

GO_Biological_Process_2023 Top pathways by permulation

Geneset	stat	num_genes	pval	p.adj	gene.vals
Negative Regulation Of Gene Expression V	0.4443979	5	5.786e-04	2.555e-02	USP7:105 HELLS:341 UHRF1:431 UHRF2:738 ZNF45:2794 NA
Transmembrane Receptor Protein Tyrosine	-0.4113276	4	8.839e-03	9.078e-02	TRIO:437 PTN:1193 PTPRD:1777 PTPRF:2041 NA NA
Striated Muscle Hypertrophy (GO:0014897)	-0.4146901	4	4.073e-03	9.377e-02	TCAP:388 MYOC:1391 RYR2:1609 HTR2B:2232 NA NA
snRNA Transcription By RNA Polymerase II	-0.4082423	4	4.295e-03	9.766e-02	SNAPC5:84 ICE2:1182 SNAPC1:1866 ZC3H8:2427 NA NA
Atrial Cardiac Muscle Cell To AV Node Ce	-0.4093389	6	5.158e-04	2.417e-02	GJA1:638 SCN3B:822 KCNQ1:1341 SCN5A:1561 GJC1:1769 KCNE5:2838
Atrial Cardiac Muscle Cell Action Potent	-0.4082423	11	2.757e-06	4.792e-04	KCNQ2:933 KCANB2:377 GJA1:638 SCN3B:822 KCNQ3:1219 KCNQ1:1341
Positive Regulation Of Peptidyl--Serine P	0.3911883	4	6.734e-03	1.295e-01	IFNG:257 LIF:403 IFNK:669 IFNE:5676 NA NA
Regulation Of Peptidyl--Serine Phosphoryl	0.3911883	4	6.734e-03	1.295e-01	IFNG:257 LIF:403 IFNK:669 IFNE:5676 NA NA
SA Node Cell Action Potentials (GO:008601	-0.3804143	5	3.219e-03	8.299e-02	CACNA1G:66 CACNA1D:583 SCN3B:822 SCN5A:1561 HCN4:6779 NA
Positive Regulation Of Opsinization (GO:	-0.3784966	4	8.747e-03	1.515e-01	COLEC11:302 COLEC10:997 PLA2G5:3134 MYO18A:3607 NA NA
Regulation Of Glycogen (Starch) Synthase	0.3685854	5	4.312e-03	9.766e-02	INPP5K:699 PPP1R3F:924 IGFB2:2372 GSK3B:2946 GSK3A:3527 NA
RIG-I Signaling Pathway (GO:0039529)	-0.3677064	4	1.086e-02	1.753e-01	RNF135:510 TRIM25:1117 OAS3:2368 PHB2:4719 NA NA
Plasma Membrane Phospholipid Scrambling	-0.3653594	5	4.664e-03	1.026e-01	PLSCR3:92 ANO7:360 P2RX7:411 PLSCR5:3087 PLSCR4:7127 NA
Organic Hydroxy Compound Catabolic Proce	0.3555406	6	2.561e-03	7.225e-02	PDXP:843 FGF23:859 HSD17B6:1256 LCT:1516 CYP2A1:1836 LDHD:7517
Establishment Of Mitotic Sister Chromati	0.3551057	6	2.592e-03	7.275e-02	STAG1:824 NIPBL:948 SMC3:1217 RAD21:2361 STAG2:2857 SMC1A:5679
Hepoxilin Biosynthetic Process (GO:00511	-0.3497193	4	1.542e-02	2.131e-01	ALOXE3:488 ALOX15B:2296 ALOX12B:2757 ALOX15:4358 NA NA
Hepoxilin Metabolic Process (GO:0051121)	-0.3497193	4	1.542e-02	2.131e-01	ALOXE3:488 ALOX15B:2296 ALOX12B:2757 ALOX15:4358 NA NA
Positive Regulation Of DNA Methylation--D	0.34390984	8	6.280e-04	2.739e-02	TASOR:349 SETDB2:437 PPHLN1:828 AT7FIP2:1595 TRIM28:2274 MORC2:2819
Cellular Response To UV--A (GO:0071492)	-0.3489810	9	2.886e-04	1.603e-02	MME:236 OPN1SW:531 PPID:596 MMP9:1060 OPN3:1133 MMP3:1808
Androgen Biosynthetic Process (GO:000670	0.3431339	7	1.667e-03	5.397e-02	MED1:333 HSD3B2:943 HSD17B3:1051 HSD17B6:1256 SRD5A1:4241 SRD5A3:4513
Detection Of Muscle Stretch (GO:003595)	-0.3431090	5	7.882e-03	1.416e-01	TCAP:388 PTK2:2125 CDH2:2549 CTNNB1:3471 CSRP3:4397 NA
Glucocorticoid Biosynthetic Process (GO:	0.3427544	3	3.976e-02	3.209e-01	CYP17A1:248 CYP21A2:3245 CYP11A1:4086 NA NA NA
Actin--Myosin Filament Sliding (GO:003327	-0.3420364	11	8.571e-05	6.505e-03	MYH8:153 MYH2:312 MYH6:664 TPM1:919 MYH4:955 TNNT2:993
Positive Regulation Of Mast Cell Activat	0.3355274	4	2.012e-02	2.368e-01	TSLP:186 SPHK2:1020 NECTIN2:3841 NR4A3:5702 NA NA
Inhibitory Postsynaptic Potential (GO:00	-0.3347499	6	4.549e-03	1.009e-01	GLRA1:402 INSYN2A:1178 NLGN3:2399 NPAS4:2963 INSYN1:3211 INSYN2B:6191
Glucocorticoid Metabolic Process (GO:000	0.3324978	5	1.003e-02	1.642e-01	CYP17A1:248 HSD11B2:2886 YWHAH:2960 CYP21A2:3245 CYP11A1:4086 NA
Regulation Of DNA Methylation--Dependent	0.3323028	14	1.673e-05	2.049e-03	TASOR:349 TET1:395 SETDB2:437 L3MBTL3:538 PPHLN1:828 SAMD1:981
Positive Regulation Of CD4--positive, CD2	0.3297362	3	4.792e-02	3.513e-01	IFNG:257 HLA--DRA:1240 KHL25:6716 NA NA NA
snRNA Modification (GO:0040031)	0.3294592	4	2.248e-02	2.452e-01	METTL18:869 NHP2:2194 MPECE:3011 METTL4:4751 NA NA
Muscle Filament Sliding (GO:0030049)	-0.3279529	10	3.281e-04	1.786e-02	MYH8:153 MYH6:664 TPM1:919 MYH4:955 TNNI2:993 MYGB8:1497
Membrane Lipid Catabolic Process (GO:004	0.3248545	7	2.917e-03	7.778e-02	SMPD2:857 MGST2:1147 PPT1:2595 SMPD1:3829 SGPL1:3217 ENPP2:3952
MHC Class II Protein Complex Assembly (G	0.3240637	7	2.986e-03	7.811e-02	HLA--DOA:66 GNAO1:967 HLA--DOB:977 HLA--DRA:1240 HLA--DPA1:4273 HLA--DMA:4357
Peptide Antigen Assembly With MHC Class	0.3240637	7	2.986e-03	7.811e-02	HLA--DOA:66 GNAO1:967 HLA--DOB:977 HLA--DRA:1240 HLA--DPA1:4273 HLA--DMA:4357
Regulation Of Thymocyte Apoptotic Proces	0.3231736	4	2.518e-02	2.613e-01	TP53:1394 BMP4:1773 ZC3H8:2427 JAK3:5719 NA NA
Chitin Catabolic Process (GO:0006030)	-0.3224901	2	1.142e-01	4.845e-01	CTBS:1223 CHIT1:4615 NA NA NA NA
Chitin Metabolic Process (GO:0006032)	-0.3224901	2	1.142e-01	4.845e-01	CTBS:1223 CHIT1:4615 NA NA NA NA
Adenylyate Cyclase--Inhibiting Serotonin R	-0.3203648	6	6.575e-03	1.284e-01	HTR1B:18 HTR1D:144 HTR1F:1671 HTR5A:4324 HTR1E:4268 HTR1A:8224
Positive Regulation Of Chemokine (C--X--C	0.3321099	4	2.660e-02	2.681e-01	TNF:1142 MHGB1:2063 TLR4:2553 LCP1:5752 NA NA
Ventricular Cardiac Muscle Cell Membrane	-0.3198836	7	3.380e-03	8.591e-02	KCNJ3:1219 KCNQ1:1341 KCNJ5:1985 KCNE1:2854 KCNE2:3086 KCNH2:4475
Positive Regulation Of Heterochromatin F	0.3197136	11	2.411e-04	1.412e-02	TASOR:349 SETDB2:437 PPHLN1:828 AT7FIP2:1595 TRIM28:2274 MORC2:2819

EnrichmentHsSymbolsFile2 Top pathways by permulation

Geneset	stat	num_genes	pval	p.adj	gene.vals
REACTOME_SPERM_MOTILITY_AND_TAXES	0.4327112	8	2.250e-05	8.743e-04	CATSPER2:12 CATSPERG:43 CATSPERB:79 CATSPERD:380 CATSPER4:812 KCNU1:1183
WP_AFLATOXIN_B1_METABOLISM	-0.4113276	2	4.392e-02	2.285e-01	EPHX1:1046 CYP1A2:1817 NA NA NA NA
MIKHAYLOVA_OXIDATIVE_STRESS_RESPONSE_VIA	0.3978723	6	7.373e-04	1.454e-02	PGAM1:38 HSPB1:317 CTSD:404 CALU:907 OAT:3537 AKR1B1:4722
REACTOME_ESTABLISHMENT_OF_SISTER_CHROMAT	0.39277351	11	6.468e-06	3.019e-04	ESCO1:1302 PDS5B:653 WAPL:762 STAG1:824 SMC3:1217 PDS5A:1375
WP_NIPBL_ROLE_IN_DNA_DAMAGE_CORNELIA_DE	0.3677627	7	7.524e-04	1.470e-02	RNF2:477 RNF168:327 H2AX:541 NIPBL:948 CBX3:3253 ATR:3509
REACTOME_MINERALOCORTICOID_BIOSYNTHESIS	0.3674805	4	1.091e-02	9.969e-02	CGA:456 HSD3B2:943 CYP21A2:3245 HSD18A:3927 NA NA
REACTOME_GLUCCORTICOID_BIOSYNTHESIS	0.3662302	6	1.891e-03	3.014e-02	CYP17A1:248 HSD3B2:943 HSD11B1:1291 HSD11B2:2886 CYP21A2:3245 SERPINA6:4378
REACTOME_PREDNISONE_ADME	0.3621584	5	5.036e-03	5.940e-02	ALB:1283 HSD11B1:1291 ABCB1:1314 HSD11B2:2886 SERPINA6:4378 NA
WP_PILOCYTIC_ASTROCYTOMA	0.3612640	6	2.179e-03	3.313e-02	SOS1:445 RAF1:861 GRB2:1307 BRAF:2046 NF1:2736 PTPN11:6081
NIKOLSKY_BREAST_CANCER_17P11_AMPLICON	0.3479529	10	1.388e-04	3.865e-03	ALDH3A2:267 LSC2:368 SLCA7A1:477 EPN2:706 RNF112:2016 SLC47A2:2297
MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_1	0.3402176	3	3.712e-02	2.096e-01	GATA1:1199 WAS:1974 TFE3:4230 NA NA NA
CHOL_ATL_ACUTE_STAGE	0.3402176	4	1.844e-02	1.383e-01	MBD1:237 MET:833 LHX2:4603 ETV1:4666 NA NA
REACTOME_MET_ACTIVATES_PTPN11	0.3369180	5	9.074e-03	8.830e-02	GAB1:418 MET:833 GRB2:1307 HGF:4558 PTPN11:6081 NA
REACTOME_FORMYL_PEPTIDE_RECEPTORS_BIND_F	-0.3347935	4	2.039e-02	1.457e-01	APP:255 HEBP1:375 ANXA1:3526 FPR2:6566 NA NA
NIKOLSKY_BREAST_CANCER_21Q22_AMPLICON	-0.3307171	14	1.831e-05	7.379e-04	PCBP3:248 COL6A1:436 DIP2A:843 SPATC1L:1211 YBEY:2156 COL6A2:2530
OHASHI_AURKA_TARGETS	0.3250838	4	2.433e-02	1.645e-01	DLGAP5:1246 TP53:1394 CDC25B:3713 MBD3:4967 NA NA
REACTOME_ELECTRIC_TRANSMISSION_ACROSS_GA	-0.3242662	5	1.203e-02	1.066e-01	PANX1:220 GJA10:1151 GJC1:1769 PANX2:1390 GJD2:5805 NA
REACTOME_LEUKOTRIENE_RECEPTORS	-0.3234565	5	1.224e-02	1.075e-01	LTBR4:528 LTBAR:1002 CYS1LTR2:1390 GPR17:3658 CYS1LTR1:7742 NA
BERGER_MBD2_TARGETS	-0.3225602	2	1.141e-01	3.839e-01	TFE2:552 CEL2A2:530 NA NA NA NA
REACTOME_COHESIN_LOADING_ONTO_CHROMATIN	0.3191736	10	4.738e-04	1.032e-02	PDS5B:653 WAPL:762 STAG1:824 NIPBL:948 SMC3:1217 PDS5A:1375
HEIDENBLAD_AMPLIFIED_IN_BONE_CANCER	0.3168598	7	3.692e-03	4.810e-02	MDM2:392 TSPAN31:763 FGF23:859 CCND2:2187 CDK4:3471 SIK1:383L:3663
WALLACE_PROSTATE_CANCER_DN	-0.3147394	5	1.479e-02	1.208e-01	GJA1:638 GPM6B:2592 LAMA4:2750 CA2V:3045 RAP1B:5993 NA
CROSBY_E2F4_TARGETS	0.3139116	6	7.744e-03	8.000e-02	CENPE:1016 CDC6:1475 BUB1B:2075 NDC80:2206 PTTG1:2529 CHEK1:8772
REACTOME_BIOSYNTHESIS_OF_MARESIN_LIKE_SP	-0.3129467	2	1.253e-01	4.054e-01	CYP1A2:1817 CYP2E1:4240 NA NA NA NA
WP_STEROID_HORMONE_PRECURSOR_BIOSYNTHESI	0.3119430	7	4.259e-03	5.300e-02	CYP17A1:248 HSD3B2:943 AKR1D1:3241 CYP21A2:3245 CYP11A1:4086 SRD5A1:4241
REACTOME_NEGATIVE_FEEDBACK_REGULATION_OF	0.3064465	6	9.330e-03	9.008e-02	MAP2K2:485 RAF1:861 MAP2K1:882 BRAF:2046 MAPK1:5771 MAPK3:8759
REACTOME_TYPE_I_HEMIDESMOSOME_ASSEMBLY	-0.3063766	11	4.337e-04	9.637e-03	PLEC:16 ITGB4:192 LAMB3:361 LAMC2:492 KRT14:721 ITGA6:2177
TURASHVILI_BREAST_NORMAL_DUCTAL_VS_LOBUL	0.3056030	6	9.527e-03	9.143e-02	EHBP1:203 RHOB1B3:725 TSPAN5:835 DCM:3763 MBTPS2:5057 ARHGEF9:8301
WP_IRINOTECAN_PATHWAY	0.3039092	4	3.527e-02	2.034e-01	SLC01B1:372 ABCB1:613 BCHE:2914 UGT1A1:8804 NA NA
REACTOME_ANDROGEN_BIOSYNTHESIS	0.3027715	9	1.658e-03	2.723e-02	CYP17A1:248 CGA:456 HSD3B2:943 HSD17B3:1051 LHB:3927 SRD5A1:4241
REACTOME_ESTROGEN_STIMULATED_SIGNALING_T	0.3024543	4	3.616e-02	2.071e-01	PDPK1:1180 NRAS:1780 KRAS:4052 MAPK1:5771 NA NA
REACTOME_ACTIVATION_OF_NOXA_AND_TRANSLOC	0.3013315	4	3.686e-02	2.090e-01	TP53:1394 E2F1:1942 TDFP1:2573 TDFP2:6958 NA NA
JL_CARCINOGENESIS_BY_KRAS_AND_STK11_UP	-0.2987281	10	1.071e-03	1.940e-02	TIAM1:143 BNC1:420 PKP1:972 KRT5:2486 LYPD3:3453 TP63:3845
REACTOME_BIOSYNTHESIS_OF_MARESIN	-0.2981846	4	3.887e-02	2.154e-01	ALOX5:278 CYP1A2:1817 CYP2E1:4240 EPHX2:6751 NA NA
SMID_BREAST_CANCER_ERBB2_DN	-0.2963027	4	4.012e-02	2.189e-01	NPY1R:566 FGFR2:1822 GABRP:3916 SOD1:3010:6899 NA NA
REACTOME_SARS_COV_1_MODULES_HOST_TRANS	0.2944289	31	1.403e-08	1.423e-06	RPS24:210 RPS5:836 RPS27L:539 RPS27:719 RPS15:945 RPS6:1023
CHEN_HOXA5_TARGETS_6HR_DN	0.2941549	5	2.272e-02	1.571e-01	ZBED8:1034 NPTXR:1397 TUBA1A:3257 FXJ1:3829 PRPF31:7140 NA
REACTOME_ROLE_OF_SECOND_MESSENGERS_IN_NE	-0.2940138	10	1.284e-03	2.215e-02	TRPC4:303 DCC:614 TRPC5:886 TRPC6:1365 NTN1:1634 TRPC3:2302
KUMAMOTO_RESPONSE_TO_NUTLIN_3A_DN	0.2927550	7	7.308e-03	7.735e-02	CNGB1:160 SPAG5:343 KIFC1:961 KIF2C:1664 CCNA2:5872 CDKN3:6861
WP_GLUCCORTICOID_BIOSYNTHESIS	0.2919065	6	1.327e-02	1.129e-01	HSD11B1:1291 HSD11B2:2886 AKR1D1:3241 CYP21A2:3245 SRD5A1:4241 SRD5A2:5297

DisGeNET Top pathways by permulation

Human metapneumovirus infection	0.4103988	5	1.482e-03	9.693e-02	TSLP:18 PIP5K1:40 TNF:1142 NCR1:2359 ISYNA1:3676 NA
Herlitz Disease	-0.4086677	5	1.552e-03	9.895e-02	ITGB4:192 LAMB3:361 LAMC2:492 ITGA6:2177 LAMA3:4062 NA
Localized vitiligo	0.4076994	2	4.582e-02	3.643e-01	TNF:1142 RBM45:1802 NA NA NA NA
Congenital pyloric atresia	-0.4069048	5	1.626e-03	1.006e-01	PLEC:16 ITGB4:192 LAMC2:492 ITGA6:2177 COL17A1:4556 NA
Bulla of lung	-0.3992733	2	5.049e-02	3.773e-01	EPHX1:1046 TIMP2:2139 NA NA NA NA
Plantar hyperkeratosis	-0.3991391	6	7.095e-04	6.446e-02	PLEC:16 ITGB4:192 LAMB3:361 LAMC2:492 LAMA3:4062 COL17A1:4556
Ineffective erythropoiesis	0.3958478	5	2.173e-03	1.099e-01	RPL26:98 COX4I2:995 KLF1:1184 GATA1:1199 SEC23B:5003 NA
Opticospinal Multiple Sclerosis	0.3894387	4	6.984e-03	1.730e-01	CD2AP:590 RBM45:1802 AQP4:1987 PLA2G7:2673 NA NA
T-lymphocyte immunodeficiency	-0.3890736	6	9.651e-04	7.910e-02	RAG1:15 CD3E:1383 LBR:1431 SFTPA1:1491 SMARCA1:12365 SIPA1:3895
Abnormality of finger	0.3884336	4	7.132e-03	1.749e-01	SIL1:679 INPP5K:699 NRAS:1780 KRAS:4052 NA NA
Epidermolysis bullosa inversa dystrophic	-0.3836865	6	1.135e-03	8.419e-02	ITGB4:192 LAMB3:361 LAMC2:492 LAMC1:1461 LAMA3:4062 COL17A1:4556
Candidiasis of the esophagus	-0.3795516	3	2.279e-02	2.815e-01	ADAM17:771 NFKB1:946 IL1B:4040 NA NA NA
EPIDERMOLYSIS BULLOSA_JUNCTIONAL_LOCAL	-0.3790536	5	3.331e-03	3.138e-01	ITGB4:192 LAMB3:361 LAMC2:492 LAMA3:4062 COL17A1:4556 NA
Adult junctional epidermolysis bullosa (-0.3790536	5	3.331e-03	3.138e-01	ITGB4:192 LAMB3:361 LAMC2:492 LAMA3:4062 COL17A1:4556 NA
Epidermolysis Bullosa Progressiva	-0.3790536	5	3.331e-03	3.138e-01	ITGB4:192 LAMB3:361 LAMC2:492 LAMA3:4062 COL17A1:4556 NA
JEB-I	-0.3790536	5	3.331e-03	3.138e-01	ITGB4:192 LAMB3:361 LAMC2:492 LAMA3:4062 COL17A1:4556 NA
Palmar hyperhidrosis	-0.3790536	5	3.331e-03	3.138e-01	ITGB4:192 LAMB3:361 LAMC2:492 LAMA3:4062 COL17A1:4556 NA
Benign neoplasm of thyroid gland	-0.3777993	3	3.242e-02	2.841e-01	APP:255 IQGAP1:1885 ALK:3706 NA NA NA
Microcystic stromal tumor	-0.3733318	5	3.838e-03	1.396e-01	MME:236 VIM:309 DICER1:1249 CTNNB1:3471 FOXL2:4831 NA
Papillary and follicular adenocarcinoma	0.3701925	5	4.146e-03	1.437e-01	EGF:390 TP53:1394 BRAF:2046 EDNR4:2564 KRAS:4052 NA
Papillary transitional cell carcinoma	0.3692013	4	1.055e-02	2.037e-01	EGF:390 ERBB2:944 TP53:1394 VEGFA:5779 NA NA
Emphyema, Pleural	0.3806963	6	1.794e-03	1.012e-01	NFKBIA:51 NFKB1:1410 NFKBIE:1433 SMCA2:2352 SMCA217 TNFRSF6B:4687
Intestinal obstruction co-occurrent and	-0.3677232	3	2.738e-02	3.046e-01	CFTF:773 MUC1:1021 SLG26A9:4520 NA NA NA
Congenital muscular hypertrophy-cerebral	0.3669450	5	4.488e-03	1.477e-01	BRD4:571 NIPBL:948 SMC3:1217 RAD21:2361 SMC1A:5679 NA
Cornelia de Lange Syndrome 3	0.3669450	5	4.488e-03	1.477e-01	BRD4:571 NIPBL:948 SMC3:1217 RAD21:2361 SMC1A:5679 NA
Liver Abscess	-0.3646719	5	4.742e-03	1.501e-01	NCF1:687 NCF2:1364 DECR1:1756 CYBB:3242 CYBA:3741 NA
Myelodysplastic syndrome, no ID- or Subty	0.3633493	6	2.054e-03	1.068e-01	TET2:791 PAFAH1B1:100 SF3B1:1469 YYHAE:1922 SETBP1:3122 FANCB:4755
Myopathy, Centronuclear, Autosomal Reces	-0.3604260	4	1.254e-02	2.177e-01	SPG8:898 AMPH:1398 BIN1:2934 DNM2:3668 NA NA
Phocomelia	0.3598469	5	5.325e-03	1.588e-01	GNAS:886 NIPBL:948 SMC3:1217 ESCO2:1311 WNT7A:6675 NA
Serous cystadenoma, borderline malignanc	0.3597996	5	5.334e-03	1.588e-01	ERBB2:944 DERL2:1888 BRAF:2046 MYC:2342 KRAS:4052 NA
Small anterior fontanelle	0.3561628	3	2.636e-02	3.238e-01	ORC1:107 MYCN:3411 ATR:350 NA NA NA
Anterior Horn Cell Disease	-0.3558228	6	2.541e-03	1.170e-01	VIM:309 PNPLA4:676 SOD1:722 GLE1:806 PRDX3:2870 SMN1:8655
Acanthamoeba Keratitis	0.3542440	2	8.270e-02	4.464e-01	ARSA:2028 TLR4:2553 NA NA NA NA