DisGeNET Top pathways by non−permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
Ciliary Motility Disorders	0.16317105	57	2.066e−05	2.027e−01	DNAH9:5 CCDC151:47 AK7:231 OFD1:243 ARMC4:370 CFAP221:399
Carcinoma, Transitional Cell	−0.05419937	324	8.510e−04	7.540e−01	ABCB1:25 BAX:52 HDAC8:61 ST13:68 TNF:80 VEGFA:95
Chronic glomerulonephritis	−0.24014893	15	1.282e−03	7.540e−01	LTA:71 TNF:80 VEGFA:95 TGFB2:552 IL6:568 BRD2:580
Congenital anomaly of cartilage	−0.37893894	6	1.307e−03	7.540e−01	TGFB2:552 TGFBR1:573 IGF1:668 COL2A1:1065 ATF2:1276 CUL7:7162.5
CONOTRUNCAL ANOMALY FACE SYNDROME	−0.20361091	21	1.241e−03	7.540e−01	HIRA:219 DGCR2:233 DGCR8:357 CRKL:438 JMJD1C:821 ESS2:849
Defective enamel matrix	0.15159146	39	1.060e−03	7.540e−01	PLEC:19 ITGA6:196 OFD1:243 STX16:261 FGFR2:470 ITGB4:525
Desmoplastic Medulloblastoma	−0.14154015	47	7.937e−04	7.540e−01	L3MBTL3:46 KDM4B:65 MYCN:114 L3MBTL2:215 S100A6:373 HIC1:551
DiGeorge Syndrome	−0.13626714	61	2.354e−04	7.540e−01	SPECC1L:89 VEGFA:95 ALB:152 HIRA:219 DGCR2:233 PRODH:253
Dysplasia of tooth enamel	0.15159146	39	1.060e−03	7.540e−01	PLEC:19 ITGA6:196 OFD1:243 STX16:261 FGFR2:470 ITGB4:525
Hepatitis B	−0.04014637	634	6.442e−04	7.540e−01	PROM1:1 AICDA:23 ABCB1:25 FABP1:47 TAT:55 LTA:71
Kartagener Syndrome	0.10614076	93	4.116e−04	7.540e−01	DNAH9:5 DNAH17:33 CCDC151:47 AK7:231 OFD1:243 ARMC4:370
Medullomyoblastoma	−0.14843277	40	1.168e−03	7.540e−01	L3MBTL3:46 KDM4B:65 MYCN:114 L3MBTL2:215 S100A6:373 HIC1:551
Melanotic medulloblastoma	−0.14843277	40	1.168e−03	7.540e−01	L3MBTL3:46 KDM4B:65 MYCN:114 L3MBTL2:215 S100A6:373 HIC1:551
Polynesian Bronchiectasis	0.18140321	35	2.053e−04	7.540e−01	CCDC151:47 OFD1:243 ARMC4:370 RSPH9:558 DNAH11:609 GAS8:657
Shprintzen syndrome	−0.16373190	33	1.139e−03	7.540e−01	HIRA:219 DGCR2:233 PRODH:253 DGCR8:357 CRKL:438 CHRNA7:791
Thin dental enamel	0.15159146	39	1.060e−03	7.540e−01	PLEC:19 ITGA6:196 OFD1:243 STX16:261 FGFR2:470 ITGB4:525
Urothelial Carcinoma	−0.06914302	206	6.511e−04	7.540e−01	HDAC8:61 TNF:80 VEGFA:95 KDR:216 DNMT3B:228 ADAM9:295
Posterior embryotoxon	−0.16578766	31	1.405e−03	7.660e−01	HIRA:219 DGCR2:233 PEX13:321 DGCR8:357 PAX6:517 JMJD1C:821
T−lymphocyte immunodeficiency	0.36908829	6	1.742e−03	8.697e−01	LBR:89 SMARCAL1:106 RAG1:273 SFTPA1:1346 CD3E:1936 SIPA1:8620.5
Ureteral obstruction	−0.08527262	113	1.773e−03	8.697e−01	FABP1:47 HSD17B6:92 VEGFA:95 IL4:126 ALB:152 KDR:216
Hepatocarcinogenesis	−0.04351578	429	2.152e−03	9.724e−01	PROM1:1 AICDA:23 BAX:52 IGF2BP2:58 KDM4B:65 ARHGAP24:79
Malignant tumor of cervix	−0.03532442	662	2.181e−03	9.724e−01	ABCB1:25 BAX:52 LTA:71 RBL1:77 ARHGAP24:79 TNF:80
46, XX Testicular Disorders of Sex Devel	−0.05232156	7	6.317e−01	9.827e−01	NR5A1:442 SOX3:7162.5 RSPO1:7162.5 SOX9:7162.5 NR0B1:7162.5 SOX10:7162.5
46, XY female	−0.09952397	16	1.682e−01	9.827e−01	PRKY:153 PRKX:462 SSRP1:851 SOX9:7162.5 NR0B1:7162.5 HSD17B3:7162.5
46,XY partial gonadal dysgenesis	−0.12553242	10	1.693e−01	9.827e−01	NR5A1:442 WT1:1145 SOX9:7162.5 NR0B1:7162.5 MAP3K1:7162.5 ZFPM2:7162.5
5,10−Methylenetetrahydrofolate reductase	−0.06813905	18	3.170e−01	9.827e−01	ABCB1:25 SERPINE1:966 GPX3:7162.5 XRCC3:7162.5 XRCC4:7162.5 MTHFR:7162.5
Abnormalities, Drug−Induced	0.08819500	4	5.413e−01	9.827e−01	EPHX1:194 WNT11:8620.5 CAT:8620.5 CRBN:8620.5 NA NA
Abortion, Habitual	−0.15721803	4	2.761e−01	9.827e−01	VEGFA:95 MTHFR:7162.5 F2:7162.5 F5:7162.5 NA NA
Abortion, Tubal	0.00676453	91	8.238e−01	9.827e−01	ECM2:18 COL6A1:121 IL16:122 IGFBP1:284 CSRNP3:300 MMP7:338
Achondrogenesis, type IB (disorder)	−0.13418858	5	2.987e−01	9.827e−01	SLC26A3:139 SLC26A2:7162.5 SLC26A5:7162.5 SLC26A4:7162.5 DCN:7162.5 NA
Acidosis, Lactic	−0.01440357	148	5.462e−01	9.827e−01	TNF:80 HSD17B6:92 COA7:127 UQCC3:188 NDUFB3:290 PRKAA1:337
ACROMESOMELIC DYSPLASIA, MAROTEAUX TYPE	−0.14788523	4	3.057e−01	9.827e−01	IGF1:668 NPPC:7162.5 NPR2:7162.5 GDF5:7162.5 NA NA
ACTH Syndrome, Ectopic	−0.04495989	5	7.277e−01	9.827e−01	CRH:7162.5 AVPR1B:7162.5 NR3C1:7162.5 PAK3:7162.5 GHSR:7162.5 NA
Acute Myeloid Leukemia, M1	−0.01588563	100	5.836e−01	9.827e−01	ASMTL:316 TNFSF10:339 ATP1B1:399 AQP9:699 HSPB1:809 SPI1:854
Acute myeloid leukemia, minimal differen	−0.03107771	18	6.481e−01	9.827e−01	ELL:8 ABCB1:25 CD34:1220 RUNX1:7162.5 FAS:7162.5 FANCB:7162.5
Adenocarcinoma of lung, stage IV	0.03827482	17	5.849e−01	9.827e−01	CD74:547 ROS1:631 EGFR:2281 MET:8620.5 TP53:8620.5 KRAS:8620.5
Adenocarcinoma, Basal Cell	−0.03031455	100	2.956e−01	9.827e−01	TNF:80 VEGFA:95 KDR:216 SMARCC1:607 EGF:719 CKB:806
Adenocarcinoma, Clear Cell	−0.02227290	91	4.634e−01	9.827e−01	ABCB1:25 VEGFA:95 ALDH1A1:167 KNG1:186 CTLA4:276 POU5F1:353
Adenocarcinoma, intestinal type	−0.04628967	12	5.788e−01	9.827e−01	BECN1:610 TP53:7162.5 KRAS:7162.5 BRAF:7162.5 CDKN2A:7162.5 MDM2:7162.5
Adenocarcinoma, metastatic	−0.10954803	12	1.889e−01	9.827e−01	ALB:152 EGF:719 MYC:890 HSPA5:7162.5 KRAS:7162.5 ERBB2:7162.5