

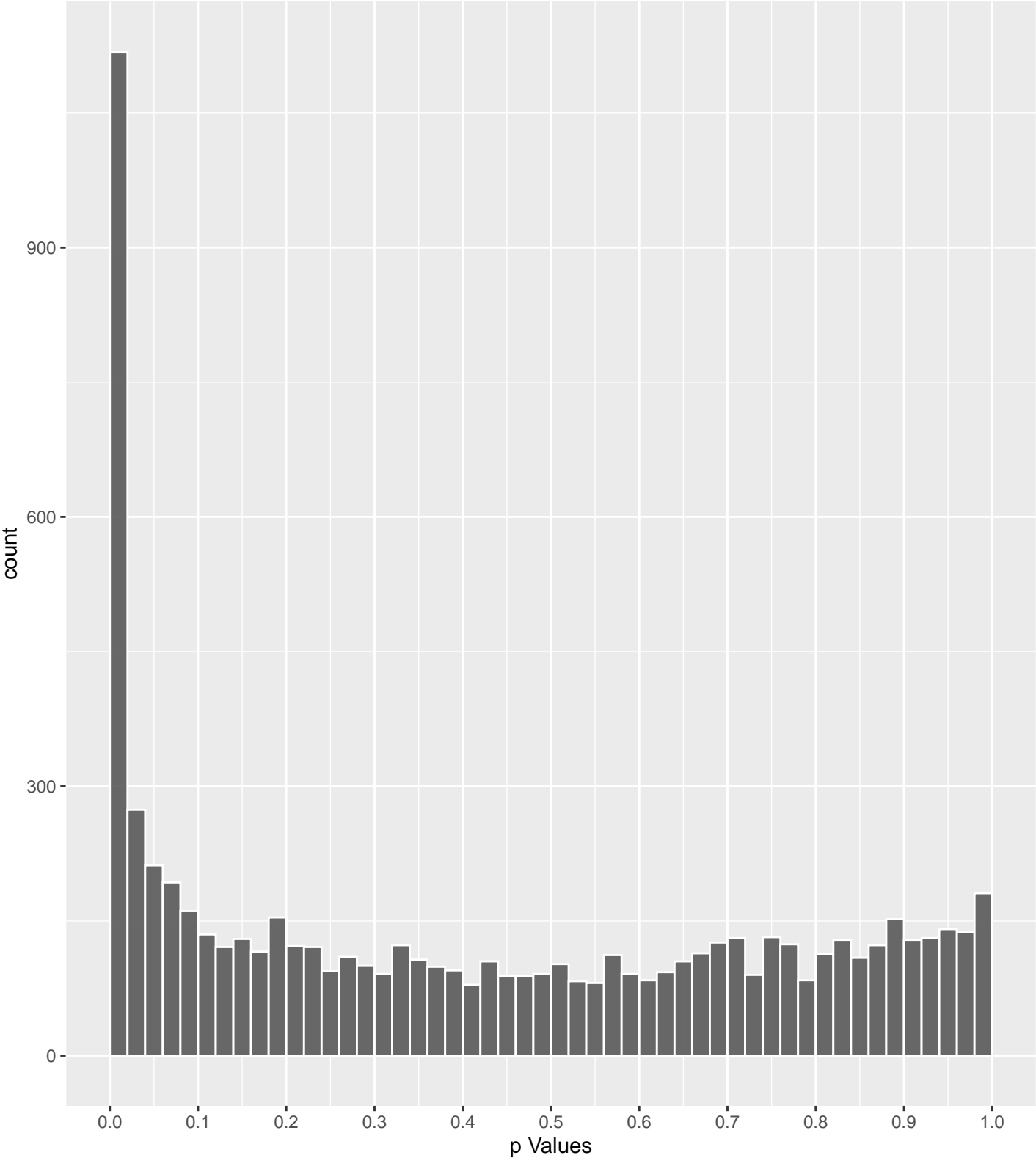
Top genes by P–value non–permulated

Gene	Rho	N	P	p.adj	qValueNoperm
SLX4	−0.3925041	390	2.823e−21	4.526e−17	6.741e−13
ADGRV1	−0.3645829	408	2.315e−19	1.856e−15	1.382e−11
BDP1	−0.3962035	304	3.375e−17	1.804e−13	7.702e−10
CEP192	−0.3427245	400	5.568e−17	2.232e−13	7.702e−10
CAMSAP2	0.3772855	327	8.063e−17	2.585e−13	7.702e−10
SPG11	−0.3279455	420	2.179e−16	5.823e−13	1.446e−09
ZBTB41	0.3843681	302	3.528e−16	8.080e−13	1.604e−09
MYO3A	−0.3369911	390	4.298e−16	8.614e−13	1.604e−09
KDM5B	0.3433639	352	3.617e−15	6.444e−12	1.067e−08
CNTN4	0.3649983	309	4.776e−15	7.657e−12	1.141e−08
ANKRD31	−0.3328298	366	7.416e−15	1.081e−11	1.464e−08
NCAN	−0.3309616	366	1.046e−14	1.398e−11	1.512e−08
DPY19L3	0.3400687	343	1.458e−14	1.761e−11	1.512e−08
DENND1B	0.3407672	341	1.538e−14	1.761e−11	1.512e−08
POLRMT	−0.3411871	339	1.705e−14	1.823e−11	1.512e−08
TRIM29	0.3421597	336	1.879e−14	1.827e−11	1.512e−08
DCHS2	−0.3103392	407	2.023e−14	1.827e−11	1.512e−08
NAV1	0.3437217	332	2.051e−14	1.827e−11	1.512e−08
ATAD5	−0.3158377	385	3.724e−14	2.986e−11	2.053e−08
PPP1R12B	0.3232234	368	3.635e−14	2.986e−11	2.053e−08
C2CD3	−0.3051371	411	4.094e−14	3.032e−11	2.053e−08
PTPRQ	−0.3024759	418	4.160e−14	3.032e−11	2.053e−08
CNTRL	−0.3009318	419	5.218e−14	3.637e−11	2.356e−08
PKD1	−0.3229155	359	7.862e−14	5.252e−11	3.260e−08
TMPRSS9	−0.3275718	347	9.203e−14	5.902e−11	3.517e−08

Top genes by Q–Value non–permulated

Gene	Rho	N	P	p.adj	qValueNoperm
SLX4	−0.3925041	390	2.823e−21	4.526e−17	6.741e−13
ADGRV1	−0.3645829	408	2.315e−19	1.856e−15	1.382e−11
BDP1	−0.3962035	304	3.375e−17	1.804e−13	7.702e−10
CAMSAP2	0.3772855	327	8.063e−17	2.585e−13	7.702e−10
CEP192	−0.3427245	400	5.568e−17	2.232e−13	7.702e−10
SPG11	−0.3279455	420	2.179e−16	5.823e−13	1.446e−09
ZBTB41	0.3843681	302	3.528e−16	8.080e−13	1.604e−09
MYO3A	−0.3369911	390	4.298e−16	8.614e−13	1.604e−09
KDM5B	0.3433639	352	3.617e−15	6.444e−12	1.067e−08
CNTN4	0.3649983	309	4.776e−15	7.657e−12	1.141e−08
ANKRD31	−0.3328298	366	7.416e−15	1.081e−11	1.464e−08
NCAN	−0.3309616	366	1.046e−14	1.398e−11	1.512e−08
TRIM29	0.3421597	336	1.879e−14	1.827e−11	1.512e−08
DCHS2	−0.3103392	407	2.023e−14	1.827e−11	1.512e−08
NAV1	0.3437217	332	2.051e−14	1.827e−11	1.512e−08
DPY19L3	0.3400687	343	1.458e−14	1.761e−11	1.512e−08
POLRMT	−0.3411871	339	1.705e−14	1.823e−11	1.512e−08
DENND1B	0.3407672	341	1.538e−14	1.761e−11	1.512e−08
ATAD5	−0.3158377	385	3.724e−14	2.986e−11	2.053e−08
C2CD3	−0.3051371	411	4.094e−14	3.032e−11	2.053e−08
PPP1R12B	0.3232234	368	3.635e−14	2.986e−11	2.053e−08
PTPRQ	−0.3024759	418	4.160e−14	3.032e−11	2.053e−08
CNTRL	−0.3009318	419	5.218e−14	3.637e−11	2.356e−08
PKD1	−0.3229155	359	7.862e−14	5.252e−11	3.260e−08
TMPRSS9	−0.3275718	347	9.203e−14	5.902e−11	3.517e−08

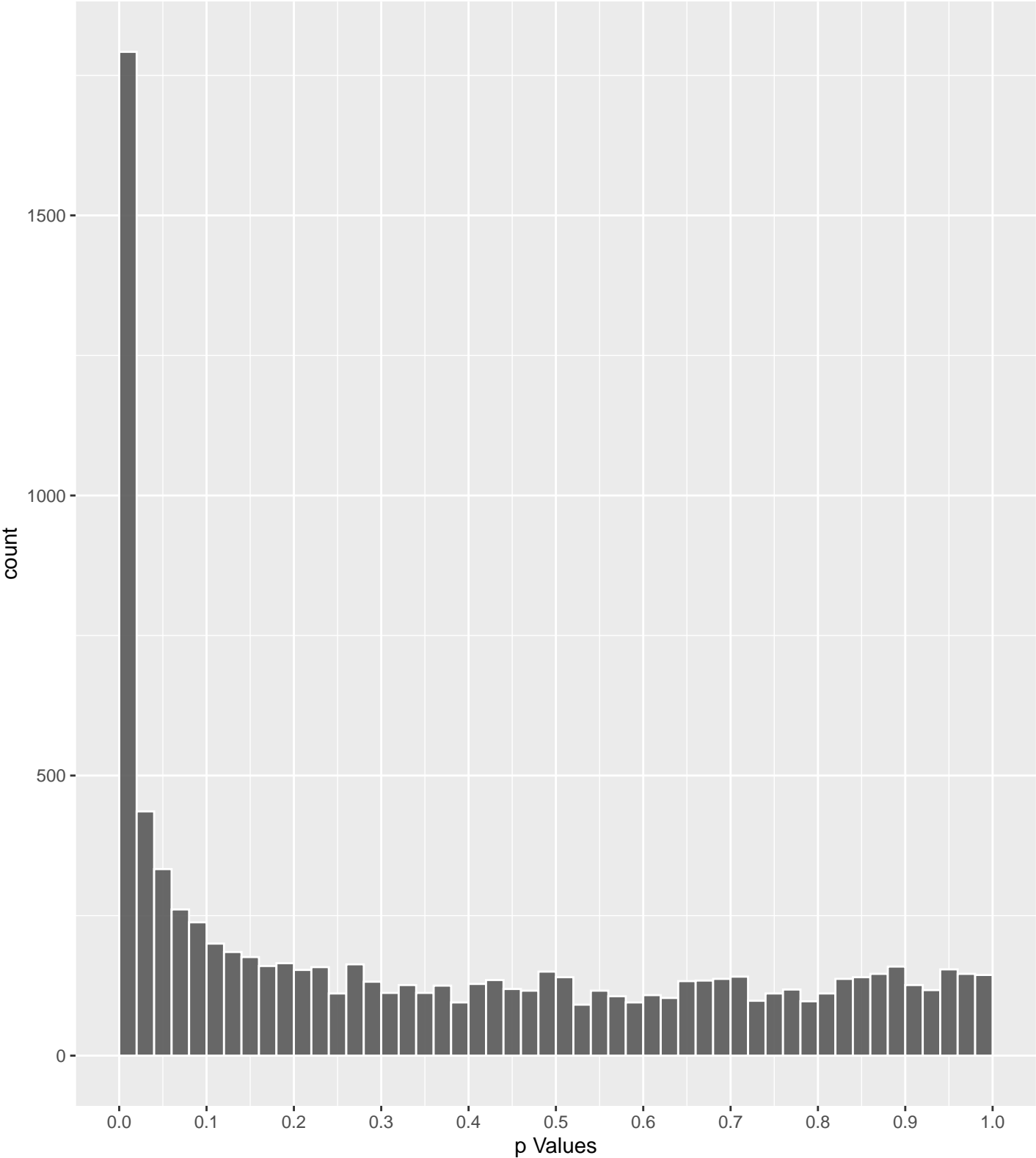
Positive Rho Non–permulated



Top Positive genes by P–value non–permulated

Gene	Rho	N	P	p.adj	qValueNoperm
CAMSAP2	0.3772855	327	8.063e−17	2.585e−13	7.702e−10
ZBTB41	0.3843681	302	3.528e−16	8.080e−13	1.604e−09
KDM5B	0.3433639	352	3.617e−15	6.444e−12	1.067e−08
CNTN4	0.3649983	309	4.776e−15	7.657e−12	1.141e−08
DPY19L3	0.3400687	343	1.458e−14	1.761e−11	1.512e−08
DENND1B	0.3407672	341	1.538e−14	1.761e−11	1.512e−08
TRIM29	0.3421597	336	1.879e−14	1.827e−11	1.512e−08
NAV1	0.3437217	332	2.051e−14	1.827e−11	1.512e−08
PPP1R12B	0.3232234	368	3.635e−14	2.986e−11	2.053e−08
TRPM1	0.3072748	379	2.729e−13	1.509e−10	7.751e−08

Positive Rho Non–permulated



Top Negative genes by P–value non–permulated

Gene	Rho	N	P	p.adj	qValueNoperm
SLX4	−0.3925041	390	2.823e−21	4.526e−17	6.741e−13
ADGRV1	−0.3645829	408	2.315e−19	1.856e−15	1.382e−11
BDP1	−0.3962035	304	3.375e−17	1.804e−13	7.702e−10
CEP192	−0.3427245	400	5.568e−17	2.232e−13	7.702e−10
SPG11	−0.3279455	420	2.179e−16	5.823e−13	1.446e−09
MYO3A	−0.3369911	390	4.298e−16	8.614e−13	1.604e−09
ANKRD31	−0.3328298	366	7.416e−15	1.081e−11	1.464e−08
NCAN	−0.3309616	366	1.046e−14	1.398e−11	1.512e−08
POLRMT	−0.3411871	339	1.705e−14	1.823e−11	1.512e−08
DCHS2	−0.3103392	407	2.023e−14	1.827e−11	1.512e−08

EnrichmentHsSymbolsFile2 Top pathways by non-permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
REACTOME_FLT3_SIGNALING_BY_CBL_MUTANTS	0.4400716	2	3.111e-02	2.707e-01	CBL:215 FLT3:1693 NA NA NA NA
WP_ULTRACONSERVED_REGION_339_MODULATION	0.4229172	2	3.830e-02	2.979e-01	CCNE2:1135 TP53:1315 NA NA NA NA
NIKOLSKY_BREAST_CANCER_19P13_AMPLICON	-0.4119433	5	1.421e-03	4.625e-02	USHBP1:34 MYO9B:154 OCEL1:747 NR2F6:1983 USE1:4141 NA
WP_NICOTINE_METABOLISM_IN_LIVER_CELLS	-0.3884488	2	5.706e-02	3.485e-01	AOX1:1420 FMO3:2141 NA NA NA NA
REACTOME_TACHYKININ_RECEPTORS_BIND_TACHY	0.3754681	5	3.640e-03	8.091e-02	TACR1:271 TAC1:346 TACR2:639 TAC3:1650 TACR3:7066 NA
REACTOME_SIGNALING_BY_MEMBRANE_TETHERED	-0.3737427	5	3.798e-03	8.297e-02	GOLGA4:486 BIN2:1068 KANK1:1309 KDR:3211 ETV6:4047 NA
BIOCARTA_TUBBY_PATHWAY	0.3645687	4	1.156e-02	1.644e-01	HTR2C:1357 TUB:1666 CHRM1:1757 PLCB1:3875 NA NA
BIOCARTA_CREM_PATHWAY	0.3635715	6	2.040e-03	6.044e-02	ADCY1:133 FHL5:967 FSHR:1583 FSHB:1884 XPO1:2615 CREM:5899
MATHEW_FANCONI_ANEMIA_GENES	-0.3524289	11	5.176e-05	4.487e-03	FANCM:45 FANCG:125 BRCA2:273 BRIP1:385 FANCE:1494 FANCD2:1744
REACTOME_INTERLEUKIN_36_PATHWAY	0.3459335	6	3.339e-03	7.712e-02	IL36G:230 IL36RN:537 IL1F10:1522 IL1RAP:2107 IL36B:3207 IL1RL2:7196
REACTOME_VITAMIN_D_CALCIFEROL_METABOLISM	-0.3299918	9	6.074e-04	2.765e-02	CUBN:189 PIAS4:387 CYP24A1:564 CYP2R1:814 CYP27B1:2762 GC:3052
REACTOME_NADE_MODULATES_DEATH_SIGNALLING	0.3259904	4	2.394e-02	2.417e-01	CASP2:261 CASP3:2024 NGF:2634 NGFR:6214 NA NA
BIOCARTA_ION_PATHWAY	0.3252157	5	1.178e-02	1.654e-01	PTK2B:385 PRKCA:1251 PRKCB:2018 PLCG1:4715 P2RY2:5624 NA
REACTOME_MUCOPOLYSACCHARIDOSES	-0.3218779	11	2.184e-04	1.337e-02	GLB1:325 NAGLU:816 GALNS:1145 ARSB:1365 HYAL1:1726 IDS:2493
REACTOME_FORMYL_PEPTIDE_RECEPTORS_BIND_F	0.3165495	4	2.832e-02	2.618e-01	ANXA1:429 FPR2:607 APP:3362 HEBP1:7369 NA NA
WP_IRINOTECAN_PATHWAY	-0.3161342	4	2.853e-02	2.623e-01	SLCO1B1:2097 ABCC1:2228 UGT1A1:3072 BCHE:4369 NA NA
WP_STEROID_HORMONE_PRECURSOR_BIOSYNTHESI	-0.3145697	7	3.947e-03	8.537e-02	CYP11A1:79 CYP17A1:94 SRD5A1:301 CYP21A2:431 HSD3B2:652 SRD5A2:5895
REACTOME_MUSCARINIC_ACETYLCHOLINE_RECEPT	0.3144163	5	1.489e-02	1.896e-01	CHRM4:1231 CHRM2:1374 CHRM3:1455 CHRM1:1757 CHRM5:9015 NA
NIKOLSKY_BREAST_CANCER_17P11_AMPLICON	0.3109563	10	6.613e-04	2.899e-02	RNF112:32 EPN2:469 ULK2:1500 ALDH3A1:1520 MAPK7:1999 ALDH3A2:2061
REACTOME_REGULATION_OF_NPAS4_GENE_TRANSC	0.3107029	4	3.178e-02	2.711e-01	NR3C1:1080 KCNIP3:1110 NPAS4:1326 PRF:8599 NA NA
REACTOME_HDL_REMODELING	0.3103429	8	2.367e-03	6.648e-02	APOA1:262 ABCG1:902 PLTP:1103 APOE:2252 LCAT:3287 LIPG:3855
REACTOME_TETRAHYDROBIPTERIN_BH4_SYNTHES	0.3093676	9	1.309e-03	4.352e-02	DHFR:616 PRKG2:1418 HSP90AA1:1687 AKT1:2785 GCH1:3200 SPR:3290
REACTOME_DOPAMINE_RECEPTORS	0.3085783	4	3.255e-02	2.750e-01	DRD5:154 DRD1:296 DRD2:872 DRD3:10944 NA NA
MCGOWAN_RSP6_TARGETS_DN	0.3082338	3	6.443e-02	3.695e-01	ELAPOR1:664 DIDO1:2637 FBXO38:5905 NA NA NA
REACTOME_VITAMINS	-0.3080159	6	8.975e-03	1.438e-01	CYP24A1:564 CYP2R1:814 CYP26C1:2380 CYP27B1:2762 CYP26B1:5217 CYP26A1:6721
SMID_BREAST_CANCER_ERBB2_DN	0.3079712	4	3.290e-02	2.765e-01	FGFR2:1677 NPY1R:1980 GABRP:2047 SOX10:6568 NA NA
REACTOME_SYNTHESIS_OF_WYBUTOSINE_AT_G37	-0.3072917	6	9.137e-03	1.460e-01	TYW1:797 LCMT2:830 TRMT5:1408 TRMT12:4191 TYW5:5647 TYW3:5673
REACTOME_SODIUM_COUPLED_SULPHATE_DI_AND	0.3052911	5	1.806e-02	2.127e-01	SLC13A3:562 SLC13A1:835 SLC13A4:3416 SLC13A5:4894 SLC13A2:5898 NA
REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHE	0.3042982	11	4.745e-04	2.386e-02	PKP1:18 DSP:97 DSG3:110 TJP1:286 DSG2:1995 CASP3:2024
REACTOME_ROLE_OF_SECOND_MESSENGERS_IN_NE	0.3027167	10	9.167e-04	3.611e-02	TRPC4:68 TRPC5:191 TRPC1:247 TRPC3:742 DCC:1749 TRPC7:1866
WP_NIPBL_ROLE_IN_DNA_DAMAGE_CORNELIA_DE	-0.3023446	7	5.600e-03	1.056e-01	RNF168:620 ATM:623 ATR:1285 CBX3:1774 H2AX:5270 NIPBL:6100
DELASERNA_TARGETS_OF_MYOD_AND_SMARCA4	0.3010511	9	1.762e-03	5.524e-02	TNNT2:77 BIN1:214 MYOG:443 MYH3:1091 TNNI2:2553 TNNT3:2809
MOOTHA_PYR	0.3009076	8	3.204e-03	7.712e-02	PDP1:1419 PDK1:1502 PDK4:1711 PDHA1:2255 PDHB:3077 PDHA2:3178
NIKOLSKY_BREAST_CANCER_7P22_AMPLICON	0.2995220	37	2.907e-10	1.257e-07	INTS1:232 TMEM184A:568 CHST12:583 ADAP1:677 IQCE:815 GPER1:1290
BIOCARTA_ALTERNATIVE_PATHWAY	0.2968848	7	6.522e-03	1.163e-01	C8A:1577 CFB:2784 C6:3070 C3:3219 C5:3607 CFD:4010
JI_CARCINOGENESIS_BY_KRAS_AND_STK11_UP	0.2962925	10	1.176e-03	4.017e-02	PKP1:18 TIAM1:233 KRT5:241 BNC1:611 COL17A1:1018 GPR87:3015
WP_ALTERNATIVE_PATHWAY_OF_FETAL_ANDROGEN	-0.2959590	9	2.107e-03	6.082e-02	CYP11A1:79 CYP17A1:94 HSD3B2:652 HSD17B3:1323 STAR:1599 HSD17B6:4021
NIKOLSKY_BREAST_CANCER_16P13_AMPLICON	-0.2939147	99	5.634e-24	3.656e-20	PKD1:15 PGAP6:77 WDR90:85 ZNF213:104 TBL3:114 PTX4:115
BIOCARTA_WNT_LRP6_PATHWAY	-0.2930406	6	1.292e-02	1.730e-01	WNT8A:792 DKK2:1397 WNT8B:1434 DKK1:2430 KREMEN2:6252 FZD1:7585
BIOCARTA_BARD1_PATHWAY	-0.2919756	8	4.237e-03	8.903e-02	FANCG:125 FANCE:1494 FANCD2:1744 FANCA:1751 FANCF:3696 BRCA1:3760

GSEA-c5-HsSymbols Top pathways by non-permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
HP_LAMELLAR_CATACT	0.4600295	5	3.671e-04	1.255e-02	HSF4:74 MIP:603 CRYBA4:687 BFSP1:868 CRYGB:966 NA
HP_GRANULOCYTIC_HYPERPLASIA	-0.4538957	5	4.395e-04	1.426e-02	TET2:92 ASXL1:598 CSF3R:603 KIT:713 IRF8:1706 NA
GOMF_STRUCTURAL_CONSTITUENT_OF_POSTSYNAP	0.4419580	3	8.016e-03	1.003e-01	ACTBL2:231 DBNL:421 ACTL9:2115 NA NA NA
GOBP_REGULATION_OF_TOLL_LIKE_RECEPTOR_7	0.4387372	3	8.487e-03	1.037e-01	RSAD2:251 SLC15A4:652 PTPN22:2022 NA NA NA
GOBP_NEGATIVE_REGULATION_OF_DENDRITIC_CE	0.4303943	3	9.822e-03	1.130e-01	ZBTB46:837 FCGR2B:906 TMEM176B:1578 NA NA NA
GOBP_ONCOSTATIN_M_MEDIATED_SIGNALING_PAT	0.4286357	5	9.017e-04	2.312e-02	PRLR:747 IL6ST:814 OSMR:936 LIFR:1297 IL13RA1:1894 NA
HP_ACHROMATOPSIA	0.4225607	4	3.421e-03	5.918e-02	ATF6:53 GNAT2:325 CNGB3:369 CNGA3:4220 NA NA
GOMF_3_BETA_HYDROXY_DELTA5_STEROID_DEHYD	-0.4176700	5	1.218e-03	2.823e-02	HSD3B2:652 SDR42E1:954 NSDHL:1272 HSD3B7:1575 SDR42E2:2159 NA
GOBP_VITAMIN_D3_METABOLIC_PROCESS	-0.4137534	3	1.306e-02	1.344e-01	CYP27A1:583 CYP2R1:814 CYP27B1:2762 NA NA NA
GOCC_DENSE_BODY	0.4101631	4	4.494e-03	7.011e-02	SND1:432 PIWIL1:707 PIWIL2:2051 ACTG1:2532 NA NA
GOBP_DOUBLE_STRAND_BREAK_REPAIR_VIA_SING	-0.4099711	8	5.928e-05	3.089e-03	SLX4:1 HELX:191 OGG1:435 SLX1A:916 SLX1B:919 RBBP8:1526
GOMF_ESTROGEN_2_HYDROXYLASE_ACTIVITY	-0.3981817	2	5.112e-02	2.861e-01	CYP1A1:407 CYP1A2:2871 NA NA NA
HP_CORTICOSPINAL_TRACT_HYPOPLASIA	0.3962975	6	7.741e-04	2.078e-02	RAI1:211 L1CAM:702 DEAF1:774 FLII:1068 PDHB:3077 IQSEC2:4116
GOBP_ADENYLATE_CYCLASE_INHIBITING_SEROTO	0.3931096	6	8.534e-04	2.216e-02	HTR5A:244 HTR1D:750 HTR1B:822 HTR1F:2014 HTR1A:2207 HTR1E:4197
GOBP_COBALAMIN_TRANSPORT	-0.3904720	7	3.465e-04	1.200e-02	CUBN:189 TCN2:1012 TCN1:1511 AMN:1768 ABCD4:1897 ABCC1:2228
GOMF_HAPTOGLOBIN_BINDING	-0.3865105	3	2.041e-02	1.739e-01	HBM:1435 HBQ1:1786 HBE1:2248 NA NA NA
GOMF_ALKALINE_PHOSPHATASE_ACTIVITY	-0.3861974	3	2.051e-02	1.744e-01	CILP2:908 ALPL:2057 CILP:2514 NA NA NA
GOBP_TETRAHYDROFOLATE_BIOSYNTHETIC_PROCE	0.3809859	3	2.228e-02	1.821e-01	DHFR:616 ATIC:1879 GCH1:3200 NA NA NA
GOBP_TOLERANCE_INDUCITION_DEPENDENT_UPON	-0.3785901	4	8.728e-03	1.053e-01	AIRE:294 FOXP3:578 CD274:3271 HAVCR2:3670 NA NA
GOMF_RRNA_CYTOSINE_METHYLTRANSFERASE_ACT	-0.3734398	4	9.686e-03	1.119e-01	NSUN5:520 NOP2:1153 METTL15:2929 NSUN4:3543 NA NA
GOBP_POSITIVE_REGULATION_OF_CELL_ADHESIO	0.3704039	2	6.961e-02	3.330e-01	CAV1:516 IL1B:3630 NA NA NA NA
GOBP_NEUROTROPHIN_PRODUCTION	0.3697537	5	4.190e-03	6.725e-02	PCSK6:465 ADORA1:912 HAP1:1498 NPY:1544 FURIN:5983 NA
HP_CONGENITAL_ADRENAL_HYPERPLASIA	-0.3691786	4	1.055e-02	1.188e-01	CYP17A1:94 HSD3B2:652 STAR:1599 POR:6066 NA NA
HP_DEFICIENT_EXCISION_OF_UV_INDUCED_PYRI	-0.3690826	5	4.259e-03	6.790e-02	FANCE:1494 FANCD2:1744 FANCA:1751 ERCC4:1771 FANCC:3779 NA
GOBP_ANTIBODY_DEPENDENT_CELLULAR_CYTOTOX	0.3671856	3	2.761e-02	2.030e-01	FCGR2B:906 FCGR1A:2393 FCGR3A:3047 NA NA NA
GOBP_NEGATIVE_REGULATION_OF_CELL_VOLUME	0.3639554	5	4.823e-03	7.291e-02	SHANK3:468 CLCN3:1361 P2RX7:1663 ANO6:3690 KCNMA1:3691 NA
GOBP_RESPONSE_TO_ERYTHROPOIETIN	-0.3639424	3	2.901e-02	2.083e-01	KIT:713 EPOR:1878 EPO:3972 NA NA NA
GOBP_CHITIN_METABOLIC_PROCESS	0.3596703	3	3.095e-02	2.161e-01	CHI3L1:909 CHIT1:1301 CTBS:4521 NA NA NA
GOMF_CHITINASE_ACTIVITY	0.3596703	3	3.095e-02	2.161e-01	CHI3L1:909 CHIT1:1301 CTBS:4521 NA NA NA
HP_ANAL_FISSURE	0.3589619	4	1.290e-02	1.335e-01	EGFR:84 ADAM17:1013 CYBC1:2268 COL7A1:5643 NA NA
GOBP_DETOXIFICATION_OF_NITROGEN_COMPOUND	0.3582595	2	7.927e-02	3.559e-01	MTARC2:1035 MTARC1:3493 NA NA NA NA
GOBP_OPERANT_CONDITIONING	0.3580901	5	5.551e-03	8.007e-02	TACR1:271 DRD1:296 TACR2:639 PDE8B:1901 AGT:8263 NA
GOBP_GONADAL_MESODERM_DEVELOPMENT	-0.3573537	2	8.003e-02	3.578e-01	AMH:353 ZFPM2:4231 NA NA NA NA
GOBP_MITOCHONDRIAL_RNA_CATABOLIC_PROCESS	-0.3566555	6	2.481e-03	4.707e-02	LRPPRC:113 PDE12:456 PNPT1:2022 SUPV3L1:2616 GRSF1:3664 SLIRP:4971
GOMF_AMINO_ACID_MONOATOMIC_CATION_ANTIPO	0.3566405	5	5.745e-03	8.162e-02	SLC25A12:1348 SLC38A3:1808 SLC38A5:1852 SLC25A13:2596 SLC32A1:3830 NA
GOMF_PHOSPHATIDYLCHOLINE_STEROL_O_ACYLTR	0.3562244	5	5.802e-03	8.228e-02	APOA1:262 APOA2:309 APOA4:2122 APOE:2252 APOA5:6543 NA
GOBP_INTERMEDIATE_FILAMENT_BUNDLE_ASSEMB	0.3528555	5	6.283e-03	8.664e-02	PKP1:18 KRT14:260 NEFM:1731 NEFL:4239 PKP2:5520 NA
HP_BLIND_VAGINA	-0.3526372	4	1.458e-02	1.445e-01	CYP17A1:94 MTM1:1608 WT1:1846 MAMLD1:5927 NA NA
HP_IMPAIRED_RENAL_CONCENTRATING_ABILITY	-0.3524944	6	2.787e-03	5.080e-02	CLCNKA:289 CLCNKB:324 CEP290:965 BSND:1459 NPHP1:4045 FAM20A:7124
GOBP_TYPE_II_HYPERSENSITIVITY	0.3500034	4	1.533e-02	1.482e-01	FCGR2B:906 FCGR1A:2393 FCGR3A:3047 C3:3219 NA NA

tissue_specific Top pathways by non-permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
putamen	0.17800805	14	2.118e-02	7.002e-02	GPR88:334 LRRC10B:846 KCNH4:927 PDE10A:1316 RGS9:1660 OPALIN:3081
Brodmann.area.9	0.12395363	180	1.292e-08	6.978e-07	HS3ST2:46 NECAB1:51 TMEM132D:111 PLPPR4:143 NETO1:170 PLPPR5:172
hippocampus.proper	0.12269144	10	1.793e-01	3.458e-01	NEUROD6:542 NTS:1423 SLC17A7:2359 OLIG2:3572 GRP:4995 NEUROG3:5735
hypothalamus	0.11760052	66	9.879e-04	1.299e-02	GRIK1:36 BRINP3:49 QRFPR:73 SCN9A:131 SYT6:168 RAB3C:203
breast	0.11055548	15	1.384e-01	2.875e-01	KRT5:241 NPY2R:881 THRSP:2581 TNN:2687 GSC:3929 HCAR1:4032
cerebral.cortex	0.08958798	107	1.444e-03	1.299e-02	FAM163B:217 KCNF1:307 MAS1:370 ADGRB1:512 NEUROD6:542 OPRL1:600
amygdala	0.08917820	9	3.544e-01	5.172e-01	NEUROD6:542 TNR:926 PTPRZ1:2055 LHFP3:2338 SLC17A7:2359 PCDH15:8738
caudate.nucleus	0.08901828	26	1.166e-01	2.518e-01	GPR37L1:116 GPR88:334 TAC1:346 RLBP1:717 LRRC10B:846 RGS14:1913
subcutaneous.adipose	-0.07829807	72	2.204e-02	7.002e-02	SIGLEC1:41 ITIH5:120 CYP1A1:407 PPARG:558 VWF:645 GPBAR1:716
nucleus.accumbens	0.06928515	99	1.773e-02	6.838e-02	GABRA5:179 DRD1:296 GPR88:334 INSYN2A:396 CDH4:452 LHFP1:507
ectocervix	-0.06905064	25	2.326e-01	3.962e-01	COL27A1:152 RIPOR3:390 PTHLH:1884 ADAMTSL5:1950 KRT34:2725 MMRN1:2913
greater.omentum	0.06869970	32	1.792e-01	3.458e-01	ADAMTS4:102 BNC1:611 GFPT2:800 ADAMTS9:1566 SPRY1:2044 THRSP:2581
sigmoid.colon	0.06454700	50	1.152e-01	2.518e-01	NTSR1:533 VIP:622 TACR2:639 GALR2:688 LIMS2:720 DPT:787
esophagus.mucosa	0.06204401	218	1.783e-03	1.317e-02	PKP1:18 DSG3:110 DSC3:121 ELF3:162 TGM1:181 KRT5:241
bladder	0.06191232	24	2.943e-01	4.610e-01	ARL14:1585 PADI3:1618 KRT13:1859 RD3:2052 SLC14A1:2786 WFDC13:3205
EBV.lymphocyte	-0.06004892	670	2.989e-07	8.069e-06	ATAD5:11 DLGAP5:22 CHAF1A:28 IL27RA:36 TCF3:43 IRAG2:56
suprapubic.skin	0.05955843	194	4.597e-03	2.758e-02	PKP1:18 DSG3:110 DSC3:121 IL37:158 IL36G:230 POU2F3:235
C1.spinal.cord	0.05598340	182	9.811e-03	4.075e-02	ZNF536:56 UGT8:207 TAF4A:210 DSCAML1:220 ANLN:255 PDE6B:355
spleen	-0.05504312	297	1.298e-03	1.299e-02	AKNA:90 PATL2:182 NLR3:267 GDF3:290 NIBAN3:302 CD40LG:395
blood	-0.05499927	275	1.951e-03	1.317e-02	MEFV:46 TREML2:70 NHS2:162 JAK3:178 DHX34:193 NLRP12:199
cortex.kidney	-0.05427193	114	4.648e-02	1.321e-01	PKHD1:86 CUBN:189 DMRT2:239 CLCNKB:324 PRODH2:541 ITGB6:551
Brodmann.area.24	0.05399343	31	2.988e-01	4.610e-01	DRD5:154 FAM189A1:308 CRH:359 NEUROD6:542 RAPGEF4:1548 TAC3:1650
leg.skin	0.05288114	217	7.888e-03	3.995e-02	TRIM29:7 TRPM1:10 PKP1:18 VSIG8:21 KLK7:72 BLMH:80
pituitary.gland	0.05256263	213	8.867e-03	3.995e-02	UNC79:114 ARC:117 PLPPR4:143 WDR17:151 IL5RA:180 BPIFA1:313
vagina	0.05092764	91	9.452e-02	2.431e-01	PKP1:18 DSG3:110 DSC3:121 KRT5:241 LEXM:272 DSC2:288
thyroid	-0.04837633	151	4.164e-02	1.249e-01	IDO2:61 PRTG:127 RGL3:235 TLE6:257 CLCNKA:289 PLA2R1:349
cerebellar.hemisphere	0.04814490	509	2.886e-04	5.194e-03	PPFIA4:26 RNF112:32 APBA2:42 MYT1:54 NDST3:58 SLC35F3:60
liver	-0.04276997	327	8.878e-03	3.995e-02	ABCC6:37 IDO2:61 SERPINA7:108 CREB3L3:112 CA5A:138 ABCB11:149
transverse.colon	-0.04068012	147	9.089e-02	2.431e-01	WNK4:29 ATP2C2:134 TJP3:410 TRPM6:723 CDX1:763 MUC4:833
left.ventricle	0.03774983	68	2.832e-01	4.610e-01	TNNT2:72 MYOM2:167 RD3L:174 LMOD2:183 TENM2:556 TCAP:593
fallopian.tube	-0.03607607	52	3.693e-01	5.205e-01	ADAMTS3:181 ADGRG4:368 CDCD17:371 GASKA1:1155 GREB1L:1571 CCDC198:1770
substantia.nigra	-0.03606965	12	6.654e-01	7.985e-01	DBX2:625 RPE65:3957 SLC6A3:5040 C10orf105:5221 RET:5611 CHRMS:7019
cerebellum	0.03577425	375	1.952e-02	7.002e-02	PPFIA4:26 RNF112:32 NOS1AP:45 MYT1:54 ANK2:70 NPPC:87
adrenal.gland	-0.03431847	108	2.202e-01	3.962e-01	ADGRV1:2 CYP11A1:79 CYP17A1:94 VHRN:255 CYP21A2:431 AMHR2:476
minor.salivary.gland	-0.03251869	69	3.518e-01	5.172e-01	PIP:303 IRX1:646 APCDD1L:1232 TCN1:1511 ENPP1:1522 PRSS8:1580
skeletal.muscle	0.03102131	238	1.032e-01	2.518e-01	CACNA1S:78 IGFN1:90 MYOM2:167 LMOD2:183 BIN1:214 SLC8A3:273
aorta	-0.02877762	154	2.211e-01	3.962e-01	HMCN1:93 VCAN:207 KCNK15:293 FBLIM1:428 SUSD5:465 GAS6:508
tibial.nerve	-0.02509548	192	2.348e-01	3.962e-01	GLI1:121 INSC:180 CUBN:189 PLXNB3:221 SOX8:381 KANK4:391
pancreas	-0.02404073	94	4.225e-01	5.704e-01	EGF:155 TMED6:525 PRODH2:541 G6PC2:972 NPHS1:1143 KCNK16:1173
lung	-0.01932338	139	4.346e-01	5.724e-01	SHROOMA:24 ABCA3:248 LRRN4:337 LAMP3:433 A2M:510 ITGB6:551