

Supplementary Table 8. KEGG pathway enrichment analysis for the 917 candidate genes.

Pathway	Count	%	p-value	Genes	Fold Enrichment	FDR
hsa04610: Complement and coagulation cascades	16	1.788	<0.001	KNG1, F11, A2M, C5, C1R, F7, C4BPA, PLG, F13B, C8B, F5, SERPINA5, KLKB1, F2, CFH, CFI	4.747	0.001
hsa00350: Tyrosine metabolism	8	0.894	0.001	GOT2, DDC, TYR, GOT1, AOX1, TPO, ADH1A, ALDH3A1	4.680	1.626
hsa01100: Metabolic pathways	82	9.162	0.001	TUSC3, IMPA1, GNPDA1, B3GALT5, DTYMK, ADH1A, PIP5K1A, PSPH, COX5A, GLDC, AFMID, GOT2, TYR, GOT1, XYLT1, CYP7A1, P4HA3, ALOX12B, TPO, PHOSPHO1, BPNT1, DDC, ALDH5A1, ACSM2A, PI4KB, PNPLA3, HAO1, NNT, PANK1, HSD11B1, ABAT, FLAD1, GALNT8, PCCB, GPAM, AKR1D1, PCCA, MDH2, ALDH9A1, SLC27A5, PLA2G5, HSD3B2, CHKA, FUT9, ENPP1, UGDH, PAH, ALDH3A1, HPSE2, CKMT2, DHODH, HSD17B6, GCSH, DMGDH, UGT8, UCK2, SPAM1, GCNT1, BDH1, HSD17B7, CHDH, NADK2, UAP1, NDUFA3, SI, ACACA, AK5, ACLY, ACACB, AK4, AK8, ADI1, RDH10, SDHC, AOX1, LIPG, UGT2B4, AGXT2, IPPK, ALG11, PLA2G4E, PC	1.377	1.766
hsa00630: Glyoxylate and dicarboxylate metabolism	7	0.782	0.002	HAO1, GCSH, PCCB, PCCA, MDH2, GLDC, AFMID	5.308	2.038
hsa04976: Bile secretion	11	1.229	0.002	ABCG8, ADCY1, ABCG5, ATP1B3, ADCY8, SLC5A1, CYP7A1, ABCC2, SLC27A5, NR1H4, SLC10A1	3.264	2.208
hsa05033: Nicotine addiction	8	0.894	0.003	GABRG2, GRIA2, GABRA4, GABRB2, GABRB1, GABRA6, GRIN2A, GRIA4	4.095	3.623
hsa04080: Neuroactive ligand-receptor interaction	25	2.793	0.004	TACR3, GABRB2, OPRK1, GABRB1, HCRTR2, EDNRB, APLNR, P2RY6, NMUR2, GRID2, ADRA2C, GHR, HTR1E, GABRG2, CCKBR, GABRA4, NPBWR1, GABRA6, GRIN2A, GRIA4, PLG, GRM4, GRIA2, PRLR, F2	1.848	5.314
hsa01130: Biosynthesis of antibiotics	20	2.235	0.007	UAP1, ACLY, AK5, AK4, PSPH, GLDC, AK8, HAO1, GOT2, GOT1, SDHC, TGDS, GCSH, PCYOX1, BPNT1, PCCB, PCCA, MDH2, HSD17B7, ALDH9A1	1.931	9.013
hsa00360:	5	0.559	0.008	GOT2, DDC, GOT1, PAH, ALDH3A1	6.022	9.852

Phenylalanine metabolism						
hsa00260: Glycine, serine and threonine metabolism	7	0.782	0.011	CHDH, GCAT, GCSH, DMGDH, AGXT2, PSPH, GLDC	3.675	13.025

Notes: Count: the number of genes involved in the pathway; %: the percentage of involved genes/total genes in the pathway; FDR: false discovery rate; KEGG: Kyoto Encyclopedia of Genes and Genomes.