

Pourkarimi et al., Figure 4- figure supplement 1

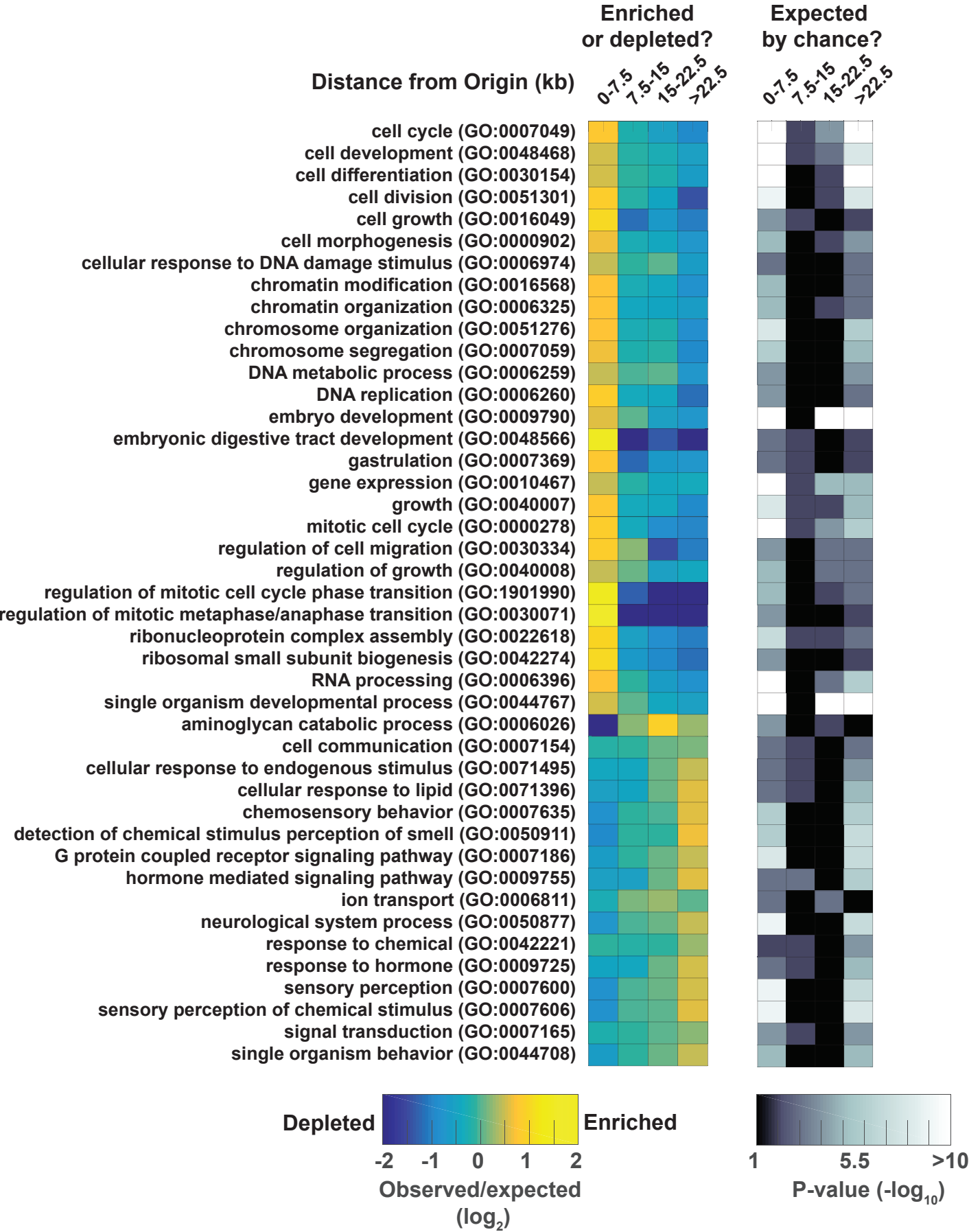


Figure 4- figure sepplement 1

Gene ontology analysis for genes at varying distances from the midpoint of a replication origin. Gene ontologies were calculated using the Gene Ontology Consortium (<http://geneontology.org/>). Select GO terms with greatest significance are shown that lie within “Biological Process” annotation datasets. Left, observed/expected \log_2 ratio is shown at varying distances from origins for each ontology term as a heatmap: color key is below – yellow indicates enrichment, blue is depletion. Right, heatmap showing the calculated p-values (hypergeometric distribution) for the data on left; color key is below.