Supplementary Information, Table S10 Gene Ontology analysis for genes identified by combining FST and population diversity ratio

General biological processes			
MF	pancreatic ribonuclease activity	4	3.25E-04
MF	cysteine-type endopeptidase inhibitor activity	6	5.58E-04
MF	endoribonuclease activity, producing 3'-phosphomonoesters	4	0.00106
MF	aryl hydrocarbon receptor binding	3	0.001368
BP	regulation of transcription, DNA-dependent	48	0.002201
MF	protein complex binding	12	0.002223
MF	endonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 3'-phosphomonoesters	4	0.004497
BP	transcription	53	0.007359
MF	endonuclease activity	7	0.009451
MF	nuclease activity	9	0.009978
MF	DNA binding	59	0.010078
MF	carboxy-lyase activity	4	0.016021
CC	gap junction	4	0.016912
BP	regulation of transcription	61	0.018409
BP	Conduct disorder and ADHD: Evaluation of conduct problems as a categorical and quantitative trait in the international multicentre ADHD genetics study	4	0.02057
CC	cell projection	23	0.024842
MF	protein heterodimerization activity	10	0.026157
BP	positive regulation of cell differentiation	10	0.031682
MF	endoribonuclease activity	4	0.03353
MF	phosphatidylinositol binding	3	0.040376
MF	zinc ion binding	55	0.042172
MF	metal ion binding	93	0.043186
CC	cell projection part	10	0.044726
MF	transition metal ion binding	65	0.044811
BP	mRNA processing	12	0.045415
BP	lymphocyte differentiation	6	0.047965
MF	transcription repressor activity	12	0.05065
BP	cell-cell recognition	3	0.05104
CC	spliceosome	7	0.052379
BP	response to abiotic stimulus	13	0.052894
MF	cation binding	93	0.053417
CC	nucleoplasm	26	0.055429
BP	regulation of insulin receptor signaling pathway	3	0.056296
BP	regulation of cell-substrate adhesion	4	0.056772
MF	ion binding	94	0.058547
CC	nucleoplasm part	18	0.060363
MF	peptidase inhibitor activity	7	0.062049
MF	helicase activity	7	0.063914
BP	enzyme linked receptor protein signaling pathway	12	0.070832
CC	intermediate filament	6	0.07852
BP	cell-cell adhesion mediated by integrin	2	0.079037
BP	cell recognition	4	0.085295
CC	intermediate filament cytoskeleton	6	0.085942

BP	nuclear import	5	0.092163
MF	vitamin B6 binding	4	0.092669
MF	pyridoxal phosphate binding	4	0.092669
MF	ribonuclease activity	4	0.09697
BP	protein palmitoylation	2	0.097804
BP	negative regulation of transcription	14	0.099958
Neurological process			
BP	central nervous system neuron development	4	0.026816
BP	negative regulation of response to stimulus	6	0.042865
BP	central nervous system neuron differentiation	4	0.044574
BP	learning or memory	6	0.069617
BP	adult behavior	5	0.089123
Metabolism and digestion			
BP	regulation of digestive system process	4	0.001221
BP	regulation of RNA metabolic process	49	0.00211
BP	regulation of intestinal cholesterol absorption	3	0.005873
KEGG	hsa00290:Valine, leucine and isoleucine biosynthesis	3	0.013699
BP	regulation of lipid transport	4	0.017029
BP	regulation of glucose import	4	0.020652
BP	response to corticosteroid stimulus	6	0.022409
BP	regulation of glucose transport	4	0.022609
BP	regulation of cellular catabolic process	5	0.031949
KEGG	hsa00500:Starch and sucrose metabolism	4	0.031989
BP	negative regulation of insulin receptor signaling pathway	3	0.036447
BP	negative regulation of intestinal phytosterol absorption	2	0.040328
BP	negative regulation of intestinal cholesterol absorption	2	0.040328
BP	negative regulation of digestive system process	2	0.040328
BP	regulation of catabolic process	6	0.041241
MF	Sitosterolemia	2	0.045369
BP	regulation of sterol transport	3	0.05104
BP	regulation of cholesterol transport	3	0.05104
BP	ribonucleotide metabolic process	7	0.056186
BP	response to glucocorticoid stimulus	5	0.064049
BP	purine ribonucleoside triphosphate metabolic process	6	0.065336
BP	negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	16	0.065937
BP	ribonucleoside triphosphate metabolic process	6	0.067458
BP	negative regulation of nitrogen compound metabolic process	16	0.072583
BP	purine nucleoside triphosphate metabolic process	6	0.076322
BP	digestion	5	0.077462
BP	nucleoside triphosphate metabolic process	6	0.095837
BP	mRNA metabolic process	12	0.099594
Regulation of developmental processes			
BP	positive regulation of developmental process	12	0.019092
BP	in utero embryonic development	8	0.056229
BP	urogenital system development	6	0.065336
BP	gastrulation with mouth forming second	3	0.06734
BP	thymus development	3	0.06734
BP	determination of symmetry	4	0.056772

BP	determination of bilateral symmetry	4	0.056772
BP	determination of left/right symmetry	4	0.053588