

SUPPORTING INFORMATION:

Supporting information to Characterization of γ -cadinene enzymes in *Ganoderma lucidum* and *Ganoderma sinensis* from Basidiomycetes provides insight into the identification of terpenoid synthases

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Table S1. The products, protein ID and exon number of published STSs from Basidiomycetes.

Species names and references	Terpene synthase	Main product(s)	Accession No / Protein ID	Number of exons
<i>Agrotype aegerita</i> [1]	Agr1	□ delta-Cadinene	MN146024	4
	Agr2	Viridiflorene	MN146025	5
	Agr3	□ alpha-Muurolene	MN146026	7
	Agr4	delta-Cadinene	MN146027	5
	Agr5	Viridiflorol	MN146028	6
	Agr6	delta-6-Protoilludene	MN146029	6
	Agr7	delta-6-Protoilludene	MN146030	6
	Agr8	□ gamma-Muurolene	MN146031	5
<i>Antrodia cinnamomea</i> [2]	AcTPS4	zonarene	EIW57364	3
	AcTPS5	T-cadinol	EJF64719	4
	AcTPS7	nerolidol	EIW53985	9
	AcTPS9	1-epi-cubenol	EIW57365	3
<i>Armillaria Gallica</i> [3]	Pro1	delta-6-protoilludene	P0DL13/ PBK84744	9

Table S1 (continued)

	CpSTS1	sterprene	LC436345	5
	CpSTS2	alpha-cubebene, delta-cadinene	LC436346	5
	CpSTS3	alpha-muurolene, delta-cadinol	LC436347	6
	CpSTS4	delta-6-protoilludene	LC436348	5
	CpSTS5	gamma-muurolene, alpha-muurolene	LC436349	4
<i>Clitopilus pseudo-pinsitus</i> [4]	CpSTS6	pentalene	LC436350	6
	CpSTS7	alpha-farnesene	LC436351	5
	CpSTS8	alloaromadendrene	LC436352	5
	CpSTS9	ledene, virifloridol	LC436353	5
	CpSTS11	9-alloaromadendrene	LC436355	5
	CpSTS12	beta-elemene, ledene, virifloridol	LC436356	5
	CpSTS13	ledene	LC436357	5
	CpSTS14	beta-elemene, beta-farnesene	LC436358	3
	CpSTS16	aristolene	LC436360	5
	CpSTS17	beta-caryophyllene	LC436361	3
	CpSTS18	gamma-cadinene	LC436362	9
<i>Coniophora puteana</i> [5]	Copu2	□ beta-Copaene	XP_007771895	3
	Copu3	Cubebol	XP_007765978	3
<i>Coprinopsis cinerea</i> [6]	Cop1	Germacrene A	EAU89322	10
	Cop2	Germacrene A	EAU85264	4
	Cop3	□ alpha-Muurolene, Germacrene A	EAU88892	7
	Cop4	□ delta-Cadinene, beta-copaene	EAU85540	5
	Cop6	□ alpha-Cuprenene	EAU89298	5
<i>Dendrothele bispora</i> [1]	Denbi1_659367	delta-6-protoilludene	JGI ID: 659367	5
	Denbi1_816208	Viridiflorol	JGI ID: 816208	5
<i>Fomitopsis pinicola</i> [7]	Fompi1	□ alpha-Cuprenene	EPT01290	5
<i>Galerina</i>	Galma_104215	□ beta-Gurjunene	JGI ID: 104215	5

<i>marginata</i> [1]				
<i>Heterobasidion annosum</i> [1]	Hetan2_454193	delta-6-protoilludene	JGI ID: 454193	5
Table S1 (continued)				
<i>Hypholoma sublateritium</i> [1]	Hypsu1_138665	delta-6-protoilludene	JGI ID: 138665	5
<i>Lignosus rhinoceros</i> [8]	GME3634	alpha-cadinol	KX281943	/
	GME3638	delta-cadinol	KX281944	/
	GME9210	ethanonaphthalene	KX281945	/
<i>Omphalotus olearius</i> [7]	Omp1	□ alpha-Muurolene	JGI ID: 1311	4
	Omp3	Germacrene A, alpha-Muurolene	JGI ID: 4636	7
	Omp4	□ delta-Cadinene	JGI ID: 1447	5
	Omp5a	□ gamma-Cadinene, epi-zonarene,	JGI ID: 2392	5
	Omp5b	gamma-Cadinene,	JGI ID: 2393	5
	Omp6	delta-6-Protoilludene	JGI ID: 4774	4
	Omp7	delta-6-Protoilludene	JGI ID: 2271	5
	Omp9	alpha-barbatene	JGI ID: 3258	4
	Omp10	trans-daucadiene	JGI ID: 3981	4
	<i>Piloderma rozeum</i> [1]	Pilcr_825684	gamma-Cadinene	JGI ID: 825684
<i>Postia placenta</i> [9]	PpSTS01	□ alpha-Muurolene, delta-Cadinene, □ beta-Elemene	JGI ID:60326	6
	PpSTS03	□ alpha-Cadinene, gamma-Cadinene	JGI ID: 99496	4
	PpSTS06	□ alpha-Gurjunene	JGI ID: 45581	6
	PpSTS08	delta-6-Protoilludene	JGI ID: 59374	5
	PpSTS10	□ delta-Cadinene	JGI ID: 98072	3
	PpSTS14	Pentalenene	JGI ID: 101549	11
	PpSTS25	linalool, myrcene	JGI ID: 125961	5
<i>Stereum hirsutum</i> [4]	ShSTS1	alpha-barbatene, beta-barbatene	JGI ID: 159379	3
	ShSTS3	beta-farnesene, alpha-farnesene	JGI ID: 122776	7
	ShSTS4	hirstene	JGI ID: 52743	15
	ShSTS5	gamma-cadinene	JGI ID: 161672	9
	ShSTS7	delta-cadinene	JGI ID: 167646	4

	ShSTS8	alpha-cubebene, 1-epi-cubenol	JGI ID: 146390	5
	ShSTS10	germacrene D, delta-cadinene	JGI ID: 111121	4
Table S1 (continued)				
	ShSTS11	alpha-cubebene, delta-cadinene	JGI ID: 128017	4
	ShSTS12	alpha-cubebene, beta-cubebene	JGI ID: 111127	4
	ShSTS13	beta-caryophyllene	JGI ID: 50042	6
	ShSTS15	delta-6-protoilludene	JGI ID: 64702	5
	ShSTS16	delta-6-protoilludene	JGI ID: 73029	5
	ShSTS17	delta-6-protoilludene	JGI ID: 69906	5
	ShSTS18	delta-6-protoilludene	JGI ID: 25180	5
Termitomyces [10]	STC4	Intermedeol	/	6
	STC9	□ gamma-Cadinene	KNZ74377	9
	STC15	Germacrene D-4-ol	KAG5727529	4
Average				5.53 (5-6)

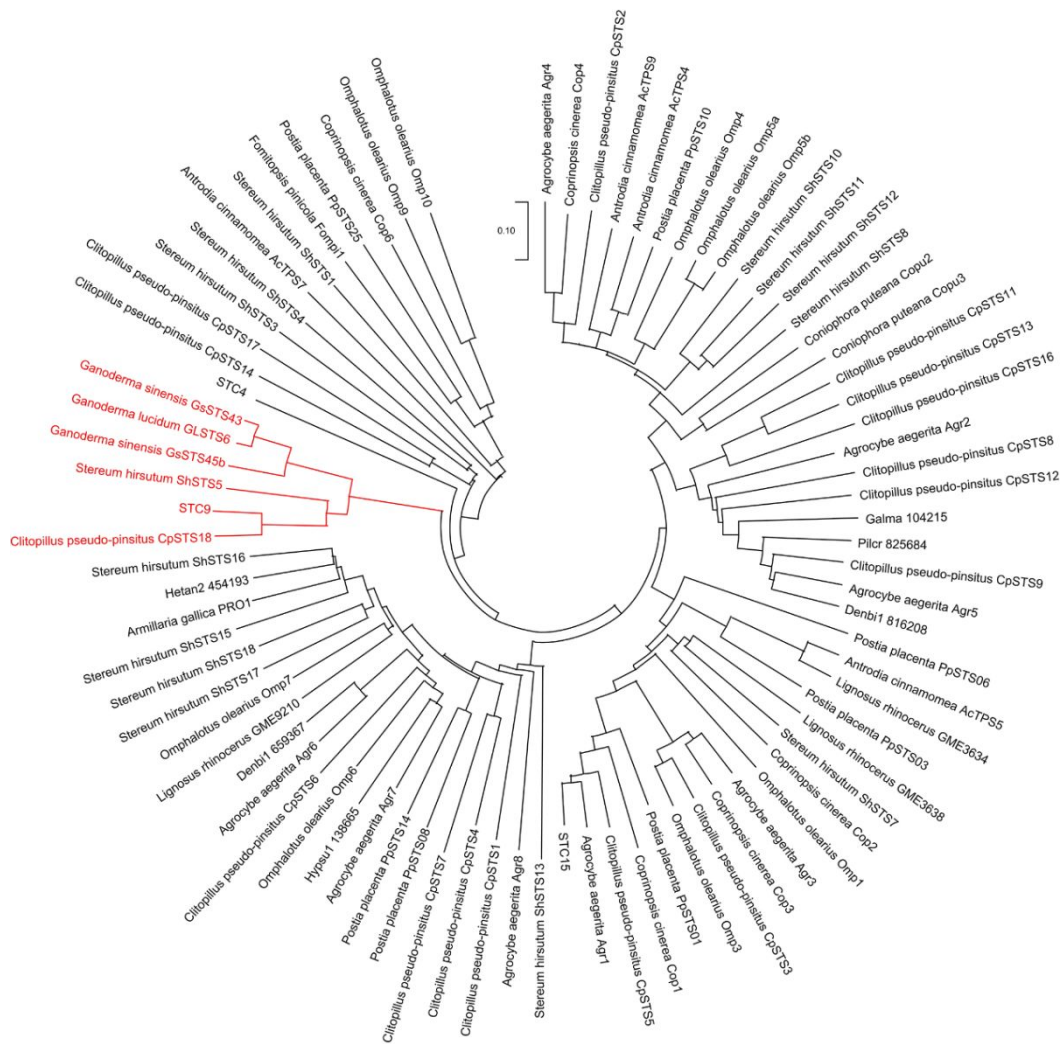


Figure S1. The phylogenetic tree of characterized STSs in Basidiomycetes. GISTS6, GsSTS43, and GsSTS45b, like STC9, CpSTS18, and ShSTS5, located in the small red branch.

Table S2. Protein sequence similarity of the STSs in the small red branch (Figure S1).

	GsSTS43	GsSTS45b	GL22395	CpSTS18	ShSTS5	STC9
GsSTS43						
GsSTS45b	0.197					
GL22395	0.038	0.203				
CpSTS18	0.465	0.491	0.471			
ShSTS5	0.461	0.478	0.467	0.417		
STC9	0.500	0.518	0.503	0.222	0.440	

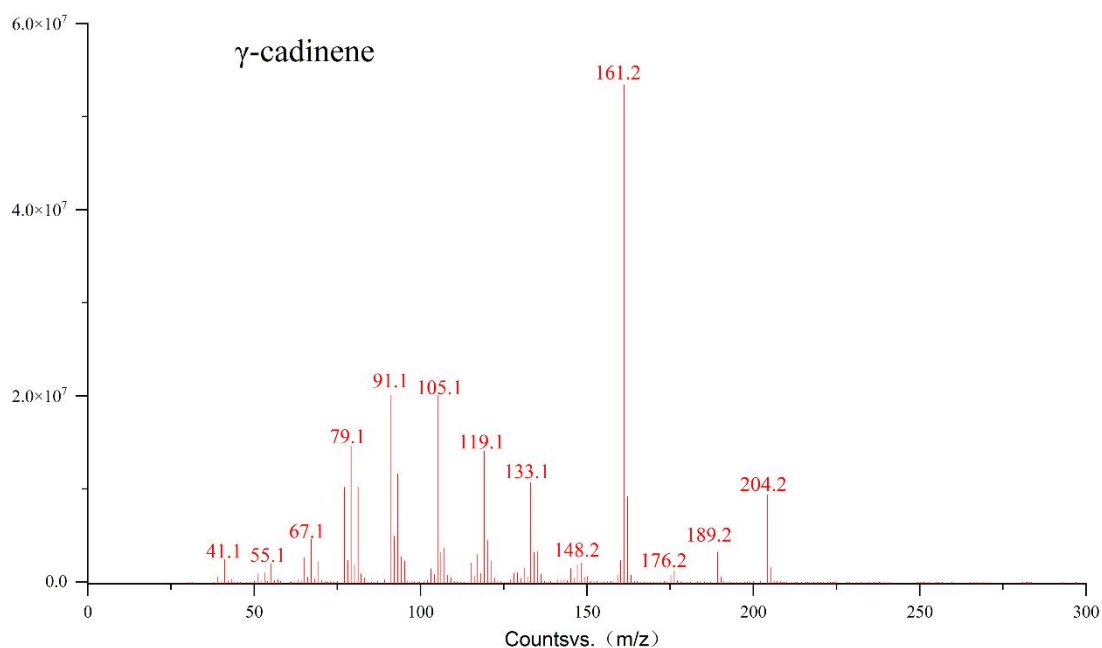


Figure S2. The MS spectra for γ -cadinene.

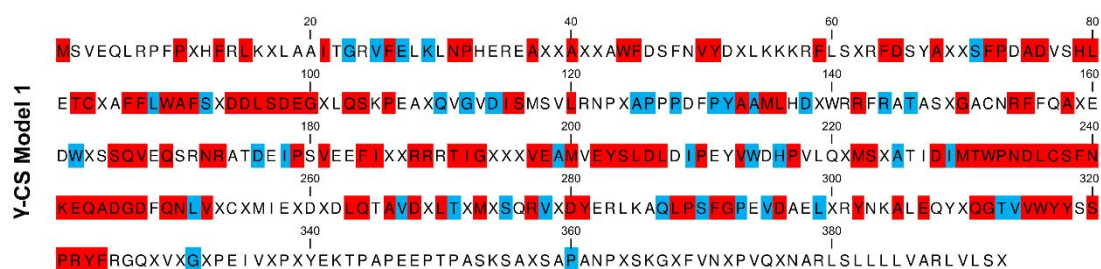


Figure S3. Model 1 was recombined according to conservative amino acid motifs of six sequences, GISTS6, GsSTS43, GsSTS45b, STC9, CpSTS18 and ShSTS5. Blue represented that > 80% amino acid motifs were the same. 100% of amino acid motifs was same in red.

Table S3. 67 sequences retrieved by Model 1 (Figure S3) in NCBI.

Description	Scientific name	Accession	comment
terpene cyclase	Moniliophthora roreri MCA 2997	ESK85067.1	1
terpenoid synthase	Gymnopus androsaceus JB14	KAE9402135.1	2
terpenoid synthase	Paxillus ammoniavirescens	KAF8837143.1	3
terpenoid synthase	Gyrodon lividus	KAF9228206.1	4
terpenoid synthase	Marasmius fiardii PR-910	KAF9255786.1	5
terpenoid synthase	Marasmius fiardii PR-910	KAF9262323.1	6

terpenoid synthase	Marasmius fiardii PR-910	KAF9266407.1	7
terpenoid synthase	Suillus variegatus	KAG1804596.1	8
terpenoid synthase	Suillus hirtellus	KAG2046364.1	9
terpenoid synthase	Suillus decipiens	KAG2064828.1	10
terpenoid synthase	Suillus weaverae	KAG2344196.1	11
terpenoid synthase	Suillus spraguei	KAG2359861.1	12
terpenoid synthase	Suillus brevipes Sb2	KAG2757286.1	13
terpenoid synthase	Rhizopogon vinicolor AM-OR11-026	OAX38211.1	14
terpenoid synthase	Obba rivulosa	OCH88150.1	15
terpene synthase	Ganoderma sinense ZZ0214-1	PIL24732.1 OK500007	16 (reannotated)
terpene synthase	Ganoderma sinense ZZ0214-1	PIL26225.1 OK500006	17
terpenoid synthase	Polyporus brumalis	RDX49040.1	18
terpenoid synthase	Lentinus tigrinus ALCF2SS1-6	RPD53648.1	19
terpenoid synthase	Lentinus tigrinus ALCF2SS1-6	RPD54775.1	20
terpenoid synthase	Dichomitus squalens	TBU24857.1	21
terpene cyclase	Steccherinum ochraceum	TCD60657.1	22
terpenoid synthase	Polyporus arcularius HHB13444	TFK81182.1	23
terpenoid synthase	Polyporus arcularius HHB13444	TFK90599.1	24
terpenoid synthase	Dendrothele bispora CBS 962.96	THU89284.1	25
terpenoid synthase	Stereum hirsutum FP-91666 SS1	XP_007309315.1	26
putative terpene cyclase	Serpula lacrymans var. lacrymans S7.9	XP_007314914.1	27
terpenoid synthase	Dichomitus squalens LYAD-421 SS1	XP_007366915.1	28

Table S3 (continued)

terpenoid synthase	Coniophora puteana RWD-64-598 SS2	XP_007773189.1	29
terpenoid synthase	Suillus fuscotomentosus	XP_041224442.1	30
terpenoid synthase	Suillus discolor	XP_041291209.1	31
putative sesquiterpene synthase	Clitopilus sp.	BBH51515.1	32
Pentalenene synthase [Termitomyces sp. J132]	Termitomyces sp. J132	KNZ74377.1	33

hypothetical protein	Termitomyces sp. Mi166#008	KAG6887643.1	34
hypothetical protein D9613_005750	Agrocybe pediades	KAF4617509.1	35
hypothetical protein D9756_001012	Leucoagaricus leucothites	KAF5363252.1	36
hypothetical protein E1B28_011602	Marasmius oreades	KAG7089978.1	37
hypothetical protein GYMLUDRAFT_239618	Gymnopus luxurians FD-317 M1	KIK65943.1	38
hypothetical protein GYMLUDRAFT_257858	Gymnopus luxurians FD-317 M1	KIK65941.1	39
hypothetical protein GYMLUDRAFT_70394	Gymnopus luxurians FD-317 M1	KIK65274.1	40
hypothetical protein H0H92_007861	Tricholoma furcatifolium	KAG6807361.1	41
hypothetical protein HYDPIDRAFT_31051	Hydnomerulius pinastri MD-312	KIJ61720.1	42
hypothetical protein HYPsudRAFT_202683	Hypholoma sublateritium FD-334 SS-4	KJA21771.1	43
hypothetical protein M404DRAFT_26981	Pisolithus tinctorius Marx 270	KIO03692.1	44
hypothetical protein PAXINDRAFT_167348	Paxillus involutus ATCC 200175	KIJ18045.1	45
hypothetical protein PAXRUDRAFT_612281	Paxillus rubicundulus Ve08.2h10	KIK91798.1	46
hypothetical protein PISMIDRAFT_685262	Pisolithus microcarpus 441	KIK17499.1	47
hypothetical protein SCLCIDRAFT_131396	Scleroderma citrinum Foug A	KIM56960.1	48
hypothetical protein WG66_13564	Moniliophthora roreri	KTB33869.1	49
isoprenoid synthase domain-containing protein	Boletus edulis	KAF8124306.1	50

Table S3 (continued)

isoprenoid synthase domain-containing protein	Cyathus striatus	KAF8991670.1	51
isoprenoid synthase domain-containing protein	Infundibulicybe gibba	KAF8883528.1	52
isoprenoid synthase domain-containing protein	Infundibulicybe gibba	KAF8883523.1	53
isoprenoid synthase domain-containing protein	Melanogaster broomeanus	KAF9232893.1	54

isoprenoid synthase domain-containing protein	Suillus americanus	KAG2039422.1	55
isoprenoid synthase domain-containing protein	Suillus ampliporus	KAG0702095.1	56
isoprenoid synthase domain-containing protein	Suillus clintonianus	XP_041202483.1	57
isoprenoid synthase domain-containing protein	Suillus cothurnatus	KAG2122404.1	58
isoprenoid synthase domain-containing protein	Suillus lakei	KAG1733514.1	59
isoprenoid synthase domain-containing protein	Suillus occidentalis	KAG1761835.1	60
isoprenoid synthase domain-containing protein	Suillus paluster	XP_041178962.1	61
isoprenoid synthase domain-containing protein	Suillus placidus	KAG1777933.1	62
isoprenoid synthase domain-containing protein	Suillus plorans	XP_041168029.1	63
isoprenoid synthase domain-containing protein	Suillus subalutaceus	XP_041248664.1	64
isoprenoid synthase domain-containing protein	Suillus tomentosus	KAG1844547.1	65
Pentalenene synthase	Termitomyces sp. T112	KAG5718178.1	66
terpenoid synthase	<i>Ganoderma lucidum</i>	OK500005	67

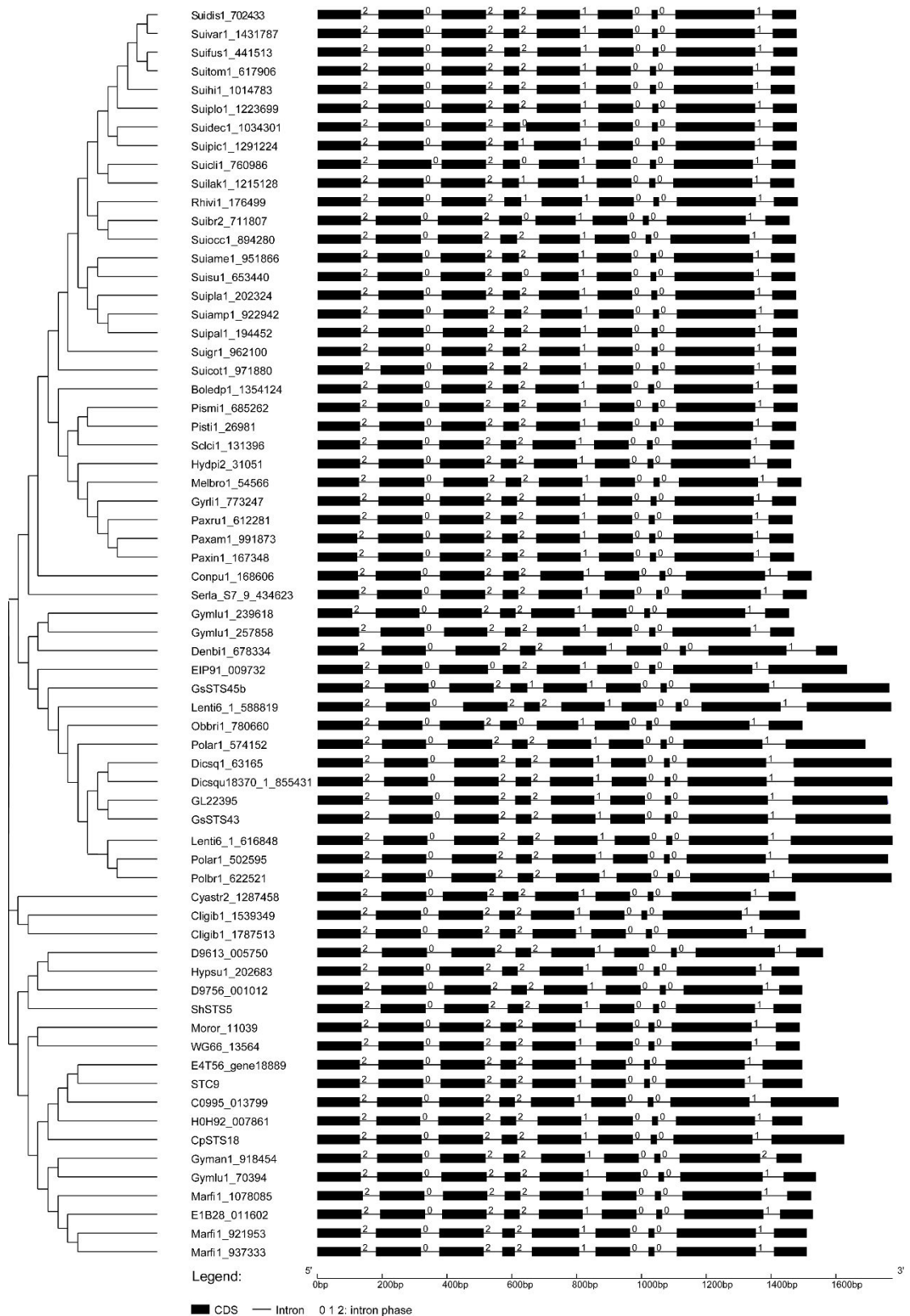


Figure S4. Gene structure-phylogenetic tree of 67 sequence were retrieved by Model 1 in NCBI and were created using GSDS (<http://gsds.gao-lab.org/>).

Table S4. Comparison of Exon/Intron Size for 67 sequences retrieved by Model 1 (Figure S3) in NCBI.

Name	Exon1	Intron1	Exon2	Intron2	Exon3	Intron3	Exon4	Intron4	Exon5	Intron5	Exon6	Intron6	Exon7	Intron7	Exon8	Intron8	Exon9	Length
Moror_11039	137	52	139	49	137	51	48	50	134	63	113	49	18	53	247	75	74	1489
Gyman1_918454	134	51	139	55	140	55	48	69	134	60	107	48	18	60	244	55	77	1494
Paxam1_991873	131	56	139	51	137	55	48	58	134	57	107	51	18	57	244	51	74	1468
Gyrl1_773247	131	57	139	50	137	54	48	59	134	55	107	57	18	56	244	56	74	1476
Marfi1_937333	134	47	139	56	137	58	39	52	146	50	107	57	18	69	244	56	101	1510
Marfi1_1078085	140	52	139	57	137	53	48	60	134	58	107	57	18	67	244	79	74	1524
Marfi1_921953	134	47	139	56	137	58	39	52	146	50	107	57	18	69	244	56	101	1510
Suivar1_1431787	134	54	139	56	137	54	48	54	134	56	107	59	18	55	244	55	74	1478
Suihi1_1014783	134	54	139	56	137	54	48	54	134	50	107	59	18	55	244	55	74	1472
Suidec1_1034301	134	54	139	56	137	53	52	19	166	56	107	59	18	55	244	56	74	1479
Suigr1_962100	134	54	139	56	137	52	48	55	134	56	107	59	18	55	244	55	74	1477
Suipic1_1291224	134	54	139	56	137	55	44	49	144	54	107	59	18	55	244	55	74	1478
Suibr2_711807	134	46	139	52	137	52	70	43	124	52	107	48	18	55	244	61	74	1456
Rhivi1_176499	134	54	139	56	137	56	48	67	125	53	107	60	18	54	244	56	74	1482
Obbri1_780660	140	48	136	53	137	49	52	62	127	51	107	52	18	56	244	60	104	1496
GsSTS45b	140	67	136	64	137	51	48	54	134	59	107	62	18	72	244	102	269	1764
GsSTS43	140	80	136	66	137	53	48	63	134	46	107	62	18	56	244	85	293	1768
Polbr1_622521	140	59	136	79	137	67	48	70	134	53	107	50	18	52	244	70	308	1772
Lenti6_1_616848	140	64	136	82	137	59	48	65	134	53	107	52	18	52	244	70	314	1775
Lenti6_1_588819	140	71	136	102	137	52	48	66	134	53	107	59	18	62	244	81	260	1770
Dicsqu18370_1_855431	140	65	136	81	137	52	48	58	134	57	107	56	18	53	244	85	302	1773
EIP91_009732	140	48	136	52	150	46	53	51	134	53	107	54	18	55	244	50	242	1633
Polar1_502595	140	60	136	79	137	61	48	64	134	53	107	50	18	52	244	70	308	1761
Polar1_574152	140	59	136	67	137	61	48	62	134	55	107	53	18	52	244	72	245	1690
Denbi1_678334	125	73	136	92	137	62	48	84	134	62	107	58	18	70	241	91	65	1603
Stehi1_161672	140	55	139	57	137	59	48	48	134	54	107	58	18	52	244	57	86	1493

Table S4 (continued)

Serla_S7_9_434623	128	55	139	58	137	54	48	63	134	55	107	67	18	61	244	68	74	1510
Dicsq1_63165	140	65	136	81	137	52	48	58	134	55	107	56	18	53	244	85	302	1771
Conpu1_168606	125	54	139	60	137	58	48	66	134	65	107	62	18	64	244	69	74	1524
Suifus1_441513	134	54	139	56	137	56	48	54	134	56	107	59	18	55	244	55	74	1480
Suidis1_702433	134	54	139	56	137	54	48	54	134	55	107	59	18	55	244	55	74	1477
CpSTS18	131	52	139	52	137	58	48	63	134	53	107	55	18	52	244	58	224	1625
STC9	131	57	139	53	137	48	48	50	134	48	107	56	18	49	244	55	122	1496
C0995_013799	131	53	139	53	137	48	48	50	134	52	107	67	18	53	244	65	209	1608
D9613_005750	134	65	139	76	134	63	48	63	134	60	107	68	18	58	244	66	83	1560
D9756_001011	140	57	139	56	143	63	48	53	134	57	107	60	18	55	244	51	71	1496
E1B28_011602	137	57	139	52	137	54	48	60	134	60	107	61	18	68	244	52	101	1529
Gymlu1_239618	107	72	136	58	134	56	48	48	134	53	107	55	18	52	241	62	74	1455
Gymlu1_257858	128	66	136	60	134	54	48	50	134	53	107	54	18	53	241	61	74	1471
Gymlu1_70394	134	51	139	59	140	55	48	60	134	71	107	54	18	50	244	65	110	1539
H0H92_007861	131	51	136	55	140	52	48	67	134	53	107	59	18	55	244	54	92	1496
Hydpi2_31051	131	58	139	50	137	51	48	53	134	55	107	55	18	54	244	54	74	1462
Hypsu1_202683	134	55	139	49	137	56	48	68	134	59	107	52	18	53	244	48	86	1487
Pisti1_26981	131	60	139	52	137	54	48	54	134	56	107	56	18	54	244	58	74	1476
Paxin1_167348	131	56	139	51	137	55	48	61	134	56	107	51	18	57	244	51	74	1470
Paxru1_612281	131	54	139	51	137	54	48	60	134	56	107	51	18	58	244	49	74	1465
Pismi1_685262	131	54	139	52	137	61	48	55	134	59	107	56	18	56	244	56	74	1481
Selci1_131396	131	54	139	52	137	52	48	50	134	56	107	56	18	60	244	59	74	1471
WG66_13564	137	52	139	49	137	51	48	50	134	63	113	49	18	53	247	75	74	1489
Boledp1_1354124	134	52	139	57	137	53	48	52	134	55	107	52	18	62	244	62	74	1480
Cyatr2_1287458	134	63	139	51	137	49	48	51	134	52	107	54	18	56	244	56	83	1476
Cligib1_1539349	134	47	139	54	137	50	48	50	134	48	107	52	18	48	244	54	125	1489
Cligib1_1787513	134	46	139	54	137	53	48	53	134	47	107	62	18	49	244	54	128	1507

Table S4 (continued)

Melbro1_54566	128	63	139	58	137	55	48	55	134	55	107	58	18	60	244	60	74	1493
Suiame1_951866	134	51	139	56	137	52	48	54	134	56	107	59	18	55	244	55	74	1473
Suiamp1_922942	134	55	139	60	137	52	48	56	134	53	107	60	18	56	244	55	74	1482
Suicli1_760986	134	54	163	32	137	52	52	59	124	52	107	60	18	55	244	58	74	1475
Suicot1_971880	140	54	136	56	137	52	48	54	134	56	107	59	18	52	244	55	74	1476
Suilak1_1215128	134	54	139	54	137	51	48	63	125	56	107	56	18	55	244	56	74	1471
Suiocc1_894280	134	46	139	52	137	56	48	63	134	46	107	50	18	59	244	69	74	1476
Suipal1_194452	134	54	139	60	137	52	48	53	134	53	107	60	18	57	244	55	74	1479
Suipla1_202324	134	54	139	56	137	52	48	54	134	56	107	59	18	56	244	55	74	1477
Suiplo1_1223699	134	54	139	56	137	54	48	55	134	56	107	59	18	55	244	55	74	1479
Suisu1_653440	134	51	139	56	137	52	61	60	115	56	107	59	18	56	244	55	74	1474
Suitom1_617906	134	54	139	56	137	54	48	54	134	50	107	59	18	55	244	55	74	1472
E4T56_gene18889	131	57	139	53	137	48	48	50	134	48	107	56	18	49	244	55	122	1496
GlSTS6	140	80	136	66	137	51	48	62	134	49	107	62	18	55	244	76	296	1761
AVERAGE	134	56	139	58	137	54	48	57	134	55	107	57	18	56	244	62	119	1535

	20	40	60	80	100							
Suimp1_922942	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	91
Suip1_194452	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	91
Suigr1_962100	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	91
Suip1a1_202324	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	91
Suik1_1215128	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	91
Rhiv1_176499	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	91
Suibr2_711807	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	91
Suiooc1_894280	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	91
Suicid1_760986	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	93
Suidec1_1034301	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	91
Suip1c1_1291224	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	91
Suime1_951866	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	91
Sulfus1_441513	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	91
Suivar1_1431787	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	91
Suidis1_702433	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	91
Suikom1_617906	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	91
Suith1_1014783	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	91
Suip1o1_1223699	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	91
Suisu1_653440	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	91
Paxam1_991873	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	90
Paxin1_167348	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	90
Paxu1_612281	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	90
Gytl1_773247	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	90
Hydp2_31051	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	90
Sclic1_131396	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	90
Melbr1_54566	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	89
Pism1_685262	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	90
Pist1_26981	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	90
Suicott1_971880	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	92
Boledp1_1354124	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	91
Seria_57_9_434623	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	89
Compul1_168606	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	88
Clipl1_1539349	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	91
Cliplb1_1787513	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	91
Cystr2_1287458	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	91
ShSt55	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	93
Merf1_921953	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	91
Merf1_937333	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	90
E1B29_011602	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	92
Merf1_1078085	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	93
Gyman1_918454	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	91
Gymu1_70394	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	91
E4T56_gene18889	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	90
STC9	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	90
C0995_013799	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	90
CpST518	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	90
Dicsq1_63165	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	93
Dicsq18730_1_855431	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	93
GL22369	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	93
GeST543	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	93
Polar1_502595	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	93
Polar1_574152	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	93
Lenf6_1_616848	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	93
Polar1_574152	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	93
Lenf6_1_588919	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	93
GeST545b	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	93
Obn1_780660	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	93
EIP91_009732	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	93
D9756_001012	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	93
Hypu1_202983	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	91
D9613_005750	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	91
Denb1_678334	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	88
H0H92_007861	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	89
Gymu1_239818	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	82
Gymu1_257858	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	82
Moror_11039	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	92
WG66_13564	QVRYEEL	PQYQDIAA	GRVCE	ELRANVHOAE	DRAAARS	NO	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS	92
Consensus	MQ--RYEELP	SQYQDIAA	ITGRV--FEL	K-VNPHQAE	DRAARAFNS	--	ISVYDDR	KSKFLNYGK	DLFAALSPD	ADLKHLETCL	AFFFWAFS--	91

	120	140	160	180	200						
Suimp1_922942	DAVAQAGHDI	SVSYVTPNPDG	SRP	QYV	YAAALYDL	LTRFRGISTV	YAYHR	Y	IR	FEAFWSSSV	166
Suip1_194452	DAVAQAGHDI	SVSYVTPNPDG	SRP	QYV	YAAALYDL	LTRFRGISTV	YAYHR	Y	IR	FEAFWSSSV	166
Suigr1_962100	DAVAQAGHDI	SVSYVTPNPDG	SRP	QYV	YAAALYDL	LTRFRGISTV	YAYHR	Y	IR	FEAFWSSSV	166
Suip1a1_202324	DAVAQAGHDI	SVSYVTPNPDG	SRP	QYV	YAAALYDL	LTRFRGISTV	YAYHR	Y	IR	FEAFWSSSV	166
Suik1_1215128	DAVAQAGHDI	SVSYVTPNPDG	SRP	QYV	YAAALYDL	LTRFRGISTV	YAYHR	Y	IR	FEAFWSSSV	163
Rhiv1_176499	DAVAQAGHDI	SVSYVTPNPDG	SRP	QYV	YAAALYDL	LTRFRGISTV	YAYHR	Y	IR	FEAFWSSSV	170
Suibr2_711807	DAVAQAGHDI	SVSYVTPNPDG	SRP	QYV	YAAALYDL	LTRFRGISTV	YAYHR	Y	IR	FEAFWSSSV	166
Suiooc1_894280	DAVAQAGHDI	SVSYVTPNPDG	SRP	QYV	YAAALYDL	LTRFRGISTV	YAYHR	Y	IR	FEAFWSSSV	166
Suicid1_760986	DAVAQAGHDI	SVSYVTPNPDG	SRP	QYV	YAAALYDL	LTRFRGISTV	YAYHR	Y	IR	FEAFWSSSV	172
Suidec1_1034301	DAVAQAGHDI	SVSYVTPNPDG	SRP	QYV	YAAALYDL	LTRFRGISTV	YAYHR	Y	IR	FEAFWSSSV	178
Suip1c1_1291224	DAVAQAGHDI	SVSYVTPNPDG	SRP	QYV	YAAALYDL	LTRFRGISTV	YAYHR	Y	IR	FEAFWSSSV	168
Suime1_951866	DAVAQAGHDI	SVSYVTPNPDG	SRP	QYV	YAAALYDL	LTRFRGISTV	YAYHR	Y	IR	FEAFWSSSV	168
Sulfus1_441513	DAVAQAGHDI	SVSYVTPNPDG	SRP	QYV	YAAALYDL	LTRFRGISTV	YAYHR	Y	IR	FEAFWSSSV	166
Suivar1_1431787	DAVAQAGHDI	SVSYVTPNPDG	SRP	QYV	YAAALYDL	LTRFRGISTV	YAYHR	Y	IR	FEAFWSSSV	166
Suidis1_702433	DAVAQAGHDI	SVSYVTPNPDG	SRP	QYV	YAAALYDL	LTRFRGISTV	YAYHR	Y	IR	FEAFWSSSV	166
Suikom1_617906	DAVAQAGHDI	SVSYVTPNPDG	SRP	QYV	YAAALYDL	LTRFRGISTV	YAYHR	Y	IR	FEAFWSSSV	166
Suith1_1014783	DAVAQAGHDI	SVSYVTPNPDG	SRP	QYV	YAAALYDL	LTRFRGISTV	YAYHR	Y	IR	FEAFWSSSV	166
Suip1o1_1223699	DAVAQAGHDI	SVSYVTPNPDG	SRP	QYV	YAAALYDL	LTRFRGISTV	YAYHR	Y			

	220	240	260	280	300						
Suimp1_922942	SRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	263
Suipal1_194452	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	263
Suigr1_962100	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	263
Suipal1_202324	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	263
Suik1_121528	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	260
Rhiv1_176499	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	263
Suibr2_711807	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	267
Suiccc1_894280	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	263
Suicr1_760986	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	269
Suidec1_1034301	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	275
Suipc1_1291224	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	265
Suime1_951866	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	263
Suifus1_441513	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	263
Suiver1_1431787	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	263
Suid1_702433	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	263
Suikom1_817906	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	263
Suith1_1014783	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	263
Suiplo1_1223699	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	263
Suisu1_853440	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	261
Paxam1_991873	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	262
Paxin1_187348	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	262
Paxu1_612281	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	262
Cytl1_773247	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	262
Hydp2_31051	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	262
Solc1_131396	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	262
Melbr1_54566	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	261
Pisml1_585262	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	262
Psh1_26581	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	262
Suicr1_971880	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	264
Boledp1_1354124	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	263
Seria_57_9_434623	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	261
Conpu1_188606	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	260
Clipl1_1539349	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	264
Clipl1_1787513	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	263
Cys2r2_1287458	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	263
SHST5	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	265
Merf1_921953	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	264
Merf1_937333	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	264
EIB29_011602	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	264
Merf1_1078085	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	265
Gyman1_918454	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	264
Gymlu1_70394	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	264
E4T6_gene16869	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	262
STC9	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	262
C0995_013799	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	262
CpST518	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	262
Dicsq1_63165	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	264
G2	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	264
GeST543	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	264
Polr1_502595	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	264
Polr1_622521	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	264
Lenf6_1_816848	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	264
Polr1_574152	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	264
Lenf6_1_586819	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	264
GeST545	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	264
Obn1_780660	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	263
EIP91_009732	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	270
D9756_001012	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	267
Hypu1_202883	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	267
D9613_005750	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	262
Denb1_878334	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	259
H0H92_007861	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	262
Gymlu1_239618	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	252
Gymlu1_257858	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	259
Moror_11039	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	267
WG66_13564	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	267
Consensus	TSRFRSDDR	MPFVDELLM	ATIGGALL	FAMVYSDD	DLDVDFE	NPIIKAMSD	TTLLMTWPN	LCSEFKQAD	GDYQLVFCI	MHERDVLG	267

	320	340	360	380	400						
Suimp1_922942	EVINLEED	NEVNDVVF	ISQFSSVD	VAEERLHL	ALNEFVDT	LWYLSRPR	RGVD	VTN	RENLVVPI	FGA	343
Suipal1_194452	EVINLEED	NEVNDVVF	ISQFSSVD	VAEERLHL	ALNEFVDT	LWYLSRPR	RGVD	VTN	RENLVVPI	FGA	343
Suigr1_962100	EVINLEED	NEVNDVVF	ISQFSSVD	VAEERLHL	ALNEFVDT	LWYLSRPR	RGVD	VTN	RENLVVPI	FGA	343
Suipal1_202324	EVINLEED	NEVNDVVF	ISQFSSVD	VAEERLHL	ALNEFVDT	LWYLSRPR	RGVD	VTN	RENLVVPI	FGA	343
Suik1_121528	EVINLEED	NEVNDVVF	ISQFSSVD	VAEERLHL	ALNEFVDT	LWYLSRPR	RGVD	VTN	RENLVVPI	FGA	340
Rhiv1_176499	EVINLEED	NEVNDVVF	ISQFSSVD	VAEERLHL	ALNEFVDT	LWYLSRPR	RGVD	VTN	RENLVVPI	FGA	347
Suibr2_711807	EVINLEED	NEVNDVVF	ISQFSSVD	VAEERLHL	ALNEFVDT	LWYLSRPR	RGVD	VTN	RENLVVPI	FGA	340
Suiccc1_894280	EVINLEED	NEVNDVVF	ISQFSSVD	VAEERLHL	ALNEFVDT	LWYLSRPR	RGVD	VTN	RENLVVPI	FGA	343
Suicr1_760986	EVINLEED	NEVNDVVF	ISQFSSVD	VAEERLHL	ALNEFVDT	LWYLSRPR	RGVD	VTN	RENLVVPI	FGA	349
Suidec1_1034301	EVINLEED	NEVNDVVF	ISQFSSVD	VAEERLHL	ALNEFVDT	LWYLSRPR	RGVD	VTN	RENLVVPI	FGA	355
Suipc1_1291224	EVINLEED	NEVNDVVF	ISQFSSVD	VAEERLHL	ALNEFVDT	LWYLSRPR	RGVD	VTN	RENLVVPI	FGA	345
Suime1_951866	EVINLEED	NEVNDVVF	ISQFSSVD	VAEERLHL	ALNEFVDT	LWYLSRPR	RGVD	VTN	RENLVVPI	FGA	342
Suifus1_441513	EVINLEED	NEVNDVVF	ISQFSSVD	VAEERLHL	ALNEFVDT	LWYLSRPR	RGVD	VTN	RENLVVPI	FGA	343
Suiver1_1431787	EVINLEED	NEVNDVVF	ISQFSSVD	VAEERLHL	ALNEFVDT	LWYLSRPR	RGVD	VTN	RENLVVPI	FGA	343
Suid1_702433	EVINLEED	NEVNDVVF	ISQFSSVD	VAEERLHL	ALNEFVDT	LWYLSRPR	RGVD	VTN	RENLVVPI	FGA	343
Suikom1_817906	EVINLEED	NEVNDVVF	ISQFSSVD	VAEERLHL	ALNEFVDT	LWYLSRPR	RGVD	VTN	RENLVVPI	FGA	343
Suith1_1014783	EVINLEED	NEVNDVVF	ISQFSSVD	VAEERLHL	ALNEFVDT	LWYLSRPR	RGVD	VTN	RENLVVPI	FGA	343
Suiplo1_1223699	EVINLEED	NEVNDVVF	ISQFSSVD	VAEERLHL	ALNEFVDT	LWYLSRPR	RGVD	VTN	RENLVVPI	FGA	343
Suisu1_853440	EVINLEED	NEVNDVVF	ISQFSSVD	VAEERLHL	ALNEFVDT	LWYLSRPR	RGVD	VTN	RENLVVPI	FGA	341
Paxam1_991873	EVINLEED	NEVNDVVF	ISQFSSVD	VAEERLHL	ALNEFVDT	LWYLSRPR	RGVD	VTN	RENLVVPI	FGA	342
Paxin1_187348	EVINLEED	NEVNDVVF	ISQFSSVD	VAEERLHL	ALNEFVDT	LWYLSRPR	RGVD	VTN	RENLVVPI	FGA	342
Paxu1_612281	EVINLEED	NEVNDVVF	ISQFSSVD	VAEERLHL	ALNEFVDT	LWYLSRPR	RGVD	VTN	RENLVVPI	FGA	342
Cytl1_7											

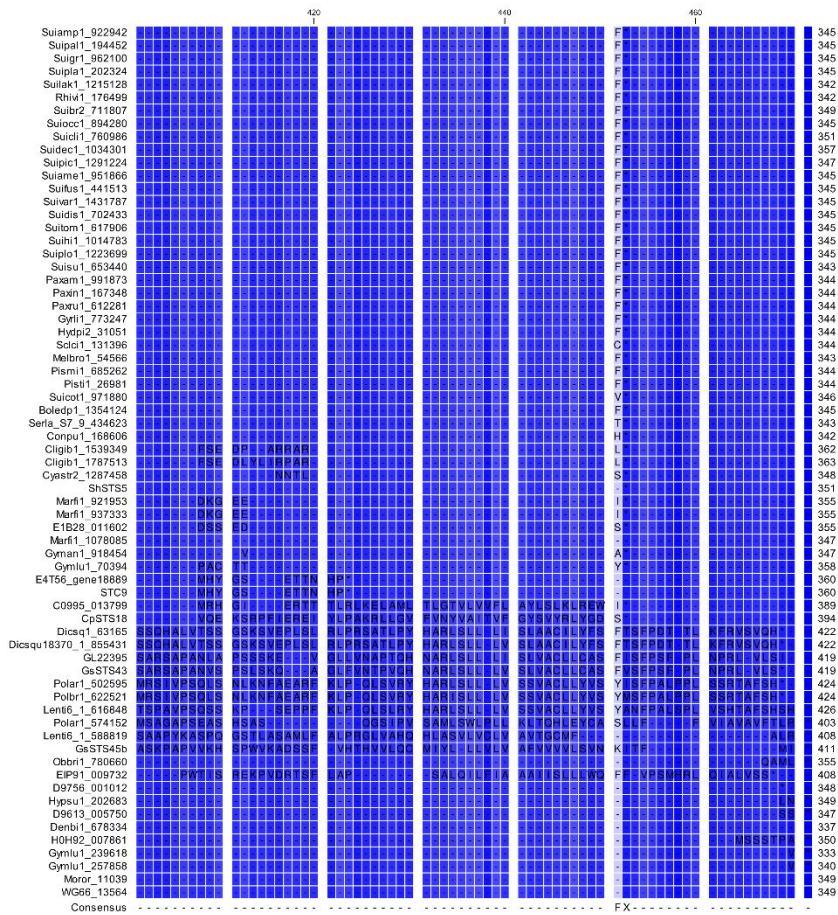


Figure S5. Amino acid sequence alignments of 67 sequences using CLC Genomics Workbench 12 software. Amino acids range from low (blue) to high (red) conservation.

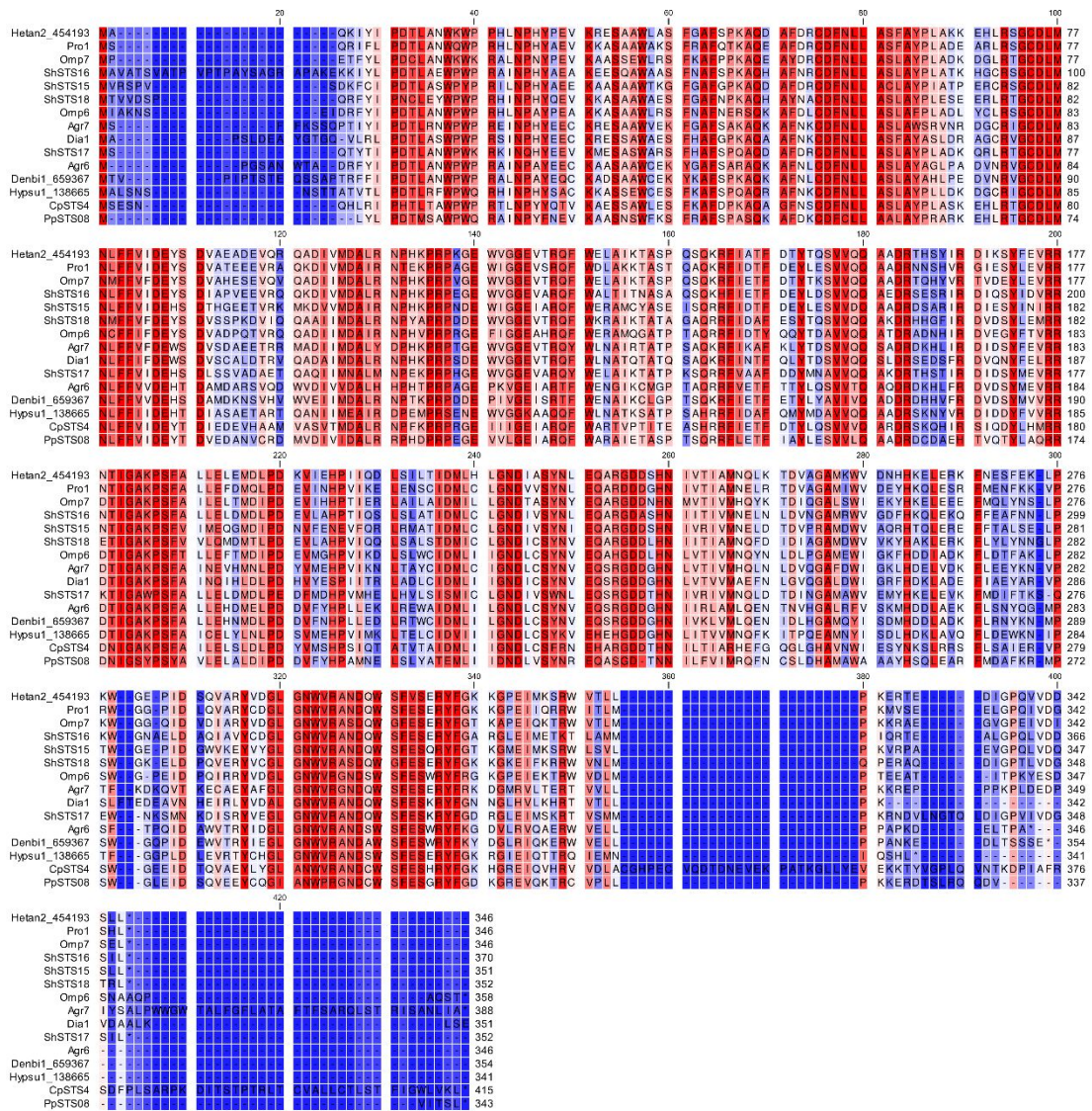


Figure S6. Amino acid sequence alignments of 15 characterized delta-6-protoilludene synthases using CLC Genomics Workbench 12 software. Amino acids range from low (blue) to high (red) conservation.

Table S5. Primers and plasmids used for cloning and expressing γ -CSs in *G. lucidum* and *G. sinensis*.

Constructed plasmids	Name	5' -3' Sequences
pGEM [®] T Easy -GsSTS43/ pet32a-GsSTS43	43-F 43-R	cgggatccATGAGCGTTCGAGCAGCTCCGTTCA ccaagctTGAAAGGACCAGCCGGGGTTGAG
pGEM [®] T Easy -GsSTS45b/ pet32a-GsSTS45b	45-F 45-R	cgggatccATGAGCATCGAACAGCTCCATC ccaagcttAATCATGAAAGTGATTTTGTGTTGAC
pGEM [®] T Easy-GISTS6/ pet32a-GISTS6	6-F 6-R	cgggatccATGAGCGTTCGAGCAGCTTCGC ccctcagTCAGATCGACAGAACGAGGCGG
Pet32a	T7 T7-Ter	TAATACGACTCACTATAGGG GCTAGTTATTGCTCAGCGG

The cloned coding sequences from *G. lucidum* and *G. sinensis*.

>GISTS6

ATGAGCGTCGAGCAGCTTCGCCATTCCCCACCCACTTCCGACTCAAGGACCTTGCAG
CAATATCCGGGCGAGTATTCGAGTTCAAGCTCAATCCGCACGAGAAGGAGGCCGCGA
AGGCGACGTATGCATGGTTTGATGGCCGCAATGTGTACCACGGTCTAAAGAAGAAGA
GATTCCTATCACACCGCTTCGACTCATATGCAGGCATGAGCTTTCGGACGCCGACGT
TTCGCATCTGGAGACCTGCATTGCGTTCTTCCTATGGGCGTTTTCGTTTGACGATCTCT
CCGACGAGGGCGCGTTGCAATCCAAGCCAGAAGCGCACCCAGGTCGGCGTGGATATCT
CCATGGAAGTCCTTCGGAATCCGACCCGCCCGCCCCCAATTTCCCTTATGCCGCGAT
GCTCCACGATATTTGGCGACGCTTTCGGGAAACCGCGAGCCCAGGGGCTTGCAACAG
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CGTACAGACGAAATTCCTCGTTGAGGAGTTCATTATCCTCCGACGCCGAACCATC
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CCCAAGTTTCGGACCTGAGGTCGACGCCGAGCTCGCACGCTACAACAAGCGATGGA
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CAAGAAGTTACCGGCATCCCCGAGATTGTCGTTCCGGTCTATGAGCGCACGACTCCG
GCCCCGGAAGAACCTACTGCACCCGCCTCCAAGTCGGCAAGGTCTGCGCCCGCAAT
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>GsSTS43

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GATTTCTCTCTCATCGTTTTGACTCATAACGCCGCATGAGTTTCCAGACGCCGACGT
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>GsSTS45a

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TCGCGCCGTGGAAGGTTGGATGCGCTCCCAGGTCGAGCAGATTTCGTAACCGGGCTAT
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GTCCATGGGTCAAGGCTGATTCGTCTTCGTCCACACACGTCGTTCTCCAGTGCAT
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>GsSTS45b

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