

Section 1

	(1)	10	20	30	40	51
Ath RGA1	(1)	MKRDHHQFQGRLSNHGTSSSSSS	ISKDKMMMKKEEDGGGNMD	DELLAVLG		
Rice	(1)	-----MKREYQEQAGSSGGGSS	ADMGSCKDKVMAGAAGEED	DELLAALG		
Pt contig5458	(1)	-----	-----	-----	LANAG	
Pt TC59241-59240	(1)					
Sm Contig 499.2	(47)	-MEDMDMLEAVYERKSRMIPVG	QGQDFQPMQWKEESAMG	MDELLAHAG		
Pp region 885000660	(1)	-----	MAYQYYPGSTRYEATGGAL	VDGQFRHAN		

Section 2

	(52)	60	70	80	90	102
Ath RGA1	(52)	YKVRSSSMAEVALKLEQLTMMSN	-----	QEDGLSHLATDTVHYNPS		
Rice	(47)	YKVRSSDMADVAQKLEQLMAMGM	GGVSAPGAADDFVSHLATDTVHYNPS			
Pt contig5458	(6)	YTVKASDLAHVAORLEQLSEIMGT	-----	QDPGISHLASEAVHYNPS		
Pt TC59241-59240	(1)			-----	RQEDGISHLSSEAVHYNPS	
Sm Contig 499.2	(51)	YNVRASDLTHVAQRLEQLDLSLL	-----	GAAPADTLAQDTVHYNPS		
Pp region 885000660	(29)	FMQPSDL	VDHLEQLHSLVLT	TVSQDSPN	FPVHHTLDAGAQ	TSNNKTS

Section 3

	(103)	110	120	130	140	153
Ath RGA1	(95)	ETYSWLDNMLSELNPPPLPASSN	GLDPVTPSP	PEICGFP		
Rice	(98)	DLSSWVESMLSELNAPLPPTPPA	PAARHASTSSTVTG			
Pt contig5458	(49)	DLAAGWIESMFGELNPGA				
Pt TC59241-59240	(21)	DLGGWIESMLSELHVEILP	TDQGFQFPQAADQSSTVREASNSVPESSTS			
Sm Contig 499.2	(92)	DLVSWIBGMLDELVEQPPATSS	DMESVVTPTITHQQQ			
Pp region 885000660	(75)	DLAAGWIDGMLDEL	SFNAGTMAA	QQRSLT	EDSLHQN	

Section 4

	(154)	160	170	180	190	204
Ath RGA1	(133)	-----	ASDY	DLKVIP		
Rice	(136)	-----	GGSGGFELPAAADSS		S	
Pt contig5458	(66)	-----	-----	DMPVPFGDRGSLIDSQVHKP		
Pt TC59241-59240	(72)	TSKGRTRVQNVQDDQYRLNGS	GAGLFEPVLD	RFSEFQLHGYPGGGVRD		
Sm Contig 499.2	(130)	-----	QQQLDFGGIPPPPPPFSSHQQQ			
Pp region 885000660	(112)	-----	-----	-----	-----	

Section 5

	(205)	210	220	230	240	255
Ath RGA1	(143)	-----	GNAIYQFPAIDSSSSSNNQNK	RKSCSSP		
Rice	(154)	-----	TYALRPISLPVATADPSAADS	ARDTKRMRTGGGSSSSSSS		
Pt contig5458	(87)	IQDDPSLSAMDLALHEYGLQFN	GSQASNPGQFSPDSDPSVRCN	TFSGPPL		
Pt TC59241-59240	(123)	NGIDRMFGNYGGLFSQVLVD	SDLLVDDPDVLC	PPQPEASPTLLQSSST		
Sm Contig 499.2	(152)	-----	GYSAFNFNVLYADQMDLSKNE	VGVASHSQ		
Pp region 885000660	(112)	-----	-----	ELASSSHDSSLD	TGSSRLPTL	

Section 6

	(256)	266	270	280	290	306
Ath RGA1	(172)	DSMVTSTSTGTGTGIGVIST	VTVTTTTTTTAAGESTRS	VIIIVDSQENGVR	LV	
Rice	(197)	SSGGGASRGSGVVEAAPPATQ	-----	AAAAANAPAVEVVVD	TQEAGR	LV
Pt contig5458	(138)	RGSDSTHTNFQARSFSAQSS	DEGSSLSSTRLTGTACQSS	INDGQESGR	LV	
Pt TC59241-59240	(174)	SSIEVQSGQDRLEEDVTGRE	QKRYRVCDELSERTVVMG	ADPHESGR	LV	
Sm Contig 499.2	(183)	IGASTTRPAPASGSSS	STSPHGIPPHAAGGMA	SAAMPTIQESDEL	SGVR	LV
Pp region 885000660	(134)	HYQNTPAVGNNFLATPOND	ASQLNANRATGAVLE	QQSPMGEDE	DN	GVRLV

Section 7

	(307)	307	320	330	340	357
Ath RGA1	(223)	HALMACAEATQONNLTALAB	ALVKOIGCLAVSQAG	---AMRKVATYFAEALA		
Rice	(243)	HALLACAEAVQENPAALAL	LVKQIPTLAASQGG	---AMRKVAAYFGEALA		
Pt contig5458	(189)	HLMLGC AEAIQRNN		---KVAS		
Pt TC59241-59240	(225)	HLMLACAEAVORGNLATARE	EMVKEVRLLASAQGG	---AMSKVATYFAEALA		
Sm Contig 499.2	(234)	HLMLACANAVORGDLAAAG	DMVAQLRMLVAHPSSSSS	AMARVATQFVEALS		
Pp region 885000660	(185)	HSLLACAESIORGNINLAL	QTLRLRIQLLSLPP	GP---MCKVATHFIDALT		

Section 8

	(358)	358	370	380	390	408
Ath RGA1	(271)	RRIYRLSEFPQ	--NQIDH	-----		C
Rice	(291)	RRVYRFRPADSTL	LD	-----		A
Pt contig5458	(208)					
Pt TC59241-59240	(273)	RRIYGFLPQDTRLRFNQN				DP
Sm Contig 499.2	(285)	RRIQNSCYNGGGGVGGGDR	QYHHHQSQQQQ	QQQQFKEESSDPGNTNNGA		
Pp region 885000660	(232)	CRIVGVAFFSSGNNV	G	-----		SNQSDS

Section 9

	(409)	409	420	430	440	459
Ath RGA1	(287)	LSDTLQMHFYETCPYLKFAH	FTANQAILEAF	BGKR	KRVHVDF	SNNOGLQWP
Rice	(308)	FADLLAHAFYESC	CPYLKFAHFTANQAILEAF	AGCHR	RVHVVD	FGKQGMQWP
Pt contig5458	(208)					
Pt TC59241-59240	(292)	LSDELQHFHYETCPYLKFAH	FIANQAILEAFSGH	QOVHVVD	FN	KOGIQWP
Sm Contig 499.2	(336)	MDLILHFFHYETCPYLKFAH	FTANQAILEALB	GHKSVHVVD	LD	QYGLQWP
Pp region 885000660	(253)	LSLLHFFHYETCPYLKFAH	FTANQAILEAFAG	QKQOVHVVD	FN	MHGLQWP

Section 10

	(460)	460	470	480	490	500	510
Ath RGA1	(338)	ALMQALALREGGPPT	FRLTGIGPPAPD	NSDHL	HEVGC	KLQALAE	AHVEFE
Rice	(359)	ALLQALALRPGGPP	SFRLTGVGPPQPD	ETDALQOVGV	KLQAF	ATIRVDFQ	
Pt contig5458	(208)						
Pt TC59241-59240	(343)	ALIQALALRPGGPP	AFRLTGIGPPQPD	GTALQOE	VCTRL	HCFAESVNV	KFS
Sm Contig 499.2	(387)	ALIQALALRPGGPP	FLRLTGIGPPQPHR	HDLL	HEIGL	KLQALADSVNV	DFA
Pp region 885000660	(304)	ALIQALALRPGGPP	FLRLTGIGPPQSGG	SDV	LQEIG	MKLQALAE	TVKVEFE

Section 11

	(511)	511	520	530	540	550	561
(389)	YRGFEVANS	SLADLDASMLE	LRPS	-----	DT	EAVAVNSVFELHKL	LGRPG-G
(410)	YRGLVAAT	TLADLEPFMLQ	PEGEADANE	EP	SVIAVNSVFELHRL	L	LAOPG---
(208)							
(394)	FRGYVAT	SLADIKPWML	DARPE	-----		EAVAVNSIL	ELHRLLED
(438)	F	GGVVAARLNDVQ	PWMLTV	RG	-----	EAVAVNSVFOMH	KALVEEPSDG
(355)	FRGVVAVK	LDLDTK	PWMLQ	ICHG	-----	EAVAVNSVF	QLHKL
							LYSASV

Section 12

	(562)	562	570	580	590	600	612
(433)	-----			IEKVLGVVKQIK	PFVIT	TVVEQESNHN	GPVFLDRF
(458)	-----			A	LEKVLGT	VHAVRPRIV	TVVEQEAHNHSGSFLDRF
(208)							
(439)	PS	-----		A	IDRVLAST	ISLKP	KILTVVEQEA
(482)	GNPAAGNGGGGRRSSP				ID	EVLR	LRVRLPKIVT
(399)	P	-----			ID	EVLR	SARALKPKISTIVE
							HEANHNQPSFLGRF

Section 13

	(613)	613	620	630	640	650	663
(467)	TESLHYYST	LFDSLEG	VPNS	-----		Q	DKVMSEVYLGKQICNL
(493)	TESLHYYST	MFDSLEG	SSSSQAELS	PSPAAGGGG	GT		DQVMSEVYLGROICNV
(208)							
(476)	TEALHYYST	VDFSLE	ARG	Q	-----		ACSE
(533)	MAALHYYST	MFDSLE	ACNLA	-----			PGSVEQMVAE
(434)	TEALHYYST	MFDSLE	ACS	P	-----		SDSS
							EQVLAEMYLGREINNI

Section 14

	(664)	664	670	680	690	700	714
(504)	VACEG	PDRVERHETIS	QWGNR	REGSSGL	APAH	HLGSNAFKQASML	SVFNSGQ
(544)	VACEGA	ERTERHETLG	QWRNRL	GRAGF	EPVHL	GSNAYKQAST	LLALFAGGD
(208)							
(516)	VACER	SERVERHEPT	LNWS	VR	LRNAGFW	PTPL	GLSNAFKQASMLSLFSGGE
(573)	VACEGA	ARTERHETL	QWR	IRMARSG	GFQ	PLYLGSNAFKQAN	MLLTFLSGD
(474)	VACEDA	ARVERHEN	IQWQ	MRMLKAGY	RPTQL	GLGN	NAFKQASMLTMFSGD

Section 15

	(715)	715	720	730	747
(555)	GYRVEE	SN	CGML	GLGWHT	TRPLITTS
(595)	GYRVEE	KE	EGCL	TGLGWHT	TRPLIATSAWRV
(208)					AAA
(567)	GYRVEE	NN	CGCL	TGLGWS	RPLIAASAWQRC
(623)	GYRVEE	KD	CGCL	TGLGWS	RPLVAASAWQCC
(524)	GYRVEE	KL	CGCL	TGLGWHT	TRPLISASAWQCA