Supplemental Figure 1. Phylogenetic relationships of InvB-related proteins by a bootstrap neighbor-joining tree analysis

The amino acid sequences of the genes listed in Supplemental Table 1 were aligned with yeast VRG4 and *Arabidopsis* GONST1 on the MUSCLE Web server (http://www.ebi.ac.uk/Tools/muscle/index.html; Edgar, 2004) and then subjected to a bootstrap neighbor-joining tree analysis by ClustalX ver. 1.83 (exclude positions with gaps = ON, correct for multiple substitutions = ON, n=10000; Thompson et al., 1997). The resulting phylogenetic tree was drawn with the unrooted version of njplot software for Macintosh (http://pbil.univ-lyon1.fr/software/njplot.html) and was then arranged by Adobe Illustrator CS3. The scale indicates the number of amino acid replacements per residue. The numbers at branch points are bootstrap percentage for 10000 repli-cates and thicker line segments are used to connect branchpoints supported by >70% bootstrap. *C. reinhardtii* GST1b is not included in the analysis because it is almost identical to GMT1a.

References

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