24.3 2882222222228 Mede 0 M-P M-c M-r M-r M-r M-r M-r M-v M-v M-v M-z M-z M-z M-z M-z 1- M2 A L L

Figure S1. The size of W1943 segment in NIL8. Blue bars indicate Guangluai 4 genomic background. Red bar indicates the W1943 genomic segment. The underside show the order of the markers used in this study and the upside numbers show the physical distance (Mb) according to Nipponbare genome chromosome 4 sequence.



Figure S2. Plant and panicle architecture of NIL8 and Guangluai 4. A, Plant architecture of NIL8 (left) and Guangluai 4 (right). B, Panicles of NIL8 with black hull (left) and Guangluai 4 with straw-white hull (right).

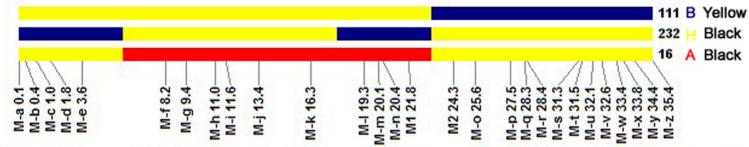


Figure S3. Some of F2 individuals used for *Bh4* primary mapping. The numbers and letters at right represent the serial number and *Bh4* genotypes of each F2 individual respectively. A: indicates SL4 (W1943) homozygous, B: indicates Guangluai4 homozygous, H: heterozygous. The genotype of *Bh4* locus of each F2 individual was judged from the corresponding F3 population. From these three individuals, the *Bh4* was localized in the region between the M1 and M2 markers.

AtAAP1	20 40 60 80 100 12 :MKSFNTEGHNHSTAESGDAYTVSDPTKNVDEDGREKRTGTWLTASAHIITAVIGSGVESLA-WAIACEWAATSILEIFSFITYFTSTMLA	
AtAAP8 AtAAP6	:MDAYNNPSAVESGDAAVKSVDDDGREKRTGTFWTASAHIITAVIGSGV SLA-WAIAC CM A TTVL AFAIITYYTSTLLA :DTNKNFDEDGRDKRTGTWMTGSAHIITAVIGSGV SLA-WAIAC CM AS PAVL AFSFITYFTSTMLA	: 83
AtAAP2 AtAAP4	MGETAAANNHRHHHHHGHQVFDVASHDFVPPQP-AFKCFDDDGRLKRTGTVWTASAHIITAVIGSGV SLA-WAIAC CW AC PAVM LFSLVTLYSSTLLS 	: 101
AtAAP3	:MUQNHQTVLAVDMPQTGGSKYLDDDGKNKRTGSVWTASAHIITAVIGSGV SLA-WATAC FW AC PVVM LFSAVTYFTSSLLA	: 85
AtAAP5 AtAAP7	:MUVQNVQDLDVLPKHSSDSFDDDGRPKRTGTVWTASAHIITAVIGSGVISLA-WAVAQTGWIGFPVAM LFSFVTFYTSTLLC: :MDIKEMDIKEDDESRVITPTELQLHDSVTARTGTLWTAVAHIITGVIGAGVISLA-WATADIGWIA-PAAL AFAGVTLLSAFLLS	: 83
AtProT1	:MTATEAKNRKINVGDGDDVVDIEIPDTAHQISSDSWFQVAFVLTTGINSAYVEGYSGTIMVPECWECVGLEIATAISLYANTLIA	: 88
AtProT2 LeProt1	:MUR GUVGL LATAISLYANTIA :MGNNRYNSPSREDKNDEEASVIIPETAHQVSNDSWFQVGVVLSMGVNSAYAHGYSGTIMVPIGNG VGL MSTIVSLYASTIMA :MEGEERGVWRWSKRDFFPEESFQSFGSYRAALSQTCSRFKNRLVSRSDDEWERFELKKQSEHEMKRG TWWDLVWFGNS IGAGIF LTOGGEAHEQAGPAT	
AtCAT5 AtCAT8	:MEGEERGYWRWSKRDFFPEESFQSFGSYRAALSQTCSRFKNRLVSRSDDENERFELKKQSEHEMKRC TWWDLVWFGFES IEAGIFWLTGQEAHEQAGPAI : MIPASMEEAHQLESRSDDLSQRRSYWRWRKQDFFPEFSFQSFSTYKSALSATCPRLADRLLSRSSDAYELDAARRESENPMRRC TWWDLLWLSFESDVGSGVFY ITGQEARVGAGPAV	
AtCAT1	:MASGGGDDGLRRRGCSCTKDDFLPEESFQSMGNYLKALKETPSRFMDRIMTRSLDSDEINEMKARSGHEMKKT TWNDLMWFG 🗗 🖬 🖬 SGIF ITGLEARNHSGPAV	: 109
AtCAT6 AtCAT7	:MEVQSSSNNGGHSSFSSLRVYLNSLSATPSRLSRRAISVSTSSDEMSRVRAVSGEQMRRT RWYDLIGLG GG VGAGVFATTGRASRLDAGPSI :MEAQYR-NHDGDTSFSSLRVYLNSLSDTPSRFSRRAVSVSTSYDEMSRVRAVSGEQMRRT RWYDLIGLG GGIGAGVFATTGRASRLYAGPSI	
AtCAT2	:CSHGHQLARA TVPHLVAIG ATICAGVY LVGTVAREHSGPSL	: 79
AtCAT3 AtCAT4	:MGCLRSLVRRKQFDSSNGKAETHHHHQQLAKA TFPHLIAIC STICAGVY LVGTVAREHSGPAL :MNSLVRRKQVDSVHLIKNDGPHQLAKK SAVDLVAIC STICAGVY LVGTVAREHTGPAL	
AtCAT9 AtLHT1	:MGGHEGFSNQRLSSATWFSHFRASALRSKSLPPPSSQTAVRSTSGDSLVRR GLFDLILLG ASIFAGVF VTGTVARDAG-PGV :MVAQAPHDDHDDEKLAAARQKEIEDWLPITSSRNAKWWYSAFHNVTAMVGAGV GLP-YAMSC WGFGIAVLLSWVITLYTMQMV	
AtANT1	:WAIKDLTATTGDSSLPLIKSPPSETTGGDRTSALQTLGNIIVSIVGTGVEGLP-YAFRIACMEAESLGVEIVGFATYYCMLLLI	: 84
Bh4 AtAUX1	:mpvgtartcmnglnalsgvgif tvp-yalsegen s-lallaavaaacwytgillc: :msegveaivandngtdqvngnrtgkdneehdgstgsnlsnflwhggsvwdawfscasnqvaqvif tlp-ysfscien si vlof fygllgswtaylis	: 55
	1 G g	
3+3301	* 140 * 160 * 180 * 200 * 220 * 24	
AtAAP1 AtAAP8	: CYRAPDPVTG-KRNYTMDVVRSYLGGRKVC CGVAQ GNLIG TIG TITASISLVAVGKSNCFHDKGHTADCTISNYPY AVFGIIQVILSQ PNFHKLSFLSI : CYRSPDSITG-TRNYNMGVVRSYLGGKKVC CGVAQ VNLVG TIG TITASISLVAIGKSNCYHDKGHKAKCSVSNYPY AAFGIVQIILSQ-PNFHKLSFLSI	: 189
AtAAP6 AtAAP2	: CYRSPDPVTG-KRNYTMEVVRSYLGGRKVQ CGLAQ GNLIG T G THASISMVAVKRSNCFHKNGHNVKCATSNTPFS IIFAIIQIILSQ PNFHNLSWLSI : CYRTGDAVSG-KRNYTMMDAVRSILGGFKFK CGLIQ LNLFG A G THAASISMMAIKRSNCFHKSGGKDPCHMSSNPYS IVFGVAEILLSQ PDFDQIWWISI	
AtAAP4	: CYRTGDPVSG-KRNYTMDAVRSILGGFRKCGLICMLNLFGTGGTAASISMMAIKRSNCFHESGGKNPCHMSSNPYGIMFGVTEILLSG-KKDFDQIWWLSI	: 180
AtAAP3 AtAAP5	: CYRSGDPISG-KRNYTMMDAVRSNLGGVKVT CGIVOLNIFG AFG TASAISMMAIKRSNCFHKSGGKDPCHMNSNPYSIAFGLVQILFSQ-PDFDQLWWLSI : CYRSGDSVTG-KRNYTMMDAIHSNLGGIKVK CGVVO VNLFGTAGG TASAISLVAIQRTSCQQMNGPNDPCHVNGNVYSIAFGIVQIIFSQ-PDFDQLWWLSI	
AtAAP7	: CYRFPDPNNGPLRINSHSGAVKLYLGKKNEIECGVVVEISLFGCGEAETHVIATCSRAIMKSNCYHRNGHNATCSYGDNNNYFEVLFGLTQIFMSQ-EPNFHNMVWLSL	: 190
AtProT1 AtProT2		
LeProt1	: LHEVGGKRHIRERDLAGFLYGRTAYLEIWALGEANLFLENEGEVEMSGSALKAFYMLFRDDHMLKLPHFEAIAGVACILFAIATPHLSALRVWLG	: 183
AtCATS AtCAT8	: LSYVVSGLSAMLSVFCYTEFAVEIPVAG-GSFAYLRIÐ GDFAA ITAGN I ESINGTAAVARAWTSYFATLINRSPNALRIKTD-SSGENLLDPIAVV IAASATIASIS : LSYAISGVSALLSVLCNAEFGVEIPVAG-GSFSYLRVÐ GDFIA IAAGN I EANNGAAGLGRSWSSYLASLVKNDSDYFRIKVDSFAKGFDLLDPVAVALLVANGIAMTG	: 233
AtCAT1 AtCAT6	: LSYVVSGVSAMLSVFCTTEFAVEIPVAG-GSFAYLRVE GDFMA IAAGN I BUVGGAAVARSWTSYFATLLNHKPEDFRIVHK GEDYSHLDPIAVG CAIICVLAVVG	: 222
AtCAT6 AtCAT7	: VSYAIAGLCALLSAFCTTEFAVHLPVAG-GAFSYIRITFGEFPA ITGAN ITGAN ITGAN TO THE SNAAVSRGFTAYLGSAFGISTSEWRFIVSG PNGFNEIDPIAVI VLAVTFVICYS	: 208
AtCAT2 AtCAT3	: LSFLIAGIAAGLSAFCAAELSSRCPSAG-SAYHYSYICTGEGVATIIGWATIPDTTGGSAVARGISPNLALIFGGEDGLPAILARHCPGLDIVVDPCAATVFVVTGLLCMG : LSFLIAGISAALSAFCAAELSSRFPSAG-SAYHYSYICTGEGVATIIGWATIPDTGGSTVARGISPNLAMIFGGEDCLPTILARHCPGLDIVVDPCAAVVFVTGLCCLG	
AtCAT4	: VSFFIAGVAAALSACCAAELASRCPSAG-SAYHYAYIC GEGIACLVGWAEVE DETAGGSAIARGITPNLASFFGGLDNLPVFLARCTEPGVGIVVDPCAALEIMIVTILLCFG	: 177
AtCAT9 AtLHT1	: ISFLLAGASCVLNALCHAELSSRFPAVVGGAYMYSYSAFNEITAELVFVC M DERGASSISRSLASYAVALLELFPALKGSIPLWMGSGKE LGGLLSLNILAPIELALLTLVLCQG : MHEMVPGKRFDRHELGQHAFGEKLGLYEVVPQQLIVEIG CVVMTGGKSLKKFHELVCDDCKPKLTYFIMIFASVHFVLSH PNFNSISGVSL	: 206
AtANT1	: CRDKLESEEGEEESKTMGDLGFKCMGTKGRYETEFLIETAOCGGSEABINFIGRNLSSIFSSYGLSMVSFILILVPIEVGLSWETSLSALSPFSI	: 180
Bh4 AtAUX1	: CMDADDAIRTYPDIGERAFGRTGRL VSAFTYVELYLATG LALEGDNLDKLFPGARVILGTVSLAGKRLFVVLVALVVAPTTWLRSLGVLAY : LYVEYRARKE-KEGKSKNHVIQWFEVLDGLGSYWKALGLAFNCTGLAFGSVIQLIACASNIYYINDHLDKRTWTYIFGACCATTVFPSFHNYRIWSF	: 150
	5 6	0.21.20200
	* 260 * 280 * 300 * 320 * 340 * 36	
AtAAP1 AtAAP8	: AAVMSFTYATIG G AIATVAGG-KVGKTSMTGTAVGVDVTAAQK WRSFQAVGD A AAAYATV IE ODT -RSSPA-ENKAKKRASLAGVSTTTFFYILCGG GYAAFGNN : AAVMSFSYASIG G AIATVASG-KIGKTELTGTVIGVDVTASEK WKLFQAIGD ASSAAFTTI IE ODT -RSSPP-ENKVSKRASLAGVSTTTVFYILCGG GYAAFGNN	
AtAAP6	ANVMSFCYASIG GISIAKAAGGGEHVRTTLTGVTVGIDVSGAEK WRTFGAIGD ABAYSTVEIE ODT -KAGPPSENKAK KRASLEGVSTTTFFYMLCGC GYAAFGOD	: 308
AtAAP2 AtAAP4	: AAVMSFTYSAIG A GIVQVAAN-GVFKGSLTGISIGTVTQTQK WRTFQALGD A AMSYSVV IE QDTV-RSPPA-ESKTSKKATK SIAVTTIFYMLCGS GYAAFG A : AAIMSFTYSAIG A GIIQVAAN-GVVKGSLTGISIGAVTQTQK WRTFQALGD A AMSYSVV IE QDTV-RSPPA-ESKTSKIATR SIAVTTFYMLCGO GYAAFG K	: 318
AtAAP3	: AAVMSFTYSSAG AGAAQUVUN-GKVKGSLTGISIGAVTETOX WRTFOALGD AGAASYSII IE IE ODTG-KSPPS-EEKTSKKATLGSVSVTTMFYMLCGO GYAAFGL	: 302
AtAAPS AtAAP7	: AAVMSFAYSAIG G GVSKVVEN-KEIKGSLTGVTVGTVTLSGTVTSSOK WRTFOSLGN AF ANSYSMI IE ODT -KSPPA-EVNT RKATFISVAVTTVFYMLCGO GYAAFG N : AAIMSFTYSFIG G ALGKIIEN-RKIEGSIRGIPAENRGEK WIVFOALGN AS SUPFSII LE ODT -RSPPA-EKOT KKAST AVFIOTFFFFCCGCFGYAAFG S	. 200
AtProT1	STELSLIVIVA V SVRDGVKT-PSRDYELQGSSLSKFFTTGAAAN VAAN-TGM PEQAT - ROPVKNMKALYFQFTAGVLPMYAVTF GYWAYGSS	: 286
LeProt1	: STILSIIVIIVA V SAKDOVNK-PERDYNIQGSSIN	: 285
AtCAT5 AtCAT8	: RKTSLLNWIASA NTLVIFFVIIAGFIHADTSNLTPFLPFGPEGVFRAAAVYGAAGGFDS ATVAEET-KNPSRDIPIG LGSMS ITVIYCLMALSLSM QKYTDI P • KRTSWINIITSMATMCTTUFTUUVCFTHEKTSNLUDFEPVGAKGUVQSAAWYGATGFDM AMAPPT-FKPSRDIPIG LGSMS ITUUVCTMALAITMUVYTTA	: 325
AtCAT1	: RKTSLLNWIASA NTLVIFFVIIAGFIHADTSNLTPFLPFGPEGVFRAAAV Y ANGGEDS AT AEET-KNPSRDIPIG LGSMS ITVIYCLMALSLSM QKYTDI P : KRTSWLNLITSM T CIIVFIVVUGFHSKTSNLVPFFPYGAKGVVQSAAV Y STGFDM AN AEET-EKPSRDIPIG VGSMS ITVVYCLMALALTM VKYTEI A : KGSSRFNYIASI H VVILFVIIAGFTKADVKNYSDFFPYG RGVFKSAAV F ANIGEDA ST AEET-KNPGRDIPIG VGSMV TTVCYCLMAVTLCL QPYQQI P	: 332
AtCATO	: KESSKVNNINTAPHARIFFVIVNOFINGUSKNUSSPANPENSGFFFGGAGVINGAAR ILSAIGTLANSTAAEN -ENVKLIPVOISGSVAFVTVLICLAAVSSST UPUDLI P BESEKUNNINTAPHARIFFVIVNOFINGUSKUSSPANPENSGFFFFGGAGVINGAAR ILSAIGTLANSTAAEN -KNOUKNITAMG GAGVILUUTU VOINAISMAN LUUTIN	: 328
AtCAT2	: KESTFAQGIVTAN N CVLLFVIVAGSYLGFKTGNPGYELPTGFFPFG DGMFAGSATYFFA IGFDS ASTAED -RNPORDLPIG GLALL CCSLYMMVSIVIVG IPYYAM P : KESTFAQGIVTTAN FVMIFVIVAGSYLGFKTGNVGYELPTGYFPFG DGMLTGSATYFFANIGFDT AS AED -KNPRRDLPLG GISLL CCLLYMNVSVVIVG VPYYAM P : KESSTVQAIVTS N CTLVFIIVVGGYLACKTGNVGYDLPSGYFPFG NGILAGSAV F SNIGFDT TSTAED -KNPORDLPLG GIALL CCILYMLLSVVVG VPYYSL P : RESSAVNSVMTATK VIVLVVICAGAFEIDVANNSFFAPNGFKAVLTGATV F SVGFDA ANSAEES-KNPORDLPIG MGSLL CISLYIGVCLVLTG VPFSLLSE	: 309
AtCAT3 AtCAT4	: KESTFAQGIVTTAN FVMIFVIVAGSYLCFKTGWVGYELPTGYFPYG DGMLTGSAT FPADIGFDT ASSAED -KNPRRDLPLGIGISLL CCLLYMMVSVVIVG VPYYAM P : KESSTVQAIVTS NCTLVFIIVVGGYLACKTGWVGYDLPSGYFPFG NGILAGSAV FSDIGFDT TSTAED -KNPCRDLPLGIGIALL CCLLYMLLSVVIVG VPYYSL P	: 298
AtCAT9	: RESSAVNSVMTATK VIVLVVICAGAFEIDVANWSPFAPNGFKAVLTGATVVFS VGFDAVANSAEES-KNPCRDLPIG MGSLL CISLYIGVCLVLTG VPFSLLSE	: 316
AtLHT1 AtANT1	: AAVMSLSYSTIAWASSASKGVQEDVQYGYKAKTTAGT FNFFSGLGD, AFAMAGHNVILE QAT PSTPEKPSKGPWRGVILAYIVVALCYFPVAL GYYIFG G : ADICNIIAMCFVIKENVEMVIEGDFSFSDRTAISSTGGLPFAGGVAV GEGFAMTLA ESSREREAFPKLLAKVLAGITFVYVLFGFCGYMAYG Q	: 293
Bh4 AtAUX1	: ADICNIIAMCFVY KENVEMVIEGDESFSDETAISST	: 250
	5	
	* * 400 *420 *460 *480	
AtAAP1 AtAAP8	: PGDFLTDFGFFEPFFLIDFANACIAVH IGAYOFFAQDIFQFMEKKCNRNYPDNKFITSEYSVNVPFLGKFNISLFR VWRTAY-VVTTTVMAMIFPFFNAI GIGAASFW : PGDFLTDFGFYEPYGLIDFANACIALH IGAYOYYAQPFFQFMEENCNKKWPQSNFINKEYSSKVPLLGKCRVNLFR VWRTCY-VVTTTFMAMIFPFFNAI GLGAFAFW	: 412
AtAAP6	: PGNFLTGFGFYEPFELIDFANVCIAVH IGAYON FCOPIFOFNESQSAKRWPDNKFITGEYKIHVPCCG-DFSINFLR VWRTSY-VVETAVNAMIFPFFNDF GIGAASFW	: 419
AtAAP2 AtAAP4	: PGNLLTGFGFYNPFELLDIANAAIVVH VGAYOFFAQPIFAFEKSVAERYPDNDFLSKEFEIRIPGFKS-PYKVNVFROVYRSGF-VVTTV SMLMPFFNDVG LGALGFW : PGNLLTGFGFYNPFELLDVANAAIVIH VGAYOFFAQPIFAFEKQAAAFFPDSDLVTKEYEIRIPGFRS-PYKVNVFRAVYRSGF-VVETTVESMLMPFFNDVG LGALGFW	: 403
AtAAP3 AtAAP5	: PGNLLTGFGFYNPYNLLDIANAAIVIH IGAYON YCOPLFAF EKQASIOFPDSEFIAKDIKIPIPGFKPLRLNVFR IWRTVF-VI TTV SMLLPFFNDV G LGALGFW : PGNLLAHGGFRNPYNLLDIANLAIVIH VGAYON YCOPLFAF EKEASRRFPESEFVTKEIKIQLFPGKPFNLNLFR VWRTFF-VMTTTI SMLMPFFNDV G LGALGFW	: 413
AtAAP7	: PGNLLTGFGFYEPFELVDFANACIVLHEVGGYGEYSOPIFAAAERSLTKKYPENKFIARFYGFKLPLLRGETVRLNPMRECLRTMY-VLETTGEAVMFPYFNEVEGEVGALAFW	: 412
AtProT1 AtProT2	: STYLLNSVNGPLOVKALANVSAILQSVISLH FASPTYEYDDTKYGIKGNPFAIKNLLFR MARGGY-IAMSTI SALLPFLGDFNS TGAVSTF : STYLLNSVSGPW/VKALANISAFLOSVISLH FASPTYEWDTKYGVKGSDLAMKNLLFRTVARGSY-IAMSTI SALLPFLGDFNS TGAISTF	: 380
LeProt1		: 379
AtCATS AtCAT8	: AAYSVAFQ-SVGMK GKYLVALGALKG TTVLL GALGQARYTTHIARTHMIPPIFALVHPKTGTPINANLLVAIPSAL AFFSGL-DV ASL SISTLFIFTM PALLVRRYVROD : AAYSVAFA-QIGMK AKYLVGICALKG TTSLL GSLGQARYTTQIARSHMIPPWFALVHPKTGTPIYATLLVTILSSI SFFTSL-EV SSVFSFATLFIFML A ALLVRYVKDV	: 443
AtCAT1	: APFSVAFS-AVGWDGAKYIVAFGALKGGTTVLLEGAIGQARYGTHIARAHMMPPWLAQVNAKTGTPINATVVMLAATALEAFFTKL-KIEADLESVSTLFIFMFGAEALLVRRYYVTGE	: 450
AtCAT6 AtCAT7	: APFSAAFRGSNGWE VTKVVGIGASFG LTSLL AMLGQARY CVIGRSRVVPFWFAKIHPKTSTPVNASTFLGIFTAA ALFTDL-NV LNI SIGTLFVFYM ANALIFRRYVPVGP : APYSAAFSKSEGWE VTRVVGIGASFG LTSLIMAMLGQARY CVIGRSRVVPIWFAKVHPKTSTPVNASAFLGIFTAV ALFTDL-NV LNI SIGTLFVFYM ANAVIFRRYVTVGY	: 446
AtCAT2 AtCAT3	: TPISSAFA-SHDMQ'AVYLITLGAVMA CSALMGALLPQPRI MAMARDGLLPSIFSDINKRTQVPVKATVATGLCAAT AFFMDV-SC AGM SVGTLLAFTM A SVLILRY-VPPD : TPISSAFS-SHGIQ'AAYLINLGAVMA CSALMGSILPQPRI MAMARDGLLPSYFSYVNQRTQVPINGTITTGVCAAI AFFMDV-SC AGM SVGTLVAFTM A SLLIVRYVPPD	
AtCAT4	: TPISSAFG-DSGMC AAVILTTGAITA CASLLGSLLAOPRIFMAMARDGLLPAFFSEISPRTQVPVKSTIAIGVLAAA AFFMDV-AQ SEM SVGTLMAFTA ACVLVLRY-VPPD	: 410
AtCAT9 AtLHT1	: APLAEAFS-SKGMK VSILISIGAVAG TTTLL GLYVQSRLYLGLGRDGLLPSIFSRIHPTLHTPLHSQIWCGIVAGV AGIFNV-HSSHI SVGTLTGYSV AACVVALRLNDKKD : EDNILMSLKKPAGLIATANIFVVIH IGSYC YAMPVFDMETLLVKKLNFRPTTLRFFVRNFY-VAATMPGCMTFPFFGGL AFFGGFAFA	: 385
AtANT1	: KDIITINLENN SAIAVQIGLCVQ IFTFF MVHPINEI EQKIKKIDWLQKHHNGYSNETGSVSKFAIFTTRIL-VVGLAA ASLVÞGFGFFAS VGSTLCA : LSQVILNLESARISSKVAIYTTLINPVTKYA VVTPIAAN EERIRGAAGKGARAVS AVRTLL-VLSTVA ALALÞFFADI AF VGSMLNV	: 383
Bh4 AtAUX1	: LSQVTLNLPSARLSSKVAIYTTLLNPVTKYA∰VVTPIAAA∰EERIRGAAGKGARAVS∰AVRTLL-VLSTVA∰ALALÞFFADLØA∰VGSMLNV : LDHSNAFSLMPKNA∰R-DAAVILMLIHQFITFGFACTPLYFVWEKVIGMHDTKSICLRALARLPVVIPIWFLAIIFPFFGPINSAVGAI∰VSFTVYIIPSLAHM∰TYRSASARQNAAEK	: 341
AtAAPI	500 520 540 560 580 60 1	
AtAAP8		1 -
AtAAP6 AtAAP2		1 1
AtAAP4		: -
AtAAP3 AtAAP5		
AtAAP7	:	: -
AtProT1 AtProT2		
LeProt1 AtCATS	PRVHL	: 501
AtCAT8	PEAGL	: 517
AtCAT1 AtCAT6	: STRUKNKFLVFLGLILASSTATAVYWALEEEGWIGYCITVPIWFLSTVAMKFLVPQ : KPWPTLCFLTLFSITSLVFTLIWKLVPEGKPKAFMLGASAVVAIAIVLSFOCVVPO	: 507
AtCAT7	: EPWPTLSFLCLFSITSILFTLVWQLAPSGPPKWFILGASTVTAIAIVQIFHCVVPQ : QPLPSSLQERIDSVSFICGETTSSGHVGTSDSSHQPLIVNNDALVDVPLIKNQEALGCLVLSEETRRIVAGWSIMFTCVGAFLLSYAASSLSFPGLIRYPLCGVGGCLLLAGLIALSSI	: 503
	: QPLPSSLQERIDSVSFICGETTSSGHVGTSDSSHQPLIVNDALVDVPLINNQEALGCIVLSEETRRIVAGMSIMFTCVGAFLLSVAASSLSFPGLINVPLCGVGGCLLLAGLIALSSI : VPLPSSLQENSSSHVGTSIBSKOPLIGKVDDSVUDKFNAPGSWUNKKNBRKFSGWSIMFTCIGNFLLSVAASSFLDGLINVGLGVGGGLILIVGLIVLCI	

AtCAT3	:	VPLPSSLQENSSSHVGTSIRSKQPLLGKVDDSVVDKENAPGSWVLNKKNRRKFAGWSIMFTCIGNFLLSYAASSFLLPGLLRYSLCGVGGLFLLVGLIVLICID	: 520
AtCAT4	:	VPLSSSSQTLSDTDESRAETENFLVDAIESSDSPLLGNETARDEKYFGKRRKIAAWSIALVCIGVLGLASAASAERLPSFPRFTICGVSAVILLGSLITLGYID	: 514
AtCAT9	:	RESSNRWISSWQEGVICLVIIACSGFGAGVFYRFSASVIFILLSVGVAVVASAVL	: 488
AtLHT1	:		: -
AtANT1	:		5 H
Bh4	:		: -
AtAUX1	:		: -

			620		640		660		680			
AtAAP1	:		LTVYF	VEMHIAQT-KIN	KYSARWIAL	KTMCYVCLI	LAAAGSIAG	LISSVKTYK	PFRTMHE		:	485
AtAAP8	:		LTVYF	VAMHIAQA-KVE	KYSRRWLAL	NLLVLVCLI	SALAAVGSIIG	LINSVKSYK	PFKNLD		:	475
AtAAP6	:		LTVYF	IEMHIAQK-KIP	KESETWINL	KILSWTCFI	VAAAGSVQG	LIQSLEDFE	PFQAP		:	481
AtAAP2	:		LTVYF	VEMYIKOR-KVE	KWSTRWVCL	OMLSVACLV	VAGVGSIAG	VMLDLKVYK	PFKSTY		:	493
AtAAP4	:		LTVYF	VEMYIROR-KVE	RWSMKWVCL	OMLSCGCLM	VAGVGSIAG	VMLDLKVYK	PFKTTY		:	466
AtAAP3	:		LTVYF	VEMYIAQK-KIP	RWSTRWVCL	OVFSLGCLV	AAAAGSIAG	VLLDLKSYK	PFRSEY		:	476
AtAAPS	:		LTVYF	VEMYIAQK-NVE	RWGTKWVCL	OVLSVTCLE	SAAAAGSVIG	IVSDLKVYK	PFQSEF		:	480
AtAAP7	:		LAVYE	VENCILOK-KIP	SWTRPWLLL	RGFSFVCLL	LSLVGSIYG	LVGAI	KFG		:	467
AtProT1	:		LTFIL	NHMYYKAK-NNB	LNAMOKLWH	WLNVVFFSL	SAAAIAAVRL	IAVDSKNFH	FADL		:	442
AtProT2	:		LTFIL	NHMYLVAM-NDE	LSLVOKLWH	WLNVCFFGL	AAAIAAVRL	ISVDSKNFH	VFADV		:	383
LeProt1	:		LTFIL	NHMYIIAK-KDB	LNSLOKSWH	WLNIVVFGO	SAAFVAALKL	TVVOTOTYH	FADL		:	441
AtCAT5	:	RTPKVWGV									:	569
AtCAT8	:	RVPKVWGV	LVPWL	SFSIAMNL-FLI	GSLGYVAFL	RFIICTMVM	LYYLFVGLHAT	YDVAHOPLE	EAKFEGER		:	590
AtCAT1	:	RAPKIWGV	LVPWL	SASIAINI-FLI	GSIDTKSFV	RFAIWTGIL	IYYVLFGLHAT	YDTAKATLKI	EKOALOKAEE	GGVVADNSCSAT	:	594
AtCAT6	:	RKPELWGV	FMPWT	CVSIFLNI-FLI	GSLDAPSYV	REGEESGLIN	LAYLFYGVHAS:	SDAEANGSE	SVKDGOVMKE	LIEV	:	583
AtCAT7	:	RIPEFWGV	LMPWT	CVSIFLNI-FLI	GSLDAPSYI	REGEESGLV	LYVFYSVHAS	TDAEGDGSL	DEKDVESLER	INRVLS	:	584
AtCAT2	:	ODDARHTFGHSGGYMC	FVPLL	IICILINM-YLI	VNLGSATWA	RVSVWLLIG	INYVFYGRKNS:	SLANAVYVT	PAHAEEIYRE	HEGSLA	:	635
AtCAT3	:	ODDARHSFGHSGGFIC	FVPLL	IVCILINM-YLI	VNLGAATWV	RVSVWLFLG	WYIFYGRRNS:	SLVNAVYVS	TAHLOEIRRT	SGHSLA	:	609
AtCAT4		EDEERHNFGHKGGFLC	FVPYL	VLCILINT-YLI	INIGAGTWI	RVLIWLLIGS	YIFYGRSHS	LLNNAVYVP	INTCTRE	TTDHLA	:	600
AtCAT9	:	HYROAYALPLGSGFSC	GVPIV	SVCIFFNI-FLF	AOLHYEAWI	REVVVSVLAT	AYALYGOYHA	DESMLDYOR	APETESDA		:	569
AtLHT1	-		TTYFL	CVIWLAIY-KPR	KYSLSWWAN	WVCIVFGLE	LSPIGGLET	IVIOAKGYK	FYS		:	445
AtANT1			LISFUL	ASYHLTLL-GPS	LNVWNKSID	VFIVICGLIF	YGTYNTIVG	V			:	432
Bh4	-										:	396
AtAUX1	;									HRL	:	485
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Figure S4. Multiple sequence alignment of the rice BH4 protein and the amino acid transporter proteins from Arabidopsis and tomato.Black and gray shading indicate 100% and 80% conserved amino acid residues, respectively. The names of proteins are indicated on left side.

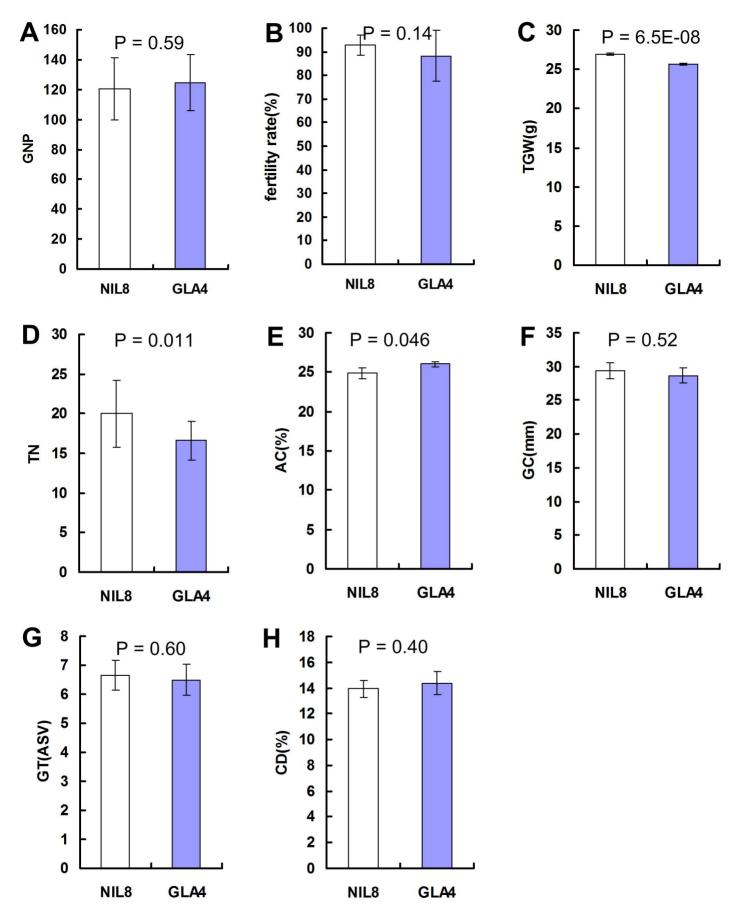


Figure S5. Comparison of grain number per panicle(GNP), fertility rate, thousand grain weight(TGW), tiller number per plant (TN), amylose content(AC), gel consistency(GC), gelatinization temperature(GT) and chalkness degree(CD) between NIL8 and Guangluai4(GLA4). For GNP, fertility rate, TN analysis, n=15; and TGW, AC, GC, GT, CT, n=3. All data are given as means ± s.e. A Student's t-test was used to generate the P values.

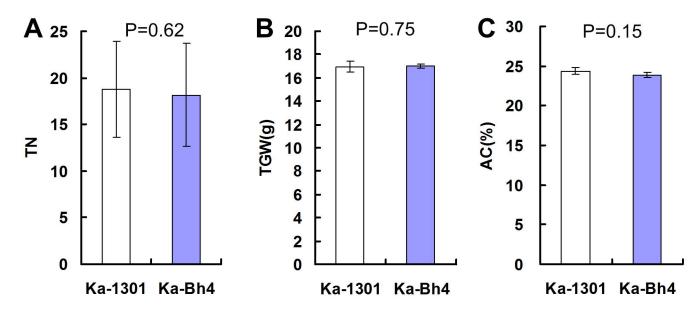


Figure S6. Comparison of TN (tiller number, A), TGW (Tousand grain weight, B) and AC (amylose content, C) between control (Ka-1301) and transgenic line(Ka-Bh4). There is no significant difference of the tree traits analyzed between control and transgenic line. This indicates the difference detected between NIL8 and GLA4 is caused by other genes. All data are given as means ± s.e. A Student's t-test was used to generate the P values.