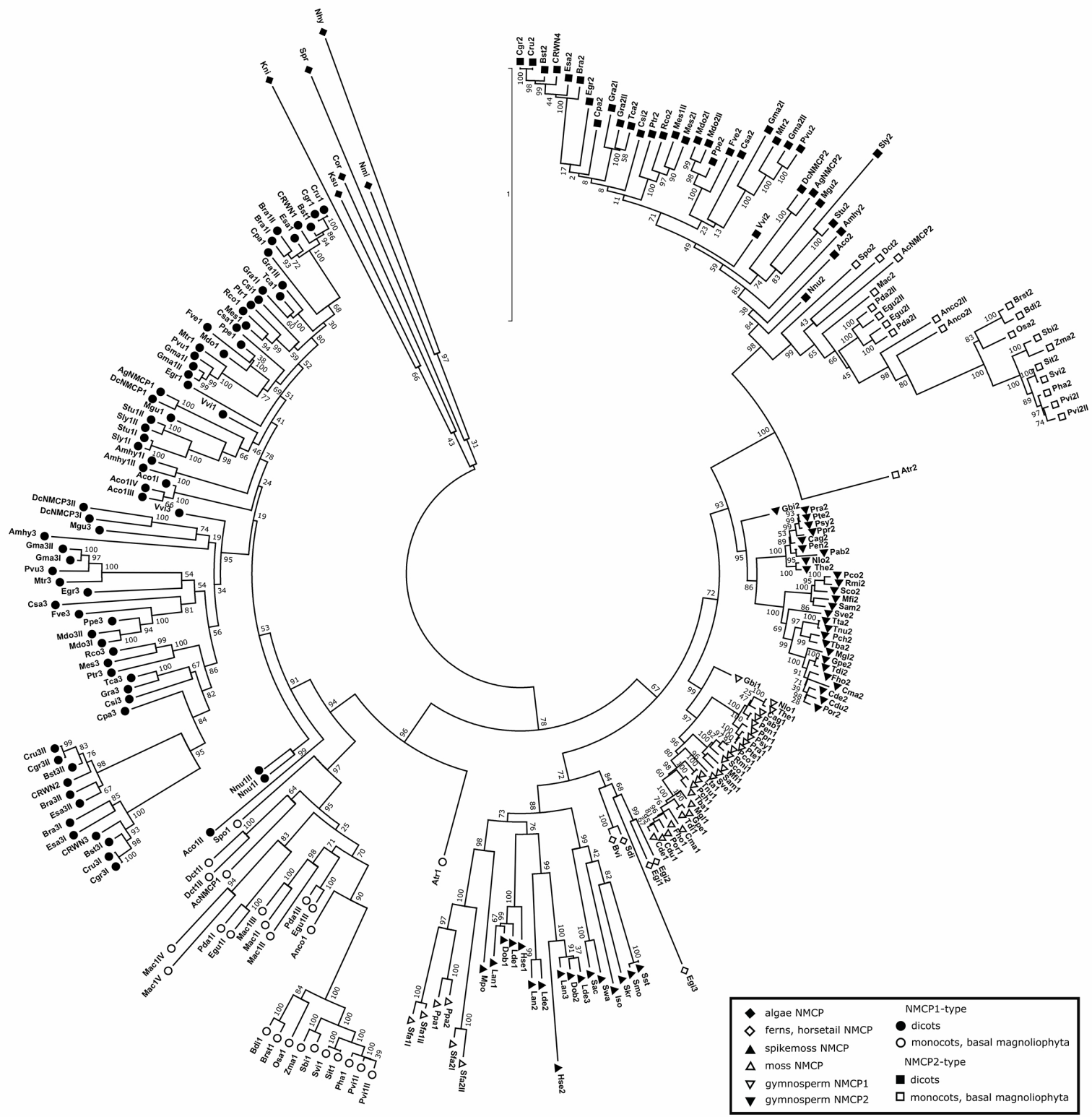

Figure S1. Phylogenetic tree of NMCP proteins (extended version with transcriptomic data). The evolutionary history was inferred by using the Maximum Likelihood method based on the JTT matrix-based model. The tree with the highest log likelihood is shown. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using a JTT model, and then selecting the topology with superior log likelihood value. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 245 amino acid sequences. All positions with less than 95% site coverage were eliminated. That is, fewer than 5% alignment gaps, missing data, and ambiguous bases were allowed at any position. There were a total of 531 positions in the final dataset. Evolutionary analyses were conducted in MEGA7. Reliability of the branches was interfered from bootstrap analyses of 1000 replicates.

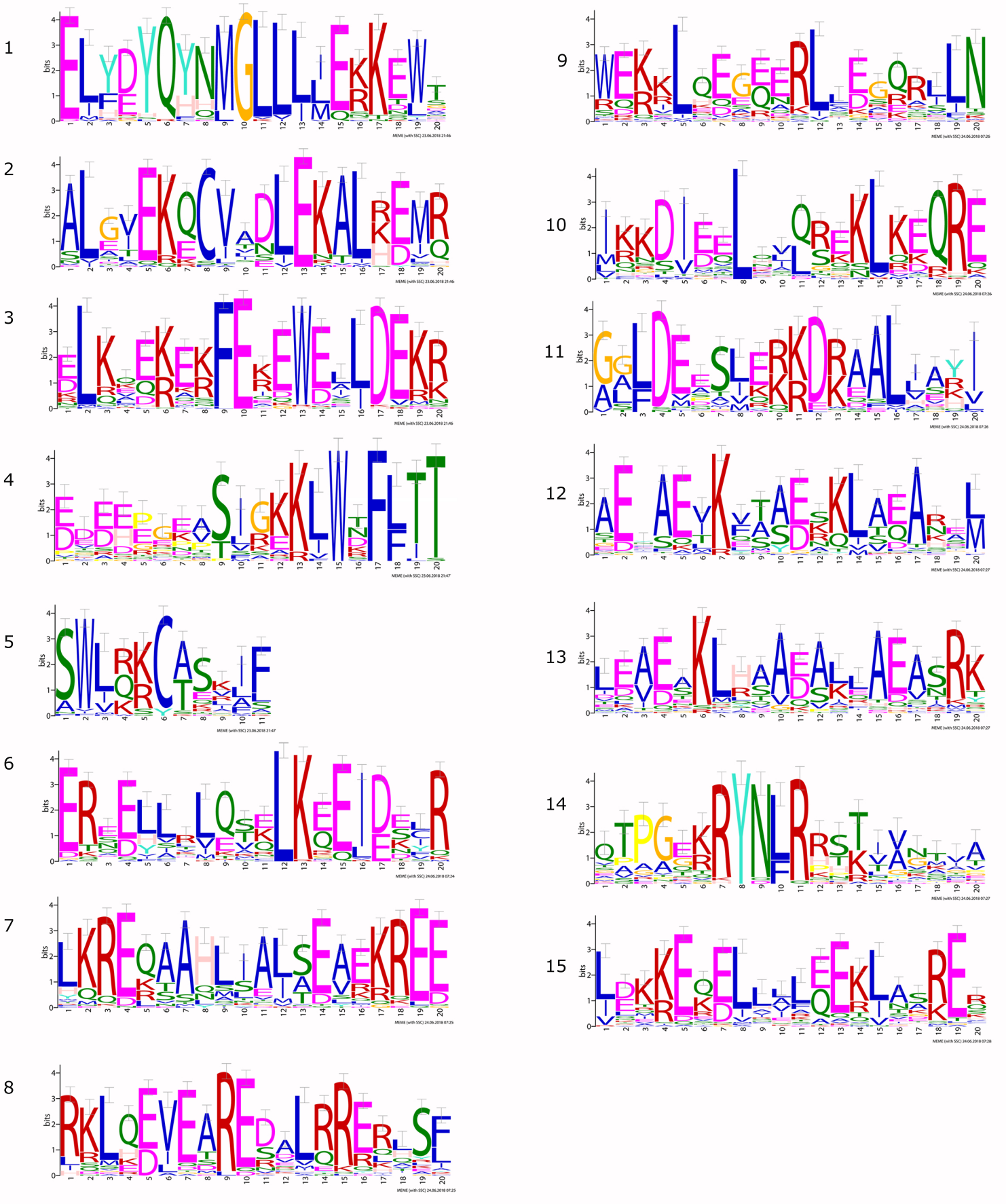

Figure S2. Regions conserved in NMCPs generated by MEME search presented as logos. The numbers correspond to the numbers designated in Table 2 from the highest score (1) to the lowest (15).

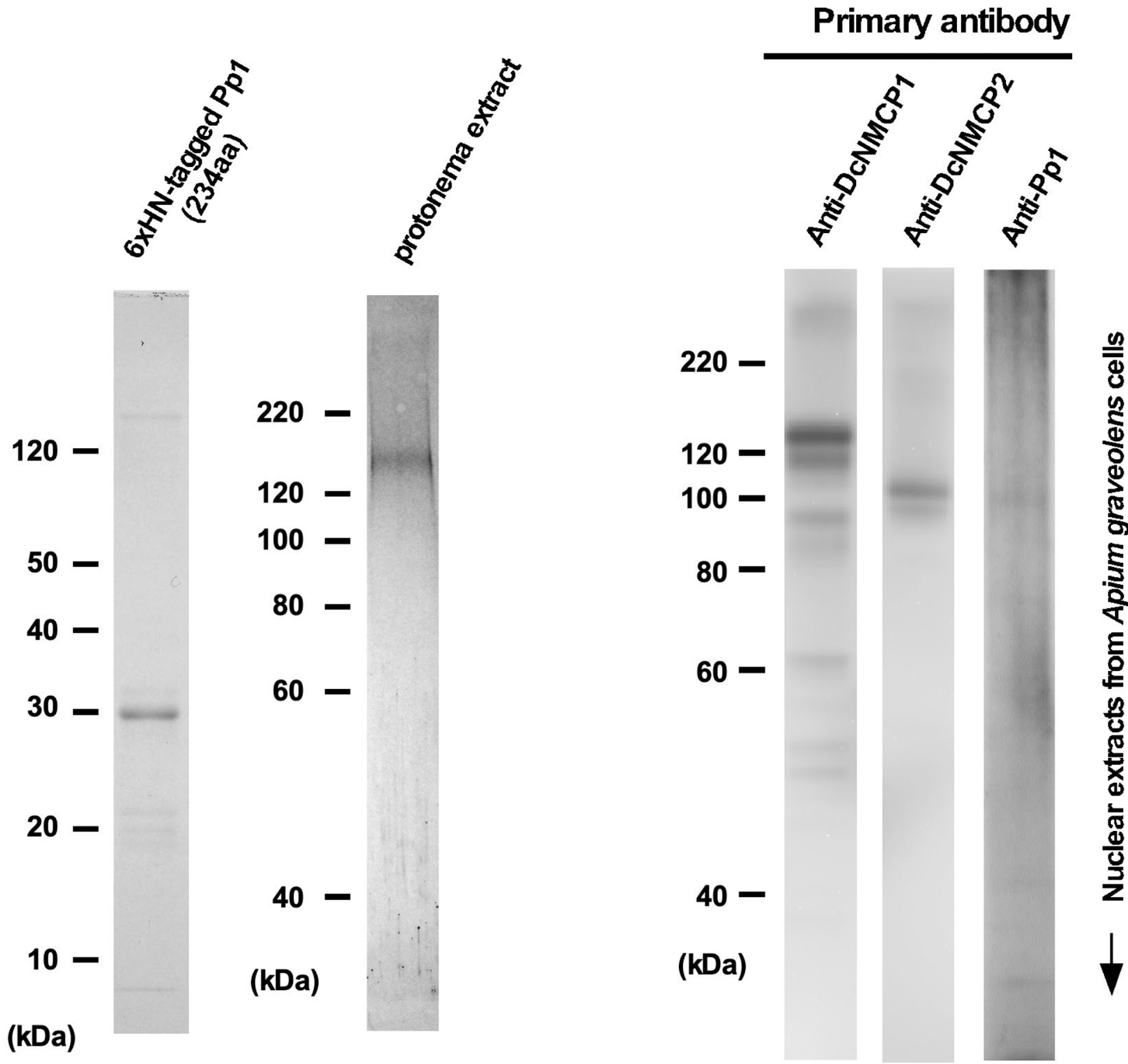

Figure S3. Validation of target specificity of the anti-PpNMCP1 antibody by western blot analysis. Starting from the left: 1st lane positive control of the immunization peptide with the anti -PpNMCP1 antibody. 2nd lane: incubation of proteins from *P patens* protonema with the anti-PpNMCP1 antibody recognizes a single band corresponding to PpNMCP1. 3rd to 5th lanes: Nuclear proteins of the dicot *Apium graveolens* incubated with antibodies against DcNMCP1 (3rd lane), DcNMCP2 (4th lane) and PpNMCP1 (5th lane). The later reveals a very weak reaction that could correspond to AgNMCP2.