

GO\_Biological\_Process\_2023 Top pathways by permutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
Fatty Acid Catabolic Process (GO:0009062)	-0.19808537	58	1.853e-07	6.390e-04	NUD77:133 ACADS:192 ACOX1:247 ABHD3:262 ACOT8:429 CPT2:489
Metal Ion Transport (GO:0030001)	0.11981291	157	2.372e-07	6.390e-04	KCNAB1:49 CAV1:65 SCN5A:231 KCNK1:269 TUSC3:321 KCNJ3:352
Potassium Ion Transport (GO:0006813)	0.13157259	119	7.495e-07	1.346e-03	KCNAB1:49 KCNH5:117 KCNH1:255 KCNK1:269 KCNJ3:352 KCNF1:373
Potassium Ion Transmembrane Transport (G	0.12008044	132	1.998e-06	2.691e-03	KCNH5:117 KCNH1:4118 KCNH1:255 KCNK1:269 SLCA2A:319 KCNJ4:362
G Protein-Coupled Receptor Signaling Pat	0.10890762	47	6.751e-06	5.196e-03	HTR1B:191 OPRM1:517 NPY1R:542 CCR1:593 HTR4:355 CHRM4:661
RNA Modification (GO:0009451)	-0.19114623	47	5.878e-06	5.196e-03	LCMT2:40 MRM1:86 DTWD1:97 PUS7L:488 WDR4:81 TRMT1:490
Regulation Of Synaptic Transmission, Glu	0.17745290	54	6.567e-06	5.196e-03	HCN1:255 GRIN1:396 CACNA2B:516 SLCA3A2:362 DRD2:954 PTK2B:961
Chemical Synaptic Transmission (GO:00072	0.07969122	254	1.333e-05	6.531e-03	CACNA1B:121 UNC119:145 GLRB:162 HTR1B:191 EXOC4:192 SNAPIN:228
Cilium Movement (GO:0030341)	0.18531102	47	1.121e-05	6.531e-03	HYDIN:46 TEXTS:146 NMES:222 SPEF2:485 CFAP70:503 SPAG6:538
Fatty Acid Beta-Oxidation (GO:0006635)	-0.13407774	47	1.282e-05	6.531e-03	DEC2:5 ACOD3:75 ACADS:411 AMACR:232 ALOX1:247 ACOT8:429
Recombinational Repair (GO:0000725)	-0.13416802	89	1.249e-05	6.531e-03	FBN1:240 SFR1:1253 ERCCA:411 RAD51D:127 ALM3:462 SVSAP1:614
Anterograde Trans-Synaptic Signaling (GO	0.09385747	180	1.488e-05	6.682e-03	CACNA1B:121 UNC119:145 GLRB:162 HTR1B:191 EXOC4:192 GRK1:396
Nuclear Membrane Organization (GO:007176	0.23828460	26	2.618e-05	1.007e-02	GPER1:198 CHMP2:699 VPS4A:855 CHMP7:1048 EENRA:287 CNMB1:1207
Regulation Of Cation Channel Activity (G	0.17230767	50	2.531e-05	1.007e-02	KCNAB1:49 CABP5:68 PIRT:180 HCN1:255 EENRA:287 CNMB1:1207
Nuclear Membrane Reassembly (GO:0031468)	0.26336210	21	2.953e-05	1.061e-02	RCC1:13 CHMP3:699 VPS4A:855 CHMP7:1048 NSF1L:1207 CHMP4C:1804
Double-Strand Break Repair Via Homologou	-0.11633290	105	3.925e-05	1.322e-02	MCMD2C:197 FBN1:240 SFR1:1253 ERCCA:411 RAD51D:127 SLX4:462
Adenylate Cyclase-Inhibiting G Protein-C	-0.10260768	46	5.172e-05	1.431e-02	HTR1B:191 OPRM1:517 NPY1R:542 CHRM4:661 HTR4:1027 OPR1L:912
Double-Strand Break Repair (GO:0006302)	-0.09297876	158	5.752e-05	1.431e-02	FBN1:240 SFR1:1253 ERCCA:411 RAD51D:127 PIAS4:453 SLX4:462
Inorganic Cation Import Across Plasma Me	0.12032186	96	4.742e-05	1.431e-02	SLCA3A:30 KCNJ1:4119 CACNA1B:121 SCN5A:231 SLCA2A:319 KCNJ3:352
Monocarboxylic Acid Transmembrane Transp	0.07115212	73	5.634e-05	1.431e-02	NNT:14 SLCA3A:30 KCNH5:117 SCN5A:231 HCN1:255 KCNJ3:352
Peptidyl-Tyrosine Phosphorylation (GO:00	0.14428612	65	5.844e-05	1.431e-02	PRP:264 TEK:416 EPHB2:470 PRLR:617 PTK2B:961 ABR3:1050
RNA Modification (GO:0006400)	-0.14408863	66	5.252e-05	1.431e-02	LCMT2:40 DTWD1:97 THUMPD2:136 TRMT4A:244 TRMT10A:369 THADA:425
Neuropeptide Signaling Pathway (GO:00072	0.14557495	63	6.541e-05	1.532e-02	GPR83:38 NTS:75 FMR1:138 GLRB:162 OPRM1:517 RXFP3:562 OPR1L:912
Regulation Of Neurotransmitter Receptor	0.18243516	39	8.136e-05	1.827e-02	SHISA8:305 PRRT1:337 OPRM1:517 CACNG7:616 PTK2B:961 CNMB1:2063
Regulation Of Monocarboxylic Acid Transme	0.14515088	61	8.952e-05	1.929e-02	HCN1:255 SHISA8:305 PRRT1:337 WNK3:346 PHB2:347 OPRM1:517
DNA Repair (GO:0006281)	-0.06879692	274	9.569e-05	1.983e-02	MUTYH:38 FBN1:240 ALKBH2:273 MGME1:274 ERCCA:411 RAD51D:127
Regulation Of Potassium Ion Transport (G	0.21065273	28	1.149e-04	2.292e-02	KCNAB1:49 KCNJ3:320 NOS1:623 VIP:789 KCNB2:851 DRD2:954
Cellular Respiration -Containing C	0.05926340	361	1.212e-04	2.332e-02	CIB2:27 IL37:74 LCP1:91 P2RY11:38 LAMTOR4:163 SELENOS:172
Protein Localization To Cell Periphery (G	0.09724065	129	1.413e-04	2.624e-02	EHOD3:9 RDX:36 CAV1:65 P2RY11:38 PRPH2:146 KCNJ3:320
Apical Protein Localization (GO:0034516)	-0.36474397	9	1.512e-04	2.716e-02	INSC:362 SHROOM3:374 SHROOM2:656 CELSR1:1785 MAL:1864 VANGL2:2086
Cardiac Conduction (GO:0061337)	0.16647691	43	1.600e-04	2.781e-02	CAV1:65 BIN1:73 SCN5A:231 HCN1:255 KCNJ3:352 SLCA1:407
Maturation Of SSU--RNA (GO:0030490)	-0.18757746	33	1.933e-04	3.254e-02	WDR4:265 NOL1:312 UTP:662 NOL11:727 SPLP2B:962 NGDN:1076
Glycophospholipid Catabolic Process (GO:	-0.35702741	9	2.082e-04	3.317e-02	GLA:857 NEU1:1230 NEU3:1277 NEU4:1372 HEXB:1598 GM2A:1985
Monocarboxylic Acid Metabolic Process (G	-0.118787246	83	2.093e-04	3.317e-02	DEC2:5 CYP11A:144 MCCC1:74 AMACR:232 NAAA:410 ACSL4:428
Mitochondrial Translation (GO:0032543)	-0.10783731	96	2.665e-04	4.102e-02	GADD45G1P:13 GFM1:37 MRPL58:71 ORSL1:172 MTIF13:419 GFM2:280
Regulation Of Cardiac Muscle Contraction	0.18851776	31	2.819e-04	4.220e-02	RG52:9 SCN5A:231 SLCA1:407 SLCA81:535 NOS1:623 PRKACA:1406
Cardiac Muscle Cell Action Potential (GO	0.19713713	28	3.069e-04	4.352e-02	SCN5A:231 SLCA1:407 SCN3B:937 DMD:1628 KCNE2:2086 PCT2:2170
RNA Methylation (GO:0030488)	-0.17415533	36	3.011e-04	4.352e-02	LCMT2:40 THUMPD2:136 TRMT4A:244 TRMT10A:369 THADA:425 WDR4:481
Fatty Acid Oxidation (GO:0019395)	-0.15139569	47	3.325e-04	4.594e-02	ACADS:192 ACOX1:247 CPT2:489 PHYH:481 ABCD4:528 HAC1:554
Regulation Of Heart Rate By Cardiac Cond	0.16748158	38	3.558e-04	4.793e-02	CAV1:65 BIN1:73 SCN5A:231 HCN1:255 KCNJ3:352 KCNH3:618

EnrichmentHsSymbolsFile2 Top pathways by permutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
NIKOLSKY_BREAST_CANCER_16P13_AMPLICON	-0.30665540	89	6.110e-26	3.964e-22	DEC2:5 RPU5D:115 WFKKM1:28 PSAP6:45 MCRIP2:81 TRAF7:102
BENPORATH_ES_WITH_HKX27ME3	0.00696593	582	2.787e-12	8.976e-09	GN1A1:5 FOXP1:25 TCEA3:47 KCNAB1:49 SLCA2A:319 KCNJ3:352
KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERAC	0.12319696	261	8.105e-12	1.753e-08	GPR83:38 P2RY11:38 GLRB:162 HTR1B:191 ADRA2C:197 GH1:270
MIKKELSEN_MFC_HCP_WITH_HKX27ME3	0.08482257	554	1.105e-11	1.793e-08	SLCA2A:319 POU2F3:105 KCNH5:117 PRDM1A:134 DKKL1:611 NCMPAP:166
REACTOME_GPCR_LIGAND_BINDING	0.09562772	397	7.231e-11	1.938e-08	NTS:75 TAS2R41:97 P2RY11:38 AVP:182 HTR1B:191 ADRA2C:197
REACTOME_CLASS_A_1_RHODOPSIN_LIKE_RECEPT	0.10826196	296	1.652e-10	1.786e-07	NTS:75 P2RY11:38 AVP:182 HTR1B:191 ADRA2C:197 GPER1:198
BLALOCK_ALZHEIMERS_DISEASE_DECN	0.05599409	1127	3.559e-10	3.299e-07	GN1A1:5 RG52:9 NNT:14 PPIA:17 KIFBP:45 KCNAB1:49
REACTOME_SIGNALING_BY_GPCR	0.07306176	624	5.846e-10	4.741e-07	GN1A1:5 RG52:9 PDE1C:20 GPR83:38 NTS:75 GPR27:90
BENPORATH_EED_TARGETS	0.05586783	922	1.196e-08	7.869e-06	GN1A1:5 FOXP1:25 TCEA3:47 KCNAB1:49 SLCA3A:80 CLIP4:107
REACTOME_G_ALPHA_1_SIGNALLING_EVENTS	0.10191345	265	2.123e-08	7.869e-06	GN1A1:5 PDE1C:20 TAS2R41:97 RG52:142 HTR1B:191 ADRA2C:197
REACTOME_NEURONAL_SYSTEM	0.08012928	379	9.413e-08	5.552e-05	KCNAB1:49 KCNH5:117 KCNJ4:118 CACNA1B:121 GLRB:162 PRKCG:215
REACTOME_AININE_LIGAND_BINDING_RECEPTORS	0.22638993	41	1.286e-07	6.936e-05	HTR1B:191 ADRA2C:197 ADRB1:282 TAAR:442 HTR4:635 CHRM4:661
REACTOME_PEPTIDE_LIGAND_BINDING_RECEPTOR	0.11656563	168	1.935e-07	9.899e-05	NTS:75 AVP:182 GPER1:198 EDNRA:287 CCR4:501 OPRM1:517
REACTOME_CARDIAC_CONDUCTION	0.13863595	119	1.801e-07	8.969e-05	SLCA3A:30 KCNJ4:118 SCN5A:231 AHCV1L:257 KCNK1:269 KCNIP3:320
CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_2	0.07630705	395	2.142e-07	9.266e-05	ODF2:16 CFA9P:19 FOXP1:25 SNTN:35 CDC65:52 DNAH6:51
REACTOME_PEROXISOMAL_LIPID_METABOLISM	-0.27479402	29	3.034e-07	1.194e-04	DEC2:5 ACOD3:75 NUDT7:133 AMACR:232 ACOX1:247 ACOT8:429
WP_GPCRS_CLASS_A_RHODOPSINLIKE	0.10357687	206	3.129e-07	1.194e-04	GPR83:38 GPR27:90 AVP:182 GPER1:198 HTR1B:191 ADRA2C:197 GPER1:198
REACTOME_POTASSIUM_CHANNELS	0.15539461	90	3.545e-07	1.278e-04	KCNAB1:49 KCNH5:117 KCNJ4:118 HCN1:255 KCNK1:269 KCNJ3:352
BENPORATH_PRC2_TARGETS	0.06175446	580	4.298e-07	1.432e-04	GN1A1:5 FOXP1:25 TCEA3:47 KCNAB1:49 TAF4A:109 CACNA1B:121
KEGG_PEROXISOME	-0.16548894	78	4.414e-07	1.432e-04	DEC2:5 ACOD3:75 PRDX5:10 PMPX:4152 AMACR:232 ACOX1:247
REACTOME_MUSCLE_CONTRACTION	0.10783909	917	5.070e-07	1.566e-04	SLCA3A:30 KCNJ4:118 TCAP:124 SCN5A:231 AHCV1L:257 KCNK1:269
BENPORATH_SUZ12_TARGETS	0.04881593	93	6.762e-07	1.774e-04	GN1A1:5 TSC22D3:11 FOXP1:25 KCNAB1:49 GPR83:38 TCEA3:47 KCNAB1:49
MEISSNER_NPC_HCP_WITH_HKX27ME3	0.00696593	331	6.834e-07	1.774e-04	GN1A1:5 GPR27:90 ADRA2C:197 SCN5A:231 TLX3:244 KCN1:255
WP_PRADERWILLI_AND_ANGELMAN_SYNDROME	0.19260982	56	6.231e-07	1.774e-04	GABRR2:521 MDMA:543 GABRR1:723 NMPX2:831 TUBGCP5:1004 FSHB:1097
WP_MONOAMINE_GPCRS	0.25438354	32	6.371e-07	1.774e-04	HTR1B:191 ADRA2C:197 ADRB1:282 HTR4:635 CHRM4:661 HTR2A:729
MIKKELSEN_NPC_HCP_WITH_HKX27ME3	0.07899812	331	8.411e-07	2.099e-04	GPR27:90 POU2F3:105 ADRA2C:197 SCN5A:231 TLX3:244 KCN1:255
SENGUPTA_NASOPHARYNGEAL_CARINOMIA_DN	0.08057649	280	1.024e-06	2.461e-04	FOXP1:25 SNTN:35 HYDIN:46 TCEA3:47 CDC65:52 CDC113:113
REACTOME_G_ALPHA_S_SIGNALLING_EVENTS	0.12198281	134	1.114e-06	2.582e-04	GPR83:38 GPR27:90 AVP:182 GPER1:198 ADRA2C:197 GPER1:198
KIM_ALL_DISORDERS_CALB1_CORR_UP	0.06281892	510	1.343e-06	3.004e-04	NDUFV1:10 KIFBP:45 KCNAB1:49 CRMP1:110 UQCQRFS:158 GLRB:162
WP_RAC1PAK1P38MP2_PATHWAY	0.16736108	66	2.604e-06	5.631e-04	STAT5B:26 CTNNB1:103 TEK:416 CRK:462 NOS1:623 DOK2:734
WP_NEUROINFLAMMATION_AND_GLUTAMATERGIC_S	0.11624503	136	2.933e-06	6.139e-04	PRKCG:215 GRK1:396 IGF1:408 NOS1:623 GRK2:668 SLCA3A:82
REACTOME_VOLTAGE_GATED_POTASSIUM_CHANNEL	0.20740768	42	3.321e-06	6.734e-04	KCNAB1:49 KCNH5:117 KCNF1:373 KCND1:460 KCND2:629 KCNKA3:788
REACTOME_PEROXISOMAL_PROTEIN_IMPORT	-0.18050965	55	3.497e-06	6.876e-04	DEC2:5 ACOD3:75 NUDT7:133 AMACR:232 ACOX1:247 ECH1:366
REACTOME_DISEASES_OF_METABOLISM	-0.08969779	223	3.894e-06	7.431e-04	NOTO1:185 CYP24A1:68 MCCC1:74 ABCA3:80 ALG1:205 SEMA5A:306
KEGG_LYSOSOME	-0.12036767	110	1.315e-05	2.437e-03	CTSB:35 LAMP3:194 ATP6V0D1:372 LAMP2:394 HVAL:1437 ARSG:525
MATZUK_SPERMATOZOEA	0.12197484	102	2.107e-05	3.796e-03	ADAD1:34 SPAG16:689 CREM:35 LDHC:106 FHL5:108 AGF61:196
REACTOME_FATTY_ACID_METABOLISM	-0.09680250	158	2.746e-05	4.815e-03	DEC2:5 HACD3:7 CYP11A:144 ACOD3:75 ACOT13:125 NUDT7:133
REACTOME_DNA_DOUBLE_STRAND_BREAK_REPAIR	-0.10518919	130	3.516e-05	6.003e-03	POLK:258 ERCC4:411 RAD51D:127 PIAS4:453 SLX4:462 BAP1:642
REACTOME_DNA_REPAIR	-0.07203303	276	3.981e-05	6.623e-03	MUTYH:38 INO80D:51 ECR4:501 POLK:258 ALKBH2:273 ERCCA:411
WP_PEPTIDE_GPCRS	0.14186422	70	4.091e-05	6.636e-03	EDNRA:287 FSHR:356 CPOR:501 OPRM1:517 NPY1R:542 CCR1:593

DisGeNET\_Top pathways by permutation

Kartagener Syndrome	0.11493733	93	1.299e-04	6.813e-02	FOXJ1:25 HYDIN:46 CDC65:52 DNAH6:52 COR2:100 TTC25:164
Post-Traumatic Stress Disorder	0.11397374	95	1.262e-04	6.813e-02	TSC22D3:11 STAT5B:26 OPRM1:517 NOS1:623 ENDOU:1641 SGK1:885
Amino Acid Metabolism, Inherited Disorder	-0.31634197	12	1.481e-04	7.269e-02	ARG1:333 D2HGDH:969 PRODH:1361 GALT:1846 MAT1A:1885 SCISBP2:2017
Diabetes Mellitus, Insulin-Dependent	0.03961672	739	2.932e-04	1.027e-01	SKIV2L:7 RG52:9 STAT5B:26 IL37:74 IDE:99 SELENOS:172
Epilepsy, Temporal Lobe	0.08367025	160	2.694e-04	1.027e-01	GN1A1:5 BIN1:73 AVP:182 HCN1:255 SLCA12:319 LG1:369
Chromatopsia 1	0.30268889	12	2.830e-04	1.027e-01	FRMD7:160 CNGA3:682 PAX6:319 PNPLA6:926 GNAT2:110 PD0EC:1325
Emotional Stress	0.35083785	9	2.876e-04	1.027e-01	AVP:182 DRD2:954 MS2H1:160 OTX1:158 RCAN1:2569 HTR2C:2725
Hodgkin Disease	0.04822324	493	2.760e-04	1.027e-01	STAT5B:26 SND1:30 FOXK1:81 EBF1:156 TP52:238 MTHFR:266
Hypernatremia	0.43291385	6	2.427e-04	1.027e-01	BSND:294 CLCNKA:501 CYP11A:1770 CLCNKB:916 HSD3B2:950 AVPR2:3198
Psychotic Disorders	0.06387430	274	2.912e-04	1.027e-01	NVS:75 CHN2:130 NDUF5A:152 AVP:182 HTR1B:191 HDAC2:212
Recurrent major depressive episodes	0.26079516	26	2.634e-04	1.027e-01	AVP:182 MTHFR:266 SNE1:552 GRM7:988 CHRM2:1096 ADORA4:1536
Diabetes Mellitus, Non-Insulin-Dependent	0.03003733	1346	3.051e-04	1.032e-01	LINC02:2 PPIA:17 STAT5B:26 CAV1:65 FAIM2:67 IL37:74
Otitis Media	-0.11326855	84	3.116e-04	1.033e-01	CTSR:95 TGIF1:116 CTRB:325 TBLX1:607 ADAMTS1:719 PHEX:798
Familial migraine	0.39144377	7	3.351e-04	1.060e-01	HTR1B:191 KNG2:2 HCN1:255 KCNKB1:857 SCN10A:1811 SLCA4:2267 ATP12A:2499
AIDS Dementia Complex	0.16683839	37	3.855e-04	1.061e-01	KCNK1:269 IGF1:408 OPRM1:517 SLCA18:356 KCNA3:788 NEURL1:178
Mental Disorders	0.06230147	281	3.466e-04	1.061e-01	MAG1:412 CADP2S:58 HTR1B:191 HTR1:266 EPHB2:470 SLITRK1:497
Neuralgia	0.11295613	83	3.809e-04	1.061e-01	PRKG2:51 HCN1:255 MDH2:290 OPRM1:517 KCNA3:788 DRD2:954
Retinal pigment epithelial mottling	0.36414748	8	3.616e-04	1.061e-01	PRPH2:148 ERCC3:424 ABCA4:915 CACNA2D4:1113 CTNS:1449 ELOVL4:1535
Tracheoesophageal Fistula	-0.15647788	43	3.876e-04	1.061e-01	CYBB:325 ERYCA1:411 SLX4:462 IGA6:504 USB1:75 FANCG:808
Bilateral cataracts (disorder)	0.10053937	103	4.311e-04	1.122e-01	CYRB44:59 CRCLY:2197 CLP4B:466 BPSF1:556 EPHA2:657 MIP:799
Hepatomegaly	-0.05667983	332	4.347e-04	1.122e-01	GM1N1:37 CYP11A:148 LRP6:153 ALG1:205 AMACR:232 AC0X1:247
Cataract, Central Sacular, With Sutureal	0.01427345	6	5.000e-04	1.198e-01	CRYBA1:297 CRYBG3:620 GJA8:832 BPSF2:310 CRYBB2:4533
Andersen Syndrome	0.21409874	22	5.003e-04	1.198e-01	SCN5A:231 MTHFR:266 KCNJ5:618 KCNA3:788 KCNJ12:958 PKRARIA:964