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1.000e+00

2.328e-03

1.010e-01

3.025e-03

8.640e-03

1.245e-04

1.928e-02

1.815e-03

1.078e-01

1.204e-01

1.166e-01

6.990e-02

1.720e-02

2.131e-01

2.988e-02

2.768e-02

1.839e-01

1.839e-01

1.537e-01 7.034e-04

PHF5A

PTCD3

ACTC1

H4C2

UBE2G1

ABCB4

ANXA11

BDNF

KLHDC2

CTNND1

TMEM116

RIMKLA

RNASE9

DHX58

TBX21

PLPP3

ARMT1

CSAD

JAK1

WIPF3

PCDHA4

SPAG5

NCOR1

0.000000

5.557042

0.000000

0.000000

0.000000

-5.054135

-3.470489

-4.856071

-4.495795

-5.843195

-4.211346

5.132478

3.433569

3.358547

-3.234726

-3.382143

-3.638144

4.255301

-3.041026

-4.048121

-4.074511

3.130740

-3.133306

4.143099

1.000000e+00

8.231524e-08

1.000000e+00

1.000000e+00

1.000000e+00

1.297036e-06

1.558537e-03

3.592126e-06

2.079314e-05

1.536268e-08

7.615610e-05

8.578565e-07

1.787073e-03

2.350599e-03

3.652786e-03

2.157682e-03

8.238288e-04

6.263051e-05

7.073214e-03

1.548911e-04

1.383337e-04

5.230994e-03

5.185467e-03

1.027932e-04 2.346e-02

4.368033 3.761123e-05 1.325e-02 1.333e-03

permP

0.000e+00

0.000e+00

0.000e+00

0.000e+00

0.000e+00

2.089e-04

3.019e-04

3.280e-04

3.511e-04

3.830e-04

3.882e-04

4.020e-04

4.309e-04

5.437e-04

7.248e-04

7.309e-04

7.724e-04

8.011e-04

8.572e-04

8.683e-04

8.800e-04

9.370e-04

1.191e-03

Top Positive genes by P-value Permulated

p.adj

4.446e-04

1.815e-03

1.078e-01

1.204e-01

1.839e-01

2.346e-02

1.325e-02

2.205e-01

1.720e-02 7.724e-04

2.441e-01 1.744e-03

0.000e+00

4.020e-04

5.437e-04

8 800e-04

1.333e-03

1.559e-03

permPValue

0.000e+00

4.020e-04

4.309e-04

5.437e-04

7.724e-04

8.800e-04

1.333e-03

1.559e-03

1.744e-03

qValueNoperm

1.000e+00

qValuePerm

0.000e+00

5.371e-01

5.371e-01

6.293e-01

6.482e-01

6.482e-01

8.042e-01

8.643e-01

9.718e-01

1.000e+00

Gene

PTCD3

TMEM116

RIMKLA

RNASE9

ARMT1

WIPF3

SPAG5

NCOR1

TRDMT1

SUPT4H1

5.557042 8.231524e-08

5.132478 8.578565e-07

3.358547 2.350599e-03

3.130740 5.230994e-03

3.013170 7.756032e-03

2.952927 9.443280e-03

1.787073e-03

6.263051e-05

1.027932e-04

3.761123e-05

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4.255301

4.143099

4.368033

permPValue

0.000e+00

0.000e+00

0.000e+00

0.000e+00

0.000e+00

2.089e-04

3.019e-04

3.280e-04

3.511e-04

3.830e-04

3.882e-04

4.020e-04

4.309e-04

5.437e-04

7.034e-04

7.248e-04

7.309e-04

7.724e-04

8.011e-04

8.572e-04

8.683e-04

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9.370e-04

1.191e-03

1.333e-03

qValueNoperm

1.000e+00

qValuePerm

0.000e+00

0.000e+00

0.000e+00

0.000e+00

0.000e+00

5.371e-01

5.371e-01

5.371e-01

5.371e-01

5.371e-01

5.371e-01

5.371e-01

5.371e-01

6.293e-01

6.482e-01

6.482e-01

6.482e-01

6.482e-01

6.482e-01

6.482e-01

6.482e-01

6.482e-01

6.602e-01

8.042e-01

8.643e-01

Gene

PHF5A

PTCD3

ACTC1

H4C2

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PKIB

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ANXA11

BDNF

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RNASE9

TBX21

DHX58

CSAD

KLHL12

ARMT1

PLPP3

WIPF3

JAK1

PCDHA4

SPAG5

NCOR1

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-3.382143

-3.234726

-3.041026

-4.048121

4.255301

-3.638144

3.130740

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4.143099

1.000000e+00

8.231524e-08

1.000000e+00

1.000000e+00

1.000000e+00

1.297036e-06

2.079314e-05

7.615610e-05

1.536268e-08

1.787073e-03

1.558537e-03

3.592126e-06

8.578565e-07

2.350599e-03

2.157682e-03

3.652786e-03

7.073214e-03

1.548911e-04

6.263051e-05

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5.230994e-03

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6.990e-02

1.839e-01

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1.839e-01

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4.368033 3.761123e-05 1.325e-02 1.333e-03

permP

0.000e+00

0.000e+00

0.000e+00

0.000e+00

0.000e+00

2.089e-04

3.511e-04

3.882e-04

3.830e-04

4.309e-04

3.019e-04

3.280e-04

4.020e-04

5.437e-04

7.248e-04

7.034e-04

8.011e-04

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8.683e-04

9.370e-04

Top Negative genes by P-value Permulated

p.adj

2.328e-03

1.010e-01

3.025e-03

1.245e-04

1.166e-01

8.640e-03 3.511e-04

1.928e-02 3.882e-04

6.990e-02 7.309e-04

-5.054135

-3.470489

-4.495795

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-3.234726

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-3.638144

ANXA11

KLHDC2

CTNND1

PKIB

TBX21

CSAD

1.297036e-06

1.558537e-03

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3.652786e-03

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8.238288e-04

-3.041026 7.073214e-03 2.131e-01 8.011e-04

permP

2.089e-04

3.019e-04

3.280e-04

3.830e-04

7.248e-04

permPValue

2.089e-04

3.019e-04

3.280e-04

3.511e-04

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3.882e-04

7.034e-04

7.248e-04

7.309e-04

8.011e-04

qValueNoperm

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qValuePerm

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0.000e+00

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3.830e-04

4.309e-04

3.019e-04

3.280e-04

4.020e-04

5.437e-04

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7.034e-04

8.011e-04

8.572e-04

7.724e-04

7.309e-04

8.800e-04

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1.191e-03

1.333e-03

qValueNoperm

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qValuePerm

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0.000e+00

0.000e+00

0.000e+00

0.000e+00

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5.371e-01

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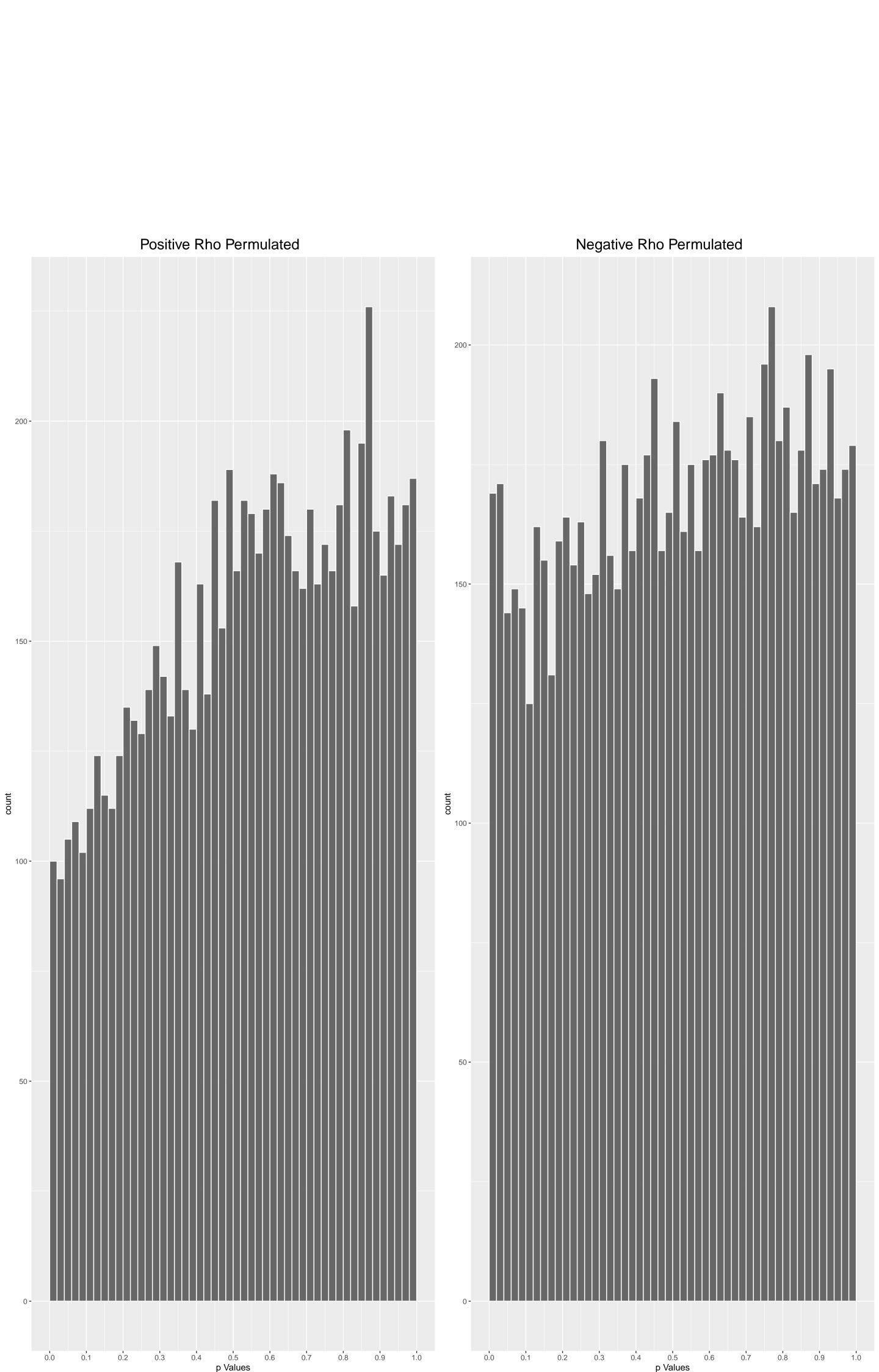
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8.042e-01

8.643e-01



Geneset	stat	num.genes	pval	p.adj	gene.vals
Very Long-Chain Fatty Acid Catabolic Pro	-0.4422393	6	1.758e-04		SLC27A2:155 SLC27A4:284 ACOX1:922 ABCD2:1256 ABCD3:1348 ABCD4:1691
Positive Regulation Of Peptidyl–Serine P	0.4105265	4	4.460e-03		LIF:380 IFNE:766 IFNK:1416 IFNG:3233 NA NA
Regulation Of Peptidyl–Serine Phosphoryl	0.4105265	4	4.460e-03		LIF:380 IFNE:766 IFNK:1416 IFNG:3233 NA NA
Cellular Response To Histamine (GO:00714	-0.3857041	6		8.464e-02	DHX8:457 GABRB2:640 GABRB3:914 DIAPH1:1773 GABRB1:2777 GABRG2:4564
Positive Regulation Of Gonad Development	-0.3750494	4	9.379e-03		SOX9:263 WT1:517 NR5A1:2590 DHX37:4732 NA NA
Positive Regulation Of Male Gonad Develo	-0.3750494	4	9.379e-03		SOX9:263 WT1:517 NR5A1:2590 DHX37:4732 NA NA
Amino–Acid Betaine Transport (GO:0015838	-0.3722803	7		6.120e-02	SLC25A29:150 SLC6A20:275 SLC22A4:439 SLC7A6:511 SLC22A5:1473 SLC6A12:531
Response To Histamine (GO:0034776)	-0.3665382	8		3.790e-02	DHX8:457 GABRB2:640 GABRB3:914 DRD3:947 DIAPH1:1773 GABRB1:2777
Regulation Of Mitochondrial mRNA Stabili	0.3638544	6		1.364e-01	FASTKD5:477 FASTKD1:925 FASTKD3:1985 FASTKD2:2508 PDE12:3360 TBRG4:3993
Positive Regulation Of Plasminogen Activ	0.3591537	7		8.038e-02	ENO1:26 HPN:292 CLEC3B:423 F12:2222 S100A10:2984 MELTF:4877
ATP Synthesis Coupled Electron Transport	0.3548545	5	5.995e-03		NDUFV1:786 NDUFB6:1014 NDUFA12:2770 NDUFV3:3028 NDUFS2:4140 NA
Negative Regulation Of B Cell Apoptotic	0.3521520	6	2.815e-03		BCL6:280 BCL10:527 NOC2L:1085 ORMDL3:1387 FOXP1:2034 IL2:9065
Long-Term Synaptic Depression (GO:006029	-0.3500000	5	6.719e-03		PLK2:738 SLC24A2:1279 PRRT1:1327 PICK1:3345 SHANK2:5447 NA
Regulation Of Collagen Fibril Organizati	0.3420706	6	3.711e-03		EMILIN1:158 EFEMP2:180 RB1:753 TNXB:1043 COLGALT1:4751 CHADL:8493
Fatty Acid Elongation, Monounsaturated F	-0.3398303	6	3.942e-03		ELOVL7:380 ELOVL3:1063 ELOVL4:1247 ELOVL2:3097 ELOVL5:4785 ELOVL6:4982
Fatty Acid Elongation, Polyunsaturated F	-0.3398303	6	3.942e-03		ELOVL7:380 ELOVL3:1063 ELOVL4:1247 ELOVL2:3097 ELOVL5:4785 ELOVL6:4982
Fatty Acid Elongation, Saturated Fatty A	-0.3398303	6	3.942e-03		ELOVL7:380 ELOVL3:1063 ELOVL4:1247 ELOVL2:3097 ELOVL5:4785 ELOVL6:4982
Fatty Acid Elongation, Unsaturated Fatty	-0.3398303	6	3.942e-03		ELOVL7:380 ELOVL3:1063 ELOVL4:1247 ELOVL2:3097 ELOVL5:4785 ELOVL6:4982
Histone Lysine Demethylation (GO:0070076	0.3309140	5		3.217e-01	KDM4C:744 KDM3B:2629 KDM6B:2798 JMJD1C:3103 KDM3A:4400 NA
Mitochondrial Translational Elongation (0.3302657	5	1.054e-02		GFM1:592 TSFM:1124 GFM2:1260 TUFM:4235 MRPL44:6555 NA
Cell Surface Pattern Recognition Recepto	-0.3266464	4	2.366e-02		COLEC10:754 EHHADH:2582 COLEC11:3615 FFAR2:4233 NA NA
Positive Regulation Of Sterol Transport	-0.3258953	4	2.398e-02		ABCB4:1 NR1H3:1971 LIPG:3257 NR1H2:6000 NA NA
Gamma–Aminobutyric Acid Transport (GO:00	-0.3233178	6		2.450e-01	SLC6A6:357 SLC6A11:619 SLC6A13:2926 SLC6A1:3482 SLC9A3R1:4439 SLC6A12:53
Glutamate Catabolic Process (GO:0006538)	-0.3188790	4	2.719e-02		GLUD1:39 GAD2:1542 GAD1:1704 GLUL:8451 NA NA
Mitochondrial Fragmentation Involved In	-0.3186327	7	3.507e-03		BAX:80 ERBB4:420 FIS1:481 MFF:963 VPS35:3470 CCAR2:5538
Regulation Of Cilium Beat Frequency (GO:	0.3148482	5	1.476e-02		CCDC40:942 CFAP43:1925 CYB5D1:2281 CFAP206:4199 DNAH11:5677 NA
Negative Regulation Of Meiotic Cell Cycl	0.3141750	4	2.954e-02		DUSP1:38 FBXO5:600 FBXO43:603 NPPC:10850 NA NA
Regulation Of Osteoclast Development (GO	0.3131473	4	3.007e-02		SIGLEC15:136 TYROBP:2171 NOTCH2:3504 FBXW7:6319 NA NA
Regulation Of Relaxation Of Muscle (GO:1	-0.3120949	3	6.117e-02		SRI:565 TIFAB:2396 NEUROG1:6158 NA NA NA
Neurotransmitter–Gated Ion Channel Clust	-0.3079538	5		4.136e-01	SHISA7:805 SHANK3:1064 GPHN:2720 NI GN1:4963 THEPL4:5954 NA
Intracellular Sequestering Of Iron Ion (-0.3073254	3	6.523e-02		FTH1:52 SRI:565 FTMT:8768 NA NA NA
Transcription Initiation At RNA Polymera	0.3063045	6	9.367e-03		TAF1C:1184 RRN3:1372 POLR1E:1835 TAF1B:1906 UBTF:6172 TAF1:6432
Negative Regulation Of Lymphocyte Apopto	0.3046263	8	2.848e-03		PIP:21 BCL6:280 NOC2L:1085 ORMDL3:1387 CCL5:1892 FOXP1:2034
Cilium Movement Involved In Cell Motilit					TEKT3:1127 RSPH9:1231 TEKT2:1391 TEKT1:1837 GAS8:2883 TEKT4:3364
Glycerol–3–Phosphate Metabolic Process (0.3032015 -0.3030835	7 5	5.469e-03 1.892e-02		GPAM:630 GPD1:2336 GK5:2502 GPAT2:3709 GCK:6747 NA
		5			
Positive Regulation Of Intracellular Est	0.3015813	5	1.952e-02		WBP2:304 KMT2D:700 PAK1:3931 YAP1:4527 PAGR1:6630 NA
Mitochondrial RNA Processing (GO:0000963	0.3010563	9	1.763e-03		PNPT1:397 FASTKD5:477 FASTKD1:925 FASTKD3:1985 FASTKD2:2508 TRMT10C:26
Podocyte Cell Migration (GO:0090521)	0.2989089	5	2.062e-02		KANK2:1771 KANK1:1888 ROCK1:1994 DAAM2:4924 TESK1:5755 NA
Negative Regulation Of Alpha–Beta T Cell	0.2982921	6	1.139e-02 2.163e-02		HFE:490 VSIR:2438 TWSG1:3129 IHH:3668 DAPL1:4453 GLI3:5442

EnrichmentHsSymbolsFile2 Top pathways by permulation

JAK1:12 PTPN11:569 IL6:957 TYK2:1799 IL6ST:4709 MAPK3:5071

JUN:1202 CRYAB:3288 HMOX1:4059 HSPB1:6833 NA NA

HM13:509 MAFK:1180 HMOX1:4059 NFE2L2:4315 BACH1:9362 NA

Compact	0404	num donos	nyal	n od:	grava vala
Geneset	stat	num.genes	pval	p.adj	gene.vals
REACTOME_FORMYL_PEPTIDE_RECEPTORS_BIND_F	-0.3863608	4	7.443e-03		APP:1047 FPR2:1347 HEBP1:2276 ANXA1:2662 NA NA
MATZUK_STEROIDOGENESIS	-0.3641491	6	2.007e-03		VDR:170 STAR:566 DHCR24:1391 CYP11A1:2512 CYP19A1:3964 NR5A2:4562
CASTELLANO_HRAS_TARGETS_DN	0.3599077	4	1.266e-02		OPRM1:583 RAMAC:676 SBF2:3158 C1QTNF12:4671 NA NA
REACTOME_RRNA_PROCESSING_IN_THE_MITOCHON	0.3575435	9		2.967e-02	PRORP:206 NSUN4:697 MRM1:1141 MRM3:1501 HSD17B10:2115 TRMT10C:2617
REACTOME_SPERM_MOTILITY_AND_TAXES	0.3533245	8			CATSPERB:28 CATSPERG:386 CATSPER4:1342 KCNU1:2451 CATSPER3:3542 CATSPERD:3640
REACTOME_RRNA_MODIFICATION_IN_THE_MITOCH	0.3487287	5	6.919e-03		NSUN4:697 MRM1:1141 MRM3:1501 TFB1M:4022 MRM2:4915 NA
WP_EFFECT_OF_INTESTINAL_MICROBIOME_ON_AN	-0.3417619	7	1.739e-03		VDR:170 NR1I2:265 CD36:694 PPARD:2995 PPARA:3331 SCARB1:4594
REACTOME_DISINHIBITION_OF_SNARE_FORMATIO	-0.3372170	5	9.013e-03		STX4:106 PRKCB:2222 STXBP3:2337 PRKCG:4141 PRKCA:4334 NA
REACTOME_FATTY_ACIDS	-0.3358945	2	9.989e-02		CYP2F1:1364 CYP4B1:3932 NA NA NA NA
REACTOME_FLT3_SIGNALING_THROUGH_SRC_FAMI	0.3354586	5	9.378e-03	2.412e-01	LCK:1423 FLT3:1841 HCK:1964 FYN:2208 SYK:5921 NA
REACTOME_ABACAVIR_TRANSMEMBRANE_TRANSPOR	-0.3283157	4	2.295e-02	3.376e-01	ABCB1:580 SLC22A3:2129 SLC22A2:2581 SLC22A1:5789 NA NA
REACTOME_ATORVASTATIN_ADME	-0.3142441	5	1.495e-02	2.795e-01	PON3:159 ABCB1:580 PON1:1819 SLCO2B1:2632 SLCO1B1:9829 NA
BIOCARTA_BBCELL_PATHWAY	0.3136387	7	4.055e-03	1.656e-01	CD40:604 FASLG:809 HLA-DRA:947 FAS:3714 CD28:4204 CD40LG:5435
TOMIDA_LUNG_CANCER_POOR_SURVIVAL	-0.2974826	5	2.123e-02	3.295e-01	TYMS:233 CKAP4:1274 DNER:1308 DAD1:6311 DLX4:7223 NA
MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_7	0.2951905	6	1.227e-02	2.672e-01	BCL6:280 MECOM:649 TFRC:1005 LPP:1063 PIK3CA:1860 EIF4A2:15061
HOFFMAN_CLOCK_TARGETS_UP	-0.2919137	7	7.478e-03	2.119e-01	CD36:694 JUN:1202 HOXA7:1767 ANXA1:2662 MIF:2840 TNFRSF11B:5092
CHEN_HOXA5_TARGETS_6HR_DN	0.2909551	5	2.424e-02	3.464e-01	ZBED8:408 TUBA1A:1992 PRPF31:4196 NPTXR:4836 FJX1:5551 NA
MATZUK_PREOVULATORY_FOLLICLE	-0.2901879	8	4.477e-03	1.741e-01	SOX3:81 SH2B1:615 IMMP2L:1297 SOD1:1571 ESR1:2584 ADAMTS1:5196
REACTOME_ERYTHROCYTES_TAKE_UP_OXYGEN_AND	-0.2893078	6	1.412e-02	2.765e-01	CA2:716 SLC4A1:1754 AQP1:2091 RHAG:2641 CA4:4955 CA1:8255
REACTOME_SYNTHESIS_OF_16_20_HYDROXYEICOS	-0.2891974	4	4.514e-02	4.493e-01	CYP2U1:1554 CYP1A1:2835 CYP1A2:3445 CYP1B1:5768 NA NA
REACTOME_ESTROGEN_STIMULATED_SIGNALING_T	0.2881538	4	4.593e-02	4.535e-01	PDPK1:250 NRAS:1928 KRAS:4814 MAPK1:6776 NA NA
WP_PHASE_I_BIOTRANSFORMATIONS_NON_P450	-0.2828663	6	1.641e-02	2.918e-01	PON3:159 PON2:321 ESD:867 PON1:1819 LIPA:3705 CES5A:14219
RAFFEL_VEGFA_TARGETS_DN	-0.2824668	5	2.870e-02	3.731e-01	HEY1:175 TLX1:540 IL18R1:2734 HES1:4636 NKX2-5:9498 NA
REACTOME_DEX_H_BOX_HELICASES_ACTIVATE_TY	-0.2790811	7	1.055e-02	2.559e-01	IRF7:1104 NFKB1:1917 DHX36:2638 NFKB2:4401 DHX9:4520 RELA:4722
REACTOME_SIGNALING_BY_MEMBRANE_TETHERED_	0.2782796	5	3.115e-02	3.894e-01	BIN2:108 GOLGA4:113 KANK1:1888 ETV6:5744 KDR:10164 NA
CROSBY_E2F4_TARGETS	0.2763827	6	1.904e-02	3.144e-01	BUB1B:680 NDC80:758 CHEK1:3852 PTTG1:4846 CENPE:5503 CDC6:6164
SASSON_FSH_RESPONSE	-0.2752988	4	5.652e-02	4.892e-01	VEGFA:290 STAR:566 FDX1:5487 GDE1:8175 NA NA
REACTOME_DISEASES_OF_BASE_EXCISION_REPAI	0.2750158	5	3.318e-02	3.972e-01	NEIL3:33 NEIL1:3712 OGG1:4565 MUTYH:4595 NTHL1:5376 NA
WP_CONVERSION_OF_ANGIOTENSINOGEN_TO_ANGI	0.2704697	3	1.047e-01	5.801e-01	CTSD:1168 ACE:4381 REN:5635 NA NA NA
TESAR_ALK_TARGETS_HUMAN_ES_5D_UP	-0.2691208	5	3.714e-02	4.242e-01	MSX1:201 PAX6:818 GBX2:1450 SOX1:3879 ZIC1:12330 NA
REACTOME_ORGANIC_ANION_TRANSPORTERS	-0.2690857	10	3.212e-03	1.555e-01	SLC25A18:26 SLC17A5:1377 SLC17A1:2067 SLC5A8:2410 SLC17A6:3312 SLC17A7:3958
REACTOME_MAPK1_ERK2_ACTIVATION	-0.2690329	9	5.190e-03	1.813e-01	JAK1:12 PTPN11:569 IL6:957 TYK2:1799 MAP2K2:4615 IL6ST:4709
GHANDHI_BYSTANDER_IRRADIATION_DN	0.2690113	11	2.005e-03	1.173e-01	EPHA4:421 CNKSR3:1256 EPHB3:1379 SLC5A3:1949 WWOX:2290 USP41:3510
BIOCARTA_PEPI_PATHWAY	0.2667094	7	1.453e-02		CELA1:1591 CELA2A:2183 CELA2B:3179 GRN:3418 ELANE:4118 CELA3B:4415
BIOCARTA_ERBB4_PATHWAY	-0.2656069	7	1.494e-02		ERBB4:420 PSEN1:1449 NRG3:1518 PRKCB:2222 ADAM17:2869 PRKCA:4334
REACTOME_NA_CL_DEPENDENT_NEUROTRANSMITTE	-0.2646073	19		1.283e-02	SLC6A14:117 SLC6A20:275 SLC6A5:320 SLC6A6:357 SLC6A11:619 SLC18A1:790
REACTOME BIOSYNTHESIS OF MARESIN LIKE SP	-0.2631695	2	1.973e-01		CYP1A2:3445 CYP2E1:4195 NA NA NA
	5.2551000	-		3.0000	

DisGeNET Top pathways by permulation

4.050e-03 1.656e-01

6.976e-02 5.225e-01

4.436e-02 4.493e-01

REACTOME_MAPK3_ERK1_ACTIVATION

STANHILL_HRAS_TRANSFROMATION_UP

REACTOME_REGULATION_OF_HMOX1_EXPRESSION_ -0.2596205

-0.2624739

-0.2617956

Geneset	stat	num.genes	pval	p.adj	gene.vals
Aspartylglucosaminuria	0.4802489	2	1.865e-02	5.158e-01	AGA:195 FN1:452 NA NA NA NA
CHORIORETINAL ATROPHY, PROGRESSIVE BIFOC	-0.4319675	3	9.559e-03	4.596e-01	RIMS1:96 ELOVL4:1247 IMPG1:1970 NA NA NA
Hyperamylasemia	-0.4180195	2	4.060e-02	5.666e-01	AMY1C:578 MYCBP:2086 NA NA NA NA
Fibrous bands	-0.3891363	5	2.582e-03	3.333e-01	BAX:80 SDHB:1050 SDS:1388 SARDH:2602 BCL2:3820 NA
CYSTIC FIBROSIS MODIFIER 1	-0.3783439	4	8.774e-03	4.568e-01	SLC6A14:117 SLC9A3:651 SLC26A9:2704 TGFB1:4367 NA NA
GLIOMA SUSCEPTIBILITY 1	0.3677490	3	2.737e-02	5.374e-01	IDH2:943 ERBB2:1624 TP53:4018 NA NA NA
Mitochondrial Complex II Deficiency	-0.3676152	6	1.818e-03	2.903e-01	SDHA:554 SDHB:1050 SDS:1388 SDHD:1694 SARDH:2602 SDHAF1:5504
Campylobacter jejuni infection	0.3626723	3	2.958e-02	5.468e-01	IRF6:1581 CD14:1613 TLR4:3653 NA NA NA
Atrial Flutter	0.3624758	5	4.999e-03	4.457e-01	NUP155:727 SCN3B:1651 TNNI3K:2330 SCN5A:3232 LMNA:3481 NA
Fibrous histiocytoma of tendon sheath	0.3612765	4	1.233e-02	4.841e-01	CSF1R:55 CSF2:739 CSF1:3475 NTRK1:4934 NA NA
Pneumonia, Viral	0.3594620	2	7.827e-02	6.508e-01	BCL6:280 ACE:4381 NA NA NA NA
Obsessions	-0.3570103	7	1.072e-03	2.503e-01	BDNF:3 SLC1A1:494 SLC6A4:1413 ESR1:2584 SCLY:3651 TAL1:3769
Abnormality of the pancreas	0.3568778	5	5.715e-03	4.462e-01	FGFR2:367 NPHP3:798 TTC37:2441 ASXL1:3479 KLHL7:4789 NA
Bacterial sepsis of newborn	-0.3542826	2	8.267e-02	6.626e-01	IL6:957 ST14:3741 NA NA NA NA
Hydroa Vacciniforme	-0.3531818	5	6.236e-03	4.462e-01	PLK2:738 CCR4:784 ERCC6:792 UVSSA:3293 ERCC8:6207 NA
Myelitis	0.3516972	5	6.457e-03	4.462e-01	AQP4:360 POU2F3:531 CSF2:739 S100B:4405 LAMC2:6238 NA
Thickening of pleura	-0.3516700	4	1.485e-02	4.913e-01	MTAP:354 SERPINE1:1952 TGFA:2876 TGFB1:4367 NA NA
Hemorrhagic Fever, Crimean	-0.3466692	3	3.755e-02	5.649e-01	CCR5:741 NFKB1:1917 ISG15:4743 NA NA NA
Intestinal Diseases, Parasitic	-0.3451175	4	1.682e-02	5.129e-01	HSP90AA1:447 MST1:1979 LMLN:3701 IL33:3845 NA NA
Central opacification of the cornea	-0.3439191	4	1.721e-02	5.129e-01	PAX6:818 FOXC1:976 PITX2:2494 CYP1B1:5768 NA NA
Thinning of Descemet membrane	-0.3439191	4	1.721e-02	5.129e-01	PAX6:818 FOXC1:976 PITX2:2494 CYP1B1:5768 NA NA
Peroxisome Biogenesis Disorder, Compleme	0.3429135	5	7.917e-03	4.541e-01	FGFR1:19 CCND1:638 ERBB2:1624 BRCA1:3438 PEX13:7256 NA
Glycogen Storage Disease Type IV	-0.3404196	8	8.553e-04	2.423e-01	DES:339 GBE1:720 KCNJ6:760 RBCK1:1265 KCNJ3:1506 KCNJ12:3322
Diamond-Blackfan Anemia 1	0.3360263	3	4.382e-02	5.718e-01	RPS7:1743 RPL11:1881 RPS19:4543 NA NA NA
Decreased size of facial bones	0.3351659	5	9.443e-03	4.596e-01	ZMPSTE24:1137 DYM:1315 CEP120:2409 LMNA:3481 FIG4:5313 NA
Flattening of facial bones	0.3351659	5	9.443e-03	4.596e-01	ZMPSTE24:1137 DYM:1315 CEP120:2409 LMNA:3481 FIG4:5313 NA
Hypoplastic facial bones	0.3351659	5	9.443e-03	4.596e-01	ZMPSTE24:1137 DYM:1315 CEP120:2409 LMNA:3481 FIG4:5313 NA
Hypotrophic facial bones	0.3351659	5	9.443e-03	4.596e-01	ZMPSTE24:1137 DYM:1315 CEP120:2409 LMNA:3481 FIG4:5313 NA
Underdevelopment of facial bones	0.3351659	5	9.443e-03	4.596e-01	ZMPSTE24:1137 DYM:1315 CEP120:2409 LMNA:3481 FIG4:5313 NA
Patchy palmoplantar keratoderma	-0.3338823	5	9.720e-03	4.596e-01	GJB3:47 GJB4:1857 GJA1:2121 DSP:3645 KDSR:5694 NA
Transposition of the Great Arteries, Dex	0.3323927	3	4.615e-02	5.775e-01	DVL2:17 MED13L:2725 HSPG2:5567 NA NA NA
Recurrent respiratory papillomatosis	0.3310264	6	4.984e-03	4.457e-01	CCL22:533 CCL1:613 CD274:850 CCL20:1456 TAP1:4991 SEC14L2:8287
Fetal Diseases	0.3271089	5	1.130e-02	4.719e-01	BCS1L:704 CHUK:707 S100A8:1986 BPI:2638 PRSS8:8209 NA
Klippel-Trenaunay-Weber Syndrome	0.3256398	5	1.168e-02	4.773e-01	ROGDI:359 PIK3CA:1860 IGF2:2496 AGGF1:3359 SMOC1:6354 NA
Calcium Pyrophosphate Dihydrate Depositi	-0.3239330	4	2.484e-02	5.273e-01	ANK1:429 CILP:1445 TGFB1:4367 ANKH:5052 NA NA
Ophthalmia, Sympathetic	0.3213816	4	2.600e-02	5.296e-01	MLANA:564 CD274:850 RBM45:5158 PDCD1:5247 NA NA
Vegetative State	-0.3206159	3	5.443e-02	5.959e-01	BDNF:3 NAGA:4223 RUNX1T1:4408 NA NA NA
Male Germ Cell Tumor	0.3201809	5	1.316e-02	4.913e-01	KIT:436 BCL10:527 FAS:3714 TP53:4018 DICER1:6191 NA
Anterior synechiae	-0.3190020	6	6.808e-03	4.462e-01	PAX6:818 FOXC1:976 PITX2:2494 OVOL2:2572 VSX1:4839 CYP1B1:5768
Anterior Horn Cell Disease	-0.3184349	6	6.907e-03	4.462e-01	PNPLA6:522 PRDX3:864 SOD1:1571 VIM:1865 GLE1:5400 SMN1:7302

GSEA-c5-HsSymbols Top pathways by permulation

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GOCC_NASCENT_POLYPEPTIDE_ASSOCIATED_COMP	0.4459899	2	2.891e-02	3.375e-01	NACA:216 BTF3:1544 NA NA NA NA
GOMF_TYPE_I_INTERFERON_RECEPTOR_BINDING	0.4329770	2	3.393e-02	3.642e-01	IFNE:766 IFNK:1416 NA NA NA NA
GOBP_REGULATION_OF_INTEGRIN_BIOSYNTHETIC	-0.4303278	3	9.834e-03	2.079e-01	TGFB2:622 NOX1:705 TMEFF2:2055 NA NA NA
GOBP_GLIAL_CELL_FATE_SPECIFICATION	-0.4157049	5	1.285e-03	6.060e-02	SOX9:263 PAX6:818 OLIG2:1606 NKX2-2:1723 ASCL1:2401 NA
GOBP_PHENYLPROPANOID_METABOLIC_PROCESS	-0.4071172	2	4.612e-02	4.120e-01	PON3:159 CYP1A1:2835 NA NA NA NA
GOBP_INTEGRIN_BIOSYNTHETIC_PROCESS	-0.4051793	4	5.005e-03	1.449e-01	TGFB2:622 NOX1:705 TMEFF2:2055 COL5A1:2741 NA NA
GOBP_NEGATIVE_REGULATION_OF_ATPASE_COUPL	0.3963285	2	5.221e-02	4.293e-01	THADA:18 TLR9:3353 NA NA NA NA
HP_ANTERIOR_BEAKING_OF_LUMBAR_VERTEBRAE	0.3935591	4	6.407e-03	1.684e-01	AGA:195 GALNS:650 GLB1:2856 GUSB:3206 NA NA
GOBP VERY LONG CHAIN FATTY ACID CATABOLI	-0.3935569	7	3.109e-04	2.129e-02	SLC27A2:155 SLC27A4:284 ACOX1:922 ABCD2:1256 ABCD3:1348 ABCD4:1691
GOBP_ESTABLISHMENT_OF_LEFT_RIGHT_ASYMMET	0.3893260	4	6.999e-03	1.732e-01	ENKUR:199 CFAP52:231 CFAP45:1333 CCDC39:5450 NA NA
GOMF_NEUTRAL_L_AMINO_ACID_SODIUM_SYMPORT	-0.3840163	8	1.689e-04	1.384e-02	SLC38A3:286 SLC6A5:320 SLC38A7:1075 SLC6A15:1451 SLC38A1:1695 SLC6A9:2106
GOBP_CELLULAR_RESPONSE_TO_AMMONIUM_ION	-0.3813600	5	3.143e-03		KCNC2:54 CPS1:351 SLC1A1:494 GRIA1:3528 ASS1:5151 NA
HP_CHRONIC_GASTRITIS	0.3808401	3	2.233e-02	3.103e-01	FOCAD:1619 IPO8:2015 ELF4:2184 NA NA NA
GOMF_RRNA_CYTOSINE_METHYLTRANSFERASE_ACT	0.3765770	4	9.092e-03		NSUN4:697 NOP2:1824 NSUN5:2490 METTL15:3019 NA NA
GOMF_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_P	-0.3737551	2	6.712e-02		CYP2U1:1554 CYP11A1:2512 NA NA NA NA
GOCC_RNA_POLYMERASE_I_COMPLEX	0.3737463	8	2.514e-04		POLR1B:560 POLR2H:784 POLR1D:1110 POLR1A:1497 POLR1E:1835 POLR2F:2332
GOMF_RNA_POLYMERASE_I_ACTIVITY	0.3737463	8	2.514e-04		POLR1B:560 POLR2H:784 POLR1D:1110 POLR1A:1497 POLR1E:1835 POLR2F:2332
GOMF_HISTAMINE_RECEPTOR_ACTIVITY	-0.3727808	6	1.565e-03		HRH4:119 HRH1:912 HTR6:1125 HRH2:1211 ZNF219:3985 HRH3:4956
HP_OSTEOLYTIC_DEFECTS_OF_THE_DISTAL_PHAL	0.3718773	5	3.977e-03		CTSK:174 ZMPSTE24:1137 BANF1:2321 MTX2:3299 LMNA:3481 NA
GOBP_RESPONSE_TO_AMMONIUM_ION	-0.3651547	6	1.950e-03		KCNC2:54 CPS1:351 SLC1A1:494 ADSS2:3481 GRIA1:3528 ASS1:5151
GOBP_TOLERANCE_INDUCTION_DEPENDENT_UPON_	0.3600764	4	1.262e-02		CD274:850 AIRE:2136 HAVCR2:2251 FOXP3:3865 NA NA
GOCC_CATSPER_COMPLEX	0.3569377	13			CATSPERB:28 CATSPERG:386 CATSPERE:447 TMEM249:895 CATSPER4:1342 C2CD6:14
GOBP SCHWANN CELL MIGRATION	0.3567895	4	1.345e-02		NF1:85 RRAS:940 CERS2:3093 RRAS2:5199 NA NA
GOBP_REGULATION_OF_GLUCOSYLCERAMIDASE_AC	-0.3564268	2	8.082e-02		SCARB2:2196 ATP13A2:2427 NA NA NA NA
HP_GLUCOCORTOCOID_INSENSITIVE_PRIMARY_HY	-0.3512252	5	6.527e-03		SCNN1G:728 SCNN1B:1634 KCNJ5:1689 CLCN2:2186 SCNN1A:5771 NA
GOBP_ICOSANOID_CATABOLIC_PROCESS	0.3507338	5	6.603e-03		DPEP2:407 DPEP1:666 ABHD16A:1224 LYPLA2:3331 HPGD:6497 NA
GOBP_C_5_METHYLATION_OF_CYTOSINE	0.3494721	5	6.800e-03		DNMT3A:525 DNMT3L:1060 DNMT1:3196 DNMT3B:3508 STPG4:3941 NA
GOMF ARYLESTERASE ACTIVITY	-0.3490835	6	3.063e-03		PON3:159 PON2:321 CA2:716 PON1:1819 APMAP:3372 CA1:8255
GOMF_OPSONIN_RECEPTOR_ACTIVITY	0.3485890	4	1.575e-02		C3AR1:1117 CD14:1613 C5AR2:2252 C5AR1:4878 NA NA
GOBP_NEGATIVE_REGULATION_OF_IRE1_MEDIATE	0.3482104	5	7.003e-03		HSPA5:626 UFL1:690 BFAR:691 DDRGK1:1046 DNAJB9:9261 NA
GOBP GLUTAMATE BIOSYNTHETIC PROCESS	-0.3459827	4	1.655e-02		GLUD1:39 GLS:2892 GLS2:2947 SLC25A12:4049 NA NA
HP HIGH FREQUENCY SENSORINEURAL HEARING	0.3456206	5	7.437e-03		CEP250:1073 ZMPSTE24:1137 ASAH1:2322 LMNA:3481 FKBP14:4542 NA
GOBP_SPINDLE_ASSEMBLY_INVOLVED_IN_FEMALE	0.3455085	6	3.378e-03		FBXO5:600 NDC80:758 SEPTIN1:2112 AURKA:2650 CCNB2:2705 TUBB8:6229
GOBP_L_GLUTAMINE_IMPORT_ACROSS_PLASMA_ME	-0.3449535	4	1.687e-02		SLC38A3:286 SLC38A1:1695 SLC38A2:3348 SLC38A5:4678 NA NA
HP_THINNING_OF_DESCEMET_MEMBRANE	-0.3431768	4 5	7.867e-02		PAX6:818 FOXC1:976 PITX2:2494 OVOL2:2572 CYP1B1:5768 NA
GOMF_GAMMA_AMINOBUTYRIC_ACID_SODIUM_CHLO	-0.3431708	5	7.867e-03 7.981e-03		SLC6A6:357 SLC6A11:619 SLC6A13:2926 SLC6A1:3482 SLC6A12:5318 NA
GOBP_LIPID_TRANSPORT_ACROSS_BLOOD_BRAIN_		5			FABP5:249 SLC27A4:284 CD36:694 SLC27A1:1019 MFSD2A:4992 APOE:8150
	-0.3412693	6	3.790e-03		
HP_LEG_DYSTONIA GOMF_OLEATE_TRANSMEMBRANE_TRANSPORTER_AC	0.3411586 -0.3406716	6 6	3.802e-03 3.852e-03		AOPEP:957 GFM2:1260 PARK7:2151 KMT2B:2667 VPS16:2809 ACTB:5651 SLC27A2:155 SLC27A4:284 CD36:694 SLC27A1:1019 MFSD2A:4992 SLC27A6:83

MGI_Mammalian_Phenotype_Level_4 Top pathways by permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
MP0004043 abnormal pH regulation	-0.25717480	14	8.725e-04	4.153e-02	RHCG:529 SLC4A10:553 SLC9A3:651 SLC26A7:749 SCNN1B:1634 HIF1AN:1831
MP0003656 abnormal erythrocyte physiolo	-0.22907123	22	2.040e-04	2.428e-02	ANK1:429 KCNN4:638 NCKAP1L:891 PFKM:1129 FECH:1669 SLC4A1:1754
MP0003136 yellow coat color	0.22042753	7	4.351e-02	2.904e-01	EDA:529 SOX2:1895 MITF:2955 ADAMTS20:3574 EDNRB:5085 OCA2:8643
MP0000566 synostosis	0.21600428	8	3.446e-02	2.690e-01	FGFR2:367 IRF6:1581 LRP5:1830 FGF9:4905 GLI3:5442 ELAVL1:5611
MP0002139 abnormal hepatobiliary system	-0.21086188	8	3.899e-02	2.770e-01	ABCB4:1 INSIG1:1946 NR1H3:1971 FABP1:4712 ALDH1A1:5488 ABCG8:5573
MP0005360 urolithiasis	-0.20441642	8	4.537e-02	2.904e-01	SLC2A9:1771 SLC7A9:2518 SLC3A1:3874 SLC26A1:4221 CAV1:4424 SLC26A6:5283
MP0005423 abnormal somatic nervous	-0.19394250	12	2.010e-02	2.057e-01	DBX1:228 CNTN2:1313 TAS1R2:1320 EGR3:3090 TAS1R1:3338 L1CAM:3511
MP0000015 abnormal ear pigmentation	0.17748517	17	1.138e-02	1.868e-01	ACD:639 POLH:742 HPS6:2001 MITF:2955 GNA11:4169 AP3B1:4341
MP0001346 abnormal lacrimal gland	-0.17262127	14	2.546e-02	2.420e-01	CTNND1:5 CCR7:665 FOXC1:976 OTX1:1016 PRLR:2013 NCDN:2249
MP0002132 abnormal respiratory system	0.15152282	14	4.985e-02	3.042e-01	CBY1:135 EDA:529 PRDX6:1988 HOXA3:2920 TLR4:3653 CFTR:4184
MP0002876 abnormal thyroid physiology	0.14793402	18	2.998e-02	2.548e-01	HPN:292 THRB:1755 RUNX2:1955 GHR:2027 AIRE:2136 MED1:2595
MP0002102 abnormal ear morphology	-0.14783594	12	7.641e-02	3.844e-01	BMP5:185 DLX6:1346 TMC1:2273 CASP3:2562 TYRP1:3165 EXT1:3578
MP0003693 abnormal embryo hatching	0.14665017	24	1.303e-02	1.951e-01	HINFP:65 ATF1:278 HSPA5:626 CDX2:1115 CDCA8:1409 RBBP8:1476
MP0003787 abnormal imprinting	0.14135940	10	1.219e-01	4.875e-01	RB1:753 ATRX:961 RASGRF1:2512 ARID4B:3389 SMCHD1:6415 ARID4A:7142
MP0002332 abnormal exercise endurance	-0.13890966	30	8.588e-03	1.849e-01	SLC6A6:357 IL6:957 PFKM:1129 APLNR:1131 PPARGC1B:1155 SLC18A3:1512
MP0005174 abnormal tail pigmentation	0.13768084	17	4.962e-02	3.042e-01	KIT:436 MITF:2955 GNA11:4169 AP3B1:4341 RPS19:4543 LYST:5027
MP0005257 abnormal intraocular pressure	-0.13655493	10	1.351e-01	4.984e-01	BEST2:725 PAX6:818 VAV2:3170 EXT1:3578 BMP4:4708 SH3PXD2B:5569
MP0004233 abnormal muscle weight	-0.13456609	16	6.265e-02	3.389e-01	SLC6A6:357 GRB10:1020 TLL2:1533 DAG1:1640 BCKDK:2387 SGCA:3412
MP0002735 abnormal chemical nociception	-0.13136611	28	1.633e-02	2.010e-01	P2RX3:643 GRIK1:866 GRIA2:2628 ADCY8:2735 HTR3A:2893 CACNA1B:3196
MP0002736 abnormal nociception after	-0.12220469	22	4.755e-02	2.978e-01	PRKAR1B:304 TRPM8:2080 CSRP2:2384 ESR1:2584 GRIA2:2628 PTGS2:3266
MP0006054 spinal hemorrhage	0.11819649	9	2.198e-01	6.028e-01	FBLN1:917 C1GALT1C1:1560 FLI1:3244 C1GALT1:4656 COL1A1:5552 TFPI:7109
MP0004147 increased porphyrin level	0.11787975	8	2.485e-01	6.327e-01	KIT:436 HFE:490 EXOC6:747 HEPH:849 HMBS:7371 KCNA1:11353
MP0001188 hyperpigmentation	0.11774674	10	1.976e-01	5.631e-01	KIT:436 BRAF:719 TERF1:3954 GNA11:4169 KRAS:4814 GNAQ:5566
MP0004185 abnormal adipocyte glucose	-0.11604225	15	1.201e-01	4.843e-01	NPY1R:40 FABP5:249 MARK2:2194 FABP4:2750 PPARG:2865 E2F1:3386
MP0003122 maternal imprinting	-0.11342580	14	1.421e-01	4.988e-01	IGF2R:1094 DIO3:1783 IGF1R:2576 SGCE:2668 DLK1:3034 MEST:3095
MP0000685 abnormal immune system	0.11269188	38	1.650e-02	2.010e-01	BCL6:280 CMKLR1:315 IL15:550 TNFSF11:872 TRAF3IP2:991 LIG4:1143
MP0004145 abnormal muscle electrophysio	0.11243865	15	1.320e-01	4.982e-01	DMD:235 SCYL1:934 TRDN:1679 CHN2:2108 FBN2:4859 HSPG2:5567
MP0004264 abnormal extraembryonic tissu	0.11238575	19	9.030e-02	4.249e-01	XBP1:227 RB1:753 HEPH:849 CUBN:954 NCOA6:1148 STK3:1477
MP0003646 muscle fatigue	0.11215582	9	2.442e-01	6.284e-01	MB:2688 NOS1:4206 COX10:4219 PPARGC1A:5304 MTMR14:6054 SLC2A4:6623
MP0008007 abnormal cellular replicative	0.11036609	29	4.006e-02	2.804e-01	TPP1:295 BRCA2:684 FLT3:1841 PA2G4:1867 BMI1:1975 MAPKAPK5:2174
MP0001756 abnormal urination	-0.10961188	81	6.958e-04	3.680e-02	VDR:170 SCNN1G:728 SLC26A7:749 AQP2:804 CLCN5:936 DRD3:947
MP0002877 abnormal melanocyte morpholog	0.10705773	10	2.414e-01	6.278e-01	KIT:436 RB1:753 MITF:2955 LMNA:3481 KRAS:4814 CDKN2A:7179
MP0001958 emphysema	0.10551453	21	9.461e-02	4.249e-01	EFEMP2:180 KL:646 CSF2:739 WWTR1:870 HCK:1964 FLNA:2607
MP0000681 abnormal thyroid gland	0.10465552	43	1.790e-02	2.010e-01	CTSK:174 FGFR2:367 SMAD2:566 FBLN1:917 HHEX:1040 THRB:1755
MP0008877 abnormal DNA methylation	0.10324618	16	1.532e-01	5.237e-01	DNMT3A:525 RB1:753 UHRF1:1665 AMHR2:1954 RASGRF1:2512 ARID4B:3389
MP0003943 abnormal hepatobiliary system	0.10149257	53	1.088e-02	1.849e-01	NF1:85 TGFBR3:184 XBP1:227 FGFR2:367 SMAD2:566 MECOM:649

4.487e-02 2.904e-01

2.761e-01 6.551e-01

1.394e-02 1.951e-01

1.306e-02 1.951e-01

ATP1B2:97 FOXN4:602 RB1:753 NR2E3:1034 RHO:1065 BHLHE23:1855

SGCB:949 SH3BP2:2003 CEBPB:2796 RYR2:4281 SYT7:4325 RELA:4722

BMP5:185 SOX9:263 AGTR2:278 NFIA:660 PAX2:789 AQP2:804

PLA2G4A:620 TGFB2:622 KCNJ6:760 DRD3:947 IL6:957 UCP2:1077

MP0006072 abnormal retinal apoptosis

MP0004510 myositis

MP0000534 abnormal ureter morphology

MP0001905 abnormal dopamine level

0.10111872

-0.09951583

-0.09892224

-0.09800629

10

52