Gene Ontology Analyses - Supplemental Data

Using the GOTree Machine web application, the 214 differentially expressed genes were categorized as being associated with specific biological processes, molecular functions and cellular compartments. Statistically significant over represented biological processes were determined using the hypergeometric test.
Downregulated Cellular Compartments

Gene count

- mitochondrion
- cytoplasmic part
- cytoplasm
- mitochondrial part
- mitochondrial membrane
- organelle inner membrane
- mitochondrial inner membrane
- organelle envelope
- organelle membrane
- envelope
- endoplasmic reticulum
- endoplasmic reticulum part
- cytosol
- endoplasmic reticulum membrane
- nuclear envelope-endoplasmic reticulum

P-Value

Gene Count  adjP
Upregulated Cellular Compartments

Gene count

P-Value

cytoplasmic part
vacuole
cytoplasm
vesicle
lytic vacuole
lysosome
cytoplasmic vesicle
apical part of cell
intracellular part
organelle

Gene Count
adjP
Upregulated Biological Processes

Gene count

- immune system process
- response to chemical stimulus
- response to organic substance
- inflammatory response
- response to stimulus
- response to steroid hormone stimulus
- regulation of immune system process
- immune response
- response to hormone stimulus
- positive regulation of cellular process

P-Value

Gene Count
adjP
Downregulated Molecular Functions

- oxidoreductase activity
- catalytic activity
- cofactor binding
- coenzyme binding
- oxidoreductase activity, acting on the CH-CH...
- electron carrier activity
- oxidoreductase activity, acting on CH-OH...
- iron ion binding
- identical protein binding
- protein homodimerization activity
Upregulated Molecular Functions

- protein binding
- carbohydrate binding
- transcription factor binding
- receptor binding
- hydrolase activity, acting on ester bonds
- transcription factor activity
- ATP binding
- transporter activity
- substrate-specific transporter activity
- nucleic acid binding