

Table S2. Gene Ontology (GO) enrichment analysis results of differentially expressed genes in neurok

"ONTOLOGY"	"ID"	"Description"	"GeneRatio"	"BgRatio"	"pvalue"	"p.adjust"	"qvalue"	"geneID"	"Cou"
GO:0062023	"CC"	"GO:0062023", "collagen-containing extracellular matrix"	"166/1537"	"429/19594"					
GO:0005201	"MF"	"GO:0005201", "extracellular matrix structural constituent"	"77/1495"	"172/18410"					
GO:0030198	"BP"	"GO:0030198", "extracellular matrix organization"	"97/1468"	"307/18800"	1.7140e-19				
GO:0043062	"BP"	"GO:0043062", "extracellular structure organization"	"97/1468"	"308/18800"	2.31e-19				
GO:0045229	"BP"	"GO:0045229", "external encapsulating structure organization"	"97/1468"	"310/18800"	2.31e-19				
GO:0005788	"CC"	"GO:0005788", "endoplasmic reticulum lumen"	"93/1537"	"311/19594"	8.084330e-19				
GO:0048018	"MF"	"GO:0048018", "receptor ligand activity"	"110/1495"	"489/18410"	2.0452777503e-19				
GO:0005539	"MF"	"GO:0005539", "glycosaminoglycan binding"	"71/1495"	"234/18410"	2.36397020e-19				
GO:0030546	"MF"	"GO:0030546", "signaling receptor activator activity"	"110/1495"	"496/18410"	6.8e-19				
GO:0048608	"BP"	"GO:0048608", "reproductive structure development"	"100/1468"	"433/18800"	1.71e-19				
GO:0061458	"BP"	"GO:0061458", "reproductive system development"	"100/1468"	"436/18800"	2.75e-19				
GO:0072562	"CC"	"GO:0072562", "blood microparticle"	"51/1537"	"147/19594"	1.26606094078442e-19				
GO:0001655	"BP"	"GO:0001655", "urogenital system development"	"83/1468"	"352/18800"	2.58415e-19				
GO:0003002	"BP"	"GO:0003002", "regionalization"	"83/1468"	"354/18800"	3.78539218084685e-20				
GO:0008201	"MF"	"GO:0008201", "heparin binding"	"54/1495"	"168/18410"	2.44444432897395e-19				
GO:0042060	"BP"	"GO:0042060", "wound healing"	"92/1468"	"429/18800"	2.12079378370603e-19				
GO:0072001	"BP"	"GO:0072001", "renal system development"	"75/1468"	"312/18800"	5.526446551e-19				
GO:0001503	"BP"	"GO:0001503", "ossification"	"90/1468"	"420/18800"	5.59087013357197e-19				
GO:0030414	"MF"	"GO:0030414", "peptidase inhibitor activity"	"56/1495"	"187/18410"	2.13435945e-19				
GO:0005581	"CC"	"GO:0005581", "collagen trimer"	"36/1537"	"86/19594"	4.83575658757844e-18				
GO:0007389	"BP"	"GO:0007389", "pattern specification process"	"95/1468"	"463/18800"	1.2791620e-19				
GO:0061134	"MF"	"GO:0061134", "peptidase regulator activity"	"62/1495"	"230/18410"	1.05106389e-19				
GO:0048568	"BP"	"GO:0048568", "embryonic organ development"	"92/1468"	"449/18800"	5.02715e-19				
GO:0010817	"BP"	"GO:0010817", "regulation of hormone levels"	"98/1468"	"496/18800"	5.4202521e-19				
GO:0010466	"BP"	"GO:0010466", "negative regulation of peptidase activity"	"66/1468"	"262/18800"	2.62e-19				
GO:0010951	"BP"	"GO:0010951", "negative regulation of endopeptidase activity"	"64/1468"	"251/18800"	2.51e-19				
GO:0004866	"MF"	"GO:0004866", "endopeptidase inhibitor activity"	"53/1495"	"180/18410"	3.9580e-19				
GO:0001656	"BP"	"GO:0001656", "metanephros development"	"36/1468"	"89/18800"	1.584792434e-19				
GO:0007548	"BP"	"GO:0007548", "sex differentiation"	"68/1468"	"281/18800"	1.71876687697106e-19				
GO:0002526	"BP"	"GO:0002526", "acute inflammatory response"	"40/1468"	"113/18800"	6.7318939e-19				
GO:0005604	"CC"	"GO:0005604", "basement membrane"	"36/1537"	"95/19594"	2.2504031272431e-19				
GO:0061135	"MF"	"GO:0061135", "endopeptidase regulator activity"	"54/1495"	"194/18410"	3.0036e-19				
GO:0042445	"BP"	"GO:0042445", "hormone metabolic process"	"59/1468"	"230/18800"	1.33319353e-19				
GO:0048562	"BP"	"GO:0048562", "embryonic organ morphogenesis"	"68/1468"	"294/18800"	2.0951e-19				
GO:0001822	"BP"	"GO:0001822", "kidney development"	"69/1468"	"303/18800"	2.95744919019876e-19				
GO:0051346	"BP"	"GO:0051346", "negative regulation of hydrolase activity"	"77/1468"	"371/18800"	3.71e-19				
GO:0048705	"BP"	"GO:0048705", "skeletal system morphogenesis"	"57/1468"	"228/18800"	1.51790e-19				
GO:0030199	"BP"	"GO:0030199", "collagen fibril organization"	"28/1468"	"62/18800"	1.9788303151e-19				
GO:0045137	"BP"	"GO:0045137", "development of primary sexual characteristics"	"57/1468"	"231/18800"	2.31e-19				
GO:0008406	"BP"	"GO:0008406", "gonad development"	"56/1468"	"226/18800"	4.08506131694463e-19				
GO:0050673	"BP"	"GO:0050673", "epithelial cell proliferation"	"85/1468"	"443/18800"	5.548733173e-19				
GO:0072006	"BP"	"GO:0072006", "nephron development"	"43/1468"	"145/18800"	7.159464572686e-19				
GO:0097529	"BP"	"GO:0097529", "myeloid leukocyte migration"	"56/1468"	"229/18800"	7.54891854e-19				
GO:0072009	"BP"	"GO:0072009", "nephron epithelium development"	"37/1468"	"111/18800"	8.929e-19				
GO:0072073	"BP"	"GO:0072073", "kidney epithelium development"	"42/1468"	"140/18800"	9.40736e-19				
GO:0045861	"BP"	"GO:0045861", "negative regulation of proteolysis"	"72/1468"	"350/18800"	1.835e-19				
GO:0030020	"MF"	"GO:0030020", "extracellular matrix structural constituent conferring tensile stren"							
GO:0060326	"BP"	"GO:0060326", "cell chemotaxis"	"67/1468"	"315/18800"	2.80416301689611e-14				

GO:0048706,"BP","GO:0048706","embryonic skeletal system development","39/1468","127/18800"
GO:0048704,"BP","GO:0048704","embryonic skeletal system morphogenesis","33/1468","94/18800"
GO:0004252,"MF","GO:0004252","serine-type endopeptidase activity","47/1495","174/18410",8.70
GO:0005125,"MF","GO:0005125","cytokine activity","56/1495","235/18410",1.26805669247511e-1
GO:0017171,"MF","GO:0017171","serine hydrolase activity","50/1495","195/18410",1.2907518537
GO:0052547,"BP","GO:0052547","regulation of peptidase activity","84/1468","456/18800",8.76496
GO:0008236,"MF","GO:0008236","serine-type peptidase activity","49/1495","191/18410",2.218774
GO:0034754,"BP","GO:0034754","cellular hormone metabolic process","40/1468","137/18800",1.10
GO:0006953,"BP","GO:0006953","acute-phase response","23/1468","48/18800",1.31717204931461
GO:0010876,"BP","GO:0010876","lipid localization","82/1468","446/18800",1.9427983961998e-13,
GO:0009636,"BP","GO:0009636","response to toxic substance","56/1468","247/18800",2.33323137
GO:0004867,"MF","GO:0004867","serine-type endopeptidase inhibitor activity","33/1495","98/1841
GO:0061138,"BP","GO:0061138","morphogenesis of a branching epithelium","47/1468","185/18800
GO:0050900,"BP","GO:0050900","leukocyte migration","74/1468","384/18800",2.64427053184633e
GO:0001763,"BP","GO:0001763","morphogenesis of a branching structure","49/1468","199/18800",
GO:0061326,"BP","GO:0061326","renal tubule development","32/1468","94/18800",2.95345694025
GO:0097530,"BP","GO:0097530","granulocyte migration","42/1468","154/18800",3.5007465089737
GO:1901681,"MF","GO:1901681","sulfur compound binding","59/1495","267/18410",9.1258226075
GO:0032963,"BP","GO:0032963","collagen metabolic process","33/1468","101/18800",4.736713227
GO:0006869,"BP","GO:0006869","lipid transport","74/1468","391/18800",6.78152096670572e-13,7
GO:0072080,"BP","GO:0072080","nephron tubule development","31/1468","91/18800",6.78634435
GO:0042730,"BP","GO:0042730","fibrinolysis","16/1468","24/18800",7.12170351478652e-13,7.865
GO:0006959,"BP","GO:0006959","humoral immune response","64/1468","317/18800",1.286565496
GO:0071621,"BP","GO:0071621","granulocyte chemotaxis","37/1468","128/18800",1.28922018221
GO:2000027,"BP","GO:2000027","regulation of animal organ morphogenesis","37/1468","129/1880
GO:0045165,"BP","GO:0045165","cell fate commitment","57/1468","266/18800",1.7326352967225
GO:0061448,"BP","GO:0061448","connective tissue development","56/1468","260/18800",2.18161
GO:0007178,"BP","GO:0007178","transmembrane receptor protein serine/threonine kinase signalin
GO:0090287,"BP","GO:0090287","regulation of cellular response to growth factor stimulus","63/146
GO:0052548,"BP","GO:0052548","regulation of endopeptidase activity","77/1468","426/18800",2.6
GO:0007369,"BP","GO:0007369","gastrulation","46/1468","190/18800",2.80713993130005e-12,2.6
GO:0008009,"MF","GO:0008009","chemokine activity","22/1495","49/18410",5.1519632098455e-1
GO:0060537,"BP","GO:0060537","muscle tissue development","74/1468","405/18800",4.09016754
GO:0061041,"BP","GO:0061041","regulation of wound healing","37/1468","133/18800",4.61185893
GO:0050878,"BP","GO:0050878","regulation of body fluid levels","71/1468","382/18800",4.8868304
GO:0048754,"BP","GO:0048754","branching morphogenesis of an epithelial tube","40/1468","153/1
GO:0150063,"BP","GO:0150063","visual system development","71/1468","383/18800",5.553606136
GO:0090092,"BP","GO:0090092","regulation of transmembrane receptor protein serine/threonine k
GO:0019838,"MF","GO:0019838","growth factor binding","38/1495","139/18410",1.379046246908
GO:0035150,"BP","GO:0035150","regulation of tube size","38/1468","142/18800",8.705644768467
GO:0015850,"BP","GO:0015850","organic hydroxy compound transport","53/1468","248/18800",1.
GO:0048880,"BP","GO:0048880","sensory system development","71/1468","389/18800",1.1816745
GO:0001649,"BP","GO:0001649","osteoblast differentiation","52/1468","241/18800",1.2435450429
GO:0048732,"BP","GO:0048732","gland development","76/1468","431/18800",1.27915592039095e
GO:0031960,"BP","GO:0031960","response to corticosteroid","40/1468","157/18800",1.339056536
GO:0007599,"BP","GO:0007599","hemostasis","50/1468","227/18800",1.39108806787289e-11,1.04
GO:0043410,"BP","GO:0043410","positive regulation of MAPK cascade","83/1468","491/18800",1.3
GO:0007517,"BP","GO:0007517","muscle organ development","64/1468","334/18800",1.424781942
GO:0046661,"BP","GO:0046661","male sex differentiation","41/1468","164/18800",1.43226175570
GO:0031093,"CC","GO:0031093","platelet alpha granule lumen","25/1537","67/19594",1.26793866

GO:1900046,"BP","GO:1900046","regulation of hemostasis","25/1468","68/18800",1.671960715609
GO:0007596,"BP","GO:0007596","blood coagulation","49/1468","221/18800",1.73072752232018e-1
GO:0061005,"BP","GO:0061005","cell differentiation involved in kidney development","23/1468","5
GO:0001228,"MF","GO:0001228","DNA-binding transcription activator activity, RNA polymerase II-s
GO:0009952,"BP","GO:0009952","anterior/posterior pattern specification","48/1468","214/18800",
GO:0030595,"BP","GO:0030595","leukocyte chemotaxis","51/1468","236/18800",1.8428062508807
GO:0004857,"MF","GO:0004857","enzyme inhibitor activity","72/1495","390/18410",2.9575241140
GO:0008083,"MF","GO:0008083","growth factor activity","41/1495","162/18410",3.1923520999626
GO:0005178,"MF","GO:0005178","integrin binding","40/1495","156/18410",3.58371193462064e-11
GO:0001216,"MF","GO:0001216","DNA-binding transcription activator activity","81/1495","466/184
GO:0034358,"CC","GO:0034358","plasma lipoprotein particle","18/1537","36/19594",2.6536350483
GO:1990777,"CC","GO:1990777","lipoprotein particle","18/1537","36/19594",2.65363504839192e-1
GO:0001654,"BP","GO:0001654","eye development","69/1468","379/18800",2.60063537775408e-1
GO:0031099,"BP","GO:0031099","regeneration","44/1468","188/18800",2.80848393853059e-11,1.1
GO:0035296,"BP","GO:0035296","regulation of tube diameter","37/1468","141/18800",3.06048755
GO:0097746,"BP","GO:0097746","blood vessel diameter maintenance","37/1468","141/18800",3.06
GO:0050678,"BP","GO:0050678","regulation of epithelial cell proliferation","69/1468","382/18800",
GO:0003012,"BP","GO:0003012","muscle system process","77/1468","449/18800",3.799859558212
GO:0050817,"BP","GO:0050817","coagulation","49/1468","226/18800",4.0432599427355e-11,2.54
GO:0001823,"BP","GO:0001823","mesonephros development","30/1468","99/18800",4.630657532
GO:0050818,"BP","GO:0050818","regulation of coagulation","25/1468","71/18800",5.00450932369
GO:0060562,"BP","GO:0060562","epithelial tube morphogenesis","62/1468","328/18800",5.378821
GO:0030193,"BP","GO:0030193","regulation of blood coagulation","24/1468","66/18800",5.559391
GO:0042063,"BP","GO:0042063","gliogenesis","57/1468","291/18800",7.65629345637811e-11,4.55
GO:0051384,"BP","GO:0051384","response to glucocorticoid","36/1468","139/18800",8.462842317
GO:0034368,"BP","GO:0034368","protein-lipid complex remodeling","16/1468","30/18800",8.96034
GO:0034369,"BP","GO:0034369","plasma lipoprotein particle remodeling","16/1468","30/18800",8.
GO:0051216,"BP","GO:0051216","cartilage development","44/1468","195/18800",1.012512246183
GO:0032994,"CC","GO:0032994","protein-lipid complex","18/1537","39/19594",1.45136721736456
GO:0031091,"CC","GO:0031091","platelet alpha granule","28/1537","91/19594",1.52996303972857
GO:0031983,"CC","GO:0031983","vesicle lumen","61/1537","327/19594",1.648767289914e-10,7.15
GO:0034364,"CC","GO:0034364","high-density lipoprotein particle","15/1537","27/19594",1.726725
GO:0070371,"BP","GO:0070371","ERK1 and ERK2 cascade","62/1468","335/18800",1.331909122604
GO:1990266,"BP","GO:1990266","neutrophil migration","34/1468","128/18800",1.34142925522902
GO:0001664,"MF","GO:0001664","G protein-coupled receptor binding","57/1495","288/18410",2.24
GO:0090596,"BP","GO:0090596","sensory organ morphogenesis","53/1468","266/18800",1.840940
GO:0031214,"BP","GO:0031214","biomineral tissue development","40/1468","170/18800",1.867639
GO:0001704,"BP","GO:0001704","formation of primary germ layer","33/1468","123/18800",1.87625
GO:1900047,"BP","GO:1900047","negative regulation of hemostasis","20/1468","49/18800",1.9595
GO:0048545,"BP","GO:0048545","response to steroid hormone","61/1468","330/18800",1.9761987
GO:0042476,"BP","GO:0042476","odontogenesis","34/1468","130/18800",2.11500657542442e-10,1
GO:0060284,"BP","GO:0060284","regulation of cell development","81/1468","500/18800",2.136320
GO:0002548,"BP","GO:0002548","monocyte chemotaxis","24/1468","70/18800",2.30143716653172
GO:0060993,"BP","GO:0060993","kidney morphogenesis","28/1468","93/18800",2.4134916333956
GO:0110148,"BP","GO:0110148","biomineralization","40/1468","172/18800",2.72301385508216e-1
GO:0072207,"BP","GO:0072207","metanephric epithelium development","14/1468","24/18800",2.7
GO:0042310,"BP","GO:0042310","vasoconstriction","26/1468","82/18800",2.96523399446375e-10,
GO:0060485,"BP","GO:0060485","mesenchyme development","57/1468","301/18800",2.992767906
GO:0001657,"BP","GO:0001657","ureteric bud development","28/1468","94/18800",3.18384183554
GO:0034367,"BP","GO:0034367","protein-containing complex remodeling","16/1468","32/18800",3

GO:1903034,"BP","GO:1903034","regulation of response to wounding","39/1468","166/18800",3.29
GO:0072028,"BP","GO:0072028","nephron morphogenesis","25/1468","77/18800",3.684165570851
GO:0070372,"BP","GO:0070372","regulation of ERK1 and ERK2 cascade","58/1468","311/18800",3.8
GO:0002685,"BP","GO:0002685","regulation of leukocyte migration","46/1468","218/18800",4.1216
GO:0072163,"BP","GO:0072163","mesonephric epithelium development","28/1468","95/18800",4.1
GO:0072164,"BP","GO:0072164","mesonephric tubule development","28/1468","95/18800",4.1814
GO:0008584,"BP","GO:0008584","male gonad development","35/1468","140/18800",4.3978262151
GO:0002237,"BP","GO:0002237","response to molecule of bacterial origin","63/1468","354/18800",
GO:0046546,"BP","GO:0046546","development of primary male sexual characteristics","35/1468","1
GO:0043010,"BP","GO:0043010","camera-type eye development","60/1468","330/18800",5.472042
GO:0070374,"BP","GO:0070374","positive regulation of ERK1 and ERK2 cascade","46/1468","220/18
GO:1905952,"BP","GO:1905952","regulation of lipid localization","37/1468","155/18800",5.7776472
GO:0042379,"MF","GO:0042379","chemokine receptor binding","24/1495","71/18410",7.12467847
GO:0034774,"CC","GO:0034774","secretory granule lumen","59/1537","322/19594",6.77419713384
GO:0035107,"BP","GO:0035107","appendage morphogenesis","35/1468","142/18800",6.656606507
GO:0035108,"BP","GO:0035108","limb morphogenesis","35/1468","142/18800",6.6566065079099e
GO:0050819,"BP","GO:0050819","negative regulation of coagulation","20/1468","52/18800",6.9527
GO:1990868,"BP","GO:1990868","response to chemokine","28/1468","97/18800",7.1198102183805
GO:1990869,"BP","GO:1990869","cellular response to chemokine","28/1468","97/18800",7.119810
GO:0060205,"CC","GO:0060205","cytoplasmic vesicle lumen","59/1537","325/19594",9.8081127113
GO:0098754,"BP","GO:0098754","detoxification","36/1468","150/18800",8.3971825919202e-10,3.4
GO:0072088,"BP","GO:0072088","nephron epithelium morphogenesis","24/1468","74/18800",8.472
GO:0060349,"BP","GO:0060349","bone morphogenesis","28/1468","98/18800",9.23273184255831e
GO:0030195,"BP","GO:0030195","negative regulation of blood coagulation","19/1468","48/18800",:
GO:0035850,"BP","GO:0035850","epithelial cell differentiation involved in kidney development","19
GO:0071772,"BP","GO:0071772","response to BMP","39/1468","173/18800",1.19236620469985e-0
GO:0071773,"BP","GO:0071773","cellular response to BMP stimulus","39/1468","173/18800",1.192
GO:0060541,"BP","GO:0060541","respiratory system development","43/1468","203/18800",1.3456
GO:0030593,"BP","GO:0030593","neutrophil chemotaxis","29/1468","106/18800",1.426201594172
GO:0045834,"BP","GO:0045834","positive regulation of lipid metabolic process","36/1468","153/18
GO:0061045,"BP","GO:0061045","negative regulation of wound healing","24/1468","76/18800",1.56
GO:0061333,"BP","GO:0061333","renal tubule morphogenesis","24/1468","76/18800",1.563371902
GO:0008202,"BP","GO:0008202","steroid metabolic process","58/1468","323/18800",1.7260566405
GO:1901654,"BP","GO:1901654","response to ketone","41/1468","190/18800",1.81346838021399e
GO:0008228,"BP","GO:0008228","opsonization","11/1468","16/18800",1.92105976161412e-09,7.21
GO:0070555,"BP","GO:0070555","response to interleukin-1","34/1468","141/18800",2.1548062216
GO:0070098,"BP","GO:0070098","chemokine-mediated signaling pathway","26/1468","89/18800",2
GO:0048736,"BP","GO:0048736","appendage development","39/1468","177/18800",2.3947290190
GO:0060173,"BP","GO:0060173","limb development","39/1468","177/18800",2.39472901903297e-
GO:0055123,"BP","GO:0055123","digestive system development","34/1468","142/18800",2.623611
GO:0072078,"BP","GO:0072078","nephron tubule morphogenesis","23/1468","72/18800",2.654176
GO:0033293,"MF","GO:0033293","monocarboxylic acid binding","25/1495","81/18410",2.74820079
GO:0060191,"BP","GO:0060191","regulation of lipase activity","26/1468","90/18800",2.8167823696
GO:0005504,"MF","GO:0005504","fatty acid binding","19/1495","49/18410",3.02721755708404e-09
GO:0048701,"BP","GO:0048701","embryonic cranial skeleton morphogenesis","18/1468","46/18800
GO:0007200,"BP","GO:0007200","phospholipase C-activating G protein-coupled receptor signaling p
GO:0072202,"BP","GO:0072202","cell differentiation involved in metanephros development","13/14
GO:0010001,"BP","GO:0010001","glial cell differentiation","44/1468","218/18800",4.221247259588
GO:0046660,"BP","GO:0046660","female sex differentiation","31/1468","124/18800",4.3133936907
GO:0001658,"BP","GO:0001658","branching involved in ureteric bud morphogenesis","20/1468","57

GO:0016485,"BP","GO:0016485","protein processing","47/1468","243/18800",5.33798926622269e-
GO:0032496,"BP","GO:0032496","response to lipopolysaccharide","58/1468","333/18800",5.566339
GO:0045785,"BP","GO:0045785","positive regulation of cell adhesion","71/1468","446/18800",6.013
GO:0048762,"BP","GO:0048762","mesenchymal cell differentiation","47/1468","244/18800",6.1208
GO:0030326,"BP","GO:0030326","embryonic limb morphogenesis","30/1468","119/18800",6.18257
GO:0035113,"BP","GO:0035113","embryonic appendage morphogenesis","30/1468","119/18800",6
GO:0072243,"BP","GO:0072243","metanephric nephron epithelium development","12/1468","21/18
GO:0072171,"BP","GO:0072171","mesonephric tubule morphogenesis","21/1468","64/18800",7.544
GO:0071674,"BP","GO:0071674","mononuclear cell migration","41/1468","199/18800",7.59073482
GO:0030509,"BP","GO:0030509","BMP signaling pathway","36/1468","162/18800",7.700649483235
GO:0042698,"BP","GO:0042698","ovulation cycle","22/1468","70/18800",8.25000113951615e-09,2.
GO:0008544,"BP","GO:0008544","epidermis development","60/1468","355/18800",9.74561213006
GO:0110110,"BP","GO:0110110","positive regulation of animal organ morphogenesis","15/1468","3
GO:0031589,"BP","GO:0031589","cell-substrate adhesion","61/1468","364/18800",1.020776332223
GO:0019216,"BP","GO:0019216","regulation of lipid metabolic process","58/1468","339/18800",1.0
GO:0030324,"BP","GO:0030324","lung development","38/1468","179/18800",1.1328103115529e-0
GO:0120254,"BP","GO:0120254","olefinic compound metabolic process","35/1468","157/18800",1.
GO:0060348,"BP","GO:0060348","bone development","44/1468","225/18800",1.15545340296783e
GO:0001667,"BP","GO:0001667","ameboidal-type cell migration","74/1468","480/18800",1.172824
GO:0060602,"BP","GO:0060602","branch elongation of an epithelium","11/1468","18/18800",1.208
GO:0072189,"BP","GO:0072189","ureter development","11/1468","18/18800",1.20822810229677e
GO:0046545,"BP","GO:0046545","development of primary female sexual characteristics","28/1468",
GO:0006936,"BP","GO:0006936","muscle contraction","59/1468","349/18800",1.28162499422846e
GO:0031406,"MF","GO:0031406","carboxylic acid binding","38/1495","173/18410",1.212862749060
GO:0005126,"MF","GO:0005126","cytokine receptor binding","51/1495","272/18410",1.335200228
GO:0022612,"BP","GO:0022612","gland morphogenesis","30/1468","123/18800",1.4148726440894
GO:0001523,"BP","GO:0001523","retinoid metabolic process","24/1468","84/18800",1.4473235496
GO:0048565,"BP","GO:0048565","digestive tract development","31/1468","130/18800",1.44895906
GO:0007422,"BP","GO:0007422","peripheral nervous system development","23/1468","78/18800",
GO:0007492,"BP","GO:0007492","endoderm development","23/1468","78/18800",1.489149377186
GO:0030178,"BP","GO:0030178","negative regulation of Wnt signaling pathway","37/1468","174/18
GO:0072210,"BP","GO:0072210","metanephric nephron development","16/1468","40/18800",1.825
GO:0098644,"CC","GO:0098644","complex of collagen trimers","12/1537","22/19594",1.602125182
GO:0035265,"BP","GO:0035265","organ growth","37/1468","175/18800",1.97214614082939e-08,5.
GO:0006721,"BP","GO:0006721","terpenoid metabolic process","26/1468","98/18800",2.009923014
GO:0030323,"BP","GO:0030323","respiratory tube development","38/1468","183/18800",2.131309
GO:1903035,"BP","GO:1903035","negative regulation of response to wounding","25/1468","92/188
GO:0008585,"BP","GO:0008585","female gonad development","27/1468","105/18800",2.22820953
GO:0030510,"BP","GO:0030510","regulation of BMP signaling pathway","27/1468","105/18800",2.2
GO:0034308,"BP","GO:0034308","primary alcohol metabolic process","27/1468","105/18800",2.228
GO:0048592,"BP","GO:0048592","eye morphogenesis","34/1468","154/18800",2.36918042400562e
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GO:0060675,"BP","GO:0060675","ureteric bud morphogenesis","20/1468","63/18800",3.232839425
GO:0033002,"BP","GO:0033002","muscle cell proliferation","44/1468","233/18800",3.42500268004
GO:0090183,"BP","GO:0090183","regulation of kidney development","14/1468","32/18800",3.6304
GO:0071813,"MF","GO:0071813","lipoprotein particle binding","14/1495","31/18410",3.616395126
GO:0071814,"MF","GO:0071814","protein-lipid complex binding","14/1495","31/18410",3.6163951
GO:0010038,"BP","GO:0010038","response to metal ion","58/1468","351/18800",3.9172632339252

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GO:0019730,"BP","GO:0019730","antimicrobial humoral response","29/1468","122/18800",4.52839
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GO:0048645,"BP","GO:0048645","animal organ formation","20/1468","65/18800",5.8377228632263
GO:1905330,"BP","GO:1905330","regulation of morphogenesis of an epithelium","20/1468","65/188
GO:0042475,"BP","GO:0042475","odontogenesis of dentin-containing tooth","24/1468","90/18800"
GO:0008217,"BP","GO:0008217","regulation of blood pressure","37/1468","183/18800",6.76119694
GO:0042627,"CC","GO:0042627","chylomicron","9/1537","13/19594",5.88218374199944e-08,1.827
GO:0071347,"BP","GO:0071347","cellular response to interleukin-1","27/1468","111/18800",7.8479
GO:0003156,"BP","GO:0003156","regulation of animal organ formation","13/1468","29/18800",7.88
GO:0001819,"BP","GO:0001819","positive regulation of cytokine production","71/1468","475/18800
GO:0014706,"BP","GO:0014706","striated muscle tissue development","45/1468","248/18800",8.24
GO:0072503,"BP","GO:0072503","cellular divalent inorganic cation homeostasis","73/1468","494/18
GO:0009954,"BP","GO:0009954","proximal/distal pattern formation","14/1468","34/18800",9.23530
GO:0051960,"BP","GO:0051960","regulation of nervous system development","67/1468","440/1880
GO:0031639,"BP","GO:0031639","plasminogen activation","12/1468","25/18800",9.7917233600535
GO:0010810,"BP","GO:0010810","regulation of cell-substrate adhesion","41/1468","217/18800",9.8
GO:0006066,"BP","GO:0006066","alcohol metabolic process","58/1468","361/18800",1.0690813008
GO:0048863,"BP","GO:0048863","stem cell differentiation","40/1468","211/18800",1.27470565140
GO:0050679,"BP","GO:0050679","positive regulation of epithelial cell proliferation","40/1468","211,
GO:0071827,"BP","GO:0071827","plasma lipoprotein particle organization","16/1468","45/18800",1
GO:0060193,"BP","GO:0060193","positive regulation of lipase activity","20/1468","68/18800",1.347
GO:0030282,"BP","GO:0030282","bone mineralization","28/1468","121/18800",1.412808971139860
GO:0007584,"BP","GO:0007584","response to nutrient","32/1468","150/18800",1.4140077516291e
GO:0048638,"BP","GO:0048638","regulation of developmental growth","54/1468","329/18800",1.43
GO:1901652,"BP","GO:1901652","response to peptide","72/1468","491/18800",1.438052605372860
GO:1905954,"BP","GO:1905954","positive regulation of lipid localization","24/1468","94/18800",1.5
GO:0060688,"BP","GO:0060688","regulation of morphogenesis of a branching structure","17/1468",
GO:0003007,"BP","GO:0003007","heart morphogenesis","45/1468","254/18800",1.6951682134855
GO:1990748,"BP","GO:1990748","cellular detoxification","27/1468","115/18800",1.7143276493857
GO:0007530,"BP","GO:0007530","sex determination","11/1468","22/18800",1.99677901152138e-0
GO:0072234,"BP","GO:0072234","metanephric nephron tubule development","10/1468","18/18800
GO:0046890,"BP","GO:0046890","regulation of lipid biosynthetic process","35/1468","175/18800",2
GO:1904888,"BP","GO:1904888","cranial skeletal system development","20/1468","70/18800",2.28
GO:0019229,"BP","GO:0019229","regulation of vasoconstriction","19/1468","64/18800",2.34749149
GO:0031638,"BP","GO:0031638","zymogen activation","19/1468","64/18800",2.34749149652957e-1
GO:0001708,"BP","GO:0001708","cell fate specification","24/1468","96/18800",2.3599369623935e-
GO:0009991,"BP","GO:0009991","response to extracellular stimulus","70/1468","479/18800",2.445
GO:0006720,"BP","GO:0006720","isoprenoid metabolic process","27/1468","117/18800",2.4934945
GO:0034612,"BP","GO:0034612","response to tumor necrosis factor","44/1468","249/18800",2.498
GO:0050920,"BP","GO:0050920","regulation of chemotaxis","41/1468","225/18800",2.72539501677
GO:0035270,"BP","GO:0035270","endocrine system development","29/1468","132/18800",2.78780
GO:0003401,"BP","GO:0003401","axis elongation","12/1468","27/18800",2.82425566838096e-07,6
GO:0097006,"BP","GO:0097006","regulation of plasma lipoprotein particle levels","22/1468","84/18
GO:0010092,"BP","GO:0010092","specification of animal organ identity","14/1468","37/18800",3.24
GO:0071542,"BP","GO:0071542","dopaminergic neuron differentiation","14/1468","37/18800",3.24
GO:0060021,"BP","GO:0060021","roof of mouth development","23/1468","91/18800",3.387100722
GO:0030169,"MF","GO:0030169","low-density lipoprotein particle binding","10/1495","18/18410",2

GO:0032602,"BP","GO:0032602","chemokine production","24/1468","98/18800",3.5667715684587
GO:0071825,"BP","GO:0071825","protein-lipid complex subunit organization","16/1468","48/18800
GO:0072079,"BP","GO:0072079","nephron tubule formation","10/1468","19/18800",3.9240561441:
GO:0032835,"BP","GO:0032835","glomerulus development","19/1468","66/18800",4.00555298334:
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GO:0003018,"BP","GO:0003018","vascular process in circulatory system","45/1468","263/18800",4.
GO:0050890,"BP","GO:0050890","cognition","50/1468","306/18800",4.74506582090745e-07,1.0070
GO:0045940,"BP","GO:0045940","positive regulation of steroid metabolic process","13/1468","33/1
GO:0048333,"BP","GO:0048333","mesodermal cell differentiation","13/1468","33/18800",4.948259
GO:0030850,"BP","GO:0030850","prostate gland development","16/1468","49/18800",4.953680826
GO:0034370,"BP","GO:0034370","triglyceride-rich lipoprotein particle remodeling","8/1468","12/18
GO:0034372,"BP","GO:0034372","very-low-density lipoprotein particle remodeling","8/1468","12/18
GO:0001570,"BP","GO:0001570","vasculogenesis","21/1468","80/18800",5.51127446246347e-07,1.
GO:0010811,"BP","GO:0010811","positive regulation of cell-substrate adhesion","27/1468","122/18
GO:0071248,"BP","GO:0071248","cellular response to metal ion","36/1468","191/18800",6.1817294
GO:0021782,"BP","GO:0021782","glial cell development","26/1468","115/18800",6.3255564610525
GO:0001527,"CC","GO:0001527","microfibril","8/1537","12/19594",5.23538114072115e-07,1.30095
GO:0005583,"CC","GO:0005583","fibrillar collagen trimer","8/1537","12/19594",5.23538114072115
GO:0098643,"CC","GO:0098643","banded collagen fibril","8/1537","12/19594",5.23538114072115e
GO:2000241,"BP","GO:2000241","regulation of reproductive process","34/1468","176/18800",6.964
GO:0004745,"MF","GO:0004745","NAD-retinol dehydrogenase activity","10/1495","19/18410",5.65:
GO:0022617,"BP","GO:0022617","extracellular matrix disassembly","18/1468","62/18800",7.017984
GO:0045664,"BP","GO:0045664","regulation of neuron differentiation","36/1468","192/18800",7.04
GO:0048839,"BP","GO:0048839","inner ear development","36/1468","192/18800",7.046299443731
GO:0097237,"BP","GO:0097237","cellular response to toxic substance","27/1468","123/18800",7.23
GO:0034375,"BP","GO:0034375","high-density lipoprotein particle remodeling","9/1468","16/18800
GO:2000696,"BP","GO:2000696","regulation of epithelial cell differentiation involved in kidney deve
GO:0014031,"BP","GO:0014031","mesenchymal cell development","22/1468","88/18800",7.428247
GO:0031128,"BP","GO:0031128","developmental induction","13/1468","34/18800",7.43975861389:
GO:0014033,"BP","GO:0014033","neural crest cell differentiation","23/1468","95/18800",7.7358340
GO:0032526,"BP","GO:0032526","response to retinoic acid","25/1468","109/18800",7.76846925420
GO:0048738,"BP","GO:0048738","cardiac muscle tissue development","41/1468","234/18800",7.98:
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GO:0051591,"BP","GO:0051591","response to cAMP","22/1468","89/18800",9.14715855848783e-0
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GO:0001890,"BP","GO:0001890","placenta development","30/1468","147/18800",9.340662565175:
GO:0060350,"BP","GO:0060350","endochondral bone morphogenesis","17/1468","57/18800",9.359
GO:0090066,"BP","GO:0090066","regulation of anatomical structure size","69/1468","487/18800",9
GO:0016209,"MF","GO:0016209","antioxidant activity","22/1495","85/18410",7.56336912381084e-
GO:0007568,"BP","GO:0007568","aging","32/1468","163/18800",1.01352897311433e-06,1.9314150
GO:0043434,"BP","GO:0043434","response to peptide hormone","60/1468","404/18800",1.021946:
GO:0038024,"MF","GO:0038024","cargo receptor activity","21/1495","79/18410",8.3313133781312
GO:0014032,"BP","GO:0014032","neural crest cell development","21/1468","83/18800",1.06699064
GO:0032368,"BP","GO:0032368","regulation of lipid transport","26/1468","118/18800",1.06981253
GO:0023061,"BP","GO:0023061","signal release","65/1468","451/18800",1.07310639892719e-06,2.
GO:0032103,"BP","GO:0032103","positive regulation of response to external stimulus","64/1468","4
GO:0004175,"MF","GO:0004175","endopeptidase activity","65/1495","432/18410",8.960385545424

GO:0032642,"BP","GO:0032642","regulation of chemokine production","23/1468","97/18800",1.145
 GO:1901342,"BP","GO:1901342","regulation of vasculature development","54/1468","351/18800",1
 GO:0002687,"BP","GO:0002687","positive regulation of leukocyte migration","29/1468","141/18800
 GO:0003206,"BP","GO:0003206","cardiac chamber morphogenesis","27/1468","126/18800",1.1939
 GO:0090189,"BP","GO:0090189","regulation of branching involved in ureteric bud morphogenesis",
 GO:0044703,"BP","GO:0044703","multi-organism reproductive process","37/1468","205/18800",1.3
 GO:0030856,"BP","GO:0030856","regulation of epithelial cell differentiation","31/1468","157/18800
 GO:0007611,"BP","GO:0007611","learning or memory","44/1468","264/18800",1.31848220347035
 GO:0090090,"BP","GO:0090090","negative regulation of canonical Wnt signaling pathway","29/1468
 GO:0048306,"MF","GO:0048306","calcium-dependent protein binding","22/1495","87/18410",1.161
 GO:0031667,"BP","GO:0031667","response to nutrient levels","64/1468","446/18800",1.508041251
 GO:0015849,"BP","GO:0015849","organic acid transport","50/1468","318/18800",1.5255373873115
 GO:0050731,"BP","GO:0050731","positive regulation of peptidyl-tyrosine phosphorylation","35/146
 GO:0030111,"BP","GO:0030111","regulation of Wnt signaling pathway","52/1468","336/18800",1.5
 GO:0045765,"BP","GO:0045765","regulation of angiogenesis","53/1468","345/18800",1.542788487
 GO:0048771,"BP","GO:0048771","tissue remodeling","33/1468","174/18800",1.5521024480172e-0
 GO:0043616,"BP","GO:0043616","keratinocyte proliferation","15/1468","47/18800",1.56456935364
 GO:0051918,"BP","GO:0051918","negative regulation of fibrinolysis","7/1468","10/18800",1.697236
 GO:0019433,"BP","GO:0019433","triglyceride catabolic process","12/1468","31/18800",1.70763338
 GO:0035115,"BP","GO:0035115","embryonic forelimb morphogenesis","12/1468","31/18800",1.707
 GO:0045766,"BP","GO:0045766","positive regulation of angiogenesis","34/1468","183/18800",1.763
 GO:1904018,"BP","GO:1904018","positive regulation of vasculature development","34/1468","183/
 GO:0006694,"BP","GO:0006694","steroid biosynthetic process","33/1468","175/18800",1.77181733
 GO:0019221,"BP","GO:0019221","cytokine-mediated signaling pathway","68/1468","486/18800",1.
 GO:0030301,"BP","GO:0030301","cholesterol transport","20/1468","79/18800",1.89557026227063
 GO:0048708,"BP","GO:0048708","astrocyte differentiation","20/1468","79/18800",1.895570262270
 GO:0098869,"BP","GO:0098869","cellular oxidant detoxification","23/1468","100/18800",2.0171672
 GO:0048593,"BP","GO:0048593","camera-type eye morphogenesis","26/1468","122/18800",2.0860
 GO:0050729,"BP","GO:0050729","positive regulation of inflammatory response","29/1468","145/18
 GO:2001236,"BP","GO:2001236","regulation of extrinsic apoptotic signaling pathway","30/1468","15
 GO:0071560,"BP","GO:0071560","cellular response to transforming growth factor beta stimulus","42
 GO:0071276,"BP","GO:0071276","cellular response to cadmium ion","13/1468","37/18800",2.28768
 GO:0003151,"BP","GO:0003151","outflow tract morphogenesis","20/1468","80/18800",2.34371786
 GO:0043588,"BP","GO:0043588","skin development","47/1468","296/18800",2.36186488496781e-0
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 GO:0046620,"BP","GO:0046620","regulation of organ growth","23/1468","101/18800",2.421235324
 GO:0007187,"BP","GO:0007187","G protein-coupled receptor signaling pathway, coupled to cyclic ni
 GO:0071280,"BP","GO:0071280","cellular response to copper ion","11/1468","27/18800",2.5591227
 GO:0010720,"BP","GO:0010720","positive regulation of cell development","47/1468","297/18800",2
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 GO:0001706,"BP","GO:0001706","endoderm formation","16/1468","55/18800",2.80995086044086e
 GO:0046683,"BP","GO:0046683","response to organophosphorus","26/1468","124/18800",2.87438
 GO:0048864,"BP","GO:0048864","stem cell development","21/1468","88/18800",2.9656482489035
 GO:0071356,"BP","GO:0071356","cellular response to tumor necrosis factor","39/1468","229/18800
 GO:0009914,"BP","GO:0009914","hormone transport","46/1468","290/18800",3.10058552564259e
 GO:0097191,"BP","GO:0097191","extrinsic apoptotic signaling pathway","38/1468","221/18800",3.1
 GO:0035136,"BP","GO:0035136","forelimb morphogenesis","13/1468","38/18800",3.229578021944
 GO:0044706,"BP","GO:0044706","multi-multicellular organism process","37/1468","213/18800",3.3
 GO:0016042,"BP","GO:0016042","lipid catabolic process","50/1468","327/18800",3.4652991695100
 GO:0005044,"MF","GO:0005044","scavenger receptor activity","15/1495","47/18410",2.552954924

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GO:0030728,"BP","GO:0030728","ovulation","10/1468","23/18800",3.63408210898075e-06,5.7676
GO:0060571,"BP","GO:0060571","morphogenesis of an epithelial fold","10/1468","23/18800",3.634
GO:1900048,"BP","GO:1900048","positive regulation of hemostasis","10/1468","23/18800",3.63408
GO:0060425,"BP","GO:0060425","lung morphogenesis","15/1468","50/18800",3.74696264366924e
GO:1902041,"BP","GO:1902041","regulation of extrinsic apoptotic signaling pathway via death dom
GO:0009410,"BP","GO:0009410","response to xenobiotic stimulus","59/1468","411/18800",3.79026
GO:0014074,"BP","GO:0014074","response to purine-containing compound","27/1468","134/18800
GO:0072330,"BP","GO:0072330","monocarboxylic acid biosynthetic process","37/1468","215/18800
GO:0071559,"BP","GO:0071559","response to transforming growth factor beta","42/1468","258/18
GO:0048251,"BP","GO:0048251","elastic fiber assembly","7/1468","11/18800",4.35097820552466e
GO:0097242,"BP","GO:0097242","amyloid-beta clearance","13/1468","39/18800",4.4994300714952
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GO:0090101,"BP","GO:0090101","negative regulation of transmembrane receptor protein serine/thi
GO:0060070,"BP","GO:0060070","canonical Wnt signaling pathway","48/1468","313/18800",4.9740
GO:0060538,"BP","GO:0060538","skeletal muscle organ development","31/1468","167/18800",5.06
GO:0010273,"BP","GO:0010273","detoxification of copper ion","8/1468","15/18800",5.3027687182
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GO:0005496,"MF","GO:0005496","steroid binding","23/1495","100/18410",3.90384622137816e-06
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GO:0048247,"BP","GO:0048247","lymphocyte chemotaxis","17/1468","64/18800",5.470791900357
GO:0198738,"BP","GO:0198738","cell-cell signaling by wnt","63/1468","454/18800",5.56641015418
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GO:0060828,"BP","GO:0060828","regulation of canonical Wnt signaling pathway","42/1468","261/1
GO:0001759,"BP","GO:0001759","organ induction","10/1468","24/18800",5.7939776452023e-06,8.
GO:0030539,"BP","GO:0030539","male genitalia development","10/1468","24/18800",5.793977645
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GO:0071294,"BP","GO:0071294","cellular response to zinc ion","10/1468","24/18800",5.793977645
GO:0050766,"BP","GO:0050766","positive regulation of phagocytosis","18/1468","71/18800",5.997
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GO:0042303,"BP","GO:0042303","molting cycle","24/1468","114/18800",6.35634073922764e-06,9.
GO:0042633,"BP","GO:0042633","hair cycle","24/1468","114/18800",6.35634073922764e-06,9.272
GO:0046889,"BP","GO:0046889","positive regulation of lipid biosynthetic process","20/1468","85/1
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GO:0048806,"BP","GO:0048806","genitalia development","14/1468","46/18800",6.5246809926498
GO:0043524,"BP","GO:0043524","negative regulation of neuron apoptotic process","28/1468","145,
GO:0046879,"BP","GO:0046879","hormone secretion","44/1468","281/18800",7.08530264134983e
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GO:0042246,"BP","GO:0042246","tissue regeneration","18/1468","72/18800",7.41812040930922e-
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GO:0062013,"BP","GO:0062013","positive regulation of small molecule metabolic process","28/1468
GO:0044060,"BP","GO:0044060","regulation of endocrine process","12/1468","35/18800",7.525209
GO:0071384,"BP","GO:0071384","cellular response to corticosteroid stimulus","16/1468","59/1880
GO:0016053,"BP","GO:0016053","organic acid biosynthetic process","48/1468","318/18800",7.7153
GO:0043691,"BP","GO:0043691","reverse cholesterol transport","9/1468","20/18800",8.011915010

GO:0071241,"BP","GO:0071241","cellular response to inorganic substance","37/1468","221/18800",
 GO:0006956,"BP","GO:0006956","complement activation","26/1468","131/18800",8.276389449330
 GO:0010043,"BP","GO:0010043","response to zinc ion","15/1468","53/18800",8.32318043503758e-
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 GO:0033574,"BP","GO:0033574","response to testosterone","13/1468","41/18800",8.42105137638
 GO:0046461,"BP","GO:0046461","neutral lipid catabolic process","13/1468","41/18800",8.42105137
 GO:0046464,"BP","GO:0046464","acylglycerol catabolic process","13/1468","41/18800",8.42105137
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 GO:0034374,"BP","GO:0034374","low-density lipoprotein particle remodeling","8/1468","16/18800'
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 GO:0022407,"BP","GO:0022407","regulation of cell-cell adhesion","62/1468","456/18800",1.260883
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 GO:0046503,"BP","GO:0046503","glycerolipid catabolic process","17/1468","68/18800",1.32171196
 GO:0060740,"BP","GO:0060740","prostate gland epithelium morphogenesis","10/1468","26/18800"
 GO:0072010,"BP","GO:0072010","glomerular epithelium development","10/1468","26/18800",1.35
 GO:1905517,"BP","GO:1905517","macrophage migration","15/1468","55/18800",1.3656822785564
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 GO:0034385,"CC","GO:0034385","triglyceride-rich plasma lipoprotein particle","9/1537","20/19594'
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 GO:0019218,"BP","GO:0019218","regulation of steroid metabolic process","22/1468","104/18800",1.
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 GO:0014002,"BP","GO:0014002","astrocyte development","13/1468","43/18800",1.5083903945244
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GO:0050433,"BP","GO:0050433","regulation of catecholamine secretion","15/1468","56/18800",1.7158
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GO:0003338,"BP","GO:0003338","metanephros morphogenesis","11/1468","32/18800",1.75809395
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GO:0006692,"BP","GO:0006692","prostanoid metabolic process","14/1468","50/18800",1.89691871
GO:0006693,"BP","GO:0006693","prostaglandin metabolic process","14/1468","50/18800",1.896918
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GO:0050432,"BP","GO:0050432","catecholamine secretion","15/1468","57/18800",2.182023730525
GO:0046883,"BP","GO:0046883","regulation of hormone secretion","37/1468","231/18800",2.2249
GO:0009953,"BP","GO:0009953","dorsal/ventral pattern formation","20/1468","92/18800",2.24112
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GO:0014013,"BP","GO:0014013","regulation of gliogenesis","21/1468","100/18800",2.45944716280
GO:0015837,"BP","GO:0015837","amine transport","21/1468","100/18800",2.45944716280657e-05
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GO:0032102,"BP","GO:0032102","negative regulation of response to external stimulus","58/1468",
GO:0002688,"BP","GO:0002688","regulation of leukocyte chemotaxis","24/1468","124/18800",2.80
GO:0010565,"BP","GO:0010565","regulation of cellular ketone metabolic process","25/1468","132/1
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GO:0060512,"BP","GO:0060512","prostate gland morphogenesis","10/1468","28/18800",2.9020240
GO:0042446,"BP","GO:0042446","hormone biosynthetic process","16/1468","65/18800",2.9032064
GO:0061687,"BP","GO:0061687","detoxification of inorganic compound","8/1468","18/18800",2.91
GO:0072077,"BP","GO:0072077","renal vesicle morphogenesis","8/1468","18/18800",2.9139878442
GO:0090190,"BP","GO:0090190","positive regulation of branching involved in ureteric bud morphog
GO:0061844,"BP","GO:0061844","antimicrobial humoral immune response mediated by antimicrobi
GO:0051937,"BP","GO:0051937","catecholamine transport","17/1468","72/18800",2.95688077597
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GO:0072311,"BP","GO:0072311","glomerular epithelial cell differentiation","9/1468","23/18800",3.
GO:1903844,"BP","GO:1903844","regulation of cellular response to transforming growth factor beta
GO:0042742,"BP","GO:0042742","defense response to bacterium","51/1468","364/18800",3.270318
GO:0055017,"BP","GO:0055017","cardiac muscle tissue growth","19/1468","87/18800",3.33138131

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GO:1901215,"BP","GO:1901215","negative regulation of neuron death","34/1468","209/18800",3.40
GO:0001755,"BP","GO:0001755","neural crest cell migration","15/1468","59/18800",3.4021308008
GO:0019842,"MF","GO:0019842","vitamin binding","28/1495","148/18410",2.01961938719829e-05
GO:0010517,"BP","GO:0010517","regulation of phospholipase activity","16/1468","66/18800",3.557
GO:0016331,"BP","GO:0016331","morphogenesis of embryonic epithelium","27/1468","150/18800"
GO:0001707,"BP","GO:0001707","mesoderm formation","17/1468","73/18800",3.57721398894056
GO:0060439,"BP","GO:0060439","trachea morphogenesis","6/1468","10/18800",3.5803806596821e
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GO:0006641,"BP","GO:0006641","triglyceride metabolic process","21/1468","103/18800",3.917969
GO:0045444,"BP","GO:0045444","fat cell differentiation","37/1468","237/18800",3.9384590339923
GO:0055102,"MF","GO:0055102","lipase inhibitor activity","8/1495","17/18410",2.3163268009404e
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GO:0002683,"BP","GO:0002683","negative regulation of immune system process","57/1468","425/1
GO:0071774,"BP","GO:0071774","response to fibroblast growth factor","23/1468","119/18800",4.1
GO:0010631,"BP","GO:0010631","epithelial cell migration","50/1468","358/18800",4.23104982559
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GO:0060420,"BP","GO:0060420","regulation of heart growth","17/1468","74/18800",4.3101195609
GO:0002673,"BP","GO:0002673","regulation of acute inflammatory response","13/1468","47/18800
GO:0071398,"BP","GO:0071398","cellular response to fatty acid","11/1468","35/18800",4.56955203
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GO:0071548,"BP","GO:0071548","response to dexamethasone","12/1468","41/18800",4.588438353
GO:1905521,"BP","GO:1905521","regulation of macrophage migration","12/1468","41/18800",4.58
GO:0001942,"BP","GO:0001942","hair follicle development","19/1468","89/18800",4.64948778408
GO:0019835,"BP","GO:0019835","cytolysis","9/1468","24/18800",4.68139320208403e-05,0.000498
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GO:0048245,"BP","GO:0048245","eosinophil chemotaxis","8/1468","19/18800",4.68889223384812e
GO:0072074,"BP","GO:0072074","kidney mesenchyme development","8/1468","19/18800",4.68889
GO:0097501,"BP","GO:0097501","stress response to metal ion","8/1468","19/18800",4.6888922338
GO:0090100,"BP","GO:0090100","positive regulation of transmembrane receptor protein serine/thr
GO:0120020,"MF","GO:0120020","cholesterol transfer activity","9/1495","22/18410",2.8146649202
GO:0009897,"CC","GO:0009897","external side of plasma membrane","61/1537","455/19594",2.628
GO:0048332,"BP","GO:0048332","mesoderm morphogenesis","17/1468","75/18800",5.1727500157
GO:1901653,"BP","GO:1901653","cellular response to peptide","50/1468","361/18800",5.26110926
GO:0051402,"BP","GO:0051402","neuron apoptotic process","37/1468","241/18800",5.6746770202
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GO:0010518,"BP","GO:0010518","positive regulation of phospholipase activity","14/1468","55/1880
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GO:0030168,"BP","GO:0030168","platelet activation","24/1468","130/18800",6.23599765196888e-1
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GO:0033344,"BP","GO:0033344","cholesterol efflux","16/1468","69/18800",6.36485832413207e-05
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 GO:0072378,"BP","GO:0072378","blood coagulation, fibrin clot formation","7/1468","15/18800",6.4
 GO:0007519,"BP","GO:0007519","skeletal muscle tissue development","27/1468","155/18800",6.42
 GO:0046942,"BP","GO:0046942","carboxylic acid transport","41/1468","279/18800",6.44208188012
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 GO:0043523,"BP","GO:0043523","regulation of neuron apoptotic process","33/1468","207/18800",6.
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 GO:0060986,"BP","GO:0060986","endocrine hormone secretion","13/1468","49/18800",6.96354461
 GO:0045236,"MF","GO:0045236","CXCR chemokine receptor binding","8/1495","18/18410",3.87252
 GO:0010469,"BP","GO:0010469","regulation of signaling receptor activity","29/1468","173/18800",7.
 GO:0060231,"BP","GO:0060231","mesenchymal to epithelial transition","8/1468","20/18800",7.280
 GO:0051480,"BP","GO:0051480","regulation of cytosolic calcium ion concentration","49/1468","356
 GO:0071377,"BP","GO:0071377","cellular response to glucagon stimulus","6/1468","11/18800",7.35
 GO:0071492,"BP","GO:0071492","cellular response to UV-A","6/1468","11/18800",7.354720066637
 GO:0072205,"BP","GO:0072205","metanephric collecting duct development","6/1468","11/18800",7.
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 GO:0007188,"BP","GO:0007188","adenylate cyclase-modulating G protein-coupled receptor signalin
 GO:0097305,"BP","GO:0097305","response to alcohol","36/1468","235/18800",7.4388139075685e-
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 GO:0022405,"BP","GO:0022405","hair cycle process","19/1468","92/18800",7.4975468047799e-05,
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 GO:0018212,"BP","GO:0018212","peptidyl-tyrosine modification","51/1468","376/18800",7.684488
 GO:0010712,"BP","GO:0010712","regulation of collagen metabolic process","12/1468","43/18800",7.
 GO:0048663,"BP","GO:0048663","neuron fate commitment","15/1468","63/18800",7.74252074768
 GO:0051047,"BP","GO:0051047","positive regulation of secretion","43/1468","300/18800",7.794321
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 GO:0098773,"BP","GO:0098773","skin epidermis development","19/1468","93/18800",8.742634715
 GO:1903053,"BP","GO:1903053","regulation of extracellular matrix organization","13/1468","50/188
 GO:0019199,"MF","GO:0019199","transmembrane receptor protein kinase activity","18/1495","79/
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 GO:0046456,"BP","GO:0046456","icosanoid biosynthetic process","14/1468","57/18800",9.2795213
 GO:0071216,"BP","GO:0071216","cellular response to biotic stimulus","38/1468","256/18800",9.46:

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GO:0060443,"BP","GO:0060443","mammary gland morphogenesis","12/1468","44/18800",9.838918
GO:0070325,"MF","GO:0070325","lipoprotein particle receptor binding","10/1495","29/18410",5.76
GO:0071375,"BP","GO:0071375","cellular response to peptide hormone stimulus","42/1468","294/1
GO:0014068,"BP","GO:0014068","positive regulation of phosphatidylinositol 3-kinase signaling","17,
GO:0042277,"MF","GO:0042277","peptide binding","47/1495","322/18410",6.09897679124907e-05
GO:0062012,"BP","GO:0062012","regulation of small molecule metabolic process","47/1468","342/1
GO:0002064,"BP","GO:0002064","epithelial cell development","32/1468","203/18800",0.000105747
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GO:0043500,"BP","GO:0043500","muscle adaptation","22/1468","118/18800",0.0001067358879557
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GO:0010743,"BP","GO:0010743","regulation of macrophage derived foam cell differentiation","10/1
GO:0046457,"BP","GO:0046457","prostanoid biosynthetic process","10/1468","32/18800",0.000106
GO:0060795,"BP","GO:0060795","cell fate commitment involved in formation of primary germ layer
GO:0019865,"MF","GO:0019865","immunoglobulin binding","9/1495","24/18410",6.372996152927
GO:0050431,"MF","GO:0050431","transforming growth factor beta binding","9/1495","24/18410",6
GO:1904062,"BP","GO:1904062","regulation of cation transmembrane transport","48/1468","352/1
GO:0045665,"BP","GO:0045665","negative regulation of neuron differentiation","16/1468","72/188
GO:0050810,"BP","GO:0050810","regulation of steroid biosynthetic process","16/1468","72/18800"
GO:1903036,"BP","GO:1903036","positive regulation of response to wounding","16/1468","72/1880
GO:0030449,"BP","GO:0030449","regulation of complement activation","8/1468","21/18800",0.000
GO:0050829,"BP","GO:0050829","defense response to Gram-negative bacterium","18/1468","87/18
GO:0031100,"BP","GO:0031100","animal organ regeneration","15/1468","65/18800",0.0001133722
GO:0060038,"BP","GO:0060038","cardiac muscle cell proliferation","14/1468","58/18800",0.000113
GO:0003073,"BP","GO:0003073","regulation of systemic arterial blood pressure","19/1468","95/188
GO:0072676,"BP","GO:0072676","lymphocyte migration","22/1468","119/18800",0.0001214476005
GO:0090257,"BP","GO:0090257","regulation of muscle system process","37/1468","250/18800",0.0
GO:0002274,"BP","GO:0002274","myeloid leukocyte activation","35/1468","232/18800",0.0001269
GO:0048660,"BP","GO:0048660","regulation of smooth muscle cell proliferation","28/1468","170/18
GO:0033555,"BP","GO:0033555","multicellular organismal response to stress","16/1468","73/18800
GO:0150076,"BP","GO:0150076","neuroinflammatory response","16/1468","73/18800",0.00013029
GO:0045104,"BP","GO:0045104","intermediate filament cytoskeleton organization","18/1468","88/1
GO:0005184,"MF","GO:0005184","neuropeptide hormone activity","10/1495","30/18410",8.017345
GO:0017147,"MF","GO:0017147","Wnt-protein binding","10/1495","30/18410",8.0173450809777e-
GO:0005507,"MF","GO:0005507","copper ion binding","15/1495","61/18410",8.10867635953047e-1
GO:0002686,"BP","GO:0002686","negative regulation of leukocyte migration","13/1468","52/18800
GO:0002675,"BP","GO:0002675","positive regulation of acute inflammatory response","9/1468","27
GO:0072012,"BP","GO:0072012","glomerulus vasculature development","9/1468","27/18800",0.000
GO:0098742,"BP","GO:0098742","cell-cell adhesion via plasma-membrane adhesion molecules","40,
GO:0006882,"BP","GO:0006882","cellular zinc ion homeostasis","11/1468","39/18800",0.000137275
GO:0045923,"BP","GO:0045923","positive regulation of fatty acid metabolic process","11/1468","39
GO:0001867,"BP","GO:0001867","complement activation, lectin pathway","6/1468","12/18800",0.0
GO:0003337,"BP","GO:0003337","mesenchymal to epithelial transition involved in metanephros mo
GO:0060442,"BP","GO:0060442","branching involved in prostate gland morphogenesis","6/1468","1
GO:0072182,"BP","GO:0072182","regulation of nephron tubule epithelial cell differentiation","6/146
GO:0006633,"BP","GO:0006633","fatty acid biosynthetic process","27/1468","162/18800",0.000139
GO:0045907,"BP","GO:0045907","positive regulation of vasoconstriction","10/1468","33/18800",0.0
GO:0045445,"BP","GO:0045445","myoblast differentiation","17/1468","81/18800",0.000143191011
GO:0030900,"BP","GO:0030900","forebrain development","50/1468","376/18800",0.000147588900

GO:0016125,"BP","GO:0016125","sterol metabolic process","26/1468","154/18800",0.00014790366
GO:0060560,"BP","GO:0060560","developmental growth involved in morphogenesis","35/1468","23/18800",0.00014790366
GO:0045103,"BP","GO:0045103","intermediate filament-based process","18/1468","89/18800",0.00014790366
GO:0097493,"MF","GO:0097493","structural molecule activity conferring elasticity","6/1495","11/18410",0.00014790366
GO:0043491,"BP","GO:0043491","protein kinase B signaling","33/1468","216/18800",0.0001533335
GO:0033674,"BP","GO:0033674","positive regulation of kinase activity","60/1468","476/18800",0.0001533335
GO:0006690,"BP","GO:0006690","icosanoid metabolic process","22/1468","121/18800",0.00015636
GO:0035987,"BP","GO:0035987","endodermal cell differentiation","12/1468","46/18800",0.00015636
GO:0001848,"MF","GO:0001848","complement binding","8/1495","20/18410",9.6194584104975e-05
GO:0035929,"BP","GO:0035929","steroid hormone secretion","8/1468","22/18800",0.00016045328
GO:0055021,"BP","GO:0055021","regulation of cardiac muscle tissue growth","15/1468","67/18800",0.00016045328
GO:0050832,"BP","GO:0050832","defense response to fungus","13/1468","53/18800",0.000166353
GO:0072132,"BP","GO:0072132","mesenchyme morphogenesis","13/1468","53/18800",0.000166353
GO:0019731,"BP","GO:0019731","antibacterial humoral response","14/1468","60/18800",0.0001671
GO:0042481,"BP","GO:0042481","regulation of odontogenesis","7/1468","17/18800",0.0001685796
GO:0072376,"BP","GO:0072376","protein activation cascade","7/1468","17/18800",0.0001685796
GO:0048659,"BP","GO:0048659","smooth muscle cell proliferation","28/1468","173/18800",0.000171
GO:0001968,"MF","GO:0001968","fibronectin binding","10/1495","31/18410",0.0001097870365337
GO:0001653,"MF","GO:0001653","peptide receptor activity","27/1495","154/18410",0.0001106726
GO:0045685,"BP","GO:0045685","regulation of glial cell differentiation","16/1468","75/18800",0.0001106726
GO:0060840,"BP","GO:0060840","artery development","20/1468","106/18800",0.000182464269214
GO:0008203,"BP","GO:0008203","cholesterol metabolic process","24/1468","139/18800",0.000184
GO:0035116,"BP","GO:0035116","embryonic hindlimb morphogenesis","9/1468","28/18800",0.000184
GO:0045177,"CC","GO:0045177","apical part of cell","56/1537","424/19594",8.35376755496219e-05
GO:0042573,"BP","GO:0042573","retinoic acid metabolic process","10/1468","34/18800",0.0001881
GO:1903532,"BP","GO:1903532","positive regulation of secretion by cell","39/1468","274/18800",0.0001881
GO:0006639,"BP","GO:0006639","acylglycerol metabolic process","23/1468","131/18800",0.000192
GO:0043627,"BP","GO:0043627","response to estrogen","15/1468","68/18800",0.000194284385054
GO:0045109,"BP","GO:0045109","intermediate filament organization","15/1468","68/18800",0.000194284385054
GO:0003197,"BP","GO:0003197","endocardial cushion development","12/1468","47/18800",0.000194284385054
GO:0042471,"BP","GO:0042471","ear morphogenesis","22/1468","123/18800",0.000199864371506
GO:0045666,"BP","GO:0045666","positive regulation of neuron differentiation","18/1468","91/18800",0.000199864371506
GO:0046916,"BP","GO:0046916","cellular transition metal ion homeostasis","21/1468","115/18800",0.000199864371506
GO:0019233,"BP","GO:0019233","sensory perception of pain","19/1468","99/18800",0.0002080980
GO:0008237,"MF","GO:0008237","metallopeptidase activity","31/1495","189/18410",0.0001294044
GO:0007498,"BP","GO:0007498","mesoderm development","23/1468","132/18800",0.00021638322
GO:0055069,"BP","GO:0055069","zinc ion homeostasis","11/1468","41/18800",0.000223846781992
GO:0120178,"BP","GO:0120178","steroid hormone biosynthetic process","11/1468","41/18800",0.000223846781992
GO:0006833,"BP","GO:0006833","water transport","8/1468","23/18800",0.000229264929432549,0
GO:0032331,"BP","GO:0032331","negative regulation of chondrocyte differentiation","8/1468","23/18800",0.000229264929432549,0
GO:0072677,"BP","GO:0072677","eosinophil migration","8/1468","23/18800",0.000229264929432549,0
GO:0009913,"BP","GO:0009913","epidermal cell differentiation","34/1468","230/18800",0.0002334
GO:0051952,"BP","GO:0051952","regulation of amine transport","18/1468","92/18800",0.00023561
GO:2001053,"BP","GO:2001053","regulation of mesenchymal cell apoptotic process","6/1468","13/18800",0.00023561
GO:0000302,"BP","GO:0000302","response to reactive oxygen species","31/1468","203/18800",0.00023561
GO:0001935,"BP","GO:0001935","endothelial cell proliferation","30/1468","194/18800",0.00024155
GO:0003044,"BP","GO:0003044","regulation of systemic arterial blood pressure mediated by a chemoreceptor","12/1468","48/18800",0.0002427
GO:0035272,"BP","GO:0035272","exocrine system development","12/1468","48/18800",0.0002427
GO:0048146,"BP","GO:0048146","positive regulation of fibroblast proliferation","12/1468","48/18800",0.0002427
GO:0035137,"BP","GO:0035137","hindlimb morphogenesis","10/1468","35/18800",0.00024506916

GO:0048008,"BP","GO:0048008","platelet-derived growth factor receptor signaling pathway","13/14
GO:0030246,"MF","GO:0030246","carbohydrate binding","40/1495","270/18410",0.0001515824930
GO:0002825,"BP","GO:0002825","regulation of T-helper 1 type immune response","9/1468","29/18800",0.0002573141032
GO:0010464,"BP","GO:0010464","regulation of mesenchymal cell proliferation","9/1468","29/18800",0.0002573141032
GO:0061437,"BP","GO:0061437","renal system vasculature development","9/1468","29/18800",0.0002573141032
GO:0061440,"BP","GO:0061440","kidney vasculature development","9/1468","29/18800",0.0002573141032
GO:0005903,"CC","GO:0005903","brush border","20/1537","102/19594",0.000112280310064272,0.000112280310064272
GO:0048511,"BP","GO:0048511","rhythmic process","41/1468","297/18800",0.00025652899956332
GO:0002076,"BP","GO:0002076","osteoblast development","7/1468","18/18800",0.0002573141032
GO:0006957,"BP","GO:0006957","complement activation, alternative pathway","7/1468","18/18800",0.0002573141032
GO:0034433,"BP","GO:0034433","steroid esterification","7/1468","18/18800",0.0002573141032534
GO:0034434,"BP","GO:0034434","sterol esterification","7/1468","18/18800",0.00025731410325343
GO:0034435,"BP","GO:0034435","cholesterol esterification","7/1468","18/18800",0.00025731410325343
GO:0060438,"BP","GO:0060438","trachea development","7/1468","18/18800",0.0002573141032534
GO:2000831,"BP","GO:2000831","regulation of steroid hormone secretion","7/1468","18/18800",0.0002573141032534
GO:0006766,"BP","GO:0006766","vitamin metabolic process","20/1468","109/18800",0.0002694267
GO:0034446,"BP","GO:0034446","substrate adhesion-dependent cell spreading","20/1468","109/18800",0.0002694267
GO:0051378,"MF","GO:0051378","serotonin binding","6/1495","12/18410",0.000170865834939512
GO:0015267,"MF","GO:0015267","channel activity","63/1495","489/18410",0.00017097284189953
GO:0055090,"BP","GO:0055090","acylglycerol homeostasis","11/1468","42/18800",0.000282090067
GO:0070328,"BP","GO:0070328","triglyceride homeostasis","11/1468","42/18800",0.000282090067
GO:0003231,"BP","GO:0003231","cardiac ventricle development","22/1468","126/18800",0.000285
GO:0022803,"MF","GO:0022803","passive transmembrane transporter activity","63/1495","490/18410",0.00017097284189953
GO:0071346,"BP","GO:0071346","cellular response to interferon-gamma","21/1468","118/18800",0.000285
GO:0050873,"BP","GO:0050873","brown fat cell differentiation","12/1468","49/18800",0.00029889
GO:0060043,"BP","GO:0060043","regulation of cardiac muscle cell proliferation","12/1468","49/18800",0.00029889
GO:0043903,"BP","GO:0043903","regulation of biological process involved in symbiotic interaction",
GO:0033627,"BP","GO:0033627","cell adhesion mediated by integrin","17/1468","86/18800",0.0003
GO:0005319,"MF","GO:0005319","lipid transporter activity","27/1495","159/18410",0.00019161129
GO:0002690,"BP","GO:0002690","positive regulation of leukocyte chemotaxis","18/1468","94/18800",0.000311
GO:0048709,"BP","GO:0048709","oligodendrocyte differentiation","18/1468","94/18800",0.000311
GO:0045121,"CC","GO:0045121","membrane raft","45/1537","326/19594",0.000147208875817955
GO:0022409,"BP","GO:0022409","positive regulation of cell-cell adhesion","40/1468","291/18800",0.000311
GO:0007190,"BP","GO:0007190","activation of adenylate cyclase activity","9/1468","30/18800",0.000311
GO:0007202,"BP","GO:0007202","activation of phospholipase C activity","9/1468","30/18800",0.000311
GO:0060325,"BP","GO:0060325","face morphogenesis","9/1468","30/18800",0.0003337469564252
GO:0004222,"MF","GO:0004222","metalloendopeptidase activity","21/1495","111/18410",0.000210
GO:0098857,"CC","GO:0098857","membrane microdomain","45/1537","327/19594",0.00015803173
GO:0009620,"BP","GO:0009620","response to fungus","14/1468","64/18800",0.0003447075403838
GO:0014015,"BP","GO:0014015","positive regulation of gliogenesis","14/1468","64/18800",0.00034
GO:0046596,"BP","GO:0046596","regulation of viral entry into host cell","11/1468","43/18800",0.00034
GO:0001892,"BP","GO:0001892","embryonic placenta development","17/1468","87/18800",0.00034
GO:0035282,"BP","GO:0035282","segmentation","19/1468","103/18800",0.000353683513531901,0.000353683513531901
GO:0070252,"BP","GO:0070252","actin-mediated cell contraction","19/1468","103/18800",0.000353683513531901
GO:0043202,"CC","GO:0043202","lysosomal lumen","19/1537","97/19594",0.000167343725940839
GO:0052372,"BP","GO:0052372","modulation by symbiont of entry into host","12/1468","50/18800",0.000353683513531901
GO:0031668,"BP","GO:0031668","cellular response to extracellular stimulus","35/1468","245/18800",0.0003692
GO:0045926,"BP","GO:0045926","negative regulation of growth","35/1468","245/18800",0.0003692
GO:0050680,"BP","GO:0050680","negative regulation of epithelial cell proliferation","26/1468","163/18800",0.0003692
GO:0035567,"BP","GO:0035567","non-canonical Wnt signaling pathway","15/1468","72/18800",0.0003692

GO:0042749,"BP","GO:0042749","regulation of circadian sleep/wake cycle","7/1468","19/18800",0.0003894109988
GO:0030238,"BP","GO:0030238","male sex determination","6/1468","14/18800",0.0003894109988
GO:0072160,"BP","GO:0072160","nephron tubule epithelial cell differentiation","6/1468","14/18800",0.0003894109988
GO:1905939,"BP","GO:1905939","regulation of gonad development","6/1468","14/18800",0.0003894109988
GO:0048644,"BP","GO:0048644","muscle organ morphogenesis","16/1468","80/18800",0.00039660
GO:0043178,"MF","GO:0043178","alcohol binding","18/1495","89/18410",0.000247364039779392,
GO:0014046,"BP","GO:0014046","dopamine secretion","10/1468","37/18800",0.000402764926258
GO:0014059,"BP","GO:0014059","regulation of dopamine secretion","10/1468","37/18800",0.000402764926258
GO:0035914,"BP","GO:0035914","skeletal muscle cell differentiation","14/1468","65/18800",0.000402764926258
GO:0006979,"BP","GO:0006979","response to oxidative stress","54/1468","433/18800",0.00041964
GO:1900024,"BP","GO:1900024","regulation of substrate adhesion-dependent cell spreading","13/1468","105/18800",0.000437332511543
GO:0014009,"BP","GO:0014009","glial cell proliferation","11/1468","44/18800",0.000437332511543
GO:0035767,"BP","GO:0035767","endothelial cell chemotaxis","9/1468","31/18800",0.00043797179
GO:1902042,"BP","GO:1902042","negative regulation of extrinsic apoptotic signaling pathway via de
GO:0003148,"BP","GO:0003148","outflow tract septum morphogenesis","8/1468","25/18800",0.00043797179
GO:0060219,"BP","GO:0060219","camera-type eye photoreceptor cell differentiation","8/1468","25/18800",0.00043797179
GO:0015872,"BP","GO:0015872","dopamine transport","12/1468","51/18800",0.000444630229080
GO:0071622,"BP","GO:0071622","regulation of granulocyte chemotaxis","12/1468","51/18800",0.000444630229080
GO:1901890,"BP","GO:1901890","positive regulation of cell junction assembly","19/1468","105/18800",0.000444630229080
GO:0048020,"MF","GO:0048020","CCR chemokine receptor binding","12/1495","47/18410",0.0002822955224930782
GO:0030500,"BP","GO:0030500","regulation of bone mineralization","16/1468","81/18800",0.000444630229080
GO:0004859,"MF","GO:0004859","phospholipase inhibitor activity","6/1495","13/18410",0.0002955224930782
GO:0039706,"MF","GO:0039706","co-receptor binding","6/1495","13/18410",0.0002955224930782
GO:0043176,"MF","GO:0043176","amine binding","6/1495","13/18410",0.000295522493078262,0.000295522493078262
GO:0007204,"BP","GO:0007204","positive regulation of cytosolic calcium ion concentration","43/1468","139/18800",0.000444630229080
GO:0045807,"BP","GO:0045807","positive regulation of endocytosis","18/1468","97/18800",0.000444630229080
GO:0055076,"BP","GO:0055076","transition metal ion homeostasis","23/1468","139/18800",0.000444630229080
GO:0033218,"MF","GO:0033218","amide binding","53/1495","402/18410",0.000310655636505521,
GO:0060389,"BP","GO:0060389","pathway-restricted SMAD protein phosphorylation","14/1468","65/18800",0.000444630229080
GO:0043292,"CC","GO:0043292","contractile fiber","35/1537","238/19594",0.000230968470879139
GO:0071682,"CC","GO:0071682","endocytic vesicle lumen","8/1537","23/19594",0.0002367353085
GO:0034185,"MF","GO:0034185","apolipoprotein binding","7/1495","18/18410",0.00032803000202
GO:0098641,"MF","GO:0098641","cadherin binding involved in cell-cell adhesion","7/1495","18/18410",0.00032803000202
GO:0020037,"MF","GO:0020037","heme binding","24/1495","139/18410",0.000329266056810624,
GO:0042886,"BP","GO:0042886","amide transport","39/1468","287/18800",0.000491850682154724
GO:0040013,"BP","GO:0040013","negative regulation of locomotion","50/1468","396/18800",0.000491850682154724
GO:0010742,"BP","GO:0010742","macrophage derived foam cell differentiation","10/1468","38/18800",0.000508761212
GO:0048246,"BP","GO:0048246","macrophage chemotaxis","10/1468","38/18800",0.000508761212
GO:0003279,"BP","GO:0003279","cardiac septum development","19/1468","106/18800",0.0005146
GO:0031102,"BP","GO:0031102","neuron projection regeneration","13/1468","59/18800",0.00051579626
GO:0046686,"BP","GO:0046686","response to cadmium ion","13/1468","59/18800",0.00051579626
GO:0001542,"BP","GO:0001542","ovulation from ovarian follicle","5/1468","10/18800",0.000520560043
GO:0015791,"BP","GO:0015791","polyol transmembrane transport","5/1468","10/18800",0.000520560043
GO:0060346,"BP","GO:0060346","bone trabecula formation","5/1468","10/18800",0.000520560043
GO:0060767,"BP","GO:0060767","epithelial cell proliferation involved in prostate gland developmen
GO:0071073,"BP","GO:0071073","positive regulation of phospholipid biosynthetic process","5/1468
GO:0090184,"BP","GO:0090184","positive regulation of kidney development","5/1468","10/18800",
GO:1905941,"BP","GO:1905941","positive regulation of gonad development","5/1468","10/18800",
GO:2000425,"BP","GO:2000425","regulation of apoptotic cell clearance","5/1468","10/18800",0.000
GO:0071383,"BP","GO:0071383","cellular response to steroid hormone stimulus","30/1468","203/18800",0.000520560043

GO:1902652,"BP","GO:1902652","secondary alcohol metabolic process","24/1468","149/18800",0.0
GO:0046622,"BP","GO:0046622","positive regulation of organ growth","12/1468","52/18800",0.000
GO:0051180,"BP","GO:0051180","vitamin transport","11/1468","45/18800",0.00053847220360353:
GO:0001701,"BP","GO:0001701","in utero embryonic development","49/1468","387/18800",0.0005
GO:0022410,"BP","GO:0022410","circadian sleep/wake cycle process","7/1468","20/18800",0.00054
GO:0042359,"BP","GO:0042359","vitamin D metabolic process","7/1468","20/18800",0.0005455072
GO:0050769,"BP","GO:0050769","positive regulation of neurogenesis","32/1468","222/18800",0.00
GO:0045600,"BP","GO:0045600","positive regulation of fat cell differentiation","14/1468","67/1880
GO:0007229,"BP","GO:0007229","integrin-mediated signaling pathway","19/1468","107/18800",0.0
GO:0060249,"BP","GO:0060249","anatomical structure homeostasis","42/1468","319/18800",0.000
GO:0071230,"BP","GO:0071230","cellular response to amino acid stimulus","15/1468","75/18800",C
GO:0010755,"BP","GO:0010755","regulation of plasminogen activation","6/1468","15/18800",0.000
GO:0034384,"BP","GO:0034384","high-density lipoprotein particle clearance","6/1468","15/18800",
GO:0072283,"BP","GO:0072283","metanephric renal vesicle morphogenesis","6/1468","15/18800",C
GO:0097152,"BP","GO:0097152","mesenchymal cell apoptotic process","6/1468","15/18800",0.0006
GO:0051271,"BP","GO:0051271","negative regulation of cellular component movement","47/1468",
GO:0033273,"BP","GO:0033273","response to vitamin","16/1468","83/18800",0.000609323205845:
GO:0090077,"BP","GO:0090077","foam cell differentiation","10/1468","39/18800",0.000636859587
GO:0006958,"BP","GO:0006958","complement activation, classical pathway","19/1468","108/18800
GO:0007218,"BP","GO:0007218","neuropeptide signaling pathway","19/1468","108/18800",0.00065
GO:0021761,"BP","GO:0021761","limbic system development","19/1468","108/18800",0.00065418:
GO:0001936,"BP","GO:0001936","regulation of endothelial cell proliferation","27/1468","178/18800
GO:0061383,"BP","GO:0061383","trabecula morphogenesis","11/1468","46/18800",0.00065840692
GO:0043394,"MF","GO:0043394","proteoglycan binding","10/1495","36/18410",0.00043260012938
GO:0002367,"BP","GO:0002367","cytokine production involved in immune response","18/1468","10
GO:2000146,"BP","GO:2000146","negative regulation of cell motility","46/1468","361/18800",0.000
GO:0032412,"BP","GO:0032412","regulation of ion transmembrane transporter activity","36/1468",
GO:0019217,"BP","GO:0019217","regulation of fatty acid metabolic process","17/1468","92/18800"
GO:0022898,"BP","GO:0022898","regulation of transmembrane transporter activity","37/1468","27:
GO:0050994,"BP","GO:0050994","regulation of lipid catabolic process","13/1468","61/18800",0.000
GO:0048566,"BP","GO:0048566","embryonic digestive tract development","9/1468","33/18800",0.0
GO:0019932,"BP","GO:0019932","second-messenger-mediated signaling","40/1468","303/18800",0
GO:0016705,"MF","GO:0016705","oxidoreductase activity, acting on paired donors, with incorporati
GO:0030879,"BP","GO:0030879","mammary gland development","22/1468","135/18800",0.000759
GO:0033762,"BP","GO:0033762","response to glucagon","7/1468","21/18800",0.0007634703999710
GO:0070167,"BP","GO:0070167","regulation of biomineral tissue development","18/1468","101/188
GO:0002697,"BP","GO:0002697","regulation of immune effector process","45/1468","353/18800",0
GO:0071320,"BP","GO:0071320","cellular response to cAMP","12/1468","54/18800",0.00077254125
GO:0010875,"BP","GO:0010875","positive regulation of cholesterol efflux","8/1468","27/18800",0.0
GO:0001837,"BP","GO:0001837","epithelial to mesenchymal transition","25/1468","162/18800",0.0
GO:0010863,"BP","GO:0010863","positive regulation of phospholipase C activity","10/1468","40/188
GO:0071229,"BP","GO:0071229","cellular response to acid chemical","16/1468","85/18800",0.00079
GO:0022408,"BP","GO:0022408","negative regulation of cell-cell adhesion","29/1468","199/18800",
GO:0032757,"BP","GO:0032757","positive regulation of interleukin-8 production","13/1468","62/18
GO:0060393,"BP","GO:0060393","regulation of pathway-restricted SMAD protein phosphorylation",
GO:0032409,"BP","GO:0032409","regulation of transporter activity","40/1468","305/18800",0.0008
GO:0051961,"BP","GO:0051961","negative regulation of nervous system development","23/1468",
GO:0031089,"CC","GO:0031089","platelet dense granule lumen","6/1537","14/19594",0.000399324
GO:0010454,"BP","GO:0010454","negative regulation of cell fate commitment","5/1468","11/18800
GO:0034115,"BP","GO:0034115","negative regulation of heterotypic cell-cell adhesion","5/1468","1:

GO:0042487,"BP","GO:0042487","regulation of odontogenesis of dentin-containing tooth","5/1468"
GO:0046689,"BP","GO:0046689","response to mercury ion","5/1468","11/18800",0.0008930707458
GO:0060272,"BP","GO:0060272","embryonic skeletal joint morphogenesis","5/1468","11/18800",0.
GO:0060433,"BP","GO:0060433","bronchus development","5/1468","11/18800",0.00089307074583
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GO:0070944,"BP","GO:0070944","neutrophil-mediated killing of bacterium","5/1468","11/18800",0.
GO:1901655,"BP","GO:1901655","cellular response to ketone","17/1468","94/18800",0.0008942046
GO:0003015,"BP","GO:0003015","heart process","35/1468","257/18800",0.000894857500461605,0
GO:0003407,"BP","GO:0003407","neural retina development","14/1468","70/18800",0.0008962894
GO:0030594,"MF","GO:0030594","neurotransmitter receptor activity","20/1495","111/18410",0.00
GO:0002921,"BP","GO:0002921","negative regulation of humoral immune response","6/1468","16/
GO:0007193,"BP","GO:0007193","adenylate cyclase-inhibiting G protein-coupled receptor signaling |
GO:1901616,"BP","GO:1901616","organic hydroxy compound catabolic process","15/1468","78/188
GO:0048730,"BP","GO:0048730","epidermis morphogenesis","9/1468","34/18800",0.000920788266
GO:0060323,"BP","GO:0060323","head morphogenesis","9/1468","34/18800",0.0009207882667369
GO:0030336,"BP","GO:0030336","negative regulation of cell migration","44/1468","346/18800",0.0
GO:0030139,"CC","GO:0030139","endocytic vesicle","45/1537","342/19594",0.00043316451342386
GO:0002573,"BP","GO:0002573","myeloid leukocyte differentiation","30/1468","210/18800",0.0009
GO:0055088,"BP","GO:0055088","lipid homeostasis","26/1468","173/18800",0.0009396357274655
GO:0035637,"BP","GO:0035637","multicellular organismal signaling","25/1468","164/18800",0.0009
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GO:0050786,"MF","GO:0050786","RAGE receptor binding","5/1495","10/18410",0.00062465314252
GO:0010543,"BP","GO:0010543","regulation of platelet activation","11/1468","48/18800",0.000965
GO:0033628,"BP","GO:0033628","regulation of cell adhesion mediated by integrin","11/1468","48/1
GO:0030016,"CC","GO:0030016","myofibril","33/1537","228/19594",0.000459486942725785,0.006
GO:0042472,"BP","GO:0042472","inner ear morphogenesis","18/1468","103/18800",0.0009718296
GO:0110149,"BP","GO:0110149","regulation of biomineralization","18/1468","103/18800",0.000971
GO:0060421,"BP","GO:0060421","positive regulation of heart growth","10/1468","41/18800",0.0009
GO:0150077,"BP","GO:0150077","regulation of neuroinflammatory response","10/1468","41/18800
GO:1905314,"BP","GO:1905314","semi-lunar valve development","10/1468","41/18800",0.0009732
GO:0007626,"BP","GO:0007626","locomotory behavior","28/1468","192/18800",0.0009870123900
GO:0008016,"BP","GO:0008016","regulation of heart contraction","30/1468","211/18800",0.001010
GO:0048661,"BP","GO:0048661","positive regulation of smooth muscle cell proliferation","17/1468"
GO:0001958,"BP","GO:0001958","endochondral ossification","8/1468","28/18800",0.001022435268
GO:0036075,"BP","GO:0036075","replacement ossification","8/1468","28/18800",0.0010224352683
GO:0050996,"BP","GO:0050996","positive regulation of lipid catabolic process","8/1468","28/18800
GO:0006939,"BP","GO:0006939","smooth muscle contraction","19/1468","112/18800",0.00103313
GO:0046597,"BP","GO:0046597","negative regulation of viral entry into host cell","7/1468","22/188
GO:1902644,"BP","GO:1902644","tertiary alcohol metabolic process","7/1468","22/18800",0.00104
GO:2000310,"BP","GO:2000310","regulation of NMDA receptor activity","7/1468","22/18800",0.001
GO:0002455,"BP","GO:0002455","humoral immune response mediated by circulating immunoglobul
GO:0014812,"BP","GO:0014812","muscle cell migration","18/1468","104/18800",0.0010911753955
GO:0005911,"CC","GO:0005911","cell-cell junction","60/1537","497/19594",0.00054890003269588
GO:0010862,"BP","GO:0010862","positive regulation of pathway-restricted SMAD protein phosphor
GO:0120009,"BP","GO:0120009","intermembrane lipid transfer","11/1468","49/18800",0.00115826
GO:0004879,"MF","GO:0004879","nuclear receptor activity","12/1495","52/18410",0.00076276314
GO:0098531,"MF","GO:0098531","ligand-activated transcription factor activity","12/1495","52/1841
GO:0004806,"MF","GO:0004806","triglyceride lipase activity","8/1495","26/18410",0.000767984486
GO:0098862,"CC","GO:0098862","cluster of actin-based cell projections","25/1537","158/19594",0.0

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 GO:0021766,"BP","GO:0021766","hippocampus development","15/1468","80/18800",0.0012002716
 GO:0006022,"BP","GO:0006022","aminoglycan metabolic process","21/1468","131/18800",0.001224
 GO:0051235,"BP","GO:0051235","maintenance of location","42/1468","331/18800",0.00124365351
 GO:0007272,"BP","GO:0007272","ensheathment of neurons","22/1468","140/18800",0.0012450624
 GO:0008366,"BP","GO:0008366","axon ensheathment","22/1468","140/18800",0.001245062472119
 GO:0050768,"BP","GO:0050768","negative regulation of neurogenesis","22/1468","140/18800",0.0012450624
 GO:0060041,"BP","GO:0060041","retina development in camera-type eye","23/1468","149/18800",0.0012450624
 GO:0060042,"BP","GO:0060042","retina morphogenesis in camera-type eye","12/1468","57/18800",0.0012450624
 GO:0003014,"BP","GO:0003014","renal system process","19/1468","114/18800",0.00128436784004
 GO:0016264,"BP","GO:0016264","gap junction assembly","6/1468","17/18800",0.001308592421980
 GO:0060192,"BP","GO:0060192","negative regulation of lipase activity","6/1468","17/18800",0.001308592421980
 GO:1904948,"BP","GO:1904948","midbrain dopaminergic neuron differentiation","6/1468","17/18800",0.001308592421980
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 GO:0010453,"BP","GO:0010453","regulation of cell fate commitment","8/1468","29/18800",0.00131636351
 GO:0010575,"BP","GO:0010575","positive regulation of vascular endothelial growth factor production",
 GO:0048265,"BP","GO:0048265","response to pain","8/1468","29/18800",0.00131636351187999,0.00131636351
 GO:0060037,"BP","GO:0060037","pharyngeal system development","8/1468","29/18800",0.00131636351
 GO:0032355,"BP","GO:0032355","response to estradiol","20/1468","123/18800",0.00132791051975
 GO:0071466,"BP","GO:0071466","cellular response to xenobiotic stimulus","25/1468","168/18800",0.00132791051975
 GO:0030858,"BP","GO:0030858","positive regulation of epithelial cell differentiation","13/1468","65/18800",0.00132791051975
 GO:0021675,"BP","GO:0021675","nerve development","15/1468","81/18800",0.0013687463922069
 GO:0048144,"BP","GO:0048144","fibroblast proliferation","15/1468","81/18800",0.0013687463922069
 GO:0060415,"BP","GO:0060415","muscle tissue morphogenesis","14/1468","73/18800",0.00137672
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 GO:0002053,"BP","GO:0002053","positive regulation of mesenchymal cell proliferation","7/1468","23/18800",0.00140170927
 GO:0042745,"BP","GO:0042745","circadian sleep/wake cycle","7/1468","23/18800",0.00140170927
 GO:0045723,"BP","GO:0045723","positive regulation of fatty acid biosynthetic process","7/1468","23/18800",0.00140170927
 GO:0046697,"BP","GO:0046697","decidualization","7/1468","23/18800",0.00140170927522299,0.00140170927
 GO:1900120,"BP","GO:1900120","regulation of receptor binding","7/1468","23/18800",0.00140170927522299,0.00140170927
 GO:0033559,"BP","GO:0033559","unsaturated fatty acid metabolic process","19/1468","115/18800",0.00140170927522299,0.00140170927
 GO:0001553,"BP","GO:0001553","luteinization","5/1468","12/18800",0.00143286473409244,0.00143286473409244
 GO:0007501,"BP","GO:0007501","mesodermal cell fate specification","5/1468","12/18800",0.00143286473409244,0.00143286473409244
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 GO:0072178,"BP","GO:0072178","nephric duct morphogenesis","5/1468","12/18800",0.00143286473409244,0.00143286473409244
 GO:0006941,"BP","GO:0006941","striated muscle contraction","26/1468","178/18800",0.001433948
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 GO:0045777,"BP","GO:0045777","positive regulation of blood pressure","9/1468","36/18800",0.001433948
 GO:0071604,"BP","GO:0071604","transforming growth factor beta production","10/1468","43/18800",0.001433948
 GO:0046906,"MF","GO:0046906","tetrapyrrole binding","24/1495","149/18410",0.00092514669040
 GO:0001838,"BP","GO:0001838","embryonic epithelial tube formation","20/1468","124/18800",0.00092514669040
 GO:0030048,"BP","GO:0030048","actin filament-based movement","21/1468","133/18800",0.001433948
 GO:0005811,"CC","GO:0005811","lipid droplet","18/1537","100/19594",0.000716498285056115,0.000716498285056115
 GO:0045604,"BP","GO:0045604","regulation of epidermal cell differentiation","12/1468","58/18800",0.000716498285056115,0.000716498285056115
 GO:0045761,"BP","GO:0045761","regulation of adenylate cyclase activity","12/1468","58/18800",0.000716498285056115,0.000716498285056115
 GO:0033138,"BP","GO:0033138","positive regulation of peptidyl-serine phosphorylation","18/1468",

GO:0043177,"MF","GO:0043177","organic acid binding","23/1495","141/18410",0.00098126061592
GO:0030104,"BP","GO:0030104","water homeostasis","13/1468","66/18800",0.0015642942333584
GO:0035924,"BP","GO:0035924","cellular response to vascular endothelial growth factor stimulus",
GO:0021510,"BP","GO:0021510","spinal cord development","17/1468","99/18800",0.001619394981
GO:0045927,"BP","GO:0045927","positive regulation of growth","34/1468","256/18800",0.0016200
GO:0008347,"BP","GO:0008347","glial cell migration","11/1468","51/18800",0.00163954756566061
GO:0032330,"BP","GO:0032330","regulation of chondrocyte differentiation","11/1468","51/18800",
GO:0043277,"BP","GO:0043277","apoptotic cell clearance","11/1468","51/18800",0.0016395475656
GO:0035148,"BP","GO:0035148","tube formation","23/1468","152/18800",0.00163976560366194,
GO:0032052,"MF","GO:0032052","bile acid binding","5/1495","11/18410",0.00106874236598296,0.
GO:0048407,"MF","GO:0048407","platelet-derived growth factor binding","5/1495","11/18410",0.0
GO:0005544,"MF","GO:0005544","calcium-dependent phospholipid binding","12/1495","54/18410"
GO:0001846,"MF","GO:0001846","opsonin binding","6/1495","16/18410",0.00111477747539847,0.
GO:0008191,"MF","GO:0008191","metalloendopeptidase inhibitor activity","6/1495","16/18410",0.
GO:0019841,"MF","GO:0019841","retinol binding","6/1495","16/18410",0.00111477747539847,0.0
GO:0031069,"BP","GO:0031069","hair follicle morphogenesis","8/1468","30/18800",0.00167367862
GO:0042744,"BP","GO:0042744","hydrogen peroxide catabolic process","8/1468","30/18800",0.001
GO:0060603,"BP","GO:0060603","mammary gland duct morphogenesis","8/1468","30/18800",0.001
GO:0061037,"BP","GO:0061037","negative regulation of cartilage development","8/1468","30/1880
GO:2001257,"BP","GO:2001257","regulation of cation channel activity","26/1468","180/18800",0.00
GO:0006805,"BP","GO:0006805","xenobiotic metabolic process","18/1468","108/18800",0.0017012
GO:0060047,"BP","GO:0060047","heart contraction","33/1468","247/18800",0.0017042780094060.
GO:0048286,"BP","GO:0048286","lung alveolus development","10/1468","44/18800",0.0017384134
GO:0051353,"BP","GO:0051353","positive regulation of oxidoreductase activity","12/1468","59/188
GO:0060395,"BP","GO:0060395","SMAD protein signal transduction","15/1468","83/18800",0.00176
GO:0003176,"BP","GO:0003176","aortic valve development","9/1468","37/18800",0.001765896049
GO:0008210,"BP","GO:0008210","estrogen metabolic process","9/1468","37/18800",0.0017658960.
GO:0014037,"BP","GO:0014037","Schwann cell differentiation","9/1468","37/18800",0.0017658960
GO:0045762,"BP","GO:0045762","positive regulation of adenylate cyclase activity","9/1468","37/188
GO:0055023,"BP","GO:0055023","positive regulation of cardiac muscle tissue growth","9/1468","37/
GO:0035051,"BP","GO:0035051","cardiocyte differentiation","23/1468","153/18800",0.0017906386
GO:0002827,"BP","GO:0002827","positive regulation of T-helper 1 type immune response","6/1468"
GO:0010759,"BP","GO:0010759","positive regulation of macrophage chemotaxis","6/1468","18/188
GO:0030730,"BP","GO:0030730","sequestering of triglyceride","6/1468","18/18800",0.00183423158
GO:0003081,"BP","GO:0003081","regulation of systemic arterial blood pressure by renin-angiotensin
GO:0022010,"BP","GO:0022010","central nervous system myelination","7/1468","24/18800",0.0018
GO:0032291,"BP","GO:0032291","axon ensheathment in central nervous system","7/1468","24/188
GO:0043567,"BP","GO:0043567","regulation of insulin-like growth factor receptor signaling pathway
GO:0048745,"BP","GO:0048745","smooth muscle tissue development","7/1468","24/18800",0.0018
GO:0051043,"BP","GO:0051043","regulation of membrane protein ectodomain proteolysis","7/1468
GO:0007044,"BP","GO:0007044","cell-substrate junction assembly","16/1468","92/18800",0.001913
GO:0005614,"CC","GO:0005614","interstitial matrix","5/1537","11/19594",0.000912177444294146,
GO:0072175,"BP","GO:0072175","epithelial tube formation","21/1468","136/18800",0.0019832731.
GO:0031526,"CC","GO:0031526","brush border membrane","12/1537","55/19594",0.000957337519
GO:0043542,"BP","GO:0043542","endothelial cell migration","36/1468","279/18800",0.0020004772
GO:0031349,"BP","GO:0031349","positive regulation of defense response","37/1468","289/18800",
GO:0008344,"BP","GO:0008344","adult locomotory behavior","14/1468","76/18800",0.0020553419
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GO:0002920,"BP","GO:0002920","regulation of humoral immune response","10/1468","45/18800",
GO:0010171,"BP","GO:0010171","body morphogenesis","10/1468","45/18800",0.002081253855498

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GO:0007159,"BP","GO:0007159","leukocyte cell-cell adhesion","46/1468","381/18800",0.00208978,
GO:0071295,"BP","GO:0071295","cellular response to vitamin","8/1468","31/18800",0.0021034896,
GO:0002020,"MF","GO:0002020","protease binding","22/1495","136/18410",0.0013979461581209,
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GO:0034109,"BP","GO:0034109","homotypic cell-cell adhesion","16/1468","93/18800",0.002146894,
GO:0051897,"BP","GO:0051897","positive regulation of protein kinase B signaling","19/1468","119/1468",
GO:0001990,"BP","GO:0001990","regulation of systemic arterial blood pressure by hormone","9/1468",
GO:0032965,"BP","GO:0032965","regulation of collagen biosynthetic process","9/1468","38/18800",
GO:1901186,"BP","GO:1901186","positive regulation of ERBB signaling pathway","9/1468","38/18800",
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GO:0051451,"BP","GO:0051451","myoblast migration","5/1468","13/18800",0.00217950600883614,
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GO:0010634,"BP","GO:0010634","positive regulation of epithelial cell migration","25/1468","174/18800",
GO:0032982,"CC","GO:0032982","myosin filament","7/1537","22/19594",0.00107394141397904,0.00107394141397904,
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GO:0032677,"BP","GO:0032677","regulation of interleukin-8 production","17/1468","102/18800",0.00217950600883614,
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GO:0001938,"BP","GO:0001938","positive regulation of endothelial cell proliferation","18/1468","11/1468",
GO:0014066,"BP","GO:0014066","regulation of phosphatidylinositol 3-kinase signaling","18/1468","11/1468",
GO:0031532,"BP","GO:0031532","actin cytoskeleton reorganization","18/1468","111/18800",0.00217950600883614,
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GO:0062197,"BP","GO:0062197","cellular response to chemical stress","41/1468","332/18800",0.00217950600883614,
GO:0034113,"BP","GO:0034113","heterotypic cell-cell adhesion","12/1468","61/18800",0.00236360,
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GO:0034764,"BP","GO:0034764","positive regulation of transmembrane transport","29/1468","213/1468",
GO:0030203,"BP","GO:0030203","glycosaminoglycan metabolic process","19/1468","120/18800",0.00217950600883614,
GO:0042552,"BP","GO:0042552","myelination","21/1468","138/18800",0.00238011339266284,0.011339266284,
GO:0032612,"BP","GO:0032612","interleukin-1 production","20/1468","129/18800",0.00238653316,
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GO:0031253,"CC","GO:0031253","cell projection membrane","43/1537","339/19594",0.0012117985,
GO:0043025,"CC","GO:0043025","neuronal cell body","57/1537","482/19594",0.0012183181415086,
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GO:0032967,"BP","GO:0032967","positive regulation of collagen biosynthetic process","7/1468","25/1468",
GO:0001894,"BP","GO:0001894","tissue homeostasis","35/1468","272/18800",0.002398409257424,
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GO:0070888,"MF","GO:0070888","E-box binding","11/1495","49/18410",0.00159171461911987,0.00159171461911987,
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GO:0021517,"BP","GO:0021517","ventral spinal cord development","10/1468","46/18800",0.002476489114,
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GO:0009799,"BP","GO:0009799","specification of symmetry","21/1468","139/18800",0.0026024196,
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 GO:0045216,"BP","GO:0045216","cell-cell junction organization","28/1468","205/18800",0.0026602
 GO:0008106,"MF","GO:0008106","alcohol dehydrogenase (NADP+) activity","7/1495","23/18410",0.
 GO:0003143,"BP","GO:0003143","embryonic heart tube morphogenesis","13/1468","70/18800",0.0
 GO:0002444,"BP","GO:0002444","myeloid leukocyte mediated immunity","17/1468","104/18800",0
 GO:0007043,"BP","GO:0007043","cell-cell junction assembly","22/1468","149/18800",0.002795990.
 GO:0015248,"MF","GO:0015248","sterol transporter activity","9/1495","36/18410",0.00188586442.
 GO:0015485,"MF","GO:0015485","cholesterol binding","11/1495","50/18410",0.0018934302143705
 GO:0048844,"BP","GO:0048844","artery morphogenesis","14/1468","79/18800",0.00298976499360
 GO:0030316,"BP","GO:0030316","osteoclast differentiation","16/1468","96/18800",0.00299477619
 GO:0031225,"CC","GO:0031225","anchored component of membrane","25/1537","169/19594",0.00
 GO:0001540,"MF","GO:0001540","amyloid-beta binding","15/1495","81/18410",0.00201592135844
 GO:0016614,"MF","GO:0016614","oxidoreductase activity, acting on CH-OH group of donors","22/14
 GO:0044403,"BP","GO:0044403","biological process involved in symbiotic interaction","36/1468","2
 GO:0010714,"BP","GO:0010714","positive regulation of collagen metabolic process","7/1468","26/1
 GO:0034377,"BP","GO:0034377","plasma lipoprotein particle assembly","7/1468","26/18800",0.003
 GO:0050995,"BP","GO:0050995","negative regulation of lipid catabolic process","7/1468","26/1880
 GO:0071549,"BP","GO:0071549","cellular response to dexamethasone stimulus","7/1468","26/1880
 GO:0090382,"BP","GO:0090382","phagosome maturation","7/1468","26/18800",0.00305857690568
 GO:1903901,"BP","GO:1903901","negative regulation of viral life cycle","7/1468","26/18800",0.0030
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 GO:0003179,"BP","GO:0003179","heart valve morphogenesis","11/1468","55/18800",0.0030910608
 GO:0010883,"BP","GO:0010883","regulation of lipid storage","11/1468","55/18800",0.00309106082
 GO:0061098,"BP","GO:0061098","positive regulation of protein tyrosine kinase activity","11/1468",
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 GO:0043200,"BP","GO:0043200","response to amino acid","18/1468","114/18800",0.003139835882
 GO:0010896,"BP","GO:0010896","regulation of triglyceride catabolic process","5/1468","14/18800",
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 GO:0004033,"MF","GO:0004033","aldo-keto reductase (NADP) activity","8/1495","30/18410",0.002
 GO:0033764,"MF","GO:0033764","steroid dehydrogenase activity, acting on the CH-OH group of dor
 GO:1903510,"BP","GO:1903510","mucopolysaccharide metabolic process","15/1468","88/18800",0.
 GO:0048167,"BP","GO:0048167","regulation of synaptic plasticity","27/1468","198/18800",0.003208
 GO:0008227,"MF","GO:0008227","G protein-coupled amine receptor activity","11/1495","51/18410
 GO:0043395,"MF","GO:0043395","heparan sulfate proteoglycan binding","6/1495","18/18410",0.00
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 GO:0051004,"BP","GO:0051004","regulation of lipoprotein lipase activity","6/1468","20/18800",0.00
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 GO:0005540,"MF","GO:0005540","hyaluronic acid binding","7/1495","24/18410",0.0023150178405.
 GO:0006937,"BP","GO:0006937","regulation of muscle contraction","24/1468","170/18800",0.00330

GO:0045598,"BP","GO:0045598","regulation of fat cell differentiation","21/1468","142/18800",0.00
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GO:0051341,"BP","GO:0051341","regulation of oxidoreductase activity","17/1468","106/18800",0.0
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GO:0001736,"BP","GO:0001736","establishment of planar polarity","13/1468","72/18800",0.003508
GO:0007164,"BP","GO:0007164","establishment of tissue polarity","13/1468","72/18800",0.003508
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GO:0044305,"CC","GO:0044305","calyx of Held","6/1537","18/19594",0.00187846763130038,0.019
GO:0031233,"CC","GO:0031233","intrinsic component of external side of plasma membrane","7/153
GO:0022836,"MF","GO:0022836","gated channel activity","43/1495","340/18410",0.002463083034
GO:0005506,"MF","GO:0005506","iron ion binding","23/1495","151/18410",0.00248263316904995
GO:0044070,"BP","GO:0044070","regulation of anion transport","15/1468","89/18800",0.00356915
GO:0001947,"BP","GO:0001947","heart looping","12/1468","64/18800",0.00358883779069591,0.01
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GO:0015250,"MF","GO:0015250","water channel activity","5/1495","13/18410",0.00259418290293
GO:0031994,"MF","GO:0031994","insulin-like growth factor I binding","5/1495","13/18410",0.00259
GO:0004601,"MF","GO:0004601","peroxidase activity","11/1495","52/18410",0.0026364471476491
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GO:0042632,"BP","GO:0042632","cholesterol homeostasis","16/1468","98/18800",0.003700903628
GO:0150115,"BP","GO:0150115","cell-substrate junction organization","16/1468","98/18800",0.003
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GO:0046209,"BP","GO:0046209","nitric oxide metabolic process","14/1468","81/18800",0.00378739
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GO:0007263,"BP","GO:0007263","nitric oxide mediated signal transduction","7/1468","27/18800",0
GO:0010758,"BP","GO:0010758","regulation of macrophage chemotaxis","7/1468","27/18800",0.00
GO:0010884,"BP","GO:0010884","positive regulation of lipid storage","7/1468","27/18800",0.00385
GO:0035640,"BP","GO:0035640","exploration behavior","7/1468","27/18800",0.0038548895742578
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GO:0008188,"MF","GO:0008188","neuropeptide receptor activity","10/1495","45/18410",0.0027774
GO:0008395,"MF","GO:0008395","steroid hydroxylase activity","9/1495","38/18410",0.0028186837
GO:0032934,"MF","GO:0032934","sterol binding","12/1495","60/18410",0.00282942994292511,0.0
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GO:0034405,"BP","GO:0034405","response to fluid shear stress","8/1468","34/18800",0.003927239
GO:0002443,"BP","GO:0002443","leukocyte mediated immunity","52/1468","457/18800",0.0039354
GO:0003281,"BP","GO:0003281","ventricular septum development","13/1468","73/18800",0.00397
GO:0019226,"BP","GO:0019226","transmission of nerve impulse","13/1468","73/18800",0.00397051
GO:0042058,"BP","GO:0042058","regulation of epidermal growth factor receptor signaling pathway"
GO:0014065,"BP","GO:0014065","phosphatidylinositol 3-kinase signaling","21/1468","144/18800",0
GO:0033135,"BP","GO:0033135","regulation of peptidyl-serine phosphorylation","21/1468","144/18
GO:0042304,"BP","GO:0042304","regulation of fatty acid biosynthetic process","10/1468","49/1880
GO:0007219,"BP","GO:0007219","Notch signaling pathway","25/1468","182/18800",0.00404802068

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GO:0045682,"BP","GO:0045682","regulation of epidermis development","12/1468","65/18800",0.00
GO:0055092,"BP","GO:0055092","sterol homeostasis","16/1468","99/18800",0.0041021583078386
GO:0042306,"BP","GO:0042306","regulation of protein import into nucleus","11/1468","57/18800",
GO:0090175,"BP","GO:0090175","regulation of establishment of planar polarity","11/1468","57/188
GO:0070696,"MF","GO:0070696","transmembrane receptor protein serine/threonine kinase binding
GO:0007173,"BP","GO:0007173","epidermal growth factor receptor signaling pathway","17/1468",
GO:2001057,"BP","GO:2001057","reactive nitrogen species metabolic process","14/1468","82/1880
GO:0006067,"BP","GO:0006067","ethanol metabolic process","6/1468","21/18800",0.00437808093
GO:0033630,"BP","GO:0033630","positive regulation of cell adhesion mediated by integrin","6/1468
GO:0060065,"BP","GO:0060065","uterus development","6/1468","21/18800",0.0043780809303576
GO:0071498,"BP","GO:0071498","cellular response to fluid shear stress","6/1468","21/18800",0.004
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GO:0150146,"BP","GO:0150146","cell junction disassembly","6/1468","21/18800",0.0043780809303
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GO:0021924,"BP","GO:0021924","cell proliferation in external granule layer","5/1468","15/18800",C
GO:0021930,"BP","GO:0021930","cerebellar granule cell precursor proliferation","5/1468","15/1880
GO:0032905,"BP","GO:0032905","transforming growth factor beta1 production","5/1468","15/1880
GO:0034116,"BP","GO:0034116","positive regulation of heterotypic cell-cell adhesion","5/1468","15
GO:0045187,"BP","GO:0045187","regulation of circadian sleep/wake cycle, sleep","5/1468","15/188
GO:0055091,"BP","GO:0055091","phospholipid homeostasis","5/1468","15/18800",0.00445787131
GO:0061307,"BP","GO:0061307","cardiac neural crest cell differentiation involved in heart developm
GO:0061308,"BP","GO:0061308","cardiac neural crest cell development involved in heart developm
GO:0072498,"BP","GO:0072498","embryonic skeletal joint development","5/1468","15/18800",0.00
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GO:0007189,"BP","GO:0007189","adenylate cyclase-activating G protein-coupled receptor signaling
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GO:0009408,"BP","GO:0009408","response to heat","17/1468","109/18800",0.00458186829674543
GO:0031669,"BP","GO:0031669","cellular response to nutrient levels","28/1468","213/18800",0.004
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GO:0015909,"BP","GO:0015909","long-chain fatty acid transport","12/1468","66/18800",0.0046580
GO:1901617,"BP","GO:1901617","organic hydroxy compound biosynthetic process","31/1468","243
GO:0021872,"BP","GO:0021872","forebrain generation of neurons","10/1468","50/18800",0.004696
GO:0030857,"BP","GO:0030857","negative regulation of epithelial cell differentiation","10/1468","5
GO:0031281,"BP","GO:0031281","positive regulation of cyclase activity","10/1468","50/18800",0.00
GO:2001238,"BP","GO:2001238","positive regulation of extrinsic apoptotic signaling pathway","10/1
GO:0042692,"BP","GO:0042692","muscle cell differentiation","45/1468","387/18800",0.004715623
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GO:0090025,"BP","GO:0090025","regulation of monocyte chemotaxis","7/1468","28/18800",0.0047
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GO:0070851,"MF","GO:0070851","growth factor receptor binding","21/1495","139/18410",0.00411
GO:0140375,"MF","GO:0140375","immune receptor activity","22/1495","148/18410",0.0041183514
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GO:2000243,"BP","GO:2000243","positive regulation of reproductive process","14/1468","85/18800
GO:0008209,"BP","GO:0008209","androgen metabolic process","7/1468","29/18800",0.0059071656
GO:0065005,"BP","GO:0065005","protein-lipid complex assembly","7/1468","29/18800",0.00590716
GO:0097421,"BP","GO:0097421","liver regeneration","7/1468","29/18800",0.00590716566792287,
GO:0030170,"MF","GO:0030170","pyridoxal phosphate binding","11/1495","55/18410",0.00417496
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GO:0072109,"BP","GO:0072109","glomerular mesangium development","5/1468","16/18800",0.006
GO:0072176,"BP","GO:0072176","nephric duct development","5/1468","16/18800",0.00607225146
GO:1903975,"BP","GO:1903975","regulation of glial cell migration","5/1468","16/18800",0.0060722
GO:2000095,"BP","GO:2000095","regulation of Wnt signaling pathway, planar cell polarity pathway"
GO:0044853,"CC","GO:0044853","plasma membrane raft","18/1537","113/19594",0.002993369334
GO:0042383,"CC","GO:0042383","sarcolemma","20/1537","131/19594",0.00302713503060421,0.02
GO:0006509,"BP","GO:0006509","membrane protein ectodomain proteolysis","9/1468","44/18800"
GO:0045840,"BP","GO:0045840","positive regulation of mitotic nuclear division","9/1468","44/1880
GO:0008076,"CC","GO:0008076","voltage-gated potassium channel complex","14/1537","79/19594"
GO:0046888,"BP","GO:0046888","negative regulation of hormone secretion","11/1468","60/18800"
GO:0055008,"BP","GO:0055008","cardiac muscle tissue morphogenesis","11/1468","60/18800",0.00
GO:0005216,"MF","GO:0005216","ion channel activity","52/1495","442/18410",0.00436767758802:
GO:0006636,"BP","GO:0006636","unsaturated fatty acid biosynthetic process","10/1468","52/18800
GO:0031103,"BP","GO:0031103","axon regeneration","10/1468","52/18800",0.0062766284861051,
GO:0070169,"BP","GO:0070169","positive regulation of biomineral tissue development","10/1468",
GO:0099172,"BP","GO:0099172","presynapse organization","10/1468","52/18800",0.006276628486
GO:0098657,"BP","GO:0098657","import into cell","30/1468","238/18800",0.00630689341614695,
GO:0051339,"BP","GO:0051339","regulation of lyase activity","13/1468","77/18800",0.0063327490:
GO:0046887,"BP","GO:0046887","positive regulation of hormone secretion","18/1468","122/18800"
GO:0019915,"BP","GO:0019915","lipid storage","14/1468","86/18800",0.00655544313282786,0.030
GO:0005667,"CC","GO:0005667","transcription regulator complex","55/1537","483/19594",0.00335
GO:0032868,"BP","GO:0032868","response to insulin","32/1468","259/18800",0.006592788097485:
GO:0015833,"BP","GO:0015833","peptide transport","31/1468","249/18800",0.0066485572536167,
GO:0044242,"BP","GO:0044242","cellular lipid catabolic process","28/1468","219/18800",0.006717:
GO:0050922,"BP","GO:0050922","negative regulation of chemotaxis","12/1468","69/18800",0.0067
GO:0070527,"BP","GO:0070527","platelet aggregation","12/1468","69/18800",0.006723263195767:
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GO:0003161,"BP","GO:0003161","cardiac conduction system development","8/1468","37/18800",0.
GO:0003203,"BP","GO:0003203","endocardial cushion morphogenesis","8/1468","37/18800",0.0067
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GO:0016684,"MF","GO:0016684","oxidoreductase activity, acting on peroxide as acceptor","11/1495
GO:0070279,"MF","GO:0070279","vitamin B6 binding","11/1495","56/18410",0.0048225490736594

GO:0004896,"MF","GO:0004896","cytokine receptor activity","16/1495","97/18410",0.00487666846
GO:0098631,"MF","GO:0098631","cell adhesion mediator activity","12/1495","64/18410",0.0049184
GO:0004993,"MF","GO:0004993","G protein-coupled serotonin receptor activity","8/1495","34/18410",0.0049859
GO:0016229,"MF","GO:0016229","steroid dehydrogenase activity","8/1495","34/18410",0.0049859
GO:0099589,"MF","GO:0099589","serotonin receptor activity","8/1495","34/18410",0.00498590097
GO:1904589,"BP","GO:1904589","regulation of protein import","11/1468","61/18800",0.007033972
GO:0031279,"BP","GO:0031279","regulation of cyclase activity","13/1468","78/18800",0.007070111
GO:0001952,"BP","GO:0001952","regulation of cell-matrix adhesion","18/1468","123/18800",0.007070111
GO:0002689,"BP","GO:0002689","negative regulation of leukocyte chemotaxis","6/1468","23/18800",0.007119675
GO:0010640,"BP","GO:0010640","regulation of platelet-derived growth factor receptor signaling pathway","6/1468","23/18800",0.007119675
GO:0016338,"BP","GO:0016338","calcium-independent cell-cell adhesion via plasma membrane cell-cell contact","6/1468","23/18800",0.007119675
GO:0036303,"BP","GO:0036303","lymph vessel morphogenesis","6/1468","23/18800",0.007119675
GO:0060444,"BP","GO:0060444","branching involved in mammary gland duct morphogenesis","6/1468","23/18800",0.007119675
GO:0072576,"BP","GO:0072576","liver morphogenesis","6/1468","23/18800",0.0071196751576544
GO:0001754,"BP","GO:0001754","eye photoreceptor cell differentiation","9/1468","45/18800",0.0071618246
GO:0042088,"BP","GO:0042088","T-helper 1 type immune response","9/1468","45/18800",0.0071618246
GO:1902622,"BP","GO:1902622","regulation of neutrophil migration","9/1468","45/18800",0.0071618246
GO:0021522,"BP","GO:0021522","spinal cord motor neuron differentiation","7/1468","30/18800",0.007195618246
GO:0034698,"BP","GO:0034698","response to gonadotropin","7/1468","30/18800",0.007195618246
GO:0051873,"BP","GO:0051873","killing by host of symbiont cells","7/1468","30/18800",0.007195618246
GO:0060045,"BP","GO:0060045","positive regulation of cardiac muscle cell proliferation","7/1468","30/18800",0.007195618246
GO:0010718,"BP","GO:0010718","positive regulation of epithelial to mesenchymal transition","10/1468","53/18800",0.00776294938410035
GO:0048260,"BP","GO:0048260","positive regulation of receptor-mediated endocytosis","10/1468","53/18800",0.00776294938410035
GO:0110151,"BP","GO:0110151","positive regulation of biomineralization","10/1468","53/18800",0.00776294938410035
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GO:0030017,"CC","GO:0030017","sarcomere","28/1537","209/19594",0.0037529267932769,0.0339
GO:0050804,"BP","GO:0050804","modulation of chemical synaptic transmission","48/1468","429/18800",0.00782079564023308
GO:1901343,"BP","GO:1901343","negative regulation of vasculature development","21/1468","152/18800",0.00782079564023308
GO:0032890,"BP","GO:0032890","regulation of organic acid transport","12/1468","70/18800",0.00782079564023308
GO:0071260,"BP","GO:0071260","cellular response to mechanical stimulus","12/1468","70/18800",0.00782079564023308
GO:0072593,"BP","GO:0072593","reactive oxygen species metabolic process","29/1468","231/18800",0.00782079564023308
GO:0050953,"BP","GO:0050953","sensory perception of light stimulus","28/1468","221/18800",0.00782079564023308
GO:0099177,"BP","GO:0099177","regulation of trans-synaptic signaling","48/1468","430/18800",0.00782079564023308
GO:0016049,"BP","GO:0016049","cell growth","53/1468","484/18800",0.00776294938410035,0.0339
GO:0046165,"BP","GO:0046165","alcohol biosynthetic process","20/1468","143/18800",0.00778535
GO:0001660,"BP","GO:0001660","fever generation","4/1468","11/18800",0.00782079564023308,0.0339
GO:0005984,"BP","GO:0005984","disaccharide metabolic process","4/1468","11/18800",0.00782079564023308
GO:0007494,"BP","GO:0007494","midgut development","4/1468","11/18800",0.00782079564023308
GO:0016102,"BP","GO:0016102","diterpenoid biosynthetic process","4/1468","11/18800",0.00782079564023308
GO:0032276,"BP","GO:0032276","regulation of gonadotropin secretion","4/1468","11/18800",0.00782079564023308
GO:0032836,"BP","GO:0032836","glomerular basement membrane development","4/1468","11/18800",0.00782079564023308
GO:0035581,"BP","GO:0035581","sequestering of extracellular ligand from receptor","4/1468","11/18800",0.00782079564023308
GO:0042670,"BP","GO:0042670","retinal cone cell differentiation","4/1468","11/18800",0.00782079564023308
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GO:0060174,"BP","GO:0060174","limb bud formation","4/1468","11/18800",0.00782079564023308
GO:0060601,"BP","GO:0060601","lateral sprouting from an epithelium","4/1468","11/18800",0.00782079564023308
GO:0060923,"BP","GO:0060923","cardiac muscle cell fate commitment","4/1468","11/18800",0.00782079564023308
GO:0061365,"BP","GO:0061365","positive regulation of triglyceride lipase activity","4/1468","11/18800",0.00782079564023308
GO:0098883,"BP","GO:0098883","synapse pruning","4/1468","11/18800",0.00782079564023308,0.0339
GO:1903977,"BP","GO:1903977","positive regulation of glial cell migration","4/1468","11/18800",0.00782079564023308

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GO:0006970,"BP","GO:0006970","response to osmotic stress","13/1468","79/18800",0.0078738164
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GO:1901184,"BP","GO:1901184","regulation of ERBB signaling pathway","13/1468","79/18800",0.00
GO:0032640,"BP","GO:0032640","tumor necrosis factor production","24/1468","182/18800",0.0079
GO:0032680,"BP","GO:0032680","regulation of tumor necrosis factor production","24/1468","182/1
GO:0043030,"BP","GO:0043030","regulation of macrophage activation","11/1468","62/18800",0.00
GO:0046530,"BP","GO:0046530","photoreceptor cell differentiation","11/1468","62/18800",0.0079
GO:1902105,"BP","GO:1902105","regulation of leukocyte differentiation","34/1468","283/18800",0.
GO:0002385,"BP","GO:0002385","mucosal immune response","8/1468","38/18800",0.00801279917
GO:0002701,"BP","GO:0002701","negative regulation of production of molecular mediator of immu
GO:0032371,"BP","GO:0032371","regulation of sterol transport","8/1468","38/18800",0.008012799
GO:0032374,"BP","GO:0032374","regulation of cholesterol transport","8/1468","38/18800",0.00801
GO:1903707,"BP","GO:1903707","negative regulation of hemopoiesis","16/1468","106/18800",0.00
GO:0046849,"BP","GO:0046849","bone remodeling","14/1468","88/18800",0.00803679772194826,
GO:0007379,"BP","GO:0007379","segment specification","5/1468","17/18800",0.008057109394175
GO:0016114,"BP","GO:0016114","terpenoid biosynthetic process","5/1468","17/18800",0.00805710
GO:0016202,"BP","GO:0016202","regulation of striated muscle tissue development","5/1468","17/1
GO:0035930,"BP","GO:0035930","corticosteroid hormone secretion","5/1468","17/18800",0.00805
GO:0048557,"BP","GO:0048557","embryonic digestive tract morphogenesis","5/1468","17/18800",C
GO:0050802,"BP","GO:0050802","circadian sleep/wake cycle, sleep","5/1468","17/18800",0.008057
GO:0051412,"BP","GO:0051412","response to corticosterone","5/1468","17/18800",0.00805710939
GO:0051580,"BP","GO:0051580","regulation of neurotransmitter uptake","5/1468","17/18800",0.00
GO:0061450,"BP","GO:0061450","trophoblast cell migration","5/1468","17/18800",0.008057109394
GO:0032755,"BP","GO:0032755","positive regulation of interleukin-6 production","15/1468","97/18
GO:0034767,"BP","GO:0034767","positive regulation of ion transmembrane transport","22/1468","1
GO:0014888,"BP","GO:0014888","striated muscle adaptation","10/1468","54/18800",0.0082420807
GO:0021545,"BP","GO:0021545","cranial nerve development","10/1468","54/18800",0.0082420807
GO:0061900,"BP","GO:0061900","glial cell activation","10/1468","54/18800",0.00824208076015417
GO:0051051,"BP","GO:0051051","negative regulation of transport","51/1468","464/18800",0.00829
GO:0032309,"BP","GO:0032309","icosanoid secretion","9/1468","46/18800",0.00830157286348697
GO:0034599,"BP","GO:0034599","cellular response to oxidative stress","34/1468","284/18800",0.00
GO:0014704,"CC","GO:0014704","intercalated disc","10/1537","49/19594",0.00416901878302496,C
GO:0014044,"BP","GO:0014044","Schwann cell development","7/1468","31/18800",0.00868082240
GO:0008330,"MF","GO:0008330","protein tyrosine/threonine phosphatase activity","4/1495","10/1
GO:0071723,"MF","GO:0071723","lipopeptide binding","4/1495","10/18410",0.0061050298773141.
GO:0051781,"BP","GO:0051781","positive regulation of cell division","14/1468","89/18800",0.00887
GO:0016048,"BP","GO:0016048","detection of temperature stimulus","6/1468","24/18800",0.00887
GO:0043501,"BP","GO:0043501","skeletal muscle adaptation","6/1468","24/18800",0.00887726119
GO:0071676,"BP","GO:0071676","negative regulation of mononuclear cell migration","6/1468","24/
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GO:2001026,"BP","GO:2001026","regulation of endothelial cell chemotaxis","6/1468","24/18800",0.
GO:0042827,"CC","GO:0042827","platelet dense granule","6/1537","21/19594",0.00447933851824!
GO:0051893,"BP","GO:0051893","regulation of focal adhesion assembly","11/1468","63/18800",0.0
GO:0090109,"BP","GO:0090109","regulation of cell-substrate junction assembly","11/1468","63/188
GO:0006865,"BP","GO:0006865","amino acid transport","20/1468","145/18800",0.00904683639692
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GO:0001954,"BP","GO:0001954","positive regulation of cell-matrix adhesion","10/1468","55/18800'

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GO:0030534,"BP","GO:0030534","adult behavior","19/1468","136/18800",0.00943644529937727,0
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GO:0055010,"BP","GO:0055010","ventricular cardiac muscle tissue morphogenesis","9/1468","47/1
GO:0060711,"BP","GO:0060711","labyrinthine layer development","9/1468","47/18800",0.0095738
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GO:0031016,"BP","GO:0031016","pancreas development","13/1468","81/18800",0.0096961329282
GO:0014897,"BP","GO:0014897","striated muscle hypertrophy","15/1468","99/18800",0.009716183
GO:0061097,"BP","GO:0061097","regulation of protein tyrosine kinase activity","14/1468","90/1880
GO:0016709,"MF","GO:0016709","oxidoreductase activity, acting on paired donors, with incorporati
GO:0004602,"MF","GO:0004602","glutathione peroxidase activity","6/1495","22/18410",0.0068104
GO:0007009,"BP","GO:0007009","plasma membrane organization","21/1468","156/18800",0.00996
GO:0001558,"BP","GO:0001558","regulation of cell growth","46/1468","415/18800",0.01015344870
GO:0009743,"BP","GO:0009743","response to carbohydrate","28/1468","226/18800",0.0101679863
GO:0050866,"BP","GO:0050866","negative regulation of cell activation","27/1468","216/18800",0.0
GO:0005372,"MF","GO:0005372","water transmembrane transporter activity","5/1495","16/18410"
GO:0042805,"MF","GO:0042805","actinin binding","8/1495","36/18410",0.0071909981249651,0.04
GO:0034702,"CC","GO:0034702","ion channel complex","36/1537","294/19594",0.00515849846463
GO:0032770,"BP","GO:0032770","positive regulation of monooxygenase activity","7/1468","32/1880
GO:0051385,"BP","GO:0051385","response to mineralocorticoid","7/1468","32/18800",0.010379111
GO:0072337,"BP","GO:0072337","modified amino acid transport","7/1468","32/18800",0.01037911
GO:0005520,"MF","GO:0005520","insulin-like growth factor binding","7/1495","29/18410",0.00730
GO:0032026,"BP","GO:0032026","response to magnesium ion","5/1468","18/18800",0.0104505239
GO:0060008,"BP","GO:0060008","Sertoli cell differentiation","5/1468","18/18800",0.010450523937
GO:0071071,"BP","GO:0071071","regulation of phospholipid biosynthetic process","5/1468","18/18
GO:0097094,"BP","GO:0097094","craniofacial suture morphogenesis","5/1468","18/18800",0.01045
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GO:0008589,"BP","GO:0008589","regulation of smoothened signaling pathway","13/1468","82/1880
GO:0006835,"BP","GO:0006835","dicarboxylic acid transport","14/1468","91/18800",0.0107424507
GO:0030216,"BP","GO:0030216","keratinocyte differentiation","22/1468","167/18800",0.01083362
GO:0051048,"BP","GO:0051048","negative regulation of secretion","22/1468","167/18800",0.01083
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GO:0003071,"BP","GO:0003071","renal system process involved in regulation of systemic arterial blo
GO:0031579,"BP","GO:0031579","membrane raft organization","6/1468","25/18800",0.0109245003
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GO:0045932,"BP","GO:0045932","negative regulation of muscle contraction","6/1468","25/18800",0
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GO:0007266,"BP","GO:0007266","Rho protein signal transduction","19/1468","138/18800",0.01096
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GO:1903555,"BP","GO:1903555","regulation of tumor necrosis factor superfamily cytokine producti
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GO:0048713,"BP","GO:0048713","regulation of oligodendrocyte differentiation","8/1468","40/1880
GO:0048483,"BP","GO:0048483","autonomic nervous system development","9/1468","48/18800",0
GO:0006705,"BP","GO:0006705","mineralocorticoid biosynthetic process","4/1468","12/18800",0.0
GO:0010642,"BP","GO:0010642","negative regulation of platelet-derived growth factor receptor sig
GO:0019627,"BP","GO:0019627","urea metabolic process","4/1468","12/18800",0.01101476109330
GO:0030656,"BP","GO:0030656","regulation of vitamin metabolic process","4/1468","12/18800",0.0
GO:0032490,"BP","GO:0032490","detection of molecule of bacterial origin","4/1468","12/18800",0.0
GO:0032908,"BP","GO:0032908","regulation of transforming growth factor beta1 production","4/14
GO:0033629,"BP","GO:0033629","negative regulation of cell adhesion mediated by integrin","4/146
GO:0034650,"BP","GO:0034650","cortisol metabolic process","4/1468","12/18800",0.011014761093
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GO:0045916,"BP","GO:0045916","negative regulation of complement activation","4/1468","12/1880
GO:0060736,"BP","GO:0060736","prostate gland growth","4/1468","12/18800",0.011014761093303
GO:0061309,"BP","GO:0061309","cardiac neural crest cell development involved in outflow tract me
GO:0061517,"BP","GO:0061517","macrophage proliferation","4/1468","12/18800",0.011014761093
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GO:1903800,"BP","GO:1903800","positive regulation of production of miRNAs involved in gene silen
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GO:0070613,"BP","GO:0070613","regulation of protein processing","11/1468","65/18800",0.011328
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GO:0016525,"BP","GO:0016525","negative regulation of angiogenesis","20/1468","149/18800",0.01

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1.80139318386679e-11,1.24988973219065e-09,8.58639774010457e-10,"HOXA11/ALX4/FOXC1/HES
6e-11,1.26243891516034e-09,8.6726071660371e-10,"CCL26/CXCL2/CTSG/SERPINE1/RARRES2/CXCL
9698e-11,1.33975842368593e-09,1.06626527271391e-09,"ITIH1/SPP2/MT3/TIMP3/SERPINA4/AVP/
57e-11,1.37727190598389e-09,1.09612089647841e-09,"IGF1/OSM/TIMP1/OGN/CXCL12/DKK1/CSF3
L,1.47583773307559e-09,1.17456587330868e-09,"IGF1/IBSP/ITGA8/FAP/CDH17/COL16A1/LTBP4/FE
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34934e-11,4.97835898059724e-09,3.41999531634758e-09,"CPS1/PTGS2/PLAT/AREG/GHR/BCHE/KL
4296796548e-11,5.15886980240736e-09,3.54400127243607e-09,"NR1H4/APOB/PLTP/LIPG/APOA4/
96034296796548e-11,5.15886980240736e-09,3.54400127243607e-09,"NR1H4/APOB/PLTP/LIPG/AP
69e-10,5.76812239615385e-09,3.96254100113109e-09,"HOXA11/SNAI2/COL11A1/FGFR3/PITX1/EPY
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419e-10,7.48434549412318e-09,5.14153893594022e-09,"CCL26/IGF1/MARCO/ROS1/FGFR2/FGFR3/
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713539e-10,1.04854781868307e-08,7.20323432448089e-09,"ATP1A2/CPS1/PTGS2/PGR/TSPO/PLAT
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587079e-10,1.47244181018043e-08,1.01152691359499e-08,"SOX8/SEMA3B/WWTR1/SNAI2/FOXC1/
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194e-07,2.08156648824487e-05,1.65664348140785e-05,"PRSS22/CPS1/MIPEP/TLL1/FAP/MMP2/CM

571832361777e-06,2.13814743704117e-05,1.46884831906279e-05,"NR1H4/SNAI2/TREM2/HMOX1/
L.17768143141226e-06,2.19024464151312e-05,1.50463766169221e-05,"TNMD/HSPB6/TBXA2R/STA
)",1.19321689169688e-06,2.20531047920362e-05,1.51498747666923e-05,"CD99/TREM2/SERPINE1,
3194827543e-06,2.20531047920362e-05,1.51498747666923e-05,"FOXC1/COL11A1/FGFR2/TGFBR3/
'10/1468","21/18800",1.29549911899665e-06,2.38477592925507e-05,1.6382752911909e-05,"SOX8
30312367261918e-06,2.39067976820847e-05,1.6423310657238e-05,"PTGS2/PGR/EPYC/COL16A1/M
)",1.30786276728779e-06,2.3912680055951e-05,1.6427351685848e-05,"PROM1/WWTR1/FOXC1/TI
e-06,2.40256757076818e-05,1.65049765821629e-05,"ATP1A2/RASGRF1/PTGS2/ITGA8/OPRK1/TREM
3","142/18800",1.38920678674974e-06,2.52294870130524e-05,1.73319617477926e-05,"WWTR1/SI
160479876969e-06,2.63103486921335e-05,2.09394549251905e-05,"TNNC1/CASQ2/MASP1/TNNT3/
.242e-06,2.72960510091027e-05,1.87516342171686e-05,"PDK4/TBXA2R/MYH13/HFE/NR1H4/CYP24
1e-06,2.75206944670996e-05,1.89059580771377e-05,"SLC7A2/ATP1A2/LRP2/SLCO1A2/SLC17A6/A
8","190/18800",1.53517063059353e-06,2.75563409035484e-05,1.8930446195848e-05,"CRLF1/IGF1
4268235114269e-06,2.75563409035484e-05,1.8930446195848e-05,"WWTR1/SNAI2/DKK3/FGFR2/FI
39379e-06,2.75563409035484e-05,1.8930446195848e-05,"TNMD/HSPB6/TBXA2R/STAB1/DCN/FOXC
5,2.76315080548326e-05,1.89820839556675e-05,"PDK4/IL20RA/FOXC1/SPP2/SEMA3C/MMP2/CST3
1428e-06,2.7762128989911e-05,1.90718169355362e-05,"SNAI2/FGFR2/FERMT1/AREG/KLF9/EREG/Z
556724699e-06,3.00055580682766e-05,2.06129908385173e-05,"APOH/SERPINE1/HRG/PLG/THBS1/
599948e-06,3.00055580682766e-05,2.06129908385173e-05,"CPS1/APOB/LIPG/APOA4/APOC3/AAD
763338599948e-06,3.00055580682766e-05,2.06129908385173e-05,"HOXA11/ALX4/HOXA13/MSX2/I
382748534334e-06,3.07930140344456e-05,2.11539513692111e-05,"HSPB6/TBXA2R/CMA1/HMOX1,
18800",1.76382748534334e-06,3.07930140344456e-05,2.11539513692111e-05,"HSPB6/TBXA2R/CN
397583e-06,3.08330399082868e-05,2.11814480406249e-05,"CFTR/NR1H4/SNAI2/DKK3/RDH8/APO
78109085173928e-06,3.08950759282467e-05,2.12240650753817e-05,"CRLF1/CCL26/NR1H4/IL20RA
e-06,3.26714212083077e-05,2.24443652911158e-05,"CFTR/MSR1/APOB/TSPO/LIPG/APOA4/APOC3,
163e-06,3.26714212083077e-05,2.24443652911158e-05,"SOX8/VIM/LAMC3/MT3/TREM2/MAG/IFN
2947842e-06,3.46568552361019e-05,2.38083037098673e-05,"MGST1/PTGS2/MT3/PTGS1/SOD3/AP
0932558538e-06,3.57262103483168e-05,2.45429211791059e-05,"SOX8/USH1C/PROM1/PAX2/FAT1
800",2.16925122548461e-06,3.70346613007026e-05,2.54417908962698e-05,"CREB3L3/TNFRSF1A/
53/18800",2.24209969536655e-06,3.81579985890684e-05,2.62134926316936e-05,"TNFRSF12A/IGF
2/1468","252/18800",2.27735013677791e-06,3.86364230101631e-05,2.65421570140227e-05,"LTBP
3796225578e-06,3.86905226616509e-05,2.65793219825244e-05,"MT3/HMOX1/MMP9/MT1G/MT2/
761207e-06,3.95146451698334e-05,2.71454714163169e-05,"FOXC1/FGFR2/TGFBR3/SEMA3C/LRP2,
06,3.96969340293348e-05,2.72706988352609e-05,"ALX4/FOXC1/NGFR/FGFR2/FOSL2/DSP/FERMT1/
e-06,4.03883395710999e-05,2.77456753734634e-05,"MIPEP/TLL1/APOH/CMA1/TLL2/TSPAN15/CTSC
199122e-06,4.04435974655941e-05,2.77836360229662e-05,"IGF1/FOXC1/YBX3/FGFR2/TGFBR3/HAN
ucleotide second messenger","18/1468","67/18800",2.44059422001172e-06,4.06415259037028e-05
71219103e-06,4.24845770502389e-05,2.91857327073256e-05,"MT3/MT1G/MT2A/SNCA/AQP2/MT1
2.59800931480954e-06,4.299824590749e-05,2.95386090452513e-05,"HOXA11/SOX8/MYOC/TRPC5,
e-06,4.38425992841298e-05,3.01186565277058e-05,"FAP/APOH/SERPINE1/HRG/PLG/THBS1/THBD,
e-06,4.62232646100484e-05,3.17541079477751e-05,"COL11A1/MMP2/MMP9/DKK1/COL12A1/FN1/
832697062e-06,4.71399685623182e-05,3.2383858280256e-05,"CFTR/CPS1/PTGS2/AQP9/PLAT/AHR
5e-06,4.84896928189306e-05,3.33110816191043e-05,"SOX8/SEMA3B/SNAI2/FOXC1/SEMA3C/FOLR
)",3.02400804867124e-06,4.92949745765324e-05,3.38642879768765e-05,"CCL26/NR1H4/YBX3/TNF
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18511376402901e-06,5.16102864997755e-05,3.54548434117569e-05,"TNFRSF12A/IGF1/SNAI2/EYA
171e-06,5.21745559843724e-05,3.5842480985102e-05,"HOXA11/ALX4/HOXA13/MSX2/RDH10/RUN
3966389260507e-06,5.37924434130316e-05,3.69539250271964e-05,"PTGS2/PGR/EPYC/COL16A1/N
07e-06,5.5650442449224e-05,3.82303191213792e-05,"CYP24A1/CPS1/APOB/MT3/LIPG/SULT2A1/R/
1369e-06,5.63297660372179e-05,4.48308234407973e-05,"STAB1/MARCO/MSR1/LOXL4/ACKR3/ME

6,5.63297660372179e-05,4.48308234407973e-05,"CRLF1/IL20RA/LTBP1/TNFRSF1A/TGFBR3/LTBP4/
1.63408210898075e-06,5.76763999231783e-05,3.96220960300046e-05,"TBXA2R/APOH/SERPINE1/S
3999231783e-05,3.96220960300046e-05,"PTGS2/AFP/PGR/MMP2/PLAT/INHBA/MMP19/TNFAIP6/E
08210898075e-06,5.76763999231783e-05,3.96220960300046e-05,"FGFR2/WNT2/BMP5/RDH10/BV
210898075e-06,5.76763999231783e-05,3.96220960300046e-05,"TBXA2R/APOH/SERPINE1/ST3GAL4
-06,5.91211715088569e-05,4.06146142625127e-05,"FGFR2/WNT2/HOXA5/TCF21/RDH10/BMP4/SO
ain receptors", "15/1468", "50/18800", 3.74696264366924e-06,5.91211715088569e-05,4.0614614262
383504199e-06,5.96305461489746e-05,4.09645405917023e-05,"TBXA2R/FMO1/CPS1/CDH1/ACSM
1", 4.14921378225408e-06,6.50885362016206e-05,4.47140292263049e-05,"CFTR/CPS1/PTGS2/AQP9
1", 4.18362475576472e-06,6.54386623647359e-05,4.49545562438728e-05,"PDK4/MLXIPL/NR1H4/AC
800", 4.21841794650765e-06,6.57927317766553e-05,4.5197792164614e-05,"LTBP1/DKK3/FGFR2/TC
-06,6.76652127824698e-05,4.6484134972514e-05,"LOX/EMILIN1/FBLN5/MFAP4/TNXB/COL3A1/THS
29e-06,6.97733969826147e-05,4.79323993742162e-05,"MARCO/MSR1/LRP2/TREM2/IFNG/CLU/C3/
173521e-06,7.24582557944845e-05,4.97768233294666e-05,"PDK4/MLXIPL/CYP24A1/ACSM2B/TNFR
e-06,7.26250958841703e-05,4.98914378696249e-05,"PTGS2/MMP2/MMP9/TIMP1/SYDE1/CALCA/S
595e-06,7.27997499516464e-05,5.00114203970154e-05,"SOX8/PAX2/SALL1/BMP4/SOX9/LIF/OSR1/
reonine kinase signaling pathway", "27/1468", "135/18800", 4.80630053706157e-06,7.368753118010!
0170230207e-06,7.60432124657028e-05,5.22395896893574e-05,"WWTR1/SNAI2/DKK3/FGFR2/FER
115312267054e-06,7.71576357743463e-05,5.30051677665599e-05,"SOX8/YBX3/PITX1/TLL2/SIX4/N
7645e-06,8.03881913258043e-05,5.52244703315713e-05,"MT3/MT1G/MT2A/MT1E/MT1X/MT1F/N
327645e-06,8.03881913258043e-05,5.52244703315713e-05,"MT3/MT1G/MT2A/MT1E/MT1X/MT1F/
, 8.22531320132235e-05,6.54622928187035e-05,"PROM1/NR1H4/ATP1A2/PGR/SULT2B1/TSPO/CALI
1610917337716e-06,8.23305666098245e-05,5.65588285809118e-05,"HFE/SNAI2/MYOC/CDH1/ERBB
16e-06,8.24733308209832e-05,5.66569036565357e-05,"CCL26/CCL7/CCL2/CCL8/CCL20/PADI2/CH25
1075e-06,8.36816993178506e-05,5.74870194870363e-05,"WWTR1/SNAI2/MYOC/DKK3/FGFR2/GPC4
18800", 5.68327792134056e-06,8.4966574890318e-05,5.83696935684061e-05,"CRLF1/GPRC5A/IGF:
8800", 5.68327792134056e-06,8.4966574890318e-05,5.83696935684061e-05,"WWTR1/SNAI2/DKK3
56748825569258e-05,5.88562814002143e-05,"HOXA11/WNT2/DKK1/FGF1/HOXC11/BMP4/SIX1/GA
2023e-06,8.56748825569258e-05,5.88562814002143e-05,"HOXA13/BMP5/HOXD13/PDGFR/LHCGI
776452023e-06,8.56748825569258e-05,5.88562814002143e-05,"TBXA2R/APOH/SERPINE1/ST3GAL4
2023e-06,8.56748825569258e-05,5.88562814002143e-05,"MT3/TSPO/GLRA2/MT1G/MT2A/MT1E/N
12935774832e-06,8.84372318368771e-05,6.07539391698467e-05,"SLC11A1/FCGR2B/TREM2/CCL2/
657599308196e-06,8.87296830265953e-05,6.09548450713686e-05,"TBXA2R/APOH/FERMT1/SERPII
144968e-06,8.87296830265953e-05,6.09548450713686e-05,"SOX8/SEMA3B/HES2/TRPC5/SEMA3C/L
27237630207547e-05,6.36986678704839e-05,"ALX4/NGFR/FGFR2/PTGS2/FERMT1/FA2H/DKK1/MSX
37630207547e-05,6.36986678704839e-05,"ALX4/NGFR/FGFR2/PTGS2/FERMT1/FA2H/DKK1/MSX2/II
8800", 6.38375423724787e-06,9.28733277741545e-05,6.38014147310681e-05,"MLXIPL/NR1H4/PTG
3379473360399e-06,9.4075863534222e-05,6.46275236322543e-05,"PDK4/MLXIPL/NR1H4/CPS1/ACS
2e-06,9.44159720112856e-05,6.48611687757927e-05,"LRP2/HOXA13/BMP5/HOXD13/PDGFR/FOX
/18800", 6.5579366410744e-06,9.46441416039858e-05,6.50179149930521e-05,"CRLF1/ERBB3/MT3
-06,0.000101983132699429,7.00595994659787e-05,"CFTR/HFE/NR1H4/OPRK1/LTBP4/OSM/RETN/T
040930922e-06,0.000106208644590427,7.29624095953221e-05,"FOXC1/FGFR2/TGFBR3/WNT2/GLI:
06,0.000106208644590427,7.29624095953221e-05,"IGF1/CPQ/PLG/MYOD1/ANXA1/TEC/GATA4/YAI
266655e-06,0.00010623285129775,8.79742557607122e-05,"CFH/PLAUR/F3/PLAU/FCN3/MBL2/THBI
", "24/1468", "115/18800", 7.44608972514659e-06,0.000106327803674125,7.30442685994105e-05,"
3", "146/18800", 7.51893412165293e-06,0.000106893520304871,7.34329003222475e-05,"MLXIPL/N
102367993e-06,0.000106893520304871,7.34329003222475e-05,"OPRK1/RETN/INHBA/AGT/REN/AG
)", 7.68708147811675e-06,0.000108907028689968,7.48161250501746e-05,"PLAT/SGK1/KLF9/PCK1/
16715471767e-06,0.000109022368254131,7.48953601496848e-05,"PDK4/MLXIPL/NR1H4/CPS1/ACS
147556e-06,0.00011291792717889,7.75715016913369e-05,"LIPG/APOA4/APOC3/APOA1/CLU/APOE/

,8.04037976326796e-06,0.000113024766957938,7.7644897672898e-05,"HFE/CDH1/PTGS2/MT3/HM
161e-06,0.00011604098367818,7.97169553723363e-05,"CFH/C8B/C6/TREM2/C7/C9/CLU/C4BPA/C4I
-06,0.000116095496171194,7.97544039515809e-05,"CPS1/MT3/TSPO/GLRA2/HAMP/MT1G/MT2A/
2318043503758e-06,0.000116095496171194,7.97544039515809e-05,"NR1H4/MSR1/APOB/TREM2/I
206e-06,0.000116262066451479,7.9868833140122e-05,"HOXA11/TBXA2R/TSPO/AVP/HOXA13/SPP
7638206e-06,0.000116262066451479,7.9868833140122e-05,"CPS1/APOB/LIPG/APOA4/APOC3/AAD
7638206e-06,0.000116262066451479,7.9868833140122e-05,"CPS1/APOB/LIPG/APOA4/APOC3/AAD/
16e-06,0.000116262066451479,7.9868833140122e-05,"MT3/SOD3/IL1A/MT1G/MT2A/SNCA/AQP2/M
7889453e-06,0.000118829490726151,8.16325828071661e-05,"VIM/COL1A1/TGFB3/BMP4/COL5A1/I
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-06,0.000122746579777647,8.43235149520851e-05,"TGFB3/MMP2/COL1A1/FHL2/MSX2/CHAD/RE
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000122915043359285,8.44392447864386e-05,"CFTR/MSR1/APOB/TSPO/PLTP/LIPG/APOA4/APOC3/
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61e-06,0.000129501166677473,8.89637298605116e-05,"WWTR1/SNAI2/MYOC/DKK3/FGFR2/GPC4,
757770717e-06,0.000131709557432796,9.04808334019208e-05,"CCL26/SLC11A1/VIM/CCL7/CCL2/C
16757770717e-06,0.000131709557432796,9.04808334019208e-05,"CCL26/TREM2/SERPINE1/RARRE
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1624e-06,0.000136544392152142,0.000108670743144205,"FMO3/FMO1/CYP24A1/FMO4/MOXD1/I
7063266e-05,0.000140163125734912,9.62882016757518e-05,"FGFR2/WNT2/HOXA5/BMP4/SOX9/F
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880852572e-05,0.000142399425412344,9.78244778769206e-05,"FGFR2/PAX2/WNT2/HOXA2/COL1
358063e-05,0.000146167491281532,0.000100413035205659,"CRLF1/ERBB3/FCGR2B/MT3/TREM2/H
5812e-05,0.000156669368108916,0.000107627534943924,"GPM6B/COMP/DKK1/CALCA/MGP/TGFB
108665576e-05,0.00016684350281127,0.000114616884881434,"SELE/HFE/PLAUR/IGF1/CDH1/FSTL3
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1245936e-05,0.000174041487611437,0.000119561701918465,"CPS1/APOB/LIPG/APOA4/APOC3/AAI
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8e-05,0.000178528321051876,0.000122644032745016,"TREM2/RARRES2/CCL2/TRPV4/LGALS3/THB
54223144923e-06,0.000179860890827403,0.000148947597825934,"APOB/APOH/APOA4/APOC3/AI
1,8.32354223144923e-06,0.000179860890827403,0.000148947597825934,"APOB/APOH/APOA4/AP
e-05,0.000181322464791494,0.000124563532431547,"MYOC/GPM6B/COL17A1/ITGA8/COL16A1/EF
109890544e-05,0.000181956786809526,0.00012499929416331,"FOXC1/COL11A1/FGFR2/TGFB3/SE
1.40726911118437e-05,0.000182641257307669,0.000125469506517814,"NR1H4/SNAI2/DKK3/APOI
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1.44255198234806e-05,0.000186326762015935,0.000128001346606038,"DKK3/DHRS9/AFP/TSPO/B
13e-05,0.000189509740238465,0.00013018796485826,"AFP/PGR/MMP2/RETN/TGFB3/INHBA/MMP
1622e-05,0.000189707758696665,0.000130323998077687,"TBXA2R/ATP1A2/MCOLN3/GNA15/TRPC
12e-05,0.000191629314910002,0.000131644054199659,"NR1H4/CLDN11/SNAI2/GABRA1/MYOC/CD
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6e-05,0.000201612740366449,0.000138502392144999,"FGFR2/CMA1/WNT2/PITX3/DKK1/WLS/PAC
-05,0.000203030190297068,0.000139476141154013,"ETV1/SEMA3B/NGFR/FGFR2/TRPC5/SEMA3C/I
74771163021e-05,0.000205312497748881,0.000141044023427286,"LIPG/RETN/IL1A/PLA2G4A/APO
1e-05,0.000207129616076946,0.000142292333602477,"GPM6B/OPRK1/HTR2A/CXCL12/SYT10/SLC22
1.66471462564109e-05,0.00020903562770231,0.000143601711021232,"IGF1/WWTR1/SNAI2/FGFR2

70142056777135e-05,0.0002131501877958,0.000146428300325741,"PDK4/MYH13/NR1H4/ATP1A2
37704041247e-05,0.000214464816228921,0.000147331413801795,"PDK4/MLXIPL/NR1H4/DKK3/DH
'317586488326e-05,0.000215951101554886,0.000148352450828929,"OPRK1/HTR2A/CXCL12/SYT10
0220914512e-05,0.000216219005882607,0.000148536493713263,"HOXA11/EYA2/PAX2/DKK1/BMP4
'037528e-05,0.00021803150336966,0.000149781629498121,"SOX8/PAX2/SALL1/CALB1/BMP4/SOX9
"113/18800",1.76052784502109e-05,0.00021803150336966,0.000149781629498121,"CPS1/NGFR/F
'18800",1.82746879798532e-05,0.000225805048737365,0.000155121840771069,"TBXA2R/NR1H4/
L942095e-05,0.000233267425547947,0.000160248287827313,"TNFRSF1A/PTGS2/PTGS1/AVP/PTGD
871942095e-05,0.000233267425547947,0.000160248287827313,"TNFRSF1A/PTGS2/PTGS1/AVP/PTG
e-05,0.000233267425547947,0.000160248287827313,"PDK4/NR1H4/CPS1/PTGS2/PLAT/SOX9/ASS1
0",1.90510351242041e-05,0.000233267425547947,0.000160248287827313,"IGF1/EPPIN/TIMP1/PLA
5,0.000235973793084331,0.000162107487683093,"PRLH/OPRK1/RETN/CALCA/OPRM1/NR4A3/MCH
5,0.000239717161474442,0.000164679078524862,"APOA4/APOC3/APOA1/APOE/APOC1/ABCA12/A
73942e-05,0.000243906498175949,0.000167557037296739,"DKK3/TSPO/SALL1/APOA1/PDGFR/NE
L85565431e-05,0.000248857787087274,0.00017095843622209,"PROM1/BMP4/NOTCH2/MYO1E/KL
800",2.05542185565431e-05,0.000248857787087274,0.00017095843622209,"PROM1/BMP4/NOTC
7923e-05,0.000253090640923749,0.000173866290065485,"SLC11A1/FCGR2B/TREM2/CCL2/IFNG/A
589e-05,0.000263009185514613,0.000180680056645586,"OPRK1/HTR2A/CXCL12/SYT10/ADORA3/H
22031409e-05,0.000267583956310789,0.000183822798010213,"CFTR/HFE/NR1H4/OPRK1/OSM/RE
912417265e-05,0.000268935494900718,0.00018475126774601,"HOXA11/TLL1/TLL2/HOXA2/GLI3/C
,0.000273873971047424,0.000226802335443276,"DCN/VCAN/GPC4/APOB/EPDR1/CTSG/RETN/OGN
5,0.000282223184328263,0.000193879543907773,"OPRK1/CMA1/CTSG/RETN/INHBA/EDN3/IL1B/C
26187480202e-05,0.000287715524645221,0.000197652630226577,"IGF1/NGFR/PTGS2/HMOX1/SLC
0427107344e-05,0.000289497804270235,0.000198877007173624,"TBXA2R/ATP1A2/MCOLN3/GNA1
43575308e-05,0.000289497804270235,0.000198877007173624,"FGFR2/TGFR3/SEMA3C/LRP2/BMI
0657e-05,0.000291258819367815,0.000200086775976801,"SOX8/LRP2/TREM2/TSPO/MAG/PTPRZ1/
,0.000291258819367815,0.000200086775976801,"SLC22A16/ATP1A2/OPRK1/AVP/HTR2A/AQP9/CX
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7e-05,0.000307742000642981,0.000211410266906097,"TBXA2R/DCN/PTGS2/FAP/FAT2/APOH/HMC
2.69259347135997e-05,0.000316102296464211,0.000217153559558018,"SEMA3B/IGF1/TRPC5/SEI
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56699719e-05,0.000319415137377727,0.00021942938989733,"HOXA11/ALX4/SALL1/GLI3/MSX2/H
429/18800",2.80727333609973e-05,0.000326886795983964,0.000224562213291197,"SEMA3B/NR
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18800",2.83408791634574e-05,0.000329143429254574,0.000226112458110078,"PDK4/MLXIPL/NR
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7042e-05,0.000333734820056885,0.000229266616960539,"FGFR2/FGFR3/COMP/MSX2/SOX9/MMP
0407042e-05,0.000333734820056885,0.000229266616960539,"FGFR2/MMP2/HOXA13/BMP4/SOX9/
6034272e-05,0.000333734820056885,0.000229266616960539,"HFE/DKK3/RDH8/HSD17B2/TSPO/BI
3987844282e-05,0.000333734820056885,0.000229266616960539,"MT3/MT1G/MT2A/MT1E/MT1X/
282e-05,0.000333734820056885,0.000229266616960539,"SOX8/PAX2/SALL1/BMP4/SOX9/LIF/WNT9
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al peptide","18/1468","79/18800",2.91678806147277e-05,0.000333734820056885,0.000229266616
084e-05,0.000337608412648823,0.000231927668237376,"OPRK1/HTR2A/CXCL12/SYT10/SLC22A2/A
9129976e-05,0.000357367652713088,0.000245501721200962,"DKK3/BMP5/APOA1/CYP11A1/STAR
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859241391e-05,0.000370271218036487,0.000254366114697334,"STAB1/NR1H4/SLC11A1/TNFRSF1/
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02433e-05,0.000379376717087432,0.000260621341415337,"GPM6B/LOX/SOX9/AGT/EMILIN1/FBLN
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1043e-05,0.000381998587012159,0.000262422493742355,"SOX8/SEMA3B/SEMA3C/FOLR1/FN1/ED
i,0.000397777209739489,0.000316576494331997,"TKTL1/MOCOS/AFM/P3H2/PYGL/CALB1/FOLR1/L
73097785166e-05,0.000397818348429832,0.000273290233526698,"SELE/GNA15/FGFR2/FGFR3/HTF
,3.55772506725866e-05,0.000397818348429832,0.000273290233526698,"SOX8/FGFR2/PAX2/LRP2
e-05,0.000397885423618061,0.000273336312331075,"HOXA11/FOXC1/EYA2/FGFR2/PAX2/ITGA8/D
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21e-05,0.000397885423618061,0.000273336312331075,"C4BPA/C4BPB/PLA2G5/FCN3/MBL2/COLE
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9e-05,0.000433230493739163,0.000297617400685946,"SOX8/WWTR1/SNAI2/PRLH/PTGS2/HTR2A/
e-05,0.000437206683677518,0.000347956986544789,"APOC3/APOC1/ANXA1/ANXA3/APOA2/ANX
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8706098556846e-05,0.000457785334422152,0.000314485899011756,"CPS1/NGFR/FGFR2/FGFR3/KI
183e-05,0.000461662130163367,0.000317149150763802,"TBXA2R/DCN/PTGS2/FAP/FAT2/APOH/HM
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)",4.32135497879034e-05,0.000468680824553374,0.000321970800233889,"CREB3L3/FCGR2B/PTGS
3139093e-05,0.000493690424854876,0.00033915170587533,"PDK4/NR1H4/CPS1/ASS1/HMGCS2/CL
35369554e-05,0.000493690424854876,0.00033915170587533,"FGFR2/WNT2/PRRX1/BMP4/SOX9/SI
369554e-05,0.000493690424854876,0.00033915170587533,"CPS1/PLAT/PCK1/ASS1/SERPINF1/CYP1
843835369554e-05,0.000493690424854876,0.00033915170587533,"TREM2/RARRES2/TRPV4/THBS1
558e-05,0.000498551763646091,0.000342491311548993,"ALX4/NGFR/FGFR2/FERMT1/DKK1/MSX2,
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e-05,0.000498551763646091,0.000342491311548993,"CCL26/CCL7/CCL2/CCL8/LGALS3/CCL11/CCL1
223384812e-05,0.000498551763646091,0.000342491311548993,"PAX2/SIX4/TCF21/BMP4/SIX1/OS
34812e-05,0.000498551763646091,0.000342491311548993,"MT3/MT1G/MT2A/MT1E/MT1X/MT1F/
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0528e-05,0.000520425799531834,0.000414188070964687,"APOB/TSPO/PLTP/APOA4/APOA1/NPC2
371225752598e-05,0.000522587996796165,0.000432769049554804,"CRLF1/SELE/HFE/MSR1/TGFBR
0817e-05,0.000547845852935668,0.000376354991358147,"HOXA11/FOXC1/EYA2/FGFR2/PAX2/ITG
271197e-05,0.000556115690035101,0.000382036141363048,"PDK4/NR1H4/IGF1/CPS1/VIM/INSRR,
6605e-05,0.000598661833015202,0.000411264168166199,"CRLF1/NGFR/ERBB3/TRPC5/MT3/TREM
.000603801239719109,0.000414794798826758,"ETV1/SEMA3B/NGFR/FGFR2/TRPC5/SEMA3C/PAX2,
424922e-05,0.000627441151520714,0.000431034766244828,"NR1H4/CYP24A1/SNAI2/HMOX1/COL:
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11864219412458e-05,0.000639268176729773,0.000439159606373664,"SNAI2/FGFR2/AREG/KLF9/Z
e-05,0.000639268176729773,0.000439159606373664,"DCN/DSP/FN1/F13A1/ANXA1/THBS1/FLG/EVF
athway","24/1468","130/18800",6.23599765196888e-05,0.000648434893328839,0.000445456887
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32408396757e-05,0.000648434893328839,0.000445456887858843,"CRLF1/GPRC5A/IGF1/INSRR/RC
i,0.000657300405359486,0.000451547250112753,"APOB/TREM2/PLTP/APOA4/APOC3/APOA1/NPC2
7e-05,0.000657300405359486,0.000451547250112753,"OPRK1/RETN/PTGDS/NR4A3/APOE/MTNR1E
8688155596e-05,0.000657300405359486,0.000451547250112753,"DKK3/BMP5/CYP11A1/CRH/CYP:

8688155596e-05,0.000657300405359486,0.000451547250112753,"FGFR2/WNT2/RDH10/BMP4/SHH/
55596e-05,0.000657300405359486,0.000451547250112753,"PAX2/CALB1/BMP4/WNT9B/SHH/AQP2/
.41268688155596e-05,0.000657300405359486,0.000451547250112753,"PAX2/SIX4/TCF21/SIX1/OSF1/
11268688155596e-05,0.000657300405359486,0.000451547250112753,"APOH/FN1/SERPINC1/F13A1/
1650433558863e-05,0.000657471483255306,0.000451664775908846,"SOX8/YBX3/PITX1/TLL2/SIX4/
2585e-05,0.000657821644061153,0.000451905326725015,"SLC7A2/ATP1A2/LRP2/SLCO1A2/SLC17A
270/18800",6.56007071511168e-05,0.000668608337291609,0.000459315487476944,"SOX8/TRPC5/
5.64008886454563e-05,0.00067549174689701,0.000464044200031167,"CRLF1/ERBB3/MT3/TREM2/
18763151599e-05,0.000676965821046239,0.000465056848316668,"HFE/EHD3/ATP1A2/PTGS2/OPRK1/
05,0.000688838340197679,0.000473212941529195,"SLC27A6/IL1A/PLA2G4A/FABP3/IL1B/PLA2G5/
946991880558e-05,0.000688838340197679,0.000473212941529195,"SOX8/PAX2/SALL1/BMP4/SOX9/
172900936805e-05,0.000699897712662311,0.0004808104253945,"FOXC1/FOLR1/NOTCH2/GATA4/Y
1848074e-05,0.000700496347123007,0.000481221670758638,"FGFR2/HOXA13/GLI3/GLI1/TCF21/SI
1848074e-05,0.000700496347123007,0.000481221670758638,"OPRK1/RETN/INHBA/IL1B/CGA/AGT/
2022269869e-05,0.000701700664353003,0.000558458179483917,"CXCL2/CXCL12/PF4V1/CXCL6/CXCL
7.2090347031765e-05,0.000723845933461803,0.000497262192590946,"HFE/GPRC5A/DKK3/RASGR
69272238181e-05,0.000729687203954266,0.000501274984316814,"PAX2/SALL1/BMP4/LIF/FZD7/V
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1472006663766e-05,0.000731686488982409,0.000502648437990794,"CPS1/GLP1R/PCK1/ASS1/GJB1/
66e-05,0.000731686488982409,0.000502648437990794,"MMP2/MMP9/TIMP1/MMP3/MME/MMP
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05,0.000735993800141878,0.00050560744196155,"CFTR/TBXA2R/CDH1/FGFR2/TGFB3/OPRK1/TSF
-05,0.000739102428187046,0.000507742983692505,"ALX4/NGFR/FGFR2/FERMT1/DKK1/MSX2/INHBA/
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83081164e-05,0.000754737917403357,0.000518484133556747,"CRLF1/GPRC5A/IGF1/INSRR/ROS1/
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589e-05,0.000757730963589078,0.000520540273738014,"GLI3/DLX2/PRRX1/SATB2/BMP4/SIX1/FO
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1468","200/18800",7.92195181060105e-05,0.000769723576283175,0.000528778867902162,"LTBP
118752979e-05,0.000778061435607728,0.000534506747299664,"CPS1/APOB/APOH/LIPG/MOGAT3,
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163258641773e-05,0.000809068248357522,0.000555807572489744,"CFTR/EHD3/OPRK1/TREM2/TS
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18410",4.88967380345998e-05,0.000835857446402782,0.000665228710103295,"INSRR/ROS1/LTBP
574417e-05,0.000882614578709657,0.00060633187303118,"FOXC1/MMP2/INHBA/MMP19/TNFAIP
14674417e-05,0.000882614578709657,0.00060633187303118,"PTGS2/PTGS1/GGT5/AVP/PTGDS/PLA
71170339703e-05,0.000898877848909601,0.000617504291116955,"TBXA2R/NR1H4/VIM/FCGR2B/C

110",5.47583715134574e-05,0.000918723788725785,0.000731179034828817,"NPFFR2/SCTR/OPRK1
375196132e-05,0.000932543402550169,0.000640631597970825,"FGFR2/PGR/GLI3/AREG/MSX2/BM
521903372761e-05,0.000949189899194935,0.000755425910245766,"APOB/DKK1/APOC3/APOA1/CI
18800",0.000101275516372095,0.000958222193366746,0.000658272219039823,"PDK4/NR1H4/CPS
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18800",0.000105326553353406,0.000993078931617826,0.0006822178368682,"PDK4/MLXIPL/NR1H
7791210896,0.000993888469596276,0.000682773967132308,"SOX8/VIM/ROS1/TNFRSF1A/FOSL2/P
30/18800",0.000106561347871406,0.000993888469596276,0.000682773967132308,"PLAUR/IGF1/S
758,0.000993888469596276,0.000682773967132308,"IGF1/MYOC/TNFRSF1A/LMCD1/HMOX1/TNNT
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.468","32/18800",0.000106881575998713,0.000993888469596276,0.000682773967132308,"MSR1/
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4,0.00369707762752968,0.00253979036457673,"CFTR/MGST1/HFE/NR1H4/CDH17/LRP2/PLTP/AQP
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143307620102,0.00383824380836394,0.00263676763744144,"FGFR2/TGFB3/SEMA3C/LRP2/SALL1/
1796266700337,0.00383824380836394,0.00263676763744144,"MMP2/TSPO/MAG/FOLR1/APOA4/P
6700337,0.00383824380836394,0.00263676763744144,"MT3/HMOX1/MMP9/MT1G/MT2A/EGFR/M
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39757536458204,0.00395286574737727,0.00271550974826633,"SOX8/IGF1/C6/FOXC1/YBX3/FGFR
45507232193058,0.00398419047318331,0.002737028970958,"PTGDS/MTNR1B/HCTR2/CRH/ADOR
32193058,0.00398419047318331,0.002737028970958,"CYP24A1/SNAI2/LRP2/IFNG/CYP27A1/CYP1
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080307,0.00457726970156523,0.00314445804370958,"MSR1/APOB/PLA2G5/CRP/AGT/AGTR1/LPL/
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319, 0.0062604347984676, 0.00430074604352658, "MMP2/CRISPLD2/DKK1/COL1A1/TGFB3/RRAS/PD
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33, 0.00633184597563705, 0.00524357042565728, "CFTR/STAB1/EHD3/SLC11A1/MARCO/EHD2/VIM/I
35255560970507, 0.00634286102252179, 0.00435737058613353, "FSTL3/TREM2/MMP9/CSF3/IFNG/
34, 0.00636459143559864, 0.00437229878059174, "MLXIPL/NR1H4/APOB/TREM2/LIPG/APOA4/APOC
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7152783, 0.00652672281270552, 0.00448367856507486, "USH1C/COL11A1/FGFR2/PAX2/ITGA8/MYO
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332839, 0.00680617425854026, 0.00467565400108224, "FOXC1/FGFR3/COL1A1/RUNX2/BMP4/MMP1
32839, 0.00680617425854026, 0.00467565400108224, "FOXC1/FGFR3/COL1A1/RUNX2/BMP4/MMP13
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,0.00128158970087226,0.00833649454461618,0.00572694183132694,"SOX8/USH1C/PROM1/CALB
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'14/1468","74/18800",0.00157825101470996,0.00981780976047159,0.00674456452989179,"DCN/F
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L,0.0101306066746785,0.00695944738300164,"TREM2/TSP0/GLI3/CCL2/MMP14/CX3CR1/P2RY12/C
.0.00163954756566061,0.0101306066746785,0.00695944738300164,"HOXA11/SNAI2/PTHLH/CHAD
66061,0.0101306066746785,0.00695944738300164,"MARCO/TREM2/CCL2/C3/ANXA1/THBS1/FCN3,
.0101306066746785,0.00695944738300164,"SOX8/FGFR2/PAX2/LRP2/SIX4/FOLR1/BMP5/SDC4/BM
.0101924271955849,0.00811178416286238,"NR1H4/PYGL/FABP1/AKR1C3/AKR1C4",5
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,0.00108991586763439,0.0102019029566769,0.00811932557839396,"CPNE6/ANXA13/ANXA10/SYT
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!295445,0.0102931235311698,0.00707109198119031,"NGFR/FGFR2/FST/KRT71/FGF7/FOXQ1/SHH/!
.67367862295445,0.0102931235311698,0.00707109198119031,"MT3/APOA4/SNCA/HBA1/HBM/GP!
167367862295445,0.0102931235311698,0.00707109198119031,"FGFR2/PGR/AREG/MSX2/AR/SOSTI
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)168686448261503,0.0103624410668701,0.00711871121643619,"EHD3/RASGRF1/TREM2/MMP9/C
.6857649536,0.0104390765714205,0.00717135769445235,"FMO1/ACSM2B/FMO4/SMOX/SULT2A1/
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!8841067,0.0106428662887766,0.00731135560974815,"FGFR2/PGR/HOXA5/TCF21/TGFB3/BMP4/LI
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90987,0.0107261834142674,0.00736859217707091,"SNAI2/TNFRSF1A/BMP4/SOX9/GATA5/GATA4/
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)0825307,0.0108642781926745,0.00746345948117754,"IGF1/TGFB3/SEMA3C/HAMP/DKK1/FOLR1,
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!30943,0.0119763083781676,0.00822739354877816,"TBXA2R/DCN/PTGS2/FAP/APOH/HMOX1/SRPX
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,0.00207488981623656,0.0123777427098434,0.00850316786306585,"FGFR2/PGR/WNT2/HOXA5/A
)00208125385549842,0.0123777427098434,0.00850316786306585,"CFH/FCGR2B/TREM2/C4BPA/C
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1,0.0126653921925755,0.0100799275611876,"FAP/TIMP3/CTSG/CST3/TIMP1/COMP/SERPINE1/COL
5812248,0.0126714242447742,0.00870491897781586,"IGF1/SIX4/MYL9/TNNT1/COMP/HAMP/TBX1
43376704,0.0127107796907093,0.00873195508374864,"CD99/PLAUR/DSP/CTSG/MYL9/COMP/FN1/
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,0.00215604134443295,0.0127107796907093,0.00873195508374864,"VIM/TGFB3/BMP4/IL6/EMILII
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,"13/18800",0.00217950600883614,0.0127656780517546,0.00876966874368792,"TNFRSF1A/FAP/C
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53/18800",0.00227284580277252,0.0132550015997898,0.00910582052562676,"GPC4/PLEKHA4/DK
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ed in apoptotic process","14/1468","77/18800",0.00233528490946095,0.0135606887660973,0.0093
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.37325945427412,0.0094339137054036,"MYOC/BCAS1/FA2H/MAG/PTPRZ1/ASPA/CLU/EGR2/PLP1/I
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09,0.0137551940417961,0.0113910428260982,"ATP1A2/NGFR/TRPC5/ITGA8/OPRK1/APOB/PVALB/C
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073042,0.0141828138507101,0.00974320195291322,"FOXC1/SEMA3C/CST3/HRG/LIF/AGT/TMBIM1/
648911473042,0.0141828138507101,0.00974320195291322,"GLI3/LBX1/FOXN4/ISL2/TBX20/SHH/GI
313041,0.014301771870467,0.0098249228316197,"ATP1A2/OPRK1/FXYD3/TREM2/ATP1B4/HTR2A/
'230039,0.0143424884858392,0.00985289402341464,"SERPINE1/F3/IL1B/LBP/CRP/CHI3L1/ANXA1/I
40452197679,0.0144856891064751,0.00995126890031314,"PDK4/IL20RA/CST3/HAMP/CALCA/THBS
",0.00258979699828134,0.0147692111219163,0.0101460407053737,"SELE/HFE/IGF1/FCGR2B/LGAL
59008592,0.01480644309916,0.0101716180468808,"FOLR1/BICC1/DAW1/BMP4/NOTCH2/GATA4/CI
L63875,0.01480644309916,0.0101716180468808,"TSPO/TGFB3/YAP1/THBS1/CYP1B1/GJB2/FOS/FOS

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 1547664501053, 0.01480644309916, 0.0101716180468808, "WNT2/PLG/NOTCH2/PLCD3/JUNB/FOSL
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 027152611303937, 0.0153232463375294, 0.0105266476181884, "FOLR1/NOTCH2/GATA4/YAP1/LBX1
 1.00278684767120693, 0.0157108537464291, 0.010792923217876, "FCGR2B/DDX1/HMOX1/CTSG/PTC
 71967864, 0.0157459956034348, 0.0108170647044252, "NR1H4/CLDN11/SNAI2/CDH19/CDH7/TRPV4
 455032, 0.0160322221889692, 0.0127594657830183, "APOB/TSPO/PLTP/APOA4/APOA1/NPC2/APOE/
 53, 0.0160322221889692, 0.0127594657830183, "PROM1/SULT2B1/TSPO/APOA4/APOC3/APOA1/NPC
 1494, 0.0168197589868918, 0.0115547105344268, "FOX1/LRP2/APOB/COMP/HOXA13/FOLR1/PRRX1
 910011, 0.0168304556485252, 0.0115620588459546, "FSTL3/TREM2/IFNG/TNFAIP6/NOTCH2/GPC3/C
 1156187602585726, 0.0168750518445882, 0.0139746802313544, "PLAUR/GPC4/FOLR1/VNN1/IGSF21
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 32885131, 0.0171753811147262, 0.0117990131281777, "MSR1/APOB/TREM2/PLIN3/C3/CRP/IL6/LPL/C
 155/18800", 0.00309106082885131, 0.0171753811147262, 0.0117990131281777, "ERBB3/AREG/NEDD
 800", 0.00311650488976439, 0.017298999449646, 0.0118839355148694, "IGF1/YBX3/FGFR2/TGFB3/
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 81038638553, 0.0176445712512041, 0.0121213338116569, "RASGRF1/PTGS2/SCTR/CALB1/PLAT/EGR
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 134533506453309, 0.0183434178006617, 0.0126014221169209, "TREM2/IFNG/CLU/APOE/TTPA/MYO
 2711, 0.0183982996799786, 0.0146425412812656, "STAB1/VCAN/ITIH1/TNFAIP6/LYVE1/HAPLN1/ACA
 6715937915552, 0.0184443993522163, 0.012670793657764, "TBXA2R/EHD3/ATP1A2/PTGS2/DSP/MY

337683763078748,0.0184787110796985,0.0126943648682256,"WWTR1/SNAI2/PTGS2/HTR2A/MED
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364593733061,0.0191034122865526,0.0131235173680522,"GPC4/PLEKHA4/DKK1/FOXF2/SFRP2/RSF
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37", "24/19594",0.00189703050080696,0.0192413093653278,0.01593424115608,"FOLR1/IGSF21/F3,
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0.0193902211306832,0.0154319756878332,"CYP24A1/HEPH/P3H2/FA2H/CYP27A1/FDX1/CYP1B1/C
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813,0.0197506698324533,0.0157188437727786,"AQP9/AQP10/AQP7/AQP2/AQP1",5
9418290293813,0.0197506698324533,0.0157188437727786,"LRP2/ITGB4/IGFBP4/IGFBP1/IGFBP6",5
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9199291399,0.0203751147769886,0.0139971419053806,"CPS1/PTGS2/TSPO/IFNG/SPR/CLU/IL1B/AS
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 ion or reduction of molecular oxygen, NAD(P)H as one donor, and incorporation of one atom of oxyge
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.20629300889435, 0.0492713793519717, 0.0338480787083604, "TNMD/STAB1/DCN/FOXC1/APOH/HO

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23A1/COL11A1/COL17A1/COL16A1/LTBP4/COL9A3/CHADL/SRPX/SRPX2/COMP/TFPI2/OGN/COL1A1/
C1/COL11A1/COL17A1/TNFRSF1A/ITGA8/FAP/COL16A1/MMP2/CCDC80/CMA1/COL9A3/TLL2/CHADI
OXC1/COL11A1/COL17A1/TNFRSF1A/ITGA8/FAP/COL16A1/MMP2/CCDC80/CMA1/COL9A3/TLL2/CH/
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MA3C/CXCL2/PTHLH/OSM/CTSG/AVP/TIMP1/RETN/HAMP/WNT2/OGN/CXCL12/DKK1/CSF3/CCL7/C
L/ITIH1/COL11A1/FGFR2/TGFBR3/EPYC/APOB/LTBP4/APOH/CCDC80/TREM2/CTSG/LIPG/CRISPLD2/C
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PAX2/HOXA9/LRP2/TLL2/TDRD1/WNT2/HOXA2/HOXA5/HOXA6/MEOX2/GLI3/DKK1/GLI1/MDFI/TBX
OB/APOH/CCDC80/CTSG/LIPG/CRISPLD2/COMP/CCL7/CCL8/PF4V1/SOD3/SMOC2/THBS4/FGF1/HRG
2/ERBB3/FGFR2/FAP/APOH/DSP/HMOX1/CTSG/FERMT1/MYL9/TIMP1/WFDC1/PLAT/COMP/TFPI2/SE
/FOXC1/FGFR2/PAX2/ITGA8/LRP2/SIX4/MMP9/SALL1/CALB1/GLI3/ACTA2/TBX18/FGF1/NID1/TCF21/
C/VCAN/GPM6B/FOXC1/COL11A1/FGFR2/FGFR3/FSTL3/PTGS2/MMP2/PTHLH/MMP9/CHRD1/COM
P/CST3/EPPIN/TIMP1/WFDC1/TFPI2/SERPINE1/AMBP/HRG/SERPINC1/SPINK4/ITIH5/SERPINA7/SLPI/
A1/COL9A3/COL1A1/COL12A1/LOX/COL10A1/COL21A1/COL5A1/EMILIN1/LUM/COL6A2/FCN3/C1QL
ES2/SEMA3C/PAX2/HOXA9/LRP2/TLL2/TDRD1/WNT2/HOXA2/HOXA5/HOXA6/MEOX2/GLI3/DKK1/FC
INA4/AVP/CST3/EPPIN/TIMP1/WFDC1/TFPI2/SERPINE1/AMBP/HRG/FN1/SERPINC1/SPINK4/ITIH5/SE
LA1/FGFR2/PAX2/ITGA8/HOXA9/TBX15/MYO3A/SIX4/SALL1/WNT2/HOXA2/HOXA5/HOXA6/RARRES2
/RDH8/AFP/OPRK1/HSD17B2/LTBP4/CMA1/OSM/TSPO/CTSG/CPQ/RETN/SULT2A1/SULT1E1/TRPV4/I
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TGS2/PAX2/MT3/TIMP3/SERPINA4/MMP9/AVP/CST3/EPPIN/TIMP1/WFDC1/TFPI2/SERPINE1/AMBP,
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X4/SALL1/CALB1/GLI3/TCF21/RDH10/HOXC11/BMP4/SOX9/SIX1/LIF/PDGFR/YAP1/OSR1/GPC3/WN
MP2/TFAP2C/COL9A3/SIX4/SALL1/RETN/HOXA13/BMP5/IL1A/TCF21/TEX11/RDH10/INHBA/MMP19/
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1/FGFR2/PAX2/ITGA8/LRP2/SIX4/MMP9/SALL1/CALB1/GLI3/ACTA2/FGF1/NID1/TCF21/RDH10/BICC1
PAX2/MT3/TIMP3/SERPINA4/MMP9/AVP/CST3/EPPIN/TIMP1/WFDC1/TFPI2/SERPINE1/AMBP/CRYAI
R2/FGFR3/HOXA9/MMP2/TBX15/SIX4/COMP/HOXA2/HOXA5/HOXA6/SFRP4/GLI3/COL1A1/TRPV4/M
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C1/YBX3/AFP/LRP2/PGR/MMP2/TFAP2C/COL9A3/SIX4/SALL1/RETN/IL1A/TCF21/TEX11/RDH10/INHBA
MMP2/TFAP2C/COL9A3/SIX4/SALL1/RETN/IL1A/TCF21/TEX11/RDH10/INHBA/MMP19/TNFAIP6/EREG
/TGFBR3/PAX2/FAP/PGR/APOH/HMOX1/SIX4/FERMT1/FGL1/WNT2/HOXA5/CXCL12/CCL2/ODAM/AI
X2/SIX4/SALL1/CALB1/GLI3/ACTA2/FGF1/NID1/TCF21/BMP4/SOX9/SIX1/LIF/HOXD11/NOTCH2/PDGF
RPINE1/RARRES2/CXCL12/CCL7/CCL2/CCL8/PF4V1/CALCA/TRPV4/THBS4/IL1A/CCL20/IL1R1/DUSP1/T
/FOXC1/PAX2/SIX4/SALL1/CALB1/GLI3/FGF1/TCF21/BMP4/SOX9/SIX1/LIF/HOXD11/NOTCH2/AGT/Y
NTR1/FOXC1/FGFR2/PAX2/SIX4/SALL1/CALB1/GLI3/FGF1/TCF21/SDC4/BMP4/SOX9/SIX1/LIF/HOXD1
PAX2/MT3/TIMP3/SERPINA4/MMP9/AVP/CST3/EPPIN/TIMP1/WFDC1/PLAT/TFPI2/SERPINE1/AMBP/
"COL23A1/COL11A1/COL17A1/COL16A1/COL9A3/COL1A1/COL12A1/COL10A1/COL21A1/COL5A1/CC
L7/CCL2/CCL8/PF4V1/CALCA/TRPV4/SMOC2/LOX/THBS4/FGF1/HRG/CCL20/PADI2/DUSP1/NR4A1/TN

GFR2/HOXA9/TBX15/SIX4/HOXA2/HOXA5/HOXA6/GLI3/COL1A1/MDFI/DLX2/PRRX1/SATB2/TGFB3/K
 /FGFR2/HOXA9/TBX15/SIX4/HOXA2/HOXA5/HOXA6/GLI3/MDFI/DLX2/PRRX1/SATB2/TGFB3/RDH10/I
 TLL2/CTSG/GZMB/MMP9/PLAT/F3/PLG/PLAU/MMP19/F10/MASP1/KLK10/MMP7/MMP13/HABP2/M
 CSF3/CCL7/CCL2/CCL8/PF4V1/AREG/IFNG/BMP5/IL1A/CCL20/SPP1/TGFB3/INHBA/NDP/CXCL6/BMP4
 G/GZMB/MMP9/PLAT/AADAC/F3/PLG/PLAU/MMP19/F10/MASP1/KLK10/MMP7/MMP13/HABP2/M
 SPP2/PTGS2/PAX2/MT3/TIMP3/SERPINA4/MMP9/AVP/CST3/EPPIN/TIMP1/WFDC1/TFPI2/SERPINE1/
 L2/CTSG/GZMB/MMP9/PLAT/F3/PLG/PLAU/MMP19/F10/MASP1/KLK10/MMP7/MMP13/HABP2/MN
 L7B2/TSPO/SULT1E1/BMP5/TTR/SPP1/RDH10/LRAT/PDGFR4/CYP1B1/CYP2C9/RBP4/CYP11A1/CRABP
 4/PCS/SAA2/IL6/AHSG/PTGES/SAA4/MBL2/CEBPA/SAA1/F2/SERPINA3/SERPINA1/ORM2/ORM1/HP",2:
 'TSPO/APOL4/PLTP/LIPG/AQP9/RETN/PLIN3/APOA4/APOC3/SLC27A6/PLSCR4/IL1A/PLA2G4A/APOA1
 L/PON3/PON2/AHR/SOD3/APOA4/ABCG2/SLC17A3/MT1G/MT2A/APOE/ASS1/ALOX5AP/TTPA/CYP1B
 WFDC1/TFPI2/SERPINE1/AMBP/HRG/SERPINC1/SPINK4/ITIH5/SERPINA7/SLPI/SERPINF1/SPINK5/AGT
 3FR2/SEMA3C/PAX2/PGR/SIX4/SALL1/WNT2/HOXA5/HOXA13/GLI3/AREG/FGF1/TCF21/MSX2/RDH10
 5G/MMP9/SERPINE1/RARRES2/CXCL12/CCL7/CCL2/CCL8/PF4V1/ST3GAL4/CALCA/TRPV4/BMP5/THBS
 4R2/SEMA3C/PAX2/PGR/SIX4/SALL1/WNT2/HOXA5/HOXA13/GLI3/AREG/FGF1/DLX2/TCF21/MSX2/RI
 X4/SALL1/CALB1/GLI3/FGF1/TCF21/BMP4/SOX9/SIX1/LIF/HOXD11/NOTCH2/AGT/YAP1/LGR5/OSR1/
 CL8/PF4V1/TRPV4/THBS4/IL1A/CCL20/IL1R1/TNFAIP6/EDN3/TREM1/CXCL6/IL1B/LBP/LGALS3/ANXA1
 GFR2/TGFB3/APOB/APOH/CCDC80/CTSG/LIPG/CRISPLD2/SULT2A1/COMP/CCL7/CCL8/PF4V1/SOD3
 CST3/COL1A1/TGFB3/MMP19/BMP4/COL5A1/IL6/MMP7/MMP13/EMILIN1/RCN3/SERPINH1/MMP3/
 APO4/PLTP/LIPG/AQP9/RETN/APOA4/APOC3/SLC27A6/PLSCR4/IL1A/PLA2G4A/APOA1/ATP10B/ABCG
 2/SIX4/SALL1/CALB1/GLI3/FGF1/TCF21/BMP4/SOX9/SIX1/LIF/HOXD11/NOTCH2/AGT/YAP1/OSR1/GP
 1ING1/FGG/FGA/FGB/THBD/F2/PROS1/SERPINB2",16
 REM2/CTSG/RARRES2/CCL2/PF4V1/IFNG/C7/C9/HRG/CLU/C4BPA/C4BPB/SLPI/TREM1/CXCL6/IL1B/C
 F4V1/TRPV4/THBS4/CCL20/TNFAIP6/EDN3/TREM1/CXCL6/IL1B/LBP/LGALS3/ANXA1/THBS1/CXCL9/X
 4GFR/PAX2/GPC4/SIX4/PLEKHA4/WNT2/DKK1/FGF1/HOXC11/RUNX2/BMP4/SOX9/SIX1/GATA5/AGT/
 X15/WNT2/HOXA2/HOXA13/POU6F2/GLI3/DKK1/TBX18/DLX2/PRRX1/SATB2/TBX22/RUNX2/BMP4/S
 11A1/FGFR3/PITX1/EPYC/PTHLH/CHADL/TIMP1/COMP/HOXA5/GLI3/ACTA2/COL1A1/TRPV4/MGP/BI
 1215e-10,"HFE/WWTR1/VIM/LTBP1/DKK3/TGFB3/FSTL3/ITGA8/AFP/LRP2/LTBP4/FERMT1/CHRD1/
 1/DKK3/NGFR/TGFB3/FSTL3/ITGA8/LRP2/MT3/LTBP4/FERMT1/CHRD1/HOXA13/SFRP4/DKK1/FOL
 1P2/PTGS2/PAX2/MT3/TIMP3/SERPINA4/MMP9/AVP/CST3/EPPIN/TIMP1/WFDC1/TFPI2/SERPINE1/A
 MMP2/KIF16B/MMP9/DKK1/COL12A1/FN1/WLS/APOA1/NR4A3/DUSP1/DUSP4/INHBA/BMP4/FOXA:
 CCL20/CXCL6/CXCL9/XCL1/CXCL14/CXCL16/CXCL3/CXCL1/CXCL8/CCL11/CCL13/CCL23/CCL16/CCL18/C
 'ERBB3/FGFR2/PITX1/TGFB3/SEMA3C/ITGA8/LRP2/TLL2/DSP/SIX4/MYH14/HAMP/WNT2/MEOX2/D
 T1/WFDC1/PLAT/SERPINE1/KANK1/ACTA2/ST3GAL4/SMOC2/HRG/F3/SERPINC1/PLG/PLAU/FOXA2/T:
 OPRK1/APOH/CTSG/AVP/MYL9/FA2H/PLAT/COMP/TFPI2/SERPINE1/PF4V1/ST3GAL4/TRPV4/SCNN1A
 2/PAX2/PGR/SIX4/SALL1/WNT2/HOXA5/GLI3/AREG/FGF1/TCF21/MSX2/RDH10/BMP4/SOX9/SIX1/H
 C3/FOXC1/PAX2/FAT1/SLC17A6/CHRD1/CALB1/WNT2/GLI3/PITX3/CRYAB/EFEMP1/DLX2/RDH10/IN
 91810612345473e-10,"HFE/LTBP1/DKK3/TGFB3/FSTL3/ITGA8/LRP2/LTBP4/FERMT1/CHRD1/HOXA
 1/TGFB3/LRP2/LTBP4/SRPX2/COL1A1/GHR/IL1R2/IL1R1/TGFB3/FGFRL1/COL5A1/ITGB4/PDGFR4/IL1
 /MMP2/AVP/HTR2A/COMP/ACTA2/SOD3/CALCA/NPR3/EDN3/APOE/CRP/MTNR1B/HTR1B/AGT/HTR
 LCO1A2/APOB/TSPO/PLTP/LIPG/HTR2A/AQP9/CXCL12/APOA4/APOC3/SYT10/SLC22A2/APOA1/SPP1
 AMC3/FOXC1/PAX2/FAT1/SLC17A6/CHRD1/CALB1/WNT2/GLI3/PITX3/CRYAB/EFEMP1/DLX2/RDH10
 /IBSP/MYOC/VCAN/FGFR2/PTHLH/HOXA2/GLI3/COL1A1/AREG/GLI1/LOX/FHL2/SPP1/SATB2/MSX2/T
 2/PITX1/TGFB3/SEMA3C/PGR/MMP2/HMOX1/TSPO/SIX4/FA2H/SALL1/FGL1/HAMP/WNT2/HOXA5,
 'BCHE/SGK1/KLF9/CPN1/PCK1/ZFP36/MYOD1/ASS1/SERPINF1/HMGCS2/ANXA1/HTR1B/IL6/IL1RN/CY
 /COMP/TFPI2/SERPINE1/PF4V1/ST3GAL4/HRG/FN1/PLA2G4A/F3/SERPINC1/PLG/PLAU/NFE2/C4BPB/
 'FGFR2/FGFR3/FCGR2B/OPRK1/MT3/TREM2/GADD45B/OSM/HTR2A/ACTA2/DKK1/CCL7/CCL2/CCL8/
 OL11A1/ERBB3/FGFR2/PITX1/TGFB3/LRP2/TLL2/DSP/SIX4/MYH14/WNT2/MEOX2/CRYAB/LOX/TNN
 3/SIX4/HOXA13/BMP5/IL1A/TCF21/TEX11/INHBA/SOX9/HOXD13/RXFP2/PDGFR4/GATA4/NR5A1/LH
 11/TGFB3/CLU/PLG/SRGN/F13A1/ISLR/THBS1/AHSG/SERPING1/ALB/IGF2/FGG/FGA/FGB/PROS1/SERI

L/ST3GAL4/HRG/F3/SERPINC1/PLG/PLAU/FOXA2/TSPAN8/APOE/PDGFRA/THBS1/SERPINC1/FGG/FGA/PLAT/COMP/TFPI2/SERPINE1/PF4V1/ST3GAL4/HRG/FN1/PLA2G4A/F3/SERPINC1/PLG/PLAU/C4BPB
L/PAX2/MMP9/SALL1/GLI3/ACTA2/TCF21/BMP4/LIF/NOTCH2/YAP1/OSR1/MYO1E/WNT9B/KLF15/SH
e-10,"ETV1/NR1H4/ALX4/FOXC1/CREB3L3/DLX3/PITX1/FOSL2/PGR/TFAP2C/SIX4/HOXA5/HOXA13/M
2/SEMA3C/HOXA9/TDRD1/WNT2/HOXA2/HOXA5/HOXA6/MEOX2/GLI3/DKK1/TBX18/WLS/MSX2/H
CCL7/CCL2/CCL8/PF4V1/CALCA/TRPV4/THBS4/CCL20/PADI2/DUSP1/TNFAIP6/EDN3/TREM1/CXC
CST3/EPPIN/TIMP1/WFDC1/TFPI2/PPP1R17/SERPINE1/AMBP/APOC3/HRG/SERPINC1/SPINK4/ITIH5/
/AREG/BMP5/THBS4/FGF1/FGF12/EFEMP1/TGFB3/INHBA/EREG/BMP4/GDF5/LIF/VGF/GDF15/NGF/
RMT1/ADAM2/COMP/PTPRZ1/CXCL12/THBS4/FGF1/FN1/SPP1/TGFB3/IL1B/TSPAN8/COL5A1/GFAP/I
DXC1/CREB3L3/DLX3/PITX1/FOSL2/PGR/TFAP2C/SIX4/HOXA5/HOXA13/MEOX2/TLX1/PITX3/GLI1/DLX
3/APOA1/CLU/APOE/APOC1/SAA2/SAA4/APOA2/LIPC/SAA1/LPL/LPA/HPR",18
L/CLU/APOE/APOC1/SAA2/SAA4/APOA2/LIPC/SAA1/LPL/LPA/HPR",18
1/PAX2/FAT1/SLC17A6/CHRD1/CALB1/WNT2/GLI3/PITX3/CRYAB/EFEMP1/DLX2/RDH10/INHBA/ND
IP/GLI3/CXCL12/FOLR1/APOA4/GLI1/PRRX1/SPP1/NR4A3/PLG/MYOD1/GFAP/ANXA1/TEC/IL6/GATA4
GS2/MMP2/AVP/HTR2A/COMP/ACTA2/SOD3/CALCA/NPR3/EDN3/APOE/CRP/MTNR1B/HTR1B/AGT/
DXC1/PTGS2/MMP2/AVP/HTR2A/COMP/ACTA2/SOD3/CALCA/NPR3/EDN3/APOE/CRP/MTNR1B/HTR
/NGFR/FGFR2/TGFB3/PAX2/PGR/APOH/HMOX1/SIX4/WNT2/HOXA5/CXCL12/CCL2/ODAM/AREG/G
C/UTS2/TNFRSF1A/LMCD1/PTGS2/DSP/HMOX1/MYL9/HTR2A/TNNT1/MYH14/COMP/HAMP/SCN1B/
COMP/TFPI2/SERPINE1/PF4V1/ST3GAL4/HRG/FN1/PLA2G4A/F3/SERPINC1/PLG/PLAU/C4BPB/F13A1,
X2/SIX4/SALL1/CALB1/GLI3/FGF1/TCF21/SDC4/BMP4/SOX9/SIX1/HOXD11/AGT/REN/OSR1/GPC3/W
4/HRG/F3/SERPINC1/PLG/PLAU/FOXA2/TSPAN8/APOE/PDGFRA/THBS1/SERPINC1/ANXA5/FGG/FGA/
3R/SIX4/SALL1/WNT2/HOXA5/GLI3/AREG/FOLR1/BMP5/FGF1/TCF21/MSX2/RDH10/SDC4/BMP4/SO
/ST3GAL4/HRG/F3/SERPINC1/PLG/PLAU/FOXA2/TSPAN8/APOE/PDGFRA/THBS1/SERPINC1/FGG/FGA
M2/TSPO/FA2H/MAG/PTPRZ1/GLI3/PITX3/ASPA/CCL2/AREG/IFNG/DLX2/CLU/EGR2/PLP1/SOX9/IL1E
F9/CPN1/PCK1/ZFP36/MYOD1/ASS1/SERPINF1/HMGCS2/ANXA1/IL6/IL1RN/CYP1B1/ANXA3/TPH2/FE
APOC3/APOA1/PLA2G5/APOE/APOC1/AGT/AGTR1/APOA2/LIPC/LPL/PLA2G2A",16
OA4/APOC3/APOA1/PLA2G5/APOE/APOC1/AGT/AGTR1/APOA2/LIPC/LPL/PLA2G2A",16
C/PTHLH/CHADL/TIMP1/COMP/HOXA5/GLI3/COL1A1/TRPV4/MGP/BMP5/GHR/EFEMP1/DLX2/PRRX
A1/CLU/APOE/APOC1/SAA2/SAA4/APOA2/LIPC/SAA1/LPL/LPA/HPR",18
B3/CLU/PLG/SRGN/F13A1/ISLR/THBS1/AHSG/SNCA/SERPINC1/CD109/ALB/IGF2/FGG/FGA/FGB/PRO
TIMP1/CRISPLD2/RETN/SERPINE1/RARRES2/SPARC/HRG/FN1/PADI2/APOA1/TTR/NPC2/TGFB3/CLU/
APOA1/CLU/APOE/APOC1/SAA2/SAA4/APOA2/LIPC/SAA1/HPR",15
MT3/TREM2/TIMP3/AVP/HTR2A/ACTA2/CCL7/CCL2/CCL8/TRPV4/OPRM1/FGF1/IL1A/CCL20/FN1/DU
THBS4/IL1A/CCL20/IL1R1/TNFAIP6/EDN3/TREM1/CXCL6/IL1B/LBP/LGALS3/CXCL9/XCL1/S100A9/CXC
2/GNA15/PRLH/CXCL2/AVP/WNT2/CXCL12/CCL7/CCL2/CCL8/PF4V1/CALCA/CCL20/EDN3/NDP/CXCL6
2/PAX2/ITGA8/FAT1/MYO3A/SIX4/CALB1/WNT2/HOXA2/GLI3/PITX3/TBX18/EFEMP1/PRRX1/BMP4/
R3/PTGS2/PTHLH/COMP/COL1A1/FAM20A/ODAM/MGP/LOX/SPP1/TGFB3/MSX2/SRGN/BMP4/SOX9
FGFR2/PAX2/ITGA8/MMP2/KIF16B/MMP9/DKK1/COL12A1/FN1/WLS/DUSP1/DUSP4/INHBA/BMP4/C
1/HRG/PLG/PLAU/TSPAN8/APOE/PDGFRA/THBS1/SERPINC1/FGG/FGA/FGB/THBD/F2/PROS1/SERPIN
COL1A1/AREG/GHR/LOX/BCHE/PADI2/SGK1/TCF21/SPP1/KLF9/NR4A3/TGFB3/CPN1/PCK1/BMP4/Z
CL1A1/FAM20A/ODAM/PERP/DLX2/TGFB3/MSX2/INHBA/RUNX2/BMP4/FST/LRP4/PDGFRA/OSR1/DL
C/TNFRSF1A/HES2/TRPC5/SEMA3C/LRP2/MT3/PTHLH/TREM2/TSPO/MAG/WNT2/PTPRZ1/GLI3/KAN
CL8/CALCA/CCL20/DUSP1/LGALS3/ANXA1/IL6/XCL1/NBL1/CX3CR1/CCL11/DEFB124/CCL13/S100A14,
ALB1/GLI3/FGF1/TCF21/BMP4/SOX9/SIX1/LIF/HOXD11/AGT/OSR1/GPC3/WNT9B/SHH/GDNF/IRX2/IR
THLH/COMP/COL1A1/FAM20A/ODAM/MGP/LOX/SPP1/TGFB3/MSX2/SRGN/BMP4/SOX9/HTN1/OMI
SOX9/LIF/YAP1/OSR1/WNT9B/LAMB2/ADIPOQ/WT1/WNT7B/POU3F3",14
P/ACTA2/EDN3/CRP/MTNR1B/HTR1B/AGT/HTR2B/AGTR1/DOCK5/HTR7/BDKRB2/DRD5/ADRA1B/FGC
/ERBB3/FGFR2/TGFB3/SEMA3C/PAX2/SIX4/WNT2/HOXA5/ACTA2/COL1A1/FOLR1/BMP5/FN1/TCF2
2/SIX4/SALL1/CALB1/GLI3/FGF1/TCF21/SDC4/BMP4/SOX9/SIX1/HOXD11/AGT/OSR1/GPC3/WNT9B/
POA4/APOC3/APOA1/PLA2G5/APOE/APOC1/AGT/AGTR1/APOA2/LIPC/LPL/PLA2G2A",16

FERMT1/WFDC1/PLAT/SERPINE1/KANK1/ACTA2/ST3GAL4/SMOC2/HRG/F3/SERPINC1/SPP1/PLG/PLA
/TCF21/BMP4/SOX9/SIX1/LIF/HOXD11/AGT/OSR1/GPC3/WNT9B/SHH/GDNF/IRX2/IRX3/ERBB4/TAC
GFR2/FGFR3/MT3/TREM2/TIMP3/HTR2A/ACTA2/CCL7/CCL2/CCL8/TRPV4/OPRM1/FGF1/IL1A/CCL20,
PINE1/RARRES2/CXCL12/CCL7/CCL2/CCL8/ST3GAL4/TRPV4/BMP5/THBS4/IL1A/CCL20/IL1R1/PADI2/C
FGFR2/PAX2/SIX4/SALL1/CALB1/GLI3/FGF1/TCF21/SDC4/BMP4/SOX9/SIX1/HOXD11/AGT/OSR1/GPC
2/PAX2/SIX4/SALL1/CALB1/GLI3/FGF1/TCF21/SDC4/BMP4/SOX9/SIX1/HOXD11/AGT/OSR1/GPC3/W
3A3/SIX4/IL1A/TCF21/TEX11/INHBA/SOX9/RXFP2/PDGFR4/GATA4/NR5A1/LHCGR/CYP1B1/DHH/LHX
4/SLC11A1/CPS1/VIM/FGFR2/FCGR2B/PTGS2/CXCL2/OPRK1/APOB/TREM2/TSPO/CTSG/HAMP/SERF
BX3/LRP2/TFAP2C/COL9A3/SIX4/IL1A/TCF21/TEX11/INHBA/SOX9/RXFP2/PDGFR4/GATA4/NR5A1/LH
XOC1/PAX2/FAT1/SLC17A6/CALB1/WNT2/GLI3/PITX3/CRYAB/EFEMP1/DLX2/RDH10/INHBA/NDP/BN
/FGFR2/FGFR3/MT3/TREM2/HTR2A/ACTA2/CCL7/CCL2/CCL8/TRPV4/OPRM1/FGF1/IL1A/CCL20/BMP
N/PLIN3/APOA4/IL1A/PLA2G4A/APOA1/SPP1/LRAT/FABP3/IL1B/C3/APOE/APOC1/CRP/AGT/IL6/TH
/PF4V1/CCL20/CXCL6/CXCL9/XCL1/CXCL14/CXCL16/CXCL3/CXCL1/CX3CR1/CXCL8/CCL11/CCL13/S100
PINA4/TIMP1/CRISPLD2/RETN/SERPINE1/RARRES2/SPARC/HRG/FN1/PADI2/APOA1/TTR/NPC2/TGFB
ALL1/HOXA13/GLI3/DKK1/PRRX1/MSX2/RDH10/HOXC11/RUNX2/BMP4/SOX9/GDF5/HOXD13/NOTCH
OXA13/GLI3/DKK1/PRRX1/MSX2/RDH10/HOXC11/RUNX2/BMP4/SOX9/GDF5/HOXD13/NOTCH2/LRP
/PLG/PLAU/TSPAN8/APOE/PDGFR4/THBS1/SERPING1/ANXA5/FGG/FGA/FGB/THBD/F2/PROS1/SERP
CCL2/CCL8/PF4V1/LOX/CCL20/PADI2/DUSP1/CXCL6/CXCL9/XCL1/ACKR3/CXCL3/CXCL1/CX3CR1/CXCL
2/CCL7/CCL2/CCL8/PF4V1/LOX/CCL20/PADI2/DUSP1/CXCL6/CXCL9/XCL1/ACKR3/CXCL3/CXCL1/CX3C
RPINA4/TIMP1/CRISPLD2/RETN/SERPINE1/RARRES2/SPARC/HRG/FN1/PADI2/APOA1/TTR/NPC2/TGF
217A3/MT1G/MT2A/APOE/ALOX5AP/FBLN5/PTGES/S100A9/FABP1/ALB/GPX8/ALDH1A1/NXN/TXND
/GLI3/FGF1/TCF21/BMP4/SOX9/SIX1/LIF/HOXD11/AGT/OSR1/GPC3/WNT9B/SHH/GDNF/IRX2/IRX3/
GLI3/COL1A1/TRPV4/GHR/TGFB3/MSX2/RUNX2/BMP4/SOX9/MMP13/SFRP2/SERPINH1/MMP14/DH
/HRG/PLG/PLAU/TSPAN8/APOE/PDGFR4/THBS1/SERPING1/FGG/FGA/FGB/THBD/F2/PROS1/SERPINI
1/WWTR1/PAX2/MMP9/SALL1/ACTA2/BMP4/LIF/NOTCH2/YAP1/OSR1/MYO1E/WNT9B/KLF15/GDNI
L3/SFRP4/DKK1/BMP5/TGFB3/SFRP5/MSX2/TNFAIP6/RUNX2/BMP4/SOX9/GDF5/GDF15/GATA5/NOT
L1/COMP/HOXA13/SFRP4/DKK1/BMP5/TGFB3/SFRP5/MSX2/TNFAIP6/RUNX2/BMP4/SOX9/GDF5/GD
/HOXA5/GLI3/GLI1/LOX/FGF1/HSD11B1/TCF21/TGFB3/RDH10/BMP4/SOX9/SIX1/FGFRL1/LIF/FOXA1/
S4/CCL20/TNFAIP6/EDN3/TREM1/CXCL6/IL1B/LBP/LGALS3/CXCL9/XCL1/S100A9/CXCL3/CXCL1/CXCL
/PTGS2/AVP/HTR2A/APOA4/IFNG/FGF1/AADAC/IL1A/APOA1/NR4A3/RDH10/FABP3/RAB38/IL1B/AP
PINE1/HRG/PLG/PLAU/TSPAN8/APOE/APCS/PDGFR4/THBS1/SERPING1/CD109/CLDN19/FGG/FGA/FG
FGF1/TCF21/BMP4/SOX9/SIX1/HOXD11/AGT/LGR5/OSR1/GPC3/WNT9B/SHH/GDNF/IRX2/IRX3/TAC
RS9/RDH8/AFP/LRP2/APOB/HSD17B2/MT3/SULT2B1/TSPO/SULT2A1/SULT1E1/APOA4/IFNG/BMP5/F
VP/PLAT/HOXA13/AHR/SGK1/SPP1/KLF9/TGFB3/PCK1/HOXD13/ASS1/SERPINF1/POSTN/HMGCS2/YA
ABL2/COLEC10/C4B",11

CCL20/IL1R2/IL1R1/PCK1/SOX9/IL1B/CHI3L1/ANXA1/IL6/IL1RN/XCL1/SNCA/ADAMTS12/TRIM63/SLC
CXCL12/CCL7/CCL2/CCL8/PF4V1/CCL20/PADI2/CXCL6/CXCL9/XCL1/ACKR3/CXCL3/CXCL1/CX3CR1/CX
L1/COMP/HOXA13/MEOX2/GLI3/DKK1/PRRX1/MSX2/RDH10/HOXC11/RUNX2/BMP4/SOX9/GDF5/H
VP/HOXA13/MEOX2/GLI3/DKK1/PRRX1/MSX2/RDH10/HOXC11/RUNX2/BMP4/SOX9/GDF5/HOXD13/
OXA13/RARRES2/GLI3/GLI1/WLS/TCF21/TGFB3/SFRP5/BMP4/HOXD13/GATA5/ASS1/PYY/BARX1/HM
LI3/FGF1/TCF21/BMP4/SOX9/SIX1/HOXD11/AGT/OSR1/GPC3/WNT9B/SHH/GDNF/IRX2/IRX3/TACST
ABP3/APOC1/ALOX5AP/CRABP2/PMP2/S100A9/FABP1/ALB/FABP7/CRABP1/ACOX2/FABP4/CYP4F11,
A/APOA4/APOC3/APOA1/PLA2G5/APOC1/PDGFR4/ANXA1/AGT/HTR2B/AGTR1/SNCA/EGFR/RHOC/A
P2/PMP2/S100A9/FABP1/ALB/FABP7/CRABP1/ACOX2/FABP4/CYP4F11/FFAR4/FABP12/GSTA1",19

/GLI3/DLX2/PRRX1/TGFB3/RDH10/RUNX2/BMP4/SIX1/PDGFR4/MMP14/WNT9B/TGFB2/FOXC2/IR
9e-08,"GNA15/OPRK1/HTR2A/CALCA/OPRM1/NPR3/NMUR2/AGT/HTR2B/HCTR2/LHCGR/AGTR1/V
PAX2/SALL1/TCF21/BMP4/LIF/YAP1/OSR1/WNT9B/GDNF/LAMB2/ADIPOQ/POU3F3",13

13/TREM2/FA2H/MAG/PTPRZ1/GLI3/ASPA/IFNG/DLX2/CLU/EGR2/PLP1/SOX9/IL1B/LIF/GFAP/ITGB4/I
ETN/INHBA/MMP19/TNFAIP6/EREG/DACH2/VGF/FST/PDGFR4/NR5A1/LHCGR/RBP4/LHX9/ADAMTS1
AX2/SIX4/SALL1/GLI3/FGF1/TCF21/BMP4/SOX9/SIX1/HOXD11/AGT/GPC3/WNT9B/SHH/GDNF/TACST

MP/SERPINE1/GLI3/PERP/BCHE/IL1R2/F3/CPN1/CPXM2/PLAU/SRGN/CPM/THBS1/DHH/REN/GSN/AC
A1/CPS1/VIM/FGFR2/PTGS2/CXCL2/OPRK1/APOB/TREM2/TSPO/CTSG/HAMP/SERPINE1/CSF3/CCL2/
FSTL3/COL16A1/CCDC80/LGALS1/CTSG/FERMT1/GLI3/CXCL12/MAP3K8/CCL2/ST3GAL4/IFNG/NEDD9
XC1/FGFR2/TGFB3/SEMA3C/PAX2/WNT2/COL1A1/FOLR1/BMP5/FN1/TCF21/TGFB3/MSX2/RDH10/
13/GLI3/DKK1/PRRX1/MSX2/RDH10/HOXC11/RUNX2/BMP4/GDF5/HOXD13/NOTCH2/LRP4/FBN2/CF
/HOXA13/GLI3/DKK1/PRRX1/MSX2/RDH10/HOXC11/RUNX2/BMP4/GDF5/HOXD13/NOTCH2/LRP4/FI
2/CALB1/SOX9/LIF/YAP1/OSR1/LAMB2/ADIPOQ/WNT7B/POU3F3",12
1/GLI3/FGF1/TCF21/BMP4/SOX9/SIX1/HOXD11/AGT/OSR1/GPC3/WNT9B/SHH/GDNF/TACSTD2/WT
2/CXCL12/CCL7/CCL2/CCL8/CALCA/TRPV4/BMP5/CCL20/PADI2/DUSP1/PLG/LGALS3/ANXA1/IL6/THBS
OXA13/SFRP4/DKK1/BMP5/TGFB3/SFRP5/MSX2/TNFAIP6/RUNX2/BMP4/GDF5/GDF15/NOTCH2/FST
A/MMP19/TNFAIP6/EREG/SERPINF1/PDGFR/NR5A1/LHCGR/CYP1B1/ADAMTS1/TIMP4/PTX3/AXL/I
17A1/FGFR2/FOSL2/PTHLH/SULT2B1/KRT31/DSP/FERMT1/FA2H/SFRP4/DKK1/GLI1/IL1A/MSX2/HOX
4/EGFR/SIX4/WNT2/DKK1/FGF1/HOXC11/BMP4/SOX9/SIX1/GATA5/GDNF/AR/CSF1",15
COL16A1/EPDR1/FAT2/TRIP6/CCDC80/FERMT1/SERPINE1/KANK1/COL1A1/NEDD9/HRG/FN1/NID1/AP
DKK3/FGFR3/PTGS2/APOB/TREM2/TSPO/AVP/HTR2A/RARRES2/APOA4/APOC3/IFNG/BMP5/FGF1/A
OX/FGF1/HSD11B1/TCF21/TGFB3/RDH10/BMP4/SOX9/LIF/FOXA1/CHI3L1/HMGCS2/PDGFR/YAP1/R
P/PTGS1/PTGDS/BMP5/PLA2G4A/TTR/RDH10/LRAT/CYP1B1/CYP2C9/RBP4/CYP11A1/EPHX1/CYP17
YC/PLS3/COMP/SFRP4/GLI3/COL1A1/TRPV4/GHR/LOX/TGFB3/MSX2/RUNX2/BMP4/SOX9/NOTCH2/C
SEMA3C/FAP/FAT2/APOH/HMOX1/MMP9/FERMT1/TIMP1/SRPX2/SYDE1/MEOX2/KANK1/ACTA2/FO
MP4/SOX9/SIX1/HOXD13/YAP1/SHH",11
/SHH/RET/EMX2",11
/MMP2/COL9A3/RETN/INHBA/MMP19/TNFAIP6/EREG/DACH2/VGF/FST/PDGFR/NR5A1/LHCGR/LH
SP/MYL9/HTR2A/TNNT1/MYH14/COMP/SCN1B/ACTA2/MYH1/CRYAB/CALCA/TRPV4/KCNA1/FGF12/
/PYGL/GLRA2/MAG/PTGDS/FOLR1/LRAT/FABP3/PCK1/APOC1/ALOX5AP/TM4SF5/CRABP2/PMP2/P4F
1/CXCL12/CSF3/CCL7/CCL2/CCL8/PF4V1/IFNG/IL1A/CCL20/TGFB3/CXCL6/IL1B/TNFSF9/LIF/NGF/TMB
XA13/GLI3/AREG/GLI1/FGF1/TGFB3/MSX2/BMP4/SOX9/HOXD13/FOXA1/NOTCH2/IL6/FGF7/EGFR/T
O/LRAT/CYP1B1/RBP4/CRABP2/DHRS3/ALDH1A1/CRABP1/CYP2S1/SDR16C5/PNLIP/CYP27C1/ADH1A
A13/RARRES2/GLI3/GLI1/TCF21/TGFB3/SFRP5/BMP4/HOXD13/GATA5/ASS1/PYY/HMGCS2/PDGFR
NEFH/FA2H/EGR2/ITGB4/NGF/RXRG/NTRK2/LGI4/RUNX1/ISL2/CLDN1/SERPINI1/CITED2/GDNF/LAM
L12A1/FN1/DUSP1/DUSP4/INHBA/HOXC11/BMP4/COL5A1/GATA4/DUSP5/COL8A1/MMP14/TBX20/S
/FERMT1/SFRP4/GLI3/DKK1/GLI1/MDFI/TBX18/SFRP5/BICC1/SOX9/APOE/BARX1/GSC/LRP4/IGFBP4/
4/SOX9/LIF/PDGFR/OSR1/WNT9B/RET/GDNF/IRX2/LAMB2/ADIPOQ/WT1",16
COL5A1/LUM/COL8A1/COL1A2/COL3A1/COL4A5/COL4A6/COL5A2",12
MP/WNT2/GLI1/MSX2/SOX9/CGA/AGT/GATA4/YAP1/MMP13/RBP4/DUSP6/FGF7/RSP02/LATS2/RU
10/LRAT/HMGCS2/CYP1B1/CYP2C9/RBP4/CRABP2/DHRS3/ALDH1A1/CRABP1/CYP2S1/SDR16C5/PNL
5/GLI3/GLI1/LOX/FGF1/HSD11B1/TCF21/TGFB3/RDH10/BMP4/SOX9/LIF/FOXA1/CHI3L1/HMGCS2/P
AT/SERPINE1/HRG/SPP1/PLG/PLAU/TSPAN8/APOE/APCS/PDGFR/THBS1/SERPING1/CD109/CLDN19
/INHBA/MMP19/TNFAIP6/EREG/VGF/FST/PDGFR/NR5A1/LHCGR/LHX9/ADAMTS1/MMP14/LHX8/P
SFRP4/DKK1/SFRP5/MSX2/TNFAIP6/BMP4/GDF5/NOTCH2/FST/GATA4/DLX1/SFRP2/GPC3/FZD1/NBL
SULT2A1/SULT1E1/BMP5/TTR/RDH10/LRAT/CYP1B1/RBP4/CYP11A1/CYP11B1/DHRS3/ALDH1A1/SDF
/GLI3/PITX3/EFEMP1/BMP4/SOX9/GNGT1/COL5A1/NOTCH2/FOXF2/RBP4/FBN2/FOXN4/COL8A1/N
BP4/DHRS3/ALDH1A1/SDR16C5/PNLIP/CYP27C1/ADH1A/AKR1C3/ADH1B/AKR1B10/ADH4/ADH1C",1
49e-07,"DCN/VCAN/CHADL/OGN/FMOD/LUM/HAPLN1/ACAN/PODN/AMBN/BGN/PRELP",12
DH10/LRAT/CYP1B1/RBP4/CRABP2/DHRS3/ALDH1A1/CRABP1/CYP2S1/SDR16C5/PNLIP/CYP27C1/AD
FGF1/TCF21/BMP4/SOX9/SIX1/HOXD11/AGT/GPC3/WNT9B/SHH/GDNF/TACSTD2/WT1/HOXB7",20
/HMOX1/MMP9/WNT2/OGN/GLI1/IFNG/NPR3/NR4A3/TGFB3/EREG/BMP4/SIX1/CNN1/APOE/HTR1
1/AGT/OSR1/RET/GDNF/ADIPOQ/TACSTD2/WT1/HOXB7",14
DE/CRP/APCS/THBS1/COLEC12/APOA2/LIPC/PCSK9/LPL",14
POE/CRP/APCS/THBS1/COLEC12/APOA2/LIPC/PCSK9/LPL",14
X1/TSPO/CPNE6/MMP9/GLRA2/AQP9/HAMP/SOD3/SYT10/KCNA1/TNNC1/IL1A/CASQ2/MT1G/MT2/

/MMP7/MMP13/MMP3/ADAMTS3/MMP14/MMP10/CLK6/PRTN3/MMP1/MMP28",16
 VMO3A/PVALB/SIX4/CALB1/HOXA2/HOXA13/GLI3/BMP5/TBX18/PRRX1/TGFB3/RDH10/SDC4/BMP4/
 F4V1/HRG/SLPI/CXCL6/SPINK5/CXCL9/CXCL14/SPON2/S100A9/CXCL3/CXCL1/DEFA4/DEFA6/WFDC13
 /NID1/TGFB1/MMP13/THBS1/ITGA11/LUM/COL6A2/SERPINH1/PCOLCE2/TNXXB/CRTAP/PODN/COL14
 3/LIF/YAP1/OSR1/WNT9B/WNT7B/POU3F3",11
 1/FOLR1/FGF1/RDH10/HOXC11/BMP4/SIX1/GATA5/TGFB2/CITED2/SHH/GDNF/AR/WT1",20
 4/WNT2/FGF1/BMP4/SOX9/SIX1/LIF/HOXD13/AGT/FGF7/ADAMTS12/GJA1/SHH/GDNF/AR/TACSTD2/
 SERPINE1/GLI3/FAM20A/ODAM/PERP/DLX2/MSX2/RUNX2/BMP4/FST/LRP4/PDGFR4/DLX1/RSPO2/I
 CMA1/PTGS1/HMOX1/CTSG/AVP/ACTA2/CALCA/GLP1R/NPR3/SGK1/EDN3/AGT/REN/AGTR1/CYP11B
 A2/LPL",9
 CCL20/IL1R2/IL1R1/PCK1/SOX9/IL1B/IL6/IL1RN/XCL1/ADAMTS12/NKX3-1/CXCL8/HAS2/FGG/FGB/CCL
 10/HOXC11/BMP4/SIX1/GATA5/CITED2/SHH/GDNF/AR/WT1",13
 /PTGS2/DDX1/TREM2/OSM/HMOX1/FERMT1/SERPINE1/TRPV4/IFNG/IL1A/IL1R1/IL1RL1/F3/NR4A3/
 RBB3/FGFR2/TGFB3/SEMA3C/LRP2/DSP/HAMP/WNT2/DKK1/GLI1/BMP5/TBX18/LOX/TNNC1/FHL2,
 1A2/MCOLN3/GNA15/TRPC5/MT3/AVP/HTR2A/CALB1/CXCL12/CCL7/CCL8/CALCA/TRPV4/GLP1R/C
 /HOXC11/LRP4/OSR1/DLX1/EN1/IRX2/IRX3/HOXC10/HOXA10",14
 RPC5/SEMA3C/LRP2/MT3/TREM2/TSPO/SRPX2/MAG/WNT2/PTPRZ1/GLI3/CXCL12/PITX3/DKK1/ASP
 /CLEC3B/FGG/FGA/FGB/ANXA2/S100A10",12
 C80/FERMT1/SERPINE1/KANK1/COL1A1/NEDD9/HRG/FN1/NID1/APOA1/PLG/HOXA7/PLAU/SDC4/R
 AOXD1/RDH8/APOB/MT3/SULT2B1/SULT2A1/MOGAT3/SULT1E1/APOA4/BMP5/FGF1/SPR/PLA2G4A,
 3C/PAX2/OSM/FOLR1/FN1/MSX2/RDH10/TRIM6/HOXA7/EDN3/RUNX2/BMP4/SOX9/SIX1/LIF/FOXA1
 /PAX2/HMOX1/WNT2/CXCL12/ODAM/AREG/BMP5/THBS4/FGF1/F3/NR4A3/NR4A1/BMP4/SOX9/NC
 POA4/APOC3/APOA1/PLA2G5/APOE/APOC1/AGT/AGTR1/APOA2/LIPC/LPL/PLA2G2A",16
 H/HTR2A/APOA4/APOA1/PLA2G5/PDGFR4/AGT/HTR2B/AGTR1/EGFR/RHOC/P2RY12/PNLIP/C5AR1/
 1/COMP/MGP/LOX/TGFB3/SRGN/BMP4/SOX9/OMD/MMP13/FBN2/OSR1/AHSG/GPC3/RSPO2/GJA1/
 1/TSPO/LIPG/HAMP/COL1A1/FOLR1/BCHE/IL1A/SPP1/LRAT/FOXA2/ASS1/POSTN/HMGCS2/GATA4/C
 GFR2/FGFR3/TGFB3/PRLH/TRPC5/SEMA3C/MT3/TLL2/SIX4/CPNE6/MAG/HAMP/WNT2/CXCL12/GLI
 3/FGFR3/PRLH/FCGR2B/PTGS2/OPRK1/MMP2/TREM2/MMP9/TIMP1/PLAT/RETN/KLF1/RARRES2/KANK
 13/IL1A/PLA2G4A/APOA1/SPP1/LRAT/FABP3/IL1B/C3/APOE/ABCA12/CRH/PTGES/GALR1/NKX3-1/LPL
 2/FGFR2/PAX2/SIX4/WNT2/BMP4/SOX9/SIX1/HOXD13/AGT/FGF7/SHH/GDNF/AR/TACSTD2/HOXB7",17
 1A3C/LRP2/DSP/WNT2/DKK1/FOLR1/BMP5/TNNC1/FHL2/MSX2/BMP4/SOX9/SIX1/FGFR1/COL5A1/C
 BCG2/APOE/AOX5AP/FBLN5/PTGES/S100A9/FABP1/ALB/GPX8/ALDH1A1/NXN/TXNDC2/NQO1/AKR
 1/D2/AR/FOXL2/WT1",11
 LB1/SOX9/LIF/YAP1/OSR1/WNT7B/POU3F3",10
 2/DKK3/PTGS2/APOB/TSPO/AVP/HTR2A/APOA4/APOC3/IFNG/BMP5/FGF1/IL1A/APOA1/RDH10/FAB
 13/DLX2/PRRX1/TGFB3/MSX2/RDH10/RUNX2/BMP4/SIX1/PDGFR4/MMP14/WNT9B/TGFB2/FOXC2/
 1/HTR2A/EDN3/MTNR1B/AGT/AGTR1/DOCK5/BDKRB2/ADRA1B/FGG/FGA/FGB/ADRA1D/HTR1A/HRH1
 14/RUNX1/C1R/CLEC3B/PRSS12/CLK1/FGG/FGA/FGB/ANXA2/S100A10/HP/HPR",19
 1/TBX18/TBX22/SOX9/FOXA2/SIX1/FOXA1/GSC/DHH/SFRP2/FZD7/ISL2/TBX20/SHH/AR/HOXC10/SO
 14/H4/CYP24A1/SNAI2/CPS1/WIP1/PRLH/PTGS2/PAX2/SCTR/MT3/HMOX1/TSPO/LIPG/HAMP/COL1A1/
 PC2/RDH10/LRAT/HMGCS2/CYP1B1/CYP2C9/RBP4/CRABP2/DHRS3/ALDH1A1/CRABP1/CYP2S1/SDR1
 SF1A/PTGS2/APOB/HAMP/CCL7/CCL2/CCL8/COL1A1/CALCA/KRT18/CCL20/APOA1/PCK1/ZFP36/MYO
 1/RARRES2/CXCL12/CCL7/CCL2/TRPV4/SMOC2/THBS4/FGF1/HRG/PADI2/F3/DUSP1/TNFAIP6/EDN3/LI
 XA5/GLI1/BMP5/APOA1/BMP4/SOX9/FOXA2/SIX1/SOX3/PDGFR4/ANXA1/CGA/IL6/NR5A1/CYP1B1/C
 10XD13/YAP1/SFRP2/SHH",12
 /TREM2/HMOX1/PLTP/LIPG/APOA4/APOC3/APOA1/PLA2G5/APOE/APOC1/AGT/AGTR1/APOA2/LIPC,
 1/WNT2/GLI3/DKK1/FGF1/HOXC11/BMP4/SIX1/GATA5/GDNF/AR",14
 XA1/LMX1B/SFRP2/RSPO2/NR4A2/FZD1/WNT9B/EN1/SHH/OTX2",14
 /TCF21/SATB2/TGFB3/INHBA/PDGFR4/FOXF2/OSR1/CSRN1/FZD1/WNT9B/DHRS3/TGFB2/SHH/OS
 1/CRP/APCS/THBS1/COLEC12/LIPC/PCSK9",10

L1RL1/TREM1/CXCL6/IL1B/LBP/IL6/KLF4/ADCYAP1/TSBP/AIRE/TLR3/LPL/DEFB124/ADIPOQ/FFAR3/AF
APOA4/APOC3/APOA1/PLA2G5/APOE/APOC1/AGT/AGTR1/APOA2/LIPC/LPL/PLA2G2A",16
B/GDNF/IRX2/IRX3",10
1/TCF21/BMP4/NOTCH2/PDGFR/OSR1/MYO1E/KLF15/RET/SERPINE1/LAMB2/FOXC2/ADIPOQ/WT:
NFRSF1A/FCGR2B/PTGS2/CMA1/TREM2/OSM/LGALS1/MMP9/WFDC1/HAMP/SERPINE1/TRPV4/IFN
/NGF/CGA/LUM/KERA/GPC3/MMP14/ACAN/DEFA4/DEFA6/MUC15/CSPG4/F2/BGN/PROS1/WNT7B/
A/TTR/INHBA/EDN3/VGF/PYY/CGA/AGT/ADCYAP1/VIP/CRH/FBN1/IGF2/PRL/CALCB/METRN1/ADIPO
S1/UTS2/FOXC1/PTGS2/SLC4A4/LRP2/MMP2/AVP/HTR2A/COMP/ACTA2/SOD3/CALCA/TRPV4/SLC22
CALB1/ADAM2/PTPRZ1/DKK1/ST3GAL4/GLP1R/BCHE/SGK1/EGR2/APOE/PPP1R1B/SERPINF1/CHL1/N
IL1A/APOA1/APOE/APOC1/CGA/AGT/AGTR1/STAR/APOA2/CES1",13
DKK1/INHBA/BMP4/ITGB4/KLF4/SFRP2/GJA1/FOXC2",13
IL1/BMP4/SOX9/HOXA10/FOXO1/SERPINF1/ANXA1/SHH/NKX3-1/AR/HOXA10",16
3/APOA1/APOE/APOA2/LIPC/LPL",8
C3/APOA1/APOE/APOA2/LIPC/LPL",8
NTRK2/MYO1E/TGFB2/CITED2/TBX20/SHH/TMEM100/HAS2/JUNB/NKX2-5/WT1/WNT7B/EMP2/AF
C80/FERMT1/NEDD9/HRG/FN1/NID1/APOA1/SDC4/RRAS/EMILIN1/COL8A1/DOCK5/DOCK1/THY1/A
O/CPNE6/MMP9/GLRA2/SYT10/KCNA1/MT1G/MT2A/SERPINF1/ALOX5AP/TPH2/SNCA/EGFR/SYT8/C
G/ASPA/IFNG/CLU/PLP1/IL1B/GFAP/ITGB4/IL6/NTRK2/NKX6-2/LGI4/MXRA8/S100A9/SHH/MAL/LAM
AP5",8
L1A2/COL3A1/COL5A2",8
L1A2/COL3A1/COL5A2",8
SYDE1/IL1A/DUSP1/MSX2/PAEP/INHBA/BMP4/SOX9/LIF/HOXA10/TEX101/SERPINF1/NR5A1/SPATA:
R16C5/ADH1A/AKR1C3/ADH1B/ADH4/ADH1C",10
T3/PLG/MMP19/IL6/MMP7/MMP13/MMP3/MMP14/PDPN/MMP10/TPSAB1/MMP1/ELANE",18
I3/CXCL12/DKK1/DLX2/BMP4/SOX9/GDF5/SIX1/FOXO1/NGF/SOX3/LBX1/DLX1/CNTN4/SFRP2/NBL1/I
GA8/MYO3A/PVALB/SIX4/CALB1/HOXA13/GLI3/TBX18/PRRX1/TGFB3/SDC4/BMP4/SOX9/SIX1/LRIG3
D3/APOA4/ABCG2/APOE/ALOX5AP/FBLN5/PTGES/S100A9/FABP1/ALB/GPX8/ALDH1A1/NXN/TXNDC
3/APOA1/APOE/APOC1/APOA2/LIPC",9
e-06,"PROM1/WWTR1/PAX2/MMP9/LIF/YAP1/OSR1/WNT9B/GDNF",9
3C/FOLR1/FN1/RDH10/EDN3/BMP4/SOX9/HTR2B/SEMA3D/PITX2/CITED2/TBX20/SHH/RET/GBX2/G
HOXC11/BMP4/SOX9/SIX1/GATA5/GDNF/AR",13
3C/FOLR1/FN1/RDH10/EDN3/BMP4/SOX9/SIX1/GSC/HTR2B/SEMA3D/PITX2/CITED2/SHH/RET/GBX2/
XA2/DKK1/COL1A1/LRAT/PCK1/SOX9/SERPINF1/KLF4/YAP1/RBP4/RXRG/OSR1/FZD7/WNT9B/BRINP:
FGFR2/TGFB3/LRP2/DSP/HAMP/WNT2/DKK1/GLI1/BMP5/TBX18/TNNC1/FHL2/MSX2/BMP4/GATA5
9/TIMP1/SYDE1/KLF1/AMBP/CALCA/SPP1/TGFB3/NDP/IL1B/LIF/ITGB4/AGT/ADCYAP1/CRH/A1CF/GJ
2/DSP/AVP/HTR2A/SCN1B/CALCA/GLP1R/TBX18/CASQ2/KCNJ5/ADORA3/EDN3/MTNR1B/AGT/GATA
P19/PCK1/VGF/ASS1/HMGCS2/FDX1/CYP1B1/REN/FOS/FOSL1/THBD/ADIPOQ/PENK/WT1/AQP1",22
H/CHADL/COMP/GLI3/EFEMP1/MSX2/TGFB1/RUNX2/BMP4/SOX9/GDF5/OSR1/SFRP2/SERPINF1/AD
5/MDFI/SPP1/PLG/NDP/LIF/NOTCH2/TTPA/RSPO3/EGFR/PLCD3/CITED2/GJB2/HTRA1/IGF2/PLAC1/JU
COL1A1/TRPV4/GHR/RUNX2/BMP4/SOX9/MMP13/SERPINF1/MMP14/TGFB2/COL3A1/TSKU/TMEM
M1/SEMA3B/ATP1A2/CPS1/UTS2/FOXC1/TPR5/PTGS2/SEMA3C/PAX2/SCTR/MMP2/MT3/AVP/HTR
/ALOX5AP/PTGES/S100A9/FABP1/ALB/GPX8/NXN/TXNDC2/NQO1/HBA1/HBM/GPX3/HBD/GSTA1/HF
JMP/HAMP/PITX3/CRYAB/CALCA/TGFB3/PCK1/ASS1/SERPINF1/AGT/NR5A1/IGFBP1/SERPINF1/GFRA
PRLH/PTGS2/OPRK1/TIMP1/PLAT/RETN/RARRES2/KANK1/CXCL12/COL1A1/AREG/TRPV4/GLP1R/GHR
3/MEGF10/TMPRSS15/COLEC12/TMPRSS3/CXCL16/ASGR2/PRSS12/FOLR2/SCARA5/LRP1B/OLR1/TM
C/FOLR1/FN1/RDH10/EDN3/BMP4/SOX9/HTR2B/SEMA3D/PITX2/CITED2/SHH/RET/GBX2/GDNF/FOX
1A/APOA1/SPP1/LRAT/FABP3/IL1B/APOE/APOC1/AGT/THBS1/REN/ABCA12/AGTR1/CRH/PTGES/APO
2A/RETN/CXCL12/SYT10/TRPV4/IFNG/OPRM1/IL1A/PLA2G4A/WLS/SPP1/ADORA3/INHBA/NR4A1/EI
3/TNFRSF1A/PTGS2/APOH/TREM2/OSM/LGALS1/SERPINE1/RARRES2/CXCL12/CCL7/TRPV4/IFNG/OP
IA1/TLL2/CTSG/GZMB/MMP9/PLAT/ADAM2/F3/ADGB/PLG/PLAU/MMP19/F10/MASP1/USP6/CLK10/

/TRPV4/IFNG/IL1RL1/CXCL6/IL1B/LBP/IL6/KLF4/ADCYAP1/TSPL/AIRE/TLR3/LPL/DEFB124/ADIPOQ/FF,
 B1/DCN/FOXC1/APOH/CMA1/HMOX1/HOXA5/SERPINE1/SMOC2/SPARC/THBS4/FGF1/HRG/IL1A/F3/
 /RARRES2/CXCL12/CCL7/CCL8/TRPV4/THBS4/IL1A/CCL20/IL1R1/EDN3/LBP/LGALS3/LYVE1/IL6/THBS1
 'SEMA3C/LRP2/DSP/WNT2/BMP5/TNNC1/FHL2/MSX2/BMP4/FGFRL1/NOTCH2/GATA4/RBP4/SFRP2/
 3/PAX2/SIX4/BMP4/SOX9/SIX1/AGT/GDNF/TACSTD2/HOXB7",10
 IMP2/PTHLH/MMP9/TIMP1/SYDE1/KLF1/AMBP/CALCA/SPP1/TGFB3/NDP/IL1B/LIF/ITGB4/AGT/ADCY
 NFRSF1A/PAX2/SULT2B1/MMP9/SERPINE1/SFRP4/IFNG/IL1A/MSX2/HOXA7/BMP4/SOX9/IL1B/ZFP36
 12/HTR2A/CALB1/ADAM2/PTPRZ1/DKK1/GLP1R/BCHE/SGK1/EGR2/APOE/PPP1R1B/SERPINF1/NGF/A
 NAI2/DKK3/FERMT1/SFRP4/GLI3/DKK1/GLI1/TBX18/SFRP5/BICC1/SOX9/APOE/LRP4/IGFBP4/SFRP2/T
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 1A1/SNAI2/CPS1/WIPI1/PRLH/PTGS2/PAX2/SCTR/MT3/HMOX1/TSPO/LIPG/HAMP/COL1A1/FOLR1/TF
 VP/SLC32A1/AQP9/SLC1A6/FOLR1/SLC22A2/SLC27A6/IL1A/PLA2G4A/ABCG2/FABP3/IL1B/PLA2G5/A
 /ERBB3/TNFRSF1A/FGFR3/TREM2/OSM/HTR2A/CSF3/AREG/IFNG/NEDD9/GHR/THBS4/EREG/LIF/LRF
 ERMT1/SALL1/PLEKHA4/SFRP4/GLI3/KANK1/DKK1/COL1A1/FOLR1/GLI1/MDFI/TBX18/WLS/SFRP5/BI
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 'FP36/NOTCH2/FST/YAP1/FGF7/CD109/SDR16C5/HAS2/PRKD1",15
 THBD/F2",7
 AC/APOA1/LIPC/LPL/PNPLA1/LIPI/PLIN5",12
 RDH10/RUNX2/CRABP2/OSR1/RSPO2/EN1/SHH/OSR2",12
 /SERPINE1/SMOC2/FGF1/IL1A/F3/IL1B/C3/RRAS/CHI3L1/GATA4/KLF4/THBS1/CYP1B1/ANXA3/SFRP2,
 1A1/HMOX1/SERPINE1/SMOC2/FGF1/IL1A/F3/IL1B/C3/RRAS/CHI3L1/GATA4/KLF4/THBS1/CYP1B1/A
 B/HSD17B2/TSPO/APOA4/IFNG/BMP5/FGF1/IL1A/APOA1/APOE/HMGCS2/CGA/CYP27A1/NR5A1/FD
 /FOXC1/TNFRSF1A/CXCL2/MT3/TREM2/OSM/CTSG/LILRB5/CXCL12/CSF3/CCL7/CCL2/CCL8/PF4V1/KI
 /APOA1/NPC2/CLU/APOE/APOC1/ABCA8/STAR/APOA2/LIPC/PCSK9/PNLIP/ANXA2/CES1",20
 3/PLP1/SOX9/IL1B/LIF/GFAP/IL6/S100A9/SHH/GPR37L1/LAMB2/F2/ROR1/C5AR1",20
 OA4/APOE/ALOX5AP/FBLN5/PTGES/S100A9/FABP1/ALB/GPX8/NXN/TXNDC2/NQO1/HBA1/HBM/GP
 L/CALB1/WNT2/GLI3/PITX3/BMP4/SOX9/NOTCH2/FOXF2/RBP4/FOXN4/COL8A1/NTRK2/THRB/THY1/
 PTGS2/TREM2/OSM/LGALS1/SERPINE1/TRPV4/IFNG/IL1RL1/IL1B/C3/LBP/ALOX5AP/AGT/IL6/NFKBIZ,
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 '1/DKK3/FGFR2/TGFB3/ITGA8/LTBP4/FERMT1/WNT2/COL1A1/FOLR1/LOX/TGFB3/FMOD/SOX9/GDI
 4/EGFR/MT1E/FOS/MT1X/AKR1C3/MT1F/MT1A/MT1M",13
 /FOLR1/MSX2/BMP4/SIX1/SFRP2/FZD1/DHRS3/TGFB2/PITX2/NPY1R/CITED2/TBX20/FOXC2/FZD2/N
 'FA2H/COMP/DKK1/COL1A1/IL1A/MSX2/HOXA7/INHBA/EREG/SOX9/ZFP36/COL5A1/ITGB4/SPINK5/F
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 MP/WNT2/GLI1/CGA/YAP1/RBP4/DUSP6/LATS2/RUNX1/TGFB2/CITED2/PI16/TBX20/IGF2/FOXC2/EF
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 1E/MT1X/MT1F/MT1A/MT1M/AQP1",11
 /LRP2/TSPO/MAG/WNT2/PTPRZ1/GLI3/CXCL12/ASPA/IFNG/NEDD9/OPRM1/FN1/APOA1/EGR2/BMP
 /F2",8
 /DUSP1/DUSP4/INHBA/COL5A1/DUSP5/COL8A1/MMP14/TBX20/SOX2/COL5A2",16
 /COL1A1/AREG/MMP19/PCK1/IL1B/VGF/ASS1/HMGCS2/FDX1/CYP1B1/REN/P2RY12/FOS/P2RY2/FO
 '1/FN1/RDH10/EDN3/BMP4/SOX9/HTR2B/SEMA3D/PITX2/CITED2/SHH/RET/GBX2/GDNF/FOXC2/ERB
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 RPV4/IFNG/TTR/SPP1/INHBA/SERPINA7/EDN3/IL1B/FOXA2/LIF/VGF/MTNR1B/ANXA1/CGA/AGT/IL6/
 2/ERBB3/TNFRSF1A/FGFR3/TIMP3/HMOX1/SRPX/SERPINE1/KRT18/IFNG/BMP5/IL1A/INHBA/BMP4/I
 X2/GDF5/CRABP2/OSR1/RSPO2/EN1/SHH/OSR2",13
 AMP2/PTHLH/MMP9/TIMP1/SYDE1/KLF1/AMBP/CALCA/SPP1/TGFB3/NDP/IL1B/LIF/ITGB4/AGT/ADC
 ARRES2/SULT1E1/APOA4/APOC3/AADAC/PLCH1/PLA2G4A/HSD11B1/APOA1/SPP1/PLBD1/PCK1/IL1B,
 GF10/TMPRSS15/COLEC12/TMPRSS3/CXCL16/PRSS12/SCARA5/TMPRSS2/DMBT1/CFI",15

COMP/GHR/IL1R2/IL1R1/IL1RL1/TGFB3/GDF5/ZFP36/IL1RN/THBS1/ACKR3/OSMR/CD109/NBL1/PDPI
 T3GAL4/HRG/F3/PLG/THBS1/THBD/F2",10
 REG/ADAMTS1",10
 4P4/HOXD13/EGFR/SHH/AR/SOSTDC1",10
 4/HRG/F3/PLG/THBS1/THBD/F2",10
 X9/LIF/FOXA1/YAP1/FGF7/RSPO2/TGFBR2/SHH/WNT7B",15
 5127e-05,"TIMP3/HMOX1/SERPINE1/BMP5/LGALS3/TMBIM1/THBS1/PMAIP1/SFRP2/ITPRIP/ATF3/F
 2B/PTGS2/SEMA3C/FMO4/MMP2/SMOX/HMOX1/TSPO/HTR2A/SULT2A1/PON3/AHR/COL1A1/LOX/I
 /PLAT/AHR/COL1A1/AREG/CASQ2/MMP19/PCK1/IL1B/VGF/ASS1/HMGCS2/FDX1/CYP1B1/REN/P2RY
 CSM2B/DHRS9/PTGS2/PTGS1/AVP/LIPG/FA2H/PTGDS/APOA4/APOC3/PLA2G4A/APOA1/RDH10/PLP1
 3FBR3/ITGA8/LTBP4/FERMT1/WNT2/COL1A1/FOLR1/LOX/TGFB3/FMOD/SOX9/GDF5/GDF15/THBS1/
 5D4",7
 APOE/LRP4/TTPA/MYOCN/MME/C5AR1",13
 SF1A/PTGS2/PTGS1/GGT5/AVP/LIPG/FA2H/PTGDS/APOA4/APOC3/SLC27A6/PLA2G4A/HAO2/APOA1
 PP1/IL1B/LIF/ITGB4/A1CF/GJA1/TGFBR2/HMX3/EMP2/APELA",16
 'WNT9B/GDNF",9
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 4T1A/MT1M",8
 /MT1A/MT1M",8
 B1/SULT1E1/APOA4/APOC3/HSD11B1/APOA1/NPC2/GC/STAR/PMP2/NR3C2/APOA2/AR/GPR183/IR
 3/FCGR2B/MMP2/CTSG/FGL1/SERPINE1/GLI3/KANK1/CXCL12/COL1A1/TRPV4/HRG/APOA1/DUSP1/
 5H/XCL1/CXCL16/GPR183/CCL11/SAA1/CCL13/CCL23/CCL16/CCL18/CCL14",17
 1/FERMT1/SALL1/PLEKHA4/WNT2/SFRP4/GLI3/KANK1/DKK1/COL1A1/FOLR1/GLI1/OPRM1/MDFI/TB
 1/ERBB3/TNFRSF1A/FGFR3/TREM2/OSM/HTR2A/CSF3/AREG/IFNG/NEDD9/GHR/THBS4/HRG/EREG/L
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 1TA5/GDNF/AR",10
 R/WNT9B/SHH/AR/WT1/SYCP2",10
 /HRG/F3/PLG/THBS1/THBD/F2",10
 MT1X/MT1F/MT1A/MT1M",10
 IFNG/APOA1/IL1B/C3/PLA2G5/FCN3/AHSG/APOA2/PTX3/MBL2/RAB31/COLEC10/C4B/C4A",18
 NE1/KANK1/ST3GAL4/SMOC2/HRG/F3/PLG/ANXA1/THBS1/CLDN1/FOXC2/THBD/F2",16
 .RP2/MT3/TREM2/TSPO/MAG/WNT2/PTPRZ1/GLI3/CXCL12/PITX3/ASPA/IFNG/OPRM1/FN1/DLX2/SP
 2/INHBA/SOX9/SPINK5/FST/LRP4/LGR5/KRT71/FGF7/EGFR/CD109/FOXQ1/SHH/TRPV3/SOSTDC1/TS
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 F2/LHCGR/RBP4/WNT9B/SHH/AXL/AR/WT1/SYCP2",14
 /HMOX1/SIX4/MAG/PTPRZ1/CCL2/TGFB3/GDF5/SIX1/APOE/CHL1/NGF/MTNR1B/DLX1/SNCA/NTRK2
 TRPV4/IFNG/SPP1/INHBA/EDN3/IL1B/FOXA2/LIF/VGF/MTNR1B/ANXA1/CGA/AGT/IL6/IL1RN/RBP4/AI
 1/SIX1/YAP1/RBP4/MEGF10/RUNX1/TGFBR2/CITED2/TBX20/SHH/FOXC2/SIX5/ERBB4/NKX2-5",18
 P1/IGFBP1/GJA1/FZD7/RUNX1/TGFBR2/CLK6/MYOZ1/ERBB4/SOX2/APOD",18
 3",7
 DCN/NGFR/FSTL3/LRP2/CHRD1/DKK1/HRG/TNFAIP6/AGT/THBS1/EMILIN1/DLX1/SFRP2/ADAMTS12
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 TR1/CRH/GJA1/GALR1/NKX3-1/OR51E2/FOXL2",12
 'ZFP36/MYOD1/ASS1/SERPINF1/HMGCS2/ANXA1/CYP1B1/FBXO32/GJB2/FAM107A/AKR1C3/AQP1",1
 M2B/DHRS9/PTGS2/PTGS1/GGT5/AVP/LIPG/FA2H/PTGDS/APOA4/APOC3/PLA2G4A/APOA1/RDH10/
 /APOA2/LIPC/CES1",9

MOX1/TSPO/CPNE6/MMP9/GLRA2/SYT10/KCNA1/MT1G/MT2A/SERPINF1/ALOX5AP/TPH2/SNCA/EGF
 BPB/IL1B/C3/MASP1/CRP/APCS/FCN3/SERPING1/VSIG4/C8A/C1R/MBL2/MFAP4/C1S/COLEC10/CFI/C
 ASS1/SLC30A2/SLC30A8/MT1E/MT1X/MT1F/MT1A/MT1M",15
 HMOX1/LIPG/APOC3/APOA1/APOE/APOC1/APOA2/LIPC/PCSK9/ADIPOQ/ANXA2",15
 1/HOXD13/HMGCS2/THBS1/NKX3-1/AR/NQO1/HOXA10",13
 AC/APOA1/APOA2/LIPC/LPL/PNPLA1/LIPI/PLIN5",13
 AC/APOA1/APOA2/LIPC/LPL/PNPLA1/LIPI/PLIN5",13
 MT1E/MT1X/MT1F/MT1A/MT1M/AQP1",13
 IL6/EMILIN1/RCN3/SERPINH1/ADAMTS3/CREB3L1/RUNX1/SERPINB7/F2",14
 1/THY1/FGG/FGA/FGB/ADIPOQ/MBP",10
 3P4/FBN2/ADAMTS1/NKX2-5",10
 V4/THBS1/MMP14/IL34/CX3CR1/P2RY12/CSF1/C5AR1",10
 APOA1/NPC2/CLU/APOE/APOC1/ABCA8/STAR/APOA2/LIPC/PCSK9/PNLIP/ANXA2/CES1",21
 MP9/FERMT1/SRPX2/MEOX2/KANK1/ACTA2/IFNG/SMOC2/SPARC/FGF1/HRG/APOA1/NR4A1/BMP4/
 /FERMT1/SALL1/PLEKHA4/WNT2/SFRP4/GLI3/KANK1/DKK1/COL1A1/FOLR1/GLI1/MDFI/TBX18/WLS/
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 IT/AGTR1/APOA2/LIPC/PLA2G2A",8
 RET/LAMB2/ADIPOQ/WT1",8
 HMOX1/CYP27A1/CYP1B1/CYP2C9/CH25H/TPH2/CYP11A1/CYP4B1/CYP17A1/CYP11B1/CYP2S1/CYP4
 OXA1/YAP1/FGF7/RCN3/THRB/SHH/WNT7B",12
 SIX4/BMP4/SOX9/SIX1/LIF/AGT/GJA1/GDNF/AR/HOXB7",12
 A1/PCK1/SOX9/SERPINF1/YAP1/OSR1/FZD7/WNT9B/BRINP3/RET/WNT7B/BRINP2/AQP1",17
 HMOX1/SIX4/MAG/PTPRZ1/PITX3/DKK1/CSF3/CCL2/IFNG/GHR/NR4A3/TGFB3/CLU/GDF5/SIX1/APOE,
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 /GATA4/YAP1/RBP4/DUSP6/RUNX1/TGFBR2/CITED2/PI16/TBX20/FOXC2/ERBB4/NKX2-5/WT1",21
 DAC/PLA2G4A/APOA1/PLA2G5/APOC1/APOA2/PLA2G4D/LIPC/LPL/PNPLA1/LIPI/PLIN5",17
 BMP4/SOX9/HOXD13/FOXA1/SHH/NKX3-1/AR",10
 I2/MYO1E/KLF15/LAMB2/FOXC2/ADIPOQ/WT1",10
 S1/EMILIN1/MMP14/IL34/CX3CR1/P2RY12/SAA1/CSF1/C5AR1/MMP28",15
 POA1/APOE/APOC1/APOA2/LPL",9
 OC3/APOA1/APOE/APOC1/APOA2/LPL",9
 PDR1/TRIP6/FERMT1/SERPINE1/HRG/FN1/NID1/HOXA7/PLAU/SDC4/RRAS/ITGB4/LYVE1/THBS1/ITGA
 MA3C/LRP2/DSP/SALL1/WNT2/HOXA13/BMP5/TNNC1/FHL2/MSX2/BMP4/FGFRL1/NOTCH2/GATA4,
 B/TSPO/APOA4/IFNG/BMP5/FGF1/IL1A/APOA1/APOE/APOC1/CGA/AGT/NR5A1/DHH/AGTR1/STAR/A
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 MP5/CYP11A1/CYP17A1/CYP11B1/AKR1C3/AKR1C4/HSD3B1/HSD3B2",12
 19/TNFAIP6/EREG/PDGFR/NR5A1/LHCGR/ADAMTS1/PTX3",14
 5/AVP/HTR2A/CALB1/CXCL12/CCL7/CCL8/FAM20A/CALCA/TRPV4/GLP1R/CASQ2/EDN3/MCHR1/APC
 H1/GPM6B/COL17A1/CDH19/GPC4/CDH7/COL16A1/TRIP6/SIX4/SRPX2/DKK1/TRPV4/HRG/CLDN16/I
 NAI2/EYA2/HMOX1/SERPINE1/BMP5/IL1A/BMP4/IL1B/LGALS3/TMBIM1/YAP1/THBS1/SFRP2/ITPRIP,
 NG/LRAT/CYP27A1/TTPA/CYP11A1/GC/CRABP1/CYP4F11/CYP4F3",13
 3FAP/IL6/S100A9/LAMB2/ROR1/C5AR1",13
 EN/AGTR1/CRH/PTGES/GALR1/NKX3-1",13
 I2/PLP1/SYPL2/SFRP2/NR4A2/FZD1/WNT9B/S100A1/EN1/SHH/OTX2/TAL2/POTEE/MBP",20
 PAX2/MMP2/MT3/NEFH/TSPO/MAG/SCN1B/HOXA2/EVX1/PTPRZ1/GLI3/CXCL12/LGI1/FOLR1/APOA
 A1/SPP1/LRAT/FABP3/IL1B/APOE/ABCA12/CRH/PTGES/GALR1/NKX3-1/ADIPOQ/ANXA2",17
 A2/ADORA3/HTR1B/AGT/SNCA/VIP/CRH/SYT8/GDNF/SNCG/KCNA2/HTR1A/MAPK15/FFAR3",19
 2/HOXA2/GLI3/AREG/GLI1/MSX2/TNFAIP6/RUNX2/BMP4/SOX9/IL6/YAP1/FBN2/SFRP2/CEBPB/TMEN

/CYP24A1/SNAI2/TNFRSF1A/WIPI1/PTGS2/HMOX1/MAG/COL1A1/FOLR1/TNFRSF8/PCK1/SOX9/IL1B
 IRS9/PTGS2/AFP/AVP/APOA4/APOC3/BMP5/APOA1/NR4A3/RDH10/FABP3/SOX9/IL1B/APOC1/ANXA
 1/ADORA3/HTR1B/AGT/SNCA/VIP/CRH/SYT8/GDNF/SNCG/KCNA2/FFAR3",15
 4/KLF4/SFRP2/FOXC2",8
 3/LIF/WNT9B/GDNF/WT1/WNT7B",11
 2/GFR2/FGFR3/KIF16B/CCL2/COL1A1/SMOC2/FGF1/FGF12/NR4A1/RUNX2/FGFRL1/ZFP36/THBS1/FGF
 1/IM/FCGR2B/CXCL2/OPRK1/TREM2/TSPO/CTSG/HAMP/SERPINE1/CSF3/CCL2/PF4V1/PLSCR4/IL1A/C
 S/PLA2G4A/IL1B/ANXA1/PTGES/HPGDS/CYP2S1/AKR1C3/AKR1C4/GSTA1",14
 GDS/PLA2G4A/IL1B/ANXA1/PTGES/HPGDS/CYP2S1/AKR1C3/AKR1C4/GSTA1",14
 /HMGCS2/CLDN1/OR51E2/LPL/ADIPOQ/FFAR3/AKR1C3/MBP/AKR1C4",16
 AT/IL1A/DUSP1/PAEP/BMP4/LIF/SERPINF1/NR5A1/GJA1/HPGDS/NKX3-1/WT1/NANOS2",16
 1R1/GDF15/PYY/NMUR2/HTR1B/AGT/HCRTR2/REN/NTRK2/EN1/NPY1R/FOS/NPW/CCK/BSX/DMBX1'
 POA2",7
 35A1/CYP1B1/CRH/CITED2/WT1",10
 15/LAMB2/FOXC2/ADIPOQ/WT1",9
 12/MYO1E/KLF15/LAMB2/FOXC2/ADIPOQ/WT1",9
 POA1/IL1B/C3/PLA2G5/FCN3/AHSG/APOA2/PTX3/MBL2/RAB31/SPHK1/ADIPOQ/COLEC10/PRTN3/C
 1R1B/AGT/SNCA/VIP/CRH/SYT8/GDNF/SNCG/KCNA2/FFAR3",15
 TN/IFNG/SPP1/INHBA/EDN3/IL1B/FOXA2/LIF/MTNR1B/ANXA1/AGT/IL6/RBP4/ADCYAP1/REN/ABCA1
 3LI1/MDFI/BMP4/HOXD11/FOXA1/GSC/LRP4/LMX1B/FOXN4/NBL1/EN1/TBX20/SHH/SOSTDC1/SOX1'
 /CSF3/PADI2/TTR/NPC2/FMOD/SDC4/C3/OMD/LUM/KERA/GC/GPC3/ACAN/RNASE2/RNASE3/CSPG4
 GA/AGT/REN/AGTR1/CRH/GJA1/CPA3/GALR1/NKX3-1/OR51E2/DRD5/FOXL2",19
 352A3/HTR2A/CXCL12/CALCA/TRPV4/FGF1/IL1A/VGF/PRDM12/HMGCS2/HTR1B/HTR2B/THBS1/BAG
 15/TRPC5/AVP/HTR2A/CALB1/CXCL12/CCL7/CCL8/CALCA/TRPV4/GLP1R/CASQ2/EDN3/MCHR1/APOE
 P5/MSX2/BMP4/FGFRL1/NOTCH2/GATA4/FZD1/DHRS3/TGFBR2/CITED2/TBX20/FZD2/NKX2-5",17
 'PITX3/ASPA/DLX2/EGR2/IL1B/LIF/GFAP/IL6/DLX1/DAAM2/NKX6-2/IL34/SHH/GPR37L1/F2",21
 (CL12/SYT10/SLC22A2/ADORA3/HTR1B/AGT/SNCA/VIP/CRH/SYT8/ADORA1/GDNF/SNCG/KCNA2/FFA
 3RA/IGF1/SNAI2/YBX3/NGFR/EYA2/PTGS2/TREM2/TIMP3/HMOX1/MMP9/AVP/SRPX/SERPINE1/CXCL
 1P2/SLCO1A2/SLC17A6/AVP/SLC52A3/SLC32A1/AQP9/SLC1A6/FOLR1/RHAG/SLC22A2/SLC27A6/IL1A,
 1X1/MMP9/FERMT1/SRPX2/MEOX2/KANK1/IFNG/SMOC2/SPARC/FGF1/HRG/APOA1/NR4A1/BMP4/S
 1A3C/MT3/PTHLH/TREM2/TSPO/MAG/KANK1/PITX3/IL1A/DLX2/SPP1/PAEP/IL1B/LRP4/IL6/TPPA/DL
 DKK1/TNFAIP6/DLX1/SFRP2/FZD1/NBL1/HTRA1/FBN1/HTRA3/SOSTDC1/GDF3/VWC2",15
 OXC11/BMP4/HOXD13/LRP4/OSR1/SFRP2/FREM2/GJA1/SHH/OSR2",15
 1H4/IGF1/TNFRSF1A/FCGR2B/SEMA3C/FAP/APOH/TREM2/WFDC1/PLAT/HAMP/SERPINE1/CCL2/HRC
 1CL7/CCL2/TRPV4/THBS4/PADI2/DUSP1/TNFAIP6/EDN3/LBP/IL6/THBS1/XCL1/IL34/NBL1/CX3CR1/CX
 1H4/DKK3/PTGS2/AVP/APOA4/APOC3/BMP5/APOA1/NR4A3/RDH10/FABP3/SOX9/IL1B/APOC1/ANX
 1/NPR3/TTR/INHBA/MCHR1/HCRTR2/LHCGR/EGFR/THRB/ALDH1A1/GALR1/AR/MC5R/GCGR",20
 '13/TGFBR2/BNC2/TSKU/OSTN",10
 /HOXD13/FOXA1/SHH/NKX3-1/AR",10
 1P5/FDX1/CYP11A1/CYP17A1/CHST9/CYP11B1/FFAR3/DIO3/HSD3B1/HSD3B2/CYP21A2",16
 /MT1F/MT1A/MT1M",8
 3B/GDNF",8
 3,"SOX8/PAX2/SIX4/SOX9/SIX1/AGT/GDNF/HOXB7",8
 3960539,"CXCL2/PF4V1/HRG/CXCL6/SPINK5/CXCL9/CXCL14/S100A9/CXCL3/CXCL1/DEFA4/DEFA6/RN
 1DORA3/HTR1B/AGT/SNCA/VIP/CRH/SYT8/GDNF/SNCG/KCNA2/MAPK15/FFAR3",17
 1/CRH/CYP17A1/CYP11B1/CYP21A2",9
 31E/KLF15/LAMB2/FOXC2/ADIPOQ/WT1",9
 1526171,"LTBP1/DKK3/TGFBR3/ITGA8/LTBP4/FERMT1/FOLR1/LOX/TGFB3/THBS1/EMILIN1/FBN2/MY
 A/TREM2/CTSG/EPPIN/HAMP/SERPINE1/RARRES2/CCL20/SLPI/TREM1/CXCL6/HTN1/VGF/LBP/CRP/SI
 1NNT2/GLI1/AGT/GATA4/YAP1/RBP4/RUNX1/TGFBR2/CITED2/PI16/TBX20/FOXC2/ERBB4/NKX2-5",19

V5/COL1A2/MFAP4/TNXB/COL3A1/HAS2/LAMB2/THSD4",13
 IX4/MAG/PTPRZ1/CSF3/CCL2/GHR/NR4A3/TGFB3/GDF5/SIX1/APOE/SERPINF1/CHL1/NGF/MTNR1B/I
 N3/BMP4/HTR2B/SEMA3D/PITX2/SHH/RET/GBX2/GDNF/ERBB4",15
 .RAT/GAD1/SDS/TTPA/RBP4/HDC/CRABP2/GC/P4HA3/TKTL2/ALAS2/ALB/ETNPPL/FOLR2/CRABP1/SP
 R2A/PLA2G5/PDGFRA/ANXA1/AGT/HTR2B/AGTR1/SNCA/EGFR/P2RY12/C5AR1/ANG",16
 !/SIX4/WNT2/FOLR1/BMP5/TBX18/RDH10/SDC4/BMP4/SOX9/SIX1/OSR1/SFRP2/FZD1/WNT9B/CITEC
 K1/WLS/INHBA/BMP4/ITGB4/KLF4/SFRP2/GJA1/TBX20/FOXC2/APELA",17
 ,6
 C10",6
 /AGT/AGTR1/APOA2",7
 ",7
 C/NID1/SPP1/TGFB1/LGALS3/THBS1/OLFML2B/FBLN2/SHH/BGN/DMBT1",15
 /MYOD1/ASS1/SERPINF1/HMGCS2/ANXA1/CYP1B1/FBXO32/GJB2/FAM107A/AQP1",14
 APOA4/APOC3/AADAC/APOA1/PCK1/C3/APOE/APOC1/APOA2/LIPC/TNXB/PCSK9/LPL/PNPLA1/LIPI/F
 /MEDAG/RETN/RARRES2/SULT1E1/TRPV4/NR4A3/MSX2/FABP3/EGR2/NR4A1/SIX1/ZFP36/LGALS12/f
 A5/ANXA2/ANXA4",8
 /NT2/HOXA5/RDH10/BMP4/SOX9/FOXA1/YAP1/RSP02/SHH",10
 :STL3/FCGR2B/TREM2/HMOX1/CTSG/FGL1/AHR/TMEM176B/GLI3/AMBP/CXCL12/CCL2/BMP5/IL1RL
 IF16B/CCL2/COL1A1/SMOC2/FGF1/FGF12/NR4A1/RUNX2/FGFRL1/ZFP36/THBS1/FGF7/CREB3L1/OTX
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 1/YAP1/RBP4/DUSP6/RUNX1/TGFB2/CITED2/PI16/TBX20/ERBB4/NKX2-5/WT1",17
 ;2/OSM/IL1B/C3/APCS/ALOX5AP/IL6/OSMR/PTGES/ADORA1/FFAR3",13
 .DN1/OR51E2/LPL/FFAR3/AKR1C3/AKR1C4",11
 IX1/FGF7/OSR1/GPC3/LMNA/TGFB2/SHH",12
 .B1/FBXO32/CLDN1/GJB2/FIBIN/TAT/AQP1",12
 L/EMILIN1/MMP14/IL34/CX3CR1/P2RY12/CSF1/C5AR1/MMP28",12
 /INHBA/SOX9/SPINK5/FST/LRP4/LGR5/KRT71/FGF7/EGFR/CD109/FOXQ1/SHH/SOSTDC1",19

 MSR1/APOB/PLA2G5/AGT/AGTR1/LPL/CSF1/PLA2G2A",8
 3/HRH1",8
 ;R1/SHH/WT1",8
 /MT1A/MT1M",8
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 !/APOE/STAR/APOA2",9
 R3/FCGR2B/GPC4/ITGA8/LRP2/WNT2/CXCL12/FOLR1/GHR/IL1R1/IL1RL1/IGSF21/F3/ABCG2/GRIA2/PI
 iA8/DKK1/WLS/INHBA/BMP4/ITGB4/KLF4/SFRP2/GJA1/TBX20/FOXC2/APELA",17
 /NGFR/FCGR2B/TREM2/PLAT/KLF1/RARRES2/KANK1/GLP1R/GHR/NR4A3/NR4A1/PCK1/IL1B/GDF15/
 I2/HMOX1/SIX4/MAG/PTPRZ1/PITX3/CCL2/TGFB3/GDF5/SIX1/APOE/CHL1/NGF/MTNR1B/DLX1/SNC
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 1A1/FOLR1/FOXA2/POSTN/FOLR2/LPL/PENK/KANK2",12
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 ZFP36/NOTCH2/YAP1/FGF7/CD109/HAS2/PRKD1",11
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 PLA2G4A/APOE/PDGFRA/TEC/IL6/CSRP1/PDPN/F2RL2/AXL/COL3A1/P2RY12/FGG/FGA/FGB/SAA1/TH
 JS1/ERBB3/FGFR2/TNFRSF1A/FGFR3/TREM2/OSM/HTR2A/CSF3/AREG/IFNG/NEDD9/GHR/THBS4/HR
 2/APOE/APOC1/ABCA8/ABCA12/APOA2/SHH/ADIPOQ/TSKU/CES1",16
 3/HTR1B/HTR2B/HCTR2/CRH/ADORA1/NLGN1/KCNA2/HTR1A/PENK/RELN",16
 17A1/CYP11B1/CYP21A2",7

H/AR/SOSTDC1",7
 2/WNT7B",7
 R1/SHH/WT1",7
 L/FGG/FGA/FGB",7
 'MYH14/MEOX2/SMYD1/TCF21/EGR2/NR4A1/SIX1/MYOD1/CHRNA1/MYOCN/RXRG/MEGF10/ATF3/C
 6/AVP/SLC32A1/AQP9/SLC1A6/FOLR1/SLC22A2/IL1A/PLA2G4A/ABCG2/SLC17A3/SLC17A1/IL1B/PLA2
 LRP2/TSPO/SRPX2/MAG/WNT2/PTPRZ1/GLI3/CXCL12/ASPA/IFNG/OPRM1/FN1/EGR2/IL1B/LIF/GFAP
 /HMOX1/SIX4/MAG/PTPRZ1/PITX3/CCL2/TGFB3/GDF5/SIX1/APOE/CHL1/NGF/MTNR1B/DLX1/SNCA/
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 APOE/NMUR2/ANXA1/THBS1/CRABP2/PMP2/PTGES/FABP1/FABP7/CRABP1/BDKRB2/FABP4/PLA2G2
 <9/LIF/WNT9B/GDNF/WT1",9
 'AP1/LBX1/FOXN4/GJA1/ZIC3/TGFB2/PITX2/CITED2/TBX20/SHH/PIFO/FOXC2/NKX2-5/APELA",18
 FRP5/BMP4/HOXD13/PDGFR/GATA4/SFRP2/EGFR/SHH",13
 /REN/AGTR1/CRH/GJA1/GALR1/NKX3-1/FOXL2",13
 CL9/CXCL3/CXCL1/CXCL8",8
 F1/FCGR2B/SERPINE1/DKK1/CCL2/AREG/IFNG/OPRM1/PLAU/EREG/CGA/CBLC/CRH/DKK2/ADORA1/I
 VNT9B/GDNF/WT1",8
 MCOLN3/GNA15/TRPC5/AVP/HTR2A/CALB1/CALCA/TRPV4/GLP1R/CASQ2/MCHR1/NMUR2/MTNR1E
 2/GCGR",6
 '1",6
 AQP2/WNT7B",6
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 BA/SOX9/SPINK5/FST/LRP4/LGR5/KRT71/FGF7/EGFR/CD109/FOXQ1/SHH/SOSTDC1",19
 SOX9/SPINK5/FST/LRP4/LGR5/KRT71/FGF7/EGFR/CD109/FOXQ1/SHH/SOSTDC1",19
 IRL1/IL1B/LBP/IL6/ADCYAP1/TSLP/AIRE/TLR3/LPL/DEFB124/ADIPOQ/FFAR3/MBP",16
 'ERBB3/FGFR2/TNFRSF1A/FGFR3/TREM2/OSM/HTR2A/CSF3/AREG/IFNG/NEDD9/GHR/THBS4/HRG/EI
 4P4/IL6/EMILIN1/CREB3L1/RUNX1/SERPINE1/MFAP4/F2",12
 'XA1/LBX1/FOXN4/DLX1/ISL2/SHH/GBX1/HOXC10/SOX1",15
 REM2/AVP/RETN/CXCL12/SYT10/IFNG/IL1A/PLA2G4A/WLS/SPP1/TGFB3/INHBA/SDC4/EDN3/IL1B/AG
 IE/STAR/APOA2",9
 09,"HOXA11/COMP/COL1A1/TRPV4/GHR/SOX9/MMP13/SERPINE1/TGFB2/TSKU",10
 3NC2/TSKU/OSTN",10
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 2/S100A6",7
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 5X2/INHBA/SOX9/SPINK5/FST/LRP4/LGR5/KRT71/FGF7/EGFR/CD109/FOXQ1/SHH/SOSTDC1",19
 DL/CST3/SOX9/AGT/IL6/EMILIN1/RUNX1/PDPN/TNXB/HAS2/ANGPTL7",13
 '1/FGFR2/FGFR3/TGFB3/LTBP4/PDGFR/EFEMP1/FGFR1/PDGFR/EGFR/NTRK2/TGFB2/RET/AXL/
 6/EREG/VGF/LHCGR/MMP14/PTX3/CEBPB/UMODL1/FOXL2/ANG",14
 2G4A/IL1B/PLA2G5/ALOX5AP/ANXA1/CYP2C9/PTGES/HPGDS/AKR1C3",14
 XCL2/OPRK1/TREM2/TSPO/CTSG/HAMP/SERPINE1/CSF3/CCL2/PF4V1/PLSCR4/IL1A/CXCL6/IL1B/ZFP

L/OPRM1/GLP1R/NPR3/MCHR1/NMUR2/RXFP2/HCRT2/LHCGR/LGR5/SSTR1/ACKR3/AGTR1/NPY1R/
 IP4/TGFB2/AR/SOSTDC1/CCL11/CSF1/BSX",12
 LU/APOE/CRP/APOA2/PCSK9/RELN",10
 1/INSRR/PLAT/RARRES2/KANK1/GLP1R/GHR/NR4A3/NR4A1/PCK1/IL1B/GDF15/ASS1/HMGCS2/AGT/
 IGF1/MYOC/ERBB3/TREM2/OSM/CSF3/FN1/SOX9/PDGFR/AGT/NTRK2/NKX3-1/ERBB4/F2/ROR1/RE
 CTR/OPRK1/CMA1/TREM2/KDEL3/CST3/CRYAB/OPRM1/GLP1R/GHR/NPR3/BCHE/FBXO2/APOA1/G
 4/IGF1/SNAI2/DKK3/PTGS2/SLC4A4/APOB/TREM2/AVP/HTR2A/RCVRN/APOA4/APOC3/IFNG/BMP5/
 GR/FAT1/HOXA5/HOXA13/ACTA2/BMP5/ARHGEF26/IL1A/BMP4/SOX9/IL1B/FOXA1/NOTCH2/YAP1/F
 5/NAI2/YBX3/EYA2/PTGS2/HMOX1/MMP9/AVP/SERPINE1/CXCL12/BMP5/VNN1/IL1A/CLU/BMP4/IL1B
 1/HAMP/TNNC1/NR4A3/IL1B/MYOD1/GATA5/AGT/MLIP/GSN/FBXO32/TRIM63/LMNA/KLF15/PI16/
 2G4A/IL1B/ANXA1/PTGES/HPGDS/AKR1C3",10
 /SOX9/SFRP2/SERPINE1/TGFB2/TSKU",10
 APOB/PLA2G5/CRP/AGT/AGTR1/LPL/ADIPOQ/CSF1/PLA2G2A",10
 4A/IL1B/ANXA1/PTGES/HPGDS/AKR1C3",10
 HOXA11/EYA2/PAX2/DKK1/BMP4/KLF4/SFRP2/FZD7/FOXC2/SOX2",10
 4A2/FCGR1A/FCER1A/LILRA2",9
 B3/THBS1/CD109/TGFB2/WF1K1/TSKU",9
 GRF1/OPRK1/FXYD3/TREM2/MMP9/HAMP/SCN1B/CCL2/KCNA1/IFNG/OPRM1/FGF12/CASQ2/PLP1/I
 LI3/DLX2/SOX9/SOX3/LBX1/DLX1/CNTN4/ISL2/SHH/GPR37L1/HES3/IRX3/SOX2",16
 B/TSPO/IFNG/BMP5/FGF1/IL1A/APOE/CGA/NR5A1/DHH/STAR/AKR1C3/CES1",16
 1/SERPINE1/KANK1/ST3GAL4/SMOC2/HRG/F3/PLG/ANXA1/THBS1/CLDN1/FOXC2/THBD/F2",16
 3/C3/SERPINE1/VSIG4",8
 SG/SERPINE1/RARRES2/TREM1/CXCL6/LBP/IL6/DEFA4/DEFA6/RNASE3/F2/PRKD1/DMBT1/ELANE/PR
 LI1/NR4A3/IL6/ANXA3/APOA2/CLDN1/TGFB2/NNMT/AXL/CEBPB",15
 /YAP1/RBP4/RUNX1/TGFB2/CITED2/TBX20/FOXC2/ERBB4/NKX2-5",14
 A/EDN3/AGT/REN/AGTR1/ADORA1/CPA3/OR51E2/KLK1/AR/DRD5/GPR37L1/ADRA1B/ADRA1D/ADR
)/PADI2/CH25H/XCL1/AIRE/CXCL16/RET/GPR183/CCL11/SAA1/CCL13/APOD/CCL23/CCL16/CCL18/CC
 NFRSF1A/LMCD1/PTGS2/DSP/MYL9/TNNT1/HAMP/CALCA/TRPV4/KCNA1/TNNC1/CASQ2/NR4A3/NR
 TSG/HAMP/PTGDS/IFNG/FN1/IL1RL1/PLA2G4A/NR4A3/CLU/CXCL6/MT1G/LBP/NOTCH2/ANXA1/IL6/
 /MMP2/HMOX1/MMP9/OGN/IFNG/NPR3/NR4A3/TGFB3/EREG/BMP4/CNN1/APOE/HTR1B/AGT/IL6/
 HBS4/MORC1/APOE/NMUR2/HMGCS2/THBS1/NR4A2/RET/HTR1A/VWA1/PENK/GABRA5/RELN",16
 J/IL1B/IL6/SNCA/MMP3/TLR3/CX3CR1/NUPR1/SPHK1/C5AR1/CD200R1L",16
 IEFH/KRT18/GFAP/KRT34/KRT7/KRT71/SHH/EVPL/KRT8/KRT4/DES/FAM83H/KRT79/KRT14/NEFL",18
 RH/CALCB/PENK/CCK",10
 R1/APCDD1L/TRABD2B",10
 /IL1A/LOXL4/SNCA/ALB/SNCG/S100A13/ANG",15
 P5/PADI2/DUSP1/HOXA7/TNFAIP6/EMILIN1/NBL1/ADORA1/APOD/MMP28",13
 SM/IL1B/C3/ALOX5AP/IL6/OSMR/FFAR3",9
 DGFRA/OSR1/SERPINE1/FOXC2/WT1",9
 ENM1/CLDN11/CDH1/CDH19/GPC4/CDH17/CDH7/FAT1/FAT2/PCDH11X/MAG/CLDN16/IGSF21/APO
 C30A8/MT1E/MT1X/MT1F/MT1A/MT1M",11
 P/APOA4/APOA1/NR4A3/IL1B/ANXA1/FABP1/ADIPOQ/PLIN5",11
 L2/MFAP4/COLEC10",6
 39466,"PAX2/SALL1/BMP4/LIF/WNT9B/GDNF",6
 /BMP4/HOXD13/SHH/NKX3-1",6
 /WTR1/PAX2/LIF/YAP1/OSR1",6
 1/AVP/LIPG/FA2H/PTGDS/APOA4/APOC3/PLA2G4A/APOA1/PLP1/IL1B/APOC1/ANXA1/CYP2C9/PTGE
 DRA1B/FGG/FGA/FGB/ADRA1D/HRH1",10
 IP4/SOX9/MYOD1/CXCL9/MYOC/BOC/MEGF10/SHH/CMTM5/SOSTDC1/GDF3",17
 LC32A1/SALL1/GLI3/CXCL12/DKK1/GLI1/KCNA1/DLX2/SATB2/INHBA/BMP4/FOXP2/GSC/SOX3/ANXA

A1/APOA4/FGF1/APOA1/NPC2/APOE/HMGCS2/CYP27A1/FDX1/CYP1B1/CYP2C9/CH25H/CYP11A1/ST
 !/TRPC5/SEMA3C/MT3/SIX4/CPNE6/SALL1/MAG/CXCL12/AREG/FGF1/FN1/SPP1/RDH10/EDN3/NRN1
 /GFAP/KRT34/KRT7/KRT71/SHH/EVPL/KRT8/KRT4/DES/FAM83H/KRT79/KRT14/NEFL",18
 2/FBLN5/FBLN2/FBN1",6
 3/CCL2/LOX/F3/SFRP5/SOX9/IL1B/F10/RRAS/GDF15/CHI3L1/GATA4/THBS1/RCN3/TPBG/EGFR/NTRK2
 L/INSRR/ROS1/ERBB3/FGFR2/FGFR3/MT3/TREM2/HTR2A/DKK1/FAM20A/AREG/CALCA/IFNG/NEDD9
 TGDS/PLA2G4A/IL1B/PLA2G5/ALOX5AP/ANXA1/CYP1B1/CYP2C9/EPHX1/PTGES/HPGDS/CYP2S1/CYP
 12A1/FN1/INHBA/COL5A1/COL8A1/MMP14/SOX2/COL5A2",12

 R1/NKX3-1",8
 4P/WNT2/GLI1/YAP1/RBP4/RUNX1/TGFB2/CITED2/PI16/TBX20/ERBB4/NKX2-5",15
 2G5/SPON2/S100A9/DEFA4/DEFA6/CLEC4E/CX3CR1/ELANE",13
 3X9/GATA5/OSR1/ACTG2/TGFB2/TBX20/TMEM100/FOXC2",13
 4EFA6/WFDC13/RNASE3/FGA/FGB/WFDC11/DMBT1/ELANE/ANG",14
 AX9",7
 3",7
 1/MMP9/OGN/IFNG/NPR3/NR4A3/TGFB3/EREG/BMP4/CNN1/APOE/HTR1B/AGT/IL6/THBS1/MYOC
 D/BS1/SFRP2/IGFBP6/LPA",10
 3/MCHR1/NMUR2/RXFP2/HCTR2/LHCGR/LGR5/SSTR1/ACKR3/AGTR1/NPY1R/F2RL2/GALR1/CX3CR
 2/EGR2/LIF/IL6/DLX1/DAAM2/NKX6-2/IL34/SHH/GPR37L1/F2/SOX1",16
 3/FOLR1/LOX/PRRX1/EGR2/BMP4/SIX1/APOE/MYOC/CITED2/SHH/NKX3-1/COL3A1/FOXC2",20
 ULT2A1/APOA4/FGF1/APOA1/NPC2/APOE/HMGCS2/CYP27A1/FDX1/CYP2C9/CH25H/CYP11A1/STAR,
 3PC3/RSPO2/SHH/OSR2",9
 FAP/LRP2/FAT1/SI/SLC52A3/PLAT/ANXA13/HAMP/FOLR1/TRPV4/KCNA1/SCNN1A/SLC22A2/FN1/AB
 S1/CYP27C1/ADH1A/AKR1C3/ADH1B/ADH1C",10
 <1/TREM2/AVP/RETN/CXCL12/SYT10/IFNG/IL1A/PLA2G4A/WLS/SPP1/TGFB3/INHBA/SDC4/EDN3/IL1
 POA4/APOC3/AADAC/PLA2G4A/APOA1/PCK1/C3/APOE/APOC1/APOA2/LIPC/TNXB/PCSK9/LPL/PNPL
 2H2/DHH/MMP14/APOA2/TGFB2/CITED2/AR/ARID5A/HOXA10",15
 34/KRT7/KRT71/SHH/KRT8/KRT4/DES/KRT79/KRT14/NEFL",15
 5OX9/GATA5/GATA4/TGFB2/CITED2/TBX20/TMEM100",12
 6IX4/HOXA2/TBX18/PRRX1/SOX9/SIX1/GSC/LRIG3/OSR1/ZIC1/OTOP1/OSR2/GBX2/CHRNA9/FZD2/HN
 X2/BMP4/GDF5/FOXA1/NGF/DLX1/NBL1/BRINP3/NEUROD1/IRX3/NKX2-5/NAP1L2/VWC2/BRINP2/K
 MT3/HEPH/HMOX1/HAMP/IFNG/MT1G/MT2A/SLC30A2/ALAS2/S100A9/SLC30A8/SCARA5/MT1E/MT
 2A/KCNA1/OPRM1/IL1A/PRDM12/NMUR2/VIP/PTGES/ADORA1/NPY1R/TMEM100/KCNA2/PENK/MM
 /CPQ/ADAM2/CPN1/CPXM2/XPNPEP2/MMP19/CPM/MMP7/MMP13/ADAMTS19/ADAM33/MMP3/
 /DKK1/WLS/INHBA/BMP4/ITGB4/KLF4/YAP1/OSR1/SFRP2/GJA1/CITED2/TBX20/SHH/FOXC2/IRX3/GI
 MT1E/MT1X/MT1F/MT1A/MT1M",11
 8MP5/CYP11A1/CYP17A1/CYP11B1/HSD3B1/HSD3B2/CYP21A2",11

 DL/EFEMP1/BMP4/SOX9/GDF5/ADAMTS12",8
 RH1",8
 2B1/DSP/FA2H/SFRP4/GLI1/IL1A/MSX2/HOXA7/EREG/BMP4/ZFP36/SPINK5/ANXA1/KRT7/KLF4/YAP1
 3YT10/ADORA3/HTR1B/AGT/SNCA/VIP/CRH/SYT8/ADORA1/GDNF/SNCG/KCNA2/FFAR3",18
 42/SOX9/GDF5/SHH",6
 5MP9/COL1A1/AREG/SOD3/CRYAB/APOA4/IL1A/NR4A3/APOE/PDGFR/ANXA1/IL6/CYP1B1/FBLN5/EC
 6TNT2/CXCL12/CCL2/SPARC/THBS4/F3/APOA1/NR4A1/BMP4/APOE/HTR2B/THBS1/AGTR1/VIP/MMP1
 84511,"CMA1/CTSG/EDN3/AGT/REN/AGTR1/CPA3/OR51E2/DRD5/ADRA1B/ADRA1D/ADRB3",12
 7GFB3/SOX9/FGF7/EGFR/SHH/NKX3-1/IGF2",12
 82/FN1/EREG/PDGFR/AGT/EGFR/SPHK1/S100A6/AQP1",12
 93/RSPO2/SHH/OSR2",10

AT/LOX/F3/NR4A3/PDGFRA/MYOCN/CSRNP1/SNCA/MYO1E/CSPG4/ADIPOQ/APOD",13
 AG/FBXO2/PPP1R3C/LGALS3/APCS/CHI3L1/LGALS12/GALNT5/FCN3/FUOM/P4HA3/CHODL/HKDC1/A
 .PLA2G4A/IL1B/ANXA1/XCL1/ARID5A/IL27",9
 IP4/SOX9/SIX1/LMNA/TGFBR2/SHH",9
 'PDGFRA/OSR1/SERPINB7/FOXC2/WT1",9
 RA/OSR1/SERPINB7/FOXC2/WT1",9
 7A3/KCNK1/TMPRSS15/MYO1E/SLC2A2/SLC6A18/DRD5/SLC6A19/PDZK1/ITLN1/ESPN/MME/AQP1",2
 ;OPRM1/KLF9/TGFB3/INHBA/EGR2/BHLHE41/MMP19/TNFAIP6/EREG/ASS1/SERPINF1/BHLHE40/MT
 EC5A",7
 4/C8A",7
 .2",7
 ",7
 POA2",7
 7B",7
 GALR1/NKX3-1",7
 A3/FOLR1/IFNG/VNN1/RDH10/LRAT/CYP27A1/TTPA/CYP11A1/GC/CRABP1/NNMT/CYP4F11/CYP4F3/
 ANK1/NEDD9/FN1/APOA1/DOCK5/DOCK1/FZD7/PDPN/MICALL2/AXL/HAS2/FGG/FGA/FGB/LAMB2/
 P9/SCN1B/TRPV4/KCNA1/SCNN1A/OPRM1/RHAG/GRIA2/KCNJ5/KCNS1/SLC17A3/NMUR2/HTR1B/KC
 DE/ADORA1/LIPC/ANGPTL4/LPL/ACSM2A",11
 DE/ADORA1/LIPC/ANGPTL4/LPL/ACSM2A",11
 MA3C/LRP2/DSP/SALL1/HOXA13/TNNC1/BMP4/FGFRL1/GATA4/MYOCN/SFRP2/FZD1/TGFBR2/CITED
 I3/TRPC5/FXYD3/GLRA2/AQP9/SCN1B/TRPV4/KCNA1/SCNN1A/OPRM1/RHAG/GRIA2/KCNJ5/KCNS1/
 3/IFNG/CCL20/ASS1/RAB20/XCL1/GSN/CLDN1/OTOP1/TLR3/CCL11/CCL13/TDGF1/CCL23/CCL16/CCL1
 .BP4/LRG1/CEBPB/METRN1/ADIPOQ/SLC2A4/FFAR4",12
 'GLI1/YAP1/RBP4/RUNX1/TGFBR2/CITED2/TBX20/ERBB4/NKX2-5",12
 .LS1/TRIM6/CXCL6/APCS/CH25H/IFITM3/FCN3/GSN/PTX3/CXCL8/TRIML2/TMPRSS2/IFITM2",13
 SERPINE1/HRG/PLAU/LIF/ITGB4/ITGA11/CYP1B1/SFRP2/RET/FBN1/P2RY12/FOXC2/ITGBL1",17
 'A6/PLSCR4/APOA1/ATP10B/NPC2/APOE/CFHR4/TTPA/RBP4/ABCA8/ABCA12/STAR/ABCA9/ABCA6/A
 L12/CCL7/TRPV4/THBS4/EDN3/LBP/IL6/THBS1/XCL1/IL34/CX3CR1/CXCL8/DEFB124/CSF1/S100A14/C
 A/DLX2/CLU/PLP1/SOX9/DLX1/DAAM2/NTRK2/NKX6-2/IL34/SHH/MAL/SOX1",18
 ;/PTGS2/TREM2/HMOX1/HTR2A/MAG/OPRM1/ABCG2/SDC4/AHNAK/CDH15/TEX101/LRP4/MYOF/CI
 .LS1/CTSG/GLI3/MAP3K8/CCL2/ST3GAL4/IFNG/VNN1/IL1A/NR4A3/PCK1/IL1B/TNFSF9/FOXA2/FOXA1
 .HCGR/LGR5/ADCYAP1/DRD5/ADRB3",9
 /EGFR/P2RY12/C5AR1/ANG",9
 3FRA/CSRNP1/PAX9",9
 AM2/MMP19/MMP7/MMP13/ADAMTS19/ADAM33/MMP3/ADAMTS12/ADAMTS1/ADAMTS3/MMP:
 A/TRPC5/PTGS2/TREM2/HMOX1/HTR2A/MAG/OPRM1/ABCG2/SDC4/AHNAK/CDH15/TEX101/LRP4/I
 2/S100A9/PTX3/DEFA4/DEFA6/CLEC4E/CX3CR1/ELANE",14
 A/EGR2/IL1B/LIF/GFAP/IL6/NKX6-2/IL34/SHH",14
 :ITM3/FCN3/GSN/PTX3/TRIML2/TMPRSS2/IFITM2",11
 F/TTPA/RSPO3/EGFR/PLCD3/CITED2/IGF2/JUNB/CEBPB/PHLDA2/SOCS3/WNT7B",17
 3/EGR2/BMP4/OSR1/SFRP2/NKX3-1/IRX2/DMRT2/FOXC2/IRX3/GDF3/WT1/TDGF1",19
 /FGF12/TNNC1/KCNJ5/MYH8/GATA4/FRMD6/GSN/SCN2B/KCNE4/GJA1/PDPN/ADORA1/KCND3/EMP
 AOD/SDC4/OMD/LUM/KERA/GC/GPC3/ACAN/CSPG4/BGN/PRELP",19
 :5H/IFITM3/FCN3/GSN/PTX3/CXCL8/TRIML2/TMPRSS2/IFITM2",12
 24A1/SNAI2/WIPI1/HMOX1/COL1A1/FOLR1/PCK1/FOXA2/MYOD1/POSTN/MYOCN/PMAIP1/SFRP2/N
 VFDC1/MAG/CRYAB/HRG/SPP1/INHBA/MT1G/MT2A/BMP4/GDF15/CGA/AGT/RBP4/OSGIN1/SFRP2/
 =R/FGFR2/TGFBR3/APOH/CCL2/SPARC/KLF9/EREG/BMP4/SOX9/GDF5/APOE/SERPINF1/THBS1/SFRP2
 DKK1/SFRP5/SFRP2/DAAM2/RSPO3/GPC3/FZD7/FZD1/WNT9B/FZD2/ROR1",15

H/ADORA1/NLGN1/KCNA2",7

IF/YAP1/OSR1",6

/WT1",6

/DSP/WNT2/TNNC1/LIF/GSC/FZD1/TBX20/COL3A1/FOXC2/FZD2/NKX2-5",16

A1/NPC2/LRAT/RBP4/CRABP2/STAR/PMP2/APOA2/CRABP1/CYP27C1/APOD/ADH4",18

8/GDNF/SNCG/KCNA2",10

1B/SNCA/SYT8/GDNF/SNCG/KCNA2",10

SIX1/MYOD1/MYOD1/MEGF10/ATF3/CITED2/FOS/NUPR1/MAFF",14

S1/TREM2/HMOX1/MMP9/PON2/COL1A1/AREG/SOD3/CRYAB/APOA4/VNN1/IL1A/NR4A3/APOE/PD

LNK1/NEDD9/APOA1/DOCK5/DOCK1/PDPN/HAS2/FGG/FGA/FGB/TACSTD2/S100A10",13

L34/PENK/CSF1",11

/EGR3/PRKD1/FGF16",9

9666154316991,"HMOX1/SERPINE1/BMP5/TMBIM1/SFRP2/ITPRIP/FGG/FGA/FGB",9

IP4/TGFB2/TBX20/NKX2-5",8

M1/SOX9/NTRK2/THRB/THY1/DIO3",8

SNCA/SYT8/GDNF/SNCG/KCNA2/MAPK15",12

P6/LBP/THBS1/XCL1/IL34/CXCL8/CSF1/S100A14/C5AR1",12

1/HRG/SDC4/AGT/TPBG/NTRK2/THY1/CLDN1/CLDN19/NLGN1/LRRN1/IRX3/SLITRK4/SLITRK2/THBS2/

L1/CCL11/CCL13/CCL23/CCL16/CCL18/CCL14",12

/BMP4/SOX9/OMD/FBN2/OSR1/AHSG/GJA1/SGMS2/OSR2/TMEM119/ISG15",16

2/ANXA4",6

TP1A2/MCOLN3/GNA15/TRPC5/AVP/HTR2A/CALCA/TRPV4/GLP1R/CASQ2/MCHR1/NMUR2/PDGFR

ALU/C3/APOE/SNCA/GPC3/AXL/RAB31/PCSK9/NLGN1/CD14/ANXA2/NTF3/APELA",18

EPH/HMOX1/HAMP/IFNG/RHAG/MT1G/MT2A/SLC30A2/ALAS2/S100A9/STEAP1/SLC30A8/SCARA5/N

OPRK1/EPDR1/CMA1/TREM2/KDEL3/PLTP/CST3/MAG/CRYAB/FOLR1/OPRM1/GLP1R/GHR/NPR3/B

/BMP5/TGFB3/INHBA/BMP4/GDF5/GDF15/EMILIN1/BMP3/TGFB2/GDF3/GDF10",14

3/FHL5/TNNC1/FHL2/CASQ2/MYOT/SDC4/AHNAK/MYOD1/TNNT3/FBP2/PDLIM4/MYH8/JPH2/BAG3/

L/HP",8

A1/S100A11/STXBP6/ANXA2/PKP3",7

ADGB/CYP27A1/CYP1B1/CYP2C9/CYP11A1/CYP4B1/CYP17A1/CYP11B1/CYP2S1/CYP4F11/CYP4F3/CYI

9/FOLR1/SLC15A3/TRPV4/IFNG/ABCG2/EDN3/IL1B/FOXA2/VGF/MTNR1B/ANXA1/IL6/IL1RN/RBP4/AI

IFR/SEMA3C/APOH/HMOX1/EPPIN/TIMP1/SERPINE1/MEOX2/KANK1/CXCL12/CCL2/BMP5/HRG/PADI

CRP/AGT/AGTR1/LPL/ADIPOQ/CSF1/PLA2G2A",10

/SAA1/CSF1/C5AR1/MMP28",10

/HOXA13/BMP5/MSX2/BMP4/FGFRL1/NOTCH2/GATA4/FZD1/DHRS3/TGFB2/CITED2/TBX20/FZD2/N

RRX1/SPP1/GFAP/KLF4/THY1/LAMB2/APOD/NEFL",13

MT1E/FOS/MT1X/AKR1C3/MT1F/MT1A/MT1M",13

X9/SERPINF1/SHH/NKX3-1/AR",5

A/FABP3/RAB38/HTR2B",5

ET",5

/WT1",5

ADI2/SGK1/TCF21/KLF9/NR4A3/PCK1/BMP4/ZFP36/MYOD1/FOXA1/ASS1/SERPINF1/HMGCS2/ANXA

T2B1/SULT2A1/APOA4/FGF1/APOA1/NPC2/APOE/HMGCS2/CYP27A1/FDX1/CYP2C9/CH25H/CYP11A1
/WNT2/GLI1/YAP1/TBX20/IGF2/ERBB4/WT1",12
3C/SLC2A2/FOLR2/SLC2A14",11
2/APOB/HSD17B2/WNT2/GLI3/BMP5/MDFI/SLC5A7/TGFB3/RDH10/PLG/LIF/NOTCH2/DSC3/PDGFR
A1/NLGN1/KCNA2",7
1A1/GC",7
NT2/PTPRZ1/GLI3/CXCL12/ASPA/IFNG/OPRM1/FN1/EGR2/IL1B/LIF/GFAP/SERPINF1/NGF/IL6/CRABP2
EDAG/RARRES2/SULT1E1/SIX1/ZFP36/SFRP2/CEBPB/LPL/METRNL/GDF3/FFAR4",14
IT1/TIMP1/NEDD9/FN1/APOA1/ITGB4/TEC/ITGA11/DOCK1/THY1/ADAMTS1/COL3A1/PRKD1/ISG15/I
/TR1/FOXC1/PRLH/PTGS2/CALB1/COMP/HAMP/HOXA13/CALCA/LOX/SPP1/PLG/SOX9/HTR1B/IL6/YA
IL1A1/SIX1/ASS1/HMGCS2/PDGFR/EGFR/NTRK2/COL1A2/COL3A1/CEBPB/COL4A6/COL5A2",15
'ANXA2/S100A10",6
/APOE/APOA2",6
9B/GDNF",6
'SHH",6
/CDH1/NGFR/TGFB3/APOH/HMOX1/EPPIN/TIMP1/SERPINE1/MEOX2/KANK1/CXCL12/CCL2/BMP5/I
DLR1/BCHE/IL1A/SPP1/LRAT/POSTN/GATA4/FOLR2/PENK/KANK2",16
'ADIPOQ/CSF1/PLA2G2A",10
.U/C4BPA/C4BPB/C3/CRP/APCS/SERPING1/C8A/C1R/MBL2/C1S/CFI/C4B/C4A",19
.LCA/OPRM1/MCHR1/PYY/NMUR2/HCTR2/SSTR1/ADCYAP1/NXPH2/NPY1R/GALR1/NTSR2/GPR139/
:NA1/DLX2/SOX3/ANXA3/DLX1/HTR5A/NEUROD1/EMX2/HAP1/TSKU/RELN/HSD3B1/HSD3B2/NEFL",;
I/HMOX1/WNT2/CXCL12/CCL2/SPARC/THBS4/F3/NR4A1/BMP4/APOE/HTR2B/THBS1/AGTR1/VIP/IGF
2/CHAD/RBP4/FBN2/ADAMTS1/NKX2-5",11
/THBS1/LPL",10
X1/IL1R1/APOA1/NR4A3/TGFB3/TRIM6/TREM1/IL1B/IL6/XCL1/APOA2/SPON2/SLAMF9/TLR3/FFAR3/
I/HMOX1/EPPIN/TIMP1/SERPINE1/MEOX2/KANK1/CXCL12/CCL2/BMP5/HRG/PADI2/DUSP1/ADORA3
TP1A2/RASGRF1/FXYD3/TREM2/MMP9/SCN1B/CCL2/KCNA1/IFNG/OPRM1/FGF12/CASQ2/KCNS1/A
'APOA4/APOC3/APOA1/NR4A3/FABP3/SOX9/IL1B/APOC1/ANXA1/SNCA/FABP1/ADIPOQ/PLIN5",17
A2/RASGRF1/FXYD3/TREM2/MMP9/SCN1B/CCL2/KCNA1/IFNG/OPRM1/FGF12/CASQ2/KCNS1/AHNA
:/APOA1/IL1B/APOC1/LGALS12/APOA2/ADORA1/FABP1/CIDEA/PLIN5",13
TCF21/PDGFR/FOX2/SHH/CXCL8",9
BB3/LMCD1/SCTR/TREM2/AHR/RASD1/GLP1R/CCL20/FHL2/CASQ2/EDN3/SOX9/APOE/NMUR2/MTN
'96310348,0.0042631305387776,"FMO3/FMO1/CYP24A1/PTGS2/FMO4/MOXD1/P3H2/PTGS1/HMO
:G/TGFB3/MSX2/BMP4/SOX9/GJA1/TGFB2/AR/SOSTDC1/CCL11/PRL/CEBPB/ERBB4/CSF1/WNT7B/B
',
MGP/TGFB3/SRGN/BMP4/SOX9/OMD/FBN2/OSR1/AHSG/GJA1/SGMS2/OSR2/CEBPB/TMEM119/ISG1
:M2/HMOX1/AHR/IFNG/IL1R1/APOA1/NR4A3/TGFB3/TRIM6/C4BPA/C4BPB/PCK1/CXCL6/IL1B/C3/PL
CYP1B1/ADIPOQ/PENK/WT1/AQP1",12
3CA8/ABCA12/ADIPOQ/CES1",8
/TGFB3/WNT2/COL1A1/BMP5/TGFB3/MSX2/BMP4/SOX9/IL1B/FOXA2/FOXA1/GSC/IL6/FOX2/SFRF
'DGFR/AGT/HTR2B/EGFR/P2RY12/C5AR1/ANG",10
IX1/ASS1/HMGCS2/PDGFR/EGFR/NTRK2/COL1A2/AQP2/COL3A1/CEBPB/COL4A6/COL5A2",16
:GL1/GLI3/CXCL12/TRPV4/APOA1/PLG/SDC4/BMP4/ASS1/LGALS3/ANXA1/IL1RN/KLF4/XCL1/ABCA12,
P/CHI3L1/IL6/APOA2/TLR3/AFAP1L2/CD14/ADIPOQ/ELANE/LILRA2",13
/DKK1/BMP5/TGFB3/INHBA/BMP4/GDF5/GDF15/EMILIN1/BMP3/TGFB2/GDF3/GDF10",13
/D3/TREM2/MMP9/SCN1B/CCL2/KCNA1/IFNG/OPRM1/FGF12/SGK1/CASQ2/KCNS1/AHNAK/MTNR1E
5/SEMA3C/MT3/TREM2/TSPO/MAG/PITX3/DKK1/DLX2/SPP1/IL1B/LRP4/IL6/DLX1/DAAM2/NKX6-2/S
/CLEC3B",6
/7/SOSTDC1",5
=4/ADIPOQ/MBP",5

'BMP4/RSPO2/CSF1",5

1/OSR2",5

KLF4/ADIPOQ/MBP",5

VE",5

ASS1/SERPINF1/POSTN/FDX1/CYP1B1/FBXO32/GJB2/AR/AKR1C3/AQP1",17

3X18/FGF12/TNNC1/CASQ2/KCNJ5/ADORA3/EDN3/AGT/GATA4/YAP1/FOXN4/GSN/SCN2B/THRB/KCNE4/FOXN4/DLX1/NTRK2/THRB/THY1/NEUROD1/IGFN1/DIO3",14

IRIA2/HTR1B/HTR2B/CHRNA1/CHRNA3/HTR7/HTR5A/ADORA1/HTR1E/DRD5/GRIK1/CHRNA9/HTR1A,3PB/SPINK5/SERPING1/VSIG4",6

7818,"MARCO/OPRK1/OPRM1/NPR3/MCHR1/HTR1B/HTR5A/ADORA1/NPY1R/HTR1E/P2RY12/GPR37/FAH/SULT2A1/SULT1E1/APOE/CYP27A1/LDHD/CYP4F11/CYP4F3/AKR1C3/DIO3/AKR1B10/ADH4",15

'SHH/SOSTDC1",9

GFRA/CSRNP1/PAX9",9

H/HMOX1/TIMP1/SERPINE1/MEOX2/KANK1/CXCL12/CCL2/BMP5/HRG/PADI2/DUSP1/ADORA3/HOXA/MSR1/LRP2/APOB/CPNE6/AVP/CSF3/RAB34/AREG/SPARC/WLS/APOA1/RAB32/GRIA2/RAB38/EREG/IL3/FOXN4/HOXA7/INHBA/TNFAIP6/MT1G/BMP4/LIF/APCS/NOTCH2/GPC3/CD109/IL34/RUNX1/TGFB2/TLR3/CD3/APOA1/NPC2/FABP3/APOE/RCN3/ABCA12/APOA2/ADORA1/LIPC/ANGPTL4/ACOX2/PCSK9/FABP4,MAG/SCN1B/KCNA1/TBX18/FGF12/CASQ2/KCNJ5/MTNR1B/AGT/CHRNA1/NTRK2/SCN2B/KCNE4/GJA4/ADH1C",5

/TEC/IL6/PDPN/FGG/THBD/F2",11

SERPINE1/HRG/PLAU/LIF/CYP1B1/SFRP2/RET/P2RY12/FOXC2",11

/FHL2/CASQ2/MYOT/SDC4/AHNAK/MYOD1/TNNT3/FBP2/PDLIM4/MYH8/JPH2/BAG3/PDLIM3/FBXO3/3A/SIX4/TBX18/PRRX1/SOX9/SIX1/LRIG3/ZIC1/OTOP1/GBX2/CHRNA9/FZD2/HMX3",18

IGN/BMP4/SOX9/OMD/FBN2/OSR1/AHSG/GJA1/SGMS2/OSR2/CEBPB/TMEM119/ISG15",18

T2/GLI1/YAP1/TBX20/ERBB4/WT1",10

P9/IL1B/IL6/MMP3/NUPR1/SPHK1/CD200R1L",10

/NOTCH2/GATA4/EMILIN1/TBX20/NKX2-5",10

/PITX3/FGF12/FOXA2/GAD1/APOE/PPP1R1B/CHL1/SNCA/CRH/ZIC1/NR4A2/LGI4/EN1/HPGDS/NPY1F/P1R/TBX18/CASQ2/KCNJ5/ADORA3/EDN3/AGT/GATA4/FOXN4/SCN2B/THRB/KCNE4/GJA1/S100A1/FGS2/MMP2/HMOX1/MMP9/NR4A3/EREG/BMP4/HTR1B/AGT/IL6/THBS1/GJA1/ADAMTS1/TGFB2/EL3/MMP14/TMEM119",8

3/MMP14/TMEM119",8

B/APOA2/ADORA1/FABP1/PLIN5",8

ACTA2/CALCA/EDN3/CNN1/NMUR2/AGT/HTR2B/MYOC/DOCK5/HTR7/ADORA1/BDKRB2/GDNF/SPHN3/GSN/PTX3/IFITM2",7

1C3/AKR1B10/AKR1C4",7

4/NLGN1/RELN",7

8B/C6/FCGR2B/TREM2/C7/C9/CLU/C4BPA/C4BPB/C3/CRP/APCS/SERPING1/C8A/C1R/MBL2/C1S/CFI/J/SIX1/ANXA1/AGT/CYP1B1/MYOC/MEGF10/DOCK5/ADAMTS1/S100A11/HAS2/ADIPOQ",18

L9/CDH7/FAT1/FAT2/DSP/HAMP/SCN1B/MYH1/KRT18/TRPV4/PERP/CLDN16/IGSF21/AHNAK/FGFRL1/6,"HFE/BMP5/TGFB3/INHBA/BMP4/GDF5/GDF15/BMP3/TGFB2/GDF3/GDF10",11

/APOE/TTPA/STAR/APOA2/TNFAIP8L3",11

XRG/THRB/NR3C2/NR4A2/NKX3-1/AR",12

3/NR4A1/NR5A1/RXRG/THRB/NR3C2/NR4A2/NKX3-1/AR",12

LIPN",8

3A/PVALB/CALB1/MYH14/FOLR1/ABCG2/SLC17A3/KCNK1/TMPRSS15/RHOC/MYO1E/SLC2A2/SLC6A

YOC/NEDD9/APOA1/DOCK5/DOCK1/HAS2/FGG/FGA/FGB/S100A10",10
GT/HTR2B/EGFR/P2RY12/C5AR1/ANG",10
A3C/LRP2/DSP/TNNC1/GATA4/SFRP2/TGFBR2/TBX20/FOXC2/NKX2-5",14
DLX1/HTR5A/NEUROD1/EMX2/TSKU/RELN/HSD3B1/HSD3B2/NEFL",15
3ST2/CHST3/ITIH5/TNFAIP6/IL1B/CHI3L1/CHIT1/LYVE1/GALNT5/CHST9/HAS2/B3GNT3/BGN/CHST6/S
A2/KDEL3/TSP0/HTR2A/PLIN3/MDFI/APOA1/CASQ2/SRGN/IL1B/C3/APOE/CRP/HTR2B/IL6/NR5A1/C
1/ASPA/CLU/EGR2/PLP1/ITGB4/DHH/RXRG/NTRK2/NKX6-2/LGI4/MPZ/KLK6/MAL/UGT8/NCMAP/MB
A/CLU/EGR2/PLP1/ITGB4/DHH/RXRG/NTRK2/NKX6-2/LGI4/MPZ/KLK6/MAL/UGT8/NCMAP/MBP",22
REM2/TSP0/MAG/PITX3/DLX2/SPP1/IL1B/LRP4/IL6/DLX1/DAAM2/NKX6-2/SEMA3D/THY1/GPR37L1
3/PAX2/CALB1/DLX2/NDP/SOX9/SERPINF1/PDGFR4/CYP1B1/RBP4/FOXN4/DLX1/NTRK2/THRB/THY1,
1/SOX9/RBP4/FOXN4/NTRK2/THRB/THY1/IGFN1/DIO3",12
V/AGTR1/GSN/MYO1E/ADORA1/OR51E2/AQP2/HAS2/ADIPOQ/AKR1C3/EMP2/AQP1",19

GPTL4/PLIN5",6
A2/FZD1/WNT9B",6
R2/GDF3",8
R/SOSTDC1/GDF3",8
GS2/IL1A/IL1B/C3/IL6/GATA4/CYP1B1/C5AR1",8
I",8
1/NKX3-1/NKX2-5",8
SX2/MYOD1/FOXA1/ASS1/ANXA1/AGT/CYP1B1/DHH/SSTR1/EGFR/HTR5A/GJB2/NQO1/PENK",20
SULT2A1/PON3/AHR/AADAC/IL1B/HTR1B/CYP1B1/CYP2C9/AOX1/EPHX1/REN/GLYAT/NAT2/TLR3/FB
X2/SULT2B1/SERPINE1/SFRP4/BMP4/SOX9/LIF/TMEM100/GDNF/ATOH8/ETV4",13
VGF/ACKR3/CITED2/RET/KCNA2/NTF3/GABRA5",15
AGT/EGFR/COL3A1/NUPR1/SPHK1/WNT7B/S100A6/AQP1",15
P/WNT2/TNNC1/FZD1/TBX20/COL3A1/FOXC2/FZD2/NKX2-5",14
1/FGFR2/FGFR3/PDGFR1/EFEMP1/FGFR1/PDGFR4/EGFR/NTRK2/RET/AXL/ERBB4",13
X1/SOX9/SIX1/TGFBR2/SHH",7
3N1/KCNA2",7
P/APOA4/APOA1/IL1B/ANXA1",7

2/ANXA2",7
VP/PTGDS/PLA2G4A/IL1B/ANXA1/CYP1B1/CYP2C9/EPHX1/PTGES/HPGDS/CYP2S1/CYP4F11/CYP4F3/

;
MBP",5
ANE",5
/LAMB2/ADIPOQ",5

3/TRPV4/FGF12/TNNC1/CASQ2/KCNJ5/NR4A1/TNNT3/MYH8/MYBPH/GATA4/CHRNA1/GSN/SCN2B/H
2,"PLAUR/MMP9/AREG/EREG/AGT/ADORA1/AFAP1L2/HAP1/BTC",9
1/OR51E2/DRD5/ADRA1B/ADRA1D",9
V1/THBS1/LUM/XCL1/SERPINF1/COL3A1/TSKU",10
G/ADGB/CYP27A1/CYP1B1/CYP2C9/CYP11A1/CYP4B1/CYP17A1/CYP11B1/CYP2S1/CYP4F11/CYP4F3/
AP5/SDC4/BMP4/SOX9/SIX1/OSR1/SFRP2/FZD1/WNT9B/CITED2/RET/GDNF/IRX2/IRX3/FZD2",20
/ACTA2/FGF12/TNNC1/KCNJ5/MYH8/GATA4/FRMD6/GSN/SCN2B/KCNE4/GJA1/MYO1E/PDPN/ADOR
/AQP7/PLIN1/PLIN4/FABP4/SDR16C5/CIDEA/PNPLA1/ANXA2/CIDEA/CES1/PLIN5",18
SX2/HOXA7/BMP4/ZFP36/ABCA12/CD109/ETV4/GDF3/MAFF",12
ADORA3/RXFP2/LHCGR/LGR5/ADCYAP1/GALR1/DRD5/ADRB3",12
!/OSM/AVP/CSF3/IFNG/TRIM6/LIF/NGF/IL6/IFNA21/SNCA/SFRP2/EGFR/NTRK2/RET/PRKD1/NTF3",18

3/ASS1/ALOX5AP/TM4SF5/CRABP2/P4HA3/S100A9/FABP1/FOLR2/CRABP1/AGXT/CYP27C1/TAT/HBA
 /ABCA12/CLDN1/AQP2/HAS2/AQP1",13
 =OXC1/SMOC2/HRG/NR4A1/MT1G/PDGFRA/ANXA1/ADAMTS12/ADAMTS3/SPHK1/EGR3/GAS1/PRK
 ISL2/TBX20/SHH/GBX1/GDNF/HOXC10/SOX1/RELN/VIT/NEFL",17
 6/AVP/HAMP/WNT2/CXCL12/LGI1/GLI1/GHR/FN1/MYOD1/NGF/YAP1/CRABP2/SFRP2/EGFR/IGFBP1,
 3PR183/CSPG4/CSF1/RELN",11
 L/GLI3/EFEMP1/RUNX2/BMP4/SOX9/GDF5/ADAMTS12",11
 /MEGF10/AXL/C4B/C4A",11
 IP4/SOX9/SIX1/OSR1/SFRP2/FZD1/WNT9B/CITED2/SHH/RET/GDNF/ATOH8/IRX2/IRX3/FZD2",23

 \2/COL3A1",5
 ^10/PLA2G4A/ANXA1/ANXA3/SYT8/PLA2G4D/ANXA5/ANXA2/ANXA4",12

 <KN2/SPOCK3",6

 SOSTDC1",8
 X3/HBD/HP",8
 DC1/CCL11/CSF1",8
 /P1/BMP4/SOX9/GDF5/ADAMTS12",8
 CL2/KCNA1/IFNG/OPRM1/FGF12/CASQ2/KCNS1/AHNAK/MTNR1B/CRH/JPH2/KCNE4/KCNS2/LRRC38
 'PON3/AHR/AADAC/CYP1B1/CYP2C9/AOX1/EPHX1/GLYAT/NAT2/CYP2S1/NQO1/UGT2B15/GSTA1",11
 ;F12/TNNC1/CASQ2/KCNJ5/ADORA3/EDN3/AGT/GATA4/FOXN4/GSN/SCN2B/THRB/KCNE4/GJA1/S10
 F/FOXA1/MYOC/ABCA12",10
 POE/AGT/HTR2B/FDX1/AGTR1/SNCA/S100A1/GDNF",12
 BA/BMP4/GDF5/GDF15/BMP3/ATOH8/FOS/GDF3/VEPH1/GDF10",15
 'EMILIN1/TBX20/NKX2-5",9
 CYP2C9/UGT2B4/UGT2B15/HSD3B1",9
 i4/LAMB2/NCMAP",9
 RXFP2/LHCGR/LGR5/ADCYAP1/DRD5/ADRB3",9
 'HAMP/WNT2/GLI1/YAP1/TBX20/ERBB4",9
 /TBX18/FHL2/BMP4/PDGFRA/AGT/GATA4/MYOC/EGFR/FZD7/LMNA/PITX2/CITED2/PI16/IRX3/NKX:
 PLA2G4A/IL1B/XCL1/ARID5A",6
 L34/CSF1/C5AR1",6

 1/CTSG/AGT/REN/AGTR1/CPA3/OR51E2",7
 !/MAL",7
 P1/NKX6-2/MAL",7
 BMP5/IGFBP4/IGFBP1/NKX3-1/IGFBP6/AR",7
 'COL3A1",7
 ;H3D19/IFNG/IL1B/APOE/TIMP4",7
 IP6/HRG/FN1/SDC4/ITGB4/THBS1/THY1/MMP14/FAM107A/RHOD/APOD/S100A10",16

 ;SDC4/BMP4/SOX9/SIX1/OSR1/SFRP2/FZD1/WNT9B/CITED2/RET/GDNF/IRX2/IRX3/FZD2",21
 ./SLC6A18/DRD5/SLC6A19/PDZK1/ITLN1/AQP1",12
 <2/MEOX2/SMOC2/SPARC/FGF1/HRG/APOA1/NR4A1/BMP4/RRAS/APOE/SERPINF1/STARD13/LGALS:
 REM2/OSM/LGALS1/SERPINE1/TRPV4/IFNG/IL1RL1/TRIM6/EREG/IL1B/C3/PLA2G5/LBP/ALOX5AP/AG
 /ZIC1/NR4A2/LGI4/EN1/GBX1/GDNF/SNCG/DMBX1",14
 REG/MSX2/AR/SOSTDC1/CCL11/CEBPB/ERBB4/CSF1/WNT7B",13
 ;4BPB/IL1B/C3/SPINK5/SERPING1/VSIG4",10
 GFRA/CSRNP1/GPC3/PAX9",10

1/D1/MEGF10/JPH2/GJA1/SHH/IGF2",10
11/GLI3/CXCL12/MAP3K8/CCL2/ST3GAL4/APOA4/IFNG/VNN1/IL1A/NR4A3/SDC4/PCK1/BMP4/IL1B/1
R2/PENK/KANK2",8
1A1/FN1/IL1R1/F3/SERPINC1/CHL1/NTRK2/TIMP4/COL1A2/BDKRB2/COL3A1/ANXA2/SERPINA1/ELA
8/LOX/FHL2/BMP4/SIX1/MYOD1/TNNT3/PDGFRA/AGT/GATA4/MYOF/SYPL2/MEGF10/CSRP1/LMNA,
'PDGFRA/IL6/MEGF10/CSRP1/PDPN/P2RY12/FGG/FGA/FGB",16
'3/F3/F10/GDF15/CHI3L1/THBS1/TPBG/EGFR/RET/IGF2/AXL/CX3CR1/P2RY12/TNFAIP8L3/FAM110C/
EDN3/AGT/REN/AGTR1/CPA3/OR51E2/DRD5",9
N1/CREB3L1/RUNX1/SERPINB7/F2",9
3/AGT/ADORA1/AFAP1L2/HAP1/BTC",9
JNX1/ISL2",5
VX1/ISL2",5

ADIPOQ",5
HADL/CST3/EMILIN1",5
SRPX2/IFNG/SMOC2/SPARC/FGF1/BMP4/SOX9/RRAS/ANXA1/AGT/THBS1/ANXA3/FGF7/DOCK5/DOC
7
3/KIF16B/SMOC2/FGF1/FGF12/RUNX2/FGFRL1/THBS1/FGF7/CREB3L1/OTX2/SHISA2/FGF16",15
I3L1/ANXA1/IL6/KLF4/APOA2/TLR3/AFAP1L2/CD14/ADIPOQ/ANXA4/ELANE/LILRA2",17
K1/SFRP2/RSPO3/GPC3/FZD7/FZD1/WNT9B/FZD2/ROR1",11
SLC5A3/ANXA13/FOLR1/TRPV4/KCNA1/SCNN1A/SLC22A2/FN1/ABCG2/SLC17A3/SLC17A1/ACY3/AN
IT2/CXCL12/THBS4/F3/NR4A1/BMP4/HTR2B/AGTR1/VIP/IGF2/LRG1/CCL11/EGR3/PRKD1/ANG/APEL
/ERBB3/TREM2/OSM/CSF3/FN1/SOX9/PDGFRA/AGT/EGFR/NTRK2/NKX3-1/ERBB4/F2/ROR1/RELN",1
EDD9/NRK/PDLIM4/NOTCH2/PDGFRA/ANXA1/FGF7/HMCN1/THSD7B/GSN/CLDN19/MICALL2/NTF3",
31581917801679,"PLAUR/PTGS2/PAX2/MT3/MMP9/AVP/CRYAB/NR4A1/KLF4/THBS1/SNCA/SFRP2/F
2/MT3/TREM2/HMOX1/TSPO/MMP9/SOD3/APOA4/TRPV4/VNN1/NR4A3/PDGFRA/ANXA1/IL6/GATA
/FGG/FGA/FGB/ADIPOQ/MBP",12
OPRM1/CRH/NLGN1/DLGAP1/PATE1/SHISA6/RELN/PRRT1/SHISA9",12
K1/TREM2/CCL2/KCNA1/IFNG/NR4A3/PLP1/EDN3/C3/AGT/CXCL9/XCL1/SNCA/GPC3/JPH2/THY1/LRI
T/HS3ST2/CHST3/ITIH5/TNFAIP6/IL1B/LYVE1/GALNT5/CHST9/HAS2/B3GNT3/BGN/CHST6/SPOCK3/CI
ITGB4/DHH/RXRG/NTRK2/NKX6-2/LGI4/MPZ/KLK6/MAL/UGT8/NCMAP/MBP",21
A1/ANXA1/IL6/PANX3/CX3CR1/SAA1/LPL/SPHK1/FFAR4/S100A13/S1PR3/ORM2/ORM1/LILRA2",20
JG/IL1R2/APOA1/ANXA1/IL6/PANX3/CX3CR1/SAA1/LPL/SPHK1/FFAR4/S100A13/S1PR3/ORM2/ORM
RP2/PLEK2/FERMT1/KANK1/FOLR1/TRPV4/SCNN1A/OPRM1/ABCG2/SLC17A3/MCHR1/KCNK1/EGFR/
PNE6/HTR2A/CALB1/SCN1B/RCVRN/CRYAB/CALCA/KCNA1/OPRM1/GHR/SLC5A7/TGFB3/GRIA2/MY
2/APOB/AVP/RAB34/AREG/WLS/RAB32/GRIA2/RAB38/EREG/APOE/ANXA3/RAB20/EGFR/FCGR1A/CC
EB3L1/RUNX1/SERPINB7/F2",7
I/PTGS2/COMP/HAMP/HOXA13/CALCA/SPP1/SOX9/IL6/YAP1/RBP4/RCN3/ABCA12/GJA1/LCN1/AZGF
/CCL2/ZFP36/IL6/YAP1/THBS1/GSN/NEUROD1/ANGPTL4/FGG/FGA/FGB/NUPR1/AKR1C3",16
'ATOX8/HES3/NEUROG2/FIGLA",11
V/STAR/APOA2/TNFAIP8L3",11
'RSPO3/AXL/FOXC2",10
BX1/HOXC10/SOX1/RELN",10
'KCNA1/CASQ2/KCNJ5/KCNS1/EDN3/MTNR1B/KCNK1/VIP/KCNE4/KCNS2/KCNJ15/LRRC38/LRRC52/A
L6/KLF4/APOA2/TLR3/AFAP1L2/CD14/ADIPOQ/ANXA4/ELANE/LILRA2",17
3/HRG/SPP1/AGT/TMBIM1/IL6/GJA1/RUNX1/TMEM119/SIGLEC15",15
S1/CTSG/FGL1/GLI3/CXCL12/MAP3K8/CCL2/ST3GAL4/IFNG/VNN1/IL1A/NR4A3/SDC4/PCK1/BMP4/IL
FC1/LBX1/FOXN4/DAAM2/GJA1/ZIC3/NBL1/TGFBR2/PITX2/CITED2/TBX20/SHH/SOSTDC1/NKX2-5/TD
3L1/MBP",9

MT1/FN1/THBS1/LUM/XCL1/SERPINB7/TSKU",9
K20/NKX2-5",8

1/SOCS3/APELA",8
L1/CXCL8/C5AR1",8
OF15/CFC1/BMP3/TDGF1",8
P1",5
/CXCL9/MYOCN/BOC/CMTM5/SOSTDC1/GDF3",11
H7/DSP/TRPV4/PERP/CLDN16/TGFB3/IL1B/AGT/RAB13/GJA1/RHOC/CLDN14/CLDN1/CLDN19/MICALL1/KR1B10/ADH4/AKR1C4",7
/FOXN4/GJA1/ZIC3/TGFB2/CITED2/TBX20/SHH/NKX2-5",13
3DS/NR4A3/TREM1/CXCL6/C3/IL6/ANXA3/FCGR1A/SPON2/CX3CR1/F2/S100A13/ELANE",17
/CLDN16/IL1B/AGT/RAB13/GJA1/RHOC/CLDN14/CLDN1/CLDN19/MICALL2/GJB2/GJB1/UGT8/IRX3/C
'STAR/APOA2",9
2/STAR/PMP2/APOA2/APOD",11
L/BMP4/SIX1/APOE/MYOCN/CITED2/COL3A1/FOXC2",14
D109/TLR3/FBN1/GPR183/FOS/JUNB/CEBPB/ANXA2/CSF1/SIGLEC15",16
/TECTB/XPNP2/NRN1/TEX101/CNTN6/CPM/CFC1/CNTN4/GPC3/GFRA1/THY1/RAET1L/ART3/CD10
B/BCHE/FBXO2/APOA1/GRIA2/CLU/APOE/NLGN1/GRIN2B",15
3/HSD17B2/SPR/HAO2/HSD11B1/RDH10/CYP27A1/DHRS3/CRYL1/LDHD/SDR16C5/CYP4F3/ADH1A/A
HTR2A/CCL8/HRG/FN1/TRIM6/PLG/TREM1/CXCL6/APOE/CRP/APCS/POU2F3/CH25H/IFITM3/FCN3/A
3L1/RUNX1/SERPINB7/F2",7
'APOC1/APOA2",7
'ADORA1/CIDEA/PLIN5",7
'FBXO32/GJB2/AQP1",7
31",7
3/IFITM2",7
/SFRP2/DAAM2/RSPO3/GPC3",7
/GATA4/EMILIN1/TGFB2/TBX20/NKX2-5",11
IDEA/CES1/PLIN5",11
9/EREG/AGT/FCGR1A/IL34/ADORA1/AFAP1L2/BTC/RELN",11
'TRPC5/CPNE6/HAMP/WNT2/CXCL12/GLI1/GHR/FN1/MYOD1/NGF/YAP1/CRABP2/TGFB2/TBX20/ISI
IX1/ASS1/HMGCS2/PDGFR/EGFR/NTRK2/COL1A2/COL3A1/CEBPB/NQO1/COL4A6/COL5A2",18
PLIN5",5

143871667,"TIMP3/THBS1/PMAIP1/ATF3/MAL",5
.KR1B10/ADH4/AKR1C4",8
0.0139588460478492,"DHRS9/RDH8/HSD17B2/HSD11B1/AKR1C3/AKR1C4/HSD3B1/HSD3B2",8
/ITI5/TNFAIP6/IL1B/CHST9/HAS2/B3GNT3/BGN/CHST6/SPOCK3/CHSY3",15
2/VGF/APOE/GFAP/AGT/UNC13C/CNTN4/IGSF11/SNCA/NTRK2/S100B/ADORA1/FAM107A/CX3CR1/I
HTR5A/HTR1E/ADRA1B/ADRA1D/HTR1A/ADRB3/HRH1",11

IC1/ANGPTL4",6
CD",6
N",7
L9/TNNT1/CALCA/TRPV4/KCNA1/TNNC1/CASQ2/NR4A1/CNN1/TNNT3/NMUR2/MYBPH/GATA4/MYC

AG/RARRES2/SULT1E1/TRPV4/MSX2/SIX1/ZFP36/LGALS12/IL6/YAP1/SFRP2/CEBPB/LPL/METRNL/AD
LA2G4A/CLU/LBP/IL6/THBS1/SNCA/VSIG4/TLR3/CX3CR1/SPHK1/C5AR1",17
/APOE/AGT/HTR2B/FDX1/AGTR1/SNCA/EGFR/S100A1/GDNF/DRD5/HP",17
DGFR/CSRP1/PAX9",10
O3/GPC3/FZD7/FZD1/WNT9B/ERBB4/FZD2/ROR1",13
O3/GPC3/FZD7/FZD1/WNT9B/ERBB4/FZD2/ROR1",13

/F10/THY1/FOLR2/CD14",7
CNA1/SCNN1A/OPRM1/GRIA2/KCNJ5/KCNS1/SLC17A3/NMUR2/HTR1B/KCNK1/CHRNA1/CHRN3/S
YP2C9/CH25H/AOX1/TPH2/CYP11A1/CYP4B1/SNCA/CYP17A1/P4HA3/CYP11B1/CYP2S1/CYP4F11/CY
L1B/HTR1B/AGT/SNCA/PTGES/ADORA1/CEBPB/PDZK1/CES1",15
ITED2/TBX20/SHH/NKX2-5",12
KCNE4/KCNS2/KCNJ15/LRRC38/LRRC52/KCNK5/KCNJ4/KCNG3/KCND3/KCNA2/KCNA4/KCNJ18",16

5
M/GPX3/HBD/GSTA1",11
RK1/OSM/HMOX1/OPRM1/INHBA/IL1B/LIF/APOE/MTNR1B/ANXA1/HTR1B/SNCA/CRH/GJA1/ADORA
1/HMOX1/IL1R1/APOA1/NR4A3/TGFB3/TRIM6/IL1B/IL6/XCL1/APOA2/SPON2/TLR3/FFAR3/ARID5A"
2/FABP3/APOE/APOA2/LIPC/PCSK9/FABP4/LPL/TSKU/CES1",16
RIP6/HRG/FN1/SDC4/ITGB4/THBS1/THY1/MMP14/FAM107A/RHOD/APOD/S100A10",16
YOD1/BHLHE40/FIGLA",8
PCK1/SOX9/ASS1/HMGCS2/NOTCH2/ANXA1/IL6/ZIC3/CLDN1/CITED2/PCSK9/CEBPB",20
/RNASE2/RNASE3/IFNLR1/FFAR3",9
2/NKX6-2/GPR37L1/F2",9
HX8/GBX2/SOX1",9
/HTR2A/CSF3/NPR3/PLCH1/FN1/SOX9/PDGFR/AGT/HTR2B/PIK3C2G/EGFR/NTRK2/PLCD3/NKX3-1/E
S1/AGT/KLF4/CYP1B1/PTX3/CX3CR1/NQO1",14
X1/MMP9/SRPX2/MEOX2/IFNG/SMOC2/SPARC/FGF1/HRG/BMP4/SOX9/RRAS/APOE/SERPINF1/STAR
YP27A1",7
/NEUROD1/FPR1",7
/C5AR1/MMP28",7
I5",7

/NKX6-2/GPR37L1/F2",7
ILIN1/RUNX1/PDPN/TNFB",7
2/SSTR1/NPY1R/GALR1/NTSR2/GPR139",10
CYP17A1/CYP11B1/CYP2S1/CYP21A2",9
AR/PMP2/APOA2/GPR183/APOD",12
SHH/NKX3-1",8
APOC3/PCSK9/ADIPOQ/ANXA2",8
ED2/HAS2",8
OX1/CTSG/GZMB/AHR/PTGDS/C7/C9/IL1R1/NR4A3/CLU/C4BPA/C4BPB/TREM1/CXCL6/IL1B/C3/CRP/
MMP4/FGFRL1/GATA4/FZD1/TGFB2/CITED2/FZD2/NKX2-5",13
/MTNR1B/AGT/CHRNA1/NTRK2/CLDN19/DRD5/KCNA2",13
1/PLAUR/GPRC5A/MMP9/AREG/EREG/AGT/CBLC/EGFR/ADORA1/AFAP1L2/HAP1/BTC",13
/OSM/HTR2A/CSF3/FN1/SOX9/PDGFR/AGT/HTR2B/PIK3C2G/EGFR/NTRK2/NKX3-1/ERBB4/F2/ROR
SM/AVP/DKK1/CSF3/IFNG/TRIM6/LIF/NGF/IL6/IFNA21/SNCA/SFRP2/EGFR/NTRK2/RET/BDKRB2/PRK
POA4/APOC3/APOA1/IL1B/APOC1/ANXA1",10
OX9/SIX1/FOXA1/GATA5/POSTN/CNTN6/NOTCH2/YAP1/DLX1/TIMP4/MMP14/TGFB2/TMEM100/A

IP/DKK1/TBX18/SMYD1/FHL2/BHLHE41/BMP4/SIX1/MYOD1/GDF15/TNNT3/PDGFRA/AGT/GATA4/M
/NOTCH2/GATA4/EMILIN1/TGFB2/TBX20/NKX2-5",12
XA7/BMP4/ZFP36/ABCA12/CD109/ETV4/GDF3/MAFF",12
P3/APOE/APOA2/LIPC/PCSK9/FABP4/LPL/TSKU/CES1",16
G/BMP4/BAG3/ZIC1/SHH/PRKD1/APOD",11
2/RSPO3/GPC3/FZD7/FZD1/WNT9B/FZD2/ROR1",11
INHBA/BMP4/GDF15/CFC1/BMP3/TGFB1",7
PRC5A/KIF16B/MMP9/AREG/EFEMP1/EREG/SOX9/AGT/CBLC/EGFR/ADORA1/FAM83B/AFAP1L2/HAP
R/CLU/IL1B/ASS1/AGT/KLF4/CYP1B1/PTX3/CX3CR1/NQO1",14
1C",6
P2/RET/P2RY12/FOXC2",6

S2",6
FERMT1/THBS1/LUM/XCL1/SERPINB7",6
/SERPINB7/WT1",6

TGFB2/CITED2/FZD2/NKX2-5",9
,5

",5
37L1",5
3A1/TSKU",5
FGB",5
ORA1/KCNA2",5

MA3C/FOLR1/BMP4/PITX2/CITED2",5
A3C/FOLR1/BMP4/PITX2/CITED2",5
R2",5
P3/RAB38/HTR2B",5
LR1",5
8,"TBXA2R/PTHLH/CALCA/OPRM1/GLP1R/RFXP2/LHCGR/CXCL9/LGR5/ADCYAP1/VIP/HTR5A/GALR1/I
F36/IL6/YAP1/THBS1/GSN/NEUROD1/TGFB2/ANGPTL4/FGG/FGA/FGB/NUPR1/AKR1C3",18
FGF1/IL1A/THBS1/BAG3/TRPV3/SCARA5/HSPB2/CD14/HSPA6/MICA",17
I2/WIPI1/HMOX1/COL1A1/FOLR1/PCK1/FOXA2/MYOD1/POSTN/PMAIP1/WNT9B/ATF3/DAPL1/ALB/
COL1A1/PLG/HOXA7/THBS1/FZD7/MMP14/FAM107A/TACSTD2/APOD",12
/NMUR2/ANXA1/THBS1/FABP1/BDKRB2/FABP4/PLA2G2A",12
KK3/MOXD1/APOB/PLTP/APOA4/IFNG/BMP5/FGF1/SPR/APOA1/PCK1/APOE/HMGCS2/CYP27A1/LHC
DLX1/LHX8/GBX2/SOX1",10
SX2/HOXA7/SOX9/YAP1/OSR1/GDF3/S1PR3",10
FP2/LHCGR/LGR5/ADCYAP1/DRD5/ADRB3",10
FIMP3/SRPX/INHBA/AGT/THBS1/PMAIP1/ATF3/RET/MAL",10
OMP/HAMP/DKK1/TBX18/LOX/SMYD1/FHL2/BHLHE41/EREG/BMP4/SOX9/SIX1/MYOD1/GDF15/TNN
LB1/CYP2C9/EPHX1/CYP2S1/CYP4F11/CYP4F3/AKR1C3",11
VDP/LIF/CITED2/GJB2/AR/JUNB/HMX3",11
/FOXL2/MFAP5",8
TR2B/HTR7/HTR5A/HTR1E/HTR1A/HRH1",8

./DEFB124/S100A14",7
/PLEK2/CPNE6/PLTP/ANXA13/PLEKHA4/ANXA10/APOA4/APOC3/SYT10/PLA2G4A/F3/APOA1/F10/PL

3600491621998,"DHRS9/RDH8/HSD17B2/SPR/HSD11B1/RDH10/CYP27A1/DHRS3/CRYL1/LDHD/SDR
 P/GLI3/GLI1/FGF1/PCK1/SOX9/ASS1/HMGCS2/NOTCH2/ANXA1/IL6/ZIC3/CLDN1/CITED2/PCSK9/CEBI
 YAB/NR4A3/ANXA1/IL6/CYP1B1/FABP1/AXL/GPR37L1/FOSL1/SPHK1/NQO1/HBA1/AQP1/HP",19
 /CXCL12/LGI1/MYOT/EGR2/EDN3/CNTN6/CHL1/NOTCH2/LHX9/CNTN4/BOC/SEMA3D/ISL2/SHH/GBX
 MA1/TREM2/PYGL/TRPV4/PCK1/FOXA2/VGF/FOXA1/SERPINF1/MTNR1B/IL6/GATA4/RBP4/ABCA12/
)PRM1/HMGCS2/HTR1B/CLDN1/CA3/CD14/NQO1/ADIPOQ/PENK/SLC2A4/GRIN2B",18
 G/FN1/PLG/TREM1/CXCL6/APOE/CRP/APCS/POU2F3/PTX3/MBL2/CX3CR1/F2/ELANE",16
 3/HTN1/XCL1/FCGR1A/CD1A/CD1B/AZGP1/DEFA4/DEFA6/CX3CR1/F2/CCL13/ELANE/MICA/KLRC3/EN
 'AGT/KLF4/CYP1B1/PTX3/CX3CR1/NQO1",13
 2/PITX2/SHH/GBX2/HAP1/SOX2/TAL2",13
 'SOD3/APOA4/NR4A3/PDGFR/ANXA1/IL6/CYP1B1/FBLN5/EGFR/FABP1/AXL/GPR37L1/FOS/SPHK1/N
 TCH2/KLF4/LBX1",9
 52R7/TAS2R9/TAS2R3/AZGP1/CST2/CST1/FFAR4/RTP5/TAS2R38",9
 /COL1A1/SOX9/ZFP36/EGFR/ERBB4/TGDF1",9
 TA4/CFC1/LBX1/FOXN4/DAAM2/GJA1/ZIC3/NBL1/TGFBR2/PITX2/CITED2/TBX20/SHH/SOSTDC1/NKX2
 /IL1A/EGR2/NMUR2/MTNR1B/AGT/IGSF11/VIP/ADORA1/TMEM100/NLGN1/DLGAP1/NCMAP/SHISA
 K1/CMA1/TREM2/PYGL/TRPV4/PCK1/FOXA2/VGF/FOXA1/SERPINF1/MTNR1B/IL6/GATA4/RBP4/ABC
 A2/EVX1/GLI3/CXCL12/LGI1/MYOT/EGR2/EDN3/CNTN6/CHL1/NOTCH2/LHX9/CNTN4/BOC/SEMA3D,

 ,"SEMA3C/FOLR1/BMP4/PITX2",4
 H/GPR37L1",4
 ",4

 /WT1",4

 .1RN",4
 DF5/SHH",4
 MP2/TDRD1/FERMT1/HOXA5/IGSF21/RAB32/MSX2/PAEP/RAB38/RUNX2/EREG/C3/FOXA1/SPINK5/U
 L/SIX1/ASS1/HMGCS2/PDGFR/EGFR/NTRK2/COL1A2/AQP2/COL3A1/CEBPB/NQO1/COL4A6/COL5A2
 A3/GJA1",5
 310",5
 IN1A/FLG/ABCA12/CLDN1/AQP2/HAS2/AQP1",11
 4/GBX1/HOXC10/SOX1",10
 /LHCGR/LGR5/ADCYAP1/DRD5/ADRB3",10
 REM2/CCL2/KCNA1/IFNG/PLP1/EDN3/AGT/CXCL9/XCL1/SNCA/JPH2/THY1/LRRC38/LRRC52/HAP1/PD
 R2B/TMEM176B/GLI3/HOXA7/INHBA/TNFAIP6/BMP4/APCS/ANXA1/RUNX1/TLR3/SHH/FBN1/ADIPO
 /MT3/TLL2/MAG/SPP1/BMP4/GDF15/CGA/RBP4/SEMA3D/TGFBR2/CITED2/PI16/MYOZ1/OSTN",17
 2B/LRP2/SERPINE1/SFRP4/DKK1/FOLR1/APOC3/CLU/C3/APOE/APOC1/HTR1B/HTR2B/ACKR3/SNCA/C
 EM119",6
 RA5",6
 HH",6

 =1/NOTCH2/IL6/CEBPB",6
 12/OSM/HTR2A/CSF3/NPR3/PLCH1/FN1/SOX9/PDGFR/AGT/HTR2B/PIK3C2G/EGFR/NTRK2/PLCD3/N
 IH/NKX3-1",8

2/KCNJ15/LRRC38/LRRC52/KCNK5/KCNJ4/KCNG3/GRIK1/KCND3/KCNA2/KCNIP1/KCNA4/AQP1/KCNJ1/ELANE/ORM2/ORM1/HP",12
1R1/EREG/IL1B/PDGFRA/IL6/IL1RN/FGF7/CBLC/TSLP/FAM83B/GDNF/BTC/ERBB4/IL1RAP/FGF16",21
R1/IL1RL1/F3/ACKR3/OSMR/FCGR1A/GFRA1/IL17RE/CX3CR1/FPR1/CCR9/IFNLR1/IL1RAP/C5AR1/CRLI2/PAX2/MT3/MMP9/AVP/CRYAB/NR4A1/KLF4/THBS1/SNCA/SFRP2/FABP1/AQP1",14
HBA/SOX9/NR5A1/VIP/CITED2/SHH/AR/MAPK15/WT1/APELA",14
L/HSD3B2",7
C1/APOA2",7

/ETNPPL/SPTLC3/AGXT/TAT",11
L/FOXN4/GJA1/ZIC3/TGFBR2/CITED2/TBX20/SHH/NKX2-5",12
'AREG/EFEMP1/EREG/SOX9/AGT/CBLC/EGFR/ADORA1/FAM83B/AFAP1L2/HAP1/BTC",18
HR/APOA1/TGFB3/C4BPA/C4BPB/LGALS3/SPINK5/ANXA1/XCL1/SERPING1/VSIG4/APOA2/CX3CR1/MIR75,"CMA1/CTSG/REN/CPA3/OR51E2",5

ITR2A/CXCL12/CALCA/PRDM12/ADORA1",5
",5

/DKK1/SFRP2/RSPO3/GPC3",5
IX1/HTR2A/CDH15/TEX101/LRP4/MYOF/TGFBR2/ADORA1B/HAS2/MAL/PRTN3/FXYD1",18
NAK/ANXA1/COL6A2/MLIP/COL6A3/KCND3/SNTB1/DES/SLC2A4/BGN/LAMA2/AQP1/FXYD1",20
L1B/APOE/MMP7/TIMP4/PRTN3",9
REG/IL1B/IGF2/BTC/SPHK1",9
'KCNS2/LRRC38/LRRC52/KCNJ4/KCNG3/KCND3/DPP10/KCNA2/KCNIP1/KCNA4",14
MTNR1B/CRH/GJA1/ADORA1/ADIPOQ/FFAR4",11
RP2/DSP/WNT2/TNNC1/TBX20/FOXC2/NKX2-5",11
LB/TRPV4/KCNA1/SCNN1A/OPRM1/RHAG/GRIA2/KCNJ5/KCNS1/SLC17A3/NMUR2/HTR1B/KCNK1/CHLA2G4A/IL1B/ANXA1/PTGES/HPGDS/AKR1C3",10
'APOD/NEFL",10
3/BMP4/FBN2/OSR1/OSR2/CEBPB/TMEM119/ISG15",10
LITRK2/IL1RAP/C5AR1",10
C1A6/FOLR1/SLC15A3/TRPV4/SCNN1A/IFNG/SLC22A2/KCNJ5/FABP3/GFAP/AGT/THBS1/SNCA/KCNJ13/RXFP2/LHCGR/LGR5/ADCYAP1/GALR1/DRD5/ADRB3",13
/INHBA/EDN3/RBP4/ADCYAP1/CRH/SLC30A8/GALR1/NKX3-1/FGG/FGA/FGB/FOXL2/FFAR4",18
.PL/CIDEA/CES1/PLIN5",14
ITX1/FOSL2/TBX15/SIX4/AHR/GLI3/TBX18/TCF21/SATB2/NR4A3/NR4A1/NFE2/RUNX2/SOX9/DACH2/ANKK1/TRPV4/GHR/EGR2/PCK1/IL1B/VGF/HMGCS2/AGT/RAB13/AHSG/IGFBP1/KLF15/OTOP1/FBP1/IG/EDN3/IL1B/FOXA2/VGF/MTNR1B/ANXA1/IL6/IL1RN/RBP4/ADCYAP1/ABCA12/VIP/CRH/GJA1/NEURAC/PLA2G4A/APOA1/PLBD1/PCK1/PLA2G5/APOC1/CYP1B1/APOA2/PLA2G4D/FABP1/LIPC/CRABP1/JSP1/TNFAIP6/THBS1/SEMA3D/NBL1/ELANE/MMP28",12
2RY12/FGG/FGA/FGB",12
.2,"TAS2R7/TAS2R9/TAS2R3/AZGP1/CST2/CST1/RTP5/TAS2R38",8
ATA4/GJA1/IRX3/NKX2-5",8
IFBR2/TBX20/TMEM100",8
FBP4/IGFBP1/NKX3-1/IGFBP6/AR",8
'TGS1/ALOX5AP/PTGES/GPX8/HBA1/HBM/GPX3/HBD/GSTA1",11
SPTLC3/AGXT/TAT",11

CKR3/OSMR/GFRA1/IL17RE/CX3CR1/CCR9/IFNLR1/IL1RAP/CRLF2",16
GA11/EMILIN1/CNTN4/S100A11/STXBP6/ANXA2/PKP3",12
7/HTR5A/HTR1E/HTR1A/HRH1",8
3/AKR1C4/HSD3B1/HSD3B2",8
TR1A/HRH1",8
G3/ZIC1/SHH/PRKD1/APOD",11
A3/RXFP2/LHCGR/LGR5/ADCYAP1/GALR1/DRD5/ADRB3",13
PINE1/HRG/HOXA7/PLAU/SDC4/RRAS/THBS1/THY1/MMP14/FAM107A/CSF1/APOD/S100A10/EMP2",
NBL1/MMP28",6
X/F3/MYOCD/SNCA/ADIPOQ/APOD",6
46072571,"CLDN11/CLDN16/CLDN14/CLDN1/CLDN19/CLDN7",6
2",6
X2/AR/CCL11/CSF1",6

NTRK2/THRB/THY1/DIO3",9
NXA1/XCL1/ARID5A/IL27",9
CL1/CXCL8/C5AR1",9
/HOXC10",7
L",7
",7
2/GLI1/YAP1/TBX20/ERBB4",7
C1/COL1A1/TGFB3/BMP4/IL1B/IL6/PDPN/TGFBR2/TBX20",10
1/SFRP4/CLU/C3/PCSK9/ANXA2/NTF3/APELA",10
2/OSR1/OSR2/CEBPB/TMEM119/ISG15",10
P1B/OLR1",5
MYOT/TNNT3/FBP2/PDLIM4/MYH8/JPH2/BAG3/PDLIM3/FBXO32/TIMP4/TRIM63/CSRP1/IGFN1/CM
/PTGS2/SCTR/HTR2A/CALB1/PLAT/RETN/DKK1/LGI1/CCL2/BCHE/SRGN/EGR2/IL1B/VGF/APOE/GFAP/
XC1/APOH/HOXA5/SERPINE1/SPARC/THBS4/HRG/SERPINF1/SPINK5/AGT/KLF4/THBS1/EMILIN1/ADA
IL1B/HTR1B/AGT/THBS1/SNCA/PTGES/ADORA1",12
3/COL1A1/TNFRSF8/SOX9/IL1B/AGT/BAG3/TLR3/AQP1",12
/SOD3/CRYAB/APOA4/CRP/AGT/THBS1/CYP11B1/FBLN5/PMAIP1/AGTR1/SNCA/MMP3/TGFBR2/DRD
2/RDH8/MYO3A/TIMP3/POU6F2/COL1A1/RCVRN/EFEMP1/SFRP5/TGFB1/RDH10/LRAT/NDP/RBP4/LI
CTR/HTR2A/CALB1/PLAT/RETN/DKK1/LGI1/CCL2/BCHE/SRGN/EGR2/IL1B/VGF/APOE/GFAP/NGF/HTR
VP/WFDC1/MAG/HAMP/CXCL12/LGI1/CRYAB/HRG/FN1/SGK1/SPP1/INHBA/EDN3/NRN1/SOX9/APOE
FGF1/SPR/APOA1/PCK1/APOE/HMGCS2/CYP27A1/LHCGR/SNCA/CYP11B1/SPTLC3/SPHK1/HRH1/CES

1",4

1",4

LIP",4

i2130998377216,0.0241904284099336,"CREB3L3/CREB3L1/ATF3/CEBPB",4
'CLDN1/TLR3/BDKRB2/LRRC8E/SLC2A4/AQP1",13
3/PDGFR/AGT/EGFR/NUPR1/SPHK1/S100A6/AQP1",13
.REG/EREG/AGT/CBLC/EGFR/ADORA1/AFAP1L2/HAP1/BTC",13
/CLU/TNFRSF8/ZFP36/LBP/IL6/THBS1/SPON2/TLR3/AXL/CX3CR1/CD14/LPL/CIDEA/ADIPOQ/ARID5A/
PO/IFNG/IL1A/CLU/TNFRSF8/ZFP36/LBP/IL6/THBS1/SPON2/TLR3/AXL/CX3CR1/CD14/LPL/CIDEA/ADI
2G4A/LBP/IL6/THBS1/SNCA/VSIG4/SPHK1",11
GT1/DLX1/NTRK2/THRB/THY1/DIO3",11
M2/TMEM176B/GLI3/IFNG/VNN1/HOXA7/INHBA/TNFAIP6/PCK1/BMP4/TNFSF9/LIF/APCS/SPINK5/N
'IFNLR1/FFAR3",8
L58,"HFE/FCGR2B/HMOX1/APOA1/TGFB3/SPINK5/XCL1/APOA2",8
'CSK9/ANXA2",8
A2/PCSK9/ANXA2",8
176B/GLI3/HOXA7/INHBA/TNFAIP6/BMP4/APCS/ANXA1/RUNX1/TLR3/SHH/FBN1/ADIPOQ",16
NOTCH2/HTR1B/IL6/GJA1/TMEM119/SIGLEC15",14

",5
/GJA1",5

H",5
,5

F",5

1B/LBP/IL6/TSLP/SPON2/TLR3/LPL/IL1RAP/ARID5A/MBP/LILRA2",15
/TREM2/CCL2/KCNA1/IFNG/PLP1/EDN3/AGT/CXCL9/XCL1/SNCA/JPH2/THY1/LRRC38/LRRC52/HAP1/
IM63/LMNA/KLF15/MYOZ1",10
:KR3/CITED2/KCNA2",10
'1/C5AR1",10
F1A/FCGR2B/PTGS2/OPRK1/OSM/HMOX1/MMP9/FERMT1/EPPIN/HTR2A/HAMP/SFRP4/CRYAB/APC
BDKRB2/PLA2G2A",9
HMOX1/MMP9/SOD3/APOA4/VNN1/NR4A3/PDGFR/ANXA1/IL6/GATA4/CYP1B1/FBLN5/SNCA/EGFR
VRAP/FXYD1",10
AP",7
USP6",4

/EREG/IL1B/HTR2B/FGF7/SHH/NKX3-1/IGF2/BTC",14
/ADORA1",6
1",6
SP1/NBL1/APOD",6

DXC1/IFNG/TRIM6/KLF4/NEUROD1",6
1/FGF16",6

;
C4/THBS1/THY1/MMP14/FAM107A/APOD/S100A10",11
-RG/SDC4/THBS1/THY1/MMP14/FAM107A/APOD/S100A10",11
SLC22A2/GFAP/HTR1B/AGT/SNCA/NTRK2/GJA1/ADORA1/SLC6A18/SLC6A5/LRRC8E/SLC6A19/SLC36/
/CXCL12/SOD3/CRYAB/IL1A/TGFB3/PLAU/PCK1/GNGT1/THBS1/MYOC/PMAIP1/NR4A2/MMP14/AI
XA7/INHBA/TNFAIP6/LIF/APCS/NOTCH2/IL34/RUNX1/TLR3/FBN1/FOS/CEBPB/ADIPOQ/CSF1",17
/SDC4/RRAS/THY1/CSF1/S100A10/EMP2",10

VE1/THY1/ELANE",8
4B",8
i/BAG3/ZIC1/SHH/PRKD1",8
RC8E/SLC2A4/AQP1",8
/FOXA2/PPP1R1B/CHL1/SNCA/ZIC1/NR4A2/LGI4/EN1/GBX1/GDNF/SNCG/DMBX1",19
1/C5AR1",9
TGFB3/LRP2/DSP/TNNC1/FOXC2/NKX2-5",9
IUNB/SOCS3/WNT7B",9
ZFP36/EGFR/ERBB4/TGDF1",9
ITCH2/TGFB2/AXL/CEBPB/PRTN3",9
2095638,"LTBP1/TGFB3/TGFB3/EMILIN1/FBN2/PRDM16/CD109/HTRA1/FBN1/HTRA3/WFIKKN2/CI
6/NKX6-2/ZIC3/NEUROD1/SHH/IGF2",13
A3/GATA5/AGT/HTR2B/GATA4/MLIP/TRIM63/LMNA/KLF15/PI16",15
D9/EREG/AGT/CBLC/FCGR1A/THY1/IL34/ADORA1/AFAP1L2/BTC/RELN",14
en","9/1495","43/18410",0.00676002691845072,0.0422385130214921,0.0336161048213339,"FMO3
A1",6
SCR4/CLU/A4GALT/COL5A1/MYOF/SYPL2/GSN/DMKN/S100A9/SPTA1/CHMP4C/FOLR2/AR/TMEM95/
P4/CPNE6/AVP/WFDC1/MAG/HAMP/CXCL12/LGI1/CRYAB/HRG/FN1/SGK1/SPP1/INHBA/APOE/NGF/
K1/APOB/CMA1/TREM2/IL1A/PCK1/IL1B/FOXA2/SERPINF1/HMGCS2/GATA4/THBS1/COL6A2/ABCA1:
FGL1/GLI3/INHBA/SDC4/BMP4/APOE/LGALS3/PDGFRA/ANXA1/EMILIN1/XCL1/VSIG4/RUNX1/SHH/A
P1",5
RAP",8
V1A/CASQ2/GRIA2/KCNJ5/KCNS1/KCNK1/CHRNA1/CHRNA3/SCN2B/KCNS2/CLIC6/LRRC38/LRRC52/T
2B/S100A1/GDNF",7
VEFL",7
Z/PDZK1",7
BP6/HTRA3",7

38/HTR2B",5

G/NPR3/TGFB3/CNN1/APOE/MYOC/VIP/ADIPOQ/APOD/ANG",12

P1/ITGB4/ITGA11/EMILIN1/ITGBL1",9
A4/CFC1/LBX1/FOXN4/DAAM2/GJA1/ZIC3/TGFB2/PITX2/CITED2/TBX20/SHH/NKX2-5/TGDF1",18
3FBR3/LRP2/DSP/TNNC1/FOXC2/IRX3/NKX2-5",10
X1/RUNX2/FOXA1/GPC3/ZIC1/SHH/OTX2/GPR37L1/GAS1",13
FAP/SNCA/NTRK2/GJA1/ADORA1/FOLR2/LRRC8E/AGXT",14
Z/ZFP36/ANXA1/KRT7/YAP1/KRT71/FLG/ABCA12/CD109/EVPL/KRT8/KRT4/ETV4/KRT79/AKR1C3/LIPN
RK1/OSM/HMOX1/OPRM1/INHBA/IL1B/LIF/APOE/MTNR1B/ANXA1/HTR1B/SNCA/CRH/GJA1/ADORA:
U6F2/COL1A1/RCVRN/EFEMP1/SFRP5/TGFB1/RDH10/LRAT/NDP/RBP4/LUM/KERA/RGS16/HMCN1/D
17,"AGT/REN/AGTR1/ADORA1/OR51E2/EMP2",6

/SOSTDC1/GDF3",6

OCK5/ADORA1",6

",6

Z/CALCA/KCNA1/PRDM12/ADORA1",6

Z/EPYC/MYO3A/SLC52A3/HTR2A/MYH14/CXCL12/COL1A1/KCNA1/SIX1/USP53/THRB/TMPRSS3/GJB2
POA1/CDC42EP1/APOE/STARD13/AGTR1/GPR174/PDPN/F2RL2/COL1A2/CDC42EP5/COL3A1/RHOD/
5/F10/RRAS/GDF15/CHI3L1/GATA4/THBS1/RCN3/TPBG/EGFR/NTRK2/RET/IGF2/AXL/CX3CR1/P2RY12

M2/TSPO/IFNG/IL1A/CLU/TNFRSF8/ZFP36/LBP/IL6/THBS1/SPON2/TLR3/AXL/CX3CR1/CD14/LPL/CIDE
.H4/IGF1/TREM2/TSPO/IFNG/IL1A/CLU/TNFRSF8/ZFP36/LBP/IL6/THBS1/SPON2/TLR3/AXL/CX3CR1/C
TR1E/HTR1A/HRH1",8
.M2/IL34/SHH/SOX1",8
R3/RET/GBX2/GDNF",9

4717,"MYOCD/SNCA/ADIPOQ/APOD",4

RPINB7/TSKU",4
'HRG/CYP1B1",4

IG4",4

17,"SEMA3C/FOLR1/BMP4/PITX2",4

1107A/CX3CR1",4
LA/PAX2/FOXC2",4
4717,"BMP4/IL6/MYOCD/EGFR",4

A1/ERBB3/MT3/HTR2A/DKK1/FAM20A/AREG/CALCA/IFNG/NEDD9/TPD52L1/GHR/FGF1/CLU/SDC4/E
INX1/CLEC3B/GAS1/ANXA2/S100A10/SPON1",11
S02/KCNS1/EDN3/MTNR1B/VIP/KCNE4/KCNS2/LRRC38/LRRC52/ADORA1/DPP10/KCNIP1",16

A5/AGT/HTR2B/GATA4/MLIP/TRIM63/LMNA/KLF15/PI16",15
A3/KCNE4/GJA1/KCNK5/KCND3/PDZK1/KCNA2/FXYD1",12
;/SERPINE1/BMP5/BMP4/FOXA1/GATA5/PYY/GATA4/YAP1/NEUROD1/CEBPB",14
;1/THY1/MMP14/FAM107A/RHOD/APOD/S100A10",13
4/OTX2/GDF3/WT1/TDGF1",10
;/SNCA/EGFR/S100A1/GDNF",10
16/NGF/KLF4/MYOCD/NEUROD1",10
DXA5/SERPINE1/SPARC/THBS4/HRG/SERPINF1/SPINK5/AGT/KLF4/THBS1/EMILIN1/ADAMTS1/CREB3I

/LTBP4/P3H2/APOH/CCDC80/CMA1/COL9A3/LGALS1/TIMP3/CHADL/CTSG/MMP9/SRPX/TIMP1/SRP
 'MGP/COL12A1/SPARC/EFEMP1/FN1/NID1/TECTB/TGFB1/FMOD/COL10A1/COL21A1/COL5A1/MATN
 L/CTSG/MMP9/FERMT1/CST3/CRISPLD2/COMP/COL1A1/COL12A1/SMOC2/LOX/NID1/TGFB1/FMOD/
 ADL/CTSG/MMP9/FERMT1/CST3/CRISPLD2/COMP/COL1A1/COL12A1/SMOC2/LOX/NID1/TGFB1/FMO
 ;/TLL2/CHADL/CTSG/MMP9/FERMT1/CST3/CRISPLD2/COMP/COL1A1/COL12A1/SMOC2/LOX/NID1/T
 'CST3/CHRD1/TIMP1/COL1A1/APOA4/COL12A1/BCHE/EVA1A/FN1/SERPINC1/APOA1/CASQ2/SPP1/
 CL2/CCL8/PF4V1/AREG/CALCA/IFNG/BMP5/THBS4/FGF1/FGF12/IL1A/CCL20/EFEMP1/APOA1/TTR/SP
 OMP/CCL7/CCL8/PF4V1/SOD3/SMOC2/THBS4/FGF1/HRG/FN1/SERPINC1/TNFAIP6/CXCL6/BMP4/FGI
 /CSF3/CCL7/CCL2/CCL8/PF4V1/AREG/CALCA/IFNG/BMP5/THBS4/FGF1/FGF12/IL1A/CCL20/EFEMP1/
 XA13/GLI3/GLI1/BMP5/MDFI/IL1A/TCF21/SPP1/TEX11/RDH10/PLG/INHBA/MMP19/TNFAIP6/NDP/E
 A13/GLI3/GLI1/BMP5/MDFI/IL1A/TCF21/SPP1/TEX11/RDH10/PLG/INHBA/MMP19/TNFAIP6/NDP/ERI
 NG1/C8A/APOA2/C1R/ACTG2/ALB/ANXA5/ANGPTL4/FGG/FGA/FGB/HSPA6/CPN2/F2/C1S/PROS1/PC
 L1/TBX18/FGF1/NID1/TCF21/RDH10/BICC1/HOXC11/SDC4/BMP4/SOX9/SIX1/LIF/HOXD11/HOXD13/FC
 18/FGF1/DLX2/WLS/MSX2/HOXA7/EGR2/BHLHE41/HOXC11/BMP4/C3/FOXA2/SIX1/HOXD11/HOXD1
 /FN1/SERPINC1/CXCL6/BMP4/FGFRL1/APOE/COL5A1/POSTN/THBS1/FGF7/RSPO3/RSPO2/ADAMTS1
 :RPINE1/GLI3/KANK1/ACTA2/COL1A1/ODAM/PF4V1/ST3GAL4/OPRM1/SMOC2/LOX/FGF1/HRG/IL1A,
 'RDH10/BICC1/HOXC11/SDC4/BMP4/SOX9/SIX1/LIF/HOXD11/ASS1/SERPINF1/HMGC52/NOTCH2/LRP
 IP/HOXA2/GLI3/DKK1/COL1A1/AREG/CALCA/GLI1/MGP/BMP5/LOX/FHL2/SPP1/SATB2/TGFB3/MSX2,
 'C3/SERPINF1/SPINK5/NGF/AGT/AHSG/SNCA/GPC3/SERPING1/SERPINH1/CD109/TIMP4/WFDC8/LCN
 .2/COL8A1/COLEC12/C1QTNF7/COL6A3/COL1A2/MBL2/COL3A1/COL22A1/COL8A2/COL6A5/ADIPOQ
 DLR1/GLI1/BMP5/MDFI/TBX18/FGF1/DLX2/WLS/SATB2/MSX2/HOXA7/BICC1/EGR2/BHLHE41/HOXC1
 :RPINA7/SLPI/C3/SERPINF1/SPINK5/NGF/AGT/AHSG/SNCA/SFRP2/GPC3/SERPING1/SERPINH1/CD109
 ?/GLI3/FOLR1/GLI1/BMP5/MDFI/TBX18/EFEMP1/DLX2/PRRX1/TCF21/SATB2/TGFB3/RDH10/PLG/HO
 IFNG/BMP5/GHR/BCHE/TTR/SPP1/RDH10/LRAT/INHBA/SERPINA7/EDN3/IL1B/FOXA2/LIF/VGF/FOXA:
 B/HRG/SERPINC1/SPINK4/ITIH5/NR4A1/SERPINA7/SLPI/C3/SERPINF1/SPINK5/NGF/AGT/KLF4/THBS1,
 /CRYAB/HRG/SERPINC1/SPINK4/ITIH5/NR4A1/SERPINA7/SLPI/C3/SERPINF1/SPINK5/NGF/AGT/KLF4/
 'SLPI/C3/SERPINF1/SPINK5/NGF/AGT/AHSG/SNCA/SERPING1/SERPINH1/CD109/TIMP4/WFDC8/LCN1
 T9B/SHH/OSR2/RET/FBN1/NKX3-1/AQP2/GDNF/IRX2/LAMB2/FOXC2/IRX3/ADIPOQ/WT1/WNT7B/PC
 TNFAIP6/ERE/REG/SOX9/DACH2/VGF/HOXD13/RXFP2/FST/PDGFR/GATA4/NR5A1/FOXF2/LHCGR/CYP1
 1R/PTGES/SAA4/FCGR1A/APOA2/ADORA1/MBL2/CEBPB/SAA1/NUPR1/F2/FFAR3/SERPINA3/SERPINA
 L/COL8A1/FREM2/ADAMTS1/LAD1/VWA2/FBN1/COL8A2/LAMB2/VWA1/ANXA2/THBS2/COL4A5/VW
 /SLPI/C3/SERPINF1/SPINK5/NGF/AGT/AHSG/SNCA/SFRP2/SERPING1/SERPINH1/CD109/TIMP4/WFDC
 3FRA/CGA/NR5A1/FDX1/CYP1B1/CYP2C9/RBP4/CYP11A1/CRABP2/REN/CYP17A1/CHST9/UGT2B4/CY
 X18/EFEMP1/DLX2/PRRX1/TCF21/SATB2/TGFB3/RDH10/HOXA7/HOXC11/RUNX2/BMP4/SOX9/SIX1/
 L/HOXC11/SDC4/BMP4/SOX9/SIX1/LIF/HOXD11/ASS1/SERPINF1/HMGC52/NOTCH2/LRP4/PDGFR/A
 B/APOC3/HRG/SERPINC1/APOA1/SPINK4/ITIH5/NR4A1/SERPINA7/SLPI/C3/APOC1/PPP1R1B/LGALS3,
 IGP/MDFI/GHR/DLX2/PRRX1/SATB2/TGFB3/MSX2/RDH10/HOXA7/HOXC11/RUNX2/BMP4/SOX9/SIX1
 TS12/ADAMTS3/COL1A2/TNXB/COL3A1/CRTAP/FOXC2/COL14A1/COLGALT2/COL5A2", 28
 A/MMP19/TNFAIP6/ERE/REG/SOX9/DACH2/VGF/RXFP2/FST/PDGFR/GATA4/NR5A1/LHCGR/CYP1B1/D
 /SOX9/VGF/RXFP2/FST/PDGFR/GATA4/NR5A1/LHCGR/CYP1B1/DHH/LHX9/RAB13/REN/OSR1/SFRP:
 REG/GLI1/BMP5/SPARC/THBS4/FGF1/F3/APOA1/KLF9/NR4A3/NR4A1/ERE/REG/BMP4/SOX9/GDF5/SIX1,
 FRA/AGT/YAP1/OSR1/GPC3/MYO1E/WNT9B/KLF15/SHH/RET/SERPINB7/GDNF/IRX2/LAMB2/FOXC2/I
 TNFAIP6/EDN3/TREM1/CXCL6/IL1B/LBP/LGALS3/ANXA1/IL6/THBS1/EMILIN1/CXCL9/XCL1/MMP14/IL
 AP1/OSR1/GPC3/MYO1E/WNT9B/KLF15/SHH/GDNF/IRX2/LAMB2/FOXC2/IRX3/ADIPOQ/TACSTD2/WT
 1/NOTCH2/AGT/YAP1/OSR1/GPC3/MYO1E/WNT9B/KLF15/SHH/RET/GDNF/IRX2/LAMB2/FOXC2/IRX:
 CRYAB/HRG/IL1R2/SERPINC1/SPINK4/ITIH5/NR4A1/SERPINA7/SLPI/C3/SERPINF1/SPINK5/NGF/AGT/
 IL6A2/COL8A1/COL6A3/COL1A2/COL3A1/COL8A2/COL6A5/COL14A1/COL4A5/COL4A6/COL5A2/COL:
 TNFAIP6/EDN3/TREM1/CXCL6/IL1B/LBP/ARHGEF16/LGALS3/PDGFR/ANXA1/IL6/THBS1/CH25H/CXCL:

IAA1217/RDH10/HOXA7/HOXC11/RUNX2/BMP4/SIX1/GSC/PDGFRA/RBP4/OSR1/DLX1/MMP14/WNT
HOXA7/HOXC11/RUNX2/BMP4/SIX1/GSC/PDGFRA/OSR1/MMP14/WNT9B/TGFB2/OSR2/FOXC2/IRX
MMP3/PRSS23/TMPRSS15/MMP14/C1R/TMPRSS3/PRSS12/HTRA1/MMP10/KLK1/KLK6/KLK11/KLK13/
IL1B/TNFSF9/GDF5/LIF/GDF15/IL6/IL1RN/IFNA21/CXCL9/XCL1/TSLP/CXCL14/BMP3/IL34/WNT9B/C
MMP3/PRSS23/TMPRSS15/MMP14/C1R/TMPRSS3/PRSS12/HTRA1/MMP10/KLK1/KLK6/KLK11/KLK13/
/AMBP/CRYAB/PERP/SLC22A2/HRG/FN1/F3/SERPINC1/SPINK4/ITIH5/NR4A1/SERPINA7/SLPI/C3/SERF
MMP3/PRSS23/TMPRSS15/MMP14/C1R/TMPRSS3/PRSS12/HTRA1/MMP10/KLK1/KLK6/KLK11/KLK13/P
P2/CYP17A1/UGT2B4/CYP11B1/DHRS3/SHH/ALDH1A1/CRABP1/CYP2S1/SDR16C5/PNLIP/CYP27C1/AI
3

/ATP10B/ABCG2/SPP1/NPC2/CLU/LRAT/FABP3/INHBA/IL1B/C3/PLA2G5/LBP/APOE/APOC1/CRP/NM
1/FBLN5/AQP10/EPHX1/PTGES/GLYAT/SCN2B/S100A9/CLDN1/FABP1/ALB/GPX8/ALDH1A1/NXN/TXN
/SERPING1/SERPINH1/CD109/WFDC8/COL6A3/SERPINI1/SERPINB7/WFDC13/WFIKN2/WFDC11/AN
/BMP4/SOX9/SIX1/HOXD11/HOXD13/FOXA1/AGT/YAP1/FGF7/SFRP2/RSPO3/GPC3/RSPO2/MMP14/
4/IL1A/CCL20/IL1R1/PADI2/DUSP1/PLG/HOXA7/TNFAIP6/EDN3/TREM1/CXCL6/IL1B/LBP/LGALS3/LY
DH10/BMP4/SOX9/SIX1/HOXD11/HOXD13/FOXA1/AGT/YAP1/FGF7/SFRP2/RSPO3/GPC3/RSPO2/MM
GPC3/WNT9B/SHH/GDNF/IRX2/IRX3/TACSTD2/WT1/WNT7B/POU3F3/HOXB7",32
L/THBS1/CXCL9/XCL1/IL34/S100A9/CXCL3/CXCL1/CXCL8/CCL11/SAA1/UMODL1/CCL13/CSF1/S100A1
/SMOC2/THBS4/FGF1/HRG/FN1/SERPINC1/CXCL6/BMP4/FGFRL1/APOE/COL5A1/POSTN/FST/THBS1/
/ADAMTS3/MMP14/CREB3L1/RUNX1/COL1A2/SERPINB7/MFAP4/MMP10/KLK6/TNXB/F2/PRTN3/MM
2/SPP1/NPC2/CLU/LRAT/FABP3/INHBA/IL1B/PLA2G5/LBP/APOE/APOC1/NMUR2/CFHR4/ANXA1/AG
C3/WNT9B/SHH/GDNF/IRX2/IRX3/TACSTD2/WT1/WNT7B/POU3F3/HOXB7",31

3/MASP1/CRP/APCS/SPINK5/NOTCH2/IL6/IFNA21/CXCL9/FCN3/CXCL14/SERPING1/VSIG4/C8A/C1R/
CL1/IL34/S100A9/CXCL3/CXCL1/CXCL8/CCL11/SAA1/CCL13/CSF1/S100A14/HRH1/C5AR1/CCL23/CCL
/FGF7/SFRP2/RSPO3/GPC3/RSPO2/FZD7/FZD1/WNT9B/CITED2/SHH/GDNF/AR/FZD2/TACSTD2/CSF1/
SOX9/FOXA2/SIX1/MYOD1/FOXA1/GATA5/GSC/NOTCH2/IL6/GATA4/KLF4/LBX1/FOXN4/DHH/DLX1/S
VP5/GHR/LOX/EFEMP1/DLX2/PRRX1/SATB2/MSX2/TGFB1/RUNX2/BMP4/SOX9/GDF5/FOXA1/COL5A
COMP/HOXA13/SFRP4/DKK1/FOLR1/BMP5/LOX/TGFB3/SFRP5/MSX2/FMOD/INHBA/TNFAIP6/RUNX
R1/SMOC2/LOX/FGF1/HRG/TGFB3/SFRP5/MSX2/TNFAIP6/RUNX2/BMP4/IL1B/GDF5/NOTCH2/FST/A
MBP/CRYAB/PERP/SLC22A2/HRG/F3/SERPINC1/SPINK4/ITIH5/NR4A1/SERPINA7/SLPI/C3/SERPINF1/S
2/COL5A1/ITGB4/GSC/IL1RN/CFC1/KLF4/DUSP5/OSR1/COL8A1/SFRP2/GPC3/GJA1/FZD7/MMP14/TG
CL14",22

KK1/GLI1/BMP5/TBX18/LOX/TNNC1/SMYD1/FHL2/TCF21/MSX2/EGR2/NR4A1/BMP4/SOX9/SIX1/MY
SPAN8/APOE/APCS/PDGFRA/ANXA1/THBS1/SERPING1/CD109/CLDN1/CLDN19/FGG/FGA/FGB/FOXC2
/SLC22A2/NPR3/HRG/FN1/PLA2G4A/F3/SERPINC1/PLG/PLAU/NFE2/C4BPB/F13A1/FOXA2/F10/TSPA
OXD11/FOXA1/AGT/YAP1/SFRP2/GPC3/RSPO2/MMP14/WNT9B/TGFB2/TBX20/SHH/NKX3-1/GBX2/
HBA/NDP/BMP4/SOX9/C3/GNGT1/COL5A1/SERPINF1/NOTCH2/MTNR1B/PDGFRA/KLF4/FOXF2/CYP1
13/SFRP4/DKK1/FOLR1/BMP5/LOX/TGFB3/SFRP5/MSX2/INHBA/TNFAIP6/BMP4/GDF5/GDF15/NOTC
RN/FGFBP2/THBS1/IGFBP4/OSMR/EGFR/IGFBP1/NTRK2/CD109/TGFB2/COL1A2/HTRA1/IGFBP6/CO
2B/AGTR1/DOCK5/HTR7/WNT9B/ADORA1/BDKRB2/DRD5/ADRA1B/FGG/FGA/FGB/ADRA1D/P2RY2/I
/NPC2/CLU/ADORA3/APOE/APOC1/HTR1B/AGT/RBP4/ABCA8/AQP10/REN/AGTR1/SNCA/VIP/STAR/C
/INHBA/NDP/BMP4/SOX9/C3/GNGT1/COL5A1/SERPINF1/NOTCH2/MTNR1B/PDGFRA/KLF4/FOXF2/C
NFAIP6/RUNX2/BMP4/SOX9/RRBP1/IL6/YAP1/ITGA11/FBN2/DHH/SFRP2/RSPO2/GJA1/BMP3/FZD1/C
/HOXA13/GLI3/AREG/GLI1/FGF1/WLS/APOA1/TCF21/TGFB3/MSX2/PCK1/BMP4/SOX9/SIX1/HOXD13/
P1B1/ANXA3/TPH2/FBXO32/TRIM63/APOA2/CLDN1/GJB2/FAM107A/FOS/FOSL1/FIBIN/ADIPOQ/WI
/F13A1/FOXA2/F10/TSPAN8/APOE/PDGFRA/TEC/IL6/THBS1/SERPING1/CSRP1/PDPN/ANXA5/F2RL2/S
TRPV4/TPD52L1/OPRM1/GHR/FGF1/IL1A/CCL20/TGFB3/EDN3/BMP4/IL1B/PLA2G5/LIF/APOE/GDF15
C1/SMYD1/TCF21/EGR2/NR4A1/BMP4/SIX1/FGFRL1/LIF/MYOD1/ASS1/GSC/ITGA11/LBX1/CHRNA1/I
CGR/CYP1B1/DHH/LHX9/RAB13/REN/SFRP2/GFRA1/GJA1/MMP14/WNT9B/TLR3/CITED2/SHH/NKX3
PINA3/SERPINA1/ORM2/ORM1",25

A/FGB/THBD/F2/PROS1/SERPINB2",25
/F13A1/FOXA2/F10/TSPAN8/APOE/PDGFR/TEC/IL6/THBS1/SERPING1/CSRP1/PDPN/ANXA5/F2RL2/
IH/GDNF/LAMB2/FOXC2/ADIPOQ/WT1/POU3F3",23
IEOX2/TLX1/PITX3/GLI1/DLX2/PRRX1/TCF21/SATB2/NR4A3/HOXA7/EGR2/NR4A1/HOXC11/CTCF/RU
XA7/BHLHE41/HOXC11/BMP4/FOXA2/HOXD13/BARX1/BHLHE40/GATA4/CFC1/OSR1/SFRP2/GPC3/Z
L6/IL1B/LBP/LGALS3/ANXA1/IL6/THBS1/CH25H/CXCL9/XCL1/IL34/NBL1/CXCL16/S100A9/CXCL3/CXCL
SERPINA7/SLPI/C3/APOC1/PPP1R1B/LGALS3/SERPINF1/SPINK5/NGF/ANXA1/AGT/ANXA3/AHSG/SNC
AGT/IL6/FGF7/OSGIN1/BMP3/IL34/CXCL1/IGF2/GDNF/BTC/AMBN/F2/GDF3/CSF1/NTF3/FGF16/TGFB
TGB4/LGALS12/THBS1/ITGA11/EMILIN1/FBLN5/SFRP2/GFRA1/THY1/MMP14/FBN1/IGF2/TNXB/COL3
2/PRRX1/TCF21/SATB2/NR4A3/HOXA7/EGR2/NR4A1/HOXC11/CTCF/RUNX2/SOX9/SIX1/HOXD13/N

P/BMP4/SOX9/GNGT1/COL5A1/SERPINF1/NOTCH2/MTNR1B/PDGFR/KLF4/FOXF2/CYP1B1/RBP4/FE
L/KLF4/YAP1/ANXA3/IGFBP1/GJA1/THY1/FZD7/APOA2/RUNX1/CLDN1/TGFB2/NNMT/AXL/KLK6/LAM
HTR2B/AGTR1/DOCK5/HTR7/ADORA1/BDKRB2/DRD5/ADRA1B/FGG/FGA/FGB/ADRA1D/P2RY2/FOX
1B/AGT/HTR2B/AGTR1/DOCK5/HTR7/ADORA1/BDKRB2/DRD5/ADRA1B/FGG/FGA/FGB/ADRA1D/P2R
LI1/BMP5/SPARC/THBS4/FGF1/F3/KLF9/NR4A3/NR4A1/EREG/BMP4/SOX9/GDF5/SIX1/ZFP36/APOE/
ACTA2/MYH1/CRYAB/CALCA/TRPV4/KCNA1/FGF12/TNNC1/CASQ2/NR4A3/KCNJ5/MYOT/SSPN/NR4
/FOXA2/F10/TSPAN8/APOE/PDGFR/TEC/IL6/THBS1/SERPING1/CSRP1/PDPN/ANXA5/F2RL2/SHH/AX
NT9B/SHH/OSR2/RET/GDNF/FOXC2/TACSTD2/WT1/HOXB7",30

'FGB/THBD/F2/PROS1/SERPINB2",25
'X9/SIX1/HOXD11/FOXA1/STARD13/NOTCH2/AGT/GATA4/YAP1/LBX1/LGR5/FOXN4/OSR1/SFRP2/GPC
'/FGB/THBD/F2/PROS1/SERPINB2",24
3/LIF/GFAP/ITGB4/ANXA1/IL6/DLX1/DAAM2/NTRK2/NKX6-2/LGI4/MMP14/IL34/MXRA8/S100A9/KLF
3XO32/TRIM63/APOA2/CLDN1/GJB2/FAM107A/FOS/FOSL1/FIBIN/ADIPOQ/WNT7B/TAT/HSD3B1/HSI

1/SATB2/MSX2/TGFB1/RUNX2/BMP4/SOX9/GDF5/MATN3/CHI3L1/MMP13/OSR1/SFRP2/RSPO2/SER

S1/THBS2/SERPINA3/SERPINA1/ORM2/ORM1",28
'PLG/SRGN/SLPI/F13A1/C3/ISLR/CHI3L1/CHIT1/THBS1/AHSG/EGFR/GSN/SERPING1/S100A11/S100A9

ISP4/BMP4/SOX9/IL1B/RRAS/PLA2G5/LIF/APOE/CHI3L1/NOTCH2/PDGFR/AGT/HTR2B/GATA4/EMIL
L3/CXCL1/CXCL8/CCL11/SAA1/UMODL1/CCL13/PRTN3/C5AR1/CCL23/CCL16/CCL18/CCL14",34
'/C3/PYY/ITGB4/AGT/CXCL9/ADCYAP1/XCL1/AGTR1/CXCL14/RSPO3/FZD7/FZD1/WNT9B/CLIC6/CXCL
'SOX9/SIX1/GNGT1/COL5A1/GSC/NOTCH2/FOXF2/RBP4/FBN2/LRIG3/FOXN4/OSR1/COL8A1/NTRK2/1
3/HTN1/OMD/MMP13/FBN2/OSR1/AHSG/GPC3/RSPO2/MEPE/GJA1/CLEC3B/OTOP1/SGMS2/COL1A2
OL5A1/ITGB4/KLF4/DUSP5/COL8A1/SFRP2/GJA1/FZD7/MMP14/TBX20/ATOH8/FOXC2/SOX2/COL5A
1B2",20

FP36/MYOD1/FOXA1/ASS1/SERPINF1/HMGCS2/ANXA1/HTR1B/IL6/IL1RN/YAP1/THBS1/CYP1B1/ANX
X1/RSPO2/LHX8/PITX2/SHH/COL1A2/OSR2/HTRA1/SOSTDC1/AMBN/CSF1/PAX9/AQP1",34
K1/CXCL12/PITX3/ASPA/IFNG/NEDD9/OPRM1/IL1A/FN1/DLX2/APOA1/SPP1/PAEP/EGR2/BHLHE41/B
'CCL23/CCL16/CCL18/CCL14",24
'X3/ERBB4/TACSTD2/WT1/WNT7B/HOXB7",28
D/MMP13/FBN2/OSR1/AHSG/GPC3/RSPO2/MEPE/GJA1/CLEC3B/OTOP1/SGMS2/COL1A2/OSR2/CEBI

G/FGA/FGB/ADRA1D/HTR1A/HRH1",26
1/TGFB3/MSX2/RDH10/EDN3/BMP4/SOX9/IL1B/FOXA2/SIX1/FOXA1/GATA5/GSC/HTR2B/IL6/GATA4,
'SHH/RET/GDNF/FOXC2/TACSTD2/WT1/HOXB7",28

\U/FOXA2/TSPAN8/APOE/APCS/PDGFR/ANXA1/KLF4/THBS1/SERPING1/CD109/CLDN1/CLDN19/FGC
 STD2/WT1/HOXB7",25
 /FN1/DUSP4/BMP4/IL1B/RRAS/PLA2G5/LIF/APOE/CHI3L1/NOTCH2/PDGFR/HTR2B/GATA4/EMILIN1
 DUSP1/HOXA7/TNFAIP6/EDN3/LBP/LGALS3/LYVE1/ANXA1/IL6/THBS1/EMILIN1/XCL1/THY1/MMP14/I
 3/WNT9B/SHH/RET/GDNF/FOXC2/TACSTD2/WT1/HOXB7",28
 'NT9B/SHH/RET/GDNF/FOXC2/TACSTD2/WT1/HOXB7",28
 9/RAB13/REN/SFRP2/GFRA1/GJA1/MMP14/TLR3/CITED2/NKX3-1/AR/NUPR1/ZFP42/WT1/AKR1C3/H
 PINE1/CSF3/CCL2/PF4V1/OPRM1/PLSCR4/IL1A/TRIM6/NR4A1/SLPI/PCK1/CXCL6/IL1B/ZFP36/LBP/ASS
 ICGR/CYP1B1/DHH/LHX9/RAB13/REN/SFRP2/GFRA1/GJA1/MMP14/TLR3/CITED2/NKX3-1/AR/NUPR1
 /P4/SOX9/SERPINF1/NOTCH2/MTNR1B/PDGFR/KLF4/FOXF2/CYP1B1/RBP4/FBN2/KERA/FOXN4/DL
 4/PLA2G5/APOE/CHI3L1/NOTCH2/PDGFR/HTR2B/GATA4/ADCYAP1/XCL1/ACKR3/TPBG/EGFR/GPR1
 3S1/REN/ABCA12/AGTR1/CRH/PTGES/APOA2/GALR1/NKX3-1/PCSK9/LPL/CIDEA/ADIPOQ/ANXA2/CES
 A14/CCL23/CCL16/CCL18/CCL14",24
 3/CLU/PLG/SRGN/SLPI/F13A1/C3/ISLR/CHI3L1/CHIT1/THBS1/AHSG/GSN/SERPING1/S100A11/S100A
 12/LRP4/FBN2/CRABP2/OSR1/SFRP2/GPC3/RSP02/FREM2/GJA1/EN1/SHH/OSR2/COL3A1/EVX2/HO
 4/FBN2/CRABP2/OSR1/SFRP2/GPC3/RSP02/FREM2/GJA1/EN1/SHH/OSR2/COL3A1/EVX2/HOXC10/H
 NB2",20
 L8/CCL11/CCR9/CCL13/CCL23/CCL16/CCL18/CCL14",28
 R1/CXCL8/CCL11/CCR9/CCL13/CCL23/CCL16/CCL18/CCL14",28
 B3/CLU/PLG/SRGN/SLPI/F13A1/C3/ISLR/CHI3L1/CHIT1/THBS1/AHSG/GSN/SERPING1/S100A11/S100
 C2/MT1E/PDZK1/NQO1/MT1X/AKR1B10/ADH4/MT1F/MT1A/MT1M/HBA1/HBM/GPX3/HBD/GSTA1/
 TACSTD2/WT1/HOXB7",24
 IRS3/TGFBR2/CITED2/OSR2/COL3A1/HAS2/TSKU/TMEM119/SP5",28
 B2",19
 F/LAMB2/FOXC2/ADIPOQ/WT1",19
 CH2/FST/GATA4/DLX1/SFRP2/GPC3/ADAMTS12/FZD1/NBL1/FSTL1/TBX20/HTRA1/FBN1/TMEM100/
 F15/GATA5/NOTCH2/FST/GATA4/DLX1/SFRP2/GPC3/ADAMTS12/FZD1/NBL1/FSTL1/TBX20/HTRA1/F
 /ASS1/CHI3L1/HMGCS2/PDGFR/YAP1/RBP4/FGF7/MYOC/RN3/ABCA12/GPC3/CRH/RSP02/THRB/
 3/CCL11/SAA1/CCL13/C5AR1/CCL23/CCL16/CCL18/CCL14",29
 OE/APOC1/PDGFR/ANXA1/CGA/AGT/HTR2B/AGTR1/STAR/APOA2/ADORA1/FABP1/P2RY12/F2/ADI
 B/MYOZ1/THBD/F2/PROS1/SERPINB2",24
 STD2/WT1/HOXB7",24
 FGF1/IL1A/HSD11B1/APOA1/SPP1/NPC2/APOE/APOC1/HMGCS2/PDGFR/CGA/AGT/CYP27A1/NR5A
 P1/FDX1/THBS1/CYP1B1/FBXO32/CLDN1/GJB2/NKX3-1/AR/FOS/FOSL1/FIBIN/NQO1/AKR1C3/MBP/T

 30A8/NKX3-1/CXCL8/HAS2/FGG/FGB/CCL11/CEBPB/CCL13/CCL23/CCL16/CCL18/CCL14",34
 CL8/CCL11/CCR9/CCL13/CCL23/CCL16/CCL18/CCL14",26
 DXD13/ITGB4/NOTCH2/LRP4/FBN2/CRABP2/OSR1/SFRP2/GPC3/RSP02/FREM2/GJA1/EN1/PITX2/SH
 /ITGB4/NOTCH2/LRP4/FBN2/CRABP2/OSR1/SFRP2/GPC3/RSP02/FREM2/GJA1/EN1/PITX2/SHH/OSR2
 HGCS2/PDGFR/GATA4/FOXF2/YAP1/MYOC/SFRP2/EGFR/ZIC3/TGFBR2/SHH/RET/IGF2/COL3A1/CX
 2/WT1/HOXB7",23
 /FFAR4/CYP27C1/AKR1C3/FABP12/AKR1C4/GSTA1",25
 APOA2/ANGPTL4/P2RY12/PNLIP/C5AR1/ANG/PLIN5",26

 K5",18
 IP/GPR174/F2RL2/CX3CR1/NTSR2/P2RY12/DRD5/ADRA1B/FPR1/ADRA1D/P2RY2/F2/GPR139/FFAR4/

 IL6/DLX1/DAAM2/NTRK2/NKX6-2/LGI4/IL34/MXRA8/S100A9/KLF15/SHH/GPR37L1/MAL/LAMB2/F2/
 L/MMP14/LHX8/PTX3/AXL/CEBPB/NUPR1/UMODL1/ZFP42/FOXL2/WT1/ANG",31
 FD2/WT1/HOXB7",20

JAMTS3/MMP14/RUNX1/C1R/CPA3/CLEC3B/PRSS12/SHH/SLC30A8/KLK1/KLK6/KLK13/PCSK9/FGG/FPF4V1/OPRM1/PLSCR4/IL1A/TRIM6/NR4A1/SLPI/PCK1/CXCL6/IL1B/ZFP36/LBP/ASS1/HMGCS2/IL6/C3/VNN1/HRG/IL1A/FN1/NID1/APOA1/NR4A3/SDC4/PCK1/IL1B/TNFSF9/FOXA2/RRAS/LIF/FOXA1/ANXEDN3/BMP4/SOX9/IL1B/FOXA2/SIX1/FOXA1/GATA5/GSC/HTR2B/IL6/FOXF2/OSR1/SFRP2/SEMA3D/FABP2/OSR1/SFRP2/GPC3/RSP02/FREM2/GJA1/EN1/SHH/OSR2/HOXC10/HOXA10",30
BN2/CRABP2/OSR1/SFRP2/GPC3/RSP02/FREM2/GJA1/EN1/SHH/OSR2/HOXC10/HOXA10",30

1/HOXB7",21

51/CH25H/XCL1/IL34/NBL1/AIRE/CXCL16/RET/CX3CR1/GPR183/CCL11/SAA1/DEFB124/CCL13/CSF1/IL6/GATA4/DLX1/SFRP2/GPC3/FZD1/NBL1/FSTL1/TBX20/HTRA1/FBN1/TMEM100/HTRA3/SOSTDC1/GDF10",22

A7/INHBA/EREG/BMP4/SOX9/ZFP36/KRT34/SPINK5/FST/EMP1/LRP4/ANXA1/KRT7/KLF4/YAP1/POU2

OA1/PLG/HOXA7/PLAU/SDC4/RRAS/ITGB4/LYVE1/THBS1/ITGA11/EMILIN1/FBLN5/COL8A1/DOCK5/CADAC/IL1A/APOA1/NR4A3/NPC2/RDH10/FABP3/RAB38/PCK1/SOX9/IL1B/C3/APOE/APOC1/LGALS12, RBP4/FGF7/MYOC/RCN3/ABCA12/GPC3/CRH/RSP02/THRB/ZIC3/MMP14/PDPN/TGFBR2/SHH/COL3A1/CYP11B1/DHRS3/ALDH1A1/CYP2S1/SDR16C5/CYP4F11/PNLIP/CYP4F3/CYP27C1/ADH1A/AKR1C3/ADH4/MMP13/SFRP2/SERPINH1/ADAMTS12/GJA1/MMP14/DHRS3/TGFBR2/PITX2/CITED2/OSR2/FBN1/IFNG/SMOC2/SPARC/FGF1/HRG/FN1/APOA1/NR4A1/SDC4/EDN3/BMP4/SOX9/RRAS/APOE/SER

IX9/ADAMTS1/MMP14/LHX8/PTX3/CEBPB/NUPR1/UMODL1/ZFP42/FOXL2/WT1/ANG",28

TNNC1/CASQ2/KCNJ5/MYOT/SSPN/NR4A1/EDN3/CNN1/TNNT3/NMUR2/MYH8/MYBPH/AGT/HTR2B/IL6/IL1A/IL1B/IL1RN/IFNA21/CXCL9/XCL1/OSMR/TSRP/CXCL14/IL34/CXCL16/TGFBR2/CXCL3/CXCL1/CX3CR1/GFBR2/SHH/NKX3-1/AR/SOSTDC1/CCL11/CEBPB/CSF1/BSX",30

/AKR1C3/ADH1B/AKR1B10/ADH4/AKR1C4/ADH1C",24

/GATA4/FOXF2/YAP1/MYOC/SFRP2/EGFR/ZIC3/TGFBR2/SHH/RET/COL3A1/CXCL8",31

B2/UGT8/EGR3/NCMAP/NTF3",23

SOX2/GDF3/PAX9/COL5A2/APELA",23

SFRP2/TPBG/IGFBP1/GPC3/LATS2/DKK2/FZD1/SHH/NXN/IGFBP6/SOSTDC1/SHISA2/SOX2/TSKU/NKX2

NX1/TGFBR2/CITED2/PI16/TBX20/SHH/IGF2/AR/BNC2/FOXC2/ERBB4/TSKU/NKX2-5/WT1/OSTN",37

IL6/IL1A/IL1B/IL1RN/IFNA21/CXCL9/XCL1/OSMR/TSRP/CXCL14/IL34/CXCL16/TGFBR2/CXCL3/CXCL1/CX3CR1/GFBR2/SHH/NKX3-1/AR/SOSTDC1/CCL11/CEBPB/CSF1/BSX",30

OGFRA/YAP1/RBP4/FGF7/MYOC/RCN3/ABCA12/GPC3/CRH/RSP02/THRB/ZIC3/MMP14/PDPN/TGFBR2/SHH/NKX3-1/AR/SOSTDC1/CCL11/CEBPB/CSF1/BSX",30

IX3/CEBPB/NUPR1/UMODL1/ZFP42/FOXL2/WT1/ANG",27

IL6/IL1A/IL1B/IL1RN/IFNA21/CXCL9/XCL1/OSMR/TSRP/CXCL14/IL34/CXCL16/TGFBR2/CXCL3/CXCL1/CX3CR1/GFBR2/SHH/NKX3-1/AR/SOSTDC1/CCL11/CEBPB/CSF1/BSX",30

R16C5/PNLIP/CYP27C1/ADH1A/AKR1C3/ADH1B/AKR1B10/ADH4/AKR1C4/ADH1C",27

TRK2/THRB/THY1/IGFN1/PITX2/CITED2/FBN1/COL8A2/TSKU/SOX1/FOXL2/DIO3/MFAP5/COL5A2",34

8

H1A/AKR1C3/ADH1B/AKR1B10/ADH4/AKR1C4/ADH1C",24

3/AGT/IL6/YAP1/THBS1/RBP4/MYOC/MEGF10/VIP/GJA1/ADAMTS1/RUNX1/TGFBR2/CITED2/TBX20

A/ASS1/SERPINF1/ALOX5AP/HMGCS2/THBS1/TPH2/SNCA/EGFR/SYT8/SLC30A2/CYP11B1/CLDN1/SHH

SOX9/SIX1/GSC/LRIG3/LGR5/OSR1/FREM2/ZIC1/NEUROD1/OTOP1/SHH/OSR2/GJB2/GBX2/CHRNA9/
3/RNASE3/CXCL8/FGA/FGB/WFDC11/F2/CCL13/DMBT1/PRTN3/ELANE/ANG",29
A1",21

/HOXB7",20
LHX8/SHH/HTRA1/SOSTDC1/AMBN/CSF1",24
31/ADORA1/CPA3/NPY1R/COL1A2/ANPEP/OR51E2/KLK1/AR/DRD5/GPR37L1/ADRA1B/ADRA1D/ADIP
_11/CEBPB/CCL13/CCL23/CCL16/CCL18/CCL14",27

CLU/TNFRSF8/TRIM6/PAEP/EREG/IL1B/C3/LBP/CHI3L1/ANXA1/AGT/HTR2B/IL6/GATA4/THBS1/CYP11
/MSX2/BMP4/GATA5/NOTCH2/PDGFA/AGT/GATA4/YAP1/RBP4/MYOC/JPH2/GJA1/FZD7/RUNX1/I
SQ2/EDN3/MT1G/MT2A/MCHR1/APOE/NMUR2/MTNR1B/PDGFA/HTR1B/AGT/HTR2B/HCTR2/CX

A/IFNG/OPRM1/FN1/DLX2/SPP1/EGR2/BHLHE41/IL1B/LIF/GFAP/SERPINF1/BHLHE40/NGF/LRP4/IL6/

RAS/THBS1/EMILIN1/COL8A1/DOCK5/DOCK1/THY1/ABI3BP/FZD7/MMP14/PDPN/FBLN2/FAM107A/I
/APOA1/TTR/NPC2/RDH10/LRAT/PCK1/APOE/HMGCS2/CYP27A1/FDX1/LHCGR/CYP1B1/CYP2C9/CH2
L/GSC/PDGFA/HTR2B/GATA4/YAP1/OSR1/SEMA3D/FZD1/PITX2/CITED2/SHH/RET/GBX2/GDNF/FOX
TCH2/HTR2B/YAP1/FGF7/OSR1/AGTR1/VIP/EGFR/FZD7/CLDN1/SHH/OSR2/HTRA1/IGF2/AR/HAS2/LI

'ANG/PLIN5",20
'CLEC3B/SGMS2/COL1A2/OSR2/TMEM119/ISG15",28
YP1B1/SFRP2/TGFB2/FOLR2/SLC6A19/LPL/NQO1/ADIPOQ/PENK/AKR1C3/KANK2/GCGR",32
I1/GHR/FN1/SPP1/BMP4/GDF5/SIX1/MYOD1/APOE/GDF15/NGF/CGA/YAP1/RBP4/DUSP6/CRABP2/L
C1/CXCL12/COL1A1/AREG/TRPV4/GLP1R/GHR/NR4A3/EGR2/NR4A1/PCK1/EREG/IL1B/VGF/GDF15/A
_/CIDEA/ADIPOQ/ANXA2/PLIN5",24
,

3ATA5/NOTCH2/HTR2B/GATA4/YAP1/LBX1/RBP4/FOXP4/SFRP2/GJA1/ADAMTS1/ZIC3/FZD1/DHRS3/
1B10/ADH4/HBA1/HBM/GPX3/HBD/GSTA1/HP",27

IP3/RAB38/PCK1/IL1B/C3/APOE/APOC1/ANXA1/CGA/HTR2B/NR5A1/DHH/STAR/SPHK1/AKR1C3/CES:
'IRX5/COLEC10",20
L",19

X2/SOX1",24
/FOLR1/TRPV4/OPRM1/GHR/BCHE/IL1A/SPP1/LRAT/PCK1/FOXA2/ZFP36/VGF/MYOD1/APOE/GDF15/
.6C5/PNLIP/CYP27C1/ADH1A/AKR1C3/ADH1B/AKR1B10/ADH4/AKR1C4/ADH1C",27
D1/ASS1/CHI3L1/THBS1/CYP1B1/XCL1/ADAMTS12/HMHB1/CXCL16/CLDN1/NKX3-1/CXCL8/FABP4/C
BP/PDGFA/IL6/THBS1/XCL1/TPBG/SEMA3D/IL34/NBL1/CX3CR1/P2RY12/CXCL8/GPR183/DEFB124/F
CRH/NKX6-2/NEUROD1/PITX2/CITED2/SHH/SOX2/NKX2-5/WT1",29

/PCSK9/LPL/ADIPOQ/ANXA2/PLA2G2A",22

IR2/BNC2/WFIKN2/FZD2",23

POD/ELANE/MBP",24

1",19

G/IL1R1/IL1RL1/APOA1/TNFAIP6/IL1B/C3/ZFP36/LBP/APOE/SERPINF1/APCS/ALOX5AP/ANXA1/AGT/I
'PRELP",25

IQ/PENK/CCK/OSTN/APELA",28

2A2/NPR3/ABCG2/EDN3/APOE/CRP/MTNR1B/HTR1B/AGT/HTR2B/AGTR1/DOCK5/HTR7/ADORA1/BD
JGF/AGT/LHCGR/TPBG/VIP/EGFR/CRH/NTRK2/AFF2/S100B/LHX8/EN1/ADORA1/FAM107A/CX3CR1/C

PELA",21

BI3BP/FBLN2/HAS2/FGG/FGA/FGB/CSF1/VWC2/S100A10/VIT/EMP2",27

YIP11B1/CLDN1/SHH/FBP1/AQP2/MT1E/NLGN1/FABP4/FOS/JUNB/NQO1/MT1X/AKR1C3/MT1F/MT1
B2/NCMAP/ROR1/C5AR1",26

22/VIP/GJA1/HPGDS/CITED2/SHH/NKX3-1/AR/NUPR1/UMODL1/MAPK15/PHLDA2/WT1/NANOS2/AP

ISL2/BRINP3/NEUROD1/SHH/RET/NLGN1/GPR37L1/HES3/IRX3/SOX2/NKX2-5/NTF3/NAP1L2/VWC2/E
LGR5/FREM2/ZIC1/NEUROD1/OTOP1/SHH/GJB2/GBX2/CHRNA9/FZD2/SOX2/TSKU/ROR1/GABRA5/I
22/NQO1/AKR1B10/ADH4/HBA1/HBM/GPX3/HBD/GSTA1/HP",27

DNF/FOXC2/ERBB4",22

/GDNF/FOXC2/ERBB4",23

3/GJB2/RET/WNT7B/BRINP2/AQP1",25

;/NOTCH2/PDGfra/AGT/GATA4/YAP1/RBP4/MYOCD/JPH2/GJA1/FZD7/RUNX1/LMNA/TGFBR2/CITE
A1/TGFBR2/CITED2/GJB2/AR/FOS/JUNB/PRL/FOSL1/THBD/HMX3/EMP2/APELA",35

4/FOXN4/AGTR1/DOCK5/SCN2B/THRB/KCNE4/GJA1/S100A1/ADORA1/BDKRB2/ADRA1B/KCND3/FGC

AMTS12/RUNX1/TGFBR2/OSR2/COL3A1/TSKU/ARID5A",25

INB/CEBPB/FOSL1/PHLDA2/SOCS3/WNT7B/MME/ANG/APELA",30

119",17

2A/COMP/MAG/KANK1/CXCL12/ACTA2/CSF3/SOD3/CALCA/TRPV4/NPR3/FN1/SPP1/EDN3/CDC42EP
",22

1/CLDN1/TGFBR2/GJB2/FOS/NQO1/PENK/KRT14/APOD/MME/MBP",32

}/NR4A3/EGR2/NR4A1/PCK1/EREG/IL1B/VGF/GDF15/ASS1/HMGCS2/ANXA1/AGT/LHCGR/CYP1B1/CY
PRSS2/DMBT1/CFI",21

C2/ERBB4",21

A2/GALR1/NKX3-1/PCSK9/ADIPOQ/ANXA2",26

DN3/IL1B/FOXA2/LIF/VGF/MTNR1B/ANXA1/HTR1B/CGA/AGT/IL6/IL1RN/UNC13C/RBP4/ADCYAP1/RE
RM1/SMOC2/THBS4/HRG/IL1RL1/F3/TRIM6/PLG/EDN3/EREG/IL1B/C3/PLA2G5/LBP/ALOX5AP/AGT/I
'TINAG/MMP7/MMP13/REN/ADAMTS19/HABP2/ADAM33/MMP3/PRSS23/ADAMTS12/TMPRSS15/A

AR3/APOD/ELANE/MBP",23
'IL1B/C3/RRAS/SERPINF1/CHI3L1/SPINK5/AGT/IL6/GATA4/KLF4/THBS1/CYP1B1/EMILIN1/ANXA3/SFRP2/XCL1/THY1/MMP14/IL34/CX3CR1/P2RY12/CXCL8/DEFB124/CSF1/S100A14/C5AR1",29
'ADAMTS1/FZD1/DHRS3/TGFBR2/CITED2/TBX20/FOXC2/FZD2/NKX2-5",27

'AP1/CRH/A1CF/GJA1/TGFBR2/CITED2/GJB2/AR/FOS/JUNB/PRL/FOSL1/THBD/MAFF/HMX3/DDO/EMILIN1/LIF/YAP1/OSR1/ABCA12/CD109/WNT9B/TMEM100/GDNF/ATOH8/CEBPB/ETV4/GDF3/MAFF/S1PR3/AGT/TPBG/VIP/EGFR/CRH/NTRK2/AFF2/S100B/LHX8/EN1/CX3CR1/DRD5/FOS/GATM/CCL11/CEBPB/ETV4/TPBG/IGFBP1/GPC3/LATS2/DKK2/FZD1/SHH/IGFBP6/SOSTDC1/SOX2/NKX2-5/SHISA6/TPBGL",29
'S100A14/S100A4/S100A2/ANXA4/S100A10/S100A6",22
'RBPV4/OPRM1/GHR/BCHE/IL1A/SPP1/LRAT/PCK1/FOXA2/ZFP36/VGF/MYOD1/APOE/GDF15/ASS1/NMUR2/POE/GFAP/NMUR2/ANXA1/HTR1B/AGT/THBS1/CRABP2/SNCA/PMP2/NTRK2/PTGES/SLC5A12/GJA1/IL14/TEC/AGT/IL6/FGF7/TSLP/FCGR1A/GFRA1/IL34/ADORA1/IGF2/AFAP1L2/CSPG4/BTC/ERBB4/ADIPOQ/CC1/SOX9/APOE/BARX1/GSC/LRP4/YAP1/LGR5/IGFBP4/SFRP2/DAAM2/TPBG/RSPO3/EGFR/IGFBP1/CEBPB/SERPINF1/CHI3L1/SPINK5/AGT/IL6/GATA4/KLF4/THBS1/CYP1B1/EMILIN1/ANXA3/SFRP2/ADAMTS1/IL6/RSPO3/GJA1/MMP14/RUNX1/AXL/CSPG4/FOXC2/TMEM119/BSX/SIGLEC15",33

/RUNX1/S100A1/TGFBR2/TLR3/ANGPTL4/CX3CR1/CXCL8/LRG1/CCL11/SPHK1/FOXC2/PRKD1/C5AR1/ANXA3/SFRP2/RUNX1/S100A1/TGFBR2/TLR3/ANGPTL4/CX3CR1/CXCL8/LRG1/CCL11/SPHK1/FOXC2/PF4/X1/CH25H/DHH/CYP11A1/STAR/CRH/CYP17A1/CYP11B1/AKR1C3/AKR1C4/CES1/HSD3B1/HSD3B2/CRT18/IFNG/GHR/IL1A/CCL20/IL1R2/IL1R1/IL1RL1/PADI2/F3/APOA1/TRIM6/CXCL6/EREG/IL1B/IL6/IL1

X3/HBD/GSTA1/HP",23
'IGFN1/PITX2/CITED2/COL8A2/TSKU/SOX1/DIO3",26
'/AGTR1/SNCA/OSMR/TSLP/S100A9/TLR3/FABP4/CEBPB/LPL/NUPR1/FFAR3/PLA2G2A",29
'1/YAP1/THBS1/PMAIP1/SFRP2/ITPRIP/LMNA/ATF3/RET/GDNF/AR/FGG/FGA/FGB/MAL",30
'F5/GDF15/THBS1/EMILIN1/FBN2/MYOC/PRDM16/XCL1/DLX1/LATS2/CD109/CLDN1/TGFBR2/CLEC3

IKX2-5",20
'FST/LRP4/ANXA1/KRT7/YAP1/LGR5/KRT71/FGF7/FLG/ABCA12/EGFR/CD109/CLDN1/FOXQ1/SHH/COL1A2/EN/GSN/SERPINF1/ADAMTS3/MMP14/RUNX1/C1R/CPA3/CLEC3B/PRSS12/SHH/SLC30A8/CLK1/CLK6,ERBB4/NKX2-5/WT1",23
'/HTR7/HTR5A/NPY1R/HTR1E/MC5R/HTR1A/ADRB3/HRH1",18

4/IL1B/LIF/MYOD1/GFAP/SERPINF1/NGF/IL6/CRABP2/DOCK5/NTRK2/NKX6-2/DOCK1/CHODL/IL34/S

SL1/THBD/ADIPOQ/PENK/WT1/AQP1",26
'IB4",21
'ASS1/CHI3L1/THBS1/CYP1B1/XCL1/ADAMTS12/HMHB1/CLDN1/NKX3-1/CXCL8/FABP4/HAS2/CCL11/S100A1/IL1RN/RBP4/ADCYAP1/REN/ABCA12/AGTR1/VIP/CRH/GJA1/NEUROD1/ADORA1/SLC30A8/GALR1/NKX2-5/IL1B/LGALS3/NGF/AGT/TMBIM1/YAP1/THBS1/PMAIP1/SFRP2/ITPRIP/BAG3/LMNA/ATF3/TLR3/RET/C

YAP1/CRH/A1CF/GJA1/TGFBR2/CITED2/GJB2/AR/FOS/JUNB/PRL/FOSL1/THBD/MAFF/HMX3/DDO/EMILIN1/PLA2G5/APOE/APOC1/LGALS12/CYP27A1/CYP1B1/APOA2/PLA2G4D/PLCD3/ADORA1/FABP1/LIPC/C

N/TGFB2/CX3CR1/SOSTDC1/CCR9/WFIKN2/TSKU/ELANE/CRLF2",29

GG/FGA/FGB/MAL",15

BCHE/AADAC/INHBA/IL1B/ASS1/HMGCS2/HTR1B/HTR2B/GATA4/THBS1/CYP1B1/CYP2C9/AOX1/DUS
/12/FOS/P2RY2/FOSL1/THBD/ADIPOQ/PENK/WT1/AQP1",27

./IL1B/APOC1/ANXA1/SDS/CYP27A1/CYP2C9/CRABP2/STAR/PTGES/HPGDS/LIPC/GATM/LPL/ACSM5/
'EMILIN1/FBN2/MYOCD/PRDM16/XCL1/DLX1/LATS2/CD109/CLDN1/TGFB2/CLEC3B/CITED2/COL1A2

./NR4A3/FABP3/PLP1/PCK1/SOX9/IL1B/C3/PLA2G5/APOC1/ALOX5AP/ANXA1/CYP1B1/CYP2C9/CYP4E

LIN1/FBN2/PRDM16/DLX1/SFRP2/CD109/FZD1/NBL1/TBX20/HTRA1/FBN1/HTRA3/SOSTDC1/WFIKN
K9/APOE/LRP4/KLF4/YAP1/LGR5/IGFBP4/SFRP2/DAAM2/TPBG/RSPO3/EGFR/IGFBP1/GPC3/RSPO2/L
GF10/ATF3/CITED2/SHH/IGF2/VAMP5/FOS/DES/NUPR1/MYOZ1/FOXL2/WT1/MAFF",31

5/APOD/CYP21A2",23

TGFB1/PLG/HOXA7/SDC4/BMP4/ASS1/LGALS3/ANXA1/IL1RN/KLF4/THBS1/CYP1B1/XCL1/ABCA12/VS

K18/WLS/SFRP5/BICC1/NDP/SOX9/APOE/BARX1/GSC/LRP4/KLF4/YAP1/LGR5/IGFBP4/SFRP2/DAAM2,
.IF/LRP4/TEC/AGT/IL6/FGF7/CBLC/SFRP2/TSLP/EGFR/FCGR1A/GFRA1/THY1/IL34/ADORA1/IGF2/AFAF
1/SOX9/APOE/LRP4/YAP1/LGR5/IGFBP4/SFRP2/DAAM2/TPBG/RSPO3/EGFR/IGFBP1/GPC3/RSPO2/LA

P1/EGR2/BHLHE41/IL1B/LIF/GFAP/SERPINF1/BHLHE40/NGF/LRP4/IL6/YAP1/CRABP2/DLX1/DAAM2/I
iKU/KRT14",24

'KRT14",24

2B/STAR/PLIN5",20

/PLP1/IL1B/PLA2G5/GAD1/APOC1/ASS1/BHMT2/ALOX5AP/ANXA1/SDS/CYP27A1/CYP2C9/CRABP2/B

./NR4A2/EN1/FOXQ1/AXL/CX3CR1/GDNF/CEBPB/NTF3/GABRA5/NEFL",28

DCYAP1/REN/ABCA12/AGTR1/VIP/CRH/GJA1/NEUROD1/ADORA1/SLC30A8/GALR1/NKX3-1/FGG/FGA

/FZD1/CREB3L1/NBL1/HTRA1/FBN1/HTRA3/SOSTDC1/SHISA2/GDF3/VWC2",24

1B/ANXA1/LHCGR/PMAIP1/SNCA/STAR/FABP1/NNMT/IGF2/ADIPOQ/HRH1/CES1/PLIN5",28

L6

PLP1/IL1B/PLA2G5/GAD1/APOC1/ASS1/BHMT2/ALOX5AP/ANXA1/SDS/CYP27A1/CYP2C9/CRABP2/B

FR/SYT8/MMP3/CYP11B1/CLDN1/SHH/FBP1/AQP2/MT1E/NLGN1/FABP4/FOS/JUNB/NQO1/MT1X/AK
4B/C4A",26

'SOX9/RRAS/APOE/SERPINF1/STARD13/LGALS12/ANXA1/AGT/KLF4/THBS1/CYP1B1/ANXA3/FGF7/RAI
'SFRP5/BICC1/NDP/SOX9/APOE/BARX1/GSC/LRP4/KLF4/YAP1/LGR5/IGFBP4/SFRP2/DAAM2/TPBG/RS
1/CCL13/IFITM2/TDGF1/CCL23/CCL16/CCL18/CCL14",27
'CXCL8/DEFB124/PRKD1/CSF1/NTF3/S100A14/FGF16/C5AR1",27

IF11/NLRP11/CYP4F3/CYP27C1/AKR1C3/AKR1C4/CYP21A2",23

/SERPINF1/CHL1/NGF/MTNR1B/DLX1/SNCA/NTRK2/NR4A2/FZD1/EN1/ADORA1/FOXQ1/AXL/CX3CR1
M119/CSF1/ISG15/GDF10",24
1/NR4A3/PLG/SDC4/PCK1/BMP4/IL1B/TNFSF9/FOXA2/FOXA1/ASS1/LGALS3/ANXA1/IL6/IL1RN/KLF4/

11/EMILIN1/FBLN5/ADAMTS12/THY1/MMP14/VWA2/FAM107A/TNXB/COL3A1/FGG/FGA/FGB/RHO
/RBP4/MYOC/SFRP2/ADAMTS1/FZD1/DHRS3/TGFBR2/CITED2/TBX20/FOXC2/FZD2/NKX2-5",30
APOA2/AKR1C3/CES1",22
/SERPINF1/CHL1/NGF/MTNR1B/DLX1/SNCA/NTRK2/THRB/NR4A2/FZD1/EN1/ADORA1/FOXQ1/AXL/C

DE/NMUR2/MTNR1B/PDGfra/HTR1B/AGT/HTR2B/HCRTR2/CXCL9/ADCYAP1/SYPL2/XCL1/ACKR3/AG
FN1/SDC4/IL1B/SIX1/ITGB4/LRP4/AGT/THBS1/RAB13/SNCA/TPBG/NTRK2/GJA1/THY1/RHOC/MMP14
/LMNA/GDNF/AR/FGG/FGA/FGB",21

4/UST/FN1/SPP1/MYOT/EGR2/PLP1/EDN3/APOE/CNTN6/CHL1/NOTCH2/NGF/LRP4/KLF4/CRABP2/LH

1119/PRKD1/FFAR4/WNT7B/OSTN/CEBPD/TWIST2/GDF10",26

/FOXA2/MYOD1/POSTN/AGT/MYOCN/PMAIP1/SFRP2/BAG3/NR4A2/WNT9B/ATF3/DAPL1/ALB/TLR3
1/CYP11A1/SNCA/BHMT/STAR/CYP17A1/CYP11B1/FABP1/CYP4F11/ADIPOQ/CYP4F3/AKR1C3/AKR1C4

7/CREB3L1/OTX2/CXCL8/EGR3/SHISA2/FGF16/TGDF1",23
<CL6/IL1B/ZFP36/LBP/ASS1/HMGCS2/IL6/CXCL9/SPON2/CXCL3/CXCL1/DEFA4/DEFA6/AXL/CX3CR1/C

",22

4B/C4A",21

.2/AGTR1/CRH/GJA1/NEUROD1/ADORA1/SLC30A8/GALR1/NKX3-1/FGG/FGA/FGB/HTR1A/ADIPOQ/F
",20
1/BGN/ANXA2/PRELP/SERPINA3/PRTN3/ELANE/ORM2",31

3/ADORA1/PLIN1/TRPV3/SCARA5/HSPB2/FOS/CD14/HSPA6/LPL/CIDEA/METRNL/FGF16/MICA",31
/NMUR2/MTNR1B/PDGFRA/HTR1B/AGT/HTR2B/HCRTR2/CXCL9/ADCYAP1/SYPL2/XCL1/ACKR3/AGTF

LR3",21
L12/TPD52L1/BMP5/VNN1/IL1A/CLU/INHBA/BMP4/IL1B/LGALS3/AGT/TMBIM1/GATA4/YAP1/THBS1
/PLA2G4A/ABCG2/SLC17A3/SLC17A1/IL1B/PLA2G5/GFAP/NMUR2/ANXA1/HTR1B/AGT/SNCA/SLC17A
5/OX9/RRAS/APOE/SERPINF1/STARD13/LGALS12/ANXA1/AGT/KLF4/THBS1/CYP1B1/ANXA3/FGF7/RAB
.X1/DAAM2/NKX6-2/SEMA3D/THY1/FBN1/GPR37L1/CCL11/F2/TACSTD2/MBP/S1PR3",31

3/PADI2/APOA1/SPP1/DUSP1/PLG/PLAU/TNFAIP6/TSPAN8/ZFP36/APOE/SERPINF1/APCS/SPINK5/PDI
CL8/DEFB124/CSF1/S100A14/C5AR1/MMP28",24
A1/SNCA/BHMT/STAR/FABP1/ADIPOQ/AKR1C3/CES1/PLIN5",25

ASE3/CXCL8/F2/CCL13/ELANE/ANG",18

/OCN/PRDM16/DLX1/LATS2/CD109/CITED2/HTRA1/FBN1/HTRA3/LRG1/WFIKKN2/CIDEA/VEPH1",25
PINK5/NOTCH2/IL6/EMILIN1/ANXA3/COLEC12/SPON2/S100A9/TLR3/DEFA4/DEFA6/MBL2/CLEC4E/W

DLX1/SNCA/NTRK2/NR4A2/FZD1/EN1/FOXQ1/AXL/CX3CR1/GDNF/CEBPB/CSF1/NTF3/GABRA5/NEFL"

TLC3/AGXT/IRX5/CYP27C1/ADH4/TAT",28

02/SHH/RET/GDNF/AR/IRX2/IRX3/FZD2/WNT7B",27

9LIN5",21

9PDGFRA/IL6/KLF4/YAP1/PRDM16/SFRP2/NR4A2/FABP4/LRG1/CEBPB/LPL/METRNL/ADIPOQ/SLC2A4/

1/PADI2/APOA1/TGFB3/DUSP1/HOXA7/INHBA/TNFAIP6/C4BPA/C4BPB/SDC4/BMP4/SOX9/LGALS3/A
12/CXCL8/EGR3/SHISA2/FGF16/TDGF1",23

4/SOX9/RRAS/APOE/SERPINF1/STARD13/LGALS12/ANXA1/AGT/KLF4/THBS1/CYP1B1/ANXA3/FGF7/R
L0",17

5/GDF15/NOTCH2/GATA4/THBS1/MYOC/DGPC3/BMP3/TGFBR2/CITED2/TBX20/LRG1/GDF3/GDF10'

LG/F10/PDGFR/ANXA1/THBS1/ITGA11/CXCL9/ACKR3/OSMR/MS4A2/GFRA1/THY1/RAET1L/CD1A/Ci

ASS1/HMGCS2/AGT/LHCGR/CYP1B1/CYP11A1/RAB13/AGTR1/AHSG/IGFBP1/GJA1/NR4A2/CYP11B1/
4/NTRK2/THRB/NR4A2/EN1/FOXQ1/AXL/CX3CR1/GDNF/PCSK9/CEBPB/NUPR1/NQO1/NTF3/GABRA5
J3/APOE/CNTN6/CHL1/NOTCH2/NGF/LRP4/CRABP2/LHX9/CNTN4/BOC/NTRK2/NR4A2/SEMA3D/THY

0CD/PRDM16/LATS2/CD109/CITED2/HTRA1/FBN1/HTRA3/LRG1/WFIKKN2/CIDEA/VEPH1",24

IBD/F2",24

G/EFEMP1/EREG/LIF/LRP4/PDGFR/TEC/AGT/IL6/FGF7/CBLC/SFRP2/TSLP/EGFR/NTRK2/FCGR1A/GFI

CITED2/SHH/IGF2/VAMP5/FOS/NUPR1/MYOZ1/FOXL2/MAFF",27
2G5/GFAP/NMUR2/ANXA1/HTR1B/AGT/SNCA/SLC17A4/NTRK2/PTGES/SLC5A12/GJA1/ADORA1/FOLF
/SERPINF1/NGF/IL6/CRABP2/TPBG/NTRK2/NKX6-2/CHODL/IL34/SHH/ISLR2/CX3CR1/NLGN1/HAP1/LI
NTRK2/NR4A2/EN1/FOXQ1/AXL/CX3CR1/GDNF/PCSK9/CEBPB/NUPR1/NQO1/NTF3/GABRA5/NEFL",3
5F12/CASQ2/PLP1/KCNS1/EDN3/AHNAK/MCHR1/LGALS3/MTNR1B/AGT/CXCL9/XCL1/OSR1/SNCA/VII
A/FABP12",20

PCSK9/NLGN1/DLGAP1/PATE1/WFIKK2/BTC/PHLDA2/SHISA6/RELN/PRRT1/SHISA9",29

3/PDGFR/AGT/HTR2B/HCRTR2/CXCL9/ADCYAP1/XCL1/ACKR3/AGTR1/SNCA/GPR174/JPH2/T

HMGC2/IL6/CXCL9/SPON2/CXCL3/CXCL1/DEFA4/DEFA6/AXL/CX3CR1/CXCL8/CD14/CEBPB/ARID5A/I
2/HTR1B/LHCGR/CXCL9/LGR5/ADCYAP1/VIP/HTR5A/ADORA1/NPY1R/GALR1/HTR1E/P2RY12/DRD5/C
/TGFB2/CA3/FOS/CD14/FOSL1/NQO1/ADIPOQ/PENK/SLC2A4/AKR1C3/CES1/HSD3B1/HSD3B2/GRIN

FEMP1/EREG/LIF/LRP4/PDGFR/TEC/AGT/IL6/FGF7/CBLC/SFRP2/TSLP/EGFR/NTRK2/FCGR1A/GFRA1,

IT/RBP4/ADCYAP1/SNCA/VIP/CRH/PTGES/ADORA1/SLC30A8/GALR1/NKX3-1/OR51E2/GDNF/NLGN1/

N2/MYOC/PRDM16/LATS2/CD109/TGFB2/CITED2/COL1A2/HTRA1/FBN1/COL3A1/FOS/HTRA3/LRC
PL/PNPLA1/LIPI/ANG/PLIN5",24

G3/ATF3/FGG/FGA/FGB/MAL",18

3/GULP1/AHSG/MEGF10/GSN/FCGR1A/DOCK1/COLEC12/APOA2/SPON2/ADORA1/PTX3/MBL2/AXL/F
B124/CSF1/APOD/S100A14/C5AR1",22

/AGT/CXCL9/XCL1/SNCA/PTGES/JPH2/THY1/LRRC38/LRRC52/ADORA1/TRPV3/GDNF/P2RY12/CEBPB,

IJ5/PLP1/KCNS1/EDN3/AHNAK/MTNR1B/AGT/CXCL9/XCL1/OSR1/SNCA/CRH/SCN2B/JPH2/KCNE4/TH
I3L1/AGT/GATA4/THBS1/USP53/GSN/BAG3/MMP14/TGFB2/TLR3/CITED2/FOS/CHRNA9/FOSL1/AQI
1/CLDN1/CLDN19/FAM107A/NLGN1/LRRN1/IRX3/SLITRK4/SLITRK2/THBS2/APOD/IL1RAP/S100A10",:

SOSTDC1/ERBB4",18

36/LBP/ASS1/HMGC2/NOTCH2/IL6/CXCL9/SPON2/CXCL3/CXCL1/DEFA4/DEFA6/AXL/CX3CR1/CXCL8

'F2RL2/GALR1/CX3CR1/BDKRB2/NTSR2/GPR37L1/FPR1/CCR9/MC5R/GPR139/GCGR",27

'LHCGR/CYP11B1/CYP11A1/RAB13/AGTR1/AHSG/IGFBP1/NR4A2/CYP11B1/OTOP1/FBP1/GJB2/VWA2/
:LN",17
RIA2/CLU/INHBA/MCHR1/LBP/APOE/NMUR2/HCRTR2/SSTR1/PTGES/CD1A/CD1B/POM121L2/NPY1R
'FGF1/APOA1/NR4A3/PPP1R3C/RDH10/FABP3/SOX9/IL1B/FOXA2/APOE/APOC1/ANXA1/LHCGR/PMA
-RMD6/RAB13/ABCA12/GJA1/MYO1E/CLDN1/AR/COL22A1/LAMB2/FOXC2/ADIPOQ/WNT7B/S1PR3",
3/LGALS3/TMBIM1/GATA4/YAP1/THBS1/ACKR3/SFRP2/ITPRIP/NR4A2/CREB3L1/LMNA/CX3CR1/BDKF
GATM/MYOZ1",22

KCNS1/EDN3/AHNAK/MTNR1B/AGT/CXCL9/XCL1/OSR1/SNCA/CRH/SCN2B/JPH2/KCNE4/THY1/KCNS2

B3/AQP1",18

:B3/EMP2",19
:L14",22
'4A1/CNN1/TNNT3/GATA5/NMUR2/MYBPH/AGT/GATA4/MYOCN/MLIP/DOCK5/FBXO32/TRIM63/LM
THBS1/ANXA3/SNCA/TSLP/VSIG4/TGFBR2/TLR3/CX3CR1/CXCL8/SPHK1/CSF1/PLA2G2A/S100A13/C5/
THBS1/MYOCN/VIP/GJA1/ADAMTS1/TGFBR2/ADIPOQ/APOD/ELANE/ANG",28

A1/MYOT/FGFRL1/CDH15/GATA5/CNTN6/DSC3/IL1RN/KLF4/HMCN1/CNTN4/IGSF11/MPZ/CLDN14/C

:S/HPGDS/LIPC/LPL/ACSM5/ACSM2A/LIPI/AKR1C3/TECRL",27

3/SSTR1/DLX1/EGFR/NTRK2/NR4A2/HTR5A/LHX8/NEUROD1/PITX2/SHH/OTX2/AXL/GBX2/COL3A1/P

AR/APOA2/CYP11B1/LIPC/PCSK9/TSKU/CES1/CYP21A2",26
/BMP4/SOX9/SIX1/HOXD13/APOE/NGF/YAP1/CRABP2/SFRP2/SEMA3D/TGFBR2/SHH/ISLR2/LAMB2/

2/RET/TMEM100/NKX3-1/IGF2/AXL/CX3CR1/P2RY12/TNFAIP8L3/FAM110C/AKR1C3",33
/TPD52L1/GHR/FGF1/CLU/SDC4/EDN3/EREG/IL1B/CHI3L1/PDGFRA/AGT/HTR2B/THBS1/ADCYAP1/SN
4F11/CYP4F3/AKR1C3/AKR1C4/GSTA1",22

)/VIP/GJA1/ADAMTS1/TGFBR2/ADIPOQ/APOD/ELANE/ANG",28

1/BDKRB2/NTSR2/GPR37L1/FPR1/CCR9/MC5R/GPR139/GCGR",27

/APOA2/CYP11B1/LIPC/PCSK9/TSKU/CES1",24

CG2/SLC17A3/SLC17A1/ACY3/CHL1/ANXA1/KCNK1/AQP10/REN/OSMR/SLC17A4/SLC5A12/KCNE4/GJ

B/AGT/RBP4/ADCYAP1/SNCA/VIP/CRH/PTGES/SLC30A8/GALR1/NKX3-1/OR51E2/GDNF/NLGN1/FGG,
A1/LIPI/ANG/PLIN5",23

AX3",22

CTD11",18

1X/MT1F/MT1A/MT1M",21

4E",19

ADAMTS12/CPB1/ADAMTS1/ADAMTS3/MMP14/CPA3/MMP10/ANPEP/NAALADL2/MME/MMP1/TRA
DF3/APELA",23

/KRT71/FLG/ABCA12/CD109/PITX2/EVPL/KRT8/KRT4/ETV4/GDF3/MAFF/KRT79/AKR1C3/LIPN",34

5FR/FABP1/AXL/GPR37L1/FOS/FOSL1/SPHK1/NQO1/APOD/AKR1C3/HBA1/AQP1/HP",31
4/IGF2/ATOH8/LRG1/CCL11/PRL/EGR3/PRKD1/ANG/APELA/NOX5",30

.CAN/GALNT14/COLEC12/ASGR2/PTX3/CLEC3B/FBP1/MBL2/CLEC3A/CLEC4E/EVA1C/OLR1/LGALS7B/I

20

NR1B/PDGFRA/NR5A1/HCRT2/LHCGR/CYP1B1/TPH2/CRH/NTRK2/HTR7/ADAMTS1/TIMP4/ADORA1

AKR1C3",20

TACSTD2/S100A10",20

:NK1/CHRNA1/AQP10/CHRNA3/SCN2B/KCNE4/GJA1/PANX3/KCNS2/KCNJ15/CLIC6/LRRC38/LRRC52/C

2/TBX20/FOXC2/FZD2/NKX2-5",22

SLC17A3/NMUR2/HTR1B/KCNK1/CHRNA1/AQP10/CHRNA3/SCN2B/KCNE4/GJA1/PANX3/KCNS2/KCN.
L8/CCL14",21

.BCA10/APOA2/FABP1/FABP4/TMEM30B/TNFAIP8L3/APOD/AKR1C4",27

5AR1",18

BLC/EGFR/SERPINH1/GJA1/THY1/CD1A/PDPN/TGFB2/SHH/RET/ADRA1B/CD14/HAS2/MAL/OLR1/PC
./ANXA1/IL6/XCL1/NFKBIZ/MEGF10/THY1/RUNX1/PDPN/TGFB2/SPTA1/CITED2/SHH/IGF2/HAS2/FG

14/MMP10/MME/MMP1/TRABD2B/MMP28",21

MYOF/CBLC/EGFR/SERPINH1/GJA1/THY1/CD1A/PDPN/TGFB2/SHH/RET/ADRA1B/CD14/HAS2/MAL/

'2",19

IR4A2/WNT9B/ATF3/DAPL1/ALB/FOLR2/AQP2/AXL/FAM107A/PCSK9/FOS/FOXA3/LPL/FOSL1/PENK/F
3PC3/GJA1/SEMA3D/TGFB2/CITED2/PI16/FBP1/MT1E/MYOZ1/WT1/MT1X/OSTN/MT1F/MT1A/MT:
!/GPC3/CD109/NKX3-1/ATOH8/AR/KRT4/PRL/NUPR1/SOX2",26

GFRA/ANXA1/IL6/GATA4/CYP1B1/FBLN5/SNCA/EGFR/MMP3/NR4A2/MMP14/FZD1/FABP1/GPX8/C

IL1RAP/S100A10",19

AGT/HTR2B/CXCL9/ADCYAP1/XCL1/ACKR3/AGTR1/SNCA/GPR174/JPH2/THY1/F2RL2/GALR1/TRPV3

MT1E/MT1X/MT1F/MT1A/MT1M",23

CHE/FBXO2/PLA2G4A/APOA1/GRIA2/CLU/INHBA/MCHR1/LBP/APOE/NMUR2/HCRTR2/SSTR1/PTGES,

GJA1/PDLIM3/FBXO32/TIMP4/TRIM63/CSRP1/IGFN1/CMYA5/DES/MYOZ1/MYBPC1/NRAP/MYL4/TP

P27C1/HBA1/HBM/HBD/CYP21A2/NOX5",24

DCYAP1/AQP10/ABCA12/VIP/CRH/GJA1/NEUROD1/ADORA1/SLC30A8/AQP7/FOLR2/FGG/FGA/FGB/F
I2/DUSP1/ADORA3/HOXA7/TNFAIP6/RRAS/APOE/SERPINF1/STARD13/KLF4/THBS1/CYP1B1/EMILIN1,

JKX2-5",19

.1/YAP1/CYP1B1/RXRG/NR3C2/FBXO32/GJB2/NKX3-1/OR51E2/FAM107A/AR/AKR1C3/KANK2/AQP1"

L/STAR/APOA2/CYP11B1/LIPC/PCSK9/TSKU/CES1",24

,/KLF4/TTPA/YAP1/RSP03/EGFR/ST8SIA6/RBM46/GJA1/ADAMTS3/MYO1E/WNT9B/PLCD3/TGFBR2/C

2/NTRK2/NKX6-2/CHODL/IL34/SHH/ISLR2/CX3CR1/HAP1/RELN/MME/NEFL",32

TGBL1/EMP2",19

.P1/RBP4/CHRNA1/RCN3/ABCA12/BAG3/GJA1/LCN1/AZGP1/NEUROD1/CLDN1/ADORA1/ALB/ALDH1.

HRG/PADI2/DUSP1/ADORA3/HOXA7/TNFAIP6/RRAS/APOE/SERPINF1/STARD13/KLF4/THBS1/CYP1B1,

'PENK/NPW",19

19

=2/ATOH8/LRG1/CCL11/PRL/EGR3/PRKD1/ANG/APELA",27

'ARID5A",18

;/HOXA7/TNFAIP6/RRAS/APOE/SERPINF1/STARD13/KLF4/THBS1/CYP1B1/EMILIN1/MYOC/SFRP2/GJ
-INAK/MTNR1B/OSR1/CRH/SCN2B/JPH2/KCNE4/KCNS2/LRRC38/LRRC52/RRAD/PCSK9/NLGN1/SLN/H

.K/MTNR1B/OSR1/SNCA/CRH/SCN2B/JPH2/KCNE4/KCNS2/LRRC38/LRRC52/RRAD/PCSK9/NLGN1/SLN

IR1B/AGT/HTR2B/THBS1/ADCYAP1/ACKR3/AGTR1/EGFR/NEUROD1/TMEM100/OR51E2/CX3CR1/P2R
X1/CYP27A1/CYP1B1/CYP2C9/CH25H/TPH2/CYP11A1/CYP4B1/CYP17A1/P4HA3/CYP11B1/CYP2S1/CY
SX/TDGF1",22

L5",18

.A2G5/LBP/LGALS3/SPINK5/ANXA1/IL6/RBP4/FCN3/XCL1/NFKBIZ/SERPING1/VSIG4/CD1A/CD1B/APO

2/PDPN/TGFBR2/TBX20/TMEM100/HAS2/S100A4",25

/VSIG4/RUNX1/SHH/B4GALNT2/FGG/CEBPB/LGALS7B/ADIPOQ/MBP/TARM1",29

3/OSR1/SNCA/CRH/SCN2B/JPH2/KCNE4/KCNS2/APOA2/LRRC38/LRRC52/RRAD/PCSK9/NLGN1/SLN/H
;EMA3D/THY1/GPR37L1/CCL11/F2/MBP",23

NE4/GJA1/S100A1/ADORA1/ADRA1B/KCND3/ADRA1D/HSPB7/DES/IRX3/NKX2-5/MYL4/APELA/FXYD1

/GABRA5/HRH1/GRIN2B",20

'L1/HTR1A/FFAR3/S1PR3",15

;

A7/TNFAIP6/RRAS/APOE/SERPINF1/STARD13/KLF4/THBS1/CYP1B1/EMILIN1/MYOCN/SFRP2/GJA1/TN-
PLA2G5/APOE/ANXA3/RAB20/RAB13/EGFR/GSN/FCGR1A/MYO1E/COLEC12/CLEC4E/RAB31/SAA1/BT-
CITED2/FBN1/GPR183/FOS/JUNB/CEBPB/ADIPOQ/ANXA2/CSF1/PRTN3/SIGLEC15",30

/LPL/PNPLA1/TSKU/ACSM2A/TLCD2/CES1",26

A1/CLDN19/DRD5/KCND3/KCNA2/IRX3/NKX2-5",25

32/TIMP4/TRIM63/CSRP1/IGFN1/CMYA5/DES/MYOZ1/MYBPC1/NRAP/MYL4/TPM2",33

R/GBX1/GDNF/SNCG/PENK/BSX/RELN/DMBX1",28

ADORA1/ADRA1B/KCND3/ADRA1D/HSPB7/DES/IRX3/NKX2-5/MYL4/APELA/FXYD1",30

ELANE",17

IK1",19

/C4B/C4A",20

L/CDC42EP1/PDLIM4/DSC3/ANXA1/FRMD6/HMCN1/RAB13/IGSF11/USP53/GJA1/PANX3/PDLIM3/MY

.18/DRD5/SLC6A19/PDZK1/EPH8L2/ITLN1/ESPN/MME/AQP1",25

POCK3/CHSY3",21
CXCL9/FBN2/XCL1/IGSF11/SNCA/GSN/JPH2/THY1/SLC30A2/NBL1/S100A9/ALB/SLC30A8/FBN1/HAP1,
P",22

/CCL11/F2/MBP",22
/NEUROD1/IGFN1/RET/LAMB2/DIO3",23

P1/NKX3-1/CYP2S1/NQO1/ADIPOQ/UGT2B15/GSTA1",25

AKR1C3/AKR1C4/GSTA1",19

CNE4/GJA1/ADORA1/ADRA1B/KCND3/NKX2-5/MYL4",26

CYP27C1/HBA1/HBM/HBD/CYP21A2/NOX5",24

A1/KCND3/EMP2",21

1/HBM/HBD/GRIN2B",23

1",14

/MMP14/CXCL16/S100A9/TGFBR2/TBX20/ISLR2/IGF2/SPHK1/ERBB4/F2/CSF1/WT1/DIO3",34

/LRRC52/RRAD/NLGN1/HAP1/SHISA6/RELN/PRRT1/SHISA9",26

8

10A1/ADORA1/ADRA1B/KCND3/ADRA1D/HSPB7/DES/IRX3/NKX2-5/MYL4/APELA/FXYD1",33

2-5/WT1/NRAP",23

12/ANXA1/AGT/KLF4/THBS1/CYP1B1/ANXA3/RAB13/FSTL1/ATOH8/FOXC2/EGR3/PRKD1/FGF16/S100
T/IL6/EMILIN1/NFKBIZ/AGTR1/SNCA/OSMR/TSLP/S100A9/TLR3/MBL2/FABP4/CEBPB/LPL/NUPR1/PE

TNFSF9/ASS1/LGALS3/ANXA1/IL6/KLF4/XCL1/NFKBIZ/THY1/VSIG4/RUNX1/S100A9/TGFBR2/SPTA1/SH

NE/MBP",22

/PI16/WFIKK2/MYOZ1/NKX2-5/NRAP",26

AKR1C3",19

K1/TGFBR2/ATOH8/HAS2/FOXC2/PRKD1/FGF16/TDGF1",25

IXA1/KCNK1/AQP10/OSMR/SLC17A4/SLC5A12/KCNE4/GJA1/THY1/PDPN/CLDN1/SLC2A2/F2RL2/SLC6A",18

8

,18

ABP1/AQP1",14

4/CYP1B1/FBLN5/SNCA/EGFR/MMP3/NR4A2/FZD1/FABP1/GPX8/GJB2/AXL/BDKRB2/GPR37L1/FOS/L

RC38/LRRC52/KLF15/HAP1/PDZK1/ITLN1/F2/ADIPOQ/RELN/FXYD1",29

HSY3",19

1/LILRA2",20

THY1/PDPN/DHRS3/MXRA8/ADORA1/SLC6A18/TTYH1/FAM107A/P2RY12/DRD5/GPR37L1/CSPG4/SLC12/OT/VGF/APOE/ASS1/PPP1R1B/SERPINF1/LRP4/KCNK1/ANXA3/ADCYAP1/SNCA/VIP/CRH/CYP17A1/GI
LEC12/CLEC4E/RAB31/BTC/FZD2/DMBT1/WNT7B/HLA-DPB1",28

1/NEUROD1/CLDN1/ALB/ALDH1A1/COL3A1/TMEM119/CSF1/POTEE/SERPINA3/LAMA2/POTEF/SIGL

DORA1/KCNK5/KCNJ4/KCNG3/KCND3/DPP10/KCNA2/KCNIP1/KCNA4/KCNU1/AQP1/KCNJ18/FXYD1",

.1B/TNFSF9/ASS1/LGALS3/ANXA1/IL6/KLF4/XCL1/NFKBIZ/THY1/VSIG4/RUNX1/TGFBR2/SPTA1/SHH/IGF1",21

L2/SVEP1/GJB2/GJB1/UGT8/IRX3/CLDN7/PKP3/PRTN3",28

LDN7/PKP3",22

9/FOLR2/CD14/ITLN1/GAS1/NTM/TDGF1",25

KR1C3/ADH1B/AKR1B10/ADH4/AKR1C4/HSD3B1/HSD3B2/ADH1C",22
GTR1/EGFR/GSN/CLDN1/PTX3/CHMP4C/MBL2/ANPEP/AXL/CX3CR1/CXCL8/TRIML2/F2/TMPRSS2/IFI

LR2/IGF2/ERBB4/CSF1/WT1/DIO3",24

DRD5/SHISA6/RELN/MME/HRH1/PRRT1/SHISA9/GRIN2B",27

DCD/DOCK5/ADORA1/ADRA1B/SPHK1/NKX2-5",24

ADIPOQ/GDF3/FFAR4",21

KCN2B/KCNE4/KCNS2/KCNJ15/CLIC6/LRRC38/LRRC52/KCNK5/TTYH1/KCNJ4/KCNG3/GRIK1/KCND3/CH
P4F3/CYP27C1/HBA1/CYP21A2",23

1/STXBP6/ADIPOQ/FFAR4",21
,16

RBB4/F2/TNFAIP8L3/ROR1/RELN",25

D13/ANXA1/AGT/KLF4/THBS1/ANXA3/FGF7/DOCK5/DOCK1/TGFBR2/ATOH8/HAS2/FOXC2/TACSTD2

APCS/IL6/ANXA3/XCL1/SERPING1/FCGR1A/C8A/CD1A/CD1B/C1R/SPON2/AIRE/AZGP1/SLAMF9/TLR3

1/RELN",21
D1/NTF3",21

GXT/HES3/FOXC2/DLK1/ANXA4/S1PR3",25

YOF/CXCL9/MYOCN/FZD7/MMP14/CSRP1/LMNA/PI16/SHH/IGF2/IRX3/MYOZ1/NKX2-5/TMEM119/W

'1/BTC",17

DRD5/ADRA1B/MRAP/ADRA1D/CALCB/MC5R/ADRB3/S1PR3/GCGR",22

'FOLR2/FAM107A/PCSK9/FOXA3/LPL/PENK/PRKD1/AKR1C3/KANK2/GCGR",28

CGR/CH25H/TPH2/HDC/SNCA/STAR/NR4A2/CYP11B1/SPTLC3/SPHK1/AKR1C3/HRH1/AKR1C4/CES1",3

IT3/PDGFR/AGT/GATA4/MYOF/CXCL9/MYOCN/SYPL2/MEGF10/FZD7/MMP14/CSRP1/LMNA/FBXO4

A2G5/APOE/APOC1/ANXA1/TEC/NR5A1/TTPA/UNC13C/THBS1/MYOF/ANXA3/PIK3C2G/SNCA/SYTL5/

16C5/ADH1A/AKR1C3/ADH1B/AKR1B10/ADH4/AKR1C4/HSD3B1/HSD3B2/ADH1C",20
PB",20

1/OTX2/RET/GBX2/GDNF/LAMB2/RELN/LAMA2",30
'HKDC1/CYP11B1/NEUROD1/KLF15/FOXA3/ADIPOQ/SLC2A4/ACSM2A/FAM3B/GCGR",31

1P2",25

1QO1/AKR1C3/AQP1",21

2-5/TDGF1",20
.6/RELN/SHISA9",20
A12/HKDC1/CYP11B1/NEUROD1/KLF15/FOXA3/ADIPOQ/SLC2A4/ACSM2A/FAM3B/GCGR",31
/ISL2/SHH/GBX1/OTX2/RET/GBX2/GDNF/LAMB2/RELN/LAMA2",30

1NC13C/REN/ADAMTS12/GJA1/NR4A2/LGI4/NFIA/TRIM58/RET/AXL/CX3CR1/FGG/RELN/ANG/NEFL",3
",19

ZK1/F2/RELN/FXYD1",21
Q",16

:XCL16/TGFBR2/RAB31/LRP1B/PCSK9/CXCL8/CD14/ADIPOQ/ANXA2/NTF3/APELA",31

IKX3-1/ERBB4/F2/ROR1/RELN",24

18",19

.F2/LILRA2",22

ICA",17

IRNA1/CHRNA3/SCN2B/KCNE4/KCNS2/KCNJ15/CLIC6/LRRC38/LRRC52/OTOP1/KCNK5/TTYH1/TRPV3/

L5/KCNK5/FOLR2/SLC6A5/TRPV3/KCNJ4/GDNF/LRRC8E/MAPK15/KCNJ18",30

/SIX1/MYOD1/GSC/GATA4/KLF4/NR5A1/FOXF2/YAP1/LBX1/PRDM16/RXRG/THRB/NR4A2/RUNX1/AT
VWA2/IGF2/RAB31/PCSK9/LPL/FOXC2/ADIPOQ/SLC2A4/SOCS3/FFAR3",32
JROD1/ADORA1/SLC30A8/FGG/FGA/FGB/FAM3B/FFAR3/FFAR4",31
/ACOX2/LPL/SPHK1/PNPLA1/ADIPOQ/LIPI/AKR1C3/AKR1B10/PLIN5",28

,18

YA5/DES/MYOZ1/NRAP/MYL4/TPM2",28
NGF/HTR1B/AGT/UNC13C/CNTN4/IGSF11/SNCA/CHRNA3/NTRK2/S100B/ADORA1/FAM107A/CX3CR:
MTS1/CREB3L1/ANGPTL7/PRL/THBS2",21

5/F2/NQO1/AKR1C3/HBA1/HBM/GPX3/PLIN5/HBD/NOX5/HP",29
JM/KERA/RGS16/HMCN1/DHRS3/CLDN19/LAMB2/IRX5/TACSTD2/CNGA1",28
1B/AGT/UNC13C/CNTN4/IGSF11/SNCA/CHRNA3/NTRK2/S100B/ADORA1/FAM107A/CX3CR1/DRD5/I
E/NGF/AGT/GATA4/YAP1/FBLN5/OSGIN1/MYOC/IGFBP4/CRABP2/AGTR1/SFRP2/EGFR/IGFBP1/GJA:
.1",20

'ORM2/ORM1/LILRA2",24
POQ/ARID5A/ORM2/ORM1/LILRA2",24

OTCH2/ANXA1/NFKBIZ/MMP14/IL34/RUNX1/TGFBR2/TLR3/SHH/FBN1/AXL/FOS/CEBPB/EGR3/ADIPC

PDZK1/F2/RELN/FXYD1",22

OC3/OPRM1/CASQ2/INHBA/IL1B/LIF/APOE/APOC1/LGALS3/MTNR1B/ANXA1/HTR1B/THBS1/OSR1/SN
I/MMP3/NR4A2/FZD1/FABP1/GPX8/GJB2/AXL/GPR37L1/FOS/SPHK1/NQO1/PENK/PRKD1/AKR1C3/AI

A2/SLC6A17",20
LAS2/LMNA/ADORA1/TGFBR2/FABP1/CITED2/NKX3-1/ANGPTL4/ADIPOQ/PENK/SLC2A4/DIO3/ANG/A

DEA/VEPH1",13

3/FMO1/FMO4/CYP27A1/CYP2C9/CH25H/CYP4F11/AKR1C3/AKR1C4",9

/TLCD2/NOX5",21

AGT/YAP1/FBLN5/OSGIN1/MYOC/IGFBP4/CRABP2/AGTR1/SFRP2/EGFR/IGFBP1/GJA1/SEMA3D/MMP2/COLEC12/APOA2/NEUROD1/TGFBR2/SLC30A8/LPL/NQO1/ADIPOQ",28

XL/FGG/CEBPB/THBD/LGALS7B/F2/MICA/TARM1",27

TYH1/KCNJ4/LRRC8E/KCNG3/KCND3/CHRNA9/CATSPER1/DPP10/KCNA2/KCNIP1/KCNA4/GABRA5/VV

√",22

1/STXBP6/ADIPOQ/FFAR4",22

0HRS3/CLDN19/LAMB2/IRX5/TACSTD2/CNGA1",27

:/CHRNA9/EP8L2/ROR1/GABRA5/ESPN/MBP",23

'EP8L2/KANK2",19

2/TNFAIP8L3/FAM110C/AKR1C3",24

:A/ADIPOQ/ARID5A/ORM2/ORM1/LILRA2",24
D14/LPL/CIDEA/ADIPOQ/ARID5A/ORM2/ORM1/LILRA2",24

DN3/EREG/IL1B/CHI3L1/AGT/HTR2B/THBS1/ADCYAP1/SNCA/EGFR/FCGR1A/IL34/ADORA1/TGFBR2/1

L1/PRL/THBS2",20

K2/FGL1/COMP/WNT2/PTPRZ1/SERPINE1/RARRES2/OGN/AMBP/CXCL12/COL1A1/SOD3/APOA4/APC
3/MATN2/CHI3L1/POSTN/THBS1/EMILIN1/OIT3/FBN2/LUM/FBLN5/COL6A2/DPT/HMCN1/COL8A1/H
PLG/MMP19/COL10A1/SOX9/COL5A1/GFAP/POSTN/SPINK5/PDGFRA/AGT/IL6/FOXF2/MMP7/MMP1
D/PLG/MMP19/COL10A1/SOX9/COL5A1/GFAP/POSTN/SPINK5/PDGFRA/AGT/IL6/FOXF2/MMP7/MM
GFBI/FMOD/PLG/MMP19/COL10A1/SOX9/COL5A1/GFAP/POSTN/SPINK5/PDGFRA/AGT/IL6/FOXF2/N
CLU/COL10A1/COL21A1/BMP4/C3/F10/VGF/APOE/COL5A1/MATN3/IL6/THBS1/IGFBP4/COL6A2/RCN
P1/TGFB3/INHBA/EDN3/NDP/CXCL6/EREGBMP4/IL1B/TNFSF9/GDF5/LIF/VGF/GDF15/PYY/LGALS3/I
FRL1/APOE/COL5A1/POSTN/LYVE1/THBS1/FGF7/HAPLN1/RSPO3/RSPO2/HABP2/ADAMTS1/ADAMTS
APOA1/TTR/SPP1/TGFB3/INHBA/EDN3/NDP/CXCL6/EREGBMP4/IL1B/TNFSF9/GDF5/LIF/VGF/GDF15
EREGBMP4/SOX9/C3/LIF/VGF/HOXD13/FOXA1/SERPINF1/RXFP2/NOTCH2/FST/PDGFRA/ANXA1/GAT
EG/BMP4/SOX9/C3/LIF/VGF/HOXD13/FOXA1/SERPINF1/RXFP2/NOTCH2/FST/PDGFRA/ANXA1/GATA4
JTEE/SERPINA3/POTEF/HBA1/HBD/C4B/ORM2/ORM1/C4A/HP/HPR",51

DXA1/ASS1/SERPINF1/HMGCS2/NOTCH2/LRP4/PDGFRA/ANXA1/AGT/YAP1/RBP4/LGR5/MYOCN/REN
3/FOXA1/GATA5/BARX1/GSC/BHLHE40/NOTCH2/LRP4/GATA4/CFC1/LMX1B/FOXN4/OSR1/DLX1/SFR
/ADAMTS3/FSTL1/PCOLCE2/CLEC3B/LIPC/FBN1/EVA1C/TNXB/CXCL8/SAA1/LPL/F2/ADAMTSL5/THBS
/FN1/PLA2G4A/F3/SERPINC1/TGFB3/MSX2/PLG/PLAU/C4BPB/SDC4/F13A1/EREGBMP4/FOXA2/F10/TSPAN
4/PDGFRA/AGT/YAP1/RBP4/LGR5/MYOCN/REN/OSR1/AGTR1/GPC3/FREM2/GFRA1/ADAMTS1/MYC
/SRGN/EGR2/TNFAIP6/RUNX2/BMP4/SOX9/RRBP1/GDF5/OMD/LRP4/IL6/YAP1/MMP13/ITGA11/FBN
11/COL6A3/SERPINI1/PI16/SERPINB7/WFDC13/CST2/CST1/WFIKKN2/CST6/UMODL1/WFDC11/ANXA2
/COLEC10/COL14A1/COL4A5/COL4A6/COL5A2/C1QTNF9B/COL28A1",36

.1/DAW1/BMP4/C3/FOXA2/SIX1/HOXD11/HOXD13/FOXA1/GATA5/BARX1/GSC/BHLHE40/NOTCH2/F
3/TIMP4/WFDC8/LCN1/COL6A3/SERPINI1/PCOLCE2/PI16/SERPINB7/NKX3-1/WFDC13/CST2/CST1/M
XA7/HOXC11/RUNX2/BMP4/SOX9/SIX1/LIF/GSC/NOTCH2/PDGFRA/GATA4/FOXF2/TPA/YAP1/LBX1/
1/MTNR1B/PDGFRA/ANXA1/CGA/AGT/IL6/IL1RN/NR5A1/FDX1/CYP1B1/CYP2C9/RBP4/CYP11A1/ADC
/AHSG/SNCA/SFRP2/GPC3/SERPING1/SERPINH1/CD109/TIMP4/WFDC8/LCN1/COL6A3/SERPINI1/FAB
THBS1/AHSG/SNCA/SFRP2/SERPING1/SERPINH1/CD109/TIMP4/WFDC8/LCN1/COL6A3/SERPINI1/FAB
/COL6A3/SERPINI1/SERPINB7/WFDC13/CST2/CST1/WFIKKN2/CST6/WFDC11/ANXA2/PROS1/SERPIN
JOU3F3",36

B1/RBP4/DHH/LHX9/RAB13/REN/OSR1/SFRP2/CYP17A1/GFRA1/GJA1/ADAMTS1/MMP14/WNT9B/LI
.1/ELANE/ORM2/ORM1/HP/HPR",40

'C2/LAMA2/COL4A6/ANG/COL28A1",36

C8/LCN1/COL6A3/SERPINI1/SERPINB7/WFDC13/CST2/CST1/WFIKKN2/CST6/WFDC11/ANXA2/PROS1/
P11B1/DHRS3/CPA3/SHH/SLC30A8/ALDH1A1/CRABP1/CYP2S1/KLK6/SDR16C5/PNLIP/FFAR3/CYP27C
/GSC/NOTCH2/PDGFRA/GATA4/FOXF2/YAP1/LBX1/RBP4/FBN2/LRIG3/FOXN4/OSR1/GJA1/ZIC1/ZIC3/
GT/YAP1/REN/OSR1/AGTR1/GPC3/FREM2/GFRA1/ADAMTS1/MYO1E/WNT9B/KLF15/SHH/OSR2/RET
/SERPINF1/APCS/SPINK5/NGF/ANXA1/AGT/KLF4/THBS1/AHSG/SNCA/SFRP2/GPC3/SERPING1/SERPIN
L/GSC/PDGFRA/CHAD/MMP13/FBN2/OSR1/CSRNP1/SFRP2/SERPINH1/MMP14/WNT9B/DHRS3/TGFB

HH/LHX9/RAB13/REN/OSR1/SFRP2/GFRA1/GJA1/ADAMTS1/MMP14/LHX8/PTX3/TLR3/CITED2/NKX3
2/GFRA1/GJA1/ADAMTS1/MMP14/LHX8/PTX3/TLR3/CITED2/NKX3-1/AR/CEBPB/NUPR1/IRX5/UMOD
/ZFP36/APOE/SERPINF1/NOTCH2/FST/HTR2B/IL6/YAP1/THBS1/LGR5/FGF7/IGFBP4/OSR1/COL8A1/A
RX3/ERBB4/ADIPOQ/TACSTD2/WT1/WNT7B/POU3F3/HOXB7",43

34/NBL1/S100A9/CXCL3/CXCL1/CX3CR1/P2RY12/CXCL8/CCL11/SAA1/UMODL1/DEFB124/CCL13/CSF
T1/WNT7B/POU3F3/HOXB7",37

3/ADIPOQ/TACSTD2/WT1/WNT7B/KANK2/POU3F3/HOXB7",42

<LF4/THBS1/AHSG/SNCA/SFRP2/GPC3/SERPING1/SERPINH1/CD109/TIMP4/WFDC8/LCN1/COL6A3/SE
28A1",22

3/XCL1/RAB13/ACKR3/AGTR1/CXCL14/TPBG/IL34/NBL1/CXCL16/S100A9/CXCL3/CXCL1/CX3CR1/CXCL

WNT9B/TGFBR2/SHH/OSR2/DMRT2/FOXC2/IRX5/HOXA4/HOXB7",39
5/HOXA4/HOXB7",33
/PCSK9/HTRA3/TPSAB1/F2/C1S/TMPRSS2/PRTN3/MMP1/TPSB2/ELANE/LPA/CFI/HP/HPR",47
XCL16/CXCL3/CXCL1/CMTM5/CXCL8/CCL11/ADIPOQ/CCL13/FAM3B/GDF3/CSF1/WNT7B/IL27/GDF10
PCSK9/HTRA3/TPSAB1/DPP10/F2/C1S/TMPRSS2/RELN/PRTN3/MMP1/TPSB2/ELANE/LPA/CFI/HP/HPI
INF1/SPINK5/NGF/AGT/KLF4/THBS1/PMAIP1/RCN3/AHSG/SNCA/SFRP2/GPC3/GSN/SERPING1/SERP
CSK9/HTRA3/TPSAB1/DPP10/F2/C1S/TMPRSS2/RELN/PRTN3/MMP1/TPSB2/ELANE/LPA/CFI/HP/HPR"
DH1A/AKR1C3/ADH1B/UGT2B15/AKR1B10/ADH4/AKR1C4/HSD3B1/HSD3B2/CYP21A2/ADH1C",40

UR2/CFHR4/ANXA1/AGT/IL6/TTPA/THBS1/RBP4/ABCA8/CRABP2/REN/GULP1/ABCA12/AGTR1/STAR/
VDC2/MT1E/FOS/PDZK1/NUPR1/NQO1/PENK/MT1X/MBP/AKR1B10/ADH4/MT1F/CES1/MT1A/MT1N
IXA2/SERPINA11/SERPINA3/SERPINA1/SERPINB2/SERPINB11/COL28A1",33
/WNT9B/TGFBR2/TBX20/SHH/NKX3-1/GBX2/GDNF/AR/CCL11/FOXC2/TACSTD2/CSF1/SOCS3/WT1/H
VE1/ANXA1/IL6/THBS1/EMILIN1/CH25H/CXCL9/XCL1/THY1/MMP14/IL34/NBL1/AIRE/CXCL16/S100A
IP14/WNT9B/TGFBR2/TBX20/SHH/NKX3-1/GBX2/GDNF/AR/CCL11/FOXC2/TACSTD2/CSF1/SOCS3/WT

4/PRTN3/HRH1/C5AR1/CCL23/CCL16/CCL18/CCL14",42
/FGF7/RSP03/RSP02/PTGES/TKTL2/ADAMTS1/ADAMTS3/FSTL1/PCOLCE2/CLEC3B/LIPC/FBN1/EVA1C
MP1/MMP28",33
T/TTPA/THBS1/RBP4/ABCA8/CRABP2/REN/GULP1/ABCA12/AGTR1/STAR/CRH/PMP2/PTGES/ABCA9/

SPON2/AIRE/S100A9/CXCL3/CXCL1/DEFA4/DEFA6/MBL2/MFAP4/WFDC13/RNASE3/CXCL8/GPR183/F
16/CCL18/CCL14",37

'WT1/ROR1/PAX9/HOXB7",37
FRP2/NKX6-2/FZD7/WNT9B/ISL2/PDPN/NEUROD1/TBX20/SHH/GBX1/AR/SOSTDC1/FOXC2/ERBB4/G
1/MATN3/CHI3L1/HMGCS2/MMP13/OSR1/SFRP2/RSP02/SERPINH1/ADAMTS12/BMP3/RUNX1/TGFE
2/BMP4/GDF5/GDF15/NOTCH2/FST/GATA4/CFC1/THBS1/EMILIN1/FBN2/MYOC/PRDM16/DLX1/SF
GT/GATA4/THBS1/EMILIN1/FBN2/MYOC/PRDM16/DLX1/SFRP2/GPC3/LATS2/ADAMTS12/ADAMTS
SPINK5/NGF/AGT/KLF4/THBS1/PMAIP1/AHSG/SNCA/SFRP2/GSN/SERPING1/SERPINH1/CD109/TIMP4
FBR2/TBX20/OTX2/ATOH8/FOXC2/ADIPOQ/SOX2/GDF3/MBP/COL5A2/APELA",46

'OD1/GATA5/NOTCH2/PDGFR/AGT/GATA4/YAP1/RBP4/CHRNA1/MYOC/RXRG/OSR1/MEGF10/JPH
2/MYOZ1/THBD/F2/PROS1/SERPINB2",37

IN8/APOE/PDGFR/TEC/IL6/THBS1/FLG/ABCA12/VIP/SERPING1/GJA1/CSRP1/PDPN/CLDN1/ADORA1
GDNF/AR/CCL11/FOXC2/TACSTD2/CSF1/WT1/HOXB7",40

LB1/RBP4/FBN2/KERA/FOXN4/DLX1/COL8A1/EGFR/NTRK2/FREM2/THRB/GJA1/THY1/WNT9B/NEURC
H2/FST/GATA4/THBS1/EMILIN1/FBN2/MYOC/PRDM16/DLX1/SFRP2/GPC3/LATS2/BMP3/CD109/FZ
IL3A1/HTRA3/WFIKN2/HAP1/TSKU/S100A13",38

FOXC2/HTR1A/ADRB3/HRH1",38

CRH/SLC5A12/SYT8/APOA2/AQP7/LIPC/GALR1/AQP2/GDNF/PCSK9/SNCG/PNLIP/KCNA2/HTR1A/MAF
YP1B1/RBP4/FBN2/KERA/FOXN4/DLX1/COL8A1/EGFR/NTRK2/FREM2/THRB/GJA1/THY1/WNT9B/NEU
CREB3L1/SHH/IGF2/JUNB/CEBPB/PENK/SOX2/TMEM119/PRKD1/FFAR4/WNT7B/OSTN/CEBPD/TWIST
/FOXA1/ASS1/SERPINF1/HMGCS2/NOTCH2/SOX3/PDGFR/ANXA1/CGA/IL6/NR5A1/CYP1B1/FGF7/E
NT7B/AKR1C3/TAT/HSD3B1/HSD3B2/AQP1/NEFL",40

SHH/AXL/COL3A1/P2RY12/FGG/FGA/FGB/CYP4F11/SAA1/THBD/F2/PROS1/SERPINA1/SERPINB2",50
;CHI3L1/NOTCH2/PDGFR/HTR2B/IL6/GATA4/THBS1/ADCYAP1/IGFBP4/XCL1/ACKR3/TPBG/EGFR/N
MYOC/RXRG/MEGF10/TAGLN/JPH2/MKX/GJA1/CHODL/FZD1/ATF3/COL6A3/CITED2/TBX20/SHH/IG
F-1/AR/NUPR1/ZFP42/WT1/SYCP2/AKR1C3/HOXA10",41

SHH/AXL/COL3A1/P2RY12/FGG/FGA/FGB/CYP4F11/SAA1/THBD/F2/PROS1/SERPINA1/SERPINB2",49

INX2/SOX9/SIX1/HOXD13/MYOD1/FOXA1/EGR4/GATA4/KLF4/FOXF2/POU2F3/PRDM16/CSRNP1/VENTX/ZIC3/NEUROD1/EN1/SHH/OTX2/NKX3-1/GBX2/EMX2/DMRT2/HES3/FOXC2/HOXC10/GDF3/WT1/HOXL1/CX3CR1/CXCL8/GPR183/CCL11/SAA1/DEFB124/CCL13/CSF1/S100A14/HRH1/C5AR1/MMP28/CCL11/IL1A/GPC3/ITPRIP/SERPING1/SERPINH1/SH3RF2/CD109/TIMP4/APOA2/WFDC8/LCN1/COL6A3/SERPINI1/MIA/GDF10",41

3A1/LAMB2/ISG15/ITGBL1/S1PR3/EMP2",40

MYOD1/FOXA1/EGR4/GATA4/KLF4/FOXF2/POU2F3/PRDM16/CSRNP1/VENTX/ZIC1/NR4A2/ZIC3/CREB

3N2/KERA/FOXN4/DLX1/COL8A1/EGFR/NTRK2/FREM2/THRB/GJA1/THY1/WNT9B/NEUROD1/IGFN1/ITGB2/CEBPB/MYOZ1/ERBB4/SOX2/APOD/NEFL",44

C2/HTR1A/ADRB3/HRH1",37

Y2/FOXC2/HTR1A/ADRB3/HRH1",37

SERPINF1/NOTCH2/HTR2B/YAP1/THBS1/FGF7/OSR1/AGTR1/SFRP2/VIP/EGFR/GPC3/FZD7/CD109/CLA1/EDN3/IL1B/MYOD1/CNN1/TNNT3/GATA5/NMUR2/MYH8/MYBPH/AGT/HTR2B/GATA4/MYOF/CHI3L/COL3A1/P2RY12/FGG/FGA/FGB/CYP4F11/SAA1/THBD/F2/PROS1/SERPINA1/SERPINB2",49

C3/RSPO2/ADAMTS12/GJA1/ZIC3/MMP14/FZD1/WNT9B/TGFBR2/CITED2/TBX20/SHH/RET/NKX3-1/G

15/SHH/CX3CR1/P2RY12/GPR183/GPR37L1/MAL/LAMB2/CSPG4/F2/PENK/SOX2/SOX1/CSF1/NCMAF3/D3B2/AQP1/NEFL",36

SERPINH1/ADAMTS12/BMP3/RUNX1/TGFBR2/OSR2/COL3A1/BGN/TSKU/WNT7B/ARID5A",44

I/SERPINI1/ALB/PTX3/CXCL1/CLEC3B/DEFA4/IGF2/RNASE2/RNASE3/LRG1/FGG/FGA/FGB/HSPA6/PEN

IN1/DUSP5/DUSP6/ADCYAP1/XCL1/ACKR3/TPBG/EGFR/ATF3/GPR183/FGG/FGA/FGB/CCL11/CHRNA9

16/ADORA1/CXCL3/CXCL1/CX3CR1/BDKRB2/CXCL8/MRAP/FPR1/CCL11/SAA1/P2RY2/CALCB/PENK/C11OR/THRB/ZIC1/THY1/IGFN1/OTOP1/PITX2/CITED2/OSR2/FBN1/GBX2/COL8A2/CHRNA9/FZD2/TSKU/SOX2/OSR2/CEBPB/AMBN/FAM83H/TMEM119/ISG15",40

2/APELA",33

1A3/TPH2/RXRG/NR3C2/FBXO32/TRIM63/APOA2/CLDN1/TGFBR2/GJB2/NKX3-1/OR51E2/FAM107A/A

3MMP4/IL1B/LIF/MYOD1/GFAP/SERPINF1/BHLHE40/NOTCH2/NGF/LRP4/IL6/TTPA/YAP1/CRABP2/DLX1

PB/AMBN/FAM83H/TMEM119/ISG15",40

/FOXF2/YAP1/OSR1/SFRP2/SEMA3D/PDPN/ACTG2/TGFBR2/PITX2/CITED2/TBX20/SHH/RET/TMEM10

3/FGA/FGB/FOXC2/MYOZ1/THBD/F2/PROS1/SERPINB2",39

./DUSP6/ADCYAP1/XCL1/ACKR3/TPBG/EGFR/ATF3/GPR183/FGG/FGA/FGB/CCL11/CHRNA9/ERBB4/A
IL34/NBL1/AIRE/ADORA1/CX3CR1/P2RY12/CXCL8/DEFB124/CSF1/APOD/S100A14/C5AR1/ELANE/MN

HOXA10",35

51/HMGCS2/IL6/CXCL9/REN/SNCA/TIMP4/SPON2/S100A9/CLDN1/CXCL3/CXCL1/DEFA4/DEFA6/GJB2,
/ZFP42/WT1/AKR1C3/HOXA10",35

41/COL8A1/EGFR/NTRK2/THRB/GJA1/THY1/WNT9B/NEUROD1/IGFN1/TGFBR2/PITX2/CITED2/SHH/O
L83/FGG/FGA/FGB/CCL11/ERBB4/CCL13/TNFAIP8L3/FFAR4/PLA2G2A/C5AR1/APELA/CCL23/CCL16/C
51/PLIN5",37

9/SERPINI1/ALB/PTX3/CXCL1/CLEC3B/DEFA4/IGF2/RNASE2/RNASE3/LRG1/FGG/FGA/FGB/HSPA6/PEI
C10/HOXA10",35
HOXA10",35

A9/SERPINI1/ALB/PTX3/CXCL1/CLEC3B/DEFA4/IGF2/RNASE2/RNASE3/LRG1/FGG/FGA/FGB/HSPA6/PI
'HP",36

HTRA3/SOSTDC1/GDF3/FAM83G/VWC2",39

7BN1/TMEM100/HTRA3/SOSTDC1/GDF3/FAM83G/VWC2",39

7ZIC3/MMP14/PDPN/TGFBR2/SHH/COL3A1/WT1/WNT7B/MME",43

POQ/TNFAIP8L3/PRKD1/CES1/PLIN5",36

1/FDX1/CYP1B1/CYP2C9/CH25H/DHH/CYP11A1/AGTR1/GC/STAR/CRH/CYP17A1/UGT2B4/APOA2/CY
7AT/HSD3B1/HSD3B2/AQP1/HOXA10/NEFL",41

4/OSR2/COL3A1/EVX2/HOXC10/HOXA10",39

2/COL3A1/EVX2/HOXC10/HOXA10",39

3L8",34

'HRH1/C5AR1",28

SOX2/SOX1/NCMAP/ROR1/RELN/C5AR1",44

GA/FGB/GAS1/ANXA2/TMPRSS2/MME/S100A10/HP/HPR/SPON1",47
XCL9/REN/SNCA/TIMP4/SPON2/S100A9/CLDN1/CXCL3/CXCL1/DEFA4/DEFA6/GJB2/AXL/CX3CR1/CXC
'A1/IL6/EMILIN1/XCL1/NFKBIZ/COL8A1/SFRP2/MEGF10/DOCK5/DOCK1/THY1/ABI3BP/RUNX1/PDPN/
PDPN/TGFBR2/PITX2/CITED2/TBX20/SHH/RET/TMEM100/GBX2/GDNF/HAS2/FOXC2/ERBB4/S100A4"

APOD/S100A14/C5AR1/CCL23/CCL16/CCL18/CCL14",41
F3/FAM83G/VWC2",36

F3/LGR5/KRT71/FGF7/CRABP2/FLG/ABCA12/EGFR/CD109/PITX2/FOXQ1/SHH/SVEP1/EVPL/AGPAT2/
DOCK1/ADAMTS12/THY1/ABI3BP/FZD7/MMP14/PDPN/FBLN2/MICALL2/VWA2/AXL/TTYH1/FAM107A
/PDGFRA/ANXA1/CGA/AGT/HTR2B/NR5A1/DHH/AGTR1/SNCA/STAR/APOA2/ADORA1/FABP1/P2RY1:
A1/WNT7B/MME",38
'ADH1B/AKR1B10/ADH4/AKR1C4/GSTA1/ADH1C",35
J1/COL3A1/HAS2/BNC2/BGN/TSKU/ANXA2/TMEM119/OSTN/SIGLEC15/SP5",44
PINF1/ITGB4/STARD13/LGALS12/ANXA1/AGT/HTR2B/KLF4/THBS1/CYP1B1/ANXA3/FGF7/RAB13/DA/

3/GATA4/MYOF/CHRNA1/MYOC/DOCK5/GSN/HTR7/SCN2B/KCNE4/GJA1/TRIM63/ADORA1/TBX20/I
AKR1C3/FABP12/AKR1C4/GSTA1/GRIN2B",38
1/CXCL8/LRG1/CCL11/PRL/CCL13/CSF1/NTF3/S100A14/IL1RAP/IL27/CRLF2/CCL23/CCL16/CCL18/CCL

2-5/SHISA6/APCDD1L/TPBGL/TRABD2B",37

3R2/SHH/COL3A1/WNT7B/MME",38

I/SHH/FOXC2/SIX5/ERBB4/ADIPOQ/NKX2-5/APOD/ELANE/ANG",44

4/SLC30A8/FBP1/AQP2/MT1E/NLGN1/FABP4/FOS/CD14/JUNB/FGG/FGA/FGB/FIBIN/NQO1/PENK/M

'FZD2/SOX2/TSKU/ROR1/GABRA5/HMX3/CEBPD",42

'OQ/FFAR3/ADRB3/EMP2/GCGR",37

B1/LUM/ADCYAP1/XCL1/TSLP/PANX3/HMHB1/APOA2/RUNX1/SPON2/AIRE/TLR3/SERPINB7/CLEC4E/
LMNA/TGFBR2/CITED2/PI16/TBX20/SHH/FOXC2/IRX3/ERBB4/NKX2-5/WT1/NRAP",45
.CL9/ADCYAP1/SYPL2/XCL1/ACKR3/AGTR1/SNCA/GPR174/JPH2/THY1/SLC30A2/S100A9/ADORA1/F2F

YAP1/RXRG/CRABP2/DLX1/DAAM2/TPBG/NTRK2/NKX6-2/LGI4/SEMA3D/THY1/CHODL/IL34/SHH/GB

-HAS2/FGG/FGA/FGB/TACSTD2/CSF1/VWC2/APOD/S100A10/VIT/EMP2",41
.5H/RBP4/CYP11A1/SNCA/STAR/APOA2/CYP11B1/DHRS3/ALDH1A1/LIPC/PCSK9/SDR16C5/SPTLC3/P
C2/ERBB4/NKX2-5/TACSTD2/SHC4",40
RG1/CCL11/EGR3/PRKD1/C5AR1/ANG/APELA",40

ATS2/SEMA3D/RUNX1/TGFBR2/NPY1R/CITED2/PI16/TBX20/ISLR2/IGF2/AR/PRL/FOXC2/MYOZ1/ERBE
SS1/SERPINF1/HMGCS2/ANXA1/AGT/MMP13/LHCGR/CYP1B1/CYP11A1/RAB13/AGTR1/AHSG/IGFBP

'TGFBR2/PITX2/NPY1R/CITED2/TBX20/SHH/TMEM100/HAS2/FOXC2/FZD2/NKX2-5",45

1/PLIN5",35

'ASS1/NMUR2/POSTN/HMGCS2/GATA4/CYP1B1/TPH2/SSTR1/MYOC/PMAIP1/SFRP2/NR4A2/WNT9

.D14/HAS2/CCL11/SPHK1/ADIPOQ/CCL13/SLC2A4/MBP/TDGF1/CCL23/CCL16/CCL18/CCL14",44
'RKD1/CSF1/NTF3/S100A14/FGF16/C5AR1/ELANE/MMP28",41

IL6/KLF4/XCL1/NFKBIZ/AGTR1/AHSG/SNCA/OSMR/TSLP/PTGES/MMP3/ADAMTS12/S100A9/ADORA1

KRB2/DRD5/ADRA1B/FGG/FGA/FGB/ADRA1D/P2RY2/FOXC2/HTR1A/SLC2A4/ADRB3/HRH1/SLC6A17'
DRD5/FOS/GATM/CCL11/CEBPB/FOSL1/SLC2A4/NTF3/GABRA5/RELN/MME/HRH1/C5AR1/PRRT1/GRII

LA/MT1M/AQP1",36

'ELA/NOX5",34

3RINP2/KCTD11",36
HMX3/CEBPD",36

D2/PI16/TBX20/FOXC2/IRX3/ERBB4/NKX2-5/WT1/NRAP",41

3/FGA/FGB/ADRA1D/HSPB7/DES/IRX3/HTR1A/NKX2-5/HRH1/MYL4/APELA/FXYD1",44

1/APOE/CRP/NGF/MTNR1B/HTR1B/AGT/HTR2B/CRABP2/AGTR1/DAAM2/DOCK5/GSN/HTR7/SEMA3

'P11A1/RAB13/AGTR1/AHSG/IGFBP1/NR4A2/TIMP4/CYP11B1/KLF15/OTOP1/FBP1/GJB2/VWA2/FBN

:N/ABCA12/AGTR1/SNCA/VIP/CHRNA3/CRH/PTGES/SYT8/GJA1/NEUROD1/ADORA1/SLC30A8/GALR1,
L6/THBS1/EMILIN1/XCL1/NFKBIZ/AGTR1/SNCA/OSMR/TSLP/TPBG/IL34/S100A9/TLR3/MBL2/CX3CR1
DAMTS1/ADAMTS3/MMP14/C1R/TMPRSS3/CAPN13/PRSS12/SHH/HTRA1/MMP10/KLK1/KLK6/KLK1:

IP2/ADAMTS1/CREB3L1/RUNX1/S100A1/TGFBR2/TLR3/ANGPTL4/CX3CR1/CXCL8/LRG1/ANGPTL7/CC

IP2/APELA",37

3",31

OSL1/SLC2A4/NTF3/GABRA5/RELN/MME/HRH1/PRRT1/GRIN2B",44

IUR2/POSTN/HMGCS2/GATA4/CYP1B1/TPH2/SSTR1/PMAIP1/SFRP2/WNT9B/ATF3/DAPL1/TGFBR2/A
'ADORA1/FABP1/SLC6A18/FABP7/FOLR2/SLC6A5/CRABP1/BDKRB2/FABP4/LRRC8E/AGXT/SLC16A11/
Q/NTF3/RELN/TDGF1",35

3PC3/RSPO2/LATS2/DKK2/FZD7/FZD1/KLF15/SHH/NXN/IGFBP6/SOSTDC1/SHISA2/SOX2/TSKU/NKX2-
/CREB3L1/RUNX1/S100A1/TGFBR2/TLR3/ANGPTL4/CX3CR1/CXCL8/LRG1/CCL11/PRL/SPHK1/FOXC2/

/AQP1/APELA",34

3KD1/C5AR1/AQP1/APELA",34

YP21A2",33

RN/IFNA21/YAP1/CXCL9/IFITM3/XCL1/ACKR3/OSMR/TSLP/IL34/IL17RE/CXCL3/CXCL1/OTOP1/AXL/C

3B/CITED2/COL1A2/HTRA1/FBN1/CX3CR1/COL3A1/FOS/HTRA3/LRG1/WFIKK2/CIDEA/PENK/VEPH1/

.1A2/EVPL/COL3A1/KRT8/KRT4/SOSTDC1/ETV4/KRT79/AKR1C3/LIPN/COL5A2",47

/KLK13/PCSK9/FGG/FGA/FGB/GAS1/ANXA2/TMPRSS2/MME/S100A10/HP/HPR/SPON1",49

HH/RET/ISLR2/CX3CR1/HAS2/FGG/FGA/FGB/HAP1/ADIPOQ/RELN/MME/S100A10/NEFL",47

PHK1/ADIPOQ/CCL13/SLC2A4/TDGF1/CCL23/CCL16/CCL18/CCL14",39

3X3-1/FGG/FGA/FGB/HTR1A/ADIPOQ/FOXL2/FAM3B/FFAR3/FFAR4",46

3DNF/AR/FGG/FGA/FGB/MAL",38

/AP2/APELA",37

:RABP1/PLIN1/ACOX2/CYP4F11/LPL/PNLIP/SPHK1/CIDEA/PNPLA1/ADIPOQ/CYP4F3/PLA2G2A/LIPI/AK

P6/EPHX1/REN/SNCA/SFRP2/GLYAT/CCNO/NAT2/TIMP4/FZD1/APOA2/NEUROD1/TGFBR2/TLR3/FBP

ACSM2A/LIPI/AKR1C3/AKR1C4/CES1/TECRL",37

2/HTRA1/FBN1/CX3CR1/COL3A1/FOS/HTRA3/LRG1/WFIKKN2/CIDEA/PENK/VEPH1/GDF10",42

31/EPHX1/SNCA/PTGES/PLA2G4D/HPGDS/FABP1/CRYL1/LIPC/CYP2S1/ACOX2/TNXB/CYP4F11/LPL/AC

2/CIDEA/GDF3/VWC2/VEPH1",27

ATS2/NR4A2/DKK2/FZD7/FZD1/WNT9B/SHH/IGFBP6/SOSTDC1/FZD2/SOX2/NKX2-5/WNT7B/SHISA6/

IG4/FZD7/MMP14/RUNX1/SHH/B4GALNT2/FAM107A/FGG/CEBPB/LGALS7B/ADIPOQ/TACSTD2/APOI

/TPBG/RSPO3/EGFR/IGFBP1/GPC3/RSPO2/LATS2/NR4A2/DKK2/FZD7/FZD1/WNT9B/KLF15/SHH/NXN
P1L2/CSPG4/BTC/ERBB4/ADIPOQ/SOCS3/NTF3/RELN/TDGF1",42

TS2/DKK2/FZD7/FZD1/SHH/IGFBP6/SOSTDC1/SOX2/NKX2-5/SHISA6/TPBGL",42

NTRK2/NKX6-2/SEMA3D/THY1/CHODL/IL34/SHH/ISLR2/CX3CR1/GPR37L1/CCL11/HES3/HAP1/F2/REL

HMT/STAR/PTGES/HPGDS/ALDH1A1/LIPC/GATM/CYP4F11/AGXT/LPL/ACSM5/ACSM2A/LIPI/AKR1C3,

/FGB/HTR1A/ADIPOQ/FOXL2/FAM3B/FFAR3/FFAR4",44

HMT/STAR/PTGES/HPGDS/ALDH1A1/LIPC/GATM/CYP4F11/AGXT/LPL/ACSM5/ACSM2A/LIPI/AKR1C3/.

CR1C3/MT1F/MT1A/MT1M/AQP1",37

B13/DAAM2/DOCK5/DOCK1/ACTG2/FSTL1/TGFBR2/ATOH8/HAS2/FOXC2/EGR3/TACSTD2/PRKD1/FG
PO3/EGFR/IGFBP1/GPC3/RSP02/LATS2/NR4A2/DKK2/FZD7/FZD1/WNT9B/KLF15/SHH/NXN/IGFBP6/

/GDNF/PCSK9/FOS/CEBPB/SNCG/NUPR1/NQO1/CSF1/NTF3/GABRA5/GRIN2B/NEFL",47

/XCL1/ABCA12/NFKBIZ/MEGF10/THY1/VSIG4/RUNX1/PDPN/TGFBR2/SPTA1/CITED2/SHH/B4GALNT2/

D/CSF1/APOD/S100A10/ITGBL1/EMP2",38

CX3CR1/GDNF/PCSK9/FOS/CEBPB/SNCG/NUPR1/NQO1/CSF1/NTF3/GABRA5/DIO3/GRIN2B/NEFL",51

TR1/SNCA/GPR174/JPH2/THY1/ADORA1/F2RL2/GALR1/TRPV3/CX3CR1/BDKRB2/DRD5/ADRA1B/FPR:
I/FZD1/CLDN14/CLDN1/IGFN1/CLDN19/MICALL2/GJB2/FAM107A/GJB1/NLGN1/RHOD/UGT8/LRRN1/

IX9/CNTN4/BOC/NTRK2/NR4A2/SEMA3D/THY1/CHODL/ISL2/S100B/SHH/GBX1/OTX2/RET/ISLR2/GB>

/FOLR2/AQP2/AXL/FAM107A/PCSK9/FOS/FOXA3/LPL/FOSL1/PENK/PRKD1/AKR1C3/KANK2/GCGR/AC310/ADH4/AKR1C4/CES1/PLIN5",35

XCL8/CD14/CEBPB/DEFB124/ARID5A/LILRA2",37

OXL2/FFAR3/FFAR4",37

31/SNCA/GPR174/JPH2/THY1/ADORA1/F2RL2/GALR1/TRPV3/CX3CR1/BDKRB2/DRD5/ADRA1B/FPR1/

/PMAIP1/ACKR3/SFRP2/NACC2/ITPRIP/NR4A2/CREB3L1/LMNA/ATF3/S100A9/RET/NKX3-1/CX3CR1/14/NTRK2/PTGES/SLC5A12/GJA1/ADORA1/SLC2A2/FOLR2/SLC6A5/SLC22A11/BDKRB2/LRRC8E/AGXT13/DAAM2/DOCK5/DOCK1/FSTL1/TGFBR2/ATOH8/HAS2/FOXC2/EGR3/TACSTD2/PRKD1/FGF16/S100

GFRA/KLF4/THBS1/SERPING1/SEMA3D/VSIG4/CD109/NBL1/ADORA1/OTOP1/CLDN19/HTRA1/FGG/F

VFDC13/RNASE3/FGA/FGB/CEBPB/WFDC11/F2/DEFB124/PRKD1/ISG15/DMBT1/PLA2G2A/S100A14/C

',34

'GDF3/FFAR4/CEBPD/GDF10",37

\PCS/SPINK5/ANXA1/THBS1/EMILIN1/XCL1/SERPING1/THY1/VSIG4/NBL1/APOA2/RUNX1/ADORA1/C
AB13/DAAM2/DOCK5/DOCK1/FSTL1/TGFBR2/ATOH8/HAS2/FOXC2/EGR3/TACSTD2/PRKD1/FGF16/S:

',23

D1B/AZGP1/ASGR2/SLAMF9/TGFBR2/ANXA5/FOLR2/CLEC4E/ANPEP/SLC22A11/SCARA5/CX3CR1/PCS
KLF15/OTOP1/FBP1/GJB2/VWA2/FBN1/IGF2/RAB31/PCSK9/LPL/FOXC2/UMODL1/ADIPOQ/SLC2A4/S
/DIO3/NEFL",37
'1/CHODL/ISL2/S100B/SHH/GBX1/OTX2/RET/ISLR2/GBX2/GDNF/LAMB2/SLITRK4/TSKU/SLITRK2/CCK/

RA1/THY1/IL34/ADORA1/RET/IGF2/AXL/AFAP1L2/CSPG4/BTC/ERBB4/ADIPOQ/SOCS3/ROR1/NTF3/RE

32/SLC6A5/BDKRB2/LRRC8E/AGXT/SLC16A11/SLC36A2/PLA2G2A/SLC6A17/AKR1C4/CES1",41
RRN1/SLITRK4/SLITRK2/THBS2/RELN/IL1RAP/MME/NEFL",40
33
P/SCN2B/JPH2/KCNE4/THY1/KCNS2/LRRC38/LRRC52/ADORA1/RRAD/TRPV3/PCSK9/SLN/HAP1/DPP1

THY1/ADORA1/F2RL2/GALR1/TRPV3/CX3CR1/BDKRB2/ADORA1B/FPR1/ADRA1D/SAA1/CCR9/HAP1/CH

LILRA2",34
3PR37L1/ADRA1B/MRAP/FPR1/ADRA1D/CALCB/MC5R/HTR1A/FFAR3/ADRB3/S1PR3/GCGR",37
V2B/NEFL",36

/THY1/IL34/ADORA1/RET/IGF2/AXL/AFAP1L2/CSPG4/BTC/ERBB4/ADIPOQ/SOCS3/ROR1/NTF3/RELN/

FGG/FGA/FGB/PRL/P2RY2/FOXL2/FFAR4/ANG/AQP1",43

31/WFIKK2/CIDEA/VEPH1/GDF10",32

3AB31/CD14/SPHK1/ADIPOQ/COLEC10/PRTN3/ELANE/C4B/C4A",44

/HAP1/PDZK1/F2/NKX2-5/RELN/LILRA2/FXYD1",40

Y1/KCNS2/KCNJ15/CLIC6/LRRC38/LRRC52/KCNK5/RRAD/KCNJ4/PCSK9/NLGN1/SLN/KCNG3/KCND3/H
P1",32
32

/CD14/CEBPB/DEFB124/ARID5A/LILRA2",38

/FBN1/IGF2/RAB31/PCSK9/LPL/FOXC2/UMODL1/ADIPOQ/SLC2A4/SOCS3/FFAR3/GCGR",42

;/GALR1/ANPEP/PPIC/NLGN1/GPR37L1/CD14/MME/ANG/GCGR/HLA-DPB1/TMEM158/PPIAL4D/GRIN
IP1/IGFBP4/SNCA/BHMT/STAR/FABP1/FBP1/NNMT/IGF2/NUPR1/ADIPOQ/PHLDA2/AKR1C3/HRH1/C
,32
RB2/GDNF/AR/FGG/FGA/FGB",35

2/LRRC38/LRRC52/RRAD/PCSK9/NLGN1/SLN/HAP1/PDZK1/DPP10/F2/KCNIP1/PRKD1/SHISA6/RELN/P

INA/ADORA1/PI16/ADRA1B/SLN/SPHK1/NKX2-5",37
AR1/CRLF2/LILRA2",35

CLDN1/IGFN1/TGFBR2/CLDN19/RET/NLGN1/LGALS7B/ADIPOQ/CLDN7/SLITRK2/IL1RAP/MBP",40

2RY12/EMX2/HAP1/ERBB4/SOX2/TSKU/SOX1/TAL2/WNT7B/RELN/POU3F3/HSD3B1/HSD3B2/AQP1/I

CCL11/CSF1/WNT7B/OSTN",35

ICA/EGFR/NTRK2/FCGR1A/IL34/ADORA1/TGFBR2/TLR3/RET/IGF2/AXL/AFAP1L2/P2RY12/PIFO/BTC/E

IA1/THY1/PDPN/CLDN1/SLC2A2/FABP1/F2RL2/SLC6A18/AQP2/SLC22A11/MAL/CSPG4/SLC6A19/PDZI
/FGA/FGB/FOXL2/FFAR4/ANG",39

BD2B/MMP28",31

ITLN1/COLEC10/KLRC3/C4B/MGAM/CLEC5A/CLEC19A",40

L/PTX3/AXL/NLGN1/HAS2/KCNA2/EGR3/ADIPOQ/GDF10",41

OTOP1/KCNK5/STEAP1/AQP7/GJB2/AQP2/TTYH1/TRPV3/KCNJ4/GJB1/LRRC8E/KCNG3/GRIK1/KCND3,

J15/CLIC6/LRRC38/LRRC52/OTOP1/KCNK5/STEAP1/AQP7/GJB2/AQP2/TTYH1/TRPV3/KCNJ4/GJB1/LR

PKZK1/ITLN1/SLC2A4/ANXA2/PRTN3/MME/S100A10/EMP2/TDGF1/FXYD1",45
G/FGA/FGB/EGR3/SOX2/ELANE/HLA-DPB1",40

'OLR1/PDZK1/ITLN1/SLC2A4/ANXA2/PRTN3/MME/S100A10/EMP2/TDGF1/FXYD1",45

'RKD1/AKR1C3/KANK2/GCGR",35
1M",35

3/MBL2/GJB2/AXL/ACOX2/GPR37L1/FOS/ANGPTL7/FOSL1/SPHK1/NQO1/ADIPOQ/PENK/PRKD1/APC

/CX3CR1/BDKRB2/ADRA1B/FPR1/ADRA1D/SAA1/CCR9/HAP1/CHRNA9/F2/PRKD1/FFAR4/C5AR1/S1P

/CD1A/CD1B/POM121L2/NPY1R/FOLR2/GALR1/ANPEP/PPIC/NLGN1/GPR37L1/CD14/MME/ANG/GC

M2",35

AM3B/FFAR3/FFAR4",39

/MYOCD/SFRP2/GJA1/SEMA3D/THY1/NBL1/ADORA1/CLDN19/CITED2/SHH/CX3CR1/COL3A1/PODN/

CITED2/TMEM100/IGF2/NXN/COL3A1/AR/TM4SF1/JUNB/CEBPB/FOSL1/PHLDA2/GDF3/SOCS3/MAFF,

A1/COL3A1/TMEM119/CSF1/POTEE/SERPINA3/LAMA2/POTEF/SIGLEC15/MBP",42

/EMILIN1/MYOCD/SFRP2/GJA1/THY1/NBL1/ADORA1/CLDN19/CITED2/SHH/CX3CR1/COL3A1/PODN/I

JA1/THY1/NBL1/ADORA1/CLDN19/CITED2/SHH/CX3CR1/COL3A1/PODN/MAPK15/ADIPOQ/TACSTD2/
AP1/PDZK1/SHISA6/RELN/PRRT1/SHISA9/FXYD1",36

I/HAP1/PDZK1/SHISA6/RELN/PRRT1/SHISA9/FXYD1",37

Y12/CXCL8/FPR1/CCR9/SPHK1/MYOZ1/FFAR4/HRH1/AQP1/GRIN2B",40
'P4F11/PHYHD1/NLRP11/CYP4F3/CYP27C1/AKR1C3/AKR1C4/CYP21A2",28

A2/SPON2/AZGP1/TLR3/MBL2/CX3CR1/COLEC10/FFAR3/ARID5A/IL27/MICA/KLRC3",45

IAP1/PDZK1/ADIPOQ/SHISA6/RELN/PRRT1/SHISA9/FXYD1",40

1",35

HY1/NBL1/ADORA1/CLDN19/CITED2/SHH/CX3CR1/COL3A1/PODN/MAPK15/ADIPOQ/TACSTD2/APOD
FC/SPHK1/FZD2/FFAR4/DMBT1/WNT7B/ELANE/HBA1/HLA-DPB1/HP",45

FO1E/CLDN14/MXRA8/S100A11/CLDN1/SLC2A2/CLDN19/STEAP1/MICALL2/AQP7/GJB2/HEPACAM/E'

/LPL/CIDEA/F2/PRKD1/CES1/PLIN5",42

0A2/EMP2/TDGF1",36

INK/FFAR3/PLA2G2A/KLRC3/LILRA2",37

-H/IGF2/CX3CR1/HAS2/CEBPB/OLR1/LGALS7B/EGR3/ELANE/HLA-DPB1/TARM1",46

IA18/AQP2/SLC22A11/MAL/CSPG4/SLC6A19/PDZK1/UMODL1/EMP2/AQP1/TDGF1/MGAM/FXYD1",4

.RRC8E/SPHK1/NQO1/PENK/SLC2A4/PRKD1/AKR1C3/AQP1",41

.C6A19/PDZK1/EPSS8L2/KCNA2/ITLN1/FFAR4/GABRA5/SHISA6/CNGA1/CYS1/SHISA9/AQP1",43
FRA1/THY1/HTR5A/TMPRSS3/S100B/BRINP3/ADORA1/SERPINI1/RET/TMEM100/CX3CR1/KCND3/SN

EC15/MBP",35

,32

GF2/HAS2/CEBPB/LGALS7B/EGR3/ELANE/HLA-DPB1/TARM1",42

TM2/IFIT1/ELANE/CLEC5A",36

IRNA9/CATSPER1/KCNA2/KCNIP1/KCNA4/GABRA5/TMC3/CNGA1/KCNU1/AQP1/KCNJ18/GRIN2B",43

;/PRKD1/FGF16/EMP2/TDGF1",36

;/MBL2/CX3CR1/F2/C1S/S100A13/ARID5A/ELANE/MICA/CFI/KLRC3/EMP2/HLA-DPB1/C4B/C4A",52

VT1/NRAP",35

31

IO/PI16/SHH/IGF2/WFIKKN2/IRX3/MYOZ1/NKX2-5/TMEM119/WT1/NRAP",45

'GSN/SYT8/JPH2/THY1/FZD7/MYO1E/APOA2/PLA2G4D/FABP1/ANXA5/AXL/STXBP6/PXDC1/FRMPD4,

'KCNJ4/LRRC8E/KCNG3/GRIK1/KCND3/CHRNA9/CATSPER1/KCNA2/KCNIP1/KCNA4/ANXA2/OTOP2/G.

F3/NEUROD1/PITX2/GFI1B/FOS/SDR16C5/JUNB/CEBPB/FOSL1/SIX5/ZFP42/SOX2/NKX2-5/FIGLA/MAI

1/DRD5/NLGN1/DLGAP1/GRIK1/SNCG/HAP1/ADIPOQ/NTF3/SHISA6/RELN/MME/LAMA2/HRH1/PRRT

NLGN1/DLGAP1/GRIK1/SNCG/HAP1/ADIPOQ/NTF3/SHISA6/RELN/MME/LAMA2/HRH1/PRRT1/SHISA6/SEMA3D/MMP14/CXCL16/S100A9/TGFBR2/PI16/FBP1/ISLR2/FAM107A/LAMB2/SPHK1/F2/FOXL2/

Q/CSF1/IL27",34

ICA/VIP/CRH/BAG3/KCNE4/GJA1/APOA2/ADORA1/SHH/RRAD/STXBP6/PCSK9/SLN/ADIPOQ/ANXA2/F

QP1",34

QP1",34

1P14/CXCL16/S100A9/PI16/FBP1/ISLR2/FAM107A/SPHK1/F2/WT1/OSTN",46

VC2/SHISA6/CNGA1/SHISA9/GRIN2B",36

TLR3/IGF2/AFAP1L2/BTC/ADIPOQ/CSF1/NTF3/RELN/ELANE/EMP2/ANG/TDGF1",44

IC3/MGP/COL12A1/SMOC2/LOX/SPARC/THBS4/HRG/EFEMP1/FN1/ANGPTL1/NID1/F3/SERPINC1/APC
APLN1/MEPE/ABI3BP/ACAN/COL6A3/FBLN2/COL1A2/FBN1/MFAP4/TNXB/COL3A1/COL22A1/FGG/FC
.3/CYP1B1/EMILIN1/LOXL4/LUM/FBLN5/DPT/HMCN1/COL8A1/SFRP2/ADAMTS19/SERPINH1/MMP3/
IP13/CYP1B1/EMILIN1/LOXL4/LUM/FBLN5/DPT/HMCN1/COL8A1/SFRP2/ADAMTS19/SERPINH1/MMF
MMP7/MMP13/CYP1B1/EMILIN1/LOXL4/LUM/FBLN5/DPT/HMCN1/COL8A1/SFRP2/ADAMTS19/SERPI
J3/COL8A1/AHSG/IGFBP1/GPC3/SERPING1/SERPINH1/P4HA3/PRSS23/MEPE/APOA2/MXRA8/COL6A3
NGF/CGA/AGT/IL6/IL1RN/IFNA21/CXCL9/FGF7/OSGIN1/ADCYAP1/XCL1/SFRP2/TSLP/CXCL14/VIP/CRH
3/ACAN/FSTL1/TGFBR2/PCOLCE2/CLEC3B/SHH/LIPC/FBN1/EVA1C/TNXB/CXCL8/SAA1/LPL/F2/BGN/A
;PYY/LGALS3/NGF/CGA/AGT/IL6/IL1RN/IFNA21/CXCL9/FGF7/OSGIN1/ADCYAP1/XCL1/SFRP2/TSLP/C
A4/NR5A1/FOXF2/TTPA/LHCGR/CYP1B1/RBP4/DHH/MYOC/LHX9/RAB13/REN/OSR1/SFRP2/RSPO3,
4/NR5A1/FOXF2/TTPA/LHCGR/CYP1B1/RBP4/DHH/MYOC/LHX9/RAB13/REN/OSR1/SFRP2/RSPO3/E

/OSR1/AGTR1/GPC3/FREM2/GFRA1/ADAMTS1/MYO1E/WNT9B/NFIA/KLF15/SHH/OSR2/RET/FBN1/S
P2/GPC3/ZIC3/NBL1/NEUROD1/EN1/PITX2/CITED2/TBX20/SHH/OTX2/NKX3-1/GBX2/GDNF/AR/EMX
2/PRELP/LIPI/ELANE/LPA/ANG/CCL23",54

I8/APOE/COL5A1/APCS/NOTCH2/PDGFRA/ANXA1/TEC/IL6/GATA4/YAP1/THBS1/MYOF/SERPING1/RH
1E/WNT9B/NFIA/KLF15/SHH/OSR2/RET/FBN1/SERPINB7/NKX3-1/AQP2/GDNF/PCSK9/EMX2/IRX2/H
J2/DHH/OSR1/AHSG/SFRP2/EGFR/GPC3/RSPO2/ADAMTS12/GJA1/BMP3/MMP14/FZD1/CREB3L1/RU
2/PROS1/SERPINA11/SPOCK3/SERPINA3/SERPINA1/SERPINB2/LPA/SERPINB11/COL28A1/C4B/C4A",5

ST/LRP4/GATA4/CFC1/LMX1B/LBX1/FOXN4/OSR1/DLX1/SFRP2/DAAM2/GPC3/GJA1/ZIC1/ZIC3/NBL1,
AL/WFIKK2/CST6/UMODL1/WFDC11/ANXA2/PROS1/SERPINA11/SPOCK3/SERPINA3/SERPINA1/SERF
RBP4/FBN2/LRIG3/FOXN4/OSR1/RSPO3/EGFR/GJA1/ZIC1/ZIC3/MMP14/WNT9B/PLCD3/NEUROD1/EI
YAP1/CRABP2/REN/ABCA12/AGTR1/VIP/CRH/CYP17A1/GJA1/CHST9/UGT2B4/CYP11B1/DHRS3/NEU
P1/PI16/SERPINB7/WFDC13/CST2/CST1/WFIKK2/CST6/WFDC11/ANXA2/PROS1/SERPINA11/SPOCK
P1/SERPINB7/WFDC13/CST2/CST1/WFIKK2/CST6/WFDC11/ANXA2/PROS1/SERPINA11/SPOCK3/SEI
A11/SPOCK3/SERPINA3/SERPINA1/SERPINB2/LPA/SERPINB11/COL28A1/C4B/C4A",53

HX8/PTX3/TLR3/CITED2/SHH/NKX3-1/AXL/AR/CEBPB/DMRT2/NUPR1/IRX5/UMODL1/ZFP42/FOXL2/V

'SERPINA11/SPOCK3/SERPINA3/SERPINA1/SERPINB2/LPA/SERPINB11/COL28A1/C4B/C4A",54
:1/ADH1A/AKR1C3/ADH1B/UGT2B15/DIO3/AKR1B10/ADH4/AKR1C4/DDO/HSD3B1/HSD3B2/CYP21A
MMP14/WNT9B/NEUROD1/TGFBR2/OTOP1/CITED2/TBX20/SHH/OSR2/FBN1/GBX2/CHRNA9/FOXC2,
'FBN1/SERPINB7/NKX3-1/AQP2/GDNF/PCSK9/IRX2/HAS2/LAMB2/FOXC2/IRX3/ERBB4/ADIPOQ/TACS
IH1/CD109/TIMP4/APOA2/WFDC8/LCN1/COL6A3/SERPINI1/FABP1/PTX3/PI16/SERPINB7/ANGPTL4/V
R2/CITED2/OSR2/COL3A1/HAS2/FOXC2/IRX5/TSKU/TMEM119/HOXA4/SP5/HOXB7",57

-1/AR/CEBPB/NUPR1/IRX5/UMODL1/ZFP42/FOXL2/WT1/AKR1C3/ANG/HOXA10",57

IL1/ZFP42/FOXL2/WT1/AKR1C3/ANG/HOXA10",56

GTR1/SFRP2/VIP/EGFR/GPC3/FZD7/CD109/MMP14/CLDN1/FABP7/SHH/OSR2/HTRA1/NKX3-1/IGF2/I

1/S100A14/PRTN3/HRH1/C5AR1/MMP28/CCL23/CCL16/CCL18/CCL14",56

ERPINI1/FABP1/PI16/SHH/SERPINB7/WFDC13/CST2/CST1/WFIKK2/CST6/WFDC11/F2/GAS1/ANXA2,

.8/GPR183/CCL11/SAA1/CCR9/EGR3/DEFB124/CCL13/PRKD1/CSF1/S100A14/FGF16/HRH1/C5AR1/M

INH1/CD109/TIMP4/WFDC8/LCN1/S100A9/COL6A3/SERPINI1/FABP1/PCOLCE2/PI16/SERPINB7/NKX3-1,49

'CRH/PMP2/PTGES/ABCA9/ABCA6/ABCA10/APOA2/FABP1/FABP7/LIPC/CRABP1/GALR1/NKX3-1/BDK
1/HBA1/HBM/GPX3/HBD/INMT/GSTA1/HP/NEFL",56

OXB7",47

9/ADORA1/CXCL3/CXCL1/RET/CX3CR1/P2RY12/CXCL8/GPR183/CCL11/SAA1/UMODL1/DEFB124/CCL1/TDGF1/HOXB7".⁴⁹

:/TNXB/CXCL8/SAA1/LPL/F2/ADAMTSL5/THBS2/PRELP/LIPI/ELANE/LPA/ANG/CCL23",59

ABCA6/ABCA10/APOA2/FABP1/FABP7/LIPC/CRABP1/GALR1/NKX3-1/BDKRB2/PCSK9/FABP4/PNLIP/A

="GA/FGB/WFDC11/F2/CCL13/C1S/COLEC10/DMBT1/PRTN3/ELANE/CFI/ANG/C4B/C4A".64

AS1/HOXC10/SOX2/SOX1/NKX2-5/GDF3/WT1/WNT7B",57

3R2/OSR2/SERPINB7/COL3A1/FOXC2/UMODL1/BGN/TSKU/CSF1/WT1/WNT7B/ARID5A",56

3P2/GPC3/LATS2/BMP3/CD109/FZD1/NBL1/FSTL1/TGFR2/CITED2/TBX20/SHH/COL1A2/HTRA1/FBN
 3/CD109/FZD1/CREB3L1/NBL1/FSTL1/CITED2/TBX20/OTX2/HTRA1/FBN1/HTRA3/LRG1/SOSTDC1/WF
 ./WFDC8/LCN1/S100A9/COL6A3/SERPINI1/FABP1/SERPINB7/NKX3-1/WFDC13/CST2/CST1/WFIKK2/

I2/GJA1/FZD7/CSRP1/RUNX1/LMNA/ATF3/TGFB2/CITED2/PI16/TBX20/SHH/IGF2/COL3A1/VAMP5/

/ANXA5/F2RL2/SHH/AQP2/AXL/COL3A1/P2RY12/HAS2/FGG/FGA/FGB/CYP4F11/PRL/SAA1/P2RY2/EF

JD1/IGFN1/TGFBR2/PITX2/CITED2/SHH/OSR2/RET/FBN1/P2RY12/COL8A2/ANGPTL7/LAMB2/FOXC2/
'D1/NBL1/FSTL1/TGFBR2/CITED2/TBX20/SHH/HTRA1/FBN1/HTRA3/LRG1/SOSTDC1/WFIKKN2/CIDEA

⁹K15/ANXA2/FFAR3/AKR1C4/CES1/AQP1",⁵³

JROD1/IGFN1/TGFBR2/PITX2/CITED2/SHH/OSR2/RET/FBN1/P2RY12/COL8A2/ANGPTL7/LAMB2/FOXO1/CTSC/CLC5A/GDF10".52

GFR/CRH/GJA1/ZIC3/AIRE/CLDN1/TGFBR2/PITX2/CITED2/SHH/NKX3-1/IGF2/AR/PCSK9/SOSTDC1/CCl

TRK2/FZD7/SH3RF2/IL34/ADORA1/TLR3/RET/IGF2/IGFBP6/AR/GPR183/GPR37L1/ADRA1B/FGG/FGA/
F2/COL3A1/VAMP5/FOS/DES/NUPR1/FOXC2/MYOZ1/EGR3/FZD2/NKX2-5/FOXL2/WT1/MAFF/LAMA:

VTX/ZIC1/NR4A2/ZIC3/CREB3L1/RUNX1/IRX6/NFIA/ATF3/NEUROD1/KLF15/TBX20/OSR2/OTX2/GFI1B
A4/TDGF1/HOXA10/HOXB7",48
23/CCL16/CCL18/CCL14",51
1/ANXA5/PI16/SERPINB7/ANGPTL4/WFDC13/SLN/CST2/CST1/WFIKKN2/CST6/UMODL1/MYOZ1/WFI

3L1/RUNX1/IRX6/NFIA/ATF3/NEUROD1/KLF15/TBX20/OSR2/OTX2/GFI1B/GBX2/AR/FOS/JUNB/CEBP

TGFB2/PITX2/CITED2/SHH/OSR2/RET/FBN1/COL8A2/ANGPTL7/LAMB2/FOXC2/SIX5/SOX2/TSKU/SO

.DN1/SHH/OSR2/HTRA1/NKX3-1/IGF2/ATOH8/AR/KRT4/HAS2/LRG1/CCL11/PRL/NUPR1/EGR3/SOX2/
RNA1/MYOC/MLIP/DOCK5/GSN/HTR7/SCN2B/KCNE4/GJA1/FBXO32/TRIM63/LMNA/ADORA1/KLF1

iBX2/GDNF/AR/IRX2/SOSTDC1/CCL11/FOXC2/IRX3/FZD2/NKX2-5/TACSTD2/CSF1/WT1/HOXB7",62

2/ROR1/RELN/C5AR1",57

IK/ANXA2/PROS1/SERPINA3/PRTN3/SERPINA1/ELANE/ORM2/ORM1/HP",61

9/ERBB4/ADIPOQ/CCL13/TNFAIP8L3/FFAR4/PLA2G2A/C5AR1/APELA/CCL23/CCL16/CCL18/CCL14",62

CL13/NPW/RTP5/WNT7B/S100A14/APELA/CCL23/CCL16/CCL18/CCL14",57
1/FOXL2/HMX3/DIO3/MFAP5/COL5A2",53

AR/FOS/FOSL1/FIBIN/ADIPOQ/WNT7B/AKR1C3/KANK2/MBP/TAT/HSD3B1/HSD3B2/AQP1/NEFL",61

./DAAM2/DOCK5/NTRK2/NKX6-2/DOCK1/SEMA3D/THY1/CHODL/IL34/TRIM58/SHH/RET/FBN1/ISLR2,

10/GBX2/GDNF/HAS2/BNC2/FOXC2/ERBB4/NKX2-5/WT1/S100A4",57

DIPOQ/CCL13/TNFAIP8L3/FFAR4/PLA2G2A/C5AR1/APELA/CCL23/CCL16/CCL18/CCL14",58
AP28",46

/AXL/CX3CR1/CXCL8/FOS/CD14/CEBPB/THBD/DEFB124/PENK/DMBT1/S100A14/ARID5A/C5AR1/ELAI
SR2/RET/FBN1/COL8A2/ANGPTL7/LAMB2/FOXC2/SIX5/TSKU/SOX1/FOXL2/WT1/WNT7B/DIO3",60
CL18/CCL14",46

VK/ANXA2/PROS1/SERPINA3/PRTN3/SERPINA1/ELANE/ORM2/ORM1/HP",59

ENK/ANXA2/PROS1/SERPINA3/PRTN3/SERPINA1/ELANE/ORM2/ORM1/HP",59

P11B1/SHH/LIPC/PCSK9/TSKU/AKR1C3/UGT2B15/AKR1C4/CES1/HSD3B1/HSD3B2/CYP21A2",58

IL8/FOS/CD14/CEBPB/THBD/PENK/S100A14/ARID5A/ELANE/LILRA2",58
/TGFB2/FBLN2/SPTA1/CITED2/SHH/RET/IGF2/P2RY12/HAS2/FGG/FGA/FGB/RHOD/SAA1/FOXC2/EG
,47

KRT8/KRT4/SOSTDC1/CST6/ETV4/GDF3/MAFF/KRT79/KRT14/AKR1C3/LIPN",60

/TNXB/COL3A1/HAS2/FGG/FGA/FGB/LAMB2/RHOD/TACSTD2/CSF1/VWC2/APOD/S100A10/ITGBL1/
2/SPHK1/CIDEA/F2/ADIPOQ/TNFAIP8L3/PRKD1/APOD/SERPINA3/AKR1C3/CES1/PLIN5",58

AM2/TPBG/GPC3/DOCK5/DOCK1/GJA1/SEMA3D/FSTL1/TGFB2/PITX2/SHH/RET/GBX2/GDNF/ATOH8

BDKRB2/GDNF/ADRA1B/KCND3/SNTB1/DES/SPHK1/NKX2-5/MYBPC1/MYL4/TPM2/FXYD1",59

.14",51

T1X/S100A16/AKR1C3/MBP/MT1F/TAT/MT1A/MT1M/AQP1",58

/AFAP1L2/AGPAT2/CD14/CEBPB/SAA1/LPL/SPHK1/DEFB124/ADIPOQ/FFAR3/ISG15/S100A13/IL1RAP,
RL2/SLC30A8/GALR1/TRPV3/CX3CR1/BDKRB2/DRD5/MT1E/ADRA1B/FPR1/ADRA1D/CCL11/SAA1/CCF
X1/ISLR2/CX3CR1/GBX2/NLGN1/GPR37L1/CCL11/HES3/HAP1/LRRN1/SLITRK4/F2/NCMAP/SLITRK2/TI
VLIP/SPHK1/TSKU/CYP27C1/ADH1A/AKR1C3/ADH1B/HRH1/AKR1B10/ADH4/AKR1C4/CES1/ADH1C",5

34/NKX2-5/CSF1/WT1/OSTN/DIO3",54
1/MMP3/GJA1/NR4A2/TIMP4/CYP11B1/KLF15/OTOP1/FBP1/GJB2/VWA2/FBN1/IGF2/RAB31/COL3A:

DB/ATF3/DAPL1/TGFBR2/ALB/FOLR2/AQP2/AXL/FAM107A/PCSK9/FOS/FOXA3/PRL/SLC6A19/LPL/FOS

.TLR3/FABP4/CEBPB/SAA1/LPL/NUPR1/SPHK1/METRNL/ADIPOQ/SOCS3/FFAR3/FFAR4/PLA2G2A/EL

",45
N2B",50

D/WNT9B/ADORA1/SPTA1/RET/ISLR2/CDC42EP5/BDKRB2/DRD5/ADRA1B/LRRC8E/FGG/FGA/FGB/AC

1/IGF2/RAB31/COL3A1/PCSK9/LPL/FOXC2/UMODL1/ADIPOQ/SLC2A4/SOCS3/FFAR3/GCGR/NEFL",60

/NKX3-1/OR51E2/GDNF/NLGN1/FGG/FGA/FGB/SNCG/KCNA2/HTR1A/ADIPOQ/FOXL2/FAM3B/FFAR3,
.P2RY12/CXCL8/FABP4/CEBPB/LPL/NUPR1/THBD/F2/DEFB124/PRKD1/CSF1/NTF3/FFAR3/PLA2G2A/!
1/KLK13/PCSK9/HTRA3/TPSAB1/NRIP3/F2/C1S/TMPRSS2/PRTN3/MME/MMP1/TPSB2/ELANE/LPA/CF

IL11/PRL/SPHK1/FOXC2/PRKD1/THBS2/C5AR1/EMP2/AQP1/APELA",54

LB/FOLR2/FAM107A/PCSK9/FOXA3/PRL/SLC6A19/LPL/NQO1/ADIPOQ/PENK/PRKD1/GDF3/AKR1C3/I
SLC6A19/SLC36A2/PLA2G2A/SLC6A17/FABP12/AKR1C4",50

5/SHISA6/APCDD1L/TPBGL/TRABD2B",52
PRKD1/THBS2/C5AR1/EMP2/AQP1/APELA",53

X3CR1/CXCL8/AGPAT2/CCL11/CCR9/SPHK1/ADIPOQ/CCL13/CSF1/IFITM2/IFNLR1/ISG15/IL1RAP/CRLF

GDF10",42

R1C3/AKR1B10/CES1/LIPN/LIPJ/PLIN5",50

'1/RET/NNMT/NKX3-1/CYP2S1/AGPAT2/FOS/EMX2/LPL/FOSL1/NQO1/ADIPOQ/UGT2B15/GSTA1",59

DIPOQ/ACSM5/ACSM2A/CYP4F3/LIPI/AKR1C3/ADH4/AKR1C4/CES1/TECRL/PLIN5/GSTA1",57

TPBGL",48

D/MBP/TARM1",47

I/IGFBP6/SOSTDC1/FZD2/SHISA2/SOX2/TSKU/NKX2-5/ROR1/WNT7B/SHISA6/APCDD1L/TPBGL/TRABI

.N/MME/MBP/NEFL",53

/AKR1C4/CES1/TECRL",48

AKR1C4/CES1/TECRL",48

F16/S100A2/KANK2/EMP2/TDGF1/APELA",53
SOSTDC1/FZD2/SHISA2/SOX2/TSKU/NKX2-5/ROR1/WNT7B/SHISA6/APCDD1L/TPBGL/TRABD2B",62

/IGF2/HAS2/FGG/FGA/FGB/CEBPB/LGALS7B/EGR3/ADIPOQ/SOX2/ELANE/MBP/HLA-DPB1/TARM1",6:

1/ADRA1D/CCL11/SAA1/CCR9/HAP1/CHRNA9/CALCB/F2/CCL13/PRKD1/FFAR4/S100A14/C5AR1/ELAI
/IRX3/ERBB4/SLITRK4/CLDN7/PKP3/SLITRK2/THBS2/APOD/IL1RAP/S100A10",58

2/GDNF/LAMB2/SLITRK4/TSKU/SLITRK2/CCK/RELN/APOD/LAMA2/S100A6/MBP/NEFL",64

2P1",46

'ADRA1D/CCL11/SAA1/CCR9/HAP1/CHRNA9/CALCB/F2/CCL13/PRKD1/FFAR4/C5AR1/ELANE/S1PR3/C

BDKRB2/GDNF/AR/FGG/FGA/FGB/MAL/NUPR1",52
/SLC2A14/SLC16A11/SLC22A10/SLC36A2/PLA2G2A/SLC6A17/AKR1C4/CES1",51
0A2/KANK2/EMP2/TDGF1/APELA",51

GA/FGB/SAA1/METRNL/MYOZ1/THBD/F2/ADIPOQ/PROS1/SOCS3/FFAR4/ISG15/ELANE/SERPINB2/M

5AR1/ELANE/PRB3/MICA/ANG/AQP1/HP",51

TOP1/TLR3/SHH/FBN1/AXL/CX3CR1/COL3A1/CEBPB/LGALS7B/ADIPOQ/ISG15/APOD/MICA/TARM1/
100A2/KANK2/EMP2/TDGF1",50

K9/NLGN1/CD14/FGG/FGA/FGB/CCR9/UMODL1/THBD/F2/SLC2A4/MICA/CRLF2/KLRC3/CD200R1L/C
OCS3/FFAR3/GCGR",50
/RELN/LAMA2/S100A6/MBP/NEFL",57

ELN/TDGF1",51

0/F2/KCNIP1/NKX2-5/PRKD1/NKAIN2/LILRA2/FXYD1",54

RNA9/CALCB/F2/PRKD1/FFAR4/C5AR1/S1PR3/GRIN2B",49

'TDGF1",51

-IAP1/PDZK1/CATSPER1/DPP10/KCNA2/F2/KCNIP1/KCNA4/PRKD1/SHISA6/RELN/PRRT1/KCNU1/SHIS,

Q2B",47

DES1/PLIN5/GCGR",47

RR1/SHISA9/FXYD1",48

NEFL",50

BB4/F2/ADIPOQ/TNFAIP8L3/PRKD1/CSF1/ROR1/NTF3/RELN/ELANE/EMP2/ANG/TDGF1",60

K1/UMODL1/INSC/C5AR1/EMP2/AQP1/TDGF1/MGAM/FXYD1",56

/CHRNA9/CATSPER1/KCNA2/KCNIP1/KCNA4/ANXA2/OTOP2/GABRA5/TMC3/GJB4/CNGA1/KCNU1/AI

.RC8E/KCNG3/GRIK1/KCND3/CHRNA9/CATSPER1/KCNA2/KCNIP1/KCNA4/ANXA2/OTOP2/GABRA5/TM

OD/AKR1C3/TAT/HBA1/GPX3/AQP1/HP",54

'R3/GRIN2B",43

3R/HLA-DPB1/TMEM158/PPIAL4D/GRIN2B",53

MAPK15/ADIPOQ/TACSTD2/APOD/SPOCK3/ELANE/MMP28",50

/FOXD3/WNT7B",49

MAPK15/ADIPOQ/TACSTD2/APOD/SPOCK3/MMP28",47

'APOD/SPOCK3/MMP28",46

/MMP28",44

VPL/VAMP5/STXBP6/GJB1/DES/KCNA2/MAPK15/CLDN7/ANXA2/PRKD1/PKP3/GJB4/NRAP/KIAA1210

ABRA5/TMC3/CNGA1/AQP1/NOX5/KCNJ18/FXYD1/GRIN2B",52

FF/BSX/ARID5A/ELANE/DMBX1/CEBPD/HOXA10",55

1/SHISA9/GRIN2B",48

3/GRIN2B",48
WT1/OSTN",53

PRKD1/FFAR4/OSTN/APOD/PRTN3",51

OA1/TGFB3/TGFB1/CLU/FMOD/PLG/ITIH5/COL10A1/SLPI/MATN4/NDP/F13A1/COL21A1/OMD/APOE,
3A/FGB/COL8A2/LAMB2/COL6A5/PODN/UMODL1/AMBN/VWA1/ADIPOQ/BGN/THBS2/THSD4/COL1.
'ADAMTS12/ABI3BP/ADAMTS1/ADAMTS3/ADAMTSL3/MMP14/MYO1E/CREB3L1/RUNX1/PDPN/OLFN
P3/ADAMTS12/ABI3BP/ADAMTS1/ADAMTS3/ADAMTSL3/MMP14/MYO1E/CREB3L1/RUNX1/PDPN/O
INH1/MMP3/ADAMTS12/ABI3BP/ADAMTS1/ADAMTS3/ADAMTSL3/MMP14/MYO1E/CREB3L1/RUNX:
3/FSTL1/ALB/GPX8/SHH/COL1A2/LIPC/FBN1/COL3A1/PCSK9/COL22A1/CRTAP/FGG/FGA/COL8A2/LA
4/BMP3/SEMA3D/IL34/NBL1/WNT9B/CXCL16/CXCL3/CXCL1/SHH/CMTM5/FBN1/IGF2/GDNF/CXCL8/
'ADAMTSL5/THBS2/PRELP/LIPI/SPOCK3/ELANE/LPA/VIT/ANG/CCL23",71
XCL14/VIP/CRH/BMP3/SEMA3D/IL34/NBL1/WNT9B/CXCL16/CXCL3/CXCL1/SHH/CMTM5/FBN1/IGF2,
/EGFR/GFRA1/GJA1/ADAMTS1/MMP14/WNT9B/PLCD3/LHX8/PTX3/TLR3/CITED2/SHH/GJB2/HTRA1/
GFR/GFRA1/GJA1/ADAMTS1/MMP14/WNT9B/PLCD3/LHX8/PTX3/TLR3/CITED2/SHH/GJB2/HTRA1/NI

;ERPINB7/NKX3-1/AQP2/GDNF/AR/PCSK9/EMX2/IRX2/HAS2/LAMB2/FOXC2/IRX3/ERBB4/ADIPOQ/TA
2/IRX2/SOSTDC1/DMRT2/HES3/PIFO/FOXC2/IRX3/HOXC10/SOX1/NKX2-5/GDF3/WT1/WNT7B/RELN,

IOC/FZD7/CD109/CSRP1/PDPN/CLDN1/TGFBR2/CLDN19/ANXA5/F2RL2/SHH/CHMP4C/AXL/EVPL/COI
AS2/LAMB2/FOXC2/IRX3/ERBB4/ADIPOQ/TACSTD2/WT1/WNT7B/MME/KANK2/POU3F3/HOXB7",75
INX1/DHRS3/CLEC3B/SGMS2/SHH/COL1A2/OSR2/CLEC3A/IGF2/JUNB/CEBPB/FOXC2/PENK/SOX2/TM
6

/NEUROD1/EN1/TGFBR2/PITX2/CITED2/TBX20/SHH/OTX2/NKX3-1/GBX2/GDNF/AR/EMX2/IRX2/SOST
PINB2/LPA/SERPINB11/COL28A1/C4B/C4A",62
N1/TGFBR2/OTOP1/PITX2/CITED2/TBX20/SHH/OSR2/FBN1/IGF2/GBX2/GDNF/CXCL8/JUNB/CEBPB/P
ROD1/ADORA1/CPA3/SHH/SLC30A8/ALDH1A1/CRABP1/GALR1/NKX3-1/CYP2S1/KLK6/SDR16C5/FGG
'3/SERPINA3/SERPINA1/SERPINB2/LPA/SERPINB11/COL28A1/C4B/AQP1/C4A",66
RPINA3/SERPINA1/SERPINB2/LPA/SERPINB11/COL28A1/C4B/AQP1/C4A",64

NT1/SYCP2/AKR1C3/ANG/HOXA10",68

2/ADH1C",59
/IRX5/FZD2/NKX2-5/FOXL2/HMX3/HOXA4/MFAP5/HOXB7",68
;TD2/WT1/WNT7B/MME/KANK2/POU3F3/HOXB7",69
NFDC13/CST2/CST1/WFIKKN2/CST6/WFDC11/ANXA2/PROS1/SERPINA11/SPOCK3/SERPINA3/SERPIN.

OR51E2/ATOH8/AR/KRT4/SDR16C5/HAS2/LRG1/COL8A2/CCL11/PRL/CEBPB/NUPR1/EGR3/SOX2/TAC

/PROS1/SERPINA11/SPOCK3/SERPINA3/SERPINA1/SERPINB2/LPA/SERPINB11/COL28A1/C4B/AQP1/C
IMP28/CCL23/CCL16/CCL18/CCL14",67

3-1/WFDC13/CST2/CST1/WFIKKN2/CST6/UMODL1/WFDC11/SOX2/ANXA2/FOX L2/PROS1/SERPINA11

.RB2/PCSK9/FABP4/LPL/PNLIP/CIDEA/ADIPOQ/TMEM30B/ANXA2/TNFAIP8L3/CIDE C/PLA2G2A/APOD

.13/CSF1/APOD/S100A14/PRTN3/HRH1/C5AR1/ELANE/MMP28/CCL23/CCL16/CCL18/CCL14",74

.DIPOQ/TMEM30B/ANXA2/TNFAIP8L3/CIDE C/PLA2G2A/APOD/FABP12/AKR1C4/LPA/CES1",74

1/TMEM100/COL3A1/ATOH8/FOS/HTRA3/LRG1/SOSTDC1/WFIKKN2/CIDEA/GDF3/FAM83G/VWC2/V
FIKKN2/CIDEA/SHISA2/GDF3/VWC2/FGF16/VEPH1",63
'CST6/WFDC11/SOX2/ANXA2/FOX L2/PROS1/SERPINA11/SPOCK3/SERPINA3/SERPINA1/SERPINB2/ME

FOS/NUPR1/FOXC2/IRX3/MYOZ1/ERBB4/NKX2-5/FOX L2/WT1/MAFF/NRAP",74

ERBB4/THBD/F2/PROS1/SERPINA1/SERPINB2/EMP2/AQP1",71

SIX5/SOX2/TSKU/SOX1/FOX L2/GDF3/WT1/WNT7B/DIO3/MFAP5/COL5A2",71
/GDF3/VWC2/VEPH1/GDF10",56

C2/SIX5/SOX2/TSKU/SOX1/FOX L2/GDF3/WT1/WNT7B/DIO3/MFAP5/COL5A2",71

.11/PRL/CEBPB/ERBB4/SOX2/NKX2-5/CSF1/WT1/WNT7B/BSX/TDGF1/HOXA10",76

/FGB/ADRA1D/CCL11/CSPG4/SPHK1/ERBB4/CCL13/SOX2/TNFAIP8L3/NTF3/FFAR4/WNT7B/PLA2G2A,
2",64

3/GBX2/AR/FOS/JUNB/CEBPB/DMRT2/FOSL1/ETV4/FOXC2/SIX5/IRX3/EGR3/HOXC10/SOX2/SOX1/NK

3C11/ANXA2/PROS1/SOCS3/SERPINA11/SPOCK3/SERPINA3/ANXA4/SERPINA1/SERPINB2/LPA/SERPIN

B/DMRT2/FOSL1/ETV4/FOXC2/SIX5/IRX3/EGR3/HOXC10/SOX2/SOX1/NKX2-5/FIGLA/FOXL2/WT1/MF

X1/FOXL2/GDF3/WT1/WNT7B/DIO3/MFAP5/COL5A2",69

TACSTD2/PRKD1/C5AR1/ANG/APELA",69

5/PI16/TBX20/BDKRB2/GDNF/ADRA1B/SLN/KCND3/GATM/SNTB1/DES/SPHK1/MYOZ1/NKX2-5/MYB

! /CX3CR1/GPR37L1/HAS2/FGG/FGA/FGB/CCL11/HES3/HAP1/F2/ADIPOQ/TACSTD2/RELN/MME/SIGLE

NE/C4B/LILRA2",63

R3/SOX2/CSF1/VWC2/ELANE/S100A10/VIT/EMP2/HLA-DPB1",71

VIT/EMP2",61

3/P2RY12/HAS2/FOXC2/ERBB4/EGR3/TACSTD2/PRKD1/FGF16/S100A2/KANK2/EMP2/TDGF1/APELA",

/ARID5A/IL27/C5AR1/ELANE/MBP/CRLF2/HLA-DPB1/ORM2/ORM1/LILRA2/NOX5/CLEC5A",71
R9/HAP1/CHRNA9/CALCB/F2/CCL13/PRKD1/FFAR4/MT1X/C5AR1/ELANE/MT1F/MT1A/MT1M/S1PR3,
HBS2/RELN/IL1RAP/MME/MBP/NEFL",67

8

1/PCSK9/LPL/FOXC2/UMODL1/ADIPOQ/SLC2A4/SOCS3/FFAR3/GCGR/NEFL",72

IL1/NQO1/ADIPOQ/PENK/PRKD1/GDF3/AKR1C3/KANK2/GCGR",70

ANE/CD200R1L",60

ORA1D/CCL11/P2RY2/FOXC2/HTR1A/WNT7B/ADRB3/HRH1/AQP1/NEFL",69

)

/FFAR4",65
S100A14/FGF16/C5AR1/KLRC3/LILRA2",64
I/HP/HPR/TRABD2B/MMP28",65

ANK2/GCGR",64

2/LILRA2/CCL23/CCL16/CCL18/CCL14",68

D2B",63

SRIN2B/CCL23/CCL14",61

IIICA/LILRA2/MMP28",58

MMP28",57

LEC19A",61

QP1/NOX5/KCNJ18/FXYD1/GRIN2B",63

AC3/GJB4/CNGA1/KCNU1/AQP1/NOX5/KCNJ18/FXYD1/GRIN2B",63

/FXYD1",60

/GDF15/COL5A1/LGALS3/MATN3/SERPINF1/ITGB4/MATN2/APCS/POSTN/ANXA1/AGT/TINAG/THBS1,4A1/COL4A5/PRELP/LAMA2/COL4A6/MFAP5/COL5A2/COL28A1/SPON1",77
VL2B/FBLN2/PTX3/COL1A2/MFAP4/MMP10/TNXB/COL3A1/COL22A1/CRTAP/HAS2/COL8A2/ANGPT1/LFML2B/FBLN2/PTX3/COL1A2/MFAP4/MMP10/TNXB/COL3A1/COL22A1/CRTAP/HAS2/COL8A2/ANG1/PDPN/OLFML2B/FBLN2/PTX3/COL1A2/MFAP4/MMP10/TNXB/COL3A1/COL22A1/CRTAP/HAS2/COLVB2/ADAMTSL1/AMBN/VWA1/F2/ARSI/PENK/ARSI/CSF1/COL14A1/WNT7B/COL4A5/SERPINA1/IL27,CCL11/PRL/BTC/CALCB/METRNL/AMBN/F2/ADIPOQ/PENK/CCL13/FAM3B/GDF3/CSF1/COLEC10/NTF

/GDNF/CXCL8/CCL11/PRL/BTC/CALCB/METRNL/AMBN/F2/ADIPOQ/PENK/CCL13/FAM3B/GDF3/CSF1,NKX3-1/IGF2/AXL/AR/GJB1/PLAC1/JUNB/CEBPB/FOSL1/NUPR1/IRX5/UMODL1/ZFP42/PHLDA2/FOXLKX3-1/IGF2/AXL/AR/GJB1/PLAC1/JUNB/CEBPB/FOSL1/NUPR1/IRX5/UMODL1/ZFP42/PHLDA2/FOXL2/

ACSTD2/WT1/WNT7B/MME/KANK2/POU3F3/HOXA10/HOXB7",83
/HOXA4/TDGF1/HOXA10/HOXB7",83

L3A1/P2RY12/DRD5/FGG/FGA/FGB/CYP4F11/SAA1/FOXC2/MYOZ1/THBD/F2/TSKU/PROS1/SERPINA1

MEM119/PRKD1/CSF1/FFAR4/ISG15/WNT7B/OSTN/COL5A2/CEBPD/TWIST2/CLEC5A/GDF10",90

TDC1/DMRT2/HES3/PIFO/FOXC2/IRX3/ERBB4/HOXC10/SOX1/NKX2-5/GDF3/WT1/WNT7B/RELN/HOX

IFO/CHRNA9/FOXC2/IRX5/FZD2/PHLDA2/NKX2-5/FOXL2/GDF3/SOCS3/WNT7B/HMX3/HOXA4/MFAP/FGA/FGB/PNLIP/HTR1A/ADIPOQ/FOXL2/FAM3B/FFAR3/FFAR4/CYP27C1/ADH1A/AKR1C3/ADH1B/U

A1/SERPINB2/LPA/SERPINB11/PLIN5/COL28A1/C4B/AQP1/C4A",77

STD2/PRKD1/C5AR1/ANG/APELA/NOX5",85

4A",72

/SPOCK3/SERPINA3/SERPINA1/SERPINB2/MBP/LPA/SERPINB11/COL28A1/C4B/AQP1/C4A/GRIN2B",8

/FABP12/AKR1C4/LPA/CES1/PLIN5",82

'EPH1/TDGF1/GDF10",70

3P/LPA/SERPINB11/COL28A1/C4B/AQP1/C4A/GRIN2B",77

/ADRB3/C5AR1/ELANE/TDGF1/APELA/CCL23/CCL16/CCL18/CCL14",83

X2-5/FIGLA/FOXL2/WT1/MAFF/SHOX/FOXD2/PAX9/CEBPD/HOXA10/HOXB7",81

JB11/COL28A1/C4B/C4A",72

MAFF/SHOX/FOXD2/PAX9/CEBPD/HOXA10/HOXB7",81

PC1/MYL4/TPM2/FXYD1",77

IC15/S100A10/MBP/S1PR3/NEFL",81

/GRIN2B/CCL23/CCL14",73

/EMILIN1/LOXL4/FBN2/LUM/FBLN5/COL6A2/FCN3/DPT/HMCN1/FLG/COL8A1/AHSG/SFRP2/HAPLN1

L7/LAMB2/TPSAB1/COL6A5/FOXC2/VWA1/WT1/THSD4/COL14A1/COL4A5/MMP1/ELANE/COL4A6/C
PTL7/LAMB2/TPSAB1/COL6A5/FOXC2/VWA1/WT1/THSD4/COL14A1/COL4A5/MMP1/ELANE/COL4A6
L8A2/ANGPTL7/LAMB2/TPSAB1/COL6A5/FOXC2/VWA1/WT1/THSD4/COL14A1/COL4A5/MMP1/ELAN
/COL4A6/COLGALT2/CES1/COL5A2/COL28A1/C4A/SPON1",93

3/CCK/WNT7B/OSTN/FGF16/IL27/TDGF1/APELA/MIA/GDF10/CCL23/CCL16/CCL18/CCL14",110

/COLEC10/NTF3/CCK/WNT7B/OSTN/FGF16/IL27/TDGF1/APELA/MIA/GDF10/CCL23/CCL16/CCL18/CC
.2/SOCS3/WT1/WNT7B/SYCP2/AKR1C3/MME/ANG/APELA/HOXA10",100

'SOCS3/WT1/WNT7B/SYCP2/AKR1C3/MME/ANG/APELA/HOXA10",100

./SERPINB2",92

CA4/TDGF1/HOXA10/HOXB7",95

5/APELA/HOXB7",92

IGT2B15/DIO3/AKR1B10/ADH4/AKR1C4/DDO/HSD3B1/HSD3B2/CYP21A2/ADH1C",98

/GPC3/SERPING1/SERPINH1/FREM2/ABI3BP/ADAMTS1/ADAMTS3/ACAN/LAD1/AZGP1/S100A9/COL6

OLGALT2/COL5A2/VIT/COL28A1/MIA/MMP28",97

i/COLGALT2/COL5A2/VIT/COL28A1/MIA/MMP28",97

IE/COL4A6/COLGALT2/COL5A2/VIT/COL28A1/MIA/MMP28",97

L14",110

5A3/FBLN2/CPA3/CLEC3B/ANXA5/SHH/COL1A2/MBL2/VWA2/HTRA1/FBN1/MFAP4/ANGPTL4/TNXB/

'COL3A1/FGG/FGA/FGB/COL8A2/ANGPTL7/LAMB2/TPSAB1/COL6A5/CSPG4/PODN/VWA1/F2/ADIPOI

Q/BGN/ANXA2/THBS2/THSD4/COL14A1/COL4A5/VWC2/PRELP/SERP