

Comprehensive analysis of cotton miRNAs response to whitefly infestation offers new insights into plant-herbivore interactions

Jiaying Li¹, J. Joe Hull², Sijia Liang¹, Qiongqiong Wang¹, Luo Chen¹, Qinghua Zhang¹, Maojun Wang¹, Xianlong Zhang¹ and Shuangxia Jin^{1*}

¹National Key Laboratory of Crop Genetic Improvement, Huazhong Agricultural University, Wuhan, Hubei 430070, P. R. China

² USDA-ARS, Arid Land Agricultural Research Center, 21881 North Cardon Lane, Maricopa, AZ 85138, USA

Supplementary Figures

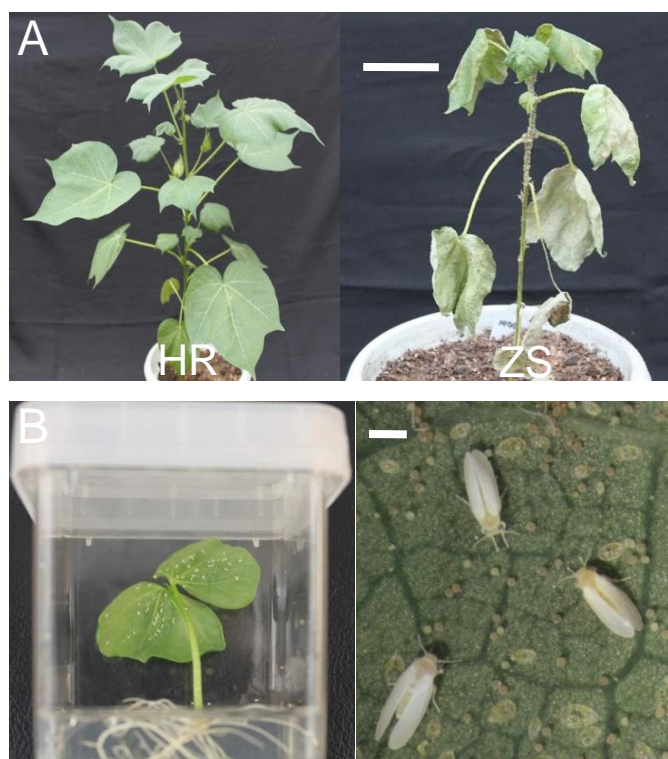


Figure S1. The phenotype during the whitefly infestation resistant and susceptible cotton cultivar. (A) The phenotype of HR and ZS cultivar after infestation 1 month. (B) The cotton plants infested by whitefly in a sealed chamber box.

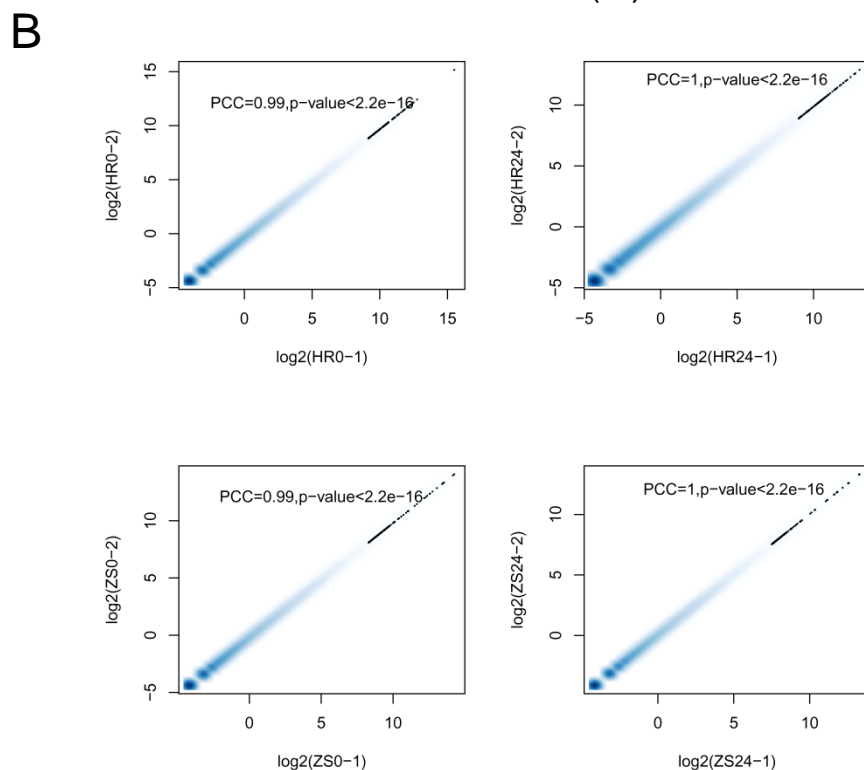
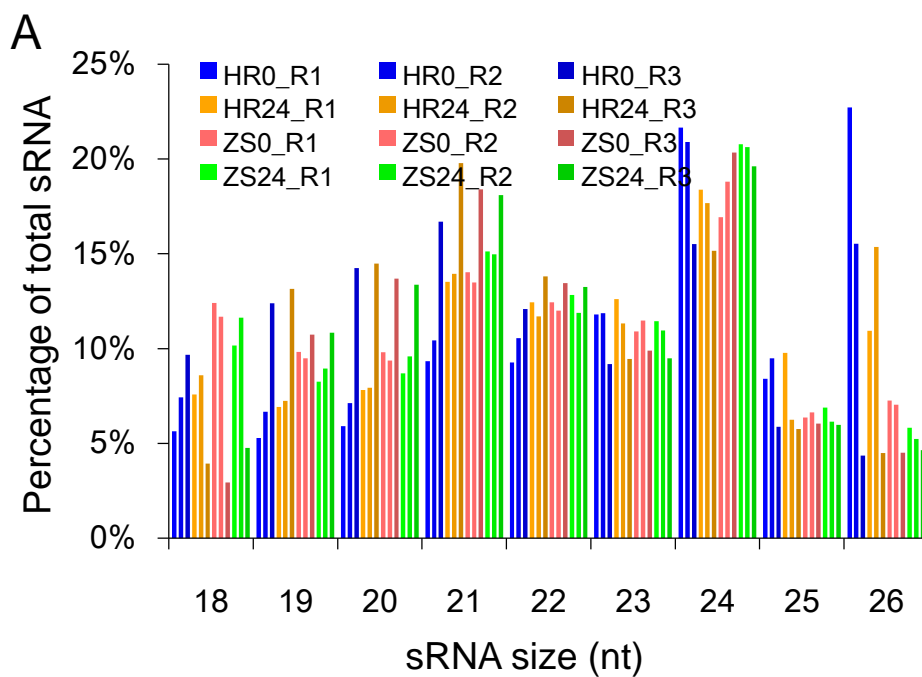


Figure S2. Distribution of sRNA reads in twelve libraries. (A) Distribution of total read lengths present in the three biological replicates. (B) All sRNA (miRNAs + siRNAs) expression level correlations were calculated by PCC in the two biological replicates.

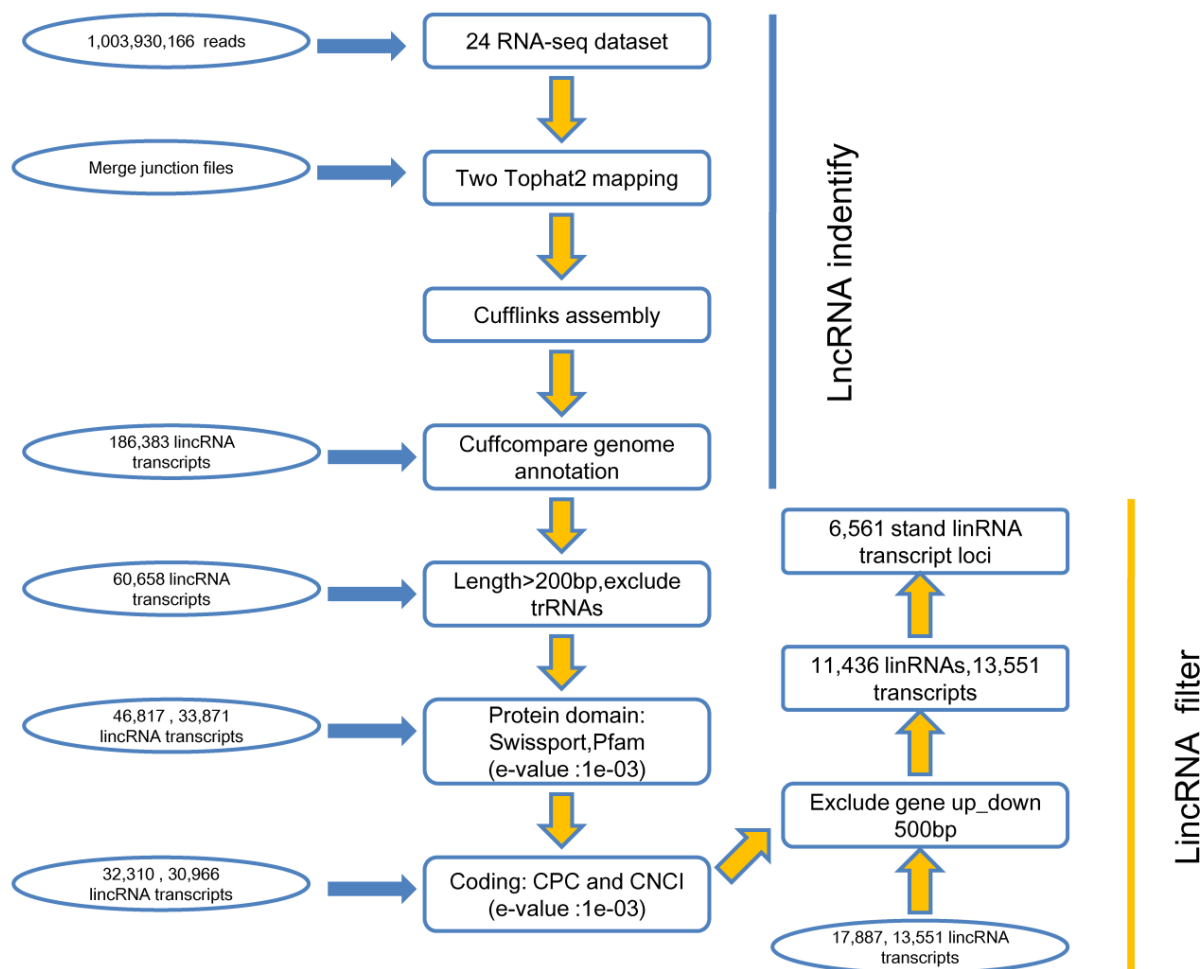


Figure S3. Schematic diagram of the integrative pipeline used for systematic identification of lincRNAs.

GhA05linc.520 → P132: miR171f-3p



GhD06linc.129 → P168 : miR8733



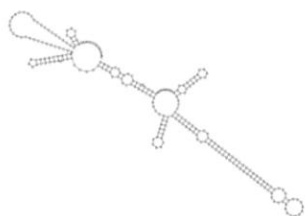
GhA05linc.451 → P181 : miR172b



GhA07linc.319 → P147:miR166b



GhA08linc.292 → P111: miR166



GhD09linc.75.2 → P187:miR390c



GhA07linc.14 → P193 : ghe-miR156d



GhA07linc.38 → P72: miR482c



Figure S4. Conserved miRNA precursors generated by lincRNAs.

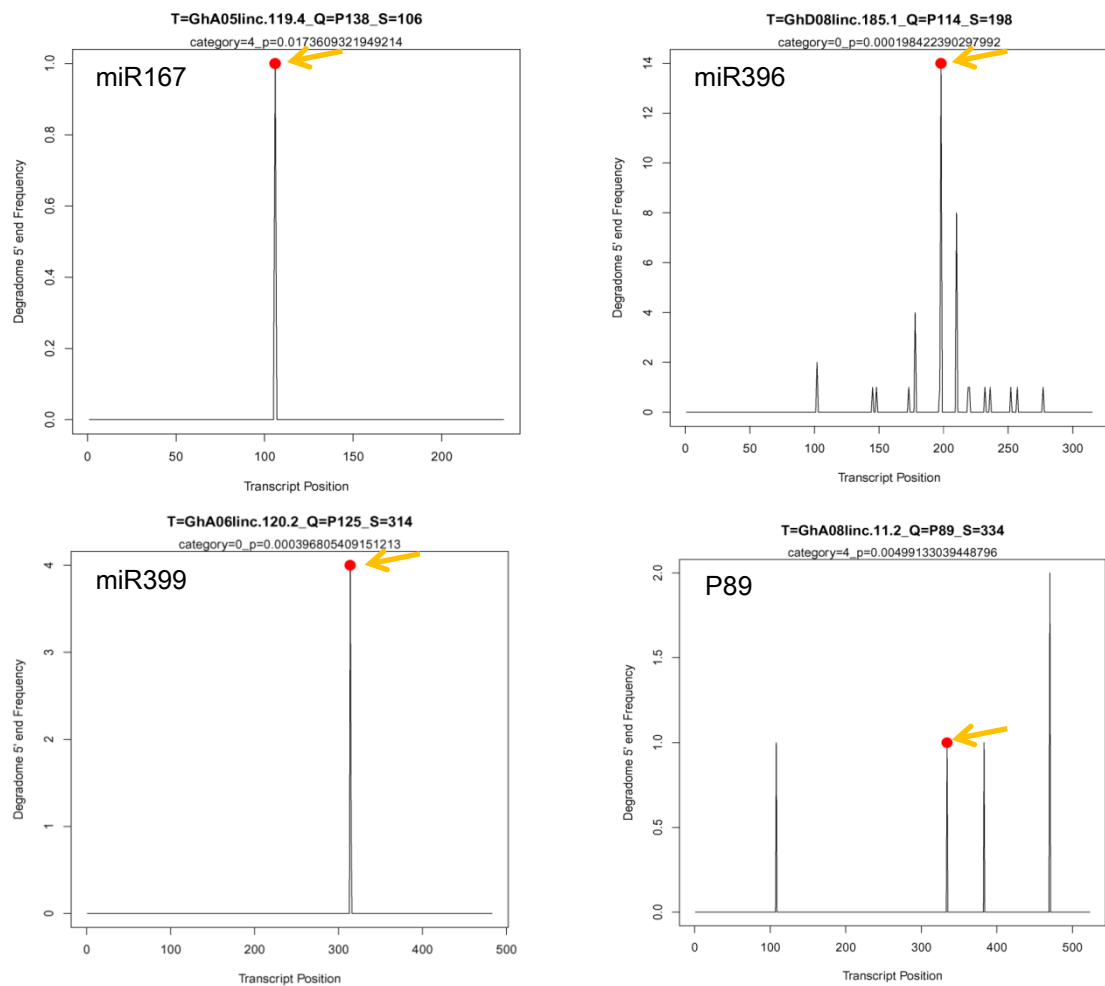


Figure S5. T-plots of the cotton miRNAs targeted by lincRNAs.

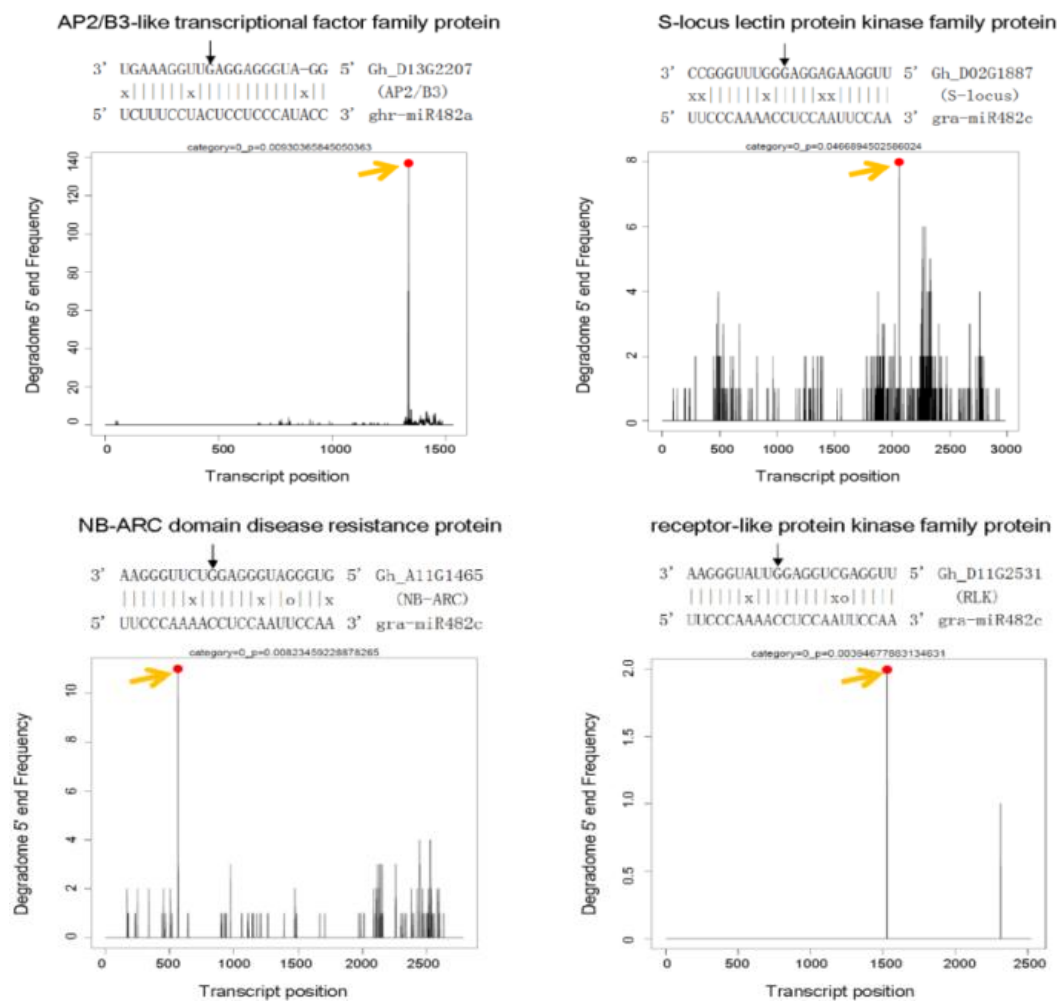


Figure S6. miR482 targets were confirmed by degradome sequencing.

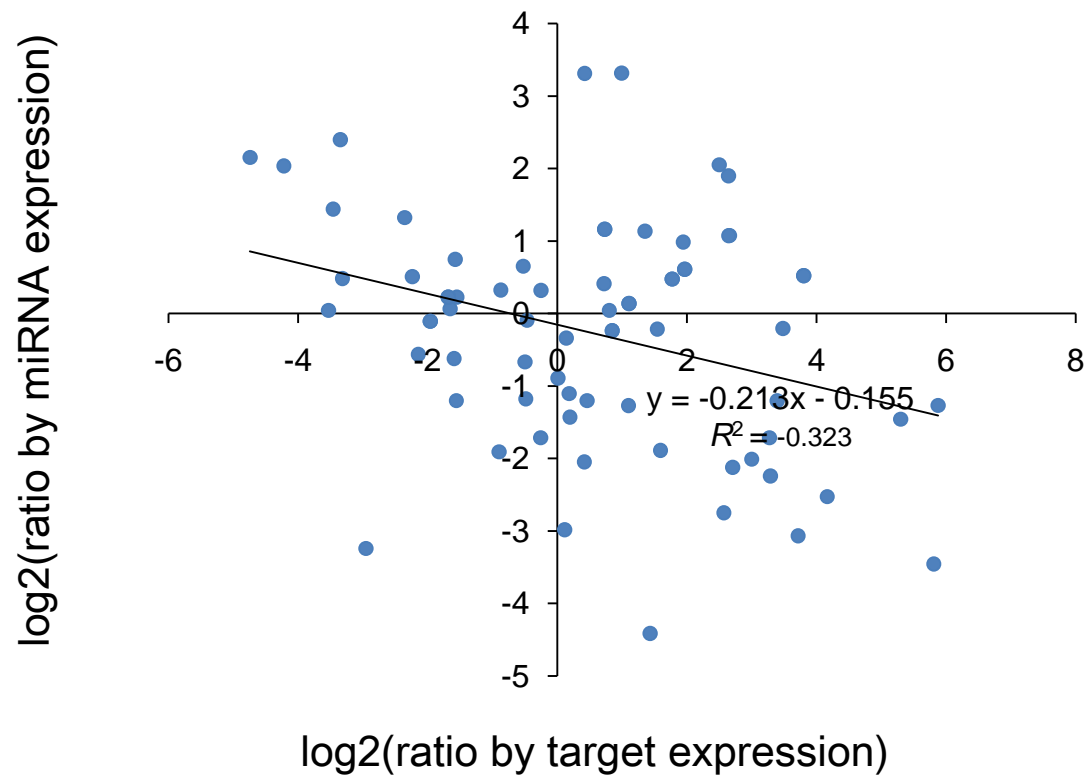


Figure S7. The expression of correlation between miRNA and their target gene.

| PHAS_ID | Nearby gene | start | end | Region | miRBase21 | miRNA_length | Target_annotation | No.of siRNA |
|---------|-------------|----------|----------|------------|---------------|--------------|-------------------|-------------|
| PHAS1 | Gh_A10G0412 | 4109823 | 4110172 | Coverexon | P138: miR167b | 21nt | ARF8 | 6 |
| PHAS2 | Gh_D10G0426 | 4000280 | 4000629 | Coverexon | P138: miR167b | 21nt | ARF8 | 6 |
| PHAS3 | Gh_D07G1901 | 46743778 | 46744190 | intergenic | P187: miR390c | 21nt | TAS3 | 11 |
| PHAS4 | Gh_A10G1561 | 85166412 | 85166845 | intergenic | P187: miR390c | 21nt | TAS3 | 14 |
| PHAS5 | Gh_A06G0606 | 15588866 | 15589509 | exon | P73 | 22nt | NB-ARC | 9 |
| PHAS6 | Gh_D06G0687 | 11881265 | 11881656 | exon | P73 | 22nt | NB-ARC | 10 |
| PHAS7 | Gh_A05G2533 | 35115948 | 35116255 | exon | P81 | 22nt | NB-ARC | 5 |
| PHAS8 | Gh_A11G0364 | 3393149 | 3393750 | exon | P79: miR482a | 22nt | CC-NBS-LRR | 16 |
| PHAS9 | Gh_D13G2207 | 58191228 | 58191535 | exon | P80: miR482a | 22nt | AP2/B3 | 8 |

Figure S8. *PHAS* genes triggered by miRNAs identified in this report

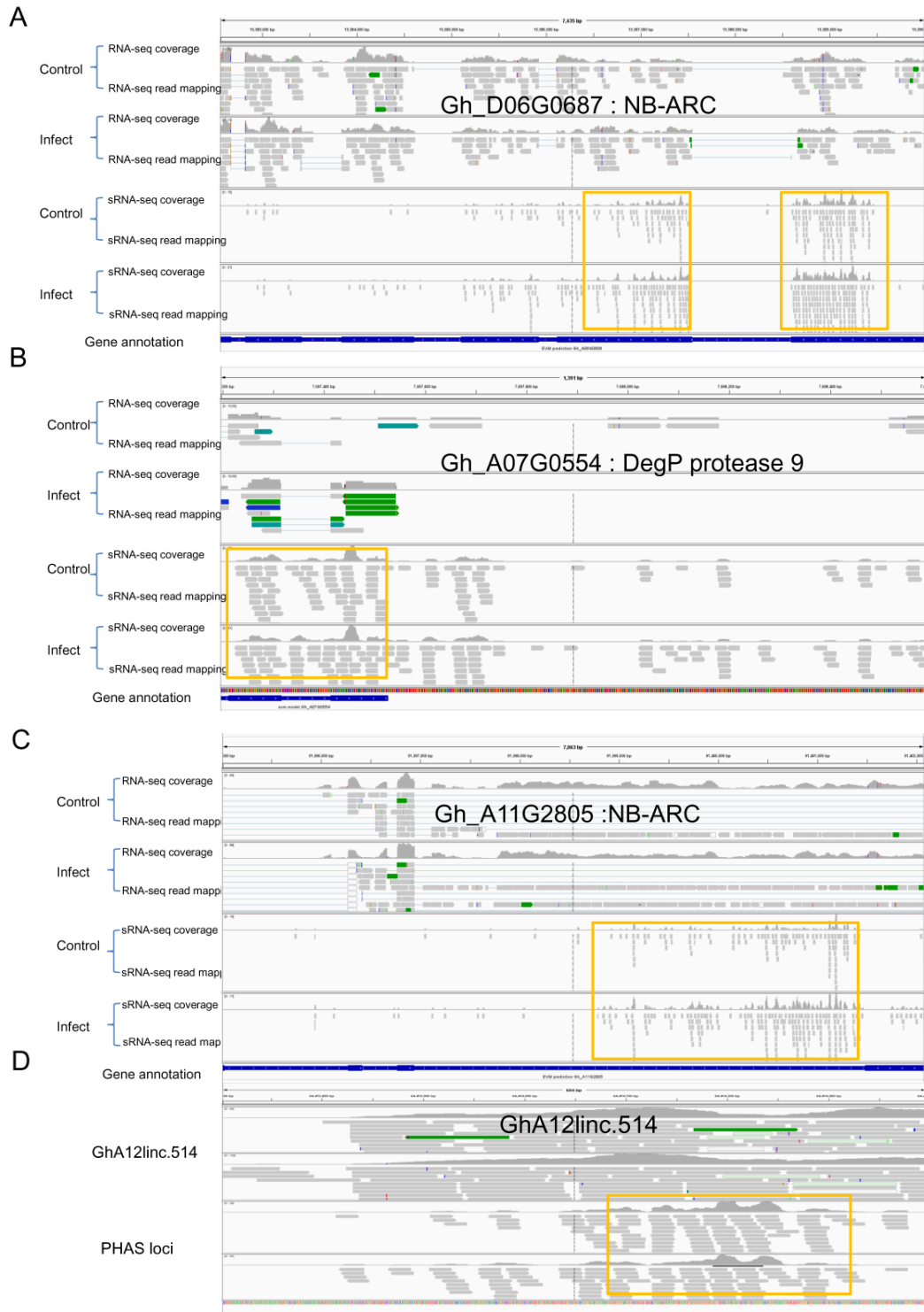


Figure S9. PhasiRNAs generated from different cotton genome regions. *A* NB-LRR protein generated phasiRNA loci in two alternative exons by a novel *P73* miRNA trigger. *B* Deg P protease-generated siRNAs from exon-intron-exon junctions. *C* NB-LRR protein generated siRNAs from a *bona fide* intron. *D* lincRNA-generated phasiRNAs.