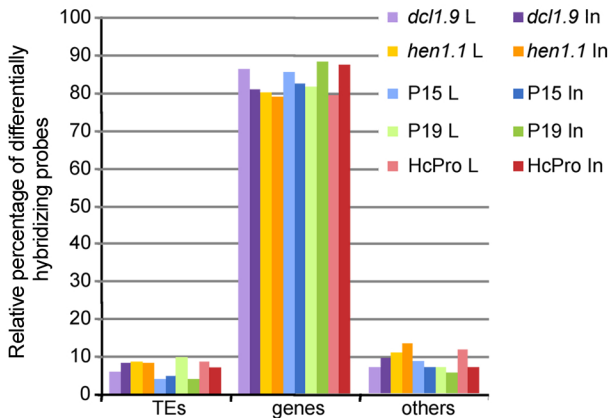


Figure S1. Arabidopsis Chromosome IV Tiling array analysis

One percent or less of the ~21000 probes present on the tiling array reported statistically significant differences in transcript accumulation in leaves or inflorescences between WT plants and transgenic plants expressing VSRs, a fraction slightly lower than between WT and *dcl1-9* or *hen1-1* mutant plants (data deposited on Gene expression omnibus (GEO): accession number GSE26739). In addition, most of these changes in transcript accumulation concerned genes and not repeat elements (A). We therefore conclude that VSRs do not detectably affect silencing of repeat elements across the Arabidopsis genome. Similarly, no difference could be detected reliably in the profiles of histone H3 dimethylated at lysine 9 (H3K9me2, a mark associated with silent repeat elements) or dimethylated at lysine 4 (H3K4me2, a typical euchromatic mark) along the entire chromosome between WT and HcPro- or WT and P19-expressing plants (B; GEO accession number GSE24692). In contrast, a small number of repeat loci exhibited statistically significant gain of H3K4me2 and/or loss of H3K9me2 in *hen1-1* mutant plants (GEO accession number GSE24692), consistent with the role of HEN1 in stabilizing all classes of small RNAs, including 24nt-long siRNA associated with repeat elements (B). Nonetheless, these chromatin changes were not associated with detectable transcript up-regulation of the corresponding repeat elements (data not shown).

A**B**