



Figure S1. Gene expression profiles of target genes

The expression levels of mRNAs analyzed by microarray hybridization at different stages of the life cycle (Miao et al. 2009) are plotted. Growing cells at three different concentrations: $\sim 1 \times 10^5$ cells/mL, $\sim 3.5 \times 10^5$ cells/mL and $\sim 1 \times 10^6$ cells/mL (Ll, Lm, and Lh, respectively); cells starved for 0, 3, 6, 9, 12, 15 and 24 hrs (S0, S3, S6, S9, S12, S15 and S24, respectively); and conjugating cells at 2, 4, 6, 8, 10 and 12 hrs post-mixing (C2, C4, C6, C8, C10 and C12, respectively) are indicated. The data were obtained from the Tetrahymena Functional Genomics Database (<http://tfgd.ihb.ac.cn/>).