Additional File 9: Parameters data from Structural Modeling in I-TASSER. Scoring function (C-score) is based on the relative clustering structural density and the consensus significance score of multiple threading templates to estimate the accuracy of the I-TASSER predictions. Numbers can vary from -5 to 2 and higher numbers are more significant. TM-score is a measure of the absolute distance between atoms of the final model in comparison with the native structure. Ideal TM-Score is higher than 0,5.

Gene	C--score	TM--score
MA_20337g0010	-1.20	0.56±0.15
Potri_018G030500_5	-0.51	0.65±0.13
Bra022578	-1.08	0.58±0.14
Os05g04180	-0.46	0.65±0.13
cassava4_1_003152	-1.71	0.51±0.15
AT3G62300.1	-1.18	0.57±0.15
AT5G13020	0.02	0.72±0.11
AT3G62300.2	-0.82	0.61±0.14