Geneset bladder vagina	stat tiss -0.160117878 0.112320956	24 6.6776	cific Top, page page 1.202e-01 1.222e-02	UPK2:1		Qn e.vals .1:306 MSX2:309 SEMA3E: :57 ENDOU:339 SULT1E1:4	
hippocampus.proper caudate.nucleus left.ventricle fallopian.tube	-0.066351284 0.061706366 0.061445305 -0.059554967	11 4.4636 26 2.7666 69 7.8516	e-01 8.654e-01 e-01 8.654e-01 e-02 6.056e-01 e-01 6.789e-01	NEUROG GF CK	:3:248 NTS:1086 NEUROI RM3:80 GPR88:95 ANO3:(MT2:54 S100A1:123 MYH	D6:4732 GRP:5569 SLC17A 334 RGS14:1114 TAC1:1336 7B:181 MYL3:321 SMPX:52 15 ADAMTS3:645 EGR1:15	7:6436 OLIG2:6778 3 AQP4:1961 20 ASB10:542
endocervix leg.skin breast suprapubic.skin	0.056094196 0.055028346 0.051782294 0.050664190	5.69364.87761941.5916	e-01 6.657e-01 e-03 1.202e-01 e-01 8.654e-01 e-02 1.718e-01	ANI LMX1B: SLC	(RD35:12 POF1B:66 RNF 125 THRSP:2823.5 GSC:3 10A6:18.5 RNF222:82 WI	IL2:209 MSX1:350 TGM2:56 222:82 EVPL:126 GGT6:13 3105 NPY2R:3277 ABCB5:4 NT4:90 EVPL:126 GGT6:13	9 FAM83F:188 003 TFAP2B:6113 9 FAM83F:188
coronary.artery skeletal.muscle pancreas ectocervix nucleus.accumbens	-0.049413688 0.046787336 0.044847150 -0.043309474 0.037904216	239 1.3776 94 1.3466 25 4.5406	e-01 8.654e-01 e-02 1.718e-01 e-01 6.789e-01 e-01 8.654e-01 e-01 8.654e-01	PYC CASR:8.5 ADRA1D	GM:42 CKMT2:54 SLC2A4 PRODH2:111 CATSPERE :1000 TSKU:1808 ADRA2	06 MYO18B:2351 COL4A1:2 :160 TNNI2:186 MSS51:194 3:132.5 GCG:299 PNLIPRP A:2027 KCNK6:2692 MATN: N5:184 ANO3:334 PENK:36	1.5 USP13:197 1:337 ONECUT1:392 2:3244 FGF10:3561
esophagus.mucosa putamen Brodmann.area.24 subcutaneous.adipos	0.037017906 0.036991357 0.034009398 e -0.033559582	15 6.2016 31 5.1286 72 3.2646	e-02 5.504e-01 e-01 9.050e-01 e-01 8.654e-01 e-01 8.654e-01	GRM3 SLC39A12 PLIN1	3:80 GPR88:95 ANO3:334 2:309 SLC25A18:478 DDN :728 FZD4:792 PNPLA2:1	:92.5 DENND2C:113 EVPL KCNH4:2081.5 RGS9:2717 I:1413 SLC6A1:2491 SHAN 203 G0S2:1241 ANGPTL4:	LRRC10B:3136 K1:2878 UPP2:3217 I301 BMP6:1369
esophagogastric.junctic aorta eye.development sigmoid.colon	-0.029175763 -0.029146938 -0.028927434	154 2.1486 67 4.1086 52 4.7166	e-01 9.240e-01 e-01 8.654e-01 e-01 8.654e-01 e-01 8.654e-01	LTBF CITI SI	P1:125 MYO1D:185 TBXA2 ED2:389 PROX1:621 FZD4 LC5A7:11 BTC:453 VIP:46	1:5763 GADL1:7900 ADCY: 2R:234 ART4:305 PMEPA1: 4:792 CDH11:879 KLF4:101 9 HLX:1387 HAND1:1822 I	368 IRAG1:428 5 MEIS2:1168 HMCN2:1911
greater.omentum spleen hypothalamus substantia.nigra cerebral.cortex	-0.027563112 -0.027230574 0.027214551 -0.026723172 0.026592321	298 1.1096 66 4.4596 12 7.4876	e-01 8.822e-01 e-01 6.657e-01 e-01 8.654e-01 e-01 9.240e-01 e-01 8.654e-01	N SYT FOXI	OX5:36 CD180:74 BLK:90 L5:312 DLX2:450 SCN9A B1:130 CHRM5:861 RPE6	4:1044 HBEGF:1150 SPRY BANK1:96 TNFRSF4:204 :484 ENKUR:556 OXT:910 5:3248 SPX:3861 SLC6A3: 1:138 KCNF1:194.5 EIF4E1	TAS1R3:235 GABRG3:1163 1464 RET:6738
C1.spinal.cord esophagus.muscularis.mu ovary adrenal.gland	-0.025345457	182 2.4236 26 6.5896 103 4.0886	e-01 8.654e-01 e-01 9.145e-01 e-01 8.654e-01 e-01 8.654e-01	GFAP: PRUNE2 WIPF3	64 FOXB1:130 HHIP:224 ::130 KCNMB1:1064 SYNI :20 BTNL2:53 KCNT2:403	SLC5A11:458 FAM222A:460 M:1698 NTN1:3444 FAM83E G C21orf62:422 CCDC170:40 G CYSLTR2:305 KCNN2:61	0 COLGALT2:599 0:3537 F2RL2:4348 86 TMEM221:727
blood pituitary.gland transverse.colon amygdala	-0.020364754 -0.019676417 0.019482835 0.018819337	276 2.5056 213 3.2726 149 4.1506	e-01 8.654e-01 e-01 8.654e-01 e-01 8.654e-01	NAA B3GN	CTSW:6 ARHGDIB:23 A(LAD2:18 RXRG:38 OTOG: LT6:30 EPS8L3:65 ETHE1	QP10:29 NFE2:32 RGS19:3 :211 ZSWIM2:308 CRYBA2 :155 GCG:299 TMEM54:41 :3438 NEUROD2:6882 SLC	3 BLK:90 455 VWA7:461 9 LGALS9C:487
transformed.skin.fibrobl tibial.nerve prostate testis	-0.013085956 -0.012034885 0.009100238	192 5.3556 38 7.9776 1381 2.9276	e-01 8.654e-01 e-01 8.763e-01 e-01 9.240e-01 e-01 8.654e-01	GFRA: NTF4 ,DN	3:55.5 SCARA5:172 SLC2 5:855 GLIS1:1119 TULP1: IAH2:8.5 CFAP45:13 SLAN	:287 SEPTIN11:382 CITED 7A6:261 GLDN:336 IL1RAF 1917 SRD5A2:2029 P2RX2: MF9:26 GSG1:37 C11orf53:	L1:443 LGI2:510 2490 SP8:2704
Geneset GOCC_9PLUS0_MOTIL GOCC_B_CELL_RECEPTO HP_APLASIA_CUTIS_CONGENIT	DR_COMPLEX -0 A_ON_TRUNK_OR_L 0	.4546269 .4107645 .3852853	4 1.637e-03 3 1.373e-03 6 1.081e-03	3 5.422e-01 2 7.190e-01 3 4.775e-01	SYK:1 ITGB4:134 PLEC:14	ENKUR:556 DNAH11:1124 1076 CD79B:1561 CD79A:1 17 KRT14:905 ITGA6:1212	707 NA NA NA ARHGAP31:1607 KRT5:7146
GOMF_ANDROGEN_ HP_BRONCHIAL_WALL_ HP_TALL_CHI GOCC_CUL4B_RING_E3_UBIQU GOMF_MELANOCORTIN_REC	THICKENING -C N 0 ITIN_LIGASE_COMP 0	.3754813 .3750714 .3738549	6 1.446e-03 5 3.676e-03 4 9.606e-03	3 7.035e-01 3 5.053e-01 3 5.954e-01 3 7.097e-01 3 7.097e-01	ABCA3:608 HYDIN: MYH8:382 N: CUL4B:5	02 TSPO:1523 SHBG:2329 1101 FNIP1:1866 SFTPC:2 SD1:975 TLK2:2008 APC2:2 83 DDB2:1421 DTL:2811 F 7 ASIP:1601 MRAP:2208 N	457 PAK2:2935 TTC26:3169 2163 OPHN1:4559 NA RBX1:3331 NA NA
HP_PECTUS_EXCAVATUM_OF_II GOBP_CELL_CELL_JUNCTIO GOBP_NEGATIVE_REGULATION GOMF_MHC_CLASS_II_RECE	NFERIOR_STERNUM 0 N_DISASSEMBLY 0 _OF_HEMATOPOIETI 0	3709487 3690699 3682289 3644865	5 4.069e-03 5 4.260e-03 4 1.075e-03	3 5.954e-01 3 5.954e-01 2 7.137e-01 2 7.137e-01	NF1:522 PTPN1 FER:751 SNAI2 ZFP36:1541	11:1349 MAP2K1:2117.5 BF 2:1530 TGFB3:2504 ABCC8 NFE2L2:1576 N4BP2L2:192 A-DOB:1690 HLA-DPA1:28	AF:2370 SOS1:4070 NA :2629 TGFBR1:3169 NA 8 TCF15:3478 NA NA
GOCC_PAR_POLARITY GOCC_B_WICH_CO GOBP_RESPONSE_TO_F HP_GENERALIZED_AMYLO	PHEROMONE -0	.3597092 .3571460 .3543741 .3534351	6 2.447e-03 2 8.258e-03	3 6.152e-01 3 5.954e-01 2 8.580e-01 2 8.370e-01	DEK:247 ERCC6:1037	6G:951 PARD6B:1738 PARI MYBBP1A:2177 DDX21:224 EM145:778 GPR180:3945 N A1:1827 GSN:2086 B2M:31	11 SF3B1:2955 SMARCA5:5185 A NA NA NA
HP_RECURRENT_NEISSERI GOBP_POSITIVE_REGULATION_ HP_ABNORMAL_MIDDLE_E GOBP_PEPTIDYL_ARGININE_	OF_EXTRACELLULA -C AR_REFLEXES 0 N_METHYLATION 0	3452500 3449578	4 1.644e-02 5 7.501e-02 5 7.551e-02	3 6.687e-01 2 7.377e-01 3 6.744e-01 3 6.744e-01	CPB2:1170 OTOF:853 PRO PRMT5:1500 PRM	8 C6:433 C5:2207 CFB:460 6.5 RGCC:2007 BMP2:2792 RP:859 AIFM1:1196 MPDU T3:1662 PRMT8:2791 NDU	2 AGT:4003 NA NA 1:1595 DIAPH3:8032 NA FAF7:3213 PRMT6:3356 NA
HP_ELEVATED_CIRCULATING_L GOBP_TRICUSPID_VALVE_M GOMF_INTERLEUKIN_2_REC GOBP_GRANULOCYTE_COLONY	ORPHOGENESIS -0 EPTOR_BINDING -0 _STIMULATING_FACT 0	.3424484 .3416423 .3396734 .3395927	4 1.795e-02 5 8.524e-02 4 1.865e-02	3 6.830e-01 2 7.377e-01 3 7.022e-01 2 7.377e-01	HEY2:429 B GATA3:576 I CD34:683	PEX19:700 PEX1:1212 PEX MPR2:2367 TGFBR2:3006 L2:1880 TIMM50:3264 IL21 TSLP:709 ISL1:4083 HAV	BMPR1A:4473 NA NA :3460 ECM1:3839 NA CR2:4879.5 NA NA
GOBP_POSITIVE_REGULATION_ GOCC_CCAAT_BINDING_FAGE GOBP_SKELETAL_MUSCLE_SATE HP_APLASIA_CUTIS_CONGENIT GOMF_PEROXISOME_TARGETIN	CTOR_COMPLEX -0 FELLITE_CELL_ACTI -0 FA_OVER_THE_SCAL 0	.3388384 .3377705 .3377407 .3374607 .3373764	6 4.165e-03 8 9.390e-04 6 4.199e-03	3 5.954e-01 3 5.954e-01 4 4.665e-01 3 5.954e-01 3 7.035e-01	NFYB:245 NFYC: EPHB1:69 GJD4:107 ITGB4:134 PLEC:	1588 ATF2:1910 ING2:2021	07 WNT7A:2913 SOX15:3455 50 DLL4:4367 UBA2:6909
HP_CONGENITAL_ADRENAL GOBP_ESTABLISHMENT_OF_LEF GOCC_MCRD_MEDIATED_MRNA GOBP_PHENYLPROPANOID_ME	HYPERPLASIA 0 FT_RIGHT_ASYMMET 0 _STABILITY_COMPLE 0		4 1.991e-02 4 2.049e-02 5 9.807e-03	2 7.450e-01 2 7.552e-01 3 7.097e-01 1 8.609e-01	POR:1825 (CFAP45:13 PAIP1:285 SYNCR	CYP17A1:2556 STAR:2615 CFAP52:173 ENKUR:556 C IP:1467 CSDE1:1538 HNRN DN3:1308 CYP1A1:4086 NA	HSD3B2:3596 NA NA CCDC39:9977 NA NA NPD:3429 PABPC1:6740 NA
GOBP_REGULATION_OF_FAS_S GOBP_HYPOTHALAMUS_CF GOBP_POSITIVE_REGULATION_CFAS_S	ELL_MIGRATION -0 OF_HYDROGEN_PER -0	.3329904 .3326495 .3326225 .3312035	5 9.990e-03 4 2.122e-03	2 8.580e-01 3 7.097e-01 2 7.566e-01 2 7.584e-01	FOXB1:130 SEI ENDOG:128	7:789 TMBIM1:1080 SMAD5 MA3E:1381 NDNF:1925 NR 4 HDAC6:1821 ABL1:2142. ABCB4:24 ABCC1:3415 A	P2:2141 NRP1:8022 NA 5 PAWR:5617 NA NA
GOBP_BRANCHED_CHAIN_AMIN GOCC_DNA_REPLICATION_FAG GOBP_CHONDROBLAST_DI	CTOR_A_COMPLEX -0	3308770 .3271269 .3271128 Nathus	3 4.970e-02 5 1130e-02	7.137e-01 8.580e-01 7.137e-01 70p.ap	I RPA	T2:1648 BCAT1:2244.5 SDS .2:380 RPA1:2077 RPA3:599 DF5:1242 CCN1:1726 FGF2 rmulatiophe.vals	50 NA NA NA
REACTOME_CHYLOMICRON REACTOME_EICOSA REACTOME_BETA_OXIDATION_OI REACTOME_BETA_OXIDATION_OI	NOIDS -0 F_DECANOYL_COA0 F_OCTANOYL_COA0	.4270646 .3748340 .3640254 .3637663	4 9.417e-03 6 2.014e-03 5 4.845e-03	4 7.207e-01 3 9.378e-01 3 7.730e-01 3 7.730e-01	TBXAS1:105- HADH:66 ACADM:3 HADH:66 ACA	DM:388 ECHS1:2401 HADI	353 PTGIS:2929 NA NA 01 HADHA:2626 HADHB:5554 HA:2626 HADHB:5554 NA
REACTOME_ALPHA_DE IBRAHIM_NRF3_ BAFNA_MUC4_TARGI WP_PILOCYTIC_ASTRO MCCOLLUM_GELDANAMYCIN_	UP -0 ETS_UP -0 DCYTOMA 0	.3598466 .3402808 .3296240 .3220873 .3179774	5 8.406e-03 3 4.799e-03 6 6.288e-03	2 9.398e-01 3 9.378e-01 2 9.398e-01 3 8.868e-01 4 7.207e-01	RPN2:1382 CM NEK NF1:522 PTPN11	1:1786 CD4:2248 PRSS3:2 MAS:1464 PSMD4:1875 HM 6:275 AVPR2:2798 SNAI1:5 I:1349 BRAF:2370 GRB2:40	OX1:3572 GCLM:4655 NA 3209 NA NA NA
REACTOME_BETA_OXIDATION_O WP_EFFECT_OF_INTESTINAL_MI REACTOME_ATORVASTA BIOCARTA_NPP1_PA	F_LAUROYL_COA_T -0 CROBIOME_ON_AN 0 TIN_ADME 0	.3153029 3106366 2876818	5 1.461e-02 7 4.423e-02 5 2.588e-02	2 9.398e-01 3 7.730e-01 2 9.398e-01 3 7.730e-01	HADH:66 ECH: NR1I2:886 VDR:12 ABCB1:3 PON3	S1:2401 HADHA:2626 ACA 275 PPARA:2537 NPC1L1:3 :1308 SLCO1B1:2894 PON	DL:4315 HADHB:5554 NA 800 PPARD:4081 CD36:4307
SCHAEFFER_PROSTATE_DEVELOR REACTOME_PREDNISO MIZUKAMI_HYPOXI WP_ALTERNATIVE_PATHWAY_OF_	PMENT_AND_CANCE 0 NE_ADME 0 A_DN -0	2848615 2820033 .2779689 2770188	5 2.738e-02 5 2.896e-02 5 3.134e-02	2 9.398e-01 2 9.398e-01 2 9.398e-01 3 7.730e-01	ZNF22:1342 S ABCB1:3 ALB:6 PDGFB:529 L	OX9:1459 CDC27:2525 PD 64 HSD11B1:605 SERPINA RP1:745 CXCL8:3229 FGF	A4:2882 IGF1R:9251 NA 6:7506 HSD11B2:9492 NA
MIKKELSEN_IPS_LCP_WITH_H3F REACTOME_CA2_ACTIVATED DONATO_CELL_CYCLE_ REACTOME_LEUKOTRIENE	O_K_CHANNELS 0 TRETINOIN -0	.2757051 2732905 .2726870 2680283	9 4.522e-03 6 2.071e-02	2 9.398e-01 3 7.730e-01 2 9.398e-01 2 9.398e-01	KCNN3:174 KCNN2:612 SKAP2:1849 AE	2.5 KCNMB1:1064 KCNN1: BI1:2513 BTG2:3242 TOB1:	JT7:5732 SLC17A7:6436 NA J408 KCNN4:2896 KCNMB4:5762 J862 ATR:5148 MNT:5488 R17:7159 CYSLTR1:8200 NA
REACTOME_TERMINAL_PATHWAY REACTOME_REGULATION_OF_NP WILSON_PROTEASES_AT_TUMOR BYSTRYKH_HEMATOPOIESIS_S	AS4_GENE_TRANSC -0 R_BONE_INTERFACE -0 STEM_CELL_FGF3 -0	.2638915 .2629308 .2599469 .2568035	4 6.855e-02 5 4.410e-02 6 2.936e-02	2 9.398e-01 2 9.398e-01 2 9.398e-01 2 9.398e-01	NR3C1:13 SERPINI2:94 C EFNB1:30 SH3RF1:34		NPAS4:9404 NA NA E:4790 ADAMTS7:6163 NA I3 POU5F1:7550 MAP2K6:9715
GALI_TP53_TARGETS_AP0 IGARASHI_ATF4_TAR0 BIOCARTA_RAN_PAT IKEDA_MIR1_TARGE	ETS_UP	2560171 .2531141 .2476446 .2472354	4 7.954e-02 4 8.626e-02 7 2.349e-02	2 9.398e-01 2 9.398e-01 2 9.430e-01 2 9.398e-01	ITFG2:67 RCC1:17 F CLCN3:1378 SMIM36	76 PDP1:4113 SFXN4:4437 RANGAP1:1865 RAN:5397 5:1628 EIF4E:1999 STK39:2	RANBP1:9078 NA NA 2773 MTSS1:3162 HSPD1:6532
BERENJENO_TRANSFORMED_BY_ BIOCARTA_NEUTROPHIL SAMOLS_TARGETS_OF_KHS LIU_CDX2_TARGET REACTOME_COBALAMIN_CB	_PATHWAY -0 SV_MIRNAS_UP -0 S_DN 0	.2448934 .2443868 .2442821 2436449 .2434498	8 1.667e-02 6 3.823e-02 5 5.917e-02	2 9.398e-01 2 9.398e-01 2 9.398e-01 2 9.398e-01 2 9.398e-01	ITGB2:129 ICAM CDH11:879 GALNT KRT14:905 K	1:807	B:4594 DAP:5978 MGST3:8442 860 CD44:3352 SELL:5686 CH:4031 GAL:4887 AK3:9584 2:2674 HES1:13763 NA 16 MMAB:4723 MMACHC:5597
REACTOME_SYNTHESIS_OF_5_E MIKHAYLOVA_OXIDATIVE_STRES BIOCARTA_SLRP_PA REACTOME_BETA_OXIDATION_OI	ICOSATETRAENOIC 0 SS_RESPONSE_VIA 0 THWAY -0	2427929 2427749 .2420635 .2415328	9 1.166e-02 6 3.944e-02 6 4.002e-02	2 9.378e-01 2 9.398e-01 2 9.398e-01 2 9.398e-01	PON2:463 PON3:13 PGAM1:165 CALU EPYC:92.5 BG	308 GPX1:1447 GPX2:1556	ALOX5:2324 ALOX5AP:2391 746 AKR1B1:6329 OAT:9840 9 FMOD:6666 DCN:9760
WP_SCFA_AND_SKELETAL_MUSO REACTOME_ARYL_HYDROCARBON Geneset GOCC_9PLUSO_MOTIL	N_RECEPTOR SIGNA GSEA-		gmb ols 123e-02	2 9.398e-01 2 9.398e-01 0 path 3 5.422e-01	ways by perm	634 ARNT:3459 AIP:3798 A	081 FFAR3:6844 PYY:11669 RNT2:4740 HSP90AB1:11524 DNAH5:1259 NA NA
GOCC_B_CELL_RECEPT(HP_APLASIA_CUTIS_CONGENIT GOMF_ANDROGEN_ HP_BRONCHIAL_WALL_	A_ON_TRUNK_OR_L 0 BINDING 0	3852853	6 1.081e-03 4 9.037e-03	2 7.190e-01 3 4.775e-01 3 7.035e-01 3 5.053e-01	ITGB4:134 PLEC:14 ALDH1A1:109	92 TSPO:1523 SHBG:2329	ARHGAP31:1607 KRT5:7146
HP_TALL_CHI GOCC_CUL4B_RING_E3_UBIQU GOMF_MELANOCORTIN_REC HP_PECTUS_EXCAVATUM_OF_II	ITIN_LIGASE_COMP 0 CEPTOR_BINDING -C NFERIOR_STERNUM 0	3750714 3738549 .3723779 3709487	4 9.606e-03 4 9.895e-03 5 4.069e-03	3 5.954e-01 3 7.097e-01 3 7.097e-01 3 5.954e-01	CUL4B:5 AGRP:149 NF1:522 PTPN1	SD1:975 TLK2:2008 APC2:283 DDB2:1421 DTL:2811 F 7 ASIP:1601 MRAP:2208 N 11:1349 MAP2K1:2117.5 BF	RBX1:3331 NA NA IRAP2:2994 NA NA RAF:2370 SOS1:4070 NA
GOBP_CELL_CELL_JUNCTIO GOBP_NEGATIVE_REGULATION GOMF_MHC_CLASS_II_RECE GOCC_PAR_POLARITY GOCC_B_WICH_CO	OF_HEMATOPOIETI 0 EPTOR_ACTIVITY 0 _COMPLEX -0	3690699 3682289 3644865 .3597092 3571460	4 1.075e-02 4 1.158e-02 5 5.341e-03	3 5.954e-01 2 7.137e-01 2 7.137e-01 3 6.152e-01 3 5.954e-01	ZFP36:1541 I HLA-DOA:243 HLA PRKCI:564 PARD	2:1530 TGFB3:2504 ABCC8 NFE2L2:1576 N4BP2L2:192 A-DOB:1690 HLA-DPA1:28 6G:951 PARD6B:1738 PARI MYBBP1A:2177 DDX21:224	8 TCF15:3478 NA NA 52.5 HLA-DRA:3972 NA NA
GOBP_RESPONSE_TO_F HP_GENERALIZED_AMYLO HP_RECURRENT_NEISSERI GOBP_POSITIVE_REGULATION_	PHEROMONE -C ID_DEPOSITION 0 AL_INFECTIONS -C	.3534351 .3495784	3 3.398e-03 5 6.784e-03	2 8.580e-01 2 8.370e-01 3 6.687e-01 2 7.377e-01	APO. C8B:98	EM145:778 GPR180:3945 N A1:1827 GSN:2086 B2M:31 8 C6:433 C5:2207 CFB:460 6.5 RGCC:2007 BMP2:2792	95 NA NA NA 9 CFI:4850 NA
HP_ABNORMAL_MIDDLE_E GOBP_PEPTIDYL_ARGININE_ HP_ELEVATED_CIRCULATING_L GOBP_TRICUSPID_VALVE_M	N_METHYLATION 0 ONG_CHAIN_FATTY -0	3452500 3449578 .3424484 .3416423	5 7.551e-03 5 8.000e-03	3 6.744e-01 3 6.744e-01 3 6.830e-01 2 7.377e-01	PRMT5:1500 PRM ABCD1:699 F	RP:859 AIFM1:1196 MPDU T3:1662 PRMT8:2791 NDU PEX19:700 PEX1:1212 PEX MPR2:2367 TGFBR2:3006	FAF7:3213 PRMT6:3356 NA 5:4881 CPT2:5280 NA
GOMF_INTERLEUKIN_2_REC GOBP_GRANULOCYTE_COLONY GOBP_POSITIVE_REGULATION_ GOCC_CCAAT_BINDING_FAC	_STIMULATING_FACT 0 OF_RESPONSE_TOC CTOR_COMPLEX -C	.3396734 3395927 .3388384 .3377705	4 1.865e-02 6 4.047e-03 6 4.165e-03	3 7.022e-01 2 7.377e-01 3 5.954e-01 3 5.954e-01	CD34:683 RIPK1:578 ENDOG:1 NFYB:245 NFYC:	1588 ATF2:1910 ING2:2021	CR2:4879.5 NA NA I2.5 FOXP1:4244 PAWR:5617 NFYA:3378 CEBPZ:6673
GOBP_SKELETAL_MUSCLE_SATE HP_APLASIA_CUTIS_CONGENIT GOMF_PEROXISOME_TARGETIN HP_CONGENITAL_ADRENAL GOBB_ESTABLISHMENT_OF_LEG	A_OVER_THE_SCAL 0 G_SEQUENCE_BINDI -0		6 4.199e-03 5 8.981e-03 4 1.991e-03	4 4.665e-01 3 5.954e-01 3 7.035e-01 2 7.450e-01	I ITGB4:134 PLEC: PEX19:700 PE POR:1825 (147 MCTP2:1043 BMS1:31 X5L:904 BABAM2:3022 PE CYP17A1:2556 STAR:2615	X7:3691 PEX5:4881 NA HSD3B2:3596 NA NA
GOBP_ESTABLISHMENT_OF_LEF GOCC_MCRD_MEDIATED_MRNA GOBP_PHENYLPROPANOID_ME GOBP_REGULATION_OF_FAS_S GOBP_HYPOTHALAMUS_CF	_STABILITY_COMPLE 0 TABOLIC_PROCESS 0 IGNALING_PATHWAY -C	3345227 3334727 3331674 .3329904 .3326495	5 9.807e-03 2 1.027e-03 3 4.575e-03	2 7.552e-01 3 7.097e-01 1 8.609e-01 2 8.580e-01 3 7.097e-01	PAIP1:285 SYNCR POI ZDHHC	CFAP52:173 ENKUR:556 (IP:1467 CSDE1:1538 HNRN DN3:1308 CYP1A1:4086 NA 7:789 TMBIM1:1080 SMAD6 MA3E:1381 NDNF:1925 NR	NPD:3429 PABPC1:6740 NA NA NA NA 5:6249 NA NA NA
GOBP_POSITIVE_REGULATION_GOBP_SPHINGOLIPID_TR. GOBP_BRANCHED_CHAIN_AMIN GOCC_DNA_REPLICATION_FAC	OF_HYDROGEN_PER -C ANSLOCATION 0 O_ACID_BIOSYNTHE 0		4 2.122e-02 4 2.178e-02 5 1.039e-02	2 7.566e-01 2 7.584e-01 2 7.137e-01 2 8.580e-01	ENDOG:128 ABCB1:3 SDS:17 BCAT	4 HDAC6:1821 ABL1:2142.4 ABCB4:24 ABCC1:3415 Al 2:1648 BCAT1:2244.5 SDS 2:380 RPA1:2077 RPA3:598	5 PAWR:5617 NA NA BCA2:7474 NA NA L:3421 ILVBL:6330 NA
MP0003787 abnormal im MP0002837 dystrophic cardia	oprinting 0.267188 ac calcinosis -0.243540	1 10 4 9	3.457e-03 4.83 1.145e-02 1.09	9e-02 S 0e-01	OP patnways I SMCHD1:119 ATRX:823 G DES:88 SLC2A4:104 M	DF5:1242 CCN1:1726.FGF DY Permulation NAS:886 ARID4B:1089 ARI YH6:664 MYBPC3:1024 MM	D4A:1422 SNRPN:4608 IP9:1060 SCG5:3692
MP0004510 myosi MP0003646 muscle fa MP0009379 abnormal foot p MP0006054 spinal hemo	-0.201897 igmentation 0.195553 orrhage 0.187457	9 5 5 3 9	2.095e-02 1.51d 3.606e-02 2.12d 1.300e-01 4.55d 5.162e-02 2.73d	3e-01 3 2e-01 0e-01 COL	SLC2A4:104 PPARGC1A:9 GNAQ:819 RPS19:279 1A1:1906 C1GALT1:2381		MB:2833 COX10:3324 7 EGFR:13579 NA 019 TFPI:4251 PSEN1:5483
MP0005083 abnormal bill MP0003121 genomic im MP0002653 abnormal ependyn MP0000678 abnormal parath MP0004233 abnormal mus	printing 0.178348 na morphology 0.175731 nyroid gland 0.175214	5 23 0 11 8 21	6.696e-02 3.12 3.113e-03 4.53 4.372e-02 2.39 5.507e-03 6.89 1.627e-02 1.29	9e-02 2e-01 9e-02	SMCHD1:119 DNMT1:200 SOX2:789 MSI1:1363 I TBX1:517 HOXA3:585 O	CKAR:3259 XYLT2:3990 AN 0 HELLS:341 ATRX:823 GN NR1H2:1803 DLL3:2185 E2 GCM2:621 PTHLH:896 CHR GRB10:1863 MTOR:1952 (IAS:886 ARID4B:1089 F5:3298 BBS1:4694 D:1133 FOXG1:1711
MP0004233 abnormal mus MP0003183 abnormal peptide MP0002277 abnormal respira MP0002254 reproductive syste MP0005275 abnormal ski	e metabolism -0.163743 tory mucosa 0.161147 em inflammat 0.153730	10 4 20 2 5	1.627e-02 1.29 7.315e-02 3.28 1.272e-02 1.14 2.340e-01 5.77 3.031e-02 2.00	5e-01 2e-01 2e-01	NCF1:687 VAV2:937 VA HESX1:225 SOX2:789 C RELB:989 PGR:379	GRB10:1863 MTOR:1952 (AV3:2303 ACE2:2935 NCST CXCR2:881 RELB:989 C3AF 5 MFGE8:5659 AIRE:6695 DL5A2:1938 DSG4:2109 DS	N:3890 TRIP11:4584 R1:1331 HOXA5:1413 EPHA1:12018 NA
MP0010386 abnormal urina MP0003136 yellow coa MP0009278 abnormal bon MP0002396 abnormal hemato	-0.145759 t color 0.142551 e marrow -0.139797	0 14 4 7 7 17	5.921e-02 2.91 1.917e-01 5.31 4.622e-02 2.50 3.145e-02 2.04	4e-01 T 9e-01 0e-01	AC1:151 CHRNB2:718 HT ADAMTS20:494 SOX2:789 LIG1:323 MMP9:1060 TS	FR3A:1222 MYLK:2380 ANX O OCA2:3435 EDA:6304 ED FC22D1:1646 RAG2:1934 H LDB1:1163 MAN2A1:1214	(A4:3282 KCNMA1:3553 NRB:6342 MITF:10332 IP1:2087 SOCS3:2644
MP0000569 abnormal digit p MP0000383 abnormal ha MP0008007 abnormal cellula MP0003950 abnormal plasma	igmentation	9 22 0 29 4 10	2.505e-01 5.79 3.216e-02 2.04 1.469e-02 1.22 1.554e-01 4.76	6e-01 1e-01 7e-01 S 0e-01	PKP3:582 KRT14:721 AD/ IRT6:115 CUL7:926 MAP/ CAV1:542 NPC1:1230 CI	EN1:3772 DOCK7:3806 HP AM17:771 DICER1:1249 FG (APK5:1376 CDKN2A:1956 DK5RAP2:1759 DMD:2293 (FR2:1822 TRPV3:1872 FLT3:2799 RAD9B:2882 GLRX:2480 TJP2:4457
MP0006292 abnormal olfact MP0000749 muscle dege MP0002877 abnormal melanoc MP0004859 abnormal synap	yte morpholog 0.127583 tic plasticity -0.126267	36 8 10 2 31	1.230e-01 4.43 8.226e-03 9.32 1.636e-01 4.83 1.518e-02 1.24	3e-02 7e-01 C 6e-01	PLEC:16 DES:88 F CDKN2A:1956 KIT:3050 KF ADD2:73 CAMK2B:132	HEX:1048 CHRD:1133 FOX HSPB2:266 MYOF:339 DYSI RAS:4052 PTPN11:6081 RA TNC:250 ADCY1:450 FOXE	F:414 BAG3:422 B27A:6218 MREG:6665 P2:648 GRIN2B:1050
MP0002876 abnormal thyroic MP0003122 maternal im MP0009780 abnormal chondro MP0005167 abnormal chamic	printing 0.122038 ocyte physiolo -0.120927 brain barrier -0.116855	2 14 2 9 4 16	6.510e-02 3.06 1.142e-01 4.34 2.093e-01 5.50 1.060e-01 4.13	6e-01 4e-01 4e-01	GNAS:886 ARID4A:1422 CAV1:542 WNT9A:2360 PTAFR:33 MMP9:1060 NO	GHR:980 HPN:1344 GFRA4 NDN:2096 IGF2:2372 MES THRA:3025 TRIP11:4584 E DS1:1203 HRH3:1485 CLCI	ST:2982 SNRPN:4608 SR1:5740 THRB:6513 N2:3412 CTNNB1:3471
MP0002735 abnormal chemical MP0000681 abnormal thyromal cardiom MP0000013 abnormal adip MP0003693 abnormal embr	oid gland 0.113348 yocyte apopto 0.110710 ose tissue 0.110375	7 43 7 37 9 15	3.602e-02 2.12 1.034e-02 1.09 2.010e-02 1.51 1.392e-01 4.70 7.525e-02 3.32	0e-01 4e-01 0e-01 C	CGA:456 TBX1:517 HC CASP8:117 AIFM1:216 ⁻ OL1A1:1906 PRKAR1A:20	' ADCY1:450 BAMBI:577 P DXA3:585 MANBA:797 HHE TFAM:220 MAPKAPK2:242 30 SMTN:2743 FSTL3:2853 ATF1:1069 PARG:1268 KIF	X:1048 CHRD:1133 MDM2:392 RAF1:861 PYY:4078 PPARG:4605
MP0010352 gastrointestinal	-		1.626e-01 4.83			MAD4:2423 PTGS2:2550 IT	

MP0010352 gastrointestinal tract polyps

MP0008260 abnormal autophagy

MP0004957 abnormal blastocyst morpholog

0.1042249

0.1034792

0.1026718

15

16

84

1.626e-01 4.837e-01

1.523e-01 4.760e-01

1.221e-03 2.325e-02

STAT3:594 SAV1:682 SMAD4:2423 PTGS2:2550 ITGB1:2961 APC:3314

PMP22:498 LRRK2:878 PTHLH:896 VCP:923 ATG9A:968 ATG5:3778 CHD8:212 CUL3:218 BRD4:571 TPT1:777 HSPA5:786 ATRX:823