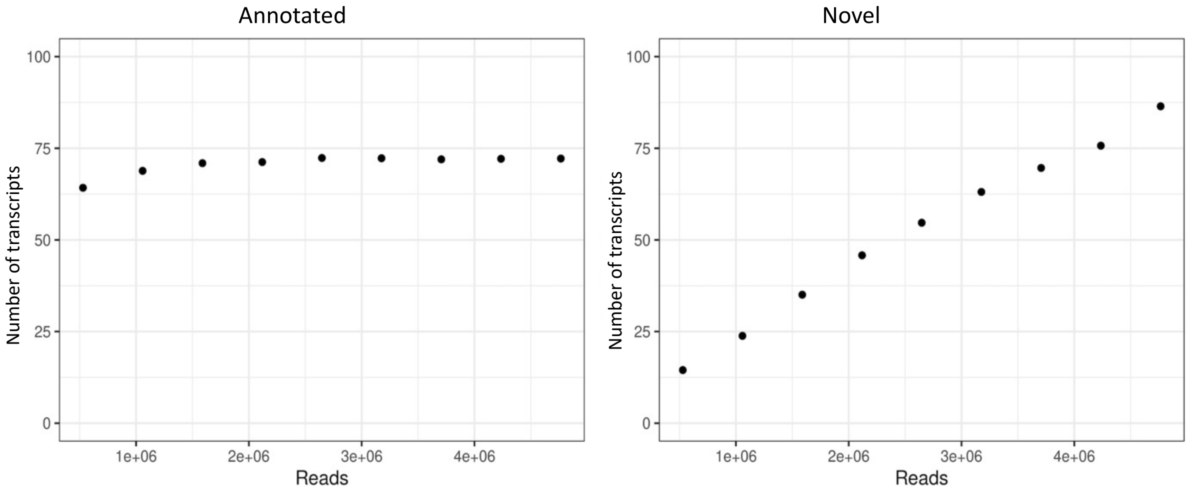

Fig S12. Saturation curves showing the number of recovered transcripts with increasing number of mapped dRNA reads. Data is shown for Pombase gene annotations (Annotated) and novel transcripts (Novel). For the curves, 0.1 to 0.9 of the total number of mapped reads were subsampled with samtools. Transcript assembly for each subsampled set of reads was performed with Stringtie2. We subsequently used the findOverlaps function of the R GenomicAlignments package to assign the assembled transcripts to predefined transcripts from the Annotated or Novel classes.