

**Functional characterisation of barley betaglucanless mutants demonstrates a unique role
for CslF6 in (1,3;1,4)- β -D-glucan biosynthesis**

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Haruyama, Oscar Larroque and Stephen A. Jobling

Supplementary material

Figure S1. Molecular mapping of the *bgl* and *HvCslF6* genes on chromosome 7H using 104 F₂ plants from a cross between ‘Bowman’ and OUM125. The black box indicates the centromere position.

Figure S2. Quantitative RT-PCR analysis of expression of the *HvCslF6* gene in various tissues and developmental stages. DAF: days after flowering. Bars indicate standard deviations.

Figure S3. Alignments of seven barley HvCslF proteins and rice OsCslF6 protein. The mutated amino acids in three *bgl* mutants (positions 253, 638 and 660) are highly conserved as highlighted in colour. The amino acids at position 590, which were mutated in some barley germplasm accessions, are not conserved.

Figure S4. Difference in appearance of leaf tip between wild type barley (‘Akashinriki’) and *HvCslF6* mutant OUM125. Images were taken from the upper leaves of plants which were heading.

Figure S5. FACE analysis of lichenase digests of cell wall extracts from various barley seedling tissues of ‘Akashinriki’ (shown in blue line) and OUM125 (shown in red line) demonstrating the absence DP3 and DP4 peaks characteristic of (1,3;1,4)- β -D-glucan in all tissues of the mutant.

Figure S6. Content of (1,3;1,4)- β -D-glucan in leaves of three sets of isogenic lines. Error bars represent the standard errors in three replications. **: significant at the 1% level by *t*-test.

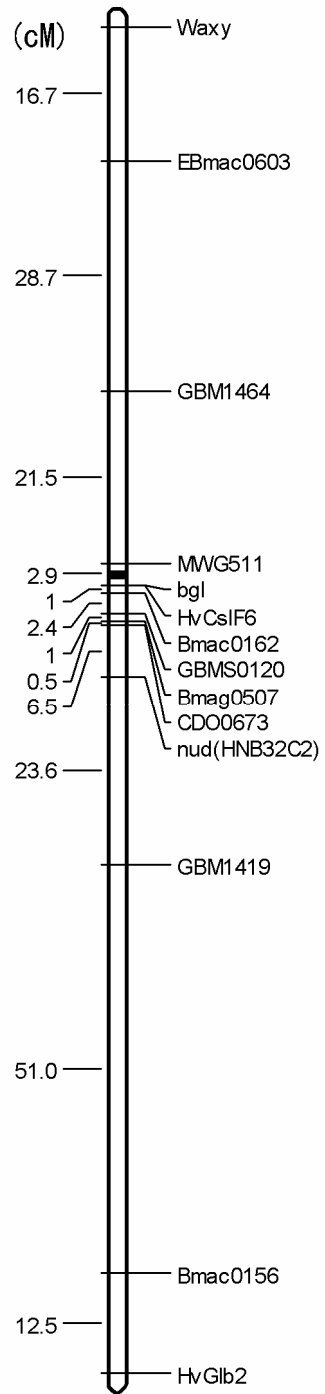


Fig. S1

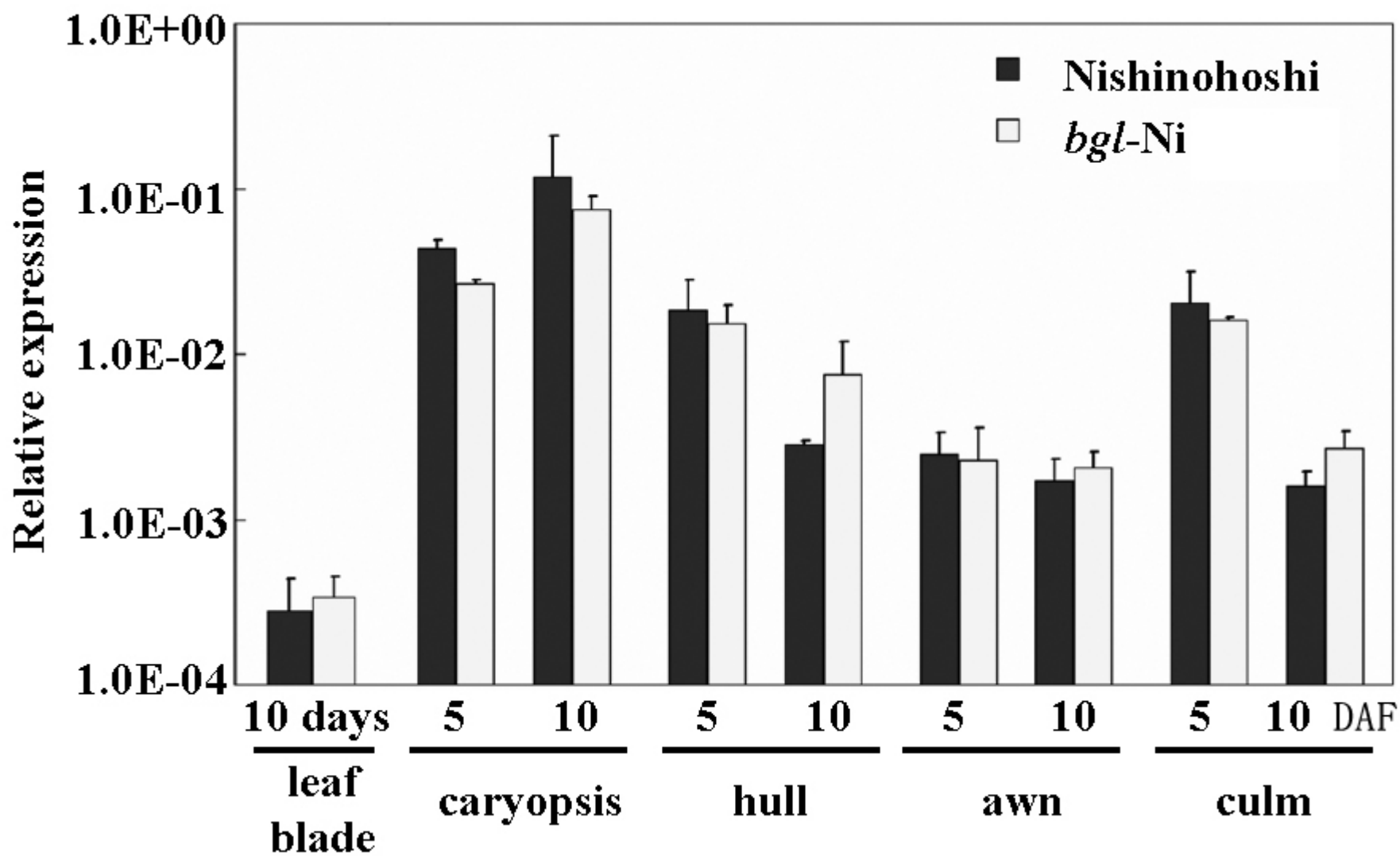


Fig. S2

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HvCs1F6 1: MAPAVAGGGRVRSNEPVAAAAAPAASGKPCVCGFQVCACTGSAAVASAASSLMDIVAMGQIGAVNDESWVGVELGEDGETDES---GAAVDDRPVFRTEKIKGVLLHPYRVLIFVRLI 117
OsCs1F6 1: MAPAVAGGGRRNNEGVNGNAAP-----ACVCGFPVCACAGAAVASAASSADMIVAAGQIGAVNDESWVAVDLSDSDDAPAAGDVQGALDDRPVFRTEKIKGVLLHPYRVLIFVRLI 115
HvCs1F10 1: -----MLSPRTDAGAGAATDLSQPLLWNRNGVHAGALVVMVVVANGHGGGDKLKGAPKAKDKYWKVDVQPDMAAAPDL--NGGGRPLLFSNRRVKNIILCPYRVLILIRVI 106
HvCs1F3 1: -----MASAAGAAGSNASLAAPLLASRE-----GGAKKPVGAKGKHWAAADK-DERRAAKESG--GEDGRPLLFRYKVKGTLHPYRALIFIRLI 83
HvCs1F9 1: -----MASPAVGGGRLADPLLAADV VVGAKDKYVWPADEREILASQSSGGGEQDGRAPLLYRTRFRVKGFFINLYRLLTLRVRI 80
HvCs1F8 1: -----MGSLAAANGAGHASNGAGVADQALALENGTGNGHKASDANRATPVQQANGSSKAAGKVS PKDKYVWAVDEGEMAAA IADGG--EDGRRPLLRYRTRFKVKGILLHPYRLLSLIRLV 112
HvCs1F4 1: -----MAPAVTRRANALRVEAPDGAESGRASLAADSPAAKRAIDAKDDVWVAAAEG-----DASGASAGNGDRPPLFRTMKVKGSILHPYRFMILVRLV 90
HvCs1F7 1: -----MLMITYIKKHIDYVATLDEKESPADEKSN-----VERLLVRTTKLTTVTIKLYRLMIVRMA 57
                          : .                               : . . : . : * : . : * :

HvCs1F6 118: AFTLFIWRIS-----HKNPDMWLWVTSICGEFVWFGFSWLLDQLPKLNPINRVPLAVLRQRFRDPDGTSTLPGLDIFVTTADPIKEPILSTANSVLSILAADYPVDRNTCYVSDDS 230
OsCs1F6 116: AFTLFIWRIE-----HKNPDMWLWVTSIAGEFVWFGFSWLLDQLPKLNPINRVPLAVLRFRFDHADGTSSLPGLDIFVTTADPIKEPILSTANSILSILAADYPVDRNTCYVSDDS 228
HvCs1F10 107: TVILFVGWRIK-----HNNSDVMWFWMMSVVADVWVWVWVSLWLSYQLPKYNPKRIPDLATLRQYDTPGRSSQLPSIDVIVTTASATDEPILYTMNCVLSILAADYHIGRCNCYLSDS 219
HvCs1F3 84: AVLLFFVWRIK-----HNKSDIMWFWTISVVGDVWVWFGFSWLLNQLPKFNPKIPDMVALRRQYDLSDGTSTLPGIDVFTTADPIDEPILYTMNCVLSILASDYPVDRACACYPDDS 196
HvCs1F9 81: VVILFFTWMR-----HRSDAMWLWVIVSGDLWFGVTVWLLNQITKLKPKRCVPSISVLREQLDQPDGSDPLPLDVFINTVDPVDEPMLYTMNSILSILATDYPVQKYATYFSDDG 193
HvCs1F8 113: AIVLFFVVRVR-----HPYADGMWLWVISMVGDVWFGVTVWLLNQVAKLNPVVRPNLALLQQQFDLPDGNLPLCLDVFINTVDPINEMPMIYTMNSISILAADYPVDKHACYLSDDG 225
HvCs1F4 91: AVVAFFAWRLK-----HKNHDGMWLWATSMVADVWVWFGFSWLLNQLPKLNPKIRVPLAALADQCG--SSGDANLPGIDIFVTTVDPVDEPILYTVNTILSILATDYPVDKYACYLSDDG 202
HvCs1F7 58: IFVLFKWRISTALAMTNGTSTARAMWTVSIAGELWFALMWVLDQLPKMQTVR-----RTVFATALESLLPTMDVFTTADPDKPPLVTVNTILSILAADYPDKLTCYVSDDG 169
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                                  253

HvCs1F6 231: GMLTYEALAESSKFATLWVPFCRKHGIEPRGPESYFELKSH-----PYMGRAQDEFVNDRRRVRKEYDEFKARINSLHDIKQRNDGYNAAIASHQGVPRPTWMADG--TQWEGTWVD 342
OsCs1F6 229: GMLTYEAMAEAKFATLWVPFCRKHAI EPRGPESYFELKSH-----PYMGRAQE EFVNDRRRVRKEYDDFKARINGLEHDIKQRSYNAAGVKDGEPRATWMADG--SQWEGTWIE 340
HvCs1F10 220: GSVLVYEALVETAKFAALWVPFCRKHQI EPRAPESYFELKGP-----LYGGTPHKEFFQDYKHLGTQYEEFKNLDMLPNTIHQRSYNAAGVKDGEPRATWMADG--TQWPGTWLD 330
HvCs1F3 197: GALIQYEALVETAKFATLWVPFCRKHCIEPRAPESYFEIEAP-----LYTGTAPEEFKNDYSSVHKEYDEFKERLDSLDAISKRSDAYNSMKT EGD--AKATWMANG--TQWPGSWID 307
HvCs1F9 194: GSLVHYEGLLLAEFASWVPFCRKHCVEPRAPESYFVAKMRG-----EYAGSAAKEFLDHRMRAAAYEEFKARLDGSAVIEQRSEACNRAANEKEGCGNATWMADG--TQWPGTWIK 307
HvCs1F8 226: GSIHYDGLELLETAKFAALWVPFCRKHSIEPRAPESYFSLNTR-----PYTGNAPQDFVNDRRHMCREYDEFKERLDALFTLIPKRSVYVNHAAAGKEG--AKATWMADG--TQWPGTWID 335
HvCs1F4 203: GTLVHYEAMIEVANFAVMWVPFCRKHCVEPRSPENYFGMKTQ-----PYVGSMA GEFMRHRRRVRREYDEFKVRIDSLSTIRQRSYNAAGVKDGEPRATWMADG--TQWPGTWIE 312
HvCs1F7 170: GALLTREA VVEARFAGLWVPFCRKHGV EPRNPEAYFSGHVKRVVSRADYKGRS WPELARRRRRVRREYEELRLRVDALHAGDVQR-----PWRSRQ----- 262
    * : : . : : . * * * : * * * * : * * * : * * : : : * : : : * : * : * : * : * : * : * : * : * : * :

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Fig. S3

HvCs1F6	343: ASENHRRGDHAGIVLVLLNHPSHRRQTGPPASADNPLDLSGVDVRLPMLVYVSREKRPGHDHQQKAGAMNALTRASALLSNSPFILNLDGDHYINNSQALRAGICFMVG-RSDTVAFAVQ	461
OsCs1F6	341: QSENHRKGDHAGIVLVLLNHPSHARQLGPPASADNPLDFSGVDVRLPMLVYVAREKRPGCNHQKAGAMNALTRASAVLSNSPFILNLDGDHYINNSQALRAGICFMLG-RSDTVAFAVQ	459
HvCs1F10	331: PAEKHRAGHHAGIVKIVQSHPEHVQPGVQESLDNPLSFDDVDVRLPMLVYVAREKSPGIEHNKKAGALNAELRISALLSNAPFFINFDCDHYINNSEALRAAVCFMLDPREGDNTGFVQ	450
HvCs1F3	308: TTEIHRKHGHAGIVKVVLDSIRGHNLGSQESTHN-LSFANTDERLPMLVYISRGKNPSYDHKKAGALNAQLRASALLSNAQFIINFDCDHYINNSQALRAAMCFMLDQRQGDNTAFVQ	426
HvCs1F9	308: PAKGHRKHGHPAILQVMLDQPSKDPDELGMASSDHPDLFSAVDVRLPMLVYIAREKRPGYDHQKAGAMNVQLRVSALLSNAPFIINFDCDHYINNSQAFRAAMCFMLDPREGDNTAFVQ	427
HvCs1F8	336: PAENHKKGQHAGIVKVLKHPSEYEPGLGASTNSPLDFSAVDVRLPMLVYISREKSPSCDHQKAGAMNVQLRVSALLTNAPFIINFDCDHYVNNKAFRAGICFMLDRREGDNTAFVQ	455
HvCs1F4	313: QVENHRRGQHAGIVQVILSHPSCKPQLGSPASTDNPLDFSVDTRLPLVYMSREKRPGYNHQQKAGAMNMRRVSALLSNAPFVNFDCDHYINNTQALRAPMCFMLDPRDQNTAFVQ	432
HvCs1F7	263: -----TPEDHAGVVEVLVDPSPCTPEP-----GVSGNLLDLSSVDVRPALVYMCREKRGRRAHHRKAGAMNALLRTSAVLSNAPIILNLDGDHYVNNKALRAGVCLMLD-RGGSVAVFVQ	373
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HvCs1F6	462: FPQRFEGVDPTDLYANHNRIFFDGLRALDGMQGPPIYVGTGCLFRRITVYGFDPPIRINVGGPCFPRLAGLFAKTKYEKPGLEMTAKAKAAPVP-----AKGKHGFLPLPKTYGKSDAF	576
OsCs1F6	460: FPQRFEGVDPTDLYANHNRIFFDGLRALDGLQGPPIYVGTGCLFRRITLYGFEPPIRINVGGPCFPRLGGMFAKNRYQKPGFEMTKPGAKPVAPPPAATVAKGKHGFLPMPKKAYGKSDAF	579
HvCs1F10	451: FPQRFNDVPTDRYGNHNRVFFDGAMYGLNGQQGPTYLGTGCMFRPLALYIDPPCWAEDIIVDSNRFG-----NSLPF	525
HvCs1F3	427: FPQRFNDVPSDRYGNHNRVFFDGTMALNGLQGSPYLGTGCMSTRRIALYIDPPDWRHDIIVDDKFKG-----SSIPF	501
HvCs1F9	428: FPQRFDDVDPTDRYCNHNRVFFDATALLGLNGIQGPSYVGTGCMFRRVALYSADPPRWRSDDAKEAKASHRPNM-----FGKSTSF	507
HvCs1F8	456: FPQRFDDVDPTDRYCNHNRVFFDATALLGLNGIQGPSYVGTGCMFRRVALYGVDPPIRWRPDDVKIVDSSSK-----FGSSESF	532
HvCs1F4	433: FPQRFDDVDPTDRYANHNRVFFDGTMLSLNGLQGPSYLTGTMFRRVTLYGMEPPRYRAENIKLVGKTYE-----FGSSTSF	509
HvCs1F7	374: FPQRFDDVDPADRYANHNRVFFDCTELGLDGLQGPPIYLTGCMFRRALYSIDPPLWWSHGDSAGKDVAAEADKFG-----VSTPFLGSV	459
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HvCs1F6	577: VDTIPRASHPSPYAAAEGIVADEATIVEAVNVTAAAFEKKTGWGKEIGWVYDVTEDVVTGYRMHIKGRSRYCSIYPHAFIGTAPINLTERLFQVLRWSTGSLEIFFSKNNPLFGSTY	696
OsCs1F6	580: ADTIPRASHPSPYAAEAA-VADEAAIAEAVMVTAAAYEKKTWGSDIGWVYGTVEDVVTGYRMHIKGRSRYCSIYPHAFIGTAPINLTERLFQVLRWSTGSLEIFFSRNNPLFGSTF	698
HvCs1F10	526: LNSVLAAIKQEEGVTLPP-PLDSDLEEMTKVVVSCSYDDSDTWGRGIGYINMATEDIVTGFRIHGGQWCSMYVTMEREAFRTGAPINLTERLRQIVRWGGSGLEMFSSHISPLFAGRR	643
HvCs1F3	502: LDSVSKAINQER-STIPP-PISETLVAEMERVVSASHDKATGWGKGVGYDYDIATEDIVTGFRIHGGQWRSMYCTMERDAFCGIAPINLTERLHQIVRWGGSGLEMFSSLNPLIGRR	618
HvCs1F9	508: INSMPTAAANQERSVPSP-----ATVGEAELADAMTCAYEDGTEWGNQVGVYNIATEDVVTGFRHRGWRSTYCAMEDAFRTGAPINLTERLYQILRWGGSGLEMFSSRFPCPLLAGRR	622
HvCs1F8	533: ISSILPAADQERSIMSPP-ALYESVMADLAHVMTCAVEDGTWGREVGVWYNIATEDVVTGFRHRGWRSMYCRMEDAFRTGAPINLTERLYQILRWGGSGLEMFSSHNCPLLAGRR	650
HvCs1F4	510: INSMPTGAIQERSITPVL-VDEALSNLDLATLMTCAVEDGTWGRDVGWYNIATEDVVTGFRMHRGWRSMYCSMEPAAFRTGAPINLTERLYQVLRWGGSGLEMFSSNALMAGRR	626
HvCs1F7	460: RAALNLRSEQRNTGTSPPCSSDAAAVGEATALVSCGYEDRTAWGREIGWYGTVEDVATGFCMHRGWRSAFCATAPDAFRGTGAPINLTDRLHQVLRWAAGSLEIFFSRNNALLAGRR	579
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HvCs1F6	697: LHPLQRVAYINITTYPFTAIFLIFYTTVPALSFVT-----GHFIVQRPTTMFYVYLIVLSTLLVIAVLEVWAGVTVFEWFRNGQFWMATASCAYLAAVCVLTKVIFRRDISFKLTS	810
OsCs1F6	699: LHPLQRVAYINITTYPFTAIFLIFYTTVPALSFVT-----GHFIVQRPTTMFYVYLIVLSTLLVIAVLEVWAGVTVFEWFRNGQFWMATASCAYLAAVLVVTKVIFRRDISFKLTS	812
HvCs1F10	644: LSLVQLRSYINFTIYPLTSLFILMYAFCPVMWLLP-----TEILIQRPYTRYIVYLIIVVAMIHVGIMFEMWAGITWLDWVRNEQFFMIGSVTAYPTAVLHMVNNLTKKGIHFRVTT	757
HvCs1F3	619: IHALQRVSYLNMTVYPTVTSFLIFLLYALSPVMWLIP-----DEVYIQRPFQYVYVFLVILMIHIGWLEIKWAGVTWLDYWRNEQFFMIGSTAYPAVLMVNNLTKKGIHFRVTS	732
HvCs1F9	623: LHPMQRVAYINMTYVSTFIFLLMYFYFPVMWLFQ-----GEFYIQRPFQTFALFVVVVIATVELIGMVEIRWAGLTLLDWRNEQFYIIGTGVYPMAMHLILRSLGKGVSFKLTA	736
HvCs1F8	651: LHPMQRVAYANMSTYVSSVFLVYFLLFPVIWIFR-----GQFYIQRPFQTYLVIVIALTELIGMVEIKWAGLTLLDWRNEQFYIIGATAVYPTAVFHVILKFLGKGVSFKLTA	764
HvCs1F4	627: IHPLQRVAYLNMTSTYIVTFILAYLFPVMWLFQ-----EQFYIQRPFQTYIMLVGVIAMIHVGIMFVWAGITLLDWRNEQFYIIGATAVYPTAVLVMALKVLTKGKIVFRLTS	740
HvCs1F7	580: LHPLQRVAYLNMTYVSTFIFLLYVCLLPALPLVTRSATMSAFSTNMPSSSTYITFAALMLTLAMVAALVLRWSGITPEGWRNEQFWMVSTAYAAAVVQVALKVLVGKEVAFKLTS	699
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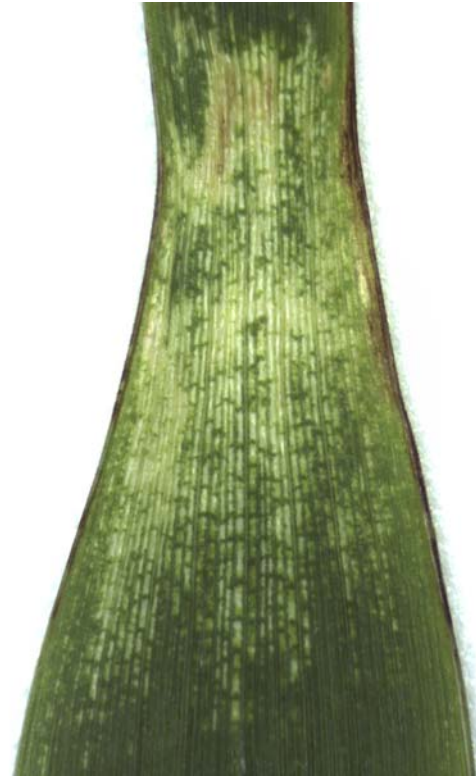
Fig. S3 continued.

HvCs1F6	811:KLPSGDEKK-----DPYADLYVVRWTPLMITPIIIIFVNIIGSAVAFAKVLDGEW----THWLKVAGGVFFNFVWLFHLYPFAKGILGKHGKTPVVVLVWVAFTFVITAVLYINIPHMHT	921
OsCs1F6	813:KLPAGDEKK-----DPYADLYVVRWTWLMITPIIIILVNIIGSAVAFAKVLDGEW----THWLKVAGGVFFNFVWLFHLYPFAKGILGKHGKTPVVVLVWVAFTFVITAVLYINIPHIHG	923
HvCs1F10	758:KQPVADTD-----DKYAEMYEVHWVPMMPAVVVLFSNILAIGVAIGKSVLYMGTWVSAQKRHGALGLLNLWIMVLLYPFALAIIGRWAKRTGILFILLPIAFLATALMYIGIHTFLL	871
HvCs1F3	733:KQTTADTN-----DKFADLYDMRWVPMLIPTTVVLIANVGAIGVAMGKTIVYMGAWTIAQKTHAALGLLNFVWIMVLLYPFALAIMGRWAKRPVILVVLLPVAFTIVCLVYVSVHILLL	846
HvCs1F9	737:KKLTGGAR-----ERLAELYDVQWVPLLVPVTVVMAVNVAAGAAAGKAIVGR--WSAAQVAGAASGLVFNWMLLLLYPFALGIMGHWSKRPYILFLVLVTAVAATASVYVALAGSLL	848
HvCs1F8	765:KQVASSTS-----DKFAELYAVQWAPMLIPTMVVIAVNVCAIGASIGKAVVGG--WSLMQMADAGLGLVFNWILVLIYPFALGMIGRWKRPYILFVILFVIAFILIALVDIAIQAMRS	876
HvCs1F4	741:KQTDACSN-----DKFADLYTVRWVPLLFPVAVLIVNVAAVGAAIGKAAAWG--FFTDQARHVLLGMVFNWILVLLYPFALGIMGWGKRPIILFVMLIMAIGAVGLVYVAFHDPYP	852
HvCs1F7	700:KRRASGSGGGVVKGRFAELYAVRWTVLMVPTAVVLAVNVASMAAAVQERRWRKG-----PAAVLATAFNWVVVHLHPFALGLMGRWSKTLSPLLLLVVAFTILSLCFLHLHML--	810
	* . *:* :*: :... : : * . . . : :	. ** *:. :*** .:*. * .: :
HvCs1F6	922:SGGKHTTVHGHHGKLVDTGLYGWLH---	947
OsCs1F6	924:PGRHGAASPSHGHSAGTKKYDFTYAWP	952
HvCs1F10	872:HFFPSMLV-----	879
HvCs1F3	847:SFLPF-----	851
HvCs1F9	849:YLHSGIKLV-----	857
HvCs1F8	877:GIVRFHFKSSGGATFPTSWGL-----	897
HvCs1F4	853:TDFSEVAASLGEASLTGPSG-----	872
HvCs1F7	810:-----	810

Fig. S3 concluded.



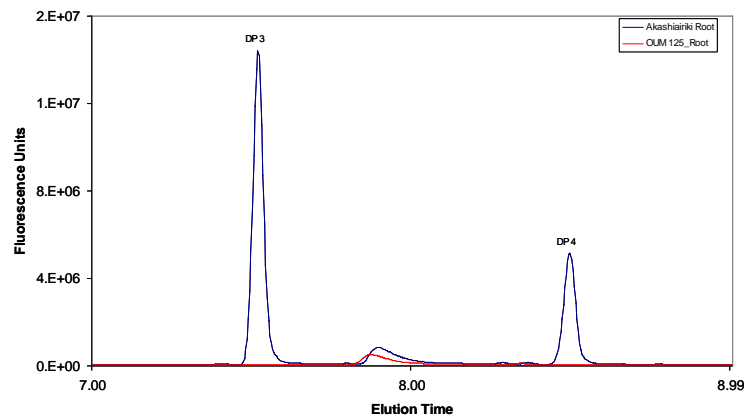
Akashinriki



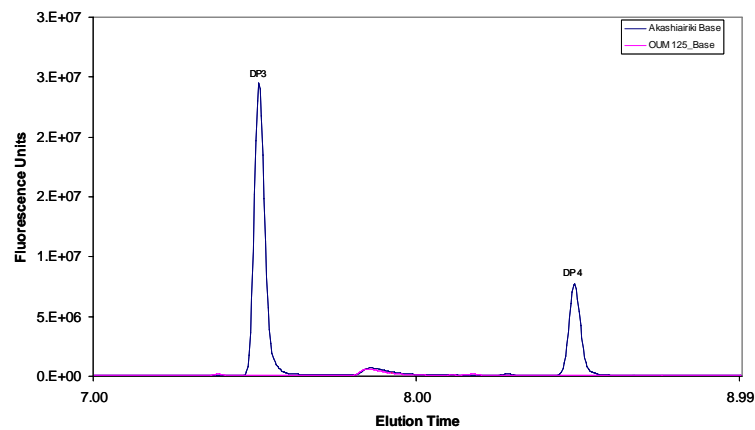
OUM125

Fig. S4

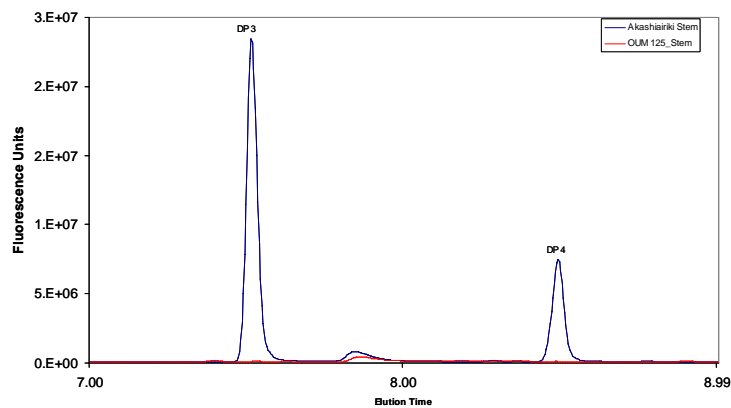
Seedling tissue - Akashiniriki vs OUM 125



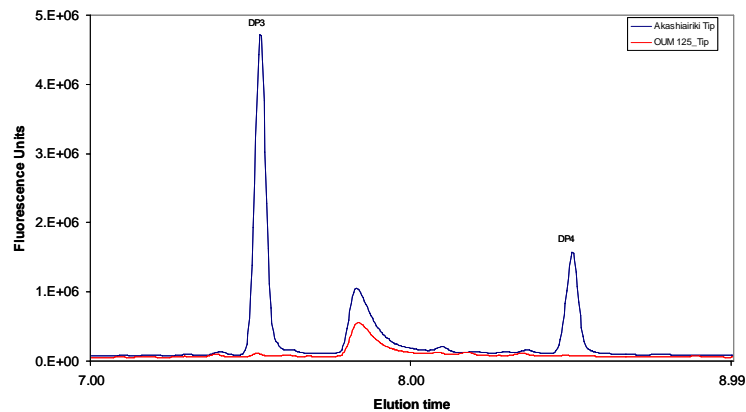
ROOT



LEAF BASE



STEM



LEAF TIP

DP3

DP4

DP3

DP4

Fig. S5

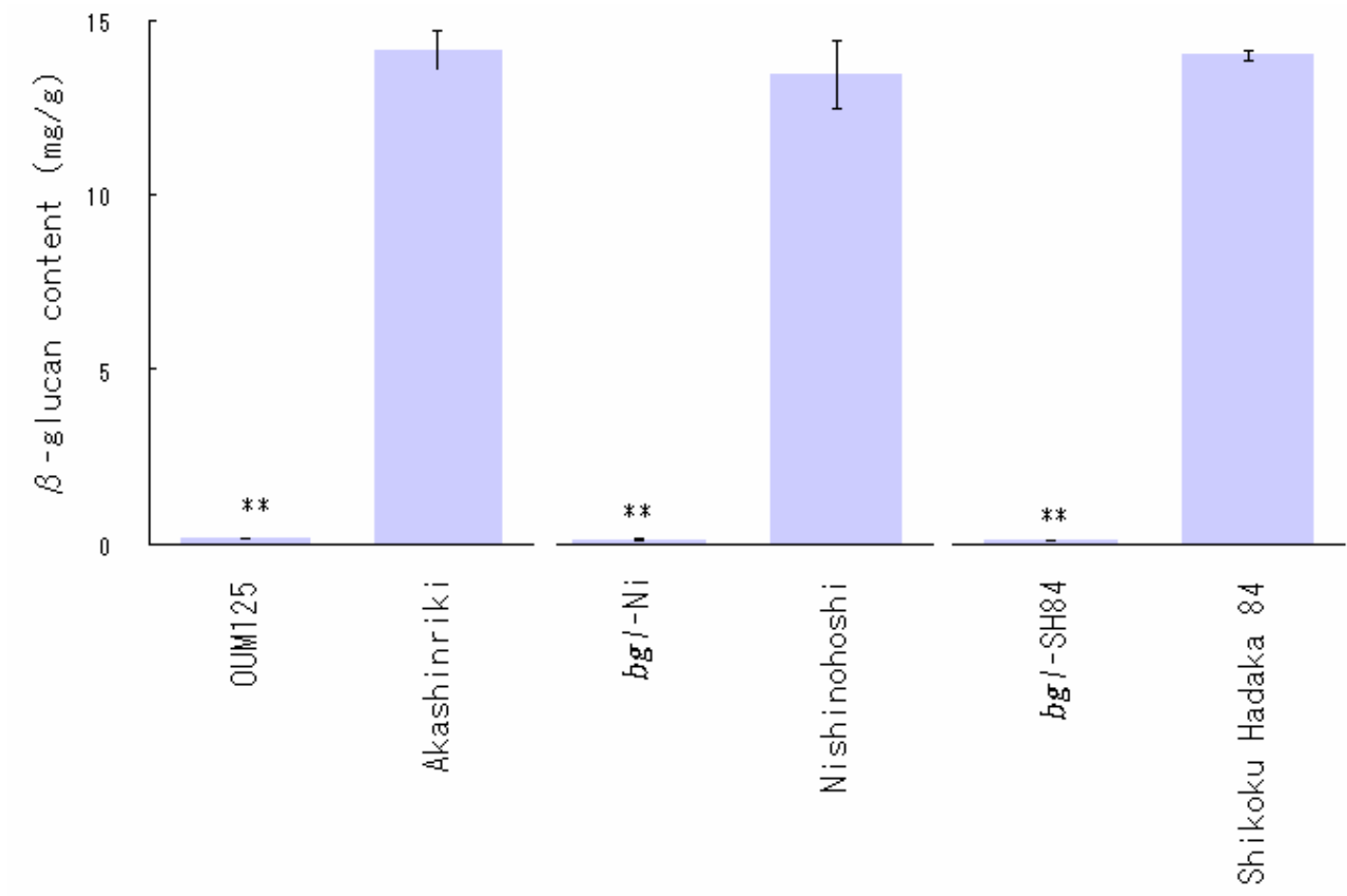


Fig. S6

Supplementary Table S1. Primer sequences used in this study.

Primer name	Primer sequence (5'-3')
Mapping	
<i>Waxy</i> (F)	TGGATCCAAATCCTGCATGT
<i>Waxy</i> (R)	CATGGTTTTGTCCGGTTTC
<i>HvGlb2</i> (F)	CTCTTGAGAATCCTCACCTTTCAT
<i>HvGlb2</i> (R)	CTCAATAAAAAGTATGCCCAAAATG

Genomic sequencing of *HvCslF6*

For amplification of the entire gene	
HvCSLF6_CP1-1F	AGAGTGAGTGCGTGCATTGAG
HvCSLF6_CP1-2R	TGTTGAGTGGATGAGTTGTTTCTT
For internal sequencing	
N8.B10-M13-RV(2)	CAATTAACCCAACAAGCACC
N8.B10-M13-RV(3)	AGTTTTTGTGAGCGTTTTATG
N8.B10-M13-RV(4)	GACTTGCCAGCTCTCTCCTT
N8.B10-M13-RV(5)	AACACATGCTACGTCTCCGA
N8.B10-M13-RV(6)	GTGGTGATAGTCGAGAGTGC
N8.B10-M13-RV(7)	GCTGCTCTCCAACCTCCCCCT
N8.B10-M13-RV(8)	AGGACGTGGTCACCGGCTAC
N8.B10-M13-RV(9)	TCACATCCAAGCTACCCTCG
N8.B10-M13-20(2)	GAATATCACCTTGGTCAGCA
N8.B10-M13-20(3)	GCCACGATCCCCCTCAGCCGC
N8.B10-M13-20(4)	CACGTACACCAGCATGGGGA
N8.B10-M13-20(5)	GAGGCCCTAACTAACCAAGA
N8.B10-M13-20(6)	AGGATGGAGAGCACCGAGTT
N8.B10-M13-20(7)	CGAGCTGGCACACTTGGC
N8.B10-M13-20(8)	AAACTCGCCGTACATAGGAT
N8.B10-M13-20(9)	TGCTTGTGGGTTAATTGTAGT

cDNA sequencing of *HvCslF6*

For amplification of the entire cDNA	
HvCSLF6_CP1-1F	AGAGTGAGTGCGTGCATTGAG
HvCSLF6_CP1-1R	TTGAGTGGATGAGTTGTTTCTTGT
For internal sequencing	
HvCslF6 F2	GTATTCCGCACCCGAGAAGAT
HvCslF6 F4	CTACGTCTCCGACGACAGTG
HvCslF6 F7	CCTCGACTGCGATCATTACA
HvCslF6 F9	AAGGGTAAGCACGGCTTCTTG
HvCslF6 F11	CTACCTGGGCATCGTGTAT
HvCslF6 R1	GAGAGGATGGGCTCCTTGAT
HvCslF6 R3	ATGAAGGGGGAGTTGGAGAG
HvCslF6 R4	GTCGAAGAAGATGCGGTTGT
HvCslF6 R6	ATGAAGGCGTGTGGGTAGAT
HvCSLF6_P28R	GCACCCAGAAGTTGAAGAAGAC

bgl.b mutant allele detection in KM27: Restriction enzyme *Bsr* FI

HvCSLF6_MPP2-1F	ATCAAGGAGCCCATCCTCTC
HvCSLF6_MPP2-1R	TTGATCCTGGCCTTGAAGTC

bgl.c mutant allele detection in KM30: Restriction enzyme *Fnu* 4HI

HvCSLF6-MPP- L	TGGGTGTACGACACCGTCA
HvCSLF6-MPP-R	GCGGAGCACCTGGAAGAG

Supplementary Table S2. Allelic variation in genomic sequences of the *HvCSLF6* gene.

Polymorphism	intron 1																	intron 2										exon 3		
nt position	174	333	412	558	620	749	752	988	1064	1137	1162	1188	1212	1398	1491	1530	1656	1737	2768	2958	3070	3133	3164	3173	3175	3262	3317	3347	4064	4801
nt change	G → A	C → T	C → A	A → G	G → C	T→ A	ins. 31	→ G	→ T	Δ 14	→ G	→ C	→ G	→ A	Δ 2	→ G	→ C	→ T	T → C	C → T	G → A	C → T	C → T	ins. 338	(CA TT) ⁿ	A → G	(T) ⁿ	T → C	G → A	T → C
aa change	no	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	A → T	no
aa position	58																												590	835
	SNP1	SNP2	SNP3	SNP4	SNP5	SNP6	indel 1	SNP7	SNP8	indel 2	SNP9	SNP10	SNP11	SNP12	indel 3	SNP13	SNP14	SNP15	SNP16	SNP17	SNP18	SNP19	SNP20	indel 4	SSR1	SNP21	indel 5	SNP22	SNP23	SNP24
OUH625	G	C	C	G	G	T	no	T	C	no	T	T	A	G	no	C	T	C	T	C	G	C	C	no	3	A	9	T	G	T
Beka	G	C	C	A	G	T	no	T	C	no	T	T	A	G	no	C	T	C	T	C	G	C	C	no	3	A	9	T	G	T
Sachiho Golden	G	C	C	A	G	T	no	T	C	no	T	T	A	G	no	C	T	C	T	C	G	C	C	no	3	A	9	T	G	T
Derkado	G	C	C	A	G	T	no	T	C	no	T	T	A	G	no	C	T	C	T	C	G	C	C	no	3	A	9	T	G	T
Haruna Nijo	G	C	C	A	G	T	no	T	C	no	T	T	A	G	no	C	T	C	T	C	G	C	C	no	3	A	9	T	G	T
OUI444	G	C	C	A	G	T	no	T	C	no	T	T	A	G	no	C	T	T	T	C	G	C	C	no	3	A	9	T	G	T
OUJ066	G	C	C	A	G	T	no	T	C	no	T	T	A	G	no	C	T	C	T	C	G	C	C	no	3	A	9	T	G	T
OUM382	G	C	C	A	G	T	no	T	C	no	T	T	A	G	no	C	T	C	T	C	G	C	C	no	3	A	9	T	G	T
M-737	G	C	C	A	G	T	no	T	C	no	T	T	A	A	no	C	T	C	T	C	G	C	C	no	3	A	9	T	G	T
CDC-Fibar	G	C	C	A	G	T	no	T	C	no	T	T	A	A	no	C	T	C	T	C	G	C	C	no	3	A	10	T	G	T
Azhul	G	C	C	A	G	T	no	T	C	no	T	T	A	A	no	C	T	C	T	C	G	C	C	no	2	A	9	T	G	T
B83-12/21/5	G	C	C	A	G	T	no	T	C	no	T	T	A	A	no	C	T	C	T	C	G	C	C	no	3	A	9	T	G	T
Minerva	G	C	C	A	G	T	no	T	C	no	T	T	A	A	no	C	T	C	T	C	G	C	C	no	3	A	9	T	G	T
OUH725	G	C	C	G	G	T	no	T	T	no	G	T	G	G	no	C	T	C	T	C	A	C	C	+	3	A	9	T	G	T
OUH737	G	C	C	G	G	T	no	T	T	no	G	T	G	G	no	C	T	C	T	C	A	C	C	+	3	A	9	T	G	T
OUH602	C	C	C	G	G	T	no	T	T	no	G	T	G	G	no	C	T	C	T	C	A	C	C	+	4	A	9	T	G	T
Nishinohoshi	G	T	C	G	G	T	no	T	T	no	G	T	G	G	no	G	T	C	T	C	A	C	C	no	3	A	9	C	G	T
OUH639	G	C	C	G	G	T	no	T	T	no	G	T	G	G	no	G	T	C	T	C	A	C	T	no	3	G	9	T	G	T
Shikoku Hadaka 84	G	C	C	G	G	T	no	T	T	no	G	T	G	G	no	G	T	C	T	C	A	C	T	no	3	G	9	T	G	T
SH 84 (lys5h)	G	C	C	G	G	T	no	T	T	no	G	T	G	G	no	G	T	C	T	C	A	C	T	no	3	G	9	T	G	T
Akashinriki	G	C	C	G	G	T	no	T	T	no	G	T	G	G	no	G	T	C	T	C	A	C	T	no	3	G	9	T	G	T
CDC-Bold	G	C	C	G	G	T	no	T	T	no	G	T	G	G	no	G	T	C	T	C	A	C	T	no	3	G	9	T	G	T
Logan	G	C	C	G	G	T	no	T	T	no	G	T	G	G	no	G	T	C	T	C	A	C	T	no	3	G	9	T	G	T
Himalaya	G	C	C	G	G	T	no	T	T	no	G	T	G	G	no	G	T	C	T	C	A	C	T	no	3	G	9	T	G	T
Bowman	G	C	C	G	G	T	no	T	T	no	G	T	G	G	no	G	T	C	T	C	A	C	T	no	3	G	9	T	G	T
Morex	G	C	C	G	G	T	no	T	T	no	G	T	G	G	no	G	C	C	T	C	A	C	T	no	3	G	9	T	G	T
Steptoe	A	C	A	G	C	T	no	G	T	Δ14	G	C	G	G	Δ2	C	T	C	C	T	G	T	C	no	3	A	9	T	A	C
OUT329	A	C	A	G	C	A	+	G	T	Δ14	G	C	G	G	Δ2	C	T	C	C	T	G	T	C	no	3	A	9	T	A	C
TR251	A	C	A	G	C	T	no	G	T	Δ14	G	C	G	G	Δ2	C	T	C	C	T	G	T	C	no	3	A	9	T	A	C