The Sucrose Synthase Gene Family in Chinese Pear (*Pyrus bretschneideri* Rehd.): Structure, Expression, and Evolution

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Table S1. The detailed information of PbSSs genes from Chinese pear.

Gene Name	Gene ID	Chromosome	Start	End	Strand	Length (bp)	Molecular weight	Theoretical PI
PbSS1	Pbr035996.1	Chr2	16772840	16776299	+	801	91910.48	5.89
PbSS2	Pbr035997.1	Chr2	16782598	16786033	+	807	92685.32	5.92
PbSS3	Pbr003107.1	Chr2	21529677	21535125	+	1072	120330.5	6.25
PbSS4	Pbr022714.1	Chr3	1322262	1324033	+	183	20747.49	4.69
PbSS5	Pbr022715.1	Chr3	1325811	1328963	+	559	63581.31	7.25
PbSS6	Pbr008035.1	Chr5	3932753	3937176	+	818	91171.68	5.62
PbSS7	Pbr028302.1	Chr6	2843943	2847973	+	867	undefined	undefined
PbSS8	Pbr042506.1	Chr8	9179789	9184899	+	962	106746.1	6.06
PbSS9	Pbr033571.1	Chr9	252260	262865	+	1142	129417.5	8.64
PbSS10	Pbr008457.1	Chr9	484297	496090	-	1142	129417.5	8.64
PbSS11	Pbr008464.1	Chr9	651911	662128	+	1119	126822.5	8.66
PbSS12	Pbr031564.1	Chr11	13021557	13025667	+	815	91557.1	6.76
PbSS13	Pbr012029.1	Chr13	9093304	9095768	-	265	29773.02	5.91
PbSS14	Pbr014902.1	Chr13	12846483	12851084	-	800	91169.09	5.7
PbSS15	Pbr027868.1	Chr15	10137257	10142745	-	1054	117624	6.15
PbSS16	Pbr034361.1	Chr15	12427951	12433933	+	1066	119481.6	6.06
PbSS17	Pbr032090.1	Chr15	13956060	13960667	-	873	97214.54	5.94
PbSS18	Pbr037395.1	Chr15	17070500	17075187	-	837	96491.85	6.41
PbSS19	Pbr012642.1	Chr17	4602903	4606969	+	844	95523.44	6.81
PbSS20	Pbr012641.1	Chr17	4613998	4626884	+	1138	128711.8	8.53
PbSS21	Pbr003395.1	scaffold1142.0	15301	18735	+	807	92644.24	5.78
PbSS22	Pbr026341.1	scaffold424.0	208844	210615	+	183	20747.49	4.69
PbSS23	Pbr026338.1	scaffold424.0	167041	168812	-	183	20747.49	4.69

Table S1. *Cont.*

PbSS24	Pbr026337.1	scaffold424.0	165212	166512	-	63	7543.7	6.72
PbSS25	Pbr003394.1	scaffold1142.0	5534	9046	+	790	90749.18	5.97
PbSS26	Pbr026342.1	scaffold424.0	212581	215680	+	566	64281.07	7.62
PbSS27	Pbr026336.1	scaffold424.0	161976	165075	-	566	64281.07	7.62
PbSS28	Pbr009578.1	scaffold160.1.1	28772	34269	+	1054	117601	6.06
PbSS29	Pbr001616.1	scaffold1046.0	32129	36123	+	856	96122.99	6.48
PbSS30	Pbr001745.1	scaffold1051.0	77	3071	-	510	57267.35	6.78

Table S2. List of sucrose synthase gene sequences used in this study

Taxon	**Sequence name**	**Accession number**	**Protein sequence**	**Protein size**
A. Angiosperms				
Dicot plants				
Arabidopsis thaliana	AtSS1	At5g20830	MANAERMITRVHSQRERLNETLVSERNEVLALLSRVEAKGKGILQQNQIIAEFEALPEQTRKKLEGGPFFDLLKSTQEAIVLPPWVALAVRPRPGVWEYLRVNLHALVVEELQPAEFLHFKEELVDGVKNGNFTLELDFEPFNASIPRPTLHKYIGNGVDFLNRHLSAKLFHDKESLLPLLKFLRLHSHQGKNLMLSEKIQNLNTLQHTLRKAEEYLAELKSETLYEEFEAKFEEIGLERGWGDNAERVLDMIRLLLDLLEAPDPCTLETFLGRVPMVFNVVILSPHGYFAQDNVLGYPDTGGQVVYILDQVRALEIEMLQRIKQQGLNIKPRILILTRLLPDAVGTTCGERLERVYDSEYCDILRVPFRTEKGIVRKWISRFEVWPYLETYTEDAAVELSKELNGKPDLIIGNYSDGNLVASLLAHKLGVTQCTIAHALEKTKYPDSDIYWKKLDDKYHFSCQFTADIFAMNHTDFIITSTFQEIAGSKETVGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADMSIYFPYTEEKRRLTKFHSEIEELLYSDVENKEHLCVLKDKKKPILFTMARLDRVKNLSGLVEWYGKNTRLRELANLVVVGGDRRKESKDNEEKAEMKKMYDLIEEYKLNGQFRWISSQMDRVRNGELYRYICDTKGAFVQPALYEAFGLTVVEAMTCGLPTFATCKGGPAEIIVHGKSGFHIDPYHGDQAADTLADFFTKCKEDPSHWDEISKGGLQRIEEKYTWQIYSQRLLTLTGVYGFWKHVSNLDRLEARRYLEMFYALKYRPLAQAVPLAQDD	808
	AtSS2	At5g49190	MANAERVITRVHSQRERLDATLVAQKNEVFALLSRVEAKGKGILQHHQIIAEFEAMPLETQKKLKGGAFFEFLRSAQEAIVLPPFVALAVRPRPGVWEYVRVNLHDLVVEELQASEYLQFKEELVDGIKNGNFTLELDFEPFNAAFPRPTLNKYIGDGVEFLNRHLSAKLFHDKESLHPLLKFLRLHSHEGKTLMLNNRIQNLNTLQHNLRKAEEYLMELKPETLYSEFEHKFQEIGLERGWGDTAERVLNMIRLLLDLLEAPDPCTLENFLGRIPMVFNVVILSPHGYFAQDNVLGYPDTGGQVVYILDQVRALETEMLQRIKQQGLNITPRILIITRLLPDAAGTTCGQRLEKVYGSQYCDILRVPFRTEKGIVRKWISRFEVWPYLETFTEDVAAEISKELQGKPDLIIGNYSDGNLVASLLAHKLGVTQCTIAHALEKTKYPDSDIYWKKLDEKYHFSCQFTADLIAMNHTDFIITSTFQEIAGSKDTVGQYESHRSFTLPGLYRVVHGIDVFDPKFNIVSPGADMSIYFAYTEEKRRLTAFHLEIEELLYSDVENEEHLCVLKDKKKPIIFTMARLDRVKNLSGLVEWYGKNTRLRELVNLVVVGGDRRKESQDNEEKAEMKKMYELIEEYKLNGQFRWISSQMNRVRNGELYRYICDTKGAFVQPALYEAFGLTVVEAMTCGLPTFATCNGGPAEIIVHGKSGFHIDPYHGDKAAESLADFFTKCKHDPSHWDQISLGGLERIQEKYTWQIYSQRLLTLTGVYGFWKHVSNLDRLESRRYLEMFYALKYRPLAQAVPLAHEE	808

Table S2. *Cont*.

	AtSS3	At4g02280	MANPKLTRVLSTRDRVQDTLSAHRNELVALLSRYVDQGKGILQPHNLIDELESVIGDDETKKSLSDGPFGEILKSAMEAIVVPPFVALAVRPRPGVWEYVRVNVFELSVEQLTVSEYLRFKEELVDGPNSDPFCLELDFEPFNANVPRPSRSSSIGNGVQFLNRHLSSVMFRNKDCLEPLLDFLRVHKYKGHPLMLNDRIQSISRLQIQLSKAEDHISKLSQETPFSEFEYALQGMGFEKGWGDTAGRVLEMMHLLSDILQAPDPSSLEKFLGMVPMVFNVVILSPHGYFGQANVLGLPDTGGQVVYILDQVRALETEMLLRIKRQGLDISPSILIVTRLIPDAKGTTCNQRLERVSGTEHTHILRVPFRSEKGILRKWISRFDVWPYLENYAQDAASEIVGELQGVPDFIIGNYSDGNLVASLMAHRMGVTQCTIAHALEKTKYPDSDIYWKDFDNKYHFSCQFTADLIAMNNADFIITSTYQEIAGTKNTVGQYESHGAFTLPGLYRVVHGIDVFDPKFNIVSPGADMTIYFPYSEETRRLTALHGSIEEMLYSPDQTDEHVGTLSDRSKPILFSMARLDKVKNISGLVEMYSKNTKLRELVNLVVIAGNIDVNKSKDREEIVEIEKMHNLMKNYKLDGQFRWITAQTNRARNGELYRYIADTRGAFAQPAFYEAFGLTVVEAMTCGLPTFATCHGGPAEIIEHGLSGFHIDPYHPEQAGNIMADFFERCKEDPNHWKKVSDAGLQRIYERYTWKIYSERLMTLAGVYGFWKYVSKLERRETRRYLEMFYILKFRDLVKTVPSTADD	809
	AtSS4	At3g43190	MPTGRFETMREWVYDAISAQRNELLSLFSRYVAQGKGILQSHQLIDEFLKTVKVDGTLEDLNKSPFMKVLQSAEEAIVLPPFVALAIRPRPGVREYVRVNVYELSVDHLTVSEYLRFKEELVNGHANGDYLLELDFEPFNATLPRPTRSSSIGNGVQFLNRHLSSIMFRNKESMEPLLEFLRTHKHDGRPMMLNDRIQNIPILQGALARAEEFLSKLPLATPYSEFEFELQGMGFERGWGDTAQKVSEMVHLLLDILQAPDPSVLETFLGRIPMVFNVVILSPHGYFGQANVLGLPDTGGQVVYILDQVRALENEMLLRIQKQGLEVIPKILIVTRLLPEAKGTTCNQRLERVSGTEHAHILRIPFRTEKGILRKWISRFDVWPYLETFAEDASNEISAELQGVPNLIIGNYSDGNLVASLLASKLGVIQCNIAHALEKTKYPESDIYWRNHEDKYHFSSQFTADLIAMNNADFIITSTYQEIAGSKNNVGQYESHTAFTMPGLYRVVHGIDVFDPKFNIVSPGADMTIYFPYSDKERRLTALHESIEELLFSAEQNDEHVGLLSDQSKPIIFSMARLDRVKNLTGLVECYAKNSKLRELANLVIVGGYIDENQSRDREEMAEIQKMHSLIEQYDLHGEFRWIAAQMNRARNGELYRYIADTKGVFVQPAFYEAFGLTVVESMTCALPTFATCHGGPAEIIENGVSGFHIDPYHPDQVAATLVSFFETCNTNPNHWVKISEGGLKRIYERYTWKKYSERLLTLAGVYAFWKHVSKLERRETRRYLEMFYSLKFRDLANSIPLATDEN	807
	AtSS5	At5g37180	MEMTSGSLGNGIPEAMGQNRGNIKRCLEKYIENGRRVMKLNELMDEMEIVINDVTQRRRVMEGDLGKILCFTQAVVIPPNVAFAVRGTPGNWQYVKVNSSNLSVEALSSTQYLKLKEFLFDENWANDENALEVDFGALDFTLPWLSLSSSIGNGLSFVSSKLGGRLNDNPQSLVDYLLSLEHQGEKLMMNETLNTARKLEMSLILADVFLSELPKDTPFQAFELRFKECGFEKGWGESAGRVKETMRILSEILQAPDPQNIDRFFARVPRIFNVVIFSVHGYFGQTDVLGLPDTGGQVVYILDQVKALEDELLQRINSQGLNFKPQILVVTRLIPDAKKTKCNQELEPIFGTKYSNILRIPFVTENGILRRWVSRFDIYPYLERFTKDATTKILDILEGKPDLIIGNYTDGNLVASLMANKLGITQATIAHALEKTKYEDSDIKWKEFDPKYHFSSQFTADLISMNSADFIIASTYQEIAGSKERAGQYESHMSFTVPGLYRVVSGINVFDPRFNIAAPGADDSIYFPFTAQDRRFTKFYTSIDELLYSQSENDEHIGYLVDKKKPIIFSMARLDVVKNLTGLTEWYAKNKRLRDLVNLVIVGGFFDASKSKDREEISEIKKMHSLIEKYQLKGQFRWITAQTDRTRNGELYRSIADTRGAFVQPAHYEAFGLTVIEAMSCGLVTFATNQGGPAEIIVDGVSGFHIDPSNGEESSDKIADFFEKSGMDPDYWNMFSNEGLQRINECYTWKIYANKVINMGSTYSYWRHLNKDQKLA	836

Table S2. *Cont.*

			KQRYIHSFYNLQYRNLVKTIPILSDIPEPPPLPPKPLVKPSASKGSKRTQPRLSFRLFGA	
	AtSS6	At1g73370	MSSSSQAMLQKSDSIAEKMPDALKQSRYHMKRCFASFVGGGKKLMKREHLMNEIEKCIEDSRERSKILEGLFGYILTCTQEAAVVPPFVALAARPNPGFWEYVKVNSGDLTVDEITATDYLKLKESVFDESWSKDENALEIDFGAIDFTSPRLSLSSSIGKGADYISKFISSKLGGKSDKLEPLLNYLLRLNHHGENLMINDDLNTVAKLQKSLMLAVIVVSTYSKHTPYETFAQRLKEMGFEKGWGDTAERVKETMIILSEVLEAPDNGKLDLLFSRLPTVFNVVIFSVHGYFGQQDVLGLPDTGGQVVYILDQVRALEEELLIRINQQGLGFKPQILVVTRLIPEARGTKCDQELEAIEGTKHSHILRVPFVTNKGVLRQWVSRFDIYPYLERFTQDATSKILQRLDCKPDLIIGNYTDGNLVASLMATKLGVTQGTIAHALEKTKYEDSDAKWKELDPKYHFSCQFTADLIAMNVTDFIITSTYQEIAGSKDRPGQYESHTAFTMPGLCRVVSGIDVFDPKFNIAAPGADQSVYFPYTEKDKRFTKFHPSIQELLYNEKDNAEHMGYLADREKPIIFSMARLDTVKNITGLVEWYGKDKRLREMANLVVVAGFFDMSKSNDREEKAEIKKMHDLIEKYKLKGKFRWIAAQTDRYRNSELYRCIADTKGVFVQPALYEAFGLTVIEAMNCGLPTFATNQGGPAEIIVDGVSGFHIDPNNGDESVTKIGDFFSKCRSDGLYWDNISKGGLKRIYECYTWKIYAEKLLKMGSLYGFWRQVNEDQKKAKKRYIEMLYNLQFKQLTKKVTIPEDKPLPLRLASLRNLLPKKTTNLGAGSKQKEVTETEKTKQKSKDGQEQHDVKVGEREVREGLLAADASERVKKVLESSEEKQKLEKMKIAYGQQHSQGASPVRNLFWSVVVCLYICYILKQRFFGANSAQEY	942
Pisum sativum	PsSS1	AJ012080	MATDRLTRVHSLRERLDETLTANRNEILALLSRIEAKGKGILQHHQVIAEFEEIPEENRQKLTDGAFGEVLRSTQEAIVLPPWVALAVRPRPGVWEYLRVNVHALVVENLQPAEFLKFKEELVDGSANGNFVLELDFEPFTASFPRPTLNKSIGNGVQFLNRHLSAKLFHDKESLHPLLEFLRLHSYKGKTLMLNDRIQNPDSLQHVLRKAEEYLGTVAPDTPYSEFEHRFQEIGLERGWGDTAERVLESIQLLLDLLEAPDPCTLETFLDRIPMVFNVVILSPHGYFAQDDVLGYPDTGGQVVYILDQVRALESEMLNRIKKQGLDIVPRILIITRLLPDAVGTTCGQRLEKVYGTEHCHILRVPFRDQKGIVRKWISRFEVWPYLETYTEDVAHELAKELQGKPDLIVGNYSDGNIVASLLAHKLGVTQCTIAHALEKTKYPESDIYWKKFEEKYHFSCQFTADLFAMNHTDFIITSTFQEIAGSKDTVGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADQTIYFPYTETSRRLTSFYPEIEELLYSTVENEEHICVLKDRSKPIIFTMARLDRVKNITGLVEWYGKNAKLRELVNLVVVAGDRRKESKDLEEKAEMKKMYEHIETYKLNGQFRWISSQMNRVRNGELYRVICDTKGAFVQPAVYEAFGLTVVEAMATGLPTFATLNGGPAEIIVHGKSGFHIDPYHGDRAADLLVEFFEKVKTDPSHWDKISQGGLQRIEEKYTWQIYSQRLLTLTGVYGFWKHVSNLDRLESRRYLEMFYALKYRKLAESVPLAVEE	806
	PsSS2	AJ001071	MSTHPKFTRVPSIRDRVQDTLSAHRNELISLLSRYVAQGKGILQPHNLIDELDNILGEDHATLDLKNGPFGQIINSAQEAIVLPPFVAIAVRPRPGVWEYVRVNVFELSVEQLSVSEYLSFKEELVEGKSNDNIILELDLEPFNASFPRPTRSSSIGNGVQFLNRHLSSNMFRNKDCLEPLLDFLRVHTYKGHALMLNDRIQSISKLQSALVKAEDHLSKLAPDTLYSEFEYELQGTGFERGWGDTAARVLEMMHLLLDILQAPDPSTLETFLGRVPMVFNVVILSPHGFFGQANVLGLPDTGGQVVYILDQVRALESEMLVRIKKQGLDFTPRILIVTRLIPDAKGTTCNQRLERVSGTEYTHILRVPFRSEKGILRKWISRFDVWPFLETFAEDVASEIAAELQCYPDFIIGNYSDGNLVASLLAYKMGVTQCTIAHALEKTKYPDSDIYWKKFEDKYHFSCQFTADLIAMNNADFIITSTYQEIAGTKNTIGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADMTIYFPYSDKEKRLTALHSSIEKLLYGTEQTDEYIGSLTDRSKPIIFSMARLDRVK	809

Table S2. *Cont.*

			NITGLVESYAKNSKLRELVNLVVVAGYIDVKKSSDREEIEEIEKMHDLMKQYNLNGEFRWITAQTNRARNGELYRYIADTKGAFVQPAFYEAFGLTVVEAMTCGLPTFATNHGGPAEIIEHGVSGFHIDPYHPDQASELLVDFFQRCKEDPNHWNKVSDGGLQRIYERYTWKIYSERLMTLAGVYSFWKYVSKLERRETRRYLEMFYILKFRDLANSVPIAKG	
	PsSS3	AJ311496	MASLTHSTSLRQRFDETLTAHRNEILSLLSRIEAKGKGILQHHQIIAEFEEIPEENRQKLVNGVFGEVLRSTQEAIVLVPFVALAVRPRPGVWEYLRVDVHGLVVDELSAAEYLKFKEELVEGSSNENFVLELDFEPFNASIPKPTQNKSIGNGVEFLNRHLSAKLFHGKESLQPLLEFLRLHNHNGKTIMVNDRIQNLNSLQHVLRKAEDYLIKIAPETPYSEFEHKFQEIGLERGWGDTAERVVETIQLLLDLLDGPDPGTLETFLGRIPMVFNVVILSPHGYFAQDNVLGYPDTGGQIVYILDQVRALEEEMLKRIKQQGLDITPRILIITRLLPDAVGTTCGQRLEKVYNTEHCHILRVPFRTEKGIVRKWISRFEVWPYLETFSEDVANELAKELQGKPDLIVGNYSDGNIVASLLAHKLGVTQCTIAHALEKTKYPESDIYWKKFDDKYHFSSQFTADLFAMNHTDFIITSTFQEIAGSKDTVGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADLSIYFPYTETERRLTSFHPDIEELLYSTVENEEHICVLKDRSKPIIFTMARLDRVKNITGLVECYGKNARLRELVNLVVVAGDRRKESKDLEEIAEMKKMYGLIETYKLNGQFRWISAQMDRIRNGELYRVICDTKGAFVQPAIYEAFGLTVIEAMSCGLPTFATCNGGPAEIIVHGKSGYHIDPYHGDRAAETLVEFFEKSKADPTYWDKISHGGLKRIHEKYTWQIYSDRLLTLTGVYGFWKHVTNLERRESKRYLEMFYALKYSKLAESVPLAVEE	804
	PsSS4	AF079851	MATDRLTRVHSLRERLDETLTANRNEILALLSRIEAKGKGILQHHQVIAEFEEIPEENRQKLTDGAFGEVLRSTQEAIVLPPWVALAVRPRPGVWEYLRVNVHALVVENLQPAEFLKFKEELVDGSANGNFVLELDFEPFTASFPRPTLNKSIGNGVQFLNRHLSAKLFHDKESLHPLLEFLRLHSYKGKTLMLNDRIQNPDSLQHVLRKAEEYLGTVAPDTPYSEFEHRFQEIGLERGWGDTAERVLESIQLLLDLLEAPDPCTLETFLDRIPMVFNVVILSPHGYFAQDDVLGYPDTGGQVVYILDQVRALESEMLNRIKKQGLDIVPRILIITRLLPDAVGTTCGQRLEKVYGTEHCHILRVPFRDQKGIVRKWISRFEVWPYLETYTEDVAHELAKELQGKPDLIVGNYSDGNIVASLLAHKLGVTQCTIAHALEKTKYPESDIYWKKFEEKYHFSCQFTADLFAMNHTDFIITSTFQEIAGSKDTVGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADQTIYFPYTETSRRLTSFYPEIEKLLYSTGGNEEHICVLKDRNKPIIFTMARLDRVKNITGLVEWYGKNAKLRELVNLVVVAGDRRKESKDLEEKAEMKKMYEHIETYKLNGQFRWISSQMNRVRNGELYRVICDTKGAFVQPAVYEAFGLTVVEAMATGLPTFATLNGGPAEIIVHGKSGFHIDPYHGDRAADLLVEFFEKVKTDPSHWDKISQGGLQRIEEKYTWQIYSQRLLTLTGVYGFWKHVSNLDRLESRRYLEMFYALKYRKLAESVPLAVEE	806
Citrus unshiu	CuSS1	AB022092	MAERALTRVHSLRERLDETLSAHRNEILALLSRIEGKGKGILQNHQLIAEFESISEENRKHLTEGAFGEVLRATQEAIVLAPWVALAVRPRPGVWEYIRVNVHALVVEELLVAEYLHFKEELVDGGSNGNFVLELDFEPFNASFPRPTLSKSIGNGVEFLNRHLSAKLFHDKESMHPLLEFLRVHCHKGKNMMLNDRIQNLNSLQHVLRKAEEYLTTVVPETPFSELALRFQEIGLERGWGDTAERALEMIQLLLDLLEAPDPCTLETFLGRIPMVFNVVILTPHGYFAQDDVVGYPDTGGQVVYILDQVRALEDEMLLRIKQQGLDITPQILIITRLLPDAVGTTCGQRLEKVYGTKYSDILRVPFRTEKGVVRKWISRFEVWPYLETYTEDVAVEIAKELQGKPDLIIGNYSDGNIVASLLAHKLGVTQCTIAHALEKTKYPDSDIYWKNLDDKYHFSCQFTADLIAMNHTDFIITSTFQEIAGSKDTVGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADMSIYFPYTEEKRRLKSFHPEIEELLYSDVENKEHLCVLKDRNKPILFTMARLDRVK	805

Table S2. *Cont.*

			NLTGLVEWYGKNAKLRELVNLVVVGGDRRKESKDLEEQAEMKKMYSLIDQNKLNGQFRWISSQMNRVRNGELYRYICETKGAFVQPALYEAFGLTVVEAMTCGLPTFATCKGGPAEIIVNGKSGYHIDPYHGEQAAEILVDFFEKCKADPSYWDKISLGGLKRIEEKYTWKIYSQRLLTLTGVYGFWKHVSNLDRLESRRYLEMFYALKYRKLAESVPLAVE	
	CuSS2	AB029401	MAERALTRVHSLRERLDETLSAHRNEILALLSRIEGKGKGILQNHQLIAEFESISEENRKHLTEGAFGEVLRATQEAIVLPPWVALAVRPRPGVWEYIRVNVHALVVEELLVAEYLHFKEELVDGGSNGNFVLELDFEPFNASFPRPTLSKSIGNGVEFLNRHLSAKLFHDKESMHPLLEFLRVHCHKGKNMMLNDRIQNLNSLQHVLRKAEEYLTTVAPETPFSELALRFQEIGLERGWGDTAERALEMIQLLLDLLEAPDPCTLETFLGRIPMVFNVVILTPHGYFAQDDVLGYPDTGGQVIYILDQVRALEDEMLLRIKQQGLDITPQILIITRLLPDAVGTTCGQRLEKVYGTKYSDILRVPFRTEKGVVRKWISRFEVWPYLETYTEDVAVEIAKELQGKPDLIIGNYSDGNIVASLLAHKLGVTQCTIAHALEKTKYPDSDIYWKNLDDKYHFSCQFTADLIAMNHTDFIITSTFQEIAGSKDTVGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADMSIYFPYTEEKRRLKSFHPEIEELLYSDVENKEHLCVLKDRNKPILFTMARLDRVKNLTGLVEWYGKNAKLRELVNLVVVGGDRRKESKDLEEQAEMKKMYSLIDQYKLNGQFRWISSQMNRVRNGELYRYICDTKGAFVQPALYEAFGLTVVEAMTCGLPTFATCKGGPAEIIVNGKSGYHIDPYHGEQAAEILVDFFEKCKADPSYWDKISLGGLKRIEEKYTWKIYSQRLLTLTGVYGFWKHVSNLDRLESRRYLEMFYALKYRKLAESVPLAVE	805
	CuSS3	AB022091	MAAPKLSRIPSIRERVEDTLSVHRNELVSLLSRYVAQGKGILQPHVLIDELDNIFGDDEGRQNLRDGPFSEVIKSAQEAIVLPPFVAIAVRPRPGVWEYVRVNVYELSVEQLSVSEYLHFKEELVDAAFNERFVLELDFEPFNATFPRPNRSSSIGNGVQFLNRHLSSSMFRNKDCLEPLLDFLRAHKYKGHLLMLNDRIQSISRLQSSLSKAEDHLSKLPPDTPFSQFEYVLQGMGFEKGWGDTAEHVLEMMHLLLDILQAPDPSTLEKFLGRLPMVFNVVILSPHGYFGQANVLGLPDTGGQVVYILDQVRALENEMLLRIKRQGLDISPKILIVTRLIPDAKGTTCNQRLERVSGTEHTHILRVPFRSEKGILRQWISRFDVWPYLETFTEDVGSEITAELQGFPDFIIGNYSDGNLVASLLAYKMGITQCTIAHALEKTKYPDSDIYWKKFDEKYHFSCQFTADLIAMNNADFIITSTYQEIAGTKNTVGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADMDIYFPYSEKQKRLTALHGSIEQLLFDPEQNDEHVGTLSDRSKPIVFSMARLDHVKNMTGLVECYGKNSRLRELVNLVVVAGYIDVNKSKDREEIAEIEKMHELMKTYKLDGQFRWIAAQTNRARNGELYRYIADTKGAFVQPAFYEAFGLTVVEAMTCGLPTFATCHGGPAEIIEHGASGFHIDPYHPDQAAELMADFFGKCKENPSHWKKISDGGLKRIYERYTWKIYSERLMTLAGVYGFWKYVSKLERRETRRYLEMFYILKFRDLVKSVPLASENQH	811
Citrus sinensis	CitSS1	Cs4g06850.1	MAERALTRVHSLRERLDETLSAHRNEILALLSRIEGKGKGILQNHQLIAEFESISEENRKHLTEGAFGEVLRATQEAIVLPPWVALAVRPRPGVWEYIRVNVHALVVEELLVAEYLHFKEELVDGGSNGNFVLELDFEPFNASFPRPTLSKSIGNGVEFLNRHLSAKLFHDKESMHPLLEFLRVHCHKGKNMMLNDRIQNLNSLQHVLRKAEEYLTTVVPETPFSELALRFQEIGLERGWGDTAERALEMIQLLLDLLEAPDPCTLETFLGRIPMVFNVVILTPHGYFAQDDVLGYPDTGGQVVYILDQVRALEDEMLLRIKQQGLDITPQILIITRLLPDAVGTTCGQRLEKVYGTKYSDILRVPFRTEKGVVRKWISRFEVWPYLETYTEDVAVEIAKELQGKPDLIIGNYSDGNIVASLLAHKLGVTQCTIAHALEKTKYPDSDIYWKNLDDKYHFSCQFTADLIAMNHTDFIITSTFQEIAGSKDTVGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADMSIYFPYTEEKRRLKSFHPEIEELLYSDVENKEHLCVLKDRNKPILFTMARLDRVK	805

Table S2. *Cont.*

			NLTGLVEWYGKNAKLRELVNLVVVGGDRRKESKDLEEQAEMKKMYSLIDQYKLNGQFRWISSQMNRVRNGELYRYICDTKGAFVQPALYEAFGLTVVEAMTCGLPTFATCKGGPAEIIVNGKSGYHIDPYHGEQAAEILVDFFEKCKADPSYWDKISLGGLKRIEEKYTWKIYSQRLLTLTGVYGFWKHVSNLDRLESRRYLEMFYALKYRKLAESVPLAVE	
	CitSS2	Cs4g06900.1	MFRFPPYFVFVCYSIERLGCGTYKRQQILSLLEAESNGAAIADVLNATQEAAVSSPWVAFAVRTSPGVWCYIRVNVQTVDVEEISVSKYLLFKEEIVDGRKSNGNFAFEVDFEPFRALPHPTLSNSIGHGMEFLNRHMSAKLFNDKESMQSLLEFLRVHSHMGKNMMLNEKIQDLGTLQSSLRMAEKYLSMLAPDTSYAEFEQKFQEIGLERGWGDNAEHVLGMIQLLLDLLQAPESSTLETFLGKIPRVFNVVIFTPHGYFAQDNVLGYPDTGGQVVYILDQVRALENEMLLRIKQQGLDITPRILIITRLLPDAVGTTCGQRVEKVYGTKYSDILRVPFRTEEGIVRKWISRFEVWPYLETFTEDVATEIIQELQCKPDLIIGNYSDGNIVASLLAHKLDVTQCTIAHALELTKYPDSDINWKKLDDKYHFSCQFTADLFAMNRTDFIITSTFQEIAGSKDTVGQYESHTAFSLPGLYRVVNGIDAFDPKFNIVSPGADMTIYFPYMEEKRRLKHFHSEIEELLYSPVENKEHLCVLKDSSKPILFTMARLDRVKNLTGLVEWYGKNAKLRELVNLVVVGGDRRKESKDLEEQAEMKKMYGLVDTYKLNGQFRWISSQMNRVRNGELYRYICDTKGAFVQPALYEAFGLTVVEAMTCGLPTFATCNGGPAEIIVHGKSGFHIDPYKGDQAAGILVDFFEKCKVDPGHWDEISQGGLKRIQEKYTWKIYSERLLNLSGVYGFWKHLSKLDSREKNRYLEMFYSLMYRKQVQTVPLAVDE	780
	CitSS3	Cs5g33470.1	MAAPKLSRIPSIRERVEDTLSVHRNELVSLLSRYVAQGKGILQPHVLIDELDNIFGDDEGRQNLRDGPFSEVIKSAQEAIVLPPFVAIAVRPRPGVWEYVRVNVYELSVEQLSVSEYLHFKEELVDAAFNERFVLELDFEPFNATFPRPNRSSSIGNGVQFLNRHLSSSMFRNKDCLEPLLDFLRAHKYKGHLLMLNDRIQSISRLQSSLSKAEDHLSKLPPDTPFSQFEYVLQGMGFEKGWGDTAEHVLEMMHLLLDILQAPDPSTLEKFLGRLPMVFNVVILSPHGYFGQANVLGLPDTGGQVVYILDQVRALENEMLLRIKRQGLDISPKILIVTRLIPDAKGTTCNQRLERVSGTEHTHILRVPFRSEKGILRQWISRFDVWPYLETFTEDVGSEITAELQGFPDFIIGNYSDGNLVASLLAYKMGITQCTIAHALEKTKYPDSDIYWKKFDEKYHFSCQFTADLIAMNNADFIITSTYQEIAGTKNTVGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADMDIYFPYSEKQKRLTALHGSIEQLLFDPEQNDEHVGTLSDRSKPIVFSMARLDHVKNMTGLVECYGKNSQLRELVNLVVVAGYIDVNKSKDREEIAEIEKMHELMKTYKLDGQFRWIAAQTNRARNGELYRYIADTKGAFVQPAFYEAFGLTVVEAMTCGLPTFATCHGGPAEIIEHGASGFHIDPYHPDQAAELMADFFGKCKENPSHWKKISDGGLKRIYERYTWKIYSERLMTLAGVYGFWKYVSKLERRETRRYLEMFYILKFRDLVKSVPLASENQH	811
	CitSS4	Cs5g16700.1	MSSSPSLKRSDTIADTMPDALRQSRYYMKKCFSRFVAKGKRLMKRHHLMDEVEKSIEDKIERGKVLEGLLGYILSSTQEAAVVPPNVAFAVRPNPGSWEYVKVNSEDLTVDGINVLEYLKFKETIFDQDWAKDENALELDFGAMDFSSPRLTLSSSIGNGVNYVSKFMSTRLSANSEKAKQFLDYLLALNHRGEQLMINDTLDTVDKLQAALIVAEVSISDLPKDTPYQEFQQRFKEWGFEKGWGNTAERVRETMRLFSEVLQAPDAAKLQVLFSRLPNMFNVVIFSPHGYFGQADVLGLPDTGGQVVYILDQVRALEEELLLRIKQQGLSVKPQILVVTRLIPNSKGTKCNQELEPIYDTKHSHILRIPFKTEQAILPQWVSRFDIYPYLGRFAQDATAKILDLMEGKPDLIIGNYSDGNLVASLMASKLGITQATIAHALEKSKYEDSDAKWKELDPKYHFSCQFTADLIAMNQTDFIITSTYQEIAGSKDRPGQYESHTAFTMPGLCRVVSGINVFDPKFNIAAPGADQSVYFPYTEKQKRLTSFHPDIEELLYSKEDNSEHIGYLADRKKPIIFSMARL	867

Table S2. *Cont.*

			DTVKNITGLTEWYGKNKRLRNMVNLVVVAGFFDPSKSHDREEIAEIKKMHTLIEKYQLQGQFRWIAAQTDRYRNGELYRCIADTKGAFVQPALYEAFGLTVIEAMNCGLPTFATNQGGPAEIIIDGVSGFHIDPNNGDESSNKIADFFEKCKTDAGYWNQMSAAGRQRIYECYTWKIYANKVLNMGSIYGFWRQINKEPKEAKQRYIQMFYSLLFRKLASNVPIKVPEPLQSAQTSPVESQQPAAATGIAKPQPPASAVIDKPNQQEKTAQQKKRHVRKTMTVI	
	CitSS5	Cs6g15930.1	MASATSLKRSDSIADNMPDALKQSRYHMKRCFVRYIEKGKRIMKLHDLMDELNEVIDDEDVRTQVLEGLLGYILCSTQEAVVMPPHVAFAIRPNPGFWEFVKVNSDDLSVEAITVTDFLKFKELVFDEDWAKDENALEVDFGAYEFSLPQLTLSSSIGNGISFVSKFVTAKLSGRQDCAQPLVDYLLSLDHQGEKLMINDNLNTAEKLQMALIVAEVSLSTLPKDTPYQKFELRFKEWGFEKGWGHTAERVRETMRSLSEVLQAPDPLHMEKFLSSLPILFNVVIFSPHGYFGQADVLGLPDTGGQVVYILDQVKALEEELLLRIKQQGLYIKPQIVVVTRLIPDARGTKCNQELEPIEGTKHSNILRVPFKTDKGILHRWVSRFDVYPYLEGFAQDATTMILELLGGKPDLIIGNYSDGNLVASLMASKLGITQATIAHALEKTKYEDSDVKWKELDPKYHFSCQFIADTIAMNATDFIIASTFQEIAGSKDRPGQYESHTAFTLPGLCRVVKGIDVLDPKFNIAAPGADQSVYFPYTEKQRRLTKFHPEIEELLYNKEDNNEHIGYLADRKKPIIFSMARLDVVKNLTGLTEWYGKNKRLRNLVNLVIVGAFFDPSKSKDREETAEIKKMHALMEKYQLKGQMRWIAAQSDRLRNGELYRCIADTKGAFVQPALYEAFGLTVIEAMNCGLPTFATNQGGPAEIIVDGVSGFHIDPYNGDESSDKIADFFEACKVDPTYWNKFSTEGLKRINECYTWKIYANKMLNMGCMYSFWKQLNKGQKLAKQRYIEMFYNLLFKNLVKNVPVPNEEAQQPMSEPAVKPQHSLRQARSSTNMLHF	839
	CitSS6	Cs9g03980.1	MPHSKLDSMRDRVQDTLSVHRNELVSLLSRYAGKGKGILQRHHLTEEMDDIVKEDEGMQKLSKSPFMKVLQSAQEAIILPPFVVLAVRPRPGVWEYVRVNVYELSVDRLNVAEYLKSKEELVEGQSGDNYVLELDLEPFNATFPRPTRSSSIGNGVQFLNRHLSSVMFRNKESLEPLLNFLRVHKHDGFVMMLNDRIQSISKLQSALQRAEEYLSKFPPDTPYSEFEFEIQGMGFERGWGDTAQRVSEMVHLLLDILQAPDPATLETFLGRIPMVFNVVIVSPHGYFGQANVLGLPDTGGQVVYILDQVRALENEMLLRIQNQGLDVIPKILIVTRLIPDAKGTTCNQRLERISGTEHTHILRVPFRTENGILRKWISRFDVWPYLETFAEDASNEIAAELQGVPDLIIGNYSDGNLVATLLSYKLGVTQCNIAHALEKTKYPDSDLYWRKFEEKYHFSSQFTADLTAMNNADFIITSTYQEIAGSKNNVGQYENHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADMCIYFPYSDKEKRLIALHGQIEDLLYDPKQNDEHVGILNDRSKPLIFSMARLDGVKNLTGLVECYGKSSKLRELVNLVVVGGYMDVKNSRDREEMAEIEKMHGLIKQYNLHGQFRWISAQMNRVRNGELYRYIADTRGVFVQPAFYEAFGLTVVEAMTCGLPTFATCHGGPAEIIEHGVSGFHIDPYHPDQVAELMIEFFEKCYNDPSHWNKISDGGLKRIYERYTWKIYSERLLTLAGVYGFWKYVSKLDRRETRRYLEMFYILKFRDLAKSVRLAVDEQH	808
Populus tomentosa	PtSS1	GU559727	MAERALTRVHSIRERVDETLKAHRNEIVALLTRIESKGKGILQHHQIVAEFEAIPEDTRKTLAGGAFAEVLRSTQEAIVVPPWIALALRPRPGVWEYIRLNVQALVVEELRVAEYLHFKEELVDGGCNGKFVLELDFEPFNASFPRPTLSKYIGNGVEFLNRHLSAKLFHDKESLHPLLAFLKVHCHKGKNMMLNDRIRNLDSLQYVLRKAEEFLSALKPDTPYSQFEHKFQEIGLERGWGDTAERVLEMIRLLLDLLEAPDPCTLETFLGRIPMVFNVVIMSPHGYFAQDNVLGYPDTGGQVVYILDQVRALENEMLQRIKKQGLDITPRILIITRLLPDAAGTTCGQRLEKVYGSEHCDILRVPFRDGKGMVRKWISRFEVWPYLETFTEDVAAEIAKELQGKPDLIIGNYSDGNIVASLLAHKLGVTECTIAHALEKTKYPDSDIYWKKFDEKYHFSCQFTADLFAMNHTDFIITSTFQEI	805

Table S2. *Cont.*

			AGSKDTVGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADESIYFPYTDEKRRLTSFHPEIDELLYSPVENEEHLCVLKDRNKPILFTMARLDRVKNLSGLVEWYGKNTKLRELVNLVVVGGDRRKESKDLEEQAEMKKMYSHIEKYNLNGQFRWISSQMNRVRNGELYRYICDTKGAFVQPALYEAFGLTVVEAMTCGLPTFATCNGGPAEIIVHGKSGFHIDPYHGEQAAELLVDFFEKCKVDPAHWDKISHGGLQRIQEKYTWQIYSQRLLTLTGVYGFWKHVSNLDRLESRRYMEMFYALKYRKLAESVPLTKE	
	PtSS2	GU559728	MAALTRVQSIRERLDETLKTHRNEIVALLTRIEGKGKGILQHHQIIAEFEAIPEEIRKILAGGAFSEVLRSTQEAIVLPPWVALAVRPRPGVWEYVRVNVQALVVEELRVAEYLHFKEELVDGGSNGNFVLELDFEPFSASFPRPTLSKYIGNGVEFLNRHLSAKLFHDKESLHPLLAFLKVHCHKGKNMMLNDRIQNLDSLQYVLRKAEEYLSSLKPETPYSQFEHKFQEIGLERGWGNTAERVLQMIQLLLDLLEAPDPCTLETFLGRIPMVFNVVIMSPHGYFAQDNVLGYPDTGGQVVYILDQVRALENEMLLRIKQQGLDIIPRILIITRLLPDAVGTTCGQRLEKVYGSEHCDILRVPFRDEKGMVRKWISRFEVWPYLETYTEDVAAEIAKELQGKPDLIIGNYSDGNVVASLLAHKLGVTECTIAHALEKTKYPDSDIYWKKFDEKYHFSCQFTADLFAMNHTDFIITSTFQEIAGSKDTVGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADESIYFPYTEEKLRLTSFHEEIEELLYSPVENDEHLCVLKDRSKPILFTMARLDRVKNLTGLVEWYGKNTKLRELANLVVVGGDRRKESKDIEEQAEMKKMYNHIEKYNLNGQFRWISSQMNRVRNGELYRYICDTKGAFVQPALYEAFGLTVVEAMTCGLPTFATCNGGPAEIIVHGKSGFHIDPYHGVQAAELLVDFFEKCKADPTYWDKISQGGLQRIQEKYTWKIYSQRLLTLTGVYGFWKHVSNLDHRESRRYLEMFYALKYRKLADSVPLTIE	803
Populus trichocarapa	PtrSS1	GU559729	MAERALTRVHSIRERVDETLKAHRNEIVALLTRIEGKGKGILQHHQIVAEFEAIPEDTRKTLAGGAFAEVLRSTQEAIVVPPWIALALRPRPGVWEYIRLNVQALVVEELRVAEYLHFKEELVDGGCNGNFVLELDFEPFNASFPRPTLSKYIGNGVEFLNRHLSAKLFHDKESLHPLLAFLKVHCHKGKNMMLNDRIRNLDSLQYVLRKAEEFLSTLKPDTPYSQFEHKFQEIGLERGWGDTAERVLEMIRLLLDLLEAPDPCTLETFLGRIPMVFNVVIMSPHGYFAQDNVLGYPDTGGQVVYILDQVRALENEMLQRIKKQGLDIIPRILIITRLLPDAVGTTCGQRLERVYGSEHCDILRVPFRDGKGMVRKWISRFEVWPYLETFTEDVAAEIAKELQGKPDLIIGNYSDGNIVASLLAHKLGVTECTIAHALEKTKYPDSDIYWKKFDEKYHFSCQFTADLFAMNHTDFIITSTFQEIAGSKDTVGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADESIYFPYTDEKRRLTSFHPEIDELLYSPVENEEHLCVLKDRNKPILFTMARLDRVKNLSGLVEWYGKNTKLRELVNLVVVGGDRRKESKDLEEQAEMKKMYSHIEKYNLNGQFRWISSQMNRVRNGELYRYICDTKGAFVQPALYEAFGLTVVEAMTCGLPTFATCNGGPAEIIVNGKSGFHIDPYHGEKAAELLVDFFEKCKVDPAHWDKISHGGLQRIQEKYTWQIYSQRLLTLTGVYGFWKHVSNLDRLESRRYMEMFYALKYRKLAESVPLTKE	805
	PtrSS2	GU559730	MSVLTRVQSIRERLDETLKTHRNEIVALLTRIEGKGKGILQHHQIIAEFEAIPEEIRKILAGGAFSEVLRSTQEAIVLPPWVALAVRPRPGVWEYVRVNVQALVVEELRVAEYLHFKEELVDGGSNGNFVLELDFEPFSASFPRPTLSKYIGNGVEFLNRHLSAKLFHDKESLHPLLAFLKVHCHKGKNMMLNDRIHNLDSLQYVLRKAEEYLSSLKPETPYSQFEHKFQEIGLERGWGNTAERVLQMIQLLLDLLEAPDPCTLETFLGRIPMVFNVVIMSPHGYFAQDNVLGYPDTGGQVVYILDQVRALESEMLLRIKQQGLDITPRILIITRLLPDAVGTTCGQRLEKVYGSEHCDILRVPFRDEKGMVRKWISRFEVWPYLETYTEDVAAEIAKELQGKPDLIIGNYSDGNVVASLLAHKLGVTECTIAHALEKTKYPDSDIYWKKFDEKYHFSCQFTADLFAMNHTDFIITSTFQEIAGSK	803

Table S2. *Cont.*

			DTVGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADESIYFPYTEKKLRLTSFHEEIEELLYSSVENDEHLCVLKDRNKPILFTMARLDRVKNLTGLVEWYGKNTKLRELANLVVVGGDRRKESKDIEEQAEMKKMYSHIEKYKLNGQFRWISSQMNRVRNGELYRYICDTKGAFVQPALYEAFGLTVVEAMTCGLPTFATCNGGPAEIIVHGKSGFHIDPYHGVQAAELLVDFFEKCKADPSYWDKISQGGLQRIQEKYTWKIYSQRLLTLTGVYGFWKHVSNLDHRESRRYLEMFYALKYRKLADSVPLTIE	
	PtrSS3	GU559731	MANPKLERIPSMRERVQDTLSANRNVLVSLLSRYVEQGKGILHPNNLIDELDNIVCDDAARLSLKDGPFSEVLKAAQEAIVLPPFVAVSIRPRPGVWEYVRVDVSQLNVEELTVSQYLRFKEELVDGPSNDPYVLELDFEPFNAAFPRPTRSSSIGNGVQYLNRHLSSNMFRNKDTLEPLLDFLRVHKYKGHALMLNDRIKSVSRLQSALLKAEEYISKLPSETLYTEFEYTFQGMGFERGWGDTAARVLEMMHLLLDILQAPDPSTLETFLGRVPMVFNVVILSPHGYFGQANVLGLPDTGGQIVYILDQVRALENEMLLRIQQQGLDFKPKILIVTRLIPDSKGTSCNQRLERVSGTEHTHILRVPFRSEHGILRKWISRFDVWPYLETFAEDAASEIVAELQGIPDFIIGNYSDGNLVASLLAYKMGVTQCTIAHALEKTKYPDSDIYWKKFDDKYHFSCQFTADVLAMNNADFIITSTYQEIAGTKTTVGQYESHTAFTLPGLYRVVHGINVFDTKFNIVSPGADMDIYFPYSDKQKRLTTLHGSIEKMLYDSEQTDDWIGTLTDKSKPIIFSMARLDRVKNISGLVECYGKNARLRELVNLVVVAGYIDVKKSNDREEILEIEKMHELMKKYKLDGQFRWLTAQTNRARNGELYRYIADTKGAFVQPAFYEAFGLTVVEAMTCGLPTFATCHGGPAEIIEHGVSGFHMDPYYPDQAAEFMADFFEKCKDDPSYWKKISDAGLQRIYERYTWKIYSERLMTLAGVYGFWKYVSKLERRETRRYLEMFYILKFRDLVKTVPLSIEDWH	811
	PtrSS4	GU559732	MATLKRSDSIADNMPEALKQSRYHMKKCFAKYIEKGRRTMKLQQLLDEMENVIDDQVERTRVLEGLLGDIWFSIQEAVVNPPYVAFSIRPSPGFWEYVKVNSANLSVEGITVTDYLKFKEMIYDENWAKDANALEVDFGAFDFSVPHLTLSSSIGNGLGFVSKFVTSKLSGRLENAQPLVDYLLSLNRQGEKLMINETLGTVGKLQMALIVAEVYLSGLAKDTPYQNFEISFKEWGFEKGWGDTAERVKETMRCLSEVLQAPDPMNMEKFLSRLPTVFNVVIFSPHGYFGQADVLGLPDTGGQVVYILDQVKALEEELLLRIKQQGLNVKPQIVVATRLIPDARGTTCNLEFEAIDGTKYSNILRVPFRVENRVLRQWVSRFDEVTTKILDLMEGKPDLIIGNYTDGNFAATLMAGKLGITQATIAHALEKTKYENSDVKWKELESKYHFPCQFMADIVAMNATDFIIASTYQEIAGSKDRTGQYESHAAFTLPGLCRVVSGVNVFDPKFNIAAPGADQSVYFPHTEKQSRFTQFNPDIEELLYSKVVNDEHIGYLEDKKKPIIFSMARLDTVKNLTGLTEWYGKNKRLRGLVNLVIVGGFFDPNKSKDREEMAEIKKMHELIEKYQLKGQIRWIAAQTDRKRNGELYRCIADTKGAFVQPALYEAFGLTVIEAMNCGLPTFATNQGGPSEIIVDGISGFHIDPKNGDESSNIIADFFEKCKVDPGHWNKYSLEGLKRINECYTWKIYANKLLNMGNVYSFWRQLNKEQKLAKQRYIQLFFNLKFRELVQSVPIPTEEAQTPASEPTARTQSSAR	815
	PtrSS5	GU559733	MATLKRSDSIADNMPEALKQSRYHMKRCFAKYIEKGRRTMKLQQLLDEMENVIDDQVERTRVLQGLLGDIWFSIQEAVVNPPYVALSIRPSPGFWEFVKVNSADLSVEGITATDYLKFKEMIYDENWAKDANALEVDFGAFDFSVPHLTLSSSIGNGLGFVSKFATSKLSGRLESAQPLVDYLLSLNHEGEKLMINETLSSVRKLRMALIVAEAYLSGLPKDTQYQNFETSFKAWGFEKGWGNTAERVKETMRCLSEVLQAPDPLNMENFFSRLPTVFNVVIFSPHGYFGQADVLGLPDTGGQVVYILDQVKALEDELLLRIEQQGLNIKPQIVVVTRLIPEARGTKCNQELESINGTKHSNILRVPFSIENKVLRQWVSRFDDVITKLLDLMQRKPDLIIGNYTDGNLAATLMASKLGITQATIAHALEKTKYENSDVKWKELDPKYHFSCQFMADTIAMNATDFIIASTYQEIAGSKDRPG	835

Table S2. *Cont.*

			QYESHASFTLPGLCRVVSGIDVFDPKFNIAAPGADQSVYFPYTEKQSRFTKFHPAIEELLYSKVVNDEHIGYLEDKKKPIIFSMARLDTVKNLTGLTEWYGKNKRLRGLVNLVIVGGFFDPNKSKDREEMAEITKMHGLIKKYRLNGQFRWIAAQTDRNRNGELYRCIADTKGAFVQPALYEAFGLTVIEAMNCGLPTFATNQGGPAEIIVDGISGFHIDPQNGDESSNIIADFFEKCKVDPGYWNKFAAEGLKRINECYTWKIYAKKLLNMGNMYSFWRQLNKEQKLAKQRYIQMLYNLQFRRLVVWSLSCNQEAWIRTAIILCHLTLLNMFIHNVFYLLLSEFNFSVYDH	
	PtrSS6	GU559734	MASQTALQRSETITESMPEALRQSRYHMKKCFSRFVAPGKRLMKRQHLMDEVDESIQDKNERQKVLEGLLGYILSCTQEAAVIPPFVAFAVRPNPGFWEYVKVNAEDLSVEGISVSEYLQLKEMVFDEKWANNENALELDFGAMDFSTPRLTLSSSIGNGVNYMSKFMSSKLSGSSEAAKPLLDYLLALNHQGENLMINQTLDTVAKLQEALIVAEVVVSAFPKDTPYQDFQQRLRELGFETGWGDTAERVKETMRLLSESLQAPYPMKLQLLFSRIPNMFNIVIFSPHGYFGQSDVLGLPDTGGQVVYILDQVRALEEELLLKIKHQGLGVKPRILVVTRLIPNAGGTKCNQEVEPIFGTQHSHIVRVPFKTEKGVLPQWVSRFDDAADKVLEHMDSKPDLIIGNYSDGNLVASLMARKLSITLGTIAHALEKTKYEDSDVKWKELDAKYHFSCQFTADMIAMNSADFIITSTYQEIAGSNVRPGQYESHTAFTMPGLCRVVSGINVFDPKFNIASPGADQSVYFPYTEKQKRLTSFHPAIEELLYSNEDNHEHIGYLADRKKPIIFSMARLDTVKNITGLTEWFGKNTKLRNLVNLVVVAGFFDPSKSNDREEIAEIKKMHALIEKYQLKGQFRWIAAQTDRYRNGELYRCIADTKGAFVQPALYEAFGLTVIEAMNCGLPTFATNQGGPAEILVDGISGFHIDPNNGDESSNKIADFFEKCKTDAEYWNKMSAAGLQRIYECYTWKIYANKVLNMGSVYGFWRQTNKEQKLAKQRYIEAFYNLQFNNLVGYCGQLVL	800
	PtrSS7	GU559735	MASAPVLKRSETIAESMPDALRQSRYHMRICFSRFVAPGRRLMKRQHIMDEVDKSIQDKNERQKVLEGLLGYILSSTQEAAVVPPFVAFAVRPNPGFWEYVKVNAEDLSVDGISVSEYLQFKEMIFDEKWASNENALEVDFGAMDFSTPRLTLSSSIGNGLNYMSKFMSSKLRGNSDAAKPLLDYLLALDHQGENLMINQALDSVSKLQAALIVAEVVVSAFPKDAPYQDFQQSLKRLGFEKGWGDTAERVKETMRMLSESLQAPEPVKLELLFSRIPNVFNIVIFSPHGYFGQSDVLGLPDTGGQIVYILDQVRALEEELLLKIRQQGLSVKPQILVITRLIPHAGGTKCNQEVEPIFGTKHSHIVRVPFKTEKGVLPQWVSRFDVYPYLERFAQDAADKVREHMDCKPDLLIGNYSDGNLVASLMAQKLGTTLGTIAHALEKTKYEDSDAKWKELDPKYHFSCQFTADMIAMNTADFIITSTYQEIAGSKNRPGQYESHVAFTMPGLCRVVSGINVFDPKFNIASPGADQTVYFPYTEKQKRLTSFHPAIEELLYNNEDNNEHIGYLADKKKPIIFSMARLDTVKNITGLTEWYGKNAKLRNLVNLVVVAGFFDPSKSNDREEIAEIKKMHSLIEKYQLKGQFRWIAAQSDRYRNGELYRCIADTKGAFIQPALYEAFGLTVIEAMNCGLPTFATNQGGPAEIIVDGISGFHIDPNNGDESSNKIADFVEKCKTDAEYWNKMSATGLQRIYECYTWKIYANKVLNMGSVYGFWRQMNKEQKLLKQRYIEAFYNLQFRNLVGYFRQLVT	810
Glycine max	GmSS1	Glyma.02G240400	MASAPALKRTDSVVDNMPDALRQSRYHMKRCFAKYLEKGRRIMKLHHLMEEMELVIDDKSERSQVLEGILGFILSSTQEAVVDPPYVAFAIRPNPGVWEFVKVSSEDLSVEAITPTDYLKFKERVHDEKWATDENSFEADFGAFDSQIPLLTLSSSIGNGLEFTSKFLTSKLTGKLEKTQAIVDYLLTLNHQGESLMINDSLNSAAKLQMALVVADAFLSGLSKDTAYQNFELRFKEWGFERGWGDTAGRVKETMRTLSEVLQAPDPMNLEKFLSNLPIIFNVVIFSVHGYFGQADVLGLPDTGGQVVYILDQVKSLEAELLLRIRQQGLNVKPQILVVTRLIPDARGTKCHHELEPISDTKHSHILRVPFQTDKGILRQWISRFDIYPYLERFTQDATAKILEFMEGKPDLVIGNYTDGNLVASLMARKLGITQG	840

Table S2. *Cont.*

			TIAHALEKTKYEDSDVKWKELDPKYHFSCQFMADTVAMNASDFIITSTYQEIAGSKDRPGQYESHAAFTLPGLCRVVSGINVFDPKFNIVAPGADQSVYFPYTEKEKRLSQFHPAIEDLLFSKVDNIEHIGYLADRRKPIIFSMARLDVVKNLSGLVEWYGKNKRLRNLVNLVIVGGFFDPSKSKDREEMAEIKKMHDLIDKYQLKGQFRWIAAQTNRYRNGELYRCIADTRGAFVQPALYEAFGLTVIEAMNCGLPTFATNQGGPAEIIVDGVSGFHIDPLNGEESSNKIADFFEKCKVNQSQWNVISEAGLQRINECYTWKIYANKMVNMGNIYTFWRQVNKEQKEAKQRYIQMFYNLIFKNLVKTVPAPSDEPQQPVGKQPSLKSRSTGRSQSRLQRLFGN	
	GmSS2	Glyma.03G216300	MSTQPKLGRISSIRDRVEDTLSAHRNELISLLSRYVAQGKGILQPHNLIDELDNIPGDDEAIVDLKNGPFGEIVKSAKEAIVLPPFVAIAVRPRPGVWEYVRVNVSDLSVEQLSISEYLSFKEELVDGKINENFVLELDFEPFNATFPRPTRSASIGNGVQFLNRHLSSIMFRNKDSLQPLLDFLRAHKYKGHALMINDRVQTISNLQSALAKTEDYLSKLASDTLYSEFEYVLQGMGFERGWGDTAERVLEMMHLLLDILQAPDPSTLETFLGRVPMVFNVVILSPHGYFGQANVLGLPDTGGQVVYILDQVRALENEMLLRIKKQGLDFTPRILIVTRLIPDAKGTTCNQRLERVSGTDHTHILRVPFRSESGTLRKWISRFDVWPYLETYAEDVASEIAAELQGYPDFIIGNYSDGNLVASLLAYKMGVTQCTIAHALEKTKYPDSDLYWKKFEDKYHFSCQFTADLIAMNNADFIITSTYQEIAGTKNTVGQYESHTGFTLPGLYRVVHGIDVFDPKFNIVSPGADMSIYFPYSEKQNRLTALHGSIEKLLFDPEQTDEYIGSLKDKSKPIIFSMARLDRVKNITGLVECFGKNSKLRELVNLVVVAGYIDVKKSSDREEIAEIEKMHELMKKYNLNGDFRWIAAQTNRARNGELYRYIADTQGAFIQPAFYEAFGLTVVEAMTCGLPTFATCHGGPAEIIEHGISGFHIDPYHPDQASELLVEFFQKSKEDPDHWKKISNGGLQRIYERYTWKIYSERLMTLAGVYSFWKYVSKLERRETRRYLEMFYILKFRDLANSVPLAKDDAS	812
	GmSS3	Glyma.09G073600	MANHPLTHSHSFRERFDETLTGHRNEILALLSRLEAKGKGILQHHQVVAEFEEIPEESRKKLQDGVFGEVLRSTQEAIVLPPFVALAVRPRPGVWEYLRVNVHMLVVDELRPAEYLRFKEELVEGSSNGNFVLELDFEPFNASFPRPTLNKSIGNGVEFLNRHLSAKLFHDKESMQPLLEFLRLHSYKGKTMMLNDKVQSLDSLQHVLRKAEEYLISVAPETPYSEFENRFREIGLERGWGDTAERVLEMIQLLLDLLEAPDPCTLETFLGRVPMVFNVVILSPHGYFAQDNVLGYPDTGGQVVYILDQVRALENEMLNRIKKQGLDITPRILIITRLLPDAVGTTCGQRLERVYDTEYCDILRVPFRTEKGIVRKWISRFEVWPYLETYTEDVALELAKELQAKPDLIVGNYSDGNIVASLLAHKLGVTQCTIAHALEKTKYPESDIYWKKFEEKYHFSCQFTADLFAMNHTDFIITSTFQEIAGSKDTVGQYESHTAFTLPGLYRVVHGIDPFDPKFNIVSPGADMGIYFPYTETERRLTEFHSDIEELLYSSVENEEHICVLKDRNKPIIFTMARLDRVKNITGLVEWYGKNARLRELVNLVVVAGDRRKESKDLEEKAEMKKMYGLIETYKLNGQFRWISSQMNRVRNGELYRVICDTRGAFVQPAVYEAFGLTVVEAMTCGLPTFATCNGGPAEIIVHGKSGYHIDPYHGDHAAEILVEFFEKSKADPSHWDKISQGGLKRIHEKYTWQIYSDRLLTLTGVYGFWKHVTNLERRESKRYLEMFYALKYRKLVYFFHYYTIQWLHL	810
	GmSS4	Glyma.09G167000	MASTASNSALKRSDSITDSMPEALKQSRFHMKRCFARFVASGKRLMKQQHVMDDAEKTVEDKVERKKLLDGMLGYIFSCTQEAAVVPPYIAFAVRPNPGFWEYIKVNADDLQVEGIEAVEYLKYKEMIFDEKWANDENALELDFGAIDFSTPRMVLSSSIGNGLNFTTKILTSRLSESSQNINPLLDYLLSLNYQGENLMIKDTLNTMPKLQQALKVAEAYVSALHKDTPYQKFEDRFKEWGFDKGWGNTAGRVKETMKLLSEVLESADPVKLESLFSRLPNMFNIVILSIHGYFGQADVLGLPDTGGQVVYILDQVRALEEELLHKIELQGLDVKPQILVVTRLIPDAKGTTCNQELEPVTHTKHSNILRVPFYTDKGMLH	921

Table S2. *Cont.*

			QWVSRFDIYPYLERFSQDATAKILELMEDKPDLIIGNYTDGNLVSSLMASKLGVTQATIAHALEKTKYEDSDAKWMAFDEKYHFSCQFTADIISMNAADFIITSTYQEIAGSKQKPGQYETHTAFTMPGLCRAVSGINVFDPKFNIAAPGADQSVYFPSTEKEQRLIAFHPAIEELLFSKDDNEEHIGFLEDMKKPIIFSMARLDKVKNLSGLVEWYARNKRLRSLVNLVVVGGFFNPAKSKDREETEEIKKMHFLMKEYNLKGQFRWIAAQTDRYRNSELYRCISDSKGAFVQPALYEAFGLTVIEAMNCGLPTFATNQGGPAEIIVDEVSGFHIDPYNGDESSDKIADFFEKCKIDSEHWNRMSKAGLQRINECYTWKIYAKKVLNMGSIYGFWKRLNKEQKLAKERYNHMFYNLQFRNLAKQVPIPSERPQDPTQMPKPSAPAPSRRPAAKARPKKVSEHGIVGAPLTLLTAAATPKIKDHPTTSGEGVSARTATSEQSGGGGGLFGLRWLVSIISFLCAIHYLLKNLDRLFTREQ	
	GmSS5	Glyma.13G114000	MATDRLTRVHSLRERLDETLTANRNEILALLSRIEAKGKGILQHHQVIAEFEEIPEENRQKLTDGAFGEVLRSTQEAIVLPPWVALAVRPRPGVWEYLRVNVHALVVEELQPAEYLHFKEELVDGSSNGNFVLELDFEPFNAAFPRPTLNKSIGNGVQFLNRHLSAKLFHDKESLHPLLEFLRLHSVKGKTLMLNDRIQNPDALQHVLRKAEEYLGTVPPETPYSEFEHKFQEIGLERGWGDNAERVLESIQLLLDLLEAPDPCTLETFLGRIPMVFNVVILSPHGYFAQDNVLGYPDTGGQVVYILDQVRALENEMLHRIKQQGLDIVPRILIITRLLPDAVGTTCGQRLEKVFGTEHSHILRVPFRTEKGIVRKWISRFEVWPYLETYTEDVAHELAKELQGKPDLIVGNYSDGNIVASLLAHKLGVTQCTIAHALEKTKYPESDIYWKKLEERYHFSCQFTADLFAMNHTDFIITSTFQEIAGSKDTVGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADQTIYFPHTETSRRLTSFHPEIEELLYSSVENEEHICVLKDRSKPIIFTMARLDRVKNITGLVEWYGKNAKLRELVNLVVVAGDRRKESKDLEEKAEMKKMYGLIETYKLNGQFRWISSQMNRVRNGELYRVICDTRGAFVQPAVYEAFGLTVVEAMTCGLPTFATCNGGPAEIIVHGKSGFHIDPYHGDRAADLLVDFFEKCKLDPTHWDKISKAGLQRIEEKYTWQIYSQRLLTLTGVYGFWKHVSNLDRRESRRYLEMFYALKYRKLAESVPLAAE	805
	GmSS6	Glyma.14G209900	MASAPALKRTDSVVDNMPDALRQSRYHMKRCFAKYLGKGRRIMKLHHLMEEMELVIDDKSERSQVLEGILGFILSSTQEAVVDPPYVAFAIRPYPGVWEFVKVSSEDLSVEAITPTDYLKFKERVHDEKWATDENSFEADFGAFDFQIPQLTLSSSIGNGLQFTSKFLTSKLTGKLEKTQAIVDYLLTLNHQGESLMINESLNSSAKLQMALVVADAFLSGLPKDTAYQNFELRFKEWGFERGWGDTAGRVKETMRTLSEVLQAPDPVNLEKFLSSLPIIFNVVIFSVHGYFGQADVLGLPDTGGQVVYILDQVKSLEAELLLRIKQQGLNVKPQILVVTRLIPDARGTKCHQELEPISDTKHSHILRVPFQTDKGILHQWISRFDIYPYLERFTQDATAKILEFMEGKPDLVIGNYTDGNLVASLMARKLGITQGTIAHALEKTKYEDSDVKWKELDPKYHFSCQFMADTVAMNASDFIITSTYQEIAGSKDRPGQYESHAAFTLPGLCRVVSGINVFDPKFNIAAPGADQSVYFPYTEKEKRLSQFHPAIEDLLFSKVDNIEHIGYLADRRKPIIFSMARLDVVKNLTGLVEWYGKNKRLRNLVNLVIVGGFFDPSKSKDREEMAEIKNMHDLIDKYQLKGQFRWIAAQTNRYRNGELYRCIADTRGAFVQPALYEAFGLTVIEAMNCGLPTFATNQGGPAEIIVDGVSGFHIDPLNGDESSNKIADFFEKCKMNQSQWNVISAAGLQRINECYTWKIYANKMVNMGNIYTFWRQVNKEQKEAKQRYIQMFYNLIFKNLVKTVPVPSDEPQQPVGKQPSLKSRSTGRSHSRLQRLFGN	840

Table S2. *Cont.*

	GmSS7	Glyma.15G182600	MANHPLTHSHSFRERFDETLTGHRNEILALLSRLEAKGKGILQHHQVVAEFEEIPEESRKKLQGGVFGEVLRSTQEAIVLPPFVALAVRPRPGVWEYLRVNVHMLVVDELLPAEYLRFKEELVEGSSNGNFVLELDFEPFNASFPRPTLNKSIGNGVEFLNRHLSAKLFHDKESMQPLLEFLRLHSYKGKTMMLNDKVQSLDSLQHVLRKAEEYLTSVAPETPYSEFENKFREIGLERGWGDIAERVLEMIQLLLDLLEAPDPCTLETFLGRVPMVFNVVILSPHGYFAQDNVLGYPDTGGQVVYILDQVRALENEMLNRIKKQGLDITPRILIITRLLPDAVGTTCGQRLERVYDTEYCDILRVPFRTEKGIVRKWISRFEVWPYLETYTEDVALELAKELQAKPDLIVGNYSDGNIVASLLAHKLGVTQCTIAHALEKTKYPESDIYWKKFEEKYHFSCQFTADLFAMNHTDFIITSTFQEIAGSKDTVGQYESHTAFTLPGLYRVVHGIDPFDPKFNIVSPGADMSIYFPYTETERRLTEFHPDIEELLYSSVENEEHICVLKDRNKPIIFTMARLDRVKNITGLVEWYGKNARLRELVNLVVVAGDRRKESKDLEEKAEMKKMYGLIETYKLNGQFRWISSQMNRVRNGELYRVICDTRGAFVQPAVYEAFGLTVVEAMTCGLPTFATCNGGPAEIIVHGKSGYHIDPYHGDRAAEILVEFFEKSKADPSHWDKISQGGLKRIHEKYTWQIYSDRLLTLTGVYGFWKHVTNLERRESKRYLEMFYALKYRKLAESVPLAIEE	806
	GmSS8	Glyma.15G151000	MPATSVRERVLDTLSRYRNEFISLLSRYVAGGKGILQPHDLLYEVEKLLEEDEGMQKLKDSPFVKELESAKEAIVLPPFVSIALRPRPGVWEYVRVDAFELSVDNLSVAEYLRLKEELVDGQCTDKYVLELDFEPFNVTLPRPTRSSSIGDGVQFLNRHLSSFMFRSKESLEPLLAFLRTHRYDGHAMMLNDRIYNLSKLQSSLAKAEELLSRLLPNAPYSDFEYELQGLGFERGWGDTAERVSEMVHLLLEILQAPDPNTLESFLGRIPMVFNVVVVSPHGYFGQANILGLPDTGGQLVYILDQVRALENEMLIKIQKQGLDVSPKILIVTRLIPEAKGTTCNQRLERVSGTEHSYILRVPFRTKNGILRKWISRFDMWPYLETFAEDASHEIAGELQGIPDLIIGNCSDGNLVATLLSYKLGITQCNIAHALEKTKHPDSDIYWKKYEDKYHFTCQFTADLIAMNNADFIITSTYQEIAGSKNNVGQYESYTAFTLPGLYRVVHGIDVFDPKFNIVSPGADMCIYFPYSDRERRLTSLHGSIEKLVYGAEQNEEHIGLLNDRSKPIIFSMARIDPVKNITGLVECFGKSSKLRELVNLVVVGGYIDVQKSTDIEEMREIEKMHNLIEEYNLHGQFRWIKAQMNRARNGELYRYIADVKGAFVQPALYEAFGLTVVEAMTCGLPTFATCHGGPAEIIEHGVSGFHIEPHHPDHVAAILINFFEQCQSDPGYWNKISDAGLRRIHERYTWKIYSERLLTLAGVYGFWKHVSKLEKRETRRYLEMFYILKFRDLVKSIPLAVN	802
	GmSS9	Glyma.16G217200	MASTAPNSALKRSDSITDSMPEALKQSRFHMKRCFARFVASGKRLMKQQHVMDDVEKTVEDKAERKKFLDGMLGYIFSCTQEAAVVPPYVAFAVRPNPGFWEYIKVNADDLQVEGIEAVEYLKYKEMIFDEKWANDENALELDFGAIDFSTPQMVLSSSIGNGLNFTTKILTSRLSGSSQSINPLLDYLLSLNYQGENLMIKDTLNTMPKLQQALKVAEAYVSALNKDTAYQKFEDRFKEWGFDKGWGNTAGRVKETMKLLSEVLESADPVKLESLFSRLPNMFNIVILSIHGYFGQADVLGLPDTGGQVVYILDQVRALEEELLHKIELQGLDVKPQILVVTRLIPDAKGTTCNQELEPVTNTKHSNILRVPFYTDKGMLRQWVSRFDIYPYLERFSQDATAKIFDLMEDKPDLIIGNYTDGNLVSSLMASKLGVTQATIAHALEKTKYEDSDAKWMAFDEKYHFSCQFTADIISMNAADFIITSTYQEIAGSKQKPGQYETHTAFTMPGLCRAVSGINVFDPKFNIAAPGADQSVYFPSTAKEQRLTSFHPAIEELLYSKDDNEEHIGLLEDMKKPIIFSMARLDKVKNLSGLVEWYARNKRLRSLVNLVVVGGFFNPAKSKDREETEEIKKMHFLMKEYNLKGQFRWIAAQTDRYRNSELYRCISDTKGAFVQPALYEAFGLTVIEAMNCGLPTFATNQGGPAEIIVDGVSGFHIDPYNGDESSDKIADFFEKCKTDSQHWNRMSKAGLQRINECYTWKIYAKKVLNMGSIYGFWRRLNREQKLAKERYIHMFYNLQFRNLAKQVPIPSETP	920

Table S2. *Cont.*

			QDPTQMPKPSAPAPSRRSAAKARPKKVSEHWIVGAPLTLLTAAATPKIKDHPTPSGEGVSEGTATSEQSGGGGLFGLRWLVPIIAFVCAIHYFLKNLDRLFTREQ	
	GmSS10	Glyma.17G045800	MATDRLTRVHSLRERLDETLTANRNEILALLSRIEAKGKGILQHHQVIAEFEEIPEENRQKLTDGAFGEVLRSTQEAIVLPPWVALAVRPRPGVWEYLKVNVHALVVEELQPAEYLHFKEELVDGSSNGNFVLELDFEPFNAAFPRPTLNKSIGNGVQFLNRHLSAKLFHDKESLHPLLEFLRLHSVKGKTLMLNDRIQNPDALQHVLRKAEEYLGTVPPETPYSEFEHKFQEIGLERGWGDNAERVLESIQLLLDLLEAPDPCTLETFLGRIPMVFNVVILSPHGYFAQDNVLGYPDTGGQVVYILDQVRALENEMLHRIKQQGLDIVPRILIITRLLPDAIGTTCGQRLEKVFGTEHSHILRVPFRTEKGIVRQWISRFEVWPYLETYTEDVAHELAKELQGKPDLIVGNYSDGNIVASLLAHKLGVTQCTIAHALEKTKYPESDIYWKKLEERYHFSCQFTADLFAMNHTDFIITSTFQEIAGSKDTVGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADQTIYFPPTETSRRLTSFHPEIEELLYSSVENEEHICVLKDRSKPIIFTMARLDRVKNITGLVEWYGKNAKLRELVNLVVVAGDRRKESKDLEEKAEMKKMYGLIETYKLNGQFRWISSQMNRVRNGELYRVICDTKGAFVQPAIYEAFGLTVVEAMTCGLPTFATCNGGPAEIIVHGKSGFHIDPYHGDRAADLLVDFFEKCKLDPTHWETISKAGLQRIEEKYTWQIYSQRLLTLTGVYGFWKHVSNLDRRESRRYLEMFYALKYRKLAESVPLAVE	805
	GmSS11	Glyma.19G212800	MSTQPKLGRIPSIRDRVEDTLSAHRNELISLLSRYVAQGRGILQPHNLIDELDNIPGDDQAIVDLKNGPFGEIVKSAKEAIVLPPFVAIAVRPRPGVWEYVRVNVSELSVEQLSVSEYLSFKEELVDGKINDNFVLELDFEPFNATFPRPTRSASIGNGVQFLNRHLSSIMFRNKDSLQPLLDFLRAHKYKGHALMLNDRIQTISKLQSALAKAEDYLSKLAHDTLYSEFEYVLQGMGFERGWGDTAERVLEMMHLLLDILQAPDPSTLETFLGRVPMVFNVAILSPHGYFGQANVLGLPDTGGQVVYILDQVRALENEMLLRIKKQGLDFTPRILIVTRLIPDAKGTTCNQRLERVSGTDHTHILRVPFRSESGTLRKWISRFDVWPYLETYAEDVASEIAAELQGYPDFIIGNYSDGNLVASLLAYKMGVTQCTIAHALEKTKYPDSDLYWKKFEDKYHFSCQFTADLIAMNNADFIITSTYQEIAGTKNTVGQYESHAGFTLPGLYRVVHGIDVFDPKFNIVSPGADMSIYFPYSEKQNRLTALHGSIEQLLFAPEQTDEYIGLLKDKSKPIIFSMARLDRVKNITGLVESFGKNSKLRELVNLVIVAGYIDVKKSSDREEIAEIEKMHELMKKYNLVGDFRWIAAQTNRARNGELYRYIADTQGAFVQPAFYEAFGLTVVEAMNCGLPTFATCHGGPAEIIEHGISGFHIDPYHPDQASQLLVEFFQKSKEDPSHWKKISDGGLQRIYERYTWKIYSERLMTLAGVYSFWKYVSKLERRETRRYLEMFYILKFRDLANSVPLAKDDAS	812
Malus domestica	MdSS7	MDP0000250070	MAERVLTRVQSLRERLDETLSAHRNEILALLSRIESKGKGFLQPHQLLAEFEEIPEANRQKLLDGAFGEVLKNTQEVIVLPPWVALAVRPRPGVWEYIRVNVHALVVEELRVAEYLQFKEELVDGSANGNFVLELDFEPFNASFPRPTLSKSIGNGVEFLNRHLSAKLFHDKESLHPLLKFLRVHCYEGRNLMLNNKIKDVNELQHVLRKAEDFLSAIAPETPYKDFEPKLQAIGLERGWGDTAGRVLEMIELLLDLLEAPDPCTLEKFLDQIPMVFNVVILSPHGYFAQDNVLGYPDTGGQVVYILDQVRALEAEMLKRVKQQGLDIIPRIIILTRLLPDAVGTTCGDRLEKVYGTEHSDILRVPFRDEKGAIVRRWISRFEVWPYLETYAEDAIKELSKEMHGKPDLIIGNYSDGNIVASLMALKLGVTQCTIAHALEKSKYPDSDLYWKKLDDSYHFSCQFTADLIAMNHTDFIITSTYQEIAGSKETVGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADMSVYFPYSEKEKRLTNFHPEIEELLYSQVENKEHLCVLKDRNKPIIFTMARLDRVKNITGLVEWYGKNAKLRELVNLVVVAGDRRKESKDNEEKAEMKKMYELIDTYKLNGQFRWISSQMNRVRNGELYRYICDTKGAFVQPAVYE	807

Table S2. *Cont.*

			AFGLTVVEAMTCGLPTFATCKGGPAEIIVHGKSGYHIDPYHGDQAAEILVDFFEKSKADPSHWDKISQGGLQRIYEKYTWQIYSQRLLTLTGVYGFWKHVSNLDRLESRRYLEMFYALKYSKLAASVPLAVEE	
	MdSS4	MDP0000872262	MAERVLTRVQSLRERLDETLSTQRNDFLALLSRIESKGKGFLQPHQLLAEFEAIPENNRQKLLDGAFGEVLKHTQEAIVLPPWVALAVRPRPGVWEYIRVNVHALALEELCVAEYLQFKEELVDGSSNGNFVLELDFQPFNASFPRPTLSKSIGNGVEFLNRHLSAKLFHDKESLHPLLEFLRVHCYEGRNMMLNNRIKNVNELQRVLRKAEDFLSSIVPRTPYKEFEPKLQAIGLERGWGDTAERVLEMIQLLLDLLEAPNPFTLEKFLGQIPMVFNVVILSPHGYFAQDHVLGFPDTGGQVVYILDQVRALESEMLKRIKQQGLDITPRIIILTRLLPDAVGTTCGDRLEKVYGCEHSDILRVPFRDKKGAIVRRWISRFEVWPYLETYAGDAITELSKEMQGKPDLIIGNYSDGNIVASLMAHXLGVTQCTIAHALEKSKYPDSDLYWKKLDENYHFSCQFTADLIAMNHTDFIITSTFQEIAGSKDTVGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADMNVYFPFSEKEKRLTHFHPEIEELLYGQVENIEHLCVLKDRNKPIIFTMARLDRVKNITGLVEWYGKNAKLRELVNLVVVAGDRRNESKDNEEKAELKKMYEXIDTYKLNGQLRWISSQMNRVRNGELYRYICDTRGAFVQPAVYEAFGLTVIEAMTCGLPTFATCKGGPAEIIVNGKSGYHIDPYHGDQAAEIXVDFFEKNKADPSHWDKISQGGLQRIYEKYTWQIYSERLLTLTGVYGFWKDVSNLDRLESRRYLEMFYALKFRKLAASVPLAVEE	807
	MdSS2	MDP0000160578	MAERALTRVQSLRERLDETLXTHRNEILALLSRIESKGKGFLQPHQLHAEFEAIPENNRQKLLDGAFGEVLKHTQEAVVLPPWVAFAVRPRPGVWEYIRVNVHALVLEELRVAEYLQFKEELVDGSSNGNFVLELDFQPFHASFPRPTLSKSIGKGVEFLNRHLSAKLFHDKESLHPLLEFLRVHCYEGRNMMLNNRIKNVNELERVLRKAEDFLSSXVPGTPYKEFEPKXQXIGLERGWGDTAERVLEMIQLLLDLIEAPDPFTLEKFLGQIPMVFNVVILSPHGYFAQDHVLGFPDTGGQVVYILDQVRALESEMLKRIKQQGLDITPRIIILTRLLPDAVGTTCGDRLEKVYGCEHSDILRVPFRDEKGXIVRRWISRFEVWPYLQTYAEDAIKELSKEMQGKPDLIIGNYSDGNIVASLMAHKLGVTQCTIAHALEKSKYPDSDLYWKKLDENYHFSCQFTADLIAMNHTDFIITSTFQEIAGSKDTVGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADKDVYFPYSEKEKRLTHFHPEIEELLYGQVENIEQLCVLKDRNKPIIFTMARLDRVKNITGLVEWYGKNAKLRELVNLLVVAGDRRNESKDNEEKAELKKMYELIDTYKLNGQLRWISSQMNRVRNGELYRYICDTRGAFVQPAVYEAFGXTVIEAMTCGLPTFATCKGGPAEIIVNGISGYHIDPYHGDQAAEILVDFFEKSKADPSHWDKISQGGLQRIYEKYTWQIYSERLLTLTGVYGFWKDVSNLDRLECRRYLEMFYALKFRKLAASVPLAVE	806
	MdSS8	MDP0000132527	MAERALTRVQSLRERLDETLXTHRNEILALLSRIESKGKGFLQPHQLHAEFEAIPENNRQKLLDGAFGEVLKHTQEAVVLPPWVAFAVRPRPGVWEYIRVNVHALVLEELRVAEYLQFKEELVDGSSNGNFVLELDFQPFHASFPRPTLSKSIGKGVEFLNRHLSAKLFHDKESLHPLLEFLRVHCYEGRNMMLNNRIKNVNELERVLRKAEDFLSSXVPGTPYKEFEPKXQXIGLERGWGDTAERVLEMIQLLLDLIEAPDPFTLEKFLGQIPMVFNVVILSPHGYFAQDHVLGFPDTGGQVVYILDQVRALESEMLKRIKQQGLDITPRIIILTRLLPDAVGTTCGDRLEKVYGCEHSDILRDAIXELSKEMQGKPDLIIGNYSDGNIVASLMAHXLGVTQCTIAHALEKSKYPDSDLYWKKLDENYHFSCQFTADLIAMNHTDFIITSTFQEIAGSKDTVGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADXXVYFPXSEKEKRLTHFHPEIEELLYGQVENIEXLCVLKDRNKPIIFTMARLDRVKNITGLVEWYGKNAKLRELVNLVVVAGDRRNESKDNEEKAELKKMYEXIDTYKLNGQLRWISSQMNRVRNGELYRYICDTRGAFVQPAVYEAFGLTVIEAMTCGLPTFATCKGGPAEIIVNGK	778

Table S2. *Cont.*

			SGYHIDPYHGDQAAEIXVDFFEKNKADPSHWDKISQGGLQRIYEKYTWQIYSERLLTLTGVYGFWKDVSNLDRLESRRYLEMFYALKFRKLAASVPLAVEE	
	MdSS5	MDP0000126946	MANRPKFTRALSLRERVEDTLSDHRNELVALLSRYLDQGKRILQPHDLIDQLDIVIGDDEAKRQLKTGPFSEVLKSAQEAIILPPYVALAVRPRPGVWDYVRVNVYELSVEELTVSEYLRFKEELVDGESSDKYALELDFEPFNAAFPRPTRSSSIGNGVQFLNRHLSSIMFRNKESLEPLLDFLKAHKYKGHPLMLNDRIQSVSKLQSALAKAEDHLSKLQPETPYSEFEYLFQGMGFERGWGDTAVHVLEMMHLLLDILQAPDPSILETFLGRIPMMFNVVILSPHGYFGQANVLGLPDTGGQASQYSSFILVLFHYLFYLYSGGIVIFYXEIVYILDQVRALEKEMLERIRLQGLDFTPRILIVTRLIPEAKGTTCNQRLERISGTEHTHILRVPFRSEKGILRKWISRFDVWPYLETFAEDAAGEIIAELQGYPDFIIGNYSDGNLVASLLAYKMGVTQCTIAHALEKTKYPDSDIYWKKFEEKYHFSTQFTADLIAMNNADFIITSTYQEIAGTKDTVGQYESHSSYTLPGQYRVVHGINVFDPKFNIVSPGADMAIYFPYSEKQKRLTSLHGSLEELLYNPDQNDVHIGTLSDRSKPIIFSMARLDQVKNMTGLVECYAKCSKLRDLANLVIVAGYIDAKKSQDREEIAEIEKMHNLMTEYKLDGQFRWISXQTNRVSNGELYRYIADTRGAFAQPAFYEAFGLTVVEAMTCGLPTFATVHGGPAEIIEHGVSGFHIDPYHPEKAAALMADFFQRCKEDPSYWNTISDAGLQRIYEKYTWKIYSERLMTLAGVYGFWKYVSKLERRETRRYLEMFYILKFRDLAKSVPEAIDDAH	841
	MdSS1	MDP0000252802	MAERALTRVQSLRERLDETLFTHRNEILALLSRIESKGKGFLQPHQLHAEFEAIPENNRQKLLDGAFGEVLKHTQEAVVLPPWVAFAVRPRPGVWEYIRVNVHALVLEELRVAEYLQFKEELVDGSSNGNFVLELDFQPFHASFPRPTLSKSIGKGVEFLNRHLSAKLFHDKESLHPLLEFLRVHCYEGRNMMLNNRIKNVNELERVLRKAEDFLSSVVPGTPYKEFEPKMQVIGLERGWGDTAERVLEMIQLLLDLIEAPDPFTLEKFLGQIPMVFNVVILSPHGYFAQDHVLGFPDTGGQVVYILDQVRALESEMLKRIKQQGLDITPRIIILTRLLPDAVGTTCGDRLEKVYGCEHSDILRVPFRDEKGAIVRRWISRFEVWPYLQTYAEDAIKELSKEMQGKPDLIIGNYSDGNIVASLMAHKLGVTQCTIAHALEKSKYPDSDLYWKKLDENYHFSCQFTADLIAMNHTDFIITSTFQEIAGSKDTVGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADKDVYFPYSEKEKRLTHFHPEIEELLYGQVENIEQLCVLKDRNKPIIFTMARLDRVKNITGLVEWYGKNAKLRELVNLLVVAGDRRNESKDNEEKAELKKMYELIDTYKLNGQLRWISSQMNRVRNGELYRYICDTRGAFVQPAVYEAFGLT	679
	MdSS6	MDP0000212593	MASTSPPSKRSDTIAETMPEALRESRFHMKKCFASFGTGKRLMKPQHIMEELEKSIEDRHERSKVLEGLLGYILSRTQEAAVVPPYVAFAVRPNPGFSEFVKVNADDLTVDGISATEYLKFKEMIFDESWANDENALELDFGAIDFSTPRMTLPSSIGNGLNFVLKSISSRLSTHASCSDYAKSLLDYLLRLNYHGENLMINESLDTVAKLQTALIQAEVLVSTLPKTTPFPSFEQRLKVLGFEKGWGDTAERVGETMRLLSEVFQAPDSVMLESLFSRLPNTFNIVIFSPHGYFGQSDVLGLPDTGGQVVYILDQVRALEEELLLRIKQQGLAVKPQILVVTRLIPDARGTKCNQELEAIIDTKHSHILRVPFRTDKGVLHQWDATSKILQHMECKPDLIIGNYSDGNLVASLIASKLGITQGTIAHALEKTKYEDSDAKWKEFDPKYHFSCQFTADIISMNCADFVITSTFQEIAGGKDRPGQYESHTAFTMPGLYRVVSGIDVFDPKFNIAAPGADQSVYFPYSEKQRRFTKFQPAIEELLYTKEENDEHIGFLADKKKPIIFSMARLDTVKNLTGLVEWFGKNKRLRNSVNLVIVGGFFDPSKSKDREEIAEIKKLHALVQAYQLSGQFRWIAAQTDRYRNGELYRCIADTKGAFVQPALYEAFGLTVIEAMNCGLPTFATNQGGPAEIIVDGVSGFHIDPNNGDESSNKIADFFEKCKTDGEYW	883

Table S2. *Cont.*

			KKMSAAGLQRINECYTWKIYANKMLNMGSTYGFWRQLRDDQKLAKETYIHMFYNLLFRKLAKNVAVPSVGYEKPAPRAVTAAVDQPTTAAASKPPQPPAAPTSAVPQLTPRVRDEGRELSQPRSRSRARCLWNCCCVILGFLIIXYYKIRNMYN	
	MdSS3	MDP0000138004	MASAAAIKGSESIADNMPDARRQSRYHMKRCFAKYXEKGRRIIKLHHLMSEMETVIDDKAERTQVLEGVLGYILCSTQEAVVIPPHVVFSIRPNPGYWEFVKVSSEDLSIEGITVRDFLKYKETLYDENWSNDENALEVDFRAIDFSTPHLTLSSSIGNGINYVTKFTTSKLAGKLENAQPLVDYLLSLNHQGEQLILNETLNTASKLQAALIVTDVHLSALPKDTPFQNFELRFKEWGFEKGWGDTAERTKETMGILAEVLQAPDPLIMDRFFSRLPTIFNVVIFSPHGYFGQADVLGLPDTGGQVVYILDQVKALEEELLVRIKQQGLTVKPQILVVTRLIPEARGTKCNQELEPINGTKYSNILRVPFRTEKGILRRWDATAKILDLMEGKPDLIIGNYTDGNLVASLMANKLGITQATIAHALEKTKYEDSDINWKXLDPKYHFSCQFLADTISMNATDFVIASTYQEIAGSKDRPGQYESHTAFTXPGLCRVVSGINVFDPKFNIAAPGADQSVYFPYAEKQKRLTSFHPAIEELLFSKEDXNEHIGFLVDRKKPIIFSMARLDIVKNITGLVEWYGKNKRLXNLVNLVVVGGFFDPSKSKDREEIAEIKKMHTLIEKYXLRGQIRWIAAQTDRNRNGELYRCIADTRGAFVQPALYEAFGLTVIEAMNCGLPTFATNQGGPAEIIVDGISGFHIDPNNGDEASNKIADFFEKSKTDAAYWDRISKAGLQRIYECYTWKIYANKVLNMGSTYTFWRQLNKEQKQAKQRYIQMFFSLQYRNLVKNVPIPSDETEQPVVPKPTAKPKTTLRHVQLS	819
	MdSS9	MDP0000277711	SNDEHVLEVDFRAIDFSTPHLTLSSSVGNGIDYVTKFTTSRLAGKLENAQPLADYLLSLNHQGEQLILNETLNTASKLQAALIVTEVYLSDLPKDTPFQNFELSFKEWGFEKGWGDTAERTKETMKILLEVLQAPDPLNMDRFFSRLPTIFNVVIFSPHGYFGQADVLGLPDTGGQVVYILDQVKAMEEELTLRIKQQGLTVKPQILVVTRLIPEARGTKCNQELEPINGTKYSNILRVPFRTEKGILRRWVSRFDIYPYLELFTQACFPSIFKFILLECSIIDFVPYDATAKILNLMEGKPDLIIGNYTDGNLVASLMANKLGITQATIAHALEKTKYEDSDINWKELDPKYHFSCQFLADTISMNATDFVIASTYQEIAGSKDRPGQYESHTAFTLPGLCRVVSGINVFDPKFNIAAPGADQSVYFPYSDKXKRLTSFYPAIEELLFSKEDXSEHLGFLVDRKKPIIFSMARLDIVKNITGLVEWYGKNKRLRNLVNLVVVGGFFDPSKSKDREEIAEIKKMHTLIEKYQLRGQIRWIAAQTDRNRNGELYRCIADTRGAFVQPALYEAFGLTVIEAMNCGLPTFATNQGGPAEIIVDGVSGFHIDPNNGDEASKKIADFFENSKTDVAYWDRFSKAGLQRIYECYTWKIYANKVLNMGSTYTFWRQLNKEQKQAKQRYIQMFFNLQYRNXVKNVPVPXDEPEQPQTTSRHHKALTVSIAKVVEVVHHYDKDCIPLKYADNMLAYIQSSKTNKTCIRRLTIPKQMKSPVYIYYQLDHFYQNHRRYVKSRSDKQLRSKSNENKTDDCAPERYTTKGVIVPCGLVAWSLFNDTYKFSVNNKQLGVSKKDITWKSDQKNKFGSDVYPKNFQSEGLIGGAKLNSSIPLSEQEDLMVWMRTAALPTFRKLYGRIEVDLEADAVVTVTIENNYNTYSFRGNKKLVLSTASWIGGKNYLLGVAYLTVGGLCLFLALAFLLLYLIKPRYVNYFTGHTVCNDQLKLDSILDNYGKFTLVFLLKWINSSTKPIFSGLLSLYIEHNRQCCIYAQAXTEMCLKLFRPFCAGLLGIYRTCLGTGVHQEDTYTRSPSMHLSIRFDLFWDNLFCH	1102
	MdSS10	MDP0000195934	MASAAAIKRSDSIADTMPDALRQSRYHMKRCFAKYIEQGRRIMKLHHLMSEMETVIDDKAERTQVLGGVLGYILCSTQEAVVVPPHVVFSIRLNPGYWEFVKVSSEDLSVEAITVRDFLKYKEALYDEKWSNDEHVLEVDFRAIDFSTPHLTLSSSIGNGIEYVTKFTTSKLAGKLENAQPLVDYLLXLNHQGEQLILNETLNTASKLQAALIVTEVYLSTLPKDTPFQNFELRFKEWGFEKGWGDTAERTKETMKILSEVLQAPDPLNMDRFFSRLPIIFNVVIFSPHGYFGQADVLGLPDTGGQVVYILDQVKAMEEELTLRIKQQGLTVKPQILVV	502

Table S2. *Cont.*

			TRLIPEARGTKCNQELEPIYGTKYSNILRVPFRTEKGILRRWDATAKILDLMEGKPDLIIGNYTDGNLVASLMANKLGITQATIAHALEKTKYENSDINWKELDPKYHFSCQFLADTISMNATDFVIASTYQEIAGSKDRPGQYESHTAFTLPGLCRVVSGIN	
Solanum tuberosum	StSS1	M18745	MAERVLTRVHSLRERVDATLAAHRNEILLFLSRIESHGKGILKPHELLAEFDAIRQDDKNKLNEHAFEELLKSTQEAIVLPPWVALAIRLRPGVWEYIRVNVNALVVEELSVPEYLQFKEELVDGASNGNFVLELDFEPFTASFPKPTLTKSIGNGVEFLNRHLSAKMFHDKESMTPLLEFLRAHHYKGKTMMLNDRIQNSNTLQNVLRKAEEYLIMLPPETPYFEFEHKFQEIGLEKGWGDTAERVLEMVCMLLDLLEAPDSCTLEKFLGRIPMVFNVVILSPHGYFAQENVLGYPDTGGQVVYILDQVPALEREMLKRIKEQGLDIIPRILIVTRLLPDAVGTTCGQRIEKVYGAEHSHILRVPFRTEKGIVRKWISRFEVWPYMETFIEDVAKEISAELQAKPDLIIGNYSEGNLAASLLAHKLGVTQCTIAHALEKTKYPDSDIYWKKFDEKYHFSSQFTADLIAMNHTDFIITSTFQEIAGSKDTVGQYESHMAFTMPGLYRVVHGINVFDPKFNIVSPGADINLYFSYSETEKRLTAFHPEIDELLYSDVENDEHLCVLKDRTKPILFTMARLDRVKNLTGLVEWYAKNPRLRGLVNLVVVGGDRRKESKDLEEQAEMKKMYELIETHNLNGQFRWISSQMNRVRNGELYRYIADTKGAFVQPAFYEAFGLTVVEAMTCGLPTFATNHGGPAEIIVHGKSGFHIDPYHGEQAADLLADFFEKCKKDPSHWETISMGGLKRIEEKYTWQIYSESLLTLAAVYGFWKHVSKLDRLEIRRYLEMFYALKYRKMAEAVPLAAE	805
	StSS2	AY205084	MAERVLTRVHSLRERLDATLAAHRNEILLFLSRIESHGKGILKPHQLLAEFESIHKEDKDKLNDHAFEEVLKSTQEAIVLPPWVALAIRLRPGVWEYVRVNVNALIVEELTVPEFLQFKEELVNGTSNDNFVLELDFEPFTASFPKPTLTKSIGNGVEFLNRHLSAKMFHDKESMTPLLEFLRVHHYKGKTMMLNDRIQNLYTLQKVLRKAEEYLTTLSPETSYSAFEHKFQEIGLERGWGDTAERVLEMICMLLDLLEAPDSCTLEKFLSRIPMVFNVVILSPHGYFAQENVLGYPDTGGQVVYILDQVPALEREMLKRIKEQGLDIKPRILIVTRLLPDAVGTTCGQRLEKVFGTEHSHILRVPFRTEKGIVRKWISRFEVWPYMETFIEDVGKEITAELQAKPDLIIGNYSEGNLAASLLAHKLGVTQCTIAHALEKTKYPDSDIYLNKFDEKYHFSAQFTADLIAMNHTDFIITSTFQEIAGSKDTVGQYESHMAFTMPGLYRVVHGIDVFDPKFNIVSPGADVNLYFPYSEKEKRLTTFHPEIEDLLFSDVENEEHLCVLKDRNKPIIFTMARLDRVKNLTGLVEWYAKNPRLRELVNLVVVGGDRRKESKDLEEQAEMKKMYELIKTHNLNGQFRWISSQMNRVRNGELYRYIADTRGAFVQPAFYEAFGLTVVEAMSCGLPTFATNQGGPAEIIVHGKSGFQIDPYHGEQAADLLADFFEKCKVDPSHWEAISEGGLKRIQEKYTWQIYSDRLLTLAAVYGFWKHVSKLDRLEIRRYLEMFYALKFRKLAQLVPLAVE	805
	StSS3	STU24088	MAERVLTRVHSLRERLDATLAAHRNEILLFLSRIESHGKGILKPHQLLAEFESIHKEDKDKLNDHAFEEVLKSTQEAIVLPPWVALAIRLRPGVWEYVRVNVNALIVEELTVPEFLQFKEELVNGTSNDNFVLELDFEPFTASFPKPTLTKSIGNGVEFLNRHLSAKMFHDKESMTPLLEFLRVHHYKGKTMMLNDRIQNLYTLQKVLRKAEEYLTTLSPETSYSAFEHKFQEIGLERGWGDTAERVLEMICMLLDLLEAPDSCTLEKFLGRIPMVFNVVILSPHGYFAQENVLGYPDTGGQVVYILDQVPALEREMLKRIKEQGLDIKPRILIVTRLLPDAVGTTCGQRLEKVFGTEHSHILRVPFRTEKGIVRKWISRFEVWPYMETFIEDVGKEITAELQAKPDLIIGNYSEGNLAASLLAHKLGVTQCTIAHALEKTKYPDSDIYLNKFDEKYHFSAQFTADLIAMNHTDFIITSTFQEIAGSKDTVGQYESHMAFTMPGLYRVVHGIDVFDPKFNIVSPGADVNLYFPYSEKEKRLTTFHPEIEDLLFSDVENEEHLCVLKDRNKPIIFTMARLDRVKNLTGLVEWYAKNPRLRELVNLVVVGGDRRKESKDLEEQAEMKKMYE	805

Table S2. *Cont.*

			LIKTHNLNGQFRWISSQMNRVRNGELYRYIADTRGAFVQPAFYEAFGLTVVEAMSCGLPTFATNQGGPAEIIVHGKSGFQIDPYHGEQAADLLADFFEKCKVDPSHWEAISEGGLKRIQEKYTWQIYSDRLLTLAAVYGFWKHVSKLDRLEIRRYLEMFYALKFRKLAQLVPLAVE	
	StSS4	STU24087	MAERVLTRVHSLRERVDATLAAHRNEILLFLSRIESHGKGILKPHELLAEFDAIRQDDKNKLNEHAFEELLKSTQEAIVLPPWVALAIRLRPGVWEYIRVNVNALVVEELSVPEYLQFKEELVDGASNGNFVLELDFEPFTASFPKPTLTKSIGNGVEFLNRHLSAKMFHDKESMTPLLEFLRAHHYKGKTMMLNDRIQNSNTLQNVLRKAEEYLIMLPPDTPYFEFEHKFQEIGLEKGWGDTAERVLEMVCMLLDLLEAPDSCTLEKFLGRIPMVFNVVILSPHGYFAQENVLGYPDTGGQVVYILDQVPALEREMLKRIKEQGLDIIPRILIVTRLLPDAVGTTCGQRIEKVYGAEHSHILRVPFRTEKGIVRKWISRFEVWPYMETFIEDVAKEISAELQAKPDLIIGNYSEGNLAASLLAHKLGVTQCTIAHALEKTKYPDSDIYWKKFDEKYHFSSQFTADLIAMNHTDFIITSTFQEIAGSKDTVGQYESHMAFTMPGLYRVVHGINVFDPKFNIVSPGADINLYFSYSETEKRLTAFHPEIDELLYSDVENDEHLCVLKDRTKPILFTMARLDRVKNLTGLVEWYAKNPRLRGLVNLVVVGGDRRKESKDLEEQAEMKKMYELIETHNLNGQFRWISSQMNRVRNGELYRYIADTKGAFVQPAFYEAFGLTVVEAMTCGLPTFATNHGGPAEIIVHGKSGFHIDPYHGEQAADLLADFFEKCKREPSHWETISTGGLKRIQEKYTWQIYSERLLTLAAVYGFWKHVSKLDRLEIRRYLEMFYALKYRKMAEAVPLAAE	805
	StSS5	AJ537575	MAERVLTRVHSLRERVDATLAAHRNEILLFLSRIESHGKGILKPHELLAEFDAIRQDDKNKLNEHAFEELLKSTQEAIVLPPWVALAIRLRPGVWEYIRVNVNALVVEELSVPEYLQFKEELVDGASNGNFVLELDFEPFTASFPKPTLTKSIGNGVEFLNRHLSAKMFHDKESMTPLLEFLRAHHYKGKTMMLNDRIQNSNTLQNVLRKAEEYLIMLSPDTPYFEFEHKFQEIGLEKGWGDTAERVLEMVCMLLDLLEAPDSCTLEKFLGRIPMVFNVVILSPHGYFAQENVLGYPDTGGQVVYILDQVPALEREMLKRIKEQGLDIIPRILIVTRLLPDAVGTTCGQRIEKVYGAEHSHILRVPFRTEKGIVRKWISRFEVWPYMETFIEDVAKEISAELQAKPDLIIGNYSEGNLAASLLAHKLGVTQCTIAHALEKTKYPDSDIYWKKFDEKYHFSSQFTADLIAMNHTDFIITSTFQEIAGSKDTVGQYESHMAFTMPGLYRVVHGINVFDPKFNIVSPGADINLYFSYSETEKRLTAFHPEIDELLYSDVENDEHLCVLKDRTKPILFTMARLDRVKNLTGLVEWYAKNPRLRGLVNLVVVGGDRRKESKDLEEQAEMKKMYELIETHNLNGQFRWISSQMNRVRNGELYRYIADTKGAFVQPAFYEAFGLTVVEAMTCGLPTFATNHGGPAEIIVHGKSGFHIDPYHGEQAADLLADFFEKCKKEPSHWETISTGGLKRIQEKYTWQIYSERLLTLAAVYGFWKHVSKLDRLEIRRYLEMFYALKYRKMAEAVPLAAE	805
Lycopersicon esculentum	LeSS1	NP_001300839.1	MAERVLTRVHRLRERVDATLCAHRNEILLFLSRIESHGKGILKPHELLAEFDAIRQDDKDKLNEHAFEELLKSTQEAIVLPPWVALAIRLRPGVWEYVRVNVNALVVEELSVPEYLQFKEELVDGASNGNFVLELDFEPFTASFPKPTLTKSIGNGVEFLNRHLSAKMFHDKESMAPLLEFLRAHHYKGKTMMLNDRIHNSNTLQNVLRKAEEYLIMLPPETPFFEFEHKFQEIGLEKGWGDTAERVLEMVCMLLDLLEAPDSCTLEKFLGRIPMVFNVVILSPHGYFAQENVLGYPDTGGQVVYILDQVPALEREMLKRIKEQGLDIIPRILIVTRLLPDAVGTTCGQRLEKVYGTEHSHILRVPFGTEKGIVRKWISRFEVWPYMETFIEDVAKEISAELQAKPDLIIGNYSEGNLAASLLAHKLGVTQCTIAHALEKTKYPDSDIYWKKFDEKYHFSSQFTADLIAMNHTDFIITSTFQEIAGSKDTVGQYESHMAFTMPGLYRVVHGINVFDPKFNIVSPGADINLYFPYSESEKRLTAFHPEIDELLYSDVENDEHLCVLKDRTKPILFTMARLDRVKNLTGLVEWYAKNPRLRGLVNLVVVGGDRRKESKDLEEQAEMKK	805

Table S2. *Cont.*

			MYELIETHNLNGQFRWISSQMNRVRNGELYRYIADTKGAFVQPAFYEAFGLTVVEAMTCGLPTFATNHGGPAEIIVHGKSGFHIDPYHGEQAADLLADFFEKCKKEPSHWETISTGGLKRIQEKYTWQIYSERLLTLAAVYGFWKHVSKLDRLEIRRYLEMFYALKYRKMAEAVPLAAE	
	LeSS2	NP_001234804.2	MAERVLTRVHRLRERVDATLAAHRNEILLFLSRIESHGKGILKPHELLAEFDAIRQDDKDKLNEHAFEELLKSTQEAIVLPPWVALAIRLRPGVWEYVRVNVNALVVEELSVPEYLQFKEELVDGASNGNFVLELDFEPFTASFPKPTLTKSIGNGVEFLNRHLSAKMFHDKESMAPLLEFLRAHHYKGKTMMLNDRIHNSNTLQNVLRKAEEYLIMLPPETPFFEFEHKFQEIGLEKGWGDTAERVLEMVCMLLDLLEAPDSCTLEKFLGRIPMVFNVVILSPHGYLAQENVLGYPDTGGQVVYILDQVPALEREMLKRIKEQGLDIIPRILIVTRLLPDAVGTTCGQRLEKVYGTEHSHILRVPFRTEKGIVRKWISRFEVWPYMETFIEDVAKEISAELQAKPDLIIGNYSEGNLAASLLAHKLGVTQCTIAHALEKTKYPDSDIYWKKFDEKYHFSSQFTADLIAMNHTDFIITSTFQEIAGSKDTVGQYESHMAFTMPGLYRVVHGINVFDPKFNIVSPGADINLYFPYSESEKRLTAFHPEIDELLYSDVENDDHLCVLKDRTKPILFTMARLDRVKNLTGLVEWYAKNPRLRGLVNLVVVGGDRRKESKDLEEQAEMKKMYELIETHNLNGQFRWISSQMNRVRNGELYRYIADTKGAFVQPAFYEAFGLTVVEAMTCGLPTFATNHGGPAEIIVHGKSGFHIDPYHGEQAADLLADFFEKCKKEPSHWETISTGGLKRIQEKYTWQIYSERLLTLAAVYGFWKHVSKLDRLEIRRYLEMFYALKYRKMAEAVPLAAE	805
	LeSS3	NP_001300840.1	MAQRVLTRVHSLRERLDATLDAHRNEILLFLSRIESHGKGILKPHQLLAEFESIQKEDKDKLNDHAFEEVLKSTQEAIVLPPWVALAIRLRPGVWEYVRVNVNALSVEELTVPEFLQFKEELVNGTSSDNFVLELDFEPFTASFPKPTLTKSIGNGVEFLNRHLSAKMFHDKESMTPLLEFLRVHHYNGKSMMLNDRIQNLYTLQKVLRKAEEYLTTLSPETSYSSFEHKFQEIGLERGWGDTAERVLEMICMLLDLLEAPDSCTLEKFLSRIPMVFNVVIPSPHGYFAQENVLGYPDTGGQVVYILDQVPALEREMLKRIKEQGLDIKPRILIVTRLLPDAVGTTCGQRLEKVFGTEHSHILRVPFRTEKGIVRKWISRFEVWPYMETFIEDVGKEITAELQAKPDLIIGNYSEGNLAASLLAHKLGVTQCTIAHALEKTKYPDSDIYLNKFDEKYHFSAQFTADLIAMNHTDFIITSTFQEIAGSKDTVGQYESHMAFTMPGLYRVVHGIDVFDPKFNIVSPGADVNLYFPYSEKEKRLTTFHPEIEDLLFSDVENEEHLCVLKDRNKPIIFTMARLDRVKNLTGLVEWYAKNPRLRELVNLVVVGGDRRKESKDLEEQAEMKKMYELIKTHNLNGQFRWISSQMNRVRNGELYRYIADTRGAFVQPAFYEAFGLTVVEAMSCGLPTFATNQGGPAEIIVHGKSGFQIDPYHGEQAADLLAEFFEKCKVDPSHWEAISKGGLKRIQEKYTWQIYSDRLLTLAAVYGFWKHVSKLDRLEIRRYLEMFYALKFRKLAELVPLAVE	805
	LeSS4	NP_001300841.1	MAQRVLTRVHSLRERLDATLDAHRNEILLFLSRIESHGKGILKPHQLLAEFESIQKEDKDKLNDHAFEEVLKSTQEAIVLPPWVALAIRLRPGVWEYVRVNVNALSVEELTVPEFLQFKEELVNGTSSDNFVLELDFEPFTASFPKPTLTKSIGNGVEFLNRHLSAKMFHDKESMTPLLEFLRVHHYNGKSMMLNDRIQNLYTLQKVLRKAEEYLTTLSPETSYSSFEHKFQEIGLERGWGDTAERVLEMICMLLDLLEAPDSCTLEKFLSRIPMVFNVVILSPHGYFAQENVLGYPDTGGQVVYILDQVPALEREMLKRIKEQGLDIKPRILIVTRLLPDAVGTTCGQRLEKVFGTEHSHILRVPFRTEKGIVRKWISRFEVWPYMETFIEDVGKEITAELQAKPDLIIGNYSEGNLAASLLAHKLGVTQCTIAHALEKTKYPDSDIYLNKFDEKYHFSAQFTADLIAMNHTDFIITSTFQEIAGSKDTVGQYESHMAFTMPGLYRVVHGIDVFDPKFNIVSPGADVNLYFPYSEKEKRLTTFHPEIEDLLFSDVENEEHLCVLKDRNKPIIFTMARLDRVKNLTGLVEWYAKNPRLRELVNLVVVGGDRRKESKDLEEQAEMKKMYE	805

Table S2. *Cont.*

			LIKTHNLNGQFRWISSQMNRVRNGELYRYIADTRGAFVQPAFYEAFGLTVVEAMSCGLPTFATNQGGPAEIIVHGKSGFQIDPYHGEQAADLLAEFFEKCKVDPSHWEAISKGGLKRIQEKYTWQIYSDRLLTLAAVYGFWKHVSKLDRLEIRRYLEMFYALKFRKLAELVPLAVE	
Pyrus bretschneideri Redh.	PbSS1	Pbr035996.1	MAERVLTRVQSLRERLDETLSTQRNDFLALLSRIESKGKGFLQPHQLLAEFEAIPENNRQKLLDGAFGEEAIVLPPWVALAVRPRPGVWEYIRVNVHALALEELCVAEYLQLKEELVDRSSNGNFVLELDFQPFNASFPRPTLSKSIGNGVQFLNRHLSAKLFHDKESLHPLLEFLRVHCYEGRNMMLNNRIKNVNELQRVLRKAEDFLSSIVPRTPYKEFEPKLQAIGLERGWGDTAERVLEMIQLLLDLLEAPNPFTLEKFLGQIPMVFNVVILSPHGYFAQDHVLGFPDTGGQVVYILDQVRALESEMLKRIKLQGLDITPRIIILTRLLPDAVGTTCGDRLEKVYGCEHSDILRVPFRDEKGAIVRRWISRFEVWPYLETYAEDAIKELSKEMQGKPDLIIGNYSDGNIVASLMAHKLGVTQCTIAHALEKSKYPDSDLYWKKLDENYHFSCQFTADLIAMNHTDFIITSTFQEIAGSKDTVGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADMSVYFPYSEKEKRLTHFHPEIEELLYSQVENIEQICVLKDRNKPIIFTMARLDRVKNITGLVEWYGKNAKLRELVNLVVAAGDHRNESKDNEEKAELKKMYELIETYKLNGQLRWISSQMNRVRNGELYRYICDTRGAFVQPAVYEAFGLTVIEAMTCGLPTFATCKGGPAEIIVNGKSGYHIDPYQGDQAAEILVDFFEKSKADPSHWDKISQGGLQRIYEKYTWQIYSERLLTLTGVYGFWKDVSNLDRLENRRYLEMFYALKFRKLAASVPLAVEE	801
	PbSS2	Pbr035997.1	MAERVLTRVQSLRERLDQTLSTQRNEILALLSRIESKGKGFLQPHQLHAEFEAIPENNRQKLLDGAFGEVLKHTQEAVVLPPWVALAVRPRPGVWEYIRVNVHALTLEELRVAEYLQFKEELVDGSSNGNFVLELDFQPFNASFPRPTLSKSIGNGVEFLNRHLSAKLFHDKESLHPLLEFLQVHCYEGRNMMLNNRIKNVNELQHVLRKAEDFLSSIVPRTPYKEFEPKLQAIGLERGWGDTAERVLEMIQLLLDLLEAPDPFTLEKFLGQIPMVFNVVILSPHGYFAQDHVLGFPDTGGQVVYILDQVRALESEMLKRIKQQGLDITPRIIILTRLLPDAVGTTCGDRLEKVYGCEHSDILRVPFRDEKGAIVRRWISRFEVWPYLETYAEDAIKELSKEMQGKPDLIIGNYSDGNIVASLMAHKLGVTQCTIAHALEKSKYPDSDLYWKKLDENYHFSCQFTADLIAMNHTDFIITSTFQEIAGTKDTVGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADMSVYFPYSEKEKRLTHFHPEIEELLYSQVENIEQICVLKDRNKPIIFTMARLDRVKNITGLVEWYGKNAKLRELVNLLVVAGDRRNESKDIEEKAELKKMYELIDTYKLNGQLRWISSQMNRVRNGELYRYICDTRGAFVQPAVYEAFGLTVIEAMTCGLPTFATCMGGPAEIIVNGKSGYHIDPYHGDQAAEILVDFFEKSKADPSHWDKISQGGLQRIYEKYTWQIYSERLLTLTGVYGFWKDVSTLDRRESRRYLEMFYALKYRKLAASVPLAVEE	807
	PbSS3	Pbr003107.1	MAGNDWINSYLEAILDVGPGLVDDAKSSLLLRERGHFSPTRYFVEEVITGFDETDLHRSWVRASATRSPQERNTRLENLCWRIWNLARQKKQLEGEESQRKAKRRLERERGRREATADMSEDLSEGEKGDTVSDMSAHGDSHRGRLPRINSVDAMETWISQQKGKKLYIVLIRHELNFNGLSFVYKYSCSLHGLIRGEQMELGRDSDTGGQVKYVVELARALGTTPGVYRVDLLTRQVSSPDVDWSYGEPTEMLTPINAEVFEEEMGESSGSYIIRIPFGPKDKYIPKEELWPHIPEFVDGALNHIMQMSKVLGEQIGGGKPVWPVAIHGHYADAGDSAALLSGALNVPMLFTGHSLGRDKLEQLLKQGRLSRDEINKTYKIMRRIEAEELALDASEIVITSTRQEIEEQWRLYNGFDPILERKLRARLRRNVSCYGRFMPRMVVIPPGMEFHHIVPHDGDMDAETEANEDHPTSPDPPIWSEIMRFFTNPRKPMILALARPDPKKNITTLVKAFGECRPLRELANLTLIMGNRDGIDEMSSTSASLLLSVLKLIDKYDLYGQVAYPKHHKQSDVPDIYRLAAKTKGVFINPAFIEPFGLTLIEAAAHGLPIVATKNGGPVDIHQVLD	1072

Table S2. *Cont.*

			NGLLIDPHDQQSIADALLKLVADKQLWARCRQNGLKNIHLFSWPEHCKTYLSRIASCKQRQPQWQRSEDGGDTSESESASDSLRDIHDLSLNLKFSMDGEKSGTSVNDSLDSEGNTADRRSKIESAVLAWSKGISRDTRRAGFSEKADHNNAGKFPVLRRRKHLIVISVDCETVTELNEITKNIFEATGKEKAEGSVGFILSTSLTIIEIRSFLVFGGLSPKDFDAYICNSGSDLYYPSINSEDRPFVVDFYYHSHIEYRWGGEGLRKTLVRWATSVNDKKTGSEAIVSAADQLSTDYCYAFEVQAPGKLPPVKELRKVLRIQALRCHVIYCQNGTRVNVIPVLASRSQALRYLYLRWGVDLSKVVVLTGECGDTDYEGLLGGLHQSVVLKGVGRNAISQLHNNRNYPLTDVLALDTSNIVQTSEGCGSDDIRASLEKLGVLKN	
	PbSS4	Pbr022714.1	MSILTPQAPPTPILYKYPISFCHVSYFPLSLSTSPPALSEHRDEEEDDDDDRRKKIESWGIALSSLAPYVDRGKGILQPHDLIDQLEHVIGDDEAKQHLKTGAFSKVLKAAQEAIILPPFVALVVRPRPGVWEYVRVNVYELSVEELTVSEYLSFKEELVDGESSDKYVLELDFRPFNATFVE	183
	PbSS5	Pbr022715.1	MLVFFPATCVQISWNGFRASLFHVLEMINLLLDILQAPDPSILETFLGRIPMVFNVIILSPHGYFGQANVLGLPDTGGQAFLIVYILDQVHALENEMLERIRRQGLDFTPRILIVTRLIPDAKGTTCNQRLEKITGTEYTHILRVPFRSEKGILRKWISRFDVLSLFGDLCSGEITAELQGYPDFIIGNYSDGNLVASMLAYKMGVTQFTADLIAMNNADFIVTSTYQEIAGTEVSRKNTVGQYESHSCFTLLRQYRVVHGINVFDPKFNIMSPGAVMTIYFPYSEKQKRLTSLHGSLEELLYDPDQNDVHIGTLSDRSKPIIFSMARLNQVKNMTGLVECYKKCSKLRDLVNLVVIAGYIDAKKSRDREEIAEIEKMHNLMKEYKLNGQFRWISSQTNRVSTGELYHYIADKRGAFAQPAFYEAFGLTVVEAMTCSPPTLATVHGGPPQIIEHGVSGFHIDPYHPEKAAALLADFFQRCKEDPSYWNTISDGGLQRIYEKCTWKIYSGRLMTLAGVYGFWKYVSKLERRETRQYLEMFHILKFRDLAKSVSRAVDDAH	559
	PbSS6	Pbr008035.1	MCWRIWHLARKKKQIAWDDARRLVKRRLDREQGRHDAEDDLSELSEGEKEKGDVSSAEPTVKDILRSKSDMPVWSDDVNKSRHLYIVLISMHGLVRGENMELGRDSDTGGQVKYVIELARALANTKGVYRVDLLTRQITSSEVDSSYGEPNEMLICPPDGSGSCGAYIVRLPCGPCYKYIPKESLWPHIPEFVDGALGHIANMARALGEEVNGGKPTWPYVIHGHYADAGEVAAHLSGALNVPMVLTGHSLSRNKFEQLLKQGRLTKEDINATYKIMRRIEGEELGLDSAEMVVTSTRQEIEEQWGLYDGFDLKLERKLRVRRRRGVSCLGRYMPRMVVIPPGMDFSYVTAHDSEGDGDLKSLIGSDRGQSKRHLPPIWSEVMRFFTNPHKPTILALSRPDPKKNTLILGNRDDIEEMSNSSSVVLTTVLRLIDKYDLYGQVAYPKHHKQLDVPDIYRLVAKTKGVFINPALVEPFGLTIIEAAAYGLPVVATKNGGPVDILKALNNGLLVDPHDQKAIEEALLKAITPITEEPLNESLKDVEDLSLRFSVEGDFKHNGELDAATRQRELIEAITRMSSSTSNVGATYGPGRRQSLFVIAIDCYDQNGDGTQVFQEILVNVKKAAGLGYGQGRVGIVLLTGSSLQDIMKAFKGCQVNIEDFDVLVCKSGSEMYYPWRDLAADADYETHIEYRWPGENVRSMVPRLARLEVGAEDDVVEYARSSSSRYLSVRWAIDLLKVVVFVGEEGDTDNEDLLTGLHKTLVPRGSVEYGSEKLIHGKDSLKREDVVPQDSPNIALVESYQAHEISAALEALGIKCF	818
	PbSS7	Pbr028302.1	MASTSSAVKRSENIAETMPDALRESHFHMKKCFASCTQEAAVVPPYVAFAVRPNPGFSEFVKVNADDLAVDGISATQYLKFKEMIFDESWANDENALEIDFGTIDFSTPRMTLPSSIGNGLNFVLKLISSRLSTHASCSDYAKPLLDYLLPLNYHGENLMINESLDTVEKLQTALIRAEVLVSTLPKTTPFPNFEQRFKVLGFEKGWGDTAERVGETMRLLSEVLQAPDSVKLASLFSRLPNTFNIVIFSPHGYFGQSNVLGLPDTGGQVVYILDQVRALEEELLLRIKQQGLAVKPQILVVTRLIPDARGTKCNQELEAVIDTKHSHILRVPFRTDKGV	867

Table S2. *Cont.*

			LRQWVSRFDIYPYLETFAQDATAKILRHMECKPDLIIGNYSDGNLVASL IASKLGITQGTIAHALEKTKYEDSDAKWKEFDPKYHFSCQFTADIISMN CADFVITSTFQEIAGGKDRPGQYESHTAFTMPGLYRVVSGIDVFDPKFN IAAPGADQSVYFPXXXXXXXVYFPYSEKQKRFTKFQPVIEELLYTKEEN DEHIGFLADQKKPIIFSMARLDTVKNLTGLVEWFGKNKRLRNLVNLVI VGGFFDPSKSKDREEIAEIKKLHALVQEYQLSGQFRWIAAQTDRYRNG ELYRCIADTKGAFVQPALYEAFGLTVIEAMNCGLPTFATNQGGPAEIIV DSVSGFHIDPNNGDESSNKIADFFEKCKTDGEYWKKMSAAGLQRINE CYTWKIYANKVLNMGSTYGFWRQLRDAQKLAKETYIHMFYNLLFRK LAKNVAVPSDGYEQPAPKAGIAAVDQRTPASKPPQPEAAPTLAIPQLT PRERDEGGELSQPRSHSRARCLWNCCCVILGLLIILYYKIRNMYN	
	PbSS8	Pbr042506.1	MIEGEEAQRVARRRLERERGRREATEDMSEDLSEGEKGDTVGDISAHG GDSTRGRMKRINSTDAMENWAGQQKEKKFYMVLHGLIRGENMELG RDSDTGGQVKYVVELARALGSMPGVYRVDLLTRQVAAPDVDWSYGE PTEMLNPLNTENSKEELGESSGAYIVRIPFGPRDKYAPKELLWPHIPEFV DGALTHIIQMSKALGEQIGGGQPVWPVAIHGHYADAGDSAALLSGAL NVPMVFTGHSLGRDKLEQLLKQGRQSREEINTTYKIMRRIEAEELTLD ASEIVITSTRQEIESQWRLYDGFDPILERKLRARIKRGVSCHGRFMPRMV VIPPGMEFHHIIPPDGDGDGEGERHDDSSISPDPPIWSEIMRFFTNPRKP MILALARADPKKNITTLVKAFGECRPLRELANLTLIMGNRDDIDEMPS TNASVLLSILKLIDRYDLYGHVAYPKHHKQSDVPDIYRLAAKTKGVFI NPAFIEPFGLTLIEAAAHGLPIVATQNGGPVDIHRVLDNGLLVDPHDQ RSIADALLKLVSDKQLWARCRQNGLKNIHLFSWPEHCKTYLTRITSCK PRQPQWQRNDADFDNSEPDSPNDSLRDIQDISLNLKLSLDGDKTEGSA ALDNALEAEDCAAGGKTKEQNAVLTLSKGVCQKAGATEKADNSSG AGKFLAFRKRKYVCVIAVDCDTTSEFTEIIEKVTEAAGKDRDAGPIGFIL STALGISEIHSLLISGGLSPSQFDAFICNSGGELYYPSSSSEDSPSGLPFVV DIDYRSHIEYRWGAEGLRKTLVRWVANFNEKKGRETVTEDVSASTNH CYAYKVKDPELIPPVKELRKLMRIQALRCHVIYSLNGTRLNVIPVLASR SQALRYLYVRWGLNLSTAVVFVGESGDTDYEGLLGGLHKTVILKGVGI GARKLHANRNYPLEHVFPNDSPNMAQSEGCSENDIRASLVKLGILKR	962
	PbSS9	Pbr033571.1	MASGAAIKRSESIADNMPDALRQSRYHMKRCFAKYIEKGRRIIKLHHL LSEMETVIDDKAERTQVLEGVLGYILCSTQEAVVIPPHVVFSIRPNPGY WEFVKVSSEDLSVVGITLRDFLKYKETLYDENWSNDENALEVDFRAID FSTPHLTLSSSIGNGINYVTKFATSKLAGKLENAQPLVDYLLSLNHQGE QLILNETLNTASKLQATLIVTEVYLSAVPKDTPFQNFELRFKEWGFEKG WGDTAERTKETMRILSEVLQAPDPLIMDRFFSRLPTIFNVVIFSPHGYFG QADVLGLPDTGGQVVYILDQVKALEEELLVRIKQQGLTVKPQILVVTR LIPEARGTKCNQELEPINGTKYSNILRVPFRTEKGILRRWDATAKILDL MEGKPDLIIGNYTDGNLVASLMANKLGITQATIAHALEKTKYEDSDIN WKELDPKYHFSCQFLADTISMNATDFVIASTYQEIAGSKDRPGQYESH TAFTLPGLCRVVSGISVFDPKFNIAAPGADQSVYFPYAEKQKRLTSFHP AIEELLFSKEDNNEHIGFLEDRKKPIIFSMARLDIVKNITGLVEWYGKN KRLRNLVNLVVVGGFFDPSKSKDREEIAEIKKMHTLIEKYQLRDQIRWI AAQTDRNRNGELYRCIADTRGAFVQPALYEAFGLTVIEAMNCGLPTF ATNQGGPAEIIVDGISGFHIDPNNGDEASNKIADFFEKSKTDAAYWDR FSKAGLQRIYECYTWKIYANKVLNMGSTYTFWRQLNKEQKQAKQRYI HMFFNLQYRNLVKNVPIPSDEPEQPVVPKPTAKPKTTLRHVQLNSQFT QQELPACKPILTPAWVILIFVAIGIVFLPIGFASLFASEHVVEIVNHYDRD CVPPNYMDNKLAYIQSSKTNKTCIRRVTIPKQMKSPVYIYYQLDHFYQ NHRRYVKSRSDGQLRSKSNEKKTDTCAPERYTANGAIVPCGLVAWSL	1142

Table S2. *Cont.*

			FNDTYKFSVNNKQLGVSKKDITWKSDPKKKFGSDVYPKNFQSGGLIGGAKLNSSIPLSEQEDLMVWMRTSTLPTFRKLYGKIEADLEADDIVTVTIENNYNTYIFGGNKKLVLSTASWIGGKNCLLGIAYLTVGGLCLFLAISFLLLYLFKPRPLGDTSYLSWNRSAPGGLIY	
	PbSS10	Pbr008457.1	MASGAAIKRSESIADNMPDALRQSRYHMKRCFAKYIEKGRRIIKLHHLLSEMETVIDDKAERTQVLEGVLGYILCSTQEAVVIPPHVVFSIRPNPGYWEFVKVSSEDLSVVGITLRDFLKYKETLYDENWSNDENALEVDFRAIDFSTPHLTLSSSIGNGINYVTKFATSKLAGKLENAQPLVDYLLSLNHQGEQLILNETLNTASKLQATLIVTEVYLSAVPKDTPFQNFELRFKEWGFEKGWGDTAERTKETMRILSEVLQAPDPLIMDRFFSRLPTIFNVVIFSPHGYFGQADVLGLPDTGGQVVYILDQVKALEEELLVRIKQQGLTVKPQILVVTRLIPEARGTKCNQELEPINGTKYSNILRVPFRTEKGILRRWDATAKILDLMEGKPDLIIGNYTDGNLVASLMANKLGITQATIAHALEKTKYEDSDINWKELDPKYHFSCQFLADTISMNATDFVIASTYQEIAGSKDRPGQYESHTAFTLPGLCRVVSGISVFDPKFNIAAPGADQSVYFPYAEKQKRLTSFHPAIEELLFSKEDNNEHIGFLEDRKKPIIFSMARLDIVKNITGLVEWYGKNKRLRNLVNLVVVGGFFDPSKSKDREEIAEIKKMHTLIEKYQLRDQIRWIAAQTDRNRNGELYRCIADTRGAFVQPALYEAFGLTVIEAMNCGLPTFATNQGGPAEIIVDGISGFHIDPNNGDEASNKIADFFEKSKTDAAYWDRFSKAGLQRIYECYTWKIYANKVLNMGSTYTFWRQLNKEQKQAKQRYIHMFFNLQYRNLVKNVPIPSDEPEQPVVPKPTAKPKTTLRHVQLNSQFTQQELPACKPILTPAWVILIFVAIGIVFLPIGFASLFASEHVVEIVNHYDRDCVPPNYMDNKLAYIQSSKTNKTCIRRVTIPKQMKSPVYIYYQLDHFYQNHRRYVKSRSDGQLRSKSNEKKTDTCAPERYTANGAIVPCGLVAWSLFNDTYKFSVNNKQLGVSKKDITWKSDPKKKFGSDVYPKNFQSGGLIGGAKLNSSIPLSEQEDLMVWMRTSTLPTFRKLYGKIEADLEADDIVTVTIENNYNTYIFGGNKKLVLSTASWIGGKNCLLGIAYLTVGGLCLFLAISFLLLYLFKPRPLGDTSYLSWNRSAPGGLIY	1142
	PbSS11	Pbr008464.1	MASGAAIKRSESIADNMPDALRQSRYHMKRCFAKYIEKGRRIIKLHHLLSEMETVIDDKAERTQVLEGVLGYILCSTQEAVVIPPHVVFSIRPNPGYWEFVKVSSEDLSVVGITLRDFLKYKETLYDENWSNDENALEVDFRAIDFSTPHLTLSSSIGNGINYVTKFATSKLAGKLENAQPLVDYLLSLNHQGEQLILNETLNTASKLQATLIVTEVYLSAVPKDTPFQNFELRFKEWGFEKGWGDTAERTKETMRILSEVLQAPDPLIMDRFFSRLPTIFNVVIFSPHGYFGQADVLGLPDTGGQVVYILDQVKALEEELLVRIKQQGLTVKPQILVVTRLIPEARGTKCNQELEPINGTKYSNILRVPFRTEKGILRRWDATAKILDLMEGKPDLIIGNYTDGNLVASLMANKLGITQATIAHALEKTKYEDSDINWKELDPKYHFSCQFLADTISMNATDFVIASTYQEIAGSKDRPGQYESHTAFTLPGLCRVVSGISVFDPKFNIAAPGADQSVYFPYAEKQKRLTSFHPAIEELLFSKEDNNEHIGFLEDRKKPIIFSMARLDIVKNITGLVEWYGKNKRLRNLVNLVVVGGFFDPSKSKDREEIAEIKKMHTLIEKYQLRDQIRWIAAQTDRNRNGELYRCIADTRGAFVQPALYEAFGLTVIEAMNCGLPTFATNQGGPAEIIVDGISGFHIDPNNGDEASNKIADFFEKSKTDAAYWDRFSKAGLQRIYECYTWKIYANKVLNMGSTYTFWRQLNKEQKQAKQRYIHMFFNLQYRNLVKNVPIPSDEPEQPVVPKPTAKPKTTLRHVILIFVAIGIVFLPIGFASLFASEHVVEIVNHYDRDCVPPNYMDNKLAYIQSSKTNKTCIRRVTIPKQMKSPVYIYYQLDHFYQNHRRYVKSRSDGQLRSKSNEKKTDTCAPERYTANGAIVPCGLVAWSLFNDTYKFSVNNKQLGVSKKDITWKSDPKKKFGSDVYPKNFQSGGLIGGAKLNSSIPLSEQEDLMVWMRTSTLPTFRKLYGKIEADLEADDIVTVTIENNYNTYIFGGNKKLVLSTASWI	1119

Table S2. *Cont.*

			GGKNCLLGIAYLTVGGLCLFLAISFLLLYLFKPRPLGDTSYLSWNRSAPGGLIY	
	PbSS12	Pbr031564.1	MASTSSAVKRSENIAETMPDALRESHFHMKKCFARLIKPQHIMEELEKSIEDRHERSKVLEGLLGYILSCTQEAAVVPPYVAFAVRPNPGFSEFVKVNADDLAVDGISATQYLKFKEMIFDESWANDENALEIDFGTIDFSTPRMTLPSSIGNGLNFVLKLISSRLSTHASCSDYAKPLLDYLLPLNYHGENLMINESLDTVEKLQTALIRAEVLVSTLPKTTPFPNFEQRFKVLGFEKGWGDTAERVGETMRLLSEVLQAPDSVKLASLFSRLPNTFNIVIFSPHGYFGQSNVLGLPDTGGQVVYILDQVRALEEELLLRIKQQGLAVKPQILVVTRLIPDARGTKCNQELEAIIDTKHSHILRVPFRTDKGVLRQWVSRFDIYPYLETFAQDATAKILRHMECKPDLIIGNYSDGNLVASLIASKLGITQGTIAHALEKTKYEDSDAKWKEFDPKYHFSCQFTADIISMNCADFVITSTFQEIAGGGFLADQKKPIIFSMARLDTVKNLTGLVEWFGKNKRLRNLVNLVIVGGFFDPSKSKDREEIAEIKKLHALVQEYQLSGQFRWIAAQTDRYRNGELYRCIADTKGAFVQPALYEAFGLTVIEAMNCGLPTFATNQGGPAEIIVDGVSGFHIDPNNGDESSNKIADFFEKCKTDGEYWKKMSAAGLQRINECYTWKIYANKVLNMGSTYGFWRQLRDAQKLATETYIHMFYNLLFRKLAKNVAVPSDGYKQPAPKAVTAAVDQRTPASKPPQPEAAPTLAIPQLTPRERDEGGELSQPRSPSRARCLWNCCCVILGLLIILYYKIRNMYN	815
	PbSS13	Pbr012029.1	MRNTIQDTLTAHRNELVLLLSRYVARGNGILLSHQMINELENVIMKGEGMQKLKDSSFSKVLQSALEAIVLAPFVAFALRPRPGVWDLKMKLSWVQRYVCDLEPFNAHFPRPTRSSSIGNGVQFLNRHLSSVIFRSKESLESLLDFLRTHKYDGYDASNEIAAELQGVPDLIIGNYSDGNLVAILKNNVGQYESYTASTLPGPYQIVHGIDVFDPKFNIVSPGADMCIYFPYSDKERRLTALHGSIEELLYGAEQKDEHIGLAIE	265
	PbSS14	Pbr014902.1	MRNTIQETLAAHRNELVSLLSRYVARGNGILQPHQMINELESVIMEDEGMQKLKDSSFSKVLQSAQEAIVLAPFVAFALRPRPGVWEYVRVNEYELSVDHLSVAEYLRFKEELMDGECNDKYVLELDLEPFNASFPRPTRSSSIGNGVQFLNRHLSSVMFRNKESLEPLLDFLRTHKHDGHAMMLNDRIQSIPRLQSALAKAEEYLSKFPATTPYSEFEFDLQGMGFERGWGDTAQRVSEMVHLLLEILQAPDPSTLENFLGRIPMVFNVVIVSPHGYFGQANVLGLPDTGGQVVYILDQVRALESEMLLRIQNQGLDVIPKILIVTRLIPDAKGTTCNQRLERVSGTEYTHILRVPFRTENGILRKWISRFDVWPYLETFAEDASNEIAAELQGVPDLIIGNYSDGNLVATLLSYKLGITQCNIAHALEKTKYPDSDIFWKKHEDKYHFSSQFTADLIAMNNADFIITSTYQEIAGSKNNVGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADMCIYFPCSDKEKRLTALHGSIEELLYGAEQNDEHIGLLSDSSKPIVFSMARLDRVKNLTGLVECYAKSAKLREMVNLVVVGGYLDVKNSRDREEIAEVEKMHDLIKKYNLSGQFRWIAAQMNRARNGELYRYIADTKGVFVQPAFYEAFGLTVVEAMTCGLPTFATCHGGPAEIIEHGSSGFHVDPYNPDQVAELLIDFFDQCQKDPGHWEKISQAGLKRIYERYTWKIYSERLLTLAGVYGFWKHVSKLERRETRRYLEMFYILKYRNLVKSIPLAVEEQH	800
	PbSS15	Pbr027868.1	MAGNDWVNSYLEAILDVGPGLDDAKSSLLLRERGRFSPTRYFVEEVITRYDETDLHRSWVRAAATARSPEERNTRLENMCWRIWNLARKKKQIEGEEAQRVARHRLERERGRREATEDMSEDLSEGEKGDTVGDISAHGGDSTRGGRMKRINSTDAVENWASQQKEQKFYMVLHGLIRGENMELGRDSDTGGQVKYVVELARALGSMPGVYRVDLLTRQVAAPDVDWSYGEPTEMLNPLNTENSKEELGESSGAYIVRIPFGPRDKYVPKELLWPHIPEFVDGALTHILQMSKALGEQIGGGQPVWPVAIHGHYADAGDSAALLSGALNVPMVFTGHSLGRDKLEQLLKQGRQSREEINTTYKIMRRIEAEELTLDASEIVITSTRQEIDSQWRLYDGFDPILERKLRARIKRGVSCHGRFMPRM	1054

Table S2. *Cont.*

			VVIPPGMEFHHIIPHDGDGDGEGERHDDSSTSPDPPIWSEIMRFFTNPRKPMILALARADPKKNITTLVKAFGECRPLRELANLTLIMGNRDDIDEMSSTNASVLLSILKLIDRYDLYGHVAYPKHHKQSDVPDIYRLAAKTKGVFINPAFIEPFGLTLIEAAAHGLPIVATQNGGPVDIHRVLDNGLLVDPHDQQSIADALLKLVSDKQLWARCRQNGLKNIHLFSWPEHCKTYLTRITSCKPRQPQWQRNEADFDNSQHDSPSDSLRDIQDISLNLKLSLDGDKTEGSAALDNALETEDRAAGGKIKEQNAVLTLSKGVCEKAGSTEKADNSSGAGKFPAFRKRKYVYVIAVDCDTTSEFTEIIEKVTEAAEKKKDAGPIGFILSTALGISEIHTLLVSGGLSPSQFDAFICNSGAELYYPSSSSEDSPSGLPFVVDLDYRSHIEYRWGAEGLRKTLVRWVANFNEKKGSETVTEDVSASTNHCYAYKVKDPALIPPVTELRRLMRIQALRCHVIYSQNGTRLNVIPVLASRSQALRYLYVRWGLNLSTAVVFVGESGDTDYEGLLGGLHKTVILKGVNSGARKLHANRNYPLEHVFPDDSPNMAQSEGCSQNDIRASLVKLGVLKR	
	PbSS16	Pbr034361.1	MAGNDWINSYLEAILDVGPGLVDDAKSSLLLRERGHFSPTRYFVEEVITGFDETDLHRSWVRAAATRSPQERNTRLENLCWRIWNLARQKKQLEGEEAQRMAKRRLERERGRREATADMSEDLSEGEKGDLVSDISAHGDSHRSKLPRINSVDAMETWISQQKGKKLYIVLIRHELNFSFYSCSLHGLIRGEQMELGRDSDTGGQVKYVVELARALGTTPGVYRVDLLTRQVSSPDVDWSYGEPTEMLTPINTEGFEEEMGESSGSYIIRIPFGPKDKYIPKEELWPHIPEFVDGALNHIMQMSKVLGEQVGGGKPVWPVAIHGHYADAGDSAALLSGALNVPMLFTGHSLGRDKLEQLLKQGRLSRDEINKTYKIMRRIEAEELALDASEIVITSTRQEIEEQWRLYDGFDPILERKLRARIRRNVSCYGRSMPRMVIIPPGMEFHHIVPHDSDMDAETEANEDHPTSPDPPIWSEIMRFFTNPRKPMILALARPDPKKNITTLVKAFGECRPLRELANLTLIMGNRDGIDEMSSTSASLLLSVLKLIDKYDLYGQVAYPKHHKQSDVPEIYRLAAKTKGVFINPAFIEPFGLTLIEAAAHGLPIVATKNGGPVDIHQVLDNGLLIDPHDQQSIADALLKLVADKQLWARCRQNGLKNIHLFSWPEHCKTYLSRIASVKQRQPHWQRSEDGGDTSESDSPSDSLRDIQDLSLNLKFSMDGEKSGTSVNDSLDSEGNTADRSCKIESAVLAWSKGISRDTRKAGFSEKADHNSAGKFPVLRRRKHLIVISVDCETITELNEITKNIFEAMGKEKAEGSVGFILSTSLTIIEIRSFLVSGGLNPNDFDAYICNSGSDLYYPSINSEERPFVVDFYYHSHIEYRWGGEGLRKTLVRWATSINDKKTGSEEIVSAADQLSTDYCYAFKVQTPGKLPSVKELRKVLRIQALRCHVIYCQNGTRVNVIPVLASRSQALRYLYLRWGVDLSKVVVVAGECGDTDYEGLLGGLHKSVVLKGVASNAISQLHTNRNYPLSDVLALDTPNIVQTSEGCGSDDIRASLEKLGVLKN	1066
	PbSS17	Pbr032090.1	MELGRDSDTGGQVKYVVELARALGTTPGVYRVDLLTRQVSSPDVDWSYGEPTEMLTPINTEGFEEEMGESSGSYIIRIPFGPKDKYIPKEELWPHIPEFVDGALNHIMQMSKVLGEQVGGGKPVWPVAIHGHYADAGDSAALLSGALNVPMLFTGHSLGRDKLEQLLKQGRLSRDEINKTYKIMRRIEAEELALDASEIVITSTRQEIEEQWRLYDGFDPILERKLRARIRRNVSCYGRSMPRMVIIPPGMEFHHIVPHDSDMDAETEANEDHPTSPDPPIWSEIMRFFTNPRKPMILALARPDPKKNITTLVKAFGECRPLRELANLTLIMGNRDGIDEMSSTSASLLLSVLKLIDKYDLYGQVAYPKHHKQSDVPEIYRLAAKTKGVFINPAFIEPFGLTLIEAAAHGLPIVATKNGGPVDIHQVLDNGLLIDPHDQQSIADALLKLVADKQLWARCRQNGLKNIHLFSWPEHCKTYLSRIASVKQRQPHWQRSEDGGDTSESDSPSDSLRDIQDLSLNLKFSMDGEKSGTSVNDSLDSEGNTADRSCKIESAVLAWSKGISRDTRKAGFSEKADHNSAGKFPVLRRRKHLIVISVDCETITELNEITKNIFEAMGKEKAEGSVGFILSTSLTIIEIRSFLVSGGLNPNDFDAYICNSGSDLYYPSINSEERPFVVDFYYHSHIEYRWGGEGLRKTLVRWATSINDKKTGSEEIVSAADQLSTD	873

Table S2. *Cont.*

			YCYAFKVQTPGKLPSVKELRKVLRIQALRCHVIYCQNGTRVNVIPVLASRSQALRYLYLRWGVDLSKVVVVAGECGDTDYEGLLGGLHKSVVLKGVASNAISQLHTNRNYPLSDVLALDTPNIVQTSEGCGSDDIRASLEKLGVLKN	
	PbSS18	Pbr037395.1	MAERVLTRVQSLRERLDETLSAHRNEILALLSRIEKKGKGFLQPHQLLAEFEEIPETNRRKLLDGAFGEVLKNTQEVIVLPPWVALAVRPRPGVWEYIRVNVHALVFEELRVAEYLQFKEELVDGSANGNFVLELDFEPFNASFPRPTLSKSIGNGVEFLNRHLSAKLFHDKESLHPLLKFLRVHCYEGRNLMLNNKINDVNELQHVLRKSEDFLSAIAPETPYKEFEPKLQAIGLERGWGDTAGRVLEMMQLLLDLLEAPDPCTLEKFLDQIPMVFNVVILSPHGYFAQDNVLGYPDTGGQVVYILDQVRALEAEMLKRVKQQGLDIIPRIIILTRLLPDAVGTTCGDRLEKVYGTEHSDILRVPFRDEKGAIVRRWISRFEVWPYLETYAEDAIKELSKEMHGKPDLIIGNYSDGNIVASLMALKLGVTQCTIAHALEKSKYPDSDLYWKKLDDSYHFSCQFTADLIAMNHTDFIITSTYQEIAGSKETVGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADMSVYFPYTEKEKRLTNFHPEIEELLYSQVENKEHLCVLKDRNKPIIFTMARLDRVKNITGLVEWYGKNAKLRELVNLVVVAGDRRKESKDNEEKDEMKKMYELIDTYKLNGQFRWISSQMNRVRNGELYRYICDTKGAFVQPAVYEAFGLTVVEAMTCGLPTFATCKGGPAEIIVHGKSGYHIDPYHGDQAAEILVDFFEKSKADPSHWDKISQAGLQRIYEKYTWQIYSQRLLTLTGVYGFWKHVSKLDRLESRRYLEMFYALKYSKLESWRAGSPAAIWRCFTPSSTASWRRLFLLLWRSERERFPK	837
	PbSS19	Pbr012642.1	MASAEAIKRSDSIADTMPDALRQSRYHMKRCFAKYIEQGRRIMKLHHLMSEMEAVIDDKDERTQVLGGVLGYILCSTQEAVVVPPHVVFSIRLDPGYWEFVKVSSEDLAVEAITVREFLKYKEALCDEKWSNDEHVLEVDFRAIDFSTPHLTLSSSIGNGIDYVTKFTTSKLAGKLDNAQPLVDYLVSLHHHGEQLILNETLNTASKLQAALIVTEVYLSALPKDTPFQNFELRFKEWGFEKGWGDTAERTQETMKILSEVLQAPDPLNMDRFLSRLPTIFNVVILSPHGYFGQADVLGLPDTGGQVVYILDQVKAMEEELTLRIKQQGLTVKPQILVVTRLIPEARGTKCNQELEPINGTKYSNILRVPFRTEKGILRRWDATAKILYLMEGKPDLIIGNYTDGNLVASLMANKLGITQATIAHALEKTKYEDSDVNWKELDPKYHFSCQFLADTISMNATDFVIASTYQEIAGSKDRPGQYESHTAFTLPGLCRVVSGINVFDPKFNIAAPGADQSVYFPYSEKQKRLTSFYPAIEELLFSKEDNSEHLGFLVDRKKPIIFSMARLDIVKNITGLVEWYGKNKRLRNLVNLVVVGGFFDPSKSKDREEIAEIKKMHTLIEKYQLRGQIRWIAAQADRNRNGELYRCIADTRGAFVQPALYEAFGLTVIEAMNCGLPTFATNQGGPAEIIVDEVSGFHIDPNNGDEASNKIADFFEKSKTDAAYWDRFSNAGLQRIYECYTWKIYANKVLNMGSTYTFWRQLNKEQKQAKQRYIQMFFNLQYRNLVKNVPVPSDEPEQPAAPKPTAKPQTTLRHLKALTVSIAKVKSKIATNGLFSIFSLKPA	844
	PbSS20	Pbr012641.1	MASAAAVKRSDSIADTMPDALRQSRYHMKRCFAKYIEKGRRIMKLHHLMSEMETVIDDKAEMTQVLEGVLGYILCSTQEAVVVPPHVVFSIRLNPGYWEFVKVSSEDLSVEAITVRDFLKYKEALYDDKWSNDEHGLEVDFRAIDFSTPHLTLSSSIGNGIHYVTKFMTSKLAGKLENAQPLVDYLLSLNHQGEQLILNETLNTALKLQAALIVTEVYLSTLPKDTPFQNFELRFKEWGFEKGWGDTAERTRETMKILSEVLQAPDPLNMDRFFSRLPTIFNVVIFSPHGYFGQADVLGLPDTGGQVVYILDQVKAMEEELTLRIKQQGLTVKPQILVVTRLIPEARGTKCNQELEQINGTKYSNILRDATAKILYLMEGKPDLIIGNYTDGNLVASLMANKLGITQATIAHALEKTKYEDSDINWKELDPKYHFSCQFLADTISMNATDFVIASTYQEIAGSKDRPGQYESHTAFTLPGLCRVVSGINVFDPKFNIAAPGADQSVYFPYSEKQKRLTSFSPAIEELLFSKED	1138

Table S2. *Cont.*

			NSEHLGFLVDRKKPIIFSMARLDIVKNITGLVEWYGKNKRLRNLVNLVVVGGFFDPSKSKDREEIAEIKKMHTLIEKYQLRGQIRWIAAQTDRNRNGELYRCIADTRGAFVQPALYEAFGLTVIEAMNCGLPTFATNQGGPAEIIVDEVSGFHIDPNNGDEASNKIADFFEKSKTDAAYWDSFSNAGLQRIYECYTWKIYANKVLNMGSTYTFWRQLNKEQKQAKQRYIQMFFNLQYRNLVKNVPVPSDEPEQPAAPKSIAKPQTTSRHLKALTVSIAKVENSKFTQQELPACKPILTPASVILIFVAIGIVFIPIGLASLFASERVVEIVHHYDKDCIPLKYADNMLAYIQSSKTNKTCVRKLTIPKQMKSPVYIYYQLDHFYQNHRRYVKSRSDKQLRSKSYENTTDDCAPERYTAKGVIVPCGLVAWSLFNDTYKFSVNNKQLGVSKKDITWKSDQKNKFGSDVYPKNFQSGGLIGGAKLNSSIPLSEQEDLMVWMRTAALPTFRKLYGRIEVDLEADAVITVTIENNYNTYSFRGNKKLVLSTASWIGGKNYLLGVAYLTVGGLCLFLALAFLLLYLIKPRPLGDISYLSWNRSASGGHIY	
	PbSS21	Pbr003395.1	MAERVLTRVQSLRERLDETLSTQRNEILALLSRIESKGKGFLQPHQLHAEFEAIPENNRQKLLDGAFGEVLKHTQEAVVLPPWVALAVRPRPGVWEYIRVNVHALTLEELRVAEYLQFKEELVDGSSNGNFVLELDFQPFNASFPRPTLSKSIGNGVEFLNRHLSAKLFHDKESLHPLLEFLQVHCYEGRNMMLNNRIKNVNELQHVLRKAEDFLTSIAPRTPYKEFEPKLQAMGLERGWGDTAERVLEMIQLLLDLLEAPDPFTLEKFLGQIPMVFNVVILSPHGYFAQDHVLGFPDTGGQVVYILDQVRALESEMLKRIKQQGLDITPRIIILTRLLPDAVGTTCGDRLEKVYGCEHSDILRVPFRDEKGAIVRRWISRFEVWPYLETYAEDAIKELSKEMQGKPDLIIGNYSDGNIVASLMAHKLGVTQCTIAHALEKSKYPDSDLYWKKLDENYHFSCQFTADLIAMNHTDFIVTSTFQEIAGTKDTVGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADMDVYFPYSEKEKRLTHFHPEIEELLYGQVENIEQLCVLKDRNKPIIFTMARLDRVKNITGLVEWYGKNAKLRELVNLLVVAGDRRNESKDIEEKAELKKMYELIDTYKLNGQLRWISSQMNRVRNGELYRYICDTRGAFVQPAVYEAFGLTVIEAMTCGLPTFATCMGGPAEIIVNGKSGYHIDPYHGDQAAEILVDFFEKSKADPSHWDKISQGGLQRIYEKYTWQIYSERLLTLTGVYGFWKDVSNLDRLESRRYLEMFYALKYRKLAASVPLAVEE	807
	PbSS22	Pbr026341.1	MSILTPQAPPTPILYKYPISFCHVSYFPLSLSTSPPALSEHRDEEEDDDDDRRKKIESWGIALSSLAPYVDRGKGILQPHDLIDQLEHVIGDDEAKQHLKTGAFSKVLKAAQEAIILPPFVALVVRPRPGVWEYVRVNVYELSVEELTVSEYLSFKEELVDGESSDKYVLELDFRPFNATFVE	183
	PbSS23	Pbr026338.1	MSILTPQAPPTPILYKYPISFCHVSYFPLSLSTSPPALSEHRDEEEDDDDDRRKKIESWGIALSSLAPYVDRGKGILQPHDLIDQLEHVIGDDEAKQHLKTGAFSKVLKAAQEAIILPPFVALVVRPRPGVWEYVRVNVYELSVEELTVSEYLSFKEELVDGESSDKYVLELDFRPFNATFVE	183
	PbSS24	Pbr026337.1	MFRNKESLKPLLDFLRAHKYKEQPLMLNERIQSESKLQSALAKAEDHLSKLQLETPYSEFEYM	63
	PbSS25	Pbr003394.1	MAERVLTRVQSLRERLDETLSTQRNDFLALLSRIESKGKGFLQPHQLLAEFEAIPENNRQKLLDGAFGEEAIVLPPWVALAVRPRPGVWEYIRVNVHALALEELCVAEYLQLKEELVDRSSNGNFVLELDFQPFNASFPRPTLSKSIGNGVQFLNRHLSAKLFHDKESLHPLLEFLRVHCYEGRNMMLNNRIKNVNELQRVLRKAEDFLSSIVPRTPYKEFEPKLQAIGLERGWGDTAERVLEMIQLLLDLLEAPNPFTLEKFLGQIPMVFNVVILSPHGYFAQDHVLGFPDTGGQVVYILDQVRALESEMLKRIKQQGLDITPRIIILTRLLPDAVGTTCGDRLEKVYGCEHSDILRVPFRDEKGAIVRRWISRFEVWPYLETYAEDAIKELSKEMQGKPDLIIGNYSDGNIVASLMAHKLGVTQCTIAHALEKSKYPDSDLYWKKLDENYHFSCQFTADLIAMNHTDFIITSTFQEIAGTKDTVGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADMSVYFPYSEKEKR	790

Table S2. *Cont.*

			LTHFHPEIEELLYSQVENIEQICVLKDRNKPIIFTMARLDRVKNITGLVEWYGKNAKLRELVNLVVAAGDRRNESKDNEEKAELKKMYELIETYKLNGQLRWISSQMNRVRNGYDLWTAHICHLQGCVIEAMTCGLPTFATCKGGPAEIIVNGKSGYHIDPYQGDQAAEILVDFFEKSKADPSHWEKISQGGLQRIYEKYTWQIYSERLLTLTGVYGFWKDVSNLDRLENRRYLEMFYALKFRKLAASVPLAVEE	
	PbSS26	Pbr026342.1	MLVFFPATCVQISWNGFRASLFHVLEMINLLLDILQAPDPSILETFLGRIPMVFNVIILSPHGYFGQANVLGLPDTGGQAFLIVYILDQVHALENEMLERIRRQGLDFTPRILIVTRLIPDAKGTTCNQRLEKITGTEYTHILRVPFRSEKGILRKWISRFDVLSLFGDLCSGEITAELQGYPDFIIGNYSDGNLVASMLAYKMGVTQFTADLIAMNNADFIVTSTYQGIAGTEVSRYIGTSYSKNTVGQYESHSCFTLLRQYRVVHGINVFDPKFNIMSPGAVMTIYFPYSEKQKRLTSLHGSLEELLYDPDQNDVHIGTLSDRSKPIIFSMARLNQVKNMTGLVECYKKCSKLRDLVNLVVIAGYIDAKKSRDREEIAEIEKMHNLMKEYKLNGQFRWISSQTNRVSTGELYHYIADKRGAFAQPAFYEAFGLTVVEAMTCSPPTLATVHGGPPQIIEHGVSGFHIDPYHPEKAAALLADFFQRCKEDPSYWNTISDGGLQRIYEKCTWKIYSGRLMTLAGVYGFWKYVSKLERRETRQYLEMFHILKFRDLAKSVSRAVDDAH	566
	PbSS27	Pbr026336.1	MLVFFPATCVQISWNGFRASLFHVLEMINLLLDILQAPDPSILETFLGRIPMVFNVIILSPHGYFGQANVLGLPDTGGQAFLIVYILDQVHALENEMLERIRRQGLDFTPRILIVTRLIPDAKGTTCNQRLEKITGTEYTHILRVPFRSEKGILRKWISRFDVLSLFGDLCSGEITAELQGYPDFIIGNYSDGNLVASMLAYKMGVTQFTADLIAMNNADFIVTSTYQGIAGTEVSRYIGTSYSKNTVGQYESHSCFTLLRQYRVVHGINVFDPKFNIMSPGAVMTIYFPYSEKQKRLTSLHGSLEELLYDPDQNDVHIGTLSDRSKPIIFSMARLNQVKNMTGLVECYKKCSKLRDLVNLVVIAGYIDAKKSRDREEIAEIEKMHNLMKEYKLNGQFRWISSQTNRVSTGELYHYIADKRGAFAQPAFYEAFGLTVVEAMTCSPPTLATVHGGPPQIIEHGVSGFHIDPYHPEKAAALLADFFQRCKEDPSYWNTISDGGLQRIYEKCTWKIYSGRLMTLAGVYGFWKYVSKLERRETRQYLEMFHILKFRDLAKSVSRAVDDAH	566
	PbSS28	Pbr009578.1	MAGNDWVNSYLEAILDVGPGLDDAKSSLLLRERGRFSPTRYFVEEVITRYDETDLHRSWVRAAATARSPEERNTRLENMCWRIWNLARKKKQIEGEEAQRVARHRLERERGRREATEDMSEDLSEGEKGDTVGDISAHGGDSTRGGRMKRINSTDAVENWTSQQKEQKFYMVLHGLIRGENMELGCDSDTGGQVKYVVELARALGSMPGVYRVDLLTRQVAAPDVDWSYGEPTEMLNPLNTENSKEELGESSGAYIVRIPFGPRDKYVPKELLWPHIPEFVDGALTHILQMSKALGEQIGGGQPVWPVAIHGHYADAGDSAALLSGALNVPMVFTGHSLGRDKLEQLLKQGRQSREEINTTYKIMRRIEAEELTLDASEIVITSTRQEIDSQWRLYDGFDPILERKLRARIKRGVSCHGRFMPRMVVIPPGMEFHHIIPHDGDGDGEGERHDDSSTSPDPPIWSEIMRFFTNPRKPMILALARADPKKNITTLVKAFGECRPLRELANLTLIMGNRDDIDEMSSTNASVLLSILKLIDRYDLYGHVAYPKHHKQSDVPDIYRLAAKTKGVFINPAFIEPFGLTLIEAAAHGLPIVVTQNGGPVDIHRVLDNGLLVDPHDQQSIADALLKLVSDKQLWARCRQNGLKNIHLFSWPEHCKTYLTRITSCKPRQPQWQRNEADFDNSQHDSPSDSLRDIQDISLNLKLSLDGDKTEGSAALDNALETEDRAAGGKIKEQNAVLTLSKGVCEKAGSTEKADNSSGAGKFPAFRKRKYVYVIAVDCDTTSEFTEIIEKVTEAAEKNKDAGPIGFIVSTALGISEIHTLLVSGGLSPSQFDAFICNSGAELYYPSSSEDSPSGLPFVVDLDYRSHIEYRWGAEGLRKTLVRWVANFNEKKGSETVTEDVSASTNHCYAYKVKDPALIPPVTELRRLMRIQALRCHVIYSQNGTRLNVIPVLASRS	1054

Table S2. *Cont.*

			QALRYLYVRWGLNLSTAVVFVGESGDTDYEGLLGGLHKTVILKGVNSGARKLHANRNYPLEHVFPDDSPNMAQSEGCSQNDIRASLVKLGVLKR	
	PbSS29	Pbr001616.1	MASTSSAVKRSENIAETMPDALRESHFHMKKCFASCTQEAAVVPPYVAFAVRPNPGFSEFVKVNADDLAVDGISATQYLKFKEMIFDESWANDENALEIDFGTIDFSTPRMTLPSSIGNGLNFVLKLISSRLSTHASCSDYAKPLLDYLLPLNYHGENLMINESLDTVEKLQTALIRAEVLVSTLPKTTPFPNFEQRFKVLGFEKGWGDTAERVGETMRLLSEVLQAPDSVKLASLFSRLPNTFNIVIFSPHGYFGQSNVLGLPDTGGQVVYILDQVRALEEELLLRIKQQGLAVKPQILVVTRLIPDARGTKCNQELEAIIDTKHSHILRVPFRTDKGVLRQWVSRFDIYPYLETFAQDATAKILRHMECKPDLIIGNYSDGNLVASLIASKLGITQGTIAHALEKTKYEDSDAKWKEFDPKYHFSCQFTADIISMNCADFVITSTFQEIAGGKDRPGQYESHTAFTMPGLYRVVSGIDVFDPKFNIAAPGADQSVYFPSSEKQKRFTKFQPVIEELLYTKEENDEHIGFLADQKKPIIFSMARLDTVKNLTGLVEWFGKNKRLRNLVNLVIVGGFFDPSKSKDREEIAEIKKLHALVQEYQLSGQFRWIAAQTDRYRNGELYRCIADTKGAFVQPALYEAFGLTVIEAMNCGLPTFATNQGGPAEIIVDGVSGFHIDPNNGDESSNKIADFFEKCKTDGEYWKKMSAAGLQRINECYTWKIYANKVLNMGSTYGFWRQLRDAQKLATETYIHMFYNLLFRKLAKNVAVPSDGYKQPAPKAVTAAVDQRTPASKPPQPEAAPTLAIPQLTPRERDEGGELSQPRSPSRARCLWNCCCVILGLLIILYYKIRNMYN	856
	PbSS30	Pbr001745.1	MGMVVQVIATRNTRERSNRLENMCWRIWHLARKKKQIAWDDARRLVKRRLDREQGRHDAEDDLSELSEGEKEKGDVSSAEPTVKDVLRSKSDMPVWSDDVNKSRHLYIVLISMHGLVRGENMELGRDSDTGGQVKYVIELARALANTKGVYRVDLLTRQITSSEVDSSYGEPNEMLICPPDGSGSCGAYIVRLPCGPCDKYIPKESFWPHTPEFVDGALSHIANMARALGEEVNGGKPTWPYVIHGHYADGGEVAAHLSGALNVPMVLTGHSLGRNKFEQLLKQGRLTKEDINATYKIMRRIEGEELGLDSAEMVVTSTRQEIEEQWGLYDGFDLKLERKLRVRRRRGVSCLGRYMPRMVVIPPGMDFSYVTAHDSEGDGDLISLIGSDRGQSKRHLPPIWSETLILGNRDDIEEMSNGSSVVLTTVLRLIDKYDLYGQVAYPKHHKQLDVPDIYRLAAKTKGVFINPALVEPFGLTIIEAAAYGLPVVATKNGGPVDILKLPHYFHKQR	510
Prunus persica	PPSUS1	ppa001535m	MAERALTRVQSLRERLDVTLSAHRNEIVALLSRIVNKGKGFMQPHELVAEFEAIPESNRQKLLDGAFGEVLTHTQEVIVLPPWVALAVRPRPGVWEYIRVNVDALVVEELQVPEYLHFKEELVDGSANGNFVLELDFEPFNASFPRPTLSKSIGNGVEFLNRHLSAKLFHDKESMHPLLEFLRVHCYKGKNMMLNDRIHNVNELQHVLRKAEDYLSTIAPETPYKQFEDKLQKLGLERGWGDTAERVLEMIQLLLDLLEAPDPCTLEKFLGQIPMVFNVVILSPHGYFAQDNVLGYPDTGGQVVYILDQVRALETEMLKRIKQQGLDITPRIIILTRLLPDAVGTTCGERLEKVYNTEYSHILRVPFRTEKGIVRRWISRFEVWPYLETYAEDAIQELSKELHGKPDLIIGNYSDGNIVASLMAHKLGVTQCTIAHALEKTKYPDSDLYWKKLDDKYHFSSQFTADLIAMNHTDFIITSTFQEIAGSKDTVGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADMSIYFPYSEKEKRLTSFHPEIEELLYSQVENKEHLCVLKDRNKPIIFTMARLDRVKNITGLVEWYGKNAKLRELVNLVVVAGDRRKESKDNEEKAEMKKMYELIDTYKLNGQFRWISSQMNRVRNGELYRVIADTKGAFVQPAVYEAFGLTVVEAMTCGLPTFATCKGGPAEIIVHGKSGYHIDPYHGDQAADILVDFFEKSRADPSHWDKISQGGLQRIYEKYTWQIYSERLLTLTGVYGFWKHVSNLDRLESRRYLEMFYALKYRKLAESVPRAEEE	806
	PPSUS2	ppa001573m	MRKSIEDTLAAHRNELVSLLSRYVDRGNGILQPHQMINELENVIAEDEGMQKLKDSPFSIVLQSAQEAIVQTPFVALALRPRPGVWEYVRVNVYELSVDLLSVAEYLWFKEELLDGECNDKYVLELDLEPFNATFPRPTRSSSIG	800

Table S2. *Cont.*

			NGVQFLNRHLSSIMFRNKESLEPLLDFLRTHKHDGHAMMLNDRIQSIPRLQSALAKAEEYLSKLLATTPYSDFEFDLQGMGFERGWGDTAQRVSEMVHLLLEILQAPDPSTLETFLGRIPMVFNVVIVSPHGYFGQANVLGLPDTGGQVVYILDQVRALENEMLLRIQNQGLDVIPKILIVTRLIPDAKGTTCNQRLERISGTEHTHILRVPFRTENGIMRKWISRFDVWPYLETFAEDASNEIAAELQGVPDLIIGNYSDGNLVATLLSNKLGISQCNIAHALEKTKYPDSDIYWKKHEDKYHFSSQFTADLIAMNNADFIITSTYQEIAGSKNNVGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADMCIYFPYSEKERRLTALHGSIEELLYGAEQNEEHIGILSDRSKPIVFSMARLDRVKNLTGLVECYGKSTKLRELVNLVVVGGYIDAKNSRDREEVAEIEKMHDLVKKYNLSGQFRWIAAQMNRARNGELYRYIADTKGVFVQPAFYEAFGLTVVEAMTCGLPTFATCHGGPAEIIEHGISGFHIDPYHQDQVAALLIDFFDQCQKHPGYWEKISEAGLKRIYERYTWKIYSERLLNLAGVYGFWKHVSKLERRETRRYLDMFYILKYRNLVKSIPLAVDEQH	
	PPSUS3	ppa002723m	MFRNKDSLEPLLDFLRAHKYKGHALMLNDRIQSIPKLQSVLGKAEDYLSKLPPETPSSEFEYVLQGMGFERGWGDNAVHVLEMMHLLLDILQAPDPSILETFLGRVPMVFNVVILSPHGYFGQANVLGLPDTGGQIVYILDQVRALENEMLHRIQRQGLDIAPRILIVTRLIPDSKGTTCNQRLERVSGTEHTHILRVPFRSEKGVLRKWISRFDVWPYLETFAEDAASELTAELQGYPDFIIGNYSDGNLVASLLAYKMGVTQCTIAHALEKTKYPDSDIYWKKFEDKYHFSSQFTADLIAMNNADFIITSTYQEIAGTKNTVGQYESHSSFTLPGQYRVVHGIDVFDPKFNIVSPGADMAIYFPYSEKTKRLTSLHGSIEELLYDPVQNDVHIGTLDDRSKPLLFSMARLDRVKNISGLVECYAKNPKLRDLVNLVVVAGYIDVKKSKDREEIEEIEKMHGLLKEYKLNGQFRWISAQNNRARNGELYRYIADTRGAFVQPALYEAFGLTVVEAMTCGLPTFATCHGGPAEIIEHGKSGFHIDPYHPEQAGALMADFFERCKEDPSYWSTFSDAGLKRIYERYTWKIYSERLMTLAGVYGFWKYVSKLERRETRRYLEMFYILKFRDLASSVPSASDE	604
	PPSUS4	ppa001845m	MGFSTYILVSLIFRCFMQEVCAGEEAIVLPPFVALAFRPRPGVWEYVRVNVYELSVDHLTVAEYLQFKEELIDGECNDNYVLELDFEPFNAAFPRPTRSSSIGNGVQYLNRHLSSIMFSKKESLEPLLDFLRTHKHDGHAMMLNDRIHSILRLQSALAKAEEYLSKFPPTTPYSEFQFDLQGMGFERGWGDTAQRVSEMVHLLLEILQAPDPSTLESFLGRIPMVFNVVIVSPHGYFGQANVLGLPDTGGQVVYILDQVRALENEMLLRIQNQGLGVIPKILIVTRLIPDAKGTTCNQRLERVSSTEHTHILRVPFRTKNGILRKWLSRFDVWPYLETFAEDASNEIAAVFQGVPDLIIGNYSDGNLVATLLSYKLGITQCNIAHALEKTKHPDFDIYWKKHEDKYHFSSQFTADLIAMNNADFIITSTYQEIAGSKNNVGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADMCIYFPYSEKERRLTALHGSIEELLYGAEQNEEHIGILSDRSKRIVFSMARLDRVKNLTGLVEFYAKSTKLRELVNLVVVGGYIDVKNCRDREEMAEIEKMHGLIKKYNLSGQFRWIVTQMNHARNGELYRYVADTKGVFVQPAFYEAFGLTVVEAMSCGLPTFATCHGGPAEIIEHGISGFHIDPYHPDQVAALLVDFFDQCQKDPGYWERISETGLKRIFERYTWKIYSERLLNLAGVYGFWKHVSKLERRETRRYLEMFYILTYRNLVSSVILPSMTQ	757
	PPSUS5	ppa017606m	MASGAAIKRSESIAESMPEALRQSRYHMKRCFAKYIEKGKRIMKLPHLMSEMETVIDDKVERNQVLEGVLGYILCSTQEAVVIPPFVVFAIRPNPGYWEFVKVSSEDLSVESITVRDYLKFKETLYDEKWSNDENTLEVDFRAIDFSTPHLTLSSSIGNGLNFVSKFTSSKLAGRLENAQPLVDYLLSLNHEGENLILNENLNTASKLQTALIVTEVYLSALPKDMPYQNFELRFKEWGFEKGWGDTAERTKETMKLLSEVLQAPDPLNLERFFSRLPIIFNVVIFSPHGYFGQADVLGLPDTGGQVVYILDQVQALEEELLLRIKQQGLTVKPQILVVTR	833

Table S2. *Cont.*

			LIPEAKGTKCNQELEPINGTKYSNILRVPFRTEKGILRRWVSRFDIYPYLELFAQDASAKVLDIMEGKPDLIIGNYSDGNLVASLMASKLGITQATIAHALEKTKYEDSDIKWKELDPKYHFSCQFLADTISMNATDFVIASTYQEIAGSKDRPGQYESHTAFTLPGLCRVVSGINVFDPKFNIAAPGADQSVYFPYTEKQKRLTSFHPAIEELLYSKEDNSEHIGFLADRKKPIIFSMARLDTVKNITGLVEWYGKNKRLRNLVNLAVVGGFFDPSKSKDREEIAEIKKMHTLIEKYQLRGQIRWIAAQTDRNRNGELYRCIADTRGAFVQPALYEAFGLTVIEAMNCGLPTFATNQGGPAEIIVDGISGFHIDPNNGDEASNKIADFFEKSKTDATYWDRFSKAGLQRIYECYTWKIYANKVLNMGSTYTFWRQLNKEQKQAKQRYIQMFFNLQYRNLVKNVPIPSDEAEQPVPKPTAKSQPTPRHVNLN	
	PPSUS6	ppa001135m	MASTPALKRSDTIAETMPDALRQSRYHMKKCFARFVAMGKRLMKMQHVMEELEKSIEDKHERSKVLEGLLGYIISSTQEAAVVPPYVAFAVRPNPGFWEFVKVNADDLAVDGITASEYLKFKEMIFDDNWANDENALEIDFGGIDFATPRMKLPSSIGNGLNFILKLISSRLATANSSDYAKPLLDYLSQLHYHGENLMINETLNTVAKLQTALIQAEVVVSTLPKDTPFPNFEHRLKELGFEKGWGDTAERVGETMKMLSEVLQAPDSAKLECFFSRLPNTFNIVIFSPHGYFGQSDVLGLPDTGGQVVYILDQVRALEEELLLRIKQQGLAVKPQILVVTRLIPDARGTKCNQELEAIINTKHSHILRVPFRTHRGILRQWLSRFDIYPYLETFAQDATAKILERMECKPDLIIGNYSDGNLVASLTAGKLGITQGTIAHALEKTKYEDSDAKWKEFDPKYHFSCQFTADIISMNSADFVITSTFQEIAGGKDRPGQYESHTAFTMPGLYRVVSGIDVFDPKFNIAAPGADQSVYFPCSEKQRRFTKFHPAIEELLYNKAENDEHIGYLADKKKPIIFSMARLDTVKNLSGLVEWFGKNKRLRSLVNLVIVGGFFDPSKSKDREEIAEIKKVHALVQEYRLTGQFRWIAAQTDRYRNGELYRCIADTRGAFVQPALYEAFGLTVIEAMNCGLPTFATNQGGPAEIIVDGVSGFHIDPNNGDESSNKIADFFEKCKTDGEYWNKMSAAGLQRIYECYTWKIYANKVLNMGSTYGFWRQLRKEQKLANQTYIHMFYSLLFRNLARNVGVPSDGFEQPTAKAITAAGQPTPVAPPTSPIPQLITPTPRERDEGLEEKQKQQQLGEPRSPTARCILNCCCVIIGFLILVYYKIRNMYNYN	898
Monocot plants				
Oryza sativa	OsSS1	Os03g0401300	MGEAAGDRVLSRLHSVRERIGDSLSAHPNELVAVFTRLVNLGKGMLQAHQIIAEYNNAISEADREKLKDGAFEDVLRSAQEGIVISPWVALAIRPRPGVWEYVRVNVSELAVELLTVPEYLQFKEQLVEEGTNNNFVLELDFEPFNASFPRPSLSKSIGNGVQFLNRHLSSKLFHDKESMYPLLNFLRAHNYKGMTMMLNDRIRSLSALQGALRKAEEHLSGLSADTPYSEFHHRFQELGLEKGWGDCAKRSQETIHLLLDLLEAPDPSTLEKFLGTIPMVFNVVIMSPHGYFAQANVLGYPDTGGQVVYILDQVRAMENEMLLRIKQQGLNITPRILIVTRLLPDATGTTCGQRLEKVLGTEHTHILRVPFRTENGIVRKWISRFEVWPYLETFTDDVAHEIAGELQANPDLIIGNYSDGNLVACLLAHKMGVTHCTIAHALEKTKYPNSDLYWKKFEDHYHFSCQFTTDLIAMNHADFIITSTFQEIAGNKDTVGQYESHMAFTMPGLYRVVHGIDVFDPKFNIVSPGADMSIYFPYSESRKRLTSLHPEIEELLYSEVDNNEHKFMLKDRNKPIIFSMARLDRVKNLTGLVELYGRNPRLQELVNLVVVCGDHGNPSKDKEEQAEFKKMFDLIEQYNLNGHIRWISAQMNRVRNGELYRYICDTKGAFVQPAFYEAFGLTVVESMTCGLPTFATAYGGPAEIIVNGVSGFHIDPYQGDKASALLVEFFEKCQEDPSHWTKISQGGLQRIEEKYTWKLYSERLMTLTGVYGFWKYVSNLERRETRRYLEMLYALKYRTMASTVPLAVEGEPSNK	816

Table S2. *Cont.*

	OsSS2	Os06g0194900	MAAKLARLHSLRERLGATFSSHPNELIALFSRYVNQGKGMLQRHQLLAEFDALIEADKEKYAPFEDILRAAQEAIVLPPWVALAIRPRPGVWDYIRVNVSELAVEELSVSEYLAFKEQLVDGHTNSNFVLELDFEPFNASFPRPSMSKSIGNGVQFLNRHLSSKLFQDKESLYPLLNFLKAHNHKGTTMMLNDRIQSLRGLQSSLRKAEEYLMGIPQDTPYSEFNHRFQELGLEKGWGDCAKRVLDTIHLLLDLLEAPDPANLEKFLGTIPMMFNVVILSPHGYFAQSNVLGYPDTGGQVVYILDQVRALENEMLLRIKQQGLDITPKILIVTRLLPDAVGTTCGQRVEKVIGTEHTDILRVPFRSENGILRKWISRFDVWPFLETYTEDVANEIMREMQAKPDLIIGNYSDGNLVATLLAHKLGVTQCTIAHALEKTKYPNSDIYLDKFDSQYHFSCQFTADLIAMNHTDFIITSTFQEIAGSKDTVGQYESHIAFTLPGLYRVVHGIDVFDPKFNIVSPGADMSVYFPYTEADKRLTAFHPEIEELLYSEVENDEHKFVLKDKNKPIIFSMARLDRVKNMTGLVEMYGKNAHLRDLANLVIVCGDHGNQSKDREEQAEFKKMYGLIDQYKLKGHIRWISAQMNRVRNGELYRYICDTKGVFVQPAFYEAFGLTVIEAMTCGLPTIATCHGGPAEIIVDGVSGLHIDPYHSDKAADILVNFFEKCKQDSTYWDNISQGGLQRIYEKYTWKLYSERLMTLTGVYGFWKYVSNLERRETRRYIEMFYALKYRSLASAVPLAVDGESTSK	808
	OsSS3	Os07g0616800	MGETTGERALTRLHSMRERIGDSLSAHTNELVAVFSRLVNQGKGMLQPHQIIAEYNAAIPEGEREKLKDSALEDVLRGAQEAIVIPPWIALAIRPRPGVWEYLRINVSQLGVEELSVPEYLQFKEQLVDGSTQNNFVLELDFEPFNASFPRPSLSKSIGNGVQFLNRHLSSKLFHDKESMYPLLNFLRAHNYKGMTMMLNDRIRSLDALQGALRKAEKHLAGITADTPYSEFHHRFQELGLEKGWGDCAQRVRETIHLLLDLLEAPEPSALEKFLGTIPMVFNVVILSPHGYFAQANVLGYPDTGGQVVYILDQVRAMENEMLLRIKQQGLNITPRILIVTRLLPDAHGTTCGQRLEKVLGTEHTHILRVPFRTENGTVRKWISRFEVWPYLETYTDDVAHEISGELQATPDLIIGNYSDGNLVACLLAHKLGVTHCTIAHALEKTKYPNSDLYWKKFEDHYHFSCQFTADLIAMNHADFIITSTFQEIAGNKETVGQYESHMAFTMPGLYRVVHGIDVFDPKFNIVSPGADMSIYFPFTESQKRLTSLHLEIEELLFSDVENTEHKFVLKDKKKPIIFSMARLDHVKNLTGLVELYGRNPRLQELVNLVVVCGDHGKESKDKEEQAEFKKMFNLIEQYNLNGHIRWISAQMNRVRNGELYRYICDMRGAFVQPALYEAFGLTVIEAMTCGLPTFATAYGGPAEIIVHGVSGYHIDPYQNDKASALLVEFFEKCQEDPNHWIKISQGGLQRIEEKYTWKLYSERLMTLSGVYGFWKYVTNLDRRETRRYLEMLYALKYRKMATTVPLAIEGEASTK	816
	OsSS4	Os03g0340500	MSGPKLDRTPSIRDRVEDTLHAHRNELVALLSKYVSQGKGILQPHHILDALDEVQSSGGRALVEGPFLDVLRSAQEAIVLPPFVAIAVRPRPGVWEYVRVNVHELSVEQLTVSEYLRFKEELVDGQYNDPYILELDFEPFNASVPRPNRSSSIGNGVQFLNRHLSSIMFRNKDCLEPLLDFLRGHRHKGHVMMLNDRIQSLGRLQSVLTKAEEHLSKLPADTPYSQFAYKFQEWGLEKGWGDTAGYVLEMIHLLLDVLQAPDPSTLETFLGRIPMIFNVVVVSPHGYFGQANVLGLPDTGGQIVYILDQVRALENEMVLRLKKQGLDFTPKILIVTRLIPEAKGTSCNQRLERISGTQHTYILRVPFRNENGILRKWISRFDVWPYLEKFAEDAAGEIAAELQGTPDFIIGNYSDGNLVASLLSYKMGITQCNIAHALEKTKYPDSDIYWTKYDEKYHFSCQFTADIIAMNNADFIITSTYQEIAGSKNTVGQYESHTAFTLPGLYRIVHGIDVFDPKFNIVSPGADMSIYFPYTEKAKRLTSLHGSLENLISDPEQNDEHIGHLDDRSKPILFSMARLDRVKNITGLVEAYAKNARLRELVNLVVVAGYNDVKKSKDREEIAEIEKMHELIKTYNLFGQFRWISAQTNRARNGELYRYIADTHGAFVQPAFYEAFGLTVVEAMTCGLPTFATVHGGPAEIIEHGISGFHIDPYHPDQAANLIADFFEQCKQDPNHWVEVSNRGLQRIYEKYTWKIYSERLMTLAGVYGFWKYVSKLERRETRRYLEMFYILKFRELAKTVPLAVDEAH	809

Table S2. *Cont.*

	OsSS5	Os04g0309600	MASKLSFKRMDSIAETMPDALRQSRYQMKRCFQRYVSKGKRLLKNQQLMEELEKSLDDKVEKEKLVEGFLGYIICSTQEAVVLPPFVAFAVRMNPGIWEYVKVHSDDLSVEGITPSEYLKFKETLYDEKWAKDDNSLEVDFGALDLSTPHLTLPSSIGNGLQFVSKFMSSKLGGKPESMKPLLDYLLTLNYRGEKLMINDTIDTVSKLQTALLLAEVFVSGLPKYTPYLKFEQRFQEWGLERGWGDTAERCKETLNCLSEVLQAPDPTNMEKFFSRVPSIFNIVIFSIHGYFGQEKVLGLPDTGGQVVYILDQVRAMEEELLQRIKQQGLHVTPKILVLTRLIPDAKGTKCNVELEPVENTKYSHILRVPFKTEDGKDLRQWVSRFDIYPYLERYAQDSCAKILDILEGKPDLIIGNYTDGNLVASLLSNKLCVTQGTIAHALEKTKYEDSDVKWREMDQKYHFSCQFTADMISMNTSDFIITSTYQEIAGSKEKPGQYEHHYAFTMPGLCRYATGINVFDPKFNIAAPGADQSIYFPFTQKQKRLTDLHPQIDELLYSKDDTDEHIGYLADRNKPIIFSMARLDKVKNKKLRDLVNLVVVAGLLDASQSKDREEIEEINKMHNLMDRYQLKGQIRWIKAQTDRVRNGELYRCIADTKGAFVQPALYEAFGLTVIEAMNCGLPTFATNQGGPAEIIIDGVSGFHVNPINDREAGIKIADFFQKCKEDPSYWNKVSTAGLQRICECYTWKIYATRVLNMGSTYSFWKTLNKEERQAKQRYLQIFYNVQYRNLAKAMARAGDQQARQTTTGVAPSEIVVRPKERKPQTRMQRILTRLAGQKPPVSE	844
	OsSS6	Os02g0831500	MAVGLRRSDSIADMMPEALRQSRYQMKRCFQRYVSQGKRLMKRQQLLDELDKSVDDKADKDQLLQGFLGYVISSTQEAAVLPPFVAFAVRMNPGIWEFVKVHSANLSVEQMTPSDYLKNKEALVDDKWGAYDDDSQLEVDFGALDLSTPHLTLPSSIGKGAHLVSRFMSSKLTDNKKPLLDYLLALSHRGDKLMINDILDTVDKLQTALLLAEVYVAGLHPDTNYSEFEQKFQEWGLEKGWGDTAETCKETLSSLSEVLQAPDPINMEKFFSTVPCVFTVVIFSIHGYFGQEKVLGMPDTGGQVVYILDQVRALEDELLQRIKQQGLNATPKILVLTRLIPEAKGTKCNVELEPIENTKHSNILRVPFKTEDGKVLPQWVSRFDIYPYLERYAQDSSVKILEILEGKPDLVIGNYTDGNLVASLLTSKLGVTQGTIAHALEKTKYEDSDIKWRELDHKYHFSCQFTADMIAMNTSDFIIASTYQEIAGSKEKPGQYESHYAFTMPGLCRYATGINVFDPKFNIAAPGADQSVYFPFTQKQKRLTDLHPQIEELLYSKEDNNEHIGHLADRSKPIIFSMARLDKIKNITGLVEWYGQNKRLRDLVNLVIVGGLLDPSQSKDREEIEEINKMHSLINKYQLVGQIRWIKGQTDRVRNGELYRCIADTKGAFVQPALYEAFGLTVIEAMNCGLPTFATNQGGPAEIIVDEVSGFHINPLNGKEASDKIADFFQKCKEDLIYWSKMSTAGLQRIYECYTWQIYATKVLNMASIYGFWRTLDKEERQAKQHYLHMFYNLQFRKLAKNVPTLGEQPAQPTESAEPNRIIPRPKERQVCPFLRNLLKKETGNN	846
Zea mays	ZmSS1	L29418	MGEGAGDRVLSRLHSVRERIGDSLSAHPNELVAVFTRLKNLGKGMLQPHQIIAEYNNAIPEAEREKLKDGAFEDVLRAAQEAIVIPPWVALAIRPRPGVWEYVRVNVSELAVEELRVPEYLQFKEQLVEEGPNNNFVLELDFEPFNASFPRPSLSKSIGNGVQFLNRHLSSKLFHDKESMYPLLNFLRAHNYKGMTMMLNDRIRSLSALQGALRKAEEHLSTLQADTPYSEFHHRFQELGLEKGWGDCAKRAQETIHLLLDLLEAPDPSTLEKFLGTIPMVFNVVILSPHGYFAQANVLGYPDTGGQVVYILDQVRAMENEMLLRIKQCGLDITPKILIVTRLLPDATGTTCGQRLEKVLGTEHCHILRVPFRTENGIVRKWISRFEVWPYLETYTDDVAHEIAGELQANPDLIIGNYSDGNLVACLLAHKMGVTHCTIAHALEKTKYPNSDLYWKKFEDHYHFSCQFTTDLIAMNHADFIITSTFQEIAGNKDTVGQYESHMAFTMPGLYRVVHGIDVFDPKFNIVSPGADLSIYFPYTESHKRLTSLHPEIEELLYSQTENTEHKFVLNDRNKPIIFSMARLDRVKNLTGLVELYGRNKRLQELVNLVVVCGDHGNPSKDKEEQAEFKKMFDLIEQYNLNGHIRWISAQMNRVRNGELYRYICDTKGAFVQPAFYEAFGLTVVEAMTCGLPTFATAYGGPAEIIVHGVSGYHIDPYQGDKASALLVDFF	816

Table S2. *Cont.*

			DKCQAEPSHWSKISQGGLQRIEEKYTWKLYSERLMTLTGVYGFWKYVSNLERRETRRYLEMLYALKYRTMASTVPVAVEGEPSSK	
	ZmSS2	L22296	MGEGAGDRVLSRLHSVRERIGDSLSAHPNELVAVFTRLKNLGKGMLQPHQIIAEYNNAIPEAEREKLKDGAFEDVLRAAQEAIVIPPWVALAIRPRPGVWEYVRVNVSELAVEELRVPEYLQFKEQLVEEGPNNNFVLELDFEPFNASFPRPSLSKSIGNGVQFLNRHLSSKLFHDKESMYPLLNFLRAHNYKGMTMMLNDRIRSLSALQGALRKAEEHLSTLQADTPYSEFHHRFQELGLEKGWGDCAKRAQETIHLLLDLLEAPDPSTLEKFLGTIPMVFNVVILSPHGYFAQANVLGYPDTGGQVVYILDQVRAMENEMLLRIKQCGLDITPKILIVTRLLPDATGTTCGQRLEKVLGTEHCHILRVPFRTENGIVRKWISRFEVWPYLETYTDDVAHEIAGELQANPDLIIGNYSDGNLVACLLAHKMGVTHCTIAHALEKTKYPNSDLYWKKFEDHYHFSCQFTTDLIAMNHADFIITSTFQEIAGNKDTVGQYESHMAFTMPGLYRVVHGIDVFDPKFNIVSPGADLSIYFPYTESHKRLTSLHPEIEELLYSQTENTEHKFVLNDRNKPIIFSMARLDRVKNLTGLVELYGRNKRLQELVNLVVVCGDHGNPSKDKEEQAEFKKMFDLIEQYNLNGHIRWISAQMNRVRNGELYRYICDTKGAFVQPAFYEAFGLTVVEAMTCGLPTFATAYGGPAEIIVHGVSGYHIDPYQGDKASALLVDFFDKCQAEPSHWSKISQGGLQRIEEKYTWKLYSERLMTLTGVYGFWKYVSNLERRETRRYLEMLYALKYRTMASTVPLAVEGEPSSK	816
	ZmSS3	BT069288	MGEGAGDRVLSRLHSVRERIGDSLSAHPNELVAVFTRLKNLGKGMLQPHQIIAEYNNAIPEAEREKLKDGAFEDVLRAAQEAIVIPPWVALAIRPRPGVWEYVRVNVSELAVEELRVPEYLQFKEQLVEEGPNNNFVLELDFEPFNASFPRPSLSKSIGNGVQFLNRHLSSKLFHDKESMYPLLNFLRAHNYKGMTMMLNDRIRSLSALQGALRKAEEHLSTLQADTPYSEFHHRFQELGLEKGWGDCAKRAQETIHLLLDLLEAPDPSTLEKFLGTIPMVFNVVILSPHGYFAQANVLGYPDTGGQVVYILDQVRAMENEMLLRIKQCGLDITPKILIVTRLLPDATGTTCGQRLEKVLGTEHCHILRVPFRTENGIVRKWISRFEVWPYLETYTDDVAHEIAGELQANPDLIIGNYSDGNLVACLLAHKMGVTHCTIAHALEKTKYPNSDLYWKKFEDHYHFSCQFTTDLIAMNHADFIITSTFQEIAGNKDTVGQYESHMAFTMPGLYRVVHGIDVFDPKFNIVSPGADLSIYFPYTESHKRLTSLHPEIEELLYSQTENTEHKFVLNDRNKPIIFSMARLDRVKNLTGLVELYGRNKRLQELVNLVVVCGDHGNPSKDKEEQAEFKKMFDLIEQYNLNGHIRWISAQMNRVRNGELYRYICDTKGAFVQPAFYEAFGLTVVEAMTCGLPTFATAYGGPAEIIVHGVSGYHIDPYQGDKASALLVDFFDKCQADPSHWSKISQGGLQRIEEKYTWKLYSERLMTLTGVYGFWKYVSNLERRETRRYLEMLYALKYRTMASTVPLAVEGEPSSK	816
	ZmSS4	NM_001111941	MAAKLTRLHSLRERLGATFSSHPNELIALFSRYVHQGKGMLQRHQLLAEFDALFDSDKEKYAPFEDILRAAQEAIVLPPWVALAIRPRPGVWDYIRVNVSELAVEELSVSEYLAFKEQLVDGQSNSNFVLELDFEPFNASFPRPSMSKSIGNGVQFLNRHLSSKLFQDKESLYPLLNFLKAHNYKGTTMMLNDRIQSLRGLQSSLRKAEEYLLSVPQDTPYSEFNHRFQELGLEKGWGDTAKRVLDTLHLLLDLLEAPDPANLEKFLGTIPMMFNVVILSPHGYFAQSNVLGYPDTGGQVVYILDQVRALENEMLLRIKQQGLDITPKILIVTRLLPDAAGTTCGQRLEKVIGTEHTDIIRVPFRNENGILRKWISRFDVWPYLETYTEDVSSEIMKEMQAKPDLIIGNYSDGNLVATLLAHKLGVTQCTIAHALEKTKYPNSDIYLDKFDSQYHFSCQFTADLIAMNHTDFIITSTFQEIAGSKDTVGQYESHIAFTLPGLYRVVHGIDVFDPKFNIVSPGADMSVYYPYTETDKRLTAFHPEIEELIYSDVENSEHKFVLKDKKKPIIFSMARLDRVKNMTGLVEMYGKNARLRELANLVIVAGDHGKESKDREEQAEFKKMYSLIDEYKLKGHIRWISAQMNRVRNGELYRYICDTKGAFVQPAFYEAFGLTVIESMTCGLPTIATCHGGPAEIIVDGVSGLHIDPYHSDKAADILVNFFDKCKADPSYWDEISQ	802

Table S2. *Cont.*

			GGLQRIYEKYTWKLYSERLMTLTGVYGFWKYVSNLERRETRRYIEMFYALKYRSLASQVPLSFD	
	ZmSS5	EU971052	MAAKLTRLHSLRERLGATFSSHPNELIALFSRYVHQGKGMLQRHQLLAEFDALFDSDKEKYAPFEDILRAAQEAIVLPPWVALAIRPRPGVWDYIRVNVSELAVEELSVSEYLAFKEQLVDGQSNSNFVLELDFEPFNASFPRPSMSKSIGNGVQFLNRHLSSKLFQDKESLYPLLNFLKAHNYKGTTMMLNDRIQSLRGLQSSLRKAEEYLLSVPQDTPYSEFNHRFQELGLEKGWGDTAKRVLDTLHLLLDLLEAPDPANLEKFLGTIPMMFNVVILSPHGYFAQSNVLGYPDTGGQVVYILDQVRALENEMLLRIKQQGLDITPKILIVTRLLPDAAGTTCGQRLEKVIGTEHTDIIRVPFRNENGILRKWISRFDVWPYLETYTEDVSSEIMKEMQAKPDLIIGNYSDGNLVATLLAHKLGVTQCTIAHALEKTKYPNSDIYLDKFDSQYHFSCQFTADLIAMNHTDFIITSTFQEIAGSKDTVGQYESHIAFTLPGLYRVVHGIDVFDPKFNIVSPGADMSVYYPYTETDKRLTAFHPEIEELINSDVENSEHKFVLKDKKKPIIFSMARLDRVKNMTGLVEMYGKNARLRELANLVIVAGDHGKESKDREEQAEFKKMYSLIDEYKLKGHIRWISAQMNRVRNGELYRYICDTKGAFVQPAFYEAFGLTVIESMTCGLPTIATCHGGPAEIIVDGVSGLHIDPYHSDKAADILVNFFDKCKADPSYWDKISQGGLQRIYEKYTWKLYSERLMTLTGVYGFWKYVSNLERRETRRYIEMFYALKYRSLASQVPLSFD	802
Triticum aestivum	TaSS1	AJ001117	MAAKLTRLHSLRERLGATFSSHPNELIALFSRYVHQGKGMLQRHQLLAEFDALFESDKEKYAPFEDILRAAQEAIVLPPWVALAIRPRPGVWDYIRVNVSELAVEELTVSEYLAFKEQLVDEHASSKFVLELDFEPFNASFPRPSMSNSIGKRVQFLNRHLSSQLFQDKESLYPLLNFLKAHYYKGTTMMLNDRIQSLRGLQSALRKAEEYLVSIPEDTPSSEFNHRFQELGLEKGWGDTAKRVHDTIHLLLDLLEAPDPASLEKFLGTIPMMFNVVILSPHGYFAQSNVLGYPDTGGQVVYILDQVRALENEMLLRIKQQGLDITPKILIVTRLLPDAVGTTCGQRLEKVIGTEHTDILRVPFRTDNGILRKWISRFDVWPYLETYTEDVANELMREMQTKPDFIIGNNSDGNLVATLLAHKLGVTQCTIAHALEKTKYPNSDIYLDKFDSQYHFSCQFTADLIAMNHTDFIITSTFQEIAGSKDSVGQYESHIAFTLPDLYRVVHGIDVFDPKFNIVPGADMTVYFPYTETDKRLTAFHSEIEELLYSDVENDEHKFVLKDRNKPIIFSMARLDRVKNMTGLVEMYGKNAHLKGFGKLVIVAGDHGKESKDREEQAEFKRMYSLIEEYKLKGHIRWISAQMNRVRNGELYRYICDTKGAFVQPAFYEAFGLTVIEVHECGLPTIATCHGGPAEIIVNGVSGLHIDPYHSDKAADILVNFFEKCSEDPSYWDKMSEGGLKRIYEKYTWKLYSERLMTLTGVYGFWKYVSNLERRETRRYLEMFYALKYRSLAAAVPLAVDGESSDN	807
	TaSS2	AJ000153	MGETAGGRALSRIHSVRERIGDSLSAHTNELVAVFSRLVNQGKGMLQPHQITAEYNAAIPEAEREKLKDTAFEDLLRGAQEAIVIPPWVALAIRPRPGVWEYVRVNVSELGVEELNVLNYLQFKEQLANGSIDNNFVLELDFEPFNASFPRPSLSKSIGNGVQFLNRHLSSKLFHDKESMYPLLNFLRAHNYKGMTMMLNDRIRSLGTLQGALRKAETHLSGLPADTPYSEFHHRFQELGLEKGWGDCAQRASETIHLLLDLLEAPDPSSLEKFLGTIPMVFNVVILSPHGYFAQANVLGYPDTGGQVVYILDQVRAMENEMLLRIKQQGLDITPKILIVTRLLPDAHGTTCGQRLEKVLGTEHTHILRVPFKTEDGIVRKWISRFEVWPYLEAYTDDVAHEIAGELQATPDLIIGNYSDGNLVACSLAHKLGVTHCIAHALEKTKYPNSDLYWKKFEDHYHFSCQFTADLIAMNHADFIITSTFQEIAGNKDTVGQYESHMAFTMPSLYRVVHGIDVFDPKFNIVSPGADMSIYFPYTEQQKRLTSLHTEIEELLFSDVENAEHKFVLKDKKKPIIFSMARLDRVKNMTGLVEMYGRNPRLQELVNLVVVCGDHGKVSKDKEEQAEFKKMFDLIEQYNLIGHIRWISAQMNRVRNGELYRYICDMKGAFVQPAFYEAFGLTVIEAMTCGLPTFATAYGGPAEIIVHGVSGYHIDPYQNDKASALLVDF	815

			FGKCQEDPSHWNKISQGGLQRIEEKYTWKLYSERLMTLSGVYRFWKYVSNLDRRETRRYLEMLYALKYRKMAATVPLAVEGETSGK	
Hordeum vulgare	HvSS1	X69931	MGETAGERALSRVHSVRERIGHSLSAHTNELVAVFSRLVNQGKGMLQPHQITAEYNAAIPEAEREKLKNTPFEDLLRGAQEAIVIPPWVALAIRPRPGVWEYVRVNVSELGVEELSVLRYLQFKEQLANGSTDNNFVLELDFGPFNASFPRPSLSKSIGNGVQFLNRHLSSKLFHDKESMYPLLNFLRAHNYKGMTMMLNDRIRSLGTLQGALRKAETHLSGLPADTPYTEFHHRFQELGLEKGWGDCAQRASETIHLLLDLLEAPDPSSLEKFLGTIPMVLNVVILSPHGYFAQANVLGYPDTGGQVVYILDQVRAMENEMLLRIKQQGLDITPKILIVTRMLPDAHGTTCGQRLEKVLGTEHTHILRVPFKTEDGIVRKWISRFEVWPYLEAYTDDVAHEIAGELQANPDLIIGNYSDGNLVACLLAHKLGVTHCTIAHALEKTKYPNSDLYWKKFEDHYHFSCQFTADLIAMNHADFIITSTFQEIAGNKDTVGQYESHMAFTMPGLYRVVHGIDVFDPKFNIVSPGADMSIYFPYTEQQKRLTSLHTEIEELLFSDVENAEHKFVLKDKKKPIIFSMARLDRVKNMTGLVEMYGRNPRLQELVNLVVVCGDHGKVSKDKEEQVEFKKMFDLIEKYNLSGHIRWISAQMNRVRNGELYRYICDMKGAFVQPAFYEAFGLTVIEAMTCGLPTFATAYGGPAEIIVNGVSGYHIDPYQNDKASALLVGFFGKCQEDPSHWNKISQGGLQRIEEKYTWKLYSERLMTLSGVYGFWKYVSNLDRRETRRYLEMLYALKYRKMAATVPLAVEGETSGE	816
	HvSS2	Y15802	MGETAGERALSRVHSVRERIGHSLSAHTNELVAVFSRLVNQGKGMLQPHQITAEYNAAIPEAEREKLKNTPFEDLLRGAQEAIVIPPWVALAIRPRPGVWEYVRVNVSELGVEELSVLRYLQFKEQLANGRTDNNFVLELDFGPFNASFPRPSLSKSIGNGVQFLNRHLSSKLFHDKESMYPLLNFLRAHNYKGMAMMLNDRIRSLGTLQGALRKAETHLSGLPADTPYSEFHHRFQELGLEKGWGDCAQRASETIHLLLDLLEAPDPSSLEKFLGTIPMVFNVVILSPHGYFAQANVLGYPDTGGQVVYILDQVRAMENEMLLRIKQQGLDITPKILIVTRMLPDAHGTTCGQRLEKVLGTEHTHILRVPFKTEDGIVRKWISRFEVWPYLEAYTDDVAHEIAGELQANPDLIIGNYSDGNLVACLLAHKLGVTHGTIAHALEKTKYPNSDLYWKKFEDHYHFSCQFTADLIAMNHADFIITSTFQEIAGKKDTVGQYESHMAFTMPGLYRVVHGIDVFDPKFNIVSPGADMSIYFPYTEQQKRLTSLHTEIEELLFSDVENAEHKFVLKDKKKPIIFSMARLDRVKNMTGLVEMYGRNPRLQELVNLVVVCGDHGKVSKDKEEQVEFKKMFDLIEKYNLSGHIRWISAQMNRVRNGELYRYICDMKGAFVQAAFYEAFGLTVIEAMTCGLPTFATAYGGPAEIIVNGVSGYHIDPYQNDKASALLVDFFGKCQEDPSHWNKISQGGLQRIEEKYTWKLYSERLMTLSGVYGFWKYVSNLDRRETRRTLKCSMPSSTAKWLQLSHWLLRARPRANDLSLPEK	823
Bambusa oldhamii	BoSS1	AF412036	MGEAAGDRVLSRLHSVRERIGDSLSAHPNELVAVFTRLVNLGKGMLQPHQIIAEYNNAIPEAEREKLKDGAFEDVLRAAQEAIVIPPWVALAIRPRPGVWEYVRVNVSELAVEELRVPEYLQFKEQLVEGSTNNNFVLELDLEPFNASFPRPSLSKSIGNGVQFLNRHLSSKLFHDKESMYPLLNFLRAHNYKGMTMMLNDRIRSLSALQGALRKAEEHLSGLSADTSYSDFHHRFQELGLEKGWGDCAKRAQETIHLLLDLLEAPDPSTLEKFLGTIPMVFNVVILSPHGYFAQANVLGYPDTGGQVVYILDQVRAMENEMLLRIKQQGLNITPRILIVTRLLPDATGTTCGQRLEKVLGTEHTHILRVPFRTENGIVRKWISRFEVWPYLETFTDDVAHEIAGELQANPDLIIGNYSDGNLVACLLAHKMGVTHCTIAHALEKTKYPNSDLYWKKFEDHYHFSCQFTTDLIAMNHADFIITSTFQEIAGNKDTVGQYESHMAFTMPGLYRVVHGIDVFDPKFNIVSPGADLSIYFPYTESHKRLTSLHPEIEELLYSDVDNHEHKFVLKDRNKPIIFSMARLDRVKNLTGLVELYGRNPRLQELVNLVVVCGDHGNPSKDKEEQAEFQKMFDLIEQYNLNGHIRWISAQMNRVRNGELYRYICDTKGAFVQPAFYEAFGLTVVESMTCGLPTFATAYGGPAEIIVHGVSGFHIDPYQGDKASALLVEFFEKCQQDHSHWTKISQGGLQRIEEKYTWKLYSERLMTLTGVYGFWKYVSNLERRETRRYLEMLYALKYRTMASTVPLAVDGEPSSK	816

Table S2. *Cont.*

	BoSS2	AF412038	MAAKLTRLHSLRERLSATFSSHPNELIALFSRYVHQGKGMLQRHQLLAEFDALIAADKEKYAPFEDILRAAQEAIVLPPWVALAIRPRPGVWDYIRVNVSELAVEELSVSEYLEFKEQLVDGHTNSNFVLELDFEPFNASFPRPSMSKSIGNGVQFLNRHLSSKLFQDKESLYPLLNFLKAHNHKGTTMMLNDRIQSLRGLQSALRKAEEYLMSFPQDTPYSEFNHRFQELGLEKGWGDTAKRVLDTIHLLLDLLEAPDPANLEKFLGTIPMTFNVVILSPHGYFAQSNVLGYPDTGGQVVYILDQVRALENEMLLRIKQQGLDITPKILIVTRLLPDAVGTTCGQRLEKVIGTEHTDILRVPFRTENGILRKWISRFDVWPFLETYTEDVANEIMREMQAKPDLIIGNYSDGNLVATLLAHKLGVTQCTIAHALEKTKYPNSDIYLDKFDSQYHFSCQFTADLIAMNHTDFIITSTFQEIAGSKDTVGQYESHIAFTLPGLYRVVHGIDVFDPKFNIVSPGADMSVYFPYTETDKRLTAFHPEIEELIYSDVENSEHKFVLKDKNKPIIFSMARLDRVKNMTGLVEMYGKNAHLRDLANLVIVAGDHGKESKDREEQAEFKRMYSLIDEYKLKGHIRWISAQMNRVRNGELYRYICDTKGVFVQPAFYEAFGLTVIESMTCGLPTIATCHGGPAEIIVDGVSGLHIDPYHSNKAADILVNFFEKCKEDPTYWDKISQGGLKRIYEKYTWKLYSERLMTLTGVYGFWKYVSNLERRETRRYLEMFYALKYRSLASAVPLAVDGDSAAN	808
	BoSS3	AF412037	MGETAGDRVLSRLHSVRERIGDSLSAHPNELVAVFTRLVNLGKGMLQPHQIIAEYNNAIPEAERDKLKDGAFEDVLRAAQEAIVIPPWVALAIRPRPGVWEYVRVNVSELAVEELRVPEYLQFKEQLVEGSTNNNFVLELDFEPFNASFPRPSLSKSIGNGVQFLNRHLSSKLFHDKESMYPLLNFLRAHNYKGMTMMLNDRIRSLSALQGALRKAEEHLSGLSADTPYSDFHHRFQELGLEKGWGDCAKRAQETIHLLLDLLEAPDPSTLEKFLGTIPMVFNVVILSPHGYFAQANVLGYPDTGGQVVYILDQVRAMENEMLLRIKQQGLNITPRILIVTRLLPDATGTTCGQRLEKVLGTEHTHILRVPFRTENGIVRKWISRFEVWPYLETFTDDVAHEIAGELQANPDLIIGNYSDGNLVACLLAHKMGVTHCTIAHALEKTKYPNSDLYWKKFEDHYHFSCQFTTDLIAMNHADFIITSTFQEIAGNKDTVGQYESHMAFTMPGLYRVVHGIDVFDPKFNIVSPGADMSIYFPYSESHKRLTSLHPEIEELLYSDVDNNEHKFVLKDRNKPIIFSMARLDRVKNLIGLVELYGRNPRLQELVNLVVVCGDHGNPSKDKEEQAEFKKMFDHIEQYNLNGHIRWISAQMNRVRNGELYRYICDTRGAFVQPAFYEAFGLTVVESMSCGLPTFATAYGGPAEIIVHGVSGFHIDPYQGDKASALLVEFFEKCQQDPAHWTKISQGGLQRIEEKYTWKLYSERLMTLTGVYGFWKYVSNLERRETRRYLEMLYALKYRKMASTVPLAVEGEPSNK	816
	BoSS4	AF412039	MAAKLTRLHSLRERLGATFSSHPNELIALFSRYVNQGKGMLQRHQLLAEFDALMDADKEKYAPFEDILRAAQEAIVLPPWVALAIRPRPGVWDYIRVNVSELAVEELSVSEYLAFKEQLVDGHTNSNFVLELDFEPFNASFPRPSMSKSIGNGVQFLNRHLSSKLFQDKESLYPLLNFLKAHNPKGKTMMLNDRIQSLRGLQSALRKAEEYLISIPQDTPCSEFNHRFQELGLEKGWGDTAKRVLDTIHLLLDLLEAPDPANLEKFLGTIPMTFNVVILSPHGYFAQSNVLGYPDTGGQVVYILDQVRALENEMLLRIKQQGLDITPKILIVTRLLPDAVGTTCGQRLEKVLGTEHTDILRVPFRTENGILRKWISRFDVWPFLETYTEDVANEIMREMQAKPDLIIGNYSDGNLVATLLAHKLGVTQCTIAHALEKTKYPNSDIYLDKFDSQYHFSCQFTADLIAMNHTDFIITSTFQEIAGSKDTVGQYESHIAFTLSGLYRVVHGIDVFDPKFNIVSPGADMSVYFPYTETDKRLTAFHPEIEELIYSDVENSEHQFVLKDKNKPIIFSMARLDRVKNMTGLVEMYGKNAHLRDLANLVVVAGDHGKESKDREEQAEFKRMYSLIEEYKLKGHIRWISAQMNRVRNGELYRYICDTRGVFVQPAFYEAFGLTVIESMTCGLPTIATCHGGPAEIIVDGVSGLHIDPYHSDKAADILVNFFEKCKEDPTYWDKISLGGLKRIYEKYTWKLYSERLMTLTGVYGFWKYVSNLERRETRRYLEMFYALKYRSLASAVPLAVDGDSVAK	808

Table S2. *Cont.*

B. Bacteria				
Nostoc punctiforme	NpSSA	AJ316589	MSELLQAVLDSEERSDLRSFLSELRQQEKKYLLRNDILNVYSEYCSKSQKPEAYYTTSELGKLIYYTQEIIQEDSNFCFIIRSKIASQEVYWLTSDLSIEPMTVQDLLDLRDRLVNKFHPNDGDLLELDFGPFYDYTPIIRDPKNIGKGVQFLNRYLSSKIFQDSKQLLENLLNFLRLHHYNGVQLLVNDRIQSQQQLSEQVKKAIGFVNNRPDDEPYEQFRFQLQSMGFEPGWGNTAARVRETLNILDELIDSADPQTLEAFISRVPMIFRIVLVSAHGWFGQEGVLGRPDTGGQVVYVLDQAKSLEKQLQEDVLLAGLEKLNVEPKVIILTRLIPNSDGTLCNQRLEKVHGTENAWILRVPLRDFNPNMTQNWISRFEFWPYLETFAIDSERELRAEFQGTPDLIVGNYTDGNLIAFLLARRLKVTQCNVAHALEKSKYLFSNLYWQELEEKYHFSLQFTADLIAMNAANFVVSSTYQEIVGTPDSVGQYESYKCFTMPELYHVTNGIELFSPKFNVVPPGVNENNYFPYTRTKDRVESDRQRLAETLFTLEDPTQIFGKLDDPNKRPLFSMARLDHIKNLTGLAECYGQSKELQEHCNLILVAGKLRVEESGDNEERDEIIKLYNIIDEYNLHGKIRWLGVRLSKTDSGEIYRVIADRQGIFVQPALFEAFGLTILESMVSGLPTFATQFGGPLEIIQDKVNGFLINPTNLDETATKIVDFITKCEQNPNYWNEISQRGIDRVYSTYTWKIHTSKLLSLARIYGFWNFTSKENREDLLRYLEALFYLIYKPRAQQLLEQHKYR	806
Lyngbya majuscule	LmSS	AY522504	LIQDVLESDEKSDLRHFTSQLKTAEPRYLLRNEILAAFNEYCTKHKKSEYFYHSSHLGKLIYYTQEIILEDESLCLIIRPKIAAKRAFRLFEDLRAQEVTPEELLDIRDRFVNRYNPKVGEVLQLDFQPFYDYSPLIRDPKNIGKGVRFLNRYLSSKLFQDPEQWLESLYGFLKVRHFHGNQLLINERIHNHQQLSEQVKLALEFVSDRPDSESYDKFRFKLQEMGFEPGWGNTASRVRETLAMLDELIDEPDDRALEQFLSRIPMIFRIVLVSVHGWFGQEGVLGRPDTGGQVVYVLDQAKSLEKQLQENLTLAGLNIQPKVIILTRLIPNNDGTRCNERLEKIKGTENAWILRVPFREFNPKVTQDWISRFEIWPYLETYAIDAEKELLAEFQGRPDLIVGNYSDGNLVAFLLARRLKVTQCNIAHALEKSKYLFSNLYWQDSEQQYHFSLQFTADLIAMNAANFIISSTYQEIVGTADSVGQYESYQNFTMPDLYHVINGIELFSPKFNVVPPGVNETVFFPYTRTQGRVASDIKRLDEFLFTLDDEAQVFGKLDYPNKRPIFSMARLDRIKNLTGLAECFGKSRKLQERCNLILIAGNLRTEDSSDSEEKAEIIKLYQIIEEYNLYGKIRWLGVRLSKSDSGEVYRVIADRHGIFVQPALFEAFGLTILESMISGLPTFGTQFGGPLEIIQDKVNGILINPTNQEEMAQKILDFVTKCEENPQYWEEISNQGIERVYSTYTWKIHTTRLLSLARIYRFWNYTSKANQEDMLRYLEALFHLIYKPRAKKLLEEHLTLPARA	804
Thermosynechococcus elongates	TeSS	NP_681838	MTCVLLKAVVESDERADLRQFSRILQLGEKRYLLRNDILDAFADYCRDQERPVPPPSESRLSKLVFYTQEIIVDNESLCWIVRPRIAQQEVCRLLVEDLTIVPMTIPELLDLRDRLVNHYHPNEGDVFEIDVQPFYDYSPIIRDAKNIGKGVEFLNRYLSSKLFQDPRQWQQNLFNFLRIHRYNGYQLLINERIRSPQHLSEQVKQALVVLSDRPPTEAYSEFRFELQNLGFEPGWGNTVARVRDTLEILDQLLDSPDHQVLEAFVSRIPMLFRIALISPHGWFGQEGVLGRPDTGGQVVYILDQVKSLEKQMREDLELAGLGVLEAQPKIIVLTRLIPNAEGTLCNQRLEKIYGTNDAWILRVPFREFNPKVTQNWISRFEIWPYLETFAIDAERELRAEFGHVPDLIIGNYSDGNLVAFLLARRLKVTQCNIAHALEKSKYLFSNLYWQDLEDKYHFSLQFTADLIAMNAANFIISSTYQEIVGTPDSIGQYESYQSFTMPDLYHVVNGIELFSPKFNVVPPGVNEQVYFPYYHYTERLEGDRQRLEELLFTLEDPQQIYGYLEAPEKRPLFSMARLDRIKNLTGLAEAFGRSKALQERCNLILVAGKLRTADSSDREEIAEIEKLYQIIHQYNLHGKIRWLGIRLPKADSGEIYRIIADRQGIFVQPALFEAFGLTILEAMISGLPTFGTRFGGPLEIIQDGVNGFYINPTHLEEMAETIVRFLEACDRDPQEWQRISKAGI	808

Table S2. *Cont.*

			ERVYSTYTWKIHCTRLLSLAKIYGFWNFSSQENREDMMRYMEALFHLLYKPRAQALLAEHLQR	
Acaryochloris marina	AmSS	NC_009925	MSQLIQAVLNSDEKTDLRQFASEVHNQPERYLLRNDILSVFDTFCEKYEKTPAFQLSSRLQKLIYYTQEILVEDENLYLIIRPKIASEEAYRLDPRELVYEQIQIDELLDLRDRFVGHYHPQEGDILEIDFRPFYDYSPVIRDPKNIGRGVQYLNRYLSSKMFEGPQQWLFSLFSFLKLHSYNGTQLLINQRIQSPEHLSECVKQAISLVGGLPPEQPYPEFRFNFQELGFEPGWGNTAARVLETLEMLDELIDSPDDQVLEAFISRIPMIFKIVLVSIHGYFGQEGVLGRPDTGGQVVYVLDQAKSLEKQLQEDLQFAGLDTLEVQPKLIILSRLIPNSEGTLCNQRLEKVHATDNVWILRVPFRELNPKYTQNWISRFEIWPYLETYAIDAERELLAEFRGLPDLIVGNYTDGNLVAFLLSRRLGVTQCNVAHALEKSKYLFSNLYWQDLEEQYHFSMQFTADLIAMNAANFIVTSTYQEIAGRPDTIGQYESYRSFTMPDLYHVVYGAELFSPKFNVVPPGVNESVYFPFTRHQERTPGDIDRLEELLFTLEDPEHVFGHLDNPGKPPLFSMARLDRIKNLTGLAECFGQHPQLQDHYNLILVAGKLRTSDSVDHEEINEIERLYRIIDQYNLHGKIRWLGVRFPKQDSGEIYRVVADHKGIFVQPALFEAFGLTVLEAMISGLPTFATRFGGPLEIIRDGIDGFYINPTHNEEIATKLLEFAKECATNPDYWQQISEQAIERVYTTYTWKIHTSRLLSLAKIYGFWNYTSREKREDMLRYIETIFYLLYKPMAKKLLAKHMDS	807

Table S3. The Ka, Ks and Ka/Ks values of PbSSs duplication gene pairs.

Duplicate genes IDs	ks	ka	Ka/ks	Purifying selection	Duplicated type
PbSS1 vs *PbSS18*	0.2407	0.0403	0.167428	Yes	Segmental
PbSS3 vs *PbSS16*	0.1352	0.0201	0.148669	Yes	Segmental
PbSS3 vs *PbSS17*	0.1308	0.0202	0.154434	Yes	Segmental
PbSS3 vs *PbSS15*	0.8614	0.1627	0.188879	Yes	Segmental
PbSS5 vs *PbSS13*	0.543	0.4424	0.814733	Yes	Segmental
PbSS8 vs *PbSS15*	0.1048	0.0191	0.182252	Yes	Segmental
PbSS10 vs *PbSS20*	0.2181	0.0407	0.186612	Yes	Segmental
PbSS12 vs *PbSS7*	0.4387	0.3837	0.87463	Yes	Segmental
PbSS15 vs *PbSS16*	0.7509	0.1816	0.241843	Yes	Tandem
PbSS25 vs *PbSS1*	0.0112	0.005	0.446429	Yes	Segmental
PbSS25 vs *PbSS18*	0.2193	0.0505	0.230278	Yes	Segmental
PbSS28 vs *PbSS3*	0.8743	0.1751	0.200275	Yes	Segmental
PbSS29 vs *PbSS7*	0.0051	0.0041	0.803922	Yes	Segmental