

# Ontology	Term Name	Binom Rank	Binom Raw P-Value	Binom FDR Q-Val	Binom Fold Enrichment	Binom Observed Region Hits	Binom Region Set Coverage	Hyper Rank	Hyper FDR Q-Val	Hyper Fold Enrichment	Hyper Observed Gene Hits	Hyper Total Genes	Hyper Gene Set Coverage
Human DHS gains (836 regions):													
GO Biological Process	regulation of action potential in neuron	7	0.00000763757	0.007823054	3.012161	22	0.02631579	115	0.007019542	3.128633	14	67	0.01192504
GO Biological Process	axon ensheathment	8	0.00000786052	0.007044991	3.636246	17	0.02033493	143	0.022543212	3.229415	11	51	0.009369676
GO Biological Process	regulation of action potential	18	0.0000417578	0.016633536	2.497522	25	0.02990431	79	0.003546283	2.994549	17	85	0.01448041
GO Biological Process	cellular response to hydrogen peroxide	22	0.0000726281	0.023670142	4.714695	10	0.01196172	139	0.018571156	4.277927	8	28	0.00681431
GO Biological Process	myelination	23	0.0000754788	0.023529683	3.306935	15	0.01794258	170	0.038235965	3.18569	10	47	0.008517888
GO Biological Process	regulation of striated muscle tissue development	29	0.000137597	0.034019722	2.411843	23	0.02751196	89	0.004115235	3.539012	13	55	0.01107325
GO Biological Process	regulation of muscle organ development	33	0.000168307	0.036568564	2.377772	23	0.02751196	101	0.005400322	3.414836	13	57	0.01107325
*No significant Disease processes identified													
Human DHS losses (286 regions):													
*No significant Biological processes identified													
*No significant Disease processes identified													
Chimpanzee DHS gains (676 regions):													
*No significant Biological processes identified													
Disease Ontology	colonic neoplasm	1	0.00000302625	0.005477516	2.121369	45	0.06656805	14	0.009633704	1.997111	35	292	0.03317536
Disease Ontology	malignant tumor of colon	2	0.0000124607	0.011276943	2.062751	42	0.06213018	29	0.019480787	1.917883	32	278	0.03033175
Disease Ontology	habitual abortion	6	0.000093841	0.028308705	11.37484	5	0.00739645	7	0.009590983	10.41351	5	8	0.004739336
Chimpanzee DHS losses (211 regions):													
*No significant Biological processes identified													
*No significant Disease processes identified													
Common DHS (1259 regions):													
*No significant Biological processes identified													
*No significant Disease processes identified													
# GREAT version 1.8	Species assembly: hg19	Association rule: Basal+extension: 5000 bp upstream, 1000 bp downstream, 1000000 bp max extension, curated regulatory domains included											

b.								
Category	Term	Count	%	PValue	Fold Enrichment	Bonferroni	Benjamini	FDR
Human Upregulated genes:								
GOTERM_BP_FAT	GO:0007155~cell adhesion	53	6.95	0.000000715	2.08	0.001611697	0.001611697	0.00124656
GOTERM_BP_FAT	GO:0022610~biological adhesion	53	6.95	0.000000726	2.07	0.001637286	0.000819	0.001266367
GOTERM_BP_FAT	GO:0016337~cell-cell adhesion	24	3.15	0.000191	2.39	0.350739019	0.13408931	0.333243188
GOTERM_BP_FAT	GO:0007156~homophilic cell adhesion	14	1.83	0.000966	2.93	0.886936744	0.420130359	1.67050329
Human Downregulated genes:								
GOTERM_BP_FAT	GO:0008585~female gonad development	12	1.42	0.000103	4.23	0.246204589	0.246204589	0.18269255
GOTERM_BP_FAT	GO:0046545~development of primary female sexual characteristics	12	1.42	0.000206	3.92	0.432997289	0.247004176	0.366419612
GOTERM_BP_FAT	GO:0046660~female sex differentiation	12	1.42	0.000206	3.92	0.432997289	0.247004176	0.366419612
GOTERM_BP_FAT	GO:0042127~regulation of cell proliferation	57	6.75	0.000279	1.63	0.536759885	0.226247521	0.496622618
GOTERM_BP_FAT	GO:0022602~ovulation cycle process	11	1.30	0.00036	4.00	0.629831591	0.219990597	0.64090748
GOTERM_BP_FAT	GO:0043523~regulation of neuron apoptosis	13	1.54	0.000591	3.26	0.804204021	0.278293272	1.049478067
GOTERM_BP_FAT	GO:0042698~ovulation cycle	11	1.30	0.000682	3.70	0.847437036	0.269015469	1.209074752
GOTERM_BP_FAT	GO:0035295~tube development	22	2.60	0.000775	2.25	0.8821305	0.26321112	1.373840222
Chimpanzee Upregulated genes:								
GOTERM_BP_FAT	GO:0045686~negative regulation of glial cell differentiation	6	0.84	0.0000213	15.34	0.054817189	0.054817189	0.037834948
GOTERM_BP_FAT	GO:0014014~negative regulation of gliogenesis	6	0.84	0.0000213	15.34	0.054817189	0.054817189	0.037834948
GOTERM_BP_FAT	GO:0045685~regulation of glial cell differentiation	7	0.98	0.000049	9.84	0.121648588	0.06279596	0.087026886
GOTERM_BP_FAT	GO:0032101~regulation of response to external stimulus	18	2.53	0.0000497	3.18	0.123219374	0.042886045	0.088227299
GOTERM_BP_FAT	GO:0014013~regulation of gliogenesis	7	0.98	0.0000666	9.37	0.161536038	0.043089984	0.118190582
GOTERM_BP_FAT	GO:0048713~regulation of oligodendrocyte differentiation	5	0.70	0.000171	15.62	0.364044143	0.086548708	0.303357002
GOTERM_BP_FAT	GO:0043062~extracellular structure organization	17	2.39	0.000225	2.93	0.448228735	0.094351136	0.398334855
GOTERM_BP_FAT	GO:0048715~negative regulation of oligodendrocyte differentiation	4	0.56	0.00082	18.75	0.885656722	0.266401115	1.445061963
Chimpanzee Downregulated genes:								
GOTERM_BP_FAT	GO:0040012~regulation of locomotion	21	2.89	0.0000606	2.80	0.153130469	0.153130469	0.108032715
GOTERM_BP_FAT	GO:0051270~regulation of cell motion	21	2.89	0.0000652	2.79	0.163766918	0.085542193	0.116243241
GOTERM_BP_FAT	GO:0030334~regulation of cell migration	19	2.62	0.000105	2.88	0.250742864	0.091739774	0.187557766
GOTERM_BP_FAT	GO:0035108~limb morphogenesis	14	1.93	0.000118	3.62	0.276560071	0.077745849	0.210316176
GOTERM_BP_FAT	GO:0035107~appendage morphogenesis	14	1.93	0.000118	3.62	0.276560071	0.077745849	0.210316176
GOTERM_BP_FAT	GO:0035113~embryonic appendage morphogenesis	13	1.79	0.000133	3.83	0.305963752	0.070442133	0.237240307
GOTERM_BP_FAT	GO:0030326~embryonic limb morphogenesis	13	1.79	0.000133	3.83	0.305963752	0.070442133	0.237240307
GOTERM_BP_FAT	GO:0048736~appendage development	14	1.93	0.000177	3.48	0.385015169	0.077830543	0.315665555
GOTERM_BP_FAT	GO:0060173~limb development	14	1.93	0.000177	3.48	0.385015169	0.077830543	0.315665555
GOTERM_BP_FAT	GO:0009954~proximal/distal pattern formation	7	0.96	0.000195	7.80	0.413349516	0.073359351	0.346239237
GOTERM_BP_FAT	GO:0001944~vasculature development	22	3.03	0.000837	2.25	0.899154027	0.249315722	1.480895953
Common genes:								
GOTERM_BP_FAT	GO:0044265~cellular macromolecule catabolic process	97	7.38	0.000000000128	1.97	0.000000361	0.000000361	0.000000229
GOTERM_BP_FAT	GO:0009057~macromolecule catabolic process	100	7.60	0.000000000736	1.88	0.00000207	0.00000104	0.00000132
GOTERM_BP_FAT	GO:0006350~transcription	210	15.97	0.00000000183	1.47	0.00000517	0.00000172	0.00000328
GOTERM_BP_FAT	GO:0034470~ncRNA processing	37	2.81	0.0000000104	2.91	0.0000294	0.00000734	0.0000186
GOTERM_BP_FAT	GO:0034660~ncRNA metabolic process	42	3.19	0.0000000104	2.68	0.0000294	0.00000588	0.0000186
GOTERM_BP_FAT	GO:0006974~response to DNA damage stimulus	56	4.26	0.0000000384	2.21	0.000108	0.0000181	0.0000688
GOTERM_BP_FAT	GO:0006396~RNA processing	73	5.55	0.0000000391	1.96	0.00011	0.0000157	0.0000699
GOTERM_BP_FAT	GO:0030163~protein catabolic process	79	6.01	0.0000000854	1.87	0.000241	0.0000301	0.000153

GOTERM_BP_FAT	GO:0044257~cellular protein catabolic process	77	5.86	0.0000000998	1.88	0.000281	0.0000313	0.000179
GOTERM_BP_FAT	GO:0051603~proteolysis involved in cellular protein catabolic process	76	5.78	0.000000174	1.86	0.000491	0.0000492	0.000312
GOTERM_BP_FAT	GO:0006399~tRNA metabolic process	26	1.98	0.000000278	3.24	0.000783	0.0000712	0.000497
GOTERM_BP_FAT	GO:0045449~regulation of transcription	237	18.02	0.000000456	1.34	0.001285375	0.000107	0.000816
GOTERM_BP_FAT	GO:0019941~modification-dependent protein catabolic process	72	5.48	0.000000565	1.84	0.001590863	0.000122	0.001009622
GOTERM_BP_FAT	GO:0043632~modification-dependent macromolecule catabolic process	72	5.48	0.000000565	1.84	0.001590863	0.000122	0.001009622
GOTERM_BP_FAT	GO:0016568~chromatin modification	42	3.19	0.00000143	2.25	0.004014057	0.000287	0.002550549
GOTERM_BP_FAT	GO:0008033~tRNA processing	19	1.44	0.00000238	3.67	0.006698326	0.000448	0.004261851
GOTERM_BP_FAT	GO:0051276~chromosome organization	61	4.64	0.00000429	1.85	0.012036859	0.000757	0.007679025
GOTERM_BP_FAT	GO:0000184~nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	11	0.84	0.0000173	5.39	0.047573698	0.002863102	0.030904642
GOTERM_BP_FAT	GO:0006402~mRNA catabolic process	13	0.99	0.0000195	4.44	0.053524232	0.003051441	0.034877696
GOTERM_BP_FAT	GO:0006259~DNA metabolic process	60	4.56	0.0000312	1.74	0.0842638	0.004622281	0.055805503
GOTERM_BP_FAT	GO:0033554~cellular response to stress	65	4.94	0.0000378	1.69	0.101051332	0.005312307	0.067531309
GOTERM_BP_FAT	GO:0000956~nuclear-transcribed mRNA catabolic process	11	0.84	0.0000773	4.62	0.195893587	0.010328371	0.138161184
GOTERM_BP_FAT	GO:0006325~chromatin organization	47	3.57	0.0000839	1.83	0.21059191	0.01069116	0.149843012
GOTERM_BP_FAT	GO:0006281~DNA repair	38	2.89	0.000102	1.97	0.250134292	0.012437706	0.182376685
GOTERM_BP_FAT	GO:0046907~intracellular transport	71	5.40	0.000107	1.59	0.260573322	0.012499563	0.19125004
GOTERM_BP_FAT	GO:0051726~regulation of cell cycle	42	3.19	0.000137	1.86	0.320117681	0.015314937	0.244373244
GOTERM_BP_FAT	GO:0008610~lipid biosynthetic process	40	3.04	0.000335	1.82	0.611513914	0.03571203	0.597780671
GOTERM_BP_FAT	GO:0006913~nucleocytoplasmic transport	24	1.83	0.000353	2.26	0.630364845	0.036189613	0.629129683
GOTERM_BP_FAT	GO:0008104~protein localization	87	6.62	0.000385	1.45	0.661981653	0.037996974	0.685459086
GOTERM_BP_FAT	GO:0051169~nuclear transport	24	1.83	0.000425	2.23	0.6984702	0.040498031	0.757374729
GOTERM_BP_FAT	GO:0015031~protein transport	77	5.86	0.000432	1.48	0.703954049	0.039762555	0.768924949
GOTERM_BP_FAT	GO:0008654~phospholipid biosynthetic process	18	1.37	0.000487	2.59	0.746959377	0.043361021	0.867647415
GOTERM_BP_FAT	GO:0006260~DNA replication	27	2.05	0.000495	2.09	0.752623939	0.042712414	0.881878892
GOTERM_BP_FAT	GO:0070647~protein modification by small protein conjugation or removal	24	1.83	0.00051	2.20	0.762625317	0.042643325	0.907815417
GOTERM_BP_FAT	GO:0045184~establishment of protein localization	77	5.86	0.000579	1.47	0.804710791	0.046901918	1.030373006
GOTERM_BP_FAT	GO:0016071~mRNA metabolic process	43	3.27	0.000733	1.71	0.873455781	0.057351501	1.302308953