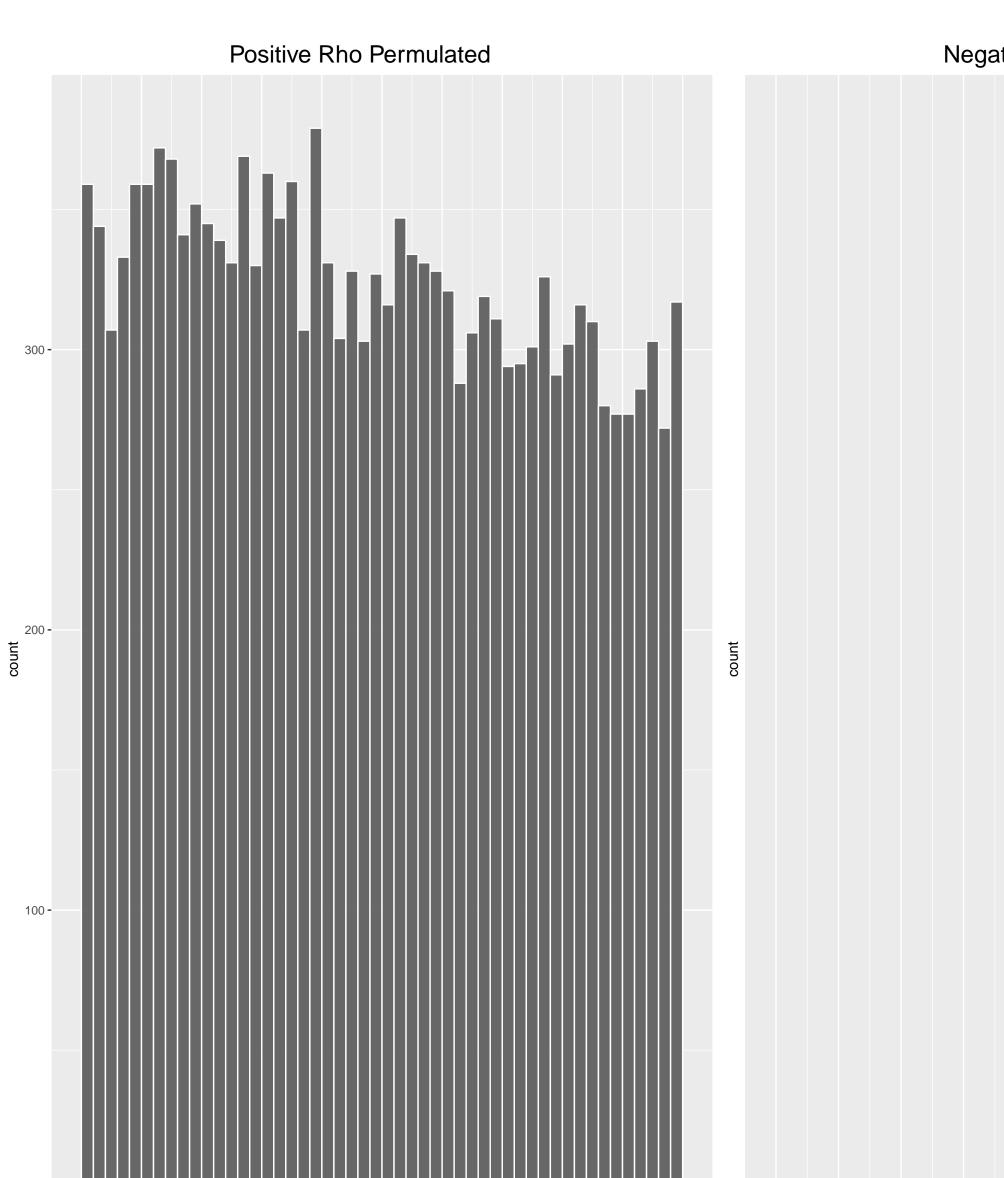
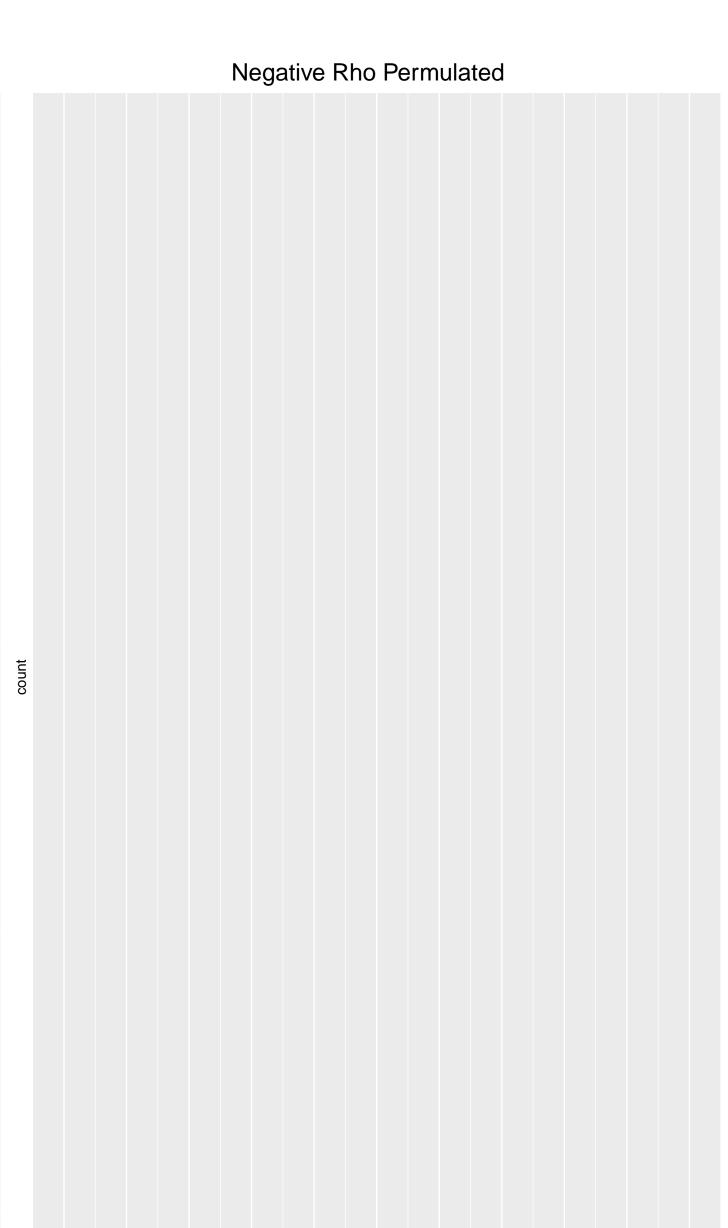
Gene	Rho	N	Р	p.adj	permP	permPValue	qValueNoperm	qValuePerm
PTCD3	0.09932340	313	1.866e-07	4.455e-05	1.515e-05	1.515e-05	9.596e-03	2.195e-01
PPFIA3	0.17794716	171	2.698e-07	5.909e-05	3.970e-04	3.970e-04	1.187e-02	6.964e-01
ABCB1	0.07230963	288	3.116e-05	1.476e-03	5.303e-04	5.303e-04	6.358e-02	6.964e-01
BAX	0.18734038	105	5.878e-05	2.279e-03	6.455e-04	6.455e-04	8.105e-02	6.964e-01
ARHGEF12	0.09204905	293	1.457e-06	1.785e-04	7.273e-04	7.273e-04	1.980e-02	6.964e-01
OFD1	0.16618570	274	1.407e-10	1.755e-07	7.394e-04	7.394e-04	2.007e-04	6.964e-01
CADPS2	0.08121832	251	3.899e-05	1.694e-03	9.606e-04	9.606e-04	6.749e-02	6.964e-01
CASR	0.09342518	251	8.477e-06	5.700e-04	1.027e-03	1.027e-03	3.515e-02	6.964e-01
DNAH2	0.21574345	312	2.693e-15	4.364e-11	1.027e-03	1.027e-03	6.486e-07	6.964e-01
TACR2	0.15034267	256	4.733e-09	2.841e-06	1.045e-03	1.045e-03	1.564e-03	6.964e-01
ZFYVE9	0.14857597	286	6.384e-10	5.747e-07	1.073e-03	1.073e-03	4.746e-04	6.964e-01
ANKRD35	0.15249551	289	2.905e-10	3.363e-07	1.118e-03	1.118e-03	3.570e-04	6.964e-01
CFAP45	0.11550068	273	1.507e-07	3.942e-05	1.285e-03	1.285e-03	9.381e-03	6.964e-01
ESYT3	0.11976678	299	1.778e-08	7.582e-06	1.297e-03	1.297e-03	2.874e-03	6.964e-01
GGTLC3	0.10623403	248	2.005e-06	2.166e-04	1.355e-03	1.355e-03	2.146e-02	6.964e-01
PTPRB	0.09626052	324	1.772e-07	4.350e-05	1.385e-03	1.385e-03	9.596e-03	6.964e-01
SDS	0.08252280	243	4.607e-05	1.924e-03	1.424e-03	1.424e-03	7.372e-02	6.964e-01
SLC10A6	0.09033010	277	3.857e-06	3.572e-04	1.427e-03	1.427e-03	3.028e-02	6.964e-01
MZF1	0.11725148	252	4.068e-07	7.434e-05	1.427e-03	1.427e-03	1.241e-02	6.964e-01
WIPF3	0.08197540	137	3.794e-03	3.631e-02	1.452e-03	1.452e-03	3.186e-01	6.964e-01
NUP88	0.18840808	267	1.310e-11	4.246e-08	1.473e-03	1.473e-03	1.262e-04	6.964e-01
ALYREF	0.14952497	96	8.231e-04	1.323e-02	1.473e-03	1.473e-03	1.949e-01	6.964e-01
SP3	0.08035184	147	2.835e-03	2.976e-02	1.509e-03	1.509e-03	2.864e-01	6.964e-01
ABCB4	0.10082176	291	4.477e-07	7.886e-05	1.570e-03	1.570e-03	1.274e-02	6.964e-01
ZNF606	0.07759741	249	6.625e-05	2.438e-03	1.591e-03	1.591e-03	8.190e-02	6.964e-01

Gene	Rho	N	Р	p.adj	permP	permPValue	qValueNoperm	qValuePerm
PTCD3	0.09932340	313	1.866e-07	4.455e-05	1.515e-05	1.515e-05	9.596e-03	2.195e-01
PYGM	0.14280726	224	1.215e-07	3.455e-05	2.330e-03	2.330e-03	9.010e-03	6.964e-01
SUPT4H1	0.42948718	25	5.777e-03	4.783e-02	1.931e-03	1.931e-03	3.623e-01	6.964e-01
PTK7	0.04657853	280	1.507e-03	1.993e-02	3.867e-03	3.867e-03	2.419e-01	6.964e-01
RARS1	0.05524878	255	8.969e-04	1.402e-02	3.133e-03	3.133e-03	2.009e-01	6.964e-01
DHX58	0.03808004	296	3.636e-03	3.521e-02	2.748e-03	2.748e-03	3.126e-01	6.964e-01
CKMT2	0.09831331	186	1.123e-04	3.468e-03	3.009e-03	3.009e-03	9.802e-02	6.964e-01
NARS1	0.07761724	243	8.341e-05	2.834e-03	3.548e-03	3.548e-03	8.826e-02	6.964e-01
SDS	0.08252280	243	4.607e-05	1.924e-03	1.424e-03	1.424e-03	7.372e-02	6.964e-01
PDCL	0.11137572	194	2.149e-05	1.106e-03	3.691e-03	3.691e-03	5.210e-02	6.964e-01
ABCB4	0.10082176	291	4.477e-07	7.886e-05	1.570e-03	1.570e-03	1.274e-02	6.964e-01
ABCB1	0.07230963	288	3.116e-05	1.476e-03	5.303e-04	5.303e-04	6.358e-02	6.964e-01
CSAD	0.03766079	260	7.619e-03	5.738e-02	3.076e-03	3.076e-03	3.959e-01	6.964e-01
NCOR1	0.09276775	285	1.901e-06	2.146e-04	1.873e-03	1.873e-03	2.146e-02	6.964e-01
SLC10A6	0.09033010	277	3.857e-06	3.572e-04	1.427e-03	1.427e-03	3.028e-02	6.964e-01
C11orf53	0.08954310	265	7.358e-06	5.165e-04	2.227e-03	2.227e-03	3.323e-02	6.964e-01
PRSS53	0.08168560	295	6.097e-06	4.796e-04	3.655e-03	3.655e-03	3.323e-02	6.964e-01
ZFYVE9	0.14857597	286	6.384e-10	5.747e-07	1.073e-03	1.073e-03	4.746e-04	6.964e-01
PIP	0.12368616	250	2.053e-07	4.685e-05	3.018e-03	3.018e-03	9.808e-03	6.964e-01
ALB	0.07914234	303	6.456e-06	4.935e-04	3.215e-03	3.215e-03	3.323e-02	6.964e-01
HPS3	0.06782127	305	3.334e-05	1.544e-03	3.127e-03	3.127e-03	6.555e-02	6.964e-01
RAB8A	0.19976468	78	4.569e-04	9.005e-03	3.630e-03	3.630e-03	1.618e-01	6.964e-01
HAS2	0.23169520	105	5.855e-06	4.721e-04	1.612e-03	1.612e-03	3.323e-02	6.964e-01
SP3	0.08035184	147	2.835e-03	2.976e-02	1.509e-03	1.509e-03	2.864e-01	6.964e-01
SPTBN5	0.13306984	284	6.645e-09	3.846e-06	3.106e-03	3.106e-03	1.828e-03	6.964e-01





Top Positive genes by P-value Permulated

_{0.5} p Values

0.0

Top Negative genes by P-value Permulated

_{0.5} p Values

0.0

1.0

0.2

Gene	Rho	N	P	p.adj	permP	permPValue	qValueNoperm	qValuePerm
PTCD3	0.09932340	313	1.866e-07	4.455e-05	1.515e-05	1.515e-05	9.596e-03	2.195e-01
PPFIA3	0.17794716	171	2.698e-07	5.909e-05	3.970e-04	3.970e-04	1.187e-02	6.964e-01
ABCB1	0.07230963	288	3.116e-05	1.476e-03	5.303e-04	5.303e-04	6.358e-02	6.964e-01
BAX	0.18734038	105	5.878e-05	2.279e-03	6.455e-04	6.455e-04	8.105e-02	6.964e-01
ARHGEF12	0.09204905	293	1.457e-06	1.785e-04	7.273e-04	7.273e-04	1.980e-02	6.964e-01
OFD1	0.16618570	274	1.407e-10	1.755e-07	7.394e-04	7.394e-04	2.007e-04	6.964e-01
CADPS2	0.08121832	251	3.899e-05	1.694e-03	9.606e-04	9.606e-04	6.749e-02	6.964e-01
CASR	0.09342518	251	8.477e-06	5.700e-04	1.027e-03	1.027e-03	3.515e-02	6.964e-01
DNAH2	0.21574345	312	2.693e-15	4.364e-11	1.027e-03	1.027e-03	6.486e-07	6.964e-01
TACR2	0.15034267	256	4.733e-09	2.841e-06	1.045e-03	1.045e-03	1.564e-03	6.964e-01

Gene	Rho	N	Р	p.adj	permP	permPValue	qValueNoperm	qValuePerm
NA	NA	NA	NA	NA	NA	NA	NA	NA
NA.1	NA	NA	NA	NA	NA	NA	NA	NA
NA.2	NA	NA	NA	NA	NA	NA	NA	NA
NA.3	NA	NA	NA	NA	NA	NA	NA	NA
NA.4	NA	NA	NA	NA	NA	NA	NA	NA
NA.5	NA	NA	NA	NA	NA	NA	NA	NA
NA.6	NA	NA	NA	NA	NA	NA	NA	NA
NA.7	NA	NA	NA	NA	NA	NA	NA	NA
NA.8	NA	NA	NA	NA	NA	NA	NA	NA
NA.9	NA	NA	NA	NA	NA	NA	NA	NA

March Column Co	Geneset bladder vagina hippocampus.proper caudate.nucleus	stat tissuena -0.160117878 24 0.112320956 91 -0.066351284 11 0.061706366 26	6.677e-03 1.202e-02 2.263e-04 1.222e-02 4.463e-01 8.654e-02 2.766e-01 8.654e-02	1 UPK2:1 2 RNI 1 NEURO	s by permulation	9 SULT1E1:410 KRT13:492 5569 SLC17A7:6436 OLIG2:6778
Section	left.ventricle fallopian.tube endocervix leg.skin breast	0.061445305 69 -0.059554967 52 0.056094196 72 0.055028346 217 0.051782294 15	7.851e-02 6.056e-0° 1.383e-01 6.789e-0° 1.009e-01 6.657e-0° 5.693e-03 1.202e-0° 4.877e-01 8.654e-0°	1 CK 1 CFAP157 1 BE 1 ANI 1 LMX1B:	MT2:54 S100A1:123 MYH7B:181 MYL3: 7:73 HOXC4:332 HOXA6:415 ADAMTS3:0 0KRB1:91 PLPP3:115 NXNL2:209 MSX1: KRD35:12 POF1B:66 RNF222:82 EVPL:1 125 THRSP:2823.5 GSC:3105 NPY2R:3	321 SMPX:520 ASB10:542 645 EGR1:1591 CRISPLD2:1650 :350 TGM2:569 PWP2:947 126 GGT6:139 FAM83F:188 277 ABCB5:4003 TFAP2B:6113
### STATES AND COLORS 1. Section 1. Sect	skeletal.muscle pancreas ectocervix nucleus.accumbens	0.046787336 239 0.044847150 94 -0.043309474 25 0.037904216 99	1.377e-02 1.718e-0° 1.346e-01 6.789e-0° 4.540e-01 8.654e-0° 1.945e-01 8.654e-0°	1 PY0 1 CASR:8.5 1 ADRA1D 1 GP	GM:42 CKMT2:54 SLC2A4:160 TNNI2:18 PRODH2:111 CATSPERB:132.5 GCG:2 :1000 TSKU:1808 ADRA2A:2027 KCNK6 R88:95 KCNIP1:158 PTPN5:184 ANO3:3	36 MSS51:194.5 USP13:197 99 PNLIPRP1:337 ONECUT1:392 6:2692 MATN2:3244 FGF10:3561 334 PENK:364 GPR6:608.5
Preserved 1970 20 20 20 20 20 20 20	Brodmann.area.24 subcutaneous.adipose esophagogastric.junction aorta	0.034009398 31 -0.033559582 72 -0.032693923 8 -0.029175763 154	5.128e-01 8.654e-0° 3.264e-01 8.654e-0° 7.489e-01 9.240e-0° 2.148e-01 8.654e-0°	1 SLC39A1 1 PLIN1 1 COL4A5: 1 LTBI	2:309 SLC25A18:478 DDN:1413 SLC6A :728 FZD4:792 PNPLA2:1203 G0S2:124 2383 BARX1:5206 NKX6–1:5763 GADL1 P1:125 MYO1D:185 TBXA2R:234 ART4:3	1:2491 SHANK1:2878 UPP2:3217 1 ANGPTL4:1301 BMP6:1369 1:7900 ADCY5:8233 HOXA4:9210 805 PMEPA1:368 IRAG1:428
Part	greater.omentum spleen hypothalamus substantia.nigra	-0.027563112 33 -0.027230574 298 0.027214551 66 -0.026723172 12	5.842e-01 8.822e-0° 1.109e-01 6.657e-0° 4.459e-01 8.654e-0° 7.487e-01 9.240e-0°	1 UPK3E 1 N 1 SY ⁻ 1 FOX	8:519 PLIN1:728 ADAMTS4:1044 HBEGF IOX5:36 CD180:74 BLK:90 BANK1:96 TI FL5:312 DLX2:450 SCN9A:484 ENKUR:5 B1:130 CHRM5:861 RPE65:3248 SPX:38	F:1150 SPRY1:2060 ATF3:2573 NFRSF4:204 TAS1R3:235 556 OXT:910 GABRG3:1163 861 SLC6A3:4464 RET:6738
	esophagus.muscularis.mucosa ovary adrenal.gland blood	0.025039952 26 0.023667029 103 0.020876066 108 -0.020364754 276	6.589e-01 9.145e-0° 4.088e-01 8.654e-0° 4.558e-01 8.654e-0° 2.505e-01 8.654e-0°	1 PRUNE2 1 WIPF3 1 ABCB1	2:130 KCNMB1:1064 SYNM:1698 NTN1:3 3:20 BTNL2:53 KCNT2:403 C21orf62:422 :3 SLC47A1:96 MGST1:262 CYSLTR2:30 CTSW:6 ARHGDIB:23 AQP10:29 NFE2	3444 FAM83D:3537 F2RL2:4348 CCDC170:436 TMEM221:727 D5 KCNN2:612.5 MAP3K15:725 2:32 RGS19:33 BLK:90
March Marc	amygdala transformed.skin.fibroblast tibial.nerve prostate	0.018819337 9 -0.014560148 259 -0.013085956 192 -0.012034885 38 0.009100238 1381	8.450e-01 9.240e-0° 4.256e-01 8.654e-0° 5.355e-01 8.763e-0° 7.977e-01 9.240e-0°	1 LHFPL3:148 1 KDELR 1 GFRA 1 NTF-	80 PCDH15:1496 PTPRZ1:3438 NEURO 3:76 PRKD1:197 SPOCD1:287 SEPTIN1 3:55.5 SCARA5:172 SLC27A6:261 GLDN 4:855 GLIS1:1119 TULP1:1917 SRD5A2:	D2:6882 SLC17A7:9770 TNR:10465 1:382 CITED2:389 MXRA5:532 N:336 IL1RAPL1:443 LGI2:510 1:2029 P2RX2:2490 SP8:2704 1:37 C11orf53:41 OVOI 1:46
Column C	GOCC_9PLUS0_MOTILE_CIL GOCC_B_CELL_RECEPTOR_CO HP_APLASIA_CUTIS_CONGENITA_ON_ GOMF_ANDROGEN_BINDII	LIUM 0.45462 DMPLEX -0.41076 _TRUNK_OR_L 0.38528 NG 0.37687	69 4 1.637e- 45 3 1.373e- 53 6 1.081e- 53 4 9.037e-	-03 5.422e-0 -02 7.190e-0 -03 4.775e-0 -03 7.035e-0	1 CFAP45:13 ENKUR:556 E 1 SYK:1076 CD79B:18 1 ITGB4:134 PLEC:147 KRT14:905 1 ALDH1A1:1092 TSPO:1523	DNAH11:1124 DNAH5:1259 NA NA 561 CD79A:1707 NA NA NA ITGA6:1212 ARHGAP31:1607 KRT5:7146 SHBG:2329 SLC39A9:3012 NA NA
Control Cont	GOCC_CUL4B_RING_E3_UBIQUITIN_L GOMF_MELANOCORTIN_RECEPTO HP_PECTUS_EXCAVATUM_OF_INFERI GOBP_CELL_CELL_JUNCTION_DIS	LIGASE_COMP 0.37385 IR_BINDING -0.3723 OR_STERNUM 0.37094 CASSEMBLY 0.36906	49 4 9.606e- 79 4 9.895e- 87 5 4.069e- 99 5 4.260e-	7.097e-0 -03 7.097e-0 -03 5.954e-0 -03 5.954e-0	CUL4B:583 DDB2:1421 AGRP:1497 ASIP:1601 I NF1:522 PTPN11:1349 MAP2 FER:751 SNAI2:1530 TGFB3:	1 DTL:2811 RBX1:3331 NA NA MRAP:2208 MRAP2:2994 NA NA K1:2117.5 BRAF:2370 SOS1:4070 NA :2504 ABCC8:2629 TGFBR1:3169 NA
19 19 19 19 19 19 19 19	GOCC_PAR_POLARITY_COM GOCC_B_WICH_COMPLE GOBP_RESPONSE_TO_PHERO HP_GENERALIZED_AMYLOID_DE	PLEX -0.35970 XX 0.35714 DMONE -0.35433 POSITION 0.35343	92 5 5.341e- 60 6 2.447e- 41 2 8.258e- 51 3 3.398e-	-03 6.152e-0 -03 5.954e-0 -02 8.580e-0 -02 8.370e-0	PRKCI:564 PARD6G:951 PARD6 DEK:247 ERCC6:1037 MYBBP1A:217 TMEM145:778 GF APOA1:1827 GSN:	6B:1738 PARD3:3725 PARD6A:4399 NA 77 DDX21:2241 SF3B1:2955 SMARCA5:5185 PR180:3945 NA NA NA NA 2086 B2M:3195 NA NA NA
Sept Perform of an order or process of a pro	HP_ABNORMAL_MIDDLE_EAR_R GOBP_PEPTIDYL_ARGININE_N_ME HP_ELEVATED_CIRCULATING_LONG_ GOBP_TRICUSPID_VALVE_MORPH	EFLEXES 0.34525 THYLATION 0.34495 CHAIN_FATTY -0.34244 OGENESIS -0.34164	5 7.501e- 78 5 7.551e- 84 5 8.000e- 23 4 1.795e-	-03 6.744e-0 -03 6.744e-0 -03 6.830e-0 -02 7.377e-0	OTOF:853 PRORP:859 AIFM1 PRMT5:1500 PRMT3:1662 PRMT ABCD1:699 PEX19:700 PE: HEY2:429 BMPR2:2367 TG	I:1196 MPDU1:1595 DIAPH3:8032 NA F8:2791 NDUFAF7:3213 PRMT6:3356 NA X1:1212 PEX5:4881 CPT2:5280 NA GFBR2:3006 BMPR1A:4473 NA NA
## COMMENTAL APPROXIMATION CHEENERS CASHADON CASHAD	GOBP_POSITIVE_REGULATION_OF_RIGOCC_CCAAT_BINDING_FACTOR_GOBP_SKELETAL_MUSCLE_SATELLITHP_APLASIA_CUTIS_CONGENITA_OVE	ESPONSE_TO_	84 6 4.047e- 05 6 4.165e- 07 8 9.390e- 07 6 4.199e-	-03 5.954e-0 -03 5.954e-0 -04 4.665e-0 -03 5.954e-0	1 RIPK1:578 ENDOG:1284 HDAC6:18 1 NFYB:245 NFYC:1588 ATF2:19 1 EPHB1:69 GJD4:1079 MEGF10:238 1 ITGB4:134 PLEC:147 MCTP2:10	821 ABL1:2142.5 FOXP1:4244 PAWR:5617 10 ING2:2021 NFYA:3378 CEBPZ:6673 81 CAPN3:2507 WNT7A:2913 SOX15:3455 043 BMS1:3150 DLL4:4367 UBA2:6909
Description Description Proceedings Proceedings Proceedings Process Proc	HP_CONGENITAL_ADRENAL_HYP GOBP_ESTABLISHMENT_OF_LEFT_RIC GOCC_MCRD_MEDIATED_MRNA_STAB GOBP_PHENYLPROPANOID_METABOI GOBP_REGULATION_OF_FAS_SIGNAL	ERPLASIA 0.33606 GHT_ASYMMET 0.33452 SILITY_COMPLE 0.33347 LIC_PROCESS 0.33316 LING_PATHWAY -0.33299	61 4 1.991e- 27 4 2.049e- 27 5 9.807e- 74 2 1.027e- 04 3 4.575e-	7.450e-0 7.552e-0 7.097e-0 8.609e-0 8.580e-0	1 POR:1825 CYP17A1:2556 1 CFAP45:13 CFAP52:173 I 1 PAIP1:285 SYNCRIP:1467 CSDE 1 PON3:1308 CYF 1 ZDHHC7:789 TMBIM1	STAR:2615 HSD3B2:3596 NA NA ENKUR:556 CCDC39:9977 NA NA 61:1538 HNRNPD:3429 PABPC1:6740 NA P1A1:4086 NA NA NA NA :1080 SMAD5:6249 NA NA NA
## # # # # # # # # # # # # # # # # # #	GOBP_POSITIVE_REGULATION_OF_HY GOBP_SPHINGOLIPID_TRANSLO GOBP_BRANCHED_CHAIN_AMINO_AC GOCC_DNA_REPLICATION_FACTOR_ GOBP_CHONDROBLAST_DIFFERE	/DROGEN_PER	25 4 2.122e- 35 4 2.178e- 70 5 1.039e- 69 3 4.970e-	7.566e-0 7.584e-0 7.137e-0 7.137e-0 7.137e-0	ENDOG:1284 HDAC6:1821 ABCB1:3 ABCB4:24 AB SDS:17 BCAT2:1648 BCAT1 RPA2:380 RPA1:20 RARA:126 GDF5:1242 CCN	1 ABL1:2142.5 PAWR:5617 NA NA BCC1:3415 ABCA2:7474 NA NA 1:2244.5 SDSL:3421 ILVBL:6330 NA 077 RPA3:5950 NA NA NA N1:1726 FGF2:5431 FGF4:5494 NA
MONING, MULE, MULE, 1949 0.0000000 0.0000000 0.0000000000	REACTOME_CHYLOMICRON_CLEAR REACTOME_EICOSANOIDS REACTOME_BETA_OXIDATION_OF_DEC REACTOME_BETA_OXIDATION_OF_OCT REACTOME_ALPHA_DEFENS	ARANCE -0.42706 S -0.37483 ANOYL_COA -0.36402 ANOYL_COA -0.36376 ANOYL_COA -0.35984	46 5 9.417e- 40 4 9.417e- 54 6 2.014e- 63 5 4.845e- 66 3 3.087e-	7.207e-0 9.378e-0 9.378e-0 7.730e-0 7.730e-0 9.398e-0	1 APOB:107 APOE:246 LDLF 1 TBXAS1:1054 CYP8B1:127 1 HADH:66 ACADM:388 MECR:218 1 HADH:66 ACADM:388 ECHS 1 ART1:1786 CD4:2:	R:1315 LIPC:1642 LDLRAP1:2603 NA 78 CYP4B1:2853 PTGIS:2929 NA NA RIS ECHS1:2401 HADHA:2626 HADHB:5554 RI:2401 HADHA:2626 HADHB:5554 NA RIS PRSS3:2772 NA NA NA
DICCORT_CAPE_PROPER_CAPE_CAPE_CAPE_CAPE_CAPE_CAPE_CAPE_CAPE	BAFNA_MUC4_TARGETS_U WP_PILOCYTIC_ASTROCYTO MCCOLLUM_GELDANAMYCIN_RESIS REACTOME_BETA_OXIDATION_OF_LAU WP_EFFECT_OF_INTESTINAL_MICROB	P -0.32962 DMA 0.32208 STANCE_UP -0.31797 ROYL_COA_T -0.31530 IOME_ON_AN 0.31063	40 3 4.799e- 73 6 6.288e- 74 9 9.550e- 29 5 1.461e- 66 7 4.423e-	-02 9.398e-0 -03 8.868e-0 -04 7.207e-0 -02 9.398e-0 -03 7.730e-0	NEK6:275 AVPR2:: NF1:522 PTPN11:1349 BRAF:2 FOXN3:339 SMPD1:717 CDH11:87 HADH:66 ECHS1:2401 HADH NR1I2:886 VDR:1275 PPARA:253	2798 SNAI1:5209 NA NA NA 2370 GRB2:4051 SOS1:4070 RAF1:4951 79 PMCH:1639 SLC16A7:1851 SULF2:2927 HA:2626 ACADL:4315 HADHB:5554 NA 37 NPC1L1:3800 PPARD:4081 CD36:4307
PRINCIPOR LEGICAL PRINCIPOR 0.0000000000000000000000000000000000	BIOCARTA_NPP1_PATHWA' SCHAEFFER_PROSTATE_DEVELOPMEN' REACTOME_PREDNISONE_AI MIZUKAMI_HYPOXIA_DN WP_ALTERNATIVE_PATHWAY_OF_FETAI	Y -0.28654 T_AND_CANCE 0.28486 DME 0.28200 -0.27796 L_ANDROGEN 0.27701	56 10 1.702e- 15 5 2.738e- 33 5 2.896e- 89 5 3.134e- 88 9 4.003e-	7.730e-0 9.398e-0 9.398e-0 9.398e-0 9.398e-0 7.730e-0	1 SPP1:566 ALPL:661 COL4A2:1158 1 ZNF22:1342 SOX9:1459 CD0 1 ABCB1:3 ALB:64 HSD11B1:6 1 PDGFB:529 LRP1:745 CXC 1 HSD17B6:150 POR:1825 HSD17B3:2	8 COL4A4:2014 ENPP1:2036 COL4A5:2383 C27:2525 PDIA4:2882 IGF1R:9251 NA 05 SERPINA6:7506 HSD11B2:9492 NA EL8:3229 FGF2:5431 CXCR1:8060 NA 2212 CYB5A:2320 CYP17A1:2556 STAR:2615
CALLITEST ANDROPOSES, STEM, CELL, FIGS 0.288905017 2.28906-20 3.9890-50 1.0840-20 3.9890-50 1.0840-20 3.9890-50 1.0840-20 3.9890-50 1.0840-20 3.9890-50 1.0840-20 3.9890-50 1.0840-20 3.9890-50 1.0840-20 3.9890-50 1.0840-20 3.9890-50 1.0840-20 3.9890-50 1.0840-20 3.9890-50 1.0840-20 3.9890-50 1.0840-20 3.9890-50 1.0840-20 3.9890-5	REACTOME_CA2_ACTIVATED_K_CF DONATO_CELL_CYCLE_TRETIF REACTOME_LEUKOTRIENE_RECF REACTOME_TERMINAL_PATHWAY_OF_C REACTOME_REGULATION_OF_NPAS4_CF	HANNELS 0.27329 NOIN -0.27268 EPTORS 0.26802 COMPLEMENT -0.26389 GENE_TRANSC -0.26293	05 9 4.522e- 70 6 2.071e- 83 5 3.792e- 15 6 2.518e- 08 4 6.855e-	7.730e-0 9.398e-0 9.398e-0 9.398e-0 9.398e-0 9.398e-0	1 KCNN3:174 KCNN2:612.5 KCNMB1:1 1 SKAP2:1849 ABI1:2513 BTG2 1 CYSLTR2:305 LTB4R:1121 LTB4 1 C8B:98 C6:433 C5:2207 1 NR3C1:1336 SRF:1407	064 KCNN1:1408 KCNN4:2896 KCNMB4:5762 2:3242 TOB1:3862 ATR:5148 MNT:5488 4R2:2034 GPR17:7159 CYSLTR1:8200 NA C8G:2879 C8A:8519.5 CLU:8826 KCNIP3:3221 NPAS4:9404 NA NA
BIOCARIA_NEUTOPHIL_PMINHAW	BYSTRYKH_HEMATOPOIESIS_STEM_ GALI_TP53_TARGETS_APOPTOT IGARASHI_ATF4_TARGETS_I BIOCARTA_RAN_PATHWAY	CELL_FGF3	35 6 2.936e- 71 7 1.898e- 41 4 7.954e- 46 4 8.626e-	-02 9.398e-0 -02 9.398e-0 -02 9.398e-0 -02 9.430e-0	EFNB1:30 SH3RF1:34 EFNB3:1512 BAX:4 GADD45A:1024 CASP8:1 ITFG2:676 PDP1:4113 RCC1:17 RANGAP1:186	PKNOX1:4813 POU5F1:7550 MAP2K6:9715 1109 BIRC3:1804 BIRC2:6062 CD40:6618 SFXN4:4437 ASB4:6782 NA NA 5 RAN:5397 RANBP1:9078 NA NA
BIOCARTIA_SIRP_PATHWAY	BIOCARTA_NEUTROPHIL_PATH SAMOLS_TARGETS_OF_KHSV_MIF LIU_CDX2_TARGETS_DN REACTOME_COBALAMIN_CBL_MET	-0.24438 RNAS_UP -0.24428 0.24364 FABOLISM -0.24344	68 8 1.667e- 21 6 3.823e- 49 5 5.917e- 98 7 2.570e-	-02 9.398e-0 -02 9.398e-0 -02 9.398e-0 -02 9.398e-0	1 ITGB2:129 ICAM1:807 ITGAL:1 1 CDH11:879 GALNT3:1721 SLC31 1 KRT14:905 KRT15:920 KRT 1 MTR:656 MTRR:1163 MMADHC:18	308 ITGAM:1860 CD44:3352 SELL:5686 IA1:3765 COCH:4031 GAL:4887 AK3:9584 IT9:2546 SOX2:2674 HES1:13763 NA IZ5 MMAA:2716 MMAB:4723 MMACHC:5597
GOCC_BLCELL_RECEPTOR_COMPLEX O_0.4107946 3 1.339-02 7.1909-01 HP_APALSAS_CUTIS CONCENTAL ON TRUNK OR L	BIOCARTA_SLRP_PATHWA' REACTOME_BETA_OXIDATION_OF_HEX WP_SCFA_AND_SKELETAL_MUSCLE_SU REACTOME_ARYL_HYDROCARBON_REC	Y -0.24206 (ANOYL_COA0.24153 JBSTRATE_ME 0.24096 CEPTOR_SIGNA 0.24061	35 6 4.002e- 28 5 6.141e- 21 6 4.094e- 43 6 4.123e-	9.398e-0 -02 9.398e-0 -02 9.398e-0 -02 9.398e-0	1 EPYC:92.5 BGN:748 KERA:1 1 HADH:66 ECHS1:2401 HADH 1 SLC2A4:160 GCG:299 FFAR2:2 ⁻¹ 1 AHR;86 PTGES3:1634 ARNT:345	213 LUM:6609 FMOD:6666 DCN:9760 A:2626 HADHB:5554 ACADS:10292 NA 149 PPARD:4081 FFAR3:6844 PYY:11669 9 AIP:3798 ARNT2:4740 HSP90AB1:11524
GOCC, CULB, RING, E3, UBIQUITIN, LICASE, COMP GOMP MELANGOCRITIN, DECEPTOR, BIDINING GOMP LELANGOCRITIN, DECEPTOR, BIDINING HP_PECTUS, EXCANATUM, OF, INFERIOR, STERNUM J3709487 5 4,089-0.3 5,934-0.1 NF1.522 PTPN1.1349 MAPXX1.217.5 BRAF.2270 SOS1-4070 NA GORP COELL, CELL, UNINGTION, DISASSMBILY GORP, NEGATIVE, REGULATION, OF, HERARDOCIET GOMP, MICC, CLASS, ILL, RECEPTOR, ACTIVITY J3849859 4 1,075-0.2 1,7139-0.1 HP. LADOX.23 HIADOS.1306 HIADOS1.2381 TOFE13-3478 NA NA GOCC, PAR, POLARITY, COMPIEX J387415 GOCC, PAR, POLARIT	GOCC_B_CELL_RECEPTOR_CO HP_APLASIA_CUTIS_CONGENITA_ON_ GOMF_ANDROGEN_BINDII HP_BRONCHIAL_WALL_THICK	DMPLEX -0.41076 _TRUNK_OR_L 0.38528 NG 0.37687 ENING -0.37548	45 3 1.373e- 53 6 1.081e- 53 4 9.037e- 13 6 1.446e-	-02 7.190e-0 -03 4.775e-0 -03 7.035e-0 -03 5.053e-0	SYK:1076 CD79B:19 1 ITGB4:134 PLEC:147 KRT14:905 1 ALDH1A1:1092 TSPO:1523 1 ABCA3:608 HYDIN:1101 FNIP1:18	561 CD79A:1707 NA NA NA ITGA6:1212 ARHGAP31:1607 KRT5:7146 SHBG:2329 SLC39A9:3012 NA NA 866 SFTPC:2457 PAK2:2935 TTC26:3169
GOCC_B.WICH_COMPLEX GOBP_RESPONSE_TO_PHEROMONE	GOMF_MELANOCORTIN_RECEPTO HP_PECTUS_EXCAVATUM_OF_INFERI GOBP_CELL_CELL_JUNCTION_DIS GOBP_NEGATIVE_REGULATION_OF_H	R_BINDING -0.37237 OR_STERNUM 0.37094 SASSEMBLY 0.36906 HEMATOPOIETI 0.36822	79 4 9.895e- 87 5 4.069e- 99 5 4.260e- 89 4 1.075e-	7.097e-0 -03 5.954e-0 -03 5.954e-0 -02 7.137e-0	AGRP:1497 ASIP:1601 I NF1:522 PTPN11:1349 MAP2 FER:751 SNAI2:1530 TGFB3: ZFP36:1541 NFE2L2:1576	MRAP:2208 MRAP2:2994 NA NA K1:2117.5 BRAF:2370 SOS1:4070 NA :2504 ABCC8:2629 TGFBR1:3169 NA N4BP2L2:1928 TCF15:3478 NA NA
GOBP_PEPTIDYL_ARGININE_N_METHYLATION	GOCC_B_WICH_COMPLE GOBP_RESPONSE_TO_PHERO HP_GENERALIZED_AMYLOID_DE HP_RECURRENT_NEISSERIAL_IN	0.35714 0MONE -0.3543 POSITION 0.35343 FECTIONS -0.3495	60 6 2.447e- 41 2 8.258e- 51 3 3.398e- 84 5 6.784e-	-03 5.954e-0 -02 8.580e-0 -02 8.370e-0 -03 6.687e-0	1 DEK:247 ERCC6:1037 MYBBP1A:217 1 TMEM145:778 GF 1 APOA1:1827 GSN: 1 C8B:98 C6:433 C5:2	PR180:3945 NA NA NA NA 2086 B2M:3195 NA NA NA 2007 CFB:4609 CFI:4850 NA
GOCC_CCAAT_BINDING_FACTOR_COMPLEX	GOBP_PEPTIDYL_ARGININE_N_ME HP_ELEVATED_CIRCULATING_LONG_ GOBP_TRICUSPID_VALVE_MORPH GOMF_INTERLEUKIN_2_RECEPTO	THYLATION 0.34495 CHAIN_FATTY -0.34244 OGENESIS -0.34164 R_BINDING -0.33967	78 5 7.551e- 84 5 8.000e- 23 4 1.795e- 34 5 8.524e-	-03 6.744e-0 -03 6.830e-0 -02 7.377e-0 -03 7.022e-0	PRMT5:1500 PRMT3:1662 PRMT ABCD1:699 PEX19:700 PE HEY2:429 BMPR2:2367 TG GATA3:576 IL2:1880 TIMM	T8:2791 NDUFAF7:3213 PRMT6:3356 NA X1:1212 PEX5:4881 CPT2:5280 NA GFBR2:3006 BMPR1A:4473 NA NA 50:3264 IL21:3460 ECM1:3839 NA
GOCC_MCRD_MEDIATED_MRNA_STABILITY_COMPLE 0.3334727 5 9.807e-03 7.097e-01 PAIP1:285 SYNCRIP:1467 CSDE1:1538 HNRNPD:3429 PABPC1:6740 NA GOBP_PHENYLPROPANOID_METABOLIC_PROCESS 0.3331674 2 1.027e-01 8.609e-01 PON3:1308 CYP1A1:4086 NA NA NA NA GOBP_REGULATION_OF_FAS_SIGNALING_PATHWAY -0.3329904 3 4.575e-02 8.580e-01 ZDHHC7:789 TMBIM1:1080 SMAD5:6249 NA NA NA GOBP_HYPOTHALAMUS_CELL_MIGRATION -0.3326495 5 9.990e-03 7.097e-01 FOXB1:130 SEMA3E:1381 NDNF:1925 NRP2:2141 NRP1:8022 NA GOBP_POSITIVE_REGULATION_OF_HYDROGEN_PER -0.3326225 4 2.122e-02 7.566e-01 ENDOG:1284 HDAC6:1821 ABL1:2142.5 PAWR:5617 NA NA GOBP_SPHINGOLIPID_TRANSLOCATION 0.3312035 4 2.178e-02 7.584e-01 ABCB1:3 ABCB4:24 ABCC1:3415 ABCA2:7474 NA NA GOBP_BRANCHED_CHAIN_AMINO_ACID_BIOSYNTHE 0.3308770 5 1.039e-02 7.137e-01 SDS:17 BCAT2:1648 BCAT1:2244.5 SDSL:3421 ILVBL:6330 NA GOCC_DNA_REPLICATION_FACTOR_A_COMPLEX -0.3271269 3 4.970e-02 8.580e-01 RPA2:380 RPA1:2077 RPA3:5950 NA NA NA GOBP_CHONDROBLAST_DIFFERENTIATION 0.3271128	GOCC_CCAAT_BINDING_FACTOR_ GOBP_SKELETAL_MUSCLE_SATELLIT HP_APLASIA_CUTIS_CONGENITA_OVE GOMF_PEROXISOME_TARGETING_SEC	COMPLEX -0.33777 E_CELL_ACTI -0.33774 ER_THE_SCAL 0.33746 QUENCE_BINDI -0.33737	05 6 4.165e- 07 8 9.390e- 07 6 4.199e- 64 5 8.981e-	-03 5.954e-0 -04 4.665e-0 -03 5.954e-0 -03 7.035e-0	1 NFYB:245 NFYC:1588 ATF2:19 1 EPHB1:69 GJD4:1079 MEGF10:238 1 ITGB4:134 PLEC:147 MCTP2:10 1 PEX19:700 PEX5L:904 BABA	10 ING2:2021 NFYA:3378 CEBPZ:6673 81 CAPN3:2507 WNT7A:2913 SOX15:3455 043 BMS1:3150 DLL4:4367 UBA2:6909 AM2:3022 PEX7:3691 PEX5:4881 NA
GOBP_BRANCHED_CHAIN_AMINO_ACID_BIOSYNTHE	GOCC_MCRD_MEDIATED_MRNA_STAB GOBP_PHENYLPROPANOID_METABOI GOBP_REGULATION_OF_FAS_SIGNAL GOBP_HYPOTHALAMUS_CELL_M	ILITY_COMPLE 0.33347 LIC_PROCESS 0.33316 LING_PATHWAY -0.33299 IGRATION -0.33264	27 5 9.807e- 74 2 1.027e- 04 3 4.575e- 95 5 9.990e-	7.097e-0 -01 8.609e-0 -02 8.580e-0 -03 7.097e-0	PAIP1:285 SYNCRIP:1467 CSDE PON3:1308 CYF ZDHHC7:789 TMBIM1 FOXB1:130 SEMA3E:1381 NI	21:1538 HNRNPD:3429 PABPC1:6740 NA P1A1:4086 NA NA NA NA :1080 SMAD5:6249 NA NA NA DNF:1925 NRP2:2141 NRP1:8022 NA
MP0002837 dystrophic cardiac calcinosis -0.2435404 9 1.145e-02 1.090e-01 DES:88 SLC2A4:104 MYH6:664 MYBPC3:1024 MMP9:1060 SCG5:3692	GOBP_BRANCHED_CHAIN_AMINO_ACGOCC_DNA_REPLICATION_FACTOR_ GOBP_CHONDROBLAST_DIFFERENCE Geneset	ID_BIOSYNTHE 0.33087 _A_COMPLEX -0.32712 ENTIATION 0.32712 Mammalian_	70 5 1.039e- 69 3 4.970e- Phen otype L	7.137e-0 -02 8.580e-0 -02 7.137e-0	SDS:17 BCAT2:1648 BCAT1 RPA2:380 RPA1:20 RARA:126 GDF5:1242 CCN OP pathways by perm	1:2244.5 SDSL:3421 ILVBL:6330 NA 077 RPA3:5950 NA NA NA N1:1726.FGF2:5431 FGF4:5494 NA
MP0003646 muscle fatigue	MP0004510 myositis MP0003646 muscle fatigue MP0009379 abnormal foot pigment MP0006054 spinal hemorrhage	-0.2109870 -0.2018970 tation 0.1955535 e 0.1874573	10 2.095e-02 1.5 9 3.606e-02 2.1 5 1.300e-01 4.5 9 5.162e-02 2.7	514e-01 123e-01 552e-01 730e-01 COL	SH3BP2:157 SYT7:394 CEBPB:1326 R SLC2A4:104 PPARGC1A:904 NOS1:1203 GNAQ:819 RPS19:2791 GNA11:373 1A1:1906 C1GALT1:2381 C1GALT1C1:26	YR2:1609 SGCB:1760 SOCS1:2131 3 MTOR:1952 MB:2833 COX10:3324 55 RPS20:4587 EGFR:13579 NA 670 FBLN1:3019 TFPI:4251 PSEN1:5483
MP0003121 genomic imprinting 0.1783485 23 3.113e-03 4.539e-02 SMCHD1:119 DNMT1:200 HELLS:341 ATRX:823 GNAS:886 ARID4B:1089 MP0002653 abnormal ependyma morphology 0.1757310 11 4.372e-02 2.392e-01 SOX2:789 MSI1:1363 NR1H2:1803 DLL3:2185 E2F5:3298 BBS1:4694 MP0000678 abnormal parathyroid gland 0.1752148 21 5.507e-03 6.899e-02 TBX1:517 HOXA3:585 GCM2:621 PTHLH:896 CHRD:1133 FOXG1:1711 MP0004233 abnormal muscle weight -0.1736810 16 1.627e-02 1.291e-01 PPARGC1A:904 NOS1:1203 GRB10:1863 MTOR:1952 CHRNE:2394 ARNTL:2668 MP0003183 abnormal peptide metabolism -0.1637430 10 7.315e-02 3.285e-01 NCF1:687 VAV2:937 VAV3:2303 ACE2:2935 NCSTN:3890 TRIP11:4584 MP0002277 abnormal respiratory mucosa 0.1611474 20 1.272e-02 1.142e-01 HESX1:225 SOX2:789 CXCR2:881 RELB:989 C3AR1:1331 HOXA5:1413	MP0002653 abnormal ependyma mor MP0000678 abnormal parathyroid of MP0004233 abnormal muscle we MP0003183 abnormal peptide metal	phology 0.1757310 gland 0.1752148 ight -0.1736810 bolism -0.1637430	11 4.372e-02 2.3 21 5.507e-03 6.8 16 1.627e-02 1.2 10 7.315e-02 3.2	392e-01 399e-02 291e-01 PF 285e-01	SOX2:789 MSI1:1363 NR1H2:1803 D TBX1:517 HOXA3:585 GCM2:621 PTH PARGC1A:904 NOS1:1203 GRB10:1863 NCF1:687 VAV2:937 VAV3:2303 ACE	DLL3:2185 E2F5:3298 BBS1:4694 HLH:896 CHRD:1133 FOXG1:1711 MTOR:1952 CHRNE:2394 ARNTL:2668 2:2935 NCSTN:3890 TRIP11:4584
MP0002254 reproductive system inflammat 0.1537302 5 2.340e-01 5.772e-01 RELB:989 PGR:3795 MFGE8:5659 AIRE:6695 EPHA1:12018 NA MP0005275 abnormal skin tensile -0.1519069 17 3.031e-02 2.004e-01 LAMC2:492 OGN:1089 COL5A2:1938 DSG4:2109 DSE:2754 COL14A1:3060 MP0010386 abnormal urinary bladder -0.1457590 14 5.921e-02 2.914e-01 TAC1:151 CHRNB2:718 HTR3A:1222 MYLK:2380 ANXA4:3282 KCNMA1:3553 MP0003136 yellow coat color 0.1425514 7 1.917e-01 5.319e-01 ADAMTS20:494 SOX2:789 OCA2:3435 EDA:6304 EDNRB:6342 MITF:10332 MP0009278 abnormal bone marrow -0.1397977 17 4.622e-02 2.500e-01 LIG1:323 MMP9:1060 TSC22D1:1646 RAG2:1934 HIP1:2087 SOCS3:2644 MP0002396 abnormal hematopoietic system 0.1357974 21 3.145e-02 2.041e-01 CASP8:117 MEOX2:1122 LDB1:1163 MAN2A1:1214 MYC:2342 CDK6:2354	MP0005275 abnormal skin tensi MP0010386 abnormal urinary blac MP0003136 yellow coat color MP0009278 abnormal bone marr	-0.1519069 dder -0.1457590 0.1425514 row -0.1397977	17 3.031e-02 2.0 14 5.921e-02 2.9 7 1.917e-01 5.3 17 4.622e-02 2.5	004e-01 914e-01 319e-01 500e-01	LAMC2:492 OGN:1089 COL5A2:1938 D FAC1:151 CHRNB2:718 HTR3A:1222 MY ADAMTS20:494 SOX2:789 OCA2:3435 L LIG1:323 MMP9:1060 TSC22D1:1646 F	SG4:2109 DSE:2754 COL14A1:3060 'LK:2380 ANXA4:3282 KCNMA1:3553 EDA:6304 EDNRB:6342 MITF:10332 RAG2:1934 HIP1:2087 SOCS3:2644
MP0000569 abnormal digit pigmentation	MP0000569 abnormal digit pigment MP0000383 abnormal hair follic MP0008007 abnormal cellular replic MP0003950 abnormal plasma mem MP0006292 abnormal olfactory pla	tation -0.1355291 le -0.1321389 cative 0.1311550 brane -0.1298324 code 0.1286637	6 2.505e-01 5.7 22 3.216e-02 2.0 29 1.469e-02 1.2 10 1.554e-01 4.7 12 1.230e-01 4.4	796e-01 041e-01 227e-01 S 760e-01 432e-01	LYST:3249 MYO5A:3671 EN1:3772 DOG PKP3:582 KRT14:721 ADAM17:771 DIC BIRT6:115 CUL7:926 MAPKAPK5:1376 C CAV1:542 NPC1:1230 CDK5RAP2:1759 HESX1:225 OTX2:951 HHEX:1048 CHI	CK7:3806 HPS5:6218 AP3B1:13469 ER1:1249 FGFR2:1822 TRPV3:1872 DKN2A:1956 FLT3:2799 RAD9B:2882 DMD:2293 GLRX:2480 TJP2:4457 RD:1133 FOXG1:1711 TCOF1:2625
MP0002877 abnormal melanocyte morpholog 0.1272998 10 1.636e-01 4.837e-01 CDKN2A:1956 KIT:3050 KRAS:4052 PTPN11:6081 RAB27A:6218 MREG:6665 MP0004859 abnormal synaptic plasticity -0.1262672 31 1.518e-02 1.246e-01 ADD2:73 CAMK2B:132 TNC:250 ADCY1:450 FOXP2:648 GRIN2B:1050 MP0002876 abnormal thyroid physiology 0.1257304 18 6.510e-02 3.068e-01 MED1:333 CGA:456 GHR:980 HPN:1344 GFRA4:3169 GNA11:3735 MP0003122 maternal imprinting 0.1220382 14 1.142e-01 4.346e-01 GNAS:886 ARID4A:1422 NDN:2096 IGF2:2372 MEST:2982 SNRPN:4608 MP0009780 abnormal chondrocyte physiolo -0.1209272 9 2.093e-01 5.504e-01 CAV1:542 WNT9A:2360 THRA:3025 TRIP11:4584 ESR1:5740 THRB:6513 MP0005167 abnormal blood-brain barrier -0.1168554 16 1.060e-01 4.134e-01 PTAFR:33 MMP9:1060 NOS1:1203 HRH3:1485 CLCN2:3412 CTNNB1:3471	MP0002877 abnormal melanocyte mo MP0004859 abnormal synaptic plas MP0002876 abnormal thyroid physi MP0003122 maternal imprinting MP0009780 abnormal chondrocyte p	orpholog 0.1272998 sticity -0.1262672 ology 0.1257304 g 0.1220382 hysiolo -0.1209272	10 1.636e-01 4.8 31 1.518e-02 1.2 18 6.510e-02 3.0 14 1.142e-01 4.3 9 2.093e-01 5.5	337e-01 (246e-01 (246	CDKN2A:1956 KIT:3050 KRAS:4052 PTF ADD2:73 CAMK2B:132 TNC:250 ADC MED1:333 CGA:456 GHR:980 HPN: GNAS:886 ARID4A:1422 NDN:2096 IG CAV1:542 WNT9A:2360 THRA:3025 TF	PN11:6081 RAB27A:6218 MREG:6665 CY1:450 FOXP2:648 GRIN2B:1050 :1344 GFRA4:3169 GNA11:3735 GF2:2372 MEST:2982 SNRPN:4608 RIP11:4584 ESR1:5740 THRB:6513
MP0002735 abnormal chemical nociception	MP0002735 abnormal chemical nocio MP0000681 abnormal thyroid gla MP0003221 abnormal cardiomyocyte MP0000013 abnormal adipose tis MP0003693 abnormal embryo hato	ception -0.1146968 and 0.1133487 apopto 0.1107107 sue 0.1103759 ching 0.1050691	28 3.602e-02 2.1 43 1.034e-02 1.0 37 2.010e-02 1.5 15 1.392e-01 4.7 24 7.525e-02 3.3	123e-01 090e-01 514e-01 700e-01 C	ADCY8:341 PROKR1:407 ADCY1:450 I CGA:456 TBX1:517 HOXA3:585 MAN CASP8:117 AIFM1:216 TFAM:220 MAI OL1A1:1906 PRKAR1A:2030 SMTN:2743 RBBP8:364 HSPA5:786 ATF1:1069 PA	BAMBI:577 PTGIR:983 GRIK1:1090 NBA:797 HHEX:1048 CHRD:1133 PKAPK2:242 MDM2:392 RAF1:861 3 FSTL3:2853 PYY:4078 PPARG:4605 RG:1268 KIF11:1497 AURKA:2108

CHD8:212 CUL3:218 BRD4:571 TPT1:777 HSPA5:786 ATRX:823

MP0004957 abnormal blastocyst morpholog

0.1026718

1.221e-03 2.325e-02