



## Supplemental Figure 2

**Supplemental Figure 2.** Phylogenetic analysis of pollen and Arabidopsis PI PLCs.

An unrooted maximum parsimony tree with bootstrap values (1000 replicates) for each node is shown. Amino acid sequences were aligned using ClustalW (Higgins et al., 1992). Phylip programs (Seqboot, Protpars and Consense; Felsenstein, 1989) were employed to create the tree and to calculate bootstrap values.

**Felsenstein, J.** (1989). PHYLIP - Phylogeny Inference Package (Version 3.2). *Caldistics* **5**, 164-166.

**Higgins, D.G., Bleasby, A.J., and Fuchs, R.** (1992). CLUSTAL V: improved software for multiple sequence alignment. *Comput. Appl. Biosci.* **8**, 189-191.