

Further fine mapping and candidate gene prediction for a new restoring fertility gene *Rf(fa)* in rice

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Electronic Supplementary Material (ESM)

The authors are fully responsible for both the content and the formal aspects of the electronic supplementary material. No editorial adjustments were made.

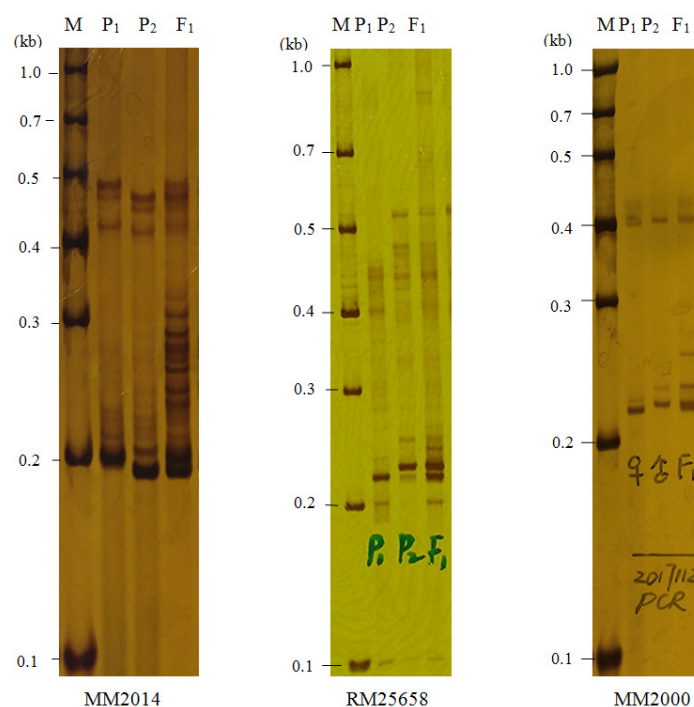


Figure S1. Polymorphism SSR markers between the two parents

M – DL1000 DNA marker; P₁ – Jinnong 1A (♀); P₂ – 9311-9 (♂); F₁ – F₁ of Jinnong 1A × 9311-9

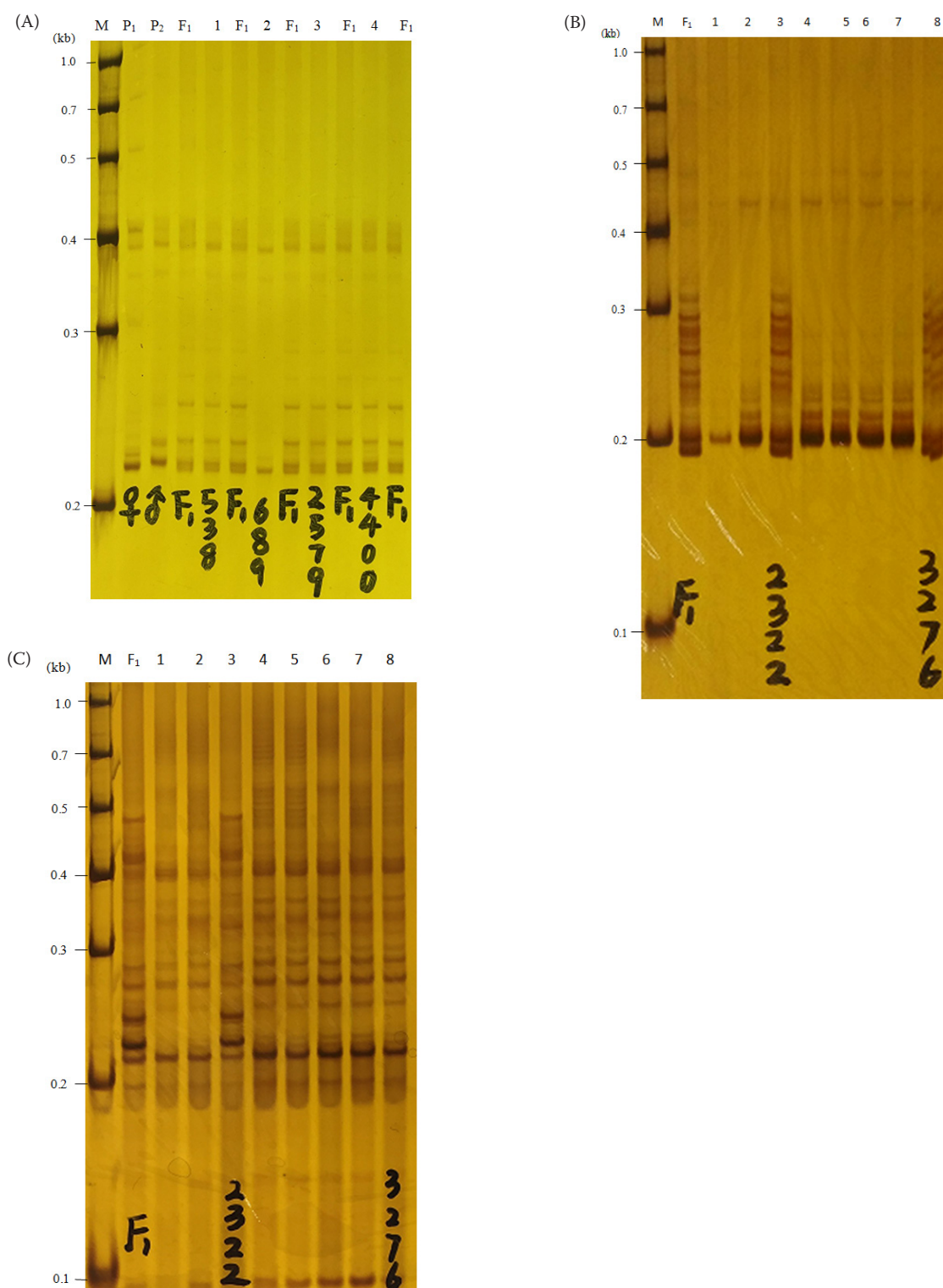


Figure S2. Plants displaying crossing-over bands at MM2000 (A), MM2014 (B) and RM25658 (C)

A: M – DL1000 DNA marker; P₁ – Jinnong 1A (♀); P₂ – 9311-9 (♂); 1, 3, 4 – recombinants (plant numbers: 538, 2579, 4400); 2 – non-crossing over plant; F₁ – F₁ of Jinnong 1A × 9311-9

B: M – DL1000 DNA marker; F₁ – F₁ of Jinnong 1A × 9311-9; 1, 2, 4~7 – non-crossing-over plants; 3, 8 – crossing over plants

C: M – DL1000 DNA marker; F₁ – F₁ of Jinnong 1A × 9311-9; 1~2, 4~8 – non-crossing over plants, 3 – crossing-over plant

<https://doi.org/10.17221/49/2022-CJGPB>

Table S1. Results of the protein sequence alignment of the predicted genes

For gene 1

protochlorophyllide reductase B, chloroplastic [Oryza sativa Japonica Group]

Sequence ID: [XP_015614945.1](#) Length: 402 Number of Matches: 1

[See 5 more title\(s\)](#) [See all Identical Proteins\(IPG\)](#)

Range 1: 1 to 244 [GenPept](#) [Graphics](#)

[▼ Next Match](#) [▲ Previous](#)

Score	Expect	Method	Identities	Positives	Gaps
421 bits(1083)	2e-148	Compositional matrix adjust.	231/244(95%)	232/244(95%)	5/244(2%)
Query 1	MALQAATTTSFPLSALSARKEGAVKDSAFGLGVRLGDGLKLETSALGLRTKRVSTSSVAIR				60
Sbjct 1	MALQAATTTSFPLSALSARKEGAVKDSAFGLGVRLGDGLKLETSALGLRTKRVSTSSVAIR				60
Query 61	AQasaavssptatpaspsGKQTLRKCTAVITGASSGLGLATAKALAETGRWHVVMGCRDF				120
Sbjct 61	AQASAAVSSPT TPASPSGKQTLRKCTAVITGASSGLGLATAKALAETGRWHVVMGCRDF				120
Query 121	LKASRAAKAAGMEKGSYTIHLDLASLDSVRQFVGNVRLGMPVDVVCNAAVYQPTAKQ				180
Sbjct 121	LKASRAAKAAGMEKGSYTIHLDLASLDSVRQFV NVRRL MPVDVVCNAAVYQPTAKQ				180
Query 181	PSFTADGFEMSVGVNHLGHFLLARELLADLTSSDYP SKRLIIVGSITGN-----GNLSPS				235
Sbjct 181	PSFTADGFEMSVGVNHLGHFLLARELLADLTSSDYP SKRLIIVGSITGN GN+ P				240
Query 236	PELG	239			
	LG				
Sbjct 241	ANLG	244			

For gene 2

protochlorophyllide reductase B, chloroplastic [Oryza sativa Japonica Group]

Sequence ID: [XP_015614945.1](#) Length: 402 Number of Matches: 1

[See 5 more title\(s\)](#) [See all Identical Proteins\(IPG\)](#)

Range 1: 228 to 402 [GenPept](#) [Graphics](#)

[▼ Next Match](#) [▲ Previous](#)

Score	Expect	Method	Identities	Positives	Gaps
375 bits(963)	6e-131	Compositional matrix adjust.	175/175(100%)	175/175(100%)	0/175(0%)
Query 4	GNTNTLAGNVPPKANLGDRLGLASGLDGVSSAMIDGGEFDGAKAYKDSKVCNMLTMQEF				63
Sbjct 228	GNTNTLAGNVPPKANLGDRLGLASGLDGVSSAMIDGGEFDGAKAYKDSKVCNMLTMQEF				287
Query 64	HRRYHGETGVTFASLYPGCIATTGLFREHVPLFRLLFPPFQKYITKGYVSEEEAGKRLAQ				123
Sbjct 288	HRRYHGETGVTFASLYPGCIATTGLFREHVPLFRLLFPPFQKYITKGYVSEEEAGKRLAQ				347
Query 124	VVSDPSLTKSGVYWSWNNNSASFENQLSEBASDPEKAKKVWELSEKLVGLADHDQ				178
Sbjct 348	VVSDPSLTKSGVYWSWNNNSASFENQLSEBASDPEKAKKVWELSEKLVGLADHDQ				402

Table S1 to be continued.

For gene 3

uncharacterized protein LOC4349005 isoform X2 [Oryza sativa Japonica Group]Sequence ID: [XP_015614617.1](#) Length: 887 Number of Matches: 1[See 4 more title\(s\)](#) [See all Identical Proteins\(IPG\)](#)Range 1: 1 to 864 [GenPept](#) [Graphics](#)[▼ Next Match](#) [▲ Previous](#)

Score	Expect	Method	Identities	Positives	Gaps
1236 bits(3198)	0.0	Compositional matrix adjust.	792/864(92%)	793/864(91%)	67/864(7%)
Query 144	MIVRTYgrrrsfsdgggggrrggggfssssQDAFEFdggeeddvlvllgssssqsshppaps				203
Sbjct 1	MIVRTYGRRRSFSDGGGGERGGGGFSSSQDAFEFDGEEEDDLVLLGSSSSQSSHPPAPS				60
Query 204	qesssMWFDEDPFPPSPrrrrrgrggggDYAEPataaaaaaaaaatSLMEABEYEGEMMESVDE				263
Sbjct 61	QESSSMWFDEDPFPPRRRRRGRGGG DYAE PATAAAAAAATSLMEABEYEGEMMESVDE				120
Query 264	ANFALDGLRATAPRRVRRASFLALLGICASAPRRRVLRAGC-----				304
Sbjct 121	ANFALDGLRATAPRRVRRASFLALLGICASAPRRRVLRAGLVQIIDAAILVLNIDPPC				180
Query 305	-----SVQENHLLDSESCVHF11k11nppvnlvDSKAPSIGSKLLGISKVQM				351
Sbjct 181	TIGAAALLFVLASDVQENHLLDSESCVHFLLKLLNPPVNLVDSKAPSIGSKLLGISKVQM				240
Query 352	LNGSNKSDCISEEILSKVEEILLSCQBIKSLDKDDKKTTRPELCPKWALLTMEKACLS				411
Sbjct 241	LNGSNKSDCISEEILSKVEEILLSCQBIKSLDKDDKKTTRPELCPKWALLTMEKACLS				300
Query 412	AVSVEETSDTVSRVGGNFKETLRELGLDLSIFDVMMDCHSTLENLIKDTSTSDLDLNEG				471
Sbjct 301	AVSVEETSDTVSRVGGNFKETLRELGLDLSIFDVMMDCHSTLENLIKDTSTSDLDLNEG				360
Query 472	SLQSAALLLCKLKILENATFLSDDNKTHLLNMSRKLYPKRSSLSFVGVIISIIELLSALS				531
Sbjct 361	SLQSAALLLCKLKILENATFLSDDNKTHLLNMSRKLYPKRSSLSFVGVIISIIELLSALS				420
Query 532	ilQNSsvssstypksskvsQQSCS-----				556
Sbjct 421	ILQNSSVSSSTYPKSSKVSQQSCSDVMGGTSFNDGKRKNSKKKNLLSNQTRHSCLSKS				480
Query 557	EVSHITISSGSDAGLSQKAFNCspssissngassgslGERHSNGGALKNIKKDRGNANPI				616
Sbjct 481	EVSHITISSGSDAGLSQKAFNCSPSISNGASSGSLGERHSNGGALKNIKKDRGNANPI				540
Query 617	RGSSGWISIRAHSSDGNREMAKRRRLSENVITDSGGGDDPFAFDVDVQEPSNWELLGPK				676
Sbjct 541	RGSSGWISIRAHSSDGNREMAKRRRLSENVITDSGGGDDPFAFDVDVQEPSNWELLGPK				600
Query 677	KKSPQKHQDKSGNGVLVASHEPDQPEDLNQSGTTSLSFAKDESSLEDCLLASVKVLMNL				736
Sbjct 601	KKSPQKHQDKSGNGVLVASHEPDQPEDLNQSGTTSLSFAKDESSLEDCLLASVKVLMNL				660
Query 737	ANDNPSGCEL IASCGGLNTMASLIMKHFPSPCFVVDNNYNTRDVNLDELSSSQNSKAHQ				796
Sbjct 661	ANDNPSGCEL IASCGGLNTMASLIMKHFPSPCFVVDNNYNTRDVNLDELSSSQNSKAHQ				720
Query 797	VKIKQLRDHELDLVAIILGLLVNVEKDSLNRVRLSSARVPVDLSQNPQSEETQRDVIAL				856
Sbjct 721	VKIKQLRDHELDLVAIILGLLVNVEKDSLNRVRLSSARVPVDLSQNPQSEETQRDVIAL				780
Query 857	LCSVFLASQGASEASGTISPDEESLMQGAREAEEMMIVEAYAALLLAFLSTESMKVRGAI				916
Sbjct 781	LCSVFLASQGASEASGTISPDEESLMQGAREAEEMMIVEAYAALLLAFLSTESMKVRGAI				840
Query 917	SSCLPNNSLKILVPALEKFTSRL 940				
Sbjct 841	SSCLPNNSLKILVPALEKFTSRL 864				

<https://doi.org/10.17221/49/2022-CJGPB>

Table S1 to be continued.

For gene 4

XS domain containing protein-like [Oryza sativa Japonica Group]

Sequence ID: [BAD26426.1](#) Length: 123 Number of Matches: 1

[See 1 more title\(s\)](#) [See all Identical Proteins\(IPG\)](#)

Range 1: 40 to 123 [GenPept](#) [Graphics](#)

[Next Match](#) [▲](#)

Score	Expect	Method	Identities	Positives	Gaps
153 bits(386)	3e-49	Compositional matrix adjust.	77/84(92%)	78/84(92%)	0/84(0%)
Query 1	MTSVRLVTNCSFLSTTRQFSNLHVGPSSHNILPVMVRMKPGIYLTRTNVPSLGGNTLAPA				60
	+T VRLVTN SFLSTT Q SNLHVGPSSHNILPVMVRMKPGIYL RTNVPSLGGNTLAPA				
Sbjct 40	VTGVRVTNRSFLSTTCQLSNLHVGPSSHNILPVMVRMKPGIYLIRTNVPSLGGNTLAPA				99
Query 61	GDERLEALVLTGWGEACVRSPVAT				84
	GDERLEALVLTGWGEACVR PVAT				
Sbjct 100	GDERLEALVLTGWGEACVRPPVAT				123

For gene 5

retrotransposon protein, putative, unclassified [Oryza sativa Japonica Group]

Sequence ID: [AAX96828.1](#) Length: 1014 Number of Matches: 3

Range 1: 1 to 309 [GenPept](#) [Graphics](#)

[Next Match](#) [▲](#) [Pre](#)

Score	Expect	Method	Identities	Positives	Gaps
461 bits(1187)	4e-146	Compositional matrix adjust.	254/320(79%)	265/320(82%)	25/320(7%)
Query 1	MARGSALLDGSVLPPSRIVSERQAGLPRRFMPESATGREIVTLGEGRPAPDYPGRSVFFL				60
	MARGSALLDGSVLPPSRIVSERQAGL RRFMPESATGREIVTLGEGRPAPDYPGRSVFFL				
Sbjct 1	MARGSALLDGSVLPPSRIVSERQAGLSRRFMPESATGREIVTLGEGRPAPDYPGRSVFFL				60
Query 61	PFAMAGLVPPFSSFFMDVLEFYDLQMAHLTPNAVMTLAIFAHLCEMFIVGRP-----F				113
	PFAMAGLVPPFSSFFMDVLEFYDLQMAHLTPNAVMTLAIFAHLCEMFIVGRP F				
Sbjct 61	PFAMAGLVPPFSSFFMDVLEFYDLQMAHLTPNAVMTLAIFAHLCEMFIVGRPSLRLFRWF				120
Query 114	FGCSGATGAGAEPLHPLRPQEVG---RLEER---LVLHPP---RRRSAPPTSEpapgaglg				166
	F + + PP VG + R L + P R++APPTSE P				
Sbjct 121	F-----TVQSVSPSVVGGCYFQPRGPVLNRYIPCALRKNAPPTSEQPPAQASS				169
Query 167	lagagRSGDGYDAVLDRLAGLRSQGLTGAMVYGDYlrrriaplqrrarGAWeyTGSedYM				226
	GDGYDAVLDRLAGLRSQGLTGAMVYGDYLRRIAPLQRRARGAWeyTGSed+				
Sbjct 170	WRAPVDLDGDGYDAVLDRLAGLRSQGLTGAMVYGDYLRRIAPLQRRARGAWeyTGSedFT				229
Query 227	RTHQGVWRWDAPEDFKIVVQVRLNLSMEASLIPQGILPLCSDPDRASILTIMAVGASE				286
	RTHQGVWRWDAPEDFKI+VQVRLNLS+EA+LIPQGILPLCSDPDRASILTIM AVGASE				
Sbjct 230	RTHQGVWRWDAPEDFKILVQVRLNLSVEAALIPQGILPLCSDPDRASILTIMAVGASE				289
Query 287	ERAPKGHDGAGGSRRGDQST				306
	ERAPKGHDGAGGSRRG+QST				
Sbjct 290	ERAPKGHDGAGGSRRGEQST				309

Table S1 to be continued.

For gene 6

retrotransposon protein, putative, unclassified [Oryza sativa Japonica Group]Sequence ID: [ABB47352.2](#) Length: 1772 Number of Matches: 2Range 1: 329 to 1664 [GenPept](#) [Graphics](#)[▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps
1766 bits(4574)	0.0	Compositional matrix adjust.	1014/1399(72%)	1061/1399(75%)	187/1399(13%)
Query 775	GDD-----RRFCQIRNTIPCI	PAHAVIYAFRGGVRRHNRMLEKIASKEPQT	TAEFLQLA	827	
Sbjct 329	GDD +RFCQ+RNTIPCI	PAHAVIYAFRGGVRRHNRMLEKIASKEPQT	TAEFLQLA	388	
Query 828	DRVARKEEAWTWNppvpvwl	rppdpplrqgzevteggrrgqSIP	TRVMSPPSRALRGP	887	
Sbjct 389	DRVARKEEAWTWN P R	DRVARKEEAWTWNSSGVAAPAGSAARS-----	ERRRRRKKRAHRGP	434	
Query 888	PKRGGLRATKRKRPPALPAGSAQ	PASGARPPHLPRLRGLSRQKFCRANeev	ggrrqer	947	
Sbjct 435	P+RGGLRATKR+RPALPAGSA+PASG	P + + + RRQER	PERGGLRATKRKRPPALPAGSARPASGVPCITPPSTTSRTAVVKS	LAERTKKEEERRQER	494
Query 948	regrSPAVPSG-----	FQEPGATATVDGGACAHVSRRSFKA	984		
Sbjct 495	REG++PA P+G	FQEPGAT+ATVDGGACAH SR S KA	REGKAPAAPAGNRRGEAKQKATAEDVDDGDDDLGFQEPGATVATVDGGACAHASRWSLKA	554	
Query 985	MKRELLAAAPTHEATRARRWSEVAL	TFDQTDHPPCVARGGQIAMVVSPTVCNVKLG	RVL I	1044	
Sbjct 555	MKRELLAAAPTH+ATRRARWSEVAL	TFDQTDHPPCVARGGQIAM+VSPTVCNVKLG	RVL	614	
Query 1045	DGGAALNILSPAADFDAIKAPGMVLRPSQPIIGVTP	PGHTWP-----	1084		
Sbjct 615	DGGAALNILSPAADFDAIKAPGMVLRPSQPIIGVTP	PGHTWPLGHIDLPTVFGGPANFRTER	674		
Query 1085	LDEDA-----	GPGGPISVHGDLKVALACLEQR	1111		
Sbjct 675	VDFDVADLSLPYNAVLGRPTLVKFMVAVHYAYLQ	MKMPGPGGPITVHGDLKVALACMEQR	734		
Query 1112	ADHLAAASKPEDGDERLGASAPATPRQRMITCDEV	VPKEDALVSFLRANADVFAWRPAD	1171		
Sbjct 735	ADHLAAASKP DERL S PA PRQRM+TCDEV	EDALVSFLRANADVFAWRPAD	791		
Query 1172	MPGVPREVIEHRLAVRPGARPVRRQAPERQAFIRER	WRDFWRPDSSVRSIRSGWR	1231		
Sbjct 792	MPGVPREVIEHRLAVRPGARPVRRHQLGRNVEAYV	DDL VVKTRNQTLLSDLAETFEELRS	851		
Query 1232	TRWSFPRRTASFG--SSRVLGLCP---	GIEANPEKIRAIERMPPSKLRDVQCVTGCM	1286		
Sbjct 852	TR FG + ++LG	GIEANPEKIRAIERMPPSKLRDVQCVTGCM	911		
Query 1287	LSRFISRLGEKALPLFKLLKRSQPTTWTEEAENAL	TQLKAYLSSPPVLVAPEPDEPLLLY	1346		
Sbjct 912	LSRFISRLGEKAL LFKLLKRSQPTTWTEEA A	TQLKAYLSSPPVLVAPEPDEPLLLY	971		
Query 1347	LAATPQVVSAAALVVERDEDNSHFALPHVPVTP	PGREGgeapepnggprpdtgvgplpA	1406		
Sbjct 972	LAATPQVVSAAALVVER+EDN H A PHPV T	PGREGGGEAPEPNGGPRPPT G GP PA	1031		
Query 1407	CQTVLGAPDPKRALRPLSPDPQDGPKATVGRPPL	SSDPEVISTEDKCAPRGCLDEECPR	1466		
Sbjct 1032	C V GAPDP	DGP AT GRP L SDPEV+ TE +CAPRG DEE P	1080		
Query 1467	DAAPSEEDRPHRKVRQRPVYFVSEALRDAKTRYP	QAQKMLYAILMASRKLRYHQAHRVTV	1526		
Sbjct 1081	DAAP BEDRP RKVQRPVYF+S+ALRDAKTRYP	QAQKMLYAILMASRKLRYHQAHRVTV	1140		
Query 1527	VTSYPLGQILHNREGTGRVVKWAIELSEFDLHFE	PRHAIKSQALADFVAEWTPAPEPVSI	1586		
Sbjct 1141	VTSYPLGQILHNREGTGRVVKWAIELSEFDLHFE	PRHAIKSQALADFVAEWTPAPEPVSV	1200		

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Table S1 to be continued.

For gene 6

Query	1587	PEASTDPSQLPHTAHVWMQFDGSLSLQGAGAGVTLTSPSGDVLRYLVRLDFRATNNMAEY	1646
Sbjct	1201	PEAS+ PSQLPHTA+VWMQFDGSLSLQGAGAGVTLTSPSGDVLRYLVRLDFRATNNMAEY	1260
Query	1647	Egllaglrvaaglgirrl1VLGDSQLVVNQVCKEYRCSDPQMDAYVRQVRRMERHFDGIE	1706
Sbjct	1261	EGLLAGLRVAAGLGIRRL1VLGDSQLVVN-----QMDAYVRQVRRMERHFDGIE	1309
Query	1707	LRHVPRRDNMIADSLRLASTRAQTTPGAFEEERLAQPSARPDPPLGETda-----	1755
Sbjct	1310	LRHVPRRDN+ADELSRLAS+RAQTTPGAFEEERL QPSARP+PLGETDA	1369
Query	1756	-----pdrpprpdREGSERVHRISKRYVLVEGTLYRRAAN	1790
Sbjct	1370	D+ DREGSERV RISKRYVLVEGTLYRRAA+	1429
Query	1791	GILLKICIPREQGVLLADIHEGECGAHSASRTLVGKAFRQGFYWPTALNDAVDLVRRCRA	1850
Sbjct	1430	G+LLKICIPREQGV LLADIHEGECGAHSASRTLVGKAFRQGFYWPTALNDAVDL RRCRA	1489
Query	1851	CQFHAKQIQPAQALQTIPLSWPFAVWGLDILGPFRRAPGGFEYLYVAIDKFTKWPEAYP	1910
Sbjct	1490	CQFHA+Q HQPAQALQ IPLSWPFAVWGLDILGPFRRAPGGFEYLYVA+DKFTKWPEAYP	1549
Query	1911	VVKIDKHSALKFIKGITARFGVFNRIITDNGTQFTSELFGDYCEDMGIKLCFASPAHPRS	1970
Sbjct	1550	V+KIDKHSALKFI+GITARFGVFNRIITDNGTQFT +	1587
Query	1971	NGQVERANSEILKGLKTKTFNILKKHGDSEWIEELPAVLWANRTTPSRATGETPPFLVYGA	2030
Sbjct	1588	AN EILKGLKTKTFNILKKHGDSEWIEELPAVLWANRTTPSRATGETPPFLVYGA	1645
Query	2031	EAVLPSELTLRSPRATMYC	2049
Sbjct	1646	EAVLPSELTLRSPRATMYC	1664

Table S1 to be continued.

For gene 7

protein Rf1, mitochondrial isoform X1 [Oryza sativa Japonica Group]Sequence ID: [XP_015614273.1](#) Length: 620 Number of Matches: 8Range 1: 35 to 378 [GenPept](#) [Graphics](#)▼ [Next Match](#)

Score	Expect	Method	Identities	Positives	Gaps
648 bits(1671)	0.0	Compositional matrix adjust.	315/345(91%)	324/345(93%)	5/34
Query 94	AEDARHVFDLLRRGRGASIVGLNCALADVARHSPAAAVSRYNRMARAGADEVTPNLCTY				153
Sbjct 35	AEDARHVFDLLRRGRGASIVGLNCALADVARHSPAAAVSRYNRMARAGADEVTPNLCTY				94
Query 154	GILIGSCCCAGRLDLGFAALGNVIKKGFRVDAIAFTPLLKGLCADKRTSDAMDIVLRMT				213
Sbjct 95	GILIGSCCCAGRLDLGFAALGNVIKKGFRVDAIAFTPLLKGLCADKRTSDAMDIVLRMT				154
Query 214	QLGCIPNVFSYNILLKGLCDENRSQEALELLHMMADDRGGGSPPDVVSYYTTVIDGFFKEG				273
Sbjct 155	QLGCIPNVFSYNILLKGLCDENRSQEALELLMMDDGGPPDVVSYYTTVI+GFFKEG				213
Query 274	DLDKAYGTYHEMLDRGILPNVVITYSSIIAALCKAQAMDKAMEVLTSMVKNGVMPNCRITY				333
Sbjct 214	DLDKAYGTYHEMLDRGILPNVVITYSSIIAALCKAQAMDKAMEVLTSMVKNGVMPNCRITY				273
Query 334	SIMHGYCSSGQPKAIGFLKKMRSDGVEPDVVITYNSLMDYLCKNGRCTEARKIFDSMTKR				393
Sbjct 274	SIVHGYCSSGQPKAIGFLKKMRSDGVEPDVVITYNSLMDYLCKNGRCTEARKMFDSMTKR				333
Query 394	GLKPEITTYGTLQGHCKEGRVIESEKLFDLMVQE----NHLLDS				434
Sbjct 334	GLKPEITTYGTLQGYATKGALVEMHGLLDLMVRNGIHPNHYVFS				378

PPR protein [Oryza sativa Indica Group]Sequence ID: [ABC42330.1](#) Length: 791 Number of Matches: 9[See 1 more title\(s\)](#) ▼ [See all Identical Proteins\(IPG\)](#)Range 1: 32 to 364 [GenPept](#) [Graphics](#)▼ [Next Match](#)

Score	Expect	Method	Identities	Positives	Gaps
627 bits(1616)	0.0	Compositional matrix adjust.	301/333(90%)	315/333(94%)	0/333
Query 95	EDARHVFDLLRRGRGASIVGLNCALADVARHSPAAAVSRYNRMARAGADEVTPNLCTY				154
Sbjct 32	EDARHVFDLLRRGRGASIVGLN ALADVAR SPAAAVSRYNRMARAGADEVTP+LCTY				91
Query 155	ILIGSCCCAGRLDLGFAALGNVIKKGFRVDAIAFTPLLKGLCADKRTSDAMDIVLRMTQ				214
Sbjct 92	ILIG CC AGRDLGFAALGNVIKKGFRVDAIAFTPLLKGLCADKRTSDAMDIVLRMT+				151
Query 215	LGCIPNVFSYNILLKGLCDENRSQEALELLHMMADDRGGGSPPDVVSYYTTVIDGFFKEGD				274
Sbjct 152	LGCIPNVFSYNILLKGLCDENRSQEALELLHMMADDRGGGSPPDVVSYYTTVI+GFFKEGD				211
Query 275	LDKAYGTYHEMLDRGILPNVVITYSSIIAALCKAQAMDKAMEVLTSMVKNGVMPNCRITYS				334
Sbjct 212	DKAY TYHEMLDRGILP+VVITY+SIIAALCKAQAMDKAMEVL+MVKNVMP+C TY S				271
Query 335	IMHGYCSSGQPKAIGFLKKMRSDGVEPDVVITYNSLMDYLCKNGRCTEARKIFDSMTKRG				394
Sbjct 272	I+HGYCSSGQPKAIGFLKKMRSDGVEPDVVITY+ LMDYLCKNGRC EARKIFDSMTKRG				331
Query 395	LKPEITTYGTLQGHCKEGRVIESEKLFDLMVQ				427
Sbjct 332	LKPEITTYGTLQGYATKGALVEMHGLLDLMVR				364

<https://doi.org/10.17221/49/2022-CJGPB>

Table S1 to be continued.

For gene 8

putative membrane-associated protein [Oryza sativa Japonica Group]

Sequence ID: [AAL58263.1](#) Length: 1219 Number of Matches: 1

Range 1: 1045 to 1168 [GenPept](#) [Graphics](#)

▼ [Next Match](#) ▲

Score	Expect	Method	Identities	Positives	Gaps
224 bits(570)	1e-66	Composition-based stats.	109/132(83%)	114/132(86%)	8/132(6%)
Query 31	VVMAGGDRGRGVECHPHRGVSAALLRPGPQALAAASWRRRETVVRSDFAAAGGVATMGDSPQ				90
Sbjct 1045	VVMAGGDRGRGVECHPH+GVSAALLRPGPQALAAASWRRRETVVRSDFAAAGGVATMGDSPQ				1104
Query 91	ALSDRLRGSVTKVWRGGAEWTAFAFARNGAAGPSQSRLPVTRNRYGVGQARIETECFFKI				150
Sbjct 1105	ALSDRL GS TKVWRGGAEWTAFAFARNGAAGPSQSRLPVTRNR Q I KI				1156
Query 151	VSGYTIRMVHRL 162				
Sbjct 1157	+ TI M+++L WATLTISMVYKL 1168				

Table S1 to be continued.

For gene 9

protein Rf1, mitochondrial [Oryza sativa Japonica Group]Sequence ID: [XP_015614275.1](#) Length: 401 Number of Matches: 4[See 2 more title\(s\)](#) [See all Identical Proteins\(IPG\)](#)Range 1: 38 to 401 [GenPept](#) [Graphics](#)[▼ Next Match](#) [▲ E](#)

Score	Expect	Method	Identities	Positives	Gaps
746 bits(1927)	0.0	Compositional matrix adjust.	363/371(98%)	363/371(97%)	7/371(1%)
Query 38	HVFDELLRRGIPDVF SYNILLNGLCDENRSQEALELLHIMADDGGDCPPDVVSYSTVING				97
Sbjct 38	HVFDELLRRGIPDVF SYNILLNGLCDENRSQEALELLHIMADDGGDCPPDVVSYSTVING				97
Query 98	FFKEGDLTKYSTYNEMLDQRISPNVVYNSIIAALCKAQTVDKAMEVLTMMVKSGVMPD				157
Sbjct 98	FFKEGDLTK-----MLDQRISPNVVYNSIIAALCKAQTVDKAMEVLTMMVKSGVMPD				150
Query 158	CMTYNSIVHGFCSGQPKAIVFLKKMRSDGVEPDVVYNSLMDYLCKNGRCTEARKIFD				217
Sbjct 151	CMTYNSIVHGFCSGQPKAIVFLKKMRSDGVEPDVVYNSLMDYLCKNGRCTEARKIFD				210
Query 218	SMTKRGLKPDITTYGTLTLLQGYATKGALVEMHGLLDLMVRNGIHPNHVVSILVCAYAKQE				277
Sbjct 211	SMTKRGLKPDITTYGTLTLLQGYATKGALVEMHGLLDLMVRNGIHPNHVVSILVCAYAKQE				270
Query 278	KVEEAMLVFSKMRQQGLNPNAVITYGTVIDVLCKSGRVEDAMLYFEQMIDEGLRPDSIVYN				337
Sbjct 271	KVEEAMLVFSKMRQQGLNPNAVITYGTVIDVLCKSGRVEDAMLYFEQMIDEGLRPDSIVYN				330
Query 338	SLIHSCLCFDKWEKAEELFLEMLDRGICLSTIFFNSIIDSHCKEGRVIESVKLFDLMVRI				397
Sbjct 331	SLIHSCLCFDKWEKAEELFLEMLDRGICLSTIFFNSIIDSHCKEGRVIESVKLFDLMVRI				390
Query 398	GVKPDIIITLGR 408				
Sbjct 391	GVKPDIIITLGR 401				

PPR protein [Oryza sativa Indica Group]Sequence ID: [BAD13709.1](#) Length: 332 Number of Matches: 3Range 1: 1 to 332 [GenPept](#) [Graphics](#)[▼ Next Match](#) [▲ Pre](#)

Score	Expect	Method	Identities	Positives	Gaps
689 bits(1778)	0.0	Compositional matrix adjust.	331/332(99%)	332/332(100%)	0/332(0%)
Query 77	MADDGGDCPPDVVSYSTVINGFFKEGDLTKYSTYNEMLDQRISPNVVYNSIIAALCKA				136
Sbjct 1	MADDGGDCPPDVVSYSTVINGFFKEGDLTKYSTYNEMLDQRISPNVVYNSIIAALCKA				60
Query 137	QTVDKAMEVLTMMVKSGVMPDCMTYNSIVHGFCSGQPKAIVFLKKMRSDGVEPDVVY				196
Sbjct 61	QTVDKAMEVLTMMVKSGVMPDCMTYNSIVHGFCSGQPKAIVFLKKMRSDGVEPDVVY				120
Query 197	NSLMDYLCKNGRCTEARKIFDSMTKRGLKPDITTYGTLTLLQGYATKGALVEMHGLLDLMVR				256
Sbjct 121	NSLMDYLCKNGRCTEARKIFDSMTKRGLKPDITTYGTLTLLQGYATKGALVEMHGLLDLMVR				180
Query 257	NGIHPNHVVSILVCAYAKQEKVEEAMLVFSKMRQQGLNPNAVITYGTVIDVLCKSGRVED				316
Sbjct 181	NGIHPNHVVSILVCAYAKQEKVEEAMLVFSKMRQQGLNPNAVITYGTVIDVLCKSGRVED				240
Query 317	AMLYFEQMIDEGLRPDSIVYNSLIHSCLCFDKWEKAEELFLEMLDRGICLSTIFFNSIID				376
Sbjct 241	AMLYFEQMIDEGLRPDSIVYNSLIHSCLCFDKWEKAEELFLEMLDRGICLSTIFFNSIID				300
Query 377	SHCKEGRVIESVKLFDLMVRIGVKPDIIITLGR 408				
Sbjct 301	SHCKEGRVIESVKLFDLMVRIGVKPDIIITLGR 332				

<https://doi.org/10.17221/49/2022-CJGPB>

Table S1 to be continued.

For gene 10

putative membrane-associated protein [Oryza sativa Japonica Group]

Sequence ID: [AAL58282.1](#) Length: 952 Number of Matches: 3

Range 1: 215 to 952 [GenPept](#) [Graphics](#)

▼ [Next Match](#) ▲ [Pre](#)

Score	Expect	Method	Identities	Positives	Gaps
817 bits(2110)	0.0	Compositional matrix adjust.	456/752(61%)	516/752(68%)	83/752(11%)
Query 194	AVSRYNRMARAGADEVTPDLCTYILIGCCCRAGRLDLGFAAL--GNVIKK-----				242
Sbjct 215	A S Y + M G + PD+ TY +I C+ +D ++ G VI+				271
Query 243	-GFRVEAITFTPLKGLCADKRTSDAMDIVLRRTTELGCIPDVFSYNNLLKGLCDENRSQ				301
Sbjct 272	G + + IT++ L+ G C + +AM + L +G P+ +Y+ L+ G C +R +				330
Query 302	EALELLHMMADDRGGGSPPDVVSNTVLNGFFKEGDSKAYSTYHEMLDRGILPDVVTYN				361
Sbjct 331	+AL L M G PD+++YN +L G F+ + A Y + + G ++ TYN				387
Query 362	SIIAALCKAQTVDKAMEGSRKRLLYFSKMRSDGVEPDVVTYNSLMDYLCKNGRCTEARKI				421
Sbjct 388	I+ LCK + D A++ + L K+ + T+N ++D L K GR EA+ +				440
Query 422	FDSMTKRG-KPEITTYGTLQGHCKEGRVIESEKLFDLMVIRIGVKPD-----IITYSTLI				475
Sbjct 441	F + + G P TY + + +G + E ++LF M G D I L				500
Query 476	DGYCLAVRLEEGSS-----VCVNSE----VQTGACGQVKEVGK				509
Sbjct 501	G + V E ++ + VN VQTGACGQVKEVGK				560
Query 510	NASEERLIVSSQEIIPDDPVSTIEALILLHSHKSTLAENHQLTTRLVVPNSKVGCCILGE				569
Sbjct 561	NASEERLIVSSQEIIPDDPVSTIEALILLHSHKSTLAENHQLTTRLVVPNSKVGCCILGE				620
Query 570	GQKVITEMRRRTGAEIRVYSKADKPKYLSFDEELVQH-----AGRAHLLSHQLLTA				620
Sbjct 621	GQKVITEMRRRTGAEIRVYSKADKPKYLSFDEELVQH AGRAHLLSHQLLTA				680
Query 621	IYVLVLRNRSIVVAEVKNNHGTAAACWALAAISK-----FIIKASVFSFALGLQ				667
Sbjct 681	IYVLVLRNRSIVVAEVKNNHGTAAACWALAAIS FIIKASVFSF LGLQ				740
Query 668	NLRTGPAHDPTVYVPVEYFSKREYPSGSSKVAPSASYERYAATTRLPNRELPSISPCAD				727
Sbjct 741	NLRTGPAHDPTVYVPVEYFSKREYPSGSSKVAPSASYERYAATTRLPN ELPSSISPCAD				800
Query 728	YMSCRSYLDQVPTDRYSNRVTLLQLGLSRAGNSNVQQLGITRAGNSNAYDYTEAAELHGR				787
Sbjct 801	YMSCRSYLDQVPTDRYSNRVTLLQLGLSRAGNSNVQQLGITRAGNSNAYDYTEAAE IHGR				860
Query 788	EDYRRLSGIQ---VALSNCGFQIVNWSLSLVVISGARVKLHEAHPGSSSEIVEIQGIPD				844
Sbjct 861	EDYRRLSG+ SNCGFQIVNWSLSLVVISGARVKLHEAHPGSSSEIVEIQGIPD				920
Query 845	QVKAAQSLQGFIGASSNSRQAPQSSRMAHYF		876		
Sbjct 921	QVKAAQSLQGFIGASSNSRQAPQSSRMAHYF		952		

Table S1 to be continued.

For gene 10

PPR protein [Oryza sativa Indica Group]Sequence ID: [ABC42330.1](#) Length: 791 Number of Matches: 3[See 1 more title\(s\)](#) ▼ [See all Identical Proteins\(IPG\)](#)Range 1: 32 to 381 [GenPept](#) [Graphics](#)▼ [Next Match](#) ▲ [Pre](#)

Score	Expect	Method	Identities	Positives	Gaps				
563 bits(1452)	0.0	Compositional matrix adjust.	280/350(80%)	293/350(83%)	29/350(8%)				
Query 158	EDARHVFD	ELLRRGRGAS	IYGLNRLADV	ARDSFPA	AAVSRYNRMARAGADEVTPDLCTYG 217				
Sbjct 32	EDARHVFD	ELLRRGRGAS	IYGLNRLADV	ARDSFPA	AAVSRYNRMARAGADEVTPDLCTYG 91				
Query 218	ILIGCCCR	AGRLDLGFA	ALGNVIKKG	FRVEAITF	TPLLKGLCADKRTSDAMDIVLRRTTE 277				
Sbjct 92	ILIGCCCR	AGRLDLGFA	ALGNVIKKG	FRV+AI	FTPLLKGLCADKRTSDAMDIVLRR TE 151				
Query 278	LGCIPDV	FSYNNLLK	GLCDENRSQ	EAL	ELLHMMADDRGGGSPPDVVS	SYNTVLNGFFKEGD 337			
Sbjct 152	LGCIPDV	FSYNNLLK	GLCDENRSQ	EAL	ELLHMMADDRGGGSPPDVVS	Y TV+NGFFKEGD 211			
Query 338	SDKAYSTY	HEMLDRG	ILPDVV	TYSIIA	ALCKAQTVDKAME-----	378			
Sbjct 212	SDKAYSTY	HEMLDRG	ILPDVV	TYSIIA	ALCKAQ +DKAME	271			
Query 379	-----G	SRKRL	-YFSKMR	SDGVEPD	VVTYNSLMDYLCKNGRC	TEARKIFDSMTKRG 429			
Sbjct 272	ILHGYS	SSGQPK	EAGFLK	KMRSDG	VEPDVVTY+ LMDYLCKNGRC	EARKIFDSMTKRG 331			
Query 430	-KPEITTY	GTL	LQGHCKE	GRVIESE	KLF	DLMVRI	GKPDII	TYSTLIDGY 478	
Sbjct 332	LKPEITTY	GTL	LQGYAT	KGALV	EMHGL	LDL	MVRNGI	HPDHYV	SILICAY 381