

Haplotypes	Wild Type Ajigasawa20_1	ms1 Ooi-7_1 (30bp deletion )
Peptide sequence	MAAIVRALIIFVLMVAESVMTQQTDAADCTDPIVSLSPCLSYMTRSAKLSIPDDDC CDSLATVINTHAGCLCELVSRDDFLGFPINQTITLSLPSTCDIQYPRELDQCIVVLPSS DGPVVQPGSNPPRRLFHPEAPSPALEAVPPVLEAPPMEVDPDQDDSPFPNVSIA <b>G</b> ALFTQSLRLRFWGSLLTAILTVGYLH	MAAIVRALIIFVLMVAESVMTQQTDAADCTDPIVSLSPCLSYMTRSAKLSIPDDDC CDSLATVINTHAGCLCELVSRDDFLGFPINQTITLSLPSTCDIQYPRELDQCIVVLPSS DGPVVQPGSNPPRRLFHPEAPSPALEAVPPVLEAPPMEVDPDQDDSPFPNVSIA <b>G</b> ALFTQSLRLRFWGSLL
Prediction of potential C-terminal GPI-modification site	Potential GPI-modification site was found. Quality of the site ..... : S Sequence position of the omega-site : <b>176</b> Score of the best site ..... : -3.28 (PValue = 2.791270e-03)	<b>None</b> potential GPI-modification site was found. Among all positions checked, sequence position 160 had the best score.

Figure S1 Results of a 30-bp deletion on the loss of potential GPI-modification sites. Peptide sequences of Ajigasawa20\_1 and Ooi-7\_1 were tested for prediction of potential GPI-modification site using big-PI Plant Predictor (Eisenhaber *et al.* 2003).

#### Reference

Eisenhaber, B. *et al.* Glycosylphosphatidylinositol lipid anchoring of plant proteins. Sensitive prediction from sequence- and genome-wide studies for Arabidopsis and rice. *Plant Physiol.* **133**, 1691–1701 (2003).