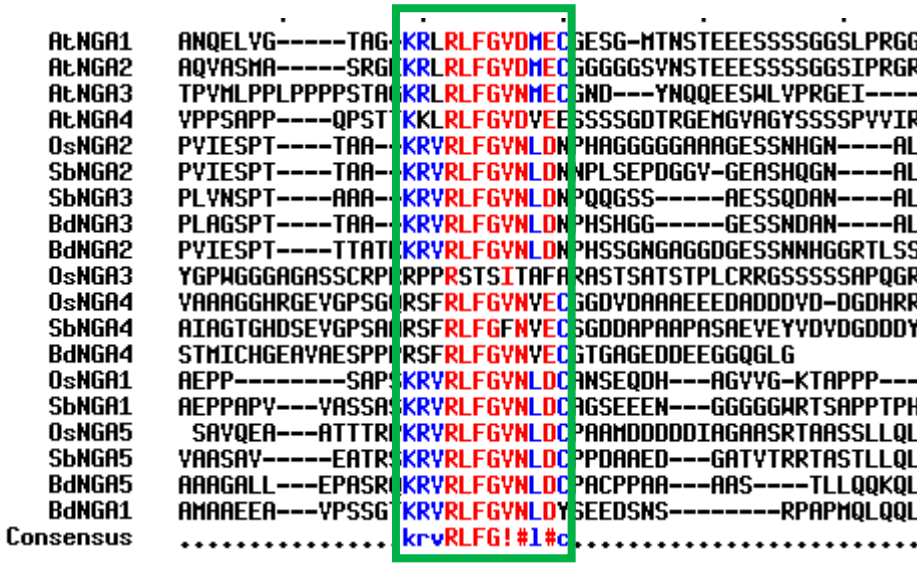


3c



3d

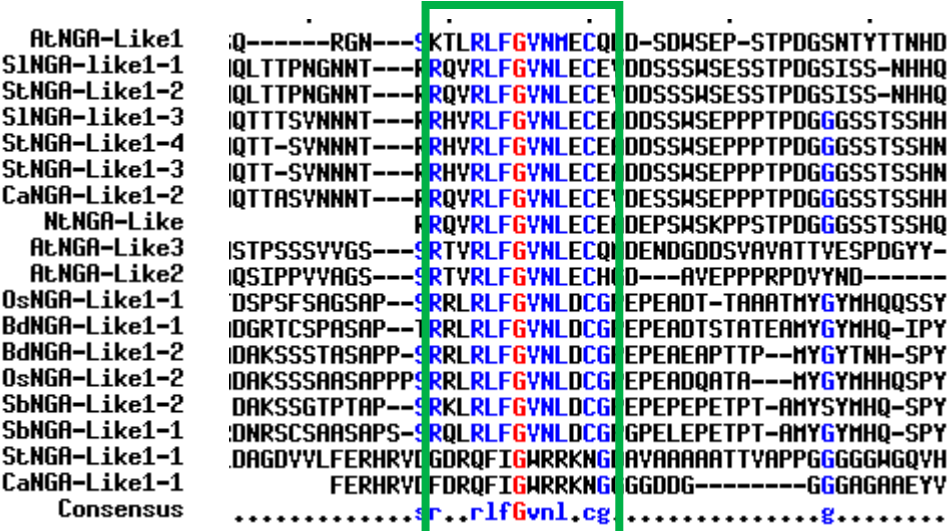


Figure S3. Multialignment of NGATHA proteins of (a) Arabidopsis; (b) Arabidopsis and tomato; (c) NGATHA proteins of Arabidopsis, rice, sorghum and Brachypodium; (d) NGATHA-Like proteins of Arabidopsis, rice, sorghum and Brachypodium, tomato, potato, capsicum and nicotiana. The B3 domain is represented in black boxes. The repressor motif RLFGV is marked in green boxes. The repressor motif RLFGV is marked in green boxes. NGA-I and NGA-II motifs are indicated in pink and yellow boxes respectively.



Figure S4. Protein motifs in the NGATHA proteins of (a) dicots, and (b) monocots

TMHMM result

```
# WEBSEQUENCE Length: 4478
# WEBSEQUENCE Number of predicted TMHs: 0
# WEBSEQUENCE Exp number of AAs in TMHs: 27.9725499999998
# WEBSEQUENCE Exp number, first 60 AAs: 0.06739
# WEBSEQUENCE Total prob of N-in: 0.01256
WEBSEQUENCE    TMHMM2.0      outside      1 4478
```

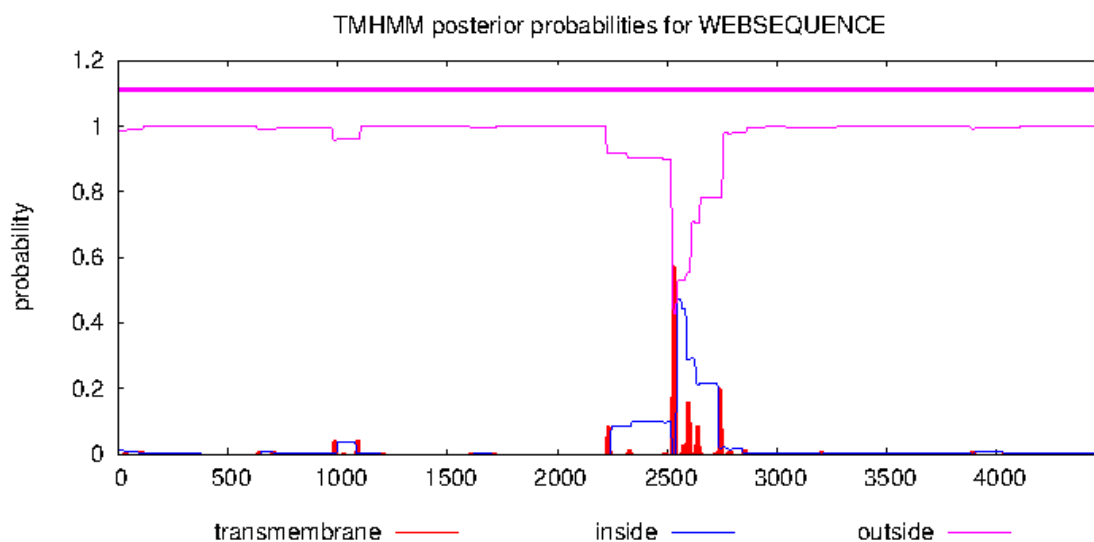


Figure S5. Analysis of transmembrane domain in the NGATHA proteins. The TMHMM analysis predicts that there are no domains embedded within the membrane.

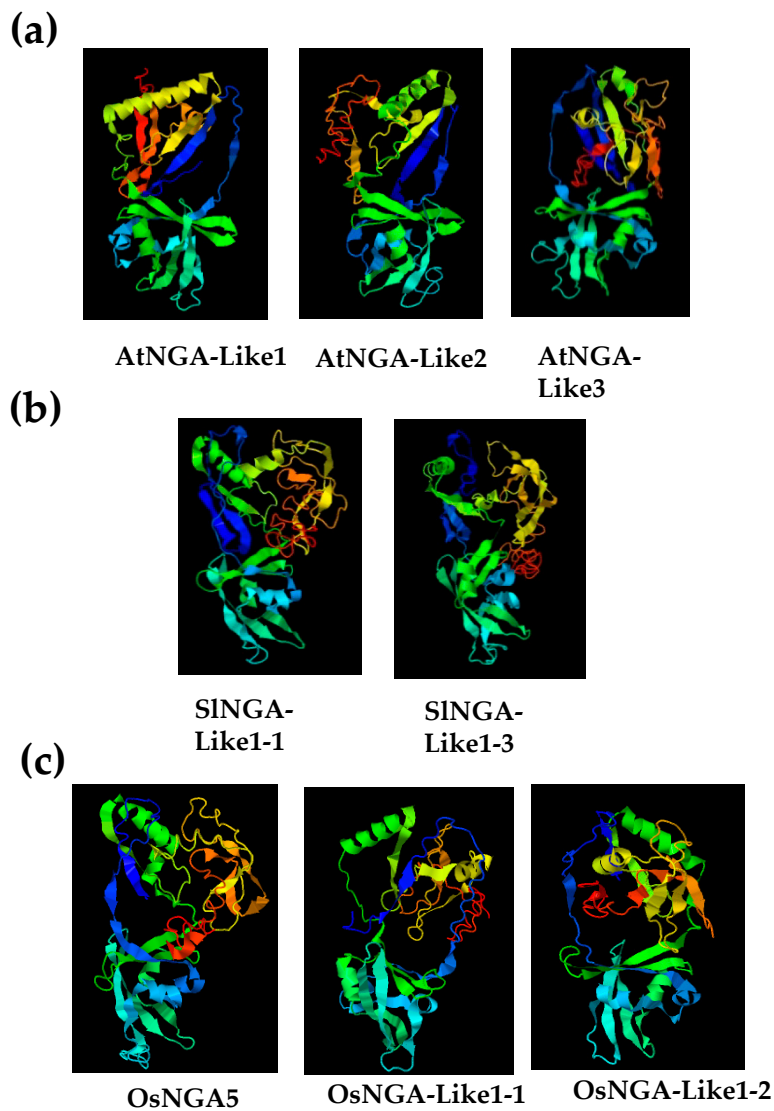


Figure S6. 3D-structure of NGATHA-Like proteins in (a) *A. thaliana*, (b) *S. lycopersicum* and (c) *O. sativa* L. Japonica. The three dimensional structures are acquired using I-TASSER (<https://zhanggroup.org/I-TASSER/>).

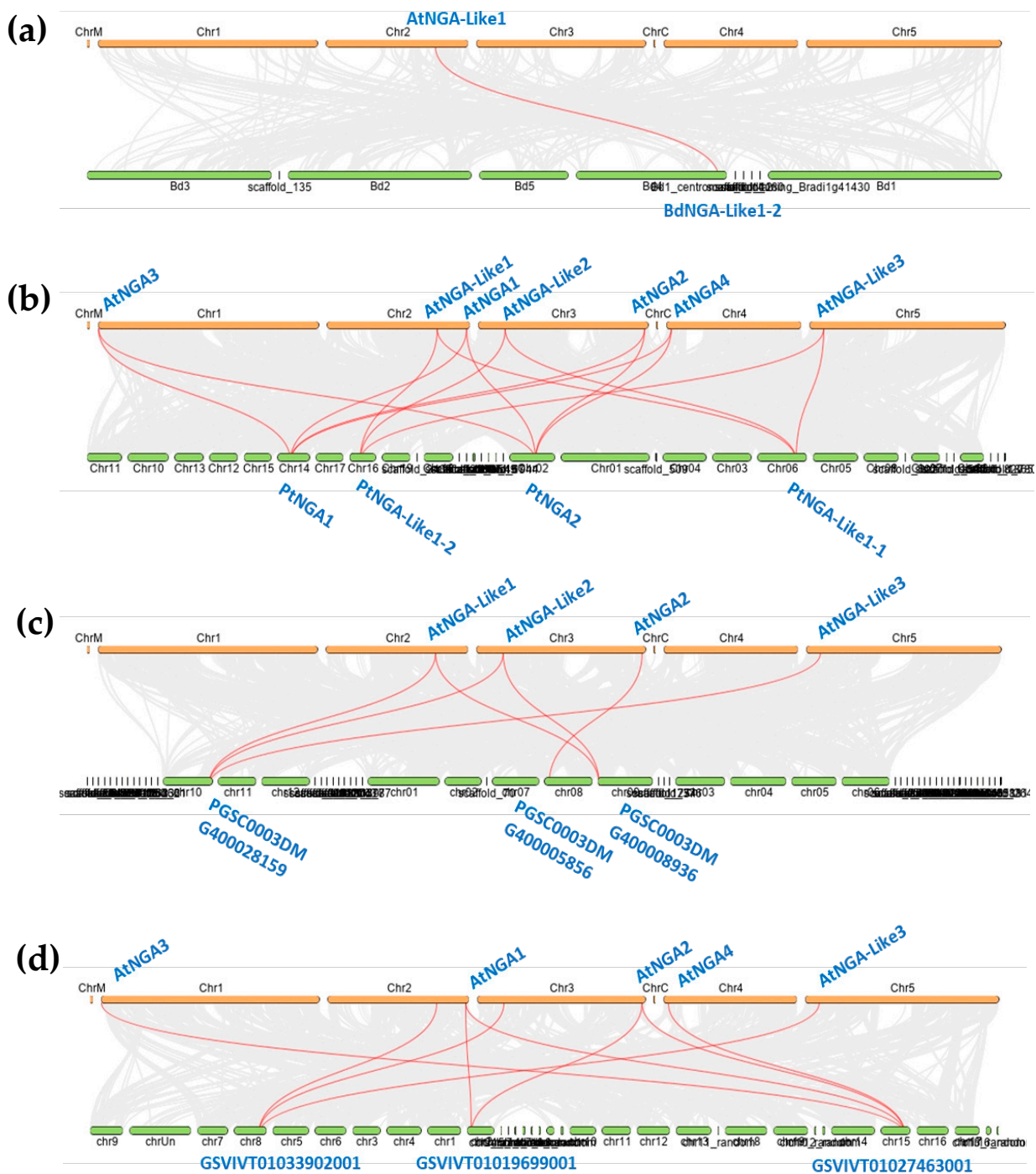


Figure S7. Gene duplication or synteny analysis of NGATHA genes in (a) *Brachypodium distachyon*; (b) *Populus trichocarpa*; (c) *S. tuberosum* and (d) *Vitis vinifera* in comparison with *A. thaliana*. The grey lines in the background represent collinear blocks between the respective genomes. The red lines indicate the syntenic gene pairs of *S. lycopersicum*, *B. rapa* and *O. sativa* L. Japonica with *A. thaliana*.