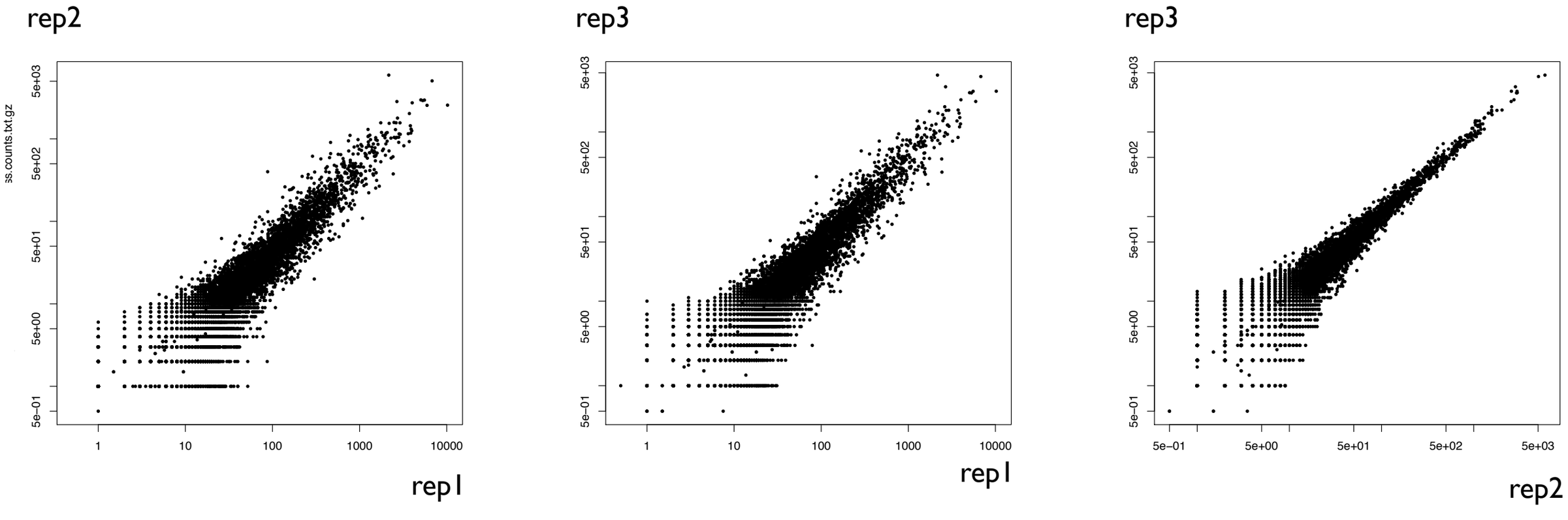


Figure S1: Scatter plots of gene expressions across the CAGE libraries (different batches) with the same barcodes. Individual dots represent quantified levels of transcript abundances.

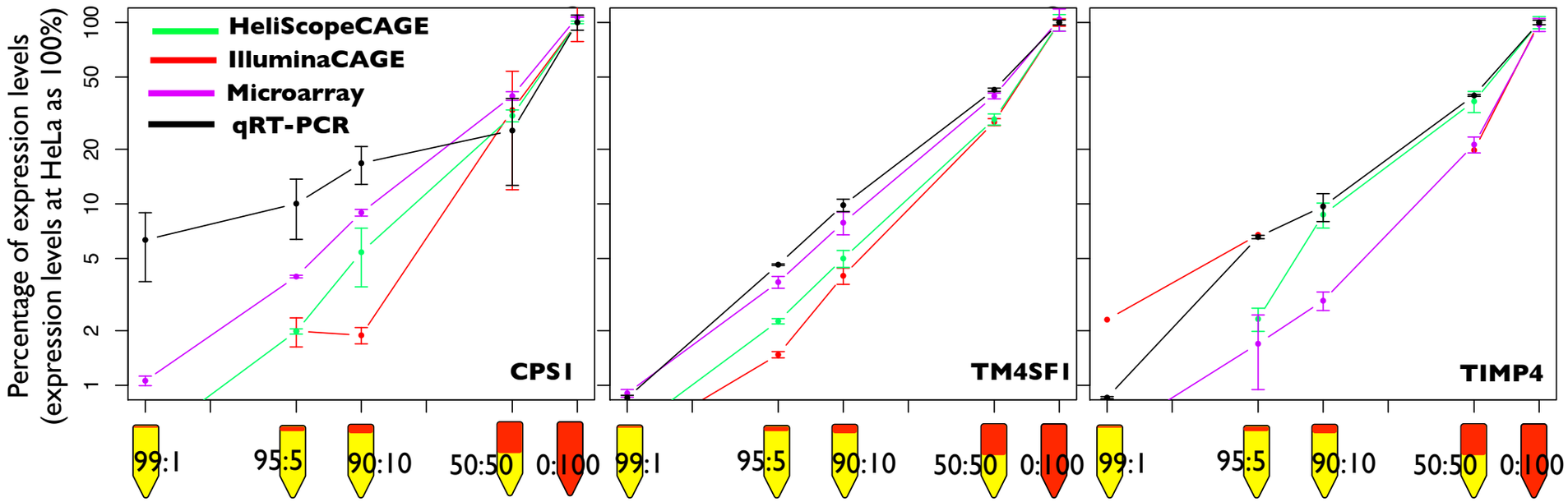


Figure S2: Quantification of gene abundance with different technologies. Different color represent different protocols, and x-axis corresponds to mixing ratio of HeLa cells.

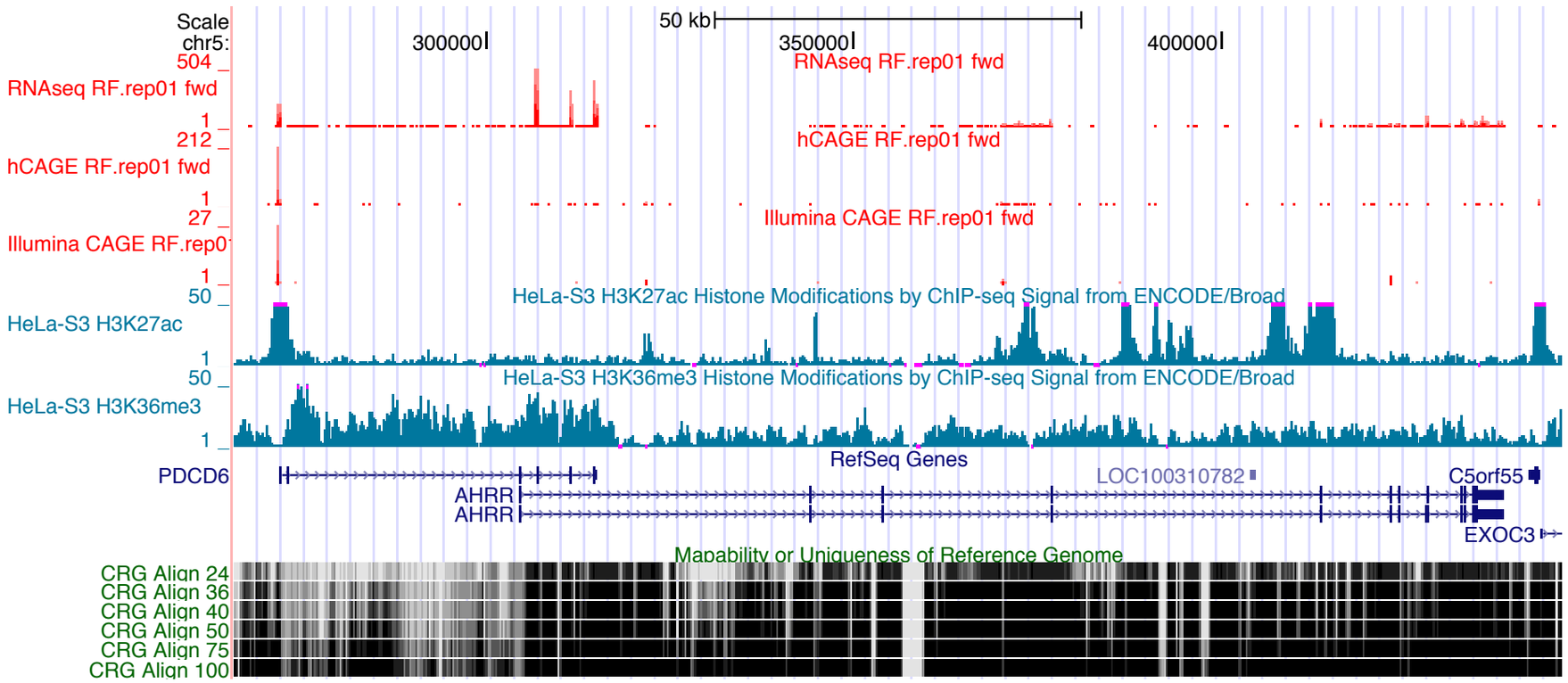


Figure S3: CAGE, RNA-seq, and chromatin marks at AHRR loci

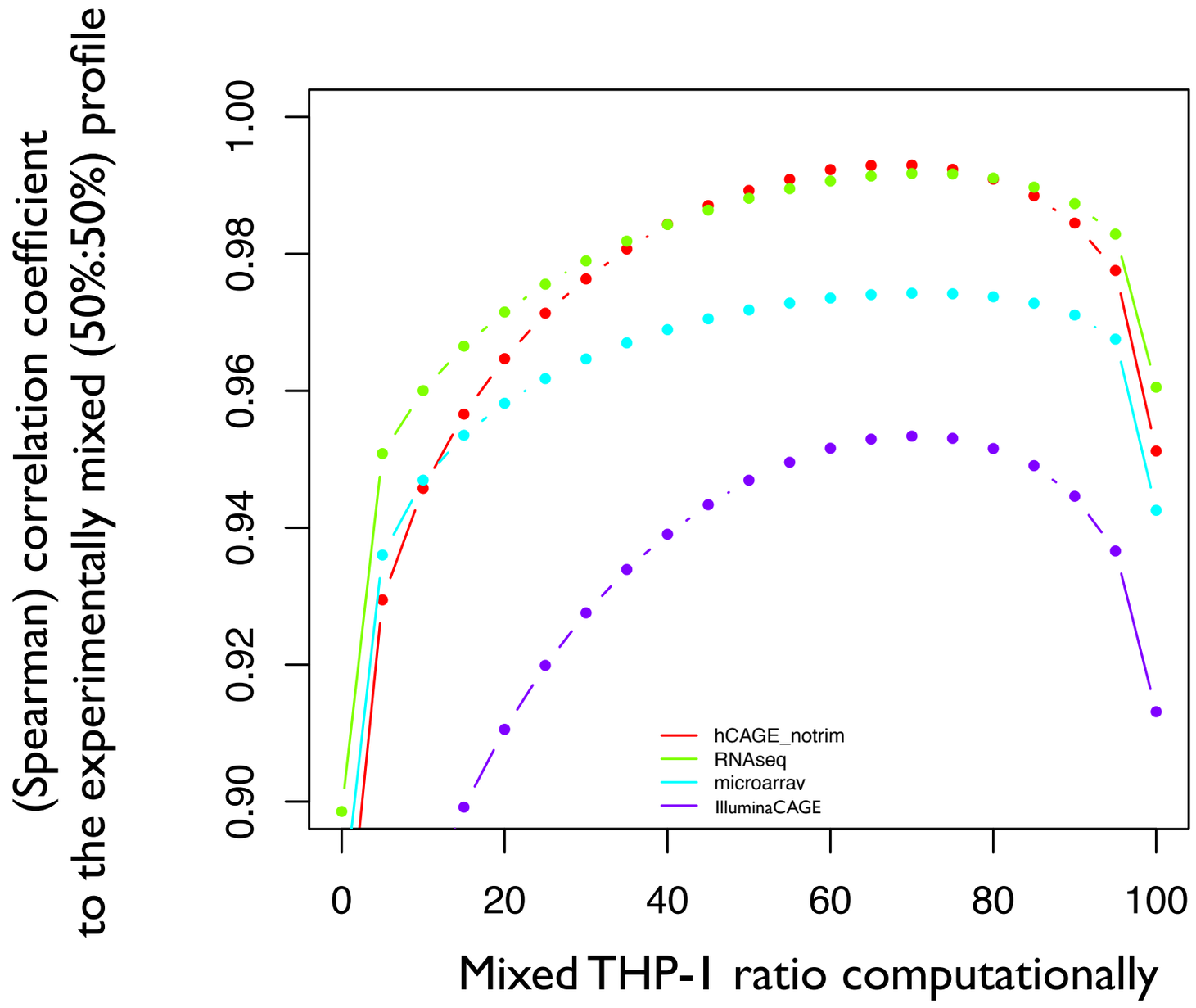


Figure S4: Comparison of computationally and experimentally mixed profiles

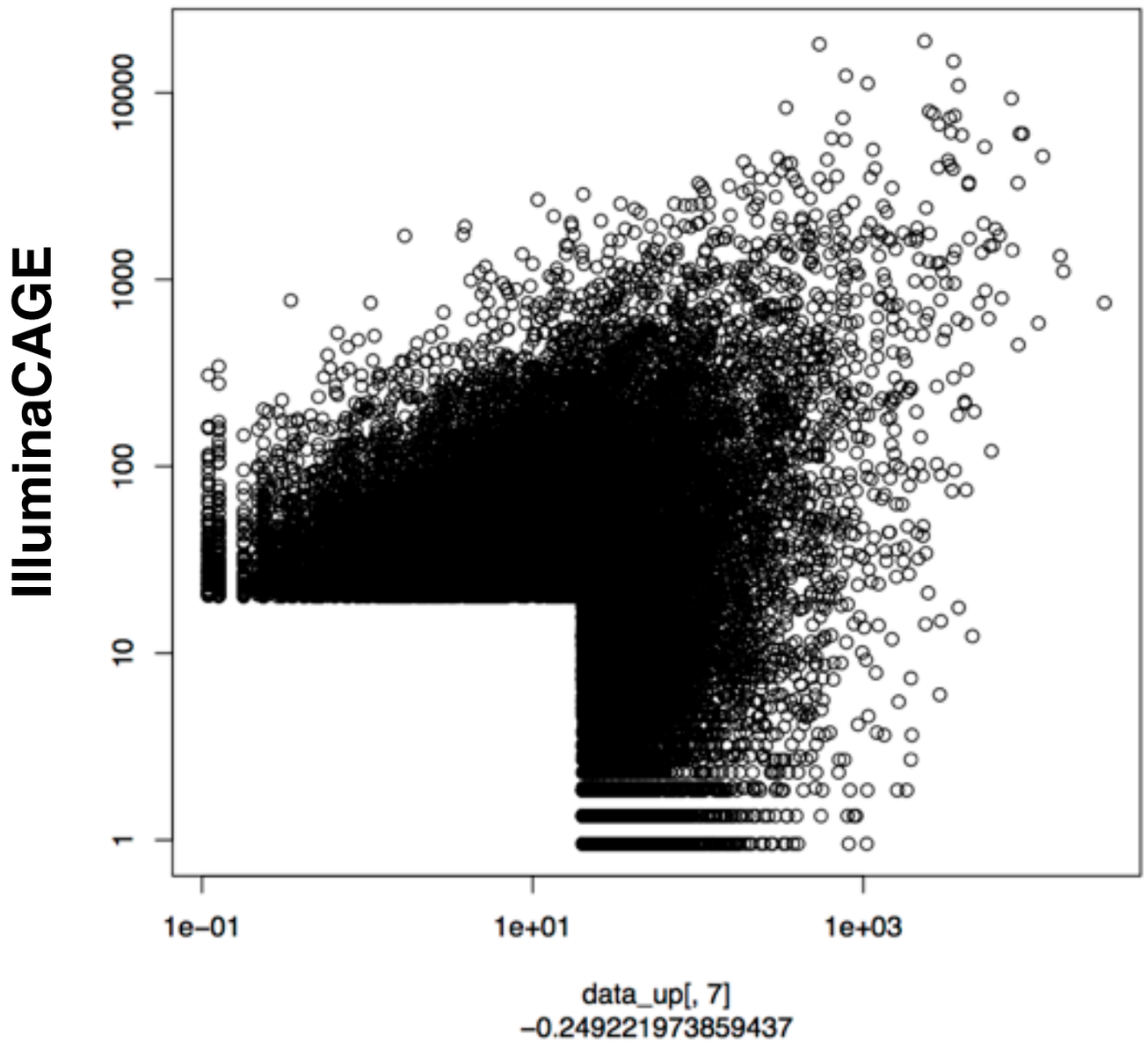


Figure S5: Scatter plot of the TSS activities in THP-1 cells,
Only TSSs with >50tpm at either technologies are shown.

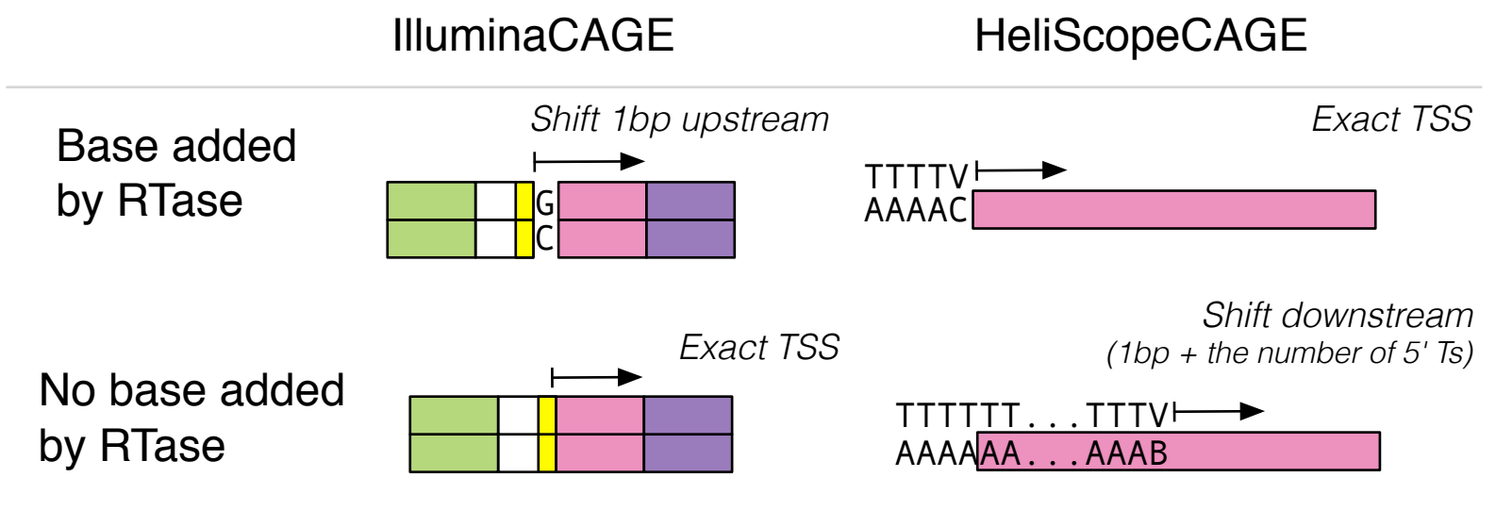


Figure S6: Schematic view of how CAGE platforms identify actual TSSs accurately or in a shift manner.

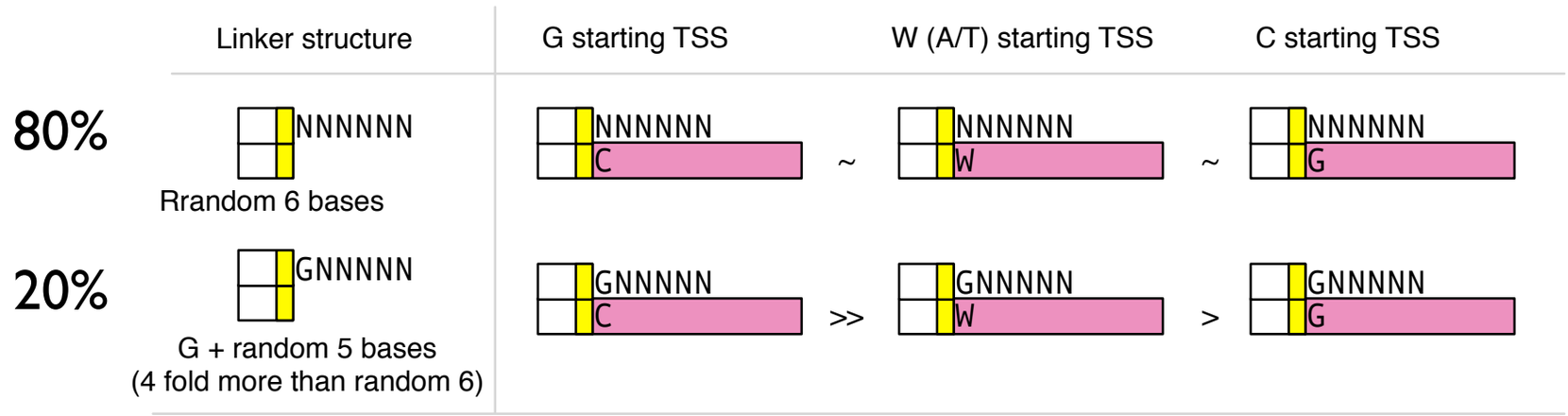


Figure S7: 5‘Linker structure in IlluminaCAGE and their ligation efficiencies that potentially affect to skewed TSS profiles

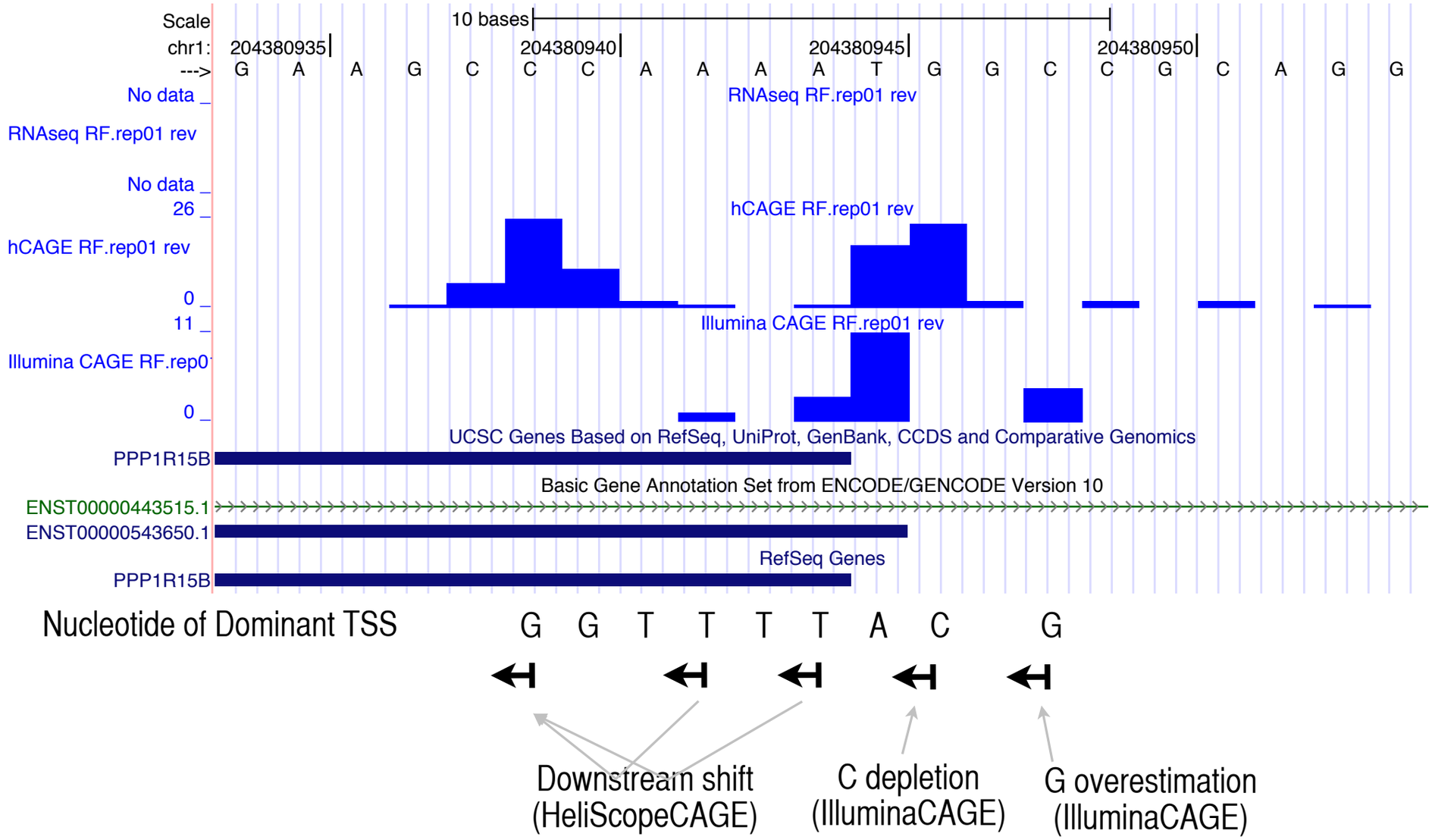


Figure S8: TSS activities at a single base pair resolution between IlluminaCAGE and HeliScopeCAGE at PPP1R15B locus

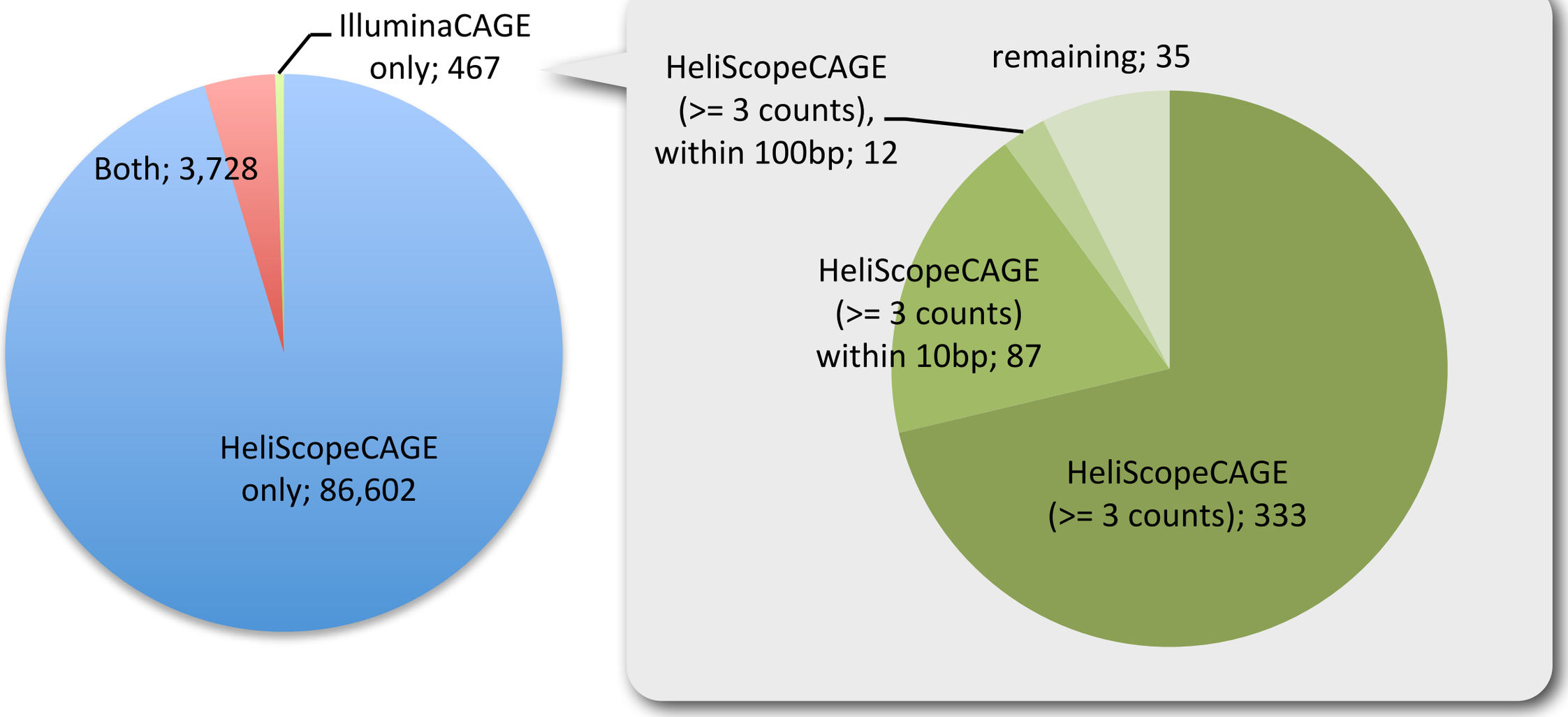


Figure S9: overlap of identified TSSs with >10 counts are shown as pie chart.

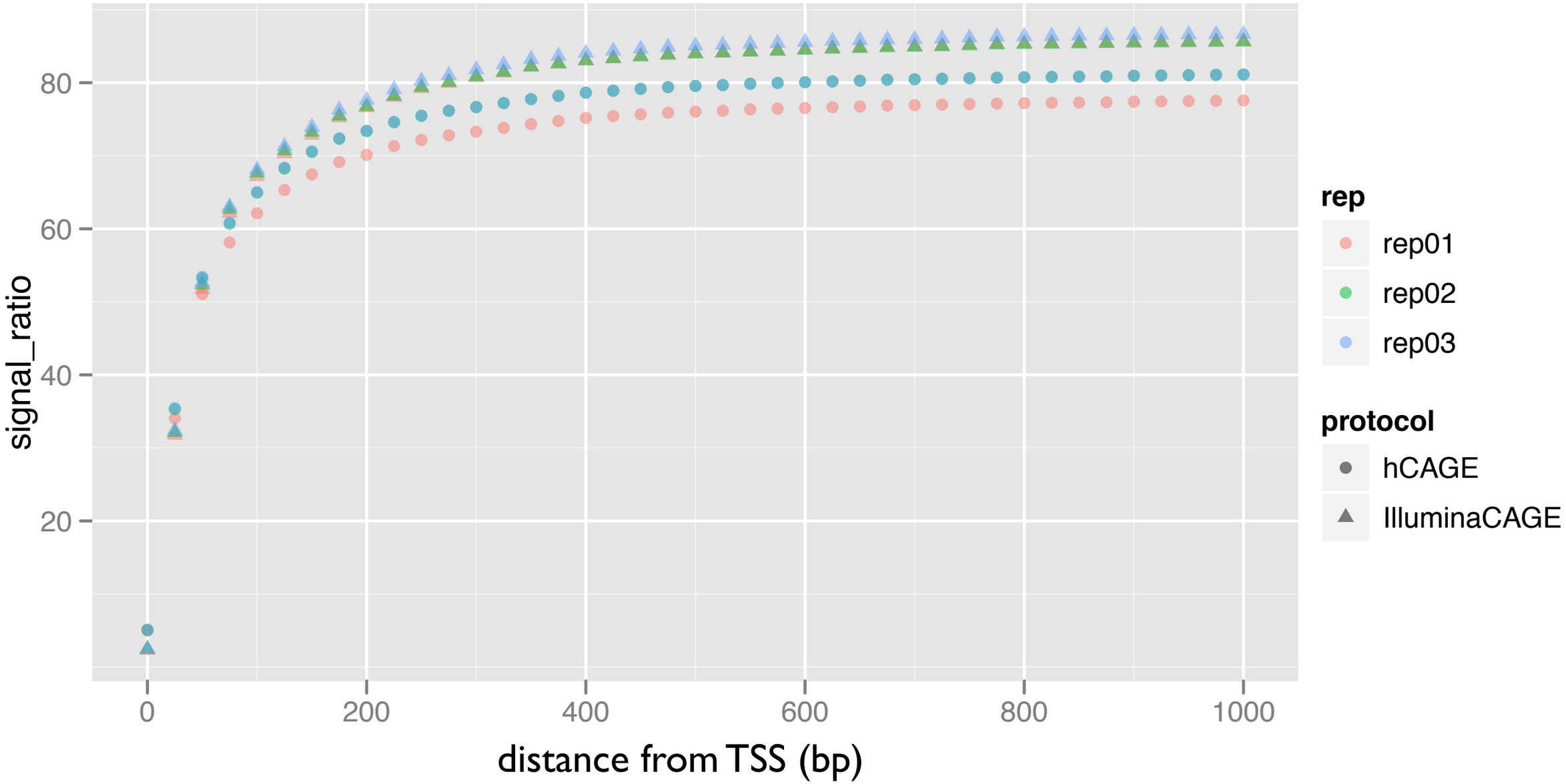
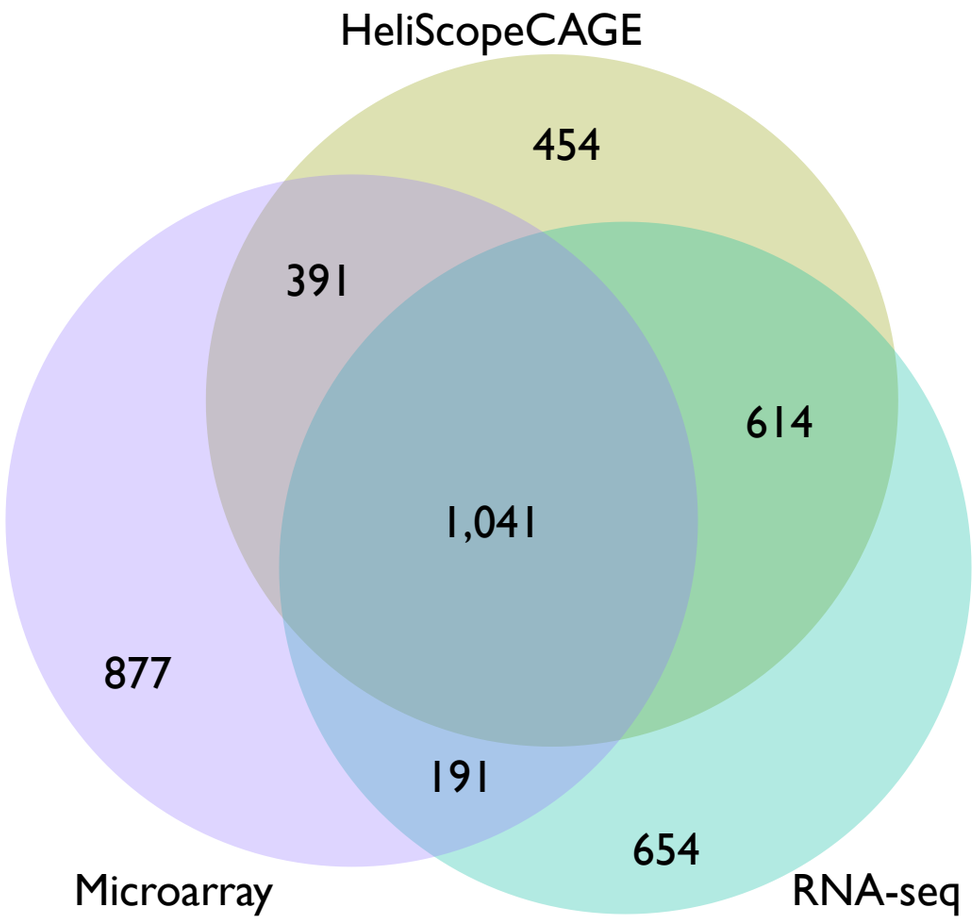
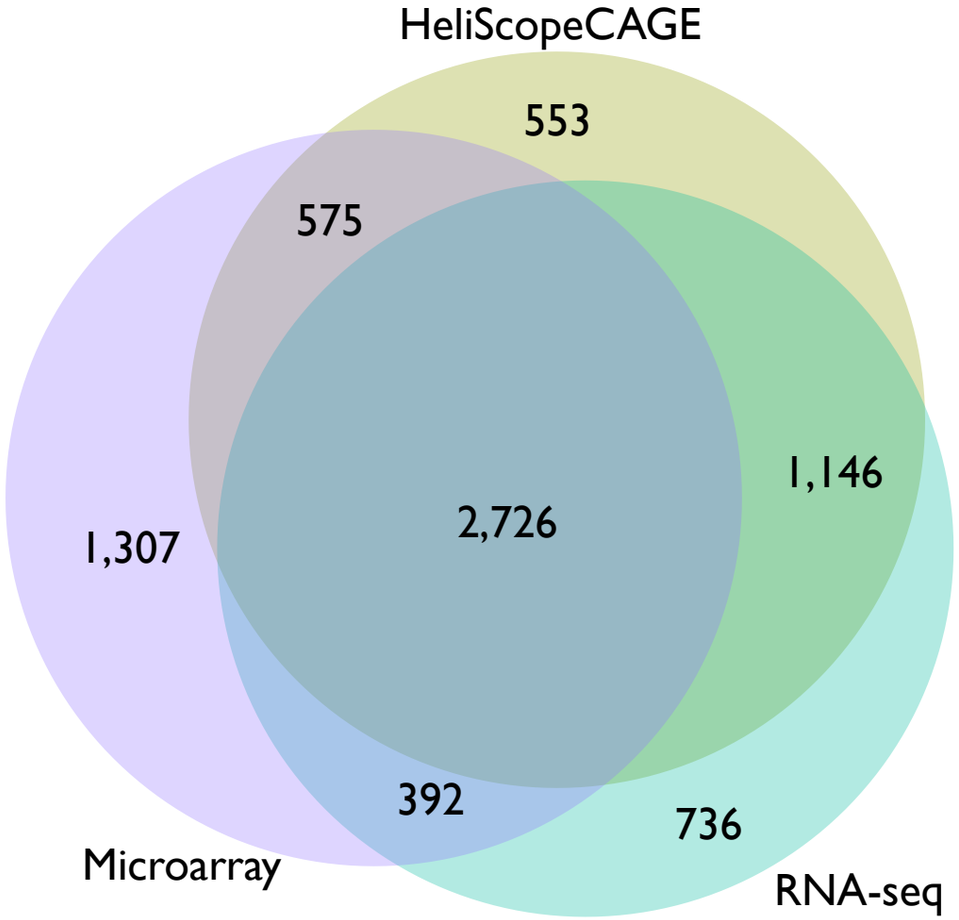


Figure S10: the ratio of CAGE reads starting from TSS proximal regions

Figure S11: complexity of detected RNA species in THP-1 and HeLa RNA



Top 2500 genes in each platform
(4,222 genes in total)



Top 5,000 genes in each platform
(7,435 genes in total)

Figure S12: Overlaps of genes detected in HeLa cells by each platform.