

Table 3:

Probe set	Baseline expression [§]	Fold-change	p-value	Annotation [#]
Potentially virulence associated				
2.m00545_at ^{*f}	4.12	0.27	0.033	cysteine proteinase, putative (GO:0006508)
52.m00148_at	0.96	0.46	0.018	lysozyme, putative
1.m00663_at	6.21	0.36	0.006	myosin calcium-binding light chain, putative (GO:0005509)
Protein kinases				
35.m00259_at	1.76	0.48	0.013	protein kinase, putative (GO:0005524)
67.m00091_x_at ^f	3.42	0.37	0.033	protein kinase, putative (GO:0005524)
99.m00190_s_at	0.39	0.46	0.040	protein kinase, putative (GO:0006468)
466.m00033_x_at	0.51	0.47	0.003	protein kinase, putative (GO:0005524)
264.m00068_at	2.29	0.44	0.029	protein kinase, putative (GO:0005524)
GTPases				
106.m00140_at	2.39	0.48	0.025	Rap Ran GTPase activating protein, putative
2.m00606_x_at	0.20	0.36	0.005	Rab family GTPase (GO:0005524)
226.m00092_at [*]	0.34	0.44	0.008	Rab family GTPase
30.m00257_at	4.28	0.50	0.023	Rab family GTPase (GO:0005524)
34.m00273_x_at	3.22	0.43	0.040	Rab family GTPase (GO:0005524)
71.m00153_x_at ^f	2.21	0.47	0.002	Rho family GTPase (GO:0005525)
8.m00366_s_at ^b	1.15	0.46	0.021	Rho GTPase activating protein, putative
171.m00089_at	4.88	0.35	0.044	GTPase activating protein, putative (GO:0003924)
Genes with decreased expression in <i>E. histolytica</i> Rahman compared to <i>E. histolytica</i> HM-1:IMSS				
108.m00122_at	32.12	0.21	0.036	hypothetical protein
136.m00107_at	1.20	0.38	0.030	hypothetical protein
22.m00298_at	4.12	0.43	0.002	hypothetical protein
297.m00061_at	5.00	0.35	0.010	hypothetical protein
32.m00239_at	0.93	0.46	0.039	N-acetylglucosaminyl transferase, putative
37.m00215_at	1.90	0.46	0.035	hypothetical protein
442.m00023_x_at	0.82	0.44	0.006	hypothetical protein
460.m00024_s_at ^c	2.18	0.27	0.015	hypothetical protein
Genes that overlap significantly with up-regulated genes from <i>in vivo</i> mouse model of amebic colitis (Gilchrist et al, 2006)				
15.m00302_at	4.05	0.41	0.030	hypothetical protein
2.m00545_at [*]	4.12	0.27	0.033	cysteine proteinase, putative (GO:0006508)
67.m00091_x_at	3.42	0.37	0.033	protein kinase, putative (GO:0005524)
71.m00153_x_at	2.21	0.47	0.002	Rho family GTPase (GO:0005525)
Miscellaneous				
338.m00049_s_at ^d	4.30	0.42	0.020	LIM domain protein (GO:0008270)
10.m00349_x_at	4.30	0.44	0.024	paxillin, putative (GO:0008270)
35.m00253_at	1.74	0.26	0.036	iron-sulfur flavoprotein, putative (GO:0006118)
646.m00021_s_at	0.36	0.40	0.009	iron-sulfur flavoprotein, putative
90.m00179_at	1.31	0.46	0.044	amino acid transporter, putative (GO:0006865)
139.m00118_at	3.90	0.44	0.048	histone H3, putative (GO:0005634)

[§]Baseline expression level in untreated *E. histolytica* HM-1:IMSS

Bold = RT-PCR

^{*}Bisulfite sequencing was done

^fThese genes were significantly up-regulated in *E. histolytica* HM-1:IMSS trophozoites passed through mice (Gilchrist et al, 2006)

[#]GO IDs where available are provided within parentheses

^b8.m00366_s_at also represents 58.m00170 (Rho GTPase activating protein, putative)

^c460.m00024_s_at also represents 353.m00048 (hypothetical protein) and 353.m00049 (hypothetical protein)

^d338.m00049_s_at also represents 321.m00056 (LIM domain protein)