Supplementary Table 5 : Transcripts and DAVID pathways correlating with the expression of CD4 in lupus kidney biopsies

Positive correlation

Transcripts

Identifier	Gene Symbol	Correlation coefficient with CD4
ILMN_1727284	CD4	1
ILMN_1772218	HLA-DPA1	0.934229063
ILMN_1778977	TYROBP	0.933302249
ILMN_1689655	HLA-DRA	0.915891173
ILMN_3228688	HLA-DRB1	0.906190291
ILMN_2157441	HLA-DRA	0.902996561
ILMN_2066066	HLA-DRB6	0.901531942
ILMN_1736567	CD74	0.900464276
ILMN_2366330	FERMT3	0.896532157
ILMN_1815895	HLA-DRB1	0.895853418
ILMN_2379644	CD74	0.890964861
ILMN_2049536	TRPV2	0.889679914
ILMN_1718936	LST1	0.886044814
ILMN_1718558	PARP12	0.883825964
ILMN_3240316	TMSB4X	0.881816413
ILMN_1683026	PSMB10	0.881679636
ILMN_2179837	BANF1	0.881663753
ILMN_1786612	PSME2	0.881166328
ILMN_1653828	CHFR	0.879799743
ILMN_1754842	DLGAP4	0.875737515
ILMN_1668039	GYPC	0.874017008
ILMN_1752340	ARF5	0.871364059
ILMN_1654319	HAPLN3	0.86967548
ILMN_2390299	PSMB8	0.868740369
ILMN_1747195	PSMB8	0.866391356
ILMN_2176063	FCGR1C	0.866366101
ILMN_2111739	MAN2C1	0.866279082
ILMN_1807277	IFI30	0.86456805
ILMN_1794473	PHF17	0.863368562
ILMN_1758250	TRAFD1	0.862805609
ILMN_1772359	LAPTM5	0.862504464
ILMN_1679809	GSTP1	0.861629683
ILMN_1651788	MAP3K11	0.861566346
ILMN_1778360	PYGB	0.861254289
ILMN_2349658	TSPO	0.860302388
ILMN_1740015	CD14	0.858368684
ILMN_1760683	SRSF9	0.857616844
ILMN_2062468	IGFBP7	0.857204295
ILMN_1715024	LSS	0.857094666
ILMN_1723706	GRAMD4	0.856571802
ILMN_1782057	ATP8B2	0.855792595
ILMN_2366041	ITM2C	0.855750662
ILMN_1761464	CD74	0.854043623
ILMN_1689968	PLEKHO2	0.853935274
ILMN_1680453	ITM2C	0.853816711
ILMN_1691892	TAGLN2	0.853601352
ILMN_1683271	TMSB4X	0.853486495
ILMN_1785005	NCF4	0.852288271
ILMN_1685005	TNFRSF1A	0.852016046
ILMN_1741371	TMEM8A	0.851368336
ILMN_1752592	HLA-DRB4	0.851148745
ILMN_2400947	CELF2	0.850982825
ILMN_2370772	EIF4G1	0.850763294
ILMN_1712950	PFN1	0.850098377
ILMN_1793950	POTEM	0.849590981
ILMN_1669550	MAD2L2	0.849558148
ILMN_1717261	HLA-DRB1	0.84901389
ILMN_1659688	LGALS3BP	0.8488395
ILMN_1660832	RPL18A	0.848663905
ILMN_1745148	ZNFX1	0.848322315
ILMN_3194911	ATF6B	0.847634385
ILMN_1775762	GNAI2	0.847561057
ILMN_1720476	PHF2	0.847273916
ILMN_1723978	LGALS1	0.846002437
ILMN_1738116	TMEM119	0.845930944
ILMN_1782538	VIM	0.845340049
ILMN_1733947	FKBP8	0.844948911
ILMN_2376108	PSMB9	0.84365789
ILMN_1687533	SEMA4D	0.843172109
ILMN_2278729	EIF3B	0.842759453
ILMN_3229210	FLJ45340	0.842202302
ILMN_1770673	AKNA	0.842092
ILMN_1653220	PITPNM1	0.841307988
ILMN_1749011	NECAP2	0.840455038
ILMN_2379734	CTBP1	0.83935087
ILMN_1695311	HLA-DMA	0.838589567
ILMN_1755733	RPLP2	0.838180672
ILMN_2387496	COAS3	0.837846899
ILMN_1786024	POLR3H	0.837564447
ILMN_1772486	ELF2	0.835726208
ILMN_2120965	NPAT	0.835607122
ILMN_1716547	NAGK	0.834757851
ILMN_1749662	GPX1	0.834646595
ILMN_1778255	FARSA	0.834189514

Pathways

Annotation Cluster 1	**Enrichment Score: 26.47**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	translational elongation	74	2.50E-42	1.00E-38
	SP_PIR_KEYWORDS	ribosome	60	2.00E-41	4.60E-39
	KEGG_PATHWAY	Ribosome	65	3.80E-35	6.60E-33
	SP_PIR_KEYWORDS	protein biosynthesis	91	4.10E-34	7.20E-32
	SP_PIR_KEYWORDS	ribonucleoprotein	114	4.80E-34	6.70E-32
	GOTERM_CC_FAT	cytosolic ribosome	59	3.20E-33	2.30E-30
	SP_PIR_KEYWORDS	ribosomal protein	85	3.10E-29	3.60E-27
	GOTERM_CC_FAT	ribosomal subunit	70	6.50E-28	2.30E-25
	GOTERM_BP_FAT	translation	122	6.60E-28	1.40E-24
	GOTERM_CC_FAT	cytosolic part	76	5.60E-27	1.30E-24
	GOTERM_MF_FAT	structural constituent of ribosome	79	6.80E-27	8.90E-24
	GOTERM_CC_FAT	ribonucleoprotein complex	160	2.50E-26	4.30E-24
	GOTERM_CC_FAT	ribosome	90	7.50E-25	8.70E-23
	GOTERM_CC_FAT	cytosolic small ribosomal subunit	30	1.80E-17	1.80E-15
	GOTERM_CC_FAT	cytosolic large ribosomal subunit	29	3.10E-17	2.70E-15
	GOTERM_CC_FAT	large ribosomal subunit	39	5.60E-17	8.70E-15
	GOTERM_MF_FAT	structural molecule activity	154	1.30E-15	5.80E-13
	GOTERM_CC_FAT	small ribosomal subunit	32	7.30E-12	3.40E-10
Annotation Cluster 2	**Enrichment Score: 10.95**		**Count**	**P_Value**	**Benjamini**
	GOTERM_CC_FAT	intracellular non-membrane-bounded organelle	477	3.80E-16	2.30E-14
	GOTERM_CC_FAT	non-membrane-bounded organelle	477	3.80E-16	2.30E-14
	GOTERM_CC_FAT	cytoskeleton	214	9.90E-03	1.30E-01
Annotation Cluster 3	**Enrichment Score: 10.64**		**Count**	**P_Value**	**Benjamini**
	GOTERM_CC_FAT	intracellular organelle lumen	343	3.90E-14	2.50E-12
	GOTERM_CC_FAT	membrane-enclosed lumen	354	6.40E-14	3.70E-12
	GOTERM_CC_FAT	organelle lumen	348	7.50E-14	4.10E-12
	GOTERM_CC_FAT	nuclear lumen	284	1.90E-12	9.40E-11
	GOTERM_CC_FAT	nucleoplasm	170	3.50E-07	1.50E-05
	GOTERM_CC_FAT	nucleolus	138	1.30E-06	4.90E-05
Annotation Cluster 4	**Enrichment Score: 6.84**		**Count**	**P_Value**	**Benjamini**
	SP_PIR_KEYWORDS	ubl conjugation	117	4.10E-08	2.20E-06
	UP_SEQ_FEATURE	cross-link:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in ubiquitin)	53	4.50E-08	8.10E-05
	SP_PIR_KEYWORDS	isopeptide bond	69	1.70E-06	5.80E-05
Annotation Cluster 5	**Enrichment Score: 5.35**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	macromolecular complex assembly	136	1.00E-07	7.20E-05
	GOTERM_BP_FAT	macromolecular complex subunit organization	138	1.70E-06	3.10E-04
	GOTERM_BP_FAT	cellular macromolecular complex assembly	73	2.10E-06	3.20E-04
	GOTERM_BP_FAT	cellular macromolecular complex subunit organization	77	1.20E-05	1.20E-03
	GOTERM_BP_FAT	protein complex assembly	99	4.10E-05	3.20E-03
	GOTERM_BP_FAT	protein complex biogenesis	99	4.10E-05	3.20E-03
Annotation Cluster 6	**Enrichment Score: 4.78**		**Count**	**P_Value**	**Benjamini**
	SP_PIR_KEYWORDS	mrna splicing	54	8.30E-08	3.90E-06
	SP_PIR_KEYWORDS	mrna processing	61	4.30E-07	1.70E-05
	GOTERM_BP_FAT	RNA splicing	69	4.80E-07	2.20E-04
	GOTERM_BP_FAT	RNA processing	114	4.80E-07	2.00E-04
	GOTERM_BP_FAT	mRNA metabolic process	83	1.00E-06	2.40E-04
	GOTERM_BP_FAT	mRNA processing	74	1.50E-06	2.90E-04
	SP_PIR_KEYWORDS	Spliceosome	30	1.70E-04	3.30E-03
	KEGG_PATHWAY	Spliceosome	34	6.70E-04	3.80E-02
	GOTERM_BP_FAT	nuclear mRNA splicing, via spliceosome	36	6.80E-04	3.10E-02
	GOTERM_BP_FAT	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	36	6.80E-04	3.10E-02
	GOTERM_BP_FAT	RNA splicing, via transesterification reactions	36	6.80E-04	3.10E-02
	GOTERM_CC_FAT	spliceosome	32	1.00E-03	2.10E-02
Annotation Cluster 7	**Enrichment Score: 4.43**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	regulation of cellular protein metabolic process	112	4.70E-10	6.50E-07
	GOTERM_BP_FAT	regulation of protein modification process	71	4.70E-07	2.40E-04
	GOTERM_BP_FAT	positive regulation of ubiquitin-protein ligase activity during mitotic cell cycle	26	7.50E-07	2.60E-04
	GOTERM_BP_FAT	positive regulation of protein metabolic process	61	7.50E-07	2.40E-04
	GOTERM_BP_FAT	negative regulation of protein modification process	37	8.50E-07	2.30E-04
	GOTERM_BP_FAT	positive regulation of cellular protein metabolic process	59	8.60E-07	2.20E-04
	GOTERM_BP_FAT	negative regulation of cellular protein metabolic process	49	9.10E-07	2.20E-04
	GOTERM_BP_FAT	negative regulation of ubiquitin-protein ligase activity during mitotic cell cycle	25	1.10E-06	2.50E-04
	GOTERM_BP_FAT	anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process	25	1.10E-06	2.50E-04
	GOTERM_BP_FAT	positive regulation of ubiquitin-protein ligase activity	26	1.40E-06	2.90E-04
	GOTERM_BP_FAT	positive regulation of protein ubiquitination	29	1.60E-06	3.10E-04
	GOTERM_BP_FAT	negative regulation of molecular function	76	1.80E-06	3.10E-04
	GOTERM_BP_FAT	regulation of ubiquitin-protein ligase activity during mitotic cell cycle	26	1.90E-06	3.00E-04
	GOTERM_BP_FAT	negative regulation of ubiquitin-protein ligase activity	25	2.10E-06	3.20E-04
	GOTERM_BP_FAT	negative regulation of ligase activity	25	2.10E-06	3.20E-04
	GOTERM_BP_FAT	negative regulation of protein metabolic process	49	3.00E-06	4.30E-04
	GOTERM_BP_FAT	positive regulation of ligase activity	26	3.40E-06	4.40E-04
	GOTERM_BP_FAT	regulation of ubiquitin-protein ligase activity	27	3.80E-06	4.80E-04
	GOTERM_BP_FAT	negative regulation of protein ubiquitination	26	4.50E-06	5.50E-04
	GOTERM_BP_FAT	regulation of protein ubiquitination	31	8.20E-06	9.20E-04
	GOTERM_BP_FAT	regulation of ligase activity	27	8.40E-06	9.20E-04
	GOTERM_BP_FAT	negative regulation of catalytic activity	63	1.50E-05	1.50E-03
	GOTERM_BP_FAT	positive regulation of protein modification process	47	1.60E-05	1.50E-03
	GOTERM_BP_FAT	proteasomal protein catabolic process	30	3.50E-05	2.90E-03
	GOTERM_BP_FAT	proteasomal ubiquitin-dependent protein catabolic process	30	3.50E-05	2.90E-03
	INTERPRO	Proteasome, alpha and beta subunits	9	9.40E-05	4.70E-02
	SP_PIR_KEYWORDS	proteasome	18	2.10E-04	4.00E-03
	INTERPRO	Proteasome, beta-type subunit, conserved site	8	2.20E-04	9.00E-02
	GOTERM_CC_FAT	proteasome complex	20	2.50E-04	6.60E-03
	SP_PIR_KEYWORDS	proteinase	9	3.90E-04	6.80E-03

Negative correlation

Transcripts

Identifier	Gene Symbol	Correlation coefficient with CD4
ILMN_1681389	C2H2 zinc finger pr	-0.40001984
ILMN_1768954	RIBC1	-0.400186083
ILMN_1699190	SORCS1	-0.400223681
ILMN_3249088	LOC93432	-0.400285215
ILMN_1680436	CSH2	-0.400299744
ILMN_1722755	KRTAP6-2	-0.400334007
ILMN_3310171	MIR210	-0.400359894
ILMN_1799903	GALNTL1	-0.400392176
ILMN_1754727	ARMCX5	-0.40044397
ILMN_1660020	LOC644662	-0.400562184
ILMN_2369826	C16orf13	-0.400562661
ILMN_2206554	SLC35F5	-0.400563498
ILMN_1853093	BG325888	-0.400578134
ILMN_2331232	TNFRSF6B	-0.400582848
ILMN_1700169	C15orf44	-0.400627977
ILMN_1771689	EXD2	-0.400641297
ILMN_1679134	NSMCE4A	-0.400646612
ILMN_1838375	BM714348	-0.400665624
ILMN_1653266	DNAJB14	-0.400749707
ILMN_1719316	TMED3	-0.400813303
ILMN_3257233	AK126616	-0.400986267
ILMN_1692276	GGPS1	-0.400992588
ILMN_1790595	TFAP2E	-0.401012982
ILMN_1734559	SORD	-0.401202426
ILMN_1698731	SEC31B	-0.401253836
ILMN_1652333	FN3KRP	-0.401355089
ILMN_2052863	RNF5	-0.401425107
ILMN_3311095	MIR643	-0.401427458
ILMN_1663263	EPHA10	-0.401468095
ILMN_3255211	KIAA2015	-0.401494305
ILMN_1676548	BZW2	-0.401528449
ILMN_1709020	MYBL2	-0.401560655
ILMN_1651341	LOC401010	-0.40162232
ILMN_3285238	BX537874	-0.40162554
ILMN_1701239	SPRR2E	-0.401647677
ILMN_2288290	CDY1B	-0.4017477
ILMN_1674297	HCFC2	-0.401754371
ILMN_1769071	XKRX	-0.40180268
ILMN_1773968	SERBP1	-0.401804507
ILMN_2222163	HIST1H3B	-0.401887856
ILMN_1781672	GAB1	-0.401901556
ILMN_1660852	ZC3H6	-0.401907906
ILMN_1736045	KCNJ16	-0.401981532
ILMN_2389528	MTL5	-0.401986801
ILMN_1805842	FHL1	-0.401998765
ILMN_1791702	SMARCA2	-0.402008017
ILMN_1806022	RNF212	-0.402016792
ILMN_1760849	NETO2	-0.402029764
ILMN_3277402	LOC441242	-0.402055879
ILMN_1732584	SHISA6	-0.40209057
ILMN_1740920	ACADSB	-0.40236063
ILMN_1727252	WNT8A	-0.402361321
ILMN_1791679	DNER	-0.402409976
ILMN_1714813	DPY19L2P2	-0.402417622
ILMN_1751036	SMAD2	-0.402457469
ILMN_1823229	BX094072	-0.4024611
ILMN_1769704	FLJ39632	-0.402484676
ILMN_2101025	ZNF75D	-0.402489395
ILMN_1724149	OCLN	-0.40249034
ILMN_2377862	RAB6A	-0.402512772
ILMN_3231804	LL0XNC01-19D8.1	-0.402512855
ILMN_3310336	MIR450A1	-0.402559411
ILMN_2203147	TMPRSS12	-0.402569462
ILMN_1726815	HIST1H3G	-0.402576019
ILMN_1745110	LAPTM4A	-0.402745881
ILMN_1781764	RPL36A	-0.402746902
ILMN_1792002	PAPPA2	-0.402751808
ILMN_1688831	SYT7	-0.402796218
ILMN_1723574	TSG1	-0.402856432
ILMN_1821279	BM678326	-0.402875566
ILMN_1877778	DA086964	-0.402971114
ILMN_1678306	NA	-0.403011806
ILMN_1769918	APBB1	-0.403049265
ILMN_3243908	SNHG7	-0.403056774
ILMN_1669486	tMDC	-0.403074616
ILMN_1908258	BF510793	-0.403134314
ILMN_2099594	SRP9	-0.403137412
ILMN_2156267	EIF2AK1	-0.403168571
ILMN_1776552	FUBP1	-0.403195196
ILMN_2174127	DCBLD2	-0.403197796
ILMN_3206565	XAGE5	-0.403233714
ILMN_1747854	GOLGA8E	-0.403251728
ILMN_1838254	NA	-0.403256259
ILMN_1662158	RPL26L1	-0.403302701

Pathways

Annotation Cluster 1	**Enrichment Score: 3.16**		**Count**	**P_Value**	**Benjamini**
	INTERPRO	Ubiquitin-conjugating enzyme/RWD-like	17	2.00E-05	4.20E-02
	SMART	UBCc	14	1.00E-04	3.50E-02
	SP_PIR_KEYWORDS	ubl conjugation pathway	81	1.30E-04	2.30E-02
	GOTERM_MF_FAT	small conjugating protein ligase activity	35	1.40E-04	4.40E-02
	SP_PIR_KEYWORDS	ligase	54	1.50E-04	2.00E-02
	GOTERM_MF_FAT	acid-amino acid ligase activity	40	1.60E-04	4.00E-02
	INTERPRO	Ubiquitin-conjugating enzyme, E2	14	2.10E-04	2.00E-01
	GOTERM_MF_FAT	ubiquitin-protein ligase activity	31	3.60E-04	7.40E-02
	GOTERM_MF_FAT	ligase activity, forming carbon-nitrogen bonds	43	3.90E-04	6.10E-02
	GOTERM_BP_FAT	protein ubiquitination	25	1.40E-03	5.70E-01
	GOTERM_BP_FAT	protein modification by small protein conjugation	26	2.80E-03	6.00E-01
	UP_SEQ_FEATURE	active site:Glycyl thioester intermediate	16	4.70E-03	9.90E-01
	GOTERM_BP_FAT	protein modification by small protein conjugation or removal	28	9.90E-03	8.80E-01
	KEGG_PATHWAY	Ubiquitin mediated proteolysis	25	1.60E-02	7.80E-01
	GOTERM_CC_FAT	ubiquitin ligase complex	16	5.60E-02	9.00E-01
Annotation Cluster 2	**Enrichment Score: 2.83**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	dephosphorylation	41	5.20E-08	1.80E-04
	GOTERM_BP_FAT	protein amino acid dephosphorylation	36	2.50E-07	4.40E-04
	GOTERM_MF_FAT	phosphoprotein phosphatase activity	41	4.70E-07	6.10E-04
	GOTERM_MF_FAT	phosphatase activity	54	6.40E-07	4.10E-04
	GOTERM_MF_FAT	protein tyrosine phosphatase activity	28	8.70E-06	3.70E-03
	SP_PIR_KEYWORDS	protein phosphatase	30	6.30E-05	1.40E-02
	UP_SEQ_FEATURE	active site:Phosphocysteine intermediate	21	3.00E-04	7.30E-01
	INTERPRO	Protein-tyrosine phosphatase, active site	22	3.20E-04	2.10E-01
	INTERPRO	Dual-specific/protein-tyrosine phosphatase, conserved region	20	7.80E-04	2.90E-01
	SMART	PTPc	12	1.30E-03	2.10E-01
	INTERPRO	Protein-tyrosine phosphatase	19	1.80E-03	4.80E-01
	INTERPRO	Protein-tyrosine phosphatase, receptor/non-receptor type	12	2.30E-03	5.20E-01
	UP_SEQ_FEATURE	domain:Tyrosine-protein phosphatase	13	2.60E-02	1.00E+00
	GOTERM_MF_FAT	protein tyrosine/serine/threonine phosphatase activity	10	4.00E-02	8.30E-01
	SP_PIR_KEYWORDS	tyrosine-specific phosphatase	7	9.90E-02	8.40E-01
	SP_PIR_KEYWORDS	phosphoric monoester hydrolase	12	1.00E-01	8.30E-01
	INTERPRO	Dual specificity phosphatase, catalytic domain	8	1.10E-01	1.00E+00
	INTERPRO	Protein-tyrosine phosphatase, dual specificity	7	1.90E-01	1.00E+00
	GOTERM_MF_FAT	transmembrane receptor protein phosphatase activity	4	3.00E-01	9.90E-01
	UP_SEQ_FEATURE	domain:Tyrosine-protein phosphatase 2	3	3.60E-01	1.00E+00
	UP_SEQ_FEATURE	domain:Tyrosine-protein phosphatase 1	3	3.60E-01	1.00E+00
	SMART	DSPc	3	8.00E-01	1.00E+00
Annotation Cluster 3	**Enrichment Score: 2.62**		**Count**	**P_Value**	**Benjamini**
	SP_PIR_KEYWORDS	ubl conjugation pathway	81	1.30E-04	2.30E-02
	GOTERM_BP_FAT	modification-dependent protein catabolic process	88	3.50E-04	2.70E-01
	GOTERM_BP_FAT	modification-dependent macromolecule catabolic process	88	3.50E-04	2.70E-01
	GOTERM_BP_FAT	proteolysis involved in cellular protein catabolic process	88	1.40E-03	5.20E-01
	GOTERM_BP_FAT	cellular protein catabolic process	88	1.70E-03	5.20E-01
	GOTERM_BP_FAT	cellular macromolecule catabolic process	102	2.30E-03	6.00E-01
	GOTERM_BP_FAT	protein catabolic process	88	4.00E-03	6.70E-01
	GOTERM_BP_FAT	macromolecule catabolic process	106	5.70E-03	7.40E-01
	GOTERM_BP_FAT	proteolysis	136	1.00E-02	8.40E-01
	GOTERM_BP_FAT	ubiquitin-dependent protein catabolic process	30	2.70E-01	9.90E-01
Annotation Cluster 4	**Enrichment Score: 2.24**		**Count**	**P_Value**	**Benjamini**
	GOTERM_CC_FAT	mitochondrion	158	4.70E-05	2.70E-02
	SP_PIR_KEYWORDS	mitochondrion	120	2.40E-04	2.30E-02
	SP_PIR_KEYWORDS	transit peptide	71	2.10E-03	1.20E-01
	UP_SEQ_FEATURE	transit peptide:Mitochondrion	70	2.30E-03	9.60E-01
	GOTERM_CC_FAT	mitochondrial part	80	2.70E-02	8.70E-01
	GOTERM_CC_FAT	mitochondrial envelope	55	9.00E-02	9.20E-01
	GOTERM_CC_FAT	mitochondrial matrix	32	9.70E-02	9.20E-01
	GOTERM_CC_FAT	mitochondrial lumen	32	9.70E-02	9.20E-01
Annotation Cluster 5	**Enrichment Score: 2.15**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	cofactor metabolic process	36	1.30E-03	5.90E-01
	GOTERM_BP_FAT	coenzyme metabolic process	29	2.80E-03	6.30E-01
	GOTERM_BP_FAT	cofactor biosynthetic process	19	1.30E-02	8.70E-01
	GOTERM_BP_FAT	coenzyme biosynthetic process	13	5.70E-02	9.80E-01
Annotation Cluster 6	**Enrichment Score: 2.04**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	water-soluble vitamin metabolic process	11	7.50E-03	8.10E-01
	GOTERM_BP_FAT	betaine metabolic process	4	1.00E-02	8.70E-01
	GOTERM_BP_FAT	carnitine metabolic process	4	1.00E-02	8.70E-01
Annotation Cluster 7	**Enrichment Score: 1.94**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	domain:Myotubularin phosphatase	6	1.10E-02	1.00E+00
	INTERPRO	Myotubularin phosphatase	6	1.20E-02	9.40E-01
	INTERPRO	Myotubularin-related	6	1.20E-02	9.40E-01
Annotation Cluster 8	**Enrichment Score: 1.43**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	carboxylic acid catabolic process	20	2.40E-02	9.60E-01
	GOTERM_BP_FAT	organic acid catabolic process	20	2.40E-02	9.60E-01
	GOTERM_BP_FAT	cellular amino acid catabolic process	13	5.20E-02	9.80E-01
	GOTERM_BP_FAT	amine catabolic process	14	6.60E-02	9.80E-01
Annotation Cluster 9	**Enrichment Score: 1.38**		**Count**	**P_Value**	**Benjamini**
	GOTERM_MF_FAT	enzyme binding	71	2.80E-02	8.40E-01
	GOTERM_MF_FAT	protein kinase binding	24	4.00E-02	8.30E-01
	GOTERM_MF_FAT	kinase binding	27	6.50E-02	8.90E-01
Annotation Cluster 10	**Enrichment Score: 1.33**		**Count**	**P_Value**	**Benjamini**
	SP_PIR_KEYWORDS	nucleotide-binding	213	2.10E-03	1.30E-01
	GOTERM_MF_FAT	nucleotide binding	276	5.40E-03	4.10E-01
	SP_PIR_KEYWORDS	atp-binding	162	2.30E-02	6.10E-01

ILMN_1728224	OGFR	0.834143823
ILMN_2400935	TAGLN	0.834136449
ILMN_1697567	TPM3	0.833912646
ILMN_2310968	RUFY1	0.833741884
ILMN_1690610	RALY	0.833051016
ILMN_1799815	XYLT2	0.832847321
ILMN_1708858	CSNK1E	0.832300175
ILMN_3237826	CNTNAP3B	0.831914342
ILMN_1679880	THOC6	0.831798261
ILMN_2391891	MAP2K5	0.831765836
ILMN_3234828	TMEM229B	0.83164614
ILMN_1742450	TAPBP	0.831521403
ILMN_1695341	KCNK10	0.831345574
ILMN_1815083	WHSC2	0.831045368
ILMN_1774733	SOCS1	0.830948173
ILMN_1681998	AP2B1	0.830807069
ILMN_2396571	GPR108	0.829917167
ILMN_1704286	FXYD5	0.829720373
ILMN_2222688	TMSB4X	0.829404615
ILMN_1727043	GLT25D1	0.82934787
ILMN_1654246	SIRT6	0.829048964
ILMN_2070052	NPIPL3	0.828694714
ILMN_1701643	GDPD5	0.828367608
ILMN_1684306	S100A4	0.828034127
ILMN_2090105	TAGLN2	0.827793534
ILMN_1745807	TMEM62	0.827749835
ILMN_3241979	TMEM179B	0.827418143
ILMN_2064606	TBC1D2B	0.827258435
ILMN_1679039	CASKIN1	0.826970028
ILMN_2410783	GAA	0.826601383
ILMN_2408987	SMARCD3	0.826251666
ILMN_1800354	CST3	0.825786839
ILMN_1787109	CLK2	0.82575294
ILMN_2382431	ANKRD36	0.824841327
ILMN_1803810	RRBP1	0.824545261
ILMN_1812327	RNF19A	0.82428379
ILMN_2155719	NBPF1	0.824018549
ILMN_1805750	IFITM3	0.823656128
ILMN_2115633	CD320	0.823505643
ILMN_1718769	ITSN1	0.823342308
ILMN_1685088	RPL36	0.823301945
ILMN_1693552	CD300A	0.823185387
ILMN_1736256	CALR	0.823016189
ILMN_1765021	TOP3B	0.822718182
ILMN_1652825	IL10RA	0.822561758
ILMN_1786823	ICAM2	0.821328086
ILMN_2200562	LOC595101	0.821150358
ILMN_1680403	SSR4	0.820979014
ILMN_1689953	CD81	0.820970821
ILMN_1761912	MGAT1	0.820751551
ILMN_1683576	MAGED2	0.81984923
ILMN_2367707	PKN1	0.818771419
ILMN_1727271	WARS	0.8183549
ILMN_1720124	RCC2	0.817782509
ILMN_2368068	TCF20	0.817716324
ILMN_1760890	SEPN1	0.817576064
ILMN_1712944	AES	0.816642821
ILMN_1754121	CSK	0.816591048
ILMN_2092756	TMEM109	0.816343494
ILMN_2159453	STXBP2	0.816323572
ILMN_3203186	AL543610	0.816262196
ILMN_1702787	SEMA4A	0.816184641
ILMN_2397776	ASB6	0.816125049
ILMN_1747556	CDK9	0.816085417
ILMN_3247325	PP13759	0.815788721
ILMN_1704753	EPAS1	0.815724159
ILMN_1756360	RPL35A	0.815498871
ILMN_2312906	MIA3	0.815209851
ILMN_1765801	GAA	0.815204248
ILMN_1765258	HLA-E	0.814863854
ILMN_1727642	MOGS	0.814624244
ILMN_3243664	NPIPL3	0.814276952
ILMN_1737074	RPS2	0.813976656
ILMN_1808860	STX5	0.813882479
ILMN_1770787	DDAH2	0.813281485
ILMN_3244065	C9orf69	0.812726623
ILMN_1760563	PRRC2A	0.812521977
ILMN_1667813	RPL7	0.812505284
ILMN_1704315	RPL27A	0.81238402
ILMN_3225505	RPS8	0.812380428
ILMN_1673352	IFITM2	0.81218353
ILMN_1685286	PPP1R12C	0.811843659
ILMN_1744912	CTTN	0.811662697
ILMN_1666976	PLD3	0.811528784
ILMN_1733511	GOLGA3	0.811321895
ILMN_1729408	C7orf28B	0.811262169
ILMN_1718044	ELAC2	0.811198184
ILMN_3251733	C19orf43	0.811058332
ILMN_1811702	GRN	0.810939309
ILMN_1759154	PABPN1	0.810934215
ILMN_1675709	ARFGAP1	0.810665935
ILMN_2403852	CYTH1	0.810197199
ILMN_1784467	NUP210	0.810119504
ILMN_1653708	CORO1B	0.809969137
ILMN_2254635	ITGAX	0.809557107
ILMN_1666635	RPS14	0.809246354

	INTERPRO	Proteasome, subunit alpha/beta	9	1.30E-03	2.40E-01
	SP_PIR_KEYWORDS	threonine protease	9	1.40E-03	2.10E-02
	GOTERM_MF_FAT	threonine-type peptidase activity	9	2.20E-03	1.20E-01
	GOTERM_MF_FAT	threonine-type endopeptidase activity	9	2.20E-03	1.20E-01
	GOTERM_CC_FAT	proteasome core complex	9	2.80E-03	4.80E-02
	GOTERM_BP_FAT	mitotic cell cycle	67	6.00E-03	1.40E-01
	KEGG_PATHWAY	Proteasome	15	7.20E-03	1.50E-01
	PIR_SUPERFAMILY	PIRSF001212:multicatalytic endopeptidase complex chain C9	4	2.00E-02	9.90E-01
	UP_SEQ_FEATURE	site:Cleavage; by autocatalysis	3	4.00E-02	9.90E-01
	INTERPRO	Peptidase T1A, proteasome beta-subunit	4	4.70E-02	9.20E-01
	GOTERM_BP_FAT	ubiquitin-dependent protein catabolic process	42	5.30E-02	5.10E-01
	PIR_SUPERFAMILY	PIRSF001214:multicatalytic endopeptidase complex chain C5	3	9.10E-02	1.00E+00
Annotation Cluster 8	**Enrichment Score: 4.36**		**Count**	**P_Value**	**Benjamini**
	SP_PIR_KEYWORDS	sh3 domain	50	3.40E-06	1.00E-04
	UP_SEQ_FEATURE	domain:SH3	41	6.30E-05	6.50E-02
	INTERPRO	Src homology-3 domain	48	8.00E-05	4.90E-02
	SMART	SH3	48	2.10E-04	4.30E-02
Annotation Cluster 9	**Enrichment Score: 4.32**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	regulation of protein kinase cascade	64	1.60E-07	9.30E-05
	GOTERM_BP_FAT	positive regulation of I-kappaB kinase/NF-kappaB cascade	29	3.50E-05	2.90E-03
	GOTERM_BP_FAT	positive regulation of protein kinase cascade	42	4.70E-05	3.50E-03
	GOTERM_BP_FAT	regulation of I-kappaB kinase/NF-kappaB cascade	30	9.20E-05	6.10E-03
	GOTERM_BP_FAT	positive regulation of cell communication	66	4.70E-04	2.40E-02
	GOTERM_BP_FAT	positive regulation of signal transduction	59	1.00E-03	4.30E-02
Annotation Cluster 10	**Enrichment Score: 4.32**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	vesicle-mediated transport	125	1.10E-08	1.20E-05
	GOTERM_BP_FAT	membrane organization	78	6.90E-05	4.90E-03
	GOTERM_BP_FAT	endocytosis	50	1.30E-04	8.50E-03
	GOTERM_BP_FAT	membrane invagination	50	1.30E-04	8.50E-03
	SP_PIR_KEYWORDS	Endocytosis	20	1.90E-02	1.60E-01
Annotation Cluster 11	**Enrichment Score: 4.23**		**Count**	**P_Value**	**Benjamini**
	GOTERM_MF_FAT	transcription factor binding	111	2.40E-08	7.80E-06
	GOTERM_MF_FAT	transcription activator activity	78	3.40E-04	3.70E-02
	GOTERM_MF_FAT	transcription cofactor activity	70	4.80E-04	4.40E-02
	GOTERM_MF_FAT	transcription coactivator activity	43	3.10E-03	1.40E-01
Annotation Cluster 12	**Enrichment Score: 4.18**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	positive regulation of cell death	91	6.60E-06	7.90E-04
	GOTERM_BP_FAT	positive regulation of apoptosis	90	7.30E-06	8.40E-04
	GOTERM_BP_FAT	regulation of apoptosis	149	9.80E-06	1.00E-03
	GOTERM_BP_FAT	positive regulation of programmed cell death	90	9.80E-06	1.00E-03
	GOTERM_BP_FAT	regulation of cell death	150	1.30E-05	1.30E-03
	GOTERM_BP_FAT	regulation of programmed cell death	149	1.70E-05	1.50E-03
	GOTERM_BP_FAT	induction of apoptosis	69	3.60E-05	2.90E-03
	GOTERM_BP_FAT	induction of programmed cell death	69	4.00E-05	3.10E-03
	GOTERM_BP_FAT	induction of apoptosis by extracellular signals	31	8.80E-05	6.00E-03
	GOTERM_BP_FAT	negative regulation of apoptosis	71	2.80E-04	1.60E-02
	GOTERM_BP_FAT	negative regulation of programmed cell death	71	4.30E-04	2.30E-02
	GOTERM_BP_FAT	negative regulation of cell death	71	4.70E-04	2.40E-02
	GOTERM_BP_FAT	anti-apoptosis	36	6.80E-02	5.80E-01
Annotation Cluster 13	**Enrichment Score: 4.17**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	protein localization	167	6.60E-07	2.50E-04
	GOTERM_BP_FAT	intracellular transport	131	8.00E-07	2.40E-04
	SP_PIR_KEYWORDS	protein transport	95	1.80E-06	5.90E-05
	GOTERM_BP_FAT	protein transport	145	3.00E-06	4.20E-04
	GOTERM_BP_FAT	establishment of protein localization	146	3.10E-06	4.20E-04
	GOTERM_BP_FAT	intracellular protein transport	71	1.40E-03	4.90E-02
	GOTERM_BP_FAT	cellular protein localization	75	3.00E-03	8.40E-02
	GOTERM_BP_FAT	cellular macromolecule localization	75	3.60E-03	9.70E-02
	SP_PIR_KEYWORDS	transport	212	2.30E-01	6.70E-01
Annotation Cluster 14	**Enrichment Score: 4.13**		**Count**	**P_Value**	**Benjamini**
	SP_PIR_KEYWORDS	endoplasmic reticulum	133	2.30E-07	9.60E-06
	GOTERM_CC_FAT	endoplasmic reticulum	168	1.30E-04	3.80E-03
	GOTERM_CC_FAT	endoplasmic reticulum part	62	1.40E-02	1.60E-01
Annotation Cluster 15	**Enrichment Score: 4.12**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	programmed cell death	117	2.30E-05	2.00E-03
	GOTERM_BP_FAT	apoptosis	115	3.00E-05	2.60E-03
	GOTERM_BP_FAT	cell death	132	5.30E-05	3.80E-03
	GOTERM_BP_FAT	death	132	7.30E-05	5.10E-03
	SP_PIR_KEYWORDS	Apoptosis	68	9.10E-04	1.50E-02
Annotation Cluster 16	**Enrichment Score: 4.12**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	short sequence motif:Prevents secretion from ER	21	1.10E-05	1.40E-02
	INTERPRO	Endoplasmic reticulum, targeting sequence	17	6.80E-05	5.60E-02
	GOTERM_CC_FAT	endoplasmic reticulum lumen	23	5.90E-04	1.40E-02
Annotation Cluster 17	**Enrichment Score: 4.11**		**Count**	**P_Value**	**Benjamini**
	SP_PIR_KEYWORDS	rna-binding	118	1.20E-10	7.30E-09
	INTERPRO	Nucleotide-binding, alpha-beta plait	52	3.70E-06	9.30E-03
	INTERPRO	RNA recognition motif, RNP-1	51	6.20E-06	7.90E-03
	SMART	RRM	51	1.90E-05	7.80E-03
	UP_SEQ_FEATURE	domain:RRM	28	8.60E-04	3.40E-01
	UP_SEQ_FEATURE	domain:RRM 2	22	8.80E-03	9.00E-01
	UP_SEQ_FEATURE	domain:RRM 1	22	8.80E-03	9.00E-01
	UP_SEQ_FEATURE	domain:RRM 3	8	4.00E-01	1.00E+00
Annotation Cluster 18	**Enrichment Score: 4.07**		**Count**	**P_Value**	**Benjamini**
	SP_PIR_KEYWORDS	lysosome	42	2.30E-07	1.00E-05
	GOTERM_CC_FAT	lysosome	50	5.90E-05	1.90E-03
	GOTERM_CC_FAT	lytic vacuole	50	5.90E-05	1.90E-03
	GOTERM_CC_FAT	vacuole	53	7.90E-04	1.70E-02
	KEGG_PATHWAY	Lysosome	29	6.70E-03	1.50E-01
Annotation Cluster 19	**Enrichment Score: 4.03**		**Count**	**P_Value**	**Benjamini**
	SP_PIR_KEYWORDS	actin-binding	55	8.70E-06	2.50E-04
	GOTERM_BP_FAT	actin cytoskeleton organization	54	1.60E-05	1.50E-03
	GOTERM_CC_FAT	actin cytoskeleton	61	3.30E-05	1.20E-03
	GOTERM_BP_FAT	actin filament-based process	55	5.10E-05	3.70E-03
	GOTERM_MF_FAT	actin binding	68	5.40E-05	1.20E-02
	GOTERM_MF_FAT	cytoskeletal protein binding	93	2.70E-04	3.10E-02
	GOTERM_BP_FAT	cytoskeleton organization	74	1.80E-02	2.80E-01

ILMN_2415267	RREB1	-0.403322364
ILMN_3301599	ZNF285A	-0.403344101
ILMN_2266595	LILRA5	-0.403391731
ILMN_1653310	ZNF580	-0.403431767
ILMN_1698148	CHD5	-0.403504114
ILMN_3242443	SNORD91B	-0.403676051
ILMN_1665970	KIAA0786	-0.403690352
ILMN_3247170	SNORD32B	-0.403796598
ILMN_3309724	MIR509-2	-0.403853321
ILMN_1666121	FKBP9	-0.40387984
ILMN_1753249	DDX10	-0.403932092
ILMN_1715416	NUP188	-0.403964757
ILMN_1690866	KBTBD10	-0.403969664
ILMN_1688971	NOL11	-0.4039802
ILMN_3239861	C10orf140	-0.404014265
ILMN_1654474	LOC647946	-0.404030321
ILMN_3187429	LOC100130071	-0.404042737
ILMN_3267319	NA	-0.404072718
ILMN_3308768	MIR302B	-0.404077099
ILMN_1694007	ADRB3	-0.404129686
ILMN_1786303	LILRA3	-0.404172836
ILMN_1872266	BM690100	-0.404185474
ILMN_1834317	AW294430	-0.404193601
ILMN_3249608	ANKLE2	-0.404204387
ILMN_1688242	C6	-0.40424357
ILMN_2328378	OSBPL3	-0.404285779
ILMN_1793894	ANAPC13	-0.404287303
ILMN_1779051	CYP2A7	-0.404336237
ILMN_1776283	LGALS12	-0.404347986
ILMN_1808907	HIST1H2BN	-0.404363208
ILMN_3235171	CCDC64B	-0.404377561
ILMN_1695687	SALL4	-0.404436407
ILMN_1796627	PKIG	-0.40463093
ILMN_1766830	RELT	-0.404642882
ILMN_1769912	OR4K14	-0.404665497
ILMN_1784367	HSPD1	-0.404668926
ILMN_1699767	PDE8A	-0.404714577
ILMN_1674587	TBC1D3C	-0.404749011
ILMN_1762531	FGF9	-0.404889035
ILMN_1900657	BM678241	-0.404905405
ILMN_3236330	DQ581928	-0.40500449
ILMN_1674719	NID1	-0.405014639
ILMN_2150187	KCTD18	-0.405032765
ILMN_1808674	CPN1	-0.405036699
ILMN_1786936	BM919382	-0.405215564
ILMN_3308861	MIR525	-0.405220568
ILMN_1728496	SYT9	-0.405235374
ILMN_2336647	NNT	-0.405246086
ILMN_1712754	NFKBIB	-0.405253738
ILMN_1797794	AK126307	-0.405264157
ILMN_1706558	TRMT61B	-0.405281547
ILMN_1657295	CPA6	-0.405305236
ILMN_1705637	ACR	-0.405319831
ILMN_1715607	CHMP4A	-0.405424093
ILMN_1674341	POTEC	-0.405475228
ILMN_1749821	MED28	-0.405529566
ILMN_3245250	CTSL1P8	-0.405576831
ILMN_1722533	KATNAL1	-0.405617181
ILMN_1728798	TEKT4P2	-0.405717756
ILMN_1693107	MLH3	-0.405770143
ILMN_1715703	DALRD3	-0.405800747
ILMN_1889942	AW450078	-0.405810082
ILMN_1658232	KDM2B	-0.405816326
ILMN_3269310	AK127969	-0.405818196
ILMN_1777024	PCDHA@	-0.40588058
ILMN_1743537	U60319	-0.405904161
ILMN_1655715	BI769462	-0.405921308
ILMN_1719471	MSH3	-0.405956289
ILMN_1812070	ABCB1	-0.406024563
ILMN_1800796	LOC100506548	-0.406049239
ILMN_1847363	LOC100288144	-0.406091118
ILMN_2120022	ARL5B	-0.406097912
ILMN_1895120	ADORA1	-0.406169421
ILMN_1685636	KCNN2	-0.406214143
ILMN_1862900	BQ447249	-0.406223415
ILMN_2216637	STK32B	-0.406277959
ILMN_3244516	C12orf51	-0.406280973
ILMN_1706901	HOXD13	-0.406310479
ILMN_1841334	CREB1	-0.406316435
ILMN_1757845	SPIRE1	-0.406331527
ILMN_1849117	AL109791	-0.406452302
ILMN_1881780	BE042871	-0.406473248
ILMN_1703229	HIATL1	-0.406506573
ILMN_1667715	NA	-0.40655125
ILMN_1741843	RD3	-0.406604417
ILMN_1670158	FAM83A	-0.40660538
ILMN_3291203	AB593110	-0.406677058
ILMN_1763670	TM2D1	-0.406693236
ILMN_1689515	CPLX3	-0.406756066
ILMN_1708363	LOXL1	-0.406841347
ILMN_1803408	KRT18	-0.406937003
ILMN_2182980	ALDH1L2	-0.406947349
ILMN_2285091	ZNF3	-0.406950351
ILMN_1768958	RASGRP1	-0.406950458
ILMN_1743357	XPNPEP2	-0.406969184
ILMN_1696590	CHST4	-0.406973918

	GOTERM_MF_FAT	purine nucleotide binding	231	2.60E-02	8.30E-01
	GOTERM_MF_FAT	purine ribonucleotide binding	219	4.50E-02	8.40E-01
	GOTERM_MF_FAT	ribonucleotide binding	219	4.50E-02	8.40E-01
	GOTERM_MF_FAT	purine nucleoside binding	192	4.80E-02	8.50E-01
	GOTERM_MF_FAT	adenyl nucleotide binding	189	5.20E-02	8.60E-01
	GOTERM_MF_FAT	nucleoside binding	192	6.10E-02	8.80E-01
	GOTERM_MF_FAT	adenyl ribonucleotide binding	177	8.40E-02	9.20E-01
	GOTERM_MF_FAT	ATP binding	175	8.50E-02	9.20E-01
	INTERPRO	Protein kinase, core	61	8.90E-02	1.00E+00
	SP_PIR_KEYWORDS	kinase	83	1.10E-01	8.50E-01
	UP_SEQ_FEATURE	binding site:ATP	63	2.60E-01	1.00E+00
	UP_SEQ_FEATURE	nucleotide phosphate-binding region:ATP	108	2.80E-01	1.00E+00
Annotation Cluster 11	**Enrichment Score: 1.28**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	negative regulation of phosphate metabolic process	11	2.70E-02	9.60E-01
	GOTERM_BP_FAT	negative regulation of phosphorus metabolic process	11	2.70E-02	9.60E-01
	GOTERM_BP_FAT	negative regulation of phosphorylation	10	4.40E-02	9.80E-01
	GOTERM_BP_FAT	negative regulation of protein amino acid phosphorylation	6	2.50E-01	9.90E-01
Annotation Cluster 12	**Enrichment Score: 1.2**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	branched chain family amino acid metabolic process	6	2.10E-02	9.50E-01
	GOTERM_BP_FAT	branched chain family amino acid catabolic process	4	1.00E-01	9.80E-01
	KEGG_PATHWAY	Valine, leucine and isoleucine degradation	9	1.10E-01	9.40E-01
Annotation Cluster 13	**Enrichment Score: 1.19**		**Count**	**P_Value**	**Benjamini**
	GOTERM_CC_FAT	autophagic vacuole	6	1.70E-02	9.20E-01
	PIR_SUPERFAMILY	PIRSF005455:microtubule-associated proteins 1 light chain 3A/3B	3	9.30E-02	1.00E+00
	INTERPRO	Light chain 3 (LC3)	3	1.60E-01	1.00E+00
Annotation Cluster 14	**Enrichment Score: 1.19**		**Count**	**P_Value**	**Benjamini**
	INTERPRO	Glutathione S-transferase, alpha class	5	5.80E-04	2.70E-01
	GOTERM_MF_FAT	transferase activity, transferring alkyl or aryl (other than methyl) groups	12	1.30E-02	6.40E-01
	INTERPRO	Glutathione S-transferase, C-terminal	7	1.90E-02	9.80E-01
	PIR_SUPERFAMILY	PIRSF000503:glutathione transferase	5	4.30E-02	1.00E+00
	GOTERM_MF_FAT	glutathione transferase activity	6	5.50E-02	8.70E-01
	UP_SEQ_FEATURE	domain:GST N-terminal	6	6.20E-02	1.00E+00
	INTERPRO	Glutathione S-transferase, N-terminal	6	7.60E-02	1.00E+00
	INTERPRO	Glutathione S-transferase, C-terminal-like	7	8.00E-02	1.00E+00
	INTERPRO	Glutathione S-transferase/chloride channel, C-terminal	7	9.10E-02	1.00E+00
	UP_SEQ_FEATURE	domain:GST C-terminal	7	1.30E-01	1.00E+00
	KEGG_PATHWAY	Glutathione metabolism	9	1.90E-01	9.40E-01
	KEGG_PATHWAY	Metabolism of xenobiotics by cytochrome P450	9	3.50E-01	9.50E-01
	KEGG_PATHWAY	Drug metabolism	9	3.90E-01	9.60E-01
	INTERPRO	Thioredoxin fold	12	5.10E-01	1.00E+00
Annotation Cluster 15	**Enrichment Score: 1.19**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	carboxylic acid biosynthetic process	24	6.10E-02	9.80E-01
	GOTERM_BP_FAT	organic acid biosynthetic process	24	6.10E-02	9.80E-01
	GOTERM_BP_FAT	fatty acid biosynthetic process	14	7.10E-02	9.80E-01
Annotation Cluster 16	**Enrichment Score: 1.17**		**Count**	**P_Value**	**Benjamini**
	SP_PIR_KEYWORDS	tyrosine-protein kinase	22	5.20E-03	2.40E-01
	INTERPRO	Tyrosine protein kinase, active site	18	2.60E-02	9.90E-01
	GOTERM_MF_FAT	protein tyrosine kinase activity	27	3.00E-02	8.40E-01
	SMART	TyrKc	19	4.20E-02	9.80E-01
	GOTERM_MF_FAT	non-membrane spanning protein tyrosine kinase activity	9	6.60E-02	8.80E-01
	INTERPRO	Tyrosine protein kinase	19	7.20E-02	1.00E+00
	INTERPRO	Protein kinase, core	61	8.90E-02	1.00E+00
	SP_PIR_KEYWORDS	tyrosine-specific protein kinase	9	1.20E-01	8.40E-01
	INTERPRO	Protein kinase, ATP binding site	56	1.70E-01	1.00E+00
	UP_SEQ_FEATURE	domain:Protein kinase	57	1.70E-01	1.00E+00
	GOTERM_MF_FAT	transmembrane receptor protein tyrosine kinase activity	8	5.80E-01	1.00E+00
Annotation Cluster 17	**Enrichment Score: 1.16**		**Count**	**P_Value**	**Benjamini**
	GOTERM_MF_FAT	lipoic acid binding	4	3.10E-02	8.20E-01
	SP_PIR_KEYWORDS	lipoyl	3	8.80E-02	8.60E-01
	INTERPRO	2-oxo acid dehydrogenase, lipoyl-binding site	3	1.30E-01	1.00E+00
Annotation Cluster 18	**Enrichment Score: 1.14**		**Count**	**P_Value**	**Benjamini**
	GOTERM_CC_FAT	organelle envelope	83	2.60E-02	8.90E-01
	GOTERM_CC_FAT	mitochondrial part	80	2.70E-02	8.70E-01
	GOTERM_CC_FAT	envelope	83	2.80E-02	8.50E-01
	GOTERM_CC_FAT	organelle inner membrane	46	5.30E-02	9.00E-01
	GOTERM_CC_FAT	organelle membrane	134	6.70E-02	9.00E-01
	GOTERM_CC_FAT	mitochondrial envelope	55	9.00E-02	9.20E-01
	GOTERM_CC_FAT	nuclear envelope	29	1.10E-01	9.20E-01
	GOTERM_CC_FAT	mitochondrial membrane	50	1.50E-01	9.30E-01
	GOTERM_CC_FAT	mitochondrial inner membrane	39	1.90E-01	9.40E-01
	SP_PIR_KEYWORDS	mitochondrion inner membrane	25	2.10E-01	9.00E-01
Annotation Cluster 19	**Enrichment Score: 1.13**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	embryonic morphogenesis	44	3.50E-02	9.70E-01
	GOTERM_BP_FAT	embryonic hindlimb morphogenesis	6	3.50E-02	9.70E-01
	GOTERM_BP_FAT	embryonic appendage morphogenesis	16	3.90E-02	9.70E-01
	GOTERM_BP_FAT	embryonic limb morphogenesis	16	3.90E-02	9.70E-01
	GOTERM_BP_FAT	limb morphogenesis	16	9.90E-02	9.80E-01
	GOTERM_BP_FAT	appendage morphogenesis	16	9.90E-02	9.80E-01
	GOTERM_BP_FAT	embryonic digit morphogenesis	6	1.20E-01	9.80E-01
	GOTERM_BP_FAT	limb development	16	1.30E-01	9.80E-01
	GOTERM_BP_FAT	appendage development	16	1.30E-01	9.80E-01
	GOTERM_BP_FAT	hindlimb morphogenesis	6	1.30E-01	9.80E-01
Annotation Cluster 20	**Enrichment Score: 1.11**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	ion homeostasis	58	1.90E-02	9.40E-01
	GOTERM_BP_FAT	chemical homeostasis	68	4.00E-02	9.70E-01
	GOTERM_BP_FAT	cation homeostasis	41	4.10E-02	9.70E-01
	GOTERM_BP_FAT	di-, tri-valent inorganic cation homeostasis	35	4.60E-02	9.80E-01
	GOTERM_BP_FAT	cellular ion homeostasis	51	5.00E-02	9.80E-01
	GOTERM_BP_FAT	cellular chemical homeostasis	51	6.30E-02	9.80E-01
	GOTERM_BP_FAT	cellular di-, tri-valent inorganic cation homeostasis	32	8.40E-02	9.80E-01
	GOTERM_BP_FAT	calcium ion homeostasis	27	9.50E-02	9.80E-01
	GOTERM_BP_FAT	cellular homeostasis	59	1.10E-01	9.70E-01
	GOTERM_BP_FAT	cellular cation homeostasis	34	1.30E-01	9.80E-01
	GOTERM_BP_FAT	metal ion homeostasis	28	1.40E-01	9.80E-01
	GOTERM_BP_FAT	homeostatic process	90	1.40E-01	9.80E-01
	GOTERM_BP_FAT	cellular calcium ion homeostasis	25	1.60E-01	9.80E-01

ILMN_2350266	FBXO46	0.809012563
ILMN_1662799	GPSM3	0.808974076
ILMN_1673357	SLA2	0.808936701
ILMN_1735180	NCSTN	0.808844231
ILMN_1814789	UBAP2L	0.808685874
ILMN_1759700	NLGN3	0.808282349
ILMN_3236904	LOC648740	0.807906427
ILMN_2109994	MIA-RAB4B	0.807572263
ILMN_1801043	GSN	0.807523537
ILMN_2397024	SPOP	0.807300201
ILMN_1715760	HUAT	0.807291519
ILMN_2103362	ARHGAP27	0.806776335
ILMN_3238633	SDHAF2	0.806667048
ILMN_1705750	TGM2	0.806331049
ILMN_2333107	AES	0.806240321
ILMN_1741148	ALDOA	0.806239454
ILMN_2376204	LTB	0.805355045
ILMN_3275345	RPS27	0.805077537
ILMN_2408039	EEF1D	0.804486489
ILMN_2375992	SPINT1	0.804384209
ILMN_1666361	SLC23A2	0.804202607
ILMN_1770454	AGRN	0.803888579
ILMN_1699598	AP2M1	0.803789511
ILMN_1709549	PLEKHM1	0.803771165
ILMN_2125747	CORO1A	0.803651999
ILMN_2111932	SERINC2	0.803473224
ILMN_1773885	DMAP1	0.803425398
ILMN_1792528	RPS25	0.803400366
ILMN_2103841	AIP	0.803367166
ILMN_2396444	CD14	0.803001296
ILMN_2116366	RPL12	0.802712608
ILMN_1724581	EDC3	0.802294496
ILMN_3246360	RPS18	0.801990001
ILMN_2372974	SIRPA	0.801909314
ILMN_2272074	TROVE2	0.801859722
ILMN_2388507	AKT1	0.80165812
ILMN_2403555	DHX30	0.801562828
ILMN_3200830	CCT6P3	0.801458582
ILMN_2402798	AP2M1	0.801281577
ILMN_3225761	RPS14	0.800977472
ILMN_1715926	RPL32	0.800936561
ILMN_1732725	PPP6R3	0.800704411
ILMN_1791447	CXCL12	0.800532308
ILMN_1803988	MCL1	0.800442675
ILMN_1671291	EIF3I	0.800439881
ILMN_1777342	PREX1	0.800420607
ILMN_1768595	DLG4	0.80029691
ILMN_1809484	TMOD3	0.800285794
ILMN_2053178	ACTG1	0.799847542
ILMN_1768505	IL13RA1	0.799728713
ILMN_1744347	DQ895289	0.799551618
ILMN_1666385	CALM3	0.799447958
ILMN_1695404	LY6E	0.799441874
ILMN_3281563	RPL12	0.799004073
ILMN_1769702	GPAA1	0.798983762
ILMN_1701655	SLC24A6	0.798848798
ILMN_2411963	RBM39	0.79857177
ILMN_1669727	WAC	0.797953256
ILMN_2218277	RPS2	0.797791526
ILMN_1719303	P4HB	0.797743734
ILMN_1662166	PTK7	0.797561568
ILMN_2247594	RPLP1	0.797244996
ILMN_1761969	DERL2	0.797224682
ILMN_2386530	RPLP1	0.796900533
ILMN_1781276	TMCO4	0.796834571
ILMN_1724994	COL4A2	0.796800999
ILMN_2080342	LGALS9C	0.796661258
ILMN_1754195	RPL31	0.796429946
ILMN_3204210	RPL10	0.796319812
ILMN_3176090	RCC2	0.796147666
ILMN_2353202	PTK7	0.796076585
ILMN_1713086	RPL27A	0.795807754
ILMN_2160819	RPS27	0.795556984
ILMN_2398847	ARHGAP17	0.795019615
ILMN_1811921	CSRP1	0.794999755
ILMN_1707336	ARPC4	0.794946569
ILMN_3198090	FAM201B	0.794946164
ILMN_1783771	UBE2Z	0.794821422
ILMN_2412214	HUAT	0.794776221
ILMN_1732885	SLX4	0.794412295
ILMN_1696839	RPS27	0.794200605
ILMN_1670305	SERPING1	0.794188549
ILMN_1802106	APOBEC3G	0.794033059
ILMN_3266186	HDAC7	0.79362989
ILMN_3290380	XRCC6	0.793356046
ILMN_1717334	VAV1	0.793019919
ILMN_1772177	ASCC3	0.793011011
ILMN_1770742	TMEM55B	0.792839673
ILMN_1746516	RPS25	0.792595871
ILMN_2061043	CD48	0.792338043
ILMN_1656868	NPIPL3	0.792295858
ILMN_1789338	SORBS3	0.792119514
ILMN_1705464	MRPL41	0.792005986
ILMN_1654289	ELK1	0.791938088

Annotation Cluster 20	**Enrichment Score: 3.67**		**Count**	**P_Value**	**Benjamini**
	GOTERM_CC_FAT	Golgi apparatus part	65	4.10E-05	1.40E-03
	SP_PIR_KEYWORDS	golgi apparatus	102	1.40E-04	2.90E-03
	GOTERM_CC_FAT	Golgi apparatus	147	1.80E-03	3.40E-02
Annotation Cluster 21	**Enrichment Score: 3.17**		**Count**	**P_Value**	**Benjamini**
	SP_PIR_KEYWORDS	chromatin regulator	48	2.50E-05	6.30E-04
	GOTERM_BP_FAT	chromatin organization	75	2.70E-04	1.50E-02
	GOTERM_BP_FAT	chromosome organization	90	6.40E-04	2.90E-02
	GOTERM_BP_FAT	chromatin modification	55	1.40E-03	5.00E-02
	GOTERM_BP_FAT	covalent chromatin modification	26	2.30E-02	3.20E-01
Annotation Cluster 22	**Enrichment Score: 3.02**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	regulation of cellular response to stress	33	1.80E-06	3.00E-04
	GOTERM_BP_FAT	regulation of stress-activated protein kinase signaling pathway	23	4.60E-05	3.50E-03
	GOTERM_BP_FAT	regulation of MAPKKK cascade	30	1.30E-04	8.40E-03
	GOTERM_BP_FAT	regulation of JNK cascade	21	1.70E-04	1.10E-02
	GOTERM_BP_FAT	activation of JUN kinase activity	12	2.30E-04	1.40E-02
	GOTERM_BP_FAT	stress-activated protein kinase signaling pathway	20	3.30E-04	1.90E-02
	GOTERM_BP_FAT	JNK cascade	19	4.10E-04	2.10E-02
	GOTERM_BP_FAT	positive regulation of kinase activity	49	8.10E-04	3.50E-02
	GOTERM_BP_FAT	MAPKKK cascade	41	8.60E-04	3.60E-02
	GOTERM_BP_FAT	positive regulation of transferase activity	50	1.10E-03	4.30E-02
	GOTERM_BP_FAT	positive regulation of JUN kinase activity	12	1.80E-03	5.90E-02
	GOTERM_BP_FAT	regulation of JUN kinase activity	13	2.00E-03	6.30E-02
	GOTERM_BP_FAT	positive regulation of protein kinase activity	46	2.10E-03	6.40E-02
	GOTERM_BP_FAT	regulation of protein amino acid phosphorylation	36	6.00E-03	1.40E-01
	GOTERM_BP_FAT	activation of MAPK activity	20	9.20E-03	1.90E-01
	GOTERM_BP_FAT	positive regulation of MAP kinase activity	23	1.30E-02	2.30E-01
	GOTERM_BP_FAT	regulation of MAP kinase activity	29	1.70E-02	2.70E-01
	GOTERM_BP_FAT	activation of protein kinase activity	21	1.10E-01	7.10E-01
Annotation Cluster 23	**Enrichment Score: 2.96**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	domain:PH	49	2.20E-04	1.80E-01
	INTERPRO	Pleckstrin homology	55	6.90E-04	2.00E-01
	SMART	PH	55	1.80E-03	1.70E-01
	INTERPRO	Pleckstrin homology-type	55	5.30E-03	5.10E-01
Annotation Cluster 24	**Enrichment Score: 2.77**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	negative regulation of macromolecule metabolic process	151	1.20E-08	1.00E-05
	GOTERM_BP_FAT	negative regulation of RNA metabolic process	71	5.50E-04	2.70E-02
	GOTERM_BP_FAT	negative regulation of gene expression	93	6.30E-04	3.00E-02
	GOTERM_BP_FAT	negative regulation of transcription, DNA-dependent	68	1.50E-03	5.10E-02
	GOTERM_BP_FAT	regulation of transcription from RNA polymerase II promoter	121	4.80E-03	1.20E-01
	GOTERM_BP_FAT	negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	89	5.00E-03	1.20E-01
	GOTERM_BP_FAT	negative regulation of nitrogen compound metabolic process	90	5.10E-03	1.30E-01
	GOTERM_BP_FAT	negative regulation of transcription	80	7.30E-03	1.60E-01
	GOTERM_BP_FAT	negative regulation of macromolecule biosynthetic process	91	1.40E-02	2.50E-01
	GOTERM_BP_FAT	negative regulation of biosynthetic process	94	1.80E-02	2.80E-01
	GOTERM_BP_FAT	negative regulation of cellular biosynthetic process	92	2.00E-02	3.00E-01
	GOTERM_BP_FAT	negative regulation of transcription from RNA polymerase II promoter	48	2.10E-02	3.10E-01
Annotation Cluster 25	**Enrichment Score: 2.74**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	positive regulation of molecular function	113	2.40E-05	2.00E-03
	GOTERM_BP_FAT	positive regulation of catalytic activity	98	2.10E-04	1.30E-02
	GOTERM_BP_FAT	protein kinase cascade	72	6.30E-04	3.00E-02
	GOTERM_BP_FAT	positive regulation of kinase activity	49	8.10E-04	3.50E-02
	GOTERM_BP_FAT	MAPKKK cascade	41	8.60E-04	3.60E-02
	GOTERM_BP_FAT	positive regulation of transferase activity	50	1.10E-03	4.30E-02
	GOTERM_BP_FAT	regulation of phosphate metabolic process	88	1.50E-03	5.10E-02
	GOTERM_BP_FAT	regulation of phosphorus metabolic process	88	1.50E-03	5.10E-02
	GOTERM_BP_FAT	regulation of phosphorylation	85	1.60E-03	5.30E-02
	GOTERM_BP_FAT	regulation of kinase activity	68	1.60E-03	5.40E-02
	GOTERM_BP_FAT	regulation of transferase activity	70	1.90E-03	6.00E-02
	GOTERM_BP_FAT	positive regulation of protein kinase activity	46	2.10E-03	6.40E-02
	GOTERM_BP_FAT	regulation of protein kinase activity	65	2.70E-03	7.70E-02
	GOTERM_BP_FAT	activation of MAPK activity	20	9.20E-03	1.90E-01
	GOTERM_BP_FAT	positive regulation of MAP kinase activity	23	1.30E-02	2.30E-01
	GOTERM_BP_FAT	regulation of MAP kinase activity	29	1.70E-02	2.70E-01
	GOTERM_BP_FAT	activation of protein kinase activity	21	1.10E-01	7.10E-01
Annotation Cluster 26	**Enrichment Score: 2.5**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	leukocyte differentiation	33	3.40E-04	1.80E-02
	GOTERM_BP_FAT	immune system development	57	5.80E-04	2.80E-02
	GOTERM_BP_FAT	leukocyte activation	51	7.30E-04	3.20E-02
	GOTERM_BP_FAT	cell activation	58	9.00E-04	3.70E-02
	GOTERM_BP_FAT	lymphocyte activation	43	1.20E-03	4.60E-02
	GOTERM_BP_FAT	hemopoietic or lymphoid organ development	53	1.30E-03	4.70E-02
	GOTERM_BP_FAT	hemopoiesis	49	1.30E-03	4.70E-02
	GOTERM_BP_FAT	T cell activation	30	1.70E-03	5.60E-02
	GOTERM_BP_FAT	lymphocyte differentiation	24	7.10E-03	1.60E-01
	GOTERM_BP_FAT	T cell selection	8	8.10E-03	1.70E-01
	GOTERM_BP_FAT	B cell activation	17	3.70E-02	4.20E-01
	GOTERM_BP_FAT	T cell differentiation	15	4.20E-02	4.50E-01
	GOTERM_BP_FAT	B cell differentiation	11	9.30E-02	6.60E-01
Annotation Cluster 27	**Enrichment Score: 2.46**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	regulation of translation	32	1.60E-03	5.30E-02
	GOTERM_BP_FAT	posttranscriptional regulation of gene expression	44	2.20E-03	6.50E-02
	SP_PIR_KEYWORDS	translation regulation	16	1.20E-02	1.10E-01
Annotation Cluster 28	**Enrichment Score: 2.41**		**Count**	**P_Value**	**Benjamini**
	SP_PIR_KEYWORDS	P-loop	27	1.20E-03	1.80E-02
	SP_PIR_KEYWORDS	nucleotide binding	25	1.80E-03	2.50E-02
	SP_PIR_KEYWORDS	GTP binding	15	2.70E-02	2.00E-01
Annotation Cluster 29	**Enrichment Score: 2.23**		**Count**	**P_Value**	**Benjamini**
	SP_PIR_KEYWORDS	diamond-blackfan anemia	7	1.90E-05	5.10E-04
	GOTERM_BP_FAT	ribonucleoprotein complex biogenesis	40	1.10E-03	4.30E-02
	GOTERM_BP_FAT	ribosomal small subunit biogenesis	7	1.30E-03	4.80E-02
	GOTERM_BP_FAT	ribosome biogenesis	29	2.10E-03	6.50E-02
	GOTERM_BP_FAT	ncRNA metabolic process	44	1.10E-02	2.10E-01
	GOTERM_BP_FAT	rRNA processing	21	1.60E-02	2.60E-01

ILMN_1732468	HSPA4L	-0.407005857
ILMN_1725833	IFLTD1	-0.407019599
ILMN_2388585	GOPC	-0.407049292
ILMN_3271312	NA	-0.407053001
ILMN_3181507	FLJ39609	-0.407059047
ILMN_1652963	C1orf194	-0.407111688
ILMN_3229447	NA	-0.407150295
ILMN_1760088	CCKBR	-0.407153725
ILMN_1678502	BC171856	-0.407198651
ILMN_1814333	SERPINI1	-0.40725014
ILMN_1711878	ENOPH1	-0.407324313
ILMN_1690984	FGF13	-0.407327647
ILMN_2269136	AGAP3	-0.407347742
ILMN_1805766	POU6F1	-0.407359125
ILMN_2389590	PRKAR1A	-0.407405283
ILMN_1785786	AK095242	-0.407418691
ILMN_1652959	ABCD2	-0.407424713
ILMN_1657959	AY227114	-0.407469618
ILMN_2179915	ARHGEF38	-0.407487438
ILMN_1725031	LHFPL1	-0.407496853
ILMN_1912334	HYDIN	-0.407511711
ILMN_1888195	BM975708	-0.407521396
ILMN_1844068	AA813722	-0.407569769
ILMN_1788349	TMEM202	-0.407577832
ILMN_2352609	OGG1	-0.407604957
ILMN_1861380	BX088900	-0.407622862
ILMN_2285952	PCDH11X	-0.407739278
ILMN_3257004	AK124173	-0.40776638
ILMN_2228180	MSRA	-0.407778609
ILMN_1808404	RHBDF1	-0.40778088
ILMN_3252969	LOC100128300	-0.407784387
ILMN_1895825	AA779998	-0.407822822
ILMN_1910511	AF086162	-0.407835417
ILMN_1815238	MAP2K3	-0.407841949
ILMN_1805826	BIVM	-0.407850446
ILMN_1676625	SS18L1	-0.407899207
ILMN_1653182	PMS2L13	-0.407937469
ILMN_1745282	RAGE	-0.407961706
ILMN_1789692	MARK2	-0.40798923
ILMN_1835451	BX097896	-0.408059017
ILMN_2358733	TAZ	-0.408073665
ILMN_3249677	DEFB105A	-0.408078649
ILMN_1803018	KIFC2	-0.408087412
ILMN_2367743	TUBG1	-0.408120759
ILMN_2234605	AGRN	-0.408132158
ILMN_1788400	KIAA2022	-0.408179235
ILMN_2283245	C9orf84	-0.408231909
ILMN_1665365	MATR3	-0.408239832
ILMN_1672582	XAGE1A	-0.408251276
ILMN_2072568	CLDN8	-0.408302394
ILMN_3305354	SP140L	-0.408316213
ILMN_2404516	PCDHGC3	-0.408330171
ILMN_1821915	BM683706	-0.408346941
ILMN_1668927	CXorf42	-0.408438586
ILMN_1656949	SLFN14	-0.408548805
ILMN_1730351	TEX19	-0.40857797
ILMN_3246388	MED14	-0.408578597
ILMN_1851451	CD515724	-0.408628143
ILMN_1710619	C17orf73	-0.408628168
ILMN_2085659	OTOGL	-0.408641693
ILMN_1759579	ZNF91	-0.408650877
ILMN_2047240	ARSA	-0.408707673
ILMN_1710204	TNFRSF4	-0.408721908
ILMN_1829919	NA	-0.408774729
ILMN_3185563	BRD7	-0.408785939
ILMN_1662738	ACSM3	-0.408798282
ILMN_2083137	LOC284379	-0.408802917
ILMN_1722127	RAD54B	-0.408840813
ILMN_1811479	SPINK6	-0.408902295
ILMN_1885165	AB072895	-0.408911619
ILMN_1807515	CSTF2T	-0.408968392
ILMN_1797893	N4BP2L2	-0.409023885
ILMN_1729645	BBC3	-0.409061858
ILMN_1714604	LOC283710	-0.409078951
ILMN_1681402	FLJ38379	-0.409124133
ILMN_2371147	BCL7C	-0.40913884
ILMN_3182885	LOC100130542	-0.409153135
ILMN_1777031	PKLR	-0.409188448
ILMN_1703470	TBX20	-0.409194416
ILMN_1700810	HSP90AA1	-0.409223405
ILMN_1730369	GOLGA6L1	-0.409241863
ILMN_1705201	FOXC2	-0.409330505
ILMN_2131467	GNAI1	-0.409332907
ILMN_2223561	CRHBP	-0.409357068
ILMN_1653927	SNORD83A	-0.409397019
ILMN_1669083	TXNRD2	-0.409400808
ILMN_2195665	PANK3	-0.409486077
ILMN_1707649	MPDZ	-0.409503458
ILMN_2359835	SFTPB	-0.409594714
ILMN_3310075	MIR1297	-0.409635001
ILMN_1808873	C9orf110	-0.409667062
ILMN_1802834	NCRNA00087	-0.409711806
ILMN_1768202	ANKRD24	-0.409739022
ILMN_3245360	FAM201B	-0.409760466

	GOTERM_BP_FAT	cellular metal ion homeostasis	26	1.90E-01	9.90E-01
Annotation Cluster 21	**Enrichment Score: 1.1**		**Count**	**P_Value**	**Benjamini**
	SMART	SH3	30	4.80E-02	9.70E-01
	SP_PIR_KEYWORDS	sh3 domain	30	7.40E-02	8.50E-01
	INTERPRO	Src homology-3 domain	30	9.50E-02	1.00E+00
	UP_SEQ_FEATURE	domain:SH3	25	1.20E-01	1.00E+00
Annotation Cluster 22	**Enrichment Score: 1.1**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	repeat:WD 7	25	2.40E-02	1.00E+00
	UP_SEQ_FEATURE	repeat:WD 6	29	4.70E-02	1.00E+00
	UP_SEQ_FEATURE	repeat:WD 5	34	4.70E-02	1.00E+00
	SMART	WD40	36	5.00E-02	9.50E-01
	UP_SEQ_FEATURE	repeat:WD 4	36	5.10E-02	1.00E+00
	INTERPRO	WD40 repeat, subgroup	34	7.80E-02	1.00E+00
	UP_SEQ_FEATURE	repeat:WD 3	36	9.30E-02	1.00E+00
	INTERPRO	WD40 repeat, region	33	9.50E-02	1.00E+00
	INTERPRO	WD40/YVTN repeat-like	40	1.00E-01	1.00E+00
	INTERPRO	WD40 repeat	36	1.10E-01	1.00E+00
	INTERPRO	WD40 repeat, conserved site	37	1.20E-01	1.00E+00
	INTERPRO	WD40 repeat 2	31	1.20E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:WD 1	36	1.30E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:WD 2	36	1.30E-01	1.00E+00
	SP_PIR_KEYWORDS	wd repeat	36	1.30E-01	8.50E-01
Annotation Cluster 23	**Enrichment Score: 1.08**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	sensory perception of sound	17	4.80E-02	9.80E-01
	GOTERM_BP_FAT	sensory perception of mechanical stimulus	17	7.60E-02	9.80E-01
	SP_PIR_KEYWORDS	deafness	15	1.60E-01	8.70E-01
Annotation Cluster 24	**Enrichment Score: 1.07**		**Count**	**P_Value**	**Benjamini**
	INTERPRO	Zinc finger, C3HC4 RING-type	35	2.60E-02	9.90E-01
	SMART	RING	40	4.00E-02	9.90E-01
	INTERPRO	Zinc finger, RING-type	40	9.00E-02	1.00E+00
	INTERPRO	Zinc finger, RING-type, conserved site	37	1.30E-01	1.00E+00
	UP_SEQ_FEATURE	zinc finger region:RING-type	25	3.60E-01	1.00E+00
Annotation Cluster 25	**Enrichment Score: 1.07**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	striated muscle cell differentiation	18	1.00E-02	8.30E-01
	GOTERM_BP_FAT	muscle cell differentiation	22	1.60E-02	9.10E-01
	GOTERM_BP_FAT	cardiac cell differentiation	8	2.40E-02	9.50E-01
	GOTERM_BP_FAT	cardiac muscle cell differentiation	7	2.90E-02	9.60E-01
	GOTERM_BP_FAT	striated muscle tissue development	20	4.50E-02	9.80E-01
	GOTERM_BP_FAT	muscle tissue development	20	6.80E-02	9.80E-01
	GOTERM_BP_FAT	muscle organ development	29	1.30E-01	9.80E-01
	GOTERM_BP_FAT	cardiac muscle tissue development	10	1.40E-01	9.80E-01
	GOTERM_BP_FAT	skeletal muscle organ development	11	1.60E-01	9.80E-01
	GOTERM_BP_FAT	skeletal muscle tissue development	11	1.60E-01	9.80E-01
	GOTERM_BP_FAT	ventricular cardiac muscle cell differentiation	3	2.90E-01	9.90E-01
	GOTERM_BP_FAT	muscle cell development	8	3.80E-01	1.00E+00
	GOTERM_BP_FAT	heart development	22	6.90E-01	1.00E+00
Annotation Cluster 26	**Enrichment Score: 1.06**		**Count**	**P_Value**	**Benjamini**
	GOTERM_MF_FAT	protein serine/threonine phosphatase activity	13	2.10E-03	2.20E-01
	GOTERM_CC_FAT	protein serine/threonine phosphatase complex	11	8.30E-03	8.10E-01
	INTERPRO	Protein phosphatase 2C, manganese/magnesium aspartate binding site	5	6.60E-02	1.00E+00
	INTERPRO	Protein phosphatase 2C	5	9.80E-02	1.00E+00
	INTERPRO	Protein phosphatase 2C, N-terminal	5	1.20E-01	1.00E+00
	SMART	PP2Cc	5	1.30E-01	9.70E-01
	SMART	PP2C_SIG	5	1.30E-01	9.70E-01
	UP_SEQ_FEATURE	metal ion-binding site:Manganese 1; via carbonyl oxygen	4	1.50E-01	1.00E+00
	INTERPRO	Protein phosphatase 2C-related	5	1.60E-01	1.00E+00
	UP_SEQ_FEATURE	metal ion-binding site:Manganese 1	5	3.10E-01	1.00E+00
	UP_SEQ_FEATURE	metal ion-binding site:Manganese 2	5	3.10E-01	1.00E+00
	UP_SEQ_FEATURE	domain:PP2C-like	3	4.00E-01	1.00E+00
Annotation Cluster 27	**Enrichment Score: 1.05**		**Count**	**P_Value**	**Benjamini**
	SP_PIR_KEYWORDS	iron-sulfur	10	3.60E-02	7.20E-01
	GOTERM_MF_FAT	iron-sulfur cluster binding	11	3.60E-02	8.40E-01
	GOTERM_MF_FAT	metal cluster binding	11	3.60E-02	8.40E-01
	UP_SEQ_FEATURE	metal ion-binding site:Iron-sulfur (4Fe-4S)	4	2.30E-01	1.00E+00
	GOTERM_MF_FAT	4 iron, 4 sulfur cluster binding	4	5.10E-01	1.00E+00
Annotation Cluster 28	**Enrichment Score: 1.04**		**Count**	**P_Value**	**Benjamini**
	GOTERM_CC_FAT	nuclear inner membrane	7	3.10E-02	8.50E-01
	GOTERM_CC_FAT	intrinsic to nuclear inner membrane	3	1.30E-01	9.30E-01
	GOTERM_CC_FAT	integral to nuclear inner membrane	3	1.30E-01	9.30E-01
	GOTERM_CC_FAT	nuclear membrane part	3	1.30E-01	9.30E-01
Annotation Cluster 29	**Enrichment Score: 1.03**		**Count**	**P_Value**	**Benjamini**
	SP_PIR_KEYWORDS	oxidoreductase	74	3.00E-02	6.70E-01
	GOTERM_BP_FAT	oxidation reduction	79	1.00E-01	9.80E-01
	GOTERM_MF_FAT	electron carrier activity	28	2.60E-01	9.90E-01
Annotation Cluster 30	**Enrichment Score: 1.01**		**Count**	**P_Value**	**Benjamini**
	SMART	BAR	5	5.40E-02	9.10E-01
	INTERPRO	BAR	5	6.60E-02	1.00E+00
	UP_SEQ_FEATURE	domain:BAR	4	2.60E-01	1.00E+00
Annotation Cluster 31	**Enrichment Score: 0.99**		**Count**	**P_Value**	**Benjamini**
	GOTERM_MF_FAT	calcium-activated potassium channel activity	5	6.80E-02	8.80E-01
	GOTERM_MF_FAT	ion gated channel activity	5	1.00E-01	9.30E-01
	GOTERM_MF_FAT	calcium activated cation channel activity	5	1.60E-01	9.70E-01
Annotation Cluster 32	**Enrichment Score: 0.99**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	domain:RWD	4	7.90E-02	1.00E+00
	SMART	RWD	4	1.10E-01	9.70E-01
	INTERPRO	RWD	4	1.30E-01	1.00E+00
Annotation Cluster 33	**Enrichment Score: 0.98**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	visual perception	31	7.40E-02	9.80E-01
	GOTERM_BP_FAT	sensory perception of light stimulus	31	7.40E-02	9.80E-01
	SP_PIR_KEYWORDS	vision	19	2.00E-01	8.90E-01
Annotation Cluster 34	**Enrichment Score: 0.98**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	phosphorus metabolic process	138	2.50E-04	2.60E-01
	GOTERM_BP_FAT	phosphate metabolic process	138	2.50E-04	2.60E-01
	INTERPRO	Protein kinase, core	61	8.90E-02	1.00E+00

ILMN_2112417	PGAM1	0.791899701
ILMN_2338785	RPS14	0.791880494
ILMN_1655935	ADCY7	0.791767264
ILMN_2064655	CXorf40A	0.791749416
ILMN_1768480	VGLL4	0.79171757
ILMN_2160005	NUMA1	0.791697747
ILMN_2389013	ADRM1	0.791673118
ILMN_1789599	C1orf151	0.791277954
ILMN_1688780	S100A4	0.791254338
ILMN_3215206	SMN1	0.79122124
ILMN_1843949	BX648950	0.79108187
ILMN_1749447	RPS9	0.791023843
ILMN_1758315	SLC9A9	0.790913175
ILMN_1736481	SECISBP2	0.790882054
ILMN_1664099	GLIS3	0.790834381
ILMN_1773964	H1FX	0.790453314
ILMN_1691165	CLSPN	0.790365162
ILMN_1764721	RPL8	0.790283302
ILMN_1767256	MBTPS1	0.790115347
ILMN_2106331	H3F3A	0.789967611
ILMN_1749372	GGT5	0.789946841
ILMN_2210581	B3GAT3	0.789941542
ILMN_1776464	PARP4	0.789653482
ILMN_2133360	RPS2	0.789516596
ILMN_1661917	RPL10	0.789486302
ILMN_1669424	YBX1	0.789406382
ILMN_1788108	TXNDC5	0.789346279
ILMN_1653469	RPL12	0.789199249
ILMN_2366634	PKM2	0.789174743
ILMN_1744604	CYBA	0.788946337
ILMN_2322972	ZFYVE27	0.788643489
ILMN_1779010	MAP3K3	0.788318762
ILMN_2316278	MAGED4B	0.788125674
ILMN_3224204	PSMG4	0.787986273
ILMN_1668748	MED15	0.787745868
ILMN_2388701	ST3GAL5	0.787653518
ILMN_1746257	DAZAP1	0.787453647
ILMN_2232177	ACTN1	0.787426614
ILMN_1712357	HNRNPK	0.78732257
ILMN_2393254	CAPNS1	0.787318113
ILMN_1781626	C1S	0.787303856
ILMN_2393144	ARL6IP4	0.787242066
ILMN_3199798	RPL10	0.78720251
ILMN_3252771	RPL18A	0.787101171
ILMN_1784717	RPS19	0.787086843
ILMN_1805448	EPB41L2	0.787047333
ILMN_1756146	WDR45	0.786862934
ILMN_1725366	SLC27A5	0.786836089
ILMN_1768470	EIF4G1	0.786670408
ILMN_1658160	FAM156B	0.786436154
ILMN_2166506	XRCC6	0.786393211
ILMN_3241970	POLR2J2	0.786362849
ILMN_1756204	RPS6KA4	0.78621872
ILMN_1802089	SYMPK	0.78581435
ILMN_1695261	RPL10	0.785808679
ILMN_1701854	GNG5	0.785772334
ILMN_1734205	RASSF1	0.785591359
ILMN_2124769	YBX1	0.785561291
ILMN_2141452	RPL18A	0.785517593
ILMN_3248247	LOC349114	0.785437791
ILMN_1770247	HOXA10-HOXA9	0.78541072
ILMN_2207363	RABAC1	0.785279134
ILMN_1779185	SPECC1L	0.785021591
ILMN_2337241	RPS15A	0.784956044
ILMN_2141444	RPL18A	0.784202608
ILMN_1804476	GMPPA	0.784199465
ILMN_1682938	ARF3	0.783963454
ILMN_2410909	AKT1	0.783637457
ILMN_1778401	HLA-B	0.783588956
ILMN_2402930	H3F3A	0.78355458
ILMN_3273641	ATF6B	0.783470309
ILMN_1782543	EEF1D	0.783369687
ILMN_3264073	RPS27	0.783236259
ILMN_3307887	PRR14L	0.783152904
ILMN_1806757	MYBBP1A	0.782903961
ILMN_1658472	APH1A	0.782749522
ILMN_1802456	DCTD	0.782597135
ILMN_1715804	PITPNA	0.782564606
ILMN_2275803	LRRC45	0.782401421
ILMN_1815682	C3orf37	0.782242486
ILMN_3217172	RPS2	0.782242413
ILMN_1691487	TRAF2	0.78212567
ILMN_1802627	PSMG3	0.782060602
ILMN_3220792	RPL13AP5	0.781908832
ILMN_1660498	RPS27	0.781890402
ILMN_1775734	SH2D3C	0.781885883
ILMN_1671494	USP5	0.781625672
ILMN_1742330	PLXNB1	0.781413669
ILMN_2402341	MAPK3	0.781178848
ILMN_1754303	RPL30	0.780884178
ILMN_1782621	RPS12	0.780762002
ILMN_1758895	CTSK	0.780723974
ILMN_1751753	IDH2	0.780715539
ILMN_1709044	TGIF2	0.780626798
ILMN_1786195	PRKACA	0.780591569

	GOTERM_BP_FAT	rRNA metabolic process	21	2.40E-02	3.30E-01
	GOTERM_BP_FAT	ncRNA processing	34	4.80E-02	4.90E-01
	SP_PIR_KEYWORDS	rrna processing	7	7.60E-01	9.80E-01
Annotation Cluster 30	**Enrichment Score: 2.2**		**Count**	**P_Value**	**Benjamini**
	SP_PIR_KEYWORDS	phosphotransferase	50	8.90E-07	3.30E-05
	GOTERM_MF_FAT	nucleotide binding	346	7.60E-05	1.20E-02
	SP_PIR_KEYWORDS	nucleotide-binding	253	1.10E-04	2.40E-03
	SP_PIR_KEYWORDS	atp-binding	203	1.90E-04	3.60E-03
	SP_PIR_KEYWORDS	kinase	114	3.30E-04	5.90E-03
	GOTERM_MF_FAT	purine ribonucleotide binding	279	1.10E-03	9.30E-02
	GOTERM_MF_FAT	ribonucleotide binding	279	1.10E-03	9.30E-02
	GOTERM_MF_FAT	ATP binding	229	1.20E-03	9.10E-02
	GOTERM_MF_FAT	adenyl ribonucleotide binding	230	1.90E-03	1.20E-01
	GOTERM_MF_FAT	purine nucleotide binding	286	2.80E-03	1.30E-01
	GOTERM_MF_FAT	adenyl nucleotide binding	237	4.80E-03	1.80E-01
	GOTERM_MF_FAT	purine nucleoside binding	240	5.20E-03	1.80E-01
	GOTERM_MF_FAT	nucleoside binding	241	5.90E-03	1.90E-01
	GOTERM_MF_FAT	protein kinase activity	100	6.40E-03	2.00E-01
	UP_SEQ_FEATURE	binding site:ATP	86	7.10E-03	8.50E-01
	GOTERM_BP_FAT	phosphorylation	130	7.70E-03	1.70E-01
	GOTERM_BP_FAT	protein amino acid phosphorylation	109	1.30E-02	2.20E-01
	UP_SEQ_FEATURE	domain:Protein kinase	74	1.40E-02	9.40E-01
	GOTERM_MF_FAT	protein serine/threonine kinase activity	72	1.50E-02	3.50E-01
	SP_PIR_KEYWORDS	serine/threonine-protein kinase	61	1.80E-02	1.50E-01
	UP_SEQ_FEATURE	nucleotide phosphate-binding region:ATP	138	2.10E-02	9.70E-01
	SP_PIR_KEYWORDS	transferase	191	3.40E-02	2.20E-01
	INTERPRO	Protein kinase, core	74	4.40E-02	9.20E-01
	GOTERM_BP_FAT	phosphate metabolic process	146	5.90E-02	5.40E-01
	GOTERM_BP_FAT	phosphorus metabolic process	146	5.90E-02	5.40E-01
	INTERPRO	Serine/threonine protein kinase, active site	55	8.00E-02	9.60E-01
	INTERPRO	Protein kinase, ATP binding site	68	9.90E-02	9.60E-01
	INTERPRO	Serine/threonine protein kinase-related	54	1.30E-01	9.80E-01
	INTERPRO	Serine/threonine protein kinase	40	1.40E-01	9.80E-01
	UP_SEQ_FEATURE	active site:Proton acceptor	89	1.70E-01	1.00E+00
	SMART	S_TKc	40	2.10E-01	9.00E-01
Annotation Cluster 31	**Enrichment Score: 2.15**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	DNA packaging	30	4.80E-04	2.40E-02
	SP_PIR_KEYWORDS	citrullination	10	6.00E-04	1.00E-02
	KEGG_PATHWAY	Systemic lupus erythematosus	28	1.10E-03	4.50E-02
	GOTERM_BP_FAT	chromatin assembly or disassembly	30	1.90E-03	6.00E-02
	GOTERM_BP_FAT	nucleosome assembly	22	2.50E-03	7.20E-02
	GOTERM_BP_FAT	chromatin assembly	22	3.90E-03	1.00E-01
	GOTERM_CC_FAT	chromatin	41	5.30E-03	7.70E-02
	INTERPRO	Histone H2A	8	6.40E-03	5.20E-01
	GOTERM_BP_FAT	protein-DNA complex assembly	22	6.70E-03	1.50E-01
	SP_PIR_KEYWORDS	chromosomal protein	29	7.60E-03	7.90E-02
	SMART	H2A	8	8.10E-03	4.30E-01
	INTERPRO	Histone core	13	8.30E-03	5.60E-01
	GOTERM_BP_FAT	nucleosome organization	22	8.70E-03	1.80E-01
	SP_PIR_KEYWORDS	nucleosome core	13	9.90E-03	9.60E-02
	GOTERM_CC_FAT	nucleosome	15	3.60E-02	2.80E-01
	PIR_SUPERFAMILY	PIRSF002048:histone H2A	6	4.20E-02	1.00E+00
	GOTERM_CC_FAT	protein-DNA complex	17	1.00E-01	5.00E-01
	INTERPRO	Histone-fold	10	2.40E-01	1.00E+00
Annotation Cluster 32	**Enrichment Score: 2.11**		**Count**	**P_Value**	**Benjamini**
	SP_PIR_KEYWORDS	GTPase activation	36	2.70E-04	5.00E-03
	UP_SEQ_FEATURE	domain:Rho-GAP	16	9.60E-03	9.10E-01
	INTERPRO	RhoGAP	16	1.80E-02	7.90E-01
	GOTERM_MF_FAT	GTPase activator activity	40	2.20E-02	4.10E-01
	SMART	RhoGAP	16	2.60E-02	5.90E-01
Annotation Cluster 33	**Enrichment Score: 2.1**		**Count**	**P_Value**	**Benjamini**
	GOTERM_CC_FAT	NuRD complex	8	6.10E-04	1.40E-02
	GOTERM_CC_FAT	chromatin remodeling complex	19	4.70E-03	7.10E-02
	GOTERM_CC_FAT	transcriptional repressor complex	12	1.60E-02	1.70E-01
	GOTERM_CC_FAT	histone deacetylase complex	10	8.80E-02	4.70E-01
Annotation Cluster 34	**Enrichment Score: 2.08**		**Count**	**P_Value**	**Benjamini**
	INTERPRO	Zinc finger, PHD-type	23	1.50E-03	2.60E-01
	INTERPRO	Zinc finger, PHD-finger	22	1.70E-03	2.60E-01
	SMART	PHD	23	2.60E-03	1.90E-01
	INTERPRO	Zinc finger, PHD-type, conserved site	21	1.10E-02	6.40E-01
	UP_SEQ_FEATURE	zinc finger region:PHD-type	12	4.40E-02	1.00E+00
	UP_SEQ_FEATURE	zinc finger region:PHD-type 1	8	9.60E-02	1.00E+00
Annotation Cluster 35	**Enrichment Score: 2.07**		**Count**	**P_Value**	**Benjamini**
	GOTERM_MF_FAT	translation factor activity, nucleic acid binding	25	1.20E-03	9.30E-02
	SP_PIR_KEYWORDS	Initiation factor	15	2.70E-03	3.50E-02
	GOTERM_BP_FAT	translational initiation	14	4.30E-03	1.10E-01
	GOTERM_MF_FAT	translation initiation factor activity	16	9.00E-03	2.50E-01
	GOTERM_CC_FAT	eukaryotic translation initiation factor 3 complex	6	4.00E-02	2.90E-01
	GOTERM_BP_FAT	regulation of translational initiation	10	8.30E-02	6.30E-01
Annotation Cluster 36	**Enrichment Score: 2.06**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	transcription, DNA-dependent	55	5.90E-03	1.40E-01
	GOTERM_BP_FAT	RNA biosynthetic process	55	7.80E-03	1.70E-01
	GOTERM_BP_FAT	transcription from RNA polymerase II promoter	44	1.40E-02	2.50E-01
Annotation Cluster 37	**Enrichment Score: 2.05**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	leukocyte mediated immunity	24	5.80E-04	2.80E-02
	GOTERM_BP_FAT	immune effector process	32	1.10E-03	4.30E-02
	GOTERM_BP_FAT	lymphocyte mediated immunity	20	1.40E-03	4.90E-02
	GOTERM_BP_FAT	B cell mediated immunity	15	1.20E-02	2.20E-01
	GOTERM_BP_FAT	immunoglobulin mediated immune response	14	2.10E-02	3.10E-01
	GOTERM_BP_FAT	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	18	2.10E-02	3.10E-01
	GOTERM_BP_FAT	adaptive immune response	18	2.10E-02	3.10E-01
	GOTERM_BP_FAT	humoral immune response mediated by circulating immunoglobulin	6	3.90E-01	9.70E-01
Annotation Cluster 38	**Enrichment Score: 2.02**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	positive regulation of immune system process	47	4.60E-03	1.20E-01
	GOTERM_BP_FAT	positive regulation of response to stimulus	46	6.40E-03	1.50E-01

ILMN_3249425	NA	-0.409768274
ILMN_1771878	SUSD5	-0.409819129
ILMN_1771538	PSCA	-0.409822459
ILMN_1805792	TRIO	-0.409832336
ILMN_1778557	CDK13	-0.409848931
ILMN_2356441	CACNG6	-0.409890521
ILMN_1745813	KIAA1279	-0.409915645
ILMN_1704302	C10orf140	-0.409982644
ILMN_1812233	KALRN	-0.410071225
ILMN_1744056	TAAR1	-0.410073148
ILMN_1674975	MANEAL	-0.410099542
ILMN_3242462	UHRF1BP1	-0.410115591
ILMN_2237746	ING3	-0.410150081
ILMN_2170353	CR613620	-0.410158071
ILMN_1782551	E2F5	-0.410291471
ILMN_1771268	BICD2	-0.410320718
ILMN_1798475	CSF2RB	-0.410331802
ILMN_1833524	CR741512	-0.410405346
ILMN_1737635	RAD1	-0.410421899
ILMN_1674050	COL8A2	-0.410447736
ILMN_2125618	SMEK3P	-0.41046641
ILMN_2380698	DSTN	-0.410473475
ILMN_2403237	CHN2	-0.410482743
ILMN_1709440	CPM	-0.410555572
ILMN_2408566	NR4A1	-0.410572275
ILMN_2352159	BBS9	-0.410576139
ILMN_2341343	AGTR1	-0.410608277
ILMN_1741592	SLC27A6	-0.410711627
ILMN_1858001	BE894306	-0.410857358
ILMN_1797318	HSPA14	-0.41086757
ILMN_1681755	DKFZp434F1622	-0.410883008
ILMN_3234959	FLJ35424	-0.410885357
ILMN_1776129	ASAH2	-0.410896677
ILMN_1774878	OTOGL	-0.410912988
ILMN_3308778	MIR488	-0.410989035
ILMN_1803033	MGST1	-0.411011975
ILMN_1673605	PRSS57	-0.411037649
ILMN_3243639	DUX2	-0.411045732
ILMN_1832208	TMEM33	-0.411119289
ILMN_1659781	CSMD3	-0.411134263
ILMN_1789294	OPRL1	-0.411163527
ILMN_1722829	HLF	-0.411183356
ILMN_1671626	DLGAP3	-0.411190821
ILMN_2386967	VPS54	-0.411256009
ILMN_1723761	ZFATAS	-0.41125828
ILMN_1810866	MRPS12	-0.411273493
ILMN_1681374	ALDOA	-0.411275026
ILMN_1812254	KIF5A	-0.411275574
ILMN_2342559	SPOCK3	-0.411286103
ILMN_2404135	RIOK3	-0.411469298
ILMN_2258977	XAGE1A	-0.41147957
ILMN_1796847	PITX2	-0.411490435
ILMN_3309299	MIR559	-0.411556847
ILMN_1652188	EPG5	-0.41159775
ILMN_1826215	LOC100128922	-0.411602097
ILMN_1695773	STK24	-0.411605734
ILMN_1695797	NCOA6	-0.411650861
ILMN_2231242	HMGB1	-0.411683661
ILMN_1740949	LRRC19	-0.411784407
ILMN_1730745	CCDC73	-0.411790568
ILMN_2390453	BCKDHB	-0.411806902
ILMN_2394193	METTL21D	-0.411876576
ILMN_1750879	TSPY3	-0.411878777
ILMN_1748899	TMED6	-0.411882633
ILMN_3243102	LOC728989	-0.41191828
ILMN_1764944	SLC6A10P	-0.411941889
ILMN_1694491	CCNG1	-0.41196735
ILMN_1849745	AI446524	-0.412009292
ILMN_1784654	RFPL3	-0.412022028
ILMN_1788895	SRD5A2	-0.412064535
ILMN_3292122	NA	-0.412077231
ILMN_1737418	ACSL6	-0.412085054
ILMN_1772207	FAM36A	-0.412100168
ILMN_3242896	DKFZp686K04236	-0.412207046
ILMN_1798615	SOHLH2	-0.412211572
ILMN_1660232	PEX5	-0.412215223
ILMN_1655905	DEFB131	-0.412233381
ILMN_1662603	NA	-0.412320857
ILMN_1689770	ARHGEF10L	-0.412336612
ILMN_1655624	LOC100130673	-0.412417419
ILMN_1653129	CSTF2	-0.412435776
ILMN_1687913	ELFN1	-0.41246446
ILMN_3273268	FAM75C1	-0.41247614
ILMN_1898826	BG564551	-0.412592797
ILMN_3201334	LOC100505502	-0.412614451
ILMN_1713613	PIAS2	-0.412670176
ILMN_2226324	BRP44L	-0.41267415
ILMN_1836193	NA	-0.412703862
ILMN_3275422	LOC648809	-0.412725089
ILMN_1662331	PDSS2	-0.412812625
ILMN_1910308	R00495	-0.41285712
ILMN_1728338	AK126539	-0.412871298
ILMN_1886639	DB027317	-0.412909083
ILMN_1856662	BM680619	-0.412938364
ILMN_1752550	NPAS3	-0.412943996

	GOTERM_BP_FAT	protein amino acid phosphorylation	82	1.10E-01	9.80E-01
	SP_PIR_KEYWORDS	kinase	83	1.10E-01	8.50E-01
	GOTERM_BP_FAT	phosphorylation	95	1.50E-01	9.80E-01
	SMART	S_TKc	32	1.60E-01	9.40E-01
	INTERPRO	Protein kinase, ATP binding site	56	1.70E-01	1.00E+00
	UP_SEQ_FEATURE	domain:Protein kinase	57	1.70E-01	1.00E+00
	GOTERM_MF_FAT	protein kinase activity	73	1.90E-01	9.80E-01
	UP_SEQ_FEATURE	active site:Proton acceptor	77	2.10E-01	1.00E+00
	SP_PIR_KEYWORDS	transferase	156	2.20E-01	9.00E-01
	UP_SEQ_FEATURE	binding site:ATP	63	2.60E-01	1.00E+00
	INTERPRO	Serine/threonine protein kinase	32	2.60E-01	1.00E+00
	UP_SEQ_FEATURE	nucleotide phosphate-binding region:ATP	108	2.80E-01	1.00E+00
	INTERPRO	Serine/threonine protein kinase-related	42	3.30E-01	1.00E+00
	GOTERM_MF_FAT	protein serine/threonine kinase activity	50	3.50E-01	9.90E-01
	SP_PIR_KEYWORDS	serine/threonine-protein kinase	41	5.20E-01	9.70E-01
	INTERPRO	Serine/threonine protein kinase, active site	38	5.60E-01	1.00E+00
Annotation Cluster 35	**Enrichment Score: 0.97**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	UDP-glucose metabolic process	3	3.10E-02	9.60E-01
	GOTERM_BP_FAT	nucleotide-sugar metabolic process	4	1.80E-01	9.80E-01
	KEGG_PATHWAY	Amino sugar and nucleotide sugar metabolism	8	2.20E-01	9.50E-01
Annotation Cluster 36	**Enrichment Score: 0.94**		**Count**	**P_Value**	**Benjamini**
	SMART	RHOD	6	8.30E-02	9.60E-01
	INTERPRO	Rhodanese-like	6	1.00E-01	1.00E+00
	UP_SEQ_FEATURE	domain:Rhodanese	5	1.70E-01	1.00E+00
Annotation Cluster 37	**Enrichment Score: 0.92**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	regulation of defense response to virus	6	4.40E-02	9.80E-01
	GOTERM_BP_FAT	regulation of defense response to virus by host	4	6.10E-02	9.80E-01
	GOTERM_BP_FAT	regulation of response to biotic stimulus	7	8.00E-02	9.80E-01
	GOTERM_BP_FAT	regulation of multi-organism process	6	2.30E-01	9.90E-01
	GOTERM_BP_FAT	regulation of immune effector process	12	5.10E-01	1.00E+00
Annotation Cluster 38	**Enrichment Score: 0.9**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	phosphatidylcholine metabolic process	6	6.40E-02	9.80E-01
	GOTERM_BP_FAT	biogenic amine metabolic process	15	1.40E-01	9.80E-01
	GOTERM_BP_FAT	ethanolamine and derivative metabolic process	7	1.50E-01	9.80E-01
	GOTERM_BP_FAT	glycerophospholipid metabolic process	17	1.80E-01	9.80E-01
Annotation Cluster 39	**Enrichment Score: 0.9**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	cerebellar granular layer formation	3	5.80E-02	9.80E-01
	GOTERM_BP_FAT	cerebellar granule cell differentiation	3	5.80E-02	9.80E-01
	GOTERM_BP_FAT	cerebellar granular layer morphogenesis	3	5.80E-02	9.80E-01
	GOTERM_BP_FAT	cerebellar granular layer development	3	5.80E-02	9.80E-01
	GOTERM_BP_FAT	cerebellar cortex morphogenesis	5	8.10E-02	9.80E-01
	GOTERM_BP_FAT	cerebellar cortex development	5	1.20E-01	9.80E-01
	GOTERM_BP_FAT	cerebellar cortex formation	4	1.30E-01	9.80E-01
	GOTERM_BP_FAT	cerebellum morphogenesis	5	1.30E-01	9.80E-01
	GOTERM_BP_FAT	cell differentiation in hindbrain	4	1.50E-01	9.80E-01
	GOTERM_BP_FAT	cerebellum development	6	2.10E-01	9.90E-01
	GOTERM_BP_FAT	hindbrain morphogenesis	5	2.20E-01	9.90E-01
	GOTERM_BP_FAT	metencephalon development	6	3.10E-01	9.90E-01
	GOTERM_BP_FAT	hindbrain development	8	4.50E-01	1.00E+00
Annotation Cluster 40	**Enrichment Score: 0.9**		**Count**	**P_Value**	**Benjamini**
	SMART	CLH	3	5.20E-02	9.30E-01
	INTERPRO	Clathrin, heavy chain/VPS, 7-fold repeat	3	5.80E-02	1.00E+00
	GOTERM_CC_FAT	Golgi-associated vesicle	6	6.50E-01	9.80E-01
Annotation Cluster 41	**Enrichment Score: 0.9**		**Count**	**P_Value**	**Benjamini**
	GOTERM_CC_FAT	chromatin	31	3.70E-02	8.20E-01
	GOTERM_CC_FAT	chromosome	57	1.80E-01	9.40E-01
	GOTERM_CC_FAT	chromosomal part	46	3.00E-01	9.50E-01
Annotation Cluster 42	**Enrichment Score: 0.89**		**Count**	**P_Value**	**Benjamini**
	SP_PIR_KEYWORDS	gtp-binding	44	7.40E-02	8.40E-01
	GOTERM_MF_FAT	guanyl ribonucleotide binding	51	7.70E-02	9.10E-01
	GOTERM_MF_FAT	guanyl nucleotide binding	51	7.70E-02	9.10E-01
	UP_SEQ_FEATURE	nucleotide phosphate-binding region:GTP	40	8.00E-02	1.00E+00
	GOTERM_MF_FAT	GTP binding	48	1.30E-01	9.50E-01
	GOTERM_MF_FAT	GTPase activity	27	2.50E-01	9.90E-01
	INTERPRO	Small GTP-binding protein	19	5.10E-01	1.00E+00
Annotation Cluster 43	**Enrichment Score: 0.85**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	hormone metabolic process	18	5.40E-02	9.80E-01
	GOTERM_BP_FAT	regulation of hormone levels	22	1.20E-01	9.70E-01
	GOTERM_BP_FAT	cellular hormone metabolic process	8	4.40E-01	1.00E+00
Annotation Cluster 44	**Enrichment Score: 0.85**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	endochondral bone morphogenesis	6	2.10E-02	9.50E-01
	GOTERM_BP_FAT	endochondral ossification	5	3.10E-02	9.60E-01
	GOTERM_BP_FAT	bone morphogenesis	6	5.30E-02	9.80E-01
	GOTERM_BP_FAT	bone development	16	3.20E-01	9.90E-01
	GOTERM_BP_FAT	ossification	15	3.30E-01	9.90E-01
	GOTERM_BP_FAT	skeletal system development	36	4.40E-01	1.00E+00
	GOTERM_BP_FAT	skeletal system morphogenesis	12	6.50E-01	1.00E+00
Annotation Cluster 45	**Enrichment Score: 0.84**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	domain:LEM	3	1.20E-01	1.00E+00
	SMART	LEM	3	1.50E-01	9.50E-01
	INTERPRO	Lamino-associated polypeptide 2/emerin	3	1.60E-01	1.00E+00
Annotation Cluster 46	**Enrichment Score: 0.84**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	zinc finger region:A20-type	3	1.20E-01	1.00E+00
	SMART	ZnF_A20	3	1.50E-01	9.50E-01
	INTERPRO	Zinc finger, A20-type	3	1.60E-01	1.00E+00
Annotation Cluster 47	**Enrichment Score: 0.83**		**Count**	**P_Value**	**Benjamini**
	KEGG_PATHWAY	Citrate cycle (TCA cycle)	8	5.10E-02	8.60E-01
	GOTERM_BP_FAT	tricarboxylic acid cycle	6	8.90E-02	9.80E-01
	GOTERM_BP_FAT	acetyl-CoA catabolic process	6	8.90E-02	9.80E-01
	GOTERM_BP_FAT	acetyl-CoA metabolic process	7	1.00E-01	9.80E-01
	GOTERM_BP_FAT	cofactor catabolic process	7	1.00E-01	9.80E-01
	GOTERM_BP_FAT	coenzyme catabolic process	6	1.30E-01	9.80E-01
	GOTERM_BP_FAT	aerobic respiration	7	1.60E-01	9.80E-01
	SP_PIR_KEYWORDS	tricarboxylic acid cycle	5	1.70E-01	8.70E-01
	GOTERM_BP_FAT	energy derivation by oxidation of organic compounds	18	3.60E-01	1.00E+00

ILMN_1676361	ARHGAP22	0.780565106
ILMN_3210538	NUDT3	0.780484257
ILMN_2101885	TUBB	0.780271925
ILMN_1687805	RPS12	0.780215735
ILMN_2392940	CEP250	0.779958173
ILMN_2368530	IL32	0.779947832
ILMN_1778226	EXTL3	0.779266044
ILMN_1703692	TUBB	0.77913614
ILMN_1770892	YY1	0.779083851
ILMN_1662174	ORMDL3	0.778951889
ILMN_2354334	ATXN2L	0.778812581
ILMN_1666078	HLA-H	0.778708791
ILMN_2141453	RPL18A	0.778578355
ILMN_2400512	PRKCSH	0.778542937
ILMN_1731233	GZMH	0.778437598
ILMN_1786347	TNPO1	0.778355095
ILMN_1726222	FLOT2	0.778227216
ILMN_1785902	C1QC	0.77808631
ILMN_2371685	UBE2E1	0.778036682
ILMN_1815656	SERINC3	0.778007044
ILMN_1772888	AX746718	0.777938563
ILMN_3247802	PRRC2B	0.777879502
ILMN_1678422	DHX58	0.777853097
ILMN_1710756	ENO1	0.777850668
ILMN_1765649	IRF3	0.77773112
ILMN_1768311	NPIPL3	0.777621226
ILMN_1750805	ARHGAP30	0.777390041
ILMN_2388155	CASP3	0.777354802
ILMN_3307693	WFDC2	0.776754166
ILMN_2177965	RPS19BP1	0.776634451
ILMN_2319414	BTF3	0.776434929
ILMN_1693352	MRPL20	0.776352647
ILMN_1652797	FAM174B	0.776220261
ILMN_2300186	DYNLL1	0.77620392
ILMN_3250389	GPAA1	0.776150121
ILMN_1758963	NADK	0.776113508
ILMN_1767509	DEF8	0.775854204
ILMN_1786197	NR2F1	0.77579258
ILMN_1810037	RUSC2	0.775662603
ILMN_1758398	GUK1	0.775375982
ILMN_1801118	SNRNP25	0.77536368
ILMN_2384544	ADAM15	0.775174467
ILMN_2330948	ARF1	0.774739379
ILMN_1711994	TCIRG1	0.77455265
ILMN_1717101	MINK1	0.774295441
ILMN_1787949	RPS15A	0.774200408
ILMN_3288161	RPS27	0.774133502
ILMN_2399503	UBN1	0.773880138
ILMN_1652768	RPS2	0.773787861
ILMN_1658411	CHD4	0.773658832
ILMN_2399036	SEPN1	0.77365667
ILMN_2215640	TUBA3D	0.773601924
ILMN_1711853	MED24	0.77351025
ILMN_1795933	CHMP7	0.773417413
ILMN_1666819	PHLDB1	0.773155687
ILMN_1792314	ACTR1A	0.773091396
ILMN_1810085	ABCF3	0.773051203
ILMN_1777296	ACTB	0.773021411
ILMN_2133675	SGSH	0.772784884
ILMN_3241462	RPS18	0.772665206
ILMN_2130180	RPL13P5	0.772606093
ILMN_2323491	NUP62	0.772599457
ILMN_1718206	KIAA0100	0.772408616
ILMN_1653498	IGSF6	0.772385033
ILMN_2309848	FXYD5	0.772374581
ILMN_2407482	ITPA	0.772308891
ILMN_2088847	OTUD5	0.771954346
ILMN_1796216	VASH1	0.771791281
ILMN_1694730	RNPEPL1	0.771732489
ILMN_1753534	RPS18	0.771545942
ILMN_2355559	PSAP	0.771455305
ILMN_2403994	RALY	0.771364184
ILMN_2038778	GAPDH	0.771202286
ILMN_1807972	MICAL1	0.771072148
ILMN_2371911	MUC1	0.771021162
ILMN_1772189	ABCD1	0.770993054
ILMN_2405592	TMEM93	0.770698287
ILMN_1664610	RPS17	0.770564138
ILMN_2112301	DRAP1	0.770554021
ILMN_1694475	GTPBP2	0.770480273
ILMN_2401978	STAT3	0.770386192
ILMN_2331062	CBFA2T2	0.77036556
ILMN_1729161	NOTCH1	0.770320625
ILMN_2208903	CD52	0.770023683
ILMN_2319994	RPL3	0.76988788
ILMN_3246962	SPECC1L	0.769831502
ILMN_3239460	OAZ2	0.769820984
ILMN_1780987	RFXANK	0.769677987
ILMN_1798819	DTNB	0.769550915
ILMN_1659800	BCL11A	0.769435097
ILMN_1730773	RPL10	0.769426962
ILMN_2392043	SPI1	0.76940794

	GOTERM_BP_FAT	positive regulation of immune response	31	7.60E-03	1.70E-01
	GOTERM_BP_FAT	activation of immune response	20	3.60E-02	4.20E-01
Annotation Cluster 39	**Enrichment Score: 1.95**		**Count**	**P_Value**	**Benjamini**
	INTERPRO	Tubulin/FtsZ, 2-layer sandwich domain	10	8.50E-04	2.10E-01
	UP_SEQ_FEATURE	site:Involved in polymerization	5	9.70E-04	3.50E-01
	GOTERM_BP_FAT	protein polymerization	16	1.20E-03	4.40E-02
	KEGG_PATHWAY	Pathogenic Escherichia coli infection	19	1.20E-03	4.00E-02
	INTERPRO	Tubulin	10	1.80E-03	2.60E-01
	INTERPRO	Tubulin/FtsZ, GTPase domain	10	1.80E-03	2.60E-01
	INTERPRO	Alpha tubulin	6	2.60E-03	3.40E-01
	INTERPRO	Tubulin, conserved site	9	5.40E-03	4.80E-01
	PIR_SUPERFAMILY	PIRSF002306:tubulin	9	6.00E-03	9.60E-01
	INTERPRO	Beta tubulin	3	4.10E-01	1.00E+00
	GOTERM_BP_FAT	microtubule-based movement	15	6.40E-01	1.00E+00
	INTERPRO	Beta tubulin, autoregulation binding site	3	6.80E-01	1.00E+00
	GOTERM_BP_FAT	microtubule-based process	28	9.00E-01	1.00E+00
Annotation Cluster 40	**Enrichment Score: 1.92**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	'de novo' protein folding	8	2.60E-03	7.60E-02
	GOTERM_BP_FAT	'de novo' posttranslational protein folding	6	2.00E-02	3.00E-01
	GOTERM_BP_FAT	chaperone mediated protein folding requiring cofactor	5	3.30E-02	4.00E-01
Annotation Cluster 41	**Enrichment Score: 1.87**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	in utero embryonic development	39	1.30E-03	4.80E-02
	GOTERM_BP_FAT	chordate embryonic development	56	4.00E-02	4.40E-01
	GOTERM_BP_FAT	embryonic development ending in birth or egg hatching	56	4.70E-02	4.80E-01
Annotation Cluster 42	**Enrichment Score: 1.85**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	erythrocyte homeostasis	15	3.40E-03	9.30E-02
	GOTERM_BP_FAT	myeloid cell differentiation	22	8.70E-03	1.80E-01
	GOTERM_BP_FAT	erythrocyte differentiation	12	2.10E-02	3.10E-01
	GOTERM_BP_FAT	homeostasis of number of cells	20	6.30E-02	5.60E-01
Annotation Cluster 43	**Enrichment Score: 1.79**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	positive regulation of developmental process	57	7.00E-04	3.10E-02
	GOTERM_BP_FAT	positive regulation of cell development	20	1.20E-03	4.50E-02
	GOTERM_BP_FAT	positive regulation of cell differentiation	48	1.20E-03	4.60E-02
	GOTERM_BP_FAT	positive regulation of cell projection organization	15	2.20E-03	6.60E-02
	GOTERM_BP_FAT	positive regulation of neurogenesis	17	3.30E-03	9.00E-02
	GOTERM_BP_FAT	regulation of cell morphogenesis	29	6.10E-03	1.40E-01
	GOTERM_BP_FAT	regulation of cell projection organization	21	1.10E-02	2.10E-01
	GOTERM_BP_FAT	regulation of cell development	40	1.10E-02	2.10E-01
	GOTERM_BP_FAT	positive regulation of axonogenesis	9	1.20E-02	2.20E-01
	GOTERM_BP_FAT	regulation of cell morphogenesis involved in differentiation	18	2.10E-02	3.10E-01
	GOTERM_BP_FAT	regulation of axonogenesis	14	3.20E-02	3.90E-01
	GOTERM_BP_FAT	regulation of neuron projection development	16	3.70E-02	4.20E-01
	GOTERM_BP_FAT	regulation of nervous system development	33	9.50E-02	6.70E-01
	GOTERM_BP_FAT	positive regulation of cellular component organization	31	1.10E-01	7.10E-01
	GOTERM_BP_FAT	regulation of axon extension	6	1.10E-01	7.20E-01
	GOTERM_BP_FAT	regulation of neurogenesis	28	1.40E-01	7.80E-01
	GOTERM_BP_FAT	positive regulation of developmental growth	5	1.50E-01	7.90E-01
	GOTERM_BP_FAT	regulation of neuron differentiation	23	1.50E-01	8.00E-01
Annotation Cluster 44	**Enrichment Score: 1.77**		**Count**	**P_Value**	**Benjamini**
	SP_PIR_KEYWORDS	elongation factor	8	9.20E-03	9.30E-02
	GOTERM_CC_FAT	eukaryotic translation elongation factor 1 complex	4	1.90E-02	1.90E-01
	GOTERM_MF_FAT	translation elongation factor activity	8	2.70E-02	4.60E-01
Annotation Cluster 45	**Enrichment Score: 1.77**		**Count**	**P_Value**	**Benjamini**
	PIR_SUPERFAMILY	PIRSF002034:ubiquitin	6	2.40E-04	2.20E-01
	INTERPRO	Ubiquitin supergroup	17	4.60E-04	1.50E-01
	UP_SEQ_FEATURE	cross-link:Glycyl lysine isopeptide (Gly-Lys) (interchain with K-? in acceptor proteins)	7	8.40E-04	3.60E-01
	UP_SEQ_FEATURE	binding site:Activating enzyme	5	9.70E-04	3.50E-01
	INTERPRO	Ubiquitin subgroup	7	1.10E-03	2.30E-01
	INTERPRO	Ubiquitin	15	1.20E-03	2.40E-01
	SMART	UBQ	15	1.80E-03	2.10E-01
	GOTERM_BP_FAT	regulation of skeletal muscle fiber development	10	3.30E-03	9.10E-02
	SP_PIR_KEYWORDS	protein degradation	8	4.90E-03	5.60E-02
	GOTERM_BP_FAT	regulation of striated muscle cell differentiation	11	6.40E-03	1.50E-01
	UP_SEQ_FEATURE	compositionally biased region:Lys-rich (highly basic)	4	6.40E-03	8.40E-01
	UP_SEQ_FEATURE	site:Essential for function	4	6.40E-03	8.40E-01
	UP_SEQ_FEATURE	chain:Ubiquitin	4	6.40E-03	8.40E-01
	UP_SEQ_FEATURE	chain:40S ribosomal protein S27a	4	6.40E-03	8.40E-01
	INTERPRO	Ribosomal protein S27a	4	7.30E-03	5.50E-01
	INTERPRO	Ribosomal protein L40e	4	7.30E-03	5.50E-01
	GOTERM_BP_FAT	regulation of synaptic growth at neuromuscular junction	5	7.60E-03	1.70E-01
	PIR_SUPERFAMILY	PIRSF038431:ribosomal protein S27Ae	4	8.90E-03	9.50E-01
	PIR_SUPERFAMILY	PIRSF002042:polyubiquitin 3	4	8.90E-03	9.50E-01
	GOTERM_BP_FAT	regulation of skeletal muscle tissue development	10	1.00E-02	2.00E-01
	GOTERM_BP_FAT	regulation of striated muscle tissue development	14	1.10E-02	2.10E-01
	GOTERM_BP_FAT	regulation of muscle development	14	1.30E-02	2.30E-01
	GOTERM_BP_FAT	negative regulation of striated muscle development	5	1.40E-02	2.40E-01
	SP_PIR_KEYWORDS	polyprotein	4	1.40E-02	1.30E-01
	GOTERM_BP_FAT	regulation of developmental growth	13	1.70E-02	2.70E-01
	GOTERM_BP_FAT	long-term strengthening of neuromuscular junction	4	1.90E-02	2.80E-01
	GOTERM_BP_FAT	negative regulation of muscle development	5	2.20E-02	3.10E-01
	GOTERM_BP_FAT	regulation of muscle cell differentiation	11	2.70E-02	3.60E-01
	GOTERM_BP_FAT	ER-associated protein catabolic process	7	8.60E-02	6.40E-01
	SP_PIR_KEYWORDS	pseudogene	4	1.10E-01	4.70E-01
	UP_SEQ_FEATURE	domain:Ubiquitin-like	9	1.30E-01	1.00E+00
	INTERPRO	Ubiquitin conserved site	8	1.30E-01	9.80E-01
	SP_PIR_KEYWORDS	thiolester bond	8	1.40E-01	5.20E-01
	GOTERM_BP_FAT	regulation of myoblast differentiation	4	1.70E-01	8.20E-01
	GOTERM_BP_FAT	negative regulation of myoblast differentiation	3	1.80E-01	8.40E-01
	GOTERM_BP_FAT	regulation of synapse structure and activity	6	2.00E-01	8.60E-01
	GOTERM_BP_FAT	regulation of synaptogenesis	5	2.10E-01	8.70E-01
	GOTERM_BP_FAT	positive regulation of synaptic transmission	7	2.90E-01	9.30E-01
	GOTERM_BP_FAT	regulation of synapse organization	5	3.00E-01	9.30E-01

ILMN_1670870	ALCAM	-0.412996776
ILMN_3210565	HIGD1A	-0.413118496
ILMN_3297876	VSTM2B	-0.413201209
ILMN_1714083	KLHL8	-0.413224445
ILMN_1712405	LOC100506085	-0.413228518
ILMN_1844361	CA944693	-0.413252565
ILMN_1713744	DKFZp761F2014	-0.413271021
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ILMN_1731498	GPR156	-0.4132939
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ILMN_3244276	LOC415056	-0.413376935
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ILMN_3249152	VSX2	-0.413576721
ILMN_1707484	GEMIN6	-0.41361845
ILMN_2158594	C10orf28	-0.413620924
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ILMN_1811927	OR2W3	-0.413698385
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ILMN_1762024	TAAR9	-0.413850833
ILMN_1763419	TOP1	-0.413943351
ILMN_2361737	TRIM36	-0.414002801
ILMN_1777214	C2orf67	-0.414030989
ILMN_1791588	S71824	-0.414126197
ILMN_1729112	CHPT1	-0.414215016
ILMN_1677824	RAB4A	-0.414219792
ILMN_1664833	MRPL50	-0.414246458
ILMN_1771523	PRKACB	-0.414298387
ILMN_3227582	AK311627	-0.414334066
ILMN_1740996	CA3	-0.414412618
ILMN_3309869	MIR504	-0.41454217
ILMN_2128967	C11orf1	-0.414555872
ILMN_2202368	RBMY2EP	-0.41459383
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ILMN_1873412	NA	-0.414885935
ILMN_2323979	WARS2	-0.415021658
ILMN_1662491	BI827797	-0.41504115
ILMN_1774110	CHN2	-0.415126523
ILMN_1766316	GOLGA8G	-0.415145923
ILMN_1679949	SLC25A23	-0.415273941
ILMN_3244461	LRRC16A	-0.415275096
ILMN_1760651	LOC253724	-0.415332144
ILMN_1685357	RTN2	-0.415368994
ILMN_1772677	CNOT4	-0.415373352
ILMN_1775486	SSPN	-0.415404417
ILMN_1807244	STGC3	-0.415416395
ILMN_1679527	IAPP	-0.415546722
ILMN_3237035	SNORA54	-0.415691542
ILMN_1777017	FOXK1	-0.415702304
ILMN_1768004	PDCD4	-0.415746344
ILMN_1725314	GBP3	-0.415820056
ILMN_2151048	STAG1	-0.415840446
ILMN_1788774	TYR	-0.415861118
ILMN_1659857	SNAP29	-0.415967834
ILMN_3237817	REXO1L1	-0.416047244
ILMN_1669443	LOC642384	-0.416063962
ILMN_1754234	ZMYND11	-0.416169894
ILMN_1713764	AK096649	-0.416181545
ILMN_1785387	ERMAP	-0.416210539
ILMN_1853280	DA778026	-0.416246306
ILMN_3309699	MIR29B1	-0.416333861
ILMN_1904400	AW136452	-0.416345798
ILMN_1724254	INSL6	-0.416350016
ILMN_1684184	DYRK2	-0.41640553
ILMN_1667388	OR13C8	-0.416488441
ILMN_1667213	DFFA	-0.416489707
ILMN_1740048	MYOD1	-0.416508333
ILMN_1683737	SNX32	-0.416513401
ILMN_1899842	ELK4	-0.41652031
ILMN_1690352	ADO	-0.416629553
ILMN_2347097	KLK15	-0.416639946
ILMN_1782938	SLC16A10	-0.416707259
ILMN_2369953	ARL4A	-0.416751669
ILMN_1797642	KIAA1569	-0.416754414
ILMN_2336585	CTAG2	-0.416795974
ILMN_1843478	AI494041	-0.416805589

	GOTERM_BP_FAT	cellular respiration	9	8.20E-01	1.00E+00
Annotation Cluster 48	**Enrichment Score: 0.81**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	myoblast fusion	4	1.00E-01	9.80E-01
	GOTERM_BP_FAT	syncytium formation by plasma membrane fusion	4	1.30E-01	9.80E-01
	GOTERM_BP_FAT	syncytium formation	4	1.80E-01	9.80E-01
	GOTERM_BP_FAT	myotube differentiation	4	2.40E-01	9.90E-01
Annotation Cluster 49	**Enrichment Score: 0.81**		**Count**	**P_Value**	**Benjamini**
	GOTERM_MF_FAT	acid-thiol ligase activity	6	5.50E-02	8.70E-01
	GOTERM_MF_FAT	ligase activity, forming carbon-sulfur bonds	7	6.20E-02	8.80E-01
	GOTERM_MF_FAT	CoA-ligase activity	3	2.10E-01	9.80E-01
	SP_PIR_KEYWORDS	fatty acid metabolism	9	3.20E-01	9.20E-01
	INTERPRO	AMP-dependent synthetase and ligase	5	4.00E-01	1.00E+00
Annotation Cluster 50	**Enrichment Score: 0.8**		**Count**	**P_Value**	**Benjamini**
	GOTERM_CC_FAT	cytoskeleton	166	6.90E-02	8.90E-01
	GOTERM_CC_FAT	cytoskeletal part	114	1.30E-01	9.20E-01
	GOTERM_CC_FAT	intracellular non-membrane-bounded organelle	290	2.60E-01	9.50E-01
	GOTERM_CC_FAT	non-membrane-bounded organelle	290	2.60E-01	9.50E-01
Annotation Cluster 51	**Enrichment Score: 0.8**		**Count**	**P_Value**	**Benjamini**
	SMART	LA	3	1.50E-01	9.50E-01
	UP_SEQ_FEATURE	domain:HTH La-type RNA-binding	3	1.60E-01	1.00E+00
	INTERPRO	RNA-binding protein Lupus La	3	1.60E-01	1.00E+00
Annotation Cluster 52	**Enrichment Score: 0.8**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	glucose metabolic process	22	1.30E-01	9.80E-01
	GOTERM_BP_FAT	monosaccharide metabolic process	30	1.40E-01	9.80E-01
	GOTERM_BP_FAT	hexose metabolic process	25	2.20E-01	9.90E-01
Annotation Cluster 53	**Enrichment Score: 0.8**		**Count**	**P_Value**	**Benjamini**
	GOTERM_CC_FAT	autophagic vacuole	6	1.70E-02	9.20E-01
	SP_PIR_KEYWORDS	autophagy	5	4.10E-01	9.40E-01
	GOTERM_BP_FAT	autophagy	5	5.80E-01	1.00E+00
Annotation Cluster 54	**Enrichment Score: 0.79**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	glutathione metabolic process	7	6.90E-02	9.80E-01
	GOTERM_BP_FAT	sulfur metabolic process	18	9.90E-02	9.80E-01
	GOTERM_BP_FAT	peptide metabolic process	10	1.00E-01	9.80E-01
	GOTERM_BP_FAT	sulfur compound biosynthetic process	9	1.50E-01	9.80E-01
	GOTERM_BP_FAT	glutathione biosynthetic process	3	2.90E-01	9.90E-01
	GOTERM_BP_FAT	peptide biosynthetic process	3	5.50E-01	1.00E+00
Annotation Cluster 55	**Enrichment Score: 0.79**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	metal ion-binding site:Iron	10	4.80E-02	1.00E+00
	SMART	PP2Ac	4	1.30E-01	9.60E-01
	INTERPRO	Serine/threonine-specific protein phosphatase and bis(5-nucleosyl)-tetraphosphatase	4	1.50E-01	1.00E+00
	INTERPRO	Metallophosphoesterase	6	1.70E-01	1.00E+00
	UP_SEQ_FEATURE	metal ion-binding site:Manganese	4	6.90E-01	1.00E+00
Annotation Cluster 56	**Enrichment Score: 0.79**		**Count**	**P_Value**	**Benjamini**
	SMART	14_3_3	3	1.50E-01	9.50E-01
	UP_SEQ_FEATURE	site:Interaction with phosphoserine on interacting protein	3	1.60E-01	1.00E+00
	INTERPRO	14-3-3 protein	3	1.60E-01	1.00E+00
	PIR_SUPERFAMILY	PIRSF000868:14-3-3	3	1.70E-01	1.00E+00
	PIR_SUPERFAMILY	PIRSF000868:14-3-3 protein	3	1.70E-01	1.00E+00
Annotation Cluster 57	**Enrichment Score: 0.78**		**Count**	**P_Value**	**Benjamini**
	GOTERM_MF_FAT	inhibitory MHC class I receptor activity	3	3.20E-02	8.20E-01
	PIR_SUPERFAMILY	PIRSF016955:killer cell immunoglobulin-like receptor	3	2.50E-01	1.00E+00
	GOTERM_MF_FAT	MHC class I receptor activity	3	5.60E-01	1.00E+00
Annotation Cluster 58	**Enrichment Score: 0.77**		**Count**	**P_Value**	**Benjamini**
	PIR_SUPERFAMILY	PIRSF036841:ring finger protein 13	3	1.30E-01	1.00E+00
	UP_SEQ_FEATURE	zinc finger region:RING-type; atypical	7	1.40E-01	1.00E+00
	UP_SEQ_FEATURE	domain:PA	4	1.50E-01	1.00E+00
	INTERPRO	Protease-associated PA	4	3.00E-01	1.00E+00
Annotation Cluster 59	**Enrichment Score: 0.77**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	centrosome cycle	6	4.40E-02	9.80E-01
	GOTERM_BP_FAT	centrosome duplication	3	2.50E-01	9.90E-01
	GOTERM_BP_FAT	centrosome organization	6	2.50E-01	9.90E-01
	GOTERM_BP_FAT	microtubule organizing center organization	6	3.10E-01	9.90E-01
Annotation Cluster 60	**Enrichment Score: 0.75**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	histone ubiquitination	5	1.20E-01	9.80E-01
	GOTERM_BP_FAT	histone monoubiquitination	3	1.60E-01	9.80E-01
	GOTERM_BP_FAT	histone H2B ubiquitination	3	2.00E-01	9.90E-01
	GOTERM_BP_FAT	protein monoubiquitination	3	2.50E-01	9.90E-01
Annotation Cluster 61	**Enrichment Score: 0.75**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	domain:COS	4	1.00E-01	1.00E+00
	INTERPRO	COS domain	4	1.30E-01	1.00E+00
	UP_SEQ_FEATURE	domain:Fibronectin type-III	8	4.30E-01	1.00E+00
Annotation Cluster 62	**Enrichment Score: 0.75**		**Count**	**P_Value**	**Benjamini**
	GOTERM_MF_FAT	phospholipase activity	14	1.00E-01	9.30E-01
	GOTERM_BP_FAT	lipid catabolic process	25	1.00E-01	9.80E-01
	GOTERM_MF_FAT	lipase activity	15	1.80E-01	9.80E-01
	GOTERM_MF_FAT	carboxylesterase activity	14	2.20E-01	9.80E-01
	SP_PIR_KEYWORDS	lipid degradation	11	4.10E-01	9.40E-01
Annotation Cluster 63	**Enrichment Score: 0.75**		**Count**	**P_Value**	**Benjamini**
	BIOCARTA	Aspirin Blocks Signaling Pathway Involved in Platelet Activation	8	2.40E-03	4.30E-01
	BIOCARTA	Erk1/Erk2 Mapk Signaling pathway	8	3.00E-02	9.70E-01
	BIOCARTA	Phospholipids as signalling intermediaries	7	3.00E-02	9.00E-01
	BIOCARTA	Roles of ?-arrestin-dependent Recruitment of Src Kinases in GPCR Signaling	6	3.70E-02	8.20E-01
	BIOCARTA	Role of ?-arrestins in the activation and targeting of MAP kinases	5	5.50E-02	8.80E-01
	BIOCARTA	CCR3 signaling in Eosinophils	6	6.70E-02	8.90E-01
	SP_PIR_KEYWORDS	signal transduction	7	1.50E-01	8.70E-01
	BIOCARTA	uCalpain and friends in Cell spread	4	1.60E-01	9.80E-01
	BIOCARTA	PKC-catalyzed phosphorylation of inhibitory phosphoprotein of myosin phosphatase	4	1.60E-01	9.80E-01
	BIOCARTA	Attenuation of GPCR Signaling	3	1.70E-01	9.70E-01
	BIOCARTA	Signaling Pathway from G-Protein Families	5	1.80E-01	9.70E-01
	BIOCARTA	Erk and PI-3 Kinase Are Necessary for Collagen Binding in Corneal Epithelia	5	2.10E-01	9.80E-01
	BIOCARTA	mCalpain and friends in Cell motility	4	2.10E-01	9.70E-01
	BIOCARTA	CXCR4 Signaling Pathway	5	2.30E-01	9.80E-01

ILMN_1700628	DDX24	0.769278801		GOTERM_BP_FAT	negative regulation of muscle cell differentiation	4	3.50E-01	9.60E-01
ILMN_2364376	ILK	0.76892612		GOTERM_BP_FAT	positive regulation of transmission of nerve impulse	7	3.60E-01	9.60E-01
ILMN_2128428	DAB2	0.76891676		GOTERM_BP_FAT	positive regulation of neurological system process	7	4.10E-01	9.70E-01
ILMN_1737170	FLII	0.768501793	**Annotation Cluster 46**	**Enrichment Score: 1.76**		**Count**	**P_Value**	**Benjamini**
ILMN_1708077	DAXX	0.768491106		GOTERM_CC_FAT	nuclear inner membrane	9	7.60E-03	1.00E-01
ILMN_1862018	ATXN7L3	0.768406132		GOTERM_CC_FAT	lamin filament	4	1.90E-02	1.90E-01
ILMN_1810844	RARRES2	0.768397201		GOTERM_CC_FAT	nuclear lamina	4	3.50E-02	2.70E-01
ILMN_1683658	FKBP1A	0.768328505	**Annotation Cluster 47**	**Enrichment Score: 1.76**		**Count**	**P_Value**	**Benjamini**
ILMN_2410986	STAT3	0.768291334		GOTERM_BP_FAT	antigen processing and presentation of peptide antigen	13	1.00E-04	6.90E-03
ILMN_1774828	VEZT	0.768213139		GOTERM_MF_FAT	MHC protein binding	12	1.20E-04	1.60E-02
ILMN_1763884	CORO7	0.768084654		UP_SEQ_FEATURE	region of interest:Alpha-1	10	2.60E-04	1.60E-01
ILMN_3232447	AI880175	0.768028287		UP_SEQ_FEATURE	region of interest:Alpha-2	10	2.60E-04	1.60E-01
ILMN_1738675	PTPN6	0.767666604		GOTERM_MF_FAT	MHC class I protein binding	9	3.60E-04	3.60E-02
ILMN_2349061	IRF7	0.767648353		KEGG_PATHWAY	Viral myocarditis	23	4.60E-04	4.00E-02
ILMN_1736178	AEBP1	0.767636916		UP_SEQ_FEATURE	domain:Ig-like C1-type	14	5.90E-04	3.00E-01
ILMN_1699603	MRPL12	0.767568354		GOTERM_BP_FAT	antigen processing and presentation	23	8.60E-04	3.70E-02
ILMN_3221499	ZNF735	0.767552558		GOTERM_BP_FAT	antigen processing and presentation of exogenous antigen	8	1.00E-03	4.10E-02
ILMN_1730084	COMT	0.767517185		UP_SEQ_FEATURE	region of interest:Connecting peptide	13	1.30E-03	4.10E-01
ILMN_2146566	CLASRP	0.76714661		UP_SEQ_FEATURE	region of interest:Alpha-3	6	2.10E-03	5.60E-01
ILMN_2189424	MRPL20	0.767071215		GOTERM_CC_FAT	MHC class I peptide loading complex	6	3.30E-03	5.40E-02
ILMN_1761155	PABPC1	0.766818243		GOTERM_BP_FAT	antigen processing and presentation of peptide antigen via MHC class I	8	4.00E-03	1.00E-01
ILMN_2393450	INF2	0.766651565		GOTERM_BP_FAT	antigen processing and presentation of exogenous peptide antigen	6	9.20E-03	1.90E-01
ILMN_1733155	GIT1	0.766626893		INTERPRO	Immunoglobulin C1-set	17	9.30E-03	5.80E-01
ILMN_1726589	CD248	0.766522016		KEGG_PATHWAY	Cell adhesion molecules (CAMs)	31	1.10E-02	1.40E-01
ILMN_2395711	ARRB2	0.766330425		KEGG_PATHWAY	Allograft rejection	12	1.30E-02	1.50E-01
ILMN_1778078	PTPRA	0.766328791		GOTERM_BP_FAT	antigen processing and presentation of peptide antigen via MHC class II	5	1.40E-02	2.40E-01
ILMN_3217815	RPS2	0.766213836		GOTERM_BP_FAT	antigen processing and presentation of exogenous peptide antigen via MHC class II	5	1.40E-02	2.40E-01
ILMN_2372922	PPP2R4	0.766156978		SMART	IGc1	17	1.40E-02	4.70E-01
ILMN_1766275	PIK3CD	0.766095938		KEGG_PATHWAY	Antigen processing and presentation	21	1.90E-02	1.70E-01
ILMN_2128750	PTTG1IP	0.765963971		PIR_SUPERFAMILY	PIRSF001990:class I histocompatibility antigen	5	2.40E-02	9.90E-01
ILMN_1677138	POLR2J2	0.765735548		SP_PIR_KEYWORDS	mhc i	5	2.40E-02	1.80E-01
ILMN_1706959	TIMM22	0.76530121		KEGG_PATHWAY	Intestinal immune network for IgA production	14	2.50E-02	2.00E-01
ILMN_1793371	KIAA0430	0.765231772		SP_PIR_KEYWORDS	mhc ii	9	2.70E-02	2.00E-01
ILMN_2038772	RPS9	0.765190139		GOTERM_MF_FAT	MHC class II receptor activity	7	2.70E-02	4.50E-01
ILMN_2058251	VIM	0.764893517		KEGG_PATHWAY	Type I diabetes mellitus	12	4.10E-02	2.60E-01
ILMN_1767651	TECPR1	0.764813359		INTERPRO	Immunoglobulin/major histocompatibility complex, conserved site	18	4.30E-02	9.20E-01
ILMN_1708743	NT5DC2	0.764702922		GOTERM_CC_FAT	TAP complex	4	5.50E-02	3.50E-01
ILMN_1791211	DOK2	0.764683695		KEGG_PATHWAY	Graft-versus-host disease	11	5.70E-02	3.30E-01
ILMN_1665384	SH3BP5L	0.764653302		GOTERM_MF_FAT	MHC class I receptor activity	6	5.70E-02	6.40E-01
ILMN_1778374	BSG	0.764583833		GOTERM_BP_FAT	antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	9	6.10E-02	5.50E-01
ILMN_3212833	RPL7A	0.764522098		GOTERM_CC_FAT	MHC protein complex	13	7.10E-02	4.20E-01
ILMN_1713491	VAMP2	0.76444178		SP_PIR_KEYWORDS	transplantation antigen	3	7.40E-02	3.70E-01
ILMN_1726392	NIN	0.7643455		INTERPRO	MHC class I, alpha chain, C-terminal	3	8.00E-02	9.50E-01
ILMN_1701558	MAP1A	0.764322918		PIR_SUPERFAMILY	PIRSF001991:class II histocompatibility antigen	7	1.30E-01	1.00E+00
ILMN_1692473	PRMT1	0.764226141		KEGG_PATHWAY	Autoimmune thyroid disease	12	1.30E-01	5.00E-01
ILMN_3192791	HNRNPM	0.764038255		KEGG_PATHWAY	Asthma	8	1.30E-01	4.90E-01
ILMN_1790797	VPS28	0.763755018		INTERPRO	MHC class II, alpha/beta chain, N-terminal	6	1.40E-01	9.80E-01
ILMN_1694504	RNF220	0.763260422		BBID	70.Signal_peptides_(MHC)_class_I_molecules	3	1.40E-01	9.90E-01
ILMN_1815261	PDIA4	0.763096431		GOTERM_CC_FAT	MHC class II protein complex	7	1.80E-01	6.50E-01
ILMN_1799062	NFKB2	0.763063543		INTERPRO	MHC class II, alpha chain, N-terminal	4	1.90E-01	9.90E-01
ILMN_1686626	DDX39B	0.762974327		INTERPRO	MHC class I, alpha chain, alpha1 and alpha2	6	2.50E-01	1.00E+00
ILMN_2408400	NSUN5	0.762875397		INTERPRO	MHC class I-like antigen recognition	6	2.70E-01	1.00E+00
ILMN_1806937	BABAM1	0.762820219		GOTERM_CC_FAT	MHC class I protein complex	6	3.20E-01	8.00E-01
ILMN_1667893	TNS3	0.762800879		UP_SEQ_FEATURE	region of interest:Beta-2	3	4.40E-01	1.00E+00
ILMN_1743655	TMED9	0.762756591		UP_SEQ_FEATURE	region of interest:Beta-1	3	4.40E-01	1.00E+00
ILMN_1683415	CAMK2D	0.762638161		INTERPRO	MHC class II, beta chain, N-terminal	3	6.50E-01	1.00E+00
ILMN_1761159	ESYT1	0.762562585	**Annotation Cluster 48**	**Enrichment Score: 1.7**		**Count**	**P_Value**	**Benjamini**
ILMN_2315979	LBH	0.76207024		UP_SEQ_FEATURE	domain:SAP	8	1.60E-02	9.40E-01
ILMN_1688749	RPS2	0.761808173		INTERPRO	DNA-binding SAP	8	2.00E-02	8.00E-01
ILMN_1674236	HSPB1	0.76179783		SMART	SAP	8	2.50E-02	6.00E-01
ILMN_1720287	E4F1	0.761696832	**Annotation Cluster 49**	**Enrichment Score: 1.7**		**Count**	**P_Value**	**Benjamini**
ILMN_1695829	TTYH2	0.76162341		GOTERM_BP_FAT	nuclear export	16	9.60E-03	1.90E-01
ILMN_1709439	CHMP1A	0.761609338		SP_PIR_KEYWORDS	translocation	17	1.40E-02	1.20E-01
ILMN_1701832	RPL19	0.761446189		GOTERM_BP_FAT	nucleic acid transport	22	1.40E-02	2.40E-01
ILMN_1780940	PPP2R5D	0.761372969		GOTERM_BP_FAT	establishment of RNA localization	22	1.40E-02	2.40E-01
ILMN_3270833	NA	0.761344641		GOTERM_BP_FAT	RNA transport	22	1.40E-02	2.40E-01
ILMN_3214389	HLA-DQB1	0.76128883		GOTERM_BP_FAT	mRNA transport	20	1.70E-02	2.70E-01
ILMN_1756445	PMF1	0.761287994		SP_PIR_KEYWORDS	nuclear pore complex	11	1.80E-02	1.50E-01
ILMN_3291098	RPL29	0.761043879		GOTERM_BP_FAT	RNA localization	22	1.90E-02	2.90E-01
ILMN_1684051	WASF2	0.760934372		GOTERM_BP_FAT	nucleobase, nucleoside, nucleotide and nucleic acid transport	24	2.10E-02	3.10E-01
ILMN_1750178	FAM21C	0.760806481		GOTERM_BP_FAT	mRNA export from nucleus	10	2.40E-02	3.30E-01
ILMN_1794740	CD151	0.76078523		SP_PIR_KEYWORDS	mRNA transport	16	2.90E-02	2.00E-01
ILMN_2349138	CDC42SE1	0.760631804		GOTERM_CC_FAT	nuclear pore	18	3.00E-02	2.50E-01
ILMN_1703622	PPIB	0.760487785		GOTERM_BP_FAT	RNA export from nucleus	11	3.70E-02	4.20E-01
ILMN_2085862	SLC15A3	0.76044275		GOTERM_CC_FAT	pore complex	20	4.50E-02	3.10E-01
ILMN_1669456	NME3	0.760377893	**Annotation Cluster 50**	**Enrichment Score: 1.67**		**Count**	**P_Value**	**Benjamini**
ILMN_1807074	MIF	0.760324495		SP_PIR_KEYWORDS	GTPase activation	36	2.70E-04	5.00E-03
ILMN_3281599	RPL3	0.76031587		GOTERM_BP_FAT	regulation of Ras protein signal transduction	42	6.00E-03	1.40E-01
ILMN_1665985	SPDYE7P	0.760107584		GOTERM_MF_FAT	small GTPase regulator activity	49	1.50E-02	3.50E-01
ILMN_2333670	RNASE1	0.759898058		GOTERM_MF_FAT	GTPase regulator activity	68	1.60E-02	3.60E-01
ILMN_2290808	RPL21	0.759883		GOTERM_MF_FAT	nucleoside-triphosphatase regulator activity	69	1.80E-02	3.70E-01
ILMN_1790455	BCAM	0.75980712		GOTERM_BP_FAT	regulation of small GTPase mediated signal transduction	46	2.00E-02	3.00E-01
ILMN_1685625	UCP2	0.75976714		GOTERM_MF_FAT	GTPase activator activity	40	2.20E-02	4.10E-01
ILMN_1773080	OAZ1	0.759708288		GOTERM_MF_FAT	enzyme activator activity	56	3.20E-02	4.90E-01
ILMN_1758823	SMARCB1	0.759572163		GOTERM_BP_FAT	regulation of Rho protein signal transduction	20	5.80E-02	5.40E-01
ILMN_1651878	EVC	0.75945475		SP_PIR_KEYWORDS	guanine-nucleotide releasing factor	19	2.00E-01	6.30E-01
ILMN_1746579	UBE2O	0.759452195		GOTERM_MF_FAT	guanyl-nucleotide exchange factor activity	23	3.10E-01	9.70E-01
ILMN_1778668	TAGLN	0.759167503	**Annotation Cluster 51**	**Enrichment Score: 1.62**		**Count**	**P_Value**	**Benjamini**

ILMN_1676118	RPL23AP7	-0.416834548		BIOCARTA	Thrombin signaling and protease-activated receptors	4	2.80E-01	9.80E-01
ILMN_3308758	MIR1207	-0.416880971		BIOCARTA	Integrin Signaling Pathway	6	3.00E-01	9.90E-01
ILMN_3244592	SNORA68	-0.41689948		BIOCARTA	Signaling of Hepatocyte Growth Factor Receptor	6	3.00E-01	9.90E-01
ILMN_1786984	DCTN3	-0.416938312		BIOCARTA	Agrin in Postsynaptic Differentiation	5	3.30E-01	9.90E-01
ILMN_3308245	MIR524	-0.41698299		BIOCARTA	Angiotensin II mediated activation of JNK Pathway via Pyk2 dependent signaling	5	3.30E-01	9.90E-01
ILMN_2321339	POLR3H	-0.417032617		BIOCARTA	?-arrestins in GPCR Desensitization	3	3.80E-01	9.90E-01
ILMN_1784630	KBTBD11	-0.41703786		BIOCARTA	Bioactive Peptide Induced Signaling Pathway	5	4.10E-01	9.90E-01
ILMN_1664994	MINPP1	-0.417089747		BIOCARTA	Cadmium induces DNA synthesis and proliferation in macrophages	3	4.20E-01	9.90E-01
ILMN_2375032	BEND3	-0.417099143		KEGG_PATHWAY	VEGF signaling pathway	10	4.60E-01	9.50E-01
ILMN_2401701	PCGF6	-0.417109376		BIOCARTA	fMLP induced chemokine gene expression in HMC-1 cells	4	5.20E-01	9.90E-01
ILMN_1675937	ANKRD9	-0.417133456		BIOCARTA	Links between Pyk2 and Map Kinases	4	5.40E-01	9.90E-01
ILMN_1687123	C21orf99	-0.417215758		KEGG_PATHWAY	ErbB signaling pathway	9	7.70E-01	9.70E-01
ILMN_1900795	AF070564	-0.417218275		KEGG_PATHWAY	Fc epsilon RI signaling pathway	6	9.50E-01	9.90E-01
ILMN_2351906	ACPT	-0.417266712	**Annotation Cluster 64**	**Enrichment Score: 0.74**		**Count**	**P_Value**	**Benjamini**
ILMN_1688234	ASS1	-0.417292674		GOTERM_BP_FAT	membrane lipid metabolic process	14	8.40E-02	9.80E-01
ILMN_2238132	TTYH2	-0.417312924		GOTERM_BP_FAT	sphingolipid metabolic process	13	9.60E-02	9.80E-01
ILMN_1694487	LOC645427	-0.417325944		GOTERM_BP_FAT	sphingoid metabolic process	8	1.90E-01	9.80E-01
ILMN_2231478	TSPYL3	-0.417374219		KEGG_PATHWAY	Sphingolipid metabolism	7	2.70E-01	9.50E-01
ILMN_3307972	SKCG-1	-0.417613374		GOTERM_BP_FAT	ceramide metabolic process	7	2.80E-01	9.90E-01
ILMN_1690704	CBY3	-0.417642185		GOTERM_MF_FAT	ceramidase activity	3	2.90E-01	9.90E-01
ILMN_2241775	TROVE2	-0.417645294	**Annotation Cluster 65**	**Enrichment Score: 0.74**		**Count**	**P_Value**	**Benjamini**
ILMN_1768489	TTTY20	-0.417647576		GOTERM_BP_FAT	nucleoside monophosphate metabolic process	11	1.60E-01	9.80E-01
ILMN_1721564	C3orf24	-0.417676562		GOTERM_BP_FAT	cGMP metabolic process	4	1.80E-01	9.80E-01
ILMN_1743104	RBM4B	-0.417694835		GOTERM_BP_FAT	cyclic nucleotide metabolic process	7	2.10E-01	9.90E-01
ILMN_3309339	MIR100	-0.417945079	**Annotation Cluster 66**	**Enrichment Score: 0.74**		**Count**	**P_Value**	**Benjamini**
ILMN_2127722	FAM174A	-0.417950893		GOTERM_MF_FAT	di-, tri-valent inorganic cation transmembrane transporter activity	8	1.20E-01	9.50E-01
ILMN_1758128	CYGB	-0.417967253		GOTERM_BP_FAT	transition metal ion transport	12	1.30E-01	9.70E-01
ILMN_3308465	MIR376A1	-0.417987753		GOTERM_BP_FAT	copper ion transport	4	2.40E-01	9.90E-01
ILMN_1797965	PDP2	-0.418011751		GOTERM_MF_FAT	transition metal ion transmembrane transporter activity	5	3.30E-01	9.90E-01
ILMN_1801467	KCNK4	-0.418029897	**Annotation Cluster 67**	**Enrichment Score: 0.73**		**Count**	**P_Value**	**Benjamini**
ILMN_1796655	SPO11	-0.418046672		SMART	BRK	3	1.10E-01	9.60E-01
ILMN_1789323	LINC00477	-0.418064903		INTERPRO	BRK domain	3	1.30E-01	1.00E+00
ILMN_1770665	HERC4	-0.418333135		INTERPRO	SNF2-related	5	4.40E-01	1.00E+00
ILMN_1727178	C11orf92	-0.418358379	**Annotation Cluster 68**	**Enrichment Score: 0.73**		**Count**	**P_Value**	**Benjamini**
ILMN_1684108	IRX4	-0.418375933		GOTERM_BP_FAT	cysteine metabolic process	3	1.30E-01	9.80E-01
ILMN_3238793	C9orf129	-0.418413663		GOTERM_BP_FAT	serine family amino acid metabolic process	6	1.30E-01	9.80E-01
ILMN_1835210	BM503295	-0.418430631		GOTERM_BP_FAT	sulfur compound biosynthetic process	9	1.50E-01	9.80E-01
ILMN_1727567	OLIG2	-0.418464054		GOTERM_BP_FAT	sulfur amino acid metabolic process	4	4.50E-01	1.00E+00
ILMN_1752214	BC141517	-0.418512538	**Annotation Cluster 69**	**Enrichment Score: 0.73**		**Count**	**P_Value**	**Benjamini**
ILMN_1749108	H1FOO	-0.418536795		SMART	FBOX	11	1.40E-01	9.60E-01
ILMN_3292711	LOC100128437	-0.418579011		INTERPRO	Cyclin-like F-box	11	2.00E-01	1.00E+00
ILMN_1705423	TBC1D29	-0.418718318		UP_SEQ_FEATURE	domain:F-box	11	2.20E-01	1.00E+00
ILMN_2394287	ATP6V0A4	-0.41874763	**Annotation Cluster 70**	**Enrichment Score: 0.72**		**Count**	**P_Value**	**Benjamini**
ILMN_1665996	BCL7A	-0.418761356		GOTERM_BP_FAT	cellular macromolecular complex subunit organization	48	6.90E-02	9.80E-01
ILMN_1879811	BI830246	-0.41877747		GOTERM_BP_FAT	cellular macromolecular complex assembly	43	7.90E-02	9.80E-01
ILMN_1720041	MAGEC1	-0.418887745		GOTERM_BP_FAT	macromolecular complex subunit organization	87	1.00E-01	9.80E-01
ILMN_3250932	SCAND2	-0.418917705		GOTERM_BP_FAT	macromolecular complex assembly	78	2.20E-01	9.90E-01
ILMN_1807579	AX747879	-0.41894642		GOTERM_BP_FAT	protein complex assembly	53	6.10E-01	1.00E+00
ILMN_2412141	TAAR2	-0.418974128		GOTERM_BP_FAT	protein complex biogenesis	53	6.10E-01	1.00E+00
ILMN_1788387	UGGT2	-0.418981141	**Annotation Cluster 71**	**Enrichment Score: 0.72**		**Count**	**P_Value**	**Benjamini**
ILMN_2402303	SSX4B	-0.419005514		SP_PIR_KEYWORDS	cGMP-binding	4	5.90E-02	8.00E-01
ILMN_1672871	CELF5	-0.419008891		UP_SEQ_FEATURE	binding site:cGMP	3	1.20E-01	1.00E+00
ILMN_1789751	MFSD1	-0.419033131		GOTERM_MF_FAT	cyclic nucleotide binding	5	2.30E-01	9.80E-01
ILMN_3310466	MIR572	-0.419052543		GOTERM_MF_FAT	cGMP binding	3	2.50E-01	9.90E-01
ILMN_1683670	SLC10A2	-0.419095638		GOTERM_MF_FAT	GMP binding	3	2.90E-01	9.90E-01
ILMN_3235046	LOC100132354	-0.419139648		SP_PIR_KEYWORDS	cGMP	4	3.80E-01	9.30E-01
ILMN_3237263	LOC728405	-0.419163003	**Annotation Cluster 72**	**Enrichment Score: 0.71**		**Count**	**P_Value**	**Benjamini**
ILMN_1723418	CEL	-0.419231993		UP_SEQ_FEATURE	domain:WW 2	8	2.80E-02	1.00E+00
ILMN_1696699	FAM184A	-0.419334626		UP_SEQ_FEATURE	domain:WW 1	8	2.80E-02	1.00E+00
ILMN_1763187	PAK4	-0.419450804		UP_SEQ_FEATURE	domain:WW 4	3	8.90E-02	1.00E+00
ILMN_2211790	ADAMTS7	-0.419468599		SMART	WW	9	1.50E-01	9.50E-01
ILMN_1730768	LOC400456	-0.419482668		INTERPRO	WW/Rsp5/WWP	9	1.90E-01	1.00E+00
ILMN_1736103	ITPR2	-0.419488284		UP_SEQ_FEATURE	domain:WW 3	3	2.40E-01	1.00E+00
ILMN_1659378	TFAP2D	-0.419502913		SMART	HECTc	5	3.00E-01	9.70E-01
ILMN_3309269	MIR557	-0.419597425		UP_SEQ_FEATURE	domain:HECT	5	3.40E-01	1.00E+00
ILMN_1683377	MDH1B	-0.419617169		INTERPRO	HECT	5	3.40E-01	1.00E+00
ILMN_2116605	COL19A1	-0.419685175		GOTERM_BP_FAT	viral reproductive process	5	9.10E-01	1.00E+00
ILMN_1697959	SLC35B4	-0.419719641		GOTERM_BP_FAT	viral reproduction	5	9.50E-01	1.00E+00
ILMN_1689059	ZNF329	-0.419720233	**Annotation Cluster 73**	**Enrichment Score: 0.71**		**Count**	**P_Value**	**Benjamini**
ILMN_1742328	IFNA14	-0.419720608		GOTERM_MF_FAT	inorganic cation transmembrane transporter activity	25	3.10E-02	8.40E-01
ILMN_1667753	PPP1R1C	-0.419810248		GOTERM_BP_FAT	ATP biosynthetic process	16	4.70E-02	9.80E-01
ILMN_1800989	HTR6	-0.419831006		GOTERM_BP_FAT	purine nucleoside triphosphate biosynthetic process	17	5.70E-02	9.80E-01
ILMN_1726391	MRPL39	-0.419864186		UP_SEQ_FEATURE	metal ion-binding site:Magnesium	19	5.90E-02	1.00E+00
ILMN_1665585	LOC100287166	-0.419965309		GOTERM_BP_FAT	nucleoside triphosphate biosynthetic process	17	7.10E-02	9.80E-01
ILMN_1759631	SERPINA4	-0.420052556		INTERPRO	ATPase, P-type phosphorylation site	8	8.10E-02	1.00E+00
ILMN_3237520	C6orf127	-0.420089566		INTERPRO	ATPase, P-type, ATPase-associated region	8	8.10E-02	1.00E+00
ILMN_1750062	PPARGC1A	-0.420099403		INTERPRO	ATPase, P-type, K/Mg/Cd/Cu/Zn/Na/Ca/Na/H-transporter	8	8.10E-02	1.00E+00
ILMN_1730504	AGPAT4	-0.420109525		GOTERM_MF_FAT	cation-transporting ATPase activity	8	8.30E-02	9.20E-01
ILMN_1691911	CDON	-0.420152051		GOTERM_BP_FAT	ATP metabolic process	17	8.70E-02	9.80E-01
ILMN_1906437	LOC100240735	-0.420360117		GOTERM_BP_FAT	purine ribonucleoside triphosphate biosynthetic process	16	9.20E-02	9.80E-01
ILMN_1691243	NA	-0.420473688		GOTERM_MF_FAT	ATPase activity, coupled to transmembrane movement of ions	13	9.30E-02	9.20E-01
ILMN_2415439	NAE1	-0.420525952		GOTERM_BP_FAT	nucleoside triphosphate metabolic process	20	9.80E-02	9.80E-01
ILMN_2229464	LRRC37A2	-0.420607237		GOTERM_BP_FAT	ribonucleoside triphosphate biosynthetic process	16	9.90E-02	9.80E-01
ILMN_1894780	H05469	-0.420641242		GOTERM_BP_FAT	ribonucleotide biosynthetic process	19	1.00E-01	9.80E-01
ILMN_1811272	AF385432	-0.420694654		GOTERM_CC_FAT	proton-transporting two-sector ATPase complex	9	1.00E-01	9.30E-01
ILMN_1762466	BBS4	-0.420729147		UP_SEQ_FEATURE	active site:4-aspartylphosphate intermediate	8	1.10E-01	1.00E+00
ILMN_1712075	KIAA0353	-0.42085462		INTERPRO	Haloacid dehalogenase-like hydrolase	8	1.10E-01	1.00E+00
ILMN_1718061	TMCO7	-0.420877648		GOTERM_MF_FAT	di-, tri-valent inorganic cation transmembrane transporter activity	8	1.20E-01	9.50E-01

ILMN_1761068	DKFZp434K1323	0.759113489		GOTERM_BP_FAT	angiogenesis	31	1.00E-02	2.00E-01
ILMN_1798224	KDM5C	0.758982766		GOTERM_BP_FAT	blood vessel morphogenesis	39	2.70E-02	3.60E-01
ILMN_1787509	PRIC285	0.758855132		GOTERM_BP_FAT	blood vessel development	44	3.00E-02	3.80E-01
ILMN_2059549	SYK	0.758671164		GOTERM_BP_FAT	vasculature development	44	4.20E-02	4.50E-01
ILMN_3248649	MYO15B	0.758428679	**Annotation Cluster 52**	**Enrichment Score: 1.61**		**Count**	**P_Value**	**Benjamini**
ILMN_1787844	C19orf10	0.758341435		GOTERM_MF_FAT	SH3 domain binding	24	2.00E-03	1.20E-01
ILMN_1756992	MUC1	0.758300389		SP_PIR_KEYWORDS	sh3-binding	13	5.80E-02	3.20E-01
ILMN_2349696	CNIH2	0.758288412		UP_SEQ_FEATURE	short sequence motif:SH3-binding	11	1.20E-01	1.00E+00
ILMN_1733799	FAM195B	0.758241702	**Annotation Cluster 53**	**Enrichment Score: 1.61**		**Count**	**P_Value**	**Benjamini**
ILMN_3241446	ODF3B	0.758165545		UP_SEQ_FEATURE	domain:BAR	7	1.20E-02	9.10E-01
ILMN_2306189	MAGED1	0.757975406		INTERPRO	BAR	6	3.20E-02	9.10E-01
ILMN_1711909	EDEM2	0.757927036		SMART	BAR	6	3.80E-02	6.80E-01
ILMN_1804530	ARPC1B	0.757887861	**Annotation Cluster 54**	**Enrichment Score: 1.61**		**Count**	**P_Value**	**Benjamini**
ILMN_1796755	ITGB5	0.757816349		INTERPRO	Ets	10	7.50E-03	5.50E-01
ILMN_1815023	PIM1	0.757678386		SMART	ETS	10	1.00E-02	4.00E-01
ILMN_2340131	MAPK10	0.757009895		UP_SEQ_FEATURE	DNA-binding region:ETS	9	1.20E-02	9.10E-01
ILMN_1768973	HIST2H2AC	0.757009777		INTERPRO	Winged helix repressor DNA-binding	26	4.10E-01	1.00E+00
ILMN_1712755	LRRC41	0.757003905	**Annotation Cluster 55**	**Enrichment Score: 1.57**		**Count**	**P_Value**	**Benjamini**
ILMN_1800317	WNT5A	0.756873715		GOTERM_MF_FAT	intramolecular oxidoreductase activity	13	2.10E-03	1.20E-01
ILMN_3246766	NPIPL3	0.75638424		UP_SEQ_FEATURE	domain:Thioredoxin 1	6	2.10E-03	5.60E-01
ILMN_1651378	AUP1	0.756316929		UP_SEQ_FEATURE	domain:Thioredoxin 2	6	2.10E-03	5.60E-01
ILMN_1812403	BCAP31	0.755498888		INTERPRO	Disulphide isomerase	5	3.10E-03	3.70E-01
ILMN_1724990	C3orf75	0.755437233		INTERPRO	Thioredoxin-like	12	3.70E-03	4.10E-01
ILMN_1810467	PPP2R1A	0.755279821		GOTERM_MF_FAT	intramolecular oxidoreductase activity, interconverting keto- and enol-groups	6	5.00E-03	1.80E-01
ILMN_2347234	PRMT1	0.755278681		GOTERM_MF_FAT	intramolecular oxidoreductase activity, transposing S-S bonds	5	2.00E-02	3.80E-01
ILMN_1802706	IDH3G	0.755274672		GOTERM_MF_FAT	protein disulfide isomerase activity	5	2.00E-02	3.80E-01
ILMN_1766222	LARP4B	0.75493525		INTERPRO	Thioredoxin-like subdomain	5	2.80E-02	8.80E-01
ILMN_1721977	NAA10	0.754893092		INTERPRO	Thioredoxin fold	20	4.70E-02	9.20E-01
ILMN_1776678	GIMAP7	0.754823661		PIR_SUPERFAMILY	PIRSF001487:protein disulfide-isomerase	4	5.70E-02	1.00E+00
ILMN_1782292	LAMP1	0.754713332		SP_PIR_KEYWORDS	Redox-active center	10	5.90E-02	3.20E-01
ILMN_1804444	PDIA2	0.754706698		GOTERM_BP_FAT	cell redox homeostasis	14	6.50E-02	5.70E-01
ILMN_2198893	MAP2K2	0.754674051		UP_SEQ_FEATURE	site:Lowers pKa of C-terminal Cys of first active site	3	7.40E-02	1.00E+00
ILMN_2114422	NOD1	0.754510983		UP_SEQ_FEATURE	site:Lowers pKa of C-terminal Cys of second active site	3	7.40E-02	1.00E+00
ILMN_1672650	PKM2	0.754413707		INTERPRO	Protein disulphide isomerase	3	8.00E-02	9.50E-01
ILMN_1806017	PSME1	0.754264268		INTERPRO	Thioredoxin domain	7	1.20E-01	9.70E-01
ILMN_1681679	TSPO	0.754116091		UP_SEQ_FEATURE	site:Contributes to redox potential value	3	2.00E-01	1.00E+00
ILMN_1689004	TNFRSF12A	0.754010636		INTERPRO	Thioredoxin, conserved site	6	2.20E-01	1.00E+00
ILMN_2399392	SIL1	0.75399574		SP_PIR_KEYWORDS	redox-active disulfide	3	2.50E-01	6.90E-01
ILMN_1775522	MAGED1	0.753701943	**Annotation Cluster 56**	**Enrichment Score: 1.53**		**Count**	**P_Value**	**Benjamini**
ILMN_1663080	LFNG	0.753468439		INTERPRO	Ribosomal protein L7Ae/L30e/S12e/Gadd45	6	7.60E-03	5.40E-01
ILMN_2206746	BGN	0.753434943		INTERPRO	Ribosomal protein L7Ae conserved site	3	4.40E-02	9.10E-01
ILMN_1677484	SNAPC4	0.753429177		INTERPRO	Ribosomal protein L7A/RS6 family	3	4.40E-02	9.10E-01
ILMN_1708881	RAB20	0.753419869		PIR_SUPERFAMILY	PIRSF002165:ribosomal protein, L7Ab/L7Aa/L7Ae/L8e types/H/ACA ribonucleoprotein complex, NHP2 subunit	3	5.00E-02	1.00E+00
ILMN_1761844	ZCCHC17	0.753381459	**Annotation Cluster 57**	**Enrichment Score: 1.5**		**Count**	**P_Value**	**Benjamini**
ILMN_1771862	TXNDC11	0.75318273		UP_SEQ_FEATURE	zinc finger region:C4-type	18	2.50E-03	5.70E-01
ILMN_1659771	RPL13AP3	0.753133201		GOTERM_BP_FAT	regulation of ARF protein signal transduction	13	9.70E-03	1.90E-01
ILMN_2410772	KEAP1	0.753047726		UP_SEQ_FEATURE	domain:Arf-GAP	9	1.50E-02	9.40E-01
ILMN_2358914	SLC35C2	0.752972172		INTERPRO	Arf GTPase activating protein	9	1.90E-02	8.00E-01
ILMN_1730670	FSTL3	0.752941615		GOTERM_BP_FAT	regulation of ARF GTPase activity	9	2.40E-02	3.30E-01
ILMN_1688959	CD27	0.752626113		SMART	ArfGap	9	2.50E-02	6.40E-01
ILMN_1772487	SUGP2	0.752475521		GOTERM_MF_FAT	ARF GTPase activator activity	9	2.60E-02	4.50E-01
ILMN_1733811	JUP	0.752368762		GOTERM_BP_FAT	regulation of GTPase activity	22	1.30E-01	7.50E-01
ILMN_3209220	NA	0.752230086		GOTERM_BP_FAT	regulation of Ras GTPase activity	19	1.40E-01	7.70E-01
ILMN_3242900	HIST2H2AA4	0.7521808		GOTERM_BP_FAT	regulation of hydrolase activity	46	4.90E-01	9.90E-01
ILMN_1778144	SLC48A1	0.752087304	**Annotation Cluster 58**	**Enrichment Score: 1.48**		**Count**	**P_Value**	**Benjamini**
ILMN_1886655	TCRVB	0.75191266		GOTERM_BP_FAT	positive regulation of adaptive immune response	12	1.40E-03	4.90E-02
ILMN_1724059	GAS2L1	0.751852332		GOTERM_BP_FAT	positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	11	3.80E-03	1.00E-01
ILMN_1796336	MAP1S	0.7517574		GOTERM_BP_FAT	positive regulation of T cell mediated immunity	7	9.00E-03	1.90E-01
ILMN_1751871	STK11	0.751726854		GOTERM_BP_FAT	positive regulation of immune effector process	13	9.70E-03	1.90E-01
ILMN_1687867	KRT8	0.751721383		GOTERM_BP_FAT	regulation of immune effector process	23	1.10E-02	2.10E-01
ILMN_1751034	ITPRIPL2	0.751612733		GOTERM_BP_FAT	regulation of adaptive immune response	15	1.20E-02	2.20E-01
ILMN_1677505	CCL21	0.751533959		GOTERM_BP_FAT	regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	14	2.40E-02	3.30E-01
ILMN_1751368	HNRNPD	0.751460303		GOTERM_BP_FAT	regulation of leukocyte mediated immunity	15	2.50E-02	3.40E-01
ILMN_1726434	UNC45A	0.751393254		GOTERM_BP_FAT	positive regulation of leukocyte mediated immunity	10	2.80E-02	3.70E-01
ILMN_1765446	EMP3	0.751337857		GOTERM_BP_FAT	positive regulation of lymphocyte mediated immunity	10	2.80E-02	3.70E-01
ILMN_1814194	TCF4	0.751320118		GOTERM_BP_FAT	regulation of lymphocyte mediated immunity	13	4.60E-02	4.80E-01
ILMN_1760143	ADRM1	0.751127854		GOTERM_BP_FAT	regulation of T cell mediated immunity	7	4.90E-02	4.90E-01
ILMN_1654563	EFNB1	0.750694334		GOTERM_BP_FAT	positive regulation of defense response	14	1.60E-01	8.10E-01
ILMN_1691942	CCNI	0.750507801		GOTERM_BP_FAT	regulation of production of molecular mediator of immune response	9	1.60E-01	8.20E-01
ILMN_1789909	TBC1D9B	0.750358301		GOTERM_BP_FAT	positive regulation of B cell mediated immunity	4	1.70E-01	8.20E-01
ILMN_2324672	USF2	0.750054682		GOTERM_BP_FAT	positive regulation of immunoglobulin mediated immune response	4	1.70E-01	8.20E-01
ILMN_1744113	SCNM1	0.750003388		GOTERM_BP_FAT	regulation of immunoglobulin mediated immune response	6	2.00E-01	8.60E-01
ILMN_1755115	RPL23	0.749719903		GOTERM_BP_FAT	regulation of B cell mediated immunity	6	2.00E-01	8.60E-01
ILMN_1716876	MED27	0.749601114	**Annotation Cluster 59**	**Enrichment Score: 1.48**		**Count**	**P_Value**	**Benjamini**
ILMN_1707810	RPS5	0.749530339		GOTERM_MF_FAT	identical protein binding	107	3.20E-03	1.40E-01
ILMN_1658283	RPL17	0.749480923		GOTERM_MF_FAT	protein dimerization activity	82	8.10E-02	7.40E-01
ILMN_1741398	TTI1	0.749391475		GOTERM_MF_FAT	protein homodimerization activity	51	1.40E-01	8.60E-01
ILMN_1773849	ATP6V0C	0.749354628	**Annotation Cluster 60**	**Enrichment Score: 1.48**		**Count**	**P_Value**	**Benjamini**
ILMN_1663113	TTLL12	0.74928163		UP_SEQ_FEATURE	domain:Saposin B-type	4	1.50E-02	9.40E-01
ILMN_1752269	ACSS1	0.749241449		INTERPRO	Saposin B	4	4.70E-02	9.20E-01

ILMN_1859744	AI939525	-0.420896686		GOTERM_BP_FAT	purine nucleotide metabolic process	26	1.30E-01	9.70E-01
ILMN_1768922	ZNF790	-0.420930585		GOTERM_BP_FAT	nucleotide biosynthetic process	26	1.30E-01	9.70E-01
ILMN_3184595	NA	-0.420965069		GOTERM_MF_FAT	calcium ion transmembrane transporter activity	4	1.30E-01	9.50E-01
ILMN_1663118	RASGEF1C	-0.421011499		GOTERM_MF_FAT	hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances	17	1.30E-01	9.60E-01
ILMN_1695108	RSPO2	-0.421060597		GOTERM_BP_FAT	ribonucleotide metabolic process	21	1.50E-01	9.80E-01
ILMN_1720274	C2orf53	-0.421112694		GOTERM_BP_FAT	purine nucleoside triphosphate metabolic process	18	1.50E-01	9.80E-01
ILMN_1672332	LOC646862	-0.42116657		GOTERM_BP_FAT	purine nucleotide biosynthetic process	21	1.50E-01	9.80E-01
ILMN_3187758	SELK	-0.421219375		GOTERM_MF_FAT	P-P-bond-hydrolysis-driven transmembrane transporter activity	18	1.50E-01	9.70E-01
ILMN_1681598	PCDHGC3	-0.421302283		GOTERM_MF_FAT	primary active transmembrane transporter activity	18	1.50E-01	9.70E-01
ILMN_1757281	GPRIN1	-0.421305186		GOTERM_CC_FAT	proton-transporting V-type ATPase complex	5	1.60E-01	9.30E-01
ILMN_1684730	POM121L2	-0.421363856		GOTERM_BP_FAT	nucleobase, nucleoside and nucleotide biosynthetic process	26	1.70E-01	9.80E-01
ILMN_3284078	KRTAP16-1	-0.421364059		GOTERM_BP_FAT	nucleobase, nucleoside, nucleotide and nucleic acid biosynthetic process	26	1.70E-01	9.80E-01
ILMN_2073969	ABHD13	-0.421375678		GOTERM_BP_FAT	purine ribonucleotide biosynthetic process	17	1.70E-01	9.80E-01
ILMN_1655117	WDR19	-0.421396867		GOTERM_BP_FAT	purine ribonucleoside triphosphate metabolic process	17	1.70E-01	9.80E-01
ILMN_2292875	EFTUD1	-0.421516702		GOTERM_BP_FAT	nitrogen compound biosynthetic process	41	1.80E-01	9.80E-01
ILMN_2351272	DZIP1	-0.421518591		INTERPRO	ATPase, P-type, phospholipid-translocating, flippase	4	1.80E-01	1.00E+00
ILMN_1669208	TSPO2	-0.421558258		GOTERM_BP_FAT	ribonucleoside triphosphate metabolic process	17	1.80E-01	9.80E-01
ILMN_3186439	NA	-0.421562546		GOTERM_MF_FAT	ATPase activity, coupled to transmembrane movement of substances	16	1.90E-01	9.80E-01
ILMN_1696407	SRSF2	-0.421579849		GOTERM_MF_FAT	phospholipid transporter activity	6	1.90E-01	9.80E-01
ILMN_1750295	ACCN5	-0.421635823		GOTERM_MF_FAT	ATPase activity, coupled to movement of substances	16	1.90E-01	9.80E-01
ILMN_1671355	SLC7A5P1	-0.421637868		GOTERM_MF_FAT	ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism	9	2.00E-01	9.80E-01
ILMN_1705177	DNAH14	-0.421685041		GOTERM_BP_FAT	purine ribonucleotide metabolic process	19	2.10E-01	9.90E-01
ILMN_1900154	BU536494	-0.421703168		GOTERM_MF_FAT	phospholipid-translocating ATPase activity	4	2.10E-01	9.80E-01
ILMN_1832920	LOC115110	-0.421741186		GOTERM_MF_FAT	aminophospholipid transporter activity	4	2.10E-01	9.80E-01
ILMN_3305933	LOC730668	-0.421755043		GOTERM_MF_FAT	monovalent inorganic cation transmembrane transporter activity	15	2.20E-01	9.80E-01
ILMN_3274006	BC153822	-0.421773219		GOTERM_BP_FAT	hydrogen transport	10	2.20E-01	9.90E-01
ILMN_1713892	C4orf34	-0.421782949		GOTERM_MF_FAT	lipid transporter activity	10	2.30E-01	9.80E-01
ILMN_1893367	BX094716	-0.421802516		SP_PIR_KEYWORDS	Hydrogen ion transport	8	2.30E-01	9.00E-01
ILMN_3308210	MIR195	-0.421824797		GOTERM_BP_FAT	ATP synthesis coupled proton transport	7	2.50E-01	9.90E-01
ILMN_1691076	TEX11	-0.421833839		GOTERM_BP_FAT	energy coupled proton transport, down electrochemical gradient	7	2.50E-01	9.90E-01
ILMN_1739045	RWDD4	-0.421861943		GOTERM_MF_FAT	calcium-transporting ATPase activity	3	2.50E-01	9.90E-01
ILMN_1726603	ATP5I	-0.421882992		GOTERM_CC_FAT	proton-transporting V-type ATPase, V1 domain	3	2.50E-01	9.50E-01
ILMN_1743319	PAFAH1B2	-0.421915585		GOTERM_MF_FAT	hydrogen ion transmembrane transporter activity	13	2.50E-01	9.90E-01
ILMN_1722559	NEUROD6	-0.421983046		GOTERM_BP_FAT	ion transmembrane transport	8	2.60E-01	9.90E-01
ILMN_1660440	FAM108B1	-0.422013607		GOTERM_BP_FAT	phospholipid transport	6	2.70E-01	9.90E-01
ILMN_3289764	SP9	-0.422021701		KEGG_PATHWAY	Vibrio cholerae infection	9	2.80E-01	9.40E-01
ILMN_2186482	TICAM2	-0.422054381		GOTERM_CC_FAT	vacuolar proton-transporting V-type ATPase complex	3	2.90E-01	9.60E-01
ILMN_1703894	SLX1A	-0.422156804		GOTERM_MF_FAT	ATPase activity	40	3.10E-01	9.90E-01
ILMN_1679318	ARSJ	-0.42220231		GOTERM_BP_FAT	proton transport	9	3.20E-01	9.90E-01
ILMN_1850240	AW262671	-0.422249302		GOTERM_CC_FAT	mitochondrial proton-transporting ATP synthase complex	4	3.40E-01	9.50E-01
ILMN_1793578	ZFP37	-0.422309081		GOTERM_MF_FAT	ATPase activity, coupled	32	3.80E-01	9.90E-01
ILMN_1774432	DTD1	-0.422310182		GOTERM_CC_FAT	proton-transporting ATP synthase complex	4	4.00E-01	9.60E-01
ILMN_1731181	TEX2	-0.422384271		SP_PIR_KEYWORDS	cf(0)	3	4.00E-01	9.40E-01
ILMN_1749375	TNFAIP8	-0.422386726		GOTERM_MF_FAT	proton-transporting ATPase activity, rotational mechanism	4	4.50E-01	1.00E+00
ILMN_2192694	EIF3M	-0.422432994		INTERPRO	ATPase, P-type cation-transporter, C-terminal	3	4.80E-01	1.00E+00
ILMN_1702889	OR2AK2	-0.422448739		GOTERM_CC_FAT	proton-transporting two-sector ATPase complex, proton-transporting domain	4	4.80E-01	9.70E-01
ILMN_2103133	PDZD11	-0.422459642		GOTERM_CC_FAT	proton-transporting ATP synthase complex, coupling factor F(o)	3	4.90E-01	9.70E-01
ILMN_2412564	NCBP2	-0.422476376		PIR_SUPERFAMILY	PIRSF001297:Na(+)/K(+)-transporting ATPase alpha chain	3	4.90E-01	1.00E+00
ILMN_1762629	ANO9	-0.422531645		GOTERM_MF_FAT	hydrogen ion transporting ATP synthase activity, rotational mechanism	3	5.20E-01	1.00E+00
ILMN_1773650	LRRN3	-0.422551983		INTERPRO	ATPase, P-type cation-transporter, N-terminal	3	5.50E-01	1.00E+00
ILMN_3234513	CCDC72	-0.422560887		GOTERM_CC_FAT	proton-transporting two-sector ATPase complex, catalytic domain	3	5.90E-01	9.70E-01
ILMN_1658083	ABT1	-0.422598472		GOTERM_BP_FAT	lipid transport	15	6.80E-01	1.00E+00
ILMN_1777476	SPDYC	-0.422601802		GOTERM_BP_FAT	lipid localization	16	7.00E-01	1.00E+00
ILMN_1685104	C9orf6	-0.422604869		KEGG_PATHWAY	Epithelial cell signaling in Helicobacter pylori infection	7	7.90E-01	9.70E-01
ILMN_1685413	ALG8	-0.422615704		KEGG_PATHWAY	Oxidative phosphorylation	13	8.00E-01	9.70E-01
ILMN_2210129	PRIM1	-0.422629432		GOTERM_BP_FAT	oxidative phosphorylation	8	9.10E-01	1.00E+00
ILMN_3262321	PATE4	-0.422634123	**Annotation Cluster 74**	**Enrichment Score: 0.7**		**Count**	**P_Value**	**Benjamini**
ILMN_1814327	AGTR1	-0.422688808		GOTERM_MF_FAT	CoA hydrolase activity	5	1.00E-01	9.30E-01
ILMN_1677608	NEUROD4	-0.422700162		GOTERM_MF_FAT	acyl-CoA thioesterase activity	4	1.30E-01	9.50E-01
ILMN_1766678	NKX2-6	-0.422777814		GOTERM_MF_FAT	palmitoyl-CoA hydrolase activity	3	2.10E-01	9.80E-01
ILMN_2046751	PGLYRP3	-0.422825113		SP_PIR_KEYWORDS	serine esterase	4	5.70E-01	9.70E-01
ILMN_1660970	ADAMTS12	-0.422826522	**Annotation Cluster 75**	**Enrichment Score: 0.7**		**Count**	**P_Value**	**Benjamini**
ILMN_3185130	LOC100128770	-0.422834069		UP_SEQ_FEATURE	site:Cleavage; by anthrax lethal factor	3	8.90E-02	1.00E+00
ILMN_1667058	CLU	-0.422855399		BBID	100.MAPK_signaling_cascades	5	9.70E-02	9.90E-01
ILMN_1713315	AMAC1L2	-0.422968903		KEGG_PATHWAY	Fc epsilon RI signaling pathway	6	9.50E-01	9.90E-01
ILMN_2156250	SOCS3	-0.423003588	**Annotation Cluster 76**	**Enrichment Score: 0.69**		**Count**	**P_Value**	**Benjamini**
ILMN_1751389	LOC100288974	-0.423129224		INTERPRO	Adenylate kinase, subfamily	3	3.10E-02	9.90E-01
ILMN_1668270	ZDHHC18	-0.423145952		INTERPRO	Adenylate kinase, zinc-finger lid region	3	3.10E-02	9.90E-01
ILMN_2233099	SSRP1	-0.423168489		PIR_SUPERFAMILY	PIRSF000734:adenylate kinase	3	9.30E-02	1.00E+00
ILMN_1778673	GOLGA7	-0.423298303		GOTERM_MF_FAT	adenylate kinase activity	3	2.10E-01	9.80E-01
ILMN_1781390	FGF17	-0.423437624		INTERPRO	Adenylate kinase	3	2.50E-01	1.00E+00
ILMN_1787658	MTMR7	-0.423600942		UP_SEQ_FEATURE	nucleotide phosphate-binding region:AMP	3	4.00E-01	1.00E+00
ILMN_1754658	CDRT1	-0.423640229		UP_SEQ_FEATURE	binding site:AMP	3	4.00E-01	1.00E+00
ILMN_1770676	CAPRIN1	-0.423673102		GOTERM_MF_FAT	nucleotide kinase activity	4	4.50E-01	1.00E+00
ILMN_1656902	HECTD3	-0.423703093		GOTERM_MF_FAT	phosphotransferase activity, phosphate group as acceptor	5	4.80E-01	1.00E+00
ILMN_2132379	TDGF1	-0.423794741		GOTERM_MF_FAT	nucleobase, nucleoside, nucleotide kinase activity	5	6.90E-01	1.00E+00
ILMN_1662482	LPPR4	-0.423823411	**Annotation Cluster 77**	**Enrichment Score: 0.69**		**Count**	**P_Value**	**Benjamini**
ILMN_1822180	AW188305	-0.42394859		GOTERM_MF_FAT	cofactor transporter activity	5	4.20E-02	8.30E-01
ILMN_1676998	SCN2B	-0.423996991		GOTERM_MF_FAT	vitamin transporter activity	4	1.30E-01	9.50E-01
ILMN_3244779	LOC100286979	-0.424107709		GOTERM_BP_FAT	vitamin transport	4	4.80E-01	1.00E+00

ILMN_1738523	MYD88	0.749143118
ILMN_3188110	C19orf60	0.749113677
ILMN_2219134	RPS15	0.749081538
ILMN_1659762	BTF3	0.748956648
ILMN_1674337	FKBP2	0.748912493
ILMN_1811624	THADA	0.748883475
ILMN_1676765	RPL18A	0.748863715
ILMN_2336902	TRIM6	0.74874964
ILMN_1754145	CAPRIN1	0.748636943
ILMN_1792256	TBX2	0.748422142
ILMN_1695598	RPL18	0.748241343
ILMN_2402272	TCEAL8	0.748072527
ILMN_1732328	RPL22	0.747994322
ILMN_1742167	TUBA1C	0.747880886
ILMN_1679520	AGPAT1	0.747821968
ILMN_1789136	SERF2	0.747787471
ILMN_1690085	STK11IP	0.747659456
ILMN_1699015	H3F3A	0.747575539
ILMN_3202432	RPSA	0.747469134
ILMN_1805161	LZTR1	0.747419021
ILMN_2175912	ITGB2	0.747379246
ILMN_1752197	PDDC1	0.747305129
ILMN_1755658	ABI3	0.747162783
ILMN_1725534	ACTN4	0.747091663
ILMN_3247781	AK097701	0.746960724
ILMN_2051519	RPL37A	0.746839627
ILMN_1702044	CNTROB	0.746622693
ILMN_1732296	ID3	0.746592473
ILMN_1689585	C20orf194	0.746450291
ILMN_2148819	TUBA1A	0.746400147
ILMN_1737344	DDX41	0.74578133
ILMN_1790891	CKAP4	0.745769159
ILMN_1803813	ASTE1	0.745701066
ILMN_3241657	TMEM204	0.745431323
ILMN_1807535	YWHAE	0.745411392
ILMN_1765371	LUC7L	0.745317437
ILMN_1677906	PTMA	0.745313514
ILMN_1681543	RHBDD1	0.745305825
ILMN_1756595	SH3TC1	0.745104216
ILMN_3243297	RPL6	0.745100352
ILMN_1689989	CDC42BPB	0.745035512
ILMN_1730940	KLHDC3	0.744992527
ILMN_1678827	SPDYE7P	0.744941915
ILMN_1683204	GMEB2	0.744705211
ILMN_2261416	CD3D	0.744578995
ILMN_2411076	MATR3	0.744547337
ILMN_2384591	HN1	0.744528533
ILMN_2335398	CECR5	0.744517035
ILMN_2408179	PRRC2A	0.744364107
ILMN_1738347	RNPEP	0.744262065
ILMN_2230624	RPL18	0.744246643
ILMN_2262288	EEF1G	0.744154237
ILMN_1703288	C19orf6	0.744096924
ILMN_1666050	TMUB1	0.743526518
ILMN_1664861	ID1	0.74342345
ILMN_1685631	MAU2	0.743354483
ILMN_1814998	POTEKP	0.743325444
ILMN_2343775	RPL38	0.743226412
ILMN_1698940	RPL15	0.74309253
ILMN_1742521	GRB2	0.743086328
ILMN_1776963	LMAN2	0.743083332
ILMN_2356284	PFDN5	0.743081719
ILMN_3248069	RPL3	0.742726182
ILMN_1724422	SELL	0.742701863
ILMN_1678235	KIAA1267	0.742578781
ILMN_2333440	TM9SF1	0.742534842
ILMN_1758100	GALR3	0.742414912
ILMN_1659744	PRMT1	0.74238718
ILMN_1694778	KRT18	0.742292768
ILMN_1699931	HCST	0.742244256
ILMN_1751530	GADD45GIP1	0.742126611
ILMN_1812392	TMSB10	0.741990104
ILMN_2054019	ISG15	0.741885968
ILMN_2095597	CDH16	0.741683981
ILMN_1809013	MYL6	0.741657101
ILMN_2154671	COX6B1	0.74161683
ILMN_1659095	RPL7A	0.741545594
ILMN_1669281	CLN3	0.741462253
ILMN_3248487	RPL7A	0.741423171
ILMN_1760089	RPS2	0.741379833
ILMN_1728626	WDR5	0.741376304
ILMN_2415011	DCTD	0.741303668
ILMN_1728049	S100A16	0.741253522
ILMN_2316540	MRPL11	0.74122786
ILMN_1738684	NRXN2	0.741223652
ILMN_1724907	NUDT3	0.740878563
ILMN_2096654	COMMD4	0.740786308
ILMN_2280548	FYB	0.740768247
ILMN_1651899	RPL19	0.740625479
ILMN_1663799	RPL32	0.740617837
ILMN_1653797	C6orf62	0.740588198
ILMN_3241136	RNASEK	0.740543971
ILMN_1775327	PKM2	0.740476148
ILMN_1786176	CD37	0.740269633
ILMN_1734184	PLBD2	0.740196157
ILMN_2207539	RPS17	0.740116232
ILMN_2321416	DIAPH1	0.740019288

	SMART	SapB	4	5.30E-02	7.30E-01
Annotation Cluster 61	**Enrichment Score: 1.48**		**Count**	**P_Value**	**Benjamini**
	GOTERM_CC_FAT	membrane-bounded vesicle	95	1.50E-02	1.60E-01
	GOTERM_CC_FAT	vesicle	108	2.60E-02	2.40E-01
	GOTERM_CC_FAT	cytoplasmic membrane-bounded vesicle	89	3.80E-02	2.80E-01
	GOTERM_CC_FAT	cytoplasmic vesicle	99	8.30E-02	4.60E-01
Annotation Cluster 62	**Enrichment Score: 1.47**		**Count**	**P_Value**	**Benjamini**
	GOTERM_CC_FAT	membrane coat	19	1.10E-03	2.20E-02
	GOTERM_CC_FAT	coated membrane	19	1.10E-03	2.20E-02
	GOTERM_CC_FAT	clathrin coat	14	1.10E-03	2.20E-02
	GOTERM_CC_FAT	clathrin adaptor complex	11	3.10E-03	5.30E-02
	GOTERM_CC_FAT	AP-type membrane coat adaptor complex	11	4.20E-03	6.40E-02
	GOTERM_CC_FAT	vesicle coat	11	2.40E-02	2.30E-01
	GOTERM_CC_FAT	Golgi-associated vesicle	12	7.00E-02	4.20E-01
	GOTERM_CC_FAT	Golgi-associated vesicle membrane	8	8.30E-02	4.60E-01
	GOTERM_CC_FAT	clathrin vesicle coat	6	9.90E-02	4.90E-01
	GOTERM_CC_FAT	coated vesicle membrane	15	1.00E-01	5.00E-01
	GOTERM_CC_FAT	vesicle membrane	26	1.50E-01	5.90E-01
	GOTERM_CC_FAT	coated vesicle	27	1.60E-01	6.10E-01
	GOTERM_CC_FAT	cytoplasmic vesicle part	30	2.20E-01	7.00E-01
	GOTERM_CC_FAT	cytoplasmic vesicle membrane	23	2.30E-01	7.00E-01
	GOTERM_CC_FAT	clathrin coated vesicle membrane	10	2.70E-01	7.60E-01
	GOTERM_CC_FAT	clathrin-coated vesicle	20	4.00E-01	8.70E-01
Annotation Cluster 63	**Enrichment Score: 1.46**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	cellular response to stress	106	1.50E-04	9.20E-03
	GOTERM_BP_FAT	DNA metabolic process	82	3.60E-02	4.20E-01
	GOTERM_BP_FAT	response to DNA damage stimulus	60	7.70E-02	6.10E-01
	SP_PIR_KEYWORDS	dna repair	30	1.10E-01	4.70E-01
	GOTERM_BP_FAT	DNA repair	44	1.80E-01	8.40E-01
	SP_PIR_KEYWORDS	DNA damage	30	2.00E-01	6.30E-01
Annotation Cluster 64	**Enrichment Score: 1.45**		**Count**	**P_Value**	**Benjamini**
	GOTERM_MF_FAT	ATPase activity	63	1.70E-03	1.10E-01
	GOTERM_MF_FAT	ATPase activity, coupled	53	2.00E-03	1.20E-01
	GOTERM_MF_FAT	ATP-dependent helicase activity	24	2.70E-03	1.30E-01
	GOTERM_MF_FAT	purine NTP-dependent helicase activity	24	2.70E-03	1.30E-01
	SP_PIR_KEYWORDS	helicase	28	4.80E-03	5.60E-02
	GOTERM_MF_FAT	RNA-dependent ATPase activity	8	1.70E-02	3.60E-01
	GOTERM_MF_FAT	helicase activity	28	1.90E-02	3.80E-01
	GOTERM_MF_FAT	RNA helicase activity	9	2.60E-02	4.50E-01
	GOTERM_MF_FAT	ATP-dependent DNA helicase activity	8	3.40E-02	5.00E-01
	GOTERM_MF_FAT	ATP-dependent RNA helicase activity	7	4.40E-02	5.80E-01
	INTERPRO	DEAD-like helicase, N-terminal	21	5.30E-02	9.20E-01
	GOTERM_MF_FAT	DNA helicase activity	10	6.40E-02	6.70E-01
	UP_SEQ_FEATURE	domain:Helicase ATP-binding	20	6.90E-02	1.00E+00
	UP_SEQ_FEATURE	short sequence motif:Q motif	9	7.10E-02	1.00E+00
	INTERPRO	DNA/RNA helicase, DEAD/DEAH box type, N-terminal	13	7.70E-02	9.60E-01
	INTERPRO	DNA/RNA helicase, C-terminal	20	7.70E-02	9.50E-01
	INTERPRO	Helicase, superfamily 1 and 2, ATP-binding	20	7.70E-02	9.50E-01
	SMART	DEXDc	21	7.70E-02	7.70E-01
	UP_SEQ_FEATURE	domain:Helicase C-terminal	19	8.00E-02	1.00E+00
	INTERPRO	RNA helicase, DEAD-box type, Q motif	9	8.70E-02	9.60E-01
	UP_SEQ_FEATURE	short sequence motif:DEAD box	8	9.60E-02	1.00E+00
	SMART	HELICc	20	1.00E-01	8.00E-01
	PIR_SUPERFAMILY	PIRSF001321:ATP-dependent RNA helicase	4	1.80E-01	1.00E+00
	GOTERM_MF_FAT	DNA-dependent ATPase activity	11	1.90E-01	9.00E-01
	INTERPRO	RNA helicase, ATP-dependent, DEAD-box, conserved site	6	3.80E-01	1.00E+00
Annotation Cluster 65	**Enrichment Score: 1.44**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	viral reproductive process	16	1.30E-02	2.30E-01
	GOTERM_BP_FAT	viral infectious cycle	12	2.10E-02	3.10E-01
	GOTERM_BP_FAT	viral reproduction	16	4.20E-02	4.50E-01
	GOTERM_BP_FAT	initiation of viral infection	6	1.50E-01	8.00E-01
Annotation Cluster 66	**Enrichment Score: 1.44**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	lung development	22	1.70E-02	2.70E-01
	GOTERM_BP_FAT	respiratory system development	23	2.40E-02	3.30E-01
	GOTERM_BP_FAT	respiratory tube development	22	2.40E-02	3.30E-01
	GOTERM_BP_FAT	tube development	35	1.80E-01	8.40E-01
Annotation Cluster 67	**Enrichment Score: 1.43**		**Count**	**P_Value**	**Benjamini**
	SP_PIR_KEYWORDS	Isomerase	28	9.10E-04	1.40E-02
	UP_SEQ_FEATURE	domain:PPIase FKBP-type	6	9.80E-03	9.00E-01
	SP_PIR_KEYWORDS	Rotamase	10	2.80E-02	2.00E-01
	INTERPRO	Peptidyl-prolyl cis-trans isomerase, FKBP-type	7	3.20E-02	9.00E-01
	GOTERM_MF_FAT	peptidyl-prolyl cis-trans isomerase activity	10	4.10E-02	5.50E-01
	GOTERM_MF_FAT	cis-trans isomerase activity	10	5.50E-02	6.40E-01
	UP_SEQ_FEATURE	domain:PPIase cyclophilin-type	4	3.70E-01	1.00E+00
	INTERPRO	Peptidyl-prolyl cis-trans isomerase, cyclophilin-type	4	5.00E-01	1.00E+00
Annotation Cluster 68	**Enrichment Score: 1.43**		**Count**	**P_Value**	**Benjamini**
	GOTERM_CC_FAT	NuRD complex	8	6.10E-04	1.40E-02
	GOTERM_CC_FAT	Sin3-type complex	3	2.90E-01	7.80E-01
	GOTERM_CC_FAT	Sin3 complex	3	2.90E-01	7.80E-01
Annotation Cluster 69	**Enrichment Score: 1.42**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	domain:FCH	7	2.70E-02	9.90E-01
	INTERPRO	Fps/Fes/Fer/CIP4 homology	7	4.10E-02	9.10E-01
	SMART	FCH	7	4.90E-02	7.50E-01
Annotation Cluster 70	**Enrichment Score: 1.41**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	negative regulation of response to stimulus	23	1.00E-02	2.00E-01
	GOTERM_BP_FAT	regulation of inflammatory response	18	1.90E-02	2.80E-01
	GOTERM_BP_FAT	negative regulation of defense response	10	4.00E-02	4.40E-01
	GOTERM_BP_FAT	negative regulation of inflammatory response	8	1.00E-01	7.00E-01
	GOTERM_BP_FAT	negative regulation of response to external stimulus	11	1.10E-01	7.20E-01
Annotation Cluster 71	**Enrichment Score: 1.39**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	regulation of cell activation	40	6.00E-04	2.90E-02
	GOTERM_BP_FAT	regulation of lymphocyte activation	35	7.40E-04	3.30E-02
	GOTERM_BP_FAT	regulation of leukocyte activation	38	8.10E-04	3.50E-02
	GOTERM_BP_FAT	regulation of T cell activation	29	1.10E-03	4.30E-02
	GOTERM_BP_FAT	positive regulation of lymphocyte activation	24	3.30E-03	9.00E-02
	GOTERM_BP_FAT	positive regulation of T cell activation	20	3.90E-03	1.00E-01
	GOTERM_BP_FAT	positive regulation of immune system process	47	4.60E-03	1.20E-01

ILMN_1787386	ADAMTS13	-0.424117354
ILMN_1675584	HTRA4	-0.42413881
ILMN_2355463	CYFIP1	-0.424204293
ILMN_1802105	STYK1	-0.424225734
ILMN_1770203	TUBGCP6	-0.42426629
ILMN_1736223	IQCH	-0.424272159
ILMN_1655348	GPR1	-0.424277053
ILMN_2079059	KRTAP4-11	-0.424298365
ILMN_1785574	HTRA2	-0.424354666
ILMN_1767542	THAP10	-0.424389436
ILMN_1693303	TAS2R41	-0.424410513
ILMN_1712999	MGAM	-0.424427509
ILMN_1859160	BX110173	-0.42445343
ILMN_1878007	FUT9	-0.424469342
ILMN_2148193	MPPED2	-0.42458187
ILMN_1801053	C15orf2	-0.424587832
ILMN_2253805	GFRA1	-0.424607489
ILMN_1901646	BX109627	-0.424864169
ILMN_2076658	MRPL1	-0.424946744
ILMN_1803673	LOC113230	-0.424988471
ILMN_1658109	LOC221442	-0.425011137
ILMN_1771233	CHMP4B	-0.425019744
ILMN_1689634	NA	-0.425068716
ILMN_1688346	ZNF800	-0.425144867
ILMN_1664216	NKIRAS1	-0.425154091
ILMN_1711069	YPEL5	-0.425170275
ILMN_2043306	EPB41L5	-0.425258071
ILMN_1672076	WFDC10B	-0.425299372
ILMN_1874770	DA691010	-0.425337705
ILMN_2195060	OR8K5	-0.425405996
ILMN_1871136	DR731427	-0.425447413
ILMN_1737685	CRLS1	-0.425494414
ILMN_1834233	AW138182	-0.425588095
ILMN_1699852	CES4A	-0.425595728
ILMN_2081863	NDUFB4	-0.425625577
ILMN_1760414	AADAC	-0.425643518
ILMN_1736510	FOXN2	-0.4256478
ILMN_1745851	LOC389676	-0.425650127
ILMN_3238823	CXorf49	-0.42571376
ILMN_2222984	NT5C1B	-0.425742622
ILMN_2286800	DNM1L	-0.425744372
ILMN_2089902	NUS1	-0.425745231
ILMN_1712751	HADHA	-0.425747776
ILMN_3244638	DDX3Y	-0.425795046
ILMN_1891885	AI219815	-0.425886906
ILMN_2306565	MTX2	-0.425912992
ILMN_1849267	DB026495	-0.425920313
ILMN_1760955	C1orf100	-0.425923315
ILMN_1754241	C16orf73	-0.425931476
ILMN_1737172	BC035647	-0.425957153
ILMN_1912185	GPC6	-0.426032637
ILMN_2178994	TUBB8	-0.42619813
ILMN_2153547	OR4C15	-0.426243844
ILMN_1700048	BX107512	-0.426253652
ILMN_1894862	AW130728	-0.426269146
ILMN_1806294	RPS6KA3	-0.426313921
ILMN_2376258	SMARCA1	-0.4264026
ILMN_3236671	CLRN2	-0.426436531
ILMN_1760798	RYR2	-0.426640324
ILMN_1769810	ARL6IP5	-0.426696823
ILMN_1703826	UNC5D	-0.426706936
ILMN_1824498	BQ889978	-0.426773639
ILMN_1782881	DLEU7	-0.426873294
ILMN_1718968	MT1E	-0.426940247
ILMN_3309965	MIRLET7F2	-0.427010655
ILMN_2405023	PPP1CB	-0.427108504
ILMN_1722527	LECT1	-0.427112236
ILMN_1903159	PPM1A	-0.427159427
ILMN_1885762	AI140602	-0.427257499
ILMN_3309799	MIR569	-0.427263382
ILMN_1788701	PSIP1	-0.427268444
ILMN_1690971	SSX3	-0.427355744
ILMN_1657977	MSRB2	-0.427383894
ILMN_1809035	SYT7	-0.427498519
ILMN_1866868	AA766245	-0.427506992
ILMN_2224454	TTY7	-0.427510999
ILMN_1741176	CHMP2B	-0.427548572
ILMN_1850372	AI798827	-0.427569658
ILMN_1813581	CNR1	-0.427593645
ILMN_1756311	UFSP2	-0.427619797
ILMN_1852040	AW263556	-0.427624859
ILMN_1657191	KRTAP10-5	-0.427635264
ILMN_1874577	LOC440117	-0.427692003
ILMN_1658825	FAM75C1	-0.427793933
ILMN_2128741	RDH11	-0.427811753
ILMN_1785379	ZNF8	-0.427831674
ILMN_2227790	GRIN2C	-0.427835691
ILMN_3241451	MRAP2	-0.427847201
ILMN_1787196	LYZL1	-0.427889431
ILMN_2052331	MYOC	-0.427896646
ILMN_1812461	WISP2	-0.427907155
ILMN_1769546	RIN2	-0.427933158
ILMN_1891857	RAB2A	-0.428033007
ILMN_1688723	MSX2P1	-0.428064247
ILMN_1887505	BX648650	-0.428068483
ILMN_1676946	AP3M2	-0.428089825
ILMN_1898130	CN291113	-0.42809942

	GOTERM_BP_FAT	cofactor transport	3	6.40E-01	1.00E+00
Annotation Cluster 78	**Enrichment Score: 0.69**		**Count**	**P_Value**	**Benjamini**
	INTERPRO	Nucleosome assembly protein (NAP)	6	2.10E-02	9.90E-01
	GOTERM_BP_FAT	nucleosome organization	16	6.40E-02	9.80E-01
	GOTERM_BP_FAT	chromatin assembly or disassembly	20	7.70E-02	9.80E-01
	GOTERM_BP_FAT	nucleosome assembly	14	1.00E-01	9.80E-01
	GOTERM_BP_FAT	DNA packaging	18	1.10E-01	9.70E-01
	GOTERM_BP_FAT	chromatin assembly	14	1.30E-01	9.70E-01
	GOTERM_BP_FAT	protein-DNA complex assembly	14	1.60E-01	9.80E-01
	SMART	H2A	4	2.90E-01	9.70E-01
	GOTERM_CC_FAT	protein-DNA complex	12	3.20E-01	9.50E-01
	INTERPRO	Histone H2A	4	3.30E-01	1.00E+00
	SP_PIR_KEYWORDS	chromosomal protein	18	3.50E-01	9.30E-01
	GOTERM_CC_FAT	nucleosome	9	3.70E-01	9.50E-01
	SP_PIR_KEYWORDS	nucleosome core	7	3.90E-01	9.30E-01
	INTERPRO	Histone-fold	7	5.20E-01	1.00E+00
	INTERPRO	Histone core	6	5.30E-01	1.00E+00
	KEGG_PATHWAY	Systemic lupus erythematosus	9	8.80E-01	9.80E-01
Annotation Cluster 79	**Enrichment Score: 0.68**		**Count**	**P_Value**	**Benjamini**
	INTERPRO	Guanine nucleotide binding protein (G-protein), alpha subunit	5	8.10E-02	1.00E+00
	PIR_SUPERFAMILY	PIRSF002400:GTP-binding regulatory protein Gs alpha chain	5	8.50E-02	1.00E+00
	SP_PIR_KEYWORDS	signal transduction	7	1.50E-01	8.70E-01
	SP_PIR_KEYWORDS	heterotrimer	6	1.60E-01	8.70E-01
	INTERPRO	G-protein alpha subunit, group I	3	2.00E-01	1.00E+00
	SP_PIR_KEYWORDS	ADP-ribosylation	6	2.60E-01	9.00E-01
	SP_PIR_KEYWORDS	GTP binding	10	2.60E-01	9.00E-01
	SP_PIR_KEYWORDS	myristylation	6	3.90E-01	9.40E-01
	SP_PIR_KEYWORDS	thiolester bond	4	7.40E-01	9.90E-01
Annotation Cluster 80	**Enrichment Score: 0.68**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	domain:DRBM 3	4	9.90E-03	1.00E+00
	GOTERM_BP_FAT	RNA interference, production of siRNA	3	3.10E-02	9.60E-01
	GOTERM_MF_FAT	double-stranded RNA binding	8	5.60E-02	8.70E-01
	UP_SEQ_FEATURE	domain:DRBM 2	4	1.20E-01	1.00E+00
	UP_SEQ_FEATURE	domain:DRBM 1	4	1.20E-01	1.00E+00
	GOTERM_BP_FAT	RNA interference	3	1.30E-01	9.80E-01
	SP_PIR_KEYWORDS	rna-mediated gene silencing	6	1.50E-01	8.60E-01
	SMART	DSRM	5	1.70E-01	9.40E-01
	INTERPRO	Double-stranded RNA binding	5	2.00E-01	1.00E+00
	GOTERM_BP_FAT	gene silencing	9	2.40E-01	9.90E-01
	INTERPRO	Double-stranded RNA-binding-like	4	2.70E-01	1.00E+00
	GOTERM_BP_FAT	posttranscriptional gene silencing by RNA	4	3.90E-01	1.00E+00
	GOTERM_BP_FAT	posttranscriptional gene silencing	4	3.90E-01	1.00E+00
	GOTERM_BP_FAT	dsRNA fragmentation	3	4.10E-01	1.00E+00
	GOTERM_BP_FAT	gene silencing by RNA	5	4.70E-01	1.00E+00
	GOTERM_BP_FAT	gene silencing by miRNA	3	5.50E-01	1.00E+00
	GOTERM_BP_FAT	regulation of gene expression, epigenetic	9	5.80E-01	1.00E+00
	GOTERM_BP_FAT	chromatin silencing	3	5.80E-01	1.00E+00
	GOTERM_BP_FAT	negative regulation of gene expression, epigenetic	3	6.70E-01	1.00E+00
	GOTERM_BP_FAT	response to dsRNA	3	7.60E-01	1.00E+00
Annotation Cluster 81	**Enrichment Score: 0.67**		**Count**	**P_Value**	**Benjamini**
	INTERPRO	Quinone oxidoreductase/zeta-crystallin, conserved site	3	1.60E-01	1.00E+00
	INTERPRO	Alcohol dehydrogenase GroES-like	4	1.80E-01	1.00E+00
	INTERPRO	Alcohol dehydrogenase, zinc-binding	4	2.70E-01	1.00E+00
	INTERPRO	Alcohol dehydrogenase superfamily, zinc-containing	4	2.70E-01	1.00E+00
Annotation Cluster 82	**Enrichment Score: 0.67**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	domain:CS	4	1.80E-01	1.00E+00
	INTERPRO	CS	4	2.40E-01	1.00E+00
	INTERPRO	CS domain	4	2.40E-01	1.00E+00
Annotation Cluster 83	**Enrichment Score: 0.67**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	short sequence motif:GXSXG	3	2.00E-01	1.00E+00
	UP_SEQ_FEATURE	domain:Patatin	3	2.00E-01	1.00E+00
	INTERPRO	Patatin	3	2.50E-01	1.00E+00
Annotation Cluster 84	**Enrichment Score: 0.66**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	cell growth	11	1.10E-01	9.70E-01
	GOTERM_BP_FAT	regulation of cell size	28	1.40E-01	9.80E-01
	GOTERM_BP_FAT	growth	19	6.70E-01	1.00E+00
Annotation Cluster 85	**Enrichment Score: 0.66**		**Count**	**P_Value**	**Benjamini**
	SP_PIR_KEYWORDS	cell junction	53	5.70E-02	8.20E-01
	GOTERM_CC_FAT	cell junction	67	7.90E-02	9.10E-01
	GOTERM_CC_FAT	postsynaptic density	12	1.40E-01	9.20E-01
	SP_PIR_KEYWORDS	synapse	26	3.00E-01	9.20E-01
	GOTERM_CC_FAT	synapse	42	3.40E-01	9.50E-01
	SP_PIR_KEYWORDS	postsynaptic cell membrane	14	3.60E-01	9.30E-01
	GOTERM_CC_FAT	synapse part	28	4.80E-01	9.70E-01
	GOTERM_CC_FAT	postsynaptic membrane	16	4.90E-01	9.70E-01
Annotation Cluster 86	**Enrichment Score: 0.66**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	negative regulation of catalytic activity	37	1.10E-01	9.80E-01
	GOTERM_BP_FAT	negative regulation of MAP kinase activity	7	1.80E-01	9.80E-01
	GOTERM_BP_FAT	negative regulation of protein kinase activity	13	2.10E-01	9.90E-01
	GOTERM_BP_FAT	negative regulation of transferase activity	14	2.10E-01	9.90E-01
	GOTERM_BP_FAT	negative regulation of kinase activity	13	2.40E-01	9.90E-01
	GOTERM_BP_FAT	regulation of protein kinase activity	38	5.10E-01	1.00E+00
Annotation Cluster 87	**Enrichment Score: 0.66**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	lipid biosynthetic process	47	2.30E-02	9.60E-01
	GOTERM_BP_FAT	organophosphate metabolic process	30	5.00E-02	9.80E-01
	GOTERM_BP_FAT	phospholipid metabolic process	28	7.00E-02	9.80E-01
	GOTERM_BP_FAT	glycerolipid biosynthetic process	14	7.70E-02	9.80E-01
	GOTERM_BP_FAT	glycerolipid metabolic process	24	8.90E-02	9.80E-01
	GOTERM_BP_FAT	preassembly of GPI anchor in ER membrane	5	9.80E-02	9.80E-01
	GOTERM_BP_FAT	phospholipid biosynthetic process	16	1.20E-01	9.70E-01
	GOTERM_BP_FAT	glycerophospholipid metabolic process	17	1.80E-01	9.80E-01
	GOTERM_BP_FAT	glycerophospholipid biosynthetic process	10	2.90E-01	9.90E-01
	GOTERM_BP_FAT	phosphoinositide biosynthetic process	6	4.20E-01	1.00E+00
	SP_PIR_KEYWORDS	gpi-anchor biosynthesis	4	4.70E-01	9.50E-01
	GOTERM_BP_FAT	GPI anchor biosynthetic process	5	4.90E-01	1.00E+00
	GOTERM_BP_FAT	protein amino acid lipidation	7	5.00E-01	1.00E+00
	GOTERM_BP_FAT	GPI anchor metabolic process	5	5.20E-01	1.00E+00

ILMN_2321064	BAX	0.739890518
ILMN_1690125	PDLIM7	0.739634415
ILMN_1765523	TOLLIP	0.739566202
ILMN_1652631	GLIPR2	0.739411309
ILMN_2337655	WARS	0.738993733
ILMN_1660869	SERF2-C15ORF63	0.738460636
ILMN_3284584	RPL10	0.738444294
ILMN_1666522	ZDHHC14	0.738322719
ILMN_1801909	IGHMBP2	0.738254491
ILMN_1670841	CPNE1	0.738134936
ILMN_1655126	LOC375133	0.738104634
ILMN_1705302	FCGRT	0.737929733
ILMN_1714622	TNRC6A	0.737815755
ILMN_1710697	BUD31	0.737719804
ILMN_1733045	RAB36	0.737485946
ILMN_2344130	PSMD4	0.737266157
ILMN_1782977	UBA52	0.73716794
ILMN_1793632	TMEM222	0.73713849
ILMN_2339863	VPS28	0.73713121
ILMN_2361427	PMS2P3	0.737126013
ILMN_1712435	NA	0.737115708
ILMN_3245403	RPL17	0.736920197
ILMN_1737586	EIF4H	0.736827318
ILMN_2351795	C18orf1	0.7367946
ILMN_2225887	ATP5EP2	0.736462159
ILMN_2309180	SMARCD3	0.736423232
ILMN_3219558	TUBA1C	0.736323324
ILMN_2389582	HNRNPL	0.736218413
ILMN_1802205	RHOB	0.736057886
ILMN_1671911	MTA1	0.736053868
ILMN_2226955	VOPP1	0.736035768
ILMN_3247452	OST4	0.736020172
ILMN_1733703	GTSE1	0.735948768
ILMN_3247906	RNF114	0.735792395
ILMN_1797530	CHCHD5	0.73573271
ILMN_2112493	DAP	0.735726116
ILMN_2320888	CXCR4	0.735719408
ILMN_1733991	UBL7	0.735629463
ILMN_1658425	DAG1	0.735618369
ILMN_2206716	JTB	0.735598805
ILMN_1742166	GRWD1	0.735534054
ILMN_1699570	TPD52L2	0.735184095
ILMN_1772113	U2AF1	0.735180067
ILMN_1675479	ZNF646	0.735157336
ILMN_1701696	SRP14	0.734987259
ILMN_1697777	TSTA3	0.734888093
ILMN_1802053	ZNF91	0.73472377
ILMN_1713394	RPS16	0.734627919
ILMN_1713402	FAM160A2	0.734529733
ILMN_2083559	KIAA0415	0.734276087
ILMN_1788099	LSM4	0.734200543
ILMN_1740395	RAVER1	0.73409799
ILMN_1738677	PRPF8	0.734073742
ILMN_2143685	CLDN7	0.733952055
ILMN_2384496	ST6GAL1	0.73394705
ILMN_1778132	C2CD2L	0.733831375
ILMN_2169025	JOSD2	0.733799154
ILMN_1756982	CLIC1	0.733788964
ILMN_2075847	ZC3H10	0.733694641
ILMN_2354391	RAB4B-EGLN2	0.733632767
ILMN_2173451	GPI	0.733626254
ILMN_1680626	PDIA6	0.733598848
ILMN_1808202	C19orf22	0.73359855
ILMN_1790951	C19orf50	0.733550828
ILMN_2293131	ARHGEF1	0.733518636
ILMN_2140389	TMEM185A	0.733435005
ILMN_2325234	PQBP1	0.733229163
ILMN_2287888	PSMC4	0.733213151
ILMN_1739794	CD3E	0.733159787
ILMN_1774334	HIGD2A	0.732927988
ILMN_1798083	CHERP	0.732905648
ILMN_1764794	PSMB2	0.732893804
ILMN_1760714	RPS3	0.732831237
ILMN_1713369	RPL13A	0.732680312
ILMN_1756696	USF2	0.732606733
ILMN_2356786	ADD1	0.732451155
ILMN_1696065	SDF4	0.732350935
ILMN_2407589	CTDP1	0.732307437
ILMN_1761138	C9orf142	0.732074295
ILMN_1737935	MACF1	0.731992143
ILMN_1690653	CDK2AP2	0.731766512
ILMN_1659905	FKBP10	0.73163287
ILMN_3202734	RPL17	0.73158821
ILMN_1742432	COBRA1	0.731556516
ILMN_1706273	MOB2	0.731546943
ILMN_1808041	RPL10A	0.731483283
ILMN_1731287	ARFGAP3	0.73135961
ILMN_2137066	ZNF7	0.731315655
ILMN_1753008	REXO1	0.731301258
ILMN_1755234	SSH3	0.731294931
ILMN_1652594	ACTR5	0.731041723
ILMN_1663444	LIN7B	0.730886503
ILMN_1754660	ZCCHC24	0.730869661
ILMN_1797362	LIMK1	0.730828199
ILMN_2376205	LTB	0.730798793
ILMN_1761797	CSTB	0.730770844

	GOTERM_BP_FAT	positive regulation of leukocyte activation	25	5.10E-03	1.20E-01
	GOTERM_BP_FAT	positive regulation of cell activation	25	9.20E-03	1.90E-01
	GOTERM_BP_FAT	positive regulation of alpha-beta T cell activation	9	1.60E-02	2.60E-01
	GOTERM_BP_FAT	regulation of T cell differentiation	13	3.10E-02	3.90E-01
	GOTERM_BP_FAT	regulation of lymphocyte differentiation	15	3.30E-02	4.00E-01
	GOTERM_BP_FAT	positive regulation of lymphocyte differentiation	10	3.40E-02	4.00E-01
	GOTERM_BP_FAT	regulation of alpha-beta T cell activation	10	4.00E-02	4.40E-01
	GOTERM_BP_FAT	regulation of lymphocyte proliferation	18	4.10E-02	4.50E-01
	GOTERM_BP_FAT	regulation of leukocyte proliferation	18	4.60E-02	4.80E-01
	GOTERM_BP_FAT	regulation of mononuclear cell proliferation	18	4.60E-02	4.80E-01
	GOTERM_BP_FAT	positive regulation of T cell differentiation	9	5.20E-02	5.00E-01
	GOTERM_BP_FAT	positive regulation of lymphocyte proliferation	13	5.20E-02	5.00E-01
	GOTERM_BP_FAT	positive regulation of leukocyte proliferation	13	5.80E-02	5.40E-01
	GOTERM_BP_FAT	positive regulation of mononuclear cell proliferation	13	5.80E-02	5.40E-01
	GOTERM_BP_FAT	regulation of T cell proliferation	13	1.10E-01	7.10E-01
	GOTERM_BP_FAT	positive regulation of alpha-beta T cell differentiation	6	1.10E-01	7.20E-01
	GOTERM_BP_FAT	regulation of B cell activation	11	1.30E-01	7.50E-01
	GOTERM_BP_FAT	positive regulation of T cell proliferation	9	1.30E-01	7.60E-01
	GOTERM_BP_FAT	positive regulation of B cell activation	8	1.40E-01	7.70E-01
	GOTERM_BP_FAT	regulation of B cell proliferation	7	1.50E-01	8.00E-01
	GOTERM_BP_FAT	regulation of production of molecular mediator of immune response	9	1.60E-01	8.20E-01
	GOTERM_BP_FAT	regulation of immunoglobulin mediated immune response	6	2.00E-01	8.60E-01
	GOTERM_BP_FAT	regulation of B cell mediated immunity	6	2.00E-01	8.60E-01
	GOTERM_BP_FAT	regulation of alpha-beta T cell differentiation	6	2.30E-01	8.90E-01
	GOTERM_BP_FAT	regulation of immunoglobulin production	6	2.50E-01	9.10E-01
	GOTERM_BP_FAT	positive regulation of B cell proliferation	5	2.70E-01	9.20E-01
	GOTERM_BP_FAT	positive regulation of isotype switching	3	3.40E-01	9.50E-01
	GOTERM_BP_FAT	positive regulation of DNA recombination	3	3.40E-01	9.50E-01
	GOTERM_BP_FAT	regulation of isotype switching	3	5.30E-01	9.90E-01
	GOTERM_BP_FAT	regulation of DNA recombination	3	8.80E-01	1.00E+00
Annotation Cluster 72	**Enrichment Score: 1.38**		**Count**	**P_Value**	**Benjamini**
	GOTERM_CC_FAT	cytoskeleton	214	9.90E-03	1.30E-01
	GOTERM_CC_FAT	microtubule cytoskeleton	87	6.10E-02	3.80E-01
	GOTERM_CC_FAT	cytoskeletal part	141	1.20E-01	5.30E-01
Annotation Cluster 73	**Enrichment Score: 1.38**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	regulation of lymphocyte activation	35	7.40E-04	3.30E-02
	GOTERM_BP_FAT	regulation of T cell activation	29	1.10E-03	4.30E-02
	GOTERM_BP_FAT	negative regulation of immune system process	22	2.10E-03	6.50E-02
	GOTERM_BP_FAT	negative regulation of cell activation	15	2.50E-02	3.40E-01
	GOTERM_BP_FAT	regulation of lymphocyte proliferation	18	4.10E-02	4.50E-01
	GOTERM_BP_FAT	negative regulation of T cell activation	11	4.30E-02	4.60E-01
	GOTERM_BP_FAT	regulation of leukocyte proliferation	18	4.60E-02	4.80E-01
	GOTERM_BP_FAT	regulation of mononuclear cell proliferation	18	4.60E-02	4.80E-01
	GOTERM_BP_FAT	negative regulation of lymphocyte activation	13	4.60E-02	4.80E-01
	GOTERM_BP_FAT	negative regulation of leukocyte activation	13	6.50E-02	5.70E-01
	GOTERM_BP_FAT	regulation of T cell proliferation	13	1.10E-01	7.10E-01
	GOTERM_BP_FAT	negative regulation of leukocyte proliferation	7	2.40E-01	9.00E-01
	GOTERM_BP_FAT	negative regulation of lymphocyte proliferation	7	2.40E-01	9.00E-01
	GOTERM_BP_FAT	negative regulation of mononuclear cell proliferation	7	2.40E-01	9.00E-01
	GOTERM_BP_FAT	negative regulation of T cell proliferation	6	2.80E-01	9.30E-01
	GOTERM_BP_FAT	regulation of activated T cell proliferation	3	4.80E-01	9.90E-01
Annotation Cluster 74	**Enrichment Score: 1.37**		**Count**	**P_Value**	**Benjamini**
	BBID	73.Integrins_and_other_cell-surface_receptors	8	1.70E-02	7.50E-01
	PIR_SUPERFAMILY	PIRSF002419:CD9 antigen	7	2.60E-02	9.90E-01
	INTERPRO	Tetraspanin, conserved site	8	3.80E-02	9.20E-01
	INTERPRO	Tetraspanin, subgroup	8	7.50E-02	9.60E-01
	INTERPRO	Tetraspanin	8	1.10E-01	9.70E-01
Annotation Cluster 75	**Enrichment Score: 1.36**		**Count**	**P_Value**	**Benjamini**
	GOTERM_CC_FAT	clathrin coat	14	1.10E-03	2.20E-02
	GOTERM_CC_FAT	clathrin adaptor complex	11	3.10E-03	5.30E-02
	GOTERM_CC_FAT	AP-type membrane coat adaptor complex	11	4.20E-03	6.40E-02
	INTERPRO	Clathrin adaptor, mu subunit, C-terminal	5	4.00E-02	9.20E-01
	INTERPRO	Clathrin adaptor, mu subunit, conserved site	4	4.70E-02	9.20E-01
	INTERPRO	Clathrin adaptor, alpha/beta/gamma-adaptin, appendage, Ig-like subdomain	4	9.40E-02	9.60E-01
	SMART	Alpha_adaptinC2	4	1.00E-01	7.90E-01
	UP_SEQ_FEATURE	domain:MHD	4	1.10E-01	1.00E+00
	INTERPRO	Clathrin adaptor, mu subunit	3	1.70E-01	9.90E-01
	PIR_SUPERFAMILY	PIRSF005992:Clathrin_mu	3	1.90E-01	1.00E+00
	PIR_SUPERFAMILY	PIRSF005992:adaptor protein complex, mu subunit	3	1.90E-01	1.00E+00
	INTERPRO	Clathrin/coatomer adaptor, adaptin-like, N-terminal	4	2.60E-01	1.00E+00
Annotation Cluster 76	**Enrichment Score: 1.32**		**Count**	**P_Value**	**Benjamini**
	GOTERM_CC_FAT	microtubule organizing center	45	3.80E-02	2.80E-01
	GOTERM_CC_FAT	centrosome	40	4.80E-02	3.30E-01
	GOTERM_CC_FAT	microtubule cytoskeleton	87	6.10E-02	3.80E-01
Annotation Cluster 77	**Enrichment Score: 1.3**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	domain:BRCT	6	2.00E-02	9.70E-01
	INTERPRO	BRCT	7	7.30E-02	9.60E-01
	SMART	BRCT	7	8.70E-02	7.90E-01
Annotation Cluster 78	**Enrichment Score: 1.29**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	domain:Bromo	9	1.50E-02	9.40E-01
	UP_SEQ_FEATURE	zinc finger region:PHD-type	12	4.40E-02	1.00E+00
	INTERPRO	Bromodomain	10	5.80E-02	9.40E-01
	SMART	BROMO	10	7.30E-02	7.70E-01
	INTERPRO	Bromodomain, conserved site	9	7.60E-02	9.60E-01
	SP_PIR_KEYWORDS	bromodomain	9	9.00E-02	4.10E-01
Annotation Cluster 79	**Enrichment Score: 1.29**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	T cell selection	8	8.10E-03	1.70E-01
	GOTERM_BP_FAT	thymic T cell selection	6	2.00E-02	3.00E-01
	GOTERM_BP_FAT	positive thymic T cell selection	4	5.30E-02	5.10E-01
	GOTERM_BP_FAT	negative thymic T cell selection	4	7.70E-02	6.10E-01
	GOTERM_BP_FAT	positive T cell selection	4	1.00E-01	7.00E-01
	GOTERM_BP_FAT	negative T cell selection	4	1.00E-01	7.00E-01
	GOTERM_BP_FAT	T cell differentiation in the thymus	7	1.40E-01	7.70E-01
Annotation Cluster 80	**Enrichment Score: 1.28**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	defense response	98	3.30E-02	4.00E-01
	GOTERM_BP_FAT	inflammatory response	55	4.20E-02	4.50E-01

ILMN_3232869	NA	-0.428259945
ILMN_1782651	NLRP14	-0.428335873
ILMN_2312386	PAIP1	-0.428363785
ILMN_1752557	NEU2	-0.428389602
ILMN_1888925	BQ184051	-0.428480908
ILMN_3259148	AB058757	-0.428515085
ILMN_1713846	PPM1H	-0.428520709
ILMN_1738217	NPIPL1	-0.428545148
ILMN_1654979	EPHA6	-0.428585569
ILMN_1658452	FAM53A	-0.428653755
ILMN_3242743	NA	-0.428786445
ILMN_3307132	AK127120	-0.428876979
ILMN_1766974	ZNF107	-0.428912359
ILMN_3300663	SLC35E2B	-0.429045317
ILMN_3272299	EML6	-0.429070749
ILMN_1769099	ZNF253	-0.429091607
ILMN_1673138	ZBTB33	-0.429101869
ILMN_1833212	C9orf130	-0.429171819
ILMN_1735062	KCNG2	-0.429236939
ILMN_1785404	FGFBP1	-0.429287969
ILMN_1758111	PIBF1	-0.429288058
ILMN_1745788	CX3CR1	-0.429344508
ILMN_1815705	LZTFL1	-0.429349175
ILMN_1726054	C13orf26	-0.429387652
ILMN_1808457	TBX18	-0.429463347
ILMN_1721741	AY358864	-0.429477547
ILMN_1729314	PRG2	-0.429508499
ILMN_1693323	C6orf162	-0.429514342
ILMN_2128923	HCCS	-0.429518411
ILMN_2376980	FSD1	-0.429532381
ILMN_1751941	TMEM106A	-0.429538597
ILMN_1763732	ZC3H13	-0.429599387
ILMN_1871756	AA609726	-0.429721419
ILMN_2415583	HS6ST2	-0.429750202
ILMN_1739178	TBXA2R	-0.429766709
ILMN_2159322	SLK	-0.429772553
ILMN_1665458	PDHA2	-0.429796515
ILMN_1916404	AI948987	-0.429803823
ILMN_1833010	BF001957	-0.429861286
ILMN_3218421	NA	-0.429888246
ILMN_1777453	NPB	-0.429982509
ILMN_1658806	SLC5A10	-0.430035052
ILMN_1767632	FLJ44838	-0.430089556
ILMN_3245659	ERI1	-0.430203769
ILMN_1845162	MYO1H	-0.430265648
ILMN_1897405	CA420307	-0.430344795
ILMN_1663932	TP53TG3b	-0.430352466
ILMN_1657680	CCDC69	-0.430402929
ILMN_1761511	APOH	-0.430404287
ILMN_2372384	MGA	-0.430417436
ILMN_1687371	LOC100131257	-0.430581356
ILMN_1756878	SLC39A9	-0.430602736
ILMN_3305180	LOC100631378	-0.43063044
ILMN_1658710	FAM19A4	-0.430731411
ILMN_1740463	AX747015	-0.430754359
ILMN_2107655	SNORD116-2	-0.430796517
ILMN_1854544	LOC100289673	-0.430803434
ILMN_3306168	MOBKL3	-0.430836961
ILMN_1758333	HMGXB4	-0.430896013
ILMN_1716803	RALYL	-0.431009779
ILMN_1846110	NA	-0.431125632
ILMN_1749009	REXO2	-0.431199544
ILMN_3239946	LOC729375	-0.431351493
ILMN_1758542	BMP1	-0.431364816
ILMN_2088825	ACAP2	-0.431389727
ILMN_1667750	SLC4A5	-0.431401101
ILMN_3177615	LOC100128816	-0.431473698
ILMN_2351902	SMN1	-0.431495602
ILMN_1686884	IL1RAP	-0.431499851
ILMN_1667561	IFRD1	-0.431546459
ILMN_1664622	EFR3B	-0.431565379
ILMN_1780625	HR	-0.431652883
ILMN_1892782	NA	-0.431655352
ILMN_1752935	TMEM30B	-0.431679243
ILMN_1775759	NRAS	-0.431696171
ILMN_1707342	LRIG1	-0.431699745
ILMN_1735278	OR13C3	-0.431743776
ILMN_1652459	ATAD3B	-0.431759749
ILMN_1798535	SMR3A	-0.43178259
ILMN_1689510	AK128283	-0.431878408
ILMN_1798853	CTSL1P2	-0.431959947
ILMN_3248970	KIAA0393	-0.431960765
ILMN_3243773	GALNTL6	-0.431978149
ILMN_3190834	ELMOD3	-0.43200874
ILMN_2300894	KCNQ2	-0.432046141
ILMN_1730931	RUFY3	-0.432060268
ILMN_3201183	NA	-0.432079676
ILMN_1766128	THAP3	-0.432087015
ILMN_1913510	AK023519	-0.432105989
ILMN_2154836	BTG3	-0.43211068
ILMN_1694917	SERPINB11	-0.432125266
ILMN_1671337	SLC2A5	-0.432162772
ILMN_1791587	OR2Y1	-0.432165773
ILMN_2221769	PRAMEF11	-0.432175952
ILMN_3272689	NA	-0.432227101
ILMN_3226405	PRAMEF11	-0.432290462

	KEGG_PATHWAY	Glycosylphosphatidylinositol(GPI)-anchor biosynthesis	4	5.40E-01	9.50E-01
	GOTERM_BP_FAT	lipoprotein biosynthetic process	7	5.90E-01	1.00E+00
	GOTERM_BP_FAT	phosphoinositide metabolic process	8	6.70E-01	1.00E+00
	GOTERM_BP_FAT	lipoprotein metabolic process	7	8.60E-01	1.00E+00
Annotation Cluster 88	**Enrichment Score: 0.65**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	glutamine metabolic process	5	1.30E-01	9.80E-01
	GOTERM_BP_FAT	glutamine family amino acid metabolic process	9	1.80E-01	9.80E-01
	KEGG_PATHWAY	Alanine, aspartate and glutamate metabolism	5	4.60E-01	9.50E-01
Annotation Cluster 89	**Enrichment Score: 0.64**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	regulation of action potential in neuron	10	1.10E-01	9.80E-01
	GOTERM_BP_FAT	myelination	7	2.10E-01	9.90E-01
	GOTERM_BP_FAT	regulation of membrane potential	18	2.50E-01	9.90E-01
	GOTERM_BP_FAT	axon ensheathment	7	2.80E-01	9.90E-01
	GOTERM_BP_FAT	ensheathment of neurons	7	2.80E-01	9.90E-01
	GOTERM_BP_FAT	regulation of action potential	10	2.90E-01	9.90E-01
Annotation Cluster 90	**Enrichment Score: 0.64**		**Count**	**P_Value**	**Benjamini**
	SMART	PTB	7	1.70E-01	9.40E-01
	INTERPRO	Phosphotyrosine interaction region	7	2.10E-01	1.00E+00
	UP_SEQ_FEATURE	domain:PID	5	3.40E-01	1.00E+00
Annotation Cluster 91	**Enrichment Score: 0.63**		**Count**	**P_Value**	**Benjamini**
	SMART	PDZ	20	1.50E-01	9.40E-01
	INTERPRO	PDZ/DHR/GLGF	20	2.30E-01	1.00E+00
	UP_SEQ_FEATURE	domain:PDZ	14	3.70E-01	1.00E+00
Annotation Cluster 92	**Enrichment Score: 0.62**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	cellular lipid catabolic process	14	5.50E-02	9.80E-01
	GOTERM_BP_FAT	fatty acid catabolic process	7	1.80E-01	9.80E-01
	GOTERM_BP_FAT	lipid oxidation	7	2.30E-01	9.90E-01
	GOTERM_BP_FAT	fatty acid oxidation	7	2.30E-01	9.90E-01
	GOTERM_BP_FAT	fatty acid beta-oxidation	4	5.80E-01	1.00E+00
	GOTERM_BP_FAT	lipid modification	8	6.10E-01	1.00E+00
Annotation Cluster 93	**Enrichment Score: 0.62**		**Count**	**P_Value**	**Benjamini**
	INTERPRO	BTB/POZ	19	1.20E-01	1.00E+00
	UP_SEQ_FEATURE	domain:BTB	20	1.60E-01	1.00E+00
	SMART	BTB	23	1.70E-01	9.30E-01
	INTERPRO	BTB/POZ-like	23	2.60E-01	1.00E+00
	INTERPRO	BTB/POZ fold	22	3.60E-01	1.00E+00
	INTERPRO	Kelch related	9	6.10E-01	1.00E+00
Annotation Cluster 94	**Enrichment Score: 0.61**		**Count**	**P_Value**	**Benjamini**
	INTERPRO	ATP-grasp fold, subdomain 2	5	9.80E-02	1.00E+00
	UP_SEQ_FEATURE	domain:ATP-grasp	3	3.60E-01	1.00E+00
	INTERPRO	ATP-grasp fold	3	4.10E-01	1.00E+00
Annotation Cluster 95	**Enrichment Score: 0.61**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	calcium ion homeostasis	27	9.50E-02	9.80E-01
	GOTERM_BP_FAT	metal ion homeostasis	28	1.40E-01	9.80E-01
	GOTERM_BP_FAT	cellular calcium ion homeostasis	25	1.60E-01	9.80E-01
	GOTERM_BP_FAT	negative regulation of sequestering of calcium ion	4	1.80E-01	9.80E-01
	GOTERM_BP_FAT	regulation of sequestering of calcium ion	4	1.80E-01	9.80E-01
	GOTERM_BP_FAT	release of sequestered calcium ion into cytosol	4	1.80E-01	9.80E-01
	GOTERM_BP_FAT	cellular metal ion homeostasis	26	1.90E-01	9.90E-01
	GOTERM_BP_FAT	calcium ion transport into cytosol	4	3.30E-01	9.90E-01
	GOTERM_BP_FAT	cytosolic calcium ion transport	4	3.60E-01	1.00E+00
	GOTERM_BP_FAT	cytosolic calcium ion homeostasis	11	8.20E-01	1.00E+00
	GOTERM_BP_FAT	elevation of cytosolic calcium ion concentration	10	8.40E-01	1.00E+00
Annotation Cluster 96	**Enrichment Score: 0.6**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	microtubule cytoskeleton organization	21	1.50E-01	9.80E-01
	GOTERM_BP_FAT	microtubule-based process	32	2.20E-01	9.90E-01
	GOTERM_BP_FAT	cytoskeleton organization	48	4.80E-01	1.00E+00
Annotation Cluster 97	**Enrichment Score: 0.6**		**Count**	**P_Value**	**Benjamini**
	SP_PIR_KEYWORDS	cytoplasmic vesicle	32	1.20E-01	8.50E-01
	GOTERM_CC_FAT	vesicle	78	2.70E-01	9.50E-01
	GOTERM_CC_FAT	membrane-bounded vesicle	66	3.10E-01	9.50E-01
	GOTERM_CC_FAT	cytoplasmic membrane-bounded vesicle	64	3.10E-01	9.50E-01
	GOTERM_CC_FAT	cytoplasmic vesicle	74	3.20E-01	9.50E-01
Annotation Cluster 98	**Enrichment Score: 0.6**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	G1/S transition of mitotic cell cycle	11	6.80E-02	9.80E-01
	GOTERM_BP_FAT	interphase of mitotic cell cycle	14	2.90E-01	9.90E-01
	GOTERM_BP_FAT	interphase	14	3.30E-01	9.90E-01
	GOTERM_BP_FAT	mitotic cell cycle	39	6.10E-01	1.00E+00
Annotation Cluster 99	**Enrichment Score: 0.59**		**Count**	**P_Value**	**Benjamini**
	SP_PIR_KEYWORDS	phenylalanine catabolism	3	1.20E-01	8.50E-01
	GOTERM_BP_FAT	L-phenylalanine metabolic process	3	1.30E-01	9.80E-01
	GOTERM_BP_FAT	L-phenylalanine catabolic process	3	1.30E-01	9.80E-01
	GOTERM_BP_FAT	tyrosine metabolic process	3	2.50E-01	9.90E-01
	GOTERM_BP_FAT	aromatic amino acid family catabolic process	3	3.70E-01	1.00E+00
	GOTERM_BP_FAT	aromatic amino acid family metabolic process	3	6.10E-01	1.00E+00
	GOTERM_BP_FAT	aromatic compound catabolic process	3	6.40E-01	1.00E+00
Annotation Cluster 100	**Enrichment Score: 0.59**		**Count**	**P_Value**	**Benjamini**
	SP_PIR_KEYWORDS	signal transduction	7	1.50E-01	8.70E-01
	BIOCARTA	How Progesterone Initiates the Oocyte Maturation	5	1.60E-01	9.70E-01
	SP_PIR_KEYWORDS	heterotrimer	6	1.60E-01	8.70E-01
	BIOCARTA	Signaling Pathway from G-Protein Families	5	1.80E-01	9.70E-01
	GOTERM_CC_FAT	heterotrimeric G-protein complex	4	6.20E-01	9.70E-01
	GOTERM_CC_FAT	extrinsic to plasma membrane	6	6.40E-01	9.80E-01
Annotation Cluster 101	**Enrichment Score: 0.59**		**Count**	**P_Value**	**Benjamini**
	GOTERM_MF_FAT	cytoskeletal protein binding	64	1.00E-01	9.40E-01
	GOTERM_MF_FAT	actin binding	38	3.80E-01	9.90E-01
	SP_PIR_KEYWORDS	actin-binding	28	4.40E-01	9.50E-01
Annotation Cluster 102	**Enrichment Score: 0.58**		**Count**	**P_Value**	**Benjamini**
	GOTERM_CC_FAT	microtubule cytoskeleton	66	2.20E-01	9.40E-01
	GOTERM_CC_FAT	microtubule	34	2.70E-01	9.60E-01
	SP_PIR_KEYWORDS	microtubule	28	3.00E-01	9.20E-01
Annotation Cluster 103	**Enrichment Score: 0.58**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	negative regulation of protein modification process	19	7.70E-02	9.80E-01
	GOTERM_BP_FAT	regulation of cellular protein metabolic process	60	1.10E-01	9.70E-01
	GOTERM_BP_FAT	regulation of protein modification process	39	1.20E-01	9.70E-01
	GOTERM_BP_FAT	positive regulation of protein metabolic process	28	4.30E-01	1.00E+00

ILMN_1657612	RPL6	0.730740614
ILMN_1737015	RPL39	0.730398658
ILMN_1802252	GAPDH	0.730307584
ILMN_1783303	HSP90AB4P	0.729849286
ILMN_1658351	FIS1	0.729722964
ILMN_1693233	KIAA0513	0.729509954
ILMN_1740385	CEP164	0.729366497
ILMN_1808395	ACAP1	0.72924889
ILMN_1785424	ABLIM1	0.72923244
ILMN_1686623	CSF1R	0.729178342
ILMN_2398388	APH1A	0.729146156
ILMN_2405009	C1orf151	0.728968729
ILMN_1803476	KCTD20	0.728749607
ILMN_1685415	HBP1	0.728599642
ILMN_1790692	GNLY	0.728549165
ILMN_1660376	RPL13A	0.728529068
ILMN_1727249	FAM21C	0.728160083
ILMN_2203950	HLA-A	0.72790687
ILMN_1745112	FAM102A	0.727886698
ILMN_1800451	MED16	0.727865169
ILMN_1651767	MKL1	0.72777291
ILMN_3279306	RPL17	0.727761711
ILMN_1652313	RNF215	0.727662846
ILMN_1752802	CLPTM1L	0.727652757
ILMN_1688381	BPTF	0.727549807
ILMN_1689456	ZBTB20	0.727509872
ILMN_2328224	MADD	0.727414894
ILMN_3302905	RPL23A	0.727227199
ILMN_1742238	SET	0.727091517
ILMN_1797005	PGLS	0.727061288
ILMN_1726169	EDF1	0.7270302
ILMN_1747589	HIST2H2AB	0.726897749
ILMN_1730797	RUNX1	0.726892018
ILMN_1736597	TKT	0.726868258
ILMN_1719972	PLXNA3	0.7267651
ILMN_1682993	NKG7	0.726748877
ILMN_2415179	CLSTN1	0.726714589
ILMN_1762787	RNF26	0.726667157
ILMN_1798867	CAMTA2	0.726639999
ILMN_1708991	CCNY	0.726567618
ILMN_2362368	U2AF1	0.726549068
ILMN_1812191	C12orf57	0.726548015
ILMN_1801504	RUNX1	0.726522574
ILMN_1669607	PHKG2	0.726478066
ILMN_1703866	SUPT5H	0.726406396
ILMN_1686725	DICER1	0.726314052
ILMN_2188533	RPL12	0.726058474
ILMN_2360710	TPM1	0.725850368
ILMN_3205656	GAPDH	0.725803486
ILMN_1735788	TRIOBP	0.725778112
ILMN_1771651	MON1B	0.725753881
ILMN_2393765	IGLL1	0.725656482
ILMN_2319996	RPL3	0.725546927
ILMN_1735827	NISCH	0.725520364
ILMN_1752755	VWF	0.725387195
ILMN_1798081	PTPRF	0.725266032
ILMN_1812616	MYO1C	0.725145118
ILMN_1785061	EPHB2	0.724979615
ILMN_1699887	ST14	0.724950309
ILMN_1803772	POLD4	0.724915578
ILMN_1675222	PLXND1	0.724852498
ILMN_1695334	PYGO2	0.72482679
ILMN_1809003	CBR1	0.724779287
ILMN_1804327	NAP1L4	0.724721866
ILMN_1790782	MED16	0.724694927
ILMN_1804652	PLEKHH3	0.724647986
ILMN_1784299	C19orf43	0.724614574
ILMN_2300396	COMMD5	0.724577438
ILMN_3242293	SPDYE7P	0.724523554
ILMN_1756674	ATP5E	0.724508499
ILMN_1718607	TSPAN4	0.724488193
ILMN_2167416	MR1	0.724215407
ILMN_2154115	PSD4	0.724198124
ILMN_1794781	VAV2	0.724195197
ILMN_1761442	WDR24	0.724169156
ILMN_1658206	OSCP1	0.724032736
ILMN_1653652	PTPRC	0.724031071
ILMN_1660810	TTC17	0.72373663
ILMN_1689445	POLR2H	0.723525328
ILMN_2393712	CTTN	0.723113826
ILMN_1730777	KRT19	0.722962193
ILMN_1708151	LAGE3	0.722882173
ILMN_1722102	ANAPC11	0.72282853
ILMN_1713990	TRIP6	0.722752855
ILMN_1789616	NUPL2	0.722659607
ILMN_1709809	NHP2L1	0.722440577
ILMN_1703305	TWF2	0.722303972
ILMN_1343295	GAPDH	0.722259911
ILMN_1782633	BOLA2B	0.722248619
ILMN_3251404	NUCKS1	0.722149451
ILMN_3235254	SPDYE8P	0.721926034
ILMN_2383489	CDK5RAP3	0.721677057
ILMN_3211187	TUBB2A	0.721569085
ILMN_2399328	COBRA1	0.72152988
ILMN_1686082	C14orf79	0.721512515
ILMN_1802458	AGTRAP	0.721494231

	GOTERM_BP_FAT	response to wounding	81	1.10E-01	7.00E-01
Annotation Cluster 81	**Enrichment Score: 1.23**		**Count**	**P_Value**	**Benjamini**
	SP_PIR_KEYWORDS	methylated carboxyl end	6	3.80E-03	4.70E-02
	SP_PIR_KEYWORDS	ADP-ribosylation	10	1.40E-02	1.20E-01
	INTERPRO	Ras small GTPase, Rho type	6	9.80E-02	9.70E-01
	SMART	RHO	6	1.10E-01	8.10E-01
	GOTERM_BP_FAT	regulation of cell projection assembly	5	2.10E-01	8.70E-01
	PIR_SUPERFAMILY	PIRSF037169:small GTPase, Rho type	4	3.30E-01	1.00E+00
Annotation Cluster 82	**Enrichment Score: 1.22**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	regulation of actin filament polymerization	15	8.80E-03	1.80E-01
	GOTERM_BP_FAT	regulation of actin cytoskeleton organization	21	1.10E-02	2.10E-01
	GOTERM_BP_FAT	regulation of actin polymerization or depolymerization	16	1.10E-02	2.10E-01
	GOTERM_BP_FAT	regulation of actin filament length	16	1.50E-02	2.50E-01
	GOTERM_BP_FAT	regulation of actin filament-based process	21	1.60E-02	2.60E-01
	GOTERM_BP_FAT	negative regulation of cellular component organization	29	1.80E-02	2.80E-01
	GOTERM_BP_FAT	barbed-end actin filament capping	4	1.90E-02	2.80E-01
	GOTERM_BP_FAT	negative regulation of actin filament polymerization	9	2.40E-02	3.30E-01
	GOTERM_BP_FAT	negative regulation of protein complex assembly	10	2.80E-02	3.70E-01
	GOTERM_BP_FAT	negative regulation of protein polymerization	9	3.00E-02	3.80E-01
	GOTERM_BP_FAT	regulation of cellular component biogenesis	28	3.10E-02	3.90E-01
	GOTERM_BP_FAT	regulation of cytoskeleton organization	27	3.20E-02	3.90E-01
	GOTERM_BP_FAT	regulation of protein polymerization	15	5.80E-02	5.40E-01
	GOTERM_BP_FAT	regulation of cellular component size	46	5.90E-02	5.40E-01
	UP_SEQ_FEATURE	repeat:Gelsolin-like 2	4	6.20E-02	1.00E+00
	UP_SEQ_FEATURE	repeat:Gelsolin-like 1	4	6.20E-02	1.00E+00
	UP_SEQ_FEATURE	repeat:Gelsolin-like 3	4	6.20E-02	1.00E+00
	INTERPRO	Gelsolin	4	6.90E-02	9.50E-01
	SMART	GEL	4	7.70E-02	7.60E-01
	GOTERM_BP_FAT	regulation of organelle organization	37	8.50E-02	6.40E-01
	INTERPRO	Gelsolin region	5	9.00E-02	9.60E-01
	GOTERM_BP_FAT	negative regulation of cytoskeleton organization	12	1.00E-01	6.90E-01
	GOTERM_BP_FAT	negative regulation of organelle organization	16	1.20E-01	7.20E-01
	GOTERM_BP_FAT	regulation of protein complex assembly	17	1.30E-01	7.60E-01
	GOTERM_BP_FAT	actin filament capping	6	1.50E-01	8.00E-01
	GOTERM_BP_FAT	negative regulation of actin filament depolymerization	6	2.00E-01	8.60E-01
	UP_SEQ_FEATURE	repeat:Gelsolin-like 4	3	2.00E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:Gelsolin-like 5	3	2.00E-01	1.00E+00
	GOTERM_BP_FAT	regulation of protein complex disassembly	10	2.20E-01	8.90E-01
	GOTERM_BP_FAT	regulation of actin filament depolymerization	6	2.80E-01	9.30E-01
	GOTERM_BP_FAT	negative regulation of protein complex disassembly	8	2.90E-01	9.30E-01
	SP_PIR_KEYWORDS	actin capping	4	4.10E-01	8.40E-01
Annotation Cluster 83	**Enrichment Score: 1.2**		**Count**	**P_Value**	**Benjamini**
	GOTERM_MF_FAT	protein complex scaffold	8	3.40E-02	5.00E-01
	GOTERM_MF_FAT	MAP-kinase scaffold activity	3	8.30E-02	7.40E-01
	GOTERM_MF_FAT	receptor signaling complex scaffold activity	6	8.70E-02	7.50E-01
Annotation Cluster 84	**Enrichment Score: 1.2**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	cell cycle	137	2.30E-04	1.40E-02
	GOTERM_BP_FAT	cell cycle process	104	3.20E-04	1.80E-02
	GOTERM_BP_FAT	mitotic cell cycle	67	6.00E-03	1.40E-01
	GOTERM_BP_FAT	cell division	50	5.10E-02	5.00E-01
	SP_PIR_KEYWORDS	cell cycle	68	5.90E-02	3.30E-01
	SP_PIR_KEYWORDS	cell division	41	7.50E-02	3.70E-01
	SP_PIR_KEYWORDS	mitosis	27	2.10E-01	6.40E-01
	GOTERM_BP_FAT	cell cycle phase	59	3.30E-01	9.50E-01
	GOTERM_BP_FAT	organelle fission	32	4.70E-01	9.80E-01
	GOTERM_BP_FAT	M phase	45	4.80E-01	9.90E-01
	GOTERM_BP_FAT	M phase of mitotic cell cycle	31	4.90E-01	9.90E-01
	GOTERM_BP_FAT	mitosis	30	5.30E-01	9.90E-01
	GOTERM_BP_FAT	nuclear division	30	5.30E-01	9.90E-01
Annotation Cluster 85	**Enrichment Score: 1.2**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	response to nutrient	29	1.50E-02	2.50E-01
	GOTERM_BP_FAT	response to nutrient levels	35	5.90E-02	5.40E-01
	GOTERM_BP_FAT	response to extracellular stimulus	38	7.00E-02	5.80E-01
	GOTERM_BP_FAT	response to vitamin	12	2.50E-01	9.00E-01
Annotation Cluster 86	**Enrichment Score: 1.2**		**Count**	**P_Value**	**Benjamini**
	GOTERM_CC_FAT	nuclear chromatin	15	1.20E-02	1.40E-01
	GOTERM_CC_FAT	heterochromatin	12	1.60E-02	1.70E-01
	GOTERM_CC_FAT	nuclear heterochromatin	8	8.30E-02	4.60E-01
	GOTERM_CC_FAT	nuclear chromosome part	22	1.30E-01	5.60E-01
	GOTERM_CC_FAT	chromosomal part	59	1.80E-01	6.40E-01
	GOTERM_CC_FAT	nuclear chromosome	27	1.80E-01	6.40E-01
Annotation Cluster 87	**Enrichment Score: 1.16**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	lymphocyte proliferation	11	4.30E-02	4.60E-01
	GOTERM_BP_FAT	mononuclear cell proliferation	11	5.70E-02	5.30E-01
	GOTERM_BP_FAT	leukocyte proliferation	11	5.70E-02	5.30E-01
	GOTERM_BP_FAT	B cell proliferation	5	8.10E-02	6.30E-01
	GOTERM_BP_FAT	T cell proliferation	7	1.40E-01	7.70E-01
Annotation Cluster 88	**Enrichment Score: 1.16**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	regulation of endocytosis	15	2.50E-02	3.40E-01
	GOTERM_BP_FAT	regulation of vesicle-mediated transport	19	7.60E-02	6.10E-01
	GOTERM_BP_FAT	positive regulation of endocytosis	7	1.70E-01	8.30E-01
Annotation Cluster 89	**Enrichment Score: 1.15**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	negative regulation of protein kinase activity	18	6.10E-02	5.50E-01
	GOTERM_BP_FAT	negative regulation of transferase activity	19	7.60E-02	6.10E-01
	GOTERM_BP_FAT	negative regulation of kinase activity	18	7.90E-02	6.10E-01
Annotation Cluster 90	**Enrichment Score: 1.13**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	domain:VWFA	13	6.60E-02	1.00E+00
	INTERPRO	von Willebrand factor, type A	16	6.80E-02	9.50E-01
	SMART	VWA	16	9.10E-02	7.90E-01
Annotation Cluster 91	**Enrichment Score: 1.13**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	immune response-regulating signal transduction	14	2.80E-02	3.60E-01
	GOTERM_BP_FAT	activation of immune response	20	3.60E-02	4.20E-01
	GOTERM_BP_FAT	immune response-regulating cell surface receptor signaling pathway	11	4.30E-02	4.60E-01
	GOTERM_BP_FAT	antigen receptor-mediated signaling pathway	9	6.10E-02	5.50E-01
	GOTERM_BP_FAT	immune response-activating signal transduction	12	7.40E-02	6.00E-01
	GOTERM_BP_FAT	B cell receptor signaling pathway	4	1.00E-01	7.00E-01

ILMN_1712523	MAP6	-0.432305905
ILMN_1798557	FAM153A	-0.432401124
ILMN_2172933	LCN12	-0.432421757
ILMN_3272764	NA	-0.432462818
ILMN_2312106	PRAMEF10	-0.432544283
ILMN_1750974	S100A9	-0.432548586
ILMN_1777905	NA	-0.432598373
ILMN_1778717	DBF4	-0.432717105
ILMN_1700306	OCIAD2	-0.432744868
ILMN_3308235	MIR608	-0.432790709
ILMN_1664660	GAGE8	-0.432836359
ILMN_2357730	CDK20	-0.432837531
ILMN_1668012	SLC25A13	-0.432843898
ILMN_3201163	NA	-0.432919028
ILMN_1668740	LOC100287221	-0.432979918
ILMN_1838702	BG188175	-0.433001122
ILMN_2343563	ANAPC11	-0.433057001
ILMN_1828245	AW070200	-0.433082296
ILMN_3251625	ZNF503	-0.433103876
ILMN_1762526	SMC1B	-0.433236043
ILMN_2120917	CTR9	-0.433242368
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ILMN_3308505	MIR129-2	-0.433300545
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ILMN_1662184	C5orf34	-0.433411696
ILMN_1881783	BX090917	-0.433445686
ILMN_1745887	FBXO21	-0.433455559
ILMN_1808110	TCEB3	-0.433517372
ILMN_1707816	ZNF527	-0.433523923
ILMN_1801891	HDX	-0.43360293
ILMN_1713983	NCRNA00169	-0.433645523
ILMN_1785564	FGF16	-0.433686112
ILMN_1781221	SPDYA	-0.433733857
ILMN_1757384	RAN	-0.433743261
ILMN_2402947	USP14	-0.433817481
ILMN_1804597	DCAF17	-0.433840165
ILMN_3183170	AK126852	-0.433857008
ILMN_2411935	KREMEN2	-0.433943196
ILMN_1697512	SLC32A1	-0.433946007
ILMN_3291253	SBF1P1	-0.43399392
ILMN_1681304	PAN3	-0.434075855
ILMN_1663980	MMP19	-0.434109157
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ILMN_1742131	CPNE7	-0.434220155
ILMN_3277282	LOC115110	-0.434238359
ILMN_2124236	C3orf42	-0.434250906
ILMN_1676893	ADCY3	-0.434311164
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ILMN_1678718	AK307134	-0.434406058
ILMN_1741200	RFX5	-0.434442976
ILMN_1655387	PRDM16	-0.434472183
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ILMN_1689098	ATP1A3	-0.434720181
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ILMN_3301502	BC112987	-0.434768092
ILMN_1667405	C9orf100	-0.434890558
ILMN_1736453	RCVRN	-0.434899172
ILMN_1913498	BM665736	-0.434907575
ILMN_2063584	CLIC4	-0.434969808
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ILMN_1849997	AK123174	-0.435027152
ILMN_1786989	NKX6-2	-0.435167323
ILMN_1772055	VARS	-0.435170074
ILMN_1670189	FAM21C	-0.435187275
ILMN_2228780	SLC5A11	-0.435200944
ILMN_3206986	NA	-0.435255744
ILMN_1780773	LOC400027	-0.435260464
ILMN_1725485	RGS17	-0.435276808
ILMN_1686832	NR6A1	-0.43546439
ILMN_1797367	TSC1	-0.435579515
ILMN_1694389	MYL10	-0.435609902
ILMN_2077008	WDR38	-0.435614998
ILMN_1804090	SLC25A10	-0.435648776
ILMN_2224230	TTTY21	-0.435666477
ILMN_1773835	ZNF585B	-0.435692079
ILMN_1680963	LOC100132686	-0.43569364
ILMN_1833415	BC021736	-0.435768477
ILMN_2136446	CTNNAL1	-0.435792767
ILMN_1711839	AK130343	-0.435813286
ILMN_1657607	NRG1	-0.435853208
ILMN_1914707	DA886662	-0.43590821
ILMN_1742787	BHLHE23	-0.435950728
ILMN_1799969	SNAPIN	-0.435967944
ILMN_2341229	CD34	-0.435985153

	GOTERM_BP_FAT	positive regulation of protein modification process	21	5.20E-01	1.00E+00
	GOTERM_BP_FAT	positive regulation of cellular protein metabolic process	25	5.90E-01	1.00E+00
	GOTERM_BP_FAT	positive regulation of protein ubiquitination	9	6.80E-01	1.00E+00
Annotation Cluster 104	**Enrichment Score: 0.58**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	energy reserve metabolic process	9	7.90E-02	9.80E-01
	SP_PIR_KEYWORDS	carbohydrate metabolism	13	9.60E-02	8.40E-01
	SP_PIR_KEYWORDS	glycogen metabolism	5	1.90E-01	8.90E-01
	SP_PIR_KEYWORDS	glycogen storage disease	4	2.60E-01	9.00E-01
	GOTERM_BP_FAT	glycogen metabolic process	6	3.10E-01	9.90E-01
	GOTERM_BP_FAT	glucan metabolic process	6	3.30E-01	9.90E-01
	GOTERM_BP_FAT	cellular glucan metabolic process	6	3.30E-01	9.90E-01
	GOTERM_BP_FAT	energy derivation by oxidation of organic compounds	18	3.60E-01	1.00E+00
	GOTERM_BP_FAT	cellular polysaccharide metabolic process	7	5.00E-01	1.00E+00
	GOTERM_BP_FAT	polysaccharide metabolic process	11	7.50E-01	1.00E+00
Annotation Cluster 105	**Enrichment Score: 0.58**		**Count**	**P_Value**	**Benjamini**
	INTERPRO	SM22/calponin	4	1.00E-01	1.00E+00
	INTERPRO	Calponin repeat	3	1.30E-01	1.00E+00
	UP_SEQ_FEATURE	domain:CH	7	2.80E-01	1.00E+00
	SMART	CH	9	3.90E-01	9.70E-01
	INTERPRO	Calponin-like actin-binding	9	4.70E-01	1.00E+00
	COG_ONTOLOGY	Cytoskeleton	4	5.40E-01	9.70E-01
Annotation Cluster 106	**Enrichment Score: 0.57**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	chromatin assembly or disassembly	20	7.70E-02	9.80E-01
	GOTERM_BP_FAT	chromatin organization	49	1.10E-01	9.70E-01
	GOTERM_BP_FAT	chromosome organization	58	2.20E-01	9.90E-01
	GOTERM_BP_FAT	covalent chromatin modification	15	4.70E-01	1.00E+00
	GOTERM_BP_FAT	chromatin modification	30	5.30E-01	1.00E+00
	SP_PIR_KEYWORDS	chromatin regulator	20	8.00E-01	9.90E-01
Annotation Cluster 107	**Enrichment Score: 0.57**		**Count**	**P_Value**	**Benjamini**
	SP_PIR_KEYWORDS	iron transport	6	8.50E-02	8.60E-01
	GOTERM_BP_FAT	cellular iron ion homeostasis	5	4.20E-01	1.00E+00
	GOTERM_BP_FAT	iron ion homeostasis	5	5.40E-01	1.00E+00
Annotation Cluster 108	**Enrichment Score: 0.57**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	repeat:Solcar 1	10	1.10E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:Solcar 2	10	1.10E-01	1.00E+00
	INTERPRO	Mitochondrial substrate/solute carrier	10	1.30E-01	1.00E+00
	PIR_SUPERFAMILY	PIRSF002458:ADP,ATP carrier protein	5	4.10E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:Solcar 3	7	4.50E-01	1.00E+00
	INTERPRO	Mitochondrial carrier protein	4	5.60E-01	1.00E+00
	INTERPRO	Mitochondrial substrate carrier	6	6.60E-01	1.00E+00
Annotation Cluster 109	**Enrichment Score: 0.57**		**Count**	**P_Value**	**Benjamini**
	GOTERM_MF_FAT	non-membrane spanning protein tyrosine kinase activity	9	6.60E-02	8.80E-01
	PIR_SUPERFAMILY	PIRSF000601:tyrosine-protein kinase, proto-oncogene SRC type	4	1.30E-01	1.00E+00
	SMART	SH2	13	4.20E-01	9.80E-01
	UP_SEQ_FEATURE	domain:SH2	12	4.30E-01	1.00E+00
	SP_PIR_KEYWORDS	SH2 domain	13	5.00E-01	9.60E-01
	INTERPRO	SH2 motif	13	5.20E-01	1.00E+00
Annotation Cluster 110	**Enrichment Score: 0.56**		**Count**	**P_Value**	**Benjamini**
	KEGG_PATHWAY	Starch and sucrose metabolism	9	9.00E-02	9.20E-01
	INTERPRO	Glycoside hydrolase, subgroup, catalytic core	6	2.70E-01	1.00E+00
	SP_PIR_KEYWORDS	glycosidase	7	8.50E-01	9.90E-01
Annotation Cluster 111	**Enrichment Score: 0.56**		**Count**	**P_Value**	**Benjamini**
	GOTERM_MF_FAT	identical protein binding	77	1.80E-01	9.80E-01
	GOTERM_MF_FAT	protein homodimerization activity	42	2.00E-01	9.80E-01
	GOTERM_MF_FAT	protein dimerization activity	58	5.70E-01	1.00E+00
Annotation Cluster 112	**Enrichment Score: 0.56**		**Count**	**P_Value**	**Benjamini**
	GOTERM_MF_FAT	cyclic nucleotide binding	5	2.30E-01	9.80E-01
	SMART	cNMP	6	2.60E-01	9.60E-01
	INTERPRO	Cyclic nucleotide-binding, conserved site	6	2.70E-01	1.00E+00
	INTERPRO	RmlC-like jelly roll fold	6	3.10E-01	1.00E+00
	INTERPRO	Cyclic nucleotide-binding	6	3.10E-01	1.00E+00
Annotation Cluster 113	**Enrichment Score: 0.56**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	central nervous system neuron axonogenesis	4	2.10E-01	9.90E-01
	GOTERM_BP_FAT	central nervous system neuron development	6	2.50E-01	9.90E-01
	GOTERM_BP_FAT	central nervous system neuron differentiation	6	4.20E-01	1.00E+00
Annotation Cluster 114	**Enrichment Score: 0.55**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	short sequence motif:DEAH box	9	6.80E-02	1.00E+00
	UP_SEQ_FEATURE	domain:Chromo 2	3	2.40E-01	1.00E+00
	UP_SEQ_FEATURE	domain:Chromo 1	3	3.60E-01	1.00E+00
	SMART	CHROMO	5	3.90E-01	9.70E-01
	INTERPRO	Chromo domain	5	4.40E-01	1.00E+00
	INTERPRO	SNF2-related	5	4.40E-01	1.00E+00
Annotation Cluster 115	**Enrichment Score: 0.55**		**Count**	**P_Value**	**Benjamini**
	PIR_SUPERFAMILY	PIRSF038059:suppressor of cytokine signaling (SOCS) 4-7	3	3.20E-02	1.00E+00
	SMART	SOCS	6	3.20E-01	9.70E-01
	UP_SEQ_FEATURE	domain:SOCS box	6	3.70E-01	1.00E+00
	INTERPRO	SOCS protein, C-terminal	6	3.80E-01	1.00E+00
	SP_PIR_KEYWORDS	Signal transduction inhibitor	5	5.30E-01	9.70E-01
	SP_PIR_KEYWORDS	growth regulation	6	6.60E-01	9.80E-01
Annotation Cluster 116	**Enrichment Score: 0.55**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	striated muscle cell differentiation	18	1.00E-02	8.30E-01
	GOTERM_BP_FAT	muscle cell development	8	3.80E-01	1.00E+00
	GOTERM_BP_FAT	striated muscle cell development	7	4.80E-01	1.00E+00
	GOTERM_BP_FAT	skeletal muscle fiber development	4	5.80E-01	1.00E+00
	GOTERM_BP_FAT	neuromuscular junction development	3	6.40E-01	1.00E+00
	GOTERM_BP_FAT	muscle fiber development	4	7.30E-01	1.00E+00
Annotation Cluster 117	**Enrichment Score: 0.55**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	DNA metabolic process	61	1.90E-01	9.90E-01
	GOTERM_BP_FAT	DNA repair	36	1.90E-01	9.80E-01
	GOTERM_BP_FAT	response to DNA damage stimulus	46	2.00E-01	9.80E-01
	SP_PIR_KEYWORDS	DNA damage	25	3.10E-01	9.20E-01
	GOTERM_BP_FAT	cellular response to stress	63	4.10E-01	1.00E+00
	SP_PIR_KEYWORDS	dna repair	21	5.30E-01	9.70E-01
Annotation Cluster 118	**Enrichment Score: 0.54**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	neurotransmitter metabolic process	5	2.00E-01	9.90E-01
	GOTERM_BP_FAT	neurotransmitter biosynthetic process	3	2.00E-01	9.90E-01

ILMN_1805812	TOR1A	0.72135148
ILMN_1683597	RPL23A	0.721261586
ILMN_2399140	RAB5C	0.721179209
ILMN_2312709	LCMT1	0.721169216
ILMN_1724532	C11orf49	0.721095522
ILMN_1656420	C16orf67	0.721013331
ILMN_1760493	LIMS2	0.720817288
ILMN_1653404	NKIRAS2	0.720628198
ILMN_1664706	HIST2H3D	0.720585865
ILMN_1765082	RBM10	0.720585208
ILMN_1770281	ERC1	0.720505797
ILMN_1657750	CNNM1	0.720505016
ILMN_2353642	ATP6V0B	0.720438369
ILMN_1813836	DARS	0.720315758
ILMN_1778111	FLJ45340	0.720312126
ILMN_2246894	EDF1	0.719921976
ILMN_3219340	RPL29	0.719689217
ILMN_1764770	OXNAD1	0.719612125
ILMN_2325763	VCAM1	0.719611096
ILMN_1656920	CRIP1	0.719097703
ILMN_1804854	CTNNA1	0.719036017
ILMN_1766125	LONP1	0.718863713
ILMN_1792571	ARHGEF15	0.718239915
ILMN_1713884	C16orf42	0.718139537
ILMN_3244029	ANKRD52	0.718026121
ILMN_3238570	EIF3CL	0.717894547
ILMN_1693430	NME1	0.717879579
ILMN_1723871	OTUB1	0.717731459
ILMN_1728845	SMARCD1	0.717617061
ILMN_1676792	RPS11	0.717603756
ILMN_1716913	TRAPPC1	0.717575633
ILMN_2252309	DPP7	0.717544221
ILMN_1779886	TBC1D14	0.717473712
ILMN_2402806	TRPC4AP	0.717451582
ILMN_1800843	SCAMP4	0.71744772
ILMN_2367384	EPHB2	0.717412277
ILMN_1812559	SLC7A6	0.71739314
ILMN_1773620	SMARCC2	0.717355946
ILMN_1745963	FOLR2	0.717254042
ILMN_1733863	FAM100A	0.71688483
ILMN_2358652	NXF1	0.716562212
ILMN_1679838	WBP5	0.716502688
ILMN_1663132	ADCK2	0.716461666
ILMN_1788689	PHIP	0.716431965
ILMN_2353697	HINFP	0.716148564
ILMN_1778560	ZNF3	0.716094649
ILMN_1801121	SENP2	0.716066822
ILMN_1814799	S100A13	0.716053904
ILMN_2336186	LCMT1	0.715848835
ILMN_2083789	C14orf105	0.715831144
ILMN_1706992	ADAMTSL1	0.715713169
ILMN_1655418	CAPNS1	0.715669409
ILMN_2233256	ZNF607	0.715587836
ILMN_1657095	STARD3	0.715563051
ILMN_1774844	MAPKAPK2	0.715444497
ILMN_2067370	SNRPF	0.715404011
ILMN_1663667	FLAD1	0.715398763
ILMN_1667432	HYAL3	0.715337448
ILMN_1794677	TMC6	0.715169627
ILMN_1731991	SCYL1	0.715144378
ILMN_1722900	EIF4A1	0.715052278
ILMN_2302716	ALDH18A1	0.714881515
ILMN_1700147	VPREB3	0.714847053
ILMN_1708728	H2AFJ	0.71481995
ILMN_1739222	ETV5	0.714815334
ILMN_2053546	RPL19	0.714641707
ILMN_2410771	KEAP1	0.714606607
ILMN_1753275	DENND1A	0.714537554
ILMN_1696749	LMNA	0.714461714
ILMN_1713006	CDC34	0.714268583
ILMN_1695851	PARVG	0.714081512
ILMN_3227912	RPL15	0.714067204
ILMN_3233179	HS6ST1	0.713988857
ILMN_1737157	GRAMD1A	0.71391632
ILMN_1685873	ZC3H7B	0.713889087
ILMN_2407434	DCLK2	0.713866359
ILMN_1744665	EP300	0.713856083
ILMN_1659029	FAM116B	0.713813112
ILMN_1664614	FAU	0.713670468
ILMN_2399694	NOMO3	0.713581054
ILMN_2396148	HIP1R	0.713567092
ILMN_3303101	AK027616	0.713366175
ILMN_2377980	PPP1CA	0.713348549
ILMN_1754199	BCL7B	0.713209495
ILMN_3307827	DNAJC4	0.713067655
ILMN_1739450	NFE2L1	0.712963889
ILMN_1716608	NGF	0.712878312
ILMN_1703949	KPNB1	0.71281946
ILMN_1716973	POLM	0.712710169
ILMN_1811313	SLIT3	0.712649869
ILMN_1704941	PPCDC	0.712647346
ILMN_2352042	MRPL4	0.712548643
ILMN_1753790	ZNF259	0.712454778

	GOTERM_BP_FAT	immune response-activating cell surface receptor signaling pathway	9	1.30E-01	7.60E-01
	GOTERM_BP_FAT	T cell receptor signaling pathway	5	3.60E-01	9.60E-01
Annotation Cluster 92	**Enrichment Score: 1.13**		**Count**	**P_Value**	**Benjamini**
	GOTERM_CC_FAT	leading edge membrane	8	2.60E-02	2.30E-01
	GOTERM_CC_FAT	ruffle membrane	5	6.50E-02	4.00E-01
	GOTERM_CC_FAT	cell projection membrane	12	2.50E-01	7.20E-01
Annotation Cluster 93	**Enrichment Score: 1.12**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	positive regulation of axonogenesis	9	1.20E-02	2.20E-01
	GOTERM_BP_FAT	positive regulation of cell growth	11	4.30E-02	4.60E-01
	GOTERM_BP_FAT	positive regulation of cell size	11	9.30E-02	6.60E-01
	GOTERM_BP_FAT	positive regulation of axon extension	4	1.00E-01	7.00E-01
	GOTERM_BP_FAT	regulation of axon extension	6	1.10E-01	7.20E-01
	GOTERM_BP_FAT	positive regulation of developmental growth	5	1.50E-01	7.90E-01
	GOTERM_BP_FAT	positive regulation of growth	15	1.60E-01	8.10E-01
Annotation Cluster 94	**Enrichment Score: 1.1**		**Count**	**P_Value**	**Benjamini**
	GOTERM_CC_FAT	cortical cytoskeleton	13	2.50E-02	2.30E-01
	GOTERM_CC_FAT	cell cortex	27	7.50E-02	4.30E-01
	GOTERM_CC_FAT	cell cortex part	16	1.40E-01	5.60E-01
	GOTERM_CC_FAT	cortical actin cytoskeleton	7	1.60E-01	6.10E-01
Annotation Cluster 95	**Enrichment Score: 1.09**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	regulation of Ras protein signal transduction	42	6.00E-03	1.40E-01
	INTERPRO	Guanine-nucleotide dissociation stimulator, CDC24, conserved site	14	4.90E-02	9.20E-01
	UP_SEQ_FEATURE	domain:DH	14	5.60E-02	1.00E+00
	GOTERM_BP_FAT	regulation of Rho protein signal transduction	20	5.80E-02	5.40E-01
	INTERPRO	Dbl homology (DH) domain	14	8.90E-02	9.60E-01
	SMART	RhoGEF	14	1.20E-01	8.00E-01
	GOTERM_MF_FAT	Rho guanyl-nucleotide exchange factor activity	14	1.50E-01	8.70E-01
	GOTERM_MF_FAT	Ras guanyl-nucleotide exchange factor activity	16	1.50E-01	8.70E-01
	SP_PIR_KEYWORDS	guanine-nucleotide releasing factor	19	2.00E-01	6.30E-01
	GOTERM_MF_FAT	guanyl-nucleotide exchange factor activity	23	3.10E-01	9.70E-01
Annotation Cluster 96	**Enrichment Score: 1.08**		**Count**	**P_Value**	**Benjamini**
	GOTERM_MF_FAT	protein tyrosine kinase activity	32	2.00E-02	3.90E-01
	SP_PIR_KEYWORDS	autophosphorylation	12	2.90E-02	2.00E-01
	INTERPRO	Tyrosine protein kinase	23	3.80E-02	9.10E-01
	SP_PIR_KEYWORDS	tyrosine-specific protein kinase	11	5.70E-02	3.20E-01
	SMART	TyrKc	23	5.70E-02	7.40E-01
	SP_PIR_KEYWORDS	tyrosine-protein kinase	20	7.20E-02	3.60E-01
	GOTERM_MF_FAT	transmembrane receptor protein tyrosine kinase activity	13	1.50E-01	8.70E-01
	GOTERM_MF_FAT	non-membrane spanning protein tyrosine kinase activity	7	4.30E-01	9.90E-01
	INTERPRO	Tyrosine protein kinase, active site	13	5.80E-01	1.00E+00
Annotation Cluster 97	**Enrichment Score: 1.08**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	regulation of cell growth	36	3.20E-02	3.90E-01
	GOTERM_BP_FAT	regulation of cellular component size	46	5.90E-02	5.40E-01
	GOTERM_BP_FAT	regulation of cell size	31	3.10E-01	9.40E-01
Annotation Cluster 98	**Enrichment Score: 1.06**		**Count**	**P_Value**	**Benjamini**
	GOTERM_MF_FAT	transcription activator activity	78	3.40E-04	3.70E-02
	GOTERM_BP_FAT	positive regulation of macromolecule metabolic process	143	1.90E-03	6.00E-02
	GOTERM_BP_FAT	regulation of transcription from RNA polymerase II promoter	121	4.80E-03	1.20E-01
	GOTERM_BP_FAT	positive regulation of macromolecule biosynthetic process	95	1.90E-01	8.60E-01
	GOTERM_BP_FAT	positive regulation of cellular biosynthetic process	98	2.30E-01	8.90E-01
	GOTERM_BP_FAT	positive regulation of biosynthetic process	99	2.50E-01	9.10E-01
	GOTERM_BP_FAT	positive regulation of nitrogen compound metabolic process	92	2.50E-01	9.10E-01
	GOTERM_BP_FAT	positive regulation of transcription, DNA-dependent	69	2.60E-01	9.10E-01
	GOTERM_BP_FAT	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	89	2.70E-01	9.20E-01
	GOTERM_BP_FAT	positive regulation of RNA metabolic process	69	2.90E-01	9.30E-01
	GOTERM_BP_FAT	positive regulation of transcription	79	3.50E-01	9.60E-01
	GOTERM_BP_FAT	positive regulation of gene expression	79	4.50E-01	9.80E-01
	GOTERM_BP_FAT	positive regulation of transcription from RNA polymerase II promoter	50	5.20E-01	9.90E-01
Annotation Cluster 99	**Enrichment Score: 1.06**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	glucose catabolic process	15	1.70E-02	2.60E-01
	SP_PIR_KEYWORDS	glycolysis	11	3.40E-02	2.30E-01
	BIOCARTA	Glycolysis Pathway	6	4.40E-02	9.10E-01
	GOTERM_BP_FAT	hexose catabolic process	15	6.40E-02	5.60E-01
	GOTERM_BP_FAT	hexose metabolic process	34	6.50E-02	5.70E-01
	SP_PIR_KEYWORDS	gluconeogenesis	6	6.90E-02	3.60E-01
	GOTERM_BP_FAT	monosaccharide catabolic process	15	7.80E-02	6.10E-01
	GOTERM_BP_FAT	glycolysis	11	8.30E-02	6.30E-01
	GOTERM_BP_FAT	cellular carbohydrate catabolic process	17	8.80E-02	6.40E-01
	GOTERM_BP_FAT	glucose metabolic process	27	1.00E-01	6.90E-01
	GOTERM_BP_FAT	alcohol catabolic process	16	1.10E-01	7.00E-01
	GOTERM_BP_FAT	monosaccharide metabolic process	35	2.00E-01	8.60E-01
	GOTERM_BP_FAT	carbohydrate catabolic process	18	2.70E-01	9.20E-01
	KEGG_PATHWAY	Glycolysis / Gluconeogenesis	10	5.60E-01	8.40E-01
Annotation Cluster 100	**Enrichment Score: 1.06**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	negative regulation of actin filament polymerization	9	2.40E-02	3.30E-01
	GOTERM_BP_FAT	negative regulation of protein polymerization	9	3.00E-02	3.80E-01
	INTERPRO	Thymosin beta-4, chordata	3	1.20E-01	9.80E-01
	INTERPRO	Thymosin beta-4	3	1.20E-01	9.80E-01
	SMART	THY	3	1.30E-01	8.10E-01
	PIR_SUPERFAMILY	PIRSF001828:Thymosin_beta	3	1.40E-01	1.00E+00
	GOTERM_BP_FAT	sequestering of actin monomers	3	1.80E-01	8.40E-01
Annotation Cluster 101	**Enrichment Score: 1.06**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	regulation of inflammatory response	18	1.90E-02	2.80E-01
	GOTERM_BP_FAT	regulation of response to external stimulus	29	6.60E-02	5.70E-01
	GOTERM_BP_FAT	positive regulation of inflammatory response	8	9.10E-02	6.60E-01
	GOTERM_BP_FAT	negative regulation of response to external stimulus	11	1.10E-01	7.20E-01
	GOTERM_BP_FAT	positive regulation of defense response	14	1.60E-01	8.10E-01
	GOTERM_BP_FAT	positive regulation of response to external stimulus	12	2.20E-01	8.80E-01
Annotation Cluster 102	**Enrichment Score: 1.04**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	T cell selection	8	8.10E-03	1.70E-01
	GOTERM_BP_FAT	thymic T cell selection	6	2.00E-02	3.00E-01
	BIOCARTA	Activation of Csk by cAMP-dependent Protein Kinase Inhibits Signaling through the T Cell Receptor	8	3.10E-02	9.40E-01
	OMIM_DISEASE	Severe combined immunodeficiency, T cell-negative, B-cell/natural killer-cell positive	3	3.30E-02	1.00E+00

ILMN_1779780	CHTF8	-0.43608213
ILMN_2264634	UTY	-0.436119098
ILMN_1670956	GCOM1	-0.436159586
ILMN_1733116	UBXN7	-0.436176279
ILMN_2225956	C4orf39	-0.436184678
ILMN_1692589	LOC728723	-0.43635144
ILMN_1725683	FUT10	-0.436355785
ILMN_3184724	C7orf58	-0.436471374
ILMN_1666881	AK125965	-0.436521652
ILMN_1691592	SUMF2	-0.436552903
ILMN_1754827	LRRC45	-0.436573051
ILMN_2355042	CLUAP1	-0.436586154
ILMN_1727909	CNTN5	-0.436599502
ILMN_1783443	ALOX15	-0.436611258
ILMN_2056975	HPRT1	-0.436637968
ILMN_1788291	LHFPL5	-0.436647352
ILMN_1748124	TSC22D3	-0.436729844
ILMN_1667948	SPATA18	-0.436771237
ILMN_1813400	CBR4	-0.436800402
ILMN_1743535	PIKFYVE	-0.43682001
ILMN_3272347	AK123101	-0.43691845
ILMN_1680967	SARNP	-0.436926238
ILMN_1684017	GYG2	-0.436933296
ILMN_2083469	IRS2	-0.436986882
ILMN_1783852	CD164	-0.437004022
ILMN_1784595	SBF2	-0.437014345
ILMN_1828111	BE466189	-0.43733202
ILMN_1718352	AK125467	-0.437372516
ILMN_1711102	B3GNT2	-0.437430702
ILMN_1670899	FBN2	-0.4374364
ILMN_1739366	TBR1	-0.437445259
ILMN_1716448	OR10A3	-0.437446785
ILMN_1691175	ADH6	-0.437499867
ILMN_3310366	MIR365-2	-0.437505934
ILMN_1799104	SPAG9	-0.437517658
ILMN_2092589	FAM5C	-0.437519592
ILMN_2260813	TSPYL2	-0.437543188
ILMN_2283814	C21orf34	-0.437632591
ILMN_1895504	LOC100288238	-0.43768678
ILMN_1727558	MRPL27	-0.437761484
ILMN_3247636	SCARNA14	-0.43778702
ILMN_1698769	FAM75D1	-0.437803395
ILMN_1905829	BC063871	-0.437810931
ILMN_1688537	OR10J3	-0.437831073
ILMN_3307858	STIM2	-0.437840772
ILMN_1681643	PCP4L1	-0.437855398
ILMN_3307149	FLJ34503	-0.437869671
ILMN_1768162	LOC100507271	-0.438037956
ILMN_1742798	TRA2B	-0.438080332
ILMN_2082130	C1orf123	-0.438107331
ILMN_1727287	PHF20L1	-0.438162845
ILMN_2166812	KIR2DS5	-0.438172997
ILMN_1818617	AL133627	-0.438185037
ILMN_1717909	ANO1	-0.43820741
ILMN_1674089	PRAMEF7	-0.438229691
ILMN_2075221	C17orf47	-0.438355282
ILMN_2408771	SPPL2B	-0.438358631
ILMN_1685580	CBLB	-0.438390951
ILMN_1700834	SLK	-0.438397889
ILMN_1779897	NPR1	-0.438416636
ILMN_2118612	FAM120C	-0.43848772
ILMN_1732154	BCAN	-0.438491018
ILMN_1796969	POU4F3	-0.438499174
ILMN_3282184	TRIM43B	-0.438517329
ILMN_1882045	CF890951	-0.438519713
ILMN_1705550	FOXD4L6	-0.438527561
ILMN_2174023	FAM75A3	-0.438533853
ILMN_1733311	PIGB	-0.438598937
ILMN_3228090	ZNF716	-0.438602769
ILMN_1675756	KCNJ15	-0.438646786
ILMN_1801240	OR5D14	-0.438664991
ILMN_1737396	PSMD14	-0.438684379
ILMN_2075578	FAM126A	-0.438752254
ILMN_1707311	CCDC54	-0.438795326
ILMN_1846742	AA459851	-0.438805928
ILMN_1753502	IGSF11	-0.438877772
ILMN_1675237	BC113726	-0.439005335
ILMN_2243687	LAMP2	-0.439021241
ILMN_1829253	AA398827	-0.439059711
ILMN_2124187	TSC22D2	-0.439276172
ILMN_3191988	NA	-0.439280143
ILMN_1657476	C7orf72	-0.439303325
ILMN_1721337	MRPS18B	-0.439338505
ILMN_1698484	RHOV	-0.439462304
ILMN_1714650	RASGRP4	-0.439485965
ILMN_1672807	CA5B	-0.43949023
ILMN_3307247	LOC440742	-0.43949744
ILMN_1853116	BC031013	-0.439545137
ILMN_3247400	LOC572558	-0.439592331
ILMN_1673493	GABRB3	-0.439654556
ILMN_1710884	OR5M10	-0.439693608
ILMN_3234910	CLIC5	-0.439718468
ILMN_1809347	SRP14	-0.439747418

	GOTERM_BP_FAT	regulation of neurotransmitter levels	8	5.70E-01	1.00E+00
Annotation Cluster 119	**Enrichment Score: 0.54**		**Count**	**P_Value**	**Benjamini**
	SP_PIR_KEYWORDS	molecular chaperone	4	1.50E-01	8.60E-01
	INTERPRO	Chaperone, tailless complex polypeptide 1	3	3.30E-01	1.00E+00
	INTERPRO	Chaperonin Cpn60/TCP-1	3	4.80E-01	1.00E+00
Annotation Cluster 120	**Enrichment Score: 0.54**		**Count**	**P_Value**	**Benjamini**
	SP_PIR_KEYWORDS	Chaperone	23	1.00E-01	8.30E-01
	GOTERM_MF_FAT	unfolded protein binding	14	4.60E-01	1.00E+00
	GOTERM_BP_FAT	protein folding	20	5.10E-01	1.00E+00
Annotation Cluster 121	**Enrichment Score: 0.54**		**Count**	**P_Value**	**Benjamini**
	SP_PIR_KEYWORDS	protein transport	66	2.20E-02	6.20E-01
	GOTERM_BP_FAT	protein localization	106	1.10E-01	9.70E-01
	GOTERM_BP_FAT	establishment of protein localization	93	1.20E-01	9.80E-01
	GOTERM_BP_FAT	protein transport	92	1.20E-01	9.80E-01
	GOTERM_BP_FAT	intracellular transport	69	6.00E-01	1.00E+00
	GOTERM_BP_FAT	cellular macromolecule localization	39	8.50E-01	1.00E+00
	GOTERM_BP_FAT	cellular protein localization	38	8.80E-01	1.00E+00
	GOTERM_BP_FAT	intracellular protein transport	33	9.20E-01	1.00E+00
	GOTERM_BP_FAT	protein targeting	18	9.20E-01	1.00E+00
Annotation Cluster 122	**Enrichment Score: 0.54**		**Count**	**P_Value**	**Benjamini**
	GOTERM_CC_FAT	cell-cell adherens junction	7	1.70E-01	9.40E-01
	GOTERM_CC_FAT	fascia adherens	3	2.90E-01	9.60E-01
	GOTERM_CC_FAT	intercalated disc	3	4.90E-01	9.70E-01
Annotation Cluster 123	**Enrichment Score: 0.54**		**Count**	**P_Value**	**Benjamini**
	SMART	R3H	3	2.60E-01	9.70E-01
	INTERPRO	Single-stranded nucleic acid binding R3H	3	2.90E-01	1.00E+00
	UP_SEQ_FEATURE	domain:R3H	3	3.20E-01	1.00E+00
Annotation Cluster 124	**Enrichment Score: 0.53**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	membrane lipid metabolic process	14	8.40E-02	9.80E-01
	GOTERM_BP_FAT	sphingolipid metabolic process	13	9.60E-02	9.80E-01
	GOTERM_BP_FAT	glycolipid metabolic process	6	2.30E-01	9.90E-01
	GOTERM_BP_FAT	glycosphingolipid metabolic process	5	2.90E-01	9.90E-01
	GOTERM_BP_FAT	sphingolipid biosynthetic process	5	4.20E-01	1.00E+00
	GOTERM_BP_FAT	membrane lipid biosynthetic process	5	4.90E-01	1.00E+00
	GOTERM_CC_FAT	intrinsic to Golgi membrane	6	5.60E-01	9.70E-01
	GOTERM_CC_FAT	integral to Golgi membrane	4	8.60E-01	9.90E-01
Annotation Cluster 125	**Enrichment Score: 0.52**		**Count**	**P_Value**	**Benjamini**
	SMART	TUDOR	5	2.30E-01	9.70E-01
	INTERPRO	Tudor domain	5	2.70E-01	1.00E+00
	UP_SEQ_FEATURE	domain:Tudor	3	3.20E-01	1.00E+00
	INTERPRO	Tudor subgroup	3	4.10E-01	1.00E+00
Annotation Cluster 126	**Enrichment Score: 0.51**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	metal ion transport	59	1.10E-01	9.70E-01
	GOTERM_BP_FAT	monovalent inorganic cation transport	41	1.40E-01	9.80E-01
	GOTERM_BP_FAT	potassium ion transport	20	3.40E-01	9.90E-01
	GOTERM_MF_FAT	alkali metal ion binding	27	3.90E-01	9.90E-01
	GOTERM_BP_FAT	sodium ion transport	16	4.00E-01	1.00E+00
	SP_PIR_KEYWORDS	Sodium transport	14	4.40E-01	9.50E-01
	SP_PIR_KEYWORDS	Sodium	14	4.40E-01	9.50E-01
	GOTERM_MF_FAT	sodium ion binding	14	4.90E-01	1.00E+00
Annotation Cluster 127	**Enrichment Score: 0.51**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	proximal/distal pattern formation	5	2.20E-01	9.90E-01
	GOTERM_BP_FAT	embryonic forelimb morphogenesis	4	3.30E-01	9.90E-01
	GOTERM_BP_FAT	forelimb morphogenesis	4	4.20E-01	1.00E+00
Annotation Cluster 128	**Enrichment Score: 0.5**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	lung development	14	2.50E-01	9.90E-01
	GOTERM_BP_FAT	respiratory tube development	14	2.80E-01	9.90E-01
	GOTERM_BP_FAT	respiratory system development	14	3.60E-01	1.00E+00
	GOTERM_BP_FAT	tube development	26	3.90E-01	1.00E+00
Annotation Cluster 129	**Enrichment Score: 0.5**		**Count**	**P_Value**	**Benjamini**
	SMART	MAM	4	2.60E-01	9.70E-01
	INTERPRO	MAM	4	3.00E-01	1.00E+00
	UP_SEQ_FEATURE	domain:MAM	3	4.00E-01	1.00E+00
Annotation Cluster 130	**Enrichment Score: 0.5**		**Count**	**P_Value**	**Benjamini**
	KEGG_PATHWAY	Retinol metabolism	9	2.50E-01	9.50E-01
	GOTERM_BP_FAT	estrogen metabolic process	3	2.90E-01	9.90E-01
	GOTERM_BP_FAT	cellular hormone metabolic process	8	4.40E-01	1.00E+00
Annotation Cluster 131	**Enrichment Score: 0.5**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	response to corticosteroid stimulus	13	1.90E-01	9.80E-01
	GOTERM_BP_FAT	response to steroid hormone stimulus	23	3.80E-01	1.00E+00
	GOTERM_BP_FAT	response to glucocorticoid stimulus	10	4.50E-01	1.00E+00
Annotation Cluster 132	**Enrichment Score: 0.5**		**Count**	**P_Value**	**Benjamini**
	SMART	RINGv	3	3.00E-01	9.70E-01
	UP_SEQ_FEATURE	zinc finger region:RING-CH-type	3	3.20E-01	1.00E+00
	INTERPRO	Zinc finger, RING-CH-type	3	3.30E-01	1.00E+00
Annotation Cluster 133	**Enrichment Score: 0.5**		**Count**	**P_Value**	**Benjamini**
	INTERPRO	C2 membrane targeting protein	17	9.30E-02	1.00E+00
	SMART	C2	18	2.00E-01	9.50E-01
	INTERPRO	C2 calcium-dependent membrane targeting	18	2.80E-01	1.00E+00
	PIR_SUPERFAMILY	PIRSF002385:B/K protein/synaptotagmin	3	4.50E-01	1.00E+00
	UP_SEQ_FEATURE	domain:C2	10	4.70E-01	1.00E+00
	UP_SEQ_FEATURE	domain:C2 2	7	5.40E-01	1.00E+00
	UP_SEQ_FEATURE	domain:C2 1	7	5.40E-01	1.00E+00
Annotation Cluster 134	**Enrichment Score: 0.49**		**Count**	**P_Value**	**Benjamini**
	GOTERM_CC_FAT	adherens junction	23	1.10E-01	9.20E-01
	GOTERM_CC_FAT	anchoring junction	25	1.10E-01	9.20E-01
	GOTERM_CC_FAT	basolateral plasma membrane	23	5.20E-01	9.70E-01
	GOTERM_CC_FAT	focal adhesion	12	5.40E-01	9.70E-01
	GOTERM_CC_FAT	cell-substrate junction	13	5.50E-01	9.70E-01
	GOTERM_CC_FAT	cell-substrate adherens junction	12	6.00E-01	9.70E-01
Annotation Cluster 135	**Enrichment Score: 0.49**		**Count**	**P_Value**	**Benjamini**
	SMART	PlsC	4	2.60E-01	9.70E-01
	SP_PIR_KEYWORDS	phospholipid biosynthesis	7	2.70E-01	9.00E-01

ILMN_2369580	C16orf35	0.712439732
ILMN_1789510	STIP1	0.712271416
ILMN_1692168	UBE2Z	0.712195695
ILMN_1813669	ANKS1A	0.712054629
ILMN_1795227	DYNLL1	0.711828081
ILMN_1728163	CTDSP1	0.71175555
ILMN_1699703	ARCN1	0.71161254
ILMN_3243700	RPS8	0.711544341
ILMN_1678329	TNRC18	0.711449205
ILMN_2121207	FAM125A	0.711383192
ILMN_1730622	EVL	0.71137422
ILMN_1803036	TARBP1	0.711245456
ILMN_1720799	TECR	0.710984938
ILMN_1721225	C20orf4	0.710812604
ILMN_3289171	RPS27	0.710729327
ILMN_1675156	CDC42	0.710657034
ILMN_1681269	DYRK4	0.710472999
ILMN_1739199	WASH2P	0.710470181
ILMN_3251100	MEF2A	0.710338722
ILMN_1760682	STAG3L2	0.710292459
ILMN_1651262	HNRNPAB	0.710229282
ILMN_1686954	RPS10	0.710030708
ILMN_1753254	SLC12A7	0.7099978
ILMN_2262198	PMS2CL	0.709931654
ILMN_1671054	HLA-A	0.709830158
ILMN_1664028	CENPB	0.709789272
ILMN_3299520	PRKCB	0.709611469
ILMN_1780298	FAM86A	0.709575137
ILMN_2181968	CBL	0.709530485
ILMN_1663313	AMY1A	0.709360339
ILMN_3238375	CENPT	0.709230526
ILMN_2380163	PTPRF	0.70890466
ILMN_1808500	CEP68	0.708828908
ILMN_3241469	RNF181	0.708644084
ILMN_1803277	MVP	0.708256704
ILMN_1774074	RXRB	0.707998818
ILMN_2378952	GPX4	0.707983345
ILMN_1675460	RPL29	0.707909625
ILMN_1760778	ENG	0.70778025
ILMN_2382829	PRDX2	0.707733136
ILMN_1802251	PTTG1IP	0.707573612
ILMN_1778684	BRE	0.707548634
ILMN_3297317	RPL13AP5	0.707479084
ILMN_1723895	GTF3C5	0.707438165
ILMN_1726245	TGFBR2	0.707408106
ILMN_1703593	BAIAP2L1	0.707253559
ILMN_3204734	PILRB	0.707071166
ILMN_1800425	SLC9A1	0.706943657
ILMN_1815057	PDGFRB	0.706935348
ILMN_1683441	NCAPD3	0.706821779
ILMN_1781281	B9D1	0.706782355
ILMN_2175712	NDUFA11	0.706759502
ILMN_1740429	FTL	0.70665256
ILMN_2112673	POTEKP	0.70663258
ILMN_2109489	GZMB	0.706494782
ILMN_3195401	GABPB1	0.706453998
ILMN_1787815	TRIB3	0.705511361
ILMN_3193623	RPL17	0.705503693
ILMN_1674608	FAM169B	0.705460214
ILMN_1726990	DOM3Z	0.705379976
ILMN_1760858	RAB8A	0.705225433
ILMN_1811104	MDSRP	0.705224441
ILMN_1655987	STAB1	0.705203827
ILMN_1719986	PIK3IP1	0.704946162
ILMN_1805999	MYO1D	0.704863137
ILMN_2334989	CCT3	0.704862075
ILMN_2151817	PFN1	0.704850406
ILMN_1779399	SNRPA	0.704760345
ILMN_1755536	PFDN5	0.704740593
ILMN_3195203	C17orf101	0.704711346
ILMN_1655563	CTIF	0.704629425
ILMN_1679482	TUBA3C	0.704415773
ILMN_1808777	EHD2	0.704360272
ILMN_1674768	LOC375133	0.704121918
ILMN_1665117	C6orf89	0.704012997
ILMN_3200362	NBPF1	0.703889553
ILMN_1795495	ERCC5	0.703843462
ILMN_1716056	LMF2	0.703729544
ILMN_1749109	PSAP	0.703548706
ILMN_1686664	MT2A	0.703502977
ILMN_1783909	COL6A2	0.70340899
ILMN_1776047	HSP90AB3P	0.703397603
ILMN_1781623	TEX264	0.703188699
ILMN_1724066	PLCB2	0.703049068
ILMN_1651544	HDAC8	0.702988239
ILMN_1721241	CYTH2	0.70288524
ILMN_1680437	EEF1G	0.702822882
ILMN_3242330	FAM65C	0.702798498
ILMN_1741491	ZNHIT1	0.702625337
ILMN_2338348	UBASH3A	0.702585529
ILMN_1733023	CCT6P1	0.702434205
ILMN_1722872	MYH9	0.702385945
ILMN_1670638	PITPNC1	0.702351978
ILMN_1809437	RHBDD2	0.702329845

	BIOCARTA	Lck and Fyn tyrosine kinases in initiation of TCR Activation	6	4.40E-02	9.10E-01
	GOTERM_CC_FAT	T cell receptor complex	5	6.50E-02	4.00E-01
	KEGG_PATHWAY	Primary immunodeficiency	10	6.80E-02	3.60E-01
	GOTERM_BP_FAT	T cell differentiation in the thymus	7	1.40E-01	7.70E-01
	SP_PIR_KEYWORDS	T-cell	7	1.60E-01	5.80E-01
	BIOCARTA	T Cytotoxic Cell Surface Molecules	5	1.90E-01	9.40E-01
	BIOCARTA	T Helper Cell Surface Molecules	5	1.90E-01	9.40E-01
	BIOCARTA	CTL mediated immune response against target cells	5	3.30E-01	9.50E-01
	BIOCARTA	HIV Induced T Cell Apoptosis	3	5.40E-01	9.80E-01
	BIOCARTA	IL 17 Signaling Pathway	4	5.80E-01	9.90E-01
Annotation Cluster 103	**Enrichment Score: 1.04**		**Count**	**P_Value**	**Benjamini**
	SP_PIR_KEYWORDS	microfilament	3	4.00E-02	2.50E-01
	INTERPRO	Actin, conserved site	6	4.20E-02	9.20E-01
	PIR_SUPERFAMILY	PIRSF002337:Actin	6	6.90E-02	1.00E+00
	INTERPRO	Actin/actin-like	8	2.20E-01	1.00E+00
	SMART	ACTIN	8	2.50E-01	9.20E-01
Annotation Cluster 104	**Enrichment Score: 1.04**		**Count**	**P_Value**	**Benjamini**
	INTERPRO	Ubiquitin-associated/translation elongation factor EF1B, N-terminal, eukaryote	10	7.50E-02	9.60E-01
	SMART	UBA	10	9.40E-02	7.90E-01
	INTERPRO	Ubiquitin-associated/translation elongation factor EF1B, N-terminal	9	9.80E-02	9.60E-01
	UP_SEQ_FEATURE	domain:UBA	9	1.00E-01	1.00E+00
Annotation Cluster 105	**Enrichment Score: 1.03**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	regulation of protein amino acid phosphorylation	36	6.00E-03	1.40E-01
	GOTERM_BP_FAT	regulation of peptidyl-tyrosine phosphorylation	16	2.90E-02	3.80E-01
	GOTERM_BP_FAT	positive regulation of peptidyl-tyrosine phosphorylation	10	1.60E-01	8.10E-01
	GOTERM_BP_FAT	positive regulation of phosphorus metabolic process	18	1.60E-01	8.10E-01
	GOTERM_BP_FAT	positive regulation of phosphate metabolic process	18	1.60E-01	8.10E-01
	GOTERM_BP_FAT	positive regulation of protein amino acid phosphorylation	15	2.80E-01	9.20E-01
	GOTERM_BP_FAT	positive regulation of phosphorylation	16	2.90E-01	9.30E-01
Annotation Cluster 106	**Enrichment Score: 1.03**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	regulation of lymphocyte apoptosis	5	6.20E-02	5.60E-01
	GOTERM_BP_FAT	regulation of B cell apoptosis	4	7.70E-02	6.10E-01
	GOTERM_BP_FAT	positive regulation of B cell apoptosis	3	8.70E-02	6.40E-01
	GOTERM_BP_FAT	apoptotic mitochondrial changes	8	1.00E-01	7.00E-01
	GOTERM_BP_FAT	apoptotic nuclear changes	7	1.20E-01	7.30E-01
	GOTERM_BP_FAT	positive regulation of lymphocyte apoptosis	3	1.30E-01	7.60E-01
Annotation Cluster 107	**Enrichment Score: 1.02**		**Count**	**P_Value**	**Benjamini**
	INTERPRO	WD40/YVTN repeat-like	50	3.40E-02	9.10E-01
	UP_SEQ_FEATURE	repeat:WD 3	43	4.10E-02	9.90E-01
	UP_SEQ_FEATURE	repeat:WD 1	44	4.50E-02	1.00E+00
	UP_SEQ_FEATURE	repeat:WD 2	44	4.50E-02	1.00E+00
	SP_PIR_KEYWORDS	wd repeat	44	4.60E-02	2.70E-01
	INTERPRO	WD40 repeat, conserved site	45	6.30E-02	9.40E-01
	INTERPRO	WD40 repeat	43	7.30E-02	9.60E-01
	UP_SEQ_FEATURE	repeat:WD 5	37	7.40E-02	1.00E+00
	INTERPRO	WD40 repeat, subgroup	39	9.00E-02	9.60E-01
	INTERPRO	WD40 repeat, region	38	1.00E-01	9.70E-01
	SMART	WD40	43	1.20E-01	8.10E-01
	INTERPRO	WD40 repeat 2	35	1.60E-01	9.90E-01
	UP_SEQ_FEATURE	repeat:WD 4	37	1.60E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:WD 6	25	4.70E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:WD 7	17	7.40E-01	1.00E+00
Annotation Cluster 108	**Enrichment Score: 1.02**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	gene silencing	16	4.90E-03	1.20E-01
	GOTERM_BP_FAT	regulation of gene expression, epigenetic	19	1.00E-02	2.00E-01
	SP_PIR_KEYWORDS	rna-mediated gene silencing	8	3.70E-02	2.40E-01
	GOTERM_BP_FAT	gene silencing by RNA	9	6.10E-02	5.50E-01
	GOTERM_CC_FAT	RNA-induced silencing complex	3	8.90E-02	4.70E-01
	GOTERM_CC_FAT	RNAi effector complex	3	8.90E-02	4.70E-01
	GOTERM_BP_FAT	RNA interference	3	1.80E-01	8.40E-01
	GOTERM_BP_FAT	posttranscriptional gene silencing	5	3.00E-01	9.30E-01
	GOTERM_BP_FAT	posttranscriptional gene silencing by RNA	5	3.00E-01	9.30E-01
	UP_SEQ_FEATURE	domain:PAZ	3	3.00E-01	1.00E+00
	INTERPRO	Argonaute and Dicer protein, PAZ	3	3.20E-01	1.00E+00
	GOTERM_BP_FAT	gene silencing by miRNA	4	3.90E-01	9.70E-01
Annotation Cluster 109	**Enrichment Score: 1.02**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	positive regulation of alpha-beta T cell activation	9	1.60E-02	2.60E-01
	GOTERM_BP_FAT	regulation of calcium-mediated signaling	7	3.90E-02	4.40E-01
	GOTERM_BP_FAT	positive regulation of calcium-mediated signaling	6	6.30E-02	5.60E-01
	GOTERM_BP_FAT	positive regulation of alpha-beta T cell proliferation	4	1.00E-01	7.00E-01
	GOTERM_BP_FAT	positive regulation of T cell proliferation	9	1.30E-01	7.60E-01
	GOTERM_BP_FAT	leukocyte adhesion	7	1.50E-01	8.00E-01
	GOTERM_BP_FAT	regulation of alpha-beta T cell proliferation	4	2.40E-01	9.00E-01
	GOTERM_BP_FAT	regulation of B cell differentiation	4	3.50E-01	9.60E-01
Annotation Cluster 110	**Enrichment Score: 1.02**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	retrograde vesicle-mediated transport, Golgi to ER	8	1.50E-02	2.50E-01
	GOTERM_BP_FAT	Golgi transport vesicle coating	5	3.30E-02	4.00E-01
	GOTERM_BP_FAT	COPI coating of Golgi vesicle	5	3.30E-02	4.00E-01
	GOTERM_BP_FAT	Golgi vesicle budding	5	3.30E-02	4.00E-01
	GOTERM_BP_FAT	vesicle targeting	7	6.00E-02	5.50E-01
	GOTERM_BP_FAT	vesicle targeting, to, from or within Golgi	5	6.20E-02	5.60E-01
	GOTERM_BP_FAT	vesicle coating	5	1.30E-01	7.50E-01
	GOTERM_CC_FAT	COPI-coated vesicle	5	1.30E-01	5.60E-01
	GOTERM_BP_FAT	establishment of vesicle localization	8	1.40E-01	7.70E-01
	GOTERM_BP_FAT	organelle localization	17	1.50E-01	7.90E-01
	GOTERM_BP_FAT	membrane budding	5	1.50E-01	7.90E-01
	GOTERM_CC_FAT	COPI vesicle coat	4	1.70E-01	6.30E-01
	GOTERM_BP_FAT	establishment of organelle localization	13	1.90E-01	8.50E-01
	GOTERM_BP_FAT	vesicle localization	8	2.10E-01	8.70E-01
	GOTERM_CC_FAT	COPI coated vesicle membrane	4	2.10E-01	6.90E-01
	GOTERM_BP_FAT	vesicle organization	9	3.80E-01	9.60E-01
Annotation Cluster 111	**Enrichment Score: 1.02**		**Count**	**P_Value**	**Benjamini**
	INTERPRO	Citron-like	5	9.00E-02	9.60E-01
	UP_SEQ_FEATURE	domain:CNH	5	9.80E-02	1.00E+00

ILMN_2232066	ABCB11	-0.439831383
ILMN_1904791	AK023763	-0.439964325
ILMN_1733746	REEP1	-0.439969482
ILMN_1690753	RBMY1A1	-0.440043788
ILMN_3311180	SKCG-1	-0.440076423
ILMN_2054271	GPR135	-0.440147566
ILMN_1651535	TMEM217	-0.440257381
ILMN_1762095	TMTC4	-0.440319827
ILMN_1742901	RSPH10B2	-0.44032704
ILMN_1738867	TYMP	-0.440363918
ILMN_3308632	MIR617	-0.440463093
ILMN_1777665	SLC22A13	-0.44047253
ILMN_1730085	LCORL	-0.440486382
ILMN_2128048	PCDHB3	-0.440506452
ILMN_3246014	C1orf130	-0.440568885
ILMN_1903082	AI769787	-0.440596157
ILMN_1685952	ACSM3	-0.44061411
ILMN_1874613	AW979088	-0.440651233
ILMN_1801943	NAV2	-0.440670235
ILMN_3240715	PP1164	-0.440698803
ILMN_3246673	AMAC1L3	-0.440776846
ILMN_1759493	ANXA8	-0.440784885
ILMN_1700763	BC153822	-0.44080103
ILMN_3255871	H03055	-0.440870857
ILMN_1790384	AK124197	-0.440932927
ILMN_3221072	GCSH	-0.440984666
ILMN_3235891	AK122833	-0.441045563
ILMN_3240446	FKHRL1P2	-0.441105629
ILMN_1712352	DOCK3	-0.441147848
ILMN_1749996	KCNN2	-0.441176515
ILMN_1728746	GAB2	-0.441220783
ILMN_3211746	AK127966	-0.441382424
ILMN_3207615	TRIM64C	-0.441408399
ILMN_1674661	CIRBP	-0.441408412
ILMN_1776240	DUSP13	-0.441446191
ILMN_3307695	THEM5	-0.441454301
ILMN_1703599	HYDIN	-0.441467537
ILMN_2143220	ANGPTL3	-0.441479773
ILMN_1712197	KCNMB3	-0.441487542
ILMN_1909135	BX952833	-0.441488486
ILMN_2361575	SNX14	-0.441488586
ILMN_1842191	AI827529	-0.441494661
ILMN_3190833	CCRL2	-0.441572955
ILMN_1737242	C8G	-0.441579568
ILMN_1796835	TMEM56	-0.441618944
ILMN_3238462	LOC100506874	-0.441622702
ILMN_2185077	C14orf39	-0.441679986
ILMN_1695949	SIGLEC12	-0.441688566
ILMN_1701565	UPK3B	-0.441726138
ILMN_3240465	DKFZp434F1719	-0.441832231
ILMN_1709360	ARAP2	-0.441844139
ILMN_3226324	BBIP1	-0.441851699
ILMN_3309349	SNHG8	-0.441876326
ILMN_1654386	C14orf182	-0.441955043
ILMN_3246694	KRTAP21-1	-0.442021286
ILMN_3308078	MIR31	-0.442027231
ILMN_1790043	NXF4	-0.442041196
ILMN_1669747	UNC13B	-0.442058824
ILMN_2344283	FMO3	-0.44211933
ILMN_1903651	BX417275	-0.442136871
ILMN_1724826	DNM1L	-0.442223782
ILMN_2402629	METTL9	-0.442227831
ILMN_3299074	NOX4	-0.442276259
ILMN_1720207	GMPPB	-0.4423306
ILMN_1797209	TSGA14	-0.442358382
ILMN_3238960	PRSS3	-0.442450719
ILMN_1811957	CAMSAP1	-0.442577249
ILMN_3215006	LOC100131831	-0.442583681
ILMN_1876466	NA	-0.442583967
ILMN_1781381	AK123658	-0.442603723
ILMN_3224820	HM801842	-0.442609643
ILMN_3249524	FLJ40434	-0.442708382
ILMN_1856044	AA909740	-0.442721675
ILMN_3307178	SPRNP1	-0.44273019
ILMN_1774256	PRSS21	-0.442745298
ILMN_1810387	PLAA	-0.442776337
ILMN_1740076	SLC16A12	-0.442777699
ILMN_1856986	BX109078	-0.442787563
ILMN_1673395	PIGO	-0.442821529
ILMN_1800611	CEP72	-0.442848258
ILMN_3309224	MIR23A	-0.442887876
ILMN_2257833	BBS7	-0.44304955
ILMN_2216815	MAP7	-0.443057762
ILMN_1744295	CDKN2A	-0.4430874
ILMN_1787716	AK125940	-0.443106683
ILMN_1660085	PRTG	-0.443168942
ILMN_1788832	MIB1	-0.4432983
ILMN_1677165	SF3B1	-0.443345965
ILMN_2121272	PDE10A	-0.443349406
ILMN_2215545	C3orf26	-0.443370626
ILMN_3251672	DSG2	-0.443408839
ILMN_1688218	RASGRP4	-0.443422307
ILMN_3211343	AX747968	-0.443453928
ILMN_3248440	SNORA81	-0.443476194

	INTERPRO	Phospholipid/glycerol acyltransferase	4	3.00E-01	1.00E+00
	UP_SEQ_FEATURE	short sequence motif:HXXXXD motif	3	5.10E-01	1.00E+00
Annotation Cluster 136	**Enrichment Score: 0.49**		**Count**	**P_Value**	**Benjamini**
	SP_PIR_KEYWORDS	fmn	4	2.30E-01	9.00E-01
	GOTERM_MF_FAT	FMN binding	3	3.70E-01	9.90E-01
	UP_SEQ_FEATURE	nucleotide phosphate-binding region:FMN	3	4.00E-01	1.00E+00
Annotation Cluster 137	**Enrichment Score: 0.48**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	angiogenesis	20	2.20E-01	9.90E-01
	SP_PIR_KEYWORDS	angiogenesis	10	2.50E-01	9.00E-01
	GOTERM_BP_FAT	blood vessel morphogenesis	26	3.10E-01	9.90E-01
	GOTERM_BP_FAT	blood vessel development	28	4.50E-01	1.00E+00
	GOTERM_BP_FAT	vasculature development	28	5.00E-01	1.00E+00
Annotation Cluster 138	**Enrichment Score: 0.48**		**Count**	**P_Value**	**Benjamini**
	BIOCARTA	AKT Signaling Pathway	5	2.10E-01	9.80E-01
	BIOCARTA	mTOR Signaling Pathway	5	3.30E-01	9.90E-01
	BIOCARTA	Inactivation of Gsk3 by AKT causes accumulation of b-catenin in Alveolar Macrophages	5	3.80E-01	9.90E-01
	BIOCARTA	Skeletal muscle hypertrophy is regulated via AKT/mTOR pathway	4	4.60E-01	9.90E-01
Annotation Cluster 139	**Enrichment Score: 0.48**		**Count**	**P_Value**	**Benjamini**
	GOTERM_MF_FAT	solute:cation antiporter activity	6	2.10E-01	9.80E-01
	GOTERM_MF_FAT	solute:hydrogen antiporter activity	5	2.30E-01	9.80E-01
	INTERPRO	Na+/H+ exchanger, subfamily	3	2.50E-01	1.00E+00
	INTERPRO	Na+/H+ exchanger, conserved region	3	2.50E-01	1.00E+00
	GOTERM_MF_FAT	monovalent cation:hydrogen antiporter activity	3	2.50E-01	9.90E-01
	GOTERM_MF_FAT	sodium:hydrogen antiporter activity	3	2.50E-01	9.90E-01
	GOTERM_MF_FAT	cation:cation antiporter activity	4	2.70E-01	9.90E-01
	INTERPRO	Cation/H+ exchanger, conserved region	3	2.90E-01	1.00E+00
	GOTERM_MF_FAT	antiporter activity	9	4.40E-01	1.00E+00
	INTERPRO	Cation/H+ exchanger	3	4.50E-01	1.00E+00
	GOTERM_BP_FAT	regulation of pH	5	4.90E-01	1.00E+00
	GOTERM_MF_FAT	solute:solute antiporter activity	7	5.20E-01	1.00E+00
	GOTERM_BP_FAT	monovalent inorganic cation homeostasis	6	5.30E-01	1.00E+00
	SP_PIR_KEYWORDS	antiport	5	5.30E-01	9.70E-01
Annotation Cluster 140	**Enrichment Score: 0.47**		**Count**	**P_Value**	**Benjamini**
	GOTERM_CC_FAT	nuclear chromatin	9	2.30E-01	9.50E-01
	GOTERM_CC_FAT	nuclear chromosome	21	2.90E-01	9.60E-01
	GOTERM_CC_FAT	nuclear chromosome part	14	5.60E-01	9.70E-01
Annotation Cluster 141	**Enrichment Score: 0.47**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	dorsal/ventral axis specification	3	2.00E-01	9.90E-01
	GOTERM_BP_FAT	axis specification	6	2.10E-01	9.90E-01
	GOTERM_BP_FAT	dorsal/ventral pattern formation	5	8.90E-01	1.00E+00
Annotation Cluster 142	**Enrichment Score: 0.47**		**Count**	**P_Value**	**Benjamini**
	INTERPRO	Acyl-CoA dehydrogenase/oxidase, N-terminal	4	1.80E-01	1.00E+00
	INTERPRO	Acyl-CoA oxidase/dehydrogenase, central region	4	2.10E-01	1.00E+00
	INTERPRO	Acyl-CoA oxidase/dehydrogenase, type1/2, C-terminal	4	2.10E-01	1.00E+00
	GOTERM_MF_FAT	acyl-CoA dehydrogenase activity	4	2.10E-01	9.80E-01
	SP_PIR_KEYWORDS	Flavoprotein	15	2.30E-01	9.00E-01
	INTERPRO	Acyl-CoA dehydrogenase, N-terminal	3	3.30E-01	1.00E+00
	GOTERM_MF_FAT	FAD binding	10	3.60E-01	9.90E-01
	INTERPRO	Acyl-CoA oxidase/dehydrogenase, type 1	3	4.10E-01	1.00E+00
	UP_SEQ_FEATURE	binding site:Substrate; via carbonyl oxygen	4	5.20E-01	1.00E+00
	SP_PIR_KEYWORDS	FAD	13	5.40E-01	9.70E-01
	UP_SEQ_FEATURE	nucleotide phosphate-binding region:FAD	7	6.30E-01	1.00E+00
	UP_SEQ_FEATURE	binding site:Substrate; via amide nitrogen	3	7.10E-01	1.00E+00
Annotation Cluster 143	**Enrichment Score: 0.47**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	domain:WH2	4	2.90E-01	1.00E+00
	SMART	WH2	4	3.50E-01	9.70E-01
	INTERPRO	Actin-binding WH2	4	3.90E-01	1.00E+00
Annotation Cluster 144	**Enrichment Score: 0.46**		**Count**	**P_Value**	**Benjamini**
	SMART	ANK	30	1.40E-01	9.60E-01
	UP_SEQ_FEATURE	repeat:ANK 9	7	1.90E-01	1.00E+00
	SP_PIR_KEYWORDS	ank repeat	30	2.30E-01	9.00E-01
	INTERPRO	Ankyrin	30	2.40E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:ANK 7	9	2.60E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:ANK 8	7	2.80E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:ANK 1	28	3.10E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:ANK 2	28	3.20E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:ANK 3	21	5.70E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:ANK 4	16	7.00E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:ANK 6	9	7.60E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:ANK 5	10	9.40E-01	1.00E+00
Annotation Cluster 145	**Enrichment Score: 0.46**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	RNA localization	15	1.70E-01	9.80E-01
	GOTERM_BP_FAT	nuclear export	9	3.00E-01	9.90E-01
	GOTERM_BP_FAT	establishment of RNA localization	13	3.30E-01	9.90E-01
	GOTERM_BP_FAT	RNA transport	13	3.30E-01	9.90E-01
	GOTERM_BP_FAT	nucleic acid transport	13	3.30E-01	9.90E-01
	SP_PIR_KEYWORDS	mRNA transport	10	3.70E-01	9.30E-01
	GOTERM_BP_FAT	nucleobase, nucleoside, nucleotide and nucleic acid transport	14	4.20E-01	1.00E+00
	GOTERM_BP_FAT	RNA export from nucleus	6	4.40E-01	1.00E+00
	GOTERM_BP_FAT	mRNA transport	10	5.80E-01	1.00E+00
Annotation Cluster 146	**Enrichment Score: 0.46**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	nucleus organization	9	1.80E-01	9.80E-01
	GOTERM_BP_FAT	DNA catabolic process, endonucleolytic	5	2.90E-01	9.90E-01
	GOTERM_BP_FAT	DNA fragmentation involved in apoptosis	4	3.30E-01	9.90E-01
	GOTERM_BP_FAT	cellular component disassembly	8	3.30E-01	9.90E-01
	GOTERM_BP_FAT	cell structure disassembly during apoptosis	4	4.50E-01	1.00E+00
	GOTERM_BP_FAT	DNA catabolic process	8	4.50E-01	1.00E+00
	GOTERM_BP_FAT	apoptotic nuclear changes	4	5.30E-01	1.00E+00
Annotation Cluster 147	**Enrichment Score: 0.46**		**Count**	**P_Value**	**Benjamini**
	BBID	26.cyclin-CDK_complexes	4	1.30E-01	9.70E-01
	SP_PIR_KEYWORDS	cell cycle control	6	2.20E-01	9.00E-01
	BIOCARTA	Cell Cycle	5	3.80E-01	9.90E-01
	GOTERM_BP_FAT	regulation of cyclin-dependent protein kinase activity	7	5.20E-01	1.00E+00
	BIOCARTA	Cyclins and Cell Cycle Regulation	4	5.20E-01	9.90E-01

ILMN_1778561	WEE1	0.702204115
ILMN_1767556	C10orf10	0.702061648
ILMN_2232936	UQCRH	0.702050315
ILMN_3239397	NA	0.701964741
ILMN_1736500	GNB2L1	0.701788952
ILMN_1668090	STK25	0.701760846
ILMN_3302356	RPS14	0.701685109
ILMN_1793386	MED12	0.701490529
ILMN_2355953	LILRB4	0.701410093
ILMN_1668721	CCND3	0.701402337
ILMN_1687358	TMPRSS4	0.701258218
ILMN_1707901	DHRS7B	0.701250343
ILMN_2149566	VPS25	0.701231327
ILMN_1766110	PHF6	0.701128861
ILMN_1775008	NCAPD2	0.701061554
ILMN_1844692	FOXO3	0.701030179
ILMN_1785711	NEDD8	0.700991782
ILMN_2111229	BZRAP1	0.700964056
ILMN_2408576	FAM129B	0.700926326
ILMN_1796900	NUDCD3	0.700843356
ILMN_1704385	H3F3A	0.700745281
ILMN_1746604	IL6ST	0.700737445
ILMN_1653165	AAMP	0.700502268
ILMN_1739640	DCHS1	0.700418729
ILMN_1813314	HIST1H2BK	0.700388564
ILMN_2258816	SAMD3	0.700323247
ILMN_3245236	FBRS	0.70027578
ILMN_1695827	PPP1CA	0.70023217
ILMN_1804601	DKFZp686O16217	0.700199015
ILMN_2119535	RIPK1	0.700166642
ILMN_1685122	COL9A2	0.699841767
ILMN_2375599	RNH1	0.699728564
ILMN_1769191	GNAS	0.699673301
ILMN_1739283	UPF2	0.699650078
ILMN_1740749	RPL7A	0.699587198
ILMN_1749345	STX5	0.699281098
ILMN_1653599	ATP5D	0.699201793
ILMN_1696485	HNRNPAB	0.699164936
ILMN_1797566	SNAP47	0.698941458
ILMN_1745994	GAS7	0.698881456
ILMN_2332990	DIABLO	0.698876969
ILMN_1778941	HNF1B	0.698762754
ILMN_1669772	LRP1	0.698624053
ILMN_2377025	TCOF1	0.698620488
ILMN_2154287	ACCS	0.698553776
ILMN_2098126	CCL5	0.698199295
ILMN_3245441	AK299972	0.698013645
ILMN_1682818	ARPC4	0.697980044
ILMN_1656720	PTPN11	0.69796538
ILMN_1807234	ZNF700	0.697893954
ILMN_1735467	NPIPL2	0.697891101
ILMN_1718303	PVRL2	0.697817979
ILMN_1658624	UBXN6	0.697334632
ILMN_1692742	DENND3	0.697137203
ILMN_1663416	RPL17	0.696919711
ILMN_2330213	CUX1	0.696826757
ILMN_1700349	ADCK4	0.696805558
ILMN_2325837	CD3D	0.696722503
ILMN_1678547	CPNE9	0.696617386
ILMN_1806242	PSD	0.69660384
ILMN_1719449	DCLK2	0.69646375
ILMN_1779735	C7orf59	0.696429547
ILMN_1758831	RNF31	0.696369303
ILMN_1658486	MRPL54	0.696355015
ILMN_1718900	KCTD2	0.696252633
ILMN_1764383	MCOLN1	0.69619835
ILMN_1714159	LUZP1	0.696176582
ILMN_1738132	HOXA11	0.696158559
ILMN_3249400	abParts	0.696156237
ILMN_1800091	RARRES1	0.696141806
ILMN_2331501	UBC	0.696126166
ILMN_2197128	OSR1	0.695965019
ILMN_1674780	SF3B1	0.695839994
ILMN_2347068	MKNK2	0.695789016
ILMN_3230608	NBPF14	0.695745547
ILMN_1804789	KIAA1967	0.695735692
ILMN_1708093	ARHGEF5	0.69559438
ILMN_3241051	RPL32	0.695479706
ILMN_1683609	UBA1	0.69538271
ILMN_1728984	PA2G4	0.695308849
ILMN_1652161	PNKD	0.695230244
ILMN_3215569	NTAN1	0.695197857
ILMN_2348090	MRPL55	0.695190001
ILMN_1734353	GPX4	0.695187585
ILMN_1682792	BYSL	0.695068912
ILMN_1795218	DHX30	0.694824287
ILMN_1704079	RBM38	0.694736392
ILMN_1699980	TSPAN18	0.694722499
ILMN_1726410	APRT	0.694565054
ILMN_2232368	PCIF1	0.694554088
ILMN_1796409	C1QB	0.694507802

	SMART	CNH	5	1.00E-01	7.90E-01
Annotation Cluster 112	**Enrichment Score: 1**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	protein modification by small protein conjugation	29	6.80E-03	1.50E-01
	GOTERM_BP_FAT	protein modification by small protein conjugation or removal	33	9.90E-03	2.00E-01
	GOTERM_BP_FAT	protein ubiquitination	24	3.70E-02	4.20E-01
	GOTERM_CC_FAT	ubiquitin ligase complex	19	5.00E-02	3.30E-01
	GOTERM_MF_FAT	small conjugating protein ligase activity	28	1.20E-01	8.30E-01
	GOTERM_MF_FAT	ubiquitin-protein ligase activity	24	1.80E-01	8.90E-01
	GOTERM_MF_FAT	acid-amino acid ligase activity	30	2.80E-01	9.60E-01
	KEGG_PATHWAY	Ubiquitin mediated proteolysis	23	4.00E-01	7.30E-01
	GOTERM_MF_FAT	ligase activity, forming carbon-nitrogen bonds	31	5.10E-01	9.90E-01
	SP_PIR_KEYWORDS	ubl conjugation pathway	60	6.50E-01	9.50E-01
Annotation Cluster 113	**Enrichment Score: 0.97**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	positive regulation of T cell mediated immunity	7	9.00E-03	1.90E-01
	GOTERM_BP_FAT	positive regulation of immune effector process	13	9.70E-03	1.90E-01
	GOTERM_BP_FAT	regulation of interleukin-2 production	9	3.60E-02	4.20E-01
	GOTERM_BP_FAT	regulation of T cell mediated immunity	7	4.90E-02	4.90E-01
	GOTERM_BP_FAT	positive regulation of production of molecular mediator of immune response	5	1.30E-01	7.50E-01
	GOTERM_BP_FAT	positive regulation of T cell cytokine production	3	1.30E-01	7.60E-01
	GOTERM_BP_FAT	regulation of production of molecular mediator of immune response	9	1.60E-01	8.20E-01
	GOTERM_BP_FAT	regulation of T cell cytokine production	3	1.80E-01	8.40E-01
	GOTERM_BP_FAT	positive regulation of immunoglobulin production	3	1.80E-01	8.40E-01
	GOTERM_BP_FAT	positive regulation of interleukin-2 production	3	2.30E-01	8.90E-01
	GOTERM_BP_FAT	regulation of immunoglobulin production	6	2.50E-01	9.10E-01
	GOTERM_BP_FAT	positive regulation of cytokine production during immune response	3	3.90E-01	9.70E-01
	GOTERM_BP_FAT	regulation of cytokine production during immune response	3	7.10E-01	1.00E+00
Annotation Cluster 114	**Enrichment Score: 0.96**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	purine nucleoside triphosphate catabolic process	8	1.50E-02	2.50E-01
	GOTERM_BP_FAT	ribonucleoside triphosphate catabolic process	7	3.10E-02	3.80E-01
	GOTERM_BP_FAT	purine ribonucleoside triphosphate catabolic process	7	3.10E-02	3.80E-01
	GOTERM_BP_FAT	nucleoside triphosphate catabolic process	8	3.10E-02	3.90E-01
	GOTERM_BP_FAT	ATP catabolic process	6	5.00E-02	4.90E-01
	GOTERM_BP_FAT	purine ribonucleotide catabolic process	7	7.30E-02	6.00E-01
	GOTERM_BP_FAT	ribonucleotide catabolic process	7	1.00E-01	6.90E-01
	GOTERM_BP_FAT	purine nucleotide catabolic process	8	1.40E-01	7.70E-01
	GOTERM_BP_FAT	heterocycle catabolic process	14	2.10E-01	8.70E-01
	GOTERM_BP_FAT	nucleobase, nucleoside, nucleotide and nucleic acid catabolic process	10	3.50E-01	9.60E-01
	GOTERM_BP_FAT	nucleobase, nucleoside and nucleotide catabolic process	10	3.50E-01	9.60E-01
	GOTERM_BP_FAT	nucleotide catabolic process	9	3.60E-01	9.60E-01
	GOTERM_BP_FAT	nitrogen compound catabolic process	11	3.90E-01	9.70E-01
	GOTERM_MF_FAT	ADP binding	4	4.50E-01	9.90E-01
Annotation Cluster 115	**Enrichment Score: 0.96**		**Count**	**P_Value**	**Benjamini**
	GOTERM_CC_FAT	integral to organelle membrane	27	1.10E-02	1.30E-01
	GOTERM_CC_FAT	intrinsic to organelle membrane	29	2.90E-02	2.50E-01
	GOTERM_CC_FAT	integral to endoplasmic reticulum membrane	11	8.80E-02	4.70E-01
	GOTERM_CC_FAT	integral to Golgi membrane	10	1.10E-01	5.10E-01
	GOTERM_CC_FAT	intrinsic to Golgi membrane	10	1.50E-01	6.00E-01
	KEGG_PATHWAY	Glycosphingolipid biosynthesis	5	1.80E-01	5.40E-01
	GOTERM_BP_FAT	glycolipid metabolic process	7	2.20E-01	8.80E-01
	GOTERM_CC_FAT	intrinsic to endoplasmic reticulum membrane	12	2.30E-01	7.10E-01
	INTERPRO	Glycosyl transferase, family 29	5	2.40E-01	1.00E+00
	GOTERM_MF_FAT	sialyltransferase activity	5	2.50E-01	9.40E-01
Annotation Cluster 116	**Enrichment Score: 0.96**		**Count**	**P_Value**	**Benjamini**
	INTERPRO	Ribosomal protein L13, eukaryotic/archaeal	3	8.00E-02	9.50E-01
	INTERPRO	Ribosomal protein L13	3	1.20E-01	9.80E-01
	PIR_SUPERFAMILY	PIRSF002181:Ribosomal_L13	3	1.40E-01	1.00E+00
Annotation Cluster 117	**Enrichment Score: 0.95**		**Count**	**P_Value**	**Benjamini**
	SP_PIR_KEYWORDS	tpr repeat	29	2.70E-02	2.00E-01
	INTERPRO	Tetratricopeptide-like helical	29	3.60E-02	9.20E-01
	UP_SEQ_FEATURE	repeat:TPR 9	8	6.30E-02	1.00E+00
	UP_SEQ_FEATURE	repeat:TPR 2	26	6.40E-02	1.00E+00
	UP_SEQ_FEATURE	repeat:TPR 1	26	6.40E-02	1.00E+00
	UP_SEQ_FEATURE	repeat:TPR 3	24	6.90E-02	1.00E+00
	UP_SEQ_FEATURE	repeat:TPR 4	18	7.40E-02	1.00E+00
	INTERPRO	Tetratricopeptide repeat	21	9.60E-02	9.60E-01
	INTERPRO	Tetratricopeptide region	21	1.20E-01	9.80E-01
	SMART	TPR	21	1.30E-01	8.10E-01
	INTERPRO	Tetratricopeptide TPR-1	17	1.90E-01	9.90E-01
	UP_SEQ_FEATURE	repeat:TPR 7	10	2.80E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:TPR 6	11	3.10E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:TPR 8	8	3.60E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:TPR 5	11	4.40E-01	1.00E+00
Annotation Cluster 118	**Enrichment Score: 0.95**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	macromolecule catabolic process	122	3.00E-02	3.80E-01
	GOTERM_BP_FAT	cellular macromolecule catabolic process	113	3.80E-02	4.30E-01
	GOTERM_BP_FAT	ubiquitin-dependent protein catabolic process	42	5.30E-02	5.10E-01
	GOTERM_BP_FAT	protein catabolic process	96	6.80E-02	5.70E-01
	GOTERM_BP_FAT	proteolysis involved in cellular protein catabolic process	91	1.00E-01	6.90E-01
	GOTERM_BP_FAT	cellular protein catabolic process	91	1.10E-01	7.10E-01
	GOTERM_BP_FAT	modification-dependent protein catabolic process	85	1.60E-01	8.10E-01
	GOTERM_BP_FAT	modification-dependent macromolecule catabolic process	85	1.60E-01	8.10E-01
	GOTERM_BP_FAT	proteolysis	144	3.70E-01	9.60E-01
	SP_PIR_KEYWORDS	ubl conjugation pathway	60	6.50E-01	9.50E-01
Annotation Cluster 119	**Enrichment Score: 0.95**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	nucleocytoplasmic transport	32	1.20E-02	2.20E-01
	GOTERM_BP_FAT	nuclear transport	32	1.40E-02	2.40E-01
	GOTERM_BP_FAT	protein targeting	41	1.50E-02	2.50E-01
	GOTERM_BP_FAT	protein localization in organelle	25	1.50E-01	7.90E-01
	GOTERM_BP_FAT	nuclear import	15	2.70E-01	9.20E-01
	GOTERM_BP_FAT	protein import into nucleus	14	3.40E-01	9.50E-01
	GOTERM_BP_FAT	protein import	20	3.60E-01	9.60E-01

ILMN_1656170	JAKMIP1	-0.443505301
ILMN_1704790	FADS6	-0.443508534
ILMN_2224955	XCL1	-0.443522363
ILMN_2051563	HIGD2B	-0.443558473
ILMN_2310703	RPS26	-0.443579728
ILMN_1686557	TIMM13	-0.443590721
ILMN_1792088	C1orf101	-0.443596714
ILMN_1679232	KIDINS220	-0.443638681
ILMN_3239673	POM121C	-0.443648152
ILMN_1677303	C5orf42	-0.443800556
ILMN_1731639	CASP3	-0.443924705
ILMN_3247979	LOC100132024	-0.44402494
ILMN_3307252	STMN1	-0.444058039
ILMN_2113417	CRYGC	-0.444089503
ILMN_1736340	ANGEL2	-0.444100488
ILMN_1699684	PBLD	-0.444269621
ILMN_3177122	LOC100127910	-0.444302694
ILMN_1804005	FBP2	-0.444370216
ILMN_2112942	KRTAP6-1	-0.444499187
ILMN_1719089	EXO1	-0.444520538
ILMN_1658563	KRT40	-0.444536418
ILMN_3249059	TRG11	-0.444563112
ILMN_3309159	MIR199B	-0.444574744
ILMN_2234187	CDO1	-0.444585031
ILMN_1672843	FBXO8	-0.444601413
ILMN_3309754	DNM3OS	-0.444611257
ILMN_1688160	WDR27	-0.444630754
ILMN_1681203	TWF1	-0.444658451
ILMN_1671366	LOC285780	-0.444681556
ILMN_1657603	AGBL1	-0.444687196
ILMN_1703091	C2orf27B	-0.444757214
ILMN_1747696	TPM3	-0.444770424
ILMN_1658548	LOC401180	-0.444803037
ILMN_1690423	SLC29A4	-0.444876832
ILMN_1907705	BM717102	-0.444902805
ILMN_1813325	PDE11A	-0.444921785
ILMN_1899048	AW295241	-0.44492497
ILMN_1800164	PPFIA1	-0.445038026
ILMN_1729179	SPATA5L1	-0.4450694
ILMN_1715376	LRRIQ3	-0.44511096
ILMN_1805180	CDAN1	-0.445111279
ILMN_1796926	PABPC5	-0.445300428
ILMN_1701831	GSTA1	-0.445338498
ILMN_3214579	LOC100131733	-0.445371657
ILMN_1750188	LAT	-0.445436292
ILMN_1748281	MAPK10	-0.445464811
ILMN_1711608	SSBP2	-0.445554373
ILMN_1710312	TMEM31	-0.445649649
ILMN_1877939	BX109006	-0.445879268
ILMN_1657870	ABL2	-0.445957138
ILMN_3204975	LOC201651	-0.446074298
ILMN_1803676	ENOSF1	-0.446170381
ILMN_3270641	HNRNPH3	-0.446179172
ILMN_1757183	LOC100192378	-0.446223234
ILMN_1814353	ARGFXP2	-0.446301019
ILMN_1692674	NKD1	-0.446349667
ILMN_2083595	BC132841	-0.446391702
ILMN_1693766	CEP135	-0.446428724
ILMN_2253286	PRKCZ	-0.446477273
ILMN_3191541	PTPRQ	-0.446495565
ILMN_1748141	AMOTL1	-0.446496285
ILMN_1685323	CXADR	-0.446526554
ILMN_2184525	LOC220115	-0.446636897
ILMN_3308500	MIR611	-0.446703416
ILMN_1823034	NA	-0.446722288
ILMN_1719998	DKFZp779O012	-0.446725303
ILMN_2393046	NHLRC3	-0.446756266
ILMN_2043265	ZFP106	-0.446806903
ILMN_3241878	RNU6ATAC	-0.446833868
ILMN_1808970	MORC1	-0.44686371
ILMN_2053567	FASTKD2	-0.446868207
ILMN_2148507	ANKRD13C	-0.447009162
ILMN_1813701	RASAL2	-0.447016925
ILMN_1776542	SLC35C2	-0.447091431
ILMN_1742009	C3orf30	-0.44712452
ILMN_1884828	AA770086	-0.447191044
ILMN_3228301	TMEM191C	-0.447193649
ILMN_1780117	CXorf48	-0.447328691
ILMN_1698849	CHRNA2	-0.447412221
ILMN_1795254	OR2T2	-0.447497026
ILMN_1806647	HEATR2	-0.447509548
ILMN_1675437	FLJ34503	-0.447512098
ILMN_3246724	CISD3	-0.447550123
ILMN_1706028	VCX3B	-0.447584249
ILMN_1663948	KIAA1013	-0.447607147
ILMN_3277872	BMS1	-0.447630518
ILMN_1781102	METTL21D	-0.447637794
ILMN_1781841	LRRN2	-0.447748083
ILMN_3245031	OR7E156P	-0.44778119
ILMN_1654766	NHEDC2	-0.447797351
ILMN_3294028	BM714821	-0.447801271

	SP_PIR_KEYWORDS	cyclin	6	6.10E-01	9.70E-01
Annotation Cluster 148	**Enrichment Score: 0.46**		**Count**	**P_Value**	**Benjamini**
	KEGG_PATHWAY	Regulation of autophagy	9	3.60E-02	9.00E-01
	INTERPRO	Four-helical cytokine, core	10	5.00E-02	1.00E+00
	INTERPRO	Interferon alpha	4	1.50E-01	1.00E+00
	SP_PIR_KEYWORDS	antiviral	4	1.70E-01	8.70E-01
	PIR_SUPERFAMILY	PIRSF001934:interferon alpha	4	2.10E-01	1.00E+00
	SMART	IFabd	4	2.30E-01	9.60E-01
	GOTERM_MF_FAT	interferon-alpha/beta receptor binding	3	2.50E-01	9.90E-01
	INTERPRO	Interferon alpha/beta/delta	4	2.70E-01	1.00E+00
	SP_PIR_KEYWORDS	leukocyte	3	4.80E-01	9.60E-01
	KEGG_PATHWAY	Antigen processing and presentation	10	5.90E-01	9.60E-01
	KEGG_PATHWAY	Autoimmune thyroid disease	6	6.90E-01	9.60E-01
	KEGG_PATHWAY	Cytosolic DNA-sensing pathway	5	8.80E-01	9.80E-01
	KEGG_PATHWAY	Natural killer cell mediated cytotoxicity	12	8.90E-01	9.80E-01
	SP_PIR_KEYWORDS	Antiviral defense	5	9.00E-01	1.00E+00
	GOTERM_BP_FAT	response to virus	9	9.00E-01	1.00E+00
	KEGG_PATHWAY	Toll-like receptor signaling pathway	8	9.40E-01	9.90E-01
	KEGG_PATHWAY	RIG-I-like receptor signaling pathway	5	9.60E-01	9.90E-01
Annotation Cluster 149	**Enrichment Score: 0.45**		**Count**	**P_Value**	**Benjamini**
	GOTERM_MF_FAT	monocarboxylic acid binding	9	2.20E-01	9.80E-01
	GOTERM_MF_FAT	fatty acid binding	6	3.80E-01	9.90E-01
	GOTERM_MF_FAT	acyl-CoA binding	3	5.20E-01	1.00E+00
Annotation Cluster 150	**Enrichment Score: 0.45**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	negative regulation of protein modification process	19	7.70E-02	9.80E-01
	GOTERM_BP_FAT	negative regulation of cellular protein metabolic process	26	9.60E-02	9.80E-01
	GOTERM_BP_FAT	regulation of protein ubiquitination	16	1.10E-01	9.80E-01
	GOTERM_BP_FAT	regulation of protein modification process	39	1.20E-01	9.70E-01
	GOTERM_BP_FAT	negative regulation of protein metabolic process	26	1.30E-01	9.80E-01
	GOTERM_BP_FAT	negative regulation of protein ubiquitination	12	1.60E-01	9.80E-01
	GOTERM_BP_FAT	proteasomal protein catabolic process	14	2.80E-01	9.90E-01
	GOTERM_BP_FAT	proteasomal ubiquitin-dependent protein catabolic process	14	2.80E-01	9.90E-01
	GOTERM_BP_FAT	regulation of ubiquitin-protein ligase activity	11	3.10E-01	9.90E-01
	GOTERM_BP_FAT	regulation of ligase activity	11	3.50E-01	1.00E+00
	GOTERM_BP_FAT	negative regulation of ubiquitin-protein ligase activity	9	4.20E-01	1.00E+00
	GOTERM_BP_FAT	negative regulation of ligase activity	9	4.20E-01	1.00E+00
	GOTERM_BP_FAT	negative regulation of ubiquitin-protein ligase activity during mitotic cell cycle	8	5.40E-01	1.00E+00
	GOTERM_BP_FAT	positive regulation of ubiquitin-protein ligase activity	8	6.20E-01	1.00E+00
	GOTERM_BP_FAT	regulation of ubiquitin-protein ligase activity during mitotic cell cycle	8	6.40E-01	1.00E+00
	GOTERM_CC_FAT	proteasome core complex	3	6.50E-01	9.80E-01
	GOTERM_BP_FAT	positive regulation of ligase activity	8	6.70E-01	1.00E+00
	GOTERM_BP_FAT	positive regulation of protein ubiquitination	9	6.80E-01	1.00E+00
	GOTERM_BP_FAT	anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process	7	7.00E-01	1.00E+00
	SP_PIR_KEYWORDS	proteasome	6	7.10E-01	9.80E-01
	GOTERM_BP_FAT	positive regulation of ubiquitin-protein ligase activity during mitotic cell cycle	7	7.40E-01	1.00E+00
	KEGG_PATHWAY	Proteasome	5	7.90E-01	9.70E-01
	GOTERM_CC_FAT	proteasome complex	6	8.00E-01	9.90E-01
Annotation Cluster 151	**Enrichment Score: 0.45**		**Count**	**P_Value**	**Benjamini**
	SMART	PTBI	3	3.40E-01	9.70E-01
	GOTERM_MF_FAT	insulin receptor binding	5	3.50E-01	9.90E-01
	UP_SEQ_FEATURE	domain:IRS-type PTB	3	3.60E-01	1.00E+00
	INTERPRO	Insulin receptor substrate-1, PTB	3	3.70E-01	1.00E+00
Annotation Cluster 152	**Enrichment Score: 0.44**		**Count**	**P_Value**	**Benjamini**
	GOTERM_MF_FAT	transmembrane receptor protein serine/threonine kinase activity	4	3.00E-01	9.90E-01
	GOTERM_MF_FAT	transforming growth factor beta receptor activity	4	3.00E-01	9.90E-01
	GOTERM_BP_FAT	BMP signaling pathway	7	3.20E-01	9.90E-01
	GOTERM_MF_FAT	growth factor binding	12	5.80E-01	1.00E+00
Annotation Cluster 153	**Enrichment Score: 0.44**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	erythrocyte differentiation	8	1.70E-01	9.80E-01
	GOTERM_BP_FAT	erythrocyte homeostasis	8	2.60E-01	9.90E-01
	GOTERM_BP_FAT	myeloid cell differentiation	11	5.30E-01	1.00E+00
	GOTERM_BP_FAT	homeostasis of number of cells	10	7.50E-01	1.00E+00
Annotation Cluster 154	**Enrichment Score: 0.44**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	muscle filament sliding	3	2.50E-01	9.90E-01
	GOTERM_BP_FAT	actin-mediated cell contraction	3	2.50E-01	9.90E-01
	GOTERM_BP_FAT	actin-myosin filament sliding	3	2.50E-01	9.90E-01
	SP_PIR_KEYWORDS	muscle protein	8	4.40E-01	9.50E-01
	GOTERM_BP_FAT	cytoskeleton-dependent intracellular transport	7	4.80E-01	1.00E+00
	GOTERM_BP_FAT	actin filament-based movement	3	7.20E-01	1.00E+00
Annotation Cluster 155	**Enrichment Score: 0.44**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	cellular protein complex disassembly	4	2.70E-01	9.90E-01
	GOTERM_BP_FAT	protein complex disassembly	4	2.70E-01	9.90E-01
	GOTERM_BP_FAT	cellular component disassembly	8	3.30E-01	9.90E-01
	GOTERM_BP_FAT	macromolecular complex disassembly	4	5.30E-01	1.00E+00
	GOTERM_BP_FAT	cellular macromolecular complex disassembly	4	5.30E-01	1.00E+00
Annotation Cluster 156	**Enrichment Score: 0.44**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	domain:Laminin EGF-like 5	3	1.20E-01	1.00E+00
	UP_SEQ_FEATURE	domain:Laminin EGF-like 1	5	2.90E-01	1.00E+00
	UP_SEQ_FEATURE	domain:Laminin EGF-like 2	5	3.10E-01	1.00E+00
	SMART	EGF_Lam	6	3.90E-01	9.70E-01
	SP_PIR_KEYWORDS	laminin egf-like domain	5	3.90E-01	9.40E-01
	UP_SEQ_FEATURE	domain:Laminin EGF-like 4	3	4.00E-01	1.00E+00
	UP_SEQ_FEATURE	domain:Laminin EGF-like 3	4	4.10E-01	1.00E+00
	INTERPRO	EGF-like, laminin	6	4.40E-01	1.00E+00
	SMART	LamNT	3	4.80E-01	9.80E-01
	UP_SEQ_FEATURE	domain:Laminin N-terminal	3	5.10E-01	1.00E+00
	INTERPRO	Laminin, N-terminal	3	5.20E-01	1.00E+00
Annotation Cluster 157	**Enrichment Score: 0.43**		**Count**	**P_Value**	**Benjamini**
	INTERPRO	Pleckstrin homology-type	36	3.20E-01	1.00E+00
	SMART	PH	31	3.30E-01	9.70E-01
	UP_SEQ_FEATURE	domain:PH	28	3.60E-01	1.00E+00

ILMN_1793934	PISD	0.694466229
ILMN_1651504	FAM193A	0.694288895
ILMN_2207533	RPS17	0.694219264
ILMN_1715705	SSNA1	0.694206495
ILMN_1796177	GIPC1	0.694146954
ILMN_2412192	CFH	0.694125476
ILMN_1673682	GATAD2A	0.694054626
ILMN_3310431	MIR874	0.6940248
ILMN_1790637	C11orf80	0.69381097
ILMN_3206132	RPS8	0.693780645
ILMN_1697448	TXNIP	0.693559306
ILMN_1771957	MAN1B1	0.693454847
ILMN_2329165	MYO1C	0.693441625
ILMN_1678605	CDC123	0.693249623
ILMN_3243238	TPSAB1	0.693151723
ILMN_1739847	EIF3D	0.693127913
ILMN_1667476	LTBR	0.692938344
ILMN_1752968	LAMB2	0.692886946
ILMN_1709880	RPLP0	0.692798447
ILMN_1747460	TMEM184B	0.692786108
ILMN_1798679	ANO9	0.692722927
ILMN_1752526	RNF144B	0.692567269
ILMN_2047511	ADAP1	0.692514576
ILMN_1814971	TCF25	0.692385924
ILMN_2406410	RHBDD2	0.692371389
ILMN_1713163	SMARCA5	0.69221211
ILMN_1701613	RARRES3	0.692141628
ILMN_1685763	WDR45L	0.692075599
ILMN_1788149	NEK11	0.691901095
ILMN_1710216	AVEN	0.691890678
ILMN_2205245	GPN2	0.691881428
ILMN_2325194	PHF6	0.691769677
ILMN_1756071	MFGE8	0.691769151
ILMN_1758055	YIF1B	0.691688991
ILMN_1729915	PILRA	0.691561592
ILMN_1724659	CIZ1	0.691559985
ILMN_1743763	TJAP1	0.691483609
ILMN_1738103	COPE	0.691473888
ILMN_1691843	RNPS1	0.691352724
ILMN_1660368	TRRAP	0.691302784
ILMN_1711414	MRPS27	0.691226588
ILMN_2127605	LRP3	0.691187833
ILMN_2070072	RPS7	0.691033314
ILMN_2382657	ARHGAP9	0.690935078
ILMN_1719286	CTSA	0.690920825
ILMN_1716983	LILRA2	0.690834909
ILMN_1700419	TMEM208	0.690780155
ILMN_1777129	CENPT	0.690667649
ILMN_3185223	NA	0.690566702
ILMN_1808059	BCAS4	0.690435278
ILMN_1723021	ICMT	0.690385327
ILMN_1782419	GNG11	0.690352743
ILMN_1660880	RNH1	0.690200071
ILMN_1672741	ITSN1	0.690177278
ILMN_1681591	PTPN1	0.690095849
ILMN_1715698	RNASEK	0.690070735
ILMN_1704015	SYNGAP1	0.690014695
ILMN_1667315	STAG3L1	0.689889352
ILMN_1779648	HIST3H2A	0.68987261
ILMN_2365544	NHP2	0.689812136
ILMN_2375825	CD37	0.689696843
ILMN_1814985	PDLIM7	0.689583877
ILMN_1745415	BBX	0.689492791
ILMN_1711699	HIP1R	0.689300878
ILMN_1809208	KIAA1543	0.689265539
ILMN_1718646	MMP15	0.689126296
ILMN_1695354	BMF	0.689124585
ILMN_1665895	LOC653160	0.689118285
ILMN_1797604	CAP1	0.689088772
ILMN_2357809	G3BP1	0.689058574
ILMN_1751330	RBCK1	0.688909808
ILMN_1800573	RPS21	0.688909574
ILMN_2303166	MBNL3	0.688885937
ILMN_2342066	METRNL	0.688755307
ILMN_2376289	DBNL	0.688464839
ILMN_1728535	COPZ1	0.688399794
ILMN_1703370	ZDHHC12	0.688352739
ILMN_1683475	TOMM40	0.688239125
ILMN_2340217	PTPRC	0.688190568
ILMN_1664012	CANT1	0.68800571
ILMN_1782257	METTL17	0.687953005
ILMN_2038773	UBC	0.687900831
ILMN_1715908	NCAPH2	0.687870665
ILMN_1783806	DTNBP1	0.687862023
ILMN_1775243	RPL35	0.687747131
ILMN_3248562	SNORD49A	0.687741596
ILMN_2139100	SHISA5	0.687558011
ILMN_1715636	EIF3B	0.687317218
ILMN_3275193	LOC643955	0.687285275
ILMN_1706539	KDM3B	0.687196685
ILMN_1755235	XPO6	0.687189921
ILMN_1799011	CEP250	0.687106734

	GOTERM_BP_FAT	protein import into nucleus, translocation	6	4.70E-01	9.80E-01
	GOTERM_BP_FAT	protein localization in nucleus	14	4.70E-01	9.80E-01
Annotation Cluster 120	**Enrichment Score: 0.95**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	positive regulation of T cell mediated immunity	7	9.00E-03	1.90E-01
	GOTERM_BP_FAT	regulation of response to biotic stimulus	9	3.00E-02	3.80E-01
	GOTERM_BP_FAT	regulation of T cell mediated immunity	7	4.90E-02	4.90E-01
	GOTERM_BP_FAT	positive regulation of response to tumor cell	3	2.90E-01	9.30E-01
	GOTERM_BP_FAT	regulation of response to tumor cell	3	2.90E-01	9.30E-01
	GOTERM_BP_FAT	positive regulation of response to biotic stimulus	3	2.90E-01	9.30E-01
	GOTERM_BP_FAT	regulation of immune response to tumor cell	3	2.90E-01	9.30E-01
	GOTERM_BP_FAT	positive regulation of immune response to tumor cell	3	2.90E-01	9.30E-01
Annotation Cluster 121	**Enrichment Score: 0.95**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	domain:SH3 1	9	6.20E-02	1.00E+00
	UP_SEQ_FEATURE	domain:SH3 2	9	7.10E-02	1.00E+00
	INTERPRO	Neutrophil cytosol factor 2	7	8.60E-02	9.60E-01
	UP_SEQ_FEATURE	domain:SH3 3	5	1.90E-01	1.00E+00
	UP_SEQ_FEATURE	domain:SH3 4	3	2.50E-01	1.00E+00
Annotation Cluster 122	**Enrichment Score: 0.94**		**Count**	**P_Value**	**Benjamini**
	GOTERM_CC_FAT	vesicle coat	11	2.40E-02	2.30E-01
	GOTERM_CC_FAT	transport vesicle	15	5.10E-02	3.30E-01
	GOTERM_CC_FAT	Golgi-associated vesicle	12	7.00E-02	4.20E-01
	GOTERM_CC_FAT	Golgi-associated vesicle membrane	8	8.30E-02	4.60E-01
	GOTERM_CC_FAT	trans-Golgi network transport vesicle	7	9.10E-02	4.70E-01
	GOTERM_CC_FAT	clathrin vesicle coat	6	9.90E-02	4.90E-01
	GOTERM_CC_FAT	AP-1 adaptor complex	3	1.40E-01	5.70E-01
	GOTERM_CC_FAT	clathrin coat of trans-Golgi network vesicle	4	2.50E-01	7.20E-01
	GOTERM_CC_FAT	transport vesicle membrane	6	2.60E-01	7.50E-01
	GOTERM_CC_FAT	clathrin coated vesicle membrane	10	2.70E-01	7.60E-01
	GOTERM_CC_FAT	trans-Golgi network transport vesicle membrane	4	2.80E-01	7.70E-01
Annotation Cluster 123	**Enrichment Score: 0.94**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	regulation of cell motion	38	1.20E-02	2.10E-01
	GOTERM_BP_FAT	negative regulation of cell motion	15	3.30E-02	4.00E-01
	GOTERM_BP_FAT	regulation of cell migration	30	8.10E-02	6.20E-01
	GOTERM_BP_FAT	regulation of locomotion	33	9.50E-02	6.70E-01
	GOTERM_BP_FAT	negative regulation of locomotion	12	1.70E-01	8.30E-01
	GOTERM_BP_FAT	negative regulation of cell migration	11	2.10E-01	8.70E-01
	GOTERM_BP_FAT	positive regulation of cell motion	17	2.20E-01	8.80E-01
	GOTERM_BP_FAT	positive regulation of cell migration	14	3.90E-01	9.70E-01
	GOTERM_BP_FAT	positive regulation of locomotion	15	4.20E-01	9.70E-01
Annotation Cluster 124	**Enrichment Score: 0.93**		**Count**	**P_Value**	**Benjamini**
	SP_PIR_KEYWORDS	cell adhesion	62	7.50E-02	3.60E-01
	GOTERM_BP_FAT	cell adhesion	103	1.50E-01	7.90E-01
	GOTERM_BP_FAT	biological adhesion	103	1.50E-01	7.90E-01
Annotation Cluster 125	**Enrichment Score: 0.92**		**Count**	**P_Value**	**Benjamini**
	GOTERM_CC_FAT	histone methyltransferase complex	9	4.00E-03	6.40E-02
	GOTERM_CC_FAT	methyltransferase complex	9	4.00E-03	6.40E-02
	GOTERM_CC_FAT	MLL5-L complex	5	1.40E-02	1.60E-01
	GOTERM_MF_FAT	protein methyltransferase activity	13	2.20E-02	4.10E-01
	SP_PIR_KEYWORDS	s-adenosyl-l-methionine	20	3.80E-02	2.40E-01
	GOTERM_BP_FAT	protein amino acid alkylation	10	6.30E-02	5.60E-01
	GOTERM_BP_FAT	protein amino acid methylation	10	6.30E-02	5.60E-01
	GOTERM_BP_FAT	biopolymer methylation	15	6.40E-02	5.60E-01
	UP_SEQ_FEATURE	binding site:S-adenosyl-L-methionine	11	8.20E-02	1.00E+00
	GOTERM_MF_FAT	histone methyltransferase activity	9	1.20E-01	8.30E-01
	GOTERM_BP_FAT	methylation	15	1.20E-01	7.40E-01
	UP_SEQ_FEATURE	region of interest:S-adenosyl-L-methionine binding	8	1.20E-01	1.00E+00
	GOTERM_MF_FAT	N-methyltransferase activity	11	1.40E-01	8.50E-01
	INTERPRO	Post-SET zinc-binding region	5	1.60E-01	9.90E-01
	INTERPRO	MLL Transcription Factor	3	1.70E-01	9.90E-01
	SMART	PostSET	5	1.80E-01	8.80E-01
	GOTERM_BP_FAT	DNA methylation	6	2.00E-01	8.60E-01
	GOTERM_BP_FAT	DNA alkylation	6	2.00E-01	8.60E-01
	GOTERM_MF_FAT	lysine N-methyltransferase activity	7	2.20E-01	9.30E-01
	GOTERM_MF_FAT	protein-lysine N-methyltransferase activity	7	2.20E-01	9.30E-01
	GOTERM_MF_FAT	histone-lysine N-methyltransferase activity	7	2.20E-01	9.30E-01
	SP_PIR_KEYWORDS	methyltransferase	22	2.20E-01	6.60E-01
	GOTERM_BP_FAT	DNA modification	7	2.60E-01	9.20E-01
	GOTERM_BP_FAT	one-carbon metabolic process	18	3.00E-01	9.40E-01
	UP_SEQ_FEATURE	domain:Post-SET	4	3.00E-01	1.00E+00
	GOTERM_BP_FAT	histone methylation	5	3.30E-01	9.50E-01
	UP_SEQ_FEATURE	domain:SET	8	3.80E-01	1.00E+00
	INTERPRO	SET	8	4.20E-01	1.00E+00
	SMART	SET	8	4.70E-01	9.70E-01
	KEGG_PATHWAY	Lysine degradation	5	9.10E-01	9.70E-01
Annotation Cluster 126	**Enrichment Score: 0.92**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	regulation of response to biotic stimulus	9	3.00E-02	3.80E-01
	GOTERM_BP_FAT	regulation of multi-organism process	8	1.00E-01	7.00E-01
	GOTERM_BP_FAT	regulation of defense response to virus	5	2.40E-01	8.90E-01
	GOTERM_BP_FAT	regulation of defense response to virus by virus	3	2.90E-01	9.30E-01
Annotation Cluster 127	**Enrichment Score: 0.91**		**Count**	**P_Value**	**Benjamini**
	GOTERM_MF_FAT	nuclear hormone receptor binding	19	7.80E-03	2.30E-01
	GOTERM_MF_FAT	hormone receptor binding	19	2.90E-02	4.60E-01
	GOTERM_BP_FAT	steroid hormone receptor signaling pathway	12	1.40E-01	7.70E-01
	GOTERM_BP_FAT	intracellular receptor-mediated signaling pathway	14	1.80E-01	8.40E-01
	GOTERM_BP_FAT	androgen receptor signaling pathway	7	3.40E-01	9.50E-01
	GOTERM_MF_FAT	androgen receptor binding	5	4.30E-01	9.90E-01
	GOTERM_MF_FAT	steroid hormone receptor binding	6	5.50E-01	1.00E+00
Annotation Cluster 128	**Enrichment Score: 0.9**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	region of interest:Beta-galactoside binding 1	3	4.00E-02	9.90E-01
	UP_SEQ_FEATURE	region of interest:Beta-galactoside binding 2	3	4.00E-02	9.90E-01
	UP_SEQ_FEATURE	domain:Galectin 2	3	1.60E-01	1.00E+00
	UP_SEQ_FEATURE	domain:Galectin 1	3	1.60E-01	1.00E+00

ILMN_2367710	PKN1	-0.447812901
ILMN_1776442	ACTRT2	-0.447958898
ILMN_1790810	HCN4	-0.448008569
ILMN_2168449	DHX15	-0.448008777
ILMN_1810684	TINAG	-0.448081753
ILMN_1665748	DCC	-0.448104212
ILMN_3244597	SNORA38	-0.448238503
ILMN_1694875	APPBP2	-0.448291002
ILMN_1805658	LTV1	-0.448317062
ILMN_1717184	MZT2B	-0.448319024
ILMN_3179396	MUC7	-0.448476914
ILMN_3308118	MIR125B1	-0.44855093
ILMN_1746871	TNRC6C	-0.448560495
ILMN_3310276	MIR425	-0.448585482
ILMN_1712019	ANKRD17	-0.448612328
ILMN_1702739	TMEM146	-0.448618825
ILMN_2399463	VAV3	-0.448622698
ILMN_1910322	LOC100131034	-0.448746157
ILMN_3199958	PCDH11Y	-0.448951354
ILMN_1706691	CCDC87	-0.448974168
ILMN_1682763	ALB	-0.448976182
ILMN_1760635	RAD51C	-0.449013202
ILMN_1733035	MZT2A	-0.449051629
ILMN_1902378	DB299844	-0.449084309
ILMN_3305763	LOC728460	-0.449111853
ILMN_3240425	LOC348926	-0.449116943
ILMN_3308415	MIR337	-0.449117699
ILMN_2399300	NAV2	-0.449153243
ILMN_1690621	GPR98	-0.449159777
ILMN_3190972	DSTNP2	-0.449177351
ILMN_1757569	GSK3A	-0.449207462
ILMN_1759879	LOC220115	-0.449216282
ILMN_1780222	SLC6A7	-0.449283042
ILMN_1681515	CRLF1	-0.44929925
ILMN_1696975	USP1	-0.449304164
ILMN_1807101	F11	-0.449321796
ILMN_2297997	LIPT1	-0.449324143
ILMN_1662453	PRDM6	-0.449338283
ILMN_1727668	LOC100131180	-0.449388055
ILMN_3310476	MIR508	-0.449438747
ILMN_1853592	TFAP2B	-0.449498603
ILMN_2382127	PPFIA1	-0.44958249
ILMN_1860789	BM974067	-0.44963838
ILMN_2077733	NAA25	-0.449639227
ILMN_1900456	NA	-0.449660815
ILMN_1790688	AHNAK2	-0.44967952
ILMN_1665714	C4orf22	-0.449681545
ILMN_2208373	TMEM164	-0.449697587
ILMN_1694182	C21orf84	-0.449779612
ILMN_1786657	LOC283682	-0.44978002
ILMN_1662243	ING1	-0.449789464
ILMN_1688504	OR1L8	-0.449815763
ILMN_1784175	KIAA1383	-0.449869106
ILMN_1868866	NA	-0.450002232
ILMN_1740837	NEUROD1	-0.450006878
ILMN_1765605	APOC4-APOC2	-0.450022578
ILMN_1684186	C1orf141	-0.450060516
ILMN_1765085	TRMT6	-0.450065208
ILMN_1708249	NR1D1	-0.45007284
ILMN_1762670	C20orf70	-0.450084734
ILMN_3244678	SNORA5B	-0.450119526
ILMN_1891042	AI807473	-0.450152778
ILMN_1704176	PSKH2	-0.450204164
ILMN_1739259	UBE4A	-0.450214582
ILMN_3251278	DPPA3	-0.450233268
ILMN_1851540	FGF12	-0.450331446
ILMN_2354478	CYFIP2	-0.450375375
ILMN_1718783	EXTL1	-0.450445943
ILMN_1674648	LOC338588	-0.450465728
ILMN_1696708	C14orf166	-0.450484354
ILMN_1814316	RBFOX1	-0.450537026
ILMN_1733419	CCNE1	-0.450620195
ILMN_1887977	BX094636	-0.450630545
ILMN_1662091	FLJ43860	-0.450695817
ILMN_2207170	WWC2	-0.450750891
ILMN_1769301	DNAH10OS	-0.450785348
ILMN_1670572	IDO2	-0.450831449
ILMN_1704101	HSF4	-0.450869197
ILMN_1766219	HGC6.1.1	-0.450961747
ILMN_1663099	UBE2B	-0.451014558
ILMN_1707137	C17orf97	-0.451016527
ILMN_1698007	CCRL1	-0.451024822
ILMN_1758943	FAM5C	-0.451070859
ILMN_2266309	CEPT1	-0.451112198
ILMN_1671398	NPAS3	-0.451124818
ILMN_1734775	TISP43	-0.45113568
ILMN_2274199	SUPT3H	-0.451147358
ILMN_1652066	SNED1	-0.451164905
ILMN_3290889	AX748201	-0.451171704
ILMN_3266944	RPS29	-0.451173746
ILMN_2082810	BRD7	-0.451181175
ILMN_1732197	MN1	-0.451273067

	INTERPRO	Pleckstrin homology	31	4.80E-01	1.00E+00
Annotation Cluster 158	**Enrichment Score: 0.43**		**Count**	**P_Value**	**Benjamini**
	GOTERM_MF_FAT	lysine N-acetyltransferase activity	8	1.00E-01	9.30E-01
	GOTERM_MF_FAT	histone acetyltransferase activity	8	1.00E-01	9.30E-01
	SP_PIR_KEYWORDS	Acyltransferase	20	2.50E-01	9.00E-01
	GOTERM_MF_FAT	acetyltransferase activity	12	2.60E-01	9.90E-01
	GOTERM_BP_FAT	histone H3 acetylation	5	2.90E-01	9.90E-01
	GOTERM_MF_FAT	N-acetyltransferase activity	10	3.20E-01	9.90E-01
	INTERPRO	Acyl-CoA N-acyltransferase	5	4.20E-01	1.00E+00
	GOTERM_BP_FAT	covalent chromatin modification	15	4.70E-01	1.00E+00
	GOTERM_MF_FAT	N-acyltransferase activity	10	5.30E-01	1.00E+00
	GOTERM_BP_FAT	histone modification	14	5.40E-01	1.00E+00
	GOTERM_BP_FAT	histone acetylation	6	5.90E-01	1.00E+00
	GOTERM_BP_FAT	protein amino acid acetylation	6	6.60E-01	1.00E+00
	GOTERM_BP_FAT	protein amino acid acylation	6	7.80E-01	1.00E+00
	GOTERM_CC_FAT	histone acetyltransferase complex	5	8.00E-01	9.90E-01
Annotation Cluster 159	**Enrichment Score: 0.43**		**Count**	**P_Value**	**Benjamini**
	SMART	GuKc	6	1.10E-01	9.60E-01
	INTERPRO	Guanylate kinase/L-type calcium channel region	6	1.30E-01	1.00E+00
	UP_SEQ_FEATURE	domain:PDZ 1	6	4.10E-01	1.00E+00
	UP_SEQ_FEATURE	domain:PDZ 2	6	4.10E-01	1.00E+00
	UP_SEQ_FEATURE	domain:PDZ 4	3	4.80E-01	1.00E+00
	UP_SEQ_FEATURE	domain:PDZ 3	4	5.80E-01	1.00E+00
	UP_SEQ_FEATURE	domain:Guanylate kinase-like	3	7.10E-01	1.00E+00
	INTERPRO	Guanylate kinase	3	7.20E-01	1.00E+00
Annotation Cluster 160	**Enrichment Score: 0.43**		**Count**	**P_Value**	**Benjamini**
	INTERPRO	Voltage-dependent calcium channel, L-type, beta subunit	3	5.80E-02	1.00E+00
	PIR_SUPERFAMILY	PIRSF015600:human voltage-dependent calcium channel beta chain	3	6.00E-02	1.00E+00
	SMART	GuKc	6	1.10E-01	9.60E-01
	INTERPRO	Guanylate kinase/L-type calcium channel region	6	1.30E-01	1.00E+00
	GOTERM_BP_FAT	di-, tri-valent inorganic cation transport	23	2.40E-01	9.90E-01
	GOTERM_BP_FAT	calcium ion transport	17	4.40E-01	1.00E+00
	KEGG_PATHWAY	Arrhythmogenic right ventricular cardiomyopathy (ARVC)	10	4.80E-01	9.50E-01
	SP_PIR_KEYWORDS	calcium transport	10	5.40E-01	9.70E-01
	GOTERM_MF_FAT	voltage-gated calcium channel activity	4	5.90E-01	1.00E+00
	GOTERM_CC_FAT	voltage-gated calcium channel complex	3	7.00E-01	9.80E-01
	KEGG_PATHWAY	Hypertrophic cardiomyopathy (HCM)	9	7.50E-01	9.70E-01
	GOTERM_MF_FAT	calcium channel activity	8	7.50E-01	1.00E+00
	SP_PIR_KEYWORDS	calcium channel	6	7.80E-01	9.90E-01
	KEGG_PATHWAY	Cardiac muscle contraction	8	7.80E-01	9.70E-01
	GOTERM_CC_FAT	calcium channel complex	3	8.00E-01	9.90E-01
	KEGG_PATHWAY	Dilated cardiomyopathy	9	8.20E-01	9.70E-01
Annotation Cluster 161	**Enrichment Score: 0.43**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	positive regulation of mesenchymal cell proliferation	4	2.70E-01	9.90E-01
	GOTERM_BP_FAT	regulation of mesenchymal cell proliferation	4	3.00E-01	9.90E-01
	GOTERM_BP_FAT	positive regulation of epithelial cell proliferation	5	6.40E-01	1.00E+00
Annotation Cluster 162	**Enrichment Score: 0.43**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	domain:VWFA 1	4	2.30E-01	1.00E+00
	UP_SEQ_FEATURE	domain:VWFA 2	4	2.60E-01	1.00E+00
	SMART	VWA	10	3.80E-01	9.70E-01
	INTERPRO	von Willebrand factor, type A	10	4.60E-01	1.00E+00
	UP_SEQ_FEATURE	domain:VWFA	7	6.50E-01	1.00E+00
Annotation Cluster 163	**Enrichment Score: 0.43**		**Count**	**P_Value**	**Benjamini**
	OMIM_DISEASE	Common variants at 30 loci contribute to polygenic dyslipidemia	9	6.40E-02	1.00E+00
	GOTERM_BP_FAT	glycerol ether biosynthetic process	4	1.50E-01	9.80E-01
	GOTERM_BP_FAT	very-low-density lipoprotein particle remodeling	3	1.60E-01	9.80E-01
	GOTERM_BP_FAT	triglyceride metabolic process	8	1.70E-01	9.80E-01
	GOTERM_BP_FAT	glycerol ether metabolic process	9	1.70E-01	9.80E-01
	GOTERM_BP_FAT	organic ether metabolic process	9	1.90E-01	9.80E-01
	GOTERM_BP_FAT	triglyceride homeostasis	3	2.00E-01	9.90E-01
	GOTERM_BP_FAT	triglyceride-rich lipoprotein particle remodeling	3	2.50E-01	9.90E-01
	GOTERM_BP_FAT	low-density lipoprotein particle remodeling	3	2.50E-01	9.90E-01
	GOTERM_BP_FAT	triglyceride biosynthetic process	3	2.50E-01	9.90E-01
	GOTERM_BP_FAT	acylglycerol metabolic process	8	2.60E-01	9.90E-01
	GOTERM_BP_FAT	neutral lipid metabolic process	8	2.80E-01	9.90E-01
	GOTERM_BP_FAT	macromolecular complex remodeling	4	3.60E-01	1.00E+00
	GOTERM_BP_FAT	protein-lipid complex remodeling	4	3.60E-01	1.00E+00
	GOTERM_BP_FAT	plasma lipoprotein particle remodeling	4	3.60E-01	1.00E+00
	OMIM_DISEASE	Genome-wide association analysis of metabolic traits in a birth cohort from a founder population	4	3.60E-01	1.00E+00
	GOTERM_BP_FAT	high-density lipoprotein particle remodeling	3	3.70E-01	1.00E+00
	GOTERM_BP_FAT	neutral lipid biosynthetic process	3	3.70E-01	1.00E+00
	GOTERM_BP_FAT	acylglycerol biosynthetic process	3	3.70E-01	1.00E+00
	GOTERM_BP_FAT	reverse cholesterol transport	3	5.20E-01	1.00E+00
	OMIM_DISEASE	Newly identified loci that influence lipid concentrations and risk of coronary artery disease	4	5.40E-01	1.00E+00
	GOTERM_BP_FAT	lipid homeostasis	6	6.40E-01	1.00E+00
	OMIM_DISEASE	Six new loci associated with blood low-density lipoprotein cholesterol, high-density lipoprotein cholesterol or triglycerides in humans	4	6.50E-01	1.00E+00
	GOTERM_CC_FAT	protein-lipid complex	4	7.40E-01	9.80E-01
	GOTERM_CC_FAT	plasma lipoprotein particle	4	7.40E-01	9.80E-01
	GOTERM_BP_FAT	regulation of foam cell differentiation	3	7.60E-01	1.00E+00
	GOTERM_CC_FAT	high-density lipoprotein particle	3	7.70E-01	9.90E-01
	GOTERM_BP_FAT	sterol transport	4	7.70E-01	1.00E+00
	GOTERM_BP_FAT	cholesterol transport	4	7.70E-01	1.00E+00
	GOTERM_BP_FAT	sterol homeostasis	4	7.80E-01	1.00E+00
	GOTERM_BP_FAT	cholesterol homeostasis	4	7.80E-01	1.00E+00
	OMIM_DISEASE	Loci influencing lipid levels and coronary heart disease risk in 16 European population cohorts	3	7.90E-01	1.00E+00
Annotation Cluster 164	**Enrichment Score: 0.43**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	amino sugar metabolic process	5	2.70E-01	9.90E-01
	GOTERM_BP_FAT	glucosamine metabolic process	4	3.60E-01	1.00E+00
	GOTERM_BP_FAT	N-acetylglucosamine metabolic process	4	3.60E-01	1.00E+00
	GOTERM_CC_FAT	intrinsic to Golgi membrane	6	5.60E-01	9.70E-01
Annotation Cluster 165	**Enrichment Score: 0.43**		**Count**	**P_Value**	**Benjamini**
	GOTERM_MF_FAT	kinase regulator activity	13	2.90E-01	9.90E-01

ILMN_1775111	SND1	0.686717255
ILMN_2113333	LGALS9B	0.686662288
ILMN_1773347	CARD14	0.686631498
ILMN_2411723	RPSA	0.686628097
ILMN_1677877	UBE2L3	0.686490093
ILMN_1745242	PLSCR1	0.686490004
ILMN_1783636	COX6A1	0.686451705
ILMN_1742001	CD160	0.686319965
ILMN_1663379	FBXL15	0.686314752
ILMN_1771447	ZNF833P	0.686283476
ILMN_2340027	TSPAN4	0.686245124
ILMN_1670037	POLR2L	0.686141665
ILMN_1679401	TRPM4	0.686131347
ILMN_1683447	RPL35	0.685977161
ILMN_1652464	TUBA3E	0.68591112
ILMN_2412024	JMJD6	0.685785596
ILMN_1655625	GPATCH1	0.685732948
ILMN_2391765	C6orf48	0.685655911
ILMN_2334193	SLC22A2	0.685628417
ILMN_1795286	C6orf47	0.685560508
ILMN_1708534	PAX8	0.685397814
ILMN_3222402	FLJ45340	0.685381068
ILMN_1815734	FCHSD2	0.685305967
ILMN_1813604	NDUFB7	0.685281181
ILMN_1749579	PKHD1	0.685128982
ILMN_2370872	GRINA	0.685109859
ILMN_1763000	ADAP2	0.685053322
ILMN_1751075	SETD4	0.684873964
ILMN_1735014	KLF6	0.684850944
ILMN_1810577	RPS4X	0.684811427
ILMN_1791067	TESK1	0.684715357
ILMN_1803686	ADA	0.684715039
ILMN_1702592	WDR73	0.684679673
ILMN_2317923	TMEM132A	0.684677645
ILMN_1746588	TALDO1	0.684628684
ILMN_1705733	RPRD2	0.684532078
ILMN_2050112	RPSA	0.684492304
ILMN_1779034	NADSYN1	0.684450156
ILMN_3191596	STAG3L2	0.684346439
ILMN_1651958	MGP	0.684329929
ILMN_1785161	CHCHD6	0.684313981
ILMN_1770719	KIAA0664	0.684275455
ILMN_2116714	SLC39A1	0.684062935
ILMN_1737805	TPCN1	0.683876536
ILMN_3207060	RPL4	0.683759877
ILMN_1666670	RBX1	0.683743884
ILMN_2359453	ERGIC3	0.68366081
ILMN_1664922	FLNB	0.683633582
ILMN_1755850	ZNF350	0.683521295
ILMN_1712975	YIF1A	0.683513172
ILMN_1795918	AGAP3	0.683504337
ILMN_1811063	RPL29	0.683283692
ILMN_1750100	TUBB8	0.683042307
ILMN_1683700	TNFSF13	0.683012708
ILMN_1700690	VAT1	0.68295504
ILMN_2268026	C15orf44	0.682931494
ILMN_1671971	KRT8	0.6829028
ILMN_1733861	ARHGEF11	0.682879575
ILMN_1814823	FTL	0.682873452
ILMN_1796912	ARHGEF7	0.682848631
ILMN_1737576	RASA1	0.682789539
ILMN_1710885	RPSA	0.682731828
ILMN_3238001	LOC349114	0.682662627
ILMN_1775939	SF3B2	0.682631349
ILMN_1715301	FXYD2	0.682449405
ILMN_1704294	CDH3	0.682098062
ILMN_1708029	TMEM8B	0.682072756
ILMN_1713993	UBAC2	0.681886723
ILMN_2286870	CSNK1D	0.681829554
ILMN_1716488	PACS1	0.681747234
ILMN_2405031	TRIM24	0.681644452
ILMN_1662409	PRR13	0.681468652
ILMN_2165753	HLA-A	0.681360286
ILMN_1664440	TP53BP1	0.681355726
ILMN_1782403	PRR11	0.681324401
ILMN_1676600	SEC24C	0.681277727
ILMN_1728197	CLDN5	0.68126484
ILMN_1696434	LAMA1	0.681250869
ILMN_1720083	EHD4	0.681179854
ILMN_1707631	MED10	0.68102544
ILMN_1701477	CCDC101	0.68098973
ILMN_1669215	SRPK2	0.680880702
ILMN_1743755	C6orf226	0.680831211
ILMN_1720941	EVC	0.680770855
ILMN_1777190	CFD	0.680639226
ILMN_2389876	TGFB1I1	0.680518629
ILMN_1704672	OBFC2B	0.680479917
ILMN_2399174	TRAK1	0.680359331
ILMN_1675124	DDX17	0.68020088
ILMN_1677532	TARDBP	0.680106053
ILMN_2103591	MORC2	0.680078405
ILMN_1663145	NOMO3	0.680036137
ILMN_2234758	SRP14	0.679898981
ILMN_2092693	LSM12	0.679857254

	INTERPRO	Galectin, carbohydrate recognition domain	4	2.90E-01	1.00E+00
	SMART	GLECT	4	3.20E-01	9.50E-01
Annotation Cluster 129	**Enrichment Score: 0.9**		**Count**	**P_Value**	**Benjamini**
	SP_PIR_KEYWORDS	Aminoacyl-tRNA synthetase	10	3.90E-02	2.50E-01
	GOTERM_MF_FAT	ligase activity, forming carbon-oxygen bonds	11	7.20E-02	7.00E-01
	GOTERM_MF_FAT	ligase activity, forming aminoacyl-tRNA and related compounds	11	7.20E-02	7.00E-01
	GOTERM_MF_FAT	aminoacyl-tRNA ligase activity	11	7.20E-02	7.00E-01
	GOTERM_BP_FAT	amino acid activation	11	7.30E-02	6.00E-01
	GOTERM_BP_FAT	tRNA aminoacylation for protein translation	11	7.30E-02	6.00E-01
	GOTERM_BP_FAT	tRNA aminoacylation	11	7.30E-02	6.00E-01
	UP_SEQ_FEATURE	short sequence motif:"KMSKS" region	5	1.20E-01	1.00E+00
	KEGG_PATHWAY	Aminoacyl-tRNA biosynthesis	10	1.50E-01	5.00E-01
	UP_SEQ_FEATURE	short sequence motif:"HIGH" region	5	1.70E-01	1.00E+00
	INTERPRO	Rossmann-like alpha/beta/alpha sandwich fold	8	2.30E-01	1.00E+00
	GOTERM_BP_FAT	tRNA metabolic process	19	2.90E-01	9.30E-01
	INTERPRO	Aminoacyl-tRNA synthetase, class II, conserved region	4	3.60E-01	1.00E+00
	INTERPRO	Aminoacyl-tRNA synthetase, class I, conserved site	5	6.40E-01	1.00E+00
Annotation Cluster 130	**Enrichment Score: 0.89**		**Count**	**P_Value**	**Benjamini**
	INTERPRO	Protein kinase C-like, phorbol ester/diacylglycerol binding	15	3.80E-02	9.10E-01
	SMART	C1	15	5.20E-02	7.40E-01
	INTERPRO	Protein kinase C, phorbol ester/diacylglycerol binding	11	9.20E-02	9.60E-01
	GOTERM_MF_FAT	diacylglycerol binding	13	1.60E-01	8.80E-01
	UP_SEQ_FEATURE	zinc finger region:Phorbol-ester/DAG-type	8	2.60E-01	1.00E+00
	UP_SEQ_FEATURE	zinc finger region:Phorbol-ester/DAG-type 2	5	2.70E-01	1.00E+00
	UP_SEQ_FEATURE	zinc finger region:Phorbol-ester/DAG-type 1	5	2.70E-01	1.00E+00
Annotation Cluster 131	**Enrichment Score: 0.89**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	glycosylation site:O-linked (Xyl...) (glycosaminoglycan)	5	7.90E-02	1.00E+00
	SP_PIR_KEYWORDS	chondroitin sulfate proteoglycan	5	1.40E-01	5.30E-01
	SP_PIR_KEYWORDS	proteoglycan	10	2.00E-01	6.30E-01
Annotation Cluster 132	**Enrichment Score: 0.89**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	positive regulation of MAPKKK cascade	11	9.30E-02	6.60E-01
	GOTERM_BP_FAT	positive regulation of stress-activated protein kinase signaling pathway	6	1.30E-01	7.60E-01
	GOTERM_BP_FAT	positive regulation of JNK cascade	5	1.80E-01	8.30E-01
Annotation Cluster 133	**Enrichment Score: 0.88**		**Count**	**P_Value**	**Benjamini**
	INTERPRO	Histone H3	3	1.20E-01	9.80E-01
	SMART	H3	3	1.30E-01	8.10E-01
	PIR_SUPERFAMILY	PIRSF002051:histone H3	3	1.40E-01	1.00E+00
Annotation Cluster 134	**Enrichment Score: 0.88**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	repeat:HEAT 3	12	3.40E-02	9.90E-01
	INTERPRO	Armadillo-like helical	24	5.00E-02	9.20E-01
	UP_SEQ_FEATURE	repeat:HEAT 7	7	6.20E-02	1.00E+00
	UP_SEQ_FEATURE	repeat:HEAT 8	6	7.10E-02	1.00E+00
	INTERPRO	HEAT	12	8.00E-02	9.60E-01
	UP_SEQ_FEATURE	repeat:HEAT 2	12	8.60E-02	1.00E+00
	UP_SEQ_FEATURE	repeat:HEAT 1	12	8.60E-02	1.00E+00
	UP_SEQ_FEATURE	repeat:HEAT 5	8	1.20E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:HEAT 4	9	1.40E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:HEAT 6	7	1.50E-01	1.00E+00
	UP_SEQ_FEATURE	domain:Importin N-terminal	4	2.40E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:HEAT 9	4	2.70E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:HEAT 10	4	2.70E-01	1.00E+00
	INTERPRO	Importin-beta, N-terminal	4	2.90E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:HEAT 11	3	3.90E-01	1.00E+00
	GOTERM_BP_FAT	protein import into nucleus, docking	4	3.90E-01	9.70E-01
Annotation Cluster 135	**Enrichment Score: 0.88**		**Count**	**P_Value**	**Benjamini**
	GOTERM_CC_FAT	organelle membrane	183	7.40E-04	1.70E-02
	GOTERM_CC_FAT	organelle envelope	103	1.30E-02	1.60E-01
	GOTERM_CC_FAT	envelope	103	1.50E-02	1.60E-01
	GOTERM_CC_FAT	organelle inner membrane	50	2.20E-01	7.00E-01
	SP_PIR_KEYWORDS	mitochondrion inner membrane	27	3.00E-01	7.50E-01
	GOTERM_CC_FAT	mitochondrial envelope	58	4.60E-01	9.00E-01
	SP_PIR_KEYWORDS	mitochondrion	102	4.90E-01	8.90E-01
	GOTERM_CC_FAT	mitochondrial part	81	5.00E-01	9.20E-01
	GOTERM_CC_FAT	mitochondrial membrane	53	5.60E-01	9.40E-01
	GOTERM_CC_FAT	mitochondrial inner membrane	41	5.80E-01	9.40E-01
	GOTERM_CC_FAT	mitochondrion	144	5.90E-01	9.40E-01
Annotation Cluster 136	**Enrichment Score: 0.88**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	natural killer cell mediated cytotoxicity	4	7.70E-02	6.10E-01
	GOTERM_BP_FAT	natural killer cell mediated immunity	4	7.70E-02	6.10E-01
	GOTERM_BP_FAT	leukocyte mediated cytotoxicity	4	1.40E-01	7.70E-01
	GOTERM_BP_FAT	cell killing	5	3.90E-01	9.70E-01
Annotation Cluster 137	**Enrichment Score: 0.85**		**Count**	**P_Value**	**Benjamini**
	KEGG_PATHWAY	Pentose phosphate pathway	8	6.90E-02	3.40E-01
	GOTERM_MF_FAT	monosaccharide binding	9	1.30E-01	8.50E-01
	GOTERM_BP_FAT	fructose metabolic process	5	1.80E-01	8.30E-01
	GOTERM_BP_FAT	fructose 6-phosphate metabolic process	3	2.30E-01	8.90E-01
Annotation Cluster 138	**Enrichment Score: 0.84**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	domain:EH	3	1.10E-01	1.00E+00
	INTERPRO	EPS15 homology (EH)	4	1.50E-01	9.90E-01
	SMART	EH	4	1.70E-01	8.70E-01
Annotation Cluster 139	**Enrichment Score: 0.84**		**Count**	**P_Value**	**Benjamini**
	INTERPRO	Calponin-like actin-binding	18	5.30E-03	4.90E-01
	SMART	CH	18	8.20E-03	3.80E-01
	UP_SEQ_FEATURE	domain:Actin-binding	7	2.70E-02	9.90E-01
	UP_SEQ_FEATURE	domain:CH 1	8	3.80E-02	9.90E-01
	UP_SEQ_FEATURE	domain:CH 2	8	3.80E-02	9.90E-01
	UP_SEQ_FEATURE	domain:CH	10	6.10E-02	1.00E+00
	INTERPRO	Actinin-type, actin-binding, conserved site	7	6.10E-02	9.40E-01
	UP_SEQ_FEATURE	repeat:Spectrin 4	6	1.00E-01	1.00E+00
	INTERPRO	Spectrin repeat	6	1.20E-01	9.70E-01
	UP_SEQ_FEATURE	repeat:Spectrin 3	6	1.20E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:Spectrin 2	6	2.00E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:Spectrin 1	6	2.00E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:Spectrin 8	4	2.00E-01	1.00E+00

ILMN_1855868	BX093310	-0.451331075
ILMN_1721727	USP6	-0.451404358
ILMN_2152828	KIF16B	-0.451493441
ILMN_2231985	HSPA13	-0.451513311
ILMN_2346451	ACTR3B	-0.45152437
ILMN_1664698	UNC119	-0.451559593
ILMN_1796813	EED	-0.451559871
ILMN_2339779	ATP6V1E1	-0.451584432
ILMN_1770245	EPB41L5	-0.451598535
ILMN_1804470	C17orf109	-0.451601199
ILMN_2179533	C4A	-0.451608326
ILMN_1839138	BU632831	-0.451610381
ILMN_1779423	MRPS14	-0.451646238
ILMN_1663156	DDX31	-0.451662968
ILMN_1718236	LL0XNC01-19D8.1	-0.451680163
ILMN_1689831	FLJ11235	-0.451680904
ILMN_1902112	AA725558	-0.451820475
ILMN_3265228	LOC653581	-0.45182171
ILMN_1686750	MGEA5	-0.451876182
ILMN_1653783	MLC1	-0.45190179
ILMN_1685260	DNM1L	-0.451901885
ILMN_3311115	MIR663B	-0.451939116
ILMN_2373073	LIG4	-0.452046064
ILMN_2204826	SEPP1	-0.452164644
ILMN_1668498	CWF19L2	-0.452190494
ILMN_1896431	AK127458	-0.452238922
ILMN_1714461	RNF14	-0.452276499
ILMN_3300937	C13orf25 v_1	-0.452305745
ILMN_1779584	UTP18	-0.452364263
ILMN_1782609	STAG2	-0.45237227
ILMN_3248146	LOC100128542	-0.452375432
ILMN_1848552	NFIB	-0.452412585
ILMN_1686804	CDK20	-0.452480917
ILMN_1862939	BX100265	-0.452678126
ILMN_1688629	ZNF274	-0.452718779
ILMN_1773850	FXC1	-0.452756995
ILMN_3236346	ZNF286B	-0.452806789
ILMN_1818248	NCRNA00160	-0.452812817
ILMN_1671642	CSNK1A1L	-0.452891287
ILMN_1808487	PLA2G12B	-0.4529136
ILMN_1731314	OR10H3	-0.452948706
ILMN_1755047	LRRC2	-0.45300658
ILMN_3247592	ZNF830	-0.453018831
ILMN_1811278	RNF186	-0.453047927
ILMN_1784395	NA	-0.453048809
ILMN_1783645	DKFZp666P158	-0.453100566
ILMN_1661940	CAMTA1	-0.453156789
ILMN_1738816	FOXO1	-0.453196211
ILMN_1659631	LOC440905	-0.453198176
ILMN_1764186	ATXN1L	-0.453309646
ILMN_1799293	MINA53	-0.453346269
ILMN_1663367	SERHL	-0.45352334
ILMN_1761438	truncated AKR	-0.453560044
ILMN_2087629	NOL4	-0.453572276
ILMN_3299416	LOC729020	-0.453577253
ILMN_3191746	BCAR4	-0.453581402
ILMN_2339748	RNF13	-0.453588655
ILMN_1786388	RNF113A	-0.45358978
ILMN_1670959	CEACAM5	-0.453723327
ILMN_1738767	PLP2	-0.453741479
ILMN_1718018	PFN3	-0.453795538
ILMN_1695969	TMPRSS15	-0.4538438
ILMN_1859672	AI638857	-0.453955341
ILMN_2149494	NPL	-0.453958514
ILMN_1698060	FLJ43860	-0.453968512
ILMN_1658605	NA	-0.454033952
ILMN_1736060	GLT6D1	-0.454051797
ILMN_3237956	ZC3H12C	-0.454075711
ILMN_1806800	TRADD	-0.454086329
ILMN_1808272	KCNJ10	-0.454187942
ILMN_1893798	CK823348	-0.454212595
ILMN_2128931	FAT2	-0.454283376
ILMN_3224722	NA	-0.454290694
ILMN_1767274	FBLL1	-0.454352567
ILMN_1690048	OR4F21	-0.454415141
ILMN_3275685	LOC727721	-0.454522545
ILMN_1752791	PARP8	-0.454564307
ILMN_1769673	ZNF655	-0.45460196
ILMN_2038777	ACTB	-0.45465125
ILMN_1880796	BE439524	-0.454668251
ILMN_3199911	BX106402	-0.454680283
ILMN_3185278	LOC100128542	-0.454783315
ILMN_1815938	TRPM3	-0.454826748
ILMN_1660400	CELF4	-0.454880016
ILMN_1717904	SORBS3	-0.454882914
ILMN_1888546	AI039233	-0.454979676
ILMN_1808238	RBPMS2	-0.455000533
ILMN_1803819	IQGAP1	-0.455007066
ILMN_1719788	LDHAL6B	-0.455027337
ILMN_1804329	TUSC2	-0.455035191
ILMN_1730477	TAS2R43	-0.45505705
ILMN_1666453	STK3	-0.45509784
ILMN_2403911	ARFIP1	-0.4551006
ILMN_1664118	CADM2	-0.455124987

	GOTERM_MF_FAT	protein kinase inhibitor activity	6	3.40E-01	9.90E-01
	GOTERM_MF_FAT	kinase inhibitor activity	6	3.60E-01	9.90E-01
	GOTERM_MF_FAT	protein kinase regulator activity	11	3.60E-01	9.90E-01
	GOTERM_MF_FAT	protein serine/threonine kinase inhibitor activity	3	5.60E-01	1.00E+00
Annotation Cluster 166	**Enrichment Score: 0.42**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	telencephalon development	10	2.50E-01	9.90E-01
	GOTERM_BP_FAT	pallium development	7	3.60E-01	1.00E+00
	GOTERM_BP_FAT	hippocampus development	4	4.20E-01	1.00E+00
	GOTERM_BP_FAT	limbic system development	5	4.40E-01	1.00E+00
	GOTERM_BP_FAT	cerebral cortex development	5	4.70E-01	1.00E+00
Annotation Cluster 167	**Enrichment Score: 0.42**		**Count**	**P_Value**	**Benjamini**
	SP_PIR_KEYWORDS	dioxygenase	10	2.50E-01	9.00E-01
	UP_SEQ_FEATURE	metal ion-binding site:Iron; catalytic	5	2.70E-01	1.00E+00
	GOTERM_MF_FAT	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	9	4.10E-01	1.00E+00
	GOTERM_MF_FAT	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen	9	4.30E-01	1.00E+00
	GOTERM_MF_FAT	L-ascorbic acid binding	3	6.70E-01	1.00E+00
Annotation Cluster 168	**Enrichment Score: 0.42**		**Count**	**P_Value**	**Benjamini**
	INTERPRO	HEAT	9	2.20E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:HEAT 14	3	2.40E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:HEAT 1	9	2.60E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:HEAT 2	9	2.60E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:HEAT 12	3	2.80E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:HEAT 13	3	2.80E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:HEAT 11	3	3.20E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:HEAT 6	5	3.90E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:HEAT 7	4	4.70E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:HEAT 4	6	4.80E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:HEAT 10	3	4.80E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:HEAT 9	3	4.80E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:HEAT 5	5	5.10E-01	1.00E+00
	INTERPRO	Armadillo-like helical	14	6.10E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:HEAT 8	3	6.10E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:HEAT 3	6	6.20E-01	1.00E+00
Annotation Cluster 169	**Enrichment Score: 0.41**		**Count**	**P_Value**	**Benjamini**
	SP_PIR_KEYWORDS	amino-acid transport	7	1.70E-01	8.70E-01
	INTERPRO	Amino acid permease-associated region	5	2.00E-01	1.00E+00
	GOTERM_BP_FAT	amino acid transport	13	2.40E-01	9.90E-01
	GOTERM_BP_FAT	amine transport	15	3.70E-01	1.00E+00
	GOTERM_BP_FAT	carboxylic acid transport	18	3.90E-01	1.00E+00
	GOTERM_BP_FAT	organic acid transport	18	4.00E-01	1.00E+00
	INTERPRO	Amino acid/polyamine transporter I	3	4.80E-01	1.00E+00
	PIR_SUPERFAMILY	PIRSF006060:AA_transporter	3	4.90E-01	1.00E+00
	GOTERM_MF_FAT	amine transmembrane transporter activity	9	5.40E-01	1.00E+00
	GOTERM_MF_FAT	L-amino acid transmembrane transporter activity	5	5.90E-01	1.00E+00
	GOTERM_MF_FAT	amino acid transmembrane transporter activity	6	7.70E-01	1.00E+00
Annotation Cluster 170	**Enrichment Score: 0.41**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	response to estradiol stimulus	8	3.50E-01	1.00E+00
	GOTERM_BP_FAT	response to steroid hormone stimulus	23	3.80E-01	1.00E+00
	GOTERM_BP_FAT	response to estrogen stimulus	13	4.40E-01	1.00E+00
Annotation Cluster 171	**Enrichment Score: 0.41**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	cell-cell signaling	69	3.00E-01	9.90E-01
	GOTERM_BP_FAT	transmission of nerve impulse	40	4.00E-01	1.00E+00
	GOTERM_BP_FAT	synaptic transmission	33	5.00E-01	1.00E+00
Annotation Cluster 172	**Enrichment Score: 0.41**		**Count**	**P_Value**	**Benjamini**
	GOTERM_CC_FAT	Sin3 complex	3	2.10E-01	9.50E-01
	GOTERM_CC_FAT	Sin3-type complex	3	2.10E-01	9.50E-01
	GOTERM_CC_FAT	NuRD complex	3	4.20E-01	9.60E-01
	GOTERM_CC_FAT	histone deacetylase complex	6	4.50E-01	9.70E-01
	GOTERM_CC_FAT	chromatin remodeling complex	8	6.50E-01	9.80E-01
	GOTERM_CC_FAT	transcriptional repressor complex	5	6.60E-01	9.80E-01
Annotation Cluster 173	**Enrichment Score: 0.41**		**Count**	**P_Value**	**Benjamini**
	GOTERM_CC_FAT	vacuole	34	1.30E-01	9.30E-01
	SP_PIR_KEYWORDS	lysosome	17	5.00E-01	9.60E-01
	GOTERM_CC_FAT	lytic vacuole	23	5.90E-01	9.70E-01
	GOTERM_CC_FAT	lysosome	23	5.90E-01	9.70E-01
Annotation Cluster 174	**Enrichment Score: 0.41**		**Count**	**P_Value**	**Benjamini**
	GOTERM_MF_FAT	gap junction channel activity	3	2.90E-01	9.90E-01
	GOTERM_MF_FAT	wide pore channel activity	3	3.30E-01	9.90E-01
	SMART	CNX	4	3.50E-01	9.70E-01
	INTERPRO	Connexins	4	3.60E-01	1.00E+00
	INTERPRO	Gap junction protein, cysteine-rich domain	4	3.60E-01	1.00E+00
	INTERPRO	Connexin, N-terminal	4	3.90E-01	1.00E+00
	INTERPRO	Connexin region	4	3.90E-01	1.00E+00
	INTERPRO	Connexin, conserved site	4	3.90E-01	1.00E+00
	PIR_SUPERFAMILY	PIRSF002292:gap junction protein	3	4.20E-01	1.00E+00
	GOTERM_CC_FAT	connexon complex	4	4.30E-01	9.60E-01
	SP_PIR_KEYWORDS	gap junction	4	4.90E-01	9.60E-01
	GOTERM_CC_FAT	gap junction	4	6.20E-01	9.70E-01
Annotation Cluster 175	**Enrichment Score: 0.4**		**Count**	**P_Value**	**Benjamini**
	GOTERM_CC_FAT	vacuolar proton-transporting V-type ATPase complex	3	2.90E-01	9.60E-01
	GOTERM_CC_FAT	vacuolar membrane	8	4.00E-01	9.60E-01
	GOTERM_CC_FAT	vacuolar part	8	5.40E-01	9.70E-01
Annotation Cluster 176	**Enrichment Score: 0.4**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	midgut development	3	9.00E-02	9.80E-01
	GOTERM_BP_FAT	morphogenesis of embryonic epithelium	9	2.70E-01	9.90E-01
	GOTERM_BP_FAT	embryonic epithelial tube formation	7	3.00E-01	9.90E-01
	GOTERM_BP_FAT	tube lumen formation	7	3.20E-01	9.90E-01
	GOTERM_BP_FAT	mesenchymal cell development	7	4.60E-01	1.00E+00
	GOTERM_BP_FAT	mesenchymal cell differentiation	7	4.60E-01	1.00E+00
	GOTERM_BP_FAT	neural crest cell differentiation	5	4.70E-01	1.00E+00
	GOTERM_BP_FAT	neural crest cell development	5	4.70E-01	1.00E+00
	GOTERM_BP_FAT	mesenchyme development	7	4.80E-01	1.00E+00
	GOTERM_BP_FAT	ameboidal cell migration	5	5.60E-01	1.00E+00
	GOTERM_BP_FAT	neural crest cell migration	3	7.20E-01	1.00E+00

ILMN_1737298	MAT2A	0.679827006
ILMN_1665943	MAP4K1	0.679808081
ILMN_1679358	ZDHHC5	0.679527043
ILMN_1677800	SGTA	0.679354713
ILMN_1673804	ZNF426	0.679337048
ILMN_1789839	GTF3C1	0.679195114
ILMN_1746968	PHF1	0.679013586
ILMN_1743910	PANK4	0.678918564
ILMN_1674038	CTSD	0.678821669
ILMN_1755883	RPS27A	0.678720553
ILMN_1709114	TAB1	0.678693357
ILMN_1768284	P2RY8	0.678472555
ILMN_1666449	LOC162427	0.678254572
ILMN_1706434	CSDAP1	0.678202914
ILMN_3248008	TUBB	0.678176598
ILMN_1700109	PTOV1	0.6781494
ILMN_1807493	ACVRL1	0.678119532
ILMN_1689446	EIF3G	0.677980343
ILMN_2391912	SEC14L1	0.677749592
ILMN_1687857	ST6GALNAC4	0.677553537
ILMN_1697544	SLC25A29	0.677453833
ILMN_1801130	STOML1	0.677406535
ILMN_1740160	PLCG1	0.677277017
ILMN_1801307	TNFSF10	0.677247548
ILMN_2147133	NBPF1	0.677063664
ILMN_1738369	TUFM	0.676960033
ILMN_1693650	FES	0.676938331
ILMN_1769705	H3F3C	0.676923188
ILMN_1661306	RPL29	0.676862337
ILMN_1786852	ZCCHC3	0.676740179
ILMN_1693986	WHAMML2	0.676705172
ILMN_1807169	TINAGL1	0.676688423
ILMN_1783226	SSR2	0.676511775
ILMN_1651385	MFN2	0.676415783
ILMN_3249419	FLJ14186	0.676375007
ILMN_1732615	ASMTL	0.676373858
ILMN_2406169	PKIG	0.676299555
ILMN_1686981	SULF2	0.676187438
ILMN_3181411	ATL1	0.67616968
ILMN_1725193	IGFBP2	0.676160599
ILMN_1654032	ZER1	0.676066546
ILMN_1675266	NAGPA	0.676063654
ILMN_3295847	RPL6	0.675929137
ILMN_1815519	EPN2	0.675922864
ILMN_1688534	EIF2B5	0.675901234
ILMN_1696757	TTC14	0.67582851
ILMN_3251728	MTMR10	0.675820703
ILMN_3283573	RPL4	0.675768654
ILMN_1675992	DST	0.67572379
ILMN_2183510	MANF	0.675488921
ILMN_1682929	SYTL2	0.675266457
ILMN_1665390	SPDYE7P	0.675218732
ILMN_2348503	PPIE	0.674954781
ILMN_1715832	PIK3R4	0.674874204
ILMN_1669433	KIAA0913	0.674832191
ILMN_1754746	CCNB3	0.67475101
ILMN_1812557	CDK5RAP3	0.674746479
ILMN_1737964	HIATL1	0.674740263
ILMN_2383419	GMEB1	0.674735708
ILMN_1768812	FXYD6	0.674594413
ILMN_1715305	TRIM6	0.674593136
ILMN_2397721	GLB1	0.674552325
ILMN_1792135	SLC35A2	0.674514242
ILMN_1666376	TRIM56	0.674371914
ILMN_1809495	COX8A	0.674359617
ILMN_2257015	AGER	0.674284093
ILMN_1710937	IFI16	0.674261606
ILMN_2124386	RGL2	0.674245626
ILMN_1734742	ARHGDIA	0.674235917
ILMN_1727041	EWSR1	0.674058724
ILMN_3238221	FLJ42627	0.674022751
ILMN_1739103	MPZL1	0.673915791
ILMN_1763452	EVI2B	0.673891872
ILMN_2326071	MYL6	0.673865263
ILMN_1732609	KIAA1539	0.673851422
ILMN_2062524	RBBP4	0.673761966
ILMN_1797298	ARMC7	0.673370934
ILMN_2160388	RPL24	0.673342293
ILMN_1688011	UPF1	0.673232877
ILMN_1785272	COL1A2	0.672931436
ILMN_1759915	ARPC1A	0.672786001
ILMN_2316806	RWDD1	0.67265973
ILMN_1660554	VWA1	0.672628474
ILMN_1805466	SOX9	0.672350778
ILMN_2058782	IFI27	0.672182059
ILMN_1804384	ASMTL	0.672147564
ILMN_3282436	EIF3F	0.672028851

	UP_SEQ_FEATURE	repeat:Spectrin 9	4	2.00E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:Spectrin 6	4	2.00E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:Spectrin 7	4	2.00E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:Spectrin 5	4	2.40E-01	1.00E+00
	INTERPRO	Spectrin/alpha-actinin	6	3.50E-01	1.00E+00
	SMART	SPEC	6	3.90E-01	9.70E-01
	UP_SEQ_FEATURE	repeat:Spectrin 16	3	4.40E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:Spectrin 17	3	4.40E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:Spectrin 14	3	4.40E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:Spectrin 15	3	4.40E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:Spectrin 12	3	4.40E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:Spectrin 13	3	4.40E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:Spectrin 11	3	4.40E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:Spectrin 10	3	4.40E-01	1.00E+00
Annotation Cluster 140	**Enrichment Score: 0.84**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	response to organic substance	123	1.90E-03	6.00E-02
	GOTERM_BP_FAT	cellular response to hormone stimulus	24	1.00E-01	6.90E-01
	GOTERM_BP_FAT	response to hormone stimulus	56	1.70E-01	8.20E-01
	GOTERM_BP_FAT	insulin receptor signaling pathway	8	2.10E-01	8.70E-01
	GOTERM_BP_FAT	response to peptide hormone stimulus	25	2.20E-01	8.80E-01
	GOTERM_BP_FAT	response to endogenous stimulus	59	2.70E-01	9.20E-01
	GOTERM_BP_FAT	cellular response to insulin stimulus	12	2.80E-01	9.20E-01
	GOTERM_BP_FAT	response to insulin stimulus	16	3.40E-01	9.50E-01
	GOTERM_BP_FAT	response to steroid hormone stimulus	23	7.90E-01	1.00E+00
Annotation Cluster 141	**Enrichment Score: 0.83**		**Count**	**P_Value**	**Benjamini**
	INTERPRO	Cell surface receptor IPT/TIG	10	2.20E-02	8.20E-01
	SMART	IPT	10	2.90E-02	6.00E-01
	INTERPRO	Plexin/semaphorin/integrin	11	5.10E-02	9.20E-01
	UP_SEQ_FEATURE	domain:IPT/TIG 3	5	6.20E-02	1.00E+00
	UP_SEQ_FEATURE	domain:IPT/TIG 2	5	6.20E-02	1.00E+00
	SMART	PSI	11	6.50E-02	7.50E-01
	UP_SEQ_FEATURE	domain:IPT/TIG 4	3	2.50E-01	1.00E+00
	INTERPRO	Plexin cytoplasmic region	3	3.20E-01	1.00E+00
	INTERPRO	Plexin	6	3.50E-01	1.00E+00
	UP_SEQ_FEATURE	domain:IPT/TIG 1	3	3.90E-01	1.00E+00
	UP_SEQ_FEATURE	domain:Sema	5	5.30E-01	1.00E+00
	INTERPRO	Semaphorin/CD100 antigen	5	5.60E-01	1.00E+00
	SMART	Sema	5	6.00E-01	9.90E-01
Annotation Cluster 142	**Enrichment Score: 0.83**		**Count**	**P_Value**	**Benjamini**
	GOTERM_CC_FAT	endoplasmic reticulum part	62	1.40E-02	1.60E-01
	GOTERM_CC_FAT	nuclear envelope-endoplasmic reticulum network	40	4.50E-01	9.00E-01
	GOTERM_CC_FAT	endoplasmic reticulum membrane	37	5.20E-01	9.20E-01
Annotation Cluster 143	**Enrichment Score: 0.83**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	negative regulation of cellular catabolic process	8	1.10E-02	2.10E-01
	GOTERM_BP_FAT	regulation of proteolysis	14	1.80E-02	2.80E-01
	GOTERM_BP_FAT	regulation of cellular catabolic process	13	9.90E-02	6.80E-01
	GOTERM_BP_FAT	positive regulation of proteolysis	7	1.00E-01	6.90E-01
	GOTERM_BP_FAT	negative regulation of catabolic process	9	1.10E-01	7.00E-01
	GOTERM_BP_FAT	positive regulation of protein catabolic process	7	1.40E-01	7.70E-01
	GOTERM_BP_FAT	negative regulation of proteolysis	6	1.50E-01	8.00E-01
	GOTERM_BP_FAT	regulation of proteasomal ubiquitin-dependent protein catabolic process	4	1.70E-01	8.20E-01
	GOTERM_BP_FAT	regulation of membrane protein ectodomain proteolysis	4	2.40E-01	9.00E-01
	GOTERM_BP_FAT	regulation of protein catabolic process	10	2.40E-01	9.00E-01
	GOTERM_BP_FAT	regulation of catabolic process	16	2.80E-01	9.20E-01
	GOTERM_BP_FAT	positive regulation of membrane protein ectodomain proteolysis	3	3.40E-01	9.50E-01
	GOTERM_BP_FAT	negative regulation of protein catabolic process	4	3.90E-01	9.70E-01
	GOTERM_BP_FAT	positive regulation of catabolic process	8	4.70E-01	9.80E-01
	GOTERM_BP_FAT	positive regulation of cellular catabolic process	6	5.20E-01	9.90E-01
Annotation Cluster 144	**Enrichment Score: 0.81**		**Count**	**P_Value**	**Benjamini**
	GOTERM_MF_FAT	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors	8	5.90E-02	6.50E-01
	GOTERM_MF_FAT	procollagen-proline dioxygenase activity	3	2.20E-01	9.30E-01
	GOTERM_MF_FAT	peptidyl-proline dioxygenase activity	3	2.70E-01	9.60E-01
Annotation Cluster 145	**Enrichment Score: 0.81**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	small GTPase mediated signal transduction	56	9.20E-03	1.90E-01
	GOTERM_MF_FAT	GTPase activity	40	1.20E-02	3.00E-01
	UP_SEQ_FEATURE	nucleotide phosphate-binding region:GTP	48	3.00E-02	9.90E-01
	UP_SEQ_FEATURE	short sequence motif:Effector region	18	6.30E-02	1.00E+00
	SP_PIR_KEYWORDS	prenylation	26	8.30E-02	3.90E-01
	SP_PIR_KEYWORDS	gtp-binding	49	9.20E-02	4.10E-01
	UP_SEQ_FEATURE	lipid moiety-binding region:S-geranylgeranyl cysteine	18	1.10E-01	1.00E+00
	GOTERM_MF_FAT	GTP binding	55	1.90E-01	9.00E-01
	GOTERM_MF_FAT	guanyl nucleotide binding	55	2.50E-01	9.40E-01
	GOTERM_MF_FAT	guanyl ribonucleotide binding	55	2.50E-01	9.40E-01
	INTERPRO	RNA polymerase sigma factor 54, interaction	3	4.10E-01	1.00E+00
	INTERPRO	Ras GTPase	19	4.40E-01	1.00E+00
	INTERPRO	Small GTP-binding protein	23	4.50E-01	1.00E+00
	INTERPRO	Ras small GTPase, Rab type	9	5.10E-01	1.00E+00
	INTERPRO	Ras	17	5.20E-01	1.00E+00
	SMART	RAB	9	5.60E-01	9.90E-01
	PIR_SUPERFAMILY	PIRSF001710:Ras-related protein Rab	3	8.60E-01	1.00E+00
Annotation Cluster 146	**Enrichment Score: 0.81**		**Count**	**P_Value**	**Benjamini**
	INTERPRO	MIF4G-like, type 3	4	1.20E-01	9.80E-01
	INTERPRO	MIF4-like, type 1/2/3	4	1.20E-01	9.80E-01
	SMART	MIF4G	4	1.40E-01	8.10E-01
	UP_SEQ_FEATURE	domain:MIF4G	3	3.00E-01	1.00E+00
Annotation Cluster 147	**Enrichment Score: 0.77**		**Count**	**P_Value**	**Benjamini**
	SP_PIR_KEYWORDS	ascorbic acid	5	2.60E-03	3.40E-02

ILMN_1866314	BX118075	-0.455172406
ILMN_1687073	KIAA0889	-0.455175667
ILMN_3294126	RPL39	-0.455194247
ILMN_1690530	FER1L5	-0.455260278
ILMN_3287849	LOC440419	-0.455368959
ILMN_3241154	POM121L1P	-0.455371985
ILMN_1713024	PCDHA@	-0.455400301
ILMN_1681728	BM665414	-0.455413589
ILMN_1659484	MAGEC3	-0.455419505
ILMN_2364819	USP44	-0.455473525
ILMN_1798206	KRTAP11-1	-0.455496613
ILMN_2175020	RPL32P3	-0.455515513
ILMN_1724211	GPRC5C	-0.455548942
ILMN_1769358	NPBWR2	-0.455582418
ILMN_2173909	ZNF14	-0.45568314
ILMN_1688633	CLCN2	-0.455761339
ILMN_1709346	CLTB	-0.455788656
ILMN_1796772	ARHGAP28	-0.455871772
ILMN_1731966	LEPR	-0.455916835
ILMN_1765132	LACTB	-0.455946565
ILMN_3264466	FAM54B	-0.456016739
ILMN_1900782	BE466650	-0.45614319
ILMN_1853881	BG118017	-0.456283849
ILMN_1890421	DB311601	-0.456297432
ILMN_1783847	FCHSD1	-0.456329456
ILMN_1768049	FOXP3	-0.45639319
ILMN_1789096	OSTalpha	-0.456407575
ILMN_1781031	CTBP2	-0.456452811
ILMN_2166706	FBXO22OS	-0.456483928
ILMN_1662865	CPPED1	-0.456486631
ILMN_1794528	KIAA1751	-0.456533986
ILMN_1805449	TAPBPL	-0.456631368
ILMN_1662880	FIS	-0.456661693
ILMN_1803454	PCGF3	-0.456663669
ILMN_1897911	BF512455	-0.456745054
ILMN_1701497	CD5L	-0.456758987
ILMN_1693092	SYNPO2	-0.456777744
ILMN_1765355	NOX1	-0.456786834
ILMN_1846922	BC042566	-0.456799136
ILMN_2059606	CCDC117	-0.456800237
ILMN_2097052	CDY2B	-0.456858401
ILMN_1818538	DA855529	-0.456915689
ILMN_1693487	OR2W1	-0.457018656
ILMN_1687875	UNC5C	-0.457030781
ILMN_1825242	AA918474	-0.457033634
ILMN_1708393	C1orf185	-0.457046349
ILMN_1699728	BTD	-0.457056385
ILMN_1814769	UGT2B15	-0.457059252
ILMN_1697289	ZNF713	-0.457227176
ILMN_1683664	FAM60A	-0.457236303
ILMN_1672325	PYDC2	-0.457251594
ILMN_1777156	GTPBP3	-0.457270138
ILMN_1708989	TBX1	-0.45730284
ILMN_1876039	AA812958	-0.457401986
ILMN_1827966	AK023961	-0.457439321
ILMN_2103720	MRPL15	-0.457675346
ILMN_1683097	RPS6KA5	-0.457741257
ILMN_1860963	BM715829	-0.457754487
ILMN_1693771	ASPH	-0.457794593
ILMN_1695991	COLQ	-0.457803983
ILMN_3235221	LOC644936	-0.457820283
ILMN_1770692	WDR12	-0.457858169
ILMN_1806492	TNR	-0.457954323
ILMN_2156687	DFNB59	-0.457999732
ILMN_1695058	SLC38A5	-0.458073392
ILMN_1818935	BQ575873	-0.458134297
ILMN_1765019	SACM1L	-0.458283138
ILMN_1728975	SCO1	-0.458447002
ILMN_1655521	DMRTA1	-0.4584615
ILMN_1694078	AY358310	-0.458474593
ILMN_1693878	GMPPA	-0.45851713
ILMN_1704497	KRT25	-0.458606697
ILMN_2206420	UGT1A1	-0.458608053
ILMN_1800612	VBP1	-0.458637544
ILMN_1843425	AF520419	-0.45864635
ILMN_1737813	ERI3	-0.458723363
ILMN_1900457	NA	-0.458852105
ILMN_2162328	PTS	-0.458860781
ILMN_2103003	OR4N3P	-0.458872091
ILMN_1673716	KIF6	-0.458876574
ILMN_1763092	MCCD1	-0.458893651
ILMN_1756721	FSCB	-0.458918457
ILMN_1688935	NA	-0.458979036
ILMN_1756102	RFX3	-0.458982059
ILMN_1680673	NT5DC1	-0.459061119
ILMN_1786658	BOLA3	-0.459127312
ILMN_1903568	CR625988	-0.459134649

	GOTERM_BP_FAT	gut development	4	7.50E-01	1.00E+00
Annotation Cluster 177	**Enrichment Score: 0.4**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	negative regulation of specific transcription from RNA polymerase II promoter	7	2.60E-01	9.90E-01
	BIOCARTA	Control of Gene Expression by Vitamin D Receptor	5	3.30E-01	9.90E-01
	GOTERM_BP_FAT	regulation of gene-specific transcription	17	3.50E-01	1.00E+00
	GOTERM_BP_FAT	negative regulation of gene-specific transcription	7	4.00E-01	1.00E+00
	GOTERM_BP_FAT	regulation of specific transcription from RNA polymerase II promoter	12	4.10E-01	1.00E+00
	GOTERM_BP_FAT	positive regulation of specific transcription from RNA polymerase II promoter	7	5.70E-01	1.00E+00
	GOTERM_BP_FAT	positive regulation of gene-specific transcription	10	5.80E-01	1.00E+00
Annotation Cluster 178	**Enrichment Score: 0.4**		**Count**	**P_Value**	**Benjamini**
	INTERPRO	Carbonic anhydrase, alpha-class, catalytic domain	4	3.00E-01	1.00E+00
	PIR_SUPERFAMILY	PIRSF001392:carbonate dehydratase	3	4.50E-01	1.00E+00
	INTERPRO	Carbonic anhydrase, alpha-class, conserved site	3	4.80E-01	1.00E+00
Annotation Cluster 179	**Enrichment Score: 0.4**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	regulation of binding	21	1.90E-01	9.90E-01
	GOTERM_BP_FAT	positive regulation of DNA binding	11	2.00E-01	9.90E-01
	GOTERM_BP_FAT	regulation of DNA binding	17	2.10E-01	9.90E-01
	GOTERM_BP_FAT	positive regulation of binding	11	3.10E-01	9.90E-01
	GOTERM_BP_FAT	positive regulation of transcription factor activity	8	4.50E-01	1.00E+00
	GOTERM_BP_FAT	regulation of transcription factor activity	12	5.40E-01	1.00E+00
	GOTERM_BP_FAT	negative regulation of binding	7	6.10E-01	1.00E+00
	GOTERM_BP_FAT	negative regulation of DNA binding	6	6.40E-01	1.00E+00
	GOTERM_BP_FAT	positive regulation of NF-kappaB transcription factor activity	5	6.40E-01	1.00E+00
	GOTERM_BP_FAT	negative regulation of transcription factor activity	5	7.20E-01	1.00E+00
Annotation Cluster 180	**Enrichment Score: 0.39**		**Count**	**P_Value**	**Benjamini**
	SP_PIR_KEYWORDS	GTP binding	10	2.60E-01	9.00E-01
	SP_PIR_KEYWORDS	P-loop	14	4.40E-01	9.50E-01
	SP_PIR_KEYWORDS	nucleotide binding	12	5.70E-01	9.70E-01
Annotation Cluster 181	**Enrichment Score: 0.39**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest	3	1.30E-01	9.80E-01
	GOTERM_BP_FAT	G1/S transition checkpoint	4	2.70E-01	9.90E-01
	GOTERM_BP_FAT	G1 DNA damage checkpoint	3	3.30E-01	9.90E-01
	GOTERM_BP_FAT	DNA damage checkpoint	7	4.00E-01	1.00E+00
	GOTERM_BP_FAT	DNA integrity checkpoint	7	4.80E-01	1.00E+00
	GOTERM_BP_FAT	mitotic cell cycle checkpoint	6	4.80E-01	1.00E+00
	GOTERM_BP_FAT	cell cycle checkpoint	11	5.00E-01	1.00E+00
	GOTERM_BP_FAT	DNA damage response, signal transduction	8	7.60E-01	1.00E+00
	GOTERM_BP_FAT	DNA damage response, signal transduction by p53 class mediator	3	7.80E-01	1.00E+00
Annotation Cluster 182	**Enrichment Score: 0.39**		**Count**	**P_Value**	**Benjamini**
	SMART	BBOX	12	9.70E-02	9.70E-01
	INTERPRO	Zinc finger, B-box	12	1.40E-01	1.00E+00
	UP_SEQ_FEATURE	zinc finger region:B box-type 2	4	2.30E-01	1.00E+00
	UP_SEQ_FEATURE	zinc finger region:B box-type	8	3.60E-01	1.00E+00
	UP_SEQ_FEATURE	zinc finger region:B box-type 1	3	3.60E-01	1.00E+00
	INTERPRO	B302 (SPRY)-like	11	4.40E-01	1.00E+00
	INTERPRO	Butyrophylin-like	8	4.90E-01	1.00E+00
	UP_SEQ_FEATURE	domain:B30.2/SPRY	10	5.00E-01	1.00E+00
	INTERPRO	SPla/RYanodine receptor SPRY	10	5.40E-01	1.00E+00
	SMART	SPRY	6	6.50E-01	9.90E-01
	INTERPRO	SPla/RYanodine receptor subgroup	6	7.10E-01	1.00E+00
	SMART	PRY	4	8.70E-01	1.00E+00
	INTERPRO	SPRY-associated	4	9.00E-01	1.00E+00
Annotation Cluster 183	**Enrichment Score: 0.39**		**Count**	**P_Value**	**Benjamini**
	GOTERM_MF_FAT	protein serine/threonine/tyrosine kinase activity	4	2.10E-01	9.80E-01
	GOTERM_MF_FAT	MAP kinase kinase activity	3	4.10E-01	1.00E+00
	BIOCARTA	MAPKinase Signaling Pathway	8	7.80E-01	1.00E+00
Annotation Cluster 184	**Enrichment Score: 0.39**		**Count**	**P_Value**	**Benjamini**
	SMART	FHA	5	3.70E-01	9.80E-01
	INTERPRO	Forkhead-associated	5	4.20E-01	1.00E+00
	UP_SEQ_FEATURE	domain:FHA	5	4.40E-01	1.00E+00
Annotation Cluster 185	**Enrichment Score: 0.39**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	positive regulation of cholesterol biosynthetic process	3	5.80E-02	9.80E-01
	GOTERM_BP_FAT	positive regulation of steroid biosynthetic process	3	1.60E-01	9.80E-01
	GOTERM_BP_FAT	regulation of cholesterol biosynthetic process	3	2.50E-01	9.90E-01
	GOTERM_BP_FAT	regulation of steroid biosynthetic process	5	2.70E-01	9.90E-01
	GOTERM_BP_FAT	positive regulation of lipid biosynthetic process	4	3.90E-01	1.00E+00
	GOTERM_BP_FAT	positive regulation of steroid metabolic process	3	4.50E-01	1.00E+00
	GOTERM_BP_FAT	regulation of lipid biosynthetic process	6	5.30E-01	1.00E+00
	GOTERM_BP_FAT	regulation of steroid metabolic process	5	5.40E-01	1.00E+00
	GOTERM_BP_FAT	positive regulation of lipid metabolic process	6	5.50E-01	1.00E+00
	GOTERM_BP_FAT	regulation of fatty acid oxidation	3	8.10E-01	1.00E+00
	GOTERM_BP_FAT	regulation of lipid metabolic process	10	8.50E-01	1.00E+00
	GOTERM_BP_FAT	regulation of cellular ketone metabolic process	5	8.70E-01	1.00E+00
	GOTERM_BP_FAT	regulation of fatty acid metabolic process	4	9.00E-01	1.00E+00
Annotation Cluster 186	**Enrichment Score: 0.39**		**Count**	**P_Value**	**Benjamini**
	GOTERM_MF_FAT	retinol dehydrogenase activity	3	2.90E-01	9.90E-01
	INTERPRO	NAD(P)-binding domain	19	3.20E-01	1.00E+00
	PIR_SUPERFAMILY	PIRSF000092:short-chain dehydrogenase	3	4.20E-01	1.00E+00
	INTERPRO	Glucose/ribitol dehydrogenase	7	5.00E-01	1.00E+00
	INTERPRO	Short-chain dehydrogenase/reductase SDR	7	6.10E-01	1.00E+00
Annotation Cluster 187	**Enrichment Score: 0.38**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	domain:MAGE	6	2.40E-01	1.00E+00
	INTERPRO	MAGE protein	6	3.10E-01	1.00E+00
	SP_PIR_KEYWORDS	tumor antigen	5	5.70E-01	9.70E-01
	PIR_SUPERFAMILY	PIRSF005491:tumor associated protein MAGE	3	6.80E-01	1.00E+00
Annotation Cluster 188	**Enrichment Score: 0.38**		**Count**	**P_Value**	**Benjamini**
	KEGG_PATHWAY	Steroid biosynthesis	5	1.10E-01	9.20E-01

ILMN_2382906	PLCG1	0.671705455
ILMN_1798189	COX7C	0.671666584
ILMN_1674640	CXCR6	0.671613346
ILMN_1686748	TMEM9	0.671499677
ILMN_1705301	TEAD4	0.671491247
ILMN_1770206	GEMIN4	0.671455025
ILMN_1713829	PTGES	0.671358329
ILMN_3267760	RPL10A	0.671099039
ILMN_2325394	MSH5	0.671069998
ILMN_1738759	PIGT	0.670970006
ILMN_1805693	GMIP	0.670826438
ILMN_3234142	LOC728855	0.670733624
ILMN_2352448	NSUN5P1	0.670725248
ILMN_1806705	ASB6	0.67072202
ILMN_1657836	PLEKHG2	0.670628443
ILMN_2214232	AIM2	0.670529878
ILMN_2383435	PSMD10	0.670509576
ILMN_1694587	EEF1B2	0.670409492
ILMN_1669362	IGFBP6	0.670382976
ILMN_2059689	TMEM54	0.670365533
ILMN_1693630	C16orf7	0.67028484
ILMN_1652412	PHKB	0.670079773
ILMN_1814966	PIAS3	0.670079012
ILMN_2220283	HNRNPA1	0.670030498
ILMN_1726025	ASXL1	0.670025962
ILMN_1694398	EIF3F	0.66986
ILMN_1657509	TSEN54	0.669749613
ILMN_1707070	PCOLCE	0.669425304
ILMN_1783728	TBRG4	0.669351647
ILMN_1677122	FAM168B	0.669104591
ILMN_2251184	ERP29	0.66903646
ILMN_1756573	NDUFA4L2	0.66902643
ILMN_1670878	YTHDC1	0.66900312
ILMN_2413064	ST6GALNAC4	0.668948591
ILMN_2316104	IQCB1	0.668866984
ILMN_3234831	RPL17	0.668859052
ILMN_1673711	HSP90AB1	0.668857289
ILMN_1807600	NPLOC4	0.66874258
ILMN_1711272	SERPING1	0.668734692
ILMN_1806908	PRKCB	0.668697411
ILMN_3268028	BMS1	0.668675846
ILMN_1758523	ABCA3	0.668606288
ILMN_1785528	DKFZp434K1323	0.668567798
ILMN_1787518	GSN	0.668482276
ILMN_1682332	GYPC	0.668413977
ILMN_1699636	ACIN1	0.668329109
ILMN_2286514	GTPBP8	0.668280969
ILMN_2041222	FLJ40504	0.66815541
ILMN_2368318	FGR	0.668110343
ILMN_1802376	FAM48A	0.668084297
ILMN_1725705	CLPP	0.667888001
ILMN_2298958	MRRF	0.667819691
ILMN_1684647	ILKAP	0.667750134
ILMN_1717524	LIPT1	0.667663108
ILMN_1673708	HDAC9	0.667521467
ILMN_2379326	MAP3K7	0.667427586
ILMN_3228639	NA	0.66726768
ILMN_1845157	TTC15	0.667206659
ILMN_2390974	DNAJB2	0.66700416
ILMN_2118773	ASAH2B	0.666966892
ILMN_1667925	PDCL3	0.6669445
ILMN_3248122	MED1	0.666930575
ILMN_1705522	SPAG1	0.666923975
ILMN_1802646	EPHB6	0.666875852
ILMN_1698307	DBNL	0.666543185
ILMN_2317751	REC8	0.666487316
ILMN_2309245	BIN1	0.666460964
ILMN_1703565	GLTSCR2	0.666450318
ILMN_1779257	CD40	0.666326866
ILMN_1773389	PLTP	0.666260043
ILMN_1679405	DDX56	0.666245243
ILMN_1790460	ZNF574	0.666229046
ILMN_1715500	SS18L1	0.666144362
ILMN_1822775	DB336446	0.665810107
ILMN_1661337	SRM	0.665496289
ILMN_2366719	NSFL1C	0.66540831
ILMN_1676721	NF2	0.665246719
ILMN_1682957	PACSIN3	0.665223496
ILMN_1793990	ID2	0.66515368
ILMN_2219351	CENPO	0.664897585
ILMN_1728355	PSMD4	0.664887716
ILMN_1727300	ZNF444	0.664871563
ILMN_3279935	RPL17	0.664831025
ILMN_1683781	ADAMTS15	0.664823528
ILMN_2367020	SEC61G	0.664759946
ILMN_1741459	CDK10	0.664736578
ILMN_1703430	CCDC94	0.664696712
ILMN_3241870	FRMD8	0.664693711
ILMN_1765876	ARHGAP24	0.664683073
ILMN_3226807	NHP2	0.664459917
ILMN_2356578	TH	0.664391026
ILMN_2339028	PKD1	0.664353106

	GOTERM_MF_FAT	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors	8	5.90E-02	6.50E-01
	SP_PIR_KEYWORDS	vitamin c	6	6.90E-02	3.60E-01
	UP_SEQ_FEATURE	domain:Fe2OG dioxygenase	6	1.00E-01	1.00E+00
	INTERPRO	Prolyl 4-hydroxylase, alpha subunit	5	1.10E-01	9.70E-01
	GOTERM_MF_FAT	L-ascorbic acid binding	6	1.20E-01	8.30E-01
	SMART	P4Hc	5	1.30E-01	8.00E-01
	INTERPRO	Oxoglutarate and iron-dependent oxygenase	5	1.60E-01	9.90E-01
	SP_PIR_KEYWORDS	dioxygenase	12	1.70E-01	5.80E-01
	UP_SEQ_FEATURE	metal ion-binding site:Iron	9	1.90E-01	1.00E+00
	GOTERM_MF_FAT	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	12	2.20E-01	9.30E-01
	GOTERM_MF_FAT	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen	12	2.40E-01	9.40E-01
	GOTERM_MF_FAT	vitamin binding	13	9.20E-01	1.00E+00
	GOTERM_MF_FAT	carboxylic acid binding	14	9.40E-01	1.00E+00
	SP_PIR_KEYWORDS	iron	24	9.90E-01	1.00E+00
	GOTERM_MF_FAT	iron ion binding	26	1.00E+00	1.00E+00
Annotation Cluster 148	**Enrichment Score: 0.77**		**Count**	**P_Value**	**Benjamini**
	SP_PIR_KEYWORDS	cell binding	7	5.80E-03	6.30E-02
	SP_PIR_KEYWORDS	collagen	18	6.10E-02	3.30E-01
	SP_PIR_KEYWORDS	hydroxyproline	9	7.00E-02	3.60E-01
	SP_PIR_KEYWORDS	triple helix	8	7.20E-02	3.60E-01
	SP_PIR_KEYWORDS	hydroxylysine	8	7.20E-02	3.60E-01
	SP_PIR_KEYWORDS	hydroxylation	13	1.40E-01	5.30E-01
	GOTERM_CC_FAT	collagen	8	1.80E-01	6.40E-01
	INTERPRO	Collagen triple helix repeat	14	2.60E-01	1.00E+00
	UP_SEQ_FEATURE	glycosylation site:O-linked (Gal...)	3	3.00E-01	1.00E+00
	UP_SEQ_FEATURE	region of interest:Triple-helical region	5	3.00E-01	1.00E+00
	UP_SEQ_FEATURE	domain:VWFA 2	4	3.40E-01	1.00E+00
	GOTERM_CC_FAT	anchoring collagen	3	3.40E-01	8.20E-01
	UP_SEQ_FEATURE	domain:VWFA 1	3	5.90E-01	1.00E+00
	SP_PIR_KEYWORDS	trimer	4	6.20E-01	9.40E-01
	SP_PIR_KEYWORDS	pyroglutamic acid	5	8.20E-01	9.90E-01
Annotation Cluster 149	**Enrichment Score: 0.77**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	DNA-binding region:ETS	9	1.20E-02	9.10E-01
	UP_SEQ_FEATURE	domain:PNT	3	3.90E-01	1.00E+00
	INTERPRO	Sterile alpha motif/pointed	3	4.10E-01	1.00E+00
	SMART	SAM_PNT	3	4.40E-01	9.70E-01
Annotation Cluster 150	**Enrichment Score: 0.76**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	regulation of macroautophagy	3	8.70E-02	6.40E-01
	GOTERM_BP_FAT	regulation of autophagy	3	1.80E-01	8.40E-01
	GOTERM_BP_FAT	regulation of response to nutrient levels	4	2.40E-01	9.00E-01
	GOTERM_BP_FAT	regulation of response to extracellular stimulus	4	2.40E-01	9.00E-01
Annotation Cluster 151	**Enrichment Score: 0.76**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	protein retention in ER lumen	4	5.30E-02	5.10E-01
	GOTERM_BP_FAT	maintenance of location	13	1.30E-01	7.60E-01
	GOTERM_BP_FAT	maintenance of protein location	10	1.70E-01	8.30E-01
	GOTERM_BP_FAT	maintenance of location in cell	9	3.00E-01	9.30E-01
	GOTERM_BP_FAT	maintenance of protein location in cell	7	4.60E-01	9.80E-01
Annotation Cluster 152	**Enrichment Score: 0.76**		**Count**	**P_Value**	**Benjamini**
	KEGG_PATHWAY	Fc gamma R-mediated phagocytosis	21	6.90E-02	3.50E-01
	KEGG_PATHWAY	Natural killer cell mediated cytotoxicity	26	1.30E-01	4.80E-01
	KEGG_PATHWAY	B cell receptor signaling pathway	16	1.50E-01	5.00E-01
	KEGG_PATHWAY	Non-small cell lung cancer	12	1.80E-01	5.50E-01
	KEGG_PATHWAY	T cell receptor signaling pathway	21	1.80E-01	5.30E-01
	KEGG_PATHWAY	Glioma	13	2.30E-01	5.80E-01
	KEGG_PATHWAY	Fc epsilon RI signaling pathway	15	2.70E-01	6.30E-01
	KEGG_PATHWAY	VEGF signaling pathway	14	3.30E-01	6.80E-01
Annotation Cluster 153	**Enrichment Score: 0.76**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	mRNA catabolic process	10	1.10E-01	7.00E-01
	SP_PIR_KEYWORDS	nonsense-mediated mrna decay	7	1.10E-01	4.70E-01
	GOTERM_BP_FAT	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	7	2.00E-01	8.60E-01
	GOTERM_BP_FAT	RNA catabolic process	12	2.30E-01	8.90E-01
	GOTERM_BP_FAT	nuclear-transcribed mRNA catabolic process	7	3.10E-01	9.40E-01
Annotation Cluster 154	**Enrichment Score: 0.76**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	regulation of T cell tolerance induction	3	1.30E-01	7.60E-01
	GOTERM_BP_FAT	positive regulation of T cell tolerance induction	3	1.30E-01	7.60E-01
	GOTERM_BP_FAT	positive regulation of tolerance induction	3	2.30E-01	8.90E-01
	GOTERM_BP_FAT	regulation of tolerance induction	3	2.30E-01	8.90E-01
Annotation Cluster 155	**Enrichment Score: 0.76**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	nucleus organization	13	3.50E-02	4.10E-01
	GOTERM_BP_FAT	DNA catabolic process, endonucleolytic	8	4.70E-02	4.80E-01
	GOTERM_BP_FAT	apoptotic nuclear changes	7	1.20E-01	7.30E-01
	GOTERM_BP_FAT	DNA catabolic process	12	1.60E-01	8.10E-01
	GOTERM_BP_FAT	cell structure disassembly during apoptosis	6	1.80E-01	8.30E-01
	GOTERM_BP_FAT	DNA fragmentation involved in apoptosis	5	2.40E-01	8.90E-01
	GOTERM_BP_FAT	cellular component disassembly	9	4.00E-01	9.70E-01
	BIOCARTA	Caspase Cascade in Apoptosis	6	5.10E-01	9.80E-01
	BIOCARTA	Apoptotic DNA fragmentation and tissue homeostasis	3	6.00E-01	9.90E-01
Annotation Cluster 156	**Enrichment Score: 0.75**		**Count**	**P_Value**	**Benjamini**
	GOTERM_CC_FAT	Golgi trans cisterna	3	8.90E-02	4.70E-01
	GOTERM_CC_FAT	Golgi stack	10	1.50E-01	6.00E-01
	GOTERM_CC_FAT	organelle subcompartment	6	2.10E-01	6.80E-01
	GOTERM_CC_FAT	Golgi cisterna	5	3.40E-01	8.20E-01
Annotation Cluster 157	**Enrichment Score: 0.75**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	ribonucleoside metabolic process	11	7.30E-02	6.00E-01
	GOTERM_BP_FAT	purine nucleoside metabolic process	8	7.80E-02	6.10E-01
	GOTERM_BP_FAT	purine ribonucleoside metabolic process	8	7.80E-02	6.10E-01
	GOTERM_BP_FAT	nucleoside biosynthetic process	3	2.90E-01	9.30E-01
	GOTERM_BP_FAT	purine nucleoside biosynthetic process	3	2.90E-01	9.30E-01
	GOTERM_BP_FAT	ribonucleoside biosynthetic process	3	2.90E-01	9.30E-01
	GOTERM_BP_FAT	purine ribonucleoside biosynthetic process	3	2.90E-01	9.30E-01
	GOTERM_BP_FAT	nucleoside metabolic process	11	3.30E-01	9.50E-01
Annotation Cluster 158	**Enrichment Score: 0.75**		**Count**	**P_Value**	**Benjamini**

ILMN_3233385	TP53TG3b	-0.459150921
ILMN_1865290	BU618600	-0.459196581
ILMN_1781517	LIPF	-0.459247504
ILMN_1769151	AK123300	-0.459405242
ILMN_1755504	CALCOCO2	-0.459428284
ILMN_1693192	PI3	-0.459617215
ILMN_1788239	AMDHD1	-0.459628056
ILMN_2105549	TMEM220	-0.45962916
ILMN_1904301	MECP2	-0.459632711
ILMN_1766377	PCDHB6	-0.459747086
ILMN_1672324	EBLN1	-0.459751472
ILMN_2388669	GRIA3	-0.459776539
ILMN_1658259	DRG1	-0.459786374
ILMN_1722620	MGC39584	-0.460016872
ILMN_1915480	BX107598	-0.460041031
ILMN_2154101	UPRT	-0.460086166
ILMN_1699447	TRAF5	-0.460093358
ILMN_1774945	NRG3	-0.460106803
ILMN_2206592	PRAMEF11	-0.46013135
ILMN_1707887	LOC644172	-0.460183384
ILMN_1746194	DUSP21	-0.460189579
ILMN_2246105	C3orf23	-0.460242904
ILMN_3280594	LOC120824	-0.460256891
ILMN_1659426	CCDC36	-0.460257243
ILMN_1726602	PPEF2	-0.460281973
ILMN_3235851	SCARNA9L	-0.460287208
ILMN_1747573	C3orf65	-0.460305301
ILMN_1688569	KCNQ1	-0.460364151
ILMN_3310760	MIR519A2	-0.46042833
ILMN_1748802	OR2B3	-0.460516029
ILMN_1768894	OR8G1	-0.46053136
ILMN_1801869	WDR75	-0.460609346
ILMN_1805404	GRIN1	-0.460622487
ILMN_1880223	AL833666	-0.460720251
ILMN_1688627	AGBL2	-0.460738451
ILMN_1775053	LOC644838	-0.460783545
ILMN_1789543	FBF1	-0.460834808
ILMN_1700771	PRUNE2	-0.460985719
ILMN_1787434	OR10H1	-0.460994076
ILMN_1704557	RPS6KB1	-0.460994943
ILMN_3234879	OTOA	-0.461058203
ILMN_2357062	IL1RAP	-0.461084253
ILMN_1660590	NA	-0.461108912
ILMN_1861767	BX118413	-0.461164416
ILMN_1698171	INCENP	-0.461225319
ILMN_1781906	RBM17	-0.461261673
ILMN_3309644	MIR139	-0.461287599
ILMN_1810335	DGKB	-0.461299486
ILMN_1675671	ICOSLG	-0.461312451
ILMN_1792107	ERCC8	-0.461406617
ILMN_2413141	C6orf162	-0.461444343
ILMN_1687316	NCDN	-0.46144502
ILMN_3243961	ZNF252	-0.461524156
ILMN_3307752	DLEU7	-0.461554441
ILMN_2351930	TRIM33	-0.46159732
ILMN_1878928	BC031939	-0.461628446
ILMN_1694634	MOGAT3	-0.461645812
ILMN_3191893	NA	-0.461676571
ILMN_1701661	CYP7B1	-0.461702175
ILMN_1725556	TMEM229A	-0.461713508
ILMN_1825421	BC033844	-0.461734635
ILMN_1813117	ITGA9	-0.461791634
ILMN_1693259	PDCD6IP	-0.46182869
ILMN_1884357	AI734261	-0.46186157
ILMN_1797408	NKAPL	-0.46188383
ILMN_1701127	CC2D1A	-0.462011904
ILMN_1890902	BF056964	-0.462012129
ILMN_1812659	ZNF705G	-0.462048694
ILMN_1724977	MDK	-0.462097864
ILMN_1815345	EIF3J	-0.462207959
ILMN_1807093	CR608006	-0.462239629
ILMN_3236316	LOC729121	-0.462288516
ILMN_1741096	FDFT1	-0.462307934
ILMN_1763202	LOC441179	-0.462376636
ILMN_2122076	GPR149	-0.462392199
ILMN_1707741	TBC1D26	-0.462413744
ILMN_1685521	KLRF1	-0.462441853
ILMN_1734707	CHST13	-0.462446699
ILMN_1907966	BI464833	-0.462450978
ILMN_3242226	LOC399939	-0.462453068
ILMN_1708110	TMEM144	-0.462466438
ILMN_2394552	WNK3	-0.462536854
ILMN_1741662	TMC5	-0.462547316
ILMN_2244484	CCBL2	-0.462603511
ILMN_1726421	METTL9	-0.462630235
ILMN_2364574	MAPK8	-0.462653224
ILMN_1750051	FAM123B	-0.462771748
ILMN_1854765	AK130706	-0.462789103
ILMN_1839665	BQ186372	-0.462810517
ILMN_1796574	BEND4	-0.462813826
ILMN_1711988	KCNK12	-0.462849309
ILMN_3248990	UBTFL1	-0.462870419

	GOTERM_BP_FAT	steroid metabolic process	26	2.30E-01	9.90E-01
	SP_PIR_KEYWORDS	sterol biosynthesis	5	2.60E-01	9.00E-01
	GOTERM_BP_FAT	steroid biosynthetic process	12	2.90E-01	9.90E-01
	SP_PIR_KEYWORDS	Steroid biosynthesis	6	4.10E-01	9.40E-01
	GOTERM_BP_FAT	sterol biosynthetic process	5	5.20E-01	1.00E+00
	SP_PIR_KEYWORDS	Cholesterol biosynthesis	3	6.10E-01	9.70E-01
	GOTERM_BP_FAT	sterol metabolic process	11	6.40E-01	1.00E+00
	SP_PIR_KEYWORDS	lipid synthesis	10	7.10E-01	9.80E-01
	GOTERM_BP_FAT	cholesterol metabolic process	9	7.70E-01	1.00E+00
	GOTERM_BP_FAT	cholesterol biosynthetic process	3	7.80E-01	1.00E+00
Annotation Cluster 189	**Enrichment Score: 0.37**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	ectoderm development	26	2.10E-01	9.90E-01
	GOTERM_BP_FAT	epidermal cell differentiation	11	2.30E-01	9.90E-01
	GOTERM_BP_FAT	keratinocyte differentiation	10	2.60E-01	9.90E-01
	GOTERM_BP_FAT	epidermis development	21	4.90E-01	1.00E+00
	SP_PIR_KEYWORDS	keratinization	5	6.10E-01	9.70E-01
	GOTERM_BP_FAT	keratinization	5	6.80E-01	1.00E+00
	GOTERM_BP_FAT	epithelial cell differentiation	11	9.30E-01	1.00E+00
Annotation Cluster 190	**Enrichment Score: 0.37**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	repeat:ANK 9	7	1.90E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:ANK 7	9	2.60E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:ANK 8	7	2.80E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:ANK 13	3	4.00E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:ANK 15	3	4.00E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:ANK 14	3	4.00E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:ANK 11	4	4.40E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:ANK 12	3	5.10E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:ANK 10	4	5.20E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:ANK 6	9	7.60E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:ANK 5	10	9.40E-01	1.00E+00
Annotation Cluster 191	**Enrichment Score: 0.37**		**Count**	**P_Value**	**Benjamini**
	INTERPRO	Four-helical cytokine, core	10	5.00E-02	1.00E+00
	KEGG_PATHWAY	Jak-STAT signaling pathway	21	2.80E-01	9.50E-01
	KEGG_PATHWAY	Autoimmune thyroid disease	6	6.90E-01	9.60E-01
	KEGG_PATHWAY	Cytokine-cytokine receptor interaction	26	8.30E-01	9.70E-01
	GOTERM_MF_FAT	cytokine activity	18	8.50E-01	1.00E+00
	SP_PIR_KEYWORDS	cytokine	16	8.60E-01	9.90E-01
Annotation Cluster 192	**Enrichment Score: 0.37**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	regulation of neuron projection development	11	2.00E-01	9.90E-01
	GOTERM_BP_FAT	regulation of cell morphogenesis	18	2.20E-01	9.90E-01
	GOTERM_BP_FAT	regulation of cell morphogenesis involved in differentiation	11	3.00E-01	9.90E-01
	GOTERM_BP_FAT	regulation of neuron differentiation	17	3.30E-01	9.90E-01
	GOTERM_BP_FAT	regulation of cell projection organization	12	3.40E-01	1.00E+00
	GOTERM_BP_FAT	negative regulation of cell projection organization	5	3.40E-01	1.00E+00
	GOTERM_BP_FAT	negative regulation of cell development	7	4.00E-01	1.00E+00
	GOTERM_BP_FAT	regulation of axonogenesis	8	4.00E-01	1.00E+00
	GOTERM_BP_FAT	negative regulation of axonogenesis	4	5.00E-01	1.00E+00
	GOTERM_BP_FAT	negative regulation of neurogenesis	6	5.30E-01	1.00E+00
	GOTERM_BP_FAT	regulation of neurogenesis	18	6.00E-01	1.00E+00
	GOTERM_BP_FAT	regulation of nervous system development	20	6.60E-01	1.00E+00
	GOTERM_BP_FAT	regulation of cell development	20	7.70E-01	1.00E+00
	GOTERM_BP_FAT	negative regulation of cellular component organization	11	9.40E-01	1.00E+00
Annotation Cluster 193	**Enrichment Score: 0.37**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	domain:PLAT	4	3.80E-01	1.00E+00
	SMART	LH2	4	4.30E-01	9.80E-01
	INTERPRO	Lipoxygenase, LH2	4	4.80E-01	1.00E+00
Annotation Cluster 194	**Enrichment Score: 0.37**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	DNA geometric change	4	3.00E-01	9.90E-01
	GOTERM_BP_FAT	DNA duplex unwinding	4	3.00E-01	9.90E-01
	GOTERM_BP_FAT	DNA unwinding during replication	3	4.50E-01	1.00E+00
	GOTERM_BP_FAT	DNA-dependent DNA replication	5	8.80E-01	1.00E+00
Annotation Cluster 195	**Enrichment Score: 0.36**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	domain:TTL	3	4.00E-01	1.00E+00
	INTERPRO	Tubulin-tyrosine ligase	3	4.50E-01	1.00E+00
	GOTERM_MF_FAT	tubulin-tyrosine ligase activity	3	4.50E-01	1.00E+00
Annotation Cluster 196	**Enrichment Score: 0.36**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	nucleoside monophosphate metabolic process	11	1.60E-01	9.80E-01
	GOTERM_BP_FAT	ribonucleoside monophosphate metabolic process	4	5.00E-01	1.00E+00
	GOTERM_BP_FAT	nucleoside monophosphate biosynthetic process	6	6.20E-01	1.00E+00
	GOTERM_BP_FAT	ribonucleoside monophosphate biosynthetic process	3	7.20E-01	1.00E+00
Annotation Cluster 197	**Enrichment Score: 0.36**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	positive regulation of osteoblast differentiation	6	1.20E-01	9.80E-01
	GOTERM_BP_FAT	regulation of osteoblast differentiation	7	3.00E-01	9.90E-01
	GOTERM_BP_FAT	regulation of bone mineralization	5	4.00E-01	1.00E+00
	GOTERM_BP_FAT	regulation of biomineral formation	5	4.40E-01	1.00E+00
	GOTERM_BP_FAT	regulation of ossification	10	4.50E-01	1.00E+00
	GOTERM_BP_FAT	positive regulation of bone mineralization	3	5.80E-01	1.00E+00
	GOTERM_BP_FAT	positive regulation of biomineral formation	3	6.10E-01	1.00E+00
	BIOCARTA	ALK in cardiac myocytes	4	7.30E-01	1.00E+00
	GOTERM_BP_FAT	positive regulation of ossification	3	7.40E-01	1.00E+00
Annotation Cluster 198	**Enrichment Score: 0.36**		**Count**	**P_Value**	**Benjamini**
	SP_PIR_KEYWORDS	hormone receptor	5	2.40E-01	9.00E-01
	GOTERM_MF_FAT	peptide hormone binding	4	5.60E-01	1.00E+00
	GOTERM_MF_FAT	hormone binding	6	6.10E-01	1.00E+00
Annotation Cluster 199	**Enrichment Score: 0.35**		**Count**	**P_Value**	**Benjamini**
	GOTERM_CC_FAT	microbody	15	2.10E-01	9.50E-01
	GOTERM_CC_FAT	peroxisome	15	2.10E-01	9.50E-01
	SP_PIR_KEYWORDS	peroxisome	12	3.40E-01	9.30E-01
	GOTERM_CC_FAT	microbody membrane	4	6.60E-01	9.80E-01
	GOTERM_CC_FAT	peroxisomal membrane	4	6.60E-01	9.80E-01
	GOTERM_CC_FAT	peroxisomal part	5	6.90E-01	9.80E-01
	GOTERM_CC_FAT	microbody part	5	6.90E-01	9.80E-01

ILMN_1781752	CLEC16A	0.664237109
ILMN_1721116	USP10	0.664217881
ILMN_2108709	ANKRD11	0.664214754
ILMN_1792344	LOC653075	0.664161733
ILMN_2391458	ACSL4	0.664146908
ILMN_2206098	ATG10	0.66410867
ILMN_1674036	BIRC7	0.664008883
ILMN_2282641	TBXAS1	0.663984355
ILMN_1714327	SETD1A	0.663932846
ILMN_1680134	CARM1	0.663893163
ILMN_1753584	KRT8	0.66375219
ILMN_1674421	TM9SF4	0.66368151
ILMN_1801845	DNAL4	0.663586189
ILMN_1741997	SNRPC	0.663274815
ILMN_2157435	DYNLRB1	0.663211701
ILMN_1653342	DUS1L	0.66306881
ILMN_1809928	COL6A2	0.662983404
ILMN_2366864	JUP	0.662950866
ILMN_1651429	SELM	0.662832499
ILMN_1769779	PTP4A3	0.662799159
ILMN_1782829	GLTSCR1	0.662699983
ILMN_1765043	RPL38	0.662686337
ILMN_2211065	TMEM91	0.662447488
ILMN_2377496	ERCC1	0.662353905
ILMN_1757631	DBNDD1	0.662336505
ILMN_1770085	BTG2	0.662251178
ILMN_2356909	MOSPD3	0.662164961
ILMN_1663577	S100PBP	0.662099212
ILMN_1746012	MBD6	0.662054439
ILMN_1783798	GAS8	0.66192612
ILMN_1659564	SEC61A1	0.66185139
ILMN_3244323	hCG_20425	0.66162293
ILMN_3286389	LOC653075	0.661591243
ILMN_1757439	RBM14	0.6612937
ILMN_1795025	NFX1	0.661171438
ILMN_1731135	RAB11B	0.661149939
ILMN_1787567	TSC22D1	0.660853624
ILMN_1775677	TYSND1	0.660845479
ILMN_1757467	H1F0	0.660696733
ILMN_3210917	SET	0.660677071
ILMN_1672908	TWIST1	0.660586019
ILMN_2189936	RPL36AL	0.660584582
ILMN_1722634	NUCB1	0.660555595
ILMN_1757134	MPV17L2	0.660542967
ILMN_1792951	ZHX2	0.660517834
ILMN_1654118	BCL2L1	0.660482004
ILMN_2134538	FTH1	0.660388058
ILMN_3244798	AV762097	0.660267415
ILMN_2227533	ABHD14B	0.660139969
ILMN_1685387	PIGR	0.660135579
ILMN_1800634	NME4	0.659963146
ILMN_1786396	ZZEF1	0.659882909
ILMN_1808047	PHC2	0.659878124
ILMN_1794072	B3GAT1	0.659796348
ILMN_2181089	VPRBP	0.659730007
ILMN_1784218	DDX23	0.659720074
ILMN_1768181	TOR3A	0.659512821
ILMN_1675239	NDUFA7	0.659483457
ILMN_1798181	IRF7	0.659434799
ILMN_3208973	LAMR1P15	0.659254689
ILMN_1682928	CPVL	0.659195443
ILMN_1651354	SPP1	0.659191842
ILMN_1801833	ARHGAP24	0.65907067
ILMN_1676128	DNMT3A	0.65906758
ILMN_1747903	DNAJC11	0.658741051
ILMN_1774584	C2orf28	0.658729134
ILMN_1653042	HSD3B7	0.658560962
ILMN_2143314	SPIB	0.658543569
ILMN_2078389	SLC4A2	0.658516728
ILMN_1762594	NOD2	0.658424222
ILMN_1753468	CD63	0.658360794
ILMN_1677104	TRAF5	0.658153809
ILMN_2374159	HERPUD1	0.658092516
ILMN_1674160	BIN1	0.65795398
ILMN_1777314	CNPY4	0.657906899
ILMN_2234016	FTH1	0.657648232
ILMN_1668185	ZNF282	0.657619621
ILMN_2358760	HPN	0.657599453
ILMN_2289593	FXYD2	0.65750512
ILMN_2129161	LRRC32	0.657495506
ILMN_1748767	H3F3A	0.65742503
ILMN_3299407	RPS8	0.657329729
ILMN_1654031	TPTE2	0.6573058
ILMN_1769787	SELO	0.657252725
ILMN_1709630	CCDC107	0.657210926
ILMN_3248975	PPP4C	0.657016089
ILMN_2263144	TMEM223	0.656826455
ILMN_1669584	ILF3	0.656789233
ILMN_1652525	FAM125B	0.656666969
ILMN_1766184	LGALS9C	0.656643706
ILMN_2352216	FBXL6	0.656535507
ILMN_1763723	PTDSS2	0.656533806
ILMN_1670256	PDK1	0.656499565
ILMN_1790909	NFE2L2	0.656085042

	GOTERM_CC_FAT	microtubule cytoskeleton	87	6.10E-02	3.80E-01
	SP_PIR_KEYWORDS	microtubule	37	6.30E-02	3.30E-01
	GOTERM_CC_FAT	microtubule	41	3.00E-01	7.80E-01
	GOTERM_BP_FAT	microtubule-based process	28	9.00E-01	1.00E+00
Annotation Cluster 159	**Enrichment Score: 0.74**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	regulation of binding	31	1.60E-02	2.60E-01
	GOTERM_BP_FAT	positive regulation of binding	16	8.30E-02	6.30E-01
	GOTERM_BP_FAT	regulation of DNA binding	22	1.10E-01	7.10E-01
	GOTERM_BP_FAT	negative regulation of binding	12	1.50E-01	7.90E-01
	GOTERM_BP_FAT	negative regulation of DNA binding	10	2.20E-01	8.90E-01
	GOTERM_BP_FAT	negative regulation of transcription factor activity	9	2.40E-01	8.90E-01
	GOTERM_BP_FAT	regulation of transcription factor activity	17	2.80E-01	9.20E-01
	GOTERM_BP_FAT	positive regulation of DNA binding	12	3.10E-01	9.40E-01
	GOTERM_BP_FAT	positive regulation of transcription factor activity	9	5.40E-01	9.90E-01
	GOTERM_BP_FAT	positive regulation of NF-kappaB transcription factor activity	6	6.40E-01	1.00E+00
Annotation Cluster 160	**Enrichment Score: 0.74**		**Count**	**P_Value**	**Benjamini**
	GOTERM_CC_FAT	leading edge membrane	8	2.60E-02	2.30E-01
	GOTERM_CC_FAT	axolemma	3	1.90E-01	6.50E-01
	GOTERM_CC_FAT	neuron projection membrane	3	2.90E-01	7.80E-01
	GOTERM_CC_FAT	axon part	7	7.50E-01	9.80E-01
Annotation Cluster 161	**Enrichment Score: 0.74**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	domain:WW	7	4.20E-02	9.90E-01
	INTERPRO	WW/Rsp5/WWP	9	3.50E-01	1.00E+00
	SMART	WW	9	4.00E-01	9.60E-01
Annotation Cluster 162	**Enrichment Score: 0.74**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	icosanoid biosynthetic process	10	1.60E-02	2.60E-01
	GOTERM_BP_FAT	unsaturated fatty acid biosynthetic process	10	2.80E-02	3.70E-01
	GOTERM_BP_FAT	icosanoid metabolic process	12	3.90E-02	4.40E-01
	GOTERM_BP_FAT	unsaturated fatty acid metabolic process	12	6.50E-02	5.70E-01
	INTERPRO	Peptidase M1, leukotriene A4 hydrolase, aminopeptidase C-terminal	3	8.00E-02	9.50E-01
	GOTERM_MF_FAT	aminopeptidase activity	8	8.20E-02	7.40E-01
	SP_PIR_KEYWORDS	Aminopeptidase	7	8.40E-02	3.90E-01
	GOTERM_BP_FAT	prostanoid metabolic process	6	9.50E-02	6.70E-01
	GOTERM_BP_FAT	prostaglandin metabolic process	6	9.50E-02	6.70E-01
	GOTERM_BP_FAT	prostanoid biosynthetic process	4	1.70E-01	8.20E-01
	GOTERM_BP_FAT	prostaglandin biosynthetic process	4	1.70E-01	8.20E-01
	INTERPRO	Peptidase M1, membrane alanine aminopeptidase	4	1.90E-01	9.90E-01
	INTERPRO	Peptidase M1, membrane alanine aminopeptidase, N-terminal	4	2.20E-01	1.00E+00
	GOTERM_BP_FAT	alkene biosynthetic process	5	2.40E-01	8.90E-01
	GOTERM_BP_FAT	leukotriene biosynthetic process	5	2.40E-01	8.90E-01
	GOTERM_MF_FAT	exopeptidase activity	13	2.80E-01	9.60E-01
	GOTERM_BP_FAT	leukotriene metabolic process	5	3.30E-01	9.50E-01
	GOTERM_BP_FAT	cellular alkene metabolic process	5	3.60E-01	9.60E-01
	GOTERM_BP_FAT	fatty acid biosynthetic process	12	4.70E-01	9.80E-01
	GOTERM_BP_FAT	carboxylic acid biosynthetic process	20	6.70E-01	1.00E+00
	GOTERM_BP_FAT	organic acid biosynthetic process	20	6.70E-01	1.00E+00
	BIOCARTA	Eicosanoid Metabolism	4	8.00E-01	1.00E+00
	GOTERM_BP_FAT	fatty acid metabolic process	22	8.80E-01	1.00E+00
	UP_SEQ_FEATURE	metal ion-binding site:Zinc; catalytic	12	8.90E-01	1.00E+00
Annotation Cluster 163	**Enrichment Score: 0.74**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	positive regulation of stress-activated protein kinase signaling pathway	6	1.30E-01	7.60E-01
	GOTERM_BP_FAT	regulation of stress-activated MAPK cascade	4	1.40E-01	7.70E-01
	GOTERM_BP_FAT	positive regulation of stress-activated MAPK cascade	3	3.40E-01	9.50E-01
Annotation Cluster 164	**Enrichment Score: 0.74**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	positive regulation of myeloid leukocyte differentiation	6	7.80E-02	6.10E-01
	GOTERM_BP_FAT	positive regulation of myeloid cell differentiation	8	1.40E-01	7.70E-01
	GOTERM_BP_FAT	regulation of myeloid leukocyte differentiation	9	1.60E-01	8.20E-01
	GOTERM_BP_FAT	positive regulation of osteoclast differentiation	3	1.80E-01	8.40E-01
	GOTERM_BP_FAT	regulation of myeloid cell differentiation	13	2.10E-01	8.70E-01
	GOTERM_BP_FAT	regulation of osteoclast differentiation	4	5.70E-01	9.90E-01
Annotation Cluster 165	**Enrichment Score: 0.73**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	heme metabolic process	7	6.00E-02	5.50E-01
	GOTERM_BP_FAT	heme biosynthetic process	6	6.30E-02	5.60E-01
	GOTERM_BP_FAT	heterocycle biosynthetic process	13	8.10E-02	6.20E-01
	GOTERM_BP_FAT	tetrapyrrole biosynthetic process	6	1.10E-01	7.20E-01
	GOTERM_BP_FAT	porphyrin biosynthetic process	6	1.10E-01	7.20E-01
	GOTERM_BP_FAT	pigment metabolic process	10	1.30E-01	7.60E-01
	GOTERM_BP_FAT	pigment biosynthetic process	9	1.30E-01	7.60E-01
	GOTERM_BP_FAT	tetrapyrrole metabolic process	7	1.70E-01	8.30E-01
	GOTERM_BP_FAT	porphyrin metabolic process	7	1.70E-01	8.30E-01
	SP_PIR_KEYWORDS	heme biosynthesis	4	2.00E-01	6.30E-01
	SP_PIR_KEYWORDS	porphyrin biosynthesis	3	3.40E-01	7.90E-01
	GOTERM_BP_FAT	cofactor biosynthetic process	13	6.40E-01	1.00E+00
	BIOCARTA	Hemoglobin's Chaperone	3	7.10E-01	1.00E+00
	KEGG_PATHWAY	Porphyrin and chlorophyll metabolism	4	8.90E-01	9.70E-01
Annotation Cluster 166	**Enrichment Score: 0.73**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	domain:MATH	4	1.70E-01	1.00E+00
	INTERPRO	MATH	4	1.90E-01	9.90E-01
	SMART	MATH	4	2.00E-01	9.00E-01
Annotation Cluster 167	**Enrichment Score: 0.72**		**Count**	**P_Value**	**Benjamini**
	GOTERM_MF_FAT	phosphatidylinositol transporter activity	3	1.30E-01	8.40E-01
	INTERPRO	Phosphatidylinositol transfer protein	3	1.70E-01	9.90E-01
	GOTERM_MF_FAT	phospholipid transporter activity	6	3.10E-01	9.70E-01
Annotation Cluster 168	**Enrichment Score: 0.72**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	domain:Ras-associating	8	1.10E-01	1.00E+00
	INTERPRO	Ras-association	8	2.30E-01	1.00E+00
	SMART	RA	8	2.70E-01	9.30E-01
Annotation Cluster 169	**Enrichment Score: 0.72**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	domain:RUN	5	1.40E-01	1.00E+00
	INTERPRO	RUN	5	2.10E-01	1.00E+00
	SMART	RUN	5	2.40E-01	9.20E-01
Annotation Cluster 170	**Enrichment Score: 0.72**		**Count**	**P_Value**	**Benjamini**
	GOTERM_CC_FAT	SWI/SNF complex	5	1.30E-01	5.60E-01
	GOTERM_CC_FAT	SWI/SNF-type complex	5	1.30E-01	5.60E-01

ILMN_1767230	AXDND1	-0.462985533
ILMN_1817255	LOC144438	-0.463031801
ILMN_1768930	U2AF2	-0.463062918
ILMN_1860288	MBTPS2	-0.463085596
ILMN_3242977	FLJ33630	-0.463121596
ILMN_1734229	SPPL2A	-0.463267776
ILMN_3292114	LOC100131510	-0.4632744
ILMN_1796583	CLRN2	-0.463348463
ILMN_1718042	ZNF549	-0.46335229
ILMN_1748819	MRPL22	-0.463357528
ILMN_1683390	FLCN	-0.463378395
ILMN_1790603	ATPAF1	-0.463427045
ILMN_1795000	OR8J3	-0.463438428
ILMN_2413259	SOCS4	-0.463474005
ILMN_2089484	CYP4F3	-0.463475685
ILMN_1661966	UGCGL1	-0.463507271
ILMN_1736630	LOC100132024	-0.46356997
ILMN_1895518	AW468861	-0.463575816
ILMN_1810330	LOC440131	-0.463577729
ILMN_1804361	SUFU	-0.4636211
ILMN_1672957	RPL32P3	-0.463641722
ILMN_1744059	DCTN6	-0.463671021
ILMN_1695036	TPPP3	-0.463706361
ILMN_1733696	IMP3	-0.463724496
ILMN_2069821	C4orf32	-0.463785453
ILMN_1660727	ENPP5	-0.463798942
ILMN_3255965	NA	-0.463835049
ILMN_2221336	QRFPR	-0.463852421
ILMN_2382717	OPN3	-0.463866346
ILMN_1724367	NDUFB1	-0.463939172
ILMN_1670625	DKFZp434A171	-0.463962596
ILMN_1774930	CDC14A	-0.463997283
ILMN_3236182	GCNT4	-0.464006634
ILMN_1742203	DYDC1	-0.464010982
ILMN_1656218	AK131040	-0.464012025
ILMN_1657436	FGFR1OP2	-0.464128654
ILMN_1750447	GOLGA6A	-0.464145869
ILMN_1808537	LRRC66	-0.464304091
ILMN_1774589	IQCC	-0.464308049
ILMN_1704255	FAM159B	-0.464316652
ILMN_2138745	C14orf37	-0.464334062
ILMN_3305788	NA	-0.464452296
ILMN_1707694	FAM22A	-0.464482571
ILMN_3235931	LOC100132287	-0.464488957
ILMN_1744701	RGSL1	-0.464522237
ILMN_1715742	SLC22A1	-0.464539519
ILMN_2334322	MIER1	-0.464542661
ILMN_1653876	SPG21	-0.464556224
ILMN_3243986	FAM72B	-0.464608865
ILMN_2211189	IKBKAP	-0.464716851
ILMN_1694952	SSX4B	-0.464773608
ILMN_1694734	RUNX1T1	-0.464779476
ILMN_1732860	FLJ26850	-0.464843623
ILMN_1751816	MCTS1	-0.464859519
ILMN_1705085	C8orf77	-0.464880181
ILMN_1687439	SNX20	-0.464892833
ILMN_1685057	SLC22A4	-0.464940871
ILMN_2060578	INSL5	-0.464970899
ILMN_1684746	IPO11	-0.465074254
ILMN_1760431	GABRR1	-0.465116271
ILMN_1660323	PDXDC1	-0.465180109
ILMN_1678246	SLC25A32	-0.465208692
ILMN_1752213	TMEM60	-0.465233708
ILMN_2189668	NUDT11	-0.465240638
ILMN_1807304	MBNL1	-0.465256516
ILMN_3282561	LOC100132272	-0.465354651
ILMN_1888015	AI525756	-0.465355237
ILMN_1785615	SUMO1P1	-0.465386407
ILMN_1672962	LOC645485	-0.465402467
ILMN_1670805	PRR20A	-0.465523449
ILMN_1717485	AL832378	-0.465565336
ILMN_3243414	LOC100133161	-0.465574713
ILMN_2410371	CD79A	-0.46560942
ILMN_1715638	GAGE8	-0.465625119
ILMN_1853210	AW117187	-0.465626213
ILMN_1765310	TCEAL2	-0.465722059
ILMN_1752728	FUCA1	-0.465825871
ILMN_1706615	SLC22A7	-0.465833951
ILMN_1741518	LOC100128035	-0.465848794
ILMN_3248228	PROX2	-0.465880704
ILMN_1849859	BU616091	-0.46589324
ILMN_1793508	C7orf36	-0.466004572
ILMN_3240893	SLMO2	-0.466006216
ILMN_1739486	BX647938	-0.466025033
ILMN_1726642	BEND3	-0.466051337
ILMN_1663131	LYST	-0.46606158
ILMN_1893697	AA532505	-0.466078333
ILMN_1868572	C6orf168	-0.466098715
ILMN_3269520	LOC100130673	-0.466099176
ILMN_1911806	BQ940594	-0.466107422
ILMN_1813344	C20orf7	-0.466112309
ILMN_3247434	LOC100128977	-0.466138241
ILMN_1729272	DIP2A	-0.466170826
ILMN_1817651	BX091227	-0.466197974

ILMN_2105966	SLC35A4	0.656083511
ILMN_1814917	TLE2	0.656022695
ILMN_2394027	CLK3	0.655989811
ILMN_2330552	CDK11A	0.655953672
ILMN_1747593	ISLR	0.655785374
ILMN_2382500	MS4A14	0.655730543
ILMN_1685433	COL8A1	0.655630543
ILMN_2390919	FBLN2	0.65550337
ILMN_2212690	ZC3H7A	0.655449582
ILMN_1654060	MKNK2	0.655429293
ILMN_1794165	PGD	0.655361599
ILMN_1757877	HCFC1R1	0.655289821
ILMN_1674811	OASL	0.655200294
ILMN_1776953	MYL9	0.655087788
ILMN_1684258	RPS28	0.655071645
ILMN_1677635	TUBA4B	0.654993849
ILMN_1744487	C1QTNF5	0.654760753
ILMN_1803846	EIF1	0.654706558
ILMN_1752249	FAM38A	0.654613797
ILMN_1684391	PLOD1	0.654601479
ILMN_2189933	RPL36AL	0.654522637
ILMN_1703718	CCT7	0.654390059
ILMN_1769129	CCL19	0.654366457
ILMN_1748812	TMEM130	0.654139742
ILMN_1712155	RPL6	0.65410387
ILMN_1810420	DYSF	0.654016911
ILMN_1712515	FOXO3	0.653909675
ILMN_1872419	AW276479	0.653862958
ILMN_1716687	TPM1	0.653662339
ILMN_1694259	NSA2	0.653494417
ILMN_1802799	AKIRIN1	0.653447736
ILMN_1675130	NFIC	0.653279278
ILMN_2241953	PILRA	0.653184116
ILMN_1730698	ODF2	0.653115176
ILMN_1719256	CKS1B	0.653075236
ILMN_1693334	P4HA1	0.653058128
ILMN_3240375	abParts	0.652854973
ILMN_1696843	NPIPL3	0.652731688
ILMN_1739840	LRRC8A	0.652657803
ILMN_1704253	C6orf106	0.652631303
ILMN_2174081	ZNF133	0.652535356
ILMN_1680274	abParts	0.652494909
ILMN_1719611	CCT6P3	0.652401612
ILMN_2347145	DCN	0.652396222
ILMN_1656082	H3F3A	0.652210278
ILMN_1778337	HNF1B	0.652195861
ILMN_1753890	IFT20	0.652166796
ILMN_1771599	PLOD2	0.65209355
ILMN_2389501	HSD11B1	0.652047615
ILMN_1689007	SUGP2	0.652012182
ILMN_1759436	NOSIP	0.651984083
ILMN_1685378	RPS7	0.651926927
ILMN_3261197	ATP5E	0.65187189
ILMN_1759419	ILVBL	0.651656546
ILMN_2082244	FOXK1	0.65164199
ILMN_1761463	EFHD2	0.651601653
ILMN_2191428	UBB	0.651552987
ILMN_1725700	MOV10	0.651521456
ILMN_1716336	CKAP5	0.651433031
ILMN_3251536	FAM127C	0.651403377
ILMN_1763603	FAM177A1	0.651364419
ILMN_1670134	FADS1	0.651333747
ILMN_1688279	PVRIG	0.651304312
ILMN_1678290	HMG20A	0.651138322
ILMN_1739508	abParts	0.651073095
ILMN_1759325	C16orf91	0.650995539
ILMN_1805519	DQ893812	0.650963974
ILMN_3235709	HNF1B	0.650881266
ILMN_1659189	C9orf89	0.650851083
ILMN_1780397	TRAF3IP3	0.650726968
ILMN_1687442	TNIK	0.65054193
ILMN_1692706	DCUN1D2	0.650508496
ILMN_2088990	CXorf21	0.650410073
ILMN_2041577	GPR172A	0.650382138
ILMN_2069128	EPB41L2	0.650359696
ILMN_1815158	GPS2	0.650296365
ILMN_1737406	KLF6	0.650223224
ILMN_1712687	PAK2	0.650203508
ILMN_2396956	AKAP13	0.65012727
ILMN_3180557	CYB561D1	0.650100296
ILMN_1766221	B4GALT1	0.650052639
ILMN_3278548	RPL7	0.650024561
ILMN_1811579	HOMER3	0.649891391
ILMN_2398432	BRMS1	0.649592127
ILMN_1802523	HS3ST5	0.649280407
ILMN_1761733	HLA-DMB	0.649268095
ILMN_1737862	PSMB4	0.649195609
ILMN_3307930	RAN	0.649149211
ILMN_1757627	ZMYND19	0.649104675
ILMN_2136133	PABPC1	0.648992521
ILMN_1695962	SLC12A9	0.648974306
ILMN_1669308	BRPF1	0.648970928
ILMN_1793522	PRKAB1	0.648924796
ILMN_1764230	GNPTG	0.648791896

	BIOCARTA	Chromatin Remodeling by hSWI/SNF ATP-dependent Complexes	5	4.20E-01	9.70E-01
Annotation Cluster 171	**Enrichment Score: 0.72**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	domain:PSI	6	9.80E-03	9.00E-01
	INTERPRO	Plexin/semaphorin/integrin	11	5.10E-02	9.20E-01
	SMART	PSI	11	6.50E-02	7.50E-01
	INTERPRO	Integrin beta subunit, N-terminal	4	6.90E-02	9.50E-01
	SMART	INB	4	7.70E-02	7.60E-01
	UP_SEQ_FEATURE	region of interest:Cysteine-rich tandem repeats	4	8.50E-02	1.00E+00
	INTERPRO	Integrin beta subunit, C-terminal	4	9.40E-02	9.60E-01
	INTERPRO	Integrin beta subunit	4	9.40E-02	9.60E-01
	GOTERM_CC_FAT	integrin complex	7	1.80E-01	6.50E-01
	INTERPRO	Integrin beta subunit, tail	3	2.20E-01	1.00E+00
	INTERPRO	Integrin beta subunit, subgroup	3	2.20E-01	1.00E+00
	PIR_SUPERFAMILY	PIRSF002512:integrin, beta subunit	3	2.40E-01	1.00E+00
	PIR_SUPERFAMILY	PIRSF002512:Integrin_B	3	2.40E-01	1.00E+00
	GOTERM_BP_FAT	integrin-mediated signaling pathway	12	3.10E-01	9.40E-01
	INTERPRO	Plexin	6	3.50E-01	1.00E+00
	SP_PIR_KEYWORDS	integrin	7	3.70E-01	8.10E-01
	UP_SEQ_FEATURE	repeat:I	4	6.30E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:IV	4	6.30E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:III	4	6.30E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:II	4	6.30E-01	1.00E+00
	GOTERM_BP_FAT	cell-matrix adhesion	12	6.40E-01	1.00E+00
	INTERPRO	EGF, extracellular	8	7.00E-01	1.00E+00
Annotation Cluster 172	**Enrichment Score: 0.71**		**Count**	**P_Value**	**Benjamini**
	GOTERM_CC_FAT	organellar large ribosomal subunit	6	8.10E-02	4.60E-01
	GOTERM_CC_FAT	mitochondrial large ribosomal subunit	6	8.10E-02	4.60E-01
	GOTERM_CC_FAT	organellar ribosome	8	4.60E-01	9.00E-01
	GOTERM_CC_FAT	mitochondrial ribosome	8	4.60E-01	9.00E-01
Annotation Cluster 173	**Enrichment Score: 0.7**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	covalent chromatin modification	26	2.30E-02	3.20E-01
	GOTERM_BP_FAT	histone modification	25	2.80E-02	3.70E-01
	GOTERM_BP_FAT	protein amino acid acetylation	10	2.40E-01	9.00E-01
	GOTERM_BP_FAT	histone acetylation	9	3.00E-01	9.30E-01
	GOTERM_CC_FAT	histone acetyltransferase complex	9	3.50E-01	8.30E-01
	GOTERM_BP_FAT	protein amino acid acylation	10	3.90E-01	9.70E-01
	GOTERM_BP_FAT	histone H4 acetylation	4	5.00E-01	9.90E-01
	GOTERM_BP_FAT	histone H3 acetylation	3	8.80E-01	1.00E+00
Annotation Cluster 174	**Enrichment Score: 0.69**		**Count**	**P_Value**	**Benjamini**
	GOTERM_CC_FAT	anchored to external side of plasma membrane	3	1.40E-01	5.70E-01
	GOTERM_CC_FAT	anchored to plasma membrane	6	1.60E-01	6.10E-01
	GOTERM_CC_FAT	intrinsic to external side of plasma membrane	3	3.90E-01	8.60E-01
Annotation Cluster 175	**Enrichment Score: 0.67**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	regulation of RNA splicing	6	1.10E-01	7.20E-01
	GOTERM_BP_FAT	regulation of mRNA processing	5	1.80E-01	8.30E-01
	GOTERM_BP_FAT	regulation of nuclear mRNA splicing, via spliceosome	3	4.80E-01	9.90E-01
Annotation Cluster 176	**Enrichment Score: 0.67**		**Count**	**P_Value**	**Benjamini**
	SP_PIR_KEYWORDS	molecular chaperone	5	6.20E-02	3.30E-01
	INTERPRO	Chaperone, tailless complex polypeptide 1	4	1.50E-01	9.90E-01
	GOTERM_CC_FAT	chaperonin-containing T-complex	3	2.40E-01	7.20E-01
	INTERPRO	Chaperonin Cpn60/TCP-1	4	2.90E-01	1.00E+00
	INTERPRO	Chaperonin TCP-1, conserved site	3	3.70E-01	1.00E+00
	PIR_SUPERFAMILY	PIRSF002584:molecular chaperone t-complex-type	3	4.00E-01	1.00E+00
Annotation Cluster 177	**Enrichment Score: 0.66**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	negative regulation of tyrosine phosphorylation of Stat3 protein	3	8.70E-02	6.40E-01
	GOTERM_BP_FAT	negative regulation of phosphate metabolic process	11	9.30E-02	6.60E-01
	GOTERM_BP_FAT	negative regulation of phosphorus metabolic process	11	9.30E-02	6.60E-01
	GOTERM_BP_FAT	negative regulation of peptidyl-tyrosine phosphorylation	4	1.00E-01	7.00E-01
	GOTERM_BP_FAT	negative regulation of protein amino acid phosphorylation	8	1.20E-01	7.30E-01
	GOTERM_BP_FAT	regulation of tyrosine phosphorylation of Stat3 protein	5	1.80E-01	8.30E-01
	GOTERM_BP_FAT	negative regulation of tyrosine phosphorylation of STAT protein	3	1.80E-01	8.40E-01
	GOTERM_BP_FAT	negative regulation of JAK-STAT cascade	3	2.30E-01	8.90E-01
	GOTERM_BP_FAT	negative regulation of phosphorylation	9	2.40E-01	8.90E-01
	GOTERM_BP_FAT	regulation of JAK-STAT cascade	7	3.40E-01	9.50E-01
	GOTERM_BP_FAT	negative regulation of protein kinase cascade	7	3.40E-01	9.50E-01
	GOTERM_BP_FAT	regulation of tyrosine phosphorylation of STAT protein	6	3.90E-01	9.70E-01
	GOTERM_BP_FAT	positive regulation of tyrosine phosphorylation of STAT protein	3	8.30E-01	1.00E+00
	GOTERM_BP_FAT	positive regulation of JAK-STAT cascade	3	8.80E-01	1.00E+00
Annotation Cluster 178	**Enrichment Score: 0.66**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	domain:W2	3	2.00E-01	1.00E+00
	INTERPRO	eIF4-gamma/eIF5/eIF2-epsilon	3	2.20E-01	1.00E+00
	SMART	eIF5C	3	2.30E-01	9.20E-01
Annotation Cluster 179	**Enrichment Score: 0.66**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	amyloid precursor protein catabolic process	5	2.20E-02	3.10E-01
	GOTERM_BP_FAT	amyloid precursor protein metabolic process	5	4.60E-02	4.80E-01
	GOTERM_BP_FAT	membrane protein ectodomain proteolysis	5	1.30E-01	7.50E-01
	GOTERM_BP_FAT	Notch receptor processing	3	1.80E-01	8.40E-01
	GOTERM_BP_FAT	glycoprotein catabolic process	5	2.10E-01	8.70E-01
	GOTERM_BP_FAT	membrane protein proteolysis	5	2.70E-01	9.20E-01
	GOTERM_BP_FAT	membrane protein intracellular domain proteolysis	3	4.40E-01	9.80E-01
	KEGG_PATHWAY	Notch signaling pathway	8	5.70E-01	8.30E-01
	SP_PIR_KEYWORDS	notch signaling pathway	4	8.90E-01	9.90E-01
	GOTERM_BP_FAT	Notch signaling pathway	5	9.30E-01	1.00E+00
Annotation Cluster 180	**Enrichment Score: 0.66**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	short sequence motif:LXXLL motif 3	4	1.40E-01	1.00E+00
	UP_SEQ_FEATURE	short sequence motif:LXXLL motif 5	3	2.00E-01	1.00E+00
	UP_SEQ_FEATURE	short sequence motif:LXXLL motif 2	5	2.40E-01	1.00E+00
	UP_SEQ_FEATURE	short sequence motif:LXXLL motif 1	5	2.40E-01	1.00E+00
	UP_SEQ_FEATURE	short sequence motif:LXXLL motif 4	3	3.00E-01	1.00E+00
Annotation Cluster 181	**Enrichment Score: 0.66**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	domain:UBX	4	2.00E-01	1.00E+00
	INTERPRO	UBX	4	2.20E-01	1.00E+00
	SMART	UBX	4	2.40E-01	9.20E-01
Annotation Cluster 182	**Enrichment Score: 0.66**		**Count**	**P_Value**	**Benjamini**

ILMN_3309614	MIR1-1	-0.466386075
ILMN_1904135	AK023536	-0.466390952
ILMN_1790062	FAM105B	-0.466414379
ILMN_1794807	CACHD1	-0.466438363
ILMN_3309814	MIR208B	-0.466441332
ILMN_1903750	U10515	-0.466481294
ILMN_1693042	WDR90	-0.46651748
ILMN_3237446	SCARNA16	-0.466536328
ILMN_2089977	FKBP9L	-0.46654968
ILMN_3235168	MUL1	-0.466593345
ILMN_1698318	LGALS14	-0.466644467
ILMN_3242059	C6orf221	-0.466701561
ILMN_1739559	FAM187B	-0.466820572
ILMN_1675695	PDS5B	-0.466856482
ILMN_1839956	NA	-0.466871559
ILMN_1785535	ARPC4	-0.466891826
ILMN_1655039	SLC27A4	-0.467008949
ILMN_1668531	BC029817	-0.467026949
ILMN_1656867	PLA2G2C	-0.467083318
ILMN_1692026	SUV420H1	-0.467086463
ILMN_1740648	CYP2D6	-0.467183257
ILMN_3242856	BEND3	-0.467188233
ILMN_1692688	RGS12	-0.467251711
ILMN_1657860	C1orf151	-0.467281156
ILMN_2353358	LGALS8	-0.467350998
ILMN_1775268	HECW2	-0.467379419
ILMN_2187727	NOC3L	-0.467394014
ILMN_1732491	OFCC1	-0.467455284
ILMN_1812100	HEATR7A	-0.46747241
ILMN_1673099	PTPN20A	-0.467494038
ILMN_3245559	CDK2AP1	-0.467548429
ILMN_1791297	LOC649305	-0.467600865
ILMN_3262015	AK024162	-0.467611758
ILMN_1875967	BG222050	-0.467630011
ILMN_1758938	SLC31A2	-0.467666404
ILMN_1693843	HELT	-0.467666816
ILMN_1753450	ATXN3L	-0.467688251
ILMN_2152387	DOCK7	-0.467929693
ILMN_3310136	MIR605	-0.467983259
ILMN_1676629	INSIG2	-0.468034473
ILMN_1714643	MGAM	-0.468041434
ILMN_1704369	LIMA1	-0.468054209
ILMN_3208428	NA	-0.468087847
ILMN_2346997	RAB23	-0.46809061
ILMN_2157544	GBF1	-0.468097319
ILMN_1729775	OPA1	-0.468130591
ILMN_2166686	NUFIP1	-0.468147386
ILMN_1853705	AW118645	-0.468161779
ILMN_1667229	HCG22	-0.468185191
ILMN_2283196	ZSWIM3	-0.4683098
ILMN_1674190	LOC100507206	-0.468312809
ILMN_1769011	KIAA1456	-0.468333468
ILMN_2352926	BPGM	-0.468335546
ILMN_1794070	ANKRD13B	-0.468526692
ILMN_3261292	EBF4	-0.46853916
ILMN_2184556	SLC4A4	-0.468540888
ILMN_1655296	UTRN	-0.468581747
ILMN_3237085	NTF4	-0.468607042
ILMN_1809639	TMEM26	-0.468622759
ILMN_1764396	HDAC4	-0.468661224
ILMN_1752843	GRM4	-0.468744452
ILMN_1793832	GRB14	-0.46876901
ILMN_3239541	BC131768	-0.468787874
ILMN_1742040	GDPD4	-0.468923703
ILMN_1667018	ACE2	-0.46894057
ILMN_3239177	MEX3A	-0.468984692
ILMN_3246909	LOC256880	-0.469011429
ILMN_1779070	APOLIV	-0.469094128
ILMN_1799299	PRPF38B	-0.469096519
ILMN_3269652	TUBBP5	-0.469115687
ILMN_1892652	DB335929	-0.469156047
ILMN_2390457	ESR2	-0.46916113
ILMN_3307791	FAM69A	-0.469177238
ILMN_1725401	DEFB104B	-0.469219297
ILMN_1670124	YDJC	-0.469274602
ILMN_1690911	C16orf87	-0.469336638
ILMN_1655165	RNF138	-0.469384277
ILMN_1722445	MC4R	-0.469395113
ILMN_1685661	RRP15	-0.469403129
ILMN_1757427	XAGE1D	-0.469407343
ILMN_1695506	DKK2	-0.469412407
ILMN_3251526	USP13	-0.46942161
ILMN_2160764	HBP1	-0.469506567
ILMN_1766643	HOPX	-0.469512928
ILMN_1677269	MAGEA2	-0.469598079
ILMN_1811277	TRIM13	-0.469626386
ILMN_1772557	SLC22A10	-0.469644149
ILMN_2301955	THAP1	-0.469789765
ILMN_3227031	MS4A18	-0.469792946
ILMN_3238130	DUX2	-0.469858965
ILMN_1739144	SI	-0.469900225
ILMN_1759690	PRB2	-0.469920712
ILMN_1757272	THAP1	-0.469989041
ILMN_1666546	DUSP14	-0.469993341

ILMN_1740587	RPS11	0.648719151
ILMN_2383306	GPATCH4	0.648604602
ILMN_1697554	SASH3	0.648502748
ILMN_1680624	CREG1	0.648359421
ILMN_1690566	RASSF4	0.648292113
ILMN_1651850	RPS16	0.648245488
ILMN_2364022	SLC16A3	0.648036352
ILMN_1790472	SLC25A28	0.647999833
ILMN_1670561	TCEAL8	0.647988804
ILMN_2364384	PPARG	0.647916434
ILMN_1758798	NPIPL2	0.647913515
ILMN_1657708	MGLL	0.647911016
ILMN_1674519	ZP2	0.647888247
ILMN_1767475	CERK	0.647765033
ILMN_1763207	BATF3	0.647689072
ILMN_1691117	DNTTIP1	0.647501964
ILMN_1780806	ANKRD36B	0.647232295
ILMN_2325168	ARRB1	0.64723057
ILMN_1659058	PPP1R10	0.647122928
ILMN_1690105	STAT1	0.646980823
ILMN_1656482	OSBPL2	0.646968308
ILMN_1774207	ANGPT2	0.646942108
ILMN_1811195	ZNF211	0.646900036
ILMN_1666269	CTSZ	0.646876047
ILMN_1766803	TUBGCP6	0.646779075
ILMN_1689932	WDR85	0.646778371
ILMN_1749722	RNF213	0.6467514
ILMN_1660341	LRPAP1	0.646609936
ILMN_1751328	FAM83H	0.646493113
ILMN_3285819	NA	0.64642578
ILMN_1743097	XRCC6	0.646388804
ILMN_1766185	AXIN1	0.646235652
ILMN_1728024	TUBG2	0.64622909
ILMN_1800261	TUBA1B	0.646190746
ILMN_1730048	C7orf26	0.646100155
ILMN_1667551	SMA4	0.646085609
ILMN_1652749	ERF	0.646050754
ILMN_2363165	TACC2	0.646049908
ILMN_1803560	LAT2	0.645981039
ILMN_1703412	LATS2	0.645972871
ILMN_1691449	CHCHD2	0.645829087
ILMN_1666169	NBR2	0.64571977
ILMN_1722820	KDELR3	0.645574177
ILMN_1665554	BRF2	0.645567397
ILMN_1731666	ZNF641	0.645527247
ILMN_2056551	RBMX2	0.64539567
ILMN_1689725	RPLP1	0.645324939
ILMN_2311166	ITGB5	0.645162054
ILMN_2294878	NSUN5	0.645125427
ILMN_3269537	RPS2	0.645118614
ILMN_1809141	ING4	0.645115556
ILMN_2194828	C16orf53	0.645004757
ILMN_1727761	GMEB1	0.644906018
ILMN_1778013	PDPR	0.644781906
ILMN_2226763	H2AFB2	0.644766692
ILMN_2305721	POMT1	0.644241239
ILMN_1715332	TTC21A	0.644098518
ILMN_1734608	ZNF77	0.644020008
ILMN_1684663	ZDHHC13	0.644014898
ILMN_2370414	CHD3	0.643992057
ILMN_3304012	NA	0.643770383
ILMN_1722059	SAFB	0.643514246
ILMN_1812769	UBXN1	0.643509069
ILMN_1769665	RAB5C	0.64348971
ILMN_1719237	SPDYE8P	0.64337813
ILMN_3307799	PSMD4	0.643136118
ILMN_1703053	ZFP91	0.643070727
ILMN_1815874	NANS	0.64306804
ILMN_1652223	WDR91	0.642961922
ILMN_2328835	IP6K2	0.642952858
ILMN_2320964	ADAR	0.642800995
ILMN_2101930	POLG	0.642760054
ILMN_1675626	PRPF38A	0.642713365
ILMN_2349129	DPP3	0.642640033
ILMN_1809889	CCDC117	0.642577425
ILMN_2357976	DDX39B	0.642577256
ILMN_1788377	COL27A1	0.642557904
ILMN_2047112	DPCD	0.642517811
ILMN_2134062	ALKBH3	0.641789203
ILMN_1691131	LSMD1	0.641742692
ILMN_1813025	AK125786	0.641719946
ILMN_1779071	FEZ1	0.641517956
ILMN_2151277	LPGAT1	0.641485064
ILMN_2056032	CD99	0.641476689
ILMN_1812067	RER1	0.641472642
ILMN_1690802	TRMT112	0.641450614
ILMN_1702065	MFSD5	0.641366445
ILMN_1716080	CBL	0.641237401
ILMN_1713301	DGCR2	0.641171187
ILMN_2325506	BCAS4	0.641168308
ILMN_1687037	IFT140	0.640959966
ILMN_2287296	SYF2	0.640923742
ILMN_3283772	GAPDH	0.640852411
ILMN_1699440	ZBTB47	0.640730326

	INTERPRO	PAK-box/P21-Rho-binding	5	1.80E-01	9.90E-01
	UP_SEQ_FEATURE	domain:CRIB	5	1.90E-01	1.00E+00
	SMART	PBD	5	2.10E-01	9.00E-01
	SP_PIR_KEYWORDS	cell shape	5	3.30E-01	7.80E-01
Annotation Cluster 183	**Enrichment Score: 0.65**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	repeat:HAT 5	4	1.40E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:HAT 4	4	1.70E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:HAT 1	4	2.00E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:HAT 3	4	2.00E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:HAT 2	4	2.00E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:HAT 7	3	2.00E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:HAT 6	3	3.00E-01	1.00E+00
	INTERPRO	RNA-processing protein, HAT helix	3	3.20E-01	1.00E+00
	SMART	HAT	3	3.40E-01	9.60E-01
Annotation Cluster 184	**Enrichment Score: 0.65**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	branching morphogenesis of a tube	13	1.40E-01	7.80E-01
	GOTERM_BP_FAT	morphogenesis of a branching structure	14	1.70E-01	8.20E-01
	GOTERM_BP_FAT	tube development	35	1.80E-01	8.40E-01
	GOTERM_BP_FAT	patterning of blood vessels	5	3.00E-01	9.30E-01
	GOTERM_BP_FAT	tube morphogenesis	19	4.10E-01	9.70E-01
Annotation Cluster 185	**Enrichment Score: 0.65**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	regulation of lipid kinase activity	4	1.40E-01	7.70E-01
	GOTERM_BP_FAT	regulation of phosphoinositide 3-kinase activity	3	1.80E-01	8.40E-01
	GOTERM_BP_FAT	positive regulation of phosphoinositide 3-kinase activity	3	1.80E-01	8.40E-01
	GOTERM_BP_FAT	positive regulation of lipid metabolic process	7	5.80E-01	9.90E-01
Annotation Cluster 186	**Enrichment Score: 0.64**		**Count**	**P_Value**	**Benjamini**
	GOTERM_MF_FAT	protein binding, bridging	19	5.30E-02	6.20E-01
	GOTERM_MF_FAT	SH3/SH2 adaptor activity	8	4.40E-01	9.90E-01
	GOTERM_MF_FAT	molecular adaptor activity	10	5.00E-01	9.90E-01
Annotation Cluster 187	**Enrichment Score: 0.64**		**Count**	**P_Value**	**Benjamini**
	INTERPRO	Tropomyosin	3	8.00E-02	9.50E-01
	GOTERM_CC_FAT	muscle thin filament tropomyosin	3	8.90E-02	4.70E-01
	PIR_SUPERFAMILY	PIRSF002327:tropomyosin	3	9.10E-02	1.00E+00
	SP_PIR_KEYWORDS	muscle protein	9	4.40E-01	8.60E-01
	GOTERM_CC_FAT	striated muscle thin filament	3	6.10E-01	9.50E-01
	SP_PIR_KEYWORDS	skeletal muscle	3	8.00E-01	9.90E-01
Annotation Cluster 188	**Enrichment Score: 0.64**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	phosphoinositide phosphorylation	5	1.30E-01	7.50E-01
	GOTERM_BP_FAT	lipid phosphorylation	5	1.50E-01	7.90E-01
	UP_SEQ_FEATURE	domain:FAT	3	1.60E-01	1.00E+00
	UP_SEQ_FEATURE	domain:FATC	3	1.60E-01	1.00E+00
	UP_SEQ_FEATURE	domain:PI3K/PI4K	5	1.70E-01	1.00E+00
	INTERPRO	PIK-related kinase, FATC	3	1.70E-01	9.90E-01
	INTERPRO	PIK-related kinase	3	1.70E-01	9.90E-01
	INTERPRO	Phosphatidylinositol 3- and 4-kinase, conserved site	5	1.80E-01	9.90E-01
	INTERPRO	Phosphatidylinositol 3- and 4-kinase, catalytic	5	1.80E-01	9.90E-01
	SMART	PI3Kc	5	2.10E-01	9.00E-01
	GOTERM_CC_FAT	phosphoinositide 3-kinase complex	3	4.90E-01	9.10E-01
	KEGG_PATHWAY	Type II diabetes mellitus	7	7.30E-01	9.10E-01
	KEGG_PATHWAY	mTOR signaling pathway	7	8.10E-01	9.30E-01
Annotation Cluster 189	**Enrichment Score: 0.64**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	response to vitamin A	9	1.80E-01	8.40E-01
	GOTERM_BP_FAT	response to vitamin	12	2.50E-01	9.00E-01
	GOTERM_BP_FAT	response to retinoic acid	7	2.60E-01	9.20E-01
Annotation Cluster 190	**Enrichment Score: 0.64**		**Count**	**P_Value**	**Benjamini**
	GOTERM_MF_FAT	transforming growth factor beta binding	4	1.30E-01	8.40E-01
	GOTERM_MF_FAT	activin binding	4	1.60E-01	8.70E-01
	GOTERM_MF_FAT	transmembrane receptor protein serine/threonine kinase activity	5	1.90E-01	9.00E-01
	GOTERM_MF_FAT	transforming growth factor beta receptor activity	5	1.90E-01	9.00E-01
	GOTERM_MF_FAT	type I transforming growth factor beta receptor binding	3	2.20E-01	9.30E-01
	GOTERM_MF_FAT	transforming growth factor beta receptor binding	4	3.80E-01	9.80E-01
	GOTERM_MF_FAT	SMAD binding	7	5.50E-01	9.90E-01
Annotation Cluster 191	**Enrichment Score: 0.64**		**Count**	**P_Value**	**Benjamini**
	GOTERM_CC_FAT	basolateral plasma membrane	35	9.50E-02	4.80E-01
	GOTERM_CC_FAT	cell-substrate junction	20	1.60E-01	6.20E-01
	GOTERM_CC_FAT	adherens junction	26	1.80E-01	6.50E-01
	GOTERM_CC_FAT	focal adhesion	18	2.00E-01	6.70E-01
	GOTERM_CC_FAT	cell-substrate adherens junction	18	2.40E-01	7.30E-01
	GOTERM_CC_FAT	anchoring junction	27	2.80E-01	7.60E-01
	GOTERM_CC_FAT	cell junction	58	9.60E-01	1.00E+00
Annotation Cluster 192	**Enrichment Score: 0.63**		**Count**	**P_Value**	**Benjamini**
	GOTERM_MF_FAT	histone deacetylase activity	5	1.20E-01	8.20E-01
	GOTERM_MF_FAT	protein deacetylase activity	5	1.20E-01	8.20E-01
	GOTERM_BP_FAT	protein amino acid deacetylation	6	1.50E-01	8.00E-01
	GOTERM_BP_FAT	histone deacetylation	5	1.80E-01	8.30E-01
	GOTERM_MF_FAT	deacetylase activity	5	1.90E-01	9.00E-01
	GOTERM_BP_FAT	chromatin silencing	5	2.10E-01	8.70E-01
	COG_ONTOLOGY	Chromatin structure and dynamics / Secondary metabolites biosynthesis, transport, and catabolism	3	2.10E-01	9.50E-01
	GOTERM_BP_FAT	negative regulation of gene expression, epigenetic	5	3.00E-01	9.30E-01
	UP_SEQ_FEATURE	region of interest:Histone deacetylase	3	3.50E-01	1.00E+00
	INTERPRO	Histone deacetylase superfamily	3	4.10E-01	1.00E+00
	GOTERM_MF_FAT	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides	7	7.70E-01	1.00E+00
Annotation Cluster 193	**Enrichment Score: 0.63**		**Count**	**P_Value**	**Benjamini**
	GOTERM_CC_FAT	vacuolar part	13	1.40E-01	5.70E-01
	GOTERM_CC_FAT	lysosomal membrane	6	2.90E-01	7.80E-01
	GOTERM_CC_FAT	vacuolar membrane	10	3.30E-01	8.10E-01
Annotation Cluster 194	**Enrichment Score: 0.62**		**Count**	**P_Value**	**Benjamini**
	BIOCARTA	Activation of Csk by cAMP-dependent Protein Kinase Inhibits Signaling through the T Cell Receptor	8	3.10E-02	9.40E-01
	BIOCARTA	Lck and Fyn tyrosine kinases in initiation of TCR Activation	6	4.40E-02	9.10E-01
	KEGG_PATHWAY	Asthma	8	1.30E-01	4.90E-01
	BIOCARTA	B Lymphocyte Cell Surface Molecules	5	1.50E-01	9.30E-01
	BIOCARTA	Bystander B Cell Activation	4	1.90E-01	9.30E-01
	BIOCARTA	Antigen Dependent B Cell Activation	4	4.20E-01	9.70E-01
	BIOCARTA	The Co-Stimulatory Signal During T-cell Activation	5	5.20E-01	9.80E-01

ILMN_1726967	TWSG1	-0.47004142
ILMN_1810107	C17orf74	-0.470054119
ILMN_1691181	TMX1	-0.470125971
ILMN_1800543	SCFD1	-0.470167777
ILMN_1688240	PHOSPHO1	-0.470177798
ILMN_1692762	NA	-0.470233624
ILMN_1670245	KLF3	-0.470269252
ILMN_3269956	NA	-0.470305978
ILMN_1726701	BC038536	-0.470319584
ILMN_1707585	SLC46A2	-0.470393928
ILMN_1881598	AW451118	-0.47039514
ILMN_1837271	CA449813	-0.470425997
ILMN_1746428	RGPD1	-0.470431857
ILMN_1745949	CEACAM21	-0.470562241
ILMN_1671890	UBTFL1	-0.470572197
ILMN_1787794	BMF	-0.470589425
ILMN_1885728	KIAA1147	-0.470634556
ILMN_1870923	AI125404	-0.470648949
ILMN_3304072	PRG4	-0.470650171
ILMN_1833175	CD242195	-0.470660412
ILMN_1914874	KRTAP25-1	-0.470678994
ILMN_1808163	C11orf24	-0.47071481
ILMN_1662413	HGSNAT	-0.470745829
ILMN_1696183	HBQ1	-0.470804271
ILMN_1671547	HMGA2	-0.470814597
ILMN_1736546	SLC16A14	-0.470840134
ILMN_1714280	FOXL2	-0.47088854
ILMN_1695181	SCRIB	-0.47089567
ILMN_1772214	CRYBA1	-0.470958407
ILMN_1861915	CA392115	-0.470972771
ILMN_2145781	RBMY2FP	-0.471052682
ILMN_1734552	LRRC20	-0.471073155
ILMN_1723141	OTUD1	-0.471203258
ILMN_1704374	BC043355	-0.471243422
ILMN_1822408	BU736534	-0.471280693
ILMN_2360047	MAGEA11	-0.47131226
ILMN_1760222	C14orf144	-0.471452385
ILMN_1803073	DNAJC12	-0.471564801
ILMN_1654340	NA	-0.471582102
ILMN_3239367	HYDIN	-0.471593006
ILMN_2229379	KIT	-0.471602468
ILMN_1751072	SRPRB	-0.471618649
ILMN_2203073	RNF151	-0.471660458
ILMN_1776337	CHORDC1	-0.471673192
ILMN_1711289	GYS1	-0.47170598
ILMN_2072622	LOC100288413	-0.471747066
ILMN_1750902	LYZL6	-0.471768405
ILMN_1867214	LOC400654	-0.471772912
ILMN_1888373	AI859116	-0.471795519
ILMN_1748719	SEC16B	-0.471795641
ILMN_1703703	AB231702	-0.471879148
ILMN_1784707	LOC644277	-0.471892068
ILMN_1681930	TMEM232	-0.471896475
ILMN_1661833	ANKRD12	-0.471917578
ILMN_1725312	RASA1	-0.471934084
ILMN_2081883	IQCK	-0.471976033
ILMN_1684494	BX248300	-0.472119338
ILMN_1784428	MGC57346	-0.472267522
ILMN_1775587	STX19	-0.472268977
ILMN_2071826	RNF152	-0.472339409
ILMN_1776112	SLC10A1	-0.472349113
ILMN_1916313	BX111153	-0.472353236
ILMN_1657790	SRSF11	-0.47235351
ILMN_1849418	AW661821	-0.472416738
ILMN_1864558	BC034632	-0.472456835
ILMN_1895935	CB242622	-0.47250937
ILMN_1668463	SON	-0.472526275
ILMN_1707312	NFIL3	-0.472577389
ILMN_2360988	SEMA6B	-0.472582451
ILMN_3240108	SNORD90	-0.472643537
ILMN_1791186	ARHGAP18	-0.472646883
ILMN_1801405	ROPN1B	-0.472689156
ILMN_2397230	USP16	-0.472716629
ILMN_1725594	FAM188A	-0.472720506
ILMN_1769104	ZCCHC10	-0.472740977
ILMN_1657873	XPO4	-0.472861561
ILMN_1886117	AI187771	-0.472952411
ILMN_2379110	WDR16	-0.472991808
ILMN_1790706	OR10C1	-0.473013376
ILMN_1676490	MIP	-0.473402353
ILMN_1881561	AI204073	-0.473448414
ILMN_2117526	DMGDH	-0.473499684
ILMN_1742534	COL4A5	-0.473529648
ILMN_2322458	OPA1	-0.473550389
ILMN_1676846	ABCE1	-0.473646518
ILMN_1685079	TELO2	-0.473665111
ILMN_1840469	BE217788	-0.473704533
ILMN_1705035	FBXL7	-0.473705225
ILMN_1695972	CCDC89	-0.473725903
ILMN_1746788	TRIM10	-0.473751454
ILMN_1847612	AA554377	-0.473759238
ILMN_1797219	CLCA1	-0.47377604
ILMN_1716680	GRM7	-0.473892278
ILMN_1782045	FKBP4	-0.473919172

ILMN_1675038	PRMT2	0.640461759
ILMN_2311989	CUTA	0.640418616
ILMN_1812721	HIP1R	0.640279458
ILMN_1789775	WDR74	0.640277022
ILMN_1680104	SLC35C1	0.640264772
ILMN_1810560	NUPR1	0.640214158
ILMN_1739946	VKORC1	0.640204728
ILMN_1701621	TYMP	0.640118228
ILMN_1689160	DPEP2	0.640066393
ILMN_3297945	UBA1	0.640064819
ILMN_3305938	SGK1	0.640042001
ILMN_1801383	SMG1	0.639796237
ILMN_1715169	HLA-DRB1	0.639780211
ILMN_2399264	sept-06	0.639680881
ILMN_1676036	TUBBP5	0.639590345
ILMN_3234841	RPL23AP7	0.639342661
ILMN_1667222	MTX1	0.639324629
ILMN_1696911	FTH1	0.63928477
ILMN_1660292	MRPS21	0.63924818
ILMN_1747204	HTRA2	0.639062979
ILMN_1761566	C5orf32	0.639011137
ILMN_1651819	GALNT11	0.638855523
ILMN_1807283	NDST1	0.638844663
ILMN_1794522	EIF5A	0.638830659
ILMN_1681356	PDE2A	0.638809858
ILMN_1745533	FAM117A	0.638766839
ILMN_1763842	PTRH1	0.638691536
ILMN_3237636	C16orf67	0.638690652
ILMN_1800420	RNF214	0.638631004
ILMN_1667716	TMEM101	0.63860242
ILMN_2302358	ABCC5	0.638320677
ILMN_1659024	TMCC2	0.638141021
ILMN_2386354	CSNK2A1	0.638134384
ILMN_1685928	WDR34	0.638101024
ILMN_1718129	MAP2K5	0.638005281
ILMN_3214532	RPL21	0.637949219
ILMN_1713749	CORO1A	0.637824404
ILMN_1738420	TMEM201	0.637608654
ILMN_1725414	ABCC6	0.637555032
ILMN_1710434	TBC1D10C	0.63752807
ILMN_1767006	PSMB8	0.637496823
ILMN_2331205	CHKB	0.637166824
ILMN_1717078	DNAJC16	0.637107692
ILMN_2161746	TRIP10	0.637068321
ILMN_1671295	MST151	0.63697052
ILMN_2342630	LPHN1	0.636968514
ILMN_1796244	CD2BP2	0.636915292
ILMN_1683082	RPUSD1	0.636882451
ILMN_1710571	PAPD5	0.636868402
ILMN_2395285	SNRNP35	0.636796035
ILMN_1736575	TRIM28	0.63665085
ILMN_1796762	CCDC102A	0.636502033
ILMN_1680091	POP7	0.63649984
ILMN_2178775	ZNF585B	0.636432
ILMN_1677237	CHCHD2	0.636380577
ILMN_1707783	CCDC72	0.636344863
ILMN_2354649	SRSF10	0.636288732
ILMN_1703538	AIF1	0.636287556
ILMN_1751958	NSUN5	0.636128946
ILMN_1876778	AI819186	0.636125063
ILMN_1670096	NRBP1	0.636123175
ILMN_1661888	MEF2A	0.635826579
ILMN_2354617	DYRK1B	0.635806682
ILMN_1756898	COQ9	0.635770368
ILMN_1736863	TMEM140	0.635741966
ILMN_1729433	LIPH	0.635610849
ILMN_1664541	POLR2J4	0.635376507
ILMN_2211800	HMGB1	0.635340699
ILMN_1709795	RAC2	0.635233284
ILMN_3236021	ANKRD36	0.635108669
ILMN_2386016	C2orf28	0.635089333
ILMN_3236752	COAS3	0.635076305
ILMN_2396991	HCST	0.635041369
ILMN_1651776	FHOD1	0.63491931
ILMN_1813682	MRPL53	0.634909454
ILMN_1767377	SMA4	0.634905945
ILMN_1666409	PSMB6	0.634878999
ILMN_1718771	CCDC24	0.634843087
ILMN_1777725	LSM14B	0.634811991
ILMN_1682960	DTNBP1	0.634762046
ILMN_2361807	OS9	0.634706209
ILMN_1712708	TRIM47	0.634688648
ILMN_1769473	SETD2	0.634566993
ILMN_2099487	C17orf108	0.634399624
ILMN_2410713	FGFR4	0.634056766
ILMN_3301749	SPNS2	0.63392257
ILMN_1695356	RNF166	0.633745788
ILMN_1762312	FOXRED1	0.633738443
ILMN_1790625	CBX3	0.633642355
ILMN_3176040	RPS27A	0.63363912
ILMN_3273456	PABPC4	0.633604509
ILMN_1722491	APRT	0.633568265
ILMN_1761996	SRSF5	0.633472161
ILMN_1740298	SIGLEC5	0.633340891
ILMN_2413779	SEZ6L2	0.633328612

	BIOCARTA	IL 5 Signaling Pathway	3	6.00E-01	9.90E-01
	BIOCARTA	Th1/Th2 Differentiation	3	9.20E-01	1.00E+00
	BIOCARTA	Cytokines and Inflammatory Response	3	9.70E-01	1.00E+00
Annotation Cluster 195	**Enrichment Score: 0.62**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	DNA damage response, signal transduction by p53 class mediator resulting in transcription of p21 class mediator	3	2.30E-01	8.90E-01
	GOTERM_BP_FAT	DNA damage response, signal transduction resulting in transcription	3	2.30E-01	8.90E-01
	GOTERM_BP_FAT	DNA damage response, signal transduction by p53 class mediator	6	2.50E-01	9.10E-01
Annotation Cluster 196	**Enrichment Score: 0.62**		**Count**	**P_Value**	**Benjamini**
	GOTERM_MF_FAT	fructose binding	3	1.70E-01	8.90E-01
	GOTERM_BP_FAT	fructose metabolic process	5	1.80E-01	8.30E-01
	GOTERM_MF_FAT	phosphofructokinase activity	3	2.20E-01	9.30E-01
	KEGG_PATHWAY	Fructose and mannose metabolism	8	2.40E-01	5.90E-01
	GOTERM_MF_FAT	carbohydrate kinase activity	4	4.80E-01	9.90E-01
Annotation Cluster 197	**Enrichment Score: 0.61**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	response to lipopolysaccharide	15	1.30E-01	7.60E-01
	GOTERM_BP_FAT	response to molecule of bacterial origin	16	1.60E-01	8.00E-01
	GOTERM_BP_FAT	response to bacterium	24	7.30E-01	1.00E+00
Annotation Cluster 198	**Enrichment Score: 0.6**		**Count**	**P_Value**	**Benjamini**
	GOTERM_CC_FAT	stress fiber	6	2.10E-01	6.80E-01
	GOTERM_CC_FAT	actin filament bundle	6	2.60E-01	7.50E-01
	GOTERM_CC_FAT	actomyosin	6	2.90E-01	7.80E-01
Annotation Cluster 199	**Enrichment Score: 0.6**		**Count**	**P_Value**	**Benjamini**
	GOTERM_MF_FAT	insulin-like growth factor binding	7	9.20E-02	7.60E-01
	SP_PIR_KEYWORDS	Growth factor binding	5	1.20E-01	4.80E-01
	INTERPRO	Insulin-like growth factor binding protein	3	1.70E-01	9.90E-01
	UP_SEQ_FEATURE	domain:Thyroglobulin type-1	4	2.00E-01	1.00E+00
	UP_SEQ_FEATURE	domain:IGFBP N-terminal	5	2.20E-01	1.00E+00
	INTERPRO	Insulin-like growth factor-binding protein, IGFBP	5	2.40E-01	1.00E+00
	SMART	IB	5	2.70E-01	9.30E-01
	INTERPRO	Thyroglobulin type-1	4	3.60E-01	1.00E+00
	SMART	TY	4	3.90E-01	9.60E-01
	INTERPRO	Insulin-like growth factor binding protein, N-terminal	3	4.60E-01	1.00E+00
	BIOCARTA	Ghrelin	3	7.50E-01	1.00E+00
Annotation Cluster 200	**Enrichment Score: 0.6**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	cell motion	73	1.10E-01	7.10E-01
	GOTERM_BP_FAT	cell migration	41	2.80E-01	9.30E-01
	GOTERM_BP_FAT	localization of cell	44	3.60E-01	9.60E-01
	GOTERM_BP_FAT	cell motility	44	3.60E-01	9.60E-01
Annotation Cluster 201	**Enrichment Score: 0.6**		**Count**	**P_Value**	**Benjamini**
	SP_PIR_KEYWORDS	antiport	8	1.40E-01	5.20E-01
	GOTERM_MF_FAT	solute:hydrogen antiporter activity	6	1.60E-01	8.80E-01
	GOTERM_MF_FAT	solute:cation antiporter activity	7	1.80E-01	8.90E-01
	GOTERM_MF_FAT	antiporter activity	12	2.50E-01	9.50E-01
	INTERPRO	Cation/H+ exchanger	4	2.60E-01	1.00E+00
	GOTERM_MF_FAT	solute:solute antiporter activity	9	3.90E-01	9.80E-01
	GOTERM_MF_FAT	cation:cation antiporter activity	3	6.60E-01	1.00E+00
Annotation Cluster 202	**Enrichment Score: 0.59**		**Count**	**P_Value**	**Benjamini**
	SP_PIR_KEYWORDS	igg-binding protein	3	2.00E-01	6.30E-01
	GOTERM_MF_FAT	IgG binding	3	2.70E-01	9.60E-01
	GOTERM_MF_FAT	immunoglobulin binding	4	3.00E-01	9.60E-01
Annotation Cluster 203	**Enrichment Score: 0.59**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	zinc finger region:C3H1-type 2	7	1.50E-01	1.00E+00
	UP_SEQ_FEATURE	zinc finger region:C3H1-type 1	7	1.50E-01	1.00E+00
	UP_SEQ_FEATURE	zinc finger region:C3H1-type 3	5	2.20E-01	1.00E+00
	INTERPRO	Zinc finger, CCCH-type	9	3.30E-01	1.00E+00
	SMART	ZnF_C3H1	9	3.80E-01	9.70E-01
	UP_SEQ_FEATURE	zinc finger region:C3H1-type 4	3	4.80E-01	1.00E+00
Annotation Cluster 204	**Enrichment Score: 0.59**		**Count**	**P_Value**	**Benjamini**
	KEGG_PATHWAY	Endometrial cancer	13	8.00E-02	3.70E-01
	KEGG_PATHWAY	Acute myeloid leukemia	14	8.50E-02	3.80E-01
	KEGG_PATHWAY	Non-small cell lung cancer	12	1.80E-01	5.50E-01
	KEGG_PATHWAY	ErbB signaling pathway	17	2.20E-01	5.90E-01
	KEGG_PATHWAY	Chronic myeloid leukemia	15	2.30E-01	5.80E-01
	KEGG_PATHWAY	Glioma	13	2.30E-01	5.80E-01
	KEGG_PATHWAY	Prostate cancer	14	5.90E-01	8.40E-01
	BIOCARTA	Trefoil Factors Initiate Mucosal Healing	5	6.40E-01	9.90E-01
	KEGG_PATHWAY	Melanoma	7	9.70E-01	9.90E-01
Annotation Cluster 205	**Enrichment Score: 0.58**		**Count**	**P_Value**	**Benjamini**
	GOTERM_MF_FAT	tumor necrosis factor receptor superfamily binding	9	3.80E-02	5.30E-01
	GOTERM_MF_FAT	tumor necrosis factor receptor binding	5	2.80E-01	9.60E-01
	INTERPRO	Tumor Necrosis Factor	3	6.50E-01	1.00E+00
	SMART	TNF	3	6.80E-01	9.90E-01
Annotation Cluster 206	**Enrichment Score: 0.58**		**Count**	**P_Value**	**Benjamini**
	SP_PIR_KEYWORDS	heterotrimer	9	1.50E-02	1.30E-01
	SP_PIR_KEYWORDS	basement membrane	9	9.00E-02	4.10E-01
	UP_SEQ_FEATURE	domain:Laminin G-like 2	7	1.30E-01	1.00E+00
	UP_SEQ_FEATURE	domain:Laminin G-like 1	7	1.30E-01	1.00E+00
	SP_PIR_KEYWORDS	laminin egf-like domain	7	1.40E-01	5.40E-01
	INTERPRO	Concanavalin A-like lectin/glucanase, subgroup	14	1.70E-01	9.90E-01
	UP_SEQ_FEATURE	domain:Laminin EGF-like 1	6	2.00E-01	1.00E+00
	UP_SEQ_FEATURE	domain:Laminin EGF-like 12	3	2.00E-01	1.00E+00
	UP_SEQ_FEATURE	domain:Laminin EGF-like 13	3	2.00E-01	1.00E+00
	UP_SEQ_FEATURE	domain:Laminin G-like 3	5	2.20E-01	1.00E+00
	INTERPRO	Laminin G, subdomain 1	3	2.20E-01	1.00E+00
	UP_SEQ_FEATURE	domain:Laminin EGF-like 2	6	2.20E-01	1.00E+00
	UP_SEQ_FEATURE	domain:Laminin G-like 4	4	2.70E-01	1.00E+00
	UP_SEQ_FEATURE	domain:Laminin G-like 5	3	3.00E-01	1.00E+00
	UP_SEQ_FEATURE	domain:Laminin EGF-like 11	3	3.00E-01	1.00E+00
	UP_SEQ_FEATURE	domain:Laminin N-terminal	4	3.00E-01	1.00E+00
	INTERPRO	Laminin, N-terminal	4	3.30E-01	1.00E+00
	INTERPRO	Laminin G	8	3.40E-01	1.00E+00
	GOTERM_CC_FAT	laminin complex	3	3.40E-01	8.20E-01
	UP_SEQ_FEATURE	domain:Laminin EGF-like 9	3	3.50E-01	1.00E+00
	SMART	LamNT	4	3.60E-01	9.60E-01
	SMART	LamG	8	3.80E-01	9.70E-01

ILMN_1735792	RHBDF2	-0.47393291
ILMN_1805720	SDHAF1	-0.474196797
ILMN_1690276	ZNF354C	-0.474207661
ILMN_1718107	MAGEA12	-0.474373924
ILMN_1671997	LOC388428	-0.474382216
ILMN_1851906	AW665857	-0.474389706
ILMN_3200421	GCSH	-0.474403659
ILMN_1719083	OR56A3	-0.474481903
ILMN_1801491	SLC26A2	-0.474556968
ILMN_1797204	WDR64	-0.474652961
ILMN_1813620	PARP6	-0.474684817
ILMN_1883255	AA470148	-0.474688734
ILMN_1810945	CYP2F1	-0.474711759
ILMN_2399431	PRPS2	-0.474736164
ILMN_1683817	UBE2Q2	-0.474750651
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ILMN_1887177	ODC1	-0.474880378
ILMN_1804277	SPRED1	-0.474888007
ILMN_1663518	FAM153A	-0.47494422
ILMN_1701933	SNCA	-0.474954669
ILMN_1709768	LOC100128818	-0.47502575
ILMN_1709937	KCNN4	-0.475037004
ILMN_1767433	TBC1D5	-0.475071976
ILMN_1816395	CR736179	-0.475104769
ILMN_1675221	DGKZ	-0.47511494
ILMN_1687315	RXRA	-0.475209409
ILMN_1735195	PRAMEF10	-0.475231117
ILMN_1681053	LOC100124692	-0.475268856
ILMN_2330112	CNIH	-0.47527494
ILMN_2262901	RUFY3	-0.475300143
ILMN_3194755	BE780475	-0.475309642
ILMN_1666617	C6orf155	-0.475310114
ILMN_1785795	METAP1	-0.475392807
ILMN_1793201	HAGHL	-0.475488259
ILMN_1776266	CRYGB	-0.475523349
ILMN_1720113	PTPRO	-0.47554397
ILMN_2295511	LUC7L	-0.475560967
ILMN_1710873	ZNF330	-0.475584244
ILMN_1653504	S1PR1	-0.475612704
ILMN_3206537	UBTFL1	-0.475718774
ILMN_1730019	BRD1	-0.475786939
ILMN_1656779	FAM75D3	-0.475792148
ILMN_2193752	MBLAC2	-0.47596555
ILMN_1785821	TDP2	-0.475976199
ILMN_1677085	RGS19	-0.476120237
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ILMN_3262976	FLJ46446	-0.476391619
ILMN_2250830	SPDYE1	-0.476483911
ILMN_1744539	GOLGA6L6	-0.476493316
ILMN_2205767	CTXN3	-0.476494973
ILMN_1665945	ACBD3	-0.476524865
ILMN_1713397	NCCRP1	-0.476528434
ILMN_1801441	RFTN2	-0.476533485
ILMN_1681437	DCXR	-0.476610378
ILMN_1811048	GPR107	-0.476657237
ILMN_1769720	STAU2	-0.4766948
ILMN_1755027	NLRP8	-0.4768509
ILMN_1911487	BX108993	-0.476867295
ILMN_1692396	CXorf58	-0.476905076
ILMN_1733298	C1orf158	-0.476910465
ILMN_2344047	ZNF398	-0.476938799
ILMN_1787115	WWTR1	-0.477014359
ILMN_2311548	PTRH2	-0.477063219
ILMN_2393461	DDO	-0.477082285
ILMN_1699610	CCT6B	-0.47708757
ILMN_3309759	VTRNA1-1	-0.477105043
ILMN_1813800	NUFIP1	-0.47711128
ILMN_1772278	TANC1	-0.477124925
ILMN_1756408	PARVA	-0.477168408
ILMN_1656492	NA	-0.477174613
ILMN_1875763	AI290919	-0.477198607
ILMN_3245038	AQP7	-0.477305008
ILMN_1787591	XPA	-0.477328145
ILMN_2359789	RAC1	-0.477341172
ILMN_1739086	SNORD43	-0.477407907
ILMN_1712945	DYNC2LI1	-0.477443501
ILMN_1666718	NA	-0.47750202
ILMN_1732269	GP6	-0.477531298
ILMN_3211615	FAM157B	-0.477705882
ILMN_1840294	D59687	-0.477751754
ILMN_3207821	FAM159B	-0.477751758
ILMN_1703074	CPD	-0.47792571
ILMN_1889752	LOC221710	-0.477944959
ILMN_2347943	ZNF384	-0.478026335
ILMN_1693891	MOGAT2	-0.478043788
ILMN_1746618	PAQR7	-0.478046776
ILMN_1827283	BX104024	-0.478067893
ILMN_1882041	H16080	-0.478091843
ILMN_1722906	SPATC1	-0.478211662
ILMN_1770725	AIF1L	-0.478256916
ILMN_2374692	WAC	-0.478357269
ILMN_3227782	MARVELD1	-0.478385219
ILMN_3271872	BX117604	-0.478402908
ILMN_1911721	AK090694	-0.478485801
ILMN_1661021	AK125823	-0.478522204

ILMN_1757604	TPM2	0.633319315
ILMN_1711566	TIMP1	0.633212006
ILMN_2408645	SPCS2	0.633097681
ILMN_2260313	CRYBA2	0.632745288
ILMN_1670948	TSR2	0.632711628
ILMN_1732717	FAM71E1	0.632684355
ILMN_3307950	CDK5RAP3	0.632539428
ILMN_1805737	PFKP	0.632511352
ILMN_1782741	CD300LB	0.632347748
ILMN_1802743	MLL2	0.632287022
ILMN_1745573	TTC13	0.63219832
ILMN_1745787	POLL	0.632127813
ILMN_2059211	KIAA0195	0.63206416
ILMN_1670844	OPN3	0.632029846
ILMN_1794333	POU2F1	0.632022883
ILMN_2088124	TMEM154	0.632022516
ILMN_1747622	CD33	0.631911285
ILMN_1717737	FKBP7	0.631692684
ILMN_1780825	RRAS	0.631667707
ILMN_1657283	ALKBH5	0.631644826
ILMN_1667408	EPB41	0.631582362
ILMN_1797384	UROS	0.631518903
ILMN_1805665	FLRT3	0.631500397
ILMN_1716651	RUNX2	0.631329228
ILMN_1775999	ATAT1	0.631328563
ILMN_2205050	PRKX	0.631309903
ILMN_1696035	ERP29	0.631292837
ILMN_3242485	TLK2	0.631292722
ILMN_2318811	RANBP3	0.63121831
ILMN_3209399	KRT18	0.631169044
ILMN_1690682	B3GALT4	0.631008398
ILMN_1665583	TUBB	0.630842464
ILMN_1789642	DNAJC5	0.630812919
ILMN_1748093	PAFAH1B3	0.630735107
ILMN_1656826	SH3RF1	0.630601495
ILMN_1679655	WDR82	0.63057194
ILMN_1808435	OGT	0.630433502
ILMN_1775224	NOS3	0.630409413
ILMN_1805512	WDR13	0.630297603
ILMN_1799387	INO80	0.630285592
ILMN_1810559	RHOQ	0.63016679
ILMN_3225784	LAMR1P15	0.630147187
ILMN_2160476	CCL22	0.630108488
ILMN_1784651	NAGA	0.629970984
ILMN_1686254	FAM127B	0.629889324
ILMN_1708375	IRF1	0.629661595
ILMN_1700031	PRAME	0.629475057
ILMN_1796316	MMP9	0.629456365
ILMN_3266666	NSA2	0.629425867
ILMN_1753524	HIST1H2AB	0.629366542
ILMN_3240793	OR2A4	0.629280973
ILMN_1770388	VPS39	0.629272951
ILMN_1760779	ENSA	0.629116444
ILMN_1728199	POLE	0.629090728
ILMN_1664644	ATG16L2	0.628866171
ILMN_1713605	RPAP1	0.628861016
ILMN_2046856	RPS15	0.628699157
ILMN_1765459	S100A13	0.628694702
ILMN_2141398	VEZT	0.628692364
ILMN_1802203	ARF1	0.628646144
ILMN_1674034	H2AFY	0.628565156
ILMN_3273198	NA	0.628544975
ILMN_2404049	RBM38	0.628471469
ILMN_1748438	POLR2G	0.628465046
ILMN_1692539	SH3BP1	0.628403344
ILMN_2280568	ANKRD36	0.628341658
ILMN_1783606	MLL5	0.628214752
ILMN_1762316	CPSF3L	0.628090266
ILMN_3228585	SLC35E2B	0.628037558
ILMN_1659845	KIAA0355	0.627971069
ILMN_3262031	BRD7	0.627869224
ILMN_2138435	MRPS27	0.627859046
ILMN_1694731	CLCN7	0.62756474
ILMN_1732151	COL6A1	0.627479873
ILMN_1676302	FAM113A	0.627434723
ILMN_2373062	RHBDF2	0.627426734
ILMN_2352190	CLIP2	0.627369784
ILMN_1719835	OSCP1	0.627332289
ILMN_1783712	C16orf88	0.627149775
ILMN_1698015	TBX1	0.627111249
ILMN_3211302	RPL17	0.627052608
ILMN_2347693	NCOA3	0.627025326
ILMN_1709486	SRPX	0.626789186
ILMN_1659792	HOXD9	0.626687339
ILMN_1661138	GON4L	0.626296389
ILMN_1673649	HYOU1	0.626285491
ILMN_1663618	STAT3	0.62627495
ILMN_1710524	PARD3	0.62626597
ILMN_2075334	HIST1H4C	0.6261659
ILMN_2377733	CASP8	0.626149099
ILMN_2334210	ITGB4	0.626009906
ILMN_1811754	NDUFB10	0.626009762
ILMN_2155480	RAB43	0.62586857
ILMN_1740170	CHCHD10	0.625863693

	UP_SEQ_FEATURE	domain:Laminin EGF-like 8	3	3.90E-01	1.00E+00
	UP_SEQ_FEATURE	domain:Laminin EGF-like 10	3	3.90E-01	1.00E+00
	GOTERM_CC_FAT	basal lamina	4	4.00E-01	8.60E-01
	INTERPRO	EGF-like, laminin	7	4.20E-01	1.00E+00
	UP_SEQ_FEATURE	domain:Laminin EGF-like 7	3	4.40E-01	1.00E+00
	INTERPRO	Laminin G, subdomain 2	7	4.40E-01	1.00E+00
	SMART	EGF_Lam	7	4.60E-01	9.70E-01
	GOTERM_CC_FAT	basement membrane	12	4.70E-01	9.00E-01
	UP_SEQ_FEATURE	domain:Laminin EGF-like 4	3	4.80E-01	1.00E+00
	UP_SEQ_FEATURE	domain:Laminin EGF-like 6	3	4.80E-01	1.00E+00
	UP_SEQ_FEATURE	domain:Laminin EGF-like 3	4	5.10E-01	1.00E+00
Annotation Cluster 207	**Enrichment Score: 0.58**		**Count**	**P_Value**	**Benjamini**
	BIOCARTA	Role of Erk5 in Neuronal Survival	7	2.50E-02	9.70E-01
	BIOCARTA	TPO Signaling Pathway	8	7.30E-02	9.40E-01
	BIOCARTA	Erk1/Erk2 Mapk Signaling pathway	10	9.00E-02	9.50E-01
	BIOCARTA	Nerve growth factor pathway (NGF)	7	9.20E-02	9.20E-01
	BIOCARTA	PDGF Signaling Pathway	9	9.20E-02	9.00E-01
	BIOCARTA	Role of ERBB2 in Signal Transduction and Oncology	8	9.30E-02	8.80E-01
	BIOCARTA	T Cell Receptor Signaling Pathway	11	1.00E-01	8.90E-01
	BIOCARTA	IGF-1 Signaling Pathway	7	1.40E-01	9.30E-01
	BIOCARTA	IL 6 signaling pathway	7	1.40E-01	9.30E-01
	BIOCARTA	Fc Epsilon Receptor I Signaling in Mast Cells	9	2.10E-01	9.30E-01
	BIOCARTA	EGF Signaling Pathway	8	2.20E-01	9.40E-01
	BIOCARTA	BCR Signaling Pathway	8	2.20E-01	9.40E-01
	BIOCARTA	EPO Signaling Pathway	6	2.60E-01	9.40E-01
	BIOCARTA	Inhibition of Cellular Proliferation by Gleevec	6	3.00E-01	9.60E-01
	BIOCARTA	Insulin Signaling Pathway	6	3.00E-01	9.60E-01
	BIOCARTA	Role of MAL in Rho-Mediated Activation of SRF	6	3.00E-01	9.60E-01
	BIOCARTA	Signaling of Hepatocyte Growth Factor Receptor	9	3.30E-01	9.50E-01
	BIOCARTA	Trka Receptor Signaling Pathway	4	3.60E-01	9.60E-01
	BIOCARTA	Growth Hormone Signaling Pathway	6	4.30E-01	9.70E-01
	BIOCARTA	Sprouty regulation of tyrosine kinase signals	4	5.80E-01	9.90E-01
	BIOCARTA	IL 2 signaling pathway	5	6.00E-01	9.90E-01
	BIOCARTA	Angiotensin II mediated activation of JNK Pathway via Pyk2 dependent signaling	6	6.20E-01	9.90E-01
	BIOCARTA	Links between Pyk2 and Map Kinases	5	7.70E-01	1.00E+00
	BIOCARTA	IL 3 signaling pathway	3	7.90E-01	1.00E+00
	BIOCARTA	Signaling Pathway from G-Protein Families	4	8.00E-01	1.00E+00
	BIOCARTA	Integrin Signaling Pathway	6	8.20E-01	1.00E+00
	BIOCARTA	Bioactive Peptide Induced Signaling Pathway	5	8.60E-01	1.00E+00
	BIOCARTA	fMLP induced chemokine gene expression in HMC-1 cells	4	8.90E-01	1.00E+00
Annotation Cluster 208	**Enrichment Score: 0.58**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	actin filament-based movement	6	1.80E-01	8.30E-01
	GOTERM_MF_FAT	actin-dependent ATPase activity	3	2.70E-01	9.60E-01
	GOTERM_BP_FAT	cytoskeleton-dependent intracellular transport	9	3.80E-01	9.60E-01
Annotation Cluster 209	**Enrichment Score: 0.58**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	negative regulation of phosphatase activity	3	8.70E-02	6.40E-01
	GOTERM_BP_FAT	regulation of dephosphorylation	6	2.50E-01	9.10E-01
	GOTERM_BP_FAT	regulation of phosphatase activity	4	4.30E-01	9.80E-01
	GOTERM_BP_FAT	regulation of phosphoprotein phosphatase activity	3	5.30E-01	9.90E-01
Annotation Cluster 210	**Enrichment Score: 0.58**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	regulation of interleukin-2 production	9	3.60E-02	4.20E-01
	GOTERM_BP_FAT	regulation of interleukin-2 biosynthetic process	5	2.40E-01	8.90E-01
	GOTERM_BP_FAT	positive regulation of cytokine biosynthetic process	8	4.50E-01	9.80E-01
	GOTERM_BP_FAT	positive regulation of interleukin-2 biosynthetic process	3	5.30E-01	9.90E-01
	GOTERM_BP_FAT	regulation of cytokine biosynthetic process	10	6.50E-01	1.00E+00
Annotation Cluster 211	**Enrichment Score: 0.57**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	UV protection	5	4.60E-02	4.80E-01
	GOTERM_BP_FAT	nucleotide-excision repair, DNA incision	3	1.80E-01	8.40E-01
	SP_PIR_KEYWORDS	xeroderma pigmentosum	3	2.50E-01	6.90E-01
	GOTERM_BP_FAT	response to UV	10	3.70E-01	9.60E-01
	GOTERM_BP_FAT	nucleotide-excision repair	9	4.40E-01	9.80E-01
	KEGG_PATHWAY	Nucleotide excision repair	8	5.00E-01	8.10E-01
	GOTERM_BP_FAT	nucleotide-excision repair, DNA damage removal	4	5.70E-01	9.90E-01
Annotation Cluster 212	**Enrichment Score: 0.57**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	domain:FCP1 homology	3	2.50E-01	1.00E+00
	INTERPRO	NLI interacting factor	3	2.70E-01	1.00E+00
	SMART	CPDc	3	2.90E-01	9.40E-01
Annotation Cluster 213	**Enrichment Score: 0.57**		**Count**	**P_Value**	**Benjamini**
	KEGG_PATHWAY	Dilated cardiomyopathy	19	1.40E-01	4.90E-01
	KEGG_PATHWAY	Arrhythmogenic right ventricular cardiomyopathy (ARVC)	14	3.50E-01	7.00E-01
	KEGG_PATHWAY	Hypertrophic cardiomyopathy (HCM)	15	4.00E-01	7.40E-01
Annotation Cluster 214	**Enrichment Score: 0.57**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	regulation of specific transcription from RNA polymerase II promoter	17	1.70E-01	8.20E-01
	GOTERM_BP_FAT	positive regulation of specific transcription from RNA polymerase II promoter	11	2.10E-01	8.70E-01
	GOTERM_BP_FAT	positive regulation of gene-specific transcription	15	2.50E-01	9.10E-01
	GOTERM_BP_FAT	negative regulation of specific transcription from RNA polymerase II promoter	8	2.90E-01	9.30E-01
	GOTERM_BP_FAT	regulation of gene-specific transcription	21	3.10E-01	9.40E-01
	GOTERM_BP_FAT	negative regulation of gene-specific transcription	8	4.50E-01	9.80E-01
Annotation Cluster 215	**Enrichment Score: 0.57**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	regulation of axonogenesis	14	3.20E-02	3.90E-01
	GOTERM_BP_FAT	negative regulation of cell projection organization	6	3.10E-01	9.40E-01
	GOTERM_BP_FAT	negative regulation of axonogenesis	5	4.20E-01	9.80E-01
	GOTERM_BP_FAT	negative regulation of neurogenesis	7	5.50E-01	9.90E-01
	GOTERM_BP_FAT	negative regulation of cell development	7	6.20E-01	1.00E+00
Annotation Cluster 216	**Enrichment Score: 0.56**		**Count**	**P_Value**	**Benjamini**
	GOTERM_MF_FAT	Rho GTPase binding	9	1.10E-01	8.10E-01
	GOTERM_MF_FAT	GTPase binding	17	3.20E-01	9.70E-01
	GOTERM_MF_FAT	Ras GTPase binding	14	3.90E-01	9.80E-01
	GOTERM_MF_FAT	small GTPase binding	15	4.20E-01	9.90E-01
Annotation Cluster 217	**Enrichment Score: 0.56**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	domain:LIM zinc-binding 3	6	1.80E-01	1.00E+00
	SP_PIR_KEYWORDS	LIM domain	12	2.30E-01	6.70E-01
	UP_SEQ_FEATURE	domain:LIM zinc-binding 1	9	2.50E-01	1.00E+00
	UP_SEQ_FEATURE	domain:LIM zinc-binding 2	9	2.50E-01	1.00E+00

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ILMN_1752646	NA	-0.478634718
ILMN_1844083	C12orf71	-0.478683997
ILMN_1765645	C17orf50	-0.478697378
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ILMN_1785731	MAPK8IP2	-0.47876775
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ILMN_1777797	AFM	-0.478952553
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ILMN_1755364	RALA	-0.479513542
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ILMN_1685696	C3orf55	-0.480089797
ILMN_1900604	BX108309	-0.480116146
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ILMN_2156971	PRY	-0.480356111
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ILMN_3309914	MIR660	-0.481319389
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ILMN_2212878	ESM1	-0.481577044
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ILMN_3297082	LOC729080	-0.481722115
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ILMN_1754137	CFHR1	-0.482074657
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ILMN_1750180	HIST1H2BB	-0.482184388
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ILMN_3308400	MIR516A2	-0.48221901

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ILMN_1792473	AIF1	0.625785042
ILMN_1708167	CDCP1	0.625724657
ILMN_1763837	ANPEP	0.625719521
ILMN_1677226	ARVCF	0.625349346
ILMN_1804117	FAM89B	0.625106039
ILMN_1716400	FOXM1	0.62490057
ILMN_1809323	C9orf125	0.62481904
ILMN_1737255	C22orf36	0.624774209
ILMN_3247661	FLJ45340	0.624768496
ILMN_1750429	DKFZp686E14208	0.624763973
ILMN_3224856	LOC100133161	0.624760764
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ILMN_1715508	NNMT	0.624649278
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ILMN_1740620	LOC161527	0.624360526
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ILMN_2109416	NAPSB	0.624179514
ILMN_1803997	SDCCAG3	0.6241661
ILMN_3214945	SMN1	0.623998723
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ILMN_1659843	DNAJC3	0.62396074
ILMN_1679693	TMEM87B	0.623894029
ILMN_1769757	C14orf104	0.62355159
ILMN_1781999	ABCF2	0.623505721
ILMN_1766593	PHRF1	0.623462305
ILMN_1685125	CR626459	0.623278424
ILMN_1714352	DMWD	0.623214998
ILMN_1793959	ADPGK	0.623188836
ILMN_1703743	AATF	0.623183471
ILMN_2049303	ECI1	0.623176948
ILMN_1746408	MIDN	0.622996925
ILMN_2383097	RPL17	0.622989389
ILMN_1794213	ABHD14A	0.622600644
ILMN_1691090	MPV17	0.622500707
ILMN_3222058	LOC349114	0.622360976
ILMN_1671005	IRF2BP2	0.622230176
ILMN_1705991	SMA4	0.62218908
ILMN_1677534	SCAP	0.622158898
ILMN_1723480	BST2	0.621860309
ILMN_2364131	TTPAL	0.621797408
ILMN_3305304	POLD2	0.621682804
ILMN_2415926	THOC3	0.621612402
ILMN_3235044	LOC100288615	0.621563462
ILMN_1705737	IMPDH2	0.621411295
ILMN_1695414	ASF1B	0.621357769
ILMN_1797594	NFAT5	0.621331236
ILMN_2292178	CLEC12A	0.621270542
ILMN_1715715	CEBPA	0.621197987
ILMN_1781099	ISY1	0.621160077
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ILMN_1693317	TTC15	0.620977594
ILMN_1771057	XAB2	0.620966852
ILMN_1674629	C9orf3	0.620953797
ILMN_1737580	PPPDE2	0.620775065
ILMN_2110271	OLFM2	0.620749721
ILMN_1741617	SCRT1	0.620644807
ILMN_1713561	C20orf103	0.620590608
ILMN_1712419	DCDC2	0.620437464
ILMN_1698803	ZAK	0.620419111
ILMN_1697218	MED22	0.620356201
ILMN_2391750	SFMBT1	0.620244592
ILMN_1672446	RPL11	0.620215588
ILMN_1728802	SDCCAG8	0.620192568
ILMN_1740938	APOE	0.620173322
ILMN_1755749	PGK1	0.620161189
ILMN_1802096	ABTB1	0.619776798
ILMN_2308689	AGBL5	0.619765569
ILMN_1716563	PRKCB	0.619755632
ILMN_2073235	FTH1	0.61970774
ILMN_1809040	LDLRAP1	0.619694508
ILMN_1688103	CTNNBIP1	0.619639588
ILMN_1797522	DUSP3	0.619567878
ILMN_1809010	PSMC3	0.619544418
ILMN_1811823	MED25	0.619513844
ILMN_1696704	TLE4	0.619392467
ILMN_1662905	NME1	0.619236939
ILMN_2370208	CMTM3	0.619107841
ILMN_1815668	GTF2I	0.619037669
ILMN_1701596	RPS20	0.618988482
ILMN_1763460	NHP2L1	0.618947575
ILMN_1676611	PHPT1	0.6188947
ILMN_1763524	LZTS2	0.618847218
ILMN_3289352	RPL6	0.618778872
ILMN_1771593	RRM1	0.618762992
ILMN_1713406	DKFZp434K1323	0.618661597
ILMN_2403730	ATP6V1H	0.618481454
ILMN_1697682	RECQL5	0.618474485
ILMN_1693438	FBXL12	0.618338249
ILMN_1668283	HYAL2	0.618273381
ILMN_1745130	RBFOX2	0.618205735
ILMN_1688000	POLDIP3	0.618165194
ILMN_2337923	TPD52L1	0.618136889
ILMN_1683234	DNAJC1	0.618045672

	INTERPRO	Zinc finger, LIM-type	12	3.10E-01	1.00E+00
	SMART	LIM	12	3.70E-01	9.60E-01
	UP_SEQ_FEATURE	domain:LIM zinc-binding 4	3	3.90E-01	1.00E+00
Annotation Cluster 218	**Enrichment Score: 0.55**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	virus-host interaction	5	2.70E-01	9.20E-01
	GOTERM_BP_FAT	intronless viral mRNA export from host nucleus	3	2.90E-01	9.30E-01
	GOTERM_CC_FAT	transcription export complex	3	2.90E-01	7.80E-01
Annotation Cluster 219	**Enrichment Score: 0.55**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	positive regulation of tumor necrosis factor production	5	1.30E-01	7.50E-01
	GOTERM_MF_FAT	peptidoglycan binding	3	3.30E-01	9.70E-01
	GOTERM_BP_FAT	regulation of tumor necrosis factor production	6	3.90E-01	9.70E-01
	GOTERM_BP_FAT	positive regulation of cytokine production	14	4.10E-01	9.70E-01
Annotation Cluster 220	**Enrichment Score: 0.55**		**Count**	**P_Value**	**Benjamini**
	INTERPRO	Phosphorylated immunoreceptor signaling ITAM	3	2.70E-01	1.00E+00
	SMART	ITAM	3	2.90E-01	9.40E-01
	UP_SEQ_FEATURE	domain:ITAM	3	3.00E-01	1.00E+00
Annotation Cluster 221	**Enrichment Score: 0.55**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	DNA-binding region:A.T hook	5	4.80E-02	1.00E+00
	INTERPRO	AT hook, DNA-binding, conserved site	4	6.80E-01	1.00E+00
	SMART	AT_hook	4	7.10E-01	9.90E-01
Annotation Cluster 222	**Enrichment Score: 0.54**		**Count**	**P_Value**	**Benjamini**
	INTERPRO	Low density lipoprotein-receptor, class A, cysteine-rich	12	4.40E-02	9.10E-01
	SMART	LDLa	12	5.80E-02	7.20E-01
	UP_SEQ_FEATURE	domain:LDL-receptor class A 1	6	2.20E-01	1.00E+00
	UP_SEQ_FEATURE	domain:LDL-receptor class A 2	6	2.20E-01	1.00E+00
	UP_SEQ_FEATURE	domain:LDL-receptor class A 4	4	3.00E-01	1.00E+00
	UP_SEQ_FEATURE	domain:LDL-receptor class A	4	4.40E-01	1.00E+00
	UP_SEQ_FEATURE	domain:CUB 1	6	4.50E-01	1.00E+00
	UP_SEQ_FEATURE	domain:CUB 2	6	4.50E-01	1.00E+00
	UP_SEQ_FEATURE	domain:LDL-receptor class A 3	4	4.80E-01	1.00E+00
	INTERPRO	CUB	6	7.90E-01	1.00E+00
	SMART	CUB	6	8.20E-01	1.00E+00
Annotation Cluster 223	**Enrichment Score: 0.54**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	cell activation during immune response	8	1.90E-01	8.50E-01
	GOTERM_BP_FAT	leukocyte activation during immune response	8	1.90E-01	8.50E-01
	GOTERM_BP_FAT	leukocyte degranulation	4	2.00E-01	8.70E-01
	GOTERM_BP_FAT	lymphocyte activation during immune response	5	2.10E-01	8.70E-01
	GOTERM_BP_FAT	T cell activation during immune response	4	2.40E-01	9.00E-01
	GOTERM_BP_FAT	myeloid leukocyte mediated immunity	4	3.20E-01	9.40E-01
	GOTERM_BP_FAT	myeloid leukocyte activation	8	4.00E-01	9.70E-01
	GOTERM_BP_FAT	regulated secretory pathway	4	4.30E-01	9.80E-01
	GOTERM_BP_FAT	myeloid cell activation during immune response	3	7.10E-01	1.00E+00
Annotation Cluster 224	**Enrichment Score: 0.54**		**Count**	**P_Value**	**Benjamini**
	GOTERM_MF_FAT	ubiquitin binding	6	2.60E-01	9.50E-01
	GOTERM_MF_FAT	small conjugating protein binding	6	2.90E-01	9.60E-01
	GOTERM_MF_FAT	polyubiquitin binding	3	3.30E-01	9.70E-01
Annotation Cluster 225	**Enrichment Score: 0.53**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	apoptotic mitochondrial changes	8	1.00E-01	7.00E-01
	BBID	127.Mito-stress	4	1.50E-01	9.60E-01
	GOTERM_BP_FAT	induction of apoptosis by intracellular signals	11	1.70E-01	8.20E-01
	GOTERM_BP_FAT	negative regulation of survival gene product expression	3	2.30E-01	8.90E-01
	GOTERM_BP_FAT	release of cytochrome c from mitochondria	5	3.00E-01	9.30E-01
	GOTERM_BP_FAT	lymphocyte apoptosis	3	3.90E-01	9.70E-01
	BIOCARTA	Role of Mitochondria in Apoptotic Signaling	6	4.30E-01	9.70E-01
	BIOCARTA	Apoptotic Signaling in Response to DNA Damage	6	4.30E-01	9.70E-01
	GOTERM_BP_FAT	regulation of survival gene product expression	4	5.40E-01	9.90E-01
	KEGG_PATHWAY	Amyotrophic lateral sclerosis (ALS)	8	7.00E-01	8.90E-01
Annotation Cluster 226	**Enrichment Score: 0.53**		**Count**	**P_Value**	**Benjamini**
	SP_PIR_KEYWORDS	myristylation	11	1.50E-02	1.30E-01
	INTERPRO	ADP-ribosylation factor	4	5.40E-01	1.00E+00
	SMART	ARF	4	5.70E-01	9.90E-01
	PIR_SUPERFAMILY	PIRSF001711:ADP-ribosylation factor	4	6.50E-01	1.00E+00
	INTERPRO	ARF/SAR superfamily	4	7.50E-01	1.00E+00
Annotation Cluster 227	**Enrichment Score: 0.53**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	epithelial to mesenchymal transition	7	2.40E-02	3.30E-01
	GOTERM_BP_FAT	mesenchymal cell differentiation	10	2.20E-01	8.90E-01
	GOTERM_BP_FAT	mesenchymal cell development	10	2.20E-01	8.90E-01
	GOTERM_BP_FAT	mesenchyme development	10	2.40E-01	9.00E-01
	GOTERM_BP_FAT	ameboidal cell migration	7	3.60E-01	9.60E-01
	GOTERM_BP_FAT	neural crest cell migration	3	8.30E-01	1.00E+00
	GOTERM_BP_FAT	neural crest cell differentiation	4	8.30E-01	1.00E+00
	GOTERM_BP_FAT	neural crest cell development	4	8.30E-01	1.00E+00
Annotation Cluster 228	**Enrichment Score: 0.53**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	domain:SAND	3	2.50E-01	1.00E+00
	INTERPRO	SAND	3	2.70E-01	1.00E+00
	SMART	SAND	3	2.90E-01	9.40E-01
	INTERPRO	SAND-like	3	4.10E-01	1.00E+00
Annotation Cluster 229	**Enrichment Score: 0.52**		**Count**	**P_Value**	**Benjamini**
	BIOCARTA	TNFR1 Signaling Pathway	11	4.80E-02	8.90E-01
	GOTERM_BP_FAT	activation of pro-apoptotic gene products	7	6.00E-02	5.50E-01
	BIOCARTA	Ceramide Signaling Pathway	7	2.10E-01	9.40E-01
	GOTERM_BP_FAT	response to tumor necrosis factor	4	2.40E-01	9.00E-01
	BIOCARTA	SODD/TNFR1 Signaling Pathway	4	2.40E-01	9.50E-01
	BIOCARTA	HIV-I Nef	13	3.20E-01	9.50E-01
	BBID	40.Deg_of_Chrom_DNA_TNF-ind_apoptosis	4	3.60E-01	1.00E+00
	BBID	150.caspase_and_NFKB_activation	5	3.70E-01	9.90E-01
	BIOCARTA	FAS signaling pathway (CD95)	8	3.90E-01	9.70E-01
	BBID	44.Sig_Trans_TNFR1-DR3-DR4_DR5	3	4.40E-01	9.90E-01
	BIOCARTA	Caspase Cascade in Apoptosis	6	5.10E-01	9.80E-01
	BIOCARTA	Induction of apoptosis through DR3 and DR4/5 Death Receptors	7	5.40E-01	9.80E-01
	BIOCARTA	Keratinocyte Differentiation	7	7.70E-01	1.00E+00
	BIOCARTA	TNF/Stress Related Signaling	3	9.60E-01	1.00E+00
Annotation Cluster 230	**Enrichment Score: 0.52**		**Count**	**P_Value**	**Benjamini**
	INTERPRO	Peptidase C1A, papain C-terminal	5	9.00E-02	9.60E-01
	INTERPRO	Peptidase C1A, papain	5	9.00E-02	9.60E-01
	SMART	Pept_C1	5	1.00E-01	7.90E-01
	PIR_SUPERFAMILY	PIRSF001182:papain	3	3.50E-01	1.00E+00

ILMN_1687046	OR10A2	-0.482291791
ILMN_2154603	ZNF830	-0.48234456
ILMN_2163835	PRDM14	-0.482390407
ILMN_3266265	LOXHD1	-0.48241216
ILMN_1798914	C1orf65	-0.482470499
ILMN_1893915	AW195332	-0.482482882
ILMN_2204726	UBR5	-0.482624112
ILMN_1760246	BSN	-0.482688544
ILMN_3249444	POM121-like 1	-0.482715865
ILMN_2260933	C20orf71	-0.48279389
ILMN_3254046	BI599339	-0.482872776
ILMN_1656495	NOTO	-0.482918493
ILMN_2073263	C11orf61	-0.482928147
ILMN_1897107	AI056628	-0.483026736
ILMN_1676239	LOC653550	-0.483077145
ILMN_1892996	BQ011293	-0.483130494
ILMN_1789112	TMEM145	-0.483306092
ILMN_2114185	C1orf104	-0.483338188
ILMN_1800935	ARV1	-0.483354924
ILMN_1663129	MAMLD1	-0.483388175
ILMN_1798166	POM121C	-0.483419832
ILMN_1686405	KDR	-0.483474217
ILMN_1736300	KIAA1445	-0.483485054
ILMN_1738009	PRRT4	-0.483507903
ILMN_1736162	GC	-0.483562334
ILMN_1770658	NEB	-0.483569172
ILMN_1798923	MYH1	-0.483623637
ILMN_1804907	OR1F2	-0.483646653
ILMN_1798690	ADAMTSL3	-0.483650903
ILMN_1685043	CYP3A7	-0.48381583
ILMN_1747205	JDP2	-0.483875267
ILMN_1655892	BE266556	-0.483941115
ILMN_1651636	CYP2A13	-0.48395582
ILMN_1840934	AJ420430	-0.484006514
ILMN_2287543	SHISA3	-0.484009161
ILMN_1797878	OR7G3	-0.48406013
ILMN_1701386	STRADB	-0.484131496
ILMN_1739925	SLC28A1	-0.484175517
ILMN_2077623	RRAS2	-0.484193122
ILMN_1762582	ARNT	-0.48421571
ILMN_1723414	HACL1	-0.484254684
ILMN_1747151	ANKRD23	-0.484305847
ILMN_1713550	LGR6	-0.484320001
ILMN_2373515	HSP90AA1	-0.484335026
ILMN_2103014	CCDC104	-0.48443129
ILMN_1662010	DLK2	-0.484441682
ILMN_1806473	BEX5	-0.484443842
ILMN_1729529	BAI1	-0.484451211
ILMN_2164173	DYDC1	-0.484452988
ILMN_3308445	MIR642A	-0.484564696
ILMN_1676289	NCAM1	-0.484626772
ILMN_1735108	ANKS6	-0.484632481
ILMN_1676997	TREX1	-0.484653136
ILMN_1753415	LY6H	-0.484671046
ILMN_1660261	TDRD6	-0.484747081
ILMN_1654637	SETD5	-0.484757961
ILMN_1817715	CK001807	-0.485010512
ILMN_1659773	PCDHA@	-0.485020768
ILMN_3235833	NA	-0.485034538
ILMN_1736533	RND2	-0.48504642
ILMN_1787988	UBE2D1	-0.485069562
ILMN_1887349	BU753709	-0.485105833
ILMN_1909276	BX105693	-0.485121211
ILMN_1658299	CCR2	-0.485137193
ILMN_1664016	ARHGEF18	-0.485320747
ILMN_1722640	LOC284801	-0.485351539
ILMN_1755419	EIF1AX	-0.485387193
ILMN_1804137	ATP11C	-0.485475747
ILMN_1710326	CLDND1	-0.485587847
ILMN_1667804	FAM182B	-0.485651718
ILMN_1803261	OPRM1	-0.48571115
ILMN_1675946	ISG20L2	-0.485805273
ILMN_1916256	TCRA	-0.485927899
ILMN_3298694	TYW1B	-0.485939855
ILMN_1661853	TRIM49L2	-0.485946961
ILMN_1778236	PTPN11	-0.485985263
ILMN_1791283	AK126240	-0.486021395
ILMN_1755369	RAB3A	-0.486053789
ILMN_1737514	KYNU	-0.486059831
ILMN_1769931	SFPQ	-0.486100916
ILMN_2101526	GGCT	-0.48622118
ILMN_1843007	BU752765	-0.486285817
ILMN_1825443	BX089525	-0.486435449
ILMN_1745567	SMA4	-0.486471918
ILMN_1680776	C12orf70	-0.486568851
ILMN_1756367	WNK3	-0.486592904
ILMN_1771841	FOSL1	-0.486604152
ILMN_1718446	FAM69B	-0.486607736
ILMN_1893852	AW340373	-0.48662648
ILMN_2112599	C16orf80	-0.486636961
ILMN_1860645	CD706264	-0.486674586
ILMN_3229515	CSN1S2BP	-0.486700829
ILMN_1749804	ADSSL1	-0.486702768
ILMN_1667707	SPCS3	-0.486768999
ILMN_1663975	CNNM2	-0.486789474
ILMN_1741812	AK056801	-0.486854333
ILMN_1752294	PCDH9	-0.486907116

ILMN_1729767	TARBP2	0.618013865
ILMN_1897310	LETM1	0.617997
ILMN_3296816	LOC338739	0.617812825
ILMN_1703433	PLSCR3	0.617624725
ILMN_1733581	C16orf35	0.617435518
ILMN_3287068	LAMR1P15	0.617378478
ILMN_2140700	CRIPAK	0.617368782
ILMN_1737644	TMEM219	0.617297151
ILMN_2396982	BCL2L12	0.617245929
ILMN_2334693	NARF	0.617237576
ILMN_2301624	MACF1	0.617220349
ILMN_2374449	SPP1	0.617132229
ILMN_1686388	TPM3	0.61705512
ILMN_2361186	PHF20L1	0.617052259
ILMN_2123402	CNPY2	0.616868674
ILMN_2370336	MS4A4A	0.616689646
ILMN_1769201	ELF3	0.616648338
ILMN_3304435	LOC728640	0.616521564
ILMN_1708936	EXOSC3	0.616501325
ILMN_1685830	SLC7A2	0.616372785
ILMN_1722738	ROGDI	0.616352259
ILMN_3243291	HNRNPA1	0.616172737
ILMN_2087656	SLCO2B1	0.616167402
ILMN_1803392	P2RX5-TAX1BP3	0.616156047
ILMN_1715947	HNRNPA1	0.616038903
ILMN_1790228	FURIN	0.615918446
ILMN_1659913	ISG20	0.615825232
ILMN_2123567	SENP2	0.615820735
ILMN_3309089	MIR196B	0.615686153
ILMN_1677314	MUC1	0.615615678
ILMN_2403458	SMARCB1	0.615568416
ILMN_1723042	CLDN3	0.615566622
ILMN_3240838	SLC25A6	0.615523631
ILMN_2041046	CKS1B	0.61551412
ILMN_1711078	CDK11A	0.615483088
ILMN_1773059	GPR124	0.615379201
ILMN_2208802	NPIPL3	0.615258485
ILMN_1693014	CEBPB	0.615145393
ILMN_1811790	FOXS1	0.615093188
ILMN_2054145	PAK1IP1	0.615027205
ILMN_1681467	RAB11FIP4	0.614937828
ILMN_1811117	DKFZp667P0924	0.614929997
ILMN_1788062	SH3GL1	0.614908688
ILMN_1695420	CLTA	0.614829608
ILMN_1654065	ATOH8	0.614814588
ILMN_1777584	KARS	0.614782688
ILMN_1755462	UGCGL1	0.614714292
ILMN_1793267	ETHE1	0.614645399
ILMN_1691717	RHBDF2	0.614571358
ILMN_1764723	SH3PXD2B	0.614105043
ILMN_2386269	U2AF1L4	0.613988701
ILMN_1738681	NUP62	0.613986277
ILMN_2203588	MYL5	0.613890043
ILMN_2299045	BMP2K	0.613754389
ILMN_1777881	TSPAN17	0.613693348
ILMN_2380850	SDCCAG3	0.613670142
ILMN_1774823	RPL34	0.613361396
ILMN_1801421	EMD	0.613312834
ILMN_1709032	FYCO1	0.613274137
ILMN_1903914	AK129699	0.613260843
ILMN_1680434	MAPK8IP1	0.613107427
ILMN_1665428	GSDMD	0.613045137
ILMN_2163723	KRT7	0.612879754
ILMN_1718537	HPS6	0.61283754
ILMN_1713037	PFKL	0.612676316
ILMN_2083066	IGLL3P	0.612643105
ILMN_1671106	GJA4	0.612628393
ILMN_1703326	GPR44	0.612590433
ILMN_2364529	EZH2	0.612517783
ILMN_1677589	hCG_1818547	0.612489948
ILMN_1738529	BCS1L	0.612305778
ILMN_1655821	CAPG	0.612230463
ILMN_1747023	PTGIR	0.612093773
ILMN_1655952	WASH3P	0.611877331
ILMN_1751161	COL7A1	0.611867
ILMN_2351298	WIPF1	0.611747531
ILMN_3246159	C20orf191	0.611726723
ILMN_2176502	UNC5B	0.611533032
ILMN_3240321	AEN	0.611496932
ILMN_3248113	SNRNP70	0.6114509
ILMN_1780769	TUBB2C	0.611443455
ILMN_3239055	TMEM208	0.611264163
ILMN_1761764	ALKBH7	0.611168576
ILMN_1725992	RAPGEF6	0.610998934
ILMN_1653278	MUC20	0.610985416
ILMN_2313730	RHOC	0.610908254
ILMN_1815718	BTRC	0.610708871
ILMN_2244841	ALDH4A1	0.610660181

	INTERPRO	Peptidase, cysteine peptidase active site	6	4.80E-01	1.00E+00
	GOTERM_MF_FAT	cysteine-type endopeptidase activity	10	5.90E-01	1.00E+00
	GOTERM_MF_FAT	cysteine-type peptidase activity	14	9.30E-01	1.00E+00
	SP_PIR_KEYWORDS	thiol protease	11	9.50E-01	1.00E+00
Annotation Cluster 231	**Enrichment Score: 0.52**		**Count**	**P_Value**	**Benjamini**
	GOTERM_MF_FAT	ATPase activity, coupled	53	2.00E-03	1.20E-01
	GOTERM_BP_FAT	purine nucleoside triphosphate metabolic process	23	7.70E-02	6.10E-01
	GOTERM_BP_FAT	purine ribonucleoside triphosphate metabolic process	22	8.60E-02	6.40E-01
	GOTERM_BP_FAT	ribonucleoside triphosphate metabolic process	22	9.20E-02	6.60E-01
	GOTERM_MF_FAT	ATPase activity, coupled to movement of substances	20	1.10E-01	8.10E-01
	GOTERM_BP_FAT	nucleoside triphosphate metabolic process	23	1.40E-01	7.70E-01
	GOTERM_BP_FAT	purine ribonucleotide metabolic process	24	1.40E-01	7.70E-01
	GOTERM_MF_FAT	P-P-bond-hydrolysis-driven transmembrane transporter activity	21	1.50E-01	8.70E-01
	GOTERM_MF_FAT	primary active transmembrane transporter activity	21	1.50E-01	8.70E-01
	GOTERM_MF_FAT	ATPase activity, coupled to transmembrane movement of substances	19	1.60E-01	8.70E-01
	GOTERM_MF_FAT	hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances	19	1.80E-01	8.90E-01
	GOTERM_BP_FAT	ATP metabolic process	18	2.20E-01	8.80E-01
	GOTERM_BP_FAT	ribonucleotide metabolic process	24	2.20E-01	8.80E-01
	GOTERM_MF_FAT	hydrogen ion transmembrane transporter activity	15	2.60E-01	9.50E-01
	GOTERM_BP_FAT	energy coupled proton transport, down electrochemical gradient	8	2.70E-01	9.20E-01
	GOTERM_BP_FAT	ATP synthesis coupled proton transport	8	2.70E-01	9.20E-01
	GOTERM_BP_FAT	purine ribonucleoside triphosphate biosynthetic process	16	3.10E-01	9.40E-01
	GOTERM_MF_FAT	cation-transporting ATPase activity	7	3.10E-01	9.70E-01
	GOTERM_BP_FAT	hydrogen transport	11	3.20E-01	9.40E-01
	GOTERM_BP_FAT	ribonucleoside triphosphate biosynthetic process	16	3.20E-01	9.50E-01
	GOTERM_BP_FAT	purine nucleoside triphosphate biosynthetic process	16	3.20E-01	9.50E-01
	GOTERM_BP_FAT	nitrogen compound biosynthetic process	47	3.30E-01	9.50E-01
	GOTERM_BP_FAT	purine nucleotide metabolic process	28	3.30E-01	9.50E-01
	GOTERM_MF_FAT	proton-transporting ATPase activity, rotational mechanism	5	3.40E-01	9.70E-01
	SP_PIR_KEYWORDS	Hydrogen ion transport	8	3.60E-01	8.00E-01
	GOTERM_MF_FAT	monovalent inorganic cation transmembrane transporter activity	16	3.60E-01	9.70E-01
	GOTERM_BP_FAT	nucleoside triphosphate biosynthetic process	16	3.70E-01	9.60E-01
	GOTERM_BP_FAT	purine ribonucleotide biosynthetic process	18	3.70E-01	9.60E-01
	GOTERM_BP_FAT	nucleobase, nucleoside and nucleotide biosynthetic process	28	4.00E-01	9.70E-01
	GOTERM_BP_FAT	nucleobase, nucleoside, nucleotide and nucleic acid biosynthetic process	28	4.00E-01	9.70E-01
	GOTERM_BP_FAT	proton transport	10	4.10E-01	9.70E-01
	GOTERM_BP_FAT	ribonucleotide biosynthetic process	18	4.70E-01	9.80E-01
	GOTERM_BP_FAT	ion transmembrane transport	8	4.70E-01	9.80E-01
	GOTERM_BP_FAT	purine nucleotide biosynthetic process	21	4.90E-01	9.90E-01
	GOTERM_BP_FAT	ATP biosynthetic process	13	5.10E-01	9.90E-01
	GOTERM_BP_FAT	oxidative phosphorylation	14	5.40E-01	9.90E-01
	GOTERM_CC_FAT	proton-transporting ATP synthase complex	4	5.50E-01	9.30E-01
	GOTERM_CC_FAT	proton-transporting two-sector ATPase complex	7	5.70E-01	9.40E-01
	GOTERM_BP_FAT	nucleotide biosynthetic process	25	5.80E-01	9.90E-01
	GOTERM_MF_FAT	ATPase activity, coupled to transmembrane movement of ions	10	6.20E-01	1.00E+00
	GOTERM_MF_FAT	hydrogen ion transporting ATP synthase activity, rotational mechanism	3	6.30E-01	1.00E+00
	GOTERM_CC_FAT	proton-transporting two-sector ATPase complex, proton-transporting domain	4	6.40E-01	9.60E-01
	GOTERM_MF_FAT	inorganic cation transmembrane transporter activity	19	6.70E-01	1.00E+00
	GOTERM_CC_FAT	proton-transporting two-sector ATPase complex, catalytic domain	3	7.10E-01	9.70E-01
	GOTERM_CC_FAT	mitochondrial proton-transporting ATP synthase complex	3	7.40E-01	9.80E-01
	GOTERM_CC_FAT	proton-transporting V-type ATPase complex	3	7.70E-01	9.80E-01
	GOTERM_CC_FAT	mitochondrial respiratory chain	8	7.70E-01	9.80E-01
	GOTERM_CC_FAT	mitochondrial membrane part	14	8.70E-01	1.00E+00
	GOTERM_BP_FAT	monovalent inorganic cation transport	22	1.00E+00	1.00E+00
Annotation Cluster 232	**Enrichment Score: 0.51**		**Count**	**P_Value**	**Benjamini**
	GOTERM_CC_FAT	BRCA1-A complex	4	5.50E-02	3.50E-01
	GOTERM_BP_FAT	G2/M transition checkpoint	5	1.50E-01	7.90E-01
	GOTERM_BP_FAT	regulation of DNA repair	5	3.30E-01	9.50E-01
	GOTERM_BP_FAT	response to ionizing radiation	10	3.90E-01	9.70E-01
	GOTERM_BP_FAT	G2/M transition DNA damage checkpoint	3	5.30E-01	9.90E-01
	GOTERM_BP_FAT	positive regulation of DNA repair	3	6.10E-01	1.00E+00
	GOTERM_BP_FAT	double-strand break repair	8	7.30E-01	1.00E+00
Annotation Cluster 233	**Enrichment Score: 0.51**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	repeat:TPR 9	8	6.30E-02	1.00E+00
	UP_SEQ_FEATURE	repeat:TPR 12	3	3.50E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:TPR 8	8	3.60E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:TPR 11	3	4.80E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:TPR 10	3	7.20E-01	1.00E+00
Annotation Cluster 234	**Enrichment Score: 0.51**		**Count**	**P_Value**	**Benjamini**
	GOTERM_CC_FAT	nuclear heterochromatin	8	8.30E-02	4.60E-01
	GOTERM_CC_FAT	sex chromatin	3	5.80E-01	9.40E-01
	GOTERM_CC_FAT	sex chromosome	3	6.10E-01	9.50E-01
Annotation Cluster 235	**Enrichment Score: 0.51**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	interphase	18	2.30E-01	8.90E-01
	GOTERM_BP_FAT	interphase of mitotic cell cycle	17	2.80E-01	9.20E-01
	GOTERM_BP_FAT	G1/S transition of mitotic cell cycle	9	4.60E-01	9.80E-01
Annotation Cluster 236	**Enrichment Score: 0.51**		**Count**	**P_Value**	**Benjamini**
	INTERPRO	D111/G-patch	5	3.00E-01	1.00E+00
	UP_SEQ_FEATURE	domain:G-patch	5	3.00E-01	1.00E+00
	SMART	G_patch	5	3.30E-01	9.60E-01
Annotation Cluster 237	**Enrichment Score: 0.51**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	respiratory burst	6	2.00E-02	3.00E-01
	SP_PIR_KEYWORDS	antioxidant	4	8.40E-02	3.90E-01
	UP_SEQ_FEATURE	active site:Cysteine sulfenic acid (-SOH) intermediate	3	1.60E-01	1.00E+00
	GOTERM_BP_FAT	cellular response to oxidative stress	9	2.00E-01	8.60E-01
	INTERPRO	Alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal allergen	3	2.20E-01	1.00E+00
	GOTERM_BP_FAT	hydrogen peroxide metabolic process	6	2.30E-01	8.90E-01
	GOTERM_MF_FAT	peroxiredoxin activity	3	2.70E-01	9.60E-01

ILMN_1780996	ETAA1	-0.486932571
ILMN_1781472	CDC42BPA	-0.486958384
ILMN_1656630	AY831680	-0.48705526
ILMN_1910805	BE326664	-0.487184216
ILMN_1701507	EHHADH	-0.487243649
ILMN_2295844	VAMP1	-0.487351562
ILMN_1748661	AKT1	-0.487363086
ILMN_1653878	CACNB2	-0.487430352
ILMN_1838137	BF514549	-0.487446463
ILMN_2373779	COPS8	-0.487453259
ILMN_1885199	AI733327	-0.487462655
ILMN_2373010	TMEM70	-0.487528536
ILMN_1749343	PLXNA4	-0.487595114
ILMN_1795822	DIS3L	-0.487704226
ILMN_3187648	BC153822	-0.487710386
ILMN_3183069	C17orf107	-0.487716017
ILMN_3269324	AK094963	-0.487768976
ILMN_1802414	CA13	-0.487832083
ILMN_1657050	ARSK	-0.487918423
ILMN_2120575	HTATSF1	-0.487960094
ILMN_1721541	WIF1	-0.488027774
ILMN_1701289	LOC146880	-0.488041555
ILMN_3236661	SDR16C5	-0.488041593
ILMN_1782937	GSTA1	-0.488137579
ILMN_1730620	ARRB1	-0.488222874
ILMN_2131123	AMY2A	-0.488223214
ILMN_1887928	BQ775960	-0.488266937
ILMN_3240173	MTSS1L	-0.488269971
ILMN_1728785	GPR116	-0.488298714
ILMN_3239408	REXO1L1	-0.48829914
ILMN_1810652	LMBRD2	-0.488340651
ILMN_3277332	OR7E14P	-0.488479804
ILMN_2052598	ARMC10	-0.48848483
ILMN_1702837	PSMD1	-0.488511173
ILMN_2076484	FAM126B	-0.488627404
ILMN_3238299	NHEDC1	-0.488701963
ILMN_1745570	KLK7	-0.488782955
ILMN_1657010	FAM90A12	-0.488823777
ILMN_1727438	KCND3	-0.488921108
ILMN_1723846	METTL21B	-0.488971905
ILMN_2059294	RTCD1	-0.48900466
ILMN_1671154	TMPRSS13	-0.489071031
ILMN_1683453	FRAS1	-0.48908457
ILMN_1664449	ALG5	-0.489181354
ILMN_1740627	TIAM2	-0.489213818
ILMN_1720235	ADSSL1	-0.489220096
ILMN_1915734	DA722162	-0.489237793
ILMN_1759448	CPZ	-0.489256511
ILMN_1679881	WRN	-0.489376618
ILMN_1708145	LOC100132966	-0.489432097
ILMN_1714782	OPRK1	-0.489484764
ILMN_1741957	RABEPK	-0.489512287
ILMN_1699562	EFCAB1	-0.48957376
ILMN_1802450	CNOT6L	-0.489641299
ILMN_1764605	FGF6	-0.489696579
ILMN_1761829	HK1	-0.489792445
ILMN_1845693	COL29A1	-0.489856182
ILMN_1780783	SOCS7	-0.489859893
ILMN_1800465	DHRS4L2	-0.49000246
ILMN_1659099	ROCK2	-0.490036548
ILMN_1766028	TBC1D26	-0.490047284
ILMN_2409596	RAB11FIP1	-0.490097181
ILMN_1803376	AEBP2	-0.490111163
ILMN_1800923	OR4M1	-0.490172709
ILMN_3251132	TMOD2	-0.49021148
ILMN_3301206	MAGIX	-0.490231692
ILMN_1665022	SMN1	-0.490261201
ILMN_1716357	AK097401	-0.490287181
ILMN_1809760	KLHL1	-0.490347764
ILMN_2156699	ACOT6	-0.490390855
ILMN_1783705	GRXCR2	-0.490566368
ILMN_1886537	AI859685	-0.490588762
ILMN_1775192	BCLAF1	-0.490633872
ILMN_1820327	NA	-0.490658947
ILMN_1726112	PKP3	-0.490763684
ILMN_1709256	PLEC	-0.490861396
ILMN_1783497	PANK1	-0.490873962
ILMN_2043109	TOP1P2	-0.490889484
ILMN_1724166	OR56B1	-0.490978835
ILMN_3191416	LOC100131199	-0.490995585
ILMN_2372681	MAGEA6	-0.491001816
ILMN_2086612	DKFZp686H12134	-0.491019129
ILMN_1703648	TMEM82	-0.491078523
ILMN_2057220	HRSP12	-0.491083967
ILMN_1781419	C11orf73	-0.491103443
ILMN_2279144	PHF16	-0.491124319
ILMN_1795673	C9orf173	-0.491212072
ILMN_1740041	HERC2P7	-0.491230771

ILMN_1653115	ECH1	0.610550226
ILMN_2043615	C17orf90	0.610447793
ILMN_1766713	HSPD1	0.610421587
ILMN_1740500	TSPYL4	0.610416845
ILMN_2376408	DPM3	0.610354929
ILMN_1677261	LZTS1	0.610230505
ILMN_2335604	SKAP1	0.610019676
ILMN_1655710	RPS25	0.610002765
ILMN_2139943	RPS3A	0.609990545
ILMN_1760509	EOMES	0.609953246
ILMN_1741259	RPS2	0.609900608
ILMN_1792733	FOXA3	0.609897719
ILMN_1738819	EFTUD2	0.609666627
ILMN_1688246	LOC642852	0.60962932
ILMN_1740742	UROD	0.609508182
ILMN_1724612	SLC25A35	0.609464329
ILMN_1726456	SLC3A2	0.609364313
ILMN_1775542	FAIM3	0.609340482
ILMN_1722524	GALNT14	0.609256221
ILMN_2340721	TMEM134	0.609251119
ILMN_1778333	MMP24	0.609094517
ILMN_3236135	FAM86B1	0.608972058
ILMN_2209260	KRTAP1-3	0.608930002
ILMN_2074258	BARD1	0.608921187
ILMN_1785060	TSPAN14	0.608864415
ILMN_2304624	EIF4H	0.608769001
ILMN_1797453	ARMC8	0.608606675
ILMN_1690064	RUNDC2B	0.608419098
ILMN_1815024	PRDX5	0.608334596
ILMN_1753241	SNTA1	0.608229652
ILMN_1694571	SPDYE7P	0.608118275
ILMN_2409055	FAM13C	0.608034601
ILMN_1717793	C19orf33	0.607808158
ILMN_3208233	RBMX	0.607798713
ILMN_1772991	MIR671	0.607705427
ILMN_1675541	EEF1B2	0.607692853
ILMN_1749448	GLMN	0.607692322
ILMN_2352131	ERBB2	0.607672202
ILMN_2380237	C1QTNF1	0.607661626
ILMN_2307656	AGTRAP	0.607639506
ILMN_1803739	RPGRIP1	0.607533186
ILMN_1698950	PWP2	0.607450684
ILMN_1699878	RAB27A	0.607376406
ILMN_1656625	RPS24	0.607255827
ILMN_2234310	GLTPD1	0.607217285
ILMN_1806320	PPFIBP1	0.607151322
ILMN_1769031	MTOR	0.607029644
ILMN_2198393	KATNA1	0.60699289
ILMN_1767253	RRP12	0.606923438
ILMN_1656904	SLC1A4	0.606869559
ILMN_1723177	ANAPC5	0.606834762
ILMN_2295506	LUC7L	0.606634645
ILMN_1789176	PSMB1	0.606591381
ILMN_1774287	CFB	0.606530067
ILMN_1768482	CD8A	0.60652102
ILMN_3292224	HNRNPA1	0.606494982
ILMN_1768773	RAB4B-EGLN2	0.606492562
ILMN_2396269	CDH24	0.606468537
ILMN_1658053	DYNLRB1	0.60636705
ILMN_1658373	PAN2	0.606187893
ILMN_1727809	STK35	0.606116094
ILMN_1682736	FT002	0.606066042
ILMN_2312296	PCBP2	0.606053262
ILMN_1759003	SNX12	0.605960101
ILMN_3224952	RPS16	0.605920918
ILMN_2169736	PGBD4	0.605797384
ILMN_1709026	C6orf145	0.605635045
ILMN_2399571	CBY1	0.605538674
ILMN_1674533	TRPV6	0.605479305
ILMN_1730734	TMEM205	0.605425575
ILMN_1654072	CX3CL1	0.605355362
ILMN_1696601	VARS	0.605345003
ILMN_2376416	UBXN11	0.605295637
ILMN_1680102	C11orf45	0.605194914
ILMN_1791840	RALBP1	0.605130631
ILMN_1766560	ANKHD1	0.605063042
ILMN_1738750	TFCP2	0.604962072
ILMN_1683980	PLEKHM2	0.604889263
ILMN_1789809	RPL13AP6	0.60471905
ILMN_1678831	GCC2	0.604660433
ILMN_2313946	CPNE7	0.604640291
ILMN_1699226	UBR4	0.604636177
ILMN_1787410	EIF6	0.604273031
ILMN_1733927	TCEB2	0.604239323
ILMN_2353732	CD8A	0.60420109
ILMN_2314080	CTAGE5	0.604185247
ILMN_1708025	RBPMS	0.604123918
ILMN_1751726	RPLP0	0.604063322
ILMN_1745217	KIAA1310	0.604058665
ILMN_1657857	TMEM14C	0.604042502
ILMN_2326737	PPIE	0.60399066
ILMN_1787879	ARL2	0.603955588
ILMN_3287687	TUBB2A	0.60380977
ILMN_3188076	RPS7	0.603804338
ILMN_1652407	ZMYND8	0.60378994
ILMN_2226917	KIAA0247	0.603714965

	GOTERM_BP_FAT	response to reactive oxygen species	13	2.80E-01	9.20E-01
	SP_PIR_KEYWORDS	peroxidase	5	3.60E-01	8.00E-01
	GOTERM_BP_FAT	cellular response to reactive oxygen species	6	3.60E-01	9.60E-01
	UP_SEQ_FEATURE	domain:Thioredoxin	6	3.70E-01	1.00E+00
	GOTERM_BP_FAT	hydrogen peroxide catabolic process	4	3.90E-01	9.70E-01
	GOTERM_MF_FAT	oxidoreductase activity, acting on peroxide as acceptor	6	3.90E-01	9.80E-01
	GOTERM_MF_FAT	peroxidase activity	6	3.90E-01	9.80E-01
	GOTERM_MF_FAT	antioxidant activity	8	4.00E-01	9.80E-01
	GOTERM_MF_FAT	glutathione peroxidase activity	3	4.20E-01	9.90E-01
	GOTERM_BP_FAT	superoxide metabolic process	5	4.20E-01	9.80E-01
	GOTERM_BP_FAT	cellular response to hydrogen peroxide	4	4.30E-01	9.80E-01
	GOTERM_BP_FAT	response to hydrogen peroxide	9	4.60E-01	9.80E-01
	GOTERM_BP_FAT	response to oxidative stress	23	5.00E-01	9.90E-01
	GOTERM_BP_FAT	oxygen and reactive oxygen species metabolic process	10	5.30E-01	9.90E-01
	GOTERM_BP_FAT	peptide metabolic process	8	5.60E-01	9.90E-01
	GOTERM_BP_FAT	response to inorganic substance	26	6.90E-01	1.00E+00
	GOTERM_BP_FAT	glutathione metabolic process	4	7.30E-01	1.00E+00
Annotation Cluster 238	**Enrichment Score: 0.5**		**Count**	**P_Value**	**Benjamini**
	INTERPRO	Octicosapeptide/Phox/Bem1p	4	2.60E-01	1.00E+00
	SMART	PB1	4	2.80E-01	9.30E-01
	UP_SEQ_FEATURE	domain:OPR	3	4.40E-01	1.00E+00
Annotation Cluster 239	**Enrichment Score: 0.5**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	DNA-binding region:Tryptophan pentad repeat	3	3.00E-01	1.00E+00
	INTERPRO	Interferon regulatory factor	3	3.20E-01	1.00E+00
	INTERPRO	Interferon regulatory factor, conserved site	3	3.20E-01	1.00E+00
	SMART	IRF	3	3.40E-01	9.60E-01
Annotation Cluster 240	**Enrichment Score: 0.5**		**Count**	**P_Value**	**Benjamini**
	GOTERM_CC_FAT	NuA4 histone acetyltransferase complex	4	2.80E-01	7.70E-01
	GOTERM_CC_FAT	H4/H2A histone acetyltransferase complex	4	3.20E-01	8.10E-01
	GOTERM_CC_FAT	histone acetyltransferase complex	9	3.50E-01	8.30E-01
Annotation Cluster 241	**Enrichment Score: 0.49**		**Count**	**P_Value**	**Benjamini**
	INTERPRO	Translation elongation factor EFTu/EF1A, domain 2	4	2.90E-01	1.00E+00
	INTERPRO	Translation elongation factor EFTu/EF1A, C-terminal	3	3.20E-01	1.00E+00
	INTERPRO	Protein synthesis factor, GTP-binding	4	3.60E-01	1.00E+00
Annotation Cluster 242	**Enrichment Score: 0.49**		**Count**	**P_Value**	**Benjamini**
	SP_PIR_KEYWORDS	SH2 domain	18	1.80E-01	6.00E-01
	INTERPRO	SH2 motif	17	3.20E-01	1.00E+00
	SMART	SH2	17	3.90E-01	9.60E-01
	UP_SEQ_FEATURE	domain:SH2	13	5.00E-01	1.00E+00
Annotation Cluster 243	**Enrichment Score: 0.49**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	short sequence motif:BH2	4	2.00E-01	1.00E+00
	INTERPRO	Apoptosis regulator Bcl-2, BH	5	3.00E-01	1.00E+00
	SMART	BCL	5	3.30E-01	9.60E-01
	UP_SEQ_FEATURE	short sequence motif:BH3	4	3.40E-01	1.00E+00
	UP_SEQ_FEATURE	short sequence motif:BH1	3	3.90E-01	1.00E+00
	INTERPRO	BCL2-like apoptosis inhibitor	3	4.60E-01	1.00E+00
Annotation Cluster 244	**Enrichment Score: 0.49**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	regulation of establishment of protein localization	22	1.10E-01	7.10E-01
	GOTERM_BP_FAT	regulation of intracellular protein transport	11	1.50E-01	8.00E-01
	GOTERM_BP_FAT	regulation of protein transport	20	1.70E-01	8.20E-01
	GOTERM_BP_FAT	regulation of protein localization	23	2.00E-01	8.60E-01
	GOTERM_BP_FAT	regulation of protein import into nucleus	9	2.20E-01	8.80E-01
	GOTERM_BP_FAT	regulation of nucleocytoplasmic transport	11	2.30E-01	8.90E-01
	GOTERM_BP_FAT	positive regulation of protein transport	12	2.60E-01	9.20E-01
	GOTERM_BP_FAT	regulation of intracellular transport	12	3.30E-01	9.50E-01
	GOTERM_BP_FAT	regulation of transcription factor import into nucleus	6	3.60E-01	9.60E-01
	GOTERM_BP_FAT	regulation of NF-kappaB import into nucleus	4	4.30E-01	9.80E-01
	GOTERM_BP_FAT	positive regulation of nucleocytoplasmic transport	4	5.70E-01	9.90E-01
	GOTERM_BP_FAT	positive regulation of intracellular transport	5	5.70E-01	9.90E-01
	GOTERM_BP_FAT	positive regulation of protein import into nucleus	3	6.80E-01	1.00E+00
	GOTERM_BP_FAT	positive regulation of transport	27	7.80E-01	1.00E+00
	GOTERM_BP_FAT	regulation of cellular localization	30	7.80E-01	1.00E+00
Annotation Cluster 245	**Enrichment Score: 0.47**		**Count**	**P_Value**	**Benjamini**
	GOTERM_MF_FAT	transcription regulator activity	223	1.50E-02	3.50E-01
	SP_PIR_KEYWORDS	Transcription	268	1.10E-01	4.70E-01
	SP_PIR_KEYWORDS	transcription regulation	259	1.70E-01	5.90E-01
	GOTERM_MF_FAT	transcription factor activity	130	3.80E-01	9.80E-01
	GOTERM_BP_FAT	regulation of RNA metabolic process	236	6.30E-01	1.00E+00
	GOTERM_BP_FAT	regulation of transcription	339	6.40E-01	1.00E+00
	GOTERM_BP_FAT	transcription	273	6.50E-01	1.00E+00
	GOTERM_BP_FAT	regulation of transcription, DNA-dependent	226	7.60E-01	1.00E+00
	GOTERM_MF_FAT	DNA binding	280	9.30E-01	1.00E+00
	SP_PIR_KEYWORDS	dna-binding	207	9.30E-01	1.00E+00
Annotation Cluster 246	**Enrichment Score: 0.47**		**Count**	**P_Value**	**Benjamini**
	INTERPRO	Ephrin, conserved site	3	2.70E-01	1.00E+00
	INTERPRO	Ephrin	3	2.70E-01	1.00E+00
	INTERPRO	Cupredoxin	3	5.40E-01	1.00E+00
Annotation Cluster 247	**Enrichment Score: 0.47**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	protein maturation	24	4.70E-02	4.80E-01
	SP_PIR_KEYWORDS	innate immunity	14	1.40E-01	5.30E-01
	GOTERM_BP_FAT	protein maturation by peptide bond cleavage	16	1.60E-01	8.00E-01
	SP_PIR_KEYWORDS	complement alternate pathway	4	2.00E-01	6.30E-01
	GOTERM_BP_FAT	humoral immune response	14	2.40E-01	9.00E-01
	GOTERM_BP_FAT	protein processing	18	3.00E-01	9.40E-01
	GOTERM_BP_FAT	acute inflammatory response	16	3.10E-01	9.40E-01
	GOTERM_BP_FAT	complement activation	8	3.10E-01	9.40E-01
	GOTERM_BP_FAT	complement activation, alternative pathway	4	3.20E-01	9.40E-01
	GOTERM_BP_FAT	activation of plasma proteins involved in acute inflammatory response	8	3.40E-01	9.50E-01
	GOTERM_BP_FAT	humoral immune response mediated by circulating immunoglobulin	6	3.90E-01	9.70E-01
	SP_PIR_KEYWORDS	complement pathway	5	4.70E-01	8.80E-01
	GOTERM_BP_FAT	complement activation, classical pathway	5	5.40E-01	9.90E-01
	BIOCARTA	Alternative Complement Pathway	3	6.00E-01	9.90E-01
	BIOCARTA	Complement Pathway	4	6.70E-01	9.90E-01
	SP_PIR_KEYWORDS	acute phase	4	7.00E-01	9.60E-01
	KEGG_PATHWAY	Complement and coagulation cascades	9	8.30E-01	9.40E-01
	SP_PIR_KEYWORDS	plasma	7	9.70E-01	1.00E+00

ILMN_1704627	BM723461	-0.491254183
ILMN_2202320	BRWD1-IT2	-0.49134899
ILMN_1813955	SERTAD3	-0.491361493
ILMN_1664448	PEX12	-0.491398755
ILMN_1725387	TMEM200A	-0.491443294
ILMN_2215043	RNF32	-0.491472247
ILMN_3225244	TSEN15	-0.491500431
ILMN_1746819	C5	-0.491523781
ILMN_1669669	KCMF1	-0.491529827
ILMN_1730032	BOK	-0.491531516
ILMN_1712066	EXPH5	-0.491583942
ILMN_1673713	LOC646168	-0.491640506
ILMN_1760412	SHISA2	-0.491661543
ILMN_1728532	FAM72A	-0.491695174
ILMN_1776524	LOC388692	-0.491724449
ILMN_1666966	IGF2	-0.491775952
ILMN_1813775	GAK	-0.491795733
ILMN_2045453	CFHR2	-0.491837928
ILMN_2107184	SNRK	-0.491846243
ILMN_1801778	MPPED1	-0.491850239
ILMN_3240993	NA	-0.491861244
ILMN_1652409	SPATA7	-0.491868132
ILMN_1664014	STOX1	-0.491884019
ILMN_1753729	KNG1	-0.491894172
ILMN_2372379	MGA	-0.49191354
ILMN_1754103	CLDN11	-0.491950576
ILMN_1800049	MAPT	-0.491972058
ILMN_1796455	RYR3	-0.49199601
ILMN_2232430	NMD3	-0.492064549
ILMN_1804328	WWP1	-0.492082006
ILMN_1703545	CSHL1	-0.492091384
ILMN_1783168	NETO1	-0.49215635
ILMN_1811478	MFI2	-0.492396909
ILMN_1780504	C19orf26	-0.492401509
ILMN_1671682	LOC554249	-0.492423831
ILMN_1791933	CCDC82	-0.49243437
ILMN_2293511	CTNND1	-0.492452557
ILMN_1695418	IQGAP3	-0.492622316
ILMN_3309939	MIR302F	-0.492627887
ILMN_3304064	DAMS	-0.492643715
ILMN_1773493	TIMM23	-0.492752372
ILMN_1740576	BC169297	-0.492798836
ILMN_1866290	BI827719	-0.492838246
ILMN_2204526	TCTEX1D4	-0.492955734
ILMN_1665630	HMGN2	-0.493048252
ILMN_1707551	AFMID	-0.49309896
ILMN_1771065	AB621825	-0.493130053
ILMN_3236481	HIGD1A	-0.493170178
ILMN_1730448	DEFB108B	-0.493405901
ILMN_1680284	ZNF681	-0.493426146
ILMN_3295874	NA	-0.493426376
ILMN_1684339	LRIT1	-0.493495651
ILMN_2177234	DEFB104B	-0.493621684
ILMN_1784302	LIPJ	-0.493629619
ILMN_1672591	SCN9A	-0.493839753
ILMN_1897796	BQ773461	-0.49387516
ILMN_3221852	LOC728405	-0.4938893
ILMN_1852041	CA391357	-0.493975241
ILMN_1669033	NCOA1	-0.493986715
ILMN_2180252	FAM70A	-0.494004826
ILMN_1737806	DKFZp686K1684	-0.494008084
ILMN_1902060	CD000292	-0.494046447
ILMN_1693674	TRDN	-0.494063022
ILMN_1774757	ZNF496	-0.494112853
ILMN_1661066	NCRNA00087	-0.494155953
ILMN_1887508	AI206543	-0.494255035
ILMN_3240586	PLD6	-0.494263446
ILMN_3241904	MAN1C1	-0.494341248
ILMN_3310548	MIR889	-0.494371811
ILMN_1656066	TNPO2	-0.494463923
ILMN_1790160	KIT	-0.49447714
ILMN_1741389	B3GNT8	-0.494486965
ILMN_3280496	RPL26	-0.494539906
ILMN_1779264	PSMG1	-0.494569709
ILMN_1669123	AK125437	-0.494589886
ILMN_1728107	GNG7	-0.494673002
ILMN_2385688	RABL2B	-0.49480939
ILMN_1770336	AGRP	-0.494880584
ILMN_2066151	TEK	-0.494902748
ILMN_1758343	LOC100129233	-0.494962869
ILMN_1788468	ARGLU1	-0.49500168
ILMN_2385161	CUL4B	-0.495108415
ILMN_3187619	NA	-0.495115324
ILMN_3205271	HMGB1	-0.495191867
ILMN_1782173	CBX3	-0.495206971
ILMN_1731518	PLD6	-0.495374389
ILMN_1740213	ELOVL7	-0.495400922
ILMN_1724234	TRPV1	-0.495465121
ILMN_1682273	SHISA3	-0.495512896
ILMN_1703408	FZD3	-0.495533114
ILMN_1658427	SMPD4	-0.495683973
ILMN_1687392	NRK	-0.495689272
ILMN_1801044	DOCK4	-0.495698258
ILMN_1911594	AV647465	-0.495711091
ILMN_2402463	SHMT1	-0.495716464
ILMN_3311045	MIR216A	-0.495721489

ILMN_3237368	MAFG	0.60368571
ILMN_1659727	CDAN1	0.603668155
ILMN_1708041	PLEKHF1	0.603557258
ILMN_1739558	CRELD1	0.603460465
ILMN_1690806	CR613620	0.603453994
ILMN_1811049	POU2AF1	0.603450557
ILMN_1767337	SFXN5	0.603394433
ILMN_1801101	ZBTB48	0.603331234
ILMN_2114876	RPL11	0.603318644
ILMN_1664243	USE1	0.603269604
ILMN_1782788	CSDA	0.603185596
ILMN_1781580	BRI3	0.60314657
ILMN_1673944	MANBAL	0.603115857
ILMN_2340565	ATP2C1	0.60311099
ILMN_1736623	NCKIPSD	0.602768278
ILMN_1786972	SARS	0.602647655
ILMN_1753312	PLXDC2	0.602556315
ILMN_1670456	RBM42	0.602512248
ILMN_2361163	SSBP3	0.602453977
ILMN_1812995	CTSL1	0.602318078
ILMN_1689868	TMEM80	0.602247033
ILMN_2387505	AP1B1	0.602218145
ILMN_1670398	BCR	0.602190015
ILMN_1691930	CBX6	0.602051977
ILMN_1790819	MEMO1	0.60194508
ILMN_2081269	OR2A9P	0.60192587
ILMN_2398903	HAX1	0.60173596
ILMN_1744822	BECN1	0.601725771
ILMN_1811682	CLIP2	0.601633363
ILMN_3247424	ADAP1	0.601546688
ILMN_1735333	NBR1	0.601467656
ILMN_3243381	MLEC	0.601423953
ILMN_1780153	QTRT1	0.601366167
ILMN_1688295	ZNF219	0.601348002
ILMN_2333367	FKBP1A	0.601345885
ILMN_1795183	RNASE1	0.601313435
ILMN_1655572	C6orf59	0.601236528
ILMN_1657435	MT1M	0.601142974
ILMN_1657884	NME1	0.601015529
ILMN_2394381	CLN3	0.600953166
ILMN_1691290	CELSR3	0.600932254
ILMN_1697864	CXorf38	0.600909598
ILMN_1747442	P4HA1	0.600816601
ILMN_1707748	PIM3	0.600742006
ILMN_2114568	GBP5	0.60068657
ILMN_2054392	PPIL1	0.600685305
ILMN_1740216	ERCC3	0.600643528
ILMN_1705783	NXF1	0.600628355
ILMN_1724194	NPEPL1	0.6006186
ILMN_1739335	OST4	0.600561463
ILMN_1711810	PNKD	0.600553256
ILMN_1774132	MAP6	0.600424134
ILMN_2339627	COPE	0.600410738
ILMN_1694950	MRPL28	0.600359062
ILMN_1719165	BRMS1	0.600342873
ILMN_1765257	CINP	0.600309571
ILMN_1750761	NCR1	0.600163747
ILMN_1726659	THOP1	0.60015062
ILMN_1652929	POGZ	0.599864672
ILMN_2394250	PLEKHA1	0.599834206
ILMN_1753482	FAM86C	0.59980756
ILMN_1785831	ZDHHC13	0.599785155
ILMN_1778991	NFIB	0.599686543
ILMN_1782098	SMO	0.599485382
ILMN_2141482	SERPINF1	0.599363814
ILMN_1656998	CHMP4B	0.599265175
ILMN_1778032	SURF6	0.599204428
ILMN_1706664	RIMKLA	0.59918758
ILMN_1753353	SLBP	0.599167167
ILMN_2372639	TRAPPC5	0.599159135
ILMN_3185709	IP6K2	0.59891642
ILMN_2400759	CPVL	0.59882385
ILMN_1658619	WWC1	0.598776047
ILMN_1718023	APEH	0.59870449
ILMN_1751431	WIBG	0.598693554
ILMN_2345353	LST1	0.59862278
ILMN_2075440	PDIA3P	0.598604353
ILMN_2242463	CTSC	0.598562706
ILMN_1787718	SLC27A1	0.598508998
ILMN_1786310	MVK	0.598455581
ILMN_1724407	TACC3	0.598432535
ILMN_1775692	EIF4G3	0.598287317
ILMN_1700541	FBLN1	0.59823139
ILMN_1745583	EXOC1	0.597884304
ILMN_1784005	RAB13	0.597832028
ILMN_1784141	JAKMIP1	0.597786862
ILMN_1789196	TPM2	0.597686251
ILMN_1677968	KIAA0649	0.597619344
ILMN_1652199	abParts	0.59756277
ILMN_2152581	STK38	0.597365722
ILMN_1696066	CARS	0.597360402
ILMN_2208413	ARHGAP15	0.59728746
ILMN_1811765	ADAMTS2	0.597227504
ILMN_1869109	NUCKS1	0.597162893
ILMN_1668960	MID1IP1	0.597094812
ILMN_1665865	IGFBP4	0.597056285
ILMN_2097546	NUDC	0.597029011

Annotation Cluster 248	**Enrichment Score: 0.47**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	domain:SEC7	4	3.00E-01	1.00E+00
	INTERPRO	SEC7-like	4	3.30E-01	1.00E+00
	SMART	Sec7	4	3.60E-01	9.60E-01
	GOTERM_MF_FAT	ARF guanyl-nucleotide exchange factor activity	4	3.80E-01	9.80E-01
Annotation Cluster 249	**Enrichment Score: 0.47**		**Count**	**P_Value**	**Benjamini**
	BIOCARTA	Role of Erk5 in Neuronal Survival	7	2.50E-02	9.70E-01
	BIOCARTA	Ras Signaling Pathway	8	7.30E-02	9.40E-01
	BIOCARTA	Inhibition of Cellular Proliferation by Gleevec	6	3.00E-01	9.60E-01
	BIOCARTA	Transcription factor CREB and its extracellular signals	5	4.70E-01	9.80E-01
	BIOCARTA	PTEN dependent cell cycle arrest and apoptosis	5	6.40E-01	9.90E-01
	BIOCARTA	Trefoil Factors Initiate Mucosal Healing	5	6.40E-01	9.90E-01
	BIOCARTA	Multiple antiapoptotic pathways from IGF-1R signaling lead to BAD phosphorylation	4	7.10E-01	1.00E+00
	BIOCARTA	Phospholipids as signalling intermediaries	4	8.50E-01	1.00E+00
	BIOCARTA	Influence of Ras and Rho proteins on G1 to S Transition	3	9.60E-01	1.00E+00
Annotation Cluster 250	**Enrichment Score: 0.47**		**Count**	**P_Value**	**Benjamini**
	GOTERM_MF_FAT	insulin receptor binding	7	1.40E-01	8.60E-01
	UP_SEQ_FEATURE	domain:IRS-type PTB	3	4.40E-01	1.00E+00
	INTERPRO	Insulin receptor substrate-1, PTB	3	4.60E-01	1.00E+00
	SMART	PTBI	3	4.80E-01	9.70E-01
Annotation Cluster 251	**Enrichment Score: 0.47**		**Count**	**P_Value**	**Benjamini**
	GOTERM_MF_FAT	DNA-directed DNA polymerase activity	7	2.20E-01	9.30E-01
	SP_PIR_KEYWORDS	dna-directed dna polymerase	5	2.40E-01	6.80E-01
	SP_PIR_KEYWORDS	nucleotidyltransferase	11	4.30E-01	8.60E-01
	GOTERM_MF_FAT	nucleotidyltransferase activity	18	4.40E-01	9.90E-01
	GOTERM_MF_FAT	DNA polymerase activity	7	4.60E-01	9.90E-01
Annotation Cluster 252	**Enrichment Score: 0.46**		**Count**	**P_Value**	**Benjamini**
	SP_PIR_KEYWORDS	extracellular matrix	41	2.20E-02	1.70E-01
	GOTERM_CC_FAT	proteinaceous extracellular matrix	43	5.70E-01	9.40E-01
	GOTERM_CC_FAT	extracellular matrix part	16	6.10E-01	9.50E-01
	GOTERM_CC_FAT	extracellular matrix	45	6.50E-01	9.60E-01
	GOTERM_CC_FAT	extracellular region part	108	9.90E-01	1.00E+00
Annotation Cluster 253	**Enrichment Score: 0.46**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	domain:ABC transporter 2	8	8.40E-02	1.00E+00
	UP_SEQ_FEATURE	domain:ABC transporter 1	8	8.40E-02	1.00E+00
	UP_SEQ_FEATURE	nucleotide phosphate-binding region:ATP 1	7	2.40E-01	1.00E+00
	UP_SEQ_FEATURE	nucleotide phosphate-binding region:ATP 2	7	2.40E-01	1.00E+00
	INTERPRO	ABC transporter-like	9	2.50E-01	1.00E+00
	PIR_SUPERFAMILY	PIRSF002775:human multidrug resistance protein cMOAT2	3	3.50E-01	1.00E+00
	INTERPRO	ATPase, AAA+ type, core	21	3.60E-01	1.00E+00
	INTERPRO	ABC transporter, conserved site	9	4.30E-01	1.00E+00
	SMART	AAA	21	4.40E-01	9.70E-01
	INTERPRO	ABC transporter integral membrane type 1	5	4.80E-01	1.00E+00
	UP_SEQ_FEATURE	domain:ABC transmembrane type-1 1	3	5.60E-01	1.00E+00
	UP_SEQ_FEATURE	domain:ABC transmembrane type-1 2	3	5.60E-01	1.00E+00
	INTERPRO	ABC transporter, transmembrane region	4	6.00E-01	1.00E+00
	COG_ONTOLOGY	Defense mechanisms	3	6.90E-01	9.80E-01
	KEGG_PATHWAY	ABC transporters	6	8.10E-01	9.40E-01
Annotation Cluster 254	**Enrichment Score: 0.46**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	cell fate specification	11	1.30E-01	7.50E-01
	GOTERM_BP_FAT	cell-cell signaling involved in cell fate specification	4	4.70E-01	9.80E-01
	GOTERM_BP_FAT	developmental induction	4	4.70E-01	9.80E-01
	GOTERM_BP_FAT	induction of an organ	3	5.30E-01	9.90E-01
Annotation Cluster 255	**Enrichment Score: 0.46**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	regulation of interleukin-10 production	4	1.70E-01	8.20E-01
	GOTERM_BP_FAT	positive regulation of interferon-gamma production	3	4.40E-01	9.80E-01
	GOTERM_BP_FAT	regulation of interferon-gamma production	5	5.70E-01	9.90E-01
Annotation Cluster 256	**Enrichment Score: 0.46**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	domain:CUE	3	3.00E-01	1.00E+00
	INTERPRO	Ubiquitin system component Cue	3	3.70E-01	1.00E+00
	SMART	CUE	3	3.90E-01	9.70E-01
Annotation Cluster 257	**Enrichment Score: 0.46**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	pentose-phosphate shunt	4	1.00E-01	7.00E-01
	GOTERM_BP_FAT	oxidoreduction coenzyme metabolic process	10	2.40E-01	9.00E-01
	GOTERM_BP_FAT	nicotinamide nucleotide metabolic process	8	2.70E-01	9.20E-01
	GOTERM_BP_FAT	nicotinamide metabolic process	8	2.70E-01	9.20E-01
	GOTERM_BP_FAT	alkaloid metabolic process	8	2.90E-01	9.30E-01
	GOTERM_BP_FAT	pyridine nucleotide metabolic process	8	3.10E-01	9.40E-01
	GOTERM_BP_FAT	cofactor metabolic process	29	3.40E-01	9.50E-01
	GOTERM_BP_FAT	NADP metabolic process	4	3.50E-01	9.60E-01
	GOTERM_BP_FAT	cellular amide metabolic process	9	4.60E-01	9.80E-01
	GOTERM_BP_FAT	coenzyme metabolic process	20	6.50E-01	1.00E+00
	GOTERM_BP_FAT	NAD metabolic process	4	6.60E-01	1.00E+00
	GOTERM_BP_FAT	secondary metabolic process	9	8.30E-01	1.00E+00
Annotation Cluster 258	**Enrichment Score: 0.45**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	cell cycle checkpoint	16	2.10E-01	8.80E-01
	GOTERM_BP_FAT	DNA damage response, signal transduction	14	2.50E-01	9.10E-01
	GOTERM_BP_FAT	DNA damage checkpoint	9	3.00E-01	9.30E-01
	GOTERM_BP_FAT	DNA integrity checkpoint	9	3.80E-01	9.60E-01
	GOTERM_BP_FAT	G2/M transition DNA damage checkpoint	3	5.30E-01	9.90E-01
	GOTERM_BP_FAT	positive regulation of DNA repair	3	6.10E-01	1.00E+00
Annotation Cluster 259	**Enrichment Score: 0.45**		**Count**	**P_Value**	**Benjamini**
	SP_PIR_KEYWORDS	calmodulin-binding	19	1.90E-01	6.30E-01
	GOTERM_MF_FAT	calmodulin binding	21	3.40E-01	9.70E-01
	UP_SEQ_FEATURE	region of interest:Calmodulin-binding	7	6.70E-01	1.00E+00
Annotation Cluster 260	**Enrichment Score: 0.45**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	endothelial cell development	3	2.30E-01	8.90E-01
	GOTERM_BP_FAT	endothelial cell differentiation	4	3.50E-01	9.60E-01
	GOTERM_BP_FAT	epithelial cell development	4	5.40E-01	9.90E-01
Annotation Cluster 261	**Enrichment Score: 0.45**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	ceramide metabolic process	9	1.80E-01	8.40E-01
	GOTERM_BP_FAT	glycolipid metabolic process	7	2.20E-01	8.80E-01
	GOTERM_BP_FAT	sphingoid metabolic process	9	2.40E-01	8.90E-01
	GOTERM_BP_FAT	glycosphingolipid metabolic process	6	2.50E-01	9.10E-01
	GOTERM_BP_FAT	membrane lipid metabolic process	14	2.70E-01	9.20E-01
	GOTERM_BP_FAT	sphingolipid metabolic process	13	2.80E-01	9.20E-01
	GOTERM_BP_FAT	sphingolipid biosynthetic process	6	3.90E-01	9.70E-01

ILMN_1678968	GEM	-0.49583411
ILMN_2128489	UQCRB	-0.495862925
ILMN_1779951	ANKRD7	-0.495895963
ILMN_1801143	LOXHD1	-0.495950648
ILMN_1792931	LYSMD1	-0.496070999
ILMN_1882560	NA	-0.496119898
ILMN_1652439	KRTAP3-1	-0.496200121
ILMN_1777657	SLC22A9	-0.496237243
ILMN_1811696	FDXR	-0.496269776
ILMN_2351262	MAPK8IP2	-0.496279996
ILMN_3305273	PSAT1	-0.496465607
ILMN_3309664	MIR300	-0.496497568
ILMN_1775646	L3MBTL4	-0.496570073
ILMN_1806655	ARHGAP6	-0.496658217
ILMN_1767649	PCDHGC3	-0.496692056
ILMN_1768205	SLFN12L	-0.496734832
ILMN_2275060	GHRHR	-0.496769983
ILMN_1771898	NBPF3	-0.49683929
ILMN_1654063	HYDIN	-0.496866963
ILMN_1874172	BX097339	-0.496884903
ILMN_3306028	BM932296	-0.497038992
ILMN_1651752	CXorf21	-0.497043976
ILMN_1779997	MEIS3	-0.497058848
ILMN_1712461	CBLN1	-0.497083712
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ILMN_1730117	TMC5	-0.497099582
ILMN_1802146	ZNF74	-0.497124265
ILMN_2200331	H2AFX	-0.497161221
ILMN_1810115	KCTD2	-0.497168956
ILMN_1701881	ZNF365	-0.497180095
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ILMN_1769752	FER1L5	-0.49731926
ILMN_1847029	CX787363	-0.497337425
ILMN_3307818	C9orf106	-0.497353678
ILMN_3240524	MFSD6	-0.497381559
ILMN_1789500	KIAA1875	-0.497394456
ILMN_1760180	MID2	-0.497448803
ILMN_1815051	API5	-0.497524899
ILMN_1652023	AGFG2	-0.49752636
ILMN_1679647	CHIA	-0.497549809
ILMN_1766320	IL3	-0.497600278
ILMN_1796595	C5orf22	-0.497606242
ILMN_1677880	MYADML2	-0.497620725
ILMN_2292863	RASA1	-0.49769163
ILMN_1837935	TNPO1	-0.497698456
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ILMN_2372398	ALDH5A1	-0.497831697
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ILMN_1810628	PRUNE2	-0.498011004
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ILMN_1888330	AI809531	-0.49823388
ILMN_1761072	AIDA	-0.498258196
ILMN_1813055	LOC401093	-0.498320978
ILMN_1890924	BX094420	-0.498340873
ILMN_1665730	ABCB10	-0.49845364
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ILMN_1754304	SNRNP48	-0.498709153
ILMN_1727134	KLHDC5	-0.498722239
ILMN_1680754	A4GNT	-0.498740105
ILMN_2212156	PPIG	-0.498827256
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ILMN_1693273	AK127961	-0.498864069
ILMN_1682224	MUC3A	-0.498944122
ILMN_1883982	KSR2	-0.498952769
ILMN_1668285	APBA1	-0.498954249
ILMN_1728734	PSG5	-0.498995267
ILMN_1765198	HEATR4	-0.499011374
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ILMN_1668657	C2orf69	-0.499078059
ILMN_2394366	FAM123A	-0.49908604
ILMN_1880704	AA484452	-0.49908693
ILMN_2130411	KDELR1	-0.499111369
ILMN_1753745	HDDC2	-0.499136784
ILMN_3283960	BC046381	-0.499165908
ILMN_1707258	UCN	-0.499198496
ILMN_1696127	KIAA0240	-0.499269975
ILMN_3182712	NA	-0.499392206
ILMN_1882000	TXLNG	-0.499400887
ILMN_2173740	ASB8	-0.499447764
ILMN_1729868	SPRYD4	-0.499449907
ILMN_1681008	CGRRF1	-0.499567087
ILMN_3296181	AX747752	-0.499615619
ILMN_3262348	IP6K2	-0.499683462
ILMN_1767837	GOLT1B	-0.499739895
ILMN_1691705	ZNF98	-0.499789902
ILMN_1699606	ASB3	-0.499801177
ILMN_1676296	PPAP2A	-0.49983008
ILMN_1753026	LPPR1	-0.499849499
ILMN_2080760	SNX22	-0.499888766

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ILMN_1658231	NACC1	0.596748414
ILMN_1703263	SP140	0.596726389
ILMN_1720053	ZFAND3	0.596671506
ILMN_1698491	MBD3	0.596636286
ILMN_1664464	PTGDS	0.596546765
ILMN_1653861	SCMH1	0.596542778
ILMN_2384133	DFFB	0.596467807
ILMN_1785618	SMTN	0.596417042
ILMN_1733932	SNUPN	0.596348252
ILMN_2211122	TRAPPC2	0.596258973
ILMN_1724341	ALG13	0.596258318
ILMN_1659240	MTMR14	0.596196159
ILMN_3238803	RASAL3	0.596116657
ILMN_2229922	C12orf35	0.595954254
ILMN_1675106	YIPF2	0.595751496
ILMN_1691436	BLVRA	0.595695716
ILMN_2392635	ABCF1	0.595633076
ILMN_1659769	MRAP	0.595605399
ILMN_1732921	ITGB8	0.595445735
ILMN_1655195	SMA4	0.595224509
ILMN_1794912	ATP5H	0.595189682
ILMN_1669966	NDUFS7	0.595163172
ILMN_1750321	TRANK1	0.595124349
ILMN_1697417	CEP170	0.595078471
ILMN_1776119	ABCC10	0.595068996
ILMN_1755710	EFNA4	0.594975865
ILMN_2399190	TNFSF13	0.594930027
ILMN_1654893	SCAMP2	0.594893003
ILMN_1769671	RYK	0.594821577
ILMN_1783843	MIIP	0.594771603
ILMN_1725612	NUP50	0.594726005
ILMN_2359456	ERGIC3	0.594530774
ILMN_1656310	IDO1	0.594441505
ILMN_1657983	TERF2IP	0.594430348
ILMN_3229467	EBPL	0.594381302
ILMN_1693762	LRRC48	0.594349265
ILMN_1808707	FSCN1	0.594316489
ILMN_1720373	SLC7A5	0.59429729
ILMN_1748651	PSMB3	0.594245679
ILMN_1738263	PIGU	0.593881209
ILMN_3234837	PKDCC	0.593854248
ILMN_1675848	MYL12A	0.593763397
ILMN_1681798	sept-06	0.593757192
ILMN_3247679	SNORA52	0.593637355
ILMN_3274666	CR601848	0.593615661
ILMN_1703228	AGFG2	0.593588092
ILMN_2094718	TPT1	0.59357182
ILMN_1660817	DDB2	0.593493035
ILMN_1782352	VENTX	0.593444383
ILMN_1900123	BX105859	0.593358623
ILMN_2220739	TMCO3	0.593357565
ILMN_2328433	NOP2	0.593329782
ILMN_1707503	C1orf144	0.593307181
ILMN_1733603	NDUFC1	0.593216444
ILMN_1676256	TPSAB1	0.593166469
ILMN_1725241	GSTK1	0.593042652
ILMN_1746578	SLC23A2	0.592968599
ILMN_1739345	C11orf48	0.592918181
ILMN_1813491	SPTLC1	0.592915828
ILMN_2109536	GOLGA8F	0.592861775
ILMN_1789733	CLIP3	0.592800721
ILMN_1711023	CDK5RAP1	0.592665156
ILMN_1771815	C20orf43	0.592601965
ILMN_1778319	DMKN	0.592557893
ILMN_1753805	PRKD2	0.592528237
ILMN_2330806	MYO18A	0.592502312
ILMN_1678966	SNRPF	0.592392402
ILMN_1681103	AQP1	0.592354606
ILMN_1810680	BOLA2B	0.592345175
ILMN_1700081	FST	0.592324328
ILMN_3247064	SNRNP40	0.592299215
ILMN_1659610	TJP3	0.591983311
ILMN_1814402	NFIC	0.591843276
ILMN_1802338	HHLA3	0.591831182
ILMN_1815366	ENGASE	0.591751019
ILMN_1678766	DYNLT1	0.591737109
ILMN_2339266	LAMA2	0.591735944
ILMN_2366391	PRDX1	0.591712015
ILMN_3179371	HNRNPK	0.591651785
ILMN_1656718	DEF8	0.591648181
ILMN_1661335	SPTBN1	0.591532043
ILMN_1727574	ZNF827	0.591502905
ILMN_1692398	CNTNAP1	0.591488393
ILMN_1769545	PRPF19	0.591463425
ILMN_1700203	KIAA1984	0.591462112
ILMN_1713901	KDELR3	0.591295624
ILMN_1682227	ZNF404	0.591250389
ILMN_1721113	HLA-C	0.591187187
ILMN_1651735	TGOLN2	0.591168427
ILMN_2255579	RAB37	0.591168292
ILMN_2048326	RPS27A	0.591032097
ILMN_1817239	DA160411	0.590962137
ILMN_3311070	MIR33B	0.590948731

	GOTERM_BP_FAT	sphingomyelin metabolic process	3	4.40E-01	9.80E-01
	GOTERM_BP_FAT	membrane lipid biosynthetic process	6	4.70E-01	9.80E-01
	GOTERM_BP_FAT	ceramide biosynthetic process	3	6.10E-01	1.00E+00
	GOTERM_BP_FAT	sphingoid biosynthetic process	3	6.40E-01	1.00E+00
	KEGG_PATHWAY	Sphingolipid metabolism	6	7.20E-01	9.00E-01
Annotation Cluster 262	**Enrichment Score: 0.45**		**Count**	**P_Value**	**Benjamini**
	GOTERM_CC_FAT	Srb-mediator complex	7	1.80E-01	6.50E-01
	GOTERM_MF_FAT	RNA polymerase II transcription mediator activity	6	3.10E-01	9.70E-01
	GOTERM_MF_FAT	general RNA polymerase II transcription factor activity	6	7.90E-01	1.00E+00
Annotation Cluster 263	**Enrichment Score: 0.44**		**Count**	**P_Value**	**Benjamini**
	BIOCARTA	Synaptic Proteins at the Synaptic Junction	7	1.20E-01	9.00E-01
	UP_SEQ_FEATURE	domain:Guanylate kinase-like	5	3.00E-01	1.00E+00
	INTERPRO	Guanylate kinase	5	3.30E-01	1.00E+00
	INTERPRO	Guanylate kinase/L-type calcium channel region	5	4.20E-01	1.00E+00
	UP_SEQ_FEATURE	domain:PDZ 3	5	4.40E-01	1.00E+00
	SMART	GuKc	5	4.50E-01	9.70E-01
	UP_SEQ_FEATURE	domain:PDZ 1	6	5.40E-01	1.00E+00
	UP_SEQ_FEATURE	domain:PDZ 2	6	5.40E-01	1.00E+00
Annotation Cluster 264	**Enrichment Score: 0.44**		**Count**	**P_Value**	**Benjamini**
	BIOCARTA	Role of Erk5 in Neuronal Survival	7	2.50E-02	9.70E-01
	BIOCARTA	The IGF-1 Receptor and Longevity	5	1.50E-01	9.30E-01
	BIOCARTA	IL-2 Receptor Beta Chain in T cell Activation	10	1.70E-01	9.30E-01
	BIOCARTA	Regulation of BAD phosphorylation	6	2.60E-01	9.40E-01
	BIOCARTA	Inhibition of Cellular Proliferation by Gleevec	6	3.00E-01	9.60E-01
	BIOCARTA	Control of skeletal myogenesis by HDAC & calcium/calmodulin-dependent kinase (CaMK)	5	4.20E-01	9.70E-01
	BIOCARTA	Growth Hormone Signaling Pathway	6	4.30E-01	9.70E-01
	BIOCARTA	Human Cytomegalovirus and Map Kinase Pathways	4	5.30E-01	9.80E-01
	BIOCARTA	Trefoil Factors Initiate Mucosal Healing	5	6.40E-01	9.90E-01
	KEGG_PATHWAY	mTOR signaling pathway	7	8.10E-01	9.30E-01
	BIOCARTA	Phospholipids as signalling intermediaries	4	8.50E-01	1.00E+00
	BIOCARTA	NFAT and Hypertrophy of the heart (Transcription in the broken heart)	5	9.50E-01	1.00E+00
	KEGG_PATHWAY	Melanoma	7	9.70E-01	9.90E-01
Annotation Cluster 265	**Enrichment Score: 0.44**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	zinc finger region:RanBP2-type	4	3.40E-01	1.00E+00
	INTERPRO	Zinc finger, RanBP2-type	5	3.60E-01	1.00E+00
	SMART	ZnF_RBZ	5	3.90E-01	9.60E-01
Annotation Cluster 266	**Enrichment Score: 0.44**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	active site:S-palmitoyl cysteine intermediate	3	3.00E-01	1.00E+00
	UP_SEQ_FEATURE	zinc finger region:DHHC-type	5	3.90E-01	1.00E+00
	INTERPRO	Zinc finger, DHHC-type	5	4.20E-01	1.00E+00
Annotation Cluster 267	**Enrichment Score: 0.44**		**Count**	**P_Value**	**Benjamini**
	INTERPRO	S100/CaBP-9k-type, calcium binding, subdomain	6	2.50E-01	1.00E+00
	PIR_SUPERFAMILY	PIRSF002353:S-100 protein	5	2.50E-01	1.00E+00
	INTERPRO	S100/CaBP-9k-type, calcium binding	6	2.70E-01	1.00E+00
	SP_PIR_KEYWORDS	EF hand	10	2.90E-01	7.50E-01
	UP_SEQ_FEATURE	calcium-binding region:1; low affinity	3	6.60E-01	1.00E+00
	UP_SEQ_FEATURE	calcium-binding region:2; high affinity	3	7.40E-01	1.00E+00
Annotation Cluster 268	**Enrichment Score: 0.43**		**Count**	**P_Value**	**Benjamini**
	BIOCARTA	Roles of ?-arrestin-dependent Recruitment of Src Kinases in GPCR Signaling	6	2.60E-01	9.40E-01
	BIOCARTA	Role of ?-arrestins in the activation and targeting of MAP kinases	5	2.80E-01	9.50E-01
	BIOCARTA	?-arrestins in GPCR Desensitization	3	7.10E-01	1.00E+00
Annotation Cluster 269	**Enrichment Score: 0.43**		**Count**	**P_Value**	**Benjamini**
	GOTERM_MF_FAT	CARD domain binding	4	5.00E-02	6.10E-01
	UP_SEQ_FEATURE	domain:CARD	4	7.00E-01	1.00E+00
	INTERPRO	Caspase Recruitment	4	7.30E-01	1.00E+00
	SMART	CARD	4	7.60E-01	1.00E+00
Annotation Cluster 270	**Enrichment Score: 0.43**		**Count**	**P_Value**	**Benjamini**
	SP_PIR_KEYWORDS	zymogen	35	3.50E-02	2.30E-01
	GOTERM_BP_FAT	proteolysis	144	3.70E-01	9.60E-01
	SP_PIR_KEYWORDS	Protease	60	4.80E-01	8.80E-01
	GOTERM_MF_FAT	endopeptidase activity	50	4.80E-01	9.90E-01
	GOTERM_MF_FAT	serine-type peptidase activity	24	5.20E-01	9.90E-01
	GOTERM_MF_FAT	serine hydrolase activity	24	5.50E-01	1.00E+00
	GOTERM_MF_FAT	peptidase activity, acting on L-amino acid peptides	69	6.50E-01	1.00E+00
	GOTERM_MF_FAT	peptidase activity	72	6.60E-01	1.00E+00
Annotation Cluster 271	**Enrichment Score: 0.43**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	endochondral bone morphogenesis	5	1.50E-01	7.90E-01
	GOTERM_BP_FAT	bone morphogenesis	5	2.70E-01	9.20E-01
	GOTERM_BP_FAT	regulation of chondrocyte differentiation	4	2.80E-01	9.20E-01
	GOTERM_BP_FAT	endochondral ossification	3	4.80E-01	9.90E-01
	GOTERM_BP_FAT	cartilage development	10	6.50E-01	1.00E+00
	GOTERM_BP_FAT	bone development	15	7.60E-01	1.00E+00
Annotation Cluster 272	**Enrichment Score: 0.43**		**Count**	**P_Value**	**Benjamini**
	PIR_SUPERFAMILY	PIRSF002583:heat shock protein, HSP90/HTPG types	3	2.40E-01	1.00E+00
	INTERPRO	ATP-binding region, ATPase-like	6	3.30E-01	1.00E+00
	SMART	HATPase_c	6	3.60E-01	9.60E-01
	INTERPRO	Heat shock protein Hsp90	3	4.60E-01	1.00E+00
	SP_PIR_KEYWORDS	stress response	9	5.50E-01	9.20E-01
Annotation Cluster 273	**Enrichment Score: 0.43**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	negative regulation of protein kinase cascade	7	3.40E-01	9.50E-01
	GOTERM_BP_FAT	negative regulation of JNK cascade	3	3.90E-01	9.70E-01
	GOTERM_BP_FAT	negative regulation of stress-activated protein kinase signaling pathway	3	3.90E-01	9.70E-01
	GOTERM_BP_FAT	negative regulation of MAPKKK cascade	4	3.90E-01	9.70E-01
Annotation Cluster 274	**Enrichment Score: 0.42**		**Count**	**P_Value**	**Benjamini**
	INTERPRO	Synaptobrevin, metazoa/fungi	3	1.70E-01	9.90E-01
	PIR_SUPERFAMILY	PIRSF005409:Synaptobrevin_euk	3	1.90E-01	1.00E+00
	UP_SEQ_FEATURE	domain:v-SNARE coiled-coil homology	3	4.40E-01	1.00E+00
	INTERPRO	Synaptobrevin	3	4.60E-01	1.00E+00
	KEGG_PATHWAY	SNARE interactions in vesicular transport	7	5.20E-01	8.20E-01
	UP_SEQ_FEATURE	topological domain:Vesicular	4	8.70E-01	1.00E+00
Annotation Cluster 275	**Enrichment Score: 0.42**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	alpha-beta T cell differentiation	4	2.80E-01	9.20E-01
	GOTERM_BP_FAT	alpha-beta T cell activation	4	4.30E-01	9.80E-01
	GOTERM_BP_FAT	positive regulation of cytokine biosynthetic process	8	4.50E-01	9.80E-01

ILMN_1740305	DLEC1	-0.500020439
ILMN_1731326	PRR23C	-0.500174805
ILMN_2390318	CIDEA	-0.500190252
ILMN_1652037	UPP2	-0.500306247
ILMN_1709112	CHM	-0.500334664
ILMN_1656939	LOC400099	-0.500350912
ILMN_1793433	RAB10	-0.500374101
ILMN_3235340	ACER2	-0.500429574
ILMN_1725910	CNTFR	-0.500460777
ILMN_2389080	IL4	-0.500470675
ILMN_1707965	LOC100192378	-0.500476814
ILMN_1728803	HMP19	-0.500650058
ILMN_1744102	AK128005	-0.50076465
ILMN_1750092	SEPSECS	-0.500796234
ILMN_2249677	LSR	-0.500799466
ILMN_2288285	CDY1B	-0.500821579
ILMN_1757807	AGXT2L1	-0.500946964
ILMN_1910948	AK091312	-0.500962313
ILMN_1716524	RAB7A	-0.500969516
ILMN_1677311	AW665104	-0.501079047
ILMN_1904256	CR736208	-0.501175829
ILMN_1860487	DA196703	-0.50126068
ILMN_1703092	RECQL4	-0.501289048
ILMN_1658675	CDH23	-0.501301003
ILMN_3237044	SNORD36B	-0.501308836
ILMN_1889144	BI047056	-0.501335765
ILMN_1681612	DMBT1	-0.501355145
ILMN_2362293	FBXO38	-0.501368591
ILMN_1720838	DECR1	-0.501409463
ILMN_1751636	ANKS3	-0.501414166
ILMN_1733736	DKFZp434O171	-0.501418873
ILMN_3261382	TMEM221	-0.501427898
ILMN_1722753	GJA5	-0.501446578
ILMN_3301607	C13orf18	-0.50145178
ILMN_1763408	CCBL2	-0.501464134
ILMN_1809456	CNTFR	-0.501489139
ILMN_2178116	MMP20	-0.501491544
ILMN_1733675	MPP1	-0.501546967
ILMN_3238854	RGPD8	-0.50156417
ILMN_1811178	SCAPER	-0.50162557
ILMN_1677734	WFDC9	-0.501635867
ILMN_1678437	FRY	-0.501709647
ILMN_2126055	ASB5	-0.501799086
ILMN_1720998	CA12	-0.501938692
ILMN_1800253	ZNF711	-0.502077217
ILMN_2372316	PKD1L2	-0.502252429
ILMN_1651966	FGFR3	-0.502280151
ILMN_2187830	CCNH	-0.502367249
ILMN_1780894	ANTXR1	-0.502368544
ILMN_1767503	GABRB3	-0.502384548
ILMN_1793367	LOC729966	-0.502430667
ILMN_1704134	NA	-0.502468582
ILMN_1737152	DAO	-0.502471485
ILMN_1796240	TRAPPC8	-0.502484582
ILMN_1788005	PLEC	-0.502554764
ILMN_1681367	ZNF642	-0.502606215
ILMN_1731644	SETDB2	-0.502630714
ILMN_1849206	DA724733	-0.50286743
ILMN_1808715	LOC389300	-0.502884306
ILMN_2153029	CGB5	-0.502896108
ILMN_1687589	CPT1A	-0.502970028
ILMN_1678493	CHN1	-0.502990482
ILMN_1794890	SLC38A4	-0.503000428
ILMN_1743131	TOX4	-0.503080498
ILMN_1704354	NCDN	-0.503166276
ILMN_1865078	AL832552	-0.503187368
ILMN_3292840	NA	-0.503234567
ILMN_1849134	BQ012728	-0.503244928
ILMN_1789395	OR9G1	-0.503280638
ILMN_1799985	C13orf40	-0.503298404
ILMN_1778617	TAF9	-0.503302636
ILMN_1684114	LOC286016	-0.50334899
ILMN_3250879	ANGPT2	-0.50342157
ILMN_1771019	MTMR4	-0.503485974
ILMN_1732127	RBKS	-0.503542201
ILMN_1715476	CKMT1B	-0.503558061
ILMN_1717869	BF355127	-0.503581393
ILMN_1695378	SREBF1	-0.503588982
ILMN_3232949	FAM71E2	-0.503604646
ILMN_3308515	SNORD116-13	-0.503673201
ILMN_1726327	AMY1A	-0.503719381
ILMN_1761946	PROM2	-0.503744174
ILMN_2406106	CACNB2	-0.503758297
ILMN_1748147	MTO1	-0.50376076
ILMN_3202710	AK126532	-0.50379613
ILMN_3251375	WBP11P1	-0.503904017
ILMN_1739751	SLC26A11	-0.503933397
ILMN_1821352	BX096603	-0.503971916
ILMN_2128358	TPP2	-0.503983841
ILMN_1736490	BC156836	-0.504065871
ILMN_1677845	RTL1	-0.504179241
ILMN_2193980	ABCB6	-0.504210152
ILMN_1678919	YOD1	-0.504221555
ILMN_1888558	AI378936	-0.504317515

ILMN_1753345	SCAMP5	0.590758952
ILMN_1741674	PPP1R9A	0.590629022
ILMN_1652445	RAC1	0.590518176
ILMN_1713985	MAF1	0.590351914
ILMN_2390472	TTC14	0.590257967
ILMN_1751028	SERPINH1	0.590117785
ILMN_1703564	DYNLRB1	0.590117538
ILMN_1669286	YWHAZ	0.59004677
ILMN_1806408	ACADVL	0.590043141
ILMN_3297644	TMEM214	0.590041971
ILMN_1757757	TM6SF2	0.590019798
ILMN_1805796	FLYWCH2	0.589967161
ILMN_2355549	GSTT2B	0.589948059
ILMN_1794726	RNF167	0.589934921
ILMN_3231621	LOC349114	0.5898661
ILMN_2221808	KIAA1647	0.589782298
ILMN_1679178	ATP5D	0.589758601
ILMN_1682099	TNFAIP8L3	0.589710944
ILMN_2379718	RAB24	0.589480592
ILMN_1739618	ZNF408	0.589416408
ILMN_1690034	SOD3	0.589350703
ILMN_1752285	RPL4	0.589153595
ILMN_2352574	ZNF274	0.589152035
ILMN_1793672	SIX5	0.588906287
ILMN_1795400	TBCD	0.58875539
ILMN_1796712	S100A10	0.588572803
ILMN_1754579	SYNE2	0.588513368
ILMN_1793017	DGKQ	0.588422207
ILMN_1687538	ETS1	0.588272491
ILMN_2403889	PRMT5	0.588156371
ILMN_3226467	AK023375	0.588112626
ILMN_1669842	CHAF1A	0.588112356
ILMN_3225634	RPL21	0.588027769
ILMN_2087080	RPL5	0.588005479
ILMN_1771697	VRK3	0.587932698
ILMN_1757914	C19orf56	0.587768615
ILMN_1757370	SMPD1	0.587614508
ILMN_1692849	ANKRD58	0.587599521
ILMN_1774259	FAM63B	0.587582795
ILMN_1653718	ZFAND2B	0.58757834
ILMN_1675612	BLCAP	0.587577099
ILMN_1699711	DEDD	0.587552608
ILMN_2368713	UBE2V1	0.587546277
ILMN_3238018	NA	0.587534546
ILMN_1663390	CDC20	0.58741237
ILMN_1751803	LSM10	0.587321385
ILMN_1656042	KIAA0319L	0.587303036
ILMN_1735594	CDC42SE2	0.587123994
ILMN_3237946	PXDN	0.587091132
ILMN_1701875	ZYX	0.587077588
ILMN_1757019	NTN4	0.586987923
ILMN_1700674	RPL23AP53	0.586936042
ILMN_2339655	MAPK7	0.586890573
ILMN_1709042	RBM4	0.586240268
ILMN_1806733	COL18A1	0.586231118
ILMN_2399208	SCAMP3	0.586092806
ILMN_2333594	SUMO2	0.586066717
ILMN_1805200	DNM1	0.585722076
ILMN_1756126	STUB1	0.585716818
ILMN_1747499	EMID1	0.585677357
ILMN_1705602	KLHL17	0.585496213
ILMN_2261600	FCGR1B	0.585489826
ILMN_3239284	B9D1	0.585467467
ILMN_1675048	IGF1R	0.585431802
ILMN_1740505	SGMS1	0.585396633
ILMN_1696420	BRD7	0.585115196
ILMN_1779015	ZNF467	0.585022866
ILMN_1762608	EPG5	0.584995895
ILMN_2369018	EVI2A	0.584911703
ILMN_1682312	CYBB	0.584603609
ILMN_1775304	DNAJB1	0.584494301
ILMN_1754179	AP1G2	0.58446575
ILMN_1652331	LOC652276	0.584330705
ILMN_1657771	CRTC2	0.584320811
ILMN_1700047	ALAS1	0.584320176
ILMN_3306742	SIGMAR1	0.584257475
ILMN_3237966	KIAA1004	0.584178941
ILMN_1728009	TMEM171	0.584157147
ILMN_1712639	AIFM2	0.584127333
ILMN_1765833	SLC9A3R2	0.584054185
ILMN_1722622	CD163	0.584036946
ILMN_1808712	RNF40	0.584013114
ILMN_1747504	AHCTF1	0.583885626
ILMN_1695821	ACTR1B	0.583828644
ILMN_1709953	DONSON	0.583715903
ILMN_2336728	DLG3	0.58366225
ILMN_3241756	FAM136A	0.583661301
ILMN_1741404	MSC	0.583638945
ILMN_3250147	ZNF626	0.583619525
ILMN_2049417	TMEM86B	0.583571334
ILMN_2391931	SLC35A2	0.583469731
ILMN_1691736	ST6GALNAC6	0.583441936
ILMN_2406873	ARFGAP1	0.583440004
ILMN_1684183	RAD9A	0.583268412
ILMN_1774596	BSCL2	0.583261012

Annotation Cluster 276	**Enrichment Score: 0.42**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	positive regulation of endocytosis	7	1.70E-01	8.30E-01
	GOTERM_BP_FAT	positive regulation of phagocytosis	3	4.80E-01	9.90E-01
	GOTERM_BP_FAT	regulation of phagocytosis	3	6.40E-01	1.00E+00
Annotation Cluster 277	**Enrichment Score: 0.42**		**Count**	**P_Value**	**Benjamini**
	SP_PIR_KEYWORDS	selenium	6	3.20E-01	7.70E-01
	GOTERM_MF_FAT	selenium binding	6	3.90E-01	9.80E-01
	SP_PIR_KEYWORDS	selenocysteine	5	4.40E-01	8.60E-01
Annotation Cluster 278	**Enrichment Score: 0.42**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	repeat:3-3	3	1.60E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:3-2	3	2.00E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:3-1	3	2.00E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:1-2	5	3.90E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:1-1	5	4.20E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:2-1	4	6.00E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:1-4	3	6.30E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:2-2	4	6.50E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:1-3	3	6.60E-01	1.00E+00
Annotation Cluster 279	**Enrichment Score: 0.42**		**Count**	**P_Value**	**Benjamini**
	INTERPRO	Single-stranded nucleic acid binding R3H	3	3.70E-01	1.00E+00
	SMART	R3H	3	3.90E-01	9.70E-01
	UP_SEQ_FEATURE	domain:R3H	3	3.90E-01	1.00E+00
Annotation Cluster 280	**Enrichment Score: 0.42**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	immunoglobulin production	7	2.00E-01	8.60E-01
	GOTERM_BP_FAT	production of molecular mediator of immune response	7	2.20E-01	8.80E-01
	GOTERM_BP_FAT	somatic diversification of immune receptors	6	2.80E-01	9.30E-01
	GOTERM_BP_FAT	somatic diversification of immunoglobulins	5	3.30E-01	9.50E-01
	GOTERM_BP_FAT	somatic hypermutation of immunoglobulin genes	3	3.40E-01	9.50E-01
	GOTERM_BP_FAT	somatic diversification of immune receptors via somatic mutation	3	3.40E-01	9.50E-01
	GOTERM_BP_FAT	immunoglobulin production during immune response	3	5.30E-01	9.90E-01
	GOTERM_BP_FAT	somatic cell DNA recombination	4	6.30E-01	1.00E+00
	GOTERM_BP_FAT	somatic diversification of immune receptors via germline recombination within a single locus	4	6.30E-01	1.00E+00
	GOTERM_BP_FAT	somatic recombination of immunoglobulin gene segments	3	7.10E-01	1.00E+00
Annotation Cluster 281	**Enrichment Score: 0.42**		**Count**	**P_Value**	**Benjamini**
	INTERPRO	26S proteasome subunit P45	3	2.20E-01	1.00E+00
	INTERPRO	ATPase, AAA-type, conserved site	6	4.30E-01	1.00E+00
	INTERPRO	ATPase, AAA-type, core	7	6.00E-01	1.00E+00
Annotation Cluster 282	**Enrichment Score: 0.42**		**Count**	**P_Value**	**Benjamini**
	INTERPRO	CS domain	4	3.30E-01	1.00E+00
	INTERPRO	CS	4	3.30E-01	1.00E+00
	UP_SEQ_FEATURE	domain:CS	3	5.20E-01	1.00E+00
Annotation Cluster 283	**Enrichment Score: 0.42**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	regulation of cell-cell adhesion	5	3.30E-01	9.50E-01
	GOTERM_BP_FAT	negative regulation of cell-cell adhesion	3	3.40E-01	9.50E-01
	GOTERM_BP_FAT	negative regulation of cell adhesion	7	5.10E-01	9.90E-01
Annotation Cluster 284	**Enrichment Score: 0.42**		**Count**	**P_Value**	**Benjamini**
	GOTERM_MF_FAT	deoxyribonuclease activity	9	6.20E-02	6.70E-01
	GOTERM_MF_FAT	nuclease activity	24	2.90E-01	9.60E-01
	SP_PIR_KEYWORDS	nuclease	15	4.00E-01	8.30E-01
	SP_PIR_KEYWORDS	Endonuclease	8	6.60E-01	9.60E-01
	GOTERM_MF_FAT	endonuclease activity	12	7.50E-01	1.00E+00
	GOTERM_MF_FAT	endoribonuclease activity	5	8.70E-01	1.00E+00
Annotation Cluster 285	**Enrichment Score: 0.41**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	repeat:UIM 2	4	2.70E-01	1.00E+00
	UP_SEQ_FEATURE	repeat:UIM 1	4	2.70E-01	1.00E+00
	INTERPRO	Ubiquitin interacting motif	4	5.40E-01	1.00E+00
	SMART	UIM	4	5.70E-01	9.90E-01
Annotation Cluster 286	**Enrichment Score: 0.41**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	domain:AGC-kinase C-terminal	9	3.50E-01	1.00E+00
	INTERPRO	AGC-kinase, C-terminal	9	3.90E-01	1.00E+00
	INTERPRO	Protein kinase, C-terminal	7	3.90E-01	1.00E+00
	SMART	S_TK_X	9	4.40E-01	9.70E-01
Annotation Cluster 287	**Enrichment Score: 0.4**		**Count**	**P_Value**	**Benjamini**
	PIR_SUPERFAMILY	PIRSF000735:nucleoside diphosphate kinase	3	9.10E-02	1.00E+00
	UP_SEQ_FEATURE	active site:Pros-phosphohistidine intermediate	3	1.60E-01	1.00E+00
	GOTERM_BP_FAT	GTP metabolic process	4	2.00E-01	8.70E-01
	SP_PIR_KEYWORDS	nucleotide metabolism	5	2.10E-01	6.40E-01
	INTERPRO	Nucleoside diphosphate kinase, core	3	2.70E-01	1.00E+00
	SMART	NDK	3	2.90E-01	9.40E-01
	GOTERM_MF_FAT	nucleoside diphosphate kinase activity	3	3.30E-01	9.70E-01
	GOTERM_BP_FAT	GTP biosynthetic process	3	3.40E-01	9.50E-01
	GOTERM_BP_FAT	UTP metabolic process	3	3.40E-01	9.50E-01
	GOTERM_BP_FAT	UTP biosynthetic process	3	3.40E-01	9.50E-01
	GOTERM_BP_FAT	pyrimidine ribonucleoside triphosphate biosynthetic process	3	3.90E-01	9.70E-01
	GOTERM_BP_FAT	pyrimidine ribonucleoside triphosphate metabolic process	3	3.90E-01	9.70E-01
	GOTERM_BP_FAT	CTP metabolic process	3	3.90E-01	9.70E-01
	GOTERM_BP_FAT	CTP biosynthetic process	3	3.90E-01	9.70E-01
	GOTERM_BP_FAT	pyrimidine nucleoside triphosphate biosynthetic process	3	4.80E-01	9.90E-01
	GOTERM_BP_FAT	pyrimidine nucleoside triphosphate metabolic process	3	5.70E-01	9.90E-01
	GOTERM_BP_FAT	pyrimidine ribonucleotide biosynthetic process	3	6.10E-01	1.00E+00
	GOTERM_MF_FAT	phosphotransferase activity, phosphate group as acceptor	5	6.30E-01	1.00E+00
	GOTERM_BP_FAT	pyrimidine ribonucleotide metabolic process	3	6.40E-01	1.00E+00
	GOTERM_MF_FAT	nucleobase, nucleoside, nucleotide kinase activity	6	6.60E-01	1.00E+00
	GOTERM_BP_FAT	pyrimidine ribonucleoside metabolic process	3	6.80E-01	1.00E+00
	GOTERM_BP_FAT	pyrimidine nucleotide metabolic process	5	7.20E-01	1.00E+00
	GOTERM_BP_FAT	pyrimidine nucleotide biosynthetic process	3	8.10E-01	1.00E+00
	GOTERM_BP_FAT	pyrimidine nucleoside metabolic process	3	8.60E-01	1.00E+00
Annotation Cluster 288	**Enrichment Score: 0.4**		**Count**	**P_Value**	**Benjamini**
	GOTERM_MF_FAT	ligand-dependent nuclear receptor transcription coactivator activity	8	1.70E-01	8.90E-01
	GOTERM_MF_FAT	vitamin D receptor binding	5	3.40E-01	9.70E-01
	GOTERM_MF_FAT	thyroid hormone receptor activator activity	3	4.20E-01	9.90E-01
	GOTERM_MF_FAT	thyroid hormone receptor coactivator activity	3	4.20E-01	9.90E-01
	GOTERM_MF_FAT	receptor regulator activity	5	5.50E-01	1.00E+00
	GOTERM_MF_FAT	receptor activator activity	3	6.60E-01	1.00E+00
Annotation Cluster 289	**Enrichment Score: 0.4**		**Count**	**P_Value**	**Benjamini**

ILMN_3283869	FRG1B	-0.504418056
ILMN_1689380	FBXO44	-0.504462622
ILMN_1749822	TSG1	-0.504471861
ILMN_1774617	NAB1	-0.504509169
ILMN_2071405	FBXL3	-0.504582884
ILMN_2277246	SDCBP2	-0.50468522
ILMN_2155816	DIRAS2	-0.504725846
ILMN_1692790	ITGB3BP	-0.504731483
ILMN_1891311	AA744242	-0.504731716
ILMN_2149292	TMEM40	-0.504769301
ILMN_1678312	DQ577523	-0.504790052
ILMN_1839750	NA	-0.504847741
ILMN_3241149	TMEM236	-0.504931745
ILMN_1665647	CD180	-0.504976282
ILMN_2092903	C20orf141	-0.505017183
ILMN_1750246	ZBTB1	-0.505081211
ILMN_1717168	PCDHGC3	-0.505165696
ILMN_2338849	BIRC7	-0.505173292
ILMN_1651495	BG620193	-0.505197916
ILMN_1758093	C14orf101	-0.505256042
ILMN_1666371	LOC648691	-0.505292078
ILMN_1837692	BF514454	-0.505393678
ILMN_1691339	CLEC1A	-0.50541832
ILMN_1788122	GSTA5	-0.505440943
ILMN_3239925	LOC25845	-0.505470946
ILMN_2192316	TOP1	-0.505474113
ILMN_1673537	WFDC3	-0.505544985
ILMN_1882519	DA375949	-0.505605368
ILMN_1720710	HSPB3	-0.505614628
ILMN_1789407	CDRT4	-0.505637331
ILMN_1701058	TATDN1	-0.505692451
ILMN_1699912	SPDYE7P	-0.50569306
ILMN_1686083	MAGEA11	-0.505733544
ILMN_1800697	LDB2	-0.505750611
ILMN_1812473	MLLT3	-0.505793252
ILMN_1682208	CACNB2	-0.505800295
ILMN_3309219	MIR940	-0.50591876
ILMN_1687291	CDNF	-0.505970514
ILMN_3201026	LOC283028	-0.505989615
ILMN_1764607	UGT1A1	-0.506011614
ILMN_1780357	PRRT1	-0.506035317
ILMN_1690693	CTPS2	-0.506115613
ILMN_3250049	SLX1B-SULT1A4	-0.506115881
ILMN_1660307	BC073927	-0.506118462
ILMN_1736078	THBS4	-0.506187408
ILMN_1655613	GSTA2	-0.506250387
ILMN_1678671	KLHL24	-0.506256116
ILMN_2356838	CEPT1	-0.506402248
ILMN_1667201	POC1B	-0.506411454
ILMN_1750724	ZNF879	-0.506459148
ILMN_3310371	MIR939	-0.506650607
ILMN_2323385	TRIM4	-0.506815613
ILMN_1810210	DACH2	-0.506844006
ILMN_1815599	FOXE3	-0.506883389
ILMN_1656915	PSD3	-0.506892145
ILMN_2244631	STEAP1	-0.507217322
ILMN_1668779	GPR17	-0.507265127
ILMN_3309059	MIR93	-0.507271921
ILMN_3246826	AQPEP	-0.507419289
ILMN_1811954	NRG1	-0.507434765
ILMN_2149053	RIF1	-0.507451582
ILMN_3308190	MIR641	-0.507556841
ILMN_1767142	ZNF280D	-0.507647473
ILMN_1700762	PBX4	-0.507694577
ILMN_1857067	BX113978	-0.507727174
ILMN_1855107	AW592785	-0.507733326
ILMN_1721011	LCN1	-0.507737077
ILMN_3250032	XPR1	-0.507775456
ILMN_1732981	ZBTB32	-0.507790524
ILMN_2379560	CDC14B	-0.507796608
ILMN_1792383	PFN4	-0.507881276
ILMN_1812678	AGMO	-0.507891165
ILMN_1720606	LRCH2	-0.507917489
ILMN_1840806	BX105881	-0.507935421
ILMN_1690733	EGF	-0.507992945
ILMN_3310176	MIR593	-0.508058914
ILMN_1825067	AW665831	-0.508074029
ILMN_2231436	FAM26D	-0.508119229
ILMN_1705153	NEFH	-0.508137843
ILMN_3253599	FIS	-0.508169014
ILMN_1894388	NA	-0.508186395
ILMN_1699576	CDON	-0.508231246
ILMN_3242507	BX282781	-0.508232021
ILMN_1728512	YWHAH	-0.508269254
ILMN_1653031	ZNF580	-0.508273812
ILMN_1681032	C16orf54	-0.508332082
ILMN_1651599	ENTPD2	-0.508369318
ILMN_1784870	CES5A	-0.508402391
ILMN_1755741	DACH1	-0.508424037
ILMN_1806633	LOC348926	-0.508486526
ILMN_3250077	EIF4E	-0.508658524
ILMN_1660007	CCDC155	-0.508674308
ILMN_1696450	KLK1	-0.508823651
ILMN_2072401	OR11H1	-0.508837063
ILMN_1672545	GIPC2	-0.508837445

ILMN_2199284	ANAPC7	0.583244201
ILMN_1812526	TGFB2	0.583193342
ILMN_1654195	GCC2	0.58318603
ILMN_3243859	NDUFB9	0.583161978
ILMN_1824052	AA909514	0.583128652
ILMN_1708900	TMEM161A	0.583087238
ILMN_1699737	TRAP1	0.582973377
ILMN_2103388	ZBTB49	0.582972897
ILMN_1708451	PIGP	0.582964946
ILMN_2371053	EFNA1	0.582640507
ILMN_3200322	TOMM20	0.582635134
ILMN_1657194	TSNAXIP1	0.582601218
ILMN_2390114	AP3D1	0.582578054
ILMN_1748290	FAM175A	0.582386104
ILMN_1695983	DDX42	0.582262468
ILMN_1668535	JOSD1	0.5822163
ILMN_1806956	ATAD5	0.58211571
ILMN_1698067	NBPF1	0.582064201
ILMN_3240721	TDG	0.582058646
ILMN_1792681	CCDC86	0.581826461
ILMN_2147078	PIWIL4	0.581793283
ILMN_1669032	PPIC	0.581734773
ILMN_1659158	SAMD3	0.581671553
ILMN_1666910	GAB1	0.581634872
ILMN_1698766	PYCARD	0.581578172
ILMN_1652198	CCM2	0.58139921
ILMN_2402556	ZHX1	0.581386367
ILMN_1797451	SRGAP2P2	0.581380395
ILMN_1738326	EIF4E2	0.58134671
ILMN_1744109	OR2A42	0.581282412
ILMN_2345908	DDX11	0.581238322
ILMN_1684699	ELF5	0.581168634
ILMN_1754839	DHX15	0.581080154
ILMN_1807662	IGF2R	0.581018055
ILMN_1761788	MOXD1	0.581016538
ILMN_1690494	RPL6	0.58095219
ILMN_2243912	RAB37	0.580889438
ILMN_1764456	TECPR2	0.580762009
ILMN_3208881	SETD8	0.580551373
ILMN_1656807	RPL27	0.580496793
ILMN_1656017	NRF1	0.580485281
ILMN_1742824	SPATA13	0.580205101
ILMN_2087646	HLX	0.580169992
ILMN_1717063	FBXO9	0.580124518
ILMN_1673638	RPS3A	0.580076467
ILMN_3243890	NDUFA2	0.580005505
ILMN_1816342	MTRNR2L1	0.579994594
ILMN_1675979	RBMS3	0.579910656
ILMN_1778064	FICD	0.57990717
ILMN_1740900	BMP4	0.579864036
ILMN_2093343	PLAC8	0.579654265
ILMN_2317658	SLC3A2	0.579638798
ILMN_1696814	SEPSECS	0.579541657
ILMN_2327947	SLC25A25	0.579425099
ILMN_1793563	DCTN1	0.579402523
ILMN_2308582	CYB5R3	0.579374741
ILMN_3183573	NA	0.579366133
ILMN_1794374	PER2	0.579321984
ILMN_1669674	CNPY3	0.579200192
ILMN_1666894	CSPG4	0.57918953
ILMN_2398711	SIRT2	0.579189159
ILMN_1676213	SRPX2	0.579188757
ILMN_2300695	IKZF3	0.579132176
ILMN_1698323	PLEKHB2	0.579119712
ILMN_1711368	TRAPPC9	0.579019574
ILMN_1749752	GAR1	0.578980616
ILMN_1666280	COX11	0.578877596
ILMN_1731609	CHMP6	0.578875738
ILMN_1695792	CUL4A	0.578854416
ILMN_1715674	ITPK1	0.578848896
ILMN_1664294	LEPRE1	0.57852179
ILMN_1704383	TRIM37	0.578495202
ILMN_1762260	C3	0.578448725
ILMN_1703153	GLYR1	0.578371372
ILMN_1791754	CPT1B	0.578284899
ILMN_1759952	PSMA5	0.578211504
ILMN_1685202	KRBA2	0.57816883
ILMN_1743130	PTGFRN	0.57808104
ILMN_1717565	CLEC18A	0.577776739
ILMN_1768969	LBR	0.577725289
ILMN_1734895	SFT2D1	0.577550675
ILMN_1798006	ANKRD35	0.577532433
ILMN_1759789	KAT5	0.577526783
ILMN_1763640	NCKAP5L	0.577469662
ILMN_2173919	MYO9A	0.577469554
ILMN_1756937	ST8SIA4	0.577436823
ILMN_3235984	FLJ45340	0.577394705
ILMN_1803624	TMEM147	0.577355314
ILMN_1673604	YIPF3	0.577327078
ILMN_2411897	KLF10	0.577230304
ILMN_2311674	ADCY6	0.577174644
ILMN_1689786	ASMTL	0.576994755
ILMN_1813840	KDM1A	0.57678522
ILMN_1651229	IPO13	0.576587199
ILMN_2133638	CTDNEP1	0.576556523
ILMN_1668249	LMF1	0.576524858
ILMN_1682864	SPSB3	0.576477684
ILMN_2124951	RBMX	0.576463745

	UP_SEQ_FEATURE	domain:GST C-terminal	7	2.00E-01	1.00E+00
	INTERPRO	Glutathione S-transferase, N-terminal	5	3.00E-01	1.00E+00
	UP_SEQ_FEATURE	domain:GST N-terminal	4	4.80E-01	1.00E+00
	INTERPRO	Glutathione S-transferase, C-terminal	4	5.00E-01	1.00E+00
	INTERPRO	Glutathione S-transferase, C-terminal-like	5	5.10E-01	1.00E+00
	INTERPRO	Glutathione S-transferase/chloride channel, C-terminal	5	5.30E-01	1.00E+00
Annotation Cluster 290	**Enrichment Score: 0.4**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	cell fate specification	11	1.30E-01	7.50E-01
	GOTERM_BP_FAT	dorsal/ventral neural tube patterning	4	2.80E-01	9.20E-01
	GOTERM_BP_FAT	neural tube patterning	4	5.40E-01	9.90E-01
	GOTERM_BP_FAT	neural tube development	10	5.50E-01	9.90E-01
	GOTERM_BP_FAT	dorsal/ventral pattern formation	5	9.60E-01	1.00E+00
Annotation Cluster 291	**Enrichment Score: 0.39**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	mitochondrial transport	12	3.00E-01	9.30E-01
	GOTERM_BP_FAT	protein localization in mitochondrion	6	4.70E-01	9.80E-01
	GOTERM_BP_FAT	protein targeting to mitochondrion	6	4.70E-01	9.80E-01
Annotation Cluster 292	**Enrichment Score: 0.39**		**Count**	**P_Value**	**Benjamini**
	INTERPRO	Chromo domain	6	3.80E-01	1.00E+00
	SMART	CHROMO	6	4.20E-01	9.70E-01
	UP_SEQ_FEATURE	domain:Chromo 1	3	4.40E-01	1.00E+00
Annotation Cluster 293	**Enrichment Score: 0.39**		**Count**	**P_Value**	**Benjamini**
	UP_SEQ_FEATURE	domain:CBS 1	4	3.70E-01	1.00E+00
	UP_SEQ_FEATURE	domain:CBS 2	4	3.70E-01	1.00E+00
	SP_PIR_KEYWORDS	CBS domain	4	4.10E-01	8.40E-01
	INTERPRO	Cystathionine beta-synthase, core	4	4.40E-01	1.00E+00
	SMART	CBS	4	4.70E-01	9.70E-01
Annotation Cluster 294	**Enrichment Score: 0.39**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	chromosome condensation	7	1.00E-01	6.90E-01
	GOTERM_BP_FAT	mitotic chromosome condensation	3	5.30E-01	9.90E-01
	GOTERM_BP_FAT	mitotic sister chromatid segregation	5	7.20E-01	1.00E+00
	GOTERM_BP_FAT	sister chromatid segregation	5	7.40E-01	1.00E+00
Annotation Cluster 295	**Enrichment Score: 0.39**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	cell morphogenesis involved in differentiation	37	2.60E-01	9.10E-01
	GOTERM_BP_FAT	cellular component morphogenesis	58	2.70E-01	9.20E-01
	GOTERM_BP_FAT	cell morphogenesis	52	2.80E-01	9.30E-01
	GOTERM_BP_FAT	neuron projection morphogenesis	32	3.00E-01	9.40E-01
	GOTERM_BP_FAT	cell part morphogenesis	37	3.70E-01	9.60E-01
	GOTERM_BP_FAT	cell projection organization	52	3.80E-01	9.60E-01
	GOTERM_BP_FAT	neuron projection development	36	4.40E-01	9.80E-01
	GOTERM_BP_FAT	axon guidance	16	4.40E-01	9.80E-01
	GOTERM_BP_FAT	cell projection morphogenesis	34	4.80E-01	9.80E-01
	GOTERM_BP_FAT	axonogenesis	27	4.90E-01	9.90E-01
	GOTERM_BP_FAT	neuron development	45	5.70E-01	9.90E-01
	GOTERM_BP_FAT	cell morphogenesis involved in neuron differentiation	27	6.60E-01	1.00E+00
	GOTERM_BP_FAT	neuron differentiation	56	6.80E-01	1.00E+00
Annotation Cluster 296	**Enrichment Score: 0.38**		**Count**	**P_Value**	**Benjamini**
	INTERPRO	Phosphoinositide 3-kinase accessory region PIK	3	3.70E-01	1.00E+00
	SMART	PI3Ka	3	3.90E-01	9.70E-01
	GOTERM_MF_FAT	inositol or phosphatidylinositol kinase activity	6	5.30E-01	9.90E-01
Annotation Cluster 297	**Enrichment Score: 0.37**		**Count**	**P_Value**	**Benjamini**
	GOTERM_BP_FAT	cell chemotaxis	8	2.50E-01	9.10E-01
	GOTERM_BP_FAT	leukocyte migration	10	3.40E-01	9.50E-01
	GOTERM_BP_FAT	leukocyte chemotaxis	6	5.50E-01	9.90E-01
	GOTERM_BP_FAT	neutrophil chemotaxis	3	7.10E-01	1.00E+00

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