

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

*Bisulfite sequencing was done

#GO IDs where available are provided within parentheses

^a763.m00027_s_at also represents 190.m00085 (hypothetical protein), 239.m00065 (hypothetical protein), 278.m00067 (hypothetical protein), 330.m00074 (hypothetical protein), 43.m00171 (hypothetical protein) and 458.m00061 (hypothetical protein)

^b36.m00220_s_at also represents 36.m00212 (hypothetical protein)

^c86.m00156_s_at also represents 119.m00135 (glutamine cyclotransferase, putative)

^d93.m00158_s_at also represents 153.m00091 (DNA mismatch repair protein mutS, putative)

^e472.m00058_s_at also represents 361.m00052 (hypothetical protein)

^f289.m00067_s_at also represents 180.m00106 (short chain dehydrogenase family protein)

^g54.m00234_s_at also represents 169.m00132 (hypothetical protein) and 406.m00049 (hypothetical protein)

^h48.m00224_s_at also represents 309.m00047 (acetyltransferase, putative)

Indicated by gray boxes are genes with significantly increased expression (p-value 0.0002) in *E. histolytica* Rahman compared to *E. histolytica* HM-1:IMSS