

Supplementary table 4: GO results of B-ChIP (GO groups marked in yellow are shown in Figure 2.1)								
	Enrichment FDR	nGenes	Pathway Genes	Fold Enrichment	Pathway	URL	Genes	
BP:GO - genes located close to the human-specific peaks (n = 437)	1.0E-70	42	137	85.54	GO:0006334 nucleosome assembly	http://amigo.geneontology.org/amigo/term/GO:0006334	H2BC11,H2BC5	
	3.7E-65	42	181	64.75	GO:0034728 nucleosome organization	http://amigo.geneontology.org/amigo/term/GO:0034728	H2BC11,H2BC5	
	1.7E-60	42	230	50.95	GO:0031497 chromatin assembly	http://amigo.geneontology.org/amigo/term/GO:0031497	H2BC11,H2BC5	
	4.1E-58	42	261	44.90	GO:0065004 protein-DNA complex assembly	http://amigo.geneontology.org/amigo/term/GO:0065004	H2BC11,H2BC5	
	3.6E-55	42	305	38.42	GO:0071824 protein-DNA complex subunit organization	http://amigo.geneontology.org/amigo/term/GO:0071824	H2BC11,H2BC5	
	2.5E-53	42	337	34.78	GO:0006338 chromatin remodeling	http://amigo.geneontology.org/amigo/term/GO:0006338	H2BC11,H2BC5	
	8.3E-40	42	701	16.72	GO:0006325 chromatin organization	http://amigo.geneontology.org/amigo/term/GO:0006325	H2BC11,H2BC5	
	5.8E-32	43	1173	10.23	GO:0051276 chromosome organization	http://amigo.geneontology.org/amigo/term/GO:0051276	H1-3,H2BC11,TU	
	2.1E-28	47	1859	7.05	GO:0065003 protein-containing complex assembly	http://amigo.geneontology.org/amigo/term/GO:0065003	H2BC11,PPAN,T	
GO:0044419 biological process involved in interspecies interaction between organisms	8.0E-05	22	1917	3.37	GO:0044419 biological process involved in interspecies interaction between organisms	http://amigo.geneontology.org/amigo/term/GO:0044419	FGR,ISG20,SPN	
	7.1E-05	8	182	12.89	GO:0032635 interleukin-6 production	http://amigo.geneontology.org/amigo/term/GO:0032635	POU2F2,SLAMF	
	7.1E-05	8	182	12.89	GO:0032675 regulation of interleukin-6 production	http://amigo.geneontology.org/amigo/term/GO:0032675	POU2F2,SLAMF	
	7.1E-05	13	629	6.06	GO:0051249 regulation of lymphocyte activation	http://amigo.geneontology.org/amigo/term/GO:0051249	ACTB,IL10,FGR	
	4.8E-05	16	928	5.06	GO:0046649 lymphocyte activation	http://amigo.geneontology.org/amigo/term/GO:0046649	CD74,LAT2,ACT	
	4.8E-05	22	1771	3.64	GO:0009607 response to biotic stimulus	http://amigo.geneontology.org/amigo/term/GO:0009607	FGR,ISG20,SPN	
	4.8E-05	22	1731	3.73	GO:0043207 response to external biotic stimulus	http://amigo.geneontology.org/amigo/term/GO:0043207	FGR,ISG20,SPN	
	4.8E-05	22	1728	3.73	GO:0051707 response to other organism	http://amigo.geneontology.org/amigo/term/GO:0051707	FGR,ISG20,SPN	
	1.2E-04	8	204	11.50	GO:0051250 negative regulation of lymphocyte activation	http://amigo.geneontology.org/amigo/term/GO:0051250	IL10,FGR,CD74	
	1.2E-04	9	285	9.26	GO:0051348 negative regulation of transferase activity	http://amigo.geneontology.org/amigo/term/GO:0051348	HEXIM1,RPL23,	
	1.2E-04	16	1073	4.37	GO:0032269 negative regulation of cellular protein metabolic process	http://amigo.geneontology.org/amigo/term/GO:0032269	HEXIM1,TNFAIP	
	1.2E-04	17	1222	4.08	GO:0044092 negative regulation of molecular function	http://amigo.geneontology.org/amigo/term/GO:0044092	HEXIM1,TNFAIP	
	1.6E-04	13	724	5.27	GO:0002694 regulation of leukocyte activation	http://amigo.geneontology.org/amigo/term/GO:0002694	ACTB,IL10,FGR	
	1.6E-04	16	1122	4.18	GO:0045321 leukocyte activation	http://amigo.geneontology.org/amigo/term/GO:0045321	CD74,LAT2,ACT	
	1.6E-04	20	1735	3.38	GO:0002682 regulation of immune system process	http://amigo.geneontology.org/amigo/term/GO:0002682	CD74,LAT2,SPN	
	1.8E-04	17	1280	3.90	GO:0001775 cell activation	http://amigo.geneontology.org/amigo/term/GO:0001775	ACTB,CD74,LAT	
	1.9E-04	8	235	9.99	GO:0002695 negative regulation of leukocyte activation	http://amigo.geneontology.org/amigo/term/GO:0002695	IL10,FGR,CD74	
	1.9E-04	9	324	8.15	GO:0002263 cell activation involved in immune response	http://amigo.geneontology.org/amigo/term/GO:0002263	CD74,SLAMF1,S	
	1.9E-04	9	320	8.25	GO:0002366 leukocyte activation involved in immune response	http://amigo.geneontology.org/amigo/term/GO:0002366	CD74,SLAMF1,S	
	1.9E-04	16	1160	4.05	GO:0051248 negative regulation of protein metabolic process	http://amigo.geneontology.org/amigo/term/GO:0051248	HEXIM1,TNFAIP	
	2.4E-04	13	788	4.84	GO:0050865 regulation of cell activation	http://amigo.geneontology.org/amigo/term/GO:0050865	ACTB,IL10,FGR	
	2.4E-04	14	922	4.45	GO:0001817 regulation of cytokine production	http://amigo.geneontology.org/amigo/term/GO:0001817	CD74,SLAMF1,F	
	2.4E-04	15	1054	4.17	GO:0050776 regulation of immune response	http://amigo.geneontology.org/amigo/term/GO:0050776	CD74,LAT2,SPN	
	2.4E-04	17	1355	3.68	GO:0098542 defense response to other organism	http://amigo.geneontology.org/amigo/term/GO:0098542	FGR,ISG20,SPN	
	2.4E-04	20	1835	3.20	GO:0042127 regulation of cell population proliferation	http://amigo.geneontology.org/amigo/term/GO:0042127	DUSP22,BTG2,F	
	2.5E-04	8	257	9.13	GO:0050866 negative regulation of cell activation	http://amigo.geneontology.org/amigo/term/GO:0050866	IL10,FGR,CD74	
	2.5E-04	14	930	4.42	GO:0001816 cytokine production	http://amigo.geneontology.org/amigo/term/GO:0001816	CD74,SLAMF1,F	
	2.5E-04	18	1529	3.45	GO:0080134 regulation of response to stress	http://amigo.geneontology.org/amigo/term/GO:0080134	CD74,DUSP22,A	
	3.2E-04	14	956	4.30	GO:0051338 regulation of transferase activity	http://amigo.geneontology.org/amigo/term/GO:0051338	CD74,HEXIM1,C	
	4.4E-04	8	283	8.29	GO:0042113 B cell activation	http://amigo.geneontology.org/amigo/term/GO:0042113	LAT2,IL10,PTPN	
	7.0E-04	13	892	4.28	GO:0006954 inflammatory response	http://amigo.geneontology.org/amigo/term/GO:0006954	PTGIR,C11TA,IL1	
	9.8E-04	11	662	4.87	GO:0042110 T cell activation	http://amigo.geneontology.org/amigo/term/GO:0042110	CD74,ACTB,SPN	
	9.8E-04	14	1078	3.81	GO:1902533 positive regulation of intracellular signal transduction	http://amigo.geneontology.org/amigo/term/GO:1902533	NEK6,CD74,DU	
	1.1E-03	10	549	5.34	GO:0002764 immune response-regulating signaling pathway	http://amigo.geneontology.org/amigo/term/GO:0002764	LAT2,TNFAIP3,F	
	1.1E-03	14	1089	3.77	GO:0032101 regulation of response to external stimulus	http://amigo.geneontology.org/amigo/term/GO:0032101	IL16,IL10,HEXIM	
	1.1E-03	10	551	5.32	GO:0031400 negative regulation of protein modification process	http://amigo.geneontology.org/amigo/term/GO:0031400	HEXIM1,TNFAIP	
	1.2E-03	9	445	5.93	GO:0030098 lymphocyte differentiation	http://amigo.geneontology.org/amigo/term/GO:0030098	ACTB,SPN,CD7	
	1.2E-03	12	826	4.26	GO:0043549 regulation of kinase activity	http://amigo.geneontology.org/amigo/term/GO:0043549	CD74,HEXIM1,C	
	1.2E-03	14	1119	3.67	GO:0002684 positive regulation of immune system process	http://amigo.geneontology.org/amigo/term/GO:0002684	CD74,LAT2,ACT	
	1.2E-03	9	457	5.78	GO:0010563 negative regulation of phosphorus metabolic process	http://amigo.geneontology.org/amigo/term/GO:0010563	HEXIM1,CDKN1	
	1.2E-03	9	456	5.79	GO:0045936 negative regulation of phosphate metabolic process	http://amigo.geneontology.org/amigo/term/GO:0045936	HEXIM1,CDKN1	
	1.2E-03	11	702	4.60	GO:0045859 regulation of protein kinase activity	http://amigo.geneontology.org/amigo/term/GO:0045859	HEXIM1,CDKN1	
	1.2E-03	12	835	4.22	GO:0043086 negative regulation of catalytic activity	http://amigo.geneontology.org/amigo/term/GO:0043086	HEXIM1,RPL23,	
	1.3E-03	8	353	6.65	GO:0002460 adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	http://amigo.geneontology.org/amigo/term/GO:0002460	SPN,CD74,PTPN	
	1.4E-03	19	1994	2.80	GO:0016310 phosphorylation	http://amigo.geneontology.org/amigo/term/GO:0016310	CD74,IKBKB,MC	
	1.4E-03	17	1645	3.03	GO:0009967 positive regulation of signal transduction	http://amigo.geneontology.org/amigo/term/GO:0009967	NEK6,CD74,DU	
	1.5E-03	18	1836	2.88	GO:0023056 positive regulation of signaling	http://amigo.geneontology.org/amigo/term/GO:0023056	NEK6,CD74,DU	
	1.5E-03	11	731	4.41	GO:0031347 regulation of defense response	http://amigo.geneontology.org/amigo/term/GO:0031347	IL10,IL16,HEXIM	
	1.7E-03	9	488	5.41	GO:0050863 regulation of T cell activation	http://amigo.geneontology.org/amigo/term/GO:0050863	ACTB,CD74,PTP	
	1.7E-03	17	1684	2.96	GO:0006468 protein phosphorylation	http://amigo.geneontology.org/amigo/term/GO:0006468	CD74,IKBKB,MC	
	2.1E-03	11	762	4.23	GO:0002252 immune effector process	http://amigo.geneontology.org/amigo/term/GO:0002252	CD74,SLAMF1,IL	
	2.1E-03	14	1213	3.39	GO:0051726 regulation of cell cycle	http://amigo.geneontology.org/amigo/term/GO:0051726	BIRC3,GADD45I	
	2.1E-03	9	507	5.21	GO:1903131 mononuclear cell differentiation	http://amigo.geneontology.org/amigo/term/GO:1903131	ACTB,CD74,ZFP	
	2.5E-03	8	403	5.82	GO:0050727 regulation of inflammatory response	http://amigo.geneontology.org/amigo/term/GO:0050727	IL10,IL16,TNFAI	

asks across all three genera

BP:GO - genes located close to overlapping peaks
(n = 82)

2.6E-03	9	525	5.03	GO:0007159 leukocyte cell-cell adhesion	http://amigo.geneontology.org/amigo/term/GO:0007159	ACTB,CD74,PTF
2.8E-03	9	533	4.95	GO:0002683 negative regulation of immune system process	http://amigo.geneontology.org/amigo/term/GO:0002683	IL10,FGR,CD74,
2.8E-03	9	534	4.94	GO:0007346 regulation of mitotic cell cycle	http://amigo.geneontology.org/amigo/term/GO:0007346	TEX14,BTG2,AC
2.8E-03	13	1102	3.46	GO:0045087 innate immune response	http://amigo.geneontology.org/amigo/term/GO:0045087	FGR,CD74,CIITA
3.6E-03	11	827	3.90	GO:0000165 MAPK cascade	http://amigo.geneontology.org/amigo/term/GO:0000165	CD74,DUSP22,I
3.6E-03	16	1641	2.86	GO:0031399 regulation of protein modification process	http://amigo.geneontology.org/amigo/term/GO:0031399	CD74,BIRC3,MO
3.7E-03	17	1830	2.73	GO:0010647 positive regulation of cell communication	http://amigo.geneontology.org/amigo/term/GO:0010647	NEK6,CD74,DUS
3.7E-03	15	1478	2.98	GO:0019220 regulation of phosphate metabolic process	http://amigo.geneontology.org/amigo/term/GO:0019220	CD74,MOB3A,H
3.7E-03	15	1479	2.98	GO:0051174 regulation of phosphorus metabolic process	http://amigo.geneontology.org/amigo/term/GO:0051174	CD74,MOB3A,H
3.9E-03	14	1318	3.12	GO:0042325 regulation of phosphorylation	http://amigo.geneontology.org/amigo/term/GO:0042325	CD74,MOB3A,H
4.0E-03	17	1857	2.69	GO:1902531 regulation of intracellular signal transduction	http://amigo.geneontology.org/amigo/term/GO:1902531	NEK6,CD74,DUS
4.1E-03	13	1165	3.27	GO:0001932 regulation of protein phosphorylation	http://amigo.geneontology.org/amigo/term/GO:0001932	CD74,MOB3A,H
4.4E-03	8	459	5.11	GO:0002697 regulation of immune effector process	http://amigo.geneontology.org/amigo/term/GO:0002697	CD74,IL10,FGR
5.3E-03	8	476	4.93	GO:0044772 mitotic cell cycle phase transition	http://amigo.geneontology.org/amigo/term/GO:0044772	TEX14,ACTB,NE
5.7E-03	8	486	4.83	GO:1903037 regulation of leukocyte cell-cell adhesion	http://amigo.geneontology.org/amigo/term/GO:1903037	ACTB,CD74,PTF
5.8E-03	9	620	4.26	GO:0001819 positive regulation of cytokine production	http://amigo.geneontology.org/amigo/term/GO:0001819	CD74,SLAMF1,F
6.8E-03	8	501	4.68	GO:0002443 leukocyte mediated immunity	http://amigo.geneontology.org/amigo/term/GO:0002443	FGR,CD74,LAT2
6.8E-03	11	935	3.45	GO:0071345 cellular response to cytokine stimulus	http://amigo.geneontology.org/amigo/term/GO:0071345	CD74,IKKB,ZF
6.8E-03	17	1987	2.51	GO:0051254 positive regulation of RNA metabolic process	http://amigo.geneontology.org/amigo/term/GO:0051254	IKKB,CIITA,AC
6.9E-03	17	1992	2.50	GO:0040011 locomotion	http://amigo.geneontology.org/amigo/term/GO:0040011	ACTB,TNFAIP3,
7.1E-03	9	645	4.09	GO:0002250 adaptive immune response	http://amigo.geneontology.org/amigo/term/GO:0002250	SPN,CD74,LAT2
7.5E-03	9	653	4.04	GO:0002521 leukocyte differentiation	http://amigo.geneontology.org/amigo/term/GO:0002521	ACTB,CD74,ZFF
8.7E-03	9	670	3.94	GO:0050778 positive regulation of immune response	http://amigo.geneontology.org/amigo/term/GO:0050778	CD74,LAT2,HEX
8.9E-03	13	1312	2.91	GO:0010628 positive regulation of gene expression	http://amigo.geneontology.org/amigo/term/GO:0010628	CD74,MED26,SL
1.2E-02	16	1937	2.42	GO:0007049 cell cycle	http://amigo.geneontology.org/amigo/term/GO:0007049	BIRC3,GADD45I
1.2E-02	11	1032	3.13	GO:0034097 response to cytokine	http://amigo.geneontology.org/amigo/term/GO:0034097	CD74,IKKB,ZF
1.5E-02	8	598	3.92	GO:0044770 cell cycle phase transition	http://amigo.geneontology.org/amigo/term/GO:0044770	TEX14,ACTB,NE
1.7E-02	8	616	3.81	GO:0022407 regulation of cell-cell adhesion	http://amigo.geneontology.org/amigo/term/GO:0022407	ACTB,CD74,PTF
1.8E-02	8	619	3.79	GO:0009611 response to wounding	http://amigo.geneontology.org/amigo/term/GO:0009611	ACTB,ZFP36,ZF
1.8E-02	9	772	3.42	GO:0008285 negative regulation of cell population proliferation	http://amigo.geneontology.org/amigo/term/GO:0008285	BTG2,PTGIR,TN
1.8E-02	11	1108	2.91	GO:0002520 immune system development	http://amigo.geneontology.org/amigo/term/GO:0002520	ACTB,CD74,ZFF
1.8E-02	11	1110	2.91	GO:0010629 negative regulation of gene expression	http://amigo.geneontology.org/amigo/term/GO:0010629	PARP15,SLAMF
2.4E-02	10	996	2.95	GO:0000278 mitotic cell cycle	http://amigo.geneontology.org/amigo/term/GO:0000278	TEX14,BTG2,AC
2.4E-02	11	1172	2.75	GO:1901698 response to nitrogen compound	http://amigo.geneontology.org/amigo/term/GO:1901698	RAB8A,ADORA2
2.5E-02	8	672	3.49	GO:0006935 chemotaxis	http://amigo.geneontology.org/amigo/term/GO:0006935	IL16,TMSB4X,CI
2.5E-02	10	1001	2.93	GO:0030097 hemopoiesis	http://amigo.geneontology.org/amigo/term/GO:0030097	ACTB,CD74,ZFF
2.5E-02	8	676	3.47	GO:0042330 taxis	http://amigo.geneontology.org/amigo/term/GO:0042330	IL16,TMSB4X,CI
2.8E-02	14	1777	2.31	GO:0048585 negative regulation of response to stimulus	http://amigo.geneontology.org/amigo/term/GO:0048585	CD74,DUSP2,SL
2.9E-02	14	1791	2.29	GO:0070727 cellular macromolecule localization	http://amigo.geneontology.org/amigo/term/GO:0070727	RAB8A,TMSB4X
2.9E-02	10	1042	2.82	GO:0048534 hematopoietic or lymphoid organ development	http://amigo.geneontology.org/amigo/term/GO:0048534	ACTB,CD74,ZFF
3.0E-02	14	1806	2.27	GO:0048870 cell motility	http://amigo.geneontology.org/amigo/term/GO:0048870	ACTB,TNFAIP3,
3.0E-02	14	1806	2.27	GO:0051674 localization of cell	http://amigo.geneontology.org/amigo/term/GO:0051674	ACTB,TNFAIP3,
3.1E-02	8	719	3.26	GO:0043408 regulation of MAPK cascade	http://amigo.geneontology.org/amigo/term/GO:0043408	CD74,DUSP22,I
3.2E-02	10	1061	2.76	GO:0010243 response to organonitrogen compound	http://amigo.geneontology.org/amigo/term/GO:0010243	RAB8A,ADORA2
3.2E-02	14	1825	2.25	GO:0045893 positive regulation of transcription DNA-templated	http://amigo.geneontology.org/amigo/term/GO:0045893	IKKB,CIITA,AC
3.2E-02	14	1825	2.25	GO:1903508 positive regulation of nucleic acid-templated transcription	http://amigo.geneontology.org/amigo/term/GO:1903508	IKKB,CIITA,AC
3.2E-02	13	1627	2.34	GO:0043067 regulation of programmed cell death	http://amigo.geneontology.org/amigo/term/GO:0043067	CD74,BIRC3,AC
3.3E-02	14	1831	2.24	GO:1902680 positive regulation of RNA biosynthetic process	http://amigo.geneontology.org/amigo/term/GO:1902680	IKKB,CIITA,AC
3.7E-02	13	1665	2.29	GO:0010558 negative regulation of macromolecule biosynthetic process	http://amigo.geneontology.org/amigo/term/GO:0010558	HEXIM1,ZFP36,
3.8E-02	10	1104	2.66	GO:0098609 cell-cell adhesion	http://amigo.geneontology.org/amigo/term/GO:0098609	ACTB,ITGAL,CD
3.9E-02	12	1483	2.37	GO:2000026 regulation of multicellular organismal development	http://amigo.geneontology.org/amigo/term/GO:2000026	BHLHE40,HES7
3.9E-02	13	1687	2.26	GO:0051240 positive regulation of multicellular organismal process	http://amigo.geneontology.org/amigo/term/GO:0051240	CD74,SLAMF1,A
4.1E-02	8	772	3.04	GO:0009617 response to bacterium	http://amigo.geneontology.org/amigo/term/GO:0009617	SPN,TNFAIP3,Z
4.2E-02	14	1916	2.14	GO:0042592 homeostatic process	http://amigo.geneontology.org/amigo/term/GO:0042592	ACTB,PIGR,PTC
4.3E-02	8	781	3.00	GO:0010564 regulation of cell cycle process	http://amigo.geneontology.org/amigo/term/GO:0010564	TEX14,ACTB,NE
4.3E-02	8	782	3.00	GO:0080135 regulation of cellular response to stress	http://amigo.geneontology.org/amigo/term/GO:0080135	CD74,DUSP22,A
4.3E-02	9	958	2.76	GO:0014070 response to organic cyclic compound	http://amigo.geneontology.org/amigo/term/GO:0014070	ZFP36,ADORA2
4.4E-02	13	1726	2.21	GO:0031327 negative regulation of cellular biosynthetic process	http://amigo.geneontology.org/amigo/term/GO:0031327	HEXIM1,ZFP36,
4.7E-02	11	1354	2.38	GO:0009968 negative regulation of signal transduction	http://amigo.geneontology.org/amigo/term/GO:0009968	CD74,DUSP2,SL
4.7E-02	13	1756	2.17	GO:0009890 negative regulation of biosynthetic process	http://amigo.geneontology.org/amigo/term/GO:0009890	HEXIM1,CIITA,Z

asks only between

6.0E-07	20	136	5.11	Path:hsa04210 Apoptosis	http://www.genomeweb.com/pathway/hsa04210	PARP2,TUBA1B
1.2E-03	10	79	4.40	Path:hsa01521 EGFR tyrosine kinase inhibitor resistance	http://www.genomeweb.com/pathway/hsa01521	FOXO3,IL6R,PR
4.2E-06	20	162	4.29	Path:hsa04630 JAK-STAT signaling pathway	http://www.genomeweb.com/pathway/hsa04630	IFNLR1,IFNAR2
6.5E-06	20	169	4.12	Path:hsa04141 Protein processing in endoplasmic reticulum	http://www.genomeweb.com/pathway/hsa04141	ATF6,SEC61G,P
3.7E-04	13	112	4.04	Path:hsa04668 TNF signaling pathway	http://www.genomeweb.com/pathway/hsa04668	MAP3K8,MAPK1
9.9E-04	12	108	3.86	Path:hsa04659 Th17 cell differentiation	http://www.genomeweb.com/pathway/hsa04659	MAPK14,HSP90

KEGG - genes located close to overlapping pecc chimpanzees and orangutans (n = 710)	2.7E-05	20	191	3.64	Path:hsa04062 Chemokine signaling pathway	http://www.genor	CCR4,CCR7,PIK
	2.8E-05	20	193	3.60	Path:hsa05202 Transcriptional misregulation in cancer	http://www.genor	DDX5,ETV6,H3-
	3.4E-04	16	161	3.46	Path:hsa05206 MicroRNAs in cancer	http://www.genor	CDK6,PDCD4,S
	3.3E-05	21	214	3.41	Path:hsa05417 Lipid and atherosclerosis	http://www.genor	TANK,MAPK14,A
	8.9E-05	19	194	3.41	Path:hsa05167 Kaposi sarcoma-associated herpesvirus infection	http://www.genor	CDK6,CCR4,MA
	4.2E-06	28	294	3.31	Path:hsa04060 Cytokine-cytokine receptor interaction	http://www.genor	CCR4,CCR7,IFN
	1.3E-05	25	266	3.27	Path:hsa05012 Parkinson disease	http://www.genor	TUBA1B,ATP5P
	4.0E-04	18	202	3.10	Path:hsa05169 Epstein-Barr virus infection	http://www.genor	CDK6,MAPK14,I
	8.9E-05	22	249	3.07	Path:hsa05132 Salmonella infection	http://www.genor	ARPC3,ARPC2,
	2.9E-04	20	232	3.00	Path:hsa05171 Coronavirus disease-COVID-19	http://www.genor	MAPK14,RPL13
	2.9E-04	21	251	2.91	Path:hsa04144 Endocytosis	http://www.genor	ARPC3,ARPC2,
	1.3E-05	30	364	2.87	Path:hsa05014 Amyotrophic lateral sclerosis	http://www.genor	TUBA1B,ATP5P
	9.1E-04	30	476	2.19	Path:hsa05022 Pathways of neurodegeneration-multiple diseases	http://www.genor	TUBA1B,ATP5P
	1.0E-03	32	530	2.10	Path:hsa05200 Pathways in cancer	http://www.genor	CDK6,GNG3,GN
genes nearest to human diffbind bins (n = 115)	1.3E-02	13	977	4.23	GO:0033365 protein localization to organelle	http://amigo.gene	SORL1,H4C13,H
	1.8E-02	17	1825	2.96	GO:0045893 positive regulation of transcription DNA-templated	http://amigo.gene	MEF2A,MED26,
	1.8E-02	17	1831	2.95	GO:1902680 positive regulation of RNA biosynthetic process	http://amigo.gene	MEF2A,MED26,
	1.8E-02	17	1825	2.96	GO:1903508 positive regulation of nucleic acid-templated transcription	http://amigo.gene	MEF2A,MED26,
	1.9E-02	14	1316	3.38	GO:0045944 positive regulation of transcription by RNA polymerase II	http://amigo.gene	MEF2A,MED26,
	2.3E-02	16	1782	2.85	GO:0034613 cellular protein localization	http://amigo.gene	SORL1,RAB8A,T
	2.3E-02	16	1791	2.84	GO:0070727 cellular macromolecule localization	http://amigo.gene	SORL1,RAB8A,T
	2.3E-02	17	1987	2.72	GO:0051254 positive regulation of RNA metabolic process	http://amigo.gene	MEF2A,MED26,
	3.3E-02	11	1001	3.49	GO:0031175 neuron projection development	http://amigo.gene	LYN,MYCBP2,C
	3.3E-02	12	1169	3.26	GO:0048666 neuron development	http://amigo.gene	LYN,MYCBP2,C
	3.3E-02	14	1483	3.00	GO:2000026 regulation of multicellular organismal development	http://amigo.gene	CST7,BATF,EGF
	3.3E-02	15	1757	2.71	GO:0022008 neurogenesis	http://amigo.gene	WNT11,LYN,MY
	3.7E-02	11	1088	3.21	GO:0009894 regulation of catabolic process	http://amigo.gene	RNF19A,SNX9,S
	3.7E-02	13	1449	2.85	GO:0030182 neuron differentiation	http://amigo.gene	WNT11,LYN,MY
	4.0E-02	11	1108	3.15	GO:0002520 immune system development	http://amigo.gene	LYN,BATF,H4C1
human nearest genes closer than 10k (n = 68)	4.1E-02	11	1124	3.11	GO:0030163 protein catabolic process	http://amigo.gene	MYLIP,RNF19A,
	4.4E-02	13	1522	2.71	GO:0048699 generation of neurons	http://amigo.gene	WNT11,LYN,MY
	7.0E-03	6	305	11.25	GO:0071824 protein-DNA complex subunit organization	http://amigo.gene	CHD2,H2BC14,H
	7.0E-03	10	977	5.85	GO:0033365 protein localization to organelle	http://amigo.gene	SORL1,H4C13,H
	1.6E-02	6	451	7.61	GO:0042176 regulation of protein catabolic process	http://amigo.gene	RNF19A,SORL1
	1.6E-02	6	386	8.89	GO:0051098 regulation of binding	http://amigo.gene	SORL1,TMSB4X
	1.7E-02	6	480	7.15	GO:0072594 establishment of protein localization to organelle	http://amigo.gene	SORL1,CDH1,N
	1.7E-02	11	1782	3.53	GO:0034613 cellular protein localization	http://amigo.gene	SORL1,RAB8A,T
	1.7E-02	11	1791	3.51	GO:0070727 cellular macromolecule localization	http://amigo.gene	SORL1,RAB8A,T
	2.6E-02	6	572	6.00	GO:0051052 regulation of DNA metabolic process	http://amigo.gene	H1-5,USP7,CDK
	2.8E-02	8	1088	4.21	GO:0009894 regulation of catabolic process	http://amigo.gene	RNF19A,SORL1
	3.4E-02	8	1138	4.02	GO:0006259 DNA metabolic process	http://amigo.gene	APOBEC3H,H1-
	3.5E-02	6	634	5.41	GO:0006897 endocytosis	http://amigo.gene	CLINT1,SORL1,
	3.8E-02	10	1825	3.13	GO:0045893 positive regulation of transcription DNA-templated	http://amigo.gene	MED26,CDH1,H
	3.8E-02	10	1831	3.12	GO:1902680 positive regulation of RNA biosynthetic process	http://amigo.gene	MED26,CDH1,H
	3.8E-02	10	1825	3.13	GO:1903508 positive regulation of nucleic acid-templated transcription	http://amigo.gene	MED26,CDH1,H