

### Supplementary data

Supplementary Table 1. Assembly results by programs. CLCAssemblyCell shows the best result that the least scaffolds number and the longest NG50.

	<b>Platanus</b>	<b>SOAPdenovo</b>	<b>CLCAssemblyCell</b>
<b># of scaffolds</b>	23,597	6,194	5,006
<b>Total length</b>	31,473,128	31,927,826	31,895,682
<b>Maximum</b>	149,695	82,365	603,101
<b>Average</b>	8,754.21	1,037.8	13,416.48
<b>N50</b>	25,707	16,255	132,918
<b>NG50</b>	25,429	16,255	132,918

Supplementary Table 2. Proteins sequences of four candidates of new polyketide synthase (PKS) genes.

<b>Name</b>	<b>Protein Sequences</b>
<b>CpPKS5</b>	<p>MEEFWDVLVQGIDTHELVPASRDHRTHTVQQEPASKNTSGTGFGCWVHDAPAFDVRFFNMSPREAPQ  VDPAQRMALLCAAEEALEQAGIVPNASSSTQKNRVGVYFGCTSNDWMETNSAQNIDTYFIPGGNRAFIPG  RINYHFKFSGPSYTIDTACSSSLTAIQLACNALWRGEVDTAIVGGTNVLTNPDMTAGLDRGHFLSRTGNC  KTFDESADGYCRGEAVVTAILKRLDDATRNDPQVAVILSVATNHNAAEADSIIRPHVQAQQDLIDSVLA  DAGVDPTSISYVEMHGTGTQVGDAAETSSVLQSLAPVNRKRSIHQPLHMGAAKANVGHGEAAAGITSLA  KVLLMMKHSKIPPHCGIKTRINSKIPDLKTRNTFIAKTALSWQRPVGDVRRVLLNNFSAAGGNTALVLE  DAPQIQSTERDPRSYPHVVAVSAKTAGSLQQLKNMIAWIGRQNLPASSVECLSYTSTARRAHYPHRVA  VSGRNLDEIKGSLQDALDQGRGVNRSKRAPRLIFAFTGQGSFAGMGSVLYASFRGFKTDIDRYDQICV  KSGLPAIRSMFTDTAAAYDDADPTVLQLTTVCLQMALVRLWRSFGLSPSAVVGHSGLGEYPALYAAGVLS  QAEVIHFVQGQRAQLLQAKCMRDTHMMLAVRCSMSDLTDLGAPGARYEISCINGRQSVIGGLKSNLQE  AALKLKERGIVSTPLDVAYAFHTSQVDPIIDPLVQLSRSMKFAEPQIIPICPAYGKVRKSAADFSDSDFIAHH  CRSTVDVAGAMADAQKEGVVDSMDACLEIGPAVVVSKMVKDALGSKTDIFATIGKDDDDWKLMTA  LSQLHSAGATIDWISYHKDFKACHRVLDLPAYSWEMKDYWMQYEHWSLRKGDPLRITGPELQSSSI  HRVIQSTLDRPDGELIVEADLNRKDLNPMVQGHKVVYVPLCTPSVYADIALTIGDHILHHFTGDDHSDKA  VEVAEMTIQSALVAKPDHILRTTVKLDKVQNTARCTFFTVDHSGKVLEQHAHCTLRVFDKEASQKKT  ALAPSIQSRMRSLDTQVGENANTFRFSRSMIYKMIGQLADFDPNYRGLVEITLDNDALDARGRVSFKDV  LGDGQFHTNPAYIDALSQGGFVMNANETVDLEKEVFVNHGWGFSQLFEPISPHKTYRSHVKMSEQKD  KLWTGDVVIFEDAKIVAVFLQVALQCVPKRLMEYIVSTANKRSGSGATTVAKPLVSAVSPAMQKQV  TTGVETRQVTTQSARVGVDSAMQIISAESGIVGDLTDESSFDEIGMDSLLCLLVNSKLRDELDELVELDS  AKFAIQLGTVGKLRSHLHQFETPVETVVTSEIVRETTSSVPAIAPTGDGVWPQIVEIISQKDDDDWKLMTA  ACFADIGVDSLILLSIWSRLRDELGIDSQSSPFLEFENLGNFKKFIVGESGDIPERSESPLEAESGSSSSSTP  PRETETPVTELSSEDEKEIPSKVVADHQPQAIPAWSLVLQGPKTATETLFLFPDGC GAATSYLWLPRI  PTTAVVAFNSPFMKTPEMVGRALEDIVTAYVTSLQTHQPHGYPYHLGGWSAGGILAYAIAQRLMADGE  EVATLQLIDSPAPTRGLDRLPDRFFDHCSVDVGFREMGSNDRANAPPKAPEWLMPHFRATIELLHDYTA  SPMPVDRQPKASIIWAGSCAFDNGLYAPLPDAGTDDQDTEGMKFLTEKRQDFGPGEWADLFPQDISVE  VMEGEHHFSMMRGEAELKSLIKDFLLSKA</p>
<b>CpPKS6</b>	<p>GTGTPGLDPLEHGAVEEVIRSSKRTTPLLIGSIKSNIGHLEGAAGLAGLIKCILMLEKGIIPNIHFDKPNKK  ISFKQVDVPTTTMAWPAGLKRRASVNSFGYGGTNAHAIVEAFFTPSLQRREEDLLSALDDGGMGSPNRR  LFVFTGHEPSAVQEVNRNYATYTKRAENTVDPNVRFDLSTYTLGSHRSKLDWAASHVANSFSELRGKL  SNTEVKA TRSSREARVGFVFTGGAQWPRMGLLEMQYTVFRESIEASDRFLSQRPD CRWSVIEELQKHD  GESHIEAPELSQPLCTILQMAMVDLLKSWQVRPVAVVGHSSGEIAAAAYCAGTITKQAAWQIAFYRGREC  ADLKTKAPELQGAMLA VGLGADGVKPYIDAIAPGHINVACINSPKSVTVSGDASEVRKLLSNLSADNVF  ARELQVENAYHSHHMKLV AEPYLRSIADV TSEKGEVSSGIKMLSSVTGRLVESSELTP EYVWQNLVSPV  HFSDAVTTMLRSSGKSSRRQRKAESA VDFLEIGPHAAALRGPLSDILKKELESVGYASMLLRGSDAVDS  AHL YCRGYPVDVATVNNFKHEARVLVDLPEYPNRSDKYWATSRLTQNFHLHRAFPHHGLLGKRMIGS  DGLYPAWRHFGLIQENPWIAEHVVHGAILYPGAGFLAMAIEAALQVAEPGREVINIRLKDVRIVKALVIK  EDEDHPEVITRFRRVESGDNDGWEFAISCSRALNEPEQHATGQIMLEYVPKEPYLSPASGLVHEARKSEY  VNLVNAATDTMEQNEFYNASRSAGLDYGPDFQGVFEMLRGTDSCCVSVKVTDRSATMLGAFESKHLI  HPTTLDAIMHSLFGAMNRGKQFTSAALPVAFDNVTISAKMPDAGATLSGFTVTKEVKEREIVADIYVSS  GDWEQPLLQMEGLRCTELPSQEATPAISTPQYAPLGSVKYRPDITLLDEGLMSYIKENCKSELTTESQSS  LYSERLRNAV AQVIDLAVFKAPTSSILQIGGFDQGLTDSLLSTLKAGACGQALTSNILDLTLEENVSQIQE  KYDSESTVSALKYDMAKSLSSQMRRGDNFVLLVTMDPQLDEERRAFLTEARKLLNPGGIFVVFDSL</p>

	<p>PNIKENPTYSFSEVRDSPSPSQRVTWESFTIEDPACEKA AVLSMQKMSVSDPIGISSRPCILRPPGEAAVINS  AVGALEDSLRAHDIEVVCTWPPDIENVRDKCVIALLDMERPFCLDDAVDFDMLRQVALQSARLLWV  CPSDDPHMAVATGWLRVLQENENVNKNYQYLALERRADGSAPCALAIKAVAMAQTEEREFIERSSGLL  NIPRWSYDPEMTRTVTDSVVSLETRDTLLGDIASGLPLRMIHAGDPEHAHFASDALRMPDELAADQVEIE  LRFVVIVDHDVVKDPGTATLHEASGIIKAVGPDVSLRPGDHVCLSFHGLSTRVVAKESICQRPVAGVKMS  EAACLPTVFATAVRALIDVARVKPRQNVLVQAGGTRIGRAVLLATASDAIVYATARDAEEVKILMGL  GVPRQNILIDGDPDIPAAATMVLTRDKGWDVIVRDTKTASATCLLPGCIAPNGAVVDVYPSGFDRMRETTI  SLMGVGSLLPEDPVLQKTVSHAVAYLRQLSTFVESFDIFPSSAVTDALSQRQSQGANRGMVLSFHHEH  KIQVSPGVKNTMQLHDEATYILAGGLGGIGRGVAKLLVDNGARNLVFLSRAGTESPAAMSLAKSMAGL  GVTVKTFACDISDEQSLMRALSECTRTMPPIRGAIQAATVIRDAVFDNYTLEQWQANLRPKVQGSWNL  HCHLPKMDMDFVMLSSIAGLIGHRSQAGYAAGNTFQDSLALRRQSQGLPAVAIDLGGMLDVGAVMEGT  ATANFSASETTWMTEAELHSIIKMCISGGIDEYATPPQVCTGIPSGGMVQLGQHEMPHFERPFV ALKH  LGTGTGATIEPTAMVDKMTPELLHRLAASNSLADAIECAAEILCAHLAERLQRAADSIDLQRLHKYGIDS  LAAVDLRTWIGKKMKADVSLFDVLAESIRELSSKIAKASELVSRDVQ</p>
<p><b>CpPKS7</b></p>	<p>MPINTPATTPESESITNTMDVVYFNSNEFPREDLQSLFRRLHNHSGKRQHPTLAHLSEATWAIKNEIQTLP  SELRQLIPPFTILSWAEATELREGLICGAVDGVLLIVAQLATYIGYVEDHPDEFCHFENTCLSGLGLGLLS  STAVLSSTRADLALAGADAVRLAFSLRIHVRSVSENLEVRDMSETPDTWAYVVDVNPAAAQKALDA  QQNKDQIPDTGKVFLSGISRTSVTVSGPPARLKTLLNKSEFFRVARIIPVYGGCLHASHVYGESDTKKI  VDTPALITPGTKACPVPIYSTTGLPYQARSALFEAVVSELLTQAIRWDTVIAGLRWDAKRRHCASSMS  LYSFGNSIPFRDLGATLKAILPAVKTTTTPNLVSWAFQVDPTDDAPRTTAQSR LAIVGMSCLPGGTTNTE  KFWEVLENGLDVFORIPADRFDIDTHYDPTGKDLNKSMTQYGCDFIDEPLDAPFNMSPREAQVVDPQ  MRLALVTA YEALERAGYVGNRTARTRLERIGTWYGOAADDYREVNQGGQEVRTYIYPGGCRAFPGRI  NYFFKAGPSYSFDTACSSGLAAIEALWNGEVDMAVAGGLNVLTPDGFAGLNGHFLTKRHNACKT  WDATADGYCRADGVGSVVIKRLDAQADNDNILGVILGAGTNHSADAVSITHPHAGHQDYLARQVLR  QAGVDPLDVSVELHGTGTRAGDHEEMQGMVDVYAPLTKRRSKEQSLHIGAAKSNVGHSESAAGTTAL  TKVLLMLQKNAIPPHIGIKMEINPRFPKDFDQRNLHIAFEETEWLCTKGGKRIAANNFGAAGGNTMML  EEAPDREILEADPRQTHIITVSAKTKVSLAANIERLIAHVEANLGINLADLGYTTTARRYHHVFRVAVAV  SDEAQLKKQLKARLEKVDLSKSVGKSGPPPIAFTFTGGQASYSKMNLELYRDSVPVREHINHLDSLAIGQ  GFPSFIPALDGSHTKDHASHPVVTQLALVCTEIALAKYWTSLGVKPDIVMGHSLGEYAAAMHVAGVITA  NEAIFMVGRRAQMLQDKCKVGSHTMMAVRASLAQIAENCAGKPYTIACVNGHVDTMSLGTQEQIDEV  SVPLQAAGLHCIKLDVAYAFHSEQTDAILDDFEAVAKSGVIFQEPKLPVISPLGKVIDFGKTLNADYVR  RFTRETVDFLSALENARQISAVGDETVWVEIGHPVCTGFVNSIHESPALVPSLRGGDSSWKTIAESMA  ALHLTGLSVDWNGFHRAFETRLRLDLPTYAFNDKNHWLPYKGTWCLTKDNESYGAENETGRASAPA  DESPRSEVQTSVQQIHDQTFSGSAGSVTMQSDLMQGDLFAAANGHRMNNCGVVTSSIHADIAITLGEY  LYRKLNPKGKTCAINVANLNVTKGLVAQSDTKSPQVFRVTITTEDIATGVANLTWQCVNDNDGNALEPF  ATANLFYGTAAEWLSSWSSISHIVQRMESLQHMAAEGTASRFRTRNMAITIFASNLDYADKRYGMKS  VVVHELEAYADIELTVKESGVWTVAPYFIDSVAHIAGFVMNCSDAIDTQKDYVYTPGWDSMR FARPLV  GGQKYRSYVKMIPSKEDPAVYKRDVYIMQEDAIVGMVGGIQFRRFRILLNKFSPDPKQGAHEAQP KV  ADPAAATRVSQKQAPL PINLPAAMPAPPVKLETAEVPTAPAPAATPLADSTTVKALALIAKEAGLDVS  DLEADAFAANLGDLSMSLVISAKLSELGVKVGGSFLDYQTIEDLKNYLDESYS</p>
<p><b>CpPKS8</b></p>	<p>MGGFYTQARYDVPNPSSPPSSLESSTKSVYMQDPIAVVGLANRLPGHSNNPTKLWQFLLRGGVAKNDP  PESRFLTGHYDGSHPHTFKTPGAMFLEDHDPADFDPAFFRTTVADAIAAMPDQQRMLLEVVEALEN  AGISLSQIDGEAFGCFVGSYAVDYMDMQRDPEDRAEGITV GAGRAILSNRISHFLNIKASMTIDTACS  GSLVSDVACRYIQTGQIEGAIVAGANLYMSPDQNMMDGPMRTASASGRCHTFDAKADGYCKSEAIN  CVILKHLDAALRDGDPRAVIRGTATNSDGWTPGIASPAEEAQA VAIRAAYAAAGITNFHETGYLECHG  TGTLAGDPVEVAAAASVLTQGR TDSNPLIGSIKSNIGHSEPAAGVSLIKGILAVEKNRNPNTFIDPNP  KIDFKGLRVEASRMSRGWPNPKRIASVNSFGYGGNAHVVLQDAESYLGDRSLAHIASFVDEYDTGNLF  DEDDEEVSNDTALARPNVFVISANDELSLKSYYKALRRHLIDPSVKIKPSDLAYTLSERRSHLFHRGFVV  ADILDQLQEDALITGKQSSPPKIGIFITGQGAQWPQMGRGLIDAYS GARPILLAGLDKALQALPEPPSWSII  DELYDPRTPDHLRLPEFSQPLVTALQLVLVLSALSEWGITPSSVVGHSSGEIAGYAAGFLTAEDIAKIAFF  RGEAAKQQQAQSEAVGMLAVGIGAEVPIYIGELSATVQIACYNKSAKSVTLSGKASDVEITRLQAD  SHFARALQVNLAHYHSTYMTAIGERYQELVERNTGKPLPGNSNVMTMYSSVTGGANSDLKDSLYWRNTM  VSPVLFNDATTELLKAENPATLMIELGPSGALAGPFSQIKNALPEHGAGVQYFAAAKRGPDVSRLFEVA  GRVFAAGGDVNIRKVNTERLVDTPADPAIIVDLPNYSWNHNSKQYWHESDASKEWRYRKYVHDDLGS  KVLGTPWSAPTFSKILDLDLDPWLKDHKMGNDIVFPAAGFCAMAIEALYQSTQVATPEGEVVSANQLN  YRLRNVTFDNALVLEESTPAKIKITTLAPSTTGSHPWYHFSVATYSDGVSREHSAGLIRLENVEPIVTD  HTANPLQTTSGKLWYKAMATAGYGFGLPFQKQLEVEATSGQRASRSLVDL TEPDSTWKGQSPYPLHP  AALDGIFQTLRISLVAGIRPNIKSVLIPAIMDDL VVFANTSRPDRGISRTTSEYVGKRRDDNKNYLSNAT  VHHPTDKKVVILQSLGLRCHRLDTGFDPLGAHTFSKLSWKRVDVTLFSLQSLSPGDFSVTADLDDLVAHR  KPVLRVLEINLDAGDTEVWFGNGNNA TRAA YRGYKFASADAAALVNAQARYEFHRA TDFALLDLAK  PLADHHHA EHDV VICKGSNLTLELATQALRNAKLLAVGGHAVFLQGT VETVSSVGHIAAPPLEADLTA  IESAGLKILTQYVFNEGQRITVSTLEDASSANATSVKLSFAGPTNLSTTIMEVNLKLGHNISVSDGAQLS  HRETVLVDELTESELLTRIDAKQWDVLQLLSSRAKIVVWTHGSQLDVTPNQGALIHGLLRTIRSEDPGL  SLTTLDVGDVPSSTQVSAISVLLRRLASLEGPIPIDTEY AERHGEIYISRVPDEKINMFKNNESLNGALQD  GSLRDQKTLVRLRAERIGTLDGLVFGEITSDELPEPNHVEVDIYAAGLNFKVRSSTDYHDTYMGIVPE  NEHLLGIEGAGVRRIASDVTTYKPGDRVVVLQGTGFANRIQASADRTHKIPDQLSYSDAATIPCYYLTS  LYGLFNLAGLQKGNVLIHSAAGGVGISA IKAQYKQAEIFVTGTEDKRRFLESEFGIPRSRMFSSRSTA  FAKEILAAATGGRGIDVILNSLTGELLDETWRICADGGTMEIGKRDILDRKQLAEMPFDRNCYRALDFS  HKQISDALVADLLSTIFDLYDQGHVEPIPIKQFSFADIPSAFAYMRGGKHIGKIVVADAPEDQVIVPIRA  GKQVTLQPEASYIIVGGLKGLCGSLAIAAMAQRGAKHLIVMSRSGVSDQRSQSIVKDCASYGCRIYDSRG  DVANIEDVKA AFSSGYPYVRGIIQGAMVLRDKPFVEMTVEDYHTTISSRVVDGTLHLHLNIAKDRGIELEFF  TLLSSISVGLGQKAQANYAAANVFMDAFANFRNTLGLRANSVDLGVIEDVGYVAEQEALQRLDDKQ  WTGISEAVLLKILDFSILQVDPINTNSRSLITGIPVQPEDSDLARDARFSSLFIPQDANSAGASSTKSDI</p>

	GKEIQAFVLLKSGAEDAALLPLVIDIVNKQLTKLRLSEPIEPAKSL SAYGLDSLASVELRNWVRHELK AGLTTLEINSAPSLTALCEKILSKLKASG
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Supplementary Table 3. The list of the 71 single-copy genes used to construct the phylogenetic tree of the order Capnodiales.

<b>Gene ID</b>	<b>Description (Determined by BLAST against UniRef 90)</b>
Cphlei28858	Uncharacterized protein
Cphlei29054	Uncharacterized protein
Cphlei29270	Peflin
Cphlei29996	Uncharacterized protein
Cphlei30124	Uncharacterized protein
Cphlei30217	Uncharacterized protein
Cphlei30237	Uncharacterized protein (Fragment)
Cphlei30563	Uncharacterized protein
Cphlei30871	Uncharacterized protein
Cphlei30973	Uncharacterized protein
Cphlei31042	Uncharacterized protein
Cphlei31148	NADH-ubiquinone oxidoreductase 14.8 kDa subunit, putative
Cphlei31204	Uncharacterized protein
Cphlei31447	Uncharacterized protein
Cphlei32061	WGS project CABT000000000 data, contig 2.2
Cphlei32084	Uncharacterized protein
Cphlei32159	Uncharacterized protein
Cphlei32290	3,4-dihydroxy-2-butanone 4-phosphate synthase
Cphlei32383	Uncharacterized protein
Cphlei32519	Uncharacterized protein (Fragment)
Cphlei32544	Uncharacterized protein
Cphlei32564	Uncharacterized protein
Cphlei32597	Uncharacterized protein
Cphlei33037	Uncharacterized protein
Cphlei33066	Uncharacterized protein
Cphlei33076	Uncharacterized protein
Cphlei33312	Ubiquinone biosynthesis protein coq4, mitochondrial
Cphlei33357	Uncharacterized protein (Fragment)
Cphlei33421	Uncharacterized protein

Cphlei33465	Uncharacterized protein
Cphlei33487	Dol-P-Man:Man(5)GlcNAc(2)-PP-Dol alpha-1,3-mannosyltransferase
Cphlei33494	Altered inheritance of mitochondria protein 24, mitochondrial
Cphlei33550	Putative secretory component protein shr3 protein
Cphlei33690	Uncharacterized protein
Cphlei33850	Uncharacterized protein
Cphlei33955	Uncharacterized protein
Cphlei34005	Uncharacterized protein
Cphlei34010	Uncharacterized protein
Cphlei34053	Uncharacterized protein
Cphlei34420	Uncharacterized protein
Cphlei34771	Uncharacterized protein
Cphlei34803	Uncharacterized protein
Cphlei34807	Uncharacterized protein
Cphlei34837	40S ribosomal protein S12
Cphlei34862	Mitochondrial import inner membrane translocase subunit TIM23
Cphlei35512	Uncharacterized protein
Cphlei35662	Mitochondria fission 1 protein
Cphlei35987	Uncharacterized protein
Cphlei36118	Uncharacterized protein
Cphlei36182	Uncharacterized protein
Cphlei36249	Uncharacterized protein
Cphlei36333	Uncharacterized protein
Cphlei36359	Uncharacterized protein
Cphlei36402	Short-chain dehydrogenase reductase family
Cphlei36495	Uncharacterized protein
Cphlei36504	Uncharacterized protein
Cphlei36528	Uncharacterized protein
Cphlei36739	Uncharacterized protein
Cphlei36878	Uncharacterized protein
Cphlei36952	Uncharacterized protein
Cphlei36990	DNA replication licensing factor mcm7
Cphlei37155	Uncharacterized protein
Cphlei37156	Uncharacterized protein

Cphlei37426	Uncharacterized protein
Cphlei37662	Uncharacterized protein
Cphlei37847	Uncharacterized protein
Cphlei37893	Uncharacterized protein
Cphlei37917	Uncharacterized protein
Cphlei38143	Uncharacterized protein
Cphlei38180	Uncharacterized protein
Cphlei38226	Uncharacterized protein