

Genome-wide analysis of cotton miRNAs during whitefly infestation offers new insights into plant-herbivore interaction

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Supplementary Figures

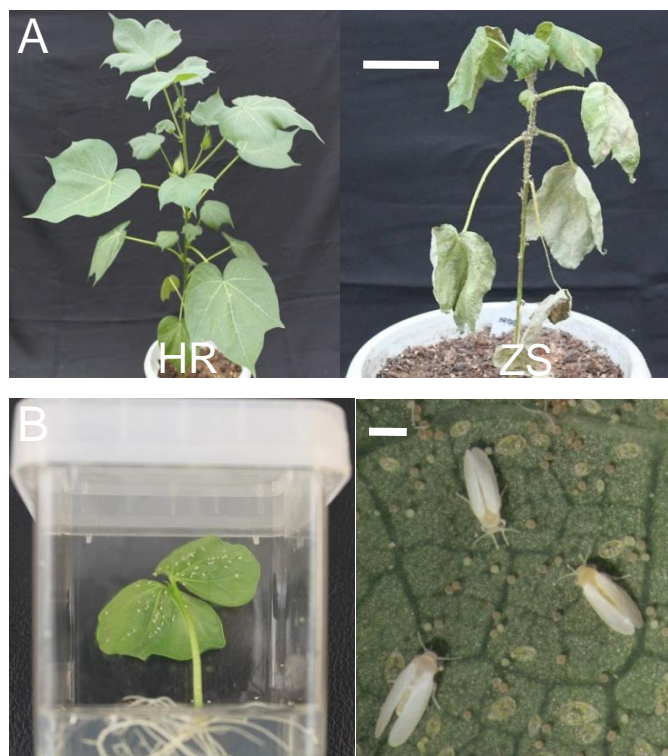


Figure S1. The phenotype during the whitefly infestation resistant and susceptible cotton cultivar. (A) The phenotype of HR and ZS cultivar after infestation 1 month. (B) The cotton plants infested by whitefly in a sealed chamber box.

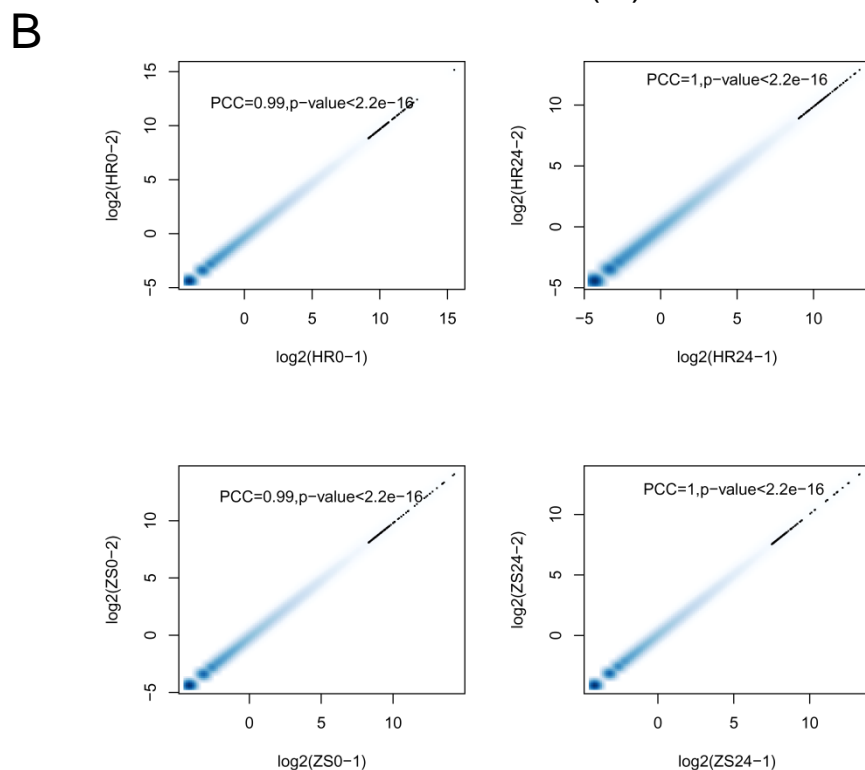
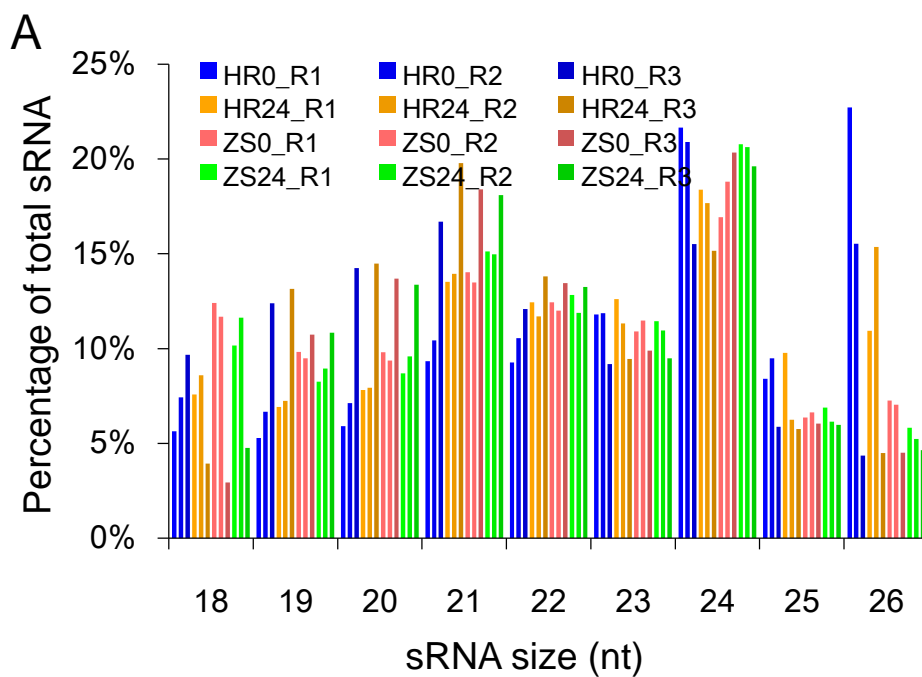


Figure S2. Distribution of sRNA reads in twelve libraries. (A) Distribution of total read lengths present in the three biological replicates. (B) All sRNA (miRNAs + siRNAs) expression level correlations were calculated by PCC in the two biological replicates.

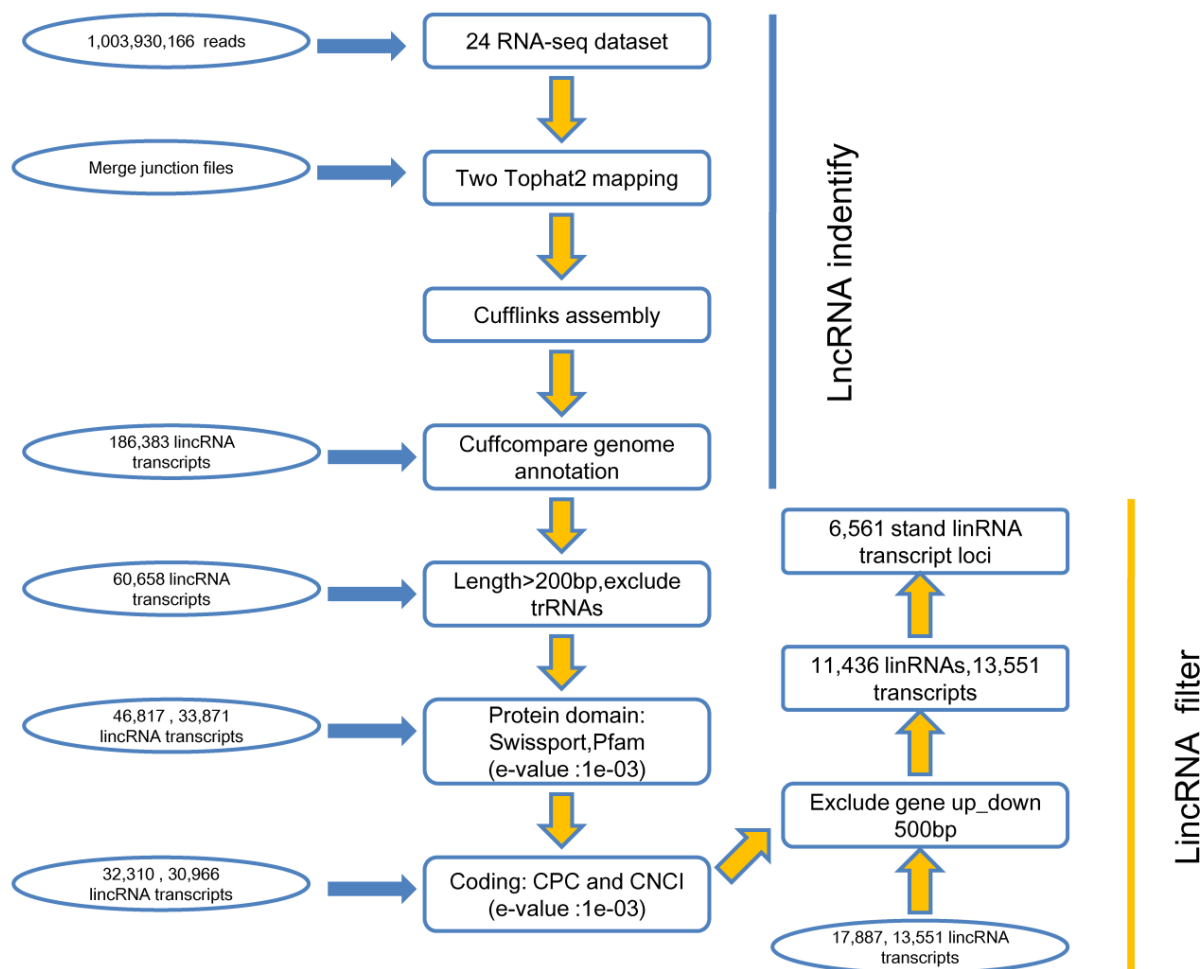


Figure S3. Schematic diagram of the integrative pipeline used for systematic identification of lincRNAs.

GhA05linc.520 → P132: miR171f-3p



GhD06linc.129 → P168 : miR8733



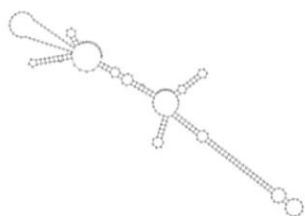
GhA05linc.451 → P181 : miR172b



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.

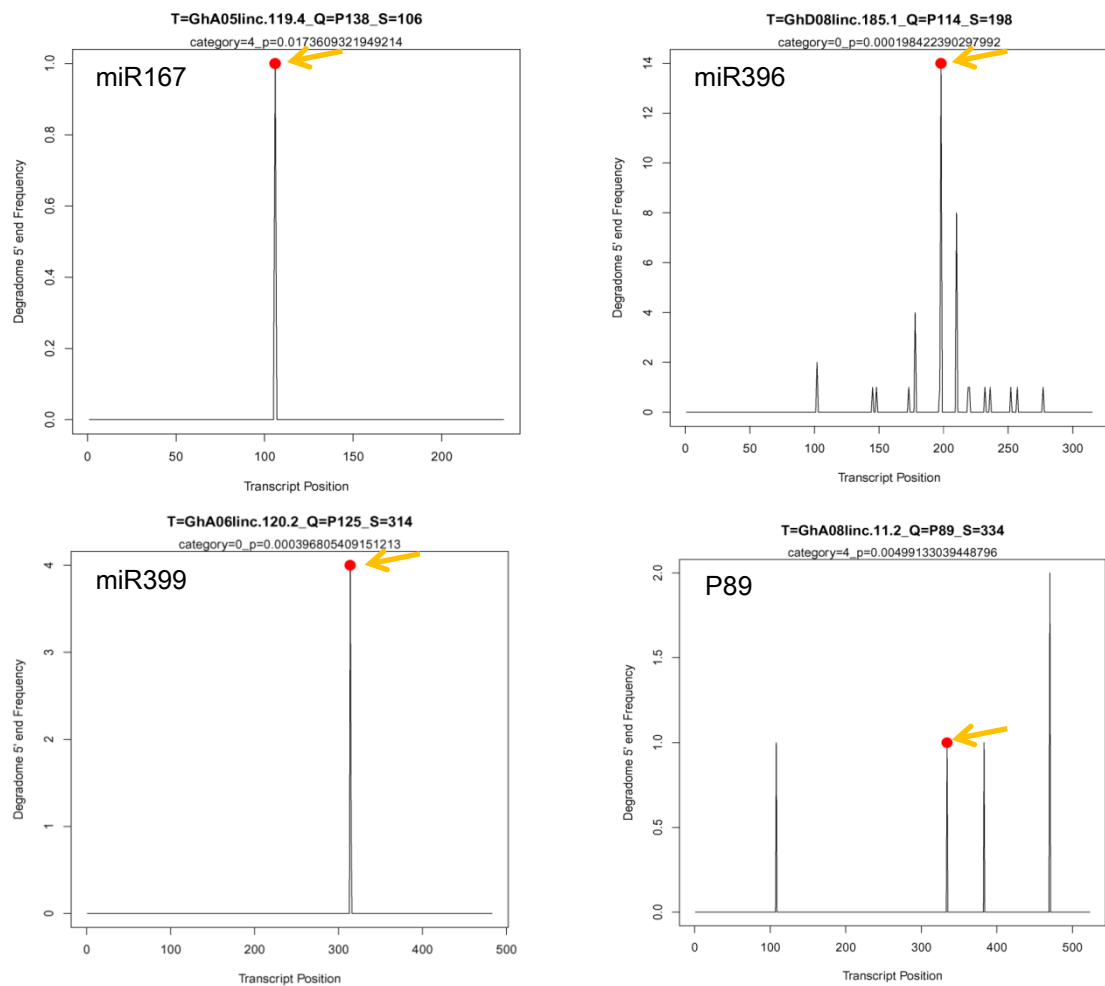


Figure S5. T-plots of the cotton miRNAs targeted by lincRNAs.

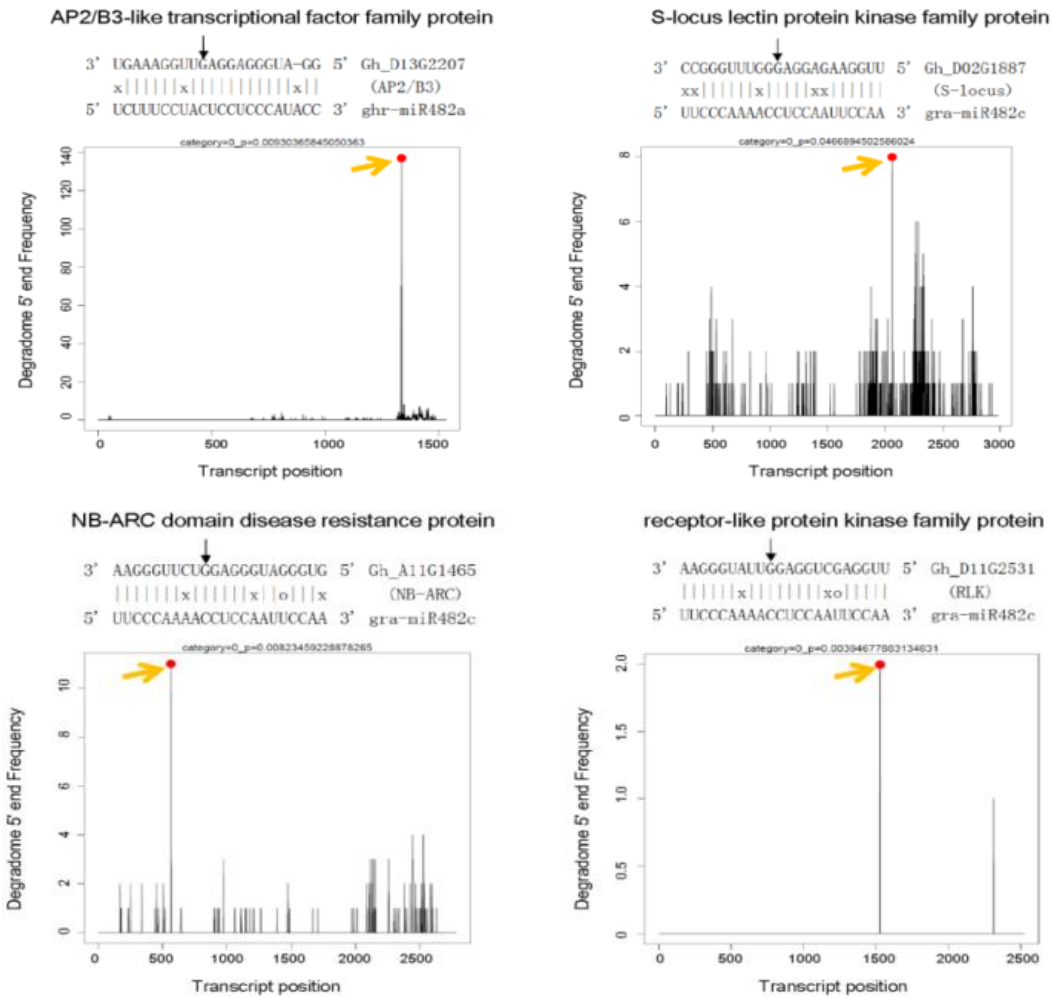


Figure S6. miR482 targets were confirmed by degradome sequencing.

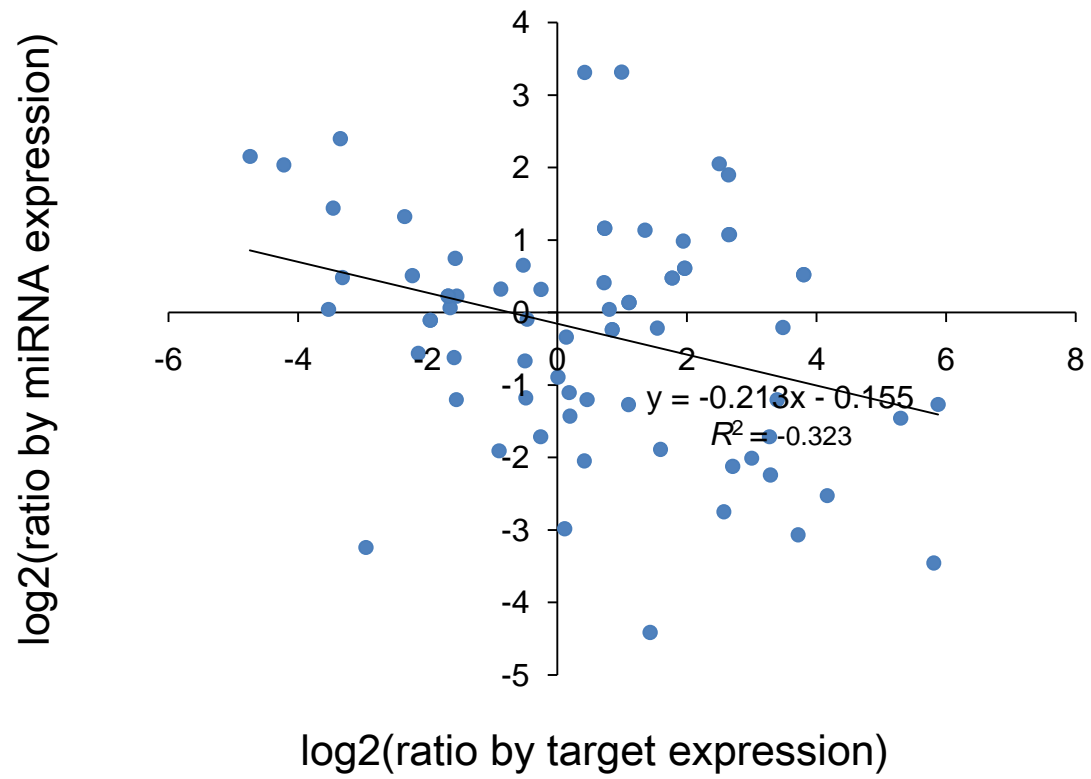


Figure S7. The expression of correlation between miRNA and their target gene.

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

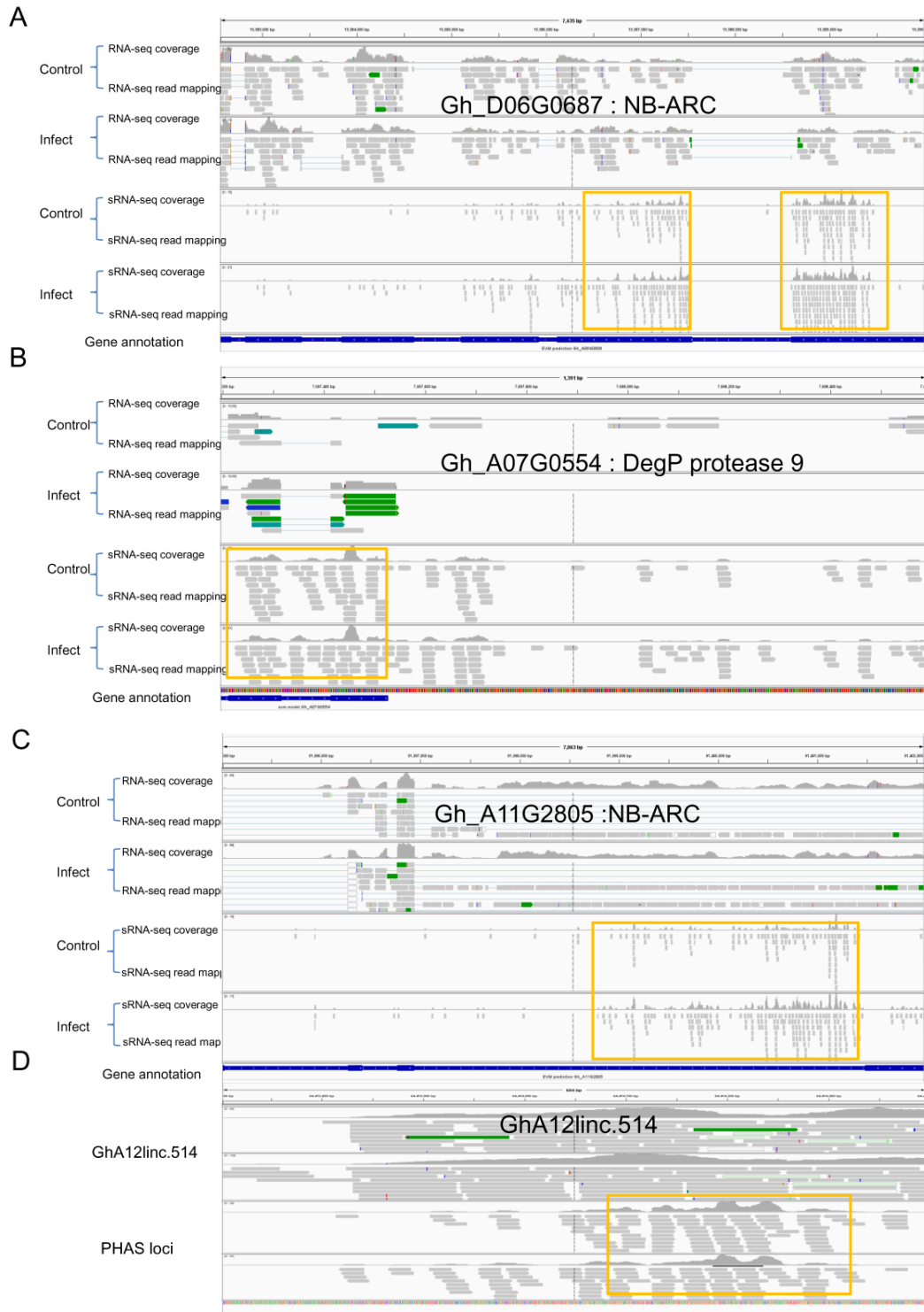


Figure S9. PhasiRNAs generated from different cotton genome regions. *A* NB-LRR protein generated phasiRNA loci in two alternative exons by a novel *P73* miRNA trigger. *B* Deg P protease-generated siRNAs from exon-intron-exon junctions. *C* NB-LRR protein generated siRNAs from a *bona fide* intron.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

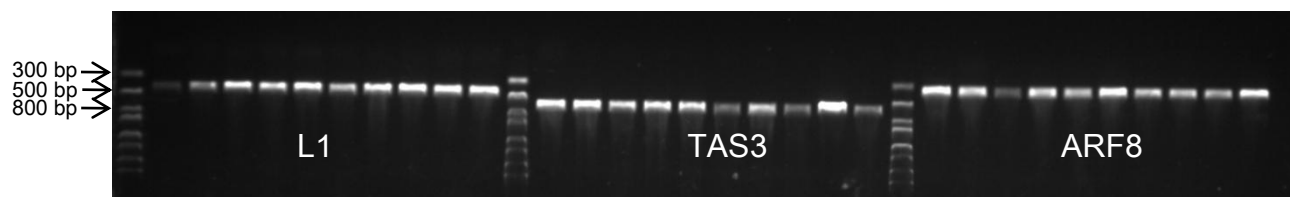


Figure S10. The VIGS vector construction.