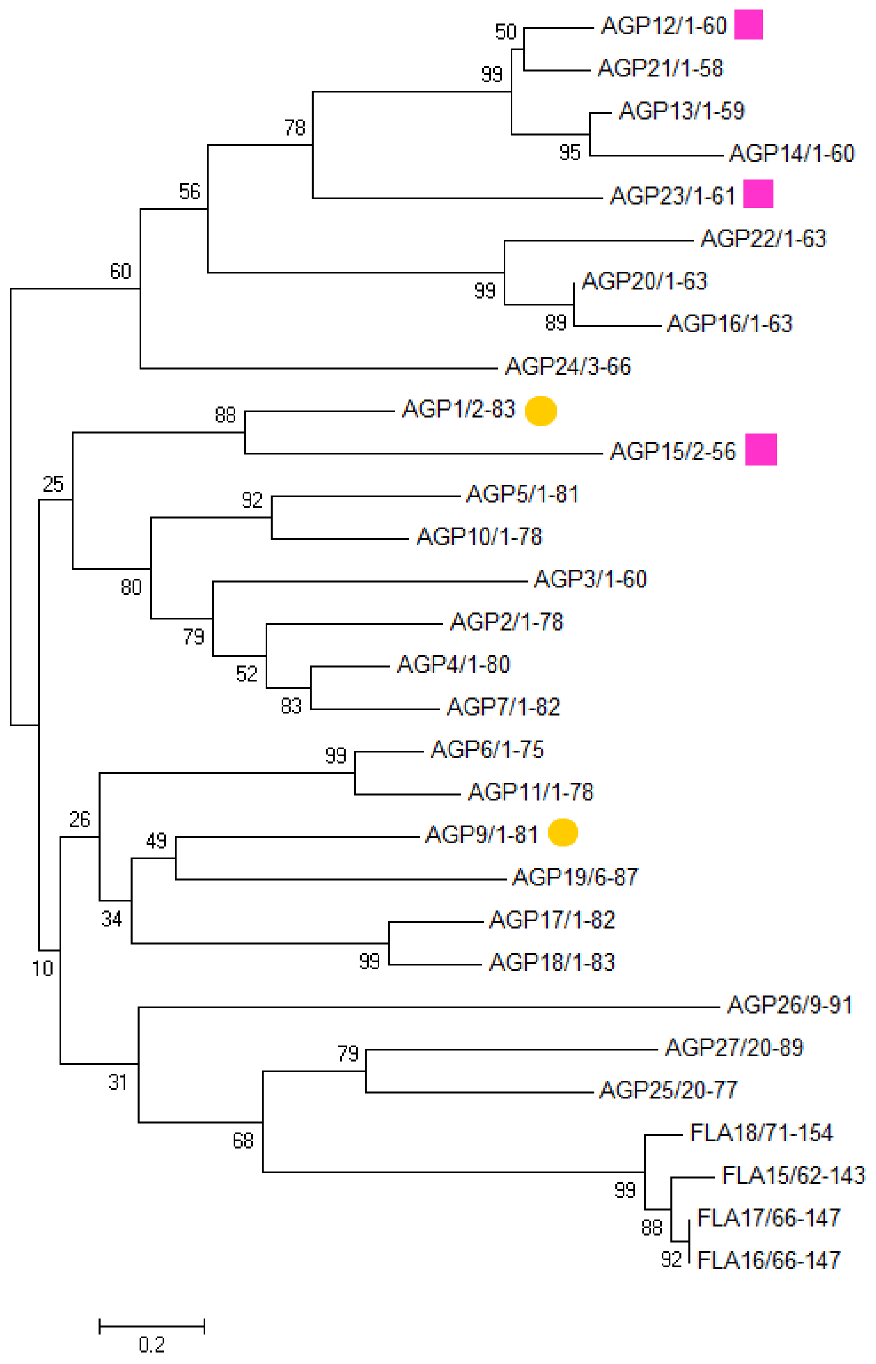
Supplemental table 1 - Primer list for AGP promoter amplification and use in GUS/GFP fusions.

Name	Locus	Primers
AGP1	At5g64310	**F CACC**GTCATATTGACTCTGAGCCATAAACTC **R** CAAAAAAGAGAGAGATTCGAATTTAGC
AGP9	At2g14890	**F CACC**ATTGGCCACAGTTCACCTGC **R** TTTTGCTTTTGCTTTTTCTCTCTG
AGP12	At3g13520	**F CACC**GTTGGGGCCACATTTGTAGT **R** CTTCTAAGTGCAAAAGAGGAG
AGP15	At5g11740	**F CACC**CCATTTTCTTTGATTGTAGCAAGTTAG **R** TTCAAAGATTTTGTTGTGAGAGATAAAG
AGP23	At3g57690	**F CACC**CATCGTGAATATTTATAGGACAAGTTTATG **R** GAGACCTGAAAGGCTTTTCTTTTC

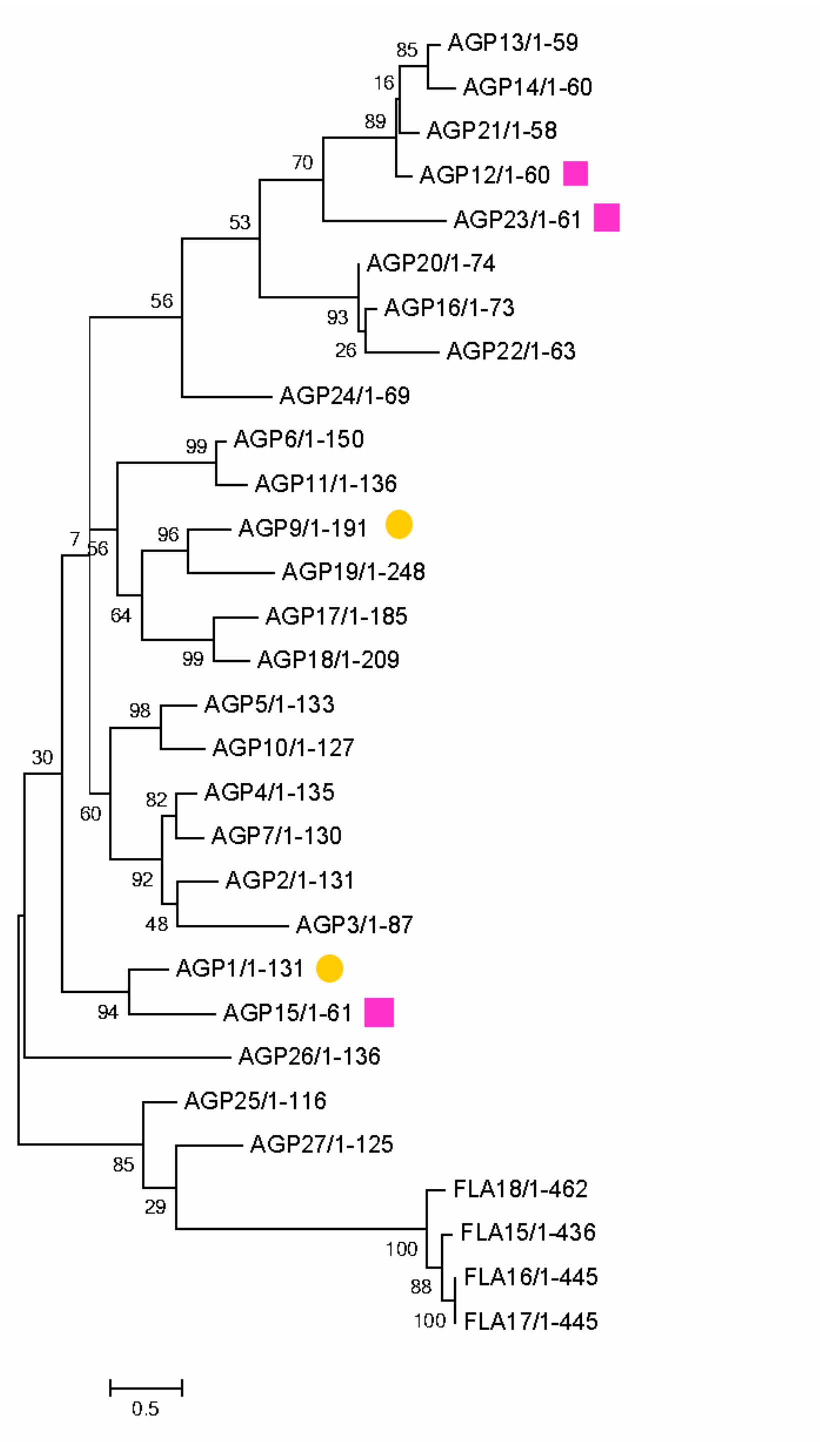
Supplemental table 2 - Primer list for the Real Time RT-PCR experiment with the selected *AGPs*.

Name	Locus	Primers
AGP1-RT	At5g64310	**F** CAAAAACACTCCCAAACCAAA **R** GGTGGTGAAGCAGAGGATTC
AGP4-RT	At5g10430	**F** TCGCCACTTCAGCACTCGCTC **R** CGGGAGCACTGCTTGGGCTC
AGP7-RT	At5g65390	**F** GAACTAGCCCCGACACCTTC **R** ACAAGTGAACCGACGACGAA
AGP9-RT	At2g14890	**F** ATCTGTATCGTCCTCATCG **R** ATGTTGTGACTGGTGGTG
AGP10-RT	At4g09030	**F** CTGCTCAACCTCCAAGAACC **R** CAAATCCGGCTAAAGATCCA
AGP12-RT	At3g13520	**F** ACAACTCATCATTCGCACCA **R** GCATCGGAAGTAGGACTTGG
AGP15-RT	At5g11740	**F** CTCAGCGTCTTTCGTGTCAG **R** GCTTCGGAATACACACGAGAC
AGP16-RT	At2g46330	**F** TCATCATTTTCGTCGGATCA **R** ACCACCATTAGCAAATACGC
AGP23-RT	At3g57690	**F** AATGGAGATGAAGAAGATTG **R** TGCAAGTAGTAGCTGAAG
AGP25-RT	At5g18690	**F** ACGAACGTTTTGGTTTTCACG **R** TCAAGAGGGGCAAACACGAC
AGP26-RT	At2g47930	**F** CAAGCGAAATGTCTCCTTCC **R** TGCTGCTTACTCGCTGTTTC
RUB1	At4g36800	**RT_147** CTGTTCACGGAACCCAATTC **RT_148** TGTCGGTCAGACCTTTTTCC
ACT8	At1g49240	**RT_861** CTCAGGTATTGCAGACCGTATGAG **RT_862** CAGAGTATGATGAAGCAGGTCCAG

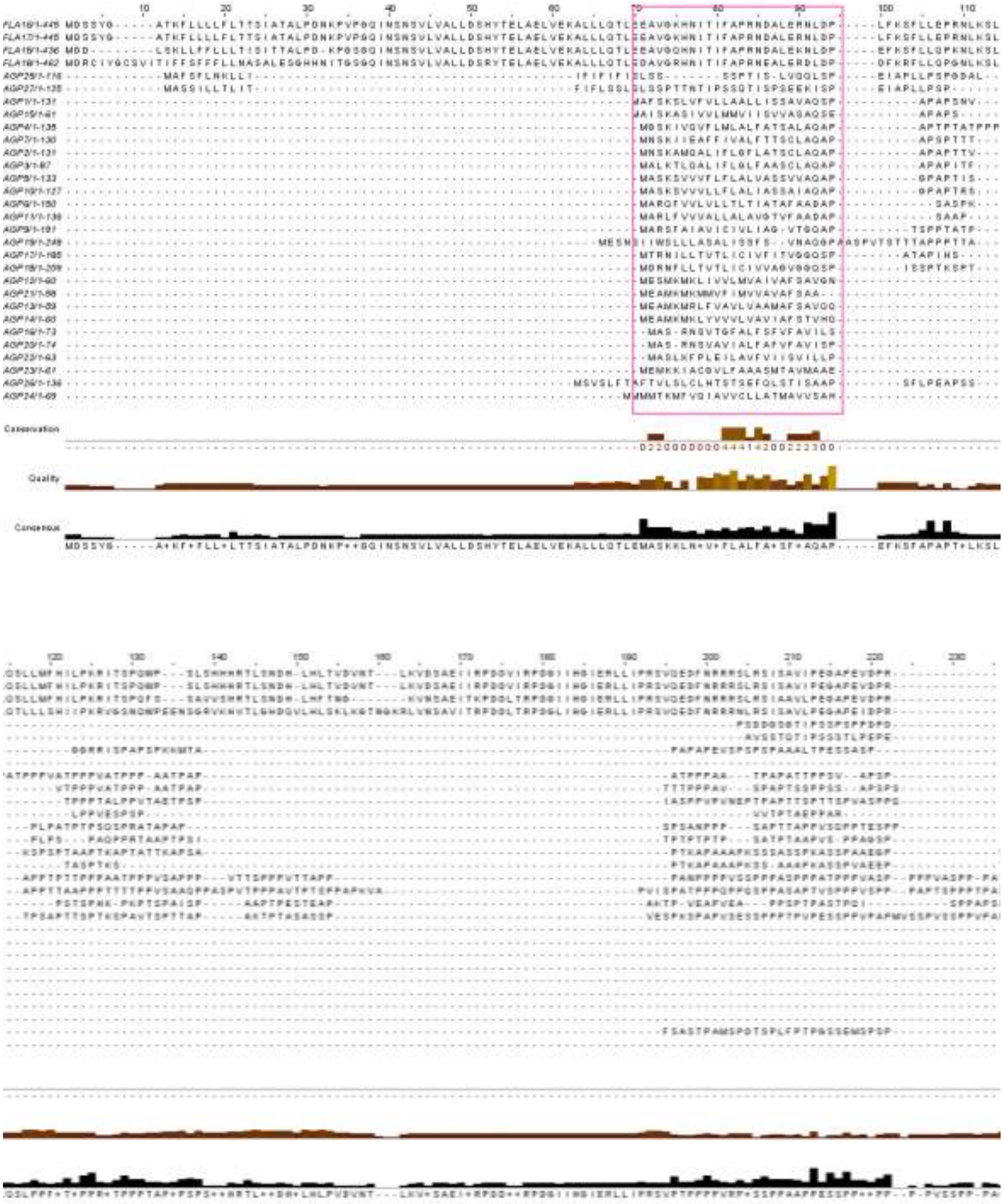
Supplemental figure 1 – Phylogenetic analysis of the AGP family in *A. thaliana*. To generate the phylogenetic tree for AGPs, the 3 blocks of most conserved amino acid sequences of AGPs coding sequences were aligned using Clustal W and manually edited using Jalview to reduce gaps. Neighbor-joining (NJ) tree was generated using the MEGA4 program. AGPs selected for further analysis are indicated by a yellow circle (classical AGPs) and a violet square (AG peptides).

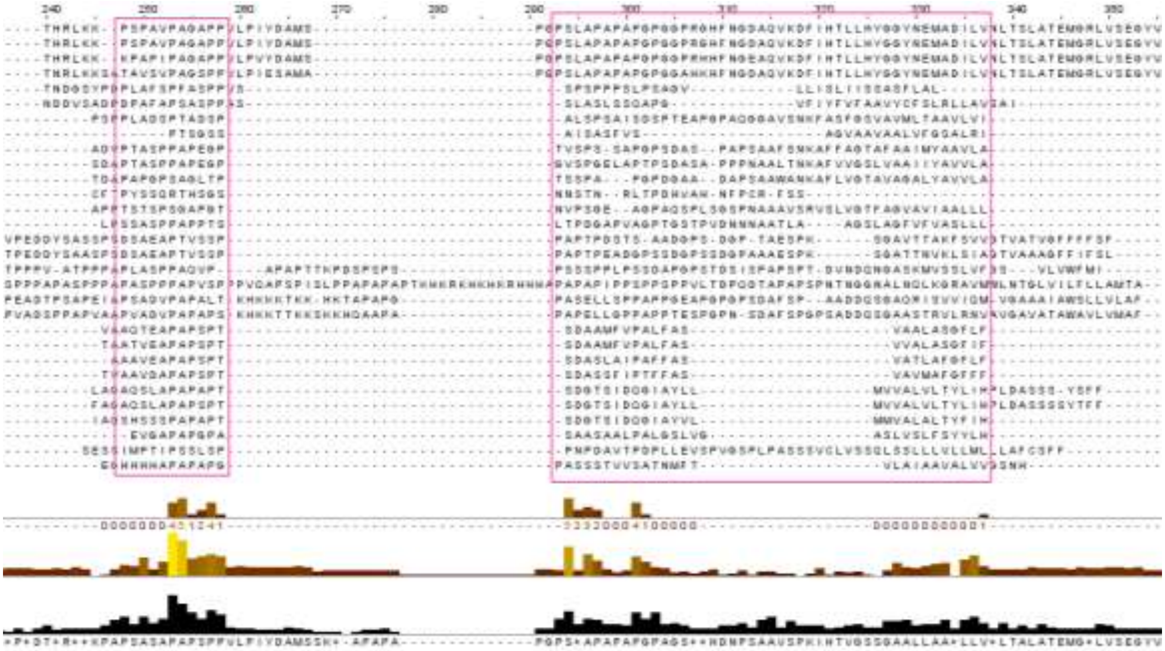


Supplemental figure 2 – Phylogenetic analysis of the AGP family in *A. thaliana*. To generate the phylogenetic tree for AGPs, the 3 blocks of most conserved amino acid sequences of AGPs coding sequences were aligned using Clustal W and manually edited using Jalview to reduce gaps. Maximum Parsimony tree was generated using the MEGA4 program. AGPs selected for further analysis are indicated by a yellow circle (classical AGPs) and a violet square (AG peptides).



Supplemental figure 3 – The amino acid sequences of AGPs coding sequences aligned using Clustal W (Thompson *et al.*, 1994) and viewed using Jalview (Clamp *et al.*, 2004). The 3 conserved blocks are highlighted by the pink rectangles.

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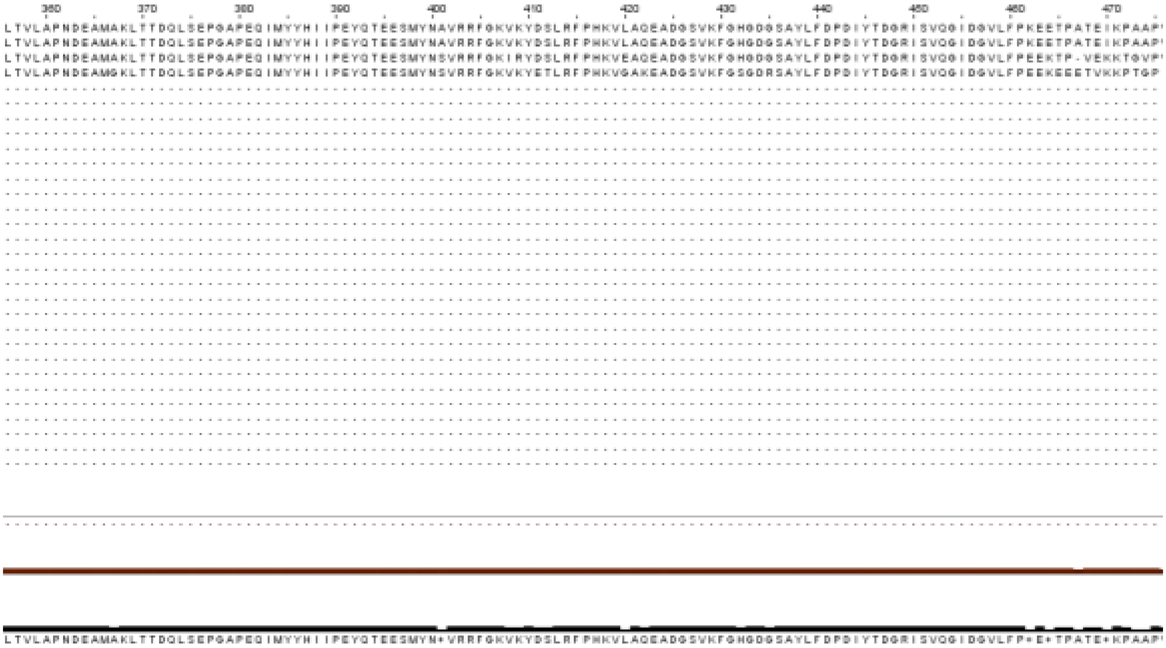
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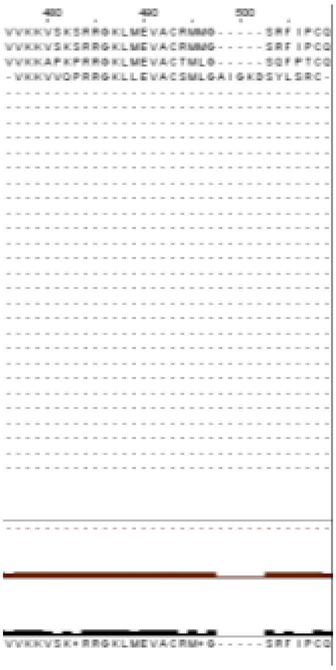
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