

**Table S2.** Functional enrichment analysis of transcripts with significantly higher additive genetic variance, dominance variance, or putative environmental variance. Functional clusters are based on inter-relationships and redundancies among GO biological processes and molecular functions, implemented in DAVID. Ad hoc descriptions of retained clusters are based on common themes/functions of constituent GO annotations. Clusters are ranked by overall enrichment score (Enrich. Score). Data pertaining to the number of GO terms, the number of candidate genes (No. Genes) and the mean fold enrichment score of constituent GO terms are also presented (95% quantiles in parentheses).

<b>Functional Cluster</b>	<b>Enrich. Score</b>	<b>No. GO Terms</b>	<b>No. Genes</b>	<b>Fold Enrichment</b>
<b>High Heritability Transcripts (fig. 1C)</b>				
cellular adhesion	2.44	3	16	3.26 (2.37 - 4.77)
ion binding	2.14	5	62	1.36 (1.24 - 1.43)
oxidation reduction	1.88	8	21	6.29 (1.87 - 14.32)
cell-matrix adhesion	1.74	3	6	6.05 (4.79 - 8.02)
epithelial development	0.94	6	7	4.16 (2.49 - 7.21)
peptidase activity	0.84	4	18	1.63 (1.22 - 2.05)
hydrolytic activity	0.76	3	6	2.83 (2.66 - 3.07)
GTPase mediated signalling	0.72	3	7	3.47 (1.75 - 6.16)
regulation of cNMP metabolism	0.68	4	3	3.53 (3.27 - 3.70)
amino acid biosynthesis	0.68	5	9	2.33 (1.45 - 3.37)
protein maturation	0.61	3	4	2.53 (2.36 - 2.67)
ion transport (channel-mediated)	0.61	10	10	2.89 (1.41 - 5.08)
morphogenesis & development of epithelial tubes	0.59	5	6	2.39 (1.44 - 3.13)
GTPase regulation	0.51	8	11	1.88 (1.17 - 3.26)
endocytosis	0.51	4	8	1.59 (0.98 - 2.15)
<b>Transcripts with only Dominance Variance (fig. 1D)</b>				
Gap junction	1.86	7	11	4.81 (2.31 - 9.44)
ion transport	1.60	5	11	3.68 (2.18 - 5.08)
organ morphogenesis & development	1.45	7	5	7.66 (2.60 - 14.55)
cell migration	1.41	8	8	4.31 (1.69 - 7.63)
translation	1.36	4	9	3.01 (1.90 - 4.56)
G-protein signalling	1.34	4	9	5.63 (3.07 - 7.85)
cell-cell signalling	1.14	3	11	2.37 (1.70 - 2.82)
protein dimerization	0.93	3	10	2.06 (1.71 - 2.43)
cell morphogenesis	0.82	12	9	2.87 (2.31 - 3.61)
cellular differentiation	0.63	3	3	3.30 (2.49 - 4.08)
<b>Transcripts with Highly Significant Non-Genetic Effects (fig. 2B)</b>				
regulation of phosphorylation	0.88	7	4	3.19 (2.72 - 3.90)
mRNA processing	0.46	6	5	2.07 (1.34 - 2.80)
ATP binding	0.46	9	8	1.39 (1.20 - 1.51)

**Table S3.** Functional enrichment analysis of transcripts putatively under directional selection.

<b>Functional Cluster</b>	<b>Enrich. Score</b>	<b>No. GO Terms</b>	<b>No. Genes</b>	<b>Fold Enrichment</b>
translation	8.92	4	99	2.31 (1.64 - 3.37)
RNA splicing	3.70	7	103	1.65 (1.52 - 1.71)
cellular macromolecule catabolism	3.28	9	138	1.42 (1.30 - 1.54)
RNA transport	2.60	11	39	1.99 (1.64 - 2.23)
regulation of protein ubiquitination	2.28	31	150	1.89 (1.24 - 2.60)
positive regulation of transcription	2.27	16	186	1.36 (1.15 - 1.52)
regulation of translation	2.01	3	66	1.54 (1.41 - 1.73)
cellular assembly	1.99	3	14	3.61 (2.63 - 4.18)
regulation of transcription cofactors	1.83	5	131	1.36 (1.25 - 1.46)
cell migration	1.65	4	38	1.49 (1.30 - 1.59)
regulation of transcription	1.41	7	234	1.15 (1.07 - 1.23)
regulation of cell growth	1.34	7	53	1.55 (1.35 - 1.79)
mitosis	1.16	3	12	3.95 (1.57 - 5.35)
SMAD-BMP signalling	1.04	3	9	2.70 (2.26 - 3.26)
amine metabolism	0.99	6	14	2.30 (1.71 - 2.51)
sex differentiation	0.99	11	25	1.67 (1.54 - 2.03)
protein modification	0.94	7	40	1.32 (1.05 - 1.65)
nucleoside metabolism	0.92	10	4	4.11 (2.64 - 5.01)
endopeptidase activity	0.90	6	53	1.31 (1.13 - 1.49)
lipid catabolism	0.89	4	7	3.55 (2.16 - 6.12)
rRNA & ncRNA processing	0.86	6	51	1.30 (1.07 - 1.49)
morphogenesis & development of epithelial tubes	0.80	14	24	2.15 (1.10 - 3.82)
muscle contraction	0.80	4	12	1.91 (1.37 - 2.73)
cytoskeleton organization	0.77	4	41	1.32 (1.21 - 1.42)
mRNA catabolism	0.76	4	10	1.72 (1.47 - 1.94)
SMAD-BMP signalling (phosphorylation mediated)	0.72	3	8	2.20 (1.75 - 2.50)
tRNA processing	0.71	5	11	2.03 (1.00 - 3.23)
GTPase regulation	0.69	14	54	1.38 (1.04 - 1.82)
nuclear membrane organization	0.69	3	4	3.70 (1.46 - 5.01)
purine metabolism	0.67	23	23	1.93 (1.15 - 3.77)
cell junction organization	0.63	4	10	1.93 (1.29 - 2.57)
GTPase binding	0.61	4	13	1.57 (1.31 - 1.96)
chromatin organization & modification	0.61	5	45	1.20 (1.11 - 1.26)
regulation of cellular catabolism (carbohydrates)	0.60	19	14	1.83 (1.20 - 2.68)
protein & histone ubiquitination	0.59	4	4	2.72 (1.57 - 3.34)
muscle contraction	0.58	4	6	2.27 (2.01 - 2.43)
hormone signalling	0.58	4	12	1.85 (1.26 - 2.69)
mesenchyme development	0.58	9	15	1.99 (1.31 - 2.61)
hormone receptor binding	0.56	7	17	1.48 (1.23 - 1.64)
thiolester activity	0.55	3	19	1.31 (1.00 - 1.54)
growth hormone signalling	0.54	3	8	2.36 (1.08 - 3.29)
regulation of erythrocyte differentiation	0.54	8	14	1.96 (1.19 - 3.49)
viral response	0.52	3	7	1.68 (1.30 - 2.29)
endocytosis	0.51	5	63	1.26 (1.06 - 1.70)
protein folding	0.50	5	23	1.81 (1.05 - 3.01)