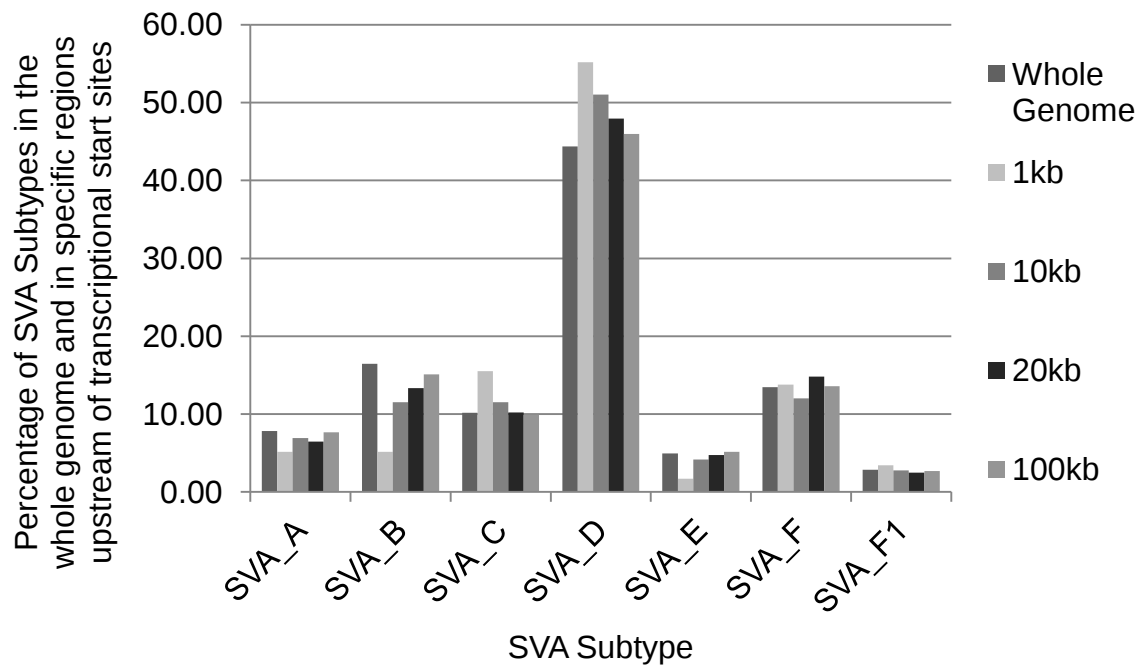


### Additional file 3

#### Distribution of SVA subtypes within 1kb, 10kb, 20kb and 100kb upstream of a transcriptional start site



The distribution of SVA subtypes within regions upstream of a transcriptional start site. There is a significant difference in the distribution of the subtypes within the first kilobase compared to the whole genome. (1kb  $\chi^2=16.30$ , df=6,  $p<0.05$ ), (10kb  $\chi^2=2.97$ , df=6,  $p=0.81$ ), (20kb  $\chi^2=1.30$ , df=6,  $p=0.97$ ), (100kb  $\chi^2=0.20$ , df=6,  $p=0.99$ ).