

Table 1 Suppl. Details of *trihelix* gene properties and their predicted subcellular localization

Protein sequence	Protein length [aa]	Mr [Da]	pI	Localization	Group	Position of chromosome
OTG22032	510	59829.6	6.59	nucleus	GT2	chr6:7235237...7238993
OTG22742	373	42144	6.28	nucleus	SH4	chr6:32194921...32197512
OTG16790	366	42155.8	4.56	nucleus	SIP	chr9:204449032...204451805
OTF90560	341	39235.4	4.41	nucleus	SIP	chr16:11593876...11595578
OTF91880	422	48340.9	6.33	nucleus	GT2	chr16:106030713...106034025
OTF93113	277	31206.5	5.02	nucleus	SH4	chr16:171802231...171803064
OTG06033	296	33826.5	9.04	nucleus	SH4	chr12:127716683...127722143
OTG06393	304	34177	5.03	nucleus	SH4	chr12:161540828...161542263
OTG06206	533	60571.2	7.35	nucleus	GT2	chr12:149666760...149670132
OTF98282	249	28518	7.97	nucleus	SIP	chr14:116606913...116608281
OTG30479	848	94437.5	8.56	chloroplast	Gδ	chr3:28044260...28055400
OTG31950	248	27742.9	4.54	nucleus	SH4	chr3:130175071...130177571
OTG32052	315	36669.8	8.66	nucleus	GT1	chr3:133853738...133856030
OTG09292	424	48173.2	7.83	nucleus	GT2	chr11:159829348...159831876
OTG09256	411	46358.5	6.02	nucleus	GT-γ	chr11:158566940...158568685
OTG07556	273	32447.4	5.78	nucleus	GT1	chr11:51680753...51684034
OTG01800	371	42716.4	5.57	nucleus	GT-γ	chr13:108199261...108200417
OTG26142	339	38796.8	4.98	nucleus	SH4	chr5:189244605...189255048
OTG26730	650	72506.7	7.5	nucleus	GT2	chr5:213209562...213212533
OTG38319	517	56287.7	7.52	nucleus	SIP	chr1:145906871...145914896
OTG38320	214	23942.7	8.48	cytoplasm	SIP	chr1:145919233...145920047
OTG38290	517	58557.1	8.53	chloroplast	GT-γ	chr1:145424097...145425737
OTF84884	345	39110	9.44	nucleus	SIP	chr17:2146913...2147950
OTF85373	254	28669.7	5.6	nucleus	SH4	chr17:20231123...20233720
OTF95801	393	44783.6	8.24	nucleus	SH4	chr15:99322589...99326807
OTF96213	396	45624.8	6.24	nucleus	GT2	chr15:128454271...128456184
OTG33983	593	65408.5	6.04	nucleus	GT2	chr2:60331789...60334707
OTG09673	632	70214.9	6.29	nucleus	GT2	chr10:6880940...6883711
OTG11003	239	28973.8	8.65	nucleus	GT1	chr10:102583846...102585202
OTG28164	596	66770.2	6.1	nucleus	SIP	chr4:76573934...76575744
OTG18952	251	30118.2	7.44	nucleus	GT1	chr8:95804336...95805233

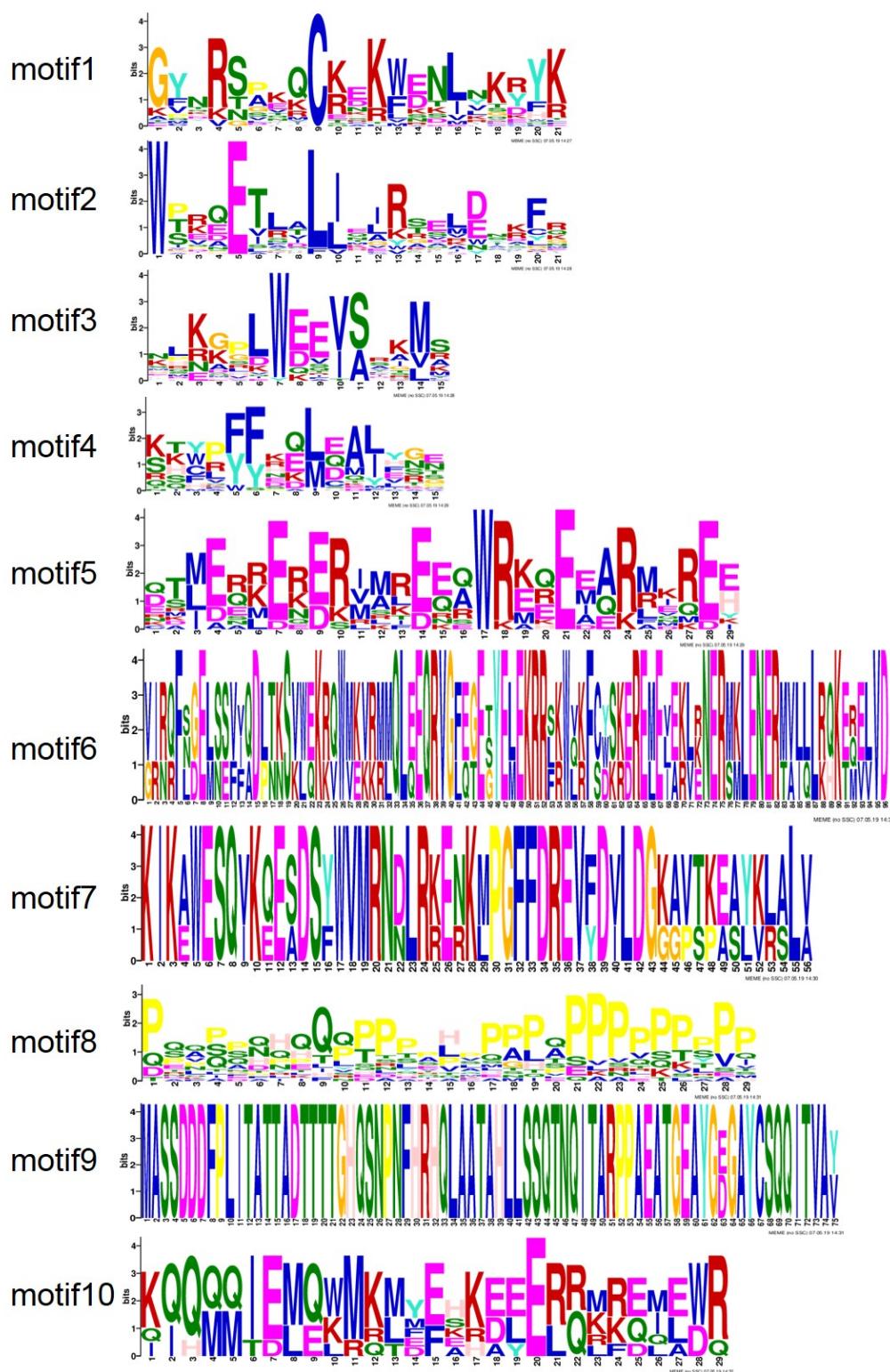


Fig. 1 Suppl. Logos of the *trihelix* protein conserved motifs of *Helianthus annuus*. A total of 10 motifs were identified by the *MEME* (multiple EM for motif elicitation) tool.

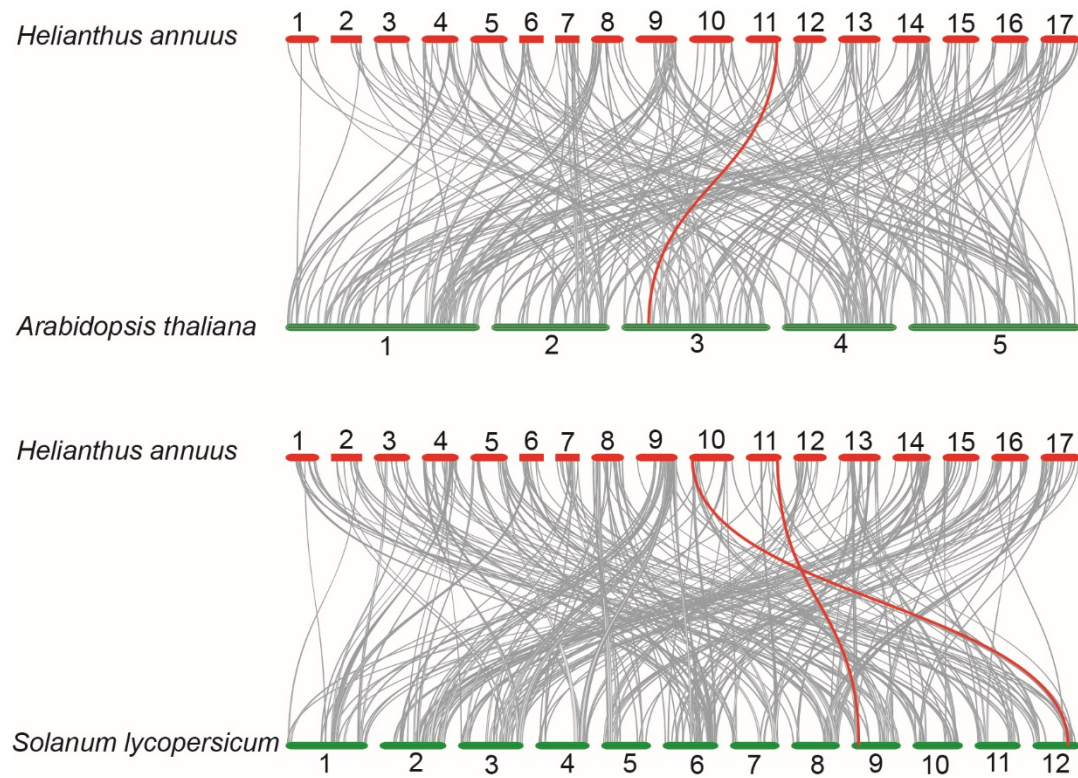


Fig. 2 Suppl. Synteny analysis of *trihelix* genes between *Helianthus annuus* and dicotyledonous plant *Arabidopsis thaliana* and dicotyledonous plant *Solanum lycopersicum*. Gray lines in the background indicate the collinear blocks within *H. annuus* and other plant genomes, while the red lines highlight the syntenic *trihelix* gene pairs. Red or green bars represent the chromosomes. The chromosome number is labeled at the top or bottom of each chromosome.