

Table 2

Functional classification of differentially expressed genes (DEGs) using PANTHER ontologies: Over- or under-represented biological processes separating delayed graft function (DGF) and primary graft function (PF) as derived on the level of differential gene expression by t-test and SAM. Categories are ranked by the p-value (comparison of expected number of genes and observed number of genes in each biological process) indicating the relevance of a particular process.

Biological Process	t-test (n=84)		SAM (n=39)	
	number of genes	p-value	number of genes	p-value
DEGs down-regulated in DGF enriched processes				
Transport	20	<0.001	8	0.001
Lipid, fatty acid and steroid metabolism	12	<0.001	5	0.006
Amino acid metabolism	7	<0.001	2	0.049
Steroid hormone metabolism	4	<0.001	2	0.002
Steroid metabolism	6	<0.001	3	0.003
Ion transport	9	<0.001	-	-
Coenzyme and prosthetic group metabolism	5	<0.001	3	0.003
Amino acid transport	3	0.001	-	-
Carbohydrate metabolism	8	0.001	-	-
Fatty acid metabolism	4	0.004	-	-
Other amino acid metabolism	2	0.005	-	-
Cation transport	6	0.005	-	-
Electron transport	4	0.010	-	-
Vitamin/cofactor transport	2	0.011	-	-
Other polysaccharide metabolism	3	0.012	-	-
Cell adhesion	6	0.017	-	-
Homeostasis	3	0.028	-	-
Extracellular transport and import	2	0.028	-	-
Anion transport	2	0.034	-	-
Sulfur metabolism	2	0.035	-	-
Proteolysis	7	0.036	-	-
Other developmental process	2	0.042	-	-
depleted processes				
Nucleoside, nucleotide and nucleic acid metabolism	5	0.042	-	-
Intracellular protein traffic	0	0.043	-	-
mRNA transcription	2	0.047	-	-
DEGs up-regulated in DGF enriched processes				
Blood circulation and gas exchange	2	<0.001	-	-
Blood clotting	2	<0.001	-	-
Immunity and defense	3	0.009	-	-