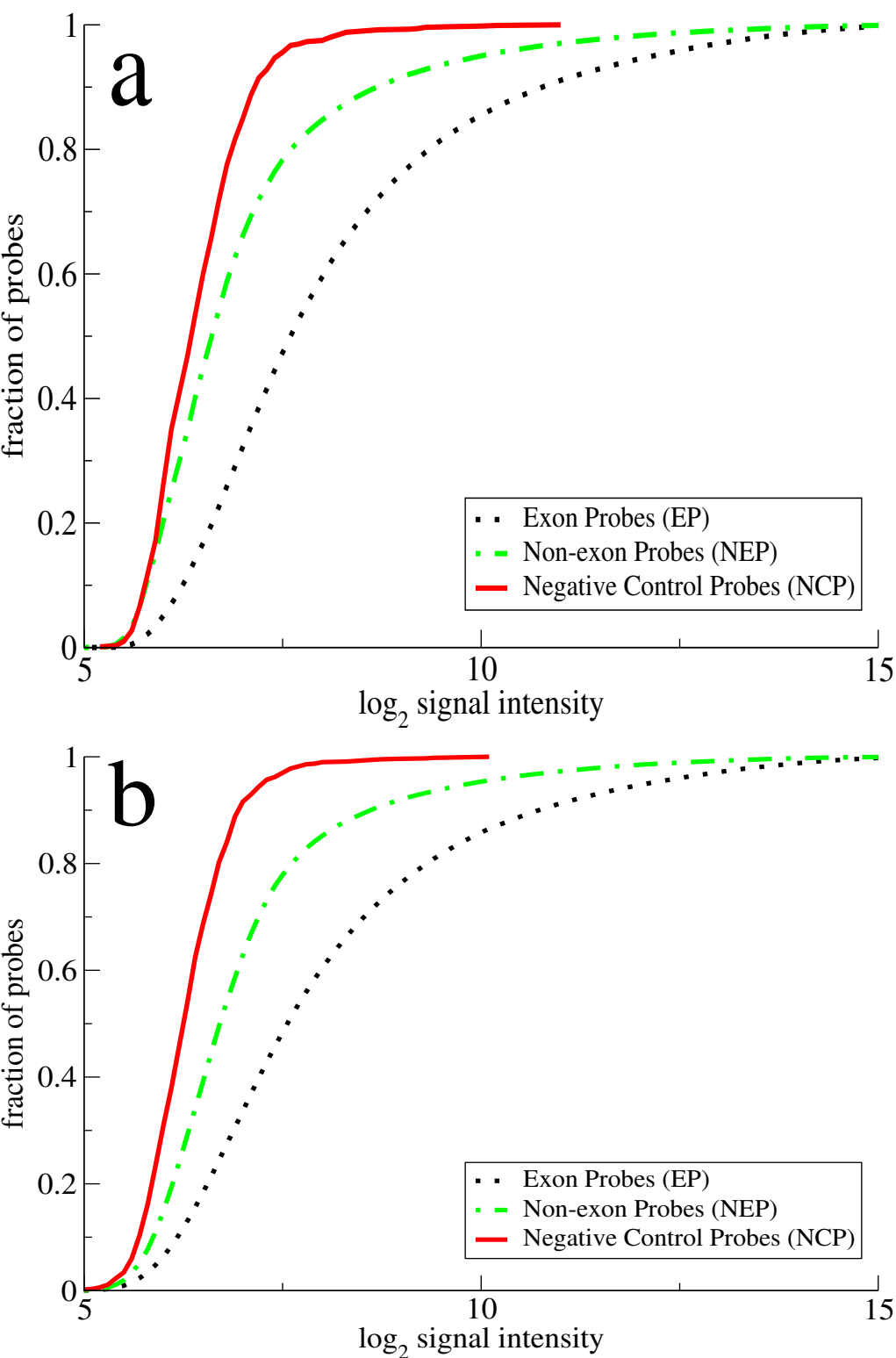
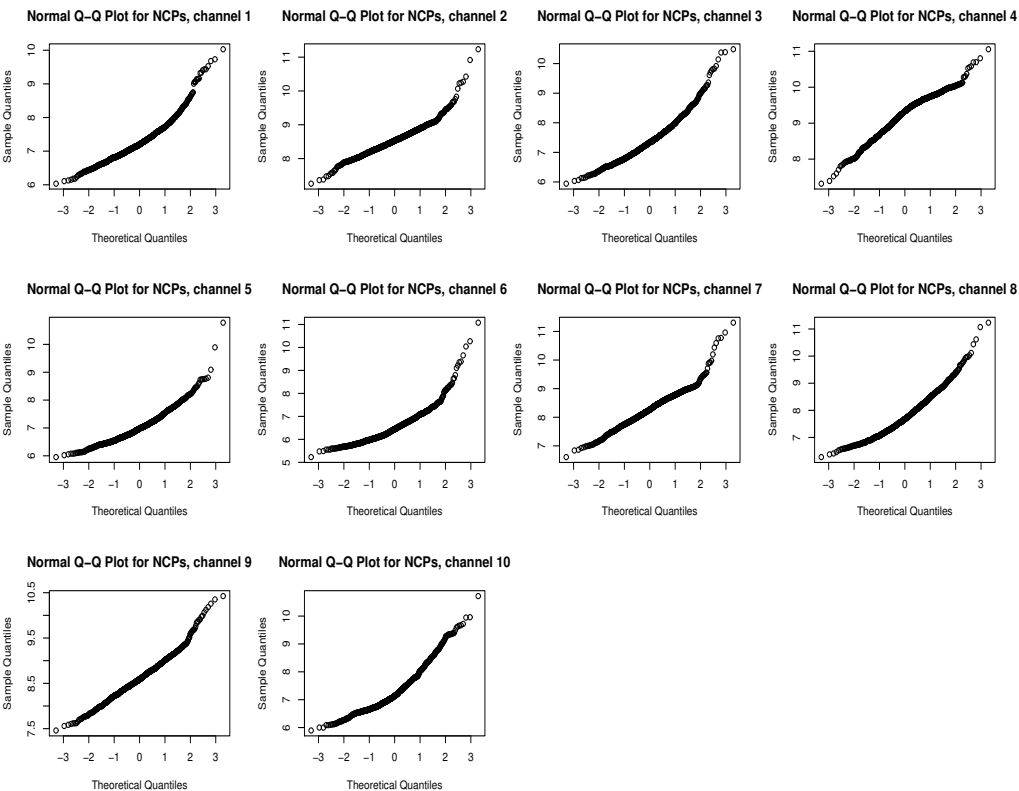


Figure S1



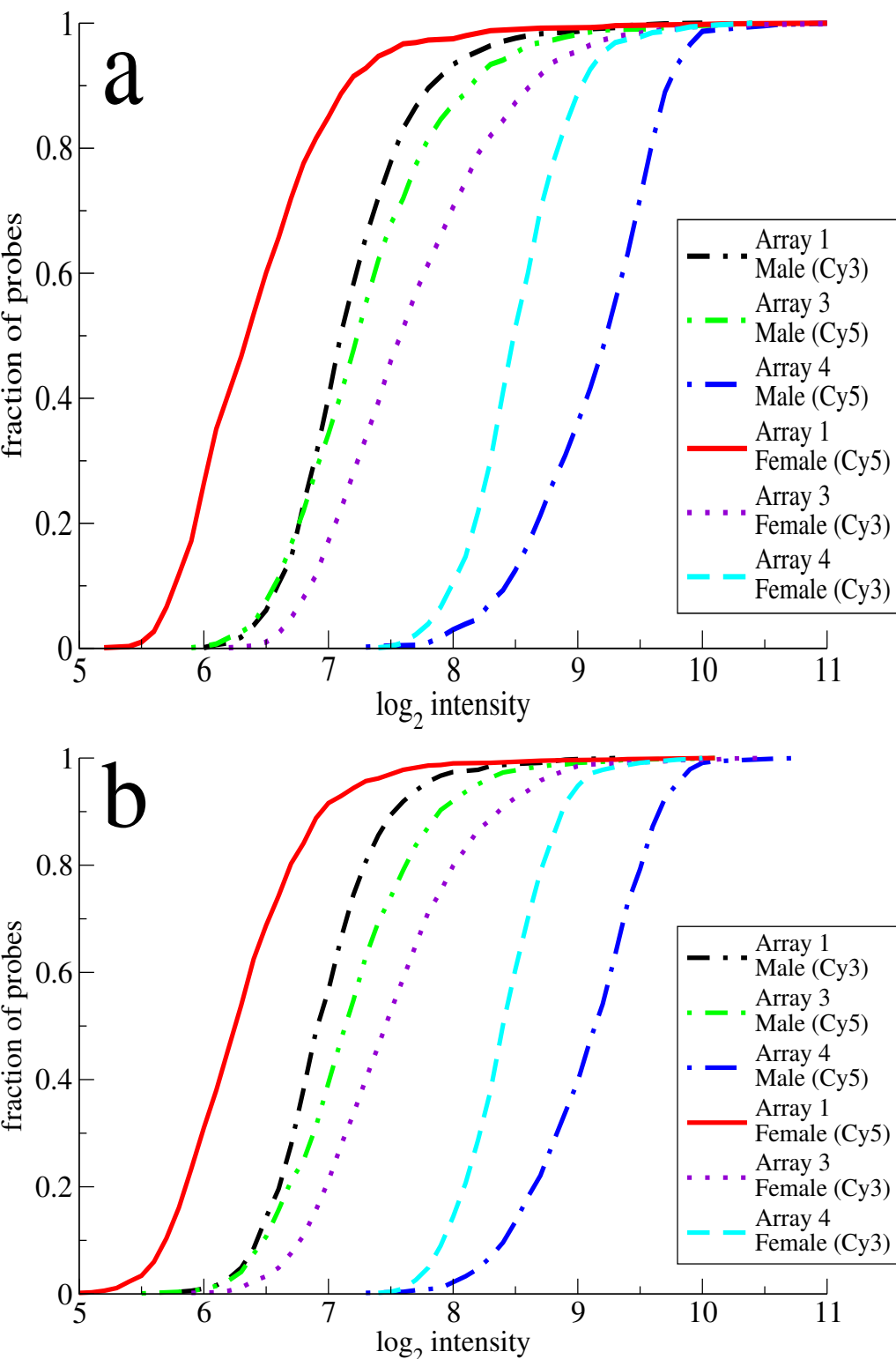
Probe population-specific differences in signal intensity are not explained by variation in probe sequence composition. Shown are cumulative distribution functions of signal intensities for annotated exons (EPs), non-exon regions (NEPs) and negative control probes (NCPs) in a representative channel either without (a) or with (b) correction using the Full Position-Specific Model. (Note that (a) is identical to Figure 1 in the main text.)

Figure S2



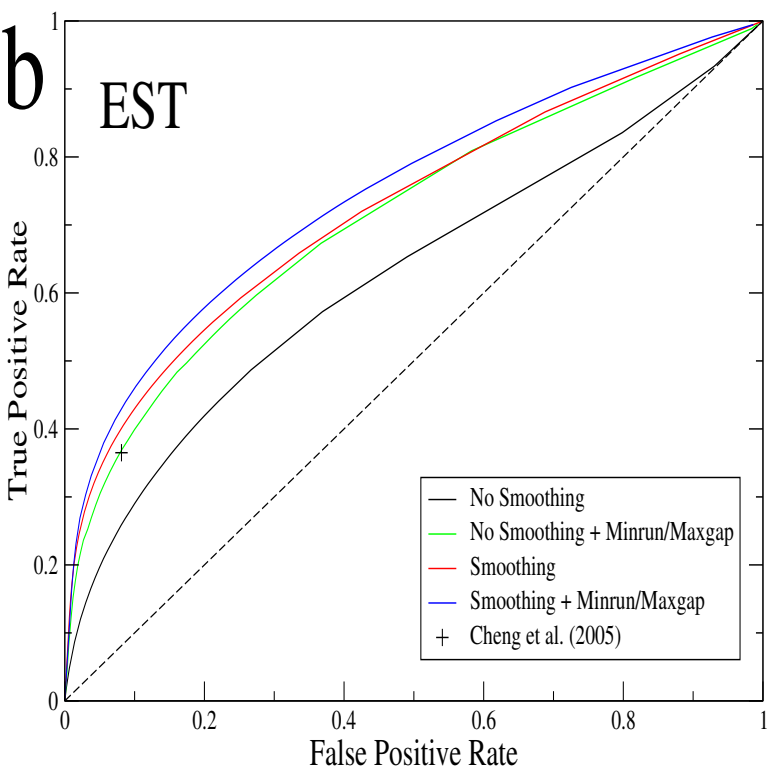
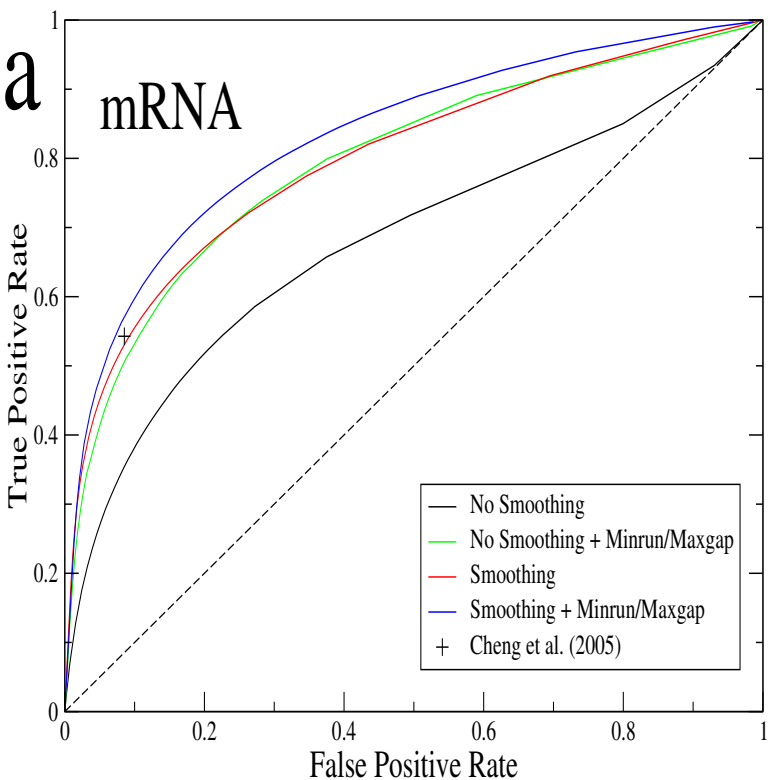
Quantile–Quantile plots comparing NCP signal intensities for different channels to a random normal distribution. All channels show deviations from normality.

Figure S3



Variation between channels in the distribution of negative control probe (NCP) signal intensities remain after sequence correction. Cumulative distribution functions of signal intensities are shown for NCPs in different channels either without (a) or with (b) correction using the Full Position-Specific Model. (Note that (a) is identical to Figure 3 in the main text.)

Figure S4



ROC curve showing true positive rate vs. false positive rate relative to mRNA (a) and EST (b) transcripts annotated in the UCSC database. The "+" symbol corresponds to the transfrags defined by Cheng et al. [10]. Lines correspond to our algorithm as applied with/without neighborhood smoothing and with/without minrun/maxgap post-processing.