

Table S3. Comparison of gene ontology (GO) terms in the differentially regulated genes between High and Low strains

Strain	Biological process	<i>P</i>	Molecular function	<i>P</i>	Cellular component	<i>P</i>
Low	Defense response	0.0335	Molecular function	0.0773	Cytoskeleton	0.0510
	Regulation of apoptosis	0.0408	G-protein receptor binding	0.0673		
	Detection of abiotic stimulus	0.0102				
	Electron transport	0.0408				
	Signal transduction	0.0728				
	Intracellular signaling cascade	0.0555				
	Response to radiation	0.0564				
	Catabolic process	0.0328	Transferase activity	0.0469	Endomembrane system	0.0117
High	Protein modification development	0.0669	Kinase binding	0.0162		
	Nervous system development	0.0555				
	Phosphate metabolic process	0.0831				
	Membrane lipid metabolic process	0.0701				

The upregulated genes in High and Low ovaries were compared using GO analysis (<http://chem.colorado.edu/knightgroup/>) in terms of the three domains of GO – biological process, molecular function and cellular component. The cutoff *P*-value is 0.10. Results with *P*<0.05 are presented in Fig. 1.