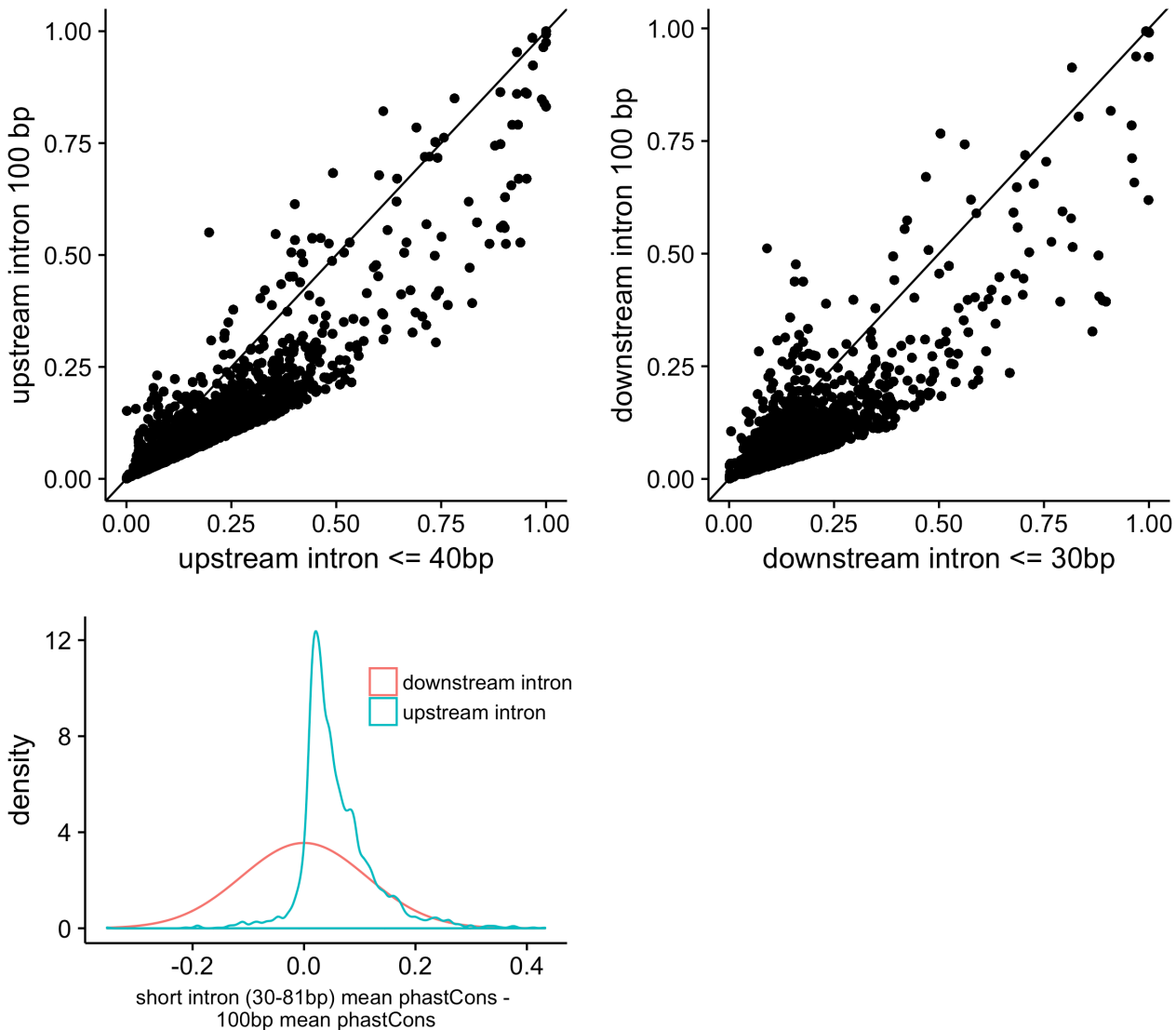
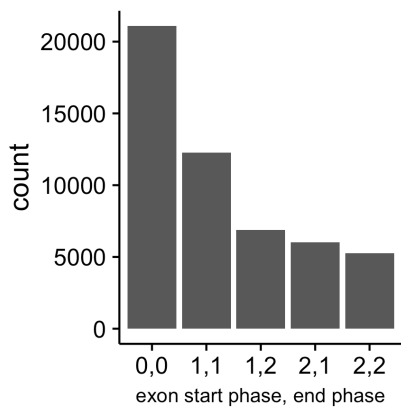


Supplementary Figures - Computational

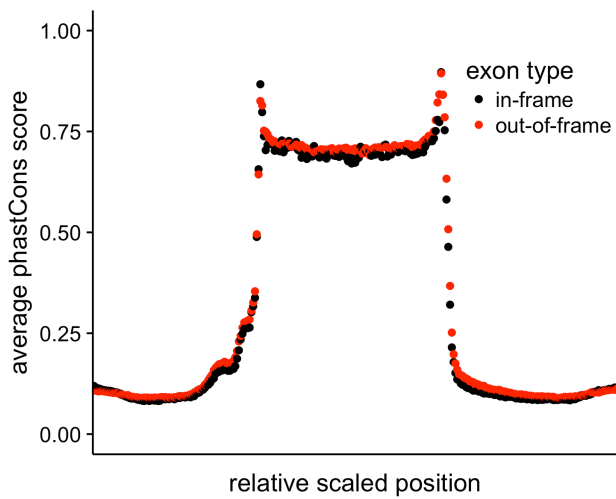
Is there a difference in conservation between our short intron context (~30bp) and longer 100bp intron context?



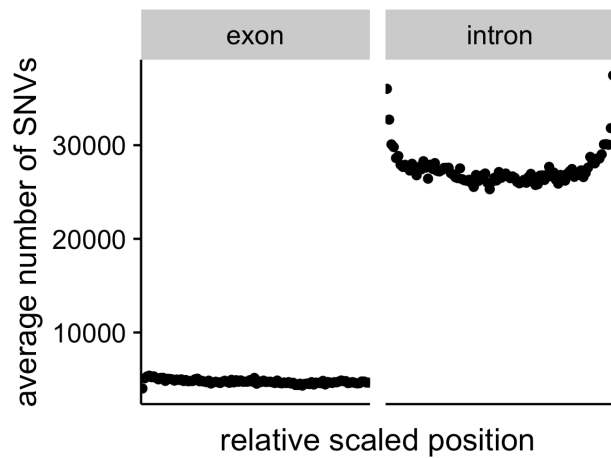
How many exons are in-frame (phase 0,0) vs. out-of-frame?

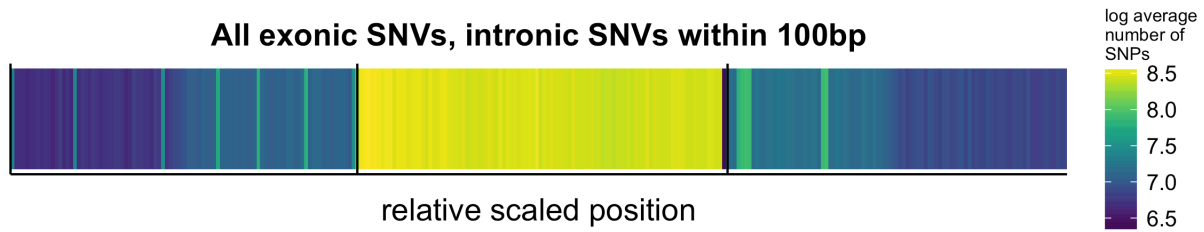


Is there a difference in conservation between exons in-frame vs. exons out-of-frame?



What is the distribution of all genomic SNVs between exons and introns?





How are other measures of exonic strength distributed in our assay?

