# Comprehensive insight into Colorectal Cancer metabolites by Human Serum Sample

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Colorectal Cancer (CRC) is the third most diagnosed cancer, accounting for the second most cancer-related deaths with poor prognostic outcomes. The current screening methods are either highly invasive (e.g., colonoscopy) or lack sufficient sensitivity (e.g., Fecal Occult Blood Test (gFOBT), Immunochemical FOBT (FIT)).

Therefore, the aim of the research is to identify highly sensitive and less invasive diagnostic biomarkers for CRC using comprehensive two-dimensional gas chromatography (GC×GC) coupled with low- and high-resolution time-of-flight mass spectrometry (TOFMS).

We thus conducted a study of 66 human serum samples representing three different groups (Adenocarcinoma (ADK), Adenoma, and Control) using GC×GC–TOFMS. We analyzed samples with two different statistically tailored sample preparation and analytical approaches for metabolomics (50 µL serum) and lipidomics (fatty acids) (25 µL serum). All serum samples were injected in a randomized order along with a QC sample (pooled human plasma) and NIST SRM 1950 to fulfill QAQC requirements.

A chemometric screening, including unsupervised (PCA, HCA) and supervised analysis (PLS-DA), univariate analysis (volcano plot), and random forest (RF) classification algorithm, was performed on both data sets. On the top selected features, receiver operating curves (ROC) were generated. The in-depth investigation of metabolic pathways and quantitative enrichment analysis (QEA) was also performed. The preliminary finding suggests the significant involvement of dysregulated fatty acid metabolism in CRC screening. The lipidomics method is also advantageous compared to the metabolomics approach as it is simpler, faster, and more easily automatable to large-scale studies.

With this viewpoint, incorporating the multi-omics metabolomics and lipidomics analytical approaches using the same sample will enable us to compare and combine the comprehensive omics information, bringing us closer to providing an in-depth understanding of the molecular and pathological level changes involved in CRC with comparison to healthy volunteers (control) and benign.