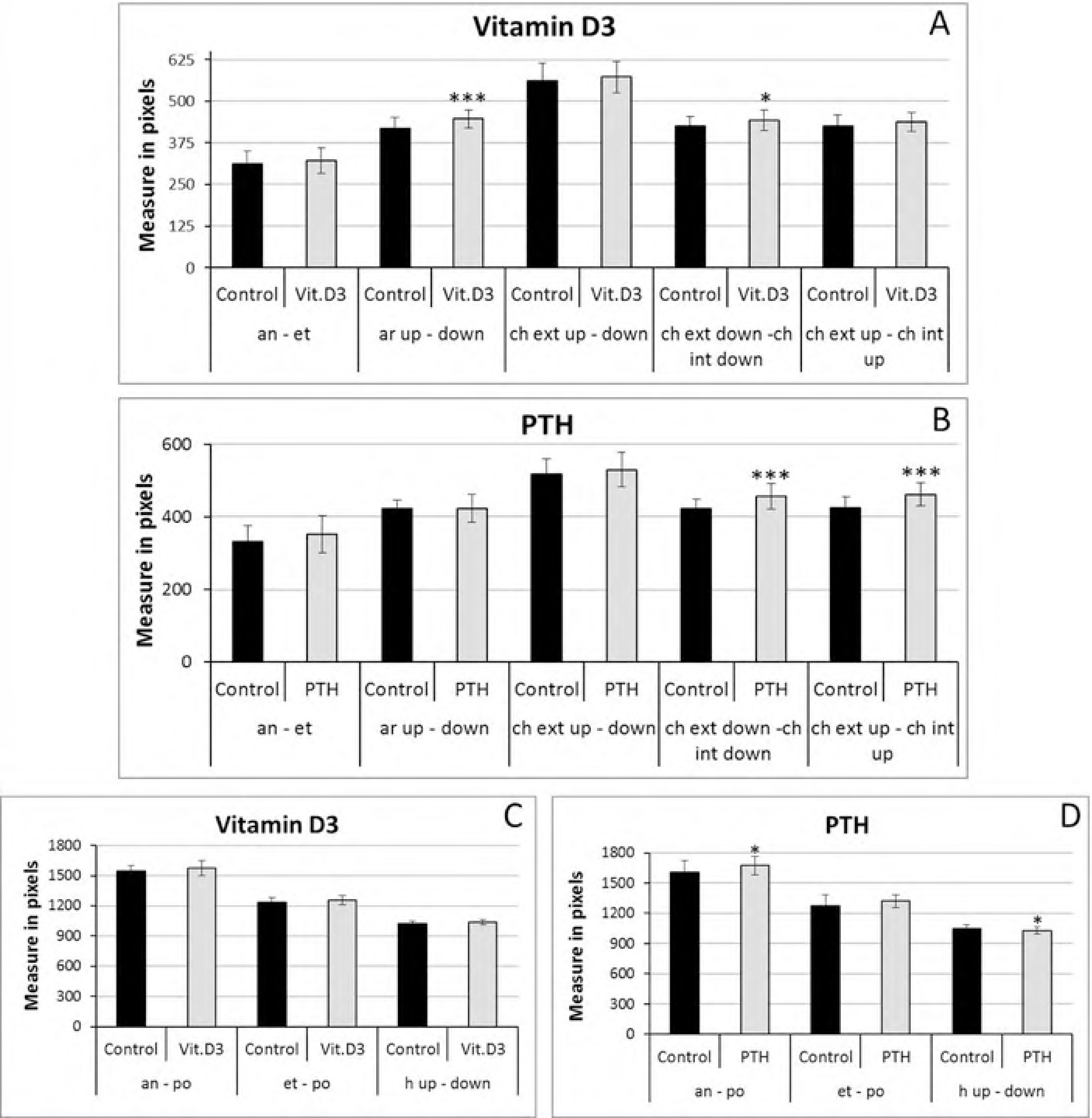
Vitamin D3
A
Measure in pixels
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500
375
250
125
0
***
*
Control
Vit.D3
Control
Vit.D3
Control
Vit.D3
Control
Vit.D3
Control
Vit.D3
an - et
ar up - down
ch ext up - down
ch ext down -ch int down
ch ext up - ch int up
PTH
B
Measure in pixels
600
400
200
0
***
***
Control
PTH
Control
PTH
Control
PTH
Control
PTH
Control
PTH
an - et
ar up - down
ch ext up - down
ch ext down -ch int down
ch ext up - ch int up
Vitamin D3
C
Measure in pixels
1800
1500
1200
900
600
300
0
Control
Vit.D3
Control
Vit.D3
Control
Vit.D3
an - po
et - po
h up - down
PTH
D
Measure in pixels
1800
1500
1200
900
600
300
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*
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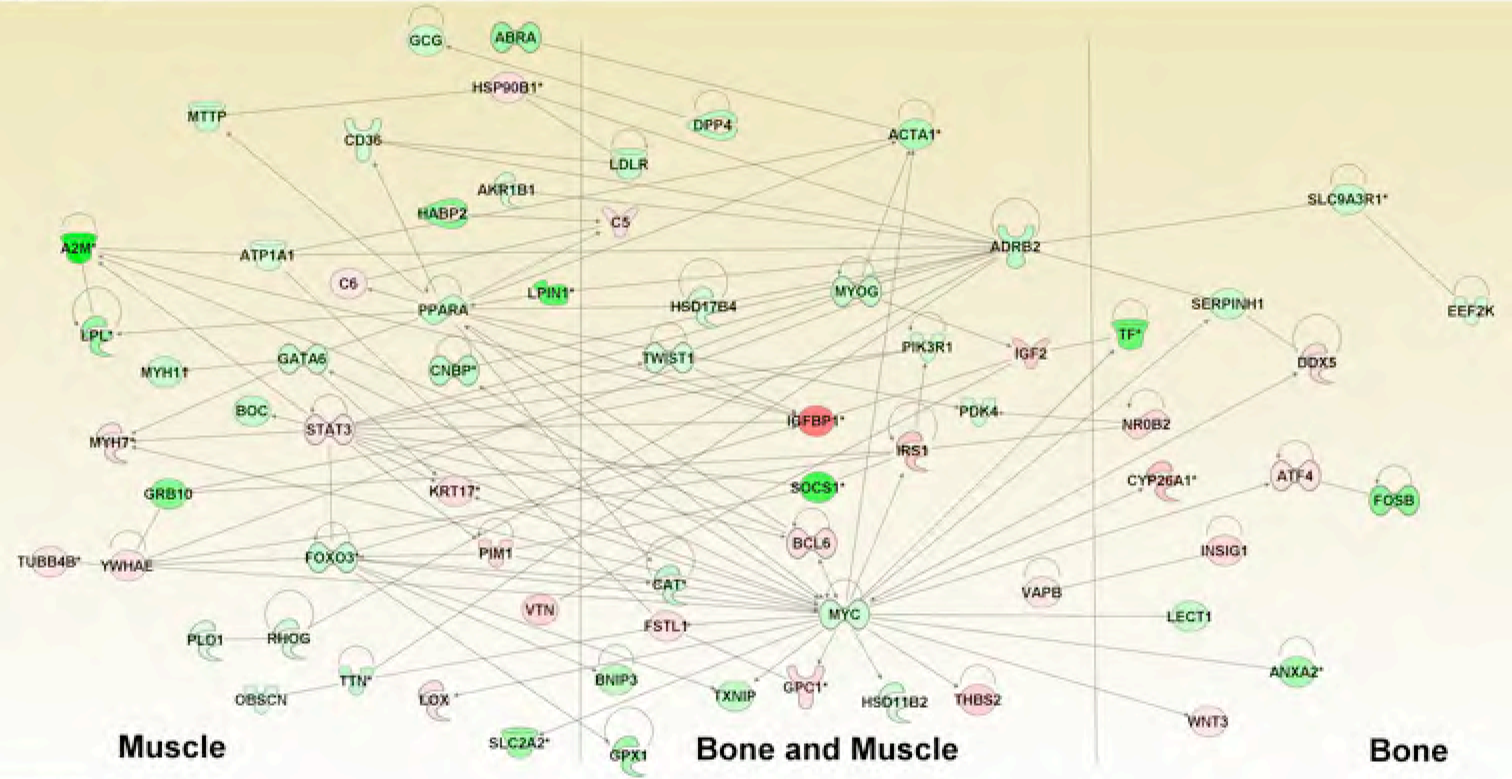
Control
PTH
Control
PTH
Control
PTH
an - po
et - po
h up - down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MTTP
CD36
DPP4
ACTA1*
LDLR
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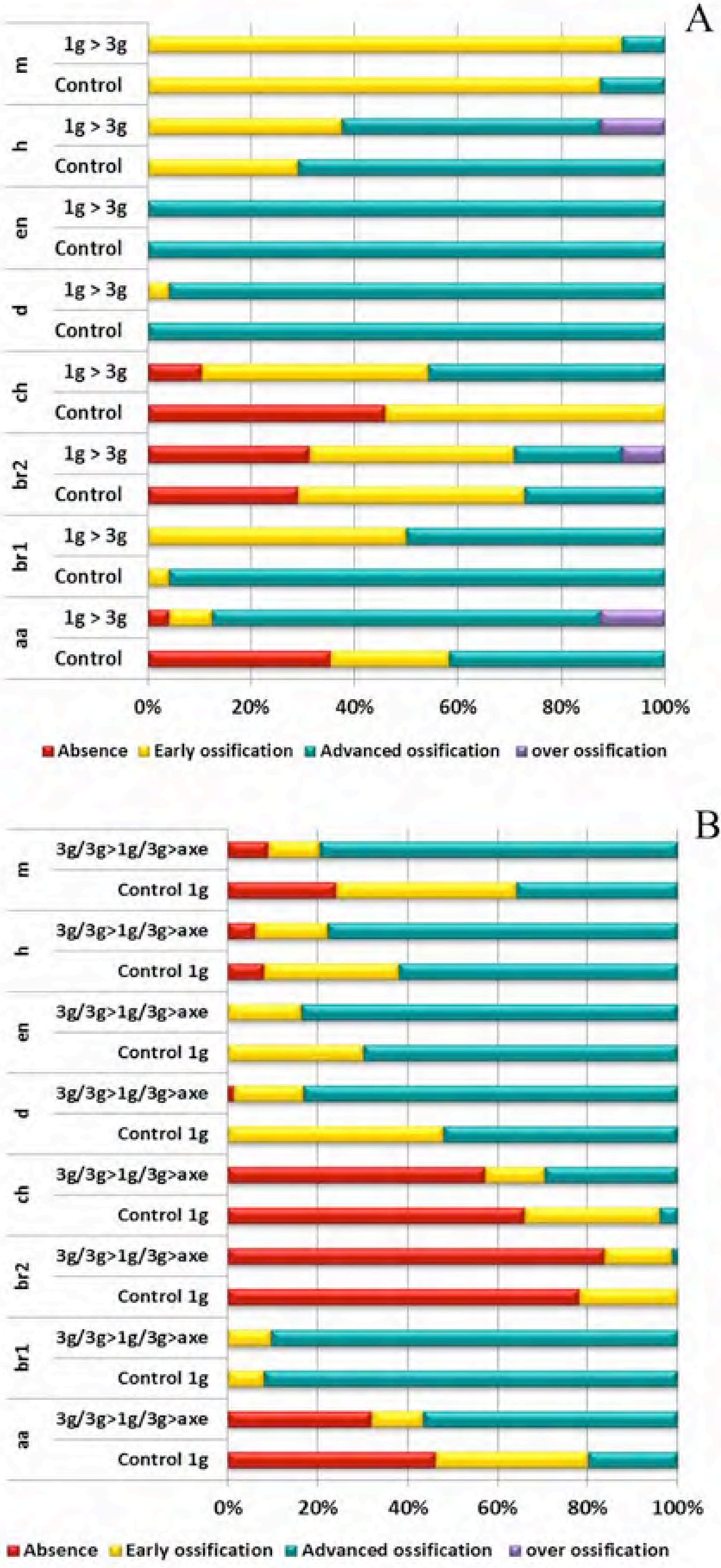
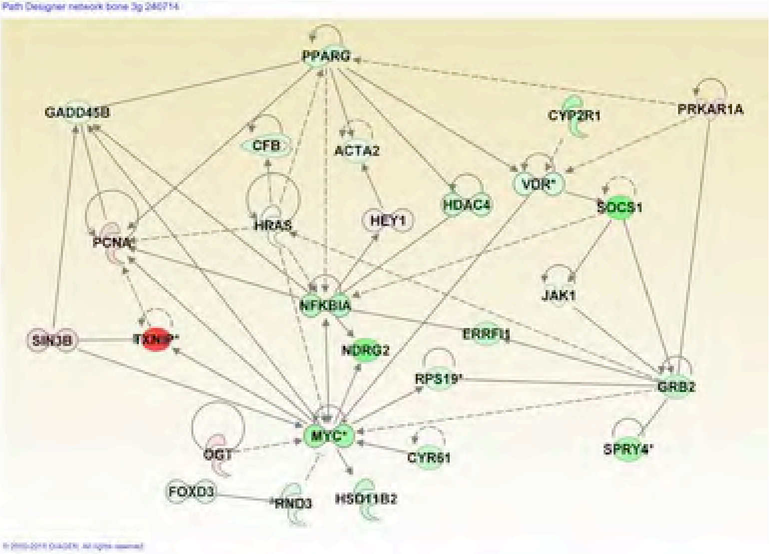
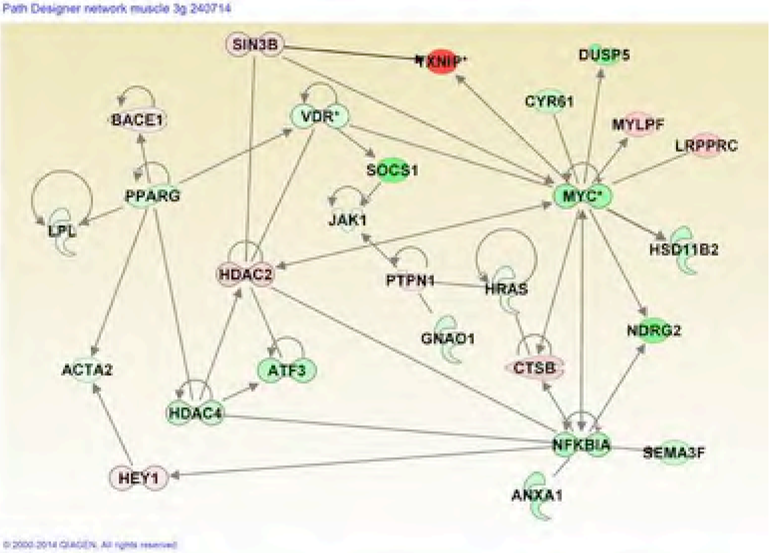
SLC9A3R1*
HABP2
C5
A2M*
ATP1A1
ADRB2
C6
LPIN1*
PPARA*
HSD17B4
MYOG
SERPINH1
EEF2K
TF*
LPL*
PIK3R1
IGF2
GATA6
CNBP*
TWIST1
DDX5
MYH11*
BOC
STAT3
IGFBP1*
PDK4
NR0B2
MYH7*
IRS1
KRT17*
CYP26A1*
ATF4
GRB10
SOCS1*
FOSB
BCL6
INSIG1
TUBB4B*
YWHAE
FOXO3*
PIM1
CAT*
VAPB
VTN
MYC
LECT1
PLD1
RHOG
FSTL1*
TTN*
BNIP3
ANXA2*
OBSCN
LOX
TXNIP
GPC1*
HSD11B2
THBS2
WNT3
SLC2A2*
GPX1
Muscle
Bone and Muscle
Bone


A
m
1g > 3g
Control
h
1g > 3g
Control
en
1g > 3g
Control
d
1g > 3g
Control
ch
1g > 3g
Control
br2
1g > 3g
Control
br1
1g > 3g
Control
aa
1g > 3g
Control
0%
20%
40%
60%
80%
100%
Absence
Early ossification
Advanced ossification
over ossification
B
m
3g/3g>1g/3g>axe
Control 1g
h
3g/3g>1g/3g>axe
Control 1g
en
3g/3g>1g/3g>axe
Control 1g
d
3g/3g>1g/3g>axe
Control 1g
ch
3g/3g>1g/3g>axe
Control 1g
br2
3g/3g>1g/3g>axe
Control 1g
br1
3g/3g>1g/3g>axe
Control 1g
aa
3g/3g>1g/3g>axe
Control 1g
0%
20%
40%
60%
80%
100%
Absence
Early ossification
Advanced ossification
over ossification

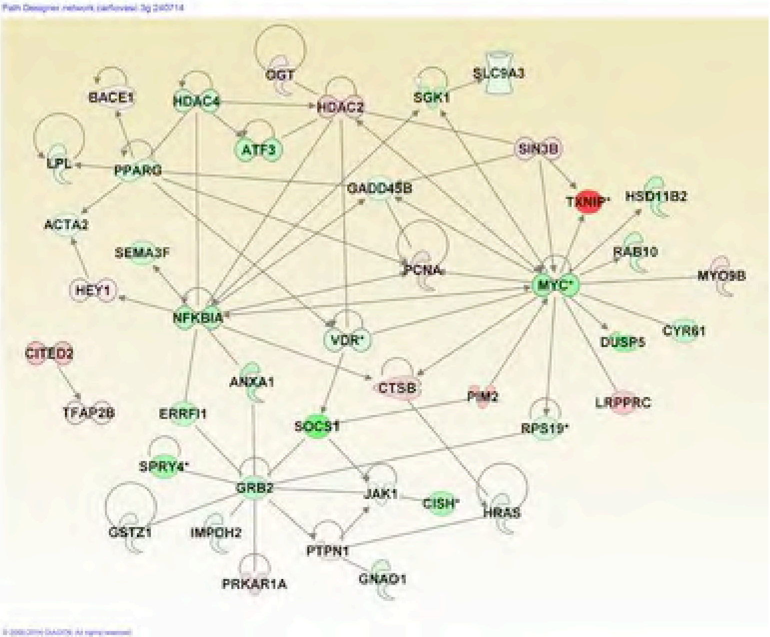
Bone

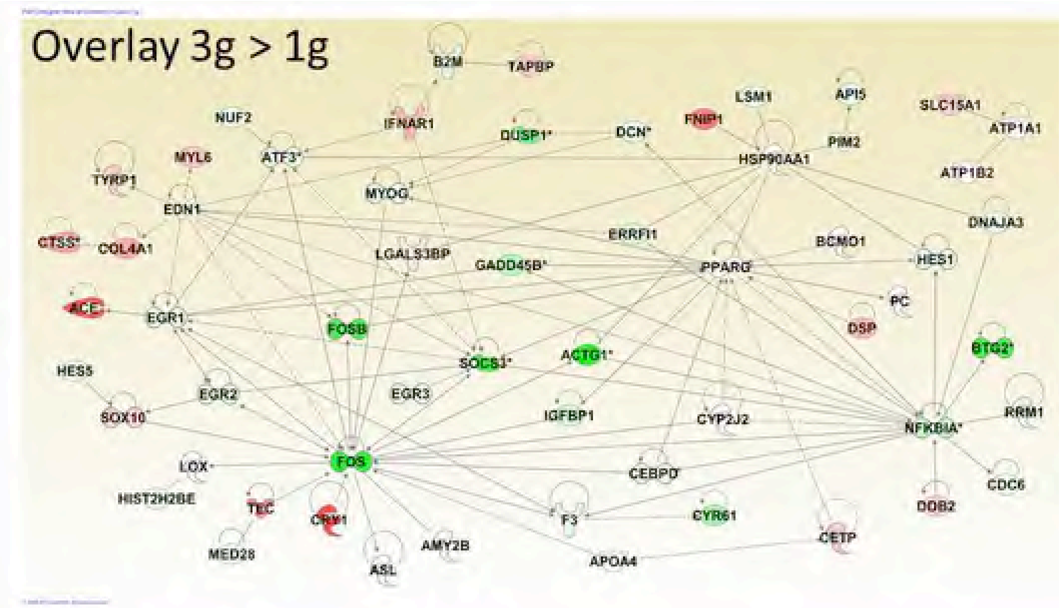


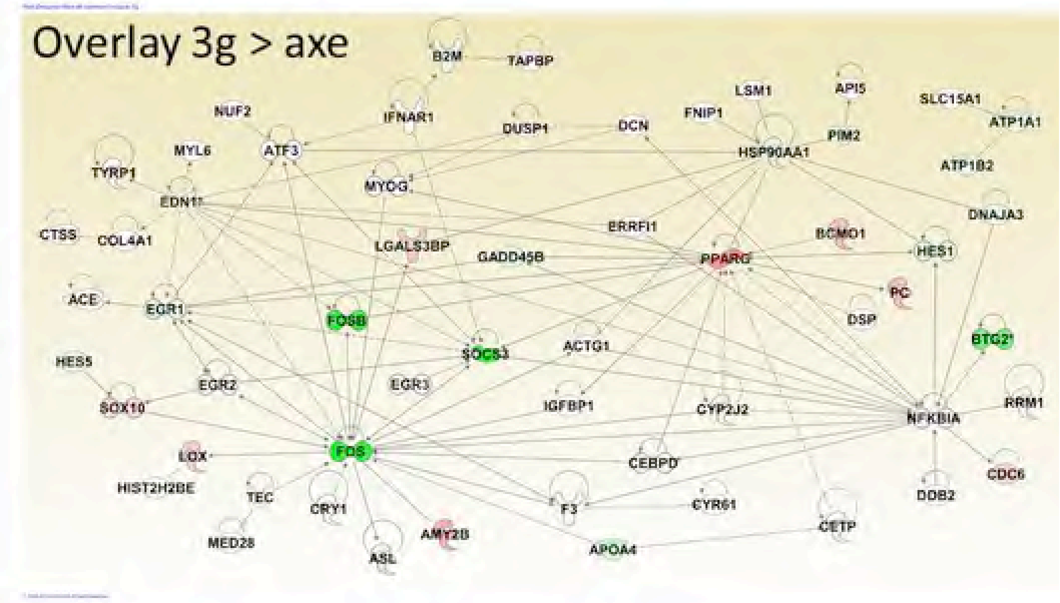
Muscle

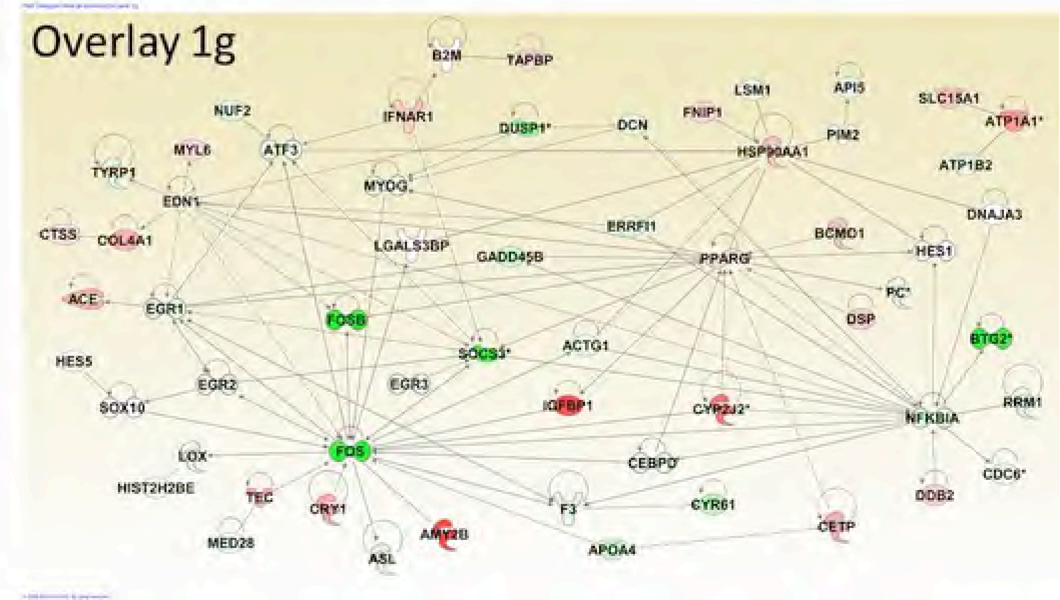


Cardio-
vascular

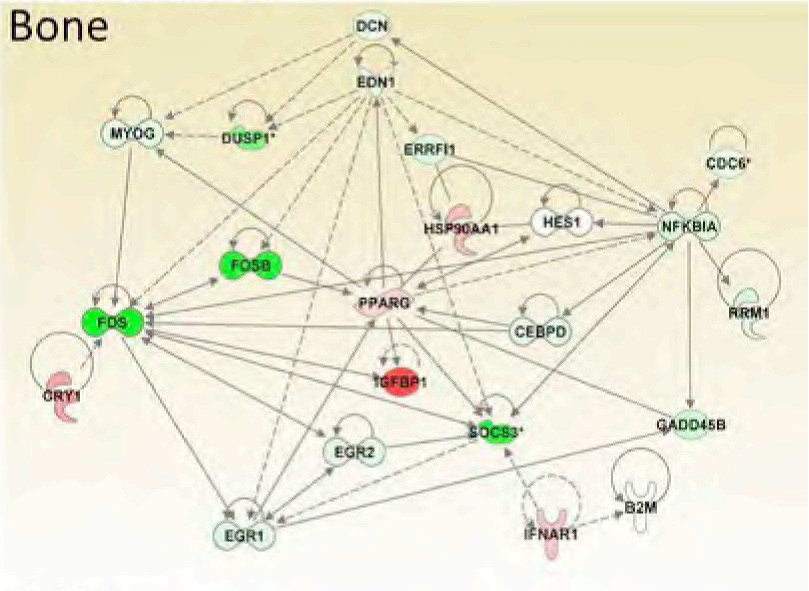



Overlay 3g > 1g

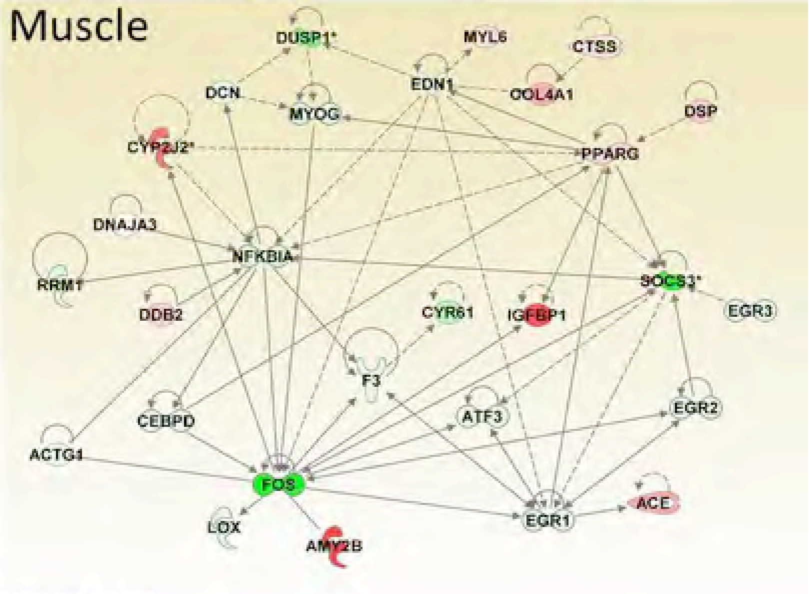

Overlay 3g > axe


Overlay 1g

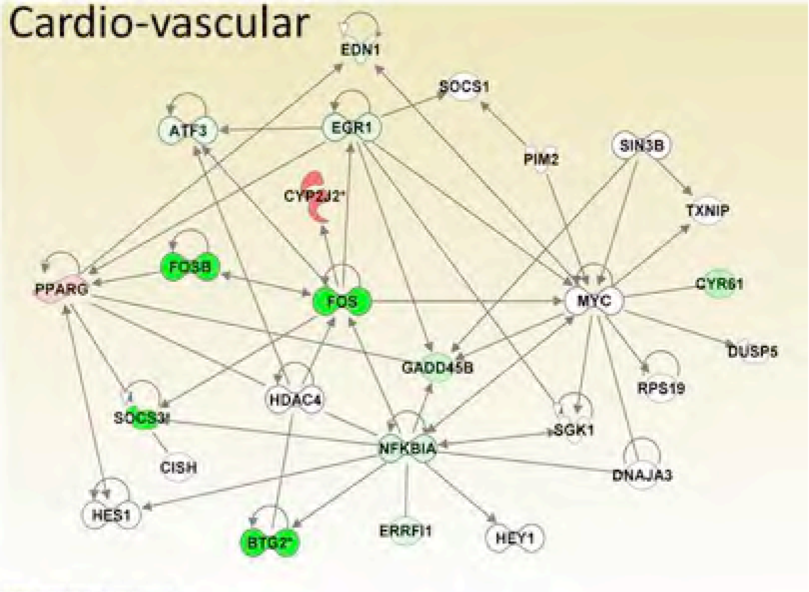
Path Designer network. all common bone lnc-axe-1g



Path Designer network all common muscle lnc-axe-1g 240714



Path Designer network cardiovasc all common lnc-axe-1g



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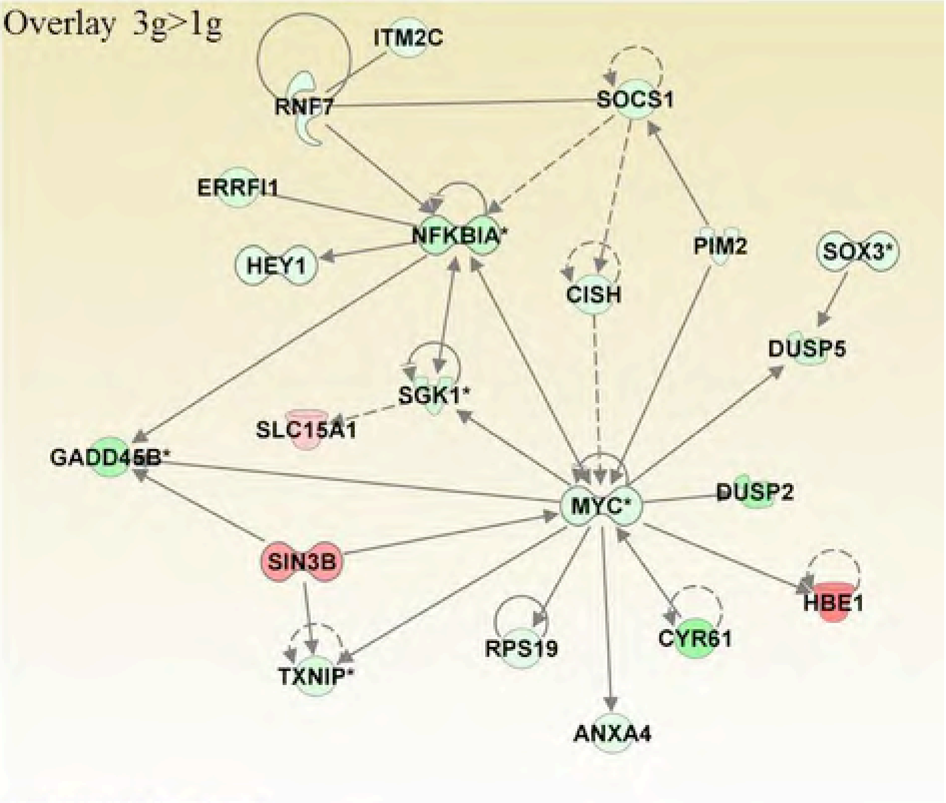

Path Designer network common gene 1g-3g 250714

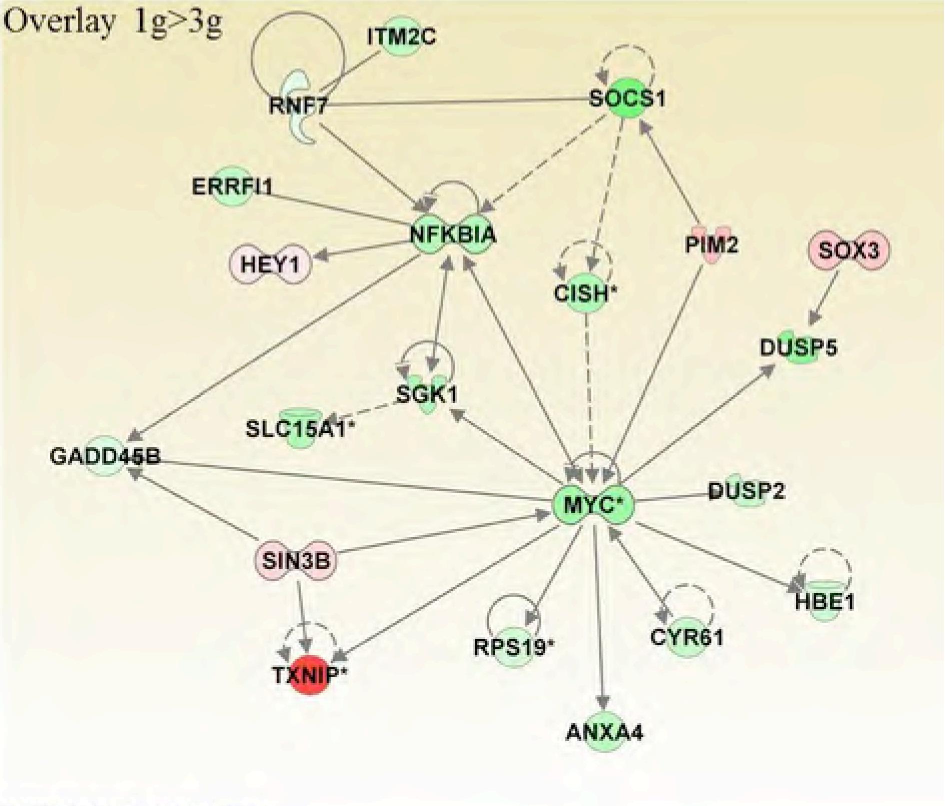

Table S1

	Primer	Forward (5' -> 3')	Reverse (5' -> 3')	Amplicon size (bp)
Housekeeping gene	**gadph**	GTGGAGTCTACTGGTGTCTTC	GTGCAGGAGGCATTGCTTACA	
Relative microgravity	btg2	GGTGTTCAGAGACGGACTCG	GAGGGTCCATTTCATGGTTG	110
	cebpb	TATGCAAGCAGCCAGTCAAC	TGGTACTGGGGCAAAGAGTC	106
	fos	GGTATTACCCGCTCAACCAG	TGACAGTTGGCACGAAAGAG	75
	fos b	TGCCGCTAAGTGTAGGAACC	CAGGCGCTCTTTCTCCTTC	130
	klf2	TGCACTTTTTCTGGATGTGG	TCCCAACTGCAATGATAGGG	127
	socs3	GGGAAGACAAGAGCCGAGAC	ACACACCAAACCCTGAGCTG	114
VitD3 and PTH	bglap	TCTTCCTGACTCCTCAGATACTAAAC	TTCCAGCCCTCTTCTGTCTC	116
	col1a1	CACAGAAGACCGGACCCTAC	CTTTGAGGCGAGGGAAGTT	
	col1a2	CGTACTTGCCGTGACATCAG	GTCTGGCCAGTAGAGAAGTCG	125
	col10a1	TGCCCATGGTGAGAGATATG	GTGCCTGGTTCTCCTGCTAC	105
	dlx5a	CCAATACCACGGAGTCAATG	GCTGTGGAGTATGAGCCGTA	
	dlx6a	AATCACCGTTTCCAGCAGAC	CGCCTTGTTTCAACAGCTTC	142
	osx	AAATCAGCTCGTGGTTCTGG	GCTGTGGACAGGTTTCTTCC	132
	pth1a	CAGGCCTCTGAGAAGCAAAC	GTTTCATCTGCAGCCAGTCC	104
	runx2b	GTGGCCACTTACCACAGAGC	TCGGAGAGTCATCCAGCTT	88
	sparc	AGGTGGAGACCGGAGAGTTT	CCCTTCTTGCAGTGATGGTT	91
	spp1	CGCCACAGTCTTCTGTGTACC	TTGAACAATTACAAGCTCTTCTGAG	76
VitD3 confirmation	cad	TCATTGGCGCAAAGACATAC	ACCCGTGATTCTGAGAGGTG	107
	cyp24a1	TGGAGATCAAACCATGGAAAG	CCGTCCAGCTTCATGACTTC	145
	fgf4	AAATCACCGGCGTACACAAC	CGTAAAGCTTCCCTTTGCTG	132
	igfbp1	TCCCGAGAGCTGGAGACC	AGCAGGTGATGCAGTGAGC	127
	slc26a3	AAGCCTACCGCAAACACAAG	CTTCATCCACCCAATGACAG	116
	slc6a18	AATGGGACAACAAGGTCCAG	CAGGTACGGGATCAGAAACG	125
	socs1	TGTATTGCCTGCTCTTGGAG	TGATTCCCTTCCACTGAACTG	
PTH confirmation	fgf4	AAATCACCGGCGTACACAAC	CGTAAAGCTTCCCTTTGCTG	132
	mcph1	TACGCCAGCTCTGAAAAACC	AACATTCGGAGTTGGTCAGC	101
	ndrg2	AAGCACCAAACCTGCTCAAC	CTCGTACGGAGCCTGATCTC	131
	nrbp2	GCATCGAGAGTGCGTACTTG	TCCACCTGCATCAGGTCCTC	142
	rxra	GAGTGGGCGAAGAGGATTC	CCTGTGGCCAACAGTATTCC	146
	slc6a18	AATGGGACAACAAGGTCCAG	CAGGTACGGGATCAGAAACG	125
Hypergravity 3g	nr1d1	CCGCAGTAGACACGAACAAC	CGAAGCAGGGTTGTGTAAGG	141
	rhcg	CGAGGAGGCAGACACTAACTG	CAGGAAGGTCATGAGGAACC	148
	socs1	TGTATTGCCTGCTCTTGGAG	TGATTCCCTTCCACTGAACTG	144
	spry4	ATCGCAACGACCTGTTCATC	AATGTGGTGAGGAACCCTTG	124
	txnip	GAGTCGGATGCGCTAAAGTC	CAGGCCTGAGAGTGATGGAG	141

Table S2

A

				Score of ossification (Y)		X^2 pearson	Logistic regression	
Structures	Treat	N	Mean	early	advanced	p-value	OR (IC 95%)	p-value
anguloarticular down	Control	28	0.75	20 (71.43%)	8 (28.57%)		1	
	VitD3	29	0.86	18 (62.07%)	11 (37.93%)	0.454	1.528 (0.503-4.642)	0.455
anguloarticular up	Control	28	0.75	7 (25.00%)	21 (75.00%)		1	
	VitD3	29	0.83	5 (17.24%)	24 (82.76%)	0.473	1.600 (0.441-5.803)	0.475
branchiostegal ray1 down	Control	28	0.54	13 (46.43%)	15 (53.57%)		1	
	VitD3	29	0.86	4 (13.76%)	25 (86.24%)	**0.007**	5.417 (1.490-19.690)	**0.010**
branchiostegal ray1 up	Control	28	0.57	12 (42.86%)	16 (57.14%)		1	
	VitD3	29	0.86	4 (13.76%)	25 (86.24%)	**0.015**	4.688 (1.285-17.096)	**0.019**
branchiostegal ray2 down	Control	28	0.21	22 (78.57%)	6 (21.43%)		1	
	VitD3	29	0.59	12 (41.38%)	17 (58.62%)	**0.004**	5.194 (1.618-16.680)	**0.006**
branchiostegal ray2 up	Control	28	0.21	22 (78.57%)	6 (21.43%)		1	
	VitD3	29	0.79	6 (20.69%)	23 (79.31%)	**<0.001**	14.056 (3.933-50.232)	**<0.001**
maxilla down	Control	28	0.36	18 (64.29%)	10 (35.71%)		1	
	VitD3	29	0.66	10 (34.48%)	19 (65.25%)	**0.024**	3.420 (1.152-10.153)	**0.027**
maxilla up	Control	28	0.29	20 (71.43%)	8 (28.57%)		1	
	VitD3	29	0.38	18 (62.07%)	11 (37.93%)	0.454	1.528 (0.503-4.642)	0.455

B

				Score of ossification (Y)			X^2 pearson	Ordinal logistic regression	
Structures	Treat	N	Mean	early	advanced	over	p-value	OR (IC 95%)	p-value
ceratohyal down	Control	28	1.71	8 (28.57%)	20 (71.43%)	0 (0%)		1	
	VitD3	29	2.21	4 (13.79%)	15 (51.72%)	10 (34.48%)	**0.002**	6.075 (1.747-21.127)	**0.005**
ceratohyal up	Control	28	1.75	7 (25%)	21 (75%)	0 (0%)		1	
	VitD3	29	2.28	2 (6.90%)	17 (58.62%)	10 (34.48%)	**0.001**	11.764 (2. 406-57.514)	**0.002**
dentary down	Control	28	1.93	2 (7.14%)	26 (92.86%)	0 (0%)		1	
	VitD3	29	2.14	0 (0%)	25 (86.21%)	4 (13.79%	0.050	/	/
dentary up	Control	28	1.93	2 (7.14%)	26 (92.86%)	0 (0%)		1	
	VitD3	29	2.17	0 (0%)	24 (82.76%)	5 (17.24%)	**0.029**	/	/
entopterygoid down	Control	28	1.86	4 (14.29%)	24 (85.71%)	0 (0%)		1	
	VitD3	29	2.48	1 (3.45%)	13 (44.83%)	15 (51.72%)	**<0.001**	33.972 (4.040-285.690)	**0.001**
entopterygoid up	Control	28	1.86	4 (14.29%)	24 (85.71%)	0 (0%)		1	
	VitD3	29	2.45	2 (6.90%)	12 (41.38%)	15 (51.72%)	**<0.001**	16.542 (3.299-82.948)	**<0.001**
hyomandibular down	Control	28	1.82	5 (17.86%)	23 (82.14%)	0 (0%)		1	
	VitD3	29	2.41	3 (10.35%)	11 (37.93%)	15 (51.72%)	**<0.001**	11.226 (2.794-45.400)	**<0.001**
hyomandibular up	Control	28	1.75	7 (25%)	21 (75%)	0 (0%)		1	
	VitD3	29	2.54	3 (10.35%)	7 (24.14%)	19 (65.52%)	**<0.001**	19.373 (4.695-79.936)	**<0.001**

Table S3

A

				Score of ossification (Y)		X^2 pearson	Logistic regression	
Structures	Treat	N	Mean	early	advanced	p-value	OR (IC 95%)	p-value
branchiostegal ray1 down	Control	29	1.00	0 (0%)	29 (100%)		1	
	PTH	27	0.93	2 (7.41%)	25 (92.59%)	0.136	/	0.995
branchiostegal ray1 up	Control	29	1.00	0 (0%)	29 (100%)		1	
	PTH	27	0.85	4 (14.81%)	23 (85.19%)	**0.031**	/	0.995
entopterygoid down	Control	29	0.97	1 (3.45%)	28 (96.55%)		1	
	PTH	27	0.41	16 (59.26%)	11 (40.74%)	**<0.001**	0.025 (0.003-0.208)	**<0.001**
entopterygoid up	Control	29	0.97	1 (3.45%)	28 (96.55%)		1	
	PTH	27	0.41	16 (59.26%)	11 (40.74%)	**<0.001**	0.025 (0.003-0.208)	**<0.001**

B

				Score of ossification (Y)			X^2 pearson	Ordinal logistic regression	
Structures	Treat	N	Mean	absence	early	advanced	p-value	OR (IC 95%)	p-value
anguloarticular down	Control	29	1.28	8 (27.59%)	5 (17.24%)	16 (55.17%)		1	
	PTH	27	0.11	25 (92.60%)	1 (3.7%)	1 (3.7%)	**<0.001**	0.031 (0.006-0.1577)	**<0.001**
anguloarticular up	Control	29	1.52	4 (13.79%)	6 (20.69%)	19 (65.52%)		1	
	PTH	27	0.04	26 (96.3%)	1 (3.7%)	0 (0%)	**<0.001**	0.006 (0.001-0.055)	**<0.001**
branchiostegal ray2 down	Control	29	1.03	6 (20.69%)	16 (55.17%)	7 (24.14%)		1	
	PTH	27	0.19	22 (81.48%)	5 (18.52%)	0 (0%)	**<0.001**	0.054 (0.014-0.201)	**<0.001**
branchiostegal ray2 up	Control	29	1.17	4 (13.79%)	16 (55.17%)	9 (31.04%)		1	
	PTH	27	0.30	19 (70.37%)	8 (29.63%)	0 (0%)	**<0.001**	0.055 (0.015-0.207)	**<0.001**
ceratohyal down	Control	29	1.66	2 (6.90%)	6 (20.69%)	21 (72.41%)		1	
	PTH	27	0.41	21 (77.78%)	1 (3.7%)	5 (18.52%)	**<0.001**	0.047 (0.013-0.169)	**<0.001**
ceratohyal up	Control	29	1.66	3 (10.35%)	4 (13.79%)	22 (75.86%)		1	
	PTH	27	0.44	19 (70.37%)	4 (14.81%)	4 (14.81%)	**<0.001**	0.052 (0.015-0.183)	**<0.001**
dentary down	Control	29	1.79	0 (0%)	6 (20.69%)	23 (79.31%)		1	
	PTH	27	0.78	8 (29.63%)	17 (62.96%)	2 (7.41%)	**<0.001**	0.018 (0.003-0.010)	**<0.001**
dentary up	Control	29	1.79	0 (0%)	6 (20.69%)	23 (79.31%)		1	
	PTH	27	0.70	10 (37.04%)	15 (55.55%)	2 (7.41%)	**<0.001**	0.018 (0.003-0.095)	**<0.001**
hyomandibular down	Control	29	1.86	0 (0%)	4 (13.79%)	25 (86.21%)		1	
	PTH	27	0.93	12 (44.44%)	5 (18.52%)	10 (37.04%)	**<0.001**	0.075 (0.020-0.282)	**<0.001**
hyomandibular up	Control	29	1.86	0 (0%)	4 (13.79%)	25 (86.21%)		1	
	PTH	27	0.96	12 (44.44%)	4 (14.81%)	11 (40.74%)	**<0.001**	0.087 (0.023-0.323)	**<0.001**
maxilla down	Control	29	1.93	1 (3.45%)	0 (0%)	28 (96.55%)		1	
	PTH	27	0.93	11 (40.74%)	7 (25.93%)	9 (33.33%)	**<0.001**	0.019 (0.002-0.163)	**<0.001**
maxilla up	Control	29	1.93	1 (3.45%)	0 (0%)	28 (96.55%)		1	
	PTH	27	1.00	8 (29.63%)	11 (40.74%)	8 (29.63%)	**<0.001**	0.017 (0.002-0.142)	**<0.001**

Symbol	Entrez Gene Name	Log Ratio VitD3	p-value	N	Type(s)
A2M	alpha-2-macroglobulin	-1.165	5.01E-02	D	transporter
A2M	alpha-2-macroglobulin	-1.793	6.14E-02	D	transporter
ACTR6	ARP6 actin-related protein 6 homolog (yeast)	-0.644	2.70E-02		transporter
AP1S1	adaptor-related protein complex 1. sigma 1 subunit	0.736	5.82E-02		transporter
APOA4	apolipoprotein A-IV	-1.756	1.63E-02	D	transporter
APOA4	apolipoprotein A-IV	-0.647	8.52E-02	D	transporter
APOA4	apolipoprotein A-IV	-1.392	1.22E-02	D	transporter
APOA4	apolipoprotein A-IV	-0.681	9.49E-02	D	transporter
ATP1A1	ATPase. Na+/K+ transporting. alpha 1 polypeptide	-0.385	7.00E-02		transporter
ATP2B3	ATPase. Ca++ transporting. plasma membrane 3	0.425	7.17E-02		transporter
ATP9B	ATPase. class II. type 9B	0.431	5.68E-02		transporter
CACNA2D2	calcium channel. voltage-dependent. alpha 2/delta subunit 2	0.384	4.79E-02		ion channel
CNGA3	cyclic nucleotide gated channel alpha 3	-0.613	4.55E-02		ion channel
FABP2	fatty acid binding protein 2. intestinal	-0.752	5.78E-02	D	transporter
FABP2	fatty acid binding protein 2. intestinal	-0.805	3.76E-02	D	transporter
FOLR1	folate receptor 1 (adult)	-1.087	2.01E-02	D	transporter
FOLR1	folate receptor 1 (adult)	-0.896	3.04E-02	D	transporter
GJB3	gap junction protein. beta 3. 31kDa	-0.483	6.57E-02		transporter
HBZ	hemoglobin. zeta	-0.594	4.10E-02	D	transporter
HBZ	hemoglobin. zeta	-0.488	3.19E-02	D	transporter
HBZ	hemoglobin. zeta	-0.629	9.27E-02	D	transporter
HBZ	hemoglobin. zeta	-0.669	8.67E-02	D	transporter
HBZ	hemoglobin. zeta	-0.673	9.16E-02	D	transporter
KCNMB2	potassium large conductance calcium-activated channel. subfamily M. beta member 2	-0.630	5.61E-02		ion channel
LDLR	low density lipoprotein receptor	-0.530	3.25E-02		transporter
MTTP	microsomal triglyceride transfer protein	-0.512	8.32E-02		transporter
PDZD3	PDZ domain containing 3	-0.903	5.77E-02		transporter
PEA15	phosphoprotein enriched in astrocytes 15	0.408	3.50E-02		transporter
PLLP	plasmolipin	-0.428	5.22E-02		transporter
Rrbp1	ribosome binding protein 1	-0.401	2.77E-02		transporter
SCN4B	sodium channel. voltage-gated. type IV. beta subunit	-0.412	3.16E-02		ion channel
SERINC5	serine incorporator 5	0.379	5.07E-02		transporter
SLC10A3	solute carrier family 10. member 3	0.474	9.07E-03		transporter
SLC11A2	solute carrier family 11 (proton-coupled divalent metal ion transporter). member 2	0.401	3.39E-02		transporter
SLC16A2	solute carrier family 16. member 2 (thyroid hormone transporter)	0.834	5.93E-02		transporter
SLC25A15	solute carrier family 25 (mitochondrial carrier; ornithine transporter) member 15	0.498	4.11E-02		transporter
SLC25A43	solute carrier family 25. member 43	-0.686	9.15E-02		transporter
SLC26A3	solute carrier family 26 (anion exchanger). member 3	-0.929	2.80E-02		transporter
SLC27A2	solute carrier family 27 (fatty acid transporter). member 2	-0.549	2.12E-02		transporter
SLC28A2	solute carrier family 28 (concentrative nucleoside transporter). member 2	-0.868	3.93E-02	D	transporter
SLC28A2	solute carrier family 28 (concentrative nucleoside transporter). member 2	-0.526	7.42E-02	D	transporter
SLC2A2	solute carrier family 2 (facilitated glucose transporter). member 2	-0.543	2.87E-02	D	transporter
SLC2A2	solute carrier family 2 (facilitated glucose transporter). member 2	-0.830	8.52E-02	D	transporter
SLC35A1	solute carrier family 35 (CMP-sialic acid transporter). member A1	0.420	6.18E-02		transporter
SLC37A4	solute carrier family 37 (glucose-6-phosphate transporter). member 4	-0.400	9.73E-02		transporter
SLC43A1	solute carrier family 43 (amino acid system L transporter). member 1	-1.042	2.47E-02	D	transporter
SLC43A1	solute carrier family 43 (amino acid system L transporter). member 1	-0.998	1.09E-02	D	transporter
SLC43A1	solute carrier family 43 (amino acid system L transporter). member 1	-1.069	3.46E-02	D	transporter
SLC43A1	solute carrier family 43 (amino acid system L transporter). member 1	-1.074	3.80E-02	D	transporter
SLC5A2	solute carrier family 5 (sodium/glucose cotransporter).	-0.451	5.70E-02		transporter

SLC5A2	solute carrier family 5 (sodium/glucose cotransporter). member 2	-0.451	5.70E-02		transporter
SLC5A9	solute carrier family 5 (sodium/sugar cotransporter). member 9	-0.744	2.82E-02		transporter
SLC6A18	solute carrier family 6 (neutral amino acid transporter). member 18	-0.461	2.93E-02		transporter
SLC6A19	solute carrier family 6 (neutral amino acid transporter). member 19	-0.769	2.22E-02		transporter
SLC6A9	solute carrier family 6 (neurotransmitter transporter. glycine). member 9	0.390	6.83E-02		transporter
SLC7A3	solute carrier family 7 (cationic amino acid transporter. y+ system). member 3	0.465	7.70E-02		transporter
SYT15	synaptotagmin XV	-0.380	5.80E-02		transporter
TCN2	transcobalamin II	-0.476	5.10E-02		transporter
TF	transferrin	-1.122	1.45E-02	D	transporter
TF	transferrin	-1.179	2.34E-02	D	transporter
TF	transferrin	-1.289	9.25E-03	D	transporter
TF	transferrin	-0.959	1.04E-02	D	transporter
TF	transferrin	-1.132	1.15E-02	D	transporter
TF	transferrin	-1.152	3.26E-02	D	transporter
TF	transferrin	-1.138	9.54E-03	D	transporter
Tmed11	transmembrane emp24 protein transport domain containing	-0.717	3.17E-02		transporter
TTPA	tocopherol (alpha) transfer protein	-0.426	9.78E-02		transporter
TTYH3	tweety family member 3	0.402	7.16E-02		ion channel
ZP3	zona pellucida glycoprotein 3 (sperm receptor)	-0.788	3.73E-02		transporter
ABRA	actin-binding Rho activating protein	-0.848	7.28E-02		transcription regulator
ANKRD33	ankyrin repeat domain 33	-0.547	7.27E-02		transcription regulator
ATF4	activating transcription factor 4	0.453	9.66E-02		transcription regulator
BCL6	B-cell CLL/lymphoma 6	0.525	4.10E-02		transcription regulator
CALCOCO1	calcium binding and coiled-coil domain 1	-1.011	8.40E-02		transcription regulator
CNBP	CCHC-type zinc finger. nucleic acid binding protein	-0.585	2.01E-02	D	transcription regulator
CNBP	CCHC-type zinc finger. nucleic acid binding protein	-0.531	3.29E-02	D	transcription regulator
CNBP	CCHC-type zinc finger. nucleic acid binding protein	-0.468	5.01E-02	D	transcription regulator
ETV4	ets variant 4	0.423	4.87E-02		transcription regulator
FOSB	FBJ murine osteosarcoma viral oncogene homolog B	-0.988	7.37E-02		transcription regulator
FOXK1	forkhead box K1	0.426	6.79E-02		transcription regulator
FOXO3	forkhead box O3	-0.386	4.34E-02	D	transcription regulator
FOXO3	forkhead box O3	-0.507	7.90E-02	D	transcription regulator
FOXO3	forkhead box O3	-0.401	4.36E-02	D	transcription regulator
FOXQ1	forkhead box Q1	0.692	4.92E-02		transcription regulator
GATA6	GATA binding protein 6	-0.460	8.38E-02		transcription regulator
GSPT1	G1 to S phase transition 1	0.438	8.68E-02		translation regulator
HIF3A	hypoxia inducible factor 3. alpha subunit	0.476	2.53E-02	D	transcription regulator
HIF3A	hypoxia inducible factor 3. alpha subunit	0.482	6.22E-02	D	transcription regulator
HIF3A	hypoxia inducible factor 3. alpha subunit	0.387	8.16E-02	D	transcription regulator
KLF11	Kruppel-like factor 11	1.451	2.42E-02	D	transcription regulator
KLF11	Kruppel-like factor 11	2.629	8.99E-03	D	transcription regulator
KLF13	Kruppel-like factor 13	1.185	2.28E-02	D	transcription regulator
KLF13	Kruppel-like factor 13	1.032	3.64E-02	D	transcription

MEIS2	Meis homeobox 2	0.393	3.99E-02		transcription regulator
MYC	v-myc avian myelocytomatosis viral oncogene homolog	-0.443	8.64E-02		transcription regulator
MYOG	myogenin (myogenic factor 4)	-0.545	1.07E-02		transcription regulator
NCOA4	nuclear receptor coactivator 4	0.464	3.89E-02	D	transcription regulator
NCOA4	nuclear receptor coactivator 4	0.467	3.06E-02	D	transcription regulator
NR0B2	nuclear receptor subfamily 0. group B. member 2	0.631	2.65E-02		ligand-dependent nuclear receptor
NRARP	NOTCH-regulated ankyrin repeat protein	0.528	8.64E-02	D	transcription regulator
NRARP	NOTCH-regulated ankyrin repeat protein	0.473	8.63E-02	D	transcription regulator
PPARA	peroxisome proliferator-activated receptor alpha	-0.556	2.94E-02		ligand-dependent nuclear receptor
RYBP	RING1 and YY1 binding protein	0.707	4.61E-02	D	transcription regulator
RYBP	RING1 and YY1 binding protein	0.548	7.74E-02	D	transcription regulator
SMARCC1	SWI/SNF related. matrix associated. actin dependent regulator of chromatin. subfamily c. member 1	0.516	8.92E-02	D	transcription regulator
SMARCC1	SWI/SNF related. matrix associated. actin dependent regulator of chromatin. subfamily c. member 1	0.578	6.43E-02	D	transcription regulator
SOX4	SRY (sex determining region Y)-box 4	0.459	4.76E-02	D	transcription regulator
SOX4	SRY (sex determining region Y)-box 4	0.395	2.72E-02	D	transcription regulator
SOX4	SRY (sex determining region Y)-box 4	0.480	9.74E-02	D	transcription regulator
STAT3	signal transducer and activator of transcription 3 (acute-phase response factor)	0.471	1.22E-02		transcription regulator
TWIST1	twist family bHLH transcription factor 1	-0.416	7.22E-02		transcription regulator
ZNF423	zinc finger protein 423	0.557	5.30E-02		transcription regulator
ADRB2	adrenoceptor beta 2. surface	-0.603	2.52E-02		G-protein coupled receptor
CD36	CD36 molecule (thrombospondin receptor)	-0.421	7.09E-02		transmembrane receptor
CUBN	cubilin (intrinsic factor-cobalamin receptor)	-0.444	3.16E-02		transmembrane receptor
GPC1	glypican 1	0.535	2.44E-02	D	transmembrane receptor
GPC1	glypican 1	0.376	2.86E-02	D	transmembrane receptor
GPR112	G protein-coupled receptor 112	-0.595	7.88E-02		G-protein coupled receptor
GPR139	G protein-coupled receptor 139	0.556	3.32E-03		G-protein coupled receptor
ITGB4	integrin. beta 4	0.535	2.90E-02		transmembrane receptor
LYVE1	lymphatic vessel endothelial hyaluronan receptor 1	0.806	6.75E-02		transmembrane receptor
OPN1LW	opsin 1 (cone pigments). long-wave-sensitive	-1.538	3.33E-03		G-protein coupled receptor
OPRL1	opiate receptor-like 1	-0.613	4.39E-02		G-protein coupled receptor
PGRMC1	progesterone receptor membrane component 1	-0.388	4.56E-02		transmembrane receptor
RELT	RELT tumor necrosis factor receptor	0.460	6.03E-02		transmembrane receptor
C5	complement component 5	0.543	8.88E-04		cytokine
EBI3	Epstein-Barr virus induced 3	-1.268	3.77E-02	D	cytokine

EBI3	Epstein-Barr virus induced 3	-1.512	3.66E-02	D	cytokine
IGF2	insulin-like growth factor 2 (somatomedin A)	0.761	9.30E-03		growth factor
PDGFC	platelet derived growth factor C	0.592	8.87E-02		growth factor
BAIAP2	BAI1-associated protein 2	0.381	3.52E-03		kinase
BCKDK	branched chain ketoacid dehydrogenase kinase	-0.413	7.09E-02		kinase
CDKN3	cyclin-dependent kinase inhibitor 3	-0.445	6.96E-02		phosphatase
CHKA	choline kinase alpha	-0.509	4.48E-02		kinase
EEF2K	eukaryotic elongation factor-2 kinase	-0.414	2.01E-02		kinase
FBP1	fructose-1.6-bisphosphatase 1	-0.551	8.30E-02	D	phosphatase
FBP1	fructose-1.6-bisphosphatase 1	-0.384	8.33E-02	D	phosphatase
FBP1	fructose-1.6-bisphosphatase 1	-0.556	7.13E-02	D	phosphatase
GNE	glucosamine (UDP-N-acetyl)-2-epimerase/N-acetylmannosamine kinase	-0.400	3.30E-02		kinase
GRK7	G protein-coupled receptor kinase 7	-0.752	6.95E-02	D	kinase
GRK7	G protein-coupled receptor kinase 7	-0.618	8.45E-02	D	kinase
LPIN1	lipin 1	-1.165	6.70E-02	D	phosphatase
LPIN1	lipin 1	-1.208	6.14E-02	D	phosphatase
LPIN1	lipin 1	-1.370	6.74E-02	D	phosphatase
MEX3B	mex-3 RNA binding family member B	0.548	8.21E-02	D	kinase
MEX3B	mex-3 RNA binding family member B	0.508	6.91E-02	D	kinase
NRBP2	nuclear receptor binding protein 2	-0.477	7.35E-02		kinase
OBSCN	obscurin. cytoskeletal calmodulin and titin-interacting RhoGEF	-0.382	5.35E-02		kinase
PCK1	phosphoenolpyruvate carboxykinase 1 (soluble)	0.511	8.54E-02	D	kinase
PCK1	phosphoenolpyruvate carboxykinase 1 (soluble)	0.577	8.54E-02	D	kinase
PCK2	phosphoenolpyruvate carboxykinase 2 (mitochondrial)	-0.632	1.94E-02	D	kinase
PCK2	phosphoenolpyruvate carboxykinase 2 (mitochondrial)	-0.668	2.59E-02	D	kinase
PDK2	pyruvate dehydrogenase kinase. isozyme 2	-0.622	1.45E-02	D	kinase
PDK2	pyruvate dehydrogenase kinase. isozyme 2	-0.700	3.27E-02	D	kinase
PDK2	pyruvate dehydrogenase kinase. isozyme 2	-0.475	5.08E-02	D	kinase
PDK4	pyruvate dehydrogenase kinase. isozyme 4	-0.455	4.37E-02		kinase
PHKA1	phosphorylase kinase. alpha 1 (muscle)	-0.449	5.97E-02		kinase
PIK3R1	phosphoinositide-3-kinase. regulatory subunit 1 (alpha)	-0.450	9.29E-02		kinase
PIM1	pim-1 oncogene	0.678	2.57E-02		kinase
PKLR	pyruvate kinase. liver and RBC	-0.759	6.79E-02	D	kinase
PKLR	pyruvate kinase. liver and RBC	-0.688	8.46E-02	D	kinase
PKLR	pyruvate kinase. liver and RBC	-0.701	9.77E-02	D	kinase
PKLR	pyruvate kinase. liver and RBC	-0.874	1.17E-02	D	kinase
PPM1H	protein phosphatase. Mg2+/Mn2+ dependent. 1H	0.446	2.87E-02		phosphatase
PPP4C	protein phosphatase 4. catalytic subunit	0.401	7.85E-03		phosphatase
PTP4A3	protein tyrosine phosphatase type IVA. member 3	0.583	4.67E-02	D	phosphatase
PTP4A3	protein tyrosine phosphatase type IVA. member 3	0.478	6.33E-02	D	phosphatase
STK19	serine/threonine kinase 19	-0.456	3.89E-02		kinase
STK39	serine threonine kinase 39	-0.426	6.98E-03	D	kinase
STK39	serine threonine kinase 39	-0.545	4.04E-02	D	kinase
TPK1	thiamin pyrophosphokinase 1	-0.481	1.69E-02		kinase
TTN	titin	-0.522	6.08E-03	D	kinase
TTN	titin	-0.424	6.24E-02	D	kinase
TTN	titin	-0.578	3.95E-02	D	kinase
TTN	titin	-0.375	2.22E-02	D	kinase
TWF2	twinfilin actin-binding protein 2	-0.418	5.80E-02		kinase
ACE2	angiotensin I converting enzyme 2	-0.407	5.38E-02		peptidase
ANPEP	alanyl (membrane) aminopeptidase	-0.444	1.22E-02		peptidase
CNDP2	CNDP dipeptidase 2 (metallopeptidase M20 family)	-0.540	4.32E-02		peptidase
CPA2	carboxypeptidase A2 (pancreatic)	-0.640	8.02E-02		peptidase
CTRB2	chymotrypsinogen B2	-0.791	4.38E-02		peptidase
CTSH	cathepsin H	-0.407	3.05E-02		peptidase
CTSS	cathepsin S	0.377	4.77E-02		peptidase
DPP4	dipeptidyl-peptidase 4	-0.628	4.78E-02		peptidase
EPHX1	epoxide hydrolase 1. microsomal (xenobiotic)	-0.725	9.10E-03	D	peptidase
EPHX1	epoxide hydrolase 1. microsomal (xenobiotic)	-0.625	1.93E-02	D	peptidase

F7	coagulation factor VII (serum prothrombin conversion accelerator)	-0.569	6.00E-02		peptidase
F9	coagulation factor IX	0.668	9.22E-03		peptidase
HABP2	hyaluronan binding protein 2	-1.004	6.57E-02		peptidase
LONP1	lon peptidase 1. mitochondrial	0.447	7.49E-02		peptidase
MMP11	matrix metallopeptidase 11 (stromelysin 3)	0.883	5.26E-03		peptidase
PAPPA	pregnancy-associated plasma protein A. pappalysin 1	0.723	3.21E-02	D	peptidase
PAPPA	pregnancy-associated plasma protein A. pappalysin 1	0.588	4.75E-02	D	peptidase
PEPD	peptidase D	-0.461	6.22E-02	D	peptidase
PEPD	peptidase D	-0.407	4.87E-03	D	peptidase
TMPRSS13	transmembrane protease. serine 13	0.378	3.67E-02		peptidase
USP14	ubiquitin specific peptidase 14 (tRNA-guanine transglycosylase)	0.491	5.08E-03		peptidase
USP37	ubiquitin specific peptidase 37	0.387	8.75E-02		peptidase
AASDHPPT	aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase	-0.541	4.88E-02	D	enzyme
AASDHPPT	aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase	-0.609	5.49E-02	D	enzyme
ACAA1	acetyl-CoA acyltransferase 1	-0.413	2.26E-02	D	enzyme
ACAA1	acetyl-CoA acyltransferase 1	-0.473	3.14E-02	D	enzyme
ACADS	acyl-CoA dehydrogenase. C-2 to C-3 short chain	-0.389	2.18E-02		enzyme
ACOX1	acyl-CoA oxidase 1. palmitoyl	-0.845	6.53E-02		enzyme
ACSF2	acyl-CoA synthetase family member 2	-0.494	2.08E-02		enzyme
ACSL3	acyl-CoA synthetase long-chain family member 3	0.467	6.01E-02		enzyme
ACTA1	actin. alpha 1. skeletal muscle	-0.526	3.90E-02	D	other
ACTA1	actin. alpha 1. skeletal muscle	-0.621	8.67E-02	D	other
ACTA1	actin. alpha 1. skeletal muscle	-0.628	3.00E-02	D	other
ACTA1	actin. alpha 1. skeletal muscle	-0.446	4.16E-02	D	other
ACTA1	actin. alpha 1. skeletal muscle	-0.694	7.54E-02	D	other
ACTA1	actin. alpha 1. skeletal muscle	-0.591	1.61E-02	D	other
AGMAT	agmatine ureohydrolase (agmatinase)	-0.429	5.74E-02		enzyme
AKR1B1	aldo-keto reductase family 1. member B1 (aldose reductase)	-0.385	3.86E-02		enzyme
ALAS2	aminolevulinate. delta-. synthase 2	-0.682	4.22E-02	D	enzyme
ALAS2	aminolevulinate. delta-. synthase 2	-0.565	7.58E-02	D	enzyme
ALDH4A1	aldehyde dehydrogenase 4 family. member A1	-0.460	1.67E-02		enzyme
ANXA2	annexin A2	-0.786	7.11E-02	D	other
ANXA2	annexin A2	-0.597	3.78E-02	D	other
ANXA2	annexin A2	-0.660	6.56E-02	D	other
AOC1	amine oxidase. copper containing 1	-0.684	4.09E-02		enzyme
ARMC2	armadillo repeat containing 2	-0.495	7.47E-02		other
ARRDC2	arrestin domain containing 2	0.376	3.89E-02		other
ATAD2B	ATPase family. AAA domain containing 2B	0.446	5.54E-02		other
ATAD3A	ATPase family. AAA domain containing 3A	0.380	5.92E-03		other
BCAT2	branched chain amino-acid transaminase 2. mitochondrial	-0.638	2.30E-02	D	enzyme
BCAT2	branched chain amino-acid transaminase 2. mitochondrial	-0.636	4.97E-02	D	enzyme
BCAT2	branched chain amino-acid transaminase 2. mitochondrial	-0.453	8.24E-02	D	enzyme
BNIP3	BCL2/adenovirus E1B 19kDa interacting protein 3	-0.599	4.91E-02		other
BOC	BOC cell adhesion associated. oncogene regulated	-0.556	2.27E-02		other
C4orf33	chromosome 4 open reading frame 33	-0.376	3.97E-02		other
C6	complement component 6	0.418	5.60E-03		other
C7	complement component 7	0.665	8.71E-02		other
CA7	carbonic anhydrase VII	-0.566	4.59E-02		enzyme
CAD	carbamoyl-phosphate synthetase 2. aspartate transcarbamylase. and dihydroorotase	0.510	9.35E-02		enzyme
CADPS	Ca++-dependent secretion activator	-0.443	8.96E-02		other
CAT	catalase	-0.515	1.71E-02	D	enzyme
CAT	catalase	-0.423	8.00E-02	D	enzyme
CCBL2	cysteine conjugate-beta lyase 2	-0.381	4.82E-02		enzyme
CCDC125	coiled-coil domain containing 125	-0.380	7.53E-02		other
CEACAM20	carcinoembryonic antigen-related cell adhesion molecule 20	-0.549	6.26E-02		other
CEP85	centrosomal protein 85kDa	-0.511	9.95E-02		other
CES1	carboxylesterase 1	-2.047	4.85E-02	D	enzyme

CES1	carboxylesterase 1	-2.244	4.64E-02	D	enzyme
CFH	complement factor H	-1.151	7.01E-02		other
CHD8	chromodomain helicase DNA binding protein 8	0.382	3.18E-02		enzyme
CHPT1	choline phosphotransferase 1	-0.441	2.47E-02		enzyme
CHST2	carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2	-0.429	7.11E-02		enzyme
CISH	cytokine inducible SH2-containing protein	-1.615	7.77E-02	D	other
CISH	cytokine inducible SH2-containing protein	-1.269	3.92E-02	D	other
CISH	cytokine inducible SH2-containing protein	-1.294	5.72E-02	D	other
CISH	cytokine inducible SH2-containing protein	-1.261	4.79E-02	D	other
CISH	cytokine inducible SH2-containing protein	-1.779	4.33E-02	D	other
CISH	cytokine inducible SH2-containing protein	-1.260	3.41E-02	D	other
CISH	cytokine inducible SH2-containing protein	-0.983	6.59E-02	D	other
CLEC4E	C-type lectin domain family 4. member E	0.422	7.50E-02	D	other
CLEC4E	C-type lectin domain family 4. member E	0.443	7.01E-02	D	other
COL9A2	collagen. type IX. alpha 2	-0.417	5.61E-02		other
CREB3L3	cAMP responsive element binding protein 3-like 3	-0.475	1.42E-02		other
CROT	carnitine O-octanoyltransferase	-1.574	5.98E-02		enzyme
CTDSPL	CTD (carboxy-terminal domain. RNA polymerase II. polypeptide A) small phosphatase-like	0.496	1.93E-02	D	other
CTDSPL	CTD (carboxy-terminal domain. RNA polymerase II. polypeptide A) small phosphatase-like	0.558	5.62E-02	D	other
CTH	cystathionase (cystathionine gamma-lyase)	-0.581	3.92E-02	D	enzyme
CTH	cystathionase (cystathionine gamma-lyase)	-0.536	7.30E-02	D	enzyme
CUZD1	CUB and zona pellucida-like domains 1	-0.562	7.23E-02	D	other
CUZD1	CUB and zona pellucida-like domains 1	-0.629	4.81E-02	D	other
CYB5R2	cytochrome b5 reductase 2	-0.437	2.99E-02		enzyme
CYP24A1	cytochrome P450. family 24. subfamily A. polypeptide 1	2.955	2.87E-03	D	enzyme
CYP24A1	cytochrome P450. family 24. subfamily A. polypeptide 1	3.160	5.18E-03	D	enzyme
CYP26A1	cytochrome P450. family 26. subfamily A. polypeptide 1	0.830	5.03E-02	D	enzyme
CYP26A1	cytochrome P450. family 26. subfamily A. polypeptide 1	0.779	2.02E-02	D	enzyme
CYP27A1	cytochrome P450. family 27. subfamily A. polypeptide 1	-0.477	7.42E-02		enzyme
Cyp2ac1	cytochrome P450. family 2. subfamily ac. polypeptide 1	0.836	1.74E-02	D	other
Cyp2ac1	cytochrome P450. family 2. subfamily ac. polypeptide 1	-0.639	9.50E-02	D	other
Cyp2ac1	cytochrome P450. family 2. subfamily ac. polypeptide 1	1.134	1.52E-02	D	other
Cyp2ac1	cytochrome P450. family 2. subfamily ac. polypeptide 1	-0.605	1.88E-02	D	other
Cyp2ac1	cytochrome P450. family 2. subfamily ac. polypeptide 1	1.069	8.69E-02	D	other
Cyp2g1	cytochrome P450. family 2. subfamily g. polypeptide 1	-0.375	5.17E-02	D	enzyme
Cyp2g1	cytochrome P450. family 2. subfamily g. polypeptide 1	-0.457	9.67E-02	D	enzyme
CYP2J2	cytochrome P450. family 2. subfamily J. polypeptide 2	-1.015	6.16E-02		enzyme
CYP3A7	cytochrome P450. family 3. subfamily A. polypeptide 7	-0.911	8.51E-02	D	enzyme
CYP3A7	cytochrome P450. family 3. subfamily A. polypeptide 7	-0.414	2.54E-02	D	enzyme
CYP8B1	cytochrome P450. family 8. subfamily B. polypeptide 1	-0.686	2.20E-02		enzyme
D1Pas1	DNA segment. Chr 1. Pasteur Institute 1	0.411	1.52E-02		other
DAO	D-amino-acid oxidase	-0.464	1.11E-02	D	enzyme
DAO	D-amino-acid oxidase	-0.576	5.06E-02	D	enzyme
DBT	dihydrolipoamide branched chain transacylase E2	-0.458	2.62E-02	D	enzyme
DBT	dihydrolipoamide branched chain transacylase E2	-0.422	4.47E-02	D	enzyme
DCLRE1B	DNA cross-link repair 1B	-0.422	3.50E-02		enzyme
DCT	dopachrome tautomerase	-0.431	1.24E-02	D	enzyme
DCT	dopachrome tautomerase	-0.410	3.93E-02	D	enzyme
DDC	dopa decarboxylase (aromatic L-amino acid decarboxylase)	-0.542	9.33E-02		enzyme
DDT	D-dopachrome tautomerase	-0.627	4.14E-02		enzyme
DDX5	DEAD (Asp-Glu-Ala-Asp) box helicase 5	0.576	9.21E-02		enzyme
DECR1	2.4-dienoyl CoA reductase 1. mitochondrial	-0.562	4.76E-02		enzyme
DHRS13	dehydrogenase/reductase (SDR family) member 13	-0.607	9.83E-02		enzyme
DHTKD1	dehydrogenase E1 and transketolase domain containing 1	-1.004	5.69E-02	D	enzyme
DHTKD1	dehydrogenase E1 and transketolase domain containing 1	-0.830	6.43E-02	D	enzyme
DHX32	DEAH (Asp-Glu-Ala-His) box polypeptide 32	0.733	2.25E-02		enzyme
DIO1	deiodinase. iodothyronine. type I	-0.573	4.26E-03	D	enzyme
DIO1	deiodinase. iodothyronine. type I	-0.609	8.94E-02	D	enzyme
DMGDH	dimethylglycine dehydrogenase	-0.462	1.64E-02		enzyme
DMRT1	doublesex and mab-3 related transcription factor 1	-0.834	2.21E-02		other

DNAJC4	DnaJ (Hsp40) homolog. subfamily C. member 4	-0.446	8.95E-02		other
DNMT3A	DNA (cytosine-5-)-methyltransferase 3 alpha	0.516	9.87E-03		enzyme
DOLPP1	dolichyldiphosphatase 1	0.390	4.27E-02		enzyme
DPYS	dihydropyrimidinase	-0.402	7.06E-02		enzyme
ELOVL2	ELOVL fatty acid elongase 2	-0.449	3.45E-02		enzyme
ETNPPL	ethanolamine-phosphate phospho-lyase	-0.751	9.08E-02		enzyme
FADS6	fatty acid desaturase 6	1.083	3.19E-02		enzyme
FAM131C	family with sequence similarity 131. member C	0.503	6.11E-02		other
FAM13A	family with sequence similarity 13. member A	-0.421	2.66E-02		other
FAM46C	family with sequence similarity 46. member C	-0.601	3.17E-02	D	other
FAM46C	family with sequence similarity 46. member C	-0.443	1.38E-02	D	other
FBXO2	F-box protein 2	-0.613	2.09E-03		enzyme
FCGBP	Fc fragment of IgG binding protein	-0.687	5.23E-02		other
FSTL1	follistatin-like 1	0.455	9.56E-03		other
GADD45A	growth arrest and DNA-damage-inducible. alpha	0.396	9.17E-02	D	other
GADD45A	growth arrest and DNA-damage-inducible. alpha	-0.941	4.59E-02	D	other
GADD45A	growth arrest and DNA-damage-inducible. alpha	-0.844	4.88E-02	D	other
GATM	glycine amidinotransferase (L-arginine:glycine amidinotransferase)	0.435	4.89E-02	D	enzyme
GATM	glycine amidinotransferase (L-arginine:glycine amidinotransferase)	0.377	5.33E-02	D	enzyme
GATM	glycine amidinotransferase (L-arginine:glycine amidinotransferase)	0.417	4.60E-02	D	enzyme
GCAT	glycine C-acetyltransferase	-0.904	2.06E-02		enzyme
GCG	glucagon	-0.492	2.42E-02		other
GCHFR	GTP cyclohydrolase I feedback regulator	-0.928	4.35E-02		other
GDA	guanine deaminase	-0.524	5.50E-02		enzyme
GGCT	gamma-glutamylcyclotransferase	0.627	3.80E-02		enzyme
GLDC	glycine dehydrogenase (decarboxylating)	-0.505	6.31E-02	D	enzyme
GLDC	glycine dehydrogenase (decarboxylating)	-0.586	2.13E-02	D	enzyme
GLDC	glycine dehydrogenase (decarboxylating)	-0.515	4.58E-02	D	enzyme
GNG10	guanine nucleotide binding protein (G protein). gamma 10	-0.561	7.18E-03		enzyme
GNPDA2	glucosamine-6-phosphate deaminase 2	0.813	2.85E-02		enzyme
GOT2	glutamic-oxaloacetic transaminase 2. mitochondrial	-0.468	2.78E-02		enzyme
GPT	glutamic-pyruvate transaminase (alanine aminotransferase)	0.392	5.25E-02	D	enzyme
GPT	glutamic-pyruvate transaminase (alanine aminotransferase)	0.590	6.83E-02	D	enzyme
GPT	glutamic-pyruvate transaminase (alanine aminotransferase)	0.490	3.04E-02	D	enzyme
GPT	glutamic-pyruvate transaminase (alanine aminotransferase)	0.632	9.35E-02	D	enzyme
GPX1	glutathione peroxidase 1	-0.770	2.77E-02		enzyme
GRB10	growth factor receptor-bound protein 10	-1.053	2.88E-02		other
GSR	glutathione reductase	0.377	6.52E-02		enzyme
GSTK1	glutathione S-transferase kappa 1	-0.415	1.97E-02		enzyme
GSTO1	glutathione S-transferase omega 1	-0.470	7.39E-02		enzyme
Gstt3	glutathione S-transferase. theta 3	0.410	1.45E-02		enzyme
HADH	hydroxyacyl-CoA dehydrogenase	-0.409	1.09E-02		enzyme
HAGH	hydroxyacylglutathione hydrolase	-0.501	2.77E-02		enzyme
HAO2	hydroxyacid oxidase 2 (long chain)	-0.441	6.52E-02		enzyme
HGD	homogentisate 1.2-dioxygenase	-0.534	7.20E-02		enzyme
HMCES	5-hydroxymethylcytosine (hmC) binding. ES cell-specific	-0.540	6.37E-02		other
HMGCL	3-hydroxymethyl-3-methylglutaryl-CoA lyase	-0.374	2.07E-02		enzyme
HNMT	histamine N-methyltransferase	-0.431	1.15E-02		enzyme
HPD	4-hydroxyphenylpyruvate dioxygenase	-0.543	8.16E-02		enzyme
HSD11B1L	hydroxysteroid (11-beta) dehydrogenase 1-like	-0.698	4.07E-02		other
HSD11B2	hydroxysteroid (11-beta) dehydrogenase 2	-0.408	5.70E-02		enzyme
HSD17B4	hydroxysteroid (17-beta) dehydrogenase 4	-0.450	4.12E-02		enzyme
HSD3B7	hydroxy-delta-5-steroid dehydrogenase. 3 beta- and steroid delta-isomerase 7	-0.406	4.16E-02		enzyme
HSP90B1	heat shock protein 90kDa beta (Grp94). member 1	0.467	7.45E-02	D	other
HSP90B1	heat shock protein 90kDa beta (Grp94). member 1	0.486	4.70E-02	D	other
IFRD1	interferon-related developmental regulator 1	0.507	3.92E-02		other
IGFBP1	insulin-like growth factor binding protein 1	1.077	3.38E-02	D	other
IGFBP1	insulin-like growth factor binding protein 1	1.774	4.67E-03	D	other
IGFBP1	insulin-like growth factor binding protein 1	1.109	2.40E-02	D	other

IGFBP1	insulin-like growth factor binding protein 1	1.120	4.72E-02	D	other
IGFBP1	insulin-like growth factor binding protein 1	1.919	3.90E-03	D	other
ING5	inhibitor of growth family. member 5	-0.734	4.22E-02		other
INSIG1	insulin induced gene 1	0.616	4.79E-02		other
IRS1	insulin receptor substrate 1	0.816	2.28E-03		enzyme
ITIH3	inter-alpha-trypsin inhibitor heavy chain 3	-0.514	9.64E-02	D	other
ITIH3	inter-alpha-trypsin inhibitor heavy chain 3	-0.528	5.99E-02	D	other
ITLN1	intelectin 1 (galactofuranose binding)	-1.274	4.88E-02		other
JAKMIP1	janus kinase and microtubule interacting protein 1	0.546	1.39E-03		other
KIAA1324	KIAA1324	-0.623	8.12E-02		other
KRT17	keratin 17	0.499	2.06E-02	D	other
KRT17	keratin 17	0.444	8.65E-02	D	other
KRT17	keratin 17	0.393	7.13E-02	D	other
KRT17	keratin 17	0.520	2.04E-02	D	other
LCT	lactase	-1.104	3.59E-02		enzyme
LECT1	leukocyte cell derived chemotaxin 1	-0.532	9.60E-02		other
LOC285556	uncharacterized LOC285556	0.570	8.68E-02		other
LOX	lysyl oxidase	0.459	6.99E-02		enzyme
LPL	lipoprotein lipase	-0.851	6.88E-02	D	enzyme
LPL	lipoprotein lipase	-0.865	9.87E-02	D	enzyme
MALRD1	MAM and LDL receptor class A domain containing 1	-0.909	3.42E-02		other
MBOAT4	membrane bound O-acyltransferase domain containing 4	-0.404	7.76E-02		enzyme
MCM7	minichromosome maintenance complex component 7	0.373	5.31E-02		enzyme
Mettl21e	methyltransferase like 21E	-0.381	9.44E-02		other
METTL7A	methyltransferase like 7A	-0.512	1.11E-02		other
MFSD4	major facilitator superfamily domain containing 4	-0.447	5.27E-02		other
MID1	midline 1 (Opitz/BBB syndrome)	0.400	5.27E-02		other
MIOX	myo-inositol oxygenase	1.245	1.48E-02		enzyme
MLEC	malectin	-0.396	2.20E-02		other
MOCS1	molybdenum cofactor synthesis 1	-0.755	6.52E-02		other
MOGAT1	monoacylglycerol O-acyltransferase 1	-0.395	9.35E-02	D	enzyme
MOGAT1	monoacylglycerol O-acyltransferase 1	-0.588	4.41E-02	D	enzyme
MOV10L1	Mov10l1. Moloney leukemia virus 10-like 1. homolog (mouse)	0.518	4.63E-03		enzyme
MYH11	myosin. heavy chain 11. smooth muscle	-0.524	8.62E-02		other
MYH7	myosin. heavy chain 7. cardiac muscle. beta	0.479	7.96E-02	D	enzyme
MYH7	myosin. heavy chain 7. cardiac muscle. beta	0.441	7.32E-02	D	enzyme
MYL3	myosin. light chain 3. alkali; ventricular. skeletal. slow	-0.396	4.13E-02		other
NEFL	neurofilament. light polypeptide	0.483	5.76E-02	D	other
NEFL	neurofilament. light polypeptide	0.497	3.51E-02	D	other
NEFL	neurofilament. light polypeptide	0.562	6.86E-02	D	other
NEIL1	nei endonuclease VIII-like 1 (E. coli)	-0.373	5.13E-02		enzyme
NEURL2	neuralized E3 ubiquitin protein ligase 2	-0.459	3.82E-02	D	other
NEURL2	neuralized E3 ubiquitin protein ligase 2	-0.492	3.83E-02	D	other
NID1	nidogen 1	-0.453	8.81E-02	D	other
NID1	nidogen 1	-0.674	5.18E-02	D	other
NIPSNAP3A	nipsnap homolog 3A (C. elegans)	-0.391	6.85E-02		other
NLGN4Y	neuroligin 4. Y-linked	0.380	9.36E-02		enzyme
NPHP3	nephronophthisis 3 (adolescent)	-0.420	4.03E-02		other
NUDT16	nudix (nucleoside diphosphate linked moiety X)-type motif 16	-0.420	6.90E-02		enzyme
OLFM4	olfactomedin 4	-0.842	4.73E-02	D	other
OLFM4	olfactomedin 4	-0.811	2.84E-03	D	other
OXCT1	3-oxoacid CoA transferase 1	0.526	6.58E-02		enzyme
PARD3	par-3 family cell polarity regulator	0.456	6.19E-02		other
PARN	poly(A)-specific ribonuclease	0.439	2.73E-02		enzyme
PBLD	phenazine biosynthesis-like protein domain containing	-0.592	9.02E-02	D	enzyme
PBLD	phenazine biosynthesis-like protein domain containing	-1.348	6.88E-02	D	enzyme
PBLD	phenazine biosynthesis-like protein domain containing	-0.630	1.21E-02	D	enzyme
PCCA	propionyl CoA carboxylase. alpha polypeptide	-0.377	2.84E-02		enzyme
PDF	peptide deformylase (mitochondrial)	0.704	4.78E-02		enzyme
PDLIM5	PDZ and LIM domain 5	0.555	2.57E-02		other

PGM1	phosphoglucomutase 1	-0.511	5.01E-02		enzyme
PKHD1L1	polycystic kidney and hepatic disease 1 (autosomal recessive)-like 1	0.483	7.58E-02	D	other
PKHD1L1	polycystic kidney and hepatic disease 1 (autosomal recessive)-like 1	0.437	3.40E-02	D	other
PLA1A	phospholipase A1 member A	-0.393	5.29E-02		enzyme
PLD1	phospholipase D1. phosphatidylcholine-specific	-0.380	1.92E-02		enzyme
PLEKHS1	pleckstrin homology domain containing. family S member 1	0.605	1.79E-02	D	other
PLEKHS1	pleckstrin homology domain containing. family S member 1	0.480	4.20E-03	D	other
Plscr2	phospholipid scramblase 2	-0.541	4.32E-02		other
PLTP	phospholipid transfer protein	1.264	8.09E-02		enzyme
POPDC3	popeye domain containing 3	-0.460	6.40E-03		other
PPAT	phosphoribosyl pyrophosphate amidotransferase	0.495	5.02E-04		enzyme
PPDPF	pancreatic progenitor cell differentiation and proliferation factor	0.451	6.11E-02		other
PRAF2	PRA1 domain family. member 2	-0.461	5.63E-02		other
PRRC2B	proline-rich coiled-coil 2B	0.455	1.60E-03		other
PRTFDC1	phosphoribosyl transferase domain containing 1	-0.464	6.13E-02		enzyme
PTGR2	prostaglandin reductase 2	-0.460	1.87E-02		enzyme
PTS	6-pyruvoyltetrahydropterin synthase	-0.818	6.19E-02		enzyme
PURG	purine-rich element binding protein G	1.842	6.83E-02		other
PYGB	phosphorylase. glycogen; brain	-0.475	5.29E-02		enzyme
RCL1	RNA terminal phosphate cyclase-like 1	0.378	8.17E-02		enzyme
RCVRN	recoverin	-0.432	7.17E-02		other
RGN	regucalcin	-0.492	6.19E-02		enzyme
RGS21	regulator of G-protein signaling 21	-0.516	8.80E-02		other
RHOG	ras homolog family member G	-0.401	9.83E-02		enzyme
RND2	Rho family GTPase 2	0.437	2.96E-02	D	enzyme
RND2	Rho family GTPase 2	0.690	1.08E-02	D	enzyme
RPE65	retinal pigment epithelium-specific protein 65kDa	-1.279	1.31E-02		enzyme
SC5D	sterol-C5-desaturase	0.680	2.80E-02		enzyme
SEPP1	selenoprotein P. plasma. 1	-0.420	8.57E-02		other
SERPINB6	serpin peptidase inhibitor. clade B (ovalbumin). member 6	-0.532	5.78E-02		other
SERPINH1	serpin peptidase inhibitor. clade H (heat shock protein 47). member 1. (collagen binding protein 1)	-0.467	6.14E-02		other
SESN1	sestrin 1	-0.811	3.88E-02	D	other
SESN1	sestrin 1	-0.697	5.81E-02	D	other
SESN1	sestrin 1	-0.780	5.69E-02	D	other
SH2D4A	SH2 domain containing 4A	0.531	7.18E-02		other
SLC16A12	solute carrier family 16. member 12	0.999	3.26E-02		other
SLC25A38	solute carrier family 25. member 38	-1.258	8.13E-02		other
SLC25A47	solute carrier family 25. member 47	-0.721	1.18E-02		other
SLC9A3R1	solute carrier family 9. subfamily A (NHE3. cation proton antiporter 3). member 3 regulator 1	-0.513	5.78E-02	D	other
SLC9A3R1	solute carrier family 9. subfamily A (NHE3. cation proton antiporter 3). member 3 regulator 1	-0.510	9.15E-02	D	other
SMPDL3B	sphingomyelin phosphodiesterase. acid-like 3B	-0.782	5.74E-02		enzyme
SNRNP25	small nuclear ribonucleoprotein 25kDa (U11/U12)	-0.392	7.20E-02		other
SOCS1	suppressor of cytokine signaling 1	-1.494	6.57E-02	D	other
SOCS1	suppressor of cytokine signaling 1	-1.321	6.60E-02	D	other
STC2	stanniocalcin 2	-1.754	1.51E-02		other
STEAP4	STEAP family member 4	0.529	5.57E-02		enzyme
STRA6	stimulated by retinoic acid 6	-0.477	3.85E-02	D	other
STRA6	stimulated by retinoic acid 6	-0.566	2.60E-02	D	other
SUCLG2	succinate-CoA ligase. GDP-forming. beta subunit	-0.419	1.63E-02		enzyme
SULT1C2	sulfotransferase family. cytosolic. 1C. member 2	-0.709	5.34E-02		enzyme
SULT2B1	sulfotransferase family. cytosolic. 2B. member 1	1.185	1.48E-02	D	enzyme
SULT2B1	sulfotransferase family. cytosolic. 2B. member 1	1.216	6.97E-03	D	enzyme
SULT2B1	sulfotransferase family. cytosolic. 2B. member 1	0.418	2.75E-02	D	enzyme
SULT2B1	sulfotransferase family. cytosolic. 2B. member 1	0.604	1.65E-02	D	enzyme
TAT	tyrosine aminotransferase	1.603	1.43E-02	D	enzyme
TAT	tyrosine aminotransferase	1.403	1.16E-02	D	enzyme
TAT	tyrosine aminotransferase	1.291	9.73E-03	D	enzyme

TAT	tyrosine aminotransferase	1.309	3.22E-03	D	enzyme
TAT	tyrosine aminotransferase	1.522	6.46E-03	D	enzyme
TECTB	tectorin beta	0.802	7.69E-02	D	other
TECTB	tectorin beta	0.897	8.15E-02	D	other
TES	testis derived transcript (3 LIM domains)	0.376	7.17E-02		other
THBS2	thrombospondin 2	0.747	4.31E-02		other
TM4SF5	transmembrane 4 L six family member 5	-0.563	3.76E-02		other
TMEM150B	transmembrane protein 150B	-0.761	6.28E-02		other
TMEM205	transmembrane protein 205	-0.422	9.97E-03		other
TMEM263	transmembrane protein 263	0.872	5.33E-02		other
TMOD4	tropomodulin 4 (muscle)	-0.456	1.97E-02		other
TMX4	thioredoxin-related transmembrane protein 4	0.383	8.02E-02		enzyme
TNNI2	troponin I type 2 (skeletal. fast)	-0.403	9.93E-02		enzyme
TP53INP1	tumor protein p53 inducible nuclear protein 1	0.429	5.74E-02		other
TREH	trehalase (brush-border membrane glycoprotein)	-0.550	7.09E-02	D	enzyme
TREH	trehalase (brush-border membrane glycoprotein)	-0.632	7.69E-02	D	enzyme
TRIM3	tripartite motif containing 3	-0.425	9.17E-02		other
TSPAN1	tetraspanin 1	-0.929	3.23E-02	D	other
TSPAN1	tetraspanin 1	-0.943	4.74E-02	D	other
TTC36	tetratricopeptide repeat domain 36	-0.420	6.46E-02		other
TTC38	tetratricopeptide repeat domain 38	-0.440	2.03E-02		other
TTC7A	tetratricopeptide repeat domain 7A	-0.426	1.23E-02		other
TUBA8	tubulin. alpha 8	0.399	9.95E-02		other
TUBB4B	tubulin. beta 4B class IVb	0.405	1.80E-02	D	other
TUBB4B	tubulin. beta 4B class IVb	0.434	4.56E-03	D	other
TUBB4B	tubulin. beta 4B class IVb	0.379	3.67E-02	D	other
TXNIP	thioredoxin interacting protein	-0.553	4.73E-02		other
UGDH	UDP-glucose 6-dehydrogenase	-0.523	3.32E-02		enzyme
UGT1A1	UDP glucuronosyltransferase 1 family. polypeptide A1	-0.922	1.56E-02	D	enzyme
UGT1A1	UDP glucuronosyltransferase 1 family. polypeptide A1	-0.864	7.69E-03	D	enzyme
UGT2A3	UDP glucuronosyltransferase 2 family. polypeptide A3	-0.398	4.79E-02		enzyme
UPB1	ureidopropionase. beta	-0.399	2.83E-02		enzyme
URAD	ureidoimidazoline (2-oxo-4-hydroxy-4-carboxy-5-) decarboxylase	-0.677	7.23E-02		enzyme
USH1C	Usher syndrome 1C (autosomal recessive. severe)	-0.820	2.63E-02		other
VAPB	VAMP (vesicle-associated membrane protein)-associated protein B and C	0.388	4.41E-02		other
VASN	vasorin	0.469	1.28E-02		other
VIL1	villin 1	-0.589	3.05E-02	D	other
VIL1	villin 1	-0.491	3.11E-02	D	other
VIL1	villin 1	-0.556	5.08E-02	D	other
VTN	vitronectin	0.649	1.11E-02		other
WNT3	wingless-type MMTV integration site family. member 3	0.408	2.90E-02		other
WSB1	WD repeat and SOCS box containing 1	-0.492	1.34E-02		other
YWHAE	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein. epsilon	0.454	5.15E-02		other
ZNF729	zinc finger protein 729	-0.465	5.26E-02		other

Table S5

Category	p-value	Number of Genes
Lipid Metabolism	3.91E-12-1.79E-02	107
Molecular Transport	3.91E-12-1.79E-02	136
Small Molecule Biochemistry	3.91E-12-1.79E-02	155
Amino Acid Metabolism	1.53E-09-1.66E-02	46
Carbohydrate Metabolism	2.86E-09-1.71E-02	88
Vitamin and Mineral Metabolism	2.54E-07-1.3E-02	40
Energy Production	3.41E-07-1.66E-02	26
Protein Synthesis	5.67E-06-1.12E-02	81
Cellular Function and Maintenance	1.98E-05-1.65E-02	76
Free Radical Scavenging	2.08E-05-1.62E-02	33
Endocrine System Development and Function	6.95E-05-1.66E-02	35
Drug Metabolism	1.75E-04-5.66E-03	12
Cellular Development	2.21E-04-1.69E-02	59
Cellular Growth and Proliferation	2.21E-04-1.74E-02	43
Hematological System Development and Function	2.21E-04-1.74E-02	48
Cell-To-Cell Signaling and Interaction	3.6E-04-1.74E-02	30
Post-Translational Modification	3.91E-04-1.66E-02	32
Protein Degradation	3.91E-04-4.87E-03	27
Embryonic Development	3.91E-04-1.66E-02	48
Organ Development	3.91E-04-1.66E-02	50
Organismal Development	3.91E-04-1.66E-02	107
Skeletal and Muscular System Development and Function	3.91E-04-1.78E-02	57
Tissue Development	3.91E-04-1.69E-02	63
Cell Cycle	8.14E-04-1.66E-02	17
Organ Morphology	9.71E-04-1.78E-02	61
Tissue Morphology	9.86E-04-1.66E-02	90
Cell Death and Survival	1.18E-03-1.6E-02	46
Cardiovascular System Development and Function	1.22E-03-1.69E-02	72
Humoral Immune Response	1.22E-03-3.57E-03	3
Hair and Skin Development and Function	1.47E-03-1.66E-02	12
Cell Morphology	2.55E-03-1.66E-02	33
Cellular Movement	2.66E-03-1.45E-02	41
Cellular Compromise	2.77E-03-1.49E-02	13
Reproductive System Development and Function	3.03E-03-1.15E-02	41
Behavior	3.17E-03-3.17E-03	15
Digestive System Development and Function	3.17E-03-1.66E-02	52
Hepatic System Development and Function	3.19E-03-5.44E-03	17
Renal and Urological System Development and Function	3.45E-03-1.54E-02	56
Organismal Functions	3.51E-03-3.51E-03	9
Protein Trafficking	3.57E-03-3.57E-03	2
Connective Tissue Development and Function	3.59E-03-1.69E-02	33
Lymphoid Tissue Structure and Development	4.48E-03-7.35E-03	10
Gene Expression	4.67E-03-1.1E-02	10
DNA Replication. Recombination. and Repair	6.15E-03-6.15E-03	7
Nucleic Acid Metabolism	6.15E-03-6.15E-03	7
Cell-mediated Immune Response	6.97E-03-7.35E-03	5
Cellular Assembly and Organization	6.97E-03-1.66E-02	14
Hematopoiesis	6.97E-03-7.35E-03	5
Cell Signaling	7.35E-03-7.35E-03	3
Nervous System Development and Function	7.65E-03-7.65E-03	4
Visual System Development and Function	7.65E-03-1.13E-02	12

Symbol	Entrez Gene Name	Log Ratio PTH	p-value	N	Type(s)
BET1L	Bet1 golgi vesicular membrane trafficking protein-like	1.210	7.53E-02		transporter
CACNB1	calcium channel. voltage-dependent. beta 1 subunit	-1.060	7.90E-02		ion channel
CLCN1	chloride channel. voltage-sensitive 1	0.797	5.64E-02		ion channel
COMMD1	copper metabolism (Murr1) domain containing 1	0.545	8.50E-02		transporter
GJA9	gap junction protein. alpha 9. 59kDa	1.750	9.39E-02		transporter
KCNK18	potassium channel. subfamily K. member 18	1.040	6.67E-02		ion channel
MB	myoglobin	-0.656	9.39E-02		transporter
MTX1	metaxin 1	-0.415	5.90E-02		transporter
NXF1	nuclear RNA export factor 1	-0.902	7.90E-02		transporter
P2RX7	purinergic receptor P2X. ligand-gated ion channel. 7	-1.420	8.96E-02		ion channel
PANX1	pannexin 1	-1.060	9.58E-02		transporter
RPH3A	rabphilin 3A homolog (mouse)	0.836	4.94E-02		transporter
SLC12A3	solute carrier family 12 (sodium/chloride transporter). member 3	-0.763	5.64E-02		transporter
SLC18A3	solute carrier family 18 (vesicular acetylcholine transporter). member 3	-1.930	5.58E-02		transporter
SLC43A1	solute carrier family 43 (amino acid system L transporter). member 1	0.405	9.81E-02		transporter
SLC6A18	solute carrier family 6 (neutral amino acid transporter). member 18	-2.300	6.63E-02		transporter
SLC7A10	solute carrier family 7 (neutral amino acid transporter light chain. asc system). member 10	-1.100	5.64E-02		transporter
SLC9A6	solute carrier family 9. subfamily A (NHE6. cation proton antiporter 6). member 6	-0.985	7.90E-02		transporter
SMC4	structural maintenance of chromosomes 4	0.376	7.83E-02		transporter
AATF	apoptosis antagonizing transcription factor	-1.050	6.63E-02		transcription regulator
CALR	calreticulin	1.060	6.36E-02		transcription regulator
DMBX1	diencephalon/mesencephalon homeobox 1	0.721	9.09E-02		transcription regulator
EEF2	eukaryotic translation elongation factor 2	0.722	9.81E-02		translation regulator
EGR1	early growth response 1	-0.725	9.91E-02		transcription regulator
EPC1	enhancer of polycomb homolog 1 (Drosophila)	-0.698	7.95E-02		transcription regulator
ESR2	estrogen receptor 2 (ER beta)	-1.250	9.81E-02		ligand-dependent nuclear receptor
FOXB2	forkhead box B2	-1.080	5.89E-02		transcription regulator
GATA4	GATA binding protein 4	0.879	8.83E-02		transcription regulator
HOXA5	homeobox A5	-0.515	7.90E-02		transcription regulator
INSM2	insulinoma-associated 2	0.732	7.64E-02		transcription regulator
IRX6	iroquois homeobox 6	0.631	7.90E-02		transcription regulator
JARID2	jumonji. AT rich interactive domain 2	-1.400	9.95E-02		transcription regulator
LDB2	LIM domain binding 2	0.597	4.94E-02	D	transcription regulator
LDB2	LIM domain binding 2	1.330	5.64E-02	D	transcription regulator
LRCH4	leucine-rich repeats and calponin homology (CH) domain containing 4	1.030	5.47E-02		transcription regulator
MXI1	MAX interactor 1. dimerization protein	0.530	7.90E-02		transcription regulator
NKX3-2	NK3 homeobox 2	0.697	7.14E-02		transcription regulator
PDLIM1	PDZ and LIM domain 1	-0.943	9.27E-02		transcription regulator
PTRF	polymerase I and transcript release factor	0.480	8.88E-02		transcription regulator
RPS9	ribosomal protein S9	0.613	7.19E-02		translation regulator
RXRA	retinoid X receptor. alpha	0.993	7.64E-02		ligand-

					dependent nuclear receptor
TAF1	TAF1 RNA polymerase II. TATA box binding protein (TBP)-associated factor. 250kDa	0.416	7.96E-02		transcription regulator
TOX2	TOX high mobility group box family member 2	0.604	7.83E-02		transcription regulator
ACKR3	atypical chemokine receptor 3	-2.210	6.67E-02		G-protein coupled receptor
AVPR1A	arginine vasopressin receptor 1A	2.150	4.94E-02		G-protein coupled receptor
CALCRL	calcitonin receptor-like	0.735	7.74E-02		G-protein coupled receptor
CHRM2	cholinergic receptor. muscarinic 2	0.500	9.48E-02		G-protein coupled receptor
CHRNA6	cholinergic receptor. nicotinic. alpha 6 (neuronal)	-2.090	6.63E-02		transmembrane receptor
GFRA1	GDNF family receptor alpha 1	1.200	9.81E-02		transmembrane receptor
GPR132	G protein-coupled receptor 132	0.973	8.14E-02		G-protein coupled receptor
HLA-B	major histocompatibility complex. class I. B	0.469	6.75E-02		transmembrane receptor
ILDR1	immunoglobulin-like domain containing receptor 1	0.788	6.63E-02		transmembrane receptor
ITGA4	integrin. alpha 4 (antigen CD49D. alpha 4 subunit of VLA-4 receptor)	0.758	8.50E-02		transmembrane receptor
LHCGR	luteinizing hormone/choriogonadotropin receptor	-1.130	9.91E-02		G-protein coupled receptor
LY75	lymphocyte antigen 75	-1.390	5.90E-02		transmembrane receptor
OR8G5	olfactory receptor. family 8. subfamily G. member 5	-2.060	9.02E-02		G-protein coupled receptor
PTHR1	parathyroid hormone receptor	0.908	6.85E-02		G-protein coupled receptor
TNFRSF1A	tumor necrosis factor receptor superfamily. member 1A	1.010	7.74E-02		transmembrane receptor
TNFRSF21	tumor necrosis factor receptor superfamily. member 21	0.782	4.94E-02		transmembrane receptor
FAM3C	family with sequence similarity 3. member C	-0.477	9.09E-02		cytokine
FGF4	fibroblast growth factor 4	-1.150	7.87E-02		growth factor
GDF9	growth differentiation factor 9	-1.900	7.90E-02		growth factor
IGF1	insulin-like growth factor 1 (somatomedin C)	1.460	8.88E-02		growth factor
INHBB	inhibin. beta B	-0.830	9.02E-02		growth factor
AK3	adenylate kinase 3	-0.557	9.09E-02		kinase
COASY	CoA synthase	-1.430	9.81E-02		kinase
DAPK3	death-associated protein kinase 3	-1.300	4.94E-02		kinase
DCLK2	doublecortin-like kinase 2	1.240	7.39E-02		kinase
EPHB2	EPH receptor B2	1.540	9.81E-02		kinase
GRK4	G protein-coupled receptor kinase 4	1.840	5.60E-02		kinase
ILKAP	integrin-linked kinase-associated serine/threonine phosphatase	-0.707	5.58E-02		phosphatase
NAGK	N-acetylglucosamine kinase	-0.816	8.83E-02		kinase
NME2	NME/NM23 nucleoside diphosphate kinase 2	0.743	8.21E-02		kinase
NRBP2	nuclear receptor binding protein 2	1.330	5.64E-02	D	kinase
RPS6KA2	ribosomal protein S6 kinase. 90kDa. polypeptide 2	-0.735	6.63E-02		kinase
SGK1	serum/glucocorticoid regulated kinase 1	-0.505	7.96E-02		kinase
SYNJ1	synaptojanin 1	-2.670	8.55E-02		phosphatase
Afg3l1	AFG3(ATPase family gene 3)-like 1 (yeast)	-4.740	3.48E-02		peptidase
CPA2	carboxypeptidase A2 (pancreatic)	-0.647	9.81E-02		peptidase
IDE	insulin-degrading enzyme	-0.623	9.09E-02		peptidase
RHBDL2	rhomboid. veinlet-like 2 (Drosophila)	-0.679	9.26E-02		peptidase
SPPL2A	signal peptide peptidase like 2A	0.542	6.63E-02		peptidase
USP24	ubiquitin specific peptidase 24	1.240	6.63E-02		peptidase
ABI1	abl-interactor 1	1.040	7.14E-02		other
ADAP2	ArfGAP with dual PH domains 2	-0.726	4.94E-02		other
ALKBH5	alkB. alkylation repair homolog 5 (E. coli)	-0.900	6.63E-02		enzyme
ANLN	anillin. actin binding protein	-1.370	8.50E-02		other
ARGLU1	arginine and glutamate rich 1	0.595	9.81E-02		other

ARHGEF11	Rho guanine nucleotide exchange factor (GEF) 11	0.750	5.97E-02	other
ARHGEF19	Rho guanine nucleotide exchange factor (GEF) 19	1.420	7.80E-02	other
ARL8B	ADP-ribosylation factor-like 8B	1.270	9.39E-02	enzyme
ARPC5	actin related protein 2/3 complex. subunit 5. 16kDa	-1.050	5.64E-02	other
ARRB2	arrestin. beta 2	-0.684	6.63E-02	other
ASPN	asporin	1.670	5.50E-02	other
ASRGL1	asparaginase like 1	-0.765	4.94E-02	enzyme
AXIN1	axin 1	0.404	9.81E-02	other
C15orf41	chromosome 15 open reading frame 41	-0.815	7.83E-02	other
C2orf40	chromosome 2 open reading frame 40	1.060	9.69E-02	other
C2orf47	chromosome 2 open reading frame 47	-0.951	6.61E-02	other
C3orf58	chromosome 3 open reading frame 58	-0.676	5.58E-02	other
C4orf29	chromosome 4 open reading frame 29	-0.904	3.48E-02	other
C7	complement component 7	1.310	4.94E-02	other
CA8	carbonic anhydrase VIII	-0.650	8.50E-02	enzyme
CAB39	calcium binding protein 39	1.540	9.51E-02	enzyme
CABLES2	Cdk5 and Abl enzyme substrate 2	0.543	8.50E-02	other
CABLES2	Cdk5 and Abl enzyme substrate 2	-2.030	9.69E-02	other
CAD	carbamoyl-phosphate synthetase 2. aspartate transcarbamylase. and dihydroorotase	-1.570	6.78E-02	enzyme
CARS	cysteinyl-tRNA synthetase	-0.417	9.09E-02	enzyme
CBY1	chibby homolog 1 (Drosophila)	2.390	4.94E-02	other
CCDC62	coiled-coil domain containing 62	0.495	9.16E-02	other
CD151	CD151 molecule (Raph blood group)	-0.709	5.64E-02	other
CDC34	cell division cycle 34	-0.878	6.85E-02	enzyme
CDIPT	CDP-diacylglycerol--inositol 3-phosphatidyltransferase	-0.583	8.83E-02	enzyme
CES1	carboxylesterase 1	0.555	4.94E-02	enzyme
CHD4	chromodomain helicase DNA binding protein 4	0.425	9.39E-02	enzyme
CNPY3	canopy FGF signaling regulator 3	-0.699	5.64E-02	other
CPLX2	complexin 2	0.392	9.69E-02	other
CS	citrate synthase	-0.682	8.83E-02	enzyme
CWC22	CWC22 spliceosome-associated protein homolog (S. cerevisiae)	0.924	8.45E-02	other
CYP21A2	cytochrome P450. family 21. subfamily A. polypeptide 2	-1.260	5.89E-02	enzyme
CYP2J2	cytochrome P450. family 2. subfamily J. polypeptide 2	-0.742	9.81E-02	enzyme
DCPS	decapping enzyme. scavenger	-0.982	9.39E-02	enzyme
DCTN1	dynactin 1	0.694	6.63E-02	other
DENND5A	DENN/MADD domain containing 5A	-1.240	7.96E-02	other
DNAJB11	DnaJ (Hsp40) homolog. subfamily B. member 11	-0.892	4.94E-02	other
DNASE1L3	deoxyribonuclease I-like 3	-0.544	8.83E-02	enzyme
EFCAB4B	EF-hand calcium binding domain 4B	1.590	6.63E-02	other
EFEMP1	EGF containing fibulin-like extracellular matrix protein 1	-2.240	7.64E-02	enzyme
EFNA1	ephrin-A1	0.450	8.44E-02	other
FAIM	Fas apoptotic inhibitory molecule	1.940	7.74E-02	other
FAM177A1	family with sequence similarity 177. member A1	-0.469	7.80E-02	other
FBLN1	fibulin 1	0.742	8.50E-02	other
FOXRED1	FAD-dependent oxidoreductase domain containing 1	-0.846	7.80E-02	other
GALNT2	polypeptide N-acetylgalactosaminyltransferase 2	-0.808	7.95E-02	enzyme
GLB1	galactosidase. beta 1	1.370	5.64E-02	enzyme
GLB1L	galactosidase. beta 1-like	0.654	9.09E-02	other
Gm16500	predicted gene 16500	-0.625	5.58E-02	other
GNAL	guanine nucleotide binding protein (G protein). alpha activating activity polypeptide. olfactory type	-0.768	9.37E-02	enzyme
GPAM	glycerol-3-phosphate acyltransferase. mitochondrial	0.894	9.39E-02	enzyme
GPC3	glypican 3	0.521	9.81E-02	other
GRAMD1B	GRAM domain containing 1B	0.924	4.94E-02	other
GRAMD1C	GRAM domain containing 1C	-0.553	4.94E-02	other
GSR	glutathione reductase	-0.847	5.64E-02	enzyme
GUCA1A	guanylate cyclase activator 1A (retina)	0.659	8.18E-02	other

GUSB	glucuronidase. beta	0.544	7.97E-02	enzyme
HARS	histidyl-tRNA synthetase	-0.929	5.64E-02	enzyme
HAUS6	HAUS augmin-like complex. subunit 6	-1.550	5.58E-02	other
HDC	histidine decarboxylase	0.796	9.16E-02	enzyme
HIST2H2AB	histone cluster 2. H2ab	2.200	5.64E-02	other
HLA-A	major histocompatibility complex. class I. A	-1.210	9.31E-02	other
Hmga2	high mobility group AT-hook 2	0.749	5.64E-02	enzyme
HSD3B7	hydroxy-delta-5-steroid dehydrogenase. 3 beta- and steroid delta-isomerase 7	-0.626	6.85E-02	enzyme
ISM2	isthmin 2	-1.630	8.83E-02	other
ITGA9	integrin. alpha 9	1.620	6.61E-02	other
KIAA1324L	KIAA1324-like	0.789	6.84E-02	other
KIF23	kinesin family member 23	1.440	6.99E-02	other
KLHDC8A	kelch domain containing 8A	0.569	7.96E-02	other
KLHL40	kelch-like family member 40	-1.080	8.45E-02	other
KRT17	keratin 17	0.961	7.64E-02	other
L3HYPDH	L-3-hydroxyproline dehydratase (trans-)	0.984	7.64E-02	enzyme
LCTL	lactase-like	-1.250	5.64E-02	enzyme
LGI1	leucine-rich. glioma inactivated 1	-1.340	6.63E-02	other
LIPH	lipase. member H	-0.666	7.39E-02	enzyme
LOC102551489	protein unc-13 homolog C-like	0.615	5.47E-02	other
LOC391722	myosin regulatory light chain 12B-like	0.561	9.39E-02	other
MARVELD1	MARVEL domain containing 1	0.596	9.81E-02	other
MCPH1	microcephalin 1	0.952	5.58E-02	other
MFAP3L	microfibrillar-associated protein 3-like	-0.835	5.64E-02	other
MLEC	malectin	-0.645	7.14E-02	other
MOCOS	molybdenum cofactor sulfurase	1.700	7.90E-02	enzyme
MRPL41	mitochondrial ribosomal protein L41	-0.438	7.14E-02	other
MSI2	musashi RNA-binding protein 2	0.945	9.81E-02	other
MTSS1	metastasis suppressor 1	-0.852	9.76E-02	other
MYO1G	myosin IG	-1.330	9.96E-02	other
NDRG2	NDRG family member 2	0.628	5.97E-02	other
OSBPL2	oxysterol binding protein-like 2	-1.130	9.16E-02	other
PALM2	paralemmin 2	1.120	7.64E-02	other
PAPL	iron/zinc purple acid phosphatase-like protein	0.867	9.69E-02	enzyme
PARP14	poly (ADP-ribose) polymerase family. member 14	0.765	5.58E-02	other
PDIA4	protein disulfide isomerase family A. member 4	-0.652	5.67E-02	enzyme
PDZD8	PDZ domain containing 8	0.876	9.03E-02	other
PHLDA2	pleckstrin homology-like domain. family A. member 2	-0.853	5.64E-02	other
PLA2G12A	phospholipase A2. group XIIA	0.779	9.39E-02	enzyme
PPIL2	peptidylprolyl isomerase (cyclophilin)-like 2	-0.408	7.90E-02	enzyme
PPP1R14C	protein phosphatase 1. regulatory (inhibitor) subunit 14C	-1.640	5.64E-02	other
PRMT1	protein arginine methyltransferase 1	-0.971	5.90E-02	enzyme
PSMD5	proteasome (prosome. macropain) 26S subunit. non-ATPase. 5	-0.915	7.70E-02	other
PTGES	prostaglandin E synthase	0.509	9.70E-02	enzyme
PTGES	prostaglandin E synthase	1.510	9.81E-02	enzyme
PTH1	parathyroid hormone	-1.320	4.94E-02	other
PTX3	pentraxin 3. long	1.820	3.48E-02	other
RAD21	RAD21 homolog (S. pombe)	1.570	6.75E-02	other
RALGDS	ral guanine nucleotide dissociation stimulator	-0.985	4.94E-02	other
RBM18	RNA binding motif protein 18	-0.655	6.72E-02	other
RHOF	ras homolog family member F (in filopodia)	-1.700	4.94E-02	enzyme
RIT1	Ras-like without CAAX 1	1.050	9.16E-02	enzyme
RPAP1	RNA polymerase II associated protein 1	-1.220	9.81E-02	other
RPL23	ribosomal protein L23	0.705	9.39E-02	other
RPL27A	ribosomal protein L27a	0.977	7.90E-02	other
RPUSD1	RNA pseudouridylate synthase domain containing 1	-0.862	5.64E-02	enzyme
SAG	S-antigen; retina and pineal gland (arrestin)	0.517	7.64E-02	other

SASH1	SAM and SH3 domain containing 1	1.970	9.25E-02		other
SCARB2	scavenger receptor class B. member 2	1.360	7.64E-02		other
SERPINE1	serpin peptidase inhibitor. clade E (nexin. plasminogen activator inhibitor type 1). member 1	-0.981	9.81E-02		other
SGCG	sarcoglycan. gamma (35kDa dystrophin-associated glycoprotein)	-1.510	3.48E-02		other
SHISA2	shisa family member 2	0.907	6.63E-02		other
SLC25A51	solute carrier family 25. member 51	-0.658	8.20E-02		other
SLC43A3	solute carrier family 43. member 3	-1.330	3.48E-02		other
SMURF2	SMAD specific E3 ubiquitin protein ligase 2	-3.370	9.30E-02		enzyme
SPTLC3	serine palmitoyltransferase. long chain base subunit 3	-1.180	6.85E-02		enzyme
SRSF1	serine/arginine-rich splicing factor 1	-0.577	7.87E-02	D	other
SRSF1	serine/arginine-rich splicing factor 1	-0.529	7.90E-02	D	other
SSB	Sjogren syndrome antigen B (autoantigen La)	-0.657	6.41E-02		enzyme
ST6GAL2	ST6 beta-galactosamide alpha-2.6-sialyltranferase 2	0.645	7.63E-02		enzyme
ST8SIA2	ST8 alpha-N-acetyl-neuraminide alpha-2.8-sialyltransferase 2	0.641	7.95E-02		enzyme
TANGO2	transport and golgi organization 2 homolog (Drosophila)	-1.460	5.58E-02		other
TBC1D1	TBC1 (tre-2/USP6. BUB2. cdc16) domain family. member 1	1.990	5.50E-02		other
TFPI	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	-2.390	5.64E-02		other
TGFBRAP1	transforming growth factor. beta receptor associated protein 1	0.705	6.75E-02		other
THOC2	THO complex 2	0.491	7.74E-02		other
TMEM181	transmembrane protein 181	2.470	4.94E-02		other
TMEM30B	transmembrane protein 30B	-1.070	9.39E-02		other
TMEM87B	transmembrane protein 87B	0.501	9.26E-02		other
TMX3	thioredoxin-related transmembrane protein 3	0.600	6.63E-02		enzyme
TPD52L1	tumor protein D52-like 1	-0.544	9.81E-02		other
TSPEAR	thrombospondin-type laminin G domain and EAR repeats	0.741	7.58E-02		other
TTC14	tetratricopeptide repeat domain 14	-0.712	6.85E-02		other
Ttc39a	tetratricopeptide repeat domain 39A	-0.906	7.14E-02		other
TXNRD3	thioredoxin reductase 3	-1.490	9.37E-02		enzyme
UNC93B1	unc-93 homolog B1 (C. elegans)	0.698	9.39E-02		other
USP32	ubiquitin specific peptidase 32	0.805	7.74E-02		enzyme
VPS37B	vacuolar protein sorting 37 homolog B (S. cerevisiae)	0.758	5.58E-02		other
VSNL1	visinin-like 1	0.441	9.25E-02		other
WDR5	WD repeat domain 5	-1.400	9.09E-02		other
XAF1	XIAP associated factor 1	0.857	6.63E-02		other
ZC3H6	zinc finger CCCH-type containing 6	0.961	8.28E-02		other
ZNF346	zinc finger protein 346	0.867	9.39E-02		other
ZNF729	zinc finger protein 729	-1.320	6.85E-02	D	other
ZNF729	zinc finger protein 729	-0.981	8.50E-02	D	other
ZNF729	zinc finger protein 729	2.170	9.16E-02	D	other

TableS7

Category	p-value	Number of Genes
Cellular Development	1.83E-04-4.02E-02	13
Connective Tissue Development and Function	1.83E-04-4.02E-02	13
Embryonic Development	1.83E-04-4.02E-02	17
Cell-To-Cell Signaling and Interaction	5.45E-04-5E-02	18
Cellular Assembly and Organization	5.45E-04-4.16E-02	13
Cellular Function and Maintenance	5.45E-04-4.16E-02	18
Hair and Skin Development and Function	5.45E-04-4.02E-02	5
Hematological System Development and Function	5.45E-04-5E-02	18
Hematopoiesis	5.45E-04-4.02E-02	5
Organ Morphology	5.45E-04-4.86E-02	22
Skeletal and Muscular System Development and Function	5.45E-04-4.02E-02	13
Tissue Development	5.45E-04-4.08E-02	25
Cellular Movement	1.15E-03-5E-02	16
Immune Cell Trafficking	1.15E-03-5E-02	15
Cell Cycle	1.78E-03-4.02E-02	10
Cell Morphology	1.78E-03-4.99E-02	19
Organ Development	1.78E-03-4.02E-02	15
Organismal Development	1.78E-03-4.86E-02	23
Respiratory System Development and Function	1.78E-03-4.02E-02	3
Tissue Morphology	1.78E-03-4.63E-02	14
Cardiovascular System Development and Function	2.65E-03-4.86E-02	16
Cellular Compromise	2.65E-03-4.02E-02	9
Cell Death and Survival	3.55E-03-4.02E-02	31
Inflammatory Response	5.07E-03-4.16E-02	13
Cellular Growth and Proliferation	5.65E-03-1.36E-02	7
Nervous System Development and Function	5.65E-03-4.02E-02	15
Small Molecule Biochemistry	6.2E-03-4.02E-02	21
Molecular Transport	7.68E-03-4.79E-02	15
Humoral Immune Response	8.35E-03-4.79E-02	5
Protein Synthesis	8.35E-03-4.79E-02	17
Cell-mediated Immune Response	8.48E-03-2.7E-02	6
Cardiovascular Disease	9.3E-03-4.49E-02	8
Digestive System Development and Function	9.3E-03-2.7E-02	3
Lymphoid Tissue Structure and Development	9.3E-03-4.49E-02	5
Carbohydrate Metabolism	1.08E-02-2.7E-02	9
Lipid Metabolism	1.11E-02-4.02E-02	8
Amino Acid Metabolism	1.36E-02-4.02E-02	2
Antimicrobial Response	1.36E-02-1.36E-02	1
Cell Signaling	1.36E-02-4.02E-02	4
Drug Metabolism	1.36E-02-2.7E-02	6
Endocrine System Development and Function	1.36E-02-1.36E-02	1
Gene Expression	1.36E-02-4.57E-02	11
Hepatic System Development and Function	1.36E-02-2.7E-02	2
Nucleic Acid Metabolism	1.36E-02-4.02E-02	5
RNA Post-Transcriptional Modification	1.36E-02-2.7E-02	1
Renal and Urological System Development and Function	1.36E-02-2.7E-02	4
Reproductive System Development and Function	1.36E-02-4.16E-02	6
Visual System Development and Function	1.36E-02-2.7E-02	2
Vitamin and Mineral Metabolism	1.36E-02-4.02E-02	4
Organismal Functions	2.18E-02-2.18E-02	2
Behavior	2.7E-02-4.02E-02	3
Free Radical Scavenging	2.7E-02-2.7E-02	1
Post-Translational Modification	2.7E-02-3.02E-02	5
Auditory and Vestibular System Development and Function	4.02E-02-4.02E-02	1
RNA Trafficking	4.02E-02-4.49E-02	2

Table S8

A

				Score of ossificaiton (Y)		X^2 pearson	Logistic regression	
Structures	Treat	N	Mean	early	advanced	p-value	OR (IC 95%)	p-value
branchiostegal ray1 down	Control	24	0.96	3 (12.50%)	21 (87.50%)		1	
	LDC 1g > 3g	24	1.00	0 (0%)	24 (100%)	0.074	/	0.995
branchiostegal ray1 up	Control	24	0.96	3 (12.50%)	21 (87.50%)		1	
	LDC 1g > 3g	24	1.00	0 (0%)	24 (100%)	0.074	/	0.995
dentary down	Control	24	1.00	0 (0%)	24 (100%)		1	
	LDC 1g > 3g	24	0.96	1 (4.17%)	23 (95.83%)	0.312	/	0.995
dentary up	Control	24	1.00	0 (0%)	24 (100%)		1	
	LDC 1g > 3g	24	0.96	1 (4.17%)	23 (95.83%)	0.312	/	0.995
entopterygoid down	Control	24	1.00	0 (0%)	24 (100%)		1	
	LDC 1g > 3g	24	1.00	0 (0%)	24 (100%)	/	/	/
entopterygoid up	Control	24	1.00	0 (0%)	24 (100%)		1	
	LDC 3 g	24	1.00	0 (0%)	24 (100%)	/	/	/
hyomandibular down	Control	24	0.71	7 (29.17%)	17 (70.83%)		1	
	LDC 1g > 3g	24	0.63	9 (37.50%)	15 (62.50%)	0.540	0.686 (0.205-2.295)	0.541
hyomandibular up	Control	24	0.71	7 (29.17%)	17 (70.83%)		1	
	LDC 3 g	24	0.63	9 (37.50%)	15 (62.50%)	0.540	0.686 (0.205-2.295)	0.541
maxilla down	Control	24	0.13	21 (87.50%)	3 (12.50%)		1	
	LDC 1g > 3g	24	0.08	22 (91.67%)	2 (8.33%)	0.637	0.636 (0.096-4.197)	0.639
maxilla up	Control	24	0.13	21 (87.50%)	3 (12.50%)		1	
	LDC 1g > 3 g	24	0.08	22 (91.67%)	2 (8.33%)	0.637	0.636 (0.096-4.197)	0.639

B

				Score of ossificaiton (Y)			X^2 pearson	Ordinal logistic regression	
Structures	Treat	N	Mean	absence	early	advanced	p-value	OR (IC 95%)	p-value
anguloarticular down	Control	24	1.08	8 (33.33%)	6 (25.00%)	10 (41.67%)		1	
	LDC 1g > 3g	24	1.83	1 (4.17%)	2 (8.33%)	21 (87.50%)	**0.003**	9.993 (2.360-42.315)	**0.002**
anguloarticular up	Control	24	1.04	9 (37.50%)	5 (20.83%)	10 (41.67%)		1	
	LDC 3 g	24	1.83	1 (4.17%)	2 (8.33%)	21 (87.50%)	**0.003**	10.249 (2.413-43.538)	**0.002**
branchiostegal ray2 down	Control	24	0.92	7 (29.17%)	12 (50.00%)	5 (20.83%)		1	
	LDC 1g > 3g	24	0.96	8 (33.33%)	9 (37.50%)	7 (29.17%)	0.661	1.094 (0.382-3.129)	0.867
branchiostegal ray2 up	Control	24	1.04	7 (29.17%)	9 (37.50%)	8 (33.33%)		1	
	LDC 3 g	24	1.00	7 (29.17%)	10 (41.67%)	7 (29.17%)	0.942	0.904 (0.319-2.568)	0.850
ceratohyal down	Control	24	0.54	11 (45.83%)	13 (54.17%)	0 (0.00%)		1	
	LDC 1g > 3g	24	1.33	3 (12.50%)	10 (41.67%)	11 (4583%)	**<0.001**	12.584 (3.063-51.701)	**<0.001**
ceratohyal up	Control	24	0.54	11 (45.8%)	13 (54.17%)	0 (0.00%)		1	
	LDC 1g > 3g	24	1.38	2 (8.33%)	11 (45.83%)	11 (45.83%)	**<0.001**	19.388 (3.831-98.128)	**<0.001**

Symbol	Entrez Gene Name	Log Ratio 1g>3g	p-value	D	Type(s)
ABCA5	ATP-binding cassette. sub-family A (ABC1). member 5	-0.223	8.38E-02		transporter
APOA4	apolipoprotein A-IV	-0.353	9.57E-02		transporter
AQP3	aquaporin 3 (Gill blood group)	-0.166	7.48E-02		transporter
HBE1	hemoglobin. epsilon 1	-0.311	7.58E-02		transporter
KCND3	potassium voltage-gated channel. Shal-related subfamily. member 3	-0.252	4.52E-02	D	ion channel
KCND3	potassium voltage-gated channel. Shal-related subfamily. member 3	-0.195	8.61E-02	D	ion channel
KPNA4	karyopherin alpha 4 (importin alpha 3)	0.149	8.59E-02		transporter
NUP133	nucleoporin 133kDa	0.188	8.61E-02	D	transporter
NUP133	nucleoporin 133kDa	0.182	9.53E-02	D	transporter
REEP5	receptor accessory protein 5	-0.280	6.37E-02		transporter
RHCG	Rh family. C glycoprotein	-0.556	4.61E-02		transporter
SCN5A	sodium channel. voltage-gated. type V. alpha subunit	-0.253	7.07E-02		ion channel
SEC23B	Sec23 homolog B (S. cerevisiae)	-0.251	7.34E-02		transporter
SEH1L	SEH1-like (S. cerevisiae)	-0.174	7.69E-02		transporter
SLC15A1	solute carrier family 15 (oligopeptide transporter). member 1	-0.485	5.01E-02	D	transporter
SLC15A1	solute carrier family 15 (oligopeptide transporter). member 1	-0.487	8.61E-02	D	transporter
SLC25A26	solute carrier family 25 (S-adenosylmethionine carrier). member 26	-0.114	7.99E-02		transporter
SLC25A43	solute carrier family 25. member 43	-0.496	6.86E-02		transporter
SLC5A6	solute carrier family 5 (sodium/multivitamin and iodide cotransporter). member 6	0.101	9.94E-02		transporter
SLC6A19	solute carrier family 6 (neutral amino acid transporter). member 19	-0.185	6.64E-02		transporter
SLC9A3	solute carrier family 9. subfamily A (NHE3. cation proton antiporter 3). member 3	-0.183	9.20E-02		ion channel
SYT11	synaptotagmin XI	-0.302	5.97E-02		transporter
VDAC3	voltage-dependent anion channel 3	-0.155	8.43E-02		ion channel
VPS9D1	VPS9 domain containing 1	-0.167	9.22E-02		transporter
ANKRD33	ankyrin repeat domain 33	-0.135	6.71E-02		transcription regulator
ATF3	activating transcription factor 3	-0.433	8.23E-02		transcription regulator
CITED2	Cbp/p300-interacting transactivator. with Glu/Asp-rich carboxy-terminal domain. 2	0.310	8.61E-02		transcription regulator
EIF5	eukaryotic translation initiation factor 5	0.222	6.64E-02		translation regulator
FOXD3	forkhead box D3	-0.213	4.52E-02		transcription regulator
FOXP4	forkhead box P4	-0.233	6.64E-02		transcription regulator
HDAC2	histone deacetylase 2	0.261	7.07E-02		transcription regulator
HDAC4	histone deacetylase 4	-0.371	6.30E-02		transcription regulator
HEY1	hes-related family bHLH transcription factor with YRPW motif 1	0.130	7.05E-02		transcription regulator
KLF7	Kruppel-like factor 7 (ubiquitous)	-0.203	5.97E-02		transcription regulator
MEIS1	Meis homeobox 1	-0.264	5.79E-02		transcription regulator
MYC	v-myc avian myelocytomatosis viral oncogene homolog	-0.587	3.95E-02	D	transcription regulator
MYC	v-myc avian myelocytomatosis viral oncogene homolog	-0.567	4.52E-02	D	transcription regulator
NFKBIA	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor. alpha	-0.475	4.52E-02		transcription regulator
NR1D1	nuclear receptor subfamily 1. group D. member 1	-1.161	5.79E-02		ligand-dependent nuclear receptor
ONECUT1	one cut homeobox 1	-0.097	9.67E-02		transcription regulator
POU3F3	POU class 3 homeobox 3	0.144	7.29E-02		transcription regulator
PPARG	peroxisome proliferator-activated receptor gamma	-0.318	9.08E-02		ligand-dependent nuclear receptor

PURA	purine-rich element binding protein A	-0.304	7.75E-02		transcription regulator
SHOX	short stature homeobox	-0.261	5.77E-02		transcription regulator
SIN3B	SIN3 transcription regulator family member B	0.216	6.79E-02		transcription regulator
SOX3	SRY (sex determining region Y)-box 3	0.298	9.51E-02		transcription regulator
TANC2	tetratricopeptide repeat. ankyrin repeat and coiled-coil containing 2	-0.155	6.64E-02		transcription regulator
TFAP2B	transcription factor AP-2 beta (activating enhancer binding protein 2 beta)	0.144	9.16E-02		transcription regulator
TOB1	transducer of ERBB2. 1	-0.325	7.13E-02		transcription regulator
VDR	vitamin D (1.25- dihydroxyvitamin D3) receptor	-0.245	5.77E-02	D	transcription regulator
VDR	vitamin D (1.25- dihydroxyvitamin D3) receptor	-0.240	6.75E-02	D	transcription regulator
ANTXR2	anthrax toxin receptor 2	-0.235	6.81E-02		transmembrane receptor
CLK4	CDC-like kinase 4	0.615	9.30E-02		kinase
CSNK1A1L	casein kinase 1. alpha 1-like	-0.237	8.43E-02		kinase
DUSP2	dual specificity phosphatase 2	-0.388	4.52E-02		phosphatase
DUSP5	dual specificity phosphatase 5	-0.695	8.43E-02		phosphatase
GRK7	G protein-coupled receptor kinase 7	-0.541	4.52E-02		kinase
IP6K2	inositol hexakisphosphate kinase 2	0.256	4.52E-02		kinase
JAK1	Janus kinase 1	-0.198	8.51E-02		kinase
MAPK4	mitogen-activated protein kinase 4	-0.111	9.30E-02		kinase
NT5C3A	5'-nucleotidase. cytosolic IIIA	0.259	6.64E-02	D	phosphatase
NT5C3A	5'-nucleotidase. cytosolic IIIA	0.264	6.95E-02	D	phosphatase
PFKFB4	6-phosphofructo-2-kinase/fructose-2.6-biphosphatase 4	-0.473	6.64E-02		kinase
PHKG1	phosphorylase kinase. gamma 1 (muscle)	-0.220	9.94E-02		kinase
PIM2	pim-2 oncogene	0.335	9.30E-02		kinase
PRKAR1A	protein kinase. cAMP-dependent. regulatory. type I. alpha	0.236	7.13E-02		kinase
PTPN1	protein tyrosine phosphatase. non-receptor type 1	0.163	7.63E-02		phosphatase
SGK1	serum/glucocorticoid regulated kinase 1	-0.517	7.07E-02		kinase
STK35	serine/threonine kinase 35	-0.634	6.30E-02		kinase
STRADA	STE20-related kinase adaptor alpha	0.177	7.07E-02		kinase
BACE1	beta-site APP-cleaving enzyme 1	0.118	8.57E-02		peptidase
CFB	complement factor B	-0.281	5.79E-02		peptidase
CTSB	cathepsin B	0.247	6.11E-02		peptidase
ENDOU	endonuclease. polyU-specific	-0.139	6.64E-02		peptidase
UCHL5	ubiquitin carboxyl-terminal hydrolase L5	0.120	9.76E-02		peptidase
USP14	ubiquitin specific peptidase 14 (tRNA-guanine transglycosylase)	0.150	9.22E-02		peptidase
USP37	ubiquitin specific peptidase 37	0.207	6.79E-02		peptidase
ACBD6	acyl-CoA binding domain containing 6	0.182	6.81E-02		other
ACTA2	actin. alpha 2. smooth muscle. aorta	-0.141	6.64E-02		other
ADD3	adducin 3 (gamma)	-0.185	8.98E-02		other
AHCY	adenosylhomocysteinase	0.149	8.98E-02		enzyme
ALAS2	aminolevulinate. delta-. synthase 2	-0.111	9.94E-02		enzyme
ALDH4A1	aldehyde dehydrogenase 4 family. member A1	-0.134	8.43E-02		enzyme
ALDH8A1	aldehyde dehydrogenase 8 family. member A1	-0.202	4.89E-02		enzyme
ANXA1	annexin A1	-0.416	5.29E-02		enzyme
ANXA4	annexin A4	-0.421	4.52E-02		other
ARL5C	ADP-ribosylation factor-like 5C	-0.700	5.19E-02		other
ARR3	arrestin 3. retinal (X-arrestin)	-0.236	6.95E-02		other
ARRDC2	arrestin domain containing 2	-0.427	6.08E-02		other
ATG10	autophagy related 10	-0.108	8.43E-02		enzyme
ATL2	atlastin GTPase 2	0.214	8.43E-02		other
B3GAT2	beta-1.3-glucuronyltransferase 2 (glucuronosyltransferase S)	-0.315	4.52E-02		enzyme
BCMO1	beta-carotene 15.15'-monooxygenase 1	-0.126	7.07E-02		enzyme

BLOC1S6	biogenesis of lysosomal organelles complex-1. subunit 6. pallidin	-0.252	8.43E-02		other
BOC	BOC cell adhesion associated. oncogene regulated	-0.167	5.74E-02		other
C10orf54	chromosome 10 open reading frame 54	-0.116	7.69E-02		other
CA10	carbonic anhydrase X	-0.274	4.52E-02	D	enzyme
CA10	carbonic anhydrase X	-0.246	6.37E-02	D	enzyme
CA10	carbonic anhydrase X	-0.328	6.64E-02	D	enzyme
CAPG	capping protein (actin filament). gelsolin-like	-0.182	6.64E-02		other
CCDC124	coiled-coil domain containing 124	-0.240	5.77E-02		other
CCDC85C	coiled-coil domain containing 85C	-0.323	8.70E-02		other
CDH7	cadherin 7. type 2	-0.190	5.77E-02		other
CEP63	centrosomal protein 63kDa	0.233	5.23E-02		other
CISH	cytokine inducible SH2-containing protein	-0.410	4.52E-02	D	other
CISH	cytokine inducible SH2-containing protein	-0.510	7.75E-02	D	other
CLDN9	claudin 9	-0.349	9.67E-02		other
CRHBP	corticotropin releasing hormone binding protein	-0.220	5.72E-02		other
CSDC2	cold shock domain containing C2. RNA binding	-0.190	6.64E-02		other
CTDSPL	CTD (carboxy-terminal domain. RNA polymerase II. polypeptide A) small phosphatase-like	-0.253	5.81E-02		other
Cyp2ac1	cytochrome P450. family 2. subfamily ac. polypeptide 1	0.114	8.43E-02		other
CYP2J2	cytochrome P450. family 2. subfamily J. polypeptide 2	0.424	6.37E-02		enzyme
CYP2R1	cytochrome P450. family 2. subfamily R. polypeptide 1	-0.465	7.48E-02		enzyme
CYR61	cysteine-rich. angiogenic inducer. 61	-0.369	5.77E-02		other
DDX18	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18	0.214	8.68E-02		enzyme
DDX51	DEAD (Asp-Glu-Ala-Asp) box polypeptide 51	0.179	7.95E-02		enzyme
ELOVL1	ELOVL fatty acid elongase 1	-0.305	4.52E-02		enzyme
EMC1	ER membrane protein complex subunit 1	0.220	5.43E-02		other
ERGIC2	ERGIC and golgi 2	-0.161	6.41E-02		other
ERRFI1	ERBB receptor feedback inhibitor 1	-0.390	6.41E-02		other
FAM78B	family with sequence similarity 78. member B	-0.241	7.69E-02		other
FBLN7	fibulin 7	-0.216	5.77E-02		other
FBXL3	F-box and leucine-rich repeat protein 3	-0.310	6.81E-02		enzyme
FITM2	fat storage-inducing transmembrane protein 2	-0.179	9.94E-02		other
FKBP5	FK506 binding protein 5	-1.230	6.86E-02		enzyme
FUCA1	fucosidase. alpha-L- 1. tissue	-0.265	7.07E-02		enzyme
GADD45B	growth arrest and DNA-damage-inducible. beta	-0.230	9.08E-02		other
GBP1	guanylate binding protein 1. interferon-inducible	0.128	8.51E-02		enzyme
GNAO1	guanine nucleotide binding protein (G protein). alpha activating activity polypeptide O	-0.278	8.43E-02		enzyme
GOT1	glutamic-oxaloacetic transaminase 1. soluble	0.218	6.95E-02		enzyme
GPR137C	G protein-coupled receptor 137C	-0.329	5.16E-02		other
GRB2	growth factor receptor-bound protein 2	-0.417	3.03E-02		other
GSTZ1	glutathione S-transferase zeta 1	-0.211	6.39E-02		enzyme
GUSB	glucuronidase. beta	-0.147	9.30E-02		enzyme
HRAS	Harvey rat sarcoma viral oncogene homolog	-0.190	8.43E-02		enzyme
HRSP12	heat-responsive protein 12	-0.162	6.81E-02		other
HSD11B2	hydroxysteroid (11-beta) dehydrogenase 2	-0.383	4.52E-02		enzyme
HSD17B12	hydroxysteroid (17-beta) dehydrogenase 12	-0.404	3.58E-02		enzyme
IGHMBP2	immunoglobulin mu binding protein 2	0.170	6.81E-02		enzyme
IMPACT	impact RWD domain protein	-0.106	8.60E-02		other
IMPDH2	IMP (inosine 5'-monophosphate) dehydrogenase 2	-0.149	6.86E-02		enzyme
ITM2C	integral membrane protein 2C	-0.401	4.52E-02		other
KCTD5	potassium channel tetramerization domain containing 5	-0.346	9.94E-02		other
KDSR	3-ketodihydrosphingosine reductase	-0.147	8.21E-02		enzyme
LPL	lipoprotein lipase	-0.197	6.64E-02		enzyme
LRIT3	leucine-rich repeat. immunoglobulin-like and transmembrane domains 3	-0.167	6.37E-02		other
LRPPRC	leucine-rich pentatricopeptide repeat containing	0.305	6.97E-02		other

MBOAT2	membrane bound O-acyltransferase domain containing 2	0.189	5.81E-02		enzyme
MED18	mediator complex subunit 18	0.222	7.01E-02	D	other
MED18	mediator complex subunit 18	0.243	7.07E-02	D	other
MGST1	microsomal glutathione S-transferase 1	-0.207	6.97E-02		enzyme
MIDN	midnolin	-0.619	6.05E-02		other
MKLN1	muskelin 1. intracellular mediator containing kelch motifs	0.183	8.61E-02		other
MTMR10	myotubularin related protein 10	0.264	8.98E-02		other
MTR	5-methyltetrahydrofolate-homocysteine methyltransferase	0.152	8.21E-02	D	enzyme
MTR	5-methyltetrahydrofolate-homocysteine methyltransferase	0.227	8.43E-02	D	enzyme
MYLPF	myosin light chain. phosphorylatable. fast skeletal muscle	0.280	4.72E-02		other
MYO9B	myosin IXB	0.190	5.18E-02		enzyme
NAP1L1	nucleosome assembly protein 1-like 1	-0.227	4.61E-02	D	other
NAP1L1	nucleosome assembly protein 1-like 1	-0.234	5.43E-02	D	other
NDC1	NDC1 transmembrane nucleoporin	0.160	6.81E-02		other
NDRG2	NDRG family member 2	-0.754	8.23E-02		other
NDUFAF5	NADH dehydrogenase (ubiquinone) complex I. assembly factor 5	-0.150	6.20E-02		other
NHLH2	nescient helix loop helix 2	-0.096	9.66E-02		other
NSA2	NSA2 ribosome biogenesis homolog (S. cerevisiae)	-0.347	6.45E-02		other
OGT	O-linked N-acetylglucosamine (GlcNAc) transferase	0.169	7.13E-02		enzyme
OLIG3	oligodendrocyte transcription factor 3	0.174	6.64E-02		other
ORC4	origin recognition complex. subunit 4	0.124	7.69E-02		other
PCDH7	protocadherin 7	-0.269	6.64E-02		other
PCDHA8	protocadherin alpha 8	-0.253	8.61E-02		other
PCNA	proliferating cell nuclear antigen	0.225	4.52E-02		enzyme
PDE6C	phosphodiesterase 6C. cGMP-specific. cone. alpha prime	0.371	8.43E-02		enzyme
PHF10	PHD finger protein 10	0.143	6.64E-02		other
PHYHIPL	phytanoyl-CoA 2-hydroxylase interacting protein-like	-0.368	5.77E-02		other
PRPF39	pre-mRNA processing factor 39	0.240	9.16E-02		other
PRPF4	pre-mRNA processing factor 4	0.129	9.91E-02		other
PRPF40A	PRP40 pre-mRNA processing factor 40 homolog A (S. cerevisiae)	0.113	9.51E-02		other
PSMD11	proteasome (prosome. macropain) 26S subunit. non-ATPase. 11	0.173	7.07E-02		other
PTCD3	pentatricopeptide repeat domain 3	0.258	4.52E-02	D	other
PTCD3	pentatricopeptide repeat domain 3	0.203	5.77E-02	D	other
PTCD3	pentatricopeptide repeat domain 3	0.253	5.81E-02	D	other
PTCD3	pentatricopeptide repeat domain 3	0.176	8.51E-02	D	other
PVALB	parvalbumin	-0.290	4.52E-02		other
PWP1	PWP1 homolog (S. cerevisiae)	0.275	4.52E-02	D	other
PWP1	PWP1 homolog (S. cerevisiae)	0.241	5.77E-02	D	other
RAB10	RAB10. member RAS oncogene family	-0.292	6.78E-02		enzyme
RABGGTB	Rab geranylgeranyltransferase. beta subunit	0.143	9.30E-02		enzyme
RFNG	RFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	0.219	9.78E-02		enzyme
RND3	Rho family GTPase 3	-0.236	8.43E-02		enzyme
RNF180	ring finger protein 180	0.197	7.07E-02		enzyme
RNF7	ring finger protein 7	-0.144	7.69E-02		enzyme
RPL14	ribosomal protein L14	-0.231	8.59E-02		other
RPS19	ribosomal protein S19	-0.218	5.43E-02	D	other
RPS19	ribosomal protein S19	-0.295	7.40E-02	D	other
RPS28	ribosomal protein S28	-0.317	4.52E-02		other
RSL24D1	ribosomal L24 domain containing 1	-0.389	7.07E-02		other
RSPO1	R-spondin 1	-0.125	8.43E-02		other
RUFY2	RUN and FYVE domain containing 2	0.188	5.79E-02		other

SEMA3F	sema domain. immunoglobulin domain (Ig). short basic domain. secreted. (semaphorin) 3F	-0.346	6.39E-02		other
SERAC1	serine active site containing 1	0.186	5.74E-02	D	other
SERAC1	serine active site containing 1	0.188	6.64E-02	D	other
SETD3	SET domain containing 3	0.219	9.94E-02		enzyme
SH3GL1	SH3-domain GRB2-like 1	-0.337	8.98E-02		other
SLTM	SAFB-like. transcription modulator	0.354	9.58E-02		other
SNF8	SNF8. ESCRT-II complex subunit	-0.111	8.43E-02	D	enzyme
SNF8	SNF8. ESCRT-II complex subunit	-0.178	9.67E-02	D	enzyme
SOCS1	suppressor of cytokine signaling 1	-0.827	4.52E-02		other
SPRY4	sprouty homolog 4 (Drosophila)	-0.497	6.11E-02	D	other
SPRY4	sprouty homolog 4 (Drosophila)	-0.569	6.37E-02	D	other
SPRYD3	SPRY domain containing 3	-0.353	4.52E-02		other
TOLLIP	toll interacting protein	-0.314	5.19E-02		other
TPD52	tumor protein D52	-0.221	9.17E-02		other
Tsc22d3	TSC22 domain family. member 3	-0.280	6.64E-02		other
TSKU	tsukushi. small leucine rich proteoglycan	-0.187	7.07E-02		other
TXNIP	thioredoxin interacting protein	0.902	2.04E-02	D	other
TXNIP	thioredoxin interacting protein	0.911	5.79E-02	D	other
UBR7	ubiquitin protein ligase E3 component n-recognin 7 (putative)	0.302	5.77E-02	D	enzyme
UBR7	ubiquitin protein ligase E3 component n-recognin 7 (putative)	0.350	7.01E-02	D	enzyme
WDR13	WD repeat domain 13	0.125	9.08E-02		other
WDR6	WD repeat domain 6	0.108	8.61E-02		other
YARS	tyrosyl-tRNA synthetase	-0.155	8.12E-02		enzyme
ZC3H11A	zinc finger CCCH-type containing 11A	0.183	5.77E-02		other
ZNF729	zinc finger protein 729	-0.158	9.47E-02		other
ZSWIM8	zinc finger. SWIM-type containing 8	-0.145	7.13E-02		other

Table S10

	microarray		**RT-PCR**	
Gene	**Fold Change**	**p-value**	**Fold Change**	**p-value**
nr1d1	0,447	0,058	0,518	< 0,001
rhcg	0,68	0,046	0,779	< 0,001
socs1	0,564	0,045	0,544	< 0,001
spry4	0,674	0,064	0,739	< 0,001
txnip	1,88	0,058	2,555	< 0,001

Table S11

Category	p-value	Number of Genes
Cellular Growth and Proliferation	$2.42^{E-07}-9.08^{E-03}$	66
Molecular Transport	$3.83^{E-07}-9.08^{E-03}$	46
Cellular Development	$3.53^{E-06}-9.08^{E-03}$	64
Embryonic Development	$1.44^{E-05}-9.08^{E-03}$	36
Cell Death and Survival	$2.1^{E-05}-9.08^{E-03}$	66
Organ Development	$2.51^{E-05}-5.47^{E-03}$	29
Organismal Development	$2.51^{E-05}-9.08^{E-03}$	57
Skeletal and Muscular System Development and Function	$2.51^{E-05}-9.08^{E-03}$	25
Tissue Development	$2.51^{E-05}-9.08^{E-03}$	50
Connective Tissue Development and Function	$3.48^{E-05}-9.08^{E-03}$	22
Nervous System Development and Function	$3.98^{E-05}-9.08^{E-03}$	14
Endocrine System Development and Function	$5.3^{E-05}-9.04^{E-03}$	19
Lipid Metabolism	$5.3^{E-05}-9.08^{E-03}$	23
Small Molecule Biochemistry	$5.3^{E-05}-9.08^{E-03}$	39
Gene Expression	$6.34^{E-05}-9.08^{E-03}$	46
Organismal Survival	$7.23^{E-05}-5.31^{E-03}$	49
Cell Morphology	$8.19^{E-05}-9.08^{E-03}$	40
Hair and Skin Development and Function	$1.16^{E-04}-9.08^{E-03}$	14
Renal and Urological System Development and Function	$1.97^{E-04}-1.67^{E-03}$	11
Reproductive System Development and Function	$1.97^{E-04}-9.08^{E-03}$	12
Tissue Morphology	$1.98^{E-04}-9.04^{E-03}$	44
Cell Cycle	$2.44^{E-04}-9.08^{E-03}$	25
Cell-To-Cell Signaling and Interaction	$2.67^{E-04}-9.08^{E-03}$	19
Cellular Assembly and Organization	$2.67^{E-04}-9.08^{E-03}$	11
Cellular Movement	$4.34^{E-04}-9.08^{E-03}$	40
Hematological System Development and Function	$4.37^{E-04}-9.08^{E-03}$	34
Hematopoiesis	$4.37^{E-04}-8.39^{E-03}$	23
Cellular Function and Maintenance	$4.86^{E-04}-9.08^{E-03}$	13
Carbohydrate Metabolism	$6.66^{E-04}-9.08^{E-03}$	23
Organ Morphology	$8.7^{E-04}-9.08^{E-03}$	24
Lymphoid Tissue Structure and Development	$1.06^{E-03}-8.47^{E-03}$	7
Cardiovascular System Development and Function	$1.14^{E-03}-9.08^{E-03}$	29
Amino Acid Metabolism	$1.67^{E-03}-9.08^{E-03}$	8
Vitamin and Mineral Metabolism	$1.83^{E-03}-9.08^{E-03}$	8
DNA Replication. Recombination. and Repair	$1.91^{E-03}-6.16^{E-03}$	15
Digestive System Development and Function	$2.26^{E-03}-9.08^{E-03}$	17
Behavior	$2.28^{E-03}-2.28^{E-03}$	5
Hepatic System Development and Function	$2.8^{E-03}-2.8^{E-03}$	7
Respiratory System Development and Function	$2.83^{E-03}-4.27^{E-03}$	2
Nucleic Acid Metabolism	$4.27^{E-03}-9.08^{E-03}$	2
Protein Synthesis	$4.27^{E-03}-9.04^{E-03}$	25
Humoral Immune Response	$6.71^{E-03}-6.71^{E-03}$	7
Post-Translational Modification	$6.94^{E-03}-6.94^{E-03}$	2
Immune Cell Trafficking	$7.97^{E-03}-9.08^{E-03}$	13
Free Radical Scavenging	$8.78^{E-03}-8.78^{E-03}$	12
Cell-mediated Immune Response	$9.08^{E-03}-9.08^{E-03}$	1
Cellular Compromise	$9.08^{E-03}-9.08^{E-03}$	1
Cellular Response to Therapeutics	$9.08^{E-03}-9.08^{E-03}$	1
Drug Metabolism	$9.08^{E-03}-9.08^{E-03}$	4

Table S12

A

				Score of ossification (Y)		X^2 Pearson	Logistic regression		
Structures	Treat	N	Mean	early	advanced	p-value	OR (IC 95%)	p-value	global p-value
branchiostegal ray1 down	3g	33	0.97	1 (3.03%)	32 96.97%)	**<0.001**	2.783 (0.238-32.556)	0.415	**0.039**
	3g > 1g	25	0.68	8 (32.00%)	17 (68%)		0.185 (0.035-0.983)	0.048	
	3g > axe	25	1.00	0 (0%)	25 (100%)		/	0.995	
	1g	25	0.92	2 (8.00%)	23 (92%)		1.00		
branchiostegal ray1 up	3g	33	0.97	1 (3.03%)	32 (97%)	**0.009**	2.783 (0.238-32.556)	0.415	0.147
	3g > 1g	25	0.76	6 (24.00%)	19 (76%)		0.275 (0.050-1.525)	0.140	
	3g > axe	25	1.00	0 (0%)	25 (100%)		/	0.995	
	1g	25	0.92	2 (8.00%)	23 (92%)		1.00		
dentary down	3g	33	0.73	9 (27.27%)	24 (72.7%)	**0.001**	2.461 (0.822-7.370)	0.842	0.190
	3g > 1g	25	1.00	0 (0%)	25 (100%)		/	0.107	
	3g > axe	25	0.80	5 (20%)	20 (80%)		3.692 (1.052-12.957)	0.995	
	1g	25	0.52	12 (48%)	13 (52%)		1.00		
dentary up	3g	33	0.73	9 (27.27%)	24 (72.7%)	**0.001**	2.461 (0.822-7.370)	0.842	0.190
	3g > 1g	25	1.00	0 (0%)	25 (100%)		/	0.107	
	3g > axe	25	0.80	5 (20%)	20 (80%)		3.692 (1.052-12.957)	0.995	
	1g	25	0.52	12 (48%)	13 (52%)		1.00		
entopterygoid down	3g	33	0.88	4 (12.12%)	29 (88%)	0.075	3.412 (0.892-13.046)	0.079	0.098
	3g > 1g	25	0.72	7 (28.00%)	18 (72%)		1.210 (0.360-4.065)	0.073	
	3g > axe	25	0.92	2 (8.00%)	23 (92%)		5.412 (1.017-28.791)	0.758	
	1g	25	0.76	8 (32.00%)	17 (68%)		1.00		
entopterygoid up	3g	33	0.88	4 (12.12%)	29 (88%)	0.226	2.819 (0.0722-11.01)	0.136	0.246
	3g > 1g	25	0.72	7 (28.00%)	18 (72%)		1.000 (0.291-3.437)	1.000	
	3g > axe	25	0.88	3 (12.00%)	22 (88%)		2.852 (0.643-12.642)	0.168	
	1g	25	0.80	7 (28.00%)	18 (72%)		1.00		

B

				Score of ossification (Y)			X^2 pearson	Ordinal logistic regression		
Structures	Variable	N	Mean	absence	early	advanced	p-value	OR (IC 95%)	p-value	global p-value
anguloarticular down	3g	33	1.12	11 (33.33%)	7 (21.21%)	15 (45.45%)	**0.005**	0.50 (0.19-1.35)	0.171	**0.045**
	3g > 1g	25	1.24	8 (32%)	3 (12%)	14 (56%)		0.38 (0.13-1.09)	0.072	
	3g > axe	25	1.44	7(28%)	0 (0%)	18 (72%)		0.21 (0.07-0.63)	0.006	
	1g	25	0.76	11 (44%)	9 (36%)	5 (20%)		1.00		
anguloarticular up	3g	33	1.09	12 (36.36%)	6 (18.18%)	15 (45.45%)	**0.008**	0.49 (0.18-1.33)	0.164	**0.035**
	3g > 1g	25	1.24	8 (32%)	3 (12%)	14 (56%)		0.35 (0.12-1.03)	0.057	
	3g > axe	25	1.44	7 (28%)	0 (0%)	18 (72%)		0.19 (0.06-0.60)	0.004	
	1g	25	0.72	12 (48%)	8 (32%)	5 (20%)		1.00		
branchiostegal ray2 down	3g	33	0.21	26 (78.79%)	7 (21.21%)	0 (0%)	0.169	0.93 (0.26-3.38)	0.912	0.405
	3g > 1g	25	0.08	24 (96%)	0 (0%)	1 (4%)		5.68 (0.63-51.07)	0.121	
	3g > axe	25	0.2	20(80%)	5 (20%)	0 (0%)		1.00 (0.25-4.01)	1.000	
	1g	25	0.2	20(80%)	5 (20%)	0 (0%)		1.00		
branchiostegal ray2 up	3g	33	0.24	26 (76.47%)	8 (23.53%)	0 (0%)	0.247	0.99 (0.29-3.34)	0.983	0.432
	3g > 1g	25	0.12	23 (92%)	1(4%)	1(4%)		3.43 (0.63-18.64)	0.153	
	3g > axe	25	0.16	21 (84%)	4 (16%)	0 (0%)		1.65 (0.40-6.76)	0.489	
	1g	25	0.24	19 (76%)	6 (24%)	0 (0%)		1.00		
ceratohyal down	3g	33	0.57	20 (60.61%)	7 (21.21%)	6 (18.18%)	**0.003**	0.74 (0.25-2.18)	0.587	0.078
	3g > 1g	25	1	12 (48%)	1 (4%)	12 (48%)		0.30 (0.10-0.91)	0.033	
	3g > axe	25	0.48	18 (72%)	2 (8%)	5 (20%)		1.08 (0.33-3.55)	0.894	
	1g	25	0.57	16 (64%)	8 (32%)	1 (4%)		1.00		
ceratohyal up	3g	33	0.67	18 (54.54%)	8 (24.24%)	7 (21.21%)	**0.011**	0.52 (0.18-1.53)	0.236	0.082
	3g > 1g	25	1.04	11 (44%)	2 (8%)	12 (48%)		0.24 (0.08-074)	0.013	
	3g > axe	25	0.64	16 (64%)	2 (8%)	7 (28%)		0.62 (019-1.97)	0.416	
	1g	25	0.36	17 (68%)	7 (28%)	1(4%)		1.00		
hyomandibular down	3g	33	1.88	0 (0%)	4 (12.12%)	29 (87.88%)	0.080	0.21 (0.06-0.78)	0.020	0.083
	3g > 1g	25	1.52	4 (16%)	4 (16%)	17 (68%)		0.83 (0.27-2.57)	0.751	
	3g > axe	25	1.52	2 (8%)	8 (32%)	15 (60%)		1.00 (0.33-3.03)	1.000	
	1g	25	1.52	2 (8%)	8 (32%)	15 (60%)		1.00		
hyomandibular up	3g	33	1.91	0 (0%)	3 (9.09%)	30 (90.91%)	0.174	0.18 (0.04-0.76)	0.020	0.140
	3g > 1g	25	1.64	3 (12%)	3 (12%)	19 (76%)		0.63 (0.19-2.09)	0.448	
	3g > axe	25	1.72	1(4%)	5 (20%)	19 (76%)		0.56 (0.17-1.91)	0.358	
	1g	25	1.56	2 (8%)	7 (28%)	16 (64%)		1.00		
maxilla down	3g	33	1.64	3 (9.09%)	6 (18.18%)	24 (72.73%)	**0.005**	0.24 (0.08-0.69)	0.008	**0.001**
	3g > 1g	25	1.76	2 (8%)	2 (8%)	21 (84%)		0.13 (0.03-0.46)	0.002	
	3g > axe	25	1.8	1 (4%)	3 (12%)	21 (84%)		0.12 (0.03-0.44)	0.001	
	1g	25	1.12	6 (24%)	10 (40%)	9 (36%)		1.00		
maxilla up	3g	33	1.57	5 (15.15%)	4 (12.12%)	24 (72.73%)	**0.001**	0.29 (0.10-0.82)	0.019	**0.003**
	3g > 1g	25	1.84	2 (8%)	0 (0%)	23 (92%)		0.07 (0.01-0.33)	0.001	
	3g > axe	25	1.68	2 (8%)	4 (16%)	19 (76%)		0.22 (0.07-0.72)	0.012	
	1g	25	1.12	6 (24%)	10 (40%)	9 (36%)		1.00		

Symbol	Entrez Gene Name	Log Ratio 1g	p-value	N	Type(s)
ABCF2	ATP-binding cassette. sub-family F (GCN20). member 2	-0.858	6.53E-02		transporter
ABCG2	ATP-binding cassette. sub-family G (WHITE). member 2	0.362	8.25E-02		transporter
ANXA6	annexin A6	-0.576	9.86E-02		ion channel
APOA4	apolipoprotein A-IV	-0.615	8.17E-02		transporter
ATP1A1	ATPase. Na+/K+ transporting. alpha 1 polypeptide	0.607	3.80E-02	D	transporter
ATP1A1	ATPase. Na+/K+ transporting. alpha 1 polypeptide	0.614	6.53E-02	D	transporter
ATP1B2	ATPase. Na+/K+ transporting. beta 2 polypeptide	-0.257	9.21E-02		transporter
ATP2B4	ATPase. Ca++ transporting. plasma membrane 4	-0.339	5.01E-02		transporter
ATP5G3	ATP synthase. H+ transporting. mitochondrial Fo complex. subunit C3 (subunit 9)	-0.185	7.86E-02		transporter
ATP6V1B2	ATPase. H+ transporting. lysosomal 56/58kDa. V1 subunit B2	0.249	9.37E-02		transporter
CACNA2D2	calcium channel. voltage-dependent. alpha 2/delta subunit 2	0.308	4.67E-02		ion channel
CACNG6	calcium channel. voltage-dependent. gamma subunit 6	0.166	5.50E-02		ion channel
EXOC7	exocyst complex component 7	0.315	8.39E-02		transporter
GABRG2	gamma-aminobutyric acid (GABA) A receptor. gamma 2	0.295	6.32E-02		ion channel
HNRNPU	heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	-0.310	5.52E-02		transporter
HSDL2	hydroxysteroid dehydrogenase like 2	-0.302	3.17E-02		transporter
KCTD12	potassium channel tetramerization domain containing 12	-0.105	9.84E-02	D	ion channel
KCTD12	potassium channel tetramerization domain containing 12	-0.150	3.96E-02	D	ion channel
NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex. 10. 42kDa	-0.382	9.76E-02		transporter
PDZK1	PDZ domain containing 1	0.779	5.18E-02		transporter
SEC14L2	SEC14-like 2 (S. cerevisiae)	0.268	9.62E-02		transporter
SLC13A2	solute carrier family 13 (sodium-dependent dicarboxylate transporter). member 2	0.674	1.62E-02		transporter
SLC14A2	solute carrier family 14 (urea transporter). member 2	-0.237	9.37E-02		transporter
SLC15A1	solute carrier family 15 (oligopeptide transporter). member 1	0.380	9.30E-02		transporter
SLC16A3	solute carrier family 16 (monocarboxylate transporter). member 3	-0.414	3.17E-02	D	transporter
SLC16A3	solute carrier family 16 (monocarboxylate transporter). member 3	-0.476	4.16E-02	D	transporter
SLC1A3	solute carrier family 1 (glial high affinity glutamate transporter). member 3	0.154	8.39E-02		transporter
SLC22A2	solute carrier family 22 (organic cation transporter). member 2	0.481	3.05E-02	D	transporter
SLC22A2	solute carrier family 22 (organic cation transporter). member 2	0.507	3.80E-02	D	transporter
SLC22A5	solute carrier family 22 (organic cation/carnitine transporter). member 5	0.174	6.83E-02		transporter
SLC25A19	solute carrier family 25 (mitochondrial thiamine pyrophosphate carrier). member 19	-0.215	3.96E-02		transporter
SLC35D1	solute carrier family 35 (UDP-GlcA/UDP-GalNAc transporter). member D1	-0.147	7.04E-02		transporter
SLC37A4	solute carrier family 37 (glucose-6-phosphate transporter). member 4	-0.353	3.19E-02	D	transporter
SLC37A4	solute carrier family 37 (glucose-6-phosphate transporter). member 4	-0.365	3.80E-02	D	transporter
SLC6A19	solute carrier family 6 (neutral amino acid transporter). member 19	0.629	9.86E-02		transporter
SNX12	sorting nexin 12	-0.205	6.83E-02		transporter
SNX16	sorting nexin 16	0.444	4.09E-02		transporter
TAPBP	TAP binding protein (tapasin)	0.241	4.57E-02		transporter
TFRC	transferrin receptor	-0.184	3.29E-02		transporter
TIMM13	translocase of inner mitochondrial membrane 13 homolog (yeast)	-0.307	6.89E-02		transporter
TMED3	transmembrane emp24 protein transport domain containing 3	-0.193	7.04E-02		transporter
TMED9	transmembrane emp24 protein transport domain containing 9	-0.259	4.49E-02		transporter
USO1	USO1 vesicle transport factor	0.161	5.41E-02		transporter
VPS33A	vacuolar protein sorting 33 homolog A (S. cerevisiae)	-0.270	7.58E-02		transporter
ANKS4B	ankyrin repeat and sterile alpha motif domain containing 4B	0.313	9.11E-02		transcription regulator
ATF3	activating transcription factor 3	-0.319	6.83E-02		transcription regulator

BTG2	BTG family. member 2	-2.106	1.04E-02	D	transcription regulator
BTG2	BTG family. member 2	-2.024	1.35E-02	D	transcription regulator
C1QBP	complement component 1. q subcomponent binding protein	0.331	6.56E-02		transcription regulator
CEBPD	CCAAT/enhancer binding protein (C/EBP). delta	-0.193	5.92E-02		transcription regulator
DLX1	distal-less homeobox 1	-0.153	9.30E-02		transcription regulator
ECD	ecdysoneless homolog (Drosophila)	0.137	5.19E-02		transcription regulator
EEF2	eukaryotic translation elongation factor 2	0.180	9.76E-02		translation regulator
EGR1	early growth response 1	-0.388	3.99E-02		transcription regulator
EGR2	early growth response 2	-0.292	4.32E-02		transcription regulator
EGR3	early growth response 3	-0.305	6.08E-02		transcription regulator
EIF3C	eukaryotic translation initiation factor 3. subunit C	0.458	2.99E-02		translation regulator
EIF4A1	eukaryotic translation initiation factor 4A1	-0.742	2.89E-02	D	translation regulator
EIF4A1	eukaryotic translation initiation factor 4A1	-0.599	3.19E-02	D	translation regulator
FOS	FBJ murine osteosarcoma viral oncogene homolog	-2.530	2.89E-02		transcription regulator
FOSB	FBJ murine osteosarcoma viral oncogene homolog B	-2.124	9.40E-03		transcription regulator
FOXQ1	forkhead box Q1	-0.411	3.99E-02	D	transcription regulator
FOXQ1	forkhead box Q1	-0.577	3.05E-02	D	transcription regulator
GTF2H4	general transcription factor IIH. polypeptide 4. 52kDa	-0.181	5.08E-02		transcription regulator
HLTF	helicase-like transcription factor	0.234	6.53E-02		transcription regulator
HSF2	heat shock transcription factor 2	0.641	5.52E-02	D	transcription regulator
HSF2	heat shock transcription factor 2	0.624	6.53E-02	D	transcription regulator
KLF11	Kruppel-like factor 11	-0.386	3.05E-02	D	transcription regulator
KLF11	Kruppel-like factor 11	-0.518	6.30E-02	D	transcription regulator
L3MBTL2	l(3)mbt-like 2 (Drosophila)	-0.173	8.96E-02		transcription regulator
MED27	mediator complex subunit 27	-0.194	6.15E-02		transcription regulator
MYBL2	v-myb avian myeloblastosis viral oncogene homolog-like 2	-0.314	2.89E-02		transcription regulator
MYCL	v-myc avian myelocytomatosis viral oncogene lung carcinoma derived homolog	0.402	6.59E-02		transcription regulator
MYOG	myogenin (myogenic factor 4)	-0.359	9.26E-02		transcription regulator
NFIL3	nuclear factor. interleukin 3 regulated	-0.370	4.69E-02		transcription regulator
NFKBIA	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor. alpha	-0.468	5.67E-02		transcription regulator
NKX2-2	NK2 homeobox 2	-0.168	9.39E-02		transcription regulator
NMI	N-myc (and STAT) interactor	0.542	5.76E-02		transcription regulator
NPAS4	neuronal PAS domain protein 4	-1.722	3.86E-02		transcription regulator
OVOL1	ovo-like zinc finger 1	-0.217	3.17E-02		transcription regulator
PDLIM1	PDZ and LIM domain 1	0.235	9.37E-02		transcription regulator
Pou3f1	POU domain. class 3. transcription factor 1	-0.113	9.24E-02		transcription regulator
PPARG	peroxisome proliferator-activated receptor gamma	0.286	3.96E-02		ligand-dependent nuclear

					receptor
PTGES2	prostaglandin E synthase 2	-0.269	9.67E-02		transcription regulator
RXRG	retinoid X receptor. gamma	0.201	7.17E-02		ligand-dependent nuclear receptor
SOX14	SRY (sex determining region Y)-box 14	-0.248	5.62E-02		transcription regulator
SQSTM1	sequestosome 1	0.587	4.57E-02		transcription regulator
TAF7	TAF7 RNA polymerase II. TATA box binding protein (TBP)-associated factor. 55kDa	-0.124	8.25E-02		transcription regulator
TRIP13	thyroid hormone receptor interactor 13	-0.240	5.52E-02		transcription regulator
YWHAB	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein. beta	-0.295	5.01E-02	D	transcription regulator
YWHAB	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein. beta	-0.230	5.87E-02	D	transcription regulator
CXCR4	chemokine (C-X-C motif) receptor 4	-0.099	7.21E-02		G-protein coupled receptor
DRD3	dopamine receptor D3	-0.172	4.88E-02		G-protein coupled receptor
F3	coagulation factor III (thromboplastin. tissue factor)	-0.352	5.52E-02		transmembrane receptor
HMMR	hyaluronan-mediated motility receptor (RHAMM)	-0.471	9.96E-02		transmembrane receptor
IFNAR1	interferon (alpha. beta and omega) receptor 1	0.354	5.45E-02		transmembrane receptor
OPN1LW	opsin 1 (cone pigments). long-wave-sensitive	-0.484	3.19E-02	D	G-protein coupled receptor
OPN1LW	opsin 1 (cone pigments). long-wave-sensitive	-0.866	3.17E-02	D	G-protein coupled receptor
TNFRSF19	tumor necrosis factor receptor superfamily. member 19	0.287	3.99E-02		transmembrane receptor
C19orf10	chromosome 19 open reading frame 10	-0.161	7.06E-02		cytokine
CMTM3	CKLF-like MARVEL transmembrane domain containing 3	-0.156	9.53E-02		cytokine
EDN1	endothelin 1	-0.268	6.66E-02		cytokine
TNFSF10	tumor necrosis factor (ligand) superfamily. member 10	0.263	7.96E-02		cytokine
GAS6	growth arrest-specific 6	0.220	6.31E-02		growth factor
NOG	noggin	-0.221	3.45E-02		growth factor
ACP2	acid phosphatase 2. lysosomal	0.343	8.19E-02		phosphatase
ACVR1	activin A receptor. type I	-0.415	3.96E-02	D	kinase
ACVR1	activin A receptor. type I	-0.351	5.32E-02	D	kinase
AURKA	aurora kinase A	-0.248	9.47E-02		kinase
AURKB	aurora kinase B	-0.532	5.92E-02		kinase
BCKDK	branched chain ketoacid dehydrogenase kinase	-0.593	3.05E-02		kinase
CCNB1	cyclin B1	-0.258	5.30E-02		kinase
CDK2	cyclin-dependent kinase 2	-0.298	4.38E-02		kinase
CDK7	cyclin-dependent kinase 7	-0.174	6.83E-02		kinase
CKB	creatine kinase. brain	0.231	3.80E-02		kinase
CLK4	CDC-like kinase 4	0.413	5.92E-02		kinase
CMPK1	cytidine monophosphate (UMP-CMP) kinase 1. cytosolic	-0.184	5.52E-02		kinase
DAK	dihydroxyacetone kinase 2 homolog (S. cerevisiae)	0.279	3.17E-02		kinase
DUSP1	dual specificity phosphatase 1	-1.383	3.05E-02	D	phosphatase
DUSP1	dual specificity phosphatase 1	-1.311	3.80E-02	D	phosphatase
DUSP2	dual specificity phosphatase 2	-0.716	2.89E-02		phosphatase
DUSP27	dual specificity phosphatase 27 (putative)	0.782	3.78E-02		phosphatase
ILK	integrin-linked kinase	-0.562	1.04E-02	D	kinase
ILK	integrin-linked kinase	-0.577	1.04E-02	D	kinase
IMPA1	inositol(myo)-1(or 4)-monophosphatase 1	-0.279	5.17E-02		phosphatase
INPP5D	inositol polyphosphate-5-phosphatase. 145kDa	0.094	9.76E-02		phosphatase
MKNK2	MAP kinase interacting serine/threonine kinase 2	0.241	8.25E-02		kinase
MYO3A	myosin IIIA	0.301	5.01E-02	D	kinase

MYO3A	myosin IIIA	0.325	6.81E-02	D	kinase
PFKFB4	6-phosphofructo-2-kinase/fructose-2.6-biphosphatase 4	-0.355	6.83E-02		kinase
PLK1	polo-like kinase 1	-0.492	3.94E-02		kinase
PPP2R2D	protein phosphatase 2. regulatory subunit B. delta	-0.209	8.40E-02		phosphatase
PPP2R4	protein phosphatase 2A activator. regulatory subunit 4	-0.169	7.17E-02		phosphatase
PPP4C	protein phosphatase 4. catalytic subunit	-0.354	9.40E-02		phosphatase
SIK2	salt-inducible kinase 2	0.635	4.71E-02		kinase
SLK	STE20-like kinase	0.192	7.57E-02		kinase
SOCS3	suppressor of cytokine signaling 3	-2.498	2.89E-02	D	phosphatase
SOCS3	suppressor of cytokine signaling 3	-2.432	3.05E-02	D	phosphatase
STK39	serine threonine kinase 39	-0.295	3.80E-02		kinase
TEC	tec protein tyrosine kinase	0.546	1.30E-02		kinase
UBLCP1	ubiquitin-like domain containing CTD phosphatase 1	-0.384	5.36E-02		phosphatase
VRK1	vaccinia related kinase 1	-0.226	8.25E-02		kinase
ACAA2	acetyl-CoA acyltransferase 2	-0.475	6.82E-02		enzyme
ACE	angiotensin I converting enzyme	0.511	7.42E-02		peptidase
ACOX1	acyl-CoA oxidase 1. palmitoyl	0.109	9.31E-02		enzyme
ACTA2	actin. alpha 2. smooth muscle. aorta	-0.411	8.89E-02		other
ACTG1	actin. gamma 1	-0.309	9.37E-02		other
ACTR2	ARP2 actin-related protein 2 homolog (yeast)	-0.134	9.26E-02		other
AGXT	alanine-glyoxylate aminotransferase	0.572	5.55E-02		enzyme
AHSG	alpha-2-HS-glycoprotein	0.427	9.44E-02		other
AKAP17A	A kinase (PRKA) anchor protein 17A	0.258	9.73E-02		other
AKIRIN1	akirin 1	-0.124	5.38E-02		enzyme
AKR1A1	aldo-keto reductase family 1. member A1 (aldehyde reductase)	-0.149	6.52E-02		enzyme
ALDH2	aldehyde dehydrogenase 2 family (mitochondrial)	-0.401	9.11E-02		enzyme
ALG8	ALG8. alpha-1.3-glucosyltransferase	-0.181	5.52E-02		enzyme
AMD1	adenosylmethionine decarboxylase 1	0.373	3.94E-02	D	enzyme
AMD1	adenosylmethionine decarboxylase 1	0.360	6.69E-02	D	enzyme
AMY2A	amylase. alpha 2A (pancreatic)	0.757	3.96E-02	D	enzyme
AMY2A	amylase. alpha 2A (pancreatic)	0.822	5.33E-02	D	enzyme
AMY2A	amylase. alpha 2A (pancreatic)	0.841	4.89E-02	D	enzyme
AMY2B	amylase. alpha 2B (pancreatic)	1.047	3.80E-02		enzyme
ANLN	anillin. actin binding protein	-0.459	7.42E-02		other
API5	apoptosis inhibitor 5	-0.301	3.99E-02		other
Arf2	ADP-ribosylation factor 2	-0.325	8.25E-02		other
ARHGDIB	Rho GDP dissociation inhibitor (GDI) beta	-0.252	8.55E-02	D	other
ARHGDIB	Rho GDP dissociation inhibitor (GDI) beta	-0.309	9.95E-02	D	other
ARHGEF28	Rho guanine nucleotide exchange factor (GEF) 28	0.214	8.25E-02		other
ARHGEF39	Rho guanine nucleotide exchange factor (GEF) 39	-0.199	9.37E-02		other
ARR3	arrestin 3. retinal (X-arrestin)	1.025	4.16E-02		other
ASL	argininosuccinate lyase	-0.218	5.65E-02		enzyme
B4GALT1	UDP-Gal:betaGlcNAc beta 1.4- galactosyltransferase. polypeptide 1	0.200	6.83E-02		enzyme
BCL2L1	BCL2-like 1	0.218	7.66E-02		other
BCO1	beta-carotene oxygenase 1	0.387	3.19E-02		enzyme
BIN1	bridging integrator 1	0.183	7.97E-02		other
BOD1	biorientation of chromosomes in cell division 1	-0.164	4.69E-02		other
BTBD6	BTB (POZ) domain containing 6	-0.349	6.52E-02		other
C10orf54	chromosome 10 open reading frame 54	0.191	3.70E-02		other
C10orf88	chromosome 10 open reading frame 88	0.108	9.16E-02		other
C12orf65	chromosome 12 open reading frame 65	-0.106	7.73E-02		other
C1orf106	chromosome 1 open reading frame 106	0.180	9.30E-02		other
C2orf40	chromosome 2 open reading frame 40	-0.281	3.96E-02		other
CA10	carbonic anhydrase X	0.145	9.30E-02		enzyme
CALU	calumenin	-0.434	3.14E-02		other
CAMK2N2	calcium/calmodulin-dependent protein kinase II inhibitor 2	0.153	7.28E-02		other
CAPRIN1	cell cycle associated protein 1	0.335	2.89E-02	D	other
CAPRIN1	cell cycle associated protein 1	0.312	4.12E-02	D	other
CASQ1	calsequestrin 1 (fast-twitch. skeletal muscle)	-0.319	4.71E-02		other
CAV3	caveolin 3	-0.217	5.62E-02		enzyme

CBWD1	COBW domain containing 1	-0.190	6.31E-02		other
CCDC25	coiled-coil domain containing 25	-0.221	9.39E-02		other
CCNA2	cyclin A2	-0.493	3.94E-02		other
CCNB2	cyclin B2	-0.250	5.41E-02		other
CCNE2	cyclin E2	-0.203	9.37E-02		other
CCNF	cyclin F	-0.250	3.29E-02		other
CD2AP	CD2-associated protein	-0.154	4.66E-02		other
CD82	CD82 molecule	-0.237	8.80E-02		other
CDA	cytidine deaminase	0.294	5.55E-02		enzyme
CDC20	cell division cycle 20	-0.379	3.19E-02		other
CDC5L	cell division cycle 5-like	0.223	6.20E-02		other
CDC6	cell division cycle 6	-0.236	5.87E-02	D	other
CDC6	cell division cycle 6	-0.167	6.29E-02	D	other
CEL	carboxyl ester lipase	1.208	4.99E-02	D	enzyme
CEL	carboxyl ester lipase	1.219	5.32E-02	D	enzyme
CEL	carboxyl ester lipase	0.998	7.78E-02	D	enzyme
CETP	cholesteryl ester transfer protein. plasma	0.495	9.64E-02		enzyme
CFB	complement factor B	0.322	3.96E-02	D	peptidase
CFB	complement factor B	0.160	7.90E-02	D	peptidase
CFP	complement factor properdin	-0.313	5.32E-02		other
CGRRF1	cell growth regulator with ring finger domain 1	-0.089	9.76E-02		other
CHAC2	ChaC. cation transport regulator homolog 2 (E. coli)	-0.128	6.99E-02		other
CHCHD4	coiled-coil-helix-coiled-coil-helix domain containing 4	-0.275	3.17E-02		enzyme
CHIA	chitinase. acidic	0.357	3.96E-02		enzyme
CHODL	chondrolectin	-0.109	8.11E-02		other
CHPF	chondroitin polymerizing factor	0.125	7.04E-02		enzyme
CKAP2	cytoskeleton associated protein 2	-0.478	3.80E-02		other
CNN3	calponin 3. acidic	-0.302	3.24E-02		other
COL4A1	collagen. type IV. alpha 1	0.481	5.49E-02		other
COL9A3	collagen. type IX. alpha 3	-0.534	8.51E-02		other
COPS8	COP9 signalosome subunit 8	-0.122	7.51E-02	D	other
COPS8	COP9 signalosome subunit 8	-0.125	9.37E-02	D	other
CPA1	carboxypeptidase A1 (pancreatic)	1.029	5.65E-02	D	peptidase
CPA1	carboxypeptidase A1 (pancreatic)	0.545	6.29E-02	D	peptidase
CPB1	carboxypeptidase B1 (tissue)	0.731	4.50E-02		peptidase
CPT2	carnitine palmitoyltransferase 2	-0.372	8.55E-02		enzyme
CRIP2	cysteine-rich protein 2	-0.211	7.06E-02		other
CRY1	cryptochrome circadian clock 1	0.557	3.96E-02		enzyme
CRYGN	crystallin. gamma N	-0.456	4.86E-02		other
CTNNBIP1	catenin. beta interacting protein 1	-0.251	3.80E-02	D	other
CTNNBIP1	catenin. beta interacting protein 1	-0.227	8.37E-02	D	other
CTRB2	chymotrypsinogen B2	0.432	7.86E-02		peptidase
CTSS	cathepsin S	0.176	9.39E-02		peptidase
CYB5A	cytochrome b5 type A (microsomal)	0.150	6.33E-02		enzyme
Cyb5r3	cytochrome b5 reductase 3	-0.140	6.83E-02		enzyme
CYP24A1	cytochrome P450. family 24. subfamily A. polypeptide 1	1.264	3.97E-02		enzyme
CYP27A1	cytochrome P450. family 27. subfamily A. polypeptide 1	0.185	4.89E-02		enzyme
Cyp2ac1	cytochrome P450. family 2. subfamily ac. polypeptide 1	0.385	7.04E-02		other
CYP2J2	cytochrome P450. family 2. subfamily J. polypeptide 2	0.233	5.92E-02	D	enzyme
CYP2J2	cytochrome P450. family 2. subfamily J. polypeptide 2	0.379	5.18E-02	D	enzyme
CYP2J2	cytochrome P450. family 2. subfamily J. polypeptide 2	0.418	2.89E-02	D	enzyme
CYP2J2	cytochrome P450. family 2. subfamily J. polypeptide 2	0.750	3.17E-02	D	enzyme
CYP2J2	cytochrome P450. family 2. subfamily J. polypeptide 2	0.806	8.37E-02	D	enzyme
CYP2J2	cytochrome P450. family 2. subfamily J. polypeptide 2	0.282	3.45E-02	D	enzyme
CYR61	cysteine-rich. angiogenic inducer. 61	-0.797	1.35E-02		other
DBT	dihydrolipoamide branched chain transacylase E2	-0.470	3.80E-02		enzyme
DCAF13	DDB1 and CUL4 associated factor 13	-0.331	5.65E-02	D	other
DCAF13	DDB1 and CUL4 associated factor 13	-0.364	6.53E-02	D	other
DCHS1	dachsous cadherin-related 1	-0.113	9.98E-02		other
DCN	decorin	-0.293	7.13E-02		other
DCUN1D1	DCN1. defective in cullin neddylation 1. domain containing 1	-0.169	7.87E-02		other

DDB2	damage-specific DNA binding protein 2. 48kDa	0.300	9.57E-02		other
DDC	dopa decarboxylase (aromatic L-amino acid decarboxylase)	-0.212	6.38E-02		enzyme
DDX4	DEAD (Asp-Glu-Ala-Asp) box polypeptide 4	0.286	9.37E-02		enzyme
DHRS1	dehydrogenase/reductase (SDR family) member 1	0.176	9.20E-02		enzyme
DLST	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)	0.180	8.66E-02		enzyme
DNAJB11	DnaJ (Hsp40) homolog. subfamily B. member 11	-0.226	4.09E-02	D	other
DNAJB11	DnaJ (Hsp40) homolog. subfamily B. member 11	-0.230	4.12E-02	D	other
DPP7	dipeptidyl-peptidase 7	0.269	7.90E-02		peptidase
DSG2	desmoglein 2	-0.230	5.33E-02		other
DSP	desmoplakin	0.324	7.86E-02		other
EBAG9	estrogen receptor binding site associated. antigen. 9	-0.137	5.18E-02		other
ECI1	enoyl-CoA delta isomerase 1	-0.406	7.86E-02		enzyme
EEPD1	endonuclease/exonuclease/phosphatase family domain containing 1	0.200	8.37E-02		other
EIF2B3	eukaryotic translation initiation factor 2B. subunit 3 gamma. 58kDa	-0.109	9.21E-02		other
ELAC2	elaC ribonuclease Z 2	0.211	7.34E-02		enzyme
ELOVL4	ELOVL fatty acid elongase 4	-0.512	3.96E-02		enzyme
ELOVL7	ELOVL fatty acid elongase 7	-1.211	1.04E-02	D	enzyme
ELOVL7	ELOVL fatty acid elongase 7	-1.199	1.30E-02	D	enzyme
ELP6	elongator acetyltransferase complex subunit 6	-0.127	6.39E-02		other
EME1	essential meiotic structure-specific endonuclease 1	-0.179	9.76E-02		other
ENDOU	endonuclease. polyU-specific	0.845	3.17E-02		peptidase
ERRFI1	ERBB receptor feedback inhibitor 1	-0.417	5.74E-02		other
ETNPPL	ethanolamine-phosphate phospho-lyase	0.254	3.85E-02		enzyme
EXOSC2	exosome component 2	-0.269	3.05E-02		enzyme
EXT2	exostosin glycosyltransferase 2	0.162	6.69E-02		enzyme
FAAH2	fatty acid amide hydrolase 2	0.350	6.83E-02		enzyme
FAIM	Fas apoptotic inhibitory molecule	-0.119	9.16E-02		other
FAM212A	family with sequence similarity 212. member A	-0.155	8.74E-02		other
FARSA	phenylalanyl-tRNA synthetase. alpha subunit	0.410	6.33E-02		enzyme
FBL	fibrillarin	-0.287	4.38E-02		other
FBXO5	F-box protein 5	-0.113	7.23E-02		enzyme
FCGBP	Fc fragment of IgG binding protein	-0.335	6.08E-02		other
FEN1	flap structure-specific endonuclease 1	-0.258	6.53E-02	D	enzyme
FEN1	flap structure-specific endonuclease 1	-0.323	7.73E-02	D	enzyme
FGL2	fibrinogen-like 2	0.172	8.29E-02		peptidase
FKBP1B	FK506 binding protein 1B. 12.6 kDa	-0.280	3.70E-02		enzyme
FNIP1	folliculin interacting protein 1	0.278	7.17E-02		other
G2E3	G2/M-phase specific E3 ubiquitin protein ligase	-0.256	4.95E-02		enzyme
G3BP1	GTPase activating protein (SH3 domain) binding protein 1	-0.360	4.50E-02		enzyme
GADD45B	growth arrest and DNA-damage-inducible. beta	-0.636	5.76E-02		other
GDI2	GDP dissociation inhibitor 2	-0.419	5.08E-02		other
GINS4	GINS complex subunit 4 (Sld5 homolog)	-0.191	6.54E-02		other
GOLGA7	golgin A7	-0.317	3.94E-02		other
GPI	glucose-6-phosphate isomerase	-0.303	6.91E-02		enzyme
GPX7	glutathione peroxidase 7	-0.184	6.95E-02		enzyme
GTPBP4	GTP binding protein 4	0.334	7.59E-02		enzyme
GYG1	glycogenin 1	0.293	6.71E-02		enzyme
H1f0	H1 histone family. member 0	-0.399	4.29E-02	D	other
H1f0	H1 histone family. member 0	-0.408	6.33E-02	D	other
HADH	hydroxyacyl-CoA dehydrogenase	-0.407	8.04E-02		enzyme
HAUS4	HAUS augmin-like complex. subunit 4	-0.307	7.90E-02		other
HGD	homogentisate 1.2-dioxygenase	0.348	9.84E-02		enzyme
HIBADH	3-hydroxyisobutyrate dehydrogenase	-0.301	3.86E-02	D	enzyme
HIBADH	3-hydroxyisobutyrate dehydrogenase	-0.338	4.57E-02	D	enzyme
HIST2H2BE	histone cluster 2. H2be	-0.321	5.52E-02		other
HLCS	holocarboxylase synthetase (biotin-(proprionyl-CoA-carboxylase (ATP-hydrolysing)) ligase)	0.443	7.80E-02		enzyme
HMBS	hydroxymethylbilane synthase	-0.213	6.83E-02		enzyme
HMGCL	3-hydroxymethyl-3-methylglutaryl-CoA lyase	-0.288	5.81E-02		enzyme

HMGCS1	3-hydroxy-3-methylglutaryl-CoA synthase 1 (soluble)	-0.372	8.25E-02		enzyme
HMGN3	high mobility group nucleosomal binding domain 3	-0.444	9.30E-02		other
HPRT1	hypoxanthine phosphoribosyltransferase 1	-0.138	7.87E-02		enzyme
HSD17B4	hydroxysteroid (17-beta) dehydrogenase 4	0.442	7.86E-02		enzyme
HSP90AA1	heat shock protein 90kDa alpha (cytosolic). class A member 1	0.382	4.50E-02		enzyme
HSP90B1	heat shock protein 90kDa beta (Grp94). member 1	-0.285	6.32E-02		other
IARS	isoleucyl-tRNA synthetase	0.736	8.66E-02		enzyme
IDH3A	isocitrate dehydrogenase 3 (NAD+) alpha	-0.307	4.95E-02		enzyme
IGFBP1	insulin-like growth factor binding protein 1	1.006	5.52E-02		other
IMP4	IMP4. U3 small nucleolar ribonucleoprotein	-0.154	4.71E-02		other
IMPDH1	IMP (inosine 5'-monophosphate) dehydrogenase 1	0.262	7.10E-02		enzyme
ING3	inhibitor of growth family. member 3	0.325	3.96E-02		other
INSIG1	insulin induced gene 1	0.307	4.32E-02		other
IRS2	insulin receptor substrate 2	0.266	2.89E-02		enzyme
KDELC2	KDEL (Lys-Asp-Glu-Leu) containing 2	-0.212	8.29E-02		other
KDM8	lysine (K)-specific demethylase 8	-0.206	4.86E-02		other
KIAA0196	KIAA0196	0.154	8.47E-02		other
KIAA1524	KIAA1524	-0.177	6.83E-02		other
KIAA1919	KIAA1919	0.203	7.18E-02		peptidase
KIF23	kinesin family member 23	-0.473	7.86E-02		other
KNTC1	kinetochore associated 1	-0.169	8.11E-02		other
KRT18	keratin 18	0.301	8.39E-02		other
LECT1	leukocyte cell derived chemotaxin 1	-1.097	9.40E-03	D	other
LECT1	leukocyte cell derived chemotaxin 1	-1.062	2.17E-02	D	other
LENG9	leukocyte receptor cluster (LRC) member 9	0.202	9.37E-02		other
LGSN	lengsin. lens protein with glutamine synthetase domain	-0.475	7.21E-02		enzyme
LIMCH1	LIM and calponin homology domains 1	0.710	3.80E-02		other
LMO7	LIM domain 7	0.281	3.86E-02		enzyme
LOX	lysyl oxidase	-0.117	9.11E-02		enzyme
LRIT1	leucine-rich repeat. immunoglobulin-like and transmembrane domains 1	0.613	3.80E-02		other
LRIT3	leucine-rich repeat. immunoglobulin-like and transmembrane domains 3	-0.232	6.91E-02		other
LRRC39	leucine rich repeat containing 39	-0.138	5.28E-02		other
LSM1	LSM1. U6 small nuclear RNA associated	-0.174	8.04E-02		other
LXN	latexin	0.312	6.83E-02		other
MANF	mesencephalic astrocyte-derived neurotrophic factor	-0.291	6.33E-02		other
MAPRE1	microtubule-associated protein. RP/EB family. member 1	-0.354	4.38E-02	D	other
MAPRE1	microtubule-associated protein. RP/EB family. member 1	-0.314	8.37E-02	D	other
MASP1	mannan-binding lectin serine peptidase 1 (C4/C2 activating component of Ra-reactive factor)	0.168	7.96E-02		peptidase
MATN1	matrilin 1. cartilage matrix protein	-0.391	4.58E-02		other
MCM10	minichromosome maintenance complex component 10	-0.152	5.78E-02		other
MCM2	minichromosome maintenance complex component 2	-0.163	4.38E-02		enzyme
MED28	mediator complex subunit 28	-0.171	9.26E-02		other
MFAP2	microfibrillar-associated protein 2	-0.287	8.11E-02		other
MOB3A	MOB kinase activator 3A	-0.119	6.53E-02		other
MOGAT1	monoacylglycerol O-acyltransferase 1	0.329	3.96E-02		enzyme
MON1A	MON1 secretory trafficking family member A	-0.298	3.05E-02		other
MOSPD2	motile sperm domain containing 2	0.201	7.51E-02		other
MPC2	mitochondrial pyruvate carrier 2	-0.326	4.50E-02	D	other
MPC2	mitochondrial pyruvate carrier 2	-0.230	9.76E-02	D	other
MSH2	mutS homolog 2	-0.303	8.51E-02		enzyme
MTFR2	mitochondrial fission regulator 2	-0.200	7.87E-02		other
MYBPH	myosin binding protein H	-0.244	4.66E-02		other
MYL6	myosin. light chain 6. alkali. smooth muscle and non-muscle	0.243	7.97E-02		other
MYL7	myosin. light chain 7. regulatory	-0.237	5.42E-02		enzyme
N6AMT1	N-6 adenine-specific DNA methyltransferase 1 (putative)	-0.256	8.47E-02		enzyme
NCAPG	non-SMC condensin I complex. subunit G	-0.275	8.11E-02		other
NCAPG2	non-SMC condensin II complex. subunit G2	-0.153	6.33E-02		other
NDC1	NDC1 transmembrane nucleoporin	-0.229	6.91E-02		other
NDC80	NDC80 kinetochore complex component	-0.224	4.34E-02		other

NDOR1	NADPH dependent diflavin oxidoreductase 1	-0.131	8.89E-02		enzyme
NDRG4	NDRG family member 4	-0.334	9.64E-02		other
NELFA	negative elongation factor complex member A	0.132	9.39E-02		other
NID1	nidogen 1	0.233	3.86E-02		other
NKAIN1	Na+/K+ transporting ATPase interacting 1	-0.259	3.71E-02		other
NOS1	nitric oxide synthase 1 (neuronal)	0.101	8.74E-02		enzyme
NPTN	neuroplastin	0.277	9.11E-02		other
NRAS	neuroblastoma RAS viral (v-ras) oncogene homolog	-0.195	4.32E-02		enzyme
NUDT18	nudix (nucleoside diphosphate linked moiety X)-type motif 18	0.182	9.96E-02		other
NUF2	NUF2. NDC80 kinetochore complex component	-0.358	5.94E-02		other
NXN	nucleoredoxin	-0.223	3.86E-02		enzyme
ORC6	origin recognition complex. subunit 6	-0.219	6.83E-02	D	other
ORC6	origin recognition complex. subunit 6	-0.243	7.04E-02	D	other
Otub1	OTU domain. ubiquitin aldehyde binding 1	-0.205	9.21E-02		enzyme
Otud5	OTU domain containing 5	0.197	7.06E-02		enzyme
PAH	phenylalanine hydroxylase	0.371	5.33E-02		enzyme
PAPD5	PAP associated domain containing 5	0.175	6.53E-02		enzyme
PC	pyruvate carboxylase	-0.226	3.05E-02	D	enzyme
PC	pyruvate carboxylase	-0.175	8.25E-02	D	enzyme
PDHX	pyruvate dehydrogenase complex. component X	0.230	8.17E-02		enzyme
PER3	period circadian clock 3	0.197	3.96E-02		other
PGM1	phosphoglucomutase 1	-0.322	4.65E-02		enzyme
PGP	phosphoglycolate phosphatase	-0.522	5.13E-02		enzyme
PGPEP1	pyroglutamyl-peptidase I	-0.124	5.52E-02		peptidase
PHF23	PHD finger protein 23	-0.151	7.04E-02		other
PIGQ	phosphatidylinositol glycan anchor biosynthesis. class Q	-0.111	8.74E-02		enzyme
PLA2G12B	phospholipase A2. group XIIB	0.153	9.85E-02		enzyme
PM20D1	peptidase M20 domain containing 1	0.460	7.34E-02		peptidase
POLR2H	polymerase (RNA) II (DNA directed) polypeptide H	-0.284	5.33E-02		enzyme
POSTN	periostin. osteoblast specific factor	-0.448	4.66E-02		other
PPP1R3B	protein phosphatase 1. regulatory subunit 3B	-0.340	6.33E-02		other
PRC1	protein regulator of cytokinesis 1	-0.247	6.91E-02		other
PRDM11	PR domain containing 11	-0.459	5.92E-02		other
PRIM1	primase. DNA. polypeptide 1 (49kDa)	-0.185	4.32E-02		enzyme
PRMT6	protein arginine methyltransferase 6	-0.242	4.32E-02		enzyme
PRPF31	pre-mRNA processing factor 31	0.118	7.42E-02		other
PRPH	peripherin	0.293	7.43E-02		other
PRRC1	proline-rich coiled-coil 1	-0.230	5.92E-02		other
PSMC6	proteasome (prosome. macropain) 26S subunit. ATPase. 6	-0.222	9.76E-02		peptidase
PSMD11	proteasome (prosome. macropain) 26S subunit. non-ATPase. 11	-0.154	8.33E-02		other
PSME3	proteasome (prosome. macropain) activator subunit 3 (PA28 gamma; Ki)	-0.354	3.29E-02		peptidase
PXMP2	peroxisomal membrane protein 2. 22kDa	-0.147	9.38E-02		other
PYGM	phosphorylase. glycogen. muscle	-0.265	4.29E-02		enzyme
RAB1A	RAB1A. member RAS oncogene family	-0.421	4.00E-02	D	enzyme
RAB1A	RAB1A. member RAS oncogene family	-0.306	6.81E-02	D	enzyme
RAC1	ras-related C3 botulinum toxin substrate 1 (rho family. small GTP binding protein Rac1)	-0.334	4.66E-02		enzyme
RAE1	ribonucleic acid export 1	-0.131	5.25E-02	D	other
RAE1	ribonucleic acid export 1	-0.156	7.10E-02	D	other
RALA	v-ral simian leukemia viral oncogene homolog A (ras related)	-0.226	8.29E-02		enzyme
RCC1	regulator of chromosome condensation 1	-0.449	6.83E-02		other
RDH13	retinol dehydrogenase 13 (all-trans/9-cis)	0.195	9.57E-02		enzyme
RGD1563307	similar to Set beta isoform	-0.302	4.88E-02	D	other
RGD1563307	similar to Set beta isoform	-0.197	7.46E-02	D	other
RGS1	regulator of G-protein signaling 1	-0.192	9.26E-02		other
RHOQ	ras homolog family member Q	-0.210	9.37E-02		enzyme
RMI2	RecQ mediated genome instability 2	-0.156	9.28E-02		other
RNASET2	ribonuclease T2	-0.369	7.80E-02		enzyme
RNF8	ring finger protein 8. E3 ubiquitin protein ligase	0.172	6.37E-02		enzyme
RNFT1	ring finger protein. transmembrane 1	-0.271	9.86E-02		other

RNLS	renalase. FAD-dependent amine oxidase	-0.519	8.29E-02		other
RPL31	ribosomal protein L31	0.236	5.52E-02		other
RPRM	reprimo. TP53 dependent G2 arrest mediator candidate	-0.207	3.80E-02		other
RPUSD2	RNA pseudouridylate synthase domain containing 2	-0.172	8.34E-02		enzyme
RRM1	ribonucleotide reductase M1	-0.398	4.81E-02		enzyme
RTCA	RNA 3'-terminal phosphate cyclase	-0.394	8.51E-02		enzyme
SAE1	SUMO1 activating enzyme subunit 1	-0.331	7.22E-02		enzyme
SAMM50	SAMM50 sorting and assembly machinery component	-0.186	5.01E-02	D	other
SAMM50	SAMM50 sorting and assembly machinery component	-0.285	7.87E-02	D	other
SCCPDH	saccharopine dehydrogenase (putative)	0.312	5.92E-02		other
SDAD1	SDA1 domain containing 1	0.250	8.39E-02		other
SEPHS1	selenophosphate synthetase 1	-0.283	4.50E-02		enzyme
SEPN1	selenoprotein N. 1	-0.394	5.91E-02		other
SERHL2	serine hydrolase-like 2	-0.181	8.80E-02		enzyme
SERPINB6	serpin peptidase inhibitor. clade B (ovalbumin). member 6	0.408	3.94E-02	D	other
SERPINB6	serpin peptidase inhibitor. clade B (ovalbumin). member 6	0.397	6.53E-02	D	other
SGPL1	sphingosine-1-phosphate lyase 1	0.324	9.26E-02		enzyme
Sh3bgr	SH3-binding domain glutamic acid-rich protein	-0.248	3.71E-02		other
SH3BGRL	SH3 domain binding glutamate-rich protein like	-0.207	3.91E-02		other
SIAE	sialic acid acetylesterase	-0.140	7.04E-02		enzyme
SLC25A47	solute carrier family 25. member 47	0.133	9.30E-02		other
SLMO2	slowmo homolog 2 (Drosophila)	-0.479	3.17E-02	D	other
SLMO2	slowmo homolog 2 (Drosophila)	-0.495	7.87E-02	D	other
SMARCAD1	SWI/SNF-related. matrix-associated actin-dependent regulator of chromatin. subfamily a. containing DEAD/H box 1	-0.414	6.56E-02		enzyme
SMPDL3B	sphingomyelin phosphodiesterase. acid-like 3B	0.280	9.11E-02		enzyme
SNRPA	small nuclear ribonucleoprotein polypeptide A	-0.213	8.74E-02		other
SNRPB2	small nuclear ribonucleoprotein polypeptide B	-0.220	3.17E-02		other
SPCS2	signal peptidase complex subunit 2 homolog (S. cerevisiae)	-0.519	5.08E-02		other
SPDL1	spindle apparatus coiled-coil protein 1	-0.360	4.66E-02		other
SRSF1	serine/arginine-rich splicing factor 1	-0.424	5.92E-02	D	other
SRSF1	serine/arginine-rich splicing factor 1	-0.368	9.28E-02	D	other
SRSF9	serine/arginine-rich splicing factor 9	-0.195	9.20E-02		enzyme
SSB	Sjogren syndrome antigen B (autoantigen La)	-0.334	9.76E-02		enzyme
ST7	suppression of tumorigenicity 7	0.268	2.89E-02		other
STARD10	StAR-related lipid transfer (START) domain containing 10	0.159	4.98E-02		other
STMN2	stathmin 2	-0.235	3.14E-02	D	other
STMN2	stathmin 2	-0.195	4.12E-02	D	other
STMN2	stathmin 2	-0.253	5.92E-02	D	other
STMN2	stathmin 2	-0.161	6.02E-02	D	other
STMN2	stathmin 2	-0.180	6.33E-02	D	other
STMN2	stathmin 2	-0.202	7.90E-02	D	other
SULT1A1	sulfotransferase family. cytosolic. 1A. phenol-preferring. member 1	0.222	4.65E-02	D	enzyme
SULT1A1	sulfotransferase family. cytosolic. 1A. phenol-preferring. member 1	0.226	5.41E-02	D	enzyme
SUMO3	small ubiquitin-like modifier 3	-0.376	7.97E-02		other
SYBU	syntabulin (syntaxin-interacting)	0.582	4.57E-02		other
TACC3	transforming. acidic coiled-coil containing protein 3	-0.500	5.67E-02		other
TAT	tyrosine aminotransferase	1.037	3.94E-02		enzyme
TCTA	T-cell leukemia translocation altered	-0.229	9.67E-02		other
TDG	thymine-DNA glycosylase	-0.372	9.83E-02		enzyme
TDO2	tryptophan 2.3-dioxygenase	0.538	6.33E-02		enzyme
TGFBI	transforming growth factor. beta-induced. 68kDa	-0.411	3.05E-02		other
TGM1	transglutaminase 1	-0.568	7.56E-02		enzyme
THOC6	THO complex 6 homolog (Drosophila)	-0.197	3.94E-02		other
THOP1	thimet oligopeptidase 1	-0.174	9.37E-02		peptidase
THYN1	thymocyte nuclear protein 1	-0.311	8.15E-02		other
TIAM1	T-cell lymphoma invasion and metastasis 1	0.150	5.65E-02		other
TMEM189	transmembrane protein 189	-0.266	2.99E-02		other
TMEM254	transmembrane protein 254	0.627	3.94E-02	D	other

TMEM254	transmembrane protein 254	0.638	5.58E-02	D	other
TMIGD1	transmembrane and immunoglobulin domain containing 1	0.365	3.29E-02		other
TMPRSS13	transmembrane protease. serine 13	0.277	7.42E-02		peptidase
TNKS	tankyrase. TRF1-interacting ankyrin-related ADP-ribose polymerase	0.151	7.09E-02		enzyme
TNR	tenascin R	0.221	5.01E-02	D	other
TNR	tenascin R	0.191	7.42E-02	D	other
TP53BP2	tumor protein p53 binding protein 2	0.365	6.89E-02		other
TRAM1	translocation associated membrane protein 1	0.319	5.41E-02		other
TRMT13	tRNA methyltransferase 13 homolog (S. cerevisiae)	-0.139	6.38E-02		other
TRMT61A	tRNA methyltransferase 61 homolog A (S. cerevisiae)	-0.149	8.37E-02		enzyme
TSPAN4	tetraspanin 4	0.635	3.94E-02		other
TSPAN6	tetraspanin 6	-0.452	6.20E-02		other
TTC5	tetratricopeptide repeat domain 5	-0.122	6.69E-02		other
TUBA1C	tubulin. alpha 1c	-0.329	8.29E-02	D	other
TUBA1C	tubulin. alpha 1c	-0.307	8.98E-02	D	other
TUBA8	tubulin. alpha 8	-0.715	5.91E-02		other
TUBB4B	tubulin. beta 4B class IVb	-0.301	2.89E-02		other
TXNDC12	thioredoxin domain containing 12 (endoplasmic reticulum)	-0.459	6.83E-02		enzyme
TYRP1	tyrosinase-related protein 1	-0.276	7.04E-02		enzyme
UCHL1	ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase)	-0.184	3.96E-02		peptidase
UFL1	UFM1-specific ligase 1	0.352	6.53E-02		other
UGCG	UDP-glucose ceramide glucosyltransferase	-0.129	8.76E-02		enzyme
UGGT2	UDP-glucose glycoprotein glucosyltransferase 2	-0.273	7.94E-02		enzyme
USP13	ubiquitin specific peptidase 13 (isopeptidase T-3)	0.290	6.53E-02		peptidase
USP28	ubiquitin specific peptidase 28	0.426	4.15E-02		peptidase
USP48	ubiquitin specific peptidase 48	0.268	3.96E-02		peptidase
UTP11L	UTP11-like. U3 small nucleolar ribonucleoprotein (yeast)	-0.181	6.71E-02		other
VMP1	vacuole membrane protein 1	-0.232	4.15E-02		other
VWA5A	von Willebrand factor A domain containing 5A	0.413	9.40E-02		other
WDR5	WD repeat domain 5	-0.335	9.16E-02		other
WRNIP1	Werner helicase interacting protein 1	-0.209	9.30E-02		enzyme
XPOT	exportin. tRNA	-0.339	8.25E-02		other
YAE1D1	Yae1 domain containing 1	-0.336	5.40E-02		other
YWHAQ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein. theta	-0.314	7.87E-02	D	other
YWHAQ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein. theta	-0.384	7.97E-02	D	other
ZBTB11	zinc finger and BTB domain containing 11	0.335	3.85E-02		other
ZBTB49	zinc finger and BTB domain containing 49	0.234	3.29E-02		other
ZFYVE27	zinc finger. FYVE domain containing 27	-0.134	5.38E-02		other
ZMYND19	zinc finger. MYND-type containing 19	-0.138	8.98E-02		other
ZNF410	zinc finger protein 410	-0.198	8.25E-02		other
ZNF729	zinc finger protein 729	-0.278	3.34E-02	D	other
ZNF729	zinc finger protein 729	-0.158	5.74E-02	D	other
ZNF729	zinc finger protein 729	-0.280	5.28E-02	D	other
ZNF800	zinc finger protein 800	-0.177	5.16E-02	D	other
ZNF800	zinc finger protein 800	-0.196	6.83E-02	D	other

Symbol	Entrez Gene Name	Log Ratio	p-value	N	Type(s)
AMBP	alpha-1-microglobulin/bikunin precursor	0.264	4.22E-02		transporter
APOA4	apolipoprotein A-IV	-0.574	9.90E-02		transporter
ATP1A1	ATPase. Na+/K+ transporting. alpha 1 polypeptide	-0.270	6.58E-02		transporter
ATP1B2	ATPase. Na+/K+ transporting. beta 2 polypeptide	-0.291	3.84E-02		transporter
ATP5J	ATP synthase. H+ transporting. mitochondrial Fo complex. subunit F6	0.179	9.90E-02		transporter
GLRB	glycine receptor. beta	0.127	9.81E-02		ion channel
GOLGA3	golgin A3	-0.113	9.10E-02		transporter
HBE1	hemoglobin. epsilon 1	0.429	9.61E-02		transporter
NSF	N-ethylmaleimide-sensitive factor	0.221	7.77E-02		transporter
RYR2	ryanodine receptor 2 (cardiac)	-0.218	9.04E-02		ion channel
SLC25A24	solute carrier family 25 (mitochondrial carrier; phosphate carrier). member 24	0.148	6.58E-02		transporter
SNX15	sorting nexin 15	0.098	9.81E-02		transporter
STX6	syntaxin 6	-0.266	9.32E-02		transporter
VPS33A	vacuolar protein sorting 33 homolog A (S. cerevisiae)	0.257	3.84E-02		transporter
BTG2	BTG family. member 2	-1.337	3.30E-02	D	transcription regulator
BTG2	BTG family. member 2	-1.504	4.80E-02	D	transcription regulator
CSHL1	chorionic somatomammotropin hormone-like 1	-0.434	5.73E-02		transcription regulator
EGR1	early growth response 1	-0.319	9.90E-02		transcription regulator
FOS	FBJ murine osteosarcoma viral oncogene homolog	-2.020	9.81E-02		transcription regulator
FOSB	FBJ murine osteosarcoma viral oncogene homolog B	-1.985	8.82E-02		transcription regulator
FOXM1	forkhead box M1	0.268	8.62E-02		transcription regulator
FOXQ1	forkhead box Q1	-0.719	3.37E-02		transcription regulator
HDAC4	histone deacetylase 4	-0.273	4.80E-02		transcription regulator
HES1	hes family bHLH transcription factor 1	-0.397	3.66E-02		transcription regulator
KLF2	Kruppel-like factor 2	-0.758	3.30E-02		transcription regulator
KLF2	Kruppel-like factor 2	-0.679	3.83E-02		transcription regulator
LHX1	LIM homeobox 1	-0.173	6.86E-02		transcription regulator
MSX2	msh homeobox 2	-0.310	3.84E-02		transcription regulator
NPAT	nuclear protein. ataxia-telangiectasia locus	0.233	6.58E-02		transcription regulator
ONECUT1	one cut homeobox 1	-0.133	6.86E-02	D	transcription regulator
ONECUT1	one cut homeobox 1	-0.126	9.17E-02	D	transcription regulator

PAX9	paired box 9	-0.226	5.32E-02		transcription regulator
PPARG	peroxisome proliferator-activated receptor gamma	0.339	9.90E-02		ligand-dependent nuclear receptor
PRPF6	pre-mRNA processing factor 6	0.130	9.39E-02		transcription regulator
SOX10	SRY (sex determining region Y)-box 10	0.120	9.21E-02		transcription regulator
TAF9	TAF9 RNA polymerase II. TATA box binding protein (TBP)-associated factor. 32kDa	-0.134	9.39E-02		transcription regulator
ACKR3	atypical chemokine receptor 3	-0.201	4.65E-02		G-protein coupled receptor
B2M	beta-2-microglobulin	-0.184	5.32E-02		transmembrane receptor
KTN1	kinectin 1 (kinesin receptor)	0.186	6.86E-02		transmembrane receptor
LGALS3BP	lectin. galactoside-binding. soluble. 3 binding protein	0.169	4.80E-02		transmembrane receptor
LRPAP1	low density lipoprotein receptor-related protein associated protein 1	0.175	6.74E-02		transmembrane receptor
OPN1LW	opsin 1 (cone pigments). long-wave-sensitive	0.198	9.55E-02		G-protein coupled receptor
TNFRSF14	tumor necrosis factor receptor superfamily. member 14	0.205	9.76E-02		transmembrane receptor
EDN1	endothelin 1	-0.175	7.78E-02	D	cytokine
EDN1	endothelin 1	-0.184	9.47E-02	D	cytokine
AGT	angiotensinogen (serpin peptidase inhibitor. clade A. member 8)	0.236	8.33E-02		growth factor
CAMK2G	calcium/calmodulin-dependent protein kinase II gamma	-0.412	3.30E-02		kinase
CKM	creatine kinase. muscle	-0.279	4.22E-02		kinase
DLG1	discs. large homolog 1 (Drosophila)	0.163	9.76E-02		kinase
GK5	glycerol kinase 5 (putative)	0.155	6.86E-02		kinase
GNE	glucosamine (UDP-N-acetyl)-2-epimerase/N-acetylmannosamine kinase	0.187	9.39E-02		kinase
MAP3K5	mitogen-activated protein kinase kinase kinase 5	-0.103	9.90E-02		kinase
NDRG1	N-myc downstream regulated 1	0.288	3.84E-02		kinase
PAK4	p21 protein (Cdc42/Rac)-activated kinase 4	-0.149	9.39E-02		kinase
PIM2	Pim-2 proto-oncogene. serine/threonine kinase	-0.451	9.61E-02		kinase
PTPN13	protein tyrosine phosphatase. non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase)	0.174	6.67E-02		phosphatase
SOCS3	suppressor of cytokine signaling 3	-2.038	8.50E-02		phosphatase
TWF2	twinfilin actin-binding protein 2	-0.188	8.44E-02		kinase
2610028H24 Rik	RIKEN cDNA 2610028H24 gene	-0.098	9.39E-02		other
ACAA1	acetyl-CoA acyltransferase 1	0.180	9.39E-02		enzyme
ACHE	acetylcholinesterase (Yt blood group)	-0.269	9.39E-02		enzyme
ACO1	aconitase 1. soluble	-0.405	4.38E-02		enzyme
ACTR10	actin-related protein 10 homolog (S. cerevisiae)	0.164	6.86E-02		other
AKTIP	AKT interacting protein	-0.098	9.61E-02		other

AMY2B	amylase. alpha 2B (pancreatic)	0.262	4.78E-02		enzyme
ANKRD9	ankyrin repeat domain 9	-0.290	8.47E-02		other
ARRDC3	arrestin domain containing 3	0.243	9.47E-02		other
ASL	argininosuccinate lyase	-0.176	4.80E-02		enzyme
ATL3	atlastin GTPase 3	-0.194	9.39E-02		other
BABAM1	BRISC and BRCA1 A complex member 1	0.184	5.29E-02		other
BCO1	beta-carotene oxygenase 1	0.189	8.01E-02		enzyme
BIN3	bridging integrator 3	-0.238	9.39E-02		other
BYSL	bystin-like	-0.147	9.39E-02		other
C14orf166	chromosome 14 open reading frame 166	0.119	9.44E-02		other
CA13	carbonic anhydrase XIII	0.174	9.39E-02		enzyme
CAP2	CAP. adenylate cyclase-associated protein. 2 (yeast)	-0.223	9.47E-02		other
CAPZA1	capping protein (actin filament) muscle Z-line. alpha 1	0.227	9.81E-02		other
CASP6	caspase 6. apoptosis-related cysteine peptidase	-0.377	3.84E-02		peptidase
CCDC93	coiled-coil domain containing 93	0.201	8.00E-02		other
CD2BP2	CD2 (cytoplasmic tail) binding protein 2	0.313	5.39E-02		other
CDC6	cell division cycle 6	0.149	9.39E-02		other
CKAP2	cytoskeleton associated protein 2	0.363	9.39E-02		other
CMTR1	cap methyltransferase 1	0.181	6.32E-02		enzyme
CRBN	cereblon	0.140	6.86E-02		enzyme
CRYL1	crystallin. lambda 1	0.338	7.15E-02		enzyme
CWC25	CWC25 spliceosome-associated protein homolog (S. cerevisiae)	0.175	6.32E-02		other
CYP26C1	cytochrome P450. family 26. subfamily C. polypeptide 1	-0.236	9.81E-02		enzyme
CYP2J2	cytochrome P450. family 2. subfamily J. polypeptide 2	-0.231	8.62E-02		enzyme
DBR1	debranching RNA lariats 1	0.142	7.63E-02		enzyme
DDX24	DEAD (Asp-Glu-Ala-Asp) box helicase 24	-0.255	3.84E-02		enzyme
DNAJA3	DnaJ (Hsp40) homolog. subfamily A. member 3	-0.330	9.53E-02		other
EFCAB14	EF-hand calcium binding domain 14	0.414	3.97E-02		other
EIF2B3	eukaryotic translation initiation factor 2B. subunit 3 gamma. 58kDa	-0.161	8.44E-02		other
ELAVL4	ELAV like neuron-specific RNA binding protein 4	-0.384	9.32E-02		other
ELOVL7	ELOVL fatty acid elongase 7	-1.122	6.86E-02	D	enzyme
ELOVL7	ELOVL fatty acid elongase 7	-1.130	8.00E-02	D	enzyme
ERGIC1	endoplasmic reticulum-golgi intermediate compartment (ERGIC) 1	0.347	4.65E-02		other
ERI1	exoribonuclease 1	0.165	8.82E-02		enzyme
ESF1	ESF1. nucleolar pre-rRNA processing protein. homolog (S. cerevisiae)	-0.274	6.37E-02	D	other
ESF1	ESF1. nucleolar pre-rRNA processing protein. homolog (S. cerevisiae)	-0.213	6.39E-02	D	other

ESF1	ESF1. nucleolar pre-rRNA processing protein. homolog (S. cerevisiae)	-0.239	6.37E-02	D	other
FAM195A	family with sequence similarity 195. member A	-0.179	5.32E-02		other
FBXL3	F-box and leucine-rich repeat protein 3	-0.157	9.39E-02		enzyme
FBXW11	F-box and WD repeat domain containing 11	0.109	9.39E-02		enzyme
FKBP5	FK506 binding protein 5	0.516	3.30E-02		enzyme
GADD45B	growth arrest and DNA-damage-inducible. beta	-0.313	9.76E-02		other
GRHL3	grainyhead-like 3 (Drosophila)	-0.152	7.15E-02		other
HES5	hes family bHLH transcription factor 5	-0.191	8.44E-02		other
HEXA	hexosaminidase A (alpha polypeptide)	-0.174	9.32E-02		enzyme
HS6ST2	heparan sulfate 6-O-sulfotransferase 2	0.175	9.39E-02		enzyme
HSP90AA1	heat shock protein 90kDa alpha (cytosolic). class A member 1	-0.233	9.04E-02		enzyme
HSPG2	heparan sulfate proteoglycan 2	-0.211	9.68E-02		enzyme
LETM2	leucine zipper-EF-hand containing transmembrane protein 2	-0.155	6.58E-02		other
LOX	lysyl oxidase	0.139	9.32E-02		enzyme
LRIT1	leucine-rich repeat. immunoglobulin-like and transmembrane domains 1	-0.257	9.88E-02		other
LSM12	LSM12 homolog (S. cerevisiae)	0.226	9.90E-02		other
MAB21L3	mab-21-like 3 (C. elegans)	0.134	6.58E-02		other
METAP1D	methionyl aminopeptidase type 1D (mitochondrial)	-0.252	9.39E-02		peptidase
METRN	meteorin. glial cell differentiation regulator	0.136	8.62E-02		other
MGME1	mitochondrial genome maintenance exonuclease 1	-0.281	6.86E-02		enzyme
MLF2	myeloid leukemia factor 2	-0.205	9.39E-02		other
MNAT1	MNAT CDK-activating kinase assembly factor 1	-0.139	8.00E-02		other
MVP	major vault protein	0.286	3.84E-02		other
NCKIPSD	NCK interacting protein with SH3 domain	-0.242	9.76E-02		other
NEIL3	nei endonuclease VIII-like 3 (E. coli)	-0.177	6.58E-02		enzyme
NIPAL4	NIPA-like domain containing 4	-0.237	9.39E-02		other
NPEPL1	aminopeptidase-like 1	0.114	9.39E-02		peptidase
Nrxn3	neurexin III	-0.228	4.16E-02		other
NUP205	nucleoporin 205kDa	0.178	4.80E-02		other
PARP1	poly (ADP-ribose) polymerase 1	0.224	8.00E-02		enzyme
PC	pyruvate carboxylase	0.205	4.65E-02		enzyme
PCDH11X	protocadherin 11 X-linked	-0.208	8.62E-02		other
PCDHA8	protocadherin alpha 8	0.506	6.22E-02	D	other
PCDHA8	protocadherin alpha 8	-0.196	9.39E-02	D	other
PDCD2L	programmed cell death 2-like	-0.158	9.39E-02		other
PDCL3	phosducin-like 3	-0.270	4.22E-02		other
PDHA1	pyruvate dehydrogenase (lipoamide) alpha 1	-0.224	7.77E-02		enzyme
PLA2G12B	phospholipase A2. group XIIB	0.222	4.78E-02		enzyme

PLA2G15	phospholipase A2. group XV	0.221	4.78E-02		enzyme
PLXDC2	plexin domain containing 2	-0.293	9.39E-02		other
POLR3B	polymerase (RNA) III (DNA directed) polypeptide B	-0.177	9.61E-02		enzyme
POPDC3	popeye domain containing 3	-0.125	7.15E-02		other
PPP1R37	protein phosphatase 1. regulatory subunit 37	0.149	7.78E-02		other
PRC1	protein regulator of cytokinesis 1	0.137	9.39E-02		other
PRPH	peripherin	0.157	8.01E-02		other
PSEN1	presenilin 1	0.176	6.46E-02		peptidase
RAB3C	RAB3C. member RAS oncogene family	0.276	7.14E-02		enzyme
RNF130	ring finger protein 130	0.196	4.80E-02		peptidase
RNF182	ring finger protein 182	-0.314	9.39E-02		enzyme
RNF34	ring finger protein 34. E3 ubiquitin protein ligase	-0.136	6.58E-02		enzyme
SCD	stearoyl-CoA desaturase (delta-9-desaturase)	-0.241	8.00E-02		enzyme
SEPT8	septin 8	0.137	6.58E-02		other
SERPINA10	serpin peptidase inhibitor. clade A (alpha-1 antiproteinase. antitrypsin). member 10	-0.463	5.25E-02		other
SERPINH1	serpin peptidase inhibitor. clade H (heat shock protein 47). member 1. (collagen binding protein 1)	-0.581	9.17E-02		other
SLBP	stem-loop binding protein	0.302	6.58E-02		other
SLMO2	slowmo homolog 2 (Drosophila)	-0.225	9.81E-02		other
SLTM	SAFB-like. transcription modulator	0.316	9.04E-02		other
SMYD5	SMYD family member 5	-0.190	4.30E-02		other
SPPL2A	signal peptide peptidase like 2A	0.202	4.22E-02		peptidase
SPTLC1	serine palmitoyltransferase. long chain base subunit 1	0.151	9.81E-02		enzyme
STC2	stanniocalcin 2	-0.358	4.78E-02		other
STMN2	stathmin 2	0.200	5.32E-02	D	other
STMN2	stathmin 2	0.134	8.91E-02	D	other
STRC	stereocilin	0.147	8.62E-02		other
TGM1	transglutaminase 1	-0.234	7.20E-02		enzyme
TMUB1	transmembrane and ubiquitin-like domain containing 1	-0.117	9.47E-02		other
TTC7A	tetratricopeptide repeat domain 7A	0.129	7.17E-02		other
TUBA1A	tubulin. alpha 1a	0.309	9.39E-02		other
UBE2QL1	ubiquitin-conjugating enzyme E2Q family-like 1	-0.672	9.39E-02		other
UGGT2	UDP-glucose glycoprotein glucosyltransferase 2	0.229	4.22E-02		enzyme
VIL1	villin 1	0.359	9.88E-02		other
VTN	vitronectin	0.274	4.22E-02	D	other
VTN	vitronectin	0.316	9.39E-02	D	other
XKR4	XK. Kell blood group complex subunit-related family. member 4	-0.230	9.32E-02		other
XPOT	exportin. tRNA	-0.119	9.57E-02		other
ZNF503	zinc finger protein 503	-0.199	9.04E-02		other
ZNF729	zinc finger protein 729	-0.123	9.39E-02		other

Symbol	Entrez Gene Name	Log Ratio	p-value	N	Type(s)
ABCA1	ATP-binding cassette, sub-family A (ABC1), member 1	-0,346	6,67E-02		transporter
ABCA4	ATP-binding cassette, sub-family A (ABC1), member 4	0,297	8,97E-02		transporter
ABCB9	ATP-binding cassette, sub-family B (MDR/TAP), member 9	0,164	6,09E-02		transporter
ABCD3	ATP-binding cassette, sub-family D (ALD), member 3	0,180	7,68E-02		transporter
ABCE1	ATP-binding cassette, sub-family E (OABP), member 1	0,118	9,61E-02		transporter
ACTR6	ARP6 actin-related protein 6 homolog (yeast)	-0,183	7,54E-02		transporter
ANKH	ANKH inorganic pyrophosphate transport regulator	-0,221	3,25E-02		transporter
AQP3	aquaporin 3 (Gill blood group)	-0,254	9,64E-02		transporter
ATP6V1C1	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1	0,103	8,42E-02		transporter
CACNG1	calcium channel, voltage-dependent, gamma subunit 1	-0,246	8,70E-02		ion channel
CACNG6	calcium channel, voltage-dependent, gamma subunit 6	-0,203	8,33E-02		ion channel
CDH17	cadherin 17, LI cadherin (liver-intestine)	0,171	8,36E-02		transporter
DDI2	DNA-damage inducible 1 homolog 2 (S. cerevisiae)	0,176	6,13E-02		transporter
FDX1L	ferredoxin 1-like	0,237	7,76E-02		transporter
GJB3	gap junction protein, beta 3, 31kDa	-0,185	8,08E-02		transporter
GPM6A	glycoprotein M6A	-0,485	9,71E-02		ion channel
GRID2	glutamate receptor, ionotropic, delta 2	0,142	8,69E-02		ion channel
HBE1	hemoglobin, epsilon 1	0,377	8,20E-02		transporter
HDLBP	high density lipoprotein binding protein	0,274	7,74E-02		transporter
HSDL2	hydroxysteroid dehydrogenase like 2	-0,188	2,44E-02		transporter
KCNC2	potassium voltage-gated channel, Shaw-related subfamily, member 2	0,163	6,03E-02		ion channel
KCNG4	potassium voltage-gated channel, subfamily G, member 4	0,189	6,03E-02		ion channel
LRRCC1	leucine rich repeat and coiled-coil centrosomal protein 1	0,175	4,25E-02		transporter
MCL1	myeloid cell leukemia 1	-0,595	3,76E-02		transporter
NPC1	Niemann-Pick disease, type C1	0,215	2,96E-02		transporter
NUP160	nucleoporin 160kDa	-0,360	6,05E-02		transporter
NUTF2	nuclear transport factor 2	-0,164	4,94E-02		transporter
RHBG	Rh family, B glycoprotein (gene/pseudogene)	-0,436	1,42E-02		transporter
RHCG	Rh family, C glycoprotein	-0,381	4,32E-02		transporter
SCAMP2	secretory carrier membrane protein 2	0,332	2,99E-02		transporter
SCARB1	scavenger receptor class B, member 1	0,110	5,13E-02		transporter
SCFD1	sec1 family domain containing 1	-0,111	7,15E-02		transporter
SCN8A	sodium channel, voltage gated, type VIII, alpha subunit	-0,224	7,81E-02		ion channel
SEC61A1	Sec61 alpha 1 subunit (S. cerevisiae)	0,183	2,85E-02		transporter
SEC63	SEC63 homolog (S. cerevisiae)	-0,144	8,09E-02		transporter
SFXN2	sideroflexin 2	-0,101	6,97E-02		transporter
SLC15A1	solute carrier family 15 (oligopeptide transporter), member 1	0,165	9,61E-02		transporter

Table S16

	1g (Inc)				3g>axe				3g>1g			
	microarray		**RT-PCR**		**microarray**		**RT-PCR**		**microarray**		**RT-PCR**	
Gene	**FC**	**p-value**	**FC**	**p-value**	**FC**	**p-value**	**FC**	**p-value**	**FC**	**p-value**	**FC**	**p-value**
btg2	0.232	0.029	0.206	< 0.001	0.353	0.048	0.335	< 0.001	0.220	0.014	0.134	< 0.001
cebpb	0.386	0.022	0.323	< 0.001	0.395	0.033	0.326	< 0.001	0.462	0.030	0.351	< 0.001
fos	0.173	0.029	0.056	< 0.001	0.247	0.098	0.202	< 0.001	0.134	0.023	0.050	< 0.001
fos b	0.229	0.009	0.494	< 0.001	0.253	0.088	0.879	< 0.001	0.237	0.036	0.311	< 0.001
klf2a	0.616	0.087	0.476	< 0.001			0.820	< 0.001	0.533	0.010	0.419	< 0.001
socs3a	0.177	0.029	0.177	< 0.001	0.244	0.085	0.289	< 0.001	0.146	0.004	0.132	< 0.001

Symbol	Entrez Gene Name	3g	3g+sim	3g>1g	1g>3g	PTH	VitD3
GADD45B	growth arrest and DNA-damage-inducible, beta	-0.85	-0.41	-0.85	-0.42		
FOSB	FBJ murine osteosarcoma viral oncogene homolog B	-2.12	-1.99	-2.38			-0.90
FOXO1	forkhead box O1	-0.58	-0.72	-0.80			0.59
EGR1	early growth response 1	-0.59	-0.33	-0.61		-0.73	
FOS	FBJ murine osteosarcoma viral oncogene homolog	-2.52	-2.62	-2.89			
SOCS3	suppressor of cytokine signaling 3	-2.56	-2.04	-2.79			
BTG2	BTG family, member 2	-2.11	-1.93	-2.19			
ELOVL7	ELOVL fatty acid elongase 7	-1.21	-1.13	-1.40			
SLIT2	slit homolog 2 (Drosophila)	-0.52	-0.43	-0.61			
LRIT1	leucine-rich repeat, immunoglobulin-like and transmembrane domains 1	0.51	-0.26	-0.17			
ZNF729	zinc finger protein 729	-0.29	-0.12		-0.16	-1.22	-0.47
CYP2J2	cytochrome P450, family 2, subfamily J, polypeptide 2	0.51	-0.33		0.43	-0.14	-1.02
APOA4	apolipoprotein A-IV	-0.62	-0.51		-0.33		-1.79
SLC6A15	solute carrier family 6 (neutral amino acid transporter), member 15	0.64		0.20	-0.16		-0.71
CYR61	cysteine-rich, angiogenic inducer, 61	-0.89		-1.16	-0.37		
DUSP2	dual specificity phosphatase 2	-0.72		-1.20	-0.59		
NFKBIZ	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, z	-0.47		-0.73	-0.38		
ERRFI1	ERBB receptor feedback inhibitor 1	-0.60		-0.53	-0.38		
ATF3	activating transcription factor 3	-0.32		-0.35	-0.62		
HBE1	hemoglobin, epsilon 1		0.60	0.38	-0.37		
PIM2	Pim-2 proto-oncogene, serine/threonine kinase		-0.45	-0.26	0.24		
[illegible]	[illegible]		0.52	-0.18	0.30		
SLC15A1	solute carrier family 15 (oligopeptide transporter), member 1	0.33		0.17	-0.60		
BCO1	beta-carotene oxygenase 1	0.39	0.19		-0.13		
OPN1LW	opsin 1 (cone pigments), long-wave-sensitive	-0.67	0.26				-1.04
MYOG	myogenin (myogenic factor 4)	-0.38		-0.51			-0.85
WDR5	WD repeat domain 5	-0.34		-0.15		-1.46	
STK38	serine/threonine kinase 38	-0.30		-0.30			-0.55
LOX	lysyl oxidase	-0.12	0.14				0.46
SPPL2B	signal peptide peptidase like 2B		0.20	0.31		0.56	
TTC19	tetratricopeptide repeat domain 19		0.13	0.27			-0.62
ATP1A1	ATPase, Na+/K+ transporting, alpha 1 polypeptide	0.61	-0.27				-0.39
IGFBP1	insulin-like growth factor binding protein 1	1.01		-0.61			1.02
[illegible]	[illegible]	-1.72		-0.47			
DUSP1	dual specificity phosphatase 1	-1.35		-1.03			
TGM1	transglutaminase 1	-0.57	-0.23				
CKAP2	cytoskeleton associated protein 2	-0.48	0.38				
LGSN	lengsin, lens protein with glutamine synthetase domain	-0.48		-0.75			
CRYGN	crystallin, gamma N	-0.56		-0.15			
H1F0	H1 histone family, member 0	-0.41		-0.61			
RRM1	ribonucleotide reductase M1	-0.40		-0.15			
EGR2	early growth response 2	-0.29		-0.62			
ANKRD9	ankyrin repeat domain 9		-0.29	-0.67			
EFCAB14	EF-hand calcium binding domain 14		0.41	0.53			
HES1	hes family bHLH transcription factor 1		-0.40	-0.13			
EXT2	exostosin glycosyltransferase 2	0.15		0.40			
FNIP1	folliculin interacting protein 1	0.28		0.45			
HSP90AA1	heat shock protein 90kDa alpha (cytosolic), class A member 1	0.58	-0.23				
COL4A1	collagen, type IV, alpha 1	0.58		0.27			
CETP	cholesteryl ester transfer protein, plasma	0.58		0.18			
ACE	angiotensin I converting enzyme	0.51		0.52			
TEC	tec protein tyrosine kinase	0.53		0.38			

Canonical Pathway	3g	3g>axe	3g>1g	1g>3g	PTH	VitD3
IGF-1 Signaling	2.77	0.72	3.87	3.89		2.24
Tight Junction Signaling	1.42	0.39	3.63	0.35	0.85	
JAK/Stat Signaling	1.59	1.01	2.03	3.51		0.65
Mitotic Roles of Polo-Like Kinase	3.83	0.98	0.31		1.19	
Prolactin Signaling	1.67	0.81	3.74	2.36		1.28
ERK/MAPK Signaling	2.41	1.15	2.01	2.14		
Glucocorticoid Receptor Signaling	2.15	1.89	1.05	2.05		0.65
Erythropoietin Signaling	1.77	0.07	2.33	2.93		0.33
ILK Signaling	2.42		3.87	0.83	0.64	2.14
GADD45 Signaling	5.10	0.63	0.57	1.90		0.38
PPAR Signaling	1.68	1.26	0.53	2.78	0.83	0.26
Remodeling of Epithelial Adherens Junctions	4.84	0.39	1.93	0.33	0.86	0.93
VEGF Signaling	1.24	0.27	3.46	1.30		0.63
Insulin Receptor Signaling	1.96	0.81	1.74	2.80	0.60	0.33
Sertoli Cell-Sertoli Cell Junction Signaling	1.65	0.73	3.05	0.40		
Epithelial Adherens Junction Signaling	3.85		1.53	0.42	0.22	1.59
CD40 Signaling	0.72	0.73	3.74	1.21	0.18	
PI3K/AKT Signaling	3.28	0.07	0.31	1.63		0.37
Growth Hormone Signaling	0.83	2.09	1.73	0.69	0.43	1.56
Cell Cycle Control of Chromosomal Replication	5.46	0.15	0.73	0.66		0.29
Role of JAK2 in Hormone-like Cytokine Signaling	1.34	0.55	1.55	2.41		1.30
Integrin Signaling	2.81		1.77	0.31	1.62	0.59
FAK Signaling	1.51	0.29	2.35	1.35		
Renin-Angiotensin Signaling	0.62	1.21	2.97	1.11		
Cell Cycle: G2/M DNA Damage Checkpoint Regulation	4.89		0.57			0.37
SAPK/JNK Signaling	0.41	2.32	1.32	0.98		
Heme Degradation	1.20		4.85			0.59
Cellular Effects of Sildenafil (Viagra)	0.76		4.25	0.40		0.50
IL-2 Signaling	0.47	0.45	1.15	2.07		0.46
Telomerase Signaling	0.95	0.85	0.99	0.88		0.52
Gα12/13 Signaling	0.99	0.21	2.15	1.89		
Agrin Interactions at Neuromuscular Junction	1.18	0.38	2.28	0.81		0.24
Neuregulin Signaling	1.26	0.79	0.68	2.07		0.57
Regulation of IL-2 Expression in Activated and Anergic T Lymphocytes	0.67	0.33	1.07	2.26		
Notch Signaling		2.52	1.65	0.61		
STAT3 Pathway	0.63	0.34	1.18	2.36		1.29
Cyclins and Cell Cycle Regulation	2.65	0.32	0.70	0.65		
Mechanisms of Viral Exit from Host Cells	2.52		1.19	0.22		
PDGF Signaling	1.90	0.12	0.71	2.03		0.44
TNFR1 Signaling	0.31	2.11	1.35	0.44	0.58	
Gap Junction Signaling	0.94		2.75	1.29		
Role of JAK1 and JAK3 in γc Cytokine Signaling	0.56	0.54	0.65	1.50		1.13
Huntington's Disease Signaling		0.80	2.08	1.23	1.23	
TNFR2 Signaling	0.83	0.61	2.02	0.81		
LXR/RXR Activation	0.64	2.47	0.32	0.52	0.72	2.97
FXR/RXR Activation	0.76	2.08		0.96	0.24	4.10
Leukocyte Extravasation Signaling	0.52		3.64			
Actin Cytoskeleton Signaling	0.60		2.23	0.67	0.32	0.51
Thyroid Cancer Signaling	1.60	0.33		2.03	0.64	
Amyloid Processing		0.46	2.42	1.71		
Mouse Embryonic Stem Cell Pluripotency			1.21	2.75		0.31
Urate Biosynthesis/Inosine 5'-phosphate Degradation	0.58		1.35	2.16		

Diseases and Bio Functions	3g	3g>ee	3g>1g	1g>3g	PTH	VitD3