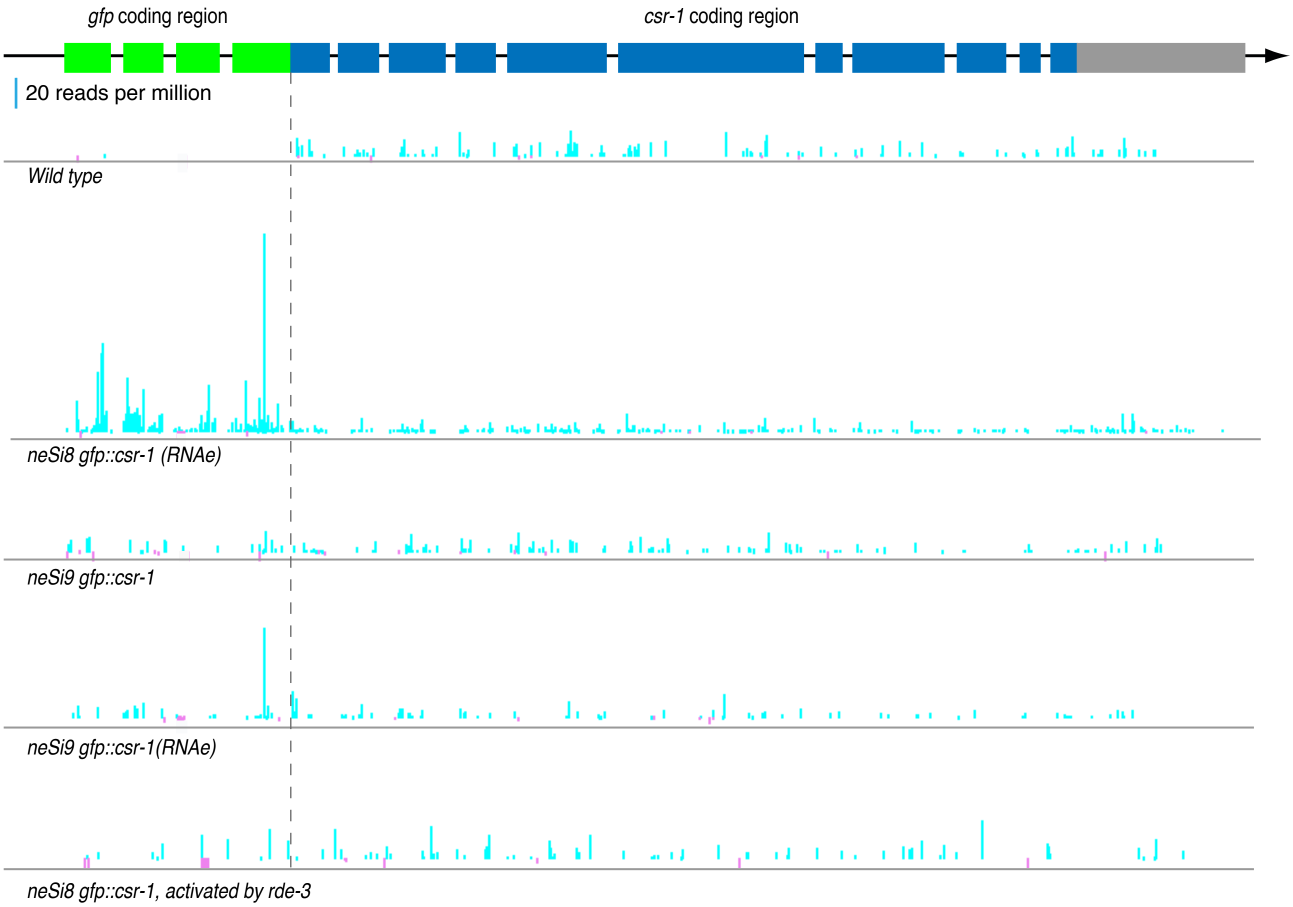

Figure S1. Small RNA profile of *gfp*::*csr-1* transgenic lines, related to Figure 3
Small RNA density along the *gfp* and *cdk-1* coding regions of wild-type and indicated transgenic lines. Vertical bars represent the 5′ nt of a small RNA, and the height of each bar indicates the number of reads that start at that position. The strand is represented by color; sense (pink) and antisense (light blue). Scale bar indicates 20 reads per million. The strain *neSi9 gfp*::*csr-1*(*RNAe*) (GFP-) was generated by crossing *neSi9 gfp*::*csr-1* (GFP+) to *neSi10 gfp*::*csr-1*(*RNAe*) (GFP-). The strain *neSi8 gfp*::*csr-1* (GFP+) was generated by crossing an *rde-3* mutation into the strain *neSi8 gfp*::*csr-1*(*RNAe*) (GFP-) and then removing the *rde-3* mutation by crossing *rde-3*; *neSi8 gfp*::*csr-1* to a wild-type strain.