

Supplementary Table S2. Enriched GO terms. Shown are Gene Ontology (GO) terms significantly enriched in 2181 genes induced (Gene Set 1) or 1896 genes repressed (Gene Set 2) in AE ($P < 0.05$; FDR < 0.05).

Gene Set 1	Enriched GO Term	P-value
Gene_Set_1_4102	immune response	3.39E-74
Gene_Set_1_4102	response to stress	1.18E-42
Gene_Set_1_4102	intracellular signaling cascade	2.62E-38
Gene_Set_1_4102	response to other organism	8.91E-38
Gene_Set_1_4102	extracellular region	1.20E-34
Gene_Set_1_4102	cell adhesion	4.93E-33
Gene_Set_1_4102	positive regulation of cellular process	1.88E-31
Gene_Set_1_4102	death	2.19E-31
Gene_Set_1_4102	enzyme regulator activity	3.82E-28
Gene_Set_1_4102	extracellular region part	6.02E-28
Gene_Set_1_4102	ATP binding	2.57E-26
Gene_Set_1_4102	cell cycle	1.18E-25
Gene_Set_1_4102	regulation of apoptosis	3.70E-25
Gene_Set_1_4102	negative regulation of cellular process	8.23E-25
Gene_Set_1_4102	peptidase activity	9.37E-25
Gene_Set_1_4102	phosphorylation	5.76E-24
Gene_Set_1_4102	protein kinase activity	1.87E-23
Gene_Set_1_4102	proteolysis	1.92E-23
Gene_Set_1_4102	extracellular matrix (sensu Metazoa)	1.31E-21
Gene_Set_1_4102	humoral immune response	1.44E-21
Gene_Set_1_4102	kinase activity	2.75E-21
Gene_Set_1_4102	endopeptidase activity	3.08E-21
Gene_Set_1_4102	cytoskeleton	1.73E-20
Gene_Set_1_4102	regulation of signal transduction	3.11E-20
Gene_Set_1_4102	protein kinase cascade	9.46E-19
Gene_Set_1_4102	cell differentiation	1.96E-18
Gene_Set_1_4102	GTPase regulator activity	4.96E-18
Gene_Set_1_4102	cytoskeleton organization and biogenesis	1.19E-17
Gene_Set_1_4102	membrane fraction	1.55E-17
Gene_Set_1_4102	regulation of cell cycle	6.49E-17
Gene_Set_1_4102	small GTPase mediated signal transduction	7.64E-17
Gene_Set_1_4102	pyrophosphatase activity	1.71E-16
Gene_Set_1_4102	cellular biosynthesis	2.11E-16
Gene_Set_1_4102	locomotion	1.26E-15
Gene_Set_1_4102	calcium ion binding	1.32E-15
Gene_Set_1_4102	protein biosynthesis	1.45E-15
Gene_Set_1_4102	receptor binding	1.65E-15
Gene_Set_1_4102	GTP binding	4.04E-15
Gene_Set_1_4102	organ development	5.10E-15
Gene_Set_1_4102	cell activation	1.19E-14
Gene_Set_1_4102	induction of apoptosis	1.78E-14
Gene_Set_1_4102	transcription factor binding	5.50E-14
Gene_Set_1_4102	transcription from RNA polymerase II promoter	5.74E-14
Gene_Set_1_4102	humoral defense mechanism (sensu Vertebrata)	6.76E-14
Gene_Set_1_4102	enzyme linked receptor protein signaling pathway	1.11E-13
Gene_Set_1_4102	protein-tyrosine kinase activity	2.21E-13
Gene_Set_1_4102	extracellular space	3.68E-13

Gene_Set_1_4102	GTPase activity	4.51E-13
Gene_Set_1_4102	transmembrane receptor protein tyrosine kinase signaling	8.11E-13
Gene_Set_1_4102	complement activation	9.17E-13
Gene_Set_1_4102	protein serine/threonine kinase activity	1.19E-12
Gene_Set_1_4102	regulation of cell proliferation	1.35E-12
Gene_Set_1_4102	antigen processing	3.57E-12
Gene_Set_1_4102	immunological synapse	4.11E-12
Gene_Set_1_4102	enzyme inhibitor activity	5.06E-12
Gene_Set_1_4102	guanyl-nucleotide exchange factor activity	5.57E-12
Gene_Set_1_4102	antigen presentation	6.57E-12
Gene_Set_1_4102	morphogenesis	7.70E-12
Gene_Set_1_4102	small GTPase regulator activity	7.83E-12
Gene_Set_1_4102	hemopoiesis	8.88E-12
Gene_Set_1_4102	serine-type peptidase activity	1.05E-11
Gene_Set_1_4102	transmembrane receptor activity	1.87E-11
Gene_Set_1_4102	T cell activation	2.41E-11
Gene_Set_1_4102	cytoskeletal part	2.42E-11
Gene_Set_1_4102	enzyme activator activity	2.59E-11
Gene_Set_1_4102	nuclear part	4.77E-11
Gene_Set_1_4102	mitotic cell cycle	4.89E-11
Gene_Set_1_4102	receptor complex	5.23E-11
Gene_Set_1_4102	cellular localization	5.41E-11
Gene_Set_1_4102	vacuole	7.78E-11
Gene_Set_1_4102	extracellular matrix structural constituent	8.43E-11
Gene_Set_1_4102	inflammatory response	8.77E-11
Gene_Set_1_4102	regulation of protein metabolism	8.77E-11
Gene_Set_1_4102	I-kappaB kinase/NF-kappaB cascade	1.13E-10
Gene_Set_1_4102	lymphocyte differentiation	1.74E-10
Gene_Set_1_4102	response to abiotic stimulus	1.76E-10
Gene_Set_1_4102	organelle lumen	3.73E-10
Gene_Set_1_4102	regulation of catalytic activity	5.04E-10
Gene_Set_1_4102	cell division	6.01E-10
Gene_Set_1_4102	Rho protein signal transduction	6.08E-10
Gene_Set_1_4102	endomembrane system	6.66E-10
Gene_Set_1_4102	lipid binding	6.77E-10
Gene_Set_1_4102	hydrolase activity, acting on ester bonds	7.10E-10
Gene_Set_1_4102	growth factor binding	8.29E-10
Gene_Set_1_4102	endoplasmic reticulum	9.08E-10

<u>Gene Set 2</u>	<u>Enriched GO Term</u>	<u>P-value</u>
Gene_Set_2_4102	lipid metabolism	5.24E-34
Gene_Set_2_4102	cellular lipid metabolism	1.07E-26
Gene_Set_2_4102	organic acid metabolism	7.63E-19
Gene_Set_2_4102	oxidoreductase activity	4.23E-13
Gene_Set_2_4102	fatty acid metabolism	5.51E-13
Gene_Set_2_4102	lipid biosynthesis	1.23E-12
Gene_Set_2_4102	generation of precursor metabolites and energy	2.10E-12
Gene_Set_2_4102	steroid metabolism	6.95E-12
Gene_Set_2_4102	coenzyme binding	1.30E-11
Gene_Set_2_4102	catabolism	7.64E-11