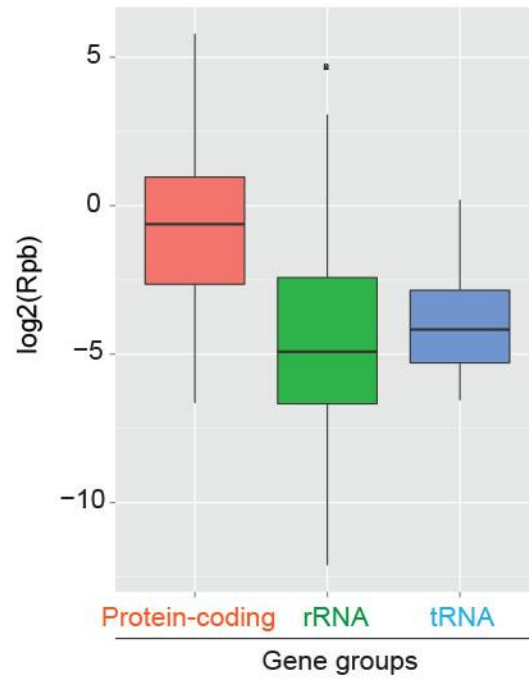## Supplementary Figure 1

Supplementary Figure 1

mNET-seq vs GRO-seq

Correlation between log2 (RPM) of Total Pol II mNET-seq and GRO-seq data for genome windows of 500kb. Both samples show very good correlation (Pearson's Correlation Coeficient (PCC) = 0.93, p-value < 2.2e-16). GRO-seq data (GEO accession number GSM1518913) and RNA-seq data used to determine gene expression (GEO accession number GSM1155630) were from previously published studies (Andersson, R. *et al. Nat. Commun.* **5**, 5336 (2014); Lacoste, N. *et al. Mol. Cell* **53**, 631-644 (2014)).

Supplementary Figure 2

Supplementary Figure 2

mNET-seq Pol II specificity

Boxplot distribution comparison of log2 reads per base (Rpb) values for Total RNA Pol II mNET-seq in expressed protein coding, tRNA and rRNA genes. For protein coding genes, only the region [TSS, TSS+100] is used, to consider a region without reads corresponding to splicing intermediates (which appear at the end of exons), and also to use a region with a size similar to that of tRNA and rRNA genes to avoid any size bias when normalizing.