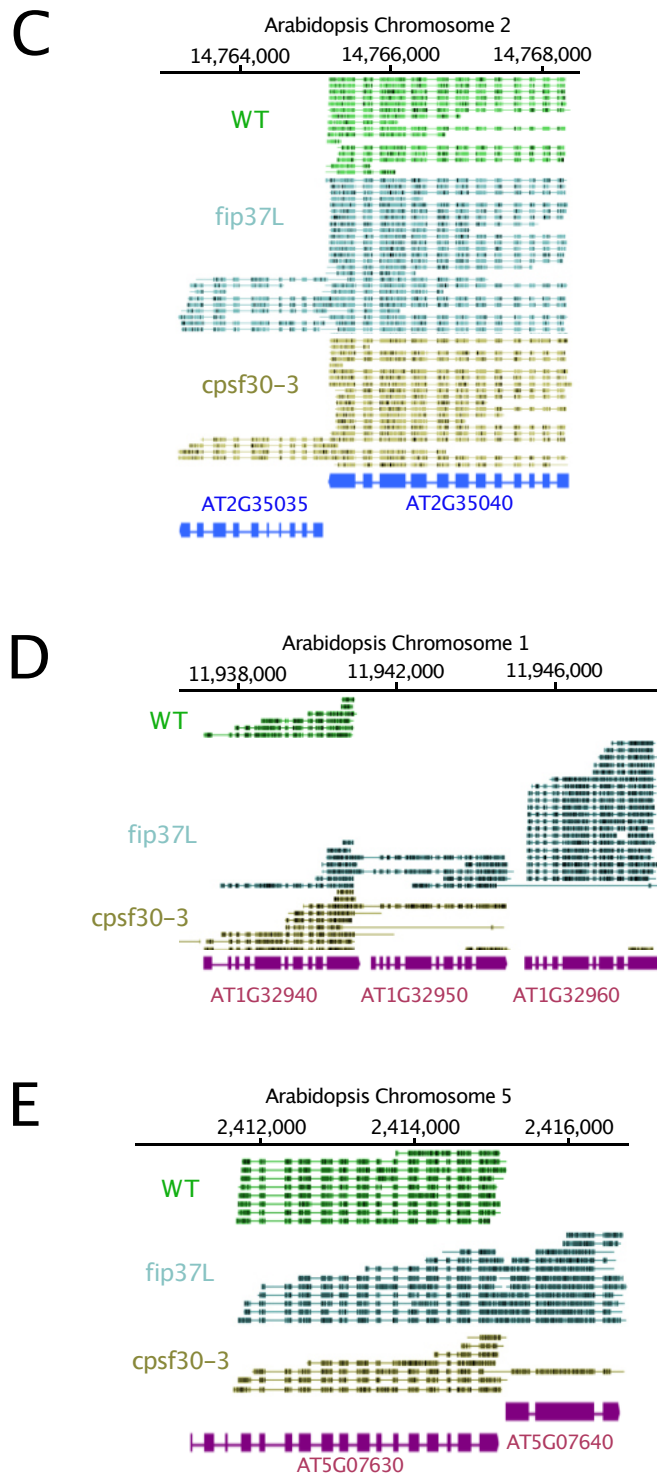


Read-through events and chimeric RNAs detected on *A. thaliana* chromosome 1, 2 and 5 in the context of fip37L and cpsf30-3 mutants. (A) Aligned reads or density profiles from both DRS (top) and *illumina* RNA-seq data (bottom) of the *AT1G71330-AT1G71340* loci displaying a read-through when the RNAs are extracted from plants harboring either the fip37L mutation, or the CPSF30-3 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-AT1G32960 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).