

Supplementary Figure S3. Amino acid sequence alignment of F2KPs from various plant species. The mutation position of Seolgaeng is highlighted in color. Bradi, *Brachypodium distachyon*; GRMZM, *Zea mays*; GSVIVP, *Vitis vinifera*; Os, *Oryza sativa*; Sb, *Sorghum bicolor*.

GSVIVP00024699001	-----MKFLFLI--FKRLPNF	14
LOC_0s03g18310	-----MAAAARSSGGMSDQLFVSIKLECPRL	26
Seolgaeng	-----MAAAARSSGGMSDQLFVSIKLECPRL	26
Bradi1g65420	-----MATAASSGGVPDHLFVSVKLESPRL	25
GRMZM5G824405	-----MASSGGISDQLFVSVKLESPHL	22
Sb01g038340	-----MASSGGISDQLFVSVKLESPRL	22
GRMZM2G021846	MGTSGSKGIDGVGAVSGVGAGAAGLGGVGAGDGGEGAAAEAWHGGAQLYVSLKMNENAL I	60
Sb09g004780	MGTSGSKSIDGVGAVSGVGAAAAGLGG--AGGEGGEGGAAEAWHGGAQLYVSLKMNENAE I	58
LOC_0s05g07130	MGTSGSKGIDGVGGVGGGAA--GLGGGEAGDGGGGVGGAAASRSHHGGAQLYVSLKMNENAR I	59
Bradi2g34580	MGTSGSKGMDGVGGVGAAAA--AGGAG--IQDEGVDGAGMESWHHGGAQLYVSLKMNENAR I	57
GSVIVP00024699001	SSLNMAPTLPCNHPLC-----YLLLLLLLLLKPVSSY	46
LOC_0s03g18310	AEMGLVPHVFGSHPVAGAWDPSKALLMEQEEAALWGLSCI VPSHRETLDFKFLKPKDNS	86
Seolgaeng	AEMGLVPHVFGSHPVAGAWDPSKALLMEQEEAALWGLSCI VPSHRETLDFKFLKPKDNS	86
Bradi1g65420	AALVFAPHLFGSHPVAGSWDPSKALPMERVAASIWELSCVLP SQHETLDFKFLVLPKGDNS	85
GRMZM5G824405	AELDLAPHLFGSHPVAGSWDPCKALPLERAATAVWEFSCVVP SQHESLDFKFLVLPKRGDN	82
Sb01g038340	AELDLAPHLFGSHPVAGSWDPCKALPLERAATSVWEFSCVVP SQHESLDFKFLVLPKREDDNS	82
GRMZM2G021846	-SGDLVPHVYGSEPI IGTWDP SRALAMERELASMMWLSFVVPD HETLDFKFLKPKDAE	119
Sb09g004780	-SGDLVPHVYGSEPI IGTWDP SRALAMERELASMMWLSFVVPD HETLDFKFLKPKDAE	117
LOC_0s05g07130	-TGDLPVHYGSEPI IGSWD PARALAMERELASMMWLSFVVPD HETLDFKFLKPKDAD	118
Bradi2g34580	-IGDLVPHVYGSEPI IGSWD PARALAMERELASMMWLSFVVPD HETLYFKFLKPKDAE	116
GSVIVP00024699001	AQTS---G---KFSLGSSLTAQKNSFWASPSGDFAFGFQQI GNGGFLLAI WFNKVPEKTI	101
LOC_0s03g18310	SHCI VEEGPDRSLVCGSNEVEIRNALFKFNDETGVVECKIFVETEL-----SPFDLAA	140
Seolgaeng	SHCI VEEGPDRSLVCGSNEVEIRNALFKFNDETGVVECKIFVETEL-----SPFDLAA	140
Bradi1g65420	SECI VEEGPNRQLCCGSNKVEMTGAVFKLSEKD-ELECKVWVETEML-----SPFDLAA	138
GRMZM5G824405	PQYI IEEGPNRPLGCQRNEFEMGNALFKLNEGKEVLECKVQVETEML-----SPIDLAA	136
Sb01g038340	SQYI IEEGPNRPLGCQRNEFEMRTAVFKLNEGKEVLECKVQIETEML-----SPFDLAA	136
GRMZM2G021846	TPCI IEEGPTRLLTGGMLEGDVRVALFKLNGDDEVLEFGVVNKADLV-----SPLELAA	173
Sb09g004780	TPCI IEEGPTRLLTGGMLEGDVRVALFKLNGDDEVLEFRVFNKADLV-----SPLELAA	171
LOC_0s05g07130	TPCI IEEGPTRHLTGGMLEGDVRIAWFKMNGDHETLEFRVFNKADIV-----SPDLAA	172
Bradi2g34580	TPCV IEEGPTRLLTGGMLEGDVRVANFRLNGDDEVLEFRVFNKADIV-----SPLELAA	170
GSVIVP00024699001	IWSANSDNPKPRGSKVE---LTTDGEFI-----LNDQKGKQMMKADLIGPGVAYAA	149
LOC_0s03g18310	SWKAHQEHLQPR-VRGAHDVIMNADSES-----	168
Seolgaeng	SWKAHQEHLQPR-VRGAHDVIMNADSES-----	168
Bradi1g65420	SWRAHQENLQPSKVRGTVDVMMNAETESRTKNGFASGLELDLEKYVVPTPNMGAGVYAA	198
GRMZM5G824405	SWRAHQEYFQPSRVRGTHDVTINPGLEGRAKNGFASGLELDLDKYVVPTPNMGSGVYAA	196
Sb01g038340	SWRAHQEYFQPSRVRGTHDVTINPGLEGRAKNGFASGLELDLEKYVVPTPNMGSGVYAA	196
GRMZM2G021846	SWRVYKENFQPSKVRGIPDISINVTPTNGAEEGSAATLELDLEHYVVPSPPTAPPNGYAA	233
Sb09g004780	SWRVYKENFQPSKVRGIPDISINVTPTNATEEGSAATLELDLEHYVVPSPPTAPPNGYAA	231
LOC_0s05g07130	SWRVFKENFQPSKVRGIPDVSINVAHAGTEDTSTESLELDLEHYVPTP-SAATSEYAA	231
Bradi2g34580	SWRVYKENFQPSQVRGIPDVSINVAHATEDGSGSLELDLEHYVVPPTP-TAPPTAYAA	229

GSV VP00024699001	MLDTGNFVLASQNSTYLWESFNHPTDT LPTQ LEQGSKLVARYSETNYSRGRFMFSLQT	209
LOC_0s03g18310	-----	168
Seolgaeng	-----	168
Bradi1g65420	NLTENPRSLLDHG--VSSN-----NDTTKGT--LQNL KGDD-----	231
GRMZM5G824405	SLTENPRSL QTG--SSSN-----NDTTKDI--LHNSTKG-----	227
Sb01g038340	NLTENPRSL QTG--SSSN-----NDTTKDI--LHSSTKG-----	227
GRMZM2G021846	NLAATPASVIQTE--ALLT-----NDILLSDG-IQSPSSVSAKLEDCT-N-----	274
Sb09g004780	NLAATPASMIQTG--ASWT-----NDILLSDG-IQSPSSVSAKLEDRSNN-----	273
LOC_0s05g07130	NLAANPASLIQTG--ALWT-----NDMLLSDG-IQSPSSATADFEDHNNC-----	273
Bradi2g34580	NLAATPASLIQPG--ALWT-----NDMLLSDG-IQSPSSASADFRDHSYH-----	271

GSV VP00024699001	DGNLVLYTTDFPMDSANFAYWESDTVSGSGLV FNQSGN YL GRNGS LNEVLPNKAST	269
LOC_0s03g18310	-----	168
Seolgaeng	-----	168
Bradi1g65420	-----AP	233
GRMZM5G824405	-----D-----SS	230
Sb01g038340	-----D-----SS	230
GRMZM2G021846	-----HKN EAWATD-----SS	286
Sb09g004780	-----KKN EAWATD-----SS	285
LOC_0s05g07130	-----NKDNVALPSD-----SF	285
Bradi2g34580	-----NKDI EASVAD-----SS	283

GSV VP00024699001	PDFYQRG LEYDGVFRQYVYPKTAGSRAGGWSSLSSEF PEN CTA TAGTSGGACGFNSY	329
LOC_0s03g18310	-----AKGADGRHVPPQEEQRA----- FVDRGVGSP-EFARPTNET SMSN	209
Seolgaeng	-----AKGADGRHVPPQEEQRA----- FVDRGVGSP-EFARPTNET SMSN	209
Bradi1g65420	PNHYA----NTEKGVDRGRHAPSQEEPR-----VFVDRGVGSP-RLSRPTNET SMGN	281
GRMZM5G824405	LNHYV-NTMKST-I---GGHASSLEEQRA-----MFVDRGVGSP-NFARPTMETFSMSN	278
Sb01g038340	SNHYV-NTMKSA-I---GGHAPSLEEQRA-----MFVDRGVGSP-NFARPTKETFSMSN	278
GRMZM2G021846	KKI QNSGL ESKSVGTFTPMQKLDGQKG-----LFVDRGVGSS-MLPKSASACSLASG	338
Sb09g004780	K---NSGL ESKSVGTFTPLQKLDGQKG-----LFVDRGVGSP-MLPKSASACSLASG	334
LOC_0s05g07130	KKLQVSGI VESKSVDTLTTLQKQDGQKG-----LFVDRGVGST-KFGKSSSACSLASG	337
Bradi2g34580	KKLQVCGMVESKSVGTL PLQKQDRQKG-----LYVDTGVVSP-KLGKSFSACALASG	335

GSV VP00024699001	CTLGDDQRPYCQCPPGYTFLDPHDQVKGCRQNFFPE CSEGSSETG-EFDFVRM-----	382
LOC_0s03g18310	I KFDSEAKDMPAAEGAVAAAADQMYGPKEDRKLA VLVGLPARGKTFTAACLTRYLRW	269
Seolgaeng	I KFDSEAKDMPAAEGAVAAAADQMYGPKEDRKLA VLVGLPARGKTFTAACLTRYLRW	269
Bradi1g65420	I KQEFKAGMPAAEGAVAAAADQMYGPKEDRKLV VLVGLPARGKTFTAACLTRYLRW	341
GRMZM5G824405	FKLDSESKGMPAAEGAVAAAADQMYGPKEDRKLA VLVGLPARGKTFTAACLTRYLRW	338
Sb01g038340	FKLDSDSKGMPAAEGAVAAAADQMYGPKEDRKLA VLVGLPARGKTFTAACLTRYLRW	338
GRMZM2G021846	FSFGSA-KTMPEAAGAVAAAADRLHGSKEDRKLA VLVGLPARGKTFTAACLTRYLRW	397
Sb09g004780	FSFGSA-KTMPEAAGAVAAAADRLHGSKEDRKLA VLVGLPARGKTFTAACLTRYLRW	393
LOC_0s05g07130	LNFGTGKQAMPEAAGAVAAAADRLHGSKEDRKLA VLVGLPARGKTFTAACLTRYLRW	397
Bradi2g34580	LSFAST-KAMPEAAGAVAAAADRLHGSKEDRKLA VLVGLPARGKTFTAACLTRYLRW	394

GSV1VP00024699001	----TNVDWPLSDYDRFQLFT-----EDECRAKLDDCFCAVAIVREGDCWKKKFPLS	431
LOC_0s03g18310	LGHETKHFNVGKYRRLKHGI NQTADFFRGDNKEGVEARNEVAALA-MEDMLSWMQEG-GQ	327
Seolgaeng	LGHETKHFNVGKYRRLKHGI NQTADFFRGDNKEGVEARNEVAALA-MEDMLSWMQEG-GQ	327
Bradi1g65420	LGHETKHFNVGKYRRLKHGTSQTADFFRGDNKEGVEARNEVAALA-MEDMLSWMQEG-GQ	399
GRMZM5G824405	LGHETKHFNVGKYRRLKHGTNQTADFFRGDNREGVEARNEVAALA-MEDMLSWMQEG-GQ	396
Sb01g038340	LGHETKHFNVGKYRRLKHGTNQTADFFRGDNREGVEARNEVAALA-MEDMLSWMQEG-GQ	396
GRMZM2G021846	LGHETRHFNVGKYRRLKLGANQSADFFRDNPGEI EARNEVAALA-MEDMIDWMNGG-GQ	455
Sb09g004780	LGHETRHFNVGKYRRLKHGANQPADFFRDNPGEI EARNEVAALA-MEDMIDWMNGG-GQ	451
LOC_0s05g07130	LGHETRHFNVGKYRRLKHGANQSADFFRDNPGEI EARNEVAALA-MEDMIDWMHGG-GQ	455
Bradi2g34580	LGHETKHFNVGKYRRLKHGANQSADFFRADNQGGI EARNEVAALA-MEDMIDWMHGG-GQ	452
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GSV1VP00024699001	NGRFDSSNGRIALIKVRKDNSTFPLGSEKQDQATLILTGSVLLGSSVLLNILLLLATAMF	491
LOC_0s03g18310	VGIFDATNS-----TRNRRNMLMKMAEGCKIIF	356
Seolgaeng	VGIFDATNS-----TRNRRNMLMKMAEGCKIIF	356
Bradi1g65420	VGICDATNS-----TRSRNMLMKMAEGCKIIF	428
GRMZM5G824405	VGIFDATNS-----TRI RRNMLMKMAEGCKIIF	425
Sb01g038340	VGIFDATNS-----TRI RRNMLMKMAEGCKIIF	425
GRMZM2G021846	VGIFDATNS-----TRKRRYMLMKMAEGNCKIIF	484
Sb09g004780	VGIFDATNS-----TRKRRYMLMKMAEGNCKIIF	480
LOC_0s05g07130	VGIFDATNS-----TRKRRYMLMKMAEGNCKIIF	484
Bradi2g34580	VGIFDATNS-----TRKRRYMLMKMAEGNCKIIF	481
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GSV1VP00024699001	IYRLNQRKPMIDESRLVMLGTNLKRFAYDE---LEEATDGFKDELGTGAFATVYKGTLAH	548
LOC_0s03g18310	LETICNDQNVLERNMRLKVQR---SPDYAEQTDFAAGVRDFKERLA---YYEKVYEPV---	408
Seolgaeng	LETICNDQNVLERNMRLKVQR---SPDYAEQTDFAAGVRDFKERLA---YYEKVYEPV---	408
Bradi1g65420	VETICNDQDVLERNIRLKVQQ---SPDYAEQTDFAAGVRDFKERLA---YYEKVYEPV---	480
GRMZM5G824405	LETLCNDQDVLERNIRLKVQQ---SPDYAEQTDFAAGVQDFKERLT---YYEKVYEPV---	477
Sb01g038340	LETLCNDQDVLERNIRLKVQQ---SPDYAEQTDFAAGVQDFKERLT---YYEKVYEPV---	477
GRMZM2G021846	LETICNDPNI IERNIRLKIQQ---SPDYAEQLDYEAGLEDKERLI---NYEKVYEPV---	536
Sb09g004780	LETICNDPNI IERNIRLKIQQ---SPDYADQPDYEAGLEDKERLI---NYEKVYEPV---	532
LOC_0s05g07130	LETICNDPNI IERNVRLKIQQ---SPDYADQPDYETGVRDFKERLA---NYEKVYEPV---	536
Bradi2g34580	LETICNDRNI IERNVRLKIQQ---SPDYADQPDYEAGLQDFLERLT---NYEKVYEPV---	533
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GSV1VP00024699001	DGNLVAVKKLDRVAGGEGDKQEFEKIVGAI GRTI HKNLVQLLGFCNKGGQHRLLVYEFMSN	608
LOC_0s03g18310	EEGS---YVKMIDMVSGTGGQLQINDISGYLPGR I---VFFLVNCHLT-----	450
Seolgaeng	EEGS---YVKMIDMVSGTGGQLQINDISGYLPGR I---VFFLVNCHLT-----	450
Bradi1g65420	EEGS---YIKMIDMVSGNGGQLQINDISGYLPGR I---VFFLVNCHLT-----	522
GRMZM5G824405	EEGS---YIKMIDMVSGKGGQLKINDISGYLPGR I---VFFLVNCHLT-----	519
Sb01g038340	EEGS---YIKMIDMVSGKGGQLKINDISGYLPGR I---VFFLVNCHLT-----	519
GRMZM2G021846	GEGS---YIKMIDMVKGQDQQLQVNNISGYLPGR I---VFFLVNSHLT-----	578
Sb09g004780	GEGS---YIKMIDMVKGQDQQLQVNNISGYLPGR I---VFFLVNSHLT-----	574
LOC_0s05g07130	QEGS---YIKMIDMVKGQGGQLQVNNISGYLPGR I---VFFLVNSHLT-----	578
Bradi2g34580	EEGS---YIKMIDMVKGQGGQLQVNNISGYLPGR I---VFFLVNSHLA-----	575
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GSV VP00024699001	GSLATFLFGNSRPSWYKRMEI LG TARGLLYLHEECS QA HGD NPQN LLDDS-L-TA	666
LOC_0s03g18310	-----PRP LLTRHGESLDNVRGR GGDSSLSETGSLYSR	485
Seolgaeng	-----PRP LLTRHGESLDNVRGR GGDSSLSETGSLYSR	485
Bradi1g65420	-----PRP LLTRHGESLDNVRGR GGDSSLSEAGGVYSR	557
GRMZM5G824405	-----PRP LLTRHGESMDNVRGR GGDSSLSEAGELYSR	554
Sb01g038340	-----PRP LLTRHGESMDNVRGR GGDSSLSEVGELYSR	554
GRMZM2G021846	-----PRP LLTRHGESLHNVRGRVGGDTVLSETGELYAK	613
Sb09g004780	-----PRP LLTRHGESLHNVRGRVGGDTVLSETGELYAK	609
LOC_0s05g07130	-----PRP LLTRHGESLHNVRGRVGGDTVLSYGELYSK	613
Bradi2g34580	-----PRP LLTRHGESLHNVRGRVGGDTVLSYNGELYAK	610
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GSV VP00024699001	RISDFGLAKLLKMDQTG-----TTTGVMGTGKYAAPEWFKKVP TFKVDVYSFGIV	717
LOC_0s03g18310	KLASF EKRLASERTAS WTSTLQRS LTAQP IGFPK QWRALDE INA-----	534
Seolgaeng	KLASF EKRLASERTAS WTSTLQRS LTAQP IGFPK QWRALDE INA-----	534
Bradi1g65420	KLASFV-EKRLKERTAS WTSTLQRT LTAHP IGFPK QWRALDE INA-----	606
GRMZM5G824405	KLASFV-EKRLKERTAS WTSTLQRT LTAHP IGFPK QWRALDE INA-----	603
Sb01g038340	KLASFV-EKRLKERTAS WTSTLQRT LTAHP IGFPK QWRALDE INA-----	603
GRMZM2G021846	KLANF EKRLKCEKTAT WTSTLQRT LTASP VGFPK QWRALDE INS-----	662
Sb09g004780	KLANF EKRLKYKTAT WTSTLQRT LTASP VGFPK QWRALDE INS-----	658
LOC_0s05g07130	KLANF EKRLKSEKTAS WTSTLQRT LTASP VGFPK QWRALDE INS-----	662
Bradi2g34580	KLANF EKRLKSEKTAT WTSTLQRT LTATP VGFPK QWRALDE INS-----	659
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GSV VP00024699001	LLELIFCRKNFEPEVEDEKQMVLGWAYDCYKEGKLDLLVGNQDEALDD KRLKEFMVVA	777
LOC_0s03g18310	----G CDGMTYDE ---KK K---PEEYESRSKDKLRYRYPGESYLDV QRLEPVI IEL	585
Seolgaeng	----G CDGMTYDE ---KK K---PEEYESRSKDKLRYRYPGESYLDV QRLEPVI IEL	585
Bradi1g65420	----G VCDGMTYDEV---KKNK---PEEYESRRKDKLRYRYPGESYLDV QRLEPVI IEL	657
GRMZM5G824405	----G VCDGMTYDE ---KSK---PEEYESRRKDKLRYRYPGESYLDV QRLEPVI IEL	654
Sb01g038340	----G VCDGMTYDE ---KSK---PEEYESRRKDKLRYRYPGESYLDV QRLEPVI IEL	654
GRMZM2G021846	----G VCDGMTYEE ---KK IM---PEEFESRRKDKLRYRYPGESYLDV QRLEPVI IEL	713
Sb09g004780	----G VCDGMTYEE ---KKNM---PEEFESRRKDKLRYRYPGESYLDV QRLEPVI IEL	709
LOC_0s05g07130	----G VCDGMTYEE ---KK VM---PEEFESRRKDKLRYRYPGESYLDV QRLEPVI IEL	713
Bradi2g34580	----G VCDGMTYEE ---KK IM---PEEYESRRKDKLRYRYPGESYLDV QRLEPVI IEL	710
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GSV VP00024699001	-----FWCTQ-----EDPSQRPTMKTMKMLEGATEVPVLQ-----	808
LOC_0s03g18310	ERQRAPVVV SHQAVLRALYAYFADKPLEE PN E PLHT I E QMGVAGVQEKRYKLMD	645
Seolgaeng	ERQRAPVVV SHQAVLRALYAYFADKPLEE PN E PLHT I E QMGVAGVQEKRYKLMD	645
Bradi1g65420	ERQRAPVVV AHQAVLRALYAYFADKPLEE VPK E PLHT I E QMGVSGVEEKRYKLMD	717
GRMZM5G824405	ERQRAPVVV AHQAVLRALYAYFADKPLEE VPN E PLHT I E QMGVAGVQEKRYKLMD	714
Sb01g038340	ERQRAPVVV AHQAVLRALYAYFADKPLEE VPN E PLHT I E QMGVAGVQEKRYKLMD	714
GRMZM2G021846	ERQRAPVVV SHQAVLRALYAYFADRPLREVPE EM PLHT I E QMGVTGVEEKRYKLMD	773
Sb09g004780	ERQRAPVVV SHQAVLRALYAYFADRPLREV PD EM PLHT I E QMGVLGVEEKRYKLMD	769
LOC_0s05g07130	ERQRAPVVV SHQAVLRALYAYFADRPLREV PD EM PLHT I E QMGVTGVEEKRYKLMD	773
Bradi2g34580	ERQRAPVVV SHQAVLRALYSYFADRPLREV PDM EM PLHT I E QMGVTGVEEKRYKLMD	770
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GSV VP00024699001	-THPH*---	812
LOC_0s03g18310	AVNSTAGI-	653
Seolgaeng	AVNSTAGI-	653
Bradi1g65420	AVNPTEI*	725
GRMZM5G824405	AIHPTAGL-	722
Sb01g038340	AIHPTAGL-	722
GRMZM2G021846	-----	773
Sb09g004780	-----	769
LOC_0s05g07130	*-----	773
Bradi2g34580	*-----	770