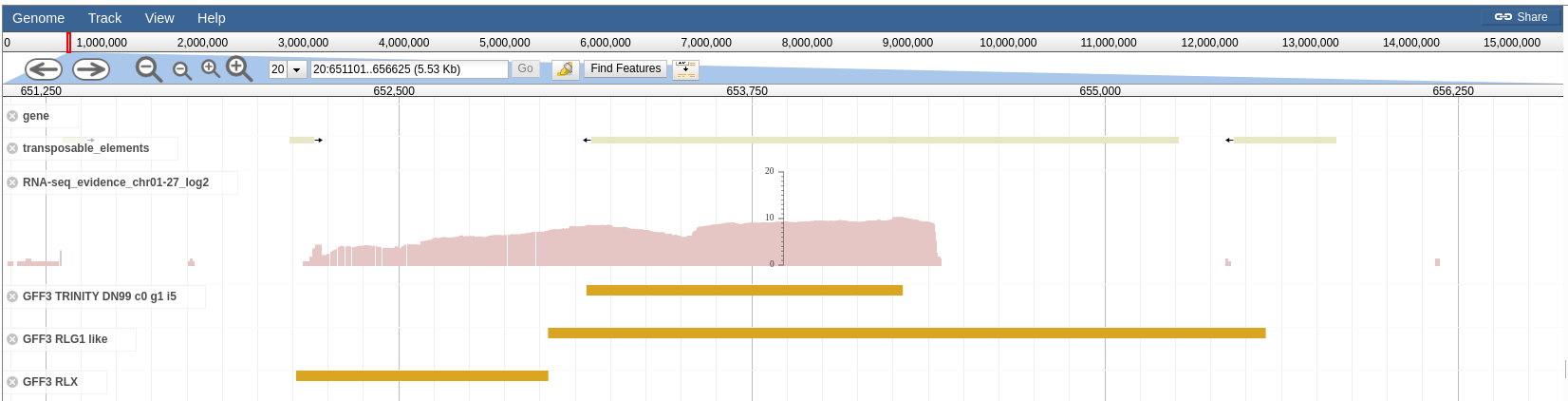
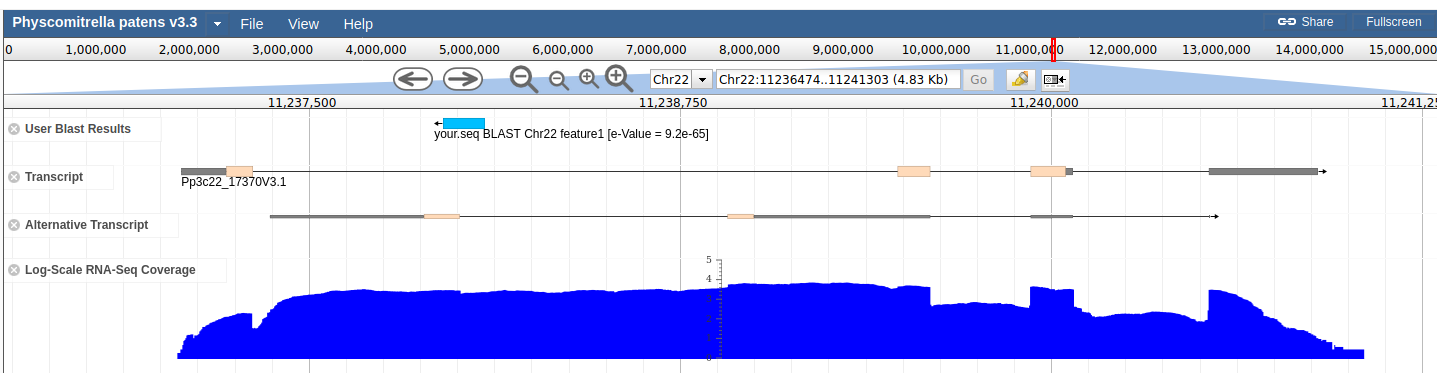


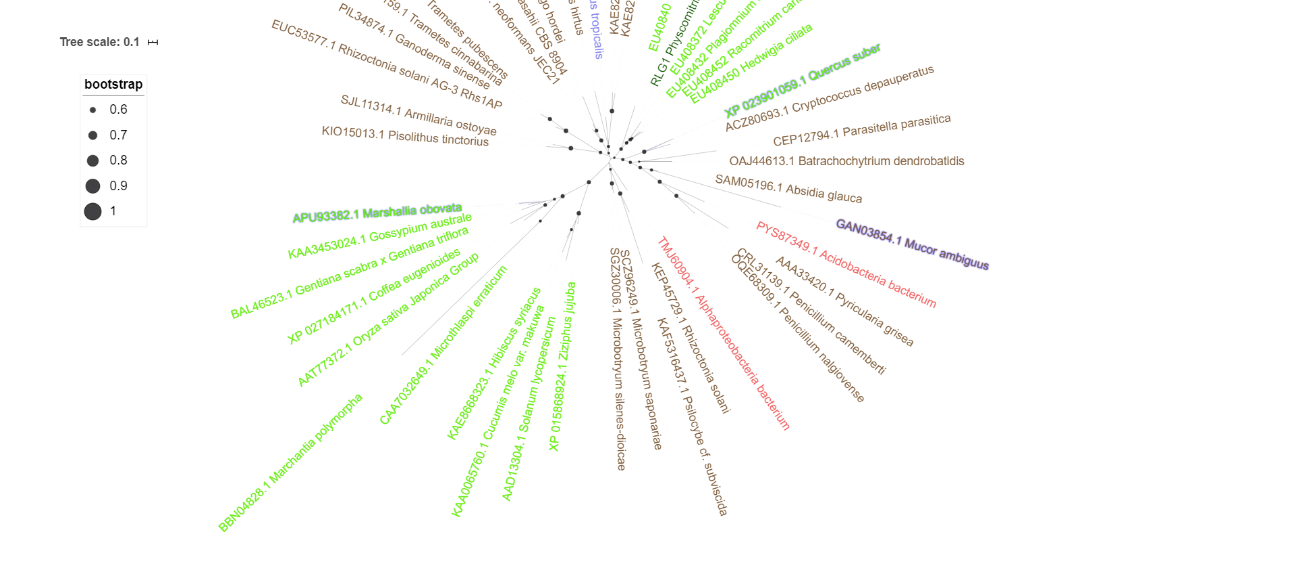
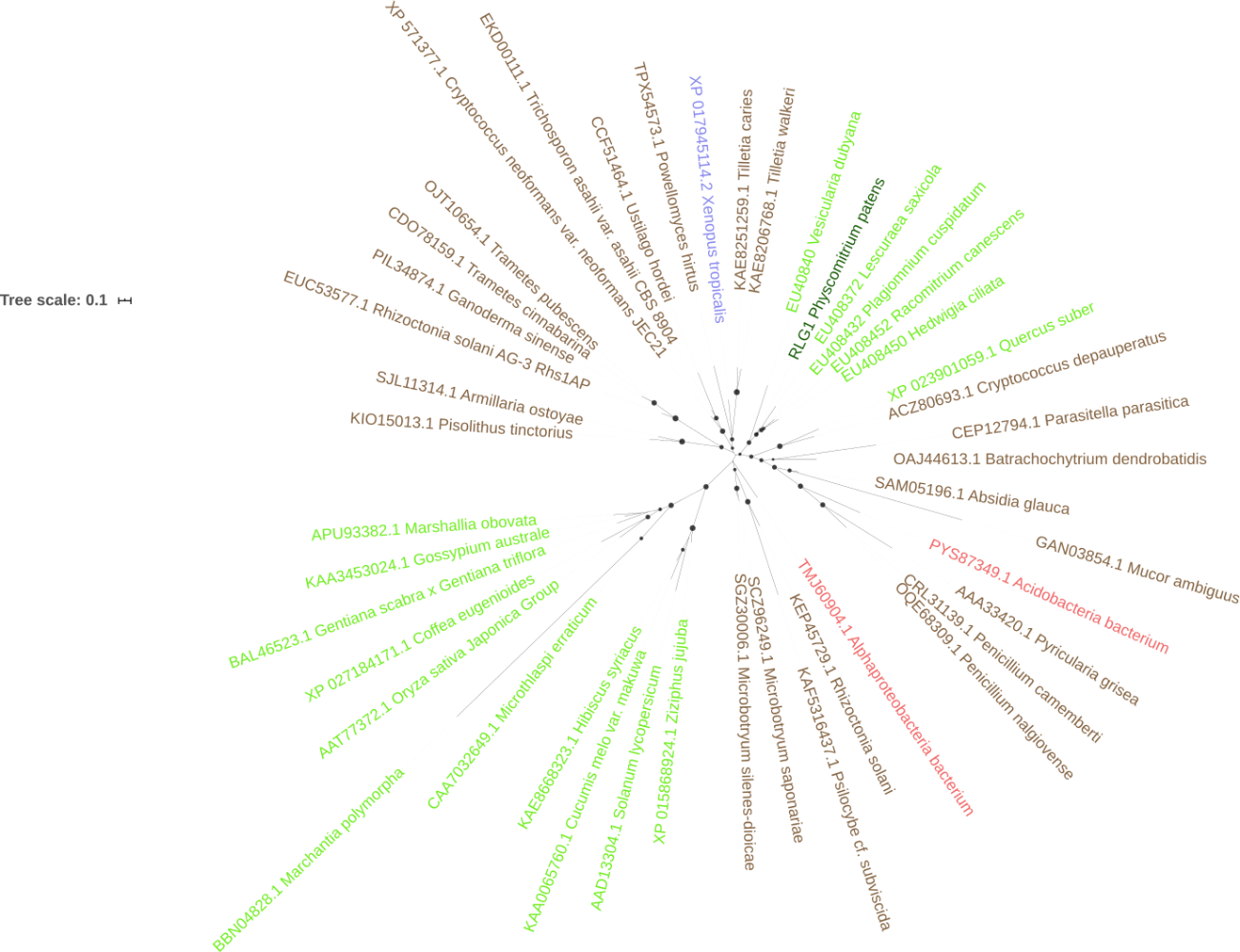
**Supplementary Figure 1: Expression of a RLC5 solo-LTR as the result of a read-through transcription from the gene Pp3c4\_32070.** Screenshot of the Phytozome genome browser showing from top to bottom, the Pp3c4\_32070 transcript, alternative transcripts, PASA Assembled EST, BLASTn best-hit of the TRINITY\_DN331\_c0\_g1\_i1, corresponding to a RLC5 solo-LTR, and the log-scale RNA-Seq coverage of the genome region.



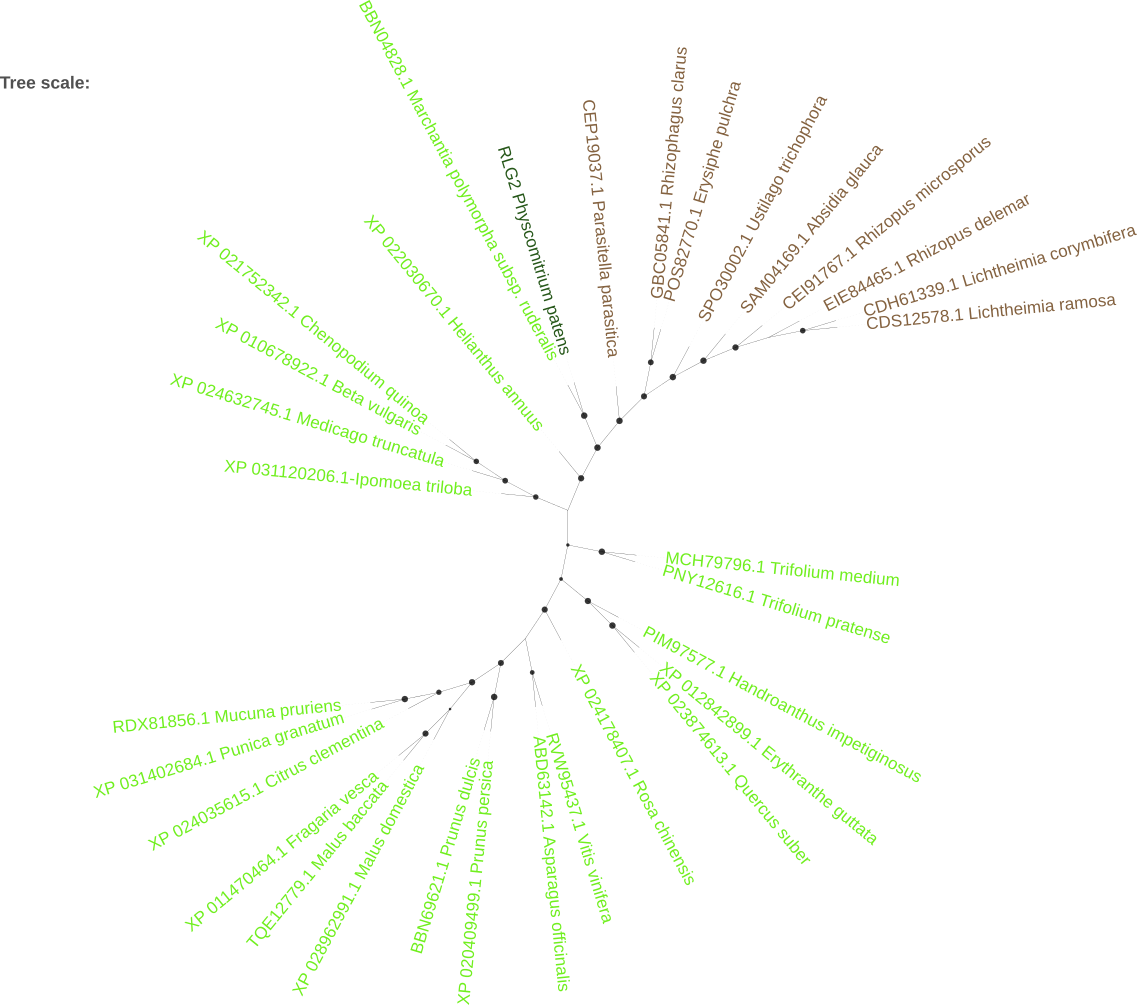
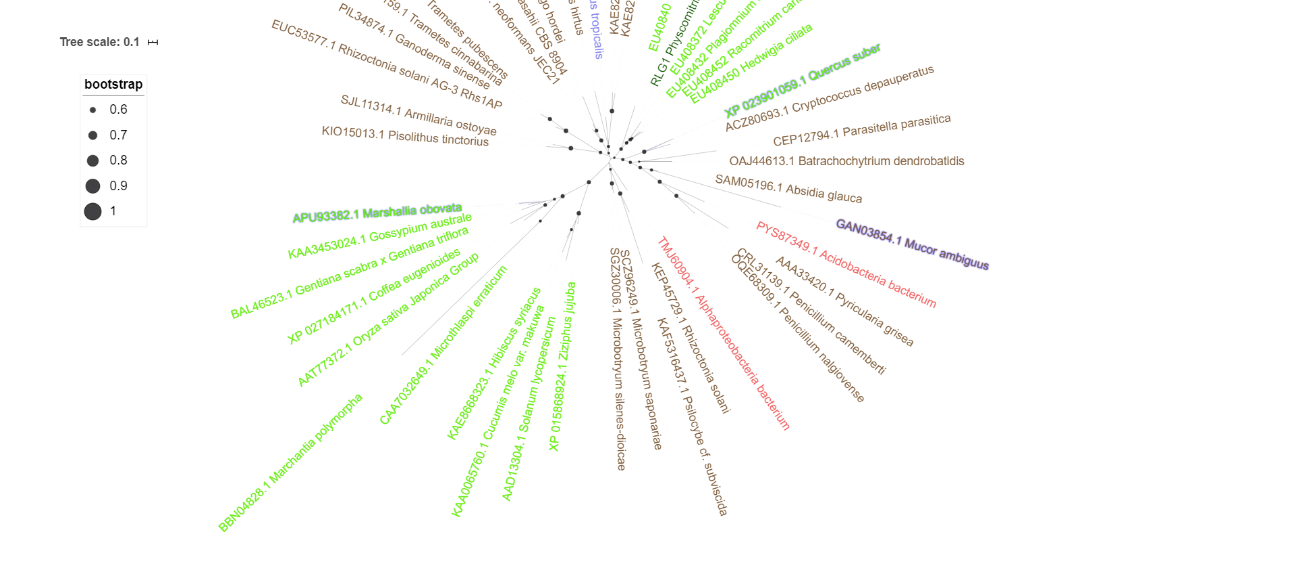
**Supplementary Figure 2: Expression of a chimeric TE sequence.** Screenshot of the COGE https://genomevolution.org/coge/) genome browser showing from top to bottom, the annotated genes in the genomic region, the TE annotation corresponding to a RLGU (unclassified Gypsy) element, the log-scale RNA-Seq coverage of the genome region, the best hit of the assembly TRINITY\_DN99\_c0\_g1\_i5, the manually curated truncated RLG1 element, and a manually curated repetitive sequence corresponding to a copy of an RLX (LTR-retrotransposon unclassified).



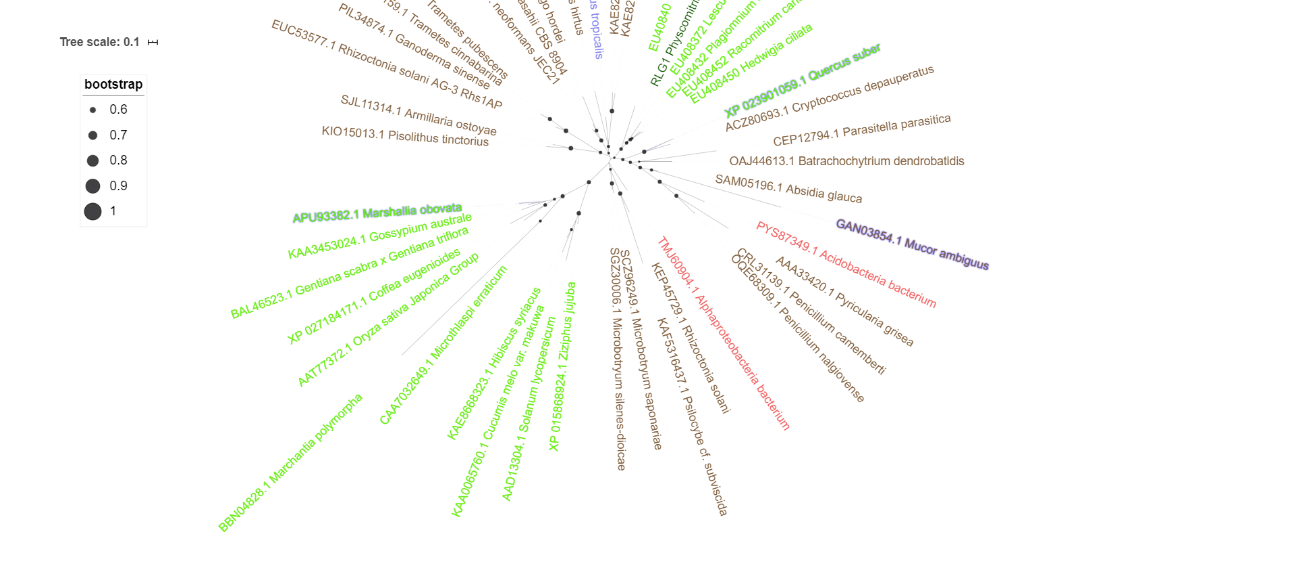
**Supplementary Figure 3: Antisense expression of a LINE inserted within an intron as a result of gene expression.** Screenshot of the Phytozome genome browser showing from top to bottom, the best hit of the assembly TRINITY\_DN734\_c0\_g1\_i1, the Pp3c22\_17370 gene annotation, the alternative transcripts, and the log-scale RNA-Seq coverage of the genome region.



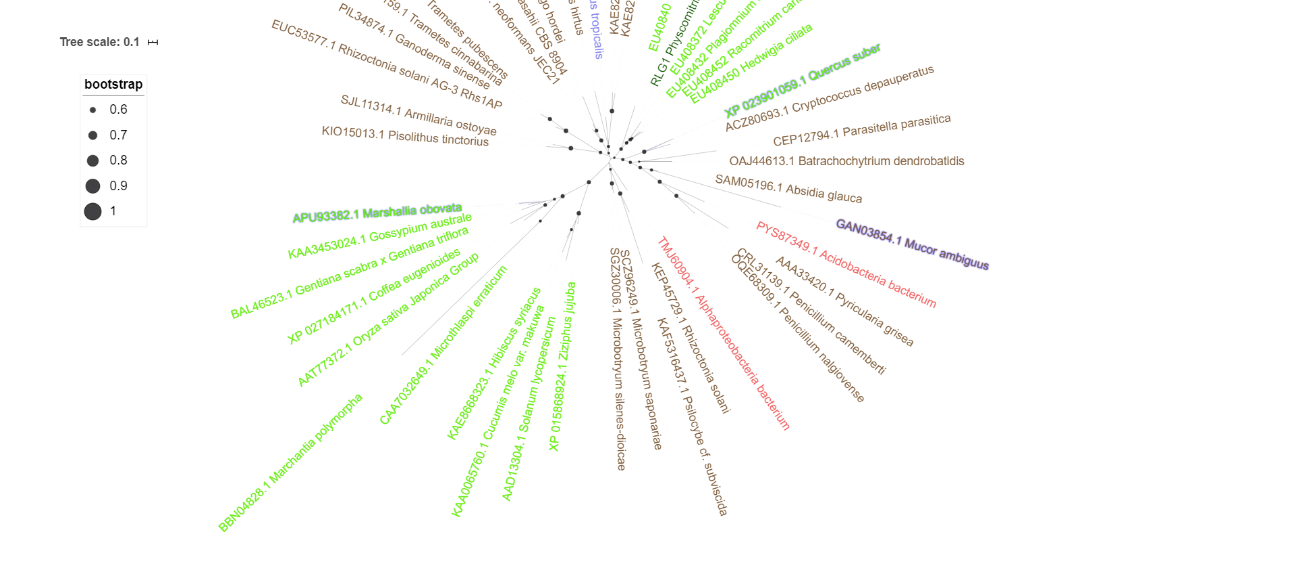
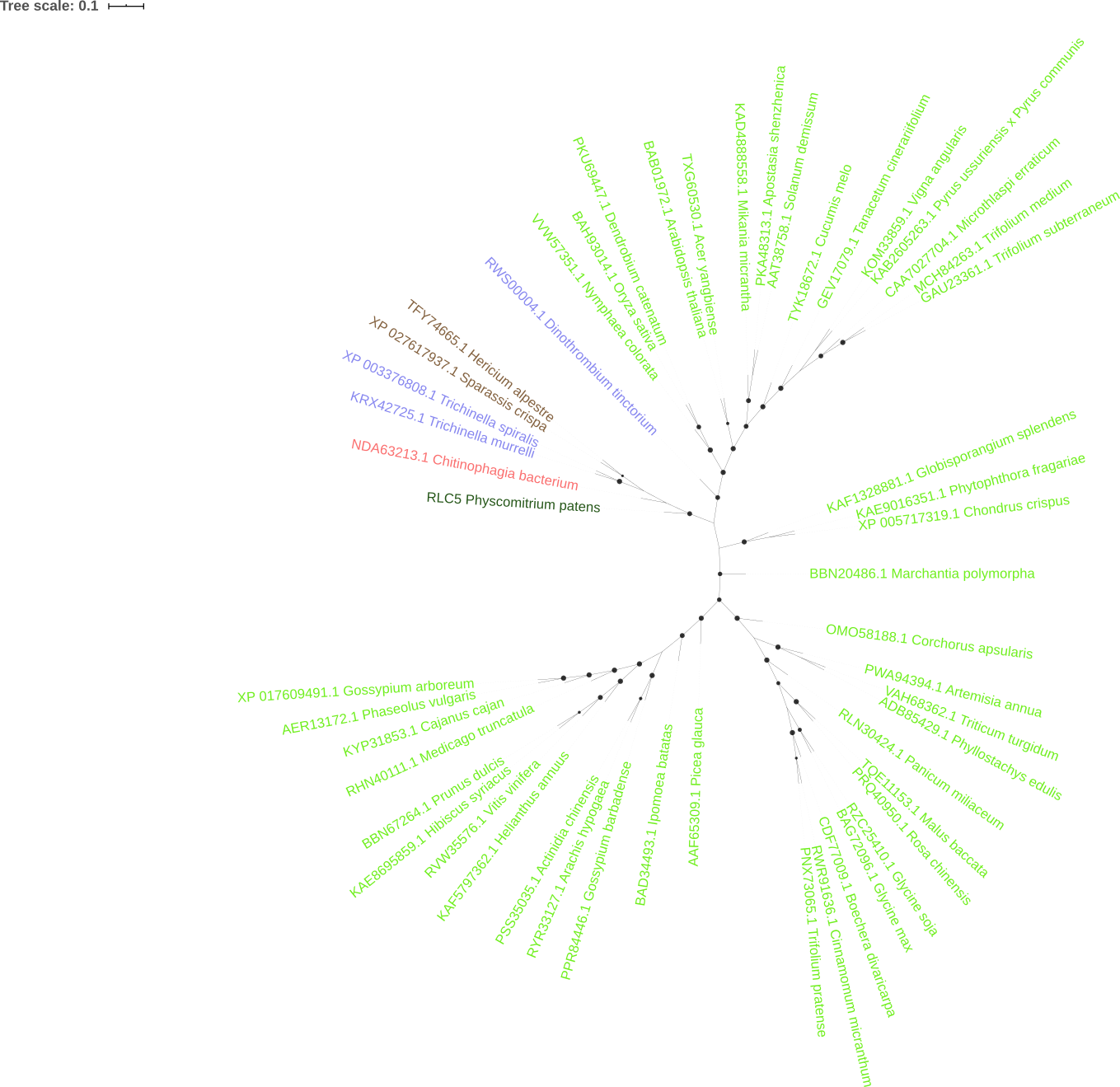
**Supplementary Figure 4: Phylogenetic analysis of the Transposable elements RLG1 proteins with those potentially encoded by plant, fungal, animals and bacterial transposable elements elements.** *P. patens* sequences are shown in dark green, plant sequences in light green, fungal sequences in brown, animal sequences in blue and bacterial sequences in red.



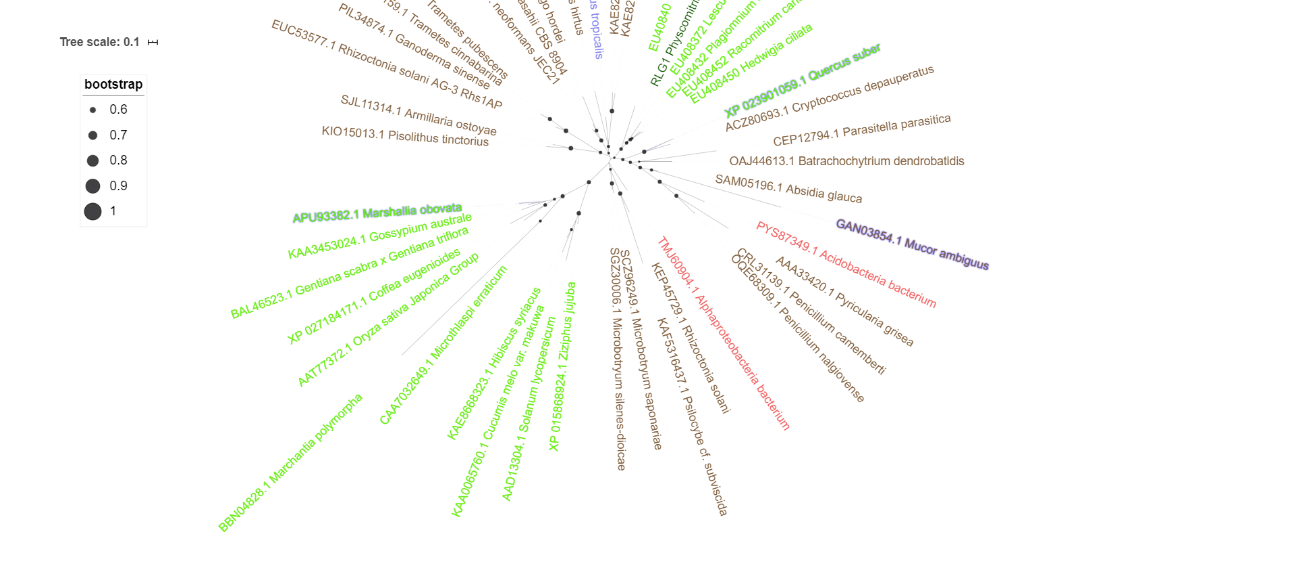
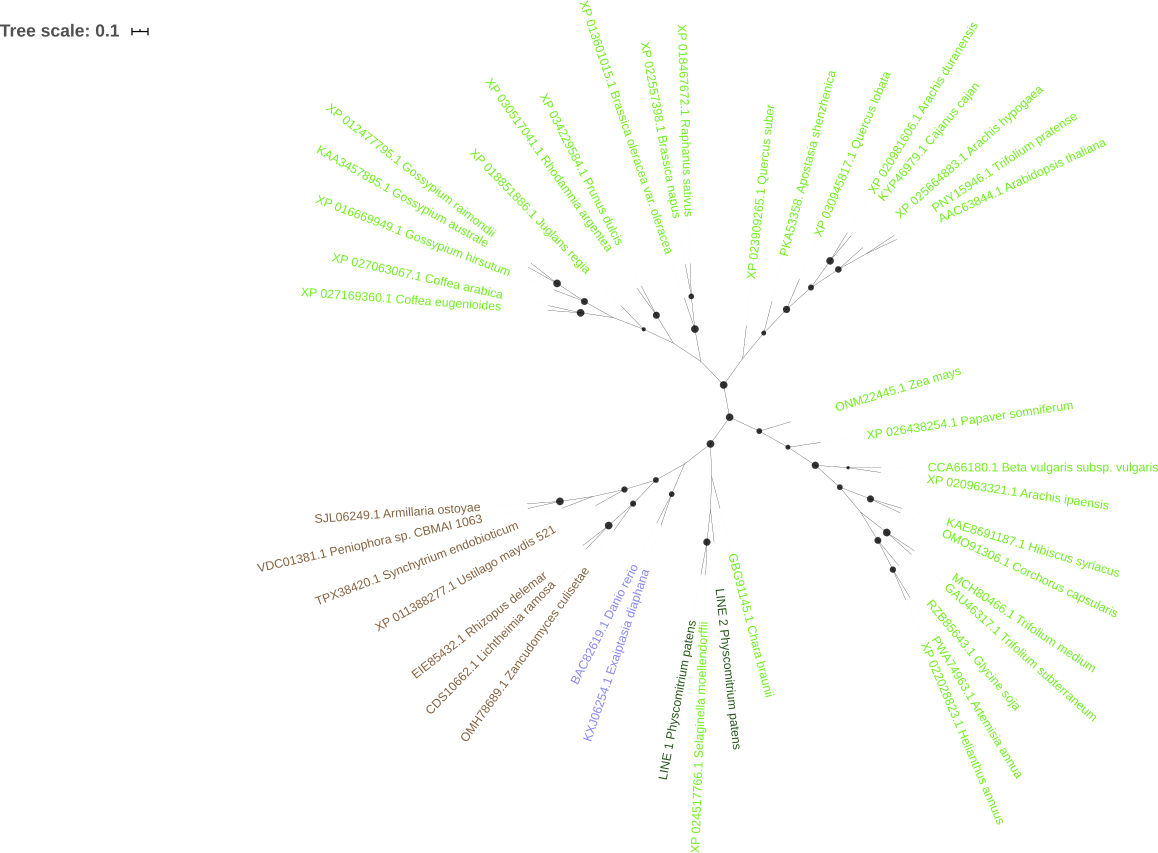
**Supplementary Figure 5: Phylogenetic analysis of the Transposable elements RLG2 proteins with those potentially encoded by plant, fungal, animals and bacterial transposable elements elements.** *P. patens* sequences are shown in dark green, plant sequences in light green, fungal sequences in brown



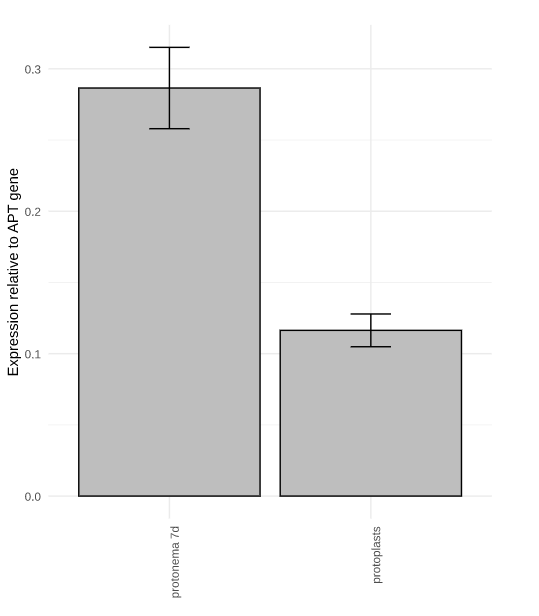
**Supplementary Figure 6: Phylogenetic analysis of the Transposable elements RLC4 proteins with those potentially encoded by plant, fungal, animals and bacterial transposable elements elements.** *P. patens* sequences are shown in dark green, plant sequences in light green, fungal sequences in brown



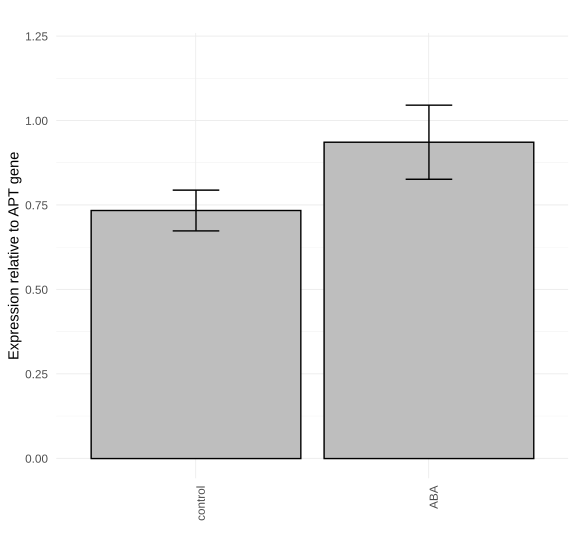
**Supplementary Figure 7: Phylogenetic analysis of the Transposable elements RLC5 proteins with those potentially encoded by plant, fungal, animals and bacterial transposable elements elements.** *P. patens* sequences are shown in dark green, plant sequences in light green, fungal sequences in brown, animal sequences in blue and bacterial sequences in red.



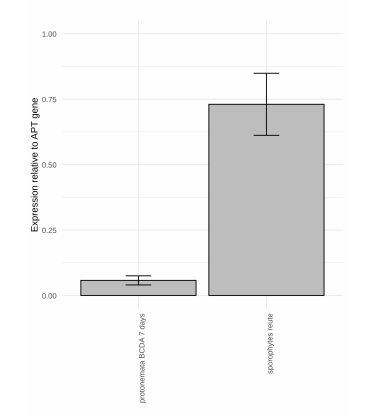
**Supplementary Figure 8: Phylogenetic analysis of the Transposable elements LINE-1 and LINE-2 proteins with those potentially encoded by plant, fungal, animals and bacterial transposable elements elements.** *P. patens* sequences are shown in dark green, plant sequences in light green, fungal sequences in brown and animal sequences in blue



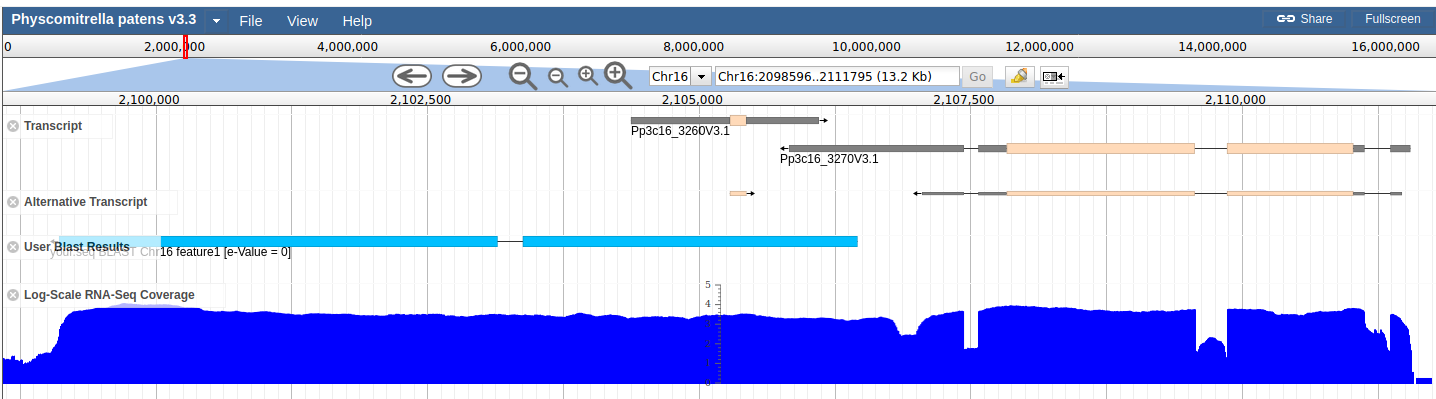
**Supplementary Figure 9:** qRT-PCR analysis of the expression of RLG1 in protonema grown for 7 days in BCDAT medium compared with the expression in protoplasts cells. The bars present the mean of three biological replicates. The standard deviation is shown.



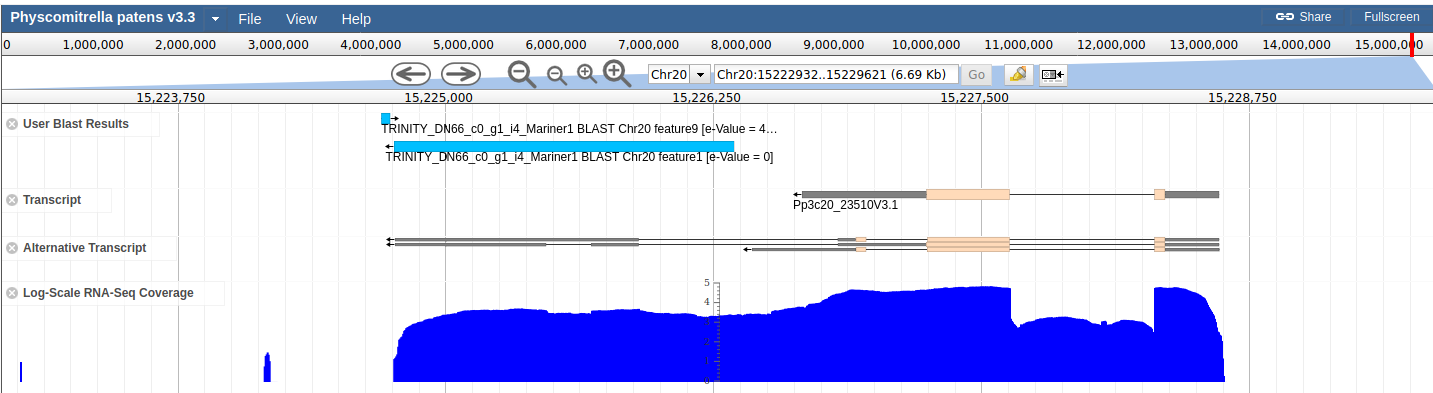
**Supplementary Figure 10: Induction of RLG2 expression by ABA.** qRT-PCR analysis of the RLG2expression in protonema grown for 7 days in BCD medium (cotrol) and protonema grown for 6 days in BCD and one additional day in 50 µM ABA (ABA). The bars present the mean of three biological replicates. The standard deviation is shown.



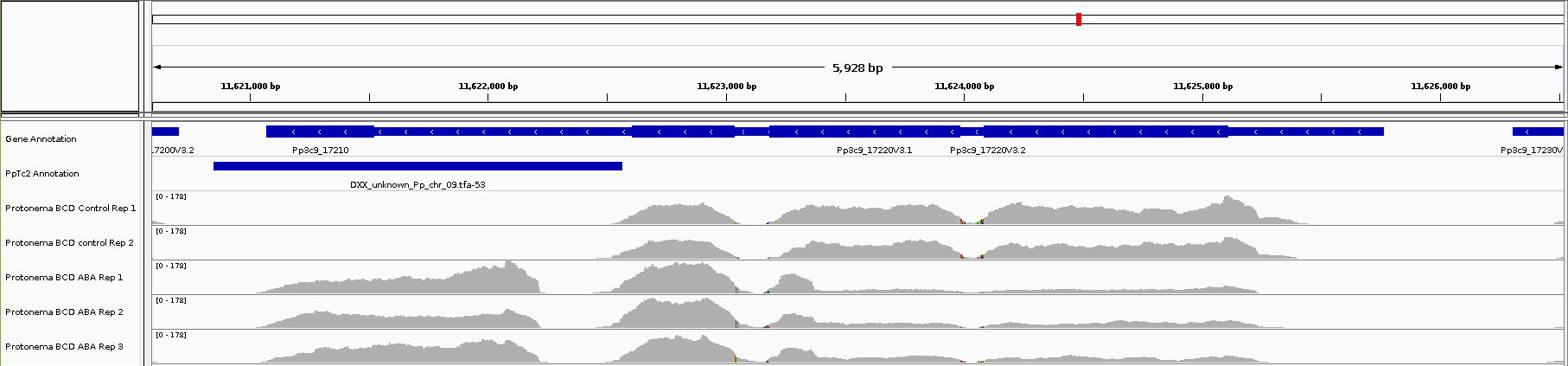
**Supplementary Figure 11:** Expression of tRLC5 elements in sporophytes. qRT-PCR analysis of the expression of tRLC5 elements in P. patens Reute sporophytes compared with its expression in protonema.



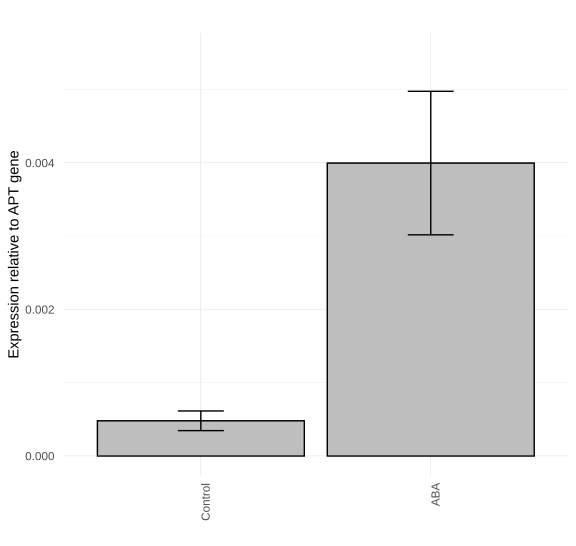
**Supplementary Figure 12:** **Expression of the LINE-2 inserted at the 3' of a gene and potentially transcribed as the result of read-through transcription.** Screenshot of the Phytozome genome browser showing from top to bottom, the Pp3c16\_3270 predicted transcripts, the annotated alternative transcripts, the nBLAST best hit of the TRINITY\_DN90\_c0\_g1\_i9 assembly, and the log-scale RNA-Seq coverage of the genome region.



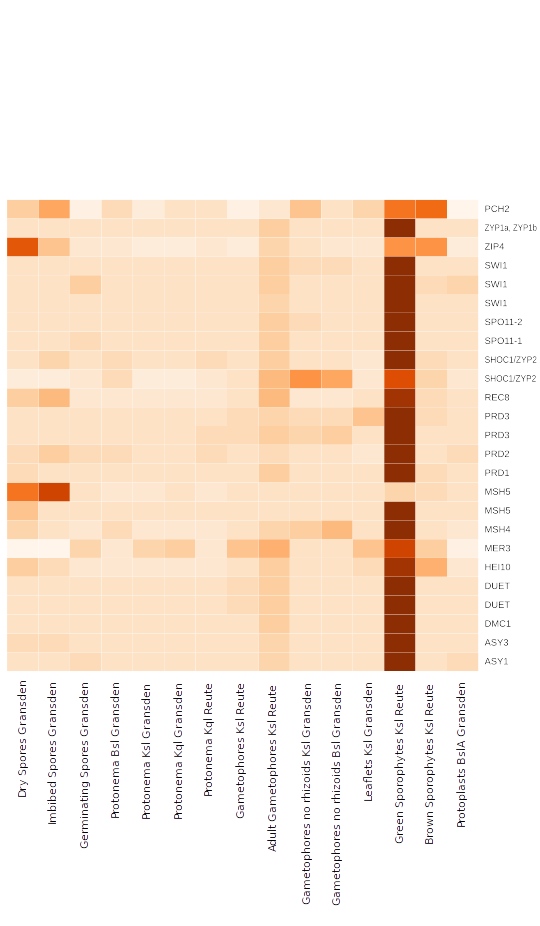
**Supplementary Figure 13:** **Expression of *PpTc1* as a result of read-through from the Pp3c20\_23510 gene.** Screenshot of the Phytozome genome browser showing from top to bottom, the best hit of the TRINITY\_DN66\_c0\_g1\_i4\_Pp\_Tc1 assembly, the Pp3c20\_23510 gene transcript, the alternative transcript of the gene track, and the log-scale RNA-Seq coverage of the genome region.



**Supplementary Figure 14:** **Expression of *PpTc2* and the Pp3c9\_17210 gene located nearby.** Screenshot of the IGV genome browser showing from top to bottom, the annotation the Pp3c9\_17210 gene, *PpTc2* annotation, RNA-Seq coverage of the genome region for two control protonema and 3 ABA-induced protonema samples.



**Supplementary Figure 15: Induction of *PpTc2* expression by ABA.** qRT-PCR analysis of the *PpTc2* expression in protonema grown for 7 days in BCD medium (control) and protonema grown for 6 days in BCD and one additional day in 50 µM ABA (ABA).



**Supplementary Figure 16: Expression of meiosis-specific genes in young sporophites.** Heat map of the expression of the meiosis-specific genes in different development conditions. The higher the expression, the darker the color.