PEATmoss (Physcomitrella Expression Atlas Tool): a unified gene expression atlas for the model plant *Physcomitrella patens*

**Supporting Information**

**Supporting results 1**

It was already shown by Wang *et al*. 2008 that *P. patens* and flowering plants share some common strategies to adapt to Pi deficiency, highlighting the importance of the PHO1 gene family. Here, we characterized the expression landscape of flowering plant orthologs in *P. patens* which are known as Pi deficiency signaling components. The custom list function of PEATmoss was used to get the expression values of candidate genes from Wang *et al*. 2008 (Figure S2A, Table S5). Further, expression differences per Pi deficiency time point were calculated (Figure S2B), clustered according to Pearson and Spearman and plotted in R (Figure S2C). The DGD1 gene family shows the highest correlation among the Pi deficiency candidates, whereas the other gene families appear to react independently to the low phosphate stimulus across the different time points. Pi deficiency caused distinct expression patterns of known phosphate deficiency responsive genes over different time points. As noted before, PHO1.1 and SQD1 respond earliest at 10dpt. In this study, PHO1.2 showed the highest response at 1dpt and its expression decreased further at later time points, whereas APS1.5 and PHO1.6 showed the highest response at 5dpt. The diverse expression patterns of the investigated genes highlight the complex signaling which takes place during Pi deficiency to slowly sense the external Pi concentration. At 10dpt the expression of Pi transporters is selectively up- or down-regulated whereas iron and other metal ion transporters are down-regulated. As noted earlier for plants, there exists an interaction of water stress and phosphate homeostasis (Kawa et al., 2016; Miura et al., 2011).

**Figure S1. Common differentially expressed genes among three Pi deficient time points.** The Venn diagram shows the overlap of up- and down-regulated (up/down) differentially expressed genes (DEGs) between the three evaluated time points (NOISeq prob > 0.9).

**Figure S2. Protonemata expression values for known phosphate deficiency responsive genes.** (A) Protonemata expression values (FPKM) from PEATmoss custom list for selected phosphate deficiency responsive genes at three different time points after transfer into Pi deficient liquid or control medium. (B) Log2(FPKM+1) expression differences for three different time points (P1-C1; P5-C5 and P10-C10) of genes as in A. (C) Pearson (lower left triangle) and Spearman (upper right triangle) correlation matrix of genes as in A.

**Figure S3. PpGML DB schema.** Genes are linked to annotations and to genes from other versions. The table “genes” stores gene names and versions, the table “gene\_gene” stores the relation between the genes from different versions, the table annotation stores the annotation IDs, terms and types, and the table “gene\_annotation” stores the relation between the genes and their annotations. Relationships between tables are displayed as one to many (1 - \*) and many to one (\* - 1).

**Figure S4.** **Correlation matrices from the phosphate deficiency experiment**. Correlation values between each replicate from the comparison between control conditions and 1 day post transfer in phosphate deficiency medium (1dpt) are shown in A, 5dpt in B and 10dpt in C respectively.

**Table S1. PEATmoss DEG output for each phosphate deficiency time point**. Up and down-regulated genes from each condition were included in separated tabs and annotations from the PpGML DB were included for all genes. M is the log2-ratio of the two conditions, D the value of the difference between conditions, prob the probability of differential expression and ranking is a summary statistic of M and D values.

**Table S2. Gene ontology analysis for Pi deficiency time point dpt1.** Gene ontology IDs, gene ontology descriptions, p-values and corrected p-values for the corresponding gene ontology category are given for each gene ontology namespace (biological process, molecular function, cellular component) either for up- or down-regulated genes and for over- or under-representation tests obtained via BiNGO (Maere *et al.,* 2005).

**Table S3. Gene ontology analysis for Pi deficiency time point dpt5.** Gene ontology IDs, gene ontology descriptions, p-values, corrected p-values, cluster frequencies, total frequencies and genes for the corresponding gene ontology category are given for each gene ontology namespace (biological process, molecular function, cellular component) either for up- or down-regulated genes and for over- or under-representation tests obtained via BiNGO (Maere *et al.,* 2005).

**Table S4. Gene ontology analysis for Pi deficiency time point dpt10.** Gene ontology IDs, gene ontology descriptions, p-values, corrected p-values, cluster frequencies, total frequencies and genes for the corresponding gene ontology category are given for each gene ontology namespace (biological process, molecular function, cellular component) either for up- or down-regulated genes and for over- or under-representation tests obtained via BiNGO (Maere *et al.,* 2005).

**Table S5. Expression of known Pi deficiency candidate genes (FPKM).** Expression values from the Pi deficiency time series for candidate genes from Wang *et al*., 2008 downloaded using the PEATmoss custom list search. Gene names and *A. thaliana* orthologs were added in extra columns.