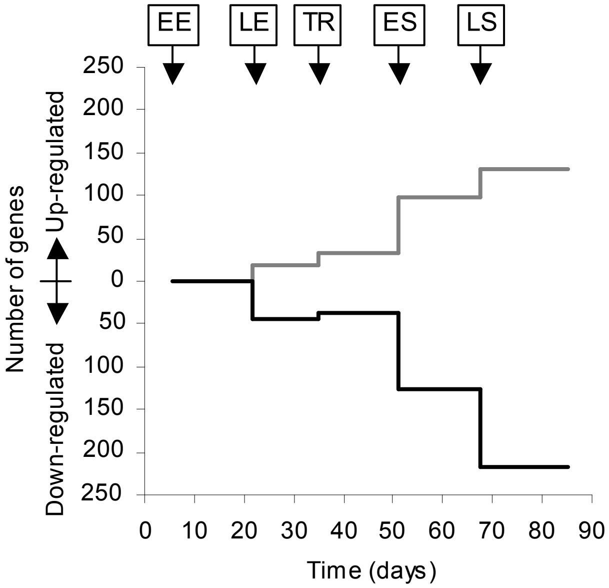

FIG S1. Total number of genes up-regulated (grey line) and down-regulated (black line) (>2-fold, FDR<0.01) at each time point relative to the expression level during the EE phase. Vertical arrows indicate time-points when cells were collected for microarray analysis. EE, early-exponential; LE, late-exponential; TR, transition; ES, early-stationary; LS, late-stationary.

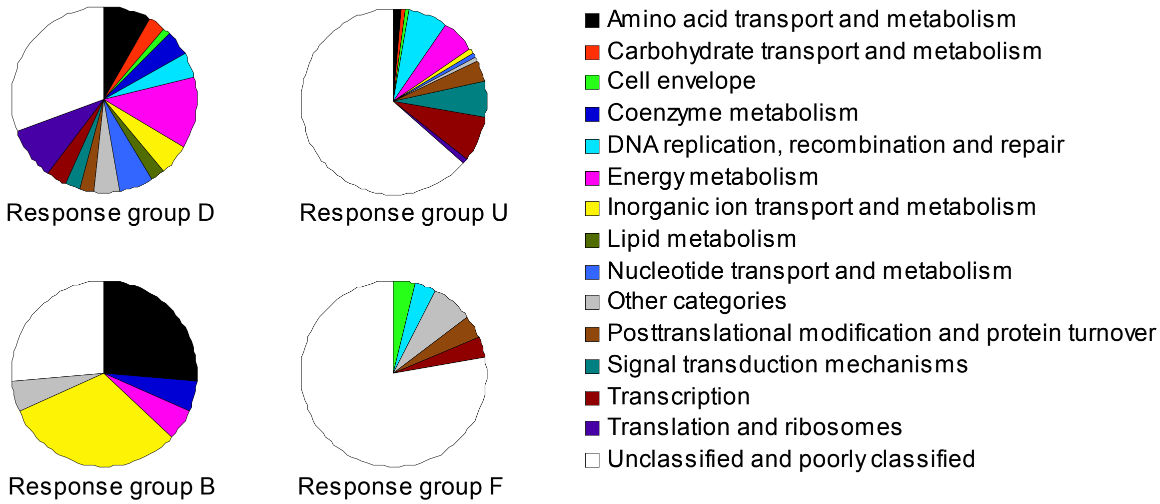

FIG S2. Distribution of clusters of orthologous gene (COG) categories within each response group. Pie areas indicate the fraction of genes from each COG category.