14hpi (Rings)

- Established and putative Maurers clefts proteins (MPM)
- Gluconeogenesis (MPM)
- Interactions between modified host cell membrane and endothelial cell (MPM)
- Fatty acid metabolism (KEGG)
- Established and putative Maurers clefts proteins (MPM)

Nominal P-value = 0.000
FDR q-value = 0.001
NES = 2.38

Nominal P-value = 0.000
FDR q-value = 0.001
NES = 2.28

Nominal P-value = 0.000
FDR q-value = 0.006
NES = 2.06

Nominal P-value = 0.001
FDR q-value = 0.015
NES = 1.99

174 genes with SD > mean SD + 2SD (SD)

26hpi (Trophozoites)

- Established and putative Maurers clefts proteins (MPM)
- Subcellular localization of proteins involved in invasion (MPM)
- Interactions between modified host cell membrane and endothelial cell (MPM)
- Gluconeogenesis (MPM)
- Methionine and polyamine metabolism (MPM)
- Genes coding for GPI-anchored membrane proteins (MPM)

Nominal P-value = 0.000
FDR q-value = 0.001
NES = 2.28

Nominal P-value = 0.000
FDR q-value = 0.003
NES = 2.22

Nominal P-value = 0.000
FDR q-value = 0.002
NES = 2.17

Nominal P-value = 0.000
FDR q-value = 0.005
NES = 2.08

Nominal P-value = 0.000
FDR q-value = 0.025
NES = 1.91

Nominal P-value = 0.000
FDR q-value = 0.048
NES = 1.83

Nominal P-value = 0.000
FDR q-value = 0.222
NES = 1.62

176 genes with SD > mean SD + 2SD (SD)

34hpi (Schizonts)

- GTPase activity (GO)
- Subcellular localization of proteins involved in invasion (MPM)
- Established and putative Maurers clefts proteins (MPM)
- Hemoglobin digestion and ferrichrotoporphyrin IX polymerization (MPM)
- Genes coding for GPI-anchored membrane proteins (MPM)
- Chaperone-assisted protein folding (MPM)
- Interactions between modified host cell membrane and endothelial cell (MPM)

Nominal P-value = 0.003
FDR q-value = 0.093
NES = 1.93

Nominal P-value = 0.000
FDR q-value = 0.061
NES = 1.88

Nominal P-value = 0.001
FDR q-value = 0.155
NES = 1.71

Nominal P-value = 0.020
FDR q-value = 0.161
NES = 1.69

Nominal P-value = 0.006
FDR q-value = 0.228
NES = 1.64

Nominal P-value = 0.024
FDR q-value = 0.223
NES = 1.61

192 genes with SD > mean SD + 2SD (SD)