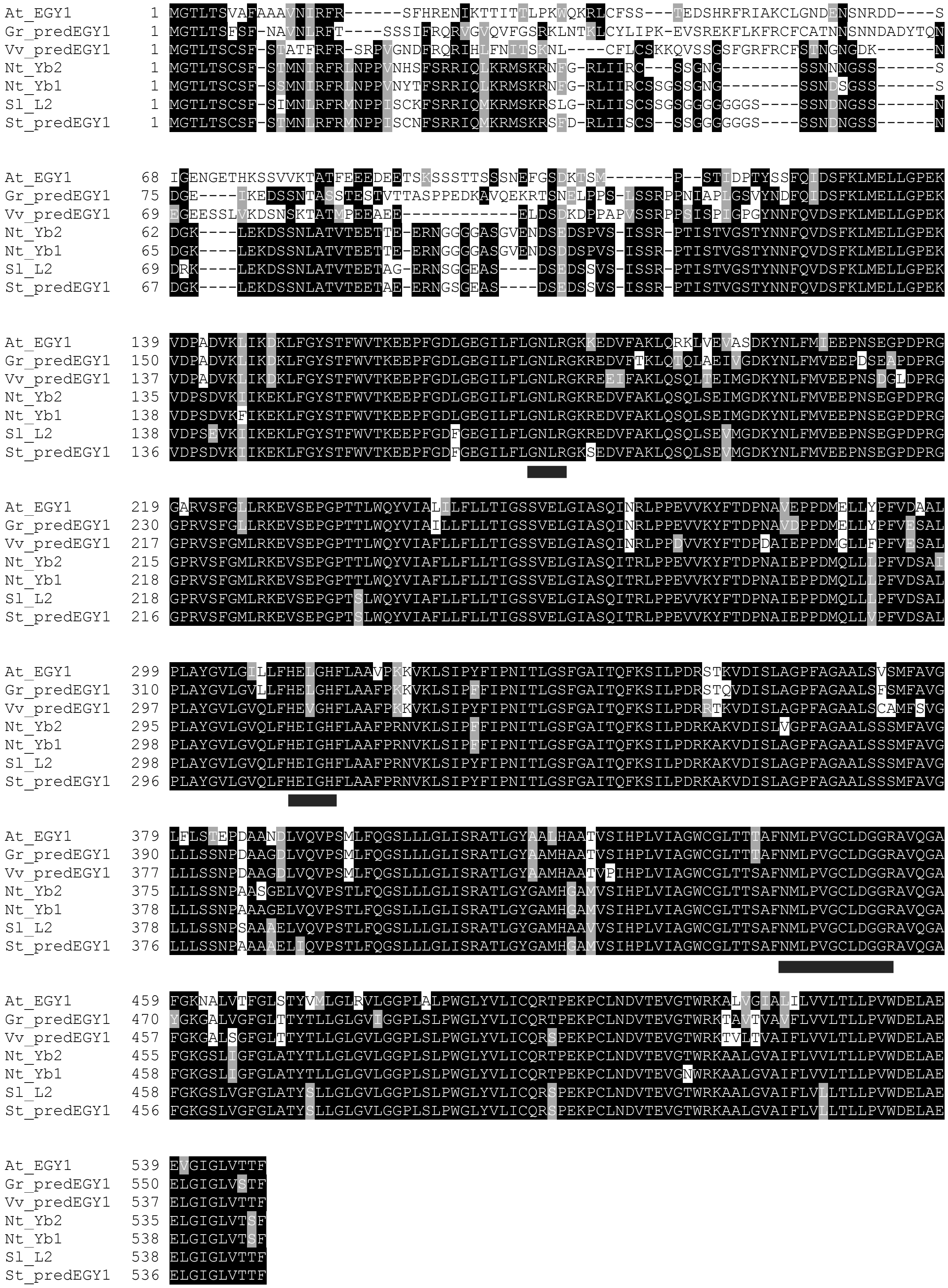

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At_EGY1        1 MGTLTSVAFAAAVNIRFR------SFHRENIKTTITTLPKWQKRLCFSS---TEDSHRFRIAKCLGNDENSNRDD----S
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Vv_predEGY1    1 MGTLTSCSF-STATFRFR-SRPVGNDFRQRIHLFNITSKNL----CFLCSKKQVSSGSFGRFRCFSTNGNGDK------N
Nt_Yb2         1 MGTLTSCSF-STMNIRFRLNPPVNHSFSRRIQLKRMSKRNFG-RLIIRC---SSGNG--------SSNNNGSS------S
Nt_Yb1         1 MGTLTSCSF-SSMNIRFRLNPPVNYTFSRRIQLKRMSKRNFG-RLIIRCSSGSSGNG--------SSNDSGSS------S
Sl_L2          1 MGTLTSCSF-SIMNLRFRMNPPISCKFSRRIQMKRMSKRSLG-RLIISCSSGSGGGGGGS----SSNDNGSS------N
St_predEGY1    1 MGTLTSCSF-STMNLRFRMNPPISCNFSRRIQMKRMSKRSFD-RLIISCS--SSGGGGGS----SSNDNGSS------N

At_EGY1       68 IGENGETHKSSVVKTATFEEEDEETSKSSSTTSSSNEFGSDKTSM-------P--STIDPTYSSFQIDSFKLMELLGPEK
Gr_predEGY1   75 DGE----IKEDSSNTASSTESTVTTASPPEDKAVQEKRTSNELPPS-LSSRPPNIAPLGSVYNDFQIDSFKLMELLGPEK
Vv_predEGY1   69 EGEESSLVKDSNSKTATMPEEAEE------------ELDSDKDPPAPVSSRPPSISPIGPGYNNFQVDSFKLMELLGPEK
Nt_Yb2        62 DGK----LEKDSSNLATVTEETTE-ERNGGGASGVENDSEDSPVS-ISSR-PTISTVGSTYNNFQVDSFKLMELLGPEK
Nt_Yb1        65 DGK----LEKDSSNLATVTEETTE-ERNGGGASGVENDSDDSPVS-ISSR-PTISTVGSTYNNFQVDSFKLMELLGPEK
Sl_L2         69 DRK----LEKDSSNLATVTEETAG-ERNSGGEAS----DSEDSSVS-ISSR-PTISTVGSTYNNFQVDSFKLMELLGPEK
St_predEGY1   67 DGK----LEKDSSNLATVTEETAE-ERNGSGEAS----DSEDSSVS-ISSR-PTISTVGSTYNNFQVDSFKLMELLGPEK

At_EGY1      139 VDPADVKLIKDKLFGYSTFWVTKEEPFGDLGEGILFLGNLRGKKEDVFAKLQRKLVEVASDKYNLFMIEEPNSEGPDPRG
Gr_predEGY1  150 VDPADVKLIKDKLFGYSTFWVTKEEPFGDLGEGILFLGNLRGKREDVFTKLQTQLAEIVGDKYNLFMVEEPDSEAPDPRG
Vv_predEGY1  137 VDPADVKLIKDKLFGYSTFWVTKEEPFGDLGEGILFLGNLRGKREEIFAKLQSQLTEIMGDKYNLFMVEEPNSDGLDPRG
Nt_Yb2       135 VDPSDVKIIKEKLFGYSTFWVTKEEPFGDLGEGILFLGNLRGKREDVFAKLQSQLSEIMGDKYNLFMVEEPNSEGPDPRG
Nt_Yb1       138 VDPSDVKFIKEKLFGYSTFWVTKEEPFGDLGEGILFLGNLRGKREDVFAKLQSQLSEIMGDKYNLFMVEEPNSEGPDPRG
Sl_L2        138 VDPSEVKIIKEKLFGYSTFWVTKEEPFGDFGEGILFLGNLRGKREDVFAKLQSQLSEVMGDKYNLFMVEEPNSEGPDPRG
St_predEGY1  136 VDPSDVKIIKEKLFGYSTFWVTKEEPFGDFGEGILFLGNLRGKSEDVFAKLQSQLSEVMGDKYNLFMVEEPNSEGPDPRG

At_EGY1      219 GARVSFGLLRKEVSEPGPTTLWQYVIALILFLLTIGSSVELGIASQINRLPPEVVKYFTDPNAVEPPDMELLYPFVDAAL
Gr_predEGY1  230 GPRVSFGLLRKEVSEPGPTTLWQYVIAILLFLLTIGSSVELGIASQINRLPPEVVKYFTDPNAVDPPDMELLYPFVESAL
Vv_predEGY1  217 GPRVSFGMLRKEVSEPGPTTLWQYVIAFLLFLLTIGSSVELGIASQINRLPPDVVKYFTDPDAIEPPDMGLLFPFVESAL
Nt_Yb2       215 GPRVSFGMLRKEVSEPGPTTLWQYVIAFLLFLLTIGSSVELGIASQITRLPPEVVKYFTDPNAIEPPDMQLLLPFVDSAI
Nt_Yb1       218 GPRVSFGMLRKEVSEPGPTTLWQYVIAFLLFLLTIGSSVELGIASQITRLPPEVVKYFTDPNAIEPPDMQLLLPFVDSAL
Sl_L2        218 GPRVSFGMLRKEVSEPGPTSLWQYVIAFLLFLLTIGSSVELGIASQITRLPPEVVKYFTDPNAIEPPDMQLLLPFVDSAL
St_predEGY1  216 GPRVSFGMLRKEVSEPGPTSLWQYVIAFLLFLLTIGSSVELGIASQITRLPPEVVKYFTDPNAIEPPDMQLLVPFVDSAL

At_EGY1      299 PLAYGVLGILLFHELGHFLAAVPKKVKLSIPYFIPNITLGSFGAITQFKSILPDRSTKVDISLAGPFAGAALSVSMFAVG
Gr_predEGY1  310 PLAYGVLGVLLFHELGHFLAAFPKKVKLSIPFFIPNITLGSFGAITQFKSILPDRSTQVDISLAGPFAGAALSFSMFAVG
Vv_predEGY1  297 PLAYGVLGVQLFHEVGHFLAAFPKKVKLSIPYFIPNITLGSFGAITQFKSILPDRRTKVDISLAGPFAGAALSCAMFSVG
Nt_Yb2       295 PLAYGVLGVQLFHEIGHFLAAFPRNVKLSIPFFIPNITLGSFGAITQFKSILPDRKAKVDISLVGPFAGAALSSSMFAVG
Nt_Yb1       298 PLAYGVLGVQLFHEIGHFLAAFPRNVKLSIPFFIPNITLGSFGAITQFKSILPDRKAKVDISLAGPFAGAALSSSMFAVG
Sl_L2        298 PLAYGVLGVQLFHEIGHFLAAFPRNVKLSIPYFIPNITLGSFGAITQFKSILPDRKAKVDISLAGPFAGAALSSSMFAVG
St_predEGY1  296 PLAYGVLGVQLFHEIGHFLAAFPRNVKLSIPYFIPNITLGSFGAITQFKSILPDRKAKVDISLAGPFAGAALSSSMFAVG

At_EGY1      379 LFLSTEPDAANDLVQVPSMLFQGSLLLGLISRATLGYAALHAATVSIHPLVIAGWCGLTTTAFNMLPVGCLDGGRAVQGA
Gr_predEGY1  390 LLLSSNPDAAGDLVQVPSMLFQGSLLLGLISRATLGYAAMHAATVSIHPLVIAGWCGLTTTAFNMLPVGCLDGGRAVQGA
Vv_predEGY1  377 LLLSSNPDAAGDLVQVPSMLFQGSLLLGLISRATLGYAAMHAATVPIHPLVIAGWCGLTTSAFNMLPVGCLDGGRAVQGA
Nt_Yb2       375 LLLSSNPAASGELVQVPSTLFQGSLLLGLISRATLGYGAMHGAMVSIHPLVIAGWCGLTTSAFNMLPVGCLDGGRAVQGA
Nt_Yb1       378 LLLSSNPAAAGELVQVPSTLFQGSLLLGLISRATLGYGAMHGAMVSIHPLVIAGWCGLTTSAFNMLPVGCLDGGRAVQGA
Sl_L2        378 LLLSSNPSAAAELVQVPSTLFQGSLLLGLISRATLGYGAMHAAVVSIHPLVIAGWCGLTTSAFNMLPVGCLDGGRAVQGA
St_predEGY1  376 LLLSSNPAAAAELIQVPSTLFQGSLLLGLISRATLGYGAMHGAMVSIHPLVIAGWCGLTTSAFNMLPVGCLDGGRAVQGA

At_EGY1      459 FGKNALVTFGLSTYVMLGLRVLGGPLALPWGLYVLICQRTPEKPCLNDVTEVGTWRKALVGIALILVVLTLLPVWDELAE
Gr_predEGY1  470 YGKGALVGFGLTTYTLLGLGVIGGPLSLPWGLYVLICQRTPEKPCLNDVTEVGTWRKTAVTVAVFLVVLTLLPVWDELAE
Vv_predEGY1  457 FGKGALSGFGLTTYTLLGLGVLGGPLSLPWGLYVLICQRSPEKPCLNDVTEVGTWRKTVLTVAIFLVVLTLLPVWDELAE
Nt_Yb2       455 FGKGSLIGFGLATYTLLGLGVLGGPLSLPWGLYVLICQRTPEKPCLNDVTEVGTWRKAALGVAIFLVVLTLLPVWDELAE
Nt_Yb1       458 FGKGSLIGFGLATYTLLGLGVLGGPLSLPWGLYVLICQRTPEKPCLNDVTEVGNWRKAALGVAIFLVVLTLLPVWDELAE
Sl_L2        458 FGKGSLVGFGLATYSLLGLGVLGGPLSLPWGLYVLICQRSPEKPCLNDVTEVGTWRKAALGVAIFLVLLTLLPVWDELAE
St_predEGY1  456 FGKGSLVGFGLATYSLLGLGVLGGPLSLPWGLYVLICQRSPEKPCLNDVTEVGTWRKAALGVAIFLVLLTLLPVWDELAE

At_EGY1      539 EVGIGLVTTF
Gr_predEGY1  550 ELGIGLVSTF
Vv_predEGY1  537 ELGIGLVTTF
Nt_Yb2       535 ELGIGLVTSF
Nt_Yb1       538 ELGIGLVTSF
Sl_L2        538 ELGIGLVTTF
St_predEGY1  536 ELGIGLVTTF
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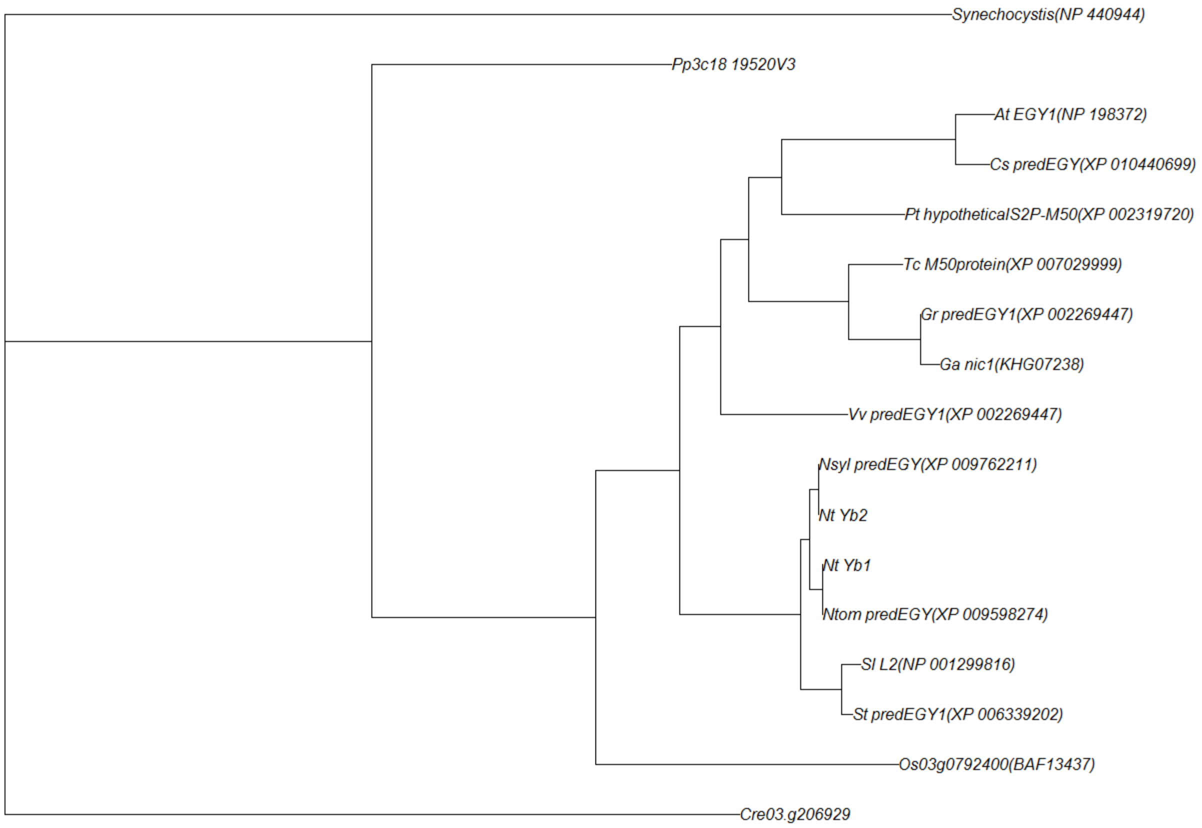
Amino acid alignments of Yb related proteins. Alignments were generated using MUSCLE. Conserved nucleotides are indicated by shaded squares. The three conserved domains, GNLR, HEXXH, and NPDG are underlined with black lines. Accession numbers are as follows: *Arabidopsis* EGY1 (NP_198372), *Gossypium raimondii* predicted EGY1 (XP_012492480), *Vitis vinifera* predicted EGY1 (XP_002269447), *S. lycopersicum* L2 (NP_001299816), *S. tuberosum* predicted EGY1 (XP_006339202).



Phylogeny of Yb_1 and Yb_2 related proteins. The dendrogram was constructed using the maximum likelihood method. GenBank accession number are given for each branch except for the Cre03.g206929 and Pp3c18_19520V3, which are based on annotations of the *Chlamydomonas reinhardtii* and *Physcomitrella patens* genomes available through the Phytozome database (www.phytozome.net).