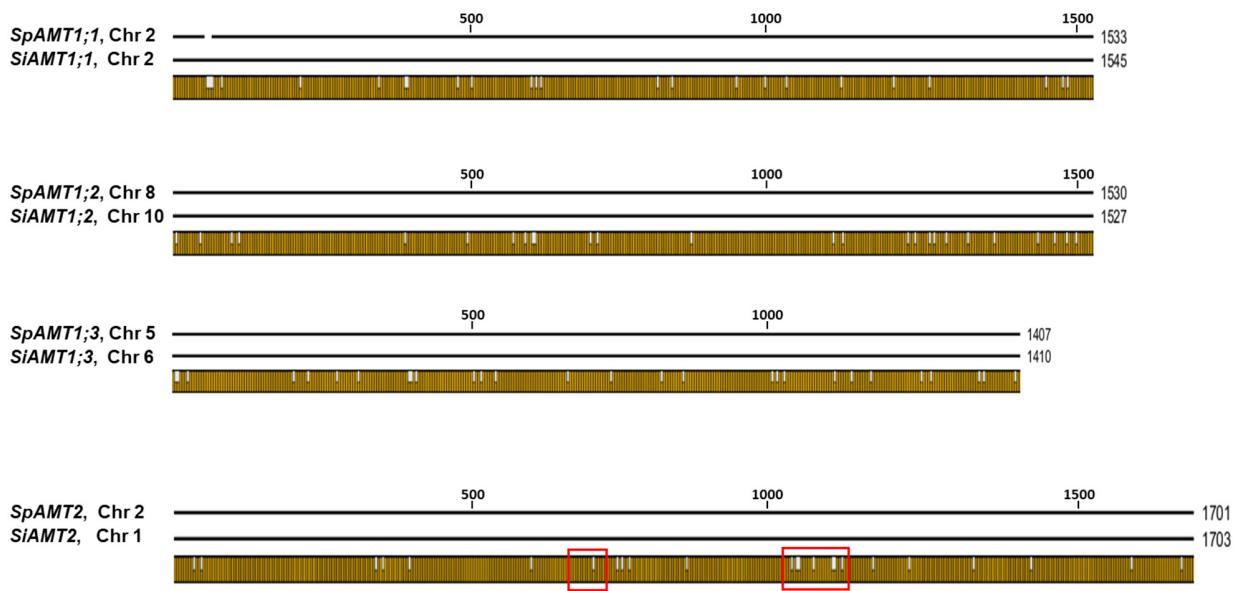


**Table S1.** List of RT-qPCR primers used for evaluating expression of *AMTs aquaporin* genes in *S. polyrhiza* line NB5548.

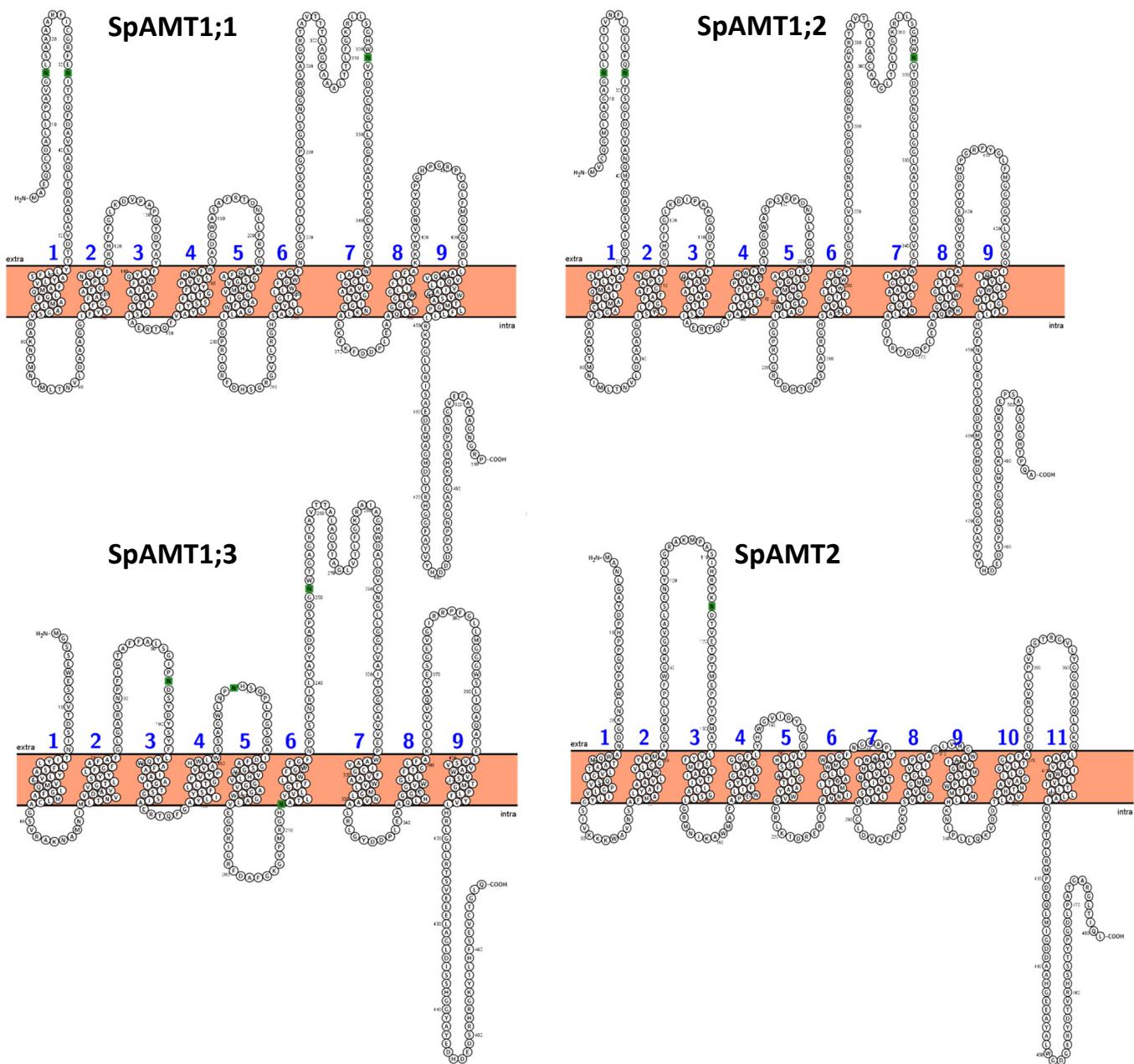
Gene	Forward primer	Reverse primer	PCR product length, bp
<i>SpAMT1;1</i>	GTTCGTCGTTATCTCATCT	GGAAAAGGAGGTGTCGGT	122
<i>SpAMT1;2</i>	TATCTCCTCTTCTCCGCGT	TTCATGGTGTCTGGCCC	92
<i>SpAMT1;3</i>	ACCCCTCTTACTACCTTT	GAATGCCCACTGGTACAGAA	147
<i>SpAMT2</i>	TCCTGAACACCAACATCTGC	AGTCCCGTCATCATTCCCTT	115
<i>SpTIP2;1</i>	TCCATGAACCCTGCTCGCT	GGTAGGCCTAGGTGTAGACAAG	127
<i>SpPIP1;2/SpPIP1;3</i>	TCGGCTTCGCAGTGTTCTT	GGACCTGGACTTGAATGGGA	218
<i>SpPIP2;2</i>	TCGCCACCATCCCTATCA	CACCAATGAAAGGCCCTA	126
<i>SpHiston3</i>	CGCAAGTACCAGAACGACAC	CGAAGAGACCCACGAGGTAG	160
<i>SpActin</i>	TGTTTCCCAAGTATCGTC	TCCCAGTTGGTGACGATT	153

**Table S2.** List of primer used for cloning *AMT* genes of *S.polyrhiza* ecotype NB5548.

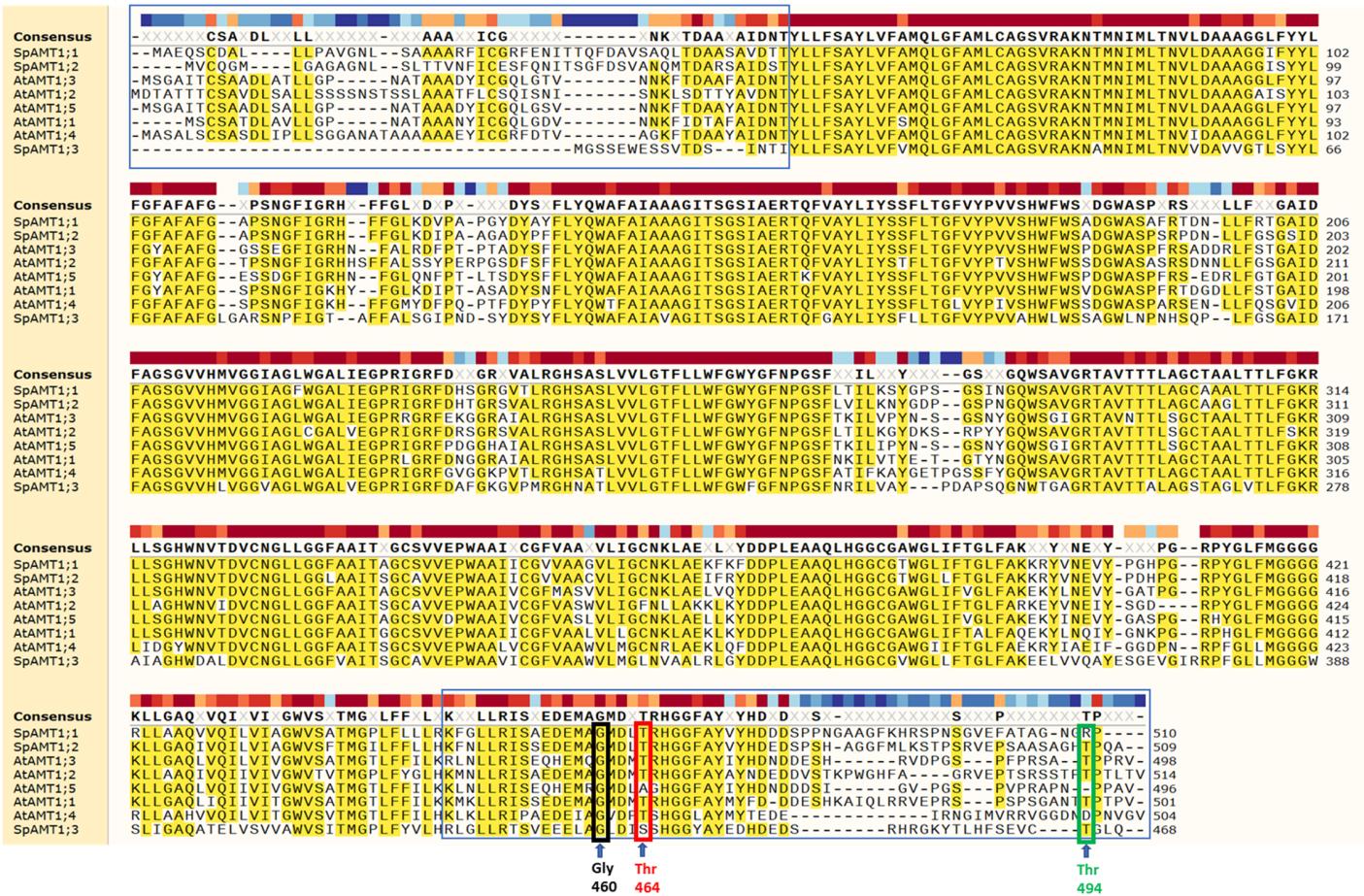
Gene	Forward primer	Reverse primer	PCR product length, bp
<i>SpAMT1;1</i>	AGAGAAGGGAGATGGCGGA	GAGAGAGAAGGTGGGAAGG	1579
<i>SpAMT1;2</i>	GGAGAGATGGGGACATGG	AAGATATCGATGGGCCAC	1689
<i>SpAMT1;3</i>	TCTCTCTGCACCTGTCTT	ACAGTTCCCAGTTGTCC	1453
<i>SpAMT2</i>	GTTGGGGTGAAGAGGATGG	AGGGAGAGAGAGAGACTAGA	1476



**Figure S1.** Schematic structure of AMT coding regions in genomes of *Spirodesla polyrhiza* (*Sp*) and *Spirodesla intermedia* (*Si*). Positions of introns in the *SpAMT2* (643-722 and 1010-1185bp) and *SiAMT2* (643-723 and 1011-1187bp) genes are marked by red boxes.



**Figure S2.** Schematic structure of AMTs of *S. polyrhiza*. Images generated by tool *Protter - visualize proteoforms* [45]



**Figure S3.** Sequence alignment of AMT1 proteins from *S. polystachya* and *A. thaliana*. Gly460, Thr464 and Thr494 reduces labeled according their position in AtAMT1;3. Non-cytoplasmic N-termini domains and the cytoplasmic C-termini domains have been shown in blue boxes.