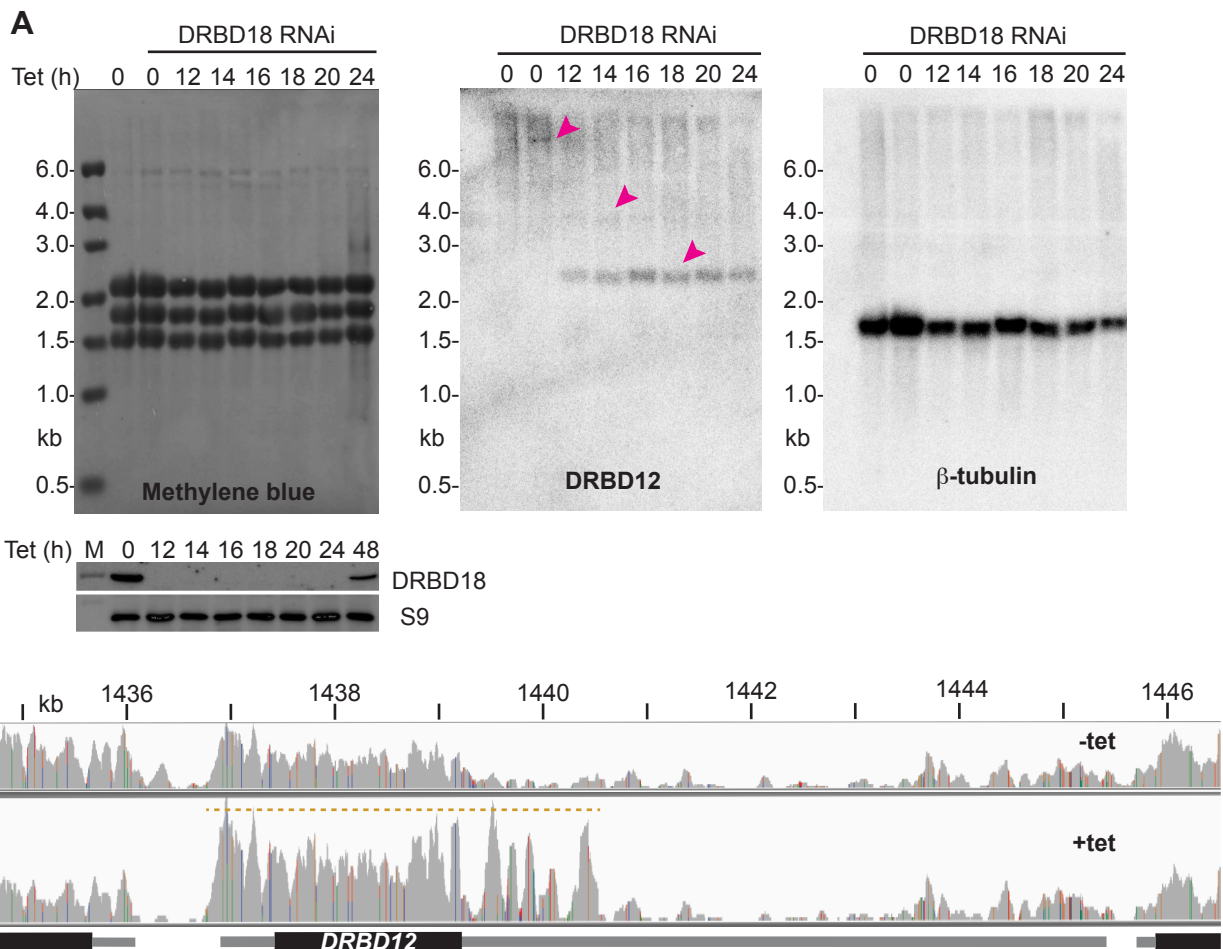




Supplementary Figure S2: Effect of *DRBD18* RNAi on *DRBD12* mRNA.

DRBD18 RNAi was induced over 24h and mRNAs encoding *DRBD12* and tubulin were compared, as in Figure 4.

A. Northern blot results were used to examine the effects of *DRBD18* RNAi on *DRBD12* mRNA. The methylene blue-stained membrane is shown on the left, with *DRBD12* hybridisation in the centre. The membrane was then stripped and hybridised with a beta-tubulin probe as a further control. Arrows indicate the different *DRBD12* signals.

B. *DRBD18* protein levels after RNAi induction, corresponding to panel (A). Ribosomal protein S9 is the loading control.

C. Reads mapped over the *DRBD12* region of the genome, without tetracycline or after 12h tetracycline addition: one replicate is shown but two others looked similar. Since the genomics viewer (88,89) shows raw reads, the heights of the "+tet" rows have been adjusted to account for (i) different scales in the viewer and (ii) the difference in total read coverage for the two samples. This ensures that mRNAs that were not affected look approximately similar. The panel predicts a *DRBD12* mRNA of about 4 kb after 12h RNAi (orange dotted line). The low level of mapped reads over the centre of the 3'-UTR might be caused by repetitive and low-complexity sequences.