SUPPLEMENTAL INFORMATION

Identification of a sesquiterpene synthase-3-hydroxy-3-methylglutaryl-CoA synthase fusion protein responsible for hirsutene biosynthesis in *S. hirsutum*

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Contents

I. Supplemental Figures

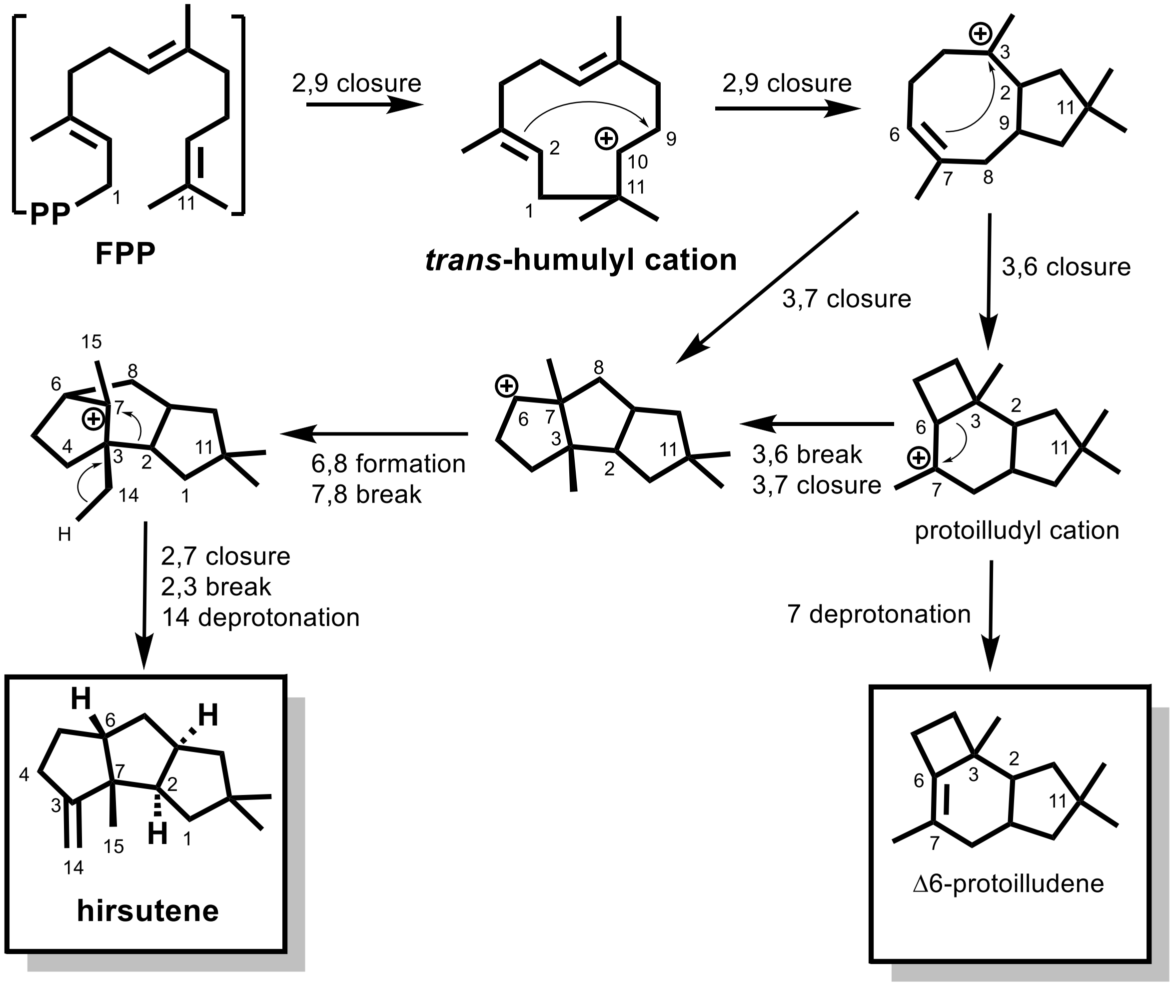


Figure S1
Possible cyclization pathway to hirsutene.
In the absence of mechanistic studies, two plausible cyclization pathways leading to hirsutene are conceivable (see also: (1)).

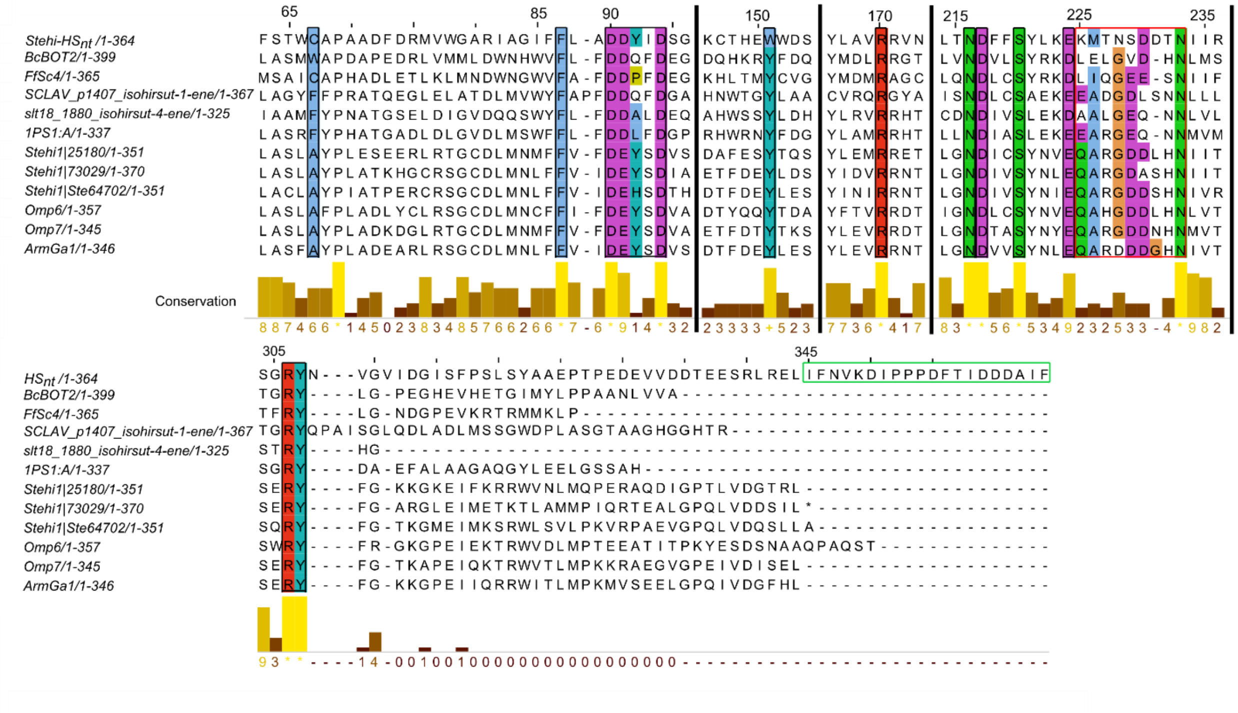
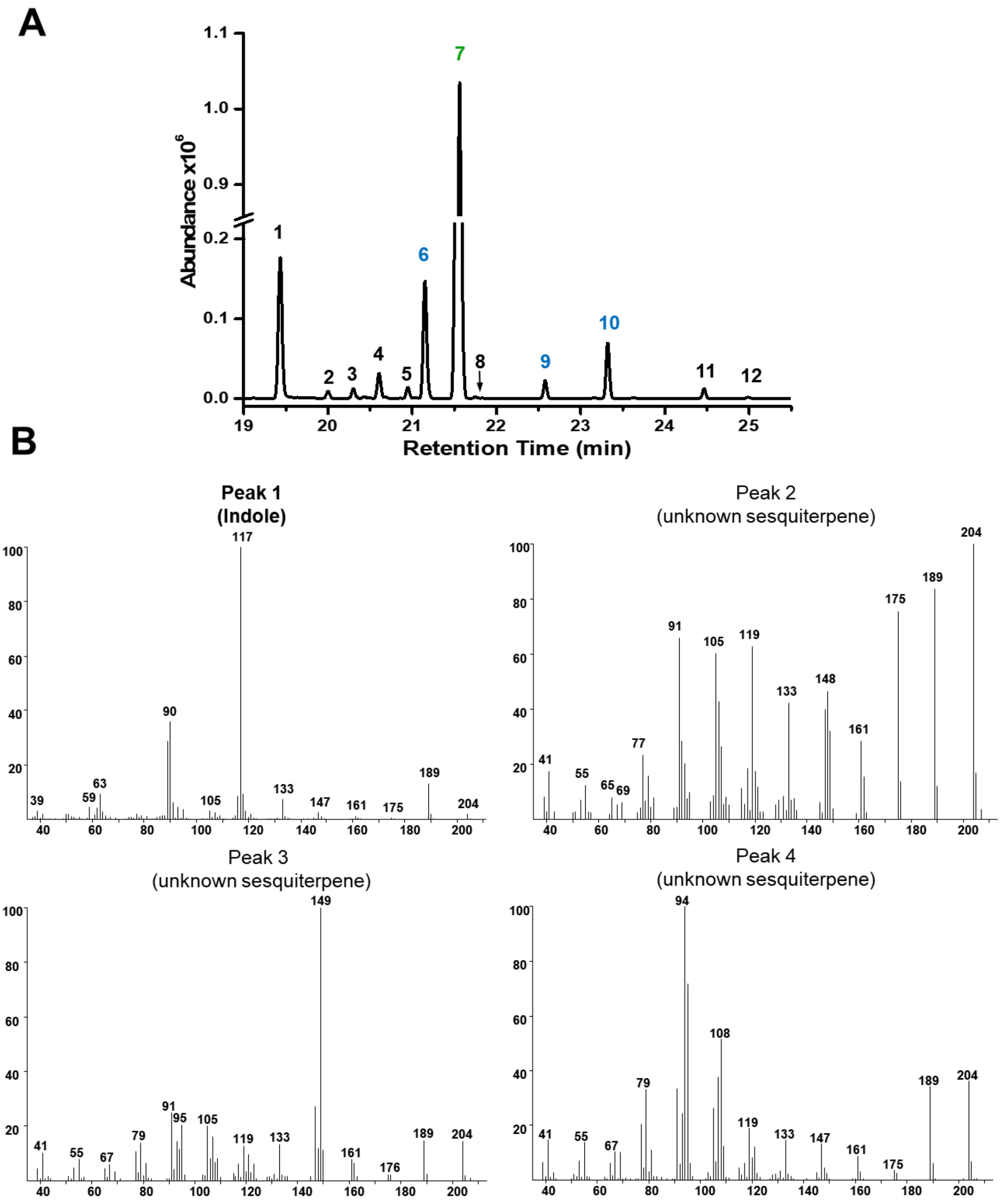


Figure S2

Sequence alignment of the N-terminal hirsutene synthase (HS$_{nt}$) domain of bifunctional HS-HMGS with functionally characterized 1, 11 cyclizing sesquiterpene synthases from fungi and bacteria. Key active site motifs of the conserved Mg^{2+} **D(D/E)**XX**(D/E)** and (**N/D**)DXX(**S/T**)XXX(**E/D**) binding motifs are boxed in black. The highly variable H-α1 loop is boxed in red. The putative 20 amino acid linker sequence between the sesquiterpene synthase and HMGS domain of HS-HMGS is boxed in green. Residue colors show physico-chemical conservation at 90% or higher using the Clustal convention. Overall physico-chemical conservation at each amino acid position is also shown graphically below the alignment, with tall yellow columns showing complete conservation (*) and short, dark yellow columns showing low conservation (1), and no bar (-) showing absence of chemical conservation (See **Figure 2** for accession numbers).



A
Abundance x10^6
1.1
1.0
0.9
0.2
0.1
0.0
Retention Time (min)
19
20
21
22
23
24
25
1
2
3
4
5
6
7
8
9
10
11
12
B
Peak 1
(Indole)
117
90
189
63
59
39
105
133
147
161
175
204
Peak 2
(unknown sesquiterpene)
204
189
175
91
105
119
133
148
161
77
41
55
65
69
Peak 3
(unknown sesquiterpene)
149
91
95
105
79
119
133
189
204
41
55
67
161
176
Peak 4
(unknown sesquiterpene)
94
108
79
189
204
41
55
67
119
133
147
161
175
100
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60
40
20
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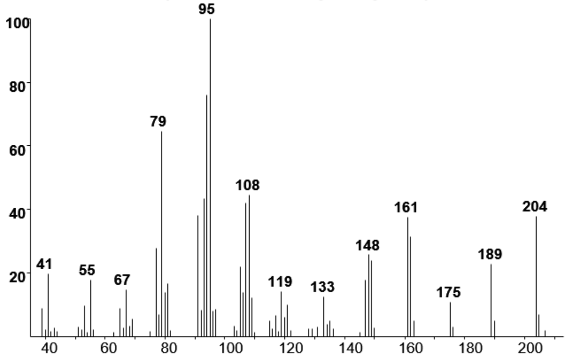
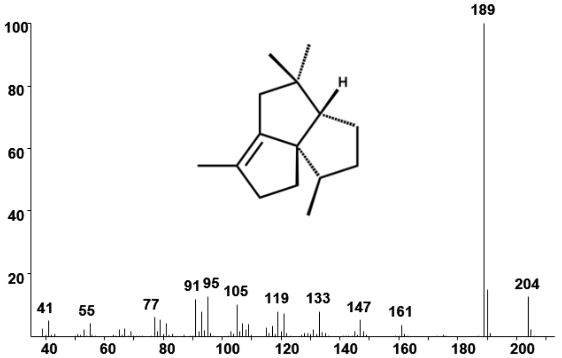
60
80
100
120
140
160
180
200

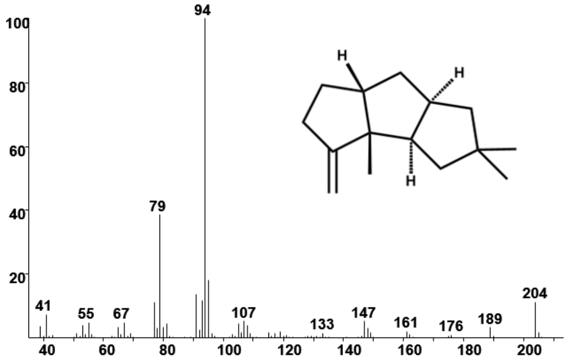
Peak 5
(unknown sesquiterpene)



Peak 6
(panaginsene)



Peak 7
(Hirsutene)



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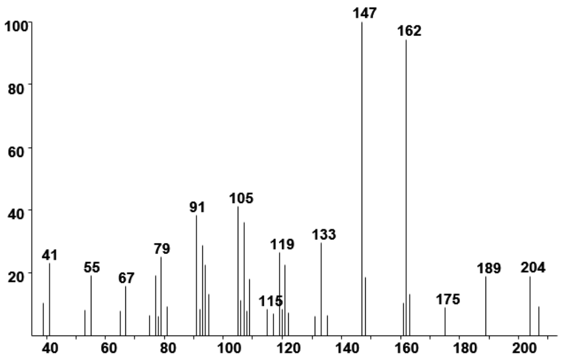
(unknown sesquiterpene)



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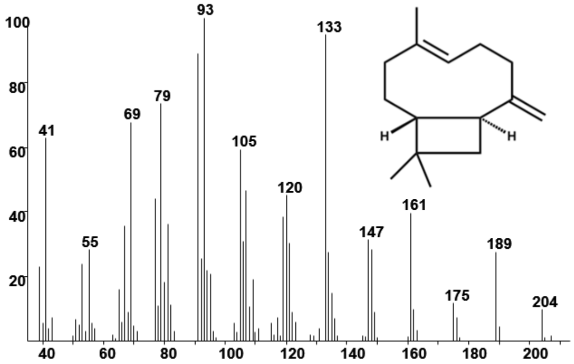
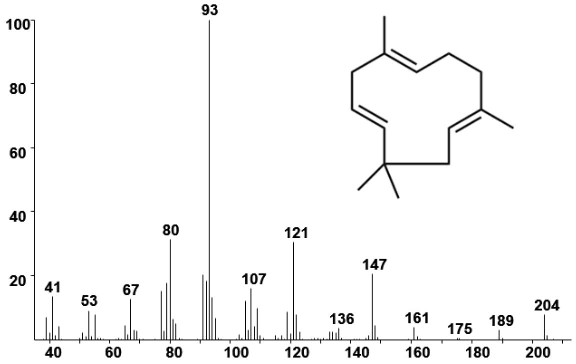
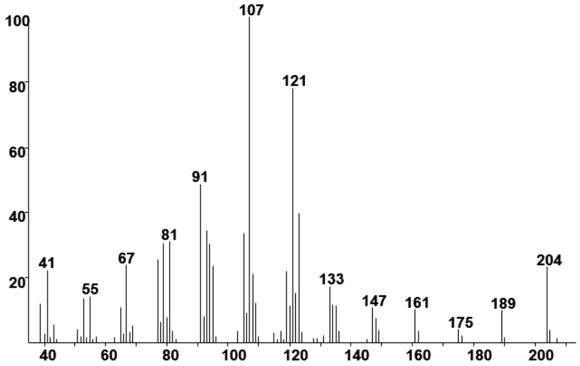
((E)-β-Caryophyllene)



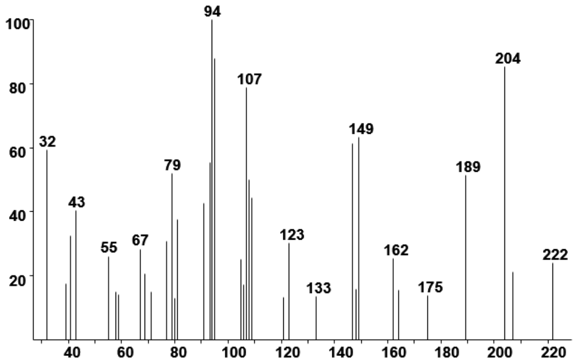
Peak 10
(α-Humulene)

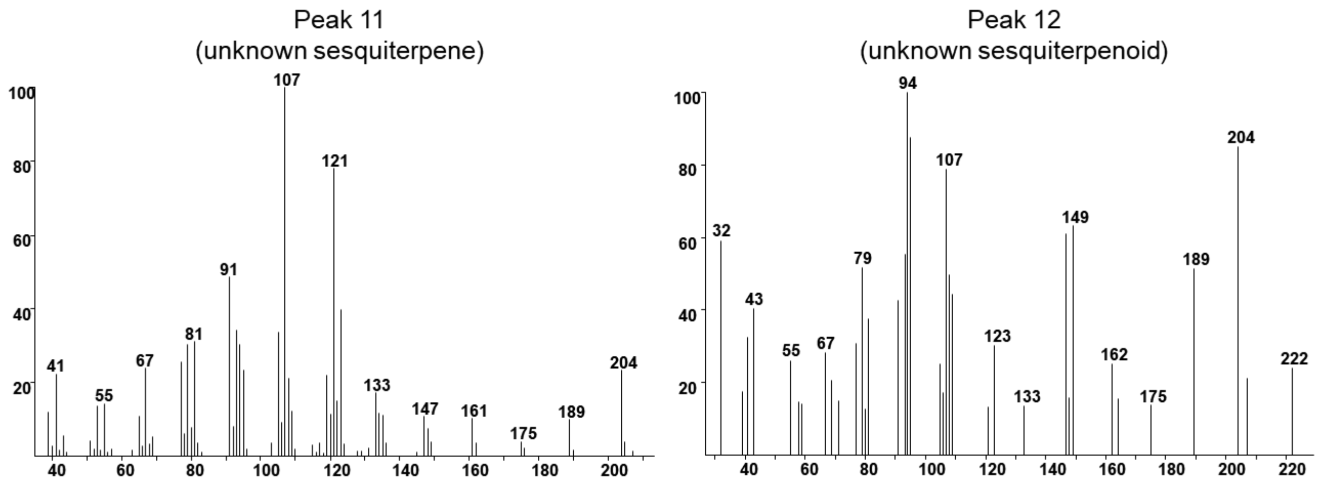


Peak 11
(unknown sesquiterpene)



Peak 12
(unknown sesquiterpenoid)




Peak 11 (unknown sesquiterpene)

Peak 12 (unknown sesquiterpenoid)

Figure S3

SPME GC-MS analysis of sesquiterpenes in the headspace of recombinant *E. coli* cultures expressing HS-HMGS. A: GC profile of separated compounds. B: EI-MS fragmentation of each peak. Peak 1 is indole, a product of *E. coli* tryptophan metabolism, and peaks 6, 7, 9, and 10 correspond to the major products panaginsene, hirsutene, (*E*)-β-caryophyllene, and α-humulene, respectively.

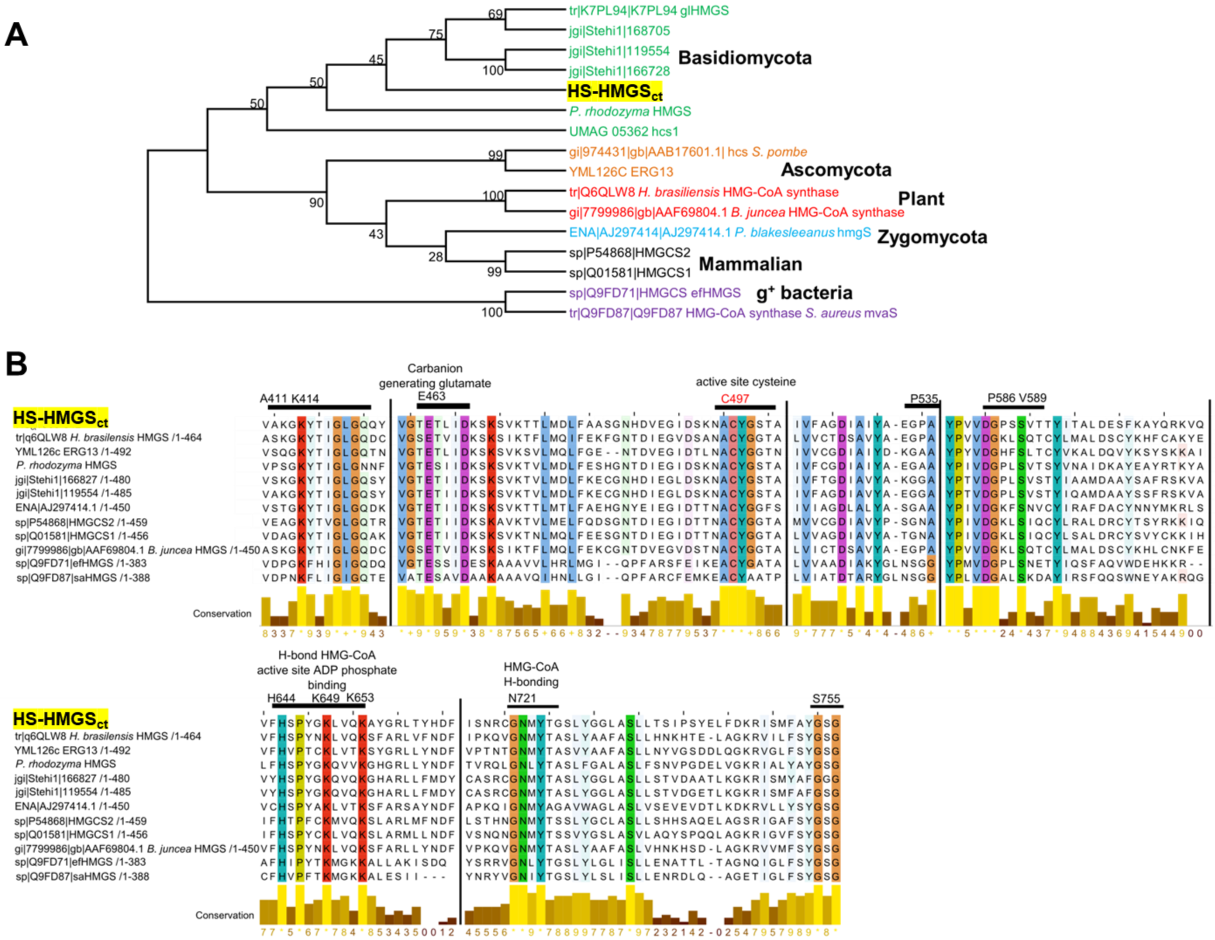


Figure S4

Phylogenetic analysis and sequence alignment of the C-terminal HMGS domain(HS-HMGS$_{ct}$) of bifunctional HS-HMGS: A: Maximum likelihood phylogenetic analysis shows that the HMGS domain (HS-HMGS residues 365-842) is most closely related to HMGS sequences from Basidiomycota (green), including *Ustilago maydis* Hcs1 (um05362) (2), *Phaffia rhodozyma* HMGS (E509999) (3), *Ganoderma lucidum* (glHMGS) (K7PL94) (4), and three putative HMGS identified in the *Stereum hirsutum* genome (jgi|Stehi1|168705 and jgi|Stehi1|119554 are clustered with protoilludene synthase Stehi1|25180 (5) whereas jgi|Stehi1|166728 is not located in a biosynthetic gene cluster, and is likely involved in the synthesis of housekeeping isoprenoids). HMGS sequences (name ID's represent accession numbers) from other phyla include representative examples from: Ascomycota (orange), plants (red), Zygomycota (blue), mammals (black) and gram-positive bacteria (purple). **B:** Sequence alignment of HS-HMGS$_{ct,}$ two putative *S. hirsutum* HMGS in sesquiterpene synthase (STS) biosynthetic gene clusters (jgi|Stehi1|168705 and jgi|Stehi1|119554), with biochemically characterized HMGS enzymes. This alignment shows conservation of catalytic motifs (horizontal bars above alignment), including the active site cysteine C497. Residue colors show residues conserved at 90% or higher using the Clustal convention to show conservation of amino acid chemical properties. Overall conservation of physicochemical properties at each position is also shown below the alignment, with tall yellow columns showing complete conservation (*) and short, dark yellow columns showing low conservation (1), and no bar (-) showing absence of conservation.

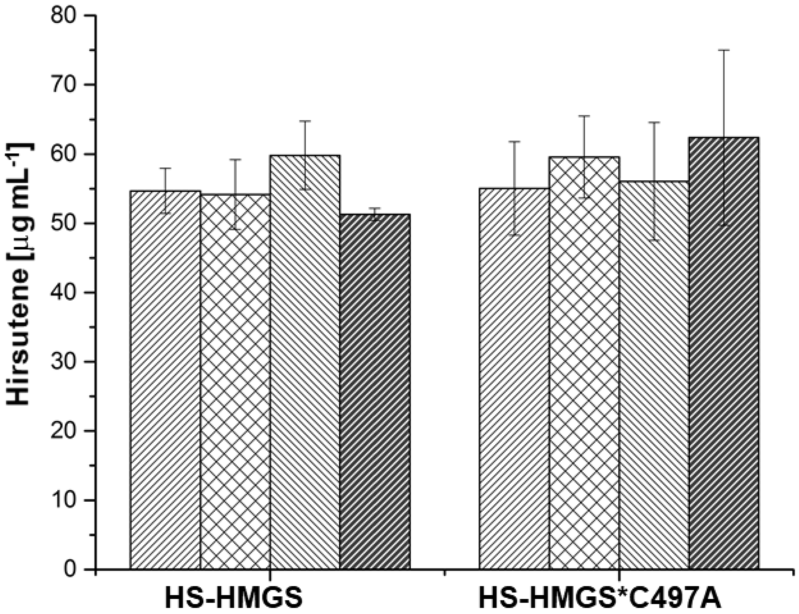


Figure S5

Hirsutene production levels of *S. cerevisiae* strains expressing wild-type HS-HMGS or mutated HS-HMGS*C497A. Four transformants (biological replicates) of *S. cerevisiae* pESC-HIS-HS-HMGS or pESC-HIS-HS-HMGS*C497A were cultivated for 48 hrs in galactose induction medium with a dodecane overlay to collect volatile hirsutene sesquiterpene product. Hirsutene production of 3 technical replicates for each biological replicate was quantified by GC-FID per mL of culture using commercially available α-caryophyllene as a standard compound.

II. Supplemental Tables

Table S1

HS-HMGS biosynthetic gene cluster protein predictions. Protein sequences from Augustus (6) gene predictions are given for each predicted open reading frame (ORF) in the biosynthetic gene clusters surrounding HS-HMGS (HS annotated as Stehi1|52743 in the *S. hirsutum* genome (7) available in the Joint Genome Initiative (JGI) Database). Genes encoding sequences highlighted in bold were amplified from cDNA. Functional annotations were done as previously described in (5).

Gene no.	**Top conserved domain(s)**	**Predicted function**	**Amino acid sequence**
1	cd06660	Aldo-keto-reductase, 2X domains, predicted gene fusion	MTSPKYPTRQLGANGPYVSAIGLGAMGIGAYYGETDYDETFKMLTYACDNGVTFWDTADIYGSSMHTSISSRDSASEAERSMMFIFPGEETLGKWFASTGRRSEIFLASKFGASGMRDESERPEAPNENGIPPPNSKPSYILRQLQRSLSLLQTDHIDLYYQHRPDPHVPVEVVLETLRPAFEDGRIRWFGISECSVDVVRRAKAVKGLGEKFICVQMEYGPFELVHERSGLLAEVEKLGVGVVAYSPLGRGLITGKFRSRADFEKGDLRLLLPRFDEANFPANVRLADQMKNLATKYNATSAQLALAWILAEHPGYIPIPGSRTIERLRENMESANLATKLSPEDIREIRDWVDKADVQGSRYPSFFQRSNECGKLEDWRGQGRLSHALLISFEGKPPIPHVCLCRLCCDYPNTKTLPTIQAHTYARQLPGRHIISCVRRSTLAPSSASALATVIQERRKGTVWVTWSYKSIATVRSSILPTQFRLESSGLMTFPTRQLGANGPFRVSLGYDAAGIGECYGKTDYDEAFKMLTYACDNGVTFWDTADIYGSSMCTSPPEGYATPVAEKRVTFVFLGEETLGKWFASTGRRSEIFLASKFGAADMRDESERPEAPNENGLPPPNSKPSYILRQLQRSLSLLQTDHIDLYYQHRPDPQVPIEVVLEALRPAFEDGRIRWFGMSECSLDVVRRAKAVDELGKKVICVQMEYGPFELVHERSGLLAEVEKLAVGVVAYSPLNRGLITGKFRSRADFEEGDHRLRLPRFSEANFPANVKLVDHMKSMAAKYNATSAQLALAWILAEHPGYIPIPGSRAIERLRENMQSAYLAAKLSPEDIREIREWVDKADVQGDRYPVIFQRPNECGKLEDWKGEY
2	cd05371	NADB_Rossman Superfamily	MAFNKVDRRYIMVQISGNTFVVSGGASGLGKGAVEVLLDGGANVVILDLNEASGSALQAEYPNRVVFPGKVDVTDSVSVDEALHQASLVFPRLSGAVLCAGIMSVGLTAALPEYSAPYGVQDIGALKKLLDVNILGTFNVAQQVSQRIVTQEQNNTTQGETGAIVLMSSYTSTDGQSGSVGYSATKGAISSMVLPMARDLARYGIRVNAIAPGVFLTPINDAFVKESTKCGEWPVRPGKPTEFGRFVAHIFENEMINGAVLRQDAALRGAISID
3	cl02310	Glycosyl hydrolase81 superfamily	MSLTLPIEEMVRLRMSVRLGTDGRLTLNMQPILPSVASSSSSSGRLQSNLKLHFNGTADATGTLCLDIWAEDDVPFSSTSSVLTPSTTDPEPAQQLPMPQSDVAPGTMPFDPSTFSFGSGYGQATDLSNFSQSNLGALSGNQWFDQNIADIDMTDTLFCELASSQSNMLWPSQFDMTQRMPPYDDITGKDMSSIISPHVDDGQAIMDALFPTPPLTETSSPIPSTSTSCQSTPDTMATLPTIPEPSPDQENINHSHSDVDDSPLPASPASTLTEEQTQGSGVPGSTSRPFPCLEPGCTLRFTRKYTRKVHMETHTRAKQQRKSFVCGVAGCGECFSRKHDRLRHEVGKHGQECEWTCRQCGRFFSSQTTLERHMMDAGHRNERVQ
4	Pfam06703	SPC25 signal peptidase 25 kDa subunit	MARGRKAANGTPETPATTNSAPDTPDSSTSARAALSLASGAGAAADRDVIKVNNANLTELKNACDDALKRFLARPDLFQQIHTHTDVRLALGWAGVFVAAGTAFYGYKVEFEESKPVMWVGLIVYMVLTTLQALYAYFIEGEIIFVGKRKTFDKRILTERITISSRTTPASSPPPSSSQLPFPLSLFTSPSTNPAPTSSKSAPAHTPPKPTITNSPSYTLNLSYIRTSSAGKSLLSKQNTLDSREYARFFDEEGVLDQEGFEAWVGGLVGALM
5	pfam13450 COG1232	NAD(P) binding 8 HemY membrane heme protein	MARPHVAIIGGGLTGLSAAFHISRALPQARITLLEKSPRLGGWVRSERVQVEDTQGNSASVVLEAGPRTLRPNAQSVLELIHLLELKDETITTPKSSLAAKSRFLHIPPRRGLLPLPHSLISLCTSPLAPLLFRAILTDLFRKPSRPQLDLSTSALSKASFPDRRSWSDDKITDETFHSFLSRRFGDAFATKFGSALVHGIYATDSRRLSVQAAFPSLWKLEEKGKGRVALGVTREIRDSILKRKEIDRKESGSEKVERATKDTISAGPTVSGSSSLASTSDATSSQSWAWEVGMSPHDPLEKSWAEKIKGAAILSFRDGMETLTRKLVKRLGEREGVEIRVGDKGQVKAIKFDDTGKLELTVGSTIDSEILRSDYIISALPIPVLSQILTNSRTSSSAKNPSLHSSDTLGPLISHLNTPPSLSTTSPTSATSTSVLVLNLVFASSSVPLHPPGFGHLIPRGPSDYHNAAKDGNDLGILGVVFDSASVEGQQDYVMSSTIIPSDHANTSLHSGDSEVGSRTESKFTKITVMLGGPYPTRPLKELSEEELLKRVLNALQHQLGLPGPLPAPVFTKMWWNEGSIPVFGVGHVEWAAEVGRRVKEAFSTPTPTEASGSGGDRLERMWVGGAGVSGVSVGDCIKSGREGARWVERMVRLEESQSLEGEAASKGMEIETEK

HS-HMGS	**cl00210 TIGR01833**	**Hirsutene synthase-HMGS bifunctional protein**	**MSETKVGKVAPFPPLPGAPYPPVRNHPRWKELYRLHDEWMMKYWPFSSEKKRARIPFMNLAGFSTWCAPAADFDRMVWGARIAGIFFLADDYIDSGKMLDRIPGFKAAATGTGPLHKEDQAEICHDIVFRAIKATSHPRTFDQLTKCTHEWWDSNIHEPFQNLDQYLAVRRVNIAMYFANAYFRYTLDINLTDEQVNHPLMREAEGIVSDHVGLTNDFFSYLKEKMTNSDDTNIIRILMDHEHLSYEEAKTVIEKKIRQKEQDFIGAGMAVLNDPELGKDREIYRWIANLQYCMGGNLAWSQESGRYNVGVIDGISFPSLSYAAEPTPEDEVVDDTEESRLRELIFNVKDIPPPDFTIDDDAIFMTNPHSHLQDNVVPLPRPENVGIIGLEVYFPKRCISIDALEDFDGVAKGKYTIGLGQQYLAFTDDREDINSFALSAVSSLLEKYNIDPRSIGRLDVGTETLIDKSKSVKTTLMDLFAASGNHDVEGIDSKNACYGSTAAVLNAVNWIESSSWDGRYAIVFAGDIAIYAEGPARPVGGAGAVALLIGPDAPLVLEPTHGSYMANTYDFYKPRMESEYPVVDGPSSVTTYITALDESFKAYQRKVQEGSSRDVPPPYANGANGKASATKSVKLSDFDYSVFHSPYGKLVQKAYGRLTYHDFVAHPTAPVYRDLPTDILSKDASATLTDKSVEKTFAAASASMYKQVVTPSLLISNRCGNMYTGSLYGGLASLLTSIPSYELFDKRISMFAYGSGCASTFFAIKVRGDTSHIKAKLDLERRLAEMDVRPCEDYVVALKLREETHNAPSYIPNDSDAGLWPGSYRLEAVDGKYRRSYTVTH**
7	pfam07110	ethD homology (likely pseudogene)	MTVRLLCFIKRLPHVSFEEFDHHWKNTHGKLVASLQPIVDGKITYTQLHVNPVASSTLQAATFPVISYDGIAEFHAETVEEILQLFGSQEYQEKVAFDEATLGFDRAAVQVMVGENHVPQPAK
8	cl12078 cl00938	**Cytochrome P450 Monooxygenase**	MANISQPLSLIQDVDFSSFSRPWSTLAIIATIALVARSALKPKRNLPPGPKGLPLVGNLFQLPQFQWLRFTEWKEEFGPIFSLNFAGQPVVVLNSHKVTTDLLGKIARPAHPEGRSQPSRPTVNYLQRSPKVLPVHVLSPFVARMTSHIFSLTRFIMASEILTGSIFIAFSSYGDLWRKLRKAAHEGLNVRAAEAYQPLQEKDAAVLVADLLKEPLYWDDHLKRSAASTVLTAVYGMEPIKSKDDPLVVRINDLMHRLVRATLPGAFLVEIFPVMKRLPEFLAPWKKEGLEWHRRDTVMFQEFMDKVRGQMKAGESKPSFAAGLIEKEKHHNLSKKEESWLAGTMFGAGAETTAAALSVFFLAMRLYPDVMRKAQAEIDSVVGRDRLPTFEDRARLPYIRAIVKEVLRWRPVGPLGLPRRAMQDDVYEGYFIPKGTLVIANVWAMNRDPTLFPDFDEFRPERFLDETGTVDVVPADTHNQGHVTFGFGRRICIGLNIANQALFIDVASTLWAASIEPALDDFGNEIVPSRNESVDEGLVVRPVPFKCKIVPRAEDVDAMLEMTEKKLVCPGGVSSGRDVEVAFFALYCTVHMQCILVYSTPGGTAKPSDYAHRFMKSPITPLVRYTGAQKSAEFVVRQGAPHIVFFARHSSFHPALDFLSPIK
9	cd05259 pfam13460	PCBER like, atypical SDR, NAD binding	MSPLPIAIVFGGSGLTGTSIVNGLLERKEFEVKVPVRPSSVDKPSVVELRNKGVAIIPVDLATASSDHLQEILRGANTVICSLVYTQLGLQHKIIEAAKAVGVPRFVPCDFGTPGRRGVRKLHDEKLDIQDAVKASGIGYTFIDVGFWYQLHLIYTDVEKAYVPWLYEASRYVYNDGLVKTAYTDLTDIGRFVARIVADPRTLNHHVRYSFSLSVFAWGEEITQQDLVNLARKYGDPNVEVIRKTTADLEALVAEAKEKKLGTLAYWDYHYSMWVLGENRAEVAKLEGALDARELYPDYKVRPLEDYAVEFYKCKLL
10	**cl12078**	**Cytochrome P450 Monooxygenase**	**MGNSSSVVSSLPESFSGPMNSLYDAAGKNAYNLVGLAVLAVAVSWFTKRPKGPFPPGPKGIPFFGNVFQLPHSFTWFKFTEWGEQYGPIVGLNMAGQPMVVLNTGKVCADLMDRRSVIYSDRPRFIMASEILTGGMLVGFANYGAVWRRLRKAAHLGLHLRAAEAYYPIEEREAAILVQDLLRDPGSWDGHIRRSIASTMFNVVYNGESLATKDDPTVAKINALMHRVVQAALPGRFLVEILPWMRYLPDWMASWKRKGKESFRQDSNMFKGFLQNVKNEVATGDYKPTFGSHLVYPGNPHGLSKDEEAWLAGIIFGAGSDSTAGTLGWFMLLMALYPEAQAKAQEEIDRVVGRHRLPNFEDRDSLPYVVALMKEVLRWHPVSPLGLPHRLTEDDWYEGYFLPKGTIVVSNIYGINRDPEFFPDPDAFRPERYYNDDEDLTKKAEFDDTHGQGHYSYGFGRRVCVGMNLANNALFINMVSILWAVNIKCPVGPDGKTIVPDRNKFIDDGLVVRPEQFQCILEPRENDVSAKLGSANAQAVY***
11	**cl12078**	**Cytochrome P450 Monooxygenase**	**MPNADLPNLVPLDPSPVIMDSIMSRPLVSTLFAADGFQLASLSALLVTVLVFVRFSKRNPSNPQNLPLPPGPRGLPVLGNLLQIPSEHYWLKFDEWIREYGPIVSINLAGKPVIILGTPKVAAELFDRRSAIYSDRPRWVLAYEILAKGMHAGVMPYGDKLRRFRKAIHAGLQPRALASYHPIEEREARIYLKEVSKNPTDFRNSVKRFTGAVIMSTTYGHTVTTFKDDKFVRRIFASAARFAGSLAPGEFMVDVFPWLWYIPSWVPGAGWKKKAAKWAQEDHELFSTMREAARANGDKQKSFISEGLSNAYGVNEEELAYIGGTISQTPDTLMSVSSCFMLAMVRWPEIQKRAQAEIDSVVGRGRFPTYADQPNLPYVTAVVKETCRWRPVAPLSVPHASTQDDVYEGYFIPAGTTVISSIWSIHRDPETYPDPDSFNPERFIDEHGNEKNTKESKAFGHHLYGFGRRLCPGATMADQAVWVFASHILWALNLDREKDEFGKEIVPDVSPLMFTSGGEASHPLPFKCKISVRPGVDDFLDEIELPTAI***
12	**cl12078**	**Cytochrome P450 Monooxygenase**	**MSLSRTDVMALLGLFLVLYLSTGYTRKAKGKLPPSPPGGLPLLGNVLQMPKRNGWLLMHEWSKTLGPIFHLNMAGQPVIVLNSNEAALELLERRSQIYSDRPRLIMTGEIMSRNLVVGFQRFSDRWKRFRKAAHAGINIRAAEAYYGIMERESALLVTELHKSPKHWDDHLQRVIASSLFTALYGGEPMLNKNDPIVEQINDCMHRLTGAALPGAFLVDVFPVLKRLPGWLYRPKGEGLNWYKKDNAMFNNWLDRVKKDMDGNTPPPSFGRVLLEAQEQFQLLDREVPWLAGSMFGAGSDATAGIMRWFMLAATLYPERIQRAQDEVDLVVGRSRLPTFDDRESMPYLRAFCREVMRWRTVAPLGVPHRLIEDDHYMGYYLPAGSIVLSNIYSINRSPEAFDDADSFKPERFLNEEGTFEVLHPETHNQGHYTFGFGRRACAGMHIANNLMFINAAHILWSFNIRKAKDAQGNEITPSATNYHDTGLIVRPHLWEVDIIPRGPEVLQVAKERFAKGI***

13	**cl19922** **cl06869**	**FAD binding 4 super family** **BBE superfamily**	**MATLLAFSAALASVYGVSAASSPYASVTASQWAALNSSVNGRLATSVPIAQPCFDAYSGIVNSNTLAPDSEACSEVQSLWTNTTYRVTQFGTYEQIWSERLNGSACDLDALDPTDPAAMNLTCTLGSIPPYYIDVTSPEDIQAALTFSNQTGVPIVIKNTGHDYLGRSSAPGSLALWTKNLLNQTFSEEFVPEGCNASVGRALTNGAGVTWIEAYKVADANNATVVGGAFPTVGASGGWLFGGGHGFLTGVNGVGADSSLQFKVVTPDGVYRIANACQNEDLFWALRGGGSGFGVVLESTIAAHPAYDIKIAVIEIQNITLDAQFEVFRVFAGLREQLAQEGWGGAFLPQYTDGTMAVTMINPTLTDEQAAATFAPVIDYVNSINGTDGILVTANGFVPGGSYLYLQENYISTVPVGLGAFIGSRLLPLSSFTSNSSLDELITAMKSGLEKVGPGEWPPMEILMDTPLLTPDSNNETSVNPVWRSSAFVMVYGVSYEYNATAADELALMQTVHDALDYVRAVTPGSGEYNNEADILQEDWQEAYWGVQYPALLAIKQKYDPYNLLTGWQYVGFDKGNSMFDRYNI***
14	cd06174	Major Facilitator Superfamily (MFS)	MSDSVEKGRSFQTPSPAGPEHNGQSSAPSSEAAAPAEPVVHIIDPNASSFRKATVLVVVCLALFIDSFNTGGMIICLNNIEEDLGQSPAIVQWILTAFNLTFGSFLLLSGRISDIYHPKPIFISGFFIVGVFGIGAGFVNNIIGLIIIRALQGIGASMTIPSAISMLTSAYTDPESRGIALTFFASAGTLGLCLGFVIGGIIVQFASWRWVFWGIACVAVPISLLSIWLIPVQSLRMNSKNKKMDYPGVATLTASIILLIFAFSQAPTFGWGTARVLAPLLVALLLLGVFFFWQTRLSDERALIPPKMWFIPNFLILILVSFSNQIYFIGPVVLYSNYYPTNYGWSPLTIGLHFLPTGIISGIICIIFPRQILRLPPKMVLVAGQLMAGVFGILYAFAYTRERYWSYTFPAMVLATAGSSVTYLVSNVGVITSVPVDKVGVGAAVFNAAQQVGSAVNVAIVTTILVETTKTDPQTPKESYHGVSSAIWWIVAIGCAEAIASAIFFRPRKNSLEGDGGEGMETQKLQARDDEVKEAVATGSAGGI
15	cd5233	SDR c Rossman superfamily NAD(P)(H) binding oxidoreductase	MSVPVEDLPVTRENDVYPGIDPKPHFEGQTYAGKVVLVTGASRGIGSEIALYYARAGASLALLSRTQAVLDKTKAHILEAAPKAQITTFVADVVDTQAIKAAVDGTVKTFGKIDIVVANAGKADPWKKPFTEYDPDNWWKTVEVNVRGVYNVAHFSLPHLGATSGYFLVIGSIGAQMRMPFASSYVLSKHAVNRLVEYIKTENPNVKTFSLNPGAIKTDMADNNPEAAPWLIDTLQLPAATALRVTSGKEDWLNGKYLSANWNLDEVEQKWKEKIIAEDALVNRLHVPV

Table S2

Stehi1|122776 gene cluster protein predictions. Protein sequences from Augustus (6) gene predictions are given for each predicted open reading frame in the biosynthetic gene clusters surrounding Stehi1|1227763 in the *S. hirsutum* genome (7) available in the Joint Genome Initiative (JGI) Database. Functional annotations were done as previously described in (5).

Gene no.	Top conserved domain(s)	Predicted function	Amino acid sequence
1	cd06174	MFS Superfamily	MPPRTNTTRRLDATQLVGLSLNLTAHKTPATPETVAPIFYHLNQEKIPRRSTRSTPYSRDSAESKTVWNAVCALNVIVACSYTISGKFNPQLDRRFLRADGWPSIWAWLMFLNDELVLKASYEQYIRDCCPQLIPQVLQVMGFSSVIRRAMIQTPGVVEFVTKKWMVEEQSPEDEAMKKDEASGWKYNEVAKLALGKLRALLAEKRADVALIGTAVNVVNYLSSTNAFEKLGSDPSPEYQDRLLYAFLVQGKIAAIVKAIAWCNKQPAENASFSDPTTRIVAFSYFSMVDDLNTMDSPVWLIQAMESGLFLAMLRSRKWVSALTTSDEQEETFSAALLSTIIPLYLLYPKVIRAARKAVKQVERLGLGTKETAGPLYGRWVVLKEIVEERARLLKQWENDVEFKGDQKLRRDYCERCSMSPAQDDGEGENTVELKRCTSCLNVFYCSKECQKAHWPRHKEDCKVRRTDMECGRRGIINKSERSLLEYIVREQVNQHKTTIADTVGSGPLLQYLVRVSLAHTPPQVTALRYNEAYPGPTKEVDWEAVLSDSEEGSDVPDSQAGSDESEENQDSDDSGSMTSEDKIAFDKKFRNMLYLEFTVPGNENPYSSSIDISFWGLPLDPL
2	Cd03386	PAP2_like protein, Aur1_like superfamily	MSSIRTSLIRTGNQLYVALLAGWARLDKSFSPRDTIQRLQKHAFSYSDLAYVFHILLATFWITIMGVPGFPLKLGIPLFYGLLLLIPFTCQFFLPFHPIASWILTFYSSRFIPTAYRPSISVSVLPTLETVLYGANISDILTRFTHPILDVFAWIPYGVAHFTLPFFVGAFLWLFRPSPVVRLWARTFGYMNLLGVIIQILFPCAAPWYEVIFGLTPADYSMLGSPGGLLRIDHLLHGSGYTVTFSNAPVVFGAFPSLHAGCATLEALFLSHFFPQTTKFVWGYASVLYWATMYLTHHYLIDVVGGACLAIAAFYVFLPDEYRGPGALAPAQGLPTNGYQYVNGGSQRSKYEIYDLEAPRTRGLGIGGGGRGNSSMITDAADFDLASDVSSPSDDEGDVGIAYRSPAIPSTPQSSVPLMGGHSGAHAGKGKGQNGSAVGGGQPRRSHKHTASIASLIRADERTEEGWSPIATGGFVIPPTPTRAEREAGSGRS
3	Cd06174 TIGR00893	MFS superfamily, D-Galactonate transporter	MIMFSVYSGHRSAPSGKVTKRYRGSTSRRIKGRCYIVPCSVLPDVLRPPVPASSPSLSGCFSLSRLLTNPLQPTFYRASAMSGKDIEKAEESYVSEKSSEGSGSPYVVDEEAERRLVKRLDMRIIPASMIIYLLCFLDRSNIGNAKVLNSDVGDSLMQTLGISNSDYLTALMIFIVGYTIFETPWTYMIKKFRPSRTLALLMFSWGLLTIILGCVTNYGGLVAVRFLLGSFEAGLFPGLVYYLTFWYTSRERAVRIALILACATLAGAFGGAIAYGVGHMNAALGHEAWRYLFWIEGVPSCVSALLVIFILPDFPENSTWLSPSDRTLASARLQGMASLGHSTITWAEAKQTLLDWRLYLHYLVYISISVPFSSISLFAPTIVAGLGYEGLDAQLFTVPPYAIAFVITVAVAWVSDRYEARAWGAFISLVIAGVSFLIEGALPGDSFKARYGMLCMAVTFSFASIPPLLSWLTANLRSTGASTLAVPLNVSIGQLGQIVGVYIFKSSEAPGYPTGHFTNAGFILEGAVVVLVLRYIYIGVAWDRLRAVEQGSGSARTQASRVSVRSRRLSPSLPTTTCDTYFTLNPVATAVENDDEGPKEYVVEEILKAKVGKRGSKKAYVRIVTYTEIRAQYSALLTCLAYEIQFVRVAYCCLNRNTTSKYAFGFWKGYGPKDNTWEPRESFASSPKLLDRFWARFDKGKPQIATLKGNEELTPGKPAVAIEDDDDDEEEEAPKRTPKAKRKSITKENPSPASTKRKRGRPSAAESTTSKRRKSNA

Stehi1 |122776	Cl00210	Isoprenoid biosynthetic C1 superfamily, predicted STS	MSAAYHVSFDMSTAKPEIPPMESFPPINVYPREAEIIKYCNNYVAEHFPFNNDAEVKHFNGMEIPAYACRVVSFARDHEKMRKVSILIVFYFIFDDWVDKNGMKLDKSTVMALLPPPSEVPIKPPQAGKMTLSDISAELYGAVRDDMPKADYDRMVNDMMEYLRVQRMAPGYNTLQELLDLRSGEVGVYVLFRYIIYAMELSVSGKELDDPLVKRAQVLGSEAGVLRNEASSYVKEVNEGSGAHNVITKLQEWSGCTEKEAMKQVLDAIEKRQEELREMCLKVTEAPHLSEDCKTFVKTIPYIVAGNTWWHHHVCLNPSTPALLLADALPLAGKVYEICRGSRGDCALEYGRVAMSLSILF
5	Pfam00348	FPP synthase	MLSSMPMPTNIPTGHAKVNGCGPKTGATNGYIALPKVTIPSGGAWTAAEEKALLEPYTYLASAPGKGVRKLLVDALNVWLQVPTEQLVVIANIVDMLHLSSLMIDDIEDSSELRRGNPGKHPISIRLGCLGPHDTLSRPAAHHVYGVPQTINTAEYVFVQAIGEVAKLRATRPDNEHGLHKIVNDELQNLHRGQGLEIIWRDSLKCPSEEEYIDMANKKTSGLLRIACRLMMGCATSNVGTDYVPLINTLGVFFQIRDDLLNLDDDEYTAKKGFAEDLSEGKFSFPIVHGIQASPSDNLILQVLKDRPTSPDMKIPAINYLRDGTHSFQYSRVVLHSLELQMKEEIARLGGNEKLSRIIKHLSVQV
6	Cl12078	P450 superfamily	MSFGVTPTLDEIALLSTLPCGVNEIRFQQSFRSFKSVKFDYYKSFWRKLIDFYPIPALTFSPLAPSKDIMLEKLFAHLSALGVTQYRLKDCALAGTYALGLVLIVRRILMGNRGSLPPGPKGWPIIKNILDIPAEYQWKTFLKWSREYRSDVISLKVPGATLVVLNTMKAVDDLMVKRSHIYSSRPRMVMLNEVMRHDWIFGIMPYGDRWRASRKLFSQYVDKNGIRPHQLTAVRRFLPRLLATGSAEDLDGKLRLVAGDFILSSAYGLDIRDADNHFVRLSQDALMSIIPGVHLGGYVVDIFPMLKHLPAWFPGAGFQRIASKSREMVYEARHAPFKFAQEQMEKGTAKPSLTSALIQSLDKDKTPDYDCRLEAVQDVFATMYLAGSETTIIAMRNFIVAVAAFPLVLKKGQMAVDSFLDGRLPTFEDRKDLPYVDALVEETLRWGGFSFIGVPHCTSEDDYYNGYFIPKGALVLANIWAVLQDENIYGPKTERFQPERFLYEDGTFNAEIDADPEFGFGRRVCPGKDVVREALWILIASFLAVFDIHDAVGEDGKPIDVDKIANLRSKSTSFLRLLPHD
7	Cl10013	Glycosyltransferase _GTB_type super family	MSSHIIAIPFSAWGHTRPAIAFLVQLLKLYPDLSTTLITAKSIEENCRAEVIFQLTSAGLKDDPRMKIVSLEANYFMGPDGYLEPMKDAYAKIVKDYPAQAVIVDLGFVPFIEHIRPLSPAETTVKIAAWWPIMVSMFHTPPLCTFNDATIGAFMMKLGGCMASGDDYLTASGKCWADEIVGKKINIPGLPEMSDYECYVQEPPFTLPSFVLTDWMKGLQQSDVLLTSSSHCLEREGIATIAKVLKAGRAVERVFAVGPLLPAESKKVLDLERTGSKAGDLNVFLDRIVQEKGPKSVLYISFGSMFYPAQPEMVFTVLRVLLGLNIPFVLVHRAESPPLPTALRESIEASPLVFLTQWGPQQYILSHPATGWFLSHCGLNSVQESLASGIPLICWPLFADQPLLSIMVSQVLNCGFELSEVRQGFGLKYRQSTGKTPTGTLEAVAEEAREVLKAAFFDQEKRAVKEEGARKMQKLLNDAWKKSGEAKKDTEAFVQFILA
8	Pfam00067	P450 superfamily	MSKRIRIFTPSDVAEHNTEESIWVSYQGKVLDVTSFLPDHPGGEEFILRHAGKDVEDVMKDADEHVHSESAYDMLEEFVIGRLGAGEMVVSDDWVPADDFHPDNTDEEKDFEKNQFLDLRKPLFRQMWYANFRAKRIISSRFISLVTSQSRRASSVLTTLSWYVIPTIWLPITAYLALRSLLQLSGFVLPLFSANPFAPFTALVSSPSGIPITSGALLSFAACFFVGNVIWTLLEYGMHRFLFHIDYYLPDKPMFLTLHFLGHGIHHYMPMDRTRLVMPPVLFTTLQAPFTRLAHTLFPASIANGIIAGSFFMYVVYDCSHYAMHHTKLPAYLRETKKYHLAHHYKNFELGFGVTSKIWDIVFNTVLPI
9	Cl01132 Pfam00173 COG3000	FA_hydroxylase superfamily, Cyt-b5, ERG3 sterol desaturase	MSKRIRIFTPSDVAEHNTEESIWVSYQGKVLDVTSFLPDHPGGEEFILRHAGKDVEDVMKDADEHVHSESAYDMLEEFVIGRLGAGEMVVSDDWVPADDFHPDNTDEEKDFEKNQFLDLRKPLFRQMWYANFSKAYYLQQVHQPRHLPEPARLFGPDYLEVFTRASWYVIPTIWLPITAYLALRSLLQLSGFVLPLFSANPFAPFTALVSSPSGIPITSGALLSFAACFFVGNVIWTLLEYGMHRFLFHIDYYLPD

			KPMFLTLHFLGHGIHHYMPMDRTRLVMPPVLFTTLQAPFTRLAHTLFPASIANGIIAGSFFMYVVYDCSHYAMHHTKLPAYLRETKKYHLAHHYKNFELGFGVTSKIWDIVFNTVLPI
10	No hits		MQNPADEIASVVKLVTTTPSPDVQKRALERDAGFRHPLCTVPSAHNSRESVIGIYQWYRIMSPKIELEVNSVSYDKEKGKVFLDVTQKFHIRFNPLPATPARLSVHLSLREENGLYYIALQEDFYHPDDLISLVIPILASPAHMALRAGAISSNIFARVFQVTFGWWQPSTGERVGSD
11	Pfam13450	NAD(P) binding, Rossman-like domain	MASSSTVRALRAVKHDIELFNQTSAKLFKQRRFLRLLNPMRVAYLLLDIFYIAIQLVILFFFKPPVPKSDELKKPFGKIAVVGAGLTGISSAAHCVSHNFDVVIFECMSAISPSVTHLKQQLTFHLVVTLASDRPGGIWAHVNKTSGLQLNSMLYRFHPSLLWSLAFPQRDDIVGEITRIWKEYRLESRTRFNVCPFSSSPSFLSSHERPIFIDVHLFFVQTPVTSAKRAPGSSSPGSKWIINDNEDEMFDAIIVTIGTCGKPQMVGFPGMPKDKAPPKKEKKGGDEKKQGKKQENGKSQEDHHEPKEKDDSPEIDSSPTQDSGSLPSPTDPRQAGAPSYSAMAKTEPTGENHVVVAQGDGADELREESPDGKRPGEPADEGNQDEDEEVYEGQLMHSSELDDKDVKGKTVVVVGSGASGVEAVETALDRGAKEAIMIARDDKWIIPRNIIVDTAISAQPFGREMPLSFLWEGFLKHWHYRGVEDLVPVDKGIYEGTPVVNDDFLQHVRSGSCTYIRGDTLRLTKSGVEVRVRPRGSKPGDKGPSHSPPPEKSNAKSNEYPIKEIKGEAVVLATGFEKPSVDFLPEDLFPGDYGRPNLYLQNFATEDWSILMTNSSYLNAIGTVGHIHIGIYTRILLIFLMDEYARPPPKDMKLWVDAIGFVKRGAKGGALGFFTYMELTIWFLLFHIFRPDRIRWVFFSMQGWGLNVNKINAKA

Table S3

Representative HMG-CoA synthase (HMGS) and reductase (HMGR) protein sequences. Sequence names and Accession numbers (JGI fungal genome database or GenBank).

<table>
<tr><th>HMG-CoA synthase sequences</th></tr>
<tr><td>HMGS domain of HS-HMGS <i>Stereum hirsutum</i> (STS gene cluster) (This study)
MTNPHSHLQDNVVPLPRPENVGIIGLEVYFPKRCISIDALEDFDGVAKGKYTIGLGQQYLAFTDDREDINSFALSAVSSLLEKYNIDPRSIGRLDVGTETLIDKSKSVKTTLMDLFAASGNHDVEGIDSKNACYGSTAAVLNAVNWIESSSWDGRYAIVFAGDIAIYAEGPARPVGGAGAVALLIGPDAPLVLEPTHGSYMANTYDFYKPRMESEYPVVDGPSSVTTYITALDESFKAYQRKVQEGSSRDVPPPYANGANGKASATKSVKLSDFDYSVFHSPYGKLVQKAYGRLTYHDFVAHPTAPVYRDLPTDILSKDASATLTDKSVEKTFAAASASMYKQVVTPSLLISNRCGNMYTGSLYGGLASLLTSIPSYELFDKRISMFAYGSGCASTFFAIKVRGDTSHIKAKLDLERRLAEMDVRPCEDYVVALKLREETHNAPSYIPNDSDAGLWPGSYRLEAVDGKYRRSYTVTH</td></tr>
<tr><td>Stehi1|166728 <i>Stereum hirsutum</i> FP-91666 SS1 (STS gene cluster)</td></tr>
<tr><td>Stehi1|119554 <i>Stereum hirsutum</i> FP-91666 SS1 (STS gene cluster)</td></tr>
<tr><td>Stehi1|168705 <i>Stereum hirsutum</i> FP-91666 SS1</td></tr>
<tr><td>NP_013580.1 HMGS1 <i>Saccharomyces cerevisiae</i> S288C</td></tr>
<tr><td>XP_002491079.1 HMGS1 <i>Komagataella phaffii</i> GS115 (<i>Pichia pastoris</i>)</td></tr>
<tr><td>Q01581.2 HMGS cytoplasmic <i>Homo sapiens</i></td></tr>
<tr><td>AAB17601.1 HMGS <i>Schizosaccharomyces pombe</i></td></tr>
<tr><td>P54868.1 HMGS mitochondrial ketogenic <i>Homo sapiens</i></td></tr>
<tr><td>AFM91095.1 HGMS <i>Ganoderma lucidum</i></td></tr>
<tr><td>XP_008038800.1 HMGS <i>Trametes versicolor</i> FP-101664 SS1</td></tr>
<tr><td>XP_001874523.1 HMGS1 <i>Laccaria bicolor</i> S238N-H82</td></tr>
<tr><td>XP_001888022.1 HMGS2 <i>Laccaria bicolor</i> S238N-H82</td></tr>
<tr><td>XP_001888015.1 HMGS3 <i>Laccaria bicolor</i> S238N-H82</td></tr>
<tr><td>EXL58785.1 HNGS1 <i>Fusarium oxysporum</i></td></tr>
<tr><td>EXL58784.1 HMGS2 <i>Fusarium oxysporum</i></td></tr>
<tr><td>EXL58783.1 HMGS3 <i>Fusarium oxysporum</i></td></tr>
<tr><td>Aspjap1|392521 HMGS1 <i>Aspergillus japonicum</i></td></tr>
<tr><td>Aspjap1|365674 HMGS2 <i>Aspergillus japonicum</i></td></tr>
<tr><td>Aspjap1|317209 HMGS3 <i>Aspergillus japonicum</i></td></tr>
<tr><td>AAG32922.1 HMGS <i>Brassica juncea</i></td></tr>
<tr><th>HMG-CoA reductase sequences</th></tr>
<tr><td>Stehi1|171644 HMGR Stereum hirsutum FP-91666 SS1</td></tr>
<tr><td>XP_008041304.1 HMGR Trametes versicolor FP-101664 SS1</td></tr>
<tr><td>XP_964546.1 HMGR <i>Neurospora crassa</i> OR74A</td></tr>
<tr><td>XP_011328582.1 HMGR <i>Fusarium graminearum</i> PH-1</td></tr>
<tr><td>XP_016270872.1 HMGR <i>Rhodotorula toruloides</i> NP11</td></tr>
<tr><td>NP_013636.1 HMGR1 <i>Saccharomyces cerevisiae</i> S288C</td></tr>
<tr><td>NP_013555.1 HMGR2 <i>Saccharomyces cerevisiae</i> S288C</td></tr>
<tr><td>AAB39277.1 HMGR <i>Schizosaccharomyces pombe</i></td></tr>
<tr><td>NP_000850.1 HMGR <i>Homo sapiens</i></td></tr>
<tr><td>NP_177775.2 HMGR1 <i>Arabidopsis thaliana</i></td></tr>
<tr><td>NP_179329.1 HMGR2 <i>Arabidopsis thaliana</i></td></tr>
<tr><td>XP_002491966.1 HMGR <i>Komagataella phaffii</i> GS115 (<i>Pichia pastoris</i>)</td></tr>
</table>

Table S4

Survey of Basidiomycota genomes in JGI's Fungal Genome Database (performed 10-2017) for duplication of mevalonate biosynthetic genes. BLAST searches (parameters: Blossom62 Scoring Matrix, 1.0 E-5, Model Proteins) were performed with HMGS, HMGR, MK, PMK and MDD sequences from *S. cerevisiae* (see Supporting Data Set for sequences). See Figure 1 for mevalonate pathway. Bold numbers denote multiple HMGS or HMGR gene copies. *Note: Individual hits were not manually verified. Some duplications may represent pseudogenes and/or allelic variants that may have been included into the filtered model protein list for certain genomes.*

Basidiomycota (307 genomes searched)	**HMGS**	**HMGR**	**MK**	**PMK**	**MDD**
Number of genomes with:					
>1 homolog	64	54	14	25	22
2	45	34	12	23	20
3	9	3	2	2	1
4	7	4	0	0	0
≥5 homologs	2	5	0	0	1
multiple copies of HMGS and/or HMGR: 85					
multiple copies of HMGS and HMGR: 18					
Genome					
Abortiporus biennis CIRM-BRFM1778 v1.0	1	1	3	1	1
Acaromyces ingoldii MCA 4198 v1.0	1	1	3	1	1
Agaricostilbum hyphaenes ATCC MYA-4628 v1.0	1	1	2	1	1
Agaricus bisporus var bisporus (H97) v2.0	1	1	2	1	1
Agaricus bisporus var. burnettii JB137-S8	1	1	2	1	1
Agrocybe pediades AH 40210 v1.0	1	1	2	1	1
Amanita muscaria Koide v1.0	1	1	2	1	1
Amanita thiersii Skay4041 v1.0	1	1	2	1	1
Amylostereum chailletii DWAch2 v1.0	**2**	1	2	1	1
Anomoporia bombycina ATCC 64506 v1.0	1	1	2	1	1
Antrodia serialis Sig1Antser10 v1.0	**2**	1	2	1	1
Antrodia sinuosa LB1 v1.0	1	1	2	1	1
Aporpium caryae L-13461	1	1	2	1	1
Armillaria cepistipes B5	1	**2**	2	1	1
Armillaria gallica 21-2 v1.0	1	1	1	1	1
Armillaria mellea DSM 3731	1	1	1	1	1
Armillaria ostoyae C18/9	1	1	1	1	1
Armillaria solidipes 28-4 v1.0	1	1	1	1	1
Artolenzites elegans CIRM-BRFM 1122 v1.0	1	1	1	1	1
Artolenzites elegans CIRM-BRFM 1663 v1.0	1	1	1	1	1
Atractiellales sp. v2.0	1	1	1	1	1
Auricularia subglabra v2.0	1	1	1	1	1
Auriculariopsis ampla NL-1724 v1.0	1	1	1	1	1
Auriscalpium vulgare FP105234-Sp v1.0	**2**	1	1	1	1
Basidioascus undulatus	1	1	1	2	1
Bjerkandera adusta v1.0	1	1	1	1	1

Basidiomycota (307 genomes searched)	**HMGS**	**HMGR**	**MK**	**PMK**	**MDD**
Bolbitius vitellinus SZMC-NL-1974 v1.0	1	**2**	1	1	1
Boletus edulis v1.0	1	1	1	1	1
Botryobasidium botryosum v1.0	1	1	1	1	1
Calocera cornea v1.0	1	1	1	1	1
Calocera viscosa v1.0	1	1	1	1	1
Cantharellus anzutake C23 v1.0	1	1	1	1	1
Ceraceosorus sp. MCA 4658 v1.0	1	1	1	1	1
Ceratobasidium sp. (anastomosis group I, AG-I) v1.0	**2**	1	1	1	1
Cerinomyces ceraceus ATCC 56525 v1.0	1	1	1	1	1
Ceriporiopsis (Gelatoporia) subvermispora B	**2**	1	1	1	1
Cerrena unicolor v1.1	1	1	1	1	1
Chionosphaera apobasidialis 52639 v1.0	1	1	1	1	1
Chionosphaera cuniculicola CBS10063 v1.0	1	1	1	1	1
Clavicorona pyxidata HHB10654 v1.0	1	1	1	1	1
Clavulina sp. PMI_390 v1.0	1	1	1	1	1
Climacocystis borealis CliBor001 v1.0	1	1	1	1	1
Clitocybe gibba IJFM A808 v1.0	**3**	1	1	1	1
Coniophora olivacea MUCL 20566 v1.0	1	1	1	1	1
Coniophora puteana v1.0	1	1	1	1	1
Coprinellus micaceus FP101781 v2.0	1	**9**	1	1	1
Coprinellus pellucidus v1.0	1	**2**	1	1	1
Coprinopsis cinerea	**2**	**2**	1	2	2
Coprinopsis cinerea AmutBmut pab1-1 v1.0	1	1	1	1	1
Coprinopsis marcescibilis CBS121175 v1.0	1	1	1	1	1
Coprinopsis sclerotiger v1.0	1	1	1	1	1
Cortinarius glaucopus AT 2004 276 v2.0	1	1	1	1	1
Crepidotus variabilis CBS 506.95 v1.0	1	1	1	1	1
Cronartium quercuum f. sp. fusiforme G11 v1.0	**2**	1	1	1	1
Crucibulum laeve CBS 166.37 v1.0	1	1	1	1	1
Cryptococcus curvatus ATCC 20509 v1.0	1	1	1	1	1
Cryptococcus neoformans var *neoformans* JEC21	**2**	1	1	1	1
Cryptococcus neoformans var. *grubii* H99	**4**	**2**	1	2	2
Cryptococcus terricola JCM 24523 v1.0	1	1	1	1	1
Cryptococcus vishniacii v1.0	1	1	1	1	1
Cryptococcus wieringae v1.0	1	1	1	1	1
Cyathus striatus AH 40144 v1.0	**2**	**2**	1	1	1
Cylindrobasidium torrendii FP15055 v1.0	1	1	1	1	1
Cystostereum murrayi CysMur001 v1.0	1	1	1	1	1
Cytidiella melzeri FP 102339 v1.0	**2**	1	1	1	1
Dacryopinax primogenitus DJM 731 SSP1 v1.0	1	1	1	1	0
Daedalea quercina v1.0	1	1	1	1	1
Dendrothele bispora CBS 962.96 v1.0	**4**	1	1	1	1
Dentipellis sp. KUC8613 v1.0	1	1	1	1	1
Dichomitus squalens CBS463.89 v1.0	1	1	1	1	1
Dichomitus squalens CBS464.89 v1.0	1	1	1	1	1

Basidiomycota (307 genomes searched)	**HMGS**	**HMGR**	**MK**	**PMK**	**MDD**
Dichomitus squalens LYAD-421 SS1 v1.0	1	1	1	1	1
Dichomitus squalens OM18370.1 v1.0	1	1	1	1	1
Dioszegia cryoxerica v1.0	1	1	1	1	1
Erythrobasidium hasegawianum ATCC 9536 v1.0	**2**	**2**	1	2	2
Exidia glandulosa v1.0	1	**2**	1	2	1
Exobasidium vaccinii MPITM v1.0	1	1	1	1	1
Fellomyces penicillatus Phaff54-35 v1.0	1	1	1	1	1
Fibroporia radiculosa TFFH 294	1	1	1	1	1
Fibulobasidium inconspicuum Phaff89-39 v1.0	1	1	1	1	1
Fibulorhizoctonia sp. CBS 109695 v1.0	1	**2**	1	1	1
Fistulina hepatica v1.0	1	1	1	1	1
Fomes fomentarius CIRM-BRFM 1821 v1.0	1	1	1	1	1
Fomitiporia mediterranea v1.0	1	1	1	2	1
Fomitopsis pinicola FP-58527 SS1 v3.0	1	1	1	1	1
Galerina marginata v1.0	1	1	1	1	1
Ganoderma sp. 10597 SS1 v1.0	1	1	1	1	1
Gautieria morchelliformis GMNE.BST v1.0	**4**	1	1	1	1
Gloeopeniophorella convolvens OM19405 v1.0	1	1	1	1	1
Gloeophyllum trabeum v1.0	**2**	1	1	1	1
Guyanagaster necrorhiza MCA 3950 v1.0	1	1	1	1	1
Gymnopilus chrysopellus PR-1187 v1.0	1	1	1	1	1
Gymnopilus junonius AH 44721 v1.0	1	1	1	1	1
Gymnopus androsaceus JB14 v1.0	**2**	**12**	1	2	1
Gymnopus earleae GB-263.02 v1.0	1	**2**	1	1	1
Gymnopus luxurians v1.0	1	1	1	2	1
Gyrodon lividus BX v1.0	1	1	1	1	1
Hebeloma cylindrosporum h7 v2.0	**3**	1	1	1	2
Heliocybe sulcata OMC1185 v1.0	1	1	1	1	1
Heterobasidion annosum v2.0	1	1	1	1	2
Heterogastridium pycnidioideum ATCC MYA-4631 v1.0	1	1	1	1	1
Hexagonia nitida CIRM-BRFM 1802 v1.0	1	1	1	1	1
Hyalopycnis blepharistoma ATCC 48560 v1.0	1	1	1	1	2
Hydnomerulius pinastri v2.0	1	1	1	1	1
Hydnopolyporus fimbriatus CBS384.51 v1.0	1	1	1	1	1
Hydnum rufescens UP504 v2.0	1	1	1	0	1
Hymenopellis radicata IJFM A160 v1.0	**4**	**2**	1	1	3
Hypholoma sublateritium v1.0	1	1	1	1	2
Irpex lacteus CCBAS Fr. 238 617/93 v1.0	**2**	1	1	0	1
Jaapia argillacea v1.0	1	1	1	1	1
Jaminaea sp. MCA 5214 v1.0	1	1	1	1	1
Kockovaella imperatae NRRL Y-17943 v1.0	0	1	1	1	1
Laccaria amethystina LaAM-08-1 v2.0	**6**	**2**	1	1	1
Laccaria bicolor v2.0	**3**	**2**	1	1	2
Lactarius quietus S23C v1.0	1	1	1	1	1
Lactifluus subvellereus BPL653 v1.0	1	1	1	1	1

Basidiomycota (307 genomes searched)	**HMGS**	**HMGR**	**MK**	**PMK**	**MDD**
Lactifluus volemus BPL652 v1.0	1	1	1	1	1
Laetiporus sulphureus var. *sulphureus* v1.0	1	1	1	1	1
Leiotrametes lactinea CIRM-BRFM 1664 v1.0	1	1	1	1	1
Leiotrametes sp BRFM 1775 v1.0	1	1	1	1	1
Lentinellus vulpinus AHS73672-sp v1.0	**2**	1	1	1	1
Lentinus tigrinus ALCF2SS1-6 v1.0	1	**2**	1	2	1
Lentinus tigrinus ALCF2SS1-7 v1.0	1	**2**	1	2	1
Lentinus tigrinus v1.0	1	**2**	1	2	1
Lepista nuda CBS 247.69 v1.0	**2**	1	1	1	1
Leucoagaricus gongylophorus	1	1	1	1	1
Leucogyrophana mollusca KUC20120723A-06 v1.0	1	1	1	1	1
Leucosporidiella creatinivora 62-1032 v1.0	1	1	1	1	0
Lycoperdon perlatum FP-102459-T v1.0	1	1	1	1	1
Macrolepiota fuliginosa MF-IS2 v1.0	1	1	1	1	1
Malassezia globosa	1	1	1	1	1
Malassezia sympodialis ATCC 42132	1	1	1	1	1
Marasmius fiardii PR-910 v1.0	**2**	1	1	1	1
Meira miltonrushii MCA 3882 v1.0	1	1	1	1	1
Melampsora allii-populina 12AY07 v1.0	1	1	1	2	1
Melampsora larici-populina v2.0	1	**2**	1	2	1
Melampsora lini CH5	1	1	1	2	1
Melanotaenium endogenum CBS481.91 v1.0	1	1	1	2	1
Meredithblackwellia eburnea MCA 4105 v1.0	1	1	1	1	1
Microbotryum lychnidis-dioicae p1A1 Lamole	1	1	1	1	1
Microbotryum violaceum p1A1 Lamole v1.0	1	1	1	1	1
Microstromatales sp. MCA 4718 v1.0	1	1	1	1	1
Mixia osmundae IAM 14324 v1.0	1	1	1	1	2
Moesziomyces aphidis DSM 70725	1	1	1	1	1
Moniliella sp. MCA 3643 v1.0	1	**2**	1	1	1
Moniliophthora perniciosa FA553	1	1	1	1	1
Mrakia frigida ATCC 22029 v1.0	1	1	1	1	1
Multifurca ochricompacta BPL690 v1.0	1	1	1	1	1
Mutinus elegans ME.BST v1.0	1	1	1	1	1
Mycena capillaripes Frankland 9286 v1.0	**3**	1	1	1	1
Mycena galopus ATCC-62051 v1.0	**4**	1	1	1	1
Mycena haematopus CBHHK189 v1.0	**3**	1	1	1	1
Mycena rosella CBHHK067 v1.0	**3**	**2**	1	1	1
Mycena sp. CBHHK59/15 v1.0	**2**	1	1	1	1
Naiadella fluitans ATCC 64713 v1.0	1	**2**	1	1	1
Naohidea sebacea CBS 8477 (P95) v1.0	1	1	1	1	2
Neolentinus lepideus v1.0	1	1	1	1	2
Obba rivulosa 3A-2 v1.0	**2**	1	1	1	1
Omphalotus olearius	1	1	1	1	1
Onnia scaura P-53A v1.0	1	1	1	1	1
Oudemansiella mucida CBS 558.79 v1.0	**2**	1	1	1	2

Basidiomycota (307 genomes searched)	**HMGS**	**HMGR**	**MK**	**PMK**	**MDD**
Panaeolus papilionaceus CIRM-BRFM 715 v1.0	1	1	1	1	1
Panellus stipticus KUC8834 v1.1	**2**	1	1	1	1
Panellus stipticus LUM v1.0	**2**	1	1	1	1
Panus rudis PR-1116 ss-1 v1.0	1	**4**	1	1	1
Paxillus adelphus Ve08.2h10 v2.0	1	1	1	1	1
Paxillus ammoniavirescens Pou09.2 v1.0	1	1	1	1	2
Paxillus involutus ATCC 200175 v1.0	1	1	1	1	1
Peniophora sp. CONTA v1.0	**2**	**2**	1	1	1
Peniophora sp. v1.0	**3**	1	1	1	1
Phanerochaete carnosa HHB-10118-Sp v1.0	1	**9**	1	0	0
Phanerochaete chrysosporium RP-78 v2.2	1	1	1	1	1
Phellinus ferrugineofuscus SpK3Phefer14 v1.0	1	**2**	1	1	1
Phlebia brevispora HHB-7030 SS6 v1.0	1	1	1	1	1
Phlebia centrifuga FBCC195	1	1	1	1	1
Phlebiopsis gigantea v1.0	1	1	1	1	0
Pholiota alnicola AH 47727 v1.0	**2**	1	1	1	1
Pholiota conissans CIRM-BRFM 674 v1.0	1	**2**	1	1	1
Piloderma croceum F 1598 v1.0	1	1	1	2	6
Piriformospora indica DSM 11827 from MPI	1	1	1	1	1
Pisolithus microcarpus 441 v1.0	1	**2**	1	1	1
Pisolithus tinctorius Marx 270 v1.0	1	**2**	1	1	1
Pleurotus eryngii ATCC 90797 v1.0	**2**	1	1	1	1
Pleurotus ostreatus PC15 v2.0	**2**	1	1	1	1
Pleurotus ostreatus PC9 v1.0	**2**	1	1	1	1
Plicaturopsis crispa v1.0	1	1	1	3	1
Pluteus cervinus NL-1719 v1.0	**2**	1	1	1	1
Polyporus arcularius v1.0	**2**	1	1	1	1
Polyporus brumalis BRFM 1820 v1.0	**2**	1	1	1	1
Porodaedalea chrysoloma FP-135951 v1.0	1	**2**	1	1	1
Porodaedalea niemelaei PN71-100-IP13 v1.0	1	1	1	1	1
Postia placenta MAD 698-R v1.0	**2**	**2**	1	2	2
Postia placenta MAD-698-R-SB12 v1.0	1	1	1	1	1
Pseudozyma antarctica T-34	1	1	1	1	1
Pseudozyma hubeiensis SY62	1	1	1	1	1
Pterula gracilis CBS309.79 v1.0	1	1	1	1	1
Puccinia coronata avenae 12NC29	**2**	**4**	1	1	2
Puccinia coronata avenae 12SD80	**2**	**4**	1	1	2
Puccinia graminis f. sp. *tritici* v2.0	1	1	1	2	2
Puccinia striiformis f. sp. *tritici* 104 E137 A-	**2**	**6**	1	2	2
Puccinia striiformis f. sp. *tritici* PST-130	1	**3**	1	1	1
Puccinia striiformis f. sp. tritici PST-78 v1.0	1	**3**	1	1	1
Puccinia triticina 1-1 BBBD Race 1	1	1	1	1	2
Punctularia strigosozonata v1.0	**2**	1	1	1	1
Pycnoporus cinnabarinus BRFM 137	1	1	1	1	1
Pycnoporus cinnabarinus CIRM-BRFM 50 v1.0	1	1	1	3	1

Basidiomycota (307 genomes searched)	**HMGS**	**HMGR**	**MK**	**PMK**	**MDD**
Pycnoporus coccineus BRFM 310 v1.0	1	1	1	2	1
Pycnoporus coccineus CIRM1662	1	1	1	1	1
Pycnoporus puniceus CIRM-BRFM 1868 v1.0	1	1	1	1	1
Pycnoporus sanguineus BRFM 1264 v1.0	1	1	1	1	1
Ramaria rubella (R. acris) UT-36052-T v1.0	1	1	1	1	2
Rhizoctonia solani AG-1 IB	**2**	1	1	1	1
Rhizopogon salebrosus TDB-379 v1.0	1	1	1	2	1
Rhizopogon vesiculosus Smith	1	1	1	1	1
Rhizopogon vinicolor AM-OR11-026 v1.0	1	1	1	1	1
Rhodocollybia butyracea AH 40177 v1.0	1	1	1	2	1
Rhodosporidium toruloides ATCC26217 v1.0	1	1	1	1	1
Rhodosporidium toruloides IFO0559_1	1	1	1	2	1
Rhodosporidium toruloides IFO0880 v2.0	1	1	1	1	1
Rhodosporidium toruloides IFO0880 v4.0	1	1	1	1	1
Rhodosporidium toruloides IFO1236_1	1	1	1	1	1
Rhodosporidium toruloides NP11	1	1	1	1	1
Rhodotorula glutinis v1.0	1	1	1	1	1
Rhodotorula graminis strain WP1 v1.1	1	1	1	1	1
Rhodotorula minuta MCA 4210 v1.0	1	1	1	1	1
Rhodotorula mucilaginosa ATCC58901 v1.0	**2**	**2**	1	1	1
Rhodotorula sp. J31 v1.0	1	1	1	1	1
Rhodotorula sp. JG-1b	1	1	1	1	1
Rickenella fibula HBK330-10 v1.0	**4**	**3**	1	1	1
Rickenella mellea v1.0 (SZMC22713)	**7**	**4**	1	1	1
Rigidoporus microporus ED310 v1.0	1	1	1	1	1
Russula brevipes BPL707 v1.0	1	1	1	1	1
Russula compacta BPL669 v1.0	**2**	1	1	1	1
Russula dissimulans BPL704 v1.0	1	1	1	1	1
Russula rugulosa BPL654 v1.0	1	1	1	1	1
Russula vinacea BPL710 v1.0	1	1	1	1	1
Schizophyllum commune H4-8 v3.0	**2**	1	1	1	1
Schizophyllum commune Loenen D v1.0	**3**	1	1	1	1
Schizophyllum commune Tattone D v1.0	**2**	1	1	1	1
Schizopora paradoxa KUC8140 v1.0	1	1	1	1	1
Scleroderma citrinum Foug A v1.0	1	1	1	1	1
Sclerogaster hysterangioides SCL2.BST v1.0	1	**2**	1	1	1
Scytinostroma sp. KUC9335 v1.0	1	1	1	1	1
Sebacina vermifera MAFF 305830 v1.0	1	1	1	1	1
Sebacina vermifera ssp. bescii v1.0	1	1	1	1	1
Septobasidium sp. PNB30-8B v1.0	1	**2**	1	1	1
Serpula himantioides (*S.lacrymans* var *shastensis*) MUCL38935 v1.0	1	1	1	1	1
Serpula lacrymans S7.3 v2.0	1	1	1	1	1
Serpula lacrymans S7.9 v2.0	1	1	1	1	1
Sirobasidium intermedium CBS7805 v1.0	1	1	1	1	1

Basidiomycota (307 genomes searched)	**HMGS**	**HMGR**	**MK**	**PMK**	**MDD**
Sistotremastrum niveocremeum HHB9708 ss-1 1.0	1	1	1	1	1
Sistotremastrum suecicum v1.0	1	1	1	1	1
Sparassis latifolia CCMJ1100 v1.0	1	1	1	1	1
Sphaerobolus stellatus v1.0	**2**	1	1	1	1
Sporidiobolus pararoseus Phaff 68-350 v1.0	1	1	1	1	1
Sporisorium reilianum SRZ2	1	1	1	1	1
Sporobolomyces linderae CBS 7893 v1.0	1	1	1	1	1
Sporobolomyces roseus v1.0	1	1	1	1	1
Stereum hirsutum FP-91666 SS1 v1.0	**4**	1	1	1	1
Suillus americanus EM31 v1.0	1	1	1	1	1
Suillus brevipes Sb2 v2.0	1	1	1	1	1
Suillus decipiens EM49 v1.0	1	1	1	1	1
Suillus granulatus EM37 v1.0	1	**2**	1	1	1
Suillus hirtellus EM16 v1.0	1	1	1	1	1
Suillus luteus UH-Slu-Lm8-n1 v3.0	1	1	1	1	1
Suillus pictus EM44 v1.0	1	1	1	1	1
Suillus subaureus MN1 v1.0	1	1	1	1	1
Suillus tomentosus FC115 v1.0	1	1	1	1	1
Testicularia cyperi MCA 3645 v1.0	1	1	1	1	1
Thanatephorus cucumeris PT424 v1.0	**2**	1	1	1	1
Thelephora ganbajun P2 v1.0	1	1	1	1	1
Tilletiaria anomala UBC 951 v1.0	1	1	1	1	1
Tilletiopsis albescens v1.0	1	1	1	1	1
Tilletiopsis sp. TKC30 v1.0	1	1	1	1	1
Tilletiopsis washingtonensis MCA 4186 v1.0	1	1	1	1	1
Trametes cingulata BRFM 1805 v1.0	1	1	1	1	1
Trametes gibbosa CIRM-BRFM 1770 v1.0	1	1	1	1	1
Trametes ljubarskyi CIRM1659 v1.0	1	1	1	1	1
Trametes maxima CIRM-BRFM 1813 v1.0	1	1	1	1	1
Trametes meyenii CIRM-BRFM 1810 v1.0	1	1	1	1	1
Trametes pubescens FBCC735	1	1	1	1	1
Trametes versicolor v1.0	1	1	1	1	1
Trametopsis cervina CIRM-BRFM 1824 v1.0	1	1	1	1	1
Tremella encephala 68-887.2 v1.0	1	1	1	1	1
Tremella mesenterica Fries v1.0	1	1	1	1	1
Trichaptum abietinum v1.0	**2**	1	1	1	1
Tricholoma matsutake 945 v3.0	1	1	1	1	1
Trichosporon asahii var. *asahii* CBS 2479	1	1	1	1	1
Trichosporon asahii var. *asahii* CBS 8904	1	1	1	1	1
Trichosporon chiarellii MYA-4694 v1.0	1	1	1	1	1
Trichosporon guehoae v1.0	1	1	1	1	1
Trichosporon oleaginosus IBC0246 v1.0	1	1	1	1	1
Tritirachium sp. CBS 265.96 v1.0	**2**	1	1	1	1
Tulasnella calospora AL13/4D v1.0	**2**	**2**	1	1	1
Tulasnella calospora UAMH 9824 v1.0	1	**2**	1	1	1

Basidiomycota (307 genomes searched)	**HMGS**	**HMGR**	**MK**	**PMK**	**MDD**
Ustilago hordei Uh4857_4	0	0	1	1	0
Ustilago maydis 521 v2.0	1	1	1	1	1
Vararia minispora EC-137 v1.0	1	**2**	1	1	1
Violaceomyces palustris SA 807 v1.0	1	1	1	1	1
Volvariella volvacea V23	1	1	1	1	1
Vuilleminia comedens VcCUCC2015_SSI3 v1.0	**2**	1	1	1	1
Vuilleminia comedens VcCUCC2015_SSI6 v1.0	**3**	1	1	1	1
Wallemia ichthyophaga EXF-994	1	1	1	1	1
Wallemia sebi v1.0	1	1	1	1	1
Wolfiporia cocos MD-104 SS10 v1.0	1	1	1	1	1
Xenasmatella vaga CBS212.54 v1.0	1	1	1	1	1
Xerocomus badius 84.06 v1.0	1	1	0	1	1

Table S5

Survey Ascomycota genomes in JGI's Fungal Genome Database (performed 10-2017) for duplication of mevalonate biosynthetic genes. BLAST searches (parameters: Blossom62 Scoring Matrix, 1.0 E-5, Model Proteins) were performed with HMGS, HMGR, MK, PMK and MDD sequences from *S. cerevisiae* (see Supporting Data Set for sequences). See Figure 1 for mevalonate pathway. Bold numbers denote multiple HMGS or HMGR gene copies. *Note: Individual hits were not manually verified. Some duplications may represent pseudogenes and/or allelic variants that may have been included into the filtered model protein list for certain genomes.*

Ascomycota (510 genomes searched)	**HMGS**	**HMGR**	**MK**	**PMK**	**MDD**
Number of genomes with:					
>1 homolog	137	150	50	6	6
2	121	92	48	5	5
3	14	21	1	1	1
4	2	31	1	0	0
≥5 homologs	0	6	0	0	0
multiple copies of HMGS and/or HMGR: 197					
multiple copies of HMGS and HMGR: 81					
Genome					
Aaosphaeria arxii CBS 175.79 v1.0	1	1	1	1	1
Acephala macrosclerotiorum EW76-UTF0540 v1.0	1	1	1	1	1
Acidomyces richmondensis BFW	1	1	1	1	1
Acidomyces richmondensis BFW	1	1	1	1	1
Acidothrix acidophila CBS 136259 v1.0	**2**	1	1	1	1
Acremonium alcalophilum v2.0	1	1	1	1	1
Acremonium chrysogenum ATCC 11550	1	1	1	1	1
Acremonium strictum DS1bioAY4a v1.0	1	1	1	1	1
Aliquandostipite khaoyaiensis CBS 118232 v1.0	1	**2**	1	1	1
Alternaria alternata 133aPRJ v1.0	1	1	1	1	1
Alternaria alternata SRC1lrK2f v1.0	1	1	1	1	1
Alternaria brassicicola	1	1	1	1	1
Amniculicola lignicola CBS 123094 v1.0	1	1	1	1	1
Amorphotheca resinae v1.0	1	1	1	1	1
Ampelomyces quisqualis HMLAC05119 v1.0	1	1	1	1	1
Anthostoma avocetta NRRL 3190 v1.0	1	1	1	1	1
Apiosordaria backusii CBS 540.89 v1.0	1	**2**	1	1	1
Apiospora montagnei NRRL 25634 v1.0	1	1	1	1	1
Aplosporella prunicola CBS 121.167 v1.0	**2**	1	1	1	1
Arthroascus fermentans 17710 v1.0	1	1	1	1	1
Arthrobotrys oligospora ATCC 24927	1	1	1	1	1
Arthroderma benhamiae CBS 112371	**2**	1	1	1	1
Ascobolus immersus RN42 v1.0	1	1	1	1	1
Ascochyta rabiei ArDII	1	**2**	1	1	1
Ascocoryne sarcoides NRRL50072	1	**2**	1	1	1
Ascodesmis nigricans CBS 389.68 v1.0	1	1	1	1	1

Ascomycota (510 genomes searched)	**HMGS**	**HMGR**	**MK**	**PMK**	**MDD**
Ascoidea rubescens NRRL Y17699 v1.0	1	1	2	1	1
Aspergillus aculeatinus CBS 121060 v1.0	**2**	**4**	2	1	1
Aspergillus aculeatus ATCC16872 v1.1	**2**	**3**	1	1	1
Aspergillus bombycis NRRL 26010	**2**	**3**	1	1	1
Aspergillus brasiliensis v1.0	**2**	**4**	1	1	1
Aspergillus brunneoviolaceus CBS 621.78 v1.0	**2**	**3**	1	1	1
Aspergillus calidoustus	1	**2**	1	1	1
Aspergillus campestris IBT 28561 v1.0	1	1	1	1	1
Aspergillus carbonarius ITEM 5010 v3	**2**	**5**	1	1	1
Aspergillus clavatus NRRL 1 from AspGD	**2**	1	1	1	1
Aspergillus costaricaensis CBS 115574 v1.0	**2**	**4**	1	1	1
Aspergillus cristatus GZAAS20.1005	1	1	2	1	1
Aspergillus ellipticus CBS 707.79 v1.0	**3**	**4**	2	1	1
Aspergillus eucalypticola CBS 122712 v1.0	**2**	**3**	1	1	1
Aspergillus fijiensis CBS 313.89 v1.0	**2**	**4**	2	1	1
Aspergillus flavus NRRL3357	**2**	**5**	1	1	1
Aspergillus fumigatus A1163	**2**	**2**	1	1	1
Aspergillus fumigatus Af293 from AspGD	**2**	**2**	1	1	1
Aspergillus glaucus v1.0	**2**	**2**	2	1	1
Aspergillus heteromorphus CBS 117.55 v1.0	**4**	**4**	2	1	1
Aspergillus homomorphus CBS 101889 v1.0	**2**	**4**	1	1	1
Aspergillus ibericus CBS 121593 v1.0	**2**	**4**	1	1	1
Aspergillus indologenus CBS 114.80 v1.0	**3**	**4**	2	1	1
Aspergillus japonicus CBS 114.51 v1.0	**3**	**4**	1	1	1
Aspergillus kawachii IFO 4308	**2**	**4**	1	1	1
Aspergillus lacticoffeatus CBS 101883 v1.0	**2**	**4**	1	1	1
Aspergillus luchuensis CBS 106.47 v1.0	**2**	**4**	1	1	1
Aspergillus neoniger CBS 115656 v1.0	**2**	**4**	1	1	1
Aspergillus nidulans	1	**2**	1	1	1
Aspergillus niger ATCC 1015 v4.0	**2**	**4**	1	1	1
Aspergillus niger CBS 513.88	**2**	**4**	1	1	1
Aspergillus niger NRRL3	**2**	**4**	1	1	1
Aspergillus niger van Tieghem ATCC 13496 v1.0	**2**	**4**	1	1	1
Aspergillus nomius NRRL 13137	**2**	**3**	2	1	1
Aspergillus novofumigatus IBT 16806 v1.0	**2**	**2**	1	1	1
Aspergillus ochraceoroseus IBT 24754 v1.0	**2**	1	1	1	1
Aspergillus ochraceoroseus SRRC1432	**2**	1	1	1	1
Aspergillus oryzae RIB40	**2**	**5**	1	1	1
Aspergillus phoenicis (Corda) Thom ATCC 13157 v1.0	**2**	**4**	1	1	1
Aspergillus piperis CBS 112811 v1.0	**2**	**4**	1	1	1
Aspergillus rambellii SRRC1468	**2**	**2**	1	1	1
Aspergillus saccharolyticus JOP 1030-1 v1.0	**2**	**2**	1	1	1
Aspergillus sclerotiicarbonarius CBS 121057 v1.0	**2**	**3**	1	1	1
Aspergillus sclerotioniger CBS115572 v1.0	**2**	**4**	1	1	1
Aspergillus steynii IBT 23096 v1.0	**2**	**2**	1	1	1

Ascomycota (510 genomes searched)	**HMGS**	**HMGR**	**MK**	**PMK**	**MDD**
Aspergillus sydowii CBS 593.65 v1.0	1	**2**	1	1	1
Aspergillus terreus NIH 2624	1	**4**	1	1	1
Aspergillus tubingensis v1.0	**2**	**4**	1	1	1
Aspergillus udagawae IFM 46973	**2**	**2**	1	1	1
Aspergillus uvarum CBS 121591 v1.0	**3**	**4**	1	1	1
Aspergillus vadensis CBS 113365 v1.0	**2**	**4**	1	1	1
Aspergillus versicolor v1.0	1	**2**	1	1	1
Aspergillus violaceofuscus CBS 115571 v1.0	**3**	**4**	1	1	1
Aspergillus wentii v1.0	**2**	**3**	2	1	1
Aspergillus zonatus v1.0	**2**	**2**	1	1	1
Aulographum hederae v2.0	1	1	1	1	1
Aureobasidium pullulans var. *melanogenum* CBS 110374	1	1	1	1	1
Aureobasidium pullulans var. *namibiae* CBS 147.97	**2**	**2**	1	1	1
Aureobasidium pullulans var. *pullulans* EXF-150	1	**2**	1	1	1
Aureobasidium pullulans var. *subglaciale* EXF-2481	**2**	**2**	1	1	1
Babjeviella inositovora NRRL Y-12698 v1.0	1	1	1	1	1
Baudoinia compniacensis UAMH 10762 (4089826) v1.0	1	1	1	1	1
Beauveria bassiana ARSEF 2860	1	1	1	1	1
Bimuria novae-zelandiae CBS 107.79 v1.0	1	1	1	1	1
Biscogniauxia nummularia v1.0	1	1	1	1	1
Bisporella sp. PMI_857 v1.0	1	**2**	1	1	1
Blastobotrys (Arxula) adeninivorans	1	1	1	1	1
Blastomyces dermatitidis SLH14081	**2**	1	1	2	2
Blumeria graminis f. sp. *tritici* 96224	1	1	1	1	1
Blumeria graminis f.sp. *hordei* DH14	1	1	1	1	1
Bombardia bombarda SMH3391-2 v1.0	**2**	1	3	1	1
Botryosphaeria dothidea	**2**	**2**	2	1	1
Botrytis cinerea v1.0	**2**	1	1	1	1
Bulgaria inquinans CBS118.31 v1.0	1	1	1	3	3
Byssochlamys spectabilis No. 5	1	**2**	1	1	1
Byssothecium circinans CBS 675.92 v1.0	**2**	**2**	2	1	1
Cadophora sp. DSE1049 v1.0	1	**2**	1	1	1
Caliciopsis orientalis	1	1	1	1	1
Caloscypha fulgens ATCC 42695 v1.0	1	1	1	1	1
Calosphaeria pulchella	0	1	1	1	1
Candida albicans SC5314	1	1	1	1	1
Candida arabinofermentans NRRL YB-2248 v1.0	1	1	1	1	1
Candida tanzawaensis NRRL Y-17324 v1.0	1	1	1	1	1
Candida tenuis NRRL Y-1498 v1.0	1	1	1	1	1
Capronia coronata CBS 617.96	1	1	1	1	1
Capronia epimyces CBS 606.96	1	1	1	1	1
Capronia semiimmersa CBS27337	1	1	1	1	1
Cenococcum geophilum 1.58 v2.0	1	1	1	1	1
Cephaloascus albidus ATCC 66658 v1.0	1	1	1	1	1
Cephaloascus fragrans 12-1022 v1.0	1	1	1	1	1

Ascomycota (510 genomes searched)	**HMGS**	**HMGR**	**MK**	**PMK**	**MDD**
Cercophora caudata CBS 606.72 v1.0	1	1	1	1	1
Cercophora newfieldiana SMH2532-1 v1.0	1	1	1	1	1
Cercospora zeae-maydis v1.0	1	**2**	1	1	1
Chaetomium globosum v1.0	1	1	1	1	1
Chaetosphaeria innumera	1	1	1	1	1
Chalara longipes BDJ v1.0	1	1	2	1	1
Choiromyces venosus 120613-1 v1.0	1	1	1	1	1
Cladonia grayi Cgr/DA2myc/ss v2.0	1	1	1	1	1
Cladophialophora bantiana CBS 173.52	1	1	1	1	1
Cladophialophora carrionii CBS 160.54	1	1	1	1	1
Cladophialophora immunda CBS83496	1	1	1	1	1
Cladophialophora psammophila CBS 110553	1	1	1	1	1
Cladophialophora yegresii CBS 114405	1	1	1	1	1
Cladorrhinum bulbillosum DJ3 v1.0	1	1	1	1	1
Cladosporium fulvum v1.0	1	1	1	1	1
Cladosporium sphaerospermum UM 843	1	1	1	1	1
Clathrospora elynae CBS 161.51 v1.0	1	1	1	1	1
Clavispora lusitaniae ATCC 42720	1	1	1	1	1
Clohesyomyces aquaticus v1.0	1	**2**	1	1	1
Clonostachys rosea CBS125111 v1.0	1	**3**	2	1	1
Coccidioides immitis RS	1	1	1	1	1
Coccodinium bartschii CBS 121709 v1.0	1	1	1	1	1
Coccomyces strobi CBS 202.91 v1.0	1	1	1	1	1
Cochliobolus carbonum 26-R-13 v1.0	1	1	1	1	1
Cochliobolus heterostrophus C4 v1.0	1	1	1	1	1
Cochliobolus heterostrophus C5 v2.0	1	1	1	1	1
Cochliobolus lunatus m118 v2.0	**2**	1	1	1	1
Cochliobolus miyabeanus ATCC 44560 v1.0	1	1	1	1	1
Cochliobolus sativus ND90Pr v1.0	1	1	1	1	1
Cochliobolus victoriae FI3 v1.0	1	1	1	1	1
Colletotrichum acutatum CBS 112980 v2.0	**2**	1	1	1	1
Colletotrichum caudatum CBS131602 v1.0	1	1	2	1	1
Colletotrichum cereale CBS 129662 v1.0	1	**2**	1	1	1
Colletotrichum eremochloae CBS129661 v1.0	**2**	**2**	1	1	1
Colletotrichum falcatum MAFF306170 v1.0	1	1	1	1	1
Colletotrichum fioriniae PJ7	**2**	1	1	1	1
Colletotrichum godetiae CBS 193.32 v1.0	**2**	**2**	1	1	1
Colletotrichum graminicola M1.001	**2**	1	2	1	1
Colletotrichum higginsianum IMI 349063	**2**	**3**	1	1	1
Colletotrichum lupini CBS 109225 v1.0	**2**	1	1	1	1
Colletotrichum navitas CBS125086 v1.0	1	1	2	1	1
Colletotrichum nymphaeae SA-01	**2**	1	1	1	1
Colletotrichum orchidophilum IMI 309357	**2**	**3**	1	1	1
Colletotrichum phormii CBS102054 v1.0	**2**	1	2	1	1
Colletotrichum salicis CBS607.94	**2**	1	1	1	1

Ascomycota (510 genomes searched)	**HMGS**	**HMGR**	**MK**	**PMK**	**MDD**
Colletotrichum simmondsii CBS122122	**2**	1	1	1	1
Colletotrichum somersetensis CBS 131599 v1.0	1	**2**	1	1	1
Colletotrichum sublineola CBS 131301 v1.0	**2**	**3**	2	1	1
Colletotrichum tofieldiae 0861	1	**2**	1	1	1
Colletotrichum zoysiae MAFF235873 v1.0	1	**2**	1	1	1
Coniella lustricola B22-T-1 v1.0	1	1	1	1	1
Coniochaeta ligniaria CBS 111746	**3**	1	1	1	1
Coniochaeta ligniaria NRRL 30616 v1.0	**3**	1	1	1	1
Coniochaeta sp. PMI_546 v1.0	1	1	1	1	1
Coniosporium apollinis CBS 100218	1	1	1	1	1
Cordyceps militaris CM01	1	1	1	1	1
Corollospora maritima CBS 119819 v2.0	**2**	1	1	1	1
Corynespora cassiicola CCP v1.0	**2**	**4**	2	1	1
Cryphonectria parasitica EP155 v2.0	**2**	1	1	1	1
Cryptodiaporthe populea CFL2025 v1.0	1	1	1	1	1
Cucurbitaria berberidis CBS 394.84 v1.0	1	1	1	1	1
Cyberlindnera jadinii NRRL Y-1542 v1.0	1	1	1	1	1
Cyphellophora europaea CBS 101466	1	1	1	1	1
Daldinia eschscholzii EC12 v1.0	1	1	1	1	1
Debaryomyces hansenii	1	1	1	1	1
Decorospora gaudefroyi v1.0	1	1	1	1	1
Dekkera bruxellensis CBS 2499 v2.0	1	1	1	1	1
Delitschia confertaspora ATCC 74209 v1.0	1	1	1	1	1
Delphinella strobiligena CBS 735.71 v1.0	1	**2**	1	1	1
Diaporthe ampelina UCDDA912	**2**	1	1	1	1
Didymella exigua CBS 183.55 v1.0	1	1	1	1	1
Didymella zeae-maydis 3018	1	**2**	1	1	1
Didymocrea sadasivanii CBS 438.65 v1.0	1	1	1	1	1
Diplodia seriata DS831	**2**	1	1	1	1
Dissoconium aciculare v1.0	1	1	1	1	1
Dothidotthia symphoricarpi v1.0	**2**	1	1	1	1
Dothistroma septosporum NZE10 v1.0	1	1	1	1	1
Elsinoe ampelina CECT 20119 v1.0	1	**2**	1	1	1
Endocarpon pusillum Z07020	**2**	1	1	1	1
Entoleuca mammata CFL468 v1.0	1	1	1	1	1
Eremomyces bilateralis CBS 781.70 v1.0	1	1	1	1	1
Eremothecium gossypii ATCC 10895	1	1	1	1	1
Erysiphe necator c	1	1	1	1	1
Eurotium rubrum v1.0	1	1	1	1	1
Eutypa lata UCREL1	1	1	1	1	1
Exophiala alcalophila ATCC 48519 v1.0	1	1	1	1	1
Exophiala alcalophila J33 v1.0	1	1	1	1	1
Exophiala aquamarina CBS 119918	1	1	1	1	1
Exophiala dermatitidis UT8656	1	1	1	1	1
Exophiala mesophila CBS40295	1	**2**	1	1	1

Ascomycota (510 genomes searched)	**HMGS**	**HMGR**	**MK**	**PMK**	**MDD**
Exophiala oligosperma CBS72588	1	1	1	1	1
Exophiala sideris CBS121828	1	**2**	1	1	1
Exophiala spinifera CBS89968	1	1	1	1	1
Exophiala xenobiotica CBS118157	1	1	1	1	1
Fonsecaea monophora CBS 269.37	1	1	1	1	1
Fonsecaea multimorphosa CBS 102226	1	1	1	1	1
Fonsecaea nubica CBS 269.64	1	**2**	1	1	1
Fonsecaea pedrosoi CBS 271.37	1	1	1	1	1
Fusarium fujikuroi IMI 58289	1	1	1	1	1
Fusarium graminearum v1.0	1	1	1	1	1
Fusarium oxysporum f. sp. *lycopersici* 4287 v2	**3**	**8**	1	1	1
Fusarium pseudograminearum CS3096	1	1	1	1	1
Fusarium redolens A4 v1.0	1	**4**	1	1	1
Fusarium verticillioides 7600 v2	**3**	1	4	1	1
Gaeumannomyces graminis var. *tritici* R3-111a-1	1	1	2	1	1
Glarea lozoyensis ATCC 20868	1	1	1	1	1
Glomerella acutata (*Colletotrichum fiorinae* MH 18) v1.0	**2**	1	1	1	1
Glomerella cingulata 23 (*Colletotrichum gloeosporoides*) v1.0	**3**	1	1	1	1
Glonium stellatum CBS 207.34 v1.0	**2**	**2**	2	1	1
Gremmeniella abietina DAOM 170408 v1.0	1	1	1	1	1
Grosmannia clavigera kw1407	1	1	1	1	1
Gymnascella aurantiaca v1.0	1	1	1	1	1
Gymnascella citrina v1.1	1	1	2	1	1
Gyromitra esculenta CBS101906 v1.0	1	1	1	1	1
Hanseniaspora valbyensis NRRL Y-1626 v1.1	1	1	1	1	1
Histoplasma capsulatum NAm1	1	1	1	1	1
Hortaea acidophila CBS 113389 v1.0	1	1	1	1	1
Hortaea werneckii EXF-2000 M0 v1.0	1	**2**	2	2	2
Hymenoscyphus varicosporoides PMI_453 v1.0	1	1	1	1	1
Hyphopichia burtonii NRRL Y-1933 v1.0	1	1	1	1	1
Hypoxylon sp. CI-4A v1.0	1	1	1	1	1
Hypoxylon sp. CO27-5 v1.0	1	1	1	1	1
Hypoxylon sp. EC38 v3.0	1	1	1	1	1
Hysterium pulicare	**2**	1	1	1	1
Ilyonectria europaea CBS 129078 v1.0	**2**	**4**	2	1	1
Ilyonectria robusta PMI_751 v1.0	**2**	**3**	2	1	1
Ilyonectria sp. v1.0	**2**	**2**	2	1	1
Kalaharituber pfeilii F3 v1.0	1	1	1	1	1
Karstenula rhodostoma CBS 690.94 v1.0	1	1	1	1	1
Kazachstania africana CBS 2517	1	**2**	1	1	1
Khuskia oryzae ATCC 28132 v1.0	**2**	1	1	1	1
Kluyveromyces lactis	1	1	1	1	1
Kuraishia capsulata CBS 1993	1	1	1	1	1
Lasiosphaeria miniovina SMH2392-1A v1.0	1	1	1	1	1
Lasiosphaeris hirsuta SMH4607-1 v1.0	1	1	1	1	1

Ascomycota (510 genomes searched)	**HMGS**	**HMGR**	**MK**	**PMK**	**MDD**
Lecythophora sp. AK0013 v1.0	1	1	1	1	1
Lentithecium fluviatile v1.0	1	1	1	1	1
Lepidopterella palustris v1.0	**2**	1	1	1	1
Leptodontium sp. PMI_412 v1.0	1	**2**	2	1	1
Leptosphaeria maculans	1	1	1	1	1
Lindgomyces ingoldianus ATCC 200398 v1.0	1	**2**	1	1	1
Lindra thalassiae JK4322 v1.0	1	1	1	1	1
Lineolata rhizophorae ATCC 16933 v1.0	1	1	1	1	1
Lipomyces starkeyi NRRL Y-11557 v1.0	1	1	1	1	1
Lizonia empirigonia CBS 542.76 v1.0	1	**6**	2	1	1
Lobaria pulmonaria Scotland v1.0	1	1	1	1	1
Lodderomyces elongisporus NRRL YB-4239	1	1	1	1	1
Lollipopaia minuta P26; CBS 116597 v1.0	1	1	1	1	1
Lophiostoma macrostomum v1.0	1	1	1	1	1
Lophiotrema nucula CBS 627.86 v1.0	1	1	1	1	1
Lophium mytilinum CBS 269.34 v1.0	1	1	1	1	1
Loramyces juncicola 46458 v1.0	1	1	2	1	1
Loramyces macrosporus CBS235.53 v1.0	1	**2**	1	1	1
Macrophomina phaseolina MS6	**3**	1	1	1	1
Macroventuria anomochaeta CBS 525.71 v1.0	1	**2**	1	1	1
Magnaporthe grisea v1.0	1	1	1	1	1
Magnaporthiopsis poae ATCC 64411	1	1	1	1	1
Mariannaea sp. PMI_226 v1.0	1	1	1	1	1
Marssonina brunnea f. sp. *multigermtubi* MB_m1	1	**2**	1	1	1
Massarina eburnea CBS 473.64 v1.0	1	1	1	1	1
Massariosphaeria phaeospora CBS 611.86 v1.0	1	1	1	1	1
Melanconium sp. NRRL 54901 v1.0	**2**	1	1	1	1
Melanomma pulvis-pyrius v1.0	1	1	2	1	1
Melanospora tiffanyae F1KG0001 v1.0	1	**2**	1	1	1
Meliniomyces bicolor E v2.0	1	**2**	1	1	1
Meliniomyces variabilis F v1.0	1	1	1	1	1
Metarhizium acridum CQMa 102	1	1	2	1	1
Metarhizium robertsii ARSEF 23	**2**	**2**	2	1	1
Metschnikowia bicuspidata NRRL YB-4993 v1.0	1	1	1	1	1
Metschnikowia fructicola 277	1	3	1	2	2
Meyerozyma guilliermondii ATCC 6260	1	1	1	2	2
Microascus trigonosporus CBS 218.31 v1.0	**2**	1	1	1	1
Microdochium bolleyi J235TASD1 v1.0	1	1	1	1	1
Microdochium trichocladiopsis CBS 623.77 v1.0	1	1	2	1	1
Microsporum canis CBS 113480	**3**	**2**	2	1	1
Microthyrium microscopicum CBS 115976 v1.0	1	1	1	1	1
Monacrosporium haptotylum CBS 200.50	1	1	1	1	1
Monascus purpureus v1.0	**2**	1	1	1	1
Monascus ruber NRRL 1597 v1.0	**2**	**2**	1	1	1
Morchella conica CCBAS932 v1.0	1	1	1	1	1

Ascomycota (510 genomes searched)	**HMGS**	**HMGR**	**MK**	**PMK**	**MDD**
Morchella importuna SCYDJ1-A1 v1.0	1	1	1	1	1
Myceliophthora heterothallica CBS 202.75 v1.0	1	1	1	1	1
Myceliophthora heterothallica CBS 203.75 v1.0	1	1	1	1	1
Myceliophthora thermophila (*Sporotrichum thermophile*) v2.0	1	1	2	1	1
Mycosphaerella graminicola v2.0	1	1	1	1	1
Myriangium duriaei CBS 260.36 v1.0	**2**	**3**	1	1	1
Myrothecium inundatum CBS 120646 v1.0	1	1	1	1	1
Mytilinidion resinicola CBS 304.34 v1.0	1	2	1	1	1
Nadsonia fulvescens var. *elongata* DSM 6958 v1.0	1	1	1	1	1
Nakaseomyces bacillisporus CBS 7720	1	1	1	1	1
Nakaseomyces delphensis CBS 2170	1	1	1	1	1
Nectria haematococca v2.0	**2**	**2**	1	1	1
Neofusicoccum parvum UCRNP2	**4**	**2**	1	1	1
Neolecta irregularis DAH-1 v1.0	1	**2**	1	2	2
Neonectria ditissima R09/05	1	1	1	1	1
Neosartorya fischeri NRRL 181	**2**	**3**	1	1	1
Neurospora crassa FGSC 73 trp-3 v1.0	1	1	1	1	1
Neurospora crassa OR74A v2.0	1	1	1	1	1
Neurospora discreta FGSC 8579 mat A	1	1	1	1	1
Neurospora tetrasperma FGSC 2508 mat A v2.0	1	1	1	1	1
Neurospora tetrasperma FGSC 2509 mat a v1.0	1	1	1	1	1
Niesslia exilis CBS 358.70 v1.0	1	**2**	1	1	1
Ogataea parapolymorpha DL-1	1	1	1	1	1
Ogataea polymorpha NCYC 495 leu1.1 v2.0	1	1	0	1	1
Oidiodendron maius Zn v1.0	1	**2**	1	1	1
Ophiobolus disseminans CBS 113818 v1.0	1	**2**	1	1	1
Ophiostoma novo-ulmi subsp. *novo-ulmi* H327	1	**2**	1	1	1
Ophiostoma piceae UAMH 11346	1	1	2	1	1
Ophiostoma piliferum	1	**2**	1	1	1
Pachysolen tannophilus NRRL Y-2460 v1.2	1	**2**	1	1	1
Paracoccidioides brasiliensis Pb03	1	1	1	1	1
Paracoccidioides brasiliensis Pb18	1	1	1	1	1
Paraconiothyrium sporulosum AP3s5-JAC2a v1.0	1	1	1	1	1
Patellaria atrata v1.0	1	1	1	1	1
Penicillium antarcticum IBT 31811	1	1	2	1	1
Penicillium bilaiae ATCC 20851 v1.0	**2**	**3**	2	1	1
Penicillium brevicompactum 1011305 v2.0	1	**2**	1	1	1
Penicillium brevicompactum AgRF18 v1.0	1	**2**	1	1	1
Penicillium canescens ATCC 10419 v1.0	1	1	2	1	1
Penicillium chrysogenum v1.0	**2**	**3**	1	1	1
Penicillium chrysogenum Wisconsin 54-1255	**2**	**3**	1	1	1
Penicillium coprophilum IBT 31321	**2**	**2**	1	1	1
Penicillium decumbens IBT 11843	1	1	1	1	1
Penicillium digitatum Pd1	1	1	1	1	1

Ascomycota (510 genomes searched)	**HMGS**	**HMGR**	**MK**	**PMK**	**MDD**
Penicillium digitatum PHI26	1	1	1	1	1
Penicillium expansum ATCC 24692 v1.0	**2**	**2**	1	1	1
Penicillium expansum d1	**2**	**2**	1	1	1
Penicillium fellutanum ATCC 48694 v1.0	**2**	**2**	1	1	1
Penicillium flavigenum IBT 14082	**2**	**3**	2	1	1
Penicillium glabrum DAOM 239074 v1.0	**2**	**2**	1	1	1
Penicillium griseofulvum PG3	**2**	**2**	1	1	1
Penicillium italicum PHI-1	1	1	1	1	1
Penicillium janthinellum ATCC 10455 v1.0	**2**	1	1	1	1
Penicillium lanosocoeruleum ATCC 48919 v1.0	**2**	**3**	1	1	1
Penicillium nalgiovense FM193	**2**	**2**	1	1	1
Penicillium oxalicum 114-2	**2**	1	1	1	1
Penicillium polonicum IBT 4502	**2**	**2**	0	1	1
Penicillium raistrickii ATCC 10490 v1.0	**2**	1	1	1	1
Penicillium solitum IBT 29525	**2**	**4**	1	1	1
Penicillium steckii IBT 24891	1	1	1	1	1
Penicillium subrubescens FBCC1632 / CBS132785	**2**	1	1	1	1
Penicillium thymicola DAOMC 180753 v1.0	**2**	**2**	2	1	1
Penicillium vulpinum IBT 29486	1	**2**	1	1	1
Periconia macrospinosa DSE2036 v1.0	**2**	**5**	1	1	1
Phaeoacremonium aleophilum UCRPA7	1	1	1	1	1
Phaeoacremonium sp. FL0889 v1.0	1	1	1	1	1
Phaeomoniella chlamydospora UCRPC4	1	1	1	1	1
Phaeosphaeriaceae sp. PMI_808 v1.0	**2**	**4**	1	1	1
Phialocephala scopiformis 5WS22E1 v1.0	1	**2**	1	1	1
Phialophora attae CBS 131958	1	1	1	1	1
Phoma tracheiphila IPT5 v1.0	1	1	1	1	1
Phyllosticta capitalensis CBS 128856 v1.0	1	1	1	1	1
Phyllosticta citriasiana v1.0	1	1	1	1	1
Phyllosticta citribraziliensis CBS 100098 v1.0	1	1	1	1	1
Phyllosticta citricarpa CBS 127454 v1.0	1	1	1	0	0
Phyllosticta citrichinaensis CBS 130529 v1.0	1	1	1	1	1
Phyllosticta sp. CPC 27169 v1.0	1	1	1	1	1
Phyllosticta sp. CPC 27913 v1.0	1	1	1	1	1
Pichia membranifaciens v2.0	1	1	1	1	1
Pichia pastoris	1	1	1	1	1
Pichia stipitis v2.0	1	1	1	1	1
Piedraia hortae v1.1	1	1	1	1	1
Plectania melastoma CBS 918.72 v1.0	1	1	1	1	1
Plectosphaerella cucumerina DS2psM2a2 v1.0	1	**2**	1	1	1
Pleomassaria siparia v1.0	1	1	1	1	1
Pneumocystis jirovecii	1	**2**	0	1	1
Podospora anserina S mat+	1	1	1	1	1
Podospora curvicolla TEP21a v1.0	1	1	1	1	1
Polychaeton citri v1.0	1	1	1	1	1

Ascomycota (510 genomes searched)	**HMGS**	**HMGR**	**MK**	**PMK**	**MDD**
Polyplosphaeria fusca CBS 125425 v1.0	1	1	1	1	1
Protomyces inouyei	1	1	1	1	1
Protomyces lactucaedebilis 12-1054 v1.0	1	1	1	1	1
Pseudocercospora (Mycosphaerella) fijiensis v2.0	1	1	1	1	1
Pseudographis elatina	1	1	1	1	1
Pseudogymnoascus destructans 20631-21	1	1	1	1	1
Pseudomassariella vexata CBS 129021 v1.0	**2**	1	1	1	1
Pseudovirgaria hyperparasitica CBS 121739 v1.0	1	1	1	1	1
Purpureocillium sp. UdeA0106 v1.0	1	**2**	1	1	1
Pyrenochaeta lycopersici ISPaVe ER 1252 v1.0	1	**2**	1	1	1
Pyrenochaeta sp. DS3sAY3a v1.0	1	**2**	1	1	1
Pyrenophora teres f. teres	1	1	1	1	1
Pyrenophora tritici-repentis	1	1	1	1	1
Pyronema confluens CBS100304	1	1	1	1	1
Rhizodiscina lignyota CBS 133067 v1.0	1	1	1	1	1
Rhizoscyphus ericae UAMH 7357 v1.0	1	1	1	1	1
Rhytidhysteron rufulum	1	1	1	1	1
Rutstroemia firma CBS 115.86 v1.0	1	1	1	1	1
Saccharata proteae CBS 121410 v1.0	1	1	1	1	1
Saccharomyces cerevisiae M3707 Dikaryon	1	**2**	1	1	1
Saccharomyces cerevisiae M3836 v1.0	1	**2**	1	1	1
Saccharomyces cerevisiae M3837 v1.0	1	**2**	1	1	1
Saccharomyces cerevisiae M3838 v1.0	1	**2**	1	1	1
Saccharomyces cerevisiae M3839 v1.0	1	**2**	1	1	1
Saccharomyces cerevisiae S288C	1	**2**	1	1	1
Saccharomyces cerevisiae YB210 v1.0	1	**2**	1	1	1
Saitoella complicata NRRL Y-17804 v1.0	1	1	1	1	1
Sarcoscypha coccinea ATCC 58028 v1.0	1	1	1	1	1
Schizosaccharomyces cryophilus OY26	1	1	1	1	1
Schizosaccharomyces japonicus yFS275	1	1	1	1	1
Schizosaccharomyces octosporus yFS286	1	1	1	1	1
Schizosaccharomyces pombe	1	1	1	1	1
Schizothecium vesticola SMH3187-1 v1.0	1	1	1	1	1
Sclerophora sanguinea CBS100924 v1.0	1	1	1	1	1
Sclerotinia sclerotiorum v1.0	**2**	1	1	1	1
Septoria musiva SO2202 v1.0	1	1	1	1	1
Septoria populicola v1.0	1	1	1	1	1
Setomelanomma holmii CBS 110217 v1.0	1	**3**	2	1	1
Setosphaeria turcica Et28A v2.0	1	**2**	1	1	1
Setosphaeria turcica NY001 v2.0	1	**2**	1	1	1
Sodiomyces alkalinus v1.0	1	1	1	1	1
Spathaspora passalidarum NRRL Y-27907 v2.0	1	1	1	1	1
Spathularia flavida	1	1	1	1	1
Sporopachydermia lactativora Phaff 68-199 v1.0	1	1	1	1	1
Sporormia fimetaria v1.0	1	1	1	1	1

Ascomycota (510 genomes searched)	**HMGS**	**HMGR**	**MK**	**PMK**	**MDD**
Stachybotrys elegans LAHC-LSPK-M15 v1.0	1	1	1	1	1
Stagonospora nodorum SN15 v2.0	1	1	1	1	1
Stagonospora sp. SRC1lsM3a v1.0	1	1	1	1	1
Stanjemonium grisellum CBS 655.79 v1.0	1	**2**	1	1	1
Stemphylium lycopersici CIDEFI-216	1	1	1	1	1
Sugiyamaella americana NRRL YB-2067 v1.0	1	1	1	1	1
Symbiotaphrina kochii v1.0	1	1	1	1	1
Sympodiomyces attinorum NRRL Y-27639 v1.0	1	1	1	1	1
Talaromyces aculeatus ATCC 10409 v1.0	1	1	1	1	1
Talaromyces marneffei ATCC 18224	**3**	1	1	1	1
Talaromyces proteolyticus PMI_201 v1.0	**2**	1	1	1	1
Talaromyces stipitatus ATCC 10500	1	1	1	1	1
Taphrina deformans	1	1	1	1	1
Teratosphaeria nubilosa CBS 116005 v1.0	**2**	1	1	1	1
Terfezia boudieri ATCC MYA-4762 v1.1	**2**	1	1	1	1
Terfezia claveryi T7 v1.0	1	1	1	1	1
Thelebolus microsporus ATCC 90970 v1.0	1	1	1	1	1
Thelebolus stercoreus	1	1	1	1	1
Thermoascus aurantiacus v1.0	1	1	1	1	1
Thermomyces lanuginosus SSBP	1	1	1	1	1
Thielavia antarctica CBS 123565 v1.0	1	1	2	1	1
Thielavia appendiculata CBS 731.68 v1.0	**2**	1	1	1	1
Thielavia arenaria CBS 508.74 v1.0	1	1	1	1	1
Thielavia hyrcaniae CBS 757.83 v1.0	1	1	1	1	1
Thielavia terrestris v2.0	1	1	1	1	1
Thozetella sp. PMI_491 v2.0	1	1	1	1	1
Tolypocladium inflatum NRRL 8044	1	1	2	1	1
Torpedospora radiata JK5252C v1.0	1	1	2	1	1
Tortispora caseinolytica Y-17796 v1.0	1	1	1	1	1
Torulaspora delbrueckii CBS 1146	1	1	1	1	1
Tothia fuscella CBS 130266 v1.0	1	1	1	1	1
Trematosphaeria pertusa CBS 122368 v1.0	**2**	1	2	1	1
Trichodelitschia bisporula CBS 262.69 v1.0	1	1	1	1	1
Trichoderma asperellum CBS 433.97 v1.0	1	1	1	1	1
Trichoderma asperellum TR356 v1.0	0	1	1	1	1
Trichoderma atroviride v2.0	1	1	1	1	1
Trichoderma citrinoviride TUCIM 6016 v4.0	1	1	1	1	1
Trichoderma gamsii T6085	1	1	1	1	1
Trichoderma harzianum CBS 226.95 v1.0	1	1	1	1	1
Trichoderma harzianum TR274 v1.0	1	1	1	1	1
Trichoderma longibrachiatum ATCC 18648 v3.0	1	1	1	1	1
Trichoderma reesei RUT C-30 v1.0	1	1	1	1	1
Trichoderma reesei v2.0	1	1	1	1	1
Trichoderma virens Gv29-8 v2.0	1	1	1	1	1
Trichomonascus petasosporus NRRL YB-2093 v1.0	1	1	1	1	1

Ascomycota (510 genomes searched)	**HMGS**	**HMGR**	**MK**	**PMK**	**MDD**
Trichophaea hybrida UTF0779 v1.0	0	0	0	0	0
Trichophyton rubrum CBS 118892	**2**	1	1	1	1
Trichophyton verrucosum HKI 0517	1	1	1	1	1
Trinosporium guianense CBS132537 v1.0	1	1	2	1	1
Truncatella angustata HP017 v1.0	1	1	1	1	1
Trypethelium eluteriae v1.0	1	1	1	1	1
Tuber borchii Tbo3840 v1.0	1	1	1	1	1
Tuber melanosporum Mel28 v1.0	**3**	1	1	1	1
Uncinocarpus reesii 1704	1	1	1	1	1
Usnea florida ATCC18376 v1.0	**2**	**2**	1	1	1
Ustilaginoidea virens	1	1	1	1	1
Valetoniellopsis laxa CBS 191.97 v1.0	1	1	1	1	1
Venturia inaequalis	1	1	1	1	1
Venturia pirina	1	1	1	1	1
Verruconis gallopava	1	1	1	1	1
Verruculina enalia CBS 304.66 v1.0	1	1	1	1	1
Verticillium alfalfae VaMs.102	1	1	1	1	1
Verticillium dahliae v1.0	1	1	1	1	1
Westerdykella ornata CBS 379.55 v1.0	**2**	1	1	1	1
Wickerhamiella domercqiae NRRL Y-6692 v1.0	1	1	1	1	1
Wickerhamomyces anomalus NRRL Y-366-8 v1.0	1	1	1	1	1
Wilcoxina mikolae CBS 423.85 v1.0	**2**	1	1	1	1
Xanthoria parietina 46-1-SA22 v1.1	1	1	1	1	1
Xylaria hypoxylon OSC100004 v1.0	1	1	1	1	1
Xylariales sp. PMI_506 v1.0	1	1	1	1	1
Xylona heveae TC161 v1.0	**2**	1	1	1	1
Yarrowia lipolytica (strain CLIB122)	1	1	1	1	1
Yarrowia lipolytica FKP355 v1.0	1	1	1	1	1
Zasmidium cellare ATCC 36951 v1.0	1	1	1	1	1
Zopfia rhizophila v1.0	1	1	1	1	1
Zygoascus hellenicus Y-7136 v1.0	1	1	1	1	1
Zygosaccharomyces rouxii CBS732	1	1	1	1	1
Zymoseptoria ardabiliae STIR04_1.1.1	1	1	1	1	1
Zymoseptoria brevis Zb18110	1	1	1	1	1
Zymoseptoria pseudotritici STIR04_2.2.1	1	1	1	1	1

Table S6

Examples of additional putative HMGS genes identified in fungal genomes from Tables S4 and S4 that are clustered or potentially fused (annotated with: ?) with predicted STS genes.

HMGS protein ID	STS protein ID	Organism	Fungal Class
114927	1602279	*Auriscalpium vulgare*	Basidiomycota
32419	324119 (HMGS fusion?)	*Hebeloma cylindrosporum*	Basidiomycota
2392737 (2701676 also in cluster)	2392761 (HMGS fusion?)	*Ricknella fibula*	Basidiomyctoa
290222	290216	*Hebeloma cylindrosporum*	Basidiomycota
6366	6367	*Macrophomina phaseolina*	Ascomycota
7969	7973	*Neofusicoccum parvum*	Ascomycota
687465	658201	*Coniochaeta ligniaria*	Ascomycota

III. Supplemental Data Set

Fungal sesquiterpene synthase genomic DNA sequences

1. Genomic Sequences obtained from published accession numbers (see also “Bioinformatic analysis”)

Name	Accession number
ARMGA1	P0DL13
FgCLM1	GU123140
FsTS	P13513
Ffsc6	HF563561.1
Ffsc4	HF563560.1
BcBOT2	AAQ16575.1
PrAS	W6Q4Q9
AtAS	Q9UR08
BcBOT2	AAQ16575.1

2. Manually re-repredicted genomic DNA sequences in this work and from (5, 8, 9):

>HS-HMGS
ATGTCTGAAACCAAAGTTGGCAAAGTTGCTCCCTTCCCCCCTCTTCCCGGCGCGCCATACCCTCCTGTTCGTAATCA
TCCGCGATGGAAAGGTATGTTCATACTCGTTATTGGCTGCTGTGTTTTTGCTTACGCCACTGCCTCAGAACTCTACA
GGCTCCATGATGAGTGGATGATGAAGTACTGGCCGTTCAGCAGCGAGAAGAAGAGGGCTCGTATTCCGTTCATGA
ACCTCGCGGGTTTCAGTACATGGTGTACGTATACAATGTGTCTCTGCTTCTACAATCCTCTAACCAGACGCATAGGT
GCACCTGCCGCTGACTTTGATCGCATGGTCTGGGGTGCCCGCATCGCTGGCATATTTTTCCTGGCCGACGATTATA
TCGACAGCGGGAAAATGTTGGACCGCATCCCAGGCTTCAAAGCGGTATGCACGTTTCTTGTATTGACTGCAGCTAC
TCGAGCCTGACGCACAATGCCGTACCTAGGCTGCCACAGGAACCGGGGTGTGTGGTTTTTCCGTATCTATAGTCTT
TTCAAGCCTTCTGAAATATCATATCTCTTCTAGCCCCTCCACAAAGAGGACCAAGCAGAGATCTGTCACGATATCGT
GTTCCGTGCCATCAAGGCAACCAGTCACCCTCGGACCTTCGACCAGCTCACGAAGTGCACACATGAGTGGTGGGA
TACGTCCATACGTTCTTCATATACTTTGACTTCCTCGATAACCCCTTGGCCGAACAACAGTTCCAACATCCACGAGCC
TTTCCAGAATCTCGACCAATATCTCGCAGTACGCCGTGTAAACATAGCCATGGTCAGTCTATGCGTTTACTACCGAT
TCGTCACGTTGCTAATATCGTCTATCCCGTTCTAGTATTTTGCGAACGGTAAGAACCAAATATAAAGACCGTGCGG
CAAATTCTAATAGCTATCATTTCAGCTTACTTCCGTTACACCCTGGACATCAACCTTACCGACGAGCAGGTCAACCA
CCCCCTGATGCGCGAAGCTGAAGGCATTGTCTCCGGTAAGAGTCTTCCGCCCATTTCAATTGATGCTGTCGTCATTA
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GACACCAACATTATCCGCATCCTAATGGACCACGAGCATCTCAGCTACGAAGAGGCGAAGACCGTCATCGAAAAG
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TCGTGAGATCTATAGGTGGATCGCGAACTTACAGTACTGTATGGGCGGTAACCTTGCTTGGTCGCAAGAGGTAAG
CGAAAATCACTATGGTATCCACGTACTCGACATCACCTAACAGTTCGTTTACAGAGCGGCAGGTATAATGTCGGTG
TCATCGATGGGATTTCGTTCCCTTCCTTGAGCTACGCGGCGGAGCCAACTCCCGAAGACGAAGTGGTCGACGACA
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GAGAAGTACAACATTGATCCGCGCAGCATCGGTCGCCTCGACGTCGGGACGGAGACTCTCATCGACAAGTCCAAG
TCTGTCAAGACAACGCTCATGGACCTTTTCGCTGCCTCGGGCAACCACGACGTCGAAGGAATCGACAGCAAGAAC

GCTTGTTATGGGTCGACGGCTGCTGTTCTGAACGCCGTCAACTGGATAGAGAGCTCGAGTTGGGACGGAAGATAC
GCTATCGTGTTTGCAGGTGATATTGCAATCTATGCGGAGGGTCCGGCCAGACCTGTCGGGGGAGCGGGAGCCGT
CGCGCTCCTGATCGGACCAGACGCACCCCTTGTTCTTGAACGTATGTCCTTTTTTGTTCTTATTGAGCCTATTGAGAC
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GGTACGCAGTTCCCCTTCGCGAGTGTTTGTTTGATTTCTCAACCTTTTTATTCGCAGACCTACCACGACTTCGTAGCC
CACCCTACTGCTCCGGTCTACAGAGATCTTCCCACCGACATTCTGAGCAAGGATGCTTCGGCAACCCTGACGGACA
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CGGGTTCATTCGTGACGTCGACAGCTATCTCGAGATGCGAAGAGAGACGATCGGCGCGAAGCCGTCGTTCGTCGT
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GACCTTCCCGACGAGGTTCTCGCCCATCCCACTATCCAATCACTTTCCCTTGCCACCATCGACATGCTTTGTCTTGGC
AACGTAAGTAACAATGCTGAGATACTCTGCACTCACCGTGCTAACCCGATGTTCTTGCTTAATAGGACATTGTCTCG
TATAACCTCGAGCAAGCTCGTGGTGATGCCAGCCACAACATCATCACCATCGTCATGAACGAGCTCAACCTCGACG
TCAACGGTGCCATGCGATGGGTAGGCGACTTCCACAAGCAGTTGGAGAAGCAATTCTTCGAGGCGTTCAACAACC

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GCAAACGACCAGTGGAGTTTCGAGAGCGAGCGCTACTTCGGGGCTAGGGGTCTTGAGATTATGGAGACGAAGAC
CCTGGCGATGATGCCTATTCAGAGGACGGAGGCATTGGGCCCTCAGCTTGTTGATGACTCCATTTTGTGA

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Fungal sesquiterpene synthase coding sequences

1. Coding sequences obtained from published accession numbers (see also “Bioinformatic analysis”)

Name	Accession number
ARMGA1	P0DL13
FgCLM1	GU123140
FsTS	P13513
Ffsc6	HF563561.1
Ffsc4	HF563560.1
BcBOT2	AAQ16575.1
PrAS	W6Q4Q9
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2. Manually re-repredicted coding sequences in this work and from (5, 8, 9):

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Accession numbers of protein sequences of *S. cerevisiae* S288c mevalonate pathway enzymes

Enzyme name	Protein name	Accession number
HMGS1 (HMG-CoA synthase)	ERG13, YML126C	P54839
HMG1 (HMG-CoA reductase)	YML075C	P12683.1
MK (mevalonate kinase)	ERG12, YMR208W	P07277.1
PMK (phosphomevalonate kinase	YMR220W	P24521.2
MVD1 (mevalonate pyrophosphate decarboxylase)	ERG8, YNR043W	AAT93171.1

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