

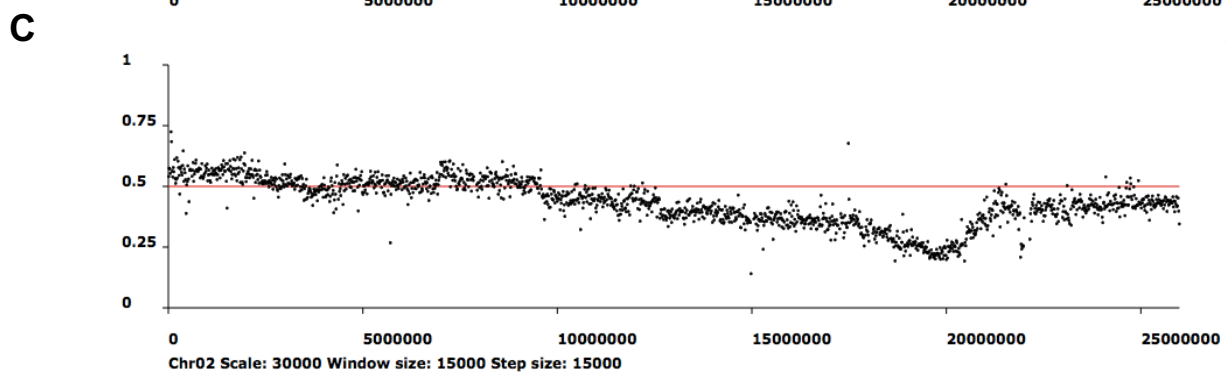
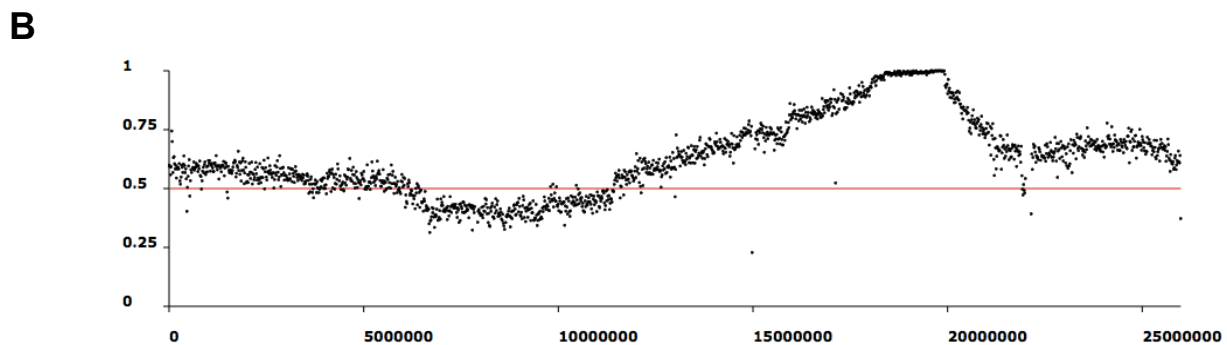
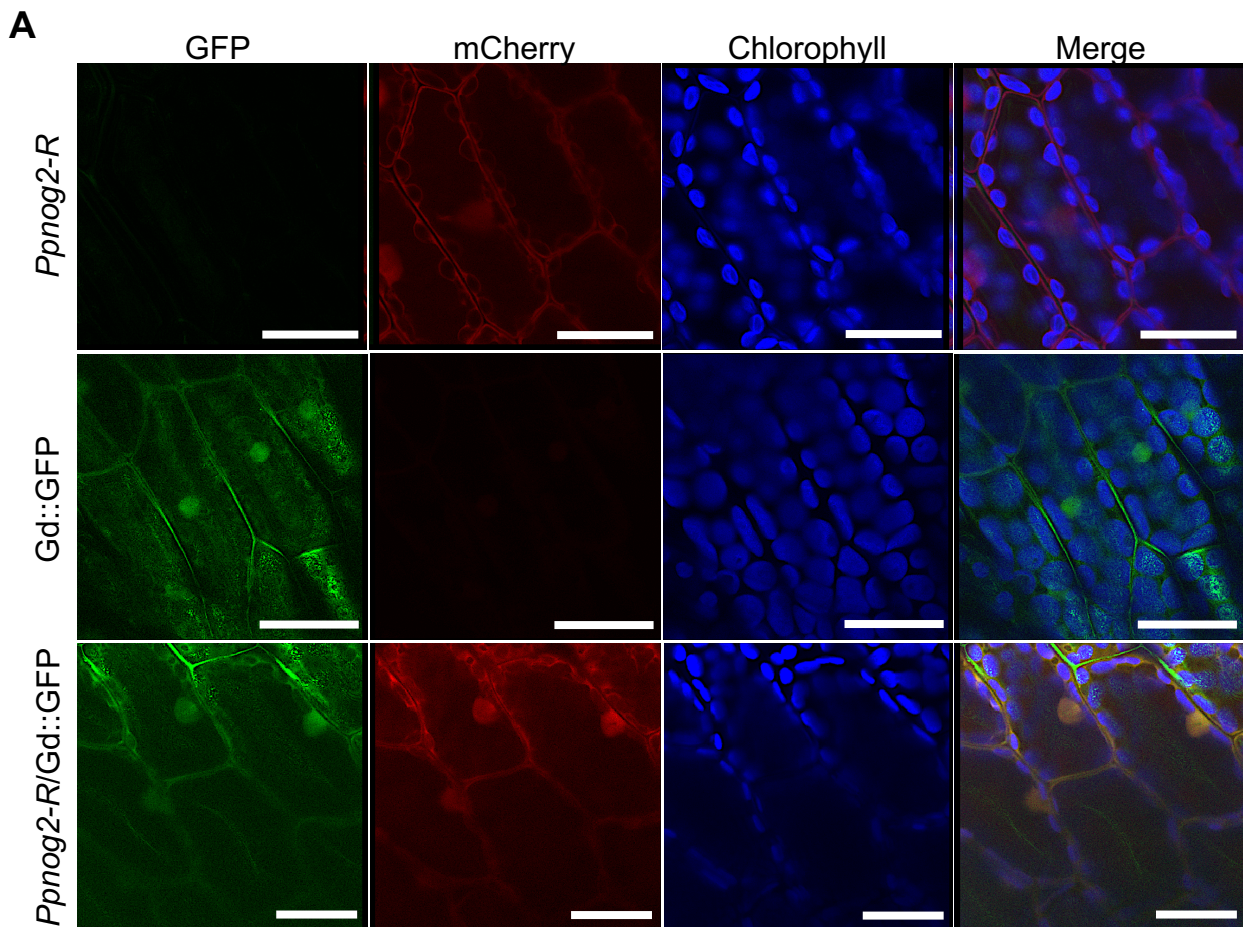


Figure S1. Bulk segregant analysis via somatic hybridization (related to Figure 3). (A) *Ppnog2-R* and Gd::GFP haploid lines and a *Ppnog2-R/Gd::GFP* diploid line. Images show green fluorescent protein (GFP, green), mCherry (red), chlorophyll autofluorescence (blue) and a merge of all four. Scale = 25 μ m. (B, C) Allele frequency plots for *Ppnog2-R* (B) and WT (C) segregants on chromosome 2 of *P. patens*.

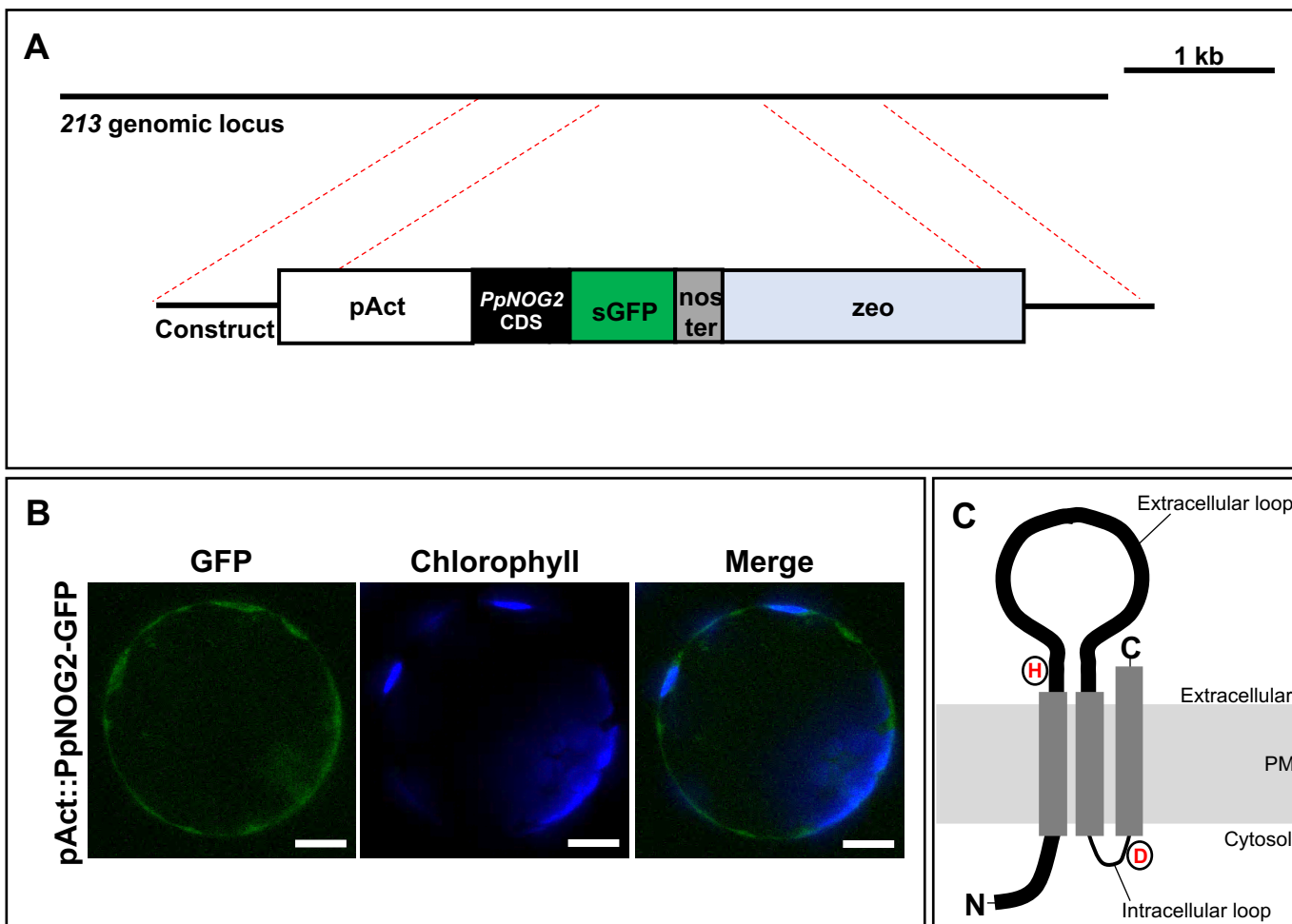


Figure S2. The PpNOG2 protein localizes at or near to the plasma membrane (related to Figure 4). A) Schematic diagram of the pAct::PpNOG2-GFP construct that was used to complement Ppnog2-R mutants. The construct was targeted to the 213 locus as shown. B) Transient expression of pAct::PpNOG2-GFP in *P. patens* protoplasts. Images show green fluorescent protein (GFP, green), chlorophyll autofluorescence and a merge of both. Scale = 10 μ m. B) Schematic of the PpNOG2 protein topology as predicted by TMpred (see **Data S1** for further details). Three transmembrane (TM) domains are predicted to exist, in addition to an extracellular loop region. The putative location of conserved aspartic acid (D) and histidine (H) have been indicated.

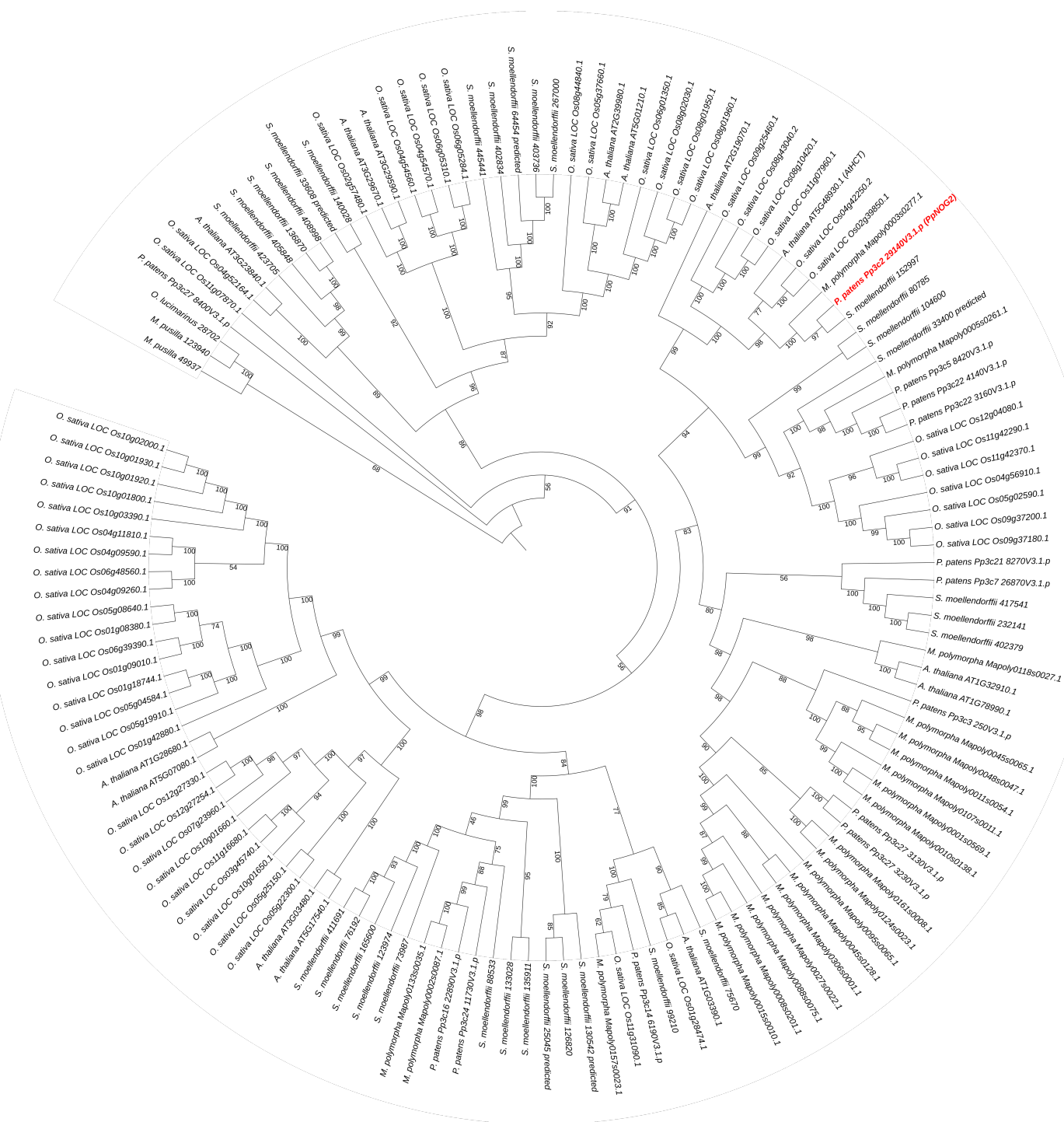


Figure S3. Maximum-likelihood phylogenetic analysis of PpNOG2-related proteins (related to Figure 4). The tree was rooted using chlorophyte sequences, and numbers correspond to bootstrap values. PpNOG2 (Pp3c2_29140) has been highlighted in red.

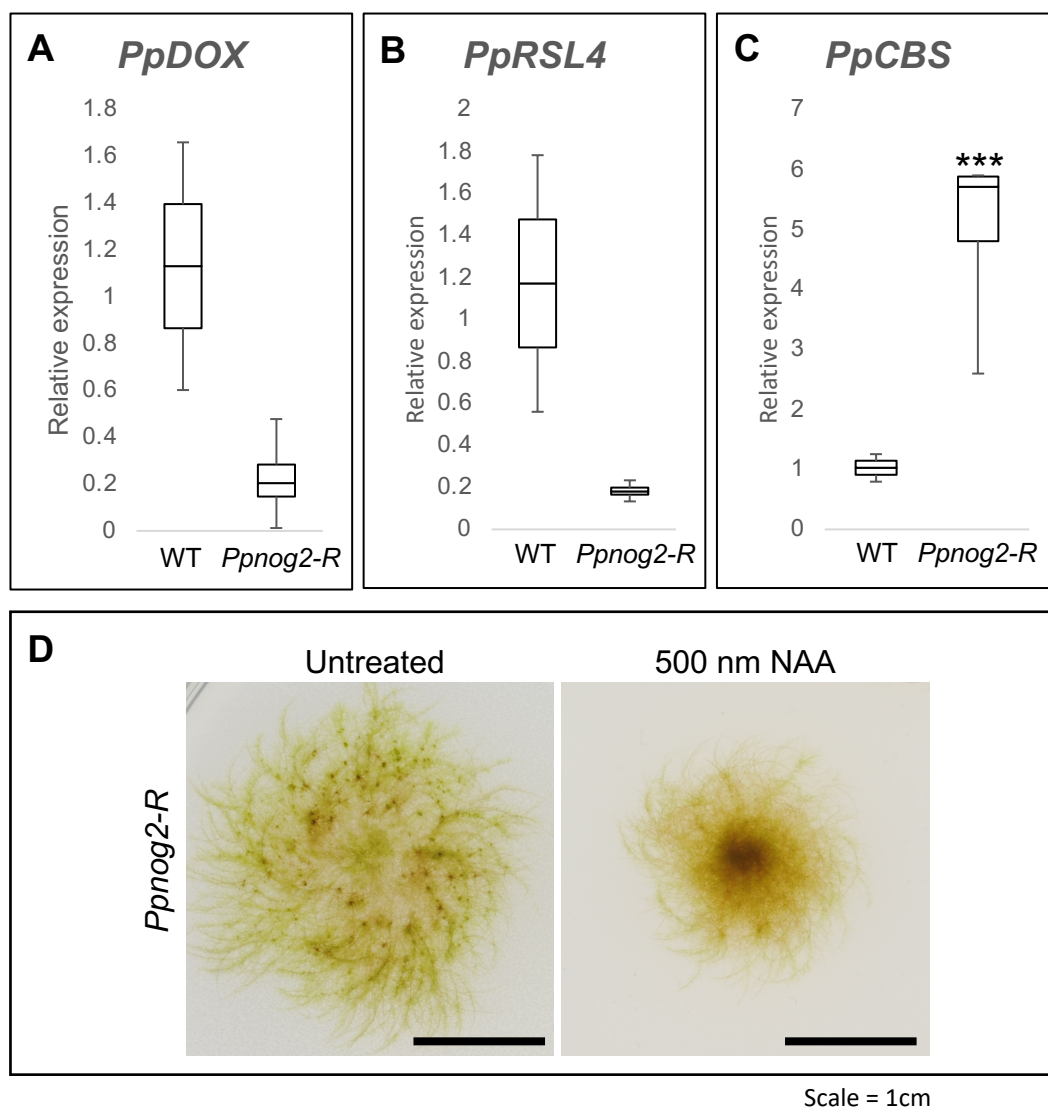


Figure S4. *PpNOG2* regulates auxin responses (related to Figure 4). (A-C) Relative transcript levels in 14 d old protonemata: *PpDOX* in WT and *Ppnog2-R* (A), *PpRSL4* in WT and *Ppnog2-R* (B), *PpCBS* in WT and *Ppnog2-R* (C) (t test $p < 0.05$ ***). (D) Representative images of 1 month old *Ppnog2-R* grown in the presence and absence of 500 nm NAA. Images show the suppression of budding when treated with NAA. Scale bar, 1cm.

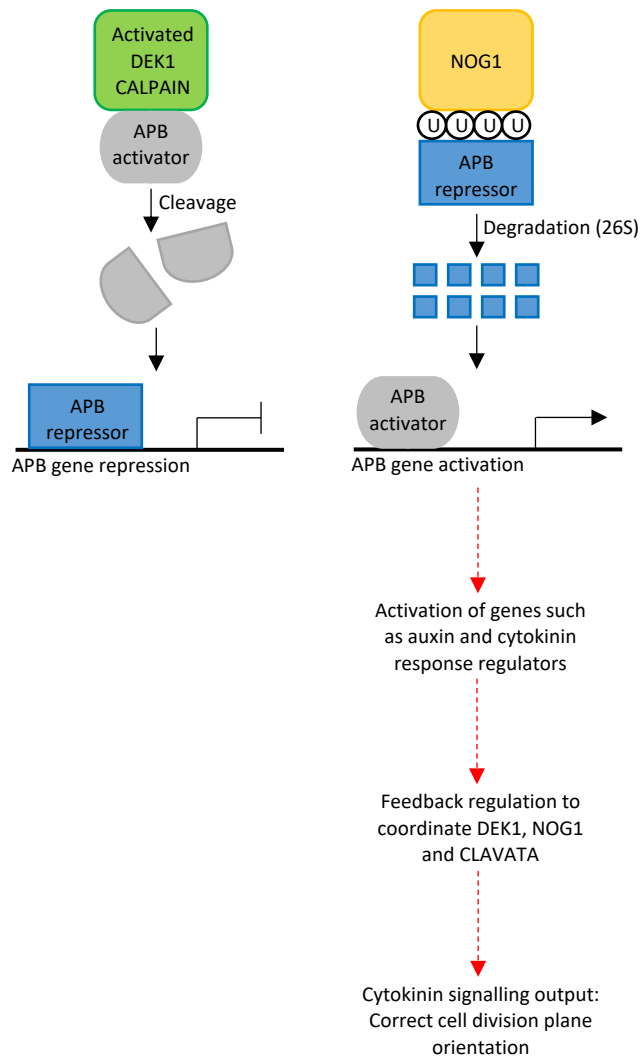


Figure S5. Previous model for 3D growth regulation in *P. patens* (related to Figure 5). Previously proposed model for 3D growth regulation suggests that PpNOG1 and PpDEK1 operate antagonistically to regulate the transcription of PpAPB genes, and then cooperate with CLAVATA to deliver correct cytokinin signalling outputs; prevent ectopic initiation of buds and ensure division planes are correctly oriented.

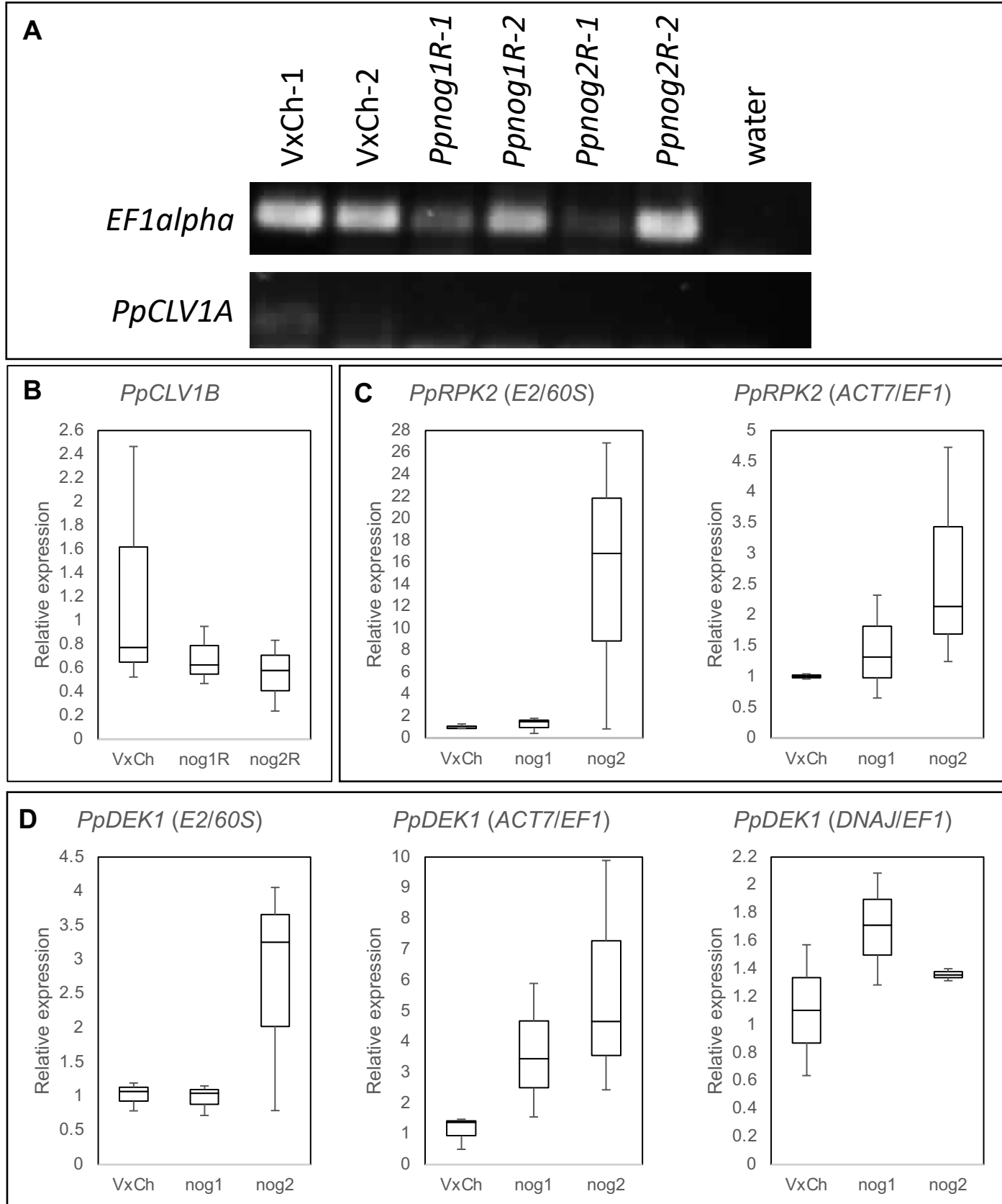


Figure S6. PpNOG1 and PpNOG2 do not act upstream of *CLAVATA* receptor genes and *DEK1* (related to Figure 6). (A) Expression of *PpCLV1A* by RT-PCR in 14 d old protonemata of WT, *Ppnog1-R* and *Ppnog2-R* compared to a control gene (*EF1alpha*). (B-D) Relative transcript levels in 14 d old protonemata: *PpCLV1B* in WT, *Ppnog1-R* and *Ppnog2-R* (B), *PpRPK2* in WT, *Ppnog1-R* and *Ppnog2-R* (C), *PpDEK1* in WT, *Ppnog1-R* and *Ppnog2-R* (D).

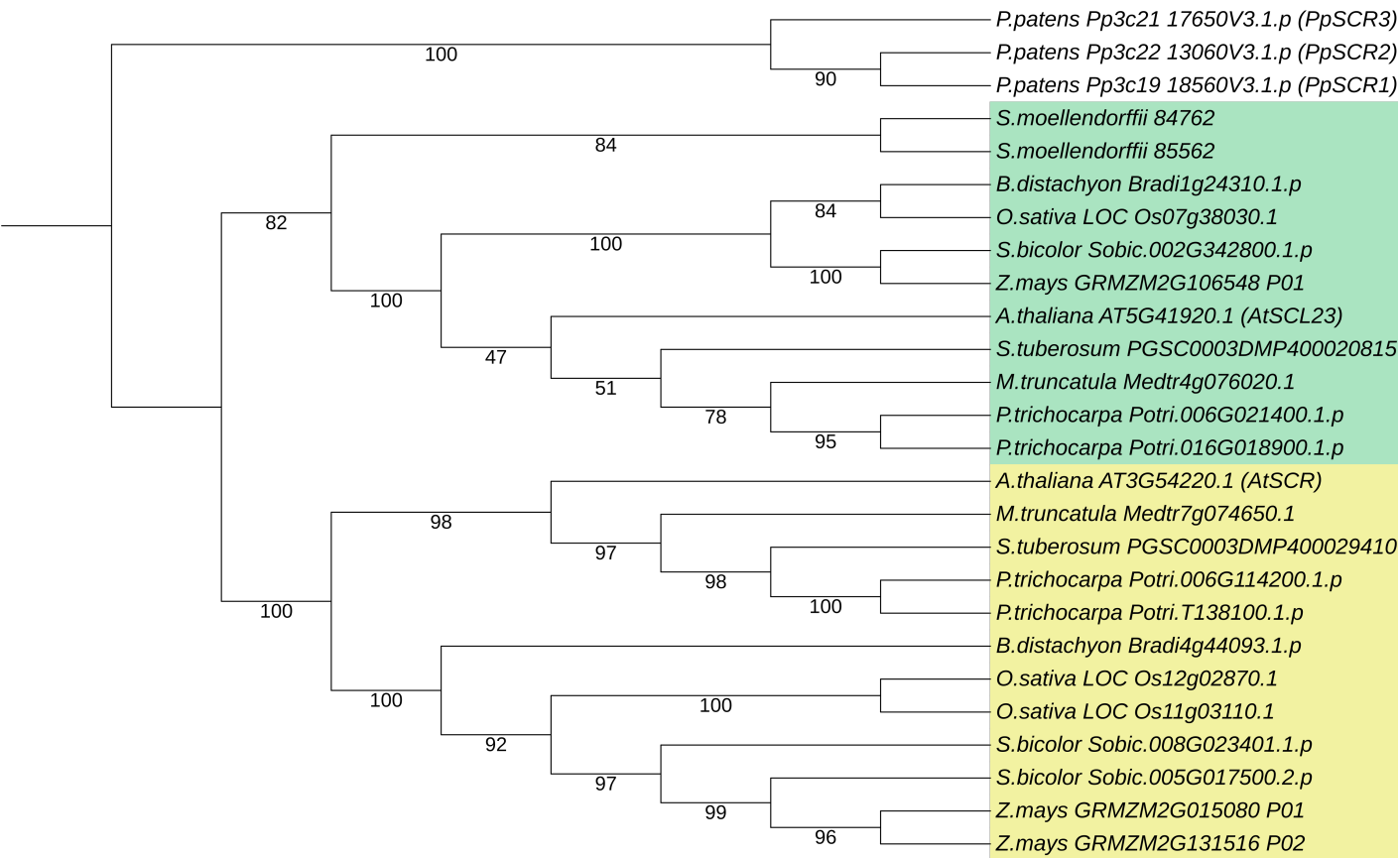


Figure S7. Maximum-likelihood phylogenetic analysis of SCR-related proteins (related to Figure 6). The tree was rooted to *P. patens* sequences, which form an outgroup. Bootstrap values are shown on branches. Green shading indicates the AtSCL23 clade and yellow shading indicates the AtSCR clade.