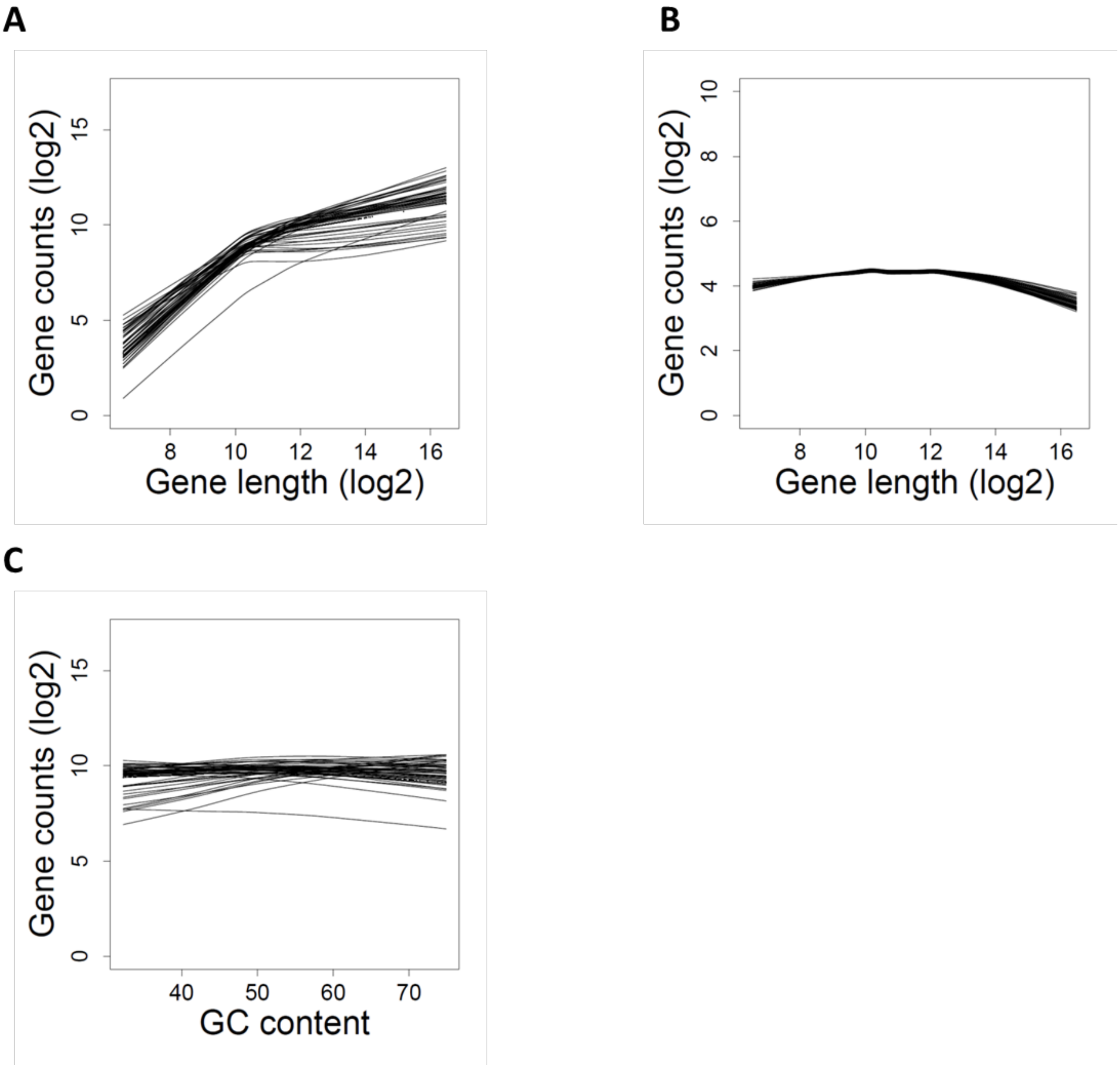
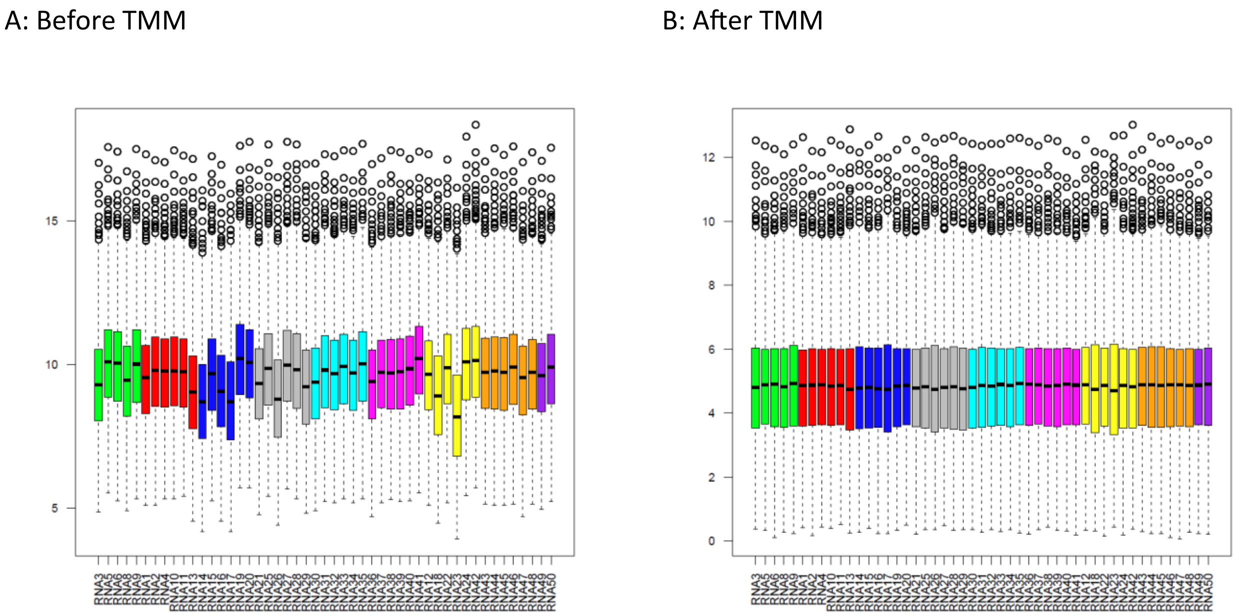
Supplementary Figure S1: Pre- and post-intrasample normalization

Panels A and B show the average expression (y-axis) of genes of a given length (x-axis) respectively before and after full-quantile normalization (see methods). Panel C shows the average expression (y-axis) of genes of a given GC-content percentage (x-axis). Lines represent sample lowess summarization.



Supplementary Figure S2: Pre- and post-intersample TMM

Gene expression distribution (y-axis) per sample (x-axis) before (panel A) and after (panel B) Trimmed Mean of M values normalization (TMM)



A: Before TMM

B: After TMM