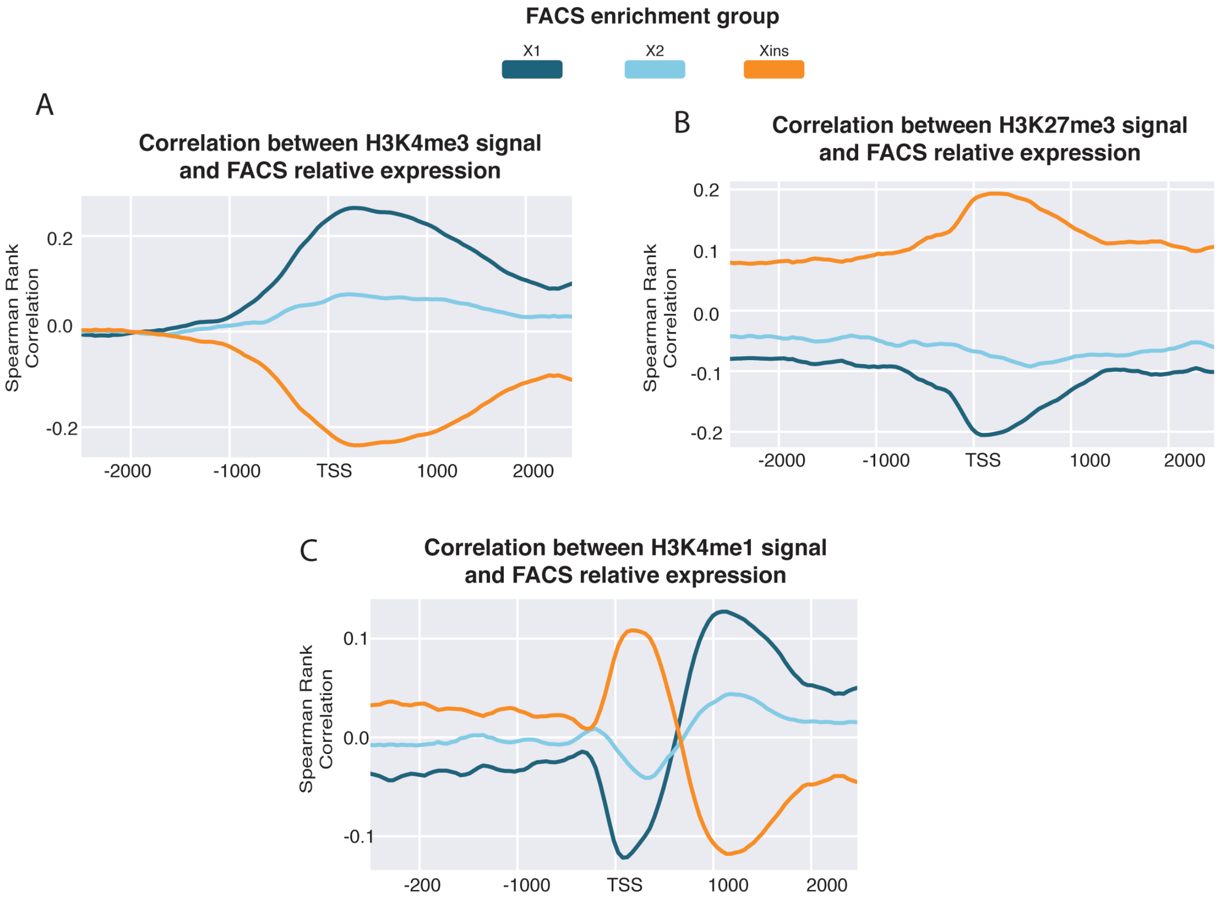
Spearman Rank Correlation Coefficients between FACS relative expression and ChIP-seq coverage normalized to input at 50bp increments 2.5kb either side of TSS.



Supplemental Figure 7: Spearman's rank correlation plots between ChIP-seq signal at each 50bp window around the TSS and the proportional expression value in X1, X2, and Xins for all annotated loci**.** A positive correlation value means that the higher the ChIP-seq signal, the higher the proportional expression value. A negative correlation means that the lower the ChIP-seq signal, the higher the proportional expression value. **A.** The profile for H3K4me3 indicates that genes with high X1 proportional expression have, on average, a high ChIP-seq signal for H3K4me3 at the TSS, whilst genes with high Xins proportional expression have a low ChIP-seq signal for H3K4me3 at the TSS. Genes with high X2 proportional expression also, on average, have H3K4me3 signal at the TSS, but the correlation is weaker than that for high X1 genes. **B.** The profile for H3K27me3 indicates that genes with a high Xins proportional expression have, on average, a high H3K27me3 signal at the TSS. Genes with a high X1 or X2 proportional expression have a lower H3K27me3 signal at the TSS. **C.** The profile for H3K4me1 indicates that higher Xins proportional expression correlates with a high H3k4me1 signal at the TSS. Genes with higher X1 proportional expression are, on average, enriched for H3K4me1 downstream of the TSS. We observe a weak negative correlation for X2 expression and H3K4me1 at the TSS, and a weak positive signal for X1 expression. This is consistent for this compartment being an admixture of genes that are almost exclusive expressed in the X2 compartment and genes that retain NB expression.