Supplementary Information, Table S9 GO categories for genes identified using SweepFinder (extra categories not presented in the main text).

	General processes		
MF	aromatase activity	6	2.41E-04
MF	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	6	3.90E-04
MF	mRNA binding	9	4.18E-04
MF	glutathione transferase activity	5	0.001685
MF	cysteine-type endopeptidase inhibitor activity	6	0.002341
MF	peptidase inhibitor activity	11	0.005357
CC	Membrane fraction	37	0.006249
CC	cell fraction	46	0.008333
MF	heme binding	9	0.009191
MF	transferase activity, transferring alkyl or aryl (other than methyl) groups	6	0.009448
MF	enzyme inhibitor activity	15	0.009496
BP	extracellular structure organization	11	0.010049
CC	insoluble fraction	37	0.010956
MF	endopeptidase inhibitor activity	10	0.012164
MF	tetrapyrrole binding	9	0.014291
MF	Framingham Heart Study 100K Project: genome-wide associations for blood pressure and arterial stiffness	4	0.015267
MF	adenyl ribonucleotide binding	56	0.016595
MF	phosphoinositide binding	8	0.022863
MF	ribonucleotide binding	65	0.023476
MF	purine ribonucleotide binding	65	0.023476
MF	nucleotide binding	77	0.027053
MF	adenyl nucleotide binding	57	0.029545
MF	hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances	8	0.036772
MF	purine nucleoside binding	57	0.037498
BP	receptor internalization	3	0.03783
CC	microsome	13	0.03809
MF	purine nucleotide binding	66	0.038889
BP	positive regulation of cell-substrate adhesion	4	0.04086
MF	nucleoside binding	57	0.041348
BP	RNA splicing	14	0.042548
CC	vesicular fraction	13	0.045237
MF	cytoskeletal protein binding	22	0.04622
MF	Ras GTPase activator activity	7	0.046805
MF	glutamate receptor activity	4	0.04925
BP	mRNA processing	15	0.051933
MF	extracellular ligand-gated ion channel activity	6	0.053977
BP	nucleotide-excision repair	5	0.054135
MF	alkane 1-monooxygenase activity	2	0.058551
MF	pyridoxal phosphate binding	5	0.060626
MF	vitamin B6 binding	5	0.060626
MF	phospholipid binding	10	0.061365
BP	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	9	0.062246
BP	RNA splicing, via transesterification reactions	9	0.062246
BP	nuclear mRNA splicing, via spliceosome	9	0.062246
BP	negative regulation of translation	4	0.062485
MF	ligand-gated channel activity	8	0.064174
MF	ligand-gated ion channel activity	8	0.064174
MF	electron carrier activity	11	0.065911
CC	non-membrane-bounded organelle	85	0.065947
CC	intracellular non-membrane-bounded organelle	85	0.065947
BP	extracellular matrix organization	7	0.066838

CC	nuclear body	10	0.069384
BP	regulation of cell adhesion	8	0.069677
MF	ionotropic glutamate receptor activity	3	0.071664
BP	positive regulation of cell adhesion	5	0.071908
CC	Cajal body	4	0.075773
MF	lipid binding	19	0.076017
MF	extracellular-glutamate-gated ion channel activity	3	0.080341
MF	GTPase activator activity	11	0.081255
CC	extracellular matrix	16	0.083184
BP	negative regulation of activin receptor signaling pathway	2	0.083383
BP	Genome-wide association analysis of susceptibility and clinical phenotype in multiple sclerosis	4	0.085307
BP	cell projection assembly	6	0.085543
MF	aryl hydrocarbon receptor binding	2	0.086532
CC	proteinaceous extracellular matrix	15	0.08953
MF	oxygen binding	4	0.090488
CC	cytoskeleton	47	0.094495
MF	SNARE binding	4	0.096408
Metabolism and motility			
BP	purine ribonucleotide metabolic process	9	0.027004
BP	purine ribonucleoside triphosphate metabolic process	8	0.032259
BP	ribonucleoside triphosphate metabolic process	8	0.033707
BP	regulation of catabolic process	7	0.05025
BP	purine nucleotide metabolic process	10	0.058845
BP	nucleobase, nucleoside and nucleotide biosynthetic process	10	0.069829
BP	response to drug	11	0.071894
CC	myosin filament	3	0.077248
BP	purine ribonucleotide biosynthetic process	7	0.080424
BP	ATP biosynthetic process	6	0.085543
MF	ATPase activity, coupled to transmembrane movement of substances	7	0.086168
BP	tRNA metabolic process	7	0.086261
CC	muscle myosin complex	3	0.086529
MF	ATP-dependent protein binding	2	0.086532
MF	ATPase activity, coupled to movement of substances	7	0.08929
BP	purine nucleotide biosynthetic process	8	0.092541
BP	lipid transport	8	0.092541
Sexual reproduction			
KEGG	hsa04114:Oocyte meiosis	7	0.059439
BP	spermatid differentiation	5	0.060924
BP	reproductive cellular process	9	0.064227
Neurological process and perception			
BP	synaptic vesicle transport	4	0.062485
BP	neurotransmitter secretion	4	0.062485
BP	behavior	19	0.065582
BP	transmission of nerve impulse	15	0.079678
CC	postsynaptic membrane	8	0.09391