		
Immunoglobulin kappa variable	IGKV4-1	P06312	LLIYWASTR	LLIYWASTR	561.8189++	561.818941	2	19.7	896.462478	y7	1	77.9	79.82		
Immunoglobulin kappa variable	IGKV4-1	P06312	LLIYWASTR	LLIYWASTR	561.8189++	561.818941	2	19.7	783.378414	y6	1	77.9	79.82		
Immunoglobulin kappa variable	IGKV4-1	P06312	LLIYWASTR	LLIYWASTR	561.8189++	561.818941	2	19.7	620.315085	y5	1	77.9	79.82		
Immunoglobulin kappa variable	IGKV4-1	P06312	LLIYWASTR	LLIYWASTR[+10.008269]	566.8231++ (heavy)	566.823076	2	19.7	906.470747	y7	1	77.9	79.82		
Immunoglobulin kappa variable	IGKV4-1	P06312	LLIYWASTR	LLIYWASTR[+10.008269]	566.8231++ (heavy)	566.823076	2	19.7	793.386683	y6	1	77.9	79.82		
Immunoglobulin kappa variable	IGKV4-1	P06312	LLIYWASTR	LLIYWASTR[+10.008269]	566.8231++ (heavy)	566.823076	2	19.7	630.323354	y5	1	77.9	79.82		
Immunoglobulin lambda consta	IGLC6	P0CF74	YAASSYLSLTPEQWK	YAASSYLSLTPEQWK	872.4331++	872.433052	2	31.2	788.39373	y6	1	90.35	87.42	3.7	5.7
Immunoglobulin lambda consta	IGLC6	P0CF74	YAASSYLSLTPEQWK	YAASSYLSLTPEQWK	872.4331++	872.433052	2	31.2	687.346051	y5	1	90.35	87.42		
Immunoglobulin lambda consta	IGLC6	P0CF74	YAASSYLSLTPEQWK	YAASSYLSLTPEQWK	872.4331++	872.433052	2	31.2	235.107718	b2	1	90.35	87.42		
Immunoglobulin lambda consta	IGLC6	P0CF74	YAASSYLSLTPEQWK	YAASSYLSLTPEQWK[+8.014199]	876.4402++ (heavy)	876.440151	2	31.2	796.407929	y6	1	90.35	87.42		
Immunoglobulin lambda consta	IGLC6	P0CF74	YAASSYLSLTPEQWK	YAASSYLSLTPEQWK[+8.014199]	876.4402++ (heavy)	876.440151	2	31.2	695.36025	y5	1	90.35	87.42		
Immunoglobulin lambda consta	IGLC6	P0CF74	YAASSYLSLTPEQWK	YAASSYLSLTPEQWK[+8.014199]	876.4402++ (heavy)	876.440151	2	31.2	235.107718	b2	1	90.35	87.42		
Immunoglobulin lambda consta	IGLC6	P0CF74	SYSCQVTHEGSTVEK	SYSC[+57.021464]QVTHEGSTVEK	571.2579+++	571.257914	3	19.2	987.474165	y9	1	14.25	16.5		
Immunoglobulin lambda consta	IGLC6	P0CF74	SYSCQVTHEGSTVEK	SYSC[+57.021464]QVTHEGSTVEK	571.2579+++	571.257914	3	19.2	749.367575	y7	1	14.25	16.5		
Immunoglobulin lambda consta	IGLC6	P0CF74	SYSCQVTHEGSTVEK	SYSC[+57.021464]QVTHEGSTVEK	571.2579+++	571.257914	3	19.2	620.324982	y6	1	14.25	16.5		
Immunoglobulin lambda consta	IGLC6	P0CF74	SYSCQVTHEGSTVEK	SYSC[+57.021464]QVTHEGSTVEK[+8.01419	573.9293+++ (heavy)	573.929314	3	19.2	995.488364	y9	1	14.25	16.5		
Immunoglobulin lambda consta	IGLC6	P0CF74	SYSCQVTHEGSTVEK	SYSC[+57.021464]QVTHEGSTVEK[+8.01419	573.9293+++ (heavy)	573.929314	3	19.2	757.381774	y7	1	14.25	16.5		
Immunoglobulin lambda consta	IGLC6	P0CF74	SYSCQVTHEGSTVEK	SYSC[+57.021464]QVTHEGSTVEK[+8.01419	573.9293+++ (heavy)	573.929314	3	19.2	628.339181	y6	1	14.25	16.5		
Sex hormone-binding globulin	SHBG	P04278	IALGGLLFPASNLR	IALGGLLFPASNLR	721.4299++	721.429918	2	25.6	917.520327	y8	1	105.33	112.16	3.6	12.2
Sex hormone-binding globulin	SHBG	P04278	IALGGLLFPASNLR	IALGGLLFPASNLR	721.4299++	721.429918	2	25.6	804.436263	y7	1	105.33	112.16		
Sex hormone-binding globulin	SHBG	P04278	IALGGLLFPASNLR	IALGGLLFPASNLR	721.4299++	721.429918	2	25.6	657.367849	y6	1	105.33	112.16		
Sex hormone-binding globulin	SHBG	P04278	IALGGLLFPASNLR	IALGGLLFPASNLR[+10.008269]	726.4341++ (heavy)	726.434053	2	25.6	927.528596	y8	1	105.33	112.16		

Sex hormone-binding globulin	SHBG	P04278	IALGGLLFPASNLR	IALGGLLFPASNLR[+10.008269]	726.4341++ (heavy)	726.434053	2	25.6	814.444532	y7	1	105.33	112.16		
Sex hormone-binding globulin	SHBG	P04278	IALGGLLFPASNLR	IALGGLLFPASNLR[+10.008269]	726.4341++ (heavy)	726.434053	2	25.6	667.376118	y6	1	105.33	112.16		
Sex hormone-binding globulin	SHBG	P04278	LPLVPALDGCLR	LPLVPALDGC[+57.021464]LR	662.3763++	662.376297	2	23.4	901.456013	y8	1	82.79	91.95		
Sex hormone-binding globulin	SHBG	P04278	LPLVPALDGCLR	LPLVPALDGC[+57.021464]LR	662.3763++	662.376297	2	23.4	211.144104	b2	1	82.79	91.95		
Sex hormone-binding globulin	SHBG	P04278	LPLVPALDGCLR	LPLVPALDGC[+57.021464]LR	662.3763++	662.376297	2	23.4	324.228168	b3	1	82.79	91.95		
Sex hormone-binding globulin	SHBG	P04278	LPLVPALDGCLR	LPLVPALDGC[+57.021464]LR	662.3763++	662.376297	2	23.4	423.296582	b4	1	82.79	91.95		
Sex hormone-binding globulin	SHBG	P04278	LPLVPALDGCLR	LPLVPALDGC[+57.021464]LR[+10.008269]	667.3804++ (heavy)	667.380432	2	23.4	911.464282	y8	1	82.79	91.95		
Sex hormone-binding globulin	SHBG	P04278	LPLVPALDGCLR	LPLVPALDGC[+57.021464]LR[+10.008269]	667.3804++ (heavy)	667.380432	2	23.4	211.144104	b2	1	82.79	91.95		
Sex hormone-binding globulin	SHBG	P04278	LPLVPALDGCLR	LPLVPALDGC[+57.021464]LR[+10.008269]	667.3804++ (heavy)	667.380432	2	23.4	324.228168	b3	1	82.79	91.95		
Sex hormone-binding globulin	SHBG	P04278	LPLVPALDGCLR	LPLVPALDGC[+57.021464]LR[+10.008269]	667.3804++ (heavy)	667.380432	2	23.4	423.296582	b4	1	82.79	91.95		
Sex hormone-binding globulin	SHBG	P04278	QAEISASAPTSLR	QAEISASAPTSLR	665.8517++	665.851698	2	23.6	889.473771	y9	1	40.5	36.88		
Sex hormone-binding globulin	SHBG	P04278	QAEISASAPTSLR	QAEISASAPTSLR	665.8517++	665.851698	2	23.6	731.404629	y7	1	40.5	36.88		
Sex hormone-binding globulin	SHBG	P04278	QAEISASAPTSLR	QAEISASAPTSLR	665.8517++	665.851698	2	23.6	573.335487	y5	1	40.5	36.88		
Sex hormone-binding globulin	SHBG	P04278	QAEISASAPTSLR	QAEISASAPTSLR	665.8517++	665.851698	2	23.6	329.14556	b3	1	40.5	36.88		
Sex hormone-binding globulin	SHBG	P04278	QAEISASAPTSLR	QAEISASAPTSLR[+10.008269]	670.8558++ (heavy)	670.855832	2	23.6	899.48204	y9	1	40.5	36.88		
Sex hormone-binding globulin	SHBG	P04278	QAEISASAPTSLR	QAEISASAPTSLR[+10.008269]	670.8558++ (heavy)	670.855832	2	23.6	741.412898	y7	1	40.5	36.88		
Sex hormone-binding globulin	SHBG	P04278	QAEISASAPTSLR	QAEISASAPTSLR[+10.008269]	670.8558++ (heavy)	670.855832	2	23.6	583.343756	y5	1	40.5	36.88		
Sex hormone-binding globulin	SHBG	P04278	QAEISASAPTSLR	QAEISASAPTSLR[+10.008269]	670.8558++ (heavy)	670.855832	2	23.6	329.14556	b3	1	40.5	36.88		
Immunoglobulin J chain	JCHAIN	P01591	SSEDPNEDIVER	SSEDPNEDIVER	695.3101++	695.31006	2	24.7	1086.506193	y9	1	24.69	23.15	2.9	5.1
Immunoglobulin J chain	JCHAIN	P01591	SSEDPNEDIVER	SSEDPNEDIVER	695.3101++	695.31006	2	24.7	971.47925	y8	1	24.69	23.15		
Immunoglobulin J chain	JCHAIN	P01591	SSEDPNEDIVER	SSEDPNEDIVER	695.3101++	695.31006	2	24.7	631.340966	y5	1	24.69	23.15		
Immunoglobulin J chain	JCHAIN	P01591	SSEDPNEDIVER	SSEDPNEDIVER	695.3101++	695.31006	2	24.7	403.229959	y3	1	24.69	23.15		
Immunoglobulin J chain	JCHAIN	P01591	SSEDPNEDIVER	SSEDPNEDIVER[+10.008269]	700.3142++ (heavy)	700.314194	2	24.7	1096.514462	y9	1	24.69	23.15		
Immunoglobulin J chain	JCHAIN	P01591	SSEDPNEDIVER	SSEDPNEDIVER[+10.008269]	700.3142++ (heavy)	700.314194	2	24.7	981.487519	y8	1	24.69	23.15		
Immunoglobulin J chain	JCHAIN	P01591	SSEDPNEDIVER	SSEDPNEDIVER[+10.008269]	700.3142++ (heavy)	700.314194	2	24.7	641.349235	y5	1	24.69	23.15		
Immunoglobulin J chain	JCHAIN	P01591	SSEDPNEDIVER	SSEDPNEDIVER[+10.008269]	700.3142++ (heavy)	700.314194	2	24.7	413.238228	y3	1	24.69	23.15		
Immunoglobulin J chain	JCHAIN	P01591	IIVPLNNR	IIVPLNNR	469.7927++	469.792726	2	16.3	712.410049	y6	1	45.29	41.17		
Immunoglobulin J chain	JCHAIN	P01591	IIVPLNNR	IIVPLNNR	469.7927++	469.792726	2	16.3	613.341635	y5	1	45.29	41.17		
Immunoglobulin J chain	JCHAIN	P01591	IIVPLNNR	IIVPLNNR	469.7927++	469.792726	2	16.3	516.288871	y4	1	45.29	41.17		
Immunoglobulin J chain	JCHAIN	P01591	IIVPLNNR	IIVPLNNR[+10.008269]	474.7969++ (heavy)	474.796861	2	16.3	722.418318	y6	1	45.29	41.17		
Immunoglobulin J chain	JCHAIN	P01591	IIVPLNNR	IIVPLNNR[+10.008269]	474.7969++ (heavy)	474.796861	2	16.3	623.349904	y5	1	45.29	41.17		
Immunoglobulin J chain	JCHAIN	P01591	IIVPLNNR	IIVPLNNR[+10.008269]	474.7969++ (heavy)	474.796861	2	16.3	526.29714	y4	1	45.29	41.17		
Immunoglobulin J chain	JCHAIN	P01591	FVYHLSDLCK	FVYHLSDLC[+57.021464]K	427.8814+++	427.881391	3	14.1	735.370552	y6	1	61.77	52.69		
Immunoglobulin J chain	JCHAIN	P01591	FVYHLSDLCK	FVYHLSDLC[+57.021464]K	427.8814+++	427.881391	3	14.1	622.286488	y5	1	61.77	52.69		
Immunoglobulin J chain	JCHAIN	P01591	FVYHLSDLCK	FVYHLSDLC[+57.021464]K	427.8814+++	427.881391	3	14.1	420.227516	y3	1	61.77	52.69		
Immunoglobulin J chain	JCHAIN	P01591	FVYHLSDLCK	FVYHLSDLC[+57.021464]K[+8.014199]	430.5528+++ (heavy)	430.55279	3	14.1	743.384751	y6	1	61.77	52.69		
Immunoglobulin J chain	JCHAIN	P01591	FVYHLSDLCK	FVYHLSDLC[+57.021464]K[+8.014199]	430.5528+++ (heavy)	430.55279	3	14.1	630.300687	y5	1	61.77	52.69		
Immunoglobulin J chain	JCHAIN	P01591	FVYHLSDLCK	FVYHLSDLC[+57.021464]K[+8.014199]	430.5528+++ (heavy)	430.55279	3	14.1	428.241715	y3	1	61.77	52.69		
Immunoglobulin J chain	JCHAIN	P01591	CYTAVVPLVYGGETK	C[+57.021464]YTAVVPLVYGGETK	828.9187++	828.918723	2	29.6	1062.582987	y10	1	70.18	74.68		
Immunoglobulin J chain	JCHAIN	P01591	CYTAVVPLVYGGETK	C[+57.021464]YTAVVPLVYGGETK	828.9187++	828.918723	2	29.6	963.514573	y9	1	70.18	74.68		
Immunoglobulin J chain	JCHAIN	P01591	CYTAVVPLVYGGETK	C[+57.021464]YTAVVPLVYGGETK	828.9187++	828.918723	2	29.6	425.148932	b3	1	70.18	74.68		
Immunoglobulin J chain	JCHAIN	P01591	CYTAVVPLVYGGETK	C[+57.021464]YTAVVPLVYGGETK[+8.01419	832.9258++ (heavy)	832.925823	2	29.6	1070.597186	y10	1	70.18	74.68		
Immunoglobulin J chain	JCHAIN	P01591	CYTAVVPLVYGGETK	C[+57.021464]YTAVVPLVYGGETK[+8.01419	832.9258++ (heavy)	832.925823	2	29.6	971.528772	y9	1	70.18	74.68		
Immunoglobulin J chain	JCHAIN	P01591	CYTAVVPLVYGGETK	C[+57.021464]YTAVVPLVYGGETK[+8.01419	832.9258++ (heavy)	832.925823	2	29.6	425.148932	b3	1	70.18	74.68		
Inter-alpha-trypsin inhibitor hea	ITIH3	Q06033	EVSFDVELPK	EVSFDVELPK	581.8032++	581.803154	2	20.5	934.488024	y8	1	61.32	73.71	4.0	6.0
Inter-alpha-trypsin inhibitor hea	ITIH3	Q06033	EVSFDVELPK	EVSFDVELPK	581.8032++	581.803154	2	20.5	700.387582	y6	1	61.32	73.71		
Inter-alpha-trypsin inhibitor hea	ITIH3	Q06033	EVSFDVELPK	EVSFDVELPK	581.8032++	581.803154	2	20.5	585.360639	y5	1	61.32	73.71		
Inter-alpha-trypsin inhibitor hea	ITIH3	Q06033	EVSFDVELPK	EVSFDVELPK[+8.014199]	585.8103++ (heavy)	585.810253	2	20.5	942.502223	y8	1	61.32	73.71		
Inter-alpha-trypsin inhibitor hea	ITIH3	Q06033	EVSFDVELPK	EVSFDVELPK[+8.014199]	585.8103++ (heavy)	585.810253	2	20.5	708.401781	y6	1	61.32	73.71		
Inter-alpha-trypsin inhibitor hea	ITIH3	Q06033	EVSFDVELPK	EVSFDVELPK[+8.014199]	585.8103++ (heavy)	585.810253	2	20.5	593.374838	y5	1	61.32	73.71		

Inter-alpha-trypsin inhibitor hea	ITIH3	Q06033	EHLVQATPENLQEAR	EHLVQATPENLQEAR	578.9638+++	578.96383	3	19.5	956.479585	y8	1	50.73	33.88		
Inter-alpha-trypsin inhibitor hea	ITIH3	Q06033	EHLVQATPENLQEAR	EHLVQATPENLQEAR	578.9638+++	578.96383	3	19.5	730.384228	y6	1	50.73	33.88		
Inter-alpha-trypsin inhibitor hea	ITIH3	Q06033	EHLVQATPENLQEAR	EHLVQATPENLQEAR	578.9638+++	578.96383	3	19.5	503.257236	y4	1	50.73	33.88		
Inter-alpha-trypsin inhibitor hea	ITIH3	Q06033	EHLVQATPENLQEAR	EHLVQATPENLQEAR[+10.008269]	582.2999+++ (heavy)	582.29992	3	19.5	966.487854	y8	1	50.73	33.88		
Inter-alpha-trypsin inhibitor hea	ITIH3	Q06033	EHLVQATPENLQEAR	EHLVQATPENLQEAR[+10.008269]	582.2999+++ (heavy)	582.29992	3	19.5	740.392497	y6	1	50.73	33.88		
Inter-alpha-trypsin inhibitor hea	ITIH3	Q06033	EHLVQATPENLQEAR	EHLVQATPENLQEAR[+10.008269]	582.2999+++ (heavy)	582.29992	3	19.5	513.265505	y4	1	50.73	33.88		
Inter-alpha-trypsin inhibitor hea	ITIH3	Q06033	DYIFGNYIER	DYIFGNYIER	645.3117++	645.311677	2	22.8	898.441743	y7	1	83.64	80.19		
Inter-alpha-trypsin inhibitor hea	ITIH3	Q06033	DYIFGNYIER	DYIFGNYIER	645.3117++	645.311677	2	22.8	751.373329	y6	1	83.64	80.19		
Inter-alpha-trypsin inhibitor hea	ITIH3	Q06033	DYIFGNYIER	DYIFGNYIER	645.3117++	645.311677	2	22.8	392.181612	b3	1	83.64	80.19		
Inter-alpha-trypsin inhibitor hea	ITIH3	Q06033	DYIFGNYIER	DYIFGNYIER[+10.008269]	650.3158++ (heavy)	650.315812	2	22.8	908.450012	y7	1	83.64	80.19		
Inter-alpha-trypsin inhibitor hea	ITIH3	Q06033	DYIFGNYIER	DYIFGNYIER[+10.008269]	650.3158++ (heavy)	650.315812	2	22.8	761.381598	y6	1	83.64	80.19		
Inter-alpha-trypsin inhibitor hea	ITIH3	Q06033	DYIFGNYIER	DYIFGNYIER[+10.008269]	650.3158++ (heavy)	650.315812	2	22.8	392.181612	b3	1	83.64	80.19		
Apolipoprotein A-I	APOA1	P02647	VQPYLDDFQK	VQPYLDDFQK	626.8141++	626.814053	2	22.1	1025.493838	y8	1	59.62	51.63	3.4	4.6
Apolipoprotein A-I	APOA1	P02647	VQPYLDDFQK	VQPYLDDFQK	626.8141++	626.814053	2	22.1	765.377745	y6	1	59.62	51.63		
Apolipoprotein A-I	APOA1	P02647	VQPYLDDFQK	VQPYLDDFQK	626.8141++	626.814053	2	22.1	228.134267	b2	1	59.62	51.63		
Apolipoprotein A-I	APOA1	P02647	VQPYLDDFQK	VQPYLDDFQK[+8.014199]	630.8212++ (heavy)	630.821152	2	22.1	1033.508037	y8	1	59.62	51.63		
Apolipoprotein A-I	APOA1	P02647	VQPYLDDFQK	VQPYLDDFQK[+8.014199]	630.8212++ (heavy)	630.821152	2	22.1	773.391944	y6	1	59.62	51.63		
Apolipoprotein A-I	APOA1	P02647	VQPYLDDFQK	VQPYLDDFQK[+8.014199]	630.8212++ (heavy)	630.821152	2	22.1	228.134267	b2	1	59.62	51.63		
Apolipoprotein A-I	APOA1	P02647	THLAPYSDELR	THLAPYSDELR	434.5543+++	434.554331	3	14.3	619.30458	y5	1	53.92	33.2		
Apolipoprotein A-I	APOA1	P02647	THLAPYSDELR	THLAPYSDELR	434.5543+++	434.554331	3	14.3	417.245609	y3	1	53.92	33.2		
Apolipoprotein A-I	APOA1	P02647	THLAPYSDELR	THLAPYSDELR	434.5543+++	434.554331	3	14.3	423.235044	b4	1	53.92	33.2		
Apolipoprotein A-I	APOA1	P02647	THLAPYSDELR	THLAPYSDELR[+10.008269]	437.8904+++ (heavy)	437.890421	3	14.3	629.312849	y5	1	53.92	33.2		
Apolipoprotein A-I	APOA1	P02647	THLAPYSDELR	THLAPYSDELR[+10.008269]	437.8904+++ (heavy)	437.890421	3	14.3	427.253878	y3	1	53.92	33.2		
Apolipoprotein A-I	APOA1	P02647	THLAPYSDELR	THLAPYSDELR[+10.008269]	437.8904+++ (heavy)	437.890421	3	14.3	423.235044	b4	1	53.92	33.2		
Apolipoprotein A-I	APOA1	P02647	QGLLPVLESFK	QGLLPVLESFK	615.8583++	615.858263	2	21.7	819.461081	y7	1	95.86	103.27		
Apolipoprotein A-I	APOA1	P02647	QGLLPVLESFK	QGLLPVLESFK	615.8583++	615.858263	2	21.7	623.339903	y5	1	95.86	103.27		
Apolipoprotein A-I	APOA1	P02647	QGLLPVLESFK	QGLLPVLESFK	615.8583++	615.858263	2	21.7	299.171381	b3	1	95.86	103.27		
Apolipoprotein A-I	APOA1	P02647	QGLLPVLESFK	QGLLPVLESFK[+8.014199]	619.8654++ (heavy)	619.865363	2	21.7	827.47528	y7	1	95.86	103.27		
Apolipoprotein A-I	APOA1	P02647	QGLLPVLESFK	QGLLPVLESFK[+8.014199]	619.8654++ (heavy)	619.865363	2	21.7	631.354102	y5	1	95.86	103.27		
Apolipoprotein A-I	APOA1	P02647	QGLLPVLESFK	QGLLPVLESFK[+8.014199]	619.8654++ (heavy)	619.865363	2	21.7	299.171381	b3	1	95.86	103.27		
Apolipoprotein A-I	APOA1	P02647	VSFLSALEEYTK	VSFLSALEEYTK	693.8612++	693.8612	2	24.6	940.462203	y8	1	109.44	111.85		
Apolipoprotein A-I	APOA1	P02647	VSFLSALEEYTK	VSFLSALEEYTK	693.8612++	693.8612	2	24.6	853.430175	y7	1	109.44	111.85		
Apolipoprotein A-I	APOA1	P02647	VSFLSALEEYTK	VSFLSALEEYTK	693.8612++	693.8612	2	24.6	782.393061	y6	1	109.44	111.85		
Apolipoprotein A-I	APOA1	P02647	VSFLSALEEYTK	VSFLSALEEYTK[+8.014199]	697.8683++ (heavy)	697.868299	2	24.6	948.476402	y8	1	109.44	111.85		
Apolipoprotein A-I	APOA1	P02647	VSFLSALEEYTK	VSFLSALEEYTK[+8.014199]	697.8683++ (heavy)	697.868299	2	24.6	861.444374	y7	1	109.44	111.85		
Apolipoprotein A-I	APOA1	P02647	VSFLSALEEYTK	VSFLSALEEYTK[+8.014199]	697.8683++ (heavy)	697.868299	2	24.6	790.40726	y6	1	109.44	111.85		
Complement component C9	C9	P02748	VVEESELAR	VVEESELAR	516.2720++	516.272021	2	18	833.399937	y7	1	20.72	20.16	7.7	2.8
Complement component C9	C9	P02748	VVEESELAR	VVEESELAR	516.2720++	516.272021	2	18	704.357344	y6	1	20.72	20.16		
Complement component C9	C9	P02748	VVEESELAR	VVEESELAR	516.2720++	516.272021	2	18	575.314751	y5	1	20.72	20.16		
Complement component C9	C9	P02748	VVEESELAR	VVEESELAR[+10.008269]	521.2762++ (heavy)	521.276155	2	18	843.408206	y7	1	20.72	20.16		
Complement component C9	C9	P02748	VVEESELAR	VVEESELAR[+10.008269]	521.2762++ (heavy)	521.276155	2	18	714.365613	y6	1	20.72	20.16		
Complement component C9	C9	P02748	VVEESELAR	VVEESELAR[+10.008269]	521.2762++ (heavy)	521.276155	2	18	585.32302	y5	1	20.72	20.16		
Complement component C9	C9	P02748	TEHYEEQIEAFK	TEHYEEQIEAFK	508.5719+++	508.571939	3	17	607.344989	y5	1	53.21	44.33		
Complement component C9	C9	P02748	TEHYEEQIEAFK	TEHYEEQIEAFK	508.5719+++	508.571939	3	17	494.260925	y4	1	53.21	44.33		
Complement component C9	C9	P02748	TEHYEEQIEAFK	TEHYEEQIEAFK	508.5719+++	508.571939	3	17	365.218332	y3	1	53.21	44.33		
Complement component C9	C9	P02748	TEHYEEQIEAFK	TEHYEEQIEAFK[+8.014199]	511.2433+++ (heavy)	511.243339	3	17	615.359188	y5	1	53.21	44.33		
Complement component C9	C9	P02748	TEHYEEQIEAFK	TEHYEEQIEAFK[+8.014199]	511.2433+++ (heavy)	511.243339	3	17	502.275124	y4	1	53.21	44.33		
Complement component C9	C9	P02748	TEHYEEQIEAFK	TEHYEEQIEAFK[+8.014199]	511.2433+++ (heavy)	511.243339	3	17	373.23253	y3	1	53.21	44.33		
Complement component C9	C9	P02748	LSPIYNLVPVK	LSPIYNLVPVK	621.8765++	621.876456	2	21.9	832.492716	y7	1	82.57	85.41		
Complement component C9	C9	P02748	LSPIYNLVPVK	LSPIYNLVPVK	621.8765++	621.876456	2	21.9	442.302396	y4	1	82.57	85.41		

Complement component C9	C9	P02748	LSPIYNLVPVK	LSPIYNLVPVK	621.8765++	621.876456	2	21.9	343.233982	y3	1	82.57	85.41		
Complement component C9	C9	P02748	LSPIYNLVPVK	LSPIYNLVPVK[+8.014199]	625.8836++ (heavy)	625.883555	2	21.9	840.506915	y7	1	82.57	85.41		
Complement component C9	C9	P02748	LSPIYNLVPVK	LSPIYNLVPVK[+8.014199]	625.8836++ (heavy)	625.883555	2	21.9	450.316595	y4	1	82.57	85.41		
Complement component C9	C9	P02748	LSPIYNLVPVK	LSPIYNLVPVK[+8.014199]	625.8836++ (heavy)	625.883555	2	21.9	351.248181	y3	1	82.57	85.41		
Complement C5	C5	P01031	VFQFLEK	VFQFLEK	455.7553++	455.755278	2	15.8	811.434866	y6	1	66.96	63.03	5.6	5.3
Complement C5	C5	P01031	VFQFLEK	VFQFLEK	455.7553++	455.755278	2	15.8	664.366452	y5	1	66.96	63.03		
Complement C5	C5	P01031	VFQFLEK	VFQFLEK	455.7553++	455.755278	2	15.8	536.307875	y4	1	66.96	63.03		
Complement C5	C5	P01031	VFQFLEK	VFQFLEK[+8.014199]	459.7624++ (heavy)	459.762378	2	15.8	819.449065	y6	1	66.96	63.03		
Complement C5	C5	P01031	VFQFLEK	VFQFLEK[+8.014199]	459.7624++ (heavy)	459.762378	2	15.8	672.380651	y5	1	66.96	63.03		
Complement C5	C5	P01031	VFQFLEK	VFQFLEK[+8.014199]	459.7624++ (heavy)	459.762378	2	15.8	544.322074	y4	1	66.96	63.03		
Complement C5	C5	P01031	IPLDLVPK	IPLDLVPK	447.7866++	447.786578	2	15.5	684.429053	y6	1	60.46	66		
Complement C5	C5	P01031	IPLDLVPK	IPLDLVPK	447.7866++	447.786578	2	15.5	571.344989	y5	1	60.46	66		
Complement C5	C5	P01031	IPLDLVPK	IPLDLVPK	447.7866++	447.786578	2	15.5	244.165568	y2	1	60.46	66		
Complement C5	C5	P01031	IPLDLVPK	IPLDLVPK[+8.014199]	451.7937++ (heavy)	451.793678	2	15.5	692.443252	y6	1	60.46	66		
Complement C5	C5	P01031	IPLDLVPK	IPLDLVPK[+8.014199]	451.7937++ (heavy)	451.793678	2	15.5	579.359188	y5	1	60.46	66		
Complement C5	C5	P01031	IPLDLVPK	IPLDLVPK[+8.014199]	451.7937++ (heavy)	451.793678	2	15.5	252.179767	y2	1	60.46	66		
Complement C5	C5	P01031	DINYVNPVIK	DINYVNPVIK	587.8270++	587.826963	2	20.7	946.535643	y8	1	52.18	57.99		
Complement C5	C5	P01031	DINYVNPVIK	DINYVNPVIK	587.8270++	587.826963	2	20.7	669.429387	y6	1	52.18	57.99		
Complement C5	C5	P01031	DINYVNPVIK	DINYVNPVIK	587.8270++	587.826963	2	20.7	343.161211	b3	1	52.18	57.99		
Complement C5	C5	P01031	DINYVNPVIK	DINYVNPVIK[+8.014199]	591.8341++ (heavy)	591.834063	2	20.7	954.549842	y8	1	52.18	57.99		
Complement C5	C5	P01031	DINYVNPVIK	DINYVNPVIK[+8.014199]	591.8341++ (heavy)	591.834063	2	20.7	677.443586	y6	1	52.18	57.99		
Complement C5	C5	P01031	DINYVNPVIK	DINYVNPVIK[+8.014199]	591.8341++ (heavy)	591.834063	2	20.7	343.161211	b3	1	52.18	57.99		
Alpha-1-antichymotrypsin	SERPINA3	P01011	LYGSEAFATDFQDSAAAK	LYGSEAFATDFQDSAAAK	946.4391++	946.439063	2	34	1271.590257	y12	1	76.35	72.58	3.2	4.3
Alpha-1-antichymotrypsin	SERPINA3	P01011	LYGSEAFATDFQDSAAAK	LYGSEAFATDFQDSAAAK	946.4391++	946.439063	2	34	1124.521844	y11	1	76.35	72.58		
Alpha-1-antichymotrypsin	SERPINA3	P01011	LYGSEAFATDFQDSAAAK	LYGSEAFATDFQDSAAAK	946.4391++	946.439063	2	34	1053.48473	y10	1	76.35	72.58		
Alpha-1-antichymotrypsin	SERPINA3	P01011	LYGSEAFATDFQDSAAAK	LYGSEAFATDFQDSAAAK[+8.014199]	950.4462++ (heavy)	950.446162	2	34	1279.604456	y12	1	76.35	72.58		
Alpha-1-antichymotrypsin	SERPINA3	P01011	LYGSEAFATDFQDSAAAK	LYGSEAFATDFQDSAAAK[+8.014199]	950.4462++ (heavy)	950.446162	2	34	1132.536043	y11	1	76.35	72.58		
Alpha-1-antichymotrypsin	SERPINA3	P01011	LYGSEAFATDFQDSAAAK	LYGSEAFATDFQDSAAAK[+8.014199]	950.4462++ (heavy)	950.446162	2	34	1061.498929	y10	1	76.35	72.58		
Alpha-1-antichymotrypsin	SERPINA3	P01011	EIGELYLPK	EIGELYLPK	531.2975++	531.297507	2	18.6	633.397024	y5	1	64.34	64.12		
Alpha-1-antichymotrypsin	SERPINA3	P01011	EIGELYLPK	EIGELYLPK	531.2975++	531.297507	2	18.6	520.31296	y4	1	64.34	64.12		
Alpha-1-antichymotrypsin	SERPINA3	P01011	EIGELYLPK	EIGELYLPK	531.2975++	531.297507	2	18.6	357.249632	y3	1	64.34	64.12		
Alpha-1-antichymotrypsin	SERPINA3	P01011	EIGELYLPK	EIGELYLPK[+8.014199]	535.3046++ (heavy)	535.304607	2	18.6	641.411223	y5	1	64.34	64.12		
Alpha-1-antichymotrypsin	SERPINA3	P01011	EIGELYLPK	EIGELYLPK[+8.014199]	535.3046++ (heavy)	535.304607	2	18.6	528.327159	y4	1	64.34	64.12		
Alpha-1-antichymotrypsin	SERPINA3	P01011	EIGELYLPK	EIGELYLPK[+8.014199]	535.3046++ (heavy)	535.304607	2	18.6	365.263831	y3	1	64.34	64.12		
Alpha-1-antichymotrypsin	SERPINA3	P01011	ITLLSALVETR	ITLLSALVETR	608.3690++	608.368995	2	21.4	888.514908	y8	1	96.53	98.01		
Alpha-1-antichymotrypsin	SERPINA3	P01011	ITLLSALVETR	ITLLSALVETR	608.3690++	608.368995	2	21.4	775.430844	y7	1	96.53	98.01		
Alpha-1-antichymotrypsin	SERPINA3	P01011	ITLLSALVETR	ITLLSALVETR	608.3690++	608.368995	2	21.4	688.398815	y6	1	96.53	98.01		
Alpha-1-antichymotrypsin	SERPINA3	P01011	ITLLSALVETR	ITLLSALVETR[+10.008269]	613.3731++ (heavy)	613.37313	2	21.4	898.523177	y8	1	96.53	98.01		
Alpha-1-antichymotrypsin	SERPINA3	P01011	ITLLSALVETR	ITLLSALVETR[+10.008269]	613.3731++ (heavy)	613.37313	2	21.4	785.439113	y7	1	96.53	98.01		
Alpha-1-antichymotrypsin	SERPINA3	P01011	ITLLSALVETR	ITLLSALVETR[+10.008269]	613.3731++ (heavy)	613.37313	2	21.4	698.407084	y6	1	96.53	98.01		
Mannose-binding protein C	MBL2	P11226	WLTFSLGK	WLTFSLGK	476.2686++	476.268553	2	16.6	765.450516	y7	1	78.19	87.59	6.1	1.2
Mannose-binding protein C	MBL2	P11226	WLTFSLGK	WLTFSLGK	476.2686++	476.268553	2	16.6	652.366452	y6	1	78.19	87.59		
Mannose-binding protein C	MBL2	P11226	WLTFSLGK	WLTFSLGK	476.2686++	476.268553	2	16.6	204.134267	y2	1	78.19	87.59		
Mannose-binding protein C	MBL2	P11226	WLTFSLGK	WLTFSLGK[+8.014199]	480.2757++ (heavy)	480.275652	2	16.6	773.464715	y7	1	78.19	87.59		
Mannose-binding protein C	MBL2	P11226	WLTFSLGK	WLTFSLGK[+8.014199]	480.2757++ (heavy)	480.275652	2	16.6	660.380651	y6	1	78.19	87.59		
Mannose-binding protein C	MBL2	P11226	WLTFSLGK	WLTFSLGK[+8.014199]	480.2757++ (heavy)	480.275652	2	16.6	212.148466	y2	1	78.19	87.59		
Mannose-binding protein C	MBL2	P11226	FQASVATPR	FQASVATPR	488.7642++	488.764166	2	17	701.394064	y7	1	20.59	25.21		
Mannose-binding protein C	MBL2	P11226	FQASVATPR	FQASVATPR	488.7642++	488.764166	2	17	630.35695	y6	1	20.59	25.21		
Mannose-binding protein C	MBL2	P11226	FQASVATPR	FQASVATPR	488.7642++	488.764166	2	17	276.134267	b2	1	20.59	25.21		
Mannose-binding protein C	MBL2	P11226	FQASVATPR	FQASVATPR[+10.008269]	493.7683++ (heavy)	493.7683	2	17	711.402333	y7	1	20.59	25.21		

Mannose-binding protein C	MBL2	P11226	FQASVATPR	FQASVATPR[+10.008269]	493.7683++ (heavy)	493.7683	2	17	640.365219	y6	1	20.59	25.21		
Mannose-binding protein C	MBL2	P11226	FQASVATPR	FQASVATPR[+10.008269]	493.7683++ (heavy)	493.7683	2	17	276.134267	b2	1	20.59	25.21		
Mannose-binding protein C	MBL2	P11226	TEGQFVDLTGNR	TEGQFVDLTGNR	668.8282++	668.828223	2	23.7	921.478856	y8	1	50.44	46.9		
Mannose-binding protein C	MBL2	P11226	TEGQFVDLTGNR	TEGQFVDLTGNR	668.8282++	668.828223	2	23.7	675.342029	y6	1	50.44	46.9		
Mannose-binding protein C	MBL2	P11226	TEGQFVDLTGNR	TEGQFVDLTGNR	668.8282++	668.828223	2	23.7	560.315085	y5	1	50.44	46.9		
Mannose-binding protein C	MBL2	P11226	TEGQFVDLTGNR	TEGQFVDLTGNR	668.8282++	668.828223	2	23.7	447.231021	y4	1	50.44	46.9		
Mannose-binding protein C	MBL2	P11226	TEGQFVDLTGNR	TEGQFVDLTGNR[+10.008269]	673.8324++ (heavy)	673.832357	2	23.7	931.487125	y8	1	50.44	46.9		
Mannose-binding protein C	MBL2	P11226	TEGQFVDLTGNR	TEGQFVDLTGNR[+10.008269]	673.8324++ (heavy)	673.832357	2	23.7	685.350298	y6	1	50.44	46.9		
Mannose-binding protein C	MBL2	P11226	TEGQFVDLTGNR	TEGQFVDLTGNR[+10.008269]	673.8324++ (heavy)	673.832357	2	23.7	570.323354	y5	1	50.44	46.9		
Mannose-binding protein C	MBL2	P11226	TEGQFVDLTGNR	TEGQFVDLTGNR[+10.008269]	673.8324++ (heavy)	673.832357	2	23.7	457.23929	y4	1	50.44	46.9		
Complement component C7	C7	P10643	ELSHLPSLYDYSAYR	ELSHLPSLYDYSAYR	605.2967+++	605.296698	3	20.5	774.341694	y6	1	82.62	77.45	4.8	6.0
Complement component C7	C7	P10643	ELSHLPSLYDYSAYR	ELSHLPSLYDYSAYR	605.2967+++	605.296698	3	20.5	659.314751	y5	1	82.62	77.45		
Complement component C7	C7	P10643	ELSHLPSLYDYSAYR	ELSHLPSLYDYSAYR	605.2967+++	605.296698	3	20.5	496.251423	y4	1	82.62	77.45		
Complement component C7	C7	P10643	ELSHLPSLYDYSAYR	ELSHLPSLYDYSAYR[+10.008269]	608.6328+++ (heavy)	608.632787	3	20.5	784.349963	y6	1	82.62	77.45		
Complement component C7	C7	P10643	ELSHLPSLYDYSAYR	ELSHLPSLYDYSAYR[+10.008269]	608.6328+++ (heavy)	608.632787	3	20.5	669.32302	y5	1	82.62	77.45		
Complement component C7	C7	P10643	ELSHLPSLYDYSAYR	ELSHLPSLYDYSAYR[+10.008269]	608.6328+++ (heavy)	608.632787	3	20.5	506.259692	y4	1	82.62	77.45		
Complement component C7	C7	P10643	VLFYVDSEK	VLFYVDSEK	550.2871++	550.287139	2	19.3	887.414525	y7	1	60.12	54.24		
Complement component C7	C7	P10643	VLFYVDSEK	VLFYVDSEK	550.2871++	550.287139	2	19.3	740.346111	y6	1	60.12	54.24		
Complement component C7	C7	P10643	VLFYVDSEK	VLFYVDSEK	550.2871++	550.287139	2	19.3	577.282782	y5	1	60.12	54.24		
Complement component C7	C7	P10643	VLFYVDSEK	VLFYVDSEK[+8.014199]	554.2942++ (heavy)	554.294239	2	19.3	895.428724	y7	1	60.12	54.24		
Complement component C7	C7	P10643	VLFYVDSEK	VLFYVDSEK[+8.014199]	554.2942++ (heavy)	554.294239	2	19.3	748.36031	y6	1	60.12	54.24		
Complement component C7	C7	P10643	VLFYVDSEK	VLFYVDSEK[+8.014199]	554.2942++ (heavy)	554.294239	2	19.3	585.296981	y5	1	60.12	54.24		
Complement component C7	C7	P10643	LTPLYELVK	LTPLYELVK	538.3235++	538.323525	2	18.9	861.508031	y7	1	83.57	80.25		
Complement component C7	C7	P10643	LTPLYELVK	LTPLYELVK	538.3235++	538.323525	2	18.9	764.455267	y6	1	83.57	80.25		
Complement component C7	C7	P10643	LTPLYELVK	LTPLYELVK	538.3235++	538.323525	2	18.9	651.371203	y5	1	83.57	80.25		
Complement component C7	C7	P10643	LTPLYELVK	LTPLYELVK[+8.014199]	542.3306++ (heavy)	542.330624	2	18.9	869.52223	y7	1	83.57	80.25		
Complement component C7	C7	P10643	LTPLYELVK	LTPLYELVK[+8.014199]	542.3306++ (heavy)	542.330624	2	18.9	772.469466	y6	1	83.57	80.25		
Complement component C7	C7	P10643	LTPLYELVK	LTPLYELVK[+8.014199]	542.3306++ (heavy)	542.330624	2	18.9	659.385402	y5	1	83.57	80.25		
Complement C3	C3	P01024	TGLQEVEVK	TGLQEVEVK	501.7769++	501.776939	2	17.5	731.393395	y6	1	28.75	28.42	6.0	2.2
Complement C3	C3	P01024	TGLQEVEVK	TGLQEVEVK	501.7769++	501.776939	2	17.5	603.334818	y5	1	28.75	28.42		
Complement C3	C3	P01024	TGLQEVEVK	TGLQEVEVK	501.7769++	501.776939	2	17.5	474.292225	y4	1	28.75	28.42		
Complement C3	C3	P01024	TGLQEVEVK	TGLQEVEVK[+8.014199]	505.7840++ (heavy)	505.784038	2	17.5	739.407594	y6	1	28.75	28.42		
Complement C3	C3	P01024	TGLQEVEVK	TGLQEVEVK[+8.014199]	505.7840++ (heavy)	505.784038	2	17.5	611.349017	y5	1	28.75	28.42		
Complement C3	C3	P01024	TGLQEVEVK	TGLQEVEVK[+8.014199]	505.7840++ (heavy)	505.784038	2	17.5	482.306424	y4	1	28.75	28.42		
Complement C3	C3	P01024	GYTQQLAFR	GYTQQLAFR	542.2827++	542.282723	2	19	634.367121	y5	1	46.95	42.92		
Complement C3	C3	P01024	GYTQQLAFR	GYTQQLAFR	542.2827++	542.282723	2	19	506.308544	y4	1	46.95	42.92		
Complement C3	C3	P01024	GYTQQLAFR	GYTQQLAFR	542.2827++	542.282723	2	19	393.22448	y3	1	46.95	42.92		
Complement C3	C3	P01024	GYTQQLAFR	GYTQQLAFR[+10.008269]	547.2869++ (heavy)	547.286857	2	19	644.37539	y5	1	46.95	42.92		
Complement C3	C3	P01024	GYTQQLAFR	GYTQQLAFR[+10.008269]	547.2869++ (heavy)	547.286857	2	19	516.316813	y4	1	46.95	42.92		
Complement C3	C3	P01024	GYTQQLAFR	GYTQQLAFR[+10.008269]	547.2869++ (heavy)	547.286857	2	19	403.232748	y3	1	46.95	42.92		
Apolipoprotein A-II	APOA2	P02652	EQLTPLIK	EQLTPLIK	471.2869++	471.286942	2	16.4	684.465438	y6	1	50.11	45.76	5.0	2.3
Apolipoprotein A-II	APOA2	P02652	EQLTPLIK	EQLTPLIK	471.2869++	471.286942	2	16.4	571.381374	y5	1	50.11	45.76		
Apolipoprotein A-II	APOA2	P02652	EQLTPLIK	EQLTPLIK	471.2869++	471.286942	2	16.4	470.333696	y4	1	50.11	45.76		
Apolipoprotein A-II	APOA2	P02652	EQLTPLIK	EQLTPLIK[+8.014199]	475.2940++ (heavy)	475.294042	2	16.4	692.479637	y6	1	50.11	45.76		
Apolipoprotein A-II	APOA2	P02652	EQLTPLIK	EQLTPLIK[+8.014199]	475.2940++ (heavy)	475.294042	2	16.4	579.395573	y5	1	50.11	45.76		
Apolipoprotein A-II	APOA2	P02652	EQLTPLIK	EQLTPLIK[+8.014199]	475.2940++ (heavy)	475.294042	2	16.4	478.347895	y4	1	50.11	45.76		
Apolipoprotein C-II	APOC2	P02655	ESLSSYWESAK	ESLSSYWESAK	643.7986++	643.7986	2	22.8	957.431238	y8	1	61.16	59.9	5.2	2.1
Apolipoprotein C-II	APOC2	P02655	ESLSSYWESAK	ESLSSYWESAK	643.7986++	643.7986	2	22.8	870.399209	y7	1	61.16	59.9		
Apolipoprotein C-II	APOC2	P02655	ESLSSYWESAK	ESLSSYWESAK	643.7986++	643.7986	2	22.8	620.303852	y5	1	61.16	59.9		
Apolipoprotein C-II	APOC2	P02655	ESLSSYWESAK	ESLSSYWESAK[+8.014199]	647.8057++ (heavy)	647.805699	2	22.8	965.445437	y8	1	61.16	59.9		

Apolipoprotein C-II	APOC2	P02655	ESLSSYWESAK	ESLSSYWESAK[+8.014199]	647.8057++ (heavy)	647.805699	2	22.8	878.413408	y7	1	61.16	59.9		
Apolipoprotein C-II	APOC2	P02655	ESLSSYWESAK	ESLSSYWESAK[+8.014199]	647.8057++ (heavy)	647.805699	2	22.8	628.318051	y5	1	61.16	59.9		
Apolipoprotein C-II	APOC2	P02655	TYLPAVDEK	TYLPAVDEK	518.2715++	518.271489	2	18.1	771.424696	y7	1	38.01	37.29		
Apolipoprotein C-II	APOC2	P02655	TYLPAVDEK	TYLPAVDEK	518.2715++	518.271489	2	18.1	658.340632	y6	1	38.01	37.29		
Apolipoprotein C-II	APOC2	P02655	TYLPAVDEK	TYLPAVDEK	518.2715++	518.271489	2	18.1	265.118283	b2	1	38.01	37.29		
Apolipoprotein C-II	APOC2	P02655	TYLPAVDEK	TYLPAVDEK[+8.014199]	522.2786++ (heavy)	522.278589	2	18.1	779.438895	y7	1	38.01	37.29		
Apolipoprotein C-II	APOC2	P02655	TYLPAVDEK	TYLPAVDEK[+8.014199]	522.2786++ (heavy)	522.278589	2	18.1	666.354831	y6	1	38.01	37.29		
Apolipoprotein C-II	APOC2	P02655	TYLPAVDEK	TYLPAVDEK[+8.014199]	522.2786++ (heavy)	522.278589	2	18.1	265.118283	b2	1	38.01	37.29		
Apolipoprotein C-III	APOC3	P02656	DALSSVQESQVAQQAR	DALSSVQESQVAQQAR	858.9292++	858.929196	2	30.7	1144.570525	y10	1	37.28	41.71	6.2	6.6
Apolipoprotein C-III	APOC3	P02656	DALSSVQESQVAQQAR	DALSSVQESQVAQQAR	858.9292++	858.929196	2	30.7	887.469354	y8	1	37.28	41.71		
Apolipoprotein C-III	APOC3	P02656	DALSSVQESQVAQQAR	DALSSVQESQVAQQAR	858.9292++	858.929196	2	30.7	573.310334	y5	1	37.28	41.71		
Apolipoprotein C-III	APOC3	P02656	DALSSVQESQVAQQAR	DALSSVQESQVAQQAR[+10.008269]	863.9333++ (heavy)	863.933331	2	30.7	1154.578794	y10	1	37.28	41.71		
Apolipoprotein C-III	APOC3	P02656	DALSSVQESQVAQQAR	DALSSVQESQVAQQAR[+10.008269]	863.9333++ (heavy)	863.933331	2	30.7	897.477623	y8	1	37.28	41.71		
Apolipoprotein C-III	APOC3	P02656	DALSSVQESQVAQQAR	DALSSVQESQVAQQAR[+10.008269]	863.9333++ (heavy)	863.933331	2	30.7	583.318603	y5	1	37.28	41.71		
Apolipoprotein C-III	APOC3	P02656	GWVTDGFSSLK	GWVTDGFSSLK	598.8009++	598.800945	2	21.1	854.425424	y8	1	72.93	75.89		
Apolipoprotein C-III	APOC3	P02656	GWVTDGFSSLK	GWVTDGFSSLK	598.8009++	598.800945	2	21.1	753.377745	y7	1	72.93	75.89		
Apolipoprotein C-III	APOC3	P02656	GWVTDGFSSLK	GWVTDGFSSLK	598.8009++	598.800945	2	21.1	244.108053	b2	1	72.93	75.89		
Apolipoprotein C-III	APOC3	P02656	GWVTDGFSSLK	GWVTDGFSSLK[+8.014199]	602.8080++ (heavy)	602.808045	2	21.1	862.439623	y8	1	72.93	75.89		
Apolipoprotein C-III	APOC3	P02656	GWVTDGFSSLK	GWVTDGFSSLK[+8.014199]	602.8080++ (heavy)	602.808045	2	21.1	761.391944	y7	1	72.93	75.89		
Apolipoprotein C-III	APOC3	P02656	GWVTDGFSSLK	GWVTDGFSSLK[+8.014199]	602.8080++ (heavy)	602.808045	2	21.1	244.108053	b2	1	72.93	75.89		
Apolipoprotein C-III	APOC3	P02656	DYWSTVK	DYWSTVK	449.7189++	449.718893	2	15.6	620.340238	y5	1	42.7	38.72		
Apolipoprotein C-III	APOC3	P02656	DYWSTVK	DYWSTVK	449.7189++	449.718893	2	15.6	434.260925	y4	1	42.7	38.72		
Apolipoprotein C-III	APOC3	P02656	DYWSTVK	DYWSTVK	449.7189++	449.718893	2	15.6	347.228896	y3	1	42.7	38.72		
Apolipoprotein C-III	APOC3	P02656	DYWSTVK	DYWSTVK[+8.014199]	453.7260++ (heavy)	453.725992	2	15.6	628.354437	y5	1	42.7	38.72		
Apolipoprotein C-III	APOC3	P02656	DYWSTVK	DYWSTVK[+8.014199]	453.7260++ (heavy)	453.725992	2	15.6	442.275124	y4	1	42.7	38.72		
Apolipoprotein C-III	APOC3	P02656	DYWSTVK	DYWSTVK[+8.014199]	453.7260++ (heavy)	453.725992	2	15.6	355.243095	y3	1	42.7	38.72		
Apolipoprotein C-IV	APOC4	P55056	ELLETVVNR	ELLETVVNR	536.8035++	536.803488	2	18.8	830.473043	y7	1	54.46	48.43	6.5	7.0
Apolipoprotein C-IV	APOC4	P55056	ELLETVVNR	ELLETVVNR	536.8035++	536.803488	2	18.8	717.388979	y6	1	54.46	48.43		
Apolipoprotein C-IV	APOC4	P55056	ELLETVVNR	ELLETVVNR	536.8035++	536.803488	2	18.8	588.346386	y5	1	54.46	48.43		
Apolipoprotein C-IV	APOC4	P55056	ELLETVVNR	ELLETVVNR[+10.008269]	541.8076++ (heavy)	541.807622	2	18.8	840.481312	y7	1	54.46	48.43		
Apolipoprotein C-IV	APOC4	P55056	ELLETVVNR	ELLETVVNR[+10.008269]	541.8076++ (heavy)	541.807622	2	18.8	727.397248	y6	1	54.46	48.43		
Apolipoprotein C-IV	APOC4	P55056	ELLETVVNR	ELLETVVNR[+10.008269]	541.8076++ (heavy)	541.807622	2	18.8	598.354655	y5	1	54.46	48.43		
Apolipoprotein C-IV	APOC4	P55056	AWFLESK	AWFLESK	440.7318++	440.731803	2	15.2	623.339903	y5	1	63.36	62.12		
Apolipoprotein C-IV	APOC4	P55056	AWFLESK	AWFLESK	440.7318++	440.731803	2	15.2	476.271489	y4	1	63.36	62.12		
Apolipoprotein C-IV	APOC4	P55056	AWFLESK	AWFLESK	440.7318++	440.731803	2	15.2	258.123703	b2	1	63.36	62.12		
Apolipoprotein C-IV	APOC4	P55056	AWFLESK	AWFLESK[+8.014199]	444.7389++ (heavy)	444.738903	2	15.2	631.354102	y5	1	63.36	62.12		
Apolipoprotein C-IV	APOC4	P55056	AWFLESK	AWFLESK[+8.014199]	444.7389++ (heavy)	444.738903	2	15.2	484.285688	y4	1	63.36	62.12		
Apolipoprotein C-IV	APOC4	P55056	AWFLESK	AWFLESK[+8.014199]	444.7389++ (heavy)	444.738903	2	15.2	258.123703	b2	1	63.36	62.12		
Apolipoprotein L1	APOL1	O14791	VTEPISAESGEQVER	VTEPISAESGEQVER	815.8996++	815.899573	2	29.1	1301.633185	y12	1	35.65	31.58	6.3	2.7
Apolipoprotein L1	APOL1	O14791	VTEPISAESGEQVER	VTEPISAESGEQVER	815.8996++	815.899573	2	29.1	1091.496357	y10	1	35.65	31.58		
Apolipoprotein L1	APOL1	O14791	VTEPISAESGEQVER	VTEPISAESGEQVER	815.8996++	815.899573	2	29.1	933.427215	y8	1	35.65	31.58		
Apolipoprotein L1	APOL1	O14791	VTEPISAESGEQVER	VTEPISAESGEQVER[+10.008269]	820.9037++ (heavy)	820.903708	2	29.1	1311.641454	y12	1	35.65	31.58		
Apolipoprotein L1	APOL1	O14791	VTEPISAESGEQVER	VTEPISAESGEQVER[+10.008269]	820.9037++ (heavy)	820.903708	2	29.1	1101.504626	y10	1	35.65	31.58		
Apolipoprotein L1	APOL1	O14791	VTEPISAESGEQVER	VTEPISAESGEQVER[+10.008269]	820.9037++ (heavy)	820.903708	2	29.1	943.435484	y8	1	35.65	31.58		
Apolipoprotein L1	APOL1	O14791	VNEPSILEMSR	VNEPSILEMSR	637.8241++	637.824094	2	22.5	932.486978	y8	1	56.78	60.27		
Apolipoprotein L1	APOL1	O14791	VNEPSILEMSR	VNEPSILEMSR	637.8241++	637.824094	2	22.5	635.318122	y5	1	56.78	60.27		
Apolipoprotein L1	APOL1	O14791	VNEPSILEMSR	VNEPSILEMSR	637.8241++	637.824094	2	22.5	522.234058	y4	1	56.78	60.27		
Apolipoprotein L1	APOL1	O14791	VNEPSILEMSR	VNEPSILEMSR[+10.008269]	642.8282++ (heavy)	642.828229	2	22.5	942.495247	y8	1	56.78	60.27		
Apolipoprotein L1	APOL1	O14791	VNEPSILEMSR	VNEPSILEMSR[+10.008269]	642.8282++ (heavy)	642.828229	2	22.5	645.326391	y5	1	56.78	60.27		
Apolipoprotein L1	APOL1	O14791	VNEPSILEMSR	VNEPSILEMSR[+10.008269]	642.8282++ (heavy)	642.828229	2	22.5	532.242327	y4	1	56.78	60.27		

Apolipoprotein L1	APOL1	O14791	LNILNNNYK	LNILNNNYK	553.3037++	553.303655	2	19.4	765.388979	y6	1	43.15	46.06		
Apolipoprotein L1	APOL1	O14791	LNILNNNYK	LNILNNNYK	553.3037++	553.303655	2	19.4	652.304915	y5	1	43.15	46.06		
Apolipoprotein L1	APOL1	O14791	LNILNNNYK	LNILNNNYK	553.3037++	553.303655	2	19.4	228.134267	b2	1	43.15	46.06		
Apolipoprotein L1	APOL1	O14791	LNILNNNYK	LNILNNNYK[+8.014199]	557.3108++ (heavy)	557.310755	2	19.4	773.403178	y6	1	43.15	46.06		
Apolipoprotein L1	APOL1	O14791	LNILNNNYK	LNILNNNYK[+8.014199]	557.3108++ (heavy)	557.310755	2	19.4	660.319114	y5	1	43.15	46.06		
Apolipoprotein L1	APOL1	O14791	LNILNNNYK	LNILNNNYK[+8.014199]	557.3108++ (heavy)	557.310755	2	19.4	228.134267	b2	1	43.15	46.06		
Attractin	ATRN	O75882	CTWLIEGQPNR	C[+57.021464]TWLIEGQPNR	687.3352++	687.335161	2	24.4	813.421342	y7	1	59.03	54.86	5.5	1.9
Attractin	ATRN	O75882	CTWLIEGQPNR	C[+57.021464]TWLIEGQPNR	687.3352++	687.335161	2	24.4	700.337278	y6	1	59.03	54.86		
Attractin	ATRN	O75882	CTWLIEGQPNR	C[+57.021464]TWLIEGQPNR	687.3352++	687.335161	2	24.4	571.294684	y5	1	59.03	54.86		
Attractin	ATRN	O75882	CTWLIEGQPNR	C[+57.021464]TWLIEGQPNR[+10.008269]	692.3393++ (heavy)	692.339295	2	24.4	823.429611	y7	1	59.03	54.86		
Attractin	ATRN	O75882	CTWLIEGQPNR	C[+57.021464]TWLIEGQPNR[+10.008269]	692.3393++ (heavy)	692.339295	2	24.4	710.345547	y6	1	59.03	54.86		
Attractin	ATRN	O75882	CTWLIEGQPNR	C[+57.021464]TWLIEGQPNR[+10.008269]	692.3393++ (heavy)	692.339295	2	24.4	581.302953	y5	1	59.03	54.86		
Attractin	ATRN	O75882	SEAACLAAGPGIR	SEAAC[+57.021464]LAAGPGIR	636.8219++	636.821886	2	22.5	914.487647	y9	1	46.12	37.38		
Attractin	ATRN	O75882	SEAACLAAGPGIR	SEAAC[+57.021464]LAAGPGIR	636.8219++	636.821886	2	22.5	754.456999	y8	1	46.12	37.38		
Attractin	ATRN	O75882	SEAACLAAGPGIR	SEAAC[+57.021464]LAAGPGIR	636.8219++	636.821886	2	22.5	641.372935	y7	1	46.12	37.38		
Attractin	ATRN	O75882	SEAACLAAGPGIR	SEAAC[+57.021464]LAAGPGIR	636.8219++	636.821886	2	22.5	570.335821	y6	1	46.12	37.38		
Attractin	ATRN	O75882	SEAACLAAGPGIR	SEAAC[+57.021464]LAAGPGIR	636.8219++	636.821886	2	22.5	499.298707	y5	1	46.12	37.38		
Attractin	ATRN	O75882	SEAACLAAGPGIR	SEAAC[+57.021464]LAAGPGIR[+10.008269]	641.8260++ (heavy)	641.826021	2	22.5	924.495916	y9	1	46.12	37.38		
Attractin	ATRN	O75882	SEAACLAAGPGIR	SEAAC[+57.021464]LAAGPGIR[+10.008269]	641.8260++ (heavy)	641.826021	2	22.5	764.465268	y8	1	46.12	37.38		
Attractin	ATRN	O75882	SEAACLAAGPGIR	SEAAC[+57.021464]LAAGPGIR[+10.008269]	641.8260++ (heavy)	641.826021	2	22.5	651.381204	y7	1	46.12	37.38		
Attractin	ATRN	O75882	SEAACLAAGPGIR	SEAAC[+57.021464]LAAGPGIR[+10.008269]	641.8260++ (heavy)	641.826021	2	22.5	580.34409	y6	1	46.12	37.38		
Attractin	ATRN	O75882	SEAACLAAGPGIR	SEAAC[+57.021464]LAAGPGIR[+10.008269]	641.8260++ (heavy)	641.826021	2	22.5	509.306976	y5	1	46.12	37.38		
Attractin	ATRN	O75882	LTLTPWVGLR	LTLTPWVGLR	578.3479++	578.347866	2	20.3	941.556713	y8	1	94.12	95.35		
Attractin	ATRN	O75882	LTLTPWVGLR	LTLTPWVGLR	578.3479++	578.347866	2	20.3	828.472649	y7	1	94.12	95.35		
Attractin	ATRN	O75882	LTLTPWVGLR	LTLTPWVGLR	578.3479++	578.347866	2	20.3	727.42497	y6	1	94.12	95.35		
Attractin	ATRN	O75882	LTLTPWVGLR	LTLTPWVGLR[+10.008269]	583.3520++ (heavy)	583.352	2	20.3	951.564982	y8	1	94.12	95.35		
Attractin	ATRN	O75882	LTLTPWVGLR	LTLTPWVGLR[+10.008269]	583.3520++ (heavy)	583.352	2	20.3	838.480918	y7	1	94.12	95.35		
Attractin	ATRN	O75882	LTLTPWVGLR	LTLTPWVGLR[+10.008269]	583.3520++ (heavy)	583.352	2	20.3	737.433239	y6	1	94.12	95.35		
Beta-2-glycoprotein 1	APOH	P02749	ATFGCHDGYSLDGPEEIECTK	ATFGC[+57.021464]HDGYSLDGPEEIEC[+57	796.0036+++	796.003585	3	27.3	1005.455738	y8	1	64.84	58.77	5.5	3.6
Beta-2-glycoprotein 1	APOH	P02749	ATFGCHDGYSLDGPEEIECTK	ATFGC[+57.021464]HDGYSLDGPEEIEC[+57	796.0036+++	796.003585	3	27.3	650.317788	y5	1	64.84	58.77		
Beta-2-glycoprotein 1	APOH	P02749	ATFGCHDGYSLDGPEEIECTK	ATFGC[+57.021464]HDGYSLDGPEEIEC[+57	796.0036+++	796.003585	3	27.3	537.233724	y4	1	64.84	58.77		
Beta-2-glycoprotein 1	APOH	P02749	ATFGCHDGYSLDGPEEIECTK	ATFGC[+57.021464]HDGYSLDGPEEIEC[+57	798.6750+++ (heavy)	798.674985	3	27.3	1013.469937	y8	1	64.84	58.77		
Beta-2-glycoprotein 1	APOH	P02749	ATFGCHDGYSLDGPEEIECTK	ATFGC[+57.021464]HDGYSLDGPEEIEC[+57	798.6750+++ (heavy)	798.674985	3	27.3	658.331987	y5	1	64.84	58.77		
Beta-2-glycoprotein 1	APOH	P02749	ATFGCHDGYSLDGPEEIECTK	ATFGC[+57.021464]HDGYSLDGPEEIEC[+57	798.6750+++ (heavy)	798.674985	3	27.3	545.247923	y4	1	64.84	58.77		
Beta-2-glycoprotein 1	APOH	P02749	CSYTEDAQCIDGTIEVPK	C[+57.021464]SYTEDAQC[+57.021464]IDGT	1043.4588++	1043.458812	2	37.5	743.429781	y7	1	59.45	65.49		
Beta-2-glycoprotein 1	APOH	P02749	CSYTEDAQCIDGTIEVPK	C[+57.021464]SYTEDAQC[+57.021464]IDGT	1043.4588++	1043.458812	2	37.5	248.069953	b2	1	59.45	65.49		
Beta-2-glycoprotein 1	APOH	P02749	CSYTEDAQCIDGTIEVPK	C[+57.021464]SYTEDAQC[+57.021464]IDGT	1043.4588++	1043.458812	2	37.5	411.133282	b3	1	59.45	65.49		
Beta-2-glycoprotein 1	APOH	P02749	CSYTEDAQCIDGTIEVPK	C[+57.021464]SYTEDAQC[+57.021464]IDGT	1047.4659++ (heavy)	1047.465912	2	37.5	751.44398	y7	1	59.45	65.49		
Beta-2-glycoprotein 1	APOH	P02749	CSYTEDAQCIDGTIEVPK	C[+57.021464]SYTEDAQC[+57.021464]IDGT	1047.4659++ (heavy)	1047.465912	2	37.5	248.069953	b2	1	59.45	65.49		
Beta-2-glycoprotein 1	APOH	P02749	CSYTEDAQCIDGTIEVPK	C[+57.021464]SYTEDAQC[+57.021464]IDGT	1047.4659++ (heavy)	1047.465912	2	37.5	411.133282	b3	1	59.45	65.49		
Beta-2-glycoprotein 1	APOH	P02749	EHSSLAFWK	EHSSLAFWK	552.7773++	552.777273	2	19.4	838.445765	y7	1	60.18	50.46		
Beta-2-glycoprotein 1	APOH	P02749	EHSSLAFWK	EHSSLAFWK	552.7773++	552.777273	2	19.4	480.260531	y3	1	60.18	50.46		
Beta-2-glycoprotein 1	APOH	P02749	EHSSLAFWK	EHSSLAFWK	552.7773++	552.777273	2	19.4	267.108781	b2	1	60.18	50.46		
Beta-2-glycoprotein 1	APOH	P02749	EHSSLAFWK	EHSSLAFWK[+8.014199]	556.7844++ (heavy)	556.784373	2	19.4	846.459964	y7	1	60.18	50.46		
Beta-2-glycoprotein 1	APOH	P02749	EHSSLAFWK	EHSSLAFWK[+8.014199]	556.7844++ (heavy)	556.784373	2	19.4	488.27473	y3	1	60.18	50.46		
Beta-2-glycoprotein 1	APOH	P02749	EHSSLAFWK	EHSSLAFWK[+8.014199]	556.7844++ (heavy)	556.784373	2	19.4	267.108781	b2	1	60.18	50.46		
C4b-binding protein beta chain	C4BPB	P20851	ALLAFQESK	ALLAFQESK	503.7820++	503.782024	2	17.6	822.435595	y7	1	48.58	48.75	5.5	3.6
C4b-binding protein beta chain	C4BPB	P20851	ALLAFQESK	ALLAFQESK	503.7820++	503.782024	2	17.6	709.351531	y6	1	48.58	48.75		
C4b-binding protein beta chain	C4BPB	P20851	ALLAFQESK	ALLAFQESK	503.7820++	503.782024	2	17.6	638.314417	y5	1	48.58	48.75		
C4b-binding protein beta chain	C4BPB	P20851	ALLAFQESK	ALLAFQESK[+8.014199]	507.7891++ (heavy)	507.789124	2	17.6	830.449794	y7	1	48.58	48.75		

C4b-binding protein beta chain	C4BPB	P20851	ALLAFQESK	ALLAFQESK[+8.014199]	507.7891++ (heavy)	507.789124	2	17.6	717.36573	y6	1	48.58	48.75		
C4b-binding protein beta chain	C4BPB	P20851	ALLAFQESK	ALLAFQESK[+8.014199]	507.7891++ (heavy)	507.789124	2	17.6	646.328616	y5	1	48.58	48.75		
C4b-binding protein beta chain	C4BPB	P20851	ESGMTMEELK	ESGMTMEELK	577.7570++	577.757032	2	20.3	750.370217	y6	1	46.12	36.3		
C4b-binding protein beta chain	C4BPB	P20851	ESGMTMEELK	ESGMTMEELK	577.7570++	577.757032	2	20.3	649.322539	y5	1	46.12	36.3		
C4b-binding protein beta chain	C4BPB	P20851	ESGMTMEELK	ESGMTMEELK	577.7570++	577.757032	2	20.3	518.282054	y4	1	46.12	36.3		
C4b-binding protein beta chain	C4BPB	P20851	ESGMTMEELK	ESGMTMEELK[+8.014199]	581.7641++ (heavy)	581.764131	2	20.3	758.384416	y6	1	46.12	36.3		
C4b-binding protein beta chain	C4BPB	P20851	ESGMTMEELK	ESGMTMEELK[+8.014199]	581.7641++ (heavy)	581.764131	2	20.3	657.336738	y5	1	46.12	36.3		
C4b-binding protein beta chain	C4BPB	P20851	ESGMTMEELK	ESGMTMEELK[+8.014199]	581.7641++ (heavy)	581.764131	2	20.3	526.296253	y4	1	46.12	36.3		
Carboxypeptidase N subunit 2	CPN2	P22792	LSNNALSGLPQGVFGK	LSNNALSGLPQGVFGK	801.4359++	801.435929	2	28.6	989.541457	y10	1	77.28	82.37	4.9	3.2
Carboxypeptidase N subunit 2	CPN2	P22792	LSNNALSGLPQGVFGK	LSNNALSGLPQGVFGK	801.4359++	801.435929	2	28.6	732.403901	y7	1	77.28	82.37		
Carboxypeptidase N subunit 2	CPN2	P22792	LSNNALSGLPQGVFGK	LSNNALSGLPQGVFGK	801.4359++	801.435929	2	28.6	351.202681	y3	1	77.28	82.37		
Carboxypeptidase N subunit 2	CPN2	P22792	LSNNALSGLPQGVFGK	LSNNALSGLPQGVFGK[+8.014199]	805.4430++ (heavy)	805.443028	2	28.6	997.555656	y10	1	77.28	82.37		
Carboxypeptidase N subunit 2	CPN2	P22792	LSNNALSGLPQGVFGK	LSNNALSGLPQGVFGK[+8.014199]	805.4430++ (heavy)	805.443028	2	28.6	740.4181	y7	1	77.28	82.37		
Carboxypeptidase N subunit 2	CPN2	P22792	LSNNALSGLPQGVFGK	LSNNALSGLPQGVFGK[+8.014199]	805.4430++ (heavy)	805.443028	2	28.6	359.21688	y3	1	77.28	82.37		
Carboxypeptidase N subunit 2	CPN2	P22792	LELLSLSK	LELLSLSK	451.7815++	451.781493	2	15.6	789.471646	y7	1	63.55	67.4		
Carboxypeptidase N subunit 2	CPN2	P22792	LELLSLSK	LELLSLSK	451.7815++	451.781493	2	15.6	660.429053	y6	1	63.55	67.4		
Carboxypeptidase N subunit 2	CPN2	P22792	LELLSLSK	LELLSLSK	451.7815++	451.781493	2	15.6	547.344989	y5	1	63.55	67.4		
Carboxypeptidase N subunit 2	CPN2	P22792	LELLSLSK	LELLSLSK	451.7815++	451.781493	2	15.6	243.133933	b2	1	63.55	67.4		
Carboxypeptidase N subunit 2	CPN2	P22792	LELLSLSK	LELLSLSK[+8.014199]	455.7886++ (heavy)	455.788592	2	15.6	797.485845	y7	1	63.55	67.4		
Carboxypeptidase N subunit 2	CPN2	P22792	LELLSLSK	LELLSLSK[+8.014199]	455.7886++ (heavy)	455.788592	2	15.6	668.443252	y6	1	63.55	67.4		
Carboxypeptidase N subunit 2	CPN2	P22792	LELLSLSK	LELLSLSK[+8.014199]	455.7886++ (heavy)	455.788592	2	15.6	555.359188	y5	1	63.55	67.4		
Carboxypeptidase N subunit 2	CPN2	P22792	LELLSLSK	LELLSLSK[+8.014199]	455.7886++ (heavy)	455.788592	2	15.6	243.133933	b2	1	63.55	67.4		
Carboxypeptidase N subunit 2	CPN2	P22792	AGGSWDLAVQER	AGGSWDLAVQER	644.8177++	644.817658	2	22.8	830.436657	y7	1	52.79	50.92		
Carboxypeptidase N subunit 2	CPN2	P22792	AGGSWDLAVQER	AGGSWDLAVQER	644.8177++	644.817658	2	22.8	715.409714	y6	1	52.79	50.92		
Carboxypeptidase N subunit 2	CPN2	P22792	AGGSWDLAVQER	AGGSWDLAVQER	644.8177++	644.817658	2	22.8	602.32565	y5	1	52.79	50.92		
Carboxypeptidase N subunit 2	CPN2	P22792	AGGSWDLAVQER	AGGSWDLAVQER[+10.008269]	649.8218++ (heavy)	649.821792	2	22.8	840.444926	y7	1	52.79	50.92		
Carboxypeptidase N subunit 2	CPN2	P22792	AGGSWDLAVQER	AGGSWDLAVQER[+10.008269]	649.8218++ (heavy)	649.821792	2	22.8	725.417983	y6	1	52.79	50.92		
Carboxypeptidase N subunit 2	CPN2	P22792	AGGSWDLAVQER	AGGSWDLAVQER[+10.008269]	649.8218++ (heavy)	649.821792	2	22.8	612.333919	y5	1	52.79	50.92		
Ceruloplasmin	CP	P00450	ALYLQYTDETFR	ALYLQYTDETFR	760.3750++	760.375006	2	27.1	1059.474165	y8	1	82.13	75.32	5.2	3.4
Ceruloplasmin	CP	P00450	ALYLQYTDETFR	ALYLQYTDETFR	760.3750++	760.375006	2	27.1	931.415587	y7	1	82.13	75.32		
Ceruloplasmin	CP	P00450	ALYLQYTDETFR	ALYLQYTDETFR	760.3750++	760.375006	2	27.1	348.191782	b3	1	82.13	75.32		
Ceruloplasmin	CP	P00450	ALYLQYTDETFR	ALYLQYTDETFR[+10.008269]	765.3791++ (heavy)	765.37914	2	27.1	1069.482434	y8	1	82.13	75.32		
Ceruloplasmin	CP	P00450	ALYLQYTDETFR	ALYLQYTDETFR[+10.008269]	765.3791++ (heavy)	765.37914	2	27.1	941.423856	y7	1	82.13	75.32		
Ceruloplasmin	CP	P00450	ALYLQYTDETFR	ALYLQYTDETFR[+10.008269]	765.3791++ (heavy)	765.37914	2	27.1	348.191782	b3	1	82.13	75.32		
Ceruloplasmin	CP	P00450	GAYPLSIEPIGVR	GAYPLSIEPIGVR	686.3852++	686.385176	2	24.3	1080.641171	y10	1	76.32	80.41		
Ceruloplasmin	CP	P00450	GAYPLSIEPIGVR	GAYPLSIEPIGVR	686.3852++	686.385176	2	24.3	870.504343	y8	1	76.32	80.41		
Ceruloplasmin	CP	P00450	GAYPLSIEPIGVR	GAYPLSIEPIGVR	686.3852++	686.385176	2	24.3	541.345657	y5	1	76.32	80.41		
Ceruloplasmin	CP	P00450	GAYPLSIEPIGVR	GAYPLSIEPIGVR[+10.008269]	691.3893++ (heavy)	691.389311	2	24.3	1090.64944	y10	1	76.32	80.41		
Ceruloplasmin	CP	P00450	GAYPLSIEPIGVR	GAYPLSIEPIGVR[+10.008269]	691.3893++ (heavy)	691.389311	2	24.3	880.512612	y8	1	76.32	80.41		
Ceruloplasmin	CP	P00450	GAYPLSIEPIGVR	GAYPLSIEPIGVR[+10.008269]	691.3893++ (heavy)	691.389311	2	24.3	551.353926	y5	1	76.32	80.41		
Ceruloplasmin	CP	P00450	EVGPTNADPVCLAK	EVGPTNADPVC[+57.021464]LAK	735.8665++	735.866491	2	26.2	802.412751	y7	1	39.31	45.34		
Ceruloplasmin	CP	P00450	EVGPTNADPVCLAK	EVGPTNADPVC[+57.021464]LAK	735.8665++	735.866491	2	26.2	687.385808	y6	1	39.31	45.34		
Ceruloplasmin	CP	P00450	EVGPTNADPVCLAK	EVGPTNADPVC[+57.021464]LAK	735.8665++	735.866491	2	26.2	491.26463	y4	1	39.31	45.34		
Ceruloplasmin	CP	P00450	EVGPTNADPVCLAK	EVGPTNADPVC[+57.021464]LAK[+8.014199	739.8736++ (heavy)	739.87359	2	26.2	810.42695	y7	1	39.31	45.34		
Ceruloplasmin	CP	P00450	EVGPTNADPVCLAK	EVGPTNADPVC[+57.021464]LAK[+8.014199	739.8736++ (heavy)	739.87359	2	26.2	695.400007	y6	1	39.31	45.34		
Ceruloplasmin	CP	P00450	EVGPTNADPVCLAK	EVGPTNADPVC[+57.021464]LAK[+8.014199	739.8736++ (heavy)	739.87359	2	26.2	499.278829	y4	1	39.31	45.34		
Clusterin	CLU	P10909	ASSIIDELFQDR	ASSIIDELFQDR	697.3515++	697.351531	2	24.7	1035.510551	y8	1	87.02	104.76	0.9	5.2
Clusterin	CLU	P10909	ASSIIDELFQDR	ASSIIDELFQDR	697.3515++	697.351531	2	24.7	922.426487	y7	1	87.02	104.76		
Clusterin	CLU	P10909	ASSIIDELFQDR	ASSIIDELFQDR	697.3515++	697.351531	2	24.7	678.35695	y5	1	87.02	104.76		
Clusterin	CLU	P10909	ASSIIDELFQDR	ASSIIDELFQDR[+10.008269]	702.3557++ (heavy)	702.355665	2	24.7	1045.51882	y8	1	87.02	104.76		

Clusterin	CLU	P10909	ASSIIDELFQDR	ASSIIDELFQDR[+10.008269]	702.3557++ (heavy)	702.355665	2	24.7	932.434756	y7	1	87.02	104.76		
Clusterin	CLU	P10909	ASSIIDELFQDR	ASSIIDELFQDR[+10.008269]	702.3557++ (heavy)	702.355665	2	24.7	688.365219	y5	1	87.02	104.76		
Clusterin	CLU	P10909	EPQDTYHYLPFSLPHR	EPQDTYHYLPFSLPHR	667.3269+++	667.32688	3	22.7	853.467898	y7	1	79.81	76.03		
Clusterin	CLU	P10909	EPQDTYHYLPFSLPHR	EPQDTYHYLPFSLPHR	667.3269+++	667.32688	3	22.7	756.415134	y6	1	79.81	76.03		
Clusterin	CLU	P10909	EPQDTYHYLPFSLPHR	EPQDTYHYLPFSLPHR	667.3269+++	667.32688	3	22.7	609.34672	y5	1	79.81	76.03		
Clusterin	CLU	P10909	EPQDTYHYLPFSLPHR	EPQDTYHYLPFSLPHR	667.3269+++	667.32688	3	22.7	409.230627	y3	1	79.81	76.03		
Clusterin	CLU	P10909	EPQDTYHYLPFSLPHR	EPQDTYHYLPFSLPHR[+10.008269]	670.6630+++ (heavy)	670.662969	3	22.7	863.476167	y7	1	79.81	76.03		
Clusterin	CLU	P10909	EPQDTYHYLPFSLPHR	EPQDTYHYLPFSLPHR[+10.008269]	670.6630+++ (heavy)	670.662969	3	22.7	766.423403	y6	1	79.81	76.03		
Clusterin	CLU	P10909	EPQDTYHYLPFSLPHR	EPQDTYHYLPFSLPHR[+10.008269]	670.6630+++ (heavy)	670.662969	3	22.7	619.354989	y5	1	79.81	76.03		
Clusterin	CLU	P10909	EPQDTYHYLPFSLPHR	EPQDTYHYLPFSLPHR[+10.008269]	670.6630+++ (heavy)	670.662969	3	22.7	419.238896	y3	1	79.81	76.03		
Clusterin	CLU	P10909	ELDESLQVAER	ELDESLQVAER	644.8226++	644.822606	2	22.8	715.409714	y6	1	45.06	40.26		
Clusterin	CLU	P10909	ELDESLQVAER	ELDESLQVAER	644.8226++	644.822606	2	22.8	602.32565	y5	1	45.06	40.26		
Clusterin	CLU	P10909	ELDESLQVAER	ELDESLQVAER	644.8226++	644.822606	2	22.8	474.267073	y4	1	45.06	40.26		
Clusterin	CLU	P10909	ELDESLQVAER	ELDESLQVAER[+10.008269]	649.8267++ (heavy)	649.82674	2	22.8	725.417983	y6	1	45.06	40.26		
Clusterin	CLU	P10909	ELDESLQVAER	ELDESLQVAER[+10.008269]	649.8267++ (heavy)	649.82674	2	22.8	612.333919	y5	1	45.06	40.26		
Clusterin	CLU	P10909	ELDESLQVAER	ELDESLQVAER[+10.008269]	649.8267++ (heavy)	649.82674	2	22.8	484.275342	y4	1	45.06	40.26		
Clusterin	CLU	P10909	LFDSDPITVTVPVEVSR	LFDSDPITVTVPVEVSR	937.4989++	937.498923	2	33.6	1296.752178	y12	1	89.49	95.26		
Clusterin	CLU	P10909	LFDSDPITVTVPVEVSR	LFDSDPITVTVPVEVSR	937.4989++	937.498923	2	33.6	886.499258	y8	1	89.49	95.26		
Clusterin	CLU	P10909	LFDSDPITVTVPVEVSR	LFDSDPITVTVPVEVSR	937.4989++	937.498923	2	33.6	686.383165	y6	1	89.49	95.26		
Clusterin	CLU	P10909	LFDSDPITVTVPVEVSR	LFDSDPITVTVPVEVSR[+10.008269]	942.5031++ (heavy)	942.503058	2	33.6	1306.760447	y12	1	89.49	95.26		
Clusterin	CLU	P10909	LFDSDPITVTVPVEVSR	LFDSDPITVTVPVEVSR[+10.008269]	942.5031++ (heavy)	942.503058	2	33.6	896.507527	y8	1	89.49	95.26		
Clusterin	CLU	P10909	LFDSDPITVTVPVEVSR	LFDSDPITVTVPVEVSR[+10.008269]	942.5031++ (heavy)	942.503058	2	33.6	696.391434	y6	1	89.49	95.26		
Coagulation factor IX	F9	P00740	NCELDVTCNIK	NC[+57.021464]ELDVTC[+57.021464]NIK	683.3105++	683.310494	2	24.2	849.413479	y7	1	40.06	39.94	4.0	4.8
Coagulation factor IX	F9	P00740	NCELDVTCNIK	NC[+57.021464]ELDVTC[+57.021464]NIK	683.3105++	683.310494	2	24.2	275.080852	b2	1	40.06	39.94		
Coagulation factor IX	F9	P00740	NCELDVTCNIK	NC[+57.021464]ELDVTC[+57.021464]NIK	683.3105++	683.310494	2	24.2	404.123445	b3	1	40.06	39.94		
Coagulation factor IX	F9	P00740	NCELDVTCNIK	NC[+57.021464]ELDVTC[+57.021464]NIK[+8.	687.3176++ (heavy)	687.317594	2	24.2	857.427678	y7	1	40.06	39.94		
Coagulation factor IX	F9	P00740	NCELDVTCNIK	NC[+57.021464]ELDVTC[+57.021464]NIK[+8.	687.3176++ (heavy)	687.317594	2	24.2	275.080852	b2	1	40.06	39.94		
Coagulation factor IX	F9	P00740	NCELDVTCNIK	NC[+57.021464]ELDVTC[+57.021464]NIK[+8.	687.3176++ (heavy)	687.317594	2	24.2	404.123445	b3	1	40.06	39.94		
Coagulation factor IX	F9	P00740	VDAFCGGSIVNEK	VDAFC[+57.021464]GGSIVNEK	698.3323++	698.332284	2	24.8	963.456407	y9	1	48.06	45.81		
Coagulation factor IX	F9	P00740	VDAFCGGSIVNEK	VDAFC[+57.021464]GGSIVNEK	698.3323++	698.332284	2	24.8	390.198324	y3	1	48.06	45.81		
Coagulation factor IX	F9	P00740	VDAFCGGSIVNEK	VDAFC[+57.021464]GGSIVNEK	698.3323++	698.332284	2	24.8	286.139747	b3	1	48.06	45.81		
Coagulation factor IX	F9	P00740	VDAFCGGSIVNEK	VDAFC[+57.021464]GGSIVNEK[+8.014199]	702.3394++ (heavy)	702.339383	2	24.8	971.470606	y9	1	48.06	45.81		
Coagulation factor IX	F9	P00740	VDAFCGGSIVNEK	VDAFC[+57.021464]GGSIVNEK[+8.014199]	702.3394++ (heavy)	702.339383	2	24.8	398.212523	y3	1	48.06	45.81		
Coagulation factor IX	F9	P00740	VDAFCGGSIVNEK	VDAFC[+57.021464]GGSIVNEK[+8.014199]	702.3394++ (heavy)	702.339383	2	24.8	286.139747	b3	1	48.06	45.81		
Coagulation factor IX	F9	P00740	SALVLQYLR	SALVLQYLR	531.8189++	531.818941	2	18.6	791.4774	y6	1	75.85	77.96		
Coagulation factor IX	F9	P00740	SALVLQYLR	SALVLQYLR	531.8189++	531.818941	2	18.6	692.408986	y5	1	75.85	77.96		
Coagulation factor IX	F9	P00740	SALVLQYLR	SALVLQYLR	531.8189++	531.818941	2	18.6	579.324922	y4	1	75.85	77.96		
Coagulation factor IX	F9	P00740	SALVLQYLR	SALVLQYLR	531.8189++	531.818941	2	18.6	272.160482	b3	1	75.85	77.96		
Coagulation factor IX	F9	P00740	SALVLQYLR	SALVLQYLR[+10.008269]	536.8231++ (heavy)	536.823076	2	18.6	801.485669	y6	1	75.85	77.96		
Coagulation factor IX	F9	P00740	SALVLQYLR	SALVLQYLR[+10.008269]	536.8231++ (heavy)	536.823076	2	18.6	702.417255	y5	1	75.85	77.96		
Coagulation factor IX	F9	P00740	SALVLQYLR	SALVLQYLR[+10.008269]	536.8231++ (heavy)	536.823076	2	18.6	589.333191	y4	1	75.85	77.96		
Coagulation factor IX	F9	P00740	SALVLQYLR	SALVLQYLR[+10.008269]	536.8231++ (heavy)	536.823076	2	18.6	272.160482	b3	1	75.85	77.96		
Coagulation factor X	F10	P00742	ACIPTGPYPCGK	AC[+57.021464]IPTGPYPC[+57.021464]GK	660.8074++	660.80739	2	23.4	976.455678	y9	1	28.97	38.31	3.7	4.4
Coagulation factor X	F10	P00742	ACIPTGPYPCGK	AC[+57.021464]IPTGPYPC[+57.021464]GK	660.8074++	660.80739	2	23.4	778.355236	y7	1	28.97	38.31		
Coagulation factor X	F10	P00742	ACIPTGPYPCGK	AC[+57.021464]IPTGPYPC[+57.021464]GK	660.8074++	660.80739	2	23.4	461.21768	y4	1	28.97	38.31		
Coagulation factor X	F10	P00742	ACIPTGPYPCGK	AC[+57.021464]IPTGPYPC[+57.021464]GK	660.8074++	660.80739	2	23.4	232.075038	b2	1	28.97	38.31		
Coagulation factor X	F10	P00742	ACIPTGPYPCGK	AC[+57.021464]IPTGPYPC[+57.021464]GK[+	664.8145++ (heavy)	664.81449	2	23.4	984.469877	y9	1	28.97	38.31		
Coagulation factor X	F10	P00742	ACIPTGPYPCGK	AC[+57.021464]IPTGPYPC[+57.021464]GK[+	664.8145++ (heavy)	664.81449	2	23.4	786.369435	y7	1	28.97	38.31		
Coagulation factor X	F10	P00742	ACIPTGPYPCGK	AC[+57.021464]IPTGPYPC[+57.021464]GK[+	664.8145++ (heavy)	664.81449	2	23.4	469.231879	y4	1	28.97	38.31		
Coagulation factor X	F10	P00742	ACIPTGPYPCGK	AC[+57.021464]IPTGPYPC[+57.021464]GK[+	664.8145++ (heavy)	664.81449	2	23.4	232.075038	b2	1	28.97	38.31		

Coagulation factor X	F10	P00742	ETYDFDIAVLR	ETYDFDIAVLR	671.3379++	671.337892	2	23.8	833.487965	y7	1	88	90.27		
Coagulation factor X	F10	P00742	ETYDFDIAVLR	ETYDFDIAVLR	671.3379++	671.337892	2	23.8	686.419551	y6	1	88	90.27		
Coagulation factor X	F10	P00742	ETYDFDIAVLR	ETYDFDIAVLR	671.3379++	671.337892	2	23.8	571.392608	y5	1	88	90.27		
Coagulation factor X	F10	P00742	ETYDFDIAVLR	ETYDFDIAVLR	671.3379++	671.337892	2	23.8	458.308544	y4	1	88	90.27		
Coagulation factor X	F10	P00742	ETYDFDIAVLR	ETYDFDIAVLR[+10.008269]	676.3420++ (heavy)	676.342026	2	23.8	843.496234	y7	1	88	90.27		
Coagulation factor X	F10	P00742	ETYDFDIAVLR	ETYDFDIAVLR[+10.008269]	676.3420++ (heavy)	676.342026	2	23.8	696.42782	y6	1	88	90.27		
Coagulation factor X	F10	P00742	ETYDFDIAVLR	ETYDFDIAVLR[+10.008269]	676.3420++ (heavy)	676.342026	2	23.8	581.400877	y5	1	88	90.27		
Coagulation factor X	F10	P00742	ETYDFDIAVLR	ETYDFDIAVLR[+10.008269]	676.3420++ (heavy)	676.342026	2	23.8	468.316813	y4	1	88	90.27		
Coagulation factor X	F10	P00742	MLEVPYVDR	MLEVPYVDR	561.2866++	561.286616	2	19.7	748.398815	y6	1	58.6	64.61		
Coagulation factor X	F10	P00742	MLEVPYVDR	MLEVPYVDR	561.2866++	561.286616	2	19.7	649.330401	y5	1	58.6	64.61		
Coagulation factor X	F10	P00742	MLEVPYVDR	MLEVPYVDR	561.2866++	561.286616	2	19.7	374.174418	b3	1	58.6	64.61		
Coagulation factor X	F10	P00742	MLEVPYVDR	MLEVPYVDR[+10.008269]	566.2908++ (heavy)	566.290751	2	19.7	758.407084	y6	1	58.6	64.61		
Coagulation factor X	F10	P00742	MLEVPYVDR	MLEVPYVDR[+10.008269]	566.2908++ (heavy)	566.290751	2	19.7	659.33867	y5	1	58.6	64.61		
Coagulation factor X	F10	P00742	MLEVPYVDR	MLEVPYVDR[+10.008269]	566.2908++ (heavy)	566.290751	2	19.7	374.174418	b3	1	58.6	64.61		
Complement C2	C2	P06681	CSSNLVLTGSSER	C[+57.021464]SSNLVLTGSSER	705.3381++	705.338097	2	25	848.447222	y8	1	39.44	29.7	5.4	2.8
Complement C2	C2	P06681	CSSNLVLTGSSER	C[+57.021464]SSNLVLTGSSER	705.3381++	705.338097	2	25	749.378808	y7	1	39.44	29.7		
Complement C2	C2	P06681	CSSNLVLTGSSER	C[+57.021464]SSNLVLTGSSER	705.3381++	705.338097	2	25	636.294744	y6	1	39.44	29.7		
Complement C2	C2	P06681	CSSNLVLTGSSER	C[+57.021464]SSNLVLTGSSER[+10.008269]	710.3422++ (heavy)	710.342232	2	25	858.455491	y8	1	39.44	29.7		
Complement C2	C2	P06681	CSSNLVLTGSSER	C[+57.021464]SSNLVLTGSSER[+10.008269]	710.3422++ (heavy)	710.342232	2	25	759.387077	y7	1	39.44	29.7		
Complement C2	C2	P06681	CSSNLVLTGSSER	C[+57.021464]SSNLVLTGSSER[+10.008269]	710.3422++ (heavy)	710.342232	2	25	646.303013	y6	1	39.44	29.7		
Complement C2	C2	P06681	AVISPGFDVFAK	AVISPGFDVFAK	625.8426++	625.842613	2	22.1	967.488358	y9	1	80.28	85.98		
Complement C2	C2	P06681	AVISPGFDVFAK	AVISPGFDVFAK	625.8426++	625.842613	2	22.1	880.45633	y8	1	80.28	85.98		
Complement C2	C2	P06681	AVISPGFDVFAK	AVISPGFDVFAK	625.8426++	625.842613	2	22.1	783.403566	y7	1	80.28	85.98		
Complement C2	C2	P06681	AVISPGFDVFAK	AVISPGFDVFAK[+8.014199]	629.8497++ (heavy)	629.849713	2	22.1	975.502558	y9	1	80.28	85.98		
Complement C2	C2	P06681	AVISPGFDVFAK	AVISPGFDVFAK[+8.014199]	629.8497++ (heavy)	629.849713	2	22.1	888.470529	y8	1	80.28	85.98		
Complement C2	C2	P06681	AVISPGFDVFAK	AVISPGFDVFAK[+8.014199]	629.8497++ (heavy)	629.849713	2	22.1	791.417765	y7	1	80.28	85.98		
Complement C2	C2	P06681	GESGGAVFLER	GESGGAVFLER	561.2829++	561.28292	2	19.7	935.494506	y9	1	48.77	40.64		
Complement C2	C2	P06681	GESGGAVFLER	GESGGAVFLER	561.2829++	561.28292	2	19.7	663.382437	y5	1	48.77	40.64		
Complement C2	C2	P06681	GESGGAVFLER	GESGGAVFLER	561.2829++	561.28292	2	19.7	564.314023	y4	1	48.77	40.64		
Complement C2	C2	P06681	GESGGAVFLER	GESGGAVFLER[+10.008269]	566.2871++ (heavy)	566.287054	2	19.7	945.502776	y9	1	48.77	40.64		
Complement C2	C2	P06681	GESGGAVFLER	GESGGAVFLER[+10.008269]	566.2871++ (heavy)	566.287054	2	19.7	673.390706	y5	1	48.77	40.64		
Complement C2	C2	P06681	GESGGAVFLER	GESGGAVFLER[+10.008269]	566.2871++ (heavy)	566.287054	2	19.7	574.322292	y4	1	48.77	40.64		
Complement C2	C2	P06681	QHLGDVLNFLPL	QHLGDVLNFLPL	683.3799++	683.379894	2	24.2	877.452642	b8	1	125.95	126.83		
Complement C2	C2	P06681	QHLGDVLNFLPL	QHLGDVLNFLPL	683.3799++	683.379894	2	24.2	1024.521056	b9	1	125.95	126.83		
Complement C2	C2	P06681	QHLGDVLNFLPL	QHLGDVLNFLPL	683.3799++	683.379894	2	24.2	1137.60512	b10	1	125.95	126.83		
Complement C2	C2	P06681	QHLGDVLNFLPL	QHL[+7.017164]GDVLNFLPL	686.8885++ (heavy)	686.888476	2	24.2	884.469806	b8	1	125.95	126.83		
Complement C2	C2	P06681	QHLGDVLNFLPL	QHL[+7.017164]GDVLNFLPL	686.8885++ (heavy)	686.888476	2	24.2	1031.53822	b9	1	125.95	126.83		
Complement C2	C2	P06681	QHLGDVLNFLPL	QHL[+7.017164]GDVLNFLPL	686.8885++ (heavy)	686.888476	2	24.2	1144.622284	b10	1	125.95	126.83		
Complement C4-B	C4B	P0C0L5	YVLPNFEVK	YVLPNFEVK	554.8055++	554.805499	2	19.5	846.47198	y7	1	68.39	74.31	3.6	3.2
Complement C4-B	C4B	P0C0L5	YVLPNFEVK	YVLPNFEVK	554.8055++	554.805499	2	19.5	733.387916	y6	1	68.39	74.31		
Complement C4-B	C4B	P0C0L5	YVLPNFEVK	YVLPNFEVK	554.8055++	554.805499	2	19.5	263.139019	b2	1	68.39	74.31		
Complement C4-B	C4B	P0C0L5	YVLPNFEVK	YVLPNFEVK[+8.014199]	558.8126++ (heavy)	558.812599	2	19.5	854.486179	y7	1	68.39	74.31		
Complement C4-B	C4B	P0C0L5	YVLPNFEVK	YVLPNFEVK[+8.014199]	558.8126++ (heavy)	558.812599	2	19.5	741.402115	y6	1	68.39	74.31		
Complement C4-B	C4B	P0C0L5	YVLPNFEVK	YVLPNFEVK[+8.014199]	558.8126++ (heavy)	558.812599	2	19.5	263.139019	b2	1	68.39	74.31		
Complement C4-B	C4B	P0C0L5	AEFQDALEK	AEFQDALEK	525.7587++	525.758746	2	18.4	850.430509	y7	1	39.87	34.71		
Complement C4-B	C4B	P0C0L5	AEFQDALEK	AEFQDALEK	525.7587++	525.758746	2	18.4	703.362095	y6	1	39.87	34.71		
Complement C4-B	C4B	P0C0L5	AEFQDALEK	AEFQDALEK	525.7587++	525.758746	2	18.4	575.303518	y5	1	39.87	34.71		
Complement C4-B	C4B	P0C0L5	AEFQDALEK	AEFQDALEK[+8.014199]	529.7658++ (heavy)	529.765846	2	18.4	858.444708	y7	1	39.87	34.71		
Complement C4-B	C4B	P0C0L5	AEFQDALEK	AEFQDALEK[+8.014199]	529.7658++ (heavy)	529.765846	2	18.4	711.376294	y6	1	39.87	34.71		
Complement C4-B	C4B	P0C0L5	AEFQDALEK	AEFQDALEK[+8.014199]	529.7658++ (heavy)	529.765846	2	18.4	583.317717	y5	1	39.87	34.71		

Complement C4-B	C4B	P0C0L5	VGDTLNLNLR	VGDTLNLNLR	557.8144++	557.814387	2	19.6	1015.553084	y9	1	56.9	56.79		
Complement C4-B	C4B	P0C0L5	VGDTLNLNLR	VGDTLNLNLR	557.8144++	557.814387	2	19.6	742.456999	y6	1	56.9	56.79		
Complement C4-B	C4B	P0C0L5	VGDTLNLNLR	VGDTLNLNLR	557.8144++	557.814387	2	19.6	629.372935	y5	1	56.9	56.79		
Complement C4-B	C4B	P0C0L5	VGDTLNLNLR	VGDTLNLNLR[+10.008269]	562.8185++ (heavy)	562.818521	2	19.6	1025.561353	y9	1	56.9	56.79		
Complement C4-B	C4B	P0C0L5	VGDTLNLNLR	VGDTLNLNLR[+10.008269]	562.8185++ (heavy)	562.818521	2	19.6	752.465268	y6	1	56.9	56.79		
Complement C4-B	C4B	P0C0L5	VGDTLNLNLR	VGDTLNLNLR[+10.008269]	562.8185++ (heavy)	562.818521	2	19.6	639.381204	y5	1	56.9	56.79		
Complement component C6	C6	P13671	GEVLDNSFTGGICK	GEVLDNSFTGGIC[+57.021464]K	748.8561++	748.856123	2	26.6	1098.488435	y10	1	59.31	58.11	2.9	3.1
Complement component C6	C6	P13671	GEVLDNSFTGGICK	GEVLDNSFTGGIC[+57.021464]K	748.8561++	748.856123	2	26.6	534.270444	y5	1	59.31	58.11		
Complement component C6	C6	P13671	GEVLDNSFTGGICK	GEVLDNSFTGGIC[+57.021464]K	748.8561++	748.856123	2	26.6	286.139747	b3	1	59.31	58.11		
Complement component C6	C6	P13671	GEVLDNSFTGGICK	GEVLDNSFTGGIC[+57.021464]K[+8.014199]	752.8632++ (heavy)	752.863222	2	26.6	1106.502634	y10	1	59.31	58.11		
Complement component C6	C6	P13671	GEVLDNSFTGGICK	GEVLDNSFTGGIC[+57.021464]K[+8.014199]	752.8632++ (heavy)	752.863222	2	26.6	542.284643	y5	1	59.31	58.11		
Complement component C6	C6	P13671	GEVLDNSFTGGICK	GEVLDNSFTGGIC[+57.021464]K[+8.014199]	752.8632++ (heavy)	752.863222	2	26.6	286.139747	b3	1	59.31	58.11		
Complement component C6	C6	P13671	ALNHLPLEYNSALYSR	ALNHLPLEYNSALYSR	620.9916+++	620.991608	3	21	609.335487	y5	1	82.87	70.41		
Complement component C6	C6	P13671	ALNHLPLEYNSALYSR	ALNHLPLEYNSALYSR	620.9916+++	620.991608	3	21	538.298373	y4	1	82.87	70.41		
Complement component C6	C6	P13671	ALNHLPLEYNSALYSR	ALNHLPLEYNSALYSR	620.9916+++	620.991608	3	21	425.214309	y3	1	82.87	70.41		
Complement component C6	C6	P13671	ALNHLPLEYNSALYSR	ALNHLPLEYNSALYSR	620.9916+++	620.991608	3	21	549.314357	b5	1	82.87	70.41		
Complement component C6	C6	P13671	ALNHLPLEYNSALYSR	ALNHLPLEYNSALYSR[+10.008269]	624.3277+++ (heavy)	624.327698	3	21	619.343756	y5	1	82.87	70.41		
Complement component C6	C6	P13671	ALNHLPLEYNSALYSR	ALNHLPLEYNSALYSR[+10.008269]	624.3277+++ (heavy)	624.327698	3	21	548.306642	y4	1	82.87	70.41		
Complement component C6	C6	P13671	ALNHLPLEYNSALYSR	ALNHLPLEYNSALYSR[+10.008269]	624.3277+++ (heavy)	624.327698	3	21	435.222578	y3	1	82.87	70.41		
Complement component C6	C6	P13671	ALNHLPLEYNSALYSR	ALNHLPLEYNSALYSR[+10.008269]	624.3277+++ (heavy)	624.327698	3	21	549.314357	b5	1	82.87	70.41		
Complement component C6	C6	P13671	SEYGAALAWEK	SEYGAALAWEK	612.7984++	612.798403	2	21.6	1008.514908	y9	1	58.81	56.96		
Complement component C6	C6	P13671	SEYGAALAWEK	SEYGAALAWEK	612.7984++	612.798403	2	21.6	845.451579	y8	1	58.81	56.96		
Complement component C6	C6	P13671	SEYGAALAWEK	SEYGAALAWEK	612.7984++	612.798403	2	21.6	717.393001	y6	1	58.81	56.96		
Complement component C6	C6	P13671	SEYGAALAWEK	SEYGAALAWEK[+8.014199]	616.8055++ (heavy)	616.805502	2	21.6	1016.529107	y9	1	58.81	56.96		
Complement component C6	C6	P13671	SEYGAALAWEK	SEYGAALAWEK[+8.014199]	616.8055++ (heavy)	616.805502	2	21.6	853.465778	y8	1	58.81	56.96		
Complement component C6	C6	P13671	SEYGAALAWEK	SEYGAALAWEK[+8.014199]	616.8055++ (heavy)	616.805502	2	21.6	725.4072	y6	1	58.81	56.96		
Complement component C6	C6	P13671	TLNICEVGTIR	TLNIC[+57.021464]EVGTIR	638.3399++	638.339912	2	22.6	1061.540805	y9	1	53.9	61.64		
Complement component C6	C6	P13671	TLNICEVGTIR	TLNIC[+57.021464]EVGTIR	638.3399++	638.339912	2	22.6	947.497878	y8	1	53.9	61.64		
Complement component C6	C6	P13671	TLNICEVGTIR	TLNIC[+57.021464]EVGTIR	638.3399++	638.339912	2	22.6	834.413814	y7	1	53.9	61.64		
Complement component C6	C6	P13671	TLNICEVGTIR	TLNIC[+57.021464]EVGTIR[+10.008269]	643.3440++ (heavy)	643.344046	2	22.6	1071.549074	y9	1	53.9	61.64		
Complement component C6	C6	P13671	TLNICEVGTIR	TLNIC[+57.021464]EVGTIR[+10.008269]	643.3440++ (heavy)	643.344046	2	22.6	957.506147	y8	1	53.9	61.64		
Complement component C6	C6	P13671	TLNICEVGTIR	TLNIC[+57.021464]EVGTIR[+10.008269]	643.3440++ (heavy)	643.344046	2	22.6	844.422083	y7	1	53.9	61.64		
Complement component C8 alp	C8A	P07357	AIDEDCSQYEPIPGSQK	AIDEDC[+57.021464]SQYEPIPGSQK	968.9333++	968.933287	2	34.8	726.414465	y7	1	39.7	42.02	5.0	2.6
Complement component C8 alp	C8A	P07357	AIDEDCSQYEPIPGSQK	AIDEDC[+57.021464]SQYEPIPGSQK	968.9333++	968.933287	2	34.8	516.277637	y5	1	39.7	42.02		
Complement component C8 alp	C8A	P07357	AIDEDCSQYEPIPGSQK	AIDEDC[+57.021464]SQYEPIPGSQK	968.9333++	968.933287	2	34.8	362.20341	y3	1	39.7	42.02		
Complement component C8 alp	C8A	P07357	AIDEDCSQYEPIPGSQK	AIDEDC[+57.021464]SQYEPIPGSQK[+8.014	972.9404++ (heavy)	972.940387	2	34.8	734.428664	y7	1	39.7	42.02		
Complement component C8 alp	C8A	P07357	AIDEDCSQYEPIPGSQK	AIDEDC[+57.021464]SQYEPIPGSQK[+8.014	972.9404++ (heavy)	972.940387	2	34.8	524.291836	y5	1	39.7	42.02		
Complement component C8 alp	C8A	P07357	AIDEDCSQYEPIPGSQK	AIDEDC[+57.021464]SQYEPIPGSQK[+8.014	972.9404++ (heavy)	972.940387	2	34.8	370.217609	y3	1	39.7	42.02		
Complement component C8 alp	C8A	P07357	MESLGITSR	MESLGITSR	497.2553++	497.255316	2	17.3	733.420279	y7	1	34.37	33.59		
Complement component C8 alp	C8A	P07357	MESLGITSR	MESLGITSR	497.2553++	497.255316	2	17.3	646.38825	y6	1	34.37	33.59		
Complement component C8 alp	C8A	P07357	MESLGITSR	MESLGITSR	497.2553++	497.255316	2	17.3	533.304186	y5	1	34.37	33.59		
Complement component C8 alp	C8A	P07357	MESLGITSR	MESLGITSR	497.2553++	497.255316	2	17.3	348.122382	b3	1	34.37	33.59		
Complement component C8 alp	C8A	P07357	MESLGITSR	MESLGITSR[+10.008269]	502.2595++ (heavy)	502.259451	2	17.3	743.428548	y7	1	34.37	33.59		
Complement component C8 alp	C8A	P07357	MESLGITSR	MESLGITSR[+10.008269]	502.2595++ (heavy)	502.259451	2	17.3	656.396519	y6	1	34.37	33.59		
Complement component C8 alp	C8A	P07357	MESLGITSR	MESLGITSR[+10.008269]	502.2595++ (heavy)	502.259451	2	17.3	543.312455	y5	1	34.37	33.59		
Complement component C8 alp	C8A	P07357	MESLGITSR	MESLGITSR[+10.008269]	502.2595++ (heavy)	502.259451	2	17.3	348.122382	b3	1	34.37	33.59		
Complement component C8 alp	C8A	P07357	AMAVEDIISR	AMAVEDIISR	552.7895++	552.789523	2	19.4	902.494172	y8	1	58.42	60.75		
Complement component C8 alp	C8A	P07357	AMAVEDIISR	AMAVEDIISR	552.7895++	552.789523	2	19.4	831.457058	y7	1	58.42	60.75		
Complement component C8 alp	C8A	P07357	AMAVEDIISR	AMAVEDIISR	552.7895++	552.789523	2	19.4	732.388644	y6	1	58.42	60.75		
Complement component C8 alp	C8A	P07357	AMAVEDIISR	AMAVEDIISR[+10.008269]	557.7937++ (heavy)	557.793658	2	19.4	912.502441	y8	1	58.42	60.75		

Complement component C8 alp	C8A	P07357	AMAVEDIISR	AMAVEDIISR[+10.008269]	557.7937++ (heavy)	557.793658	2	19.4	841.465327	y7	1	58.42	60.75			
Complement component C8 alp	C8A	P07357	AMAVEDIISR	AMAVEDIISR[+10.008269]	557.7937++ (heavy)	557.793658	2	19.4	742.396913	y6	1	58.42	60.75			
Complement component C8 alp	C8A	P07357	LGSLGAACEQTQTEGAK	LGSLGAAC[+57.021464]EQTQTEGAK	860.9122++	860.912158	2	30.8	1350.59542	y13	1	27.98	26.22			
Complement component C8 alp	C8A	P07357	LGSLGAACEQTQTEGAK	LGSLGAAC[+57.021464]EQTQTEGAK	860.9122++	860.912158	2	30.8	1222.536842	y11	1	27.98	26.22			
Complement component C8 alp	C8A	P07357	LGSLGAACEQTQTEGAK	LGSLGAAC[+57.021464]EQTQTEGAK	860.9122++	860.912158	2	30.8	1151.499728	y10	1	27.98	26.22			
Complement component C8 alp	C8A	P07357	LGSLGAACEQTQTEGAK	LGSLGAAC[+57.021464]EQTQTEGAK[+8.01	864.9193++ (heavy)	864.919257	2	30.8	1358.609618	y13	1	27.98	26.22			
Complement component C8 alp	C8A	P07357	LGSLGAACEQTQTEGAK	LGSLGAAC[+57.021464]EQTQTEGAK[+8.01	864.9193++ (heavy)	864.919257	2	30.8	1230.551041	y11	1	27.98	26.22			
Complement component C8 alp	C8A	P07357	LGSLGAACEQTQTEGAK	LGSLGAAC[+57.021464]EQTQTEGAK[+8.01	864.9193++ (heavy)	864.919257	2	30.8	1159.513927	y10	1	27.98	26.22			
Complement component C8 bet	C8B	P07358	CEGFVCAQTGR	C[+57.021464]EGFVC[+57.021464]AQTGR	642.7766++	642.776622	2	22.7	995.472725	y9	1	27.53	24.91	2.0	4.9	
Complement component C8 bet	C8B	P07358	CEGFVCAQTGR	C[+57.021464]EGFVC[+57.021464]AQTGR	642.7766++	642.776622	2	22.7	791.382848	y7	1	27.53	24.91			
Complement component C8 bet	C8B	P07358	CEGFVCAQTGR	C[+57.021464]EGFVC[+57.021464]AQTGR	642.7766++	642.776622	2	22.7	692.314434	y6	1	27.53	24.91			
Complement component C8 bet	C8B	P07358	CEGFVCAQTGR	C[+57.021464]EGFVC[+57.021464]AQTGR[+	647.7808++ (heavy)	647.780756	2	22.7	1005.480994	y9	1	27.53	24.91			
Complement component C8 bet	C8B	P07358	CEGFVCAQTGR	C[+57.021464]EGFVC[+57.021464]AQTGR[+	647.7808++ (heavy)	647.780756	2	22.7	801.391117	y7	1	27.53	24.91			
Complement component C8 bet	C8B	P07358	CEGFVCAQTGR	C[+57.021464]EGFVC[+57.021464]AQTGR[+	647.7808++ (heavy)	647.780756	2	22.7	702.322703	y6	1	27.53	24.91			
Complement component C8 bet	C8B	P07358	LPLEYSYGEYR	LPLEYSYGEYR	695.3379++	695.337892	2	24.7	1179.53168	y9	1	66.47	61.91			
Complement component C8 bet	C8B	P07358	LPLEYSYGEYR	LPLEYSYGEYR	695.3379++	695.337892	2	24.7	1066.447616	y8	1	66.47	61.91			
Complement component C8 bet	C8B	P07358	LPLEYSYGEYR	LPLEYSYGEYR	695.3379++	695.337892	2	24.7	937.405023	y7	1	66.47	61.91			
Complement component C8 bet	C8B	P07358	LPLEYSYGEYR	LPLEYSYGEYR	695.3379++	695.337892	2	24.7	774.341694	y6	1	66.47	61.91			
Complement component C8 bet	C8B	P07358	LPLEYSYGEYR	LPLEYSYGEYR[+10.008269]	700.3420++ (heavy)	700.342026	2	24.7	1189.539949	y9	1	66.47	61.91			
Complement component C8 bet	C8B	P07358	LPLEYSYGEYR	LPLEYSYGEYR[+10.008269]	700.3420++ (heavy)	700.342026	2	24.7	1076.455885	y8	1	66.47	61.91			
Complement component C8 bet	C8B	P07358	LPLEYSYGEYR	LPLEYSYGEYR[+10.008269]	700.3420++ (heavy)	700.342026	2	24.7	947.413292	y7	1	66.47	61.91			
Complement component C8 bet	C8B	P07358	LPLEYSYGEYR	LPLEYSYGEYR[+10.008269]	700.3420++ (heavy)	700.342026	2	24.7	784.349963	y6	1	66.47	61.91			
Complement component C8 gar	C8G	P07360	LDGICWQVR	LDGIC[+57.021464]WQVR	573.7899++	573.789858	2	20.2	748.355905	y5	1	62.79	65.95	4.3	5.6	
Complement component C8 gar	C8G	P07360	LDGICWQVR	LDGIC[+57.021464]WQVR	573.7899++	573.789858	2	20.2	588.325256	y4	1	62.79	65.95			
Complement component C8 gar	C8G	P07360	LDGICWQVR	LDGIC[+57.021464]WQVR	573.7899++	573.789858	2	20.2	286.139747	b3	1	62.79	65.95			
Complement component C8 gar	C8G	P07360	LDGICWQVR	LDGIC[+57.021464]WQVR[+10.008269]	578.7940++ (heavy)	578.793992	2	20.2	758.364174	y5	1	62.79	65.95			
Complement component C8 gar	C8G	P07360	LDGICWQVR	LDGIC[+57.021464]WQVR[+10.008269]	578.7940++ (heavy)	578.793992	2	20.2	598.333525	y4	1	62.79	65.95			
Complement component C8 gar	C8G	P07360	LDGICWQVR	LDGIC[+57.021464]WQVR[+10.008269]	578.7940++ (heavy)	578.793992	2	20.2	286.139747	b3	1	62.79	65.95			
Complement component C8 gar	C8G	P07360	QLYGDTGVLGR	QLYGDTGVLGR	589.8118++	589.811844	2	20.8	937.473771	y9	1	48.57	45.76			
Complement component C8 gar	C8G	P07360	QLYGDTGVLGR	QLYGDTGVLGR	589.8118++	589.811844	2	20.8	774.410442	y8	1	48.57	45.76			
Complement component C8 gar	C8G	P07360	QLYGDTGVLGR	QLYGDTGVLGR	589.8118++	589.811844	2	20.8	602.362036	y6	1	48.57	45.76			
Complement component C8 gar	C8G	P07360	QLYGDTGVLGR	QLYGDTGVLGR	589.8118++	589.811844	2	20.8	345.22448	y3	1	48.57	45.76			
Complement component C8 gar	C8G	P07360	QLYGDTGVLGR	QLYGDTGVLGR[+10.008269]	594.8160++ (heavy)	594.815979	2	20.8	947.48204	y9	1	48.57	45.76			
Complement component C8 gar	C8G	P07360	QLYGDTGVLGR	QLYGDTGVLGR[+10.008269]	594.8160++ (heavy)	594.815979	2	20.8	784.418711	y8	1	48.57	45.76			
Complement component C8 gar	C8G	P07360	QLYGDTGVLGR	QLYGDTGVLGR[+10.008269]	594.8160++ (heavy)	594.815979	2	20.8	612.370305	y6	1	48.57	45.76			
Complement component C8 gar	C8G	P07360	QLYGDTGVLGR	QLYGDTGVLGR[+10.008269]	594.8160++ (heavy)	594.815979	2	20.8	355.232748	y3	1	48.57	45.76			
Complement component C8 gar	C8G	P07360	SLPVSDSVLSGFEQR	SLPVSDSVLSGFEQR	810.9150++	810.915026	2	28.9	1224.585506	y11	1	81.33	83.85			
Complement component C8 gar	C8G	P07360	SLPVSDSVLSGFEQR	SLPVSDSVLSGFEQR	810.9150++	810.915026	2	28.9	836.426093	y7	1	81.33	83.85			
Complement component C8 gar	C8G	P07360	SLPVSDSVLSGFEQR	SLPVSDSVLSGFEQR	810.9150++	810.915026	2	28.9	723.342029	y6	1	81.33	83.85			
Complement component C8 gar	C8G	P07360	SLPVSDSVLSGFEQR	SLPVSDSVLSGFEQR	810.9150++	810.915026	2	28.9	636.31	y5	1	81.33	83.85			
Complement component C8 gar	C8G	P07360	SLPVSDSVLSGFEQR	SLPVSDSVLSGFEQR[+10.008269]	815.9192++ (heavy)	815.919161	2	28.9	1234.593775	y11	1	81.33	83.85			
Complement component C8 gar	C8G	P07360	SLPVSDSVLSGFEQR	SLPVSDSVLSGFEQR[+10.008269]	815.9192++ (heavy)	815.919161	2	28.9	846.434362	y7	1	81.33	83.85			
Complement component C8 gar	C8G	P07360	SLPVSDSVLSGFEQR	SLPVSDSVLSGFEQR[+10.008269]	815.9192++ (heavy)	815.919161	2	28.9	733.350298	y6	1	81.33	83.85			
Complement component C8 gar	C8G	P07360	SLPVSDSVLSGFEQR	SLPVSDSVLSGFEQR[+10.008269]	815.9192++ (heavy)	815.919161	2	28.9	646.318269	y5	1	81.33	83.85			
Complement component C8 gar	C8G	P07360	VQEAHLTEDQIFYFPK	VQEAHLTEDQIFYFPK	655.6633+++	655.663269	3	22.3	814.449788	y6	1	90.59	81.93			
Complement component C8 gar	C8G	P07360	VQEAHLTEDQIFYFPK	VQEAHLTEDQIFYFPK	655.6633+++	655.663269	3	22.3	701.365724	y5	1	90.59	81.93			
Complement component C8 gar	C8G	P07360	VQEAHLTEDQIFYFPK	VQEAHLTEDQIFYFPK	655.6633+++	655.663269	3	22.3	554.29731	y4	1	90.59	81.93			
Complement component C8 gar	C8G	P07360	VQEAHLTEDQIFYFPK	VQEAHLTEDQIFYFPK	655.6633+++	655.663269	3	22.3	391.233982	y3	1	90.59	81.93			
Complement component C8 gar	C8G	P07360	VQEAHLTEDQIFYFPK	VQEAHLTEDQIFYFPK[+8.014199]	658.3347+++ (heavy)	658.334669	3	22.3	822.463987	y6	1	90.59	81.93			
Complement component C8 gar	C8G	P07360	VQEAHLTEDQIFYFPK	VQEAHLTEDQIFYFPK[+8.014199]	658.3347+++ (heavy)	658.334669	3	22.3	709.379923	y5	1	90.59	81.93			

Complement component C8 gar	C8G	P07360	VQEAHLTEDQIFYFPK	VQEAHLTEDQIFYFPK[+8.014199]	658.3347+++ (heavy)	658.334669	3	22.3	562.311509	y4	1	90.59	81.93		
Complement component C8 gar	C8G	P07360	VQEAHLTEDQIFYFPK	VQEAHLTEDQIFYFPK[+8.014199]	658.3347+++ (heavy)	658.334669	3	22.3	399.248181	y3	1	90.59	81.93		
Complement factor B	CFB	P00751	YGLVTYATYPK	YGLVTYATYPK	638.3346++	638.334621	2	22.6	942.49311	y8	1	66.66	59.81	7.1	5.1
Complement factor B	CFB	P00751	YGLVTYATYPK	YGLVTYATYPK	638.3346++	638.334621	2	22.6	843.424696	y7	1	66.66	59.81		
Complement factor B	CFB	P00751	YGLVTYATYPK	YGLVTYATYPK	638.3346++	638.334621	2	22.6	334.176132	b3	1	66.66	59.81		
Complement factor B	CFB	P00751	YGLVTYATYPK	YGLVTYATYPK[+8.014199]	642.3417++ (heavy)	642.34172	2	22.6	950.507309	y8	1	66.66	59.81		
Complement factor B	CFB	P00751	YGLVTYATYPK	YGLVTYATYPK[+8.014199]	642.3417++ (heavy)	642.34172	2	22.6	851.438895	y7	1	66.66	59.81		
Complement factor B	CFB	P00751	YGLVTYATYPK	YGLVTYATYPK[+8.014199]	642.3417++ (heavy)	642.34172	2	22.6	334.176132	b3	1	66.66	59.81		
Complement factor B	CFB	P00751	DLLYIGK	DLLYIGK	411.2420++	411.242004	2	14.1	593.365724	y5	1	53.17	55.29		
Complement factor B	CFB	P00751	DLLYIGK	DLLYIGK	411.2420++	411.242004	2	14.1	480.28166	y4	1	53.17	55.29		
Complement factor B	CFB	P00751	DLLYIGK	DLLYIGK	411.2420++	411.242004	2	14.1	229.118283	b2	1	53.17	55.29		
Complement factor B	CFB	P00751	DLLYIGK	DLLYIGK[+8.014199]	415.2491++ (heavy)	415.249103	2	14.1	601.379923	y5	1	53.17	55.29		
Complement factor B	CFB	P00751	DLLYIGK	DLLYIGK[+8.014199]	415.2491++ (heavy)	415.249103	2	14.1	488.295859	y4	1	53.17	55.29		
Complement factor B	CFB	P00751	DLLYIGK	DLLYIGK[+8.014199]	415.2491++ (heavy)	415.249103	2	14.1	229.118283	b2	1	53.17	55.29		
Complement factor B	CFB	P00751	ALFVSEEEK	ALFVSEEEK	526.2689++	526.268947	2	18.4	867.409439	y7	1	43.01	34.8		
Complement factor B	CFB	P00751	ALFVSEEEK	ALFVSEEEK	526.2689++	526.268947	2	18.4	720.341026	y6	1	43.01	34.8		
Complement factor B	CFB	P00751	ALFVSEEEK	ALFVSEEEK	526.2689++	526.268947	2	18.4	621.272612	y5	1	43.01	34.8		
Complement factor B	CFB	P00751	ALFVSEEEK	ALFVSEEEK[+8.014199]	530.2760++ (heavy)	530.276046	2	18.4	875.423638	y7	1	43.01	34.8		
Complement factor B	CFB	P00751	ALFVSEEEK	ALFVSEEEK[+8.014199]	530.2760++ (heavy)	530.276046	2	18.4	728.355225	y6	1	43.01	34.8		
Complement factor B	CFB	P00751	ALFVSEEEK	ALFVSEEEK[+8.014199]	530.2760++ (heavy)	530.276046	2	18.4	629.286811	y5	1	43.01	34.8		
Complement factor H	CFH	P08603	SSNLIILEEHLK	SSNLIILEEHLK	465.9329+++	465.932919	3	15.4	881.509094	y7	1	78.41	68.63	4.9	2.5
Complement factor H	CFH	P08603	SSNLIILEEHLK	SSNLIILEEHLK	465.9329+++	465.932919	3	15.4	768.42503	y6	1	78.41	68.63		
Complement factor H	CFH	P08603	SSNLIILEEHLK	SSNLIILEEHLK	465.9329+++	465.932919	3	15.4	655.340966	y5	1	78.41	68.63		
Complement factor H	CFH	P08603	SSNLIILEEHLK	SSNLIILEEHLK[+8.014199]	468.6043+++ (heavy)	468.604319	3	15.4	889.523293	y7	1	78.41	68.63		
Complement factor H	CFH	P08603	SSNLIILEEHLK	SSNLIILEEHLK[+8.014199]	468.6043+++ (heavy)	468.604319	3	15.4	776.439229	y6	1	78.41	68.63		
Complement factor H	CFH	P08603	SSNLIILEEHLK	SSNLIILEEHLK[+8.014199]	468.6043+++ (heavy)	468.604319	3	15.4	663.355165	y5	1	78.41	68.63		
Complement factor H	CFH	P08603	LSYTCEGGFR	LSYTC[+57.021464]EGGFR	595.2690++	595.268955	2	21	989.414542	y8	1	43.14	37.9		
Complement factor H	CFH	P08603	LSYTCEGGFR	LSYTC[+57.021464]EGGFR	595.2690++	595.268955	2	21	826.351213	y7	1	43.14	37.9		
Complement factor H	CFH	P08603	LSYTCEGGFR	LSYTC[+57.021464]EGGFR	595.2690++	595.268955	2	21	725.303535	y6	1	43.14	37.9		
Complement factor H	CFH	P08603	LSYTCEGGFR	LSYTC[+57.021464]EGGFR[+10.008269]	600.2731++ (heavy)	600.27309	2	21	999.422811	y8	1	43.14	37.9		
Complement factor H	CFH	P08603	LSYTCEGGFR	LSYTC[+57.021464]EGGFR[+10.008269]	600.2731++ (heavy)	600.27309	2	21	836.359482	y7	1	43.14	37.9		
Complement factor H	CFH	P08603	LSYTCEGGFR	LSYTC[+57.021464]EGGFR[+10.008269]	600.2731++ (heavy)	600.27309	2	21	735.311804	y6	1	43.14	37.9		
Complement factor H-related pı	CFHR2	P36980	ITCAEEGWSPTPK	ITC[+57.021464]AEEGWSPTPK	738.3454++	738.345391	2	26.3	901.441408	y8	1	45.27	37.73	6.4	3.3
Complement factor H-related pı	CFHR2	P36980	ITCAEEGWSPTPK	ITC[+57.021464]AEEGWSPTPK	738.3454++	738.345391	2	26.3	772.398815	y7	1	45.27	37.73		
Complement factor H-related pı	CFHR2	P36980	ITCAEEGWSPTPK	ITC[+57.021464]AEEGWSPTPK	738.3454++	738.345391	2	26.3	529.298038	y5	1	45.27	37.73		
Complement factor H-related pı	CFHR2	P36980	ITCAEEGWSPTPK	ITC[+57.021464]AEEGWSPTPK[+8.014199]	742.3525++ (heavy)	742.352491	2	26.3	909.455607	y8	1	45.27	37.73		
Complement factor H-related pı	CFHR2	P36980	ITCAEEGWSPTPK	ITC[+57.021464]AEEGWSPTPK[+8.014199]	742.3525++ (heavy)	742.352491	2	26.3	780.413014	y7	1	45.27	37.73		
Complement factor H-related pı	CFHR2	P36980	ITCAEEGWSPTPK	ITC[+57.021464]AEEGWSPTPK[+8.014199]	742.3525++ (heavy)	742.352491	2	26.3	537.312237	y5	1	45.27	37.73		
Complement factor H-related pı	CFHR2	P36980	LVYPSCEEK	LVYPSC[+57.021464]EEK	562.7683++	562.768257	2	19.8	912.376759	y7	1	24.08	24.23		
Complement factor H-related pı	CFHR2	P36980	LVYPSCEEK	LVYPSC[+57.021464]EEK	562.7683++	562.768257	2	19.8	749.313431	y6	1	24.08	24.23		
Complement factor H-related pı	CFHR2	P36980	LVYPSCEEK	LVYPSC[+57.021464]EEK	562.7683++	562.768257	2	19.8	652.260667	y5	1	24.08	24.23		
Complement factor H-related pı	CFHR2	P36980	LVYPSCEEK	LVYPSC[+57.021464]EEK[+8.014199]	566.7754++ (heavy)	566.775356	2	19.8	920.390958	y7	1	24.08	24.23		
Complement factor H-related pı	CFHR2	P36980	LVYPSCEEK	LVYPSC[+57.021464]EEK[+8.014199]	566.7754++ (heavy)	566.775356	2	19.8	757.32763	y6	1	24.08	24.23		
Complement factor H-related pı	CFHR2	P36980	LVYPSCEEK	LVYPSC[+57.021464]EEK[+8.014199]	566.7754++ (heavy)	566.775356	2	19.8	660.274866	y5	1	24.08	24.23		
Complement factor I	CFI	P05156	VTYTSQEDLVEK	VTYTSQEDLVEK	706.3512++	706.351196	2	25.1	1211.579024	y10	1	39.82	33.95	3.8	2.4
Complement factor I	CFI	P05156	VTYTSQEDLVEK	VTYTSQEDLVEK	706.3512++	706.351196	2	25.1	1048.515696	y9	1	39.82	33.95		
Complement factor I	CFI	P05156	VTYTSQEDLVEK	VTYTSQEDLVEK	706.3512++	706.351196	2	25.1	947.468017	y8	1	39.82	33.95		
Complement factor I	CFI	P05156	VTYTSQEDLVEK	VTYTSQEDLVEK[+8.014199]	710.3583++ (heavy)	710.358296	2	25.1	1219.593223	y10	1	39.82	33.95		
Complement factor I	CFI	P05156	VTYTSQEDLVEK	VTYTSQEDLVEK[+8.014199]	710.3583++ (heavy)	710.358296	2	25.1	1056.529895	y9	1	39.82	33.95		
Complement factor I	CFI	P05156	VTYTSQEDLVEK	VTYTSQEDLVEK[+8.014199]	710.3583++ (heavy)	710.358296	2	25.1	955.482216	y8	1	39.82	33.95		

Complement factor I	CFI	P05156	GLETSLAECTFTK	GLETSLAEC[+57.021464]TFTK	728.8530++	728.853049	2	25.9	969.470994	y8	1	60.39	61.7		
Complement factor I	CFI	P05156	GLETSLAECTFTK	GLETSLAEC[+57.021464]TFTK	728.8530++	728.853049	2	25.9	856.38693	y7	1	60.39	61.7		
Complement factor I	CFI	P05156	GLETSLAECTFTK	GLETSLAEC[+57.021464]TFTK	728.8530++	728.853049	2	25.9	785.349816	y6	1	60.39	61.7		
Complement factor I	CFI	P05156	GLETSLAECTFTK	GLETSLAEC[+57.021464]TFTK[+8.014199]	732.8601++ (heavy)	732.860148	2	25.9	977.485193	y8	1	60.39	61.7		
Complement factor I	CFI	P05156	GLETSLAECTFTK	GLETSLAEC[+57.021464]TFTK[+8.014199]	732.8601++ (heavy)	732.860148	2	25.9	864.401129	y7	1	60.39	61.7		
Complement factor I	CFI	P05156	GLETSLAECTFTK	GLETSLAEC[+57.021464]TFTK[+8.014199]	732.8601++ (heavy)	732.860148	2	25.9	793.364015	y6	1	60.39	61.7		
Complement factor I	CFI	P05156	IVIEYVDR	IVIEYVDR	503.7820++	503.782024	2	17.6	794.404294	y6	1	49.21	47.92		
Complement factor I	CFI	P05156	IVIEYVDR	IVIEYVDR	503.7820++	503.782024	2	17.6	681.32023	y5	1	49.21	47.92		
Complement factor I	CFI	P05156	IVIEYVDR	IVIEYVDR	503.7820++	503.782024	2	17.6	552.277637	y4	1	49.21	47.92		
Complement factor I	CFI	P05156	IVIEYVDR	IVIEYVDR[+10.008269]	508.7862++ (heavy)	508.786159	2	17.6	804.412563	y6	1	49.21	47.92		
Complement factor I	CFI	P05156	IVIEYVDR	IVIEYVDR[+10.008269]	508.7862++ (heavy)	508.786159	2	17.6	691.328499	y5	1	49.21	47.92		
Complement factor I	CFI	P05156	IVIEYVDR	IVIEYVDR[+10.008269]	508.7862++ (heavy)	508.786159	2	17.6	562.285906	y4	1	49.21	47.92		
Complement factor I	CFI	P05156	VFSLQWGEVK	VFSLQWGEVK	596.8217++	596.821681	2	21	946.499258	y8	1	77.16	81.91		
Complement factor I	CFI	P05156	VFSLQWGEVK	VFSLQWGEVK	596.8217++	596.821681	2	21	746.383165	y6	1	77.16	81.91		
Complement factor I	CFI	P05156	VFSLQWGEVK	VFSLQWGEVK	596.8217++	596.821681	2	21	618.324588	y5	1	77.16	81.91		
Complement factor I	CFI	P05156	VFSLQWGEVK	VFSLQWGEVK[+8.014199]	600.8288++ (heavy)	600.82878	2	21	954.513457	y8	1	77.16	81.91		
Complement factor I	CFI	P05156	VFSLQWGEVK	VFSLQWGEVK[+8.014199]	600.8288++ (heavy)	600.82878	2	21	754.397364	y6	1	77.16	81.91		
Complement factor I	CFI	P05156	VFSLQWGEVK	VFSLQWGEVK[+8.014199]	600.8288++ (heavy)	600.82878	2	21	626.338787	y5	1	77.16	81.91		
Ficolin-3	FCN3	O75636	TFAHYATFR	TFAHYATFR	557.2774++	557.27744	2	19.6	865.431512	y7	1	52.68	35.9	4.4	5.8
Ficolin-3	FCN3	O75636	TFAHYATFR	TFAHYATFR	557.2774++	557.27744	2	19.6	794.394398	y6	1	52.68	35.9		
Ficolin-3	FCN3	O75636	TFAHYATFR	TFAHYATFR	557.2774++	557.27744	2	19.6	657.335487	y5	1	52.68	35.9		
Ficolin-3	FCN3	O75636	TFAHYATFR	TFAHYATFR[+10.008269]	562.2816++ (heavy)	562.281575	2	19.6	875.439781	y7	1	52.68	35.9		
Ficolin-3	FCN3	O75636	TFAHYATFR	TFAHYATFR[+10.008269]	562.2816++ (heavy)	562.281575	2	19.6	804.402667	y6	1	52.68	35.9		
Ficolin-3	FCN3	O75636	TFAHYATFR	TFAHYATFR[+10.008269]	562.2816++ (heavy)	562.281575	2	19.6	667.343756	y5	1	52.68	35.9		
Ficolin-3	FCN3	O75636	YGIDWASGR	YGIDWASGR	512.7460++	512.745973	2	17.9	861.421342	y8	1	50.26	51.68		
Ficolin-3	FCN3	O75636	YGIDWASGR	YGIDWASGR	512.7460++	512.745973	2	17.9	691.315814	y6	1	50.26	51.68		
Ficolin-3	FCN3	O75636	YGIDWASGR	YGIDWASGR	512.7460++	512.745973	2	17.9	390.209558	y4	1	50.26	51.68		
Ficolin-3	FCN3	O75636	YGIDWASGR	YGIDWASGR[+10.008269]	517.7501++ (heavy)	517.750108	2	17.9	871.429611	y8	1	50.26	51.68		
Ficolin-3	FCN3	O75636	YGIDWASGR	YGIDWASGR[+10.008269]	517.7501++ (heavy)	517.750108	2	17.9	701.324083	y6	1	50.26	51.68		
Ficolin-3	FCN3	O75636	YGIDWASGR	YGIDWASGR[+10.008269]	517.7501++ (heavy)	517.750108	2	17.9	400.217827	y4	1	50.26	51.68		
Gelsolin	GSN	P06396	HVVPNEVVVQR	HVVPNEVVVQR	425.9104+++	425.910449	3	14	501.314357	y4	1	38.85	25.84	3.7	1.1
Gelsolin	GSN	P06396	HVVPNEVVVQR	HVVPNEVVVQR	425.9104+++	425.910449	3	14	402.245943	y3	1	38.85	25.84		
Gelsolin	GSN	P06396	HVVPNEVVVQR	HVVPNEVVVQR	425.9104+++	425.910449	3	14	676.3413	b6	1	38.85	25.84		
Gelsolin	GSN	P06396	HVVPNEVVVQR	HVVPNEVVVQR[+10.008269]	429.2465+++ (heavy)	429.246539	3	14	511.322626	y4	1	38.85	25.84		
Gelsolin	GSN	P06396	HVVPNEVVVQR	HVVPNEVVVQR[+10.008269]	429.2465+++ (heavy)	429.246539	3	14	412.254212	y3	1	38.85	25.84		
Gelsolin	GSN	P06396	HVVPNEVVVQR	HVVPNEVVVQR[+10.008269]	429.2465+++ (heavy)	429.246539	3	14	676.3413	b6	1	38.85	25.84		
Gelsolin	GSN	P06396	SEDCFILDHGK	SEDC[+57.021464]FILDHGK	440.8678+++	440.86781	3	14.5	682.38825	y6	1	48.13	37.75		
Gelsolin	GSN	P06396	SEDCFILDHGK	SEDC[+57.021464]FILDHGK	440.8678+++	440.86781	3	14.5	569.304186	y5	1	48.13	37.75		
Gelsolin	GSN	P06396	SEDCFILDHGK	SEDC[+57.021464]FILDHGK	440.8678+++	440.86781	3	14.5	456.220122	y4	1	48.13	37.75		
Gelsolin	GSN	P06396	SEDCFILDHGK	SEDC[+57.021464]FILDHGK[+8.014199]	443.5392+++ (heavy)	443.53921	3	14.5	690.402449	y6	1	48.13	37.75		
Gelsolin	GSN	P06396	SEDCFILDHGK	SEDC[+57.021464]FILDHGK[+8.014199]	443.5392+++ (heavy)	443.53921	3	14.5	577.318385	y5	1	48.13	37.75		
Gelsolin	GSN	P06396	SEDCFILDHGK	SEDC[+57.021464]FILDHGK[+8.014199]	443.5392+++ (heavy)	443.53921	3	14.5	464.234321	y4	1	48.13	37.75		
Gelsolin	GSN	P06396	QTQVSVLPEGGETPLFK	QTQVSVLPEGGETPLFK	915.4858++	915.485816	2	32.8	1187.630666	y11	1	82.81	82.48		
Gelsolin	GSN	P06396	QTQVSVLPEGGETPLFK	QTQVSVLPEGGETPLFK	915.4858++	915.485816	2	32.8	1074.546602	y10	1	82.81	82.48		
Gelsolin	GSN	P06396	QTQVSVLPEGGETPLFK	QTQVSVLPEGGETPLFK	915.4858++	915.485816	2	32.8	504.318046	y4	1	82.81	82.48		
Gelsolin	GSN	P06396	QTQVSVLPEGGETPLFK	QTQVSVLPEGGETPLFK[+8.014199]	919.4929++ (heavy)	919.492915	2	32.8	1195.644865	y11	1	82.81	82.48		
Gelsolin	GSN	P06396	QTQVSVLPEGGETPLFK	QTQVSVLPEGGETPLFK[+8.014199]	919.4929++ (heavy)	919.492915	2	32.8	1082.560801	y10	1	82.81	82.48		
Gelsolin	GSN	P06396	QTQVSVLPEGGETPLFK	QTQVSVLPEGGETPLFK[+8.014199]	919.4929++ (heavy)	919.492915	2	32.8	512.332245	y4	1	82.81	82.48		
Gelsolin	GSN	P06396	AGALNSNDAFVLK	AGALNSNDAFVLK	660.3513++	660.351334	2	23.4	1007.515636	y9	1	64.37	58.87		
Gelsolin	GSN	P06396	AGALNSNDAFVLK	AGALNSNDAFVLK	660.3513++	660.351334	2	23.4	893.472708	y8	1	64.37	58.87		

Gelsolin	GSN	P06396	AGALNSNDAFVLK	AGALNSNDAFVLK	660.3513++	660.351334	2	23.4	806.44068	y7	1	64.37	58.87			
Gelsolin	GSN	P06396	AGALNSNDAFVLK	AGALNSNDAFVLK	660.3513++	660.351334	2	23.4	692.397753	y6	1	64.37	58.87			
Gelsolin	GSN	P06396	AGALNSNDAFVLK	AGALNSNDAFVLK[+8.014199]	664.3584++ (heavy)	664.358433	2	23.4	1015.529835	y9	1	64.37	58.87			
Gelsolin	GSN	P06396	AGALNSNDAFVLK	AGALNSNDAFVLK[+8.014199]	664.3584++ (heavy)	664.358433	2	23.4	901.486907	y8	1	64.37	58.87			
Gelsolin	GSN	P06396	AGALNSNDAFVLK	AGALNSNDAFVLK[+8.014199]	664.3584++ (heavy)	664.358433	2	23.4	814.454879	y7	1	64.37	58.87			
Gelsolin	GSN	P06396	AGALNSNDAFVLK	AGALNSNDAFVLK[+8.014199]	664.3584++ (heavy)	664.358433	2	23.4	700.411952	y6	1	64.37	58.87			
Haptoglobin-related protein	HPR	P00739	VVLHPNYHQVDIGLIK	VVLHPNYHQVDIGLIK	615.6842+++	615.684227	3	20.8	885.540394	y8	1	82.13	64.36	6.4	4.3	
Haptoglobin-related protein	HPR	P00739	VVLHPNYHQVDIGLIK	VVLHPNYHQVDIGLIK	615.6842+++	615.684227	3	20.8	757.481817	y7	1	82.13	64.36			
Haptoglobin-related protein	HPR	P00739	VVLHPNYHQVDIGLIK	VVLHPNYHQVDIGLIK	615.6842+++	615.684227	3	20.8	543.38646	y5	1	82.13	64.36			
Haptoglobin-related protein	HPR	P00739	VVLHPNYHQVDIGLIK	VVLHPNYHQVDIGLIK	615.6842+++	615.684227	3	20.8	449.28708	b4	1	82.13	64.36			
Haptoglobin-related protein	HPR	P00739	VVLHPNYHQVDIGLIK	VVLHPNYHQVDIGLIK[+8.014199]	618.3556+++ (heavy)	618.355627	3	20.8	893.554593	y8	1	82.13	64.36			
Haptoglobin-related protein	HPR	P00739	VVLHPNYHQVDIGLIK	VVLHPNYHQVDIGLIK[+8.014199]	618.3556+++ (heavy)	618.355627	3	20.8	765.496016	y7	1	82.13	64.36			
Haptoglobin-related protein	HPR	P00739	VVLHPNYHQVDIGLIK	VVLHPNYHQVDIGLIK[+8.014199]	618.3556+++ (heavy)	618.355627	3	20.8	551.400659	y5	1	82.13	64.36			
Haptoglobin-related protein	HPR	P00739	VVLHPNYHQVDIGLIK	VVLHPNYHQVDIGLIK[+8.014199]	618.3556+++ (heavy)	618.355627	3	20.8	449.28708	b4	1	82.13	64.36			
Haptoglobin-related protein	HPR	P00739	VGYVSGWGQSDNFK	VGYVSGWGQSDNFK	772.3624++	772.36243	2	27.5	1125.495963	y10	1	67.74	60.82			
Haptoglobin-related protein	HPR	P00739	VGYVSGWGQSDNFK	VGYVSGWGQSDNFK	772.3624++	772.36243	2	27.5	795.363158	y7	1	67.74	60.82			
Haptoglobin-related protein	HPR	P00739	VGYVSGWGQSDNFK	VGYVSGWGQSDNFK	772.3624++	772.36243	2	27.5	320.160482	b3	1	67.74	60.82			
Haptoglobin-related protein	HPR	P00739	VGYVSGWGQSDNFK	VGYVSGWGQSDNFK[+8.014199]	776.3695++ (heavy)	776.369529	2	27.5	1133.510162	y10	1	67.74	60.82			
Haptoglobin-related protein	HPR	P00739	VGYVSGWGQSDNFK	VGYVSGWGQSDNFK[+8.014199]	776.3695++ (heavy)	776.369529	2	27.5	803.377357	y7	1	67.74	60.82			
Haptoglobin-related protein	HPR	P00739	VGYVSGWGQSDNFK	VGYVSGWGQSDNFK[+8.014199]	776.3695++ (heavy)	776.369529	2	27.5	320.160482	b3	1	67.74	60.82			
Haptoglobin-related protein	HPR	P00739	SPVGVQPILNEHTFCVGMSK	SPVGVQPILNEHTFC[+57.021464]VGMSK	734.0345+++	734.034491	3	25.1	1309.566368	y11	1	89.52	80.39			
Haptoglobin-related protein	HPR	P00739	SPVGVQPILNEHTFCVGMSK	SPVGVQPILNEHTFC[+57.021464]VGMSK	734.0345+++	734.034491	3	25.1	929.421935	y8	1	89.52	80.39			
Haptoglobin-related protein	HPR	P00739	SPVGVQPILNEHTFCVGMSK	SPVGVQPILNEHTFC[+57.021464]VGMSK	734.0345+++	734.034491	3	25.1	422.206781	y4	1	89.52	80.39			
Haptoglobin-related protein	HPR	P00739	SPVGVQPILNEHTFCVGMSK	SPVGVQPILNEHTFC[+57.021464]VGMSK[+8	736.7059+++ (heavy)	736.705891	3	25.1	1317.580567	y11	1	89.52	80.39			
Haptoglobin-related protein	HPR	P00739	SPVGVQPILNEHTFCVGMSK	SPVGVQPILNEHTFC[+57.021464]VGMSK[+8	736.7059+++ (heavy)	736.705891	3	25.1	937.436134	y8	1	89.52	80.39			
Haptoglobin-related protein	HPR	P00739	SPVGVQPILNEHTFCVGMSK	SPVGVQPILNEHTFC[+57.021464]VGMSK[+8	736.7059+++ (heavy)	736.705891	3	25.1	430.22098	y4	1	89.52	80.39			
Heparin cofactor 2	SERPIND1	P05546	YEITTIHNLFR	YEITTIHNLFR	469.5857+++	469.585743	3	15.6	686.373269	y5	1	85.61	74.87	3.6	4.4	
Heparin cofactor 2	SERPIND1	P05546	YEITTIHNLFR	YEITTIHNLFR	469.5857+++	469.585743	3	15.6	549.314357	y4	1	85.61	74.87			
Heparin cofactor 2	SERPIND1	P05546	YEITTIHNLFR	YEITTIHNLFR	469.5857+++	469.585743	3	15.6	293.113198	b2	1	85.61	74.87			
Heparin cofactor 2	SERPIND1	P05546	YEITTIHNLFR	YEITTIHNLFR[+10.008269]	472.9218+++ (heavy)	472.921832	3	15.6	696.381538	y5	1	85.61	74.87			
Heparin cofactor 2	SERPIND1	P05546	YEITTIHNLFR	YEITTIHNLFR[+10.008269]	472.9218+++ (heavy)	472.921832	3	15.6	559.322626	y4	1	85.61	74.87			
Heparin cofactor 2	SERPIND1	P05546	YEITTIHNLFR	YEITTIHNLFR[+10.008269]	472.9218+++ (heavy)	472.921832	3	15.6	293.113198	b2	1	85.61	74.87			
Heparin cofactor 2	SERPIND1	P05546	SVNDLYIQK	SVNDLYIQK	540.2902++	540.290213	2	18.9	893.472708	y7	1	40.43	33.86			
Heparin cofactor 2	SERPIND1	P05546	SVNDLYIQK	SVNDLYIQK	540.2902++	540.290213	2	18.9	551.318774	y4	1	40.43	33.86			
Heparin cofactor 2	SERPIND1	P05546	SVNDLYIQK	SVNDLYIQK	540.2902++	540.290213	2	18.9	388.255445	y3	1	40.43	33.86			
Heparin cofactor 2	SERPIND1	P05546	SVNDLYIQK	SVNDLYIQK[+8.014199]	544.2973++ (heavy)	544.297313	2	18.9	901.486907	y7	1	40.43	33.86			
Heparin cofactor 2	SERPIND1	P05546	SVNDLYIQK	SVNDLYIQK[+8.014199]	544.2973++ (heavy)	544.297313	2	18.9	559.332973	y4	1	40.43	33.86			
Heparin cofactor 2	SERPIND1	P05546	SVNDLYIQK	SVNDLYIQK[+8.014199]	544.2973++ (heavy)	544.297313	2	18.9	396.269644	y3	1	40.43	33.86			
Heparin cofactor 2	SERPIND1	P05546	QFPILLDFK	QFPILLDFK	560.8237++	560.823692	2	19.7	845.513117	y7	1	93.99	109.12			
Heparin cofactor 2	SERPIND1	P05546	QFPILLDFK	QFPILLDFK	560.8237++	560.823692	2	19.7	635.376289	y5	1	93.99	109.12			
Heparin cofactor 2	SERPIND1	P05546	QFPILLDFK	QFPILLDFK	560.8237++	560.823692	2	19.7	294.181218	y2	1	93.99	109.12			
Heparin cofactor 2	SERPIND1	P05546	QFPILLDFK	QFPILLDFK[+8.014199]	564.8308++ (heavy)	564.830792	2	19.7	853.527316	y7	1	93.99	109.12			
Heparin cofactor 2	SERPIND1	P05546	QFPILLDFK	QFPILLDFK[+8.014199]	564.8308++ (heavy)	564.830792	2	19.7	643.390488	y5	1	93.99	109.12			
Heparin cofactor 2	SERPIND1	P05546	QFPILLDFK	QFPILLDFK[+8.014199]	564.8308++ (heavy)	564.830792	2	19.7	302.195417	y2	1	93.99	109.12			
Heparin cofactor 2	SERPIND1	P05546	NYNLVESLK	NYNLVESLK	540.2902++	540.290213	2	18.9	802.466895	y7	1	52.87	54.74			
Heparin cofactor 2	SERPIND1	P05546	NYNLVESLK	NYNLVESLK	540.2902++	540.290213	2	18.9	575.339903	y5	1	52.87	54.74			
Heparin cofactor 2	SERPIND1	P05546	NYNLVESLK	NYNLVESLK	540.2902++	540.290213	2	18.9	278.113532	b2	1	52.87	54.74			
Heparin cofactor 2	SERPIND1	P05546	NYNLVESLK	NYNLVESLK[+8.014199]	544.2973++ (heavy)	544.297313	2	18.9	810.481094	y7	1	52.87	54.74			
Heparin cofactor 2	SERPIND1	P05546	NYNLVESLK	NYNLVESLK[+8.014199]	544.2973++ (heavy)	544.297313	2	18.9	583.354102	y5	1	52.87	54.74			
Heparin cofactor 2	SERPIND1	P05546	NYNLVESLK	NYNLVESLK[+8.014199]	544.2973++ (heavy)	544.297313	2	18.9	278.113532	b2	1	52.87	54.74			

Histidine-rich glycoprotein	HRG	P04196	DGYLFQLLR	DGYLFQLLR	562.8086++	562.808573	2	19.8	789.498135	y6	1	100.51	107.1	2.1	5.1
Histidine-rich glycoprotein	HRG	P04196	DGYLFQLLR	DGYLFQLLR	562.8086++	562.808573	2	19.8	676.414071	y5	1	100.51	107.1		
Histidine-rich glycoprotein	HRG	P04196	DGYLFQLLR	DGYLFQLLR	562.8086++	562.808573	2	19.8	336.119011	b3	1	100.51	107.1		
Histidine-rich glycoprotein	HRG	P04196	DGYLFQLLR	DGYLFQLLR[+10.008269]	567.8127++ (heavy)	567.812708	2	19.8	799.506404	y6	1	100.51	107.1		
Histidine-rich glycoprotein	HRG	P04196	DGYLFQLLR	DGYLFQLLR[+10.008269]	567.8127++ (heavy)	567.812708	2	19.8	686.42234	y5	1	100.51	107.1		
Histidine-rich glycoprotein	HRG	P04196	DGYLFQLLR	DGYLFQLLR[+10.008269]	567.8127++ (heavy)	567.812708	2	19.8	336.119011	b3	1	100.51	107.1		
Histidine-rich glycoprotein	HRG	P04196	DSPVLIDFFEDTER	DSPVLIDFFEDTER	841.8990++	841.899042	2	30.1	1171.526595	y9	1	116.14	118.52		
Histidine-rich glycoprotein	HRG	P04196	DSPVLIDFFEDTER	DSPVLIDFFEDTER	841.8990++	841.899042	2	30.1	1058.442531	y8	1	116.14	118.52		
Histidine-rich glycoprotein	HRG	P04196	DSPVLIDFFEDTER	DSPVLIDFFEDTER	841.8990++	841.899042	2	30.1	399.187425	b4	1	116.14	118.52		
Histidine-rich glycoprotein	HRG	P04196	DSPVLIDFFEDTER	DSPVLIDFFEDTER[+10.008269]	846.9032++ (heavy)	846.903176	2	30.1	1181.534864	y9	1	116.14	118.52		
Histidine-rich glycoprotein	HRG	P04196	DSPVLIDFFEDTER	DSPVLIDFFEDTER[+10.008269]	846.9032++ (heavy)	846.903176	2	30.1	1068.4508	y8	1	116.14	118.52		
Histidine-rich glycoprotein	HRG	P04196	DSPVLIDFFEDTER	DSPVLIDFFEDTER[+10.008269]	846.9032++ (heavy)	846.903176	2	30.1	399.187425	b4	1	116.14	118.52		
Histidine-rich glycoprotein	HRG	P04196	GGEGTGYFVDFSVR	GGEGTGYFVDFSVR	745.8492++	745.849155	2	26.5	1089.536371	y9	1	79.46	81.31		
Histidine-rich glycoprotein	HRG	P04196	GGEGTGYFVDFSVR	GGEGTGYFVDFSVR	745.8492++	745.849155	2	26.5	869.451579	y7	1	79.46	81.31		
Histidine-rich glycoprotein	HRG	P04196	GGEGTGYFVDFSVR	GGEGTGYFVDFSVR	745.8492++	745.849155	2	26.5	623.314751	y5	1	79.46	81.31		
Histidine-rich glycoprotein	HRG	P04196	GGEGTGYFVDFSVR	GGEGTGYFVDFSVR[+10.008269]	750.8533++ (heavy)	750.85329	2	26.5	1099.54464	y9	1	79.46	81.31		
Histidine-rich glycoprotein	HRG	P04196	GGEGTGYFVDFSVR	GGEGTGYFVDFSVR[+10.008269]	750.8533++ (heavy)	750.85329	2	26.5	879.459848	y7	1	79.46	81.31		
Histidine-rich glycoprotein	HRG	P04196	GGEGTGYFVDFSVR	GGEGTGYFVDFSVR[+10.008269]	750.8533++ (heavy)	750.85329	2	26.5	633.32302	y5	1	79.46	81.31		
Immunoglobulin heavy constan	IGHA1	P01876	DASGVTFTWTPSSGK	DASGVTFTWTPSSGK	770.8675++	770.867545	2	27.5	1111.541851	y10	1	61.59	66.8	3.8	1.5
Immunoglobulin heavy constan	IGHA1	P01876	DASGVTFTWTPSSGK	DASGVTFTWTPSSGK	770.8675++	770.867545	2	27.5	863.425758	y8	1	61.59	66.8		
Immunoglobulin heavy constan	IGHA1	P01876	DASGVTFTWTPSSGK	DASGVTFTWTPSSGK	770.8675++	770.867545	2	27.5	475.251088	y5	1	61.59	66.8		
Immunoglobulin heavy constan	IGHA1	P01876	DASGVTFTWTPSSGK	DASGVTFTWTPSSGK[+8.014199]	774.8746++ (heavy)	774.874644	2	27.5	1119.55605	y10	1	61.59	66.8		
Immunoglobulin heavy constan	IGHA1	P01876	DASGVTFTWTPSSGK	DASGVTFTWTPSSGK[+8.014199]	774.8746++ (heavy)	774.874644	2	27.5	871.439957	y8	1	61.59	66.8		
Immunoglobulin heavy constan	IGHA1	P01876	DASGVTFTWTPSSGK	DASGVTFTWTPSSGK[+8.014199]	774.8746++ (heavy)	774.874644	2	27.5	483.265287	y5	1	61.59	66.8		
Immunoglobulin heavy constan	IGHA1	P01876	TFTCTAAYPESK	TFTC[+57.021464]TAAYPESK	688.3136++	688.31356	2	24.4	866.425424	y8	1	36.38	30.12		
Immunoglobulin heavy constan	IGHA1	P01876	TFTCTAAYPESK	TFTC[+57.021464]TAAYPESK	688.3136++	688.31356	2	24.4	765.377745	y7	1	36.38	30.12		
Immunoglobulin heavy constan	IGHA1	P01876	TFTCTAAYPESK	TFTC[+57.021464]TAAYPESK	688.3136++	688.31356	2	24.4	460.240189	y4	1	36.38	30.12		
Immunoglobulin heavy constan	IGHA1	P01876	TFTCTAAYPESK	TFTC[+57.021464]TAAYPESK[+8.014199]	692.3207++ (heavy)	692.320659	2	24.4	874.439623	y8	1	36.38	30.12		
Immunoglobulin heavy constan	IGHA1	P01876	TFTCTAAYPESK	TFTC[+57.021464]TAAYPESK[+8.014199]	692.3207++ (heavy)	692.320659	2	24.4	773.391944	y7	1	36.38	30.12		
Immunoglobulin heavy constan	IGHA1	P01876	TFTCTAAYPESK	TFTC[+57.021464]TAAYPESK[+8.014199]	692.3207++ (heavy)	692.320659	2	24.4	468.254388	y4	1	36.38	30.12		
Immunoglobulin heavy constan	IGHA1	P01876	TPLTATLSK	TPLTATLSK	466.2766++	466.276575	2	16.2	733.445431	y7	1	32.11	30.4		
Immunoglobulin heavy constan	IGHA1	P01876	TPLTATLSK	TPLTATLSK	466.2766++	466.276575	2	16.2	620.361367	y6	1	32.11	30.4		
Immunoglobulin heavy constan	IGHA1	P01876	TPLTATLSK	TPLTATLSK	466.2766++	466.276575	2	16.2	519.313689	y5	1	32.11	30.4		
Immunoglobulin heavy constan	IGHA1	P01876	TPLTATLSK	TPLTATLSK[+8.014199]	470.2837++ (heavy)	470.283674	2	16.2	741.45963	y7	1	32.11	30.4		
Immunoglobulin heavy constan	IGHA1	P01876	TPLTATLSK	TPLTATLSK[+8.014199]	470.2837++ (heavy)	470.283674	2	16.2	628.375566	y6	1	32.11	30.4		
Immunoglobulin heavy constan	IGHA1	P01876	TPLTATLSK	TPLTATLSK[+8.014199]	470.2837++ (heavy)	470.283674	2	16.2	527.327888	y5	1	32.11	30.4		
Immunoglobulin heavy variable	IGHV3-23	P01764	AEDTAVYYCAK	AEDTAVYYC[+57.021464]AK	645.7872++	645.787178	2	22.8	803.375637	y6	1	21.23	25.7	5.9	0.9
Immunoglobulin heavy variable	IGHV3-23	P01764	AEDTAVYYCAK	AEDTAVYYC[+57.021464]AK	645.7872++	645.787178	2	22.8	704.307223	y5	1	21.23	25.7		
Immunoglobulin heavy variable	IGHV3-23	P01764	AEDTAVYYCAK	AEDTAVYYC[+57.021464]AK	645.7872++	645.787178	2	22.8	541.243895	y4	1	21.23	25.7		
Immunoglobulin heavy variable	IGHV3-23	P01764	AEDTAVYYCAK	AEDTAVYYC[+57.021464]AK[+8.014199]	649.7943++ (heavy)	649.794277	2	22.8	811.389836	y6	1	21.23	25.7		
Immunoglobulin heavy variable	IGHV3-23	P01764	AEDTAVYYCAK	AEDTAVYYC[+57.021464]AK[+8.014199]	649.7943++ (heavy)	649.794277	2	22.8	712.321422	y5	1	21.23	25.7		
Immunoglobulin heavy variable	IGHV3-23	P01764	AEDTAVYYCAK	AEDTAVYYC[+57.021464]AK[+8.014199]	649.7943++ (heavy)	649.794277	2	22.8	549.258094	y4	1	21.23	25.7		
Insulin-like growth factor-bindi	IGFALS	P35858	LEYLLLSR	LEYLLLSR	503.8002++	503.800217	2	17.6	764.466501	y6	1	77.62	73.32	6.3	4.7
Insulin-like growth factor-bindi	IGFALS	P35858	LEYLLLSR	LEYLLLSR	503.8002++	503.800217	2	17.6	601.403172	y5	1	77.62	73.32		
Insulin-like growth factor-bindi	IGFALS	P35858	LEYLLLSR	LEYLLLSR	503.8002++	503.800217	2	17.6	488.319108	y4	1	77.62	73.32		
Insulin-like growth factor-bindi	IGFALS	P35858	LEYLLLSR	LEYLLLSR	503.8002++	503.800217	2	17.6	375.235044	y3	1	77.62	73.32		
Insulin-like growth factor-bindi	IGFALS	P35858	LEYLLLSR	LEYLLLSR[+10.008269]	508.8044++ (heavy)	508.804351	2	17.6	774.47477	y6	1	77.62	73.32		
Insulin-like growth factor-bindi	IGFALS	P35858	LEYLLLSR	LEYLLLSR[+10.008269]	508.8044++ (heavy)	508.804351	2	17.6	611.411441	y5	1	77.62	73.32		
Insulin-like growth factor-bindi	IGFALS	P35858	LEYLLLSR	LEYLLLSR[+10.008269]	508.8044++ (heavy)	508.804351	2	17.6	498.327377	y4	1	77.62	73.32		
Insulin-like growth factor-bindi	IGFALS	P35858	LEYLLLSR	LEYLLLSR[+10.008269]	508.8044++ (heavy)	508.804351	2	17.6	385.243313	y3	1	77.62	73.32		

Insulin-like growth factor-bindi	IGFALS	P35858	DFALQNPSAVPR	DFALQNPSAVPR	657.8437++	657.843676	2	23.3	740.404963	y7	1	53.29	55.25			
Insulin-like growth factor-bindi	IGFALS	P35858	DFALQNPSAVPR	DFALQNPSAVPR	657.8437++	657.843676	2	23.3	626.362036	y6	1	53.29	55.25			
Insulin-like growth factor-bindi	IGFALS	P35858	DFALQNPSAVPR	DFALQNPSAVPR	657.8437++	657.843676	2	23.3	263.102633	b2	1	53.29	55.25			
Insulin-like growth factor-bindi	IGFALS	P35858	DFALQNPSAVPR	DFALQNPSAVPR	657.8437++	657.843676	2	23.3	334.139747	b3	1	53.29	55.25			
Insulin-like growth factor-bindi	IGFALS	P35858	DFALQNPSAVPR	DFALQNPSAVPR[+10.008269]	662.8478++ (heavy)	662.84781	2	23.3	750.413232	y7	1	53.29	55.25			
Insulin-like growth factor-bindi	IGFALS	P35858	DFALQNPSAVPR	DFALQNPSAVPR[+10.008269]	662.8478++ (heavy)	662.84781	2	23.3	636.370305	y6	1	53.29	55.25			
Insulin-like growth factor-bindi	IGFALS	P35858	DFALQNPSAVPR	DFALQNPSAVPR[+10.008269]	662.8478++ (heavy)	662.84781	2	23.3	263.102633	b2	1	53.29	55.25			
Insulin-like growth factor-bindi	IGFALS	P35858	DFALQNPSAVPR	DFALQNPSAVPR[+10.008269]	662.8478++ (heavy)	662.84781	2	23.3	334.139747	b3	1	53.29	55.25			
Inter-alpha-trypsin inhibitor hea	ITIH1	P19827	EVAFDLEIPK	EVAFDLEIPK	580.8135++	580.813521	2	20.4	932.50876	y8	1	76.87	83.06	3.3	1.7	
Inter-alpha-trypsin inhibitor hea	ITIH1	P19827	EVAFDLEIPK	EVAFDLEIPK	580.8135++	580.813521	2	20.4	714.403232	y6	1	76.87	83.06			
Inter-alpha-trypsin inhibitor hea	ITIH1	P19827	EVAFDLEIPK	EVAFDLEIPK	580.8135++	580.813521	2	20.4	599.376289	y5	1	76.87	83.06			
Inter-alpha-trypsin inhibitor hea	ITIH1	P19827	EVAFDLEIPK	EVAFDLEIPK[+8.014199]	584.8206++ (heavy)	584.820621	2	20.4	940.522959	y8	1	76.87	83.06			
Inter-alpha-trypsin inhibitor hea	ITIH1	P19827	EVAFDLEIPK	EVAFDLEIPK[+8.014199]	584.8206++ (heavy)	584.820621	2	20.4	722.417431	y6	1	76.87	83.06			
Inter-alpha-trypsin inhibitor hea	ITIH1	P19827	EVAFDLEIPK	EVAFDLEIPK[+8.014199]	584.8206++ (heavy)	584.820621	2	20.4	607.390488	y5	1	76.87	83.06			
Inter-alpha-trypsin inhibitor hea	ITIH1	P19827	AAISGENAGLVR	AAISGENAGLVR	579.3173++	579.317294	2	20.4	902.46902	y9	1	40.12	29.09			
Inter-alpha-trypsin inhibitor hea	ITIH1	P19827	AAISGENAGLVR	AAISGENAGLVR	579.3173++	579.317294	2	20.4	629.372935	y6	1	40.12	29.09			
Inter-alpha-trypsin inhibitor hea	ITIH1	P19827	AAISGENAGLVR	AAISGENAGLVR	579.3173++	579.317294	2	20.4	714.341694	b8	1	40.12	29.09			
Inter-alpha-trypsin inhibitor hea	ITIH1	P19827	AAISGENAGLVR	AAISGENAGLVR[+10.008269]	584.3214++ (heavy)	584.321428	2	20.4	912.477289	y9	1	40.12	29.09			
Inter-alpha-trypsin inhibitor hea	ITIH1	P19827	AAISGENAGLVR	AAISGENAGLVR[+10.008269]	584.3214++ (heavy)	584.321428	2	20.4	639.381204	y6	1	40.12	29.09			
Inter-alpha-trypsin inhibitor hea	ITIH1	P19827	AAISGENAGLVR	AAISGENAGLVR[+10.008269]	584.3214++ (heavy)	584.321428	2	20.4	714.341694	b8	1	40.12	29.09			
Inter-alpha-trypsin inhibitor hea	ITIH1	P19827	QYYEGSEIVVAGR	QYYEGSEIVVAGR	735.8648++	735.864805	2	26.2	1179.600428	y11	1	56.39	47.19			
Inter-alpha-trypsin inhibitor hea	ITIH1	P19827	QYYEGSEIVVAGR	QYYEGSEIVVAGR	735.8648++	735.864805	2	26.2	1016.5371	y10	1	56.39	47.19			
Inter-alpha-trypsin inhibitor hea	ITIH1	P19827	QYYEGSEIVVAGR	QYYEGSEIVVAGR	735.8648++	735.864805	2	26.2	887.494506	y9	1	56.39	47.19			
Inter-alpha-trypsin inhibitor hea	ITIH1	P19827	QYYEGSEIVVAGR	QYYEGSEIVVAGR[+10.008269]	740.8689++ (heavy)	740.86894	2	26.2	1189.608697	y11	1	56.39	47.19			
Inter-alpha-trypsin inhibitor hea	ITIH1	P19827	QYYEGSEIVVAGR	QYYEGSEIVVAGR[+10.008269]	740.8689++ (heavy)	740.86894	2	26.2	1026.545369	y10	1	56.39	47.19			
Inter-alpha-trypsin inhibitor hea	ITIH1	P19827	QYYEGSEIVVAGR	QYYEGSEIVVAGR[+10.008269]	740.8689++ (heavy)	740.86894	2	26.2	897.502776	y9	1	56.39	47.19			
Inter-alpha-trypsin inhibitor hea	ITIH2	P19823	VVNNSPQPQNVVFDVQIPK	VVNNSPQPQNVVFDVQIPK	708.0479+++	708.047894	3	24.2	945.540394	y8	1	75.87	85.89	4.1	4.4	
Inter-alpha-trypsin inhibitor hea	ITIH2	P19823	VVNNSPQPQNVVFDVQIPK	VVNNSPQPQNVVFDVQIPK	708.0479+++	708.047894	3	24.2	846.47198	y7	1	75.87	85.89			
Inter-alpha-trypsin inhibitor hea	ITIH2	P19823	VVNNSPQPQNVVFDVQIPK	VVNNSPQPQNVVFDVQIPK	708.0479+++	708.047894	3	24.2	739.373329	b7	1	75.87	85.89			
Inter-alpha-trypsin inhibitor hea	ITIH2	P19823	VVNNSPQPQNVVFDVQIPK	VVNNSPQPQNVVFDVQIPK[+8.014199]	710.7193+++ (heavy)	710.719294	3	24.2	953.554593	y8	1	75.87	85.89			
Inter-alpha-trypsin inhibitor hea	ITIH2	P19823	VVNNSPQPQNVVFDVQIPK	VVNNSPQPQNVVFDVQIPK[+8.014199]	710.7193+++ (heavy)	710.719294	3	24.2	854.486179	y7	1	75.87	85.89			
Inter-alpha-trypsin inhibitor hea	ITIH2	P19823	VVNNSPQPQNVVFDVQIPK	VVNNSPQPQNVVFDVQIPK[+8.014199]	710.7193+++ (heavy)	710.719294	3	24.2	739.373329	b7	1	75.87	85.89			
Inter-alpha-trypsin inhibitor hea	ITIH2	P19823	FLHVPDTFEGHFDGVPVISK	FLHVPDTFEGHFDGVPVISK	747.7161+++	747.716144	3	25.6	543.350074	y5	1	99.43	91.33			
Inter-alpha-trypsin inhibitor hea	ITIH2	P19823	FLHVPDTFEGHFDGVPVISK	FLHVPDTFEGHFDGVPVISK	747.7161+++	747.716144	3	25.6	398.218666	b3	1	99.43	91.33			
Inter-alpha-trypsin inhibitor hea	ITIH2	P19823	FLHVPDTFEGHFDGVPVISK	FLHVPDTFEGHFDGVPVISK	747.7161+++	747.716144	3	25.6	497.28708	b4	1	99.43	91.33			
Inter-alpha-trypsin inhibitor hea	ITIH2	P19823	FLHVPDTFEGHFDGVPVISK	FLHVPDTFEGHFDGVPVISK[+8.014199]	750.3875+++ (heavy)	750.387544	3	25.6	551.364273	y5	1	99.43	91.33			
Inter-alpha-trypsin inhibitor hea	ITIH2	P19823	FLHVPDTFEGHFDGVPVISK	FLHVPDTFEGHFDGVPVISK[+8.014199]	750.3875+++ (heavy)	750.387544	3	25.6	398.218666	b3	1	99.43	91.33			
Inter-alpha-trypsin inhibitor hea	ITIH2	P19823	FLHVPDTFEGHFDGVPVISK	FLHVPDTFEGHFDGVPVISK[+8.014199]	750.3875+++ (heavy)	750.387544	3	25.6	497.28708	b4	1	99.43	91.33			
Inter-alpha-trypsin inhibitor hea	ITIH2	P19823	IQPSGGTNINEALLR	IQPSGGTNINEALLR	791.9310++	791.931011	2	28.2	1341.712104	y13	1	64.91	56.77			
Inter-alpha-trypsin inhibitor hea	ITIH2	P19823	IQPSGGTNINEALLR	IQPSGGTNINEALLR	791.9310++	791.931011	2	28.2	1157.627312	y11	1	64.91	56.77			
Inter-alpha-trypsin inhibitor hea	ITIH2	P19823	IQPSGGTNINEALLR	IQPSGGTNINEALLR	791.9310++	791.931011	2	28.2	715.409714	y6	1	64.91	56.77			
Inter-alpha-trypsin inhibitor hea	ITIH2	P19823	IQPSGGTNINEALLR	IQPSGGTNINEALLR[+10.008269]	796.9351++ (heavy)	796.935145	2	28.2	1351.720373	y13	1	64.91	56.77			
Inter-alpha-trypsin inhibitor hea	ITIH2	P19823	IQPSGGTNINEALLR	IQPSGGTNINEALLR[+10.008269]	796.9351++ (heavy)	796.935145	2	28.2	1167.635581	y11	1	64.91	56.77			
Inter-alpha-trypsin inhibitor hea	ITIH2	P19823	IQPSGGTNINEALLR	IQPSGGTNINEALLR[+10.008269]	796.9351++ (heavy)	796.935145	2	28.2	725.417983	y6	1	64.91	56.77			
Inter-alpha-trypsin inhibitor hea	ITIH2	P19823	FYNQVSTPLLR	FYNQVSTPLLR	669.3642++	669.364244	2	23.7	785.487965	y7	1	73.42	65.75			
Inter-alpha-trypsin inhibitor hea	ITIH2	P19823	FYNQVSTPLLR	FYNQVSTPLLR	669.3642++	669.364244	2	23.7	686.419551	y6	1	73.42	65.75			
Inter-alpha-trypsin inhibitor hea	ITIH2	P19823	FYNQVSTPLLR	FYNQVSTPLLR	669.3642++	669.364244	2	23.7	498.339844	y4	1	73.42	65.75			
Inter-alpha-trypsin inhibitor hea	ITIH2	P19823	FYNQVSTPLLR	FYNQVSTPLLR[+10.008269]	674.3684++ (heavy)	674.368379	2	23.7	795.496234	y7	1	73.42	65.75			
Inter-alpha-trypsin inhibitor hea	ITIH2	P19823	FYNQVSTPLLR	FYNQVSTPLLR[+10.008269]	674.3684++ (heavy)	674.368379	2	23.7	696.42782	y6	1	73.42	65.75			
Inter-alpha-trypsin inhibitor hea	ITIH2	P19823	FYNQVSTPLLR	FYNQVSTPLLR[+10.008269]	674.3684++ (heavy)	674.368379	2	23.7	508.348113	y4	1	73.42	65.75			

L-selectin	SELL	P14151	AEIEYLEK	AEIEYLEK	497.7582++	497.758215	2	17.4	794.429447	y6	1	40.39	36.52	4.7	11.7
L-selectin	SELL	P14151	AEIEYLEK	AEIEYLEK	497.7582++	497.758215	2	17.4	681.345383	y5	1	40.39	36.52		
L-selectin	SELL	P14151	AEIEYLEK	AEIEYLEK	497.7582++	497.758215	2	17.4	552.302789	y4	1	40.39	36.52		
L-selectin	SELL	P14151	AEIEYLEK	AEIEYLEK[+8.014199]	501.7653++ (heavy)	501.765314	2	17.4	802.443646	y6	1	40.39	36.52		
L-selectin	SELL	P14151	AEIEYLEK	AEIEYLEK[+8.014199]	501.7653++ (heavy)	501.765314	2	17.4	689.359582	y5	1	40.39	36.52		
L-selectin	SELL	P14151	AEIEYLEK	AEIEYLEK[+8.014199]	501.7653++ (heavy)	501.765314	2	17.4	560.316988	y4	1	40.39	36.52		
L-selectin	SELL	P14151	SYYWIGIR	SYYWIGIR	529.2769++	529.276909	2	18.5	807.451185	y6	1	84.78	77.18		
L-selectin	SELL	P14151	SYYWIGIR	SYYWIGIR	529.2769++	529.276909	2	18.5	644.387856	y5	1	84.78	77.18		
L-selectin	SELL	P14151	SYYWIGIR	SYYWIGIR	529.2769++	529.276909	2	18.5	458.308544	y4	1	84.78	77.18		
L-selectin	SELL	P14151	SYYWIGIR	SYYWIGIR[+10.008269]	534.2810++ (heavy)	534.281044	2	18.5	817.459454	y6	1	84.78	77.18		
L-selectin	SELL	P14151	SYYWIGIR	SYYWIGIR[+10.008269]	534.2810++ (heavy)	534.281044	2	18.5	654.396125	y5	1	84.78	77.18		
L-selectin	SELL	P14151	SYYWIGIR	SYYWIGIR[+10.008269]	534.2810++ (heavy)	534.281044	2	18.5	468.316813	y4	1	84.78	77.18		
Lumican	LUM	P51884	SLEDLQLTHNK	SLEDLQLTHNK	433.2297+++	433.229736	3	14.3	612.346386	y5	1	42.78	36.99	5.5	2.3
Lumican	LUM	P51884	SLEDLQLTHNK	SLEDLQLTHNK	433.2297+++	433.229736	3	14.3	499.262322	y4	1	42.78	36.99		
Lumican	LUM	P51884	SLEDLQLTHNK	SLEDLQLTHNK	433.2297+++	433.229736	3	14.3	398.214643	y3	1	42.78	36.99		
Lumican	LUM	P51884	SLEDLQLTHNK	SLEDLQLTHNK[+8.014199]	435.9011+++ (heavy)	435.901136	3	14.3	620.360585	y5	1	42.78	36.99		
Lumican	LUM	P51884	SLEDLQLTHNK	SLEDLQLTHNK[+8.014199]	435.9011+++ (heavy)	435.901136	3	14.3	507.276521	y4	1	42.78	36.99		
Lumican	LUM	P51884	SLEDLQLTHNK	SLEDLQLTHNK[+8.014199]	435.9011+++ (heavy)	435.901136	3	14.3	406.228842	y3	1	42.78	36.99		
Lumican	LUM	P51884	ISNIPDEYFK	ISNIPDEYFK	613.3086++	613.308603	2	21.6	1112.525866	y9	1	60.76	60.77		
Lumican	LUM	P51884	ISNIPDEYFK	ISNIPDEYFK	613.3086++	613.308603	2	21.6	798.366846	y6	1	60.76	60.77		
Lumican	LUM	P51884	ISNIPDEYFK	ISNIPDEYFK	613.3086++	613.308603	2	21.6	315.166296	b3	1	60.76	60.77		
Lumican	LUM	P51884	ISNIPDEYFK	ISNIPDEYFK[+8.014199]	617.3157++ (heavy)	617.315703	2	21.6	1120.540065	y9	1	60.76	60.77		
Lumican	LUM	P51884	ISNIPDEYFK	ISNIPDEYFK[+8.014199]	617.3157++ (heavy)	617.315703	2	21.6	806.381045	y6	1	60.76	60.77		
Lumican	LUM	P51884	ISNIPDEYFK	ISNIPDEYFK[+8.014199]	617.3157++ (heavy)	617.315703	2	21.6	315.166296	b3	1	60.76	60.77		
Lumican	LUM	P51884	ILGPLSYSK	ILGPLSYSK	489.2869++	489.286942	2	17	751.398481	y7	1	48.64	48.97		
Lumican	LUM	P51884	ILGPLSYSK	ILGPLSYSK	489.2869++	489.286942	2	17	694.377017	y6	1	48.64	48.97		
Lumican	LUM	P51884	ILGPLSYSK	ILGPLSYSK	489.2869++	489.286942	2	17	484.240189	y4	1	48.64	48.97		
Lumican	LUM	P51884	ILGPLSYSK	ILGPLSYSK[+8.014199]	493.2940++ (heavy)	493.294042	2	17	759.41268	y7	1	48.64	48.97		
Lumican	LUM	P51884	ILGPLSYSK	ILGPLSYSK[+8.014199]	493.2940++ (heavy)	493.294042	2	17	702.391216	y6	1	48.64	48.97		
Lumican	LUM	P51884	ILGPLSYSK	ILGPLSYSK[+8.014199]	493.2940++ (heavy)	493.294042	2	17	492.254388	y4	1	48.64	48.97		
Mannan-binding lectin serine p	MASP2	O00187	WTLTAPPGYR	WTLTAPPGYR	581.3062++	581.306198	2	20.4	874.478128	y8	1	60.43	64.49	8.5	16.0
Mannan-binding lectin serine p	MASP2	O00187	WTLTAPPGYR	WTLTAPPGYR	581.3062++	581.306198	2	20.4	761.394064	y7	1	60.43	64.49		
Mannan-binding lectin serine p	MASP2	O00187	WTLTAPPGYR	WTLTAPPGYR	581.3062++	581.306198	2	20.4	660.346386	y6	1	60.43	64.49		
Mannan-binding lectin serine p	MASP2	O00187	WTLTAPPGYR	WTLTAPPGYR	581.3062++	581.306198	2	20.4	589.309272	y5	1	60.43	64.49		
Mannan-binding lectin serine p	MASP2	O00187	WTLTAPPGYR	WTLTAPPGYR[+10.008269]	586.3103++ (heavy)	586.310332	2	20.4	884.486397	y8	1	60.43	64.49		
Mannan-binding lectin serine p	MASP2	O00187	WTLTAPPGYR	WTLTAPPGYR[+10.008269]	586.3103++ (heavy)	586.310332	2	20.4	771.402333	y7	1	60.43	64.49		
Mannan-binding lectin serine p	MASP2	O00187	WTLTAPPGYR	WTLTAPPGYR[+10.008269]	586.3103++ (heavy)	586.310332	2	20.4	670.354655	y6	1	60.43	64.49		
Mannan-binding lectin serine p	MASP2	O00187	WTLTAPPGYR	WTLTAPPGYR[+10.008269]	586.3103++ (heavy)	586.310332	2	20.4	599.317541	y5	1	60.43	64.49		
Pigment epithelium-derived fac	SERPINF1	P36955	LAAAVSNFGYDLYR	LAAAVSNFGYDLYR	780.3963++	780.396272	2	27.8	1233.589864	y10	1	84.42	81.14	3.7	2.5
Pigment epithelium-derived fac	SERPINF1	P36955	LAAAVSNFGYDLYR	LAAAVSNFGYDLYR	780.3963++	780.396272	2	27.8	1134.52145	y9	1	84.42	81.14		
Pigment epithelium-derived fac	SERPINF1	P36955	LAAAVSNFGYDLYR	LAAAVSNFGYDLYR	780.3963++	780.396272	2	27.8	786.37808	y6	1	84.42	81.14		
Pigment epithelium-derived fac	SERPINF1	P36955	LAAAVSNFGYDLYR	LAAAVSNFGYDLYR[+10.008269]	785.4004++ (heavy)	785.400407	2	27.8	1243.598133	y10	1	84.42	81.14		
Pigment epithelium-derived fac	SERPINF1	P36955	LAAAVSNFGYDLYR	LAAAVSNFGYDLYR[+10.008269]	785.4004++ (heavy)	785.400407	2	27.8	1144.529719	y9	1	84.42	81.14		
Pigment epithelium-derived fac	SERPINF1	P36955	LAAAVSNFGYDLYR	LAAAVSNFGYDLYR[+10.008269]	785.4004++ (heavy)	785.400407	2	27.8	796.386349	y6	1	84.42	81.14		
Pigment epithelium-derived fac	SERPINF1	P36955	ALYYDLISSPDIHGTYK	ALYYDLISSPDIHGTYK	652.6632+++	652.663157	3	22.2	1104.532014	y10	1	97.88	80.83		
Pigment epithelium-derived fac	SERPINF1	P36955	ALYYDLISSPDIHGTYK	ALYYDLISSPDIHGTYK	652.6632+++	652.663157	3	22.2	930.467957	y8	1	97.88	80.83		
Pigment epithelium-derived fac	SERPINF1	P36955	ALYYDLISSPDIHGTYK	ALYYDLISSPDIHGTYK	652.6632+++	652.663157	3	22.2	605.304186	y5	1	97.88	80.83		
Pigment epithelium-derived fac	SERPINF1	P36955	ALYYDLISSPDIHGTYK	ALYYDLISSPDIHGTYK[+8.014199]	655.3346+++ (heavy)	655.334557	3	22.2	1112.546213	y10	1	97.88	80.83		
Pigment epithelium-derived fac	SERPINF1	P36955	ALYYDLISSPDIHGTYK	ALYYDLISSPDIHGTYK[+8.014199]	655.3346+++ (heavy)	655.334557	3	22.2	938.482156	y8	1	97.88	80.83		
Pigment epithelium-derived fac	SERPINF1	P36955	ALYYDLISSPDIHGTYK	ALYYDLISSPDIHGTYK[+8.014199]	655.3346+++ (heavy)	655.334557	3	22.2	613.318385	y5	1	97.88	80.83		

Pigment epithelium-derived fac	SERPINF1	P36955	TVQAVLTVPK	TVQAVLTVPK	528.3266++	528.326599	2	18.5	855.529829	y8	1	45.68	47.68		
Pigment epithelium-derived fac	SERPINF1	P36955	TVQAVLTVPK	TVQAVLTVPK	528.3266++	528.326599	2	18.5	727.471252	y7	1	45.68	47.68		
Pigment epithelium-derived fac	SERPINF1	P36955	TVQAVLTVPK	TVQAVLTVPK	528.3266++	528.326599	2	18.5	557.365724	y5	1	45.68	47.68		
Pigment epithelium-derived fac	SERPINF1	P36955	TVQAVLTVPK	TVQAVLTVPK[+8.014199]	532.3337++ (heavy)	532.333698	2	18.5	863.544028	y8	1	45.68	47.68		
Pigment epithelium-derived fac	SERPINF1	P36955	TVQAVLTVPK	TVQAVLTVPK[+8.014199]	532.3337++ (heavy)	532.333698	2	18.5	735.485451	y7	1	45.68	47.68		
Pigment epithelium-derived fac	SERPINF1	P36955	TVQAVLTVPK	TVQAVLTVPK[+8.014199]	532.3337++ (heavy)	532.333698	2	18.5	565.379923	y5	1	45.68	47.68		
Pigment epithelium-derived fac	SERPINF1	P36955	LQSLFDSPDFSK	LQSLFDSPDFSK	692.3432++	692.343174	2	24.6	1142.536431	y10	1	78.26	75.67		
Pigment epithelium-derived fac	SERPINF1	P36955	LQSLFDSPDFSK	LQSLFDSPDFSK	692.3432++	692.343174	2	24.6	680.324982	y6	1	78.26	75.67		
Pigment epithelium-derived fac	SERPINF1	P36955	LQSLFDSPDFSK	LQSLFDSPDFSK	692.3432++	692.343174	2	24.6	593.292953	y5	1	78.26	75.67		
Pigment epithelium-derived fac	SERPINF1	P36955	LQSLFDSPDFSK	LQSLFDSPDFSK[+8.014199]	696.3503++ (heavy)	696.350274	2	24.6	1150.55063	y10	1	78.26	75.67		
Pigment epithelium-derived fac	SERPINF1	P36955	LQSLFDSPDFSK	LQSLFDSPDFSK[+8.014199]	696.3503++ (heavy)	696.350274	2	24.6	688.339181	y6	1	78.26	75.67		
Pigment epithelium-derived fac	SERPINF1	P36955	LQSLFDSPDFSK	LQSLFDSPDFSK[+8.014199]	696.3503++ (heavy)	696.350274	2	24.6	601.307152	y5	1	78.26	75.67		
Plasma protease C1 inhibitor	SERPING1	P05155	TNLESILSYPK	TNLESILSYPK	632.8428++	632.84281	2	22.3	1049.587738	y9	1	71.35	80.97	5.3	3.9
Plasma protease C1 inhibitor	SERPING1	P05155	TNLESILSYPK	TNLESILSYPK	632.8428++	632.84281	2	22.3	936.503674	y8	1	71.35	80.97		
Plasma protease C1 inhibitor	SERPING1	P05155	TNLESILSYPK	TNLESILSYPK	632.8428++	632.84281	2	22.3	807.461081	y7	1	71.35	80.97		
Plasma protease C1 inhibitor	SERPING1	P05155	TNLESILSYPK	TNLESILSYPK[+8.014199]	636.8499++ (heavy)	636.84991	2	22.3	1057.601937	y9	1	71.35	80.97		
Plasma protease C1 inhibitor	SERPING1	P05155	TNLESILSYPK	TNLESILSYPK[+8.014199]	636.8499++ (heavy)	636.84991	2	22.3	944.517873	y8	1	71.35	80.97		
Plasma protease C1 inhibitor	SERPING1	P05155	TNLESILSYPK	TNLESILSYPK[+8.014199]	636.8499++ (heavy)	636.84991	2	22.3	815.47528	y7	1	71.35	80.97		
Plasma protease C1 inhibitor	SERPING1	P05155	GVTSVSQIFHSPDLAIR	GVTSVSQIFHSPDLAIR	609.6635+++	609.663492	3	20.6	908.494841	y8	1	82.33	86.72		
Plasma protease C1 inhibitor	SERPING1	P05155	GVTSVSQIFHSPDLAIR	GVTSVSQIFHSPDLAIR	609.6635+++	609.663492	3	20.6	771.435929	y7	1	82.33	86.72		
Plasma protease C1 inhibitor	SERPING1	P05155	GVTSVSQIFHSPDLAIR	GVTSVSQIFHSPDLAIR	609.6635+++	609.663492	3	20.6	684.403901	y6	1	82.33	86.72		
Plasma protease C1 inhibitor	SERPING1	P05155	GVTSVSQIFHSPDLAIR	GVTSVSQIFHSPDLAIR	609.6635+++	609.663492	3	20.6	472.324194	y4	1	82.33	86.72		
Plasma protease C1 inhibitor	SERPING1	P05155	GVTSVSQIFHSPDLAIR	GVTSVSQIFHSPDLAIR[+10.008269]	612.9996+++ (heavy)	612.999581	3	20.6	918.50311	y8	1	82.33	86.72		
Plasma protease C1 inhibitor	SERPING1	P05155	GVTSVSQIFHSPDLAIR	GVTSVSQIFHSPDLAIR[+10.008269]	612.9996+++ (heavy)	612.999581	3	20.6	781.444198	y7	1	82.33	86.72		
Plasma protease C1 inhibitor	SERPING1	P05155	GVTSVSQIFHSPDLAIR	GVTSVSQIFHSPDLAIR[+10.008269]	612.9996+++ (heavy)	612.999581	3	20.6	694.41217	y6	1	82.33	86.72		
Plasma protease C1 inhibitor	SERPING1	P05155	GVTSVSQIFHSPDLAIR	GVTSVSQIFHSPDLAIR[+10.008269]	612.9996+++ (heavy)	612.999581	3	20.6	482.332463	y4	1	82.33	86.72		
Plasma protease C1 inhibitor	SERPING1	P05155	FQPTLLTLPR	FQPTLLTLPR	593.3531++	593.353148	2	20.9	910.572029	y8	1	80.89	84.13		
Plasma protease C1 inhibitor	SERPING1	P05155	FQPTLLTLPR	FQPTLLTLPR	593.3531++	593.353148	2	20.9	599.387522	y5	1	80.89	84.13		
Plasma protease C1 inhibitor	SERPING1	P05155	FQPTLLTLPR	FQPTLLTLPR	593.3531++	593.353148	2	20.9	276.134267	b2	1	80.89	84.13		
Plasma protease C1 inhibitor	SERPING1	P05155	FQPTLLTLPR	FQPTLLTLPR[+10.008269]	598.3573++ (heavy)	598.357283	2	20.9	920.580298	y8	1	80.89	84.13		
Plasma protease C1 inhibitor	SERPING1	P05155	FQPTLLTLPR	FQPTLLTLPR[+10.008269]	598.3573++ (heavy)	598.357283	2	20.9	609.395791	y5	1	80.89	84.13		
Plasma protease C1 inhibitor	SERPING1	P05155	FQPTLLTLPR	FQPTLLTLPR[+10.008269]	598.3573++ (heavy)	598.357283	2	20.9	276.134267	b2	1	80.89	84.13		
Plasminogen	PLG	P00747	QLGAGSIEECAAK	QLGAGSIEEC[+57.021464]AAK	667.3245++	667.324459	2	23.6	1092.499	y11	1	25.73	31.92	6.0	0.4
Plasminogen	PLG	P00747	QLGAGSIEECAAK	QLGAGSIEEC[+57.021464]AAK	667.3245++	667.324459	2	23.6	964.440422	y9	1	25.73	31.92		
Plasminogen	PLG	P00747	QLGAGSIEECAAK	QLGAGSIEEC[+57.021464]AAK	667.3245++	667.324459	2	23.6	707.302866	y6	1	25.73	31.92		
Plasminogen	PLG	P00747	QLGAGSIEECAAK	QLGAGSIEEC[+57.021464]AAK[+8.014199]	671.3316++ (heavy)	671.331558	2	23.6	1100.513199	y11	1	25.73	31.92		
Plasminogen	PLG	P00747	QLGAGSIEECAAK	QLGAGSIEEC[+57.021464]AAK[+8.014199]	671.3316++ (heavy)	671.331558	2	23.6	972.454621	y9	1	25.73	31.92		
Plasminogen	PLG	P00747	QLGAGSIEECAAK	QLGAGSIEEC[+57.021464]AAK[+8.014199]	671.3316++ (heavy)	671.331558	2	23.6	715.317065	y6	1	25.73	31.92		
Plasminogen	PLG	P00747	HSIFTPETNPR	HSIFTPETNPR	433.5544+++	433.554442	3	14.3	713.357679	y6	1	41.16	28.03		
Plasminogen	PLG	P00747	HSIFTPETNPR	HSIFTPETNPR	433.5544+++	433.554442	3	14.3	487.262322	y4	1	41.16	28.03		
Plasminogen	PLG	P00747	HSIFTPETNPR	HSIFTPETNPR	433.5544+++	433.554442	3	14.3	485.250694	b4	1	41.16	28.03		
Plasminogen	PLG	P00747	HSIFTPETNPR	HSIFTPETNPR[+10.008269]	436.8905+++ (heavy)	436.890532	3	14.3	723.365948	y6	1	41.16	28.03		
Plasminogen	PLG	P00747	HSIFTPETNPR	HSIFTPETNPR[+10.008269]	436.8905+++ (heavy)	436.890532	3	14.3	497.270591	y4	1	41.16	28.03		
Plasminogen	PLG	P00747	HSIFTPETNPR	HSIFTPETNPR[+10.008269]	436.8905+++ (heavy)	436.890532	3	14.3	485.250694	b4	1	41.16	28.03		
Plasminogen	PLG	P00747	NPDGDVGGPWCYTTNPR	NPDGDVGGPWC[+57.021464]YTTNPR	953.4129++	953.412856	2	34.2	1308.578982	y11	1	56.68	58.3		
Plasminogen	PLG	P00747	NPDGDVGGPWCYTTNPR	NPDGDVGGPWC[+57.021464]YTTNPR	953.4129++	953.412856	2	34.2	1194.536054	y9	1	56.68	58.3		
Plasminogen	PLG	P00747	NPDGDVGGPWCYTTNPR	NPDGDVGGPWC[+57.021464]YTTNPR	953.4129++	953.412856	2	34.2	588.31	y5	1	56.68	58.3		
Plasminogen	PLG	P00747	NPDGDVGGPWCYTTNPR	NPDGDVGGPWC[+57.021464]YTTNPR[+10.	958.4170++ (heavy)	958.416991	2	34.2	1318.587251	y11	1	56.68	58.3		
Plasminogen	PLG	P00747	NPDGDVGGPWCYTTNPR	NPDGDVGGPWC[+57.021464]YTTNPR[+10.	958.4170++ (heavy)	958.416991	2	34.2	1204.544323	y9	1	56.68	58.3		
Plasminogen	PLG	P00747	NPDGDVGGPWCYTTNPR	NPDGDVGGPWC[+57.021464]YTTNPR[+10.	958.4170++ (heavy)	958.416991	2	34.2	598.318269	y5	1	56.68	58.3		

Plasminogen	PLG	P00747	EAQLPVIENK	EAQLPVIENK	570.8166++	570.816595	2	20.1	699.403566	y6	1	42.81	40.8		
Plasminogen	PLG	P00747	EAQLPVIENK	EAQLPVIENK	570.8166++	570.816595	2	20.1	503.282388	y4	1	42.81	40.8		
Plasminogen	PLG	P00747	EAQLPVIENK	EAQLPVIENK	570.8166++	570.816595	2	20.1	329.14556	b3	1	42.81	40.8		
Plasminogen	PLG	P00747	EAQLPVIENK	EAQLPVIENK[+8.014199]	574.8237++ (heavy)	574.823695	2	20.1	707.417765	y6	1	42.81	40.8		
Plasminogen	PLG	P00747	EAQLPVIENK	EAQLPVIENK[+8.014199]	574.8237++ (heavy)	574.823695	2	20.1	511.296587	y4	1	42.81	40.8		
Plasminogen	PLG	P00747	EAQLPVIENK	EAQLPVIENK[+8.014199]	574.8237++ (heavy)	574.823695	2	20.1	329.14556	b3	1	42.81	40.8		
Pregnancy zone protein	PZP	P20742	SLFTDLVAEK	SLFTDLVAEK	561.8057++	561.805696	2	19.7	922.488024	y8	1	85.81	85.73	3.5	7.2
Pregnancy zone protein	PZP	P20742	SLFTDLVAEK	SLFTDLVAEK	561.8057++	561.805696	2	19.7	775.41961	y7	1	85.81	85.73		
Pregnancy zone protein	PZP	P20742	SLFTDLVAEK	SLFTDLVAEK	561.8057++	561.805696	2	19.7	674.371932	y6	1	85.81	85.73		
Pregnancy zone protein	PZP	P20742	SLFTDLVAEK	SLFTDLVAEK[+8.014199]	565.8128++ (heavy)	565.812796	2	19.7	930.502223	y8	1	85.81	85.73		
Pregnancy zone protein	PZP	P20742	SLFTDLVAEK	SLFTDLVAEK[+8.014199]	565.8128++ (heavy)	565.812796	2	19.7	783.433809	y7	1	85.81	85.73		
Pregnancy zone protein	PZP	P20742	SLFTDLVAEK	SLFTDLVAEK[+8.014199]	565.8128++ (heavy)	565.812796	2	19.7	682.386131	y6	1	85.81	85.73		
Pregnancy zone protein	PZP	P20742	TLLVEAEGIEQEK	TLLVEAEGIEQEK	729.8879++	729.887946	2	25.9	1131.552809	y10	1	70.3	62.41		
Pregnancy zone protein	PZP	P20742	TLLVEAEGIEQEK	TLLVEAEGIEQEK	729.8879++	729.887946	2	25.9	1032.484395	y9	1	70.3	62.41		
Pregnancy zone protein	PZP	P20742	TLLVEAEGIEQEK	TLLVEAEGIEQEK	729.8879++	729.887946	2	25.9	903.441802	y8	1	70.3	62.41		
Pregnancy zone protein	PZP	P20742	TLLVEAEGIEQEK	TLLVEAEGIEQEK	729.8879++	729.887946	2	25.9	703.362095	y6	1	70.3	62.41		
Pregnancy zone protein	PZP	P20742	TLLVEAEGIEQEK	TLLVEAEGIEQEK[+8.014199]	733.8950++ (heavy)	733.895045	2	25.9	1139.567008	y10	1	70.3	62.41		
Pregnancy zone protein	PZP	P20742	TLLVEAEGIEQEK	TLLVEAEGIEQEK[+8.014199]	733.8950++ (heavy)	733.895045	2	25.9	1040.498594	y9	1	70.3	62.41		
Pregnancy zone protein	PZP	P20742	TLLVEAEGIEQEK	TLLVEAEGIEQEK[+8.014199]	733.8950++ (heavy)	733.895045	2	25.9	911.456001	y8	1	70.3	62.41		
Pregnancy zone protein	PZP	P20742	TLLVEAEGIEQEK	TLLVEAEGIEQEK[+8.014199]	733.8950++ (heavy)	733.895045	2	25.9	711.376294	y6	1	70.3	62.41		
Pregnancy zone protein	PZP	P20742	AVGYLITGYQR	AVGYLITGYQR	620.8379++	620.837862	2	21.9	850.478128	y7	1	59.57	57.35		
Pregnancy zone protein	PZP	P20742	AVGYLITGYQR	AVGYLITGYQR	620.8379++	620.837862	2	21.9	737.394064	y6	1	59.57	57.35		
Pregnancy zone protein	PZP	P20742	AVGYLITGYQR	AVGYLITGYQR	620.8379++	620.837862	2	21.9	624.31	y5	1	59.57	57.35		
Pregnancy zone protein	PZP	P20742	AVGYLITGYQR	AVGYLITGYQR	620.8379++	620.837862	2	21.9	523.262322	y4	1	59.57	57.35		
Pregnancy zone protein	PZP	P20742	AVGYLITGYQR	AVGYLITGYQR[+10.008269]	625.8420++ (heavy)	625.841997	2	21.9	860.486397	y7	1	59.57	57.35		
Pregnancy zone protein	PZP	P20742	AVGYLITGYQR	AVGYLITGYQR[+10.008269]	625.8420++ (heavy)	625.841997	2	21.9	747.402333	y6	1	59.57	57.35		
Pregnancy zone protein	PZP	P20742	AVGYLITGYQR	AVGYLITGYQR[+10.008269]	625.8420++ (heavy)	625.841997	2	21.9	634.318269	y5	1	59.57	57.35		
Pregnancy zone protein	PZP	P20742	AVGYLITGYQR	AVGYLITGYQR[+10.008269]	625.8420++ (heavy)	625.841997	2	21.9	533.270591	y4	1	59.57	57.35		
Serotransferrin	TF	P02787	HSTIFENLANK	HSTIFENLANK	637.3304++	637.330401	2	22.5	1136.594615	y10	1	65.97	41.24	5.7	2.0
Serotransferrin	TF	P02787	HSTIFENLANK	HSTIFENLANK	637.3304++	637.330401	2	22.5	688.36243	y6	1	65.97	41.24		
Serotransferrin	TF	P02787	HSTIFENLANK	HSTIFENLANK	637.3304++	637.330401	2	22.5	225.098216	b2	1	65.97	41.24		
Serotransferrin	TF	P02787	HSTIFENLANK	HSTIFENLANK	637.3304++	637.330401	2	22.5	829.383893	b7	1	65.97	41.24		
Serotransferrin	TF	P02787	HSTIFENLANK	HSTIFENLANK[+8.014199]	641.3375++ (heavy)	641.337501	2	22.5	1144.608814	y10	1	65.97	41.24		
Serotransferrin	TF	P02787	HSTIFENLANK	HSTIFENLANK[+8.014199]	641.3375++ (heavy)	641.337501	2	22.5	696.376629	y6	1	65.97	41.24		
Serotransferrin	TF	P02787	HSTIFENLANK	HSTIFENLANK[+8.014199]	641.3375++ (heavy)	641.337501	2	22.5	225.098216	b2	1	65.97	41.24		
Serotransferrin	TF	P02787	HSTIFENLANK	HSTIFENLANK[+8.014199]	641.3375++ (heavy)	641.337501	2	22.5	829.383893	b7	1	65.97	41.24		
Serotransferrin	TF	P02787	EFQLFSSPHGK	EFQLFSSPHGK	426.2155+++	426.215538	3	14	612.31	y6	1	55.5	51.1		
Serotransferrin	TF	P02787	EFQLFSSPHGK	EFQLFSSPHGK	426.2155+++	426.215538	3	14	525.277972	y5	1	55.5	51.1		
Serotransferrin	TF	P02787	EFQLFSSPHGK	EFQLFSSPHGK	426.2155+++	426.215538	3	14	438.245943	y4	1	55.5	51.1		
Serotransferrin	TF	P02787	EFQLFSSPHGK	EFQLFSSPHGK[+8.014199]	428.8869+++ (heavy)	428.886938	3	14	620.324199	y6	1	55.5	51.1		
Serotransferrin	TF	P02787	EFQLFSSPHGK	EFQLFSSPHGK[+8.014199]	428.8869+++ (heavy)	428.886938	3	14	533.292171	y5	1	55.5	51.1		
Serotransferrin	TF	P02787	EFQLFSSPHGK	EFQLFSSPHGK[+8.014199]	428.8869+++ (heavy)	428.886938	3	14	446.260142	y4	1	55.5	51.1		
Serotransferrin	TF	P02787	YLGEEYVK	YLGEEYVK	500.7529++	500.752932	2	17.5	837.43526	y7	1	43	41.65		
Serotransferrin	TF	P02787	YLGEEYVK	YLGEEYVK	500.7529++	500.752932	2	17.5	724.351196	y6	1	43	41.65		
Serotransferrin	TF	P02787	YLGEEYVK	YLGEEYVK	500.7529++	500.752932	2	17.5	538.287139	y4	1	43	41.65		
Serotransferrin	TF	P02787	YLGEEYVK	YLGEEYVK[+8.014199]	504.7600++ (heavy)	504.760032	2	17.5	845.449459	y7	1	43	41.65		
Serotransferrin	TF	P02787	YLGEEYVK	YLGEEYVK[+8.014199]	504.7600++ (heavy)	504.760032	2	17.5	732.365395	y6	1	43	41.65		
Serotransferrin	TF	P02787	YLGEEYVK	YLGEEYVK[+8.014199]	504.7600++ (heavy)	504.760032	2	17.5	546.301338	y4	1	43	41.65		
Serum amyloid A-4 protein	SAA4	P35542	EALQGVGDMGR	EALQGVGDMGR	566.7744++	566.774405	2	19.9	819.377762	y8	1	39.01	32.86	6.9	2.5
Serum amyloid A-4 protein	SAA4	P35542	EALQGVGDMGR	EALQGVGDMGR	566.7744++	566.774405	2	19.9	691.319185	y7	1	39.01	32.86		

Serum amyloid A-4 protein	SAA4	P35542	EALQGVGDMGR	EALQGVGDMGR	566.7744++	566.774405	2	19.9	535.229307	y5	1	39.01	32.86		
Serum amyloid A-4 protein	SAA4	P35542	EALQGVGDMGR	EALQGVGDMGR[+10.008269]	571.7785++ (heavy)	571.778539	2	19.9	829.386031	y8	1	39.01	32.86		
Serum amyloid A-4 protein	SAA4	P35542	EALQGVGDMGR	EALQGVGDMGR[+10.008269]	571.7785++ (heavy)	571.778539	2	19.9	701.327454	y7	1	39.01	32.86		
Serum amyloid A-4 protein	SAA4	P35542	EALQGVGDMGR	EALQGVGDMGR[+10.008269]	571.7785++ (heavy)	571.778539	2	19.9	545.237576	y5	1	39.01	32.86		
Serum amyloid A-4 protein	SAA4	P35542	AYWDIMISNHQNSNR	AYWDIMISNHQNSNR	616.9530+++	616.953048	3	20.9	1069.513344	y9	1	67.04	69.44		
Serum amyloid A-4 protein	SAA4	P35542	AYWDIMISNHQNSNR	AYWDIMISNHQNSNR	616.9530+++	616.953048	3	20.9	956.42928	y8	1	67.04	69.44		
Serum amyloid A-4 protein	SAA4	P35542	AYWDIMISNHQNSNR	AYWDIMISNHQNSNR	616.9530+++	616.953048	3	20.9	869.397252	y7	1	67.04	69.44		
Serum amyloid A-4 protein	SAA4	P35542	AYWDIMISNHQNSNR	AYWDIMISNHQNSNR	616.9530+++	616.953048	3	20.9	755.354325	y6	1	67.04	69.44		
Serum amyloid A-4 protein	SAA4	P35542	AYWDIMISNHQNSNR	AYWDIMISNHQNSNR	616.9530+++	616.953048	3	20.9	618.295413	y5	1	67.04	69.44		
Serum amyloid A-4 protein	SAA4	P35542	AYWDIMISNHQNSNR	AYWDIMISNHQNSNR[+10.008269]	620.2891+++ (heavy)	620.289138	3	20.9	1079.521613	y9	1	67.04	69.44		
Serum amyloid A-4 protein	SAA4	P35542	AYWDIMISNHQNSNR	AYWDIMISNHQNSNR[+10.008269]	620.2891+++ (heavy)	620.289138	3	20.9	966.437549	y8	1	67.04	69.44		
Serum amyloid A-4 protein	SAA4	P35542	AYWDIMISNHQNSNR	AYWDIMISNHQNSNR[+10.008269]	620.2891+++ (heavy)	620.289138	3	20.9	879.405521	y7	1	67.04	69.44		
Serum amyloid A-4 protein	SAA4	P35542	AYWDIMISNHQNSNR	AYWDIMISNHQNSNR[+10.008269]	620.2891+++ (heavy)	620.289138	3	20.9	765.362594	y6	1	67.04	69.44		
Serum amyloid A-4 protein	SAA4	P35542	AYWDIMISNHQNSNR	AYWDIMISNHQNSNR[+10.008269]	620.2891+++ (heavy)	620.289138	3	20.9	628.303682	y5	1	67.04	69.44		
Serum amyloid P-component	APCS	P02743	AYSLFSYNTQGR	AYSLFSYNTQGR	703.8386++	703.83859	2	25	972.45337	y8	1	59.44	63.8	8.2	2.2
Serum amyloid P-component	APCS	P02743	AYSLFSYNTQGR	AYSLFSYNTQGR	703.8386++	703.83859	2	25	825.384956	y7	1	59.44	63.8		
Serum amyloid P-component	APCS	P02743	AYSLFSYNTQGR	AYSLFSYNTQGR	703.8386++	703.83859	2	25	738.352928	y6	1	59.44	63.8		
Serum amyloid P-component	APCS	P02743	AYSLFSYNTQGR	AYSLFSYNTQGR[+10.008269]	708.8427++ (heavy)	708.842725	2	25	982.461639	y8	1	59.44	63.8		
Serum amyloid P-component	APCS	P02743	AYSLFSYNTQGR	AYSLFSYNTQGR[+10.008269]	708.8427++ (heavy)	708.842725	2	25	835.393225	y7	1	59.44	63.8		
Serum amyloid P-component	APCS	P02743	AYSLFSYNTQGR	AYSLFSYNTQGR[+10.008269]	708.8427++ (heavy)	708.842725	2	25	748.361197	y6	1	59.44	63.8		
Serum amyloid P-component	APCS	P02743	DNELLVYK	DNELLVYK	497.2662++	497.266207	2	17.3	522.32861	y4	1	52.15	46.54		
Serum amyloid P-component	APCS	P02743	DNELLVYK	DNELLVYK	497.2662++	497.266207	2	17.3	409.244546	y3	1	52.15	46.54		
Serum amyloid P-component	APCS	P02743	DNELLVYK	DNELLVYK	497.2662++	497.266207	2	17.3	310.176132	y2	1	52.15	46.54		
Serum amyloid P-component	APCS	P02743	DNELLVYK	DNELLVYK[+8.014199]	501.2733++ (heavy)	501.273306	2	17.3	530.342809	y4	1	52.15	46.54		
Serum amyloid P-component	APCS	P02743	DNELLVYK	DNELLVYK[+8.014199]	501.2733++ (heavy)	501.273306	2	17.3	417.258745	y3	1	52.15	46.54		
Serum amyloid P-component	APCS	P02743	DNELLVYK	DNELLVYK[+8.014199]	501.2733++ (heavy)	501.273306	2	17.3	318.190331	y2	1	52.15	46.54		
Serum amyloid P-component	APCS	P02743	VGEYSLYIGR	VGEYSLYIGR	578.8035++	578.803488	2	20.3	871.467229	y7	1	60.33	58.13		
Serum amyloid P-component	APCS	P02743	VGEYSLYIGR	VGEYSLYIGR	578.8035++	578.803488	2	20.3	708.403901	y6	1	60.33	58.13		
Serum amyloid P-component	APCS	P02743	VGEYSLYIGR	VGEYSLYIGR	578.8035++	578.803488	2	20.3	508.287808	y4	1	60.33	58.13		
Serum amyloid P-component	APCS	P02743	VGEYSLYIGR	VGEYSLYIGR[+10.008269]	583.8076++ (heavy)	583.807622	2	20.3	881.475498	y7	1	60.33	58.13		
Serum amyloid P-component	APCS	P02743	VGEYSLYIGR	VGEYSLYIGR[+10.008269]	583.8076++ (heavy)	583.807622	2	20.3	718.41217	y6	1	60.33	58.13		
Serum amyloid P-component	APCS	P02743	VGEYSLYIGR	VGEYSLYIGR[+10.008269]	583.8076++ (heavy)	583.807622	2	20.3	518.296077	y4	1	60.33	58.13		
Tetranectin	CLEC3B	P05452	LDTLAQEVALLK	LDTLAQEVALLK	657.3874++	657.387385	2	23.3	871.524744	y8	1	91.31	91.49	5.7	3.6
Tetranectin	CLEC3B	P05452	LDTLAQEVALLK	LDTLAQEVALLK	657.3874++	657.387385	2	23.3	800.48763	y7	1	91.31	91.49		
Tetranectin	CLEC3B	P05452	LDTLAQEVALLK	LDTLAQEVALLK	657.3874++	657.387385	2	23.3	330.165962	b3	1	91.31	91.49		
Tetranectin	CLEC3B	P05452	LDTLAQEVALLK	LDTLAQEVALLK[+8.014199]	661.3945++ (heavy)	661.394484	2	23.3	879.538943	y8	1	91.31	91.49		
Tetranectin	CLEC3B	P05452	LDTLAQEVALLK	LDTLAQEVALLK[+8.014199]	661.3945++ (heavy)	661.394484	2	23.3	808.501829	y7	1	91.31	91.49		
Tetranectin	CLEC3B	P05452	LDTLAQEVALLK	LDTLAQEVALLK[+8.014199]	661.3945++ (heavy)	661.394484	2	23.3	330.165962	b3	1	91.31	91.49		
Tetranectin	CLEC3B	P05452	EQQALQTVCLK	EQQALQTVC[+57.021464]LK	659.3452++	659.345194	2	23.3	748.402186	y6	1	46.62	39.13		
Tetranectin	CLEC3B	P05452	EQQALQTVCLK	EQQALQTVC[+57.021464]LK	659.3452++	659.345194	2	23.3	620.343609	y5	1	46.62	39.13		
Tetranectin	CLEC3B	P05452	EQQALQTVCLK	EQQALQTVC[+57.021464]LK	659.3452++	659.345194	2	23.3	420.227516	y3	1	46.62	39.13		
Tetranectin	CLEC3B	P05452	EQQALQTVCLK	EQQALQTVC[+57.021464]LK[+8.014199]	663.3523++ (heavy)	663.352294	2	23.3	756.416385	y6	1	46.62	39.13		
Tetranectin	CLEC3B	P05452	EQQALQTVCLK	EQQALQTVC[+57.021464]LK[+8.014199]	663.3523++ (heavy)	663.352294	2	23.3	628.357808	y5	1	46.62	39.13		
Tetranectin	CLEC3B	P05452	EQQALQTVCLK	EQQALQTVC[+57.021464]LK[+8.014199]	663.3523++ (heavy)	663.352294	2	23.3	428.241715	y3	1	46.62	39.13		
Tetranectin	CLEC3B	P05452	CFLAFTQTK	C[+57.021464]FLAFTQTK	558.2813++	558.281334	2	19.6	808.45633	y7	1	58.6	62.9		
Tetranectin	CLEC3B	P05452	CFLAFTQTK	C[+57.021464]FLAFTQTK	558.2813++	558.281334	2	19.6	695.372266	y6	1	58.6	62.9		
Tetranectin	CLEC3B	P05452	CFLAFTQTK	C[+57.021464]FLAFTQTK	558.2813++	558.281334	2	19.6	624.335152	y5	1	58.6	62.9		
Tetranectin	CLEC3B	P05452	CFLAFTQTK	C[+57.021464]FLAFTQTK[+8.014199]	562.2884++ (heavy)	562.288434	2	19.6	816.470529	y7	1	58.6	62.9		
Tetranectin	CLEC3B	P05452	CFLAFTQTK	C[+57.021464]FLAFTQTK[+8.014199]	562.2884++ (heavy)	562.288434	2	19.6	703.386465	y6	1	58.6	62.9		
Tetranectin	CLEC3B	P05452	CFLAFTQTK	C[+57.021464]FLAFTQTK[+8.014199]	562.2884++ (heavy)	562.288434	2	19.6	632.349351	y5	1	58.6	62.9		

Tetranectin	CLEC3B	P05452	TFHEASEDCISR	TFHEASEDC[+57.021464]ISR	484.5455+++	484.545507	3	16.1	650.292636	y5	1	29.06	18.46		
Tetranectin	CLEC3B	P05452	TFHEASEDCISR	TFHEASEDC[+57.021464]ISR	484.5455+++	484.545507	3	16.1	375.235044	y3	1	29.06	18.46		
Tetranectin	CLEC3B	P05452	TFHEASEDCISR	TFHEASEDC[+57.021464]ISR	484.5455+++	484.545507	3	16.1	386.18228	b3	1	29.06	18.46		
Tetranectin	CLEC3B	P05452	TFHEASEDCISR	TFHEASEDC[+57.021464]ISR[+10.008269]	487.8816+++ (heavy)	487.881597	3	16.1	660.300905	y5	1	29.06	18.46		
Tetranectin	CLEC3B	P05452	TFHEASEDCISR	TFHEASEDC[+57.021464]ISR[+10.008269]	487.8816+++ (heavy)	487.881597	3	16.1	385.243313	y3	1	29.06	18.46		
Tetranectin	CLEC3B	P05452	TFHEASEDCISR	TFHEASEDC[+57.021464]ISR[+10.008269]	487.8816+++ (heavy)	487.881597	3	16.1	386.18228	b3	1	29.06	18.46		
Thyroxine-binding globulin	SERPINA7	P05543	TEDSSSFLIDK	TEDSSSFLIDK	621.2984++	621.298432	2	21.9	1011.499317	y9	1	53.5	43.95	3.1	6.3
Thyroxine-binding globulin	SERPINA7	P05543	TEDSSSFLIDK	TEDSSSFLIDK	621.2984++	621.298432	2	21.9	375.223811	y3	1	53.5	43.95		
Thyroxine-binding globulin	SERPINA7	P05543	TEDSSSFLIDK	TEDSSSFLIDK	621.2984++	621.298432	2	21.9	231.097548	b2	1	53.5	43.95		
Thyroxine-binding globulin	SERPINA7	P05543	TEDSSSFLIDK	TEDSSSFLIDK[+8.014199]	625.3055++ (heavy)	625.305532	2	21.9	1019.513516	y9	1	53.5	43.95		
Thyroxine-binding globulin	SERPINA7	P05543	TEDSSSFLIDK	TEDSSSFLIDK[+8.014199]	625.3055++ (heavy)	625.305532	2	21.9	383.23801	y3	1	53.5	43.95		
Thyroxine-binding globulin	SERPINA7	P05543	TEDSSSFLIDK	TEDSSSFLIDK[+8.014199]	625.3055++ (heavy)	625.305532	2	21.9	231.097548	b2	1	53.5	43.95		
Thyroxine-binding globulin	SERPINA7	P05543	NALALFVLPK	NALALFVLPK	543.3395++	543.339509	2	19	787.507637	y7	1	95.36	100.07		
Thyroxine-binding globulin	SERPINA7	P05543	NALALFVLPK	NALALFVLPK	543.3395++	543.339509	2	19	716.470524	y6	1	95.36	100.07		
Thyroxine-binding globulin	SERPINA7	P05543	NALALFVLPK	NALALFVLPK	543.3395++	543.339509	2	19	186.087317	b2	1	95.36	100.07		
Thyroxine-binding globulin	SERPINA7	P05543	NALALFVLPK	NALALFVLPK	543.3395++	543.339509	2	19	299.171381	b3	1	95.36	100.07		
Thyroxine-binding globulin	SERPINA7	P05543	NALALFVLPK	NALALFVLPK[+8.014199]	547.3466++ (heavy)	547.346609	2	19	795.521836	y7	1	95.36	100.07		
Thyroxine-binding globulin	SERPINA7	P05543	NALALFVLPK	NALALFVLPK[+8.014199]	547.3466++ (heavy)	547.346609	2	19	724.484723	y6	1	95.36	100.07		
Thyroxine-binding globulin	SERPINA7	P05543	NALALFVLPK	NALALFVLPK[+8.014199]	547.3466++ (heavy)	547.346609	2	19	186.087317	b2	1	95.36	100.07		
Thyroxine-binding globulin	SERPINA7	P05543	NALALFVLPK	NALALFVLPK[+8.014199]	547.3466++ (heavy)	547.346609	2	19	299.171381	b3	1	95.36	100.07		
Vitronectin	VTN	P04004	GQYCYELDEK	GQYC[+57.021464]YELDEK	652.7768++	652.77681	2	23.1	1119.466303	y8	1	36.66	33.52	3.2	5.0
Vitronectin	VTN	P04004	GQYCYELDEK	GQYC[+57.021464]YELDEK	652.7768++	652.77681	2	23.1	956.402974	y7	1	36.66	33.52		
Vitronectin	VTN	P04004	GQYCYELDEK	GQYC[+57.021464]YELDEK	652.7768++	652.77681	2	23.1	796.372326	y6	1	36.66	33.52		
Vitronectin	VTN	P04004	GQYCYELDEK	GQYC[+57.021464]YELDEK[+8.014199]	656.7839++ (heavy)	656.78391	2	23.1	1127.480502	y8	1	36.66	33.52		
Vitronectin	VTN	P04004	GQYCYELDEK	GQYC[+57.021464]YELDEK[+8.014199]	656.7839++ (heavy)	656.78391	2	23.1	964.417173	y7	1	36.66	33.52		
Vitronectin	VTN	P04004	GQYCYELDEK	GQYC[+57.021464]YELDEK[+8.014199]	656.7839++ (heavy)	656.78391	2	23.1	804.386525	y6	1	36.66	33.52		
Vitronectin	VTN	P04004	FEDGVLDPDYPR	FEDGVLDPDYPR	711.8304++	711.830431	2	25.3	875.425758	y7	1	58.85	61.61		
Vitronectin	VTN	P04004	FEDGVLDPDYPR	FEDGVLDPDYPR	711.8304++	711.830431	2	25.3	647.314751	y5	1	58.85	61.61		
Vitronectin	VTN	P04004	FEDGVLDPDYPR	FEDGVLDPDYPR	711.8304++	711.830431	2	25.3	435.235044	y3	1	58.85	61.61		
Vitronectin	VTN	P04004	FEDGVLDPDYPR	FEDGVLDPDYPR[+10.008269]	716.8346++ (heavy)	716.834566	2	25.3	885.434027	y7	1	58.85	61.61		
Vitronectin	VTN	P04004	FEDGVLDPDYPR	FEDGVLDPDYPR[+10.008269]	716.8346++ (heavy)	716.834566	2	25.3	657.32302	y5	1	58.85	61.61		
Vitronectin	VTN	P04004	FEDGVLDPDYPR	FEDGVLDPDYPR[+10.008269]	716.8346++ (heavy)	716.834566	2	25.3	445.243313	y3	1	58.85	61.61		
Vitronectin	VTN	P04004	DWHGVPGQVDAAMAGR	DWHGVPGQVDAAMAGR	556.2633+++	556.263334	3	18.7	691.319185	y7	1	55.45	61.17		
Vitronectin	VTN	P04004	DWHGVPGQVDAAMAGR	DWHGVPGQVDAAMAGR	556.2633+++	556.263334	3	18.7	505.255128	y5	1	55.45	61.17		
Vitronectin	VTN	P04004	DWHGVPGQVDAAMAGR	DWHGVPGQVDAAMAGR	556.2633+++	556.263334	3	18.7	595.262322	b5	1	55.45	61.17		
Vitronectin	VTN	P04004	DWHGVPGQVDAAMAGR	DWHGVPGQVDAAMAGR[+10.008269]	559.5994+++ (heavy)	559.599423	3	18.7	701.327454	y7	1	55.45	61.17		
Vitronectin	VTN	P04004	DWHGVPGQVDAAMAGR	DWHGVPGQVDAAMAGR[+10.008269]	559.5994+++ (heavy)	559.599423	3	18.7	515.263397	y5	1	55.45	61.17		
Vitronectin	VTN	P04004	DWHGVPGQVDAAMAGR	DWHGVPGQVDAAMAGR[+10.008269]	559.5994+++ (heavy)	559.599423	3	18.7	595.262322	b5	1	55.45	61.17		
Vitronectin	VTN	P04004	SIAQYWLGCPAPGHL	SIAQYWLGC[+57.021464]PAPGHL	835.4114++	835.4114	2	29.8	808.377034	y8	1	90.7	96.11		
Vitronectin	VTN	P04004	SIAQYWLGCPAPGHL	SIAQYWLGC[+57.021464]PAPGHL	835.4114++	835.4114	2	29.8	591.324922	y6	1	90.7	96.11		
Vitronectin	VTN	P04004	SIAQYWLGCPAPGHL	SIAQYWLGC[+57.021464]PAPGHL	835.4114++	835.4114	2	29.8	423.235044	y4	1	90.7	96.11		
Vitronectin	VTN	P04004	SIAQYWLGCPAPGHL	SIAQYWL[+7.017164]GC[+57.021464]PAPGH	838.9200++ (heavy)	838.919982	2	29.8	808.377034	y8	1	90.7	96.11		
Vitronectin	VTN	P04004	SIAQYWLGCPAPGHL	SIAQYWL[+7.017164]GC[+57.021464]PAPGH	838.9200++ (heavy)	838.919982	2	29.8	591.324922	y6	1	90.7	96.11		
Vitronectin	VTN	P04004	SIAQYWLGCPAPGHL	SIAQYWL[+7.017164]GC[+57.021464]PAPGH	838.9200++ (heavy)	838.919982	2	29.8	423.235044	y4	1	90.7	96.11		
Enolase 1	ENO1	P00924	VNQIGTLSESIK	VNQIGTLSESIK	644.8590++	644.858991	2	22.8	834.456724	y8	1	49	47.98	NA	NA
Enolase 1	ENO1	P00924	VNQIGTLSESIK	VNQIGTLSESIK	644.8590++	644.858991	2	22.8	563.303518	y5	1	49	47.98		
Enolase 1	ENO1	P00924	VNQIGTLSESIK	VNQIGTLSESIK	644.8590++	644.858991	2	22.8	342.177195	b3	1	49	47.98		
Enolase 1	ENO1	P00924	VNQIGTLSESIK	VNQIGTLSESIK[+8.014199]	648.8661++ (heavy)	648.866091	2	22.8	842.470923	y8	1	49	47.98		
Enolase 1	ENO1	P00924	VNQIGTLSESIK	VNQIGTLSESIK[+8.014199]	648.8661++ (heavy)	648.866091	2	22.8	571.317717	y5	1	49	47.98		
Enolase 1	ENO1	P00924	VNQIGTLSESIK	VNQIGTLSESIK[+8.014199]	648.8661++ (heavy)	648.866091	2	22.8	342.177195	b3	1	49	47.98		

Supplementary Table 5. Biomarker pairs to predict short-term relapse

Gene name 1	Gene name 2	STORI (n=)	SPARE (n=)	c-statistic (CI) development dataset (STORI)	c-statistic (CI) development dataset (SPARE)	Mean c-statistic (CI) development datasets (STORI and SPARE)	c-statistic (CI) validation dataset (STORI)	c-statistic (CI) validation dataset (SPARE)	Mean c-statistic (CI) validation datasets (STORI and SPARE)
CLEC4C	ITGA11	102	63	0.78 (0.64-0.87)	0.87 (0.75-0.95)	0.82 (0.73-0.89)	0.75 (0.73-0.77)	0.85 (0.78-0.86)	0.8 (0.76-0.81)
FC	HP	77	44	0.83 (0.72-0.92)	0.79 (0.64-0.96)	0.81 (0.71-0.9)	0.78 (0.62-0.83)	0.79 (0.78-0.8)	0.79 (0.7-0.81)
FC	F9	77	44	0.77 (0.62-0.89)	0.83 (0.68-0.96)	0.8 (0.7-0.9)	0.75 (0.54-0.77)	0.81 (0.79-0.82)	0.78 (0.67-0.79)
CLEC4C	SAA1	101	63	0.71 (0.55-0.84)	0.87 (0.76-0.95)	0.79 (0.69-0.87)	0.68 (0.51-0.69)	0.88 (0.4-0.88)	0.77 (0.53-0.79)
IL6_PEA_IR	HP	101	63	0.8 (0.7-0.87)	0.79 (0.64-0.92)	0.8 (0.71-0.87)	0.78 (0.56-0.8)	0.77 (0.72-0.78)	0.77 (0.66-0.78)
KLRD1	HP	101	63	0.77 (0.64-0.86)	0.81 (0.7-0.92)	0.79 (0.71-0.86)	0.75 (0.73-0.76)	0.79 (0.74-0.8)	0.77 (0.74-0.78)
ITGA11	HP	101	63	0.77 (0.65-0.87)	0.8 (0.66-0.92)	0.79 (0.7-0.87)	0.75 (0.69-0.77)	0.79 (0.77-0.8)	0.77 (0.74-0.78)
CLEC4C	HP	101	63	0.76 (0.62-0.88)	0.82 (0.7-0.92)	0.79 (0.7-0.88)	0.75 (0.69-0.76)	0.8 (0.73-0.82)	0.77 (0.73-0.78)
CLEC4C	CRP_SRM	101	63	0.74 (0.6-0.86)	0.84 (0.74-0.92)	0.79 (0.7-0.86)	0.71 (0.6-0.74)	0.82 (0.63-0.83)	0.77 (0.66-0.78)
IL6_PEA_cytokin	HP	102	63	0.78 (0.68-0.88)	0.79 (0.66-0.92)	0.79 (0.71-0.87)	0.77 (0.69-0.78)	0.76 (0.67-0.8)	0.76 (0.71-0.79)
FCRL6	HP	101	63	0.75 (0.62-0.85)	0.84 (0.72-0.94)	0.79 (0.71-0.87)	0.73 (0.66-0.75)	0.81 (0.72-0.84)	0.76 (0.71-0.79)
MILR1	HP	101	63	0.77 (0.66-0.9)	0.81 (0.68-0.94)	0.79 (0.71-0.88)	0.74 (0.67-0.76)	0.79 (0.72-0.8)	0.76 (0.71-0.78)
SAA1	APCS	102	67	0.7 (0.57-0.82)	0.84 (0.71-0.93)	0.77 (0.68-0.86)	0.7 (0.57-0.71)	0.83 (0.66-0.83)	0.76 (0.67-0.77)
hsCRP	APCS	98	67	0.75 (0.61-0.86)	0.81 (0.69-0.92)	0.78 (0.69-0.87)	0.74 (0.65-0.75)	0.79 (0.71-0.8)	0.76 (0.7-0.77)
ITGA11	APCS	101	63	0.74 (0.62-0.85)	0.81 (0.69-0.92)	0.78 (0.69-0.85)	0.73 (0.68-0.74)	0.8 (0.77-0.82)	0.76 (0.73-0.77)
FC	CP	77	44	0.74 (0.6-0.87)	0.84 (0.69-0.98)	0.79 (0.68-0.88)	0.73 (0.57-0.74)	0.8 (0.56-0.83)	0.76 (0.63-0.78)
ITGA11	C4B	101	63	0.72 (0.59-0.83)	0.86 (0.76-0.95)	0.79 (0.71-0.86)	0.7 (0.6-0.71)	0.83 (0.55-0.88)	0.76 (0.61-0.79)
FC	APCS	77	44	0.74 (0.59-0.87)	0.9 (0.79-0.99)	0.82 (0.73-0.91)	0.71 (0.47-0.74)	0.81 (0.57-0.88)	0.76 (0.61-0.8)
FC	SERPIND1	77	44	0.74 (0.59-0.86)	0.84 (0.69-0.97)	0.79 (0.69-0.88)	0.71 (0.51-0.74)	0.82 (0.61-0.84)	0.76 (0.64-0.79)
HP	PZP	101	67	0.77 (0.66-0.87)	0.79 (0.64-0.9)	0.78 (0.7-0.86)	0.76 (0.66-0.77)	0.76 (0.68-0.77)	0.76 (0.71-0.77)
hsCRP	CCL4	98	63	0.79 (0.66-0.89)	0.75 (0.57-0.87)	0.77 (0.66-0.85)	0.78 (0.41-0.79)	0.74 (0.6-0.76)	0.76 (0.57-0.77)
hsCRP	HP	98	67	0.79 (0.68-0.88)	0.77 (0.65-0.89)	0.78 (0.7-0.85)	0.76 (0.61-0.81)	0.76 (0.72-0.77)	0.76 (0.68-0.78)
CCL4	HP	102	63	0.77 (0.67-0.86)	0.78 (0.65-0.9)	0.78 (0.69-0.86)	0.76 (0.67-0.76)	0.76 (0.73-0.78)	0.76 (0.71-0.77)
CRP_SRM	APCS	102	67	0.75 (0.62-0.85)	0.81 (0.68-0.92)	0.78 (0.69-0.86)	0.72 (0.64-0.75)	0.79 (0.7-0.8)	0.75 (0.69-0.77)
FC	C5	77	44	0.8 (0.67-0.9)	0.76 (0.58-0.93)	0.78 (0.67-0.88)	0.79 (0.52-0.8)	0.73 (0.7-0.79)	0.75 (0.62-0.79)

hsCRP	ITGA11	98	63	0.76 (0.64-0.87)	0.77 (0.59-0.91)	0.76 (0.65-0.85)	0.74 (0.63-0.77)	0.77 (0.68-0.79)	0.75 (0.68-0.77)
IL15	HP	102	63	0.75 (0.63-0.86)	0.83 (0.74-0.92)	0.8 (0.71-0.87)	0.73 (0.69-0.74)	0.78 (0.62-0.83)	0.75 (0.67-0.78)
ITGA11	CP	101	63	0.71 (0.58-0.82)	0.83 (0.68-0.93)	0.77 (0.67-0.84)	0.69 (0.6-0.7)	0.82 (0.61-0.83)	0.75 (0.63-0.76)
CLEC4C	HPR	101	63	0.72 (0.59-0.84)	0.85 (0.71-0.96)	0.78 (0.69-0.86)	0.68 (0.64-0.7)	0.83 (0.68-0.84)	0.75 (0.67-0.77)
CCL4	CRP_SRM	102	63	0.78 (0.66-0.87)	0.74 (0.55-0.88)	0.76 (0.65-0.84)	0.77 (0.4-0.78)	0.74 (0.6-0.77)	0.75 (0.56-0.77)
SAA1	C4B	102	67	0.67 (0.53-0.8)	0.86 (0.74-0.95)	0.76 (0.67-0.84)	0.65 (0.48-0.65)	0.86 (0.34-0.87)	0.75 (0.49-0.76)
HP	SAA1	102	67	0.76 (0.63-0.86)	0.77 (0.62-0.9)	0.77 (0.67-0.84)	0.74 (0.56-0.75)	0.76 (0.64-0.78)	0.75 (0.65-0.76)
hsCRP	CLEC4C	98	63	0.74 (0.6-0.86)	0.84 (0.74-0.93)	0.79 (0.7-0.86)	0.68 (0.58-0.74)	0.83 (0.55-0.84)	0.75 (0.61-0.79)
CLEC4C	F9	101	63	0.74 (0.6-0.85)	0.82 (0.69-0.94)	0.78 (0.68-0.86)	0.72 (0.7-0.73)	0.79 (0.71-0.82)	0.75 (0.71-0.77)
IFNG	HP	102	63	0.8 (0.67-0.9)	0.78 (0.67-0.91)	0.79 (0.71-0.87)	0.75 (0.59-0.8)	0.76 (0.69-0.78)	0.75 (0.67-0.78)
MILR1	APCS	101	63	0.76 (0.61-0.87)	0.8 (0.67-0.93)	0.78 (0.69-0.86)	0.74 (0.64-0.76)	0.77 (0.68-0.79)	0.75 (0.68-0.77)
FC	C2	77	44	0.71 (0.57-0.86)	0.82 (0.67-0.97)	0.77 (0.67-0.87)	0.7 (0.57-0.71)	0.81 (0.59-0.82)	0.75 (0.63-0.76)
HP	CP	102	67	0.76 (0.65-0.86)	0.78 (0.64-0.9)	0.77 (0.69-0.84)	0.75 (0.66-0.76)	0.75 (0.69-0.77)	0.75 (0.7-0.76)
hsCRP	C4B	98	67	0.76 (0.63-0.86)	0.82 (0.7-0.93)	0.79 (0.69-0.86)	0.7 (0.56-0.77)	0.8 (0.56-0.81)	0.75 (0.63-0.78)
KLRD1	APCS	101	63	0.73 (0.61-0.84)	0.81 (0.71-0.91)	0.77 (0.69-0.85)	0.72 (0.68-0.73)	0.78 (0.63-0.81)	0.75 (0.67-0.77)
hsCRP	IL6_PEA_cytokine	98	63	0.76 (0.57-0.86)	0.75 (0.49-0.89)	0.75 (0.6-0.84)	0.75 (0.39-0.76)	0.76 (0.59-0.77)	0.75 (0.56-0.76)
CRP_SRM	HP	102	67	0.77 (0.65-0.87)	0.77 (0.64-0.89)	0.77 (0.69-0.85)	0.74 (0.58-0.79)	0.75 (0.74-0.77)	0.75 (0.67-0.77)
FCRL6	APCS	101	63	0.7 (0.58-0.81)	0.84 (0.73-0.93)	0.77 (0.68-0.84)	0.69 (0.64-0.7)	0.81 (0.64-0.83)	0.75 (0.66-0.77)
HP	F9	102	67	0.77 (0.63-0.87)	0.77 (0.63-0.89)	0.77 (0.68-0.85)	0.74 (0.68-0.76)	0.75 (0.72-0.76)	0.75 (0.71-0.76)
LAMP3	HP	101	63	0.76 (0.63-0.87)	0.77 (0.65-0.91)	0.77 (0.68-0.86)	0.73 (0.66-0.75)	0.77 (0.71-0.78)	0.75 (0.71-0.76)
CLEC4C	APCS	101	63	0.71 (0.59-0.82)	0.82 (0.69-0.94)	0.77 (0.68-0.85)	0.7 (0.67-0.7)	0.8 (0.71-0.81)	0.75 (0.7-0.75)
IL6_PEA_cytokin	CP	102	63	0.69 (0.55-0.8)	0.83 (0.7-0.93)	0.75 (0.66-0.83)	0.67 (0.56-0.71)	0.83 (0.38-0.85)	0.74 (0.53-0.77)
CLEC4C	CP	101	63	0.71 (0.57-0.83)	0.84 (0.72-0.94)	0.77 (0.69-0.85)	0.68 (0.66-0.69)	0.81 (0.68-0.82)	0.74 (0.68-0.75)
IL6_PEA_cytokin	CRP_SRM	102	63	0.76 (0.59-0.85)	0.75 (0.45-0.89)	0.75 (0.59-0.84)	0.74 (0.36-0.76)	0.77 (0.62-0.77)	0.74 (0.55-0.76)
DCTN1	HP	101	63	0.77 (0.66-0.87)	0.79 (0.64-0.93)	0.78 (0.69-0.86)	0.74 (0.61-0.76)	0.75 (0.72-0.77)	0.74 (0.68-0.76)
IL7	HP	102	63	0.75 (0.62-0.85)	0.83 (0.7-0.93)	0.79 (0.7-0.86)	0.71 (0.61-0.74)	0.79 (0.55-0.82)	0.74 (0.62-0.77)
HP	APCS	102	67	0.76 (0.65-0.86)	0.81 (0.7-0.91)	0.78 (0.71-0.86)	0.73 (0.65-0.76)	0.76 (0.64-0.8)	0.74 (0.67-0.77)
CCL4	CP	102	63	0.69 (0.57-0.8)	0.84 (0.72-0.94)	0.77 (0.68-0.83)	0.67 (0.57-0.69)	0.82 (0.51-0.83)	0.74 (0.59-0.76)
NCR1	HP	101	63	0.75 (0.62-0.85)	0.79 (0.64-0.9)	0.77 (0.67-0.86)	0.72 (0.68-0.74)	0.76 (0.65-0.8)	0.74 (0.68-0.77)
CEASE_phase1	CEASE_phase1	83	46	NA	NA	NA	0.74	0.74	0.74

FC	CFB	77	44	0.72 (0.58-0.85)	0.79 (0.65-0.94)	0.76 (0.65-0.86)	0.69 (0.49-0.72)	0.79 (0.56-0.82)	0.74 (0.59-0.76)
IL6_PEA_IR	F9	101	63	0.74 (0.61-0.83)	0.79 (0.64-0.92)	0.76 (0.67-0.85)	0.73 (0.53-0.75)	0.76 (0.69-0.77)	0.74 (0.64-0.75)
HP	SERPING1	102	67	0.75 (0.64-0.84)	0.8 (0.64-0.92)	0.77 (0.68-0.85)	0.73 (0.64-0.74)	0.76 (0.66-0.79)	0.74 (0.68-0.76)
HP	LRG1	102	67	0.75 (0.62-0.85)	0.77 (0.62-0.89)	0.76 (0.67-0.84)	0.73 (0.69-0.74)	0.75 (0.68-0.77)	0.74 (0.7-0.75)
ITGA11	HPR	101	63	0.69 (0.58-0.82)	0.83 (0.67-0.96)	0.76 (0.66-0.85)	0.67 (0.63-0.69)	0.81 (0.6-0.83)	0.74 (0.63-0.75)
CP	APCS	102	67	0.72 (0.6-0.82)	0.8 (0.67-0.92)	0.76 (0.66-0.84)	0.71 (0.67-0.72)	0.77 (0.6-0.8)	0.74 (0.66-0.76)
HP	SERPINA3	102	67	0.75 (0.62-0.85)	0.77 (0.62-0.89)	0.76 (0.67-0.84)	0.73 (0.67-0.74)	0.76 (0.7-0.76)	0.74 (0.7-0.75)
HP	ITIH3	102	67	0.75 (0.63-0.86)	0.77 (0.62-0.88)	0.76 (0.68-0.84)	0.74 (0.68-0.74)	0.74 (0.71-0.75)	0.74 (0.71-0.75)
IL15	F9	102	63	0.74 (0.61-0.85)	0.8 (0.63-0.93)	0.77 (0.66-0.86)	0.73 (0.71-0.74)	0.75 (0.61-0.78)	0.74 (0.67-0.76)
IL6_PEA_IR	APCS	101	63	0.73 (0.61-0.83)	0.8 (0.66-0.94)	0.77 (0.67-0.85)	0.72 (0.54-0.73)	0.77 (0.57-0.78)	0.74 (0.6-0.75)
KLRD1	ITGA11	102	63	0.77 (0.64-0.88)	0.77 (0.63-0.89)	0.77 (0.68-0.85)	0.74 (0.67-0.76)	0.73 (0.71-0.75)	0.74 (0.7-0.75)
FCRL6	ITGA11	102	63	0.74 (0.61-0.84)	0.78 (0.65-0.88)	0.75 (0.68-0.84)	0.72 (0.66-0.73)	0.76 (0.71-0.78)	0.74 (0.7-0.75)
HP	C5	102	67	0.75 (0.63-0.86)	0.76 (0.62-0.89)	0.76 (0.67-0.84)	0.74 (0.61-0.75)	0.74 (0.66-0.75)	0.74 (0.66-0.75)
HGF	HP	102	63	0.76 (0.64-0.85)	0.81 (0.71-0.91)	0.78 (0.71-0.85)	0.74 (0.66-0.74)	0.74 (0.64-0.8)	0.74 (0.67-0.77)
hsCRP	F9	98	67	0.76 (0.61-0.89)	0.75 (0.59-0.89)	0.75 (0.64-0.86)	0.74 (0.58-0.76)	0.74 (0.71-0.75)	0.74 (0.66-0.75)
HP	CPN2	102	67	0.75 (0.63-0.85)	0.76 (0.63-0.88)	0.76 (0.67-0.83)	0.74 (0.6-0.75)	0.74 (0.67-0.75)	0.73 (0.66-0.75)
KLRD1	CRP_SRM	101	63	0.76 (0.61-0.88)	0.75 (0.61-0.87)	0.75 (0.66-0.84)	0.75 (0.57-0.76)	0.73 (0.6-0.76)	0.73 (0.62-0.76)
CCL13	HP	102	63	0.75 (0.62-0.85)	0.81 (0.69-0.92)	0.77 (0.69-0.86)	0.72 (0.57-0.75)	0.76 (0.65-0.8)	0.73 (0.65-0.77)
PZP	APCS	101	67	0.71 (0.6-0.82)	0.79 (0.66-0.92)	0.75 (0.67-0.83)	0.7 (0.6-0.72)	0.78 (0.65-0.8)	0.73 (0.66-0.75)
KLRD1	F9	101	63	0.76 (0.62-0.88)	0.76 (0.63-0.9)	0.76 (0.67-0.85)	0.74 (0.64-0.75)	0.74 (0.69-0.75)	0.73 (0.69-0.75)
NCR1	ITGA11	102	63	0.73 (0.62-0.85)	0.78 (0.62-0.89)	0.75 (0.65-0.84)	0.71 (0.67-0.73)	0.76 (0.67-0.79)	0.73 (0.69-0.76)
HP	C3	102	67	0.75 (0.62-0.85)	0.76 (0.61-0.88)	0.75 (0.66-0.83)	0.73 (0.59-0.75)	0.75 (0.65-0.76)	0.73 (0.66-0.75)
HP	HPR	102	67	0.76 (0.65-0.87)	0.77 (0.61-0.92)	0.76 (0.67-0.86)	0.72 (0.63-0.76)	0.75 (0.73-0.75)	0.73 (0.69-0.75)
CLEC4C	MILR1	102	63	0.73 (0.59-0.85)	0.8 (0.65-0.94)	0.76 (0.66-0.85)	0.68 (0.65-0.7)	0.78 (0.66-0.81)	0.73 (0.67-0.75)
ITGA11	C5	101	63	0.75 (0.63-0.84)	0.76 (0.63-0.88)	0.76 (0.67-0.84)	0.73 (0.64-0.75)	0.74 (0.72-0.76)	0.73 (0.69-0.74)
IL6_PEA_IR	ITGA11	102	63	0.73 (0.6-0.84)	0.77 (0.57-0.91)	0.74 (0.64-0.84)	0.72 (0.53-0.74)	0.75 (0.64-0.77)	0.73 (0.63-0.75)
IL6_PEA_cytokin	APCS	102	63	0.71 (0.59-0.82)	0.79 (0.64-0.93)	0.75 (0.65-0.84)	0.71 (0.62-0.71)	0.77 (0.66-0.8)	0.73 (0.66-0.75)
HP	C8B	102	67	0.76 (0.63-0.85)	0.77 (0.63-0.9)	0.76 (0.68-0.84)	0.73 (0.64-0.75)	0.74 (0.68-0.76)	0.73 (0.68-0.75)
HP	C2	102	67	0.75 (0.62-0.85)	0.77 (0.61-0.88)	0.76 (0.67-0.84)	0.73 (0.64-0.74)	0.75 (0.67-0.76)	0.73 (0.68-0.75)
MILR1	F9	101	63	0.77 (0.66-0.87)	0.78 (0.6-0.93)	0.77 (0.67-0.86)	0.73 (0.63-0.77)	0.73 (0.67-0.75)	0.73 (0.68-0.75)

ITGA11	CRP_SRM	101	63	0.74 (0.61-0.84)	0.76 (0.58-0.91)	0.75 (0.63-0.84)	0.69 (0.58-0.75)	0.78 (0.69-0.78)	0.73 (0.67-0.76)
HPR	APCS	102	67	0.71 (0.6-0.82)	0.81 (0.68-0.92)	0.77 (0.69-0.84)	0.7 (0.61-0.72)	0.77 (0.68-0.8)	0.73 (0.68-0.75)
MASP1	HP	101	63	0.78 (0.67-0.87)	0.79 (0.63-0.92)	0.78 (0.69-0.87)	0.75 (0.47-0.77)	0.72 (0.65-0.75)	0.73 (0.59-0.75)
HP	ITIH1	102	67	0.75 (0.63-0.85)	0.76 (0.62-0.89)	0.75 (0.67-0.84)	0.72 (0.65-0.74)	0.74 (0.69-0.75)	0.73 (0.68-0.74)
ITIH3	APCS	102	67	0.72 (0.61-0.83)	0.79 (0.66-0.9)	0.76 (0.67-0.83)	0.72 (0.67-0.72)	0.75 (0.65-0.78)	0.73 (0.68-0.75)
FC	SERPINA3	77	44	0.73 (0.56-0.87)	0.77 (0.59-0.96)	0.75 (0.63-0.87)	0.7 (0.42-0.74)	0.77 (0.53-0.79)	0.73 (0.57-0.76)
IL6_PEA_IR	MILR1	102	63	0.78 (0.67-0.89)	0.76 (0.59-0.89)	0.76 (0.66-0.86)	0.73 (0.55-0.77)	0.74 (0.56-0.8)	0.73 (0.61-0.78)
hsCRP	ITIH2	98	67	0.78 (0.62-0.89)	0.73 (0.55-0.86)	0.75 (0.64-0.85)	0.75 (0.54-0.77)	0.71 (0.62-0.73)	0.73 (0.62-0.75)
IL6_PEA_IR	HPR	101	63	0.73 (0.6-0.83)	0.83 (0.65-0.97)	0.78 (0.66-0.87)	0.69 (0.49-0.72)	0.79 (0.42-0.81)	0.73 (0.55-0.76)
ITGA11	ITIH3	101	63	0.72 (0.59-0.85)	0.76 (0.6-0.89)	0.74 (0.63-0.83)	0.71 (0.64-0.72)	0.75 (0.69-0.77)	0.73 (0.68-0.74)
HP	ORM1	102	67	0.76 (0.64-0.86)	0.76 (0.6-0.88)	0.76 (0.67-0.84)	0.73 (0.68-0.74)	0.74 (0.64-0.75)	0.73 (0.68-0.74)
HP	ITIH2	102	67	0.75 (0.63-0.85)	0.76 (0.61-0.89)	0.75 (0.67-0.83)	0.73 (0.65-0.74)	0.74 (0.68-0.75)	0.73 (0.69-0.74)
ITGA11	C8B	101	63	0.7 (0.57-0.83)	0.79 (0.65-0.9)	0.75 (0.66-0.83)	0.69 (0.65-0.7)	0.77 (0.62-0.78)	0.73 (0.65-0.74)
FCRL6	F9	101	63	0.72 (0.59-0.83)	0.79 (0.62-0.92)	0.76 (0.65-0.85)	0.7 (0.63-0.71)	0.76 (0.64-0.78)	0.73 (0.67-0.74)
hsCRP	C5	98	67	0.8 (0.68-0.89)	0.71 (0.55-0.86)	0.75 (0.66-0.84)	0.77 (0.45-0.8)	0.7 (0.58-0.73)	0.73 (0.58-0.76)
hsCRP	C8B	98	67	0.77 (0.63-0.87)	0.74 (0.59-0.89)	0.75 (0.66-0.84)	0.73 (0.6-0.77)	0.74 (0.58-0.78)	0.73 (0.63-0.77)
FC	CLU	77	44	0.74 (0.6-0.87)	0.81 (0.64-0.97)	0.78 (0.65-0.89)	0.69 (0.39-0.73)	0.77 (0.57-0.83)	0.73 (0.57-0.78)
HP	CLU	102	67	0.75 (0.62-0.85)	0.76 (0.63-0.88)	0.75 (0.67-0.83)	0.73 (0.58-0.74)	0.74 (0.67-0.75)	0.73 (0.65-0.74)
IL6_PEA_IR	CP	101	63	0.72 (0.6-0.82)	0.82 (0.65-0.93)	0.77 (0.67-0.84)	0.7 (0.41-0.73)	0.79 (0.48-0.84)	0.73 (0.54-0.77)
LRG1	APCS	102	67	0.69 (0.57-0.8)	0.8 (0.67-0.92)	0.75 (0.66-0.84)	0.68 (0.67-0.68)	0.78 (0.66-0.79)	0.73 (0.67-0.74)
FC	VTN	77	44	0.71 (0.57-0.86)	0.86 (0.72-0.96)	0.78 (0.69-0.88)	0.66 (0.49-0.69)	0.8 (0.44-0.84)	0.73 (0.54-0.76)
CRP_SRM	C4B	102	67	0.73 (0.61-0.84)	0.81 (0.68-0.93)	0.77 (0.68-0.86)	0.67 (0.52-0.75)	0.79 (0.45-0.8)	0.73 (0.54-0.76)
CLEC4C	LRG1	101	63	0.71 (0.54-0.84)	0.8 (0.69-0.91)	0.75 (0.66-0.84)	0.68 (0.63-0.69)	0.78 (0.63-0.79)	0.73 (0.66-0.74)
IL6_PEA_IR	CRP_SRM	101	63	0.76 (0.64-0.86)	0.72 (0.48-0.89)	0.74 (0.62-0.84)	0.75 (0.33-0.76)	0.7 (0.56-0.75)	0.73 (0.51-0.75)
ITGA11	CCL4	101	63	0.7 (0.57-0.82)	0.77 (0.61-0.89)	0.74 (0.63-0.83)	0.7 (0.61-0.72)	0.76 (0.61-0.78)	0.73 (0.65-0.75)
ITGA11	F9	101	63	0.73 (0.61-0.84)	0.77 (0.61-0.91)	0.75 (0.65-0.84)	0.71 (0.62-0.73)	0.74 (0.72-0.76)	0.73 (0.68-0.74)
FCRL6	CRP_SRM	101	63	0.76 (0.63-0.87)	0.75 (0.58-0.89)	0.75 (0.65-0.85)	0.71 (0.47-0.77)	0.75 (0.59-0.77)	0.73 (0.59-0.77)
CLEC4C	C5	101	63	0.72 (0.6-0.84)	0.77 (0.63-0.92)	0.74 (0.65-0.84)	0.7 (0.66-0.71)	0.75 (0.64-0.77)	0.72 (0.66-0.74)
CCL4	APCS	102	63	0.73 (0.61-0.84)	0.79 (0.64-0.91)	0.76 (0.66-0.84)	0.71 (0.61-0.73)	0.74 (0.66-0.75)	0.72 (0.65-0.74)
F9	APCS	102	67	0.71 (0.59-0.82)	0.8 (0.66-0.92)	0.76 (0.66-0.84)	0.7 (0.65-0.71)	0.76 (0.65-0.78)	0.72 (0.67-0.74)

hsCRP	IL6_PEA_IR	98	63	0.75 (0.62-0.85)	0.73 (0.48-0.89)	0.74 (0.62-0.84)	0.75 (0.34-0.76)	0.71 (0.55-0.75)	0.72 (0.51-0.75)
NCR1	F9	101	63	0.73 (0.6-0.85)	0.76 (0.58-0.92)	0.74 (0.64-0.85)	0.72 (0.65-0.73)	0.73 (0.66-0.75)	0.72 (0.67-0.74)
IL6_PEA_cytokin	HPR	102	63	0.66 (0.54-0.78)	0.82 (0.65-0.96)	0.74 (0.63-0.84)	0.65 (0.57-0.67)	0.8 (0.35-0.83)	0.72 (0.5-0.74)
hsCRP	PZP	97	67	0.77 (0.62-0.88)	0.75 (0.51-0.88)	0.75 (0.61-0.84)	0.73 (0.42-0.76)	0.75 (0.54-0.76)	0.72 (0.54-0.76)
HP	C9	102	67	0.75 (0.62-0.86)	0.77 (0.61-0.88)	0.76 (0.67-0.84)	0.71 (0.6-0.74)	0.74 (0.67-0.75)	0.72 (0.66-0.75)
hsCRP	MILR1	98	63	0.8 (0.68-0.89)	0.75 (0.6-0.9)	0.77 (0.67-0.86)	0.71 (0.51-0.82)	0.73 (0.62-0.78)	0.72 (0.61-0.79)
hsCRP	IFNG	98	63	0.8 (0.65-0.9)	0.74 (0.54-0.89)	0.76 (0.64-0.86)	0.77 (0.36-0.8)	0.69 (0.57-0.73)	0.72 (0.5-0.76)
MILR1	HPR	101	63	0.67 (0.54-0.82)	0.84 (0.71-0.96)	0.76 (0.67-0.85)	0.65 (0.61-0.66)	0.8 (0.33-0.82)	0.72 (0.48-0.74)
hsCRP	KLRD1	98	63	0.76 (0.61-0.88)	0.76 (0.62-0.88)	0.76 (0.66-0.85)	0.73 (0.55-0.76)	0.74 (0.56-0.77)	0.72 (0.6-0.76)
IL6_PEA_IR	C4B	101	63	0.75 (0.63-0.84)	0.8 (0.59-0.95)	0.78 (0.65-0.86)	0.68 (0.49-0.74)	0.76 (0.56-0.78)	0.72 (0.59-0.76)
MILR1	C4B	101	63	0.74 (0.6-0.86)	0.8 (0.62-0.94)	0.77 (0.67-0.86)	0.71 (0.58-0.73)	0.74 (0.59-0.76)	0.72 (0.62-0.74)
CCL4	HPR	102	63	0.67 (0.55-0.79)	0.82 (0.66-0.94)	0.74 (0.64-0.84)	0.65 (0.59-0.66)	0.8 (0.46-0.81)	0.72 (0.55-0.73)
ITGA11	SERPINA3	101	63	0.71 (0.59-0.84)	0.76 (0.6-0.9)	0.74 (0.64-0.83)	0.7 (0.64-0.72)	0.75 (0.65-0.76)	0.72 (0.64-0.74)
FCRL6	HPR	101	63	0.65 (0.53-0.78)	0.83 (0.71-0.93)	0.74 (0.65-0.82)	0.63 (0.61-0.64)	0.81 (0.51-0.83)	0.72 (0.57-0.73)
hsCRP	ITIH1	98	67	0.77 (0.62-0.88)	0.73 (0.55-0.88)	0.75 (0.63-0.85)	0.74 (0.49-0.77)	0.72 (0.63-0.73)	0.72 (0.59-0.74)
ITGA11	CFB	101	63	0.69 (0.56-0.81)	0.79 (0.63-0.91)	0.74 (0.64-0.82)	0.68 (0.51-0.68)	0.78 (0.52-0.8)	0.72 (0.59-0.74)
FC	C3	77	44	0.73 (0.58-0.86)	0.72 (0.53-0.95)	0.72 (0.59-0.86)	0.69 (0.44-0.71)	0.77 (0.59-0.8)	0.72 (0.58-0.75)
FC	C4B	77	44	0.75 (0.58-0.87)	0.93 (0.81-1)	0.83 (0.74-0.91)	0.62 (0.47-0.72)	0.82 (0.52-0.89)	0.72 (0.56-0.79)
LAMP3	ITGA11	102	63	0.76 (0.64-0.85)	0.76 (0.62-0.87)	0.76 (0.66-0.83)	0.71 (0.61-0.74)	0.73 (0.67-0.76)	0.72 (0.67-0.75)
hsCRP	DCTN1	98	63	0.75 (0.61-0.86)	0.76 (0.5-0.91)	0.75 (0.61-0.85)	0.71 (0.34-0.76)	0.74 (0.67-0.75)	0.72 (0.54-0.75)
NCR1	APCS	101	63	0.71 (0.59-0.82)	0.79 (0.64-0.92)	0.75 (0.65-0.84)	0.7 (0.66-0.7)	0.75 (0.62-0.77)	0.72 (0.65-0.74)
CCL4	F9	102	63	0.71 (0.6-0.82)	0.77 (0.63-0.91)	0.74 (0.65-0.83)	0.71 (0.63-0.72)	0.73 (0.66-0.76)	0.72 (0.67-0.73)
SAA1	CP	102	67	0.7 (0.54-0.83)	0.78 (0.53-0.91)	0.74 (0.6-0.83)	0.69 (0.5-0.7)	0.77 (0.41-0.78)	0.72 (0.54-0.74)
ITGA11	C2	101	63	0.7 (0.58-0.83)	0.79 (0.63-0.89)	0.74 (0.65-0.82)	0.68 (0.48-0.69)	0.78 (0.5-0.79)	0.72 (0.57-0.74)
MILR1	C5	101	63	0.75 (0.63-0.87)	0.75 (0.58-0.9)	0.75 (0.65-0.85)	0.73 (0.61-0.74)	0.73 (0.64-0.73)	0.72 (0.64-0.74)
IL7	CRP_SRM	102	63	0.71 (0.56-0.83)	0.8 (0.64-0.92)	0.75 (0.65-0.84)	0.65 (0.56-0.68)	0.81 (0.45-0.82)	0.72 (0.55-0.75)
ITGA11	IL6_PEA_cytokine	101	63	0.7 (0.57-0.82)	0.76 (0.56-0.9)	0.73 (0.61-0.83)	0.69 (0.61-0.71)	0.75 (0.53-0.77)	0.72 (0.61-0.74)
IL6_PEA_IR	C5	101	63	0.76 (0.64-0.86)	0.72 (0.56-0.86)	0.74 (0.63-0.82)	0.75 (0.49-0.76)	0.7 (0.62-0.71)	0.72 (0.6-0.73)
IL15	APCS	102	63	0.71 (0.59-0.81)	0.8 (0.66-0.93)	0.75 (0.67-0.83)	0.7 (0.68-0.7)	0.74 (0.56-0.79)	0.72 (0.63-0.74)
hsCRP	CLU	98	67	0.76 (0.63-0.88)	0.74 (0.6-0.87)	0.75 (0.66-0.84)	0.7 (0.53-0.76)	0.75 (0.6-0.77)	0.72 (0.62-0.76)

CLEC4C	C4B	101	63	0.68 (0.55-0.82)	0.8 (0.59-0.97)	0.74 (0.62-0.86)	0.65 (0.62-0.66)	0.79 (0.65-0.8)	0.72 (0.65-0.73)
LAMP3	APCS	101	63	0.73 (0.61-0.83)	0.77 (0.64-0.91)	0.75 (0.66-0.84)	0.69 (0.64-0.71)	0.75 (0.66-0.77)	0.72 (0.66-0.73)
KLRD1	CP	101	63	0.72 (0.61-0.83)	0.81 (0.69-0.92)	0.76 (0.68-0.84)	0.69 (0.53-0.72)	0.74 (0.57-0.8)	0.72 (0.62-0.75)
SERPINA3	APCS	102	67	0.7 (0.56-0.81)	0.78 (0.65-0.91)	0.74 (0.66-0.83)	0.68 (0.67-0.69)	0.75 (0.59-0.76)	0.72 (0.64-0.72)
HP	C4B	102	67	0.75 (0.62-0.85)	0.82 (0.71-0.93)	0.78 (0.7-0.86)	0.71 (0.65-0.73)	0.74 (0.55-0.78)	0.72 (0.62-0.75)
hsCRP	IL7	98	63	0.72 (0.56-0.85)	0.81 (0.66-0.92)	0.76 (0.66-0.85)	0.64 (0.57-0.7)	0.81 (0.45-0.83)	0.72 (0.54-0.76)
IL6_PEA_cytokin	F9	102	63	0.72 (0.6-0.82)	0.78 (0.62-0.91)	0.75 (0.65-0.84)	0.7 (0.62-0.72)	0.73 (0.66-0.8)	0.72 (0.67-0.75)
SAA1	HPR	102	67	0.72 (0.59-0.84)	0.76 (0.54-0.93)	0.73 (0.63-0.84)	0.7 (0.53-0.72)	0.74 (0.5-0.75)	0.72 (0.57-0.73)
ITGA11	SAA1	101	63	0.68 (0.55-0.82)	0.76 (0.58-0.89)	0.73 (0.61-0.82)	0.68 (0.52-0.69)	0.76 (0.51-0.76)	0.72 (0.59-0.72)
C8B	APCS	102	67	0.7 (0.57-0.81)	0.8 (0.66-0.92)	0.75 (0.66-0.83)	0.68 (0.64-0.7)	0.75 (0.61-0.77)	0.72 (0.64-0.73)
IL7	HPR	102	63	0.65 (0.53-0.77)	0.89 (0.79-0.96)	0.77 (0.69-0.84)	0.62 (0.61-0.62)	0.82 (0.45-0.89)	0.72 (0.53-0.75)
IL15	CRP_SRM	102	63	0.76 (0.6-0.87)	0.73 (0.53-0.88)	0.74 (0.62-0.84)	0.73 (0.54-0.78)	0.74 (0.54-0.77)	0.72 (0.58-0.77)
CLEC4C	PZP	100	63	0.69 (0.55-0.82)	0.81 (0.67-0.92)	0.74 (0.65-0.84)	0.66 (0.64-0.67)	0.77 (0.5-0.79)	0.72 (0.58-0.73)
ITGA11	C3	101	63	0.71 (0.58-0.81)	0.76 (0.63-0.91)	0.74 (0.64-0.82)	0.68 (0.54-0.7)	0.76 (0.58-0.77)	0.72 (0.6-0.73)
SAA1	SERPIND1	102	67	0.68 (0.53-0.78)	0.8 (0.63-0.92)	0.74 (0.63-0.82)	0.66 (0.49-0.67)	0.79 (0.37-0.81)	0.72 (0.47-0.74)
ITGA11	SERPIND1	101	63	0.7 (0.58-0.82)	0.81 (0.66-0.92)	0.75 (0.65-0.84)	0.65 (0.51-0.69)	0.79 (0.59-0.8)	0.72 (0.61-0.74)
CLU	APCS	102	67	0.69 (0.58-0.8)	0.79 (0.66-0.91)	0.74 (0.65-0.82)	0.68 (0.65-0.69)	0.75 (0.58-0.77)	0.72 (0.62-0.72)
hsCRP	HGF	98	63	0.76 (0.61-0.87)	0.83 (0.66-0.92)	0.79 (0.68-0.87)	0.7 (0.47-0.76)	0.81 (0.54-0.85)	0.71 (0.54-0.79)
HP	CFB	102	67	0.75 (0.62-0.86)	0.75 (0.63-0.88)	0.76 (0.66-0.84)	0.73 (0.63-0.74)	0.71 (0.58-0.75)	0.71 (0.64-0.74)
F9	HPR	102	67	0.73 (0.61-0.83)	0.78 (0.61-0.92)	0.75 (0.65-0.84)	0.7 (0.58-0.73)	0.74 (0.67-0.75)	0.71 (0.65-0.73)
CLEC4C	SERPIND1	101	63	0.67 (0.53-0.82)	0.83 (0.7-0.94)	0.75 (0.66-0.84)	0.64 (0.62-0.66)	0.78 (0.32-0.82)	0.71 (0.48-0.74)
CLEC4C	SERPINA3	101	63	0.71 (0.55-0.83)	0.78 (0.65-0.92)	0.74 (0.64-0.83)	0.68 (0.62-0.68)	0.76 (0.63-0.77)	0.71 (0.64-0.73)
C4B	APCS	102	67	0.69 (0.57-0.8)	0.81 (0.65-0.95)	0.75 (0.64-0.84)	0.67 (0.66-0.69)	0.75 (0.63-0.78)	0.71 (0.64-0.73)
LAMP3	F9	101	63	0.74 (0.62-0.85)	0.75 (0.59-0.9)	0.74 (0.64-0.84)	0.71 (0.63-0.73)	0.72 (0.66-0.73)	0.71 (0.67-0.73)
IL7	CP	102	63	0.66 (0.52-0.79)	0.85 (0.74-0.94)	0.75 (0.67-0.83)	0.62 (0.59-0.65)	0.82 (0.4-0.87)	0.71 (0.51-0.75)
CLEC4C	C3	101	63	0.69 (0.56-0.81)	0.77 (0.58-0.95)	0.73 (0.61-0.84)	0.66 (0.64-0.68)	0.77 (0.62-0.78)	0.71 (0.61-0.73)
IFNG	CRP_SRM	102	63	0.79 (0.66-0.9)	0.74 (0.53-0.89)	0.76 (0.63-0.85)	0.77 (0.26-0.8)	0.69 (0.52-0.73)	0.71 (0.47-0.76)
hsCRP	hsCRP	109	69	NA	NA	NA	0.75	0.68	0.71
ITGA11	PZP	100	63	0.69 (0.57-0.81)	0.78 (0.61-0.89)	0.73 (0.63-0.81)	0.67 (0.62-0.68)	0.76 (0.56-0.78)	0.71 (0.61-0.73)
CRP_SRM	F9	102	67	0.73 (0.59-0.86)	0.75 (0.59-0.89)	0.74 (0.63-0.84)	0.7 (0.54-0.75)	0.73 (0.66-0.74)	0.71 (0.63-0.74)

FC	CLEC4C	76	43	0.79 (0.61-0.9)	0.92 (0.79-1)	0.85 (0.75-0.93)	0.59 (0.54-0.72)	0.85 (0.5-0.88)	0.71 (0.54-0.79)
NCR1	HPR	101	63	0.7 (0.59-0.79)	0.82 (0.67-0.94)	0.76 (0.66-0.84)	0.65 (0.58-0.69)	0.78 (0.52-0.81)	0.71 (0.59-0.75)
MILR1	CRP_SRM	101	63	0.78 (0.67-0.88)	0.73 (0.59-0.89)	0.76 (0.66-0.85)	0.69 (0.52-0.8)	0.73 (0.64-0.78)	0.71 (0.61-0.78)
DCTN1	CRP_SRM	101	63	0.74 (0.6-0.85)	0.75 (0.48-0.91)	0.75 (0.59-0.84)	0.69 (0.33-0.76)	0.75 (0.67-0.76)	0.71 (0.54-0.75)
CCL4	C5	102	63	0.75 (0.64-0.84)	0.73 (0.58-0.86)	0.74 (0.65-0.82)	0.73 (0.57-0.74)	0.7 (0.62-0.72)	0.71 (0.63-0.72)
CFB	APCS	102	67	0.69 (0.57-0.81)	0.76 (0.61-0.88)	0.72 (0.63-0.81)	0.67 (0.65-0.68)	0.75 (0.6-0.77)	0.71 (0.64-0.73)
SAA1	F9	102	67	0.7 (0.55-0.83)	0.75 (0.58-0.91)	0.72 (0.61-0.83)	0.68 (0.52-0.7)	0.74 (0.58-0.75)	0.71 (0.61-0.72)
F9	PZP	101	67	0.71 (0.59-0.83)	0.77 (0.61-0.9)	0.74 (0.62-0.83)	0.7 (0.57-0.71)	0.73 (0.63-0.75)	0.71 (0.61-0.72)
SAA1	PZP	101	67	0.69 (0.53-0.82)	0.77 (0.45-0.89)	0.73 (0.54-0.82)	0.67 (0.41-0.69)	0.76 (0.47-0.77)	0.71 (0.52-0.73)
HGF	HPR	102	63	0.65 (0.53-0.77)	0.85 (0.72-0.96)	0.75 (0.66-0.83)	0.64 (0.61-0.65)	0.78 (0.33-0.83)	0.71 (0.48-0.74)
HGF	APCS	102	63	0.7 (0.57-0.81)	0.8 (0.66-0.94)	0.75 (0.65-0.83)	0.68 (0.64-0.69)	0.74 (0.6-0.79)	0.71 (0.63-0.74)
C2	APCS	102	67	0.69 (0.56-0.81)	0.77 (0.63-0.9)	0.73 (0.63-0.82)	0.68 (0.65-0.69)	0.74 (0.56-0.77)	0.71 (0.62-0.72)
NCR1	CP	101	63	0.69 (0.57-0.8)	0.81 (0.66-0.93)	0.75 (0.66-0.83)	0.66 (0.59-0.67)	0.76 (0.54-0.81)	0.71 (0.59-0.74)
ITIH2	APCS	102	67	0.69 (0.57-0.81)	0.78 (0.64-0.91)	0.73 (0.64-0.83)	0.68 (0.64-0.69)	0.75 (0.58-0.77)	0.71 (0.62-0.73)
FCRL6	CP	101	63	0.68 (0.56-0.8)	0.8 (0.68-0.92)	0.74 (0.65-0.82)	0.67 (0.54-0.69)	0.77 (0.58-0.8)	0.71 (0.61-0.74)
SERPIND1	APCS	102	67	0.69 (0.57-0.8)	0.81 (0.68-0.91)	0.75 (0.65-0.83)	0.68 (0.59-0.69)	0.74 (0.56-0.79)	0.71 (0.61-0.74)
CP	F9	102	67	0.71 (0.58-0.83)	0.78 (0.61-0.9)	0.74 (0.64-0.83)	0.7 (0.59-0.72)	0.73 (0.61-0.75)	0.71 (0.64-0.73)
C3	APCS	102	67	0.69 (0.56-0.81)	0.78 (0.64-0.91)	0.74 (0.64-0.81)	0.68 (0.59-0.69)	0.75 (0.55-0.78)	0.71 (0.61-0.73)
ITGA11	LRG1	101	63	0.7 (0.57-0.83)	0.74 (0.58-0.87)	0.72 (0.62-0.81)	0.69 (0.65-0.7)	0.73 (0.63-0.74)	0.71 (0.65-0.72)
C4B	HPR	102	67	0.69 (0.58-0.79)	0.81 (0.68-0.94)	0.75 (0.66-0.84)	0.67 (0.62-0.68)	0.75 (0.65-0.77)	0.71 (0.65-0.72)
KLRD1	HPR	101	63	0.7 (0.58-0.81)	0.82 (0.67-0.93)	0.76 (0.66-0.84)	0.65 (0.6-0.69)	0.77 (0.55-0.81)	0.71 (0.6-0.73)
ITIH1	APCS	102	67	0.68 (0.56-0.8)	0.78 (0.65-0.91)	0.73 (0.63-0.82)	0.68 (0.62-0.69)	0.74 (0.55-0.76)	0.71 (0.61-0.72)
KLRD1	C5	101	63	0.74 (0.64-0.84)	0.73 (0.62-0.84)	0.74 (0.65-0.81)	0.72 (0.64-0.74)	0.7 (0.62-0.71)	0.71 (0.66-0.72)
hsCRP	CPN2	98	67	0.76 (0.63-0.86)	0.72 (0.54-0.87)	0.74 (0.63-0.83)	0.7 (0.44-0.77)	0.72 (0.62-0.73)	0.71 (0.57-0.75)
CLEC4C	C8B	101	63	0.71 (0.57-0.82)	0.76 (0.58-0.92)	0.73 (0.62-0.83)	0.67 (0.6-0.69)	0.75 (0.63-0.77)	0.71 (0.61-0.72)
IL7	APCS	102	63	0.69 (0.56-0.81)	0.83 (0.7-0.93)	0.76 (0.67-0.84)	0.66 (0.6-0.68)	0.77 (0.49-0.81)	0.71 (0.56-0.74)
IL13	HP	102	63	0.76 (0.65-0.85)	0.78 (0.65-0.9)	0.77 (0.69-0.86)	0.73 (0.65-0.76)	0.69 (0.62-0.76)	0.71 (0.65-0.75)
hsCRP	C2	98	67	0.75 (0.62-0.86)	0.73 (0.56-0.88)	0.74 (0.64-0.84)	0.69 (0.5-0.76)	0.75 (0.62-0.76)	0.71 (0.6-0.76)
IL15	HPR	102	63	0.67 (0.53-0.79)	0.82 (0.7-0.93)	0.74 (0.65-0.83)	0.64 (0.62-0.66)	0.78 (0.48-0.81)	0.71 (0.56-0.73)
DCTN1	F9	101	63	0.74 (0.61-0.84)	0.77 (0.61-0.91)	0.75 (0.65-0.84)	0.69 (0.56-0.73)	0.72 (0.71-0.73)	0.71 (0.64-0.73)

ITGA11	IL7	101	63	0.69 (0.57-0.82)	0.79 (0.66-0.88)	0.74 (0.66-0.82)	0.67 (0.55-0.68)	0.77 (0.4-0.78)	0.71 (0.53-0.73)
ITGA11	IL15	101	63	0.71 (0.58-0.83)	0.76 (0.62-0.88)	0.74 (0.65-0.81)	0.69 (0.67-0.7)	0.72 (0.56-0.77)	0.71 (0.62-0.73)
CLEC4C	ITIH3	101	63	0.69 (0.54-0.82)	0.78 (0.63-0.91)	0.73 (0.64-0.83)	0.66 (0.53-0.67)	0.76 (0.65-0.77)	0.71 (0.62-0.72)
FCRL6	C5	101	63	0.72 (0.61-0.82)	0.77 (0.67-0.88)	0.75 (0.67-0.82)	0.7 (0.53-0.71)	0.73 (0.56-0.79)	0.71 (0.61-0.75)
IL6_PEA_cytokin	SERPIND1	102	63	0.66 (0.53-0.76)	0.82 (0.66-0.93)	0.74 (0.64-0.81)	0.63 (0.53-0.66)	0.79 (0.32-0.82)	0.71 (0.48-0.74)
CLEC4C	DCTN1	102	63	0.71 (0.59-0.83)	0.8 (0.64-0.93)	0.75 (0.66-0.85)	0.68 (0.54-0.7)	0.73 (0.57-0.81)	0.71 (0.61-0.75)
KLRD1	C4B	101	63	0.71 (0.59-0.83)	0.78 (0.61-0.94)	0.75 (0.64-0.84)	0.68 (0.61-0.7)	0.74 (0.57-0.75)	0.71 (0.61-0.72)
CP	C4B	102	67	0.7 (0.58-0.8)	0.78 (0.64-0.92)	0.74 (0.65-0.83)	0.67 (0.6-0.68)	0.75 (0.56-0.75)	0.71 (0.61-0.72)
MILR1	CP	101	63	0.71 (0.57-0.84)	0.78 (0.63-0.92)	0.74 (0.63-0.84)	0.67 (0.51-0.7)	0.75 (0.58-0.79)	0.71 (0.61-0.74)
MILR1	SAA1	101	63	0.75 (0.63-0.86)	0.72 (0.55-0.87)	0.74 (0.63-0.82)	0.73 (0.51-0.74)	0.7 (0.53-0.77)	0.71 (0.59-0.75)
IL6_PEA_cytokin	C5	102	63	0.75 (0.63-0.84)	0.72 (0.57-0.87)	0.73 (0.63-0.82)	0.72 (0.62-0.74)	0.69 (0.58-0.73)	0.7 (0.62-0.73)
IFNG	APCS	102	63	0.72 (0.57-0.84)	0.78 (0.65-0.9)	0.75 (0.66-0.83)	0.69 (0.58-0.71)	0.74 (0.63-0.77)	0.7 (0.63-0.74)
IL15	CP	102	63	0.69 (0.54-0.8)	0.79 (0.64-0.92)	0.74 (0.64-0.83)	0.66 (0.63-0.67)	0.75 (0.52-0.8)	0.7 (0.59-0.73)
F9	C2	102	67	0.72 (0.59-0.84)	0.75 (0.58-0.89)	0.73 (0.62-0.84)	0.69 (0.62-0.71)	0.72 (0.67-0.74)	0.7 (0.66-0.72)
HP	VTN	102	67	0.75 (0.61-0.86)	0.79 (0.67-0.9)	0.77 (0.69-0.85)	0.69 (0.54-0.74)	0.73 (0.59-0.78)	0.7 (0.6-0.75)
hsCRP	LAMP3	98	63	0.75 (0.62-0.86)	0.71 (0.53-0.87)	0.73 (0.61-0.83)	0.72 (0.32-0.76)	0.69 (0.63-0.73)	0.7 (0.5-0.73)
CCL4	SERPIND1	102	63	0.68 (0.58-0.78)	0.8 (0.69-0.91)	0.74 (0.67-0.82)	0.64 (0.56-0.68)	0.78 (0.51-0.8)	0.7 (0.57-0.73)
ITIH3	F9	102	67	0.71 (0.58-0.84)	0.75 (0.61-0.88)	0.73 (0.64-0.82)	0.69 (0.65-0.7)	0.72 (0.7-0.73)	0.7 (0.68-0.71)
LAMP3	CRP_SRM	101	63	0.75 (0.62-0.86)	0.7 (0.53-0.85)	0.72 (0.62-0.83)	0.73 (0.32-0.76)	0.69 (0.59-0.73)	0.7 (0.5-0.74)
CRP_SRM	C5	102	67	0.77 (0.64-0.86)	0.71 (0.55-0.85)	0.73 (0.64-0.82)	0.73 (0.42-0.77)	0.7 (0.6-0.73)	0.7 (0.56-0.74)
CPN2	APCS	102	67	0.68 (0.56-0.79)	0.8 (0.67-0.91)	0.74 (0.65-0.82)	0.68 (0.63-0.68)	0.74 (0.58-0.79)	0.7 (0.62-0.73)
F9	SERPING1	102	67	0.71 (0.59-0.81)	0.8 (0.65-0.9)	0.75 (0.66-0.83)	0.69 (0.59-0.7)	0.72 (0.57-0.77)	0.7 (0.62-0.73)
hsCRP	CRP_SRM	98	67	0.76 (0.56-0.89)	0.69 (0.38-0.86)	0.72 (0.57-0.82)	0.68 (0.23-0.76)	0.73 (0.52-0.76)	0.7 (0.48-0.75)
SAA1	C5	102	67	0.73 (0.59-0.85)	0.71 (0.53-0.87)	0.72 (0.61-0.82)	0.72 (0.48-0.73)	0.7 (0.54-0.72)	0.7 (0.58-0.73)
CP	C8B	102	67	0.7 (0.57-0.82)	0.77 (0.62-0.91)	0.73 (0.64-0.82)	0.68 (0.62-0.69)	0.72 (0.52-0.76)	0.7 (0.59-0.73)
CCL4	LRG1	102	63	0.71 (0.57-0.82)	0.74 (0.59-0.85)	0.72 (0.63-0.81)	0.7 (0.52-0.72)	0.73 (0.52-0.74)	0.7 (0.58-0.73)
F9	ITIH2	102	67	0.72 (0.59-0.84)	0.76 (0.61-0.9)	0.73 (0.64-0.84)	0.69 (0.58-0.72)	0.72 (0.65-0.73)	0.7 (0.64-0.73)
IL6_PEA_IR	FCRL6	102	63	0.72 (0.6-0.83)	0.73 (0.59-0.87)	0.73 (0.63-0.81)	0.68 (0.44-0.73)	0.74 (0.57-0.75)	0.7 (0.57-0.74)
IL17F	HP	102	63	0.78 (0.67-0.87)	0.77 (0.63-0.89)	0.78 (0.69-0.86)	0.73 (0.64-0.77)	0.67 (0.56-0.75)	0.7 (0.64-0.75)
ITGA11	CPN2	101	63	0.7 (0.58-0.82)	0.75 (0.61-0.88)	0.73 (0.64-0.81)	0.68 (0.58-0.68)	0.73 (0.5-0.75)	0.7 (0.58-0.71)

CLEC4C	C2	101	63	0.68 (0.53-0.81)	0.79 (0.6-0.94)	0.73 (0.61-0.84)	0.64 (0.61-0.65)	0.77 (0.48-0.78)	0.7 (0.56-0.71)
MILR1	KLRD1	102	63	0.73 (0.59-0.88)	0.74 (0.59-0.88)	0.73 (0.63-0.84)	0.71 (0.64-0.72)	0.7 (0.59-0.71)	0.7 (0.63-0.71)
ORM1	APCS	102	67	0.69 (0.56-0.8)	0.78 (0.64-0.92)	0.73 (0.64-0.82)	0.67 (0.66-0.69)	0.73 (0.56-0.78)	0.7 (0.61-0.73)
MILR1	SERPINA3	101	63	0.74 (0.6-0.87)	0.73 (0.55-0.91)	0.74 (0.63-0.84)	0.69 (0.51-0.74)	0.7 (0.67-0.73)	0.7 (0.6-0.73)
SERPING1	APCS	102	67	0.69 (0.55-0.8)	0.84 (0.71-0.93)	0.76 (0.67-0.83)	0.67 (0.6-0.68)	0.74 (0.52-0.83)	0.7 (0.59-0.75)
CLEC4C	CLU	101	63	0.67 (0.54-0.8)	0.79 (0.66-0.92)	0.72 (0.64-0.83)	0.64 (0.6-0.65)	0.77 (0.54-0.78)	0.7 (0.58-0.71)
IL6_PEA_IR	LRG1	101	63	0.74 (0.61-0.82)	0.72 (0.52-0.87)	0.73 (0.62-0.82)	0.71 (0.38-0.73)	0.72 (0.51-0.73)	0.7 (0.54-0.73)
CLEC4C	CFB	101	63	0.68 (0.54-0.81)	0.77 (0.6-0.93)	0.72 (0.62-0.82)	0.64 (0.6-0.65)	0.76 (0.54-0.78)	0.7 (0.58-0.71)
hsCRP	ITIH3	98	67	0.75 (0.61-0.86)	0.72 (0.54-0.86)	0.73 (0.62-0.82)	0.71 (0.43-0.76)	0.71 (0.6-0.74)	0.7 (0.55-0.74)
CCL4	C4B	102	63	0.69 (0.58-0.79)	0.79 (0.59-0.94)	0.74 (0.62-0.84)	0.65 (0.56-0.69)	0.76 (0.54-0.77)	0.7 (0.58-0.72)
CRP_SRM	PZP	101	67	0.74 (0.61-0.86)	0.75 (0.51-0.88)	0.74 (0.6-0.83)	0.68 (0.42-0.75)	0.74 (0.54-0.76)	0.7 (0.52-0.75)
CCL4	SAA1	102	63	0.72 (0.52-0.84)	0.71 (0.5-0.84)	0.71 (0.59-0.81)	0.71 (0.41-0.74)	0.7 (0.49-0.72)	0.7 (0.51-0.72)
LRG1	F9	102	67	0.7 (0.58-0.82)	0.75 (0.6-0.89)	0.73 (0.63-0.82)	0.68 (0.64-0.69)	0.72 (0.68-0.73)	0.7 (0.67-0.71)
C9	APCS	102	67	0.68 (0.54-0.8)	0.78 (0.63-0.91)	0.73 (0.62-0.82)	0.68 (0.57-0.69)	0.72 (0.58-0.77)	0.7 (0.61-0.73)
F9	C8B	102	67	0.7 (0.59-0.82)	0.77 (0.62-0.9)	0.73 (0.64-0.82)	0.68 (0.64-0.69)	0.72 (0.67-0.73)	0.7 (0.67-0.71)
FCRL6	C4B	101	63	0.67 (0.55-0.79)	0.79 (0.63-0.94)	0.73 (0.63-0.83)	0.65 (0.63-0.66)	0.75 (0.53-0.76)	0.7 (0.59-0.71)
SERPINA3	F9	102	67	0.71 (0.58-0.83)	0.75 (0.6-0.89)	0.73 (0.63-0.82)	0.68 (0.64-0.69)	0.72 (0.69-0.73)	0.7 (0.67-0.71)
ITGA11	ITIH1	101	63	0.7 (0.57-0.83)	0.74 (0.58-0.89)	0.72 (0.63-0.82)	0.68 (0.58-0.69)	0.72 (0.51-0.74)	0.7 (0.59-0.71)
C3	F9	102	67	0.7 (0.57-0.82)	0.76 (0.58-0.9)	0.73 (0.63-0.83)	0.69 (0.58-0.7)	0.72 (0.65-0.74)	0.7 (0.63-0.72)
C8B	PZP	101	67	0.69 (0.56-0.81)	0.75 (0.61-0.9)	0.72 (0.62-0.82)	0.68 (0.61-0.69)	0.72 (0.53-0.75)	0.7 (0.59-0.71)
FC	PZP	77	44	0.75 (0.61-0.87)	0.81 (0.56-0.94)	0.78 (0.65-0.86)	0.7 (0.39-0.74)	0.76 (0.4-0.81)	0.7 (0.48-0.76)
CLEC4C	FCRL6	102	63	0.67 (0.55-0.81)	0.79 (0.65-0.93)	0.73 (0.64-0.82)	0.63 (0.59-0.65)	0.77 (0.56-0.81)	0.7 (0.59-0.72)
FC	ITGA11	76	43	0.78 (0.63-0.9)	0.73 (0.52-0.93)	0.76 (0.63-0.87)	0.72 (0.41-0.78)	0.68 (0.62-0.7)	0.7 (0.54-0.74)
C4B	C8B	102	67	0.66 (0.53-0.78)	0.81 (0.61-0.95)	0.73 (0.61-0.84)	0.64 (0.62-0.64)	0.76 (0.46-0.78)	0.7 (0.55-0.71)
DCTN1	APCS	101	63	0.73 (0.61-0.82)	0.79 (0.64-0.93)	0.76 (0.67-0.84)	0.67 (0.59-0.73)	0.74 (0.59-0.75)	0.7 (0.62-0.73)
hsCRP	CP	98	67	0.76 (0.61-0.88)	0.74 (0.54-0.9)	0.75 (0.63-0.85)	0.65 (0.52-0.76)	0.76 (0.59-0.77)	0.7 (0.59-0.76)
IL6_PEA_IR	SERPIND1	101	63	0.72 (0.59-0.81)	0.82 (0.69-0.94)	0.77 (0.68-0.84)	0.67 (0.43-0.71)	0.76 (0.41-0.8)	0.7 (0.5-0.75)
C4B	PZP	101	67	0.7 (0.57-0.8)	0.78 (0.6-0.92)	0.73 (0.63-0.84)	0.66 (0.58-0.69)	0.73 (0.62-0.76)	0.7 (0.64-0.71)
IL7	F9	102	63	0.7 (0.58-0.82)	0.8 (0.66-0.9)	0.75 (0.66-0.83)	0.67 (0.55-0.69)	0.74 (0.5-0.78)	0.7 (0.57-0.73)
LRG1	C4B	102	67	0.66 (0.53-0.79)	0.79 (0.68-0.92)	0.73 (0.64-0.83)	0.64 (0.59-0.66)	0.75 (0.44-0.77)	0.7 (0.54-0.71)

HGF	F9	102	63	0.71 (0.58-0.82)	0.8 (0.68-0.92)	0.76 (0.66-0.84)	0.69 (0.59-0.71)	0.7 (0.64-0.8)	0.7 (0.65-0.74)
IL7	C4B	102	63	0.66 (0.53-0.78)	0.82 (0.61-0.96)	0.74 (0.62-0.85)	0.63 (0.59-0.64)	0.77 (0.43-0.8)	0.7 (0.53-0.72)
FCRL6	SERPINA3	101	63	0.67 (0.54-0.8)	0.77 (0.64-0.89)	0.72 (0.63-0.82)	0.65 (0.6-0.67)	0.74 (0.53-0.76)	0.7 (0.59-0.71)
NCR1	C4B	101	63	0.68 (0.54-0.8)	0.78 (0.59-0.95)	0.73 (0.61-0.84)	0.66 (0.58-0.67)	0.74 (0.48-0.76)	0.7 (0.57-0.71)
CLEC4C	IL6_PEA_cytokine	101	63	0.7 (0.56-0.82)	0.79 (0.62-0.94)	0.74 (0.64-0.84)	0.61 (0.61-0.74)	0.77 (0.44-0.78)	0.7 (0.52-0.76)
APCS	VTN	102	67	0.69 (0.55-0.8)	0.8 (0.68-0.91)	0.74 (0.64-0.82)	0.66 (0.6-0.68)	0.73 (0.5-0.78)	0.7 (0.57-0.73)
C8B	HPR	102	67	0.69 (0.58-0.8)	0.78 (0.61-0.93)	0.73 (0.63-0.83)	0.67 (0.59-0.69)	0.73 (0.59-0.76)	0.69 (0.62-0.72)
MILR1	LRG1	101	63	0.72 (0.59-0.85)	0.73 (0.58-0.88)	0.73 (0.62-0.82)	0.68 (0.54-0.71)	0.72 (0.63-0.73)	0.69 (0.61-0.72)
KLRD1	SERPIND1	101	63	0.69 (0.57-0.79)	0.83 (0.7-0.91)	0.76 (0.68-0.83)	0.65 (0.59-0.67)	0.74 (0.52-0.82)	0.69 (0.57-0.74)
hsCRP	FCRL6	98	63	0.75 (0.61-0.88)	0.75 (0.58-0.9)	0.75 (0.64-0.85)	0.69 (0.44-0.77)	0.74 (0.55-0.77)	0.69 (0.56-0.76)
MILR1	C8B	101	63	0.71 (0.57-0.84)	0.75 (0.6-0.89)	0.73 (0.62-0.84)	0.68 (0.6-0.69)	0.72 (0.6-0.73)	0.69 (0.63-0.71)
C5	APCS	102	67	0.72 (0.6-0.82)	0.78 (0.64-0.9)	0.75 (0.66-0.83)	0.69 (0.59-0.72)	0.7 (0.51-0.76)	0.69 (0.59-0.73)
FCRL6	SERPIND1	101	63	0.64 (0.54-0.74)	0.84 (0.74-0.92)	0.74 (0.66-0.81)	0.61 (0.58-0.62)	0.78 (0.48-0.84)	0.69 (0.54-0.73)
IL6_PEA_cytokin	C4B	102	63	0.71 (0.59-0.8)	0.79 (0.59-0.95)	0.75 (0.63-0.85)	0.63 (0.6-0.73)	0.76 (0.59-0.78)	0.69 (0.6-0.75)
IL6_PEA_IR	SAA1	101	63	0.75 (0.57-0.85)	0.69 (0.5-0.87)	0.71 (0.6-0.82)	0.71 (0.34-0.75)	0.68 (0.56-0.7)	0.69 (0.51-0.72)
NCR1	CRP_SRM	101	63	0.74 (0.57-0.86)	0.7 (0.54-0.85)	0.72 (0.61-0.82)	0.7 (0.42-0.75)	0.7 (0.5-0.73)	0.69 (0.54-0.73)
FC	FC	85	47				0.72	0.67	0.69
KLRD1	SAA1	101	63	0.71 (0.56-0.83)	0.71 (0.54-0.86)	0.71 (0.6-0.81)	0.7 (0.45-0.71)	0.69 (0.49-0.7)	0.69 (0.54-0.71)
CCL13	HPR	102	63	0.65 (0.52-0.77)	0.83 (0.7-0.94)	0.74 (0.64-0.83)	0.62 (0.58-0.63)	0.77 (0.45-0.82)	0.69 (0.53-0.72)
MILR1	ITGA11	102	63	0.71 (0.58-0.84)	0.75 (0.61-0.88)	0.73 (0.64-0.82)	0.68 (0.64-0.69)	0.71 (0.66-0.73)	0.69 (0.66-0.71)
NCR1	C5	101	63	0.72 (0.61-0.82)	0.74 (0.6-0.89)	0.73 (0.64-0.82)	0.72 (0.6-0.72)	0.68 (0.58-0.72)	0.69 (0.62-0.72)
DCTN1	CP	101	63	0.71 (0.57-0.83)	0.8 (0.62-0.92)	0.75 (0.64-0.84)	0.68 (0.45-0.71)	0.73 (0.5-0.79)	0.69 (0.52-0.74)
hsCRP	SAA1	98	67	0.74 (0.52-0.86)	0.71 (0.44-0.86)	0.72 (0.56-0.82)	0.7 (0.31-0.76)	0.71 (0.5-0.73)	0.69 (0.49-0.74)
ITGA11	HGF	101	63	0.69 (0.57-0.81)	0.81 (0.66-0.93)	0.75 (0.66-0.84)	0.68 (0.56-0.7)	0.72 (0.46-0.85)	0.69 (0.56-0.77)
ITGA11	CLU	101	63	0.7 (0.57-0.82)	0.73 (0.57-0.88)	0.72 (0.61-0.8)	0.68 (0.58-0.69)	0.71 (0.59-0.73)	0.69 (0.61-0.71)
LAMP3	CP	101	63	0.71 (0.59-0.83)	0.8 (0.66-0.92)	0.76 (0.66-0.84)	0.68 (0.49-0.69)	0.73 (0.5-0.8)	0.69 (0.57-0.74)
CLEC4C	IFNG	101	63	0.75 (0.6-0.89)	0.79 (0.58-0.93)	0.76 (0.65-0.87)	0.7 (0.43-0.75)	0.69 (0.63-0.75)	0.69 (0.54-0.74)
F9	ITIH1	102	67	0.72 (0.58-0.83)	0.75 (0.61-0.89)	0.73 (0.64-0.83)	0.68 (0.56-0.72)	0.71 (0.62-0.73)	0.69 (0.62-0.72)
ITGA11	IFNG	101	63	0.8 (0.67-0.89)	0.74 (0.6-0.87)	0.76 (0.67-0.85)	0.68 (0.49-0.77)	0.71 (0.65-0.75)	0.69 (0.6-0.74)
hsCRP	SERPIND1	98	67	0.75 (0.61-0.87)	0.79 (0.63-0.9)	0.77 (0.67-0.85)	0.64 (0.45-0.74)	0.78 (0.45-0.79)	0.69 (0.54-0.76)

MILR1	ITIH3	101	63	0.75 (0.6-0.88)	0.73 (0.6-0.86)	0.74 (0.63-0.83)	0.68 (0.55-0.75)	0.71 (0.57-0.72)	0.69 (0.6-0.73)
CLEC4C	LAMP3	102	63	0.7 (0.55-0.84)	0.77 (0.6-0.91)	0.73 (0.63-0.83)	0.67 (0.51-0.68)	0.72 (0.49-0.76)	0.69 (0.53-0.72)
FC	C8B	77	44	0.75 (0.6-0.88)	0.69 (0.54-0.87)	0.72 (0.61-0.83)	0.71 (0.43-0.75)	0.69 (0.62-0.7)	0.69 (0.54-0.72)
FC	CRP_SRM	77	44	0.76 (0.6-0.89)	0.74 (0.43-0.94)	0.75 (0.58-0.86)	0.65 (0.24-0.77)	0.73 (0.63-0.75)	0.69 (0.49-0.76)
IL6_PEA_IR	DCTN1	102	63	0.73 (0.6-0.83)	0.71 (0.5-0.88)	0.72 (0.6-0.81)	0.71 (0.5-0.74)	0.68 (0.59-0.72)	0.69 (0.58-0.73)
LAMP3	HPR	101	63	0.73 (0.62-0.83)	0.81 (0.66-0.94)	0.77 (0.68-0.85)	0.62 (0.53-0.71)	0.78 (0.56-0.8)	0.69 (0.58-0.74)
MILR1	SERPIND1	101	63	0.68 (0.54-0.82)	0.8 (0.64-0.95)	0.74 (0.63-0.85)	0.64 (0.56-0.66)	0.75 (0.36-0.78)	0.69 (0.49-0.72)
FC	LRG1	77	44	0.73 (0.55-0.86)	0.74 (0.55-0.89)	0.74 (0.61-0.83)	0.71 (0.37-0.73)	0.71 (0.51-0.73)	0.69 (0.52-0.73)
SERPINA3	HPR	102	67	0.7 (0.59-0.81)	0.76 (0.58-0.92)	0.73 (0.62-0.83)	0.66 (0.61-0.7)	0.73 (0.63-0.74)	0.69 (0.63-0.71)
ITGA11	ORM1	101	63	0.72 (0.59-0.84)	0.74 (0.59-0.86)	0.73 (0.62-0.82)	0.69 (0.59-0.71)	0.71 (0.59-0.74)	0.69 (0.62-0.72)
hsCRP	IL15	98	63	0.76 (0.6-0.87)	0.75 (0.54-0.89)	0.75 (0.63-0.84)	0.65 (0.52-0.78)	0.74 (0.53-0.77)	0.69 (0.56-0.77)
ITGA11	C9	101	63	0.7 (0.58-0.84)	0.74 (0.59-0.87)	0.72 (0.63-0.81)	0.68 (0.6-0.71)	0.7 (0.64-0.74)	0.69 (0.62-0.72)
ITGA11	ITIH2	101	63	0.69 (0.57-0.81)	0.74 (0.58-0.87)	0.72 (0.61-0.81)	0.68 (0.57-0.68)	0.72 (0.51-0.73)	0.69 (0.59-0.7)
CLEC4C	CPN2	101	63	0.67 (0.54-0.8)	0.77 (0.64-0.91)	0.72 (0.63-0.82)	0.63 (0.58-0.65)	0.76 (0.41-0.78)	0.69 (0.52-0.71)
CLEC4C	IL7	101	63	0.68 (0.54-0.81)	0.78 (0.6-0.93)	0.72 (0.62-0.83)	0.62 (0.6-0.66)	0.76 (0.36-0.79)	0.69 (0.49-0.72)
C4B	SERPIND1	102	67	0.66 (0.54-0.76)	0.8 (0.68-0.93)	0.73 (0.64-0.81)	0.63 (0.62-0.64)	0.75 (0.49-0.77)	0.69 (0.56-0.7)
HP	SERPIND1	102	67	0.75 (0.63-0.85)	0.78 (0.64-0.9)	0.77 (0.68-0.84)	0.68 (0.51-0.74)	0.72 (0.56-0.76)	0.69 (0.58-0.74)
hsCRP	VTN	98	67	0.76 (0.61-0.87)	0.77 (0.62-0.89)	0.76 (0.67-0.84)	0.62 (0.52-0.76)	0.78 (0.58-0.78)	0.69 (0.6-0.77)
CLEC4C	ITIH1	101	63	0.67 (0.54-0.8)	0.78 (0.61-0.94)	0.73 (0.63-0.83)	0.63 (0.58-0.65)	0.76 (0.52-0.79)	0.69 (0.58-0.71)
CCL13	F9	102	63	0.7 (0.58-0.82)	0.79 (0.64-0.92)	0.74 (0.65-0.84)	0.68 (0.57-0.69)	0.72 (0.6-0.74)	0.69 (0.62-0.71)
MILR1	NCR1	102	63	0.72 (0.59-0.84)	0.74 (0.61-0.86)	0.73 (0.63-0.82)	0.68 (0.61-0.7)	0.7 (0.54-0.73)	0.69 (0.61-0.72)
DCTN1	C5	101	63	0.76 (0.66-0.84)	0.72 (0.55-0.88)	0.74 (0.64-0.82)	0.7 (0.52-0.76)	0.68 (0.62-0.7)	0.69 (0.58-0.72)
F9	C4B	102	67	0.7 (0.58-0.81)	0.81 (0.66-0.95)	0.76 (0.65-0.85)	0.66 (0.63-0.68)	0.72 (0.5-0.78)	0.69 (0.57-0.72)
MILR1	LAMP3	102	63	0.74 (0.61-0.87)	0.71 (0.57-0.86)	0.73 (0.63-0.82)	0.69 (0.54-0.72)	0.7 (0.64-0.71)	0.69 (0.61-0.71)
IL6_PEA_IR	KLRD1	102	63	0.74 (0.62-0.85)	0.68 (0.52-0.85)	0.71 (0.6-0.81)	0.72 (0.43-0.74)	0.69 (0.57-0.7)	0.69 (0.55-0.72)
CRP_SRM	ITIH3	102	67	0.73 (0.58-0.84)	0.71 (0.53-0.86)	0.72 (0.6-0.81)	0.69 (0.41-0.75)	0.71 (0.59-0.75)	0.69 (0.53-0.74)
C9	F9	102	67	0.69 (0.56-0.82)	0.76 (0.58-0.89)	0.72 (0.61-0.83)	0.68 (0.55-0.69)	0.7 (0.65-0.73)	0.69 (0.62-0.71)
CCL13	APCS	102	63	0.68 (0.56-0.8)	0.81 (0.69-0.92)	0.75 (0.66-0.82)	0.67 (0.55-0.68)	0.72 (0.51-0.82)	0.69 (0.57-0.75)
KLRD1	SERPINA3	101	63	0.71 (0.57-0.82)	0.73 (0.58-0.87)	0.72 (0.61-0.82)	0.69 (0.6-0.7)	0.69 (0.55-0.73)	0.69 (0.6-0.71)
MILR1	FCRL6	102	63	0.7 (0.54-0.86)	0.72 (0.56-0.87)	0.71 (0.59-0.82)	0.69 (0.56-0.7)	0.69 (0.44-0.71)	0.69 (0.55-0.7)

IFNG	F9	102	63	0.76 (0.64-0.87)	0.76 (0.59-0.91)	0.76 (0.65-0.86)	0.65 (0.54-0.75)	0.73 (0.63-0.74)	0.69 (0.6-0.74)
CLEC4C	VTN	101	63	0.67 (0.53-0.81)	0.83 (0.7-0.94)	0.74 (0.66-0.84)	0.6 (0.57-0.64)	0.78 (0.37-0.81)	0.69 (0.48-0.72)
CRP_SRM	C8B	102	67	0.73 (0.6-0.84)	0.74 (0.58-0.88)	0.73 (0.63-0.82)	0.69 (0.54-0.75)	0.71 (0.51-0.77)	0.69 (0.58-0.75)
IL15	C5	102	63	0.72 (0.59-0.82)	0.72 (0.57-0.86)	0.72 (0.63-0.81)	0.71 (0.63-0.72)	0.68 (0.53-0.7)	0.69 (0.6-0.71)
ORM1	F9	102	67	0.71 (0.58-0.84)	0.76 (0.57-0.9)	0.73 (0.61-0.83)	0.67 (0.58-0.7)	0.7 (0.61-0.73)	0.69 (0.62-0.71)
C5	F9	102	67	0.72 (0.59-0.82)	0.76 (0.6-0.9)	0.74 (0.63-0.84)	0.68 (0.6-0.71)	0.69 (0.62-0.74)	0.69 (0.63-0.72)
F9	CFB	102	67	0.72 (0.59-0.83)	0.75 (0.59-0.88)	0.73 (0.62-0.83)	0.67 (0.6-0.71)	0.71 (0.58-0.73)	0.69 (0.62-0.71)
hsCRP	SERPINA3	98	67	0.73 (0.57-0.85)	0.73 (0.55-0.87)	0.72 (0.61-0.83)	0.68 (0.48-0.76)	0.74 (0.57-0.78)	0.69 (0.55-0.77)
CLEC4C	NCR1	102	63	0.68 (0.54-0.81)	0.76 (0.59-0.91)	0.72 (0.62-0.82)	0.63 (0.51-0.66)	0.74 (0.41-0.77)	0.69 (0.53-0.71)
IL6_PEA_IR	SERPINA3	101	63	0.74 (0.6-0.84)	0.7 (0.49-0.88)	0.72 (0.61-0.83)	0.71 (0.37-0.74)	0.68 (0.54-0.7)	0.69 (0.52-0.72)
CLEC4C	KLRD1	102	63	0.7 (0.58-0.82)	0.77 (0.61-0.92)	0.74 (0.64-0.84)	0.66 (0.48-0.68)	0.73 (0.56-0.78)	0.69 (0.58-0.72)
CPN2	F9	102	67	0.71 (0.57-0.84)	0.76 (0.62-0.88)	0.73 (0.62-0.83)	0.68 (0.56-0.7)	0.7 (0.58-0.73)	0.69 (0.6-0.71)
DCTN1	ITGA11	102	63	0.71 (0.58-0.84)	0.74 (0.59-0.88)	0.73 (0.63-0.82)	0.69 (0.58-0.71)	0.68 (0.67-0.71)	0.69 (0.63-0.7)
HGF	CP	102	63	0.69 (0.54-0.8)	0.81 (0.68-0.93)	0.75 (0.65-0.82)	0.65 (0.54-0.67)	0.76 (0.37-0.81)	0.69 (0.5-0.73)
LAMP3	C5	101	63	0.73 (0.61-0.83)	0.71 (0.58-0.84)	0.71 (0.64-0.8)	0.7 (0.58-0.71)	0.68 (0.62-0.71)	0.69 (0.62-0.7)
MILR1	ITIH1	101	63	0.68 (0.54-0.83)	0.78 (0.62-0.91)	0.73 (0.63-0.83)	0.65 (0.54-0.66)	0.73 (0.41-0.76)	0.69 (0.52-0.71)
CRP_SRM	CLU	102	67	0.74 (0.6-0.85)	0.74 (0.6-0.87)	0.73 (0.63-0.83)	0.65 (0.49-0.72)	0.74 (0.49-0.77)	0.68 (0.56-0.74)
LAMP3	SAA1	101	63	0.7 (0.56-0.83)	0.68 (0.51-0.83)	0.69 (0.58-0.8)	0.69 (0.34-0.7)	0.69 (0.49-0.71)	0.68 (0.5-0.7)
CRP_SRM	ITIH2	102	67	0.73 (0.6-0.85)	0.72 (0.55-0.85)	0.72 (0.62-0.82)	0.67 (0.48-0.74)	0.71 (0.56-0.73)	0.68 (0.57-0.73)
CLU	F9	102	67	0.72 (0.61-0.83)	0.75 (0.6-0.88)	0.73 (0.64-0.83)	0.67 (0.55-0.72)	0.71 (0.6-0.73)	0.68 (0.62-0.72)
MILR1	CFB	101	63	0.69 (0.54-0.82)	0.76 (0.57-0.91)	0.72 (0.61-0.83)	0.66 (0.5-0.67)	0.72 (0.45-0.75)	0.68 (0.53-0.71)
SERPINA3	C4B	102	67	0.66 (0.52-0.8)	0.79 (0.64-0.92)	0.72 (0.63-0.83)	0.64 (0.62-0.65)	0.73 (0.48-0.76)	0.68 (0.56-0.7)
FCRL6	SAA1	101	63	0.69 (0.54-0.81)	0.72 (0.51-0.86)	0.7 (0.58-0.8)	0.67 (0.48-0.68)	0.7 (0.5-0.74)	0.68 (0.54-0.71)
IFNG	CP	102	63	0.76 (0.64-0.87)	0.8 (0.67-0.91)	0.78 (0.68-0.86)	0.68 (0.42-0.76)	0.7 (0.46-0.78)	0.68 (0.51-0.75)
LRG1	HPR	102	67	0.7 (0.58-0.81)	0.75 (0.57-0.91)	0.72 (0.61-0.82)	0.65 (0.57-0.7)	0.72 (0.64-0.73)	0.68 (0.62-0.71)
ITIH3	C4B	102	67	0.65 (0.53-0.8)	0.78 (0.63-0.92)	0.72 (0.62-0.83)	0.63 (0.6-0.65)	0.74 (0.44-0.77)	0.68 (0.54-0.71)
MASP1	APCS	101	63	0.76 (0.62-0.85)	0.77 (0.62-0.92)	0.77 (0.67-0.85)	0.7 (0.51-0.75)	0.67 (0.58-0.72)	0.68 (0.58-0.72)
CP	HPR	102	67	0.69 (0.55-0.81)	0.75 (0.58-0.91)	0.72 (0.61-0.82)	0.64 (0.59-0.68)	0.73 (0.61-0.74)	0.68 (0.59-0.71)
MILR1	C3	101	63	0.7 (0.57-0.82)	0.76 (0.6-0.92)	0.73 (0.63-0.83)	0.67 (0.58-0.68)	0.71 (0.52-0.73)	0.68 (0.59-0.7)
FCRL6	LRG1	101	63	0.69 (0.55-0.81)	0.75 (0.61-0.85)	0.72 (0.63-0.8)	0.66 (0.55-0.68)	0.73 (0.54-0.75)	0.68 (0.59-0.71)

IFNG	C5	102	63	0.77 (0.64-0.87)	0.71 (0.57-0.84)	0.74 (0.65-0.82)	0.68 (0.5-0.76)	0.69 (0.65-0.7)	0.68 (0.59-0.73)
CCL4	SERPINA3	102	63	0.69 (0.55-0.81)	0.74 (0.57-0.87)	0.71 (0.61-0.81)	0.68 (0.46-0.69)	0.71 (0.54-0.73)	0.68 (0.56-0.71)
CLEC4C	IL15	101	63	0.68 (0.54-0.81)	0.77 (0.54-0.91)	0.72 (0.59-0.81)	0.64 (0.57-0.65)	0.74 (0.51-0.77)	0.68 (0.57-0.71)
ITIH3	CP	102	67	0.7 (0.58-0.82)	0.74 (0.57-0.88)	0.72 (0.62-0.81)	0.66 (0.49-0.68)	0.72 (0.55-0.74)	0.68 (0.57-0.71)
IL7	C5	102	63	0.71 (0.59-0.81)	0.77 (0.6-0.9)	0.74 (0.65-0.82)	0.66 (0.56-0.7)	0.72 (0.44-0.76)	0.68 (0.54-0.72)
NCR1	LRG1	101	63	0.68 (0.54-0.82)	0.74 (0.62-0.86)	0.71 (0.62-0.8)	0.67 (0.57-0.68)	0.71 (0.5-0.76)	0.68 (0.57-0.71)
CLEC4C	C9	101	63	0.7 (0.55-0.83)	0.76 (0.6-0.91)	0.73 (0.63-0.83)	0.67 (0.46-0.7)	0.7 (0.61-0.77)	0.68 (0.58-0.73)
NCR1	SERPIND1	101	63	0.67 (0.53-0.78)	0.81 (0.68-0.92)	0.74 (0.65-0.82)	0.65 (0.57-0.66)	0.73 (0.4-0.8)	0.68 (0.51-0.73)
MILR1	IL6_PEA_cytokine	101	63	0.72 (0.58-0.85)	0.73 (0.55-0.89)	0.72 (0.6-0.83)	0.66 (0.51-0.75)	0.7 (0.52-0.8)	0.68 (0.55-0.76)
IL7	SERPIND1	102	63	0.63 (0.51-0.74)	0.85 (0.74-0.93)	0.74 (0.66-0.81)	0.6 (0.58-0.61)	0.77 (0.21-0.83)	0.68 (0.41-0.72)
KLRD1	PZP	100	63	0.72 (0.62-0.81)	0.73 (0.57-0.87)	0.72 (0.63-0.81)	0.7 (0.45-0.71)	0.67 (0.51-0.71)	0.68 (0.54-0.71)
KLRD1	LRG1	101	63	0.72 (0.58-0.82)	0.72 (0.58-0.84)	0.71 (0.61-0.8)	0.69 (0.52-0.7)	0.68 (0.55-0.71)	0.68 (0.58-0.7)
IL6_PEA_cytokin	LRG1	102	63	0.7 (0.56-0.81)	0.72 (0.51-0.86)	0.71 (0.59-0.82)	0.64 (0.43-0.72)	0.73 (0.49-0.77)	0.68 (0.54-0.73)
DCTN1	C4B	101	63	0.7 (0.57-0.81)	0.8 (0.6-0.95)	0.75 (0.63-0.84)	0.67 (0.52-0.69)	0.71 (0.55-0.74)	0.68 (0.59-0.7)
SAA1	CLU	102	67	0.67 (0.5-0.81)	0.74 (0.58-0.88)	0.7 (0.59-0.81)	0.64 (0.47-0.66)	0.74 (0.43-0.75)	0.68 (0.48-0.7)
F9	SERPIND1	102	67	0.7 (0.57-0.82)	0.79 (0.65-0.9)	0.75 (0.65-0.83)	0.67 (0.51-0.69)	0.72 (0.56-0.76)	0.68 (0.58-0.72)
ITIH3	HPR	102	67	0.72 (0.61-0.82)	0.75 (0.56-0.91)	0.73 (0.62-0.83)	0.66 (0.55-0.7)	0.71 (0.63-0.73)	0.68 (0.61-0.71)
HGF	C4B	102	63	0.67 (0.53-0.78)	0.79 (0.58-0.97)	0.73 (0.6-0.83)	0.63 (0.61-0.66)	0.73 (0.45-0.78)	0.68 (0.54-0.71)
IL6_PEA_IR	ITIH3	101	63	0.74 (0.6-0.86)	0.67 (0.48-0.85)	0.7 (0.59-0.8)	0.72 (0.34-0.74)	0.65 (0.6-0.68)	0.68 (0.49-0.71)
MILR1	CCL4	101	63	0.71 (0.56-0.83)	0.72 (0.56-0.86)	0.72 (0.61-0.81)	0.66 (0.52-0.7)	0.7 (0.52-0.71)	0.68 (0.56-0.7)
DCTN1	HPR	101	63	0.71 (0.56-0.82)	0.83 (0.67-0.95)	0.77 (0.66-0.86)	0.61 (0.53-0.7)	0.76 (0.48-0.79)	0.68 (0.55-0.74)
IL15	SERPIND1	102	63	0.65 (0.53-0.76)	0.83 (0.67-0.95)	0.74 (0.64-0.83)	0.62 (0.61-0.62)	0.74 (0.43-0.81)	0.68 (0.52-0.71)
CRP_SRM	SAA1	102	67	0.73 (0.49-0.85)	0.71 (0.41-0.87)	0.71 (0.54-0.82)	0.68 (0.32-0.75)	0.73 (0.49-0.74)	0.68 (0.5-0.74)
C5	PZP	101	67	0.72 (0.61-0.82)	0.71 (0.56-0.84)	0.72 (0.63-0.81)	0.7 (0.45-0.72)	0.67 (0.56-0.7)	0.68 (0.54-0.71)
NCR1	SAA1	101	63	0.68 (0.53-0.82)	0.7 (0.52-0.82)	0.69 (0.58-0.79)	0.66 (0.45-0.66)	0.7 (0.44-0.72)	0.68 (0.52-0.69)
MILR1	C2	101	63	0.69 (0.53-0.84)	0.74 (0.59-0.9)	0.72 (0.61-0.82)	0.66 (0.5-0.68)	0.71 (0.38-0.72)	0.68 (0.51-0.69)
KLRD1	ITIH3	101	63	0.72 (0.6-0.83)	0.69 (0.56-0.82)	0.71 (0.61-0.79)	0.7 (0.55-0.72)	0.67 (0.6-0.69)	0.68 (0.59-0.7)
CRP_SRM	CPN2	102	67	0.74 (0.6-0.84)	0.72 (0.54-0.86)	0.72 (0.62-0.81)	0.66 (0.37-0.75)	0.72 (0.52-0.73)	0.68 (0.54-0.74)
hsCRP	CCL13	98	63	0.73 (0.6-0.85)	0.74 (0.56-0.9)	0.73 (0.62-0.83)	0.65 (0.48-0.75)	0.71 (0.54-0.77)	0.68 (0.57-0.74)
CRP_SRM	ITIH1	102	67	0.73 (0.59-0.85)	0.73 (0.55-0.88)	0.73 (0.62-0.84)	0.66 (0.43-0.75)	0.72 (0.53-0.73)	0.68 (0.54-0.73)

IL15	C4B	102	63	0.67 (0.53-0.79)	0.77 (0.57-0.94)	0.72 (0.6-0.83)	0.65 (0.63-0.65)	0.71 (0.51-0.75)	0.68 (0.58-0.7)
SERPINA3	CP	102	67	0.69 (0.57-0.81)	0.74 (0.58-0.88)	0.72 (0.62-0.8)	0.67 (0.55-0.69)	0.69 (0.56-0.73)	0.68 (0.58-0.71)
LAMP3	C4B	101	63	0.69 (0.56-0.82)	0.76 (0.57-0.93)	0.73 (0.62-0.84)	0.65 (0.56-0.67)	0.7 (0.56-0.74)	0.68 (0.59-0.69)
CLEC4C	HGF	101	63	0.68 (0.53-0.81)	0.78 (0.59-0.93)	0.72 (0.61-0.83)	0.64 (0.5-0.66)	0.75 (0.34-0.77)	0.68 (0.49-0.71)
C4B	CFB	102	67	0.65 (0.53-0.78)	0.77 (0.58-0.92)	0.71 (0.61-0.8)	0.62 (0.61-0.63)	0.73 (0.43-0.75)	0.68 (0.53-0.69)
CLEC4C	CCL4	101	63	0.71 (0.59-0.83)	0.78 (0.6-0.92)	0.74 (0.65-0.84)	0.62 (0.55-0.71)	0.76 (0.54-0.77)	0.68 (0.57-0.73)
C2	C4B	102	67	0.65 (0.53-0.77)	0.78 (0.58-0.94)	0.72 (0.6-0.81)	0.62 (0.62-0.63)	0.73 (0.47-0.76)	0.68 (0.55-0.69)
CRP_SRM	HPR	102	67	0.76 (0.63-0.87)	0.74 (0.54-0.91)	0.75 (0.64-0.85)	0.64 (0.5-0.78)	0.71 (0.6-0.72)	0.68 (0.6-0.74)
IL15	LRG1	102	63	0.68 (0.54-0.81)	0.72 (0.56-0.84)	0.7 (0.6-0.8)	0.67 (0.57-0.68)	0.71 (0.53-0.74)	0.68 (0.58-0.71)
IL15	SAA1	102	63	0.69 (0.54-0.82)	0.68 (0.51-0.82)	0.68 (0.58-0.78)	0.66 (0.48-0.69)	0.7 (0.48-0.73)	0.68 (0.55-0.71)
KLRD1	C3	101	63	0.71 (0.59-0.82)	0.73 (0.58-0.87)	0.72 (0.62-0.81)	0.68 (0.55-0.71)	0.69 (0.56-0.71)	0.68 (0.59-0.71)
C3	HPR	102	67	0.67 (0.55-0.78)	0.75 (0.56-0.92)	0.71 (0.6-0.81)	0.65 (0.53-0.66)	0.72 (0.52-0.73)	0.67 (0.56-0.69)
CLEC4C	ORM1	101	63	0.69 (0.54-0.83)	0.77 (0.58-0.91)	0.72 (0.61-0.83)	0.65 (0.46-0.67)	0.71 (0.44-0.76)	0.67 (0.54-0.71)
C4B	SERPING1	102	67	0.65 (0.54-0.77)	0.78 (0.57-0.92)	0.72 (0.6-0.81)	0.63 (0.58-0.64)	0.73 (0.49-0.75)	0.67 (0.55-0.69)
NCR1	SERPINA3	101	63	0.67 (0.53-0.81)	0.74 (0.59-0.9)	0.7 (0.59-0.81)	0.64 (0.59-0.65)	0.71 (0.46-0.75)	0.67 (0.55-0.7)
hsCRP	IL13	98	63	0.78 (0.65-0.89)	0.75 (0.48-0.9)	0.76 (0.62-0.86)	0.73 (0.22-0.78)	0.62 (0.61-0.66)	0.67 (0.42-0.71)
HPR	SERPIND1	102	67	0.65 (0.53-0.77)	0.77 (0.6-0.91)	0.71 (0.61-0.8)	0.63 (0.57-0.64)	0.73 (0.51-0.74)	0.67 (0.57-0.69)
CLU	C4B	102	67	0.66 (0.51-0.78)	0.8 (0.65-0.94)	0.73 (0.64-0.82)	0.62 (0.6-0.63)	0.73 (0.4-0.77)	0.67 (0.51-0.7)
ITGA11	VTN	101	63	0.7 (0.58-0.82)	0.8 (0.66-0.89)	0.75 (0.65-0.82)	0.64 (0.44-0.68)	0.76 (0.4-0.78)	0.67 (0.49-0.73)
IL6_PEA_IR	MASP1	102	63	0.77 (0.64-0.86)	0.68 (0.5-0.87)	0.72 (0.62-0.83)	0.75 (0.24-0.77)	0.61 (0.58-0.63)	0.67 (0.42-0.69)
HPR	PZP	101	67	0.65 (0.52-0.77)	0.74 (0.57-0.91)	0.69 (0.58-0.8)	0.63 (0.54-0.64)	0.72 (0.43-0.74)	0.67 (0.53-0.69)
SAA1	C8B	102	67	0.66 (0.49-0.78)	0.74 (0.53-0.89)	0.7 (0.57-0.8)	0.63 (0.48-0.65)	0.75 (0.39-0.76)	0.67 (0.47-0.7)
LRG1	CP	102	67	0.68 (0.55-0.79)	0.74 (0.55-0.88)	0.71 (0.6-0.81)	0.64 (0.51-0.67)	0.73 (0.51-0.74)	0.67 (0.55-0.7)
C2	HPR	102	67	0.66 (0.54-0.77)	0.75 (0.58-0.91)	0.71 (0.6-0.81)	0.64 (0.6-0.65)	0.71 (0.5-0.73)	0.67 (0.57-0.68)
SAA1	ITIH1	102	67	0.66 (0.52-0.81)	0.73 (0.54-0.89)	0.7 (0.59-0.8)	0.64 (0.45-0.65)	0.71 (0.48-0.72)	0.67 (0.51-0.68)
hsCRP	C3	98	67	0.76 (0.61-0.88)	0.69 (0.51-0.86)	0.72 (0.62-0.83)	0.67 (0.42-0.76)	0.69 (0.56-0.71)	0.67 (0.53-0.73)
hsCRP	MASP1	98	63	0.78 (0.63-0.9)	0.71 (0.52-0.87)	0.74 (0.62-0.84)	0.68 (0.38-0.78)	0.67 (0.61-0.73)	0.67 (0.53-0.75)
LAMP3	SERPINA3	101	63	0.7 (0.56-0.83)	0.74 (0.6-0.85)	0.71 (0.61-0.8)	0.66 (0.49-0.68)	0.72 (0.54-0.75)	0.67 (0.58-0.71)
FCRL6	C8B	101	63	0.66 (0.54-0.79)	0.76 (0.62-0.89)	0.71 (0.62-0.81)	0.64 (0.56-0.65)	0.72 (0.5-0.75)	0.67 (0.57-0.7)
CPN2	C4B	102	67	0.65 (0.55-0.78)	0.78 (0.62-0.93)	0.72 (0.62-0.82)	0.63 (0.59-0.64)	0.73 (0.42-0.75)	0.67 (0.52-0.69)

SERPINA3	PZP	101	67	0.69 (0.56-0.81)	0.71 (0.55-0.87)	0.7 (0.58-0.8)	0.67 (0.48-0.69)	0.68 (0.54-0.69)	0.67 (0.56-0.69)
ORM1	C4B	102	67	0.66 (0.53-0.79)	0.78 (0.59-0.92)	0.72 (0.61-0.82)	0.63 (0.59-0.64)	0.72 (0.45-0.76)	0.67 (0.54-0.7)
IL6_PEA_cytokin	SAA1	102	63	0.69 (0.49-0.82)	0.7 (0.41-0.86)	0.69 (0.53-0.8)	0.66 (0.32-0.73)	0.7 (0.42-0.71)	0.67 (0.48-0.71)
HGF	SERPIND1	102	63	0.63 (0.51-0.74)	0.8 (0.67-0.92)	0.71 (0.62-0.8)	0.6 (0.55-0.61)	0.77 (0.26-0.79)	0.67 (0.43-0.7)
FCRL6	C3	101	63	0.66 (0.54-0.77)	0.76 (0.61-0.92)	0.71 (0.6-0.8)	0.64 (0.54-0.65)	0.73 (0.49-0.77)	0.67 (0.55-0.71)
NCR1	PZP	100	63	0.68 (0.54-0.79)	0.74 (0.57-0.88)	0.71 (0.61-0.8)	0.65 (0.49-0.67)	0.69 (0.43-0.76)	0.67 (0.52-0.71)
CLU	HPR	102	67	0.65 (0.54-0.76)	0.77 (0.61-0.92)	0.71 (0.61-0.81)	0.63 (0.54-0.64)	0.71 (0.54-0.74)	0.67 (0.58-0.69)
FC	KLRD1	76	43	0.76 (0.56-0.9)	0.77 (0.59-0.92)	0.76 (0.63-0.87)	0.69 (0.41-0.76)	0.65 (0.54-0.71)	0.67 (0.52-0.73)
LRG1	PZP	101	67	0.67 (0.52-0.79)	0.73 (0.54-0.84)	0.69 (0.58-0.79)	0.65 (0.5-0.66)	0.71 (0.46-0.72)	0.67 (0.51-0.69)
KLRD1	C8B	101	63	0.7 (0.58-0.82)	0.72 (0.58-0.87)	0.71 (0.62-0.81)	0.67 (0.58-0.7)	0.67 (0.57-0.71)	0.67 (0.6-0.7)
FC	HPR	77	44	0.8 (0.63-0.9)	0.74 (0.52-0.98)	0.76 (0.62-0.9)	0.61 (0.47-0.79)	0.74 (0.69-0.76)	0.67 (0.6-0.77)
FC	ITIH1	77	44	0.73 (0.57-0.89)	0.72 (0.53-0.94)	0.73 (0.59-0.86)	0.67 (0.29-0.72)	0.67 (0.56-0.69)	0.67 (0.48-0.7)
CLEC4C	CCL13	101	63	0.67 (0.53-0.81)	0.76 (0.62-0.92)	0.71 (0.62-0.83)	0.63 (0.53-0.66)	0.73 (0.38-0.77)	0.67 (0.51-0.71)
MILR1	IFNG	101	63	0.77 (0.62-0.89)	0.71 (0.54-0.85)	0.74 (0.64-0.83)	0.66 (0.52-0.78)	0.68 (0.52-0.71)	0.67 (0.56-0.73)
ITGA11	CCL13	101	63	0.7 (0.59-0.81)	0.73 (0.6-0.86)	0.71 (0.63-0.8)	0.66 (0.6-0.69)	0.69 (0.51-0.72)	0.67 (0.58-0.7)
IL6_PEA_IR	LAMP3	102	63	0.76 (0.65-0.85)	0.65 (0.48-0.84)	0.71 (0.6-0.81)	0.72 (0.31-0.76)	0.65 (0.56-0.66)	0.67 (0.47-0.71)
C9	HPR	102	67	0.7 (0.57-0.82)	0.74 (0.55-0.91)	0.72 (0.6-0.83)	0.66 (0.57-0.71)	0.7 (0.59-0.72)	0.67 (0.59-0.71)
CFB	HPR	102	67	0.66 (0.54-0.77)	0.74 (0.58-0.9)	0.7 (0.59-0.8)	0.64 (0.6-0.65)	0.71 (0.52-0.72)	0.67 (0.57-0.68)
IL7	SAA1	102	63	0.64 (0.51-0.78)	0.77 (0.59-0.9)	0.7 (0.59-0.82)	0.6 (0.45-0.61)	0.76 (0.36-0.78)	0.67 (0.44-0.69)
ORM1	PZP	101	67	0.71 (0.55-0.83)	0.71 (0.58-0.83)	0.71 (0.61-0.79)	0.7 (0.48-0.71)	0.66 (0.48-0.71)	0.67 (0.56-0.71)
SERPIND1	PZP	101	67	0.64 (0.51-0.75)	0.77 (0.61-0.9)	0.7 (0.61-0.79)	0.61 (0.51-0.63)	0.75 (0.33-0.76)	0.67 (0.44-0.69)
IL6_PEA_IR	CLEC4C	102	63	0.75 (0.63-0.84)	0.75 (0.54-0.93)	0.75 (0.64-0.85)	0.65 (0.52-0.76)	0.73 (0.52-0.77)	0.67 (0.56-0.76)
IL6_PEA_IR	PZP	100	63	0.73 (0.59-0.82)	0.75 (0.56-0.89)	0.73 (0.62-0.82)	0.7 (0.35-0.73)	0.66 (0.51-0.77)	0.67 (0.47-0.74)
C5	HPR	102	67	0.72 (0.61-0.82)	0.74 (0.56-0.91)	0.73 (0.63-0.83)	0.65 (0.54-0.71)	0.7 (0.57-0.71)	0.67 (0.58-0.7)
FCRL6	ITIH3	101	63	0.68 (0.56-0.81)	0.72 (0.6-0.85)	0.7 (0.62-0.8)	0.65 (0.56-0.67)	0.71 (0.52-0.74)	0.67 (0.57-0.7)
HPR	VTN	102	67	0.65 (0.54-0.77)	0.78 (0.63-0.91)	0.72 (0.62-0.81)	0.63 (0.52-0.64)	0.72 (0.47-0.76)	0.67 (0.53-0.7)
CRP_SRM	SERPINA3	102	67	0.72 (0.57-0.84)	0.71 (0.53-0.88)	0.71 (0.6-0.82)	0.65 (0.43-0.75)	0.74 (0.53-0.79)	0.67 (0.53-0.76)
IL6_PEA_cytokin	SERPINA3	102	63	0.71 (0.58-0.82)	0.7 (0.49-0.88)	0.7 (0.59-0.81)	0.64 (0.43-0.72)	0.7 (0.54-0.75)	0.67 (0.53-0.73)
CCL4	PZP	101	63	0.66 (0.49-0.79)	0.79 (0.63-0.9)	0.72 (0.6-0.81)	0.66 (0.46-0.67)	0.7 (0.46-0.79)	0.67 (0.48-0.73)
LRG1	SERPIND1	102	67	0.66 (0.53-0.78)	0.77 (0.62-0.89)	0.71 (0.61-0.81)	0.63 (0.52-0.65)	0.73 (0.43-0.75)	0.67 (0.53-0.7)

C5	CP	102	67	0.72 (0.59-0.81)	0.74 (0.56-0.88)	0.73 (0.62-0.81)	0.68 (0.54-0.71)	0.66 (0.53-0.73)	0.67 (0.57-0.72)
SAA1	CPN2	102	67	0.67 (0.52-0.79)	0.72 (0.55-0.85)	0.69 (0.58-0.78)	0.64 (0.48-0.66)	0.71 (0.45-0.72)	0.67 (0.49-0.69)
HGF	CRP_SRM	102	63	0.75 (0.6-0.85)	0.82 (0.65-0.91)	0.78 (0.66-0.86)	0.67 (0.44-0.75)	0.74 (0.47-0.84)	0.67 (0.51-0.78)
CLEC4C	ITIH2	101	63	0.67 (0.54-0.81)	0.75 (0.6-0.92)	0.71 (0.62-0.82)	0.62 (0.57-0.65)	0.74 (0.49-0.77)	0.67 (0.55-0.7)
IL6_PEA_IR	C8B	101	63	0.75 (0.62-0.84)	0.68 (0.49-0.88)	0.72 (0.6-0.83)	0.71 (0.3-0.75)	0.65 (0.55-0.68)	0.67 (0.47-0.71)
hsCRP	HPR	98	67	0.75 (0.61-0.86)	0.74 (0.54-0.91)	0.75 (0.63-0.84)	0.63 (0.46-0.77)	0.71 (0.5-0.72)	0.67 (0.57-0.74)
hsCRP	NCR1	98	63	0.74 (0.6-0.86)	0.71 (0.54-0.86)	0.73 (0.62-0.82)	0.66 (0.43-0.75)	0.68 (0.49-0.73)	0.67 (0.52-0.72)
MASP1	F9	101	63	0.76 (0.63-0.87)	0.76 (0.58-0.91)	0.76 (0.63-0.86)	0.68 (0.46-0.76)	0.64 (0.57-0.72)	0.67 (0.56-0.73)
LRG1	C5	102	67	0.72 (0.59-0.82)	0.7 (0.53-0.83)	0.71 (0.61-0.79)	0.7 (0.48-0.71)	0.66 (0.51-0.7)	0.67 (0.55-0.7)
ORM1	CP	102	67	0.71 (0.57-0.83)	0.74 (0.56-0.88)	0.72 (0.61-0.81)	0.67 (0.5-0.7)	0.69 (0.51-0.75)	0.67 (0.55-0.71)
MASP1	CRP_SRM	101	63	0.77 (0.63-0.87)	0.7 (0.5-0.87)	0.73 (0.62-0.83)	0.66 (0.38-0.77)	0.67 (0.57-0.74)	0.67 (0.53-0.75)
MILR1	VTN	101	63	0.68 (0.54-0.82)	0.8 (0.66-0.92)	0.74 (0.65-0.84)	0.62 (0.49-0.65)	0.73 (0.33-0.78)	0.67 (0.47-0.71)
CP	CLU	102	67	0.67 (0.55-0.79)	0.75 (0.61-0.89)	0.71 (0.61-0.8)	0.64 (0.57-0.67)	0.71 (0.48-0.75)	0.67 (0.56-0.7)
MILR1	CLU	101	63	0.68 (0.55-0.81)	0.74 (0.57-0.9)	0.71 (0.6-0.82)	0.64 (0.53-0.66)	0.71 (0.51-0.72)	0.67 (0.56-0.69)
LAMP3	PZP	100	63	0.72 (0.56-0.84)	0.74 (0.58-0.88)	0.72 (0.61-0.82)	0.68 (0.43-0.72)	0.67 (0.46-0.75)	0.67 (0.51-0.71)
C3	C4B	102	67	0.66 (0.54-0.77)	0.78 (0.59-0.94)	0.72 (0.61-0.82)	0.64 (0.57-0.65)	0.7 (0.43-0.75)	0.67 (0.53-0.7)
IL6_PEA_IR	IL15	101	63	0.73 (0.6-0.85)	0.67 (0.51-0.87)	0.7 (0.59-0.81)	0.7 (0.35-0.74)	0.66 (0.51-0.71)	0.67 (0.48-0.72)
MILR1	C9	101	63	0.72 (0.58-0.86)	0.71 (0.54-0.88)	0.72 (0.61-0.81)	0.65 (0.47-0.72)	0.69 (0.6-0.7)	0.67 (0.57-0.7)
ORM1	HPR	102	67	0.7 (0.57-0.81)	0.75 (0.56-0.91)	0.72 (0.6-0.82)	0.64 (0.57-0.69)	0.7 (0.56-0.72)	0.67 (0.58-0.7)
CCL4	ITIH3	102	63	0.71 (0.59-0.84)	0.67 (0.51-0.81)	0.69 (0.58-0.79)	0.7 (0.35-0.71)	0.65 (0.59-0.68)	0.67 (0.5-0.69)
KLRD1	C9	101	63	0.71 (0.56-0.84)	0.7 (0.56-0.82)	0.7 (0.6-0.8)	0.69 (0.51-0.72)	0.66 (0.55-0.69)	0.67 (0.56-0.7)
FCRL6	CFB	101	63	0.64 (0.53-0.76)	0.78 (0.66-0.9)	0.71 (0.62-0.79)	0.62 (0.56-0.64)	0.72 (0.44-0.78)	0.67 (0.53-0.71)
CPN2	HPR	102	67	0.66 (0.54-0.78)	0.76 (0.57-0.91)	0.7 (0.59-0.81)	0.62 (0.58-0.64)	0.71 (0.42-0.73)	0.67 (0.52-0.68)
IL13	CRP_SRM	102	63	0.77 (0.64-0.87)	0.75 (0.44-0.89)	0.75 (0.58-0.85)	0.7 (0.23-0.77)	0.62 (0.61-0.66)	0.67 (0.42-0.71)
CP	PZP	101	67	0.68 (0.52-0.79)	0.75 (0.56-0.89)	0.71 (0.58-0.8)	0.65 (0.43-0.67)	0.73 (0.43-0.73)	0.67 (0.52-0.7)
IL6_PEA_cytokin	CFB	102	63	0.68 (0.52-0.78)	0.73 (0.5-0.9)	0.71 (0.57-0.8)	0.59 (0.5-0.69)	0.74 (0.37-0.77)	0.67 (0.48-0.72)
IFNG	IL15	102	63	0.76 (0.62-0.88)	0.64 (0.47-0.79)	0.7 (0.59-0.8)	0.7 (0.39-0.76)	0.64 (0.59-0.64)	0.67 (0.51-0.7)
IFNG	SAA1	102	63	0.75 (0.57-0.88)	0.69 (0.46-0.85)	0.72 (0.56-0.83)	0.69 (0.27-0.75)	0.67 (0.47-0.68)	0.67 (0.46-0.71)
C5	SERPINA3	102	67	0.71 (0.59-0.83)	0.68 (0.54-0.82)	0.69 (0.61-0.8)	0.69 (0.42-0.71)	0.65 (0.55-0.67)	0.67 (0.53-0.68)
SAA1	C3	102	67	0.67 (0.51-0.8)	0.7 (0.52-0.88)	0.68 (0.56-0.8)	0.65 (0.46-0.67)	0.68 (0.49-0.69)	0.66 (0.52-0.67)

C9	C4B	102	67	0.64 (0.52-0.79)	0.77 (0.59-0.93)	0.71 (0.6-0.82)	0.64 (0.56-0.65)	0.7 (0.44-0.75)	0.66 (0.53-0.7)
ITIH3	C5	102	67	0.72 (0.6-0.83)	0.67 (0.55-0.81)	0.69 (0.61-0.79)	0.69 (0.49-0.71)	0.65 (0.59-0.66)	0.66 (0.56-0.68)
C4B	ITIH1	102	67	0.65 (0.53-0.78)	0.78 (0.61-0.93)	0.72 (0.61-0.82)	0.63 (0.59-0.64)	0.71 (0.45-0.75)	0.66 (0.54-0.69)
IL6_PEA_cytokin	C2	102	63	0.68 (0.5-0.79)	0.72 (0.5-0.89)	0.7 (0.57-0.8)	0.65 (0.53-0.68)	0.71 (0.42-0.73)	0.66 (0.49-0.7)
MILR1	CPN2	101	63	0.68 (0.53-0.83)	0.73 (0.55-0.9)	0.7 (0.59-0.82)	0.64 (0.49-0.65)	0.7 (0.34-0.72)	0.66 (0.48-0.68)
FC	ITIH2	77	44	0.73 (0.57-0.88)	0.71 (0.54-0.88)	0.72 (0.6-0.84)	0.66 (0.33-0.7)	0.69 (0.51-0.71)	0.66 (0.5-0.7)
IL17F	F9	102	63	0.75 (0.64-0.85)	0.74 (0.56-0.9)	0.74 (0.64-0.84)	0.68 (0.56-0.75)	0.66 (0.53-0.7)	0.66 (0.59-0.71)
C4B	VTN	102	67	0.66 (0.52-0.79)	0.79 (0.65-0.93)	0.73 (0.64-0.82)	0.6 (0.56-0.62)	0.74 (0.38-0.77)	0.66 (0.49-0.69)
ITIH3	PZP	101	67	0.69 (0.56-0.82)	0.7 (0.55-0.83)	0.7 (0.6-0.78)	0.67 (0.44-0.69)	0.67 (0.51-0.7)	0.66 (0.54-0.69)
MILR1	HGF	101	63	0.67 (0.53-0.81)	0.75 (0.56-0.9)	0.71 (0.6-0.82)	0.64 (0.51-0.65)	0.71 (0.32-0.74)	0.66 (0.47-0.69)
FC	DCTN1	76	43	0.76 (0.59-0.89)	0.7 (0.46-0.94)	0.73 (0.57-0.86)	0.66 (0.27-0.78)	0.67 (0.6-0.71)	0.66 (0.47-0.73)
hsCRP	FC	83	46	0.76 (0.61-0.9)	0.71 (0.41-0.9)	0.73 (0.57-0.85)	0.61 (0.25-0.77)	0.72 (0.68-0.73)	0.66 (0.48-0.74)
KLRD1	CFB	101	63	0.69 (0.56-0.8)	0.76 (0.65-0.88)	0.72 (0.64-0.81)	0.66 (0.57-0.68)	0.68 (0.53-0.77)	0.66 (0.58-0.72)
IL13	F9	102	63	0.72 (0.6-0.83)	0.76 (0.58-0.91)	0.73 (0.63-0.84)	0.68 (0.63-0.72)	0.65 (0.58-0.66)	0.66 (0.62-0.69)
C8B	SERPIND1	102	67	0.66 (0.55-0.78)	0.78 (0.65-0.91)	0.72 (0.64-0.8)	0.64 (0.57-0.65)	0.7 (0.49-0.76)	0.66 (0.55-0.7)
IL15	SERPINA3	102	63	0.66 (0.52-0.81)	0.75 (0.57-0.89)	0.7 (0.59-0.81)	0.64 (0.58-0.65)	0.69 (0.51-0.73)	0.66 (0.58-0.69)
FC	MILR1	76	43	0.79 (0.61-0.92)	0.73 (0.53-0.91)	0.76 (0.62-0.87)	0.62 (0.44-0.78)	0.71 (0.56-0.73)	0.66 (0.56-0.75)
CCL13	C4B	102	63	0.64 (0.53-0.77)	0.82 (0.68-0.95)	0.73 (0.64-0.82)	0.62 (0.57-0.63)	0.71 (0.42-0.78)	0.66 (0.51-0.7)
FCRL6	IL7	101	63	0.64 (0.53-0.75)	0.78 (0.65-0.89)	0.71 (0.61-0.79)	0.61 (0.55-0.61)	0.73 (0.31-0.77)	0.66 (0.46-0.69)
ITIH3	SERPIND1	102	67	0.67 (0.54-0.8)	0.77 (0.61-0.89)	0.72 (0.63-0.8)	0.63 (0.54-0.66)	0.71 (0.48-0.75)	0.66 (0.54-0.7)
SAA1	ITIH2	102	67	0.67 (0.53-0.81)	0.7 (0.53-0.85)	0.68 (0.57-0.79)	0.64 (0.44-0.65)	0.69 (0.48-0.71)	0.66 (0.51-0.68)
CRP_SRM	SERPIND1	102	67	0.74 (0.59-0.84)	0.78 (0.62-0.9)	0.76 (0.66-0.84)	0.6 (0.43-0.73)	0.77 (0.38-0.79)	0.66 (0.47-0.75)
LAMP3	LRG1	101	63	0.7 (0.54-0.82)	0.73 (0.6-0.84)	0.71 (0.62-0.79)	0.66 (0.48-0.68)	0.69 (0.55-0.74)	0.66 (0.56-0.71)
CRP_SRM	C9	102	67	0.71 (0.55-0.83)	0.7 (0.52-0.86)	0.71 (0.58-0.81)	0.67 (0.34-0.75)	0.69 (0.5-0.75)	0.66 (0.5-0.74)
IL6_PEA_cytokin	C8B	102	63	0.71 (0.58-0.83)	0.68 (0.5-0.87)	0.7 (0.58-0.81)	0.67 (0.31-0.74)	0.67 (0.47-0.67)	0.66 (0.48-0.7)
HPR	ITIH1	102	67	0.66 (0.54-0.77)	0.75 (0.56-0.9)	0.7 (0.59-0.8)	0.63 (0.56-0.64)	0.7 (0.5-0.72)	0.66 (0.54-0.68)
MILR1	PZP	100	63	0.67 (0.52-0.8)	0.72 (0.56-0.89)	0.7 (0.58-0.8)	0.64 (0.44-0.66)	0.68 (0.34-0.71)	0.66 (0.48-0.68)
KLRD1	C2	101	63	0.7 (0.57-0.81)	0.73 (0.6-0.88)	0.72 (0.62-0.81)	0.67 (0.56-0.7)	0.67 (0.56-0.71)	0.66 (0.59-0.7)
CRP_SRM	CP	102	67	0.73 (0.6-0.85)	0.73 (0.54-0.9)	0.73 (0.61-0.83)	0.59 (0.49-0.74)	0.75 (0.46-0.76)	0.66 (0.53-0.75)
C4B	ITIH2	102	67	0.66 (0.54-0.78)	0.78 (0.61-0.93)	0.72 (0.61-0.82)	0.62 (0.58-0.64)	0.71 (0.45-0.75)	0.66 (0.53-0.69)

CP	SERPIND1	102	67	0.68 (0.53-0.78)	0.76 (0.61-0.89)	0.72 (0.62-0.81)	0.61 (0.53-0.66)	0.72 (0.39-0.75)	0.66 (0.5-0.7)
KLRD1	LAMP3	102	63	0.71 (0.59-0.82)	0.68 (0.56-0.8)	0.7 (0.61-0.77)	0.68 (0.55-0.69)	0.65 (0.57-0.66)	0.66 (0.58-0.67)
NCR1	C8B	101	63	0.68 (0.55-0.8)	0.69 (0.52-0.89)	0.69 (0.58-0.81)	0.67 (0.37-0.68)	0.66 (0.51-0.69)	0.66 (0.5-0.68)
IL6_PEA_cytokin	C3	102	63	0.68 (0.53-0.79)	0.69 (0.49-0.9)	0.68 (0.55-0.79)	0.66 (0.38-0.69)	0.68 (0.48-0.7)	0.66 (0.5-0.69)
hsCRP	LRG1	98	67	0.73 (0.54-0.86)	0.71 (0.53-0.86)	0.72 (0.58-0.83)	0.64 (0.49-0.76)	0.73 (0.56-0.77)	0.66 (0.54-0.76)
CFB	SERPIND1	102	67	0.64 (0.51-0.75)	0.75 (0.61-0.89)	0.7 (0.6-0.78)	0.62 (0.57-0.64)	0.71 (0.29-0.74)	0.66 (0.45-0.69)
FC	IL15	77	43	0.74 (0.59-0.88)	0.67 (0.46-0.87)	0.7 (0.57-0.83)	0.68 (0.35-0.75)	0.64 (0.56-0.69)	0.66 (0.5-0.7)
IL13	APCS	102	63	0.72 (0.61-0.82)	0.77 (0.64-0.9)	0.74 (0.65-0.82)	0.68 (0.63-0.73)	0.64 (0.6-0.7)	0.66 (0.62-0.69)
CP	CFB	102	67	0.67 (0.54-0.78)	0.73 (0.57-0.87)	0.7 (0.6-0.8)	0.64 (0.52-0.66)	0.71 (0.49-0.73)	0.66 (0.54-0.69)
CCL4	C3	102	63	0.69 (0.55-0.79)	0.69 (0.51-0.92)	0.69 (0.57-0.81)	0.66 (0.34-0.68)	0.67 (0.49-0.67)	0.66 (0.5-0.68)
CCL13	CP	102	63	0.67 (0.54-0.79)	0.78 (0.62-0.91)	0.72 (0.63-0.83)	0.61 (0.55-0.66)	0.71 (0.45-0.8)	0.66 (0.52-0.72)
IL6_PEA_IR	C3	101	63	0.72 (0.58-0.82)	0.7 (0.48-0.9)	0.71 (0.58-0.82)	0.69 (0.38-0.73)	0.65 (0.53-0.68)	0.66 (0.51-0.7)
KLRD1	CPN2	101	63	0.69 (0.59-0.8)	0.76 (0.61-0.87)	0.73 (0.63-0.81)	0.63 (0.5-0.68)	0.7 (0.46-0.75)	0.66 (0.53-0.71)
HPR	ITIH2	102	67	0.65 (0.54-0.77)	0.74 (0.55-0.91)	0.69 (0.58-0.8)	0.62 (0.56-0.64)	0.7 (0.47-0.71)	0.66 (0.54-0.67)
FCRL6	C9	101	63	0.68 (0.54-0.82)	0.73 (0.61-0.84)	0.71 (0.61-0.8)	0.63 (0.52-0.69)	0.71 (0.52-0.75)	0.66 (0.55-0.72)
SERPIND1	VTN	102	67	0.63 (0.51-0.74)	0.77 (0.64-0.89)	0.7 (0.61-0.79)	0.6 (0.54-0.61)	0.72 (0.28-0.77)	0.66 (0.43-0.69)
C5	C8B	102	67	0.72 (0.6-0.84)	0.7 (0.54-0.87)	0.71 (0.61-0.8)	0.7 (0.51-0.72)	0.64 (0.53-0.67)	0.66 (0.57-0.69)
CCL4	C2	102	63	0.68 (0.53-0.79)	0.72 (0.54-0.9)	0.7 (0.59-0.8)	0.65 (0.44-0.66)	0.68 (0.45-0.7)	0.66 (0.51-0.68)
MILR1	ITIH2	101	63	0.67 (0.53-0.83)	0.74 (0.57-0.89)	0.71 (0.58-0.82)	0.63 (0.48-0.66)	0.69 (0.39-0.74)	0.66 (0.51-0.69)
HGF	SAA1	102	63	0.66 (0.53-0.81)	0.85 (0.68-0.94)	0.75 (0.64-0.84)	0.64 (0.44-0.66)	0.78 (0.35-0.86)	0.66 (0.41-0.76)
FCRL6	PZP	100	63	0.67 (0.55-0.79)	0.73 (0.57-0.85)	0.7 (0.59-0.78)	0.65 (0.48-0.67)	0.69 (0.48-0.74)	0.66 (0.53-0.7)
CP	C2	102	67	0.67 (0.55-0.79)	0.75 (0.58-0.88)	0.71 (0.6-0.8)	0.64 (0.55-0.66)	0.69 (0.48-0.74)	0.66 (0.55-0.7)
LRG1	C8B	102	67	0.66 (0.54-0.8)	0.71 (0.58-0.85)	0.69 (0.59-0.78)	0.64 (0.58-0.65)	0.67 (0.47-0.72)	0.66 (0.55-0.68)
LAMP3	ITIH3	101	63	0.69 (0.56-0.82)	0.69 (0.55-0.79)	0.69 (0.6-0.78)	0.66 (0.52-0.67)	0.67 (0.6-0.69)	0.66 (0.58-0.68)
MASP1	ITGA11	102	63	0.72 (0.59-0.82)	0.74 (0.59-0.88)	0.73 (0.62-0.81)	0.67 (0.44-0.72)	0.64 (0.55-0.72)	0.66 (0.54-0.7)
KLRD1	ITIH1	101	63	0.7 (0.56-0.81)	0.71 (0.57-0.87)	0.71 (0.61-0.81)	0.66 (0.52-0.69)	0.67 (0.49-0.71)	0.66 (0.55-0.69)
IL6_PEA_IR	C2	101	63	0.72 (0.58-0.82)	0.72 (0.49-0.89)	0.72 (0.58-0.81)	0.68 (0.38-0.73)	0.65 (0.47-0.7)	0.66 (0.5-0.71)
CP	ITIH1	102	67	0.67 (0.52-0.81)	0.74 (0.58-0.87)	0.71 (0.6-0.81)	0.64 (0.55-0.66)	0.69 (0.49-0.75)	0.66 (0.56-0.7)
LAMP3	C8B	101	63	0.7 (0.57-0.82)	0.7 (0.55-0.87)	0.7 (0.61-0.81)	0.65 (0.47-0.68)	0.67 (0.56-0.7)	0.66 (0.55-0.68)
MILR1	IL15	101	63	0.69 (0.51-0.84)	0.68 (0.5-0.85)	0.68 (0.55-0.79)	0.67 (0.47-0.67)	0.65 (0.38-0.68)	0.66 (0.51-0.67)

KLRD1	CCL4	101	63	0.71 (0.58-0.82)	0.69 (0.53-0.84)	0.7 (0.59-0.8)	0.68 (0.44-0.71)	0.66 (0.55-0.69)	0.66 (0.53-0.7)
FCRL6	VTN	101	63	0.63 (0.52-0.75)	0.83 (0.72-0.93)	0.73 (0.65-0.8)	0.59 (0.55-0.61)	0.72 (0.38-0.82)	0.66 (0.48-0.71)
DCTN1	ITIH3	101	63	0.7 (0.57-0.82)	0.69 (0.54-0.84)	0.7 (0.59-0.79)	0.67 (0.5-0.69)	0.64 (0.6-0.68)	0.66 (0.57-0.68)
HGF	C8B	102	63	0.67 (0.55-0.78)	0.73 (0.53-0.92)	0.7 (0.59-0.8)	0.67 (0.44-0.7)	0.66 (0.4-0.73)	0.66 (0.48-0.71)
DCTN1	LRG1	101	63	0.68 (0.55-0.8)	0.71 (0.54-0.86)	0.7 (0.58-0.8)	0.66 (0.44-0.68)	0.68 (0.53-0.71)	0.66 (0.55-0.69)
CRP_SRM	C3	102	67	0.74 (0.59-0.84)	0.68 (0.5-0.85)	0.71 (0.6-0.82)	0.64 (0.38-0.75)	0.68 (0.55-0.73)	0.66 (0.52-0.72)
hsCRP	C9	98	67	0.73 (0.55-0.85)	0.7 (0.53-0.86)	0.71 (0.59-0.82)	0.67 (0.42-0.76)	0.69 (0.46-0.74)	0.66 (0.49-0.74)
IL6_PEA_cytokin	PZP	101	63	0.66 (0.42-0.77)	0.78 (0.53-0.9)	0.71 (0.56-0.8)	0.62 (0.42-0.69)	0.76 (0.31-0.79)	0.66 (0.44-0.73)
CPN2	CP	102	67	0.67 (0.54-0.81)	0.74 (0.58-0.88)	0.7 (0.59-0.81)	0.64 (0.57-0.67)	0.68 (0.48-0.73)	0.66 (0.55-0.7)
NCR1	C3	101	63	0.68 (0.56-0.79)	0.69 (0.5-0.9)	0.68 (0.56-0.8)	0.67 (0.42-0.68)	0.65 (0.52-0.67)	0.66 (0.52-0.67)
IFNG	SERPINA3	102	63	0.71 (0.56-0.85)	0.72 (0.56-0.86)	0.71 (0.59-0.81)	0.65 (0.32-0.71)	0.67 (0.54-0.7)	0.66 (0.49-0.69)
CRP_SRM	LRG1	102	67	0.72 (0.55-0.83)	0.71 (0.53-0.86)	0.72 (0.6-0.81)	0.65 (0.46-0.76)	0.71 (0.54-0.77)	0.66 (0.53-0.75)
SAA1	ITIH3	102	67	0.67 (0.52-0.8)	0.68 (0.49-0.82)	0.67 (0.56-0.77)	0.64 (0.41-0.66)	0.68 (0.5-0.69)	0.65 (0.49-0.67)
KLRD1	VTN	101	63	0.69 (0.54-0.81)	0.81 (0.69-0.9)	0.75 (0.66-0.82)	0.62 (0.53-0.68)	0.7 (0.44-0.8)	0.65 (0.51-0.72)
HGF	C5	102	63	0.72 (0.6-0.81)	0.73 (0.58-0.87)	0.72 (0.63-0.81)	0.67 (0.52-0.71)	0.66 (0.52-0.72)	0.65 (0.55-0.7)
C3	CP	102	67	0.68 (0.54-0.8)	0.73 (0.58-0.9)	0.7 (0.59-0.81)	0.63 (0.53-0.68)	0.69 (0.51-0.75)	0.65 (0.55-0.71)
SERPINA3	SERPIND1	102	67	0.66 (0.54-0.79)	0.76 (0.61-0.89)	0.71 (0.62-0.8)	0.62 (0.53-0.65)	0.7 (0.46-0.74)	0.65 (0.54-0.69)
CCL13	C5	102	63	0.7 (0.58-0.82)	0.73 (0.57-0.87)	0.72 (0.61-0.81)	0.66 (0.54-0.71)	0.67 (0.51-0.71)	0.65 (0.54-0.7)
LAMP3	CCL4	101	63	0.72 (0.59-0.83)	0.64 (0.5-0.79)	0.68 (0.59-0.79)	0.7 (0.29-0.72)	0.62 (0.55-0.65)	0.65 (0.46-0.68)
KLRD1	CLU	101	63	0.69 (0.56-0.8)	0.74 (0.58-0.87)	0.71 (0.61-0.8)	0.66 (0.55-0.68)	0.66 (0.51-0.72)	0.65 (0.57-0.69)
KLRD1	IFNG	101	63	0.73 (0.57-0.86)	0.65 (0.47-0.8)	0.69 (0.58-0.79)	0.68 (0.28-0.72)	0.63 (0.62-0.64)	0.65 (0.45-0.68)
hsCRP	ORM1	98	67	0.73 (0.57-0.86)	0.69 (0.51-0.84)	0.71 (0.59-0.81)	0.66 (0.39-0.76)	0.61 (0.55-0.73)	0.65 (0.51-0.73)
IL6_PEA_IR	C9	101	63	0.71 (0.56-0.83)	0.65 (0.46-0.86)	0.68 (0.55-0.8)	0.69 (0.3-0.73)	0.63 (0.54-0.64)	0.65 (0.46-0.68)
NCR1	ITIH3	101	63	0.68 (0.55-0.81)	0.69 (0.55-0.84)	0.69 (0.59-0.78)	0.65 (0.55-0.66)	0.67 (0.52-0.69)	0.65 (0.57-0.67)
DCTN1	SERPINA3	101	63	0.67 (0.55-0.8)	0.72 (0.55-0.88)	0.7 (0.59-0.8)	0.64 (0.47-0.67)	0.67 (0.54-0.7)	0.65 (0.56-0.68)
FC	CPN2	77	44	0.71 (0.57-0.85)	0.72 (0.55-0.93)	0.72 (0.61-0.85)	0.61 (0.43-0.7)	0.7 (0.53-0.78)	0.65 (0.53-0.73)
IL7	LRG1	102	63	0.65 (0.51-0.78)	0.75 (0.62-0.87)	0.7 (0.6-0.79)	0.59 (0.54-0.62)	0.73 (0.3-0.77)	0.65 (0.44-0.68)
IL6_PEA_cytokin	VTN	102	63	0.63 (0.51-0.75)	0.8 (0.66-0.91)	0.71 (0.62-0.8)	0.58 (0.48-0.62)	0.75 (0.25-0.8)	0.65 (0.41-0.7)
C2	SERPIND1	102	67	0.64 (0.51-0.74)	0.76 (0.62-0.89)	0.7 (0.61-0.79)	0.6 (0.57-0.61)	0.71 (0.32-0.74)	0.65 (0.46-0.68)
C9	C5	102	67	0.7 (0.57-0.82)	0.67 (0.53-0.81)	0.68 (0.6-0.78)	0.68 (0.46-0.71)	0.63 (0.57-0.64)	0.65 (0.54-0.67)

IL17F	APCS	102	63	0.73 (0.61-0.82)	0.78 (0.64-0.91)	0.75 (0.66-0.83)	0.67 (0.58-0.72)	0.64 (0.53-0.72)	0.65 (0.58-0.7)
MASP1	C5	101	63	0.77 (0.67-0.86)	0.71 (0.56-0.86)	0.74 (0.65-0.83)	0.7 (0.38-0.77)	0.61 (0.56-0.65)	0.65 (0.5-0.7)
LAMP3	C3	101	63	0.7 (0.59-0.82)	0.69 (0.51-0.87)	0.7 (0.59-0.8)	0.64 (0.5-0.68)	0.67 (0.56-0.71)	0.65 (0.57-0.69)
CCL4	C8B	102	63	0.69 (0.55-0.81)	0.67 (0.5-0.87)	0.68 (0.57-0.8)	0.67 (0.32-0.68)	0.64 (0.53-0.67)	0.65 (0.49-0.67)
IL7	PZP	101	63	0.62 (0.49-0.76)	0.81 (0.7-0.92)	0.72 (0.62-0.8)	0.57 (0.56-0.59)	0.73 (0.22-0.8)	0.65 (0.4-0.69)
CLU	SERPIND1	102	67	0.64 (0.5-0.74)	0.77 (0.62-0.89)	0.7 (0.61-0.79)	0.6 (0.57-0.63)	0.7 (0.35-0.75)	0.65 (0.47-0.68)
FCRL6	IL6_PEA_cytokine	101	63	0.65 (0.55-0.78)	0.71 (0.54-0.86)	0.68 (0.58-0.78)	0.61 (0.49-0.69)	0.7 (0.47-0.75)	0.65 (0.53-0.71)
DCTN1	C3	101	63	0.7 (0.56-0.81)	0.73 (0.51-0.92)	0.72 (0.59-0.82)	0.65 (0.46-0.7)	0.67 (0.52-0.7)	0.65 (0.53-0.69)
KLRD1	IL6_PEA_cytokine	101	63	0.71 (0.58-0.82)	0.67 (0.48-0.86)	0.69 (0.58-0.79)	0.64 (0.38-0.72)	0.65 (0.51-0.71)	0.65 (0.5-0.7)
IL7	ITIH3	102	63	0.67 (0.54-0.81)	0.72 (0.57-0.86)	0.7 (0.6-0.8)	0.61 (0.55-0.65)	0.7 (0.33-0.72)	0.65 (0.47-0.68)
HGF	SERPINA3	102	63	0.66 (0.54-0.79)	0.74 (0.58-0.89)	0.7 (0.61-0.8)	0.64 (0.45-0.67)	0.68 (0.36-0.72)	0.65 (0.48-0.69)
LAMP3	IL7	101	63	0.7 (0.55-0.81)	0.75 (0.57-0.88)	0.72 (0.62-0.81)	0.63 (0.54-0.68)	0.69 (0.43-0.75)	0.65 (0.53-0.7)
IL15	PZP	101	63	0.68 (0.49-0.81)	0.7 (0.55-0.84)	0.69 (0.57-0.79)	0.67 (0.55-0.68)	0.64 (0.38-0.74)	0.65 (0.52-0.7)
hsCRP	SERPING1	98	67	0.75 (0.62-0.87)	0.72 (0.49-0.9)	0.73 (0.61-0.84)	0.63 (0.38-0.76)	0.65 (0.56-0.72)	0.65 (0.5-0.73)
F9	VTN	102	67	0.75 (0.61-0.88)	0.77 (0.62-0.89)	0.76 (0.66-0.86)	0.64 (0.47-0.74)	0.67 (0.46-0.73)	0.65 (0.51-0.72)
FCRL6	CCL4	101	63	0.66 (0.53-0.79)	0.72 (0.58-0.85)	0.69 (0.59-0.78)	0.63 (0.45-0.67)	0.69 (0.47-0.72)	0.65 (0.53-0.69)
LRG1	ITIH1	102	67	0.67 (0.53-0.8)	0.7 (0.54-0.84)	0.69 (0.57-0.79)	0.63 (0.53-0.66)	0.68 (0.5-0.7)	0.65 (0.55-0.68)
IL13	CP	102	63	0.7 (0.58-0.8)	0.82 (0.68-0.94)	0.76 (0.66-0.84)	0.65 (0.56-0.7)	0.64 (0.38-0.71)	0.65 (0.48-0.69)
C9	CP	102	67	0.66 (0.52-0.8)	0.73 (0.54-0.88)	0.7 (0.58-0.79)	0.63 (0.46-0.67)	0.69 (0.49-0.74)	0.65 (0.54-0.7)
SERPINA3	C8B	102	67	0.66 (0.53-0.78)	0.7 (0.55-0.87)	0.68 (0.59-0.78)	0.63 (0.58-0.64)	0.67 (0.44-0.69)	0.65 (0.52-0.66)
MASP1	LAMP3	102	63	0.75 (0.62-0.85)	0.67 (0.49-0.84)	0.71 (0.61-0.81)	0.69 (0.27-0.74)	0.62 (0.54-0.63)	0.65 (0.44-0.68)
FCRL6	C2	101	63	0.63 (0.51-0.77)	0.76 (0.63-0.89)	0.7 (0.6-0.79)	0.61 (0.56-0.63)	0.69 (0.46-0.75)	0.65 (0.53-0.68)
FC	ITIH3	77	44	0.71 (0.55-0.86)	0.66 (0.48-0.86)	0.69 (0.56-0.82)	0.65 (0.3-0.7)	0.65 (0.57-0.7)	0.65 (0.47-0.69)
C5	SERPING1	102	67	0.72 (0.6-0.82)	0.68 (0.52-0.85)	0.7 (0.6-0.8)	0.67 (0.47-0.7)	0.64 (0.53-0.68)	0.65 (0.54-0.69)
IL6_PEA_cytokin	ITIH3	102	63	0.71 (0.56-0.84)	0.67 (0.49-0.84)	0.69 (0.57-0.79)	0.62 (0.32-0.72)	0.67 (0.48-0.69)	0.65 (0.49-0.7)
CFB	PZP	101	67	0.65 (0.52-0.76)	0.71 (0.56-0.87)	0.68 (0.58-0.78)	0.62 (0.49-0.65)	0.69 (0.36-0.73)	0.65 (0.48-0.68)
hsCRP	CFB	98	67	0.74 (0.56-0.86)	0.7 (0.54-0.86)	0.72 (0.6-0.82)	0.57 (0.48-0.76)	0.71 (0.44-0.76)	0.65 (0.53-0.75)
DCTN1	KLRD1	102	63	0.7 (0.56-0.81)	0.68 (0.53-0.85)	0.69 (0.58-0.79)	0.66 (0.4-0.69)	0.63 (0.61-0.64)	0.65 (0.51-0.66)
FCRL6	CLU	101	63	0.63 (0.52-0.75)	0.77 (0.63-0.89)	0.7 (0.61-0.78)	0.61 (0.56-0.62)	0.69 (0.41-0.77)	0.65 (0.5-0.69)
SAA1	SERPINA3	102	67	0.66 (0.5-0.79)	0.71 (0.43-0.88)	0.68 (0.53-0.79)	0.63 (0.42-0.65)	0.72 (0.43-0.74)	0.65 (0.45-0.69)

CP	ITIH2	102	67	0.67 (0.54-0.8)	0.73 (0.56-0.87)	0.7 (0.6-0.8)	0.62 (0.57-0.66)	0.68 (0.49-0.74)	0.65 (0.56-0.7)
CCL4	VTN	102	63	0.65 (0.51-0.78)	0.78 (0.65-0.9)	0.71 (0.62-0.79)	0.6 (0.49-0.63)	0.72 (0.3-0.76)	0.65 (0.44-0.69)
IFNG	CCL4	102	63	0.77 (0.61-0.88)	0.63 (0.46-0.81)	0.7 (0.59-0.81)	0.7 (0.24-0.77)	0.61 (0.48-0.62)	0.65 (0.42-0.69)
IL7	VTN	102	63	0.6 (0.5-0.72)	0.8 (0.69-0.9)	0.7 (0.63-0.79)	0.54 (0.54-0.55)	0.75 (0.23-0.79)	0.65 (0.38-0.67)
MASP1	HPR	101	63	0.7 (0.56-0.81)	0.84 (0.71-0.94)	0.77 (0.68-0.84)	0.61 (0.45-0.66)	0.7 (0.49-0.76)	0.65 (0.54-0.69)
IL6_PEA_IR	ITIH1	101	63	0.71 (0.56-0.81)	0.74 (0.54-0.93)	0.72 (0.6-0.83)	0.62 (0.37-0.72)	0.69 (0.46-0.74)	0.65 (0.51-0.72)
MILR1	ORM1	101	63	0.75 (0.59-0.86)	0.69 (0.55-0.86)	0.72 (0.61-0.82)	0.65 (0.47-0.73)	0.65 (0.55-0.66)	0.65 (0.54-0.69)
LRG1	SERPINA3	102	67	0.67 (0.53-0.79)	0.7 (0.53-0.83)	0.68 (0.58-0.78)	0.63 (0.47-0.65)	0.67 (0.46-0.69)	0.65 (0.53-0.67)
DCTN1	SAA1	101	63	0.65 (0.51-0.78)	0.68 (0.45-0.85)	0.67 (0.54-0.78)	0.63 (0.35-0.66)	0.66 (0.46-0.67)	0.65 (0.51-0.66)
CPN2	SERPIND1	102	67	0.64 (0.52-0.75)	0.76 (0.62-0.89)	0.7 (0.61-0.79)	0.6 (0.57-0.61)	0.69 (0.34-0.75)	0.65 (0.47-0.68)
SERPIND1	ITIH1	102	67	0.63 (0.5-0.75)	0.76 (0.62-0.89)	0.7 (0.61-0.79)	0.61 (0.57-0.62)	0.69 (0.37-0.74)	0.65 (0.49-0.68)
KLRD1	IL7	101	63	0.69 (0.55-0.8)	0.74 (0.58-0.88)	0.72 (0.61-0.8)	0.63 (0.55-0.67)	0.68 (0.36-0.73)	0.65 (0.48-0.69)
NCR1	VTN	101	63	0.65 (0.52-0.77)	0.78 (0.65-0.91)	0.72 (0.63-0.81)	0.62 (0.53-0.64)	0.69 (0.36-0.77)	0.65 (0.48-0.7)
CRP_SRM	SERPING1	102	67	0.73 (0.59-0.84)	0.71 (0.48-0.9)	0.71 (0.59-0.83)	0.63 (0.37-0.75)	0.67 (0.52-0.74)	0.65 (0.5-0.73)
SAA1	C2	102	67	0.65 (0.5-0.8)	0.75 (0.54-0.89)	0.7 (0.57-0.79)	0.62 (0.46-0.65)	0.75 (0.42-0.76)	0.65 (0.44-0.7)
FCRL6	LAMP3	102	63	0.69 (0.55-0.81)	0.7 (0.56-0.83)	0.69 (0.59-0.77)	0.62 (0.44-0.67)	0.67 (0.53-0.7)	0.65 (0.53-0.68)
CCL4	CFB	102	63	0.67 (0.53-0.78)	0.73 (0.56-0.88)	0.7 (0.59-0.79)	0.63 (0.45-0.66)	0.68 (0.44-0.7)	0.65 (0.51-0.68)
FC	C9	77	44	0.7 (0.56-0.85)	0.71 (0.52-0.89)	0.7 (0.58-0.83)	0.65 (0.31-0.71)	0.66 (0.48-0.76)	0.65 (0.47-0.72)
NCR1	IFNG	101	63	0.72 (0.59-0.85)	0.64 (0.49-0.8)	0.68 (0.58-0.78)	0.68 (0.29-0.72)	0.61 (0.58-0.62)	0.64 (0.45-0.67)
ITIH3	SERPINA3	102	67	0.66 (0.54-0.81)	0.69 (0.54-0.83)	0.68 (0.58-0.78)	0.64 (0.48-0.66)	0.66 (0.52-0.67)	0.64 (0.53-0.66)
IFNG	C4B	102	63	0.73 (0.59-0.85)	0.77 (0.56-0.94)	0.75 (0.63-0.86)	0.58 (0.51-0.71)	0.71 (0.57-0.75)	0.64 (0.57-0.72)
C5	C4B	102	67	0.71 (0.59-0.81)	0.78 (0.61-0.92)	0.74 (0.64-0.84)	0.65 (0.54-0.7)	0.65 (0.4-0.75)	0.64 (0.5-0.7)
IL15	C8B	102	63	0.66 (0.52-0.78)	0.71 (0.54-0.88)	0.68 (0.57-0.79)	0.64 (0.53-0.65)	0.67 (0.49-0.71)	0.64 (0.55-0.67)
KLRD1	MASP1	102	63	0.75 (0.64-0.85)	0.66 (0.52-0.84)	0.71 (0.62-0.81)	0.71 (0.28-0.74)	0.59 (0.55-0.62)	0.64 (0.43-0.67)
IL13	HPR	102	63	0.66 (0.58-0.77)	0.81 (0.65-0.94)	0.74 (0.64-0.82)	0.63 (0.57-0.67)	0.67 (0.28-0.75)	0.64 (0.45-0.69)
DCTN1	HGF	101	63	0.67 (0.55-0.79)	0.76 (0.62-0.91)	0.72 (0.62-0.81)	0.65 (0.46-0.67)	0.65 (0.52-0.77)	0.64 (0.54-0.71)
NCR1	CPN2	101	63	0.67 (0.55-0.78)	0.73 (0.56-0.88)	0.7 (0.6-0.79)	0.63 (0.51-0.65)	0.67 (0.43-0.71)	0.64 (0.53-0.68)
HGF	LRG1	102	63	0.67 (0.52-0.79)	0.76 (0.63-0.89)	0.72 (0.63-0.81)	0.64 (0.45-0.66)	0.7 (0.33-0.75)	0.64 (0.47-0.7)
IFNG	LRG1	102	63	0.74 (0.59-0.87)	0.71 (0.54-0.83)	0.72 (0.61-0.81)	0.66 (0.3-0.73)	0.64 (0.47-0.69)	0.64 (0.47-0.69)
IFNG	SERPIND1	102	63	0.74 (0.59-0.86)	0.8 (0.67-0.92)	0.76 (0.68-0.85)	0.61 (0.44-0.7)	0.71 (0.42-0.77)	0.64 (0.49-0.72)

IL6_PEA_IR	CPN2	101	63	0.73 (0.6-0.82)	0.71 (0.54-0.87)	0.72 (0.61-0.81)	0.65 (0.36-0.74)	0.67 (0.44-0.71)	0.64 (0.5-0.72)
CCL13	CRP_SRM	102	63	0.73 (0.58-0.86)	0.73 (0.55-0.88)	0.73 (0.61-0.82)	0.6 (0.42-0.75)	0.69 (0.48-0.77)	0.64 (0.52-0.74)
DCTN1	IL6_PEA_cytokine	101	63	0.67 (0.55-0.81)	0.7 (0.45-0.87)	0.68 (0.55-0.79)	0.65 (0.37-0.72)	0.63 (0.54-0.77)	0.64 (0.51-0.72)
DCTN1	C8B	101	63	0.65 (0.53-0.79)	0.72 (0.56-0.87)	0.69 (0.58-0.79)	0.63 (0.54-0.64)	0.65 (0.55-0.69)	0.64 (0.57-0.66)
CRP_SRM	ORM1	102	67	0.72 (0.57-0.85)	0.69 (0.52-0.85)	0.7 (0.58-0.81)	0.67 (0.39-0.75)	0.61 (0.55-0.73)	0.64 (0.52-0.73)
ITGA11	IL13	101	63	0.71 (0.59-0.82)	0.76 (0.61-0.87)	0.73 (0.64-0.81)	0.66 (0.6-0.73)	0.61 (0.6-0.66)	0.64 (0.6-0.67)
IL7	C8B	102	63	0.65 (0.53-0.77)	0.7 (0.53-0.9)	0.68 (0.57-0.79)	0.61 (0.47-0.63)	0.69 (0.34-0.7)	0.64 (0.46-0.66)
FCRL6	ITIH1	101	63	0.64 (0.54-0.76)	0.75 (0.62-0.86)	0.69 (0.61-0.78)	0.6 (0.55-0.63)	0.69 (0.43-0.74)	0.64 (0.51-0.68)
FCRL6	CPN2	101	63	0.64 (0.54-0.76)	0.76 (0.61-0.88)	0.7 (0.61-0.79)	0.6 (0.54-0.62)	0.69 (0.42-0.75)	0.64 (0.51-0.68)
DCTN1	LAMP3	102	63	0.71 (0.57-0.84)	0.68 (0.48-0.83)	0.7 (0.57-0.79)	0.65 (0.35-0.7)	0.64 (0.58-0.65)	0.64 (0.49-0.67)
CLEC4C	MASP1	102	63	0.77 (0.64-0.87)	0.71 (0.54-0.91)	0.74 (0.62-0.85)	0.7 (0.31-0.76)	0.58 (0.54-0.74)	0.64 (0.44-0.73)
LRG1	CPN2	102	67	0.65 (0.51-0.78)	0.71 (0.56-0.85)	0.68 (0.58-0.78)	0.62 (0.54-0.64)	0.69 (0.43-0.7)	0.64 (0.52-0.67)
FC	NCR1	76	43	0.75 (0.57-0.89)	0.69 (0.53-0.86)	0.71 (0.59-0.83)	0.66 (0.37-0.75)	0.63 (0.54-0.67)	0.64 (0.48-0.7)
LRG1	CLU	102	67	0.65 (0.51-0.79)	0.71 (0.56-0.85)	0.68 (0.58-0.78)	0.62 (0.54-0.65)	0.68 (0.39-0.7)	0.64 (0.51-0.67)
MASP1	SAA1	101	63	0.74 (0.59-0.85)	0.7 (0.49-0.9)	0.71 (0.59-0.83)	0.64 (0.27-0.74)	0.65 (0.48-0.71)	0.64 (0.46-0.72)
C9	PZP	101	67	0.65 (0.51-0.78)	0.72 (0.53-0.84)	0.69 (0.56-0.78)	0.64 (0.47-0.66)	0.67 (0.45-0.72)	0.64 (0.5-0.68)
IL7	C3	102	63	0.64 (0.52-0.77)	0.72 (0.52-0.93)	0.68 (0.55-0.8)	0.6 (0.54-0.62)	0.69 (0.31-0.71)	0.64 (0.45-0.66)
NCR1	CFB	101	63	0.66 (0.53-0.78)	0.71 (0.56-0.88)	0.69 (0.58-0.79)	0.65 (0.48-0.66)	0.65 (0.46-0.69)	0.64 (0.51-0.67)
FC	MASP1	76	43	0.79 (0.63-0.9)	0.73 (0.42-0.99)	0.75 (0.57-0.91)	0.66 (0.22-0.78)	0.62 (0.56-0.67)	0.64 (0.41-0.72)
LAMP3	CFB	101	63	0.69 (0.57-0.81)	0.7 (0.55-0.86)	0.7 (0.6-0.8)	0.65 (0.45-0.66)	0.65 (0.49-0.69)	0.64 (0.53-0.67)
CRP_SRM	C2	102	67	0.71 (0.56-0.84)	0.73 (0.55-0.88)	0.72 (0.61-0.82)	0.63 (0.41-0.75)	0.72 (0.5-0.76)	0.64 (0.51-0.74)
IL6_PEA_cytokin	CLU	102	63	0.65 (0.48-0.78)	0.72 (0.53-0.89)	0.68 (0.57-0.8)	0.61 (0.53-0.67)	0.68 (0.39-0.77)	0.64 (0.48-0.71)
NCR1	ITIH1	101	63	0.66 (0.53-0.79)	0.73 (0.56-0.9)	0.7 (0.59-0.81)	0.64 (0.51-0.67)	0.65 (0.47-0.71)	0.64 (0.54-0.69)
LAMP3	SERPIND1	101	63	0.69 (0.56-0.81)	0.79 (0.65-0.92)	0.74 (0.65-0.83)	0.6 (0.45-0.66)	0.69 (0.4-0.77)	0.64 (0.49-0.7)
CCL13	SERPIND1	102	63	0.62 (0.49-0.73)	0.8 (0.64-0.93)	0.71 (0.61-0.79)	0.59 (0.54-0.61)	0.7 (0.33-0.79)	0.64 (0.46-0.7)
NCR1	C2	101	63	0.66 (0.53-0.78)	0.71 (0.54-0.91)	0.68 (0.57-0.8)	0.63 (0.49-0.65)	0.65 (0.47-0.69)	0.64 (0.5-0.67)
hsCRP	IL17F	98	63	0.78 (0.63-0.89)	0.71 (0.5-0.89)	0.74 (0.63-0.85)	0.69 (0.31-0.79)	0.59 (0.53-0.7)	0.64 (0.46-0.71)
IFNG	HPR	102	63	0.76 (0.62-0.86)	0.81 (0.65-0.94)	0.78 (0.68-0.87)	0.6 (0.47-0.72)	0.69 (0.33-0.78)	0.64 (0.47-0.72)
IL7	SERPINA3	102	63	0.65 (0.52-0.78)	0.75 (0.58-0.89)	0.7 (0.59-0.8)	0.58 (0.53-0.64)	0.7 (0.35-0.74)	0.64 (0.46-0.68)
SERPIND1	ITIH2	102	67	0.64 (0.52-0.74)	0.76 (0.6-0.89)	0.7 (0.61-0.79)	0.6 (0.57-0.61)	0.68 (0.37-0.75)	0.64 (0.48-0.68)

SERPINA3	ITIH1	102	67	0.66 (0.52-0.8)	0.7 (0.55-0.85)	0.68 (0.58-0.78)	0.64 (0.52-0.64)	0.66 (0.49-0.68)	0.64 (0.55-0.66)
IL6_PEA_IR	CFB	101	63	0.72 (0.58-0.82)	0.74 (0.46-0.91)	0.73 (0.58-0.82)	0.67 (0.36-0.72)	0.65 (0.37-0.72)	0.64 (0.47-0.71)
DCTN1	CFB	101	63	0.66 (0.55-0.79)	0.73 (0.54-0.9)	0.7 (0.58-0.81)	0.64 (0.43-0.65)	0.68 (0.46-0.7)	0.64 (0.51-0.67)
IL6_PEA_IR	ORM1	101	63	0.74 (0.62-0.85)	0.65 (0.48-0.86)	0.7 (0.59-0.81)	0.68 (0.27-0.75)	0.61 (0.53-0.62)	0.64 (0.43-0.68)
IL6_PEA_IR	CLU	101	63	0.72 (0.58-0.84)	0.74 (0.57-0.89)	0.73 (0.63-0.82)	0.67 (0.42-0.72)	0.63 (0.43-0.73)	0.64 (0.49-0.71)
CLEC4C	SERPING1	101	63	0.67 (0.52-0.82)	0.72 (0.55-0.91)	0.7 (0.58-0.82)	0.61 (0.45-0.66)	0.68 (0.48-0.77)	0.64 (0.51-0.7)
IL7	CFB	102	63	0.61 (0.51-0.73)	0.78 (0.6-0.92)	0.69 (0.59-0.79)	0.56 (0.55-0.59)	0.72 (0.27-0.77)	0.64 (0.42-0.67)
MILR1	IL7	101	63	0.68 (0.53-0.8)	0.77 (0.63-0.89)	0.72 (0.62-0.82)	0.64 (0.49-0.65)	0.68 (0.43-0.75)	0.64 (0.51-0.7)
IL15	C3	102	63	0.66 (0.53-0.78)	0.71 (0.51-0.91)	0.68 (0.56-0.8)	0.63 (0.54-0.64)	0.65 (0.49-0.7)	0.64 (0.55-0.67)
LRG1	ITIH3	102	67	0.66 (0.52-0.8)	0.7 (0.54-0.81)	0.68 (0.58-0.77)	0.62 (0.48-0.66)	0.67 (0.46-0.69)	0.64 (0.52-0.67)
LAMP3	ITIH1	101	63	0.71 (0.59-0.82)	0.72 (0.57-0.87)	0.71 (0.62-0.81)	0.63 (0.5-0.69)	0.66 (0.49-0.7)	0.64 (0.54-0.69)
FCRL6	IFNG	101	63	0.72 (0.57-0.84)	0.67 (0.51-0.81)	0.69 (0.58-0.78)	0.64 (0.3-0.71)	0.63 (0.61-0.65)	0.64 (0.47-0.67)
KLRD1	ITIH2	101	63	0.7 (0.57-0.81)	0.7 (0.59-0.83)	0.7 (0.61-0.79)	0.65 (0.52-0.68)	0.65 (0.48-0.69)	0.64 (0.53-0.68)
LAMP3	C2	101	63	0.69 (0.55-0.81)	0.71 (0.54-0.88)	0.69 (0.59-0.81)	0.61 (0.49-0.67)	0.66 (0.52-0.71)	0.64 (0.53-0.68)
NCR1	MASP1	102	63	0.72 (0.61-0.84)	0.69 (0.49-0.87)	0.71 (0.58-0.82)	0.68 (0.3-0.71)	0.63 (0.54-0.65)	0.64 (0.45-0.68)
FCRL6	HGF	101	63	0.63 (0.52-0.75)	0.77 (0.64-0.9)	0.7 (0.61-0.79)	0.6 (0.49-0.62)	0.7 (0.42-0.79)	0.64 (0.5-0.7)
LAMP3	IL6_PEA_cytokine	101	63	0.72 (0.58-0.82)	0.65 (0.48-0.83)	0.69 (0.58-0.79)	0.66 (0.29-0.76)	0.65 (0.49-0.67)	0.64 (0.47-0.71)
IL7	ITIH1	102	63	0.61 (0.5-0.75)	0.78 (0.63-0.9)	0.7 (0.61-0.79)	0.56 (0.55-0.57)	0.72 (0.26-0.76)	0.64 (0.41-0.66)
ITIH3	C8B	102	67	0.66 (0.53-0.8)	0.67 (0.52-0.84)	0.67 (0.58-0.77)	0.64 (0.48-0.66)	0.63 (0.51-0.65)	0.64 (0.51-0.65)
NCR1	CLU	101	63	0.65 (0.53-0.77)	0.76 (0.6-0.9)	0.7 (0.61-0.8)	0.64 (0.56-0.65)	0.65 (0.44-0.73)	0.64 (0.52-0.69)
DCTN1	MILR1	102	63	0.69 (0.56-0.81)	0.69 (0.52-0.86)	0.69 (0.58-0.8)	0.65 (0.43-0.68)	0.62 (0.55-0.65)	0.64 (0.52-0.65)
ITGA11	SERPING1	101	63	0.71 (0.59-0.83)	0.75 (0.57-0.9)	0.73 (0.62-0.82)	0.64 (0.54-0.71)	0.62 (0.55-0.73)	0.64 (0.57-0.7)
IL15	VTN	102	63	0.62 (0.5-0.75)	0.8 (0.65-0.92)	0.71 (0.62-0.8)	0.57 (0.57-0.58)	0.7 (0.38-0.79)	0.64 (0.47-0.68)
IL6_PEA_IR	NCR1	102	63	0.71 (0.58-0.81)	0.65 (0.47-0.85)	0.68 (0.57-0.79)	0.67 (0.29-0.72)	0.62 (0.52-0.64)	0.64 (0.46-0.67)
ORM1	SERPIND1	102	67	0.66 (0.52-0.78)	0.76 (0.62-0.89)	0.71 (0.61-0.8)	0.62 (0.52-0.65)	0.65 (0.42-0.74)	0.64 (0.52-0.69)
LRG1	C3	102	67	0.67 (0.56-0.79)	0.69 (0.54-0.86)	0.68 (0.58-0.78)	0.62 (0.49-0.66)	0.67 (0.49-0.71)	0.64 (0.54-0.68)
C3	PZP	101	67	0.66 (0.52-0.78)	0.71 (0.53-0.88)	0.68 (0.57-0.79)	0.63 (0.47-0.65)	0.66 (0.45-0.71)	0.64 (0.51-0.68)
HGF	ITIH3	102	63	0.69 (0.55-0.82)	0.73 (0.57-0.88)	0.71 (0.61-0.8)	0.61 (0.43-0.69)	0.69 (0.38-0.73)	0.64 (0.47-0.7)
NCR1	C9	101	63	0.65 (0.52-0.8)	0.68 (0.51-0.87)	0.67 (0.54-0.79)	0.65 (0.38-0.66)	0.64 (0.48-0.67)	0.64 (0.5-0.66)
ORM1	C5	102	67	0.72 (0.6-0.83)	0.67 (0.54-0.81)	0.69 (0.6-0.78)	0.66 (0.48-0.71)	0.62 (0.53-0.64)	0.64 (0.53-0.67)

LAMP3	C9	101	63	0.7 (0.55-0.83)	0.67 (0.5-0.81)	0.68 (0.58-0.78)	0.65 (0.41-0.69)	0.64 (0.51-0.67)	0.64 (0.51-0.68)
IL17F	C5	102	63	0.76 (0.65-0.85)	0.7 (0.55-0.84)	0.73 (0.64-0.81)	0.68 (0.54-0.75)	0.59 (0.53-0.65)	0.64 (0.56-0.69)
IL7	C2	102	63	0.62 (0.5-0.74)	0.74 (0.56-0.91)	0.68 (0.58-0.79)	0.57 (0.55-0.59)	0.7 (0.29-0.72)	0.63 (0.43-0.65)
C5	CPN2	102	67	0.72 (0.6-0.82)	0.68 (0.54-0.82)	0.7 (0.61-0.79)	0.66 (0.46-0.71)	0.63 (0.43-0.65)	0.63 (0.51-0.67)
IL6_PEA_IR	IFNG	101	63	0.77 (0.63-0.89)	0.63 (0.44-0.83)	0.7 (0.57-0.81)	0.65 (0.24-0.77)	0.62 (0.59-0.64)	0.63 (0.43-0.7)
C2	PZP	101	67	0.65 (0.5-0.78)	0.73 (0.58-0.86)	0.69 (0.58-0.78)	0.62 (0.51-0.65)	0.67 (0.35-0.73)	0.63 (0.48-0.69)
C8B	ITIH1	102	67	0.65 (0.54-0.78)	0.72 (0.57-0.87)	0.68 (0.59-0.78)	0.63 (0.54-0.64)	0.65 (0.45-0.68)	0.63 (0.54-0.66)
IL13	SERPINA3	102	63	0.67 (0.54-0.81)	0.76 (0.6-0.89)	0.72 (0.61-0.81)	0.62 (0.55-0.68)	0.65 (0.58-0.68)	0.63 (0.5-0.67)
SERPINA3	CPN2	102	67	0.65 (0.53-0.78)	0.7 (0.55-0.84)	0.67 (0.58-0.76)	0.63 (0.51-0.65)	0.66 (0.42-0.67)	0.63 (0.5-0.66)
IL6_PEA_cytokin	ITIH1	102	63	0.63 (0.5-0.76)	0.71 (0.53-0.94)	0.67 (0.56-0.79)	0.58 (0.48-0.65)	0.7 (0.36-0.76)	0.63 (0.47-0.69)
IL13	C5	102	63	0.73 (0.63-0.83)	0.71 (0.54-0.85)	0.72 (0.63-0.81)	0.69 (0.27-0.74)	0.58 (0.54-0.6)	0.63 (0.43-0.66)
SAA1	CFB	102	67	0.64 (0.47-0.78)	0.76 (0.48-0.89)	0.7 (0.54-0.8)	0.63 (0.48-0.65)	0.74 (0.39-0.77)	0.63 (0.44-0.71)
CCL4	ITIH1	102	63	0.65 (0.51-0.78)	0.73 (0.54-0.91)	0.69 (0.57-0.8)	0.59 (0.47-0.65)	0.69 (0.39-0.72)	0.63 (0.49-0.67)
IFNG	ITIH3	102	63	0.75 (0.62-0.88)	0.66 (0.49-0.78)	0.7 (0.61-0.79)	0.64 (0.25-0.76)	0.62 (0.61-0.64)	0.63 (0.43-0.69)
LAMP3	CLU	101	63	0.69 (0.57-0.81)	0.72 (0.58-0.86)	0.7 (0.61-0.8)	0.62 (0.52-0.67)	0.65 (0.48-0.7)	0.63 (0.52-0.68)
MASP1	CCL4	101	63	0.73 (0.61-0.83)	0.68 (0.5-0.87)	0.71 (0.6-0.82)	0.72 (0.28-0.73)	0.58 (0.52-0.66)	0.63 (0.42-0.69)
IL15	ITIH3	102	63	0.67 (0.53-0.8)	0.69 (0.55-0.81)	0.68 (0.58-0.77)	0.62 (0.52-0.64)	0.65 (0.51-0.69)	0.63 (0.55-0.66)
DCTN1	FCRL6	102	63	0.66 (0.54-0.78)	0.7 (0.54-0.88)	0.68 (0.57-0.78)	0.61 (0.4-0.65)	0.66 (0.49-0.68)	0.63 (0.51-0.66)
CLEC4C	IL13	101	63	0.68 (0.56-0.82)	0.79 (0.61-0.92)	0.73 (0.62-0.83)	0.63 (0.53-0.68)	0.63 (0.34-0.69)	0.63 (0.49-0.67)
DCTN1	C2	101	63	0.68 (0.56-0.8)	0.73 (0.55-0.88)	0.7 (0.59-0.8)	0.65 (0.42-0.66)	0.66 (0.46-0.67)	0.63 (0.49-0.66)
LRG1	ITIH2	102	67	0.66 (0.53-0.78)	0.67 (0.53-0.81)	0.67 (0.57-0.76)	0.61 (0.52-0.65)	0.65 (0.46-0.69)	0.63 (0.52-0.67)
IL7	CLU	102	63	0.62 (0.5-0.74)	0.79 (0.68-0.89)	0.7 (0.63-0.79)	0.57 (0.55-0.59)	0.7 (0.23-0.78)	0.63 (0.4-0.68)
IL6_PEA_cytokin	CPN2	102	63	0.65 (0.52-0.77)	0.71 (0.52-0.87)	0.68 (0.56-0.79)	0.58 (0.5-0.7)	0.71 (0.31-0.74)	0.63 (0.44-0.71)
DCTN1	SERPIND1	101	63	0.68 (0.57-0.78)	0.8 (0.64-0.93)	0.74 (0.64-0.82)	0.6 (0.48-0.67)	0.71 (0.41-0.77)	0.63 (0.48-0.71)
NCR1	IL7	101	63	0.65 (0.52-0.77)	0.72 (0.53-0.9)	0.68 (0.57-0.79)	0.6 (0.51-0.62)	0.67 (0.31-0.72)	0.63 (0.45-0.66)
CCL13	SERPINA3	102	63	0.64 (0.51-0.79)	0.72 (0.55-0.91)	0.69 (0.57-0.8)	0.57 (0.47-0.64)	0.68 (0.37-0.72)	0.63 (0.48-0.67)
MASP1	C8B	101	63	0.72 (0.6-0.82)	0.72 (0.53-0.92)	0.72 (0.6-0.83)	0.66 (0.31-0.71)	0.62 (0.5-0.66)	0.63 (0.47-0.68)
IFNG	C8B	102	63	0.74 (0.59-0.85)	0.68 (0.51-0.86)	0.71 (0.59-0.81)	0.64 (0.32-0.72)	0.63 (0.43-0.65)	0.63 (0.47-0.68)
MASP1	IFNG	101	63	0.81 (0.68-0.9)	0.63 (0.46-0.82)	0.72 (0.6-0.82)	0.68 (0.2-0.81)	0.59 (0.54-0.63)	0.63 (0.39-0.71)
CPN2	C8B	102	67	0.65 (0.51-0.78)	0.71 (0.56-0.86)	0.68 (0.58-0.78)	0.63 (0.54-0.64)	0.66 (0.4-0.68)	0.63 (0.52-0.66)

CLU	PZP	101	67	0.64 (0.49-0.77)	0.73 (0.58-0.87)	0.69 (0.58-0.77)	0.6 (0.5-0.63)	0.7 (0.3-0.72)	0.63 (0.44-0.67)
ITIH3	ITIH1	102	67	0.68 (0.55-0.81)	0.68 (0.54-0.83)	0.68 (0.58-0.78)	0.62 (0.47-0.67)	0.65 (0.45-0.67)	0.63 (0.53-0.67)
HGF	VTN	102	63	0.6 (0.49-0.73)	0.81 (0.68-0.93)	0.71 (0.63-0.8)	0.55 (0.52-0.56)	0.71 (0.21-0.8)	0.63 (0.38-0.68)
KLRD1	HGF	101	63	0.68 (0.55-0.79)	0.75 (0.59-0.89)	0.72 (0.61-0.81)	0.64 (0.45-0.67)	0.63 (0.45-0.75)	0.63 (0.5-0.7)
C5	C3	102	67	0.71 (0.58-0.81)	0.67 (0.53-0.83)	0.69 (0.6-0.79)	0.64 (0.47-0.71)	0.63 (0.55-0.64)	0.63 (0.55-0.67)
IL7	CPN2	102	63	0.61 (0.51-0.75)	0.79 (0.66-0.9)	0.7 (0.63-0.8)	0.56 (0.56-0.58)	0.69 (0.25-0.78)	0.63 (0.4-0.67)
CCL4	CLU	102	63	0.65 (0.51-0.77)	0.73 (0.59-0.89)	0.69 (0.59-0.79)	0.61 (0.5-0.65)	0.65 (0.37-0.73)	0.63 (0.48-0.67)
ITGA11	IL17F	101	63	0.75 (0.64-0.85)	0.73 (0.57-0.88)	0.74 (0.64-0.83)	0.68 (0.56-0.73)	0.58 (0.56-0.63)	0.63 (0.57-0.66)
SAA1	VTN	102	67	0.65 (0.5-0.79)	0.8 (0.63-0.9)	0.72 (0.61-0.81)	0.61 (0.46-0.62)	0.76 (0.38-0.8)	0.63 (0.43-0.71)
IFNG	C3	102	63	0.72 (0.6-0.85)	0.69 (0.5-0.87)	0.7 (0.59-0.82)	0.61 (0.39-0.71)	0.66 (0.5-0.68)	0.63 (0.49-0.69)
CCL4	C9	102	63	0.67 (0.52-0.82)	0.64 (0.49-0.82)	0.66 (0.55-0.77)	0.65 (0.33-0.68)	0.61 (0.47-0.63)	0.63 (0.47-0.65)
HPR	SERPING1	102	67	0.66 (0.55-0.78)	0.79 (0.58-0.92)	0.72 (0.6-0.81)	0.59 (0.51-0.65)	0.67 (0.47-0.76)	0.63 (0.52-0.69)
C3	C8B	102	67	0.66 (0.54-0.78)	0.68 (0.51-0.9)	0.67 (0.55-0.78)	0.64 (0.4-0.65)	0.63 (0.47-0.67)	0.63 (0.51-0.66)
ORM1	SERPINA3	102	67	0.66 (0.53-0.8)	0.69 (0.53-0.84)	0.67 (0.58-0.78)	0.63 (0.45-0.64)	0.63 (0.48-0.67)	0.63 (0.52-0.65)
C5	C2	102	67	0.73 (0.62-0.84)	0.68 (0.55-0.84)	0.71 (0.61-0.8)	0.64 (0.39-0.73)	0.61 (0.54-0.64)	0.63 (0.5-0.67)
SERPINA3	C3	102	67	0.66 (0.53-0.79)	0.68 (0.52-0.84)	0.67 (0.58-0.78)	0.62 (0.47-0.65)	0.64 (0.51-0.67)	0.63 (0.52-0.66)
KLRD1	ORM1	101	63	0.69 (0.55-0.81)	0.66 (0.55-0.79)	0.67 (0.58-0.77)	0.65 (0.44-0.67)	0.62 (0.52-0.64)	0.63 (0.51-0.65)
LAMP3	CPN2	101	63	0.69 (0.56-0.83)	0.7 (0.55-0.84)	0.69 (0.6-0.8)	0.61 (0.39-0.66)	0.65 (0.43-0.69)	0.63 (0.49-0.66)
CLU	C8B	102	67	0.64 (0.52-0.77)	0.74 (0.61-0.88)	0.69 (0.6-0.78)	0.61 (0.54-0.63)	0.65 (0.42-0.71)	0.63 (0.51-0.67)
DCTN1	NCR1	102	63	0.67 (0.54-0.8)	0.68 (0.5-0.86)	0.68 (0.56-0.79)	0.63 (0.37-0.66)	0.64 (0.5-0.65)	0.63 (0.49-0.65)
HGF	C3	102	63	0.65 (0.53-0.76)	0.73 (0.53-0.92)	0.7 (0.58-0.81)	0.62 (0.44-0.64)	0.66 (0.41-0.73)	0.63 (0.48-0.68)
CCL13	C8B	102	63	0.65 (0.53-0.78)	0.72 (0.57-0.87)	0.68 (0.59-0.79)	0.63 (0.5-0.64)	0.66 (0.37-0.69)	0.63 (0.48-0.66)
DCTN1	PZP	100	63	0.68 (0.53-0.82)	0.71 (0.5-0.88)	0.7 (0.59-0.8)	0.66 (0.43-0.68)	0.66 (0.48-0.7)	0.63 (0.48-0.69)
IFNG	PZP	101	63	0.76 (0.64-0.86)	0.74 (0.49-0.85)	0.75 (0.61-0.82)	0.68 (0.3-0.78)	0.64 (0.45-0.73)	0.63 (0.44-0.73)
CCL13	LRG1	102	63	0.65 (0.52-0.79)	0.71 (0.55-0.86)	0.68 (0.57-0.77)	0.57 (0.51-0.67)	0.68 (0.34-0.71)	0.63 (0.47-0.68)
CRP_SRM	VTN	102	67	0.72 (0.59-0.85)	0.76 (0.62-0.89)	0.74 (0.65-0.83)	0.52 (0.45-0.69)	0.73 (0.39-0.78)	0.63 (0.45-0.72)
ITIH3	CLU	102	67	0.66 (0.52-0.8)	0.72 (0.57-0.85)	0.69 (0.59-0.78)	0.61 (0.53-0.66)	0.65 (0.42-0.68)	0.62 (0.52-0.66)
C3	SERPIND1	102	67	0.65 (0.53-0.74)	0.77 (0.62-0.91)	0.71 (0.62-0.8)	0.6 (0.52-0.64)	0.67 (0.37-0.75)	0.62 (0.48-0.69)
NCR1	LAMP3	102	63	0.68 (0.54-0.82)	0.64 (0.51-0.78)	0.66 (0.57-0.77)	0.63 (0.36-0.67)	0.62 (0.4-0.65)	0.62 (0.49-0.65)
CCL4	CPN2	102	63	0.66 (0.54-0.79)	0.71 (0.56-0.86)	0.69 (0.58-0.79)	0.61 (0.47-0.66)	0.68 (0.35-0.7)	0.62 (0.47-0.67)

IL17F	CP	102	63	0.71 (0.58-0.82)	0.81 (0.67-0.93)	0.76 (0.67-0.84)	0.63 (0.51-0.7)	0.65 (0.51-0.71)	0.62 (0.54-0.69)
LAMP3	IL15	101	63	0.68 (0.52-0.83)	0.65 (0.5-0.82)	0.67 (0.56-0.77)	0.62 (0.38-0.66)	0.63 (0.48-0.69)	0.62 (0.49-0.66)
KLRD1	NCR1	102	63	0.69 (0.57-0.79)	0.68 (0.54-0.82)	0.69 (0.6-0.78)	0.63 (0.51-0.66)	0.62 (0.5-0.66)	0.62 (0.54-0.66)
IL15	CFB	102	63	0.64 (0.5-0.77)	0.73 (0.54-0.88)	0.68 (0.58-0.79)	0.62 (0.58-0.63)	0.63 (0.47-0.71)	0.62 (0.54-0.67)
ORM1	LRG1	102	67	0.66 (0.53-0.79)	0.69 (0.54-0.81)	0.68 (0.56-0.76)	0.62 (0.45-0.65)	0.65 (0.47-0.7)	0.62 (0.51-0.66)
SERPINA3	ITIH2	102	67	0.65 (0.53-0.79)	0.67 (0.53-0.82)	0.66 (0.57-0.77)	0.61 (0.55-0.64)	0.64 (0.45-0.67)	0.62 (0.52-0.65)
C5	ITIH2	102	67	0.72 (0.6-0.82)	0.66 (0.54-0.81)	0.69 (0.6-0.79)	0.65 (0.44-0.71)	0.61 (0.52-0.63)	0.62 (0.52-0.67)
IL6_PEA_IR	VTN	101	63	0.7 (0.57-0.81)	0.81 (0.67-0.92)	0.75 (0.66-0.83)	0.62 (0.41-0.69)	0.67 (0.34-0.78)	0.62 (0.45-0.72)
FCRL6	NCR1	102	63	0.64 (0.53-0.77)	0.7 (0.56-0.83)	0.67 (0.58-0.76)	0.61 (0.52-0.61)	0.65 (0.45-0.68)	0.62 (0.52-0.65)
HGF	CPN2	102	63	0.62 (0.51-0.76)	0.73 (0.58-0.88)	0.68 (0.58-0.78)	0.58 (0.49-0.6)	0.68 (0.29-0.73)	0.62 (0.43-0.66)
CLU	CFB	102	67	0.62 (0.49-0.74)	0.72 (0.57-0.86)	0.67 (0.57-0.77)	0.59 (0.55-0.6)	0.66 (0.32-0.7)	0.62 (0.45-0.65)
IL6_PEA_IR	ITIH2	101	63	0.7 (0.57-0.82)	0.7 (0.52-0.88)	0.7 (0.59-0.81)	0.62 (0.36-0.72)	0.64 (0.48-0.69)	0.62 (0.5-0.69)
C2	C8B	102	67	0.65 (0.54-0.78)	0.7 (0.53-0.89)	0.67 (0.57-0.79)	0.62 (0.48-0.63)	0.64 (0.46-0.68)	0.62 (0.51-0.65)
FCRL6	ITIH2	101	63	0.63 (0.52-0.76)	0.74 (0.62-0.85)	0.69 (0.6-0.77)	0.59 (0.54-0.6)	0.67 (0.4-0.74)	0.62 (0.49-0.67)
ORM1	C8B	102	67	0.65 (0.52-0.78)	0.68 (0.53-0.84)	0.67 (0.57-0.78)	0.63 (0.42-0.64)	0.63 (0.41-0.66)	0.62 (0.49-0.65)
ITIH3	VTN	102	67	0.66 (0.52-0.79)	0.77 (0.63-0.88)	0.71 (0.63-0.8)	0.58 (0.5-0.65)	0.68 (0.34-0.76)	0.62 (0.46-0.69)
CP	VTN	102	67	0.68 (0.53-0.81)	0.77 (0.62-0.9)	0.72 (0.62-0.82)	0.57 (0.46-0.66)	0.69 (0.38-0.77)	0.62 (0.47-0.7)
DCTN1	C9	101	63	0.67 (0.54-0.82)	0.66 (0.49-0.84)	0.67 (0.56-0.78)	0.63 (0.38-0.68)	0.62 (0.56-0.64)	0.62 (0.49-0.65)
LRG1	C2	102	67	0.65 (0.51-0.78)	0.71 (0.56-0.86)	0.68 (0.58-0.77)	0.6 (0.48-0.63)	0.67 (0.45-0.73)	0.62 (0.51-0.68)
C9	SERPIND1	102	67	0.65 (0.52-0.78)	0.76 (0.61-0.89)	0.71 (0.61-0.8)	0.6 (0.47-0.66)	0.67 (0.4-0.74)	0.62 (0.48-0.69)
SERPINA3	SERPING1	102	67	0.65 (0.53-0.78)	0.69 (0.51-0.88)	0.67 (0.56-0.78)	0.61 (0.42-0.65)	0.67 (0.44-0.68)	0.62 (0.48-0.66)
CP	SERPING1	102	67	0.69 (0.56-0.8)	0.71 (0.52-0.87)	0.7 (0.59-0.8)	0.62 (0.48-0.68)	0.63 (0.48-0.73)	0.62 (0.51-0.7)
IL6_PEA_IR	CCL4	101	63	0.73 (0.59-0.83)	0.62 (0.46-0.84)	0.68 (0.57-0.79)	0.68 (0.27-0.74)	0.57 (0.54-0.6)	0.62 (0.42-0.66)
IL6_PEA_IR	IL6_PEA_cytokine	101	63	0.73 (0.6-0.83)	0.63 (0.44-0.84)	0.68 (0.56-0.79)	0.67 (0.28-0.72)	0.57 (0.32-0.59)	0.62 (0.42-0.65)
MASP1	ITIH3	101	63	0.71 (0.58-0.84)	0.68 (0.53-0.84)	0.7 (0.6-0.79)	0.66 (0.31-0.71)	0.6 (0.54-0.63)	0.62 (0.45-0.67)
ITIH1	PZP	101	67	0.64 (0.51-0.77)	0.7 (0.56-0.84)	0.67 (0.57-0.76)	0.6 (0.48-0.63)	0.66 (0.36-0.74)	0.62 (0.47-0.67)
IL7	IL15	102	63	0.63 (0.51-0.74)	0.74 (0.58-0.89)	0.69 (0.58-0.79)	0.58 (0.56-0.59)	0.67 (0.33-0.74)	0.62 (0.46-0.66)
ITIH3	C3	102	67	0.67 (0.53-0.81)	0.66 (0.51-0.83)	0.67 (0.57-0.76)	0.63 (0.43-0.65)	0.63 (0.52-0.64)	0.62 (0.51-0.65)
CLU	VTN	102	67	0.61 (0.51-0.74)	0.76 (0.63-0.87)	0.68 (0.6-0.76)	0.56 (0.54-0.58)	0.69 (0.26-0.75)	0.62 (0.41-0.66)
FCRL6	ORM1	101	63	0.64 (0.51-0.78)	0.69 (0.56-0.83)	0.67 (0.57-0.78)	0.6 (0.51-0.63)	0.65 (0.46-0.7)	0.62 (0.52-0.66)

IFNG	C2	102	63	0.72 (0.57-0.84)	0.71 (0.53-0.86)	0.71 (0.6-0.81)	0.61 (0.41-0.69)	0.67 (0.47-0.69)	0.62 (0.5-0.68)
MASP1	C4B	101	63	0.72 (0.59-0.83)	0.76 (0.56-0.94)	0.74 (0.62-0.84)	0.64 (0.47-0.71)	0.6 (0.54-0.72)	0.62 (0.52-0.69)
C9	C8B	102	67	0.65 (0.52-0.8)	0.67 (0.52-0.85)	0.66 (0.57-0.77)	0.63 (0.42-0.66)	0.63 (0.47-0.65)	0.62 (0.5-0.65)
IL13	LRG1	102	63	0.66 (0.54-0.79)	0.74 (0.53-0.85)	0.7 (0.58-0.79)	0.61 (0.47-0.66)	0.65 (0.35-0.66)	0.62 (0.47-0.65)
LRG1	VTN	102	67	0.65 (0.51-0.79)	0.77 (0.62-0.88)	0.71 (0.61-0.8)	0.56 (0.48-0.62)	0.7 (0.34-0.76)	0.62 (0.45-0.68)
LAMP3	ITIH2	101	63	0.69 (0.58-0.82)	0.69 (0.56-0.82)	0.69 (0.6-0.78)	0.6 (0.5-0.67)	0.64 (0.5-0.68)	0.62 (0.53-0.67)
IL6_PEA_IR	CCL13	101	63	0.71 (0.58-0.83)	0.68 (0.49-0.85)	0.69 (0.59-0.8)	0.65 (0.35-0.72)	0.58 (0.5-0.67)	0.62 (0.47-0.68)
NCR1	ITIH2	101	63	0.66 (0.54-0.78)	0.71 (0.57-0.86)	0.68 (0.58-0.79)	0.62 (0.47-0.65)	0.64 (0.46-0.68)	0.62 (0.52-0.66)
DCTN1	CCL4	101	63	0.64 (0.51-0.78)	0.66 (0.48-0.85)	0.66 (0.54-0.76)	0.63 (0.4-0.66)	0.61 (0.58-0.64)	0.62 (0.5-0.64)
IL15	C9	102	63	0.65 (0.51-0.79)	0.67 (0.52-0.83)	0.66 (0.56-0.78)	0.62 (0.46-0.64)	0.63 (0.5-0.68)	0.62 (0.51-0.66)
IL17F	CRP_SRM	102	63	0.78 (0.65-0.88)	0.7 (0.48-0.89)	0.74 (0.62-0.85)	0.66 (0.29-0.78)	0.56 (0.52-0.69)	0.62 (0.45-0.7)
CFB	VTN	102	67	0.62 (0.51-0.75)	0.76 (0.63-0.86)	0.68 (0.6-0.77)	0.56 (0.53-0.59)	0.68 (0.26-0.75)	0.62 (0.41-0.66)
HGF	IL7	102	63	0.61 (0.49-0.73)	0.74 (0.55-0.89)	0.67 (0.56-0.77)	0.55 (0.51-0.56)	0.7 (0.26-0.74)	0.62 (0.4-0.65)
LRG1	SERPING1	102	67	0.65 (0.52-0.78)	0.69 (0.49-0.84)	0.67 (0.55-0.78)	0.58 (0.43-0.65)	0.66 (0.43-0.71)	0.62 (0.49-0.67)
CPN2	CFB	102	67	0.62 (0.51-0.75)	0.69 (0.54-0.85)	0.66 (0.56-0.75)	0.59 (0.53-0.6)	0.65 (0.34-0.67)	0.62 (0.46-0.63)
CCL13	C3	102	63	0.63 (0.52-0.76)	0.75 (0.57-0.91)	0.69 (0.59-0.79)	0.6 (0.53-0.62)	0.65 (0.38-0.73)	0.62 (0.48-0.67)
ITIH3	CPN2	102	67	0.66 (0.54-0.8)	0.69 (0.56-0.82)	0.68 (0.59-0.77)	0.6 (0.51-0.66)	0.65 (0.42-0.66)	0.62 (0.51-0.65)
C8B	ITIH2	102	67	0.65 (0.51-0.77)	0.68 (0.53-0.85)	0.66 (0.56-0.77)	0.62 (0.53-0.64)	0.63 (0.42-0.66)	0.62 (0.51-0.65)
HGF	CFB	102	63	0.63 (0.49-0.75)	0.73 (0.57-0.9)	0.68 (0.58-0.79)	0.61 (0.49-0.62)	0.65 (0.31-0.72)	0.62 (0.45-0.67)
LAMP3	IFNG	101	63	0.77 (0.62-0.88)	0.66 (0.49-0.8)	0.71 (0.61-0.8)	0.61 (0.28-0.76)	0.62 (0.61-0.64)	0.62 (0.45-0.69)
NCR1	CCL4	101	63	0.67 (0.55-0.78)	0.65 (0.52-0.81)	0.66 (0.56-0.76)	0.62 (0.34-0.67)	0.62 (0.44-0.63)	0.61 (0.48-0.65)
HGF	C2	102	63	0.64 (0.47-0.77)	0.75 (0.57-0.92)	0.69 (0.57-0.8)	0.6 (0.51-0.62)	0.64 (0.29-0.74)	0.61 (0.44-0.67)
C5	ITIH1	102	67	0.71 (0.58-0.83)	0.69 (0.55-0.84)	0.7 (0.61-0.8)	0.63 (0.46-0.71)	0.61 (0.48-0.65)	0.61 (0.52-0.67)
IL7	ITIH2	102	63	0.61 (0.49-0.73)	0.75 (0.61-0.87)	0.68 (0.59-0.78)	0.55 (0.53-0.56)	0.69 (0.28-0.73)	0.61 (0.41-0.64)
DCTN1	CPN2	101	63	0.67 (0.54-0.79)	0.72 (0.53-0.86)	0.69 (0.58-0.79)	0.61 (0.46-0.68)	0.62 (0.45-0.7)	0.61 (0.49-0.68)
IL15	CPN2	102	63	0.64 (0.5-0.76)	0.72 (0.54-0.88)	0.67 (0.56-0.79)	0.59 (0.56-0.6)	0.64 (0.43-0.72)	0.61 (0.51-0.65)
NCR1	IL6_PEA_cytokine	101	63	0.66 (0.53-0.78)	0.64 (0.5-0.83)	0.65 (0.54-0.76)	0.61 (0.36-0.68)	0.63 (0.41-0.65)	0.61 (0.48-0.66)
MILR1	MASP1	102	63	0.72 (0.61-0.82)	0.68 (0.47-0.85)	0.7 (0.58-0.8)	0.65 (0.33-0.7)	0.58 (0.52-0.69)	0.61 (0.46-0.68)
C8B	CFB	102	67	0.65 (0.53-0.78)	0.71 (0.55-0.88)	0.68 (0.58-0.78)	0.63 (0.52-0.63)	0.61 (0.41-0.69)	0.61 (0.5-0.66)
IL6_PEA_cytokin	C9	102	63	0.67 (0.52-0.81)	0.65 (0.47-0.85)	0.66 (0.54-0.78)	0.59 (0.33-0.7)	0.63 (0.46-0.67)	0.61 (0.47-0.67)

MILR1	CCL13	101	63	0.67 (0.52-0.84)	0.68 (0.52-0.85)	0.68 (0.56-0.8)	0.61 (0.44-0.67)	0.62 (0.38-0.66)	0.61 (0.49-0.65)
ITIH3	C2	102	67	0.65 (0.51-0.8)	0.69 (0.54-0.84)	0.67 (0.57-0.76)	0.61 (0.49-0.65)	0.63 (0.44-0.66)	0.61 (0.52-0.65)
C8B	VTN	102	67	0.65 (0.52-0.78)	0.78 (0.64-0.92)	0.71 (0.62-0.8)	0.61 (0.52-0.62)	0.63 (0.38-0.75)	0.61 (0.49-0.68)
SERPINA3	CLU	102	67	0.64 (0.52-0.79)	0.72 (0.59-0.86)	0.68 (0.59-0.78)	0.61 (0.51-0.64)	0.63 (0.35-0.69)	0.61 (0.48-0.66)
CCL13	CFB	102	63	0.61 (0.49-0.75)	0.76 (0.6-0.91)	0.69 (0.58-0.78)	0.56 (0.54-0.6)	0.66 (0.29-0.74)	0.61 (0.43-0.66)
LAMP3	ORM1	101	63	0.69 (0.55-0.82)	0.65 (0.51-0.79)	0.67 (0.57-0.77)	0.62 (0.37-0.67)	0.62 (0.5-0.64)	0.61 (0.48-0.65)
CCL4	ORM1	102	63	0.69 (0.53-0.82)	0.64 (0.51-0.8)	0.67 (0.55-0.77)	0.66 (0.32-0.69)	0.6 (0.43-0.62)	0.61 (0.44-0.65)
IL13	SERPIND1	102	63	0.66 (0.55-0.75)	0.79 (0.65-0.91)	0.72 (0.64-0.81)	0.6 (0.53-0.67)	0.62 (0.23-0.67)	0.61 (0.41-0.65)
SERPINA3	C2	102	67	0.64 (0.51-0.79)	0.71 (0.55-0.83)	0.68 (0.58-0.78)	0.61 (0.5-0.63)	0.62 (0.4-0.69)	0.61 (0.51-0.66)
MASP1	SERPINA3	101	63	0.74 (0.62-0.85)	0.71 (0.56-0.87)	0.72 (0.63-0.82)	0.64 (0.32-0.74)	0.59 (0.54-0.61)	0.61 (0.46-0.67)
HGF	CLU	102	63	0.62 (0.5-0.74)	0.76 (0.63-0.9)	0.69 (0.6-0.79)	0.59 (0.53-0.6)	0.64 (0.25-0.76)	0.61 (0.42-0.68)
FC	ORM1	77	44	0.72 (0.55-0.88)	0.66 (0.46-0.87)	0.69 (0.56-0.82)	0.62 (0.31-0.72)	0.62 (0.5-0.69)	0.61 (0.45-0.7)
FC	IL6_PEA_IR	76	43	0.75 (0.59-0.88)	0.68 (0.4-0.92)	0.71 (0.55-0.85)	0.6 (0.25-0.75)	0.64 (0.56-0.65)	0.61 (0.45-0.7)
FC	FCRL6	76	43	0.74 (0.57-0.89)	0.71 (0.52-0.91)	0.72 (0.6-0.85)	0.59 (0.27-0.74)	0.64 (0.53-0.67)	0.61 (0.44-0.69)
IL15	C2	102	63	0.64 (0.51-0.78)	0.72 (0.53-0.9)	0.68 (0.57-0.79)	0.6 (0.59-0.6)	0.63 (0.41-0.7)	0.61 (0.5-0.65)
SAA1	LRG1	102	67	0.66 (0.49-0.78)	0.72 (0.45-0.85)	0.69 (0.52-0.78)	0.63 (0.39-0.65)	0.71 (0.45-0.75)	0.61 (0.45-0.69)
ORM1	ITIH3	102	67	0.67 (0.54-0.79)	0.65 (0.52-0.77)	0.66 (0.56-0.75)	0.63 (0.38-0.65)	0.61 (0.47-0.63)	0.61 (0.49-0.64)
SAA1	C9	102	67	0.66 (0.51-0.81)	0.66 (0.46-0.85)	0.66 (0.54-0.79)	0.63 (0.41-0.66)	0.68 (0.48-0.69)	0.61 (0.49-0.67)
IL17F	HPR	102	63	0.69 (0.56-0.8)	0.83 (0.66-0.97)	0.75 (0.66-0.85)	0.6 (0.54-0.66)	0.62 (0.49-0.75)	0.61 (0.53-0.68)
IL13	C4B	102	63	0.68 (0.56-0.79)	0.76 (0.57-0.93)	0.72 (0.61-0.82)	0.63 (0.58-0.68)	0.59 (0.55-0.65)	0.61 (0.52-0.65)
IFNG	C9	102	63	0.7 (0.54-0.84)	0.66 (0.47-0.82)	0.68 (0.56-0.77)	0.61 (0.28-0.73)	0.63 (0.5-0.65)	0.61 (0.45-0.68)
ITIH3	ITIH2	102	67	0.67 (0.51-0.8)	0.65 (0.53-0.79)	0.66 (0.57-0.76)	0.61 (0.45-0.67)	0.63 (0.44-0.66)	0.61 (0.51-0.65)
MASP1	LRG1	101	63	0.74 (0.59-0.85)	0.7 (0.54-0.84)	0.72 (0.6-0.81)	0.63 (0.35-0.74)	0.59 (0.51-0.64)	0.61 (0.46-0.67)
DCTN1	IFNG	101	63	0.75 (0.62-0.86)	0.65 (0.45-0.82)	0.7 (0.58-0.8)	0.6 (0.29-0.76)	0.62 (0.59-0.66)	0.61 (0.45-0.69)
DCTN1	VTN	101	63	0.67 (0.56-0.79)	0.79 (0.64-0.91)	0.73 (0.63-0.81)	0.57 (0.45-0.66)	0.69 (0.39-0.75)	0.61 (0.45-0.69)
NCR1	HGF	101	63	0.64 (0.51-0.77)	0.73 (0.54-0.88)	0.69 (0.56-0.79)	0.61 (0.48-0.63)	0.64 (0.3-0.72)	0.61 (0.45-0.67)
ITIH3	C9	102	67	0.66 (0.53-0.8)	0.65 (0.52-0.79)	0.65 (0.57-0.75)	0.61 (0.4-0.66)	0.61 (0.51-0.63)	0.61 (0.5-0.64)
IL15	ITIH1	102	63	0.64 (0.49-0.77)	0.72 (0.56-0.88)	0.68 (0.57-0.78)	0.59 (0.56-0.61)	0.63 (0.46-0.7)	0.61 (0.53-0.65)
PZP	VTN	101	67	0.63 (0.5-0.76)	0.77 (0.62-0.89)	0.7 (0.6-0.79)	0.56 (0.45-0.61)	0.68 (0.25-0.76)	0.61 (0.4-0.68)
CLEC4C	IL17F	101	63	0.7 (0.58-0.83)	0.77 (0.58-0.92)	0.73 (0.63-0.83)	0.63 (0.49-0.68)	0.58 (0.49-0.71)	0.61 (0.52-0.68)

IL17F	SERPIND1	102	63	0.67 (0.55-0.77)	0.82 (0.68-0.92)	0.74 (0.65-0.81)	0.6 (0.49-0.66)	0.63 (0.43-0.71)	0.61 (0.51-0.67)
CPN2	VTN	102	67	0.62 (0.51-0.74)	0.76 (0.62-0.87)	0.69 (0.6-0.78)	0.56 (0.55-0.57)	0.66 (0.27-0.75)	0.61 (0.42-0.65)
IL6_PEA_cytokin	IL15	102	63	0.67 (0.49-0.8)	0.62 (0.46-0.86)	0.64 (0.53-0.78)	0.62 (0.51-0.71)	0.6 (0.42-0.7)	0.61 (0.48-0.69)
CCL13	ITIH3	102	63	0.65 (0.53-0.8)	0.68 (0.55-0.82)	0.66 (0.57-0.76)	0.58 (0.48-0.64)	0.64 (0.41-0.66)	0.61 (0.49-0.65)
C5	CLU	102	67	0.72 (0.61-0.82)	0.71 (0.57-0.85)	0.72 (0.62-0.8)	0.62 (0.44-0.7)	0.6 (0.44-0.67)	0.61 (0.5-0.67)
LAMP3	HGF	101	63	0.69 (0.56-0.81)	0.72 (0.56-0.87)	0.71 (0.6-0.81)	0.62 (0.39-0.69)	0.64 (0.44-0.72)	0.61 (0.45-0.69)
IFNG	CFB	102	63	0.73 (0.57-0.85)	0.71 (0.56-0.85)	0.72 (0.62-0.81)	0.61 (0.38-0.71)	0.62 (0.45-0.69)	0.61 (0.48-0.69)
CPN2	CLU	102	67	0.62 (0.5-0.75)	0.73 (0.57-0.86)	0.67 (0.58-0.77)	0.58 (0.54-0.58)	0.63 (0.32-0.71)	0.61 (0.45-0.64)
CLU	C2	102	67	0.63 (0.49-0.75)	0.72 (0.58-0.86)	0.67 (0.58-0.76)	0.59 (0.56-0.6)	0.62 (0.32-0.69)	0.61 (0.46-0.64)
LAMP3	CCL13	101	63	0.69 (0.53-0.82)	0.68 (0.53-0.83)	0.68 (0.58-0.78)	0.59 (0.41-0.67)	0.64 (0.42-0.69)	0.61 (0.48-0.67)
LAMP3	VTN	101	63	0.69 (0.57-0.82)	0.77 (0.64-0.88)	0.73 (0.64-0.82)	0.56 (0.48-0.65)	0.65 (0.38-0.76)	0.61 (0.46-0.68)
C9	ITIH1	102	67	0.64 (0.5-0.79)	0.66 (0.52-0.82)	0.65 (0.55-0.76)	0.6 (0.44-0.63)	0.63 (0.41-0.64)	0.61 (0.5-0.63)
MILR1	IL17F	101	63	0.7 (0.58-0.83)	0.71 (0.56-0.88)	0.71 (0.61-0.81)	0.62 (0.42-0.68)	0.6 (0.43-0.62)	0.61 (0.49-0.64)
HGF	ITIH1	102	63	0.61 (0.5-0.74)	0.75 (0.59-0.9)	0.68 (0.59-0.79)	0.56 (0.5-0.58)	0.65 (0.27-0.75)	0.61 (0.42-0.66)
C8B	SERPING1	102	67	0.65 (0.52-0.78)	0.69 (0.5-0.86)	0.67 (0.56-0.79)	0.61 (0.43-0.64)	0.62 (0.47-0.67)	0.61 (0.48-0.65)
MASP1	IL6_PEA_cytokine	101	63	0.73 (0.6-0.83)	0.64 (0.46-0.86)	0.69 (0.58-0.81)	0.7 (0.28-0.76)	0.54 (0.44-0.64)	0.61 (0.41-0.68)
C9	SERPINA3	102	67	0.64 (0.51-0.8)	0.69 (0.54-0.84)	0.67 (0.56-0.77)	0.61 (0.4-0.64)	0.63 (0.42-0.67)	0.61 (0.48-0.65)
CCL13	ITIH1	102	63	0.62 (0.49-0.75)	0.74 (0.59-0.88)	0.69 (0.58-0.79)	0.57 (0.53-0.62)	0.64 (0.37-0.71)	0.61 (0.48-0.66)
DCTN1	ITIH1	101	63	0.68 (0.56-0.79)	0.73 (0.57-0.89)	0.7 (0.59-0.8)	0.59 (0.47-0.67)	0.64 (0.42-0.67)	0.61 (0.48-0.66)
C5	CFB	102	67	0.74 (0.61-0.86)	0.68 (0.55-0.83)	0.71 (0.62-0.8)	0.64 (0.4-0.72)	0.58 (0.46-0.64)	0.6 (0.48-0.66)
ITIH1	ITIH2	102	67	0.62 (0.52-0.75)	0.69 (0.55-0.84)	0.66 (0.57-0.75)	0.58 (0.44-0.62)	0.63 (0.39-0.69)	0.6 (0.49-0.65)
IL6_PEA_IR	SERPING1	101	63	0.75 (0.63-0.84)	0.67 (0.49-0.9)	0.71 (0.6-0.83)	0.59 (0.26-0.75)	0.61 (0.51-0.63)	0.6 (0.44-0.69)
KLRD1	IL13	101	63	0.71 (0.6-0.81)	0.69 (0.56-0.82)	0.7 (0.61-0.79)	0.64 (0.54-0.7)	0.57 (0.54-0.61)	0.6 (0.54-0.65)
KLRD1	CCL13	101	63	0.68 (0.55-0.79)	0.68 (0.53-0.83)	0.68 (0.58-0.78)	0.59 (0.43-0.67)	0.62 (0.52-0.66)	0.6 (0.51-0.65)
CFB	ITIH1	102	67	0.62 (0.51-0.75)	0.69 (0.54-0.86)	0.66 (0.56-0.76)	0.59 (0.54-0.61)	0.63 (0.36-0.66)	0.6 (0.48-0.63)
IL13	SAA1	102	63	0.69 (0.53-0.82)	0.67 (0.42-0.86)	0.68 (0.53-0.8)	0.61 (0.31-0.69)	0.6 (0.39-0.64)	0.6 (0.45-0.65)
KLRD1	IL15	101	63	0.69 (0.56-0.79)	0.64 (0.51-0.77)	0.66 (0.57-0.76)	0.62 (0.39-0.67)	0.6 (0.47-0.63)	0.6 (0.48-0.65)
DCTN1	CLU	101	63	0.67 (0.55-0.79)	0.72 (0.55-0.88)	0.69 (0.59-0.78)	0.61 (0.44-0.66)	0.64 (0.46-0.68)	0.6 (0.48-0.66)
SERPINA3	VTN	102	67	0.64 (0.52-0.79)	0.76 (0.65-0.88)	0.7 (0.61-0.79)	0.56 (0.5-0.62)	0.66 (0.3-0.74)	0.6 (0.44-0.67)
IL15	CLU	102	63	0.63 (0.51-0.75)	0.76 (0.6-0.91)	0.69 (0.59-0.79)	0.59 (0.57-0.6)	0.61 (0.43-0.73)	0.6 (0.51-0.66)

CPN2	C2	102	67	0.63 (0.52-0.76)	0.7 (0.54-0.85)	0.66 (0.57-0.76)	0.58 (0.54-0.6)	0.63 (0.35-0.67)	0.6 (0.46-0.63)
C5	SERPIND1	102	67	0.71 (0.59-0.81)	0.76 (0.61-0.89)	0.73 (0.65-0.82)	0.6 (0.46-0.66)	0.61 (0.39-0.71)	0.6 (0.49-0.67)
IL6_PEA_IR	IL7	101	63	0.71 (0.56-0.82)	0.71 (0.52-0.89)	0.71 (0.59-0.81)	0.61 (0.3-0.72)	0.6 (0.34-0.69)	0.6 (0.45-0.68)
ITIH2	PZP	101	67	0.63 (0.5-0.78)	0.69 (0.53-0.82)	0.67 (0.56-0.77)	0.59 (0.45-0.61)	0.63 (0.34-0.71)	0.6 (0.45-0.65)
IL17F	SERPINA3	102	63	0.71 (0.58-0.83)	0.72 (0.51-0.86)	0.71 (0.59-0.81)	0.6 (0.45-0.7)	0.6 (0.5-0.66)	0.6 (0.51-0.67)
IL6_PEA_cytokin	ITIH2	102	63	0.63 (0.51-0.76)	0.68 (0.52-0.88)	0.65 (0.55-0.77)	0.58 (0.48-0.64)	0.65 (0.34-0.71)	0.6 (0.46-0.66)
SERPINA3	CFB	102	67	0.64 (0.52-0.78)	0.7 (0.55-0.86)	0.67 (0.57-0.77)	0.6 (0.5-0.64)	0.6 (0.46-0.71)	0.6 (0.51-0.66)
C2	VTN	102	67	0.62 (0.52-0.74)	0.76 (0.63-0.87)	0.69 (0.61-0.78)	0.56 (0.52-0.58)	0.66 (0.26-0.75)	0.6 (0.4-0.66)
C2	CFB	102	67	0.62 (0.52-0.75)	0.68 (0.53-0.84)	0.65 (0.56-0.75)	0.6 (0.52-0.61)	0.6 (0.37-0.66)	0.6 (0.47-0.63)
C2	ITIH1	102	67	0.63 (0.52-0.76)	0.69 (0.55-0.85)	0.66 (0.56-0.76)	0.6 (0.53-0.62)	0.61 (0.37-0.65)	0.6 (0.48-0.63)
KLRD1	SERPING1	101	63	0.69 (0.56-0.79)	0.66 (0.5-0.85)	0.67 (0.56-0.78)	0.61 (0.42-0.67)	0.61 (0.48-0.64)	0.6 (0.49-0.65)
ITIH3	SERPING1	102	67	0.66 (0.54-0.8)	0.65 (0.48-0.81)	0.66 (0.56-0.76)	0.6 (0.41-0.65)	0.61 (0.5-0.65)	0.6 (0.5-0.64)
FCRL6	MASP1	102	63	0.71 (0.58-0.82)	0.69 (0.53-0.83)	0.7 (0.6-0.8)	0.63 (0.32-0.7)	0.59 (0.5-0.67)	0.6 (0.45-0.67)
FCRL6	IL15	101	63	0.62 (0.5-0.76)	0.68 (0.53-0.81)	0.65 (0.55-0.74)	0.58 (0.44-0.59)	0.63 (0.44-0.67)	0.6 (0.5-0.63)
FC	SERPING1	77	44	0.75 (0.58-0.87)	0.68 (0.47-0.95)	0.71 (0.58-0.87)	0.56 (0.26-0.75)	0.65 (0.57-0.68)	0.6 (0.45-0.7)
IFNG	ITIH1	102	63	0.72 (0.57-0.85)	0.69 (0.53-0.86)	0.71 (0.6-0.82)	0.56 (0.31-0.68)	0.66 (0.43-0.67)	0.6 (0.46-0.67)
CCL4	ITIH2	102	63	0.64 (0.51-0.76)	0.68 (0.53-0.84)	0.66 (0.56-0.77)	0.57 (0.43-0.64)	0.64 (0.35-0.67)	0.6 (0.46-0.64)
LAMP3	IL13	101	63	0.7 (0.58-0.83)	0.68 (0.4-0.82)	0.69 (0.54-0.8)	0.63 (0.3-0.7)	0.57 (0.55-0.64)	0.6 (0.43-0.65)
IFNG	CLU	102	63	0.73 (0.59-0.85)	0.7 (0.56-0.86)	0.72 (0.61-0.81)	0.58 (0.36-0.69)	0.65 (0.41-0.7)	0.6 (0.46-0.68)
CPN2	PZP	101	67	0.63 (0.49-0.77)	0.7 (0.53-0.86)	0.66 (0.55-0.77)	0.6 (0.45-0.61)	0.61 (0.33-0.7)	0.6 (0.45-0.65)
FCRL6	CCL13	101	63	0.62 (0.49-0.75)	0.7 (0.55-0.86)	0.66 (0.56-0.77)	0.57 (0.46-0.6)	0.64 (0.44-0.67)	0.6 (0.5-0.63)
CPN2	ITIH1	102	67	0.62 (0.51-0.75)	0.7 (0.57-0.84)	0.66 (0.57-0.76)	0.57 (0.5-0.59)	0.63 (0.34-0.67)	0.6 (0.46-0.63)
CCL13	C2	102	63	0.62 (0.49-0.75)	0.75 (0.61-0.88)	0.68 (0.59-0.77)	0.57 (0.53-0.6)	0.64 (0.3-0.71)	0.6 (0.44-0.65)
DCTN1	IL7	101	63	0.66 (0.54-0.78)	0.73 (0.57-0.87)	0.7 (0.59-0.79)	0.6 (0.49-0.67)	0.61 (0.41-0.73)	0.6 (0.49-0.69)
MILR1	IL13	101	63	0.68 (0.56-0.8)	0.71 (0.52-0.86)	0.69 (0.59-0.8)	0.63 (0.33-0.68)	0.56 (0.31-0.59)	0.6 (0.44-0.62)
SERPIND1	SERPING1	102	67	0.64 (0.51-0.75)	0.76 (0.58-0.9)	0.7 (0.6-0.79)	0.58 (0.48-0.62)	0.61 (0.33-0.75)	0.6 (0.45-0.68)
LRG1	C9	102	67	0.66 (0.5-0.82)	0.7 (0.52-0.82)	0.68 (0.57-0.78)	0.61 (0.37-0.64)	0.62 (0.45-0.69)	0.6 (0.48-0.66)
C9	CPN2	102	67	0.64 (0.51-0.78)	0.68 (0.53-0.83)	0.66 (0.56-0.77)	0.58 (0.42-0.63)	0.62 (0.39-0.66)	0.6 (0.47-0.64)
MASP1	SERPIND1	101	63	0.72 (0.59-0.83)	0.8 (0.65-0.92)	0.76 (0.66-0.84)	0.59 (0.39-0.7)	0.6 (0.48-0.72)	0.6 (0.49-0.68)
FCRL6	SERPING1	101	63	0.63 (0.51-0.76)	0.69 (0.53-0.86)	0.66 (0.56-0.76)	0.57 (0.45-0.61)	0.63 (0.41-0.67)	0.6 (0.48-0.63)

LAMP3	SERPING1	101	63	0.68 (0.55-0.81)	0.67 (0.5-0.87)	0.67 (0.57-0.8)	0.59 (0.38-0.67)	0.62 (0.46-0.66)	0.6 (0.49-0.65)
IL7	CCL4	102	63	0.64 (0.51-0.77)	0.71 (0.54-0.87)	0.68 (0.56-0.78)	0.57 (0.43-0.64)	0.64 (0.3-0.7)	0.59 (0.43-0.65)
CCL13	VTN	102	63	0.6 (0.49-0.73)	0.79 (0.65-0.91)	0.7 (0.6-0.79)	0.55 (0.52-0.57)	0.64 (0.26-0.79)	0.59 (0.41-0.67)
FC	LAMP3	76	43	0.83 (0.67-0.93)	0.67 (0.47-0.86)	0.75 (0.61-0.86)	0.57 (0.18-0.83)	0.59 (0.56-0.66)	0.59 (0.38-0.73)
DCTN1	ITIH2	101	63	0.67 (0.54-0.78)	0.69 (0.53-0.85)	0.68 (0.58-0.77)	0.58 (0.45-0.66)	0.62 (0.46-0.64)	0.59 (0.49-0.65)
MASP1	C3	101	63	0.71 (0.58-0.82)	0.72 (0.54-0.93)	0.71 (0.6-0.84)	0.61 (0.33-0.71)	0.58 (0.5-0.63)	0.59 (0.46-0.66)
ITIH3	CFB	102	67	0.65 (0.53-0.8)	0.69 (0.55-0.83)	0.67 (0.58-0.77)	0.59 (0.46-0.66)	0.61 (0.46-0.69)	0.59 (0.5-0.66)
IL13	ITIH3	102	63	0.67 (0.56-0.8)	0.68 (0.52-0.8)	0.67 (0.58-0.77)	0.61 (0.33-0.67)	0.58 (0.46-0.59)	0.59 (0.45-0.63)
CFB	ITIH2	102	67	0.62 (0.51-0.75)	0.67 (0.53-0.84)	0.65 (0.56-0.74)	0.58 (0.53-0.6)	0.61 (0.37-0.66)	0.59 (0.47-0.62)
IL15	CCL4	102	63	0.66 (0.5-0.8)	0.64 (0.48-0.81)	0.65 (0.53-0.77)	0.62 (0.37-0.65)	0.61 (0.44-0.66)	0.59 (0.46-0.65)
DCTN1	ORM1	101	63	0.66 (0.53-0.8)	0.65 (0.47-0.82)	0.65 (0.54-0.76)	0.62 (0.36-0.64)	0.58 (0.53-0.61)	0.59 (0.47-0.62)
CCL13	PZP	101	63	0.62 (0.49-0.76)	0.71 (0.55-0.88)	0.67 (0.56-0.77)	0.57 (0.47-0.6)	0.64 (0.33-0.71)	0.59 (0.44-0.64)
IL7	C9	102	63	0.62 (0.51-0.77)	0.72 (0.55-0.87)	0.67 (0.57-0.78)	0.56 (0.43-0.6)	0.64 (0.32-0.7)	0.59 (0.43-0.64)
ITIH2	VTN	102	67	0.6 (0.5-0.72)	0.76 (0.63-0.88)	0.68 (0.6-0.77)	0.55 (0.53-0.56)	0.63 (0.26-0.76)	0.59 (0.4-0.66)
MASP1	IL15	101	63	0.71 (0.58-0.82)	0.63 (0.49-0.81)	0.67 (0.57-0.78)	0.65 (0.3-0.7)	0.54 (0.47-0.58)	0.59 (0.42-0.63)
CCL13	CCL4	102	63	0.66 (0.5-0.79)	0.67 (0.52-0.83)	0.66 (0.55-0.76)	0.61 (0.41-0.65)	0.61 (0.38-0.67)	0.59 (0.46-0.65)
ORM1	ITIH1	102	67	0.66 (0.52-0.79)	0.67 (0.53-0.82)	0.66 (0.57-0.76)	0.6 (0.5-0.65)	0.6 (0.43-0.64)	0.59 (0.51-0.64)
IL13	VTN	102	63	0.63 (0.54-0.74)	0.79 (0.67-0.9)	0.71 (0.63-0.78)	0.55 (0.51-0.62)	0.63 (0.23-0.68)	0.59 (0.39-0.63)
MASP1	CP	101	63	0.73 (0.59-0.84)	0.77 (0.6-0.91)	0.75 (0.64-0.84)	0.58 (0.43-0.73)	0.58 (0.49-0.79)	0.59 (0.48-0.72)
C3	ITIH1	102	67	0.64 (0.52-0.76)	0.69 (0.54-0.86)	0.67 (0.58-0.77)	0.6 (0.45-0.62)	0.59 (0.41-0.65)	0.59 (0.49-0.63)
CRP_SRM	CFB	102	67	0.71 (0.53-0.84)	0.7 (0.53-0.87)	0.71 (0.58-0.81)	0.55 (0.39-0.74)	0.61 (0.39-0.76)	0.59 (0.45-0.72)
NCR1	ORM1	101	63	0.64 (0.51-0.8)	0.65 (0.5-0.82)	0.64 (0.55-0.76)	0.61 (0.39-0.62)	0.6 (0.41-0.63)	0.59 (0.48-0.62)
KLRD1	FCRL6	102	63	0.69 (0.55-0.81)	0.68 (0.53-0.82)	0.68 (0.59-0.77)	0.59 (0.38-0.67)	0.6 (0.46-0.66)	0.59 (0.48-0.65)
C9	ITIH2	102	67	0.64 (0.51-0.8)	0.63 (0.51-0.79)	0.64 (0.55-0.75)	0.58 (0.42-0.62)	0.6 (0.4-0.62)	0.59 (0.49-0.61)
C9	C3	102	67	0.64 (0.51-0.79)	0.64 (0.48-0.83)	0.64 (0.55-0.76)	0.6 (0.38-0.64)	0.61 (0.44-0.63)	0.59 (0.49-0.63)
C2	ITIH2	102	67	0.62 (0.51-0.74)	0.67 (0.53-0.83)	0.65 (0.55-0.75)	0.59 (0.53-0.61)	0.6 (0.39-0.64)	0.59 (0.48-0.62)
FC	CCL4	77	43	0.76 (0.61-0.89)	0.64 (0.44-0.86)	0.71 (0.57-0.83)	0.55 (0.25-0.75)	0.65 (0.56-0.69)	0.59 (0.45-0.71)
C3	CLU	102	67	0.65 (0.52-0.77)	0.72 (0.59-0.88)	0.68 (0.59-0.77)	0.6 (0.42-0.64)	0.58 (0.35-0.68)	0.59 (0.47-0.64)
CPN2	ITIH2	102	67	0.62 (0.51-0.75)	0.68 (0.55-0.82)	0.65 (0.56-0.76)	0.56 (0.52-0.58)	0.62 (0.35-0.66)	0.59 (0.46-0.61)
ORM1	CPN2	102	67	0.65 (0.52-0.77)	0.68 (0.55-0.82)	0.67 (0.57-0.76)	0.57 (0.48-0.63)	0.6 (0.38-0.66)	0.59 (0.47-0.64)

CCL13	SAA1	102	63	0.64 (0.51-0.79)	0.67 (0.52-0.84)	0.66 (0.55-0.78)	0.55 (0.38-0.65)	0.6 (0.38-0.7)	0.59 (0.47-0.65)
C3	C2	102	67	0.65 (0.52-0.76)	0.66 (0.52-0.84)	0.66 (0.56-0.75)	0.61 (0.41-0.62)	0.58 (0.41-0.64)	0.59 (0.49-0.63)
IL6_PEA_cytokin	IL7	102	63	0.62 (0.51-0.74)	0.71 (0.54-0.88)	0.67 (0.56-0.77)	0.56 (0.46-0.65)	0.66 (0.3-0.7)	0.59 (0.43-0.66)
LRG1	CFB	102	67	0.64 (0.5-0.78)	0.69 (0.53-0.85)	0.67 (0.56-0.77)	0.6 (0.44-0.64)	0.57 (0.46-0.72)	0.59 (0.49-0.67)
IL7	CCL13	102	63	0.61 (0.51-0.73)	0.75 (0.6-0.88)	0.68 (0.58-0.78)	0.55 (0.52-0.56)	0.63 (0.28-0.73)	0.59 (0.41-0.64)
HGF	ITIH2	102	63	0.61 (0.5-0.75)	0.72 (0.57-0.89)	0.67 (0.57-0.78)	0.56 (0.5-0.57)	0.63 (0.29-0.72)	0.59 (0.42-0.64)
DCTN1	IL15	101	63	0.65 (0.51-0.78)	0.64 (0.49-0.82)	0.64 (0.55-0.75)	0.59 (0.37-0.63)	0.59 (0.47-0.63)	0.59 (0.48-0.62)
IL6_PEA_cytokin	CCL4	102	63	0.67 (0.47-0.81)	0.63 (0.44-0.82)	0.65 (0.52-0.77)	0.6 (0.32-0.71)	0.59 (0.4-0.62)	0.59 (0.41-0.65)
IL13	PZP	101	63	0.65 (0.53-0.77)	0.8 (0.52-0.91)	0.73 (0.58-0.81)	0.56 (0.36-0.66)	0.62 (0.21-0.64)	0.58 (0.37-0.64)
ORM1	SAA1	102	67	0.65 (0.5-0.79)	0.66 (0.47-0.83)	0.65 (0.53-0.78)	0.6 (0.37-0.65)	0.62 (0.47-0.7)	0.58 (0.45-0.66)
IL6_PEA_IR	IL17F	101	63	0.75 (0.61-0.85)	0.62 (0.44-0.83)	0.68 (0.58-0.8)	0.67 (0.25-0.75)	0.49 (0.48-0.57)	0.58 (0.37-0.64)
CCL13	C9	102	63	0.63 (0.49-0.78)	0.68 (0.51-0.85)	0.66 (0.54-0.77)	0.55 (0.34-0.67)	0.62 (0.37-0.65)	0.58 (0.45-0.65)
C9	CLU	102	67	0.63 (0.51-0.79)	0.7 (0.55-0.85)	0.67 (0.56-0.77)	0.58 (0.42-0.62)	0.61 (0.34-0.67)	0.58 (0.46-0.64)
CCL13	CLU	102	63	0.61 (0.49-0.73)	0.73 (0.57-0.89)	0.68 (0.57-0.78)	0.56 (0.51-0.59)	0.61 (0.34-0.7)	0.58 (0.45-0.64)
C3	CPN2	102	67	0.63 (0.52-0.76)	0.69 (0.53-0.84)	0.66 (0.55-0.77)	0.59 (0.45-0.62)	0.59 (0.36-0.67)	0.58 (0.46-0.64)
ORM1	C9	102	67	0.64 (0.51-0.79)	0.63 (0.5-0.8)	0.64 (0.54-0.75)	0.6 (0.36-0.65)	0.58 (0.48-0.64)	0.58 (0.46-0.64)
MASP1	ITIH1	101	63	0.71 (0.59-0.82)	0.71 (0.56-0.88)	0.71 (0.62-0.81)	0.58 (0.31-0.69)	0.59 (0.43-0.65)	0.58 (0.45-0.66)
IL17F	C4B	102	63	0.69 (0.57-0.81)	0.78 (0.57-0.95)	0.74 (0.61-0.84)	0.6 (0.54-0.68)	0.57 (0.5-0.64)	0.58 (0.54-0.63)
MILR1	SERPING1	101	63	0.71 (0.57-0.84)	0.67 (0.49-0.88)	0.69 (0.57-0.82)	0.61 (0.41-0.68)	0.54 (0.48-0.65)	0.58 (0.48-0.65)
HGF	IL15	102	63	0.62 (0.49-0.76)	0.7 (0.5-0.88)	0.66 (0.54-0.77)	0.57 (0.52-0.58)	0.62 (0.3-0.71)	0.58 (0.43-0.64)
CLU	ITIH1	102	67	0.62 (0.51-0.75)	0.72 (0.57-0.86)	0.67 (0.57-0.76)	0.58 (0.5-0.59)	0.59 (0.34-0.69)	0.58 (0.46-0.63)
DCTN1	MASP1	102	63	0.74 (0.6-0.84)	0.67 (0.51-0.83)	0.7 (0.6-0.8)	0.62 (0.27-0.74)	0.54 (0.52-0.61)	0.58 (0.4-0.65)
ORM1	VTN	102	67	0.63 (0.49-0.77)	0.75 (0.62-0.87)	0.69 (0.6-0.78)	0.55 (0.5-0.61)	0.61 (0.31-0.75)	0.58 (0.44-0.66)
MASP1	CLU	101	63	0.72 (0.58-0.82)	0.7 (0.56-0.86)	0.71 (0.6-0.82)	0.61 (0.31-0.7)	0.57 (0.46-0.62)	0.58 (0.43-0.64)
IL13	C3	102	63	0.66 (0.56-0.78)	0.68 (0.47-0.88)	0.67 (0.55-0.78)	0.6 (0.34-0.66)	0.56 (0.38-0.58)	0.58 (0.44-0.61)
MASP1	C9	101	63	0.74 (0.59-0.84)	0.66 (0.51-0.83)	0.7 (0.59-0.8)	0.59 (0.3-0.74)	0.57 (0.54-0.6)	0.58 (0.44-0.66)
FC	CCL13	77	43	0.74 (0.57-0.9)	0.69 (0.47-0.89)	0.71 (0.57-0.84)	0.6 (0.27-0.73)	0.57 (0.5-0.67)	0.58 (0.42-0.66)
C3	ITIH2	102	67	0.65 (0.53-0.77)	0.66 (0.52-0.82)	0.65 (0.56-0.75)	0.59 (0.41-0.63)	0.58 (0.43-0.62)	0.58 (0.49-0.62)
IL15	ITIH2	102	63	0.62 (0.48-0.77)	0.68 (0.54-0.83)	0.65 (0.56-0.76)	0.56 (0.53-0.57)	0.59 (0.44-0.66)	0.58 (0.5-0.61)
IL6_PEA_cytokin	CCL13	102	63	0.64 (0.49-0.77)	0.66 (0.5-0.83)	0.65 (0.52-0.76)	0.58 (0.38-0.69)	0.61 (0.35-0.67)	0.58 (0.44-0.65)

HGF	C9	102	63	0.64 (0.52-0.79)	0.71 (0.52-0.88)	0.68 (0.57-0.79)	0.6 (0.41-0.63)	0.61 (0.33-0.69)	0.58 (0.42-0.65)
IL6_PEA_IR	IL13	101	63	0.76 (0.64-0.86)	0.64 (0.43-0.87)	0.71 (0.58-0.82)	0.68 (0.24-0.76)	0.47 (0.46-0.56)	0.58 (0.35-0.63)
ORM1	C3	102	67	0.66 (0.53-0.79)	0.64 (0.51-0.81)	0.65 (0.55-0.76)	0.59 (0.38-0.64)	0.59 (0.46-0.6)	0.58 (0.48-0.62)
IFNG	ORM1	102	63	0.71 (0.55-0.85)	0.62 (0.49-0.77)	0.66 (0.56-0.77)	0.55 (0.29-0.73)	0.6 (0.53-0.64)	0.58 (0.45-0.67)
C9	VTN	102	67	0.62 (0.5-0.78)	0.76 (0.62-0.87)	0.69 (0.6-0.79)	0.54 (0.44-0.59)	0.62 (0.29-0.74)	0.58 (0.41-0.65)
IL6_PEA_cytokin	ORM1	102	63	0.69 (0.54-0.82)	0.62 (0.47-0.85)	0.66 (0.55-0.78)	0.58 (0.31-0.73)	0.59 (0.4-0.64)	0.58 (0.42-0.67)
ORM1	ITIH2	102	67	0.65 (0.51-0.78)	0.64 (0.52-0.78)	0.65 (0.55-0.75)	0.57 (0.47-0.63)	0.58 (0.43-0.61)	0.58 (0.49-0.61)
HGF	PZP	101	63	0.62 (0.47-0.76)	0.78 (0.64-0.92)	0.7 (0.6-0.78)	0.54 (0.47-0.6)	0.62 (0.24-0.77)	0.58 (0.39-0.66)
ORM1	CLU	102	67	0.63 (0.51-0.77)	0.7 (0.56-0.85)	0.67 (0.58-0.77)	0.59 (0.48-0.62)	0.58 (0.37-0.68)	0.58 (0.47-0.64)
CCL13	IFNG	102	63	0.72 (0.56-0.85)	0.65 (0.49-0.83)	0.69 (0.57-0.79)	0.57 (0.32-0.72)	0.62 (0.47-0.66)	0.58 (0.43-0.67)
IL17F	LRG1	102	63	0.71 (0.6-0.81)	0.71 (0.53-0.84)	0.71 (0.6-0.8)	0.58 (0.42-0.7)	0.56 (0.51-0.64)	0.58 (0.49-0.64)
NCR1	IL15	101	63	0.63 (0.49-0.77)	0.65 (0.51-0.8)	0.65 (0.54-0.74)	0.57 (0.39-0.61)	0.59 (0.42-0.66)	0.58 (0.46-0.63)
IL13	CPN2	102	63	0.63 (0.53-0.75)	0.72 (0.55-0.88)	0.68 (0.58-0.77)	0.55 (0.39-0.62)	0.6 (0.25-0.62)	0.58 (0.4-0.61)
NCR1	CCL13	101	63	0.63 (0.51-0.77)	0.69 (0.54-0.83)	0.66 (0.57-0.76)	0.58 (0.5-0.61)	0.58 (0.37-0.65)	0.58 (0.48-0.63)
SAA1	SERPING1	102	67	0.65 (0.49-0.79)	0.66 (0.46-0.88)	0.65 (0.53-0.79)	0.56 (0.38-0.65)	0.6 (0.42-0.7)	0.58 (0.47-0.65)
CLU	ITIH2	102	67	0.61 (0.51-0.74)	0.71 (0.56-0.86)	0.66 (0.58-0.75)	0.58 (0.51-0.59)	0.58 (0.33-0.68)	0.58 (0.45-0.63)
IL13	C8B	102	63	0.67 (0.53-0.79)	0.67 (0.46-0.85)	0.67 (0.55-0.78)	0.61 (0.33-0.67)	0.54 (0.4-0.58)	0.58 (0.44-0.61)
IL15	ORM1	102	63	0.64 (0.5-0.8)	0.63 (0.49-0.8)	0.63 (0.52-0.75)	0.58 (0.42-0.62)	0.57 (0.44-0.61)	0.58 (0.48-0.61)
C9	SERPING1	102	67	0.63 (0.51-0.78)	0.63 (0.48-0.8)	0.63 (0.53-0.74)	0.57 (0.35-0.66)	0.61 (0.46-0.65)	0.57 (0.45-0.64)
HGF	CCL13	102	63	0.61 (0.48-0.74)	0.71 (0.55-0.88)	0.66 (0.56-0.77)	0.56 (0.47-0.59)	0.62 (0.29-0.72)	0.57 (0.41-0.65)
MASP1	ORM1	101	63	0.72 (0.58-0.83)	0.63 (0.49-0.82)	0.68 (0.58-0.78)	0.59 (0.29-0.72)	0.56 (0.52-0.57)	0.57 (0.42-0.64)
MASP1	C2	101	63	0.71 (0.57-0.82)	0.7 (0.52-0.88)	0.7 (0.58-0.81)	0.59 (0.34-0.7)	0.56 (0.46-0.6)	0.57 (0.44-0.63)
IFNG	SERPING1	102	63	0.73 (0.59-0.86)	0.63 (0.46-0.83)	0.68 (0.55-0.8)	0.54 (0.3-0.71)	0.62 (0.51-0.63)	0.57 (0.44-0.67)
IFNG	CPN2	102	63	0.72 (0.58-0.84)	0.72 (0.55-0.86)	0.71 (0.61-0.8)	0.5 (0.36-0.72)	0.68 (0.4-0.72)	0.57 (0.42-0.69)
MASP1	CFB	101	63	0.73 (0.59-0.83)	0.72 (0.54-0.89)	0.72 (0.6-0.82)	0.57 (0.37-0.72)	0.58 (0.5-0.64)	0.57 (0.46-0.67)
ITIH1	VTN	102	67	0.6 (0.51-0.73)	0.76 (0.62-0.87)	0.68 (0.6-0.76)	0.56 (0.52-0.57)	0.59 (0.26-0.74)	0.57 (0.41-0.65)
IL6_PEA_cytokin	IFNG	102	63	0.77 (0.62-0.88)	0.62 (0.41-0.83)	0.7 (0.57-0.82)	0.53 (0.23-0.77)	0.62 (0.45-0.64)	0.57 (0.42-0.7)
DCTN1	CCL13	101	63	0.67 (0.53-0.79)	0.66 (0.5-0.83)	0.66 (0.55-0.77)	0.59 (0.38-0.65)	0.58 (0.47-0.61)	0.57 (0.46-0.62)
IL13	CLU	102	63	0.65 (0.53-0.76)	0.7 (0.56-0.87)	0.68 (0.57-0.78)	0.57 (0.45-0.63)	0.56 (0.32-0.61)	0.57 (0.45-0.61)
IL17F	CFB	102	63	0.67 (0.54-0.79)	0.72 (0.55-0.88)	0.7 (0.59-0.79)	0.58 (0.42-0.68)	0.56 (0.46-0.63)	0.57 (0.48-0.64)

FC	IL6_PEA_cytokine	77	43	0.73 (0.54-0.87)	0.68 (0.4-0.92)	0.7 (0.54-0.85)	0.54 (0.28-0.73)	0.63 (0.55-0.65)	0.57 (0.45-0.68)
MASP1	IL7	101	63	0.71 (0.58-0.82)	0.73 (0.56-0.9)	0.72 (0.62-0.82)	0.6 (0.39-0.7)	0.58 (0.36-0.69)	0.57 (0.43-0.67)
ORM1	C2	102	67	0.64 (0.48-0.78)	0.66 (0.52-0.84)	0.65 (0.55-0.76)	0.57 (0.49-0.62)	0.59 (0.41-0.64)	0.57 (0.48-0.62)
CCL13	ITIH2	102	63	0.61 (0.5-0.74)	0.7 (0.55-0.85)	0.66 (0.56-0.76)	0.55 (0.51-0.57)	0.6 (0.35-0.66)	0.57 (0.45-0.61)
MASP1	ITIH2	101	63	0.71 (0.58-0.82)	0.68 (0.55-0.85)	0.69 (0.6-0.8)	0.58 (0.31-0.7)	0.57 (0.44-0.62)	0.57 (0.43-0.64)
MASP1	CPN2	101	63	0.71 (0.56-0.82)	0.69 (0.52-0.86)	0.69 (0.59-0.8)	0.6 (0.31-0.71)	0.54 (0.43-0.64)	0.57 (0.42-0.65)
CCL13	CPN2	102	63	0.61 (0.49-0.74)	0.7 (0.52-0.87)	0.65 (0.54-0.76)	0.54 (0.5-0.57)	0.6 (0.34-0.69)	0.57 (0.44-0.62)
DCTN1	SERPING1	101	63	0.67 (0.55-0.8)	0.65 (0.48-0.87)	0.67 (0.55-0.78)	0.58 (0.36-0.65)	0.58 (0.5-0.61)	0.57 (0.45-0.62)
IFNG	ITIH2	102	63	0.71 (0.57-0.85)	0.67 (0.55-0.82)	0.7 (0.59-0.79)	0.54 (0.32-0.68)	0.64 (0.4-0.65)	0.57 (0.43-0.66)
IL17F	C3	102	63	0.68 (0.56-0.79)	0.67 (0.48-0.86)	0.68 (0.56-0.77)	0.6 (0.44-0.67)	0.53 (0.48-0.63)	0.57 (0.49-0.63)
IL7	IFNG	102	63	0.72 (0.57-0.86)	0.72 (0.54-0.87)	0.72 (0.6-0.82)	0.54 (0.35-0.67)	0.63 (0.32-0.69)	0.57 (0.43-0.66)
IL17F	C8B	102	63	0.68 (0.55-0.81)	0.68 (0.5-0.86)	0.68 (0.57-0.8)	0.62 (0.36-0.67)	0.51 (0.48-0.64)	0.57 (0.44-0.63)
C3	CFB	102	67	0.63 (0.52-0.75)	0.7 (0.53-0.87)	0.67 (0.57-0.77)	0.6 (0.42-0.62)	0.55 (0.35-0.66)	0.57 (0.44-0.63)
FC	HGF	77	43	0.73 (0.56-0.87)	0.91 (0.8-1)	0.82 (0.72-0.91)	0.51 (0.39-0.64)	0.65 (0.3-0.83)	0.57 (0.39-0.7)
KLRD1	IL17F	101	63	0.72 (0.57-0.82)	0.66 (0.5-0.82)	0.68 (0.59-0.78)	0.62 (0.31-0.71)	0.51 (0.5-0.58)	0.56 (0.41-0.62)
IL6_PEA_IR	HGF	101	63	0.73 (0.6-0.83)	0.71 (0.49-0.88)	0.72 (0.59-0.82)	0.61 (0.27-0.74)	0.54 (0.33-0.7)	0.56 (0.39-0.67)
MASP1	HGF	101	63	0.72 (0.62-0.82)	0.68 (0.5-0.88)	0.7 (0.6-0.81)	0.61 (0.3-0.72)	0.54 (0.45-0.59)	0.56 (0.41-0.63)
IL13	CFB	102	63	0.65 (0.54-0.76)	0.7 (0.52-0.85)	0.67 (0.57-0.77)	0.58 (0.42-0.65)	0.54 (0.34-0.59)	0.56 (0.45-0.6)
IL7	ORM1	102	63	0.65 (0.5-0.78)	0.73 (0.57-0.86)	0.69 (0.57-0.78)	0.54 (0.42-0.59)	0.61 (0.3-0.7)	0.56 (0.41-0.63)
IL17F	ITIH3	102	63	0.68 (0.56-0.82)	0.66 (0.51-0.8)	0.67 (0.58-0.77)	0.61 (0.35-0.67)	0.51 (0.49-0.59)	0.56 (0.43-0.61)
C3	VTN	102	67	0.64 (0.52-0.76)	0.77 (0.63-0.89)	0.7 (0.62-0.79)	0.55 (0.45-0.62)	0.58 (0.28-0.75)	0.56 (0.41-0.66)
SERPING1	PZP	101	67	0.68 (0.55-0.79)	0.67 (0.45-0.85)	0.67 (0.55-0.79)	0.52 (0.38-0.67)	0.58 (0.47-0.7)	0.56 (0.47-0.67)
LAMP3	IL17F	101	63	0.72 (0.58-0.84)	0.66 (0.5-0.81)	0.69 (0.58-0.79)	0.61 (0.3-0.7)	0.51 (0.48-0.61)	0.56 (0.4-0.63)
IFNG	VTN	102	63	0.71 (0.57-0.84)	0.79 (0.66-0.91)	0.75 (0.66-0.83)	0.54 (0.41-0.64)	0.59 (0.34-0.77)	0.56 (0.41-0.68)
FCRL6	IL13	101	63	0.65 (0.56-0.76)	0.71 (0.55-0.84)	0.67 (0.58-0.76)	0.57 (0.44-0.65)	0.56 (0.34-0.59)	0.56 (0.45-0.6)
MASP1	IL13	101	63	0.73 (0.62-0.82)	0.66 (0.49-0.9)	0.7 (0.58-0.81)	0.63 (0.27-0.72)	0.5 (0.46-0.52)	0.56 (0.37-0.61)
IL13	IFNG	102	63	0.75 (0.6-0.87)	0.62 (0.4-0.82)	0.68 (0.56-0.8)	0.59 (0.25-0.75)	0.52 (0.5-0.55)	0.56 (0.38-0.64)
C3	SERPING1	102	67	0.64 (0.51-0.76)	0.67 (0.49-0.89)	0.66 (0.55-0.77)	0.59 (0.39-0.62)	0.53 (0.42-0.64)	0.56 (0.45-0.63)
IL13	C2	102	63	0.65 (0.52-0.78)	0.69 (0.49-0.89)	0.67 (0.55-0.78)	0.58 (0.46-0.65)	0.53 (0.36-0.58)	0.56 (0.47-0.6)
IL13	ITIH1	102	63	0.64 (0.54-0.76)	0.7 (0.52-0.88)	0.67 (0.57-0.78)	0.56 (0.37-0.63)	0.55 (0.34-0.59)	0.56 (0.45-0.59)

C9	C2	102	67	0.62 (0.5-0.78)	0.68 (0.54-0.85)	0.65 (0.55-0.77)	0.55 (0.43-0.61)	0.61 (0.39-0.64)	0.56 (0.47-0.62)
NCR1	SERPING1	101	63	0.64 (0.52-0.77)	0.67 (0.52-0.85)	0.66 (0.55-0.78)	0.57 (0.38-0.63)	0.55 (0.41-0.64)	0.56 (0.45-0.62)
C5	VTN	102	67	0.73 (0.62-0.83)	0.76 (0.63-0.86)	0.74 (0.66-0.82)	0.54 (0.41-0.63)	0.58 (0.34-0.7)	0.56 (0.43-0.63)
IL17F	C2	102	63	0.66 (0.53-0.78)	0.69 (0.51-0.87)	0.68 (0.56-0.77)	0.59 (0.44-0.66)	0.52 (0.43-0.62)	0.56 (0.48-0.62)
ITIH1	SERPING1	102	67	0.63 (0.52-0.76)	0.7 (0.55-0.83)	0.67 (0.57-0.75)	0.54 (0.44-0.6)	0.59 (0.33-0.67)	0.55 (0.43-0.63)
IL17F	VTN	102	63	0.66 (0.53-0.77)	0.79 (0.64-0.9)	0.72 (0.63-0.8)	0.53 (0.46-0.62)	0.56 (0.31-0.69)	0.55 (0.43-0.63)
IL7	IL13	102	63	0.63 (0.55-0.74)	0.71 (0.54-0.88)	0.67 (0.57-0.77)	0.54 (0.48-0.62)	0.57 (0.31-0.63)	0.55 (0.42-0.61)
IL13	C9	102	63	0.64 (0.52-0.79)	0.64 (0.46-0.82)	0.64 (0.54-0.76)	0.58 (0.36-0.64)	0.56 (0.41-0.57)	0.55 (0.43-0.6)
ORM1	CFB	102	67	0.63 (0.49-0.78)	0.67 (0.52-0.84)	0.65 (0.55-0.76)	0.57 (0.46-0.63)	0.55 (0.43-0.65)	0.55 (0.47-0.63)
FC	SAA1	77	44	0.71 (0.54-0.87)	0.66 (0.39-0.89)	0.68 (0.52-0.82)	0.45 (0.28-0.71)	0.67 (0.63-0.68)	0.55 (0.47-0.69)
C2	SERPING1	102	67	0.63 (0.5-0.76)	0.68 (0.5-0.86)	0.66 (0.55-0.77)	0.58 (0.44-0.61)	0.51 (0.34-0.67)	0.55 (0.46-0.63)
HGF	ORM1	102	63	0.66 (0.52-0.78)	0.72 (0.54-0.89)	0.68 (0.57-0.8)	0.53 (0.41-0.67)	0.56 (0.34-0.71)	0.55 (0.41-0.66)
IL17F	SAA1	102	63	0.67 (0.52-0.8)	0.64 (0.47-0.84)	0.65 (0.54-0.77)	0.58 (0.33-0.68)	0.52 (0.45-0.54)	0.55 (0.42-0.6)
CCL13	ORM1	102	63	0.62 (0.51-0.76)	0.66 (0.52-0.83)	0.65 (0.54-0.76)	0.55 (0.41-0.6)	0.58 (0.39-0.63)	0.55 (0.44-0.6)
SERPING1	VTN	102	67	0.61 (0.51-0.75)	0.77 (0.62-0.89)	0.69 (0.6-0.78)	0.54 (0.46-0.57)	0.56 (0.24-0.77)	0.55 (0.39-0.66)
IL17F	CLU	102	63	0.65 (0.53-0.76)	0.7 (0.53-0.86)	0.67 (0.57-0.78)	0.57 (0.41-0.63)	0.52 (0.44-0.63)	0.55 (0.46-0.61)
FC	IL13	77	43	0.73 (0.58-0.87)	0.65 (0.42-0.91)	0.69 (0.55-0.83)	0.61 (0.26-0.74)	0.57 (0.43-0.59)	0.55 (0.37-0.66)
MASP1	VTN	101	63	0.71 (0.58-0.82)	0.78 (0.63-0.89)	0.74 (0.64-0.82)	0.53 (0.4-0.69)	0.56 (0.33-0.74)	0.55 (0.42-0.66)
IL13	ITIH2	102	63	0.63 (0.54-0.77)	0.68 (0.53-0.84)	0.66 (0.56-0.77)	0.55 (0.38-0.62)	0.54 (0.33-0.58)	0.55 (0.44-0.59)
MASP1	CCL13	101	63	0.7 (0.57-0.81)	0.67 (0.49-0.86)	0.68 (0.57-0.8)	0.56 (0.3-0.7)	0.52 (0.49-0.61)	0.55 (0.41-0.63)
CPN2	SERPING1	102	67	0.62 (0.51-0.75)	0.68 (0.51-0.84)	0.65 (0.55-0.76)	0.56 (0.43-0.59)	0.54 (0.34-0.66)	0.55 (0.44-0.62)
IL17F	CPN2	102	63	0.65 (0.53-0.77)	0.74 (0.59-0.89)	0.7 (0.61-0.79)	0.53 (0.4-0.62)	0.56 (0.33-0.67)	0.54 (0.42-0.62)
CFB	SERPING1	102	67	0.62 (0.5-0.75)	0.7 (0.53-0.88)	0.67 (0.56-0.77)	0.55 (0.45-0.62)	0.52 (0.35-0.7)	0.54 (0.43-0.64)
FCRL6	IL17F	101	63	0.66 (0.52-0.78)	0.69 (0.55-0.83)	0.67 (0.58-0.78)	0.56 (0.37-0.64)	0.54 (0.4-0.57)	0.54 (0.45-0.59)
IL17F	ITIH1	102	63	0.66 (0.54-0.78)	0.7 (0.53-0.87)	0.68 (0.58-0.78)	0.55 (0.4-0.64)	0.52 (0.4-0.61)	0.54 (0.45-0.61)
IL13	CCL4	102	63	0.71 (0.53-0.81)	0.63 (0.45-0.81)	0.67 (0.54-0.78)	0.6 (0.29-0.7)	0.49 (0.44-0.54)	0.54 (0.38-0.61)
IL6_PEA_cytokin	SERPING1	102	63	0.69 (0.56-0.79)	0.64 (0.46-0.88)	0.67 (0.56-0.79)	0.47 (0.33-0.74)	0.58 (0.45-0.65)	0.54 (0.43-0.67)
NCR1	IL13	101	63	0.67 (0.57-0.78)	0.64 (0.47-0.8)	0.65 (0.54-0.76)	0.58 (0.32-0.66)	0.5 (0.4-0.56)	0.54 (0.41-0.58)
CCL13	IL15	102	63	0.61 (0.47-0.76)	0.65 (0.51-0.81)	0.63 (0.54-0.74)	0.53 (0.5-0.57)	0.54 (0.38-0.63)	0.54 (0.46-0.59)
ORM1	SERPING1	102	67	0.62 (0.5-0.76)	0.62 (0.47-0.81)	0.62 (0.53-0.74)	0.55 (0.39-0.62)	0.55 (0.44-0.6)	0.54 (0.45-0.6)

DCTN1	IL17F	101	63	0.7 (0.57-0.81)	0.66 (0.48-0.86)	0.68 (0.57-0.79)	0.58 (0.31-0.69)	0.49 (0.48-0.58)	0.54 (0.4-0.6)
DCTN1	IL13	101	63	0.68 (0.57-0.79)	0.65 (0.45-0.82)	0.67 (0.55-0.76)	0.58 (0.32-0.67)	0.5 (0.48-0.54)	0.54 (0.4-0.59)
CLU	SERPING1	102	67	0.62 (0.5-0.75)	0.75 (0.58-0.89)	0.68 (0.59-0.78)	0.56 (0.45-0.6)	0.53 (0.28-0.74)	0.54 (0.41-0.66)
MASP1	IL17F	101	63	0.71 (0.57-0.83)	0.66 (0.48-0.86)	0.68 (0.58-0.79)	0.59 (0.3-0.7)	0.48 (0.46-0.51)	0.54 (0.39-0.6)
IL17F	PZP	101	63	0.68 (0.54-0.8)	0.73 (0.53-0.89)	0.7 (0.58-0.8)	0.53 (0.33-0.68)	0.54 (0.39-0.64)	0.54 (0.43-0.63)
IL17F	ITIH2	102	63	0.65 (0.54-0.78)	0.67 (0.5-0.83)	0.66 (0.56-0.77)	0.55 (0.39-0.62)	0.52 (0.39-0.59)	0.54 (0.45-0.6)
IL7	SERPING1	102	63	0.64 (0.52-0.76)	0.72 (0.53-0.89)	0.68 (0.57-0.78)	0.51 (0.43-0.61)	0.55 (0.31-0.7)	0.53 (0.4-0.64)
NCR1	IL17F	101	63	0.67 (0.53-0.79)	0.65 (0.5-0.82)	0.66 (0.55-0.77)	0.57 (0.36-0.65)	0.48 (0.45-0.59)	0.53 (0.42-0.58)
ITIH2	SERPING1	102	67	0.63 (0.51-0.75)	0.65 (0.5-0.82)	0.64 (0.54-0.74)	0.53 (0.43-0.58)	0.52 (0.36-0.65)	0.53 (0.43-0.6)
IL6_PEA_cytokin	IL13	102	63	0.72 (0.52-0.84)	0.63 (0.39-0.84)	0.67 (0.52-0.8)	0.5 (0.24-0.76)	0.56 (0.38-0.61)	0.53 (0.37-0.66)
CCL4	SERPING1	102	63	0.67 (0.53-0.8)	0.65 (0.5-0.85)	0.67 (0.57-0.77)	0.51 (0.35-0.67)	0.56 (0.42-0.62)	0.53 (0.43-0.62)
MASP1	SERPING1	101	63	0.71 (0.58-0.81)	0.64 (0.49-0.86)	0.67 (0.58-0.8)	0.52 (0.3-0.7)	0.53 (0.49-0.55)	0.53 (0.42-0.62)
IL17F	C9	102	63	0.7 (0.58-0.82)	0.62 (0.47-0.81)	0.66 (0.56-0.78)	0.54 (0.3-0.71)	0.5 (0.49-0.6)	0.53 (0.4-0.61)
IL17F	IL7	102	63	0.66 (0.55-0.77)	0.71 (0.51-0.87)	0.69 (0.57-0.79)	0.53 (0.41-0.62)	0.52 (0.38-0.68)	0.53 (0.45-0.61)
IL13	CCL13	102	63	0.63 (0.52-0.74)	0.71 (0.52-0.85)	0.67 (0.56-0.76)	0.5 (0.41-0.6)	0.61 (0.26-0.62)	0.53 (0.35-0.59)
IL17F	CCL4	102	63	0.68 (0.53-0.83)	0.64 (0.48-0.84)	0.66 (0.56-0.78)	0.56 (0.32-0.68)	0.49 (0.46-0.51)	0.53 (0.4-0.59)
HGF	SERPING1	102	63	0.64 (0.5-0.75)	0.66 (0.49-0.88)	0.65 (0.55-0.77)	0.47 (0.42-0.63)	0.51 (0.35-0.7)	0.52 (0.43-0.64)
HGF	CCL4	102	63	0.63 (0.5-0.76)	0.72 (0.53-0.89)	0.68 (0.56-0.79)	0.54 (0.36-0.66)	0.48 (0.32-0.7)	0.52 (0.38-0.67)
HGF	IL13	102	63	0.65 (0.54-0.76)	0.73 (0.51-0.9)	0.69 (0.57-0.79)	0.5 (0.39-0.66)	0.54 (0.3-0.59)	0.52 (0.37-0.6)
IL15	SERPING1	102	63	0.64 (0.5-0.78)	0.63 (0.5-0.83)	0.63 (0.53-0.75)	0.52 (0.42-0.61)	0.51 (0.43-0.58)	0.52 (0.44-0.58)
IL6_PEA_cytokin	IL17F	102	63	0.64 (0.52-0.76)	0.62 (0.44-0.84)	0.63 (0.52-0.75)	0.51 (0.3-0.72)	0.52 (0.45-0.54)	0.51 (0.41-0.62)
C9	CFB	102	67	0.61 (0.47-0.77)	0.66 (0.53-0.85)	0.64 (0.54-0.76)	0.52 (0.42-0.62)	0.48 (0.42-0.66)	0.51 (0.43-0.62)
HGF	IL17F	102	63	0.64 (0.51-0.75)	0.73 (0.5-0.91)	0.68 (0.56-0.79)	0.49 (0.42-0.59)	0.55 (0.36-0.59)	0.51 (0.42-0.57)
IL6_PEA_cytokin	HGF	102	63	0.63 (0.49-0.77)	0.72 (0.5-0.9)	0.68 (0.53-0.79)	0.52 (0.39-0.72)	0.47 (0.27-0.73)	0.51 (0.37-0.7)
IL13	IL15	102	63	0.64 (0.5-0.77)	0.59 (0.43-0.75)	0.61 (0.5-0.72)	0.54 (0.41-0.61)	0.47 (0.41-0.53)	0.51 (0.44-0.55)
IL13	ORM1	102	63	0.66 (0.55-0.8)	0.62 (0.45-0.78)	0.64 (0.54-0.75)	0.55 (0.33-0.65)	0.46 (0.44-0.5)	0.51 (0.4-0.56)
FC	IL7	77	43	0.71 (0.56-0.85)	0.72 (0.48-0.92)	0.71 (0.57-0.84)	0.5 (0.31-0.69)	0.53 (0.35-0.69)	0.51 (0.35-0.67)
IL17F	IFNG	102	63	0.79 (0.66-0.9)	0.62 (0.45-0.8)	0.7 (0.6-0.82)	0.53 (0.21-0.79)	0.48 (0.46-0.58)	0.51 (0.34-0.64)
CCL13	SERPING1	102	63	0.61 (0.49-0.75)	0.66 (0.51-0.86)	0.64 (0.53-0.76)	0.51 (0.42-0.59)	0.51 (0.39-0.61)	0.51 (0.43-0.58)
IL17F	IL15	102	63	0.65 (0.51-0.79)	0.65 (0.5-0.84)	0.65 (0.55-0.76)	0.49 (0.43-0.64)	0.53 (0.36-0.55)	0.5 (0.41-0.59)

IL17F	ORM1	102	63	0.67 (0.54-0.8)	0.62 (0.47-0.8)	0.64 (0.54-0.76)	0.53 (0.34-0.66)	0.46 (0.44-0.52)	0.5 (0.4-0.57)
HGF	IFNG	102	63	0.71 (0.56-0.86)	0.69 (0.51-0.87)	0.7 (0.57-0.82)	0.37 (0.35-0.7)	0.55 (0.4-0.71)	0.49 (0.38-0.66)
FC	IFNG	77	43	0.72 (0.53-0.89)	0.64 (0.43-0.86)	0.68 (0.54-0.82)	0.47 (0.27-0.73)	0.54 (0.5-0.63)	0.49 (0.39-0.65)
FC	IL17F	77	43	0.78 (0.63-0.9)	0.68 (0.44-0.92)	0.73 (0.59-0.87)	0.52 (0.21-0.79)	0.44 (0.43-0.57)	0.49 (0.32-0.66)
MASP1	PZP	100	63	0.71 (0.56-0.82)	0.68 (0.5-0.83)	0.69 (0.58-0.79)	0.44 (0.33-0.71)	0.53 (0.43-0.67)	0.49 (0.42-0.64)
IL17F	CCL13	102	63	0.63 (0.5-0.75)	0.69 (0.5-0.86)	0.66 (0.55-0.77)	0.51 (0.41-0.58)	0.51 (0.33-0.57)	0.49 (0.39-0.56)
IL17F	SERPING1	102	63	0.65 (0.52-0.77)	0.65 (0.46-0.88)	0.65 (0.53-0.77)	0.44 (0.37-0.62)	0.41 (0.37-0.56)	0.45 (0.37-0.54)
IL17F	IL13	102	63	0.64 (0.53-0.76)	0.62 (0.44-0.83)	0.63 (0.52-0.74)	0.38 (0.34-0.64)	0.44 (0.42-0.51)	0.42 (0.38-0.54)
IL13	SERPING1	102	63	0.64 (0.53-0.76)	0.66 (0.49-0.87)	0.65 (0.55-0.77)	0.43 (0.36-0.59)	0.38 (0.33-0.55)	0.41 (0.35-0.55)

Supplementary Table 6. Biomarker pairs to predict mid/long-term relapse

Gene name 1	Gene name 2	STORI (n=)	SPARE (n=)	c-statistic (CI) development dataset (STORI)	c-statistic (CI) development dataset (SPARE)	Mean c-statistic (CI) development datasets (STORI and SPARE)	c-statistic (CI) validation dataset (STORI)	c-statistic (CI) validation dataset (SPARE)	Mean c-statistic (CI) validation datasets (STORI and SPARE)
FLT3LG	TNF	73	53	0.69 (0.58-0.78)	0.72 (0.58-0.83)	0.7 (0.61-0.78)	0.67 (0.62-0.68)	0.69 (0.65-0.71)	0.68 (0.65-0.69)
SIT1	FLT3LG	73	53	0.69 (0.59-0.78)	0.7 (0.55-0.83)	0.69 (0.6-0.78)	0.67 (0.52-0.68)	0.67 (0.64-0.69)	0.67 (0.6-0.68)
FLT3LG	SERPINA4	73	53	0.69 (0.58-0.79)	0.69 (0.53-0.83)	0.68 (0.59-0.78)	0.68 (0.47-0.69)	0.67 (0.62-0.68)	0.67 (0.57-0.69)
CXCL9	FLT3LG	73	53	0.69 (0.6-0.79)	0.69 (0.52-0.82)	0.69 (0.6-0.77)	0.67 (0.44-0.7)	0.67 (0.65-0.69)	0.67 (0.55-0.69)
FLT3LG	IFNG	73	53	0.74 (0.65-0.84)	0.69 (0.53-0.82)	0.71 (0.62-0.79)	0.68 (0.44-0.74)	0.66 (0.63-0.67)	0.67 (0.55-0.7)
FLT3LG	IL17C	73	53	0.67 (0.57-0.77)	0.67 (0.51-0.81)	0.67 (0.58-0.76)	0.66 (0.39-0.66)	0.67 (0.61-0.68)	0.66 (0.53-0.67)
FGF2	FLT3LG	73	53	0.68 (0.57-0.77)	0.78 (0.64-0.88)	0.72 (0.64-0.8)	0.61 (0.57-0.67)	0.71 (0.56-0.76)	0.66 (0.58-0.71)
FLT3LG	C8A	73	53	0.67 (0.57-0.76)	0.7 (0.56-0.83)	0.68 (0.6-0.77)	0.66 (0.47-0.67)	0.66 (0.57-0.69)	0.66 (0.55-0.67)
FGF2	ORM1	73	53	0.61 (0.52-0.71)	0.76 (0.63-0.87)	0.69 (0.6-0.76)	0.59 (0.56-0.6)	0.73 (0.4-0.75)	0.66 (0.49-0.67)
IL10_PEA_IR	FLT3LG	73	53	0.68 (0.57-0.77)	0.69 (0.58-0.82)	0.69 (0.61-0.77)	0.66 (0.58-0.68)	0.66 (0.61-0.68)	0.66 (0.61-0.68)
FLT3LG	ORM1	73	53	0.67 (0.56-0.76)	0.71 (0.57-0.84)	0.69 (0.6-0.77)	0.66 (0.55-0.66)	0.67 (0.55-0.69)	0.66 (0.59-0.68)
SIT1	SERPINA4	73	53	0.69 (0.6-0.79)	0.68 (0.53-0.81)	0.68 (0.6-0.77)	0.67 (0.44-0.69)	0.65 (0.62-0.66)	0.66 (0.54-0.67)
FLT3LG	VEGFA	73	53	0.67 (0.56-0.77)	0.69 (0.55-0.82)	0.68 (0.59-0.77)	0.66 (0.54-0.67)	0.66 (0.57-0.68)	0.66 (0.59-0.68)
FLT3LG	APOA1	73	53	0.66 (0.56-0.77)	0.69 (0.53-0.82)	0.67 (0.59-0.75)	0.65 (0.52-0.67)	0.66 (0.6-0.67)	0.65 (0.57-0.67)
FGF2	ITGA6	74	53	0.59 (0.51-0.68)	0.76 (0.6-0.88)	0.67 (0.59-0.75)	0.57 (0.55-0.57)	0.74 (0.31-0.76)	0.65 (0.44-0.67)
FLT3LG	IL15	73	53	0.67 (0.55-0.77)	0.67 (0.51-0.81)	0.67 (0.58-0.76)	0.66 (0.45-0.67)	0.65 (0.59-0.66)	0.65 (0.54-0.66)
FLT3LG	C4BPB	73	53	0.67 (0.56-0.77)	0.7 (0.57-0.82)	0.68 (0.61-0.76)	0.65 (0.56-0.66)	0.66 (0.54-0.68)	0.65 (0.58-0.67)
SH2D1A	FLT3LG	73	53	0.67 (0.56-0.77)	0.69 (0.55-0.81)	0.68 (0.6-0.76)	0.64 (0.57-0.67)	0.66 (0.6-0.67)	0.65 (0.6-0.67)
FGF2	HSD11B1	74	53	0.59 (0.51-0.68)	0.77 (0.64-0.87)	0.68 (0.6-0.75)	0.57 (0.56-0.58)	0.73 (0.33-0.76)	0.65 (0.45-0.67)
SIT1	TNF	73	53	0.67 (0.57-0.78)	0.67 (0.54-0.79)	0.67 (0.6-0.75)	0.66 (0.5-0.67)	0.65 (0.57-0.66)	0.65 (0.57-0.66)
FLT3LG	CLU	73	53	0.67 (0.57-0.77)	0.68 (0.54-0.81)	0.67 (0.59-0.75)	0.65 (0.5-0.67)	0.66 (0.57-0.67)	0.65 (0.57-0.67)
FGF2	SIT1	74	53	0.68 (0.58-0.77)	0.76 (0.59-0.87)	0.71 (0.63-0.8)	0.6 (0.57-0.66)	0.7 (0.64-0.72)	0.65 (0.61-0.68)
FGF2	SERPINA4	73	53	0.63 (0.53-0.72)	0.77 (0.64-0.88)	0.7 (0.62-0.79)	0.61 (0.57-0.63)	0.69 (0.54-0.75)	0.65 (0.57-0.69)
FLT3LG	CFB	73	53	0.66 (0.55-0.76)	0.69 (0.55-0.82)	0.67 (0.59-0.76)	0.64 (0.5-0.67)	0.66 (0.61-0.68)	0.65 (0.57-0.67)
FGF2	TNF	73	53	0.64 (0.54-0.73)	0.75 (0.62-0.86)	0.69 (0.61-0.77)	0.6 (0.57-0.62)	0.69 (0.61-0.74)	0.64 (0.6-0.67)

FGF2	CLU	73	53	0.6 (0.51-0.71)	0.76 (0.63-0.87)	0.68 (0.6-0.76)	0.59 (0.57-0.59)	0.7 (0.46-0.75)	0.64 (0.52-0.67)
SIT1	CXCL9	73	53	0.69 (0.59-0.78)	0.66 (0.48-0.8)	0.67 (0.58-0.76)	0.64 (0.36-0.7)	0.65 (0.6-0.67)	0.64 (0.5-0.68)
TNF	SERPINA4	73	53	0.65 (0.55-0.73)	0.69 (0.56-0.81)	0.67 (0.58-0.75)	0.62 (0.5-0.65)	0.67 (0.57-0.68)	0.64 (0.57-0.66)
FGF2	VEGFA	73	53	0.6 (0.5-0.69)	0.74 (0.6-0.85)	0.67 (0.58-0.74)	0.59 (0.56-0.6)	0.69 (0.43-0.73)	0.64 (0.51-0.66)
IL10_PEA_IR	SIT1	74	53	0.69 (0.59-0.78)	0.66 (0.52-0.79)	0.68 (0.59-0.75)	0.66 (0.48-0.68)	0.62 (0.6-0.63)	0.64 (0.55-0.66)
FLT3LG	MBL2	73	53	0.66 (0.56-0.76)	0.7 (0.57-0.82)	0.68 (0.59-0.75)	0.63 (0.55-0.66)	0.65 (0.57-0.67)	0.64 (0.58-0.66)
FGF2	CFB	73	53	0.61 (0.52-0.71)	0.74 (0.59-0.85)	0.67 (0.58-0.74)	0.58 (0.56-0.59)	0.69 (0.48-0.73)	0.64 (0.53-0.66)
FGF2	CXCL9	73	53	0.64 (0.54-0.73)	0.73 (0.58-0.85)	0.69 (0.6-0.77)	0.57 (0.54-0.62)	0.7 (0.61-0.72)	0.64 (0.6-0.67)
ITGA6	FLT3LG	73	53	0.66 (0.56-0.76)	0.71 (0.55-0.82)	0.68 (0.6-0.77)	0.61 (0.51-0.66)	0.68 (0.52-0.7)	0.63 (0.55-0.68)
FGF2	APOA1	73	53	0.61 (0.51-0.7)	0.75 (0.6-0.88)	0.68 (0.6-0.76)	0.59 (0.57-0.6)	0.68 (0.51-0.75)	0.63 (0.54-0.67)
SIT1	C8A	73	53	0.66 (0.56-0.76)	0.66 (0.53-0.79)	0.66 (0.58-0.75)	0.65 (0.4-0.67)	0.63 (0.58-0.66)	0.63 (0.52-0.66)
SIT1	IFNG	73	53	0.71 (0.62-0.8)	0.65 (0.49-0.79)	0.68 (0.6-0.76)	0.65 (0.32-0.72)	0.62 (0.61-0.63)	0.63 (0.47-0.67)
IL10_PEA_IR	ORM1	73	53	0.66 (0.55-0.75)	0.66 (0.53-0.83)	0.66 (0.57-0.75)	0.64 (0.4-0.66)	0.63 (0.57-0.64)	0.63 (0.51-0.65)
CDSN	SIT1	74	53	0.69 (0.61-0.78)	0.66 (0.53-0.77)	0.68 (0.59-0.75)	0.67 (0.47-0.69)	0.62 (0.56-0.65)	0.63 (0.54-0.66)
FGF2	MBL2	73	53	0.6 (0.5-0.7)	0.77 (0.66-0.89)	0.68 (0.6-0.76)	0.58 (0.57-0.59)	0.68 (0.43-0.75)	0.63 (0.5-0.67)
HSD11B1	FLT3LG	73	53	0.66 (0.55-0.76)	0.71 (0.55-0.84)	0.68 (0.59-0.77)	0.61 (0.47-0.66)	0.65 (0.53-0.7)	0.63 (0.54-0.68)
FGF2	C8A	73	53	0.62 (0.53-0.71)	0.74 (0.6-0.85)	0.68 (0.6-0.75)	0.58 (0.53-0.6)	0.69 (0.5-0.72)	0.63 (0.53-0.66)
SERPINA4	C4BPB	73	56	0.64 (0.55-0.74)	0.68 (0.54-0.82)	0.66 (0.58-0.75)	0.62 (0.48-0.63)	0.64 (0.57-0.66)	0.63 (0.55-0.64)
PLXNA4	FLT3LG	73	53	0.66 (0.55-0.76)	0.72 (0.58-0.84)	0.69 (0.6-0.77)	0.62 (0.48-0.66)	0.64 (0.53-0.7)	0.63 (0.54-0.68)
IL10_PEA_IR	SERPINA4	73	53	0.68 (0.57-0.78)	0.66 (0.52-0.81)	0.67 (0.58-0.75)	0.65 (0.46-0.67)	0.61 (0.59-0.64)	0.63 (0.53-0.65)
SIT1	IL15	73	53	0.65 (0.55-0.75)	0.66 (0.51-0.78)	0.66 (0.57-0.74)	0.64 (0.45-0.65)	0.62 (0.56-0.65)	0.63 (0.53-0.64)
IL10_PEA_IR	CXCL9	73	53	0.67 (0.58-0.76)	0.63 (0.42-0.83)	0.65 (0.54-0.76)	0.61 (0.33-0.68)	0.65 (0.6-0.66)	0.63 (0.49-0.66)
SIT1	VEGFA	73	53	0.65 (0.55-0.75)	0.66 (0.53-0.79)	0.66 (0.58-0.74)	0.62 (0.47-0.65)	0.63 (0.59-0.65)	0.63 (0.55-0.65)
SIT1	APOA1	73	53	0.65 (0.56-0.75)	0.66 (0.52-0.78)	0.65 (0.57-0.73)	0.63 (0.44-0.65)	0.62 (0.61-0.63)	0.63 (0.54-0.64)
TNF	VEGFA	73	53	0.64 (0.53-0.75)	0.67 (0.54-0.79)	0.66 (0.57-0.74)	0.62 (0.47-0.64)	0.65 (0.52-0.66)	0.63 (0.54-0.65)
SIT1	CLU	73	53	0.65 (0.55-0.74)	0.66 (0.51-0.78)	0.65 (0.57-0.73)	0.63 (0.44-0.65)	0.62 (0.61-0.63)	0.63 (0.53-0.64)
FGF2	C4BPB	73	53	0.61 (0.52-0.7)	0.74 (0.59-0.85)	0.67 (0.58-0.75)	0.58 (0.53-0.6)	0.68 (0.45-0.73)	0.63 (0.51-0.66)
CDSN	FLT3LG	73	53	0.71 (0.61-0.79)	0.67 (0.54-0.8)	0.69 (0.61-0.77)	0.63 (0.48-0.7)	0.61 (0.58-0.65)	0.63 (0.54-0.67)
FGF2	SH2D1A	74	53	0.63 (0.54-0.72)	0.73 (0.55-0.85)	0.68 (0.58-0.75)	0.59 (0.56-0.61)	0.66 (0.56-0.72)	0.63 (0.57-0.66)
SERPINA4	C8A	73	56	0.66 (0.56-0.75)	0.65 (0.51-0.81)	0.66 (0.57-0.74)	0.63 (0.35-0.66)	0.62 (0.56-0.64)	0.62 (0.49-0.65)

ORM1	SERPINA4	73	56	0.63 (0.53-0.73)	0.68 (0.55-0.82)	0.66 (0.57-0.74)	0.63 (0.46-0.66)	0.63 (0.5-0.66)	0.62 (0.52-0.66)
SIT1	CFB	73	53	0.65 (0.55-0.75)	0.68 (0.55-0.81)	0.67 (0.58-0.75)	0.63 (0.49-0.65)	0.62 (0.55-0.67)	0.62 (0.55-0.66)
SIT1	C4BPB	73	53	0.65 (0.55-0.75)	0.67 (0.54-0.79)	0.66 (0.57-0.74)	0.63 (0.47-0.65)	0.62 (0.53-0.65)	0.62 (0.54-0.65)
SIT1	ORM1	73	53	0.64 (0.53-0.74)	0.72 (0.58-0.83)	0.68 (0.6-0.76)	0.64 (0.54-0.65)	0.61 (0.51-0.69)	0.62 (0.56-0.67)
PLXNA4	SIT1	74	53	0.65 (0.55-0.74)	0.69 (0.53-0.8)	0.67 (0.58-0.74)	0.61 (0.46-0.65)	0.64 (0.58-0.66)	0.62 (0.54-0.65)
SH2D1A	SIT1	74	53	0.66 (0.57-0.75)	0.66 (0.52-0.79)	0.66 (0.57-0.74)	0.63 (0.49-0.65)	0.62 (0.57-0.64)	0.62 (0.55-0.64)
SIT1	MBL2	73	53	0.66 (0.57-0.75)	0.66 (0.53-0.8)	0.66 (0.58-0.74)	0.63 (0.43-0.65)	0.61 (0.57-0.63)	0.62 (0.52-0.64)
FGF2	PLXNA4	74	53	0.6 (0.51-0.69)	0.74 (0.6-0.85)	0.67 (0.59-0.74)	0.58 (0.55-0.58)	0.66 (0.36-0.73)	0.62 (0.47-0.65)
HSD11B1	SIT1	74	53	0.65 (0.56-0.75)	0.68 (0.55-0.81)	0.67 (0.59-0.75)	0.61 (0.45-0.65)	0.63 (0.55-0.67)	0.62 (0.53-0.65)
SH2D1A	SERPINA4	73	53	0.65 (0.55-0.73)	0.66 (0.54-0.79)	0.65 (0.58-0.73)	0.62 (0.47-0.64)	0.62 (0.56-0.63)	0.62 (0.53-0.64)
SIT1	IL17C	73	53	0.67 (0.58-0.75)	0.64 (0.5-0.78)	0.66 (0.57-0.73)	0.63 (0.35-0.66)	0.61 (0.58-0.62)	0.62 (0.48-0.64)
IL10_PEA_IR	C8A	73	53	0.66 (0.55-0.75)	0.64 (0.48-0.81)	0.64 (0.56-0.74)	0.62 (0.36-0.65)	0.63 (0.58-0.64)	0.62 (0.49-0.64)
CXCL9	TNF	73	53	0.65 (0.54-0.76)	0.64 (0.47-0.79)	0.65 (0.54-0.75)	0.59 (0.36-0.65)	0.65 (0.54-0.67)	0.62 (0.5-0.65)
IL10_PEA_IR	TNF	73	53	0.67 (0.57-0.76)	0.64 (0.52-0.78)	0.65 (0.58-0.74)	0.64 (0.44-0.66)	0.6 (0.58-0.62)	0.62 (0.52-0.64)
TNF	ORM1	73	53	0.63 (0.5-0.73)	0.68 (0.54-0.81)	0.65 (0.56-0.73)	0.61 (0.52-0.61)	0.63 (0.41-0.66)	0.62 (0.5-0.63)
FGF2	IL10_PEA_IR	74	53	0.63 (0.53-0.74)	0.75 (0.6-0.88)	0.69 (0.6-0.77)	0.58 (0.52-0.6)	0.65 (0.48-0.73)	0.61 (0.53-0.66)
IL10_PEA_IR	SH2D1A	74	53	0.66 (0.55-0.76)	0.63 (0.5-0.78)	0.64 (0.56-0.74)	0.64 (0.46-0.65)	0.61 (0.57-0.63)	0.61 (0.53-0.64)
TNF	C4BPB	73	53	0.64 (0.52-0.74)	0.65 (0.53-0.79)	0.64 (0.56-0.73)	0.61 (0.41-0.63)	0.62 (0.47-0.63)	0.61 (0.5-0.63)
CXCL9	SERPINA4	73	53	0.64 (0.54-0.73)	0.64 (0.47-0.8)	0.64 (0.54-0.72)	0.6 (0.38-0.64)	0.62 (0.59-0.65)	0.61 (0.5-0.63)
TNF	IL15	73	53	0.62 (0.48-0.73)	0.66 (0.53-0.78)	0.64 (0.55-0.72)	0.61 (0.55-0.62)	0.61 (0.4-0.65)	0.61 (0.5-0.63)
SERPINA4	CFB	73	56	0.64 (0.54-0.74)	0.64 (0.51-0.78)	0.64 (0.55-0.73)	0.62 (0.41-0.64)	0.61 (0.58-0.62)	0.61 (0.5-0.62)
TNF	APOA1	73	53	0.63 (0.51-0.74)	0.65 (0.53-0.78)	0.64 (0.55-0.72)	0.61 (0.43-0.63)	0.62 (0.52-0.64)	0.61 (0.52-0.63)
IL10_PEA_IR	IFNG	73	53	0.71 (0.62-0.8)	0.62 (0.44-0.78)	0.66 (0.56-0.76)	0.6 (0.29-0.71)	0.61 (0.6-0.62)	0.61 (0.45-0.66)
FGF2	IL17C	73	53	0.64 (0.53-0.74)	0.75 (0.59-0.85)	0.69 (0.6-0.76)	0.57 (0.54-0.59)	0.65 (0.5-0.71)	0.61 (0.54-0.64)
SH2D1A	TNF	73	53	0.64 (0.54-0.75)	0.64 (0.52-0.77)	0.64 (0.56-0.72)	0.62 (0.48-0.64)	0.61 (0.54-0.62)	0.61 (0.53-0.63)
FGF2	IL15	73	53	0.59 (0.46-0.69)	0.76 (0.63-0.87)	0.68 (0.59-0.74)	0.58 (0.57-0.58)	0.63 (0.43-0.74)	0.61 (0.5-0.66)
IL10_PEA_IR	APOA1	73	53	0.65 (0.54-0.75)	0.64 (0.53-0.78)	0.65 (0.56-0.73)	0.61 (0.42-0.64)	0.6 (0.58-0.63)	0.61 (0.51-0.63)
CEASE_phase1	CEASE_phase1	56	40	NA	NA	NA	0.66	0.56	0.61
IFNG	SERPINA4	73	53	0.66 (0.57-0.75)	0.63 (0.5-0.78)	0.65 (0.57-0.74)	0.61 (0.34-0.66)	0.6 (0.59-0.61)	0.61 (0.47-0.63)
ORM1	APOA1	73	56	0.61 (0.49-0.72)	0.68 (0.55-0.8)	0.64 (0.56-0.72)	0.61 (0.49-0.62)	0.61 (0.44-0.65)	0.61 (0.51-0.63)

VEGFA	SERPINA4	73	53	0.62 (0.53-0.71)	0.66 (0.53-0.79)	0.64 (0.56-0.73)	0.6 (0.44-0.61)	0.61 (0.53-0.63)	0.61 (0.52-0.62)
CDSN	TNF	73	53	0.69 (0.58-0.78)	0.63 (0.52-0.76)	0.66 (0.58-0.74)	0.65 (0.39-0.68)	0.57 (0.52-0.62)	0.61 (0.48-0.64)
IFNG	IL15	73	53	0.7 (0.61-0.8)	0.58 (0.43-0.74)	0.64 (0.55-0.72)	0.62 (0.33-0.69)	0.59 (0.57-0.61)	0.6 (0.47-0.65)
SERPINA4	CLU	73	56	0.62 (0.52-0.72)	0.65 (0.53-0.79)	0.64 (0.56-0.72)	0.6 (0.41-0.61)	0.61 (0.51-0.63)	0.6 (0.51-0.62)
IL10_PEA_IR	CFB	73	53	0.63 (0.53-0.74)	0.65 (0.49-0.82)	0.64 (0.54-0.74)	0.58 (0.4-0.63)	0.63 (0.57-0.64)	0.6 (0.51-0.63)
IL10_PEA_IR	C4BPB	73	53	0.63 (0.53-0.73)	0.64 (0.51-0.8)	0.63 (0.55-0.73)	0.61 (0.39-0.62)	0.61 (0.56-0.62)	0.6 (0.5-0.62)
TNF	CFB	73	53	0.62 (0.52-0.72)	0.66 (0.54-0.79)	0.64 (0.56-0.73)	0.58 (0.45-0.61)	0.62 (0.43-0.65)	0.6 (0.5-0.63)
FGF2	IFNG	73	53	0.67 (0.57-0.77)	0.76 (0.62-0.86)	0.71 (0.63-0.78)	0.56 (0.52-0.59)	0.65 (0.62-0.67)	0.6 (0.58-0.62)
ORM1	CLU	73	56	0.62 (0.48-0.74)	0.66 (0.53-0.79)	0.64 (0.54-0.74)	0.62 (0.46-0.67)	0.59 (0.41-0.63)	0.6 (0.48-0.64)
VEGFA	ORM1	73	53	0.6 (0.46-0.71)	0.67 (0.54-0.82)	0.64 (0.54-0.73)	0.58 (0.51-0.62)	0.63 (0.36-0.65)	0.6 (0.47-0.63)
IL15	SERPINA4	73	53	0.62 (0.52-0.72)	0.65 (0.5-0.8)	0.63 (0.54-0.72)	0.61 (0.42-0.62)	0.59 (0.52-0.64)	0.6 (0.5-0.63)
APOA1	C8A	73	56	0.64 (0.54-0.75)	0.63 (0.51-0.78)	0.63 (0.56-0.72)	0.59 (0.37-0.65)	0.6 (0.56-0.61)	0.6 (0.48-0.63)
IL10_PEA_IR	VEGFA	73	53	0.63 (0.52-0.73)	0.65 (0.49-0.79)	0.64 (0.54-0.72)	0.59 (0.39-0.63)	0.62 (0.5-0.65)	0.6 (0.49-0.63)
SERPINA4	APOA1	73	56	0.62 (0.51-0.71)	0.65 (0.52-0.78)	0.63 (0.55-0.72)	0.59 (0.41-0.61)	0.61 (0.5-0.62)	0.6 (0.51-0.61)
IL17C	SERPINA4	73	53	0.64 (0.54-0.74)	0.63 (0.49-0.79)	0.64 (0.55-0.73)	0.59 (0.37-0.63)	0.6 (0.54-0.62)	0.6 (0.49-0.62)
IL10_PEA_IR	CLU	73	53	0.63 (0.52-0.74)	0.64 (0.51-0.78)	0.63 (0.55-0.71)	0.59 (0.39-0.63)	0.6 (0.56-0.63)	0.6 (0.5-0.62)
TNF	C8A	73	53	0.63 (0.54-0.73)	0.63 (0.51-0.77)	0.63 (0.55-0.72)	0.61 (0.39-0.62)	0.59 (0.53-0.62)	0.6 (0.49-0.61)
CDSN	SERPINA4	73	53	0.67 (0.58-0.76)	0.64 (0.52-0.78)	0.66 (0.58-0.75)	0.61 (0.37-0.66)	0.59 (0.54-0.6)	0.6 (0.48-0.63)
PLXNA4	SERPINA4	73	53	0.62 (0.52-0.71)	0.68 (0.54-0.8)	0.65 (0.57-0.72)	0.6 (0.44-0.62)	0.6 (0.48-0.65)	0.6 (0.49-0.63)
CDSN	IL10_PEA_IR	74	53	0.68 (0.58-0.76)	0.63 (0.5-0.77)	0.65 (0.57-0.74)	0.61 (0.34-0.66)	0.58 (0.55-0.61)	0.59 (0.46-0.63)
FC	FC	57	41	0.67	0.52	0.59	0.67	0.52	0.59
IL10_PEA_IR	IL15	73	53	0.64 (0.52-0.74)	0.62 (0.5-0.77)	0.63 (0.54-0.72)	0.6 (0.41-0.63)	0.59 (0.53-0.62)	0.59 (0.5-0.61)
HSD11B1	CXCL9	73	53	0.61 (0.52-0.71)	0.65 (0.5-0.83)	0.63 (0.53-0.74)	0.53 (0.42-0.61)	0.66 (0.42-0.7)	0.59 (0.47-0.64)
SERPINA4	MBL2	73	56	0.62 (0.52-0.71)	0.65 (0.52-0.8)	0.64 (0.55-0.73)	0.59 (0.43-0.61)	0.6 (0.47-0.61)	0.59 (0.5-0.61)
IL10_PEA_IR	MBL2	73	53	0.63 (0.52-0.74)	0.64 (0.51-0.8)	0.63 (0.54-0.73)	0.59 (0.39-0.63)	0.6 (0.5-0.62)	0.59 (0.49-0.62)
PLXNA4	TNF	73	53	0.62 (0.51-0.72)	0.66 (0.54-0.78)	0.64 (0.55-0.73)	0.56 (0.45-0.61)	0.63 (0.38-0.64)	0.59 (0.47-0.62)
HSD11B1	TNF	73	53	0.63 (0.52-0.73)	0.64 (0.52-0.78)	0.63 (0.56-0.72)	0.58 (0.44-0.61)	0.62 (0.42-0.63)	0.59 (0.5-0.62)
IL10_PEA_IR	IL17C	73	53	0.66 (0.55-0.76)	0.61 (0.43-0.78)	0.63 (0.53-0.74)	0.61 (0.34-0.66)	0.58 (0.56-0.62)	0.59 (0.46-0.63)
ITGA6	IL10_PEA_IR	74	53	0.64 (0.53-0.74)	0.67 (0.52-0.83)	0.65 (0.55-0.75)	0.56 (0.42-0.62)	0.63 (0.45-0.67)	0.59 (0.5-0.64)
HSD11B1	SH2D1A	74	53	0.59 (0.5-0.69)	0.67 (0.54-0.81)	0.63 (0.54-0.71)	0.57 (0.53-0.58)	0.62 (0.44-0.66)	0.59 (0.5-0.61)

C4BPB	CLU	73	56	0.62 (0.52-0.73)	0.63 (0.51-0.8)	0.63 (0.55-0.73)	0.59 (0.4-0.63)	0.6 (0.47-0.62)	0.59 (0.49-0.62)
TNF	CLU	73	53	0.62 (0.52-0.73)	0.64 (0.54-0.75)	0.63 (0.56-0.72)	0.58 (0.43-0.61)	0.6 (0.49-0.64)	0.59 (0.51-0.62)
HSD11B1	IL10_PEA_IR	74	53	0.64 (0.53-0.74)	0.65 (0.52-0.8)	0.64 (0.55-0.74)	0.57 (0.41-0.63)	0.61 (0.5-0.63)	0.59 (0.5-0.63)
CXCL9	IL15	73	53	0.63 (0.49-0.73)	0.59 (0.44-0.77)	0.6 (0.51-0.71)	0.6 (0.38-0.65)	0.59 (0.51-0.66)	0.59 (0.49-0.64)
TNF	MBL2	73	53	0.62 (0.52-0.72)	0.64 (0.54-0.78)	0.63 (0.55-0.72)	0.58 (0.43-0.62)	0.6 (0.45-0.64)	0.59 (0.5-0.62)
CDSN	CXCL9	73	53	0.65 (0.56-0.75)	0.61 (0.42-0.76)	0.63 (0.53-0.72)	0.62 (0.35-0.65)	0.57 (0.5-0.62)	0.59 (0.45-0.63)
APOA1	C4BPB	73	56	0.61 (0.51-0.72)	0.63 (0.52-0.78)	0.62 (0.55-0.71)	0.59 (0.41-0.61)	0.59 (0.5-0.6)	0.59 (0.49-0.61)
IFNG	APOA1	73	53	0.65 (0.55-0.76)	0.61 (0.47-0.75)	0.63 (0.55-0.73)	0.56 (0.35-0.65)	0.61 (0.58-0.63)	0.59 (0.48-0.63)
CXCL9	VEGFA	73	53	0.62 (0.53-0.72)	0.62 (0.45-0.78)	0.62 (0.52-0.72)	0.55 (0.41-0.62)	0.63 (0.55-0.64)	0.59 (0.51-0.62)
CXCL9	MBL2	73	53	0.62 (0.51-0.72)	0.63 (0.47-0.81)	0.63 (0.54-0.72)	0.55 (0.4-0.61)	0.62 (0.42-0.67)	0.58 (0.48-0.63)
FGF2	CDSN	74	53	0.65 (0.55-0.74)	0.75 (0.6-0.86)	0.7 (0.62-0.77)	0.58 (0.5-0.61)	0.6 (0.52-0.69)	0.58 (0.53-0.64)
CDSN	SH2D1A	74	53	0.66 (0.56-0.74)	0.62 (0.51-0.76)	0.64 (0.56-0.72)	0.61 (0.37-0.64)	0.57 (0.54-0.59)	0.58 (0.46-0.61)
ITGA6	SIT1	74	53	0.66 (0.57-0.75)	0.68 (0.53-0.81)	0.67 (0.58-0.74)	0.56 (0.45-0.65)	0.6 (0.51-0.67)	0.58 (0.51-0.65)
CXCL9	C4BPB	73	53	0.63 (0.5-0.73)	0.61 (0.46-0.78)	0.62 (0.52-0.72)	0.56 (0.38-0.63)	0.61 (0.46-0.63)	0.58 (0.48-0.62)
IFNG	TNF	73	53	0.68 (0.58-0.76)	0.64 (0.48-0.77)	0.66 (0.56-0.74)	0.54 (0.37-0.67)	0.62 (0.49-0.64)	0.58 (0.48-0.65)
ITGA6	SERPINA4	73	53	0.62 (0.53-0.71)	0.66 (0.52-0.8)	0.64 (0.55-0.72)	0.57 (0.43-0.61)	0.61 (0.43-0.63)	0.58 (0.48-0.61)
CLU	C8A	73	56	0.65 (0.55-0.74)	0.62 (0.49-0.77)	0.63 (0.57-0.72)	0.59 (0.35-0.66)	0.58 (0.54-0.59)	0.58 (0.46-0.62)
CXCL9	ORM1	73	53	0.61 (0.5-0.74)	0.66 (0.49-0.8)	0.63 (0.53-0.74)	0.57 (0.38-0.64)	0.61 (0.41-0.65)	0.58 (0.47-0.64)
VEGFA	APOA1	73	53	0.6 (0.51-0.7)	0.64 (0.52-0.76)	0.62 (0.54-0.7)	0.57 (0.47-0.59)	0.6 (0.45-0.61)	0.58 (0.5-0.6)
HSD11B1	SERPINA4	73	53	0.62 (0.53-0.71)	0.68 (0.53-0.81)	0.64 (0.56-0.73)	0.58 (0.44-0.61)	0.61 (0.46-0.66)	0.58 (0.49-0.63)
APOA1	CFB	73	56	0.6 (0.5-0.72)	0.63 (0.52-0.77)	0.62 (0.53-0.71)	0.57 (0.44-0.59)	0.59 (0.45-0.6)	0.58 (0.5-0.59)
IFNG	VEGFA	73	53	0.65 (0.55-0.74)	0.62 (0.46-0.76)	0.63 (0.54-0.73)	0.54 (0.35-0.64)	0.62 (0.6-0.63)	0.58 (0.48-0.63)
CXCL9	APOA1	73	53	0.62 (0.52-0.73)	0.62 (0.47-0.78)	0.62 (0.54-0.71)	0.56 (0.39-0.62)	0.61 (0.52-0.65)	0.58 (0.49-0.62)
IFNG	C4BPB	73	53	0.66 (0.55-0.75)	0.61 (0.49-0.77)	0.63 (0.55-0.73)	0.54 (0.36-0.65)	0.63 (0.47-0.64)	0.58 (0.48-0.64)
SH2D1A	VEGFA	73	53	0.59 (0.51-0.69)	0.65 (0.52-0.79)	0.62 (0.54-0.71)	0.57 (0.48-0.58)	0.59 (0.41-0.61)	0.58 (0.49-0.59)
HSD11B1	ORM1	73	53	0.58 (0.48-0.69)	0.67 (0.53-0.82)	0.63 (0.53-0.72)	0.56 (0.49-0.6)	0.61 (0.36-0.65)	0.58 (0.45-0.62)
TNF	IL17C	73	53	0.65 (0.54-0.75)	0.62 (0.47-0.75)	0.63 (0.54-0.72)	0.58 (0.37-0.64)	0.58 (0.5-0.62)	0.58 (0.47-0.62)
SH2D1A	CXCL9	73	53	0.64 (0.54-0.73)	0.61 (0.44-0.75)	0.63 (0.54-0.71)	0.56 (0.37-0.64)	0.59 (0.55-0.63)	0.58 (0.48-0.62)
CDSN	C4BPB	73	53	0.65 (0.55-0.74)	0.62 (0.51-0.77)	0.63 (0.56-0.72)	0.59 (0.36-0.64)	0.57 (0.5-0.61)	0.57 (0.46-0.62)
CDSN	ORM1	73	53	0.64 (0.54-0.73)	0.65 (0.53-0.8)	0.65 (0.56-0.74)	0.61 (0.38-0.63)	0.55 (0.47-0.63)	0.57 (0.47-0.63)

SH2D1A	APOA1	73	53	0.62 (0.51-0.72)	0.62 (0.5-0.74)	0.62 (0.54-0.7)	0.58 (0.43-0.61)	0.57 (0.55-0.59)	0.57 (0.49-0.59)
HSD11B1	IFNG	73	53	0.67 (0.57-0.77)	0.64 (0.5-0.8)	0.66 (0.57-0.75)	0.53 (0.36-0.64)	0.62 (0.46-0.64)	0.57 (0.47-0.63)
PLXNA4	IL10_PEA_IR	74	53	0.63 (0.52-0.74)	0.67 (0.54-0.81)	0.65 (0.56-0.73)	0.56 (0.41-0.62)	0.6 (0.45-0.64)	0.57 (0.47-0.62)
IFNG	ORM1	73	53	0.67 (0.56-0.76)	0.66 (0.49-0.79)	0.66 (0.55-0.75)	0.53 (0.37-0.64)	0.61 (0.44-0.65)	0.57 (0.47-0.63)
CDSN	APOA1	73	53	0.65 (0.55-0.73)	0.62 (0.5-0.74)	0.63 (0.56-0.71)	0.58 (0.38-0.63)	0.56 (0.53-0.59)	0.57 (0.47-0.6)
VEGFA	C4BPB	73	53	0.59 (0.48-0.7)	0.63 (0.51-0.78)	0.61 (0.54-0.71)	0.57 (0.43-0.6)	0.59 (0.41-0.6)	0.57 (0.47-0.6)
IL15	APOA1	73	53	0.6 (0.47-0.71)	0.62 (0.5-0.74)	0.61 (0.52-0.69)	0.58 (0.45-0.61)	0.56 (0.44-0.6)	0.57 (0.49-0.6)
SH2D1A	ORM1	73	53	0.59 (0.49-0.7)	0.66 (0.53-0.79)	0.63 (0.53-0.71)	0.59 (0.47-0.61)	0.56 (0.41-0.63)	0.57 (0.49-0.62)
SH2D1A	C4BPB	73	53	0.6 (0.5-0.71)	0.63 (0.51-0.78)	0.61 (0.54-0.7)	0.58 (0.42-0.59)	0.58 (0.42-0.6)	0.57 (0.48-0.6)
CDSN	C8A	73	53	0.65 (0.57-0.75)	0.61 (0.5-0.76)	0.63 (0.56-0.72)	0.58 (0.35-0.65)	0.57 (0.54-0.59)	0.57 (0.46-0.61)
HSD11B1	CFB	73	53	0.57 (0.5-0.66)	0.66 (0.52-0.81)	0.62 (0.54-0.71)	0.53 (0.48-0.55)	0.62 (0.36-0.65)	0.57 (0.44-0.6)
VEGFA	CFB	73	53	0.57 (0.48-0.68)	0.64 (0.51-0.79)	0.6 (0.52-0.69)	0.54 (0.46-0.56)	0.61 (0.39-0.63)	0.57 (0.46-0.59)
PLXNA4	ORM1	73	53	0.58 (0.47-0.69)	0.7 (0.57-0.83)	0.64 (0.55-0.72)	0.56 (0.49-0.59)	0.6 (0.32-0.69)	0.57 (0.42-0.63)
CXCL9	C8A	73	53	0.64 (0.54-0.74)	0.59 (0.45-0.77)	0.62 (0.53-0.72)	0.57 (0.37-0.63)	0.57 (0.54-0.62)	0.57 (0.46-0.61)
SH2D1A	C8A	73	53	0.62 (0.52-0.73)	0.62 (0.52-0.75)	0.62 (0.54-0.7)	0.59 (0.38-0.63)	0.56 (0.48-0.59)	0.57 (0.46-0.6)
CXCL9	CLU	73	53	0.61 (0.53-0.7)	0.61 (0.44-0.76)	0.61 (0.51-0.7)	0.54 (0.4-0.61)	0.61 (0.49-0.65)	0.57 (0.49-0.62)
IL15	ORM1	73	53	0.58 (0.42-0.7)	0.66 (0.51-0.81)	0.62 (0.5-0.71)	0.59 (0.48-0.59)	0.55 (0.37-0.63)	0.57 (0.47-0.61)
ITGA6	CXCL9	73	53	0.61 (0.52-0.71)	0.65 (0.48-0.8)	0.63 (0.54-0.72)	0.54 (0.45-0.59)	0.61 (0.39-0.67)	0.57 (0.46-0.62)
CDSN	IL15	73	53	0.64 (0.54-0.73)	0.6 (0.48-0.74)	0.62 (0.54-0.7)	0.59 (0.38-0.63)	0.54 (0.48-0.58)	0.57 (0.46-0.6)
ITGA6	VEGFA	73	53	0.58 (0.48-0.68)	0.7 (0.55-0.82)	0.64 (0.55-0.72)	0.57 (0.53-0.59)	0.57 (0.34-0.68)	0.57 (0.45-0.63)
ITGA6	TNF	73	53	0.62 (0.51-0.72)	0.67 (0.54-0.81)	0.65 (0.56-0.73)	0.56 (0.48-0.6)	0.58 (0.38-0.67)	0.57 (0.48-0.62)
IL17C	C4BPB	73	53	0.62 (0.52-0.73)	0.6 (0.46-0.78)	0.61 (0.52-0.72)	0.56 (0.39-0.61)	0.59 (0.47-0.61)	0.57 (0.46-0.61)
SH2D1A	CFB	73	53	0.59 (0.5-0.7)	0.62 (0.51-0.77)	0.61 (0.53-0.69)	0.57 (0.43-0.6)	0.57 (0.44-0.59)	0.56 (0.48-0.59)
ORM1	MBL2	73	56	0.58 (0.47-0.69)	0.67 (0.54-0.81)	0.63 (0.54-0.71)	0.55 (0.49-0.59)	0.57 (0.36-0.65)	0.56 (0.46-0.61)
SH2D1A	CLU	73	53	0.58 (0.49-0.69)	0.62 (0.52-0.74)	0.61 (0.53-0.68)	0.56 (0.46-0.57)	0.58 (0.45-0.59)	0.56 (0.49-0.58)
CXCL9	IFNG	73	53	0.64 (0.54-0.74)	0.57 (0.38-0.75)	0.6 (0.51-0.72)	0.52 (0.34-0.65)	0.62 (0.59-0.63)	0.56 (0.48-0.63)
HSD11B1	C4BPB	73	53	0.58 (0.48-0.69)	0.66 (0.51-0.83)	0.62 (0.53-0.71)	0.53 (0.46-0.58)	0.6 (0.38-0.63)	0.56 (0.45-0.6)
ITGA6	IFNG	73	53	0.65 (0.56-0.75)	0.64 (0.51-0.79)	0.64 (0.56-0.73)	0.54 (0.42-0.58)	0.61 (0.45-0.62)	0.56 (0.47-0.59)
HSD11B1	VEGFA	73	53	0.57 (0.48-0.66)	0.65 (0.53-0.8)	0.61 (0.53-0.69)	0.53 (0.49-0.54)	0.6 (0.38-0.63)	0.56 (0.45-0.58)
ITGA6	APOA1	73	53	0.59 (0.48-0.7)	0.66 (0.51-0.79)	0.62 (0.54-0.71)	0.53 (0.46-0.56)	0.61 (0.38-0.63)	0.56 (0.45-0.59)

APOA1	MBL2	73	56	0.6 (0.49-0.68)	0.63 (0.51-0.79)	0.61 (0.53-0.7)	0.55 (0.44-0.57)	0.58 (0.42-0.6)	0.56 (0.48-0.58)
ITGA6	HSD11B1	74	53	0.57 (0.49-0.66)	0.67 (0.53-0.81)	0.62 (0.54-0.71)	0.54 (0.49-0.55)	0.59 (0.36-0.64)	0.56 (0.45-0.59)
SH2D1A	IFNG	73	53	0.66 (0.57-0.76)	0.6 (0.48-0.73)	0.63 (0.55-0.72)	0.55 (0.34-0.66)	0.56 (0.54-0.61)	0.56 (0.46-0.62)
CXCL9	CFB	73	53	0.6 (0.51-0.71)	0.61 (0.46-0.77)	0.61 (0.52-0.71)	0.53 (0.41-0.6)	0.59 (0.46-0.63)	0.56 (0.48-0.61)
APOA1	CLU	73	56	0.59 (0.49-0.69)	0.62 (0.52-0.75)	0.6 (0.53-0.69)	0.55 (0.44-0.57)	0.58 (0.47-0.6)	0.56 (0.49-0.58)
HSD11B1	APOA1	73	53	0.59 (0.5-0.69)	0.65 (0.51-0.8)	0.62 (0.54-0.7)	0.53 (0.47-0.57)	0.6 (0.39-0.63)	0.56 (0.47-0.59)
IL17C	ORM1	73	53	0.62 (0.5-0.73)	0.64 (0.51-0.78)	0.63 (0.53-0.72)	0.58 (0.39-0.62)	0.56 (0.42-0.59)	0.56 (0.45-0.59)
MBL2	C4BPB	73	56	0.58 (0.48-0.69)	0.64 (0.51-0.8)	0.61 (0.53-0.72)	0.56 (0.43-0.58)	0.57 (0.41-0.59)	0.56 (0.47-0.58)
SH2D1A	IL15	73	53	0.59 (0.47-0.7)	0.61 (0.5-0.75)	0.6 (0.51-0.68)	0.59 (0.46-0.6)	0.53 (0.42-0.59)	0.56 (0.48-0.59)
IFNG	C8A	73	53	0.65 (0.55-0.75)	0.59 (0.46-0.76)	0.62 (0.54-0.71)	0.53 (0.35-0.65)	0.59 (0.55-0.61)	0.56 (0.46-0.62)
ORM1	CFB	73	56	0.57 (0.47-0.69)	0.66 (0.51-0.8)	0.61 (0.52-0.7)	0.56 (0.48-0.58)	0.57 (0.35-0.65)	0.56 (0.44-0.61)
VEGFA	CLU	73	53	0.57 (0.49-0.66)	0.63 (0.51-0.76)	0.6 (0.52-0.68)	0.54 (0.47-0.55)	0.58 (0.43-0.6)	0.56 (0.48-0.57)
HSD11B1	MBL2	73	53	0.57 (0.49-0.67)	0.65 (0.52-0.81)	0.61 (0.53-0.7)	0.53 (0.47-0.54)	0.59 (0.38-0.63)	0.56 (0.45-0.58)
PLXNA4	APOA1	73	53	0.58 (0.48-0.68)	0.66 (0.53-0.78)	0.62 (0.54-0.71)	0.55 (0.47-0.56)	0.57 (0.37-0.64)	0.56 (0.45-0.6)
IL17C	APOA1	73	53	0.61 (0.5-0.72)	0.61 (0.46-0.73)	0.61 (0.52-0.68)	0.54 (0.4-0.59)	0.57 (0.49-0.59)	0.55 (0.48-0.58)
VEGFA	MBL2	73	53	0.57 (0.49-0.67)	0.63 (0.51-0.8)	0.6 (0.52-0.7)	0.54 (0.48-0.56)	0.58 (0.4-0.61)	0.55 (0.47-0.58)
HSD11B1	CLU	73	53	0.58 (0.5-0.67)	0.64 (0.51-0.8)	0.61 (0.53-0.71)	0.54 (0.46-0.55)	0.59 (0.38-0.63)	0.55 (0.46-0.59)
IL15	C8A	73	53	0.6 (0.47-0.7)	0.62 (0.51-0.77)	0.61 (0.52-0.7)	0.6 (0.41-0.6)	0.52 (0.44-0.61)	0.55 (0.45-0.6)
SH2D1A	MBL2	73	53	0.59 (0.51-0.7)	0.63 (0.51-0.81)	0.61 (0.54-0.71)	0.56 (0.46-0.58)	0.56 (0.41-0.59)	0.55 (0.48-0.58)
VEGFA	C8A	73	53	0.6 (0.49-0.72)	0.62 (0.5-0.77)	0.62 (0.53-0.71)	0.54 (0.4-0.62)	0.58 (0.49-0.59)	0.55 (0.47-0.6)
MBL2	CFB	73	56	0.57 (0.49-0.68)	0.64 (0.51-0.78)	0.61 (0.53-0.69)	0.54 (0.47-0.56)	0.58 (0.41-0.61)	0.55 (0.46-0.58)
CDSN	VEGFA	73	53	0.66 (0.54-0.75)	0.61 (0.49-0.74)	0.63 (0.55-0.72)	0.57 (0.43-0.65)	0.54 (0.51-0.55)	0.55 (0.48-0.59)
IL15	C4BPB	73	53	0.58 (0.45-0.71)	0.63 (0.5-0.78)	0.61 (0.51-0.71)	0.58 (0.42-0.6)	0.53 (0.39-0.61)	0.55 (0.47-0.59)
CDSN	MBL2	73	53	0.64 (0.54-0.73)	0.62 (0.5-0.78)	0.63 (0.55-0.72)	0.57 (0.38-0.63)	0.54 (0.5-0.57)	0.55 (0.46-0.59)
PLXNA4	CXCL9	73	53	0.61 (0.52-0.71)	0.65 (0.48-0.78)	0.63 (0.54-0.72)	0.5 (0.42-0.61)	0.61 (0.41-0.63)	0.55 (0.45-0.61)
PLXNA4	SH2D1A	74	53	0.58 (0.49-0.69)	0.64 (0.52-0.77)	0.61 (0.54-0.69)	0.53 (0.45-0.58)	0.57 (0.38-0.63)	0.55 (0.46-0.59)
CLU	CFB	73	56	0.58 (0.5-0.68)	0.61 (0.5-0.75)	0.6 (0.52-0.68)	0.55 (0.43-0.58)	0.55 (0.46-0.58)	0.55 (0.49-0.57)
IFNG	CLU	73	53	0.66 (0.57-0.74)	0.6 (0.45-0.72)	0.63 (0.54-0.71)	0.52 (0.34-0.66)	0.58 (0.55-0.61)	0.55 (0.46-0.62)
ORM1	C4BPB	73	56	0.59 (0.45-0.7)	0.67 (0.52-0.85)	0.63 (0.52-0.73)	0.57 (0.46-0.58)	0.55 (0.35-0.66)	0.55 (0.45-0.62)
IFNG	CFB	73	53	0.65 (0.54-0.76)	0.61 (0.45-0.77)	0.63 (0.53-0.73)	0.51 (0.35-0.63)	0.59 (0.49-0.61)	0.55 (0.47-0.61)

CDSN	CLU	73	53	0.64 (0.54-0.73)	0.6 (0.5-0.71)	0.62 (0.55-0.69)	0.55 (0.38-0.63)	0.54 (0.53-0.56)	0.55 (0.46-0.59)
CDSN	CFB	73	53	0.63 (0.54-0.73)	0.61 (0.5-0.76)	0.62 (0.55-0.71)	0.55 (0.38-0.62)	0.55 (0.5-0.58)	0.55 (0.46-0.59)
IL15	IL17C	73	53	0.61 (0.47-0.71)	0.57 (0.44-0.72)	0.59 (0.49-0.68)	0.55 (0.39-0.62)	0.55 (0.47-0.58)	0.55 (0.46-0.59)
IFNG	MBL2	73	53	0.66 (0.54-0.77)	0.62 (0.46-0.81)	0.64 (0.54-0.76)	0.51 (0.33-0.67)	0.59 (0.47-0.62)	0.55 (0.46-0.63)
HSD11B1	PLXNA4	74	53	0.57 (0.5-0.65)	0.69 (0.56-0.82)	0.63 (0.55-0.7)	0.51 (0.47-0.54)	0.58 (0.32-0.69)	0.55 (0.41-0.61)
HSD11B1	IL17C	73	53	0.61 (0.5-0.71)	0.64 (0.49-0.79)	0.62 (0.53-0.71)	0.51 (0.42-0.59)	0.58 (0.42-0.62)	0.55 (0.46-0.59)
PLXNA4	C4BPB	73	53	0.58 (0.48-0.68)	0.65 (0.53-0.79)	0.62 (0.53-0.7)	0.53 (0.43-0.58)	0.56 (0.36-0.64)	0.54 (0.43-0.6)
CDSN	IFNG	73	53	0.67 (0.58-0.78)	0.58 (0.44-0.71)	0.63 (0.55-0.72)	0.55 (0.33-0.68)	0.53 (0.51-0.61)	0.54 (0.42-0.63)
ITGA6	CDSN	74	53	0.64 (0.54-0.74)	0.65 (0.52-0.78)	0.64 (0.56-0.74)	0.55 (0.43-0.61)	0.56 (0.42-0.61)	0.54 (0.46-0.6)
HSD11B1	C8A	73	53	0.6 (0.5-0.7)	0.64 (0.52-0.81)	0.62 (0.54-0.72)	0.52 (0.41-0.6)	0.57 (0.41-0.62)	0.54 (0.45-0.6)
ITGA6	ORM1	73	53	0.58 (0.46-0.69)	0.68 (0.53-0.83)	0.63 (0.53-0.73)	0.53 (0.51-0.58)	0.54 (0.33-0.67)	0.54 (0.43-0.61)
IL15	CLU	73	53	0.57 (0.45-0.68)	0.6 (0.48-0.72)	0.58 (0.5-0.67)	0.54 (0.46-0.57)	0.55 (0.44-0.57)	0.54 (0.48-0.56)
MBL2	C8A	73	56	0.6 (0.49-0.7)	0.63 (0.51-0.8)	0.61 (0.53-0.71)	0.56 (0.4-0.6)	0.54 (0.43-0.6)	0.54 (0.45-0.59)
SH2D1A	IL17C	73	53	0.62 (0.53-0.72)	0.59 (0.47-0.72)	0.61 (0.53-0.68)	0.55 (0.38-0.61)	0.53 (0.52-0.56)	0.54 (0.46-0.57)
CDSN	IL17C	73	53	0.66 (0.57-0.77)	0.57 (0.44-0.71)	0.62 (0.54-0.7)	0.54 (0.34-0.65)	0.54 (0.52-0.55)	0.54 (0.44-0.6)
PLXNA4	IFNG	73	53	0.65 (0.55-0.76)	0.64 (0.49-0.78)	0.65 (0.56-0.73)	0.49 (0.38-0.62)	0.6 (0.47-0.62)	0.54 (0.46-0.61)
VEGFA	IL17C	73	53	0.62 (0.52-0.73)	0.61 (0.46-0.75)	0.62 (0.51-0.71)	0.51 (0.38-0.61)	0.57 (0.48-0.59)	0.54 (0.47-0.59)
CDSN	HSD11B1	74	53	0.64 (0.54-0.73)	0.64 (0.52-0.79)	0.64 (0.56-0.72)	0.53 (0.41-0.62)	0.56 (0.46-0.61)	0.54 (0.47-0.6)
PLXNA4	CLU	73	53	0.57 (0.5-0.65)	0.65 (0.53-0.76)	0.61 (0.54-0.68)	0.53 (0.47-0.54)	0.55 (0.38-0.62)	0.54 (0.45-0.58)
IL15	MBL2	73	53	0.56 (0.44-0.67)	0.6 (0.49-0.79)	0.59 (0.5-0.69)	0.55 (0.47-0.56)	0.54 (0.4-0.6)	0.54 (0.47-0.58)
PLXNA4	CFB	73	53	0.57 (0.5-0.66)	0.64 (0.52-0.79)	0.6 (0.53-0.68)	0.51 (0.47-0.54)	0.57 (0.37-0.64)	0.54 (0.43-0.58)
ITGA6	SH2D1A	74	53	0.59 (0.5-0.7)	0.67 (0.51-0.8)	0.63 (0.54-0.72)	0.55 (0.47-0.58)	0.53 (0.38-0.65)	0.54 (0.46-0.6)
IL15	VEGFA	73	53	0.55 (0.44-0.66)	0.63 (0.5-0.76)	0.59 (0.5-0.68)	0.55 (0.51-0.56)	0.52 (0.41-0.61)	0.54 (0.48-0.58)
C4BPB	CFB	73	56	0.58 (0.48-0.68)	0.62 (0.51-0.78)	0.6 (0.52-0.69)	0.54 (0.43-0.58)	0.54 (0.41-0.6)	0.54 (0.47-0.58)
HSD11B1	IL15	73	53	0.56 (0.44-0.67)	0.63 (0.51-0.78)	0.6 (0.5-0.69)	0.52 (0.5-0.57)	0.54 (0.37-0.63)	0.54 (0.45-0.58)
IL15	CFB	73	53	0.56 (0.44-0.68)	0.63 (0.5-0.8)	0.6 (0.51-0.7)	0.54 (0.48-0.59)	0.53 (0.37-0.61)	0.54 (0.45-0.59)
PLXNA4	VEGFA	73	53	0.57 (0.49-0.67)	0.66 (0.54-0.78)	0.62 (0.55-0.69)	0.52 (0.45-0.57)	0.55 (0.36-0.64)	0.53 (0.44-0.58)
ITGA6	IL17C	73	53	0.59 (0.5-0.7)	0.64 (0.49-0.78)	0.62 (0.53-0.71)	0.53 (0.47-0.54)	0.54 (0.39-0.61)	0.53 (0.46-0.57)
ITGA6	CLU	73	53	0.57 (0.49-0.67)	0.65 (0.52-0.78)	0.61 (0.53-0.7)	0.52 (0.46-0.55)	0.56 (0.37-0.62)	0.53 (0.43-0.58)
IL17C	CLU	73	53	0.61 (0.52-0.72)	0.6 (0.46-0.72)	0.61 (0.52-0.68)	0.51 (0.39-0.61)	0.55 (0.48-0.58)	0.53 (0.47-0.58)

ITGA6	MBL2	73	53	0.57 (0.48-0.68)	0.65 (0.5-0.8)	0.61 (0.53-0.71)	0.53 (0.48-0.54)	0.53 (0.36-0.64)	0.53 (0.44-0.59)
IL17C	C8A	73	53	0.63 (0.54-0.73)	0.58 (0.45-0.75)	0.61 (0.53-0.7)	0.52 (0.38-0.62)	0.54 (0.51-0.57)	0.53 (0.45-0.59)
IL17C	MBL2	73	53	0.61 (0.52-0.71)	0.62 (0.47-0.79)	0.61 (0.53-0.71)	0.5 (0.4-0.6)	0.57 (0.4-0.59)	0.53 (0.44-0.58)
ITGA6	C4BPB	73	53	0.58 (0.48-0.69)	0.67 (0.53-0.82)	0.63 (0.53-0.72)	0.53 (0.44-0.57)	0.54 (0.38-0.63)	0.53 (0.44-0.58)
C8A	CFB	73	56	0.6 (0.51-0.71)	0.61 (0.49-0.77)	0.61 (0.53-0.7)	0.53 (0.39-0.61)	0.52 (0.48-0.59)	0.53 (0.45-0.58)
PLXNA4	IL15	73	53	0.55 (0.44-0.67)	0.66 (0.51-0.8)	0.61 (0.51-0.69)	0.53 (0.5-0.56)	0.52 (0.34-0.64)	0.53 (0.44-0.59)
C4BPB	C8A	73	56	0.61 (0.5-0.71)	0.62 (0.51-0.79)	0.61 (0.54-0.71)	0.55 (0.4-0.6)	0.51 (0.45-0.59)	0.53 (0.43-0.58)
ITGA6	CFB	73	53	0.56 (0.48-0.66)	0.64 (0.51-0.79)	0.6 (0.52-0.69)	0.52 (0.47-0.54)	0.53 (0.37-0.63)	0.53 (0.45-0.58)
ITGA6	IL15	73	53	0.55 (0.44-0.67)	0.64 (0.5-0.78)	0.6 (0.5-0.69)	0.54 (0.51-0.56)	0.51 (0.37-0.63)	0.52 (0.45-0.58)
CXCL9	IL17C	73	53	0.62 (0.51-0.72)	0.55 (0.37-0.75)	0.59 (0.48-0.7)	0.45 (0.39-0.61)	0.61 (0.53-0.62)	0.52 (0.48-0.61)
PLXNA4	MBL2	73	53	0.56 (0.48-0.67)	0.69 (0.56-0.83)	0.63 (0.55-0.71)	0.51 (0.47-0.53)	0.54 (0.34-0.67)	0.52 (0.42-0.59)
hsCRP	hsCRP	76	57	0.53	0.52	0.52	0.53	0.52	0.52
PLXNA4	C8A	73	53	0.61 (0.49-0.71)	0.65 (0.53-0.78)	0.63 (0.55-0.71)	0.51 (0.41-0.61)	0.54 (0.38-0.64)	0.52 (0.43-0.6)
PLXNA4	IL17C	73	53	0.61 (0.52-0.71)	0.64 (0.47-0.78)	0.62 (0.52-0.71)	0.5 (0.4-0.59)	0.56 (0.4-0.61)	0.52 (0.44-0.58)
MBL2	CLU	73	56	0.58 (0.5-0.68)	0.61 (0.51-0.78)	0.6 (0.53-0.69)	0.53 (0.46-0.55)	0.55 (0.42-0.59)	0.52 (0.45-0.56)
IL17C	CFB	73	53	0.61 (0.51-0.72)	0.6 (0.45-0.75)	0.61 (0.52-0.69)	0.51 (0.4-0.59)	0.55 (0.46-0.57)	0.52 (0.46-0.57)
ITGA6	C8A	73	53	0.6 (0.49-0.71)	0.66 (0.52-0.81)	0.63 (0.54-0.73)	0.54 (0.41-0.58)	0.52 (0.37-0.63)	0.52 (0.44-0.59)
ORM1	C8A	73	56	0.59 (0.46-0.7)	0.66 (0.53-0.82)	0.63 (0.52-0.72)	0.56 (0.41-0.6)	0.48 (0.4-0.63)	0.52 (0.44-0.61)
CDSN	PLXNA4	74	53	0.64 (0.54-0.73)	0.64 (0.52-0.77)	0.64 (0.56-0.72)	0.51 (0.38-0.62)	0.53 (0.42-0.57)	0.51 (0.44-0.58)
ITGA6	PLXNA4	74	53	0.56 (0.48-0.66)	0.71 (0.55-0.84)	0.63 (0.54-0.72)	0.47 (0.46-0.54)	0.52 (0.31-0.69)	0.5 (0.38-0.6)
IFNG	IL17C	73	53	0.65 (0.54-0.75)	0.54 (0.4-0.73)	0.6 (0.5-0.71)	0.4 (0.34-0.65)	0.57 (0.53-0.62)	0.49 (0.45-0.62)

Supplementary Table 7. Biomarker pairs to predict relapse during the whole follow-up period

Gene name 1	Gene name 2	STORI (n=)	SPARE (n=)	c-statistic (CI) development dataset (STORI)	c-statistic (CI) development dataset (SPARE)	Mean c-statistic (CI) development datasets (STORI and SPARE)	c-statistic (CI) validation dataset (STORI)	c-statistic (CI) validation dataset (SPARE)	Mean c-statistic (CI) validation datasets (STORI and SPARE)
SIT1	HP	101	63	0.69 (0.62-0.77)	0.68 (0.57-0.78)	0.68 (0.62-0.75)	0.68 (0.57-0.69)	0.67 (0.63-0.68)	0.67 (0.61-0.68)
CEASE_phase1	CEASE_phase1	83	46	NA	NA	NA	0.70	0.63	0.66
HP	APOA1	102	67	0.7 (0.61-0.77)	0.66 (0.55-0.77)	0.68 (0.61-0.75)	0.69 (0.6-0.7)	0.65 (0.61-0.66)	0.66 (0.62-0.68)
FLT3LG	HP	102	63	0.69 (0.6-0.76)	0.66 (0.57-0.77)	0.68 (0.61-0.75)	0.68 (0.61-0.69)	0.65 (0.63-0.66)	0.66 (0.63-0.67)
hsCRP	HP	98	67	0.68 (0.59-0.76)	0.65 (0.54-0.76)	0.66 (0.59-0.73)	0.68 (0.54-0.69)	0.65 (0.6-0.66)	0.66 (0.59-0.67)
CRP_SRM	HP	102	67	0.67 (0.58-0.75)	0.65 (0.54-0.76)	0.66 (0.59-0.73)	0.67 (0.53-0.68)	0.64 (0.62-0.66)	0.66 (0.58-0.67)
MILR1	HP	101	63	0.71 (0.62-0.78)	0.64 (0.53-0.76)	0.68 (0.61-0.74)	0.68 (0.46-0.71)	0.63 (0.6-0.64)	0.65 (0.55-0.67)
HP	SAA1	102	67	0.67 (0.59-0.75)	0.65 (0.52-0.77)	0.66 (0.59-0.73)	0.66 (0.51-0.68)	0.65 (0.6-0.66)	0.65 (0.58-0.66)
HP	C2	102	67	0.67 (0.59-0.74)	0.66 (0.54-0.75)	0.66 (0.59-0.73)	0.66 (0.57-0.67)	0.65 (0.62-0.66)	0.65 (0.6-0.66)
FC	HP	77	44	0.74 (0.66-0.82)	0.63 (0.47-0.76)	0.68 (0.6-0.76)	0.68 (0.26-0.75)	0.62 (0.61-0.63)	0.65 (0.44-0.69)
hsCRP	SIT1	98	63	0.67 (0.56-0.75)	0.66 (0.56-0.78)	0.66 (0.59-0.73)	0.65 (0.55-0.67)	0.66 (0.56-0.67)	0.65 (0.58-0.67)
MASP1	HP	101	63	0.69 (0.61-0.76)	0.65 (0.54-0.76)	0.67 (0.6-0.74)	0.67 (0.48-0.69)	0.63 (0.61-0.64)	0.65 (0.56-0.66)
HP	LRG1	102	67	0.67 (0.59-0.74)	0.66 (0.55-0.77)	0.66 (0.6-0.73)	0.66 (0.56-0.67)	0.64 (0.6-0.66)	0.65 (0.6-0.66)
IL13	HP	102	63	0.68 (0.6-0.75)	0.64 (0.5-0.75)	0.66 (0.58-0.73)	0.67 (0.34-0.68)	0.64 (0.57-0.64)	0.65 (0.49-0.66)
TNF	HP	102	63	0.67 (0.59-0.74)	0.65 (0.55-0.75)	0.66 (0.6-0.72)	0.66 (0.56-0.67)	0.64 (0.61-0.65)	0.65 (0.6-0.66)
HP	C8B	102	67	0.67 (0.6-0.75)	0.65 (0.55-0.75)	0.66 (0.59-0.73)	0.67 (0.56-0.68)	0.64 (0.6-0.64)	0.65 (0.59-0.66)
VEGFA	HP	102	63	0.67 (0.59-0.75)	0.65 (0.53-0.75)	0.66 (0.6-0.73)	0.66 (0.49-0.68)	0.64 (0.62-0.65)	0.65 (0.57-0.66)
HP	ITIH3	102	67	0.67 (0.59-0.75)	0.66 (0.55-0.76)	0.66 (0.59-0.73)	0.66 (0.57-0.67)	0.64 (0.61-0.65)	0.65 (0.6-0.66)
C5	APOA1	102	67	0.68 (0.59-0.75)	0.66 (0.54-0.77)	0.66 (0.6-0.74)	0.67 (0.63-0.68)	0.63 (0.57-0.65)	0.65 (0.61-0.66)
HP	C8A	102	67	0.67 (0.59-0.74)	0.65 (0.56-0.76)	0.66 (0.6-0.73)	0.66 (0.55-0.67)	0.64 (0.61-0.64)	0.65 (0.59-0.65)
HP	SERPING1	102	67	0.67 (0.6-0.74)	0.66 (0.54-0.76)	0.67 (0.59-0.73)	0.66 (0.53-0.67)	0.64 (0.61-0.64)	0.65 (0.59-0.66)
KLRD1	HP	101	63	0.67 (0.59-0.75)	0.65 (0.55-0.75)	0.66 (0.6-0.73)	0.66 (0.54-0.67)	0.63 (0.6-0.64)	0.65 (0.58-0.65)
HP	HPR	102	67	0.68 (0.59-0.74)	0.66 (0.56-0.76)	0.66 (0.6-0.73)	0.65 (0.53-0.67)	0.64 (0.62-0.65)	0.65 (0.59-0.66)
IL15	HP	102	63	0.67 (0.58-0.74)	0.68 (0.57-0.79)	0.67 (0.61-0.74)	0.65 (0.63-0.66)	0.64 (0.59-0.68)	0.65 (0.62-0.67)
SIT1	CRP_SRM	101	63	0.66 (0.55-0.74)	0.66 (0.55-0.77)	0.66 (0.59-0.73)	0.65 (0.53-0.67)	0.66 (0.56-0.67)	0.64 (0.58-0.67)

HP	CLU	102	67	0.67 (0.59-0.75)	0.64 (0.54-0.75)	0.66 (0.59-0.72)	0.66 (0.5-0.67)	0.63 (0.55-0.65)	0.64 (0.57-0.66)
HP	SERPINA4	102	67	0.69 (0.62-0.76)	0.65 (0.55-0.75)	0.67 (0.61-0.74)	0.68 (0.51-0.69)	0.62 (0.59-0.65)	0.64 (0.56-0.66)
HP	C3	102	67	0.67 (0.58-0.75)	0.65 (0.54-0.75)	0.66 (0.59-0.72)	0.66 (0.52-0.67)	0.64 (0.59-0.65)	0.64 (0.58-0.66)
HP	C5	102	67	0.66 (0.58-0.74)	0.65 (0.55-0.76)	0.66 (0.59-0.72)	0.66 (0.54-0.67)	0.63 (0.6-0.65)	0.64 (0.58-0.66)
HP	SERPINA3	102	67	0.67 (0.59-0.74)	0.65 (0.54-0.75)	0.66 (0.6-0.73)	0.65 (0.55-0.67)	0.64 (0.61-0.65)	0.64 (0.59-0.66)
FLT3LG	HPR	102	63	0.64 (0.55-0.73)	0.69 (0.57-0.8)	0.66 (0.59-0.74)	0.63 (0.57-0.64)	0.66 (0.58-0.68)	0.64 (0.59-0.66)
HP	C4BPB	102	67	0.67 (0.59-0.74)	0.65 (0.53-0.76)	0.66 (0.59-0.73)	0.66 (0.55-0.67)	0.63 (0.59-0.65)	0.64 (0.58-0.66)
IFNG	HP	102	63	0.71 (0.63-0.78)	0.65 (0.54-0.75)	0.68 (0.61-0.74)	0.65 (0.5-0.71)	0.63 (0.62-0.64)	0.64 (0.57-0.67)
NCR1	HP	101	63	0.67 (0.59-0.74)	0.66 (0.55-0.77)	0.67 (0.6-0.73)	0.65 (0.58-0.67)	0.64 (0.59-0.67)	0.64 (0.6-0.66)
HSD11B1	HP	101	63	0.68 (0.59-0.75)	0.65 (0.54-0.76)	0.66 (0.59-0.73)	0.65 (0.55-0.67)	0.64 (0.61-0.65)	0.64 (0.59-0.65)
HP	ITIH2	102	67	0.66 (0.58-0.74)	0.65 (0.55-0.75)	0.66 (0.59-0.72)	0.65 (0.54-0.67)	0.64 (0.59-0.64)	0.64 (0.59-0.65)
CDSN	HP	101	63	0.67 (0.59-0.74)	0.66 (0.55-0.77)	0.66 (0.59-0.74)	0.65 (0.51-0.67)	0.64 (0.59-0.65)	0.64 (0.57-0.66)
HP	ORM1	102	67	0.67 (0.59-0.75)	0.66 (0.57-0.76)	0.67 (0.6-0.74)	0.66 (0.57-0.67)	0.63 (0.56-0.66)	0.64 (0.59-0.66)
IL6_PEA_cytokine	HP	102	63	0.69 (0.61-0.76)	0.64 (0.5-0.75)	0.66 (0.58-0.73)	0.66 (0.4-0.68)	0.62 (0.6-0.63)	0.64 (0.52-0.65)
HGF	HP	102	63	0.67 (0.58-0.75)	0.64 (0.54-0.75)	0.66 (0.59-0.72)	0.66 (0.49-0.67)	0.63 (0.61-0.64)	0.64 (0.56-0.65)
FLT3LG	C5	102	63	0.65 (0.56-0.74)	0.67 (0.55-0.77)	0.66 (0.59-0.73)	0.65 (0.56-0.66)	0.64 (0.55-0.67)	0.64 (0.59-0.66)
IFNG	IL15	102	63	0.73 (0.64-0.79)	0.6 (0.47-0.72)	0.66 (0.59-0.73)	0.67 (0.43-0.71)	0.61 (0.6-0.62)	0.64 (0.52-0.67)
IL6_PEA_IR	HP	101	63	0.68 (0.6-0.76)	0.65 (0.53-0.76)	0.66 (0.59-0.74)	0.65 (0.48-0.68)	0.63 (0.61-0.63)	0.64 (0.55-0.66)
HP	APCS	102	67	0.67 (0.58-0.74)	0.65 (0.55-0.76)	0.66 (0.59-0.73)	0.65 (0.54-0.67)	0.64 (0.54-0.65)	0.64 (0.57-0.65)
CCL4	HP	102	63	0.67 (0.59-0.75)	0.64 (0.54-0.75)	0.66 (0.59-0.73)	0.65 (0.43-0.67)	0.63 (0.59-0.64)	0.64 (0.52-0.66)
CLEC4C	HP	101	63	0.67 (0.59-0.74)	0.65 (0.54-0.77)	0.66 (0.59-0.73)	0.65 (0.51-0.67)	0.63 (0.56-0.65)	0.64 (0.57-0.65)
NCR1	HPR	101	63	0.63 (0.55-0.7)	0.68 (0.56-0.78)	0.65 (0.58-0.72)	0.62 (0.55-0.63)	0.66 (0.56-0.67)	0.64 (0.58-0.65)
FC	C5	77	44	0.7 (0.62-0.78)	0.63 (0.49-0.75)	0.67 (0.59-0.74)	0.67 (0.37-0.72)	0.61 (0.57-0.62)	0.64 (0.49-0.67)
FC	FC	85	47	NA	NA	NA	0.70	0.58	0.64
ITGA11	HP	101	63	0.68 (0.6-0.75)	0.64 (0.52-0.74)	0.66 (0.6-0.72)	0.66 (0.45-0.68)	0.62 (0.59-0.64)	0.64 (0.54-0.65)
IL10_PEA_IR	HP	101	63	0.69 (0.6-0.76)	0.64 (0.47-0.77)	0.67 (0.58-0.74)	0.64 (0.5-0.69)	0.63 (0.61-0.64)	0.64 (0.56-0.66)
HP	ITIH1	102	67	0.66 (0.58-0.74)	0.65 (0.55-0.75)	0.66 (0.6-0.72)	0.64 (0.51-0.67)	0.64 (0.58-0.64)	0.64 (0.57-0.65)
SIT1	HPR	101	63	0.64 (0.55-0.71)	0.68 (0.56-0.79)	0.66 (0.59-0.72)	0.62 (0.56-0.63)	0.66 (0.58-0.67)	0.64 (0.59-0.65)
C4B	APOA1	102	67	0.64 (0.56-0.72)	0.73 (0.6-0.85)	0.68 (0.61-0.76)	0.62 (0.54-0.64)	0.66 (0.54-0.73)	0.63 (0.57-0.68)
hsCRP	C8B	98	67	0.67 (0.54-0.76)	0.64 (0.54-0.75)	0.65 (0.57-0.73)	0.67 (0.46-0.69)	0.61 (0.5-0.64)	0.63 (0.53-0.66)

SH2D1A	HP	101	63	0.67 (0.59-0.75)	0.64 (0.52-0.75)	0.65 (0.59-0.72)	0.65 (0.45-0.67)	0.63 (0.6-0.64)	0.63 (0.53-0.65)
FLT3LG	CRP_SRM	102	63	0.65 (0.57-0.75)	0.64 (0.52-0.75)	0.65 (0.58-0.72)	0.65 (0.54-0.66)	0.62 (0.57-0.67)	0.63 (0.58-0.66)
CCL13	HP	102	63	0.67 (0.59-0.75)	0.66 (0.56-0.77)	0.66 (0.59-0.73)	0.65 (0.53-0.67)	0.63 (0.57-0.66)	0.63 (0.57-0.66)
PLXNA4	HP	101	63	0.66 (0.57-0.74)	0.66 (0.55-0.76)	0.66 (0.6-0.73)	0.63 (0.47-0.67)	0.64 (0.61-0.65)	0.63 (0.55-0.65)
FLT3LG	IFNG	102	63	0.7 (0.61-0.8)	0.61 (0.49-0.73)	0.66 (0.58-0.73)	0.66 (0.4-0.71)	0.61 (0.6-0.62)	0.63 (0.5-0.66)
SIT1	C5	101	63	0.62 (0.53-0.7)	0.68 (0.57-0.79)	0.65 (0.58-0.72)	0.61 (0.59-0.62)	0.65 (0.54-0.68)	0.63 (0.58-0.65)
IL17C	HP	102	63	0.67 (0.58-0.74)	0.64 (0.53-0.74)	0.66 (0.59-0.72)	0.65 (0.41-0.68)	0.61 (0.58-0.64)	0.63 (0.51-0.65)
SIT1	LRG1	101	63	0.64 (0.55-0.71)	0.66 (0.55-0.77)	0.65 (0.58-0.71)	0.63 (0.55-0.63)	0.64 (0.56-0.66)	0.63 (0.58-0.64)
hsCRP	C4B	98	67	0.63 (0.53-0.72)	0.71 (0.57-0.82)	0.67 (0.58-0.74)	0.6 (0.53-0.63)	0.69 (0.39-0.71)	0.63 (0.49-0.67)
HP	PZP	101	67	0.66 (0.58-0.74)	0.65 (0.55-0.76)	0.66 (0.59-0.73)	0.65 (0.55-0.66)	0.62 (0.56-0.65)	0.63 (0.57-0.65)
HP	F9	102	67	0.66 (0.57-0.74)	0.66 (0.56-0.77)	0.66 (0.6-0.73)	0.64 (0.5-0.67)	0.63 (0.55-0.65)	0.63 (0.56-0.65)
hsCRP	FLT3LG	98	63	0.65 (0.56-0.74)	0.64 (0.52-0.75)	0.65 (0.57-0.72)	0.64 (0.56-0.65)	0.62 (0.57-0.67)	0.63 (0.59-0.65)
F9	APOA1	102	67	0.65 (0.55-0.73)	0.67 (0.55-0.79)	0.66 (0.59-0.73)	0.64 (0.57-0.65)	0.63 (0.55-0.66)	0.63 (0.58-0.65)
FGF2	CRP_SRM	101	63	0.62 (0.53-0.7)	0.71 (0.45-0.8)	0.66 (0.54-0.72)	0.58 (0.47-0.62)	0.69 (0.53-0.7)	0.63 (0.54-0.66)
HP	CFB	102	67	0.67 (0.59-0.75)	0.66 (0.55-0.76)	0.66 (0.6-0.73)	0.65 (0.51-0.67)	0.62 (0.55-0.64)	0.63 (0.56-0.65)
CXCL9	HP	102	63	0.71 (0.63-0.78)	0.65 (0.52-0.75)	0.68 (0.6-0.74)	0.64 (0.48-0.71)	0.62 (0.6-0.63)	0.63 (0.55-0.67)
FC	LAMP3	76	43	0.7 (0.6-0.79)	0.63 (0.51-0.75)	0.67 (0.59-0.74)	0.64 (0.42-0.7)	0.62 (0.5-0.64)	0.63 (0.51-0.67)
SAA1	C4B	102	67	0.59 (0.49-0.68)	0.72 (0.59-0.86)	0.65 (0.58-0.73)	0.57 (0.5-0.58)	0.72 (0.35-0.74)	0.63 (0.43-0.66)
IL17F	HP	102	63	0.68 (0.6-0.75)	0.63 (0.48-0.74)	0.65 (0.56-0.72)	0.65 (0.41-0.67)	0.6 (0.57-0.64)	0.63 (0.51-0.65)
LAMP3	HPR	101	63	0.61 (0.51-0.69)	0.69 (0.58-0.78)	0.65 (0.58-0.71)	0.6 (0.55-0.62)	0.67 (0.47-0.69)	0.63 (0.54-0.65)
IL15	CRP_SRM	102	63	0.64 (0.5-0.73)	0.64 (0.52-0.76)	0.64 (0.55-0.71)	0.65 (0.56-0.67)	0.62 (0.49-0.66)	0.63 (0.53-0.66)
LAMP3	HP	101	63	0.67 (0.59-0.74)	0.66 (0.55-0.75)	0.66 (0.58-0.72)	0.65 (0.48-0.67)	0.61 (0.55-0.65)	0.63 (0.55-0.66)
FCRL6	HP	101	63	0.67 (0.59-0.74)	0.68 (0.56-0.78)	0.67 (0.61-0.74)	0.63 (0.52-0.67)	0.63 (0.57-0.66)	0.63 (0.57-0.65)
HPR	APOA1	102	67	0.64 (0.55-0.73)	0.66 (0.53-0.76)	0.65 (0.57-0.72)	0.62 (0.57-0.64)	0.63 (0.58-0.64)	0.63 (0.59-0.64)
NCR1	C5	101	63	0.63 (0.53-0.71)	0.67 (0.56-0.77)	0.65 (0.58-0.72)	0.63 (0.58-0.64)	0.63 (0.49-0.66)	0.63 (0.56-0.65)
FLT3LG	LRG1	102	63	0.65 (0.56-0.74)	0.63 (0.52-0.75)	0.64 (0.57-0.71)	0.64 (0.46-0.65)	0.62 (0.59-0.62)	0.63 (0.54-0.64)
hsCRP	FGF2	98	63	0.61 (0.51-0.69)	0.71 (0.47-0.81)	0.66 (0.54-0.72)	0.58 (0.49-0.61)	0.69 (0.5-0.71)	0.63 (0.53-0.65)
CRP_SRM	C4B	102	67	0.62 (0.52-0.71)	0.7 (0.57-0.81)	0.66 (0.59-0.73)	0.59 (0.51-0.63)	0.68 (0.38-0.7)	0.63 (0.48-0.66)
HP	CP	102	67	0.66 (0.58-0.75)	0.66 (0.56-0.78)	0.66 (0.6-0.73)	0.65 (0.46-0.67)	0.61 (0.55-0.64)	0.63 (0.53-0.65)
HP	CPN2	102	67	0.67 (0.6-0.76)	0.65 (0.56-0.75)	0.66 (0.61-0.73)	0.65 (0.46-0.68)	0.62 (0.55-0.64)	0.62 (0.53-0.65)

LAMP3	FLT3LG	101	63	0.63 (0.54-0.72)	0.67 (0.57-0.77)	0.65 (0.59-0.72)	0.62 (0.55-0.63)	0.63 (0.55-0.67)	0.62 (0.58-0.65)
CRP_SRM	APOA1	102	67	0.65 (0.55-0.72)	0.63 (0.53-0.75)	0.64 (0.57-0.7)	0.65 (0.48-0.66)	0.61 (0.54-0.62)	0.62 (0.54-0.64)
LRG1	APOA1	102	67	0.66 (0.57-0.74)	0.63 (0.53-0.73)	0.64 (0.58-0.71)	0.65 (0.52-0.66)	0.6 (0.55-0.63)	0.62 (0.55-0.64)
C8B	APOA1	102	67	0.66 (0.58-0.74)	0.62 (0.52-0.73)	0.64 (0.57-0.71)	0.66 (0.39-0.67)	0.6 (0.56-0.61)	0.62 (0.49-0.64)
FGF2	HP	101	63	0.66 (0.56-0.74)	0.68 (0.5-0.79)	0.67 (0.57-0.74)	0.6 (0.49-0.67)	0.63 (0.62-0.67)	0.62 (0.56-0.66)
SIT1	F9	101	63	0.62 (0.54-0.69)	0.69 (0.58-0.78)	0.65 (0.58-0.71)	0.6 (0.56-0.61)	0.65 (0.52-0.68)	0.62 (0.56-0.64)
FLT3LG	F9	102	63	0.63 (0.55-0.72)	0.65 (0.53-0.77)	0.64 (0.57-0.72)	0.62 (0.54-0.63)	0.63 (0.53-0.64)	0.62 (0.57-0.63)
SAA1	HPR	102	67	0.63 (0.54-0.71)	0.64 (0.52-0.76)	0.64 (0.55-0.71)	0.61 (0.48-0.63)	0.63 (0.49-0.64)	0.62 (0.53-0.64)
IL15	HPR	102	63	0.6 (0.5-0.69)	0.67 (0.54-0.77)	0.64 (0.56-0.7)	0.6 (0.58-0.62)	0.65 (0.46-0.66)	0.62 (0.52-0.64)
SIT1	SAA1	101	63	0.64 (0.55-0.71)	0.64 (0.52-0.75)	0.64 (0.56-0.7)	0.63 (0.47-0.64)	0.62 (0.56-0.65)	0.62 (0.54-0.64)
MILR1	SIT1	102	63	0.66 (0.57-0.74)	0.63 (0.52-0.74)	0.64 (0.58-0.71)	0.63 (0.39-0.65)	0.62 (0.57-0.63)	0.62 (0.5-0.64)
CRP_SRM	C8B	102	67	0.65 (0.53-0.74)	0.63 (0.53-0.74)	0.64 (0.56-0.72)	0.65 (0.48-0.67)	0.6 (0.5-0.64)	0.62 (0.54-0.65)
HPR	ORM1	102	67	0.63 (0.53-0.71)	0.66 (0.57-0.76)	0.64 (0.58-0.71)	0.61 (0.54-0.63)	0.64 (0.54-0.65)	0.62 (0.55-0.64)
HP	VTN	102	67	0.67 (0.58-0.75)	0.65 (0.56-0.75)	0.66 (0.59-0.73)	0.65 (0.47-0.67)	0.6 (0.54-0.64)	0.62 (0.53-0.65)
CRP_SRM	APCS	102	67	0.63 (0.52-0.71)	0.64 (0.54-0.75)	0.63 (0.56-0.7)	0.61 (0.52-0.63)	0.64 (0.45-0.65)	0.62 (0.52-0.64)
hsCRP	C5	98	67	0.64 (0.53-0.73)	0.64 (0.52-0.74)	0.64 (0.55-0.71)	0.64 (0.5-0.65)	0.63 (0.52-0.64)	0.62 (0.54-0.64)
CLEC4C	CRP_SRM	101	63	0.63 (0.53-0.71)	0.67 (0.51-0.78)	0.65 (0.56-0.72)	0.6 (0.47-0.62)	0.66 (0.42-0.68)	0.62 (0.49-0.65)
C8B	HPR	102	67	0.64 (0.55-0.71)	0.65 (0.54-0.77)	0.65 (0.57-0.71)	0.63 (0.51-0.64)	0.63 (0.53-0.64)	0.62 (0.56-0.64)
hsCRP	hsCRP	109	69	NA	NA	NA	0.64	0.60	0.62
CXCL9	FLT3LG	102	63	0.69 (0.61-0.77)	0.61 (0.5-0.73)	0.65 (0.58-0.72)	0.64 (0.39-0.7)	0.6 (0.57-0.62)	0.62 (0.49-0.65)
NCR1	CRP_SRM	101	63	0.63 (0.53-0.72)	0.64 (0.54-0.75)	0.64 (0.56-0.71)	0.63 (0.55-0.64)	0.63 (0.49-0.64)	0.62 (0.55-0.64)
FGF2	C4B	101	63	0.58 (0.49-0.66)	0.73 (0.57-0.85)	0.65 (0.56-0.73)	0.55 (0.54-0.57)	0.68 (0.29-0.73)	0.62 (0.42-0.64)
HP	C9	102	67	0.66 (0.59-0.75)	0.68 (0.57-0.77)	0.67 (0.61-0.74)	0.6 (0.5-0.67)	0.64 (0.58-0.66)	0.62 (0.56-0.66)
hsCRP	APOA1	98	67	0.64 (0.54-0.71)	0.63 (0.52-0.75)	0.63 (0.56-0.7)	0.63 (0.51-0.65)	0.61 (0.53-0.62)	0.62 (0.55-0.63)
PLXNA4	HPR	101	63	0.59 (0.51-0.69)	0.69 (0.58-0.78)	0.64 (0.58-0.71)	0.58 (0.52-0.59)	0.66 (0.45-0.68)	0.62 (0.5-0.64)
CLEC4C	HPR	101	63	0.6 (0.53-0.68)	0.67 (0.55-0.77)	0.64 (0.57-0.7)	0.59 (0.54-0.61)	0.65 (0.43-0.66)	0.62 (0.5-0.63)
FLT3LG	C8B	102	63	0.62 (0.55-0.72)	0.65 (0.54-0.77)	0.64 (0.57-0.71)	0.61 (0.51-0.63)	0.63 (0.57-0.64)	0.62 (0.56-0.63)
MILR1	C5	101	63	0.67 (0.59-0.74)	0.64 (0.51-0.75)	0.65 (0.58-0.72)	0.64 (0.39-0.67)	0.61 (0.56-0.64)	0.62 (0.5-0.65)
IL6_PEA_cytokine	C4B	102	63	0.6 (0.46-0.68)	0.68 (0.54-0.83)	0.64 (0.53-0.72)	0.56 (0.54-0.6)	0.68 (0.37-0.69)	0.62 (0.46-0.64)
hsCRP	APCS	98	67	0.63 (0.52-0.71)	0.64 (0.54-0.75)	0.64 (0.56-0.7)	0.61 (0.53-0.62)	0.63 (0.46-0.65)	0.62 (0.53-0.63)

hsCRP	MILR1	98	63	0.67 (0.59-0.75)	0.61 (0.51-0.73)	0.65 (0.57-0.72)	0.65 (0.4-0.69)	0.59 (0.55-0.6)	0.62 (0.49-0.64)
SAA1	C5	102	67	0.62 (0.47-0.71)	0.63 (0.51-0.75)	0.63 (0.53-0.7)	0.62 (0.46-0.63)	0.63 (0.45-0.64)	0.62 (0.5-0.63)
NCR1	C8B	101	63	0.63 (0.54-0.71)	0.64 (0.53-0.75)	0.63 (0.56-0.71)	0.64 (0.45-0.65)	0.6 (0.51-0.62)	0.62 (0.52-0.63)
LAMP3	C4B	101	63	0.59 (0.49-0.67)	0.7 (0.58-0.81)	0.64 (0.56-0.71)	0.56 (0.56-0.57)	0.67 (0.32-0.69)	0.62 (0.44-0.63)
NCR1	MASP1	102	63	0.63 (0.54-0.71)	0.65 (0.52-0.77)	0.64 (0.56-0.71)	0.61 (0.43-0.62)	0.63 (0.57-0.65)	0.62 (0.52-0.63)
C4B	HPR	102	67	0.61 (0.52-0.68)	0.69 (0.57-0.8)	0.65 (0.57-0.71)	0.59 (0.56-0.6)	0.64 (0.46-0.68)	0.62 (0.52-0.64)
NCR1	C4B	101	63	0.6 (0.52-0.68)	0.7 (0.56-0.82)	0.65 (0.57-0.73)	0.59 (0.56-0.6)	0.64 (0.4-0.69)	0.62 (0.49-0.64)
FC	LRG1	77	44	0.69 (0.6-0.77)	0.62 (0.48-0.74)	0.65 (0.57-0.72)	0.66 (0.3-0.7)	0.58 (0.56-0.6)	0.62 (0.44-0.64)
C5	HPR	102	67	0.62 (0.54-0.69)	0.65 (0.54-0.76)	0.64 (0.56-0.7)	0.61 (0.54-0.62)	0.63 (0.56-0.64)	0.62 (0.56-0.63)
FC	CFB	77	44	0.68 (0.59-0.76)	0.64 (0.49-0.79)	0.66 (0.57-0.74)	0.62 (0.38-0.68)	0.63 (0.55-0.65)	0.62 (0.5-0.66)
MILR1	CRP_SRM	101	63	0.67 (0.59-0.75)	0.61 (0.49-0.74)	0.64 (0.57-0.72)	0.65 (0.39-0.68)	0.58 (0.55-0.61)	0.62 (0.49-0.64)
NCR1	LRG1	101	63	0.63 (0.54-0.72)	0.65 (0.54-0.75)	0.64 (0.56-0.71)	0.62 (0.52-0.63)	0.62 (0.51-0.64)	0.62 (0.55-0.63)
NCR1	IFNG	101	63	0.67 (0.59-0.75)	0.61 (0.48-0.72)	0.64 (0.57-0.72)	0.61 (0.35-0.67)	0.62 (0.59-0.63)	0.62 (0.49-0.65)
HSD11B1	HPR	101	63	0.6 (0.52-0.68)	0.67 (0.54-0.77)	0.64 (0.57-0.7)	0.59 (0.54-0.6)	0.64 (0.53-0.65)	0.62 (0.55-0.62)
VEGFA	HPR	102	63	0.6 (0.51-0.68)	0.67 (0.55-0.76)	0.63 (0.56-0.7)	0.59 (0.5-0.59)	0.65 (0.5-0.66)	0.62 (0.52-0.63)
KLRD1	CRP_SRM	101	63	0.64 (0.54-0.74)	0.63 (0.51-0.74)	0.64 (0.55-0.71)	0.63 (0.42-0.65)	0.62 (0.5-0.64)	0.62 (0.51-0.64)
CRP_SRM	HPR	102	67	0.65 (0.55-0.73)	0.64 (0.52-0.75)	0.64 (0.57-0.72)	0.61 (0.52-0.66)	0.62 (0.59-0.63)	0.62 (0.56-0.64)
LRG1	HPR	102	67	0.63 (0.55-0.71)	0.64 (0.54-0.75)	0.64 (0.57-0.71)	0.61 (0.5-0.63)	0.62 (0.56-0.63)	0.62 (0.55-0.63)
NCR1	F9	101	63	0.61 (0.52-0.69)	0.65 (0.54-0.77)	0.63 (0.56-0.7)	0.6 (0.54-0.6)	0.63 (0.48-0.64)	0.61 (0.54-0.62)
IL13	HPR	102	63	0.6 (0.51-0.68)	0.66 (0.52-0.76)	0.62 (0.55-0.69)	0.59 (0.43-0.6)	0.65 (0.56-0.65)	0.61 (0.51-0.62)
CRP_SRM	C5	102	67	0.63 (0.53-0.72)	0.64 (0.52-0.74)	0.63 (0.56-0.7)	0.62 (0.51-0.64)	0.62 (0.51-0.64)	0.61 (0.53-0.64)
hsCRP	FC	83	46	0.71 (0.61-0.79)	0.6 (0.42-0.74)	0.66 (0.56-0.73)	0.62 (0.28-0.73)	0.61 (0.6-0.61)	0.61 (0.44-0.67)
MILR1	C8B	101	63	0.67 (0.59-0.75)	0.61 (0.51-0.73)	0.64 (0.58-0.71)	0.65 (0.36-0.67)	0.59 (0.56-0.6)	0.61 (0.47-0.63)
C5	SERPINA4	102	67	0.69 (0.61-0.77)	0.63 (0.53-0.73)	0.66 (0.6-0.73)	0.64 (0.46-0.7)	0.59 (0.55-0.61)	0.61 (0.52-0.65)
F9	SERPINA4	102	67	0.65 (0.55-0.75)	0.65 (0.55-0.78)	0.65 (0.58-0.73)	0.62 (0.48-0.65)	0.61 (0.54-0.64)	0.61 (0.54-0.64)
SIT1	C4B	101	63	0.6 (0.52-0.68)	0.72 (0.59-0.84)	0.66 (0.58-0.74)	0.58 (0.55-0.59)	0.64 (0.48-0.72)	0.61 (0.53-0.65)
FC	C3	77	44	0.68 (0.59-0.76)	0.62 (0.48-0.76)	0.65 (0.56-0.73)	0.61 (0.36-0.68)	0.62 (0.56-0.63)	0.61 (0.48-0.65)
CDSN	HPR	101	63	0.59 (0.5-0.67)	0.69 (0.57-0.79)	0.64 (0.57-0.71)	0.57 (0.53-0.59)	0.66 (0.52-0.68)	0.61 (0.55-0.63)
FC	FLT3LG	77	43	0.69 (0.59-0.79)	0.65 (0.51-0.78)	0.67 (0.58-0.76)	0.63 (0.42-0.68)	0.61 (0.5-0.62)	0.61 (0.51-0.65)
FGF2	HPR	101	63	0.59 (0.51-0.67)	0.7 (0.58-0.8)	0.64 (0.57-0.72)	0.57 (0.52-0.59)	0.66 (0.48-0.7)	0.61 (0.52-0.64)

HPR	APCS	102	67	0.62 (0.53-0.69)	0.65 (0.55-0.76)	0.63 (0.56-0.7)	0.61 (0.52-0.61)	0.62 (0.52-0.63)	0.61 (0.54-0.62)
CLEC4C	C4B	101	63	0.58 (0.5-0.66)	0.69 (0.55-0.82)	0.64 (0.56-0.71)	0.56 (0.53-0.57)	0.67 (0.31-0.7)	0.61 (0.43-0.63)
FLT3LG	C4B	102	63	0.62 (0.54-0.7)	0.69 (0.55-0.83)	0.66 (0.57-0.73)	0.6 (0.54-0.61)	0.63 (0.51-0.69)	0.61 (0.55-0.65)
HGF	HPR	102	63	0.6 (0.51-0.68)	0.67 (0.55-0.76)	0.63 (0.56-0.69)	0.59 (0.49-0.6)	0.64 (0.48-0.65)	0.61 (0.52-0.62)
C2	C4B	102	67	0.58 (0.49-0.66)	0.7 (0.57-0.82)	0.64 (0.56-0.71)	0.56 (0.53-0.57)	0.66 (0.31-0.7)	0.61 (0.43-0.63)
PLXNA4	C4B	101	63	0.58 (0.5-0.66)	0.7 (0.57-0.82)	0.64 (0.57-0.71)	0.57 (0.53-0.58)	0.66 (0.33-0.69)	0.61 (0.45-0.63)
TNF	HPR	102	63	0.6 (0.51-0.67)	0.67 (0.55-0.77)	0.63 (0.56-0.7)	0.58 (0.55-0.59)	0.64 (0.53-0.66)	0.61 (0.55-0.62)
SIT1	C8B	101	63	0.63 (0.55-0.71)	0.64 (0.53-0.74)	0.63 (0.57-0.7)	0.62 (0.49-0.64)	0.6 (0.55-0.63)	0.61 (0.55-0.63)
FLT3LG	SAA1	102	63	0.62 (0.54-0.72)	0.62 (0.51-0.74)	0.62 (0.55-0.7)	0.61 (0.49-0.62)	0.61 (0.6-0.63)	0.61 (0.55-0.62)
SERPIND1	APOA1	102	67	0.64 (0.55-0.71)	0.67 (0.57-0.77)	0.65 (0.58-0.72)	0.59 (0.53-0.63)	0.63 (0.54-0.66)	0.61 (0.56-0.64)
hsCRP	CDSN	98	63	0.63 (0.53-0.72)	0.64 (0.52-0.78)	0.64 (0.56-0.72)	0.59 (0.49-0.65)	0.65 (0.53-0.68)	0.61 (0.53-0.66)
CCL13	HPR	102	63	0.6 (0.51-0.68)	0.67 (0.56-0.77)	0.63 (0.56-0.7)	0.59 (0.52-0.59)	0.64 (0.46-0.67)	0.61 (0.52-0.63)
F9	HPR	102	67	0.61 (0.53-0.69)	0.66 (0.56-0.77)	0.63 (0.57-0.7)	0.59 (0.52-0.6)	0.63 (0.52-0.64)	0.61 (0.54-0.62)
FC	ORM1	77	44	0.7 (0.59-0.78)	0.63 (0.49-0.76)	0.66 (0.58-0.75)	0.63 (0.32-0.7)	0.6 (0.52-0.61)	0.61 (0.46-0.65)
CXCL9	HPR	102	63	0.68 (0.6-0.75)	0.67 (0.53-0.77)	0.68 (0.59-0.74)	0.58 (0.45-0.68)	0.64 (0.51-0.66)	0.61 (0.52-0.67)
SIT1	APCS	101	63	0.62 (0.53-0.7)	0.63 (0.54-0.74)	0.63 (0.56-0.69)	0.61 (0.52-0.62)	0.62 (0.53-0.63)	0.61 (0.56-0.62)
hsCRP	IL15	98	63	0.63 (0.48-0.72)	0.65 (0.52-0.77)	0.64 (0.55-0.71)	0.62 (0.53-0.64)	0.6 (0.43-0.66)	0.61 (0.51-0.65)
hsCRP	NCR1	98	63	0.63 (0.51-0.71)	0.64 (0.54-0.75)	0.64 (0.56-0.7)	0.6 (0.55-0.63)	0.63 (0.49-0.64)	0.61 (0.53-0.63)
C5	C2	102	67	0.63 (0.53-0.71)	0.63 (0.5-0.74)	0.63 (0.55-0.7)	0.61 (0.51-0.62)	0.61 (0.53-0.62)	0.61 (0.53-0.62)
KLRD1	HPR	101	63	0.61 (0.53-0.7)	0.67 (0.54-0.76)	0.64 (0.56-0.7)	0.59 (0.5-0.61)	0.64 (0.51-0.66)	0.61 (0.52-0.63)
MASP1	HPR	101	63	0.62 (0.54-0.7)	0.67 (0.54-0.77)	0.64 (0.57-0.71)	0.59 (0.43-0.61)	0.63 (0.57-0.65)	0.61 (0.52-0.63)
IL13	C5	102	63	0.62 (0.49-0.7)	0.63 (0.5-0.74)	0.62 (0.54-0.69)	0.61 (0.39-0.61)	0.62 (0.45-0.62)	0.61 (0.48-0.62)
MILR1	FLT3LG	101	63	0.66 (0.58-0.75)	0.61 (0.51-0.72)	0.64 (0.57-0.71)	0.63 (0.4-0.66)	0.59 (0.55-0.6)	0.61 (0.49-0.63)
SAA1	APCS	102	67	0.6 (0.5-0.69)	0.64 (0.53-0.75)	0.62 (0.54-0.69)	0.59 (0.48-0.6)	0.64 (0.44-0.64)	0.61 (0.49-0.62)
hsCRP	HPR	98	67	0.64 (0.54-0.73)	0.64 (0.51-0.75)	0.64 (0.57-0.71)	0.6 (0.51-0.66)	0.62 (0.59-0.63)	0.61 (0.55-0.64)
IL6_PEA_cytokine	HPR	102	63	0.61 (0.51-0.69)	0.66 (0.53-0.77)	0.63 (0.55-0.7)	0.58 (0.55-0.61)	0.65 (0.44-0.65)	0.61 (0.51-0.63)
IL6_PEA_IR	HPR	101	63	0.61 (0.53-0.69)	0.66 (0.54-0.77)	0.64 (0.56-0.71)	0.6 (0.45-0.62)	0.63 (0.44-0.66)	0.61 (0.51-0.63)
FLT3LG	APCS	102	63	0.62 (0.54-0.71)	0.64 (0.53-0.77)	0.63 (0.56-0.71)	0.61 (0.51-0.62)	0.61 (0.51-0.64)	0.61 (0.55-0.63)
IL7	HP	102	63	0.68 (0.61-0.76)	0.65 (0.55-0.76)	0.67 (0.6-0.74)	0.64 (0.48-0.69)	0.58 (0.51-0.63)	0.61 (0.53-0.65)
CP	C4B	102	67	0.58 (0.49-0.66)	0.69 (0.57-0.81)	0.63 (0.56-0.71)	0.56 (0.55-0.57)	0.66 (0.32-0.68)	0.61 (0.44-0.62)

NCR1	SAA1	101	63	0.61 (0.52-0.69)	0.63 (0.51-0.74)	0.62 (0.55-0.69)	0.6 (0.48-0.61)	0.62 (0.48-0.64)	0.61 (0.51-0.62)
FGF2	C5	101	63	0.62 (0.53-0.7)	0.68 (0.52-0.78)	0.65 (0.56-0.72)	0.58 (0.52-0.61)	0.63 (0.41-0.69)	0.61 (0.49-0.64)
CDSN	C4B	101	63	0.58 (0.49-0.66)	0.69 (0.55-0.82)	0.63 (0.55-0.72)	0.56 (0.54-0.57)	0.65 (0.34-0.69)	0.61 (0.45-0.63)
LRG1	APCS	102	67	0.62 (0.51-0.7)	0.64 (0.54-0.76)	0.63 (0.55-0.7)	0.6 (0.5-0.61)	0.62 (0.44-0.64)	0.61 (0.51-0.62)
CCL4	HPR	102	63	0.6 (0.51-0.68)	0.67 (0.55-0.76)	0.63 (0.56-0.7)	0.58 (0.43-0.6)	0.64 (0.5-0.67)	0.61 (0.52-0.63)
IL15	LRG1	102	63	0.62 (0.5-0.71)	0.64 (0.51-0.74)	0.63 (0.54-0.69)	0.62 (0.48-0.64)	0.59 (0.47-0.64)	0.61 (0.51-0.64)
FLT3LG	ORM1	102	63	0.63 (0.54-0.72)	0.64 (0.53-0.74)	0.63 (0.56-0.7)	0.61 (0.5-0.62)	0.61 (0.53-0.62)	0.61 (0.55-0.62)
SIT1	ORM1	101	63	0.62 (0.53-0.71)	0.65 (0.55-0.74)	0.63 (0.57-0.7)	0.62 (0.53-0.62)	0.61 (0.53-0.63)	0.61 (0.55-0.63)
MILR1	ORM1	101	63	0.68 (0.61-0.76)	0.61 (0.51-0.73)	0.65 (0.58-0.72)	0.64 (0.38-0.68)	0.57 (0.54-0.6)	0.61 (0.48-0.64)
FLT3LG	ITIH3	102	63	0.63 (0.55-0.72)	0.62 (0.53-0.73)	0.63 (0.57-0.69)	0.61 (0.47-0.63)	0.61 (0.54-0.62)	0.61 (0.54-0.62)
MILR1	APOA1	101	63	0.67 (0.58-0.74)	0.6 (0.51-0.7)	0.63 (0.56-0.7)	0.64 (0.36-0.66)	0.58 (0.54-0.59)	0.61 (0.47-0.62)
hsCRP	VEGFA	98	63	0.63 (0.51-0.73)	0.62 (0.51-0.76)	0.63 (0.54-0.7)	0.61 (0.41-0.63)	0.61 (0.46-0.63)	0.61 (0.5-0.63)
CXCL9	IL15	102	63	0.69 (0.59-0.76)	0.58 (0.46-0.7)	0.63 (0.56-0.7)	0.66 (0.39-0.71)	0.56 (0.53-0.59)	0.61 (0.47-0.64)
IL15	C5	102	63	0.62 (0.5-0.7)	0.66 (0.53-0.76)	0.64 (0.56-0.71)	0.62 (0.55-0.63)	0.59 (0.49-0.66)	0.61 (0.53-0.64)
MASP1	C5	101	63	0.65 (0.57-0.74)	0.64 (0.53-0.75)	0.64 (0.57-0.72)	0.61 (0.45-0.66)	0.61 (0.57-0.62)	0.61 (0.51-0.64)
FLT3LG	CFB	102	63	0.61 (0.54-0.7)	0.64 (0.53-0.75)	0.63 (0.56-0.7)	0.6 (0.5-0.61)	0.61 (0.53-0.64)	0.61 (0.54-0.62)
IL6_PEA_cytokine	C5	102	63	0.63 (0.51-0.71)	0.63 (0.51-0.75)	0.63 (0.55-0.71)	0.6 (0.48-0.62)	0.62 (0.49-0.63)	0.61 (0.51-0.62)
NCR1	CFB	101	63	0.6 (0.52-0.68)	0.65 (0.54-0.75)	0.62 (0.56-0.7)	0.6 (0.52-0.61)	0.62 (0.47-0.64)	0.61 (0.53-0.62)
ITIH3	HPR	102	67	0.62 (0.55-0.7)	0.65 (0.54-0.76)	0.64 (0.56-0.71)	0.6 (0.48-0.62)	0.62 (0.56-0.63)	0.61 (0.54-0.63)
HGF	C4B	102	63	0.58 (0.47-0.67)	0.68 (0.55-0.81)	0.63 (0.55-0.71)	0.56 (0.53-0.59)	0.66 (0.33-0.68)	0.61 (0.44-0.63)
C5	C8B	102	67	0.63 (0.55-0.72)	0.63 (0.52-0.74)	0.63 (0.56-0.7)	0.63 (0.46-0.64)	0.59 (0.51-0.61)	0.61 (0.52-0.62)
C4B	ORM1	102	67	0.6 (0.5-0.69)	0.7 (0.57-0.82)	0.64 (0.57-0.72)	0.57 (0.55-0.59)	0.65 (0.33-0.69)	0.61 (0.45-0.63)
hsCRP	CRP_SRM	98	67	0.61 (0.47-0.7)	0.6 (0.47-0.73)	0.61 (0.51-0.68)	0.6 (0.42-0.63)	0.6 (0.43-0.64)	0.61 (0.5-0.63)
IL15	F9	102	63	0.59 (0.47-0.68)	0.68 (0.55-0.8)	0.63 (0.55-0.71)	0.6 (0.57-0.6)	0.62 (0.35-0.67)	0.61 (0.47-0.63)
HPR	CFB	102	67	0.6 (0.53-0.68)	0.65 (0.54-0.76)	0.62 (0.56-0.69)	0.59 (0.52-0.6)	0.62 (0.53-0.63)	0.61 (0.53-0.61)
FCRL6	HPR	101	63	0.59 (0.51-0.68)	0.69 (0.58-0.77)	0.64 (0.57-0.7)	0.58 (0.5-0.59)	0.64 (0.42-0.68)	0.61 (0.5-0.63)
NCR1	APCS	101	63	0.61 (0.52-0.69)	0.64 (0.53-0.75)	0.62 (0.56-0.7)	0.61 (0.5-0.61)	0.61 (0.46-0.63)	0.61 (0.52-0.62)
MASP1	SIT1	102	63	0.63 (0.54-0.71)	0.62 (0.51-0.76)	0.62 (0.56-0.7)	0.61 (0.39-0.62)	0.61 (0.58-0.62)	0.61 (0.5-0.62)
HP	MBL2	102	67	0.67 (0.58-0.74)	0.69 (0.57-0.8)	0.68 (0.61-0.75)	0.59 (0.52-0.67)	0.63 (0.55-0.66)	0.61 (0.55-0.65)
LAMP3	APOA1	101	63	0.64 (0.55-0.72)	0.63 (0.53-0.74)	0.63 (0.57-0.7)	0.64 (0.51-0.65)	0.58 (0.51-0.62)	0.61 (0.53-0.63)

hsCRP	KLRD1	98	63	0.63 (0.52-0.72)	0.63 (0.51-0.75)	0.63 (0.54-0.7)	0.62 (0.44-0.63)	0.62 (0.48-0.63)	0.61 (0.5-0.63)
NCR1	SIT1	102	63	0.62 (0.53-0.7)	0.64 (0.53-0.74)	0.63 (0.56-0.69)	0.61 (0.53-0.62)	0.61 (0.55-0.62)	0.61 (0.55-0.62)
IL13	C4B	102	63	0.58 (0.45-0.65)	0.67 (0.54-0.8)	0.62 (0.53-0.7)	0.56 (0.55-0.57)	0.65 (0.38-0.67)	0.61 (0.46-0.62)
FC	CRP_SRM	77	44	0.7 (0.61-0.78)	0.6 (0.42-0.76)	0.65 (0.55-0.73)	0.61 (0.29-0.72)	0.59 (0.59-0.62)	0.6 (0.44-0.66)
C4B	CFB	102	67	0.58 (0.49-0.66)	0.69 (0.56-0.81)	0.63 (0.56-0.71)	0.57 (0.53-0.57)	0.65 (0.33-0.69)	0.6 (0.45-0.63)
SIT1	FLT3LG	101	63	0.61 (0.54-0.7)	0.62 (0.53-0.74)	0.62 (0.56-0.69)	0.6 (0.48-0.61)	0.61 (0.57-0.63)	0.6 (0.55-0.62)
MILR1	HPR	101	63	0.64 (0.56-0.72)	0.66 (0.54-0.77)	0.65 (0.58-0.72)	0.61 (0.45-0.64)	0.6 (0.53-0.65)	0.6 (0.52-0.64)
HPR	SERPINA4	102	67	0.63 (0.54-0.73)	0.65 (0.54-0.76)	0.64 (0.56-0.71)	0.62 (0.49-0.64)	0.6 (0.51-0.64)	0.6 (0.52-0.63)
MILR1	NCR1	102	63	0.66 (0.57-0.73)	0.62 (0.51-0.72)	0.64 (0.57-0.7)	0.64 (0.41-0.65)	0.58 (0.54-0.61)	0.6 (0.49-0.63)
ITIH1	APOA1	102	67	0.63 (0.56-0.7)	0.64 (0.54-0.75)	0.64 (0.58-0.7)	0.6 (0.51-0.62)	0.61 (0.55-0.63)	0.6 (0.55-0.62)
IL13	FLT3LG	102	63	0.61 (0.52-0.7)	0.63 (0.52-0.73)	0.62 (0.55-0.7)	0.6 (0.41-0.6)	0.62 (0.54-0.63)	0.6 (0.51-0.61)
SIT1	IFNG	101	63	0.72 (0.64-0.79)	0.6 (0.49-0.72)	0.66 (0.6-0.73)	0.61 (0.3-0.72)	0.6 (0.58-0.62)	0.6 (0.45-0.66)
APCS	APOA1	102	67	0.65 (0.56-0.72)	0.63 (0.53-0.73)	0.64 (0.57-0.7)	0.61 (0.53-0.64)	0.59 (0.55-0.62)	0.6 (0.55-0.63)
SH2D1A	HPR	101	63	0.59 (0.51-0.67)	0.67 (0.54-0.77)	0.63 (0.55-0.7)	0.58 (0.49-0.59)	0.65 (0.5-0.66)	0.6 (0.53-0.62)
CXCL9	IFNG	102	63	0.68 (0.59-0.76)	0.56 (0.41-0.71)	0.62 (0.53-0.71)	0.6 (0.31-0.69)	0.6 (0.57-0.62)	0.6 (0.45-0.64)
FC	F9	77	44	0.67 (0.59-0.76)	0.64 (0.52-0.78)	0.66 (0.58-0.73)	0.6 (0.4-0.67)	0.63 (0.51-0.64)	0.6 (0.49-0.64)
MASP1	CRP_SRM	101	63	0.65 (0.55-0.73)	0.62 (0.48-0.75)	0.63 (0.55-0.72)	0.59 (0.43-0.65)	0.62 (0.54-0.66)	0.6 (0.51-0.65)
hsCRP	MASP1	98	63	0.64 (0.53-0.73)	0.62 (0.48-0.76)	0.63 (0.54-0.71)	0.59 (0.45-0.64)	0.63 (0.52-0.66)	0.6 (0.51-0.65)
IL10_PEA_IR	HPR	101	63	0.61 (0.53-0.71)	0.66 (0.51-0.77)	0.64 (0.56-0.71)	0.58 (0.52-0.61)	0.62 (0.6-0.65)	0.6 (0.56-0.62)
FC	APCS	77	44	0.69 (0.59-0.77)	0.62 (0.47-0.76)	0.65 (0.56-0.74)	0.62 (0.34-0.7)	0.6 (0.56-0.61)	0.6 (0.47-0.65)
HSD11B1	C5	101	63	0.62 (0.52-0.71)	0.63 (0.53-0.75)	0.63 (0.56-0.7)	0.61 (0.5-0.62)	0.6 (0.51-0.63)	0.6 (0.53-0.62)
IL13	CRP_SRM	102	63	0.62 (0.49-0.71)	0.6 (0.44-0.75)	0.61 (0.52-0.7)	0.61 (0.39-0.63)	0.61 (0.45-0.62)	0.6 (0.47-0.62)
FLT3LG	APOA1	102	63	0.63 (0.55-0.71)	0.61 (0.52-0.72)	0.62 (0.56-0.69)	0.62 (0.48-0.62)	0.6 (0.54-0.61)	0.6 (0.53-0.61)
hsCRP	TNF	98	63	0.61 (0.51-0.7)	0.62 (0.52-0.74)	0.62 (0.54-0.69)	0.6 (0.45-0.63)	0.61 (0.53-0.63)	0.6 (0.52-0.62)
LAMP3	C5	101	63	0.62 (0.5-0.7)	0.65 (0.55-0.74)	0.63 (0.56-0.7)	0.6 (0.53-0.61)	0.61 (0.44-0.65)	0.6 (0.52-0.62)
KLRD1	C5	101	63	0.63 (0.54-0.71)	0.63 (0.54-0.74)	0.63 (0.57-0.7)	0.62 (0.5-0.63)	0.6 (0.51-0.62)	0.6 (0.53-0.62)
hsCRP	IL13	98	63	0.63 (0.48-0.71)	0.6 (0.45-0.75)	0.61 (0.52-0.7)	0.62 (0.39-0.62)	0.6 (0.43-0.61)	0.6 (0.48-0.61)
CDSN	C5	101	63	0.61 (0.52-0.69)	0.65 (0.54-0.76)	0.63 (0.55-0.71)	0.59 (0.49-0.61)	0.62 (0.48-0.64)	0.6 (0.52-0.62)
CLEC4C	C5	101	63	0.62 (0.52-0.69)	0.64 (0.54-0.75)	0.63 (0.56-0.7)	0.6 (0.53-0.61)	0.62 (0.42-0.64)	0.6 (0.5-0.62)
ITGA11	C4B	101	63	0.63 (0.53-0.71)	0.69 (0.56-0.83)	0.66 (0.58-0.74)	0.58 (0.44-0.63)	0.67 (0.35-0.68)	0.6 (0.45-0.65)

hsCRP	C4BPB	98	67	0.64 (0.53-0.72)	0.62 (0.51-0.75)	0.63 (0.55-0.71)	0.62 (0.47-0.65)	0.61 (0.48-0.64)	0.6 (0.52-0.64)
hsCRP	C8A	98	67	0.64 (0.55-0.72)	0.63 (0.52-0.74)	0.63 (0.56-0.71)	0.62 (0.44-0.65)	0.61 (0.47-0.64)	0.6 (0.5-0.64)
FGF2	SAA1	101	63	0.56 (0.48-0.65)	0.68 (0.43-0.81)	0.62 (0.49-0.7)	0.54 (0.45-0.57)	0.66 (0.43-0.68)	0.6 (0.49-0.62)
SIT1	CFB	101	63	0.6 (0.51-0.68)	0.66 (0.54-0.77)	0.63 (0.56-0.7)	0.6 (0.55-0.6)	0.63 (0.51-0.65)	0.6 (0.54-0.62)
SERPINA3	HPR	102	67	0.62 (0.53-0.69)	0.64 (0.52-0.76)	0.63 (0.55-0.7)	0.59 (0.46-0.61)	0.62 (0.52-0.63)	0.6 (0.52-0.62)
C5	ORM1	102	67	0.62 (0.52-0.71)	0.63 (0.54-0.74)	0.63 (0.56-0.7)	0.62 (0.5-0.63)	0.61 (0.47-0.62)	0.6 (0.52-0.62)
C3	HPR	102	67	0.61 (0.53-0.68)	0.64 (0.53-0.75)	0.63 (0.55-0.69)	0.59 (0.51-0.6)	0.62 (0.52-0.63)	0.6 (0.53-0.62)
IFNG	APOA1	102	63	0.7 (0.62-0.77)	0.58 (0.45-0.71)	0.65 (0.56-0.72)	0.62 (0.29-0.71)	0.59 (0.55-0.62)	0.6 (0.44-0.66)
hsCRP	ITIH1	98	67	0.62 (0.52-0.71)	0.64 (0.52-0.76)	0.63 (0.55-0.71)	0.6 (0.49-0.63)	0.62 (0.49-0.64)	0.6 (0.53-0.63)
F9	C4B	102	67	0.58 (0.5-0.67)	0.69 (0.57-0.82)	0.64 (0.57-0.71)	0.57 (0.54-0.57)	0.64 (0.37-0.69)	0.6 (0.47-0.63)
VEGFA	C5	102	63	0.62 (0.52-0.7)	0.63 (0.53-0.73)	0.62 (0.55-0.69)	0.6 (0.47-0.61)	0.61 (0.51-0.63)	0.6 (0.51-0.62)
hsCRP	ITIH2	98	67	0.62 (0.52-0.72)	0.62 (0.52-0.73)	0.62 (0.55-0.7)	0.61 (0.49-0.63)	0.6 (0.48-0.62)	0.6 (0.52-0.62)
IL15	C4B	102	63	0.58 (0.48-0.66)	0.69 (0.56-0.83)	0.63 (0.55-0.72)	0.57 (0.56-0.58)	0.63 (0.31-0.7)	0.6 (0.44-0.64)
TNF	CRP_SRM	102	63	0.61 (0.51-0.7)	0.62 (0.51-0.74)	0.61 (0.54-0.69)	0.6 (0.44-0.63)	0.62 (0.52-0.63)	0.6 (0.52-0.62)
FGF2	CFB	101	63	0.58 (0.5-0.66)	0.69 (0.52-0.81)	0.63 (0.54-0.71)	0.55 (0.5-0.57)	0.65 (0.33-0.7)	0.6 (0.44-0.63)
FLT3LG	SERPINA3	102	63	0.62 (0.54-0.71)	0.62 (0.51-0.75)	0.62 (0.55-0.7)	0.61 (0.45-0.61)	0.61 (0.53-0.62)	0.6 (0.52-0.62)
MASP1	FLT3LG	101	63	0.63 (0.54-0.72)	0.61 (0.5-0.75)	0.62 (0.55-0.7)	0.61 (0.4-0.63)	0.6 (0.57-0.61)	0.6 (0.5-0.62)
HSD11B1	C4B	101	63	0.59 (0.5-0.68)	0.68 (0.56-0.81)	0.63 (0.57-0.72)	0.58 (0.54-0.58)	0.63 (0.35-0.68)	0.6 (0.46-0.63)
LRG1	C8B	102	67	0.63 (0.53-0.71)	0.62 (0.52-0.72)	0.62 (0.56-0.69)	0.62 (0.41-0.63)	0.59 (0.51-0.62)	0.6 (0.5-0.62)
VEGFA	CRP_SRM	102	63	0.63 (0.5-0.72)	0.63 (0.51-0.75)	0.63 (0.54-0.7)	0.61 (0.4-0.63)	0.61 (0.46-0.64)	0.6 (0.5-0.63)
LAMP3	CRP_SRM	101	63	0.62 (0.5-0.71)	0.64 (0.53-0.74)	0.63 (0.55-0.7)	0.61 (0.52-0.63)	0.59 (0.45-0.64)	0.6 (0.51-0.63)
HP	SERPIND1	102	67	0.7 (0.62-0.77)	0.65 (0.56-0.76)	0.68 (0.61-0.75)	0.62 (0.42-0.69)	0.6 (0.51-0.64)	0.6 (0.5-0.66)
NCR1	ITGA11	102	63	0.66 (0.56-0.74)	0.62 (0.51-0.73)	0.64 (0.57-0.7)	0.61 (0.41-0.66)	0.59 (0.57-0.6)	0.6 (0.5-0.63)
MASP1	CXCL9	101	63	0.69 (0.6-0.77)	0.61 (0.44-0.75)	0.65 (0.56-0.73)	0.62 (0.32-0.69)	0.61 (0.52-0.63)	0.6 (0.44-0.66)
HGF	C5	102	63	0.62 (0.51-0.7)	0.63 (0.51-0.73)	0.62 (0.55-0.69)	0.6 (0.49-0.61)	0.61 (0.5-0.62)	0.6 (0.51-0.61)
MILR1	LRG1	101	63	0.67 (0.59-0.75)	0.6 (0.5-0.71)	0.63 (0.57-0.7)	0.63 (0.36-0.67)	0.57 (0.55-0.59)	0.6 (0.46-0.62)
FC	NCR1	76	43	0.69 (0.6-0.78)	0.63 (0.5-0.74)	0.66 (0.58-0.73)	0.62 (0.38-0.69)	0.6 (0.52-0.62)	0.6 (0.47-0.64)
LRG1	C5	102	67	0.62 (0.52-0.71)	0.62 (0.52-0.73)	0.62 (0.55-0.69)	0.61 (0.47-0.62)	0.61 (0.5-0.62)	0.6 (0.51-0.62)
PLXNA4	C5	101	63	0.62 (0.53-0.7)	0.66 (0.54-0.77)	0.64 (0.56-0.7)	0.59 (0.48-0.62)	0.62 (0.42-0.65)	0.6 (0.5-0.63)
IL6_PEA_IR	C4B	101	63	0.61 (0.5-0.7)	0.68 (0.54-0.83)	0.64 (0.55-0.73)	0.55 (0.47-0.61)	0.65 (0.37-0.68)	0.6 (0.46-0.64)

APCS	SERPINA4	102	67	0.64 (0.56-0.72)	0.62 (0.52-0.73)	0.63 (0.57-0.7)	0.63 (0.46-0.64)	0.58 (0.52-0.6)	0.6 (0.52-0.62)
FLT3LG	C3	102	63	0.62 (0.53-0.7)	0.63 (0.52-0.76)	0.62 (0.55-0.7)	0.6 (0.53-0.62)	0.6 (0.53-0.62)	0.6 (0.56-0.61)
NCR1	APOA1	101	63	0.64 (0.56-0.71)	0.62 (0.51-0.73)	0.63 (0.56-0.7)	0.62 (0.46-0.63)	0.59 (0.56-0.61)	0.6 (0.52-0.62)
TNF	C5	102	63	0.61 (0.53-0.7)	0.63 (0.52-0.74)	0.62 (0.55-0.69)	0.6 (0.5-0.61)	0.6 (0.53-0.62)	0.6 (0.53-0.61)
IFNG	APCS	102	63	0.67 (0.59-0.74)	0.62 (0.49-0.73)	0.64 (0.57-0.71)	0.58 (0.37-0.65)	0.63 (0.55-0.64)	0.6 (0.5-0.64)
ITGA11	CRP_SRM	101	63	0.65 (0.53-0.73)	0.61 (0.48-0.74)	0.63 (0.55-0.71)	0.63 (0.4-0.66)	0.58 (0.48-0.63)	0.6 (0.49-0.64)
IL15	SAA1	102	63	0.61 (0.49-0.7)	0.6 (0.48-0.72)	0.6 (0.52-0.68)	0.6 (0.5-0.61)	0.61 (0.5-0.62)	0.6 (0.53-0.62)
MASP1	C8B	101	63	0.64 (0.54-0.72)	0.61 (0.51-0.75)	0.63 (0.56-0.71)	0.62 (0.38-0.64)	0.58 (0.54-0.6)	0.6 (0.48-0.62)
hsCRP	CCL13	98	63	0.62 (0.53-0.72)	0.64 (0.51-0.76)	0.63 (0.56-0.7)	0.59 (0.49-0.63)	0.61 (0.47-0.64)	0.6 (0.52-0.63)
CXCL9	C5	102	63	0.68 (0.58-0.75)	0.63 (0.52-0.74)	0.65 (0.58-0.72)	0.6 (0.42-0.67)	0.6 (0.51-0.62)	0.6 (0.49-0.65)
IFNG	HPR	102	63	0.69 (0.61-0.76)	0.66 (0.53-0.77)	0.68 (0.6-0.74)	0.58 (0.45-0.67)	0.63 (0.5-0.64)	0.6 (0.49-0.65)
MILR1	LAMP3	102	63	0.65 (0.56-0.72)	0.63 (0.52-0.75)	0.64 (0.57-0.71)	0.63 (0.4-0.64)	0.58 (0.53-0.64)	0.6 (0.5-0.64)
ITGA11	C8B	101	63	0.64 (0.57-0.72)	0.61 (0.49-0.72)	0.63 (0.56-0.7)	0.63 (0.38-0.64)	0.58 (0.5-0.59)	0.6 (0.48-0.61)
SIT1	ITIH3	101	63	0.62 (0.53-0.69)	0.63 (0.54-0.73)	0.62 (0.56-0.68)	0.6 (0.47-0.61)	0.61 (0.54-0.63)	0.6 (0.53-0.62)
ITGA11	SIT1	102	63	0.65 (0.55-0.73)	0.61 (0.51-0.73)	0.63 (0.56-0.7)	0.61 (0.4-0.65)	0.59 (0.57-0.6)	0.6 (0.5-0.62)
CP	APOA1	102	67	0.62 (0.53-0.7)	0.67 (0.55-0.78)	0.64 (0.56-0.71)	0.61 (0.53-0.62)	0.6 (0.44-0.65)	0.6 (0.51-0.63)
SIT1	C3	101	63	0.6 (0.51-0.68)	0.65 (0.54-0.76)	0.63 (0.56-0.7)	0.59 (0.54-0.6)	0.62 (0.53-0.64)	0.6 (0.55-0.62)
hsCRP	IFNG	98	63	0.68 (0.6-0.77)	0.62 (0.47-0.75)	0.65 (0.57-0.73)	0.6 (0.33-0.69)	0.61 (0.53-0.62)	0.6 (0.47-0.65)
CRP_SRM	C4BPB	102	67	0.64 (0.53-0.73)	0.62 (0.51-0.74)	0.63 (0.55-0.71)	0.62 (0.45-0.65)	0.61 (0.48-0.64)	0.6 (0.51-0.64)
C4B	SERPIND1	102	67	0.57 (0.49-0.66)	0.69 (0.57-0.8)	0.63 (0.56-0.71)	0.56 (0.55-0.57)	0.64 (0.32-0.68)	0.6 (0.44-0.62)
IL17C	HPR	102	63	0.63 (0.54-0.71)	0.67 (0.54-0.77)	0.65 (0.57-0.71)	0.56 (0.49-0.64)	0.64 (0.53-0.65)	0.6 (0.52-0.64)
HPR	C8A	102	67	0.62 (0.53-0.69)	0.64 (0.52-0.76)	0.63 (0.55-0.7)	0.59 (0.48-0.61)	0.62 (0.51-0.63)	0.6 (0.52-0.62)
ITIH3	APCS	102	67	0.61 (0.52-0.69)	0.63 (0.53-0.75)	0.62 (0.56-0.69)	0.61 (0.43-0.62)	0.6 (0.44-0.62)	0.6 (0.5-0.62)
IL6_PEA_cytokine	CFB	102	63	0.6 (0.47-0.67)	0.64 (0.49-0.79)	0.62 (0.52-0.7)	0.56 (0.41-0.59)	0.64 (0.36-0.66)	0.6 (0.45-0.62)
LAMP3	F9	101	63	0.59 (0.48-0.68)	0.65 (0.55-0.76)	0.62 (0.54-0.68)	0.58 (0.53-0.59)	0.62 (0.38-0.65)	0.6 (0.48-0.61)
NCR1	C3	101	63	0.61 (0.52-0.68)	0.63 (0.52-0.76)	0.62 (0.55-0.69)	0.61 (0.49-0.61)	0.6 (0.49-0.61)	0.6 (0.52-0.61)
F9	ORM1	102	67	0.6 (0.51-0.69)	0.65 (0.54-0.75)	0.62 (0.55-0.69)	0.58 (0.49-0.59)	0.63 (0.38-0.64)	0.6 (0.48-0.62)
C4B	SERPINA4	102	67	0.65 (0.55-0.74)	0.69 (0.57-0.82)	0.67 (0.59-0.74)	0.57 (0.51-0.65)	0.63 (0.54-0.7)	0.6 (0.54-0.66)
C4B	CLU	102	67	0.61 (0.5-0.7)	0.68 (0.57-0.82)	0.64 (0.57-0.72)	0.56 (0.53-0.61)	0.63 (0.38-0.69)	0.6 (0.48-0.63)
F9	APCS	102	67	0.59 (0.5-0.68)	0.65 (0.53-0.76)	0.62 (0.55-0.69)	0.58 (0.48-0.59)	0.63 (0.38-0.64)	0.6 (0.48-0.61)

NCR1	FLT3LG	101	63	0.61 (0.54-0.71)	0.65 (0.53-0.74)	0.63 (0.56-0.7)	0.6 (0.54-0.62)	0.59 (0.56-0.65)	0.6 (0.55-0.63)
IFNG	C5	102	63	0.69 (0.6-0.76)	0.64 (0.53-0.75)	0.66 (0.59-0.73)	0.56 (0.44-0.68)	0.64 (0.58-0.65)	0.6 (0.53-0.66)
HGF	FLT3LG	102	63	0.62 (0.54-0.7)	0.62 (0.5-0.76)	0.62 (0.55-0.69)	0.6 (0.46-0.61)	0.61 (0.54-0.62)	0.6 (0.53-0.61)
KLRD1	C4B	101	63	0.61 (0.52-0.68)	0.69 (0.56-0.82)	0.64 (0.57-0.73)	0.58 (0.52-0.6)	0.63 (0.39-0.69)	0.6 (0.48-0.64)
MILR1	IFNG	101	63	0.72 (0.65-0.79)	0.59 (0.44-0.71)	0.65 (0.58-0.73)	0.61 (0.29-0.72)	0.61 (0.54-0.62)	0.6 (0.44-0.67)
C4B	APCS	102	67	0.59 (0.5-0.67)	0.68 (0.56-0.8)	0.63 (0.57-0.71)	0.58 (0.56-0.59)	0.62 (0.37-0.68)	0.6 (0.47-0.63)
VEGFA	C4B	102	63	0.58 (0.47-0.66)	0.68 (0.54-0.81)	0.62 (0.54-0.71)	0.56 (0.52-0.57)	0.64 (0.34-0.67)	0.6 (0.45-0.62)
IFNG	CRP_SRM	102	63	0.7 (0.6-0.77)	0.62 (0.46-0.75)	0.65 (0.57-0.74)	0.59 (0.32-0.7)	0.61 (0.54-0.62)	0.6 (0.46-0.65)
LAMP3	SIT1	102	63	0.6 (0.52-0.68)	0.66 (0.55-0.76)	0.63 (0.57-0.69)	0.59 (0.53-0.6)	0.6 (0.5-0.66)	0.6 (0.54-0.63)
C5	APCS	102	67	0.61 (0.51-0.7)	0.62 (0.52-0.74)	0.62 (0.55-0.69)	0.61 (0.51-0.61)	0.59 (0.46-0.61)	0.6 (0.52-0.61)
IL6_PEA_IR	FLT3LG	101	63	0.63 (0.55-0.72)	0.62 (0.51-0.73)	0.63 (0.56-0.7)	0.6 (0.44-0.64)	0.6 (0.54-0.61)	0.6 (0.51-0.62)
IL17F	HPR	102	63	0.6 (0.51-0.69)	0.68 (0.52-0.79)	0.64 (0.55-0.71)	0.56 (0.52-0.6)	0.64 (0.47-0.67)	0.6 (0.51-0.63)
ITGA11	FLT3LG	101	63	0.65 (0.56-0.74)	0.6 (0.51-0.73)	0.63 (0.56-0.7)	0.61 (0.4-0.65)	0.59 (0.54-0.6)	0.6 (0.49-0.62)
IL6_PEA_cytokine	LRG1	102	63	0.63 (0.52-0.71)	0.6 (0.47-0.73)	0.62 (0.52-0.69)	0.6 (0.37-0.63)	0.6 (0.46-0.6)	0.6 (0.48-0.61)
APCS	ORM1	102	67	0.6 (0.5-0.69)	0.64 (0.53-0.75)	0.62 (0.55-0.69)	0.58 (0.49-0.59)	0.61 (0.4-0.63)	0.6 (0.5-0.61)
HPR	ITIH2	102	67	0.59 (0.51-0.68)	0.64 (0.53-0.75)	0.62 (0.55-0.69)	0.58 (0.49-0.59)	0.62 (0.48-0.63)	0.6 (0.52-0.61)
FGF2	F9	101	63	0.57 (0.5-0.66)	0.69 (0.48-0.79)	0.63 (0.53-0.7)	0.55 (0.48-0.56)	0.65 (0.36-0.68)	0.6 (0.45-0.62)
C4B	ITIH2	102	67	0.59 (0.5-0.68)	0.68 (0.56-0.82)	0.64 (0.56-0.71)	0.56 (0.52-0.59)	0.63 (0.37-0.69)	0.6 (0.46-0.63)
hsCRP	ITGA11	98	63	0.65 (0.51-0.73)	0.61 (0.48-0.74)	0.63 (0.55-0.71)	0.63 (0.39-0.66)	0.58 (0.45-0.63)	0.6 (0.48-0.64)
NCR1	ORM1	101	63	0.6 (0.51-0.69)	0.63 (0.52-0.74)	0.62 (0.55-0.69)	0.59 (0.5-0.6)	0.6 (0.45-0.62)	0.6 (0.51-0.61)
LAMP3	CFB	101	63	0.59 (0.48-0.67)	0.64 (0.55-0.75)	0.62 (0.55-0.69)	0.58 (0.53-0.58)	0.62 (0.38-0.64)	0.6 (0.48-0.61)
hsCRP	F9	98	67	0.62 (0.52-0.71)	0.64 (0.53-0.77)	0.64 (0.56-0.71)	0.59 (0.5-0.63)	0.63 (0.42-0.65)	0.6 (0.49-0.63)
IL6_PEA_IR	C5	101	63	0.63 (0.52-0.72)	0.64 (0.52-0.76)	0.63 (0.56-0.71)	0.6 (0.44-0.63)	0.6 (0.46-0.62)	0.6 (0.5-0.62)
SAA1	C8B	102	67	0.62 (0.48-0.71)	0.62 (0.5-0.74)	0.62 (0.52-0.69)	0.62 (0.44-0.63)	0.62 (0.47-0.62)	0.6 (0.5-0.62)
HPR	ITIH1	102	67	0.59 (0.52-0.68)	0.64 (0.53-0.75)	0.62 (0.55-0.68)	0.58 (0.48-0.59)	0.62 (0.46-0.63)	0.6 (0.51-0.61)
hsCRP	HSD11B1	98	63	0.64 (0.52-0.73)	0.63 (0.52-0.76)	0.63 (0.55-0.71)	0.59 (0.48-0.65)	0.61 (0.5-0.64)	0.6 (0.52-0.64)
hsCRP	CXCL9	98	63	0.66 (0.57-0.75)	0.61 (0.48-0.73)	0.63 (0.55-0.71)	0.63 (0.35-0.66)	0.6 (0.51-0.61)	0.6 (0.47-0.63)
IL6_PEA_cytokine	CRP_SRM	102	63	0.62 (0.5-0.7)	0.63 (0.47-0.75)	0.62 (0.53-0.7)	0.58 (0.38-0.63)	0.61 (0.45-0.63)	0.6 (0.5-0.62)
C4B	SERPING1	102	67	0.58 (0.49-0.66)	0.68 (0.54-0.8)	0.63 (0.56-0.71)	0.56 (0.54-0.57)	0.63 (0.35-0.68)	0.6 (0.46-0.62)
HPR	CLU	102	67	0.59 (0.51-0.68)	0.64 (0.53-0.75)	0.62 (0.55-0.69)	0.58 (0.49-0.59)	0.62 (0.48-0.63)	0.6 (0.52-0.61)

MASP1	C4B	101	63	0.62 (0.53-0.71)	0.68 (0.54-0.81)	0.65 (0.56-0.72)	0.57 (0.45-0.62)	0.61 (0.49-0.68)	0.6 (0.51-0.64)
ITGA11	HPR	101	63	0.63 (0.54-0.71)	0.66 (0.54-0.75)	0.64 (0.57-0.71)	0.59 (0.44-0.62)	0.61 (0.52-0.65)	0.6 (0.51-0.63)
LRG1	C4B	102	67	0.61 (0.52-0.69)	0.69 (0.57-0.81)	0.65 (0.57-0.72)	0.58 (0.5-0.6)	0.63 (0.37-0.68)	0.6 (0.47-0.64)
hsCRP	IL6_PEA_cytokine	98	63	0.62 (0.51-0.7)	0.62 (0.46-0.75)	0.62 (0.52-0.69)	0.59 (0.39-0.63)	0.61 (0.43-0.63)	0.6 (0.49-0.62)
ORM1	APOA1	102	67	0.64 (0.55-0.72)	0.62 (0.52-0.73)	0.63 (0.57-0.7)	0.63 (0.44-0.64)	0.57 (0.52-0.62)	0.6 (0.5-0.62)
CCL4	C5	102	63	0.62 (0.51-0.71)	0.63 (0.51-0.74)	0.63 (0.55-0.7)	0.6 (0.4-0.62)	0.6 (0.48-0.62)	0.6 (0.49-0.62)
ITGA11	C5	101	63	0.64 (0.56-0.73)	0.63 (0.53-0.73)	0.64 (0.56-0.7)	0.61 (0.4-0.64)	0.59 (0.48-0.63)	0.6 (0.49-0.63)
C5	SERPINA3	102	67	0.61 (0.51-0.7)	0.62 (0.51-0.73)	0.61 (0.55-0.69)	0.6 (0.47-0.61)	0.6 (0.49-0.61)	0.6 (0.51-0.61)
MILR1	C4B	101	63	0.66 (0.58-0.73)	0.67 (0.53-0.81)	0.66 (0.59-0.74)	0.61 (0.43-0.65)	0.6 (0.45-0.65)	0.6 (0.51-0.64)
IFNG	C8B	102	63	0.69 (0.61-0.77)	0.6 (0.47-0.71)	0.65 (0.58-0.72)	0.59 (0.32-0.69)	0.6 (0.56-0.62)	0.6 (0.46-0.65)
FLT3LG	C4BPB	102	63	0.63 (0.54-0.72)	0.62 (0.52-0.73)	0.62 (0.55-0.7)	0.6 (0.47-0.62)	0.59 (0.53-0.6)	0.6 (0.52-0.61)
KLRD1	SIT1	102	63	0.63 (0.54-0.71)	0.61 (0.52-0.72)	0.62 (0.56-0.68)	0.61 (0.43-0.62)	0.59 (0.57-0.59)	0.6 (0.51-0.61)
IL13	LRG1	102	63	0.61 (0.51-0.69)	0.61 (0.47-0.72)	0.6 (0.53-0.68)	0.6 (0.41-0.6)	0.61 (0.46-0.61)	0.6 (0.48-0.61)
CP	HPR	102	67	0.59 (0.5-0.68)	0.65 (0.54-0.77)	0.62 (0.55-0.7)	0.58 (0.5-0.59)	0.62 (0.4-0.66)	0.6 (0.48-0.62)
C2	HPR	102	67	0.6 (0.53-0.68)	0.64 (0.5-0.75)	0.62 (0.54-0.69)	0.59 (0.48-0.59)	0.61 (0.52-0.63)	0.6 (0.52-0.61)
SERPIND1	SERPINA4	102	67	0.62 (0.52-0.69)	0.67 (0.57-0.76)	0.64 (0.58-0.7)	0.6 (0.48-0.62)	0.6 (0.51-0.65)	0.6 (0.53-0.63)
SAA1	APOA1	102	67	0.62 (0.54-0.7)	0.6 (0.49-0.71)	0.61 (0.54-0.68)	0.61 (0.4-0.62)	0.58 (0.54-0.59)	0.59 (0.49-0.6)
CRP_SRM	F9	102	67	0.62 (0.53-0.71)	0.64 (0.54-0.77)	0.63 (0.56-0.71)	0.58 (0.49-0.63)	0.62 (0.42-0.64)	0.59 (0.49-0.63)
FCRL6	C4B	101	63	0.58 (0.5-0.67)	0.71 (0.58-0.83)	0.64 (0.57-0.72)	0.56 (0.53-0.57)	0.63 (0.32-0.71)	0.59 (0.44-0.63)
MASP1	LAMP3	102	63	0.62 (0.5-0.7)	0.64 (0.52-0.75)	0.63 (0.55-0.7)	0.59 (0.41-0.62)	0.62 (0.4-0.63)	0.59 (0.49-0.62)
MILR1	CXCL9	101	63	0.72 (0.64-0.78)	0.58 (0.47-0.7)	0.65 (0.59-0.72)	0.62 (0.29-0.72)	0.57 (0.54-0.58)	0.59 (0.43-0.64)
hsCRP	ITIH3	98	67	0.63 (0.53-0.72)	0.62 (0.52-0.75)	0.62 (0.56-0.71)	0.6 (0.46-0.63)	0.6 (0.49-0.62)	0.59 (0.5-0.62)
FLT3LG	C8A	102	63	0.62 (0.54-0.71)	0.61 (0.52-0.73)	0.62 (0.55-0.69)	0.6 (0.45-0.62)	0.59 (0.53-0.61)	0.59 (0.51-0.61)
KLRD1	C8B	101	63	0.64 (0.55-0.72)	0.61 (0.52-0.72)	0.62 (0.56-0.69)	0.63 (0.38-0.63)	0.57 (0.52-0.59)	0.59 (0.48-0.61)
FLT3LG	SERPIND1	102	63	0.61 (0.53-0.7)	0.68 (0.58-0.8)	0.65 (0.58-0.71)	0.59 (0.53-0.6)	0.6 (0.49-0.68)	0.59 (0.53-0.64)
FLT3LG	CP	102	63	0.61 (0.53-0.7)	0.66 (0.55-0.78)	0.64 (0.57-0.71)	0.61 (0.51-0.62)	0.59 (0.44-0.67)	0.59 (0.51-0.63)
HSD11B1	CRP_SRM	101	63	0.63 (0.53-0.73)	0.62 (0.51-0.75)	0.63 (0.55-0.71)	0.59 (0.47-0.65)	0.61 (0.5-0.64)	0.59 (0.52-0.64)
hsCRP	HGF	98	63	0.63 (0.52-0.72)	0.62 (0.49-0.76)	0.63 (0.54-0.7)	0.6 (0.47-0.63)	0.6 (0.48-0.62)	0.59 (0.5-0.62)
CCL4	C4B	102	63	0.59 (0.47-0.67)	0.68 (0.53-0.82)	0.63 (0.54-0.72)	0.56 (0.48-0.59)	0.64 (0.34-0.68)	0.59 (0.45-0.62)
CCL13	C4B	102	63	0.58 (0.49-0.66)	0.7 (0.57-0.8)	0.64 (0.56-0.71)	0.56 (0.55-0.56)	0.63 (0.33-0.68)	0.59 (0.44-0.62)

CLEC4C	F9	101	63	0.58 (0.51-0.67)	0.64 (0.54-0.77)	0.62 (0.55-0.69)	0.57 (0.52-0.57)	0.63 (0.36-0.64)	0.59 (0.46-0.61)
MILR1	APCS	101	63	0.66 (0.58-0.74)	0.61 (0.52-0.74)	0.64 (0.57-0.71)	0.63 (0.38-0.66)	0.57 (0.48-0.61)	0.59 (0.47-0.63)
HGF	CRP_SRM	102	63	0.63 (0.51-0.72)	0.62 (0.49-0.76)	0.62 (0.54-0.7)	0.6 (0.45-0.63)	0.6 (0.47-0.62)	0.59 (0.49-0.62)
F9	C2	102	67	0.58 (0.5-0.67)	0.66 (0.51-0.77)	0.62 (0.54-0.69)	0.56 (0.48-0.57)	0.63 (0.36-0.67)	0.59 (0.46-0.62)
CRP_SRM	ITIH3	102	67	0.62 (0.53-0.71)	0.62 (0.52-0.74)	0.62 (0.55-0.7)	0.59 (0.44-0.63)	0.6 (0.48-0.63)	0.59 (0.51-0.62)
CRP_SRM	C8A	102	67	0.62 (0.53-0.71)	0.62 (0.51-0.74)	0.62 (0.54-0.7)	0.61 (0.44-0.64)	0.6 (0.47-0.64)	0.59 (0.5-0.63)
ITGA11	LRG1	101	63	0.64 (0.54-0.72)	0.61 (0.48-0.72)	0.62 (0.54-0.69)	0.62 (0.37-0.64)	0.58 (0.51-0.6)	0.59 (0.47-0.62)
MASP1	ORM1	101	63	0.63 (0.55-0.73)	0.63 (0.51-0.77)	0.63 (0.56-0.71)	0.59 (0.4-0.63)	0.61 (0.49-0.62)	0.59 (0.5-0.62)
KLRD1	FLT3LG	101	63	0.63 (0.54-0.7)	0.61 (0.52-0.71)	0.62 (0.55-0.68)	0.61 (0.42-0.62)	0.58 (0.53-0.59)	0.59 (0.5-0.6)
DCTN1	HPR	101	63	0.6 (0.52-0.68)	0.73 (0.62-0.83)	0.66 (0.59-0.73)	0.57 (0.48-0.59)	0.63 (0.33-0.72)	0.59 (0.44-0.65)
IFNG	LRG1	102	63	0.69 (0.6-0.76)	0.61 (0.45-0.71)	0.64 (0.56-0.72)	0.59 (0.32-0.68)	0.6 (0.56-0.62)	0.59 (0.46-0.64)
hsCRP	LAMP3	98	63	0.62 (0.5-0.71)	0.64 (0.53-0.74)	0.63 (0.54-0.7)	0.6 (0.52-0.62)	0.58 (0.43-0.63)	0.59 (0.51-0.62)
CDSN	F9	101	63	0.59 (0.5-0.67)	0.65 (0.54-0.78)	0.62 (0.55-0.69)	0.57 (0.5-0.57)	0.63 (0.48-0.65)	0.59 (0.51-0.61)
NCR1	SERPINA3	101	63	0.6 (0.51-0.69)	0.63 (0.51-0.74)	0.61 (0.54-0.69)	0.59 (0.46-0.6)	0.6 (0.49-0.63)	0.59 (0.51-0.61)
CDSN	C8B	101	63	0.63 (0.53-0.71)	0.62 (0.51-0.76)	0.62 (0.55-0.71)	0.6 (0.4-0.63)	0.59 (0.5-0.63)	0.59 (0.5-0.62)
hsCRP	IL17F	98	63	0.63 (0.52-0.72)	0.59 (0.43-0.74)	0.61 (0.52-0.7)	0.59 (0.42-0.63)	0.59 (0.5-0.62)	0.59 (0.5-0.62)
LAMP3	APCS	101	63	0.6 (0.49-0.68)	0.64 (0.55-0.75)	0.62 (0.55-0.69)	0.59 (0.53-0.59)	0.61 (0.38-0.65)	0.59 (0.48-0.62)
CLEC4C	LRG1	101	63	0.62 (0.52-0.71)	0.64 (0.52-0.75)	0.63 (0.56-0.7)	0.6 (0.41-0.61)	0.61 (0.41-0.64)	0.59 (0.48-0.62)
KLRD1	LRG1	101	63	0.63 (0.55-0.71)	0.61 (0.51-0.71)	0.62 (0.55-0.69)	0.61 (0.4-0.63)	0.59 (0.5-0.59)	0.59 (0.49-0.61)
HSD11B1	IFNG	101	63	0.69 (0.61-0.77)	0.6 (0.46-0.72)	0.64 (0.56-0.71)	0.57 (0.32-0.69)	0.62 (0.57-0.62)	0.59 (0.47-0.65)
CDSN	CRP_SRM	101	63	0.62 (0.52-0.71)	0.64 (0.51-0.78)	0.63 (0.55-0.71)	0.57 (0.48-0.64)	0.62 (0.49-0.68)	0.59 (0.51-0.65)
FGF2	LRG1	101	63	0.61 (0.52-0.7)	0.67 (0.47-0.78)	0.64 (0.53-0.71)	0.57 (0.44-0.6)	0.62 (0.46-0.67)	0.59 (0.5-0.63)
IL6_PEA_cytokine	FLT3LG	102	63	0.62 (0.53-0.7)	0.62 (0.51-0.75)	0.62 (0.55-0.7)	0.59 (0.44-0.62)	0.59 (0.56-0.63)	0.59 (0.51-0.62)
SIT1	SERPINA3	101	63	0.61 (0.53-0.69)	0.63 (0.5-0.75)	0.62 (0.55-0.69)	0.59 (0.46-0.61)	0.61 (0.51-0.64)	0.59 (0.52-0.62)
IL13	C8B	102	63	0.62 (0.51-0.7)	0.59 (0.47-0.72)	0.61 (0.53-0.68)	0.61 (0.39-0.61)	0.58 (0.49-0.59)	0.59 (0.47-0.6)
F9	CFB	102	67	0.58 (0.51-0.66)	0.64 (0.55-0.76)	0.61 (0.54-0.68)	0.57 (0.51-0.57)	0.62 (0.38-0.64)	0.59 (0.47-0.6)
HPR	SERPING1	102	67	0.6 (0.51-0.68)	0.65 (0.52-0.75)	0.62 (0.54-0.69)	0.58 (0.48-0.59)	0.61 (0.48-0.63)	0.59 (0.51-0.61)
IL13	F9	102	63	0.58 (0.48-0.67)	0.62 (0.47-0.76)	0.6 (0.51-0.68)	0.57 (0.43-0.58)	0.62 (0.42-0.63)	0.59 (0.49-0.6)
CLEC4C	FLT3LG	101	63	0.61 (0.53-0.7)	0.64 (0.53-0.76)	0.62 (0.56-0.7)	0.6 (0.47-0.61)	0.59 (0.5-0.64)	0.59 (0.53-0.62)
hsCRP	SERPING1	98	67	0.63 (0.53-0.71)	0.63 (0.51-0.76)	0.63 (0.55-0.7)	0.59 (0.45-0.63)	0.6 (0.46-0.63)	0.59 (0.51-0.62)

IL10_PEA_IR	C8B	101	63	0.63 (0.52-0.72)	0.61 (0.45-0.74)	0.62 (0.52-0.7)	0.59 (0.4-0.64)	0.61 (0.56-0.63)	0.59 (0.5-0.63)
hsCRP	C2	98	67	0.63 (0.51-0.72)	0.6 (0.46-0.75)	0.61 (0.52-0.7)	0.57 (0.45-0.63)	0.62 (0.49-0.66)	0.59 (0.51-0.65)
C5	SERPING1	102	67	0.62 (0.54-0.7)	0.62 (0.5-0.73)	0.62 (0.54-0.69)	0.6 (0.47-0.62)	0.59 (0.49-0.62)	0.59 (0.51-0.61)
SH2D1A	CRP_SRM	101	63	0.63 (0.52-0.72)	0.61 (0.49-0.73)	0.62 (0.54-0.7)	0.59 (0.46-0.65)	0.6 (0.49-0.61)	0.59 (0.52-0.63)
APOA1	CFB	102	67	0.62 (0.55-0.7)	0.62 (0.51-0.74)	0.62 (0.56-0.69)	0.61 (0.48-0.62)	0.58 (0.55-0.6)	0.59 (0.53-0.61)
FC	IL15	77	43	0.68 (0.57-0.78)	0.61 (0.45-0.74)	0.64 (0.55-0.72)	0.63 (0.41-0.7)	0.55 (0.53-0.6)	0.59 (0.48-0.64)
NCR1	IL10_PEA_IR	102	63	0.59 (0.51-0.67)	0.63 (0.44-0.76)	0.61 (0.52-0.69)	0.57 (0.43-0.6)	0.62 (0.58-0.63)	0.59 (0.52-0.61)
MILR1	CFB	101	63	0.65 (0.56-0.72)	0.64 (0.52-0.76)	0.64 (0.57-0.72)	0.61 (0.39-0.64)	0.59 (0.5-0.64)	0.59 (0.48-0.63)
hsCRP	CLU	98	67	0.63 (0.52-0.71)	0.62 (0.52-0.73)	0.63 (0.55-0.69)	0.6 (0.48-0.63)	0.59 (0.45-0.63)	0.59 (0.5-0.63)
MILR1	KLRD1	102	63	0.66 (0.57-0.74)	0.59 (0.5-0.69)	0.62 (0.56-0.69)	0.64 (0.36-0.66)	0.55 (0.54-0.57)	0.59 (0.45-0.61)
CXCL9	CRP_SRM	102	63	0.66 (0.57-0.74)	0.61 (0.47-0.73)	0.63 (0.55-0.71)	0.63 (0.35-0.66)	0.59 (0.5-0.61)	0.59 (0.47-0.63)
CRP_SRM	LRG1	102	67	0.62 (0.52-0.71)	0.62 (0.51-0.74)	0.62 (0.55-0.69)	0.58 (0.46-0.64)	0.61 (0.49-0.63)	0.59 (0.51-0.63)
FLT3LG	TNF	102	63	0.61 (0.52-0.69)	0.61 (0.51-0.72)	0.61 (0.55-0.69)	0.59 (0.45-0.6)	0.59 (0.54-0.6)	0.59 (0.52-0.6)
NCR1	ITIH3	101	63	0.61 (0.52-0.68)	0.63 (0.52-0.74)	0.62 (0.55-0.7)	0.6 (0.43-0.61)	0.6 (0.49-0.62)	0.59 (0.51-0.61)
HPR	VTN	102	67	0.6 (0.52-0.68)	0.65 (0.54-0.75)	0.62 (0.55-0.69)	0.58 (0.46-0.59)	0.62 (0.44-0.63)	0.59 (0.49-0.61)
C8B	SERPINA4	102	67	0.65 (0.55-0.73)	0.61 (0.51-0.72)	0.63 (0.56-0.7)	0.63 (0.36-0.67)	0.56 (0.52-0.57)	0.59 (0.46-0.62)
HP	C4B	102	67	0.68 (0.6-0.75)	0.7 (0.58-0.81)	0.69 (0.62-0.76)	0.62 (0.56-0.66)	0.56 (0.48-0.67)	0.59 (0.54-0.65)
CLEC4C	CFB	101	63	0.58 (0.5-0.66)	0.65 (0.53-0.76)	0.61 (0.55-0.68)	0.56 (0.47-0.58)	0.63 (0.37-0.64)	0.59 (0.46-0.61)
CRP_SRM	SERPING1	102	67	0.62 (0.52-0.71)	0.63 (0.51-0.75)	0.62 (0.55-0.7)	0.59 (0.44-0.63)	0.6 (0.47-0.63)	0.59 (0.51-0.62)
HPR	C4BPB	102	67	0.61 (0.53-0.68)	0.63 (0.52-0.74)	0.62 (0.55-0.7)	0.59 (0.46-0.61)	0.6 (0.51-0.62)	0.59 (0.53-0.61)
F9	CLU	102	67	0.6 (0.51-0.68)	0.64 (0.54-0.77)	0.62 (0.55-0.7)	0.59 (0.49-0.6)	0.61 (0.44-0.65)	0.59 (0.5-0.62)
hsCRP	SH2D1A	98	63	0.63 (0.51-0.73)	0.61 (0.49-0.74)	0.62 (0.54-0.7)	0.59 (0.46-0.65)	0.6 (0.46-0.61)	0.59 (0.52-0.62)
VTN	APOA1	102	67	0.63 (0.55-0.7)	0.65 (0.55-0.76)	0.64 (0.58-0.71)	0.6 (0.51-0.61)	0.59 (0.51-0.64)	0.59 (0.53-0.62)
ITIH3	APOA1	102	67	0.64 (0.57-0.71)	0.59 (0.51-0.69)	0.62 (0.56-0.67)	0.62 (0.4-0.64)	0.56 (0.54-0.58)	0.59 (0.48-0.61)
HSD11B1	LRG1	101	63	0.62 (0.53-0.72)	0.62 (0.52-0.75)	0.62 (0.55-0.7)	0.59 (0.44-0.62)	0.61 (0.5-0.62)	0.59 (0.51-0.62)
SIT1	SERPIND1	101	63	0.59 (0.5-0.67)	0.67 (0.57-0.78)	0.63 (0.56-0.7)	0.56 (0.53-0.58)	0.63 (0.47-0.66)	0.59 (0.51-0.62)
CLEC4C	SAA1	101	63	0.59 (0.51-0.67)	0.67 (0.47-0.79)	0.63 (0.52-0.71)	0.57 (0.43-0.58)	0.67 (0.4-0.68)	0.59 (0.44-0.63)
MILR1	C4BPB	101	63	0.67 (0.59-0.75)	0.59 (0.51-0.72)	0.63 (0.57-0.7)	0.63 (0.35-0.67)	0.56 (0.54-0.57)	0.59 (0.45-0.62)
SERPINA3	C4B	102	67	0.58 (0.5-0.67)	0.69 (0.56-0.81)	0.63 (0.56-0.71)	0.56 (0.47-0.57)	0.63 (0.35-0.68)	0.59 (0.45-0.63)
APOA1	C8A	102	67	0.65 (0.58-0.72)	0.6 (0.5-0.7)	0.62 (0.56-0.69)	0.62 (0.37-0.65)	0.57 (0.55-0.57)	0.59 (0.46-0.61)

C8B	APCS	102	67	0.63 (0.53-0.71)	0.63 (0.52-0.74)	0.63 (0.56-0.7)	0.61 (0.43-0.63)	0.58 (0.44-0.62)	0.59 (0.5-0.62)
FC	SERPIND1	77	44	0.67 (0.58-0.76)	0.64 (0.47-0.79)	0.65 (0.56-0.73)	0.58 (0.36-0.68)	0.63 (0.53-0.65)	0.59 (0.48-0.66)
IL10_PEA_IR	C5	101	63	0.62 (0.54-0.71)	0.62 (0.48-0.75)	0.62 (0.54-0.7)	0.58 (0.47-0.62)	0.6 (0.59-0.61)	0.59 (0.54-0.62)
C3	APOA1	102	67	0.64 (0.55-0.71)	0.6 (0.51-0.76)	0.62 (0.55-0.71)	0.61 (0.41-0.63)	0.57 (0.55-0.59)	0.59 (0.49-0.61)
MILR1	ITIH3	101	63	0.67 (0.58-0.75)	0.59 (0.5-0.71)	0.63 (0.56-0.7)	0.62 (0.34-0.67)	0.56 (0.55-0.57)	0.59 (0.45-0.61)
F9	ITIH2	102	67	0.59 (0.52-0.69)	0.64 (0.53-0.77)	0.62 (0.55-0.7)	0.57 (0.48-0.59)	0.62 (0.41-0.64)	0.59 (0.49-0.61)
ITIH3	C5	102	67	0.61 (0.53-0.7)	0.62 (0.52-0.73)	0.61 (0.55-0.68)	0.59 (0.46-0.61)	0.6 (0.49-0.61)	0.59 (0.52-0.61)
SH2D1A	C5	101	63	0.61 (0.5-0.7)	0.63 (0.51-0.74)	0.62 (0.55-0.69)	0.59 (0.48-0.61)	0.6 (0.49-0.62)	0.59 (0.53-0.61)
TNF	C4B	102	63	0.57 (0.5-0.65)	0.68 (0.55-0.81)	0.62 (0.55-0.71)	0.56 (0.53-0.57)	0.62 (0.37-0.68)	0.59 (0.46-0.62)
C4B	ITIH1	102	67	0.59 (0.48-0.67)	0.68 (0.56-0.81)	0.63 (0.56-0.7)	0.56 (0.52-0.57)	0.63 (0.34-0.68)	0.59 (0.45-0.62)
C5	F9	102	67	0.61 (0.53-0.69)	0.64 (0.53-0.76)	0.62 (0.55-0.69)	0.58 (0.51-0.61)	0.61 (0.44-0.63)	0.59 (0.5-0.62)
CCL13	C5	102	63	0.61 (0.51-0.7)	0.64 (0.53-0.76)	0.62 (0.55-0.69)	0.59 (0.52-0.62)	0.6 (0.44-0.63)	0.59 (0.52-0.62)
C5	ITIH2	102	67	0.62 (0.54-0.71)	0.62 (0.52-0.72)	0.62 (0.56-0.68)	0.61 (0.45-0.62)	0.58 (0.5-0.6)	0.59 (0.51-0.61)
APCS	CFB	102	67	0.59 (0.49-0.68)	0.62 (0.52-0.73)	0.6 (0.54-0.68)	0.58 (0.47-0.59)	0.6 (0.4-0.62)	0.59 (0.49-0.6)
LAMP3	C8B	101	63	0.62 (0.5-0.7)	0.63 (0.54-0.74)	0.62 (0.56-0.69)	0.6 (0.44-0.62)	0.57 (0.42-0.63)	0.59 (0.5-0.62)
SAA1	F9	102	67	0.58 (0.5-0.67)	0.63 (0.52-0.76)	0.61 (0.53-0.69)	0.57 (0.48-0.58)	0.63 (0.44-0.64)	0.59 (0.47-0.61)
ITGA11	ORM1	101	63	0.65 (0.54-0.73)	0.62 (0.5-0.74)	0.64 (0.55-0.71)	0.61 (0.4-0.65)	0.59 (0.44-0.61)	0.59 (0.48-0.63)
IL15	APCS	102	63	0.6 (0.47-0.68)	0.64 (0.52-0.76)	0.62 (0.54-0.7)	0.6 (0.52-0.61)	0.58 (0.38-0.64)	0.59 (0.49-0.62)
IL17F	C5	102	63	0.63 (0.52-0.71)	0.63 (0.48-0.75)	0.63 (0.54-0.7)	0.59 (0.46-0.63)	0.59 (0.51-0.62)	0.59 (0.5-0.61)
HGF	F9	102	63	0.58 (0.5-0.67)	0.65 (0.51-0.76)	0.61 (0.54-0.69)	0.55 (0.47-0.59)	0.63 (0.37-0.64)	0.59 (0.46-0.61)
ITIH3	C8B	102	67	0.62 (0.53-0.71)	0.6 (0.52-0.71)	0.61 (0.54-0.68)	0.61 (0.39-0.63)	0.57 (0.49-0.58)	0.59 (0.48-0.6)
hsCRP	CLEC4C	98	63	0.62 (0.52-0.71)	0.67 (0.51-0.79)	0.64 (0.56-0.72)	0.59 (0.46-0.62)	0.61 (0.38-0.68)	0.59 (0.47-0.65)
FLT3LG	C2	102	63	0.61 (0.53-0.7)	0.61 (0.49-0.74)	0.61 (0.54-0.69)	0.59 (0.45-0.6)	0.59 (0.53-0.61)	0.59 (0.51-0.6)
FGF2	ORM1	101	63	0.58 (0.5-0.69)	0.67 (0.48-0.78)	0.63 (0.53-0.7)	0.55 (0.46-0.59)	0.63 (0.35-0.67)	0.59 (0.45-0.62)
FLT3LG	VEGFA	102	63	0.62 (0.53-0.7)	0.6 (0.51-0.73)	0.61 (0.55-0.69)	0.59 (0.44-0.6)	0.59 (0.54-0.6)	0.59 (0.51-0.6)
APCS	CLU	102	67	0.6 (0.51-0.68)	0.62 (0.53-0.73)	0.61 (0.55-0.68)	0.59 (0.44-0.59)	0.6 (0.46-0.62)	0.59 (0.5-0.6)
hsCRP	CCL4	98	63	0.64 (0.51-0.73)	0.62 (0.49-0.74)	0.63 (0.53-0.7)	0.59 (0.37-0.65)	0.59 (0.47-0.62)	0.59 (0.47-0.63)
VEGFA	LRG1	102	63	0.62 (0.51-0.7)	0.61 (0.5-0.72)	0.62 (0.53-0.69)	0.6 (0.4-0.61)	0.59 (0.43-0.61)	0.59 (0.48-0.61)
F9	C8B	102	67	0.61 (0.53-0.7)	0.65 (0.54-0.75)	0.63 (0.56-0.7)	0.59 (0.49-0.62)	0.6 (0.41-0.64)	0.59 (0.5-0.62)
CRP_SRM	C2	102	67	0.61 (0.51-0.7)	0.61 (0.46-0.75)	0.61 (0.51-0.7)	0.58 (0.44-0.63)	0.62 (0.49-0.67)	0.59 (0.51-0.64)

hsCRP	C3	98	67	0.62 (0.52-0.72)	0.62 (0.52-0.74)	0.62 (0.55-0.7)	0.58 (0.48-0.63)	0.61 (0.48-0.62)	0.59 (0.52-0.62)
ITIH3	F9	102	67	0.59 (0.51-0.68)	0.65 (0.54-0.76)	0.62 (0.55-0.69)	0.57 (0.47-0.59)	0.62 (0.41-0.64)	0.59 (0.49-0.61)
NCR1	LAMP3	102	63	0.59 (0.5-0.67)	0.63 (0.53-0.73)	0.61 (0.54-0.67)	0.58 (0.52-0.59)	0.6 (0.41-0.62)	0.59 (0.49-0.6)
IL6_PEA_cytokine	ORM1	102	63	0.63 (0.45-0.72)	0.61 (0.48-0.73)	0.62 (0.51-0.7)	0.59 (0.37-0.64)	0.59 (0.44-0.6)	0.59 (0.47-0.62)
FLT3LG	ITIH1	102	63	0.61 (0.54-0.7)	0.66 (0.54-0.77)	0.64 (0.57-0.71)	0.59 (0.5-0.6)	0.6 (0.51-0.66)	0.59 (0.53-0.62)
KLRD1	APOA1	101	63	0.64 (0.56-0.72)	0.58 (0.5-0.69)	0.61 (0.56-0.68)	0.62 (0.39-0.64)	0.56 (0.54-0.57)	0.59 (0.48-0.6)
LAMP3	IL10_PEA_IR	102	63	0.59 (0.5-0.68)	0.62 (0.44-0.77)	0.61 (0.52-0.69)	0.58 (0.44-0.59)	0.61 (0.46-0.63)	0.59 (0.5-0.61)
CLEC4C	C8B	101	63	0.62 (0.53-0.7)	0.62 (0.51-0.74)	0.62 (0.55-0.69)	0.61 (0.39-0.62)	0.58 (0.43-0.62)	0.59 (0.48-0.62)
IL6_PEA_IR	SIT1	102	63	0.62 (0.53-0.71)	0.61 (0.49-0.72)	0.61 (0.55-0.69)	0.6 (0.4-0.62)	0.58 (0.55-0.59)	0.59 (0.49-0.6)
MILR1	IL15	101	63	0.64 (0.56-0.72)	0.58 (0.48-0.69)	0.61 (0.55-0.68)	0.64 (0.39-0.65)	0.55 (0.5-0.58)	0.59 (0.47-0.61)
MASP1	APCS	101	63	0.63 (0.53-0.72)	0.61 (0.5-0.74)	0.62 (0.55-0.7)	0.6 (0.41-0.63)	0.58 (0.49-0.59)	0.59 (0.49-0.61)
KLRD1	APCS	101	63	0.61 (0.52-0.7)	0.61 (0.52-0.74)	0.61 (0.55-0.68)	0.6 (0.41-0.61)	0.58 (0.45-0.6)	0.59 (0.49-0.6)
MASP1	LRG1	101	63	0.64 (0.55-0.73)	0.61 (0.49-0.74)	0.63 (0.55-0.7)	0.59 (0.37-0.64)	0.58 (0.55-0.6)	0.59 (0.48-0.62)
CXCL9	C8B	102	63	0.69 (0.61-0.76)	0.59 (0.48-0.7)	0.64 (0.57-0.71)	0.62 (0.32-0.69)	0.55 (0.53-0.56)	0.59 (0.44-0.62)
MASP1	SAA1	101	63	0.62 (0.52-0.71)	0.62 (0.45-0.76)	0.62 (0.52-0.7)	0.56 (0.38-0.62)	0.63 (0.48-0.64)	0.59 (0.49-0.63)
LRG1	F9	102	67	0.61 (0.52-0.7)	0.64 (0.53-0.76)	0.63 (0.55-0.7)	0.58 (0.45-0.61)	0.62 (0.41-0.64)	0.59 (0.48-0.62)
hsCRP	LRG1	98	67	0.63 (0.51-0.73)	0.62 (0.52-0.74)	0.62 (0.55-0.7)	0.59 (0.46-0.64)	0.61 (0.47-0.63)	0.59 (0.49-0.63)
IL17F	C4B	102	63	0.59 (0.49-0.67)	0.7 (0.54-0.84)	0.64 (0.55-0.72)	0.55 (0.52-0.59)	0.62 (0.35-0.7)	0.59 (0.45-0.63)
CCL13	CRP_SRM	102	63	0.62 (0.51-0.73)	0.64 (0.51-0.75)	0.63 (0.55-0.71)	0.58 (0.47-0.63)	0.6 (0.45-0.64)	0.59 (0.5-0.63)
IL15	C8B	102	63	0.62 (0.5-0.7)	0.64 (0.53-0.76)	0.63 (0.55-0.7)	0.61 (0.47-0.62)	0.57 (0.49-0.64)	0.59 (0.52-0.63)
FC	C4B	77	44	0.69 (0.59-0.77)	0.72 (0.55-0.88)	0.7 (0.61-0.79)	0.55 (0.44-0.63)	0.64 (0.47-0.71)	0.59 (0.49-0.65)
SIT1	CXCL9	101	63	0.71 (0.62-0.78)	0.61 (0.49-0.72)	0.66 (0.59-0.73)	0.58 (0.35-0.71)	0.6 (0.55-0.61)	0.59 (0.47-0.66)
LAMP3	C3	101	63	0.6 (0.48-0.67)	0.64 (0.52-0.75)	0.61 (0.54-0.69)	0.58 (0.51-0.59)	0.6 (0.39-0.64)	0.59 (0.48-0.61)
LRG1	SERPINA3	102	67	0.6 (0.51-0.69)	0.62 (0.51-0.73)	0.61 (0.54-0.68)	0.58 (0.42-0.61)	0.59 (0.5-0.6)	0.59 (0.5-0.6)
SIT1	IL15	101	63	0.6 (0.51-0.68)	0.62 (0.52-0.74)	0.61 (0.54-0.68)	0.59 (0.51-0.59)	0.59 (0.51-0.62)	0.59 (0.54-0.6)
KLRD1	F9	101	63	0.61 (0.52-0.69)	0.64 (0.53-0.76)	0.63 (0.56-0.7)	0.58 (0.47-0.61)	0.61 (0.42-0.63)	0.59 (0.49-0.62)
C4B	VTN	102	67	0.6 (0.5-0.69)	0.68 (0.56-0.8)	0.64 (0.56-0.72)	0.55 (0.51-0.59)	0.63 (0.34-0.68)	0.59 (0.44-0.62)
HPR	PZP	101	67	0.6 (0.5-0.68)	0.65 (0.53-0.75)	0.62 (0.55-0.69)	0.58 (0.47-0.6)	0.6 (0.39-0.63)	0.59 (0.48-0.61)
IL17C	C4B	102	63	0.6 (0.52-0.68)	0.67 (0.51-0.81)	0.64 (0.54-0.71)	0.56 (0.44-0.59)	0.63 (0.36-0.67)	0.59 (0.46-0.62)
FCRL6	C5	101	63	0.61 (0.53-0.7)	0.67 (0.57-0.77)	0.64 (0.58-0.71)	0.6 (0.48-0.61)	0.59 (0.43-0.68)	0.59 (0.5-0.64)

SIT1	C8A	101	63	0.61 (0.54-0.7)	0.61 (0.52-0.73)	0.62 (0.55-0.69)	0.59 (0.43-0.62)	0.59 (0.53-0.6)	0.59 (0.51-0.6)
CXCL9	LRG1	102	63	0.66 (0.58-0.75)	0.6 (0.48-0.72)	0.63 (0.56-0.7)	0.61 (0.34-0.67)	0.57 (0.48-0.6)	0.59 (0.45-0.63)
HPR	SERPIND1	102	67	0.6 (0.52-0.69)	0.65 (0.56-0.76)	0.63 (0.56-0.69)	0.57 (0.48-0.59)	0.62 (0.45-0.63)	0.59 (0.5-0.61)
CRP_SRM	C3	102	67	0.62 (0.51-0.71)	0.61 (0.52-0.74)	0.62 (0.55-0.69)	0.58 (0.48-0.63)	0.61 (0.47-0.62)	0.59 (0.51-0.62)
IL17F	CRP_SRM	102	63	0.64 (0.52-0.72)	0.59 (0.42-0.74)	0.61 (0.51-0.7)	0.58 (0.4-0.64)	0.59 (0.51-0.61)	0.59 (0.49-0.62)
MILR1	F9	101	63	0.65 (0.58-0.72)	0.63 (0.52-0.77)	0.64 (0.57-0.72)	0.6 (0.4-0.65)	0.58 (0.48-0.63)	0.59 (0.48-0.63)
PLXNA4	F9	101	63	0.58 (0.5-0.67)	0.65 (0.54-0.77)	0.62 (0.54-0.69)	0.56 (0.47-0.57)	0.62 (0.37-0.65)	0.59 (0.46-0.6)
SH2D1A	F9	101	63	0.58 (0.5-0.66)	0.65 (0.53-0.77)	0.62 (0.55-0.69)	0.57 (0.47-0.57)	0.61 (0.41-0.64)	0.59 (0.49-0.6)
FC	SERPINA3	77	44	0.67 (0.57-0.76)	0.61 (0.47-0.76)	0.64 (0.56-0.72)	0.6 (0.34-0.67)	0.58 (0.56-0.59)	0.59 (0.45-0.62)
CRP_SRM	ITIH2	102	67	0.61 (0.53-0.7)	0.62 (0.52-0.73)	0.61 (0.55-0.69)	0.58 (0.47-0.62)	0.61 (0.48-0.62)	0.59 (0.51-0.62)
NCR1	HSD11B1	102	63	0.6 (0.52-0.68)	0.62 (0.52-0.73)	0.61 (0.55-0.68)	0.59 (0.5-0.6)	0.59 (0.47-0.61)	0.59 (0.52-0.6)
IL15	ORM1	102	63	0.6 (0.48-0.7)	0.63 (0.52-0.73)	0.61 (0.53-0.69)	0.6 (0.47-0.6)	0.58 (0.4-0.62)	0.59 (0.49-0.61)
NCR1	C8A	101	63	0.61 (0.52-0.68)	0.62 (0.52-0.73)	0.62 (0.55-0.69)	0.6 (0.41-0.61)	0.59 (0.48-0.6)	0.59 (0.5-0.61)
HSD11B1	APCS	101	63	0.61 (0.5-0.7)	0.62 (0.52-0.73)	0.61 (0.54-0.69)	0.59 (0.49-0.61)	0.59 (0.42-0.6)	0.59 (0.5-0.6)
VTN	SERPINA4	102	67	0.64 (0.55-0.71)	0.65 (0.55-0.75)	0.64 (0.58-0.7)	0.58 (0.46-0.63)	0.6 (0.51-0.63)	0.59 (0.52-0.63)
CLEC4C	ORM1	101	63	0.6 (0.51-0.69)	0.64 (0.53-0.76)	0.62 (0.54-0.69)	0.58 (0.44-0.6)	0.6 (0.36-0.65)	0.58 (0.47-0.62)
NCR1	IL13	101	63	0.59 (0.5-0.66)	0.62 (0.5-0.73)	0.6 (0.53-0.67)	0.57 (0.43-0.58)	0.6 (0.46-0.61)	0.58 (0.51-0.59)
F9	SERPING1	102	67	0.58 (0.51-0.67)	0.64 (0.53-0.76)	0.61 (0.55-0.68)	0.56 (0.48-0.57)	0.61 (0.41-0.64)	0.58 (0.48-0.6)
CDSN	APCS	101	63	0.59 (0.51-0.67)	0.63 (0.52-0.75)	0.61 (0.53-0.69)	0.57 (0.45-0.6)	0.61 (0.48-0.62)	0.58 (0.5-0.61)
HSD11B1	C8B	101	63	0.62 (0.53-0.71)	0.62 (0.51-0.73)	0.62 (0.55-0.7)	0.59 (0.41-0.62)	0.58 (0.5-0.6)	0.58 (0.5-0.61)
CCL4	CRP_SRM	102	63	0.64 (0.5-0.73)	0.62 (0.49-0.74)	0.62 (0.53-0.7)	0.58 (0.36-0.65)	0.6 (0.47-0.63)	0.58 (0.47-0.63)
IL17C	C5	102	63	0.63 (0.55-0.71)	0.63 (0.52-0.74)	0.63 (0.55-0.7)	0.6 (0.39-0.63)	0.58 (0.5-0.62)	0.58 (0.49-0.62)
C3	C4B	102	67	0.58 (0.5-0.66)	0.69 (0.56-0.81)	0.63 (0.56-0.71)	0.57 (0.5-0.58)	0.62 (0.36-0.68)	0.58 (0.46-0.63)
IL6_PEA_cytokine	F9	102	63	0.58 (0.49-0.67)	0.63 (0.51-0.77)	0.61 (0.53-0.69)	0.55 (0.44-0.59)	0.62 (0.39-0.64)	0.58 (0.46-0.61)
CRP_SRM	ITIH1	102	67	0.62 (0.51-0.7)	0.63 (0.52-0.75)	0.63 (0.55-0.7)	0.58 (0.46-0.62)	0.61 (0.46-0.64)	0.58 (0.5-0.62)
VEGFA	F9	102	63	0.58 (0.49-0.67)	0.64 (0.53-0.76)	0.61 (0.54-0.69)	0.55 (0.47-0.58)	0.62 (0.38-0.63)	0.58 (0.46-0.6)
IFNG	SAA1	102	63	0.68 (0.59-0.77)	0.59 (0.42-0.74)	0.64 (0.54-0.72)	0.56 (0.32-0.69)	0.62 (0.56-0.63)	0.58 (0.46-0.65)
HSD11B1	F9	101	63	0.59 (0.51-0.68)	0.63 (0.51-0.77)	0.61 (0.53-0.69)	0.57 (0.51-0.59)	0.6 (0.45-0.63)	0.58 (0.51-0.61)
IL6_PEA_cytokine	C8B	102	63	0.65 (0.51-0.72)	0.59 (0.48-0.7)	0.62 (0.53-0.69)	0.61 (0.35-0.65)	0.56 (0.49-0.58)	0.58 (0.45-0.61)
C5	CLU	102	67	0.64 (0.54-0.72)	0.62 (0.51-0.72)	0.63 (0.56-0.7)	0.61 (0.45-0.64)	0.58 (0.47-0.6)	0.58 (0.51-0.62)

hsCRP	IL10_PEA_IR	98	63	0.64 (0.53-0.74)	0.59 (0.44-0.75)	0.62 (0.52-0.71)	0.56 (0.44-0.67)	0.61 (0.58-0.62)	0.58 (0.52-0.64)
LAMP3	ORM1	101	63	0.6 (0.48-0.69)	0.64 (0.54-0.75)	0.62 (0.54-0.7)	0.59 (0.5-0.59)	0.58 (0.39-0.64)	0.58 (0.48-0.61)
TNF	LRG1	102	63	0.6 (0.5-0.69)	0.61 (0.51-0.72)	0.6 (0.53-0.67)	0.59 (0.4-0.61)	0.59 (0.48-0.6)	0.58 (0.49-0.6)
CLEC4C	APCS	101	63	0.59 (0.5-0.67)	0.62 (0.53-0.74)	0.61 (0.54-0.68)	0.58 (0.45-0.59)	0.59 (0.38-0.63)	0.58 (0.48-0.61)
MASP1	IFNG	101	63	0.71 (0.61-0.78)	0.6 (0.43-0.73)	0.65 (0.56-0.73)	0.57 (0.29-0.71)	0.61 (0.55-0.62)	0.58 (0.44-0.66)
SERPINA3	F9	102	67	0.58 (0.5-0.68)	0.65 (0.53-0.77)	0.62 (0.54-0.69)	0.56 (0.47-0.58)	0.62 (0.39-0.64)	0.58 (0.47-0.61)
SERPINA3	APCS	102	67	0.6 (0.49-0.69)	0.62 (0.52-0.74)	0.61 (0.54-0.68)	0.59 (0.44-0.59)	0.6 (0.41-0.62)	0.58 (0.49-0.6)
C8B	ORM1	102	67	0.63 (0.52-0.71)	0.63 (0.52-0.74)	0.62 (0.55-0.7)	0.61 (0.4-0.62)	0.57 (0.49-0.62)	0.58 (0.5-0.62)
SH2D1A	C4B	101	63	0.58 (0.49-0.66)	0.69 (0.56-0.83)	0.63 (0.55-0.71)	0.56 (0.5-0.57)	0.62 (0.36-0.69)	0.58 (0.45-0.63)
FC	HPR	77	44	0.69 (0.6-0.78)	0.63 (0.51-0.77)	0.66 (0.59-0.74)	0.55 (0.38-0.69)	0.62 (0.54-0.64)	0.58 (0.5-0.66)
C4B	C8B	102	67	0.62 (0.52-0.7)	0.69 (0.56-0.81)	0.65 (0.57-0.72)	0.58 (0.53-0.61)	0.58 (0.39-0.68)	0.58 (0.48-0.64)
APOA1	CLU	102	67	0.62 (0.54-0.69)	0.61 (0.52-0.73)	0.62 (0.55-0.69)	0.6 (0.49-0.61)	0.58 (0.5-0.6)	0.58 (0.52-0.6)
FC	C2	77	44	0.67 (0.58-0.75)	0.61 (0.44-0.77)	0.64 (0.54-0.73)	0.58 (0.33-0.67)	0.59 (0.55-0.61)	0.58 (0.46-0.64)
MASP1	APOA1	101	63	0.63 (0.54-0.72)	0.61 (0.49-0.75)	0.62 (0.54-0.7)	0.6 (0.38-0.63)	0.57 (0.54-0.6)	0.58 (0.48-0.61)
FLT3LG	SERPING1	102	63	0.61 (0.53-0.69)	0.61 (0.5-0.73)	0.61 (0.54-0.69)	0.59 (0.45-0.61)	0.58 (0.51-0.59)	0.58 (0.51-0.6)
CPN2	C4B	102	67	0.61 (0.52-0.7)	0.68 (0.57-0.81)	0.65 (0.58-0.73)	0.56 (0.5-0.6)	0.61 (0.43-0.68)	0.58 (0.48-0.62)
ITIH2	APOA1	102	67	0.62 (0.55-0.69)	0.61 (0.52-0.71)	0.61 (0.55-0.69)	0.59 (0.48-0.61)	0.58 (0.52-0.6)	0.58 (0.52-0.6)
IL10_PEA_IR	CRP_SRM	101	63	0.63 (0.53-0.74)	0.6 (0.44-0.75)	0.62 (0.52-0.71)	0.56 (0.44-0.67)	0.61 (0.58-0.62)	0.58 (0.52-0.64)
MASP1	F9	101	63	0.61 (0.52-0.71)	0.64 (0.52-0.76)	0.63 (0.56-0.71)	0.57 (0.42-0.62)	0.6 (0.48-0.63)	0.58 (0.5-0.62)
CCL4	FLT3LG	102	63	0.61 (0.54-0.7)	0.64 (0.52-0.75)	0.62 (0.55-0.7)	0.59 (0.43-0.62)	0.58 (0.57-0.62)	0.58 (0.5-0.6)
CDSN	FLT3LG	101	63	0.61 (0.53-0.7)	0.62 (0.52-0.75)	0.62 (0.55-0.69)	0.58 (0.48-0.61)	0.6 (0.55-0.6)	0.58 (0.53-0.6)
FLT3LG	IL17C	102	63	0.62 (0.53-0.71)	0.61 (0.51-0.73)	0.61 (0.54-0.69)	0.59 (0.39-0.62)	0.58 (0.55-0.59)	0.58 (0.48-0.6)
LRG1	C4BPB	102	67	0.62 (0.53-0.71)	0.62 (0.51-0.72)	0.62 (0.55-0.69)	0.6 (0.41-0.62)	0.58 (0.48-0.62)	0.58 (0.5-0.62)
IFNG	ORM1	102	63	0.68 (0.59-0.76)	0.62 (0.46-0.73)	0.65 (0.57-0.72)	0.54 (0.33-0.67)	0.62 (0.53-0.63)	0.58 (0.48-0.64)
SIT1	IL13	101	63	0.59 (0.51-0.67)	0.61 (0.51-0.72)	0.6 (0.53-0.67)	0.57 (0.43-0.58)	0.6 (0.53-0.6)	0.58 (0.51-0.59)
C5	C3	102	67	0.61 (0.51-0.69)	0.63 (0.51-0.74)	0.62 (0.55-0.69)	0.58 (0.49-0.61)	0.6 (0.46-0.61)	0.58 (0.52-0.61)
LRG1	ITIH3	102	67	0.61 (0.52-0.69)	0.61 (0.51-0.71)	0.61 (0.55-0.68)	0.59 (0.41-0.61)	0.58 (0.45-0.6)	0.58 (0.5-0.6)
ORM1	CFB	102	67	0.59 (0.5-0.69)	0.64 (0.52-0.75)	0.61 (0.54-0.69)	0.58 (0.48-0.6)	0.6 (0.4-0.62)	0.58 (0.49-0.61)
PLXNA4	LRG1	101	63	0.61 (0.51-0.7)	0.64 (0.53-0.76)	0.63 (0.56-0.69)	0.58 (0.45-0.61)	0.61 (0.41-0.64)	0.58 (0.48-0.62)
SIT1	CP	101	63	0.59 (0.49-0.66)	0.69 (0.58-0.82)	0.64 (0.56-0.71)	0.57 (0.55-0.58)	0.59 (0.43-0.68)	0.58 (0.5-0.63)

C5	C4BPB	102	67	0.61 (0.52-0.7)	0.62 (0.52-0.74)	0.62 (0.55-0.69)	0.61 (0.45-0.61)	0.58 (0.47-0.61)	0.58 (0.49-0.61)
CLEC4C	NCR1	102	63	0.59 (0.52-0.66)	0.63 (0.5-0.75)	0.61 (0.54-0.69)	0.57 (0.47-0.58)	0.6 (0.41-0.63)	0.58 (0.48-0.61)
HSD11B1	FLT3LG	101	63	0.61 (0.53-0.69)	0.62 (0.51-0.73)	0.62 (0.55-0.69)	0.58 (0.47-0.61)	0.59 (0.53-0.62)	0.58 (0.51-0.61)
C5	CFB	102	67	0.62 (0.53-0.71)	0.63 (0.52-0.73)	0.62 (0.55-0.69)	0.59 (0.47-0.62)	0.58 (0.48-0.62)	0.58 (0.51-0.61)
C5	PZP	101	67	0.61 (0.51-0.7)	0.63 (0.51-0.73)	0.62 (0.54-0.7)	0.59 (0.45-0.62)	0.59 (0.39-0.63)	0.58 (0.49-0.62)
FGF2	IL6_PEA_cytokine	101	63	0.57 (0.45-0.65)	0.67 (0.41-0.79)	0.62 (0.48-0.69)	0.53 (0.44-0.59)	0.63 (0.35-0.66)	0.58 (0.44-0.61)
IL15	APOA1	102	63	0.61 (0.52-0.7)	0.59 (0.5-0.69)	0.6 (0.54-0.67)	0.61 (0.44-0.63)	0.56 (0.5-0.59)	0.58 (0.5-0.61)
hsCRP	CFB	98	67	0.62 (0.52-0.72)	0.63 (0.48-0.75)	0.62 (0.53-0.7)	0.56 (0.48-0.63)	0.61 (0.42-0.66)	0.58 (0.48-0.64)
LAMP3	HSD11B1	102	63	0.59 (0.5-0.68)	0.64 (0.53-0.75)	0.61 (0.55-0.68)	0.57 (0.52-0.59)	0.59 (0.4-0.65)	0.58 (0.49-0.61)
CDSN	ORM1	101	63	0.6 (0.5-0.69)	0.64 (0.52-0.76)	0.62 (0.54-0.7)	0.58 (0.46-0.61)	0.6 (0.46-0.63)	0.58 (0.49-0.61)
LRG1	SERPING1	102	67	0.61 (0.52-0.7)	0.61 (0.5-0.72)	0.61 (0.55-0.68)	0.59 (0.41-0.61)	0.59 (0.46-0.6)	0.58 (0.49-0.6)
IFNG	CFB	102	63	0.68 (0.59-0.76)	0.64 (0.49-0.77)	0.66 (0.57-0.74)	0.55 (0.35-0.64)	0.62 (0.53-0.63)	0.58 (0.48-0.63)
C8B	C4BPB	102	67	0.63 (0.53-0.7)	0.62 (0.51-0.72)	0.62 (0.55-0.69)	0.61 (0.38-0.63)	0.57 (0.47-0.59)	0.58 (0.48-0.61)
VEGFA	C8B	102	63	0.62 (0.52-0.7)	0.6 (0.51-0.71)	0.61 (0.53-0.68)	0.59 (0.38-0.63)	0.57 (0.48-0.59)	0.58 (0.48-0.61)
LRG1	ORM1	102	67	0.61 (0.51-0.71)	0.63 (0.52-0.73)	0.62 (0.54-0.69)	0.6 (0.44-0.62)	0.57 (0.44-0.62)	0.58 (0.49-0.62)
MASP1	CFB	101	63	0.62 (0.53-0.71)	0.64 (0.51-0.76)	0.63 (0.55-0.71)	0.56 (0.43-0.62)	0.61 (0.47-0.62)	0.58 (0.5-0.62)
FGF2	APCS	101	63	0.59 (0.5-0.67)	0.67 (0.47-0.79)	0.63 (0.53-0.7)	0.55 (0.48-0.59)	0.61 (0.35-0.67)	0.58 (0.45-0.62)
CRP_SRM	SERPINA3	102	67	0.61 (0.51-0.71)	0.62 (0.49-0.74)	0.62 (0.54-0.7)	0.56 (0.43-0.63)	0.59 (0.47-0.64)	0.58 (0.51-0.63)
C2	C8B	102	67	0.62 (0.52-0.7)	0.61 (0.5-0.72)	0.61 (0.54-0.69)	0.6 (0.4-0.63)	0.57 (0.5-0.58)	0.58 (0.49-0.6)
hsCRP	VTN	98	67	0.63 (0.51-0.71)	0.63 (0.53-0.74)	0.63 (0.55-0.7)	0.59 (0.47-0.63)	0.6 (0.44-0.65)	0.58 (0.48-0.64)
NCR1	FGF2	102	63	0.59 (0.51-0.67)	0.69 (0.5-0.81)	0.64 (0.53-0.71)	0.55 (0.51-0.58)	0.61 (0.39-0.68)	0.58 (0.47-0.63)
TNF	C8B	102	63	0.61 (0.52-0.7)	0.6 (0.51-0.71)	0.61 (0.54-0.67)	0.6 (0.4-0.62)	0.57 (0.53-0.58)	0.58 (0.48-0.6)
IL6_PEA_cytokine	APCS	102	63	0.6 (0.46-0.68)	0.6 (0.49-0.74)	0.6 (0.51-0.68)	0.58 (0.41-0.6)	0.59 (0.42-0.6)	0.58 (0.49-0.6)
C3	C8B	102	67	0.62 (0.52-0.7)	0.61 (0.51-0.73)	0.61 (0.55-0.69)	0.6 (0.41-0.62)	0.56 (0.5-0.59)	0.58 (0.49-0.6)
PLXNA4	ORM1	101	63	0.6 (0.5-0.7)	0.67 (0.56-0.78)	0.63 (0.55-0.71)	0.57 (0.49-0.59)	0.61 (0.36-0.66)	0.58 (0.46-0.62)
C4B	PZP	101	67	0.58 (0.48-0.67)	0.68 (0.55-0.8)	0.63 (0.54-0.71)	0.55 (0.54-0.56)	0.61 (0.34-0.68)	0.58 (0.45-0.62)
CDSN	LRG1	101	63	0.61 (0.52-0.7)	0.62 (0.51-0.73)	0.62 (0.54-0.69)	0.58 (0.43-0.61)	0.6 (0.48-0.62)	0.58 (0.49-0.61)
IFNG	C4B	102	63	0.68 (0.6-0.75)	0.68 (0.53-0.81)	0.68 (0.6-0.75)	0.52 (0.46-0.63)	0.65 (0.47-0.68)	0.58 (0.5-0.64)
SAA1	CFB	102	67	0.58 (0.48-0.68)	0.65 (0.47-0.79)	0.61 (0.51-0.7)	0.57 (0.49-0.59)	0.65 (0.39-0.67)	0.58 (0.45-0.63)
PLXNA4	CRP_SRM	101	63	0.63 (0.51-0.72)	0.64 (0.52-0.77)	0.63 (0.55-0.71)	0.57 (0.48-0.62)	0.61 (0.41-0.63)	0.58 (0.48-0.62)

MILR1	SERPINA3	101	63	0.67 (0.59-0.75)	0.59 (0.49-0.72)	0.63 (0.56-0.7)	0.6 (0.35-0.66)	0.56 (0.53-0.58)	0.58 (0.46-0.62)
CDSN	SIT1	102	63	0.6 (0.52-0.67)	0.63 (0.52-0.73)	0.62 (0.55-0.68)	0.57 (0.46-0.58)	0.6 (0.52-0.62)	0.58 (0.52-0.6)
CCL13	C8B	102	63	0.62 (0.52-0.71)	0.62 (0.52-0.73)	0.62 (0.55-0.69)	0.59 (0.43-0.62)	0.58 (0.44-0.6)	0.58 (0.49-0.61)
FLT3LG	IL15	102	63	0.61 (0.51-0.7)	0.6 (0.51-0.71)	0.61 (0.54-0.68)	0.59 (0.44-0.61)	0.57 (0.51-0.59)	0.58 (0.5-0.59)
IL15	CFB	102	63	0.58 (0.47-0.66)	0.66 (0.53-0.79)	0.61 (0.54-0.7)	0.58 (0.55-0.59)	0.58 (0.37-0.67)	0.58 (0.47-0.62)
CLEC4C	IFNG	101	63	0.68 (0.59-0.75)	0.63 (0.42-0.76)	0.65 (0.54-0.73)	0.56 (0.32-0.67)	0.6 (0.59-0.61)	0.58 (0.46-0.64)
hsCRP	SERPINA4	98	67	0.63 (0.53-0.72)	0.61 (0.51-0.72)	0.62 (0.55-0.69)	0.59 (0.46-0.64)	0.58 (0.49-0.61)	0.58 (0.5-0.62)
DCTN1	SIT1	102	63	0.61 (0.52-0.68)	0.7 (0.58-0.81)	0.65 (0.58-0.72)	0.54 (0.51-0.6)	0.62 (0.4-0.67)	0.58 (0.46-0.62)
hsCRP	PLXNA4	98	63	0.62 (0.51-0.71)	0.64 (0.52-0.76)	0.63 (0.54-0.71)	0.57 (0.5-0.62)	0.6 (0.39-0.63)	0.58 (0.48-0.62)
C5	C8A	102	67	0.61 (0.52-0.69)	0.63 (0.51-0.72)	0.62 (0.55-0.68)	0.6 (0.47-0.61)	0.58 (0.47-0.61)	0.58 (0.5-0.61)
TNF	F9	102	63	0.58 (0.5-0.65)	0.63 (0.53-0.76)	0.6 (0.54-0.68)	0.56 (0.48-0.57)	0.61 (0.43-0.63)	0.58 (0.49-0.59)
LAMP3	FGF2	102	63	0.59 (0.48-0.67)	0.66 (0.5-0.77)	0.62 (0.53-0.7)	0.55 (0.5-0.58)	0.62 (0.35-0.66)	0.58 (0.44-0.62)
ITGA11	ITIH3	101	63	0.64 (0.54-0.72)	0.59 (0.48-0.72)	0.62 (0.53-0.69)	0.59 (0.37-0.64)	0.58 (0.5-0.59)	0.58 (0.47-0.61)
CXCL9	APOA1	102	63	0.69 (0.61-0.76)	0.57 (0.48-0.69)	0.63 (0.57-0.7)	0.6 (0.33-0.69)	0.56 (0.55-0.57)	0.58 (0.44-0.63)
PLXNA4	APCS	101	63	0.6 (0.49-0.68)	0.64 (0.53-0.76)	0.62 (0.55-0.69)	0.58 (0.46-0.6)	0.59 (0.38-0.64)	0.58 (0.47-0.61)
IL10_PEA_IR	FLT3LG	101	63	0.61 (0.53-0.7)	0.6 (0.45-0.74)	0.6 (0.52-0.69)	0.57 (0.46-0.61)	0.58 (0.55-0.6)	0.58 (0.51-0.6)
C2	APCS	102	67	0.59 (0.5-0.68)	0.62 (0.49-0.73)	0.6 (0.53-0.67)	0.58 (0.45-0.59)	0.59 (0.41-0.61)	0.58 (0.49-0.6)
FCRL6	CRP_SRM	101	63	0.63 (0.52-0.71)	0.66 (0.53-0.76)	0.64 (0.56-0.71)	0.59 (0.45-0.62)	0.6 (0.44-0.66)	0.58 (0.48-0.64)
ITGA11	APCS	101	63	0.63 (0.53-0.71)	0.61 (0.51-0.73)	0.62 (0.55-0.7)	0.59 (0.39-0.62)	0.58 (0.43-0.6)	0.58 (0.48-0.61)
NCR1	SERPIND1	101	63	0.59 (0.51-0.66)	0.67 (0.57-0.77)	0.63 (0.56-0.69)	0.57 (0.53-0.58)	0.59 (0.39-0.67)	0.58 (0.48-0.62)
IL10_PEA_IR	CXCL9	101	63	0.7 (0.61-0.78)	0.58 (0.38-0.78)	0.64 (0.54-0.74)	0.54 (0.3-0.71)	0.63 (0.55-0.64)	0.58 (0.46-0.67)
IL10_PEA_IR	CFB	101	63	0.58 (0.5-0.66)	0.62 (0.48-0.77)	0.6 (0.51-0.69)	0.55 (0.47-0.58)	0.61 (0.55-0.64)	0.58 (0.53-0.6)
hsCRP	SERPINA3	98	67	0.62 (0.5-0.72)	0.62 (0.49-0.75)	0.62 (0.54-0.7)	0.56 (0.45-0.63)	0.59 (0.46-0.63)	0.58 (0.5-0.63)
HGF	C8B	102	63	0.63 (0.53-0.71)	0.6 (0.49-0.72)	0.61 (0.53-0.69)	0.61 (0.37-0.64)	0.57 (0.5-0.58)	0.58 (0.47-0.61)
SERPINA3	APOA1	102	67	0.63 (0.56-0.72)	0.59 (0.5-0.71)	0.61 (0.55-0.68)	0.6 (0.39-0.64)	0.56 (0.53-0.57)	0.58 (0.47-0.6)
HSD11B1	SIT1	102	63	0.6 (0.52-0.67)	0.61 (0.52-0.73)	0.61 (0.54-0.67)	0.57 (0.48-0.59)	0.59 (0.55-0.6)	0.58 (0.53-0.59)
C5	C4B	102	67	0.61 (0.52-0.69)	0.68 (0.56-0.8)	0.65 (0.57-0.72)	0.58 (0.52-0.61)	0.59 (0.39-0.68)	0.58 (0.48-0.63)
IL6_PEA_cytokine	CXCL9	102	63	0.67 (0.58-0.75)	0.56 (0.43-0.7)	0.61 (0.53-0.69)	0.61 (0.34-0.66)	0.55 (0.54-0.56)	0.58 (0.44-0.6)
ITGA6	HP	101	63	0.68 (0.59-0.74)	0.72 (0.6-0.81)	0.69 (0.62-0.75)	0.6 (0.48-0.64)	0.56 (0.51-0.64)	0.58 (0.51-0.63)
SERPINA3	C8B	102	67	0.62 (0.52-0.7)	0.61 (0.51-0.72)	0.61 (0.54-0.68)	0.6 (0.39-0.63)	0.57 (0.5-0.59)	0.58 (0.48-0.6)

FGF2	HGF	101	63	0.57 (0.49-0.67)	0.67 (0.41-0.79)	0.62 (0.49-0.69)	0.53 (0.47-0.58)	0.63 (0.35-0.66)	0.58 (0.43-0.61)
IL6_PEA_IR	CRP_SRM	101	63	0.63 (0.5-0.71)	0.62 (0.47-0.75)	0.62 (0.53-0.7)	0.56 (0.43-0.63)	0.6 (0.45-0.63)	0.58 (0.49-0.62)
FC	MASP1	76	43	0.7 (0.56-0.78)	0.63 (0.45-0.79)	0.66 (0.56-0.75)	0.61 (0.3-0.69)	0.55 (0.53-0.6)	0.58 (0.43-0.62)
ITGA11	IL15	101	63	0.64 (0.52-0.72)	0.59 (0.48-0.7)	0.61 (0.53-0.68)	0.63 (0.39-0.64)	0.55 (0.47-0.59)	0.58 (0.47-0.61)
KLRD1	ORM1	101	63	0.61 (0.52-0.7)	0.62 (0.52-0.72)	0.61 (0.55-0.68)	0.59 (0.41-0.61)	0.58 (0.45-0.6)	0.58 (0.49-0.6)
ITIH3	C4B	102	67	0.59 (0.51-0.67)	0.68 (0.56-0.8)	0.64 (0.57-0.71)	0.56 (0.49-0.58)	0.6 (0.38-0.68)	0.58 (0.47-0.63)
KLRD1	CFB	101	63	0.6 (0.52-0.68)	0.64 (0.53-0.75)	0.62 (0.56-0.69)	0.58 (0.46-0.61)	0.59 (0.47-0.63)	0.58 (0.5-0.62)
NCR1	PLXNA4	102	63	0.59 (0.51-0.66)	0.67 (0.56-0.79)	0.63 (0.56-0.69)	0.55 (0.52-0.58)	0.61 (0.38-0.66)	0.58 (0.47-0.61)
LRG1	C3	102	67	0.61 (0.52-0.69)	0.61 (0.51-0.73)	0.61 (0.54-0.68)	0.58 (0.44-0.61)	0.59 (0.47-0.63)	0.58 (0.5-0.61)
IL10_PEA_IR	C4B	101	63	0.59 (0.5-0.67)	0.68 (0.53-0.81)	0.63 (0.55-0.71)	0.55 (0.51-0.59)	0.6 (0.44-0.67)	0.58 (0.49-0.61)
LRG1	C8A	102	67	0.61 (0.52-0.7)	0.6 (0.51-0.7)	0.61 (0.54-0.67)	0.6 (0.41-0.61)	0.57 (0.49-0.61)	0.58 (0.48-0.6)
NCR1	C2	101	63	0.59 (0.51-0.67)	0.61 (0.5-0.74)	0.61 (0.53-0.68)	0.58 (0.44-0.6)	0.59 (0.46-0.6)	0.58 (0.5-0.6)
FCRL6	F9	101	63	0.58 (0.51-0.66)	0.68 (0.56-0.8)	0.63 (0.56-0.7)	0.56 (0.48-0.57)	0.61 (0.35-0.68)	0.58 (0.45-0.62)
FGF2	C3	101	63	0.58 (0.49-0.66)	0.67 (0.44-0.79)	0.63 (0.52-0.7)	0.55 (0.46-0.57)	0.6 (0.34-0.67)	0.58 (0.45-0.62)
NCR1	CXCL9	101	63	0.67 (0.59-0.75)	0.61 (0.5-0.71)	0.64 (0.57-0.7)	0.59 (0.35-0.67)	0.57 (0.55-0.58)	0.58 (0.46-0.62)
CLEC4C	LAMP3	102	63	0.58 (0.49-0.66)	0.64 (0.53-0.75)	0.61 (0.54-0.68)	0.56 (0.5-0.58)	0.61 (0.37-0.64)	0.58 (0.46-0.61)
IL17F	F9	102	63	0.59 (0.5-0.68)	0.63 (0.48-0.76)	0.61 (0.52-0.69)	0.56 (0.44-0.59)	0.6 (0.4-0.63)	0.58 (0.48-0.6)
HGF	LRG1	102	63	0.61 (0.52-0.71)	0.6 (0.48-0.71)	0.61 (0.53-0.68)	0.58 (0.4-0.61)	0.58 (0.47-0.6)	0.58 (0.48-0.6)
MASP1	C4BPB	101	63	0.63 (0.55-0.72)	0.6 (0.49-0.75)	0.62 (0.55-0.7)	0.58 (0.38-0.62)	0.59 (0.53-0.6)	0.58 (0.48-0.61)
CRP_SRM	SERPINA4	102	67	0.64 (0.54-0.73)	0.62 (0.51-0.72)	0.63 (0.56-0.7)	0.59 (0.43-0.66)	0.57 (0.5-0.62)	0.58 (0.5-0.63)
DCTN1	HP	101	63	0.68 (0.6-0.76)	0.72 (0.6-0.82)	0.7 (0.63-0.76)	0.57 (0.49-0.66)	0.58 (0.48-0.68)	0.58 (0.51-0.64)
FLT3LG	CLU	102	63	0.61 (0.53-0.7)	0.61 (0.52-0.73)	0.61 (0.55-0.69)	0.58 (0.46-0.6)	0.57 (0.51-0.61)	0.58 (0.51-0.6)
NCR1	IL6_PEA_cytokine	101	63	0.59 (0.5-0.67)	0.61 (0.49-0.72)	0.6 (0.52-0.68)	0.56 (0.42-0.59)	0.6 (0.45-0.6)	0.58 (0.5-0.59)
MILR1	C3	101	63	0.64 (0.56-0.72)	0.62 (0.51-0.75)	0.63 (0.57-0.71)	0.6 (0.39-0.64)	0.57 (0.5-0.61)	0.58 (0.48-0.62)
C8B	C8A	102	67	0.62 (0.52-0.7)	0.65 (0.53-0.77)	0.63 (0.56-0.71)	0.59 (0.45-0.63)	0.57 (0.45-0.65)	0.58 (0.5-0.63)
SERPIND1	ORM1	102	67	0.59 (0.5-0.69)	0.66 (0.57-0.76)	0.63 (0.56-0.7)	0.57 (0.5-0.59)	0.6 (0.36-0.66)	0.58 (0.47-0.62)
NCR1	CDSN	102	63	0.58 (0.51-0.66)	0.65 (0.52-0.76)	0.61 (0.54-0.69)	0.56 (0.48-0.58)	0.61 (0.51-0.64)	0.58 (0.52-0.61)
CDSN	SAA1	101	63	0.59 (0.51-0.68)	0.63 (0.48-0.76)	0.61 (0.53-0.69)	0.56 (0.45-0.58)	0.64 (0.45-0.66)	0.58 (0.47-0.62)
CRP_SRM	CLU	102	67	0.62 (0.51-0.71)	0.62 (0.52-0.73)	0.62 (0.55-0.69)	0.59 (0.46-0.63)	0.58 (0.45-0.63)	0.58 (0.5-0.62)
MILR1	SAA1	101	63	0.67 (0.59-0.75)	0.58 (0.47-0.71)	0.63 (0.55-0.7)	0.61 (0.34-0.68)	0.56 (0.53-0.57)	0.58 (0.45-0.62)

SIT1	C2	101	63	0.59 (0.5-0.67)	0.62 (0.51-0.74)	0.61 (0.54-0.68)	0.58 (0.48-0.58)	0.59 (0.53-0.61)	0.58 (0.52-0.59)
HSD11B1	ORM1	101	63	0.6 (0.51-0.7)	0.62 (0.52-0.73)	0.61 (0.53-0.69)	0.58 (0.46-0.61)	0.59 (0.43-0.61)	0.58 (0.49-0.61)
ITGA11	CFB	101	63	0.62 (0.52-0.7)	0.65 (0.51-0.76)	0.63 (0.54-0.7)	0.58 (0.41-0.62)	0.59 (0.42-0.65)	0.58 (0.46-0.63)
ITGA11	APOA1	101	63	0.62 (0.54-0.71)	0.58 (0.48-0.7)	0.61 (0.53-0.68)	0.6 (0.38-0.63)	0.55 (0.51-0.57)	0.58 (0.47-0.59)
IL17F	FLT3LG	102	63	0.6 (0.52-0.69)	0.61 (0.48-0.74)	0.61 (0.53-0.69)	0.57 (0.43-0.6)	0.58 (0.54-0.6)	0.58 (0.5-0.59)
IL13	APOA1	102	63	0.6 (0.52-0.68)	0.59 (0.49-0.7)	0.6 (0.53-0.67)	0.58 (0.43-0.59)	0.58 (0.52-0.59)	0.58 (0.5-0.59)
FLT3LG	VTN	102	63	0.61 (0.54-0.7)	0.64 (0.54-0.76)	0.63 (0.56-0.7)	0.58 (0.5-0.6)	0.59 (0.48-0.64)	0.58 (0.52-0.61)
FC	APOA1	77	44	0.71 (0.62-0.79)	0.59 (0.47-0.71)	0.65 (0.58-0.72)	0.58 (0.31-0.73)	0.58 (0.54-0.61)	0.58 (0.44-0.66)
SIT1	C4BPB	101	63	0.61 (0.53-0.69)	0.6 (0.52-0.72)	0.61 (0.55-0.68)	0.58 (0.45-0.6)	0.58 (0.54-0.59)	0.58 (0.5-0.59)
CDSN	IFNG	101	63	0.68 (0.6-0.76)	0.6 (0.43-0.72)	0.64 (0.54-0.72)	0.55 (0.32-0.67)	0.6 (0.54-0.63)	0.58 (0.46-0.64)
hsCRP	IL17C	98	63	0.64 (0.54-0.72)	0.61 (0.48-0.74)	0.62 (0.54-0.7)	0.59 (0.38-0.63)	0.57 (0.51-0.6)	0.58 (0.47-0.61)
IL10_PEA_IR	ORM1	101	63	0.62 (0.53-0.72)	0.62 (0.46-0.74)	0.62 (0.53-0.71)	0.56 (0.4-0.63)	0.59 (0.56-0.6)	0.58 (0.5-0.61)
CCL13	LRG1	102	63	0.6 (0.52-0.69)	0.62 (0.52-0.72)	0.61 (0.54-0.68)	0.56 (0.41-0.61)	0.59 (0.43-0.6)	0.58 (0.49-0.6)
NCR1	C4BPB	101	63	0.61 (0.52-0.69)	0.62 (0.52-0.73)	0.61 (0.54-0.68)	0.59 (0.42-0.6)	0.58 (0.48-0.6)	0.58 (0.49-0.6)
LAMP3	IL13	101	63	0.58 (0.46-0.68)	0.63 (0.45-0.74)	0.6 (0.51-0.68)	0.57 (0.43-0.58)	0.61 (0.37-0.63)	0.58 (0.44-0.6)
VEGFA	APCS	102	63	0.59 (0.48-0.68)	0.61 (0.5-0.72)	0.6 (0.53-0.67)	0.58 (0.43-0.59)	0.59 (0.41-0.61)	0.58 (0.49-0.59)
TNF	CFB	102	63	0.57 (0.49-0.65)	0.63 (0.52-0.76)	0.6 (0.53-0.67)	0.56 (0.47-0.57)	0.6 (0.42-0.63)	0.58 (0.49-0.6)
CCL4	F9	102	63	0.58 (0.5-0.68)	0.63 (0.53-0.76)	0.61 (0.54-0.68)	0.56 (0.41-0.59)	0.6 (0.4-0.63)	0.58 (0.47-0.6)
FLT3LG	PZP	101	63	0.61 (0.52-0.71)	0.62 (0.5-0.75)	0.61 (0.53-0.7)	0.59 (0.44-0.62)	0.57 (0.38-0.63)	0.58 (0.48-0.61)
SIT1	CCL13	101	63	0.59 (0.51-0.66)	0.62 (0.53-0.73)	0.61 (0.54-0.67)	0.56 (0.5-0.58)	0.59 (0.5-0.61)	0.58 (0.52-0.59)
CXCL9	APCS	102	63	0.66 (0.58-0.74)	0.62 (0.49-0.73)	0.64 (0.57-0.71)	0.57 (0.37-0.66)	0.59 (0.5-0.61)	0.58 (0.47-0.63)
LAMP3	IL6_PEA_cytokine	101	63	0.6 (0.45-0.69)	0.62 (0.48-0.73)	0.6 (0.51-0.69)	0.57 (0.44-0.62)	0.59 (0.41-0.61)	0.58 (0.48-0.61)
C2	CFB	102	67	0.57 (0.5-0.65)	0.63 (0.52-0.73)	0.6 (0.54-0.67)	0.56 (0.48-0.56)	0.6 (0.4-0.62)	0.58 (0.47-0.59)
FC	ITIH1	77	44	0.67 (0.56-0.77)	0.62 (0.47-0.75)	0.65 (0.55-0.72)	0.57 (0.36-0.67)	0.58 (0.55-0.61)	0.58 (0.47-0.63)
NCR1	ITIH1	101	63	0.59 (0.52-0.67)	0.65 (0.54-0.76)	0.62 (0.55-0.68)	0.58 (0.5-0.59)	0.59 (0.44-0.64)	0.58 (0.49-0.61)
MILR1	IL6_PEA_cytokine	101	63	0.66 (0.57-0.74)	0.57 (0.44-0.7)	0.61 (0.54-0.69)	0.62 (0.34-0.67)	0.54 (0.49-0.57)	0.58 (0.43-0.61)
CCL13	FLT3LG	102	63	0.61 (0.52-0.7)	0.62 (0.52-0.74)	0.62 (0.55-0.68)	0.6 (0.47-0.61)	0.57 (0.49-0.62)	0.58 (0.51-0.61)
FGF2	SERPINA3	101	63	0.57 (0.49-0.66)	0.68 (0.43-0.79)	0.62 (0.5-0.7)	0.54 (0.45-0.57)	0.61 (0.35-0.67)	0.58 (0.44-0.61)
C3	ORM1	102	67	0.6 (0.5-0.69)	0.62 (0.51-0.75)	0.61 (0.54-0.68)	0.58 (0.45-0.6)	0.59 (0.41-0.62)	0.58 (0.49-0.6)
hsCRP	IL6_PEA_IR	98	63	0.61 (0.5-0.7)	0.62 (0.48-0.75)	0.62 (0.53-0.7)	0.57 (0.45-0.62)	0.6 (0.44-0.63)	0.58 (0.48-0.62)

IL6_PEA_IR	F9	101	63	0.59 (0.5-0.68)	0.64 (0.52-0.77)	0.62 (0.54-0.7)	0.57 (0.44-0.6)	0.61 (0.4-0.63)	0.58 (0.48-0.61)
FC	CP	77	44	0.68 (0.59-0.77)	0.66 (0.5-0.81)	0.67 (0.59-0.76)	0.59 (0.35-0.67)	0.56 (0.5-0.64)	0.58 (0.46-0.63)
C2	APOA1	102	67	0.63 (0.55-0.71)	0.59 (0.49-0.72)	0.61 (0.54-0.69)	0.59 (0.39-0.62)	0.56 (0.54-0.58)	0.58 (0.48-0.6)
SIT1	ITIH1	101	63	0.59 (0.52-0.66)	0.66 (0.54-0.77)	0.63 (0.56-0.69)	0.56 (0.51-0.58)	0.59 (0.46-0.66)	0.57 (0.5-0.61)
PLXNA4	SIT1	102	63	0.6 (0.51-0.67)	0.64 (0.54-0.78)	0.62 (0.55-0.7)	0.56 (0.49-0.59)	0.6 (0.51-0.64)	0.57 (0.53-0.61)
CCL13	F9	102	63	0.58 (0.49-0.66)	0.66 (0.54-0.76)	0.61 (0.55-0.69)	0.55 (0.53-0.57)	0.6 (0.39-0.64)	0.57 (0.47-0.6)
IL10_PEA_IR	F9	101	63	0.6 (0.51-0.68)	0.63 (0.46-0.76)	0.61 (0.51-0.7)	0.55 (0.48-0.59)	0.6 (0.56-0.62)	0.57 (0.52-0.6)
C3	F9	102	67	0.58 (0.5-0.66)	0.64 (0.54-0.76)	0.61 (0.54-0.68)	0.55 (0.47-0.57)	0.6 (0.37-0.64)	0.57 (0.47-0.6)
KLRD1	NCR1	102	63	0.6 (0.52-0.68)	0.62 (0.52-0.72)	0.61 (0.54-0.67)	0.58 (0.42-0.59)	0.58 (0.47-0.61)	0.57 (0.48-0.6)
FLT3LG	ITIH2	102	63	0.62 (0.53-0.7)	0.63 (0.52-0.75)	0.62 (0.55-0.7)	0.58 (0.49-0.61)	0.58 (0.5-0.63)	0.57 (0.52-0.61)
FGF2	SIT1	102	63	0.6 (0.52-0.67)	0.65 (0.49-0.77)	0.63 (0.53-0.7)	0.55 (0.51-0.58)	0.59 (0.51-0.63)	0.57 (0.53-0.6)
ITIH3	ORM1	102	67	0.61 (0.51-0.7)	0.62 (0.52-0.73)	0.61 (0.54-0.68)	0.59 (0.42-0.6)	0.57 (0.44-0.6)	0.57 (0.49-0.6)
CP	ORM1	102	67	0.6 (0.48-0.7)	0.66 (0.54-0.78)	0.63 (0.55-0.71)	0.58 (0.48-0.6)	0.58 (0.34-0.67)	0.57 (0.46-0.63)
SERPING1	APCS	102	67	0.6 (0.49-0.68)	0.62 (0.51-0.74)	0.61 (0.54-0.68)	0.58 (0.44-0.59)	0.58 (0.42-0.62)	0.57 (0.49-0.6)
CLEC4C	SIT1	102	63	0.6 (0.51-0.67)	0.63 (0.53-0.77)	0.61 (0.55-0.69)	0.57 (0.47-0.59)	0.59 (0.49-0.64)	0.57 (0.51-0.6)
SIT1	TNF	101	63	0.59 (0.52-0.66)	0.6 (0.51-0.71)	0.6 (0.53-0.66)	0.57 (0.43-0.58)	0.58 (0.54-0.59)	0.57 (0.51-0.58)
FGF2	C8B	101	63	0.61 (0.52-0.69)	0.66 (0.47-0.77)	0.63 (0.52-0.7)	0.55 (0.48-0.62)	0.59 (0.42-0.64)	0.57 (0.49-0.62)
C9	HPR	102	67	0.63 (0.54-0.72)	0.65 (0.54-0.76)	0.64 (0.57-0.71)	0.56 (0.42-0.63)	0.59 (0.48-0.62)	0.57 (0.49-0.62)
LRG1	ITIH1	102	67	0.61 (0.52-0.69)	0.63 (0.51-0.74)	0.62 (0.55-0.69)	0.58 (0.42-0.61)	0.59 (0.44-0.62)	0.57 (0.48-0.61)
CCL4	LRG1	102	63	0.62 (0.51-0.71)	0.6 (0.5-0.71)	0.61 (0.53-0.68)	0.58 (0.37-0.63)	0.58 (0.46-0.59)	0.57 (0.47-0.61)
HGF	CFB	102	63	0.58 (0.49-0.66)	0.64 (0.51-0.75)	0.61 (0.53-0.68)	0.55 (0.47-0.58)	0.61 (0.38-0.63)	0.57 (0.47-0.6)
IL10_PEA_IR	LRG1	101	63	0.63 (0.54-0.72)	0.6 (0.45-0.74)	0.61 (0.53-0.7)	0.56 (0.41-0.63)	0.59 (0.57-0.61)	0.57 (0.5-0.61)
HGF	APCS	102	63	0.6 (0.48-0.69)	0.61 (0.5-0.72)	0.6 (0.53-0.68)	0.59 (0.43-0.6)	0.58 (0.42-0.59)	0.57 (0.49-0.59)
FC	KLRD1	76	43	0.68 (0.58-0.76)	0.61 (0.49-0.74)	0.65 (0.57-0.72)	0.6 (0.33-0.67)	0.56 (0.52-0.58)	0.57 (0.45-0.62)
IL6_PEA_IR	LRG1	101	63	0.63 (0.53-0.71)	0.61 (0.49-0.72)	0.62 (0.54-0.69)	0.59 (0.41-0.63)	0.58 (0.45-0.6)	0.57 (0.48-0.61)
TNF	APCS	102	63	0.59 (0.49-0.67)	0.61 (0.52-0.73)	0.6 (0.53-0.67)	0.57 (0.44-0.6)	0.58 (0.44-0.6)	0.57 (0.5-0.59)
NCR1	CCL13	101	63	0.59 (0.51-0.66)	0.63 (0.53-0.74)	0.61 (0.55-0.67)	0.57 (0.49-0.58)	0.58 (0.44-0.61)	0.57 (0.5-0.59)
KLRD1	MASP1	102	63	0.63 (0.54-0.72)	0.59 (0.48-0.73)	0.61 (0.54-0.69)	0.6 (0.37-0.63)	0.55 (0.52-0.58)	0.57 (0.46-0.61)
KLRD1	CXCL9	101	63	0.67 (0.58-0.75)	0.58 (0.46-0.69)	0.62 (0.55-0.69)	0.59 (0.34-0.66)	0.57 (0.52-0.58)	0.57 (0.45-0.62)
FCRL6	SIT1	102	63	0.59 (0.52-0.67)	0.64 (0.54-0.75)	0.62 (0.56-0.68)	0.56 (0.48-0.59)	0.59 (0.49-0.63)	0.57 (0.51-0.6)

F9	ITIH1	102	67	0.59 (0.51-0.67)	0.64 (0.54-0.76)	0.61 (0.55-0.68)	0.56 (0.49-0.58)	0.61 (0.4-0.63)	0.57 (0.47-0.6)
APOA1	C4BPB	102	67	0.63 (0.56-0.71)	0.58 (0.51-0.68)	0.61 (0.56-0.68)	0.6 (0.38-0.63)	0.55 (0.54-0.56)	0.57 (0.46-0.59)
NCR1	SERPING1	101	63	0.59 (0.51-0.67)	0.62 (0.49-0.74)	0.6 (0.54-0.67)	0.58 (0.46-0.58)	0.58 (0.46-0.6)	0.57 (0.5-0.59)
CCL13	CFB	102	63	0.57 (0.5-0.66)	0.66 (0.53-0.78)	0.61 (0.55-0.69)	0.55 (0.5-0.57)	0.6 (0.38-0.65)	0.57 (0.46-0.61)
FC	SIT1	76	43	0.71 (0.63-0.79)	0.59 (0.48-0.73)	0.65 (0.58-0.73)	0.55 (0.29-0.72)	0.59 (0.54-0.6)	0.57 (0.44-0.66)
CDSN	CFB	101	63	0.57 (0.49-0.65)	0.64 (0.53-0.77)	0.6 (0.53-0.68)	0.55 (0.47-0.57)	0.61 (0.41-0.63)	0.57 (0.47-0.6)
FGF2	SERPIND1	101	63	0.56 (0.48-0.64)	0.68 (0.53-0.79)	0.62 (0.53-0.69)	0.53 (0.51-0.54)	0.62 (0.33-0.68)	0.57 (0.43-0.61)
hsCRP	SERPIND1	98	67	0.63 (0.52-0.71)	0.66 (0.54-0.77)	0.64 (0.57-0.71)	0.57 (0.47-0.62)	0.6 (0.39-0.67)	0.57 (0.45-0.64)
CXCL9	SAA1	102	63	0.65 (0.56-0.74)	0.57 (0.45-0.7)	0.62 (0.53-0.7)	0.58 (0.35-0.66)	0.57 (0.54-0.57)	0.57 (0.46-0.61)
DCTN1	C4B	101	63	0.57 (0.49-0.66)	0.75 (0.62-0.86)	0.66 (0.59-0.73)	0.55 (0.52-0.57)	0.6 (0.26-0.74)	0.57 (0.41-0.65)
SIT1	SERPING1	101	63	0.59 (0.51-0.67)	0.63 (0.51-0.73)	0.61 (0.54-0.67)	0.57 (0.46-0.58)	0.58 (0.53-0.62)	0.57 (0.51-0.6)
MILR1	IL13	101	63	0.64 (0.55-0.72)	0.59 (0.45-0.7)	0.61 (0.53-0.68)	0.6 (0.38-0.64)	0.56 (0.48-0.56)	0.57 (0.44-0.6)
ITIH2	APCS	102	67	0.59 (0.5-0.67)	0.62 (0.53-0.73)	0.6 (0.54-0.67)	0.58 (0.44-0.59)	0.58 (0.42-0.61)	0.57 (0.49-0.6)
LRG1	C2	102	67	0.61 (0.51-0.69)	0.59 (0.47-0.71)	0.6 (0.52-0.68)	0.58 (0.41-0.6)	0.58 (0.46-0.62)	0.57 (0.49-0.61)
CLEC4C	C3	101	63	0.58 (0.5-0.65)	0.62 (0.51-0.76)	0.6 (0.53-0.68)	0.56 (0.45-0.57)	0.59 (0.37-0.64)	0.57 (0.47-0.6)
SAA1	SERPIND1	102	67	0.58 (0.49-0.66)	0.66 (0.52-0.78)	0.62 (0.54-0.69)	0.57 (0.48-0.58)	0.64 (0.42-0.68)	0.57 (0.45-0.63)
C2	ORM1	102	67	0.59 (0.5-0.69)	0.63 (0.52-0.73)	0.6 (0.53-0.68)	0.56 (0.46-0.59)	0.59 (0.4-0.61)	0.57 (0.48-0.6)
MASP1	C3	101	63	0.62 (0.51-0.71)	0.62 (0.5-0.75)	0.62 (0.55-0.7)	0.56 (0.4-0.62)	0.59 (0.45-0.6)	0.57 (0.49-0.6)
SERPINA4	CLU	102	67	0.61 (0.52-0.7)	0.62 (0.53-0.72)	0.62 (0.55-0.68)	0.6 (0.41-0.62)	0.56 (0.47-0.6)	0.57 (0.48-0.61)
PLXNA4	CFB	101	63	0.57 (0.49-0.65)	0.64 (0.53-0.78)	0.61 (0.54-0.68)	0.54 (0.49-0.58)	0.61 (0.38-0.64)	0.57 (0.46-0.6)
VEGFA	CFB	102	63	0.58 (0.48-0.66)	0.63 (0.51-0.75)	0.6 (0.53-0.68)	0.56 (0.44-0.58)	0.59 (0.39-0.64)	0.57 (0.47-0.6)
IL10_PEA_IR	APCS	101	63	0.6 (0.52-0.69)	0.6 (0.45-0.74)	0.6 (0.52-0.69)	0.56 (0.45-0.61)	0.59 (0.58-0.6)	0.57 (0.52-0.6)
SERPINA3	ORM1	102	67	0.59 (0.5-0.7)	0.63 (0.52-0.74)	0.61 (0.54-0.69)	0.59 (0.44-0.59)	0.59 (0.4-0.62)	0.57 (0.48-0.6)
SERPING1	ORM1	102	67	0.59 (0.5-0.69)	0.62 (0.52-0.73)	0.61 (0.53-0.69)	0.57 (0.44-0.59)	0.58 (0.42-0.61)	0.57 (0.49-0.6)
IL6_PEA_IR	C8B	101	63	0.64 (0.52-0.72)	0.6 (0.49-0.72)	0.62 (0.54-0.69)	0.6 (0.37-0.65)	0.55 (0.48-0.57)	0.57 (0.45-0.61)
IFNG	C3	102	63	0.68 (0.6-0.75)	0.62 (0.46-0.75)	0.65 (0.56-0.72)	0.53 (0.36-0.67)	0.62 (0.54-0.64)	0.57 (0.48-0.64)
SIT1	HGF	101	63	0.59 (0.51-0.67)	0.61 (0.51-0.72)	0.6 (0.53-0.67)	0.57 (0.44-0.58)	0.58 (0.53-0.6)	0.57 (0.51-0.58)
DCTN1	APOA1	101	63	0.61 (0.52-0.69)	0.71 (0.59-0.82)	0.66 (0.58-0.74)	0.56 (0.51-0.6)	0.59 (0.39-0.68)	0.57 (0.47-0.62)
HSD11B1	CFB	101	63	0.58 (0.5-0.67)	0.63 (0.52-0.75)	0.61 (0.54-0.68)	0.56 (0.48-0.58)	0.59 (0.44-0.63)	0.57 (0.5-0.6)
HGF	ORM1	102	63	0.61 (0.49-0.7)	0.61 (0.49-0.72)	0.61 (0.52-0.69)	0.58 (0.41-0.62)	0.58 (0.42-0.6)	0.57 (0.48-0.6)

SH2D1A	LRG1	101	63	0.62 (0.53-0.7)	0.6 (0.51-0.72)	0.61 (0.54-0.68)	0.58 (0.42-0.62)	0.58 (0.5-0.6)	0.57 (0.49-0.6)
IL17C	CRP_SRM	102	63	0.64 (0.53-0.72)	0.61 (0.46-0.74)	0.62 (0.54-0.7)	0.58 (0.38-0.63)	0.57 (0.51-0.62)	0.57 (0.47-0.61)
CRP_SRM	ORM1	102	67	0.61 (0.5-0.73)	0.64 (0.52-0.75)	0.63 (0.54-0.71)	0.62 (0.49-0.64)	0.54 (0.48-0.65)	0.57 (0.5-0.64)
IL17C	C8B	102	63	0.62 (0.53-0.7)	0.6 (0.5-0.71)	0.61 (0.54-0.68)	0.59 (0.39-0.62)	0.55 (0.5-0.57)	0.57 (0.47-0.59)
SIT1	APOA1	101	63	0.62 (0.54-0.68)	0.61 (0.52-0.72)	0.61 (0.56-0.68)	0.57 (0.46-0.6)	0.57 (0.56-0.59)	0.57 (0.51-0.59)
NCR1	TNF	101	63	0.6 (0.51-0.66)	0.61 (0.51-0.71)	0.6 (0.54-0.67)	0.58 (0.47-0.59)	0.56 (0.51-0.6)	0.57 (0.51-0.59)
FC	CLU	77	44	0.67 (0.58-0.77)	0.6 (0.45-0.73)	0.64 (0.54-0.72)	0.57 (0.32-0.68)	0.58 (0.56-0.6)	0.57 (0.45-0.63)
C5	ITIH1	102	67	0.62 (0.53-0.7)	0.62 (0.52-0.73)	0.62 (0.56-0.68)	0.58 (0.44-0.61)	0.57 (0.47-0.61)	0.57 (0.5-0.61)
SH2D1A	FLT3LG	101	63	0.61 (0.52-0.69)	0.61 (0.52-0.74)	0.61 (0.54-0.68)	0.56 (0.47-0.6)	0.58 (0.52-0.6)	0.57 (0.51-0.59)
SH2D1A	C8B	101	63	0.62 (0.52-0.7)	0.6 (0.49-0.7)	0.61 (0.53-0.68)	0.59 (0.39-0.62)	0.56 (0.49-0.57)	0.57 (0.47-0.59)
SIT1	IL6_PEA_cytokine	101	63	0.6 (0.51-0.69)	0.6 (0.49-0.71)	0.6 (0.53-0.67)	0.57 (0.41-0.61)	0.57 (0.54-0.59)	0.57 (0.49-0.59)
ITGA11	IFNG	101	63	0.72 (0.63-0.79)	0.58 (0.44-0.72)	0.65 (0.56-0.73)	0.55 (0.3-0.73)	0.61 (0.53-0.62)	0.57 (0.45-0.67)
MILR1	C8A	101	63	0.67 (0.59-0.75)	0.59 (0.5-0.7)	0.63 (0.56-0.7)	0.61 (0.36-0.67)	0.54 (0.52-0.55)	0.57 (0.45-0.61)
KLRD1	SAA1	101	63	0.61 (0.52-0.7)	0.59 (0.48-0.7)	0.6 (0.53-0.67)	0.58 (0.39-0.62)	0.57 (0.51-0.59)	0.57 (0.48-0.59)
C3	APCS	102	67	0.59 (0.5-0.67)	0.62 (0.51-0.73)	0.6 (0.53-0.68)	0.58 (0.47-0.59)	0.57 (0.42-0.6)	0.57 (0.49-0.59)
CXCL9	ORM1	102	63	0.66 (0.57-0.75)	0.61 (0.48-0.73)	0.64 (0.57-0.71)	0.58 (0.34-0.67)	0.56 (0.5-0.6)	0.57 (0.45-0.63)
VEGFA	ORM1	102	63	0.61 (0.48-0.7)	0.61 (0.51-0.71)	0.61 (0.53-0.68)	0.58 (0.41-0.61)	0.58 (0.42-0.59)	0.57 (0.48-0.6)
F9	SERPIND1	102	67	0.58 (0.5-0.67)	0.65 (0.55-0.77)	0.62 (0.55-0.69)	0.56 (0.48-0.57)	0.61 (0.38-0.65)	0.57 (0.46-0.61)
LAMP3	LRG1	101	63	0.61 (0.5-0.69)	0.64 (0.53-0.74)	0.62 (0.55-0.69)	0.6 (0.49-0.61)	0.56 (0.44-0.64)	0.57 (0.49-0.62)
CLEC4C	SERPIND1	101	63	0.56 (0.49-0.64)	0.64 (0.53-0.76)	0.6 (0.54-0.67)	0.54 (0.52-0.55)	0.6 (0.37-0.64)	0.57 (0.45-0.59)
PLXNA4	C8B	101	63	0.62 (0.53-0.7)	0.66 (0.55-0.76)	0.64 (0.56-0.7)	0.57 (0.44-0.62)	0.57 (0.43-0.66)	0.57 (0.48-0.63)
C8B	ITIH2	102	67	0.62 (0.53-0.7)	0.6 (0.51-0.71)	0.61 (0.54-0.68)	0.59 (0.39-0.63)	0.56 (0.49-0.58)	0.57 (0.48-0.6)
CLEC4C	MILR1	102	63	0.64 (0.57-0.72)	0.62 (0.49-0.76)	0.63 (0.56-0.71)	0.6 (0.38-0.64)	0.56 (0.44-0.64)	0.57 (0.46-0.63)
LRG1	ITIH2	102	67	0.61 (0.52-0.69)	0.61 (0.51-0.71)	0.61 (0.54-0.67)	0.58 (0.42-0.6)	0.57 (0.45-0.6)	0.57 (0.49-0.6)
IL13	CFB	102	63	0.58 (0.46-0.66)	0.62 (0.47-0.76)	0.6 (0.51-0.68)	0.57 (0.43-0.57)	0.59 (0.43-0.63)	0.57 (0.49-0.6)
CPN2	HPR	102	67	0.61 (0.52-0.7)	0.65 (0.55-0.77)	0.63 (0.56-0.7)	0.58 (0.44-0.61)	0.58 (0.43-0.63)	0.57 (0.49-0.61)
LAMP3	IL15	101	63	0.58 (0.47-0.67)	0.66 (0.53-0.78)	0.62 (0.54-0.69)	0.57 (0.54-0.58)	0.57 (0.33-0.67)	0.57 (0.45-0.62)
CCL13	APOA1	102	63	0.61 (0.53-0.68)	0.61 (0.51-0.72)	0.61 (0.55-0.68)	0.59 (0.43-0.59)	0.57 (0.48-0.59)	0.57 (0.48-0.59)
NCR1	SH2D1A	102	63	0.59 (0.51-0.67)	0.6 (0.5-0.72)	0.6 (0.53-0.67)	0.57 (0.46-0.59)	0.58 (0.48-0.6)	0.57 (0.51-0.59)
F9	PZP	101	67	0.58 (0.49-0.67)	0.64 (0.52-0.77)	0.61 (0.54-0.68)	0.55 (0.45-0.57)	0.59 (0.37-0.64)	0.57 (0.46-0.6)

CCL13	IFNG	102	63	0.68 (0.6-0.77)	0.6 (0.45-0.72)	0.64 (0.56-0.71)	0.55 (0.33-0.68)	0.62 (0.5-0.64)	0.57 (0.47-0.66)
FC	CLEC4C	76	43	0.69 (0.58-0.76)	0.66 (0.51-0.8)	0.67 (0.59-0.76)	0.55 (0.43-0.68)	0.62 (0.45-0.67)	0.57 (0.47-0.66)
CXCL9	ITIH3	102	63	0.65 (0.56-0.73)	0.58 (0.48-0.7)	0.61 (0.55-0.69)	0.59 (0.35-0.66)	0.56 (0.53-0.57)	0.57 (0.45-0.61)
MASP1	IL13	101	63	0.61 (0.49-0.7)	0.61 (0.46-0.75)	0.61 (0.52-0.7)	0.58 (0.39-0.61)	0.62 (0.46-0.62)	0.57 (0.47-0.62)
LAMP3	ITIH3	101	63	0.59 (0.5-0.68)	0.63 (0.53-0.73)	0.61 (0.55-0.68)	0.58 (0.44-0.59)	0.58 (0.4-0.61)	0.57 (0.48-0.6)
FCRL6	FLT3LG	101	63	0.6 (0.53-0.69)	0.64 (0.54-0.73)	0.62 (0.56-0.69)	0.56 (0.49-0.6)	0.58 (0.48-0.62)	0.57 (0.5-0.61)
C3	SERPINA4	102	67	0.64 (0.54-0.72)	0.6 (0.5-0.73)	0.62 (0.55-0.7)	0.59 (0.38-0.64)	0.56 (0.51-0.57)	0.57 (0.46-0.6)
ITIH1	ORM1	102	67	0.59 (0.49-0.69)	0.63 (0.54-0.73)	0.61 (0.55-0.68)	0.57 (0.48-0.59)	0.59 (0.39-0.62)	0.57 (0.48-0.6)
IL6_PEA_cytokine	C3	102	63	0.59 (0.48-0.68)	0.6 (0.48-0.74)	0.59 (0.51-0.67)	0.56 (0.42-0.59)	0.59 (0.43-0.6)	0.57 (0.49-0.59)
ITGA11	CXCL9	101	63	0.7 (0.59-0.77)	0.57 (0.45-0.69)	0.63 (0.55-0.7)	0.59 (0.32-0.7)	0.55 (0.54-0.57)	0.57 (0.44-0.63)
SH2D1A	APCS	101	63	0.6 (0.49-0.67)	0.62 (0.52-0.74)	0.6 (0.54-0.68)	0.58 (0.44-0.59)	0.58 (0.42-0.61)	0.57 (0.49-0.6)
F9	C4BPB	102	67	0.6 (0.52-0.68)	0.64 (0.54-0.76)	0.62 (0.55-0.69)	0.56 (0.45-0.59)	0.59 (0.4-0.63)	0.57 (0.48-0.61)
LAMP3	C2	101	63	0.58 (0.47-0.67)	0.62 (0.5-0.74)	0.6 (0.53-0.67)	0.57 (0.47-0.58)	0.58 (0.39-0.61)	0.57 (0.48-0.6)
IL17C	LRG1	102	63	0.61 (0.52-0.71)	0.6 (0.48-0.71)	0.61 (0.52-0.68)	0.59 (0.4-0.61)	0.56 (0.46-0.6)	0.57 (0.47-0.6)
LAMP3	CDSN	102	63	0.57 (0.48-0.66)	0.63 (0.54-0.74)	0.61 (0.53-0.68)	0.56 (0.5-0.59)	0.59 (0.4-0.62)	0.57 (0.47-0.6)
F9	C8A	102	67	0.59 (0.51-0.66)	0.64 (0.54-0.77)	0.62 (0.55-0.69)	0.56 (0.47-0.58)	0.59 (0.39-0.64)	0.57 (0.47-0.6)
IL15	C3	102	63	0.58 (0.47-0.66)	0.63 (0.51-0.77)	0.6 (0.53-0.68)	0.58 (0.51-0.59)	0.56 (0.39-0.63)	0.57 (0.49-0.6)
IL6_PEA_IR	APCS	101	63	0.6 (0.49-0.69)	0.62 (0.49-0.74)	0.61 (0.53-0.7)	0.59 (0.41-0.6)	0.58 (0.41-0.59)	0.57 (0.47-0.59)
IL10_PEA_IR	SIT1	102	63	0.6 (0.52-0.67)	0.6 (0.46-0.73)	0.6 (0.52-0.68)	0.56 (0.46-0.59)	0.58 (0.57-0.59)	0.57 (0.52-0.59)
SAA1	C3	102	67	0.59 (0.49-0.69)	0.62 (0.48-0.75)	0.6 (0.52-0.69)	0.58 (0.45-0.6)	0.61 (0.48-0.62)	0.57 (0.49-0.61)
IL6_PEA_IR	NCR1	102	63	0.6 (0.52-0.68)	0.62 (0.5-0.73)	0.61 (0.53-0.68)	0.57 (0.42-0.6)	0.57 (0.46-0.6)	0.57 (0.49-0.6)
CCL13	ORM1	102	63	0.59 (0.5-0.69)	0.63 (0.53-0.74)	0.61 (0.54-0.69)	0.56 (0.45-0.59)	0.58 (0.41-0.61)	0.57 (0.49-0.59)
KLRD1	ITGA11	102	63	0.67 (0.56-0.75)	0.58 (0.49-0.68)	0.62 (0.56-0.69)	0.6 (0.34-0.67)	0.53 (0.52-0.56)	0.57 (0.44-0.6)
KLRD1	ITIH3	101	63	0.62 (0.53-0.7)	0.6 (0.5-0.69)	0.6 (0.54-0.67)	0.58 (0.39-0.62)	0.56 (0.5-0.58)	0.57 (0.47-0.6)
MILR1	C2	101	63	0.64 (0.56-0.72)	0.59 (0.48-0.72)	0.62 (0.55-0.69)	0.59 (0.36-0.64)	0.54 (0.52-0.59)	0.57 (0.45-0.6)
CRP_SRM	CFB	102	67	0.61 (0.51-0.7)	0.63 (0.49-0.75)	0.62 (0.53-0.7)	0.56 (0.46-0.63)	0.59 (0.42-0.66)	0.57 (0.46-0.64)
C8B	SERPING1	102	67	0.62 (0.53-0.7)	0.6 (0.5-0.72)	0.61 (0.54-0.69)	0.59 (0.4-0.62)	0.56 (0.48-0.57)	0.57 (0.48-0.6)
KLRD1	C3	101	63	0.61 (0.52-0.69)	0.61 (0.51-0.74)	0.61 (0.55-0.69)	0.58 (0.43-0.62)	0.57 (0.47-0.59)	0.57 (0.49-0.6)
NCR1	HGF	101	63	0.59 (0.5-0.67)	0.61 (0.5-0.73)	0.6 (0.52-0.67)	0.57 (0.48-0.59)	0.59 (0.46-0.61)	0.57 (0.5-0.6)
TNF	SAA1	102	63	0.57 (0.49-0.67)	0.6 (0.47-0.72)	0.59 (0.52-0.66)	0.55 (0.41-0.59)	0.59 (0.51-0.6)	0.57 (0.48-0.59)

SERPING1	APOA1	102	67	0.62 (0.54-0.69)	0.6 (0.49-0.71)	0.61 (0.54-0.68)	0.58 (0.41-0.61)	0.57 (0.53-0.59)	0.57 (0.49-0.59)
CXCL9	C4B	102	63	0.67 (0.58-0.74)	0.67 (0.54-0.82)	0.67 (0.58-0.75)	0.54 (0.42-0.66)	0.62 (0.46-0.68)	0.57 (0.47-0.66)
TNF	ORM1	102	63	0.59 (0.49-0.69)	0.61 (0.52-0.72)	0.6 (0.53-0.67)	0.58 (0.42-0.6)	0.57 (0.43-0.59)	0.57 (0.49-0.59)
MASP1	IL15	101	63	0.61 (0.49-0.7)	0.59 (0.48-0.73)	0.6 (0.52-0.68)	0.58 (0.4-0.6)	0.58 (0.42-0.59)	0.57 (0.46-0.59)
IL13	ORM1	102	63	0.6 (0.45-0.69)	0.61 (0.49-0.73)	0.61 (0.52-0.68)	0.59 (0.41-0.59)	0.58 (0.45-0.61)	0.57 (0.48-0.6)
FGF2	FLT3LG	101	63	0.61 (0.52-0.7)	0.67 (0.49-0.79)	0.64 (0.54-0.72)	0.55 (0.48-0.6)	0.57 (0.48-0.66)	0.57 (0.51-0.62)
ORM1	SERPINA4	102	67	0.61 (0.52-0.71)	0.63 (0.52-0.72)	0.62 (0.55-0.69)	0.59 (0.41-0.63)	0.56 (0.46-0.6)	0.57 (0.48-0.61)
IL6_PEA_IR	MILR1	102	63	0.66 (0.56-0.75)	0.58 (0.49-0.71)	0.62 (0.56-0.69)	0.59 (0.35-0.67)	0.54 (0.5-0.57)	0.57 (0.45-0.61)
CLEC4C	APOA1	101	63	0.61 (0.54-0.68)	0.62 (0.51-0.74)	0.62 (0.55-0.69)	0.58 (0.44-0.6)	0.57 (0.46-0.62)	0.57 (0.49-0.61)
MILR1	HSD11B1	102	63	0.64 (0.56-0.72)	0.6 (0.5-0.72)	0.62 (0.56-0.69)	0.58 (0.37-0.64)	0.57 (0.51-0.57)	0.57 (0.47-0.6)
C8B	CFB	102	67	0.62 (0.52-0.7)	0.63 (0.52-0.74)	0.62 (0.55-0.69)	0.59 (0.41-0.62)	0.55 (0.48-0.61)	0.57 (0.47-0.61)
MASP1	ITIH3	101	63	0.62 (0.53-0.71)	0.61 (0.49-0.74)	0.61 (0.54-0.69)	0.57 (0.39-0.62)	0.56 (0.54-0.59)	0.57 (0.47-0.6)
LAMP3	PLXNA4	102	63	0.57 (0.49-0.67)	0.65 (0.54-0.76)	0.61 (0.54-0.68)	0.53 (0.5-0.58)	0.61 (0.37-0.64)	0.57 (0.45-0.6)
hsCRP	SAA1	98	67	0.6 (0.45-0.71)	0.6 (0.47-0.73)	0.6 (0.51-0.68)	0.6 (0.44-0.63)	0.58 (0.49-0.61)	0.57 (0.48-0.62)
FCRL6	C8B	101	63	0.62 (0.52-0.7)	0.64 (0.54-0.74)	0.63 (0.56-0.7)	0.57 (0.42-0.62)	0.56 (0.43-0.63)	0.57 (0.48-0.61)
C8B	PZP	101	67	0.62 (0.51-0.7)	0.61 (0.5-0.73)	0.62 (0.54-0.69)	0.59 (0.4-0.62)	0.55 (0.39-0.6)	0.57 (0.46-0.6)
IL6_PEA_IR	APOA1	101	63	0.61 (0.53-0.7)	0.58 (0.47-0.69)	0.6 (0.53-0.67)	0.6 (0.39-0.62)	0.55 (0.5-0.56)	0.57 (0.46-0.59)
IL15	SERPINA3	102	63	0.58 (0.48-0.68)	0.63 (0.51-0.74)	0.6 (0.53-0.69)	0.58 (0.47-0.6)	0.56 (0.41-0.62)	0.57 (0.49-0.61)
ITIH2	ORM1	102	67	0.59 (0.51-0.7)	0.62 (0.52-0.72)	0.6 (0.54-0.68)	0.57 (0.46-0.59)	0.58 (0.42-0.61)	0.57 (0.48-0.6)
HSD11B1	CXCL9	101	63	0.67 (0.58-0.75)	0.58 (0.48-0.72)	0.63 (0.56-0.7)	0.56 (0.33-0.67)	0.58 (0.52-0.6)	0.57 (0.46-0.63)
LAMP3	SERPING1	101	63	0.58 (0.48-0.67)	0.64 (0.53-0.75)	0.61 (0.54-0.69)	0.56 (0.49-0.59)	0.58 (0.39-0.62)	0.57 (0.47-0.6)
LAMP3	VEGFA	101	63	0.58 (0.47-0.68)	0.64 (0.53-0.73)	0.61 (0.53-0.68)	0.56 (0.47-0.58)	0.59 (0.38-0.63)	0.57 (0.45-0.6)
NCR1	CCL4	101	63	0.59 (0.51-0.67)	0.63 (0.52-0.73)	0.61 (0.54-0.68)	0.55 (0.43-0.61)	0.58 (0.44-0.61)	0.57 (0.49-0.6)
LAMP3	HGF	101	63	0.59 (0.47-0.67)	0.63 (0.52-0.73)	0.6 (0.53-0.68)	0.56 (0.49-0.59)	0.59 (0.39-0.62)	0.57 (0.46-0.6)
PLXNA4	C3	101	63	0.58 (0.49-0.66)	0.65 (0.53-0.77)	0.61 (0.55-0.68)	0.55 (0.47-0.57)	0.6 (0.38-0.64)	0.57 (0.46-0.6)
FC	ITIH2	77	44	0.67 (0.58-0.77)	0.6 (0.48-0.73)	0.64 (0.56-0.71)	0.56 (0.34-0.68)	0.58 (0.54-0.59)	0.57 (0.46-0.63)
CRP_SRM	SERPIND1	102	67	0.62 (0.53-0.71)	0.66 (0.54-0.77)	0.64 (0.57-0.71)	0.56 (0.46-0.62)	0.59 (0.39-0.67)	0.57 (0.45-0.64)
CCL13	APCS	102	63	0.59 (0.48-0.67)	0.62 (0.52-0.74)	0.61 (0.54-0.68)	0.57 (0.47-0.59)	0.58 (0.42-0.63)	0.57 (0.49-0.6)
C5	CP	102	67	0.61 (0.51-0.7)	0.64 (0.52-0.76)	0.62 (0.55-0.71)	0.59 (0.46-0.61)	0.55 (0.43-0.63)	0.57 (0.49-0.61)
IL17F	LRG1	102	63	0.62 (0.52-0.71)	0.6 (0.41-0.74)	0.61 (0.5-0.69)	0.56 (0.38-0.62)	0.57 (0.5-0.6)	0.57 (0.47-0.61)

HSD11B1	SAA1	101	63	0.59 (0.51-0.68)	0.61 (0.5-0.73)	0.6 (0.53-0.68)	0.56 (0.43-0.59)	0.6 (0.48-0.62)	0.57 (0.49-0.6)
FC	CDSN	76	43	0.69 (0.58-0.78)	0.59 (0.46-0.72)	0.64 (0.56-0.72)	0.56 (0.3-0.7)	0.58 (0.53-0.59)	0.57 (0.44-0.64)
C8B	ITIH1	102	67	0.61 (0.52-0.7)	0.63 (0.53-0.73)	0.62 (0.55-0.69)	0.58 (0.43-0.62)	0.56 (0.47-0.61)	0.57 (0.48-0.61)
CLEC4C	HSD11B1	102	63	0.58 (0.51-0.67)	0.63 (0.52-0.74)	0.6 (0.54-0.67)	0.56 (0.46-0.57)	0.59 (0.38-0.63)	0.57 (0.46-0.59)
MASP1	SERPINA3	101	63	0.62 (0.53-0.72)	0.6 (0.49-0.73)	0.61 (0.54-0.69)	0.58 (0.38-0.62)	0.57 (0.49-0.58)	0.57 (0.47-0.6)
MILR1	SH2D1A	102	63	0.64 (0.55-0.72)	0.59 (0.49-0.7)	0.61 (0.54-0.68)	0.59 (0.39-0.63)	0.55 (0.5-0.56)	0.57 (0.46-0.59)
CLEC4C	IL10_PEA_IR	102	63	0.58 (0.5-0.67)	0.63 (0.42-0.76)	0.61 (0.49-0.69)	0.54 (0.42-0.59)	0.61 (0.45-0.63)	0.57 (0.47-0.6)
MILR1	ITIH1	101	63	0.63 (0.55-0.72)	0.63 (0.52-0.75)	0.63 (0.56-0.71)	0.57 (0.39-0.64)	0.59 (0.46-0.62)	0.57 (0.47-0.62)
CXCL9	C3	102	63	0.66 (0.57-0.73)	0.61 (0.48-0.74)	0.63 (0.56-0.71)	0.57 (0.35-0.66)	0.56 (0.52-0.6)	0.57 (0.47-0.62)
MILR1	ITGA11	102	63	0.64 (0.56-0.72)	0.57 (0.47-0.69)	0.61 (0.54-0.68)	0.61 (0.37-0.64)	0.52 (0.51-0.54)	0.57 (0.44-0.58)
IL6_PEA_cytokine	SERPIND1	102	63	0.56 (0.46-0.64)	0.65 (0.51-0.78)	0.6 (0.53-0.68)	0.52 (0.48-0.56)	0.61 (0.37-0.65)	0.57 (0.45-0.6)
CCL4	C8B	102	63	0.62 (0.5-0.71)	0.6 (0.5-0.7)	0.61 (0.54-0.68)	0.6 (0.38-0.63)	0.55 (0.48-0.59)	0.57 (0.46-0.6)
CLEC4C	ITGA11	102	63	0.64 (0.5-0.72)	0.63 (0.47-0.76)	0.63 (0.53-0.71)	0.59 (0.37-0.64)	0.57 (0.37-0.63)	0.57 (0.41-0.63)
IL17F	APCS	102	63	0.61 (0.48-0.69)	0.62 (0.46-0.73)	0.61 (0.52-0.69)	0.57 (0.41-0.61)	0.56 (0.43-0.61)	0.57 (0.49-0.6)
IL6_PEA_IR	ORM1	101	63	0.62 (0.46-0.72)	0.62 (0.5-0.73)	0.62 (0.52-0.69)	0.58 (0.4-0.63)	0.57 (0.44-0.59)	0.57 (0.46-0.61)
IL17F	CFB	102	63	0.58 (0.48-0.66)	0.64 (0.47-0.76)	0.61 (0.51-0.69)	0.54 (0.42-0.59)	0.59 (0.41-0.63)	0.57 (0.46-0.6)
KLRD1	IL13	101	63	0.59 (0.5-0.68)	0.6 (0.46-0.71)	0.6 (0.52-0.66)	0.58 (0.41-0.59)	0.59 (0.47-0.6)	0.57 (0.47-0.59)
CDSN	C3	101	63	0.57 (0.5-0.66)	0.62 (0.51-0.77)	0.6 (0.53-0.68)	0.55 (0.45-0.56)	0.6 (0.43-0.62)	0.57 (0.48-0.59)
IL13	APCS	102	63	0.6 (0.46-0.68)	0.59 (0.48-0.72)	0.59 (0.51-0.67)	0.59 (0.41-0.6)	0.57 (0.47-0.58)	0.57 (0.47-0.59)
LAMP3	ITGA11	102	63	0.64 (0.5-0.72)	0.62 (0.5-0.72)	0.63 (0.54-0.69)	0.59 (0.41-0.64)	0.56 (0.41-0.61)	0.57 (0.46-0.61)
SIT1	CCL4	101	63	0.6 (0.51-0.68)	0.6 (0.51-0.71)	0.6 (0.54-0.66)	0.57 (0.39-0.62)	0.57 (0.52-0.59)	0.57 (0.47-0.6)
FCRL6	IFNG	101	63	0.68 (0.59-0.75)	0.61 (0.49-0.71)	0.64 (0.57-0.7)	0.53 (0.37-0.67)	0.6 (0.52-0.62)	0.57 (0.48-0.63)
LAMP3	CCL13	101	63	0.58 (0.48-0.67)	0.63 (0.53-0.74)	0.61 (0.53-0.68)	0.56 (0.5-0.58)	0.57 (0.38-0.63)	0.57 (0.47-0.6)
ITIH1	APCS	102	67	0.59 (0.5-0.67)	0.62 (0.53-0.74)	0.6 (0.55-0.67)	0.57 (0.47-0.59)	0.58 (0.41-0.61)	0.57 (0.49-0.6)
hsCRP	ORM1	98	67	0.61 (0.51-0.72)	0.64 (0.52-0.76)	0.63 (0.54-0.7)	0.61 (0.49-0.63)	0.51 (0.49-0.65)	0.57 (0.51-0.64)
CP	F9	102	67	0.58 (0.5-0.66)	0.66 (0.54-0.78)	0.62 (0.55-0.7)	0.56 (0.47-0.57)	0.57 (0.38-0.66)	0.57 (0.47-0.61)
CLEC4C	MASP1	102	63	0.61 (0.51-0.71)	0.62 (0.49-0.75)	0.61 (0.53-0.69)	0.57 (0.38-0.62)	0.57 (0.4-0.63)	0.57 (0.46-0.62)
FGF2	IL13	101	63	0.55 (0.48-0.63)	0.66 (0.41-0.77)	0.6 (0.48-0.68)	0.53 (0.47-0.54)	0.61 (0.37-0.66)	0.57 (0.44-0.6)
SAA1	LRG1	102	67	0.59 (0.48-0.7)	0.61 (0.48-0.72)	0.6 (0.52-0.68)	0.58 (0.4-0.61)	0.61 (0.45-0.62)	0.57 (0.48-0.61)
CDSN	ITIH1	101	63	0.56 (0.49-0.64)	0.65 (0.54-0.77)	0.61 (0.54-0.68)	0.52 (0.48-0.55)	0.61 (0.37-0.65)	0.56 (0.45-0.6)

FC	VTN	77	44	0.67 (0.58-0.77)	0.63 (0.5-0.77)	0.65 (0.58-0.73)	0.57 (0.37-0.65)	0.56 (0.51-0.64)	0.56 (0.46-0.63)
KLRD1	IL6_PEA_cytokine	101	63	0.61 (0.51-0.68)	0.57 (0.46-0.69)	0.59 (0.52-0.66)	0.57 (0.39-0.61)	0.56 (0.49-0.57)	0.56 (0.46-0.59)
CDSN	CXCL9	101	63	0.66 (0.58-0.74)	0.6 (0.47-0.73)	0.63 (0.55-0.71)	0.58 (0.35-0.67)	0.55 (0.51-0.6)	0.56 (0.45-0.62)
LAMP3	SERPIND1	101	63	0.58 (0.47-0.67)	0.65 (0.56-0.76)	0.62 (0.55-0.69)	0.55 (0.48-0.58)	0.59 (0.36-0.65)	0.56 (0.45-0.61)
HSD11B1	C3	101	63	0.58 (0.5-0.67)	0.61 (0.51-0.74)	0.6 (0.53-0.68)	0.56 (0.46-0.58)	0.58 (0.44-0.6)	0.56 (0.49-0.58)
SH2D1A	CFB	101	63	0.58 (0.48-0.65)	0.63 (0.51-0.75)	0.6 (0.52-0.68)	0.56 (0.46-0.56)	0.59 (0.4-0.63)	0.56 (0.48-0.59)
MASP1	C8A	101	63	0.63 (0.54-0.71)	0.6 (0.49-0.73)	0.61 (0.54-0.69)	0.57 (0.39-0.62)	0.57 (0.53-0.59)	0.56 (0.47-0.6)
FGF2	ITIH1	101	63	0.56 (0.49-0.64)	0.66 (0.49-0.77)	0.61 (0.53-0.68)	0.52 (0.5-0.54)	0.61 (0.35-0.65)	0.56 (0.44-0.59)
SAA1	C4BPB	102	67	0.61 (0.5-0.7)	0.59 (0.48-0.73)	0.6 (0.52-0.68)	0.57 (0.39-0.61)	0.6 (0.5-0.61)	0.56 (0.49-0.61)
VEGFA	C3	102	63	0.58 (0.49-0.66)	0.61 (0.51-0.73)	0.6 (0.53-0.67)	0.56 (0.43-0.57)	0.58 (0.42-0.59)	0.56 (0.48-0.58)
IL17F	C8B	102	63	0.63 (0.52-0.71)	0.59 (0.44-0.72)	0.61 (0.52-0.68)	0.59 (0.38-0.63)	0.54 (0.51-0.57)	0.56 (0.46-0.6)
IL17F	ORM1	102	63	0.6 (0.49-0.7)	0.61 (0.44-0.74)	0.61 (0.51-0.69)	0.56 (0.41-0.6)	0.56 (0.42-0.6)	0.56 (0.48-0.59)
FCRL6	APCS	101	63	0.59 (0.5-0.67)	0.65 (0.55-0.77)	0.62 (0.55-0.69)	0.57 (0.49-0.59)	0.57 (0.37-0.64)	0.56 (0.46-0.61)
SERPINA4	CFB	102	67	0.63 (0.55-0.71)	0.62 (0.52-0.73)	0.63 (0.56-0.69)	0.58 (0.44-0.63)	0.56 (0.51-0.6)	0.56 (0.49-0.61)
LAMP3	ITIH1	101	63	0.58 (0.47-0.67)	0.65 (0.55-0.74)	0.62 (0.54-0.68)	0.55 (0.49-0.59)	0.59 (0.36-0.64)	0.56 (0.45-0.61)
FGF2	CP	101	63	0.56 (0.48-0.64)	0.71 (0.53-0.82)	0.64 (0.54-0.7)	0.54 (0.48-0.55)	0.6 (0.28-0.73)	0.56 (0.41-0.63)
MILR1	TNF	101	63	0.64 (0.55-0.72)	0.58 (0.49-0.69)	0.61 (0.55-0.67)	0.61 (0.37-0.63)	0.53 (0.5-0.55)	0.56 (0.45-0.59)
HSD11B1	SERPIND1	101	63	0.57 (0.49-0.66)	0.64 (0.54-0.75)	0.61 (0.54-0.67)	0.55 (0.51-0.57)	0.58 (0.37-0.63)	0.56 (0.46-0.59)
CLEC4C	FGF2	102	63	0.56 (0.5-0.64)	0.69 (0.47-0.79)	0.63 (0.52-0.69)	0.53 (0.49-0.54)	0.61 (0.34-0.67)	0.56 (0.43-0.6)
CRP_SRM	SAA1	102	67	0.59 (0.45-0.7)	0.6 (0.47-0.73)	0.6 (0.5-0.68)	0.59 (0.45-0.63)	0.58 (0.48-0.62)	0.56 (0.49-0.62)
IL6_PEA_IR	CFB	101	63	0.6 (0.49-0.69)	0.66 (0.5-0.8)	0.63 (0.53-0.7)	0.54 (0.43-0.6)	0.61 (0.35-0.65)	0.56 (0.45-0.62)
LAMP3	IFNG	101	63	0.69 (0.6-0.76)	0.64 (0.48-0.74)	0.66 (0.58-0.73)	0.52 (0.35-0.66)	0.62 (0.48-0.63)	0.56 (0.47-0.64)
ITGA11	C3	101	63	0.62 (0.53-0.71)	0.61 (0.49-0.74)	0.62 (0.53-0.69)	0.56 (0.39-0.62)	0.57 (0.41-0.6)	0.56 (0.44-0.6)
NCR1	IL17F	101	63	0.59 (0.51-0.67)	0.61 (0.44-0.72)	0.6 (0.51-0.67)	0.56 (0.42-0.59)	0.57 (0.49-0.6)	0.56 (0.49-0.59)
FCRL6	CFB	101	63	0.58 (0.5-0.65)	0.67 (0.57-0.77)	0.62 (0.56-0.69)	0.56 (0.49-0.57)	0.58 (0.36-0.67)	0.56 (0.45-0.61)
LAMP3	CXCL9	101	63	0.67 (0.58-0.75)	0.62 (0.51-0.72)	0.64 (0.57-0.71)	0.58 (0.36-0.66)	0.55 (0.47-0.59)	0.56 (0.45-0.62)
TNF	APOA1	102	63	0.6 (0.53-0.68)	0.58 (0.5-0.68)	0.59 (0.54-0.65)	0.58 (0.42-0.59)	0.55 (0.53-0.56)	0.56 (0.48-0.57)
SAA1	ITIH1	102	67	0.58 (0.49-0.66)	0.62 (0.5-0.75)	0.6 (0.52-0.67)	0.55 (0.45-0.57)	0.61 (0.46-0.62)	0.56 (0.47-0.59)
CCL4	CFB	102	63	0.59 (0.46-0.67)	0.64 (0.52-0.77)	0.61 (0.53-0.69)	0.56 (0.41-0.59)	0.59 (0.39-0.63)	0.56 (0.45-0.61)
IFNG	SERPINA3	102	63	0.67 (0.59-0.76)	0.6 (0.46-0.73)	0.64 (0.54-0.72)	0.52 (0.32-0.68)	0.61 (0.52-0.62)	0.56 (0.46-0.64)

MASP1	HSD11B1	102	63	0.6 (0.5-0.69)	0.61 (0.49-0.76)	0.6 (0.53-0.68)	0.55 (0.4-0.61)	0.61 (0.46-0.63)	0.56 (0.47-0.61)
IL10_PEA_IR	SAA1	101	63	0.6 (0.52-0.7)	0.57 (0.41-0.75)	0.59 (0.5-0.69)	0.51 (0.39-0.63)	0.61 (0.59-0.63)	0.56 (0.5-0.62)
F9	VTN	102	67	0.6 (0.52-0.7)	0.64 (0.55-0.76)	0.62 (0.56-0.7)	0.57 (0.44-0.61)	0.59 (0.39-0.63)	0.56 (0.48-0.62)
TNF	C3	102	63	0.58 (0.5-0.66)	0.6 (0.52-0.74)	0.59 (0.53-0.67)	0.56 (0.45-0.57)	0.57 (0.47-0.6)	0.56 (0.5-0.58)
CXCL9	CFB	102	63	0.66 (0.58-0.74)	0.63 (0.51-0.76)	0.65 (0.56-0.72)	0.56 (0.36-0.66)	0.58 (0.48-0.61)	0.56 (0.46-0.62)
CLEC4C	ITIH3	101	63	0.6 (0.52-0.67)	0.62 (0.5-0.76)	0.61 (0.54-0.68)	0.56 (0.42-0.58)	0.59 (0.39-0.63)	0.56 (0.45-0.6)
FGF2	ITIH3	101	63	0.58 (0.49-0.67)	0.66 (0.47-0.77)	0.62 (0.51-0.69)	0.55 (0.44-0.58)	0.58 (0.39-0.65)	0.56 (0.45-0.6)
CRP_SRM	PZP	101	67	0.64 (0.52-0.73)	0.61 (0.46-0.75)	0.62 (0.53-0.71)	0.6 (0.4-0.67)	0.53 (0.4-0.63)	0.56 (0.46-0.63)
NCR1	IL15	101	63	0.58 (0.5-0.66)	0.62 (0.5-0.74)	0.6 (0.53-0.67)	0.57 (0.45-0.58)	0.56 (0.49-0.63)	0.56 (0.49-0.6)
CCL4	APCS	102	63	0.6 (0.46-0.69)	0.61 (0.51-0.73)	0.61 (0.53-0.69)	0.57 (0.39-0.61)	0.56 (0.41-0.61)	0.56 (0.47-0.6)
KLRD1	SERPINA3	101	63	0.61 (0.52-0.7)	0.6 (0.5-0.71)	0.6 (0.54-0.67)	0.58 (0.4-0.61)	0.56 (0.44-0.57)	0.56 (0.47-0.59)
MILR1	SERPINA4	101	63	0.66 (0.58-0.74)	0.58 (0.5-0.69)	0.62 (0.56-0.69)	0.6 (0.35-0.66)	0.53 (0.51-0.54)	0.56 (0.44-0.6)
SIT1	VEGFA	101	63	0.59 (0.5-0.66)	0.59 (0.5-0.7)	0.59 (0.52-0.66)	0.56 (0.44-0.58)	0.58 (0.52-0.59)	0.56 (0.51-0.58)
MILR1	MASP1	102	63	0.64 (0.56-0.72)	0.6 (0.44-0.74)	0.62 (0.53-0.7)	0.61 (0.38-0.63)	0.55 (0.45-0.58)	0.56 (0.45-0.6)
IFNG	SERPING1	102	63	0.69 (0.6-0.76)	0.59 (0.42-0.74)	0.64 (0.55-0.73)	0.52 (0.33-0.67)	0.61 (0.51-0.64)	0.56 (0.46-0.64)
CP	APCS	102	67	0.6 (0.49-0.68)	0.64 (0.54-0.76)	0.62 (0.55-0.7)	0.59 (0.47-0.59)	0.55 (0.36-0.66)	0.56 (0.46-0.62)
ITGA6	HPR	101	63	0.6 (0.51-0.68)	0.75 (0.64-0.84)	0.67 (0.6-0.74)	0.53 (0.5-0.57)	0.59 (0.38-0.74)	0.56 (0.45-0.64)
FCRL6	NCR1	102	63	0.59 (0.51-0.66)	0.64 (0.54-0.73)	0.61 (0.55-0.68)	0.55 (0.47-0.58)	0.58 (0.42-0.62)	0.56 (0.48-0.6)
HGF	C3	102	63	0.58 (0.49-0.66)	0.61 (0.5-0.75)	0.6 (0.52-0.67)	0.55 (0.45-0.58)	0.58 (0.42-0.6)	0.56 (0.48-0.59)
FCRL6	LRG1	101	63	0.61 (0.52-0.69)	0.65 (0.54-0.75)	0.63 (0.56-0.69)	0.57 (0.45-0.61)	0.57 (0.43-0.65)	0.56 (0.47-0.62)
NCR1	VEGFA	101	63	0.59 (0.48-0.66)	0.62 (0.52-0.73)	0.6 (0.53-0.67)	0.55 (0.46-0.58)	0.59 (0.47-0.61)	0.56 (0.5-0.59)
MASP1	SERPIND1	101	63	0.61 (0.51-0.7)	0.65 (0.53-0.76)	0.63 (0.55-0.7)	0.54 (0.43-0.61)	0.58 (0.39-0.64)	0.56 (0.46-0.62)
FLT3LG	SERPINA4	102	63	0.63 (0.53-0.72)	0.61 (0.52-0.73)	0.62 (0.56-0.7)	0.56 (0.47-0.63)	0.56 (0.51-0.58)	0.56 (0.5-0.6)
FCRL6	ORM1	101	63	0.59 (0.5-0.69)	0.66 (0.56-0.76)	0.63 (0.55-0.7)	0.55 (0.49-0.59)	0.58 (0.35-0.66)	0.56 (0.45-0.61)
LRG1	SERPINA4	102	67	0.64 (0.55-0.72)	0.61 (0.51-0.72)	0.62 (0.55-0.69)	0.57 (0.41-0.64)	0.56 (0.49-0.59)	0.56 (0.47-0.61)
CCL4	ORM1	102	63	0.61 (0.47-0.71)	0.61 (0.5-0.72)	0.61 (0.53-0.69)	0.57 (0.39-0.62)	0.56 (0.44-0.6)	0.56 (0.46-0.6)
NCR1	CP	101	63	0.58 (0.5-0.66)	0.68 (0.56-0.79)	0.63 (0.56-0.7)	0.57 (0.53-0.58)	0.55 (0.35-0.69)	0.56 (0.46-0.63)
MILR1	IL17F	101	63	0.64 (0.55-0.72)	0.59 (0.43-0.73)	0.61 (0.52-0.69)	0.58 (0.37-0.63)	0.55 (0.52-0.58)	0.56 (0.45-0.6)
LAMP3	SERPINA3	101	63	0.59 (0.49-0.68)	0.63 (0.52-0.74)	0.61 (0.54-0.68)	0.57 (0.47-0.58)	0.57 (0.37-0.65)	0.56 (0.47-0.61)
KLRD1	IFNG	101	63	0.67 (0.58-0.74)	0.57 (0.43-0.7)	0.62 (0.54-0.69)	0.54 (0.32-0.67)	0.58 (0.55-0.61)	0.56 (0.45-0.63)

FCRL6	APOA1	101	63	0.61 (0.53-0.68)	0.63 (0.52-0.73)	0.62 (0.55-0.68)	0.55 (0.45-0.6)	0.57 (0.46-0.62)	0.56 (0.49-0.6)
CCL13	C3	102	63	0.58 (0.5-0.65)	0.63 (0.52-0.75)	0.6 (0.54-0.68)	0.55 (0.49-0.56)	0.58 (0.4-0.61)	0.56 (0.47-0.58)
hsCRP	PZP	97	67	0.63 (0.52-0.72)	0.6 (0.46-0.75)	0.61 (0.52-0.7)	0.59 (0.42-0.63)	0.52 (0.39-0.63)	0.56 (0.46-0.62)
IFNG	C4BPB	102	63	0.67 (0.59-0.75)	0.58 (0.47-0.7)	0.63 (0.56-0.7)	0.52 (0.33-0.68)	0.61 (0.56-0.62)	0.56 (0.46-0.64)
PLXNA4	FLT3LG	101	63	0.6 (0.52-0.68)	0.66 (0.53-0.8)	0.63 (0.56-0.71)	0.54 (0.48-0.6)	0.58 (0.46-0.67)	0.56 (0.49-0.61)
MILR1	FCRL6	102	63	0.63 (0.55-0.72)	0.62 (0.52-0.72)	0.63 (0.55-0.69)	0.58 (0.39-0.63)	0.54 (0.46-0.6)	0.56 (0.47-0.61)
LAMP3	SERPINA4	101	63	0.61 (0.52-0.7)	0.62 (0.52-0.73)	0.61 (0.55-0.68)	0.6 (0.42-0.62)	0.53 (0.45-0.59)	0.56 (0.47-0.6)
KLRD1	HSD11B1	102	63	0.6 (0.52-0.68)	0.6 (0.52-0.71)	0.6 (0.54-0.67)	0.57 (0.42-0.59)	0.57 (0.47-0.59)	0.56 (0.49-0.59)
SIT1	CLU	101	63	0.58 (0.5-0.66)	0.63 (0.53-0.74)	0.61 (0.54-0.68)	0.56 (0.48-0.58)	0.56 (0.51-0.62)	0.56 (0.51-0.59)
IL15	ITIH3	102	63	0.59 (0.49-0.67)	0.61 (0.5-0.72)	0.6 (0.53-0.67)	0.58 (0.45-0.59)	0.55 (0.44-0.61)	0.56 (0.49-0.6)
SERPING1	CFB	102	67	0.57 (0.5-0.65)	0.62 (0.52-0.73)	0.6 (0.54-0.66)	0.56 (0.47-0.57)	0.57 (0.43-0.62)	0.56 (0.47-0.59)
MASP1	SH2D1A	102	63	0.59 (0.5-0.69)	0.61 (0.48-0.74)	0.6 (0.52-0.68)	0.55 (0.4-0.6)	0.59 (0.48-0.6)	0.56 (0.47-0.6)
ITGA11	C4BPB	101	63	0.65 (0.56-0.73)	0.58 (0.49-0.68)	0.62 (0.55-0.68)	0.58 (0.36-0.65)	0.54 (0.51-0.56)	0.56 (0.45-0.6)
FC	ITIH3	77	44	0.67 (0.56-0.77)	0.59 (0.48-0.74)	0.63 (0.55-0.72)	0.58 (0.36-0.68)	0.54 (0.52-0.61)	0.56 (0.45-0.62)
SIT1	IL17F	101	63	0.61 (0.52-0.68)	0.61 (0.45-0.74)	0.61 (0.52-0.67)	0.55 (0.41-0.6)	0.57 (0.56-0.6)	0.56 (0.49-0.59)
ITIH3	SERPINA3	102	67	0.59 (0.51-0.68)	0.59 (0.49-0.71)	0.59 (0.52-0.67)	0.57 (0.41-0.59)	0.56 (0.44-0.58)	0.56 (0.48-0.58)
CXCL9	SERPIND1	102	63	0.66 (0.58-0.74)	0.65 (0.53-0.77)	0.66 (0.59-0.73)	0.53 (0.41-0.65)	0.59 (0.47-0.65)	0.56 (0.47-0.64)
FC	IL13	77	43	0.68 (0.59-0.78)	0.57 (0.44-0.72)	0.63 (0.55-0.72)	0.57 (0.32-0.68)	0.56 (0.48-0.56)	0.56 (0.43-0.62)
FC	PZP	77	44	0.7 (0.6-0.79)	0.61 (0.44-0.76)	0.65 (0.55-0.75)	0.58 (0.32-0.7)	0.54 (0.49-0.6)	0.56 (0.42-0.63)
IFNG	ITIH3	102	63	0.67 (0.58-0.75)	0.58 (0.45-0.71)	0.63 (0.55-0.7)	0.54 (0.32-0.68)	0.58 (0.55-0.61)	0.56 (0.45-0.63)
CP	SERPINA4	102	67	0.62 (0.53-0.69)	0.64 (0.53-0.77)	0.63 (0.55-0.7)	0.56 (0.44-0.62)	0.56 (0.49-0.64)	0.56 (0.48-0.61)
CDSN	ITIH3	101	63	0.59 (0.51-0.67)	0.6 (0.5-0.72)	0.6 (0.53-0.67)	0.55 (0.42-0.59)	0.58 (0.46-0.6)	0.56 (0.49-0.59)
CP	C8B	102	67	0.62 (0.52-0.7)	0.65 (0.54-0.77)	0.63 (0.56-0.71)	0.59 (0.42-0.62)	0.53 (0.44-0.63)	0.56 (0.47-0.61)
IL7	FLT3LG	102	63	0.6 (0.51-0.68)	0.63 (0.52-0.74)	0.61 (0.55-0.69)	0.58 (0.45-0.6)	0.56 (0.46-0.6)	0.56 (0.49-0.59)
ITGA11	SERPINA4	101	63	0.65 (0.54-0.74)	0.58 (0.48-0.68)	0.61 (0.55-0.68)	0.59 (0.34-0.66)	0.54 (0.5-0.54)	0.56 (0.44-0.6)
CXCL9	SERPINA3	102	63	0.66 (0.58-0.74)	0.6 (0.46-0.72)	0.63 (0.55-0.7)	0.57 (0.34-0.66)	0.57 (0.48-0.6)	0.56 (0.44-0.62)
ITIH1	SERPINA4	102	67	0.61 (0.54-0.68)	0.62 (0.53-0.73)	0.62 (0.55-0.68)	0.56 (0.43-0.61)	0.57 (0.5-0.62)	0.56 (0.48-0.6)
SIT1	VTN	101	63	0.59 (0.52-0.66)	0.66 (0.56-0.77)	0.63 (0.57-0.7)	0.55 (0.5-0.58)	0.57 (0.46-0.65)	0.56 (0.5-0.6)
LAMP3	TNF	101	63	0.58 (0.48-0.67)	0.62 (0.51-0.73)	0.6 (0.53-0.67)	0.58 (0.49-0.59)	0.55 (0.4-0.61)	0.56 (0.48-0.6)
KLRD1	C8A	101	63	0.61 (0.53-0.69)	0.59 (0.5-0.69)	0.6 (0.54-0.66)	0.59 (0.4-0.61)	0.54 (0.5-0.55)	0.56 (0.47-0.58)

FGF2	IFNG	101	63	0.68 (0.59-0.75)	0.68 (0.4-0.8)	0.68 (0.52-0.75)	0.51 (0.37-0.68)	0.61 (0.56-0.63)	0.56 (0.49-0.65)
ITGA11	HSD11B1	102	63	0.63 (0.52-0.71)	0.59 (0.5-0.72)	0.61 (0.54-0.68)	0.56 (0.39-0.62)	0.57 (0.46-0.58)	0.56 (0.47-0.6)
MILR1	IL10_PEA_IR	102	63	0.62 (0.52-0.71)	0.57 (0.45-0.72)	0.59 (0.52-0.67)	0.58 (0.38-0.63)	0.54 (0.52-0.58)	0.56 (0.46-0.6)
APCS	C4BPB	102	67	0.61 (0.5-0.69)	0.62 (0.52-0.74)	0.61 (0.54-0.69)	0.59 (0.44-0.6)	0.56 (0.39-0.62)	0.56 (0.48-0.6)
HGF	APOA1	102	63	0.6 (0.52-0.68)	0.58 (0.48-0.7)	0.59 (0.53-0.66)	0.58 (0.41-0.6)	0.55 (0.51-0.57)	0.56 (0.48-0.58)
NCR1	VTN	101	63	0.59 (0.51-0.66)	0.65 (0.54-0.75)	0.61 (0.55-0.68)	0.56 (0.5-0.58)	0.56 (0.41-0.63)	0.56 (0.48-0.6)
LAMP3	SAA1	101	63	0.58 (0.48-0.69)	0.63 (0.49-0.74)	0.61 (0.52-0.69)	0.6 (0.45-0.61)	0.56 (0.45-0.64)	0.56 (0.48-0.62)
NCR1	ITIH2	101	63	0.59 (0.51-0.67)	0.63 (0.52-0.74)	0.61 (0.54-0.68)	0.58 (0.46-0.59)	0.56 (0.44-0.62)	0.56 (0.49-0.6)
PLXNA4	IFNG	101	63	0.68 (0.6-0.76)	0.63 (0.49-0.76)	0.66 (0.57-0.73)	0.5 (0.38-0.66)	0.62 (0.53-0.63)	0.56 (0.48-0.64)
SAA1	ITIH3	102	67	0.6 (0.5-0.68)	0.59 (0.49-0.71)	0.6 (0.52-0.67)	0.57 (0.41-0.6)	0.58 (0.49-0.59)	0.56 (0.49-0.59)
HSD11B1	SERPINA3	101	63	0.59 (0.5-0.7)	0.6 (0.5-0.73)	0.6 (0.53-0.67)	0.56 (0.42-0.59)	0.57 (0.44-0.59)	0.56 (0.48-0.58)
FC	PLXNA4	76	43	0.67 (0.57-0.76)	0.67 (0.49-0.79)	0.67 (0.57-0.75)	0.53 (0.39-0.65)	0.58 (0.45-0.66)	0.56 (0.45-0.64)
MASP1	ITGA11	102	63	0.63 (0.53-0.72)	0.59 (0.46-0.73)	0.61 (0.53-0.68)	0.59 (0.38-0.62)	0.53 (0.46-0.58)	0.56 (0.45-0.59)
hsCRP	FCRL6	98	63	0.63 (0.52-0.72)	0.66 (0.53-0.76)	0.64 (0.56-0.71)	0.57 (0.44-0.62)	0.55 (0.38-0.66)	0.56 (0.46-0.63)
FC	SERPING1	77	44	0.68 (0.58-0.77)	0.61 (0.45-0.75)	0.64 (0.56-0.73)	0.55 (0.35-0.68)	0.57 (0.54-0.6)	0.56 (0.46-0.63)
ITGA11	SERPINA3	101	63	0.63 (0.52-0.71)	0.59 (0.47-0.72)	0.61 (0.53-0.69)	0.58 (0.38-0.63)	0.56 (0.46-0.59)	0.56 (0.44-0.6)
ITIH3	C3	102	67	0.59 (0.51-0.67)	0.6 (0.5-0.72)	0.6 (0.53-0.67)	0.57 (0.42-0.59)	0.57 (0.48-0.59)	0.56 (0.49-0.58)
KLRD1	LAMP3	102	63	0.6 (0.5-0.69)	0.63 (0.53-0.73)	0.61 (0.55-0.68)	0.59 (0.42-0.6)	0.55 (0.41-0.62)	0.56 (0.47-0.6)
IFNG	F9	102	63	0.68 (0.6-0.76)	0.65 (0.52-0.77)	0.66 (0.59-0.74)	0.51 (0.4-0.65)	0.62 (0.45-0.65)	0.56 (0.47-0.64)
IL6_PEA_cytokine	ITIH3	102	63	0.6 (0.51-0.69)	0.58 (0.46-0.7)	0.59 (0.52-0.66)	0.56 (0.4-0.61)	0.57 (0.48-0.57)	0.56 (0.46-0.59)
KLRD1	IL10_PEA_IR	102	63	0.6 (0.52-0.68)	0.58 (0.42-0.73)	0.59 (0.5-0.67)	0.56 (0.4-0.61)	0.56 (0.55-0.58)	0.56 (0.48-0.59)
NCR1	CLU	101	63	0.59 (0.5-0.67)	0.63 (0.53-0.73)	0.61 (0.55-0.68)	0.57 (0.48-0.58)	0.56 (0.48-0.62)	0.56 (0.5-0.6)
IFNG	C8A	102	63	0.67 (0.58-0.75)	0.58 (0.44-0.7)	0.63 (0.54-0.7)	0.53 (0.33-0.68)	0.59 (0.55-0.62)	0.56 (0.45-0.64)
IL10_PEA_IR	IFNG	101	63	0.69 (0.61-0.78)	0.57 (0.39-0.75)	0.63 (0.53-0.74)	0.51 (0.3-0.7)	0.61 (0.58-0.62)	0.56 (0.45-0.65)
CXCL9	F9	102	63	0.66 (0.58-0.74)	0.63 (0.5-0.76)	0.65 (0.57-0.73)	0.55 (0.39-0.66)	0.57 (0.48-0.63)	0.56 (0.46-0.64)
IL7	HPR	102	63	0.62 (0.52-0.7)	0.67 (0.56-0.77)	0.64 (0.57-0.71)	0.56 (0.5-0.6)	0.56 (0.46-0.65)	0.56 (0.5-0.6)
C8B	SERPIND1	102	67	0.61 (0.51-0.7)	0.65 (0.54-0.75)	0.63 (0.56-0.7)	0.58 (0.47-0.62)	0.54 (0.42-0.63)	0.56 (0.48-0.61)
FGF2	CXCL9	101	63	0.66 (0.58-0.74)	0.66 (0.42-0.77)	0.66 (0.54-0.74)	0.53 (0.35-0.66)	0.58 (0.49-0.63)	0.56 (0.47-0.64)
IL10_PEA_IR	SERPIND1	101	63	0.56 (0.48-0.65)	0.64 (0.5-0.76)	0.6 (0.52-0.68)	0.53 (0.49-0.56)	0.59 (0.42-0.63)	0.56 (0.48-0.58)
CDSN	SERPIND1	101	63	0.55 (0.47-0.63)	0.66 (0.55-0.77)	0.6 (0.54-0.68)	0.52 (0.51-0.54)	0.59 (0.36-0.66)	0.56 (0.44-0.6)

KLRD1	C4BPB	101	63	0.61 (0.52-0.69)	0.59 (0.5-0.69)	0.6 (0.54-0.67)	0.58 (0.4-0.6)	0.54 (0.5-0.56)	0.56 (0.47-0.58)
FGF2	C2	101	63	0.56 (0.49-0.65)	0.66 (0.45-0.78)	0.61 (0.5-0.68)	0.53 (0.46-0.55)	0.59 (0.36-0.65)	0.56 (0.44-0.59)
SAA1	C2	102	67	0.57 (0.48-0.67)	0.58 (0.42-0.75)	0.58 (0.49-0.68)	0.52 (0.43-0.57)	0.61 (0.46-0.64)	0.56 (0.46-0.61)
IL6_PEA_IR	MASP1	102	63	0.63 (0.52-0.71)	0.59 (0.48-0.73)	0.61 (0.53-0.69)	0.56 (0.38-0.63)	0.58 (0.49-0.59)	0.56 (0.46-0.6)
ORM1	C8A	102	67	0.6 (0.5-0.69)	0.62 (0.52-0.72)	0.61 (0.54-0.68)	0.57 (0.42-0.59)	0.57 (0.42-0.61)	0.56 (0.48-0.6)
MASP1	SERPING1	101	63	0.6 (0.49-0.7)	0.6 (0.47-0.74)	0.6 (0.53-0.68)	0.55 (0.4-0.61)	0.58 (0.43-0.6)	0.56 (0.46-0.6)
FGF2	APOA1	101	63	0.6 (0.52-0.67)	0.66 (0.45-0.79)	0.63 (0.52-0.71)	0.55 (0.46-0.59)	0.57 (0.46-0.65)	0.56 (0.49-0.6)
SIT1	C9	101	63	0.63 (0.54-0.73)	0.6 (0.5-0.71)	0.62 (0.55-0.69)	0.55 (0.38-0.63)	0.58 (0.5-0.59)	0.56 (0.46-0.61)
C3	CFB	102	67	0.58 (0.5-0.66)	0.64 (0.52-0.74)	0.61 (0.54-0.68)	0.56 (0.46-0.57)	0.57 (0.41-0.63)	0.56 (0.46-0.59)
CXCL9	C4BPB	102	63	0.68 (0.59-0.75)	0.58 (0.47-0.7)	0.63 (0.56-0.7)	0.57 (0.33-0.67)	0.55 (0.54-0.57)	0.56 (0.44-0.61)
PLXNA4	SERPIND1	101	63	0.56 (0.49-0.62)	0.65 (0.53-0.77)	0.6 (0.54-0.67)	0.53 (0.51-0.54)	0.59 (0.37-0.64)	0.56 (0.45-0.59)
MASP1	TNF	101	63	0.62 (0.52-0.71)	0.6 (0.49-0.73)	0.6 (0.54-0.68)	0.56 (0.39-0.62)	0.56 (0.51-0.58)	0.56 (0.47-0.6)
LRG1	SERPIND1	102	67	0.61 (0.52-0.7)	0.66 (0.55-0.76)	0.63 (0.57-0.7)	0.56 (0.44-0.59)	0.58 (0.41-0.66)	0.56 (0.46-0.62)
MILR1	SERPING1	101	63	0.65 (0.57-0.72)	0.58 (0.47-0.72)	0.62 (0.55-0.69)	0.59 (0.36-0.64)	0.53 (0.51-0.55)	0.56 (0.44-0.59)
FGF2	VTN	101	63	0.55 (0.5-0.64)	0.67 (0.5-0.78)	0.62 (0.53-0.68)	0.53 (0.49-0.54)	0.6 (0.34-0.67)	0.56 (0.43-0.6)
PZP	ORM1	101	67	0.59 (0.47-0.69)	0.64 (0.53-0.75)	0.61 (0.54-0.69)	0.58 (0.44-0.59)	0.54 (0.35-0.64)	0.56 (0.46-0.61)
C8B	CLU	102	67	0.63 (0.53-0.72)	0.61 (0.52-0.71)	0.62 (0.55-0.69)	0.59 (0.39-0.63)	0.53 (0.48-0.58)	0.56 (0.46-0.6)
LAMP3	C4BPB	101	63	0.6 (0.49-0.68)	0.63 (0.52-0.73)	0.61 (0.54-0.69)	0.58 (0.43-0.59)	0.55 (0.39-0.62)	0.56 (0.48-0.6)
FC	CCL13	77	43	0.68 (0.59-0.77)	0.59 (0.46-0.73)	0.63 (0.56-0.73)	0.57 (0.33-0.67)	0.54 (0.52-0.58)	0.56 (0.44-0.61)
CXCL9	C8A	102	63	0.67 (0.58-0.74)	0.57 (0.48-0.69)	0.62 (0.56-0.69)	0.57 (0.34-0.67)	0.54 (0.53-0.56)	0.56 (0.44-0.61)
SH2D1A	ORM1	101	63	0.59 (0.49-0.69)	0.61 (0.51-0.73)	0.6 (0.53-0.68)	0.56 (0.44-0.59)	0.56 (0.42-0.6)	0.56 (0.48-0.59)
IL17C	APCS	102	63	0.6 (0.51-0.68)	0.61 (0.5-0.72)	0.61 (0.53-0.67)	0.57 (0.41-0.59)	0.56 (0.41-0.58)	0.56 (0.48-0.58)
SIT1	ITIH2	101	63	0.6 (0.53-0.67)	0.63 (0.53-0.75)	0.62 (0.55-0.68)	0.56 (0.47-0.58)	0.56 (0.49-0.63)	0.56 (0.51-0.6)
ORM1	C4BPB	102	67	0.6 (0.5-0.69)	0.64 (0.51-0.74)	0.62 (0.54-0.69)	0.57 (0.45-0.6)	0.59 (0.4-0.61)	0.56 (0.47-0.6)
ITGA11	C8A	101	63	0.64 (0.54-0.71)	0.58 (0.49-0.68)	0.61 (0.54-0.68)	0.58 (0.37-0.63)	0.54 (0.5-0.55)	0.56 (0.45-0.59)
FCRL6	LAMP3	102	63	0.58 (0.49-0.66)	0.65 (0.54-0.76)	0.61 (0.55-0.69)	0.54 (0.49-0.58)	0.57 (0.36-0.64)	0.56 (0.45-0.6)
SH2D1A	SAA1	101	63	0.6 (0.5-0.69)	0.59 (0.46-0.72)	0.59 (0.52-0.67)	0.54 (0.43-0.61)	0.57 (0.49-0.59)	0.56 (0.48-0.59)
IL15	C8A	102	63	0.59 (0.47-0.68)	0.61 (0.5-0.73)	0.6 (0.52-0.67)	0.59 (0.46-0.6)	0.53 (0.46-0.61)	0.56 (0.49-0.6)
CCL13	ITIH3	102	63	0.58 (0.51-0.67)	0.61 (0.51-0.72)	0.6 (0.54-0.66)	0.55 (0.43-0.58)	0.57 (0.42-0.59)	0.56 (0.48-0.58)
SIT1	SERPINA4	101	63	0.62 (0.54-0.69)	0.62 (0.52-0.73)	0.62 (0.55-0.69)	0.55 (0.42-0.61)	0.56 (0.53-0.57)	0.56 (0.49-0.59)

IL13	ITIH3	102	63	0.6 (0.49-0.68)	0.59 (0.47-0.71)	0.59 (0.52-0.66)	0.59 (0.41-0.6)	0.57 (0.48-0.58)	0.56 (0.46-0.59)
FC	HSD11B1	76	43	0.69 (0.6-0.77)	0.59 (0.47-0.73)	0.64 (0.57-0.72)	0.56 (0.31-0.69)	0.56 (0.53-0.59)	0.56 (0.44-0.63)
IL6_PEA_IR	FGF2	102	63	0.58 (0.47-0.68)	0.66 (0.44-0.79)	0.62 (0.49-0.71)	0.53 (0.44-0.59)	0.59 (0.35-0.65)	0.56 (0.43-0.61)
LAMP3	C8A	101	63	0.6 (0.49-0.68)	0.63 (0.53-0.73)	0.61 (0.55-0.68)	0.58 (0.44-0.6)	0.55 (0.4-0.62)	0.56 (0.48-0.6)
MASP1	IL6_PEA_cytokine	101	63	0.61 (0.5-0.72)	0.58 (0.45-0.73)	0.6 (0.51-0.69)	0.57 (0.38-0.62)	0.57 (0.48-0.59)	0.56 (0.45-0.6)
C5	SERPIND1	102	67	0.62 (0.52-0.7)	0.65 (0.54-0.74)	0.63 (0.56-0.7)	0.56 (0.48-0.62)	0.56 (0.4-0.63)	0.56 (0.47-0.61)
CLEC4C	CXCL9	101	63	0.67 (0.58-0.75)	0.62 (0.46-0.76)	0.65 (0.55-0.72)	0.55 (0.34-0.66)	0.57 (0.48-0.64)	0.56 (0.43-0.64)
SERPINA3	CFB	102	67	0.58 (0.49-0.67)	0.63 (0.51-0.74)	0.61 (0.53-0.68)	0.55 (0.45-0.58)	0.58 (0.41-0.63)	0.56 (0.46-0.6)
PLXNA4	SAA1	101	63	0.59 (0.5-0.68)	0.63 (0.51-0.76)	0.61 (0.53-0.69)	0.55 (0.43-0.57)	0.61 (0.42-0.64)	0.56 (0.45-0.6)
SERPIND1	CFB	102	67	0.57 (0.49-0.65)	0.65 (0.54-0.76)	0.61 (0.55-0.68)	0.56 (0.49-0.57)	0.56 (0.37-0.64)	0.56 (0.46-0.6)
MILR1	HGF	101	63	0.64 (0.55-0.72)	0.58 (0.47-0.7)	0.6 (0.53-0.68)	0.58 (0.37-0.64)	0.53 (0.49-0.55)	0.56 (0.45-0.59)
C4B	C8A	102	67	0.59 (0.49-0.67)	0.69 (0.55-0.8)	0.64 (0.56-0.71)	0.57 (0.5-0.58)	0.54 (0.36-0.68)	0.56 (0.46-0.63)
IL13	C3	102	63	0.58 (0.47-0.65)	0.6 (0.47-0.73)	0.59 (0.5-0.67)	0.56 (0.43-0.57)	0.57 (0.45-0.59)	0.56 (0.48-0.58)
ITGA11	SAA1	101	63	0.62 (0.52-0.71)	0.57 (0.44-0.69)	0.59 (0.51-0.68)	0.58 (0.38-0.62)	0.54 (0.45-0.58)	0.56 (0.46-0.6)
CLEC4C	SERPINA3	101	63	0.58 (0.51-0.67)	0.62 (0.48-0.75)	0.6 (0.53-0.68)	0.55 (0.44-0.58)	0.58 (0.38-0.63)	0.56 (0.45-0.6)
SH2D1A	C3	101	63	0.58 (0.49-0.66)	0.61 (0.51-0.74)	0.59 (0.53-0.67)	0.56 (0.45-0.57)	0.57 (0.44-0.59)	0.55 (0.49-0.58)
HSD11B1	IL6_PEA_cytokine	101	63	0.58 (0.49-0.66)	0.58 (0.46-0.73)	0.58 (0.5-0.66)	0.53 (0.43-0.6)	0.58 (0.46-0.62)	0.55 (0.47-0.59)
IL6_PEA_IR	HSD11B1	102	63	0.6 (0.5-0.69)	0.61 (0.49-0.73)	0.6 (0.52-0.68)	0.56 (0.4-0.61)	0.57 (0.46-0.61)	0.55 (0.46-0.6)
APCS	C8A	102	67	0.6 (0.5-0.69)	0.62 (0.53-0.74)	0.61 (0.54-0.68)	0.58 (0.44-0.6)	0.56 (0.42-0.61)	0.55 (0.47-0.6)
FGF2	SERPING1	101	63	0.56 (0.49-0.64)	0.66 (0.46-0.78)	0.61 (0.5-0.68)	0.53 (0.46-0.55)	0.6 (0.35-0.66)	0.55 (0.44-0.6)
C5	CPN2	102	67	0.64 (0.55-0.73)	0.63 (0.52-0.73)	0.64 (0.57-0.71)	0.59 (0.42-0.65)	0.53 (0.44-0.6)	0.55 (0.47-0.61)
MILR1	CCL13	101	63	0.64 (0.55-0.72)	0.59 (0.49-0.71)	0.61 (0.55-0.68)	0.59 (0.36-0.64)	0.52 (0.46-0.56)	0.55 (0.44-0.58)
CLEC4C	ITIH1	101	63	0.56 (0.5-0.64)	0.64 (0.53-0.76)	0.6 (0.54-0.67)	0.52 (0.5-0.54)	0.59 (0.36-0.65)	0.55 (0.44-0.59)
IL10_PEA_IR	C3	101	63	0.59 (0.5-0.67)	0.6 (0.42-0.74)	0.59 (0.49-0.68)	0.55 (0.45-0.59)	0.56 (0.51-0.59)	0.55 (0.5-0.58)
IL6_PEA_cytokine	APOA1	102	63	0.6 (0.51-0.68)	0.57 (0.46-0.68)	0.59 (0.51-0.65)	0.56 (0.39-0.61)	0.55 (0.48-0.56)	0.55 (0.47-0.58)
TNF	ITIH3	102	63	0.58 (0.5-0.66)	0.59 (0.5-0.71)	0.58 (0.53-0.65)	0.55 (0.43-0.58)	0.56 (0.51-0.57)	0.55 (0.49-0.57)
LRG1	PZP	101	67	0.61 (0.51-0.7)	0.61 (0.5-0.73)	0.61 (0.53-0.69)	0.57 (0.42-0.62)	0.54 (0.39-0.61)	0.55 (0.46-0.6)
MILR1	ITIH2	101	63	0.63 (0.55-0.71)	0.6 (0.52-0.71)	0.62 (0.56-0.69)	0.56 (0.37-0.63)	0.56 (0.48-0.58)	0.55 (0.46-0.6)
IL6_PEA_IR	CXCL9	101	63	0.66 (0.58-0.75)	0.58 (0.45-0.72)	0.62 (0.54-0.7)	0.57 (0.34-0.66)	0.55 (0.51-0.58)	0.55 (0.44-0.61)
LAMP3	IL17F	101	63	0.59 (0.47-0.68)	0.62 (0.46-0.73)	0.6 (0.51-0.68)	0.56 (0.43-0.6)	0.55 (0.4-0.61)	0.55 (0.47-0.59)

ITIH1	ITIH2	102	67	0.57 (0.51-0.65)	0.63 (0.52-0.74)	0.6 (0.53-0.67)	0.54 (0.47-0.55)	0.58 (0.4-0.64)	0.55 (0.46-0.59)
FGF2	HSD11B1	102	63	0.57 (0.51-0.65)	0.67 (0.49-0.79)	0.62 (0.52-0.69)	0.53 (0.47-0.54)	0.58 (0.35-0.67)	0.55 (0.44-0.6)
DCTN1	C5	101	63	0.61 (0.51-0.69)	0.71 (0.59-0.81)	0.66 (0.58-0.73)	0.56 (0.5-0.61)	0.55 (0.33-0.69)	0.55 (0.44-0.64)
CLEC4C	IL6_PEA_cytokine	101	63	0.57 (0.46-0.65)	0.65 (0.49-0.77)	0.61 (0.52-0.69)	0.54 (0.45-0.57)	0.57 (0.36-0.64)	0.55 (0.45-0.6)
MASP1	SERPINA4	101	63	0.63 (0.54-0.72)	0.59 (0.48-0.72)	0.61 (0.53-0.69)	0.54 (0.38-0.63)	0.55 (0.51-0.59)	0.55 (0.46-0.6)
FLT3LG	C9	102	63	0.64 (0.55-0.74)	0.61 (0.51-0.72)	0.62 (0.56-0.7)	0.54 (0.39-0.64)	0.57 (0.51-0.59)	0.55 (0.48-0.61)
SERPINA4	C8A	102	67	0.63 (0.54-0.71)	0.58 (0.5-0.69)	0.61 (0.54-0.67)	0.57 (0.38-0.63)	0.54 (0.51-0.55)	0.55 (0.46-0.59)
HSD11B1	ITIH3	101	63	0.59 (0.51-0.68)	0.6 (0.51-0.71)	0.6 (0.53-0.66)	0.56 (0.42-0.59)	0.56 (0.47-0.58)	0.55 (0.49-0.58)
FCRL6	FGF2	102	63	0.56 (0.5-0.63)	0.68 (0.49-0.8)	0.62 (0.52-0.69)	0.53 (0.48-0.53)	0.59 (0.33-0.68)	0.55 (0.42-0.6)
ITIH1	CFB	102	67	0.57 (0.5-0.64)	0.63 (0.53-0.73)	0.6 (0.54-0.66)	0.55 (0.48-0.57)	0.57 (0.4-0.62)	0.55 (0.47-0.59)
ITIH3	C4BPB	102	67	0.61 (0.51-0.69)	0.59 (0.51-0.69)	0.6 (0.54-0.67)	0.58 (0.4-0.61)	0.55 (0.48-0.57)	0.55 (0.47-0.59)
NCR1	IL17C	101	63	0.61 (0.53-0.69)	0.63 (0.49-0.72)	0.62 (0.54-0.69)	0.54 (0.39-0.62)	0.57 (0.5-0.6)	0.55 (0.48-0.6)
PLXNA4	ITIH1	101	63	0.56 (0.49-0.63)	0.65 (0.54-0.76)	0.6 (0.55-0.67)	0.53 (0.5-0.54)	0.58 (0.37-0.64)	0.55 (0.44-0.59)
FC	IL17F	77	43	0.7 (0.6-0.79)	0.57 (0.37-0.76)	0.63 (0.52-0.74)	0.54 (0.3-0.69)	0.56 (0.53-0.61)	0.55 (0.42-0.64)
ITGA11	F9	101	63	0.62 (0.53-0.71)	0.63 (0.51-0.75)	0.63 (0.54-0.7)	0.55 (0.4-0.62)	0.57 (0.39-0.62)	0.55 (0.46-0.6)
HSD11B1	APOA1	101	63	0.6 (0.52-0.67)	0.6 (0.51-0.71)	0.6 (0.54-0.67)	0.55 (0.44-0.59)	0.56 (0.5-0.59)	0.55 (0.49-0.58)
SAA1	C8A	102	67	0.59 (0.49-0.69)	0.59 (0.48-0.72)	0.59 (0.52-0.67)	0.57 (0.41-0.6)	0.58 (0.5-0.59)	0.55 (0.48-0.59)
ITIH3	C2	102	67	0.59 (0.51-0.67)	0.59 (0.49-0.72)	0.59 (0.53-0.66)	0.56 (0.42-0.59)	0.56 (0.45-0.58)	0.55 (0.48-0.58)
IFNG	C2	102	63	0.68 (0.6-0.76)	0.58 (0.42-0.74)	0.63 (0.53-0.72)	0.5 (0.34-0.68)	0.62 (0.54-0.63)	0.55 (0.47-0.65)
IFNG	SERPIND1	102	63	0.68 (0.59-0.77)	0.65 (0.54-0.76)	0.67 (0.59-0.74)	0.52 (0.42-0.63)	0.6 (0.45-0.65)	0.55 (0.46-0.63)
SH2D1A	SIT1	102	63	0.62 (0.53-0.7)	0.6 (0.51-0.71)	0.61 (0.55-0.68)	0.54 (0.44-0.61)	0.55 (0.53-0.59)	0.55 (0.5-0.59)
KLRD1	TNF	101	63	0.6 (0.51-0.68)	0.58 (0.5-0.67)	0.59 (0.53-0.65)	0.58 (0.41-0.59)	0.54 (0.5-0.56)	0.55 (0.47-0.57)
ITIH3	CFB	102	67	0.59 (0.5-0.67)	0.63 (0.51-0.74)	0.61 (0.53-0.67)	0.55 (0.44-0.59)	0.58 (0.42-0.62)	0.55 (0.48-0.6)
IL13	SAA1	102	63	0.56 (0.48-0.66)	0.56 (0.42-0.72)	0.57 (0.48-0.66)	0.55 (0.44-0.56)	0.57 (0.48-0.57)	0.55 (0.48-0.57)
LAMP3	ITIH2	101	63	0.59 (0.48-0.68)	0.63 (0.54-0.73)	0.61 (0.54-0.67)	0.56 (0.47-0.59)	0.56 (0.39-0.62)	0.55 (0.46-0.6)
LRG1	CFB	102	67	0.62 (0.52-0.7)	0.61 (0.51-0.74)	0.62 (0.55-0.69)	0.57 (0.41-0.62)	0.55 (0.48-0.64)	0.55 (0.47-0.62)
LRG1	CLU	102	67	0.62 (0.52-0.71)	0.61 (0.52-0.72)	0.61 (0.54-0.68)	0.58 (0.41-0.61)	0.54 (0.44-0.6)	0.55 (0.46-0.6)
IL17C	F9	102	63	0.59 (0.51-0.67)	0.63 (0.5-0.75)	0.61 (0.53-0.69)	0.55 (0.41-0.58)	0.57 (0.4-0.62)	0.55 (0.47-0.59)
CLEC4C	IL15	101	63	0.57 (0.47-0.65)	0.6 (0.47-0.75)	0.59 (0.5-0.67)	0.56 (0.49-0.57)	0.56 (0.36-0.64)	0.55 (0.45-0.6)
CDSN	APOA1	101	63	0.6 (0.53-0.67)	0.61 (0.51-0.72)	0.6 (0.54-0.67)	0.55 (0.43-0.59)	0.57 (0.47-0.6)	0.55 (0.49-0.58)

NCR1	SERPINA4	101	63	0.6 (0.52-0.68)	0.61 (0.51-0.72)	0.61 (0.54-0.68)	0.58 (0.42-0.6)	0.53 (0.5-0.58)	0.55 (0.47-0.58)
MASP1	C2	101	63	0.61 (0.51-0.7)	0.6 (0.48-0.73)	0.6 (0.52-0.68)	0.55 (0.4-0.61)	0.57 (0.45-0.58)	0.55 (0.47-0.59)
CLEC4C	CCL13	101	63	0.57 (0.49-0.66)	0.63 (0.5-0.75)	0.6 (0.52-0.67)	0.55 (0.46-0.56)	0.57 (0.38-0.63)	0.55 (0.46-0.59)
SIT1	IL7	101	63	0.58 (0.5-0.65)	0.62 (0.52-0.72)	0.6 (0.54-0.66)	0.55 (0.47-0.58)	0.56 (0.44-0.6)	0.55 (0.48-0.59)
IL13	SERPINA3	102	63	0.58 (0.46-0.66)	0.6 (0.46-0.74)	0.59 (0.5-0.67)	0.56 (0.43-0.57)	0.58 (0.44-0.61)	0.55 (0.45-0.59)
ITIH2	CFB	102	67	0.58 (0.5-0.66)	0.62 (0.52-0.73)	0.6 (0.54-0.67)	0.55 (0.47-0.57)	0.57 (0.43-0.62)	0.55 (0.49-0.59)
CCL13	SERPINA3	102	63	0.57 (0.5-0.66)	0.61 (0.5-0.73)	0.59 (0.53-0.67)	0.54 (0.44-0.57)	0.57 (0.41-0.6)	0.55 (0.47-0.58)
MASP1	HGF	101	63	0.62 (0.51-0.71)	0.59 (0.47-0.72)	0.61 (0.53-0.68)	0.56 (0.38-0.62)	0.56 (0.48-0.58)	0.55 (0.46-0.6)
IL10_PEA_IR	IL15	101	63	0.56 (0.47-0.65)	0.59 (0.47-0.73)	0.58 (0.5-0.66)	0.55 (0.46-0.57)	0.56 (0.46-0.6)	0.55 (0.49-0.58)
C5	VTN	102	67	0.63 (0.54-0.71)	0.63 (0.53-0.74)	0.63 (0.56-0.69)	0.57 (0.44-0.64)	0.55 (0.43-0.61)	0.55 (0.47-0.62)
hsCRP	CPN2	98	67	0.62 (0.51-0.7)	0.64 (0.52-0.75)	0.63 (0.54-0.7)	0.57 (0.45-0.63)	0.55 (0.4-0.63)	0.55 (0.46-0.62)
MILR1	CLU	101	63	0.63 (0.55-0.71)	0.58 (0.5-0.71)	0.61 (0.55-0.69)	0.58 (0.37-0.63)	0.53 (0.48-0.56)	0.55 (0.45-0.59)
ITIH3	C8A	102	67	0.6 (0.51-0.68)	0.58 (0.51-0.68)	0.59 (0.53-0.66)	0.57 (0.4-0.6)	0.54 (0.46-0.57)	0.55 (0.47-0.58)
IL17C	ORM1	102	63	0.61 (0.51-0.7)	0.61 (0.5-0.72)	0.61 (0.54-0.69)	0.57 (0.4-0.6)	0.55 (0.41-0.59)	0.55 (0.46-0.59)
CDSN	SERPINA3	101	63	0.59 (0.5-0.68)	0.61 (0.49-0.74)	0.6 (0.53-0.69)	0.54 (0.42-0.58)	0.59 (0.44-0.6)	0.55 (0.47-0.59)
IFNG	VEGFA	102	63	0.65 (0.55-0.75)	0.56 (0.45-0.71)	0.6 (0.53-0.7)	0.51 (0.33-0.68)	0.6 (0.56-0.62)	0.55 (0.46-0.64)
IL10_PEA_IR	ITIH3	101	63	0.6 (0.52-0.69)	0.6 (0.43-0.73)	0.6 (0.51-0.68)	0.53 (0.4-0.61)	0.58 (0.54-0.6)	0.55 (0.49-0.6)
SERPINA4	C4BPB	102	67	0.63 (0.54-0.72)	0.58 (0.49-0.68)	0.61 (0.54-0.68)	0.56 (0.38-0.63)	0.54 (0.51-0.55)	0.55 (0.46-0.58)
PLXNA4	SERPINA3	101	63	0.58 (0.5-0.67)	0.65 (0.52-0.77)	0.61 (0.54-0.69)	0.54 (0.45-0.58)	0.58 (0.37-0.64)	0.55 (0.45-0.61)
DCTN1	F9	101	63	0.58 (0.51-0.67)	0.71 (0.57-0.82)	0.65 (0.57-0.72)	0.53 (0.48-0.56)	0.58 (0.31-0.7)	0.55 (0.42-0.62)
MILR1	VEGFA	101	63	0.64 (0.55-0.72)	0.58 (0.49-0.68)	0.61 (0.54-0.67)	0.58 (0.37-0.64)	0.53 (0.5-0.54)	0.55 (0.44-0.58)
ORM1	CLU	102	67	0.61 (0.48-0.71)	0.62 (0.53-0.72)	0.62 (0.54-0.69)	0.57 (0.45-0.61)	0.54 (0.42-0.61)	0.55 (0.48-0.6)
HGF	CXCL9	102	63	0.67 (0.58-0.75)	0.57 (0.43-0.7)	0.62 (0.54-0.7)	0.54 (0.34-0.66)	0.55 (0.52-0.59)	0.55 (0.45-0.62)
LAMP3	CCL4	101	63	0.59 (0.45-0.69)	0.62 (0.51-0.72)	0.61 (0.52-0.68)	0.57 (0.39-0.61)	0.55 (0.38-0.62)	0.55 (0.46-0.61)
IL10_PEA_IR	APOA1	101	63	0.6 (0.52-0.67)	0.58 (0.41-0.72)	0.59 (0.5-0.67)	0.54 (0.43-0.59)	0.56 (0.53-0.58)	0.55 (0.49-0.58)
SIT1	IL17C	101	63	0.62 (0.55-0.71)	0.62 (0.5-0.72)	0.62 (0.55-0.68)	0.54 (0.38-0.63)	0.57 (0.54-0.59)	0.55 (0.47-0.6)
IL10_PEA_IR	C8A	101	63	0.6 (0.52-0.68)	0.59 (0.42-0.74)	0.6 (0.5-0.68)	0.52 (0.4-0.61)	0.59 (0.52-0.61)	0.55 (0.48-0.6)
DCTN1	IFNG	101	63	0.68 (0.6-0.76)	0.69 (0.58-0.82)	0.69 (0.62-0.76)	0.5 (0.44-0.61)	0.59 (0.38-0.67)	0.55 (0.44-0.62)
DCTN1	FLT3LG	101	63	0.6 (0.52-0.69)	0.7 (0.58-0.81)	0.66 (0.57-0.73)	0.54 (0.5-0.6)	0.56 (0.36-0.67)	0.55 (0.45-0.61)
FC	IFNG	77	43	0.7 (0.59-0.79)	0.58 (0.43-0.73)	0.64 (0.54-0.73)	0.51 (0.3-0.7)	0.59 (0.57-0.6)	0.55 (0.44-0.65)

IL15	SERPIND1	102	63	0.56 (0.46-0.65)	0.67 (0.56-0.79)	0.62 (0.54-0.69)	0.55 (0.54-0.56)	0.55 (0.34-0.66)	0.55 (0.44-0.6)
VTN	ORM1	102	67	0.59 (0.5-0.68)	0.64 (0.54-0.74)	0.62 (0.54-0.68)	0.55 (0.47-0.59)	0.55 (0.38-0.63)	0.55 (0.46-0.6)
hsCRP	CP	98	67	0.62 (0.51-0.7)	0.62 (0.49-0.77)	0.62 (0.54-0.7)	0.57 (0.46-0.63)	0.53 (0.41-0.66)	0.55 (0.47-0.63)
IL7	C5	102	63	0.61 (0.51-0.69)	0.64 (0.53-0.74)	0.62 (0.54-0.7)	0.58 (0.47-0.62)	0.53 (0.42-0.62)	0.55 (0.48-0.61)
FCRL6	C3	101	63	0.58 (0.51-0.66)	0.66 (0.54-0.78)	0.62 (0.55-0.69)	0.56 (0.46-0.57)	0.56 (0.36-0.66)	0.55 (0.45-0.61)
PLXNA4	APOA1	101	63	0.6 (0.53-0.67)	0.64 (0.53-0.77)	0.62 (0.55-0.69)	0.56 (0.48-0.59)	0.56 (0.45-0.62)	0.55 (0.49-0.6)
SERPINA3	SERPINA4	102	67	0.62 (0.53-0.72)	0.59 (0.48-0.7)	0.61 (0.54-0.68)	0.56 (0.38-0.62)	0.55 (0.49-0.57)	0.55 (0.46-0.59)
CXCL9	C2	102	63	0.66 (0.58-0.74)	0.58 (0.44-0.73)	0.62 (0.53-0.7)	0.55 (0.35-0.66)	0.55 (0.55-0.57)	0.55 (0.45-0.61)
FLT3LG	CPN2	102	63	0.61 (0.52-0.69)	0.64 (0.52-0.75)	0.62 (0.55-0.69)	0.56 (0.46-0.61)	0.55 (0.42-0.6)	0.55 (0.47-0.59)
FC	IL10_PEA_IR	76	43	0.7 (0.6-0.79)	0.58 (0.39-0.77)	0.64 (0.53-0.74)	0.52 (0.29-0.71)	0.58 (0.52-0.61)	0.55 (0.44-0.65)
IL15	C4BPB	102	63	0.59 (0.48-0.68)	0.6 (0.51-0.72)	0.6 (0.52-0.68)	0.59 (0.43-0.59)	0.52 (0.45-0.58)	0.55 (0.47-0.58)
MASP1	ITIH1	101	63	0.6 (0.5-0.7)	0.63 (0.5-0.75)	0.62 (0.54-0.69)	0.52 (0.4-0.6)	0.6 (0.41-0.62)	0.55 (0.45-0.6)
FC	C4BPB	77	44	0.71 (0.62-0.79)	0.59 (0.46-0.73)	0.65 (0.57-0.73)	0.52 (0.3-0.71)	0.58 (0.54-0.59)	0.55 (0.44-0.65)
MILR1	IL17C	101	63	0.66 (0.58-0.75)	0.56 (0.44-0.67)	0.61 (0.53-0.68)	0.57 (0.33-0.67)	0.53 (0.51-0.55)	0.55 (0.43-0.6)
IL10_PEA_IR	SERPINA3	101	63	0.62 (0.53-0.7)	0.58 (0.42-0.74)	0.6 (0.51-0.68)	0.52 (0.4-0.61)	0.58 (0.54-0.6)	0.55 (0.49-0.59)
IL6_PEA_IR	C3	101	63	0.59 (0.49-0.69)	0.61 (0.49-0.75)	0.6 (0.52-0.68)	0.55 (0.41-0.59)	0.57 (0.43-0.59)	0.55 (0.47-0.59)
HPR	MBL2	102	67	0.62 (0.53-0.7)	0.67 (0.55-0.79)	0.65 (0.57-0.72)	0.53 (0.46-0.61)	0.58 (0.39-0.66)	0.55 (0.44-0.62)
SERPIND1	APCS	102	67	0.6 (0.49-0.68)	0.64 (0.54-0.76)	0.62 (0.55-0.69)	0.57 (0.46-0.59)	0.55 (0.37-0.64)	0.55 (0.46-0.61)
IL6_PEA_cytokine	C4BPB	102	63	0.63 (0.48-0.7)	0.56 (0.46-0.68)	0.6 (0.51-0.67)	0.58 (0.37-0.63)	0.54 (0.49-0.57)	0.55 (0.44-0.59)
HGF	ITIH3	102	63	0.61 (0.5-0.7)	0.58 (0.49-0.71)	0.59 (0.53-0.67)	0.54 (0.39-0.61)	0.57 (0.47-0.58)	0.55 (0.47-0.59)
ITIH3	SERPING1	102	67	0.59 (0.51-0.67)	0.6 (0.49-0.71)	0.6 (0.53-0.66)	0.55 (0.42-0.59)	0.55 (0.45-0.58)	0.55 (0.47-0.58)
MASP1	VEGFA	101	63	0.62 (0.5-0.71)	0.59 (0.48-0.73)	0.6 (0.53-0.69)	0.55 (0.39-0.61)	0.57 (0.47-0.59)	0.55 (0.46-0.6)
CCL13	CXCL9	102	63	0.66 (0.58-0.74)	0.6 (0.49-0.73)	0.63 (0.56-0.71)	0.54 (0.36-0.66)	0.56 (0.47-0.6)	0.55 (0.44-0.63)
KLRD1	SERPIND1	101	63	0.59 (0.51-0.67)	0.65 (0.55-0.75)	0.62 (0.55-0.68)	0.55 (0.47-0.58)	0.55 (0.37-0.64)	0.55 (0.46-0.6)
KLRD1	FGF2	102	63	0.6 (0.51-0.68)	0.66 (0.47-0.77)	0.63 (0.52-0.7)	0.54 (0.42-0.59)	0.55 (0.39-0.65)	0.55 (0.46-0.6)
IL17F	C3	102	63	0.58 (0.49-0.66)	0.58 (0.43-0.73)	0.58 (0.49-0.67)	0.55 (0.42-0.58)	0.55 (0.45-0.59)	0.55 (0.48-0.57)
NCR1	C9	101	63	0.62 (0.53-0.72)	0.61 (0.51-0.72)	0.62 (0.55-0.69)	0.58 (0.38-0.63)	0.53 (0.45-0.6)	0.55 (0.45-0.6)
SERPINA3	C3	102	67	0.58 (0.5-0.67)	0.6 (0.49-0.73)	0.59 (0.52-0.67)	0.55 (0.43-0.58)	0.56 (0.46-0.59)	0.55 (0.48-0.58)
IL15	C2	102	63	0.57 (0.47-0.66)	0.6 (0.49-0.75)	0.58 (0.51-0.68)	0.56 (0.48-0.59)	0.54 (0.39-0.62)	0.55 (0.48-0.59)
IL17F	SERPIND1	102	63	0.56 (0.48-0.64)	0.66 (0.51-0.76)	0.61 (0.52-0.67)	0.52 (0.47-0.56)	0.58 (0.36-0.64)	0.55 (0.44-0.59)

SIT1	PZP	100	63	0.58 (0.48-0.65)	0.63 (0.51-0.75)	0.6 (0.52-0.67)	0.54 (0.49-0.57)	0.56 (0.43-0.62)	0.55 (0.48-0.59)
IL10_PEA_IR	CP	101	63	0.56 (0.48-0.64)	0.63 (0.46-0.77)	0.6 (0.5-0.68)	0.53 (0.47-0.56)	0.58 (0.4-0.61)	0.55 (0.46-0.58)
FCRL6	MASP1	102	63	0.6 (0.51-0.7)	0.63 (0.5-0.75)	0.62 (0.54-0.69)	0.54 (0.41-0.6)	0.57 (0.4-0.62)	0.55 (0.45-0.61)
HSD11B1	CP	101	63	0.56 (0.48-0.65)	0.64 (0.54-0.77)	0.61 (0.53-0.68)	0.55 (0.5-0.57)	0.55 (0.34-0.66)	0.55 (0.44-0.61)
TNF	IL15	102	63	0.56 (0.47-0.64)	0.59 (0.5-0.7)	0.58 (0.51-0.65)	0.55 (0.5-0.56)	0.55 (0.44-0.58)	0.55 (0.5-0.57)
FGF2	CCL13	101	63	0.56 (0.49-0.65)	0.66 (0.45-0.77)	0.61 (0.5-0.68)	0.53 (0.47-0.54)	0.57 (0.36-0.65)	0.55 (0.44-0.59)
PZP	APOA1	101	67	0.61 (0.51-0.68)	0.6 (0.46-0.72)	0.6 (0.52-0.67)	0.56 (0.44-0.6)	0.53 (0.43-0.58)	0.55 (0.47-0.59)
HSD11B1	ITIH1	101	63	0.57 (0.5-0.66)	0.63 (0.52-0.75)	0.6 (0.53-0.68)	0.54 (0.49-0.55)	0.57 (0.38-0.63)	0.55 (0.45-0.59)
CLEC4C	PLXNA4	102	63	0.56 (0.5-0.63)	0.66 (0.55-0.78)	0.61 (0.54-0.68)	0.52 (0.5-0.55)	0.57 (0.34-0.66)	0.55 (0.43-0.6)
SERPIND1	CLU	102	67	0.55 (0.48-0.64)	0.64 (0.53-0.75)	0.6 (0.54-0.66)	0.54 (0.52-0.55)	0.56 (0.38-0.63)	0.55 (0.46-0.59)
PLXNA4	IL6_PEA_cytokine	101	63	0.56 (0.47-0.63)	0.64 (0.5-0.77)	0.6 (0.51-0.67)	0.5 (0.47-0.57)	0.59 (0.36-0.64)	0.55 (0.43-0.59)
MASP1	CCL13	101	63	0.6 (0.49-0.69)	0.61 (0.48-0.74)	0.6 (0.52-0.68)	0.55 (0.4-0.61)	0.57 (0.43-0.58)	0.55 (0.47-0.59)
SERPIND1	ITIH2	102	67	0.56 (0.49-0.64)	0.65 (0.55-0.76)	0.61 (0.54-0.67)	0.53 (0.5-0.55)	0.56 (0.37-0.64)	0.55 (0.45-0.59)
IL6_PEA_cytokine	IL15	102	63	0.58 (0.41-0.68)	0.57 (0.44-0.72)	0.57 (0.47-0.66)	0.55 (0.49-0.62)	0.52 (0.41-0.61)	0.55 (0.47-0.6)
LAMP3	SH2D1A	102	63	0.57 (0.48-0.66)	0.61 (0.51-0.72)	0.59 (0.52-0.67)	0.55 (0.48-0.58)	0.56 (0.4-0.62)	0.55 (0.47-0.59)
MASP1	FGF2	102	63	0.6 (0.51-0.69)	0.67 (0.48-0.78)	0.63 (0.53-0.7)	0.53 (0.43-0.6)	0.57 (0.36-0.65)	0.55 (0.44-0.61)
IL17F	SERPINA3	102	63	0.59 (0.5-0.69)	0.59 (0.41-0.74)	0.59 (0.49-0.68)	0.53 (0.41-0.59)	0.57 (0.42-0.6)	0.55 (0.46-0.59)
CDSN	C4BPB	101	63	0.59 (0.5-0.68)	0.61 (0.5-0.74)	0.6 (0.53-0.68)	0.53 (0.41-0.59)	0.58 (0.46-0.61)	0.55 (0.47-0.6)
VEGFA	APOA1	102	63	0.6 (0.52-0.68)	0.57 (0.49-0.67)	0.59 (0.53-0.65)	0.56 (0.42-0.59)	0.55 (0.52-0.56)	0.55 (0.48-0.57)
MILR1	CDSN	102	63	0.63 (0.54-0.71)	0.6 (0.49-0.72)	0.61 (0.54-0.69)	0.57 (0.38-0.63)	0.55 (0.43-0.58)	0.55 (0.44-0.59)
IL6_PEA_cytokine	SAA1	102	63	0.58 (0.47-0.68)	0.57 (0.43-0.71)	0.58 (0.49-0.66)	0.55 (0.4-0.62)	0.55 (0.49-0.56)	0.55 (0.46-0.58)
VEGFA	SAA1	102	63	0.58 (0.48-0.68)	0.59 (0.46-0.72)	0.58 (0.5-0.67)	0.54 (0.39-0.61)	0.56 (0.46-0.59)	0.55 (0.47-0.59)
ITGA11	TNF	101	63	0.62 (0.51-0.7)	0.57 (0.49-0.67)	0.59 (0.53-0.65)	0.56 (0.39-0.61)	0.53 (0.49-0.54)	0.55 (0.46-0.57)
CCL4	APOA1	102	63	0.6 (0.53-0.69)	0.58 (0.49-0.7)	0.59 (0.53-0.66)	0.55 (0.38-0.62)	0.54 (0.52-0.56)	0.55 (0.46-0.58)
IL15	SERPING1	102	63	0.56 (0.45-0.66)	0.59 (0.48-0.71)	0.58 (0.49-0.66)	0.56 (0.48-0.58)	0.54 (0.43-0.57)	0.55 (0.47-0.57)
LAMP3	CP	101	63	0.58 (0.47-0.67)	0.67 (0.56-0.79)	0.63 (0.55-0.7)	0.55 (0.5-0.58)	0.53 (0.32-0.68)	0.55 (0.44-0.62)
LAMP3	CLU	101	63	0.59 (0.48-0.67)	0.62 (0.53-0.72)	0.6 (0.53-0.67)	0.56 (0.49-0.6)	0.53 (0.39-0.62)	0.55 (0.47-0.6)
APCS	VTN	102	67	0.59 (0.5-0.67)	0.62 (0.52-0.74)	0.61 (0.54-0.68)	0.56 (0.45-0.59)	0.55 (0.39-0.61)	0.55 (0.47-0.6)
IL6_PEA_IR	LAMP3	102	63	0.6 (0.48-0.69)	0.62 (0.49-0.74)	0.61 (0.52-0.69)	0.57 (0.43-0.61)	0.56 (0.4-0.61)	0.55 (0.45-0.61)
FCRL6	ITGA11	102	63	0.63 (0.51-0.72)	0.61 (0.51-0.72)	0.62 (0.54-0.69)	0.54 (0.4-0.63)	0.57 (0.41-0.6)	0.55 (0.45-0.61)

MASP1	IL10_PEA_IR	102	63	0.59 (0.5-0.7)	0.59 (0.45-0.74)	0.59 (0.5-0.68)	0.54 (0.39-0.62)	0.55 (0.52-0.59)	0.55 (0.46-0.59)
TNF	SERPINA3	102	63	0.57 (0.49-0.66)	0.59 (0.49-0.71)	0.58 (0.51-0.66)	0.55 (0.42-0.58)	0.55 (0.44-0.59)	0.55 (0.47-0.58)
IL17C	CFB	102	63	0.59 (0.52-0.68)	0.63 (0.51-0.76)	0.61 (0.53-0.68)	0.56 (0.41-0.59)	0.55 (0.4-0.63)	0.55 (0.46-0.6)
IL10_PEA_IR	ITIH1	101	63	0.58 (0.49-0.66)	0.62 (0.49-0.74)	0.6 (0.52-0.67)	0.49 (0.47-0.57)	0.6 (0.41-0.61)	0.55 (0.46-0.59)
IFNG	ITIH1	102	63	0.68 (0.6-0.76)	0.62 (0.5-0.74)	0.65 (0.59-0.72)	0.49 (0.38-0.66)	0.62 (0.47-0.63)	0.55 (0.46-0.64)
CLEC4C	SERPING1	101	63	0.56 (0.49-0.64)	0.62 (0.48-0.74)	0.59 (0.51-0.66)	0.54 (0.46-0.55)	0.56 (0.37-0.63)	0.55 (0.45-0.59)
CLEC4C	TNF	101	63	0.57 (0.49-0.65)	0.62 (0.5-0.76)	0.59 (0.52-0.68)	0.55 (0.45-0.56)	0.55 (0.38-0.64)	0.55 (0.46-0.6)
ITIH3	SERPIND1	102	67	0.59 (0.51-0.67)	0.65 (0.55-0.76)	0.62 (0.56-0.68)	0.55 (0.47-0.57)	0.56 (0.38-0.64)	0.55 (0.46-0.6)
CCL13	SAA1	102	63	0.58 (0.49-0.68)	0.59 (0.48-0.72)	0.59 (0.52-0.67)	0.54 (0.42-0.58)	0.57 (0.49-0.58)	0.55 (0.48-0.58)
CLEC4C	CDSN	102	63	0.56 (0.49-0.63)	0.62 (0.52-0.75)	0.59 (0.52-0.67)	0.52 (0.48-0.54)	0.57 (0.38-0.63)	0.55 (0.45-0.58)
FGF2	VEGFA	101	63	0.56 (0.46-0.65)	0.66 (0.44-0.77)	0.61 (0.49-0.68)	0.53 (0.44-0.56)	0.58 (0.35-0.66)	0.55 (0.44-0.6)
PLXNA4	ITIH3	101	63	0.59 (0.51-0.67)	0.64 (0.53-0.77)	0.62 (0.54-0.68)	0.55 (0.45-0.58)	0.57 (0.4-0.63)	0.55 (0.45-0.6)
CXCL9	SERPINA4	102	63	0.68 (0.6-0.76)	0.57 (0.47-0.69)	0.63 (0.57-0.69)	0.56 (0.32-0.69)	0.53 (0.52-0.54)	0.55 (0.42-0.61)
KLRD1	CDSN	102	63	0.59 (0.51-0.67)	0.6 (0.5-0.72)	0.59 (0.53-0.67)	0.54 (0.41-0.59)	0.55 (0.48-0.58)	0.55 (0.48-0.58)
CXCL9	TNF	102	63	0.66 (0.58-0.75)	0.57 (0.46-0.69)	0.62 (0.55-0.69)	0.54 (0.34-0.66)	0.55 (0.54-0.56)	0.55 (0.44-0.61)
TNF	SERPIND1	102	63	0.56 (0.49-0.63)	0.64 (0.55-0.75)	0.6 (0.54-0.67)	0.54 (0.5-0.55)	0.56 (0.38-0.63)	0.55 (0.46-0.59)
FGF2	TNF	101	63	0.55 (0.48-0.63)	0.65 (0.45-0.78)	0.6 (0.5-0.68)	0.53 (0.47-0.54)	0.57 (0.36-0.66)	0.55 (0.44-0.59)
MASP1	IL17F	101	63	0.61 (0.49-0.7)	0.6 (0.44-0.75)	0.6 (0.51-0.69)	0.54 (0.39-0.61)	0.55 (0.45-0.6)	0.55 (0.47-0.59)
HSD11B1	C8A	101	63	0.59 (0.51-0.68)	0.59 (0.51-0.71)	0.59 (0.53-0.67)	0.55 (0.42-0.59)	0.55 (0.47-0.57)	0.55 (0.47-0.57)
PLXNA4	IL13	101	63	0.54 (0.47-0.62)	0.63 (0.48-0.76)	0.59 (0.51-0.66)	0.53 (0.48-0.53)	0.57 (0.37-0.63)	0.55 (0.44-0.58)
C3	C2	102	67	0.57 (0.5-0.65)	0.58 (0.47-0.71)	0.58 (0.5-0.66)	0.55 (0.44-0.57)	0.54 (0.44-0.57)	0.54 (0.48-0.57)
PZP	APCS	101	67	0.59 (0.48-0.68)	0.61 (0.51-0.73)	0.6 (0.53-0.68)	0.57 (0.43-0.58)	0.54 (0.37-0.63)	0.54 (0.47-0.6)
ITGA11	VEGFA	101	63	0.63 (0.51-0.7)	0.57 (0.47-0.68)	0.6 (0.52-0.67)	0.57 (0.36-0.64)	0.52 (0.49-0.54)	0.54 (0.44-0.58)
HGF	SAA1	102	63	0.59 (0.49-0.68)	0.58 (0.45-0.72)	0.59 (0.5-0.68)	0.56 (0.41-0.59)	0.54 (0.5-0.6)	0.54 (0.46-0.59)
IL13	SERPIND1	102	63	0.55 (0.45-0.63)	0.63 (0.5-0.75)	0.59 (0.52-0.67)	0.54 (0.45-0.56)	0.56 (0.39-0.63)	0.54 (0.46-0.59)
SAA1	SERPINA4	102	67	0.6 (0.51-0.68)	0.58 (0.48-0.7)	0.59 (0.53-0.66)	0.55 (0.4-0.61)	0.54 (0.49-0.56)	0.54 (0.47-0.58)
HSD11B1	IL10_PEA_IR	102	63	0.59 (0.51-0.67)	0.59 (0.43-0.74)	0.59 (0.5-0.67)	0.52 (0.42-0.58)	0.57 (0.53-0.6)	0.54 (0.49-0.58)
FCRL6	SAA1	101	63	0.59 (0.5-0.67)	0.62 (0.49-0.74)	0.61 (0.53-0.68)	0.55 (0.44-0.58)	0.58 (0.45-0.63)	0.54 (0.47-0.6)
CPN2	F9	102	67	0.62 (0.54-0.71)	0.65 (0.54-0.76)	0.63 (0.57-0.71)	0.55 (0.43-0.61)	0.53 (0.44-0.62)	0.54 (0.46-0.6)
CCL13	TNF	102	63	0.57 (0.5-0.65)	0.61 (0.51-0.72)	0.59 (0.53-0.65)	0.55 (0.46-0.56)	0.55 (0.43-0.59)	0.54 (0.48-0.57)

CXCL9	ITIH1	102	63	0.66 (0.58-0.74)	0.62 (0.5-0.74)	0.64 (0.57-0.71)	0.51 (0.37-0.66)	0.59 (0.47-0.61)	0.54 (0.44-0.63)
FGF2	IL15	101	63	0.56 (0.47-0.65)	0.68 (0.51-0.8)	0.61 (0.51-0.69)	0.54 (0.51-0.56)	0.55 (0.32-0.68)	0.54 (0.43-0.61)
FC	SH2D1A	76	43	0.69 (0.58-0.77)	0.59 (0.47-0.71)	0.64 (0.56-0.71)	0.54 (0.32-0.69)	0.56 (0.52-0.57)	0.54 (0.44-0.63)
VEGFA	ITIH3	102	63	0.59 (0.5-0.68)	0.58 (0.5-0.69)	0.59 (0.52-0.66)	0.54 (0.41-0.6)	0.55 (0.45-0.57)	0.54 (0.47-0.58)
IL6_PEA_IR	IFNG	101	63	0.69 (0.61-0.77)	0.57 (0.44-0.72)	0.63 (0.54-0.71)	0.5 (0.32-0.69)	0.6 (0.54-0.62)	0.54 (0.45-0.64)
CXCL9	PZP	101	63	0.68 (0.59-0.76)	0.6 (0.4-0.73)	0.64 (0.53-0.72)	0.56 (0.31-0.69)	0.53 (0.48-0.61)	0.54 (0.42-0.62)
MASP1	CLU	101	63	0.6 (0.49-0.7)	0.59 (0.48-0.72)	0.6 (0.52-0.67)	0.54 (0.4-0.6)	0.56 (0.47-0.58)	0.54 (0.45-0.59)
CLEC4C	IL13	101	63	0.55 (0.47-0.63)	0.62 (0.45-0.75)	0.59 (0.5-0.66)	0.53 (0.47-0.54)	0.56 (0.38-0.63)	0.54 (0.45-0.59)
MASP1	PLXNA4	102	63	0.61 (0.52-0.7)	0.63 (0.49-0.77)	0.62 (0.54-0.7)	0.53 (0.41-0.61)	0.55 (0.39-0.61)	0.54 (0.46-0.6)
IL10_PEA_IR	SERPING1	101	63	0.58 (0.5-0.67)	0.59 (0.46-0.73)	0.59 (0.5-0.67)	0.52 (0.42-0.58)	0.57 (0.49-0.61)	0.54 (0.48-0.59)
HSD11B1	IL15	101	63	0.56 (0.48-0.65)	0.6 (0.49-0.7)	0.58 (0.51-0.65)	0.55 (0.48-0.57)	0.54 (0.43-0.58)	0.54 (0.48-0.57)
ITIH3	ITIH1	102	67	0.59 (0.51-0.68)	0.61 (0.52-0.72)	0.6 (0.54-0.67)	0.54 (0.43-0.59)	0.56 (0.43-0.61)	0.54 (0.47-0.6)
C3	SERPING1	102	67	0.58 (0.49-0.66)	0.6 (0.47-0.72)	0.59 (0.51-0.66)	0.55 (0.44-0.57)	0.54 (0.44-0.57)	0.54 (0.47-0.57)
IL6_PEA_IR	SAA1	101	63	0.59 (0.47-0.7)	0.58 (0.47-0.71)	0.59 (0.5-0.67)	0.55 (0.39-0.61)	0.55 (0.49-0.57)	0.54 (0.47-0.58)
HSD11B1	SERPING1	101	63	0.57 (0.49-0.68)	0.6 (0.49-0.72)	0.59 (0.52-0.66)	0.54 (0.43-0.57)	0.55 (0.43-0.58)	0.54 (0.46-0.57)
IL6_PEA_IR	KLRD1	102	63	0.61 (0.52-0.7)	0.59 (0.49-0.69)	0.6 (0.53-0.66)	0.55 (0.4-0.61)	0.54 (0.48-0.56)	0.54 (0.46-0.58)
CRP_SRM	CP	102	67	0.63 (0.5-0.72)	0.62 (0.49-0.77)	0.63 (0.54-0.71)	0.57 (0.44-0.64)	0.52 (0.4-0.66)	0.54 (0.46-0.63)
C4BPB	CFB	102	67	0.59 (0.5-0.67)	0.63 (0.52-0.76)	0.61 (0.54-0.69)	0.56 (0.43-0.59)	0.54 (0.42-0.63)	0.54 (0.46-0.6)
IL6_PEA_IR	ITIH3	101	63	0.61 (0.52-0.7)	0.59 (0.49-0.72)	0.6 (0.53-0.67)	0.55 (0.39-0.61)	0.55 (0.46-0.57)	0.54 (0.46-0.59)
FGF2	ITIH2	101	63	0.56 (0.49-0.64)	0.65 (0.46-0.77)	0.6 (0.51-0.68)	0.53 (0.48-0.54)	0.57 (0.36-0.65)	0.54 (0.44-0.59)
ITGA11	IL6_PEA_cytokine	101	63	0.63 (0.46-0.7)	0.55 (0.43-0.67)	0.59 (0.49-0.66)	0.58 (0.37-0.63)	0.53 (0.46-0.53)	0.54 (0.43-0.58)
ITGA11	IL10_PEA_IR	102	63	0.61 (0.51-0.7)	0.57 (0.4-0.73)	0.59 (0.5-0.67)	0.53 (0.39-0.61)	0.56 (0.51-0.59)	0.54 (0.47-0.59)
FGF2	CLU	101	63	0.55 (0.48-0.64)	0.66 (0.44-0.78)	0.6 (0.5-0.68)	0.53 (0.47-0.54)	0.57 (0.35-0.66)	0.54 (0.44-0.59)
C4B	C4BPB	102	67	0.59 (0.49-0.67)	0.7 (0.57-0.82)	0.64 (0.56-0.72)	0.56 (0.52-0.59)	0.53 (0.34-0.68)	0.54 (0.45-0.63)
FGF2	CDSN	102	63	0.55 (0.48-0.63)	0.66 (0.45-0.78)	0.61 (0.5-0.68)	0.51 (0.49-0.53)	0.58 (0.36-0.66)	0.54 (0.43-0.59)
KLRD1	CCL4	101	63	0.61 (0.49-0.7)	0.58 (0.49-0.69)	0.59 (0.52-0.66)	0.54 (0.39-0.62)	0.55 (0.46-0.56)	0.54 (0.45-0.58)
IL7	C4B	102	63	0.58 (0.49-0.66)	0.69 (0.54-0.84)	0.63 (0.54-0.72)	0.55 (0.49-0.57)	0.54 (0.37-0.68)	0.54 (0.45-0.62)
KLRD1	HGF	101	63	0.6 (0.5-0.68)	0.58 (0.47-0.7)	0.59 (0.51-0.66)	0.54 (0.41-0.6)	0.55 (0.48-0.59)	0.54 (0.47-0.59)
C8B	VTN	102	67	0.62 (0.53-0.71)	0.63 (0.53-0.73)	0.63 (0.56-0.7)	0.57 (0.44-0.63)	0.51 (0.45-0.61)	0.54 (0.47-0.6)
SERPINA4	APOA1	102	67	0.61 (0.52-0.68)	0.58 (0.5-0.69)	0.59 (0.53-0.67)	0.55 (0.41-0.6)	0.53 (0.49-0.55)	0.54 (0.47-0.57)

CDSN	IL15	101	63	0.56 (0.48-0.64)	0.6 (0.49-0.73)	0.58 (0.51-0.67)	0.52 (0.49-0.56)	0.56 (0.4-0.61)	0.54 (0.46-0.58)
SH2D1A	APOA1	101	63	0.6 (0.52-0.67)	0.58 (0.48-0.68)	0.59 (0.52-0.65)	0.54 (0.42-0.59)	0.55 (0.53-0.56)	0.54 (0.49-0.57)
HGF	ITIH1	102	63	0.55 (0.48-0.63)	0.63 (0.51-0.73)	0.59 (0.52-0.66)	0.51 (0.48-0.53)	0.59 (0.39-0.61)	0.54 (0.44-0.57)
SERPIND1	SERPING1	102	67	0.56 (0.48-0.64)	0.64 (0.52-0.75)	0.6 (0.53-0.66)	0.53 (0.49-0.55)	0.55 (0.37-0.63)	0.54 (0.45-0.59)
FC	TNF	77	43	0.68 (0.58-0.76)	0.59 (0.48-0.71)	0.63 (0.55-0.71)	0.54 (0.33-0.68)	0.54 (0.52-0.56)	0.54 (0.44-0.61)
FGF2	C8A	101	63	0.58 (0.5-0.66)	0.66 (0.43-0.78)	0.62 (0.51-0.69)	0.54 (0.45-0.58)	0.56 (0.37-0.65)	0.54 (0.45-0.6)
NCR1	PZP	100	63	0.58 (0.5-0.66)	0.63 (0.51-0.75)	0.61 (0.53-0.68)	0.55 (0.45-0.57)	0.54 (0.35-0.65)	0.54 (0.45-0.6)
ITGA6	CRP_SRM	101	63	0.62 (0.52-0.71)	0.67 (0.55-0.78)	0.64 (0.57-0.72)	0.56 (0.47-0.6)	0.53 (0.39-0.68)	0.54 (0.47-0.63)
CRP_SRM	VTN	102	67	0.62 (0.52-0.71)	0.63 (0.52-0.74)	0.63 (0.55-0.69)	0.56 (0.45-0.62)	0.55 (0.43-0.65)	0.54 (0.46-0.63)
CLEC4C	C2	101	63	0.57 (0.5-0.64)	0.61 (0.48-0.75)	0.59 (0.51-0.67)	0.54 (0.45-0.55)	0.58 (0.38-0.63)	0.54 (0.44-0.59)
SERPING1	SERPINA4	102	67	0.61 (0.51-0.7)	0.59 (0.49-0.69)	0.6 (0.53-0.67)	0.56 (0.4-0.61)	0.54 (0.48-0.57)	0.54 (0.45-0.58)
FC	C8B	77	44	0.7 (0.6-0.78)	0.59 (0.47-0.73)	0.64 (0.57-0.72)	0.54 (0.3-0.71)	0.54 (0.51-0.58)	0.54 (0.42-0.63)
IFNG	TNF	102	63	0.69 (0.59-0.77)	0.58 (0.46-0.71)	0.63 (0.56-0.7)	0.48 (0.32-0.69)	0.6 (0.52-0.62)	0.54 (0.45-0.65)
CLU	CFB	102	67	0.58 (0.49-0.66)	0.62 (0.51-0.73)	0.6 (0.53-0.67)	0.55 (0.45-0.59)	0.54 (0.44-0.62)	0.54 (0.48-0.6)
IL13	C8A	102	63	0.59 (0.46-0.67)	0.58 (0.47-0.71)	0.59 (0.51-0.66)	0.58 (0.42-0.59)	0.55 (0.49-0.56)	0.54 (0.46-0.57)
IL7	CRP_SRM	102	63	0.61 (0.51-0.72)	0.64 (0.53-0.75)	0.62 (0.55-0.7)	0.53 (0.46-0.65)	0.55 (0.42-0.62)	0.54 (0.47-0.61)
CPN2	APCS	102	67	0.61 (0.51-0.69)	0.63 (0.54-0.76)	0.62 (0.55-0.69)	0.56 (0.42-0.6)	0.54 (0.45-0.57)	0.54 (0.48-0.58)
KLRD1	C2	101	63	0.6 (0.51-0.68)	0.59 (0.46-0.72)	0.59 (0.52-0.67)	0.54 (0.4-0.6)	0.55 (0.46-0.58)	0.54 (0.47-0.59)
CDSN	C8A	101	63	0.59 (0.51-0.67)	0.6 (0.5-0.73)	0.59 (0.53-0.68)	0.53 (0.42-0.58)	0.57 (0.46-0.6)	0.54 (0.47-0.59)
KLRD1	SERPINA4	101	63	0.61 (0.52-0.69)	0.58 (0.5-0.69)	0.6 (0.54-0.66)	0.56 (0.39-0.61)	0.52 (0.51-0.55)	0.54 (0.46-0.57)
ITIH2	SERPINA4	102	67	0.61 (0.53-0.68)	0.59 (0.5-0.68)	0.6 (0.55-0.66)	0.55 (0.41-0.6)	0.55 (0.49-0.56)	0.54 (0.47-0.58)
CLEC4C	C8A	101	63	0.59 (0.51-0.67)	0.61 (0.5-0.75)	0.6 (0.53-0.68)	0.55 (0.41-0.6)	0.54 (0.39-0.63)	0.54 (0.46-0.6)
CDSN	HSD11B1	102	63	0.56 (0.49-0.65)	0.61 (0.51-0.73)	0.58 (0.52-0.66)	0.52 (0.47-0.54)	0.57 (0.46-0.6)	0.54 (0.48-0.57)
CCL4	C3	102	63	0.59 (0.46-0.68)	0.6 (0.49-0.73)	0.6 (0.52-0.68)	0.56 (0.4-0.59)	0.55 (0.44-0.59)	0.54 (0.45-0.59)
CDSN	SERPING1	101	63	0.56 (0.49-0.65)	0.6 (0.47-0.74)	0.58 (0.5-0.67)	0.53 (0.46-0.56)	0.56 (0.41-0.61)	0.54 (0.46-0.58)
IL6_PEA_cytokine	SERPINA3	102	63	0.6 (0.47-0.68)	0.57 (0.44-0.72)	0.58 (0.49-0.67)	0.56 (0.4-0.61)	0.57 (0.45-0.59)	0.54 (0.44-0.59)
MILR1	SERPIND1	101	63	0.63 (0.55-0.71)	0.64 (0.53-0.76)	0.64 (0.57-0.71)	0.57 (0.39-0.63)	0.54 (0.44-0.62)	0.54 (0.45-0.61)
FCRL6	CXCL9	101	63	0.66 (0.58-0.75)	0.61 (0.49-0.72)	0.64 (0.56-0.7)	0.53 (0.36-0.66)	0.54 (0.49-0.59)	0.54 (0.45-0.62)
HGF	IFNG	102	63	0.66 (0.57-0.75)	0.57 (0.43-0.7)	0.61 (0.52-0.69)	0.5 (0.33-0.67)	0.59 (0.54-0.62)	0.54 (0.45-0.64)
IL17C	APOA1	102	63	0.62 (0.55-0.69)	0.58 (0.49-0.68)	0.6 (0.54-0.66)	0.55 (0.39-0.62)	0.54 (0.53-0.56)	0.54 (0.46-0.58)

ITIH3	SERPINA4	102	67	0.62 (0.53-0.69)	0.59 (0.5-0.69)	0.6 (0.54-0.66)	0.56 (0.39-0.62)	0.53 (0.5-0.56)	0.54 (0.46-0.58)
MILR1	CCL4	101	63	0.65 (0.56-0.73)	0.57 (0.48-0.68)	0.61 (0.54-0.68)	0.56 (0.36-0.65)	0.52 (0.51-0.53)	0.54 (0.44-0.59)
VEGFA	SERPIND1	102	63	0.55 (0.46-0.63)	0.65 (0.53-0.75)	0.6 (0.53-0.67)	0.53 (0.47-0.54)	0.56 (0.36-0.64)	0.54 (0.44-0.59)
KLRD1	ITIH1	101	63	0.6 (0.52-0.68)	0.62 (0.52-0.73)	0.61 (0.54-0.68)	0.53 (0.44-0.6)	0.55 (0.41-0.62)	0.54 (0.46-0.6)
PZP	CFB	101	67	0.58 (0.49-0.66)	0.62 (0.51-0.75)	0.6 (0.53-0.68)	0.55 (0.45-0.57)	0.55 (0.37-0.63)	0.54 (0.45-0.59)
CLEC4C	C4BPB	101	63	0.59 (0.51-0.67)	0.61 (0.5-0.74)	0.6 (0.53-0.68)	0.55 (0.42-0.59)	0.54 (0.37-0.63)	0.54 (0.44-0.6)
CXCL9	SERPING1	102	63	0.67 (0.58-0.75)	0.59 (0.46-0.72)	0.63 (0.55-0.71)	0.53 (0.34-0.66)	0.55 (0.54-0.56)	0.54 (0.45-0.61)
IL15	ITIH1	102	63	0.56 (0.46-0.65)	0.64 (0.51-0.75)	0.6 (0.51-0.67)	0.54 (0.51-0.57)	0.55 (0.37-0.63)	0.54 (0.45-0.59)
PLXNA4	HGF	101	63	0.56 (0.49-0.64)	0.63 (0.52-0.77)	0.6 (0.53-0.67)	0.52 (0.47-0.53)	0.57 (0.38-0.63)	0.54 (0.44-0.58)
IL6_PEA_IR	ITGA11	102	63	0.63 (0.48-0.72)	0.57 (0.46-0.69)	0.6 (0.52-0.67)	0.58 (0.37-0.63)	0.51 (0.47-0.54)	0.54 (0.43-0.58)
IL6_PEA_cytokine	C8A	102	63	0.62 (0.5-0.7)	0.57 (0.46-0.68)	0.6 (0.52-0.67)	0.58 (0.38-0.62)	0.53 (0.46-0.55)	0.54 (0.44-0.58)
IL10_PEA_IR	C4BPB	101	63	0.6 (0.52-0.69)	0.58 (0.45-0.72)	0.59 (0.51-0.68)	0.54 (0.4-0.6)	0.55 (0.51-0.59)	0.54 (0.47-0.58)
C9	C8B	102	67	0.63 (0.53-0.72)	0.61 (0.52-0.72)	0.62 (0.55-0.69)	0.56 (0.37-0.64)	0.55 (0.43-0.58)	0.54 (0.45-0.6)
CDSN	CCL13	101	63	0.56 (0.49-0.64)	0.6 (0.5-0.71)	0.58 (0.52-0.66)	0.53 (0.47-0.55)	0.56 (0.43-0.58)	0.54 (0.47-0.56)
HSD11B1	CCL13	101	63	0.56 (0.49-0.64)	0.62 (0.5-0.72)	0.59 (0.52-0.65)	0.53 (0.47-0.54)	0.56 (0.42-0.59)	0.54 (0.47-0.56)
KLRD1	PLXNA4	102	63	0.6 (0.51-0.68)	0.63 (0.53-0.76)	0.62 (0.54-0.69)	0.54 (0.41-0.59)	0.56 (0.39-0.62)	0.54 (0.45-0.59)
CCL13	IL15	102	63	0.57 (0.46-0.66)	0.6 (0.49-0.73)	0.59 (0.51-0.66)	0.55 (0.51-0.57)	0.53 (0.41-0.59)	0.54 (0.48-0.57)
IL10_PEA_IR	IL6_PEA_cytokine	101	63	0.58 (0.49-0.67)	0.54 (0.39-0.74)	0.57 (0.47-0.67)	0.5 (0.39-0.61)	0.58 (0.54-0.6)	0.54 (0.48-0.59)
TNF	C4BPB	102	63	0.59 (0.51-0.67)	0.58 (0.5-0.69)	0.58 (0.53-0.66)	0.56 (0.42-0.58)	0.52 (0.48-0.54)	0.54 (0.47-0.56)
IFNG	SERPINA4	102	63	0.69 (0.61-0.76)	0.57 (0.47-0.7)	0.63 (0.56-0.7)	0.54 (0.31-0.7)	0.53 (0.51-0.6)	0.54 (0.42-0.63)
CP	CFB	102	67	0.58 (0.49-0.66)	0.64 (0.53-0.76)	0.6 (0.54-0.68)	0.56 (0.46-0.57)	0.53 (0.37-0.65)	0.54 (0.46-0.6)
CLEC4C	KLRD1	102	63	0.6 (0.52-0.68)	0.62 (0.51-0.75)	0.61 (0.54-0.68)	0.55 (0.42-0.59)	0.55 (0.41-0.63)	0.54 (0.45-0.6)
DCTN1	LRG1	101	63	0.61 (0.51-0.7)	0.71 (0.59-0.82)	0.66 (0.59-0.73)	0.54 (0.5-0.58)	0.54 (0.32-0.69)	0.54 (0.43-0.62)
HSD11B1	HGF	101	63	0.57 (0.49-0.65)	0.59 (0.5-0.71)	0.58 (0.52-0.65)	0.54 (0.45-0.56)	0.55 (0.44-0.57)	0.54 (0.48-0.56)
FC	SERPINA4	77	44	0.7 (0.6-0.78)	0.59 (0.46-0.73)	0.64 (0.57-0.72)	0.53 (0.29-0.71)	0.56 (0.51-0.58)	0.54 (0.42-0.64)
CDSN	C2	101	63	0.57 (0.48-0.64)	0.6 (0.49-0.74)	0.58 (0.51-0.67)	0.52 (0.45-0.55)	0.58 (0.41-0.6)	0.54 (0.45-0.58)
KLRD1	CCL13	101	63	0.6 (0.52-0.68)	0.6 (0.5-0.71)	0.6 (0.54-0.67)	0.55 (0.41-0.59)	0.54 (0.45-0.57)	0.54 (0.46-0.58)
CXCL9	CP	102	63	0.67 (0.58-0.75)	0.66 (0.5-0.78)	0.66 (0.58-0.73)	0.55 (0.35-0.66)	0.52 (0.45-0.62)	0.54 (0.42-0.62)
KLRD1	IL17F	101	63	0.6 (0.5-0.68)	0.58 (0.43-0.71)	0.59 (0.51-0.67)	0.55 (0.4-0.6)	0.54 (0.46-0.58)	0.54 (0.46-0.58)
VEGFA	SERPINA3	102	63	0.59 (0.48-0.67)	0.59 (0.47-0.72)	0.59 (0.5-0.67)	0.53 (0.42-0.58)	0.56 (0.41-0.6)	0.54 (0.44-0.58)

KLRD1	SERPING1	101	63	0.6 (0.51-0.68)	0.59 (0.48-0.71)	0.59 (0.52-0.67)	0.57 (0.41-0.6)	0.54 (0.45-0.56)	0.54 (0.46-0.57)
CCL4	ITIH3	102	63	0.61 (0.5-0.7)	0.58 (0.49-0.7)	0.59 (0.52-0.66)	0.55 (0.38-0.62)	0.55 (0.47-0.56)	0.54 (0.44-0.59)
IFNG	CP	102	63	0.68 (0.59-0.76)	0.67 (0.46-0.78)	0.67 (0.57-0.74)	0.53 (0.36-0.65)	0.56 (0.43-0.64)	0.54 (0.43-0.62)
CCL13	SERPIND1	102	63	0.56 (0.48-0.64)	0.65 (0.53-0.76)	0.6 (0.54-0.67)	0.53 (0.5-0.54)	0.55 (0.37-0.64)	0.54 (0.45-0.59)
FGF2	IL10_PEA_IR	102	63	0.56 (0.49-0.65)	0.67 (0.42-0.81)	0.62 (0.48-0.7)	0.51 (0.46-0.55)	0.58 (0.4-0.66)	0.54 (0.45-0.59)
SH2D1A	IFNG	101	63	0.69 (0.6-0.77)	0.57 (0.45-0.69)	0.63 (0.56-0.7)	0.48 (0.32-0.69)	0.59 (0.53-0.62)	0.54 (0.45-0.64)
ITGA11	C2	101	63	0.62 (0.5-0.71)	0.58 (0.44-0.73)	0.6 (0.51-0.68)	0.55 (0.39-0.61)	0.56 (0.44-0.59)	0.54 (0.44-0.59)
hsCRP	IL7	98	63	0.62 (0.51-0.72)	0.64 (0.52-0.75)	0.63 (0.55-0.7)	0.53 (0.45-0.65)	0.55 (0.42-0.62)	0.54 (0.47-0.6)
CRP_SRM	CPN2	102	67	0.62 (0.52-0.72)	0.64 (0.51-0.75)	0.63 (0.56-0.7)	0.56 (0.44-0.64)	0.52 (0.41-0.63)	0.54 (0.45-0.61)
FCRL6	IL10_PEA_IR	102	63	0.57 (0.49-0.66)	0.61 (0.44-0.73)	0.59 (0.5-0.67)	0.51 (0.44-0.57)	0.57 (0.42-0.61)	0.54 (0.47-0.58)
ITGA11	CCL13	101	63	0.62 (0.51-0.7)	0.59 (0.48-0.71)	0.61 (0.53-0.68)	0.56 (0.39-0.62)	0.53 (0.44-0.57)	0.54 (0.44-0.58)
IL10_PEA_IR	IL13	101	63	0.57 (0.49-0.64)	0.57 (0.39-0.74)	0.56 (0.47-0.67)	0.47 (0.45-0.56)	0.61 (0.54-0.62)	0.54 (0.5-0.59)
IL17F	SAA1	102	63	0.58 (0.5-0.68)	0.55 (0.41-0.72)	0.57 (0.48-0.66)	0.52 (0.41-0.6)	0.55 (0.5-0.6)	0.54 (0.47-0.59)
CCL13	C8A	102	63	0.59 (0.51-0.68)	0.6 (0.52-0.71)	0.59 (0.53-0.67)	0.55 (0.43-0.59)	0.55 (0.44-0.57)	0.54 (0.47-0.57)
CCL13	C4BPB	102	63	0.59 (0.5-0.68)	0.6 (0.52-0.72)	0.6 (0.52-0.67)	0.54 (0.45-0.6)	0.54 (0.44-0.57)	0.54 (0.48-0.58)
CPN2	C8B	102	67	0.61 (0.52-0.7)	0.62 (0.52-0.73)	0.62 (0.55-0.69)	0.57 (0.41-0.64)	0.53 (0.44-0.57)	0.54 (0.45-0.59)
IL6_PEA_cytokine	SERPINA4	102	63	0.61 (0.52-0.69)	0.56 (0.46-0.68)	0.59 (0.52-0.66)	0.57 (0.36-0.64)	0.52 (0.46-0.53)	0.54 (0.44-0.58)
HSD11B1	C2	101	63	0.57 (0.5-0.66)	0.59 (0.5-0.72)	0.58 (0.52-0.66)	0.53 (0.44-0.57)	0.55 (0.43-0.58)	0.54 (0.47-0.57)
FCRL6	CDSN	102	63	0.55 (0.5-0.62)	0.63 (0.53-0.74)	0.59 (0.54-0.66)	0.51 (0.49-0.52)	0.56 (0.39-0.61)	0.54 (0.45-0.56)
FCRL6	SERPIND1	101	63	0.56 (0.49-0.63)	0.68 (0.57-0.79)	0.62 (0.56-0.68)	0.52 (0.5-0.54)	0.55 (0.32-0.68)	0.54 (0.42-0.61)
CCL13	ITIH1	102	63	0.56 (0.48-0.64)	0.65 (0.54-0.75)	0.6 (0.53-0.67)	0.52 (0.49-0.54)	0.56 (0.38-0.64)	0.54 (0.44-0.58)
C9	APOA1	102	67	0.65 (0.57-0.74)	0.57 (0.48-0.67)	0.61 (0.56-0.67)	0.55 (0.35-0.65)	0.53 (0.51-0.54)	0.54 (0.44-0.59)
CDSN	VTN	101	63	0.55 (0.48-0.64)	0.64 (0.53-0.76)	0.6 (0.53-0.67)	0.52 (0.49-0.54)	0.55 (0.38-0.63)	0.54 (0.44-0.58)
C9	C5	102	67	0.62 (0.52-0.72)	0.65 (0.54-0.75)	0.64 (0.57-0.7)	0.53 (0.44-0.62)	0.55 (0.38-0.64)	0.54 (0.44-0.6)
IL13	C4BPB	102	63	0.6 (0.45-0.68)	0.58 (0.47-0.7)	0.58 (0.51-0.66)	0.58 (0.41-0.59)	0.54 (0.48-0.55)	0.54 (0.45-0.57)
IL15	CP	102	63	0.56 (0.44-0.65)	0.68 (0.53-0.8)	0.61 (0.53-0.7)	0.55 (0.54-0.57)	0.53 (0.29-0.71)	0.54 (0.42-0.63)
HGF	SERPIND1	102	63	0.55 (0.49-0.63)	0.64 (0.54-0.75)	0.6 (0.54-0.67)	0.53 (0.49-0.54)	0.55 (0.36-0.64)	0.54 (0.44-0.59)
TNF	ITIH1	102	63	0.56 (0.49-0.63)	0.63 (0.52-0.74)	0.59 (0.53-0.66)	0.52 (0.49-0.53)	0.57 (0.4-0.61)	0.54 (0.46-0.57)
MILR1	VTN	101	63	0.63 (0.56-0.72)	0.62 (0.52-0.75)	0.63 (0.56-0.7)	0.56 (0.37-0.63)	0.54 (0.45-0.61)	0.54 (0.44-0.6)
MASP1	CDSN	102	63	0.59 (0.5-0.7)	0.6 (0.49-0.73)	0.6 (0.52-0.68)	0.52 (0.41-0.61)	0.56 (0.45-0.58)	0.54 (0.47-0.59)

MASP1	PZP	100	63	0.63 (0.53-0.73)	0.6 (0.44-0.74)	0.61 (0.52-0.7)	0.54 (0.38-0.62)	0.54 (0.45-0.59)	0.54 (0.43-0.6)
IL17C	C3	102	63	0.6 (0.52-0.68)	0.6 (0.49-0.73)	0.6 (0.53-0.68)	0.54 (0.4-0.59)	0.55 (0.43-0.59)	0.54 (0.46-0.58)
ITGA11	HGF	101	63	0.63 (0.5-0.71)	0.57 (0.44-0.69)	0.6 (0.51-0.67)	0.56 (0.37-0.63)	0.52 (0.47-0.58)	0.54 (0.43-0.59)
MILR1	PZP	100	63	0.65 (0.56-0.73)	0.58 (0.44-0.71)	0.61 (0.53-0.69)	0.59 (0.36-0.64)	0.49 (0.4-0.54)	0.54 (0.42-0.59)
CXCL9	VEGFA	102	63	0.66 (0.57-0.74)	0.56 (0.46-0.69)	0.61 (0.54-0.69)	0.53 (0.34-0.66)	0.55 (0.53-0.56)	0.54 (0.44-0.6)
CDSN	IL13	101	63	0.54 (0.45-0.62)	0.6 (0.48-0.71)	0.57 (0.5-0.65)	0.51 (0.47-0.52)	0.59 (0.41-0.59)	0.54 (0.46-0.55)
MILR1	FGF2	102	63	0.63 (0.54-0.71)	0.67 (0.46-0.79)	0.64 (0.54-0.72)	0.55 (0.39-0.63)	0.52 (0.44-0.65)	0.54 (0.46-0.6)
SERPINA3	C8A	102	67	0.59 (0.49-0.67)	0.59 (0.5-0.69)	0.59 (0.52-0.66)	0.56 (0.42-0.59)	0.53 (0.48-0.57)	0.54 (0.46-0.57)
C3	C8A	102	67	0.59 (0.51-0.67)	0.59 (0.51-0.73)	0.59 (0.52-0.67)	0.55 (0.42-0.59)	0.53 (0.47-0.58)	0.54 (0.46-0.58)
IL15	IL17C	102	63	0.6 (0.48-0.69)	0.58 (0.48-0.7)	0.59 (0.51-0.66)	0.55 (0.43-0.61)	0.54 (0.44-0.57)	0.54 (0.47-0.58)
IL6_PEA_cytokine	ITIH1	102	63	0.55 (0.46-0.64)	0.62 (0.5-0.75)	0.59 (0.51-0.66)	0.49 (0.46-0.56)	0.58 (0.39-0.63)	0.54 (0.44-0.58)
FC	IL7	77	43	0.7 (0.6-0.78)	0.58 (0.46-0.72)	0.64 (0.56-0.72)	0.54 (0.29-0.72)	0.53 (0.51-0.55)	0.54 (0.41-0.63)
IL6_PEA_IR	C4BPB	101	63	0.63 (0.51-0.71)	0.59 (0.49-0.7)	0.61 (0.53-0.69)	0.55 (0.38-0.62)	0.54 (0.48-0.55)	0.54 (0.45-0.58)
IL10_PEA_IR	VTN	101	63	0.57 (0.5-0.65)	0.61 (0.46-0.75)	0.59 (0.51-0.66)	0.5 (0.46-0.55)	0.58 (0.42-0.59)	0.54 (0.46-0.57)
MASP1	ITIH2	101	63	0.6 (0.51-0.7)	0.6 (0.49-0.73)	0.6 (0.53-0.68)	0.53 (0.4-0.6)	0.57 (0.43-0.59)	0.54 (0.45-0.59)
CDSN	ITIH2	101	63	0.56 (0.48-0.64)	0.62 (0.51-0.74)	0.59 (0.52-0.66)	0.51 (0.48-0.54)	0.56 (0.4-0.61)	0.54 (0.45-0.57)
HSD11B1	C4BPB	101	63	0.59 (0.51-0.68)	0.59 (0.51-0.71)	0.59 (0.53-0.67)	0.54 (0.42-0.59)	0.54 (0.44-0.56)	0.54 (0.47-0.57)
FC	IL6_PEA_cytokine	77	43	0.68 (0.58-0.78)	0.59 (0.43-0.73)	0.64 (0.54-0.72)	0.52 (0.32-0.68)	0.55 (0.53-0.57)	0.54 (0.43-0.61)
IL6_PEA_IR	IL15	101	63	0.6 (0.46-0.69)	0.59 (0.48-0.72)	0.59 (0.51-0.67)	0.59 (0.42-0.61)	0.53 (0.44-0.61)	0.54 (0.46-0.6)
CP	SERPIND1	102	67	0.55 (0.47-0.63)	0.65 (0.54-0.76)	0.6 (0.53-0.67)	0.54 (0.49-0.55)	0.54 (0.34-0.66)	0.54 (0.44-0.6)
PLXNA4	C2	101	63	0.56 (0.49-0.64)	0.63 (0.5-0.76)	0.6 (0.52-0.67)	0.51 (0.46-0.55)	0.58 (0.39-0.62)	0.54 (0.44-0.58)
IL10_PEA_IR	HGF	101	63	0.57 (0.49-0.66)	0.57 (0.4-0.73)	0.57 (0.48-0.66)	0.51 (0.43-0.57)	0.58 (0.51-0.59)	0.54 (0.49-0.58)
C3	C4BPB	102	67	0.6 (0.51-0.67)	0.6 (0.5-0.72)	0.6 (0.53-0.67)	0.56 (0.41-0.59)	0.54 (0.45-0.57)	0.54 (0.46-0.58)
ITIH3	ITIH2	102	67	0.59 (0.51-0.67)	0.59 (0.51-0.7)	0.59 (0.53-0.66)	0.55 (0.42-0.59)	0.54 (0.45-0.59)	0.54 (0.46-0.58)
FC	HGF	77	43	0.68 (0.58-0.77)	0.62 (0.48-0.76)	0.65 (0.56-0.73)	0.52 (0.36-0.66)	0.55 (0.52-0.58)	0.54 (0.45-0.61)
SERPINA3	C2	102	67	0.57 (0.5-0.67)	0.59 (0.46-0.72)	0.58 (0.51-0.67)	0.53 (0.43-0.57)	0.55 (0.43-0.59)	0.54 (0.45-0.57)
MASP1	CCL4	101	63	0.61 (0.48-0.7)	0.59 (0.47-0.74)	0.6 (0.52-0.69)	0.52 (0.39-0.61)	0.57 (0.46-0.58)	0.54 (0.44-0.59)
FCRL6	SERPINA3	101	63	0.58 (0.5-0.67)	0.63 (0.53-0.74)	0.61 (0.54-0.68)	0.55 (0.45-0.56)	0.55 (0.38-0.62)	0.54 (0.45-0.59)
HGF	IL15	102	63	0.57 (0.47-0.66)	0.58 (0.46-0.7)	0.57 (0.49-0.64)	0.54 (0.48-0.57)	0.54 (0.43-0.57)	0.54 (0.47-0.57)
IL10_PEA_IR	CCL13	101	63	0.57 (0.49-0.66)	0.6 (0.45-0.74)	0.59 (0.5-0.66)	0.53 (0.45-0.55)	0.57 (0.44-0.59)	0.54 (0.47-0.57)

SH2D1A	ITIH3	101	63	0.59 (0.51-0.67)	0.59 (0.5-0.7)	0.59 (0.53-0.66)	0.53 (0.42-0.59)	0.55 (0.48-0.57)	0.54 (0.47-0.58)
DCTN1	ORM1	101	63	0.59 (0.5-0.7)	0.71 (0.59-0.82)	0.64 (0.58-0.73)	0.52 (0.51-0.58)	0.55 (0.31-0.69)	0.54 (0.42-0.61)
FCRL6	HSD11B1	102	63	0.56 (0.5-0.64)	0.65 (0.54-0.74)	0.6 (0.55-0.67)	0.53 (0.49-0.55)	0.55 (0.37-0.64)	0.54 (0.45-0.59)
CRP_SRM	MBL2	102	67	0.61 (0.52-0.7)	0.66 (0.53-0.78)	0.63 (0.56-0.71)	0.55 (0.45-0.62)	0.51 (0.43-0.66)	0.54 (0.46-0.63)
C5	MBL2	102	67	0.61 (0.52-0.69)	0.66 (0.54-0.79)	0.63 (0.56-0.71)	0.53 (0.46-0.61)	0.55 (0.42-0.65)	0.54 (0.46-0.61)
PLXNA4	IL15	101	63	0.56 (0.48-0.64)	0.64 (0.52-0.78)	0.6 (0.53-0.68)	0.53 (0.52-0.56)	0.54 (0.36-0.64)	0.54 (0.45-0.59)
MILR1	CP	101	63	0.64 (0.56-0.73)	0.64 (0.52-0.77)	0.64 (0.56-0.71)	0.6 (0.37-0.63)	0.5 (0.41-0.61)	0.54 (0.42-0.6)
DCTN1	C8B	101	63	0.62 (0.51-0.7)	0.7 (0.59-0.8)	0.66 (0.58-0.72)	0.53 (0.5-0.61)	0.54 (0.32-0.68)	0.54 (0.43-0.61)
HGF	C4BPB	102	63	0.6 (0.49-0.69)	0.58 (0.48-0.7)	0.59 (0.52-0.67)	0.55 (0.41-0.6)	0.53 (0.47-0.56)	0.54 (0.46-0.57)
IL10_PEA_IR	C2	101	63	0.57 (0.5-0.65)	0.58 (0.41-0.74)	0.57 (0.48-0.66)	0.51 (0.43-0.57)	0.57 (0.53-0.59)	0.54 (0.49-0.57)
FGF2	SH2D1A	102	63	0.55 (0.49-0.63)	0.64 (0.48-0.77)	0.6 (0.51-0.67)	0.52 (0.48-0.53)	0.56 (0.35-0.65)	0.54 (0.44-0.58)
CLEC4C	CCL4	101	63	0.58 (0.46-0.66)	0.63 (0.52-0.75)	0.6 (0.53-0.68)	0.53 (0.42-0.58)	0.56 (0.37-0.63)	0.54 (0.44-0.59)
FC	CPN2	77	44	0.68 (0.58-0.77)	0.6 (0.47-0.73)	0.64 (0.56-0.72)	0.51 (0.34-0.68)	0.56 (0.53-0.62)	0.54 (0.45-0.62)
IL13	CCL13	102	63	0.55 (0.47-0.64)	0.62 (0.48-0.74)	0.58 (0.51-0.65)	0.52 (0.47-0.54)	0.55 (0.39-0.62)	0.54 (0.45-0.58)
PLXNA4	CXCL9	101	63	0.66 (0.57-0.74)	0.63 (0.49-0.76)	0.64 (0.56-0.72)	0.5 (0.36-0.66)	0.57 (0.46-0.61)	0.54 (0.45-0.62)
VTN	CFB	102	67	0.57 (0.5-0.65)	0.63 (0.53-0.74)	0.6 (0.54-0.67)	0.54 (0.47-0.58)	0.54 (0.41-0.63)	0.54 (0.46-0.59)
FGF2	CCL4	101	63	0.58 (0.45-0.67)	0.67 (0.42-0.77)	0.61 (0.49-0.7)	0.52 (0.41-0.58)	0.57 (0.36-0.66)	0.54 (0.43-0.6)
PLXNA4	C4BPB	101	63	0.59 (0.51-0.68)	0.63 (0.51-0.76)	0.61 (0.54-0.68)	0.53 (0.44-0.59)	0.54 (0.4-0.61)	0.54 (0.46-0.59)
PZP	SERPINA4	101	67	0.6 (0.5-0.68)	0.59 (0.48-0.74)	0.6 (0.53-0.67)	0.56 (0.42-0.59)	0.51 (0.37-0.61)	0.54 (0.44-0.58)
C4B	MBL2	102	67	0.59 (0.51-0.68)	0.7 (0.57-0.82)	0.65 (0.57-0.72)	0.54 (0.45-0.58)	0.54 (0.34-0.68)	0.54 (0.42-0.62)
KLRD1	VEGFA	101	63	0.6 (0.5-0.68)	0.58 (0.49-0.68)	0.59 (0.53-0.65)	0.53 (0.41-0.59)	0.54 (0.46-0.55)	0.54 (0.47-0.57)
CLEC4C	VEGFA	101	63	0.56 (0.48-0.64)	0.62 (0.5-0.75)	0.59 (0.51-0.67)	0.53 (0.46-0.55)	0.55 (0.37-0.63)	0.54 (0.43-0.59)
C2	SERPINA4	102	67	0.63 (0.56-0.71)	0.58 (0.47-0.71)	0.61 (0.54-0.69)	0.54 (0.37-0.63)	0.54 (0.51-0.57)	0.54 (0.45-0.59)
LAMP3	VTN	101	63	0.58 (0.49-0.67)	0.64 (0.55-0.74)	0.61 (0.54-0.68)	0.54 (0.48-0.59)	0.53 (0.37-0.63)	0.54 (0.45-0.6)
IL17F	ITIH1	102	63	0.56 (0.48-0.65)	0.63 (0.47-0.75)	0.59 (0.51-0.66)	0.5 (0.46-0.55)	0.57 (0.38-0.62)	0.54 (0.44-0.57)
HGF	SERPINA3	102	63	0.59 (0.48-0.68)	0.58 (0.47-0.7)	0.59 (0.51-0.66)	0.54 (0.42-0.58)	0.55 (0.44-0.58)	0.54 (0.46-0.57)
HSD11B1	PLXNA4	102	63	0.57 (0.5-0.65)	0.63 (0.52-0.76)	0.6 (0.54-0.67)	0.52 (0.47-0.54)	0.55 (0.38-0.63)	0.54 (0.44-0.58)
IL10_PEA_IR	SH2D1A	102	63	0.56 (0.48-0.64)	0.58 (0.44-0.73)	0.57 (0.48-0.65)	0.48 (0.46-0.55)	0.58 (0.48-0.61)	0.53 (0.48-0.57)
PLXNA4	SERPING1	101	63	0.56 (0.48-0.64)	0.64 (0.52-0.76)	0.6 (0.52-0.67)	0.52 (0.46-0.55)	0.55 (0.38-0.63)	0.53 (0.45-0.58)
FGF2	C4BPB	101	63	0.6 (0.5-0.69)	0.66 (0.46-0.77)	0.62 (0.52-0.7)	0.53 (0.42-0.59)	0.54 (0.38-0.65)	0.53 (0.45-0.6)

CPN2	APOA1	102	67	0.6 (0.52-0.67)	0.63 (0.52-0.75)	0.61 (0.54-0.69)	0.54 (0.47-0.59)	0.53 (0.41-0.6)	0.53 (0.47-0.58)
KLRD1	IL15	101	63	0.6 (0.5-0.68)	0.58 (0.49-0.68)	0.59 (0.52-0.65)	0.56 (0.41-0.59)	0.53 (0.45-0.56)	0.53 (0.46-0.57)
SERPIND1	ITIH1	102	67	0.56 (0.48-0.63)	0.65 (0.55-0.75)	0.6 (0.54-0.66)	0.53 (0.5-0.54)	0.54 (0.37-0.63)	0.53 (0.45-0.58)
ITGA11	IL13	101	63	0.62 (0.49-0.7)	0.58 (0.44-0.69)	0.6 (0.51-0.67)	0.58 (0.4-0.62)	0.54 (0.46-0.54)	0.53 (0.43-0.58)
CDSN	IL6_PEA_cytokine	101	63	0.56 (0.47-0.63)	0.58 (0.46-0.71)	0.57 (0.49-0.65)	0.51 (0.44-0.59)	0.57 (0.44-0.58)	0.53 (0.47-0.57)
CXCL9	CLU	102	63	0.67 (0.59-0.74)	0.58 (0.48-0.7)	0.62 (0.56-0.7)	0.52 (0.34-0.66)	0.54 (0.5-0.59)	0.53 (0.44-0.62)
MILR1	IL7	101	63	0.63 (0.55-0.7)	0.6 (0.5-0.72)	0.62 (0.55-0.68)	0.57 (0.37-0.63)	0.5 (0.48-0.55)	0.53 (0.44-0.58)
C4BPB	C8A	102	67	0.59 (0.51-0.67)	0.58 (0.5-0.68)	0.59 (0.53-0.65)	0.55 (0.4-0.6)	0.52 (0.49-0.55)	0.53 (0.46-0.57)
HSD11B1	VTN	101	63	0.56 (0.5-0.66)	0.62 (0.52-0.73)	0.6 (0.53-0.67)	0.53 (0.49-0.55)	0.55 (0.38-0.62)	0.53 (0.45-0.58)
DCTN1	CRP_SRM	101	63	0.63 (0.52-0.72)	0.73 (0.59-0.83)	0.67 (0.6-0.75)	0.54 (0.5-0.59)	0.52 (0.31-0.74)	0.53 (0.42-0.64)
KLRD1	CLU	101	63	0.59 (0.51-0.68)	0.58 (0.5-0.69)	0.59 (0.53-0.65)	0.55 (0.41-0.59)	0.52 (0.47-0.56)	0.53 (0.46-0.57)
SAA1	ITIH2	102	67	0.57 (0.5-0.66)	0.59 (0.49-0.71)	0.58 (0.52-0.65)	0.54 (0.44-0.57)	0.57 (0.47-0.59)	0.53 (0.47-0.58)
CLEC4C	HGF	101	63	0.56 (0.48-0.65)	0.6 (0.47-0.75)	0.58 (0.51-0.66)	0.54 (0.45-0.55)	0.53 (0.37-0.63)	0.53 (0.44-0.59)
IL13	C2	102	63	0.56 (0.46-0.64)	0.6 (0.45-0.74)	0.57 (0.49-0.67)	0.55 (0.44-0.56)	0.55 (0.44-0.6)	0.53 (0.45-0.58)
CCL13	C2	102	63	0.56 (0.49-0.64)	0.61 (0.47-0.73)	0.58 (0.52-0.66)	0.53 (0.46-0.55)	0.56 (0.43-0.58)	0.53 (0.46-0.56)
TNF	C8A	102	63	0.57 (0.5-0.66)	0.58 (0.5-0.68)	0.58 (0.52-0.65)	0.54 (0.42-0.59)	0.52 (0.49-0.53)	0.53 (0.47-0.56)
SERPIND1	VTN	102	67	0.56 (0.49-0.64)	0.64 (0.54-0.74)	0.6 (0.54-0.66)	0.54 (0.5-0.54)	0.54 (0.37-0.63)	0.53 (0.45-0.58)
CCL13	SERPINA4	102	63	0.6 (0.52-0.69)	0.6 (0.5-0.72)	0.6 (0.54-0.67)	0.57 (0.41-0.59)	0.51 (0.45-0.56)	0.53 (0.45-0.57)
SH2D1A	SERPIND1	101	63	0.55 (0.48-0.63)	0.64 (0.53-0.75)	0.6 (0.53-0.66)	0.52 (0.49-0.55)	0.55 (0.37-0.63)	0.53 (0.45-0.58)
SERPINA3	SERPIND1	102	67	0.58 (0.5-0.67)	0.65 (0.55-0.76)	0.61 (0.55-0.68)	0.52 (0.46-0.56)	0.55 (0.37-0.63)	0.53 (0.43-0.59)
HSD11B1	TNF	101	63	0.57 (0.5-0.66)	0.58 (0.5-0.69)	0.58 (0.52-0.65)	0.53 (0.45-0.56)	0.53 (0.46-0.56)	0.53 (0.49-0.55)
IL17F	ITIH3	102	63	0.6 (0.5-0.68)	0.57 (0.43-0.7)	0.59 (0.5-0.66)	0.54 (0.39-0.6)	0.53 (0.48-0.56)	0.53 (0.46-0.57)
VEGFA	C4BPB	102	63	0.6 (0.49-0.68)	0.58 (0.49-0.68)	0.59 (0.52-0.66)	0.55 (0.41-0.59)	0.53 (0.47-0.54)	0.53 (0.46-0.56)
CXCL9	ITIH2	102	63	0.67 (0.59-0.74)	0.59 (0.49-0.71)	0.63 (0.57-0.69)	0.51 (0.35-0.66)	0.55 (0.48-0.59)	0.53 (0.43-0.62)
HSD11B1	SH2D1A	102	63	0.56 (0.49-0.64)	0.61 (0.51-0.73)	0.59 (0.52-0.66)	0.51 (0.47-0.54)	0.56 (0.43-0.61)	0.53 (0.47-0.57)
VEGFA	ITIH1	102	63	0.55 (0.46-0.64)	0.62 (0.51-0.72)	0.59 (0.52-0.65)	0.5 (0.47-0.54)	0.57 (0.4-0.61)	0.53 (0.44-0.56)
ITGA6	LRG1	101	63	0.62 (0.53-0.71)	0.64 (0.53-0.75)	0.63 (0.56-0.7)	0.53 (0.43-0.6)	0.54 (0.38-0.62)	0.53 (0.45-0.59)
TNF	CP	102	63	0.56 (0.49-0.63)	0.65 (0.54-0.78)	0.61 (0.53-0.68)	0.54 (0.49-0.55)	0.53 (0.33-0.66)	0.53 (0.43-0.6)
FCRL6	ITIH3	101	63	0.59 (0.51-0.67)	0.63 (0.52-0.73)	0.61 (0.55-0.67)	0.54 (0.43-0.58)	0.53 (0.42-0.62)	0.53 (0.46-0.59)
IL10_PEA_IR	CLU	101	63	0.56 (0.48-0.64)	0.57 (0.41-0.72)	0.56 (0.49-0.65)	0.5 (0.45-0.55)	0.57 (0.48-0.59)	0.53 (0.48-0.56)

IL17F	APOA1	102	63	0.61 (0.52-0.69)	0.56 (0.43-0.7)	0.59 (0.5-0.66)	0.53 (0.39-0.61)	0.52 (0.51-0.56)	0.53 (0.45-0.58)
CCL4	CXCL9	102	63	0.67 (0.58-0.76)	0.57 (0.46-0.71)	0.62 (0.55-0.7)	0.53 (0.33-0.67)	0.54 (0.5-0.58)	0.53 (0.43-0.61)
IL7	C8B	102	63	0.61 (0.51-0.71)	0.6 (0.51-0.71)	0.6 (0.53-0.68)	0.57 (0.38-0.62)	0.53 (0.43-0.57)	0.53 (0.45-0.59)
CLEC4C	SERPINA4	101	63	0.61 (0.52-0.68)	0.61 (0.5-0.74)	0.61 (0.53-0.69)	0.55 (0.41-0.61)	0.51 (0.46-0.62)	0.53 (0.45-0.59)
PLXNA4	C8A	101	63	0.59 (0.51-0.67)	0.64 (0.53-0.76)	0.62 (0.55-0.68)	0.52 (0.44-0.58)	0.54 (0.39-0.64)	0.53 (0.45-0.6)
LAMP3	IL17C	101	63	0.61 (0.5-0.68)	0.62 (0.5-0.73)	0.61 (0.54-0.68)	0.54 (0.4-0.6)	0.55 (0.39-0.61)	0.53 (0.44-0.59)
IL17C	SERPIND1	102	63	0.59 (0.5-0.67)	0.64 (0.52-0.74)	0.62 (0.53-0.68)	0.52 (0.42-0.58)	0.55 (0.37-0.61)	0.53 (0.44-0.59)
CDSN	IL10_PEA_IR	102	63	0.57 (0.49-0.65)	0.6 (0.45-0.73)	0.58 (0.5-0.66)	0.5 (0.45-0.55)	0.57 (0.46-0.59)	0.53 (0.47-0.57)
C8B	MBL2	102	67	0.62 (0.52-0.71)	0.62 (0.52-0.74)	0.62 (0.55-0.69)	0.52 (0.4-0.63)	0.54 (0.43-0.59)	0.53 (0.45-0.59)
IL6_PEA_IR	C8A	101	63	0.62 (0.51-0.7)	0.58 (0.48-0.69)	0.6 (0.53-0.67)	0.55 (0.38-0.62)	0.53 (0.47-0.54)	0.53 (0.44-0.58)
CLEC4C	FCRL6	102	63	0.56 (0.49-0.63)	0.65 (0.52-0.77)	0.6 (0.54-0.67)	0.52 (0.48-0.54)	0.54 (0.35-0.65)	0.53 (0.44-0.59)
IL6_PEA_IR	IL10_PEA_IR	102	63	0.6 (0.53-0.7)	0.57 (0.42-0.74)	0.59 (0.5-0.68)	0.5 (0.39-0.61)	0.56 (0.49-0.59)	0.53 (0.47-0.59)
SAA1	SERPINA3	102	67	0.57 (0.46-0.69)	0.58 (0.46-0.72)	0.57 (0.5-0.67)	0.52 (0.42-0.59)	0.5 (0.48-0.6)	0.53 (0.46-0.59)
C2	SERPIND1	102	67	0.56 (0.49-0.64)	0.65 (0.52-0.75)	0.6 (0.53-0.67)	0.52 (0.48-0.54)	0.54 (0.37-0.63)	0.53 (0.44-0.58)
IL10_PEA_IR	SERPINA4	101	63	0.61 (0.52-0.69)	0.58 (0.42-0.72)	0.59 (0.51-0.68)	0.53 (0.4-0.6)	0.53 (0.51-0.57)	0.53 (0.46-0.58)
HSD11B1	CCL4	101	63	0.58 (0.47-0.67)	0.59 (0.49-0.71)	0.58 (0.51-0.65)	0.52 (0.42-0.58)	0.55 (0.43-0.57)	0.53 (0.45-0.57)
HGF	C8A	102	63	0.6 (0.5-0.67)	0.58 (0.49-0.68)	0.59 (0.52-0.66)	0.54 (0.41-0.59)	0.53 (0.48-0.55)	0.53 (0.45-0.57)
CP	SERPING1	102	67	0.56 (0.46-0.65)	0.63 (0.5-0.76)	0.59 (0.51-0.68)	0.55 (0.47-0.56)	0.52 (0.35-0.65)	0.53 (0.45-0.6)
ITGA11	IL17F	101	63	0.64 (0.48-0.72)	0.56 (0.43-0.71)	0.6 (0.5-0.68)	0.56 (0.37-0.63)	0.51 (0.47-0.55)	0.53 (0.42-0.58)
KLRD1	CP	101	63	0.6 (0.51-0.68)	0.66 (0.54-0.78)	0.63 (0.56-0.7)	0.56 (0.43-0.59)	0.52 (0.33-0.68)	0.53 (0.44-0.62)
IL17F	CXCL9	102	63	0.67 (0.58-0.75)	0.55 (0.4-0.7)	0.61 (0.53-0.7)	0.52 (0.34-0.66)	0.55 (0.53-0.56)	0.53 (0.43-0.61)
PLXNA4	CCL13	101	63	0.56 (0.49-0.65)	0.63 (0.52-0.76)	0.6 (0.53-0.67)	0.52 (0.49-0.55)	0.54 (0.38-0.62)	0.53 (0.45-0.58)
ITGA11	SH2D1A	102	63	0.62 (0.51-0.7)	0.58 (0.49-0.7)	0.6 (0.52-0.67)	0.53 (0.4-0.61)	0.55 (0.47-0.56)	0.53 (0.46-0.58)
IL15	SERPINA4	102	63	0.59 (0.5-0.68)	0.59 (0.49-0.69)	0.59 (0.52-0.66)	0.53 (0.43-0.61)	0.51 (0.45-0.55)	0.53 (0.46-0.57)
CCL13	SERPING1	102	63	0.56 (0.49-0.66)	0.6 (0.5-0.71)	0.58 (0.51-0.65)	0.53 (0.46-0.54)	0.54 (0.43-0.57)	0.53 (0.47-0.55)
CCL4	SERPIND1	102	63	0.57 (0.45-0.66)	0.64 (0.53-0.75)	0.6 (0.52-0.68)	0.53 (0.43-0.58)	0.55 (0.38-0.63)	0.53 (0.44-0.59)
FC	FCRL6	76	43	0.68 (0.59-0.77)	0.62 (0.49-0.75)	0.65 (0.57-0.73)	0.53 (0.33-0.66)	0.54 (0.48-0.6)	0.53 (0.43-0.61)
TNF	SERPINA4	102	63	0.59 (0.5-0.67)	0.58 (0.5-0.67)	0.58 (0.53-0.65)	0.55 (0.42-0.58)	0.51 (0.5-0.53)	0.53 (0.47-0.55)
LRG1	MBL2	102	67	0.6 (0.51-0.69)	0.63 (0.52-0.74)	0.62 (0.54-0.68)	0.53 (0.44-0.6)	0.54 (0.42-0.61)	0.53 (0.45-0.6)
IL13	IL15	102	63	0.54 (0.44-0.65)	0.57 (0.46-0.67)	0.56 (0.48-0.63)	0.56 (0.52-0.56)	0.5 (0.46-0.56)	0.53 (0.5-0.56)

FGF2	IL17F	101	63	0.56 (0.47-0.65)	0.66 (0.44-0.77)	0.61 (0.5-0.68)	0.51 (0.45-0.55)	0.55 (0.35-0.66)	0.53 (0.42-0.59)
C3	CLU	102	67	0.59 (0.5-0.67)	0.6 (0.5-0.72)	0.59 (0.53-0.68)	0.55 (0.42-0.59)	0.55 (0.44-0.57)	0.53 (0.46-0.57)
FC	FGF2	76	43	0.67 (0.58-0.76)	0.73 (0.6-0.84)	0.7 (0.63-0.78)	0.53 (0.46-0.57)	0.52 (0.41-0.71)	0.53 (0.46-0.63)
IL6_PEA_IR	TNF	101	63	0.59 (0.48-0.68)	0.58 (0.48-0.7)	0.59 (0.51-0.66)	0.54 (0.41-0.59)	0.54 (0.47-0.56)	0.53 (0.46-0.57)
IFNG	CLU	102	63	0.69 (0.6-0.76)	0.58 (0.46-0.71)	0.64 (0.56-0.71)	0.49 (0.32-0.69)	0.57 (0.49-0.62)	0.53 (0.43-0.63)
IL17C	SAA1	102	63	0.6 (0.51-0.69)	0.58 (0.44-0.71)	0.59 (0.51-0.67)	0.53 (0.4-0.6)	0.53 (0.5-0.6)	0.53 (0.45-0.58)
CDSN	TNF	101	63	0.56 (0.49-0.63)	0.59 (0.5-0.72)	0.57 (0.52-0.65)	0.52 (0.47-0.54)	0.54 (0.45-0.57)	0.53 (0.48-0.55)
ITIH1	SERPING1	102	67	0.56 (0.49-0.63)	0.61 (0.5-0.71)	0.58 (0.52-0.65)	0.5 (0.46-0.55)	0.56 (0.41-0.59)	0.53 (0.45-0.56)
ITGA6	IFNG	101	63	0.69 (0.6-0.77)	0.63 (0.49-0.76)	0.66 (0.58-0.73)	0.5 (0.39-0.59)	0.56 (0.47-0.63)	0.53 (0.47-0.6)
ITGA6	FLT3LG	101	63	0.61 (0.53-0.69)	0.65 (0.55-0.75)	0.63 (0.56-0.7)	0.52 (0.45-0.6)	0.54 (0.42-0.63)	0.53 (0.47-0.59)
LRG1	VTN	102	67	0.62 (0.53-0.71)	0.63 (0.53-0.74)	0.63 (0.55-0.69)	0.55 (0.42-0.62)	0.51 (0.41-0.63)	0.53 (0.45-0.61)
MASP1	IL17C	101	63	0.64 (0.52-0.72)	0.59 (0.46-0.73)	0.61 (0.53-0.69)	0.51 (0.36-0.64)	0.56 (0.49-0.58)	0.53 (0.45-0.6)
SERPINA3	C4BPB	102	67	0.59 (0.5-0.68)	0.59 (0.49-0.7)	0.59 (0.52-0.68)	0.55 (0.41-0.59)	0.54 (0.45-0.58)	0.53 (0.45-0.58)
FCRL6	ITIH1	101	63	0.56 (0.49-0.63)	0.66 (0.55-0.77)	0.61 (0.54-0.67)	0.51 (0.5-0.53)	0.55 (0.35-0.66)	0.53 (0.43-0.59)
PLXNA4	TNF	101	63	0.55 (0.49-0.62)	0.62 (0.51-0.75)	0.59 (0.53-0.65)	0.51 (0.48-0.53)	0.55 (0.39-0.61)	0.53 (0.45-0.56)
CLEC4C	IL17F	101	63	0.56 (0.49-0.64)	0.6 (0.44-0.75)	0.58 (0.5-0.67)	0.51 (0.45-0.55)	0.55 (0.39-0.63)	0.53 (0.44-0.58)
C9	C4B	102	67	0.61 (0.52-0.71)	0.69 (0.56-0.81)	0.65 (0.57-0.73)	0.53 (0.41-0.59)	0.54 (0.34-0.68)	0.53 (0.41-0.62)
CLEC4C	CP	101	63	0.56 (0.48-0.64)	0.67 (0.55-0.78)	0.62 (0.54-0.69)	0.54 (0.49-0.55)	0.52 (0.33-0.67)	0.53 (0.43-0.61)
IL6_PEA_IR	CCL13	101	63	0.59 (0.48-0.69)	0.59 (0.49-0.72)	0.59 (0.51-0.67)	0.56 (0.42-0.59)	0.52 (0.44-0.57)	0.53 (0.45-0.57)
IL6_PEA_IR	SERPINA3	101	63	0.6 (0.49-0.7)	0.59 (0.47-0.72)	0.6 (0.52-0.68)	0.55 (0.4-0.61)	0.54 (0.45-0.57)	0.53 (0.45-0.58)
IL10_PEA_IR	ITIH2	101	63	0.57 (0.49-0.66)	0.59 (0.45-0.73)	0.58 (0.5-0.66)	0.48 (0.45-0.55)	0.58 (0.44-0.61)	0.53 (0.46-0.57)
CDSN	CP	101	63	0.55 (0.47-0.62)	0.66 (0.53-0.79)	0.6 (0.53-0.68)	0.51 (0.49-0.55)	0.54 (0.34-0.66)	0.53 (0.43-0.6)
IL10_PEA_IR	IL17F	101	63	0.56 (0.47-0.64)	0.56 (0.4-0.74)	0.56 (0.46-0.66)	0.48 (0.44-0.55)	0.58 (0.5-0.59)	0.53 (0.49-0.57)
ITGA6	C5	101	63	0.62 (0.53-0.71)	0.7 (0.58-0.8)	0.66 (0.59-0.73)	0.54 (0.49-0.58)	0.52 (0.41-0.68)	0.53 (0.47-0.61)
KLRD1	SH2D1A	102	63	0.6 (0.51-0.68)	0.58 (0.49-0.69)	0.59 (0.53-0.66)	0.52 (0.41-0.6)	0.55 (0.47-0.56)	0.53 (0.46-0.57)
ITGA6	C4B	101	63	0.59 (0.51-0.68)	0.73 (0.62-0.84)	0.66 (0.59-0.73)	0.53 (0.47-0.57)	0.53 (0.29-0.73)	0.53 (0.41-0.63)
C3	ITIH2	102	67	0.58 (0.5-0.66)	0.6 (0.51-0.72)	0.59 (0.53-0.67)	0.55 (0.43-0.58)	0.53 (0.45-0.57)	0.53 (0.47-0.57)
CLEC4C	VTN	101	63	0.56 (0.5-0.64)	0.64 (0.53-0.75)	0.6 (0.54-0.67)	0.51 (0.49-0.54)	0.55 (0.37-0.63)	0.53 (0.44-0.58)
PLXNA4	IL10_PEA_IR	102	63	0.57 (0.49-0.65)	0.62 (0.46-0.76)	0.59 (0.5-0.68)	0.49 (0.46-0.54)	0.58 (0.41-0.6)	0.53 (0.45-0.56)
CP	C4BPB	102	67	0.59 (0.49-0.68)	0.63 (0.52-0.76)	0.61 (0.54-0.69)	0.56 (0.43-0.6)	0.49 (0.37-0.63)	0.53 (0.45-0.61)

HGF	SERPINA4	102	63	0.6 (0.52-0.68)	0.57 (0.48-0.7)	0.59 (0.52-0.66)	0.54 (0.41-0.59)	0.51 (0.5-0.54)	0.53 (0.46-0.55)
LRG1	CP	102	67	0.62 (0.52-0.71)	0.63 (0.51-0.75)	0.62 (0.55-0.7)	0.55 (0.4-0.61)	0.49 (0.4-0.64)	0.53 (0.44-0.61)
IL6_PEA_IR	SERPINA4	101	63	0.62 (0.53-0.7)	0.58 (0.49-0.69)	0.6 (0.53-0.67)	0.55 (0.36-0.64)	0.52 (0.49-0.53)	0.53 (0.44-0.58)
CLEC4C	ITIH2	101	63	0.56 (0.5-0.64)	0.62 (0.51-0.75)	0.59 (0.53-0.66)	0.51 (0.48-0.54)	0.54 (0.38-0.63)	0.53 (0.44-0.58)
IL6_PEA_IR	SERPIND1	101	63	0.58 (0.48-0.67)	0.65 (0.53-0.78)	0.61 (0.54-0.7)	0.53 (0.44-0.59)	0.55 (0.38-0.63)	0.53 (0.42-0.6)
DCTN1	CXCL9	101	63	0.66 (0.58-0.74)	0.7 (0.56-0.82)	0.68 (0.6-0.75)	0.51 (0.42-0.63)	0.55 (0.39-0.66)	0.53 (0.44-0.62)
SAA1	CLU	102	67	0.58 (0.48-0.66)	0.59 (0.49-0.73)	0.59 (0.51-0.66)	0.55 (0.44-0.58)	0.5 (0.45-0.61)	0.53 (0.47-0.59)
DCTN1	CFB	101	63	0.57 (0.49-0.65)	0.72 (0.6-0.83)	0.65 (0.57-0.72)	0.53 (0.51-0.56)	0.52 (0.29-0.71)	0.53 (0.41-0.63)
SERPINA3	ITIH1	102	67	0.58 (0.49-0.67)	0.61 (0.5-0.74)	0.59 (0.53-0.67)	0.54 (0.44-0.57)	0.53 (0.41-0.61)	0.53 (0.46-0.58)
IL6_PEA_cytokine	CCL13	102	63	0.57 (0.46-0.67)	0.59 (0.46-0.72)	0.58 (0.5-0.66)	0.54 (0.43-0.6)	0.54 (0.44-0.57)	0.53 (0.46-0.57)
KLRD1	VTN	101	63	0.59 (0.51-0.68)	0.63 (0.53-0.74)	0.61 (0.55-0.67)	0.53 (0.44-0.59)	0.52 (0.39-0.62)	0.53 (0.45-0.6)
C3	SERPIND1	102	67	0.57 (0.48-0.65)	0.64 (0.54-0.76)	0.61 (0.54-0.68)	0.53 (0.48-0.56)	0.52 (0.38-0.63)	0.53 (0.45-0.59)
hsCRP	ITGA6	98	63	0.64 (0.52-0.73)	0.67 (0.56-0.78)	0.66 (0.58-0.72)	0.54 (0.46-0.6)	0.52 (0.37-0.68)	0.53 (0.45-0.62)
IL6_PEA_IR	CDSN	102	63	0.57 (0.49-0.67)	0.59 (0.47-0.71)	0.58 (0.5-0.66)	0.53 (0.42-0.58)	0.54 (0.44-0.58)	0.53 (0.46-0.57)
NCR1	IL7	101	63	0.58 (0.49-0.66)	0.63 (0.51-0.74)	0.61 (0.53-0.67)	0.54 (0.46-0.58)	0.51 (0.43-0.6)	0.53 (0.47-0.59)
IL7	F9	102	63	0.59 (0.51-0.68)	0.64 (0.53-0.76)	0.61 (0.55-0.69)	0.53 (0.46-0.59)	0.52 (0.4-0.62)	0.53 (0.46-0.6)
FGF2	IL17C	101	63	0.59 (0.5-0.67)	0.67 (0.42-0.79)	0.62 (0.5-0.71)	0.5 (0.41-0.57)	0.55 (0.34-0.66)	0.53 (0.42-0.59)
SAA1	SERPING1	102	67	0.57 (0.46-0.67)	0.6 (0.46-0.73)	0.58 (0.5-0.67)	0.56 (0.42-0.58)	0.5 (0.47-0.59)	0.53 (0.45-0.58)
DCTN1	C3	101	63	0.58 (0.5-0.65)	0.71 (0.57-0.81)	0.64 (0.57-0.71)	0.54 (0.49-0.56)	0.53 (0.32-0.68)	0.53 (0.42-0.61)
ITGA11	SERPING1	101	63	0.64 (0.51-0.71)	0.58 (0.49-0.7)	0.61 (0.54-0.68)	0.53 (0.38-0.63)	0.53 (0.47-0.55)	0.53 (0.45-0.58)
IL13	ITIH1	102	63	0.55 (0.46-0.63)	0.61 (0.48-0.72)	0.58 (0.49-0.65)	0.51 (0.47-0.53)	0.54 (0.41-0.61)	0.53 (0.46-0.57)
CXCL9	MBL2	102	63	0.65 (0.58-0.74)	0.63 (0.53-0.76)	0.65 (0.58-0.72)	0.49 (0.38-0.65)	0.55 (0.44-0.62)	0.53 (0.44-0.63)
ITIH3	CP	102	67	0.59 (0.51-0.67)	0.64 (0.52-0.77)	0.61 (0.54-0.68)	0.54 (0.43-0.58)	0.52 (0.37-0.62)	0.53 (0.44-0.59)
LAMP3	PZP	100	63	0.58 (0.47-0.67)	0.63 (0.52-0.74)	0.6 (0.52-0.68)	0.56 (0.44-0.58)	0.5 (0.35-0.63)	0.53 (0.44-0.6)
MASP1	VTN	101	63	0.6 (0.51-0.71)	0.63 (0.5-0.74)	0.61 (0.54-0.68)	0.51 (0.42-0.61)	0.56 (0.4-0.61)	0.53 (0.44-0.6)
HSD11B1	VEGFA	101	63	0.57 (0.48-0.65)	0.58 (0.5-0.7)	0.58 (0.52-0.65)	0.53 (0.44-0.56)	0.54 (0.45-0.56)	0.53 (0.47-0.56)
HSD11B1	ITIH2	101	63	0.56 (0.5-0.65)	0.6 (0.52-0.72)	0.59 (0.53-0.66)	0.52 (0.47-0.54)	0.54 (0.42-0.59)	0.53 (0.46-0.56)
CDSN	CLU	101	63	0.55 (0.47-0.63)	0.6 (0.51-0.72)	0.57 (0.51-0.65)	0.52 (0.47-0.53)	0.55 (0.41-0.6)	0.53 (0.46-0.56)
FCRL6	PLXNA4	102	63	0.55 (0.49-0.62)	0.64 (0.53-0.76)	0.6 (0.53-0.66)	0.51 (0.5-0.52)	0.54 (0.38-0.62)	0.53 (0.44-0.57)
SH2D1A	IL15	101	63	0.55 (0.46-0.64)	0.59 (0.51-0.71)	0.57 (0.51-0.64)	0.53 (0.48-0.57)	0.54 (0.43-0.57)	0.53 (0.48-0.56)

DCTN1	ITIH3	101	63	0.59 (0.51-0.67)	0.7 (0.56-0.82)	0.64 (0.57-0.71)	0.53 (0.5-0.57)	0.53 (0.31-0.68)	0.53 (0.42-0.6)
KLRD1	ITIH2	101	63	0.6 (0.52-0.68)	0.61 (0.51-0.7)	0.6 (0.54-0.66)	0.53 (0.42-0.59)	0.53 (0.44-0.59)	0.53 (0.45-0.58)
CXCL9	VTN	102	63	0.66 (0.58-0.75)	0.63 (0.5-0.75)	0.65 (0.57-0.72)	0.51 (0.37-0.66)	0.52 (0.47-0.64)	0.53 (0.44-0.63)
C9	APCS	102	67	0.61 (0.51-0.71)	0.63 (0.53-0.73)	0.62 (0.55-0.69)	0.55 (0.4-0.61)	0.53 (0.39-0.6)	0.53 (0.43-0.59)
IL10_PEA_IR	TNF	101	63	0.56 (0.48-0.63)	0.58 (0.42-0.73)	0.57 (0.48-0.65)	0.49 (0.45-0.55)	0.55 (0.52-0.59)	0.53 (0.49-0.56)
DCTN1	NCR1	102	63	0.59 (0.51-0.67)	0.72 (0.58-0.84)	0.65 (0.58-0.73)	0.53 (0.51-0.56)	0.52 (0.33-0.7)	0.53 (0.43-0.62)
IL6_PEA_IR	SERPING1	101	63	0.6 (0.47-0.7)	0.59 (0.47-0.73)	0.59 (0.51-0.68)	0.53 (0.39-0.61)	0.53 (0.44-0.6)	0.53 (0.44-0.6)
TNF	SERPING1	102	63	0.56 (0.49-0.63)	0.59 (0.49-0.71)	0.58 (0.52-0.64)	0.53 (0.46-0.54)	0.53 (0.44-0.58)	0.53 (0.47-0.56)
FGF2	SERPINA4	101	63	0.59 (0.51-0.67)	0.66 (0.45-0.77)	0.62 (0.52-0.7)	0.54 (0.42-0.58)	0.51 (0.43-0.63)	0.53 (0.47-0.59)
IFNG	ITIH2	102	63	0.68 (0.6-0.76)	0.59 (0.47-0.71)	0.64 (0.56-0.71)	0.47 (0.35-0.67)	0.6 (0.47-0.62)	0.53 (0.45-0.64)
CDSN	HGF	101	63	0.56 (0.48-0.63)	0.58 (0.47-0.7)	0.57 (0.5-0.64)	0.52 (0.47-0.53)	0.55 (0.43-0.57)	0.53 (0.47-0.55)
F9	MBL2	102	67	0.59 (0.51-0.67)	0.69 (0.57-0.8)	0.64 (0.56-0.71)	0.51 (0.46-0.57)	0.53 (0.36-0.67)	0.53 (0.43-0.6)
CDSN	PLXNA4	102	63	0.55 (0.47-0.62)	0.63 (0.53-0.75)	0.59 (0.53-0.66)	0.5 (0.49-0.51)	0.55 (0.39-0.61)	0.53 (0.44-0.56)
CLEC4C	CLU	101	63	0.56 (0.49-0.64)	0.61 (0.51-0.74)	0.59 (0.52-0.66)	0.52 (0.47-0.55)	0.53 (0.38-0.63)	0.53 (0.45-0.58)
FCRL6	C8A	101	63	0.59 (0.51-0.67)	0.62 (0.52-0.73)	0.61 (0.54-0.68)	0.53 (0.43-0.58)	0.53 (0.42-0.62)	0.53 (0.46-0.59)
HGF	CCL13	102	63	0.57 (0.47-0.66)	0.59 (0.48-0.71)	0.58 (0.5-0.66)	0.54 (0.44-0.57)	0.54 (0.44-0.57)	0.53 (0.46-0.56)
FC	VEGFA	77	43	0.7 (0.6-0.78)	0.59 (0.48-0.73)	0.65 (0.57-0.72)	0.51 (0.32-0.68)	0.54 (0.52-0.57)	0.53 (0.43-0.61)
HSD11B1	CLU	101	63	0.56 (0.49-0.65)	0.59 (0.51-0.7)	0.58 (0.52-0.65)	0.54 (0.46-0.54)	0.53 (0.44-0.57)	0.53 (0.47-0.55)
C3	ITIH1	102	67	0.58 (0.5-0.65)	0.62 (0.52-0.73)	0.6 (0.53-0.66)	0.53 (0.44-0.57)	0.52 (0.43-0.6)	0.53 (0.46-0.57)
IL6_PEA_IR	IL6_PEA_cytokine	101	63	0.59 (0.42-0.7)	0.57 (0.45-0.72)	0.57 (0.47-0.66)	0.56 (0.41-0.6)	0.5 (0.4-0.6)	0.53 (0.42-0.58)
SH2D1A	ITIH1	101	63	0.55 (0.49-0.63)	0.62 (0.51-0.73)	0.59 (0.53-0.65)	0.51 (0.48-0.53)	0.55 (0.39-0.62)	0.53 (0.45-0.56)
CCL4	SAA1	102	63	0.58 (0.46-0.7)	0.58 (0.47-0.71)	0.58 (0.5-0.66)	0.52 (0.38-0.62)	0.52 (0.48-0.6)	0.53 (0.45-0.6)
IL15	VTN	102	63	0.56 (0.48-0.65)	0.65 (0.52-0.76)	0.6 (0.54-0.67)	0.53 (0.51-0.56)	0.53 (0.36-0.64)	0.53 (0.44-0.58)
ITGA11	FGF2	102	63	0.61 (0.5-0.69)	0.65 (0.43-0.77)	0.63 (0.51-0.71)	0.52 (0.4-0.61)	0.53 (0.37-0.65)	0.53 (0.42-0.6)
SERPINA3	ITIH2	102	67	0.58 (0.5-0.67)	0.59 (0.49-0.7)	0.59 (0.52-0.66)	0.53 (0.44-0.57)	0.54 (0.43-0.58)	0.53 (0.46-0.57)
ITGA11	CDSN	102	63	0.61 (0.5-0.71)	0.6 (0.48-0.71)	0.61 (0.52-0.68)	0.52 (0.38-0.62)	0.56 (0.42-0.58)	0.53 (0.43-0.59)
ITGA11	ITIH1	101	63	0.62 (0.51-0.7)	0.62 (0.51-0.73)	0.62 (0.54-0.68)	0.5 (0.39-0.61)	0.57 (0.41-0.6)	0.53 (0.44-0.59)
IL6_PEA_cytokine	SERPING1	102	63	0.58 (0.44-0.67)	0.58 (0.44-0.73)	0.58 (0.48-0.67)	0.54 (0.4-0.61)	0.56 (0.42-0.61)	0.53 (0.43-0.6)
CP	C8A	102	67	0.58 (0.5-0.66)	0.64 (0.52-0.76)	0.61 (0.53-0.68)	0.55 (0.43-0.58)	0.49 (0.37-0.63)	0.53 (0.46-0.59)
HSD11B1	PZP	100	63	0.57 (0.49-0.65)	0.61 (0.47-0.74)	0.59 (0.52-0.67)	0.54 (0.45-0.55)	0.53 (0.37-0.6)	0.53 (0.44-0.57)

C2	C8A	102	67	0.58 (0.5-0.67)	0.59 (0.47-0.71)	0.58 (0.51-0.66)	0.53 (0.42-0.58)	0.52 (0.47-0.57)	0.53 (0.47-0.57)
ITGA6	F9	101	63	0.59 (0.5-0.68)	0.69 (0.57-0.8)	0.64 (0.56-0.71)	0.53 (0.48-0.55)	0.53 (0.34-0.67)	0.53 (0.43-0.6)
IL17F	IFNG	102	63	0.69 (0.61-0.77)	0.56 (0.4-0.73)	0.62 (0.53-0.71)	0.49 (0.31-0.68)	0.55 (0.52-0.62)	0.53 (0.42-0.63)
CPN2	SERPIND1	102	67	0.58 (0.49-0.67)	0.64 (0.54-0.74)	0.61 (0.55-0.68)	0.53 (0.48-0.57)	0.52 (0.39-0.62)	0.53 (0.46-0.58)
IL6_PEA_IR	ITIH1	101	63	0.57 (0.48-0.67)	0.63 (0.52-0.75)	0.6 (0.53-0.67)	0.51 (0.42-0.58)	0.56 (0.4-0.63)	0.53 (0.44-0.59)
ITGA11	SERPIND1	101	63	0.62 (0.51-0.7)	0.64 (0.53-0.76)	0.63 (0.55-0.7)	0.53 (0.42-0.61)	0.55 (0.36-0.63)	0.53 (0.41-0.6)
IL13	SERPINA4	102	63	0.59 (0.5-0.67)	0.58 (0.46-0.69)	0.59 (0.52-0.66)	0.55 (0.43-0.59)	0.54 (0.47-0.54)	0.53 (0.45-0.56)
hsCRP	DCTN1	98	63	0.62 (0.51-0.72)	0.73 (0.59-0.83)	0.67 (0.6-0.75)	0.53 (0.5-0.58)	0.52 (0.3-0.73)	0.53 (0.41-0.64)
IL15	C9	102	63	0.61 (0.49-0.72)	0.59 (0.5-0.69)	0.6 (0.52-0.68)	0.54 (0.4-0.63)	0.5 (0.45-0.57)	0.53 (0.44-0.59)
IL17C	C4BPB	102	63	0.62 (0.52-0.69)	0.57 (0.47-0.7)	0.59 (0.53-0.67)	0.51 (0.39-0.61)	0.53 (0.48-0.56)	0.53 (0.45-0.58)
DCTN1	SERPINA4	101	63	0.6 (0.51-0.68)	0.69 (0.55-0.81)	0.64 (0.56-0.72)	0.53 (0.47-0.59)	0.52 (0.35-0.63)	0.52 (0.43-0.58)
MILR1	C9	101	63	0.68 (0.59-0.75)	0.58 (0.49-0.69)	0.63 (0.57-0.69)	0.53 (0.33-0.67)	0.52 (0.51-0.54)	0.52 (0.43-0.6)
FCRL6	C4BPB	101	63	0.59 (0.5-0.68)	0.63 (0.53-0.73)	0.61 (0.54-0.68)	0.52 (0.42-0.58)	0.52 (0.39-0.62)	0.52 (0.45-0.58)
HGF	TNF	102	63	0.56 (0.49-0.65)	0.58 (0.48-0.7)	0.57 (0.51-0.64)	0.51 (0.45-0.56)	0.53 (0.45-0.58)	0.52 (0.47-0.56)
DCTN1	HSD11B1	102	63	0.56 (0.49-0.66)	0.7 (0.57-0.8)	0.63 (0.56-0.7)	0.53 (0.5-0.55)	0.53 (0.32-0.68)	0.52 (0.41-0.61)
SIT1	CPN2	101	63	0.58 (0.51-0.66)	0.66 (0.55-0.76)	0.62 (0.55-0.69)	0.53 (0.47-0.58)	0.52 (0.44-0.63)	0.52 (0.47-0.58)
FCRL6	IL15	101	63	0.56 (0.47-0.65)	0.61 (0.5-0.72)	0.59 (0.51-0.66)	0.53 (0.51-0.57)	0.53 (0.38-0.61)	0.52 (0.45-0.58)
IL6_PEA_cytokine	TNF	102	63	0.57 (0.46-0.64)	0.57 (0.46-0.7)	0.57 (0.5-0.64)	0.51 (0.42-0.61)	0.54 (0.47-0.57)	0.52 (0.47-0.58)
C3	PZP	101	67	0.57 (0.49-0.66)	0.61 (0.48-0.73)	0.59 (0.52-0.67)	0.54 (0.45-0.57)	0.52 (0.37-0.62)	0.52 (0.43-0.58)
DCTN1	APCS	101	63	0.6 (0.5-0.69)	0.7 (0.57-0.81)	0.65 (0.57-0.72)	0.53 (0.48-0.59)	0.52 (0.31-0.69)	0.52 (0.42-0.62)
ITGA11	CLU	101	63	0.62 (0.49-0.7)	0.57 (0.49-0.67)	0.6 (0.52-0.66)	0.53 (0.39-0.61)	0.52 (0.46-0.54)	0.52 (0.44-0.57)
HSD11B1	IL17C	101	63	0.59 (0.51-0.68)	0.59 (0.47-0.71)	0.59 (0.52-0.66)	0.51 (0.4-0.6)	0.55 (0.44-0.56)	0.52 (0.45-0.57)
SAA1	ORM1	102	67	0.57 (0.45-0.69)	0.64 (0.48-0.76)	0.6 (0.51-0.69)	0.59 (0.48-0.6)	0.48 (0.42-0.64)	0.52 (0.46-0.62)
SERPINA3	SERPING1	102	67	0.58 (0.49-0.67)	0.59 (0.48-0.71)	0.58 (0.51-0.66)	0.54 (0.43-0.57)	0.51 (0.44-0.57)	0.52 (0.46-0.57)
ITIH3	PZP	101	67	0.59 (0.5-0.68)	0.6 (0.48-0.72)	0.59 (0.53-0.67)	0.55 (0.42-0.58)	0.52 (0.39-0.58)	0.52 (0.42-0.58)
CDSN	SERPINA4	101	63	0.59 (0.51-0.67)	0.6 (0.51-0.71)	0.59 (0.54-0.66)	0.53 (0.42-0.58)	0.53 (0.48-0.57)	0.52 (0.47-0.56)
MILR1	ITGA6	102	63	0.63 (0.53-0.72)	0.64 (0.53-0.74)	0.63 (0.56-0.71)	0.51 (0.41-0.61)	0.53 (0.41-0.59)	0.52 (0.44-0.59)
C9	F9	102	67	0.6 (0.52-0.71)	0.67 (0.55-0.79)	0.64 (0.56-0.71)	0.51 (0.42-0.59)	0.54 (0.35-0.64)	0.52 (0.41-0.6)
SH2D1A	CCL13	101	63	0.56 (0.47-0.66)	0.59 (0.48-0.71)	0.58 (0.51-0.65)	0.54 (0.45-0.55)	0.53 (0.43-0.57)	0.52 (0.47-0.55)
CPN2	SERPINA4	102	67	0.6 (0.52-0.68)	0.62 (0.52-0.72)	0.61 (0.54-0.68)	0.52 (0.43-0.6)	0.52 (0.4-0.58)	0.52 (0.45-0.58)

IL7	APCS	102	63	0.6 (0.5-0.69)	0.61 (0.51-0.73)	0.6 (0.54-0.69)	0.55 (0.43-0.61)	0.52 (0.43-0.59)	0.52 (0.46-0.58)
FCRL6	IL6_PEA_cytokine	101	63	0.56 (0.47-0.63)	0.61 (0.46-0.73)	0.59 (0.5-0.65)	0.5 (0.46-0.57)	0.53 (0.38-0.63)	0.52 (0.44-0.58)
CLEC4C	SH2D1A	102	63	0.56 (0.48-0.64)	0.6 (0.49-0.75)	0.58 (0.51-0.66)	0.51 (0.46-0.54)	0.53 (0.37-0.63)	0.52 (0.44-0.58)
CPN2	ORM1	102	67	0.59 (0.5-0.69)	0.64 (0.53-0.74)	0.62 (0.55-0.69)	0.54 (0.44-0.6)	0.51 (0.38-0.61)	0.52 (0.44-0.6)
ITIH3	VTN	102	67	0.58 (0.51-0.67)	0.64 (0.53-0.75)	0.61 (0.54-0.68)	0.53 (0.44-0.58)	0.52 (0.39-0.63)	0.52 (0.45-0.6)
IL6_PEA_cytokine	C2	102	63	0.58 (0.47-0.66)	0.56 (0.42-0.73)	0.57 (0.48-0.66)	0.52 (0.43-0.58)	0.57 (0.44-0.59)	0.52 (0.45-0.58)
SERPIND1	C4BPB	102	67	0.59 (0.48-0.67)	0.63 (0.53-0.75)	0.61 (0.54-0.69)	0.54 (0.44-0.58)	0.5 (0.38-0.63)	0.52 (0.45-0.59)
PLXNA4	CP	101	63	0.55 (0.48-0.63)	0.65 (0.53-0.79)	0.6 (0.53-0.67)	0.53 (0.5-0.55)	0.52 (0.33-0.67)	0.52 (0.43-0.6)
CXCL9	C9	102	63	0.66 (0.57-0.75)	0.57 (0.47-0.7)	0.62 (0.54-0.69)	0.51 (0.35-0.66)	0.53 (0.51-0.56)	0.52 (0.44-0.61)
CCL4	IFNG	102	63	0.68 (0.6-0.77)	0.58 (0.45-0.71)	0.63 (0.55-0.71)	0.46 (0.31-0.7)	0.6 (0.52-0.62)	0.52 (0.43-0.65)
SAA1	PZP	101	67	0.58 (0.49-0.67)	0.61 (0.44-0.75)	0.59 (0.5-0.68)	0.54 (0.43-0.58)	0.5 (0.39-0.64)	0.52 (0.45-0.6)
hsCRP	MBL2	98	67	0.62 (0.52-0.71)	0.66 (0.53-0.78)	0.64 (0.57-0.72)	0.53 (0.42-0.63)	0.51 (0.43-0.66)	0.52 (0.45-0.61)
IL17C	ITIH1	102	63	0.59 (0.5-0.67)	0.62 (0.5-0.73)	0.6 (0.53-0.67)	0.5 (0.41-0.57)	0.56 (0.39-0.6)	0.52 (0.44-0.57)
FCRL6	TNF	101	63	0.56 (0.49-0.63)	0.61 (0.51-0.72)	0.59 (0.53-0.65)	0.52 (0.48-0.54)	0.53 (0.4-0.6)	0.52 (0.46-0.57)
FC	IL6_PEA_IR	76	43	0.69 (0.59-0.78)	0.6 (0.46-0.74)	0.64 (0.56-0.73)	0.49 (0.34-0.68)	0.55 (0.52-0.56)	0.52 (0.44-0.61)
FCRL6	SERPING1	101	63	0.56 (0.49-0.63)	0.64 (0.51-0.74)	0.6 (0.53-0.67)	0.51 (0.47-0.55)	0.53 (0.38-0.62)	0.52 (0.44-0.58)
ITIH1	CLU	102	67	0.56 (0.48-0.65)	0.61 (0.51-0.71)	0.58 (0.53-0.65)	0.52 (0.47-0.54)	0.53 (0.41-0.59)	0.52 (0.46-0.56)
SH2D1A	SERPINA3	101	63	0.58 (0.49-0.67)	0.59 (0.48-0.7)	0.58 (0.51-0.66)	0.52 (0.43-0.57)	0.54 (0.44-0.57)	0.52 (0.47-0.57)
VEGFA	C8A	102	63	0.59 (0.5-0.67)	0.57 (0.49-0.67)	0.59 (0.52-0.65)	0.53 (0.41-0.59)	0.53 (0.47-0.54)	0.52 (0.46-0.56)
IL10_PEA_IR	VEGFA	101	63	0.57 (0.48-0.65)	0.56 (0.42-0.73)	0.56 (0.48-0.66)	0.49 (0.44-0.56)	0.56 (0.5-0.59)	0.52 (0.49-0.57)
IL15	ITIH2	102	63	0.56 (0.47-0.65)	0.6 (0.5-0.72)	0.58 (0.51-0.66)	0.52 (0.5-0.57)	0.52 (0.41-0.59)	0.52 (0.46-0.57)
IFNG	PZP	101	63	0.69 (0.59-0.77)	0.61 (0.4-0.73)	0.64 (0.53-0.73)	0.49 (0.32-0.69)	0.56 (0.49-0.62)	0.52 (0.43-0.63)
C2	C4BPB	102	67	0.59 (0.49-0.67)	0.58 (0.47-0.7)	0.58 (0.51-0.67)	0.54 (0.41-0.59)	0.51 (0.47-0.58)	0.52 (0.46-0.57)
C8A	CFB	102	67	0.58 (0.5-0.66)	0.62 (0.52-0.74)	0.6 (0.54-0.67)	0.56 (0.42-0.58)	0.5 (0.45-0.62)	0.52 (0.45-0.59)
PLXNA4	VTN	101	63	0.55 (0.49-0.63)	0.63 (0.53-0.76)	0.6 (0.53-0.66)	0.52 (0.49-0.53)	0.52 (0.38-0.62)	0.52 (0.44-0.57)
FGF2	PLXNA4	102	63	0.56 (0.48-0.64)	0.67 (0.49-0.79)	0.62 (0.52-0.69)	0.52 (0.46-0.54)	0.54 (0.34-0.66)	0.52 (0.42-0.59)
FC	IL17C	77	43	0.68 (0.58-0.77)	0.57 (0.41-0.72)	0.62 (0.53-0.71)	0.51 (0.33-0.68)	0.54 (0.53-0.56)	0.52 (0.43-0.61)
KLRD1	IL17C	101	63	0.62 (0.53-0.7)	0.58 (0.47-0.68)	0.6 (0.53-0.66)	0.52 (0.39-0.61)	0.52 (0.49-0.56)	0.52 (0.45-0.57)
HSD11B1	IL17F	101	63	0.56 (0.49-0.64)	0.59 (0.45-0.72)	0.58 (0.49-0.65)	0.51 (0.45-0.55)	0.54 (0.44-0.57)	0.52 (0.47-0.55)
hsCRP	C9	98	67	0.63 (0.52-0.74)	0.63 (0.51-0.74)	0.63 (0.54-0.71)	0.46 (0.41-0.64)	0.58 (0.4-0.61)	0.52 (0.42-0.62)

PLXNA4	SERPINA4	101	63	0.59 (0.5-0.67)	0.62 (0.52-0.76)	0.61 (0.53-0.68)	0.52 (0.45-0.59)	0.52 (0.44-0.59)	0.52 (0.46-0.58)
MASP1	CP	101	63	0.59 (0.51-0.69)	0.65 (0.49-0.77)	0.62 (0.53-0.69)	0.53 (0.41-0.61)	0.56 (0.35-0.65)	0.52 (0.42-0.6)
CDSN	SH2D1A	102	63	0.55 (0.47-0.62)	0.59 (0.49-0.7)	0.57 (0.5-0.64)	0.49 (0.48-0.51)	0.55 (0.43-0.58)	0.52 (0.46-0.54)
SH2D1A	CXCL9	101	63	0.67 (0.58-0.75)	0.57 (0.45-0.69)	0.62 (0.55-0.69)	0.49 (0.35-0.67)	0.54 (0.52-0.56)	0.52 (0.45-0.61)
HGF	C2	102	63	0.57 (0.48-0.65)	0.58 (0.45-0.73)	0.57 (0.5-0.66)	0.52 (0.44-0.56)	0.53 (0.42-0.59)	0.52 (0.45-0.57)
CCL13	CP	102	63	0.56 (0.48-0.65)	0.66 (0.53-0.78)	0.61 (0.53-0.67)	0.53 (0.49-0.55)	0.51 (0.33-0.68)	0.52 (0.43-0.6)
CCL4	SERPINA3	102	63	0.59 (0.47-0.69)	0.59 (0.48-0.72)	0.59 (0.51-0.67)	0.52 (0.41-0.59)	0.56 (0.43-0.59)	0.52 (0.43-0.58)
IL7	LRG1	102	63	0.62 (0.52-0.71)	0.61 (0.51-0.72)	0.61 (0.54-0.69)	0.54 (0.4-0.62)	0.48 (0.43-0.6)	0.52 (0.45-0.59)
FC	CCL4	77	43	0.69 (0.59-0.78)	0.59 (0.47-0.73)	0.64 (0.56-0.72)	0.5 (0.34-0.66)	0.55 (0.53-0.57)	0.52 (0.44-0.61)
NCR1	CPN2	101	63	0.58 (0.49-0.66)	0.65 (0.54-0.75)	0.61 (0.54-0.68)	0.54 (0.48-0.58)	0.5 (0.4-0.61)	0.52 (0.46-0.58)
TNF	VEGFA	102	63	0.56 (0.49-0.64)	0.57 (0.49-0.68)	0.56 (0.51-0.64)	0.51 (0.44-0.56)	0.54 (0.46-0.55)	0.52 (0.47-0.55)
FC	C8A	77	44	0.69 (0.6-0.77)	0.59 (0.48-0.72)	0.64 (0.57-0.71)	0.5 (0.32-0.69)	0.55 (0.5-0.6)	0.52 (0.42-0.62)
CRP_SRM	C9	102	67	0.63 (0.51-0.73)	0.62 (0.51-0.74)	0.63 (0.54-0.71)	0.47 (0.41-0.63)	0.57 (0.41-0.62)	0.52 (0.42-0.62)
CPN2	CFB	102	67	0.59 (0.5-0.67)	0.63 (0.53-0.74)	0.61 (0.54-0.68)	0.54 (0.45-0.59)	0.51 (0.41-0.61)	0.52 (0.46-0.58)
SH2D1A	C8A	101	63	0.59 (0.5-0.67)	0.58 (0.5-0.69)	0.59 (0.52-0.66)	0.52 (0.42-0.58)	0.53 (0.47-0.54)	0.52 (0.46-0.56)
HSD11B1	IL13	101	63	0.56 (0.48-0.65)	0.58 (0.48-0.7)	0.57 (0.51-0.64)	0.53 (0.46-0.54)	0.55 (0.47-0.56)	0.52 (0.48-0.55)
TNF	C2	102	63	0.57 (0.5-0.64)	0.57 (0.47-0.72)	0.57 (0.51-0.66)	0.51 (0.45-0.56)	0.53 (0.45-0.57)	0.52 (0.47-0.56)
IFNG	IL17C	102	63	0.68 (0.58-0.76)	0.56 (0.41-0.72)	0.62 (0.52-0.71)	0.45 (0.32-0.69)	0.59 (0.53-0.63)	0.52 (0.45-0.64)
PZP	C8A	101	67	0.58 (0.49-0.67)	0.59 (0.47-0.72)	0.59 (0.52-0.66)	0.55 (0.43-0.58)	0.52 (0.39-0.6)	0.52 (0.44-0.57)
C3	CP	102	67	0.57 (0.49-0.66)	0.63 (0.52-0.76)	0.6 (0.53-0.68)	0.55 (0.45-0.56)	0.51 (0.36-0.64)	0.52 (0.44-0.59)
FC	SAA1	77	44	0.67 (0.57-0.77)	0.59 (0.43-0.76)	0.63 (0.54-0.72)	0.48 (0.35-0.65)	0.55 (0.52-0.62)	0.52 (0.45-0.61)
PLXNA4	IL17F	101	63	0.56 (0.48-0.63)	0.63 (0.48-0.76)	0.6 (0.51-0.67)	0.49 (0.45-0.55)	0.55 (0.38-0.62)	0.52 (0.43-0.57)
IL15	CLU	102	63	0.55 (0.46-0.65)	0.61 (0.51-0.72)	0.58 (0.51-0.66)	0.53 (0.51-0.57)	0.51 (0.4-0.61)	0.52 (0.46-0.57)
IL13	SERPING1	102	63	0.56 (0.44-0.64)	0.58 (0.47-0.72)	0.57 (0.49-0.65)	0.55 (0.44-0.56)	0.51 (0.44-0.58)	0.52 (0.46-0.56)
IL17F	VTN	102	63	0.56 (0.48-0.64)	0.63 (0.45-0.75)	0.59 (0.5-0.67)	0.49 (0.46-0.55)	0.55 (0.38-0.62)	0.52 (0.43-0.57)
IL17F	SERPING1	102	63	0.56 (0.48-0.65)	0.59 (0.44-0.75)	0.57 (0.49-0.67)	0.52 (0.44-0.56)	0.53 (0.42-0.58)	0.52 (0.45-0.55)
PLXNA4	ITIH2	101	63	0.56 (0.49-0.63)	0.63 (0.53-0.75)	0.59 (0.53-0.66)	0.52 (0.48-0.53)	0.52 (0.39-0.61)	0.52 (0.45-0.57)
CP	PZP	101	67	0.57 (0.47-0.68)	0.65 (0.48-0.77)	0.61 (0.52-0.68)	0.56 (0.42-0.59)	0.5 (0.36-0.64)	0.52 (0.42-0.61)
IL7	CFB	102	63	0.58 (0.49-0.66)	0.64 (0.53-0.76)	0.61 (0.53-0.68)	0.53 (0.45-0.58)	0.52 (0.41-0.63)	0.52 (0.45-0.58)
IL17F	CCL13	102	63	0.56 (0.48-0.65)	0.61 (0.46-0.74)	0.58 (0.5-0.67)	0.52 (0.45-0.55)	0.54 (0.4-0.6)	0.52 (0.45-0.56)

CLEC4C	IL17C	101	63	0.6 (0.52-0.68)	0.63 (0.45-0.75)	0.61 (0.52-0.69)	0.5 (0.4-0.6)	0.55 (0.37-0.61)	0.52 (0.41-0.59)
ITIH3	CLU	102	67	0.59 (0.5-0.67)	0.6 (0.51-0.72)	0.6 (0.53-0.66)	0.55 (0.42-0.58)	0.5 (0.44-0.59)	0.52 (0.45-0.58)
DCTN1	IL10_PEA_IR	102	63	0.56 (0.48-0.64)	0.71 (0.54-0.82)	0.64 (0.54-0.7)	0.5 (0.47-0.53)	0.54 (0.32-0.66)	0.52 (0.41-0.59)
HGF	SERPING1	102	63	0.56 (0.47-0.65)	0.59 (0.46-0.71)	0.58 (0.5-0.66)	0.52 (0.44-0.56)	0.54 (0.42-0.58)	0.52 (0.45-0.56)
FCRL6	CCL13	101	63	0.56 (0.48-0.65)	0.63 (0.52-0.74)	0.6 (0.53-0.67)	0.53 (0.46-0.54)	0.52 (0.39-0.61)	0.52 (0.44-0.57)
MILR1	PLXNA4	102	63	0.63 (0.54-0.72)	0.63 (0.51-0.76)	0.63 (0.56-0.71)	0.53 (0.37-0.63)	0.52 (0.42-0.6)	0.52 (0.43-0.58)
IL17F	CP	102	63	0.56 (0.47-0.64)	0.64 (0.45-0.77)	0.6 (0.5-0.68)	0.51 (0.46-0.56)	0.53 (0.34-0.66)	0.52 (0.42-0.59)
IL7	ORM1	102	63	0.6 (0.5-0.69)	0.62 (0.51-0.73)	0.61 (0.53-0.69)	0.55 (0.42-0.59)	0.49 (0.42-0.6)	0.52 (0.45-0.59)
C2	ITIH1	102	67	0.56 (0.49-0.64)	0.61 (0.49-0.71)	0.58 (0.52-0.65)	0.5 (0.46-0.55)	0.53 (0.42-0.59)	0.52 (0.45-0.56)
CCL4	C4BPB	102	63	0.61 (0.49-0.7)	0.58 (0.48-0.69)	0.59 (0.52-0.66)	0.52 (0.39-0.61)	0.52 (0.48-0.53)	0.52 (0.45-0.57)
CP	ITIH1	102	67	0.55 (0.48-0.64)	0.64 (0.53-0.76)	0.59 (0.53-0.67)	0.52 (0.49-0.55)	0.51 (0.35-0.66)	0.52 (0.43-0.59)
IL15	VEGFA	102	63	0.56 (0.44-0.66)	0.58 (0.49-0.69)	0.57 (0.49-0.64)	0.51 (0.48-0.57)	0.54 (0.45-0.56)	0.52 (0.47-0.56)
HSD11B1	SERPINA4	101	63	0.59 (0.51-0.67)	0.6 (0.5-0.71)	0.59 (0.53-0.66)	0.52 (0.42-0.58)	0.52 (0.44-0.59)	0.52 (0.45-0.57)
ITGA6	C8B	101	63	0.62 (0.53-0.71)	0.66 (0.54-0.76)	0.63 (0.56-0.7)	0.53 (0.43-0.61)	0.5 (0.4-0.63)	0.52 (0.45-0.6)
IL6_PEA_IR	FCRL6	102	63	0.58 (0.48-0.67)	0.62 (0.49-0.73)	0.6 (0.52-0.67)	0.51 (0.43-0.58)	0.53 (0.39-0.62)	0.52 (0.43-0.59)
LAMP3	IL7	101	63	0.57 (0.48-0.66)	0.64 (0.54-0.76)	0.61 (0.54-0.68)	0.55 (0.47-0.58)	0.5 (0.38-0.62)	0.52 (0.45-0.59)
SERPINA3	CP	102	67	0.58 (0.49-0.66)	0.64 (0.51-0.77)	0.61 (0.54-0.69)	0.55 (0.44-0.57)	0.51 (0.36-0.64)	0.52 (0.43-0.6)
SERPIND1	C8A	102	67	0.58 (0.49-0.66)	0.64 (0.53-0.75)	0.61 (0.54-0.67)	0.53 (0.47-0.58)	0.5 (0.39-0.63)	0.52 (0.46-0.59)
LRG1	CPN2	102	67	0.62 (0.52-0.71)	0.63 (0.52-0.73)	0.62 (0.55-0.69)	0.55 (0.41-0.62)	0.49 (0.4-0.61)	0.52 (0.44-0.59)
FC	C9	77	44	0.67 (0.58-0.77)	0.59 (0.46-0.73)	0.63 (0.56-0.71)	0.51 (0.32-0.69)	0.53 (0.5-0.58)	0.52 (0.42-0.62)
CCL13	ITIH2	102	63	0.56 (0.49-0.65)	0.61 (0.52-0.71)	0.59 (0.53-0.65)	0.5 (0.47-0.55)	0.52 (0.41-0.59)	0.52 (0.45-0.56)
CCL13	VTN	102	63	0.56 (0.49-0.65)	0.63 (0.53-0.75)	0.59 (0.53-0.67)	0.51 (0.47-0.54)	0.52 (0.38-0.62)	0.52 (0.45-0.57)
FLT3LG	MBL2	102	63	0.64 (0.54-0.72)	0.66 (0.55-0.77)	0.64 (0.58-0.71)	0.52 (0.44-0.61)	0.52 (0.41-0.61)	0.52 (0.45-0.58)
IL10_PEA_IR	CCL4	101	63	0.58 (0.49-0.67)	0.57 (0.42-0.73)	0.57 (0.48-0.66)	0.47 (0.4-0.59)	0.57 (0.5-0.59)	0.52 (0.47-0.58)
SH2D1A	C4BPB	101	63	0.59 (0.49-0.68)	0.59 (0.5-0.7)	0.59 (0.52-0.67)	0.51 (0.42-0.58)	0.53 (0.47-0.56)	0.52 (0.46-0.57)
CDSN	VEGFA	101	63	0.55 (0.48-0.63)	0.58 (0.49-0.7)	0.57 (0.5-0.64)	0.5 (0.47-0.52)	0.54 (0.44-0.57)	0.52 (0.47-0.54)
ORM1	MBL2	102	67	0.61 (0.51-0.7)	0.64 (0.53-0.76)	0.62 (0.56-0.7)	0.51 (0.44-0.61)	0.52 (0.4-0.63)	0.52 (0.44-0.59)
IL6_PEA_IR	PLXNA4	102	63	0.58 (0.49-0.67)	0.64 (0.51-0.76)	0.61 (0.52-0.68)	0.53 (0.44-0.59)	0.51 (0.38-0.63)	0.52 (0.43-0.6)
CCL4	C8A	102	63	0.6 (0.5-0.68)	0.58 (0.49-0.68)	0.59 (0.52-0.65)	0.52 (0.41-0.59)	0.52 (0.48-0.54)	0.52 (0.45-0.56)
TNF	ITIH2	102	63	0.55 (0.49-0.63)	0.59 (0.51-0.7)	0.57 (0.52-0.64)	0.5 (0.48-0.53)	0.54 (0.43-0.57)	0.52 (0.46-0.54)

IL7	APOA1	102	63	0.61 (0.54-0.68)	0.6 (0.49-0.71)	0.61 (0.54-0.67)	0.55 (0.41-0.6)	0.49 (0.44-0.56)	0.52 (0.45-0.57)
FCRL6	SH2D1A	102	63	0.55 (0.48-0.63)	0.62 (0.51-0.73)	0.59 (0.52-0.65)	0.51 (0.47-0.53)	0.52 (0.39-0.61)	0.52 (0.45-0.56)
FC	CXCL9	77	43	0.69 (0.6-0.79)	0.58 (0.44-0.72)	0.64 (0.55-0.72)	0.48 (0.31-0.69)	0.56 (0.5-0.58)	0.52 (0.43-0.63)
MASP1	ITGA6	102	63	0.6 (0.51-0.7)	0.67 (0.54-0.78)	0.64 (0.55-0.71)	0.5 (0.41-0.6)	0.52 (0.34-0.66)	0.52 (0.41-0.61)
IL6_PEA_IR	C2	101	63	0.59 (0.49-0.68)	0.58 (0.46-0.72)	0.59 (0.5-0.67)	0.53 (0.41-0.59)	0.52 (0.46-0.59)	0.52 (0.45-0.58)
CCL13	IL17C	102	63	0.59 (0.5-0.68)	0.59 (0.45-0.72)	0.59 (0.52-0.66)	0.5 (0.41-0.59)	0.55 (0.43-0.58)	0.52 (0.44-0.58)
CCL4	ITIH1	102	63	0.56 (0.44-0.65)	0.62 (0.52-0.73)	0.59 (0.52-0.67)	0.49 (0.43-0.56)	0.54 (0.39-0.61)	0.52 (0.43-0.57)
PLXNA4	VEGFA	101	63	0.55 (0.47-0.63)	0.63 (0.51-0.76)	0.59 (0.52-0.66)	0.51 (0.46-0.53)	0.53 (0.38-0.62)	0.52 (0.44-0.57)
PZP	C4BPB	101	67	0.59 (0.46-0.68)	0.6 (0.49-0.72)	0.59 (0.51-0.67)	0.56 (0.42-0.59)	0.49 (0.38-0.6)	0.52 (0.42-0.58)
C2	SERPING1	102	67	0.57 (0.48-0.65)	0.6 (0.45-0.73)	0.58 (0.49-0.66)	0.52 (0.45-0.56)	0.54 (0.41-0.59)	0.52 (0.44-0.57)
CDSN	IL17C	101	63	0.59 (0.5-0.67)	0.58 (0.46-0.71)	0.59 (0.51-0.66)	0.49 (0.41-0.59)	0.56 (0.47-0.58)	0.52 (0.46-0.58)
APCS	MBL2	102	67	0.6 (0.5-0.69)	0.67 (0.55-0.79)	0.64 (0.57-0.72)	0.52 (0.45-0.59)	0.52 (0.35-0.66)	0.52 (0.43-0.59)
ITGA11	IL17C	101	63	0.63 (0.53-0.71)	0.56 (0.45-0.68)	0.59 (0.52-0.66)	0.52 (0.38-0.62)	0.51 (0.5-0.53)	0.52 (0.44-0.57)
IL17F	ITIH2	102	63	0.56 (0.49-0.64)	0.59 (0.43-0.72)	0.57 (0.48-0.65)	0.49 (0.46-0.54)	0.54 (0.42-0.58)	0.52 (0.45-0.55)
IL6_PEA_IR	CLEC4C	102	63	0.58 (0.48-0.66)	0.62 (0.5-0.75)	0.6 (0.52-0.67)	0.51 (0.43-0.58)	0.51 (0.38-0.63)	0.52 (0.44-0.6)
LRG1	C9	102	67	0.62 (0.51-0.71)	0.63 (0.52-0.74)	0.62 (0.54-0.7)	0.5 (0.39-0.61)	0.55 (0.42-0.61)	0.52 (0.42-0.6)
CCL13	VEGFA	102	63	0.56 (0.47-0.65)	0.59 (0.49-0.71)	0.58 (0.51-0.65)	0.53 (0.45-0.55)	0.54 (0.43-0.57)	0.51 (0.46-0.56)
IL17F	IL15	102	63	0.55 (0.45-0.64)	0.61 (0.49-0.73)	0.58 (0.51-0.66)	0.51 (0.47-0.56)	0.52 (0.41-0.59)	0.51 (0.46-0.56)
FC	MBL2	77	44	0.67 (0.59-0.76)	0.6 (0.48-0.75)	0.64 (0.56-0.72)	0.47 (0.35-0.68)	0.55 (0.51-0.6)	0.51 (0.44-0.62)
PLXNA4	IL17C	101	63	0.59 (0.51-0.67)	0.62 (0.46-0.76)	0.6 (0.52-0.68)	0.49 (0.41-0.58)	0.54 (0.39-0.61)	0.51 (0.42-0.58)
DCTN1	MILR1	102	63	0.63 (0.55-0.72)	0.69 (0.55-0.81)	0.66 (0.58-0.73)	0.53 (0.39-0.6)	0.52 (0.36-0.62)	0.51 (0.42-0.58)
ITGA11	ITIH2	101	63	0.62 (0.51-0.7)	0.59 (0.5-0.69)	0.6 (0.53-0.67)	0.5 (0.39-0.62)	0.53 (0.44-0.57)	0.51 (0.43-0.59)
FCRL6	C2	101	63	0.57 (0.5-0.65)	0.63 (0.49-0.76)	0.6 (0.52-0.68)	0.51 (0.45-0.55)	0.53 (0.38-0.63)	0.51 (0.43-0.58)
CCL13	CLU	102	63	0.56 (0.48-0.65)	0.6 (0.5-0.71)	0.58 (0.52-0.65)	0.52 (0.46-0.55)	0.51 (0.42-0.58)	0.51 (0.46-0.55)
IFNG	MBL2	102	63	0.67 (0.58-0.75)	0.63 (0.52-0.75)	0.65 (0.58-0.72)	0.45 (0.37-0.66)	0.55 (0.46-0.63)	0.51 (0.44-0.63)
CDSN	IL17F	101	63	0.56 (0.48-0.64)	0.59 (0.43-0.73)	0.57 (0.49-0.66)	0.49 (0.45-0.54)	0.53 (0.44-0.58)	0.51 (0.46-0.55)
FGF2	IL7	101	63	0.57 (0.49-0.65)	0.66 (0.45-0.78)	0.61 (0.51-0.69)	0.52 (0.45-0.55)	0.51 (0.38-0.65)	0.51 (0.43-0.59)
DCTN1	CDSN	102	63	0.55 (0.47-0.62)	0.69 (0.56-0.81)	0.62 (0.54-0.69)	0.51 (0.51-0.52)	0.52 (0.32-0.68)	0.51 (0.42-0.59)
SH2D1A	SERPING1	101	63	0.56 (0.47-0.64)	0.61 (0.49-0.73)	0.58 (0.5-0.65)	0.51 (0.46-0.54)	0.51 (0.41-0.6)	0.51 (0.45-0.57)
KLRD1	PZP	100	63	0.6 (0.5-0.69)	0.6 (0.44-0.72)	0.6 (0.51-0.68)	0.55 (0.41-0.59)	0.5 (0.38-0.6)	0.51 (0.43-0.58)

ITIH1	VTN	102	67	0.55 (0.5-0.63)	0.62 (0.53-0.72)	0.59 (0.53-0.65)	0.51 (0.49-0.53)	0.52 (0.39-0.61)	0.51 (0.45-0.56)
TNF	VTN	102	63	0.55 (0.49-0.63)	0.62 (0.53-0.72)	0.59 (0.53-0.66)	0.51 (0.48-0.53)	0.52 (0.39-0.62)	0.51 (0.45-0.56)
IL17C	ITIH3	102	63	0.6 (0.52-0.69)	0.59 (0.48-0.7)	0.59 (0.53-0.67)	0.5 (0.4-0.6)	0.53 (0.46-0.58)	0.51 (0.45-0.57)
IL6_PEA_cytokine	IFNG	102	63	0.71 (0.61-0.78)	0.55 (0.41-0.72)	0.63 (0.54-0.72)	0.43 (0.3-0.7)	0.6 (0.53-0.62)	0.51 (0.45-0.65)
PLXNA4	SH2D1A	102	63	0.54 (0.48-0.62)	0.64 (0.52-0.77)	0.59 (0.52-0.67)	0.48 (0.47-0.52)	0.54 (0.37-0.64)	0.51 (0.42-0.57)
FCRL6	HGF	101	63	0.56 (0.48-0.65)	0.63 (0.5-0.74)	0.59 (0.52-0.66)	0.51 (0.48-0.55)	0.52 (0.37-0.63)	0.51 (0.44-0.58)
VEGFA	SERPINA4	102	63	0.6 (0.52-0.68)	0.57 (0.49-0.67)	0.58 (0.52-0.65)	0.53 (0.4-0.6)	0.5 (0.49-0.51)	0.51 (0.45-0.55)
FC	DCTN1	76	43	0.67 (0.57-0.76)	0.7 (0.56-0.85)	0.68 (0.6-0.77)	0.52 (0.44-0.59)	0.49 (0.41-0.67)	0.51 (0.44-0.61)
ITGA11	ITGA6	102	63	0.62 (0.51-0.7)	0.63 (0.52-0.75)	0.63 (0.54-0.7)	0.5 (0.4-0.61)	0.52 (0.39-0.6)	0.51 (0.42-0.59)
IL17C	CP	102	63	0.6 (0.51-0.68)	0.65 (0.48-0.78)	0.62 (0.53-0.7)	0.52 (0.41-0.59)	0.53 (0.34-0.67)	0.51 (0.41-0.61)
HGF	VEGFA	102	63	0.54 (0.46-0.63)	0.57 (0.46-0.69)	0.56 (0.48-0.63)	0.48 (0.47-0.53)	0.53 (0.44-0.56)	0.51 (0.46-0.55)
IL17F	C4BPB	102	63	0.6 (0.51-0.68)	0.59 (0.44-0.71)	0.59 (0.51-0.68)	0.53 (0.4-0.59)	0.5 (0.47-0.56)	0.51 (0.44-0.57)
MASP1	IL7	101	63	0.61 (0.51-0.71)	0.61 (0.49-0.73)	0.61 (0.53-0.68)	0.52 (0.39-0.61)	0.52 (0.42-0.58)	0.51 (0.43-0.59)
IL17C	SERPINA4	102	63	0.61 (0.52-0.69)	0.57 (0.47-0.68)	0.59 (0.53-0.66)	0.51 (0.39-0.61)	0.51 (0.5-0.53)	0.51 (0.45-0.56)
FCRL6	SERPINA4	101	63	0.59 (0.51-0.67)	0.61 (0.52-0.72)	0.6 (0.54-0.67)	0.51 (0.42-0.58)	0.52 (0.44-0.58)	0.51 (0.46-0.56)
IFNG	VTN	102	63	0.67 (0.58-0.76)	0.64 (0.5-0.75)	0.65 (0.57-0.72)	0.47 (0.37-0.64)	0.55 (0.44-0.63)	0.51 (0.43-0.61)
ITIH2	C8A	102	67	0.59 (0.51-0.68)	0.58 (0.51-0.67)	0.59 (0.53-0.65)	0.51 (0.42-0.59)	0.52 (0.45-0.55)	0.51 (0.45-0.56)
SH2D1A	C2	101	63	0.56 (0.48-0.65)	0.58 (0.48-0.71)	0.57 (0.5-0.65)	0.51 (0.45-0.55)	0.53 (0.44-0.58)	0.51 (0.47-0.56)
MILR1	CPN2	101	63	0.65 (0.56-0.74)	0.62 (0.5-0.72)	0.63 (0.56-0.7)	0.55 (0.36-0.64)	0.48 (0.42-0.56)	0.51 (0.41-0.57)
VTN	CLU	102	67	0.54 (0.48-0.63)	0.61 (0.52-0.72)	0.58 (0.52-0.64)	0.51 (0.49-0.52)	0.51 (0.4-0.61)	0.51 (0.45-0.56)
ITGA11	PZP	100	63	0.64 (0.54-0.72)	0.59 (0.45-0.71)	0.61 (0.54-0.69)	0.56 (0.37-0.64)	0.48 (0.39-0.57)	0.51 (0.4-0.58)
CCL13	CCL4	102	63	0.57 (0.46-0.68)	0.59 (0.49-0.71)	0.58 (0.51-0.66)	0.53 (0.42-0.58)	0.54 (0.44-0.57)	0.51 (0.44-0.57)
PLXNA4	CLU	101	63	0.55 (0.48-0.62)	0.62 (0.51-0.75)	0.58 (0.52-0.65)	0.52 (0.49-0.54)	0.51 (0.4-0.61)	0.51 (0.45-0.57)
PLXNA4	CCL4	101	63	0.56 (0.45-0.65)	0.63 (0.5-0.75)	0.59 (0.52-0.67)	0.5 (0.42-0.57)	0.54 (0.39-0.62)	0.51 (0.42-0.57)
SERPING1	C4BPB	102	67	0.6 (0.51-0.67)	0.59 (0.49-0.71)	0.59 (0.52-0.66)	0.54 (0.42-0.59)	0.5 (0.44-0.56)	0.51 (0.44-0.56)
IFNG	C9	102	63	0.67 (0.57-0.76)	0.57 (0.43-0.71)	0.62 (0.53-0.7)	0.44 (0.32-0.67)	0.58 (0.52-0.62)	0.51 (0.44-0.63)
VEGFA	SERPING1	102	63	0.56 (0.47-0.65)	0.59 (0.49-0.7)	0.58 (0.5-0.65)	0.52 (0.44-0.56)	0.53 (0.43-0.57)	0.51 (0.45-0.56)
IL10_PEA_IR	PZP	100	63	0.57 (0.49-0.67)	0.57 (0.42-0.72)	0.57 (0.48-0.66)	0.48 (0.44-0.56)	0.55 (0.41-0.59)	0.51 (0.45-0.56)
CCL4	IL15	102	63	0.58 (0.43-0.68)	0.59 (0.49-0.71)	0.58 (0.49-0.66)	0.51 (0.44-0.59)	0.53 (0.43-0.57)	0.51 (0.45-0.57)
ITIH1	C4BPB	102	67	0.59 (0.5-0.68)	0.6 (0.52-0.7)	0.6 (0.53-0.67)	0.52 (0.42-0.58)	0.51 (0.42-0.58)	0.51 (0.44-0.57)

FCRL6	CP	101	63	0.56 (0.48-0.62)	0.68 (0.56-0.8)	0.62 (0.55-0.69)	0.53 (0.5-0.54)	0.5 (0.3-0.7)	0.51 (0.41-0.62)
IL6_PEA_IR	VEGFA	101	63	0.59 (0.45-0.69)	0.57 (0.48-0.7)	0.58 (0.5-0.66)	0.51 (0.41-0.59)	0.51 (0.47-0.54)	0.51 (0.45-0.57)
ITIH2	SERPING1	102	67	0.56 (0.48-0.64)	0.58 (0.46-0.69)	0.57 (0.51-0.64)	0.51 (0.46-0.54)	0.53 (0.44-0.56)	0.51 (0.46-0.55)
SH2D1A	TNF	101	63	0.55 (0.48-0.62)	0.58 (0.49-0.69)	0.56 (0.5-0.63)	0.49 (0.47-0.54)	0.53 (0.46-0.54)	0.51 (0.48-0.53)
HGF	IL13	102	63	0.54 (0.46-0.63)	0.58 (0.45-0.7)	0.56 (0.48-0.63)	0.49 (0.47-0.54)	0.53 (0.46-0.55)	0.51 (0.47-0.53)
SAA1	C9	102	67	0.61 (0.47-0.72)	0.58 (0.47-0.71)	0.6 (0.5-0.68)	0.48 (0.38-0.62)	0.54 (0.46-0.59)	0.51 (0.44-0.58)
VEGFA	C2	102	63	0.57 (0.48-0.65)	0.57 (0.46-0.71)	0.57 (0.5-0.65)	0.5 (0.44-0.56)	0.54 (0.43-0.58)	0.51 (0.44-0.56)
SIT1	MBL2	101	63	0.62 (0.53-0.69)	0.63 (0.53-0.75)	0.63 (0.56-0.69)	0.49 (0.41-0.6)	0.53 (0.42-0.61)	0.51 (0.45-0.58)
DCTN1	C4BPB	101	63	0.59 (0.5-0.68)	0.69 (0.54-0.81)	0.64 (0.55-0.71)	0.52 (0.47-0.58)	0.5 (0.32-0.68)	0.51 (0.42-0.6)
CDSN	CCL4	101	63	0.56 (0.46-0.66)	0.59 (0.49-0.71)	0.57 (0.51-0.66)	0.49 (0.42-0.57)	0.54 (0.43-0.57)	0.51 (0.45-0.56)
ITGA6	SAA1	101	63	0.59 (0.51-0.68)	0.64 (0.51-0.76)	0.61 (0.54-0.69)	0.52 (0.42-0.56)	0.49 (0.38-0.62)	0.51 (0.44-0.58)
IL6_PEA_IR	IL13	101	63	0.58 (0.45-0.68)	0.58 (0.44-0.72)	0.58 (0.49-0.66)	0.55 (0.42-0.58)	0.51 (0.43-0.57)	0.51 (0.44-0.56)
ITIH1	C8A	102	67	0.58 (0.5-0.67)	0.6 (0.51-0.7)	0.59 (0.54-0.66)	0.51 (0.42-0.58)	0.51 (0.44-0.59)	0.51 (0.45-0.56)
DCTN1	MASP1	102	63	0.6 (0.5-0.69)	0.7 (0.58-0.81)	0.65 (0.56-0.72)	0.52 (0.46-0.61)	0.49 (0.32-0.66)	0.51 (0.41-0.6)
SERPING1	VTN	102	67	0.56 (0.49-0.64)	0.62 (0.51-0.73)	0.59 (0.52-0.65)	0.51 (0.47-0.54)	0.5 (0.39-0.61)	0.51 (0.45-0.56)
CXCL9	IL17C	102	63	0.65 (0.57-0.74)	0.56 (0.42-0.69)	0.61 (0.53-0.69)	0.48 (0.34-0.66)	0.53 (0.53-0.57)	0.51 (0.44-0.6)
TNF	CLU	102	63	0.55 (0.48-0.63)	0.58 (0.5-0.68)	0.57 (0.51-0.63)	0.52 (0.47-0.53)	0.51 (0.46-0.56)	0.51 (0.47-0.54)
FCRL6	IL17F	101	63	0.55 (0.49-0.63)	0.61 (0.48-0.74)	0.59 (0.51-0.66)	0.49 (0.47-0.54)	0.53 (0.38-0.62)	0.51 (0.43-0.56)
SERPING1	C8A	102	67	0.59 (0.5-0.66)	0.59 (0.47-0.72)	0.59 (0.51-0.67)	0.53 (0.42-0.59)	0.5 (0.42-0.56)	0.51 (0.44-0.56)
FCRL6	IL13	101	63	0.54 (0.47-0.61)	0.64 (0.52-0.75)	0.59 (0.52-0.66)	0.51 (0.49-0.52)	0.5 (0.36-0.64)	0.51 (0.44-0.57)
DCTN1	ITGA11	102	63	0.62 (0.5-0.7)	0.69 (0.54-0.81)	0.65 (0.56-0.72)	0.5 (0.41-0.6)	0.51 (0.33-0.65)	0.51 (0.4-0.59)
IL17F	C2	102	63	0.57 (0.49-0.65)	0.57 (0.44-0.72)	0.57 (0.49-0.66)	0.49 (0.43-0.56)	0.53 (0.44-0.58)	0.51 (0.45-0.56)
SH2D1A	CP	101	63	0.55 (0.47-0.63)	0.65 (0.52-0.79)	0.6 (0.53-0.68)	0.52 (0.49-0.55)	0.5 (0.32-0.68)	0.51 (0.42-0.61)
IL13	CLU	102	63	0.54 (0.44-0.63)	0.58 (0.46-0.68)	0.56 (0.48-0.62)	0.52 (0.46-0.53)	0.51 (0.45-0.55)	0.51 (0.47-0.53)
C2	ITIH2	102	67	0.56 (0.49-0.65)	0.58 (0.48-0.7)	0.57 (0.51-0.65)	0.49 (0.46-0.55)	0.52 (0.44-0.58)	0.51 (0.46-0.55)
CP	ITIH2	102	67	0.55 (0.48-0.63)	0.64 (0.53-0.76)	0.6 (0.53-0.67)	0.53 (0.48-0.55)	0.49 (0.36-0.64)	0.51 (0.44-0.59)
SAA1	VTN	102	67	0.57 (0.49-0.66)	0.63 (0.49-0.74)	0.59 (0.52-0.67)	0.54 (0.46-0.57)	0.47 (0.43-0.63)	0.51 (0.46-0.59)
CP	CLU	102	67	0.55 (0.47-0.63)	0.64 (0.53-0.76)	0.59 (0.53-0.67)	0.54 (0.49-0.55)	0.49 (0.35-0.65)	0.51 (0.44-0.6)
IL17F	C8A	102	63	0.6 (0.5-0.67)	0.57 (0.41-0.71)	0.59 (0.49-0.67)	0.51 (0.4-0.6)	0.51 (0.48-0.56)	0.51 (0.45-0.56)
FGF2	PZP	100	63	0.56 (0.48-0.64)	0.67 (0.44-0.78)	0.61 (0.5-0.68)	0.52 (0.45-0.54)	0.5 (0.34-0.66)	0.51 (0.41-0.59)

SH2D1A	SERPINA4	101	63	0.59 (0.51-0.67)	0.58 (0.49-0.69)	0.59 (0.53-0.65)	0.51 (0.41-0.58)	0.52 (0.48-0.55)	0.51 (0.45-0.56)
ITGA6	SIT1	102	63	0.61 (0.52-0.69)	0.66 (0.54-0.77)	0.64 (0.57-0.7)	0.49 (0.42-0.6)	0.52 (0.46-0.64)	0.51 (0.46-0.58)
IL10_PEA_IR	IL17C	101	63	0.6 (0.51-0.7)	0.55 (0.42-0.71)	0.58 (0.49-0.68)	0.46 (0.38-0.61)	0.57 (0.5-0.58)	0.51 (0.45-0.58)
IL13	TNF	102	63	0.54 (0.47-0.62)	0.58 (0.48-0.67)	0.56 (0.51-0.62)	0.51 (0.47-0.52)	0.54 (0.46-0.55)	0.51 (0.47-0.53)
IL6_PEA_IR	HGF	101	63	0.59 (0.46-0.68)	0.57 (0.47-0.69)	0.58 (0.49-0.66)	0.51 (0.41-0.59)	0.51 (0.47-0.53)	0.51 (0.45-0.56)
C3	VTN	102	67	0.58 (0.5-0.66)	0.63 (0.52-0.74)	0.6 (0.54-0.67)	0.51 (0.44-0.58)	0.51 (0.4-0.6)	0.51 (0.44-0.57)
ITGA11	CCL4	101	63	0.62 (0.48-0.72)	0.56 (0.47-0.68)	0.59 (0.51-0.66)	0.51 (0.36-0.63)	0.51 (0.47-0.53)	0.51 (0.43-0.57)
CP	C2	102	67	0.56 (0.48-0.64)	0.64 (0.48-0.78)	0.6 (0.51-0.67)	0.52 (0.46-0.55)	0.49 (0.35-0.65)	0.51 (0.43-0.59)
ITIH2	C4BPB	102	67	0.59 (0.51-0.68)	0.58 (0.5-0.68)	0.59 (0.53-0.66)	0.52 (0.41-0.59)	0.49 (0.45-0.55)	0.51 (0.45-0.56)
CLU	C8A	102	67	0.6 (0.51-0.68)	0.59 (0.5-0.69)	0.59 (0.53-0.66)	0.52 (0.4-0.6)	0.51 (0.46-0.54)	0.51 (0.44-0.55)
HSD11B1	C9	101	63	0.62 (0.53-0.73)	0.59 (0.49-0.7)	0.61 (0.54-0.68)	0.48 (0.38-0.62)	0.54 (0.45-0.57)	0.51 (0.44-0.58)
FGF2	C9	101	63	0.61 (0.52-0.71)	0.66 (0.44-0.79)	0.63 (0.52-0.71)	0.49 (0.39-0.6)	0.52 (0.38-0.62)	0.51 (0.43-0.58)
ITGA6	APCS	101	63	0.6 (0.5-0.69)	0.69 (0.58-0.8)	0.65 (0.58-0.72)	0.52 (0.47-0.56)	0.49 (0.33-0.67)	0.51 (0.42-0.6)
MASP1	C9	101	63	0.64 (0.56-0.74)	0.59 (0.48-0.73)	0.62 (0.54-0.7)	0.49 (0.35-0.64)	0.52 (0.49-0.58)	0.51 (0.43-0.6)
DCTN1	IL15	101	63	0.55 (0.47-0.65)	0.71 (0.55-0.82)	0.63 (0.54-0.71)	0.52 (0.51-0.53)	0.49 (0.3-0.69)	0.51 (0.41-0.6)
SAA1	CP	102	67	0.57 (0.48-0.66)	0.65 (0.48-0.79)	0.61 (0.52-0.7)	0.56 (0.47-0.57)	0.45 (0.42-0.67)	0.51 (0.45-0.62)
FCRL6	VTN	101	63	0.55 (0.49-0.63)	0.67 (0.55-0.78)	0.61 (0.54-0.68)	0.51 (0.5-0.52)	0.5 (0.33-0.67)	0.51 (0.42-0.59)
IL6_PEA_cytokine	HGF	102	63	0.55 (0.44-0.64)	0.56 (0.44-0.69)	0.56 (0.47-0.63)	0.5 (0.42-0.61)	0.52 (0.46-0.54)	0.51 (0.46-0.57)
NCR1	ITGA6	102	63	0.61 (0.52-0.68)	0.65 (0.54-0.76)	0.63 (0.56-0.69)	0.51 (0.44-0.59)	0.5 (0.4-0.62)	0.51 (0.45-0.58)
C9	SERPINA4	102	67	0.64 (0.55-0.74)	0.57 (0.49-0.66)	0.61 (0.55-0.67)	0.5 (0.35-0.65)	0.51 (0.51-0.53)	0.51 (0.43-0.58)
VEGFA	CP	102	63	0.54 (0.47-0.64)	0.67 (0.51-0.78)	0.61 (0.52-0.68)	0.54 (0.47-0.55)	0.48 (0.33-0.67)	0.51 (0.42-0.61)
FCRL6	VEGFA	101	63	0.55 (0.47-0.63)	0.62 (0.51-0.72)	0.59 (0.52-0.65)	0.5 (0.47-0.53)	0.51 (0.39-0.61)	0.51 (0.44-0.56)
IL6_PEA_IR	CLU	101	63	0.57 (0.47-0.68)	0.59 (0.49-0.71)	0.58 (0.51-0.66)	0.52 (0.41-0.59)	0.47 (0.45-0.55)	0.51 (0.44-0.56)
IL6_PEA_IR	CCL4	101	63	0.59 (0.44-0.69)	0.57 (0.46-0.72)	0.58 (0.49-0.66)	0.52 (0.4-0.6)	0.49 (0.45-0.55)	0.5 (0.43-0.56)
KLRD1	C9	101	63	0.63 (0.53-0.72)	0.58 (0.49-0.68)	0.61 (0.53-0.67)	0.49 (0.37-0.63)	0.51 (0.49-0.55)	0.5 (0.43-0.58)
CP	VTN	102	67	0.55 (0.49-0.64)	0.64 (0.53-0.76)	0.6 (0.53-0.67)	0.52 (0.48-0.55)	0.49 (0.33-0.66)	0.5 (0.42-0.59)
FCRL6	CLU	101	63	0.55 (0.48-0.63)	0.63 (0.52-0.73)	0.59 (0.53-0.65)	0.51 (0.49-0.52)	0.5 (0.37-0.62)	0.5 (0.44-0.57)
SERPING1	CLU	102	67	0.56 (0.48-0.64)	0.59 (0.49-0.7)	0.57 (0.51-0.64)	0.51 (0.46-0.54)	0.49 (0.44-0.56)	0.5 (0.45-0.55)
PLXNA4	PZP	100	63	0.56 (0.49-0.63)	0.62 (0.5-0.76)	0.59 (0.52-0.67)	0.52 (0.46-0.54)	0.49 (0.37-0.62)	0.5 (0.44-0.57)
IL10_PEA_IR	C9	101	63	0.63 (0.54-0.72)	0.57 (0.42-0.72)	0.6 (0.5-0.69)	0.47 (0.37-0.62)	0.53 (0.47-0.59)	0.5 (0.43-0.58)

IL7	C3	102	63	0.58 (0.49-0.65)	0.6 (0.5-0.74)	0.59 (0.52-0.67)	0.54 (0.45-0.57)	0.47 (0.43-0.59)	0.5 (0.46-0.57)
IL6_PEA_cytokine	VEGFA	102	63	0.55 (0.45-0.65)	0.56 (0.45-0.69)	0.56 (0.48-0.63)	0.48 (0.41-0.6)	0.51 (0.45-0.56)	0.5 (0.45-0.57)
ITGA6	ORM1	101	63	0.6 (0.51-0.69)	0.65 (0.53-0.75)	0.63 (0.54-0.7)	0.5 (0.45-0.57)	0.51 (0.37-0.63)	0.5 (0.43-0.58)
NCR1	MBL2	101	63	0.61 (0.53-0.69)	0.65 (0.54-0.77)	0.63 (0.56-0.7)	0.5 (0.41-0.6)	0.5 (0.4-0.63)	0.5 (0.44-0.58)
C4BPB	CLU	102	67	0.61 (0.51-0.69)	0.59 (0.5-0.69)	0.6 (0.53-0.67)	0.52 (0.4-0.6)	0.49 (0.44-0.52)	0.5 (0.44-0.55)
DCTN1	TNF	101	63	0.55 (0.48-0.63)	0.69 (0.56-0.8)	0.62 (0.55-0.68)	0.51 (0.5-0.52)	0.49 (0.32-0.68)	0.5 (0.42-0.59)
SH2D1A	IL13	101	63	0.54 (0.46-0.63)	0.58 (0.47-0.69)	0.56 (0.49-0.63)	0.48 (0.46-0.53)	0.52 (0.46-0.54)	0.5 (0.47-0.53)
IL17C	SERPINA3	102	63	0.59 (0.5-0.68)	0.59 (0.46-0.7)	0.59 (0.51-0.66)	0.5 (0.4-0.59)	0.53 (0.44-0.56)	0.5 (0.43-0.56)
FC	ITGA11	76	43	0.7 (0.6-0.78)	0.58 (0.43-0.73)	0.64 (0.55-0.73)	0.47 (0.3-0.71)	0.54 (0.48-0.57)	0.5 (0.41-0.63)
HGF	CP	102	63	0.55 (0.47-0.64)	0.66 (0.52-0.79)	0.6 (0.52-0.68)	0.54 (0.47-0.55)	0.47 (0.34-0.67)	0.5 (0.42-0.6)
IL10_PEA_IR	IL7	101	63	0.57 (0.48-0.65)	0.6 (0.43-0.74)	0.58 (0.48-0.66)	0.47 (0.45-0.55)	0.53 (0.43-0.59)	0.5 (0.45-0.56)
ITGA6	ITIH3	101	63	0.6 (0.51-0.68)	0.63 (0.52-0.74)	0.61 (0.54-0.69)	0.5 (0.42-0.57)	0.51 (0.39-0.6)	0.5 (0.43-0.56)
IL17F	TNF	102	63	0.57 (0.49-0.65)	0.57 (0.43-0.72)	0.57 (0.49-0.65)	0.49 (0.43-0.57)	0.51 (0.48-0.55)	0.5 (0.46-0.55)
CDSN	PZP	100	63	0.55 (0.48-0.65)	0.6 (0.48-0.73)	0.58 (0.5-0.65)	0.49 (0.47-0.53)	0.52 (0.39-0.59)	0.5 (0.44-0.55)
HGF	IL17F	102	63	0.56 (0.47-0.65)	0.56 (0.42-0.71)	0.56 (0.47-0.64)	0.48 (0.45-0.54)	0.51 (0.45-0.56)	0.5 (0.46-0.54)
IL7	ITIH3	102	63	0.59 (0.51-0.67)	0.6 (0.51-0.71)	0.59 (0.53-0.66)	0.52 (0.42-0.58)	0.48 (0.42-0.58)	0.5 (0.44-0.57)
SH2D1A	VTN	101	63	0.55 (0.49-0.63)	0.62 (0.51-0.73)	0.59 (0.53-0.65)	0.5 (0.48-0.52)	0.5 (0.39-0.61)	0.5 (0.45-0.56)
IL6_PEA_IR	IL17F	101	63	0.59 (0.47-0.69)	0.55 (0.42-0.72)	0.57 (0.48-0.66)	0.51 (0.4-0.6)	0.49 (0.45-0.55)	0.5 (0.44-0.57)
FCRL6	ITIH2	101	63	0.56 (0.49-0.63)	0.64 (0.53-0.74)	0.6 (0.54-0.66)	0.5 (0.49-0.51)	0.5 (0.37-0.63)	0.5 (0.43-0.57)
CCL4	SERPING1	102	63	0.57 (0.45-0.66)	0.59 (0.48-0.72)	0.58 (0.49-0.66)	0.5 (0.41-0.58)	0.52 (0.44-0.57)	0.5 (0.44-0.56)
MASP1	CPN2	101	63	0.6 (0.51-0.69)	0.62 (0.49-0.74)	0.61 (0.53-0.68)	0.51 (0.4-0.61)	0.49 (0.41-0.58)	0.5 (0.43-0.58)
ITGA11	C9	101	63	0.64 (0.55-0.73)	0.57 (0.48-0.68)	0.61 (0.53-0.68)	0.49 (0.37-0.64)	0.51 (0.49-0.53)	0.5 (0.44-0.58)
DCTN1	LAMP3	102	63	0.57 (0.49-0.67)	0.7 (0.58-0.81)	0.64 (0.57-0.72)	0.51 (0.51-0.57)	0.48 (0.3-0.7)	0.5 (0.41-0.61)
FCRL6	IL17C	101	63	0.59 (0.5-0.68)	0.6 (0.49-0.71)	0.6 (0.52-0.66)	0.49 (0.41-0.58)	0.52 (0.4-0.6)	0.5 (0.43-0.56)
IL17F	CLU	102	63	0.55 (0.46-0.64)	0.57 (0.42-0.71)	0.56 (0.48-0.64)	0.49 (0.45-0.55)	0.52 (0.44-0.56)	0.5 (0.45-0.55)
IL17F	SERPINA4	102	63	0.59 (0.5-0.67)	0.57 (0.42-0.72)	0.58 (0.49-0.66)	0.51 (0.41-0.59)	0.49 (0.47-0.53)	0.5 (0.44-0.55)
HGF	CLU	102	63	0.55 (0.46-0.64)	0.58 (0.49-0.68)	0.56 (0.51-0.64)	0.51 (0.46-0.54)	0.49 (0.45-0.55)	0.5 (0.47-0.54)
IL7	SERPIND1	102	63	0.56 (0.48-0.65)	0.65 (0.54-0.75)	0.6 (0.54-0.67)	0.52 (0.48-0.54)	0.49 (0.38-0.63)	0.5 (0.45-0.57)
DCTN1	KLRD1	102	63	0.59 (0.51-0.67)	0.69 (0.57-0.81)	0.64 (0.57-0.71)	0.52 (0.48-0.56)	0.48 (0.33-0.66)	0.5 (0.42-0.6)
SH2D1A	HGF	101	63	0.55 (0.47-0.64)	0.57 (0.47-0.68)	0.56 (0.49-0.63)	0.49 (0.45-0.54)	0.52 (0.46-0.54)	0.5 (0.47-0.53)

SERPINA3	CLU	102	67	0.59 (0.5-0.68)	0.6 (0.49-0.71)	0.59 (0.52-0.67)	0.52 (0.42-0.58)	0.49 (0.43-0.58)	0.5 (0.44-0.56)
VTN	C8A	102	67	0.58 (0.5-0.66)	0.62 (0.53-0.72)	0.6 (0.54-0.67)	0.52 (0.43-0.58)	0.49 (0.41-0.59)	0.5 (0.45-0.56)
DCTN1	SERPINA3	101	63	0.58 (0.49-0.67)	0.7 (0.58-0.81)	0.64 (0.57-0.72)	0.52 (0.5-0.57)	0.48 (0.32-0.68)	0.5 (0.42-0.61)
ITGA6	APOA1	101	63	0.61 (0.53-0.69)	0.64 (0.52-0.75)	0.62 (0.55-0.69)	0.48 (0.41-0.58)	0.52 (0.4-0.61)	0.5 (0.44-0.57)
DCTN1	ITIH1	101	63	0.56 (0.48-0.63)	0.7 (0.58-0.8)	0.63 (0.56-0.69)	0.52 (0.51-0.52)	0.49 (0.32-0.68)	0.5 (0.42-0.6)
IL17C	C8A	102	63	0.6 (0.52-0.68)	0.58 (0.47-0.68)	0.59 (0.51-0.66)	0.48 (0.4-0.59)	0.52 (0.48-0.53)	0.5 (0.46-0.56)
ITGA11	CP	101	63	0.63 (0.49-0.7)	0.65 (0.51-0.78)	0.64 (0.54-0.72)	0.55 (0.38-0.61)	0.47 (0.35-0.64)	0.5 (0.39-0.61)
SAA1	MBL2	102	67	0.59 (0.49-0.67)	0.63 (0.49-0.77)	0.61 (0.53-0.69)	0.53 (0.43-0.58)	0.47 (0.43-0.64)	0.5 (0.44-0.59)
ITIH3	C9	102	67	0.61 (0.51-0.72)	0.6 (0.5-0.71)	0.61 (0.54-0.68)	0.47 (0.39-0.61)	0.53 (0.44-0.57)	0.5 (0.43-0.57)
CCL4	SERPINA4	102	63	0.6 (0.5-0.69)	0.58 (0.49-0.69)	0.59 (0.52-0.65)	0.5 (0.4-0.6)	0.5 (0.49-0.51)	0.5 (0.45-0.55)
FCRL6	CCL4	101	63	0.57 (0.44-0.65)	0.62 (0.5-0.73)	0.59 (0.51-0.66)	0.5 (0.42-0.58)	0.49 (0.39-0.61)	0.5 (0.43-0.58)
SH2D1A	ITIH2	101	63	0.55 (0.49-0.63)	0.59 (0.5-0.69)	0.57 (0.51-0.63)	0.49 (0.48-0.52)	0.5 (0.43-0.57)	0.5 (0.46-0.54)
ITGA6	IL10_PEA_IR	102	63	0.57 (0.49-0.66)	0.64 (0.49-0.76)	0.6 (0.52-0.68)	0.47 (0.44-0.52)	0.52 (0.38-0.61)	0.5 (0.43-0.56)
ITIH3	MBL2	102	67	0.6 (0.51-0.68)	0.6 (0.51-0.72)	0.6 (0.54-0.67)	0.47 (0.41-0.59)	0.51 (0.42-0.57)	0.5 (0.44-0.57)
IL17C	SERPING1	102	63	0.59 (0.49-0.68)	0.58 (0.46-0.71)	0.59 (0.52-0.66)	0.49 (0.41-0.58)	0.52 (0.44-0.56)	0.5 (0.44-0.56)
IL6_PEA_IR	ITIH2	101	63	0.58 (0.5-0.67)	0.6 (0.49-0.71)	0.59 (0.52-0.66)	0.5 (0.41-0.59)	0.49 (0.43-0.57)	0.5 (0.44-0.57)
CLEC4C	DCTN1	102	63	0.55 (0.48-0.64)	0.72 (0.6-0.83)	0.64 (0.57-0.71)	0.54 (0.51-0.55)	0.47 (0.3-0.7)	0.5 (0.41-0.62)
C9	ORM1	102	67	0.61 (0.52-0.71)	0.64 (0.53-0.75)	0.63 (0.56-0.7)	0.51 (0.4-0.62)	0.47 (0.39-0.62)	0.5 (0.41-0.6)
SERPINA3	PZP	101	67	0.58 (0.48-0.67)	0.59 (0.45-0.72)	0.58 (0.51-0.66)	0.54 (0.44-0.56)	0.48 (0.36-0.58)	0.5 (0.43-0.56)
SH2D1A	IL6_PEA_cytokine	101	63	0.55 (0.45-0.64)	0.57 (0.44-0.68)	0.56 (0.48-0.63)	0.48 (0.42-0.6)	0.51 (0.45-0.56)	0.5 (0.46-0.56)
MBL2	CFB	102	67	0.58 (0.5-0.67)	0.66 (0.54-0.77)	0.62 (0.55-0.69)	0.49 (0.45-0.56)	0.49 (0.37-0.65)	0.5 (0.43-0.58)
IL6_PEA_cytokine	CLU	102	63	0.54 (0.45-0.65)	0.56 (0.44-0.71)	0.55 (0.48-0.64)	0.51 (0.43-0.59)	0.48 (0.43-0.58)	0.5 (0.45-0.56)
CCL4	TNF	102	63	0.57 (0.46-0.66)	0.57 (0.48-0.68)	0.57 (0.5-0.64)	0.49 (0.41-0.59)	0.51 (0.48-0.53)	0.5 (0.45-0.56)
ITGA6	SERPINA3	101	63	0.59 (0.5-0.67)	0.65 (0.51-0.76)	0.62 (0.54-0.69)	0.49 (0.43-0.56)	0.52 (0.37-0.62)	0.5 (0.42-0.57)
IL6_PEA_cytokine	IL17F	102	63	0.56 (0.43-0.65)	0.53 (0.39-0.7)	0.54 (0.46-0.64)	0.46 (0.43-0.58)	0.53 (0.46-0.55)	0.5 (0.45-0.56)
IL6_PEA_cytokine	ITIH2	102	63	0.56 (0.48-0.65)	0.59 (0.46-0.71)	0.57 (0.5-0.65)	0.48 (0.44-0.59)	0.49 (0.42-0.59)	0.5 (0.45-0.57)
VTN	C4BPB	102	67	0.59 (0.5-0.67)	0.61 (0.52-0.72)	0.6 (0.54-0.67)	0.51 (0.42-0.58)	0.48 (0.4-0.6)	0.5 (0.45-0.57)
VEGFA	ITIH2	102	63	0.56 (0.47-0.64)	0.59 (0.49-0.7)	0.57 (0.5-0.64)	0.49 (0.46-0.53)	0.51 (0.43-0.57)	0.5 (0.45-0.54)
IL13	ITIH2	102	63	0.55 (0.47-0.63)	0.59 (0.46-0.71)	0.57 (0.49-0.64)	0.5 (0.48-0.52)	0.49 (0.42-0.59)	0.5 (0.46-0.55)
ITIH2	VTN	102	67	0.55 (0.49-0.63)	0.62 (0.51-0.72)	0.59 (0.53-0.64)	0.51 (0.49-0.52)	0.49 (0.4-0.6)	0.5 (0.45-0.56)

DCTN1	SERPING1	101	63	0.56 (0.48-0.64)	0.69 (0.55-0.8)	0.62 (0.54-0.69)	0.52 (0.49-0.54)	0.48 (0.32-0.68)	0.5 (0.42-0.6)
DCTN1	SERPIND1	101	63	0.56 (0.48-0.63)	0.72 (0.6-0.82)	0.63 (0.56-0.7)	0.53 (0.51-0.54)	0.47 (0.29-0.71)	0.5 (0.41-0.62)
C9	C4BPB	102	67	0.61 (0.51-0.72)	0.57 (0.49-0.68)	0.59 (0.53-0.67)	0.48 (0.38-0.62)	0.51 (0.49-0.53)	0.5 (0.44-0.57)
CCL4	C2	102	63	0.57 (0.46-0.67)	0.58 (0.47-0.71)	0.58 (0.5-0.66)	0.47 (0.42-0.58)	0.52 (0.44-0.58)	0.5 (0.44-0.57)
HGF	ITIH2	102	63	0.56 (0.49-0.64)	0.6 (0.49-0.69)	0.58 (0.51-0.64)	0.49 (0.47-0.53)	0.5 (0.43-0.57)	0.5 (0.45-0.55)
IL17C	VTN	102	63	0.59 (0.5-0.68)	0.62 (0.5-0.74)	0.6 (0.53-0.68)	0.49 (0.41-0.56)	0.52 (0.38-0.59)	0.5 (0.42-0.56)
CPN2	CP	102	67	0.58 (0.49-0.67)	0.65 (0.54-0.77)	0.62 (0.54-0.68)	0.53 (0.44-0.56)	0.48 (0.36-0.63)	0.5 (0.43-0.58)
CCL4	CP	102	63	0.56 (0.46-0.66)	0.65 (0.5-0.78)	0.6 (0.51-0.68)	0.54 (0.42-0.57)	0.47 (0.34-0.67)	0.5 (0.41-0.6)
LAMP3	C9	101	63	0.61 (0.51-0.71)	0.63 (0.54-0.74)	0.62 (0.55-0.69)	0.5 (0.42-0.62)	0.47 (0.4-0.61)	0.5 (0.42-0.59)
MILR1	MBL2	101	63	0.63 (0.55-0.71)	0.64 (0.52-0.76)	0.64 (0.57-0.7)	0.51 (0.38-0.63)	0.48 (0.42-0.59)	0.5 (0.42-0.58)
C2	CLU	102	67	0.56 (0.48-0.65)	0.59 (0.45-0.71)	0.58 (0.51-0.66)	0.51 (0.44-0.56)	0.5 (0.42-0.58)	0.5 (0.44-0.56)
IL13	VEGFA	102	63	0.54 (0.44-0.65)	0.58 (0.47-0.69)	0.56 (0.48-0.64)	0.47 (0.45-0.53)	0.52 (0.43-0.57)	0.5 (0.45-0.55)
SH2D1A	CLU	101	63	0.54 (0.47-0.63)	0.58 (0.48-0.69)	0.56 (0.51-0.63)	0.5 (0.47-0.53)	0.49 (0.45-0.55)	0.5 (0.47-0.53)
VEGFA	VTN	102	63	0.55 (0.48-0.63)	0.63 (0.52-0.73)	0.59 (0.53-0.66)	0.5 (0.47-0.54)	0.49 (0.38-0.61)	0.5 (0.44-0.56)
SAA1	CPN2	102	67	0.58 (0.5-0.66)	0.62 (0.49-0.75)	0.6 (0.53-0.67)	0.52 (0.43-0.58)	0.46 (0.4-0.62)	0.5 (0.44-0.58)
CLEC4C	PZP	100	63	0.56 (0.5-0.65)	0.63 (0.44-0.75)	0.6 (0.51-0.67)	0.51 (0.47-0.54)	0.48 (0.36-0.64)	0.5 (0.43-0.58)
CLEC4C	C9	101	63	0.62 (0.52-0.72)	0.62 (0.5-0.76)	0.62 (0.54-0.69)	0.48 (0.39-0.61)	0.5 (0.38-0.62)	0.5 (0.41-0.59)
CCL13	PZP	101	63	0.56 (0.48-0.66)	0.61 (0.48-0.73)	0.59 (0.51-0.66)	0.51 (0.46-0.55)	0.48 (0.38-0.61)	0.5 (0.43-0.56)
IL10_PEA_IR	CPN2	101	63	0.57 (0.49-0.64)	0.61 (0.45-0.75)	0.59 (0.5-0.67)	0.47 (0.45-0.55)	0.5 (0.4-0.59)	0.5 (0.43-0.55)
DCTN1	C2	101	63	0.56 (0.48-0.63)	0.69 (0.55-0.8)	0.62 (0.55-0.69)	0.52 (0.5-0.55)	0.47 (0.32-0.68)	0.5 (0.42-0.6)
IL15	PZP	101	63	0.56 (0.44-0.65)	0.6 (0.48-0.71)	0.57 (0.49-0.65)	0.54 (0.5-0.56)	0.45 (0.34-0.61)	0.5 (0.43-0.58)
ITGA6	CXCL9	101	63	0.67 (0.59-0.75)	0.64 (0.52-0.77)	0.66 (0.58-0.73)	0.49 (0.37-0.64)	0.46 (0.43-0.63)	0.5 (0.42-0.59)
ITGA11	PLXNA4	102	63	0.63 (0.51-0.71)	0.62 (0.49-0.76)	0.62 (0.54-0.7)	0.51 (0.37-0.61)	0.49 (0.39-0.61)	0.5 (0.39-0.57)
DCTN1	C8A	101	63	0.58 (0.49-0.66)	0.69 (0.57-0.8)	0.64 (0.56-0.71)	0.52 (0.48-0.57)	0.47 (0.32-0.65)	0.5 (0.42-0.58)
ITIH3	CPN2	102	67	0.59 (0.5-0.67)	0.62 (0.52-0.73)	0.6 (0.53-0.67)	0.5 (0.42-0.58)	0.48 (0.4-0.57)	0.5 (0.43-0.56)
FCRL6	PZP	100	63	0.56 (0.48-0.65)	0.63 (0.5-0.74)	0.59 (0.52-0.67)	0.51 (0.46-0.54)	0.48 (0.34-0.65)	0.49 (0.42-0.58)
IL6_PEA_IR	VTN	101	63	0.57 (0.48-0.67)	0.62 (0.51-0.74)	0.6 (0.53-0.68)	0.52 (0.43-0.59)	0.48 (0.4-0.61)	0.49 (0.43-0.58)
IL17F	IL13	102	63	0.56 (0.44-0.64)	0.53 (0.37-0.7)	0.54 (0.45-0.63)	0.45 (0.44-0.56)	0.54 (0.45-0.56)	0.49 (0.45-0.55)
IL7	SAA1	102	63	0.59 (0.51-0.68)	0.6 (0.49-0.73)	0.6 (0.52-0.67)	0.5 (0.41-0.59)	0.49 (0.42-0.58)	0.49 (0.44-0.56)
PLXNA4	IL7	101	63	0.55 (0.47-0.64)	0.65 (0.53-0.77)	0.61 (0.53-0.67)	0.52 (0.46-0.53)	0.48 (0.36-0.62)	0.49 (0.43-0.57)

LAMP3	ITGA6	102	63	0.6 (0.49-0.69)	0.67 (0.54-0.77)	0.63 (0.55-0.7)	0.51 (0.47-0.58)	0.47 (0.35-0.65)	0.49 (0.42-0.59)
IL6_PEA_IR	CP	101	63	0.58 (0.48-0.68)	0.66 (0.5-0.78)	0.62 (0.53-0.69)	0.54 (0.42-0.59)	0.46 (0.34-0.67)	0.49 (0.4-0.61)
VEGFA	CLU	102	63	0.54 (0.45-0.64)	0.57 (0.49-0.67)	0.56 (0.5-0.63)	0.49 (0.45-0.54)	0.47 (0.46-0.54)	0.49 (0.46-0.53)
IL6_PEA_IR	PZP	100	63	0.6 (0.48-0.7)	0.59 (0.45-0.72)	0.59 (0.51-0.67)	0.53 (0.4-0.6)	0.47 (0.38-0.61)	0.49 (0.4-0.57)
IL13	CXCL9	102	63	0.66 (0.58-0.75)	0.56 (0.42-0.69)	0.61 (0.53-0.69)	0.43 (0.35-0.67)	0.56 (0.5-0.56)	0.49 (0.43-0.61)
PLXNA4	C9	101	63	0.61 (0.52-0.71)	0.64 (0.51-0.79)	0.63 (0.55-0.72)	0.46 (0.4-0.61)	0.52 (0.37-0.6)	0.49 (0.41-0.58)
IL6_PEA_IR	SH2D1A	102	63	0.58 (0.47-0.67)	0.57 (0.47-0.68)	0.58 (0.5-0.65)	0.48 (0.42-0.59)	0.51 (0.46-0.54)	0.49 (0.45-0.55)
FC	MILR1	76	43	0.73 (0.62-0.8)	0.59 (0.48-0.72)	0.66 (0.59-0.74)	0.47 (0.28-0.73)	0.52 (0.5-0.53)	0.49 (0.4-0.62)
C9	C8A	102	67	0.61 (0.52-0.71)	0.58 (0.5-0.67)	0.6 (0.52-0.66)	0.48 (0.39-0.61)	0.51 (0.47-0.53)	0.49 (0.44-0.56)
HGF	VTN	102	63	0.55 (0.48-0.64)	0.63 (0.52-0.74)	0.59 (0.53-0.66)	0.5 (0.48-0.53)	0.49 (0.38-0.62)	0.49 (0.44-0.57)
HSD11B1	IL7	101	63	0.56 (0.49-0.64)	0.62 (0.52-0.72)	0.59 (0.53-0.65)	0.52 (0.46-0.54)	0.48 (0.4-0.59)	0.49 (0.44-0.55)
IL7	CXCL9	102	63	0.69 (0.6-0.77)	0.59 (0.47-0.71)	0.64 (0.57-0.72)	0.48 (0.3-0.7)	0.51 (0.46-0.54)	0.49 (0.4-0.6)
ITGA6	CFB	101	63	0.58 (0.5-0.66)	0.68 (0.56-0.78)	0.63 (0.56-0.69)	0.51 (0.47-0.55)	0.49 (0.36-0.66)	0.49 (0.42-0.59)
KLRD1	IL7	101	63	0.6 (0.5-0.68)	0.6 (0.5-0.7)	0.6 (0.52-0.67)	0.52 (0.41-0.59)	0.46 (0.43-0.56)	0.49 (0.43-0.56)
ITGA6	C3	101	63	0.59 (0.5-0.67)	0.66 (0.53-0.78)	0.62 (0.54-0.7)	0.51 (0.46-0.56)	0.48 (0.37-0.63)	0.49 (0.44-0.58)
CDSN	C9	101	63	0.61 (0.52-0.72)	0.6 (0.51-0.71)	0.61 (0.54-0.68)	0.46 (0.39-0.6)	0.53 (0.44-0.57)	0.49 (0.44-0.57)
IL7	SERPINA3	102	63	0.58 (0.5-0.68)	0.6 (0.5-0.72)	0.59 (0.52-0.67)	0.49 (0.43-0.57)	0.47 (0.43-0.58)	0.49 (0.44-0.56)
LAMP3	CPN2	101	63	0.59 (0.49-0.68)	0.64 (0.54-0.73)	0.61 (0.54-0.68)	0.52 (0.46-0.6)	0.45 (0.38-0.62)	0.49 (0.44-0.58)
IL6_PEA_cytokine	CCL4	102	63	0.54 (0.41-0.67)	0.57 (0.44-0.7)	0.55 (0.48-0.64)	0.46 (0.4-0.6)	0.51 (0.44-0.56)	0.49 (0.43-0.58)
FC	ITGA6	76	43	0.67 (0.58-0.76)	0.63 (0.5-0.77)	0.66 (0.56-0.74)	0.47 (0.37-0.62)	0.49 (0.47-0.63)	0.49 (0.43-0.58)
C2	PZP	101	67	0.56 (0.48-0.65)	0.59 (0.43-0.75)	0.58 (0.49-0.67)	0.5 (0.45-0.55)	0.47 (0.37-0.63)	0.49 (0.41-0.57)
TNF	PZP	101	63	0.56 (0.48-0.65)	0.59 (0.45-0.73)	0.58 (0.5-0.66)	0.5 (0.46-0.54)	0.48 (0.37-0.61)	0.49 (0.43-0.56)
C9	C3	102	67	0.61 (0.52-0.71)	0.6 (0.5-0.74)	0.61 (0.54-0.68)	0.47 (0.39-0.6)	0.51 (0.42-0.57)	0.49 (0.43-0.56)
SERPINA3	VTN	102	67	0.58 (0.5-0.67)	0.63 (0.52-0.74)	0.6 (0.54-0.67)	0.51 (0.45-0.56)	0.49 (0.4-0.61)	0.49 (0.43-0.57)
IL17F	VEGFA	102	63	0.55 (0.47-0.65)	0.56 (0.43-0.71)	0.56 (0.48-0.64)	0.46 (0.44-0.55)	0.51 (0.47-0.55)	0.49 (0.46-0.54)
HGF	CCL4	102	63	0.56 (0.46-0.66)	0.58 (0.47-0.7)	0.57 (0.5-0.65)	0.49 (0.41-0.59)	0.5 (0.43-0.57)	0.49 (0.43-0.57)
IL17C	C2	102	63	0.59 (0.5-0.67)	0.57 (0.45-0.72)	0.58 (0.5-0.66)	0.45 (0.41-0.58)	0.52 (0.44-0.58)	0.49 (0.44-0.56)
FCRL6	C9	101	63	0.61 (0.52-0.71)	0.61 (0.5-0.73)	0.61 (0.54-0.69)	0.47 (0.4-0.61)	0.49 (0.41-0.6)	0.49 (0.43-0.57)
SH2D1A	VEGFA	101	63	0.55 (0.46-0.64)	0.58 (0.48-0.68)	0.56 (0.5-0.63)	0.47 (0.45-0.54)	0.51 (0.45-0.55)	0.49 (0.46-0.53)
C9	ITIH1	102	67	0.61 (0.52-0.72)	0.6 (0.5-0.7)	0.6 (0.54-0.67)	0.46 (0.4-0.59)	0.49 (0.42-0.58)	0.49 (0.43-0.56)

ITGA6	ITIH1	101	63	0.57 (0.5-0.66)	0.7 (0.6-0.79)	0.64 (0.57-0.7)	0.49 (0.47-0.5)	0.49 (0.31-0.66)	0.49 (0.4-0.58)
KLRD1	ITGA6	102	63	0.62 (0.52-0.69)	0.63 (0.52-0.75)	0.62 (0.55-0.69)	0.5 (0.4-0.57)	0.48 (0.39-0.61)	0.49 (0.43-0.56)
IL7	SERPINA4	102	63	0.61 (0.52-0.69)	0.6 (0.51-0.71)	0.6 (0.54-0.67)	0.51 (0.4-0.6)	0.47 (0.44-0.54)	0.49 (0.43-0.54)
SH2D1A	IL17F	101	63	0.55 (0.47-0.63)	0.57 (0.43-0.72)	0.57 (0.48-0.64)	0.46 (0.44-0.54)	0.51 (0.45-0.56)	0.49 (0.45-0.54)
ITGA11	VTN	101	63	0.63 (0.51-0.71)	0.62 (0.51-0.73)	0.62 (0.54-0.69)	0.49 (0.4-0.61)	0.49 (0.39-0.6)	0.49 (0.41-0.59)
CCL4	VTN	102	63	0.56 (0.46-0.65)	0.61 (0.5-0.72)	0.58 (0.52-0.66)	0.5 (0.43-0.55)	0.47 (0.39-0.61)	0.49 (0.43-0.57)
FGF2	CPN2	101	63	0.55 (0.48-0.64)	0.67 (0.5-0.78)	0.61 (0.53-0.68)	0.52 (0.47-0.53)	0.47 (0.34-0.66)	0.49 (0.42-0.59)
CPN2	ITIH1	102	67	0.57 (0.49-0.65)	0.62 (0.52-0.73)	0.6 (0.54-0.66)	0.49 (0.45-0.54)	0.48 (0.4-0.57)	0.49 (0.44-0.54)
IL6_PEA_cytokine	VTN	102	63	0.55 (0.46-0.64)	0.62 (0.48-0.75)	0.58 (0.51-0.65)	0.5 (0.46-0.58)	0.43 (0.39-0.62)	0.49 (0.44-0.58)
IL17C	ITIH2	102	63	0.59 (0.5-0.68)	0.59 (0.48-0.69)	0.59 (0.52-0.65)	0.47 (0.41-0.58)	0.52 (0.43-0.56)	0.49 (0.43-0.55)
SH2D1A	IL17C	101	63	0.58 (0.51-0.68)	0.57 (0.46-0.68)	0.58 (0.51-0.65)	0.46 (0.41-0.59)	0.51 (0.47-0.53)	0.49 (0.45-0.55)
IFNG	CPN2	102	63	0.69 (0.59-0.77)	0.63 (0.48-0.75)	0.66 (0.57-0.73)	0.42 (0.33-0.67)	0.55 (0.41-0.63)	0.49 (0.4-0.62)
IL13	VTN	102	63	0.54 (0.46-0.62)	0.62 (0.48-0.73)	0.58 (0.5-0.65)	0.51 (0.47-0.53)	0.46 (0.38-0.62)	0.49 (0.44-0.57)
APOA1	MBL2	102	67	0.63 (0.54-0.71)	0.6 (0.51-0.72)	0.62 (0.55-0.69)	0.48 (0.37-0.63)	0.5 (0.42-0.55)	0.49 (0.42-0.57)
HSD11B1	CPN2	101	63	0.56 (0.49-0.65)	0.62 (0.51-0.73)	0.59 (0.53-0.66)	0.5 (0.47-0.54)	0.47 (0.38-0.58)	0.49 (0.43-0.55)
ITIH2	CLU	102	67	0.55 (0.48-0.63)	0.59 (0.5-0.7)	0.57 (0.52-0.64)	0.51 (0.48-0.52)	0.46 (0.43-0.56)	0.49 (0.46-0.54)
IL13	CCL4	102	63	0.55 (0.43-0.66)	0.58 (0.45-0.7)	0.56 (0.48-0.64)	0.45 (0.43-0.57)	0.49 (0.43-0.58)	0.49 (0.44-0.56)
IL7	IFNG	102	63	0.7 (0.61-0.78)	0.6 (0.46-0.72)	0.65 (0.56-0.72)	0.46 (0.3-0.7)	0.51 (0.44-0.61)	0.49 (0.39-0.62)
IL13	CP	102	63	0.54 (0.45-0.64)	0.66 (0.46-0.79)	0.6 (0.49-0.68)	0.54 (0.45-0.56)	0.43 (0.34-0.67)	0.49 (0.42-0.61)
CPN2	VTN	102	67	0.57 (0.49-0.66)	0.62 (0.52-0.73)	0.6 (0.54-0.67)	0.5 (0.46-0.56)	0.47 (0.4-0.56)	0.49 (0.44-0.55)
DCTN1	IL17F	101	63	0.55 (0.47-0.63)	0.7 (0.56-0.81)	0.62 (0.55-0.69)	0.51 (0.5-0.55)	0.46 (0.32-0.68)	0.49 (0.41-0.6)
SERPINA3	MBL2	102	67	0.58 (0.5-0.67)	0.61 (0.5-0.73)	0.6 (0.53-0.66)	0.48 (0.43-0.57)	0.48 (0.41-0.59)	0.49 (0.43-0.55)
ITIH1	PZP	101	67	0.55 (0.47-0.63)	0.61 (0.5-0.72)	0.58 (0.51-0.65)	0.5 (0.49-0.51)	0.47 (0.37-0.62)	0.49 (0.43-0.56)
KLRD1	CPN2	101	63	0.6 (0.51-0.68)	0.63 (0.53-0.74)	0.62 (0.55-0.69)	0.5 (0.4-0.6)	0.46 (0.4-0.6)	0.49 (0.42-0.56)
MBL2	C8A	102	67	0.6 (0.51-0.68)	0.6 (0.5-0.73)	0.6 (0.52-0.67)	0.49 (0.41-0.59)	0.48 (0.42-0.56)	0.49 (0.43-0.54)
CCL4	CLU	102	63	0.56 (0.45-0.65)	0.58 (0.5-0.69)	0.57 (0.5-0.64)	0.49 (0.42-0.57)	0.47 (0.46-0.54)	0.49 (0.45-0.54)
IL7	IL15	102	63	0.55 (0.47-0.65)	0.63 (0.49-0.74)	0.59 (0.51-0.67)	0.52 (0.48-0.57)	0.44 (0.39-0.58)	0.49 (0.45-0.55)
IL7	SERPING1	102	63	0.57 (0.47-0.65)	0.59 (0.48-0.71)	0.58 (0.51-0.66)	0.51 (0.43-0.57)	0.45 (0.43-0.56)	0.49 (0.44-0.54)
C3	MBL2	102	67	0.59 (0.5-0.67)	0.63 (0.51-0.75)	0.61 (0.54-0.69)	0.49 (0.43-0.57)	0.48 (0.38-0.61)	0.48 (0.43-0.56)
DCTN1	CP	101	63	0.55 (0.47-0.63)	0.72 (0.6-0.82)	0.64 (0.56-0.7)	0.54 (0.51-0.55)	0.43 (0.27-0.73)	0.48 (0.4-0.63)

CCL4	ITIH2	102	63	0.56 (0.46-0.65)	0.59 (0.5-0.7)	0.58 (0.51-0.64)	0.47 (0.42-0.57)	0.48 (0.43-0.57)	0.48 (0.44-0.54)
CCL13	C9	102	63	0.6 (0.51-0.72)	0.6 (0.5-0.72)	0.6 (0.53-0.68)	0.45 (0.37-0.62)	0.51 (0.43-0.56)	0.48 (0.41-0.57)
IL6_PEA_cytokine	IL13	102	63	0.56 (0.4-0.66)	0.55 (0.37-0.7)	0.55 (0.44-0.64)	0.44 (0.41-0.59)	0.52 (0.46-0.55)	0.48 (0.45-0.56)
SH2D1A	CCL4	101	63	0.56 (0.44-0.66)	0.58 (0.47-0.7)	0.57 (0.49-0.64)	0.47 (0.42-0.57)	0.5 (0.45-0.56)	0.48 (0.45-0.53)
IL7	C4BPB	102	63	0.59 (0.49-0.68)	0.61 (0.49-0.72)	0.6 (0.53-0.68)	0.51 (0.42-0.58)	0.44 (0.42-0.57)	0.48 (0.42-0.55)
DCTN1	IL17C	101	63	0.58 (0.5-0.68)	0.69 (0.55-0.81)	0.64 (0.56-0.72)	0.5 (0.46-0.56)	0.46 (0.32-0.68)	0.48 (0.4-0.59)
SERPIND1	PZP	101	67	0.55 (0.47-0.64)	0.64 (0.53-0.75)	0.6 (0.53-0.66)	0.52 (0.5-0.53)	0.45 (0.36-0.64)	0.48 (0.44-0.58)
CCL13	CPN2	102	63	0.57 (0.49-0.66)	0.62 (0.51-0.73)	0.59 (0.52-0.66)	0.48 (0.45-0.56)	0.48 (0.39-0.57)	0.48 (0.43-0.54)
PZP	VTN	101	67	0.55 (0.48-0.64)	0.62 (0.5-0.73)	0.59 (0.52-0.65)	0.5 (0.48-0.52)	0.46 (0.37-0.62)	0.48 (0.43-0.56)
CCL4	VEGFA	102	63	0.56 (0.44-0.66)	0.57 (0.47-0.68)	0.56 (0.48-0.64)	0.47 (0.41-0.58)	0.49 (0.47-0.53)	0.48 (0.45-0.54)
IL17C	CLU	102	63	0.59 (0.5-0.68)	0.57 (0.48-0.69)	0.58 (0.51-0.65)	0.46 (0.4-0.58)	0.51 (0.45-0.53)	0.48 (0.43-0.54)
CLEC4C	IL7	101	63	0.56 (0.48-0.64)	0.61 (0.5-0.75)	0.59 (0.52-0.67)	0.5 (0.46-0.54)	0.45 (0.42-0.62)	0.48 (0.45-0.57)
IL10_PEA_IR	MBL2	101	63	0.58 (0.49-0.68)	0.64 (0.48-0.75)	0.61 (0.52-0.68)	0.45 (0.43-0.55)	0.5 (0.39-0.61)	0.48 (0.41-0.54)
IL7	C8A	102	63	0.59 (0.5-0.68)	0.59 (0.5-0.7)	0.59 (0.52-0.66)	0.5 (0.41-0.59)	0.46 (0.42-0.54)	0.48 (0.42-0.54)
DCTN1	CCL13	101	63	0.55 (0.47-0.64)	0.69 (0.57-0.81)	0.62 (0.55-0.69)	0.52 (0.51-0.54)	0.45 (0.32-0.67)	0.48 (0.42-0.6)
DCTN1	FCRL6	102	63	0.55 (0.49-0.62)	0.71 (0.57-0.83)	0.63 (0.55-0.7)	0.51 (0.51-0.52)	0.45 (0.3-0.7)	0.48 (0.41-0.61)
IL6_PEA_cytokine	CP	102	63	0.55 (0.44-0.64)	0.66 (0.47-0.79)	0.6 (0.5-0.68)	0.53 (0.44-0.58)	0.41 (0.32-0.69)	0.48 (0.42-0.62)
IL6_PEA_IR	IL7	101	63	0.58 (0.48-0.69)	0.59 (0.47-0.7)	0.59 (0.51-0.66)	0.49 (0.4-0.6)	0.47 (0.43-0.52)	0.48 (0.42-0.55)
ITGA6	CDSN	102	63	0.56 (0.49-0.64)	0.63 (0.52-0.74)	0.6 (0.53-0.66)	0.48 (0.46-0.51)	0.48 (0.39-0.6)	0.48 (0.43-0.54)
IL17F	CCL4	102	63	0.57 (0.45-0.67)	0.57 (0.43-0.71)	0.57 (0.48-0.65)	0.44 (0.41-0.58)	0.51 (0.45-0.56)	0.48 (0.43-0.56)
C9	SERPING1	102	67	0.6 (0.52-0.7)	0.59 (0.47-0.7)	0.59 (0.52-0.67)	0.47 (0.39-0.61)	0.48 (0.43-0.55)	0.48 (0.43-0.56)
DCTN1	CLU	101	63	0.55 (0.47-0.62)	0.7 (0.56-0.81)	0.62 (0.55-0.69)	0.52 (0.51-0.52)	0.44 (0.32-0.68)	0.48 (0.42-0.6)
ITGA6	HSD11B1	102	63	0.57 (0.51-0.66)	0.65 (0.54-0.75)	0.61 (0.55-0.68)	0.49 (0.44-0.54)	0.46 (0.38-0.63)	0.48 (0.42-0.57)
C2	VTN	102	67	0.56 (0.5-0.65)	0.62 (0.5-0.73)	0.59 (0.53-0.66)	0.49 (0.45-0.55)	0.46 (0.39-0.61)	0.48 (0.43-0.56)
ITGA11	IL7	101	63	0.63 (0.51-0.71)	0.59 (0.48-0.7)	0.61 (0.53-0.68)	0.5 (0.37-0.63)	0.45 (0.44-0.54)	0.48 (0.41-0.56)
CPN2	SERPING1	102	67	0.56 (0.48-0.64)	0.6 (0.48-0.72)	0.58 (0.51-0.65)	0.48 (0.46-0.55)	0.46 (0.41-0.57)	0.48 (0.44-0.55)
CXCL9	CPN2	102	63	0.67 (0.59-0.75)	0.62 (0.5-0.74)	0.65 (0.57-0.71)	0.46 (0.34-0.67)	0.48 (0.44-0.59)	0.48 (0.41-0.59)
IL7	TNF	102	63	0.56 (0.49-0.63)	0.59 (0.5-0.71)	0.58 (0.52-0.65)	0.48 (0.45-0.55)	0.46 (0.43-0.56)	0.48 (0.44-0.53)
IL7	CP	102	63	0.55 (0.48-0.63)	0.66 (0.54-0.79)	0.61 (0.53-0.68)	0.5 (0.47-0.55)	0.44 (0.34-0.66)	0.48 (0.42-0.57)
KLRD1	FCRL6	102	63	0.62 (0.54-0.71)	0.62 (0.51-0.72)	0.62 (0.55-0.69)	0.48 (0.38-0.59)	0.47 (0.4-0.55)	0.48 (0.41-0.55)

DCTN1	SAA1	101	63	0.58 (0.51-0.67)	0.7 (0.58-0.82)	0.64 (0.56-0.72)	0.52 (0.43-0.56)	0.44 (0.31-0.69)	0.48 (0.41-0.61)
DCTN1	SH2D1A	102	63	0.55 (0.47-0.63)	0.7 (0.59-0.81)	0.62 (0.56-0.7)	0.51 (0.51-0.52)	0.44 (0.31-0.69)	0.48 (0.41-0.6)
DCTN1	ITIH2	101	63	0.55 (0.49-0.63)	0.69 (0.57-0.81)	0.62 (0.56-0.69)	0.52 (0.5-0.52)	0.44 (0.32-0.68)	0.48 (0.42-0.6)
IL6_PEA_cytokine	PZP	101	63	0.58 (0.45-0.67)	0.58 (0.38-0.73)	0.57 (0.47-0.67)	0.48 (0.41-0.6)	0.47 (0.38-0.62)	0.48 (0.4-0.58)
CDSN	IL7	101	63	0.57 (0.48-0.64)	0.6 (0.5-0.73)	0.58 (0.51-0.66)	0.49 (0.46-0.53)	0.46 (0.42-0.58)	0.48 (0.45-0.54)
CPN2	C8A	102	67	0.6 (0.51-0.68)	0.61 (0.51-0.72)	0.61 (0.54-0.67)	0.47 (0.41-0.59)	0.48 (0.42-0.52)	0.48 (0.43-0.54)
IL6_PEA_IR	ITGA6	102	63	0.58 (0.49-0.67)	0.63 (0.5-0.74)	0.6 (0.53-0.68)	0.49 (0.41-0.56)	0.46 (0.39-0.61)	0.48 (0.42-0.55)
SERPINA3	CPN2	102	67	0.59 (0.5-0.68)	0.62 (0.5-0.74)	0.6 (0.53-0.68)	0.49 (0.42-0.57)	0.46 (0.4-0.58)	0.48 (0.42-0.56)
CDSN	CPN2	101	63	0.55 (0.48-0.63)	0.62 (0.51-0.74)	0.59 (0.52-0.65)	0.49 (0.48-0.52)	0.47 (0.39-0.59)	0.48 (0.44-0.54)
FGF2	MBL2	101	63	0.57 (0.5-0.66)	0.7 (0.54-0.83)	0.64 (0.55-0.71)	0.5 (0.44-0.53)	0.46 (0.32-0.69)	0.48 (0.4-0.59)
CPN2	C4BPB	102	67	0.6 (0.5-0.69)	0.61 (0.51-0.71)	0.6 (0.53-0.68)	0.49 (0.41-0.59)	0.46 (0.41-0.52)	0.48 (0.43-0.53)
LAMP3	MBL2	101	63	0.59 (0.5-0.69)	0.67 (0.57-0.79)	0.63 (0.56-0.71)	0.49 (0.45-0.58)	0.46 (0.33-0.67)	0.48 (0.4-0.59)
HGF	IL17C	102	63	0.61 (0.51-0.7)	0.57 (0.44-0.69)	0.59 (0.52-0.67)	0.44 (0.39-0.61)	0.52 (0.45-0.53)	0.48 (0.44-0.56)
IL7	CCL13	102	63	0.57 (0.48-0.66)	0.62 (0.52-0.73)	0.59 (0.53-0.66)	0.5 (0.46-0.55)	0.43 (0.4-0.58)	0.48 (0.44-0.55)
IL7	IL13	102	63	0.54 (0.45-0.63)	0.59 (0.46-0.72)	0.57 (0.49-0.64)	0.49 (0.48-0.53)	0.46 (0.42-0.56)	0.48 (0.45-0.52)
MBL2	C4BPB	102	67	0.6 (0.51-0.69)	0.61 (0.51-0.73)	0.6 (0.54-0.68)	0.48 (0.4-0.6)	0.47 (0.41-0.57)	0.48 (0.42-0.55)
C9	SERPINA3	102	67	0.61 (0.53-0.7)	0.59 (0.49-0.71)	0.6 (0.53-0.67)	0.46 (0.39-0.6)	0.48 (0.43-0.57)	0.48 (0.42-0.56)
IL13	IFNG	102	63	0.7 (0.62-0.77)	0.53 (0.38-0.73)	0.62 (0.53-0.72)	0.34 (0.32-0.7)	0.62 (0.54-0.62)	0.48 (0.43-0.66)
TNF	C9	102	63	0.6 (0.51-0.7)	0.57 (0.49-0.67)	0.59 (0.52-0.65)	0.44 (0.4-0.6)	0.51 (0.48-0.53)	0.48 (0.44-0.56)
SERPING1	PZP	101	67	0.55 (0.46-0.63)	0.6 (0.47-0.72)	0.57 (0.49-0.65)	0.52 (0.46-0.54)	0.42 (0.37-0.61)	0.48 (0.42-0.56)
ITGA11	MBL2	101	63	0.63 (0.52-0.71)	0.65 (0.52-0.77)	0.64 (0.55-0.71)	0.5 (0.38-0.6)	0.44 (0.38-0.63)	0.48 (0.4-0.58)
ITGA6	C8A	101	63	0.6 (0.51-0.69)	0.64 (0.53-0.75)	0.62 (0.54-0.69)	0.48 (0.41-0.55)	0.47 (0.39-0.61)	0.47 (0.43-0.55)
IL6_PEA_IR	C9	101	63	0.62 (0.52-0.73)	0.58 (0.47-0.69)	0.6 (0.52-0.67)	0.46 (0.37-0.63)	0.49 (0.46-0.5)	0.47 (0.42-0.56)
SH2D1A	PZP	100	63	0.55 (0.47-0.65)	0.59 (0.47-0.71)	0.57 (0.5-0.64)	0.48 (0.46-0.52)	0.47 (0.36-0.59)	0.47 (0.42-0.54)
ITGA6	SERPIND1	101	63	0.57 (0.49-0.65)	0.71 (0.59-0.81)	0.64 (0.57-0.7)	0.49 (0.48-0.51)	0.45 (0.31-0.69)	0.47 (0.4-0.59)
TNF	IL17C	102	63	0.6 (0.5-0.68)	0.56 (0.46-0.68)	0.58 (0.51-0.65)	0.43 (0.41-0.59)	0.51 (0.48-0.53)	0.47 (0.45-0.55)
IL7	ITIH1	102	63	0.56 (0.48-0.65)	0.63 (0.52-0.74)	0.6 (0.53-0.66)	0.48 (0.46-0.53)	0.46 (0.39-0.61)	0.47 (0.43-0.55)
DCTN1	IL7	101	63	0.55 (0.47-0.63)	0.7 (0.59-0.81)	0.63 (0.56-0.69)	0.51 (0.48-0.52)	0.44 (0.32-0.67)	0.47 (0.42-0.59)
IL6_PEA_IR	IL17C	101	63	0.62 (0.52-0.71)	0.58 (0.47-0.69)	0.6 (0.52-0.67)	0.44 (0.38-0.62)	0.5 (0.47-0.53)	0.47 (0.43-0.56)
SH2D1A	C9	101	63	0.62 (0.52-0.71)	0.58 (0.49-0.68)	0.6 (0.53-0.66)	0.45 (0.39-0.61)	0.5 (0.47-0.52)	0.47 (0.43-0.55)

PLXNA4	CPN2	101	63	0.56 (0.48-0.63)	0.64 (0.51-0.76)	0.6 (0.52-0.67)	0.51 (0.46-0.52)	0.43 (0.37-0.62)	0.47 (0.42-0.56)
IL13	IL17C	102	63	0.6 (0.49-0.69)	0.57 (0.44-0.69)	0.58 (0.5-0.66)	0.42 (0.41-0.6)	0.53 (0.47-0.54)	0.47 (0.44-0.56)
C9	ITIH2	102	67	0.61 (0.52-0.71)	0.58 (0.49-0.67)	0.59 (0.53-0.66)	0.44 (0.4-0.6)	0.49 (0.44-0.54)	0.47 (0.43-0.55)
IL17C	PZP	101	63	0.59 (0.48-0.68)	0.56 (0.42-0.71)	0.58 (0.49-0.66)	0.43 (0.41-0.58)	0.49 (0.4-0.59)	0.47 (0.41-0.56)
KLRD1	MBL2	101	63	0.61 (0.52-0.7)	0.63 (0.52-0.75)	0.62 (0.55-0.69)	0.47 (0.4-0.58)	0.48 (0.39-0.58)	0.47 (0.42-0.54)
ITGA6	IL15	101	63	0.56 (0.48-0.66)	0.63 (0.51-0.73)	0.6 (0.52-0.67)	0.47 (0.46-0.57)	0.46 (0.38-0.61)	0.47 (0.42-0.54)
DCTN1	VTN	101	63	0.55 (0.49-0.64)	0.71 (0.58-0.82)	0.63 (0.56-0.7)	0.52 (0.51-0.52)	0.43 (0.3-0.69)	0.47 (0.41-0.6)
MASP1	MBL2	101	63	0.63 (0.52-0.72)	0.64 (0.52-0.77)	0.63 (0.56-0.72)	0.47 (0.37-0.59)	0.48 (0.39-0.61)	0.47 (0.39-0.56)
C3	CPN2	102	67	0.59 (0.51-0.68)	0.63 (0.5-0.74)	0.61 (0.53-0.68)	0.52 (0.42-0.59)	0.43 (0.4-0.52)	0.47 (0.42-0.53)
C9	MBL2	102	67	0.6 (0.5-0.7)	0.61 (0.5-0.72)	0.6 (0.53-0.68)	0.46 (0.4-0.6)	0.48 (0.43-0.57)	0.47 (0.42-0.55)
IL17F	PZP	101	63	0.56 (0.46-0.65)	0.56 (0.4-0.73)	0.56 (0.47-0.65)	0.46 (0.44-0.55)	0.45 (0.4-0.59)	0.47 (0.43-0.55)
HGF	PZP	101	63	0.55 (0.46-0.64)	0.59 (0.44-0.73)	0.57 (0.47-0.66)	0.5 (0.46-0.54)	0.43 (0.39-0.59)	0.47 (0.44-0.55)
C9	SERPIND1	102	67	0.61 (0.52-0.71)	0.66 (0.56-0.77)	0.63 (0.56-0.7)	0.47 (0.41-0.59)	0.46 (0.36-0.63)	0.47 (0.4-0.57)
DCTN1	C9	101	63	0.61 (0.51-0.71)	0.69 (0.56-0.81)	0.65 (0.57-0.72)	0.5 (0.41-0.56)	0.43 (0.33-0.65)	0.47 (0.39-0.58)
IL13	CPN2	102	63	0.55 (0.46-0.63)	0.62 (0.48-0.74)	0.58 (0.51-0.66)	0.49 (0.47-0.53)	0.45 (0.38-0.61)	0.47 (0.43-0.55)
DCTN1	PLXNA4	102	63	0.55 (0.47-0.63)	0.7 (0.57-0.81)	0.62 (0.55-0.69)	0.51 (0.51-0.53)	0.43 (0.32-0.68)	0.47 (0.41-0.6)
C9	C2	102	67	0.61 (0.52-0.71)	0.59 (0.47-0.72)	0.6 (0.52-0.68)	0.44 (0.4-0.6)	0.5 (0.43-0.56)	0.47 (0.43-0.56)
ITIH2	PZP	101	67	0.56 (0.48-0.64)	0.59 (0.47-0.72)	0.57 (0.5-0.65)	0.49 (0.47-0.52)	0.44 (0.38-0.6)	0.47 (0.43-0.55)
IL15	CPN2	102	63	0.56 (0.47-0.67)	0.65 (0.53-0.76)	0.6 (0.53-0.68)	0.51 (0.48-0.57)	0.41 (0.35-0.58)	0.47 (0.43-0.55)
HGF	C9	102	63	0.61 (0.52-0.72)	0.58 (0.48-0.69)	0.59 (0.52-0.67)	0.44 (0.39-0.61)	0.5 (0.46-0.53)	0.47 (0.43-0.55)
CLEC4C	MBL2	101	63	0.58 (0.51-0.67)	0.66 (0.53-0.78)	0.62 (0.54-0.69)	0.46 (0.44-0.55)	0.47 (0.34-0.66)	0.47 (0.4-0.57)
IL17F	IL17C	102	63	0.6 (0.5-0.68)	0.57 (0.43-0.72)	0.59 (0.5-0.67)	0.42 (0.4-0.57)	0.5 (0.45-0.56)	0.47 (0.43-0.54)
VEGFA	IL17C	102	63	0.6 (0.5-0.68)	0.57 (0.46-0.68)	0.58 (0.5-0.65)	0.42 (0.4-0.6)	0.51 (0.48-0.53)	0.47 (0.44-0.55)
HGF	IL7	102	63	0.56 (0.48-0.64)	0.58 (0.47-0.7)	0.57 (0.5-0.65)	0.48 (0.45-0.55)	0.44 (0.42-0.54)	0.47 (0.44-0.52)
IL7	C2	102	63	0.56 (0.48-0.64)	0.59 (0.48-0.72)	0.58 (0.51-0.66)	0.48 (0.45-0.55)	0.44 (0.42-0.57)	0.47 (0.44-0.53)
IL13	PZP	101	63	0.54 (0.45-0.62)	0.61 (0.39-0.76)	0.57 (0.46-0.66)	0.49 (0.48-0.53)	0.45 (0.36-0.64)	0.47 (0.42-0.58)
CLEC4C	ITGA6	102	63	0.57 (0.51-0.65)	0.65 (0.52-0.77)	0.61 (0.54-0.68)	0.49 (0.44-0.54)	0.44 (0.36-0.64)	0.47 (0.42-0.57)
DCTN1	FGF2	102	63	0.56 (0.49-0.65)	0.7 (0.55-0.82)	0.63 (0.55-0.71)	0.51 (0.47-0.53)	0.44 (0.29-0.71)	0.47 (0.39-0.61)
IL6_PEA_cytokine	IL7	102	63	0.57 (0.48-0.67)	0.58 (0.46-0.7)	0.58 (0.5-0.65)	0.47 (0.41-0.61)	0.44 (0.43-0.54)	0.47 (0.43-0.54)
CLEC4C	CPN2	101	63	0.57 (0.5-0.65)	0.64 (0.53-0.75)	0.6 (0.54-0.67)	0.49 (0.45-0.56)	0.41 (0.38-0.63)	0.47 (0.42-0.56)

ITIH1	MBL2	102	67	0.57 (0.49-0.66)	0.63 (0.52-0.76)	0.6 (0.53-0.67)	0.45 (0.43-0.54)	0.47 (0.39-0.61)	0.47 (0.41-0.54)
ITGA6	SERPING1	101	63	0.57 (0.5-0.66)	0.65 (0.53-0.76)	0.61 (0.54-0.68)	0.47 (0.45-0.53)	0.46 (0.36-0.63)	0.47 (0.41-0.56)
DCTN1	HGF	101	63	0.55 (0.47-0.64)	0.71 (0.59-0.81)	0.63 (0.56-0.7)	0.53 (0.5-0.54)	0.4 (0.31-0.69)	0.47 (0.41-0.61)
ITGA11	CPN2	101	63	0.63 (0.5-0.71)	0.62 (0.49-0.73)	0.62 (0.54-0.7)	0.49 (0.38-0.62)	0.41 (0.4-0.57)	0.47 (0.39-0.56)
PZP	CLU	101	67	0.55 (0.48-0.64)	0.59 (0.47-0.7)	0.57 (0.5-0.64)	0.5 (0.48-0.52)	0.43 (0.38-0.6)	0.47 (0.44-0.55)
FCRL6	IL7	101	63	0.56 (0.48-0.65)	0.63 (0.52-0.74)	0.6 (0.53-0.67)	0.49 (0.46-0.55)	0.43 (0.38-0.59)	0.46 (0.44-0.54)
ITGA6	SH2D1A	102	63	0.56 (0.49-0.64)	0.64 (0.52-0.75)	0.6 (0.53-0.67)	0.47 (0.46-0.51)	0.45 (0.38-0.61)	0.46 (0.43-0.54)
TNF	CPN2	102	63	0.56 (0.49-0.63)	0.61 (0.51-0.73)	0.59 (0.53-0.66)	0.48 (0.46-0.54)	0.44 (0.4-0.58)	0.46 (0.43-0.53)
IL15	MBL2	102	63	0.57 (0.48-0.67)	0.64 (0.52-0.76)	0.61 (0.53-0.69)	0.48 (0.45-0.57)	0.42 (0.36-0.63)	0.46 (0.41-0.55)
HSD11B1	MBL2	101	63	0.6 (0.51-0.68)	0.64 (0.53-0.74)	0.62 (0.55-0.69)	0.46 (0.41-0.58)	0.46 (0.39-0.61)	0.46 (0.41-0.54)
ITGA6	C9	101	63	0.61 (0.53-0.71)	0.63 (0.52-0.74)	0.62 (0.55-0.69)	0.46 (0.39-0.56)	0.45 (0.4-0.56)	0.46 (0.42-0.54)
IL7	VTN	102	63	0.56 (0.49-0.64)	0.62 (0.53-0.73)	0.59 (0.53-0.66)	0.48 (0.46-0.53)	0.43 (0.4-0.6)	0.46 (0.43-0.54)
SERPINA4	MBL2	102	67	0.63 (0.54-0.72)	0.6 (0.51-0.72)	0.62 (0.55-0.69)	0.45 (0.37-0.62)	0.48 (0.42-0.52)	0.46 (0.41-0.56)
VEGFA	PZP	101	63	0.55 (0.47-0.63)	0.6 (0.43-0.73)	0.57 (0.48-0.65)	0.49 (0.46-0.53)	0.43 (0.39-0.61)	0.46 (0.43-0.55)
CPN2	CLU	102	67	0.56 (0.48-0.64)	0.61 (0.52-0.72)	0.59 (0.52-0.66)	0.49 (0.46-0.54)	0.42 (0.4-0.56)	0.46 (0.44-0.54)
CDSN	MBL2	101	63	0.59 (0.48-0.67)	0.64 (0.53-0.76)	0.61 (0.54-0.69)	0.45 (0.43-0.55)	0.47 (0.39-0.61)	0.46 (0.41-0.53)
DCTN1	IL13	101	63	0.54 (0.45-0.63)	0.69 (0.55-0.81)	0.62 (0.53-0.69)	0.53 (0.51-0.54)	0.4 (0.32-0.69)	0.46 (0.42-0.61)
ITGA6	IL17C	101	63	0.59 (0.51-0.67)	0.62 (0.5-0.74)	0.61 (0.53-0.68)	0.45 (0.43-0.51)	0.47 (0.38-0.59)	0.46 (0.41-0.53)
IL7	CLU	102	63	0.56 (0.48-0.64)	0.6 (0.5-0.72)	0.58 (0.52-0.65)	0.48 (0.47-0.53)	0.43 (0.41-0.55)	0.46 (0.44-0.52)
SH2D1A	IL7	101	63	0.56 (0.48-0.64)	0.58 (0.48-0.7)	0.57 (0.51-0.64)	0.46 (0.45-0.54)	0.45 (0.43-0.54)	0.46 (0.44-0.51)
CCL4	PZP	101	63	0.57 (0.46-0.68)	0.58 (0.45-0.71)	0.58 (0.49-0.65)	0.46 (0.42-0.57)	0.44 (0.38-0.6)	0.46 (0.41-0.55)
SERPING1	MBL2	102	67	0.58 (0.5-0.66)	0.62 (0.5-0.73)	0.6 (0.52-0.67)	0.47 (0.44-0.55)	0.44 (0.4-0.58)	0.46 (0.42-0.54)
FCRL6	ITGA6	102	63	0.57 (0.5-0.65)	0.66 (0.54-0.76)	0.61 (0.55-0.68)	0.48 (0.46-0.51)	0.44 (0.36-0.64)	0.46 (0.42-0.56)
VEGFA	C9	102	63	0.61 (0.51-0.72)	0.57 (0.48-0.67)	0.59 (0.52-0.66)	0.42 (0.39-0.61)	0.5 (0.49-0.52)	0.46 (0.44-0.56)
DCTN1	CCL4	101	63	0.56 (0.47-0.66)	0.69 (0.57-0.81)	0.63 (0.55-0.7)	0.51 (0.47-0.52)	0.41 (0.32-0.68)	0.46 (0.41-0.59)
ITGA6	IL17F	101	63	0.56 (0.49-0.65)	0.63 (0.49-0.75)	0.6 (0.52-0.67)	0.48 (0.44-0.52)	0.45 (0.38-0.61)	0.46 (0.42-0.54)
ITGA6	SERPINA4	101	63	0.61 (0.52-0.69)	0.64 (0.53-0.75)	0.62 (0.54-0.69)	0.46 (0.4-0.57)	0.46 (0.39-0.57)	0.46 (0.41-0.53)
C9	PZP	101	67	0.61 (0.51-0.72)	0.58 (0.44-0.71)	0.6 (0.51-0.68)	0.42 (0.38-0.61)	0.49 (0.39-0.56)	0.46 (0.4-0.56)
ITGA6	ITIH2	101	63	0.57 (0.5-0.66)	0.66 (0.55-0.76)	0.62 (0.55-0.68)	0.47 (0.46-0.47)	0.45 (0.36-0.62)	0.46 (0.41-0.55)
FCRL6	CPN2	101	63	0.56 (0.48-0.64)	0.66 (0.55-0.77)	0.61 (0.55-0.68)	0.49 (0.47-0.52)	0.43 (0.35-0.61)	0.46 (0.42-0.55)

IL6_PEA_IR	DCTN1	102	63	0.58 (0.47-0.67)	0.7 (0.6-0.81)	0.64 (0.57-0.71)	0.52 (0.46-0.57)	0.39 (0.32-0.68)	0.46 (0.41-0.61)
IL13	C9	102	63	0.61 (0.51-0.72)	0.57 (0.47-0.69)	0.59 (0.52-0.67)	0.41 (0.4-0.61)	0.51 (0.45-0.53)	0.46 (0.43-0.56)
C2	MBL2	102	67	0.57 (0.49-0.66)	0.61 (0.49-0.74)	0.59 (0.52-0.67)	0.45 (0.44-0.56)	0.45 (0.41-0.59)	0.46 (0.43-0.53)
FGF2	ITGA6	102	63	0.56 (0.49-0.64)	0.68 (0.52-0.79)	0.62 (0.54-0.69)	0.49 (0.46-0.52)	0.43 (0.33-0.68)	0.46 (0.41-0.59)
DCTN1	CPN2	101	63	0.55 (0.48-0.64)	0.71 (0.6-0.81)	0.63 (0.57-0.7)	0.52 (0.48-0.52)	0.4 (0.32-0.68)	0.46 (0.41-0.6)
ITGA6	IL6_PEA_cytokine	101	63	0.56 (0.47-0.66)	0.63 (0.5-0.75)	0.59 (0.52-0.67)	0.46 (0.45-0.53)	0.44 (0.39-0.61)	0.46 (0.42-0.55)
DCTN1	VEGFA	101	63	0.55 (0.46-0.65)	0.69 (0.57-0.8)	0.62 (0.54-0.69)	0.51 (0.48-0.54)	0.39 (0.32-0.68)	0.46 (0.41-0.6)
SH2D1A	CPN2	101	63	0.55 (0.47-0.63)	0.61 (0.51-0.72)	0.58 (0.52-0.65)	0.48 (0.47-0.51)	0.43 (0.4-0.56)	0.46 (0.43-0.52)
SERPIND1	MBL2	102	67	0.57 (0.5-0.67)	0.7 (0.57-0.81)	0.63 (0.56-0.71)	0.45 (0.44-0.54)	0.45 (0.31-0.68)	0.46 (0.38-0.56)
ITGA6	CCL13	101	63	0.57 (0.5-0.66)	0.66 (0.53-0.77)	0.61 (0.54-0.69)	0.47 (0.45-0.51)	0.44 (0.36-0.62)	0.46 (0.41-0.55)
IL7	VEGFA	102	63	0.55 (0.47-0.63)	0.6 (0.5-0.71)	0.57 (0.5-0.64)	0.48 (0.44-0.54)	0.43 (0.4-0.55)	0.46 (0.43-0.52)
IL17F	IL7	102	63	0.57 (0.48-0.66)	0.58 (0.41-0.73)	0.57 (0.48-0.66)	0.45 (0.43-0.56)	0.44 (0.41-0.56)	0.46 (0.43-0.52)
IL7	ITIH2	102	63	0.56 (0.48-0.65)	0.61 (0.51-0.72)	0.59 (0.52-0.65)	0.47 (0.45-0.53)	0.43 (0.41-0.57)	0.46 (0.44-0.52)
CCL4	IL17C	102	63	0.61 (0.48-0.7)	0.57 (0.46-0.69)	0.59 (0.5-0.66)	0.4 (0.39-0.61)	0.5 (0.47-0.53)	0.46 (0.43-0.56)
IL17C	CPN2	102	63	0.58 (0.5-0.68)	0.61 (0.46-0.72)	0.6 (0.51-0.67)	0.47 (0.4-0.56)	0.44 (0.4-0.57)	0.46 (0.41-0.53)
IL6_PEA_IR	CPN2	101	63	0.58 (0.48-0.67)	0.62 (0.5-0.74)	0.6 (0.53-0.68)	0.47 (0.41-0.59)	0.42 (0.39-0.56)	0.45 (0.41-0.53)
CCL13	MBL2	102	63	0.58 (0.5-0.67)	0.67 (0.54-0.77)	0.62 (0.55-0.69)	0.46 (0.45-0.54)	0.44 (0.35-0.63)	0.45 (0.4-0.55)
CPN2	ITIH2	102	67	0.56 (0.49-0.64)	0.61 (0.51-0.72)	0.58 (0.53-0.65)	0.48 (0.46-0.52)	0.42 (0.41-0.53)	0.45 (0.44-0.51)
IL7	CCL4	102	63	0.56 (0.47-0.65)	0.59 (0.5-0.71)	0.58 (0.51-0.64)	0.46 (0.41-0.57)	0.44 (0.42-0.53)	0.45 (0.42-0.52)
IL6_PEA_cytokine	C9	102	63	0.63 (0.51-0.73)	0.56 (0.45-0.68)	0.59 (0.51-0.67)	0.41 (0.37-0.62)	0.5 (0.44-0.52)	0.45 (0.42-0.56)
ITGA6	TNF	101	63	0.57 (0.5-0.65)	0.63 (0.52-0.75)	0.6 (0.54-0.67)	0.47 (0.45-0.52)	0.43 (0.39-0.6)	0.45 (0.43-0.54)
IL17F	C9	102	63	0.62 (0.51-0.72)	0.57 (0.43-0.72)	0.59 (0.51-0.68)	0.41 (0.37-0.61)	0.48 (0.47-0.54)	0.45 (0.42-0.55)
IL6_PEA_cytokine	IL17C	102	63	0.62 (0.51-0.71)	0.55 (0.43-0.68)	0.59 (0.5-0.67)	0.39 (0.38-0.61)	0.51 (0.43-0.52)	0.45 (0.41-0.56)
ITGA6	VTN	101	63	0.57 (0.5-0.66)	0.68 (0.56-0.77)	0.62 (0.55-0.69)	0.48 (0.47-0.48)	0.43 (0.34-0.66)	0.45 (0.41-0.56)
C9	CLU	102	67	0.62 (0.54-0.72)	0.6 (0.51-0.7)	0.61 (0.55-0.67)	0.43 (0.38-0.61)	0.45 (0.43-0.55)	0.45 (0.41-0.54)
ITGA6	C4BPB	101	63	0.61 (0.51-0.7)	0.64 (0.52-0.75)	0.62 (0.54-0.71)	0.47 (0.4-0.55)	0.43 (0.39-0.6)	0.45 (0.41-0.55)
ITGA6	C2	101	63	0.57 (0.5-0.66)	0.65 (0.52-0.76)	0.61 (0.54-0.68)	0.47 (0.43-0.52)	0.43 (0.38-0.61)	0.45 (0.42-0.55)
ITGA6	HGF	101	63	0.57 (0.48-0.66)	0.63 (0.51-0.75)	0.6 (0.53-0.67)	0.47 (0.44-0.52)	0.42 (0.39-0.6)	0.45 (0.42-0.54)
C9	VTN	102	67	0.61 (0.53-0.71)	0.63 (0.52-0.72)	0.62 (0.55-0.69)	0.45 (0.4-0.58)	0.44 (0.39-0.58)	0.45 (0.4-0.55)
C9	CFB	102	67	0.61 (0.52-0.7)	0.65 (0.53-0.76)	0.63 (0.56-0.7)	0.44 (0.4-0.56)	0.45 (0.37-0.61)	0.45 (0.4-0.55)

IL6_PEA_IR	MBL2	101	63	0.6 (0.49-0.69)	0.62 (0.51-0.74)	0.61 (0.54-0.68)	0.46 (0.4-0.59)	0.44 (0.39-0.59)	0.45 (0.4-0.53)
VEGFA	CPN2	102	63	0.55 (0.47-0.64)	0.62 (0.51-0.73)	0.59 (0.51-0.66)	0.47 (0.46-0.53)	0.42 (0.38-0.56)	0.45 (0.42-0.53)
HGF	CPN2	102	63	0.56 (0.48-0.64)	0.62 (0.5-0.73)	0.59 (0.52-0.66)	0.48 (0.47-0.53)	0.41 (0.38-0.57)	0.45 (0.43-0.53)
ITGA6	CP	101	63	0.56 (0.49-0.65)	0.7 (0.58-0.8)	0.63 (0.55-0.7)	0.48 (0.47-0.52)	0.42 (0.3-0.68)	0.45 (0.39-0.59)
CPN2	C2	102	67	0.59 (0.5-0.68)	0.62 (0.48-0.73)	0.6 (0.52-0.68)	0.47 (0.42-0.56)	0.42 (0.39-0.54)	0.45 (0.41-0.52)
IL17C	C9	102	63	0.61 (0.52-0.72)	0.57 (0.47-0.69)	0.59 (0.53-0.67)	0.4 (0.39-0.61)	0.48 (0.47-0.52)	0.45 (0.43-0.55)
PLXNA4	MBL2	101	63	0.57 (0.5-0.66)	0.7 (0.58-0.8)	0.63 (0.57-0.7)	0.47 (0.44-0.52)	0.42 (0.32-0.66)	0.45 (0.38-0.57)
ITIH2	MBL2	102	67	0.58 (0.5-0.66)	0.62 (0.52-0.74)	0.6 (0.53-0.67)	0.44 (0.43-0.54)	0.44 (0.39-0.59)	0.45 (0.41-0.52)
IL7	IL17C	102	63	0.59 (0.51-0.69)	0.6 (0.47-0.71)	0.6 (0.52-0.67)	0.44 (0.39-0.59)	0.43 (0.4-0.53)	0.45 (0.4-0.52)
CCL4	C9	102	63	0.62 (0.52-0.72)	0.59 (0.49-0.71)	0.6 (0.53-0.68)	0.39 (0.38-0.62)	0.49 (0.43-0.51)	0.44 (0.41-0.56)
CPN2	PZP	101	67	0.56 (0.48-0.64)	0.62 (0.48-0.74)	0.59 (0.51-0.66)	0.48 (0.46-0.53)	0.41 (0.38-0.59)	0.44 (0.43-0.53)
IL6_PEA_cytokine	CPN2	102	63	0.56 (0.46-0.64)	0.62 (0.49-0.75)	0.59 (0.51-0.67)	0.47 (0.44-0.58)	0.41 (0.38-0.62)	0.44 (0.42-0.55)
C9	CP	102	67	0.61 (0.52-0.72)	0.65 (0.53-0.77)	0.63 (0.55-0.71)	0.45 (0.39-0.59)	0.43 (0.36-0.61)	0.44 (0.38-0.54)
TNF	MBL2	102	63	0.58 (0.5-0.67)	0.63 (0.53-0.74)	0.61 (0.54-0.67)	0.45 (0.43-0.56)	0.42 (0.39-0.59)	0.44 (0.41-0.53)
CCL4	CPN2	102	63	0.56 (0.47-0.65)	0.62 (0.5-0.74)	0.59 (0.52-0.66)	0.46 (0.42-0.56)	0.41 (0.39-0.59)	0.44 (0.41-0.52)
HGF	MBL2	102	63	0.58 (0.49-0.66)	0.63 (0.51-0.74)	0.6 (0.53-0.67)	0.45 (0.44-0.55)	0.42 (0.39-0.61)	0.44 (0.42-0.53)
IL6_PEA_cytokine	MBL2	102	63	0.58 (0.48-0.67)	0.62 (0.48-0.74)	0.6 (0.52-0.67)	0.45 (0.42-0.58)	0.43 (0.4-0.6)	0.44 (0.41-0.53)
CP	MBL2	102	67	0.58 (0.49-0.67)	0.67 (0.55-0.8)	0.62 (0.55-0.69)	0.44 (0.42-0.54)	0.42 (0.33-0.64)	0.44 (0.38-0.55)
IL7	PZP	101	63	0.57 (0.48-0.65)	0.62 (0.47-0.73)	0.59 (0.51-0.66)	0.46 (0.45-0.54)	0.41 (0.37-0.54)	0.44 (0.41-0.52)
IL7	C9	102	63	0.62 (0.52-0.72)	0.6 (0.5-0.72)	0.61 (0.53-0.69)	0.43 (0.38-0.61)	0.43 (0.42-0.5)	0.44 (0.41-0.53)
ITGA6	VEGFA	101	63	0.56 (0.48-0.65)	0.64 (0.52-0.76)	0.6 (0.54-0.67)	0.47 (0.45-0.49)	0.41 (0.38-0.61)	0.44 (0.42-0.54)
ITGA6	CLU	101	63	0.56 (0.49-0.65)	0.66 (0.54-0.77)	0.61 (0.54-0.68)	0.46 (0.46-0.49)	0.41 (0.35-0.62)	0.44 (0.41-0.55)
SH2D1A	MBL2	101	63	0.57 (0.5-0.67)	0.62 (0.5-0.74)	0.6 (0.52-0.67)	0.45 (0.44-0.52)	0.42 (0.39-0.6)	0.44 (0.42-0.52)
VEGFA	MBL2	102	63	0.57 (0.49-0.67)	0.61 (0.51-0.74)	0.59 (0.52-0.66)	0.45 (0.44-0.53)	0.43 (0.39-0.59)	0.44 (0.42-0.52)
FCRL6	MBL2	101	63	0.58 (0.5-0.66)	0.66 (0.54-0.78)	0.62 (0.55-0.68)	0.45 (0.44-0.52)	0.41 (0.35-0.64)	0.44 (0.4-0.55)
DCTN1	IL6_PEA_cytokine	101	63	0.55 (0.46-0.64)	0.71 (0.58-0.82)	0.63 (0.55-0.7)	0.51 (0.49-0.53)	0.36 (0.29-0.71)	0.44 (0.4-0.61)
VTN	MBL2	102	67	0.58 (0.5-0.67)	0.68 (0.55-0.79)	0.63 (0.56-0.71)	0.44 (0.43-0.52)	0.43 (0.33-0.64)	0.44 (0.38-0.54)
IL17F	CPN2	102	63	0.56 (0.49-0.65)	0.64 (0.47-0.77)	0.6 (0.51-0.68)	0.46 (0.44-0.53)	0.41 (0.36-0.59)	0.44 (0.4-0.53)
ITGA6	CCL4	101	63	0.57 (0.47-0.66)	0.63 (0.52-0.75)	0.6 (0.53-0.67)	0.46 (0.44-0.55)	0.41 (0.38-0.6)	0.44 (0.42-0.54)
MBL2	CLU	102	67	0.58 (0.5-0.67)	0.64 (0.54-0.75)	0.61 (0.55-0.68)	0.43 (0.42-0.53)	0.42 (0.38-0.58)	0.44 (0.4-0.52)

IL7	CPN2	102	63	0.57 (0.49-0.65)	0.63 (0.52-0.74)	0.6 (0.53-0.67)	0.46 (0.44-0.52)	0.4 (0.39-0.52)	0.43 (0.42-0.49)
CCL4	MBL2	102	63	0.58 (0.48-0.67)	0.62 (0.5-0.74)	0.6 (0.52-0.67)	0.44 (0.4-0.54)	0.42 (0.39-0.59)	0.43 (0.41-0.51)
IL13	MBL2	102	63	0.58 (0.49-0.67)	0.65 (0.51-0.77)	0.61 (0.53-0.68)	0.44 (0.44-0.55)	0.42 (0.36-0.64)	0.43 (0.4-0.54)
ITGA6	IL13	101	63	0.55 (0.49-0.65)	0.68 (0.56-0.79)	0.62 (0.55-0.69)	0.47 (0.46-0.47)	0.4 (0.33-0.68)	0.43 (0.4-0.57)
DCTN1	PZP	100	63	0.55 (0.47-0.65)	0.7 (0.57-0.82)	0.63 (0.54-0.7)	0.51 (0.5-0.52)	0.35 (0.31-0.69)	0.43 (0.41-0.6)
IL17F	MBL2	102	63	0.59 (0.49-0.68)	0.63 (0.47-0.76)	0.61 (0.51-0.69)	0.43 (0.4-0.54)	0.42 (0.37-0.59)	0.43 (0.39-0.53)
IL7	MBL2	102	63	0.58 (0.49-0.67)	0.63 (0.53-0.75)	0.61 (0.54-0.67)	0.44 (0.42-0.5)	0.41 (0.38-0.51)	0.43 (0.41-0.49)
C9	CPN2	102	67	0.62 (0.54-0.73)	0.62 (0.52-0.73)	0.62 (0.55-0.7)	0.42 (0.37-0.59)	0.42 (0.39-0.52)	0.43 (0.39-0.53)
IL17C	MBL2	102	63	0.6 (0.51-0.68)	0.64 (0.53-0.76)	0.62 (0.54-0.69)	0.43 (0.4-0.57)	0.4 (0.38-0.6)	0.42 (0.39-0.53)
PZP	MBL2	101	67	0.59 (0.49-0.67)	0.62 (0.47-0.74)	0.6 (0.52-0.68)	0.43 (0.41-0.56)	0.41 (0.39-0.55)	0.42 (0.4-0.5)
DCTN1	ITGA6	102	63	0.56 (0.49-0.65)	0.71 (0.6-0.83)	0.64 (0.57-0.71)	0.49 (0.46-0.5)	0.36 (0.29-0.7)	0.42 (0.38-0.59)
DCTN1	MBL2	101	63	0.57 (0.49-0.66)	0.73 (0.6-0.83)	0.65 (0.57-0.72)	0.5 (0.44-0.52)	0.35 (0.29-0.68)	0.42 (0.38-0.58)
ITGA6	PZP	100	63	0.56 (0.49-0.65)	0.66 (0.55-0.78)	0.61 (0.55-0.68)	0.47 (0.46-0.48)	0.37 (0.35-0.63)	0.42 (0.41-0.55)
ITGA6	IL7	101	63	0.58 (0.5-0.67)	0.64 (0.52-0.76)	0.61 (0.53-0.68)	0.44 (0.43-0.47)	0.39 (0.38-0.58)	0.42 (0.4-0.5)
ITGA6	MBL2	101	63	0.58 (0.5-0.67)	0.66 (0.55-0.77)	0.62 (0.55-0.68)	0.45 (0.44-0.5)	0.37 (0.35-0.63)	0.41 (0.4-0.54)
ITGA6	PLXNA4	102	63	0.58 (0.49-0.68)	0.67 (0.56-0.78)	0.63 (0.56-0.69)	0.45 (0.42-0.49)	0.37 (0.34-0.66)	0.41 (0.38-0.56)
ITGA6	CPN2	101	63	0.57 (0.49-0.66)	0.66 (0.54-0.76)	0.61 (0.55-0.68)	0.45 (0.45-0.47)	0.37 (0.36-0.55)	0.41 (0.41-0.51)
CPN2	MBL2	102	67	0.59 (0.5-0.68)	0.66 (0.55-0.78)	0.62 (0.56-0.7)	0.43 (0.42-0.49)	0.37 (0.35-0.5)	0.41 (0.38-0.48)

Supplementary Table 8. Individual biomarker to predict short-term relapse

Gene names	Dataset	STORI (n=)	SPARE (n=)	c-statistic development dataset (STORI)	c-statistic development dataset (SPARE)	Mean c-statistic development datasets (STORI and SPARE)	c-statistic validation dataset (STORI)	c-statistic validation dataset (SPARE)	Mean c-statistic validation datasets (STORI and SPARE)
HP	SRM	102	67	0.74	0.75	0.74	0.74	0.75	0.74
CEASE_phase1	clinical	83	46	NA	NA	NA	0.74	0.74	0.74
CRP	SRM	102	67	0.75	0.73	0.74	0.75	0.73	0.74
APCS	SRM	102	67	0.68	0.76	0.72	0.68	0.76	0.72
hsCRP	clinical	109	69	0.75	0.68	0.71	0.75	0.68	0.71
CLEC4C	PEA_IR	102	63	0.65	0.77	0.71	0.65	0.77	0.71
F9	SRM	102	67	0.69	0.72	0.71	0.69	0.72	0.71
FC	clinical	85	47	0.72	0.67	0.69	0.72	0.67	0.69
ITGA11	PEA_IR	102	63	0.68	0.71	0.69	0.68	0.71	0.69
CP	SRM	102	67	0.66	0.72	0.69	0.66	0.72	0.69
C4B	SRM	102	67	0.63	0.75	0.69	0.63	0.75	0.69
IFNG	PEA_cytokine	102	63	0.73	0.62	0.67	0.73	0.62	0.67
SERPIND1	SRM	102	67	0.60	0.74	0.67	0.60	0.74	0.67
HPR	SRM	102	67	0.62	0.72	0.67	0.62	0.72	0.67
SAA1	SRM	102	67	0.65	0.68	0.67	0.65	0.68	0.67
C5	SRM	102	67	0.70	0.63	0.67	0.70	0.63	0.67
LRG1	SRM	102	67	0.63	0.69	0.66	0.63	0.69	0.66
MILR1	PEA_IR	102	63	0.65	0.66	0.66	0.65	0.66	0.66
LAMP3	PEA_IR	102	63	0.67	0.64	0.65	0.67	0.64	0.65
PZP	SRM	101	67	0.61	0.69	0.65	0.61	0.69	0.65
VTN	SRM	102	67	0.56	0.74	0.65	0.56	0.74	0.65
IL6	PEA_cytokine	102	63	0.69	0.60	0.65	0.69	0.60	0.65
KLRD1	PEA_IR	102	63	0.66	0.63	0.65	0.66	0.63	0.65
SERPINA3	SRM	102	67	0.63	0.66	0.65	0.63	0.66	0.65
C8B	SRM	102	67	0.63	0.66	0.64	0.63	0.66	0.64

ITIH3	SRM	102	67	0.64	0.63	0.64	0.64	0.63	0.64
CLU	SRM	102	67	0.58	0.68	0.63	0.58	0.68	0.63
CFB	SRM	102	67	0.60	0.66	0.63	0.60	0.66	0.63
IL7	PEA_cytokine	102	63	0.55	0.70	0.63	0.55	0.70	0.63
CCL4	PEA_cytokine	102	63	0.65	0.60	0.62	0.65	0.60	0.62
C2	SRM	102	67	0.60	0.64	0.62	0.60	0.64	0.62
FCRL6	PEA_IR	102	63	0.59	0.65	0.62	0.59	0.65	0.62
DCTN1	PEA_IR	102	63	0.62	0.61	0.62	0.62	0.61	0.62
MASP1	PEA_IR	102	63	0.70	0.54	0.62	0.70	0.54	0.62
CPN2	SRM	102	67	0.57	0.66	0.61	0.57	0.66	0.61
NCR1	PEA_IR	102	63	0.61	0.62	0.61	0.61	0.62	0.61
HGF	PEA_cytokine	102	63	0.52	0.70	0.61	0.52	0.70	0.61
C9	SRM	102	67	0.60	0.62	0.61	0.60	0.62	0.61
C3	SRM	102	67	0.61	0.59	0.60	0.61	0.59	0.60
ITIH1	SRM	102	67	0.57	0.63	0.60	0.57	0.63	0.60
ITIH2	SRM	102	67	0.56	0.61	0.59	0.56	0.61	0.59
ORM1	SRM	102	67	0.60	0.57	0.58	0.60	0.57	0.58
CCL13	PEA_cytokine	102	63	0.53	0.61	0.57	0.53	0.61	0.57
IL15	PEA_cytokine	102	63	0.57	0.55	0.56	0.57	0.55	0.56
IL13	PEA_cytokine	102	63	0.60	0.45	0.53	0.40	0.55	0.47
SERPING1	SRM	102	67	0.58	0.49	0.54	0.42	0.51	0.47
IL17F	PEA_cytokine	102	63	0.59	0.49	0.54	0.41	0.51	0.46

Supplementary Table 9. Individual biomarker to predict mid/long-term relapse

Gene names	Dataset	STORI (n=)	SPARE (n=)	c-statistic development dataset (STORI)	c-statistic development dataset (SPARE)	Mean c-statistic development datasets (STORI and SPARE)	c-statistic validation dataset (STORI)	c-statistic validation dataset (SPARE)	Mean c-statistic validation datasets (STORI and SPARE)
FLT3LG	PEA_cytokine	73	53	0.66	0.66	0.66	0.66	0.66	0.66
FGF2	PEA_IR	74	53	0.57	0.73	0.65	0.57	0.73	0.65
SIT1	PEA_IR	74	53	0.65	0.62	0.63	0.65	0.62	0.63
TNF	PEA_cytokine	73	53	0.61	0.62	0.61	0.61	0.62	0.61
SERPINA4	SRM	73	56	0.61	0.61	0.61	0.61	0.61	0.61
CEASE_phase1	clinical	56	40	NA	NA	NA	0.66	0.56	0.61
ORM1	SRM	73	56	0.58	0.63	0.60	0.58	0.63	0.60
ITGA6	PEA_IR	74	53	0.54	0.63	0.59	0.54	0.63	0.59
APOA1	SRM	73	56	0.57	0.60	0.58	0.57	0.60	0.58
CDSN	PEA_IR	74	53	0.62	0.54	0.58	0.62	0.54	0.58
HSD11B1	PEA_IR	74	53	0.53	0.62	0.57	0.53	0.62	0.57
C4BPB	SRM	73	56	0.58	0.56	0.57	0.58	0.56	0.57
SH2D1A	PEA_IR	74	53	0.58	0.56	0.57	0.58	0.56	0.57
C8A	SRM	73	56	0.60	0.54	0.57	0.60	0.54	0.57
MBL2	SRM	73	56	0.54	0.59	0.56	0.54	0.59	0.56
VEGFA	PEA_cytokine	73	53	0.54	0.58	0.56	0.54	0.58	0.56
CFB	SRM	73	56	0.53	0.59	0.56	0.53	0.59	0.56
CLU	SRM	73	56	0.54	0.55	0.55	0.54	0.55	0.55
IL15	PEA_cytokine	73	53	0.44	0.53	0.49	0.56	0.47	0.51
CXCL9	PEA_cytokine	73	53	0.60	0.39	0.49	0.40	0.62	0.51
IL10	PEA_cytokine	73	53	0.54	0.50	0.52	0.46	0.50	0.48
IFNG	PEA_cytokine	73	53	0.66	0.39	0.52	0.34	0.62	0.48
IL17C	PEA_cytokine	73	53	0.61	0.45	0.53	0.39	0.55	0.47
PLXNA4	PEA_IR	74	53	0.50	0.64	0.57	0.50	0.36	0.43

Supplementary Table 10. Individual biomarker to predict relapse during the whole follow-up period

Gene names	Dataset	STORI (n=)	SPARE (n=)	c-statistic development dataset (STORI)	c-statistic development dataset (SPARE)	Mean c-statistic development datasets (STORI and SPARE)	c-statistic validation dataset (STORI)	c-statistic validation dataset (SPARE)	Mean c-statistic validation datasets (STORI and SPARE)
CEASE_phase1	clinical	83	46	NA	NA	NA	0.70	0.63	0.66
IFNG	PEA_cytokine	102	63	0.69	0.62	0.65	0.69	0.62	0.65
HP	SRM	102	67	0.67	0.64	0.65	0.67	0.64	0.65
FC	clinical	85	47	0.70	0.58	0.64	0.70	0.58	0.64
C4B	SRM	102	67	0.56	0.68	0.62	0.56	0.68	0.62
hsCRP	clinical	109	69	0.64	0.60	0.62	0.64	0.60	0.62
CRP	SRM	102	67	0.63	0.61	0.62	0.63	0.61	0.62
C5	SRM	102	67	0.61	0.60	0.61	0.61	0.60	0.61
HPR	SRM	102	67	0.59	0.62	0.61	0.59	0.62	0.61
CXCL9	PEA_cytokine	102	63	0.66	0.55	0.61	0.66	0.55	0.61
LRG1	SRM	102	67	0.60	0.60	0.60	0.60	0.60	0.60
F9	SRM	102	67	0.57	0.63	0.60	0.57	0.63	0.60
LAMP3	PEA_IR	102	63	0.58	0.61	0.59	0.58	0.61	0.59
C8B	SRM	102	67	0.62	0.57	0.59	0.62	0.57	0.59
ORM1	SRM	102	67	0.59	0.60	0.59	0.59	0.60	0.59
CP	SRM	102	67	0.55	0.64	0.59	0.55	0.64	0.59
FLT3LG	PEA_cytokine	102	63	0.60	0.58	0.59	0.60	0.58	0.59
MASP1	PEA_IR	102	63	0.60	0.58	0.59	0.60	0.58	0.59
CFB	SRM	102	67	0.56	0.62	0.59	0.56	0.62	0.59
APCS	SRM	102	67	0.59	0.59	0.59	0.59	0.59	0.59
NCR1	PEA_IR	102	63	0.58	0.60	0.59	0.58	0.60	0.59
FGF2	PEA_IR	102	63	0.52	0.65	0.59	0.52	0.65	0.59
SIT1	PEA_IR	102	63	0.59	0.59	0.59	0.59	0.59	0.59
CLEC4C	PEA_IR	102	63	0.54	0.63	0.58	0.54	0.63	0.58
MILR1	PEA_IR	102	63	0.63	0.53	0.58	0.63	0.53	0.58

SERPIND1	SRM	102	67	0.53	0.63	0.58	0.53	0.63	0.58
SAA1	SRM	102	67	0.57	0.57	0.57	0.57	0.57	0.57
KLRD1	PEA_IR	102	63	0.59	0.55	0.57	0.59	0.55	0.57
APOA1	SRM	102	67	0.59	0.55	0.57	0.59	0.55	0.57
ITIH3	SRM	102	67	0.58	0.56	0.57	0.58	0.56	0.57
SERPINA3	SRM	102	67	0.57	0.57	0.57	0.57	0.57	0.57
PLXNA4	PEA_IR	102	63	0.51	0.62	0.56	0.51	0.62	0.56
C3	SRM	102	67	0.56	0.57	0.56	0.56	0.57	0.56
ITGA11	PEA_IR	102	63	0.61	0.52	0.56	0.61	0.52	0.56
C2	SRM	102	67	0.55	0.58	0.56	0.55	0.58	0.56
VTN	SRM	102	67	0.51	0.61	0.56	0.51	0.61	0.56
FCRL6	PEA_IR	102	63	0.51	0.60	0.56	0.51	0.60	0.56
C8A	SRM	102	67	0.58	0.53	0.55	0.58	0.53	0.55
CCL13	PEA_cytokine	102	63	0.54	0.57	0.55	0.54	0.57	0.55
IL15	PEA_cytokine	102	63	0.56	0.54	0.55	0.56	0.54	0.55
C4BPB	SRM	102	67	0.59	0.52	0.55	0.59	0.52	0.55
SERPING1	SRM	102	67	0.54	0.56	0.55	0.54	0.56	0.55
HSD11B1	PEA_IR	102	63	0.54	0.55	0.55	0.54	0.55	0.55
ITIH1	SRM	102	67	0.51	0.59	0.55	0.51	0.59	0.55
SERPINA4	SRM	102	67	0.58	0.51	0.54	0.58	0.51	0.54
CDSN	PEA_IR	102	63	0.51	0.57	0.54	0.51	0.57	0.54
TNF	PEA_cytokine	102	63	0.53	0.53	0.53	0.53	0.53	0.53
HGF	PEA_cytokine	102	63	0.53	0.53	0.53	0.53	0.53	0.53
IL17F	PEA_cytokine	102	63	0.54	0.44	0.49	0.47	0.56	0.51
SH2D1A	PEA_IR	102	63	0.49	0.53	0.51	0.49	0.53	0.51
IL10	PEA_cytokine	102	63	0.51	0.51	0.51	0.49	0.49	0.49
VEGFA	PEA_cytokine	102	63	0.47	0.49	0.48	0.47	0.49	0.48
CLU	SRM	102	67	0.48	0.55	0.52	0.52	0.45	0.48
ITIH2	SRM	102	67	0.50	0.55	0.53	0.50	0.45	0.47
IL13	PEA_cytokine	102	63	0.48	0.46	0.47	0.48	0.46	0.47

IL17C	PEA_cytokine	102	63	0.60	0.48	0.54	0.40	0.53	0.46
IL6	PEA_cytokine	102	63	0.61	0.49	0.55	0.39	0.51	0.45
C9	SRM	102	67	0.61	0.49	0.55	0.40	0.51	0.45
IL7	PEA_cytokine	102	63	0.53	0.57	0.55	0.47	0.43	0.45
CCL4	PEA_cytokine	102	63	0.58	0.53	0.55	0.42	0.47	0.45
PZP	SRM	101	67	0.49	0.61	0.55	0.51	0.39	0.45
CPN2	SRM	102	67	0.53	0.59	0.56	0.47	0.41	0.44
MBL2	SRM	102	67	0.55	0.58	0.57	0.45	0.42	0.43
ITGA6	PEA_IR	102	63	0.52	0.62	0.57	0.48	0.38	0.43
DCTN1	PEA_IR	102	63	0.49	0.68	0.59	0.51	0.32	0.41