

Table S3. KEGG pathway enrichment analysis results of differentially expressed genes in neuroblastoma

"ID"	"Description"	"GeneRatio"	"BgRatio"	"pvalue"	"p.adjust"	"qvalue"	"geneID"	"Count"
hsa04610,"hsa04610"	"Complement and coagulation cascades - Homo sapiens (human)"	"40/785"	"103/8388"	"0.0001257"	"0.0001257"	"0.0001257"	"hsa04610"	40
hsa04080,"hsa04080"	"Neuroactive ligand-receptor interaction - Homo sapiens (human)"	"76/785"	"242/8388"	"0.0001257"	"0.0001257"	"0.0001257"	"hsa04080"	76
hsa04060,"hsa04060"	"Cytokine-cytokine receptor interaction - Homo sapiens (human)"	"65/785"	"225/8388"	"0.0001257"	"0.0001257"	"0.0001257"	"hsa04060"	65
hsa04974,"hsa04974"	"Protein digestion and absorption - Homo sapiens (human)"	"32/785"	"103/8388"	"0.0001257"	"0.0001257"	"0.0001257"	"hsa04974"	32
hsa04979,"hsa04979"	"Cholesterol metabolism - Homo sapiens (human)"	"20/785"	"51/8388"	"9.852E-05"	"9.852E-05"	"9.852E-05"	"hsa04979"	20
hsa04061,"hsa04061"	"Viral protein interaction with cytokine and cytokine receptor - Homo sapiens (human)"	"27/785"	"89/8388"	"1.84E-04"	"1.84E-04"	"1.84E-04"	"hsa04061"	27
hsa04512,"hsa04512"	"ECM-receptor interaction - Homo sapiens (human)"	"27/785"	"89/8388"	"1.84E-04"	"1.84E-04"	"1.84E-04"	"hsa04512"	27
hsa03320,"hsa03320"	"PPAR signaling pathway - Homo sapiens (human)"	"23/785"	"75/8388"	"1.684E-04"	"1.684E-04"	"1.684E-04"	"hsa03320"	23
hsa05146,"hsa05146"	"Amoebiasis - Homo sapiens (human)"	"27/785"	"102/8388"	"4.165364575600E-05"	"4.165364575600E-05"	"4.165364575600E-05"	"hsa05146"	27
hsa04657,"hsa04657"	"IL-17 signaling pathway - Homo sapiens (human)"	"24/785"	"94/8388"	"3.654E-05"	"3.654E-05"	"3.654E-05"	"hsa04657"	24
hsa05202,"hsa05202"	"Transcriptional misregulation in cancer - Homo sapiens (human)"	"37/785"	"114/8388"	"0.0001257"	"0.0001257"	"0.0001257"	"hsa05202"	37
hsa04614,"hsa04614"	"Renin-angiotensin system - Homo sapiens (human)"	"10/785"	"23/8388"	"1.79E-04"	"1.79E-04"	"1.79E-04"	"hsa04614"	10
hsa05150,"hsa05150"	"Staphylococcus aureus infection - Homo sapiens (human)"	"23/785"	"96/8388"	"0.0001257"	"0.0001257"	"0.0001257"	"hsa05150"	23
hsa04151,"hsa04151"	"PI3K-Akt signaling pathway - Homo sapiens (human)"	"57/785"	"354/8388"	"2.0001257E-05"	"2.0001257E-05"	"2.0001257E-05"	"hsa04151"	57
hsa00830,"hsa00830"	"Retinol metabolism - Homo sapiens (human)"	"17/785"	"68/8388"	"0.0001257"	"0.0001257"	"0.0001257"	"hsa00830"	17
hsa04913,"hsa04913"	"Ovarian steroidogenesis - Homo sapiens (human)"	"14/785"	"51/8388"	"0.0001257"	"0.0001257"	"0.0001257"	"hsa04913"	14
hsa04668,"hsa04668"	"TNF signaling pathway - Homo sapiens (human)"	"23/785"	"114/8388"	"0.0001257"	"0.0001257"	"0.0001257"	"hsa04668"	23
hsa04933,"hsa04933"	"AGE-RAGE signaling pathway in diabetic complications - Homo sapiens (human)"	"23/785"	"114/8388"	"0.0001257"	"0.0001257"	"0.0001257"	"hsa04933"	23
hsa00140,"hsa00140"	"Steroid hormone biosynthesis - Homo sapiens (human)"	"15/785"	"62/8388"	"0.0001257"	"0.0001257"	"0.0001257"	"hsa00140"	15
hsa05144,"hsa05144"	"Malaria - Homo sapiens (human)"	"13/785"	"50/8388"	"0.0005134843103052E-05"	"0.0005134843103052E-05"	"0.0005134843103052E-05"	"hsa05144"	13
hsa04927,"hsa04927"	"Cortisol synthesis and secretion - Homo sapiens (human)"	"15/785"	"65/8388"	"0.0001257"	"0.0001257"	"0.0001257"	"hsa04927"	15
hsa04978,"hsa04978"	"Mineral absorption - Homo sapiens (human)"	"14/785"	"60/8388"	"0.0010268E-05"	"0.0010268E-05"	"0.0010268E-05"	"hsa04978"	14
hsa04510,"hsa04510"	"Focal adhesion - Homo sapiens (human)"	"33/785"	"203/8388"	"0.001118660E-05"	"0.001118660E-05"	"0.001118660E-05"	"hsa04510"	33
hsa04350,"hsa04350"	"TGF-beta signaling pathway - Homo sapiens (human)"	"19/785"	"98/8388"	"0.0001257"	"0.0001257"	"0.0001257"	"hsa04350"	19
hsa05323,"hsa05323"	"Rheumatoid arthritis - Homo sapiens (human)"	"18/785"	"93/8388"	"0.002159E-05"	"0.002159E-05"	"0.002159E-05"	"hsa05323"	18
hsa00590,"hsa00590"	"Arachidonic acid metabolism - Homo sapiens (human)"	"13/785"	"61/8388"	"0.0001257"	"0.0001257"	"0.0001257"	"hsa00590"	13
hsa05133,"hsa05133"	"Pertussis - Homo sapiens (human)"	"15/785"	"76/8388"	"0.004039407058779E-05"	"0.004039407058779E-05"	"0.004039407058779E-05"	"hsa05133"	15
hsa04934,"hsa04934"	"Cushing syndrome - Homo sapiens (human)"	"25/785"	"155/8388"	"0.004734E-05"	"0.004734E-05"	"0.004734E-05"	"hsa04934"	25
hsa00980,"hsa00980"	"Metabolism of xenobiotics by cytochrome P450 - Homo sapiens (human)"	"11/785"	"46/8388"	"0.0001257"	"0.0001257"	"0.0001257"	"hsa00980"	11
hsa05171,"hsa05171"	"Coronavirus disease - COVID-19 - Homo sapiens (human)"	"34/785"	"232/8388"	"0.0001257"	"0.0001257"	"0.0001257"	"hsa05171"	34
hsa04010,"hsa04010"	"MAPK signaling pathway - Homo sapiens (human)"	"42/785"	"302/8388"	"0.0001257"	"0.0001257"	"0.0001257"	"hsa04010"	42
hsa00982,"hsa00982"	"Drug metabolism - cytochrome P450 - Homo sapiens (human)"	"14/785"	"72/8388"	"0.0001257"	"0.0001257"	"0.0001257"	"hsa00982"	14
hsa04926,"hsa04926"	"Relaxin signaling pathway - Homo sapiens (human)"	"21/785"	"129/8388"	"0.0001257"	"0.0001257"	"0.0001257"	"hsa04926"	21
hsa05418,"hsa05418"	"Fluid shear stress and atherosclerosis - Homo sapiens (human)"	"22/785"	"113/8388"	"0.0001257"	"0.0001257"	"0.0001257"	"hsa05418"	22
hsa04062,"hsa04062"	"Chemokine signaling pathway - Homo sapiens (human)"	"28/785"	"192/8388"	"0.0001257"	"0.0001257"	"0.0001257"	"hsa04062"	28
hsa00430,"hsa00430"	"Taurine and hypotaurine metabolism - Homo sapiens (human)"	"5/785"	"16/8388"	"0.0001257"	"0.0001257"	"0.0001257"	"hsa00430"	5
hsa04380,"hsa04380"	"Osteoclast differentiation - Homo sapiens (human)"	"20/785"	"128/8388"	"0.0001257"	"0.0001257"	"0.0001257"	"hsa04380"	20
hsa00350,"hsa00350"	"Tyrosine metabolism - Homo sapiens (human)"	"8/785"	"36/8388"	"0.016137E-05"	"0.016137E-05"	"0.016137E-05"	"hsa00350"	8
hsa04975,"hsa04975"	"Fat digestion and absorption - Homo sapiens (human)"	"9/785"	"43/8388"	"0.0001257"	"0.0001257"	"0.0001257"	"hsa04975"	9
hsa04726,"hsa04726"	"Serotonergic synapse - Homo sapiens (human)"	"18/785"	"115/8388"	"0.0201E-05"	"0.0201E-05"	"0.0201E-05"	"hsa04726"	18
hsa04977,"hsa04977"	"Vitamin digestion and absorption - Homo sapiens (human)"	"6/785"	"24/8388"	"0.0001257"	"0.0001257"	"0.0001257"	"hsa04977"	6
hsa04020,"hsa04020"	"Calcium signaling pathway - Homo sapiens (human)"	"32/785"	"240/8388"	"0.0001257"	"0.0001257"	"0.0001257"	"hsa04020"	32
hsa05204,"hsa05204"	"Chemical carcinogenesis - DNA adducts - Homo sapiens (human)"	"12/785"	"51/8388"	"0.0001257"	"0.0001257"	"0.0001257"	"hsa05204"	12
hsa05205,"hsa05205"	"Proteoglycans in cancer - Homo sapiens (human)"	"28/785"	"205/8388"	"0.02E-05"	"0.02E-05"	"0.02E-05"	"hsa05205"	28
hsa04024,"hsa04024"	"cAMP signaling pathway - Homo sapiens (human)"	"30/785"	"225/8388"	"0.02E-05"	"0.02E-05"	"0.02E-05"	"hsa04024"	30
hsa05217,"hsa05217"	"Basal cell carcinoma - Homo sapiens (human)"	"11/785"	"63/8388"	"0.030460E-05"	"0.030460E-05"	"0.030460E-05"	"hsa05217"	11
hsa05219,"hsa05219"	"Bladder cancer - Homo sapiens (human)"	"8/785"	"41/8388"	"0.03372523244E-05"	"0.03372523244E-05"	"0.03372523244E-05"	"hsa05219"	8
hsa04390,"hsa04390"	"Hippo signaling pathway - Homo sapiens (human)"	"22/785"	"157/8388"	"0.03E-05"	"0.03E-05"	"0.03E-05"	"hsa04390"	22

hsa05215,"hsa05215","Prostate cancer - Homo sapiens (human)","15/785","97/8388",0.0352738188
hsa04976,"hsa04976","Bile secretion - Homo sapiens (human)","14/785","89/8388",0.03615904443
hsa05134,"hsa05134","Legionellosis - Homo sapiens (human)","10/785","57/8388",0.036961613264
hsa05165,"hsa05165","Human papillomavirus infection - Homo sapiens (human)","41/785","331/8388",0.036961613264
hsa04925,"hsa04925","Aldosterone synthesis and secretion - Homo sapiens (human)","15/785","98/8388",0.036961613264
hsa04923,"hsa04923","Regulation of lipolysis in adipocytes - Homo sapiens (human)","10/785","58/8388",0.036961613264
hsa04936,"hsa04936","Alcoholic liver disease - Homo sapiens (human)","20/785","142/8388",0.0412
hsa04145,"hsa04145","Phagosome - Homo sapiens (human)","21/785","152/8388",0.044471213839
hsa04918,"hsa04918","Thyroid hormone synthesis - Homo sapiens (human)","12/785","75/8388",0.044471213839
hsa05143,"hsa05143","African trypanosomiasis - Homo sapiens (human)","7/785","37/8388",0.0527
hsa02010,"hsa02010","ABC transporters - Homo sapiens (human)","8/785","45/8388",0.054838610
hsa04964,"hsa04964","Proximal tubule bicarbonate reclamation - Homo sapiens (human)","5/785","26/8388",0.054838610
hsa00120,"hsa00120","Primary bile acid biosynthesis - Homo sapiens (human)","4/785","17/8388",0.067706
hsa00910,"hsa00910","Nitrogen metabolism - Homo sapiens (human)","4/785","17/8388",0.067706
hsa04750,"hsa04750","Inflammatory mediator regulation of TRP channels - Homo sapiens (human)","12/785","86/8388",0.067706
hsa00130,"hsa00130","Ubiquinone and other terpenoid-quinone biosynthesis - Homo sapiens (human)","14/785","99/8388",0.067706
hsa04640,"hsa04640","Hematopoietic cell lineage - Homo sapiens (human)","14/785","99/8388",0.067706
hsa00790,"hsa00790","Folate biosynthesis - Homo sapiens (human)","5/785","26/8388",0.08968990
hsa04950,"hsa04950","Maturity onset diabetes of the young - Homo sapiens (human)","5/785","26/8388",0.08968990
hsa05332,"hsa05332","Graft-versus-host disease - Homo sapiens (human)","7/785","42/8388",0.092
hsa04514,"hsa04514","Cell adhesion molecules - Homo sapiens (human)","20/785","157/8388",0.092
hsa05226,"hsa05226","Gastric cancer - Homo sapiens (human)","19/785","149/8388",0.1014301103
hsa00650,"hsa00650","Butanoate metabolism - Homo sapiens (human)","5/785","27/8388",0.10203
hsa04742,"hsa04742","Taste transduction - Homo sapiens (human)","12/785","86/8388",0.1035900
hsa04064,"hsa04064","NF-kappa B signaling pathway - Homo sapiens (human)","14/785","104/8388",0.1035900
hsa04310,"hsa04310","Wnt signaling pathway - Homo sapiens (human)","21/785","171/8388",0.118
hsa04270,"hsa04270","Vascular smooth muscle contraction - Homo sapiens (human)","17/785","134/8388",0.118
hsa00250,"hsa00250","Alanine, aspartate and glutamate metabolism - Homo sapiens (human)","6/785","30/8388",0.118
hsa04960,"hsa04960","Aldosterone-regulated sodium reabsorption - Homo sapiens (human)","6/785","30/8388",0.118
hsa05322,"hsa05322","Systemic lupus erythematosus - Homo sapiens (human)","17/785","136/8388",0.118
hsa05410,"hsa05410","Hypertrophic cardiomyopathy - Homo sapiens (human)","12/785","90/8388",0.118
hsa00591,"hsa00591","Linoleic acid metabolism - Homo sapiens (human)","5/785","30/8388",0.1436728
hsa01523,"hsa01523","Antifolate resistance - Homo sapiens (human)","5/785","30/8388",0.1436728
hsa05142,"hsa05142","Chagas disease - Homo sapiens (human)","13/785","102/8388",0.155621960
hsa05310,"hsa05310","Asthma - Homo sapiens (human)","5/785","31/8388",0.15896098039262,0.5
hsa00480,"hsa00480","Glutathione metabolism - Homo sapiens (human)","8/785","57/8388",0.1596
hsa00260,"hsa00260","Glycine, serine and threonine metabolism - Homo sapiens (human)","6/785","30/8388",0.1596
hsa05033,"hsa05033","Nicotine addiction - Homo sapiens (human)","6/785","40/8388",0.16643309
hsa04810,"hsa04810","Regulation of actin cytoskeleton - Homo sapiens (human)","26/785","229/8388",0.16643309
hsa05140,"hsa05140","Leishmaniasis - Homo sapiens (human)","10/785","77/8388",0.18036376173
hsa05417,"hsa05417","Lipid and atherosclerosis - Homo sapiens (human)","24/785","215/8388",0.2103
hsa04931,"hsa04931","Insulin resistance - Homo sapiens (human)","13/785","108/8388",0.2081986
hsa04630,"hsa04630","JAK-STAT signaling pathway - Homo sapiens (human)","19/785","166/8388",0.2103
hsa00860,"hsa00860","Porphyrin metabolism - Homo sapiens (human)","6/785","43/8388",0.2103
hsa04940,"hsa04940","Type I diabetes mellitus - Homo sapiens (human)","6/785","43/8388",0.2103
hsa04014,"hsa04014","Ras signaling pathway - Homo sapiens (human)","26/785","236/8388",0.2159
hsa00592,"hsa00592","alpha-Linolenic acid metabolism - Homo sapiens (human)","4/785","26/8388",0.2159
hsa04530,"hsa04530","Tight junction - Homo sapiens (human)","19/785","169/8388",0.2316986587
hsa00601,"hsa00601","Glycosphingolipid biosynthesis - lacto and neolacto series - Homo sapiens (human)","5/785","36/8388",0.2316986587
hsa00512,"hsa00512","Mucin type O-glycan biosynthesis - Homo sapiens (human)","5/785","36/8388",0.2316986587

hsa04550,"hsa04550","Signaling pathways regulating pluripotency of stem cells - Homo sapiens (human)", "7/785", "56/8388", 0.274240

hsa04340,"hsa04340","Hedgehog signaling pathway - Homo sapiens (human)", "7/785", "56/8388", 0.274240

hsa00514,"hsa00514","Other types of O-glycan biosynthesis - Homo sapiens (human)", "6/785", "47/8388", 0.274240

hsa00620,"hsa00620","Pyruvate metabolism - Homo sapiens (human)", "6/785", "47/8388", 0.274240

hsa04973,"hsa04973","Carbohydrate digestion and absorption - Homo sapiens (human)", "6/785", "47/8388", 0.274240

hsa05414,"hsa05414","Dilated cardiomyopathy - Homo sapiens (human)", "11/785", "96/8388", 0.285

hsa04392,"hsa04392","Hippo signaling pathway - multiple species - Homo sapiens (human)", "4/785", "67/8388", 0.285

hsa00010,"hsa00010","Glycolysis / Gluconeogenesis - Homo sapiens (human)", "8/785", "67/8388", 0.285

hsa05224,"hsa05224","Breast cancer - Homo sapiens (human)", "16/785", "147/8388", 0.2995008281

hsa00030,"hsa00030","Pentose phosphate pathway - Homo sapiens (human)", "4/785", "30/8388", 0.30

hsa04659,"hsa04659","Th17 cell differentiation - Homo sapiens (human)", "12/785", "108/8388", 0.30

hsa04915,"hsa04915","Estrogen signaling pathway - Homo sapiens (human)", "15/785", "138/8388", 0.30

hsa00532,"hsa00532","Glycosaminoglycan biosynthesis - chondroitin sulfate / dermatan sulfate - Homo sapiens (human)", "8/785", "69/8388", 0.3165205551

hsa04924,"hsa04924","Renin secretion - Homo sapiens (human)", "8/785", "69/8388", 0.3165205551

hsa01521,"hsa01521","EGFR tyrosine kinase inhibitor resistance - Homo sapiens (human)", "9/785", "70/8388", 0.3165205551

hsa00052,"hsa00052","Galactose metabolism - Homo sapiens (human)", "4/785", "31/8388", 0.32925

hsa04917,"hsa04917","Prolactin signaling pathway - Homo sapiens (human)", "8/785", "70/8388", 0.32925

hsa04814,"hsa04814","Motor proteins - Homo sapiens (human)", "20/785", "193/8388", 0.349201209

hsa04972,"hsa04972","Pancreatic secretion - Homo sapiens (human)", "11/785", "102/8388", 0.35695

hsa05218,"hsa05218","Melanoma - Homo sapiens (human)", "8/785", "72/8388", 0.36002359534057

hsa00561,"hsa00561","Glycerolipid metabolism - Homo sapiens (human)", "7/785", "62/8388", 0.36002359534057

hsa04970,"hsa04970","Salivary secretion - Homo sapiens (human)", "10/785", "93/8388", 0.37122402

hsa00051,"hsa00051","Fructose and mannose metabolism - Homo sapiens (human)", "4/785", "33/8388", 0.37122402

hsa04611,"hsa04611","Platelet activation - Homo sapiens (human)", "13/785", "124/8388", 0.3761286

hsa04670,"hsa04670","Leukocyte transendothelial migration - Homo sapiens (human)", "12/785", "114/8388", 0.3761286

hsa04620,"hsa04620","Toll-like receptor signaling pathway - Homo sapiens (human)", "11/785", "104/8388", 0.3761286

hsa05130,"hsa05130","Pathogenic Escherichia coli infection - Homo sapiens (human)", "20/785", "197/8388", 0.3761286

hsa04928,"hsa04928","Parathyroid hormone synthesis, secretion and action - Homo sapiens (human)", "15/785", "148/8388", 0.3761286

hsa04072,"hsa04072","Phospholipase D signaling pathway - Homo sapiens (human)", "15/785", "148/8388", 0.3761286

hsa04911,"hsa04911","Insulin secretion - Homo sapiens (human)", "9/785", "86/8388", 0.4144019450

hsa00040,"hsa00040","Pentose and glucuronate interconversions - Homo sapiens (human)", "4/785", "33/8388", 0.4144019450

hsa05152,"hsa05152","Tuberculosis - Homo sapiens (human)", "18/785", "180/8388", 0.42000068082

hsa04713,"hsa04713","Circadian entrainment - Homo sapiens (human)", "10/785", "97/8388", 0.4232

hsa04371,"hsa04371","Apelin signaling pathway - Homo sapiens (human)", "14/785", "139/8388", 0.4

hsa04930,"hsa04930","Type II diabetes mellitus - Homo sapiens (human)", "5/785", "46/8388", 0.4334

hsa05412,"hsa05412","Arrhythmogenic right ventricular cardiomyopathy - Homo sapiens (human)", "17/785", "171/8388", 0.434192729325

hsa05164,"hsa05164","Influenza A - Homo sapiens (human)", "17/785", "171/8388", 0.434192729325

hsa00500,"hsa00500","Starch and sucrose metabolism - Homo sapiens (human)", "4/785", "36/8388", 0.434192729325

hsa04540,"hsa04540","Gap junction - Homo sapiens (human)", "9/785", "88/8388", 0.4419480056806

hsa00360,"hsa00360","Phenylalanine metabolism - Homo sapiens (human)", "2/785", "16/8388", 0.44

hsa05216,"hsa05216","Thyroid cancer - Homo sapiens (human)", "4/785", "37/8388", 0.46037069951

hsa05032,"hsa05032","Morphine addiction - Homo sapiens (human)", "9/785", "91/8388", 0.4829363

hsa05230,"hsa05230","Central carbon metabolism in cancer - Homo sapiens (human)", "7/785", "70/8388", 0.4829363

hsa05030,"hsa05030","Cocaine addiction - Homo sapiens (human)", "5/785", "49/8388", 0.489764379

hsa04730,"hsa04730","Long-term depression - Homo sapiens (human)", "6/785", "60/8388", 0.496158

hsa05222,"hsa05222","Small cell lung cancer - Homo sapiens (human)", "9/785", "92/8388", 0.496451

hsa00565,"hsa00565","Ether lipid metabolism - Homo sapiens (human)", "5/785", "50/8388", 0.50809

hsa05225,"hsa05225","Hepatocellular carcinoma - Homo sapiens (human)", "16/785", "168/8388", 0.5

hsa04724,"hsa04724","Glutamatergic synapse - Homo sapiens (human)", "11/785", "115/8388", 0.516

hsa04744,"hsa04744","Phototransduction - Homo sapiens (human)", "3/785", "29/8388", 0.51864642

hsa05207,"hsa05207","Chemical carcinogenesis - receptor activation - Homo sapiens (human)","20/785","167/8388",0.69420
 hsa00270,"hsa00270","Cysteine and methionine metabolism - Homo sapiens (human)","5/785","52/8388",0.561686407
 hsa04961,"hsa04961","Endocrine and other factor-regulated calcium reabsorption - Homo sapiens (human)","4/785","42/8388",0.5624
 hsa05210,"hsa05210","Colorectal cancer - Homo sapiens (human)","8/785","86/8388",0.561686407
 hsa00380,"hsa00380","Tryptophan metabolism - Homo sapiens (human)","4/785","42/8388",0.5624
 hsa05321,"hsa05321","Inflammatory bowel disease - Homo sapiens (human)","6/785","65/8388",0.5624
 hsa00071,"hsa00071","Fatty acid degradation - Homo sapiens (human)","4/785","43/8388",0.58154
 hsa04215,"hsa04215","Apoptosis - multiple species - Homo sapiens (human)","3/785","32/8388",0.58154
 hsa04962,"hsa04962","Vasopressin-regulated water reabsorption - Homo sapiens (human)","4/785","43/8388",0.58154
 hsa04727,"hsa04727","GABAergic synapse - Homo sapiens (human)","8/785","89/8388",0.60165316
 hsa04022,"hsa04022","cGMP-PKG signaling pathway - Homo sapiens (human)","15/785","167/8388",0.60165316
 hsa00220,"hsa00220","Arginine biosynthesis - Homo sapiens (human)","2/785","22/8388",0.623708
 hsa00340,"hsa00340","Histidine metabolism - Homo sapiens (human)","2/785","22/8388",0.623708
 hsa00920,"hsa00920","Sulfur metabolism - Homo sapiens (human)","1/785","10/8388",0.62586793
 hsa04920,"hsa04920","Adipocytokine signaling pathway - Homo sapiens (human)","6/785","69/8388",0.6361
 hsa05031,"hsa05031","Amphetamine addiction - Homo sapiens (human)","6/785","69/8388",0.6361
 hsa05167,"hsa05167","Kaposi sarcoma-associated herpesvirus infection - Homo sapiens (human)","1/785","10/8388",0.62586793
 hsa05120,"hsa05120","Epithelial cell signaling in Helicobacter pylori infection - Homo sapiens (human)","6/785","69/8388",0.6361
 hsa00534,"hsa00534","Glycosaminoglycan biosynthesis - heparan sulfate / heparin - Homo sapiens (human)","4/785","42/8388",0.5624
 hsa04672,"hsa04672","Intestinal immune network for IgA production - Homo sapiens (human)","4/785","42/8388",0.5624
 hsa04115,"hsa04115","p53 signaling pathway - Homo sapiens (human)","6/785","73/8388",0.69043
 hsa04012,"hsa04012","ErbB signaling pathway - Homo sapiens (human)","7/785","85/8388",0.69420
 hsa04666,"hsa04666","Fc gamma R-mediated phagocytosis - Homo sapiens (human)","8/785","97/8388",0.701
 hsa04728,"hsa04728","Dopaminergic synapse - Homo sapiens (human)","11/785","132/8388",0.701
 hsa05330,"hsa05330","Allograft rejection - Homo sapiens (human)","3/785","38/8388",0.70383203
 hsa04071,"hsa04071","Sphingolipid signaling pathway - Homo sapiens (human)","10/785","121/8388",0.70383203
 hsa04152,"hsa04152","AMPK signaling pathway - Homo sapiens (human)","10/785","121/8388",0.70383203
 hsa05231,"hsa05231","Choline metabolism in cancer - Homo sapiens (human)","8/785","98/8388",0.70383203
 hsa01230,"hsa01230","Biosynthesis of amino acids - Homo sapiens (human)","6/785","75/8388",0.70383203
 hsa04260,"hsa04260","Cardiac muscle contraction - Homo sapiens (human)","7/785","87/8388",0.70383203
 hsa05160,"hsa05160","Hepatitis C - Homo sapiens (human)","13/785","157/8388",0.720105788337
 hsa04210,"hsa04210","Apoptosis - Homo sapiens (human)","11/785","136/8388",0.7384982700140
 hsa05100,"hsa05100","Bacterial invasion of epithelial cells - Homo sapiens (human)","6/785","77/8388",0.7384982700140
 hsa04916,"hsa04916","Melanogenesis - Homo sapiens (human)","8/785","101/8388",0.7405652843
 hsa04725,"hsa04725","Cholinergic synapse - Homo sapiens (human)","9/785","113/8388",0.742390
 hsa00600,"hsa00600","Sphingolipid metabolism - Homo sapiens (human)","4/785","53/8388",0.743
 hsa05320,"hsa05320","Autoimmune thyroid disease - Homo sapiens (human)","4/785","53/8388",0.743
 hsa00533,"hsa00533","Glycosaminoglycan biosynthesis - keratan sulfate - Homo sapiens (human)","9/785","115/8388",0.760856
 hsa01200,"hsa01200","Carbon metabolism - Homo sapiens (human)","9/785","115/8388",0.760856
 hsa00603,"hsa00603","Glycosphingolipid biosynthesis - globo and isoglobo series - Homo sapiens (human)","1/785","10/8388",0.62586793
 hsa00604,"hsa00604","Glycosphingolipid biosynthesis - ganglio series - Homo sapiens (human)","1/785","10/8388",0.62586793
 hsa04015,"hsa04015","Rap1 signaling pathway - Homo sapiens (human)","17/785","210/8388",0.77
 hsa00983,"hsa00983","Drug metabolism - other enzymes - Homo sapiens (human)","6/785","80/8388",0.77
 hsa04664,"hsa04664","Fc epsilon RI signaling pathway - Homo sapiens (human)","5/785","68/8388",0.77
 hsa00053,"hsa00053","Ascorbate and aldarate metabolism - Homo sapiens (human)","2/785","30/8388",0.77
 hsa00630,"hsa00630","Glyoxylate and dicarboxylate metabolism - Homo sapiens (human)","2/785","30/8388",0.77
 hsa04261,"hsa04261","Adrenergic signaling in cardiomyocytes - Homo sapiens (human)","12/785","131/8388",0.79
 hsa04068,"hsa04068","FoxO signaling pathway - Homo sapiens (human)","10/785","131/8388",0.79
 hsa04922,"hsa04922","Glucagon signaling pathway - Homo sapiens (human)","8/785","107/8388",0.79
 hsa00410,"hsa00410","beta-Alanine metabolism - Homo sapiens (human)","2/785","31/8388",0.800

hsa04935,"hsa04935","Growth hormone synthesis, secretion and action - Homo sapiens (human)","9/785","121/8388",0.812
hsa04919,"hsa04919","Thyroid hormone signaling pathway - Homo sapiens (human)","9/785","121/8388",0.812
hsa00450,"hsa00450","Selenocompound metabolism - Homo sapiens (human)","1/785","17/8388",0.812
hsa04066,"hsa04066","HIF-1 signaling pathway - Homo sapiens (human)","8/785","109/8388",0.812
hsa04370,"hsa04370","VEGF signaling pathway - Homo sapiens (human)","4/785","59/8388",0.8154
hsa01522,"hsa01522","Endocrine resistance - Homo sapiens (human)","7/785","98/8388",0.823228
hsa05145,"hsa05145","Toxoplasmosis - Homo sapiens (human)","8/785","112/8388",0.8349389165
hsa04910,"hsa04910","Insulin signaling pathway - Homo sapiens (human)","10/785","137/8388",0.8
hsa04710,"hsa04710","Circadian rhythm - Homo sapiens (human)","2/785","34/8388",0.840857047
hsa05161,"hsa05161","Hepatitis B - Homo sapiens (human)","12/785","162/8388",0.841066220919
hsa05214,"hsa05214","Glioma - Homo sapiens (human)","5/785","75/8388",0.843149626438324,0.8
hsa04213,"hsa04213","Longevity regulating pathway - multiple species - Homo sapiens (human)","4/785","64/8388",0.85
hsa05220,"hsa05220","Chronic myeloid leukemia - Homo sapiens (human)","5/785","76/8388",0.85
hsa00330,"hsa00330","Arginine and proline metabolism - Homo sapiens (human)","3/785","50/8388",0.86
hsa00100,"hsa00100","Steroid biosynthesis - Homo sapiens (human)","1/785","20/8388",0.8601977
hsa00670,"hsa00670","One carbon pool by folate - Homo sapiens (human)","1/785","20/8388",0.86
hsa04929,"hsa04929","GnRH secretion - Homo sapiens (human)","4/785","64/8388",0.86176812681
hsa00760,"hsa00760","Nicotinate and nicotinamide metabolism - Homo sapiens (human)","2/785","16/8388",0.86
hsa04625,"hsa04625","C-type lectin receptor signaling pathway - Homo sapiens (human)","7/785","98/8388",0.86
hsa04612,"hsa04612","Antigen processing and presentation - Homo sapiens (human)","5/785","78/8388",0.86
hsa04721,"hsa04721","Synaptic vesicle cycle - Homo sapiens (human)","5/785","78/8388",0.866540
hsa00770,"hsa00770","Pantothenate and CoA biosynthesis - Homo sapiens (human)","1/785","21/8388",0.86
hsa04912,"hsa04912","GnRH signaling pathway - Homo sapiens (human)","6/785","93/8388",0.8787
hsa05221,"hsa05221","Acute myeloid leukemia - Homo sapiens (human)","4/785","67/8388",0.8844
hsa00513,"hsa00513","Various types of N-glycan biosynthesis - Homo sapiens (human)","2/785","39/8388",0.88
hsa05166,"hsa05166","Human T-cell leukemia virus 1 infection - Homo sapiens (human)","16/785","225/8388",0.88
hsa00900,"hsa00900","Terpenoid backbone biosynthesis - Homo sapiens (human)","1/785","23/8388",0.88
hsa04723,"hsa04723","Retrograde endocannabinoid signaling - Homo sapiens (human)","10/785","155/8388",0.88
hsa05163,"hsa05163","Human cytomegalovirus infection - Homo sapiens (human)","16/785","225/8388",0.88
hsa04216,"hsa04216","Ferroptosis - Homo sapiens (human)","2/785","41/8388",0.90739976952607
hsa00564,"hsa00564","Glycerophospholipid metabolism - Homo sapiens (human)","6/785","99/8388",0.90739976952607
hsa05415,"hsa05415","Diabetic cardiomyopathy - Homo sapiens (human)","14/785","203/8388",0.9
hsa05223,"hsa05223","Non-small cell lung cancer - Homo sapiens (human)","4/785","72/8388",0.91
hsa05213,"hsa05213","Endometrial cancer - Homo sapiens (human)","3/785","58/8388",0.91830186
hsa04932,"hsa04932","Non-alcoholic fatty liver disease - Homo sapiens (human)","10/785","155/8388",0.91830186
hsa04218,"hsa04218","Cellular senescence - Homo sapiens (human)","10/785","156/8388",0.928029
hsa04971,"hsa04971","Gastric acid secretion - Homo sapiens (human)","4/785","76/8388",0.934243
hsa05212,"hsa05212","Pancreatic cancer - Homo sapiens (human)","4/785","76/8388",0.934243573
hsa04650,"hsa04650","Natural killer cell mediated cytotoxicity - Homo sapiens (human)","8/785","109/8388",0.934243573
hsa04217,"hsa04217","Necroptosis - Homo sapiens (human)","10/785","159/8388",0.937393806286
hsa05132,"hsa05132","Salmonella infection - Homo sapiens (human)","17/785","249/8388",0.93888
hsa04621,"hsa04621","NOD-like receptor signaling pathway - Homo sapiens (human)","12/785","181/8388",0.93888
hsa00310,"hsa00310","Lysine degradation - Homo sapiens (human)","3/785","63/8388",0.94261016
hsa04520,"hsa04520","Adherens junction - Homo sapiens (human)","5/785","93/8388",0.94390217
hsa00280,"hsa00280","Valine, leucine and isoleucine degradation - Homo sapiens (human)","2/785","34/8388",0.94390217
hsa00020,"hsa00020","Citrate cycle (TCA cycle) - Homo sapiens (human)","1/785","30/8388",0.9478
hsa05135,"hsa05135","Yersinia infection - Homo sapiens (human)","8/785","137/8388",0.95040810
hsa00520,"hsa00520","Amino sugar and nucleotide sugar metabolism - Homo sapiens (human)","2/785","34/8388",0.95040810
hsa00510,"hsa00510","N-Glycan biosynthesis - Homo sapiens (human)","2/785","50/8388",0.955140
hsa05110,"hsa05110","Vibrio cholerae infection - Homo sapiens (human)","2/785","50/8388",0.955140

hsa04146,"hsa04146","Peroxisome - Homo sapiens (human)","4/785","82/8388",0.95564049834382
 hsa01240,"hsa01240","Biosynthesis of cofactors - Homo sapiens (human)","9/785","153/8388",0.95
 hsa00640,"hsa00640","Propanoate metabolism - Homo sapiens (human)","1/785","32/8388",0.9571
 hsa04136,"hsa04136","Autophagy - other - Homo sapiens (human)","1/785","32/8388",0.957165698
 hsa04921,"hsa04921","Oxytocin signaling pathway - Homo sapiens (human)","9/785","154/8388",0.
 hsa04130,"hsa04130","SNARE interactions in vesicular transport - Homo sapiens (human)","1/785",
 hsa04662,"hsa04662","B cell receptor signaling pathway - Homo sapiens (human)","4/785","84/8388
 hsa04150,"hsa04150","mTOR signaling pathway - Homo sapiens (human)","9/785","156/8388",0.96
 hsa03020,"hsa03020","RNA polymerase - Homo sapiens (human)","1/785","34/8388",0.9648361893
 hsa04622,"hsa04622","RIG-I-like receptor signaling pathway - Homo sapiens (human)","3/785","71/
 hsa04211,"hsa04211","Longevity regulating pathway - Homo sapiens (human)","4/785","89/8388",0
 hsa00562,"hsa00562","Inositol phosphate metabolism - Homo sapiens (human)","3/785","73/8388",
 hsa01524,"hsa01524","Platinum drug resistance - Homo sapiens (human)","3/785","73/8388",0.972
 hsa04613,"hsa04613","Neutrophil extracellular trap formation - Homo sapiens (human)","11/785",
 hsa01250,"hsa01250","Biosynthesis of nucleotide sugars - Homo sapiens (human)","1/785","37/8388
 hsa04623,"hsa04623","Cytosolic DNA-sensing pathway - Homo sapiens (human)","3/785","75/8388"
 hsa05340,"hsa05340","Primary immunodeficiency - Homo sapiens (human)","1/785","38/8388",0.9
 hsa05020,"hsa05020","Prion disease - Homo sapiens (human)","17/785","273/8388",0.97719617878
 hsa04658,"hsa04658","Th1 and Th2 cell differentiation - Homo sapiens (human)","4/785","92/8388"
 hsa05162,"hsa05162","Measles - Homo sapiens (human)","7/785","139/8388",0.979826973972492,
 hsa05208,"hsa05208","Chemical carcinogenesis - reactive oxygen species - Homo sapiens (human)",
 hsa04360,"hsa04360","Axon guidance - Homo sapiens (human)","10/785","182/8388",0.9802044763
 hsa05416,"hsa05416","Viral myocarditis - Homo sapiens (human)","2/785","60/8388",0.9805004052
 hsa05010,"hsa05010","Alzheimer disease - Homo sapiens (human)","25/785","384/8388",0.9836625
 hsa05017,"hsa05017","Spinocerebellar ataxia - Homo sapiens (human)","7/785","143/8388",0.9841
 hsa05034,"hsa05034","Alcoholism - Homo sapiens (human)","10/785","187/8388",0.984858169896
 hsa03050,"hsa03050","Proteasome - Homo sapiens (human)","1/785","46/8388",0.98924852244853
 hsa04720,"hsa04720","Long-term potentiation - Homo sapiens (human)","2/785","67/8388",0.9892
 hsa04722,"hsa04722","Neurotrophin signaling pathway - Homo sapiens (human)","5/785","119/838
 hsa04660,"hsa04660","T cell receptor signaling pathway - Homo sapiens (human)","4/785","104/838
 hsa05235,"hsa05235","PD-L1 expression and PD-1 checkpoint pathway in cancer - Homo sapiens (hu
 hsa04137,"hsa04137","Mitophagy - animal - Homo sapiens (human)","2/785","72/8388",0.99302748
 hsa04144,"hsa04144","Endocytosis - Homo sapiens (human)","13/785","251/8388",0.995282600675
 hsa04330,"hsa04330","Notch signaling pathway - Homo sapiens (human)","1/785","59/8388",0.997
 hsa04914,"hsa04914","Progesterone-mediated oocyte maturation - Homo sapiens (human)","3/785'
 hsa05131,"hsa05131","Shigellosis - Homo sapiens (human)","12/785","247/8388",0.9973547867801
 hsa01232,"hsa01232","Nucleotide metabolism - Homo sapiens (human)","2/785","85/8388",0.9977
 hsa03250,"hsa03250","Viral life cycle - HIV-1 - Homo sapiens (human)","1/785","63/8388",0.997999
 hsa03420,"hsa03420","Nucleotide excision repair - Homo sapiens (human)","1/785","63/8388",0.99
 hsa05206,"hsa05206","MicroRNAs in cancer - Homo sapiens (human)","16/785","310/8388",0.99805
 hsa05022,"hsa05022","Pathways of neurodegeneration - multiple diseases - Homo sapiens (human)"
 hsa03013,"hsa03013","Nucleocytoplasmic transport - Homo sapiens (human)","3/785","108/8388",
 hsa04114,"hsa04114","Oocyte meiosis - Homo sapiens (human)","4/785","131/8388",0.9987725179
 hsa05211,"hsa05211","Renal cell carcinoma - Homo sapiens (human)","1/785","69/8388",0.9988961
 hsa05014,"hsa05014","Amyotrophic lateral sclerosis - Homo sapiens (human)","19/785","364/8388"
 hsa03015,"hsa03015","mRNA surveillance pathway - Homo sapiens (human)","2/785","97/8388",0.9
 hsa04070,"hsa04070","Phosphatidylinositol signaling system - Homo sapiens (human)","2/785","97/
 hsa04120,"hsa04120","Ubiquitin mediated proteolysis - Homo sapiens (human)","4/785","142/8388
 hsa05016,"hsa05016","Huntington disease - Homo sapiens (human)","14/785","306/8388",0.999524
 hsa05203,"hsa05203","Viral carcinogenesis - Homo sapiens (human)","7/785","204/8388",0.999730

hsa04142,"hsa04142","Lysosome - Homo sapiens (human)","3/785","132/8388",0.99976963996969
hsa05169,"hsa05169","Epstein-Barr virus infection - Homo sapiens (human)","6/785","202/8388",0.9999999999999999
hsa04141,"hsa04141","Protein processing in endoplasmic reticulum - Homo sapiens (human)","4/785","128/8388",0.9999999999999999
hsa00230,"hsa00230","Purine metabolism - Homo sapiens (human)","2/785","128/8388",0.9999999999999999
hsa05170,"hsa05170","Human immunodeficiency virus 1 infection - Homo sapiens (human)","6/785","202/8388",0.9999999999999999
hsa04140,"hsa04140","Autophagy - animal - Homo sapiens (human)","2/785","141/8388",0.9999999999999999
hsa04714,"hsa04714","Thermogenesis - Homo sapiens (human)","6/785","232/8388",0.9999999999999999
hsa04110,"hsa04110","Cell cycle - Homo sapiens (human)","2/785","157/8388",0.9999999999999999
hsa05012,"hsa05012","Parkinson disease - Homo sapiens (human)","7/785","266/8388",0.9999999999999999
hsa00190,"hsa00190","Oxidative phosphorylation - Homo sapiens (human)","1/785","134/8388",0.9999999999999999
hsa03008,"hsa03008","Ribosome biogenesis in eukaryotes - Homo sapiens (human)","2/785","164/8388",0.9999999999999999
hsa04740,"hsa04740","Olfactory transduction - Homo sapiens (human)","15/785","439/8388",0.9999999999999999
hsa03040,"hsa03040","Spliceosome - Homo sapiens (human)","1/785","157/8388",0.9999999999999999

ma, showing significantly enriched signaling pathways and biological processes.

86/8388",2.29004712904422e-19,7.12204657132753e-17,6.12286285028666e-17,"CFH/PLAUR/C8B,
'367/8388",1.13667152367099e-11,1.76752421930839e-09,1.519550352697e-09,"TBXA2R/GABRA1,
'95/8388",2.34173866822163e-11,2.42760241938976e-09,2.08702323413437e-09,"TNFRSF12A/CCL
'388",4.47924700407326e-10,3.48261454566696e-08,2.9940229974595e-08,"ATP1A2/COL23A1/COL
'39481424635e-09,6.12818957446123e-07,5.26843849014437e-07,"LRP2/APOB/APOH/TSP0/PLTP/L
'(human)",29/785",100/8388",1.70818357059313e-08,8.19915008536882e-07,7.04885470192479
'1546786487401e-08,8.19915008536882e-07,7.04885470192479e-07,"IBSP/LAMC3/ITGA8/COL9A3/C
'20415498761e-07,6.54734365251433e-06,5.62878757061648e-06,"PLTP/APOC3/SLC27A6/APOA1/F
'108e-07,1.43936487001292e-05,1.2374299440964e-05,"C8B/LAMC3/GNA15/CXCL2/CTSG/COL1A1/IF
'10396606939e-06,0.00011364263344758,9.76992007770133e-05,"PTGS2/CXCL2/MMP9/CSF3/CCL
'193/8388",1.67079100708756e-05,0.000432156015133947,0.000371526917732349,"HOXA11/ETV1,
'9521392171189e-05,0.000432156015133947,0.000371526917732349,"CMA1/CTSG/AGT/REN/AGTR
'8",1.80643993464351e-05,0.000432156015133947,0.000371526917732349,"CFH/FCGR2B/KRT31/K
'170590300069283e-05,0.000601097023725335,0.000516766437726299,"IGF1/IBSP/LAMC3/CREB3L
'731863913153,0.0026068406451327,0.0022411153286976,"DHRS9/RDH8/RDH10/LRAT/CYP2C9/AO
'1169329420938703,0.00329134061949603,0.00282958374463359,"IGF1/PTGS2/HSD17B2/PLA2G4A,
'300961107654389,0.00530959817792074,0.00456469093650996,"SELE/CREB3L3/TNFRSF1A/PTGS2,
'an)",21/785",100/8388",0.000307307933127245,0.00530959817792074,0.00456469093650996,"S
'10,0.000454933684032041,0.00744654609126129,0.00640183688333176,"HSD17B2/SULT2B1/SULT1E
'181,0.00798468102524712,0.00686447446408112,"SELE/COMP/CSF3/CCL2/IFNG/THBS4/TGFB3/IL1B
'3",0.000777471507711013,0.0115139828046726,0.00989863473476678,"CREB3L3/NR4A1/AGT/NR5
'39788232234,0.0145166018819204,0.0124800029717643,"ATP1A2/CYBRD1/HEPH/HMOX1/ATP1B4/
'07090341,0.0151262296543896,0.0130041033413943,"IGF1/IBSP/LAMC3/RASGRF1/ITGA8/COL9A3,
'00161355473762752,0.0209089801417566,0.0179755659367277,"DCN/LTBP1/HAMP/IFNG/BMP5/
'991645420523,0.026869360690313,0.023099738078658,"CXCL2/CXCL12/CCL2/IFNG/IL1A/CCL20/TG
'300362913507139365,0.0434100387385933,0.0373198505317404,"PTGS2/PTGS1/GGT5/PTGDS/PL
'103,0.0465279850103807,0.0400003661960965,"IL1A/C4BPA/C4BPB/CXCL6/IL1B/C3/IL6/SERPING1/C
'94478391052,0.0525917081355776,0.0452133825230553,"CREB3L3/WNT2/AHR/RASD1/NR4A1/AG
'5/785",78/8388",0.00521108382560645,0.0558843817159864,0.0480441122215622,"MGST1/SULT
'38",0.0054231889826062,0.0561549595413859,0.0482767294754172,"C8B/C6/TNFRSF1A/CSF3/CCL
'0559743969705133,0.0561549595413859,0.0482767294754172,"IGF1/RASGRF1/NGFR/ERBB3/FGFR
'/8388",0.00617932257734215,0.0600552912985441,0.0516298662712141,"FMO3/MGST1/FMO1/FI
'30825609900780909,0.0778074785281402,0.0668915198718823,"GNA15/CREB3L3/MMP2/MMP9/
'9/8388",0.00966671716065198,0.0884220304989049,0.07601690894135,"SELE/MGST1/TNFRSF1A/
'",0.0116979925284365,0.103945019324107,0.0893621083375296,"CCL26/CXCL2/CXCL12/CCL7/CCL
'8388",0.0129007746034012,0.111448358379382,0.0958127704463127,"FMO3/FMO1/FMO4/GGT5,
'1151203394709526,0.12709258312071,0.109262197030497,"TNFRSF1A/FCGR2B/FOSL2/TREM2/LILF
'0053028043,0.129405391738373,0.111250531398026,"FAH/AOX1/HPD/ADH1A/ADH1B/ADH4/TAT/
'0162276857806963,0.129405391738373,0.111250531398026,"APOB/MOGAT3/APOA4/APOA1/PLA:
'517565784829,0.155067546712279,0.133312428041695,"PTGS2/PTGS1/HTR2A/PLA2G4A/DUSP1/K
'8",0.0204429884733229,0.155067546712279,0.133312428041695,"APOB/SLC52A3/APOA4/APOA1/
'0251326912186495,0.181923716136556,0.156400825515943,"TBXA2R/MCOLN3/GNA15/ERBB3/FG
'69/8388",0.0251534398516782,0.181923716136556,0.156400825515943,"MGST1/PTGS2/SULT2A1/
'62139452290988,0.18528493105113,0.159290480578734,"PLAUR/DCN/IGF1/ERBB3/MMP2/TIMP3,
'294551902405969,0.203568092551681,0.175008615698517,"CFTR/ATP1A2/CREB3L3/MYL9/ATP1B4
'16932368952,0.205940773840748,0.177048422932984,"GADD45B/WNT2/GLI3/GLI1/BMP4/FZD7/FZ
'28544,0.222145199501934,0.190979457348083,"CDH1/FGFR3/MMP2/MMP9/THBS1/EGFR/CXCL8/I
'352373349020648,0.222145199501934,0.190979457348083,"WWTR1/SNAI2/CDH1/AFP/WNT2/SER

3033133,0.222145199501934,0.190979457348083,"IGF1/INSRR/CREB3L3/FGFR2/MMP9/PLAT/IL1R2
70522,0.222145199501934,0.190979457348083,"CFTR/NR1H4/ATP1A2/SCTR/SLC4A4/SLCO1A2/ATP
9048,0.222145199501934,0.190979457348083,"CXCL2/IL1B/C3/IL6/CXCL3/CXCL1/CXCL8/CD14/HSP
88",0.0371432487913201,0.222145199501934,0.190979457348083,"IBSP/LAMC3/CREB3L3/TNFRSF
'8388",0.0382007289151344,0.224158994200128,0.192710727794323,"ATP1A2/CREB3L3/ATP1B4/k
8388",0.0410738334007614,0.233408940387327,0.200662957720024,"PTGS2/PTGS1/CGA/ADORA1
2781084286269,0.233408940387327,0.200662957720024,"TNFRSF1A/CXCL2/IL1B/C3/LBP/IL6/IFNA2
3493,0.244011663994182,0.209778177879581,"MRC2/MARCO/MSR1/FCGR2B/COMP/THBS4/C3/TI
04472239500858,0.244011663994182,0.209778177879581,"ATP1A2/CREB3L3/LRP2/ATP1B4/TTR/SE
'527328920064,0.282863791886448,0.243179567233569,"SELE/IFNG/APOA1/IL1B/IL6/HBA1/HPR",7
2388627,0.289064538716717,0.248510383598057,"CFTR/ABCB5/ABCG2/ABCA8/ABCA12/ABCA9/AB
'23/8388",0.057700846084058,0.299082718869034,0.257123068514925,"ATP1A2/SLC4A4/ATP1B4/
1.0677060566937108,0.339622316641033,0.291975185062862,"CYP27A1/CH25H/ACOX2/AKR1C4",4
0566937108,0.339622316641033,0.291975185062862,"CPS1/CA12/CA1/CA3",4
, "14/785", "98/8388", 0.071506511078183, 0.352992459449443, 0.303469570824703, "IGF1/HTR2A/TI
an)", "3/785", "11/8388", 0.0762643898387091, 0.365936873699124, 0.314597955388653, "HPD/NQO1
076481983249013, 0.365936873699124, 0.314597955388653, "CSF3/IL1A/IL1R2/IL1R1/IL1B/IL6/FCGR
115206036, 0.41632178168519, 0.357914139610893, "MOCOS/SPR/TPH2/AKR1C3/AKR1B10", 5
'8388", 0.0896899015206036, 0.41632178168519, 0.357914139610893, "PAX4/FOXA2/NEUROD1/SLC2
26882205539225, 0.423912302827498, 0.364439752642358, "GZMB/IFNG/IL1A/IL1B/IL6/HLA-DPB1/KI
154929429126808, 0.430410220954257, 0.370026048814964, "CD99/SELE/CLDN11/VCAN/CDH1/ITGA
353561, 0.445928520138121, 0.383367216500534, "CDH1/FGFR2/CDH17/GADD45B/WNT2/FGF1/TGFI
30146612815, 0.445928520138121, 0.383367216500534, "ACSM2B/GAD1/HMGCS2/ACSM5/ACSM2A"
31453608, 0.445928520138121, 0.383367216500534, "GABRA1/ENTPD2/SCNN1A/TAS2R7/TAS2R9/TA
'", 0.104671324662646, 0.445928520138121, 0.383367216500534, "TNFRSF1A/PTGS2/CXCL2/GADD45
3633640265215, 0.498581920574078, 0.428633636235627, "GPC4/WNT2/SFRP4/DKK1/SFRP5/SERPINI
4/8388", 0.120498164461158, 0.499665721965601, 0.429565386289601, "AVP/MYL9/MYH14/ACTA2/(
85", "37/8388", 0.126950569570158, 0.512748404367782, 0.440812640749422, "CPS1/ASPA/GAD1/AS
5", "37/8388", 0.126950569570158, 0.512748404367782, 0.440812640749422, "IGF1/ATP1A2/ATP1B4/
3", 0.132780964366025, 0.523256949169497, 0.449846894869021, "C8B/C6/CTSG/IFNG/C7/C9/C3/FC
'", 0.132917360078425, 0.523256949169497, 0.449846894869021, "IGF1/ITGA8/TNNC1/TGFB3/ITGB4/
67288385232, 0.551632924420637, 0.474241877823124, "PLA2G4A/PLA2G5/CYP2C9/PLA2G4D/PLA2G
38385232, 0.551632924420637, 0.474241877823124, "FOLR1/ABCG2/IL1B/IL6/FOLR2", 5
1274288, 0.590224751771994, 0.507419485361606, "GNA15/TNFRSF1A/SERPINE1/CCL2/IFNG/TGFB3/I
192211502983875, 0.509127506373005, "MS4A2/RNASE3/CCL11/FCER1A/HLA-DPB1", 5
354232317188, 0.592211502983875, 0.509127506373005, "MGST1/GGT5/HPGDS/GPX8/ANPEP/OPLAI
, "40/8388", 0.166433092729406, 0.601868509754016, 0.517429688534507, "DMGDH/SDS/BHMT/ALA
2729406, 0.601868509754016, 0.517429688534507, "GABRA1/SLC17A6/SLC32A1/GRIA2/GABRA5/GRI
88", 0.173448746003613, 0.620029425369238, 0.533042728190173, "C8B/INSRR/C6/FGFR2/FGFR3/IT
2235, 0.63742193066733, 0.547995161243871, "PTGS2/IFNG/IL1A/TGFB3/IL1B/C3/FCGR2A/FCGR1A/I
08138589588648, 0.703486695995815, 0.604791405594642, "SELE/TNFRSF1A/CXCL2/APOB/MMP9/C
41796691, 0.703486695995815, 0.604791405594642, "MLXIPL/CREB3L3/TNFRSF1A/PYGL/SLC27A6/PF
0.208599712698592, 0.703486695995815, 0.604791405594642, "IL20RA/OSM/CSF3/IFNG/GHR/LIF/GI
7404268845, 0.703486695995815, 0.604791405594642, "CP/HEPH/HMOX1/UGT2B4/ALAS2/UGT2B15
67404268845, 0.703486695995815, 0.604791405594642, "GZMB/IFNG/IL1A/IL1B/GAD1/HLA-DPB1", 6
378617225699, 0.714567552736089, 0.614317679454955, "IGF1/RASGRF1/NGFR/FGFR2/FGFR3/FGF1,
, "0.221814267027737, 0.72614986363817, 0.624275056233187, "PLA2G4A/PLA2G5/PLA2G4D/PLA2G
08105, 0.750607113106466, 0.645301088945819, "CFTR/CLDN11/YBX3/MYL9/MYH14/CLDN16/TUBA
man)", "4/785", "27/8388", 0.242646287969462, 0.773546859299039, 0.665022515694554, "ST3GAL4/
8", 0.24375431579198, 0.773546859299039, 0.665022515694554, "ST6GALNAC2/GALNTL5/GALNT5/G

nan)", "16/785", "143/8388", 0.262132520801687, 0.823466807770956, 0.707938971649426, "IGF1/FG
267398725743761, 0.828047517775989, 0.711877033390087, "LRP2/GLI3/GLI1/DHH/BOC/SHH/GAS1
3388", 0.274240817784331, 0.828047517775989, 0.711877033390087, "GALNTL5/GALNT5/ST6GAL2/G
817784331, 0.828047517775989, 0.711877033390087, "PCK1/LDHD/ADH1A/ADH1B/ADH4/ADH1C", 6
7/8388", 0.274240817784331, 0.828047517775989, 0.711877033390087, "ATP1A2/SI/ATP1B4/HKDC1,
210853916998, 0.845335247142362, 0.726739389995464, "IGF1/ITGA8/TNNC1/TGFB3/ITGB4/AGT/IT
, "29/8388", 0.285466553633775, 0.845335247142362, 0.726739389995464, "WWTR1/YAP1/FRMD6/L
288120695167493, 0.845335247142362, 0.726739389995464, "PCK1/FBP2/HKDC1/FBP1/ADH1A/ADH
98345, 0.870511752987714, 0.748383771395767, "IGF1/PGR/GADD45B/WNT2/FGF1/NOTCH2/FGF7/I
307280964369383, 0.875183411041503, 0.752400021677244, "TKTL1/FBP2/TKTL2/FBP1", 4
19463215314529, 0.875183411041503, 0.752400021677244, "AHR/IFNG/IL1R1/IL1B/IL6/RXRG/RUNX1,
1.309550402619181, 0.875183411041503, 0.752400021677244, "CREB3L3/PGR/MMP2/KRT31/MMP9,
mo sapiens (human)", "3/785", "21/8388", 0.31319401111427, 0.877086220160344, 0.7540358772067
35093, 0.877086220160344, 0.754035877206727, "EDN3/AGT/ADCYAP1/REN/AGTR1/ADORA1/ADRB3
79/8388", 0.318684060701347, 0.877086220160344, 0.754035877206727, "IGF1/ERBB3/FGFR2/FGFR3
4295328903, 0.894932387035105, 0.76937832562842, "SI/HKDC1/AKR1B10/MGAM", 4
30923551476003, 0.894932387035105, 0.76937832562842, "CGA/LHCGR/CYP17A1/SLC2A2/FOS/PRL/
1884519, 0.936220485121426, 0.804873932038728, "MYH13/KIF16B/MYO3A/MYL9/TNNT1/MYH14/A
19821315774, 0.941032701694099, 0.809011021256731, "CFTR/ATP1A2/SCTR/SLC4A4/ATP1B4/PLA2G
1, 0.941032701694099, 0.809011021256731, "IGF1/CDH1/GADD45B/FGF1/PDGFRA/FGF7/EGFR/FGF16
173606114462, 0.941032701694099, 0.809011021256731, "LIPG/MOGAT3/LIPC/AGPAT2/LPL/PNLIP/A
0027869, 0.956862056609271, 0.822619605275867, "ATP1A2/CST3/ATP1B4/HTN1/ADRA1B/CST2/CS
388", 0.373369390198782, 0.956862056609271, 0.822619605275867, "FBP2/HKDC1/FBP1/AKR1B10", 4
388680556, 0.956862056609271, 0.822619605275867, "TBXA2R/PTGS1/COL1A1/PLA2G4A/FCGR2A/PL
14/8388", 0.378819238875636, 0.956862056609271, 0.822619605275867, "CD99/CLDN11/MMP2/MM
/8388", 0.381514131895658, 0.956862056609271, 0.822619605275867, "MAP3K8/SPP1/IL1B/LBP/IL6/
7/8388", 0.384799940226535, 0.957382251283618, 0.823066819516125, "CLDN11/TNFRSF1A/MYH14,
1)", "11/785", "106/8388", 0.406216707104178, 0.999999828628807, 0.859705386602528, "CYP24A1/C
/8388", 0.412621494679043, 0.999999828628807, 0.859705386602528, "AVP/PLA2G4A/RRAS/PDGFRA
177903, 0.999999828628807, 0.859705386602528, "ATP1A2/CREB3L3/ATP1B4/GLP1R/ADCYAP1/CREB
, "35/8388", 0.417240033611845, 0.999999828628807, 0.859705386602528, "UGT2B4/CRYL1/UGT2B1
4811, 0.999999828628807, 0.859705386602528, "MRC2/TNFRSF1A/FCGR2B/IFNG/IL1A/TGFB3/IL1B/C
44992014057, 0.999999828628807, 0.859705386602528, "RASD1/GRIA2/KCNJ5/GNG11/GNGT1/MTN
27759822668896, 0.999999828628807, 0.859705386602528, "CDH1/PLAT/SERPINE1/ACTA2/SPP1/RR
158204258354, 0.999999828628807, 0.859705386602528, "HKDC1/SLC2A2/ADIPOQ/SLC2A4/SOCS3", 5
"8/785", "77/8388", 0.433475041307398, 0.999999828628807, 0.859705386602528, "ITGA8/DSP/ITGB4
559, 0.999999828628807, 0.859705386602528, "TNFRSF1A/CCL2/IFNG/IL1A/PLG/IL1B/IL6/IFNA21/NX
, 0.438925748339328, 0.999999828628807, 0.859705386602528, "SI/PYGL/HKDC1/MGAM", 4
169, 0.999999828628807, 0.859705386602528, "HTR2A/TUBA4A/PDGFRA/HTR2B/EGFR/TUBA3E/GJA1,
19588633418034, 0.999999828628807, 0.859705386602528, "HPD/TAT", 2
5108, 0.999999828628807, 0.859705386602528, "CDH1/GADD45B/RXRG/RET", 4
9120328, 0.999999828628807, 0.859705386602528, "GABRA1/SLC32A1/OPRM1/KCNJ5/GNG11/GNGT
8388", 0.486040653667304, 0.999999828628807, 0.859705386602528, "FGFR2/FGFR3/PDGFRA/EGFR/
161627, 0.999999828628807, 0.859705386602528, "CREB3L3/GRIA2/PPP1R1B/CREB3L1/GRIN2B", 5
3599507715, 0.999999828628807, 0.859705386602528, "IGF1/PPP1R17/PLA2G4A/GRIA2/CRH/PLA2G4
.00045808, 0.999999828628807, 0.859705386602528, "LAMC3/PTGS2/GADD45B/FN1/RXRG/LAMB2/C
15118347672, 0.999999828628807, 0.859705386602528, "PLA2G4A/PLA2G5/PLA2G4D/UGT8/PLA2G2/
509755938986834, 0.999999828628807, 0.859705386602528, "MGST1/GADD45B/HMOX1/WNT2/TGF
1624281941977, 0.999999828628807, 0.859705386602528, "SLC17A6/SLC1A6/PLA2G4A/GRIA2/GNG1
4911204, 0.999999828628807, 0.859705386602528, "RCVRN/GNGT1/CNGA1", 3

785", "212/8388", 0.520110376521437, 0.999999828628807, 0.859705386602528, "MGST1/CREB3L3/P
'8388", 0.543920264690891, 0.999999828628807, 0.859705386602528, "BHMT2/SDS/BHMT/MAT1A/T
uman)", "5/785", "53/8388", 0.56136423847538, 0.999999828628807, 0.859705386602528, "ATP1A2/
253643, 0.999999828628807, 0.859705386602528, "GADD45B/AREG/TGFB3/EREG/PMAIP1/EGFR/TGF
118048604039, 0.999999828628807, 0.859705386602528, "CYP1B1/AOX1/TPH2/INMT", 4
576690633920365, 0.999999828628807, 0.859705386602528, "IFNG/IL1A/TGFB3/IL1B/IL6/HLA-DPB1"
4420456332, 0.999999828628807, 0.859705386602528, "ADH1A/ADH1B/ADH4/ADH1C", 4
58703954142418, 0.999999828628807, 0.859705386602528, "NGFR/TNFRSF1A/PMAIP1", 3
, "44/8388", 0.600181001336207, 0.999999828628807, 0.859705386602528, "CREB3L3/AVP/CREB3L1/
59760922, 0.999999828628807, 0.859705386602528, "GABRA1/SLC32A1/GNG11/GNGT1/GAD1/GNG1
, 0.606606954732689, 0.999999828628807, 0.859705386602528, "ATP1A2/CREB3L3/MYL9/ATP1B4/A
005571075, 0.999999828628807, 0.859705386602528, "CPS1/ASS1", 2
005571075, 0.999999828628807, 0.859705386602528, "ASPA/HDC", 2
0753237, 0.999999828628807, 0.859705386602528, "SELENBP1", 1
3", 0.636179671706123, 0.999999828628807, 0.859705386602528, "TNFRSF1A/PCK1/RXRG/ADIPOQ/S
179671706123, 0.999999828628807, 0.859705386602528, "CREB3L3/GRIA2/PPP1R1B/CREB3L1/FOS/G
17/785", "194/8388", 0.650076946765557, 0.999999828628807, 0.859705386602528, "TNFRSF1A/PTGS
n)", "6/785", "70/8388", 0.650255204647263, 0.999999828628807, 0.859705386602528, "CXCL2/PTPR
human)", "2/785", "24/8388", 0.671433774751214, 0.999999828628807, 0.859705386602528, "HS3ST2
'85", "49/8388", 0.685487849886636, 0.999999828628807, 0.859705386602528, "CXCL12/IL6/CCR9/HL
5410478218, 0.999999828628807, 0.859705386602528, "IGF1/GADD45B/SERPINE1/PERP/THBS1/PM
04560882201, 0.999999828628807, 0.859705386602528, "ERBB3/AREG/EREG/EGFR/BTC/ERBB4/SHC4
388", 0.698323093038026, 0.999999828628807, 0.859705386602528, "FCGR2B/PLA2G4A/FCGR2A/GS
976444965613, 0.999999828628807, 0.859705386602528, "CREB3L3/GRIA2/KCNJ5/GNG11/GNGT1/P
0075891, 0.999999828628807, 0.859705386602528, "GZMB/IFNG/HLA-DPB1", 3
8", 0.706996662869731, 0.999999828628807, 0.859705386602528, "TNFRSF1A/ADORA3/MS4A2/ADO
06996662869731, 0.999999828628807, 0.859705386602528, "CFTR/IGF1/CREB3L3/PCK1/FBP2/CREB3
1.709280083039891, 0.999999828628807, 0.859705386602528, "SLC22A2/SLC5A7/PLA2G4A/PDGFR
15466762029889, 0.999999828628807, 0.859705386602528, "TKTL1/CPS1/ASS1/SDS/TKTL2/MAT1A",
17386539380484, 0.999999828628807, 0.859705386602528, "ATP1A2/ATP1B4/TNNC1/CASQ2/COX7A
239, 0.999999828628807, 0.859705386602528, "CLDN11/TNFRSF1A/IFNG/CLDN16/IFNA21/EGFR/CLDI
67, 0.999999828628807, 0.859705386602528, "TNFRSF1A/GADD45B/GZMB/TUBA4A/NGF/PMAIP1/TL
'88", 0.739069277296359, 0.999999828628807, 0.859705386602528, "CDH1/ARHGAP10/ARHGEF26/FI
18468, 0.999999828628807, 0.859705386602528, "CREB3L3/WNT2/FZD7/FZD1/CREB3L1/WNT9B/FZC
103368306, 0.999999828628807, 0.859705386602528, "CREB3L3/SLC5A7/GNG11/GNGT1/CREB3L1/K
883477622367, 0.999999828628807, 0.859705386602528, "SGMS2/SPTLC3/UGT8/SPHK1", 4
.743883477622367, 0.999999828628807, 0.859705386602528, "GZMB/CGA/IFNA21/HLA-DPB1", 4
1/785", "14/8388", 0.747602559387057, 0.999999828628807, 0.859705386602528, "CHST6", 1
977133281, 0.999999828628807, 0.859705386602528, "TKTL1/CPS1/HAO2/FBP2/SDS/TKTL2/HKDC1/F
uman)", "1/785", "15/8388", 0.771262935656601, 0.999999828628807, 0.859705386602528, "A4GALT"
'85", "15/8388", 0.771262935656601, 0.999999828628807, 0.859705386602528, "ST6GALNAC5", 1
1361728626646, 0.999999828628807, 0.859705386602528, "IGF1/CDH1/NGFR/FGFR2/FGFR3/FGF1/R
'88", 0.771793833510128, 0.999999828628807, 0.859705386602528, "MGST1/NAT2/UGT2B4/UGT2B15
, 0.775422312850487, 0.999999828628807, 0.859705386602528, "PLA2G4A/ALOX5AP/MS4A2/PLA2G4
388", 0.785594458668548, 0.999999828628807, 0.859705386602528, "UGT2B4/UGT2B15", 2
"30/8388", 0.785594458668548, 0.999999828628807, 0.859705386602528, "HAO2/AGXT", 2
154/8388", 0.788473260877296, 0.999999828628807, 0.859705386602528, "ATP1A2/CREB3L3/ATP1B
4683322070459, 0.999999828628807, 0.859705386602528, "IGF1/GADD45B/SGK1/TGFB3/PCK1/IL6/E
.795946092588623, 0.999999828628807, 0.859705386602528, "CREB3L3/PYGL/PCK1/FBP2/CREB3L1/
0812025097484, 0.999999828628807, 0.859705386602528, "SMOX/GAD1", 2

3/785", "120/8388", 0.802885267181757, 0.999999828628807, 0.859705386602528, "IGF1/CREB3L3/G
 8388", 0.81059060145683, 0.999999828628807, 0.859705386602528, "ATP1A2/ATP1B4/BMP4/NOTCH
 1.812144619553141, 0.999999828628807, 0.859705386602528, "INMT", 1
 304377038216, 0.999999828628807, 0.859705386602528, "IGF1/HMOX1/TIMP1/SERPINE1/IFNG/IL6/
 49877379261, 0.999999828628807, 0.859705386602528, "PTGS2/PLA2G4A/PLA2G4D/SPHK1", 4
 37900352, 0.999999828628807, 0.859705386602528, "IGF1/MMP2/MMP9/NOTCH2/EGFR/FOS/SHC4"
 40025, 0.999999828628807, 0.859705386602528, "LAMC3/TNFRSF1A/IFNG/TGFB3/LAMB2/HSPA6/LA
 37172647639469, 0.999999828628807, 0.859705386602528, "PYGL/PPP1R3C/PCK1/TRIP10/FBP2/HKI
 112437, 0.999999828628807, 0.859705386602528, "BHLHE41/BHLHE40", 2
 178, 0.999999828628807, 0.859705386602528, "CREB3L3/MMP9/TGFB3/EGR2/IL6/IFNA21/CREB3L1/
 999999828628807, 0.859705386602528, "IGF1/GADD45B/PDGFR/EGFR/SHC4", 5
 /785", "62/8388", 0.844578726472148, 0.999999828628807, 0.859705386602528, "IGF1/CRYAB/FOXA2
 1297690962993, 0.999999828628807, 0.859705386602528, "GADD45B/TGFB3/RUNX1/TGFB2/SHC4"
 3", 0.859494905177822, 0.999999828628807, 0.859705386602528, "SMOX/P4HA3/GATM", 3
 95916654, 0.999999828628807, 0.859705386602528, "CYP24A1", 1
 0197795916654, 0.999999828628807, 0.859705386602528, "ALDH1L1", 1
 18882, 0.999999828628807, 0.859705386602528, "TRPC5/SPP1/KCNJ5/CGA", 4
 '36/8388", 0.863346722775352, 0.999999828628807, 0.859705386602528, "AOX1/NNMT", 2
 104/8388", 0.866299995255172, 0.999999828628807, 0.859705386602528, "PTGS2/EGR2/IL1B/RRAS/
 8388", 0.866540495259867, 0.999999828628807, 0.859705386602528, "IFNG/HSPA6/KLRC3/HLA-DPB:
 495259867, 0.999999828628807, 0.859705386602528, "SLC17A6/SLC32A1/SLC1A6/UNC13C/SLC6A5",
 388", 0.873312605931643, 0.999999828628807, 0.859705386602528, "VNN1", 1
 765569746793, 0.999999828628807, 0.859705386602528, "MMP2/PLA2G4A/CGA/EGFR/MMP14/PLA2
 192394036099, 0.999999828628807, 0.859705386602528, "DUSP6/FCGR1A/RUNX1/CD14", 4
 /8388", 0.891659918132055, 0.999999828628807, 0.859705386602528, "CHST9/MGAT4D", 2
 222/8388", 0.894624294414379, 0.999999828628807, 0.859705386602528, "CREB3L3/TNFRSF1A/TSP
 8", 0.89597061036313, 0.999999828628807, 0.859705386602528, "HMGCS2", 1
 148/8388", 0.897028141676336, 0.999999828628807, 0.859705386602528, "GABRA1/PTGS2/SLC17A6,
 8388", 0.905498926790689, 0.999999828628807, 0.859705386602528, "CREB3L3/TNFRSF1A/PTGS2/CX
 6, 0.999999828628807, 0.859705386602528, "CP/HMOX1", 2
 8", 0.911722081900476, 0.999999828628807, 0.859705386602528, "PLA2G4A/PLA2G5/PLA2G4D/ETNI
 15012788478184, 0.999999828628807, 0.859705386602528, "PDK4/MMP2/CMA1/MMP9/COL1A1/T
 5170669748429, 0.999999828628807, 0.859705386602528, "GADD45B/RXR/EGFR/RET", 4
 52071723, 0.999999828628807, 0.859705386602528, "CDH1/GADD45B/EGFR", 3
 88", 0.924652450003778, 0.999999828628807, 0.859705386602528, "MLXIPL/TNFRSF1A/IL1A/IL1B/IL6
 9985333145, 0.999999828628807, 0.859705386602528, "GADD45B/SERPINE1/TRPV4/IL1A/TGFB3/RR
 573591841, 0.999999828628807, 0.859705386602528, "CFTR/ATP1A2/ATP1B4/KCNJ15", 4
 591841, 0.999999828628807, 0.859705386602528, "GADD45B/TGFB3/EGFR/TGFB2", 4
 32/8388", 0.935831032839418, 0.999999828628807, 0.859705386602528, "GZMB/IFNG/IFNA21/RAET
 5969, 0.999999828628807, 0.859705386602528, "TNFRSF1A/PYGL/IFNG/IL1A/PLA2G4A/IL1B/IFNA21/I
 35083296616, 0.999999828628807, 0.859705386602528, "TNFRSF1A/MYL9/ARHGEF26/AHNAK/IL1B/R
 6/8388", 0.940125458213815, 0.999999828628807, 0.859705386602528, "CXCL2/TRIP6/CCL2/IL1B/IL6
 6918084, 0.999999828628807, 0.859705386602528, "SMYD1/PRDM16/COLGALT2", 3
 3115952, 0.999999828628807, 0.859705386602528, "SNAI2/CDH1/MYL9/EGFR/TGFB2", 5
 , "48/8388", 0.947178167540947, 0.999999828628807, 0.859705386602528, "HMGCS2/AOX1", 2
 24586491312, 0.999999828628807, 0.859705386602528, "PCK1", 1
 0808036, 0.999999828628807, 0.859705386602528, "CCL2/FN1/IL1B/IL6/FCGR2A/DOCK1/CXCL8/FOS"
 785", "49/8388", 0.951314259387143, 0.999999828628807, 0.859705386602528, "CHIT1/HKDC1", 2
 2065812531, 0.999999828628807, 0.859705386602528, "ST6GAL2/MGAT4D", 2
 140065812531, 0.999999828628807, 0.859705386602528, "CFTR/KDEL3", 2

27,0.999999828628807,0.859705386602528,"HAO2/ACOX2/AGXT/DDO",4
622799546588,0.999999828628807,0.859705386602528,"SPR/MAT1A/UGT2B4/HPD/ALAS2/DHRS3,
165698146226,0.999999828628807,0.859705386602528,"ACSS3",1
3146226,0.999999828628807,0.859705386602528,"WIPI1",1
958405844263298,0.999999828628807,0.859705386602528,"PTGS2/MYL9/PLA2G4A/KCNJ5/EGFR/F
'33/8388",0.961189743976194,0.999999828628807,0.859705386602528,"VAMP5",1
3",0.961206163724995,0.999999828628807,0.859705386602528,"FCGR2B/LILRB5/FOS/LILRA2",4
247366851894,0.999999828628807,0.859705386602528,"IGF1/TNFRSF1A/WNT2/SGK1/FZD7/FZD1/
35702,0.999999828628807,0.859705386602528,"POLR2J2",1
8388",0.96799874104626,0.999999828628807,0.859705386602528,"IFNA21/CXCL8/ISG15",3
1.972412802214476,0.999999828628807,0.859705386602528,"IGF1/CREB3L3/CREB3L1/ADIPOQ",4
,0.972435952444722,0.999999828628807,0.859705386602528,"PLCH1/PIK3C2G/PLCD3",3
435952444722,0.999999828628807,0.859705386602528,"MGST1/PMAIP1/GSTA1",3
190/8388",0.97339582061061,0.999999828628807,0.859705386602528,"CTSG/AQP9/C3/FCGR2A/F
8",0.973847581486442,0.999999828628807,0.859705386602528,"HKDC1",1
,0.976285937441474,0.999999828628807,0.859705386602528,"IL1B/IL6/IFNA21",3
76305927616623,0.999999828628807,0.859705386602528,"AIRE",1
36312,0.999999828628807,0.859705386602528,"C8B/C6/CREB3L3/C7/C9/IL1A/IL1B/TUBA4A/IL6/TU
,0.977599085973691,0.999999828628807,0.859705386602528,"IFNG/NOTCH2/FOS/HLA-DPB1",4
0.999999828628807,0.859705386602528,"FCGR2B/IL1A/IL1B/IL6/IFNA21/FOS/HSPA6",7
"13/785", "223/8388",0.980134403558614,0.999999828628807,0.859705386602528,"MGST1/HMOX
350654,0.999999828628807,0.859705386602528,"SEMA3B/TRPC5/SEMA3C/MYL9/CXCL12/RRAS/BC
295961,0.999999828628807,0.859705386602528,"LAMA2/HLA-DPB1",2
519865581,0.999999828628807,0.859705386602528,"TNFRSF1A/WIPI1/PTGS2/WNT2/DKK1/IL1A/IL
27415868404,0.999999828628807,0.859705386602528,"WIPI1/SLC1A6/GRIA2/MYOD1/KCND3/RELN
01,0.999999828628807,0.859705386602528,"CREB3L3/GNG11/GNGT1/PPP1R1B/CRH/NTRK2/CREB3
36,0.999999828628807,0.859705386602528,"IFNG",1
62538443753,0.999999828628807,0.859705386602528,"GRIA2/GRIN2B",2
8",0.989606590412706,0.999999828628807,0.859705386602528,"NGFR/NGF/NTRK2/SHC4/NTF3",5
38",0.990499256765603,0.999999828628807,0.859705386602528,"MAP3K8/IFNG/TEC/FOS",4
man)", "3/785", "89/8388",0.991965301140095,0.999999828628807,0.859705386602528,"IFNG/EGF
37155111,0.999999828628807,0.859705386602528,"RRAS/CITED2",2
5474,0.999999828628807,0.859705386602528,"EHD3/EHD2/FGFR2/FGFR3/FOLR1/PDGFR4/CBLC/EC
027814137143,0.999999828628807,0.859705386602528,"NOTCH2",1
, "102/8388",0.9971685726454,0.999999828628807,0.859705386602528,"IGF1/PGR/SPDYC",3
.19,0.999999828628807,0.859705386602528,"TNFRSF1A/WIPI1/MYL9/IL1R1/IL1B/C3/EGFR/DOCK1/
71362995828,0.999999828628807,0.859705386602528,"ENTPD2/GDA",2
775830877,0.999999828628807,0.859705386602528,"ELL2",1
7999775830877,0.999999828628807,0.859705386602528,"POLR2J2",1
50721403729,0.999999828628807,0.859705386602528,"CYP24A1/VIM/ERBB3/FGFR3/PTGS2/TIMP3
, "28/785", "476/8388",0.9982556095755,0.999999828628807,0.859705386602528,"TNFRSF1A/WIPI
0.998267996735614,0.999999828628807,0.859705386602528,"NXF3/POM121L2/NXF2B",3
171654,0.999999828628807,0.859705386602528,"IGF1/PGR/AR/SPDYC",4
125282738,0.999999828628807,0.859705386602528,"TGFB3",1
,0.998949320848084,0.999999828628807,0.859705386602528,"TNFRSF1A/WIPI1/NEFH/GRIA2/TUE
999236876968697,0.999999828628807,0.859705386602528,"NXF3/NXF2B",2
'8388",0.999236876968697,0.999999828628807,0.859705386602528,"PIK3C2G/PLCD3",2
,0.99948582074754,0.999999828628807,0.859705386602528,"FBXO2/CBLC/AIRE/SOCS3",4
4226023762,0.999999828628807,0.859705386602528,"CREB3L3/WIPI1/GRIA2/TUBA4A/TUBA3E/CRI
093420416,0.999999828628807,0.859705386602528,"CREB3L3/EGR2/C3/PMAIP1/GSN/CREB3L1/EG

1,0.999999828628807,0.859705386602528,"SLC11A1/CTSG/NPC2",3
999915223180117,0.999999828628807,0.859705386602528,"VIM/GADD45B/IL6/IFNA21/ISG15/HLA
5","171/8388",0.999951977842495,0.999999828628807,0.859705386602528,"CRYAB/FBXO2/RRBP1
174434807,0.999999828628807,0.859705386602528,"ENTPD2/GDA",2
","212/8388",0.999960801534564,0.999999828628807,0.859705386602528,"TNFRSF1A/GNG11/GN
536176207,0.999999828628807,0.859705386602528,"WIP1/RRAS",2
133334,0.999999828628807,0.859705386602528,"CREB3L3/PRDM16/CREB3L1/COX7A1/PLIN1/ADRB
3,0.999999828628807,0.859705386602528,"GADD45B/TGFB3",2
10373793,0.999999828628807,0.859705386602528,"DUSP1/TUBA4A/SNCA/TUBA3E/COX7A1/TUBB6
199998287676895,0.999999828628807,0.859705386602528,"COX7A1",1
3388",0.99999844527226,0.999999828628807,0.859705386602528,"NXF3/NXF2B",2
999777395547,0.999999828628807,0.859705386602528,"OR1Q1/OR51E2/OR1L3/OR10AD1/OR52V
807,0.999999828628807,0.859705386602528,"HSPA6",1

/C6/PLAT/SERPINE1/C7/C9/F3/SERPINC1/CLU/PLG/PLAU/C4BPA/C4BPB/F13A1/C3/F10/MASP1/CFHF
 /UTS2/NPFFR2/PRLH/SCTR/OPRK1/TSPO/CTSG/AVP/GLRA2/GPR50/HTR2A/CALCA/OPRM1/GLP1R/G
 .26/IL20RA/NGFR/TNFRSF1A/CXCL2/OSM/CXCL12/CSF3/CCL7/CCL2/CCL8/PF4V1/IFNG/BMP5/GHR/IL
 11A1/COL17A1/COL16A1/COL9A3/ATP1B4/COL1A1/COL12A1/XPNPEP2/COL10A1/COL21A1/COL5A1
 .JPG/APOA4/APOC3/APOA1/NPC2/APOE/APOC1/CYP27A1/STAR/APOA2/LIPC/ANGPTL4/PCSK9/LPL/L
 e-07,"CCL26/IL20RA/TNFRSF1A/CXCL2/CXCL12/CCL7/CCL2/CCL8/PF4V1/CCL20/CXCL6/IL6/CXCL9/XCL
 :OMP/COL1A1/THBS4/FN1/SPP1/SDC4/ITGB4/CHAD/THBS1/ITGA11/COL6A2/FREM2/MEPE/COL6A3,
 :ABP3/PCK1/HMGCS2/CYP27A1/RXRG/APOA2/FABP1/FABP7/AQP7/PLIN1/PLIN4/ANGPTL4/ACOX2/F
 =NG/C9/FN1/IL1R2/IL1R1/TGFB3/IL1B/IL6/C8A/CD1A/CD1B/CXCL3/CXCL1/COL1A2/COL3A1/CXCL8/C
 7/CCL2/IFNG/CCL20/CXCL6/IL1B/IL6/MMP13/MMP3/S100A9/IL17RE/CXCL3/CXCL1/CXCL8/FOS/CCL1
 /PROM1/IGF1/NGFR/HOXA9/GADD45B/GZMB/SIX4/MMP9/PLAT/TLX1/IL1R2/NR4A3/PLAU/RUNX2/!
 1/CPA3/ANPEP/KLK1/MRGPRD/MME",10
 RT18/PLG/C3/MASP1/KRT34/FCGR2A/FCGR1A/C1R/DEFA4/DEFA6/MBL2/FPR1/FGG/C1S/KRT14/C5A
 3/NGFR/ERBB3/FGFR2/FGFR3/ITGA8/COL9A3/OSM/COMP/CSF3/COL1A1/AREG/GHR/THBS4/FGF1/F
 X1/UGT2B4/DHRS3/ALDH1A1/CYP2S1/SDR16C5/CYP27C1/ADH1A/ADH1B/UGT2B15/ADH4/ADH1C",
 /CGA/LHCGR/CYP1B1/CYP11A1/STAR/CYP17A1/PLA2G4D/AKR1C3/HSD3B1/HSD3B2",14
 /CXCL2/MMP9/MAP3K8/CCL2/CCL20/CXCL6/IL1B/LIF/IL6/MMP3/MMP14/CREB3L1/CXCL3/CXCL1/FC
 ELE/MMP2/SERPINE1/CCL2/COL1A1/IL1A/FN1/F3/TGFB3/IL1B/AGT/IL6/AGTR1/PLCD3/TGFB2/COL:
 E1/HSD11B1/CYP1B1/CYP11A1/CYP17A1/UGT2B4/CYP11B1/AKR1C3/UGT2B15/AKR1C4/HSD3B1/HSE
 3/IL6/THBS1/CXCL8/THBS2/HBA1",13
 5A1/CYP11A1/AGTR1/STAR/CYP17A1/CREB3L1/CYP11B1/MRAP/KCNA4/HSD3B1/HSD3B2/CYP21A2",
 /MT1G/MT2A/STEAP1/MT1E/SLC6A19/MT1X/MT1F/MT1A/MT1M",14
 /MYL9/COMP/COL1A1/THBS4/FN1/SPP1/ITGB4/EMP1/PDGFRA/CHAD/THBS1/ITGA11/COL6A2/EGFR
 TGFB3/FMOD/INHBA/BMP4/GDF5/FST/THBS1/EMP3/NBL1/TGFB2/PITX2/FBN1/TGIF1/THSD4",19
 iFB3/CXCL6/IL1B/IL6/MMP3/CXCL3/CXCL1/CXCL8/FOS/CSF1/MMP1/HLA-DPB1",18
 A2G4A/PLA2G5/CYP2C9/PTGES/PLA2G4D/HPGDS/CYP4F3/PLA2G2A/AKR1C3",13
 C1R/CXCL8/FOS/CD14/C1S/C4B/C4A",15
 T/NR5A1/CYP11A1/AGTR1/EGFR/STAR/CRH/CYP17A1/FZD7/FZD1/CREB3L1/WNT9B/CYP11B1/MRAP
 2A1/HSD11B1/CYP1B1/CYP2C9/EPHX1/UGT2B4/HPGDS/CYP2S1/ADH1A/ADH1B/UGT2B15/ADH4/G
 .2/C7/C9/F13A1/IL1B/C3/MASP1/IL6/IFNA21/FCGR2A/AGTR1/EGFR/MMP3/C8A/C1R/TLR3/MBL2/CX
 :2/TNFRSF1A/FGFR3/GADD45B/MAP3K8/AREG/FGF1/IL1A/IL1R1/PLA2G4A/TGFB3/DUSP1/DUSP4/NF
 MO4/CYP2C9/AOX1/UGT2B4/HPGDS/ADH1A/ADH1B/UGT2B15/ADH4/GSTA1/ADH1C",14
 ACTA2/COL1A1/GNG11/GNGT1/RXFP2/MMP13/EGFR/CREB3L1/TGFB2/COL1A2/COL3A1/FOS/GNG:
 /MMP2/HMOX1/MMP9/PLAT/CCL2/TRPV4/IFNG/IL1A/IL1R2/IL1R1/DUSP1/SDC4/BMP4/IL1B/ASS1/F
 .2/CCL8/PF4V1/CCL20/CXCL6/GNG11/GNGT1/CXCL9/XCL1/CXCL14/CXCL16/CXCL3/CXCL1/CX3CR1/C
 /GAD1",5
 3B5/IFNG/IL1A/IL1R1/FHL2/IL1B/TEC/FCGR2A/FCGR1A/TGFB2/FOS/JUNB/FOSL1/CSF1/SOCS3/LILRA
 ADH1C",8
 2G5/FABP1/AGPAT2/PNLIP/PLA2G2A",9
 CNJ5/GNG11/GNGT1/HTR1B/HTR2B/CYP2C9/TPH2/HTR7/HTR5A/PLA2G4D/HTR1E/GNG12/HTR1A",:
 'LRAT/PNLIP",6
 iFR2/FGFR3/HTR2A/FGF1/TNNC1/CASQ2/NGF/PDGFRA/HTR2B/LHCGR/FGF7/AGTR1/EGFR/NTRK2/H
 /HSD11B1/CYP1B1/CYP2C9/EPHX1/NAT2/UGT2B4/HPGDS/UGT2B15/GSTA1",12
 /MMP9/WNT2/COL1A1/FN1/PLAU/SDC4/RRAS/THBS1/LUM/EGFR/GPC3/FZD7/FZD1/WNT9B/SHH/Ci
 /GLI3/GLI1/GLP1R/GRIA2/EDN3/SOX9/RRAS/PPP1R1B/HTR1B/CGA/LHCGR/SSTR1/ADCYAP1/VIP/CRF
 D1/WNT9B/SHH/FZD2/WNT7B",11
 MMP1",8
 PINE1/AREG/BMP5/FGF1/TGFB3/BMP4/GDF5/YAP1/FRMD6/LATS2/FZD7/FZD1/WNT9B/TGFB2/FZC

/PLAU/PDGFR/EGFR/MMP3/CREB3L1/NKX3-1/AR/TMPRSS2",15
 '1B4/AQP9/SULT2A1/ABCG2/EPHX1/UGT2B4/UGT2B15/AQP1",14
 A6/EEF1G",10
 1A/HES2/PTGS2/ITGA8/COL9A3/COMP/WNT2/COL1A1/THBS4/FN1/SPP1/ITGB4/NOTCH2/CHAD/IFN.
 (CNJ5/NR4A1/AGT/CYP11A1/AGTR1/STAR/NR4A2/CREB3L1/PRKD1/HSD3B1/HSD3B2/CYP21A2",15
 /NPY1R/AQP7/PLIN1/FABP4/CIDEA/ADRB3",10
 21/FABP1/CXCL3/CXCL1/CXCL8/CD14/ADIPOQ/ADH1A/ADH1B/C5AR1/ADH4/C4B/C4A/ADH1C",20
 UBA4A/THBS1/FCGR2A/FCGR1A/TUBA3E/COLEC12/C1R/MBL2/CD14/OLR1/TUBB6/THBS2/TUBA3C/H
 ERPINA7/CGA/CREB3L1/ASGR2/ALB/GPX8/GPX3",12
 7
 CA6/ABCA10",8
 PCK1/AQP1",5
 1

 RPV4/IL1R1/PLA2G4A/IL1B/NGF/HTR2B/PLA2G4D/TRPV3/BDKRB2/P2RY2/IL1RAP/HRH1",14
 L/TAT",3
 1A/CD1A/CD1B/ANPEP/CD14/CSF1/MME/HLA-DPB1",14

 A2/FOXA3",5
 IR2DL3",7
 8/MAG/CLDN16/SDC4/CDH15/IGSF11/MPZ/CLDN14/CLDN1/CLDN19/NLGN1/SLITRK4/CLDN7/SLITRK
 B3/FGF7/RXRG/EGFR/FZD7/FZD1/WNT9B/TGFB2/SHH/FZD2/SHC4/WNT7B/FGF16",19
 ,5
 AS2R3/HTR1B/KCNK5/HTR1E/HTR1A/GABRA5/TAS2R38",12
 B/CXCL12/IL1R1/PLAU/IL1B/LBP/CXCL3/CXCL1/CXCL8/CD14/CCL13",14
 F1/MMP7/LGR5/SFRP2/DAAM2/RSPO3/RSPO2/DKK2/FZD7/FZD1/WNT9B/FOSL1/FZD2/ROR1/WNT7
 CALCA/PLA2G4A/EDN3/PLA2G5/AGT/AGTR1/PLA2G4D/ACTG2/ADRA1B/ADRA1D/CALCB/PLA2G2A/K
 S1/AGXT/DDO",6
 /SCNN1A/SGK1/NR3C2",6
 GR2A/FCGR1A/C8A/C1R/C1S/ELANE/HLA-DPB1/C4B/C4A/GRIN2B",17
 AGT/IL6/ITGA11/LMNA/DES/LAMA2/TPM2",12
 32A",5

 IL1B/C3/IL6/TGFB2/BDKRB2/CXCL8/FOS",13

 H/GPX3/GSTA1",8
 S2/GATM/AGXT",6
 N2B",6
 GA8/MYL9/MYH14/CXCL12/C7/FGF1/C9/FN1/RRAS/ITGB4/PDGFR/ITGA11/FGF7/EGFR/GSN/DOCK1
 FOS/HLA-DPB1",10
 CL2/APOA4/APOA1/IL1B/LBP/IL6/IFNA21/POU2F3/CYP2C9/RXRG/MMP3/CXCL3/CXCL1/CXCL8/FOS/
 P1R3C/PCK1/AGT/IL6/CREB3L1/SLC2A2/SLC2A4/SOCS3",13
 FAP/PDGFR/IL6/IFNA21/AOX1/OSMR/TSRP/EGFR/PRL/SOCS3/IFNLR1/IL27/CRLF2",19
 ",6
 ;
 /PLA2G4A/RRAS/PLA2G5/GNG11/GNGT1/NGF/PDGFR/FGF7/EGFR/NTRK2/HTR7/PLA2G4D/IGF2/GN
 2A",4
 4A/GATA4/RAB13/TUBA3E/CD1A/CD1B/RUNX1/CLDN14/CLDN1/CLDN19/MICALL2/CLDN7/TUBA3C",
 /A4GALT/ABO/B3GNT3",4
 iALNT14/B3GNT3",5

FR2/FGFR3/LHX5/WNT2/INHBA/BMP4/LIF/KLF4/FZD7/ZIC3/FZD1/WNT9B/FZD2/SOX2/WNT7B",16
",7

iALNT14/GXYLT2/COLGALT2",6

/SLC2A2/MGAM",6

GA11/LMNA/DES/LAMA2/TPM2",11

.ATS2",4

11B/ADH4/ADH1C",8

EGFR/FZD7/FZD1/WNT9B/FOS/FZD2/SHC4/WNT7B/FGF16",16

/TGFB2/FOS/IL1RAP/IL27/HLA-DPB1",12

/KRT18/OPRM1/KCNJ5/KRT34/EGFR/CREB3L1/FOS/HSPA6/SHC4/KRT14",15

'27,"UST/CHST3/CHSY3",3

/AQP1",8

3/PDGFRA/IL6/EGFR/AXL/SHC4",9

'SOCS3/SHC4",8

CTA2/MYH1/TNNC1/TUBA4A/TNNT3/MYH8/TUBA3E/MYO1E/ACTG2/TUBB6/KIF19/TUBA3C/MYL4/T

i5/CPB1/CPA3/PNLIP/CCK/PLA2G2A",11

5",8

KR1B10",7

T1/ADRA1D/DMBT1/ADRB3",10

↓

.A2G4D/COL1A2/COL3A1/P2RY12/FGG/FGA/FGB/F2",13

IP9/MYL9/CXCL12/CLDN16/THY1/CLDN14/CLDN1/CLDN19/CLDN7",12

/IFNA21/CXCL9/TLR3/CXCL8/FOS/CD14",11

/CLDN16/IL1R1/IL1B/TUBA4A/IL6/FCGR2A/TUBA3E/MYO1E/CLDN14/CLDN1/CLDN19/CXCL8/FOS/TU

REB3L3/PTHLH/RUNX2/MMP13/RXRG/EGFR/NR4A2/MMP14/CREB3L1/FOS",11

4/AGT/AGTR1/EGFR/MS4A2/PLA2G4D/CXCL8/AGPAT2/SPHK1/FCER1A/F2/SHC4",15

3L1/SLC2A2/CCK/KCNU1",9

5/AKR1B10",4

3/LBP/IL6/IFNA21/FCGR2A/FCGR1A/CLEC4E/CD14/CEBPB/SPHK1/HLA-DPB1",18

R1B/ADCYAP1/FOS/GNG12/GRIN2B",10

AS/GNG11/GNGT1/AGTR1/PLIN1/GNG12/SPHK1/MYL4/APELA",14

5

4/ITGA11/GJA1/LMNA/DES/LAMA2",8

.F3/TLR3/CXCL8/TPSAB1/TMPRSS2/SOCS3/TPSB2/HLA-DPB1/NXF2B",17

/TUBB6/TUBA3C",9

Γ1/ADORA1/GNG12/GABRA5",9

'HKDC1/SLC2A2/RET",7

4D",6

COL4A5/LAMA2/COL4A6",9

A",5

3B/EGFR/FZD7/FZD1/WNT9B/TGFB2/IGF2/FZD2/NQO1/SHC4/WNT7B/GSTA1",16

1/GNGT1/PLA2G4D/DLGAP1/GRIK1/GNG12/GRIN2B",11

'GR/AHR/NOTCH2/KLF4/CYP1B1/FGF7/RXRG/EPHX1/EGFR/UGT2B4/CREB3L1/AR/FOS/CHRNA9/ADRI
[AT",5
ATP1B4/CALB1/KLK1/BDKRB2",5
FBR2/FOS",8

',6

'AQP2",4
.2/HAP1/GABRA5",8
(DORA3/GATA4/AGTR1/CREB3L1/ADORA1/BDKRB2/ADRA1B/ADRA1D/ADRB3/CNGA1/KCNU1",15

.LC2A4/SOCS3",6
iRIN2B",6
S2/CXCL2/C3/GNG11/GNGT1/ZFP36/IL6/IFNA21/CXCL3/CXCL1/TLR3/CXCL8/FOS/GNG12/MICA/CD20
Z1/EGFR/CXCL3/CXCL1/CXCL8",6
!/EXTL1",2
.A-DPB1",4
\IP1",6
l",7
N/FCGR1A/DOCK1/PLA2G4D/SPHK1",8
PP1R1B/CREB3L1/DRD5/FOS/GNG12/GRIN2B",11

RA1/SGMS2/BDKRB2/SPTLC3/SPHK1/FCER1A/S1PR3",10
L1/FBP1/CIDEA/ADIPOQ/SLC2A4",10
'SLC44A3/EGFR/PLA2G4D/FOS",8
.6
\1/MYL4/TPM2",7
N14/CLDN1/CLDN19/TLR3/CLDN7/SOCS3/IFIT1",13
JBA3E/LMNA/SPTA1/FOS/TUBA3C",11
N1/DOCK1/SHC4",6
)2/WNT7B",8
CNJ4/FOS/GNG12/KCNJ18",9

BP1/AGXT",9
,1

.RAS/NGF/PDGFR/THBS1/FGF7/EGFR/FPR1/PRKD1/CSF1/FGF16/GRIN2B",17
i/CES1/GSTA1",6
4D/FCER1A",5

4/SCN1B/TNNC1/AGT/AGTR1/CREB3L1/ADRA1B/ADRA1D/MYL4/TPM2",12
EGFR/FBXO32/TGFBR2/SLC2A4",10
SLC2A2/FBP1/GCGR",8

HR/SSTR1/CREB3L1/FOS/JUNB/SOCS3/SHC4",9
+2/GATA4/RXRG/THRB/PLCD3/DIO3",9

'EGFR/HKDC1",8

',7

MA2/HLA-DPB1",8

DC1/FBP1/SLC2A4/SOCS3/SHC4",10

TGFBR2/TLR3/CXCL8/FOS/EGR3",12

2/HSPA6",4

',5

IL6/CLEC4E/EGR3",7

1/KIR2DL3",5

,5

2G4D",6

O/IL1R2/IL1R1/TGFB3/MSX2/EGR2/ZFP36/IL6/MMP7/CREB3L1/TGFBR2/FOS/FOSL1/HLA-DPB1",16

/SLC32A1/GRIA2/KCNJ5/GNG11/GNGT1/GNG12/GABRA5",10

CL12/CCL2/IL1R1/IL1B/GNG11/GNGT1/PDGFR/IL6/IFNA21/EGFR/CREB3L1/CXCL8/GNG12",16

PPL/AGPAT2/PLA2G2A",6

GFB3/AGT/REN/AGTR1/COX7A1/TGFBR2/COL1A2/COL3A1/SLC2A4",14

5/COX7A1/CXCL8/FOS/ADIPOQ/SOCS3",10

AS/IL6/GATA4/TGFBR2/CXCL8",10

'1L/SHC4/MICA/KLRC3/KIR2DL3",8

PLA2G4D/TLR3/CHMP4C",10

IRAS/TUBA4A/IL6/PIK3C2G/TUBA3E/CXCL8/FOS/CD14/TUBB6/ANXA2/S100A10/TUBA3C",17

i/IFNA21/ANTXR2/CXCL3/CXCL1/DEFA4/DEFA6/CXCL8",12

",8

/SDR16C5/NQO1/UGT2B15",9

PLA2G4D/KCNJ4/FOS/KCNJ18",9

WNT9B/FZD2/WNT7B",9

CGR1A/FPR1/FGG/FGA/FGB/C5AR1/ELANE",11

JBA3E/C8A/CREB3L1/COX7A1/HSPA6/TUBB6/TUBA3C/GRIN2B",17

1/AHR/CYP1B1/EPHX1/EGFR/COX7A1/FOS/NQO1/PRKD1/AKR1C3/AKR1C4/GSTA1",13
C/SEMA3D/SHH/RHOD",10

1B/TUBA4A/APOE/IL6/SNCA/TUBA3E/DKK2/FZD7/FZD1/WNT9B/COX7A1/LPL/TUBB6/FZD2/CSF1/WNT9B/GRIN2B",7
3L1/GNG12/SHC4/GRIN2B",10

;

R/FOS",3

FR/TGFBR2/CHMP4C/FOLR2/RAB31/HSPA6",13

HKDC1/PLCD3/CXCL8/CD14",12

/HMOX1/MMP9/PLAU/NOTCH2/PDGFRA/THBS1/CYP1B1/EGFR/TNXB/SHC4",16
I1/PTGS2/NEFH/WNT2/DKK1/IL1A/GRIA2/IL1B/TUBA4A/IL6/SNCA/TUBA3E/DKK2/FZD7/FZD1/WNT9B/GRIN2B",14

3A4A/NXF3/TUBA3E/POM121L2/COX7A1/GPX8/HAP1/TUBB6/ERBB4/TUBA3C/GPX3/ANG/NXF2B/GRIN2B",14

EB3L1/COX7A1/GPX8/HAP1/TUBB6/TUBA3C/GPX3/POLR2J2/GRIN2B",14
iR3",7

\\-DPB1",6
1/HSPA6",4

GT1/IFNA21/FOS/GNG12",6

3",6

5/TUBA3C",7

V1/OR2T33/OR2T8/OR1E1/OR52E4/OR4M2/OR56A3/OR52B6/OR2C3/OR2W3/OR52B2",15

R4/SERPING1/VSIG4/C8A/C1R/F2RL2/MBL2/BDKRB2/FGG/FGA/FGB/THBD/F2/C1S/PROS1/SERPINA1,
HR/GRIA2/ADORA3/PLG/EDN3/C3/MCHR1/VGF/PYY/NMUR2/RXFP2/MTNR1B/HTR1B/CGA/AGT/HTF
.1A/CCL20/IL1R2/IL1R1/IL1RL1/TGFB3/TNFRSF8/INHBA/CXCL6/BMP4/IL1B/TNFSF9/GDF5/LIF/GDF15,
./COL6A2/COL8A1/CPB1/COL6A3/CPA3/KCNK5/COL1A2/COL3A1/COL22A1/COL8A2/COL6A5/SLC6A1
_PA",20
L1/ACKR3/CXCL14/IL34/CXCL3/CXCL1/CX3CR1/CXCL8/CCL11/CCR9/CCL13/CSF1/CCL23/CCL16/CCL18,
/COL1A2/TNXB/LAMB2/COL6A5/THBS2/COL4A5/RELN/LAMA2/COL4A6",27
ABP4/OLR1/LPL/ADIPOQ/MMP1/PLIN5",23
D14/LAMB2/COL4A5/LAMA2/COL4A6",27
.1/CEBPB/FOSL1/MAPK15/MMP1",24
SSX1/SIX1/IL6/DUSP6/RXRG/NFKBIZ/MMP3/FCGR1A/RUNX1/TGFBR2/DEFA4/DEFA6/CXCL8/CD14/CE

AR1/CFI/HLA-DPB1/C4B/C4A",23
N1/SGK1/SPP1/NR4A1/PCK1/EREG/GNG11/GNGT1/ITGB4/NGF/PDGFR/IL6/CHAD/IFNA21/THBS1/I
17

JS/JUNB/CEBPB/CSF1/SOCS3",23
1A2/COL3A1/CXCL8/THBD/COL4A5/COL4A6",21
3B2/CYP21A2",15

15

./DOCK1/COL6A3/COL1A2/TNXB/LAMB2/COL6A5/SHC4/THBS2/COL4A5/RELN/LAMA2/COL4A6/EMP2

/FZD2/KCNA4/WNT7B/HSD3B1/HSD3B2/CYP21A2",25
STA1/ADH1C",15
CL8/FOS/FGG/FGA/FGB/F2/C1S/TMPRSS2/ISG15/MMP1/C5AR1/C4B/C4A",34
R4A1/EREG/IL1B/RRAS/NGF/PDGFR/DUSP5/DUSP6/FGF7/EGFR/NTRK2/PLA2G4D/TGFBR2/RET/IGF2

12/SHC4/COL4A5/MMP1/COL4A6",21
OS/THBD/NQO1/GSTA1",22
KCL8/CCL11/GNG12/CCR9/CCL13/SHC4/CCL23/CCL16/CCL18/CCL14",28

2",20

18

TR7/HTR5A/PLCD3/RET/BDKRB2/GDNF/DRD5/ADRA1B/ADRA1D/SPHK1/ERBB4/ADRB3/FGF16/HRH1

OL1A2/IGF2/HSPB2/ERBB4/FZD2/WNT7B/TWIST2",28
-I/CREB3L1/ADORA1/NPY1R/HTR1E/DRD5/FOS/HTR1A/CNGA1/FXYD1/GRIN2B",30

2/SOX2/WNT7B",22

A21/THBS1/ITGA11/COL6A2/EGFR/FZD7/FZD1/CREB3L1/WNT9B/COL6A3/TLR3/COL1A2/TNXB/LAME

HLA-DPB1",21

2/HLA-DPB1",20

B/APCDD1L",21
.CNU1",17

L/C8A/BDKRB2/GNG12/F2/FGF16",26

CD14/HSPA6/OLR1/MMP1",24

VG12/CSF1/SHC4/NTF3/PLA2G2A/FGF16/GRIN2B",26
,19

PM2",20

BB6/F2/CLDN7/TUBA3C",20

B3/FGF16/UGT2B15/GSTA1",20

OR1L",17

WNT7B/MME/TUBA3C/GRIN2B",25

B/COX7A1/GPX8/HAP1/TUBB6/FZD2/CSF1/WNT7B/TUBA3C/GPX3/GRIN2B/NEFL",28

GRIN2B/NEFL",19

/C5AR1/SERPINB2/CFI/C4B/C4A",40
2B/HCTR2/LHCGR/CHRNA1/SSTR1/ADCYAP1/AGTR1/VIP/CHRNA3/CRH/HTR7/THRB/HTR5A/ADORA/
/NGF/IL6/IL1RN/IFNA21/CXCL9/XCL1/ACKR3/OSMR/TSLP/CXCL14/BMP3/IL34/CXCL16/TGFB2/IL17F
9/SLC36A2/COL14A1/COL4A5/MME/COL4A6/COL5A2/COL28A1",32

/CCL14",29

:BPB/ETV4/NUPR1/TMPRSS2/WT1/ELANE/HOXA10",37

TGA11/FGF7/COL6A2/OSMR/EGFR/NTRK2/CREB3L1/COL6A3/COL1A2/IGF2/TNFB/LAMB2/PRL/GNG1

2",33

!/GDNF/FOS/CD14/GNG12/HSPA6/ERBB4/CSF1/NTF3/IL1RAP/FGF16",42

",32

32/COL6A5/HES3/FZD2/THBS2/ISG15/WNT7B/COL4A5/RELN/LAMA2/COL4A6",41

A1/NPY1R/F2RL2/GALR1/BDKRB2/HTR1E/NTSR2/DRD5/ADRA1B/FPR1/PATE1/GRIK1/ADRA1D/PRL/C
E/CXCL3/CXCL1/CX3CR1/CXCL8/CCL11/PRL/CCR9/CCL13/GDF3/CSF1/IFNLR1/IL1RAP/IL27/CRLF2/GD

L2/COL6A5/ERBB4/CSF1/NTF3/THBS2/COL4A5/RELN/FGF16/LAMA2/COL4A6",57

HRNA9/P2RY2/CALCB/MC5R/HTR1A/F2/PENK/NPW/GABRA5/CCK/ADRB3/HRH1/C5AR1/S1PR3/GCGI
F10/CCL23/CCL16/CCL18/CCL14",65

R/PATE3/APELA/GRIN2B",76