



Fig S3. Total and full length dRNA reads. The plot shows the total number of dRNA reads mapped to annotated transcripts of different size (counts) and the estimated number of full length reads. Each dRNA read corresponds to a native transcript. Bins are the following: [71.0 - 633.2), [633.2 - 923.4), [923.4 - 1175.0), [1175.0 - 1395.0), [1395.0 - 1637.0), [1637.0 - 1911.2), [1911.2 - 2227.4), [2227.4 - 2695.0), [2695.0 - 3444.6), [3444.6 - 15022.0] nucleotides. Number of transcripts with mapped reads: N=6,453 (out of 7,006 annotated transcripts).