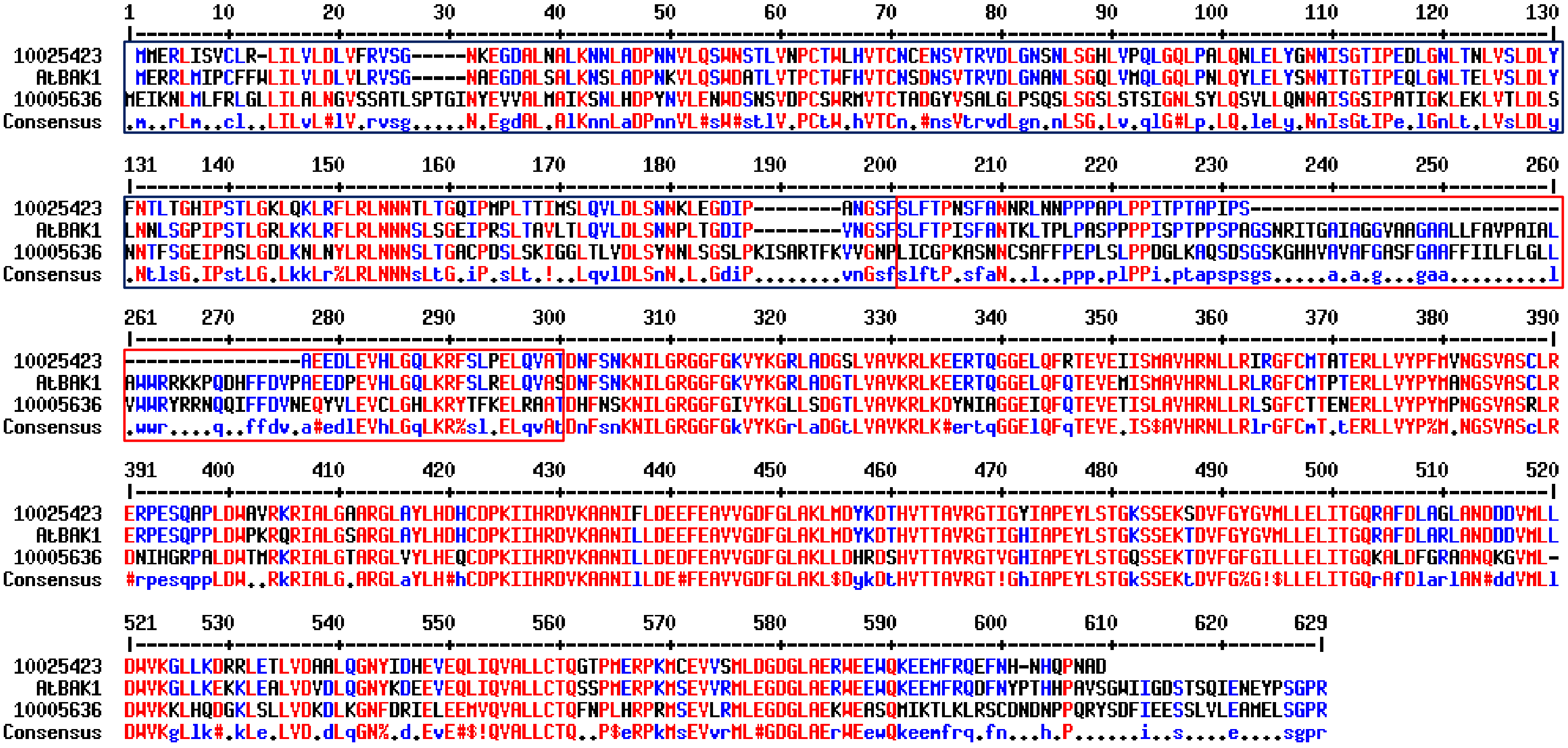

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           1       10        20        30        40        50        60        70        80        90       100       110       120       130
           |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  10025423  MMERLISVCLR-LILVLDLVFRVSG-----NKEGDALNALKNNLADPNNVLQSWNSTLVNPCTWLHVTCNCENSVTRVDLGNSNLSGHLVPQLGQLPALQNLELYGNNISGTIPEDLGNLTNLVSLDLY
    AtBAK1  MERRLMIPCFFWLILVLDLVLRVSG-----NAEGDALSALKNSLADPNKVLQSWDATLVTPCTWFHVTCNSDNSVTRVDLGNANLSGQLVMQLGQLPNLQYLELYSNNITGTIPEQLGNLTELVSLDLY
  10005636 MEIKNLMLFRLGLLILALNGVSSATLSPTGINYEVVALMAIKSNLHDPYNVLENWDSNSVDPCSWRMVTCTADGYVSALGLPSQSLSGSLSTSIGNLSYLQSVLLQNNAISGSIPATIGKLEKLVTLDLS
 Consensus .m..rLm..cl..LILvL#lV.rvsg.....N.EgdAL.AlKnnLaDPnnVL#sW#stlV.PCtW.hVTCn.#nsVtrvdLgn.nLSG.Lv.qlG#Lp.LQ.leLy.NnIsGtIPe.lGnLt.LVsLDLy

           131    140       150       160       170       180       190       200       210       220       230       240       250       260
           |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  10025423 FNTLTGHIPSTLGKLQKLRFLRLNNNTLTGQIPMPLTTIMSLQVLDLSNNKLEGDIP--------ANGSFSLFTPNSFANNRLNNPPPAPLPPITPTAPIPS----------------------------
    AtBAK1 LNNLSGPIPSTLGRLKKLRFLRLNNNSLSGEIPRSLTAVLTLQVLDLSNNPLTGDIP--------VNGSFSLFTPISFANTKLTPLPASPPPPISPTPPSPAGSNRITGAIAGGVAAGAALLFAVPAIAL
  10005636 NNTFSGEIPASLGDLKNLNYLRLNNNSLTGACPDSLSKIGGLTLVDLSYNNLSGSLPKISARTFKVVGNPLICGPKASNNCSAFFPEPLSLPPDGLKAQSDSGSKGHHVAVAFGASFGAAFFIILFLGLL
 Consensus .NtlsG.IPstLG.LkkLr%LRLNNNsLtG.iP.sLt.!..LqvlDLSnN.L.GdiP........vnGsfslftP.sfaN..l..ppp.plPPi.ptapspsgs.....a.a.g...gaa.........l

           261    270       280       290       300       310       320       330       340       350       360       370       380       390
           |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  10025423 ----------------AEEDLEVHLGQLKRFSLPELQVATDNFSNKNILGRGGFGKVYKGRLADGSLVAVKRLKEERTQGGELQFRTEVEIISMAVHRNLLRIRGFCMTATERLLVYPFMVNGSVASCLR
    AtBAK1 AWWRRKKPQDHFFDVPAEEDPEVHLGQLKRFSLRELQVASDNFSNKNILGRGGFGKVYKGRLADGTLVAVKRLKEERTQGGELQFQTEVEMISMAVHRNLLRLRGFCMTPTERLLVYPYMANGSVASCLR
  10005636 VWWRYRRNQQIFFDVNEQYVLEVCLGHLKRYTFKELRAATDHFNSKNILGRGGFGIVYKGLLSDGTLVAVKRLKDYNIAGGEIQFQTEVETISLAVHRNLLRLSGFCTTENERLLVYPYMPNGSVASRLR
 Consensus .wwr....q..ffdv.a#edlEVhLGqLKR%sl.ELqvAtDnFsnKNILGRGGFGkVYKGrLaDGtLVAVKRLK#ertqGGElQFqTEVE.IS$AVHRNLLRlrGFCmT.tERLLVYP%M.NGSVAScLR

           391    400       410       420       430       440       450       460       470       480       490       500       510       520
           |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  10025423 ERPESQAPLDWAVRKRIALGAARGLAYLHDHCDPKIIHRDVKAANIFLDEEFEAVVGDFGLAKLMDYKDTHVTTAVRGTIGYIAPEYLSTGKSSEKSDVFGYGVMLLELITGQRAFDLAGLANDDDVMLL
    AtBAK1 ERPESQPPLDWPKRQRIALGSARGLAYLHDHCDPKIIHRDVKAANILLDEEFEAVVGDFGLAKLMDYKDTHVTTAVRGTIGHIAPEYLSTGKSSEKTDVFGYGVMLLELITGQRAFDLARLANDDDVMLL
  10005636 DNIHGRPALDWTMRKRIALGTARGLVYLHEQCDPKIIHRDVKAANILLDEDFEAVVGDFGLAKLLDHRDSHVTTAVRGTVGHIAPEYLSTGQSSEKTDVFGFGILLLELITGQKALDFGRAANQKGVML-
 Consensus #rpesqppLDW..RkRIALG.ARGLaYLH#hCDPKIIHRDVKAANIlLDE#FEAVVGDFGLAKL$DykDtHVTTAVRGT!GhIAPEYLSTGkSSEKtDVFG%G!$LLELITGQrAfDlarlAN#ddVMLl

           521    530       540       550       560       570       580       590       600       610       620      629
           |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+--------|
  10025423 DWVKGLLKDRRLETLVDAALQGNYIDHEVEQLIQVALLCTQGTPMERPKMCEVVSMLDGDGLAERWEEWQKEEMFRQEFNH-NHQPNAD
    AtBAK1 DWVKGLLKEKKLEALVDVDLQGNYKDEEVEQLIQVALLCTQSSPMERPKMSEVVRMLEGDGLAERWEEWQKEEMFRQDFNYPTHHPAVSGWIIGDSTSQIENEYPSGPR
  10005636 DWVKKLHQDGKLSLLVDKDLKGNFDRIELEEMVQVALLCTQFNPLHRPRMSEVLRMLEGDGLAEKWEASQMIKTLKLRSCDNDNPPQRYSDFIEESSLVLEAMELSGPR
 Consensus DWVKgLlk#.kLe.LVD.dLqGN%.d.EvE#$!QVALLCTQ..P$eRPkMsEVvrML#GDGLAErWEewQkeemfrq.fn...h.P......i..s....e....sgpr
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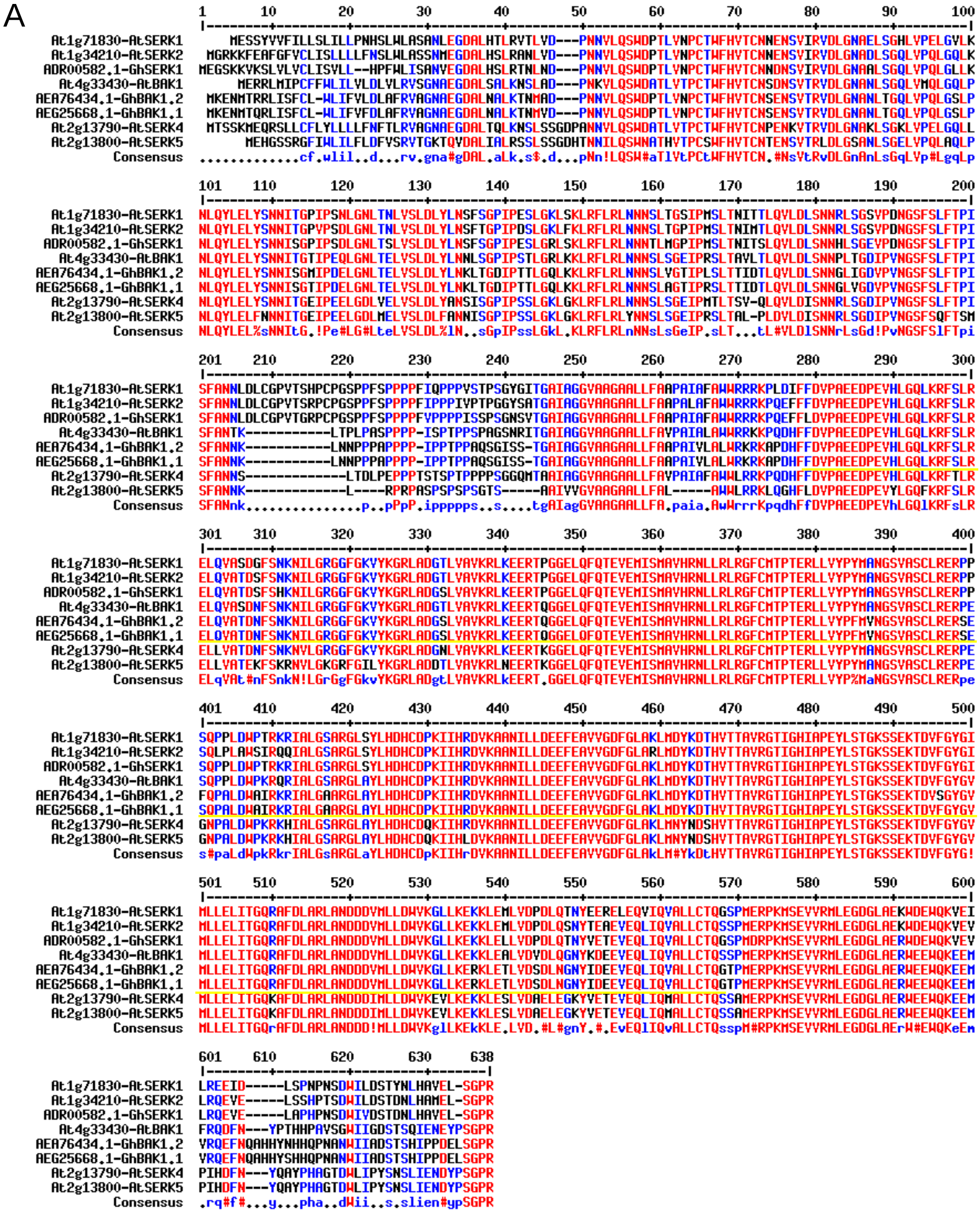
Figure S1. Sequence alignment of *Arabidopsis* AtBAK1 with *G. raimondii* SERK 10025423 and 10005636. The amino acid sequences were used for the alignment. The sequences squared in blue are LRR domain and the sequences squared in red conserved are transmembrane and juxtamembrane domains. The alignment was performed using Multalin website (http://multalin.toulouse.inra.fr/multalin/) with a hierarchical clustering approach.



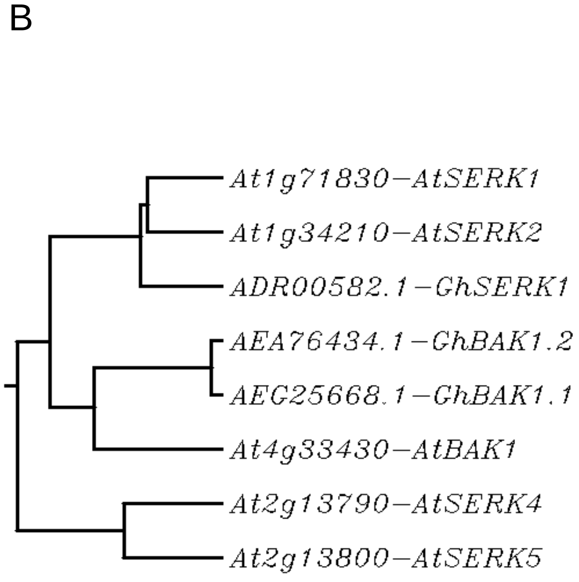


Figure S2. Sequence alignment (A) and phylogenetic analysis (B) of *Arabidopsis* SERK (AtSERK) and *G. hirsutum* SERK (GhSERK) family members. The amino acid sequences were used for the alignment. The alignment was performed using Multalin website (http://multalin.toulouse.inra.fr/multalin/) with a hierarchical clustering approach, and the phylogenetic tree was constructed using CLUSTALW and rooted phylogenetic tree (http://www.genome.jp/tools/clustalw/). AEA76434.1 was originally named as GhSERK2. The nucleotide sequence in *pTRV2-BAK1* vector corresponds to the residues that are underlined in yellow (A), which are almost identical between GhBAK1.1 and GhBAK1.2.