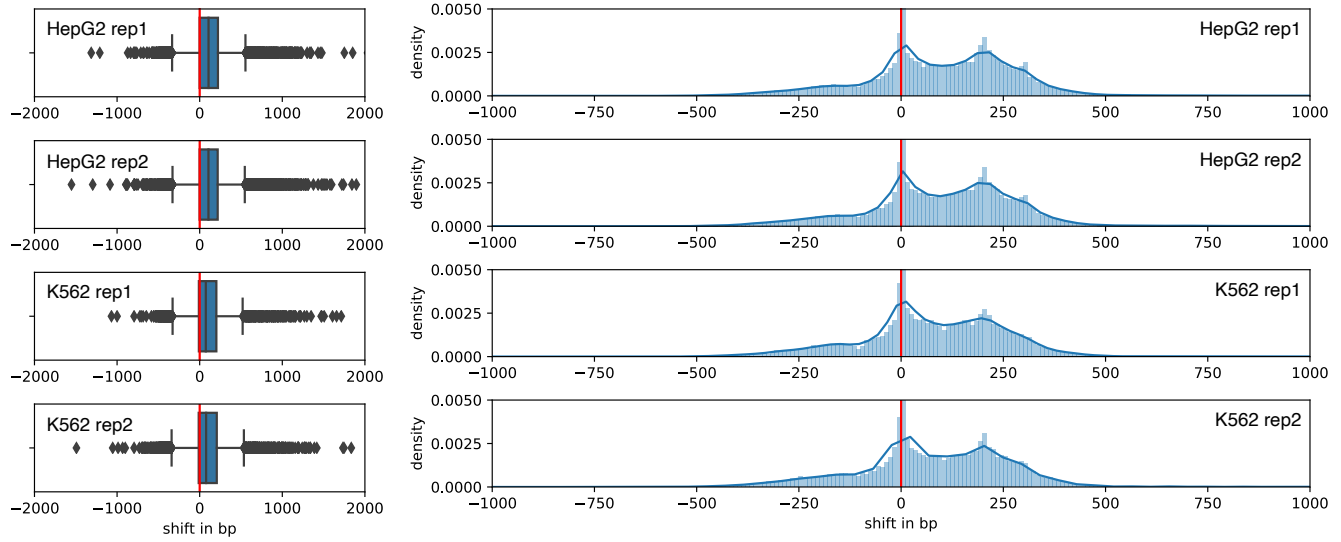
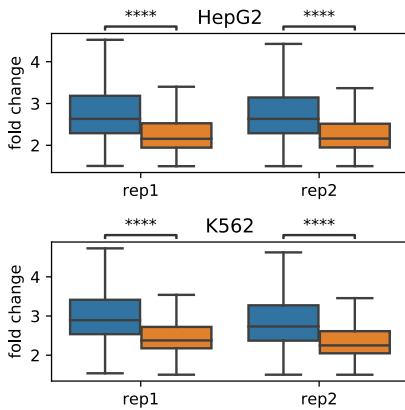


Figure S1

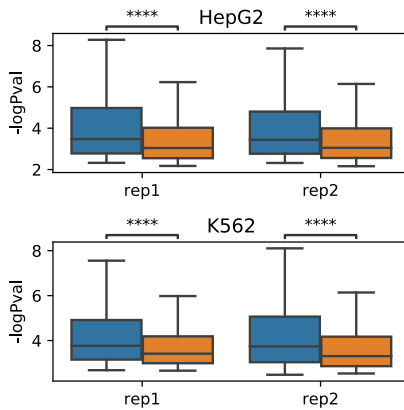
A



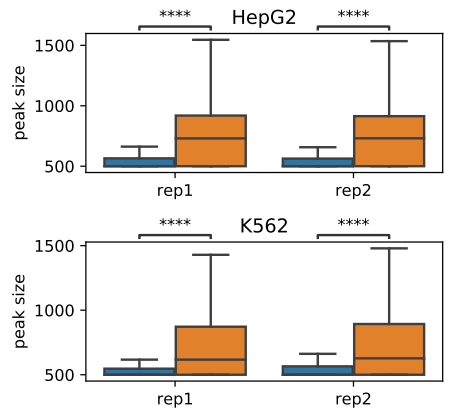
B



C



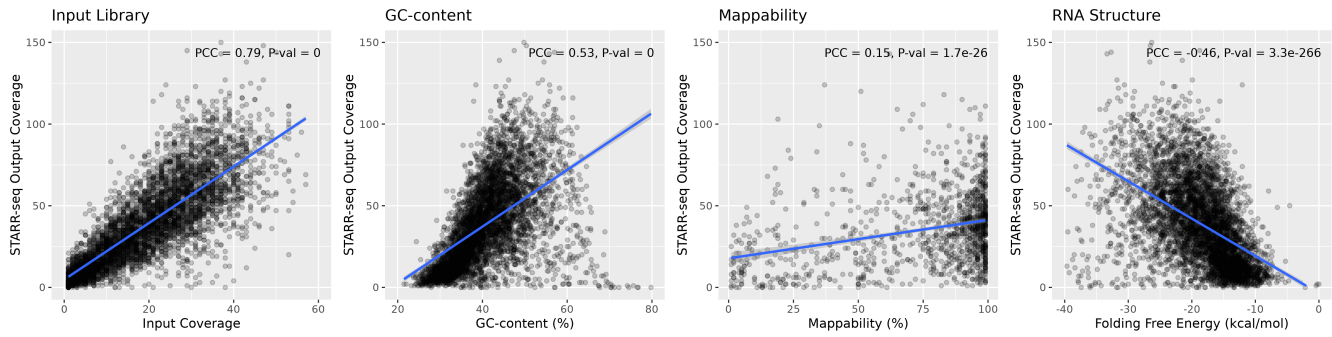
D



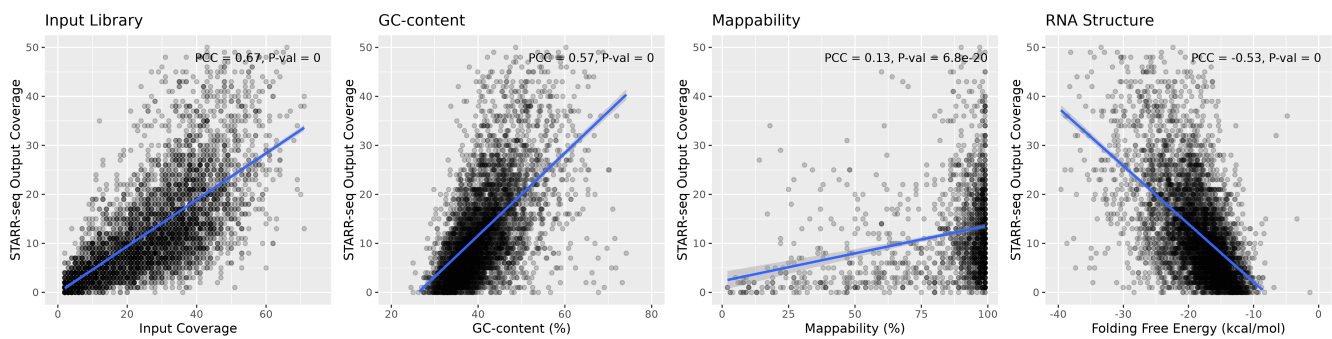
Fragment Center  
Read Start

**Figure S2**

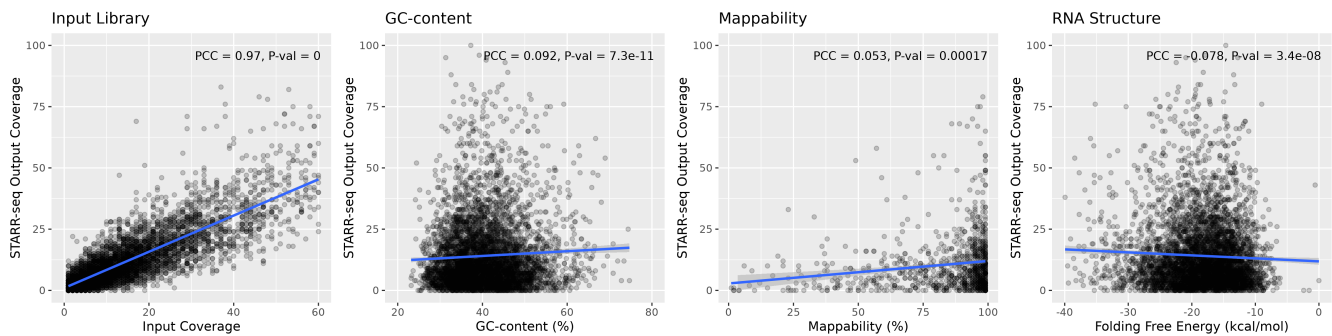
**A K562 ORI-WG-STARR-seq**



**B HeLa-S3 untreated WG-STARR-seq (Muerdter 2018)**



**C GM12878 HiDRA ATAC-STARR-seq (Wang 2018)**



**D K562 Cap-STARR-seq (Rathert 2015)**

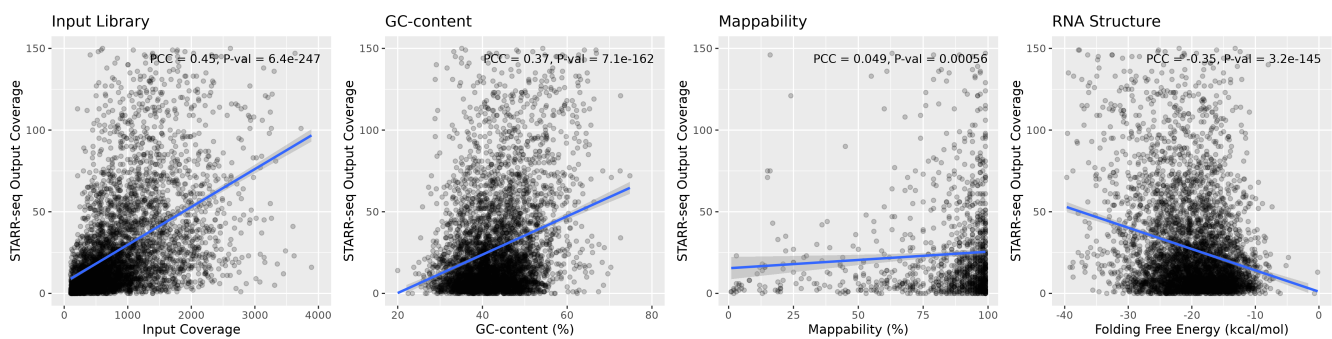
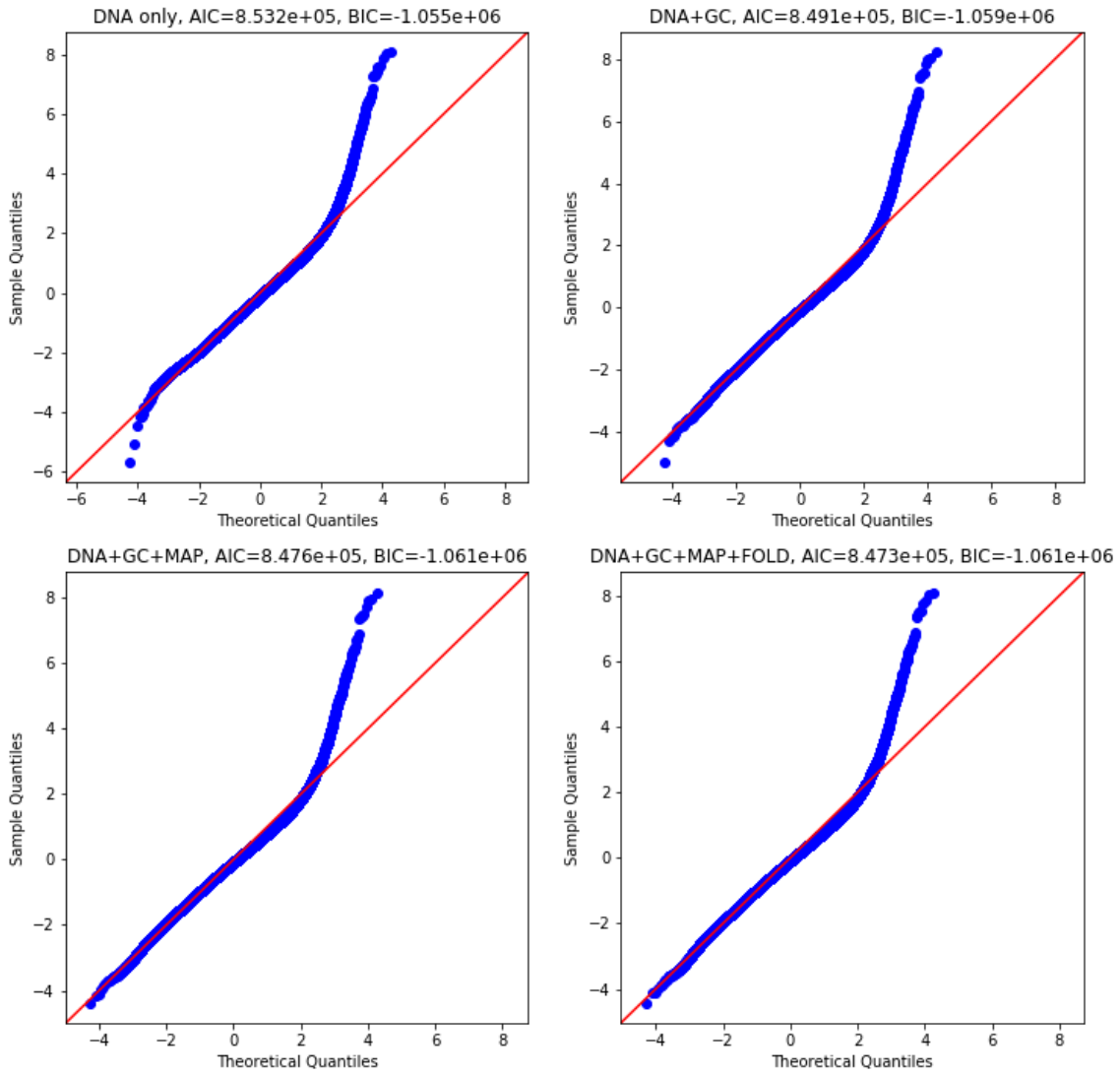
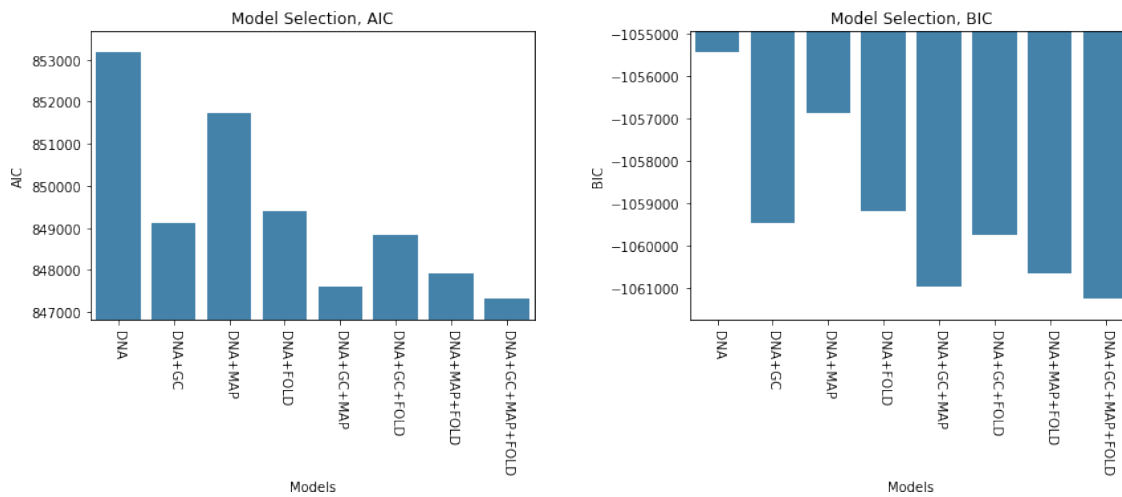


Figure S3

A

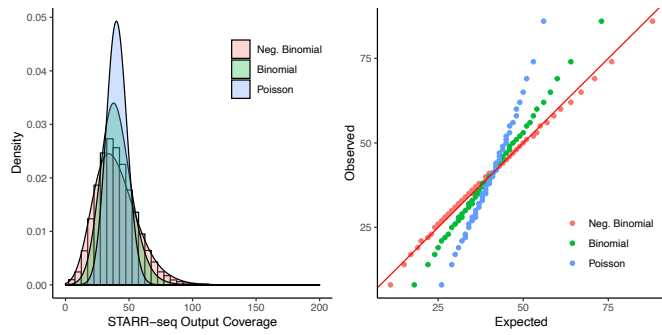


B

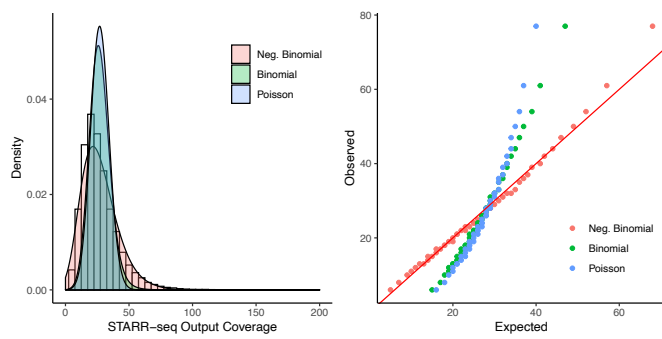


**Figure S4**

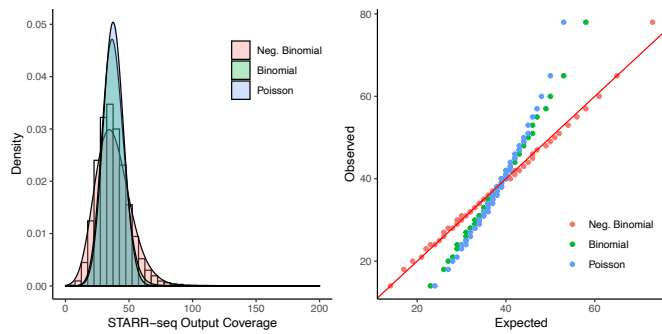
**A K562 ORI-WG-STARR-seq**



**B HeLa-S3 untreated WG-STARR-seq (Muerdter 2018)**



**C GM12878 HiDRA ATAC-STARR-seq (Wang 2018)**



**D K562 Cap-STARR-seq (Rathert 2015)**

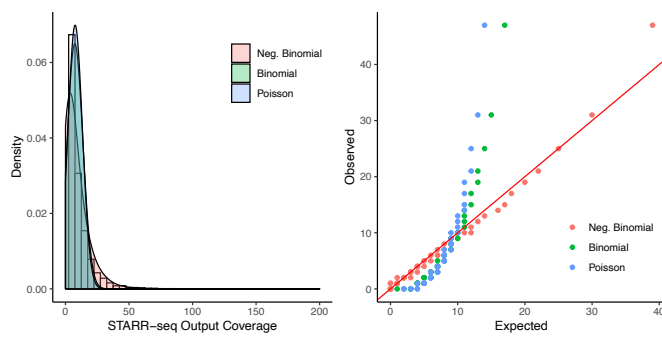
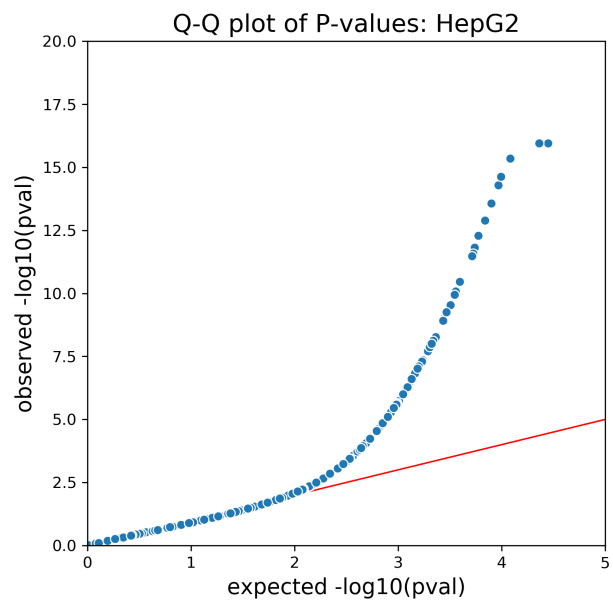




Figure S5

A



B

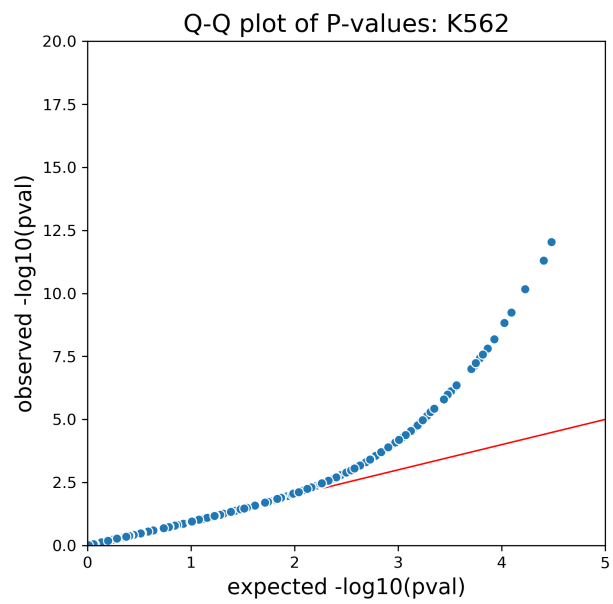
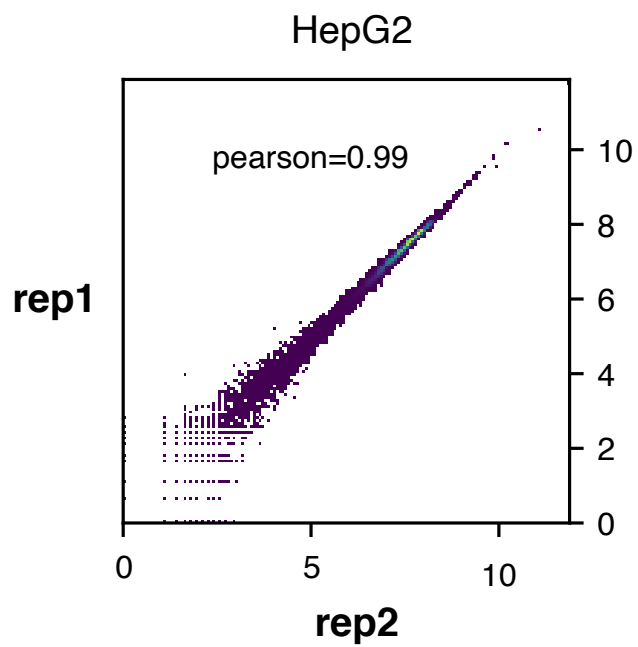
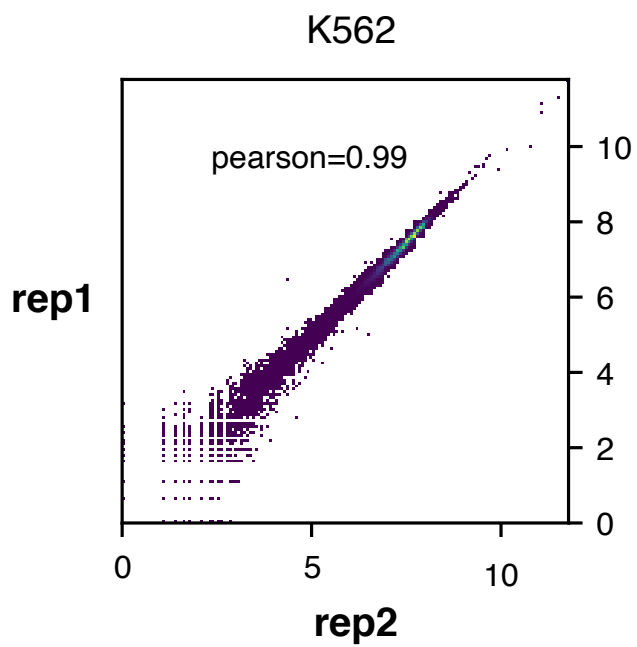


Figure S6

A

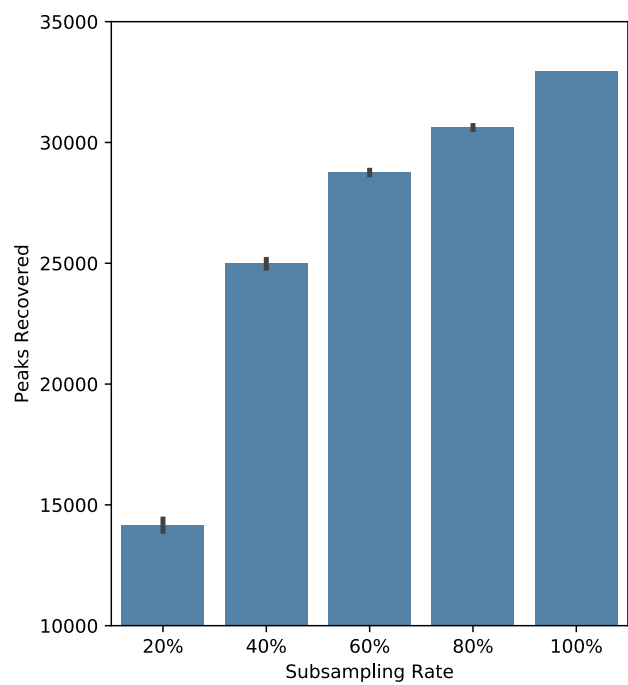


B



**Figure S7**

**A**



**B**

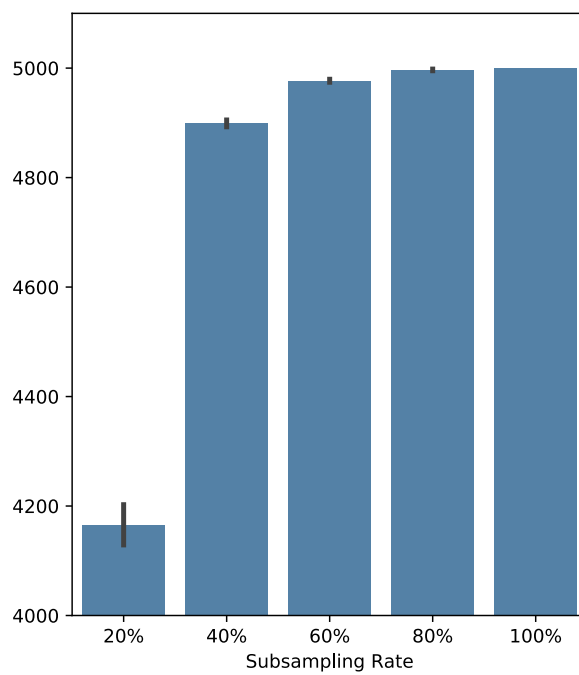
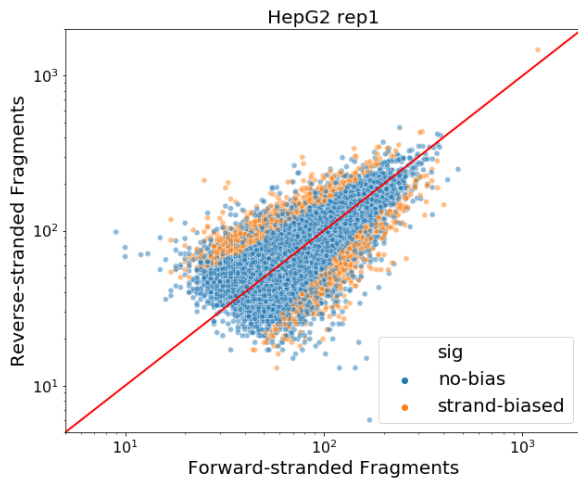
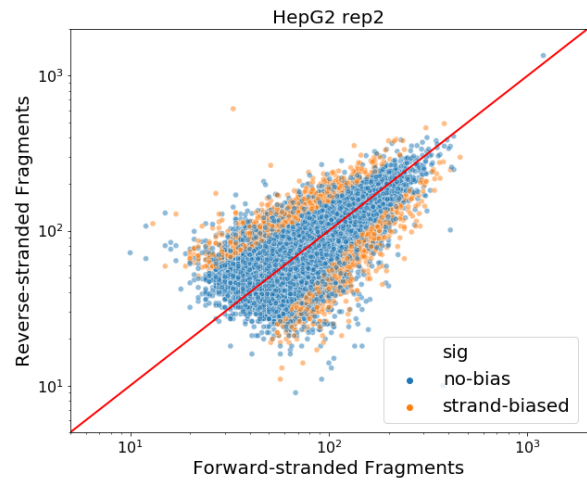


Figure S8

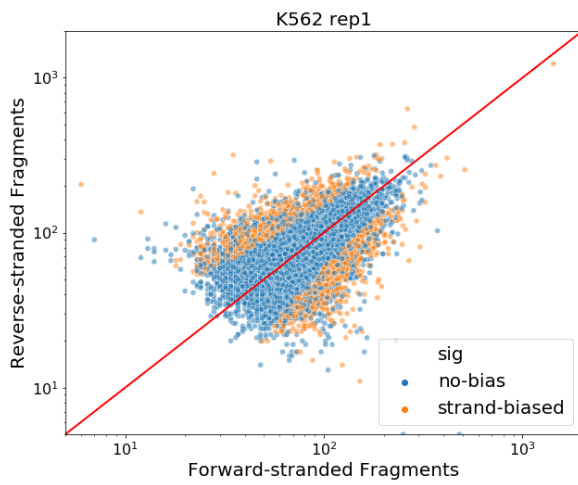
A



B



C



D

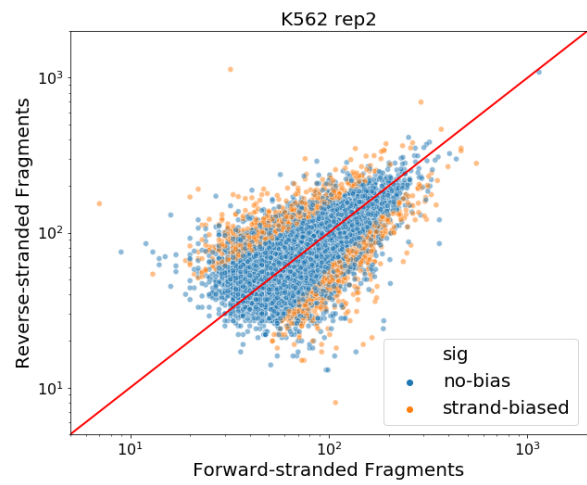


Figure S9

chr8:127,200,000-129,800,000

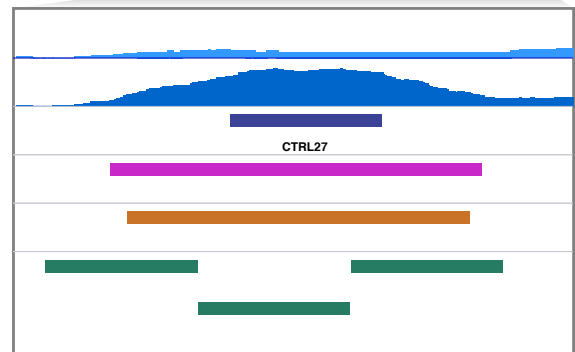
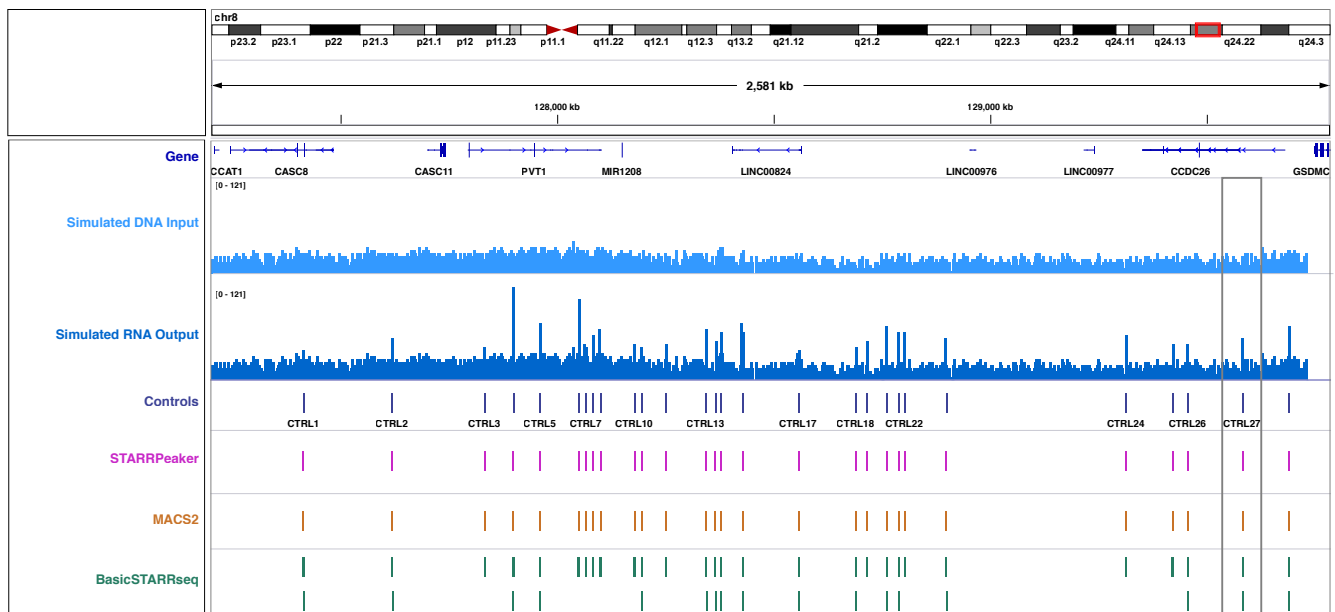


Figure S10

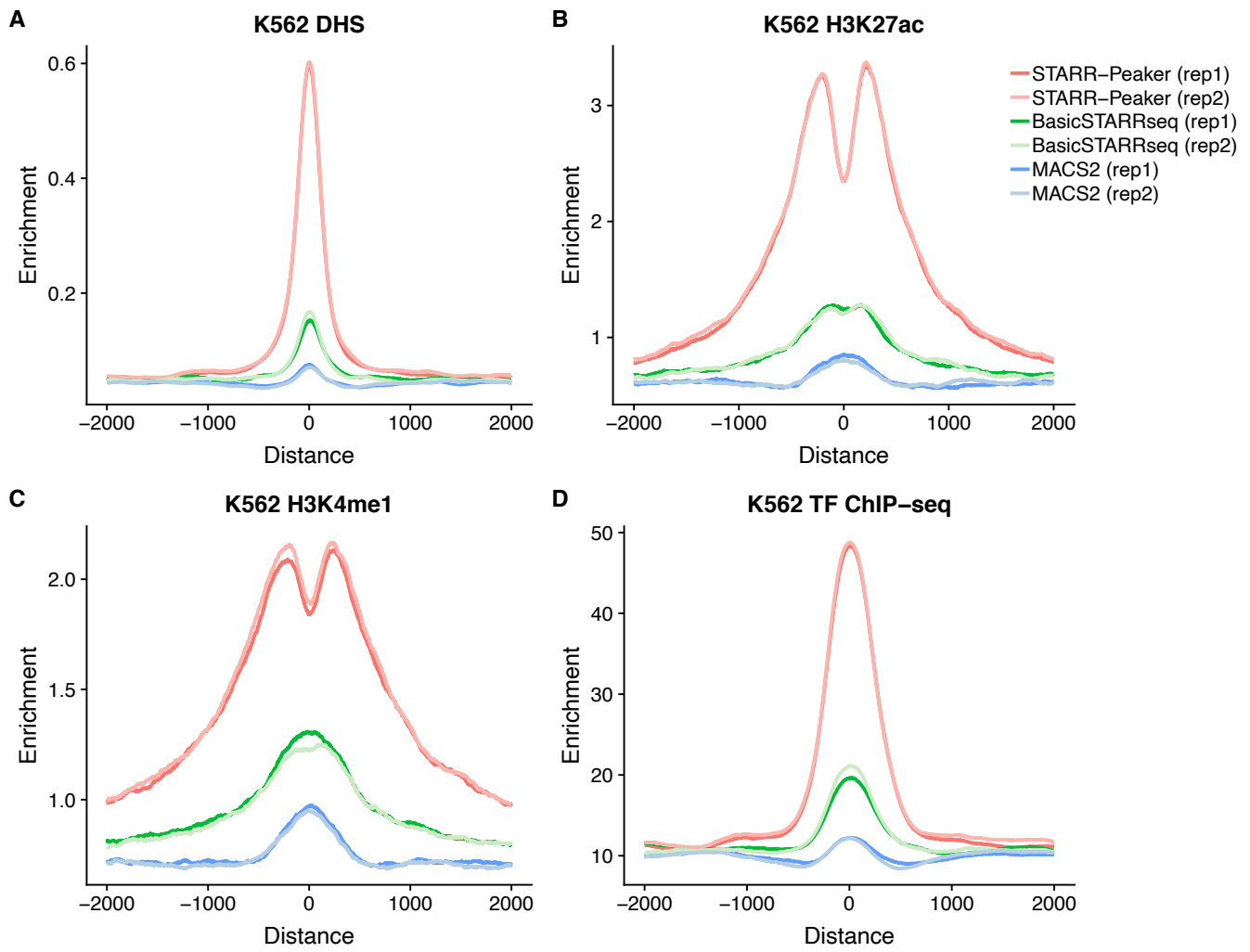
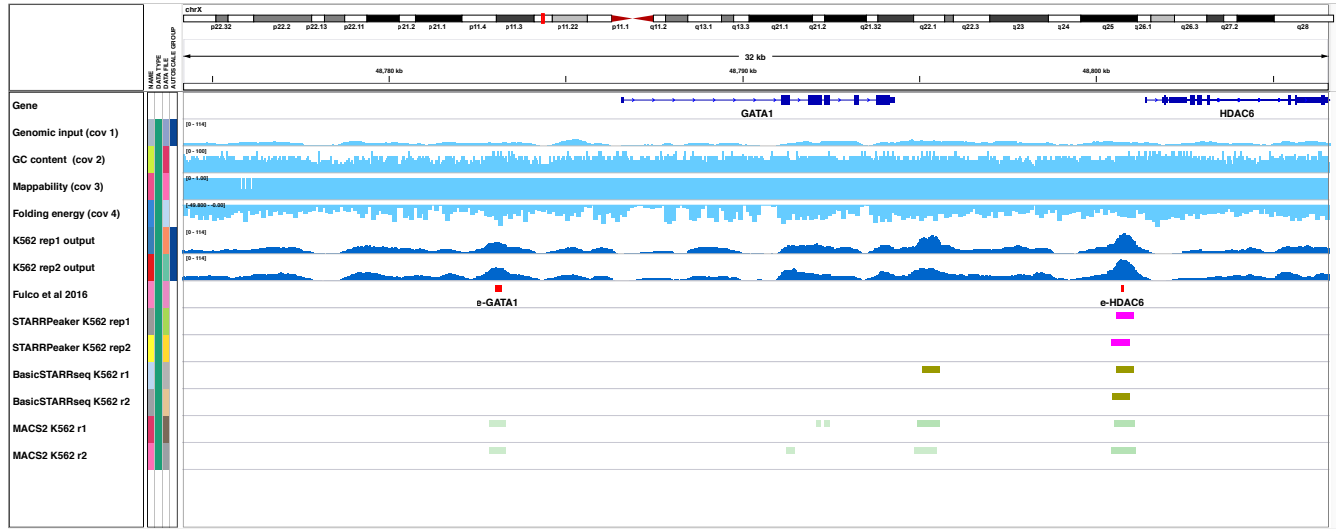
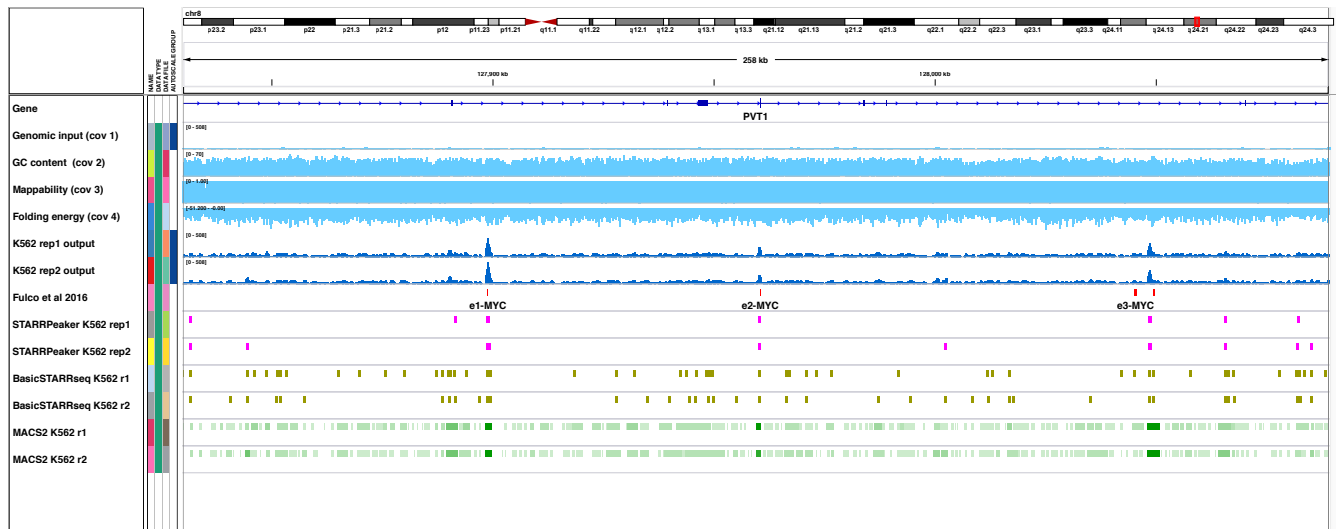


Figure S11

**A** GATA1 locus chrX:48774179-48806695



**B** MYC locus chr8:127830000-128090000



**C** MYC locus chr8:129550000-129720000

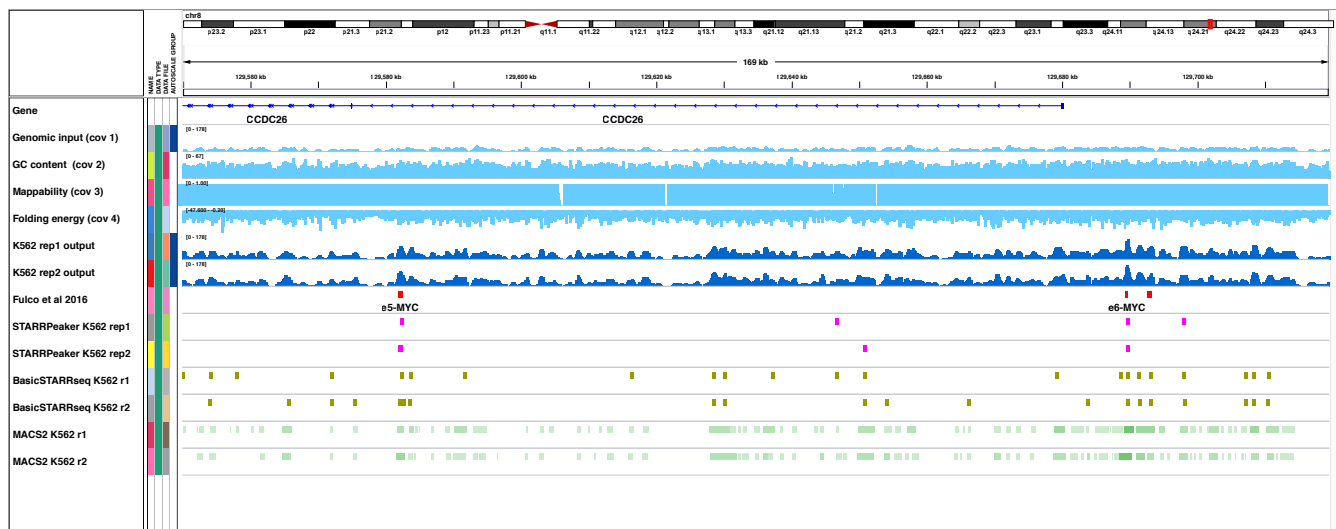


Figure S12

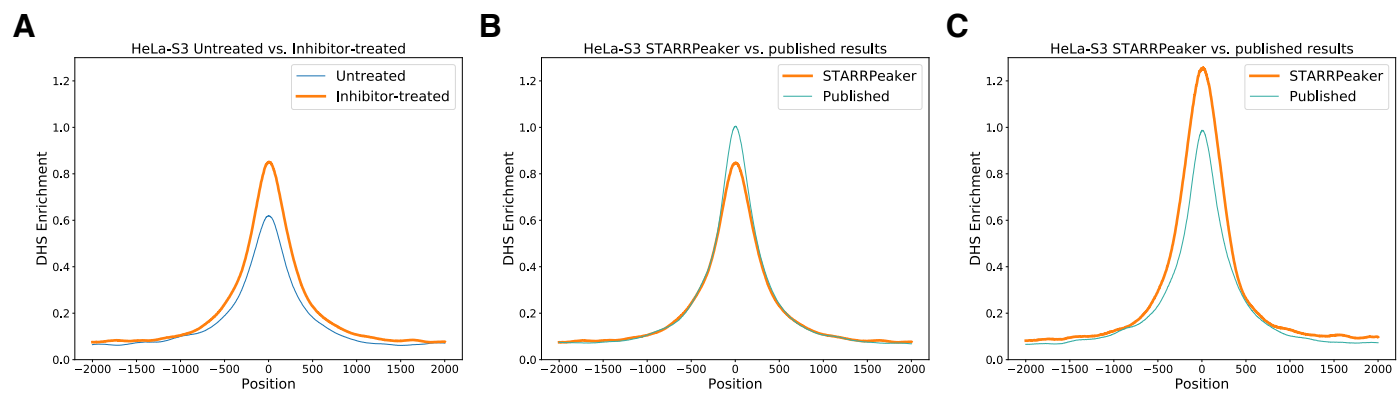




Figure S13

