



Figure S1. Banding pattern of product from Marker I with BpuEI digestion (A); and banding pattern of product from Marker II (B). Lanes 1-8: PCR amplification of rice with low AAC; Lane 9-15: PCR amplification of rice with high AAC; M: 100 bp molecular weight marker and N: negative control.

	reference	MAILLGDVLAPLP IALNLEYAAAIATPPDPALLGRRYHLRRC AAAARQDDEEEGEQE QEG-	59
1	KhaoJampi	MAILLGDVLAPLP IALNLEYAATIAMPDPDALLGRRYHLRRAAARKMMKKKATETMLEK	60
2	NguangChahng	MAILLGDVLAPLP IALNLEYAATIAMPDPDALLGRRHHLRRAAARKMMKKKATETMLEK	60
3	TahKhui	MAILLGDVLAPLP IALNLEYAATIAMPDPDALLGRRYHLRRAAARKMMKKKATETMLEK	60
4	KhaoGawDiaw	MAILLGDVLAPLP IALNLEYAATIAMPDPDALLGRRYHLRRAAARKMMKKKATETMLEK	60
5	HawmSurin	MAILLGDVLAPLP IALNLEYTATIAMPDPDALLGRRHHLRRAAARKMMKKKATETMLEK	60
6	JekChuey	MAILLGDVLAPLP IALNLEYTAAIATPPDPALLGRRYHLRRC AAAARQDDEEEGEQE QEG-	59
7	LaiMaejo	MAILLGDVLAPLP IALNLEYTAAIATPPDPALLGRRYHLRRC AAAARQDDEEEGEQE QEG-	59
8	NiawKhiawNgoo	MAILLGDVLAPLP IALNLEYTAAIATPPDPALLGRRYHLRRC AAAARQDDEEEGEQE QEG-	59
9	NiawDamHawmPooKhiaw	MAILLGDVLAPLP IALNLEYAAAIATPPDPALLGRRYHLRRC AAAARQDDEEEGEQE QEG-	59
10	LawdGwian	MAILLGDVLAPLP IALNLEYTAAIATPPDPALLGRRYHLRRC AAAARQDDEEEGEQE QEG-	59
	reference	-HG--NYVGKSTPKVPQLV NELQNRPLTAKPDIQRPLTNQNR SQMVL PWFSPRFC PMWRL	116
1	KhaoJampi	VHRRSLNLSTSYKIVP*-----	76
2	NguangChahng	VHRRSLNLSSSYKIVPQPQNQISNVP*-----	86
3	TahKhui	VHRRSLNLSSSYKIVPQPQNQISNVP*-----	86
4	KhaoGawDiaw	VHRRSLNLSTSYKIVP*-----	76
5	HawmSurin	VHRRSLNLSSSYKIVPQPQNQISNVP*-----	86
6	JekChuey	-HG--NYVRKSTSKVPQLV IELQNRPP TAKPDIQRPLTNQNR SQMVL PWFSPRFC PM*--	113
7	LaiMaejo	-HG--NYVRKSTSKVPQLV IELQNRPP TAKPDIQRPLTNQNR SQMVPV PWF*-----	106
8	NiawKhiawNgoo	-HG--NYVRKSTSKVPQLV IELQNRPP TAKPDIQRPLTNQNR SQMVPV PWF*-----	106
9	NiawDamHawmPooKhiaw	-HG--NYVRKSTSKVPQLV NELQNRPLTAKPDIQRPLTNQNR SQMVL PWFSPRFC PM*--	113
10	LawdGwian	-HG--NYVRKSTSKVPQLV IELQNRPP TAKPDIQRPLTNQNR SQMVPV PWF*-----	106
	reference	SQRGTHVDSIYQAATSTLNTMISTAITRCGRYLQRRSRH NAPS YLRSSSATRTISLSSA	176
1	KhaoJampi	-----	76
2	NguangChahng	-----	86
3	TahKhui	-----	86
4	KhaoGawDiaw	-----	76
5	HawmSurin	-----	86
6	JekChuey	-----	113
7	LaiMaejo	-----	106
8	NiawKhiawNgoo	-----	106
9	NiawDamHawmPooKhiaw	-----	113
10	LawdGwian	-----	106
	reference	STSAVAAPALMRHKSRSASLSLPRSVKLLGVSGMDAAP TMTMTAETMSAPSESGSGGET	236
1	KhaoJampi	-----	76
2	NguangChahng	-----	86
3	TahKhui	-----	86
4	KhaoGawDiaw	-----	76
5	HawmSurin	-----	86
6	JekChuey	-----	113
7	LaiMaejo	-----	106
8	NiawKhiawNgoo	-----	106
9	NiawDamHawmPooKhiaw	-----	113
10	LawdGwian	-----	106
	reference	TTTTLLGFGVG DGSQRRRCSA*	257
1	KhaoJampi	-----	76
2	NguangChahng	-----	86
3	TahKhui	-----	86
4	KhaoGawDiaw	-----	76
5	HawmSurin	-----	86
6	JekChuey	-----	113
7	LaiMaejo	-----	106
8	NiawKhiawNgoo	-----	106
9	NiawDamHawmPooKhiaw	-----	113
10	LawdGwian	-----	106

Figure S2. Sequence alignment of LOC_Os01g65810 in 10 rice cultivars with 5 high AAC (row 1-5) and 5 low ACC (row 6-10); *Nipponbare* rice was used as a reference genome sequence.

	reference	MSALTTSQLATSATGFGIADRSAPSSLLRHGFQGLKPRSPAGGDATSLSVTTTSARATPKQ	60
1	KhaoJampi	MSALTTSQLATSATGFGIADRSAPSSLLRHGFQGLKPRSPAGGDATSLSVTTTSARATPKQ	60
2	NguangChahng	MSALTTSQLATSATGFGIADRSAPSSLLRHGFQGLKPRSPAGGDATSLSVTTTSARATPKQ	60
3	TahKhui	MSALTTSQLATSATGFGIADRSAPSSLLRHGFQGLKPRSPAGGDATSLSVTTTSARATPKQ	60
4	KhaoGawDiaw	MSALTTSQLATSATGFGIADRSAPSSLLRHGFQGLKPRSPAGGDATSLSVTTTSARATPKQ	60
5	HawmSurin	MSALTTSQLATSATGFGIADRSAPSSLLRHGFQGLKPRSPAGGDATSLSVTTTSARATPKQ	60
6	JekChuey	MSALTTSQLATSATGFGIADRSAPSSLLRHGFQGLKPTGSRASSPAAPPAATRRRSA*--	57
7	LaiMaejo	MSALTTSQLATSATGFGIADRSAPSSLLRHGFQGLKPTGSRASSPAAPPAATRRRSA*--	57
8	NiawKhiawNgoo	MSALTTSQLATSATGFGIADRSAPSSLLRHGFQGLKPTGSRASSPAAPPAATRRRSA*--	57
9	NiawDamHawmPooKhiaw	MSALTTSQLATSATGFGIADRSAPSSLLRHGFQGLKPTGSRASSPAAPPAATRRRSA*--	57
10	LawdGwian	MSALTTSQLATSATGFGIADRSAPSSLLRHGFQGLKPTGSRASSPAAPPAATRRRSA*--	57

	reference	QRSVQSGSRRFSPVVVYATGAGMNVVFGAEMAPWSKTGGLGDVLGGLPPAMAANGHRVM	120
1	KhaoJampi	QRSVQSGSRRFSPVVVYATGAGMNVVFGAEMAPWSKTGGLGDVLGGLPPAMAANGHRVM	120
2	NguangChahng	QRSVQSGSRRFSPVVVYATGAGMNVVFGAEMAPWSKTGGLGDVLGGLPPAMAANGHRVM	120
3	TahKhui	QRSVQSGSRRFSPVVVYATGAGMNVVFGAEMAPWSKTGGLGDVLGGLPPAMAANGHRVM	120
4	KhaoGawDiaw	QRSVQSGSRRFSPVVVYATGAGMNVVFGAEMAPWSKTGGLGDVLGGLPPAMAANGHRVM	120
5	HawmSurin	QRSVQSGSRRFSPVVVYATGAGMNVVFGAEMAPWSKTGGLGDVLGGLPPAMAANGHRVM	120
6	JekChuey	-----	57
7	LaiMaejo	-----	57
8	NiawKhiawNgoo	-----	57
9	NiawDamHawmPooKhiaw	-----	57
10	LawdGwian	-----	57

	reference	VISPRYDQYKDAWDTSVVAEIKVADRYERVRFFHCYKRGVDRVFDHPSFLEKVVWGKTGE	180
1	KhaoJampi	VISPRYDQYKDAWDTSVVAEIKVADRYERVRFFHCYKRGVDRVFDHPSFLEKVVWGKTGE	180
2	NguangChahng	VISPRYDQYKDAWDTSVVAEIKVADRYERVRFFHCYKRGVDRVFDHPSFLEKVVWGKTGE	180
3	TahKhui	VISPRYDQYKDAWDTSVVAEIKVADRYERVRFFHCYKRGVDRVFDHPSFLEKVVWGKTGE	180
4	KhaoGawDiaw	VISPRYDQYKDAWDTSVVAEIKVADRYERVRFFHCYKRGVDRVFDHPSFLEKVVWGKTGE	180
5	HawmSurin	VISPRYDQYKDAWDTSVVAEIKVADRYERVRFFHCYKRGVDRVFDHPSFLEKVVWGKTGE	180
6	JekChuey	-----	57
7	LaiMaejo	-----	57
8	NiawKhiawNgoo	-----	57
9	NiawDamHawmPooKhiaw	-----	57
10	LawdGwian	-----	57

	reference	KIYGPDVGVDYKDNQMRFSLLCQAALAPRILNLNNNPYFKGTYGEDVVFVNCNDWHTGPL	240
1	KhaoJampi	KIYGPDVGVDYKDNQMRFSLLCQAALAPRILNLNNNPYFKGTYGEDVVFVNCNDWHTGPL	240
2	NguangChahng	KIYGPDVGVDYKDNQMRFSLLCQAALAPRILNLNNNPYFKGTYGEDVVFVNCNDWHTGPL	240
3	TahKhui	KIYGPDVGVDYKDNQMRFSLLCQAALAPRILNLNNNPYFKGTYGEDVVFVNCNDWHTGPL	240
4	KhaoGawDiaw	KIYGPDVGVDYKDNQMRFSLLCQAALAPRILNLNNNPYFKGTYGEDVVFVNCNDWHTGPL	240
5	HawmSurin	KIYGPDVGVDYKDNQMRFSLLCQAALAPRILNLNNNPYFKGTYGEDVVFVNCNDWHTGPL	240
6	JekChuey	-----	57
7	LaiMaejo	-----	57
8	NiawKhiawNgoo	-----	57
9	NiawDamHawmPooKhiaw	-----	57
10	LawdGwian	-----	57

	reference	ASYLKNNYQPNGIYRNAKVAFCIHNNISYQGRFAFEDYPELNLSEFRSSSDFIDGYDTPV	300
1	KhaoJampi	ASYLKNNYQPNGIYRNAKVAFCIHNNISYQGRFAFEDYPELNLSEFRSSSDFIDGYDTPV	300
2	NguangChahng	ASYLKNNYQPNGIYRNAKVAFCIHNNISYQGRFAFEDYPELNLSEFRSSSDFIDGYDTPV	300
3	TahKhui	ASYLKNNYQPNGIYRNAKVAFCIHNNISYQGRFAFEDYPELNLSEFRSSSDFIDGYDTPV	300
4	KhaoGawDiaw	ASYLKNNYQPNGIYRNAKVAFCIHNNISYQGRFAFEDYPELNLSEFRSSSDFIDGYDTPV	300
5	HawmSurin	ASYLKNNYQPNGIYRNAKVAFCIHNNISYQGRFAFEDYPELNLSEFRSSSDFIDGYDTPV	300
6	JekChuey	-----	57
7	LaiMaejo	-----	57
8	NiawKhiawNgoo	-----	57
9	NiawDamHawmPooKhiaw	-----	57
10	LawdGwian	-----	57

	reference	EGRKINWMKAGILEADRVLTVPYYAEELISGIARGCELDNIMRLTGITGIVNGMDVSEW	360
1	KhaoJampi	EGRKINWMKAGILEADRVLTVPYYAEELISGIARGCELDNIMRLTGITGIVNGMDVSEW	360
2	NguangChahng	EGRKINWMKAGILEADRVLTVPYYAEELISGIARGCELDNIMRLTGITGIVNGMDVSEW	360
3	TahKhui	EGRKINWMKAGILEADRVLTVPYYAEELISGIARGCELDNIMRLTGITGIVNGMDVSEW	360
4	KhaoGawDiaw	EGRKINWMKAGILEADRVLTVPYYAEELISGIARGCELDNIMRLTGITGIVNGMDVSEW	360
5	HawmSurin	EGRKINWMKAGILEADRVLTVPYYAEELISGIARGCELDNIMRLTGITGIVNGMDVSEW	360
6	JekChuey	-----	57
7	LaiMaejo	-----	57
8	NiawKhiawNgoo	-----	57
9	NiawDamHawmPooKhiaw	-----	57
10	LawdGwian	-----	57

reference	DPSKDKYITAKYDATTAEAKALNKEALQAEAGLPVDRKIPLIAFIGRLEEQKGPDMVMAA	420
1 KhaoJampi	DPSKDKYITAKYDATTAEAKALNKEALQAEAGLPVDRKIPLIAFIGRLEEQKGSVMMAA	420
2 NguangChahng	DPSKDKYITAKYDATTAEAKALNKEALQAEAGLPVDRKIPLIAFIGRLEEQKGSVMMAA	420
3 TahKhui	DPSKDKYITAKYDATTAEAKALNKEALQAEAGLPVDRKIPLIAFIGRLEEQKGSVMMAA	420
4 KhaoGawDiaw	DPSKDKYITAKYDATTAEAKALNKEALQAEAGLPVDRKIPLIAFIGRLEEQKGSVMMAA	420
5 HawmSurin	DPSKDKYITAKYDATTAEAKALNKEALQAEAGLPVDRKIPLIAFIGRLEEQKGSVMMAA	420
6 JekChuey	-----	57
7 LaiMaejo	-----	57
8 NiawKhiawNgoo	-----	57
9 NiawDamHawmPooKhiaw	-----	57
10 LawdGwian	-----	57
reference	AIPELMQEDVQIVLLGTGKKKFEKLLKSMEEEKYPGKVRVVKFNAPLAHLIMAGADVLAV	480
1 KhaoJampi	AIPELMQEDVQIVLLGTGKKKFEKLLKSMEEEKYPGKVRVVKFNAPLAHLIMAGADVLAV	480
2 NguangChahng	AIPELMQEDVQIVLLGTGKKKFEKLLKSMEEEKYPGKVRVVKFNAPLAHLIMAGADVLAV	480
3 TahKhui	AIPELMQEDVQIVLLGTGKKKFEKLLKSMEEEKYPGKVRVVKFNAPLAHLIMAGADVLAV	480
4 KhaoGawDiaw	AIPELMQEDVQIVLLGTGKKKFEKLLKSMEEEKYPGKVRVVKFNAPLAHLIMAGADVLAV	480
5 HawmSurin	AIPELMQEDVQIVLLGTGKKKFEKLLKSMEEEKYPGKVRVVKFNAPLAHLIMAGADVLAV	480
6 JekChuey	-----	57
7 LaiMaejo	-----	57
8 NiawKhiawNgoo	-----	57
9 NiawDamHawmPooKhiaw	-----	57
10 LawdGwian	-----	57
reference	PSRFEPGLIQLQGMRYGTPCACASTGGLVDTVIEGKTGFHMGRLSVDCCKVVEPSDVKKV	540
1 KhaoJampi	PSRFEPGLIQLQGMRYGTPCACASTGGLVDTVIEGKTGFHMGRLSVDCCKVVEPSDVKKV	540
2 NguangChahng	PSRFEPGLIQLQGMRYGTPCACASTGGLVDTVIEGKTGFHMGRLSVDCCKVVEPSDVKKV	540
3 TahKhui	PSRFEPGLIQLQGMRYGTPCACASTGGLVDTVIEGKTGFHMGRLSVDCCKVVEPSDVKKV	540
4 KhaoGawDiaw	PSRFEPGLIQLQGMRYGTPCACASTGGLVDTVIEGKTGFHMGRLSVDCCKVVEPSDVKKV	540
5 HawmSurin	PSRFEPGLIQLQGMRYGTPCACASTGGLVDTVIEGKTGFHMGRLSVDCCKVVEPSDVKKV	540
6 JekChuey	-----	57
7 LaiMaejo	-----	57
8 NiawKhiawNgoo	-----	57
9 NiawDamHawmPooKhiaw	-----	57
10 LawdGwian	-----	57
reference	AATLKRAIKVVGTPAYEEMVRNCMNQDLQSWKGPKNWENVLLGLGVAGSAPGIEGDEIAP	600
1 KhaoJampi	AATLKRAIKVVGTPAYEEMVRNCMNQDLQSWKGPKNWENVLLGLGVAGSAPGIEGDEIAP	600
2 NguangChahng	AATLKRAIKVVGTPAYEEMVRNCMNQDLQSWKGPKNWENVLLGLGVAGSAPGIEGDEIAP	600
3 TahKhui	AATLKRAIKVVGTPAYEEMVRNCMNQDLQSWKGPKNWENVLLGLGVAGSAPGIEGDEIAP	600
4 KhaoGawDiaw	AATLKRAIKVVGTPAYEEMVRNCMNQDLQSWKGPKNWENVLLGLGVAGSAPGIEGDEIAP	600
5 HawmSurin	AATLKRAIKVVGTPAYEEMVRNCMNQDLQSWKGPKNWENVLLGLGVAGSAPGIEGDEIAP	600
6 JekChuey	-----	57
7 LaiMaejo	-----	57
8 NiawKhiawNgoo	-----	57
9 NiawDamHawmPooKhiaw	-----	57
10 LawdGwian	-----	57
reference	LAKENVAAP*	609
1 KhaoJampi	LAKENVAAP*	609
2 NguangChahng	LAKENVAAP*	609
3 TahKhui	LAKENVAAP*	609
4 KhaoGawDiaw	LAKENVAAP*	609
5 HawmSurin	LAKENVAAP*	609
6 JekChuey	-----	57
7 LaiMaejo	-----	57
8 NiawKhiawNgoo	-----	57
9 NiawDamHawmPooKhiaw	-----	57
10 LawdGwian	-----	57

Figure S3 Sequence alignment of LOC_Os06g04200 in 10 rice cultivars with high AAC (row 1-5) and low ACC (row 6-10); *Nipponbare* rice was used as a reference genome sequence.