

Table S3: Sequencing and alignment of RNA-seq libraries.

For each replicate, the total number of reads sequenced, number of reads that passed filter, number of reads after clipping, number of reads that did not align to the ribosomal genes, and number of reads that aligned to the dm3 reference genome are shown in the table.

Library	Total reads	Passed filter	After clipping	Non-ribosomal	Mapped reads
NHS_rep1	46630399	33051180	27992112	24951251	21164958
NHS_rep2	29432765	20630727	17824656	17553278	15403098
30minHS_rep1	26881631	19246449	16839161	16345216	14286713
30minHS_rep2	29492622	20610831	18993871	18270231	15925348