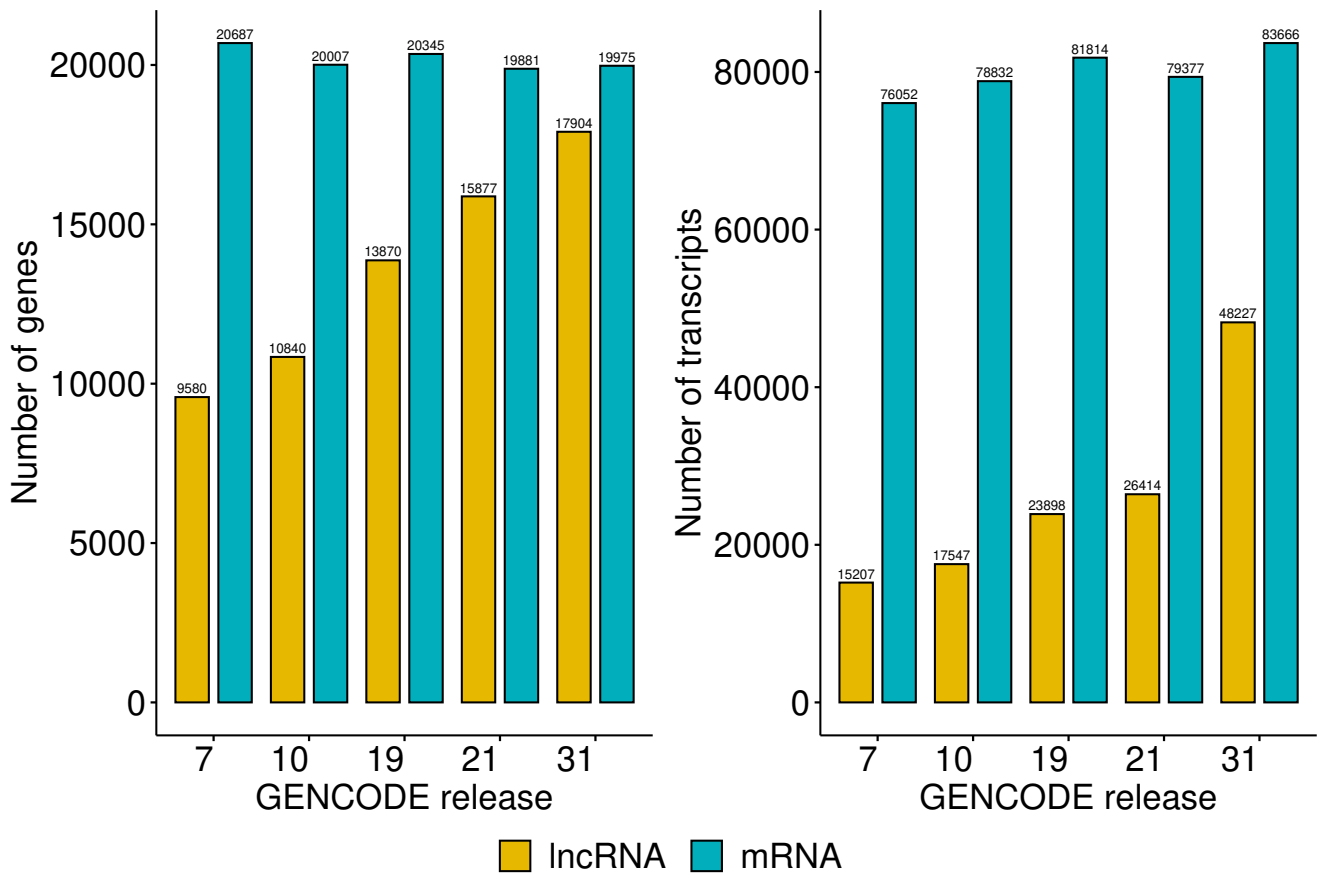# Additional file 1: Supplementary figures
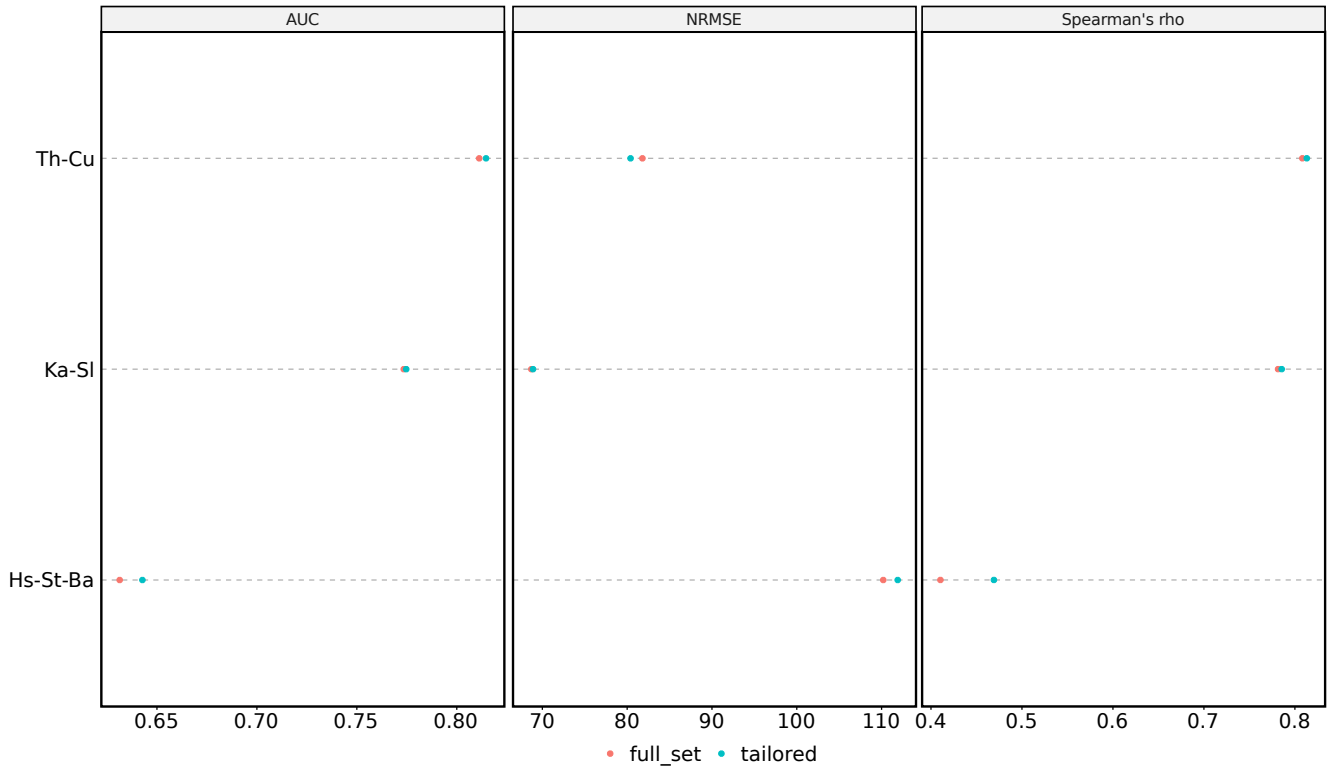
Supplementary figures

Figure S1. Growth of GENCODE gene annotation. The left and right panels show the number of gene loci and transcripts annotated in GENOCDE gene annotation, respectively. Only the past major releases and the latest release 31 at the time of writing are included. Colors indicate RNA types.

Figure S2. Comparison of metrics with full set and tailored annotation on DE step. Three metrics evaluated analysis results with full set gene annotations and tailored gene annotations: AUC, RMSE, and Spearman's rho. These metrics were calculated for all transcripts expressed. Colors indicate the annotation used. Abbreviations indicate combinations of the following tools: Hs-St-Ba; HISAT-StringTie-Ballgown, Ka-Sl; Kallisto-Sleuth, Th-Cu; Tophat2-Cufflinks. For STAR-RSEM-EBSeq has not been tested because the analysis with the tailored annotation failed.