SUPPLEMENTARY DATA

Fɪɢ. S1. Comparison of the NTα-Gal amino acid sequence with the sequences of six other plant α-Gals. Amino acids, which are completely conserved, are marked with asterisks, and the highly conserved amino acids are marked with dots or double dots; gaps left to improve the alignment are indicated with -. Numbers refer to amino acid residues at the end of the respective lines. Species' names are abbreviated at the left and are represented with accession numbers and percent conservation values: LEαGal = *Lycopersicon esculentum*, Q9SP05, 83%; CAαGal = *Coffea arabica*, Q5DUH8, 82%; VVαGal = *Vitis vinifera*, D7TXW5, 73%; OSαGal = *Oryza sativa*, Q9FXT4; PSαGal = *Picea sitchensis*, D5ADT9, 68%; ATαGal = *Arabidopsis thaliana*, Q8RX86, 73%.

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ntagal  ----------MPPTLKLLLWCCLCLCGVITTTYARPQLRNLIIADSNSTTSNAYIRRSLLSNGLGRTPQMGWSSWNHFACNIEEKMIRETADAMVSTGLASLGYEYVN-IDDCWAELNRDSQGNMVPKSSTFPSGIKALADYVHG 134
Q9SP05  ----------MSSTSPLLLWCCLCLS--LATVYARLQPRNLIVN-SN-LSVNEFNRRNLLGNGLGQTPQMGWSSWNHFGCNIDENIIKGTADAMVHTGLASLGYEYIN-IDDCWAEANRDSQGNMVAKGSTFPSGIKALADYVHG 130
Q5DUH8  MAAAYYYLFSSKKATQKLVLRASLLMLLCFLTVENVGASARRMVKS--PGTEDYTRRSLLANGLGLTPPMGWNSWNHFSCNLDEKLIRETADAMASKGLAALGYKYIN-LDDCWAELNRDSQGNLVPKGSTFPSGIKALADYVHS 142
D7TXW5  -----------------MAHDQISIPLLLFLICTLSAATVNHATLTGKFRENGAMKRKLLDNGPGQTPQMGWNSYNHFPCKLSEELIHQTADAMVSTGLSALGYKYINLVDDCWAELNRDSKGNLVPKASIFPSGMKALADYVHS 128
Q9FXT4  ----MARASSSSSPPSPRLLLLLLLVAVAATLLPEAAALGNFTAESRGARWRSRRARRRAFENGLGRTPQMGWNSWNHFYCGINEQIIRETADALVNTGLAKLGYQYVN-IDDCWAEYSRDSQGNFVPNRQTFPSGIKALADYVHA 140
D5ADT9  -----------------MKMVSVFLVALFLIGFWDQ------------TNGGRPIHRHLSSNGLGKTPQMGWNSWNHFGCNIDENIIRGTADAMVSTGLSKVGYEYVN-IDDCWGELNRDAQGNLVAKASTFPSGMKALVDYVHS 115
Q8RX86  -----------------MVLLSFSLRFIAFTLT---------ITLT--QIADGFQSRMLMNNGLALSPQMGWNSWNHFQCNINETLIKQTADAMVSSGLSAIGYKYIN-IDDCWGELKRDSQGSLVAKASTFPSGIKALSDYVHS 116
                                :              *    **  .  :* ***.*-*** * .:* -*: ****:. .**- -**-*-* -****.* .** ..*-.* . .  ****-*** ****.

ntagal  KGLKLGIYSDAGSQTCSKQMPGSLGHEEQDAKTFASWGVDYLKYDNCNNENRSPRERYPIMSKALQNSGRAIFYSLCEWGDDDPATWASSVGNSWRTTGDISDNWDSMTSRADMNDKWASYAGPGGWNDPDMLEVGNGGMTTAEY 279
Q9SP05  KGLKLGVYSDAGTQTCSKQMPGSLGHEEQDAKTFASWGVDYLKYDNCTNEDRSPRERYPIMSNALQNSGRAIFYSMCEWGDDNPATWASSVGNSWRTTGDITDDWNSMTSRADLNDQWASYAGPGGWNDPDMLEVGNGGMSFGEY 275
Q5DUH8  KGLKLGIYSDAGTQTCSKTMPGSLGHEEQDAKTFASWGVDYLKYDNCNDNNISPKERYPIMSKALLNSGRSIFFSLCEWGDEDPATWAKEVGNSWRTTGDIDDSWSSMTSRADMNDKWASYAGPGGWNDPDMLEVGNGGMTTTEY 287
D7TXW5  KGLKIGIYADAGTLTCSKTMPGSLNYEEQDANTFASWGIDYLKYDNCHNNGLSPQERYSNMSKALLNTGRPIFYSLCEWGQDNPATWASSIGNSWRTTGDIKDTWESMTSHADLNDVWASYAGPGGWNDPDMLEVGNGGMSTEEY 273
Q9FXT4  KGLKLGIYSDAGSQTCSNKMPGSLDHEEQDVKTFASWGVDYLKYDNCNDAGRSVMERYTRMSNAMKTYGKNIFFSLCEWGKENPATWAGRMGNSWRTTGDIADNWGSMTSRADENDQWAAYAGPGGWNDPDMLEVGNGGMSEAEY 285
D5ADT9  KGLKLGIYSDAGYYTCSKTMPGSLGYEEQDAKTFASWGIDYLKYDNCFNNGTNPQERYPKMSEALSNAGCPIFYSMCEWGDQNPATWGPKIANSWRTTGDIQDNWDSITSRADQNDQWAAYAGPGGWNDPDMLEVGNGNMSTVEY 260
Q8RX86  KGLKLGIYSDAGTLTCSQTMPGSLGHEEQDAKTFASWGIDYLKYDNCENTGTSPRERYPKMSKALLNSGRSIFFSLCEWGQEDPATWAGDIGNSWRTTGDIQDNWKSMTLIADQNDRWASYARPGSWNDPDMLEVGNGGMTKEEY 261
        ****-*-*-***  ***- ***** -**** -******-******** : . . *** **-*: - * **-*-**** .:-****. -: ********* * * *-* ** ** **-** ** -************ *:- **

ntagal  RSHFSIWALAKAPLIIGCDLRSMDQTAHEILSNKEVIAVNQDKLGVQGKKVKQNGDLEVWAGPLSGKRLAMVLWNRSSSKADITAYWSDIGLDSSTVVDARDLWAHSTKGS-VKGQLSASIDSHDCRMYVLTPTK- 413
Q9SP05  RSHFSIWALVKAPLIIGCDLRSMDNTAHDILSNPEVIAVNQDKLGVQGKKVKQYGDLEVWAGPLSGKRVAVVLWNRGSYKADITAYWSDIGLDYSTLVDARDLWAHSTKGS-VKGQLSASVESHDCSMYVLTPKK- 409
Q5DUH8  RSHFSIWALAKAPLLIGCDIRSIDGATFQLLSNAEVIAVNQDKLGVQGKKVKTYGDLEVWAGPLSGKRVAVALWNRGSSTATITAYWSDVGLPSTAVVNARDLWAHSTEKS-VKGQISAAVDAHDSKMYVLTPQ- 420
D7TXW5  RSHFSIWALAKAPLLIGCDIRSMDNETFELLSNKEVIEVNQDKLGAQGKKVKKTGDLEVWSGPLSDNRVAVVLWNRESSEATIIADWSDIGLNSSAVVDARDLWTHSTIYS-IRHQLKATVEAHACKMYALTPH- 406
Q9FXT4  RSHFSIWALAKAPLLIGCDVRSMSQQTKNILSNSEVIAVNQDSLGVQGKKVQSDNGLEVWAGPLSNNRKAVVLWNRQSYQATITAHWSNIGLAGSVAVTARDLWAHSSFAA--QGQISASVAPHDCKMYVLTPN- 417
D5ADT9  RSHFSIWALMKAPLLIGCDIRSATSETLEILSNSEVINVNQDPLGVQGKKVSQQGDLEVWAGPLSNNRVAVILWNRSTSQDAITANWGAIGLPSDAIVQARDLWAHSYLPSDLQGSLTSTVDSHDVKMYILTLSSG 396
Q8RX86  MSHFSIWALAKAPLLIGCDLRSMDKVTFELLSNKEVIAVNQDKLGIQGKKVKKEGDLEVWAGPLSKKRVAVILWNRGSASANITARWAEIGLNSSDIVNARDLWEHSTYSC-VKKQLSALVEPHACKMYTLTRRKA 396
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