

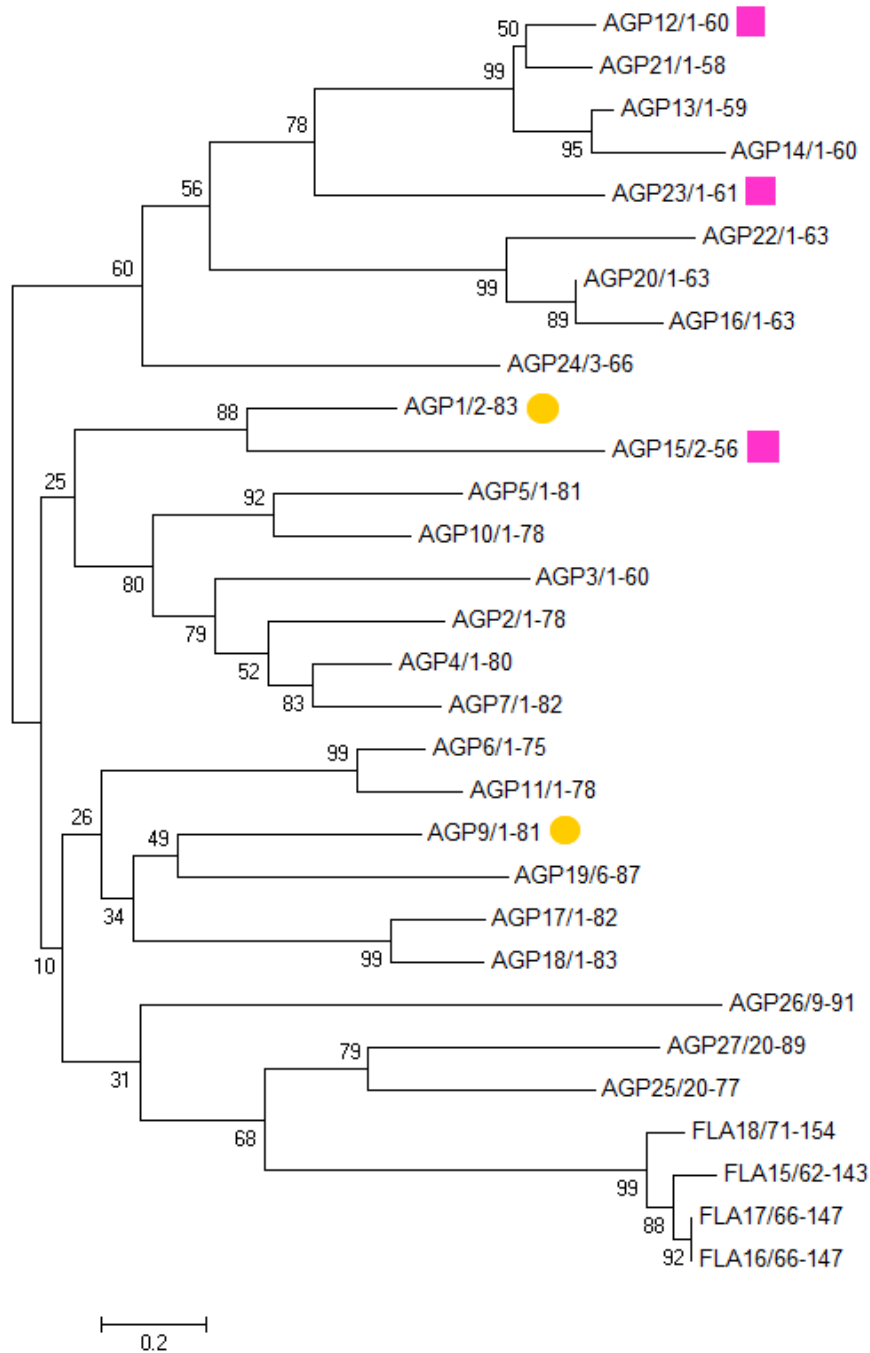
Supplemental table 1 - Primer list for AGP promoter amplification and use in GUS/GFP fusions.

Name	Locus	Primers
AGP1	At5g64310	F CACCGTCATATTGACTCTGAGCCATAAACTC R CAAAAAAGAGAGAGATTCTGAATTTAGC
AGP9	At2g14890	F CACCATTGGCCACAGTTCACCTGC R TTTTGCTTTTGCTTTTCTCTCTG
AGP12	At3g13520	F CACCGTTGGGGCCACATTTGTAGT R CTTCTAAGTGCAAAAGAGGAG
AGP15	At5g11740	F CACCCCATTTTCTTTGATTGTAGCAAGTTAG R TTCAAAGATTTTGTGAGAGATAAAG
AGP23	At3g57690	F CACCCATCGTGAATATTTATAGGACAAGTTTATG R GAGACCTGAAAGGCTTTTCTTTTC

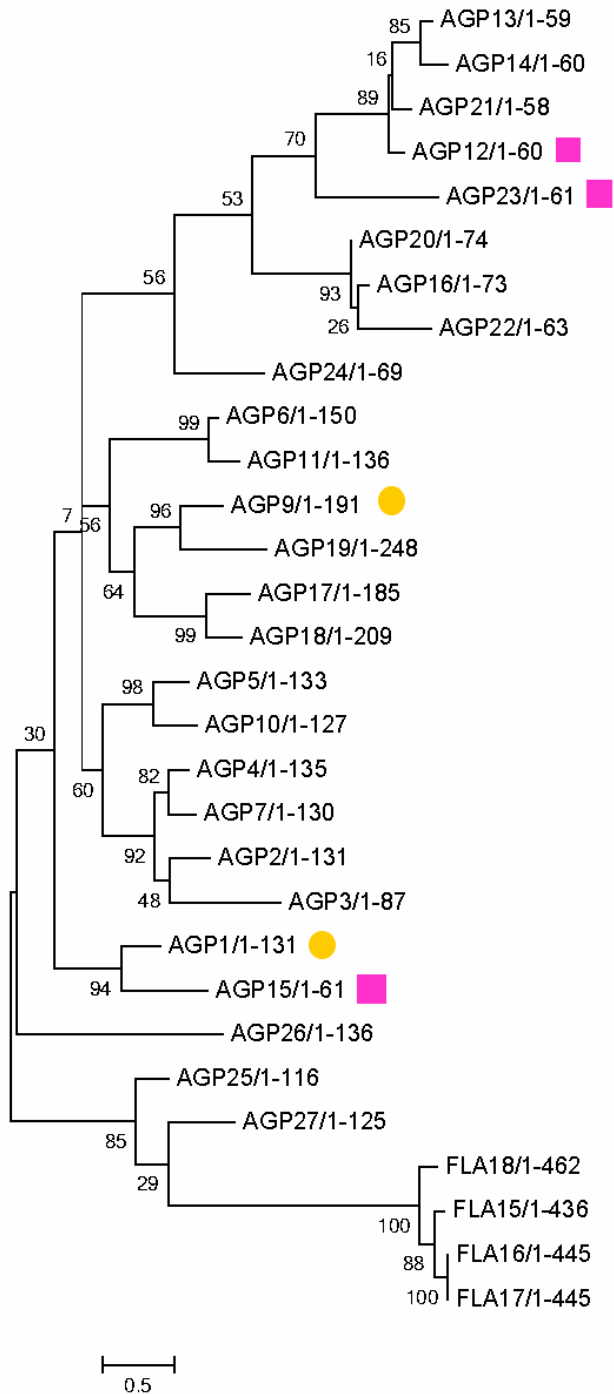
Supplemental table 2 - Primer list for the Real Time RT-PCR experiment with the selected *AGPs*.

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 CTCAGCGTCTTTTCGTGTCAG R GCTTCGGAATACACACGAGAC
AGP16-RT	At2g46330	F TCATCATTTTCGTCCGATCA R ACCACCATTAGCAAATACGC
AGP23-RT	At3g57690	F AATGGAGATGAAGAAGATTG R TGCAAGTAGTAGCTGAAG
AGP25-RT	At5g18690	F ACGAACGTTTTGGTTTTACG R TCAAGAGGGGCAAACACGAC
AGP26-RT	At2g47930	F CAAGCGAAATGTCTCCTTCC R TGCTGCTTACTCGCTGTTTC
RUB1	At4g36800	RT_147 CTGTTACGGAACCCAATTC RT_148 TGTCGGTCAGACCTTTTTCC
ACT8	At1g49240	RT_861 CTCAGGTATTGCAGACCGTATGAG RT_862 CAGAGTATGATGAAGCAGGTCCAG

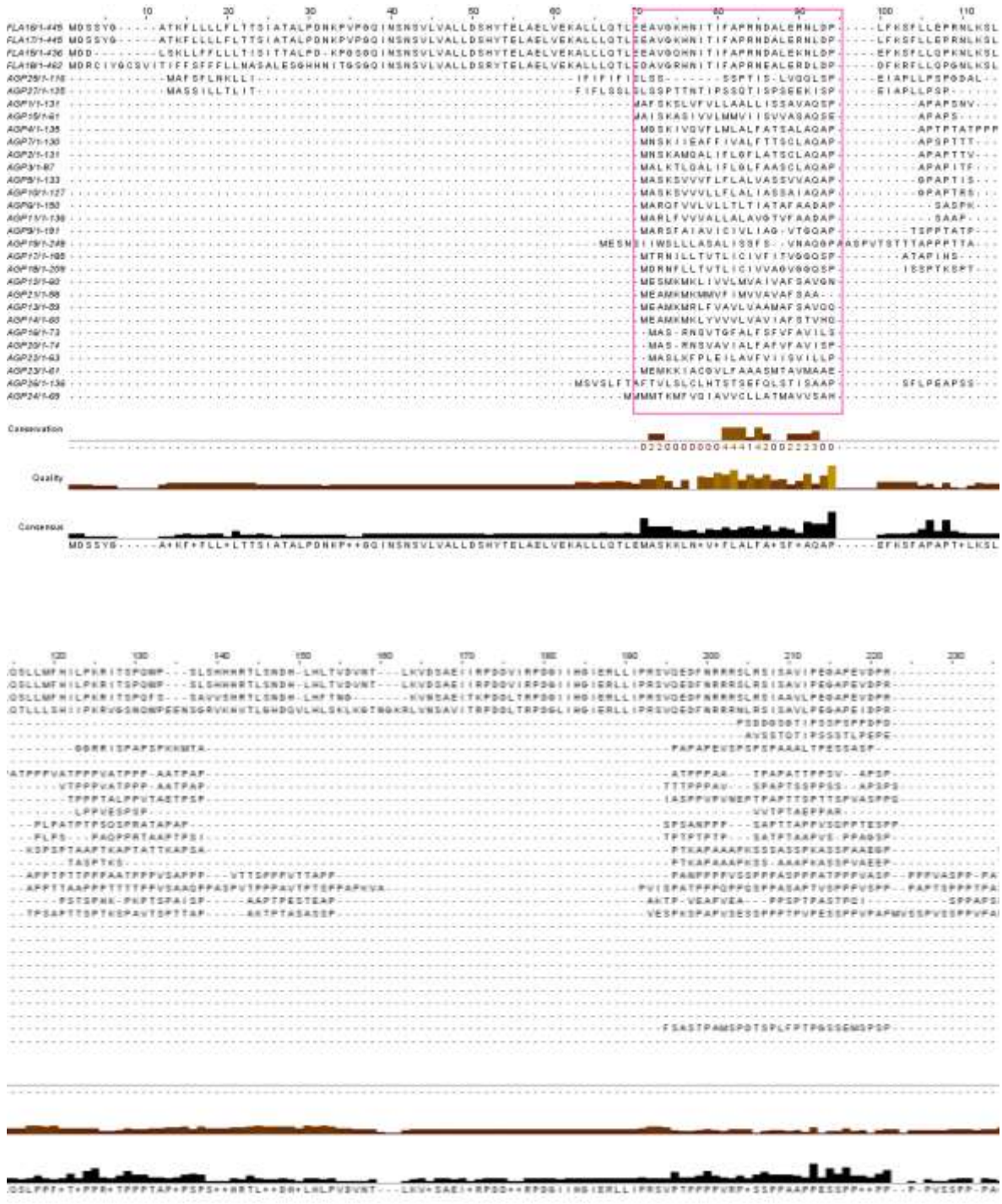
Supplemental figure 1 – Phylogenetic analysis of the AGP family in *A. thaliana*. To generate the phylogenetic tree for AGPs, the 3 blocks of most conserved amino acid sequences of AGPs coding sequences were aligned using Clustal W and manually edited using Jalview to reduce gaps. Neighbor-joining (NJ) 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).



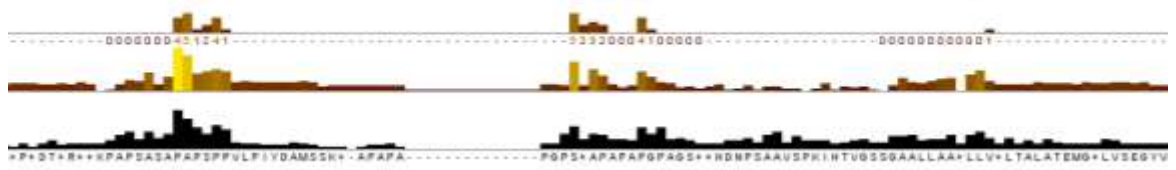
Supplemental figure 3 – The amino acid sequences of AGPs coding sequences aligned using Clustal W (Thompson *et al.*, 1994) and viewed using Jalview (Clamp *et al.*, 2004). The 3 conserved blocks are highlighted by the pink rectangles.



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240      230      220      210      200      190      180      170      160      150      140      130
---THRLKK- PSPA VPA GAPP LP IVDAMS - PPSLAPAPAPGPGGPRHFGGDAQVKDFHTLLRKYGGYEMADILVNLTLATEMGRRLVSEGVV
---THRLKK- PSPA VPA GAPP LP IVDAMS - PPSLAPAPAPGPGGPRHFGGDAQVKDFHTLLRKYGGYEMADILVNLTLATEMGRRLVSEGVV
---THRLKK- PPAI PPA GAPP LP IVDAMS - PPSLAPAPAPGPGGPRHFGGDAQVKDFHTLLRKYGGYEMADILVNLTLATEMGRRLVSEGVV
---THRLKK- TAUSVPAGSPF LP IESAMA - PPSLAPAPAPGPGGAKHFGGDAQVKDFHTLLRKYGGYEMADILVNLTLATEMGRRLVSEGVV
---TRDQVDFPPLAFSPFASFP- S- SPPPPPSGAPG- LLISL I I S G S F L A L -
---PSPFLADSPFASFP- S- SLASLSSGAPG- VFIYFVYAAVYCFSLRLLAVDAI
---PSPFLADSPFASFP- S- ALSFSAIISDSPTEARPPADGGAVEMKFASTGSSAVMLFAAVLVI
---ADPTASPPAPGSP- S- A I S A S F V E - A G V A A V A A L V F G S L R I -
---ADPTASPPAPGSP- S- TVSPK- SAQPSSDAS- PAPSAAF SNAFAQTAFASIMYAVLA
---ADPTASPPAPGSP- S- SVSPGELAPTPSDASA- PPNAAALTNKAFVVGSLVAAI IYAVVLA
---TDAPAPGPAQLTP- S- TSSPA- PPDQAA- DAPSAAWANKAFVGTAVVAAALYAVVLA
---CFPYSQRTHGGS- S- NSTN- RLTPDRUAN- NFPGR- FSS-
---APRTSSTSPGAPRT- S- NVPSDE- AQAQSPLSGSPNAAAVSRVSLVGTABAVVIAALLL
---LSSASPPAPPTG- S- LTPGGAPVAGPTGSGTPVDNNNAATLA- AGSLAGFVTVASLLL
VPEDDYSASSPDSAEAPTUSGP- S- PAPTSDSIS- AADGPG- DDP- TAESPK- S- SGAUTAKF SVVTVATVQFFFFSF
TPEDDYSAGSPDSAEAPTUSGP- S- PAPTSEADGPGSSDGPSSDGPAAASGPK- S- SGAATNFKLSIAGTVAAAGFFIFSL
TPPRV-ATPPPAPLASPPAQVP- S- APAPTTKPDSPEP- S- PDSPPPLPSSDAPSPSTDSISPAPEPT- DUNDDGNSASKMVSLLVPS- VLWVMI
SPPPAPASPPPAPASPPPAPVSP- S- PVDAPS I I S L P P A P A P A P T M M R E R K H K H R H M A -
PEAGTFSAPZ I P S A D V P A P A L T - K H K H K T K - K H T A P A P G - P A S E L L P P P A P P S E A P G P P S D A F S P - A A D D G S G A O M I S V V I G M - V G A A A I A W S L L V L A F -
PVASDPPAPVAAAPVADVPAPAPS- S- K H K H T K K S H K H Q A A P A - P A P A P I P P I P P G P P V L T D P Q G T A P A P S P N T B G G K A L B O L K G R A V U M L N T G L V I L T L L A M T A -
---VAQTEAPAPSP- S- SDAAMPVPALFAS- S- VVALASGTFP- S- VUGAVATAWAVLVMAF
---TAATVEAPAPSP- S- SDAAMPVPALFAS- S- VVALASGTFP- S-
---AAVEAPAPSP- S- SDAASLIPAFFAS- S- VATLAFGFLP- S-
---TAAVDAPAPSP- S- SDAASGTFPFFAS- S- VAMMFGFFP- S-
---LAAQSLAPAPAPT- S- SDGTSIDGIAVLL- S- MUVVALVLTVMPLDASSS- YEFF
---FAAQLAPAPAPT- S- SDGTSIDGIAVLL- S- MUVVALVLTVMPLDASSS- YTF
---LAAHSSAPAPAPT- S- SDGTSIDGIAVLL- S- MUVVALVLTVMPL
---CVGAPAPGPA- S- DAASAAIPALGSLVG- S- ASLVSLSFVYLH- S-
SBSIMPTIPSSLSP- S- PNPDAVTPDRLLEVPVQSPFLPASSEVGLVSSQLSLLLVLLMLLAFCSFP- S-
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LTVLAPNDEAMAKLTTDQLESPGAPGIMYYHI IPEYGTESMYNAVRRFGKVKYDLSLRFPHKVLAGEADGSSVNFSGHGGSSAYLFDPSIYTDGRI SVGGIDGVLFPKEETPATEIKPAAP
LTVLAPNDEAMAKLTTDQLESPGAPGIMYYHI IPEYGTESMYNAVRRFGKIRYDLSLRFPHKVLAGEADGSSVNFSGHGGSSAYLFDPSIYTDGRI SVGGIDGVLFPKEETPATEIKPAAP
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