Supplemental Table 3

Gene Families Upregulated Following OPB -/- Infection

Protein Family	Count	Fold Change	P-Value
Cytokine secretion	3	15.36	0.014
Positive regulation of Ras protein signal transduction	4	14.62	0.002
Positive regulation of cell adhesion	4	11.37	0.004
Positive regulation of small GTPase mediated signal transduction	4	10.24	0.006
Regulation of protein secretion	4	8.53	0.010
Cytokines and Inflammatory Response	3	8.09	0.047
Positive regulation of phosphorylation	4	7.87	0.012
Positive regulation of phosphate metabolic process	4	7.31	0.015
Protein secretion	6	6.40	0.002
Inositol or phosphatidylinositol phosphatase activity	5	4.46	0.024
Ubiquitin thiolesterase activity	6	3.48	0.027
Ubiquitin-specific protease activity	6	3.33	0.033
Small conjugating protein-specific protease activity	6	3.19	0.038
Protein ubiquitination	6	3.13	0.041
Thiolester hydrolase activity	7	3.01	0.027
Vasculature development	13	2.77	0.002
Growth factor activity	7	2.73	0.042
Blood vessel development	12	2.58	0.006
Blood vessel morphogenesis	10	2.56	0.016

Supplemental Table 3. Gene families upregulated following OPB -/- infection. DAVID analysis was performed to identify families and pathways of proteins that were significantly upregulated in macrophages infected by OPB knockout *Leishmania*. Protein families that were over-represented in the hit set with a fold change greater than 2.5 and a p-value less that 0.05 are listed.