

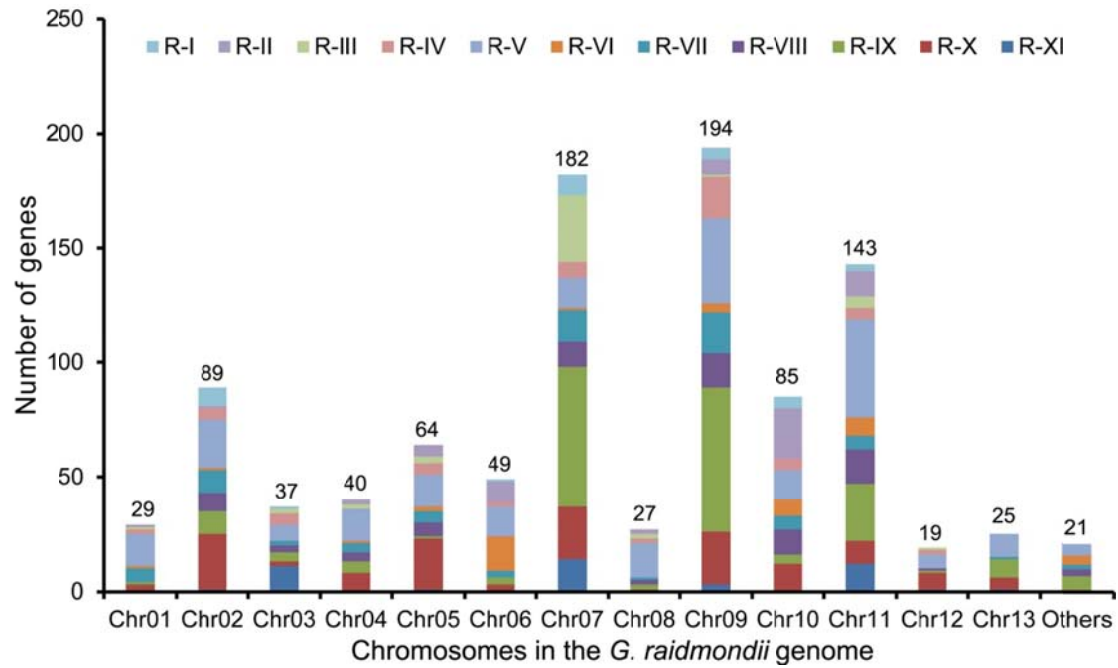


Figure S1 The statistics of RGA genes in *G. raidmondii* chromosomes. The 11 families (R-I–R-XI) of RGA genes are marked in different colours. The X-axis represents the chromosomes of the *G. raidmondii* genome (Chr01 to Chr13), and ‘Others’ represents the RGA genes that cannot be mapped to chromosomes at present. The Y-axis represents the number of genes.

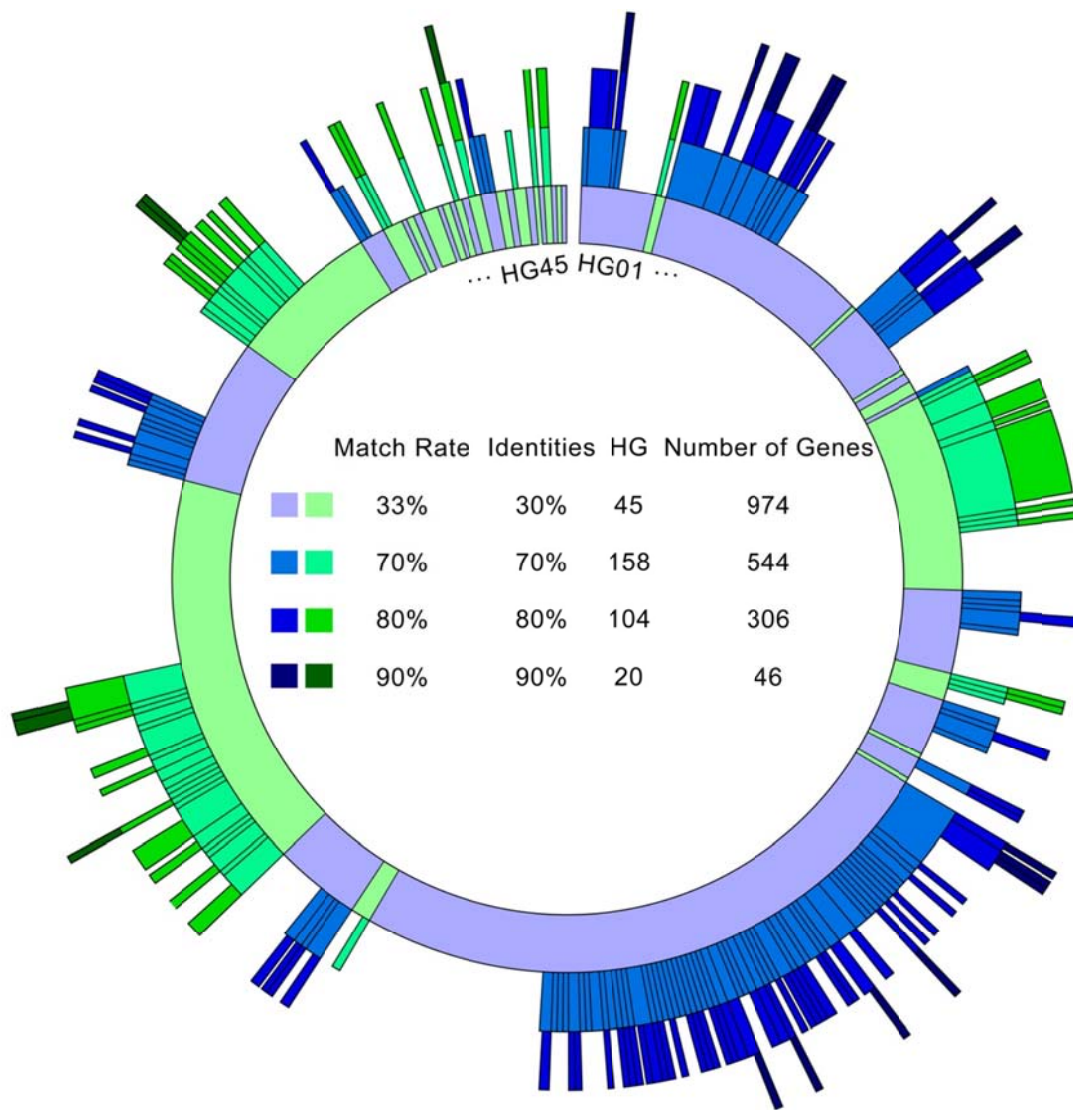
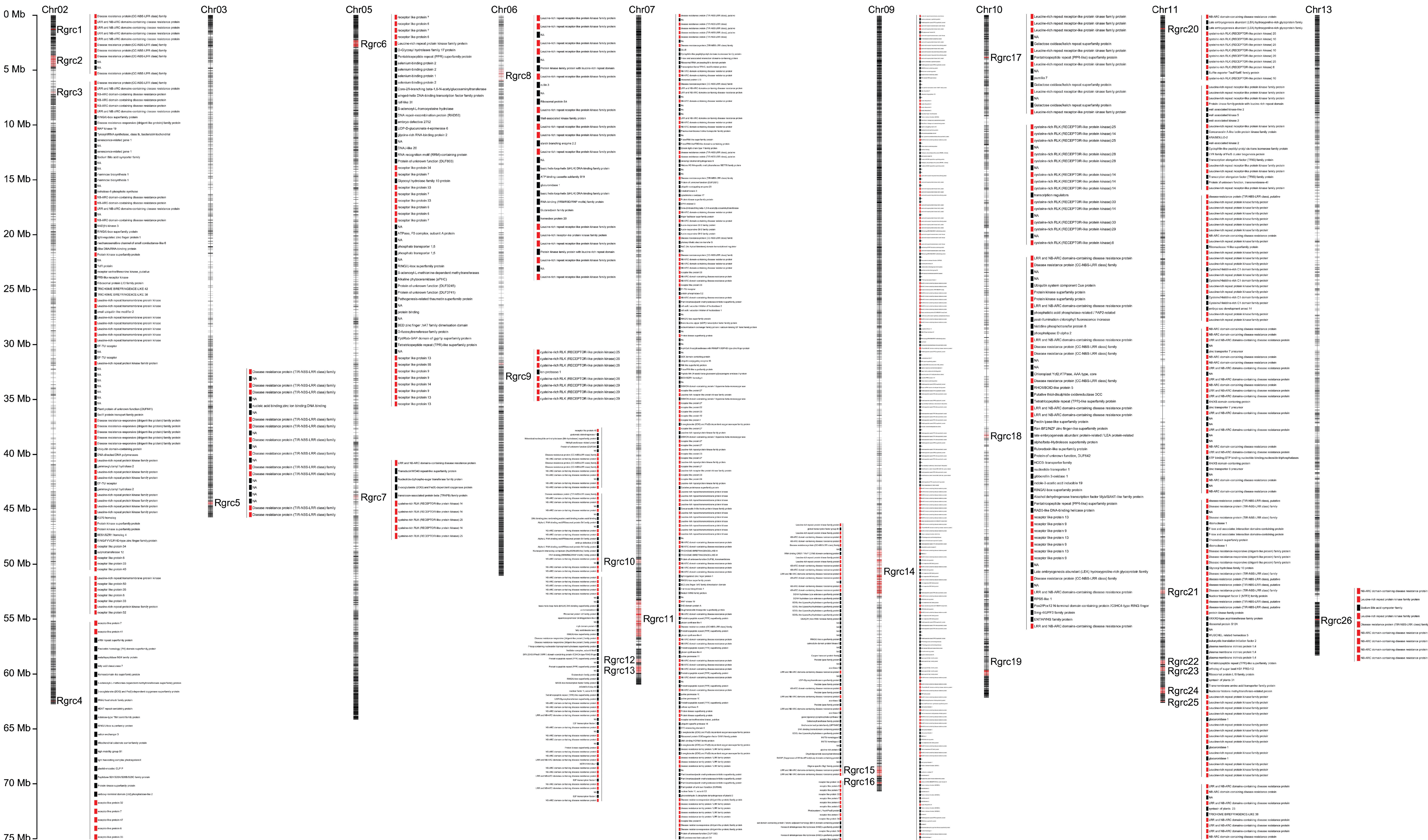


Figure S2 Homology clustering of RGA genes in the *G. raimondii* genome.

Homology clustering was filtered using four conditions based on the match rates and identities among the RGA genes. Homology groups from HG01 to HG45 are arranged clockwise, the homology group intervals are differentiated by green and blue in series, according to the clustering conditions of match rate $\geq 33\%$ and identities $\geq 30\%$.



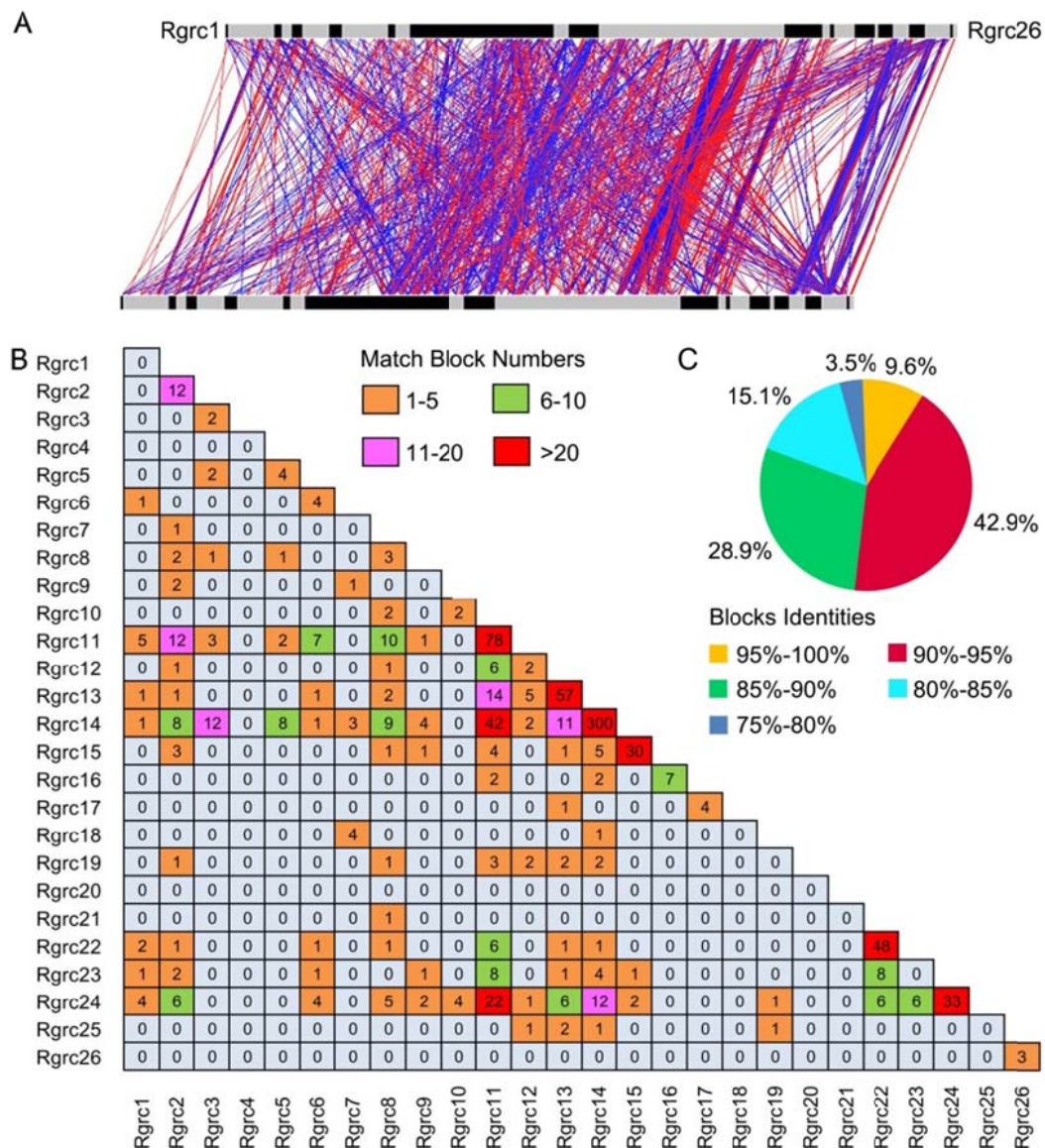


Figure S4 Homology analysis of Rgrcs in the *G. raimondii* genome. (A) Homology analysis of the Rgrcs' chimeric sequence. The chimeric sequence connected the Rgrc sequences in a series from Chr01 to Chr13 and was compared using the BlastN program (Version 2.2.23), ignoring self-matches and filtering out similarity blocks less than 3 kb in length. The forward-forward matches are marked with red lines, and the forward-reverse matches are marked with blue lines. **(B)** A statistical analysis of the similarity blocks among 26 Rgrcs. The lengths of the similarity blocks is greater than 3 kb. **(C)** Distribution of the identities of homology blocks

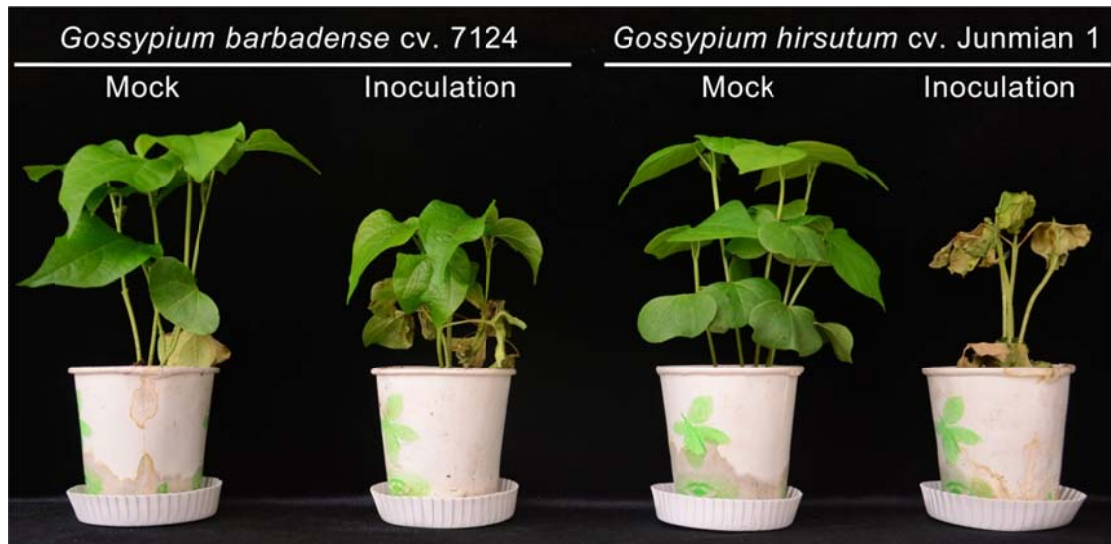


Figure S5 Cotton inoculated with *V. dahliae*. Two-week-old seedlings of the resistant cultivar *G. barbadense* cv. 7124 and the susceptible cultivar *G. hirsutum* cv. Jummian1 inoculated with the high virulence V991 defoliating strain of *V. dahliae* (5×10^6 spores/ml). The phenotypes were investigated three weeks after inoculation in this study.

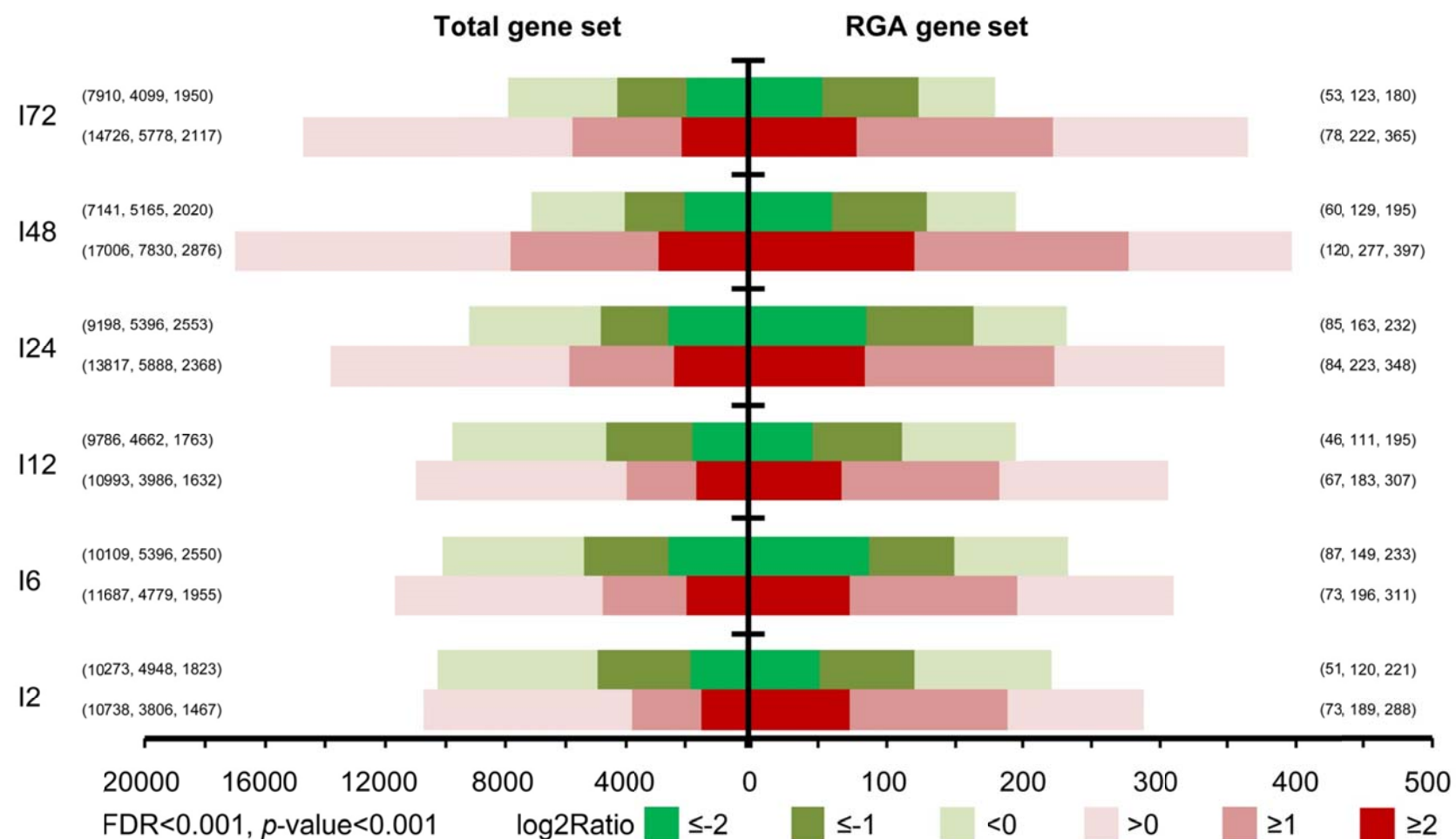


Figure S6 Statistical analysis of the DEGs in cotton inoculated with *V. dahliae*. The left side is the DEGs of all the genes in the *G. raimondii*

genome and the right side is the RGA gene set. The X-axis represents numbers of DEGs. 'I2–I72' represents the six inoculation time points (in hours). The numbers in the brackets from left to right represent the number of DEGs with more than a two-fold and a four-fold change, respectively, compared with mock-inoculated,. Red represents up-regulation and green represents down-regulation.

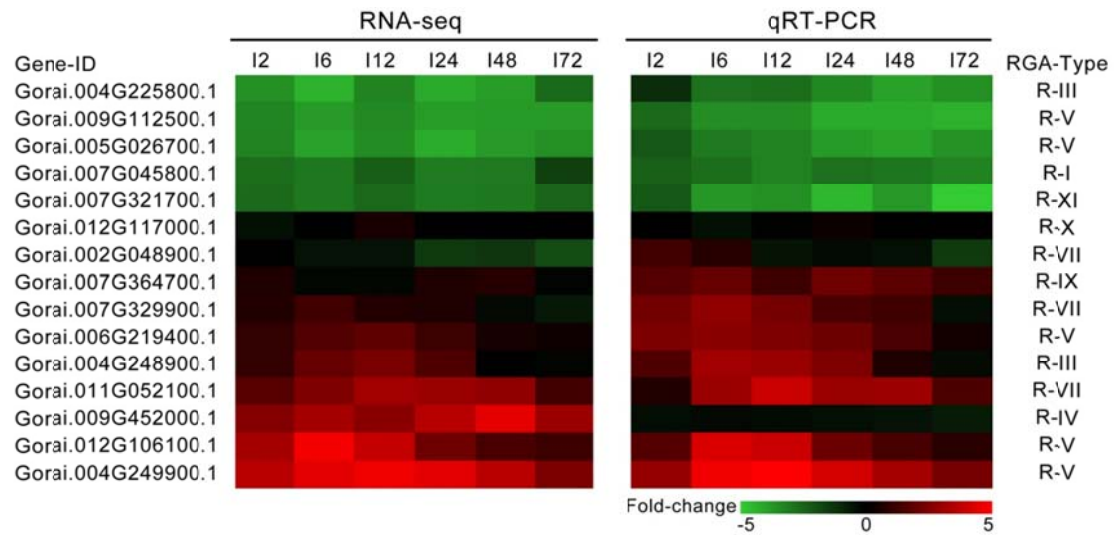


Figure S7 Differentially expressed RGA genes confirmed by qRT-PCR. In total, 15 differentially expressed RGA genes were randomly selected for qRT-PCR validation. The left side is the DEGs determined using RNA-seq and right side is the validation results using qRT-PCR.

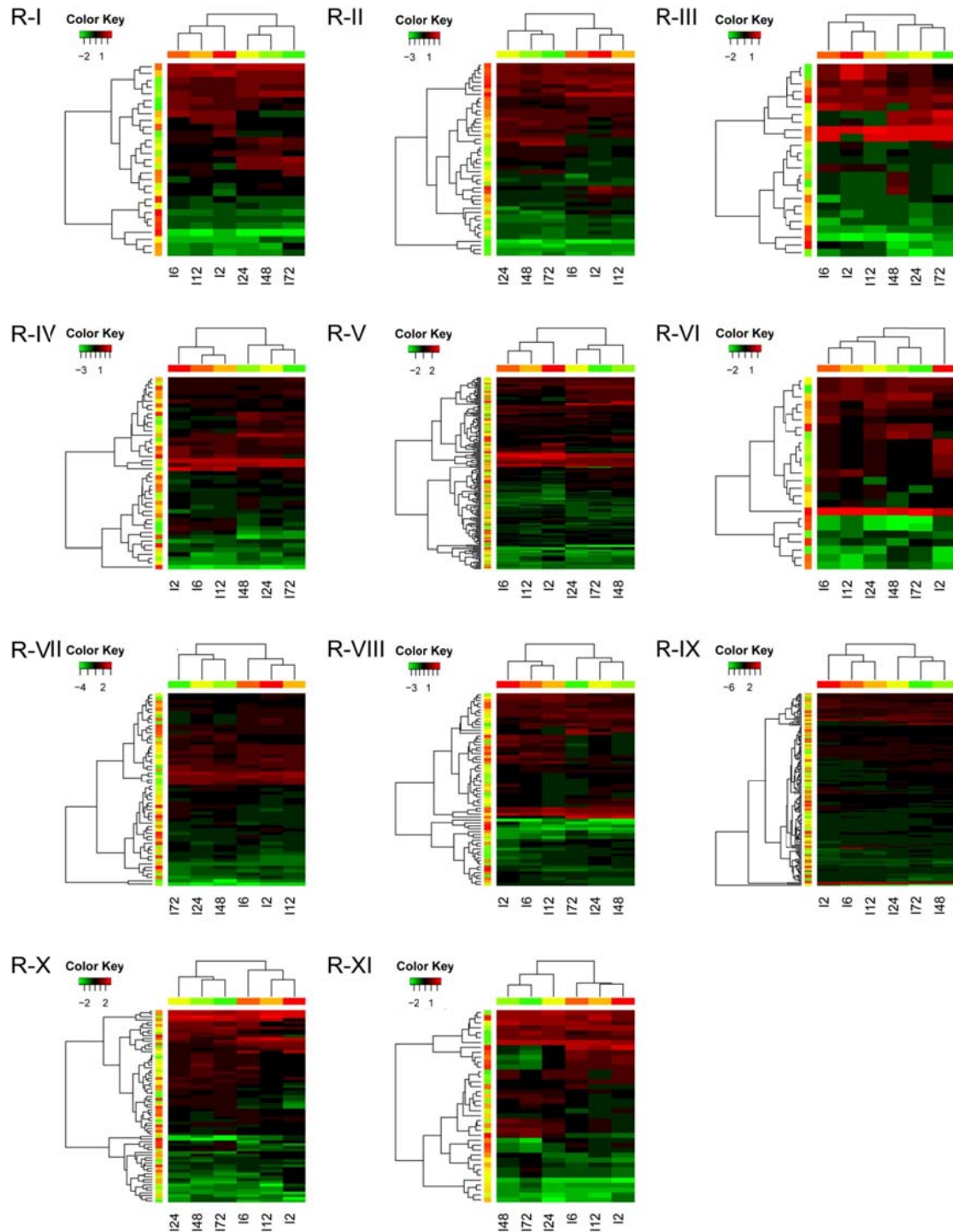


Figure S8 Expression pattern analysis of the response of 11 RGA gene families to *V. dahliae*. The filter conditions are $FDR < 0.001$ and $p < 0.001$. R-I–R-XI represents the 11 RGA gene families. ‘12–172’ represents the six inoculation time points.

analysis were screened by $\text{FDR} < 0.001$, $p < 0.001$, and $\log_2\text{Ratio} \geq |1.0|$ at all six inoculation time points. The thin lines represent the expression change of $\log_2\text{Ratio} \geq |1.0|$, and the thick lines represent the expression change of $\log_2\text{Ratio} \geq |2.0|$.

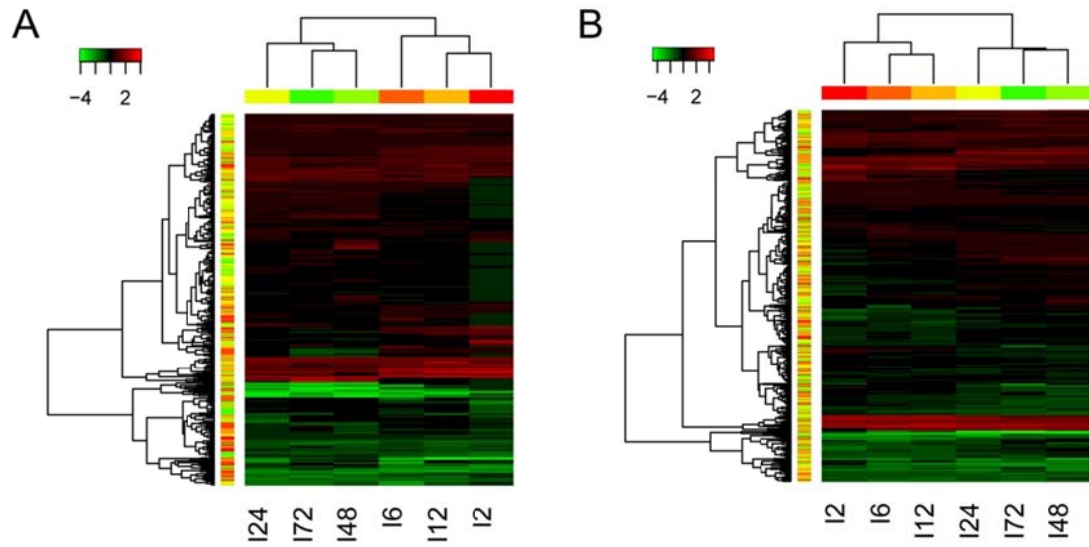


Figure S10 Clustering of DEGs encoded in Rgrcs. (A) The expression pattern analysis of RGA genes in Rgrcs. **(B)** The expression pattern analysis of other genes, not encoding RGA genes in Rgrcs. I2–I72' represents the six inoculation time points.