Supplementary Figure 3 | Increase of genomic coverage and accuracy by iterative integration. Iterative integration of transcripts, derived from various growth conditions, with RNA polymerase binding regions (RBRs) resulted in increased genomic coverage and accuracy **(a, b, c)**, genes of interest are highlighted in red. Iteration of data from various growth conditions (log phase, red; heat-shocked, blue; stationary phase, orange) also allowed for determination of condition-specific transcripts, such as *yjcC* **(b)** and *ybaE* **(c)** from stationary growth phase, and *soxR* **(b)** from heat-shocked cells.