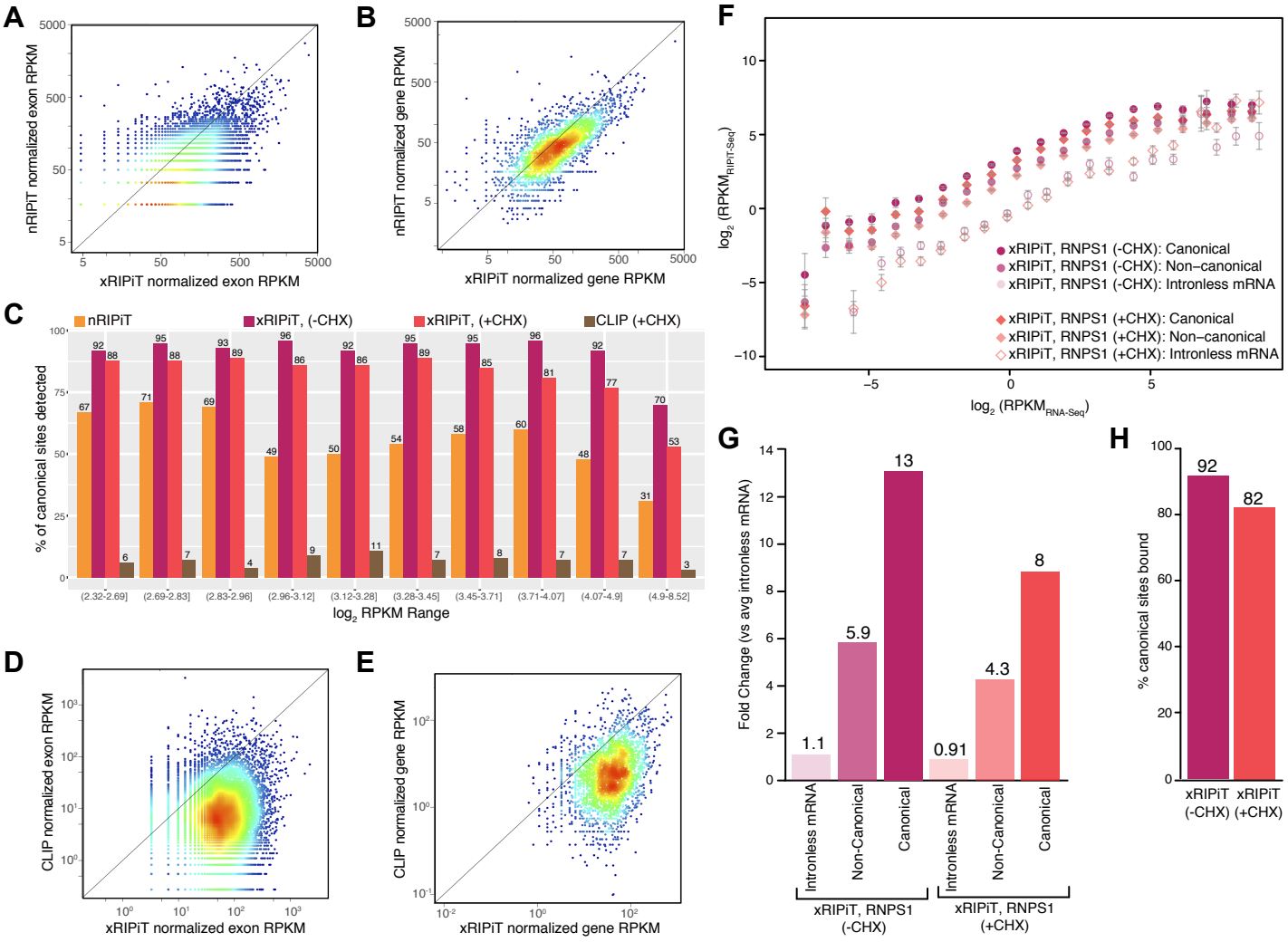
Supplemental Fig. 6



Supplemental Fig. 6. Quantification of RNPS1 occupancy by nRIPiT, xRIPiT and CLIP.
A. Scatter-plot of RNPS1 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 RNPS1 nRIPiT and xRIPiT.
C. Bar-plots showing percent of canonical regions where 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. Scatter-plot as in A comparing normalized RPKM at each canonical site detected in RNPS1 xRIPiT and CLIP.
E. Scatter-plot as in B comparing gene level normalized RPKM between RNPS1 xRIPiT and CLIP.
F. 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).
G. Comparison of the linear fit coefficients (or intercepts, in log space) of the six classes in (F). Classes are labeled on the bottom.
H. Percentage of all canonical EJC regions where read depth is ≥2-fold as compared to intronless gene read counts in the indicated datasets.