Supplemental Table 1. Phenotype rescue of *hyl1* mutants by deletion mutants of *HYL1* within T1 populations[*]

Deletion mutants	Plants observed	Plants rescued	Percentage of rescue	Percentage of non-rescue
HYL1	112	81	72	28
HYL1D1	89	0	0	100
HYL1D12	146	124	85	15
HYL1D12N	121	110	91	9
HYL1D2N	22	0	0	100
HYL1D2NP	13	0	0	100
HYL1D12P	65	55	84	16
HYL1D2NP	21	0	0	100
HYL1D12P	17	12	72	28
H-HYL1	34	26	81	19
H-HYL1D1	18	0	0	100
H-HYL1D12	33	26	79	21
H-HYL1D12N	12	9	75	25

[*] *HYL1D1* (corresponding to HYL1 lacking its dsRBD2, NLS and PPI domain), *HYL1D12* (HYL1 lacking its NLS and PPI), *HYL1D12N* (HYL1 lacking its PPI), *HYL1D2N* (HYL1 lacking its N-terminal dsRBD1 and PPI), *HYL1D2NP* (HYL1 lacking its N-terminal dsRBD1) and *HYL1D12P* (HYL1 lacking its NLS) under the control of the 35S promoter.

H-HYL1 (corresponding to HYL1), *H-HYL1D1* (corresponding to HYL1 lacking its dsRBD2, NLS and PPI), *H-HYL1D12* (HYL1 lacking its NLS and PPI), and *H-HYL1D12N* (HYL1 lacking its PPI) under the control of the native promoter of *HYL1*.