## Figure S8. Potential trans-targets of siRNAs derived from transposable elements, repeats and TASIRNA-target loci

The AGO1-IP approach was combined to the use of a second, high-stringency filter for genes that are up-regulated (>1.5 fold) in common in the three VSR lines. This allowed identification and qRT-PCR-based validation of At4g22470 (encoding an extensin-like protein) as being a possible target for a 22nt-long siRNA derived from a unique HELITRON locus on chromosome 4 (A). This siRNA is clearly nested into a larger population of 24nt siRNAs generally thought to promote heterochromatin formation and TGS of transposable elements in cis, via AGO4 or AGO6. This example thus illustrates how detailed analyses might unravel additional trans-targeting potential for such heterochromatic loci via the production of AGO1-loaded siRNA variants. The same high-stringency filter allowed identification of putative novel targets for TAS loci, including TAS2 (B), and notably unraveled a potential for *trans*-targeting by 21nt-long siRNAs produced from known TAS3 target transcripts. These include members of the pentatricopeptide-repeat (PPR) protein gene family (e.g. At1g63130), of which some were previously shown to support second waves of RDR6/DCL4-dependent siRNA production following their primary cleavage by discrete tasiRNA species, as in the example depicted in panel C. In this case, two distinct PPR-derived siRNAs show extensive complementary target sites within the ORF of the latex allergen-like protein At2g26560, which they likely contribute to regulate post-transcriptionally as assessed by qRT-PCR. Combining the AGO1-IP approach to a query of a genomic hairpin database was also successful in identifying novel transposable elements-derived IRs as sources of 20-21nt-long siRNAs with a potential to inhibit gene expression in *trans* (D-E).

