



Figure S1 Mapping specificity in RNA-Seq expression profiles. Histograms of (a) average expression (edgeR counts per million) and (b) read mapping positions across samples. (c) Number of mapped reads vs. mean mapping position ($R^2 = 0.28$, $p < 2.2 \times 10^{-16}$). This illustrates the relationship between the number of reads that map to a particular scaffold and the mean mapping position of those reads. (d) The relationship between edgeR counts per million and scaffold length ($R = 0.30$, $p < 2.2 \times 10^{-16}$).