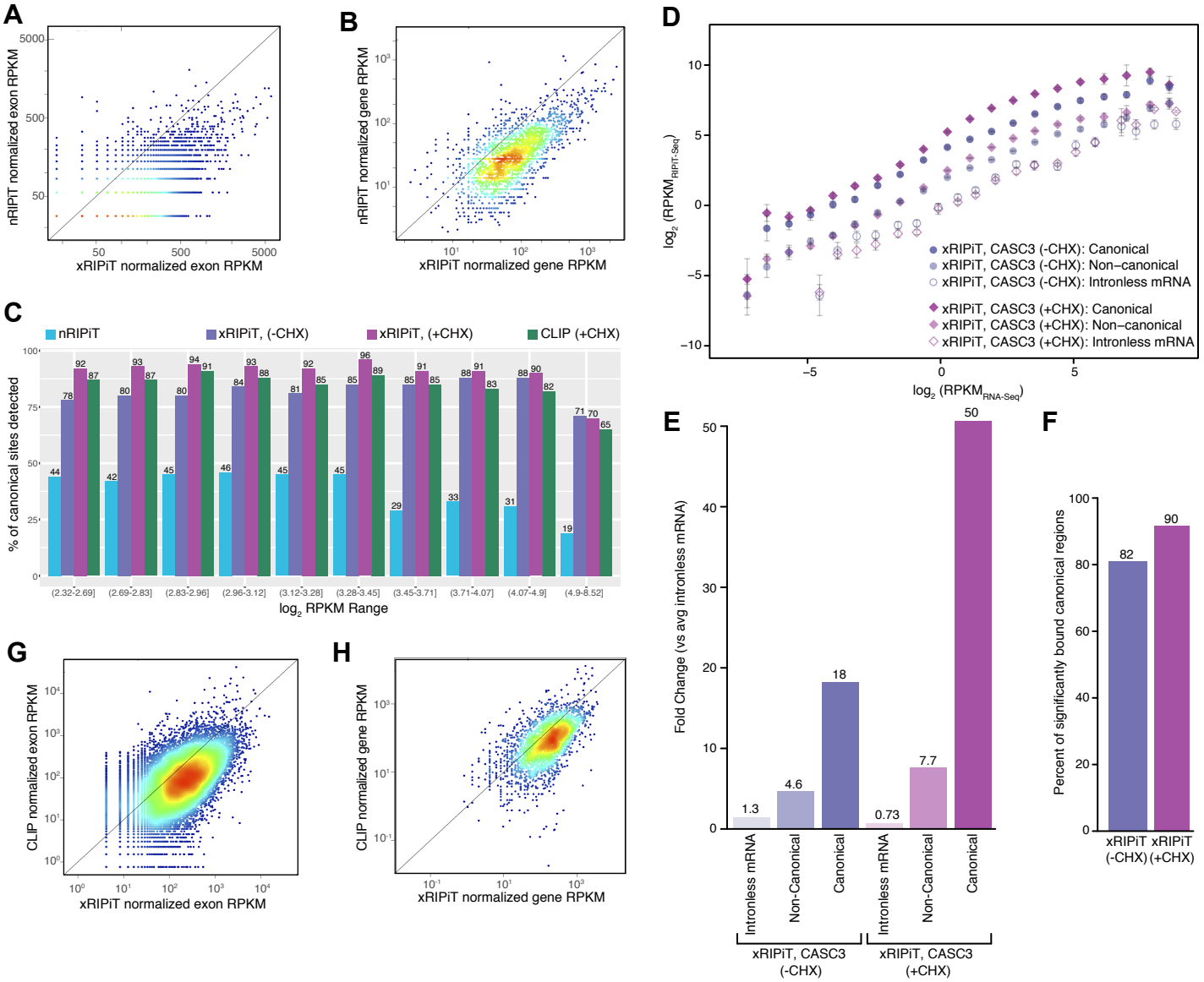
Supplemental Fig. 4



Supplemental Fig. 4. Quantification of CACS3 occupancy by nRIPiT, xRIPiT and CLIP.
A. Scatter-plot of CACS3 nRIPiT versus xRIPiT read densities (RPKM) at individual canonical sites normalized to intronless genes. Heatmap colors indicate plot density (red = most dense, blue = least dense). The diagonal represents canonical sites where nRIPiT and xRIPiT yield equal RPKM counts.
B. Scatter-plot as in A comparing gene level normalized RPKM (sum of RPKM for all canonical sites) between CASC3 nRIPiT and xRIPiT.
C. Bar-plots showing percent of canonical regions where CASC3 RIPiT or CLIP read counts are ≥2-fold over counts in intronless genes in the same expression range bin (921-922 canonical sites/bin).
D. Comparison of gene-level CASC3 read density ($RPKM_{RIPiT\text{-}Seq}$) in cycloheximide (CHX) treated xRIPiT (+CHX, diamonds) and untreated xRIPiT (circles) for canonical (darker-shaded shapes) and non-canonical regions (lighter-shaded shapes), and for intronless genes (empty shapes).
E. Comparison of the linear fit coefficients (or intercepts, in log space) of the six classes in (D). Classes are labeled on the bottom.
F. Percent of all canonical EJC regions where read depth is ≥2-fold as compared to intronless gene read counts in the indicated datasets.
G. Scatter-plot as in A comparing normalized RPKM at each canonical site detected in CASC3 xRIPiT and CLIP.
H. Scatter-plot as in B comparing gene level normalized RPKM between CASC3 xRIPiT and CLIP.