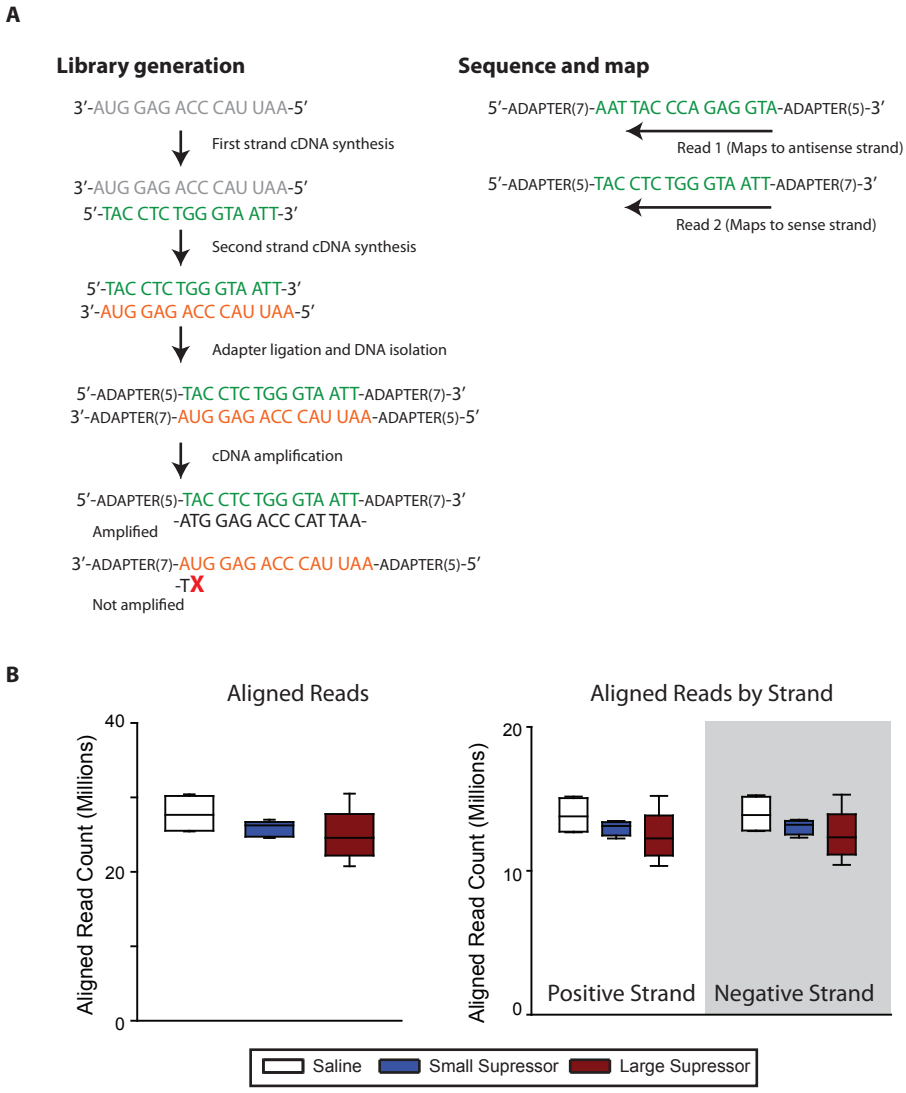

Supplemental Figure 1: A) Schematic of stranded RNA-Seq library preparation and analysis. After first and second strand cDNA synthesis adapters are ligated and then during the subsequent amplification only the forward strand is amplified. This ensures that all inserts are in 5′ to 3′ direction, corresponding to the original RNA. After pared end sequencing, alignment of Read 1 is therefore only in reverse (again, corresponding to the original RNA) and Read 2 is in a forward orientation. By ensuring the directionality of the library the original strand of the genome from which the RNA is produced can be determined. **B)** Aligned read numbers and originating strand. Across all three groups an average of ~30 million reads where aligned, with equal numbers aligning to the positive and negative genomic strands. **C)** Match status of aligned reads. The majority of the paired reads aligned normal fashion (both reads in proper direction within the expected distance). For small numbers of reads one of the mate pairs did not align (mate missing), was in the opposite orientation (mate flip) or aligned to a different chromosome (translocated).