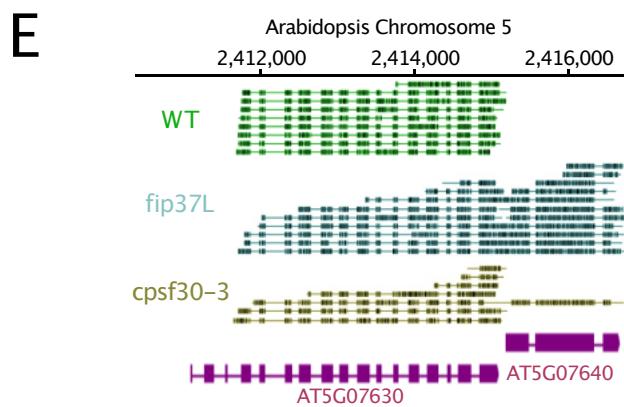
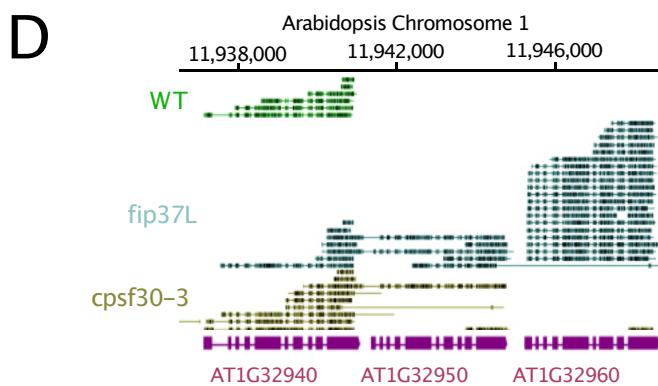
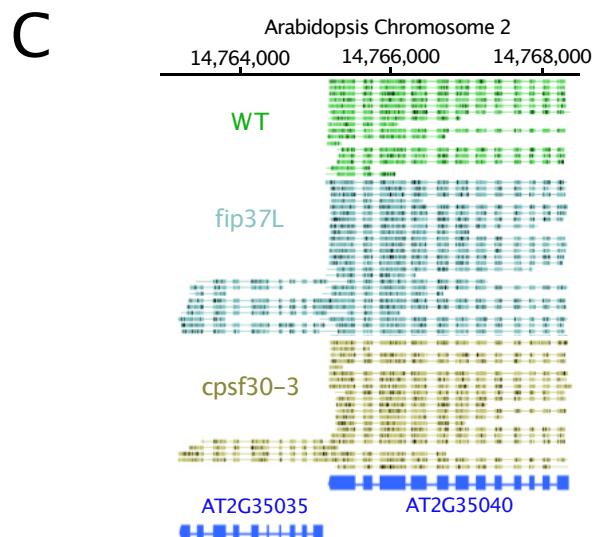


Read-through events and chimeric RNAs detected on *A. thaliana* chromosome 1, 2 and 5 in the context of *fip37L* and *cpsf30-3* mutants. (A) Aligned reads or density profiles from both DRS (top) and *illumina* RNA-seq data (bottom) of the *AT1G71330-AT1G71340* loci displaying a read-through when the RNAs are extracted from plants harboring either the *fip37L* mutation, or the *CPSF30L* mutation which specifically abrogates the *CPSF30L* mRNA production (see S1D Fig). The *illumina* RNA-seq data are represented by sashimi plots showing the differential splicing outcomes on the introns, in the backgrounds of these mutations. (B) Aligned reads or density profiles from both Nanopore RNA-sequencing (top) and *illumina* RNA-seq data (bottom) of the *AT1G29550- AT1G29560* loci. Similar description as in (A).



Read-through events and chimeric RNAs detected on *A. thaliana* chromosome 1, 2 and 5 in the context of *fip37L* and *cpsf30-3* mutants. (C) Aligned reads or density profiles from both Nanopore RNA-sequencing (top) and *illumina* RNA-seq data (bottom) of the *AT2G35035-AT2G35040* loci. Similar description as in (A). (D) Aligned reads or density profiles from both Nanopore RNA-sequencing (top) and *illumina* RNA-seq data (bottom) of the *AT1G32940-AT1G32950* loci. Similar description as in (A). (E) Aligned reads or density profiles from both Nanopore RNA-sequencing (top) and *illumina* RNA-seq data (bottom) of the *AT5G07630-AT5G07640* loci. Similar description as in (A).