

SUPPLEMENTARY INFORMATION

Supplementary Table S2. GO analysis for the 289 overlapping genes based on DAVID database.

ID	Category	Term	Genes	PValue
1	BP	GO:0055114~oxidation reduction	HSD3B2, CYP24A1, ME3, SORD, ADHFE1, CYP2C44, PAH, HIBADH, MTHFD1, ALDH1A1, PECR, CYP4A12A, FMO1, MIOX, CYP2J11, HAAO, BC089597, ALDH4A1, BDH2, DAO, NQO1, BDH1, SARDH, HPD, NOX4, GCDH, SUOX, AKR1E1, QDPR, CMAH, HGD, FADS2, AKR1C21, PPARGC1A, TET1, DDO, NNT, HAO2, CYP2D26, HSD11B2, DIO1, RDH16, CYP4A14, STEAP1, DCXR, PRODH	1.18E-17
2	BP	GO:0055085~transmembrane transport	SLC12A6, SLC2A13, SLC5A2, SLC12A1, SLC5A1, SLC22A7, SLC22A8, RHBG, SLC7A9, AQP6, SLC26A4, SLC23A1, SLC16A7, SLC2A4, RHCg, SLC7A1, SLC25A10, SLC2A2, SLC16A9, SLC5A9, SLC13A2, SLC25A37, SLC13A3, SLC46A1, SLC5A12	1.28E-07
3	BP	GO:0005996~monosaccharide metabolic process	PDK2, SLC37A4, PDK4, CMAH, PGAM2, ADIPOQ, HIBADH, PCK1, GALM, G6PC, PPP1R1A, GYS2, MYC, DCXR, XYLb	1.25E-06
4	BP	GO:0006814~sodium ion transport	SLC12A6, SLC5A2, SLC23A1, SLC12A1, SLC5A1, SLC9A3, SLC5A9, SLC13A2, SLC13A3, SLC10A2, SLC4A4, SLC5A12	3.05E-06
5	BP	GO:0015758~glucose transport	SLC5A2, G6PC, SLC2A4, SLC2A2, SLC5A1, SLC37A4, STXBP4	3.22E-06
6	BP	GO:0008645~hexose transport	SLC5A2, G6PC, SLC2A4, SLC2A2, SLC5A1, SLC37A4, STXBP4	4.95E-06
7	BP	GO:0015749~monosaccharide transport	SLC5A2, G6PC, SLC2A4, SLC2A2, SLC5A1, SLC37A4, STXBP4	6.06E-06
8	BP	GO:0006006~glucose metabolic process	PDK2, G6PC, PPP1R1A, PDK4, SLC37A4, GYS2, PGAM2, ADIPOQ, MYC, DCXR, HIBADH, PCK1	9.16E-06
9	BP	GO:0006811~ion transport	SLC5A2, GABRB3, SLC9A3, SLC5A1, RHBG, KCNIP2, KCNJ1, SLC23A1, WNK4, CHRNA4, SLC4A1, SLC4A4, SLC12A6, SLC12A1, PTGER3, SLC22A7, SLC22A8, SLC10A2, SLC26A4, NNT, SLC16A7, RHCg, SLC5A9, SLC25A37, SLC13A2, SLC13A3, STEAP1, SLC5A12	1.00E-05
10	BP	GO:0019318~hexose metabolic process	PDK2, SLC37A4, PDK4, PGAM2, ADIPOQ, HIBADH, PCK1, G6PC, GALM, PPP1R1A, GYS2, MYC, DCXR	1.01E-05
11	BP	GO:0016054~organic acid catabolic process	MTHFD1, HGD, GSTZ1, BDH2, PAH, ADIPOQ, SARDH, HPD, PRODH	3.04E-05
12	BP	GO:0046395~carboxylic acid catabolic process	MTHFD1, HGD, GSTZ1, BDH2, PAH, ADIPOQ, SARDH, HPD, PRODH	3.04E-05
13	BP	GO:0008643~carbohydrate transport	SLC2A13, SLC5A2, G6PC, SLC2A4, SLC2A2, SLC5A1, SLC37A4, STXBP4	3.25E-05
14	BP	GO:0006732~coenzyme metabolic process	MTHFD1, FOLH1, ACSS1, HNF4A, PDK4, HAAO, ACSS2, SCP2, DCXR, HIBADH, ACOT3	6.39E-05
15	BP	GO:0006559~L-phenylalanine catabolic process	HGD, GSTZ1, PAH, HPD	6.64E-05
16	BP	GO:0046942~carboxylic acid transport	SLC23A1, SLC7A1, SLC7A9, SLC13A3, SLC10A2, SLC6A19, SLC1A1, SLC46A1, SLC7A12	1.28E-04
17	BP	GO:0015849~organic acid transport	SLC23A1, SLC7A1, SLC7A9, SLC13A3, SLC10A2, SLC6A19, SLC1A1, SLC46A1, SLC7A12	1.37E-04
18	BP	GO:0009063~cellular amino acid catabolic process	MTHFD1, HGD, GSTZ1, PAH, SARDH, HPD, PRODH	1.59E-04
19	BP	GO:0006820~anion transport	SLC26A4, SLC12A6, SLC12A1, PTGER3, SLC16A7, WNK4, SLC22A7, SLC4A1, SLC10A2, SLC4A4	1.61E-04
20	BP	GO:0006558~L-phenylalanine metabolic process	HGD, GSTZ1, PAH, HPD	1.82E-04
21	BP	GO:0015672~monovalent inorganic cation transport	SLC12A6, SLC5A2, SLC12A1, SLC9A3, SLC5A1, SLC10A2, KCNIP2, KCNJ1, SLC23A1, NNT, SLC13A2, SLC5A9, SLC13A3, SLC4A4, SLC5A12	2.17E-04
22	BP	GO:0055067~monovalent inorganic cation homeostasis	SLC26A4, BSND, RHCg, AQP11, SLC9A3, SLC4A4	2.55E-04
23	BP	GO:0016053~organic acid biosynthetic process	ACSM3, MTHFD1, PECR, ACSM1, BHMT2, AMACR, FADS2, ALDH4A1, PAH, PRODH	2.96E-04
24	BP	GO:0046394~carboxylic acid biosynthetic process	ACSM3, MTHFD1, PECR, ACSM1, BHMT2, AMACR, FADS2, ALDH4A1, PAH, PRODH	2.96E-04
25	BP	GO:0006812~cation transport	SLC12A6, SLC5A2, SLC12A1, SLC5A1, SLC9A3, RHBG, SLC10A2, KCNIP2, KCNJ1, SLC23A1, NNT, RHCg, SLC5A9, SLC25A37, SLC13A2, CHRNA4, SLC13A3, SLC4A4, STEAP1, SLC5A12	3.18E-04

26	BP	GO:0006570~tyrosine metabolic process	HGD, GSTZ1, PAH, HPD	3.81E-04
27	BP	GO:0009310~amine catabolic process	MTHFD1, HGD, GSTZ1, PAH, SARDH, HPD, PRODH	4.43E-04
28	BP	GO:0051186~cofactor metabolic process	MTHFD1, FOLH1, ACSS1, HNF4A, PDK4, HAAO, ACSS2, SCP2, DCXR, HIBADH, ACOT3	4.58E-04
29	BP	GO:0009074~aromatic amino acid family catabolic process	HGD, GSTZ1, PAH, HPD	5.18E-04
30	BP	GO:0030001~metal ion transport	SLC12A6, SLC5A2, SLC12A1, SLC5A1, SLC9A3, SLC10A2, KCNIP2, KCNJ1, SLC23A1, SLC25A37, SLC13A2, CHRNA4, SLC5A9, SLC13A3, SLC4A4, STEAP1, SLC5A12	0.0011507 4
31	BP	GO:0006885~regulation of pH	SLC26A4, RHCG, AQP11, SLC9A3, SLC4A4	0.0011712 3
32	BP	GO:0048878~chemical homeostasis	PTGER3, SLC9A3, SLC37A4, PTH1R, SYPL2, ADIPOQ, SLC26A4, BSND, G6PC, SLC2A4, RHCG, AQP11, WNK4, CHRNA4, SLC4A4	0.0013641 2
33	BP	GO:0019439~aromatic compound catabolic process	HGD, GSTZ1, PAH, HPD	0.0013657 9
34	BP	GO:0015698~inorganic anion transport	SLC26A4, SLC12A6, SLC12A1, PTGER3, WNK4, SLC4A1, SLC4A4	0.0016162 8
35	BP	GO:0006631~fatty acid metabolic process	ACSM3, PECR, ACSM1, CYP4A12A, HAO2, FADS2, BDH2, ADIPOQ, ACSM5, ACOT3	0.0019793 2
36	BP	GO:0055080~cation homeostasis	SLC26A4, BSND, PTGER3, RHCG, AQP11, SLC9A3, SLC37A4, PTH1R, SLC4A4, SYPL2	0.0019793 2
37	BP	GO:0006572~tyrosine catabolic process	HGD, GSTZ1, HPD	0.0022194 7
38	BP	GO:0006112~energy reserve metabolic process	G6PC, KL, PPP1R1A, SLC37A4, GYS2	0.0022903 3
39	BP	GO:0015711~organic anion transport	PTGER3, SLC16A7, SLC22A7, SLC10A2, SLC4A4	0.0027859
40	BP	GO:0008202~steroid metabolic process	HSD3B2, CYP24A1, G6PC, CUBN, AMACR, SLC37A4, HSD11B2, OSBPL10, AKR1C21	0.0031647
41	BP	GO:0006085~acetyl-CoA biosynthetic process	ACSS1, PDK4, ACSS2	0.003296
42	BP	GO:0009072~aromatic amino acid family metabolic process	HGD, GSTZ1, PAH, HPD	0.0037338 8
43	BP	GO:0015980~energy derivation by oxidation of organic compounds	G6PC, KL, PPP1R1A, SLC37A4, GYS2, PPARGC1A, PCK1	0.0037395 5
44	BP	GO:0009749~response to glucose stimulus	HNF4A, SLC37A4, GYS2, ADIPOQ	0.0042756 1
45	BP	GO:0009746~response to hexose stimulus	HNF4A, SLC37A4, GYS2, ADIPOQ	0.0042756 1
46	BP	GO:0034284~response to monosaccharide stimulus	HNF4A, SLC37A4, GYS2, ADIPOQ	0.0042756 1
47	BP	GO:0008652~cellular amino acid biosynthetic process	MTHFD1, BHMT2, ALDH4A1, PAH, PRODH	0.0043354 3
48	BP	GO:0050801~ion homeostasis	SLC26A4, BSND, PTGER3, RHCG, AQP11, WNK4, SLC9A3, SLC37A4, PTH1R, CHRNA4, SLC4A4, SYPL2	0.0051477
49	BP	GO:0006090~pyruvate metabolic process	G6PC, ME3, PDK4, PCK1	0.0061763 7
50	BP	GO:0006091~generation of precursor metabolites and energy	G6PC, KL, PPP1R1A, SLC37A4, CMAH, GYS2, FADS2, PGAM2, STEAP1, PPARGC1A, PCK1	0.0065299 4
51	BP	GO:0009743~response to carbohydrate stimulus	HNF4A, SLC37A4, GYS2, ADIPOQ	0.0069049 7
52	BP	GO:0048596~embryonic camera-type eye morphogenesis	ALDH1A1, BMP7, PROX1	0.0095005 6
53	BP	GO:0008610~lipid biosynthetic process	ACSM3, ALDH1A1, HSD3B2, PECR, ACSM1, AMACR, ST8SIA1, FADS2, AKR1C21, RDH16, PCK1	0.0117183 3
54	BP	GO:0015837~amine transport	SLC7A1, SLC6A4, SLC7A9, SLC6A19, SLC46A1, SLC7A12	0.0129460 2
55	BP	GO:0006073~cellular glucan metabolic process	G6PC, PPP1R1A, SLC37A4, GYS2	0.0134105 9
56	BP	GO:0044042~glucan metabolic process	G6PC, PPP1R1A, SLC37A4, GYS2	0.0134105 9
57	BP	GO:0005977~glycogen metabolic process	G6PC, PPP1R1A, SLC37A4, GYS2	0.0134105 9
58	BP	GO:0009108~coenzyme biosynthetic process	MTHFD1, ACSS1, PDK4, HAAO, ACSS2	0.0160634 3
59	BP	GO:0048048~embryonic eye morphogenesis	ALDH1A1, BMP7, PROX1	0.0184631
60	BP	GO:0006766~vitamin metabolic process	ALDH1A1, CYP24A1, HAAO, LRP2, RDH16	0.0206240 1
61	BP	GO:0031076~embryonic camera-type eye development	ALDH1A1, BMP7, PROX1	0.0210934 5

62	BP	GO:0033500~carbohydrate homeostasis	G6PC, SLC2A4, SLC37A4, ADIPOQ	0.0224853
63	BP	GO:0042593~glucose homeostasis	G6PC, SLC2A4, SLC37A4, ADIPOQ	0.0224853
64	BP	GO:0006865~amino acid transport	SLC7A1, SLC7A9, SLC6A19, SLC46A1, SLC7A12	0.0226490 7
65	BP	GO:0001822~kidney development	AGTR1A, LHX1, AQP11, SLC5A1, WWTR1, BMP7	0.0233741 7
66	BP	GO:0001655~urogenital system development	SFRP1, AGTR1A, LHX1, AQP11, SLC5A1, WWTR1, BMP7	0.0238219 1
67	BP	GO:0046849~bone remodeling	NOX4, PTH1R, SPP2	0.0238693 3
68	BP	GO:0009309~amine biosynthetic process	MTHFD1, BHMT2, ALDH4A1, PAH, PRODH	0.0247912 7
69	BP	GO:0014070~response to organic cyclic substance	SLC22A8, SLC37A4, ABAT, CHRNA4	0.0255602 9
70	BP	GO:0051180~vitamin transport	SLC23A1, SLC2A2, SLC46A1	0.0267857 7
71	BP	GO:0044264~cellular polysaccharide metabolic process	G6PC, PPP1R1A, SLC37A4, GYS2	0.0271782 2
72	BP	GO:0008284~positive regulation of cell proliferation	ADM, LHX1, FGF9, PTH1R, ST8SIA1, ID4, EGF, FGF1, PROX1, MYC	0.0292871 4
73	BP	GO:0048568~embryonic organ development	ALDH1A1, ADM, FGF9, CHST11, KRT8, BMP7, PROX1, MYC, CYR61	0.0308343
74	BP	GO:0042592~homeostatic process	NOX4, PTGER3, SLC9A3, SLC37A4, PTH1R, SYPL2, ADIPOQ, SLC26A4, BSND, G6PC, SLC2A4, RHCG, AQP11, WNK4, CHRNA4, SLC4A4	0.0325045 9
75	BP	GO:0060348~bone development	FGF9, PTH1R, WWTR1, BMP7, PAPSS2, IGFBP5	0.0337348 2
76	BP	GO:0001649~osteoblast differentiation	FGF9, PTH1R, WWTR1, IGFBP5	0.0341832 4
77	BP	GO:0048771~tissue remodeling	NOX4, PTH1R, SEMA3C, SPP2	0.0341832 4
78	BP	GO:0006637~acyl-CoA metabolic process	HNF4A, SCP2, ACOT3	0.0363303 9
79	BP	GO:0016051~carbohydrate biosynthetic process	B3GAT2, G6PC, CHST11, GYS2, PCK1	0.0372975 8
80	BP	GO:0002062~chondrocyte differentiation	FGF9, CHST11, PTH1R	0.0397616
81	BP	GO:0006898~receptor-mediated endocytosis	CUBN, SLC9A3, LRP2	0.0397616
82	BP	GO:0009066~aspartate family amino acid metabolic process	MTHFD1, BHMT2, DDO	0.0433102
83	BP	GO:0042732~D-xylose metabolic process	DCXR, XYLB	0.0447985 2
84	BP	GO:0015696~ammonium transport	RHCG, RHBG	0.0447985 2
85	BP	GO:0015712~hexose phosphate transport	G6PC, SLC37A4	0.0447985 2
86	BP	GO:0015760~glucose-6-phosphate transport	G6PC, SLC37A4	0.0447985 2
87	BP	GO:0010817~regulation of hormone levels	ALDH1A1, IL1RN, HSD11B2, DIO1, RDH16, DDO	0.0452952 7
88	BP	GO:0006873~cellular ion homeostasis	BSND, PTGER3, RHCG, AQP11, WNK4, SLC37A4, PTH1R, CHRNA4, SYPL2	0.0455698 6
89	BP	GO:0050878~regulation of body fluid levels	PTGER3, F2RL1, APOH, HSD11B2, PAPSS2	0.0462594
90	BP	GO:0042445~hormone metabolic process	ALDH1A1, HSD11B2, DIO1, RDH16, DDO	0.0478597 5
91	BP	GO:0051188~cofactor biosynthetic process	MTHFD1, ACSS1, PDK4, HAAO, ACSS2	0.0494905 1
92	CC	GO:0005903~brush border	SLC5A2, CUBN, SLC2A2, SLC5A1, SLC9A3, PTH1R, LRP2, PDZK1, DCXR	5.38E-08
93	CC	GO:0031980~mitochondrial lumen	GCDH, PDK2, ME3, PDK4, ACSM3, MCCC2, ACSM1, ACSS1, ALDH4A1, ABAT, BDH1, SARDH, ACSM5, PRODH	1.77E-06
94	CC	GO:0005759~mitochondrial matrix	GCDH, PDK2, ME3, PDK4, ACSM3, MCCC2, ACSM1, ACSS1, ALDH4A1, ABAT, BDH1, SARDH, ACSM5, PRODH	1.77E-06
95	CC	GO:0016324~apical plasma membrane	SLC26A4, SLC12A6, SLC12A1, CUBN, SLC6A20B, RHCG, SLC5A1, SLC9A3, LRP2, SLC10A2, SLC46A1, HSD3B2, CYP24A1, ME3, ADHFE1, HINT2, BPHL, CLYBL, HIBADH, KEG1, MTHFD1, MCCC2, PECR, EFHD1, ACSS1, PXMP2, GSTZ1, ALDH4A1, BDH1, SARDH, AADAT, GCDH, SUOX, SHMT1, PDK2, GATM, PDK4, AMACR, QDPR, GLYCTK, ACSM3, ACSM1,	3.46E-06
96	CC	GO:0005739~mitochondrion		3.57E-05

			NNT, SLC25A10, NIPSNAP1, HAO2, SLC25A37, ABAT, SCP2, ACSM5, PRODH, D10JHU81E	
97	CC	GO:0045177~apical part of cell	SLC26A4, SLC12A6, SLC12A1, CUBN, SLC6A20B, RHCG, SLC5A1, SLC9A3, LRP2, SLC10A2, SLC46A1	5.70E-05
98	CC	GO:0044429~mitochondrial part	GCDH, PDK2, SUOX, ME3, GATM, PDK4, ACSM3, MCCC2, EFHD1, ACSS1, ACSM1, NNT, SLC25A10, NIPSNAP1, ABAT, ALDH4A1, SLC25A37, SARDH, BDH1, ACSM5, PRODH	2.29E-04
99	CC	GO:0005886~plasma membrane	CCKAR, SLC5A2, GABRB3, SLC6A20B, SLC15A2, TLN2, SLC5A1, SLC9A3, SLC6A4, F2RL1, AQP6, KCNIP2, VEPH1, SLC23A1, SLC2A4, AQP11, SLC2A2, WNK4, CHRNA4, SLC4A1, SLC4A4, CEACAM2, DPEP1, SLC12A6, RAP2B, PTGER3, SLC22A7, TIMD2, SLC22A8, ARHGAP24, SLC7A12, SLC26A4, BSND, FOLH1, RHCG, AGTR1A, RAB17, CAR4, FRAS1, PTH1R, IL4RA, RHBG, MME, KRT8, CLEC2H, EGF, EHD3, CSF1R, NOX4, CUBN, SLC12A1, KL, SLC6A13, ITGA1, CELSR2, SLC10A2, SLC6A19, SAMD4, RAB31, SLC16A7, PKP2, SLC16A9, LRP8, LRP2, PDZK1, SLC46A1, DCXR, SLC5A12	3.53E-04
10 0	CC	GO:0000267~cell fraction	ACY1, SORD, SLC15A2, SLC37A4, FADS2, SAMD4, AADAC, G6PC, CYP4A12A, SLC16A7, SLC2A4, FMO1, HSD11B2, MEP1B, CYP2D26, GYS2, CHRNA4, SLC13A3, DIO1, LRP2, CYP4A14, RDH16	4.65E-04
10 1	CC	GO:0005792~microsome	AADAC, G6PC, CYP4A12A, SLC2A4, FMO1, SLC37A4, HSD11B2, CYP2D26, DIO1, CYP4A14, RDH16	4.71E-04
10 2	CC	GO:0042598~vesicular fraction	AADAC, G6PC, CYP4A12A, SLC2A4, FMO1, SLC37A4, HSD11B2, CYP2D26, DIO1, CYP4A14, RDH16	6.14E-04
10 3	CC	GO:0005626~insoluble fraction	SLC15A2, SLC37A4, FADS2, SAMD4, AADAC, G6PC, CYP4A12A, SLC16A7, SLC2A4, FMO1, HSD11B2, MEP1B, CYP2D26, GYS2, CHRNA4, SLC13A3, DIO1, LRP2, CYP4A14, RDH16	6.78E-04
10 4	CC	GO:0044459~plasma membrane part	FRAS1, SLC5A2, GABRB3, SLC6A20B, SLC15A2, TLN2, SLC9A3, SLC5A1, SLC6A4, PTH1R, RHBG, AQP6, VEPH1, SLC23A1, SLC2A4, WNK4, CHRNA4, SLC4A1, CLEC2H, SLC4A4, EHD3, SLC12A6, NOX4, RAP2B, CUBN, SLC12A1, SLC22A7, SLC6A13, ITGA1, ARHGAP24, SLC10A2, SAMD4, SLC6A19, SLC26A4, BSND, FOLH1, RAB31, RHCG, PKP2, RAB17, LRP2, PDZK1, SLC46A1	8.00E-04
10 5	CC	GO:0005624~membrane fraction	SLC15A2, SLC37A4, FADS2, SAMD4, AADAC, G6PC, CYP4A12A, SLC16A7, SLC2A4, FMO1, HSD11B2, MEP1B, CYP2D26, CHRNA4, SLC13A3, DIO1, LRP2, CYP4A14, RDH16	0.0011707 6
10 6	CC	GO:0031526~brush border membrane	SLC5A2, SLC9A3, PTH1R, PDZK1	0.0012333 7
10 7	CC	GO:0042579~microbody	PECR, AMACR, HAO2, PXMP2, DAO, DDO, SCP2, ACOT3	0.0012685 3
10 8	CC	GO:0005777~peroxisome	PECR, AMACR, HAO2, PXMP2, DAO, DDO, SCP2, ACOT3	0.0012685 3
10 9	CC	GO:0016323~basolateral plasma membrane	SLC12A6, NOX4, BSND, SLC23A1, TLN2, PTH1R, RHBG, SLC4A1, ARHGAP24	0.0017480 3
11 0	CC	GO:0042995~cell projection	SLC12A6, SLC5A2, CCK, CUBN, GABRB3, TLN2, SLC5A1, SLC9A3, PTH1R, ARHGAP24, SAMD4, IFT122, PVALB, SLC2A2, FABP7, LRP2, PDZK1, MYC, DCXR, DPEP1	0.0018403 5
11 1	CC	GO:0005887~integral to plasma membrane	SLC6A20B, SLC15A2, SLC22A7, SLC6A4, SLC6A13, ITGA1, RHBG, AQP6, SLC6A19, BSND, FOLH1, SLC2A4, RHCG, CHRNA4, SLC4A4, CLEC2H	0.0208270 4
11 2	CC	GO:0031226~intrinsic to plasma membrane	SLC6A20B, SLC15A2, SLC22A7, SLC6A4, SLC6A13, ITGA1, RHBG, AQP6, SLC6A19, BSND, FOLH1, SLC2A4, RHCG, CHRNA4, SLC4A4, CLEC2H	0.0282017 8
11 3	CC	GO:0031253~cell projection membrane	SLC5A2, SLC9A3, PTH1R, PDZK1	0.0299695 7
11 4	CC	GO:0005743~mitochondrial inner membrane	GCDH, EFHD1, NNT, GATM, SLC25A10, NIPSNAP1, PDK4, SLC25A37, BDH1, PRODH	0.0448420 8
11 5	MF	GO:0015293~symporter activity	SLC12A6, SLC5A2, SLC2A13, SLC12A1, SLC6A20B, SLC15A2, SLC5A1, SLC6A4, SLC6A13, SLC10A2, SLC6A19, SLC23A1, SLC16A7, SLC2A4, SLC16A9, SLC13A2, SLC13A3, SLC4A4, SLC1A1, SLC5A12	3.19E-13
11 6	MF	GO:0015294~solute:cation symporter activity	SLC12A6, SLC2A13, SLC5A2, SLC12A1, SLC6A20B, SLC2A4, SLC5A1, SLC6A4, SLC6A13, SLC13A3, SLC4A4, SLC10A2, SLC1A1, SLC6A19	1.25E-10
11 7	MF	GO:0015370~solute:sodium symporter activity	SLC5A2, SLC6A20B, SLC5A1, SLC6A13, SLC6A4, SLC13A3, SLC10A2, SLC6A19, SLC1A1	6.12E-07

11 8	MF	GO:0048037~cofactor binding	AADAT, NOX4, GCDH, SUOX, SHMT1, ME3, PAH, HIBADH, HNF4A, FMO1, HAO2, HSD11B2, ABAT, BDH2, NQO1, STEAP1	3.80E-06
11 9	MF	GO:0009055~electron carrier activity	NOX4, GCDH, SUOX, CYP24A1, CYP2C44, CMAH, CYP4A12A, NNT, HAO2, CYP2J11, CYP2D26, NQO1, CYP4A14, STEAP1	2.37E-05
12 0	MF	GO:0051119~sugar transmembrane transporter activity	SLC2A13, SLC5A2, SLC2A4, SLC2A2, SLC5A1, SLC37A4	3.42E-05
12 1	MF	GO:0005506~iron ion binding	NOX4, SUOX, CYP24A1, CYP2C44, CMAH, FADS2, HGD, PAH, TET1, CYP4A12A, MIOX, CYP2J11, HAAO, CYP2D26, SLC25A37, CYP4A14, STEAP1, HPD	4.05E-05
12 2	MF	GO:0031402~sodium ion binding	SLC5A2, SLC23A1, SLC12A1, SLC5A1, SLC5A9, SLC13A2, SLC13A3, SLC10A2, SLC4A4, SLC5A12	4.17E-05
12 3	MF	GO:0050662~coenzyme binding	NOX4, GCDH, SUOX, ME3, HNF4A, FMO1, HAO2, HSD11B2, BDH2, NQO1, STEAP1, HIBADH	5.57E-05
12 4	MF	GO:0015149~hexose transmembrane transporter activity	SLC5A2, SLC2A4, SLC2A2, SLC5A1, SLC37A4	5.77E-05
12 5	MF	GO:0015145~monosaccharide transmembrane transporter activity	SLC5A2, SLC2A4, SLC2A2, SLC5A1, SLC37A4	7.77E-05
12 6	MF	GO:0031420~alkali metal ion binding	SLC12A6, SLC5A2, SLC23A1, SLC12A1, SLC5A1, SLC5A9, SLC13A2, SLC13A3, KCNIP2, SLC10A2, SLC4A4, SLC5A12, KCNJ1	1.27E-04
12 7	MF	GO:0016878~acid-thiol ligase activity	ACSM3, ACSM1, ACSS1, ACSS2, ACSM5	1.32E-04
12 8	MF	GO:0015296~anion:cation symporter activity	SLC12A6, SLC12A1, SLC13A3, SLC4A4, SLC1A1	1.68E-04
12 9	MF	GO:0008509~anion transmembrane transporter activity	SLC26A4, SLC12A6, BSND, SLC12A1, GABRB3, SLC22A7, SLC13A3, SLC4A1, SLC4A4, SLC1A1	2.52E-04
13 0	MF	GO:0005355~glucose transmembrane transporter activity	SLC5A2, SLC2A4, SLC2A2, SLC5A1	3.22E-04
13 1	MF	GO:0005275~amine transmembrane transporter activity	SLC7A1, SLC6A13, SLC6A4, SLC7A9, SLC6A19, SLC1A1, SLC7A12	5.14E-04
13 2	MF	GO:0016645~oxidoreductase activity, acting on the CH-NH group of donors	MTHFD1, QDPR, ALDH4A1, SARDH, PRODH	6.34E-04
13 3	MF	GO:0016877~ligase activity, forming carbon-sulfur bonds	ACSM3, ACSM1, ACSS1, ACSS2, ACSM5	9.89E-04
13 4	MF	GO:0015171~amino acid transmembrane transporter activity	SLC7A1, SLC6A13, SLC7A9, SLC6A19, SLC1A1, SLC7A12	0.0012153 2
13 5	MF	GO:0047760~butyrate-CoA ligase activity	ACSM3, ACSM1, ACSM5	0.0025002 9
13 6	MF	GO:0046906~tetrapyrrole binding	CYP24A1, SUOX, CYP4A12A, CUBN, CYP2C44, CYP2J11, FADS2, CYP2D26, CYP4A14	0.0030845 3
13 7	MF	GO:0005328~neurotransmitter:sodium symporter activity	SLC6A20B, SLC6A13, SLC6A4, SLC6A19	0.0038354 6
13 8	MF	GO:0005343~organic acid:sodium symporter activity	SLC6A13, SLC13A3, SLC10A2, SLC1A1	0.0050601 6
13 9	MF	GO:0005326~neurotransmitter transporter activity	SLC6A20B, SLC6A13, SLC6A4, SLC6A19	0.0050601 6
14 0	MF	GO:0016405~CoA-ligase activity	ACSM1, ACSS1, ACSS2	0.0086262 8
14 1	MF	GO:0020037~heme binding	CYP24A1, SUOX, CYP4A12A, CYP2C44, CYP2J11, FADS2, CYP2D26, CYP4A14	0.0087349 7
14 2	MF	GO:0016646~oxidoreductase activity, acting on the CH-NH group of donors, NAD or NADP as acceptor	MTHFD1, QDPR, ALDH4A1	0.0236150 4
14 3	MF	GO:0016701~oxidoreductase activity, acting on single donors with incorporation of molecular oxygen	MIOX, HAAO, HGD, TET1, HPD	0.0250672 5
14 4	MF	GO:0043167~ion binding	SLC5A2, CYP24A1, GLB1L, GABRB3, SLC5A1, KCNIP2, CALB1, CLYBL, PTER, EFHD1, ASPA, SLC23A1, PVALB, CYP2J11, MIOX, SLC4A4, DPEP1, HPD, SLC12A6, SUOX, EGFL6, CAR12, CMAH, SLC26A4, FOLH1, RAB11FIP3, HNF4A, CYP2D26, RAD18, SLC25A37, CAR4, STEAP1, NEK6, FRAS1, ME3, SORD, ADHFE1, CYP2C44, ENPP3, MME, PAH, KCNJ1, STK32B, CYP4A12A, TCEA3, LHX1, HAAO, GALNT11, EGF, EHD3, NOX4, BHMT2, ACY1, SLC12A1, CUBN, KL, PM20D1, ITGA1, ESRRG, HGD, FADS2, CELSR2, SLC10A2, TET1, PCK1, B3GAT2, ACSM3, ACSM1, RNF152, SLC13A2, MEP1B, SLC5A9, LRP8, SLC13A3, LRP2, CYP4A14, ACSM5, SLC5A12	0.0250784 5
14 5	MF	GO:0005496~steroid binding	HNF4A, ESRRG, HSD11B2, CALB1	0.0280338 6

14	MF	GO:0005104~fibroblast growth factor receptor binding	KL, IL1RN, FGF1	0.0299511
6				7
14	MF	GO:0005412~glucose:sodium symporter activity	SLC5A2, SLC5A1	0.0319513
7				4
14	MF	GO:0003858~3-hydroxybutyrate dehydrogenase activity	BDH2, BDH1	0.0319513
8				4
14	MF	GO:0003884~D-amino-acid oxidase activity	DAO, DDO	0.0319513
9				4
15	MF	GO:0051183~vitamin transporter activity	SLC23A1, SLC2A2, SLC46A1	0.0333436
0				7
15	MF	GO:0051287~NAD or NADH binding	ME3, HSD11B2, BDH2, HIBADH	0.0336368
1				3
15	MF	GO:0016712~oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced flavin or flavoprotein as one donor, and incorporation of one atom of oxygen	CYP4A12A, CYP2C44, CYP2J11, CYP2D26	0.0336368
2				3
15	MF	GO:0043169~cation binding	SLC5A2, CYP24A1, GLB1L, SLC5A1, KCNIP2, CALB1, CLYBL, PTER, EFHD1, ASPA, SLC23A1, PVALB, CYP2J11, MIOX, SLC4A4, DPEP1, HPD, SLC12A6, SUOX, EGFL6, CAR12, CMAH, FOLH1, RAB11FIP3, HNF4A, CYP2D26, RAD18, SLC25A37, CAR4, STEAP1, NEK6, FRAS1, ME3, SORD, ADHFE1, CYP2C44, ENPP3, MME, PAH, KCNJ1, STK32B, CYP4A12A, TCEA3, LHX1, HAAO, GALNT11, EGF, EHD3, NOX4, BHMT2, ACY1, SLC12A1, CUBN, KL, PM20D1, ITGA1, ESRRG, HGD, FADS2, CELSR2, SLC10A2, TET1, PCK1, B3GAT2, ACSM3, ACSM1, RNF152, SLC13A2, MEP1B, SLC5A9, LRP8, SLC13A3, LRP2, CYP4A14, ACSM5, SLC5A12	0.0369175
3				7
15	MF	GO:0008201~heparin binding	FGF9, APOH, BMP7, FGF1, CYR61	0.0448919
4				5
15	MF	GO:0019842~vitamin binding	AADAT, SHMT1, CUBN, ABAT, CALB1, SLC46A1	0.0459225
5				2
15	MF	GO:0051739~ammonia transporter activity	RHCG, RHBG	0.0475438
6				8
15	MF	GO:0005520~insulin-like growth factor binding	IGFBP4, CYR61, IGFBP5	0.0482819
7				4
15	MF	GO:0016651~oxidoreductase activity, acting on NADH or NADPH	NOX4, NNT, MIOX, NQO1	0.0487789
8				5