

**Supplementary Table 1 : Transcripts and pathways up-regulated in SLE compared to control renal biopsies**

Differences in (Log2-transformed, mean-centered) gene expression between lupus and control biopsies were analyzed using a moderated t test with Benjamini-Hochberg correction for multiple comparisons (*p* value threshold set to 0.05). Pathway analyses were performed using DAVID software. Enrichment scores are  $-\log_{10} p$  values, calculated by modified Fisher Exact test by comparing proportions of transcripts belonging to a given pathway in the tested gene list compared to the whole transcriptome.[14, 15]

**Transcripts**

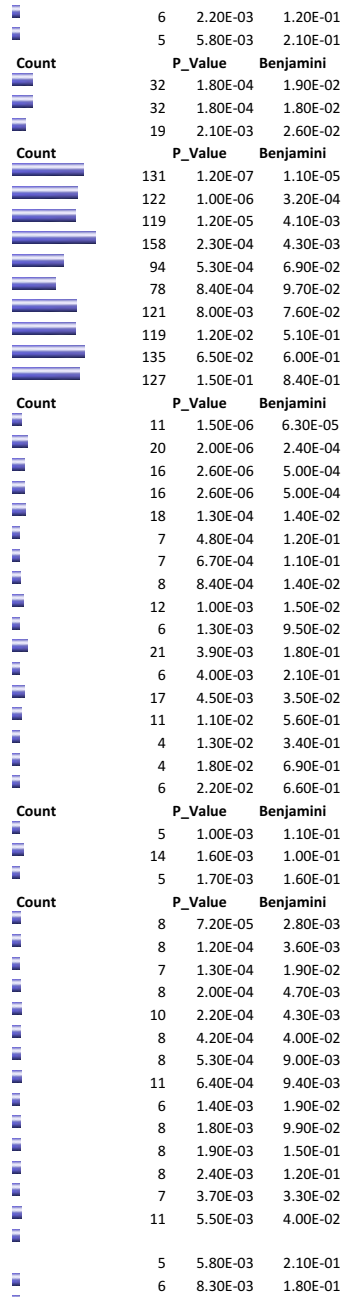
Identifier	[Control]	[SLE]	Gene Symbol
ILMN_2054019	-1.8367431	0.8733817	ISG15
ILMN_3240375	-1.9034421	0.8672207	abParts
ILMN_1739508	-1.7163734	0.8066571	abParts
ILMN_2103107	-1.8484101	0.6729792	ADAMDEC1
ILMN_1778977	-0.7100609	0.62325823	TYROBP
ILMN_1704286	-0.7749682	0.619152	FXD5
ILMN_2170814	-2.5021515	0.6106421	LAMP3
ILMN_1680274	-1.6995718	0.5754184	abParts
ILMN_1652199	-1.6970621	0.57067966	abParts
ILMN_2083066	-2.5462198	0.5612969	IGLL3P
ILMN_1674228	-0.9006702	0.55473113	abParts
ILMN_1659913	-0.8059585	0.5446736	ISG20
ILMN_1672606	-0.7296701	0.5338008	OAS1
ILMN_1695851	-0.8407382	0.532421	PARVG
ILMN_2146766	-0.7411417	0.5317069	FABP5
ILMN_1696302	-0.8049086	0.5251267	FABP5
ILMN_1886655	-1.267512	0.5189515	TCRVB
ILMN_1752899	-0.6961275	0.518324	BCL11A
ILMN_2325837	-0.9341917	0.5164521	CD3D
ILMN_1779852	-0.8254615	0.5040414	FABP5L3
ILMN_1754507	-2.2113416	0.4878948	IRF4
ILMN_1682993	-0.8189868	0.48173356	NKG7
ILMN_1714602	-1.0103395	0.46908656	CD86
ILMN_1710734	-0.9052631	0.45434737	GZMK
ILMN_1791759	-1.2359245	0.45214474	CXCL10
ILMN_1801246	-1.8158823	0.44969594	IFITM1
ILMN_1677505	-0.8335129	0.4461307	CCL21
ILMN_2231928	-2.2008712	0.4434064	MX2
ILMN_2375825	-0.4494968	0.44047216	CD37
ILMN_1719759	-1.0855303	0.43799433	TNC
ILMN_1790761	-1.575065	0.43785053	POSTN
ILMN_2232121	-1.0042269	0.43288076	GPR65
ILMN_2135272	-0.969066	0.43147218	GIMAP2
ILMN_1728106	-1.2595581	0.4270727	TNF
ILMN_3249667	-0.7323164	0.42657584	HLA-DQA1
ILMN_2254635	-2.3059683	0.41904867	ITGAX
ILMN_3266606	-1.1168858	0.4060247	FABP5
ILMN_2208903	-0.7734711	0.38791603	CD52
ILMN_1769229	-1.2805104	0.38425326	BCL2A1
ILMN_1787509	-0.9047725	0.3832354	PRIC285
ILMN_2179083	-0.9967498	0.3825167	LOXL4
ILMN_1749006	-0.8976072	0.37745827	RCS1
ILMN_2061043	-1.1870687	0.37040937	CD48
ILMN_1758067	-1.4429107	0.367198	RG54
ILMN_1806908	-1.0466263	0.36677915	PRKCB
ILMN_1662843	-1.2426662	0.36529452	CD53
ILMN_1682312	-0.6436449	0.3637218	CYBB
ILMN_1798181	-1.2807904	0.35389298	IRF7
ILMN_1780368	-1.1570473	0.35253793	GPR18
ILMN_1693452	-1.0383923	0.35075316	GAL3ST4

**Pathways**

Annotation Cluster	Enrichment Score	Count	P_Value	Benjamini
Annotation Cluster 1	Enrichment Score: 8.52	GOTERM_BP_FAT	<a href="#">defense response</a>	42 2.20E-10 1.60E-07
		GOTERM_BP_FAT	<a href="#">response to wounding</a>	38 5.10E-10 2.70E-07
		GOTERM_BP_FAT	<a href="#">inflammatory response</a>	25 2.40E-07 6.40E-05
Annotation Cluster 2	Enrichment Score: 6.1	SP_PIR_KEYWORDS	<a href="#">signal</a>	115 1.90E-10 6.90E-08
		UP_SEQ_FEATURE	signal peptide	115 2.80E-10 3.70E-07
		SP_PIR_KEYWORDS	<a href="#">disulfide bond</a>	102 7.20E-09 8.90E-07
		UP_SEQ_FEATURE	disulfide bond	98 2.70E-08 1.80E-05
		SP_PIR_KEYWORDS	<a href="#">glycoprotein</a>	131 1.20E-07 1.10E-05
		UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	119 1.20E-05 4.10E-03
		GOTERM_CC_FAT	<a href="#">extracellular region part</a>	41 6.90E-05 7.20E-03
		GOTERM_CC_FAT	<a href="#">extracellular space</a>	31 2.60E-04 1.20E-02
		GOTERM_CC_FAT	<a href="#">extracellular region</a>	67 4.30E-04 1.70E-02
		SP_PIR_KEYWORDS	<a href="#">Secreted</a>	53 1.00E-03 1.50E-02
Annotation Cluster 3	Enrichment Score: 4.85	GOTERM_BP_FAT	<a href="#">cell activation</a>	27 1.10E-09 4.50E-07
		GOTERM_BP_FAT	<a href="#">leukocyte activation</a>	22 9.60E-08 3.40E-05
		GOTERM_BP_FAT	<a href="#">T cell activation</a>	16 1.20E-07 3.50E-05
		GOTERM_BP_FAT	<a href="#">lymphocyte activation</a>	19 4.40E-07 1.00E-04
		GOTERM_BP_FAT	<a href="#">immune system development</a>	20 1.20E-05 2.20E-03
		GOTERM_BP_FAT	<a href="#">hemopoietic or lymphoid organ development</a>	19 1.90E-05 3.10E-03
		GOTERM_BP_FAT	<a href="#">hemopoiesis</a>	18 2.00E-05 2.80E-03
		GOTERM_BP_FAT	<a href="#">T cell differentiation</a>	8 5.60E-04 4.40E-02
		GOTERM_BP_FAT	<a href="#">leukocyte differentiation</a>	11 6.50E-04 4.80E-02
		GOTERM_BP_FAT	<a href="#">lymphocyte differentiation</a>	8 7.80E-03 2.40E-01
GOTERM_BP_FAT	<a href="#">T cell selection</a>	3 6.50E-02 5.70E-01		
Annotation Cluster 4	Enrichment Score: 4.59	SP_PIR_KEYWORDS	<a href="#">lipoprotein</a>	34 6.60E-07 4.10E-05
		UP_SEQ_FEATURE	lipid moiety-binding region:S-palmitoyl cysteine	14 7.40E-05 1.20E-02
		SP_PIR_KEYWORDS	<a href="#">palmitate</a>	14 3.50E-04 6.20E-03
Annotation Cluster 5	Enrichment Score: 4.12	GOTERM_CC_FAT	<a href="#">plasma membrane part</a>	81 1.90E-06 2.90E-04
		GOTERM_CC_FAT	<a href="#">intrinsic to plasma membrane</a>	48 9.50E-05 7.40E-03
		GOTERM_CC_FAT	<a href="#">integral to plasma membrane</a>	46 2.20E-04 1.40E-02
		UP_SEQ_FEATURE	topological domain:Extracellular	78 8.40E-04 9.70E-02
Annotation Cluster 6	Enrichment Score: 3.95	UP_SEQ_FEATURE	domain:SH3	15 1.30E-05 3.60E-03
		SP_PIR_KEYWORDS	<a href="#">sh3 domain</a>	15 8.30E-05 1.80E-03
		INTERPRO	<a href="#">Src homology-3 domain</a>	15 1.10E-04 1.80E-02
		SMART	<a href="#">SH3</a>	15 1.40E-03 2.10E-01
		GOTERM_BP_FAT	<a href="#">positive regulation of response to stimulus</a>	20 1.20E-06 2.60E-04
Annotation Cluster 7	Enrichment Score: 3.64	GOTERM_BP_FAT	<a href="#">positive regulation of immune response</a>	14 2.00E-05 3.00E-03
		GOTERM_BP_FAT	<a href="#">positive regulation of immune system process</a>	18 2.20E-05 2.90E-03
		GOTERM_BP_FAT	<a href="#">immune effector process</a>	13 4.20E-05 5.10E-03
		GOTERM_BP_FAT	<a href="#">activation of immune response</a>	10 2.30E-04 2.10E-02
		GOTERM_BP_FAT	<a href="#">leukocyte mediated immunity</a>	9 6.20E-04 4.70E-02
		GOTERM_BP_FAT	<a href="#">immune response-activating signal transduction</a>	7 9.60E-04 6.70E-02
		GOTERM_BP_FAT	<a href="#">immune response-regulating signal transduction</a>	7 1.40E-03 8.50E-02
		GOTERM_BP_FAT	<a href="#">immune response-activating cell surface receptor signaling pathway</a>	6 1.60E-03 9.10E-02

ILMN_2369018	-1.3167466	0.34742686	EV12A
ILMN_1772964	-1.1127529	0.33681542	CCL8
ILMN_2217574	-0.6778461	0.33079284	FABP5L3
ILMN_1760509	-1.4685779	0.33047506	EOMES
ILMN_1673357	-0.7304227	0.32993287	SLA2
ILMN_1687301	-1.5809488	0.32957417	VCAN
ILMN_1728923	-0.9579498	0.32915558	F2RL2
ILMN_1656310	-0.4940499	0.32283896	IDO1
ILMN_1801504	-0.9557369	0.32217026	RUNX1
ILMN_1749362	-1.1738353	0.31501293	CD28
ILMN_1677827	-1.610075	0.31439185	TLR7
ILMN_1723480	-1.4555889	0.31439024	BST2
ILMN_1674402	-0.6813584	0.30988973	TMEM71
ILMN_1675640	-0.99256	0.308559	OAS1
ILMN_2145670	-1.3313366	0.30529922	TNC
ILMN_2085862	-1.3194237	0.30307707	SLC15A3
ILMN_1802708	-0.8654579	0.30057782	BTN3A1
ILMN_2058782	-1.6705484	0.29868892	IFI27
ILMN_2412192	-0.5491448	0.29791167	CFH
ILMN_1740633	-1.1358054	0.29771525	PRF1
ILMN_2202894	-1.643364	0.29721236	F2RL2
ILMN_3302919	-0.7347454	0.29306167	MYOF
ILMN_1657871	-2.23516	0.29136372	RSAD2
ILMN_1662358	-2.3834696	0.2906471	MX1
ILMN_1780533	-1.423368	0.29047525	RNASE6
ILMN_3237946	-0.7705273	0.28753045	PXDN
ILMN_1691364	-1.4878128	0.28612438	STAT1
ILMN_2042651	-1.6108624	0.2831158	EV12B
ILMN_2066849	-1.3265369	0.28190893	FAM26F
ILMN_1724533	-0.9776902	0.28160933	LY96
ILMN_2105441	-1.7997382	0.27848127	IGJ
ILMN_2413808	-1.3141	0.27765673	CD53
ILMN_3234828	-0.3738681	0.27627262	TMEM229B
ILMN_1684040	-1.7639973	0.27530622	THEMIS
ILMN_1778723	-1.2069848	0.2744472	AMICA1
ILMN_1685275	-0.6273471	0.2738763	MCAM
ILMN_3306672	-0.7661769	0.27119064	PATL2
ILMN_2326512	-1.8256159	0.26943186	CASP1
ILMN_2353732	-1.9275862	0.26927188	CD8A
ILMN_1734740	-1.1187886	0.26920912	GPR65
ILMN_2307861	-1.0338793	0.26916945	COL6A3
ILMN_1768595	-0.8213046	0.26846257	DLG4
ILMN_2098126	-0.7770375	0.2672991	CCL5
ILMN_3220934	-0.5118439	0.26631477	NCRNA00152
ILMN_2146761	-0.4733385	0.26463622	FABP5
ILMN_1723486	-0.8193373	0.26113445	HK2
ILMN_1731644	-0.4773678	0.2600093	SETDB2
ILMN_2184184	-0.9364551	0.2593097	ANXA1
ILMN_1765446	-0.651159	0.2588973	EMP3
ILMN_1736729	-0.4527157	0.25189105	OAS2
ILMN_1695590	-1.5135725	0.25181645	ADRB2
ILMN_1731418	-1.4074057	0.25135908	SP110
ILMN_1737918	-0.7864966	0.25117314	C1QA
ILMN_1706483	-1.0443532	0.250543	C1orf116
ILMN_1808657	-0.6577458	0.25034893	FMO3
ILMN_1677997	-0.9073625	0.2456177	MAZ

	GOTERM_BP_FAT	<a href="#">immune response-regulating cell surface receptor signaling pathway</a>
	GOTERM_BP_FAT	<a href="#">antigen receptor-mediated signaling pathway</a>
<b>Annotation Cluster 8</b>	<b>Enrichment Score: 3.39</b>	
	GOTERM_BP_FAT	<a href="#">cell adhesion</a>
	GOTERM_BP_FAT	<a href="#">biological adhesion</a>
	SP_PIR_KEYWORDS	<a href="#">cell adhesion</a>
<b>Annotation Cluster 9</b>	<b>Enrichment Score: 3.39</b>	
	SP_PIR_KEYWORDS	<a href="#">glycoprotein</a>
	GOTERM_CC_FAT	<a href="#">plasma membrane</a>
	UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)
	SP_PIR_KEYWORDS	<a href="#">membrane</a>
	UP_SEQ_FEATURE	topological domain:Cytoplasmic
	UP_SEQ_FEATURE	topological domain:Extracellular
	SP_PIR_KEYWORDS	<a href="#">transmembrane</a>
	UP_SEQ_FEATURE	transmembrane region
	GOTERM_CC_FAT	<a href="#">intrinsic to membrane</a>
	GOTERM_CC_FAT	<a href="#">integral to membrane</a>
<b>Annotation Cluster 10</b>	<b>Enrichment Score: 3.32</b>	
	SP_PIR_KEYWORDS	<a href="#">chemotaxis</a>
	KEGG_PATHWAY	<a href="#">Chemokine signaling pathway</a>
	GOTERM_BP_FAT	<a href="#">taxis</a>
	GOTERM_BP_FAT	<a href="#">chemotaxis</a>
	GOTERM_BP_FAT	<a href="#">locomotory behavior</a>
	GOTERM_MF_FAT	<a href="#">chemokine activity</a>
	GOTERM_MF_FAT	<a href="#">chemokine receptor binding</a>
	SP_PIR_KEYWORDS	<a href="#">inflammatory response</a>
	SP_PIR_KEYWORDS	<a href="#">cytokine</a>
	INTERPRO	<a href="#">Small chemokine, interleukin-8-like</a>
	GOTERM_BP_FAT	<a href="#">behavior</a>
	SMART	<a href="#">SCY</a>
	KEGG_PATHWAY	<a href="#">Cytokine-cytokine receptor interaction</a>
	GOTERM_MF_FAT	<a href="#">cytokine activity</a>
	INTERPRO	<a href="#">Small chemokine, C-C group, conserved site</a>
	PIR_SUPERFAMILY	PIRSF001950:small inducible chemokine, C/CC types
	BBID	<a href="#">109.Chemokine families</a>
<b>Annotation Cluster 11</b>	<b>Enrichment Score: 2.85</b>	
	UP_SEQ_FEATURE	domain:Ig-like V-type 2
	INTERPRO	<a href="#">Immunoglobulin V-set</a>
	UP_SEQ_FEATURE	domain:Ig-like V-type 1
<b>Annotation Cluster 12</b>	<b>Enrichment Score: 2.54</b>	
	KEGG_PATHWAY	<a href="#">Allograft rejection</a>
	KEGG_PATHWAY	<a href="#">Graft-versus-host disease</a>
	UP_SEQ_FEATURE	domain:Ig-like C1-type
	KEGG_PATHWAY	<a href="#">Type I diabetes mellitus</a>
	KEGG_PATHWAY	<a href="#">Viral myocarditis</a>
	INTERPRO	<a href="#">Immunoglobulin C1-set</a>
	KEGG_PATHWAY	<a href="#">Intestinal immune network for IgA production</a>
	KEGG_PATHWAY	<a href="#">Systemic lupus erythematosus</a>
	KEGG_PATHWAY	<a href="#">Asthma</a>
	INTERPRO	<a href="#">Immunoglobulin/major histocompatibility complex, conserved site</a>
	SMART	<a href="#">IGc1</a>
	GOTERM_BP_FAT	<a href="#">antigen processing and presentation</a>
	KEGG_PATHWAY	<a href="#">Autoimmune thyroid disease</a>
	KEGG_PATHWAY	<a href="#">Cell adhesion molecules (CAMs)</a>
	KEGG_PATHWAY	<a href="#">antigen processing and presentation of peptide or polysaccharide antigen via MHC class II</a>
	GOTERM_BP_FAT	<a href="#">class II</a>
	GOTERM_CC_FAT	<a href="#">MHC protein complex</a>



ILMN_1753064	-0.6260933	0.24519011	TTC13	SP_PIR_KEYWORDS	<a href="#">mhc ii</a>	4	2.30E-02	1.60E-01
ILMN_1655077	-0.7821897	0.24446805	PRDM1	PIR_SUPERFAMILY	PIRSF001991:class II histocompatibility antigen	4	2.40E-02	7.10E-01
ILMN_2148785	-0.5040276	0.24378406	GBP1	GOTERM_CC_FAT	<a href="#">MHC class II protein complex</a>	4	2.50E-02	4.00E-01
ILMN_1682799	-1.0445333	0.24377693	STAMBPL1	KEGG_PATHWAY	<a href="#">Antigen processing and presentation</a>	7	3.60E-02	1.80E-01
ILMN_1750246	-0.6299647	0.24340005	ZBTB1	GOTERM_MF_FAT	<a href="#">MHC class II receptor activity</a>	3	6.40E-02	5.90E-01
ILMN_2203271	-2.2243528	0.24243772	FPR3	INTERPRO	<a href="#">MHC class II, alpha/beta chain, N-terminal</a>	3	7.10E-02	7.00E-01
ILMN_2131467	-0.397852	0.24238987	GNAI1	UP_SEQ_FEATURE	region of interest:Connecting peptide	3	1.80E-01	9.90E-01
ILMN_1701195	-0.8428546	0.24176498	PLA2G7	<b>Annotation Cluster 13</b>	<b>Enrichment Score: 2.29</b>	<b>Count</b>	<b>P_Value</b>	<b>Benjamini</b>
ILMN_2150196	-0.8684133	0.24121656	LRRC25	INTERPRO	<a href="#">Immunoglobulin-like fold</a>	31	8.10E-07	5.60E-04
ILMN_1686623	-1.1544287	0.24103889	CSF1R	INTERPRO	<a href="#">Immunoglobulin-like</a>	29	1.10E-06	3.70E-04
ILMN_1773079	-1.0618627	0.24067923	COL3A1	SP_PIR_KEYWORDS	<a href="#">Immunoglobulin domain</a>	26	8.70E-06	2.90E-04
ILMN_1738675	-0.5899928	0.24046308	PTPN6	INTERPRO	<a href="#">Immunoglobulin subtype</a>	18	3.80E-04	4.30E-02
ILMN_2145033	-1.5628619	0.23933251	CCR5	INTERPRO	<a href="#">Immunoglobulin V-set</a>	14	1.60E-03	1.00E-01
ILMN_2055156	-0.7168464	0.23903461	PAG1	UP_SEQ_FEATURE	domain:Ig-like C2-type 1	11	5.00E-03	3.60E-01
ILMN_1668411	-0.741487	0.23653066	FHL2	UP_SEQ_FEATURE	domain:Ig-like C2-type 2	11	5.20E-03	3.40E-01
ILMN_2390586	-0.9880923	0.23087709	SP100	SMART	<a href="#">IG</a>	18	5.80E-03	2.20E-01
ILMN_1795158	-0.4236481	0.23035878	FGR	UP_SEQ_FEATURE	domain:Ig-like C2-type 5	4	9.70E-02	9.50E-01
ILMN_1781155	-0.792679	0.22834751	LYN	UP_SEQ_FEATURE	domain:Ig-like C2-type 3	6	9.80E-02	9.50E-01
ILMN_2148944	-0.5236613	0.22767676	ADCY4	INTERPRO	<a href="#">Immunoglobulin</a>	8	1.10E-01	8.20E-01
ILMN_2355953	-0.4987555	0.22675383	LILRB4	UP_SEQ_FEATURE	domain:Ig-like C2-type 4	4	1.90E-01	9.90E-01
ILMN_1769129	-2.6877906	0.22659782	CCL19	INTERPRO	<a href="#">Immunoglobulin subtype 2</a>	5	5.90E-01	1.00E+00
ILMN_1654586	-0.5864834	0.22578712	RASA3	INTERPRO	<a href="#">Immunoglobulin I-set</a>	3	7.70E-01	1.00E+00
ILMN_2393765	-3.0009851	0.22573021	IGLL1	SMART	<a href="#">IGc2</a>	5	7.90E-01	1.00E+00
ILMN_1800787	-0.8008962	0.22567444	RFTN1	<b>Annotation Cluster 14</b>	<b>Enrichment Score: 2.29</b>	<b>Count</b>	<b>P_Value</b>	<b>Benjamini</b>
ILMN_1716246	-1.1581569	0.22510645	FRZB	INTERPRO	<a href="#">Guanylate-binding protein, C-terminal</a>	4	2.60E-04	3.60E-02
ILMN_1803825	-1.177887	0.22443794	CXCL12	PIR_SUPERFAMILY	PIRSF005552:guanine nucleotide-binding protein 1	4	4.60E-04	8.90E-02
ILMN_1748538	-0.6969305	0.22319187	ALDH1A2	INTERPRO	<a href="#">Guanylate-binding protein, N-terminal</a>	4	1.20E-03	9.60E-02
ILMN_1712505	-0.6336315	0.22281049	KDEL1C1	GOTERM_MF_FAT	<a href="#">GTPase activity</a>	10	4.40E-02	4.90E-01
ILMN_2262044	-0.9458075	0.22100846	PARP10	SP_PIR_KEYWORDS	<a href="#">prenylation</a>	4	6.00E-01	9.40E-01
ILMN_1808405	-1.3138167	0.22031488	HLA-DQA1	<b>Annotation Cluster 15</b>	<b>Enrichment Score: 2.26</b>	<b>Count</b>	<b>P_Value</b>	<b>Benjamini</b>
ILMN_1672661	-0.6772578	0.21959968	SP110	GOTERM_BP_FAT	<a href="#">mast cell activation</a>	4	5.50E-04	4.50E-02
ILMN_1751079	-0.8478336	0.21942043	TAP1	GOTERM_BP_FAT	<a href="#">cell activation during immune response</a>	6	1.10E-03	7.20E-02
ILMN_1669703	-1.0861342	0.21830858	TNK2	GOTERM_BP_FAT	<a href="#">leukocyte activation during immune response</a>	6	1.10E-03	7.20E-02
ILMN_2331087	-0.6249117	0.21772788	MS4A7	GOTERM_BP_FAT	<a href="#">myeloid leukocyte activation</a>	6	3.30E-03	1.60E-01
ILMN_1842448	-0.6529515	0.21661535	AI866653	GOTERM_BP_FAT	<a href="#">mast cell degranulation</a>	3	4.70E-03	1.90E-01
ILMN_1661594	-0.6992096	0.21564007	C2orf42	GOTERM_BP_FAT	<a href="#">mast cell mediated immunity</a>	3	4.70E-03	1.90E-01
ILMN_1733579	-0.8560787	0.21515703	EVI2A	GOTERM_BP_FAT	<a href="#">myeloid cell activation during immune response</a>	4	6.80E-03	2.20E-01
ILMN_2105919	-0.5137864	0.21502116	FGF2	GOTERM_BP_FAT	<a href="#">leukocyte degranulation</a>	3	2.80E-02	4.30E-01
ILMN_2344283	-1.2531308	0.21422459	FMO3	GOTERM_BP_FAT	<a href="#">myeloid leukocyte mediated immunity</a>	3	4.20E-02	4.70E-01
ILMN_1705247	-0.4828205	0.21087095	ACSL5	GOTERM_BP_FAT	<a href="#">regulated secretory pathway</a>	3	5.90E-02	5.50E-01
ILMN_1763452	-1.3882258	0.2101784	EVI2B	<b>Annotation Cluster 16</b>	<b>Enrichment Score: 2.26</b>	<b>Count</b>	<b>P_Value</b>	<b>Benjamini</b>
ILMN_2049766	-0.819701	0.21005131	NFE2L3	UP_SEQ_FEATURE	glycosylation site:O-linked (Gal...)	5	1.80E-05	4.10E-03
ILMN_1791447	-0.6749299	0.20970264	CXCL12	SP_PIR_KEYWORDS	<a href="#">triple helix</a>	7	2.90E-05	8.80E-04
ILMN_1797001	-1.04925	0.20879143	DDX58	SP_PIR_KEYWORDS	<a href="#">hydroxylysine</a>	7	2.90E-05	8.80E-04
ILMN_2066858	-1.0778518	0.20609286	TNFSF13B	SP_PIR_KEYWORDS	<a href="#">pyroglutamic acid</a>	8	3.20E-05	9.10E-04
ILMN_3238525	-0.840078	0.20518312	CARD17	GOTERM_MF_FAT	<a href="#">platelet-derived growth factor binding</a>	5	6.60E-05	3.40E-02
ILMN_1671404	-0.3086096	0.20476213	SVIL	SP_PIR_KEYWORDS	<a href="#">hydroxyproline</a>	7	8.10E-05	1.90E-03
ILMN_1771385	-0.9513072	0.2039975	GBP4	SP_PIR_KEYWORDS	<a href="#">trimer</a>	6	1.40E-04	2.90E-03
ILMN_2107068	-0.4971687	0.20379758	HOXA2	GOTERM_CC_FAT	<a href="#">collagen</a>	6	9.50E-04	3.30E-02
ILMN_1710923	-0.852091	0.20088993	SLAMF7	GOTERM_CC_FAT	<a href="#">fibrillar collagen</a>	4	2.00E-03	5.10E-02
ILMN_1701877	-0.7365986	0.19854017	AXL	SP_PIR_KEYWORDS	<a href="#">hydroxylation</a>	7	2.90E-03	3.20E-02
ILMN_1662026	-2.3509529	0.19770975	BTK	SP_PIR_KEYWORDS	<a href="#">collagen</a>	8	2.90E-03	3.10E-02
ILMN_2081682	-0.3063551	0.19752866	SMAP2	KEGG_PATHWAY	<a href="#">ECM-receptor interaction</a>	9	3.20E-03	3.10E-02
ILMN_1776723	-0.6018739	0.19542946	PHF11	SP_PIR_KEYWORDS	<a href="#">skin</a>	3	3.80E-03	3.80E-02
ILMN_1811301	-0.5809573	0.19494492	INPP5E	PIR_SUPERFAMILY	PIRSF002255:collagen alpha 1(I) chain	3	5.60E-03	4.30E-01
ILMN_2162860	-0.6841633	0.19357748	SLFN11	UP_SEQ_FEATURE	propeptide:N-terminal propeptide	3	5.70E-03	3.40E-01
ILMN_1795762	-1.6215433	0.19356228	PLEK	KEGG_PATHWAY	<a href="#">Focal adhesion</a>	14	6.40E-03	4.30E-02

ILMN_ID	Score	Gene	Condition
ILMN_1769118	-0.6864126	0.19338933	sept-09
ILMN_1775486	-0.9369748	0.19133283	SSPN
ILMN_2376205	-1.2679341	0.19055454	LTB
ILMN_1802157	-0.4378756	0.19053373	THOC1
ILMN_1761733	-1.1943467	0.19034739	HLA-DMB
ILMN_1766411	-0.4739769	0.19005528	AP1S2
ILMN_1702301	-0.8188756	0.18990526	DOCK10
ILMN_2355831	-0.7947089	0.18943101	FHL2
ILMN_1693009	-0.6449313	0.18806794	FGL2
ILMN_2335072	-0.6986206	0.18791698	TAF1C
ILMN_1682428	-0.4835178	0.18789467	HENMT1
ILMN_1653438	-0.5087999	0.18765485	PHF14
ILMN_1742307	-0.6138526	0.18763377	MEST
ILMN_1803560	-1.0579265	0.18705413	LAT2
ILMN_2196328	-0.9337432	0.18687055	POSTN
ILMN_1674706	-0.5913538	0.18563332	MTHFD2
ILMN_1699217	-0.7707384	0.18500535	C1orf96
ILMN_1653856	-1.3466251	0.18485016	UBASH3B
ILMN_1701789	-2.004902	0.18479297	IFIT3
ILMN_1758315	-1.0181562	0.18420744	SLC9A9
ILMN_1750961	-0.8616837	0.18414715	TM6SF1
ILMN_1728639	-0.5478027	0.18408255	FCGR3B
ILMN_1706779	-0.5501093	0.18396571	LIG1
ILMN_1685680	-0.7034726	0.18370552	SPATA1
ILMN_2175912	-0.9459248	0.18345703	ITGB2
ILMN_1738027	-0.4626849	0.18197875	BRCA1
ILMN_3236858	-0.5093583	0.18181755	NYNRIN
ILMN_2114568	-0.8746334	0.18175074	GBP5
ILMN_2373831	-0.9518257	0.18167904	BTN3A3
ILMN_1674250	-1.2010549	0.1805769	NCKAP1L
ILMN_1771057	-0.7285394	0.18004651	XAB2
ILMN_2399523	-0.495345	0.17881615	JAG2
ILMN_1768482	-2.152835	0.17718779	CD8A
ILMN_2120273	-0.5052606	0.17538813	AP1S2
ILMN_2112580	-0.7201615	0.17467757	FCGR3A
ILMN_1797342	-0.6990012	0.17328602	FNBP1
ILMN_1682761	-0.5960339	0.17276324	C17orf87
ILMN_1684352	-0.5583657	0.17271927	TRIM45
ILMN_3307841	-1.1468112	0.17166331	AGR2
ILMN_2415144	-1.261158	0.17139485	SP110
ILMN_1717261	-0.5074661	0.17112969	HLA-DRB1
ILMN_2123743	-0.851247	0.17013052	FCER1G
ILMN_2320513	-0.6221451	0.1697949	APBB3
ILMN_1672611	-1.1591105	0.16951554	CDH11
ILMN_1750400	-0.8579902	0.16903764	C19orf66
ILMN_1677608	-0.9510541	0.16882162	NEUROD4
ILMN_2109708	-1.0622737	0.16779476	TYMP
ILMN_2053527	-1.2896768	0.16774197	PARP9
ILMN_1854031	-1.0422922	0.16767006	CD729290
ILMN_1716552	-0.3899185	0.16749883	ENAH
ILMN_1751572	-0.9353575	0.16673219	TLE1
ILMN_1790529	-1.4788342	0.16615602	LUM
ILMN_2163873	-0.9824466	0.16482532	FNDC1
ILMN_1693766	-0.5237026	0.16480169	CEP135
ILMN_1781373	-1.2364535	0.16454612	IFIH1
ILMN_1794594	-0.4929295	0.16383012	RASGRP2
ILMN_1697377	-0.733766	0.16293058	ANKRD36B

Annotation Cluster	Enrichment Score	Gene	Condition
Annotation Cluster 17	Enrichment Score: 2.14	INTERPRO	Collagen triple helix repeat
		GOTERM_BP_FAT	extracellular matrix organization
		SP_PIR_KEYWORDS	extracellular matrix
		UP_SEQ_FEATURE	propeptide:C-terminal propeptide
		UP_SEQ_FEATURE	region of interest:Triple-helical region
		SP_PIR_KEYWORDS	Ehlers-Danlos syndrome
		UP_SEQ_FEATURE	domain:Fibrillar collagen NC1
		INTERPRO	Fibrillar collagen, C-terminal
		GOTERM_BP_FAT	collagen fibril organization
		GOTERM_BP_FAT	skin development
		GOTERM_MF_FAT	growth factor binding
		GOTERM_BP_FAT	extracellular structure organization
		SMART	COLF1
		GOTERM_MF_FAT	extracellular matrix structural constituent
		GOTERM_CC_FAT	extracellular matrix
		GOTERM_CC_FAT	extracellular matrix part
		GOTERM_CC_FAT	proteinaceous extracellular matrix
		GOTERM_BP_FAT	odontogenesis
		GOTERM_BP_FAT	epidermis development
		GOTERM_BP_FAT	ectoderm development
		GOTERM_MF_FAT	structural molecule activity
Annotation Cluster 18	Enrichment Score: 2	SP_PIR_KEYWORDS	trimer
		UP_SEQ_FEATURE	domain:VWFC
		INTERPRO	von Willebrand factor, type C
		SMART	VWC
Annotation Cluster 19	Enrichment Score: 1.99	GOTERM_MF_FAT	identical protein binding
		GOTERM_MF_FAT	protein dimerization activity
		GOTERM_MF_FAT	protein homodimerization activity
Annotation Cluster 20	Enrichment Score: 1.94	INTERPRO	Pleckstrin homology-type
		INTERPRO	Pleckstrin homology
		GOTERM_MF_FAT	GTPase regulator activity
		GOTERM_MF_FAT	nucleoside-triphosphatase regulator activity
		UP_SEQ_FEATURE	domain:PH
		GOTERM_MF_FAT	GTPase activator activity
		SMART	PH
		GOTERM_MF_FAT	enzyme activator activity
		SP_PIR_KEYWORDS	GTPase activation
Annotation Cluster 21	Enrichment Score: 1.93	GOTERM_BP_FAT	circulatory system process
		GOTERM_BP_FAT	blood circulation
		GOTERM_BP_FAT	regulation of blood pressure
Annotation Cluster 22	Enrichment Score: 1.87	SP_PIR_KEYWORDS	SH2 domain
		INTERPRO	SH2 motif
		SMART	SH2
		UP_SEQ_FEATURE	domain:SH2
		KEGG_PATHWAY	Jak-STAT signaling pathway
Annotation Cluster 23	Enrichment Score: 1.82	SP_PIR_KEYWORDS	myristylation
		SP_PIR_KEYWORDS	blocked amino end
		SP_PIR_KEYWORDS	thiolester bond
		GOTERM_BP_FAT	response to organic substance
		GOTERM_BP_FAT	response to hormone stimulus

Count	P_Value	Benjamini
7	6.80E-03	2.40E-01
8	8.20E-03	2.50E-01
12	9.00E-03	8.10E-02
3	1.00E-02	4.80E-01
4	1.00E-02	4.70E-01
3	1.90E-02	1.40E-01
3	1.90E-02	5.60E-01
3	2.00E-02	4.20E-01
4	2.60E-02	4.30E-01
4	2.60E-02	4.30E-01
7	2.80E-02	4.60E-01
9	2.80E-02	4.30E-01
3	3.20E-02	4.30E-01
6	4.10E-02	4.90E-01
14	4.20E-02	5.30E-01
7	4.50E-02	5.30E-01
13	5.20E-02	5.50E-01
4	1.20E-01	7.10E-01
7	2.20E-01	8.60E-01
7	2.80E-01	9.00E-01
13	7.40E-01	1.00E+00
6	1.40E-04	2.90E-03
4	5.20E-03	3.50E-01
4	4.60E-02	5.70E-01
4	8.60E-02	6.70E-01
27	1.90E-03	1.80E-01
21	1.60E-02	5.10E-01
14	3.30E-02	4.70E-01
19	4.30E-05	9.70E-03
14	4.00E-03	1.60E-01
17	1.70E-02	4.90E-01
17	2.00E-02	4.60E-01
11	2.10E-02	5.80E-01
11	2.40E-02	4.50E-01
14	3.00E-02	4.40E-01
14	3.40E-02	4.60E-01
8	4.00E-02	2.40E-01
12	2.90E-03	1.40E-01
12	2.90E-03	1.40E-01
5	1.80E-01	8.10E-01
9	1.70E-03	2.40E-02
9	1.80E-03	1.00E-01
9	8.40E-03	2.50E-01
7	1.30E-02	5.10E-01
5	6.80E-01	9.30E-01
5	7.30E-03	7.10E-02
7	1.00E-02	8.60E-02
4	3.40E-02	2.10E-01
30	1.30E-03	8.20E-02
16	1.70E-02	3.70E-01

ILMN_2053345	-1.0464411	0.16142471	KCNT2	GOTERM_BP_FAT	<a href="#">response to endogenous stimulus</a>	16	3.60E-02	4.40E-01
ILMN_2348788	-0.8400175	0.16100022	CD44	GOTERM_BP_FAT	<a href="#">response to steroid hormone stimulus</a>	9	6.30E-02	5.70E-01
ILMN_2129927	-0.4411718	0.16062467	EXT1	<b>Annotation Cluster 24</b>	<b>Enrichment Score: 1.82</b>	<b>Count</b>	<b>P_Value</b>	<b>Benjamini</b>
ILMN_1754894	-0.6684889	0.16053428	C1orf162	GOTERM_BP_FAT	<a href="#">immune effector process</a>	13	4.20E-05	5.10E-03
ILMN_1671565	-0.8811511	0.15950754	RNASET2	GOTERM_BP_FAT	<a href="#">leukocyte mediated immunity</a>	9	6.20E-04	4.70E-02
ILMN_1665738	-0.5216289	0.15925722	FLI1	GOTERM_BP_FAT	<a href="#">lymphocyte mediated immunity</a>	6	1.90E-02	4.00E-01
ILMN_1777325	-0.8521843	0.15826768	STAT1	GOTERM_BP_FAT	<a href="#">adaptive immune response</a>	5	9.10E-02	6.50E-01
ILMN_1858599	-0.3757296	0.15665687	RBM43	GOTERM_BP_FAT	<a href="#">adaptive immune response based on somatic recombination of immune receptors</a>	5	9.10E-02	6.50E-01
ILMN_1803429	-1.1652212	0.15593497	CD44	GOTERM_BP_FAT	<a href="#">built from immunoglobulin superfamily domains</a>	4	1.30E-01	7.30E-01
ILMN_1690105	-1.3125963	0.15538809	STAT1	GOTERM_BP_FAT	<a href="#">B cell mediated immunity</a>	3	3.40E-01	9.30E-01
ILMN_1698551	-0.4980893	0.1544606	RCN1	<b>Annotation Cluster 25</b>	<b>Enrichment Score: 1.8</b>	<b>Count</b>	<b>P_Value</b>	<b>Benjamini</b>
ILMN_1760027	-0.6957563	0.15445444	WAS	GOTERM_BP_FAT	<a href="#">response to defenses of other organism during symbiotic interaction</a>	3	1.60E-02	3.60E-01
ILMN_1689518	-0.6729684	0.15435107	PECAM1	GOTERM_BP_FAT	<a href="#">response to host defenses</a>	3	1.60E-02	3.60E-01
ILMN_1752046	-0.8322395	0.15407388	SH2B3	GOTERM_BP_FAT	<a href="#">response to host</a>	3	1.60E-02	3.60E-01
ILMN_1808590	-1.0341556	0.1538482	GUCY1A3	<b>Annotation Cluster 26</b>	<b>Enrichment Score: 1.78</b>	<b>Count</b>	<b>P_Value</b>	<b>Benjamini</b>
ILMN_1667947	-0.5844314	0.15268582	NPY1R	GOTERM_BP_FAT	<a href="#">exocytosis</a>	9	4.00E-03	1.80E-01
ILMN_1797425	-0.5200506	0.15247124	DDX55	GOTERM_BP_FAT	<a href="#">secretion by cell</a>	12	6.40E-03	2.20E-01
ILMN_3252608	-0.7166695	0.15206487	HCRP1	GOTERM_BP_FAT	<a href="#">secretion</a>	13	3.50E-02	4.50E-01
ILMN_1699496	-0.3706721	0.15120575	PHF21A	GOTERM_BP_FAT	<a href="#">vesicle-mediated transport</a>	19	8.90E-02	6.50E-01
ILMN_2309848	-1.0085205	0.15017693	FXYD5	<b>Annotation Cluster 27</b>	<b>Enrichment Score: 1.76</b>	<b>Count</b>	<b>P_Value</b>	<b>Benjamini</b>
ILMN_1726565	-0.4903091	0.15010406	PIK3R2	GOTERM_BP_FAT	<a href="#">regulation of cytokine production</a>	12	2.30E-03	1.20E-01
ILMN_2401770	-0.6743532	0.14875394	PHF14	GOTERM_BP_FAT	<a href="#">positive regulation of multicellular organismal process</a>	11	4.50E-02	4.80E-01
ILMN_1714523	-0.6782292	0.14785935	HEPH	GOTERM_BP_FAT	<a href="#">positive regulation of cytokine production</a>	6	4.90E-02	5.10E-01
ILMN_2376723	-1.4681809	0.14697123	CDKN2B	<b>Annotation Cluster 28</b>	<b>Enrichment Score: 1.65</b>	<b>Count</b>	<b>P_Value</b>	<b>Benjamini</b>
ILMN_1811313	-0.6984525	0.1466987	SLIT3	GOTERM_BP_FAT	<a href="#">antigen processing and presentation</a>	8	2.40E-03	1.20E-01
ILMN_3259146	-0.9624002	0.14500356	BST2	GOTERM_BP_FAT	<a href="#">antigen processing and presentation of exogenous peptide antigen</a>	3	2.30E-02	4.20E-01
ILMN_1713751	-0.9840141	0.14473715	ADAM19	GOTERM_BP_FAT	<a href="#">antigen processing and presentation of exogenous antigen</a>	3	3.70E-02	4.50E-01
ILMN_1699931	-1.003425	0.14460169	HCST	GOTERM_BP_FAT	<a href="#">antigen processing and presentation of peptide antigen</a>	3	1.30E-01	7.30E-01
ILMN_1725678	-1.1343282	0.14421207	GFRA1	<b>Annotation Cluster 29</b>	<b>Enrichment Score: 1.63</b>	<b>Count</b>	<b>P_Value</b>	<b>Benjamini</b>
ILMN_1704665	-0.68296	0.14387353	GPM6B	GOTERM_BP_FAT	<a href="#">positive regulation of cytokine biosynthetic process</a>	6	4.00E-03	1.80E-01
ILMN_1742544	-0.6991372	0.14363457	MEF2C	GOTERM_BP_FAT	<a href="#">regulation of cytokine biosynthetic process</a>	7	5.80E-03	2.10E-01
ILMN_1659075	-0.8373866	0.14355	HLA-DOA	GOTERM_BP_FAT	<a href="#">positive regulation of interleukin-2 biosynthetic process</a>	3	3.20E-02	4.40E-01
ILMN_1697409	-0.5747517	0.14324132	TNFRSF14	GOTERM_BP_FAT	<a href="#">regulation of interleukin-2 biosynthetic process</a>	3	6.50E-02	5.70E-01
ILMN_1810836	-0.5323594	0.1430238	PDE5A	GOTERM_BP_FAT	<a href="#">regulation of interleukin-2 production</a>	3	1.40E-01	7.60E-01
ILMN_1897405	-0.4541245	0.1429059	CA420307	<b>Annotation Cluster 30</b>	<b>Enrichment Score: 1.63</b>	<b>Count</b>	<b>P_Value</b>	<b>Benjamini</b>
ILMN_2103761	-0.32567	0.14212725	TLE4	SP_PIR_KEYWORDS	<a href="#">gtp-binding</a>	14	1.50E-02	1.20E-01
ILMN_1805842	-0.3127734	0.14195496	FHL1	UP_SEQ_FEATURE	nucleotide phosphate-binding region:GTP	13	1.60E-02	5.40E-01
ILMN_1694325	-0.6372663	0.14186426	NFIX	GOTERM_MF_FAT	<a href="#">guanyl ribonucleotide binding</a>	16	2.20E-02	4.50E-01
ILMN_1735764	-0.6439887	0.14098056	HTR2B	GOTERM_MF_FAT	<a href="#">guanyl nucleotide binding</a>	16	2.20E-02	4.50E-01
ILMN_1790149	-0.9141578	0.14082532	HGF	GOTERM_MF_FAT	<a href="#">GTP binding</a>	15	3.60E-02	4.60E-01
ILMN_1779324	-1.1017444	0.14040168	GZMA	GOTERM_MF_FAT	<a href="#">GTPase activity</a>	10	4.40E-02	4.90E-01
ILMN_2115005	-1.0511112	0.13994657	FGD2	<b>Annotation Cluster 31</b>	<b>Enrichment Score: 1.62</b>	<b>Count</b>	<b>P_Value</b>	<b>Benjamini</b>
ILMN_1764571	-0.7244104	0.13976014	ARHGAP23	GOTERM_BP_FAT	<a href="#">cell motion</a>	22	2.00E-03	1.10E-01
ILMN_1754249	-1.7247378	0.13942018	TARP	GOTERM_BP_FAT	<a href="#">localization of cell</a>	14	1.90E-02	3.90E-01
ILMN_1796409	-1.4578474	0.1390564	C1QB	GOTERM_BP_FAT	<a href="#">cell motility</a>	14	1.90E-02	3.90E-01
ILMN_1768551	-0.7304808	0.13891879	PATL2	GOTERM_BP_FAT	<a href="#">cell migration</a>	13	2.00E-02	4.00E-01
ILMN_2061565	-0.8066601	0.13852021	PLCH2	GOTERM_BP_FAT	<a href="#">leukocyte migration</a>	5	3.70E-02	4.50E-01
ILMN_1653028	-0.7519424	0.1373429	COL4A1	GOTERM_BP_FAT	<a href="#">neuron development</a>	10	3.40E-01	9.30E-01
ILMN_2255133	-2.1671016	0.13648851	BCL11A	<b>Annotation Cluster 32</b>	<b>Enrichment Score: 1.62</b>	<b>Count</b>	<b>P_Value</b>	<b>Benjamini</b>
ILMN_1796629	-0.806825	0.13480131	EDNRA	GOTERM_BP_FAT	<a href="#">skeletal system development</a>	15	1.10E-02	3.10E-01
ILMN_3252556	-0.9037436	0.13330415	CARD16	GOTERM_BP_FAT	<a href="#">osteoblast differentiation</a>	5	1.40E-02	3.30E-01
ILMN_1748473	-0.7021659	0.13273199	GIMAP4	GOTERM_BP_FAT	<a href="#">ossification</a>	8	1.40E-02	3.40E-01
ILMN_2388547	-1.5174031	0.13248418	EPST11	GOTERM_BP_FAT	<a href="#">bone development</a>	8	1.90E-02	3.90E-01
ILMN_1818617	-0.9279863	0.13082033	AL133627	GOTERM_BP_FAT	<a href="#">biomineral formation</a>	3	2.00E-01	8.30E-01
ILMN_1668374	-0.4292723	0.12997523	ITGB5	<b>Annotation Cluster 33</b>	<b>Enrichment Score: 1.61</b>	<b>Count</b>	<b>P_Value</b>	<b>Benjamini</b>
ILMN_1804571	-0.5105165	0.1295662	ZKSCAN4	UP_SEQ_FEATURE	repeat:HAT 5	3	1.90E-02	5.60E-01

ILMN_1848095	-0.8107949	0.12893517	NA
ILMN_1695640	-1.2297163	0.12878244	PTPN22
ILMN_1682165	-0.5414724	0.12867746	NT5C2
ILMN_2222688	-0.4617698	0.12545523	TMSB4X
ILMN_3222425	-0.4439984	0.12462959	LOC729852
ILMN_1768394	-0.2999259	0.12444508	ARPC5
ILMN_1814022	-0.4016976	0.12436828	NR1H3
ILMN_3238116	-0.571442	0.12429227	NBPF11
ILMN_1711383	-0.4462715	0.12396342	STK4
ILMN_1812926	-0.5183303	0.12353233	ANTXR2
ILMN_1805448	-0.4803053	0.12333091	EPB41L2
ILMN_1656111	-0.3010579	0.12267488	MYLIP
ILMN_1752520	-0.6901116	0.12224111	SLFN11
ILMN_1791873	-0.6042855	0.12214205	COG1
ILMN_1690921	-0.475829	0.12163639	STAT2
ILMN_1737833	-0.5696403	0.12110119	ATN1
ILMN_2326509	-2.0144005	0.120608	CASP1
ILMN_2208413	-1.40638	0.1202912	ARHGAP15
ILMN_1727402	-0.9682615	0.11974773	HCLS1
ILMN_1711617	-0.8764327	0.11954744	GMFG
ILMN_1777998	-0.769028	0.11922558	ARHGAP25
ILMN_1662932	-1.3524692	0.11833018	LCP1
ILMN_1815154	-0.3131096	0.11772004	MYH10
ILMN_1739541	-0.5683731	0.11725833	NMI
ILMN_1815673	-0.8984177	0.11664414	DKK3
ILMN_1813753	-0.8199365	0.11578794	PTN
ILMN_2364521	-0.8218051	0.11534408	AXL
ILMN_1663080	-1.0312574	0.11457998	LFNG
ILMN_1803423	-0.8187965	0.11438009	ARHGEP6
ILMN_1738832	-0.9569222	0.11290038	SACS
ILMN_1747968	-0.5250922	0.11259931	RBM33
ILMN_1718063	-0.3632585	0.11231238	LIPA
ILMN_1698419	-0.3359468	0.1099484	NCOR2
ILMN_3300663	-0.4206458	0.10986987	SLC35E2B
ILMN_2347805	-0.4750857	0.10956416	EXOC1
ILMN_2229877	-0.8076528	0.10956222	PCDH18
ILMN_1810910	-0.8282412	0.10938713	CFH
ILMN_2077406	-0.7479565	0.10932532	CCDC18
ILMN_3245625	-0.3613911	0.10917917	RFK7
ILMN_1728478	-0.4733229	0.10900313	CXCL16
ILMN_1806790	-0.5863853	0.10892174	ROBO1
ILMN_2253732	-0.8138144	0.10890111	ST8SIA4
ILMN_3240586	-0.4137484	0.10812488	PLD6
ILMN_3242725	-0.5643714	0.10779354	KIF26A
ILMN_2246328	-1.1970055	0.10777731	PTPN22
ILMN_1705442	-0.6908666	0.10772623	CMTM3
ILMN_1733538	-0.8262795	0.10733758	RGS10
ILMN_3243185	-0.5303395	0.10715491	RERGL
ILMN_1795930	-0.8828546	0.10697748	PTGER4
ILMN_1802109	-0.6104525	0.10639039	KLHL29
ILMN_1665686	-0.5991011	0.10587843	FAM38B
ILMN_1761941	-0.5115597	0.1056436	FAM198B
ILMN_1683494	-0.6096175	0.10531268	TMEM154
ILMN_1655595	-0.3709378	0.10528863	SERPINE2
ILMN_2317581	-0.6959561	0.10484695	SHANK3
ILMN_1776213	-0.681404	0.10361286	RGMB

		UP_SEQ_FEATURE	repeat:HAT 4
		UP_SEQ_FEATURE	repeat:HAT 3
		UP_SEQ_FEATURE	repeat:HAT 1
		UP_SEQ_FEATURE	repeat:HAT 2
<b>Annotation Cluster 34</b>	<b>Enrichment Score: 1.6</b>		
		SP_PIR_KEYWORDS	<a href="#">LIM domain</a>
		INTERPRO	<a href="#">Zinc finger, LIM-type</a>
		UP_SEQ_FEATURE	domain:LIM zinc-binding 2
		UP_SEQ_FEATURE	domain:LIM zinc-binding 1
		SMART	<a href="#">LIM</a>
		UP_SEQ_FEATURE	domain:LIM zinc-binding 3
<b>Annotation Cluster 35</b>	<b>Enrichment Score: 1.58</b>		
		SP_PIR_KEYWORDS	<a href="#">heparin-binding</a>
		GOTERM_MF_FAT	<a href="#">glycosaminoglycan binding</a>
		GOTERM_MF_FAT	<a href="#">polysaccharide binding</a>
		GOTERM_MF_FAT	<a href="#">pattern binding</a>
		GOTERM_MF_FAT	<a href="#">heparin binding</a>
		GOTERM_MF_FAT	<a href="#">carbohydrate binding</a>
<b>Annotation Cluster 36</b>	<b>Enrichment Score: 1.56</b>		
		GOTERM_BP_FAT	<a href="#">regulation of programmed cell death</a>
		GOTERM_BP_FAT	<a href="#">regulation of cell death</a>
		GOTERM_BP_FAT	<a href="#">induction of apoptosis</a>
		GOTERM_BP_FAT	<a href="#">induction of programmed cell death</a>
		GOTERM_BP_FAT	<a href="#">positive regulation of apoptosis</a>
		GOTERM_BP_FAT	<a href="#">positive regulation of programmed cell death</a>
		GOTERM_BP_FAT	<a href="#">positive regulation of cell death</a>
		GOTERM_BP_FAT	<a href="#">regulation of apoptosis</a>
<b>Annotation Cluster 37</b>	<b>Enrichment Score: 1.55</b>		
		INTERPRO	<a href="#">Zinc finger, PHD-type</a>
		INTERPRO	<a href="#">Zinc finger, PHD-type, conserved site</a>
		INTERPRO	<a href="#">Zinc finger, PHD-finger</a>
		SMART	<a href="#">PHD</a>
		UP_SEQ_FEATURE	zinc finger region:PHD-type
		INTERPRO	<a href="#">Zinc finger, RING-type</a>
		SMART	<a href="#">RING</a>
<b>Annotation Cluster 38</b>	<b>Enrichment Score: 1.53</b>		
		SP_PIR_KEYWORDS	<a href="#">cytoskeleton</a>
		GOTERM_MF_FAT	<a href="#">cytoskeletal protein binding</a>
		SP_PIR_KEYWORDS	<a href="#">actin-binding</a>
		GOTERM_MF_FAT	<a href="#">actin binding</a>
		GOTERM_MF_FAT	<a href="#">actin filament binding</a>
		GOTERM_CC_FAT	<a href="#">actin cytoskeleton</a>
<b>Annotation Cluster 39</b>	<b>Enrichment Score: 1.52</b>		
		INTERPRO	<a href="#">Bromodomain</a>
		SMART	<a href="#">BROMO</a>
		INTERPRO	<a href="#">Bromodomain, conserved site</a>
		SP_PIR_KEYWORDS	<a href="#">bromodomain</a>
		UP_SEQ_FEATURE	domain:Bromo
<b>Annotation Cluster 40</b>	<b>Enrichment Score: 1.52</b>		
		GOTERM_BP_FAT	<a href="#">integrin-mediated signaling pathway</a>
		INTERPRO	<a href="#">von Willebrand factor, type A</a>
		GOTERM_CC_FAT	<a href="#">integrin complex</a>
		SP_PIR_KEYWORDS	<a href="#">integrin</a>
		SMART	<a href="#">VWA</a>
		UP_SEQ_FEATURE	domain:VWFA
<b>Annotation Cluster 41</b>	<b>Enrichment Score: 1.5</b>		

Count	P_Value	Benjamini
3	2.30E-02	5.90E-01
3	2.70E-02	6.40E-01
3	2.70E-02	6.40E-01
3	2.70E-02	6.40E-01
6	1.30E-02	1.10E-01
6	1.60E-02	3.60E-01
5	1.80E-02	5.30E-01
5	1.80E-02	5.30E-01
6	4.20E-02	4.90E-01
3	8.80E-02	9.50E-01
6	9.40E-03	8.20E-02
9	1.20E-02	5.00E-01
9	2.00E-02	4.50E-01
9	2.00E-02	4.50E-01
7	2.60E-02	4.60E-01
11	2.60E-01	9.10E-01
28	2.20E-02	4.10E-01
28	2.30E-02	4.20E-01
14	2.60E-02	4.30E-01
14	2.60E-02	4.20E-01
17	3.00E-02	4.40E-01
17	3.10E-02	4.40E-01
17	3.30E-02	4.40E-01
27	3.30E-02	4.40E-01
8	2.20E-03	1.00E-01
8	2.70E-03	1.10E-01
7	7.20E-03	2.40E-01
8	9.00E-03	2.30E-01
4	8.60E-02	9.50E-01
7	5.50E-01	1.00E+00
7	7.90E-01	1.00E+00
23	8.60E-03	7.90E-02
20	1.60E-02	5.20E-01
11	2.60E-02	1.80E-01
14	2.80E-02	4.70E-01
5	2.90E-02	4.50E-01
9	2.50E-01	9.10E-01
5	8.20E-03	2.50E-01
5	2.00E-02	3.90E-01
4	3.50E-02	5.60E-01
4	4.20E-02	2.40E-01
3	1.10E-01	9.50E-01
7	4.40E-03	1.80E-01
6	2.10E-02	4.30E-01
4	2.50E-02	4.00E-01
4	4.80E-02	2.60E-01
6	5.50E-02	5.60E-01
4	1.30E-01	9.70E-01
Count	P_Value	Benjamini

Gene ID	Score 1	Score 2	Score 3	Gene Name	Category	Count	P_Value	Benjamini
ILMN_1791702	-0.2409067	0.10345653	SMARCA2	GOTERM_BP_FAT	<a href="#">positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains</a>	4	2.80E-02	4.30E-01
ILMN_2042595	-0.5229749	0.10331385	PCM1	GOTERM_BP_FAT	<a href="#">positive regulation of adaptive immune response</a>	4	3.00E-02	4.40E-01
ILMN_1740430	-0.310527	0.10329175	SLC2A4RG	GOTERM_BP_FAT	<a href="#">regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains</a>	5	3.30E-02	4.40E-01
ILMN_1739428	-1.0048952	0.10326946	IFIT2	GOTERM_BP_FAT	<a href="#">regulation of adaptive immune response</a>	5	3.50E-02	4.40E-01
ILMN_2408851	-0.7082942	0.102796	ARHGAP30	<b>Annotation Cluster 42</b> <b>Enrichment Score: 1.5</b>		<b>Count</b>	<b>P_Value</b>	<b>Benjamini</b>
ILMN_1677239	-0.4022552	0.10207376	CCDC14	GOTERM_BP_FAT	<a href="#">negative regulation of transcription, DNA-dependent</a>	17	5.80E-03	2.10E-01
ILMN_1670926	-0.9411953	0.10141872	CHST15	GOTERM_BP_FAT	<a href="#">negative regulation of transcription from RNA polymerase II promoter</a>	14	6.30E-03	2.20E-01
ILMN_1652000	-0.5560677	0.10119058	FAM156B	GOTERM_BP_FAT	<a href="#">negative regulation of RNA metabolic process</a>	17	6.80E-03	2.30E-01
ILMN_2230892	-0.6070417	0.10088368	IL10RB	GOTERM_BP_FAT	<a href="#">negative regulation of biosynthetic process</a>	23	8.50E-03	2.60E-01
ILMN_2157951	-0.4193257	0.10070315	STX6	GOTERM_BP_FAT	<a href="#">negative regulation of cellular biosynthetic process</a>	22	1.30E-02	3.30E-01
ILMN_1691444	-0.5584114	0.10005394	UHRF2	GOTERM_BP_FAT	<a href="#">regulation of transcription from RNA polymerase II promoter</a>	26	1.90E-02	3.90E-01
ILMN_1697268	-0.836865	0.09821321	EMILIN2	GOTERM_BP_FAT	<a href="#">negative regulation of nitrogen compound metabolic process</a>	20	2.20E-02	4.10E-01
ILMN_1749915	-0.5981271	0.09710187	C1orf63	GOTERM_BP_FAT	<a href="#">negative regulation of transcription</a>	18	2.70E-02	4.20E-01
ILMN_1703477	-0.5192355	0.09669668	ARHGEF2	GOTERM_BP_FAT	<a href="#">negative regulation of macromolecule biosynthetic process</a>	20	3.50E-02	4.50E-01
ILMN_2171289	-1.8790541	0.09620509	SAMSN1	GOTERM_BP_FAT	<a href="#">negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process</a>	19	3.60E-02	4.40E-01
ILMN_1684497	-0.630926	0.09565401	PYROXD2	GOTERM_BP_FAT	<a href="#">negative regulation of gene expression</a>	18	5.50E-02	5.50E-01
ILMN_1734543	-0.692723	0.09520887	PTPRE	GOTERM_BP_FAT	<a href="#">negative regulation of macromolecule metabolic process</a>	21	1.90E-01	8.20E-01
ILMN_3307926	-0.5134761	0.09490384	ADRBK1	GOTERM_BP_FAT	<a href="#">regulation of transcription, DNA-dependent</a>	41	4.70E-01	9.70E-01
ILMN_1709795	-1.5240674	0.09409073	RAC2	GOTERM_BP_FAT	<a href="#">regulation of RNA metabolic process</a>	41	5.30E-01	9.80E-01
ILMN_1716264	-1.9172883	0.09344087	ANKRD1	<b>Annotation Cluster 43</b> <b>Enrichment Score: 1.49</b>		<b>Count</b>	<b>P_Value</b>	<b>Benjamini</b>
ILMN_1898682	-0.3377023	0.09318444	PHIP	INTERPRO	<a href="#">Interferon regulatory factor-3</a>	3	7.90E-03	2.50E-01
ILMN_2069128	-0.5487559	0.09207791	EPB41L2	UP_SEQ_FEATURE	<a href="#">DNA-binding region:Tryptophan pentad repeat</a>	3	1.30E-02	5.00E-01
ILMN_1691539	-0.5962633	0.0919627	LAT	INTERPRO	<a href="#">Interferon regulatory factor</a>	3	1.30E-02	3.50E-01
ILMN_2167805	-0.7360011	0.09138069	LUM	INTERPRO	<a href="#">Interferon regulatory factor, conserved site</a>	3	1.30E-02	3.50E-01
ILMN_3230435	-0.5040896	0.09065887	VOPP1	SMART	<a href="#">IRF</a>	3	2.20E-02	3.80E-01
ILMN_1893633	-0.8568681	0.08968221	LOC439949	INTERPRO	<a href="#">SMAD domain-like</a>	3	3.50E-02	5.50E-01
ILMN_1694840	-0.8034787	0.0894372	MATN2	GOTERM_MF_FAT	<a href="#">RNA polymerase II transcription factor activity</a>	8	2.90E-01	9.30E-01
ILMN_1741942	-0.398401	0.08924177	STX16	INTERPRO	<a href="#">Winged helix repressor DNA-binding</a>	6	3.20E-01	9.80E-01
ILMN_1776157	-0.7247066	0.08898276	sept-04	<b>Annotation Cluster 44</b> <b>Enrichment Score: 1.47</b>		<b>Count</b>	<b>P_Value</b>	<b>Benjamini</b>
ILMN_1666775	-0.7897341	0.08870249	CACNA1C	GOTERM_BP_FAT	<a href="#">actin cytoskeleton organization</a>	11	2.90E-02	4.30E-01
ILMN_1707695	-2.0889034	0.08849268	IFIT1	GOTERM_BP_FAT	<a href="#">cytoskeleton organization</a>	17	3.30E-02	4.40E-01
ILMN_1887174	-0.5456803	0.08846726	KIAA0146	GOTERM_BP_FAT	<a href="#">actin filament-based process</a>	11	4.20E-02	4.70E-01
ILMN_1742789	-0.891553	0.0884307	LPXN	<b>Annotation Cluster 45</b> <b>Enrichment Score: 1.46</b>		<b>Count</b>	<b>P_Value</b>	<b>Benjamini</b>
ILMN_1767665	-0.9345106	0.08790112	GPX8	GOTERM_BP_FAT	<a href="#">regulation of cell activation</a>	11	5.60E-03	2.10E-01
ILMN_2082273	-0.4205569	0.08783904	RG55	GOTERM_BP_FAT	<a href="#">regulation of lymphocyte activation</a>	10	5.60E-03	2.10E-01
ILMN_1799487	-0.5319377	0.08777045	N4BP2L1	GOTERM_BP_FAT	<a href="#">negative regulation of immune system process</a>	7	1.00E-02	2.90E-01
ILMN_2398159	-0.8470689	0.0872646	DKK3	GOTERM_BP_FAT	<a href="#">regulation of leukocyte activation</a>	10	1.20E-02	3.10E-01
ILMN_2098947	-0.4422655	0.08719556	AKO95700	GOTERM_BP_FAT	<a href="#">negative regulation of lymphocyte activation</a>	4	1.20E-01	7.10E-01
ILMN_1794782	-0.7457796	0.0850738	ABCG1	GOTERM_BP_FAT	<a href="#">negative regulation of leukocyte activation</a>	4	1.30E-01	7.40E-01
ILMN_1745607	-0.7011312	0.08489525	A2M	GOTERM_BP_FAT	<a href="#">negative regulation of cell activation</a>	4	1.50E-01	7.70E-01
ILMN_1666785	-0.3553518	0.08374754	SYNE1	GOTERM_BP_FAT	<a href="#">negative regulation of T cell activation</a>	3	2.40E-01	8.70E-01
ILMN_2148459	-0.6083047	0.08253118	B2M	<b>Annotation Cluster 46</b> <b>Enrichment Score: 1.43</b>		<b>Count</b>	<b>P_Value</b>	<b>Benjamini</b>
ILMN_1791912	-0.6120568	0.08252943	SIDT2	INTERPRO	<a href="#">Tumour necrosis factor-like</a>	6	2.00E-03	1.00E-01
ILMN_2086470	-0.5840968	0.08087385	PDGFRA	INTERPRO	<a href="#">Tumor Necrosis Factor</a>	3	4.50E-02	5.80E-01
ILMN_1678841	-0.740746	0.08058992	UBD	SMART	<a href="#">TNF</a>	3	7.10E-02	6.30E-01
ILMN_2057981	-0.6686943	0.07909441	FAM164A	GOTERM_MF_FAT	<a href="#">tumor necrosis factor receptor binding</a>	3	7.70E-02	6.30E-01
ILMN_1898518	-0.7783019	0.07836554	GFRA1	GOTERM_MF_FAT	<a href="#">tumor necrosis factor receptor superfamily binding</a>	3	1.50E-01	7.80E-01
ILMN_1911042	-0.320335	0.07807413	PIP4K2A	<b>Annotation Cluster 47</b> <b>Enrichment Score: 1.42</b>		<b>Count</b>	<b>P_Value</b>	<b>Benjamini</b>
ILMN_1806752	-0.5997548	0.07768083	PLEKHH2	GOTERM_BP_FAT	<a href="#">response to nutrient</a>	9	1.30E-02	3.20E-01
ILMN_1795181	-1.0102658	0.07754815	DDX60	GOTERM_BP_FAT	<a href="#">response to vitamin A</a>	5	1.40E-02	3.30E-01
ILMN_1757552	-0.418643	0.0775457	PTRF	GOTERM_BP_FAT	<a href="#">response to extracellular stimulus</a>	11	2.50E-02	4.20E-01
ILMN_1687501	-1.0911491	0.07745464	MOXD1	GOTERM_BP_FAT	<a href="#">response to vitamin</a>	5	5.80E-02	5.50E-01
ILMN_1706643	-0.6055509	0.07680008	COL6A3	GOTERM_BP_FAT	<a href="#">response to nutrient levels</a>	9	7.10E-02	6.00E-01
ILMN_1665909	-0.297439	0.07678253	LASP1	GOTERM_BP_FAT	<a href="#">response to retinoic acid</a>	3	1.60E-01	8.00E-01

ILMN_1703487	-0.4389223	0.07673918	LMO4
ILMN_1799672	-0.4509294	0.07661649	CROCC
ILMN_1731086	-0.4449785	0.07578874	ISL2
ILMN_3241046	-1.3381329	0.07547525	MYBL1
ILMN_1713449	-0.8047564	0.07521348	TBX3
ILMN_2323944	-0.4712394	0.07488582	FAM110A
ILMN_1657683	-0.5632711	0.07470582	C1orf198
ILMN_1732799	-0.6397462	0.07385269	CD34
ILMN_1651826	-0.8626967	0.07272068	BASP1
ILMN_3245066	-0.3758309	0.07259768	DENND4B
ILMN_1742618	-3.0690904	0.071611	XAF1
ILMN_1715392	-0.4913739	0.06900385	PRPF3
ILMN_1673933	-0.4612814	0.06829594	NPIP
ILMN_1794470	-0.4384409	0.06795633	ANKFY1
ILMN_1678842	-0.9679654	0.06760374	THBS2
ILMN_1652512	-0.5816504	0.06735905	C2CD2
ILMN_2122103	-0.4310925	0.06677511	ETS1
ILMN_1663195	-0.5292518	0.06537721	MCM7
ILMN_2407389	-0.6593715	0.06515683	GPNMB
ILMN_2224143	-0.3779939	0.06345493	MCM3
ILMN_1808634	-0.3223416	0.06081992	DRAM2
ILMN_1829768	-1.0059533	0.05623433	BC047110
ILMN_1693538	-0.3450073	0.0555692	STK36
ILMN_1764709	-0.5225451	0.05520299	MAFB
ILMN_1778691	-0.5633244	0.05478557	TIA1
ILMN_1731224	-1.1919034	0.05411996	PARP9
ILMN_3244110	-0.426818	0.05406091	FAM156B
ILMN_1678961	-0.4991477	0.05171973	FRMD4A
ILMN_1864685	-0.7294178	0.04989669	BC062365
ILMN_1708006	-0.8261792	0.0494976	MICA
ILMN_3207230	-0.5748084	0.04940914	LOC283588
ILMN_2104356	-1.2947727	0.04938726	COL1A2
ILMN_2131523	-0.8579557	0.04890701	SACS
ILMN_1677038	-1.0649506	0.04827893	C7orf58
ILMN_1660844	-0.5447026	0.04755662	INTS4
ILMN_2277334	-0.5340706	0.04749291	KCNK2
ILMN_3236156	-0.3006278	0.04617408	OSTC
ILMN_1774077	-0.7700593	0.0439755	GBP2
ILMN_1658926	-0.5617282	0.04273477	NOTCH3
ILMN_1750075	-0.4129226	0.04257144	DMTF1
ILMN_1651346	-0.824809	0.04253814	TICAM2
ILMN_1668526	-1.3196023	0.04111992	GVIN1
ILMN_1701308	-1.2155994	0.03902149	COL1A1
ILMN_1773059	-0.6809862	0.03829685	GPR124
ILMN_1662773	-0.4721382	0.03742247	SNURF-SNRPN
ILMN_2396991	-1.237827	0.03555138	HCST
ILMN_1809094	-0.8183383	0.03473254	AX747733
ILMN_2131177	-0.6153819	0.03458107	GUCY1A3
ILMN_1782412	-1.0307853	0.03383414	IRX2
ILMN_2223941	-0.5435536	0.03249535	FBLN5
ILMN_1666594	-1.4824603	0.03224498	IRF8
ILMN_2129234	-0.3020076	0.03192231	TMEM47
ILMN_1760062	-2.460666	0.03003611	IFI44
ILMN_3300358	-0.7018808	0.02966945	ZNF84
ILMN_1721704	-0.3054528	0.02947792	FNTA
ILMN_2383693	-0.404843	0.02874064	UPF2
ILMN_2233366	-0.453265	0.0280124	ASAP1

**Annotation Cluster 48 Enrichment Score: 1.42**

INTERPRO	<a href="#">Tumour necrosis factor-like</a>
SP_PIR_KEYWORDS	<a href="#">collagen</a>
UP_SEQ_FEATURE	domain:C1q
INTERPRO	<a href="#">Complement C1q protein</a>
UP_SEQ_FEATURE	domain:Collagen-like
SMART	<a href="#">C1Q</a>

**Annotation Cluster 49 Enrichment Score: 1.41**

GOTERM_BP_FAT	<a href="#">regulation of T cell activation</a>
GOTERM_BP_FAT	<a href="#">regulation of cell activation</a>
GOTERM_BP_FAT	<a href="#">regulation of lymphocyte activation</a>
GOTERM_BP_FAT	<a href="#">regulation of leukocyte activation</a>
GOTERM_BP_FAT	<a href="#">regulation of T cell proliferation</a>
GOTERM_BP_FAT	<a href="#">regulation of lymphocyte proliferation</a>
GOTERM_BP_FAT	<a href="#">regulation of leukocyte proliferation</a>
GOTERM_BP_FAT	<a href="#">regulation of mononuclear cell proliferation</a>

**Annotation Cluster 50 Enrichment Score: 1.39**

GOTERM_BP_FAT	<a href="#">positive regulation of defense response</a>
GOTERM_BP_FAT	<a href="#">regulation of inflammatory response</a>
GOTERM_BP_FAT	<a href="#">positive regulation of inflammatory response</a>
GOTERM_BP_FAT	<a href="#">positive regulation of response to external stimulus</a>
GOTERM_BP_FAT	<a href="#">regulation of response to external stimulus</a>
GOTERM_BP_FAT	<a href="#">regulation of acute inflammatory response</a>

**Annotation Cluster 51 Enrichment Score: 1.39**

UP_SEQ_FEATURE	propeptide:Removed in mature form
UP_SEQ_FEATURE	lipid moiety-binding region:GPI-anchor amidated serine
SP_PIR_KEYWORDS	<a href="#">gpi-anchor</a>
GOTERM_CC_FAT	<a href="#">anchored to membrane</a>
SP_PIR_KEYWORDS	<a href="#">phosphatidylinositol linkage</a>

**Annotation Cluster 52 Enrichment Score: 1.32**

GOTERM_BP_FAT	<a href="#">apoptosis</a>
GOTERM_BP_FAT	<a href="#">cell death</a>
GOTERM_BP_FAT	<a href="#">programmed cell death</a>
GOTERM_BP_FAT	<a href="#">death</a>
SP_PIR_KEYWORDS	<a href="#">Apoptosis</a>

**Annotation Cluster 53 Enrichment Score: 1.29**

SP_PIR_KEYWORDS	<a href="#">GTPase activation</a>
UP_SEQ_FEATURE	domain:Rho-GAP
INTERPRO	<a href="#">RhoGAP</a>
SMART	<a href="#">RhoGAP</a>

**Annotation Cluster 54 Enrichment Score: 1.26**

GOTERM_BP_FAT	<a href="#">regulation of immune effector process</a>
GOTERM_BP_FAT	<a href="#">regulation of defense response to virus</a>
GOTERM_BP_FAT	<a href="#">regulation of response to biotic stimulus</a>
GOTERM_BP_FAT	<a href="#">regulation of multi-organism process</a>

**Annotation Cluster 55 Enrichment Score: 1.26**

UP_SEQ_FEATURE	domain:EGF-like 9
UP_SEQ_FEATURE	domain:EGF-like 8
UP_SEQ_FEATURE	domain:EGF-like 7
UP_SEQ_FEATURE	domain:EGF-like 3
INTERPRO	<a href="#">EGF-like region, conserved site</a>
SP_PIR_KEYWORDS	<a href="#">egf-like domain</a>
INTERPRO	<a href="#">EGF-like, type 3</a>
INTERPRO	<a href="#">EGF</a>
INTERPRO	<a href="#">EGF-like calcium-binding</a>
UP_SEQ_FEATURE	domain:EGF-like 5
UP_SEQ_FEATURE	domain:EGF-like 6; calcium-binding

Count	P_Value	Benjamini
6	2.00E-03	1.00E-01
8	2.90E-03	3.10E-02
3	1.30E-01	9.70E-01
3	1.30E-01	8.50E-01
3	1.60E-01	9.80E-01
3	2.00E-01	8.30E-01
9	4.40E-03	1.90E-01
11	5.60E-03	2.10E-01
10	5.60E-03	2.10E-01
10	1.20E-02	3.10E-01
4	1.60E-01	7.80E-01
4	2.80E-01	9.00E-01
4	2.80E-01	9.10E-01
4	2.80E-01	9.10E-01
6	2.30E-02	4.10E-01
6	2.60E-02	4.30E-01
4	2.80E-02	4.30E-01
5	5.30E-02	5.30E-01
8	6.30E-02	5.70E-01
3	7.80E-02	6.20E-01
11	1.70E-02	5.40E-01
5	2.30E-02	5.90E-01
7	4.00E-02	2.30E-01
10	5.60E-02	5.60E-01
3	1.30E-01	4.90E-01
22	2.60E-02	4.30E-01
25	2.90E-02	4.30E-01
22	3.00E-02	4.40E-01
25	3.00E-02	4.40E-01
10	3.50E-01	7.70E-01
8	4.00E-02	2.40E-01
5	4.10E-02	7.80E-01
5	4.50E-02	5.80E-01
5	9.70E-02	6.70E-01
8	7.00E-03	2.30E-01
3	6.50E-02	5.70E-01
3	1.30E-01	7.40E-01
3	1.50E-01	7.70E-01
5	1.00E-03	1.10E-01
4	1.30E-02	4.90E-01
4	1.60E-02	5.40E-01
6	1.70E-02	5.50E-01
12	3.50E-02	5.70E-01
10	4.10E-02	2.40E-01
9	4.20E-02	5.90E-01
7	4.30E-02	5.90E-01
6	4.40E-02	5.90E-01
4	4.80E-02	8.20E-01
3	8.80E-02	9.50E-01



ILMN_1666208	-0.7825285	0.02779676	MIS18BP1
ILMN_2328094	-0.7981768	0.02583879	DACT1
ILMN_1792506	-0.616087	0.02408154	PLA1A
ILMN_1790136	-0.4774218	0.02381867	C20orf20
ILMN_2402172	-0.7193549	0.02330241	sept-04
ILMN_1807042	-0.8996551	0.02306721	MARCKS
ILMN_1812473	-0.5861107	0.02185519	MLLT3
ILMN_1717934	-0.7884955	0.02136703	SYT11
ILMN_1767448	-0.5449091	0.01176193	LHFP
ILMN_1701441	-0.8963832	0.01134446	LPAR1
ILMN_1755727	-0.4310157	0.01116782	KDM5B
ILMN_1836958	-0.7591832	0.01066616	BM703456
ILMN_2395373	-0.711017	0.00998119	GABBR1
ILMN_1678143	-0.7815368	0.00972039	ARHGDI1
ILMN_1789007	-1.7765667	0.0091216	APOC1
ILMN_1778238	-0.4870963	0.00862525	UTP6
ILMN_1742230	-0.6534504	0.0061385	BAZ1A
ILMN_3231881	-0.358492	0.0047442	PTMA
ILMN_1711894	-1.7565196	0.00328988	MYB
ILMN_1691731	-1.3722534	-0.04E-04	PARP14
ILMN_1753101	-1.2060335	-0.0021272	VTCN1
ILMN_2344650	-0.5655251	-0.003253	N4BP2L1
ILMN_1714809	-0.4781135	-0.0040298	RPIA
ILMN_3220952	-0.9335808	-0.0156769	ANKRD36
ILMN_2325028	-0.8411629	-0.0159033	ODF2L
ILMN_1700448	-0.9654986	-0.0248813	SIM2
ILMN_1830984	-0.8059158	-0.0326325	BF509118
ILMN_1736670	-0.9749128	-0.0442319	PPP1R3C
ILMN_2088437	-1.4015719	-0.0448213	CX3CR1
ILMN_1710937	-1.2329658	-0.0533357	IFI16
ILMN_1706502	-0.7579128	-0.0572491	EIF2AK2
ILMN_2351466	-2.0834424	-0.0743181	NTM
ILMN_1663866	-1.4258738	-0.081615	TGFB1
ILMN_1723912	-3.1892138	-0.1006719	IFI44L
ILMN_1835092	-2.9079618	-0.1650913	IFI44L

	UP_SEQ_FEATURE	domain:EGF-like 1
	UP_SEQ_FEATURE	domain:EGF-like 2
	SMART	<a href="#">EGF_CA</a>
	UP_SEQ_FEATURE	domain:EGF-like 4
	INTERPRO	<a href="#">EGF-like</a>
	INTERPRO	<a href="#">EGF-like calcium-binding conserved site</a>
	INTERPRO	<a href="#">EGF-type aspartate/asparagine hydroxylation conserved site</a>
	INTERPRO	<a href="#">EGF calcium-binding</a>
	UP_SEQ_FEATURE	domain:EGF-like 6
	SMART	<a href="#">EGF</a>
<b>Annotation Cluster 56</b>	<b>Enrichment Score: 1.26</b>	
	BIOCARTA	<a href="#">Neutrophil and Its Surface Molecules</a>
	BIOCARTA	<a href="#">Adhesion Molecules on Lymphocyte</a>
	BIOCARTA	<a href="#">Monocyte and its Surface Molecules</a>
<b>Annotation Cluster 57</b>	<b>Enrichment Score: 1.22</b>	
	GOTERM_CC_FAT	<a href="#">endosome membrane</a>
	GOTERM_CC_FAT	<a href="#">endosomal part</a>
	GOTERM_CC_FAT	<a href="#">endosome</a>
<b>Annotation Cluster 58</b>	<b>Enrichment Score: 1.21</b>	
	GOTERM_BP_FAT	<a href="#">positive regulation of protein amino acid phosphorylation</a>
	GOTERM_BP_FAT	<a href="#">positive regulation of phosphorylation</a>
	GOTERM_BP_FAT	<a href="#">positive regulation of phosphate metabolic process</a>
	GOTERM_BP_FAT	<a href="#">positive regulation of phosphorus metabolic process</a>
	GOTERM_BP_FAT	<a href="#">positive regulation of cellular protein metabolic process</a>
	GOTERM_BP_FAT	<a href="#">positive regulation of protein metabolic process</a>
	GOTERM_BP_FAT	<a href="#">positive regulation of protein modification process</a>
	GOTERM_BP_FAT	<a href="#">regulation of peptidyl-tyrosine phosphorylation</a>
	GOTERM_BP_FAT	<a href="#">positive regulation of peptidyl-tyrosine phosphorylation</a>
	GOTERM_BP_FAT	<a href="#">regulation of protein amino acid phosphorylation</a>
	GOTERM_BP_FAT	<a href="#">regulation of phosphorus metabolic process</a>
	GOTERM_BP_FAT	<a href="#">regulation of phosphate metabolic process</a>
	GOTERM_BP_FAT	<a href="#">regulation of phosphorylation</a>
	GOTERM_BP_FAT	<a href="#">regulation of protein modification process</a>
	GOTERM_BP_FAT	<a href="#">regulation of cellular protein metabolic process</a>
<b>Annotation Cluster 59</b>	<b>Enrichment Score: 1.2</b>	
	KEGG_PATHWAY	<a href="#">Fc epsilon RI signaling pathway</a>
	KEGG_PATHWAY	<a href="#">B cell receptor signaling pathway</a>
	BIOCARTA	<a href="#">Fc Epsilon Receptor I Signaling in Mast Cells</a>
	KEGG_PATHWAY	<a href="#">VEGF signaling pathway</a>
<b>Annotation Cluster 60</b>	<b>Enrichment Score: 1.19</b>	
	GOTERM_MF_FAT	<a href="#">phosphoinositide phospholipase C activity</a>
	GOTERM_MF_FAT	<a href="#">phospholipase C activity</a>
	GOTERM_MF_FAT	<a href="#">lipase activity</a>
	GOTERM_MF_FAT	<a href="#">peptide receptor activity</a>
	GOTERM_MF_FAT	<a href="#">peptide receptor activity, G-protein coupled</a>
	GOTERM_MF_FAT	<a href="#">phospholipase activity</a>
	GOTERM_MF_FAT	<a href="#">phosphoric diester hydrolase activity</a>
<b>Annotation Cluster 61</b>	<b>Enrichment Score: 1.09</b>	
	INTERPRO	<a href="#">FERM/acyl-CoA-binding protein, 3-helical bundle</a>
	INTERPRO	<a href="#">FERM domain</a>
	INTERPRO	<a href="#">FERM central domain</a>
	UP_SEQ_FEATURE	domain:FERM
	INTERPRO	<a href="#">Band 4.1 domain</a>
	INTERPRO	<a href="#">FERM conserved site</a>
	INTERPRO	<a href="#">Band 4.1 subgroup</a>
	INTERPRO	<a href="#">FERM, N-terminal</a>
	SMART	<a href="#">B41</a>
<b>Annotation Cluster 62</b>	<b>Enrichment Score: 1.08</b>	

Count	6	9.30E-02	9.50E-01
Count	5	1.00E-01	9.50E-01
Count	6	1.10E-01	6.80E-01
Count	4	1.10E-01	9.50E-01
Count	8	1.10E-01	8.20E-01
Count	5	1.30E-01	8.50E-01
Count	5	1.30E-01	8.50E-01
Count	4	1.80E-01	8.90E-01
Count	3	2.10E-01	9.90E-01
Count	8	2.70E-01	9.00E-01
Count	3	4.20E-02	8.40E-01
Count	3	5.30E-02	8.20E-01
Count	3	7.60E-02	8.70E-01
Count	5	3.70E-02	5.00E-01
Count	5	3.70E-02	5.00E-01
Count	11	1.60E-01	8.60E-01
Count	7	1.40E-02	3.30E-01
Count	7	2.10E-02	4.00E-01
Count	7	2.30E-02	4.20E-01
Count	7	2.30E-02	4.20E-01
Count	11	3.40E-02	4.50E-01
Count	11	4.40E-02	4.80E-01
Count	9	5.60E-02	5.40E-01
Count	5	6.30E-02	5.70E-01
Count	4	8.50E-02	6.40E-01
Count	8	8.90E-02	6.50E-01
Count	16	1.20E-01	7.20E-01
Count	16	1.20E-01	7.20E-01
Count	15	1.50E-01	7.70E-01
Count	10	2.10E-01	8.40E-01
Count	14	2.60E-01	8.80E-01
Count	8	8.00E-03	5.10E-02
Count	7	2.30E-02	1.20E-01
Count	4	1.30E-01	8.60E-01
Count	3	6.60E-01	9.20E-01
Count	4	1.70E-02	4.50E-01
Count	4	3.00E-02	4.60E-01
Count	6	6.90E-02	6.10E-01
Count	6	1.10E-01	7.00E-01
Count	6	1.10E-01	7.00E-01
Count	5	1.10E-01	7.00E-01
Count	5	1.10E-01	7.10E-01
Count	4	5.50E-02	6.30E-01
Count	4	6.80E-02	6.90E-01
Count	4	6.80E-02	6.90E-01
Count	4	7.10E-02	9.10E-01
Count	4	7.90E-02	7.10E-01
Count	4	7.90E-02	7.10E-01
Count	3	8.90E-02	7.50E-01
Count	3	1.20E-01	8.40E-01
Count	4	1.40E-01	7.30E-01
Count		P_Value	Benjamini

	GOTERM_BP_FAT	<a href="#">positive regulation of cell motion</a>		7	2.10E-02	4.10E-01
	GOTERM_BP_FAT	<a href="#">regulation of cell motion</a>		10	2.80E-02	4.30E-01
	INTERPRO	<a href="#">Small chemokine, C-X-C, conserved site</a>		3	4.50E-02	5.80E-01
	GOTERM_BP_FAT	<a href="#">positive regulation of cell migration</a>		5	1.30E-01	7.40E-01
	GOTERM_BP_FAT	<a href="#">positive regulation of locomotion</a>		5	1.70E-01	8.10E-01
	GOTERM_BP_FAT	<a href="#">regulation of cell migration</a>		7	1.70E-01	8.10E-01
	GOTERM_BP_FAT	<a href="#">regulation of locomotion</a>		7	2.50E-01	8.80E-01
<b>Annotation Cluster 63</b>	<b>Enrichment Score: 1.06</b>		<b>Count</b>		<b>P_Value</b>	<b>Benjamini</b>
	GOTERM_BP_FAT	<a href="#">myeloid cell differentiation</a>		8	4.50E-03	1.80E-01
	GOTERM_BP_FAT	<a href="#">homeostasis of number of cells</a>		5	1.80E-01	8.10E-01
	GOTERM_BP_FAT	<a href="#">erythrocyte differentiation</a>		3	2.50E-01	8.80E-01
	GOTERM_BP_FAT	<a href="#">erythrocyte homeostasis</a>		3	3.00E-01	9.10E-01
<b>Annotation Cluster 64</b>	<b>Enrichment Score: 1.02</b>		<b>Count</b>		<b>P_Value</b>	<b>Benjamini</b>
	UP_SEQ_FEATURE	repeat:IV		3	9.50E-02	9.50E-01
	UP_SEQ_FEATURE	repeat:II		3	9.50E-02	9.50E-01
	UP_SEQ_FEATURE	repeat:III		3	9.50E-02	9.50E-01
	UP_SEQ_FEATURE	repeat:I		3	9.50E-02	9.50E-01
<b>Annotation Cluster 65</b>	<b>Enrichment Score: 1.02</b>		<b>Count</b>		<b>P_Value</b>	<b>Benjamini</b>
	GOTERM_BP_FAT	<a href="#">regulation of transcription from RNA polymerase II promoter</a>		26	1.90E-02	3.90E-01
	GOTERM_BP_FAT	<a href="#">positive regulation of macromolecule metabolic process</a>		29	2.50E-02	4.20E-01
	GOTERM_BP_FAT	<a href="#">positive regulation of biosynthetic process</a>		24	3.50E-02	4.40E-01
	GOTERM_BP_FAT	<a href="#">positive regulation of specific transcription from RNA polymerase II promoter</a>		5	3.70E-02	4.50E-01
	GOTERM_BP_FAT	<a href="#">positive regulation of gene-specific transcription</a>		6	4.30E-02	4.80E-01
	GOTERM_BP_FAT	<a href="#">positive regulation of macromolecule biosynthetic process</a>		22	5.60E-02	5.40E-01
	GOTERM_BP_FAT	<a href="#">regulation of specific transcription from RNA polymerase II promoter</a>		6	5.70E-02	5.50E-01
	GOTERM_BP_FAT	<a href="#">regulation of gene-specific transcription</a>		7	7.70E-02	6.20E-01
	GOTERM_BP_FAT	<a href="#">positive regulation of cellular biosynthetic process</a>		22	8.20E-02	6.30E-01
	GOTERM_BP_FAT	<a href="#">positive regulation of gene expression</a>		19	9.30E-02	6.60E-01
	GOTERM_BP_FAT	<a href="#">positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process</a>		19	1.50E-01	7.70E-01
	GOTERM_BP_FAT	<a href="#">positive regulation of transcription, DNA-dependent</a>		15	1.70E-01	8.00E-01
	GOTERM_BP_FAT	<a href="#">positive regulation of RNA metabolic process</a>		15	1.80E-01	8.20E-01
	GOTERM_BP_FAT	<a href="#">positive regulation of nitrogen compound metabolic process</a>		19	1.80E-01	8.20E-01
	GOTERM_BP_FAT	<a href="#">positive regulation of transcription</a>		17	1.90E-01	8.10E-01
	GOTERM_BP_FAT	<a href="#">negative regulation of specific transcription from RNA polymerase II promoter</a>		3	2.30E-01	8.60E-01
	GOTERM_BP_FAT	<a href="#">negative regulation of gene-specific transcription</a>		3	2.90E-01	9.10E-01
	GOTERM_MF_FAT	<a href="#">transcription activator activity</a>		12	2.90E-01	9.30E-01
	GOTERM_BP_FAT	<a href="#">positive regulation of transcription from RNA polymerase II promoter</a>		11	3.00E-01	9.20E-01
<b>Annotation Cluster 66</b>	<b>Enrichment Score: 1.01</b>		<b>Count</b>		<b>P_Value</b>	<b>Benjamini</b>
	UP_SEQ_FEATURE	domain:PARP catalytic		3	4.40E-02	8.00E-01
	INTERPRO	<a href="#">Poly(ADP-ribose) polymerase, catalytic region</a>		3	4.50E-02	5.80E-01
	GOTERM_MF_FAT	<a href="#">transferase activity, transferring pentosyl groups</a>		4	8.00E-02	6.30E-01
	GOTERM_MF_FAT	<a href="#">NAD+ ADP-ribosyltransferase activity</a>		3	1.00E-01	7.00E-01
	SP_PIR_KEYWORDS	<a href="#">nad</a>		5	5.20E-01	9.00E-01
<b>Annotation Cluster 67</b>	<b>Enrichment Score: 1.01</b>		<b>Count</b>		<b>P_Value</b>	<b>Benjamini</b>
	GOTERM_MF_FAT	<a href="#">protein binding, bridging</a>		6	5.60E-02	5.50E-01
	GOTERM_MF_FAT	<a href="#">SH3/SH2 adaptor activity</a>		4	9.20E-02	6.70E-01
	GOTERM_MF_FAT	<a href="#">molecular adaptor activity</a>		4	1.80E-01	8.30E-01