

GO_Biological_Process_2023 Top pathways by non-permutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
Skin Development (GO:0043588)	0.17289050	66	1.210e-06	6.545e-03	DSP:51 OPN3:367 ITGB4:406 MED1:466 COL3A1:815 EVPL:861
NADH Dehydrogenase Complex Assembly (GO:018430286)	0.18430286	49	8.153e-06	1.469e-02	TMEM126B:9 NDUF41:1112 ECSIT:136 NDUFAF1:152 NDUFB8:335 NDUFB5:419
Mitochondrial Respiratory Chain Complex	0.18430286	49	8.153e-06	1.469e-02	TMEM126B:9 NDUF41:1112 ECSIT:136 NDUFAF1:152 NDUFB8:335 NDUFB5:419
Calcium Ion Transmembrane Import Into Cy	0.13956176	79	1.829e-05	2.073e-02	TRPV6:52 CACNA11:278 CACNA1S:283 CACNA1E:310 SLC24A4:313 CACNA1G:528
Calcium Ion Transmembrane Transport (GO:014010667)	0.14010667	78	1.917e-05	2.073e-02	TRPM5:19 TRPV6:52 SLC24A3:237 CACNA1S:283 SLC24A4:313 ATP2C2:397
Keratinoctyte Differentiation (GO:0030216)	0.18654782	40	4.483e-05	4.040e-02	DSP:51 OPN3:367 MED1:466 EVPL:861 KRT16:1278 TGM1:1291
Natural Killer Cell Activation Involved	0.24586600	22	6.564e-05	4.436e-02	IFNA5:414 IFNA10:985 IFNA1:1066 IFNA2:1093 FCGR3A:1832 IFNA7:2164
Regulation Of Peptidyl-Serine Phosphoryl	0.27234135	18	6.338e-05	4.436e-02	IFNA5:414 IFNA10:985 IFNA1:1066 IFNA2:1093 IFNG:1395 IFNA7:2164
Positive Regulation Of Intracellular Tra	0.18140351	39	8.901e-05	5.347e-02	SORL1:6 SPAG5:369 MBD1:686 NEDD4:1044 PRR5L:1322 KIF20B:1349
Epidermis Development (GO:0008544)	0.11824992	84	1.819e-04	7.632e-02	DSP:51 HOXB13:169 FLOT2:610 EVPL:861 LCE2B:935 MANSCA:968
Intermediate Filament Organization (GO:013516074)	0.13516074	65	1.659e-04	7.632e-02	PKP1:12 DSP:51 KRT17:196 KRT80:222 KRT20:247 DES:402
mRNA Methylation (GO:0080009)	0.15675803	15	1.976e-04	7.632e-02	TRMT61B:632 TRMT10C:646 METTL8:787 NSUN2:1916 CMTR1:1970 TRMT61A:2821
Mitochondrial Respiratory Chain Complex	0.11951587	82	1.855e-04	7.632e-02	TMEM126B:9 NDUF41:1112 ECSIT:136 NDUFAF1:152 NDUFB8:335 NDUFB5:419
Positive Regulation Of Peptidyl-Serine P	0.26217905	17	1.824e-04	7.632e-02	IFNA5:414 IFNA10:985 IFNA1:1066 IFNA2:1093 IFNG:1395 IFNA7:2164 IFNA14:2417
Epidermal Cell Differentiation (GO:000099	0.14786169	52	2.273e-04	7.951e-02	DSP:51 OPN3:367 MED1:466 EVPL:861 OVOL3:1046 KRT16:1278
Homophilic Cell Adhesion Via Plasma Memb	0.13678365	60	2.500e-04	7.951e-02	SDK1:32 TRO:59 DSG2:195 ITGB1:346 NEXN:371 LICAM:594
Positive Regulation Of Neuron Apoptotic	-0.22115776	23	2.416e-04	7.951e-02	ITGAM:427 FBXW7:508 BAX:877 TFA2PA:1104 TNF:1615 CDK5R1:2334
Regulation Of Protein Localization To Nu	-0.14268264	51	4.263e-04	1.281e-01	PARP9:167 KAT7:263 DTX3L:369 YVHAZ:437 OTUD7B:839 TYK2:887
Internal Protein Amino Acid Acetylation	-0.35641964	8	4.811e-04	1.369e-01	KAT7:263 MAPT:350 NAA10:955 KAT5:1702 KAT2A:2218 KAT2B:2985
Calcium Ion Transport (GO:0006816)	0.09393830	110	6.753e-04	1.826e-01	TRPM5:19 TRPV6:52 SLC24A3:237 CACNA1S:283 SLC24A4:313 ATP2C2:397
Actin-Miosin Filament Sliding (GO:003327	0.30312187	10	9.027e-04	2.236e-01	MYH2:16 MYL6B:461 TNNT2:704 MYH3:783 MYH4:944 MYH8:3483
Calcium Ion Import Across Plasma Membran	0.16092912	34	1.168e-03	2.236e-01	TRPV6:52 CACNA11:278 CACNA1S:283 CACNA1E:310 SLC24A4:313 CACNA1G:528
Gene Expression (GO:0010487)	-0.05890262	266	9.807e-04	2.236e-01	RBM39:16.5 RPS4Y2:16.5 GSPT2:98 CHTOP:128 MRPS21:169 EXOSC9:198
Lymphocyte Activation Involved In Immune	0.19584182	23	1.151e-03	2.236e-01	IFNA5:414 IFNA10:985 IFNA1:1066 IFNA2:1093 IFNA7:2164 IFNA14:2417
mRNA Modification (GO:0016556)	0.18349639	27	9.681e-04	2.236e-01	TRMT61B:632 TRMT10C:646 METTL8:787 PUS7L:1000 DKC1:1209 NSUN2:1916
Natural Killer Cell Activation (GO:00301	0.14090453	44	1.227e-03	2.236e-01	IFNA5:414 IFNA10:985 IFNA1:1066 IFNA2:1093 CD2:1483 NCR3:13615
Protein Insertion Into ER Membrane (GO:0	-0.17779637	28	1.226e-03	2.236e-01	MMGT1:252 TRAM1:1127 CDC47:1414 RAB5F:1611 GET3:1771 EMC4:2305.5
Regulation Of Vesicle Size (GO:0097494)	-0.24282030	14	1.241e-03	2.236e-01	BLOC1S1:1154 KXD1:1893 BORCS28:2110 BORCS7:2355 RAB5A:2966 AP2M1:3456
Semaphorin-Plexin Signaling Pathway Invo	-0.06325284	12	1.083e-03	2.236e-01	PLXNC1:766 PLXNA4:842 PLXNB2:1102 PLXNB3:2191 SEMA3A:2999 PLXNA1:3281
Transcription Initiation At RNA Polymera	-0.10953066	73	1.224e-03	2.236e-01	MED20:142 TAF11L:538 GFP2H2:722 GTF2B:735 TAF11L:572 MED30:927
Mitotic Sister Chromatid Segregation (GO	0.08903716	109	1.339e-03	2.263e-01	DLGAP5:27 KIF18A:78 CTF192:96 KIF22:192 OFD1:224 KIF2C:231
Regulation Of Neuron Migration (GO:00012	0.17516094	28	1.339e-03	2.263e-01	KIF26A:120 TNN:456 COL3A1:815 ULK4:962 IGSF10:1014 PLXNB2:1102
ERBB Signaling Pathway (GO:0038127)	0.12674094	53	1.422e-03	2.330e-01	PTK2:705 AKT1:1040 PLCG1:1068 PLC1:8177 EGFR:1249 PIK3C2A:1328
mRNA Processing (GO:0006397)	-0.06716858	187	1.575e-03	2.505e-01	RBM22:16.5 MTRER:135 SFPO:265 VDRB8:321 CPSF7:699 SART3:847
Positive Regulation Of Calcium Ion Trans	0.14187187	41	1.677e-03	2.591e-01	CASQ1:277 GPER1:336 CAPN3:834 CEMIP:909 P2RX7:1001 PLOG1:1068
Muscle Contraction (GO:0006936)	0.09468339	91	1.817e-03	2.730e-01	MYH2:16 MYH13:89 MYOF:243 CACNA1S:283 DES:402 MYH1:438
Establishment Or Maintenance Of Apical/B	0.18325259	24	1.889e-03	2.734e-01	PATJ:228 SCRIB:258 PARDB3B:633 DLG3:1710 LGLL1:1783 OOEFP:1819
Negative Regulation Of Inflammatory Resp	-0.08650726	107	2.016e-03	2.734e-01	TRIM65:45 FNDCA1:133 TNFAIP6:278 AP0A1:286 IL2D2:322 PRKCD:357
Presynaptic Active Zone Organization (GO	-0.39910733	5	1.996e-03	2.734e-01	ERC2:277 ERC1:545 CAST:2550 PCLD:2855 RAB3A:3194 NA
Regulation Of Smooth Muscle Contraction	0.19941021	20	2.022e-03	2.734e-01	CTTN:279 TACR2:615 PLCE1:1177 KCNB2:1411 SETD3:1793 CHRM2:1938

EnrichmentHsSymbolsFile2 Top pathways by non-permutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
HOUNKPE_HOUSEKEEPING_GENES	-0.06632010	1063	3.793e-13	2.463e-09	ARL8B:16.5 CAB39:16.5 CUL3:16.5 TMEM203:16.5 PDCD7:54 PSMD10:76
REACTOME_METABOLISM_OF_RNA	-0.07958533	645	6.273e-12	2.037e-08	RBM39:16.5 RBM22:16.5 SNRPC:16.5 PSAP2:16.5 PDCD7:54 PSMD10:76
REACTOME_KERATINIZATION	0.12923156	214	7.558e-11	1.636e-07	PKP1:12 DSP:51 KRTAP6:1.55 KRTAP10:1.163 KRTAP10:3.164 DSG2:195
REACTOME_FORMATION_OF_THE_CORNFIFIED_ENVE	0.15619422	128	1.065e-09	1.730e-06	PKP1:12 DSP:51 DSG2:195 KRT17:196 KRT80:222 KRT20:247
BLALOCK_ALZHEIMERS_DISEASE_DN	-0.05241809	1180	1.672e-09	2.172e-06	CAB39:16.5 STAM:16.5 NQO1:16.5 TBPL1:16.5 MEMO1:16.5 SEC61A2:16.5
REACTOME_CELLULAR_RESPONSES_TO_STIMULI	-0.06327535	749	4.334e-09	4.020e-06	CUL3:16.5 NQO1:16.5 H2AC18:16.5 H2BC3:16.5 RPS4Y2:16.5 AKT3:34.5
DIAZ_CHRONIC_MYELOGENOUS_LEUKEMIA_UP	-0.04846457	1329	3.933e-09	4.020e-06	CAB39:16.5 STAM:16.5 RBM39:16.5 TBPL1:16.5 PSMD10:76 SAV1:103
NIKOLSKY_BREAST_CANCER_7P22_AMPLICON	0.27003870	37	3.116e-08	1.003e-05	INTS1:203 GPER1:336 ZFAND2A:357 SNX8:722 MAD1L1:854 AP521:942
MARTENS_TRETINOIN_RESPONSE_DN	-0.06179440	733	3.190e-08	1.003e-05	TRIM65:45 OR7G2:55 HDGF:77 IRAK3:105 ATGAD:107 CHMP2A:119
REACTOME_INFECTIOUS_DISEASE	-0.05651316	876	1.610e-08	1.045e-05	CUL3:16.5 STAM:16.5 H2AC18:16.5 H2BC3:16.5 RPS4Y2:16.5 AKT3:34.5
REACTOME_POST_TRANSLATIONAL_PROTEIN_MODI	-0.04114297	1379	3.715e-07	2.027e-04	CUL3:16.5 STAM:16.5 H2AC18:16.5 TRAPP2C:16.5 WDR48:16.5 COP22:46.2
REACTOME_REGULATION_OF_EXPRESSION_OF_SLI	-0.12190487	146	3.748e-07	2.027e-04	RPS4Y2:16.5 PSMD10:76 GSPT2:98 RPLP0:232 PSMB6:282 NUP35:541
PUJANA_BRCA1_PCC_NETWORK	-0.03907607	1514	4.714e-07	2.355e-04	RAP1B:16.5 TBPL1:16.5 SNRPC:16.5 FAM120A:41.5 MMP20:48 BRAF:67
HSIAO_HOUSEKEEPING_GENES	-0.07799012	349	5.994e-07	2.780e-04	H2AC18:16.5 PSD:64 CD164:65 STOM:176 AARS1:184 RPLP0:232
SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_D	-0.05830100	573	1.977e-06	8.560e-04	CD164:65 YME1L1:106 CNOT2:181 ARPC5L:196 CCNC:216 RPL7A:218
DANG_BOUND_BY_MYC	-0.04443417	1001	2.237e-06	9.080e-04	RBM39:16.5 H2AC18:16.5 CD164:65 PSMD10:76 HMOX1:122 CNPY2:163
BENPORATH_MYC_MAX_TARGETS	-0.05146216	727	2.511e-06	9.592e-04	RBM39:16.5 H2AC18:16.5 CD164:65 PSMD10:76 SAV1:103 MED20:142
REACTOME_UB_SPECIFIC_PROCESSING_PROTEASE	-0.09202678	214	3.566e-06	1.286e-03	H2AC18:16.5 WDR48:16.5 H2BC3:16.5 PSMD10:76 USP17L24:209 H2AC12:233
REACTOME_TRANSCRIPTIONAL_REGULATION_BY_R	-0.08916174	221	5.046e-06	1.725e-03	H2AC18:16.5 H2BC3:16.5 PSMD10:76 KMT2D:172 GPAM:178 PSMB6:282
REACTOME_PROCESSING_OF_CAPPED_INTRON_CON	-0.08315536	250	6.116e-06	1.986e-03	RBM39:16.5 RBM22:16.5 SNRPC:16.5 PDCD7:54 CHTOP:128 MTRX1:135
REACTOME_METABOLISM_OF_AMINO_ACIDS_AND_D	-0.07042644	347	6.804e-06	2.008e-03	NQO1:16.5 RPS4Y2:16.5 PSMD10:76 BCKDK9:1 RPLP0:232 OAZ3:235
REACTOME_SARS_COV_1_INFECTION	-0.11858563	121	6.694e-06	2.008e-03	RPS4Y2:16.5 CHMP2A:119 PARP9:167 NMI:201 ST3GAL4:289 YVHAZ:437
REACTOME_RUNX1_REGULATES_TRANSCRIPTION_O	-0.12133523	114	7.708e-06	2.176e-03	H2AC18:16.5 H2BC3:16.5 PSMD10:76 PSMB6:282 H2BC10:447 UTP14A:538
REACTOME_RRNA_PROCESSING	-0.09366094	182	1.334e-05	3.609e-03	RPS4Y2:16.5 MTRX1:135 EXOSC9:198 RPLP0:232 WDR3:437 NUP35:541
FLORIO_NEOCORTEX_BASAL_RADIAL_GLIA_DN	0.09138953	186	1.749e-05	4.542e-03	MKI67:14 DLGAP5:27 PARPBP:76 KIF18A:78 SG02:135 KIF22:192
DAZARD_RESPONSE_TO_UV_SCC_UP	-0.12310743	100	2.115e-05	5.528e-03	CCNC:216 TACSTD2:225 KYAT3:379 YVHAZ:437 PMAIP1:548 MAP2K1:558
REACTOME_CYCLIN_A_CDK4_ASSOCIATED_EVENTS	-0.13648570	80	2.452e-05	5.897e-03	AKT3:34.5 PSMD10:76 PSMB6:282 PSMA4:492 MNAT1:728 RBL2:790
BRUINS_UVC_RESPONSE_LATE	-0.03767346	1077	3.311e-05	7.194e-03	ARL8B:16.5 CAB39:16.5 MEMO1:16.5 TRAPP2C:16.5 COP22:16.5 TCF19:50
REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_P	-0.12561462	92	3.144e-05	7.194e-03	SEC61A2:16.5 RPS4Y2:16.5 RPLP0:232 RPL36:769 SSR3:891 RPL3L:897
REACTOME_TRANSCRIPTIONAL_REGULATION_BY_R	-0.11112684	117	3.324e-05	7.194e-03	AKT3:34.5 PSMD10:76 PSMB6:282 RUNC2:429.5 PSMA4:492 FBXW7:508
REACTOME_INFLUENZA_INFECTION	-0.10309685	132	4.354e-05	9.122e-03	RPS4Y2:16.5 RPLP0:232 KPNA4:296 SLC25A6:299 NUP35:541 SEC13:623
REACTOME_TCF_DEPENDENT_SIGNALING_IN_RESP	-0.08093447	214	4.573e-05	9.279e-03	CUL3:16.5 H2AC18:16.5 H2BC3:16.5 PSMD10:76 KMT2D:172 CENK1G:257
REACTOME_HIV_INFECTION	-0.08053257	215	4.788e-05	9.422e-03	PSMD10:76 CHMP2A:119 TAF1:519 PSMB6:282 SLC25A6:299 LCK:360
REACTOME_HCMV_LATE_EVENTS	-0.11552157	103	5.133e-05	9.805e-03	H2AC18:16.5 H2BC3:16.5 CHMP2A:119 H2AC12:233 H2BC10:447 NUP35:541
THUM_SYSTOLIC_HEART_FAILURE_UP	-0.05969294	389	5.497e-05	1.020e-02	ARL8B:16.5 CP:102 IRF8:109 ZNF672:200 KPNA4:296 FAS:361
REACTOME_SPERM_MOTILITY_AND_TAXES	0.08618630	9	6.567e-05	1.057e-02	CATSPER2:99 CATSPERB:536 CATSPER3:587 CATSPERD:760 CATSPERG:1188 HVCN1:2106
REACTOME_SIGNALING_BY_ROBO_RECEPTORS	-0.08404975	188	7.161e-05	1.057e-02	RPS4Y2:16.5 PSMD10:76 GSPT2:98 RPLP0:232 PSMB6:282 PSMA4:492
REACTOME_OTHER_SEMAPHORIN_INTERACTIONS	0.27149927	18	6.661e-05	1.057e-02	SEMA7A:97 ITGB1:346 PLXNC1:766 PLXNA4:842 PTPRC:1714 SEMA4D:2068
REACTOME_ESTROGEN_DEPENDENT_GENE_EXPRESS	-0.10093025	131	6.696e-05	1.057e-02	H2AC18:16.5 H2BC3:16.5 GPAM:178 STAG2:347 H2BC10:447 SP1:593
REACTOME_NONSENSE_MEDIATED_DECAY_NMD	-0.11948685	93	6.860e-05	1.057e-02	RPS4Y2:16.5 GSPT2:98 RPLP0:232 RPL36:769 RPL3L:897 RPS3:948.5

DisGeNET Top pathways by non-permutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
Cerebral Ischemia	-0.07316557	240	9.904e-05	4.867e-01	ASIC1:16.5 KCNK3:56 REN:132 KCN1J:13.171 BDNF:193 CREB1:221
Esophagitis	-0.14786041	58	9.914e-05	4.867e-01	NQO1:16.5 PDLIM3:188 PLCL1:242 YVHAZ:437 IL10:581 GPHN:900.5
Bell Palsy	0.11296138	87	2.742e-04	4.921e-01	SMCHD1:293 COL6A1:294 DES:402 DNA2:425 SLC18A3:454 MGME1:485
Erythrodermatoderma	0.16605376	41	2.353e-04	4.921e-01	DSP:51 DSG2:195 KRT17:196 DES:402 SLURP1:458 GJBA:521
Leukokeratosis	0.21915410	23	2.750e-04	4.921e-01	KRT17:196 CTTN:279 CTC1:756 DKC1:1209 KRT16:1278 AKT:1302
Thyroid Agenesis	-0.20101517	27	3.007e-04	4.921e-01	FOXE1:70 THRA:346 PRKARIA:637 TSHB:870 LHXA:1055 DUXO2:1201
Stiff-Person Syndrome	-0.27551525	14	3.581e-04	5.023e-01	GAD1:63 GP6:514.5 GPHN:900.5 NUDT10:2115 SLC6A5:2189 HLA-DQB1:2574
Anaphylaxis (non medication)	-0.16535181	38	4.218e-04	5.176e-01	CD63:306 F9:423 IL10:581 HACD1:668 STAT6:823 TM7SF2:1153
Abnormality of the skull	0.11904777	68	6.928e-04	5.233e-01	CENPJ:337 ESCO2:567 CEP152:831 CENPE:846 IFT122:880 RBBP8:1122
Facial Paresis	0.10632062	88	5.729e-04	5.233e-01	SMCHD1:293 COL6A1:294 DES:402 DNA2:425 SLC18A3:454 MGME1:485
Hyperdiploid B Acute Lymphoblastic Leuke	-0.18773742	28	5.865e-04	5.233e-01	CEBPE:154 KRAB1:970 CD191:991 ASPG:1413 PIP4K2A:1568 TTNF:1615
Long Qt Syndrome 2	0.29593776	11	6.773e-04	5.233e-01	GOLGA2:250 KCNH2:663 ALG10:923 KCNQ1:2351 SCN5A:3466 KCNE1:3620
Sarcoma	-0.04123981	605	5.862e-04	5.233e-01	NQO1:16.5 BRAF:67 HDGF:77 LIN28A:78
Facial muscle weakness of muscles innerv	0.10447054	84	9.434e-04	6.617e-01	SMCHD1:293 COL6A1:294 DES:402 DNA2:425 SLC18A3:454 MGME1:485
46, XX Testicular Disorders of Sex Devel	-0.24074597	9	1.238e-02	6.715e-01	SOX10:694 FOLX2:1561 NR5A1:2066 SOX9:351 AR:3201 RSP01:4096
Bulbo cavernosus Reflex, Decreased	0.32153499	5	1.277e-02	6.715e-01	PMP22:1991 CHRN2B:2399 TTPA:2852 ABAT:4487 ATXN7:5003 NA
Child Development Disorders, Specific	0.15439931	23	1.038e-02	6.715e-01	CHRNA4:732 DRD2:964 KNTN1:1030 KCNQ2:1366 SLG6A8:1549 SHANK3:1682
Conjunctivitis, recurrent	-0.11712136	39	1.140e-02	6.715e-01	BLNK:551 ERCC6:765 CD19:991 TP63:1069 XPC:1332 SAT1:1846
Creatinine measurement, serum (procedure	0.09668360	63	7.993e-03	6.715e-01	WDR72:93 ALMS1:194 PTFN1:2280 CACNA1S:283 CDK12:382 SPATA5L1:520
Epilepsy, Rolandic	0.13180789	30	1.248e-02	6.715e-01	KCNQ3:240 SNIP1:1205 RBFOX3:1299 KCNQ2: