

**Supplemental Data. Georg et al. (2014). Plant Cell 10.1105/tpc.114.129767**

Whole genome expression plot. Both strands of the respective chromosomal regions are shown with the location of annotated (protein coding) genes (blue boxes), antisense RNAs (red), and intergenic sRNA genes (yellow). RNAseq read numbers for primary transcripts (cf. [1]) are plotted in dark gray; reads for all transcripts are in light gray, given in  $\log_2$  scale (right y-axis). The scale for the microarray data are given at the left y-axis. All probes of a single RNA feature are connected by lines. Signals derived from individual microarray probes are represented by green (WT) and blue (*psrR1*<sup>+</sup>) squares, respectively. Color gradation pictures the chronological sequence of the experiment.



































































































































































































































































































































































































































































































































































































































































































































































































































