

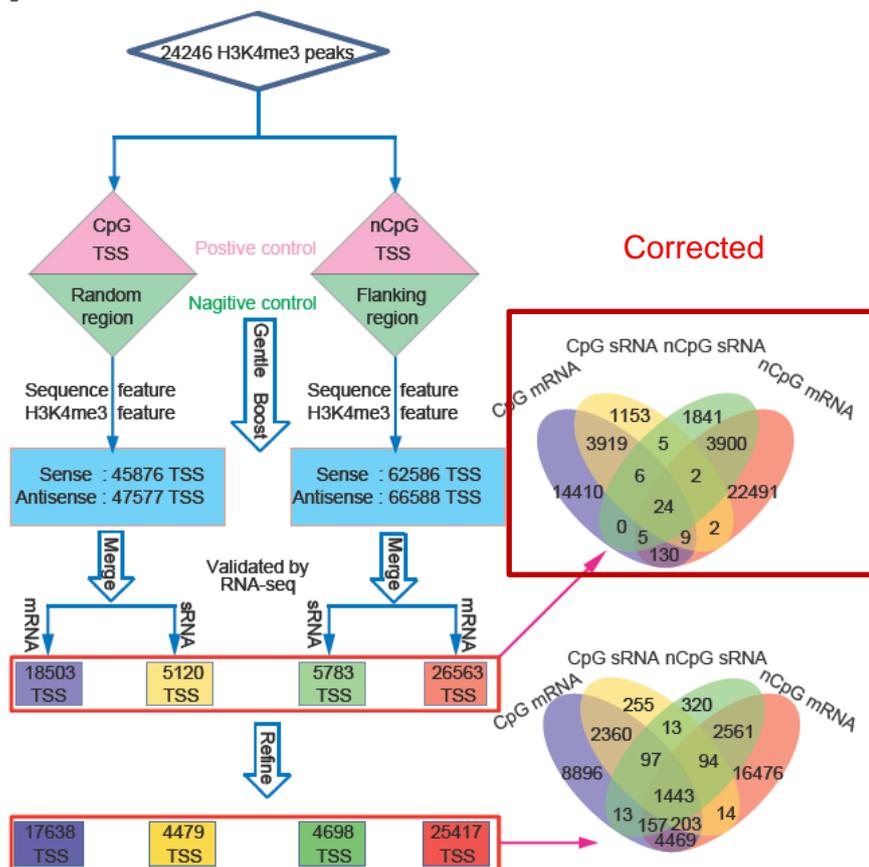
Errata

After publication, we found 2 minor mistakes in Liu Y, *et al.* (2011) Ab initio identification of transcription start sites in the Rhesus macaque genome by histone modification and RNA-Seq, *Nucleic acids research*, 39 (4), 1408-1418.

Although the two mistakes do not change any of the conclusions of the paper, we have corrected them below:

1: In Figure1, the numbers in the upper Venn diagram should be corrected as in the figure below:

Figure 1



2: In the legend of Supplemental Figure S1, the number of H3K4me3 peaks should be **24246**, as shown below:

Supplemental Figure 1. The average profile of normalized H3K4me3 ChIP-Seq tag counts for different sets of TSS annotations in the [-2 kb, +2 kb] region. “CpG/non-CpG annotation in peak” means the annotated TSSs in the **24246** H3K4me3 peak regions, while “CpG/non-CpG annotation” refers to all previously annotated TSSs.