

Supplementary Table S3. Amino acid sequences of CmoGS and CsaGS proteins used for phylogenetic tree construction

		gene
		ID or
		abbre
		viatio
species	n	amino-acid sequence
grape	VvGS1.1	MALLSDLINLNLSETTEKVIVEYIWVGGSGMDLRSKARTLSGPVSDPAKLPKWNYDGSSTGQAPGEDSEVILYPQAIKDPFRRGNNILVMCDYTPAGEPIPTNKRCAAKIFSHPDVAAEVPWYGIEQYETLLQKEVKWPIGWPGVGGFPGQGPYYCGIGADKAWGRDIVDAHYKAC
		LYAGINISGINGEVMPGQWEYQVGPSVGISAGDELWVSRYILERITEIAGVVSFDPKPIQGDWNGAGAHTNYSTKSMRNDGGFEVIKKAIEKLGRLHKEHIAAYGEGNERRLTGRHETADINTFLWGVANRGASIRVGRDTEKAGKGYFEDRRPASNMDPYVVTSMIAETITLWKP
		MAHITAPSVQCQVRVPTSSFTARPMTAKLWNSLLLNQRKKGTSRSSARFRLALQSESSTVNRLKDLLNLDITPYTDKIIAEYIWGGSGIDLRSKSRITSKPVKHPSELPKWNYDGSSTGQAPGEDSEVILYPQAIKDPFRGGNNILVICDSYTPAGEPIPTNKRHGAEEFSSQKVINEV
		PWYGIEQYETLLQTNVKWPLGWPGGYPGQGPYYCGAGADKSFGRDISDAHYKACLYAGINISGTNGEVMPGQWEYQVGPSVGIEAGDHIWCSRYILERITEQAGVVLSLDPKPIEGDWNGAGCHTNYSTKSMREDGGFEVIKAILNLSLRHEVHISAYGEGNERRLTGKHETASI
	VvGS2a	DTFSWGVANRGCSIRVGRDTEKNGKGYLEDRRPASNMDPYVVTSLLAETITLWEPTLEAEALAAQKLSLKV
	VvGS1.3	MSLLADLQNINLSDSTEKIIAEYIWGGSGMDLRSKARTLSGPVTGPAQLPKWNYDGSSTGQAPGEDSEVILYPQAIKDPFRGGNNILVMCDAYTPGGEPIPTNKRFAAKIFSHPEVTAEEPWYGIEQYETLLQKDVNWPLGWPGVGGFPGQGPYYCGIGADKAFGRDIVDAHYKACL
		YAGINISGINGEVMPGQWEFQVGPAVGISAGDELWVARYILERITEIAGVVVSFDPKPIKGDWNGAGAHTNYSTKSMRNTGGYDVIIKKAIEKLGRLHKEHISAYGEGNERRLTGRHETADINTFCWGVANRGASIRVGRDTEKEGKGYFEDRRPASNMDPYVVTSMIAETITLWKP
		MAQILAPSTQWQMRMTKNPANASPFITKMWGSLFLKQKTGTAKFSTKFRVCASKSESSTVNRLDDLNMDIRPYTDKIIAEYVWIGGTGIDLRSKSRITSKPVEHPSELPKWNYDGSSTGQAPGEDSEVILYPQAIKDPFRGGNNILVICDSYTPAGEPIPTNKRHRAAEIFNGKKVIDE
		VPWFGIEQYETLLQPNVKWPLGWPGVGAYPGQGPYYCAAGADKSFGRDISDAHYKACLYAGINISGTNGEVMPGQWEYQVGPSVGIEAGDHIWCSRYILERITEQAGVVLTLDPKPIEGDWNGAGCHTNYSTKSMREDGGYELIKKAILNLSLRHKEHISAYGEGNERRLTGKHETAN
	VvGS2b	INTFSWGVANRGCSVRVGRDTEKQKGYLEDRRPASNMDPYIVTSLLAETITLWEPTLEAEALAAQKLALKV
	VvGS1.2	MALLSDLINLNLSDVTEKIIAEYIWGGSGMDLRSKARTLSGPVSDPHKLPKWNYDGSSTGQAPGEDSEVILYPQAIKDPFRRGNNILVMCDAYTPAGEPIPTNKRHNAAKIFSHPDVLAETWYGIEQYETLLQNSVKWPIGWPGVGGYPGQGPYYCGIGADKAFGRDIVDSHYKACL
rice	OsGS1.3	YAGINISGINGEVMPGQWEFQVGPSVGISAGDELWVARYILERITEIAGVVVSFDPKPIQGDWNGAGAHTNYSTKSMRNDGGYEIIKKAIEKLGRLHKEHIAAYGEGNERRLTGRHETADINTFLWGVANRGASIRVGRDTEKEGKGYFEDRRPASNMDPYVVTSMIAETITLWKP
		MSSSLTDLVNLDLSESTDKVIAEYIWGGTGMDVRSKARTLSGPVDDPSKLPKWNFDGSSTGQATGDDSEVILHPQAIFRDPFRKGKNILVMCDCYAPNGEPIPTNNRYNAARIFSHPDVKAEEPWYGIEQYETLLQKHINWPLGWPLGGYPGQGPYYCAAGADKSYGRDIVDAHY
		KACLFAGINISGINAEVMPGQWEFQIGPVVGVSAGDHVWVARYILERITEIAGVVVSFDPKPIPGDWNGAGAHTNYSTKSMRSNGGYEVIKKAIEKLGMRHREHIAAYGDGNERRLTGRHETADINNFWGVANRGASVRVGRDTEKDGGKGYFEDRRPASNMDPYLVTAMIAETITL
		WEP SHGHGQSN GK
	OsGS2	MAQAVVPAMQCQVGAVRARPAAAAAAGGRVWGVRRTRGRGTSGRFVMAVSTETTGVVTRMEQLLNMDTTPFTDKIIAEYIWGGTGIDLRSKSRITSKPVEDPSELPKWNYDGSSTGQAPGEDSEVILYPQAIKDPFRGGNNILVMCDYTPAGEPIPTNKRNAAQVSDPKVVS
		QVPWFQIEQYETLLQRDVNWPLGWPGGYPGQGPYYCAVGSDKSFGRDISDAHYKACLYAGINISGTNGEVMPGQWEYQVGPSVGIEAGDHIWISRYILERITEQAGVVLTLDPKPIQGDWNGAGCHTNYSTKSMREDGGFEVIKAILNLSLRHDLHISAYGEGNERRLTGLHETA
		SIDNFSWGVANRGCSIRVGRDTEAKGKGYLEDRRPASNMDPYVVTALLAETITLWEPTLEAEVLAACKLALKV
		MASLTDLVNLNLSDTTEKIIAEYIWGGSGMDLRSKARTLSGPVTDPSKLPKWNFDGSSTGQAPGEDSEVILYPQAIKDPFRKGNNILVMCDYTPAGEPIPTNKRHNAAKIFSSPEVASEEPWYGIEQYETLLQKDINWPLGWPGVGGFPGQGPYYCGIGADKSFGRDIVDSHYKACLY
	OsGS1.1	AGINISGINGEVMPGQWEFQVGPSVGISAGQVWVARYILERITEIAGVVVSFDPKPIPGDWNGAGAHTNYSTKSMRNDGGYEIIKSAIEKLGRLHKEHISAYGEGNERRLTGRHETADINTFSWGVANRGASVRVGRETEQNGKGYFEDRRPASNMDPYIVTSMIAETITIIWKP

OsGS1.2	N	MANLTDLVNLDSCSDKIIAEYIWVGGSGIDLRSKARTVKGPITDVSQLPKWN YDGSSTGQAPGEDSEVILYPQAIFKDPFRRGDNILVMCDCTPQGEPIPTNKRHSAAKIFSHPDVVAEVPWYGIEQEYTLQKDVNWPLGWPVGGFPGQGPYYCAAGAEKAFGRDIVDAHYKAC
		IYAGINISGINGEVMPGQWEFQVGPSVGIAAADQVWVARYILERVTEVAGVVLSDLPKPIPGDWNGAGAHTNFTSKSMREPGGYEVIKKAIDKLALRHKEHIAAYGEGNERRLTGRHETADINTFKWGVANRGASIRVGRDTEKEGKGYFEDRRPASNMDPYVVTGMIAETTLWKQ
ZmGS2		MAQAVVPAMQCRVGVKAAAGRVWSAGRTRTGRGGASPGFKVMAVSTGSTGVVPRLEQLLNMDTPYTDK VIAEYIWVGGSGIDIRSKRTISKPVEDPSELPKWN YDGSSTGQAPGEDSEVILYPQAIFKDPFRGNNVLVICDITYPQGEPLTNKRHRAAQIFSDPKVAEQVPWFG
		IEQEYTLQKDVNWPLGWPVGGFPGQGPYYCAVGADKSFGRDISDAHYKACLYAGINISGTNGEVMPGQWEYQVGPSVGIEAGDHIWISRYILERITEQAGVVLTLDPKPIQGDWNGAGCHTNYSTKTMREDGGFEEIKRAILNLSLRHDLHISAYGEGNERRLTGKHETASIGTFSW
ZmGS1.2		GVANRGCSIRVGRDTEAKGKGYLEDRRPASNMDPYIVTGLLAETTLWQPSLEAEALAAKKLALKV
		MALLSDLINLDSGRTGKIIAEYIWVGGSGMDVRSKARTLSGPVDDPSKLPKWNFDGSSTGQAPGDDSEVILCPRAIFRDPFRKGQNILVMCDCTEPNGEPIPSNKRHGAAKIFSHPDVKAEEPWFIEQEYTLQKDTKWPLGWLPGGYPGPQGPYYCAVGADKSYGRDIVDAHYKAC
maize	ZmGS1.5	LYAGIDISGINGEVMPGQWEFQVGPVGSAGDQLWVARYILERITEIAGVVVSFDPKPIPGDWNGAGAHTNYSTKSMRSDGGYEVIKKAIGKLGLRHREHIAAYGDGNERRLTGRHETADINTFVWGVANRGASVRVGRDTEKEGKGYFEDRRPASNMDPYVVTSLIAETTMLWEP
		SHSNGDGKGAAAP
ZmGS1.3		MASLTDLVNLDSDCTDRIIAEYIWVGGSGIDLRSKARVMCDCTYPQGEPIPSNKRYKAATVFSHPDVAEVPWYGIEQEYTLQKDVSWPLGWPVGGYPGPQGPYYCAAGADKAFGRDVDAHYKACLYAGINISGINGEVMPGQWEFQVGPSVGISAGDEIWVARYILERITEMA
		GIVLSDLPKPIKGDWNGAGAHTNYSTKSMREAGGYEVIKAEIKLGRHREHIAAYGEGNERRLTGRHETADINTFKWGVANRGASIRVGRDTEKEGKGYFEDRRPASNMDPYVVTGMIAETTLWKGN
ZmGS1.4		MACLTDLVNLDSDNTEKIIAEYIWIGSGMDLRSKARTLSGPVTDPSKLPKWN YDGSSTGQAPGEDSEVILYPQAIFKDPFRRGNNILVMCDCTYPAGEPIPTNKRYYNAAKIFSSPEVAAEEPWYGIEQEYTLQKDTNWPLGWPIGGFPGPQGPYYCGIGAESFGRDIVDAHYKACL
		YAGINISGINGEVMPGQWEFQVGPSVGISSGDQVWVARYILERITEIAGVVVTFDPKPIPGDWNGAGAHTNYSTESMRKEGGYEVIKAAIEKLKL RHREHIAAYGEGNERRLTGRHETADINTFSWGVANRGASVRVGRETEQNGKGYFEDRRPASNMDPYVVTSMIAETTIHWKP
ZmGS1.1		MACLTDLVNLDSDTEKIIAEYIWIGSGMDLRSKARTLPGPVTDP SKLPKWN YDGSSTGQAPGEDSEVILYPQAIFKDPFRRGNNILVMCDCTYPAGEPIPTNKRYSAAKIFSSLEVAEEPWYGIEQEYTLQKDTNWPLGWPIGGFPGPQGPYYCGIGAESFGRDIVDAHYKACLY
		AGINISGINGEVMPGQWEFQVGPSVGISSGDQVWVARYILERITEIAGVVVTFDPKPIPGDWNGAGAHTNYSTESMRKEGGYEVIKAAIEKLKL RHKEHIAAYGEGNERRLTGRHETADINTFSWGVANRGASVRVGRETEQNGKGYFEDRRPASNMDPYVVTSMIAETTIVWKP
Arabidopsis thaliana	AtGS1.2	MASLTDLVNLDSDCTDRIIAEYIWIGTGIDLRSKARTVKGPITDPSQLPKWN YDGSSTGQAPGEDSEVILYPQAIFKDPFRKGNHILVMCDCTYPQGEPIPTNKRYSAAKVFSHPDVAEVPWYGIEQEYTLQKDVSWPLGWPVGGYPGPQGPYYCAAGADKAFGRDVDAHYKA
		CLYAGINISGINGEVMPGQWEFQVGPSVGISAGDEIWVARYILERITEMAGIVLSDLPKPIKGDWNGAGAHTNYSTKSMREAGGYEVIKAAIDKLGRHKEHIAAYGEGNERRLTGRHETADINTFKWGVANRGASIRVGRDTEREGKGYFEDRRPASNMDPYVVTGMIAETTLWNG
AtGS1.3		MSLLADLVNLDISDNSEKIIAEYIWVGGSGMDMRSKARTLPGPVTDP SKLPKWN YDGSSTGQAPGQDSEVILYPQAIFKDPFRRGNNILNVFYRFQVMCDAYTPAGEPIPTNKRHAAAEIFANPDVIAEVPWYGIEQEYTLQKDVNWPLGWPIGGFPGPQGPYYCSIGADKSFGRDIV
		DAHYKASLYAGINISGINGEVMPGQWEFQVGPSVGISAADDEIWIARYILERITEIAGVVVSFDPKPIPGDWNGAGAHTNYSTKSMREEGGYEIHKAEIKLGLRHKEHISAYGEGNERRLTGHHETADINTFLWGVANRGASIRVGRDTEKEGKGYFEDRRPASNMDPYVVTSMIAETTL
AtGS1.5		MTSPLSDLLNLDLSDTKIIAEYIWIGSGMDIRSKARTLPGPVSNPTKLPKWN YDGSSTDQAAGDDSEVILYPQAIFKDPFRKGNNILVMCDAYRPAGDPIPTNRRHKAVKIFDHPNVKAEEPWFIEQEYTLKKDVKWPLGWLPGGFPGPQGPYYCAVGADKAFGRDIVDAHYKAC
		LYSGLSIGGANGEVMPGQWEFQISPTVGIGAGDQLWVARYILERITEICGVIVSFDPKPIQGDWNGAAHTNFTSKSMRKDGGLD LIKEAIKKLEVKKHQHIAAYGEGNERRLTGKHETADINTFSWGVADRGASVRVGRDTEKEGKGYFEDRRPSSNMDPYLVTSMAIETTL
AtGS1.3		MSLLSDLVNLDATGKIIAEYIWIGSGMDIRSKARTLPGPVTDP SKLPKWN YDGSSTGQAAGEDSEVILYPQAIFKDPFRKGNNILVMCDAYTPAGDPIPTNKRHNAAKIFSHPDVAKEEPWYGIEQEYTLMQKDVNWPIGWVPGGYPGPQGPYYCGVGADKAIGRDIVDAHYKA
		CLYAGIGISGINGEVMPGQWEFQVGPVEGISSGDQVWVARYLLERITEISGVIVSFDPKPIPGDWNGAGAHCNYSTKTMRNDGGLEVIKKAIGKLQLKHKEHIAAYGEGNERRLTGKHETADINTFSWGVANRGASVRVGRDTEKEGKGYFEDRRPASNMDPYVVTSMIAETTLG

AiGS1.4	MSSLADLINLSDSTDQIIAEYIWIGSGLDMRSKARTLPGPVTDPSQLPKWNYDGSSTGQAPGDDSEVIIYPQAIKDPFRRGNNILVMCDAYTPAGEPIPTNKRHAAAKIFEDPSVVAETWYGIEQEYTLQKDIKWPGWPGVGGFPGPGPYPCYGVGADKAFGRDIVDSHYKACL
	YAGINVSGTNGEVMPGQWEFQVGPTVGIAAADQVWVARYILERITELAGVLSLDPKPIPGDWNGAGAHTNYSTKSMREDDGGYEVIIKAEIKLGRHKEHIAAYGEGNERRLTGKHETADINTFLWGVANRGASIRVGRDTEQAGKGYFEDRRPASNMDPYTVTSMIAESTILWKP
	MAQILAASPTCQMRVPKHSSVIASSSKLWSSVVLKQKKQSNNKVRGRVLAQSDNSTVNRVETLLNLDTKPYSDRIIAEYIWIGSGIDLRSKSRTIEKPVEDPSELPKWNYDGSSTGQAPGEDSEVILYPQAIFRDPFRGGNNILVICDTWTPAGEPIPTNKRKAAAEIFSNNKKVSGEVP
	WFGIEQEYTLQQNVKWPLGWPVGAFPGPGQPYPCYGVGADKIWRDISDAHYKACLYAGINISGTNGEVMPGQWEFQVGPSVIGDAGDHVWCARYLLERITEQAGVVLTLDPKPIEGDWNGAGCHTNYSTKSMREEGGFEVIKKAILNLSLRHKEHISAYGEGNERRLTGKHETASI
AiGS2	DQFSWGVANRGCSIRVGRDTEAKGKGYLEDRRPASNMDPYIVTSLLAETTLWEPTLEAEALAAQKLSLNV
AiGS1.1	MSLVSDLINLNSDSTDKIIAEYIWVGSGMDMRKARTLPGPVTDPSQLPKWNYDGSSTGQAPGEDSEVILYPQAIKDPFRRGNNILVMCDAYTPAGEPIPTNKRHAAAKVFSNPDVAAEVPWYGIEQEYTLQKDVKWPGWPGIGYPGPQGPYYCGIGADKSFGRDIVDSHYKA
	CLYAGINISGINGEVMPGQWEFQVGPAVGISAADIEWVARYILERITEIAGVVVSFDPKPIPGDWNGAGAHCNYSTKSMREEGGYEIikkaIDKLGRLHKEHIAAYGEGNERRLTGHETADINTFLWGVANRGASIRVGRDTEKEGKGYFEDRRPASNMDPYIVTSMIAETTLWNP
	MNCLLELGFSLSDAVLLSRLFCRLLSHQAPHFNASLSLSLSLSPAFAPSSASLAMSLLSDLINLNLTDSTDKIIAEYVWIGSGLDRSKARTLPGPVTDPAKLPKWNYDGSSTNQAPGDDSEVILYPQAIKDPFRRGNNILVMCDAYTPSGEPIPTNKRFAAKIFSHADVVAEEPWY
	GIEQEYTLQKDVHWPLGWPVGGFPGPGQGPYYCGTGADKAFGRDIVDAHYKACLYAGVNISGINGEVMPGQWEYQVGPTVGIAAGDQVWISRYILERITEIAGVVSFDPKPIKGDWNGAGAHTNYSTKSMRNDGGIDVIKAEIKLGRHKLHIAAYGEGNERRLTGRHETADINTF
CmoCh08G004920	SWGVANRGASVRVGRDTEQAGKGKLL
CmoCh14G017140	MAQILAPSVQWQLRTKQTSMSASSITPKMWSLLLLKQSSKVAVKSSAKFRVLALKSDGSTINRMEELNLDVTPYTDKIIAEYIWIGSGIDLRSKSRTISKVPEHSELPKWNYDGSSTGQAPGEDSEVILYPQAIKDPFRGGNNILVICDAYTPAGEPIPTNKRHRAAEIFSNNKKVVEIIP
	WYGIEQEYTLQTNVKWPLGWPVGAYPGPGQPYPCYGVGADKSFGRDISDAHYKACLYAGINISGTNGEVMPGQWEYQVGPSVIGAGDHIWCSRYILERITEQAGVVLTLDPKPIEGDWNGAGCHTNYSTKSMREEGGFDVIKKAILNLSLRHNEHISAYGEGNERRLTGKHETASIN
	TFSWGVANRGCSIRVGRDTEKQKGKGYLEDRRPASNMDPYVVTSLLAETTLWEPTLEAEALAAQKLSLKV
	MSSLDLINLSLCDYTDKIVAEYIWVGSGKDVRSKARTISEYVSDPSKLPKWNYDGSSTGQAPGEDSEVILYPQAIFRDPFRRGNNILVICDSYTPAGEPIPTNKRHAAAKIFSHPDVVAEEPWYGIEQEYTLQKDVKWPIGWPIGGFPGPGPYPCYAGADKTFGRDIVDAHYKACLF
CmoCh15G007570	AGVNISGINGEVMPGQWEFQVGPSVGISADELWVARYILERITEIAGVVSFDPKPIPGDWNGAGAHTNYSTKSMRKEGGYEVIIKAEIKLGRHKEHIAAYGEGNERRLTGRHETADINTFLWGVANRGASIRVGRDTEKSGKGYFEDRRPASNMDPYTVTSMIAETTLWKP
pumpkin	MSVLSDLVNLSDSTDKIVAEYIWIGSGMDLRKARTLCGPVSDPSDVPKWSYDGSSTGQASGEDSEVILYPQAIFRDPFRRGNNILVLCDAYTAAGEPIPTNKRDAAAKIFSHPDVAAEVPWYGIEQYENLLQKDGPPYPCYGVGADKAFGRDISEAHYKACLYAGINISGINGEVMPG
	QWEFQVGPSVGISAGDEMWWARYILERITEIAGVVLCFDPKPIQGDWSVACADINYSTKSMRDDGGIKVIRKAEIKLGRHKEHIAAYREGNKRRLNGQHETNDINTFSWGVANRCASVRVGRDTEKKKGKGYFEDRRLPSNMDPYVATAMIAETTLWKP
	MSLLSDLINLNLTDTEKIIAEYVWIGSGLDRSKARTLPGPVTDPAKLPKWNYDGSSTNQATGDNSEVILHPQAVFKDPFRRGNNILVMCDAYTSAGEPIPTNRFNAAKIFSEPDVVAEEPWFIEQEYTLQKQDTRWPLGWPVGGFPGPGQGPYYCGTGADKAFGRDIVDAHYKAC
	LYAGINISGINGEVMPGQWEFQVGPTVGASGDQIWIARYILERITEMAGVVLTFDPKPVQGDWNGAGAHANYSTKSMRDDGGIEVIKAEIKLSLRHKEHIAAYGEGNERRLTGRHETADINNFSGWVANRGASVRVGRDTEKAGKGKVLRGSKASFEHGSRLRGDFHDRNRNHSVE
CmoCh17G009640	ALNRLNRTTALWLQFVSPFDAFNCS
CmoCh06G014450	MVVGSSLYLYLPAIFIPLFIRHYRRRNPLLGLIFLPLSGTSLVQEMAQILAPSTQCQLRTKQSSMGGSPITPKMWSSLLMKQSKKGGVKSSAKFRVLALKSDGSTINRMEDLLKLDVTPYTDKIIAEYIWIGSGIDLRSKSRTISKVPEHSELPKWNYDGSSTGQAPGEDSEVILYPQAI
	FKDPRGGNNILVICDAYTPAGEPIPTNKRHRAAEIFSNNKKVVEVPWYGIEQEYTLQTNVKWPLGWPVGAYPGPGQPYPCYGVGADKSFGRDISDAHYKACLYAGINISGTNGEVMPGQWEFQVGPSVIGAGDHIWCARYILERITEQAGVVSLSLDPKPIEGDWNGAGCHTNYSTK
	SMREEGGFEVIKKAILNLSLRHKEHISAYGEGNERRLTGKHETASINSFSGWVANRGCSIRVGRDTEKEGKGYLEDRRPASNMDPYVVTSLLAESTLLWEPTLEAEALAAQKLALKV
	MSLLSDLVNLSDSTEKIIAEYIWIGSGLDIRSKARTLSGPVSDPSELPKWNYDGSSTGQAPGKDSEVILHPQAIFRDPFRRGNNILVVCDAYTPAGEPIPTNKRHAAAKIFNHPEVSAEVPWYGIEQEYTLQKDIKWPIGWPIGGFPGPGQGPYYCGVGDKAFGRDIVDAHYKACLYA
CmoCh14G008450	GVNISGINGEVMPGQWEFQVGPSVGISAGDELWVARYILERITEIAGVALSFDPKPIQGDWNGAGAHTNYSTKSMRNEGGYEVIIKAIQKLEYRHEKHIAAYGEGNERRLTGRHETADINTFSWGVANRGASVRVGRDTEKEGKGYFEDRRPASNMDPYVVTSMIAETTLWKP

PiGS1.1-831163		MSLLSDLINLNSDSTEKIIAEYLWIGGSGDIRSKARTLSGPVSDPAKLPKWNYDGSSTGQAPGQDSEVILYPQAIFRDPFRRGNNILVICDAYTPAGEIPTNKRCDAAKIFSHPEVVAEKPWYGLEQEYTLQKDVKWPLGWPIGGYPGPQGPYYCGIGVDKAFGRDIVDAHAKACLY
		AGINISGINGEVMPGQWEFQVGPSVGISAGDELWAARYILERITEVAGVLSFDPKPIQGDWNGAGAHTNSTESMRNEGGEYIIKKAIEKLGRLHKEHIAAYEGGNERRLTGRHETADINTFKWGVADR GASIRVGRDTEKEGKGYFEDRRPASNMDPYVVTSMIAETTILWKP
		MSLLSDLINLNSDSTEKIIAEYIWVGSGMDIRSKGRTLPGPVSDPSKLPKWNYDGSSTGQAPGEDSEVILYPQAIKDPFRRGNNILVICDITYTPAGEIPTNKRCKAAKIFSHPDVVAEVPWYGLEQEYTLQKDVKWPLGWPIGGYPGPQGPYYCGAGVDKAFGRDIVDAHAKACLY
PiGS1.1-710678		YAGINISGINGEVMPGQWEFQVGPSVGISSGDELWAARYILERITEVAGVLSFDPKPIQGDWNGAGAHTNSTKSMRNEGGEYIKKAIEKLGRLHKEHIAAYEGGNERRLTGRHETADINTFKWGVANRGASIRVGRDTEKEGKGYFEDRRPASNMDPYVVTSMIAETTILWKP
		MSLLNDLINLNSDTEKIIAEYLWIGGSGMDLRSKARTLPGPVTDPAKLPKWNYDGSSTGQAPGEDSEVILYPQAIKDPFRRGNNILVMCDAYTPAGEIPTNKRFAAKIFSNPAIAAEEPWFIEQEYTLQKDINWPLGWVPVGGFPGPQGPYYCGVGADKSFGRDIVDSHYKACLY
		AGINISGINGEVMPGQWEFQVGAIGISAGDEVWVARYILERIAEIAGVVVSFDPKPIPGDWNGAGAHTNSTKSMRNDGGFAVIKKAIEKLGRLHKEHIAAYEGGNERRLTGRHETADINTFSWGVANRGASVRVGRDTEKDGKGYFEDRRPASNMDPYVVTSMVAETTIIWKP
poplar	PiGS1.2-716066	MSLLNDLINLNSDTEKIIAEYLWIGGSGMDLRSKARTLPGPVTDPAELPKWNFDGSSTGQAPGDDSEVILYPQSIFKDPFRRGNNILVMCDAYTPAGEIPTNKRFAAQIFSDPVVAEEPWYGIEQEYTLQKDINWPLGWVPVGGFPGPQGPYYCSVGADKSFGRDIVDAHAKACLY
		AGINISGINGEVMPGQWEFQVGPSVGISAGDEVWVARYILERIAELAGVVVSFDPKPIPGDWNGAGAHTNSTKSMRNEGGLAVIKKAIEKLGRLHKEHIAAYEGGNERRLTGRHETADINTFSWGVANRGASIRVGRDTEKEGKGYFEDRRPASNMDPYVVTSMIAETTIIWRP
		MSLLTDLINLNSDTTDKIIAEYIWVGSGMDLRSKARTLDGAVSDPQKLPKWNYDGSSTGQAPGEDSEVILYPQAIKDPFRRGNNILVMCDAYTPAGEIPTNKRHSAKIFSHPDVVAEVPWYGLEQEYTLQKDLKWPLGWVPVGGYPGPQGPYYCGAGADKAFGRDIVDSHYKA
PiGS1.3-827781		CLYAGINISGINGEVMPGQWEFQVGPSVGISAGDELWVARYILERITEIAGVVVSFDPKPIPGDWNGAGAHTNSTKSMRNDGGFEIHKKAIGKLQLRHKEHIAAYEGGNERRLTGRHETADIHTFSWGVANRGASVRVGRDTEKEGKGYFEDRRPASNMDPYVVTSMIAETTILWKP
		MSLLSDLINLNSDTTDKIIAEYIWVGSGMDLRSKARTLNGVVSDDPHKLPKWNYDGSSTGQAPGEDSEVILYPQAIKDPFRRGNNILVMCDAYTPAGEIPTNKRNYAAKIFSHPDVVAEVPWYGIEQEYTLQKDLKWPIGWVPVGGYPGPQGPYYCGAGADKAFGRDIVDSHYKA
		CLYAGINISGINGEVMPGQWGFQVGPSVGISAGDELWVARYILERITEIAGVVVSFDPKPIPGDWNGAGAHTNSTKSMRNDGGFEVIKKAIGKLQLKHKEHIAAYEGGNERRLTGRHETADINTFSWGVANRGASVRVGRDTEKAGKGYFEDRRPASNMDPYVVTSMIADTTILWKP
PiGS1.3-834185		MAQILAPSSQWQMRIAKNSAPACPMTAKMWSSLVLKQNKKGIAKSSAKFRVFAKSENSTINRMEDLLDLTPYTDKIIAEYIWIGSGIDLRSKTSRTISKPIEHPSELPKWNYDGSSTGQAPGEDSEVILYPQAIKDPFRRGNNILVMCDITYTPQGEPIPTNKRHRAAEIFSNNKVIDE
		VPWFIEQEYTLQTNVKWPLGWVPVGGYPGPQGPYYCGAGADKSFGRDISDAHAKACMYAGINISGTNGEVMPGQWEYQVGPSVGIDAGDHIWISRYILERITEQAGVVLSDLPKPIEGDWNGAGCHTNYSTKTMREEGGFEAIKKAILNLSLRHKEHISAYEGGNERRLTGKHETAS
		IdTFswGVANRGCSIRVGRETEKQGKGYLEDRRPASNMDPYIVTSLLAETTILYEPTLEAEALAAQKLSMNV
Csa3G150160		MAQILAPSTQWQLRTKLTPMSSSPITPKMWSSILLKQNKKGAVKSSSKYRVLSVRSEGGTINRMEDLLNLDVTPYTDKIIAEYIWIGSGIDLRSKTSRTISKPIEHPSELPKWNYDGSSTGQAPGEDSEVILYPQAIKDPFRRGNNILVICDAYTPAGVPIPTNKRHRAAEIFSNNKVVDEIP
		WYGIEQEYTLQTNVKWPLGWVPVGAYPGPQGPYYCGVGADKSFGRDISDAHAKACLYAGINISGTNGEVMPGQWEYQVGPSVGIEAGDHIWISRYILERITEQAGVVLSDLPKPIEGDWNGAGCHTNYSTKSMREEGGFEVIKKAAILNLSLRHKEHISAYEGGNERRLTGKHETASINT
		FSWGVANRGCSIRVGRDTEKQGKGYLEDRRPASNMDPYVVTSLLAETTILWEPTLEAEALAAQKLSLKV
cucumber	Csa3G304140	MSLLSDLVNLNSDSTEKIIAEYIWVGSGMDLRSKARTLSGPVSDPSKLPKWNYDGSSTGQAPGEDSEVILYPQAIFRDPFRRGNNILVVCITYTPAGEIPTNKRHAAKIFSHPDVVAEVPWYGIEQEYTLQKDVKWPIGWPIGGFPGPQGPYYCGVGDKAFGRDIVDAHAKACLY
		YAGVNISGINGEVMPGQWEFQVGPSVGISAGDEIWVARYILERITEIAGVLSFDPKPIQGDWNGAGAHTNSTKSMREEGGYEVIKKAIEKLGRLHKEHIAAYEGGNERRLTGRHETADIHTFSWGVANRGASVRVGRDTEKEGKGYFEDRRPASNMDPYVVTSMVAETTILWKP
		MSSLSDLINLNLCDFTDKIIAEYIWVGSGKDVRSKARTISGPISDPSKLPKWNYDGSSTGQAPGQDSEVILYPQAIFRDPFRRGNNILVICDSYTPGGEIPTNKRHGAAKIFSHPDVVAEEPWYGIEQEYTLQKDVNWPIGWPIGGFPGPQGPYYCGAGADKTFGRDIVDAHAKACLYA
Csa5G410730		GVNISGINGEVMPGQWEFQVGPSVGISADELWVARYILERITEMAGVLSFDPKPIQGDWNGAGAHTNSTKSMRGEYEVIKKAIEKLGVRHKEHIAAYGDGNERRLTGRHETADINTFLWGVANRGASIRVGRDTEKAGKGYFEDRRPASNMDPYVTVSMIAETTILWNP
		MSLLSDLINLNLNTTEKIIAEYVWIGGSGDLRSKARTLPGPVTDPAKLPKWNYDGSSTNQAPGDDSEVIIYPQAVFKDPFRRGNNILVMCDAYTPAGEIPTNKRFAAKIFSNPDVVAEEPWYGIEQEYTLQKDIHWPLGWPTGGFPGPQGPYYCGTGADKAFGRDIVDSHYKACLY
		YAGINISGINGEVMPGQWEYQVGPVTGVIASGDQLWMSRYILERITEIAGVVVTFDPKPIQGDWNGAGAHTNSTKSMRNDGGINVIKKAIEKLSLRHKEHIAAYEGGNERRLTGRHETADINTFSWGVANRGASVRVGRDTEKAGKGYFEDRRPASNMDPYVVTSMIAETTILGKP