

Supplementary Table 7 : Transcripts and DAVID pathways correlating with expression of CD3 in lupus kidney biopsies

Positive correlation				Negative correlation			
Transcripts	Pathways			Transcripts	Pathways		
Identifier	Gene Symbol	Correlation coefficient with CD3		Identifier	Gene Symbol	Correlation coefficient with CD3	
ILMN_2325873	CD3D	1		ILMN_1726667	LOC728758	-0.4000032	
ILMN_2061043	CD48	0.905183649		ILMN_1767032	DDI1	-0.400066325	
ILMN_2261416	CD3D	0.880984568		ILMN_3307863	TAO3C	-0.400088253	
ILMN_1886655	TCRVB	0.875380574		ILMN_1840934	A4220430	-0.400098378	
ILMN_1655800	BCL11A	0.861258356		ILMN_3235584	TRIM66	-0.400112323	
ILMN_2098126	CCL5	0.853134526		ILMN_2145760	YIPF4	-0.400116748	
ILMN_1716651	RUNX2	0.839003672		ILMN_2146648	PRB3	-0.400169733	
ILMN_329520	PKRKB	0.838813012		ILMN_1692825	PSMG1	-0.400176912	
ILMN_1770673	ANXA	0.83418713		ILMN_1907812	BX119471	-0.400196296	
ILMN_1665943	MAP4K1	0.830396057		ILMN_3248052	NCCP91	-0.400210194	
ILMN_1673357	SLA2	0.828638555		ILMN_1660730	SLC7A3	-0.400203553	
ILMN_2208903	CD52	0.824780534		ILMN_2295698	AFG3L1	-0.400443702	
ILMN_2254635	ITGAX	0.811373324		ILMN_1752283	ITCH	-0.400444333	
ILMN_1731233	GZMH	0.806929173		ILMN_1767178	LOC146880	-0.400491102	
ILMN_1769129	CCL19	0.805805201		ILMN_1709142	PURA	-0.400693024	
ILMN_2376204	LTB	0.805671563		ILMN_1813350	HSD11B2	-0.400701446	
ILMN_1806908	PKRKB	0.804641104		ILMN_2278518	WATC2BP	-0.400724215	
ILMN_1794386	IL2RG	0.791218525		ILMN_1670918	INSR	-0.40077098	
ILMN_1786176	CD37	0.791172895		ILMN_1652164	UNC93B1	-0.400807543	
ILMN_1659075	HLA-DQA	0.789961811		ILMN_1879135	BM673749	-0.401053769	
ILMN_1758085	ARHGAP30	0.789946281		ILMN_1727272	CTCB12	-0.401088379	
ILMN_2353733	CDBA	0.788912749		ILMN_1675523	PPAP2C	-0.401219234	
ILMN_1768284	PRYB	0.785638873		ILMN_1673537	WFD3C	-0.401428233	
ILMN_2340217	PTPRC	0.785485884		ILMN_1756311	UFSF2	-0.401502034	
ILMN_3214389	HLA-DQB1	0.785218182		ILMN_2415949	MRRF	-0.40159747	
ILMN_1691341	IL7R	0.784804795		ILMN_2246188	SLC45A2	-0.401677326	
ILMN_1763452	EYV2B	0.783038697		ILMN_1776325	UBE2Q1	-0.401841236	
ILMN_2376205	F1B	0.780843066		ILMN_2389568	SDW6	-0.401857034	
ILMN_1738675	PTPN6	0.780070703		ILMN_1742275	ZNF1	-0.401857034	
ILMN_2393765	IGLL1	0.78007563		ILMN_3238793	C9orf129	-0.40193216	
ILMN_2157441	HLA-DRA	0.779288567		ILMN_1772873	PLCJ2	-0.401938593	
ILMN_2196550	C13orf18	0.778303127		ILMN_3226405	PRAMEF11	-0.402033476	
ILMN_1804601	DNF2P686D16G	0.775621629		ILMN_1987861	BMS5070	-0.402129106	
ILMN_2400747	C12orf1	0.773692814		ILMN_2089838	TRAF3IP2	-0.402167298	
ILMN_2143314	SP1B	0.773692781		ILMN_1743441	GSTP7	-0.402186142	
ILMN_1768482	CDBA	0.771129432		ILMN_1706065	FAM182A	-0.402215847	
ILMN_2309848	FXYD5	0.77024314		ILMN_1700042	TIN2	-0.402283739	
ILMN_1704286	FXYD5	0.770242943		ILMN_1849418	AW661821	-0.40233352	
ILMN_2378253	CD37	0.769482881		ILMN_3294277	CYP4F24P	-0.402349711	
ILMN_1680466	FAM181N1	0.767923121		ILMN_2260133	TMEM1614	-0.402352748	
ILMN_1676924	CD247	0.767126598		ILMN_1733035	M2T2A	-0.40257141	
ILMN_1695025	CD2	0.766718855		ILMN_1658152	MAP3K10	-0.402590451	
ILMN_1700428	HLA-DOB	0.765918173		ILMN_1712339	ZNF276	-0.402627478	
ILMN_1697554	SH3G3	0.764417308		ILMN_1812461	WISP2	-0.40264155	
ILMN_2208413	ARHGAP15	0.763687084		ILMN_2134888	TUBE1	-0.402689098	
ILMN_1756507	HRF4	0.763024234		ILMN_1756273	ATRN14G3	-0.402793831	
ILMN_1737974	CD3E	0.758439012		ILMN_1788267	PPP1R4D	-0.402876165	
ILMN_1811049	POU2AF1	0.755417112		ILMN_2206224	ORAM2	-0.402891662	
ILMN_1682993	NG7	0.755323021		ILMN_1712943	CCKC	-0.40290978	
ILMN_1710734	GZMK	0.753469918		ILMN_1779597	CIDEC	-0.402971794	
ILMN_1653305	PTPRC	0.752709707		ILMN_1804907	OR1F2	-0.403005451	
ILMN_1803886	ADA	0.752556696		ILMN_1851487	A051233	-0.403002551	
ILMN_1677505	CCL21	0.752131606		ILMN_1704176	PSN91	-0.403037388	
ILMN_1762594	NOD2	0.751679484		ILMN_1690689	A0207883	-0.403054195	
ILMN_1773388	C13orf18	0.749302367		ILMN_3185794	LOC100125556	-0.403106213	
ILMN_1779257	CD40	0.748078332		ILMN_3250153	REP2	-0.403146906	
ILMN_2114568	GBPS	0.747336346		ILMN_1652188	EPGS	-0.403154388	
ILMN_1781626	C1S	0.746386111		ILMN_1805372	A1798827	-0.403338422	
ILMN_2083066	IGLL3P	0.745838169		ILMN_3243578	LOC348120	-0.403358976	
ILMN_1802106	AP0BCE3G	0.7452804		ILMN_1759879	LOC220115	-0.403403636	
ILMN_1724422	SELL	0.74420065		ILMN_1806710	ESPN	-0.403422886	
ILMN_2246328	PPN2D2	0.743332805		ILMN_1813712	NA	-0.40345686	
ILMN_2175912	ITGB2	0.743016506		ILMN_1724211	GRPSC1	-0.403517298	
ILMN_1688959	CD27	0.742592537		ILMN_1727798	MOSP1D1	-0.403533644	
ILMN_1739508	abPars	0.742273943		ILMN_1659224	FMN1	-0.403546244	
ILMN_1685675	UCP2	0.741491632		ILMN_2154654	PTP4A1	-0.403636181	
ILMN_1662799	GPM3M3	0.741472537		ILMN_3311045	MIR216A	-0.403738395	
ILMN_2412192	CFH	0.741262487		ILMN_3247792	LOC100169752	-0.403765568	
ILMN_1779324	GZMA	0.74074612		ILMN_3291253	SFBP1P1	-0.403821065	
ILMN_2093343	PLAC8	0.738757748		ILMN_3239946	LOC729375	-0.403829371	
ILMN_1713561	CD20orf103	0.737266474		ILMN_1764090	AK4	-0.404040144	
ILMN_2304328	TF5A1	0.737163562		ILMN_3251751	MFSD9B	-0.404149001	
ILMN_1761733	HLA-DMB	0.736745071		ILMN_1874673	BM681652	-0.404243205	
ILMN_1745356	CXCL9	0.735582717		ILMN_1727606	C12orf59	-0.404301321	
ILMN_1652631	IGLPR2	0.734206859		ILMN_1771538	PSCA	-0.404331358	
ILMN_1695851	PARVG	0.733408869		ILMN_1841564	CD51T297	-0.404352664	
ILMN_1766509	EOMES	0.732844369		ILMN_1731959	TULP3	-0.40446544	
ILMN_2120565	PTPRB	0.731933562		ILMN_3247979	LOC100105873	-0.404494901	
ILMN_2168217	GRP183	0.727406789		ILMN_1749612	MMP1L1	-0.404543366	
ILMN_1797822	SELL13	0.727060476		ILMN_1810552	CAV3	-0.404603466	
ILMN_2345353	LS1T1	0.726210713		ILMN_2104141	FGOS	-0.404645123	
ILMN_1772359	LAP7M5	0.726004222		ILMN_3269324	A094963	-0.404848263	
ILMN_1680274	abPars	0.725307949		ILMN_3241218	ANKK1	-0.404869986	
ILMN_1733579	EV12A	0.725160501		ILMN_3284127	TRIM64B	-0.404885171	
ILMN_1763487	CTLA4	0.725124087		ILMN_3282032	USP17L2	-0.404892803	
ILMN_1717261	HLA-DRB1	0.724374021		ILMN_1706225	N4BP1	-0.404993058	

Gene	Feature	Category	Count	P-Value	Benjamini
ILMN_1718936	LS1T	0.67224888			
ILMN_1777998	ARHGAP25	0.67202644			
ILMN_1782057	ATPB82	0.67191762			
ILMN_2232688	TMS6X	0.67164519			
ILMN_1772218	HLA-DPA1	0.67092724			
ILMN_2379644	CD74	0.67025327			
ILMN_2109416	NAPS8	0.67015396			
ILMN_1756937	STB5A4	0.66891267			
ILMN_3226868	HLA-DPB1	0.66664054			
ILMN_1653498	GSF6	0.66610252			
ILMN_1691290	CLLSR3	0.66581008			
ILMN_2060606	HLA-DRB6	0.66543107			
ILMN_1676528	BTN3A2	0.665034585			
ILMN_2113333	LGALS9B	0.664937888			
ILMN_1685403	MMP7	0.66473021			
ILMN_1700795	RAC2	0.66403783			
ILMN_2249920	FYN	0.662901355			
ILMN_1710434	TBC1D10C	0.662466513			
ILMN_1653026	PLAC8	0.661502048			
ILMN_1712134	VAV1	0.661396887			
ILMN_1814194	TCF4	0.661347794			
ILMN_3249400	abParts	0.660118602			
ILMN_1734346	STGAL5	0.659938916			
ILMN_1723684	DARC	0.659105387			
ILMN_1797362	ILMK1	0.658908964			
ILMN_2167416	MRI1	0.658025234			
ILMN_2201678	FSTL1	0.658754384			
ILMN_1695640	PTPN22	0.658512971			
ILMN_1660368	TRRAP	0.658380229			
ILMN_1690139	KIAA748	0.65829327			
ILMN_1716983	ILKRA2	0.657877054			
ILMN_1718552	CKCL13	0.657876289			
ILMN_1768016	TNFRSF17	0.657768889			
ILMN_1761788	MOXD1	0.657081246			
ILMN_2388155	CASP3	0.656504153			
ILMN_1778723	AMICA1	0.656465201			
ILMN_1812392	TMSB10	0.656166009			
ILMN_2331525	PRKD2	0.655512294			
ILMN_3232447	ARHBD175	0.655153418			
ILMN_1707070	PCOLCE	0.654474893			
ILMN_1734200	RASSF1	0.654311811			
ILMN_1795762	CDC102A	0.654372052			
ILMN_1678143	ARHGDB3	0.6543491914			
ILMN_2342271	BC1L1A	0.654351229			
ILMN_1666078	HLA-H	0.652991422			
ILMN_1679379	RHMS5	0.652287815			
ILMN_1696907	CTCF	0.65223877			
ILMN_1733998	DHRS9	0.652071693			
ILMN_2395711	ARRB2	0.651877828			
ILMN_2347145	DCN	0.65133399			
ILMN_1676256	TSPAB1	0.651275576			
ILMN_1702787	SEMA4A	0.650728045			
ILMN_1763907	CENPW	0.650074396			
ILMN_1773352	CCLS1	0.649943939			
ILMN_2176063	FCGR1C	0.649641219			
ILMN_1770085	BTG2	0.649211721			
ILMN_1713058	PSY92P	0.648615032			
ILMN_2369018	EV12A	0.648472613			
ILMN_1814895	PDLIM7	0.646894802			
ILMN_1761464	CD74	0.646714479			
ILMN_1765258	HLA-E	0.646113068			
ILMN_2192072	MMP7	0.646035365			
ILMN_2193233	MZB1	0.644949722			
ILMN_2079655	KLRB1	0.644921487			
ILMN_2348788	CD44	0.644575991			
ILMN_2164476	CLL12	0.644223203			
ILMN_1700147	VPREB3	0.644050661			
ILMN_1759312	AMPD1	0.643717364			
ILMN_1665761	BC1L1B	0.642540306			
ILMN_3219558	TUBA1C	0.642395865			
ILMN_2117508	CTHRC1	0.642089036			
ILMN_3234841	RP123AP7	0.640238317			
ILMN_1800368	NKOR1-1	0.640073624			
ILMN_1719759	TNC	0.638694332			
ILMN_1716547	NAGK	0.638512775			
ILMN_1687888	BTN3A1	0.638139215			
ILMN_1691693	FCRH3	0.63761599			
ILMN_2074358	BARD1	0.63761065			
ILMN_2087692	CYBB01	0.63699207			
ILMN_1727402	HCLS1	0.635139063			
ILMN_2074432	OR2A2	0.635033426			
ILMN_2316236	HOPX	0.634952281			
ILMN_1653220	PITPNM1	0.633781969			
ILMN_1798379	ITIH4	0.633384125			
ILMN_1685387	PIGR	0.632940527			
ILMN_1864900	MIAT	0.632288927			
ILMN_2095549	SYK	0.632054354			
ILMN_1719905	TLR10	0.632037054			
ILMN_1785272	COL1A2	0.631449596			
ILMN_1774555	domain:protein kinase		90	2.50E-07	2.50E-04
ILMN_1774555	ILMAA		90	2.50E-07	2.50E-04
ILMN_1809931	NRD1		94	3.30E-07	7.60E-04
ILMN_1666140	PRY7		100	3.50E-07	3.00E-04
ILMN_1830083	OR338706		90	5.70E-07	6.40E-04
ILMN_3308748	MIR346		46	2.70E-06	7.80E-05
ILMN_1689504	G30R18		111	3.60E-06	6.30E-04
ILMN_1714643	MGAM		152	3.50E-06	3.30E-03
ILMN_1888037	CA41597		71	1.30E-05	2.60E-04
ILMN_1689809	DG6P12		196	1.30E-05	2.50E-04
ILMN_1712161	RCO1		241	1.30E-05	3.40E-04
ILMN_2219681	RRP2		40	2.30E-05	2.50E-03
ILMN_1716822	KRTAP9-2		137	3.40E-05	1.60E-03
ILMN_1743187	C6orf120		68	4.10E-05	1.50E-02
ILMN_1696162	MME		161	4.40E-05	1.90E-03
ILMN_2320850	URE2D3		161	4.40E-05	1.90E-03
ILMN_1784359	CNN3		107	4.70E-05	2.20E-02
ILMN_1750624	KRXG		79	9.70E-05	7.90E-03
ILMN_2200210	G1A10		67	1.10E-04	3.20E-02
ILMN_1651848	ITSN1		266	3.40E-04	2.20E-02
ILMN_2381730	EGF7		266	3.40E-04	2.20E-02
ILMN_1739886	HNFA4		219	3.50E-04	2.10E-02
ILMN_1846567	IX107471		318	3.90E-04	2.20E-02
ILMN_1654013	CL7orf28		193	6.00E-04	7.20E-03
ILMN_1764120	IGF2AS		219	7.40E-04	3.50E-02
ILMN_1813775	GAK		49	7.80E-04	1.00E-01
ILMN_1836627	ABO9874		272	1.00E-03	4.80E-02
ILMN_1861915	CAS92115		229	1.80E-03	7.20E-02
ILMN_3286751	LOC284648		230	2.10E-03	7.50E-02
ILMN_1802649	C11orf58		225	2.30E-03	7.50E-02
ILMN_2062793	SRAL		49	9.0E-03	4.0E-01
ILMN_1655537	ING1		9	P-Value	Benjamini
ILMN_1699216	FLJ45721		52	2.60E-05	1.30E-03
ILMN_2195665	PANX3		61	3.40E-05	1.60E-03
ILMN_3230032	KPR1		61	5.20E-05	2.30E-03
ILMN_3310775	MIR1323		16	1.60E-07	2.00E-05
ILMN_1714884	GHRHR		16	1.60E-07	2.00E-05
ILMN_1784176	ABCA5		15	1.40E-05	7.60E-04
ILMN_1786125	CNNA2		9	7.60E-05	3.00E-03
ILMN_2293607	PM2D01		8	8.70E-05	3.30E-03
ILMN_1779370	ARHGEP9		6	1.10E-03	2.60E-02
ILMN_1755869	OR5T11		6	1.10E-03	2.60E-02
ILMN_1904931	KCNQ5		57	4.60E-08	1.90E-06
ILMN_1743635	ALG1A		68	7.70E-05	2.20E-03
ILMN_3245464	NCRM5		64	8.40E-05	2.30E-03
ILMN_1764286	TEE3		153	4.10E-04	9.10E-03
ILMN_1703826	UNC5D		16	3.70E-03	6.10E-02
ILMN_3310775	MIR1328		153	4.10E-04	9.10E-03
ILMN_1908889	CB32373		29	6.40E-07	7.00E-05
ILMN_2321301	GRIN1		37	3.30E-06	2.60E-04
ILMN_1726752	APTX		23	1.90E-05	1.00E-03
ILMN_1758196	LOC619207		18	2.60E-04	7.50E-03
ILMN_3286312	NEK2		22	2.80E-04	7.90E-03
ILMN_1760088	CNCR		22	2.80E-04	7.90E-03
ILMN_1691106	CDV3		16	1.60E-03	3.60E-02
ILMN_1740920	ACAD9B		64	1.00E-08	2.00E-06
ILMN_1633006	CNS151		34	1.00E-07	1.40E-05
ILMN_1803676	INOSF1		34	1.00E-07	1.40E-05
ILMN_1793578	ZFP37		25	1.00E-06	1.00E-04
ILMN_3200717	LOC643387		23	4.90E-06	3.40E-04
ILMN_1687291	CDFP		93	1.10E-05	6.40E-04
ILMN_1675873	GLCSF3		93	1.10E-05	6.40E-04
ILMN_2396702	GRIN2		90	1.10E-05	6.60E-04
ILMN_2404539	CDorf30		31	1.30E-05	7.10E-04
ILMN_1821517	K64709		50	3.00E-05	1.40E-03
ILMN_1723874	MPP5E		51	3.70E-05	1.70E-03
ILMN_2111387	IL0V16		105	5.20E-05	2.30E-03
ILMN_1813645	MIR5051		52	5.20E-05	2.20E-03
ILMN_1811555	C6orf119		35	7.00E-05	2.90E-03
ILMN_3306691	LOC729467		20	1.30E-04	4.30E-03
ILMN_1907700	AAS51223		67	1.40E-04	4.70E-03
ILMN_1740185	TPMT		19	1.60E-04	5.30E-03
ILMN_1685689	LGALS9C		27	1.90E-04	5.90E-03
ILMN_1754708	TWE2		41	2.00E-04	6.10E-03
ILMN_1682399	CLOCK		68	2.30E-04	6.90E-03
ILMN_2122669	TOPORS		92	2.60E-04	7.50E-03
ILMN_2156953	ZFAND6		23	2.60E-04	7.50E-03
ILMN_2162819	UGT2B11		69	4.40E-04	1.30E-02
ILMN_1814046	NFYF		12	1.00E-03	2.40E-02
ILMN_1800898	ARG2		10	2.70E-03	5.20E-02
ILMN_1717094	ZNF618		12	3.70E-03	6.60E-02
ILMN_3236192	NA		19	1.60E-01	7.50E-01
ILMN_1718718	MKKS		13	9.60E-08	1.50E-03
ILMN_1746457	GTF3C2		10	2.60E-05	2.60E-03
ILMN_3249588	NSG1A2		7	2.00E-04	4.90E-03
ILMN_3239408	REXO111		5	5.80E-03	8.40E-02
ILMN_3298163	CR594811		23	4.60E-06	1.20E-04
ILMN_2234605	AGRN		12	3.00E-05	1.30E-03
ILMN_1698745	CLRN1		12	3.00E-05	1.30E-03
IL					

Gene	Enrichment Score	Category	Count	P-Value	Benjamini	Gene	P-Value	Benjamini
ILMN_2062714	0.63094981	SP_PIR_KEYWORDS	14	1.10E-05	2.30E-04	ILMN_1654430	AK129671	-0.412605565
ILMN_1773059	GPR124	SP_PIR_KEYWORDS	14	1.10E-05	2.30E-04	ILMN_1384433	LOC100130285	-0.412605565
ILMN_1663080	LFGN	SP_PIR_KEYWORDS	15	2.00E-05	3.70E-04	ILMN_1793832	GRB14	-0.412609831
ILMN_1803396	TARB11	UP_SEQ_FEATURE	7	1.20E-04	4.10E-02	ILMN_1601882	CTP	-0.412715763
ILMN_1653828	CHFR	GOTERM_CC_FAT	14	1.50E-04	3.60E-03	ILMN_1816458	DB298233	-0.412747859
ILMN_2101885	TUBB	SP_PIR_KEYWORDS	24	2.10E-04	3.00E-03	ILMN_1775138	PEG3	-0.412824696
ILMN_1764788	TNFRSF18	SP_PIR_KEYWORDS	11	1.26E-04	3.60E-03	ILMN_1800923	ORAM1	-0.412857678
ILMN_1712419	DCDC2	INTERPRO	22	5.20E-04	8.70E-02	ILMN_1740728	SMTN1L	-0.412909528
ILMN_1803988	MCL1	UP_SEQ_FEATURE	9	2.40E-03	4.40E-01	ILMN_1843648	AWR73324	-0.413007328
ILMN_1662483	CDS3	GOTERM_MF_FAT	7	2.40E-03	4.10E-02	ILMN_1752381	DNAC13	-0.413130352
ILMN_2226955	VOPPP1	GOTERM_CC_FAT	26	3.70E-03	6.10E-02	ILMN_1810233	UGT2B11	-0.413038655
ILMN_2202283	HRRNP1A1	Annotation Cluster 23	Enrichment Score: 3.83			ILMN_3309374	MIR1301	-0.413065195
ILMN_1681679	TSPD	GOTERM_BP_FAT	35	2.90E-08	4.30E-06	ILMN_3237665	LRTOMT	-0.413133146
ILMN_1719986	PKCIP1	GOTERM_BP_FAT	19	4.10E-03	7.20E-02	ILMN_1796337	CXCL17	-0.413215692
ILMN_2373062	RHBDF2	GOTERM_BP_FAT	12	2.80E-02	7.90E-01	ILMN_2151281	GABARAPL1	-0.413219986
ILMN_1687301	VCAN	Annotation Cluster 24	Enrichment Score: 3.77			ILMN_1666510	SNRPB-SNRPN	-0.413232596
ILMN_1798316	MMP9	GOTERM_MF_FAT	103	1.00E-07	3.20E-05	ILMN_2231177	OR7E24	-0.41332793
ILMN_1672417	PTPRCAP	GOTERM_MF_FAT	66	5.20E-04	2.80E-02	ILMN_1756779	CLTC	-0.413379014
ILMN_2384544	ADAM15	GOTERM_MF_FAT	70	2.00E-03	7.40E-02	ILMN_3262909	C6orf176	-0.413382783
ILMN_1807042	MARCKS	GOTERM_MF_FAT	39	7.90E-03	1.90E-01	ILMN_1916599	LOC100133985	-0.413388093
ILMN_1764362	LYR	Annotation Cluster 25	Enrichment Score: 3.59			ILMN_2284157	CLDN18	-0.413403205
ILMN_1652825	ILDR4	GOTERM_BP_FAT	65	5.50E-10	2.60E-07	ILMN_1903282	AT69787	-0.413431488
ILMN_1673708	HDAC9	GOTERM_BP_FAT	45	4.20E-07	4.70E-05	ILMN_1808769	Clorf97	-0.413446668
ILMN_1815895	HLA-DRB1	GOTERM_BP_FAT	41	8.00E-07	8.30E-05	ILMN_1730575	GLIC	-0.413471068
ILMN_2098847	AKO9700	GOTERM_BP_FAT	45	2.00E-06	1.80E-04	ILMN_3225978	NA	-0.413478373
ILMN_1674228	abPp4t5	GOTERM_BP_FAT	32	2.30E-06	2.00E-04	ILMN_1808983	BC071719	-0.413514628
ILMN_1784610	TMEM2	GOTERM_BP_FAT	24	2.60E-06	2.20E-04	ILMN_1752562	ENFR2	-0.413517126
ILMN_1767556	ITOF10	GOTERM_BP_FAT	32	6.50E-06	4.10E-04	ILMN_1795673	Ctsorf173	-0.413685852
ILMN_1792323	HDC	GOTERM_BP_FAT	29	9.10E-06	5.60E-04	ILMN_1790810	HCN4	-0.413705885
ILMN_1780368	GPR18	GOTERM_BP_FAT	24	2.40E-05	1.20E-03	ILMN_1802628	PPAPDC2	-0.413715285
ILMN_1805027	KLC3	GOTERM_BP_FAT	21	3.80E-05	1.70E-03	ILMN_2413264	SOCS4	-0.413735775
ILMN_1705442	OMTM3	GOTERM_BP_FAT	25	4.70E-05	2.10E-03	ILMN_1673234	PKDREJ	-0.413858526
ILMN_1774733	SOCS1	GOTERM_BP_FAT	25	4.70E-05	2.10E-03	ILMN_1737345	HDDC2	-0.413894248
ILMN_2309180	SMARCD3	GOTERM_BP_FAT	24	1.10E-04	3.90E-03	ILMN_1769416	TIN	-0.413924612
ILMN_1683980	PLEKHM2	GOTERM_BP_FAT	14	1.50E-04	4.80E-03	ILMN_2406304	PDRN3	-0.413983308
ILMN_3239033	TG	GOTERM_BP_FAT	14	2.00E-04	6.30E-03	ILMN_2393688	SYN1	-0.413995013
ILMN_2330307	SLC43A3	GOTERM_BP_FAT	17	2.60E-04	7.60E-03	ILMN_2046315	GABARAPL2	-0.414003193
ILMN_2300140	LOC65638	GOTERM_BP_FAT	17	2.60E-04	7.60E-03	ILMN_1695601	A098920	-0.414089787
GOTERM_1700268	PTGDR	GOTERM_BP_FAT	18	2.60E-04	7.50E-03	ILMN_1817612	HA554377	-0.414087167
ILMN_1750321	TRANK1	GOTERM_BP_FAT	18	2.60E-04	7.50E-03	ILMN_1695924	NDUF4F4	-0.414344572
ILMN_1715760	HUAT	GOTERM_BP_FAT	12	2.70E-04	7.60E-03	ILMN_3270493	FAM75A3	-0.41445667
ILMN_1679880	THOC6	GOTERM_BP_FAT	17	6.70E-04	1.70E-02	ILMN_1690796	OR4F21	-0.414544236
ILMN_1778401	HLA-B	GOTERM_BP_FAT	12	1.00E-03	3.40E-02	ILMN_3100300	MIR1265	-0.41468888
ILMN_1696004	LRRK1	GOTERM_BP_FAT	12	1.30E-03	3.10E-02	ILMN_1813741	KCNJ16	-0.414769556
ILMN_2328776	MTS1	GOTERM_BP_FAT	10	2.70E-03	5.20E-02	ILMN_1719857	GRIPAP1	-0.414775116
ILMN_1728272	MYH9	GOTERM_BP_FAT	16	6.90E-03	1.10E-01	ILMN_1725556	TMEM229A	-0.414776159
ILMN_1669447	PYHIN1	GOTERM_BP_FAT	8	7.50E-03	1.10E-01	ILMN_1674678	RMBY1A1	-0.41486818
ILMN_1676361	ARHGAP22	GOTERM_BP_FAT	11	1.70E-02	2.10E-01	ILMN_1669367	LOC100130827	-0.414944988
ILMN_2413779	SEZ6L2	GOTERM_BP_FAT	8	2.70E-02	2.90E-01	ILMN_1723846	METTL21B	-0.414963649
ILMN_1688780	S100A4	GOTERM_BP_FAT	6	2.90E-02	3.00E-01	ILMN_1664001	ARF5	-0.415177798
ILMN_1693552	CD300A	GOTERM_BP_FAT	6	3.80E-02	3.50E-01	ILMN_3237226	MBO3L2	-0.415237183
ILMN_1727761	GMEB1	GOTERM_BP_FAT	4	4.40E-02	3.90E-01	ILMN_1751615	COQ10B	-0.415264295
ILMN_2122374	FAM49B	GOTERM_BP_FAT	6	8.90E-02	5.80E-01	ILMN_3238159	MAOA	-0.415279276
ILMN_1733937	MMD	GOTERM_BP_FAT	4	1.40E-01	7.30E-01	ILMN_2300898	SEMA6B	-0.415324484
ILMN_2400030	PTPN2	GOTERM_BP_FAT	3	3.00E-01	9.20E-01	ILMN_1661417	MAGED2	-0.415345173
ILMN_1702229	CECR6	Annotation Cluster 26	Enrichment Score: 3.52			ILMN_1808085	ALD4283	-0.415354593
ILMN_2391458	ACSL4	SP_PIR_KEYWORDS	53	3.30E-06	9.20E-05	ILMN_1730401	LOC442421	-0.415372318
ILMN_1708167	CDCP1	GOTERM_MF_FAT	63	1.30E-04	9.20E-03	ILMN_2178994	TUBB8	-0.4153855
ILMN_1729351	ZHX2	GOTERM_CC_FAT	50	2.80E-03	4.80E-02	ILMN_1677885	DNAH14	-0.415424878
ILMN_1769769	H3F3C	GOTERM_MF_FAT	80	8.70E-03	1.70E-01	ILMN_1776412	RTKAP10-11	-0.415431221
ILMN_1742450	TARBP	Annotation Cluster 27	Enrichment Score: 3.43			ILMN_1764175	GPD1	-0.415493143
ILMN_1722622	CD163	UP_SEQ_FEATURE	48	5.30E-05	2.20E-02	ILMN_1783835	ZNF845	-0.415497474
ILMN_2360710	TPM1	INTERPRO	54	1.90E-04	3.90E-02	ILMN_3307777	RETNL8	-0.415508894
ILMN_1701643	GDPD5	INTERPRO	56	5.70E-04	8.30E-02	ILMN_2153495	WNT7B	-0.415526638
ILMN_1786358	Chorf68	SMART	54	3.20E-03	2.20E-01	ILMN_1747854	GOLGA8E	-0.415553681
ILMN_1683926	PSMB10	Annotation Cluster 28	Enrichment Score: 3.42			ILMN_1783705	GRXCR2	-0.415578478
ILMN_1711383	STX4	GOTERM_BP_FAT	41	8.50E-08	1.20E-05	ILMN_2142353	GRTP1	-0.415616858
ILMN_1765446	EMP3	GOTERM_BP_FAT	17	1.90E-03	3.90E-02	ILMN_1691466	YES1	-0.415623012
ILMN_1684040	THEM5	GOTERM_BP_FAT	14	2.80E-03	5.30E-02	ILMN_1747696	TPM3	-0.415637933
ILMN_1740298	SIGLEC5	GOTERM_BP_FAT	8	4.80E-02	4.10E-01	ILMN_1809844	MMP26	-0.415701214
ILMN_1780773	RPL10	Annotation Cluster 29	Enrichment Score: 3.37			ILMN_2054971	HPR1A1	-0.415706793
ILMN_1699440	ZBTB47	SP_PIR_KEYWORDS	44	4.60E-05	7.50E-04	ILMN_3250909	AL137495	-0.416026249
ILMN_2368318	FOR	domainSH3	38	1.00E-04	4.00E-02	ILMN_1732468	HSPA4L	-0.416155751
ILMN_2231051	TCF1L2	INTERPRO	42	8.50E-04	1.10E-01	ILMN_2110094	CFC1	-0.416202827
ILMN_1662932	LCP1	SMART	42	8.00E-03	4.10E-01	ILMN_1725098	RTN4R12	-0.416237184
ILMN_2089990	C1orf21	Annotation Cluster 30	Enrichment Score: 3.28			ILMN_1755120	MAM1A2	-0.416249794
ILMN_1316471	AT768	GOTERM_BP_FAT	52	1.70E-04	5.60E-03	ILMN_3219905	CR2	-0.416260998
ILMN_1690985	STK11P	GOTERM_BP_FAT	50	3.40E-04	9.30E-03	ILMN_1662333	FN3KRP	-0.416397568
ILMN_2143685	CLDN7	GOTERM_BP_FAT	34	4.20E-04	1.10E-02	ILMN_1747207	EYA1	-0.416439267
ILMN_1688401	POCD2	GOTERM_BP_FAT	41	3.20E-03	5.80E-02	ILMN_1662438	SOD1	-0.416442406
ILMN_1774077	GBP2	Annotation Cluster 31	Enrichment Score: 3.18			ILMN_1682495	FOXP1	-0.416638683
ILMN_1658888	PPP1R14B	GOTERM_BP_FAT	26	9.90E-05	3.50E-03	ILMN_1798315	SMR3A	-0.416678713
ILMN_2408851	ARHGAP39	GOTERM_BP_FAT	25	8.30E-04	2.10E-02	ILMN_1739582	HOXD40	-0.416687613
ILMN_2352303	RASSF7	GOTERM_BP_FAT	14	1.40E-03	3.20E-02	ILMN_1729868	SPRYD4	-0.416704212
ILMN_1778977	TYROBP	GOTERM_BP_FAT	15	1.70E-03	3.70E-02	ILMN_1862900	BQ447249	-0.416720569
ILMN_2151277	LPGAT1	Annotation Cluster 32	Enrichment Score: 3.09			ILMN_1672742	ARHGAP23	-0.416730482
ILMN_3235514	GPR183	GOTERM_BP_FAT	94	2.50E-06	2.10E-04	ILMN_1732127	RBK5	-0.416752108
ILMN_2227195	CDC05C	GOTERM_BP_FAT	50	4.70E-03	7.90E-02	ILMN_2274191	PNTA	-0.416793198
ILMN_2389346	ACT11493	GOTERM_BP_FAT	54	6.00E-03	9.70E-02	ILMN_1705562	CR5	-0.416795786
ILMN_1736567	CD74	GOTERM_BP_FAT	54	6.00E-03	9.70E-02	ILMN_3251171	DNASEL1	-0.416969036
ILMN_1737146	TRAM1	Annotation Cluster 33	Enrichment Score: 3.08			ILMN_2122926	VNIR2	-0.416990785
ILMN_1737935	MACF1	GOTERM_MF_FAT	111	4.30E-05	4.00E-03	ILMN_1769091	PRCP	-0.417067754
ILMN_1790562	EYA3	GOTERM_MF_FAT	90	1.10E-03	4.60E-02	ILMN_1753287	DLL3	-0.417101695
ILMN_1713829	PTGES	GOTERM_MF_FAT	55	1.30E-03	2.60E-01	ILMN_1662914	CTAGE5	-0.417154243
ILMN_2040730	S100B10	Annotation Cluster 34	Enrichment Score: 3.07			ILMN_1672545	GIPC2	-0.417163992
ILMN_1704380	INC11	GOTERM_BP_FAT	25	7.10E-05	2.90E-03	ILMN_1663620	GLYCAM1	-0.417174223

ILMN_1790692	GNLY	0.603689842	GOTERM_BP_FAT	response to lipopolysaccharide	21	7.0E-04	1.90E-02
ILMN_1654586	RASA3	0.603376818	GOTERM_BP_FAT	response to bacterium	36	1.10E-02	1.50E-01
ILMN_1748767	H3FA3	0.603376677	Annotation Cluster 35			Enrichment Score: 3.07	Count
ILMN_2082035	GALNT1	0.603323079	GOTERM_BP_FAT	regulation of cytokine production	4	1.20E-05	7.10E-04
ILMN_1752520	SLFN11	0.603231831	GOTERM_BP_FAT	positive regulation of cytokine production	21	5.60E-03	9.10E-02
ILMN_2056032	CD99	0.603123207	GOTERM_BP_FAT	positive regulation of multicellular organism process	44	8.80E-03	1.30E-01
ILMN_3209399	KRT18	0.603098497	Annotation Cluster 36			Enrichment Score: 3.06	Count
ILMN_1701558	MAP1A	0.603086915	SP_PIR_KEYWORDS	tyrosine-protein kinase	29	2.10E-05	3.70E-04
ILMN_2347234	PRMT1	0.602918858	GOTERM_MF_FAT	protein tyrosine kinase activity	40	2.30E-05	2.50E-03
ILMN_1768595	DIGA	0.602696042	INTERPRO	tyrosine protein kinase	29	1.68E-01	3.90E-01
ILMN_1809400	FAM49B	0.602608444	SP_PIR_KEYWORDS	tyrosine-specific protein kinase	15	4.90E-04	6.30E-03
ILMN_1652198	CCM2	0.602568861	GOTERM_MF_FAT	non-membrane spanning protein tyrosine kinase activity	14	6.80E-04	3.40E-02
ILMN_2415162	sepi-O1	0.601925714	SMART	TyrK	29	1.30E-03	2.20E-01
ILMN_1750678	TMD4	0.601850364	GOTERM_BP_FAT	peptidyl-tyrosine modification	15	1.40E-03	3.20E-02
ILMN_1697864	Cxorf38	0.601731587	SP_PIR_KEYWORDS	autophosphorylation	14	2.00E-03	1.90E-02
ILMN_1803560	LAT2	0.601483034	GOTERM_BP_FAT	peptidyl-tyrosine dephosphorylation	14	2.80E-03	5.30E-02
ILMN_1796216	VASH1	0.601372713	INTERPRO	Tyrosine protein kinase, active site	21	7.80E-03	4.70E-01
ILMN_1730777	KRT19	0.601322531	GOTERM_MF_FAT	transmembrane receptor protein tyrosine kinase activity	13	9.80E-02	7.40E-01
ILMN_1649968	PLEKHQ2	0.601230939	Annotation Cluster 37			Enrichment Score: 2.95	Count
ILMN_2140055	LAMA4	0.601035403	SP_PIR_KEYWORDS	signal	450	4.20E-08	1.80E-06
ILMN_1791447	CXCL12	0.600986897	UP_SEQ_FEATURE	signal peptide	450	6.80E-08	8.60E-05
ILMN_2348905	CTLA4	0.600403943	GOTERM_CC_FAT	extracellular region part	153	4.10E-04	9.10E-03
ILMN_1766275	PIK3CD	0.600270687	UP_SEQ_FEATURE	disulfide bond	361	1.40E-03	3.20E-01
ILMN_1785005	NC4	0.599983751	SP_PIR_KEYWORDS	disulfide bond	371	1.60E-03	1.60E-02
ILMN_1783909	COL6A2	0.599978988	GOTERM_CC_FAT	extracellular space	104	1.50E-02	1.70E-01
ILMN_2383964	CDC4	0.599760922	SP_PIR_KEYWORDS	Secreted	213	2.20E-02	1.50E-01
ILMN_1718194	MYB	0.599614447	SP_PIR_KEYWORDS	glycoprotein	509	4.90E-02	2.60E-01
ILMN_1746565	CD6	0.59927011	GOTERM_CC_FAT	extracellular region	256	2.70E-01	7.70E-01
ILMN_2319913	DGKA	0.599105464	UP_SEQ_FEATURE	glycosylation site-N-linked (GlcNAc...)	468	3.10E-01	1.00E+00
ILMN_1481798	sepi-O6	0.598834561	Annotation Cluster 38			Enrichment Score: 2.86	Count
ILMN_1691717	RHDZF2	0.598843015	GOTERM_BP_FAT	lymphocyte proliferation	15	3.10E-04	8.60E-03
ILMN_1757877	HCFC1R1	0.598804869	GOTERM_BP_FAT	mononuclear cell proliferation	15	5.30E-04	1.40E-02
ILMN_1683597	RPL23A	0.598585478	GOTERM_BP_FAT	lymphocyte proliferation	15	5.30E-04	1.40E-02
ILMN_1768197	ROD1	0.598554081	GOTERM_BP_FAT	T cell proliferation	10	3.60E-03	6.50E-02
ILMN_1736178	ALBP1	0.598076355	GOTERM_BP_FAT	B cell proliferation	6	1.50E-02	1.90E-01
ILMN_1777242	PREX1	0.598062135	Annotation Cluster 39			Enrichment Score: 2.84	Count
ILMN_1787345	FKBP11	0.597939093	GOTERM_BP_FAT	regulation of myeloid cell differentiation	23	1.90E-05	1.00E-03
ILMN_1742001	CD160	0.597871141	GOTERM_BP_FAT	positive regulation of myeloid cell differentiation	14	7.20E-05	2.80E-03
ILMN_3294339	LOC100131289	0.597150836	GOTERM_BP_FAT	regulation of myeloid leukocyte differentiation	15	2.30E-04	6.90E-03
ILMN_1736180	FRTA1	0.59667339	GOTERM_BP_FAT	positive regulation of myeloid leukocyte differentiation	9	7.00E-04	1.80E-02
ILMN_1782538	VIM	0.596233172	GOTERM_BP_FAT	regulation of osteoclast differentiation	9	3.30E-03	6.00E-02
ILMN_2336953	LAT2	0.596065383	GOTERM_BP_FAT	positive regulation of osteoclast differentiation	4	2.80E-02	2.80E-01
ILMN_1682799	STAMBP1L1	0.596032895	GOTERM_BP_FAT	positive regulation of macrophage differentiation	4	2.80E-02	2.90E-01
ILMN_3241756	FAM136A	0.595989307	GOTERM_BP_FAT	regulation of macrophage differentiation	5	3.70E-02	3.50E-01
ILMN_1676448	WDFY1	0.595422899	Annotation Cluster 40			Enrichment Score: 2.8	Count
ILMN_2370553	GASL2	0.59503625	GOTERM_BP_FAT	actin cytoskeleton organization	48	1.70E-04	5.60E-03
ILMN_1788108	TNND5	0.594645028	GOTERM_BP_FAT	actin filament-based process	49	4.30E-04	1.10E-02
ILMN_1789599	C1orf151	0.594455471	GOTERM_BP_FAT	actin filament organization	18	5.40E-03	8.90E-02
ILMN_2340027	TSPAN4	0.593819557	GOTERM_BP_FAT	cytoskeleton organization	70	1.50E-02	1.90E-01
ILMN_2365465	XBP1	0.593775767	Annotation Cluster 41			Enrichment Score: 2.78	Count
ILMN_3253579	HUAS8	0.592503306	GOTERM_BP_FAT	macromolecular complex assembly	113	2.50E-04	7.40E-03
ILMN_2179837	BANF1	0.59143982	GOTERM_BP_FAT	macromolecular complex subunit organization	117	6.30E-04	1.60E-02
ILMN_1676128	DMNT3A	0.591163242	GOTERM_BP_FAT	cellular macromolecular complex subunit organization	63	2.80E-03	5.40E-02
ILMN_1709747	DOG	0.591080607	GOTERM_BP_FAT	protein complex assembly	84	3.10E-03	5.70E-02
ILMN_1758418	TNFSF13B	0.590937067	GOTERM_BP_FAT	protein complex biogenesis	84	3.10E-03	5.70E-02
ILMN_3286904	LOC648740	0.590877737	GOTERM_BP_FAT	cellular macromolecular complex assembly	56	5.00E-03	8.40E-02
ILMN_1692398	CNTNAP1	0.590772255	Annotation Cluster 42			Enrichment Score: 2.77	Count
ILMN_2370414	CHD3	0.590717352	GOTERM_BP_FAT	regulation of cellular protein metabolic process	95	1.20E-06	1.10E-04
ILMN_1715508	NAMPT	0.590544477	GOTERM_BP_FAT	regulation of protein modification process	64	6.10E-06	3.90E-04
ILMN_17707491	FAM30A	0.590449224	GOTERM_BP_FAT	regulation of protein amino acid phosphorylation	40	1.00E-04	3.60E-03
ILMN_1803392	PDRX3-TAX1BP1	0.590227142	GOTERM_BP_FAT	regulation of peptidyl-tyrosine phosphorylation	19	1.10E-03	2.50E-02
ILMN_1724686	CLDN1	0.590032246	GOTERM_BP_FAT	positive regulation of protein metabolic process	47	1.70E-03	3.70E-02
ILMN_1797875	ALDXSAP	0.589490815	GOTERM_BP_FAT	positive regulation of protein modification process	38	2.10E-03	4.30E-02
ILMN_2407434	DCLK2	0.588966034	GOTERM_BP_FAT	positive regulation of cellular protein metabolic process	45	2.20E-03	4.50E-02
ILMN_2278636	CLX1	0.588620616	GOTERM_BP_FAT	positive regulation of peptidyl-tyrosine phosphorylation	12	2.40E-02	2.70E-01
ILMN_1748448	TNKN4B	0.58851918	GOTERM_BP_FAT	positive regulation of phosphorus metabolic process	20	3.40E-02	3.30E-01
ILMN_3289508	CR604709	0.587948602	GOTERM_BP_FAT	positive regulation of phosphate metabolic process	20	3.40E-02	3.30E-01
ILMN_1799011	CEP250	0.587896074	GOTERM_BP_FAT	positive regulation of phosphorylation	19	4.70E-02	4.00E-01
ILMN_1751368	HNRNP0	0.587671895	GOTERM_BP_FAT	positive regulation of protein amino acid phosphorylation	17	7.40E-02	5.30E-01
ILMN_1811851	PRRX1	0.587388866	Annotation Cluster 43			Enrichment Score: 2.68	Count
ILMN_1708858	CNSK1E	0.587219559	GOTERM_BP_FAT	negative regulation of response to stimulus	30	5.70E-06	3.70E-04
ILMN_1709486	SRPX	0.587180055	GOTERM_BP_FAT	regulation of inflammatory response	21	6.40E-04	1.60E-02
ILMN_1761801	ZNF761	0.586840497	GOTERM_BP_FAT	negative regulation of defense response	11	9.40E-03	1.40E-01
ILMN_2159774	CFP2B1	0.586478776	GOTERM_BP_FAT	negative regulation of inflammatory response	9	3.00E-02	3.00E-01
ILMN_1672589	SEDM4B	0.586456275	GOTERM_BP_FAT	negative regulation of response to external stimulus	12	3.70E-02	3.50E-01
ILMN_1795449	ERCC5	0.586305673	Annotation Cluster 44			Enrichment Score: 2.66	Count
ILMN_1777190	CFD	0.586088619	GOTERM_BP_FAT	chordate embryonic development	60	1.90E-03	3.90E-02
ILMN_2310968	RUFY1	0.585874794	GOTERM_BP_FAT	embryonic development ending in birth or egg hatching	60	2.30E-03	4.60E-02
ILMN_1670101	CLEC2D	0.585592886	GOTERM_BP_FAT	regulation in utero embryonic development	36	2.50E-03	4.90E-02
ILMN_3240321	AIN	0.585538891	Annotation Cluster 45			Enrichment Score: 2.61	Count
ILMN_3258832	CLL4L2	0.58547926	SP_PIR_KEYWORDS	basement membrane	13	7.20E-04	8.40E-03
ILMN_2412214	HUAT	0.58523934	GOTERM_CC_FAT	extracellular matrix part	26	3.70E-03	6.10E-02
ILMN_1703692	TUBB	0.585076042	GOTERM_CC_FAT	basement membrane	19	5.50E-03	8.20E-02
ILMN_3235647	SK1	0.585035279	Annotation Cluster 46			Enrichment Score: 2.61	Count
ILMN_1742025	OLFM1	0.584576844	GOTERM_BP_FAT	viral reproductive process	19	3.20E-04	9.00E-03
ILMN_2384597	FN1	0.583722392	GOTERM_BP_FAT	viral infectious cycle	14	1.40E-03	3.20E-02
ILMN_1712867	PAK2	0.583487565	GOTERM_BP_FAT	viral reproduction	19	1.90E-03	3.90E-02
ILMN_2413808	CD53	0.583416615	GOTERM_BP_FAT	inhibition of viral infection	7	4.40E-02	3.90E-01
ILMN_2141482	SERPINF1	0.583322678	Annotation Cluster 47			Enrichment Score: 2.57	Count
ILMN_1789639	FMOD	0.583148575	GOTERM_BP_FAT	regulation of lymphocyte activation	41	8.00E-07	8.30E-05
ILMN_1798874	TMEM85	0.58261848	GOTERM_BP_FAT	negative regulation of immune system process	27	3.60E-06	2.80E-04
ILMN_1756457	FAF1	0.582299734	GOTERM_BP_FAT	regulation of mononuclear cell proliferation	25	4.70E-05	2.10E-03
ILMN_3176090	RCC2	0.58228734	GOTERM_BP_FAT	regulation of leukocyte proliferation	25	4.70E-05	2.10E-03
ILMN_1765876	ARHGAP24	0.582135806	GOTERM_BP_FAT	regulation of lymphocyte proliferation	24	1.10E-04	3.90E-03

ILMN_1665435	GPER	-0.41717648	ILMN_1790692	GNLY	-0.417193327
ILMN_1719753	VGLL1	-0.417193327	ILMN_1790692	GNLY	-0.417193327
ILMN_1750092	SEPS1C5	-0.417318057	ILMN_1889669	C17orf107	-0.417368407
ILMN_1889669	C17orf107	-0.417368407	ILMN_1728965	C11orf57	-0.417516536
ILMN_1728965	C11orf57	-0.417516536	ILMN_1872769	BX103063	-0.417517017
ILMN_1872769	BX103063	-0.417517017	ILMN_3230215	TXO2	-0.417517707
ILMN_3230215	TXO2	-0.417517707	ILMN_1666403	GC5X	-0.417535439
ILMN_1666403	GC5X	-0.417535439	ILMN_2136737	OHS01M2	-0.417537723
ILMN_2136737	OHS01M2	-0.417537723	ILMN_1668531	BC029817	-0.417629361
ILMN_1668531	BC029817	-0.417629361	ILMN_1756393	VYWA5E2	-0.417629432
ILMN_1756393	VYWA5E2	-0.417629432	ILMN_2149292	TMEM40	-0.417642781
ILMN_2149292	TMEM40	-0.417642781	ILMN_1785095	ATP9V0E2	-0.417649878
ILMN_1785095	ATP9V0E2	-0.417649878	ILMN_3273383	AI661701	-0.41771717
ILMN_3273383	AI661701	-0.41771717	ILMN_1775569	CRISP2	-0.417746142
ILMN_1775569	CRISP2	-0.417746142	ILMN_2075221	C17orf47	-0.41779733
ILMN_2075221	C17orf47	-0.41779733	ILMN_1788530	ADPRHL1	-0.417812312
ILMN_1788530	ADPRHL1	-0.417812312	ILMN_1666364	CDC10A	-0.417819305
ILMN_1666364	CDC10A	-0.417819305	ILMN_1750018	SELL12	-0.417830011
ILMN_1750018	SELL12	-0.417830011	ILMN_1910784	AI809077	-0.41801807
ILMN_1910784	AI809077	-0.41801807	ILMN_1756693	ARHGAP17	-0.418053307
ILMN_1756693	ARHGAP17	-0.418053307	ILMN_1668416	MRFPS18C	-0.418109576
ILMN_1668416	MRFPS18C	-0.418109576	ILMN_1710219	CALCR	-0.418120921
ILMN_1710219	CALCR	-0.418120921	ILMN_2158548	NACA2	-0.418227739
ILMN_2158548	NACA2	-0.418227739	ILMN_2406656	GAT343	-0.41833134
ILMN_2406656	GAT343	-0.41833134	ILMN_1764043	TTL	-0.418349306
ILMN_1764043	TTL	-0.418349306	ILMN_3226181	NUDT7	-0.418363416
ILMN_3226181	NUDT7	-0.418363416	ILMN_1804248	FDP5	-0.418368569
ILMN_1804248	FDP5	-0.418368569	ILMN_1757281	GPRN1	-0.418415109
ILMN_1757281	GPRN1	-0.418415109	ILMN_1779412	ORD1A4	-0.41841626
ILMN_1779412	ORD1A4	-0.41841626	ILMN_1784678	PBX1	-0.418431071
ILMN_1784678	PBX1	-0.418431071	ILMN_1766920	EP400L	-0.418538419
ILMN_1766920	EP400L	-0.418538419	ILMN_1824784	BX111027	-0.418561031
ILMN_1824784	BX111027	-0.418561031	ILMN_16800		

ILMN_1739103	MPZL1	0.567073062	INTERPRO	Nucleotide-binding, alpha-beta plati	39	5.10E-03	3.70E-01	ILMN_1744539	GOLGA6L6	-0.427124594
ILMN_1739496	PRRX1	0.566988682	SMART	RBM	39	2.80E-02	6.10E-01	ILMN_3299074	NODX4	-0.427196511
ILMN_1789302	CIQC	0.566623932	UP_SEQ_FEATURE	domain:RRM 3	10	9.70E-02	1.00E+00	ILMN_1744056	TAMR1	-0.427200336
ILMN_1684306	S100B4	0.566364041	UP_SEQ_FEATURE	domain:RRM	19	1.10E-01	1.00E+00	ILMN_1663054	TNXCCL1	-0.427215149
ILMN_1758895	CTSK	0.566225952	Annotation Cluster 55	Enrichment Score: 2.3	Count	P_Value	Benjamini	ILMN_2342841	ATFPH	-0.427239372
ILMN_2400935	TAGLN	0.565933422		B cell receptor signaling pathway	26	2.90E-05	3.00E-04	ILMN_1732140	ABCC11	-0.427369785
ILMN_1782403	PRR11	0.565643498		Fc epsilon RI signaling pathway	23	1.20E-03	8.70E-03	ILMN_1713550	IGR6	-0.427382452
ILMN_1656998	CHMP4B	0.565633187		VEG signaling pathway	16	1.20E-01	3.30E-01	ILMN_1783333	C16orf61	-0.427497362
ILMN_1704333	PLSCR3	0.565592831		Non-small cell lung cancer	12	1.50E-01	3.90E-01	ILMN_1803452	CRCT1	-0.427555688
ILMN_1307796	KZFS	0.565447866	Annotation Cluster 56	Enrichment Score: 2.28	Count	P_Value	Benjamini	ILMN_1794989	TME4B1B	-0.427608874
ILMN_1719449	DCLK2	0.565426547		short sequence motif:Prevents secretion from ER	15	4.40E-03	5.50E-01	ILMN_1778500	FXC1	-0.427689506
ILMN_1790637	C11orf80	0.565344718		Endoplasmic reticulum targeting sequence	13	4.50E-03	3.50E-01	ILMN_1683755	SOX13	-0.427755615
ILMN_2371685	UBE2E1	0.565285802		Endoplasmic reticulum lumen	19	7.30E-03	9.80E-02	ILMN_1695418	IQGAP3	-0.427775092
ILMN_1669362	IGFBP6	0.565148947	Annotation Cluster 57	Enrichment Score: 2.28	Count	P_Value	Benjamini	ILMN_1732189	SYCE1	-0.427866552
ILMN_2313079	NLRP1	0.564825946		T cell selection	10	1.80E-04	5.70E-03	ILMN_1773898	NBPY3	-0.427871066
ILMN_1698344	CTH	0.564747154		negative T cell selection	6	2.30E-03	4.60E-02	ILMN_1684196	NR1B3	-0.427883388
ILMN_2103362	ARHGAP27	0.564712021		thymic T cell selection	7	2.70E-03	5.20E-02	ILMN_1778611	GBAS	-0.428005127
ILMN_2161577	KC16	0.564709362		negative thymic T cell selection	5	1.00E-02	1.50E-01	ILMN_1783546	CARDK	-0.428044385
ILMN_1652512	C2CD2	0.564640359		T cell differentiation in the thymus	9	1.30E-02	1.80E-01	ILMN_1775716	GOLGA8G	-0.428109839
ILMN_2388419	GMEB1	0.564210631		positive T cell selection	5	1.70E-02	2.10E-01	ILMN_1808494	ITH2	-0.428129218
ILMN_1688453	TM6C	0.564180717		positive thymic T cell selection	4	4.40E-02	3.90E-01	ILMN_1744614	PLEKHG6	-0.428199197
ILMN_1677104	TBAF5	0.564123125	Annotation Cluster 58	Enrichment Score: 2.27	Count	P_Value	Benjamini	ILMN_2044645	CGR1	-0.428243293
ILMN_1800261	TUBA1B	0.563732432		T cell receptor complex	7	1.60E-03	3.10E-02	ILMN_1800500	BBS1	-0.428294225
ILMN_1749372	GGT5	0.563558012		regulation of calcium-mediated signaling	8	7.50E-03	1.10E-01	ILMN_1819158	U03241	-0.428377976
ILMN_2184184	ANXA1	0.563465251		positive regulation of calcium-mediated signaling	7	1.30E-02	1.70E-01	ILMN_1785069	KIAA1845	-0.428401812
ILMN_1324079	OR2A4	0.563448369	Annotation Cluster 59	Enrichment Score: 2.26	Count	P_Value	Benjamini	ILMN_3226841	AK302451	-0.428542024
ILMN_1658823	SAMD3	0.563312409		regulation of inflammatory response	21	6.40E-04	1.60E-02	ILMN_1657478	MAOGL2	-0.428581789
ILMN_1728809	BHLHE41	0.563117144		regulation of response to external stimulus	33	3.00E-03	5.70E-02	ILMN_1784302	LIPI	-0.428598261
ILMN_1772991	MIR671	0.563015281		positive regulation of inflammatory response	10	7.90E-03	1.20E-01	ILMN_1752793	SAP18	-0.428631753
ILMN_1761463	EFHD2	0.562964442		positive regulation of response to external stimulus	16	9.30E-03	1.40E-01	ILMN_1691884	STC2	-0.428656605
ILMN_1805519	DOB93812	0.56265291		negative regulation of response to external stimulus	12	3.70E-02	3.50E-01	ILMN_2363744	PACRG	-0.428713503
ILMN_1762899	EGR1	0.5625233075	Annotation Cluster 60	Enrichment Score: 2.22	Count	P_Value	Benjamini	ILMN_1710075	FAM89A	-0.428759811
ILMN_1741404	MSC	0.562517704		regulation of transcription from RNA polymerase II promoter	124	1.00E-04	3.60E-03	ILMN_1741970	IJP	-0.428896141
ILMN_1788689	PHP	0.562079612		positive regulation of macromolecule metabolic process	142	1.20E-04	4.10E-03	ILMN_3274344	NA	-0.428901316
ILMN_1781824	FASLG	0.561847819		transcription activator activity	70	2.00E-03	7.40E-02	ILMN_1658806	SLCSA10	-0.428919358
ILMN_1706541	FBN1	0.561618666		positive regulation of cellular biosynthetic process	110	2.40E-03	4.70E-02	ILMN_1738601	GLS1	-0.428913688
ILMN_2206722	FER1L4	0.561580205		positive regulation of biosynthetic process	111	2.60E-03	5.20E-02	ILMN_3301551	LPA	-0.428930777
ILMN_2159453	STXB2	0.561259059		positive regulation of macromolecule biosynthetic process	104	4.10E-03	7.20E-02	ILMN_3193266	NA	-0.429343629
ILMN_1678605	CDC123	0.561180066		positive regulation of nitrogen compound metabolic process	99	1.30E-02	1.80E-01	ILMN_1836172	CN28601	-0.429376193
ILMN_1791067	TESK1	0.561090609		positive regulation of gene expression	90	1.50E-02	1.90E-01	ILMN_1746952	SLC25A48	-0.42940315
ILMN_1760347	SRGN	0.560746241		positive regulation of nucleobase, nucleotide, nucleoside and nucleic acid metabolic process	95	1.90E-02	2.30E-01	ILMN_1701881	ZNF365	-0.429405299
ILMN_1810559	RHOQ	0.56049631		positive regulation of transcription	86	2.60E-02	2.80E-01	ILMN_1811345	GLYAT	-0.429439288
ILMN_2255133	BCL11A	0.560445274		positive regulation of transcription, DNA-dependent	73	3.60E-02	3.40E-01	ILMN_2171102	MSL2	-0.429444173
ILMN_1777296	ACTB	0.560083048		positive regulation of RNA metabolic process	73	4.20E-02	3.80E-01	ILMN_1792423	LOC644961	-0.429464603
ILMN_1778360	PYG8	0.560076557		positive regulation of transcription from RNA polymerase II promoter	54	1.40E-01	7.10E-01	ILMN_1704943	GNP3	-0.429574677
ILMN_1715332	TTCC1A	0.560059309	Annotation Cluster 61	Enrichment Score: 2.07	Count	P_Value	Benjamini	ILMN_3273340	HCG_2014417	-0.429757556
ILMN_2392043	SP1	0.5600262049		nucleus	588	4.50E-10	2.70E-08	ILMN_2413473	GH2	-0.429859627
ILMN_2085862	SLC15A3	0.559642175		regulation of transcription from RNA polymerase II promoter	124	1.00E-04	3.60E-03	ILMN_2387952	FAM1348	-0.42989879
ILMN_1773964	H1FX	0.559634508		transcription regulator activity	217	2.20E-03	7.40E-02	ILMN_1776826	ARHGAP42	-0.4299703
ILMN_1745242	PLSCR1	0.559399187		Transcription	266	4.50E-03	3.90E-02	ILMN_3249291	F2	-0.430079256
ILMN_1687533	SEMA4D	0.558835195		transcription regulator activity	259	6.40E-03	5.30E-02	ILMN_3248305	NTNS	-0.430144778
ILMN_1691662	LOC10101266	0.558677748		transcription factor activity	135	4.30E-02	5.30E-01	ILMN_2191634	RPL37	-0.430299327
ILMN_1698307	DNK1	0.558623005		transcription	273	1.60E-01	7.70E-01	ILMN_2317658	RGN	-0.430313299
ILMN_1778064	KICD	0.558502593		dna-binding	219	1.90E-01	5.80E-01	ILMN_3277282	LOC115110	-0.430386399
ILMN_2076640	KIHDRS1	0.558396359		regulation of transcription	329	3.00E-01	9.10E-01	ILMN_1702700	AF257770	-0.430393088
ILMN_1673682	GATAO2A	0.558386315		regulation of RNA metabolic process	227	4.20E-01	9.70E-01	ILMN_1804509	DPPYSL5	-0.430454543
ILMN_1760563	PRRC2A	0.55831406		DNA binding	281	5.00E-01	9.90E-01	ILMN_1846922	BCD42566	-0.430566404
ILMN_1775762	GNAQ2	0.55803172		regulation of transcription, DNA-dependent	216	5.90E-01	9.90E-01	ILMN_3289997	AATK	-0.430589892
ILMN_2398274	PCARD	0.557936114	Annotation Cluster 62	Enrichment Score: 2.06	Count	P_Value	Benjamini	ILMN_1771811	LOC33622	-0.430609188
ILMN_1746408	MIND	0.557904658		taxis	39	3.90E-05	1.70E-03	ILMN_1675819	FAM101A	-0.430709189
ILMN_1770247	HOXA10-HOXA10.5	0.557814311		chemotaxis	39	3.90E-05	1.70E-03	ILMN_3251467	LRRCS5	-0.430856072
ILMN_3266186	HDAC7	0.557527385		inflammatory response	21	2.00E-04	2.80E-03	ILMN_1729453	TSPAN9	-0.430859832
ILMN_2114422	NOD1	0.557283755		Small chemokine, interleukin-8-like	14	5.40E-04	8.40E-02	ILMN_3242059	C6orf221	-0.430860923
ILMN_2379326	MAP3K7	0.557021827		chemokine activity	15	6.80E-04	3.50E-02	ILMN_3390959	MIR93	-0.430882004
ILMN_1662768	NHEK2	0.556802758		chemokine regulation of RNA metabolic process	15	1.40E-03	5.70E-02	ILMN_1807344	STG23	-0.430997736
ILMN_1785061	EPH2E	0.556615308		SMART	14	1.80E-03	1.60E-01	ILMN_1766643	HOPX	-0.431033918
ILMN_1751161	COL7A1	0.556580643		chemotaxis	18	1.80E-03	1.80E-02	ILMN_1748694	NHSL2	-0.431047539
ILMN_1809751	EIF2C3	0.55647979		Cytokine-cytokine receptor interaction	52	1.50E-02	6.80E-02	ILMN_1661173	TRIP4	-0.431057639
ILMN_1706643	COL6A3	0.556342419		locomotory behavior	47	1.60E-02	2.00E-01	ILMN_1658123	DAZ2	-0.431068658
ILMN_1772177	ASC3	0.556308469		PMSF002522-CXC chemokine	6	2.50E-02	9.90E-01	ILMN_1729650	PEXY	-0.431101071
ILMN_1801043	GN	0.556269459		Small chemokine, C-X-C, conserved site	6	4.00E-02	8.40E-01	ILMN_1815967	MG212050	-0.431122926
ILMN_2104536	COL1A2	0.5560443		Small chemokine, C-X-C	5	5.60E-02	9.00E-01	ILMN_1669393	GGT1	-0.431134004
ILMN_1737344	DOXA1	0.556015692		109 Chemokine_families	13	6.10E-02	1.00E+00	ILMN_1877317	AW294700	-0.431142663
ILMN_2335604	SKAP1	0.556009613		cytokine	27	9.80E-02	4.00E-01	ILMN_1756767	E1FSB	-0.431156047
ILMN_1906187	LOC283070	0.555788016		Small chemokine, C-C group, conserved site	6	1.60E-01	9.90E-01	ILMN_3203534	LOC100132474	-0.431207172
ILMN_1737683	FGG	0.555710428		PMSF001950-small inducible chemokine, C/CX types	6	1.60E-01	1.00E+00	ILMN_2401884	IL25	-0.431221288
ILMN_1735467	NRP12	0.555517486		cytokine activity	29	1.80E-01	8.70E-01	ILMN_1656170	IKMMP1	-0.431231211
ILMN_1689725	RPLP1	0.55534293		behavior	65	2.00E-01	8.20E-01	ILMN_1885583	AK129941	-0.431226915
ILMN_3247064	SNRNP40	0.555169482		Small chemokine, C-X-C/Interleukin-8	4	2.20E-01	9.90E-01	ILMN_1806633	LOC348926	-0.431368407
ILMN_1748283	PIM2	0.554839431						ILMN_1667030	HSPB1	-0.431374866
ILMN_1701596	RPS20	0.554803793						ILMN_1691047	EPNSL2	-0.431379754
ILMN_2338243	NUT1	0.554605791						ILMN_1802942	AJ292264	-0.431439344

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