Supplementary Table 3. Over-represented GO terms of TAS-implicated genes. A variety of over-represented terms suggests that complex networks shape these quantitative traits.

Trait	GO group	Go terms	Percentage among candidates	Percentage among genome	GO annotation
Length	Biological process	GO:0016192	3.409%	0.207%	Vesicle-mediated transport
		GO:0006886	3.409%	0.390%	Intracellular protein transport
		GO:0007165	2.273%	0.293%	Signal transduction
		GO:0015031	2.273%	0.333%	Protein transport
	Cellular component	GO:0030117	3.409%	0.065%	Membrane coat
	Molecular function	GO:0008565	2.273%	0.085%	Protein transporter activity
		GO:0016788	2.273%	0.155%	Hydrolase activity, acting on ester bonds
		GO:0003924	2.273%	0.271%	GTPase activity
		GO:0004672	5.682%	1.392%	Protein kinase activity
Width	Biological process	GO:0007242	4.167%	0.064%	Intracellular signaling cascade
		GO:0006413	4.167%	0.076%	Translational initiation
		GO:0006629	8.333%	0.360%	Lipid metabolic process
		GO:0009725	6.250%	0.053%	Response to hormone stimulus
		GO:0045449	6.250%	0.952%	Regulation of transcription
	Molecular function	GO:0003743	4.167%	0.081%	Translation initiation factor activity
		GO:0004629	4.167%	0.018%	Phospholipase C activity
		GO:0008081	8.333%	0.058%	Phosphoric diester hydrolase activity
Angle	Biological process	GO:0006355	9.677%	1.646%	Regulation of transcription, DNA-dependent
	Cellular component	GO:0005634	9.677%	2.656%	Nucleus
	Molecular function	GO:0046983	6.452%	0.601%	Protein dimerization activity
		GO:0043565	6.452%	0.763%	Sequence-specific DNA binding
DTA	Biological process	GO:0030001	3.333%	0.165%	Metal ion transport
		GO:0006355	6.667%	1.646%	Regulation of transcription, DNA-dependent
	Molecular function	GO:0046873	3.333%	0.040%	Metal ion transmembrane transporter activity
		GO:0046983	6.667%	0.601%	Protein dimerization activity
		GO:0043565	6.667%	0.763%	Sequence-specific DNA binding
		GO:0003700	6.667%	1.051%	Transcription factor activity
		GO:0003676	8.333%	2.049%	Nucleic acid binding
DTS	Biological process	GO:0009239	2.239%	0.096%	Enterobactin biosynthetic process
	Biological process	GO:0050826	7.463%	1.349%	Response to freezing
		GO:0042309	7.463%	1.349%	Homoiothermy
		GO:0008152	8.209%	2.274%	Metabolic process
		GO:0006915	1.493%	0.120%	Apoptosis
	Cellular component	GO:0005761	1.493%	0.012%	Mitochondrial ribosome
		GO:0005576	3.731%	0.338%	Extracellular region
		GO:0015935	1.493%	0.069%	Small ribosomal subunit
	Molecular function	GO:0004867	3.731%	0.092%	Serine-type endopeptidase inhibitor activity
		GO:0008667	2.239%	0.096%	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase activity
		GO:0016829	1.493%	0.069%	Lyase activity
		GO:0050825	7.463%	1.349%	Ice binding
		GO:0005488	5.970%	1.585%	Binding
		GO:0000287	1.493%	0.163%	Magnesium ion binding
		GO:0003824	6.716%	2.407%	Catalytic activity

Significant level is corrected with the Bonferroni method at $P < 0.05$. After the analysis of 80 TAS-implicated genes, only GO terms associated with more than one candidate genes were tabulated to avoid false-positive findings.