

Figure S1. Exon/intron structure of Arabidopsis secondary cell wall CESA genes.

Exons are shown as boxes (white boxes for UTRs and black boxes for CDS regions) while the introns are shown as lines. Positions of the T-DNA insertion in the mutants used in the study are indicated by arrowhead.



Figure S2. Phenotypes of the cesa mutants and wild type control.

- A. Plant height
- B. Cellulose content
- C. Rosette appearance
- D. Inflorescence stem.

Error bars shown in (A) and (B), are SEM. Rosette photos (C) were taken when the plants were 21 days old while the photos of primary inflorescence stem severed at rosette level (D) were taken at 7 week stage.



**Figure S3**. Height of different *cesa* mutant plants transformed with WT CESA genes. Error bars are SEM. Significance levels from univariate ANOVA between the genotype and the mutant background are shown; \*\*\* Significant at 0.001.

Promoter	Gene	Mutant				Plan	t hei	ght (	%)						Cel	lulos	se co	onte	nt (%	6)		
	CESA4	cesa4 <sup>irx5-4</sup>	179	121	112	108	94	90	72	68	45	0	108	35	27	16	7	NA	91	11	2	61
pCESA7	CESA7	cesa7 <sup>irx3-7</sup>	208	178	149	149	139	139	129	104	94	89	NA	118	110	89	145	95	82	97	84	108
	CESA8	cesa8 <sup>irx1-7</sup>	182	174	103	99	95	95	66	61	61	57	82	128	81	57	50	78	17	57	61	52
0504.4	CESA4	cesa4 <sup>irx5-4</sup>	106	96	96	72	69	54	19				98	55	85	92	57	84	78			
pCESA4	CESA8	cesa8 <sup>irx1-7</sup>	104	82	75	71	71	64	53	28			81	64	57	54	54	57	49	58		
0=0.1.0	CESA4	cesa4 <sup>irx5-4</sup>	93	93	43	21							51	65	59	28						
PUESA8	CESA8	cesa8 <sup>irx1-7</sup>	88	81	70	70	63	60	35				96	82	81	89	54	72	53			

Figure S4. Complementation of secondary cell wall cesa mutants using different promoters.

CESA4 and 8 were expressed under control of all three SCW CESA promoters. Plant height (%) and cellulose content (%) data is shown for up to 10 independent lines. Plant height (%) = (Plant height of the line – plant height of the background mutant)/(Plant height of Col0 WT– plant height of the background mutant) \*100. Data is colour coded and signifies the % complementation: dark green: >60%, green: 40-60%, light green: 12.5-40%, white: <12.5%.



Figure S5. Classification of CESA proteins into 6 classes.

The trees is based upon 449 sequences from Phytozome that have been manually curated. The clades were named based on the Arabidopsis members which are indicated with green dots in the tree above. The table on the right lists the number of proteins in each CESA class for all the species used in the analysis.





A global alignment of 449 CESA proteins from 43 species was produced as shown in Figure S5. Class specificity scores were calculated at each amino acid position in the global alignment exactly as described in Carroll and Specht (2011). The scores for the 3 SCW CESA classes, CESA4, 7 and 8 were plotted. The curves were smoothed by taking average scores for a sliding window of 10 amino acids.



**Figure S7**. Schematic representation of CESA proteins showing the location of the regions used in this study.

- A. Linear representation of a CESA proteins with the 9 regions used in this study shown as boxes with grey fill and black lines. The name of each region is indicated inside each box. The length of each box is proportional to actual region size in amino acids. Position of the PCR and CSR regions described in Veragara and Carpita (2001) is shown above it. A linear representation of the regions involved in the multi-region swap experiments- VRS, CRS and LOOP, are indicated below.
- B. A cartoon representation of the 9 regions and their predicted topology.

		NI		ZN		
AtCesA7		MEASAGT.VAGSHNRNE VVTHNHE	EPKPLKNLDGOF	TCTTVECDTEVAONECCEPACE	POVEYERRECTONOPOOKTRYKETRGSPE	VEGD
AtCesA4	÷	MPNTMAS	FDDEHRHSSESAKLOKVCCDE	VKDDDNGOTEVACHVOVYPVCK	PCYEYERSNENKCCPOONTLYKRHKGSPK	TAGD
AtCesA8	÷	MVPS	RSP ONTOCEP	IGVKSNGEFFVACHEOSFPICK	ACLEVEFKEGREICLECGNPYDEN	
RsBcsA	:					
				VKI		
AtCesA7	:	EDEEDIDDIEYEFNIEHEQDKHKH	SABAMLYGKMSYGRGPBDDEN	GRFPPVIAG-GHSGEFPVGGGY	GNGEHGLHKRVHPYPSSEAGSEGG	RERM
AtCesA4	:	EENNGPDDSDDELNIKYRQDGSSI	honfaygsengdynskoowrp	NGRAFSSIGSVLGKDFEAER	DGYTDAE	/KERV
AtCesA8	:	VFDDVETKTSKTQSIV	PTQTNNTSQDSGIHAR	HISTVSTIDSELNDE	YGNPIW	<i>I</i> KNRV
RsBcsA	:				MIVRAKARSPIRVVP	VLLF
					TM1	
AtCesA7	:	DWKLQHG-NLGPEBDDDP	ijMGi ID	EARQPLSRKVPIASSKINPYRM	VIVARIVIIIAVEIRYRIJINEVHDAI	GIWL
AtCesA4	:	DKWKARQEKRGI	QTN DKEDDE⊐EY∎DA	EARQPLWRKVPISSSKISPYRI	VIVIRIVIIIVEFER-ERIIITE-AKDAY	PLWL
AtCesA8	:	ESWADAKDAASKKKKKDEKATAAS	HEAQIPT OHME TPPNTES	GATDVISVVIPIPRTKINSYRI		GLWL
RSBCSA	:	LLWVOLLVPPOrLA	AAPVAPSAOGLIAL	SOVVINALLKEFODKMVPRHI	I SAOSMINORIMEWRIEETI PEPAILDASE	LFA
			1			_
AtCesA7	:	TSVICEIWFAVSWILDOFPKWFPI	ERETYLDRLSIRVEREGEPNM	LAPVDVFVSTVDPLKEPPLVTS	NTVLSILAMDYPYPKISCYVSDDGASMLT	FESL
AtCesA4	:	ISVICEIWFALSWILDOFPKWFPI	NRETYLDRLSMRFERDGEKNK	LAPVDVFVSTVDPLKEPPIITA	NTILSILAVDYPVNKVSCYVSDDGASML	FDTL
AtCesA8	:	TSVICEIWFAVSWVLDOFPKWSPI	NRETYIDRLSARFEREGEOSO	LAAVDOFVSTVDPLKEPPLITA	NTVLSILALDYPVDKVSCYVSDDGAAMLS	FESL
RsBcsA	:	LLFAVETESISIEFINGELSADET	DRPFPRPLQFE	LPTVDILVPSYNEPADMLS	VTLAAAKNYIYEARLRTVVLODDG	
				^D1		
AtCesA7	:	SETAEFARKWVPFCKKFSIEPRAP	EMYFTLKVDYLQDKVHPTFVK	ERRAMKREYEEFKVRINAQVAK	ASKVPLEGWIMQDGTPWPGNNTKDHPGMI	QVFL
AtCesA4	:	SETSEFARRWVPFCKKYNVEPRAP	EFYFSEKIDYLKDKVQTTFVK	DRRAMKREYEEFKVRINALVAK	AQKKPEEGWVMQDGTPWPGNNTRDHPGMI	<b>QVYL</b>
AtCesA8	:	VETADFARKWVPFCKKYSIEPRAP	EFYFSLKIDYLRDKVQPSFVK	ERRAMKRDYEEFKIRMNALVAK	AQKTPEEGWTMQDGTSWPGNNTRDHPGMI	QVFL
RsBcsA	:		GTDQRCMSPDPELAQ	KAQER <u>RRE</u> LQQLCRE <mark>D</mark> G		
AtCosA7		CHSCCEDVECHET.DDT.VVVSDEKD	PGEOHHKKAGAMN AT VEVAC	UT TINA DEMINI DODHVANINSKA	VERAMONTANDO TOKINOVO EPOPEDOT	
AtCesA4	:	GKEGAED TO GNEL DEL VYVSREKR	PGVAHHKKAGAMI AMVRVSA	VI.TNAPEMINI.DCDHVINNSKA	TRESMOTIMDPOLGKKLOV/OFPORFDGI	т
AtCes A8	:	GYSGARD TEGNEL PRIVYVSREKR	PGYOHHKKAGADN-ALVRVSA	VI.TNA PETINI. DCDHVVNNSKA	VREAMCETMDRVVGODVCEVOEPOREDGI	DK
RsBcsA	:	VVYSTRER-	NEHAKAGNMSAATER	I.KGELWWEDADHWPSRDET	ARTVGYEVEDBDUFTVOTEHEFINE	PTO
	•					
					VR2	
					VR2	
AtCesA7	:	NDRYANRN <mark>T</mark> VFFDINMKGI	DGIQGPVYVGTGCVFKROALY	GYBPEKGPKRPKMISC	VR2	GR
AtCesA7 AtCesA4	:	NDRYANRNIVFFDINMKGL NDRYANRNIVFFDINMRGL	DGIQGPVYVGTGCVFKROALY DGIQGPVYVGTGCVFNRPALY	GYPEKGEKRPKMISC GYPEPVSEKRKKMICDCWPSWI	VR2 -geope	GR KKKT
AtCesA7 AtCesA4 AtCesA8	::	NDRYANRN <mark>IVFFDINMKGL</mark> NDRYANRNIVFFDINMRGL SDRYANRNIVFFDVNMRGL	DGIQGPVYVGTGCVFKROALY DGIQGPVYVGTGCVFNROALY DGIQGPVYVGTGTVFRROALY	GYPEKGEKRPKMISC GYPEVSEKRKKMTCDCWPSWI GYSEPSKTRILPQSSSSS	VR2 -gcpc -gcggnrnhksdsskkksgikslfski 	GR KKKT KKQP
AtCesA7 AtCesA4 AtCesA8 RsBcsA	::	NDRYANRNIVFFDINMKGL NDRYANRNIVFFDINMRGL SDRYANRNIVFFDVNMRGL RNLALGDR <mark>CPPPN</mark> EMFYGKIHRGI	DGIQGPVYVGTGCVFKROALY DGIQGPVYVGTGCVFNRPALY DGIQGPVYVGTGTVFRROALY DRWGCAFFCGSAAVIRRRALD	GYPERGERRPRMISC GYPEVSERRERMICDCWPSWI GYSERSKERILPQSSSSS EAG	VR2 -gcpc ccccgggnrnhksdsskkksgikslfski cccltk	GR KKKT KKQP
AtCesA7 AtCesA4 AtCesA8 RsBcsA	::	NDRYANRNIVFFDINMKGI NDRYANRNIVFFDINMRGI SDRYANRNIVFFDVNMRGI RNLALGDR <mark>CPPENEMFY</mark> GKIHRGI	DGIQGPVYVGTGCVFKROALY DGIQGPVYVGTGCVFNRPALY DGIQGPVYVGTGTVFRROALY DRWGGAFFCGSAAVIRRRALD	GY PEKGEKSPKMISC GY PEVSEK KKMICDCWPSWI GYSPESKERILPOSSSSS EAG	VR2 -gcpc ccccgggnrnhksdsskkksgikslfskl cccltk	GR KKKT KKQP
AtCesA7 AtCesA4 AtCesA8 RsBcsA	::	NDRYANRNIVFFDINMKGI NDRYANRNIVFFDINMRGI SDRYANRNIVFFDVNMRGI RNLALGDR <mark>CPPBNEMFY</mark> GKIHRGI	DGIQGPVYVGTGCVFKROALY DGIQGPVYVGTGCVFNRPALY DGIQGPVYVGTGTVFRROALY DRWGGAFFCGSAAVIRRRALD	GY PEKGEKSPKMISC GY PEVSEKSKKMICDCWPSWI GYSPFSKERILPQSSSSS EAG	VR2 -GCPCF CCCCGGGNRNHKSDSSKKKSGIKSLFSKI CCCLTK	GR KKKT KKQP
AtCesA7 AtCesA4 AtCesA8 RsBcsA AtCesA7	: : : : : : : : : : : : : : : : : : : :	NDRYANRN IVFFDINMKGI NDRYANRN IVFFDINMRGI SDRYANRN IVFFDVNMRGI RNLALGDRCPPENEMFY GKIHRGI 	DGIQGPVYVGTGCVFKROALY DGIQGPVYVGTGCVFNRPALY DGIQGPVYVGTGTVFRROALY DRWGCAFFCGSAAVIRRRALD	GY PEKGER PKMISC GY PEVSER KKM CDCWPSWI GYSPESKER ILPOSSSSS EAG	VR2	GR KKKT KKQP
AtCesA7 AtCesA4 AtCesA8 RsBcsA AtCesA7 AtCesA4	: : : : : : : : : : : : : : : : : : : :	NDRYANRN TVFFDINMKGL NDRYANRN IVFFDINMRGL SDRYANRN IVFFDVNMRGL RNLALGDRCPPENEMFY GKIHRGL RRKNKKFSKNDM GDVAA KKKSDDKTVSSYSKRSSTEATED	DGIQGPVYVGTGCVFKROALY DGIQGPVYVGTGCVFNRDALY DGIQGPVYVGTGTVFRROALY DRWGCAFFCGSAAVIRRRALD LGGABCDKEHIMS IFDIECLEGYDDIFKSSIMS	GY PEKGEKR PKMISC GY PEVSEK KKM CDCWPSWI GYSPESK RILPQSSSS EAG	VR2	GR KKKT KKQP 
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AtCesA7 AtCesA8 RsBcsA AtCesA7 AtCesA4 AtCesA8 RsBcsA		NDRYANRN TVFFDINMKGI NDRYANRN TVFFDINMRGI SDRYANRN TVFFDVNMRGI RNLALGDRCPPENEMFYGK IHRGI RRKNKKFSKNDM GDVAA KKKSDDK TSSYSRKRSSTEA DDSEIYKDAKREELDAAIFN	DGIQGPVYVGTGCVFKROALY DGIQGPVYVGTGCVFNRPALY DGIQGPVYVGTGTVFROALY DRWCGAFFCGSAAVLRRRALD LCGAECDREHIMS LEDIEEGLEGYDELEKCSIMS LGDIDNYDEYDRSMLIS	GYPPEKGEKRPKMISC	VR2 -GC-PC	GR KKKT KKQP WGTE WGKE WGKE
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AtCesA7 AtCesA4 AtCesA8 RsBcsA AtCesA7 AtCesA4 AtCesA8 RsBcsA	: : : : : : : : : : : : : : : : : : : :	NDRYANRN IVFFDINMKGI NDRYANRN IVFFDINMRGI SDRYANRN IVFFDVMMRGI RNLALGDRCPPENEMFYGKIHRGI 	DGIQGPVYVGTGCVFKROALY DGIQGPVYVGTGCVFNRDALY DGIQGPVYVGTGTVFROALY DRWGGAFFCGSAAVIRRRALD LCGAECDKEHLMS LEDIBEGLEGYDBLEKSSIMS LGDIDNYDEYDRSMLIS	GYPPEKGEKRPKMISC GYPPPVSEKRKKMTCDCWPSWI GYSPESKERILPQSSSSS EAG	VR2	GR KKKT KKQP WGTE WGKE
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AtCesA7 AtCesA4 AtCesA8 RsBcsA AtCesA7 AtCesA4 AtCesA8 RsBcsA AtCesA7 AtCesA7 AtCesA7		NDRYANRN TVFFD INMKGL NDRYANRN IVFFD INMKGL SDRYANRN IVFFD INMRGL RNLALGDRCPPEN EMFY GKIHRGI 	DGIQGPVYVGTGCVFKROALY DGIQGPVYVGTGCVFNROALY DGIQGPVYVGTGTVFRROALY DRWGCAFFCGSAAVIRRALD IGGAEGDKEHIMS IEDIEECLEGYDEIEKSIMS LGDIDNYDEYDRSMLIS SIYCMPKRPAFKGSAPINLSD SVYCMPKRPAFKGSAPINLSD	GYPPEKGEKRPKMISC GYPPEVSEKRKKMTCDCWPSWI GYSPESKERILPQSSSSS EAG DMNFEKTFGQSSIFVTSTIME OKNFEKREGMSEVFIASTIMEN OTSFEKTFGISTVFIESTIMEN RINQVLRWALGSVEIFFSRHC	VR2 -GC-PCF CCC-CGGGNRNHKSDSSKKKSGIKSLFSKI CCC-LTK	GR KKKT KKQP WGTE WGKE WGKE PLLA
AtCesA7 AtCesA8 RsBcsA AtCesA7 AtCesA7 AtCesA4 AtCesA8 RsBcsA AtCesA7 AtCesA7 AtCesA4 AtCesA8		NDRYANRN TVFFDINMKGL SDRYANRN IVFFDINMRGL SDRYANRN IVFFDINMRGL RNLALGDRCPPENEMFYGKIHRGL 	DGIQGPVYVGTGCVFKROALY DGIQGPVYVGTGCVFNRDALY DGIQGPVYVGTGTVFRROALY DRWGCAFFCGSAAVIRRAID LGGABGDKEHIMS LEDIBEGLEGYDBIEKSSIMS LGDIDNYDBYDRSMIIS SIYCMPKRPAFKGSAPINLSD SIYCMPKRPAFKGSAPINLSD SIYCMPKRPAFKGSAPINLSD	GY PEKGERR PKMI SC GY PEVSEK KKM CD CWPSWI GYSPESK PRILPQ SS S EAG	VR2 -GC PCF CCC CGGGNRNHKSDSSKKKSGIKSLFSKI CCC LTK	GR
AtCesA7 AtCesA8 RsBcsA AtCesA7 AtCesA4 AtCesA8 RsBcsA AtCesA7 AtCesA7 AtCesA4 AtCesA8 RsBcsA		NDRYANRN TVFFDINMKGL SDRYANRN TVFFDINMRGL RNLALGDRCPPENEMFYGKIHRGL 	DGIQGPVYVGTGCVFKROALY DGIQGPVYVGTGCVFNRPALY DGIQGPVYVGTGTVFRROALY DRWGCAFFCGSAAVIRRAID LGOLDNDKEHIMS LGDIDNYDEYDRSMIIS SIYCMPKRPAFKGSAPINLSD SIYCMPKRPAFKGSAPINLSD SIYCMPLRPAFKGSAPINLSD SIYCMPLRPAFKGSAPINLSD SIYCMPLRPAFKGSAPINLSD	GYSPEKGERRPKMISC GYSPEVSEKRKKMTCDCWPSWI GYSPESKERILPQSSSS EAG	VR2 -GC PC	GR KKKT KKQP WGTE WGKE WGKE PLLA PLLA VRM
AtCesA7 AtCesA8 RsBcsA AtCesA7 AtCesA4 AtCesA8 RsBcsA AtCesA7 AtCesA7 AtCesA8 RsBcsA		NDRYANRN TVFFDINMKGI NDRYANRN TVFFDINMRGI RNIALGDRCPPENEMFYGKIHRGI RRKNKKFSKNDMGDVAA KKKSDKTVSSYSKRSSTEAIFD QDPSEIYADAKREEIDAAIFN CU LGWIYGSITEDILTGFKMHCRGWR IGWIYGSITEDILTGFKMHCRGWR IGWIYGSITEDILTGFKMHCRGWR GFAGETITEDAETALEIHSRGWK	DGIQGPVYVGTGCVFKROALY DGIQGPVYVGTGCVFNRPALY DGIQGPVYVGTGTVFRROALY DRWGCAFFCGSAAVLRRRALD LGDIDN	GYSPEKGERRPKMISC GYSPEYSEKRKKMTCDCWPSWI GYSPESKERILPQSSSS EAG	VR2 -GC PC	GR RKKT KKQP WGKE WGKE WGKE PILA PILA PILA
AtCesA7 AtCesA8 RsBcsA AtCesA7 AtCesA4 AtCesA8 RsBcsA AtCesA7 AtCesA7 AtCesA8 RsBcsA		NDRYANRN TVFFDINMKGI NDRYANRN TVFFDINMKGI SDRYANRN TVFFDINMRGI RNIAIGDRCPPENEMFYGKIHRGI RRKNKKFSKNDM GDVAA KKKSDDKT SSYSRKRSSTEAIFD QDPSEIYKDAKREEIDAAIFN CI IGWIYGSITEDIIITGFKMHCRGWR IGWIYGSITEDIIITGFKMHCRGWR IGWIYGSITEDIIITGFKMHCRGWR IGWIYGSITEDIIITGFKMHCRGWR	DGIQGPVYVGTGVFKROALY DGIQGPVYVGTGVFNRPALY DGIQGPVYVGTGVFRROALY DRWCGAFECGSAAVLRRRALD LGGAECDREHIMS LEDIEEGLEGYDELEKSSIMS LGDIDNYDEYDRSMLIS SIYCMPKRPAFKGSAPINLSD SIYCMPKRPAFKGSAPINLSD SIYCMPTRPAFKGSAPINLSD SIYCMPTRPAFKGSAPINLSD SIYCMPTRPAFKGSAPINLSD	GYSPEKGERRPKMISC GYSPEYSEKRKKMTCDCWPSWI GYSPESKERILPQSSSSS EAG	VR2 GC PC	GR RKKT KKQP WGTE WGKE WGKE DILA PLLA VRM
AtCesA7 AtCesA8 RsBcsA AtCesA7 AtCesA7 AtCesA8 RsBcsA AtCesA7 AtCesA8 RsBcsA AtCesA8 RsBcsA		NDRYANRN TVFFDINMKGI NDRYANRN TVFFDINMRGI RNIALGDRCPPENEMFYGKIHRGI SRKNKKFSKNDM GDVAA KKKSDDKT SSYSKRSSTEATFD QDPSEIYKDAKREELDAAIFN CHUYGSITEDILTGFKMHCRGWR IGWIYGSITEDILTGFKMHCRGWR IGWIYGSITEDILTGFKMHCRGWR GFAGETITEDAETALEIHSRGWK	DGIQGPVYVGTGCVFKROALY DGIQGPVYVGTGCVFNPALY DGIQGPVYVGTGCVFNPALY DRWCGAFFCGSAAVLRRRALD LGGAEGDREHIMS LEDIBEGLEGYDEIEKSIMS LGDIDNYDEYDRSMLIS SIYCMPKRPAFKGSAPINLSD SVYCMPKRPAFKGSAPINLSD SIYCMPIRPAFKGSAPINLSD SIYCMPIRPAFKGSAPINLSD SIYCMPIRPAFKGSAPINLSD SIYCMPIRPAFKGSAPINLSD SIYCMPIRPAFKGSAPINLSD SIYCMPIRPAFKGSAPINLSD	GYSPEKGERR PKMISC GYSPEVSEKRKKMTCDCWPSWI GYSPESKERILPOSSSSS EAG	VR2 GC PC	GR RKKT KKQP WGTB WGKE WGKE DILLA DILLA DILLA DILLA DILLA
AtCesA7 AtCesA4 AtCesA8 RsBcsA AtCesA7 AtCesA4 AtCesA8 RsBcsA AtCesA7 AtCesA4 AtCesA8 RsBcsA AtCesA7 AtCesA7 AtCesA7 AtCesA7		NDRYANRN TVFFDINMKGL NDRYANRN TVFFDINMRGL SDRYANRN TVFFDYNMRGL RNLALGDRCPPENEMFYGKIHRGL 	DGIQGPVYVGTGCVFKROALY DGIQGPVYVGTGCVFNPALY DGIQGPVYVGTGTVFROALY DRWGGAFECGSAAVIRRRAID LGGAEGDREHIMS LEDIBEGIBGYDBIEKSSIMS LGDIDNYDEYDRSMLIS SIYCMPKRPAFKGSAPINLSD SVYCMPKRPAFKGSAPINLSD SIYCMPIRPAFKGSAPINLSD SIYCMPIRPAFKGSAPINLSD SIYCMPIRPAFKGSAPINLSD SIYCMPIRPAFKGSAPINLSD SIYCMPIRPAFKGSAPINLSD SIYCMPIRPAFKGSAPINLSD SIYCMPIRPAFKGSAPINLSD SIYCMPIRPAFKGSAPINLSD	GYPPEKGERR PKMISC GYPPPVSERRKKMTCDCWPSWI GYSPESKERILPQSSSSS EAG	VR2 -GC PC	GR RKKT KKOP WGTE WGKE WGKE DILA PILA VRMM
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AtCesA7 AtCesA8 RsBcsA AtCesA7 AtCesA7 AtCesA8 RsBcsA AtCesA7 AtCesA7 AtCesA4 AtCesA8 RsBcsA AtCesA7 AtCesA7 AtCesA4 AtCesA8 RsBcsA AtCesA7		NDRYANRN TVFFDINMKGI SDRYANRN TVFFDINMKGI RNIALGDRCPPENEMFYGKIHRGI 	DGIQGPVYVGTGCVFKROALY DGIQGPVYVGTGCVFNRFALY DGIQGPVYVGTGTVFRROALY DRWGCAFFCGSAAVIRRAID IGGABGDKEHIMS IEDIBECIEGYDBIEKSSIMS IGDIDNYDEYDRSMIIS SIGDIDNYDEYDRSMIIS SIYCMPKRPAFKGSAPINLSD	GYOPEKGERR PKMISC GYPPEVSEK KKM CDCWPSWI GYSPESKERILPQSSSS	CC CC CG CON CONTRACT OF CC CC CG CON CONTRACT OF CC CC CG CON CONTRACT OF CC CC CC CG CON CONTRACT OF	GR KKKT KKQP WGKE WGKE WGKE DELLA PLLA PLLA VRMM
AtCesA7 AtCesA8 RsBcsA AtCesA7 AtCesA7 AtCesA4 AtCesA8 RsBcsA AtCesA7 AtCesA7 AtCesA4 AtCesA8 RsBcsA AtCesA7 AtCesA4 AtCesA8 RsBcsA AtCesA7 AtCesA4 AtCesA8 RsBcsA		NDRYANRN TVFFDINMKGI SDRYANRN TVFFDINMKGI RNIALGDRCPPENEMFYGKIHRGI 	DGIQGPVYVGTGVFKRALY DGIQGPVYVGTGVFKRALY DGIQGPVYVGTGVFRRALY DRWGCAFFCGSAAVIRRALD IGGAEGDKEHIMS IEDIBE GEGYDDIEKSSIMS IEDIDNYDEYDRSMIIS SIYCMPKRPAFKGSAPINLSD SVYCMPKRPAFKGSAPINLSD SIYCMPI	GY OPEKGERR PKMI SC	CC CC CGGRNRNHKSDSSKKKSGIKSLFSKI CC CC CGGRNRNHKSDSSKKKSGIKSLFSKI CC LTK- GGLPEATNTSSLIKEAIHVISCGYEDKTE GGLPEATNTSSLIKEAIHVISCGYEDKTE GGVPDSVNPSTLIKEAIHVISCGYEEKTE IWYGYKGCKLKWLEREAYANTTIYPFTST IWYAGC-KLKILERLAYINTIVYPFTST IWYCSGGRLKLLQRLAYINTIVYPFTST IWYCSGGRLKLLQRLAYINTIVYPFTST IHYCCGGCKLKWLEREAYANTTIYPFTST IWYCSGGRLKLLQRLAYINTIVYPFTST IHYCCGGCKLKULGUDNFTVTSKATDT HLFAVYQGLLKILAGIDTNFTVTSKATDT HLFAVYQGLLKILAGIDTNFTVTSKATDT HLFAVYQGLLKILAGIDTNFTVTSKATDT INFAVYQGLLKILAGIDTNFTVTSKATDT INFAVYQGLLKILAGIDTNFTVTSKATDT INFAVYQGLLKILAGIDTNFTVTSKATDT GRQNRTPTIVVLWSILLASIFSLIWVRID GRQNRTPTIVIWSVLLASIFSLIWVRID DRSVILVVGGWAVINVLVGFALRAV ferent CESA protein regions	CR
AtCesA7 AtCesA8 RsBcsA AtCesA7 AtCesA4 AtCesA8 RsBcsA AtCesA7 AtCesA4 AtCesA8 RsBcsA AtCesA7 AtCesA7 AtCesA4 AtCesA8 RsBcsA AtCesA7 AtCesA7 AtCesA7 AtCesA7 AtCesA7 AtCesA7 AtCesA7 AtCesA7 AtCesA7 AtCesA7 AtCesA7 AtCesA7		NDRYANRN TVFFDINMKGI NDRYANRN TVFFDINMKGI RNIALGDRCPPENEMFYGKIHRGI RNIALGDRCPPENEMFYGKIHRGI KKKSDDKT.SSYSKRSSTEAIFD QDPSEIYDDAKREEDAAIFN CU LGWIYGSITEDILTGFKMHCRGWR IGWIYGSITEDILTGFKMHCRGWR IGWIYGSITEDILTGFKMHCRGWR GFAGETITEDAETALEIHSRGWC YCILPAICLLTD-KFIMEPISTA YCTIPAVCLLTG-KFIIFTINNFA YCTIPAVCLLTG-KFIIFTINNFA YCTIPAVCLLTG-KFIIFTINNFA YCTIPAUCLLTG-KFIIFTINNFA YCTIPAUCLLTG-KFIIFTINNFA YCTIPAUCLLTG-KFIIFTINNFA YCTIPAUCLLTG-KFIIFTINNFA YCTIPAUCLLTG-KFIIFTINNFA YCTIPAUCLLTG-KFIIFTINNFA YCTIPAUCLLTG-KFIIFTINNFA YCTIPAUCLLTG-KFIIFTINNFA YCTIPAUCLLTG-KFIIFTINNFA YCTIPAUCLLTG-KFIIFTINNFA YCTIPAUCLLTG-KFIIFTINNFA YCTIPAUCLLTG-KFIIFTINNFA YCTIPAUCLLTG-KFIIFTINNFA YCTIPAUCLLTG-KFIIFTINNFA YCTIPAUCLLTG-KFIIFTINNFA YCTIPAUCLLTG-KFIIFTINNFA YCTIPAUCLLTG-KFIIFTINNFA YCTIPAUCLLTG-KFIIFTINNFA	DGIQGPVYVGTGVFKROALY DGIQGPVYVGTGVFKROALY DGIQGPVYVGTGVFRROALY DRWGCAFFCGSAAVIRRALD LGGAEGDREHIMS LEDIEE CLEGYDEIEKSSMSG LGDIDNYDEYDRSMISS SIYCMPKRPAFKGSAPINLSD SIYCMPKRPAFKGSAPINLSD SIYCMPTRPAFKGSAPINLSD SIY	GY OPEKGERR PKMI SC	CGVPPSSSAVLKEATHVISCGYEDKTE GGVPPSSSAVLKEATHVISCGYEDKTE GGLBEATTTSSLIKEATHVISCGYEDKTE GGLBEATTTSSLIKEATHVISCGYEKTE GGVPDSVNPSTLIKEATHVISCGYEKTE IMYGYKGGKLKWLERJAYANTTIYPFTST IMYGCSGGRLKLLQRLAYINTIVYPFTST IMYCCSGGRLKLLQRLAYINTIVYPFTST IFRRCLGIAQRICYLNSMSFWFFFI HLFAVVQGLLKILAGIDTNFTVTSKATDT HLFAVVQGLLKILAGIDTNFTVTSKATDT HLFAVVQGLLKILAGIDTNFTVTSKATDT HLFAVVQGLLKILAGIDTNFTVTSKATDT IMFQCSGGRLKLLQRLAYINTIVYPFTST GRQNRTPTIVVIWSVLLASIFSLLWVRID GRQNRTPTIVVIWSVLLASIFSLLWVRID GRQNRTPTIVVIWSVLLASIFSLLWVRID GRQNRTPTIVVIWSVLLASIFSLLWVRID GRQNRTPTIVVIWSVLLASIFSLLWVRID GRQNRTPTIVVIWSVLLASIFSLLWVRID GRQNRTPTIVVIWSVLLASIFSLLWVRID GRQNRTPTIVVIWSVLLASIFSLLWVRID IGRONTPTIVIWSVLLASIFSLWVRID IGRONTPTIVIWSVLLASIFSLWVRID IGRONTPTIVIWSVLLASIFSLWVRID IGRONTPTIVIWSVLLASIFSLWVRID IGRONTPTIVIWSVLLASIFSLWVRID IGRONTPTIVIWSVLLASIFSLWVRID IGRONTPTIVIWSVLLASIFSLWVRID IGRONTPTIVIWSVLLASIFSLWVRID IGRONTPTIVIWSVLLASIFSLWVRID IGRONTPTIVIWSVLLASIFSLWVRID IGRONTPTIVIWSVLLASIFSLWVRID IGRONTPTIVIWSVLLASIFSLWVRID IGRONTPTIVIWSVLLASIFSLWVRID IGRONTPTIVIKSVLASIFSLWVRID IGRONTPTIVIKSVLLASIFSLWVRID IGRONTPTIVIKSVL	GR RKKT KKQP WGKE WGKE DILA PILA PILA VRM

the double headed arrows above the alignment.

## Single region swaps

CESA7 <sub>NT CESA4</sub>	NZN VR1 TM	CR1	VR2 CR2	тм с
CESA7 <sub>ZN_CESA4</sub>	NZN VR1 TM	CR1	VR2 CR2	тм с
CESA7 <sub>VR1_CESA4</sub>	NZN VR1 TM	CR1	VR2 CR2	тм с
CESA7 <sub>TM1_CESA4</sub>	NZN VR1 TM	CR1	VR2 CR2	тм с
CESA7 <sub>CR1_CESA4</sub>	NZN VR1 TM	CR1	VR2 CR2	тм с
CESA7 <sub>VR2_CESA4</sub>	NZN VR1 TM	CR1	VR2 CR2	2 TM
CESA7 <sub>CR2_CESA4</sub>	NZN VR1 TM	CR1	VR2 CR2	тм с
CESA7 <sub>TM2_CESA4</sub>	NZN VR1 TM	CR1	VR2 CR2	тм с
CESA7 <sub>CT_CESA4</sub>	NZN VR1 TM	CR1	VR2 CR2	тм с

CESA7<sub>NT\_CESA8</sub> CESA7<sub>ZN\_CESA8</sub> CESA7<sub>VR1\_CESA8</sub> CESA7<sub>TM1\_CESA8</sub> CESA7<sub>CR1\_CESA8</sub> CESA7<sub>CR2\_CESA8</sub> CESA7<sub>CR2\_CESA8</sub> CESA7<sub>TM2\_CESA8</sub>

	VZN VR1 TI	И	CR1	VR2 CR2	ТМ	С
	N ZN VR1	гм	CR1	VR2 CR2	ТМ	C
	N ZN VR1 TI	М	CR1	VR2 CR2	ТМ	С
,	NZN VR1	ΓM	CR1	VR2 CR2	ТМ	C
	NZN VR1	ГΜ	CR1	VR2 CR2	ТМ	C
	NZN VR1	гм	CR1	VR2 CR2	2 TM	C
	NZN VR1	ΓМ	CR1	VR2 CR2	ТМ	C
3	NZN VR1	ГΜ	CR1	VR2 CR2	TM	C
	NZN VR1	ГМ	CR1	VR2 CR2	ТМ	C

CESA4 <sub>NT CESA7</sub>	NZN VR1 TM	CR1
CESA4	NZN VR1 TM	CR1
CESA4 <sub>VR1_CESA7</sub>	NZN VR1 TM	CR1
CESA4	NZN VR1 TM	CR1
CESA4 <sub>CR1_CESA7</sub>	NZN VR1 TM	CR1
CESA4 <sub>VR2_CESA7</sub>	NZN VR1 TM	CR1
CESA4 <sub>CR2_CESA7</sub>	NZN VR1 TM	CR1
CESA4 <sub>TM2_CESA7</sub>	NZN VR1 TM	CR1
CESA4 <sub>CT_CESA7</sub>	NZN VR1 TM	CR1
-		

L TM	CR1		VR	2	CR2	TI	vi c
ТМ	CR1	1	VR2	: 0	CR2	TⅣ	1 C
ТМ	CR1		VR2	2	CR2	TN	/I C
тм	CR1	V	28	CR	2	ТМ	С
тм	CR1	VF	2	CR	2	ТМ	С
ТМ	CR1	VR	2 CF	2	1	M	C
тм	CR1	V	<b>R2</b>	CR	2	ТМ	С
ТМ	CR1	V	R2	CR	2	ТМ	С
ТΜ	CR1		VR2		CR2	TN	l C

CESA8<sub>NT\_CESA7</sub> CESA8<sub>ZN\_CESA7</sub> CESA8<sub>TM1\_CESA7</sub> CESA8<sub>CR1\_CESA7</sub> CESA8<sub>CR2\_CESA7</sub> CESA8<sub>CR2\_CESA7</sub> CESA8<sub>TM2\_CESA7</sub>

NZN VR1 TM	CR1	VR2 CR2	TM	C
ZN VR1 TM	CR1	VR2 CR2	TM	С
ZN VR1 TM	CR1	VR2 CR2	TM	C
ZN VR1 TM	CR1	VR2 CR2	ТМ	С
ZN VR1 TM	CR1	VR2 CR2	TM	С
ZN VR1 TM	CR1	VR2 CR2	ТМ	С
ZN VR1 TM	CR1	VR2 CR2	TM	С
ZN VR1 TM	CR1	VR2 CR2	ТМ	C
ZN VR1 TM	CR1	VR2 CR2	TM	С

## Multi-region swaps

CESA4 <sub>CRS_CESA7</sub> CESA4 <sub>CRS_CESA8</sub>	NZN VR1 TM NZN VR1 TM	CR1 CR1	VR2 CR2 TM C	CESA7 <sub>CRS_CESA4</sub> CESA7 <sub>CRS_CESA8</sub>	N ZN VR N ZN VR	1 TM 1 TM	CR1 CR1	VR2 CR2 VR2 CR2	TM TM	
CESA4 <sub>VRS_CESA7</sub> CESA4 <sub>VRS_CESA8</sub>	NZM VR1 TM	CR1 CR1	VR2 CR2 TM C VR2 CR2 TM C	CESA7 <sub>VRS_CESA4</sub> CESA7 <sup>VRS_CESA8</sup>	N ZN VR1 N ZN VR1	тм	CR1 CR1	VR2 CR2	TM TM C	C
CESA4 <sub>LOOP_CESA7</sub> CESA4 <sub>LOOP_CESA8</sub>	NZN VR1 TM	CR1 CR1	VR2 CR2 TM C	CESA7 <sub>LOOP_CESA4</sub> CESA7 <sub>LOOP_CESA8</sub>	N ZN VR	1 TM	CR1 CR1	VR2 CR2	TM TM	c c
CESA8 <sub>CRS_CESA4</sub> CESA8 <sub>CRS_CESA7</sub>	ZN VR1 TM ZN VR1 TM	CR1 CR1	VR2 CR2 TM C VR2 CR2 TM C		KEY	CESA4	(IRX5)			
CESA8 <sub>VRS_CESA4</sub> CESA8 <sub>VRS_CESA7</sub>	ZN VR1 TM	CR1 CR1	VR2 CR2 TM C			CESA7 CESA8	(IRX3) (IRX1)			
CESA8 <sub>LOOP_CESA4</sub> CESA8 <sub>LOOP_CESA7</sub>	ZN VR1 TM ZN VR1 TM	CR1 CR1	VR2 CR2 TM C							

**Figure S9**. Schematic representation of the swap constructs used in this study. All region lengths are proportional to their respective amino acid size.



**Figure S10**. Analysis of protein expression in the swap constructs used in this study. Level of expression was measured for CESA7 (A) or CESA4 (B) using quantitative western blot analysis. Crudes extracts prepared from 3 independent lines for each CESA7<sub>CESA4</sub> construct and probed with anti-CESA7 antibody while the crude extracts prepared from three independent lines for each CESA4<sub>CESA7</sub> construct were probed with anti-CESA4 antibody (green bands). All extracts were also simultaneously probed with anti-HSP73 antibody to normalise for loading variations (red bands). HSP73 normalised signals were then expressed as percentage of Col0 WT. Protein expression (%WT) was plotted against cellulose content (%WT) to produce Figure 7.

Pogion	AtCesA0	4	AtCesA0	7	AtCesA08		
Region	coordinates	length	coordinates	length	coordinates	length	
NT	aa 1-22	22	aa 1-36	36	aa 1-8	8	
Zn	aa 23-72	50	aa 37-86	50	aa 9-58	50	
VR1	aa 73-197	125	aa 87-220	134	aa 59-166	108	
TM1-2	aa 198-265	68	aa 221-288	68	aa 167-234	68	
CR1	aa 266-583	318	aa 289-606	318	aa 235-552	318	
VR2	aa 584-720	137	aa 607-698	92	aa 553-655	103	
CR2	aa 721-802	82	aa 699-780	82	aa 656-737	82	
TM3-8	aa 803-1030	228	aa 781-1007	227	aa 738-964	227	
СТ	aa 1031-1049	19	aa 1008-1026	19	aa 965-985	21	
CRS	CR1+CR2	400	CR1+CR2	400	CR1+CR2	400	
VRS	VR1+VR2	262	VR1+VR2	226	VR1+VR2	211	
LOOP	CR1+VR2+CR2	537	CR1+VR2+CR2	492	CR1+VR2+CR2	503	
TOTAL		1049		1026		985	

**Table S1.** Protein coordinates for regions of AtCESA4, 7 and 8 used in the swapconstructs.

Swap Name	Primer BF	Primer CF			
CESA7 <sup>NT_CESA4</sup>	gttttcccagtcacgacgttgtaaaacgacggccag	tcattctcggctaagatttgtgagatatgtggagat			
CESA7 <sup>ZN_CESA4</sup>	aatctagatggacaattctgcaaagtctgtggcgat	caatgcaacactctttacaagcgtctcagaggaagc			
CESA7 <sup>VR1_CESA4</sup>	cagtgtaagactcgttacaaacgccacaaaggctct	ctagatgctgaagcaagacagccactctcgcggaaa			
CESA7 <sup>TM1_CESA4</sup>	ctgatcgacgaggcacggcaacctctctggagaaaa	cttgatcagttcccgaaatggttccctattgaacgt			
CESA7 <sup>CR1_CESA4</sup>	cttgatcagttccccaagtggtttccgattaaccga	agaccagcattatacGGAtatgaaccaccaaagggt			
CESA7 <sup>VR2_CESA4</sup>	cgacaagctctgtatGGAtacgaacctccggtatcg	tcgttgatcaaagaagctatccatgtcataagctgc			
CESA7 <sup>CR2_CESA4</sup>	gtgctccttaaagaggcaattcatgttattagctgt	atcttctttagtcgtcatagtcctctctggtatggc			
CESA7 <sup>TM3_CESA4</sup>	atatttttcagccggcactgtcctttgtggtatgct	ttggtttgggttcggattgatccttttgtgctcaag			
CESA7 <sup>CT_CESA4</sup>	ttgctttgggtaagaattgatccgttcttgccgaaa	-			
CESA7 <sup>NT_CESA8</sup>	gttttcccagtcacgacgttgtaaaacgacggccag	gagtctaggtctcccatctgtgagatatgtggagat			
CESA7 <sup>ZN_CESA8</sup>	aatctagatggacaattctgcaacacttgtggtgaa	cgttgcggcaatccttacaagcgtctcagaggaagc			
CESA7 <sup>VR1_CESA8</sup>	cagtgtaagactcgttacgatgagaatgtgtttgat	acagaatctggtgctacacagccactctcgcggaaa			
CESA7 <sup>TM1_CESA8</sup>	ctgatcgacgaggcacgggatgtgctttcggttgtg	ttggatcagttccctaaatggttccctattgaacgt			
CESA7 <sup>CR1_CESA8</sup>	cttgatcagttccccaagtggtctcctattaaccga	agacaagcactttacggatatgaaccaccaaagggt			
CESA7 <sup>VR2_CESA8</sup>	cgacaagctctgtatGGTtacagtccaccttcaaaa	acgctcatcaaagaagctatccatgtcataagctgc			
CESA7 <sup>CR2_CESA8</sup>	gtgctccttaaagaggcaattcatgtcattagctgt	atcttccttagccgacatagtcctctctggtatggc			
CESA7 <sup>TM3_CESA8</sup>	atatttttcagccggcactgtcctttgtggtacggt	cttgtttgggttcgtatcgatccttttgtgctcaag			
CESA7 <sup>CT_CESA8</sup>	ttgctttgggtaagaattaatcctttcgtctccaaa	-			
CESA4 <sup>NT_CESA7</sup>	gttttcccagtcacgacgttgtaaaacgacggccag	aatctagatggacaattctgcaaagtctgtggcgat			
CESA4 <sup>ZN_CESA7</sup>	tcattctcggctaagatttgtgagatatgtggagat	cagtgtaagactcgttacaaacgccacaaaggctct			
CESA4 <sup>VR1_CESA7</sup>	caatgcaacactctttacaagcgtctcagaggaagc	ctgatcgacgaggcacggcaacctctctggagaaaa			
CESA4 <sup>TM1_CESA7</sup>	ctagatgctgaagcaagacagccactctcgcggaaa	cttgatcagttccccaagtggtttccgattaaccga			
CESA4 <sup>CR1_CESA7</sup>	cttgatcagttcccgaaatggttccctattgaacgt	cgacaagctctgtatGGAtacgaacctccggtatcg			
CESA4 <sup>VR2_CESA7</sup>	agaccagcattatacGGAtatgaaccaccaaagggt	gtgctccttaaagaggcaattcatgttattagctgt			
CESA4 <sup>CR2_CESA7</sup>	tcgttgatcaaagaagctatccatgtcataagctgc	atatttttcagccggcactgtcctttgtggtatgct			
CESA4 <sup>TM3_CESA7</sup>	atcttctttagtcgtcatagtcctctctggtatggc	ttgctttgggtaagaattgatccgttcttgccgaaa			
CESA4 <sup>CT_CESA7</sup>	ttggtttgggttcggattgatccttttgtgctcaag	-			
CESA8 <sup>NT_CESA7</sup>	gttttcccagtcacgacgttgtaaaacgacggccag	aatctagatggacaattctgcaacacttgtggtgaa			
CESA8 <sup>ZN_CESA7</sup>	gagtctaggtctcccatctgtgagatatgtggagat	cagtgtaagactcgttacgatgagaatgtgtttgat			
CESA8 <sup>VR1_CESA7</sup>	cgttgcggcaatccttacaagcgtctcagaggaagc	ctgatcgacgaggcacgggatgtgctttcggttgtg			
CESA8 <sup>TM1_CESA7</sup>	acagaatctggtgctacacagccactctcgcggaaa	cttgatcagttccccaagtggtctcctattaaccga			
CESA8 <sup>CR1_CESA7</sup>	ttggatcagttccctaaatggttccctattgaacgt	cgacaagctctgtatGGTtacagtccaccttcaaaa			
CESA8 <sup>VR2_CESA7</sup>	agacaagcactttacggatatgaaccaccaaagggt	gtgctccttaaagaggcaattcatgtcattagctgt			
CESA8 <sup>CR2_CESA7</sup>	acgctcatcaaagaagctatccatgtcataagctgc	atatttttcagccggcactgtcctttgtggtacggt			
CESA8 <sup>TM3_CESA7</sup>	atcttccttagccgacatagtcctctctggtatggc	ttgctttgggtaagaattaatcctttcgtctccaaa			

CESA8 <sup>CT_CESA7</sup>	cttgtttgggttcgtatcgatccttttgtgctcaag	-
CESA4 <sup>CRS_CESA7</sup>	cgacaagctctgtatGGAtacgaacctccggtatcg	tcaactttgatggaagaaggaggattgccggaggcg
CESA4 <sup>CRS_CESA8</sup>	agacaagcactttacggatacgaacctccggtatcg	tctactcttatggagaatggaggattgccggaggcg
CESA4 <sup>VRS_CESA7</sup>	agaccagcattatacGGAtatgaaccaccaaagggt	tcaactttgatggaagaaggaggattgccggaggcg
CESA4 <sup>VRS_CESA8</sup>	agaccagcattatacGGAtacagtccaccttcaaaa	tctactcttatggagaatggaggattgccggaggcg
CESA4 <sup>LOOP_CESA7</sup>	cttgatcagttcccgaaatggttccctattgaacgt	atatttttcagccggcactgtcctttgtggtatgct
CESA4 <sup>LOOP_CESA8</sup>	cttgatcagttcccgaaatggtctcctattaaccga	atcttccttagccgacattgtcctttgtggtatgct
CESA7 <sup>CRS_CESA4</sup>	agaccagcattatacGGAtatgaaccaccaaagggt	tcgacgttgatggagaacggtggtgttcctccgtca
CESA7 <sup>CRS_CESA8</sup>	agacaagcactttacggatatgaaccaccaaagggt	tctactcttatggagaatggtggtgttcctccgtca
CESA7 <sup>VRS_CESA4</sup>	cgacaagctctgtatGGAtacgaacctccggtatcg	tcgacgttgatggagaacggtggtgttcctccgtca
CESA7 <sup>VRS_CESA8</sup>	cgacaagctctgtatGGTtacagtccaccttcaaaa	tctactcttatggagaatggtggtgttcctccgtca
CESA7 <sup>LOOP_CESA4</sup>	cttgatcagttccccaagtggtttccgattaaccga	atcttctttagtcgtcatagtcctctctggtatggc
CESA7 <sup>LOOP_CESA8</sup>	cttgatcagttccccaagtggtctcctattaaccga	atcttccttagccgacatagtcctctctggtatggc
CESA8 <sup>CRS_CESA4</sup>	agaccagcattatacGGAtacagtccaccttcaaaa	tcgacgttgatggagaacggcggtgttcccgactct
CESA8 <sup>CRS_CESA7</sup>	cgacaagctctgtatGGTtacagtccaccttcaaaa	tcaactttgatggaagaaggcggtgttcccgactct
CESA8 <sup>VRS_CESA4</sup>	agacaagcactttacggatacgaacctccggtatcg	tcgacgttgatggagaacggcggtgttcccgactct
CESA8 <sup>VRS_CESA7</sup>	agacaagcactttacggatatgaaccaccaaagggt	tcaactttgatggaagaaggcggtgttcccgactct
CESA8 <sup>LOOP_CESA4</sup>	ttggatcagttccctaaatggtttccgattaaccga	atcttctttagtcgtcattgtcctttgtggtacggt
CESA8 <sup>LOOP_CESA7</sup>	ttggatcagttccctaaatggttccctattgaacgt	atatttttcagccggcactgtcctttgtggtacggt
CESA8 <sup>VR1_CESA4</sup>	cgttgcggcaatccttacaaacgccacaaaggctct	ctagatgctgaagcaagagatgtgctttcggttgtg
CESA4 <sup>VR1_CESA8</sup>	caatgcaacactctttacgatgagaatgtgtttgat	acagaatctggtgctacacaacctctctggagaaaa

 Table S2. List of primers used in this study.

were For each swap, upto 6 primers used. Two general primers, MF (GTTTTCCCAGTCACGACGTTGTAAAACGACGGCCAG) MR and (CAGGAAACAGCTATGACCATGTAATACGACTCACTA) were used in all swaps. Either 2 or 4 swap specific primers were used for each swap. Primer BF and CR have complementary sequences BR and CR respectively. Here we have listed sequence for BF and CF primers only.