Supplementary Figure S1. Distribution of differentially expressed genes.

X-axis indicate average log CPM (counts per million) values, which can be understood as measuring expression level. Y-axis indicate log FC (fold change) values. LogCPM is the log counts per million, which is the log difference between control and 50 mM samples. The red dots represent genes with a FDR < 0.05 and a differential expression in 50 mM NaCl > two-fold their expression in control conditions. The black dots indicate non-differentially expressed genes.

Supplementary Figure S2. Gene ontology (GO) enrichment analysis.

Enrichment of GO terms in differentially expressed genes in 50 mM NaCl conditions. Z-score of each GO terms upregulated in 50 mM NaCl condition is represented by positive numbers and downregulated is represented by negative numbers.

Supplementary Table S1. Summary of sequencing reads after filtering.

Supplementary Table S2. Gene expression data based on the RNA-Seq analysis of *Marchantia polymorpha* grown in salinity-stress conditions.

Supplementary Table S3. Subsets of differentially expressed genes (DEGs) in *Marchantia polymorpha* grown in control or salinity-stress conditions (50 mM NaCl).

Up- and downregulated DEGs annotated by Swiss-Prot, filtered by *p*-value, and an adjusted FDR < 0.05.

Supplementary Table S4. Salinity stress-responsive TF genes annotated using the Plant TFDB.

Up- and downregulated DEGs in *Marchantia polymorpha* grown on 50 mM NaCl vs. control conditions, filtered by *p*-value, and an adjusted FDR < 0.05

Supplementary Table S5. Salinity stress-responsive TF genes annotated using the Plant TFDB.