Category	Cluster	Classification	Term's name	Number of genes
Inbreds up-regulated, protective configuration	Cluster 1, ES: 2.25	GOTERM_BP_FAT	RNA processing	60
		KEGG_PATHWAY	Spliceosome	40
		GOTERM_CC_FAT	Small nuclear ribonucleoprotein complex	22
	Cluster 2: ES: 2.04	GOTERM_BP_FAT	RNA localization	20
		GOTERM_BP_FAT	Nucleocytoplasmic transport	19
		GOTERM_BP_FAT	mRNA export from nucleus	11
	Cluster 3: ES: 1.76	GOTERM_CC_FAT	Extracellular region	46
		UP_SEQ_FEATURE	Signal peptide	44
		SP_PIR_KEYWORDS	Glycoprotein	25
	Cluster 4, ES: 1.44	GOTERM_BP_FAT	Cell surface receptor linked signal transduction	24
		GOTERM_MF_FAT	Hormone activity	16
		GOTERM_BP_FAT	G-protein coupled receptor protein signaling pathway	11
Inbreds down-regulated, protective configuration	Cluster 1, ES: 2.36	GOTERM_BP_FAT	Phosphate metabolic process	121
		GOTERM_CC_FAT	Mitochondrion	116
		GOTERM_BP_FAT	Energy derivation by oxidation of organic compounds	55
	Cluster 2, ES: 2.03	GOTERM_MF_FAT	Nucleotide binding	149
		GOTERM_MF_FAT	ATP binding	101
		INTERPRO	Protein kinase, ATP binding site	40
	Cluster 3, ES: 1.44	GOTERM_BP_FAT	Protein amino acid phosphorylation	50
		INTERPRO	Serine/threonine protein kinase-related	35
		UP_SEQ_FEATURE	Active site:Proton acceptor	25

Table S1 (cont.)

Inbreds up-regulated, non-protective configuration	Cluster 1, ES: 1.35	SMART	JHBP	5
		INTERPRO	Hormone binding	5
		INTERPRO	Odorant binding protein	5

Cluster annotation analysis of the probe sets showing the most extreme Student's *t* values in the test of inbreds' *vs.* controls' expression (1846 and 1860 probes for the positive and negative *t* values respectively), using as background all probes in the same expression pattern. The lists of functional terms shown are not exhaustive, we chose three informative and less redundant terms in each cluster. No significant clusters were found in the analysis of down-regulated probes having non-protective configurations. ES: Enrichment Score.