Figure S7: Comparison between known SDs and SDs identified by SDquest.
Total length (depending on percent identity) of SDs identified only by SDquest but missed in known SDs (blue) and known SDs missed by SDquest (red) in human (hg19 assembly, (A)) and mouse (mm8 assembly, (B)) genomes. Known SDs were defined based on the statistics used for reanalyzing known SDs. If an SD aligns to more than two segments in a genome, its percent identity is defined as the maximum percent identity among all these alignments.