

Supplementary Table 6 : Transcripts and DAVID pathways correlating with the expression of CD19 in lupus kidney biopsies

Positive correlation

Transcripts	Pathways						
Identifier	Gene Symbol	Correlation coefficient with CD19	Annotation Cluster 1	Enrichment Score: 1.59	Count	P_Value	Benjamini
ILMN_1782704	CD19	1	GOTERM_BP_FAT	positive regulation of response to stimulus	15	3.20E-04	4.20E-01
ILMN_1670796	EXOC10	0.702812214	GOTERM_BP_FAT	immune response-activating cell surface receptor signaling pathway	6	1.10E-03	4.60E-01
ILMN_1707467	CD19	0.67181409	GOTERM_BP_FAT	immune response-activating cell surface receptor signaling pathway	6	1.10E-03	4.60E-01
ILMN_1744604	CSA2G	0.661518537	GOTERM_BP_FAT	immune response-activating signal transduction	6	3.90E-03	6.20E-01
ILMN_1801639	IARS	0.65669978	GOTERM_BP_FAT	antigen receptor-mediated signaling pathway	5	4.20E-03	6.00E-01
ILMN_1710738	RC3H2	0.639705115	GOTERM_BP_FAT	immune response-regulating signal transduction	6	5.30E-03	6.10E-01
ILMN_1676649	AQP4	0.636286637	GOTERM_BP_FAT	positive regulation of immune response	9	9.20E-03	6.30E-01
ILMN_1737005	C19orf61	0.629717163	GOTERM_BP_FAT	immune system development	3	1.10E-02	6.40E-01
ILMN_2067895	CXCL11	0.611598413	GOTERM_BP_FAT	B cell receptor signaling pathway	3	1.30E-02	6.70E-01
ILMN_1692100	ZNFX5	0.603116686	GOTERM_BP_FAT	hemopoiesis	11	2.20E-02	7.60E-01
ILMN_2343105	UPI1	0.600465605	GOTERM_BP_FAT	hemopoiesis activation	11	2.50E-02	7.70E-01
ILMN_2324989	HEBP	0.597809229	GOTERM_BP_FAT	hemopoiesis in lymphoid organ development	11	3.80E-02	8.30E-01
ILMN_1792800	LCN6	0.59731921	GOTERM_BP_FAT	lymphocyte differentiation	6	4.20E-02	8.30E-01
ILMN_1762233	EFCAB5	0.596276524	GOTERM_BP_FAT	lymphocyte activation	9	4.90E-02	8.60E-01
ILMN_1693909	FGI2	0.588673504	GOTERM_BP_FAT	positive regulation of immune system process	10	5.20E-02	8.50E-01
ILMN_1654504	LEC7A	0.58445182	GOTERM_BP_FAT	cell activation	11	6.60E-02	8.60E-01
ILMN_2323992	CLEC7A	0.582179211	GOTERM_BP_FAT	T cell activation	6	1.10E-01	9.10E-01
ILMN_1679428	CH2C	0.580816001	GOTERM_BP_FAT	B cell activation	5	1.50E-01	9.40E-01
ILMN_1714709	OLFM1	0.580398138	GOTERM_BP_FAT	B cell activation	4	2.00E-01	9.50E-01
ILMN_1811650	DUS2L	0.579509835	GOTERM_BP_FAT	B cell-mediated immunity	4	2.50E-01	9.60E-01
ILMN_1801214	KIAA1826	0.577368078	GOTERM_BP_FAT	B cell differentiation	5	2.70E-01	9.70E-01
ILMN_1675583	SPG7	0.574873335	GOTERM_BP_FAT	myeloid cell maturation	4	2.90E-01	9.70E-01
ILMN_1702861	SGCD	0.573883839	GOTERM_BP_FAT	T cell differentiation	3	3.80E-01	9.80E-01
ILMN_1727578	DNF2p6E14208	0.571462004					
ILMN_1813836	DARS	0.571423103					
ILMN_18178043	BEND7	0.57109928					
ILMN_1795939	BOLL	0.567126703					
ILMN_1715526	SMAD3	0.565537039					
ILMN_2264788	PPP2R2B	0.564927962					
ILMN_3248521	UBXN8	0.562552263					
ILMN_1793476	PKCDBP	0.562535933					
ILMN_1669497	OSBP1L	0.562041021					
ILMN_1700510	CLEC7A	0.561024471					
ILMN_2370692	ANZF1	0.560713765					
ILMN_1782729	CLEC11	0.559580851					
ILMN_2063925	CTNBL1	0.558651714					
ILMN_2228155	OR175	0.557469081					
ILMN_1790780	HEP7	0.556295205					
ILMN_2345650	DUSP22	0.551687061					
ILMN_2048822	NUDC2	0.5503595					
ILMN_1751141	RG512	0.550235013					
ILMN_1761069	UVVAG	0.549976948					
ILMN_1737441	H4I19	0.547914182					
ILMN_1662843	CD53	0.547048404					
ILMN_1705093	ORCS	0.544483991					
ILMN_3237878	LIRA3	0.54378515					
ILMN_3247679	SNORA52	0.543084213					
ILMN_2310005	HEBP7E	0.542495963					
ILMN_2391912	SEC14L1	0.542677621					
ILMN_3187210	LOC100129186	0.541839661					
ILMN_1716195	HST1H2BG	0.539937919					
ILMN_1771801	SIRP	0.534895709					
ILMN_1662626	RTK	0.534640654					
ILMN_1711005	CDC25A	0.53359152					
ILMN_1784655	TLCD1	0.532587096					
ILMN_2413808	CD53	0.530488128					
ILMN_1660654	DCCA2	0.529068327					
ILMN_1677997	MAZ	0.526841235					
ILMN_1709795	RAC2	0.526317493					
ILMN_1708538	LOC642426	0.526196486					
ILMN_1720771	STK11	0.524749533					
ILMN_1798061	ZFYH2E	0.52311731					
ILMN_2148459	B2M	0.522971476					
ILMN_1740903	C7orf49	0.522634271					
ILMN_1766916	RPA33	0.521331799					
ILMN_2062832	THR1	0.52086732					
ILMN_1750088	WTK2	0.520027163					
ILMN_1746683	GOLGA6	0.51964193					
ILMN_1891368	BSF2640A	0.518246066					
ILMN_1769606	PW1L4	0.517111048					
ILMN_1731349	HOKA13	0.516937368					
ILMN_2400663	AKAP9	0.516517228					
ILMN_1740655	GRIN2D	0.515347665					
ILMN_1690706	SNRPB	0.514297548					
ILMN_2208455	DNHD1	0.513973644					
ILMN_1805235	SNRPB	0.513523236					
ILMN_1782810	ARPM1	0.511765168					
ILMN_1685682	PCNA	0.511204234					
ILMN_2077550	RACGAP1	0.510994819					
ILMN_2188451	HST1H2AH	0.510065216					
ILMN_1731742	TNFRSF3C	0.509004925					
ILMN_1728832	E1F4H	0.509377268					
ILMN_3239965	IDO1	0.507541614					
ILMN_1662427	PTPA43	0.507278362					
ILMN_1665049	SPG11	0.505735806					
ILMN_1694956	SCN5A	0.505649413					
ILMN_1696004	LRK1	0.504011077					
ILMN_3240594	RNU4ATC	0.503873937					
ILMN_1700380	ATP6VOA2	0.503509227					
ILMN_1789955	C2orf60	0.503054238					
ILMN_1712608	BSP1	0.502865678					

Negative correlation

Transcripts	Pathways						
Identifier	Gene Symbol	Correlation coefficient with CD19	Annotation Cluster 1	Enrichment Score: 1.43	Count	P_Value	Benjamini
ILMN_1808163	C11orf24	-0.400014			17	1.90E-03	1.80E-01
ILMN_1768856	CHAT	-0.400110384			21	5.20E-03	5.70E-01
ILMN_1808523	CD19	-0.400067072			16	6.90E-03	4.20E-01
ILMN_1772409	FAM20A	-0.400269582			18	8.30E-03	1.00E-00
ILMN_1726693	LIPK	-0.400353994			16	9.60E-03	1.00E-00
ILMN_1762952	ARTN	-0.400376425			16	1.30E-02	9.40E-01
ILMN_1774427	CALCOCC1	-0.400395592			16	1.50E-02	1.00E-00
ILMN_1812607	NRXN1S69	-0.400420066			13	2.90E-02	9.30E-01
ILMN_1790603	ATPAF1	-0.40061016			39	3.70E-02	8.20E-01
ILMN_1851972	BM973882	-0.400735148			45	5.30E-02	1.00E-00
ILMN_1832209	AA906426	-0.400781929			20	5.90E-02	1.00E-00
ILMN_1791114	CR1	-0.400864931			22	6.00E-02	8.30E-01
ILMN_1807935	AW297864	-0.400885775			23	6.60E-02	8.40E-01
ILMN_1866217	DA162273	-0.400924414			19	7.70E-02	1.00E-00
ILMN_1718884	MAGF1	-0.401120574			22	7.90E-02	1.00E-00
ILMN_1721994	HP54	-0.401274698			39	9.50E-02	1.00E-00
ILMN_1849859	BU616091	-0.401380272			19	9.60E-02	1.00E-00
ILMN_1812607	MARK4CH	-0.401329648			23	1.20E-01	1.00E-00
ILMN_1652164	UNC93B1	-0.40150875			27	1.50E-01	1.00E-00
ILMN_1691849	LIN7C	-0.401956556			46	1.80E-01	9.20E-01
ILMN_2184575	CN02	-0.402066709			53	3.30E-01	1.00E-00
ILMN_3231538	NA	-0.402078693					
ILMN_1814793	C4A40405	-0.402290388					
ILMN_1848474	A1218484	-0.402409857					
ILMN_1685985	EEF1A1	-0.402424309					
ILMN_1776685	CD19	-0.402614594					
ILMN_1768719	RHDH1	-0.402672924					
ILMN_1878107	SMAD3	-0.402731029					
ILMN_1703158	SFI1	-0.402716638					
ILMN_1754592	EDARADD	-0.402765471					
ILMN_3254666	ZNF737	-0.40278136					
ILMN_1649507	FAM90A13	-0.40288402					
ILMN_2137464	DVL3	-0.402950311					
ILMN_1654112	PAD60A	-0.403230385					
ILMN_1715814	LMAN1	-0.403478126					
ILMN_1758173	TMEH9	-0.403564978					
ILMN_1657483	SEC23B	-0.40379332					
ILMN_1759496	RAC2	-0.40395145					
ILMN_1662347	MANEAL	-0.404158458					
ILMN_1749641	F80G3	-0.404401919					
ILMN_1668814	CENPM	-0.404500121					
ILMN_1725157	NEKG	-0.405051017					
ILMN_1747412	LOC100137379	-0.405037049					
ILMN_1749821	MED2B	-0.405432328					
ILMN_1520627	INTS6	-0.405438379					
ILMN_1711765	NA	-0.405443898					
ILMN_1655498	FAM57B	-0.405897785					
ILMN_2398907	RTN4S2	-0.405957384					
ILMN_2113326	RNASE3	-0.405967213					
ILMN_1681884	LOC100506049	-0.405979469					
ILMN_1665338	PTPR8	-0.405985831					
ILMN_3309339	MIR100	-0.406011311	</				

ILMN_171462	MNS1	0.431008159
ILMN_1309021	MNR12	0.430991173
ILMN_2400940	LMN1	0.429588009
ILMN_1768293	NUP155	0.430658083
ILMN_1700939	RLP13	0.430524784
ILMN_1689136	LOC644962	0.430472491
ILMN_2190069	DEFB10	0.430215916
ILMN_1774735	DDI1	0.429588009
ILMN_1741044	NSC	0.429138614
ILMN_1696110	TUBGCP3	0.429108896
ILMN_1623632	UGR6	0.429042515
ILMN_1813275	UP_SEQ_FEATURE	0.428980584
ILMN_1670746	ROU1	0.428903195
ILMN_1804332	GPI137	0.428795066
ILMN_1746435	HST1H1E	0.428635775
ILMN_1885891	BM671563	0.428438276
ILMN_1693966	IG20I2	0.428373748
ILMN_2272096	LOC10129520	0.428232646
ILMN_1695311	HLA-DMA	0.428230583
ILMN_1794534	CDC81	0.428081229
ILMN_1788108	TXNDC5	0.428014073
ILMN_1831041	MKR24-1	0.427740054
ILMN_1884640	THEM5	0.426239289
ILMN_1766487	LRRK25	0.426242434
ILMN_1710571	PAPF5	0.426395341
ILMN_2370882	ACSL5	0.426284596
ILMN_1676797	Cbr073	0.426252875
ILMN_1882267	CCD106	0.426203769
ILMN_1729475	LOC10131551	0.425476218
ILMN_1666633	BCO1000	0.425459315
ILMN_1862043	BG188151	0.425258138
ILMN_2290628	L16	0.425137294
ILMN_1697736	EVX2C	0.424770044
ILMN_1791282	SELL13	0.424596312
ILMN_2339796	CDC16	0.424593842
ILMN_1724230	FRG1	0.424403582
ILMN_1686097	TOP2A	0.424343713
ILMN_221246	TFPIIIP2	0.424121176
ILMN_1749560	LOC10125366	0.424025366
ILMN_1802360	KRTAP5-2	0.423763128
ILMN_1729058	SCAMP1	0.423141884
ILMN_1759075	TNFRSF13B	0.42277624
ILMN_1731548	IT1	0.422616435
ILMN_1887103	XAR8	0.422590908
ILMN_2181223	MPHOSPH10	0.422569347
ILMN_1798977	GRP97	0.422474237
ILMN_1719870	FAM7D3	0.422423589
ILMN_2291571	GUS1	0.422384735
ILMN_2095920	IT1A4	0.421945936
ILMN_1695356	RNF166	0.421808771
ILMN_1763060	LTN1	0.421494761
ILMN_1764320	Cbr058	0.421330844
ILMN_1787576	HDAFX	0.421085118
ILMN_1708283	SNOB412	0.420898115
ILMN_1694367	SNOB358	0.420504917
ILMN_1665559	CDK2	0.420458794
ILMN_1792518	STX7	0.4203618
ILMN_1803873	KDSM8	0.419947086
ILMN_2398939	MSP	0.419890914
ILMN_1759991	NOL12	0.419695951
ILMN_2285648	KCNIP4	0.419609131
ILMN_1721629	ZNF108	0.419213255
ILMN_1803941	TBC1D15	0.419049336
ILMN_2360766	AKO57422	0.418547832
ILMN_2324948	LOC10013000	0.418535332
ILMN_1660624	LMR2	0.418327976
ILMN_1728199	POLE	0.417829312
ILMN_1758233	PSMB9	0.417782787
ILMN_2188833	CD69	0.417727537
ILMN_1748283	PRM2	0.417202514
ILMN_1852407	ZNF108	0.417126986
ILMN_1860540	AA709087	0.416988159
ILMN_1677446	UBE2V1	0.416940628
ILMN_2410262	MTRM14	0.416759803
ILMN_1695443	YSK4	0.416534872
ILMN_1660594	YAP1	0.416504911
ILMN_2338613	SNOB826	0.415597573
ILMN_1804339	CAMK1G	0.41582568
ILMN_1728923	F2RL2	0.415431461
ILMN_1707858	H2AF2	0.415342164
ILMN_2170735	ZNF451	0.415323771
ILMN_1700718	GAGE8	0.415052743
ILMN_1659801	ATP6V1C1	0.414864623
ILMN_1667803	OR56A1	0.414581723
ILMN_2299862	KCNH1	0.414248429
ILMN_2305082	NAP	0.414020911
ILMN_2102021	GRP19	0.4138424
ILMN_2170157	VCY	0.413769351
ILMN_3251455	RHOQ	0.413724277
ILMN_1667771	GRB10	0.413639371
ILMN_2337734	TNRC18	0.413572603
ILMN_2093931	SNJ2	0.413464971
ILMN_3229033	TDG	0.413359861
ILMN_2408968	UVELD	0.413130778
ILMN_1694584	CLTC1	0.412978643
ILMN_2301385	COX6A8B	0.412865873
ILMN_1704164	ATP13A2	0.412700613
ILMN_2095610	ANXA8	0.412623539
ILMN_1708537	RBP1	0.41244957
ILMN_2350077	HEBP2	0.411635372

GOTERM_MF_FAT	translational iron binding	64	1.70E-01	9.80E-01
SP_PIR_KEYWORDS	metal binding	65	2.20E-01	8.40E-01
GOTERM_MF_FAT	metal ion binding	83	6.60E-01	1.00E-00
GOTERM_MF_FAT	metal ion binding	82	6.60E-01	1.00E-00
GOTERM_MF_FAT	ion binding	84	6.60E-01	1.00E-00
Annotation Cluster 29 Enrichment Score: 0.74				
Count	P_Value	Benjamini		
KEGG_PATHWAY	Gamma B-mediated phagocytosis	6	4.90E-02	6.10E-01
KEGG_PATHWAY	ILK signaling pathway	4	2.30E-01	9.30E-01
KEGG_PATHWAY	Chemokine signaling pathway	4	4.50E-01	9.50E-01
Annotation Cluster 30 Enrichment Score: 0.72				
Count	P_Value	Benjamini		
INTERPRO	STER1A alpha motif type	5	6.80E-02	1.00E-00
UP_SEQ_FEATURE	domain SAM	4	2.10E-01	1.00E-00
INTERPRO	STER1A alpha motif SAM	4	2.80E-01	1.00E-00
SMART	SMART	4	3.30E-01	1.00E-00
Annotation Cluster 31 Enrichment Score: 0.71				
Count	P_Value	Benjamini		
GOTERM_CC_FAT	condensed chromosome	7	4.30E-02	7.70E-01
GOTERM_CC_FAT	condensed chromosome, centromeric region	3	3.80E-01	9.50E-01
GOTERM_CC_FAT	chromosome, centromeric region	4	4.50E-01	9.40E-01
Annotation Cluster 32 Enrichment Score: 0.71				
Count	P_Value	Benjamini		
GOTERM_BP_FAT	cell death	22	5.70E-02	8.60E-01
GOTERM_BP_FAT	death	22	5.90E-02	8.60E-01
GOTERM_BP_FAT	apoptosis	17	1.60E-01	9.40E-01
GOTERM_BP_FAT	positive regulation of apoptosis	13	1.70E-01	9.40E-01
GOTERM_BP_FAT	positive regulation of programmed cell death	13	1.70E-01	9.40E-01
GOTERM_BP_FAT	positive regulation of cell death	13	1.70E-01	9.40E-01
GOTERM_BP_FAT	programmed cell death	17	1.70E-01	9.40E-01
GOTERM_BP_FAT	regulation of programmed cell death	21	2.10E-01	9.50E-01
GOTERM_BP_FAT	regulation of cell death	21	2.10E-01	9.50E-01
GOTERM_BP_FAT	regulation of apoptosis	20	2.70E-01	9.50E-01
SP_PIR_KEYWORDS	Apoptosis	10	3.30E-01	9.00E-01
GOTERM_BP_FAT	induction of apoptosis	7	6.30E-01	1.00E-00
GOTERM_BP_FAT	induction of programmed cell death	7	6.30E-01	1.00E-00
Annotation Cluster 33 Enrichment Score: 0.7				
Count	P_Value	Benjamini		
GOTERM_BP_FAT	membrane organization	13	1.60E-02	9.50E-01
GOTERM_BP_FAT	membrane invagination	8	1.60E-01	9.40E-01
GOTERM_BP_FAT	endocytosis	8	1.60E-01	9.40E-01
GOTERM_BP_FAT	vesicle-mediated transport	15	2.80E-01	9.70E-01
SP_PIR_KEYWORDS	Endocytosis	3	5.60E-01	9.70E-01
Annotation Cluster 34 Enrichment Score: 0.66				
Count	P_Value	Benjamini		
GOTERM_BP_FAT	stem cell development	5	1.50E-01	9.40E-01
GOTERM_BP_FAT	reproductive cellular process	6	2.30E-01	9.60E-01
GOTERM_BP_FAT	seamless differentiation	3	3.20E-01	9.70E-01
Annotation Cluster 35 Enrichment Score: 0.64				
Count	P_Value	Benjamini		
GOTERM_BP_FAT	response to ionizing radiation	5	1.30E-02	9.50E-01
GOTERM_BP_FAT	response to radiation	7	2.20E-01	9.50E-01
GOTERM_BP_FAT	response to light stimulus	5	3.00E-01	9.70E-01
GOTERM_BP_FAT	response to UV	3	3.30E-01	9.70E-01
GOTERM_BP_FAT	response to oxidative stress	5	4.20E-01	9.90E-01
GOTERM_BP_FAT	response to abiotic stimulus	4	6.00E-01	1.00E-00
Annotation Cluster 36 Enrichment Score: 0.63				
Count	P_Value	Benjamini		
GOTERM_BP_FAT	regulation of behavior	4	6.50E-02	8.70E-01
GOTERM_BP_FAT	regulation of chemotaxis	3	1.30E-01	9.20E-01
GOTERM_BP_FAT	positive regulation of behavior	3	1.50E-01	9.40E-01
GOTERM_BP_FAT	positive regulation of response to external stimulus	3	1.70E-01	9.40E-01
GOTERM_BP_FAT	regulation of locomotion	5	5.50E-01	9.90E-01
GOTERM_BP_FAT	regulation of response to external stimulus	4	6.30E-01	1.00E-00
Annotation Cluster 37 Enrichment Score: 0.61				
Count	P_Value	Benjamini		
GOTERM_BP_FAT	regulation of cellular response to stress	7	1.80E-02	7.30E-01
GOTERM_BP_FAT	regulation of stress-activated protein kinase signaling pathway	5	5.10E-02	8.50E-01
GOTERM_BP_FAT	regulation of protein kinase cascade	10	6.60E-02	8.70E-01
GOTERM_BP_FAT	positive regulation of stress-activated protein kinase signaling pathway	3	6.60E-02	8.60E-01
GOTERM_BP_FAT	pathway	7	2.00E-01	9.20E-01
GOTERM_BP_FAT	positive regulation of protein kinase cascade	12	1.30E-01	9.20E-01
GOTERM_BP_FAT	regulation of protein kinase cascade	4	1.40E-01	9.30E-01
GOTERM_BP_FAT	regulation of MAPK cascade	5	1.80E-01	9.40E-01
GOTERM_BP_FAT	positive regulation of signal transduction	9	2.50E-01	9.60E-01
GOTERM_BP_FAT	positive regulation of protein kinase activity	14	2.50E-01	9.60E-01
GOTERM_BP_FAT	positive regulation of molecular function	15	3.00E-01	9.70E-01
GOTERM_BP_FAT	MAPKXX cascade	6	3.10E-01	9.70E-01
GOTERM_BP_FAT	regulation of MAP kinase activity	5	3.20E-01	9.70E-01
GOTERM_BP_FAT	positive regulation of MAP kinase activity	4	3.40E-01	9.80E-01
GOTERM_BP_FAT	regulation of phosphorylation	12	3.90E-01	9.80E-01
GOTERM_BP_FAT	positive regulation of cell communication	9	3.50E-01	9.80E-01
GOTERM_BP_FAT	regulation of fibroblast metabolic process	12	3.90E-01	9.80E-01
GOTERM_BP_FAT	regulation of aldehyde metabolic process	12	3.90E-01	9.80E-01
GOTERM_BP_FAT	regulation of protein kinase activity	5	4.05E-01	9.90E-01
GOTERM_BP_FAT	positive regulation of protein kinase activity	6	4.70E-01	9.90E-01
GOTERM_BP_FAT	activation of MAPK activity	3	5.00E-01	9.90E-01
GOTERM_BP_FAT	positive regulation of kinase activity	6	5.00E-01	9.90E-01
GOTERM_BP_FAT	positive regulation of transferase activity	6	5.30E-01	9.90E-01
GOTERM_BP_FAT	regulation of protein kinase activity	7	5.80E-01	1.00E-00
GOTERM_BP_FAT	regulation of kinase activity	8	5.80E-01	1.00E-00
GOTERM_BP_FAT	regulation of transferase activity	8	6.30E-01	1.00E-00
Annotation Cluster 38 Enrichment Score: 0.6				
Count	P_Value	Benjamini		
GOTERM_BP_FAT	cell cycle checkpoint	5	1.10E-01	9.00E-01
GOTERM_BP_FAT	DNA damage checkpoint	3	2.50E-01	9.60E-01
GOTERM_BP_FAT	DNA replication checkpoint	3	2.80E-01	9.70E-01
GOTERM_BP_FAT	DNA damage response, signal transduction	3	4.80E-01	9.90E-01
Annotation Cluster 39 Enrichment Score: 0.6				
Count	P_Value	Benjamini		
UP_SEQ_FEATURE	repeat:LR 1	11	9.70E-02	1.00E-00
UP_SEQ_FEATURE	repeat:LR 2	11	1.00E-01	1.00E-00
SP_PIR_KEYWORDS	Repeat:R1 repeat	11	1.00E-01	1.00E-00
UP_SEQ_FEATURE	repeat:LR 6	8	1.20E-01	1.00E-00
UP_SEQ_FEATURE	repeat:LR 7	7	1.40E-01	1.00E-00
UP_SEQ_FEATURE	repeat:LR 8	6	1.70E-01	1.00E-00
UP_SEQ_FEATURE	repeat:LR 9	6	1.70E-01	1.00E-00
UP_SEQ_FEATURE	repeat:LR 10	6	2.20E-01	1.00E-00
UP_SEQ_FEATURE	repeat:LR 4	8	2.30E-01	1.00E-00
UP_SEQ_FEATURE	repeat:LR 3	9	2.30E-01	1.00E-00
UP_SEQ_FEATURE	repeat:LR 15	3	2.60E-01	1.00E-00

ILMN_1713533	TKTL2	-0.456411638
ILMN_1722673	PCNB4	-0.456518866
ILMN_2397846	SHCB	-0.456525276
ILMN_1694210	HMGCS1	-0.456808213
ILMN_1797201	KRTAP10-2	-0.456892062
ILMN_1803033	MGST1	-0.456907348
ILMN_1882015	BG951912	-0.457277256
ILMN_1732426	CHH1	-0.457273916
ILMN_1694210	HMGCS1	-0.457301515
ILMN_2299221	DMRT1	-0.458401704
ILMN_3228746	GDPD5	-0.458663417
ILMN_3247514	Chro772	-0.458737446
ILMN_1811068	CABYR	-0.458873874
ILMN_249067	KLC1	-0.459023749
ILMN_1694952	SSX4B	-0.459820308
ILMN_1886510	VPF53	-0.459946356
ILMN_1672074	SHS4B	-0.459984469
ILMN_1714222	PLEKHN1	-0.460330044
ILMN_2045220	ORAM17	-0.462080688
ILMN_1652819	OPA3	-0.461070186
ILMN_1784477	PLEKHG5	-0.461842968
ILMN_1797169	ORAM47	-0.462159392
ILMN_1749381	ACRNOA0164	-0.463432659
ILMN_1787015	RGS18L1	-0.463836142
ILMN_1661653	DET1	-0.463887314
ILMN_1715669	TPST1	-0.464112925
ILMN_1766230	IL3	-0.464214463
ILMN_1724669	RUNX1T1	-0.464272871
ILMN_1765216	RNF67	-0.464370886
ILMN_1691349	LOC100133050	-0.465743359
ILMN_3204668	BM921547	-0.466246826
ILMN_1724427	ORM2	-0.466336793
ILMN_1667416	TRIM74	-0.466688975
ILMN_1667416	TRIM74	-0.466767484
ILMN_1803850	TPSAP15	-0.466868713
ILMN_1778188	TPP3	-0.467235425
ILMN_1669669	KCMF1	-0.468208107
ILMN_1791297	LOC6494905	-0.468284027
ILMN_1765216	RNF67	-0.468298964
ILMN_1660963	CCN	-0.469449678
ILMN_1728684	PELP1	-0.469451343
ILMN_1669676	SERP2	-0.469531274
ILMN_1748859	TCF61	-0.469596959
ILMN_1668454	RGS18	-0.470380115
ILMN_1722070	AP0C3	-0.470889218

ILMN_2367070	ACOT9	0.411621491	UP_SEQ_FEATURE	repeat:LRR 9	5	2.70E-01	1.00E+00
ILMN_1739599	ADPKC	0.411551885	UP_SEQ_FEATURE	repeat:LRR 11	4	3.20E-01	1.00E+00
ILMN_1702585	SET	0.410437891	UP_SEQ_FEATURE	repeat:LRR 10	3	3.00E-01	1.00E+00
ILMN_1705025	UBE2L6	0.41043696	UP_SEQ_FEATURE	repeat:LRR 10	4	4.00E-01	1.00E+00
ILMN_1666544	ARRDC4	0.410299623	INTERPRO	leucine-rich repeat	6	4.20E-01	1.00E+00
ILMN_1703072	CREB3	0.410127395	UP_SEQ_FEATURE	repeat:LRR 12	3	4.40E-01	1.00E+00
ILMN_2328874	GHI1	0.40991692	UP_SEQ_FEATURE	repeat:LRR 12	3	5.40E-01	1.00E+00
ILMN_2083066	IGLBP3	0.409854039	INTERPRO	leucine-rich repeat, typical subtype	3	7.40E-01	1.00E+00
ILMN_1731318	TEK9	0.409851572	SMART	SH_17P	7	8.00E-01	1.00E+00
ILMN_1731294	GRP179	0.409845377					
ILMN_2353161	MSLN	0.409743974	GOTERM_BP_FAT	macromolecule catabolic process	23	7.10E-02	8.70E-01
ILMN_1692276	GGPS1	0.409741762	GOTERM_BP_FAT	cellular macromolecule catabolic process	21	9.90E-02	8.90E-01
ILMN_1725338	LOC421	0.409383367	GOTERM_BP_FAT	modification-dependent macromolecule catabolic process	15	2.70E-01	9.70E-01
ILMN_1753716	EF2B1	0.409269843	GOTERM_BP_FAT	ubiquitin-dependent protein catabolic process	15	2.70E-01	9.70E-01
ILMN_1692703	CYLC1	0.409159735	GOTERM_BP_FAT	protein catabolic process	16	2.70E-01	9.70E-01
ILMN_1697315	GNAT1	0.409157737	GOTERM_BP_FAT	proteolysis	25	3.00E-01	9.70E-01
ILMN_2124585	GREM1	0.409134098	GOTERM_BP_FAT	proteolysis involved in cellular protein catabolic process	15	3.30E-01	9.70E-01
ILMN_1795662	C16orf82	0.409120346	GOTERM_BP_FAT	cellular protein catabolic process	15	3.30E-01	9.70E-01
ILMN_1865559	NA	0.40911403	GOTERM_BP_FAT	ubiquitin-dependent protein catabolic process	7	3.60E-01	9.80E-01
ILMN_1769245	GLP1R1	0.408664533	SP_PIR_KEYWORDS	tbl1 conjugation pathway	10	6.70E-01	9.80E-01
ILMN_1745787	POLL	0.408625575					
ILMN_1731891	UBN8N	0.408286108	GOTERM_MF_FAT	protein dimerization activity	16	1.30E-01	9.60E-01
ILMN_1792384	HABP4	0.407685749	GOTERM_MF_FAT	protein homodimerization activity	7	2.50E-01	9.80E-01
ILMN_1739127	C18orf12	0.407682369	GOTERM_MF_FAT	protein homodimerization activity	8	5.20E-01	1.00E+00
ILMN_2198376	PSMA4	0.407664738					
ILMN_1785635	BRD3	0.407648554	GOTERM_CC_FAT	vacuole	8	2.30E-01	9.40E-01
ILMN_1710989	LOC653061	0.407498806	GOTERM_CC_FAT	lysine vacuole	7	2.40E-01	9.40E-01
ILMN_1716276	CLC4	0.40712232	GOTERM_CC_FAT	vacuole	7	2.40E-01	9.40E-01
ILMN_1732909	ALGO	0.407093866	SP_PIR_KEYWORDS	ALGO	5	3.30E-01	9.80E-01
ILMN_1781285	DUSP1	0.406902549					
ILMN_1656073	MYL12A	0.406726282	GOTERM_CC_FAT	nuclear envelope	11	7.70E-03	9.20E-01
ILMN_1307911	AKR1C1L1	0.406725627	GOTERM_CC_FAT	endomembrane system	24	3.70E-02	8.30E-01
ILMN_1777637	SFN1L	0.406596464	GOTERM_CC_FAT	cytosolic envelope	18	1.10E-01	8.70E-01
ILMN_1842024	AP08	0.406571539	GOTERM_CC_FAT	cytoskeleton	18	1.10E-01	8.50E-01
ILMN_1786759	C11orf10	0.40631992	GOTERM_CC_FAT	mitochondrial outer membrane	4	2.60E-01	9.40E-01
ILMN_2391333	CYP20A1	0.406255936	GOTERM_CC_FAT	organelle outer membrane	4	3.40E-01	9.50E-01
ILMN_1755383	LRRC1	0.406147992	GOTERM_CC_FAT	outer membrane	4	3.60E-01	9.50E-01
ILMN_1781886	LOC441179	0.406050934	GOTERM_BP_FAT	mitochondrial transport	3	4.10E-01	9.80E-01
ILMN_1754474	CTNS	0.405780245	GOTERM_CC_FAT	mitochondrial membrane	7	8.00E-01	9.90E-01
ILMN_1818247	BGT2200	0.405548267	GOTERM_CC_FAT	mitochondrion	19	8.20E-01	1.00E+00
ILMN_1672876	MF12	0.405536726	GOTERM_CC_FAT	mitochondrial envelope	7	8.40E-01	1.00E+00
ILMN_2223887	OTOR	0.405483694	GOTERM_CC_FAT	organelle inner membrane	7	8.90E-01	1.00E+00
ILMN_1804877	CASP9	0.405220992	GOTERM_CC_FAT	mitochondrial inner membrane	4	9.40E-01	1.00E+00
ILMN_1751744	ANKE1	0.405142271	GOTERM_CC_FAT	mitochondrial part	8	9.50E-01	1.00E+00
ILMN_1736013	CIB3	0.405045801					
ILMN_1797172	ERCC1	0.40492722					
ILMN_1825159	BCO40587	0.404779777	GOTERM_BP_FAT	development of primary male sexual characteristics	4	1.40E-01	9.30E-01
ILMN_2320513	APBB8	0.404759708	GOTERM_BP_FAT	reproductive development process	9	1.80E-01	9.40E-01
ILMN_1654626	RHIC1	0.404310246	GOTERM_BP_FAT	male sex differentiation	3	2.00E-01	9.50E-01
ILMN_1666173	TCF20	0.404306377	GOTERM_BP_FAT	ovarian follicle development	5	2.50E-01	9.60E-01
ILMN_1719103	UBE2CBP	0.404270406	GOTERM_BP_FAT	development of primary sexual characteristics	5	2.50E-01	9.60E-01
ILMN_3247462	GLRX3	0.404262335	GOTERM_BP_FAT	male gonad development	3	2.80E-01	9.70E-01
ILMN_1872838	KRC	0.404023974	GOTERM_BP_FAT	ovulation cycle process	3	3.60E-01	9.80E-01
ILMN_1771870	FAM98C	0.403926393	GOTERM_BP_FAT	sex differentiation	5	3.60E-01	9.80E-01
ILMN_2371169	ZYX	0.403829212	GOTERM_BP_FAT	female gonad development	3	3.70E-01	9.80E-01
ILMN_1794677	TMC6	0.403568806	GOTERM_BP_FAT	ovulation cycle	3	3.90E-01	9.80E-01
ILMN_3221888	NAP1L6	0.403346727	GOTERM_BP_FAT	ovulation development	4	3.90E-01	9.80E-01
ILMN_1658034	AGAP4	0.403320514	GOTERM_BP_FAT	development of primary female sexual characteristics	3	4.10E-01	9.80E-01
ILMN_1656832	DNAH2	0.403249612	GOTERM_BP_FAT	female sex differentiation	3	4.10E-01	9.80E-01
ILMN_2337789	MARCK2	0.402882346	GOTERM_BP_FAT	cytoskeletal process	4	4.80E-01	9.90E-01
ILMN_2258816	SAMD3	0.402753993					
ILMN_1809434	XBP1	0.402522842					
ILMN_1682894	TMTM191C	0.402252341	GOTERM_BP_FAT	positive regulation of multicellular organism growth	3	9.00E-02	8.90E-01
ILMN_2346328	PRF1A2	0.40219246	GOTERM_BP_FAT	positive regulation of multicellular organismal process	8	2.20E-01	9.50E-01
ILMN_1798819	DTN8	0.402090183	GOTERM_BP_FAT	regulation of multicellular organism growth	3	3.50E-01	9.80E-01
ILMN_1758731	CYP2J2	0.401988843	GOTERM_BP_FAT	positive regulation of growth	3	4.80E-01	9.90E-01
ILMN_1713290	GLT1B1	0.401922033	GOTERM_BP_FAT	regulation of growth	6	8.20E-01	1.00E+00
ILMN_1792489	ARPC2	0.401765464					
ILMN_1732108	UTS2	0.401759314	GOTERM_BP_FAT	intracellular transport	19	1.20E-01	9.10E-01
ILMN_1699170	C5orf45	0.401731224	GOTERM_BP_FAT	cytoscytoplasmic transport	6	2.10E-01	9.50E-01
ILMN_1661516	POLR2J2	0.401728439	GOTERM_BP_FAT	nuclear transport	6	2.10E-01	9.50E-01
ILMN_1744316	TATD3	0.401568886	GOTERM_BP_FAT	nuclear import into nucleus	4	2.50E-01	9.60E-01
ILMN_1795852	CNVE1	0.401484807	GOTERM_BP_FAT	nuclear import	4	2.80E-01	9.60E-01
ILMN_1307505	SCC2A24	0.401360557	GOTERM_BP_FAT	protein import	5	2.70E-01	9.70E-01
ILMN_1708427	KPNA3	0.401324064	GOTERM_BP_FAT	nuclear transport	19	2.80E-01	9.70E-01
ILMN_2249720	LAT2	0.401288081	GOTERM_CC_FAT	spore complex	4	2.90E-01	9.50E-01
ILMN_2116714	SCBP1A	0.401101157	GOTERM_BP_FAT	establishment of protein localization	19	2.90E-01	9.70E-01
ILMN_2112499	DNK2	0.400838952	GOTERM_BP_FAT	protein localization in nucleus	4	3.80E-01	9.70E-01
ILMN_1800530	AGAP1	0.400828558	GOTERM_BP_FAT	cellular protein localization	11	3.20E-01	9.70E-01
ILMN_1848913	AF33971	0.400713874	GOTERM_BP_FAT	cellular macromolecule localization	11	3.20E-01	9.70E-01
ILMN_2387784	DEAF1	0.400383077	GOTERM_BP_FAT	nuclear localization in organelle	5	3.40E-01	9.80E-01
ILMN_1700276	JKAMP	0.40033307	GOTERM_BP_FAT	intracellular protein transport	10	3.40E-01	9.80E-01
ILMN_1880867	C10orf90	0.400251815	GOTERM_BP_FAT	nuclear localization	20	4.20E-01	9.80E-01
ILMN_1732176	UMSF1	0.400195786	GOTERM_BP_FAT	protein targeting	6	4.40E-01	9.80E-01
			GOTERM_CC_FAT	nuclear pore	3	4.70E-01	9.60E-01
			GOTERM_MF_FAT	protein transporter activity	3	5.30E-01	1.00E+00
			SP_PIR_KEYWORDS	protein transport	9	7.40E-01	9.90E-01

Annotation Cluster 40 Enrichment Score: 0.6

Annotation Cluster 41 Enrichment Score: 0.59

Annotation Cluster 42 Enrichment Score: 0.59

Annotation Cluster 43 Enrichment Score: 0.54

Annotation Cluster 44 Enrichment Score: 0.54

Annotation Cluster 45 Enrichment Score: 0.51

Annotation Cluster 46 Enrichment Score: 0.5

Annotation Cluster 47 Enrichment Score: 0.5

Annotation Cluster 48 Enrichment Score: 0.49

Annotation Cluster 49 Enrichment Score: 0.48

ILMN_3239440	GAGE12	0.498620978					
ILMN_1705151	SF3A3	0.49905569					
ILMN_1670997	TRK1	0.499097962					
ILMN_320552	HA	0.500834021					
ILMN_1709173	HMMB1	0.501234397					
ILMN_1810321	LELP1	0.50174155					
ILMN_167486	ORZAG2	0.502128613					
ILMN_1865716	LOC729451	0.502154851					
ILMN_1681316	CDC623	0.502449563					
ILMN_1658710	FAM19A4	0.503125341					
ILMN_1890734	LOC728800	0.503446465					
ILMN_2120210	RCAN2	0.503736306					
ILMN_2342651	OR11H12	0.503778823					
ILMN_212620	IWAL1	0.50438704					
ILMN_234350	BTBD3	0.50526904					
ILMN_1812461	WISF2	0.505656004					
ILMN_1703984	TIGD6	0.507203973					
ILMN_1917221	C11orf95	0.507431219					
ILMN_2133000	SORBS7	0.508590702					
ILMN_1676595	O2B514	0.509240129					
ILMN_1706077	DFB125	0.510224806					
ILMN_1709256	PLEC	0.510517158					
ILMN_1662897	ERCC4	0.510839735					
ILMN_1723520	AKAP1	0.510964944					
ILMN_3238670	SNORA47	0.514421232					
ILMN_1724699	ACAD8	0.515617146					
ILMN_1810834	MHS5	0.515937514					
ILMN_2145423	DETI1	0.51647993					
ILMN_2310770	HR23H14	0.516920004					
ILMN_1799717	ZNF398	0.519114585					
ILMN_1698484	RHOV	0.51954689					
ILMN_1720469	BMS1P4	0.520098002					
ILMN_1881717	ODC1	0.521206241					
ILMN_1721436	AKAP1	0.52124306					
ILMN_1878029	AKO1020	0.524101498					
ILMN_1656553	LOC653160	0.524826462					
ILMN_2410428	LOC728407	0.526161999					
ILMN_2225151	DNM6	0.526251713					
ILMN_1848617	RNKL3	0.529239283					
ILMN_1737517	RPL29	0.529959857					
ILMN_3268675	LOC100130880	0.530107625					
ILMN_1761260	CBLL1	0.530463957					
ILMN_1855673	A0027195	0.531761296					
ILMN_1656955	PCN9	0.531823119					
ILMN_1912611	FLJ41130	0.531824292					
ILMN_3189252	PLXNA4	0.534148487					
ILMN_1679782	BLOC1S2	0.537333163					
ILMN_3239748	RIR3	0.537666675					
ILMN_1700611	OR4K1	0.537848669					
ILMN_1909183	CR740230	0.539205077					
ILMN_1892243	AA720941	0.540135289					
ILMN_1744118	ASTN2	0.54130381					
ILMN_1825623	CHRNA9	0.542777646					
ILMN_1738223	Geov708	0.544470215					
ILMN_1740217	HAC1	0.546408172					
ILMN_1890521	BF109917	0.548907753					
ILMN_2347334	C20orf71	0.551456754					
ILMN_3239775	ODZ4	0.553806604					

GOTERM_BP_FAT	antigen processing and presentation	4	2.40E-01	9.60E-01
INTERPRO	immunoglobulin/heparin hyaluronate complex conserved site	4	2.50E-01	1.00E+00
GOTERM_CC_FAT	MHC protein complex	3	3.10E-01	9.50E-01
KEGG_PATHWAY	Antigen processing and presentation	3	5.30E-01	9.60E-01
INTERPRO	immunoglobulin-like fold	8	9.30E-01	1.00E+00
INTERPRO	immunoglobulin-like	7	9.40E-01	1.00E+00
Annotation Cluster 50	Enrichment Score: 0.48	Count	P_Value	Benjamini
SP_PIR_KEYWORDS	nuclease	5	1.50E-01	7.80E-01
GOTERM_MF_FAT	nuclease activity	5	4.00E-01	9.90E-01
GOTERM_MF_FAT	endonuclease activity	3	6.00E-01	1.00E+00
Annotation Cluster 51	Enrichment Score: 0.47	Count	P_Value	Benjamini
SP_PIR_KEYWORDS	rna-binding	16	1.10E-01	7.10E-01
GOTERM_MF_FAT	RNA binding	17	3.80E-01	9.90E-01
UP_SEQ_FEATURE	domain-RRM	4	4.10E-01	1.00E+00
INTERPRO	RNA recognition motif_RNP_1	6	4.10E-01	1.00E+00
INTERPRO	Nucleotide-binding_alpha-beta_fold	6	4.20E-01	1.00E+00
SMART	RRM	6	4.70E-01	1.00E+00
Annotation Cluster 52	Enrichment Score: 0.47	Count	P_Value	Benjamini
GOTERM_BP_FAT	homeostasis of number of cells	6	5.20E-02	8.50E-01
KEGG_PATHWAY	intestinal immune network for IgA production	4	8.30E-02	6.60E-01
GOTERM_BP_FAT	regulation of B cell activation	3	2.80E-01	9.70E-01
GOTERM_BP_FAT	regulation of lymphocyte activation	5	3.50E-01	9.80E-01
GOTERM_BP_FAT	regulation of leukocyte activation	5	4.30E-01	9.90E-01
GOTERM_BP_FAT	positive regulation of T cell activation	3	4.60E-01	9.90E-01
GOTERM_BP_FAT	regulation of cell activation	5	4.70E-01	9.90E-01
GOTERM_BP_FAT	positive regulation of lymphocyte activation	3	5.90E-01	1.00E+00
GOTERM_BP_FAT	positive regulation of leukocyte activation	3	6.30E-01	1.00E+00
GOTERM_BP_FAT	positive regulation of cell activation	3	6.60E-01	1.00E+00
GOTERM_BP_FAT	regulation of T cell activation	3	6.90E-01	1.00E+00
Annotation Cluster 53	Enrichment Score: 0.47	Count	P_Value	Benjamini
GOTERM_MF_FAT	transcription activator activity	12	2.10E-01	9.80E-01
GOTERM_MF_FAT	transcription coactivator activity	7	2.70E-01	9.80E-01
SP_PIR_KEYWORDS	activator	13	3.20E-01	9.00E-01
GOTERM_MF_FAT	transcription cofactor activity	9	4.50E-01	1.00E+00
GOTERM_MF_FAT	transcription factor binding	11	5.90E-01	1.00E+00

GOTERM_BP_FAT	positive regulation of transcription	12	4.80E-01	1.00E+00
GOTERM_BP_FAT	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	13	5.00E-01	1.00E+00
GOTERM_BP_FAT	positive regulation of cellular biosynthetic process	14	5.30E-01	1.00E+00
GOTERM_BP_FAT	positive regulation of transcription, DNA-dependent	10	5.30E-01	1.00E+00
GOTERM_BP_FAT	positive regulation of biosynthetic process	14	5.30E-01	1.00E+00
GOTERM_BP_FAT	positive regulation of nitrogen compound metabolic process	13	5.40E-01	1.00E+00
GOTERM_BP_FAT	positive regulation of RNA metabolic process	10	5.40E-01	1.00E+00
GOTERM_BP_FAT	positive regulation of macromolecule metabolic process	16	6.40E-01	1.00E+00
GOTERM_BP_FAT	positive regulation of transcription from RNA polymerase II promoter	6	8.30E-01	1.00E+00
Annotation Cluster 54	Enrichment Score: 0.26	Count	P_Value	Benjamini
GOTERM_BP_FAT	negative regulation of protein modification process	4	3.80E-01	1.00E+00
GOTERM_BP_FAT	negative regulation of protein ubiquitination	3	4.00E-01	1.00E+00
GOTERM_BP_FAT	negative regulation of cellular protein metabolic process	5	4.00E-01	1.00E+00
GOTERM_BP_FAT	negative regulation of protein metabolic process	5	4.60E-01	1.00E+00
GOTERM_BP_FAT	regulation of protein ubiquitination	3	5.60E-01	1.00E+00
GOTERM_BP_FAT	negative regulation of molecular function	7	5.90E-01	1.00E+00
GOTERM_BP_FAT	regulation of protein modification process	6	6.50E-01	1.00E+00
GOTERM_BP_FAT	negative regulation of catalytic activity	5	7.60E-01	1.00E+00
GOTERM_BP_FAT	regulation of cellular protein metabolic process	7	8.80E-01	1.00E+00
Annotation Cluster 55	Enrichment Score: 0.26	Count	P_Value	Benjamini
GOTERM_BP_FAT	ribosome biogenesis	6	3.20E-01	1.00E+00
GOTERM_BP_FAT	ribosome biosynthetic process	4	5.70E-01	1.00E+00
SP_PIR_KEYWORDS	ribosyltransferase	3	9.00E-01	1.00E+00
Annotation Cluster 56	Enrichment Score: 0.26	Count	P_Value	Benjamini
SP_PIR_KEYWORDS	ribosylase	12	1.50E-01	9.20E-01
GOTERM_BP_FAT	negative regulation of cellular biosynthetic process	13	3.90E-01	1.00E+00
GOTERM_BP_FAT	negative regulation of biosynthetic process	13	3.80E-01	1.00E+00
GOTERM_BP_FAT	negative regulation of macromolecule metabolic process	16	3.90E-01	1.00E+00
GOTERM_BP_FAT	negative regulation of macromolecule biosynthetic process	12	4.40E-01	1.00E+00
GOTERM_BP_FAT	negative regulation of transcription from RNA polymerase II promoter	6	5.60E-01	1.00E+00
GOTERM_BP_FAT	regulation of transcription from RNA polymerase II promoter	14	6.00E-01	1.00E+00
GOTERM_BP_FAT	negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	10	6.20E-01	1.00E+00
GOTERM_BP_FAT	negative regulation of nitrogen compound metabolic process	10	6.30E-01	1.00E+00
GOTERM_MF_FAT	transcription repressor activity	6	6.90E-01	1.00E+00
GOTERM_BP_FAT	negative regulation of gene expression	9	7.30E-01	1.00E+00
GOTERM_MF_FAT	transcription repressor activity	3	7.50E-01	1.00E+00
GOTERM_BP_FAT	chromatin modification	5	7.50E-01	1.00E+00
GOTERM_BP_FAT	negative regulation of transcription, DNA-dependent	6	8.00E-01	1.00E+00
GOTERM_BP_FAT	negative regulation of RNA metabolic process	6	8.10E-01	1.00E+00
GOTERM_BP_FAT	negative regulation of transcription	7	8.60E-01	1.00E+00
Annotation Cluster 57	Enrichment Score: 0.26	Count	P_Value	Benjamini
GOTERM_BP_FAT	negative regulation of signal transduction	6	3.90E-01	1.00E+00
GOTERM_BP_FAT	negative regulation of cell communication	6	4.90E-01	1.00E+00
GOTERM_MF_FAT	enzyme activator activity	5	8.60E-01	1.00E+00
Annotation Cluster 58	Enrichment Score: 0.26	Count	P_Value	Benjamini
SP_PIR_KEYWORDS	activator	16	4.70E-02	7.80E-01
SP_PIR_KEYWORDS	nucleus	77	5.40E-01	9.80E-01
GOTERM_MF_FAT	DNA binding	43	5.00E-01	1.00E+00
GOTERM_BP_FAT	regulation of RNA metabolic process	33	6.60E-01	1.00E+00
GOTERM_MF_FAT	transcription regulator activity	27	6.60E-01	1.00E+00
GOTERM_BP_FAT	regulation of transcription, DNA-dependent	32	6.80E-01	1.00E+00
SP_PIR_KEYWORDS	dna-binding	32	6.90E-01	9.90E-01
SP_PIR_KEYWORDS	Transcription	35	7.20E-01	9.90E-01
SP_PIR_KEYWORDS	transcription regulation	34	7.40E-01	9.90E-01
GOTERM_BP_FAT	transcription	36	7.90E-01	1.00E+00
GOTERM_MF_FAT	transcription factor activity	16	7.90E-01	1.00E+00
GOTERM_BP_FAT	regulation of transcription	44	8.30E-01	1.00E+00
Annotation Cluster 59	Enrichment Score: 0.25	Count	P_Value	Benjamini
GOTERM_BP_FAT	chromatin assembly or disassembly	4	4.20E-01	1.00E+00
GOTERM_BP_FAT	nucleosome assembly	3	4.70E-01	1.00E+00
GOTERM_BP_FAT	chromatin assembly	3	4.80E-01	1.00E+00
GOTERM_BP_FAT	protein-DNA complex assembly	3	5.10E-01	1.00E+00
GOTERM_BP_FAT	nucleosome organization	3	5.20E-01	1.00E+00
GOTERM_BP_FAT	DNA packaging	3	6.40E-01	1.00E+00
GOTERM_BP_FAT	cellular macromolecular complex subunit organization	7	6.60E-01	1.00E+00
GOTERM_BP_FAT	cellular macromolecular complex assembly	6	7.10E-01	1.00E+00
GOTERM_BP_FAT	chromatin organization	7	7.10E-01	1.00E+00
Annotation Cluster 60	Enrichment Score: 0.25	Count	P_Value	Benjamini
GOTERM_CC_FAT	nuclear speck	4	3.10E-01	1.00E+00
GOTERM_CC_FAT	nuclear body	4	6.30E-01	1.00E+00
GOTERM_CC_FAT	nucleoplasm part	8	9.10E-01	1.00E+00
Annotation Cluster 61	Enrichment Score: 0.24	Count	P_Value	Benjamini
GOTERM_CC_FAT	condensed chromosome	4	4.50E-01	1.00E+00
GOTERM_BP_FAT	M phase of meiotic cell cycle	3	5.50E-01	1.00E+00
GOTERM_BP_FAT	meiosis	3	5.50E-01	1.00E+00
GOTERM_BP_FAT	meiotic cell cycle	3	5.60E-01	1.00E+00
GOTERM_BP_FAT	M phase	7	5.80E-01	1.00E+00
GOTERM_BP_FAT	cell cycle phase	7	7.90E-01	1.00E+00
Annotation Cluster 62	Enrichment Score: 0.24	Count	P_Value	Benjamini
GOTERM_BP_FAT	carboxylic acid catabolic process	4	3.40E-01	1.00E+00
GOTERM_BP_FAT	organic acid catabolic process	4	3.40E-01	1.00E+00
GOTERM_BP_FAT	cellular amino acid catabolic process	3	3.60E-01	1.00E+00
GOTERM_BP_FAT	amine catabolic process	3	4.30E-01	1.00E+00
UP_SEQ_FEATURE	transit peptide/Mitochondrion	7	8.50E-01	1.00E+00
SP_PIR_KEYWORDS	transit peptide	7	8.60E-01	1.00E+00
GOTERM_CC_FAT	mitochondrial matrix	3	9.30E-01	1.00E+00
GOTERM_CC_FAT	mitochondrial lumen	3	9.30E-01	1.00E+00