

Table S1A. primers used in the generation of hybrids and single mutants			
Primer	Fw/ Re	Description	Primer sequence
CCH_TS2 3_fw	Fw	primer used to amplify total ORFs from cDNA library of <i>C. camphora</i>	atatggatcctATGGACTCCATGGAGGTACGCCGCTCTG
CCH_TS2 3_re	Re	primer used to amplify total ORFs from cDNA library of <i>C. camphora</i>	atatgcgccgcTCATCCCAAGTTGATGGATTCTTCAATGGCACTG
CCH054	Fw	ATG-TS23 (cloning gene only)	ATGGACTCCATGGAGGTACGCC
CCH055	Re	ATG-TS23 (cloning gene only)	TCATCCCAAGTTGATGGATTCTTTC
CCH055.1	Re	ATG-TS23 (cloning gene only, NO TGA)	TCCCAAGTTGATGGATTCTTTC
CCH201	Fw	pARC259 FW sequencing	TCCTCGCCCTTGCTCACCAT
CCH202	Re	pARC259 RE sequencing	CTATTCTAGTCGACCTGCAG
CCH203	Fw	pGD625 FW sequencing	CAAGCTTATCGATACCGTCG
CCH204	Re	pGD625 RE sequencing	TTTGAACGACTCGAGCTCGG
CCH attB1 FW	Fw	gateway attB1 site added to CiCaMS/CiCaSSy variants	GGGGACAAGTTTGTACAAAAAAGCAGGCTCAATG GACTCCATGGAGGTACGCC
CCH attB2 RE	Re	gateway attB2 site added to CiCaMS/CiCaSSy variants	GGGGACCACTTTGTACAAGAAAGCTGGGTATAATC CCAAGTTGATGGATTCTTTC
Hybrids fragments			
CCH001	Fw	commercial ACYCDuetUP1	GGATCTCGACGCTCTCCCT
CCH002	Re	commercial ACYCDuetDOWN	GATTATGCGGCCGTGTACAA
CCH003	Re	complement reverse of CCH001 with overlapping sites for CiCaMS/CiCaSSy	TCCTAATGCAGGAGTCGCATAAGGGAGAGCGTCGA GATCC
CCH004	Fw	complement reverse of CCH002 with overlapping sites for CiCaMS/CiCaSSy	TCGAACAGAAAGTAATCGTATTGTACACGGCCGCA TAATC
CCH056	Fw	F2/F4:FW	CCTCCGTTGGGCATCGATCATATTTTCGAC
CCH057	Re	F1/F3/F6/F8:RE	GTCGAAATATGATCGATGCCAACGGAGG
CCH058	Fw	F6/F8: FW	GTACTIONTCGGGAAGCTCAATGGTTCAACAG
CCH059	Re	F5/F7:RE	CTGTTGAACCATTGAGCTTCCCGAAAGTAC
CCH062	Fw	F10/F12: FW	CTACAAGACATCACACAGCCACACCATCTG
CCH063	Re	F9/F11: RE	CAGATGGTGTGGCTGTGTGATGTCTTGTAG
CCH091	Fw	F15/F17 FW	ACTTGCTTGATTTTGC AAAGCTAGATTTCAACAGGG TGCA
CCH093	Re	F15/F17 RE	CTGGCAAACCATGCACATCATAAAAGTCATCC
CCH094	Re	F32/F34_FW	TGCACCCTGTTGAAATCTAGC
CCH095	Fw	F19/20/21/22	TCCTTTTACAGCGATGGATGACTTTTATGATGTGC ATGG
CCH102	Fw	F25 (CiCaSSy: H14)_FW	CTGCACATCTTGGCGTGA AAAGTGAAGCCATCTTG GAGGAAGCTCAG

CCH103	Re	F25 (CiCaSSy: H14)_RE	CACTTTTCACGCCAAGATGTGCAGCCTCATAACAAGC TCAAAAGTC
CCH104	Fw	F26 (CiCaMS: H13)_FW	CTGTACGTCTTAGCGTCAAAGGTGAAGCCATCTTG GAGGAAGCTCAG
CCH105	Re	F26 (CiCaMS: H13)_RE	CACCTTTGACGCTAAGACGTACAGCCTCATAACAAGC TCAAAAGTC
CCH106	Fw	F32/F34_FW	GTGAAGCCATCTTGAGGAAGCTCAGGTCTTCTC
CCH107	Re	F31/F33_RE	GAGAAGACCTGAGCTTCCTCCAAGATGGCTTCAC
Single mutants (description indicates the point mutation in the parental enzyme)			
CCH118	Fw	V401A CiCaMS FW	AGTCTCAGTTGGGG C GCCTTGCTATTGGGCCTCTC ATAC
CCH119	Re	V401A CiCaMS RE	TAGCAAGGG C CCCCAACTGAGACTAAAGCATTGT CTAAATAC
CCH120	Fw	A401V CiCaSSy FW	AGTCTCAGTTGGGGTGCCTTTGTATTGGGTCTCTC ATAC
CCH121	Re	A401V CiCaSSy RE	TACAAAGGG C ACCCCAACTGAGACTAAAGCATTGT CTAAATAC
CCH122	Fw	L403F CiCaMS FW	AGTCTCAGTTGGGGTGCCTTTCTATTGGGCCTCTC ATAC
CCH123	Re	L403F CiCaMS RE	TAG A AAGGGCACCCCAACTGAGACTAAAGCATTGT CTAAATAC
CCH124	Fw	F403L CiCaSSy FW	AGTCTCAGTTGGGGCGCCCTT G TATTGGGTCTCTC ATAC
CCH125	Re	F403L CiCaSSy-RE	TAC C AAGGGCGCCCAACTGAGACTAAAGCATTGT CTAAATAC
CCH126	Fw	L404V CiCaMS FW	AGTCTCAGTTGGGGTGCCTT G TATTGGGCCTCTC ATAC
CCH127	Re	L404V CiCaMS RE	TAC C AAGGGCACCCCAACTGAGACTAAAGCATTGT CTAAATAC
CCH128	Fw	V404L CiCaSSy FW	AGTCTCAGTTGGGGCGCCCTTTCTATTGGGTCTCTC ATAC
CCH129	Re	V404L CiCaSSy RE	TAG A AAGGGCGCCCAACTGAGACTAAAGCATTGT CTAAATAC
CCH130	Fw	H415Q CiCaMS FW	ATGATACAACAACA A ATATCAAAGGCGGAAATTGA TTTAATCCCCGAAG
CCH131	Re	H415Q CiCaMS RE	TCCTTTGATATTTGTTGTTGTATCATGGGGTATGAG AGGCCCAATAGCAAG
CCH132	Fw	Q415H CiCaSSy FW	ATGATACAACAACATATATCAAAGGAGGAAATTGA TTTAATCCCCGAAG
CCH133	Re	Q415H CiCaSSy RE	TCCTTTGATAT A TGTTGTTGTATCATGGGGTATGAG AGACCCAATACAAAG
CCH134	Fw	A419E CiCaMS FW	CAACATATATCAAAG G AGGAAATTGATTTAATCCCC GAAG
CCH135	Re	A419E CiCaMS RE	CAATTTCTCCTTTGATATATGTTGTTGTATCATGGG GTATG
CCH136	Fw	E419A CiCaSSy FW	CAACAAATATCAAAG G CGGAAATTGATTTAATCCCC GAAG
CCH137	Re	E419A CiCaSSy RE	CAATTT C GCCTTTGATATTTGTTGTTGTATCATGGG GTATG

CCH142	Fw	S267N CiCaMS FW	ACAGACTATTGGAGAA ACC ATCTCTTTTCAATTGGAG TGGTTG
CCH143	Re	S267N CiCaMS RE	AAGAGATGG TTCT CCAATAGTCTGTCTCGGAAGAA CCCCATC
CCH144	Fw	N267S CiCaSSy FW	ACAGACTATTGGAGAG GC ATCTCTTTTCAATTGCAG TGGTTG
CCH145	Re	N267S CiCaSSy RE	AAGAGATGG CTCT CCAATAGTCTGTCTCGGAAGAA CCCCATC
CCH146	Fw	G273A CiCaMS FW	TCTCTTTTCAATTG C AGTGGTTGTCGAGCCTCAATA CTCCAG
CCH147	Re	G273A CiCaMS RE	GACAACCACT G CAATTGAAAAGAGATGGCTCTCCA ATAGTCTG
CCH148	Fw	A273G CiCaSSy FW	TCTCTTTTCAATTG G AGTGGTTGTCGAGCCTCAATA CTCCAG
CCH149	Re	A273G CiCaSSy RE	GACAACCACT CCA ATTGAAAAGAGATGGTTCTCCA ATAGTCTG
CCH150	Fw	L291I CiCaMS FW	CAAAGCC ATAG TCCTTTTACAGCGATGGATGACTT TTATGATG
CCH151	Re	L291I CiCaMS RE	CCATCGCTGTGAAAAGGACTATGGCTTTGGTAATT GCTACTCTGC
CCH152	Fw	I291L CiCaSSy FW	CAAAAGCC CTAG TCCTTATGACAGCAATGGATGAC TTTTATGATG
CCH153	Re	I291L CiCaSSy RE	CCATTGCTGT CATA AGGACTAGGGCTTTTGTAAATG CTACTCTAC
CCH154	Fw	F294M CiCaMS FW	CAAAGCC CTAG TCCTT ATG ACAGCGATGGATGACT TTTATGATG
CCH155	Re	F294M CiCaMS RE	CCATCGCTGT GCAT AGGACTAGGGCTTTGGTAATT GCTACTCTGC
CCH156	Fw	M294F CiCaSSy FW	CAAAAGCC ATAG TCCTTTT CAC AGCAATGGATGACT TTTTATGATG
CCH157	Re	M294 CiCaSSy RE	CCATTGCTGT GAAA AGGACTATGGCTTTTGTAAATG CTACTCTAC
CCH158	Fw	E308D CiCaMS FW	ATGGTTTGCCAGATGAGCTGAAAGTCTT CAC GGAC ACCG
CCH159	Re	E308D CiCaMS RE	TTCAGCT CA TCTGGCAAACCATGCACATCATAAAAG TCATCC
CCH160	Fw	D308E CiCaSSy FW	ATGGTTTGCCAGAG G AGCTAAAAGTCTT CAC GGAC ACCG
CCH161	Re	D308E CiCaSSy RE	TTTAGCT CTCT GGCAAACCATGCACATCATAAAAG TCATCC
CCH205	Fw	N442D CiCaMS FW	GACTATAT G ATGATTTGGCCACTTCAAAGGCTGAG C
CCH206	Re	N442D CiCaMS RE	CCAAATCAT CAT ATAGTCGAAATATGATCGATGCC
CCH207	Fw	D442N CiCaSSy FW	GACTATATA A ATGATTTGGCCACTTCAAAGGCTGAG C
CCH208	Re	D442N CiCaSSy RE	CCAAATC ATT ATATAGTCGAAATATGATCGATGCC

MS _F 40	CiCaMS- derived Synthetic fragment containing 6 residue substitutions from CiCaSSy (S267N:F294M :V401A:L403F: L404V:N442D)	GCTAGATTTCAACAGGGTGCAAATGCTGTACCAAAGTGAAGGAATTATC AATGTGGTGGGAATTGCTGGGGTTACCAGAGAAGATGGGGTTCTCCGAGACA GACTATTGGAGAAcCATCTCTTTTCAATTGGAGTGGTTGTCGAGCCTCAACTCC CAGTGCAGAGTAGCAATTACCAAAGCCCTAGTCCTTATgACAGCGATGGATGACT TTTATGATGTGCATGGTTTGCCAGAGGAGCTGAAAGTCTTCACGGACACCGTTAA TCGGTGGGATTTAGAGGGAATTGATCAACTACCAGAGTATATGAAGCTGTACTA CTTGGCGTTATATAATAACAACCAATGAGACGGCATAACATCATCCTCAAGGAGAA GGGATTCAATGCTACACATTATCTGAAGAAACTGTGGGCAATGCAAAGTAACTC GTACTTTTCGGGAAGCTCAATGGTTCAACAGTGGTTACATACCTAAATTTGATGAG TATTTAGACAATGCTTTAGTCTCAGTTGGGGcGCCCTTgTATTGGCCTCTCATAC CCCATGATACAACAACATATATCAAAGGCGGAAATTGATTTAATCCCCGAAGATC TAAATCTCCTCCGTTGGGCATCGATCATATTTGACTATATgATGATTTGG
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Table S2. Hybrid fragment design. The primer used to obtain each fragment are listed, together with their length.

Construct	Fragment s	Template	Primer (Fw+Re)	Fragment length (bp)
SSy_R1	F9	CiCaMS	pAC_UP1 + CCH063	358
	F10	CiCaSSy	CCH062 + CCH002	1566
MS_R1	F11	CiCaSSy	pAC_UP1 + CCH063	358
	F12	CiCaMS	CCH062 + CCH002	1566
MS_R2	F26 *	CiCaMS	CCH104 + CCH103	5634
SSy_R2	F25 *	CiCaSSy	CCH104 + CCH104	5634
MS_R3	F31	CiCaMS	CCH001 + CCH107	678
	F32	CiCaSSy	CCH106 + CCH094	229
	F35	CiCaMS	CCH091 + CCH002	1061
SSy_R3	F33	CiCaSSy	CCH001 + CCH107	678
	F34	CiCaMS	CCH106 + CCH094	229
	F36	CiCaSSy	CCH091 + CCH002	1061
MS_R4	F16	CiCaMS	pAC_UP1 + CCH094	873
	F15	CiCaSSy	CCH091 + CCH93	234
	F19	CiCaMS	CCH095 + CCH002	831
SSy_R4	F18	CiCaSSy	pAC_UP1 + CCH094	873
	F17	CiCaMS	CCH091 + CCH93	234
	F20	CiCaSSy	CCH095 + pAC_DOWN1	831
MS_R5	F5	CiCaMS	pAC_UP1 + CCH059	1317
	F6	CiCaSSy	CCH058 + CCH057	203
	F4	CiCaMS	CCH056 + CCH002	433
SSy_R5	F7	CiCaSSy	pAC_UP1 + CCH059	1317
	F8	CiCaMS	CCH058 + CCH057	203
	F2	CiCaSSy	CCH056 + CCH002	433
MS_R6	F1	CiCaMS	CCH001 + CCH057	1490
	F2	CiCaSSy	CCH056 + CCH002	433
SSy_R6	F3	CiCaSSy	CCH001 + CCH057	1490
	F4	CiCaMS	CCH056 + CCH002	433
SSy_R1R5	F9	CiCaMS	pAC_UP1 + CCH063	358
	F13	SSy_R5	CCH062 + pAC_DOWN1	1566
MS_R1R5	F11	CiCaSSy	pAC_UP1 + CCH063	358
	F14	MS_R5	CCH062 + pAC_DOWN1	1566
MS_R2R5	F26 *	MS_R5	CCH104 + CCH105	5634
SSy_R2R5	F25 *	SSy_R5	CCH104 + CCH106	5634
MS_R3R5	F31	CiCaMS	CCH001 + CCH107	678
	F32	CiCaSSy	CCH106 + CCH094	229
	F37	MS_R5	CCH091 + CCH002	1061
SSy_R3R5	F33	CiCaSSy	CCH001 + CCH107	678
	F34	CiCaMS	CCH106 + CCH094	229

	F38	SSy_R5	CCH091 + CCH002	1061
MS_R4R5	F16	CiCaMS	pAC_UP1 + CCH094	873
	F15	CiCaSSy	CCH091 + CCH93	234
	F21	MS_R5	CCH095 + CCH002	831
SSy_R4R5	F18	CiCaSSy	pAC_UP1 + CCH094	873
	F17	CiCaMS	CCH091 + CCH93	234
	F22	SSy_R5	CCH095 + CCH002	831
*Quick change PCR on whole template plasmid				

Table S3. List of mutants, including primers used for Q5 quick change PCR. The full gBlock sequence used to obtain MS_6S is also reported.

Region	Mutant	Primer pair	Single mutation	Template	Primer sequence (Fw/Re)	
R4	MS_S267N	CCH142	S267N	CiCaMS	ACAGACTATTGGAGAAACCATCTCTTTTCAATTGGAGTGGTTG	
		CCH143			AAGAGATGGTTCTCCAATAGTCTGTCTCGGAAGAACC CCATC	
	MS_273A	CCH146	G273A		TCTCTTTTCAATTGCAGTGGTTGTCGAGCCTCAATACT CCCAG	
		CCH147			GACAACCACTGCAATTGAAAAGAGATGGCTCTCCAAT AGTCTG	
	MS_L291I	CCH150	L291I		CAAAGCCATAGTCCTTTTACAGCGATGGATGACTTTT ATGATG	
		CCH151			CCATCGCTGTGAAAAGGACTATGGCTTTGGTAATTGC TACTCTGC	
	MS_F294M	CCH154	F294M		CAAAGCCCTAGTCCTTATGACAGCGATGGATGACTTT TATGATG	
		CCH155			CCATCGCTGTGCATAGGACTAGGGCTTTGGTAATTGC TACTCTGC	
	MS_E308D	CCH158	E308D		ATGGTTTGCCAGATGAGCTGAAAGTCTTCACGGACAC CG	
		CCH159			TTCAGCTCATCTGGCAAACCATGCACATCATAAAAGT CATCC	
	R5	MS_V401A	CCH118		V401A	CTCAGTTGGGGCGCCCTTGCTATTGGCCTCTCATA CCCATGATAC
			CCH119			GAGGCCCAATAGCAAGGGCGCCCAACTGAGACTAA AGCATTGTC
		MS_L403F	CCH122		L403F	CTCAGTTGGGGTGCCTTTCTATTGGCCTCTCATA CCATGATAC
			CCH123			GAGGCCCAATAGAAAGGGCACCCCAACTGAGACTAA AGCATTGTC
MS_L404V		CCH126	L404V	CTCAGTTGGGGTGCCTTTGGTATTGGCCTCTCATA CCCATGATAC		
		CCH127		GAGGCCCAATACCAAGGGCACCCCAACTGAGACTAA AGCATTGTC		
MS_H415Q		CCH130	H415Q	ATGATACAACAACAATATCAAAGGCGAAATTGATT TAATC		
		CCH131		TCCTTTGATATTTGTTGTTGTATCATGGGGTATGAGA GGCC		
MS_A419E		CCH134	A419E	CAACATATATCAAAGGAGGAAATTGATTTAATCCCC GAAGATC		
		CCH135		AATCAATTCCTCCTTTGATATATGTTGTTGTATCATG GGGTATG		
R6		MS_R4R5_N442D	CCH205	N442D	MS_R4 R5	GACTATATGATGATTTGGCCACTTCAAAGGCTGAGC
			CCH206			CCAAATCATCATATAGTCGAAATATGATCGATGCC
R4		SSy_N267S	CCH144	N267S	CiCaSsy	ACAGACTATTGGAGAGCCATCTCTTTTCAATTGCAGT GGTTG
			CCH145			AAGAGATGGCTCTCCAATAGTCTGTCTCGGAAGAACC CCATC
	SSy_A273G	CCH148	A273G	TCTCTTTTCAATTGGAGTGGTTGTCGAGCCTCAATACT CCCAG		

		CCH149			GACAACCACTCCAATTGAAAAGAGATGGTTCTCCAAT AGTCTG	
	SSy_I291L	CCH152	I291L		CAAAAGCCCTAGTCCTTATGACAGCAATGGATGACTT TTATGATG	
		CCH153			CCATTGCTGTCATAAGGACTAGGGCTTTTGTAAATTGCT ACTCTAC	
	SSy_M294F	CCH156	M294F		CAAAAGCCATAGTCCTTTTACAGCAATGGATGACTT TTATGATG	
		CCH157			CCATTGCTGTGAAAAGGACTATGGCTTTTGTAAATTGC TACTCTAC	
	SSy_D308E	CCH160	D308E		ATGGTTTGCCAGAGGAGCTAAAAGTCTTCACGGACAC CG	
		CCH161			TTTAGCTCCTCTGGCAAACCATGCACATCATAAAAGTC ATCC	
R5	SSy_A401V	CCH120	A401V		CTCAGTTGGGGTGCCCTTTGTATTGGGTCTCTCATACC CCATGATAC	
		CCH121			GAGACCCAATACAAAGGGCACCCCAACTGAGACTAA AGCATTGTC	
	SSy_F403L	CCH124	F403L		CTCAGTTGGGGCGCCCTTGGTATTGGGTCTCTCATAC CCCATGATAC	
		CCH125			GAGACCCAATACCAAGGGCGCCCAACTGAGACTAA AGCATTGTC	
	SSy_V404L	CCH128	V404L		CTCAGTTGGGGCGCCCTTTCTATTGGGTCTCTCATACC CCATGATAC	
		CCH129			GAGACCCAATAGAAAGGGCGCCCAACTGAGACTAA AGCATTGTC	
	SSy_Q415H	CCH132	Q415H		ATGATACAACAACATATATCAAAGGAGGAAATTGATT TAATC	
		CCH133			TCCTTTGATATATGTTGTTGTATCATGGGGTATGAGA GACC	
	SSy_E419A	CCH136	E419A		CAACAAATATCAAAGGCGGAAATTGATTTAATCCCCG AAGATC	
		CCH137			AATCAATTTCCGCCTTTGATATTTGTTGTTGTATCATG GGGTATG	
	R6	SSy_D442	CCH207	D442N	CiCaSsy	GACTATATAATGATTTGGCCAATTCAAAGGCTGAGC
			CCH208			CCAAATCATTATATAGTCGAAATATGATCGATGCC

MS	MS	S267N:F 294M:V 401A:L4 03F:L40 4V:N442 D	Ci Ca M S	GCTAGATTTCAACAGGGTGCAAATGCTGTACCAAAGTGAAGGAATTATCAAT GTGGTGGGAATTGCTGGGGTTACCAGAGAAGATGGGGTTCTCCGAGACAGACTATT GGAGAAcCATCTCTTTTCAATTGGAGTGGTTGTCGAGCCTCAATACTCCCAGTGCAGA GTAGCAATTACCAAAGCCCTAGTCCTTATgACAGCGATGGATGACTTTTATGATGTGC ATGGTTTGCCAGAGGAGCTGAAAGTCTTCACGGACACCGTAAATCGGTGGGATTTAG AGGGAATTGATCAACTACCAGAGTATATGAAGCTGTACTACTTGGCGTTATATAATAC AACCAATGAGACGGCATAATCATCCTCAAGGAGAAGGGATTCAATGCTACACATTA TCTGAAGAAACTGTGGGCAATGCAAAGTAACTCGTACTTTCCGGGAAGCTCAATGGTT CAACAGTGGTTACATACCTAAATTTGATGAGTATTTAGACAATGCTTTAGTCTCAGTTG GGGcGCCCTTgTATTGGGCCTCTCATACCCCATGATACAACAACATATCAAAGGCG GAAATTGATTTAATCCCCGAAGATCTAAATCTCCTCCGTTGGGCATCGATCATATTTCCG ACTATATgATGATTTGG
_6S	_F 40			