SUPPLEMENTAL MATERIALS

Figure S1: Reproducibility between sequencing lanes.
A) Scatter plot of read counts for each ERCC transcript in two different lanes of one human RNA-Seq library with 2% ERCC spike-ins (K562 A+ Repl.1 library 7). B) Scatter plot of fold deviation between lanes versus read counts for a given ERCC RNA. C) Distribution of regression residuals from a Poisson log-linear model

Figure S2: Histograms of ERCC control GC-content and RNA length.

Table S1
Summary characteristics of ERCC RNAs used in this study.

Table S2
All RNA-seq libraries used in this study with RNA sample information, accession numbers and mapping statistics.

ERCC sequences
Pairwise alignment of the ERCC reference sequence used in this study to the corresponding genbank records (indicated in Table S1)

Supplemental Methods