

EnrichmentHsSymbolsFile2 Top pathways by permlutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
DIAZ_CHRONIC_MYELOGENOUS_LEUKEMIA_UP	-0.05987105	1101	3.658e-11	2.372e-07	SAV1:2 IQGAP2:7 COMT:10 CCT6A:20 HADHB:24 TBCB:25
DODD_NASOPHARYNGEAL_CARCI	0.05090702	1409	3.131e-10	8.542e-07	CEP19:2 MARCFH4:4 FND01:18 D
SCHLOSSER_SERUM_RESPONSE_DN	-0.07905333	542	3.952e-10	8.542e-07	CMTR1:4 NAGPA:12 EPB42:42 CD2AP:69 LRP1:91 CDK7:118
PUJANA_BRCA1_PCC_NETWORK	-0.05260838	1222	1.072e-09	1.738e-06	SLC14A2:1 CARM1:18 CCT6A:20 SLC6A6:53 NUP62:63 CD2AP:69
JOHNSTONE_PARVB_TARGETS_3_DN	-0.06812868	667	2.613e-09	3.098e-06	MIS18BP1:29 SLC6A6:53 ATG3:59
STARKE_HYPOCAEMIA_22011_DELETION_DN	-0.38364159	20	2.866e-09	3.098e-06	PRODH:8 COMT:10 ARVCF:32 TRMT2A:62 RTN4R:102
DACOSTA_UV_RESPONSE_VIA_ERCC3_DN	-0.06289883	735	8.587e-09	7.748e-06	WDFY3:17 CD2AP:69 CENPE:74 WDHD1:88
BUYTAERT_PHOTOYNAMIC_THERAPY_STRESS_UP	-0.06524128	676	9.558e-09	7.748e-06	WDFY3:17 KDM4B:21 DNAJB4:52 SLC6A6:53
RODRIGUES_THYROID_CARCI	-0.07046444	570	1.121e-08	8.078e-06	SPIRE1:8 CCT6A:20 MCOLN3:23 ELOV
WP_22Q112_COPY_NUMBER_VARIATION_SYNDROME	-0.16862472	95	1.389e-08	8.564e-06	PRODH:8 COMT:10 ARVCF:32 TRMT2A:62
ZHANG_BREAST_CANCER_PROG	-0.08766323	357	1.453e-08	8.564e-06	MIS18BP1:29 CNOT6:58 RIDA:65
RODRIGUES_THYROID_CARCI	-0.07163072	521	2.670e-08	1.443e-05	SPIRE1:6 CCT6A:20 ADAM9:47 ELOV
NIKOLSKY_BREAST_CANCER_12Q24_AMPLICON	0.40594170	15	5.230e-08	2.609e-05	NOC4L:116 GALNT9:313 POLE:580
SENGUPTA_NASOPHARYNGEAL_CARCI	0.09500764	273	7.177e-08	3.324e-05	ANKRD35:26 DNAI2:36 TOGARAM2:73
DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN	-0.07740417	400	1.232e-07	5.327e-05	CD2AP:69 CENPE:74 MGLL:99
DAZARD_RESPONSE_TO_UV_NHEK_DN	-0.09530322	258	1.475e-07	5.978e-05	WDFY3:17 WDHD1:88 WAPL:123
HSIAO_LIVER_SPECIFIC_GENES	-0.10049184	196	1.294e-06	4.937e-04	TM4SF4:16 TAT:33 SLC38A3:38
FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_UV	-0.06969136	409	1.484e-06	5.345e-04	COMT:10 WDFY3:17 TBCB:25
DODD_NASOPHARYNGEAL_CARCI	-0.04315541	1082	2.225e-06	7.596e-04	CCT6A:20 NUP62:63 RIDA:65
NIKOLSKY_BREAST_CANCER_1Q21_AMPLICON	0.24114948	32	2.356e-06	7.639e-04	TRIM46:71 SCMP3:152 HCN3:311
HAMAI_APOPTOSIS_VIA_TRAIL_UP	-0.05688001	556	2.590e-06	7.998e-04	IQGAP2:7 MIS18BP1:29 ADAM9:47
ENK_UV_RESPONSE_KERATINOCYTE_DN	-0.06929358	392	2.756e-06	8.123e-04	CD2AP:69 BCAT2:101 RXYLT1:108
HOUNKPE_HOUSEKEEPING_GENES	-0.04844210	821	2.996e-06	8.447e-04	SAV1:2 CMTR1:4 COMT:10 KDM4B:21
OSMAN_BLADDER_CANCER_UP	-0.07550291	320	3.708e-06	9.945e-04	PTGER2:137 ATP11B:139
SENESE_HDAC3_TARGETS_UP	-0.06932866	380	3.834e-06	9.945e-04	SAV1:2 SPIRE1:6 IQGAP2:7
DEURIG_T_CELL_PRAVIMYCIN_TYTIC_LEUKEMIA_DN	-0.08404865	243	6.184e-06	2.645e-03	KLHL2:97 ADGRG3:1770
REACTOME_METABOLISM_OF_LIPIDS	-0.05190981	647	7.773e-06	1.967e-03	CYP11A1:14 CARM1:18 HADHB:24
REACTOME_METABOLISM_OF_AMINO_ACIDS_AND_OTHER_AMINO_ACIDS	-0.07699113	283	8.676e-06	2.056e-03	PRODH:8 TAT:33 RIDA:65
IBRAHIM_NRF2_UP	-0.06153676	438	1.114e-05	2.491e-03	CCT6A:20 ME1:37 DNAJB4:52
REACTOME_CLASS_A_1_RHO	0.07394779	295	1.331e-05	2.877e-03	PROKR1:17 RFXP3:35
SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6	-0.06650115	363	1.464e-05	2.902e-03	ELOV:6:55 NUP62:63
NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON	0.11555900	118	1.476e-05	2.902e-03	FND01:18 PTK6:122
MITSIADES_RESPONSE_TO_APLIDIN_DN	-0.08721012	207	1.592e-05	3.129e-03	BUB1:76 GINS1:105
IVANOVA_HEMATOPOIESIS_MATURE_CELL	-0.07987326	245	1.753e-05	3.343e-03	CMTR1:4 TM4SF4:16
CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_2	0.06444975	377	1.881e-05	3.420e-03	CEP19:2 DZIP1:6
MILLI_PSEUDOPODIA_HAPTOTAXIS_UP	-0.06336575	390	1.898e-05	3.420e-03	DNAJB4:52
WP_METHIONINE_METABOLISM_LEADING_TO_SULFUR_METHIONINE	-0.36689445	11	2.514e-05	4.406e-03	BHMT:153 AHCY:195
SHEN_SMARCA2_TARGETS_UP	-0.06604083	335	3.491e-05	5.958e-03	WDFY3:17 ATG3:59
KEGG_ARRHYTHMOGENIC_RIGHT_VENTRICULAR_CARDIAC_ARRHYTHMOGENIC_RIGHT_VENTRICULAR_CARD	0.14689327	66	3.716e-05	6.025e-03	CACNG4:85 EMD:104

DisGeNET Top pathways by permlutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
Ciliary Motility Disorders	0.20709555	55	1.109e-07	1.023e-03	DNAH11:19 DNAI2:36
DiGeorge Syndrome	-0.19898041	57	2.088e-07	1.023e-03	PRODH:8 COMT:10
Impaired T cell function	-0.35315601	17	4.649e-07	1.519e-03	COMT:10 ARVCF:32
Posterior embryotoxon	-0.25495313	31	9.072e-07	2.223e-03	COMT:10 ARVCF:32
Seborrheic dermatitis	-0.31300806	20	1.267e-06	2.484e-03	COMT:10 ARVCF:32
Embryotoxon	-0.25222446	30	1.758e-06	2.873e-03	COMT:10 ARVCF:32
Polynesian Bronchiectasis	0.23541034	34	2.054e-06	2.876e-03	DNAH11:19 DNAI2:36
Tetany	-0.30203645	20	2.939e-06	3.602e-03	COMT:10 ARVCF:32
22q11.1 Deletion Syndrome	-0.31090120	18	4.979e-06	5.424e-03	PRODH:8 COMT:10
22q11.1 partial monosomy syndrome	-0.38897459	11	7.942e-06	7.788e-03	COMT:10 ARVCF:32
Thyrosy	-0.10341521	156	8.794e-06	7.837e-03	LPL:67 ALB:80
Small earlobe	-0.33504955	13	2.886e-05	2.357e-02	COMT:10 ARVCF:32
Shprintzen syndrome	-0.21873454	30	3.401e-05	2.498e-02	PRODH:8 COMT:10
Dysseborrheic dermatitis	-0.30832704	15	3.567e-05	2.498e-02	COMT:10 ARVCF:32
Hereditary spherocytosis	-0.24775670	23	3.924e-05	2.565e-02	SLC4A1:27
Reticulocyte count (procedure)	-0.09306753	160	5.113e-05	3.022e-02	IQGAP2:7
Occipital myelomeningocele	-0.38935050	9	5.241e-05	3.022e-02	COMT:10 ARVCF:32
Abnormality of the tonsils	-0.34467567	11	7.557e-05	4.116e-02	COMT:10 ARVCF:32
Anemia, Sickle Cell	-0.08760053	169	8.976e-05	4.543e-02	COMT:10
Ewings sarcoma	-0.06934227	271	9.268e-05	4.543e-02	PAK3:39
Kartagener Syndrome	0.11965410	88	1.072e-04	4.956e-02	DNAH11:19 DNAI2:36
Anemia, hereditary spherocytic hemolytic	-0.49417932	5	1.297e-04	4.956e-02	SLC4A1:27
Spherocytosis	-0.49417932	5	1.297e-04	4.956e-02	SLC4A1:27
Congenital atresia of nasopharynx	0.34929518	10	1.310e-04	4.956e-02	DNAH11:19
Other specified congenital malformations	0.34929518	10	1.310e-04	4.956e-02	DNAH11:19
Mental deficiency	-0.03846442	890	1.314e-04	4.956e-02	PRODH:8
Poor school performance	-0.03912154	849	1.415e-04	5.126e-02	PRODH:8
Upward slant of palpebral fissure	-0.10595977	108	1.464e-04	5.126e-02	COMT:10 ARVCF:32
Solid Neoplasm	-0.04382415	658	1.536e-04	5.194e-02	TAT:33
Liver neoplasms	-0.03547721	1006	1.916e-04	6.261e-02	IQGAP2:7
Hepatocarcinogenesis	-0.05426389	395	2.393e-04	7.355e-02	KDM4B:21
Increased variability in muscle fiber di	0.21663236	24	2.402e-04	7.358e-02	TCAP:145
Pain, Postoperative	-0.22973681	21	2.688e-04	7.770e-02	COMT:10
Bilateral cataracts (disorder)	-0.10549628	100	2.737e-04	7.770e-02	ADAM9:47
Breast adenocarcinoma	-0.08948599	139	2.798e-04	7.770e-02	CASP8:191
Fabry Disease	-0.16580585	40	2.874e-04	7.770e-02	MANBA:142
Leukemia, Myelocytic, Acute	-0.03105901	1265	2.970e-04	7.770e-02	TAT:33
Abnormality of aortic arch	-0.11474135	11	3.012e-04	7.770e-02	COMT:10 ARVCF:32
CONOTRUNCAL ANOMALY FACE SYNDROME	-0.22508768	21	3.572e-04	8.859e-02	COMT:10 ARVCF:32
Malignant neoplasm of lung	-0.02630665	1805	3.617e-04	8.859e-02	COMT:10

customGeneSet Top pathways by permlutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
expressionDirectionalSelection	0.05710956	33	4.544e-01	7.646e-01	KAT8:208
NALFDGWAS	-0.05873016	14	5.097e-01	7.646e-01	GPAM:1197
HumanLocalAdaptionDietAll	-0.02127660	12	8.212e-01	8.212e-01	GPX1:743
NA	NA	NA	NA	NA	NA
NA.1	NA	NA	NA	NA	NA
NA.2	NA	NA	NA	NA	NA
NA.3	NA	NA	NA	NA	NA
NA.4	NA	NA	NA	NA	NA
NA.5	NA	NA	NA	NA	NA
NA.6	NA	NA	NA	NA	NA
NA.7	NA	NA	NA	NA	NA
NA.8	NA	NA	NA	NA	NA
NA.9	NA	NA	NA	NA	NA
NA.10	NA	NA	NA	NA	NA
NA.11	NA	NA	NA	NA	NA
NA.12	NA	NA	NA	NA	NA
NA.13	NA	NA	NA	NA	NA
NA.14	NA	NA	NA	NA	NA
NA.15	NA	NA	NA	NA	NA
NA.16	NA	NA	NA	NA	NA
NA.17	NA	NA	NA	NA	NA
NA.18	NA	NA	NA	NA	NA
NA.19	NA	NA	NA	NA	NA
NA.20	NA	NA	NA	NA	NA
NA.21	NA	NA	NA	NA	NA
NA.22	NA	NA	NA	NA	NA
NA.23	NA	NA	NA	NA	NA
NA.24	NA	NA	NA	NA	NA
NA.25	NA	NA	NA	NA	NA
NA.26	NA	NA	NA	NA	NA
NA.27	NA	NA	NA	NA	NA
NA.28	NA	NA	NA	NA	NA
NA.29	NA	NA	NA	NA	NA
NA.30	NA	NA	NA	NA	NA
NA.31	NA	NA	NA	NA	NA
NA.32	NA	NA	NA	NA	NA
NA.33	NA	NA	NA	NA	NA
NA.34	NA	NA	NA	NA	NA
NA.35	NA	NA	NA	NA	NA
NA.36	NA	NA	NA	NA	NA

GO\_Biological\_Process\_2023 Top pathways by permlutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
Cilium Movement (GO:0003341)	0.25969962	47	7.519e-10	4.045e-06	DNAH11:19 DNAI2:36 SPAG7:128 TEKT2:365 DNAH4:45 CFAP206:481
Axoneme Assembly (GO:0035082)	0.25692897	30	1.125e-06	3.027e-03	LRGUK:141 SPAG7:127 CDG65:326 PNAH6:481 SPNCA9:748 STK36:928
Regulation Of DNA-templated Transcription	-0.03634291	1447	7.452e-06	9.913e-03	CARM1:18 TCFC15:19 GTF2R:154 NUP62:63 NSD1:106 ZNF628:149
Cilium-Dependent Cell Motility (GO:006002)	0.31091204	17	9.111e-06	9.913e-03	DNAH3:232 CDG65:326 TEKT2:365 TEKT1:374 TEKT1:397 TEKT1:402 GAS8:1163
Axonemal Dynein Complex Assembly (GO:007002)	0.26722391	23	9.213e-06	9.913e-03	DNAI2:36 CDG65:326 PNAH7:128 DNAH11:1027 TC12:1033 DNAH1:1176
Neuroepithelial Signaling Pathway (GO:000702)	0.15797528	63	1.480e-05	1.327e-02	SORCS1:16 RFXP3:35 GRN45:226 LTBAR:329 OPRK1:635 GALS3:697
Regulation Of Heart Rate By Cardiac Conduction	0.20221682	37	2.100e-05	1.614e-02	SCN5A:49 KNCN3:97 HCN3:311 KNCN4:554 KNCN2:821 KNCN2:878
Muscle Contraction (GO:0006936)	0.12909370	82	5.460e-05	3.672e-02	CHRNA2:42 EMD:104 LMOB3:204 CASQ2:245 LTBAR:329 CHRN2:514
Regulation Of DNA Metabolic Process (GO:0006936)	-0.11567172	97	8.504e-05	5.084e-02	TERF2:152 USP37:477 RBBP5F:58 EPM1:537 CAC MYC:858 ASTR5:1006
Positive Regulation Of Chemotaxis (GO:0006936)	-0.17416692	41	1.152e-04	5.803e-02	LGMN:174 HSPB1:301 CLC1:939 SCPI:339 LKX:146 VEGFA:464
Fatty Acid Transport (GO:0015908)	-0.18547569	36	1.187e-04	5.803e-02	SLC02A1:46 SLC27A4:11 SLC22A6:600 FAR1:96 ACSL1:1041 PPARD:1166
Regulation Of Gene Expression (GO:0010406)	-0.03928959	829	1.593e-04	7.071e-02	CARM1:18 BTNL9:36 GTF2R:154 LRP1:91 NSD1:106 PRKAG1:107
Cardiac Conduction (GO:0061337)	0.16773310	42	1.709e-04	7.071e-02	SCN5A:49 KNCN3:97 HCN3:311 KNCN4:554 KNCN2:821 KNCN2:878
Cilium Movement Involved In Cell Motility	0.39809113	7	2.650e-04	1.002e-01	TEKT2:365 TEKT5:791 GAS8:1163 TEKT3:1764 TEKT1:2092 TEKT2:2462
Alpha-Amino Acid Biosynthetic Process (GO:0006936)	-0.33043891	10	2.968e-04	1.002e-01	ATG3:101 SDS:167 SLSL:348 LIVL5:61 CPS1:909 MTHFD:1060
Protein Modification By Small Protein Complex	-0.06437081	272	2.979e-04	1.002e-01	BCAT2:101 CUL4B:96 KDHL2:297 DTX2:234 UPR1:241 RHLK:2555
Cilium Assembly (GO:0060271)	0.06933779	218	4.434e-04	1.403e-01	CEP19:2 TMEM236:36 C9orf126:36 FEF4:42 AVIL:114
Vesicle-Mediated Transport Between Endosomes	-0.26597376	23	6.300e-04	1.763e-01	SNX16:387 PTNP3:102 RAB7A:108 HOOK2:1220 PKP3R4:1354 BECN1:1697
Motile Cilium Assembly (GO:0044458)	0.26330544	14	6.481e-04	1.763e-01	E2F4:92 SPAG7:127 BBOF1:1683 RHP59:2259 CDC39:2633 MDC05:2794
Negative Regulation Of Cellular Compartment	-0.10187651	94	6.555e-04	1.763e-01	LRP1:91 ASAP1:100 CLU11:114 PTPP:127 CLC1:939 CRR3:344
Nitrogen Compound Transport (GO:0071705)	-0.08130372	146	7.209e-04	1.847e-01	SLC38A3:38 SLC6A6:53 RHAG:75 SLC44:177 ATP1B:139 RHG:202
Early Endosome To Late Endosome Transport	-0.20462387	22	9.007e-04	1.959e-01	SNX16:387 PTNP3:102 RAB7A:108 HOOK2:1220 PKP3R4:1354 BECN1:1697
Ventricular Cardiac Muscle Cell Action Potential	0.25589950	14	9.174e-04	1.959e-01	SCN5A:49 KNCN4:554 KNCN2:821 KNCN2:878 PKP2:1022 KNCN1:1830
Negative Regulation Of Apoptotic Process	-0.05015361	375	9.347e-04	1.959e-01	NUP62:63 ALB:80 PEBM4:110 TSPY:124 LGMN:174 GCLC:215
Regulation Of Protein Phosphorylation (GO:0006936)	-0.06464198	221	9.775e-04	1.959e-01	NSD1:106 HSPB1:301 TBCAM1:312 CLU12:359 AXIN1:360 FKBP:382
Fatty Acid Catabolic Process (GO:0006936)	-0.12524595	58	9.814e-04	1.959e-01	HADHB:24 NUOT7:86 ALCA1:141 EHHAHD:260 PEX2:407 PLAG2:6125
Negative Regulation Of Macromolecular Biosynthesis	-0.10220580	75	9.831e-04	1.959e-01	RIDA:65 EIF2AK2:183 CAPRN1:443 ARK1B1:559 PAX2:407 TPO2:722
Mesodermal Cell Differentiation (GO:004048)	0.33067506	8	1.201e-03	2.307e-01	ITGA3:358 ITGB4:351 ITGB1:1752 HMG2:2252 ITGB3:299 KDM6B:3320
Diol Biosynthetic Process (GO:0034312)	-0.17828241	14	1.295e-03	2.390e-01	ACER1:184 ODR6:640 SPHK1:125 SPHK2:944 SPTLC2:1933 ACER2:2283
Anterograde Trans-Synaptic Signaling (GO:0006936)	0.07241974	166	1.332e-03	2.390e-01	CHRNA2:42 DLG4:135 CHRNA14:43 RPS6K4:1154 CHRNA2:167 GABRR2:179
Regulation Of Interleukin-2 Production (GO:0006936)	-0.14541368	40	1.472e-03	2.405e-01	HOMER3:111 CDBO:172 LIF:214 TNFAIP3:492 CDB6:503 RPS3:307
Striated Muscle Contraction (GO:0006941)	0.13278812	48	1.474e-03	2.405e-01	CLU:114 TCAAP:145 LMO3D:304 DMD:228 CASQ2:245 TNIN3:582
Positive Regulation Of Receptor-Mediated Signaling	-0.15114112	37	1.475e-03	2.405e-01	SCN5A:49 SLC6:326 CLC1:939 VEGFA:464 RAB21:969 NRP1:1021
Cellular Response To Acetylcholine (GO:0006936)	0.30402751	9	1.588e-03	2.492e-01	LY6G6D:430 CHRN2:514 CHRNA3:1025 LY6H:1055 RORC2:1193 UPR1:2263
Branched-Chain Amino Acid Metabolic Process	-0.23496089	15	1.632e-03	2.492e-01	BCAT2:101 BCKMHA:1038 D13P99 PC8B2:1515 HIBK2:2033 MCCO2:1224
Positive Regulation Of Endothelial Cell Proliferation	-0.26213167	12	1.668e-03	2.492e-01	LGMN:174 HSPB1:301 VEGFA:464 MELT:628 P2X4:2164 KDR:2330
Response To Peptidoglycan (GO:0032494)	-0.40472332	5	1.723e-03	2.506e-01	INAVA:402 ILK:430 IRAK3:721 IFI5:2460 RLEA:2:974 NA
Protein Ubiquitination (GO:0016567)	-0.050412199	329	1.795e-03	2.521e-01	ATG3:59 CUL4B:96 KHLH2:297 PILP2:154 NFRF8:228 DTX2:234
Monocarboxylic Acid Transport (GO:001517)	-0.11458399	62	1.827e-03	2.521e-01	SLC10A2:95 SLC27A4:11 SLC10A1:369 UPR1:616625 SLC01A2:681 FAPB6:916
Negative Regulation Of Leukocyte Proliferation	-0.44710420	4	1.955e-03	2.521e-01	TNFAIP3:492 LIL3:359 UPR9:986 LVE1:1062 NA