Pourkarimi et al., Figure 4- figure supplement 2

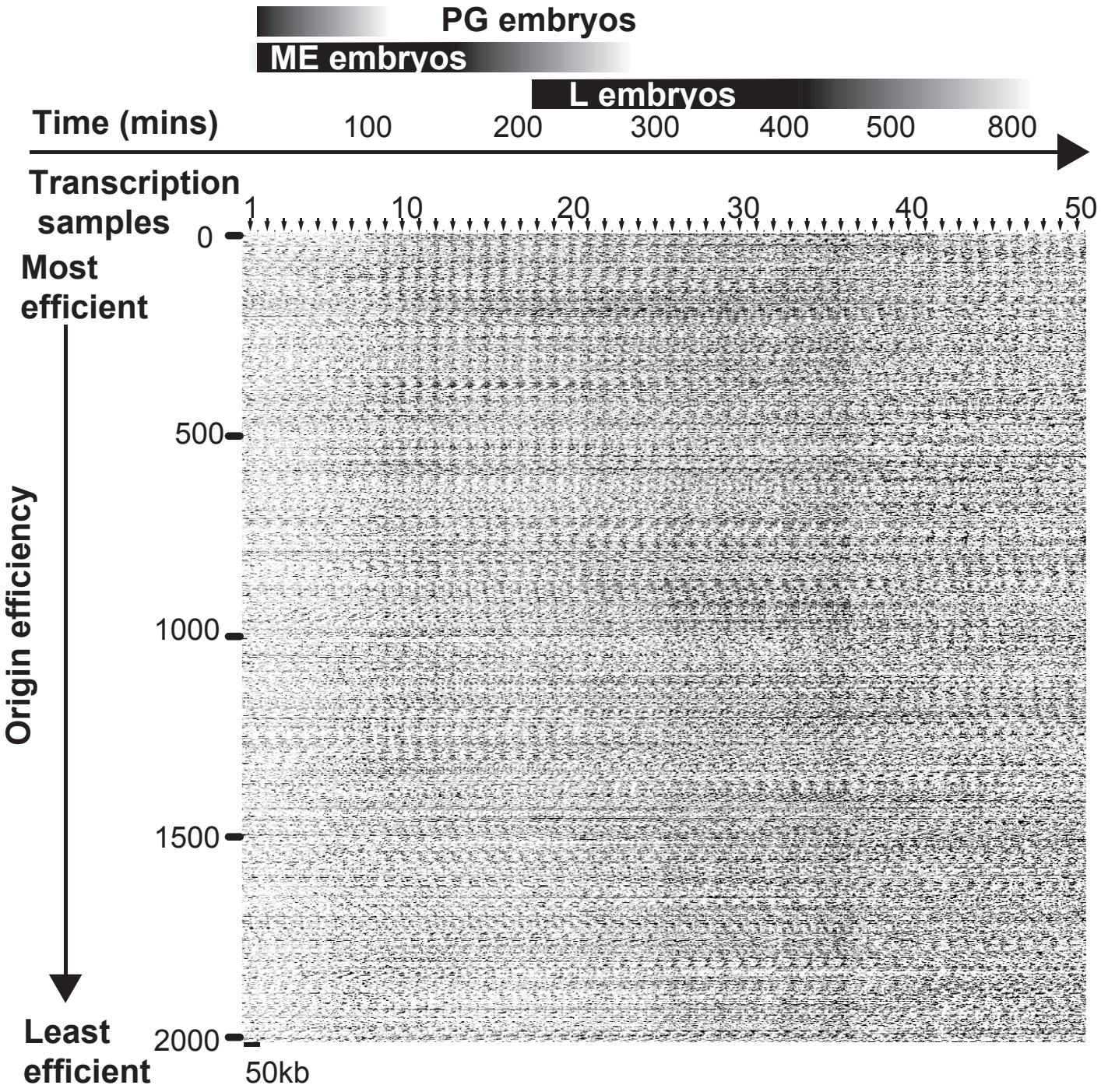

Figure 4- figure supplement 2

Heatmap showing the relationship between transcribed genes and replication origins through embryogenesis. Normalized data from each of the 50 time points from the whole embryo transcriptome (16) was plotted relative to the positions of the most efficient ~2000 replication origins. Origins are ranked from most efficient (0, top) to least efficient (2000, bottom). Genes within +/- 25kb from the origin are shaded according to their relative level of expression; origin midpoints are indicated by arrows. Sample numbers and relative time through embryogenesis are shown above.