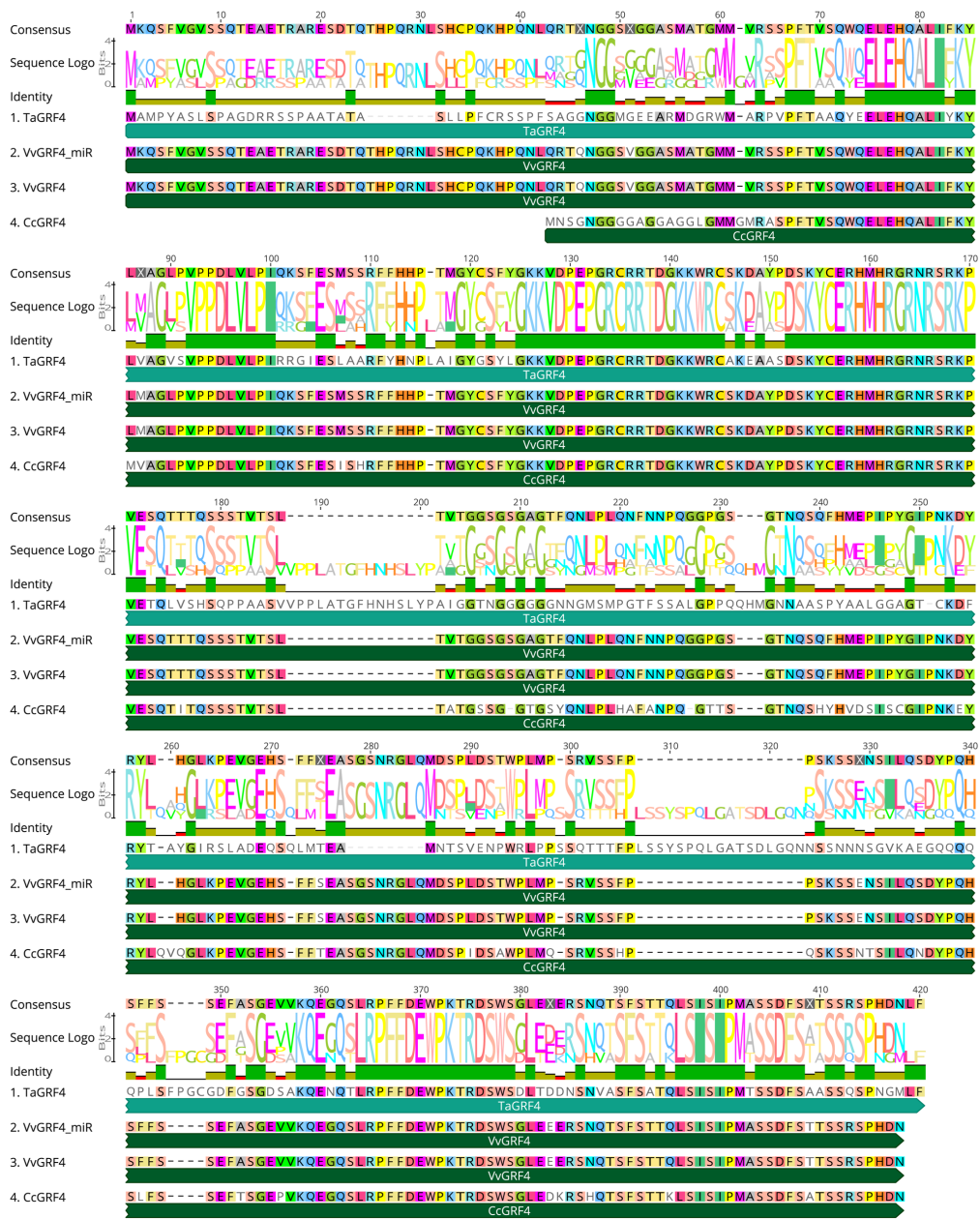


Overexpression of chimeric GRF4-GIF1 improves regeneration efficiency in diploid *Fragaria vesca* Hawaii 4.

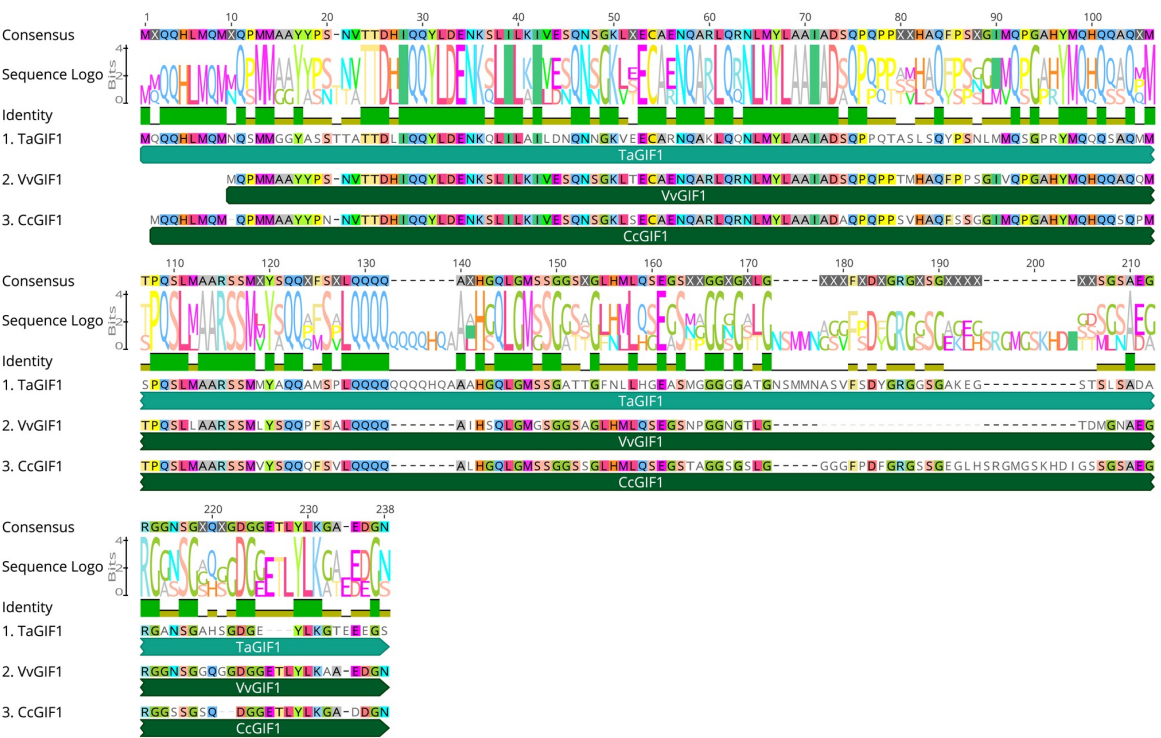
Esther Rosales Sanchez^{1,2}, R. Jordan Price², Federico Marangelli^{1,2}, Kirsty McLeary², Richard J. Harrison^{2,3}, Anindya Kundu^{2*}

Supplementary figure S1



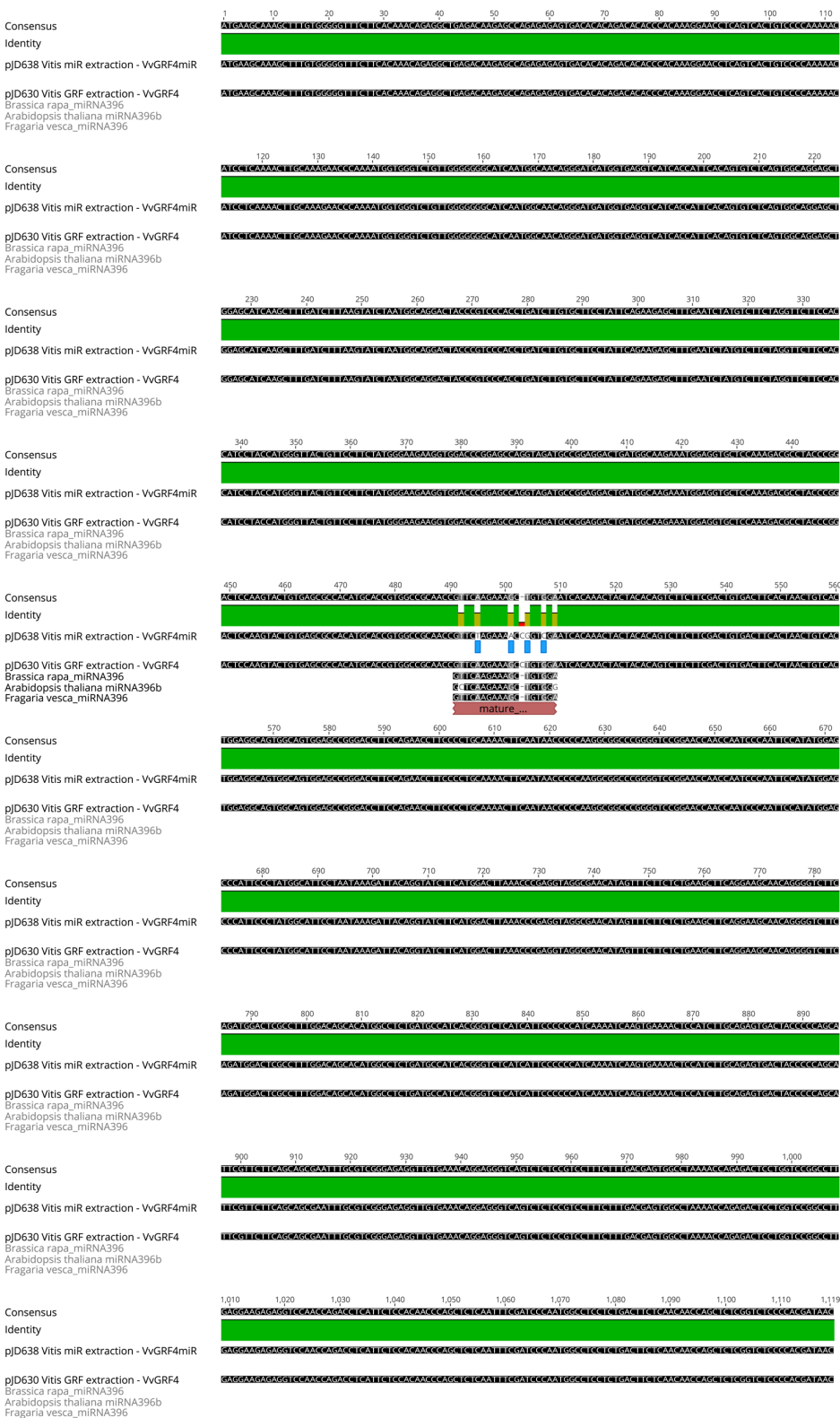
Supplementary figure S1: Protein alignment of GRF among *C. clementina*, *T. aestivum* and *V. vinifera*. Conserved amino acids among the sequences are showed in the identity row as green.

Supplementary figure S2



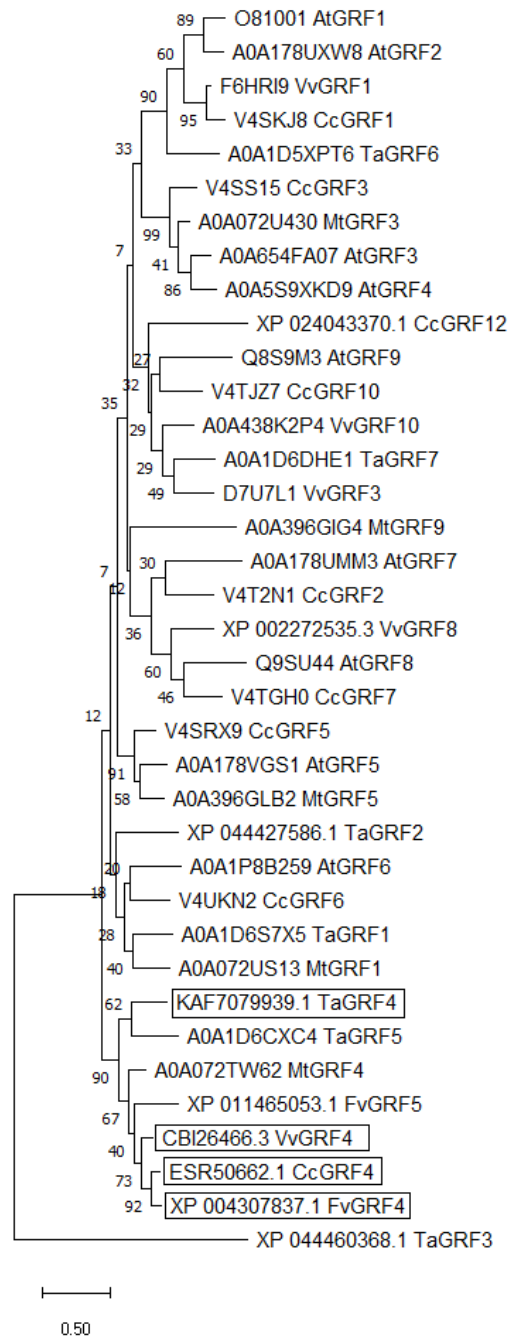
Supplementary figure S2: Protein alignment of GIF among *C. clementina*, *T. aestivum* and *V. vinifera*. Conserved amino acids among the sequences are showed in the identity row as green.

Supplementary figure S3



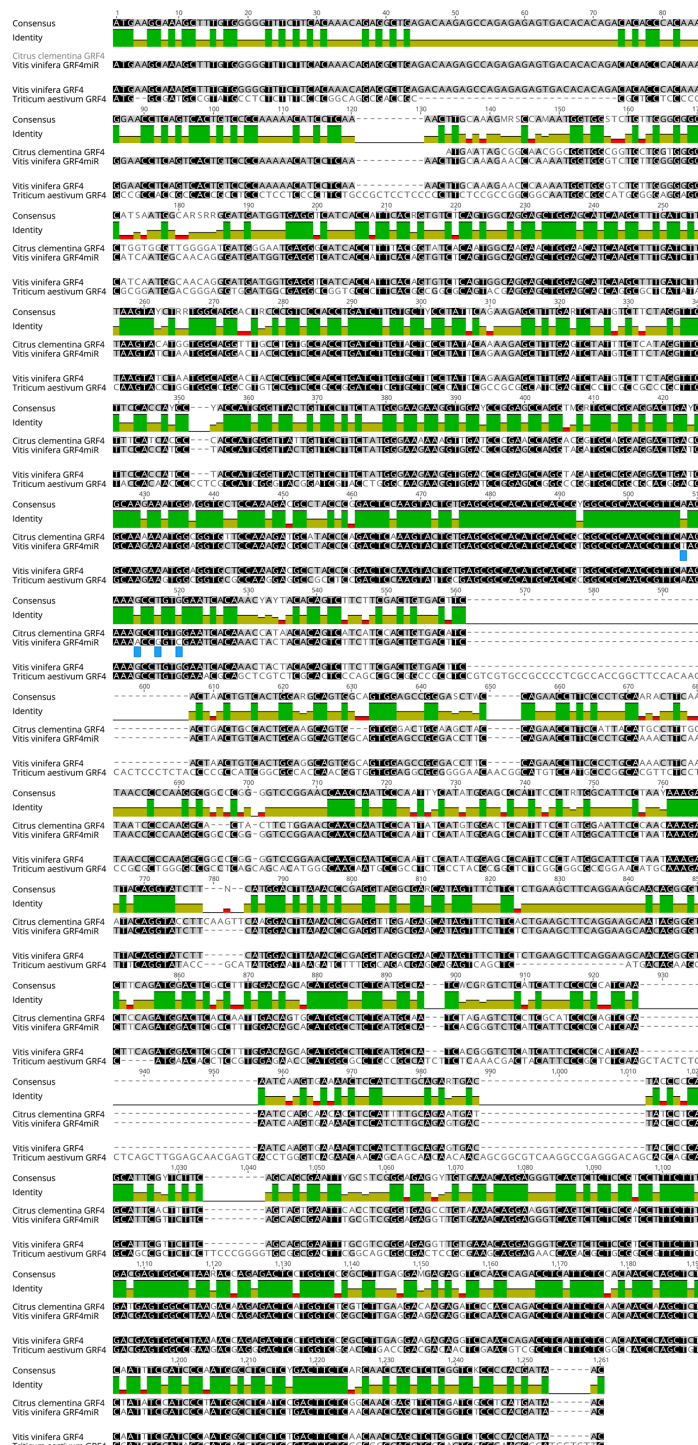
Supplementary figure S3: *miR396* conserved site in *VitisGRF4*. The alignment also indicate the presence of *Fragaria vesca miR396*, *Arabidopsis miR396b* and *Brassica rapa miR396*

Supplementary figure S4



Supplementary figure S4: Consensus phylogenetic tree inferred from 1000 replicates using Maximum Likelihood method of GRF proteins in *Arabidopsis thaliana*, *Citrus x clementina*, *Fragaria vesca*, *Medicago truncatula*, *Triticum aestivum* and *Vitis vinifera*.

Supplementary figure S5



Supplementary figure S5: GRF4 nucleotide sequence alignment between *C. clementina*, *T. aestivum* and *V. vinifera*. Conserved bases among the sequences are colored as black and are showed in the identity row as green. Blue boxes indicate the mutated *miR396* target nucleotides.