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Mapping the whole *Escherichia coli* K-12 transcriptome at single nucleotide resolution

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We have examined the whole transcriptome of *Escherichia coli* K-12 at the single nucleotide level by ultra-high-throughput RNA sequencing (RNA-Seq). Cells were grown in batch cultures in MOPS glucose minimal medium at 37°C under rigorously controlled conditions in a fermenter. Samples were taken throughout logarithmic (log) growth phase, at the end of the log growth phase, and following the transition into stationary phase. RNAs were subjected to RNA-Seq on an ABI Solid 4 platform; we obtained more than 310 million paired-ends, 75-bp reads. Excellent correlation exists among replicate logarithmic phase samples; and the data are generally of very high quality. Our data allowed identification of transcription start sites (TSS) for nearly all previously recognized genes turned on in the stationary phase and revealed a number of previously unknown genes that are similarly induced. We also found a large number of previously uncharacterized operons and unrecognized members of known operons, as well as many instances of weak transcription termination resulting in read-through transcription of downstream genes or generation of anti-sense RNA from adjacent coding sequences. We observed many short anti-sense RNAs in regulatory regions that appear to arise from independent TSSs not associated with regulatory regions of neighboring genes. All of these features have been cataloged.

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