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_CARCINOMA_UP	0.05090702	1409	3.131e-10	8.542e-07	CEP19:2 MARCHF4:4 FNDC11:8 DNAH11:19 ANKRD35:26 DNAI2:36
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 CENPE:74 BUB1:76 WDHD1:88
STARK_HYPPOCAMPUS_22Q11_DELETION_DN	-0.38364159	20	2.866e-09	3.098e-06	PRODH:8 COMT:10 ARVCF:32 TRMT2A:62 RTN4R:102 TANGO2:251
DACOSTA_UV_RESPONSE_VIA_ERCC3_DN	-0.06289883	735	8.587e-09	7.748e-06	WDFY3:17 CD2AP:69 CENPE:74 WDHD1:88 MGLL:99 GINS1:105
BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP	-0.06524128	676	9.558e-09	7.748e-06	WDFY3:17 KDM4B:21 DNAJB4:52 SLC6A6:53 GTF2IRD1:54 ARPP19:66
RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_U	-0.07044644	570	1.121e-08	8.078e-06	SPIRE1:6 CCT6A:20 MCOLN3:23 ELOVL6:55 CENPE:74 WDHD1:88
WP_22Q112_COPY_NUMBER_VARIATION_SYNDROME	-0.16862472	95	1.389e-08	8.564e-06	PRODH:8 COMT:10 ARVCF:32 TRMT2A:62 SLC7A4:87 RTN4R:102
ZHANG_BREAST_CANCER_PROGENITORS_UP	-0.08766323	357	1.453e-08	8.564e-06	MIS18BP1:29 CNOT6:58 RIDA:65 ARPP19:66 CD2AP:69 BUB1:76
RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFE	-0.07163072	521	2.670e-08	1.443e-05	SPIRE1:6 CCT6A:20 ADAM9:47 ELOVL6:55 WDHD1:88 CUL4B:96
NIKOLSKY_BREAST_CANCER_12Q24_AMPLICON	0.40594170	15	5.230e-08	2.609e-05	NOC4L:116 GALNT9:313 POLE:580 SFSWAP:595 ULK1:660 CHFR:712
SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN	0.09500764	273	7.177e-08	3.324e-05	ANKRD35:26 DNAI2:36 TOGARAM2:73 CCDC81:130 IFT172:131 CFAP45:132
DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN	-0.07740417	400	1.232e-07	5.327e-05	CD2AP:69 CENPE:74 MGLL:99 GINS1:105 EHBP1:109 WAPL:123
DAZARD_RESPONSE_TO_UV_NHEK_DN	-0.09530322	258	1.475e-07	5.978e-05	WDFY3:17 WDHD1:88 WAPL:123 DST:188 MTCL1:190 CASP8:191
HSIAO_LIVER_SPECIFIC_GENES	-0.10049184	196	1.294e-06	4.937e-04	TM4SF4:16 TAT:33 SLC38A3:38 ITIH2:49 RIDA:65 ALB:80
FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_	-0.06969136	409	1.484e-06	5.345e-04	COMT:10 WDFY3:17 TBCB:25 CD2AP:69 CLU:114 ACOT13:140
DODD_NASOPHARYNGEAL_CARCINOMA_DN	-0.04315541	1082	2.225e-06	7.596e-04	CCT6A:20 NUP62:63 RIDA:65 ARPP19:66 CENPE:74 BUB1:76
NIKOLSKY_BREAST_CANCER_1Q21_AMPLICON	0.24114948	32	2.356e-06	7.639e-04	TRIM46:71 SCAMP3:152 HCN3:311 TDRKH:323 FLAD1:538 THBS3:1093
HAMAI_APOPTOSIS_VIA_TRAIL_UP	-0.05868001	556	2.590e-06	7.998e-04	IQGAP2:7 MIS18BP1:29 ADAM9:47 ZNF654:61 CENPE:74 WDHD1:88
ENK_UV_RESPONSE_KERATINOCYTE_DN	-0.06929358	392	2.756e-06	8.123e-04	CD2AP:69 BCAT2:101 RXYLT1:108 RARS1:166 PFKM:194 IMPA1:208
HOUNKPE_HOUSEKEEPING_GENES	-0.04844210	821	2.996e-06	8.447e-04	SAV1:2 CMTR1:4 COMT:10 KDM4B:21 TBCB:25 ATG3:59
OSMAN_BLADDER_CANCER_UP	-0.07550291	320	3.708e-06	9.945e-04	PTGER2:137 ATP11B:139 G2E3:186 KBTBD6:240 APPL1:310 FAM107B:320
SENESE_HDAC3_TARGETS_UP	-0.06932856	380	3.834e-06	9.945e-04	SAV1:2 SPIRE1:6 IQGAP2:7 PTPRB:34 SLC6A6:53 CUL4B:96
DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN	-0.08440465	243	6.194e-06	1.545e-03	KLHL2:97 ADGRG1:170 ABCB1:209 HEG1:261 SFI1:315 PTPRM:353
REACTOME_METABOLISM_OF_LIPIDS	-0.05190881	647	7.773e-06	1.867e-03	CYP11A1:14 CARM1:18 HADHB:24 ME1:37 GBA2:45 ELOVL6:55
REACTOME_METABOLISM_OF_AMINO_ACIDS_AND_D	-0.07699113	283	8.876e-06	2.056e-03	PRODH:8 TAT:33 RIDA:65 NAGS:77 BCAT2:101 ARG1:125
IBRAHIM_NRF2_UP	-0.06153676	438	1.114e-05	2.491e-03	CCT6A:20 ME1:37 DNAJB4:52 MTMR12:64 FTH1:89 RXYLT1:108
REACTOME_CLASS_A_1_RHODOPSIN_LIKE_RECEPT	0.07394779	295	1.331e-05	2.877e-03	PROKR1:17 RXFP3:35 GNRH1:106 DRD2:170 ADRB3:200 GPR37:226
SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6	-0.06650115	363	1.464e-05	2.992e-03	ELOVL6:55 NUP62:63 ARPP19:66 CENPE:74 BUB1:76 WDHD1:88
NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICO	0.11559790	118	1.476e-05	2.992e-03	FNDC11:8 PTK6:122 CHRNA4:143 ABHD16B:249 CASS4:467 TCFL5:540
MITSIADES_RESPONSE_TO_APLIDIN_DN	-0.08721012	207	1.592e-05	3.129e-03	BUB1:76 GINS1:105 EIF2AK2:183 AHCY:195 ATP13A3:210 SUGP2:233
IVANOVA_HEMATOPOIESIS_MATURE_CELL	-0.07987326	245	1.753e-05	3.343e-03	CMTR1:4 TM4SF4:16 SLC4A1:27 RHAG:75 PGLYRP1:83 SPTB:85
CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_2	0.06444975	377	1.881e-05	3.420e-03	CEP19:2 DZIP1:6 DNAH11:19 TOGARAM2:73 CFAP45:132 CEP41:138
MILI_PSEUDOPODIA_HAPTOTAXIS_UP	-0.06336575	390	1.898e-05	3.420e-03	DNAJB4:52 ARPP19:66 CD2AP:69 BUB1:76 CUL4B:96 CISD1:164
WP_METHIONINE_METABOLISM_LEADING_TO_SULF	-0.36689445	11	2.514e-05	4.406e-03	BHMT:153 AHCY:195 CSAD:494 CBS:621 MAT1A:666 GNMT:868
SHEN_SMARCA2_TARGETS_UP	-0.06604083	335	3.491e-05	5.958e-03	WDFY3:17 ATG3:59 CUL4B:96 EIF2AK2:183 RAB23:238 VPS13C:364
KEGG_ARRHYTHMOGENIC_RIGHT_VENTRICULAR_CA	0.14689327	66	3.716e-05	6.025e-03	CACNG4:85 EMD:104 DMD:228 CACNA2D3:346 ITGA3:358 ACTN1:405
WP_ARRHYTHMOGENIC_RIGHT_VENTRICULAR_CARD	0.14689327	66	3.716e-05	6.025e-03	CACNG4:85 EMD:104 DMD:228 CACNA2D3:346 ITGA3:358 ACTN1:405

## DisGeNET Top pathways by permulation

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 CCDC65:326 DNAH9:435 DNAH5:728 SPEF2:820
DiGeorge Syndrome	-0.19898041	57	2.088e-07	1.023e-03	PRODH:8 COMT:10 ARVCF:32 ALB:80 SPECC1L:151 NDST1:327
Impaired T cell function	-0.35315601	17	4.649e-07	1.519e-03	COMT:10 ARVCF:32 TNFRSF13B:258 UFD1:383 UMPS:428 CD19:565
Posterior embryotoxon	-0.25495313	31	9.072e-07	2.223e-03	COMT:10 ARVCF:32 UFD1:383 PEX2:407 JAG1:993 HIRA:1025
Seborrheic dermatitis	-0.31300806	20	1.267e-06	2.484e-03	COMT:10 ARVCF:32 SLCO2A1:46 UFD1:383 HIRA:1025 TBX1:1600
Embryotoxon	-0.25222446	30	1.758e-06	2.873e-03	COMT:10 ARVCF:32 UFD1:383 PEX2:407 JAG1:993 HIRA:1025
Polynesian Bronchiectasis	0.23541034	34	2.054e-06	2.876e-03	DNAH11:19 DNAI2:36 CCDC65:326 DNAH5:728 STK36:928 RSPH3:1118
Tetany	-0.30203645	20	2.939e-06	3.602e-03	COMT:10 ARVCF:32 SLC12A1:221 CASR:265 UFD1:383 TRPM6:904
22q11 Deletion Syndrome	-0.31090120	18	4.979e-06	5.424e-03	PRODH:8 COMT:10 ARVCF:32 UFD1:383 CXCR4:425 ZDHHC8:434
22q11 partial monosomy syndrome	-0.38897450	11	7.942e-06	7.786e-03	COMT:10 ARVCF:32 UFD1:383 PI4KA:789 HIRA:1025 TBX1:1600
Trisomy	-0.10341521	156	8.794e-06	7.837e-03	LPL:67 ALB:80 PAX5:231 MDM2:345 IL6:430 LTBR:454
Small earlobe	-0.33504955	13	2.886e-05	2.357e-02	COMT:10 ARVCF:32 UFD1:383 KCTD1:694 HIRA:1025 TBX1:1600
Shprintzen syndrome	-0.21873424	30	3.401e-05	2.498e-02	PRODH:8 COMT:10 ARVCF:32 UFD1:383 HIRA:1025 DGCR6L:1305
Dysseborrheic dermatitis	-0.30832704	15	3.567e-05	2.498e-02	COMT:10 ARVCF:32 SLCO2A1:46 UFD1:383 HIRA:1025 TBX1:1600
Hereditary spherocytosis	-0.24775670	23	3.924e-05	2.565e-02	SLC4A1:27 EPB42:42 SPTB:85 ANK1:119 SPTA1:135 SDS:167
Reticulocyte count (procedure)	-0.09306753	160	5.113e-05	3.022e-02	IQGAP2:7 SLC4A1:27 CD2AP:69 SPTB:85 ANK1:119 SPTA1:135
Occipital myelomeningocele	-0.38935500	9	5.241e-05	3.022e-02	COMT:10 ARVCF:32 UFD1:383 HIRA:1025 TBX1:1600 GP1BB:2218
Abnormality of the tonsils	-0.34467567	11	7.557e-05	4.116e-02	COMT:10 ARVCF:32 UFD1:383 HIRA:1025 TBX1:1600 GP1BB:2218
Anemia, Sickle Cell	-0.08760053	169	8.976e-05	4.543e-02	COMT:10 ALB:80 HBE1:124 SPTA1:135 KEL:275 RHD:296
Ewings sarcoma	-0.06934227	271	9.268e-05	4.543e-02	PAK3:39 LRP1:91 CASP8:191 ABCB1:209 LOX:227 FCGRT:291
Kartagener Syndrome	0.11965410	88	1.072e-04	4.956e-02	DNAH11:19 DNAI2:36 CFTR:81 DNAH3:232 CCDC65:326 DNAH9:435
Anemia, hereditary spherocytic hemolytic	-0.49417932	5	1.297e-04	4.956e-02	SLC4A1:27 EPB42:42 SPTB:85 ANK1:119 SPTA1:135 NA
Spherocytosis	-0.49417932	5	1.297e-04	4.956e-02	SLC4A1:27 EPB42:42 SPTB:85 ANK1:119 SPTA1:135 NA
Congenital atresia of nasopharynx	0.34929518	10	1.310e-04	4.956e-02	DNAH11:19 DNAH5:728 GAS8:1163 DRC1:1213 ARMC4:1815 DNAI1:2131
Other specified congenital malformations	0.34929518	10	1.310e-04	4.956e-02	DNAH11:19 DNAH5:728 GAS8:1163 DRC1:1213 ARMC4:1815 DNAI1:2131
Mental deficiency	-0.03846442	890	1.314e-04	4.956e-02	PRODH:8 TAT:33 PAK3:39 CLCNKB:50 CLCNKA:51 GTF2IRD1:54
Poor school performance	-0.03912154	849	1.415e-04	5.126e-02	PRODH:8 TAT:33 PAK3:39 CLCNKB:50 CLCNKA:51 GTF2IRD1:54
Upward slant of palpebral fissure	-0.10595977	108	1.464e-04	5.126e-02	COMT:10 ARVCF:32 EHMT1:273 UFD1:383 PEX2:407 CDK13:417
Solid Neoplasm	-0.04382415	658	1.536e-04	5.194e-02	TAT:33 LPL:67 BUB1:76 ALB:80 PGLYRP1:83 ANK1:119
Liver neoplasms	-0.03547721	1006	1.916e-04	6.261e-02	IQGAP2:7 COMT:10 KDM4B:21 TAT:33 LPL:67 ALB:80
Hepatocarcinogenesis	-0.05426388	395	2.393e-04	7.358e-02	KDM4B:21 NUP62:63 ALB:80 CLU:114 PTGES:117 ARG1:125
Increased variability in muscle fiber di	0.21663236	24	2.402e-04	7.358e-02	TCAP:145 ITGA7:555 SELENON:829 TWNK:1469 SQSTM1:2146 COL6A1:2205
Pain, Postoperative	-0.22973881	21	2.688e-04	7.770e-02	COMT:10 TRPV1:133 ABCB1:209 LIF:566 SCN9A:735 AP3B1:962
Bilateral cataracts (disorder)	-0.10549628	100	2.737e-04	7.770e-02	ADAM9:47 PAX5:231 CASR:265 MGST1:333 IFNGR1:341 GSTO1:389
Breast adenocarcinoma	-0.08948959	139	2.798e-04	7.770e-02	CASP8:191 ABCB1:209 GCLC:215 HSPB1:301 MDM2:345 VEGFA:446
Fabry Disease	-0.16580585	40	2.874e-04	7.770e-02	MANBA:142 ABCB1:209 NAGA:287 VCAM1:305 IL6:430 VEGFA:446
Leukemia, Myelocytic, Acute	-0.03105901	1265	2.970e-04	7.770e-02	TAT:33 PAK3:39 RHEBL1:60 BUB1:76 WDHD1:88 LRP1:91
Abnormality of aortic arch	-0.31474135	11	3.012e-04	7.770e-02	COMT:10 ARVCF:32 UFD1:383 HIRA:1025 TBX1:1600 GP1BB:2218
CONOTRUNCAL ANOMALY FACE SYNDROME	-0.22508768	21	3.572e-04	8.859e-02	COMT:10 ARVCF:32 UFD1:383 HIRA:1025 DGCR6:1380 TBX1:1600

4.544e-01 7.646e-01 KAT8:208 LGALS2:1682 FEN1:1923 ZNF646:2085 HSD17B8:2335 KHK:2485

customGeneSet Top pathways by permulation

1805 3.617e-04 8.859e-02

-0.02630665

COMT:10 KDM4B:21 BPIFB1:31 TAT:33 ADAM9:47 DNAJB4:52

Malignant neoplasm of lung

Geneset

Geneset

Cilium Movement (GO:0003341)

Axoneme Assembly (GO:0035082)

Regulation Of DNA-templated Transcriptio

Cilium-Dependent Cell Motility (GO:00602

GOCC\_CHROMOSOME

Axonemal Dynein Complex Assembly (GO:007 0.26722391

stat

0.25969962

0.25692897

-0.03634291

0.31091204

30

17

1447

expressionDirectionalSelection 0.05710956

expressionDirectionalSelection	0.007 10000	33		7.0406-01	NATO.200 EGALGZ.1002 TENT.1925 ZNI 040.2005 TIGDT/ Do.2555 NTN.240
NAFLDGWAS	-0.05873016	14	5.097e-01	7.646e-01	GPAM:1197 GID4:1580 MTTP:1967 INSR:2158 TRIB1:4372 TOR1B:5652
HumanLocalAdaptionDietAll	-0.02127660	12	8.212e-01	8.212e-01	GPX1:743 LCT:884 SLC22A4:1656 SEPSECS:4429 TRIP4:6368 GPX3:834
NA	NA	NA	NA	NA	NA NA NA NA NA
NA.1	NA	NA	NA	NA	NA NA NA NA NA
NA.2	NA	NA	NA	NA	NA NA NA NA NA
NA.3	NA	NA	NA	NA	NA NA NA NA NA
NA.4	NA	NA	NA	NA	NA NA NA NA NA
NA.5	NA	NA	NA	NA	NA NA NA NA NA
NA.6	NA	NA	NA	NA	NA NA NA NA NA
NA.7	NA	NA	NA	NA	NA NA NA NA NA
NA.8	NA	NA	NA	NA	NA NA NA NA NA
NA.9	NA	NA	NA	NA	NA NA NA NA NA
NA.10	NA	NA	NA	NA	NA NA NA NA NA
NA.11	NA	NA	NA	NA	NA NA NA NA NA
NA.12	NA	NA	NA	NA	NA NA NA NA NA
NA.13	NA	NA	NA	NA	NA NA NA NA NA
NA.14	NA	NA	NA	NA	NA NA NA NA NA
NA.15	NA	NA	NA	NA	NA NA NA NA NA
NA.16	NA	NA	NA	NA	NA NA NA NA NA
NA.17	NA	NA	NA	NA	NA NA NA NA NA
NA.18	NA	NA	NA	NA	NA NA NA NA NA
NA.19	NA	NA	NA	NA	NA NA NA NA NA
NA.20	NA	NA	NA	NA	NA NA NA NA NA
NA.21	NA	NA	NA	NA	NA NA NA NA NA
NA.22	NA	NA	NA	NA	NA NA NA NA NA
NA.23	NA	NA	NA	NA	NA NA NA NA NA
NA.24	NA	NA	NA	NA	NA NA NA NA NA
NA.25	NA	NA	NA	NA	NA NA NA NA NA
NA.26	NA	NA	NA	NA	NA NA NA NA NA
NA.27	NA	NA	NA	NA	NA NA NA NA NA
NA.28	NA	NA	NA	NA	NA NA NA NA NA
NA.29	NA	NA	NA	NA	NA NA NA NA NA
NA.30	NA	NA	NA	NA	NA NA NA NA NA
NA.31	NA	NA	NA	NA	NA NA NA NA NA
NA.32	NA	NA	NA	NA	NA NA NA NA NA
NA.33	NA	NA	NA	NA	NA NA NA NA NA
NA.34	NA	NA	NA	NA	NA NA NA NA NA
NA.35	NA	NA	NA	NA	NA NA NA NA NA
NA.36	NA	NA	NA	NA	NA NA NA NA NA

7.519e-10 4.045e-06

1.125e-06 3.027e-03

9.111e-06 9.913e-03

9.213e-06 9.913e-03

7.452e-06 9.913e-03

DNAH11:19 DNAI2:36 SPAG17:247 TEKT2:365 DNAH9:435 CFAP206:481

LRGUK:141 SPAG17:247 CCDC65:326 CFAP206:481 SPACA9:748 STK36:928

CARM1:18 TCF15:19 GTF2IRD1:54 NUP62:63 NSD1:106 ZNF628:149

DNAH3:232 CCDC65:326 TEKT2:365 TEKT5:791 DNAH17:1027 GAS8:1163 DNAI2:36 CCDC65:326 DNAH5:728 DNAH17:1027 TTC12:1033 DNAH1:1176

GO\_Biological\_Process\_2023 Top pathways by permulation

Neuropeptide Signaling Pathway (GO:00072	0.15797528	63	1.480e-05	1.327e-02	SORCS1:16 RXFP3:35 GPR37:226 LTB4R:329 OPRK1:635 GALR3:697
Regulation Of Heart Rate By Cardiac Cond	0.20221682	37	2.100e-05	1.614e-02	SCN5A:49 KCND3:97 HCN3:311 KCNE4:554 KCNE2:821 KCNH2:878
Muscle Contraction (GO:0006936)	0.12909370	82	5.460e-05	3.672e-02	CHRNE:42 EMD:104 LMOD3:204 CASQ2:245 LTB4R:329 CHRND:514
Regulation Of DNA Metabolic Process (GO:	-0.11567172	97	8.504e-05	5.084e-02	TERF2:152 USP37:477 RBBP6:587 ESCO1:647 MYC:858 ACTR5:1006
Positive Regulation Of Chemotaxis (GO:00	-0.17416692	41	1.152e-04	5.803e-02	LGMN:174 HSPB1:301 CCL19:329 PPM1F:339 IL6:430 VEGFA:446
Fatty Acid Transport (GO:0015908)	-0.18547566	36	1.187e-04	5.803e-02	SLCO2A1:46 SLC27A4:141 SLC22A6:660 FABP6:916 ACSL1:1041 PPARD:1166
Regulation Of Gene Expression (GO:001046	-0.03928959	829	1.593e-04	7.071e-02	CARM1:18 BTNL9:36 GTF2IRD1:54 LRP1:91 NSD1:106 PRKAG1:107
Cardiac Conduction (GO:0061337)	0.16773310	42	1.709e-04	7.071e-02	SCN5A:49 KCND3:97 HCN3:311 KCNE4:554 KCNE2:821 KCNH2:878
Cilium Movement Involved In Cell Motilit	0.39809113	7	2.650e-04	1.002e-01	TEKT2:365 TEKT5:791 GAS8:1163 TEKT3:1764 TEKT1:2092 TEKT4:2462
Alpha-Amino Acid Biosynthetic Process (G	-0.33043891	10	2.968e-04	1.002e-01	BCAT2:101 SDS:167 SDSL:384 ILVBL:561 CPS1:909 MTHFD1:2006
Protein Modification By Small Protein Co	-0.06407081	272	2.979e-04	1.002e-01	ATG3:59 CUL4B:96 KLHL2:97 DTX2:234 UBR1:241 KLHL25:255
Cilium Assembly (GO:0060271)	0.06933779	218	4.434e-04	1.403e-01	CEP19:2 TMEM216:3 DZIP1:6 DNAI2:36 E2F4:92 AVIL:112
Vesicle-Mediated Transport Between Endos	-0.20597376	23	6.300e-04	1.763e-01	SNX16:367 PTPN23:1022 RAB7A:1088 HOOK2:1270 PIK3R4:1354 BECN1:1697
Motile Cilium Assembly (GO:0044458)	0.26330544	14	6.481e-04	1.763e-01	E2F4:92 SPAG17:247 BBOF1:1683 RSPH9:2559 CCDC39:2623 MCIDAS:2794
Positive Regulation Of Cellular Componen	-0.10187651	94	6.555e-04	1.763e-01	LRP1:91 ASAP1:100 CLU:114 TPPP:127 CCL19:329 CRB3:344
Nitrogen Compound Transport (GO:0071705)	-0.08130372	146	7.209e-04	1.847e-01	SLC38A3:38 SLC6A6:53 RHAG:75 SLC7A4:87 ATP11B:139 RHCG:202
Early Endosome To Late Endosome Transpor	-0.20452387	22	9.007e-04	1.959e-01	SNX16:367 PTPN23:1022 RAB7A:1088 HOOK2:1270 PIK3R4:1354 BECN1:1697
Ventricular Cardiac Muscle Cell Action P	0.25589950	14	9.174e-04	1.959e-01	SCN5A:49 KCNE4:554 KCNE2:821 KCNH2:878 PKP2:1022 KCNQ1:1830
Negative Regulation Of Apoptotic Process	-0.05015361	375	9.347e-04	1.959e-01	NUP62:63 ALB:80 TMBIM4:110 CLU:114 LGMN:174 GCLC:215
Regulation Of Protein Phosphorylation (G	-0.06464198	221	9.775e-04	1.959e-01	NSD1:106 HSPB1:301 PECAM1:312 TSPYL2:359 AXIN1:360 FKBP8:382
Fatty Acid Catabolic Process (GO:0009062	-0.12524595	58	9.814e-04	1.959e-01	HADHB:24 NUDT7:86 SLC27A4:141 EHHADH:260 PEX2:407 PLA2G15:422
Negative Regulation Of Macromolecule Bio	-0.11020580	75	9.831e-04	1.959e-01	RIDA:65 EIF2AK2:183 CAPRIN1:443 AKR1B1:559 PATL2:603 TSPO:722
Mesodermal Cell Differentiation (GO:0048	0.33067506	8	1.201e-03	2.307e-01	ITGA3:358 ITGB4:951 ITGB1:1752 HMGA2:2252 ITGB3:2909 KDM6B:3230
Diol Biosynthetic Process (GO:0034312)	-0.24836416	14	1.295e-03	2.390e-01	ACER1:184 QDPR:640 SPHK1:725 SPHK2:943 SPTLC2:1933 ACER2:2283
Anterograde Trans-Synaptic Signaling (GO	0.07241974	166	1.332e-03	2.390e-01	CHRNE:42 DLG4:135 CHRNA4:143 RPS6KA1:154 CHRNA2:167 GABRR2:179
Regulation Of Interleukin-2 Production (	-0.14541368	40	1.472e-03	2.405e-01	HOMER3:111 CD80:172 IL17F:214 TNFAIP3:492 CD86:503 RPS3:907
Striated Muscle Contraction (GO:0006941)	0.13276812	48	1.474e-03	2.405e-01	SCN5A:49 TCAP:145 LMOD3:204 DMD:228 CASQ2:245 TNNI3:582
Positive Regulation Of Receptor-Mediated	-0.15114112	37	1.475e-03	2.405e-01	CLU:114 CD63:326 CCL19:329 VEGFA:446 RAB21:989 FMR1:1021
Cellular Response To Acetylcholine (GO:1	0.30402751	9	1.588e-03	2.492e-01	LY6G6D:430 CHRND:514 CHRM3:1023 LY6H:1052 ROCK2:1193 LYPD1:2631
Branched-Chain Amino Acid Metabolic Proc	-0.23496089	15	1.632e-03	2.492e-01	BCAT2:101 BCKDHA:1038 DBT:1399 PCCB:2152 HIBCH:2203 MCCC1:2244
Positive Regulation Of Endothelial Cell	-0.26213167	12	1.668e-03	2.492e-01	LGMN:174 HSPB1:301 VEGFA:446 MET:668 P2RX4:2164 KDR:2810
Response To Peptidoglycan (GO:0032494)	-0.40472332	5	1.723e-03	2.506e-01	INAVA:402 IL6:430 IRAK3:721 IRF5:2460 RELA:2974 NA
Protein Ubiquitination (GO:0016567)	-0.05041259	329	1.795e-03	2.521e-01	ATG3:59 CUL4B:96 KLHL2:97 PPIL2:154 RNF8:228 DTX2:234
Monocarboxylic Acid Transport (GO:001571	-0.11458389	62	1.827e-03	2.521e-01	SLC10A2:95 SLC27A4:141 SLC10A1:369 UGT1A6:625 SLCO1A2:681 FABP6:916
Negative Regulation Of Leukocyte Prolife	-0.44710420	4	1.955e-03	2.522e-01	TNFAIP3:492 IL33:554 ENPP3:986 LYN:1062 NA NA
Negative Regulation of Leukocyte Frome	-0.447 10420	4	1.955e=05	2.3226-01	TINFAIF 3.492 IL33.334 ENFF3.900 ETIN.1002 IVA IVA

GSEA-c5-HsSymbols Top pathways by permulation

Cerieset	Stat	num.genes	Pvai	p.auj	gene.vais
GOCC_CILIUM	0.09555095	623	6.795e-16	1.078e-11	CEP19:2 TMEM216:3 DZIP1:6 DNAH11:19 TPPP2:33 DNAI2:36
GOBP_CILIUM_MOVEMENT	0.18074911	157	6.156e-15	4.884e-11	DZIP1:6 DNAH11:19 TPPP2:33 DNAI2:36 TMF1:95 ATP1A4:123
GOCC_MOTILE_CILIUM	0.15261536	209	3.324e-14	1.758e-10	DNAH11:19 TPPP2:33 DNAI2:36 SAXO1:99 ACTL7A:101 ATP1A4:123
GOCC_9PLUS2_MOTILE_CILIUM	0.18178260	140	1.235e-13	4.899e-10	DNAH11:19 TPPP2:33 DNAI2:36 SAXO1:99 ATP1A4:123 IFT172:131
GOBP_CILIUM_OR_FLAGELLUM_DEPENDENT_CELL_	0.17880709	128	3.055e-12	9.694e-09	DZIP1:6 DNAH11:19 TPPP2:33 TMF1:95 ATP1A4:123 CFAP45:132
GOBP_AXONEME_ASSEMBLY	0.22834182	74	1.152e-11	3.048e-08	DNAI2:36 LRGUK:141 SPAG17:247 CCDC65:326 TEKT2:365 CFAP206:481
GOBP_SPERM_MOTILITY	0.17530259	107	3.921e-10	8.887e-07	DZIP1:6 DNAH11:19 TPPP2:33 TMF1:95 ATP1A4:123 CFAP45:132
GOBP_ORGANONITROGEN_COMPOUND_CATABOLIC_P	-0.05391880	1117	2.148e-09	3.951e-06	PRODH:8 COMT:10 TAT:33 GBA2:45 ADAM9:47 USP30:48
GOBP_MICROTUBULE_BUNDLE_FORMATION	0.17154411	102	2.241e-09	3.951e-06	TPPP2:33 DNAI2:36 AAAS:63 TRIM46:71 LRGUK:141 FES:198
GOCC_AXONEME	0.15554971	122	3.117e-09	4.947e-06	DNAH11:19 DNAI2:36 SAXO1:99 IFT172:131 CFAP45:132 AK8:168
GOBP_CILIUM_ORGANIZATION	0.08889188	375	4.057e-09	5.852e-06	CEP19:2 TMEM216:3 DZIP1:6 DNAI2:36 E2F4:92 SAXO1:99
GOBP_MICROTUBULE_BASED_MOVEMENT	0.09229572	338	6.402e-09	8.466e-06	DZIP1:6 DNAH11:19 TPPP2:33 DNAI2:36 TRIM46:71 TMF1:95
HP_ABNORMAL_SPERM_MOTILITY	0.17828241	87	9.344e-09	1.141e-05	DZIP1:6 DNAH11:19 DNAI2:36 CFAP45:132 TTC21A:240 SPAG17:247
GOBP_LIPID_METABOLIC_PROCESS	-0.04778256	1194	4.547e-08	5.153e-05	COMT:10 CYP11A1:14 ANGPTL8:22 HADHB:24 BPNT1:26 AVPR1A:28
GOCC_DYNEIN_COMPLEX	0.25171237	38	7.981e-08	8.443e-05	DNAH11:19 DNAI2:36 DYNC2LI1:190 DNAH3:232 CCDC65:326 DNAH10:368
GOBP_MOTILE_CILIUM_ASSEMBLY	0.19877875	59	1.308e-07	1.297e-04	DZIP1:6 E2F4:92 SPAG17:247 CFAP206:481 CFAP69:669 SPEF2:820
GOBP_ALPHA_AMINO_ACID_METABOLIC_PROCESS	-0.11007972	193	1.437e-07	1.341e-04	PRODH:8 TAT:33 RIDA:65 NAGS:77 BCAT2:101 ARG1:125
GOBP_ORGANIC_ACID_CATABOLIC_PROCESS	-0.09928539	236	1.620e-07	1.428e-04	PRODH:8 HADHB:24 TAT:33 RIDA:65 NUDT7:86 BCAT2:101
GOBP_MALE_GAMETE_GENERATION	0.07071490	470	1.790e-07	1.495e-04	DZIP1:6 TPPP2:33 ZBTB16:47 RAI14:62 CFTR:81 SPPL2C:90
GOCC_SUPRAMOLECULAR_POLYMER	0.05504118	769	2.764e-07	2.193e-04	DNAH11:19 TPPP2:33 DNAI2:36 NEXN:45 SCN5A:49 TOGARAM2:73
HP_INFERTILITY	0.10683192	189	4.353e-07	3.289e-04	CEP19:2 DZIP1:6 DNAH11:19 DNAI2:36 CFTR:81 GNRH1:106
GOCC_TRANSFERASE_COMPLEX	-0.05918915	629	5.049e-07	3.521e-04	ELOVL6:55 ATG3:59 CUL4B:96 KLHL2:97 PRKAG1:107 CDK7:118
GOBP_ALPHA_AMINO_ACID_CATABOLIC_PROCESS	-0.15393324	89	5.324e-07	3.521e-04	PRODH:8 TAT:33 RIDA:65 BCAT2:101 ARG1:125 IDO2:165
GOMF_MINUS_END_DIRECTED_MICROTUBULE_MOTO	0.36176534	16	5.451e-07	3.521e-04	DNAH11:19 DNAH3:232 DNAH10:368 DNAH9:435 DYNC2H1:487 DNAH5:728
GOCC_AXONEMAL_DYNEIN_COMPLEX	0.36152226	16	5.548e-07	3.521e-04	DNAI2:36 DNAH3:232 CCDC65:326 DNAH9:435 DNAH5:728 DNAH17:1027
GOBP_NEUROPEPTIDE_SIGNALING_PATHWAY	0.14430626	99	7.198e-07	4.393e-04	SORCS1:16 PROKR1:17 RXFP3:35 GPR37:226 LTB4R:329 OPRK1:635
HP_CHRONIC_SINUSITIS	0.19820968	52	7.739e-07	4.548e-04	DNAH11:19 DNAI2:36 CFTR:81 CFAP45:132 CCDC65:326 DNAH9:435
HP_ABNORMAL_ATRIAL_ARRANGEMENT	0.22010494	42	8.069e-07	4.573e-04	DNAH11:19 DNAI2:36 CCDC65:326 DNAH9:435 DNAH5:728 SPEF2:820
GOBP_SMALL_MOLECULE_CATABOLIC_PROCESS	-0.07539102	362	9.408e-07	5.148e-04	PRODH:8 HADHB:24 BPNT1:26 TAT:33 RIDA:65 NUDT7:86
GOBP_SPERMATID_DIFFERENTIATION	0.11259537	159	1.009e-06	5.338e-04	DZIP1:6 CFTR:81 SPPL2C:90 TMF1:95 ACTL7A:101 ADAD1:105
HP_NASAL_CONGESTION	0.20190902	48	1.316e-06	6.738e-04	DNAH11:19 DNAI2:36 CCDC65:326 DNAH9:435 DNAH5:728 SPEF2:820
GOBP_AXONEMAL_DYNEIN_COMPLEX_ASSEMBLY	0.26814276	27	1.423e-06	7.058e-04	DNAI2:36 CCDC65:326 TEKT2:365 DAW1:708 DNAH5:728 DNAH17:1027
HP_SPHEROCYTOSIS	-0.49091204	8	1.522e-06	7.105e-04	SLC4A1:27 EPB42:42 RHAG:75 SPTB:85 ANK1:119 SPTA1:135
GOCC_CHROMATIN	-0.04525291	1015	1.522e-06	7.105e-04	TCF15:19 NSD1:106 WAPL:123 CUX2:150 DDX21:155 KMT5C:162
GOBP_POSITIVE_REGULATION_OF_CELL_CYCLE_P	-0.09534216	214	1.635e-06	7.412e-04	NUP62:63 CUL4B:96 BRD4:181 WIZ:282 MEPCE:290 MDM2:345
HP_ABSENT_SPERM_FLAGELLA	0.30918588	20	1.699e-06	7.489e-04	DZIP1:6 TTC21A:240 DNAH10:368 SPEF2:820 TTC29:983 DNAH17:1027
GOBP_ORGANIC_ACID_METABOLIC_PROCESS	-0.04900783	840	1.850e-06	7.730e-04	PRODH:8 HADHB:24 BPNT1:26 SLC4A1:27 AVPR1A:28 TAT:33
HP_DECREASED_FERTILITY_IN_MALES	0.11260181	151	1.871e-06	7.730e-04	DZIP1:6 DNAH11:19 DNAI2:36 CFTR:81 TTC21A:240 SPAG17:247
GOBP_MICROTUBULE_BASED_PROCESS	0.05149941	754	1.900e-06	7.730e-04	CEP19:2 DZIP1:6 PHLDB1:12 DNAH11:19 TPPP2:33 DNAI2:36
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