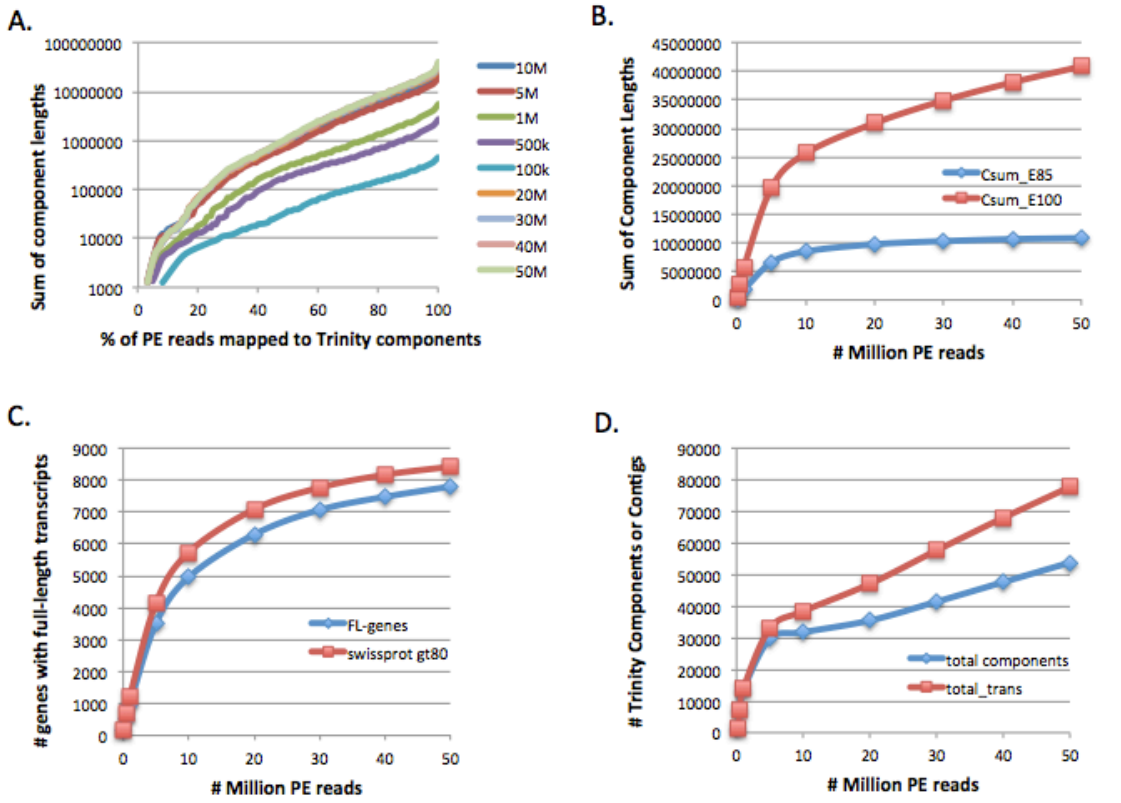

Evaluating assembly completeness for the Mouse dendritic cell transcriptome. (a) Sum of Trinity component lengths (Y axis) at different percent of PE reads mapped to Trinity components (X axis). The RSEM Trinity components 'genes.results' output file was sorted descendingly by effective fragment counts and sums of component lengths were reported according to the percent of total number of fragments mapped. (b) The sum of component lengths (Y axis) for the points in (a) corresponding to 85% and 100%, labeled as Csum_E85 (blue) and Csum_E100 (red), respectively, at different numbers of PE reads assembled by Trinity (X axis). (c) The number of transcripts (Y axis) having either having the CDS fully represented by a single BLAT alignment at 99% identity and at most 1% indel (FL genes, blue) or as matching a Swissprot protein entry covering at least 80% of the top hit's protein length in a single BLASTX match (swissprot_gt80, red) at different numbers of PE reads assembled by Trinity (X axis). (d) The number of Trinity components (blue) or transcript contigs (red) (Y axis) at different numbers of PE reads assembled by Trinity (X axis).