

Table S1: Localization of the genes encoding enzymes of the astaxanthin biosynthetic pathway in the draft genomes of *P. australis* and *P. tasmanica*.

Gene	Contig (node) in <i>P. australis</i> PYCC 6859	Contig (node) in <i>P. tasmanica</i> PYCC 6858
IDI - isopentenyl pyrophosphate isomerase	NODE_365_length_5288_cov_17.8917_ID_729	NODE_103_length_61302_cov_20.3239_ID_205
crtE - geranylgeranyl pyrophosphate synthase	NODE_17_length_156497_cov_17.9011_ID_33	NODE_17_length_123067_cov_19.576_ID_33
crtYB - phytoene synthase and lycopene cyclase	NODE_304_length_11423_cov_19.2003_ID_607	NODE_183_length_38676_cov_19.0123_ID_365
crtI - phytoene desaturase	NODE_59_length_89386_cov_21.141_ID_117	NODE_27_length_106799_cov_20.9276_ID_53
crtS - astaxanthin synthetase	NODE_63_length_84228_cov_17.8916_ID_125	NODE_273_length_20701_cov_20.2642_ID_545
crtR - cytochrome P450 reductase	NODE_182_length_35959_cov_18.3017_ID_363	NODE_137_length_52196_cov_20.5677_ID_273

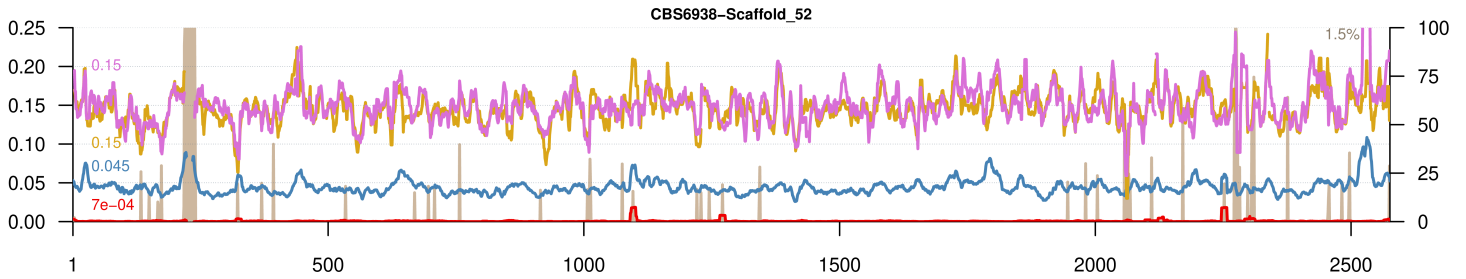
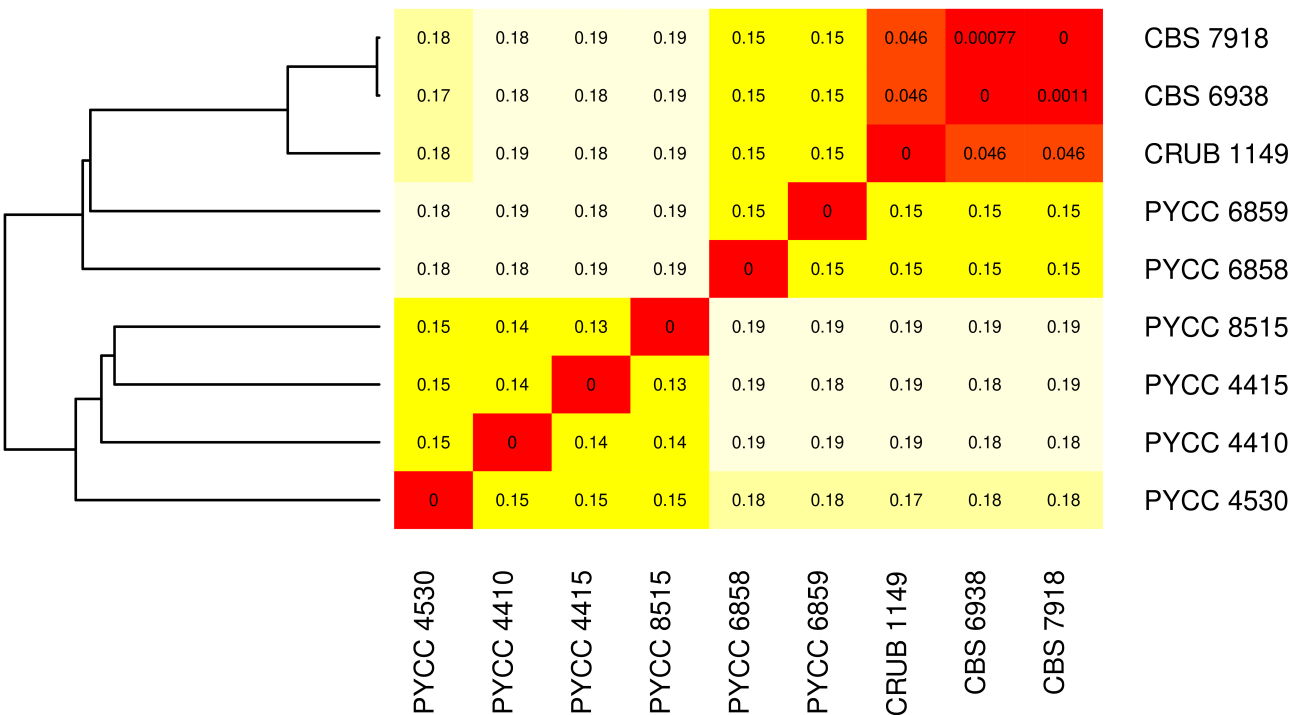
A**B**

Figure S1. (A) Sequence similarity between the new species *Phaffia australis* and *P. tasmanica* and *P. rhodozyma* along the longest scaffold (scaffold 52) of *P. rhodozyma* CBS 6938. The left scale represents the divergence measured by a sliding window approach to *P. rhodozyma* CBS 7918 (red), *P. rhodozyma* CRUB 1149 (blue), *P. australis* PYCC 6859 (yellow) and *P. tasmanica* PYCC 6858 (magenta). The mean divergence value for each strain is shown using the color-codes indicated above. The right Y scale represents the percentage of Ns in the reference sequence, which are indicated as grey bars (1.5% of the scaffold sequence corresponded to Ns). (B) Genomic sequence divergence using an alignment-free method. Heat map and clustering with pairwise distances (Kr values) between the draft genomes of *P. rhodozyma* CBS 7918, CRUB 1149 and CBS 6938, *P. tasmanica* PYCC 6858, *P. australis* PYCC 6859, *C. bisporidii* PYCC 4415, *C. macerans* PYCC 8515, *C. capitatum* PYCC 4530 and *C. ferigula* PYCC 4410

A)

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      10      20      30      40      50      60      70
....|....|....|....|....|....|....|....|....|....|....|....|....|
crtE_CBS 7918 MDYANILTAIPLFTFPQDDIVLLEPYHYLGKNPGKEIRSQIEAFNYWLDVKKEDLEVIQNVVGMMLHTAS
crtE_PYCC 6859 MDYANILTAIPLFTFPQDDIVLLEPYHYLGKNPGKEIRSQIEAFNYWLDVKKEDLEVIQNVVGMMLHTAS
crtE_PYCC 6858 MDYANILTAIPLFTFPQDDIVLLEPYHYLGKNPGKEIRSQIEAFNYWLDVKKEDLEVIQNVVGMMLHTAS
Clustal Consensus *****:*****:*****:*****:*****:*****:*****

      80      90      100     110     120     130     140
....|....|....|....|....|....|....|....|....|....|....|....|....|
crtE_CBS 7918 LLMDDVEDSSVLRGSPVAHLIYGIPTQINTANYVYFLAYQEIFKLRPTPIPMPIPPSSASLQSSVSSA
crtE_PYCC 6859 LLMDDVEDSSVLRGSPVAHLIYGIPTQINTANYVYFLAYQEIFKLRPTPTPTPIPPSSASLQSSVSSA
crtE_PYCC 6858 LLMDDVEDSSVLRGSPVAHLIYGIPTQINTANYVYFLAYQEIFKLRPTPTPIPMPIPPSSASLQSSVSSA
Clustal Consensus ***** * * *:*****

      150     160     170     180     190     200     210
....|....|....|....|....|....|....|....|....|....|....|....|....|
crtE_CBS 7918 SSSSSASSENGGTSTPNSQIPFSKDYLDKVIDEMLSLHRGQGLELFWRDSLTCPEEEYVKMVLGKTG
crtE_PYCC 6859 SSSSTSSDHGGTSTPNSQIPFSKDYLDKVIDEMLSLHRGQGLELFWRDSLTCPEEEYVKMVLGKTG
crtE_PYCC 6858 SSFSSISSENGGTSTPNSQIPFSKDYLDKVIDEMLSLHRGQGLELFWRDSLTCPEEEYVKMVLGKTG
Clustal Consensus ** * *:*****

      220     230     240     250     260     270     280
....|....|....|....|....|....|....|....|....|....|....|....|....|
crtE_CBS 7918 GLFRIAVRLMMAKSECDIDFVQLVNLISYFQIRDDYMNLSQSEYAHNKNFAEDLTEGKFDTLQKSTSP
crtE_PYCC 6859 GLFRIAVRLMMAKSECDIDFVQLVNLISYFQIRDDYMNLSQSEYAHNKNFAEDLTEGKFDTLQKSTSP
crtE_PYCC 6858 GLFRIAVRLMMAKSECDIDFVQLVNLISYFQIRDDYMNLSQSEYAHNKNFAEDLTEGKFDTLQKSTSP
Clustal Consensus *****:*****:*****:*****:*****:*****

      290     300     310     320     330     340     350
....|....|....|....|....|....|....|....|....|....|....|....|....|
crtE_CBS 7918 EILHHCVNYMRTETHSFEYTRDVLNLTSGALERELDRLQGEFAEFGSRMDIGDLDEGKAGKNVLEAIL
crtE_PYCC 6859 EILHHCVNYMRTETHSFEYTRDVLNLTSGALERELDRLQGEFAEFGSRMDIGDLDEGKAGKNVLEAIL
crtE_PYCC 6858 EILHHCVNYMRTETNSFEYTRDVLNLTSGALERELNRLQGEFAEAGSRMDIGDEAEKAGKNVLEAIL
Clustal Consensus *****:*****:*****.*** ***.****:* * :* :*:*****:***

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....|...
crtE_CBS 7918 KKLADIPL
crtE_PYCC 6859 KKLADIPL
crtE_PYCC 6858 KRLADIPL
Clustal Consensus *:*****

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      10      20      30      40      50      60      70
....|....|....|....|....|....|....|....|....|....|....|....|....|
Idi_CBS 7918  MSMNPVPPAEVIRTEGLSLEEYDEEQVRLMEERICILVNPDDVAYGEASKTCHLMSNINAPKDLLHRAF
Idi_PYCC 6859  MSMNPVPPAEVIRTEGLSLEEYDEEQVRLMEERICILVNPDDVAYGEASKTCHLMSNINAPKDLLHRAF
Idi_PYCC 6858  MSKPSVATPAEIRTEGLSLEEYDEEQVRLMEERICILVNPDDVAYGEASKTCHLMSNINAPKDLLHRAF
Clustal Consensus ** * :.***:***:*****:*****:*****:*****:*****

      80      90      100     110     120     130     140
....|....|....|....|....|....|....|....|....|....|....|....|....|
Idi_CBS 7918  VFLFRPSDGALLQRRADEKITFPGMWNTNTCCSHPLSIKGEVEEENQIGVRRASRKLEHELGVPTSSTP
Idi_PYCC 6859  VFLFRPSDGALLQRRADEKITFPGMWNTNTCCSHPLSIKGEVEEENQIGVRRASRKLEHELGVPTSATP
Idi_PYCC 6858  VFLFRPSDGALLQRRADEKITFPGMWNTNTCCSHPLSIKGEIEEENQMGVRRASRKLEHELGVPTSSTP
Clustal Consensus *****:*****:*****:*****:*****:*****:*****

      150     160     170     180     190     200     210
....|....|....|....|....|....|....|....|....|....|....|....|....|
Idi_CBS 7918  PDSFTYLTRIHYLAPSDGLWGEHEIDYILFSTTPTTEHTGNPNEVSDTRYVTKPELQAMFEDESNSFTPW
Idi_PYCC 6859  PDSFTYLTKIHYLAPSDGLWGEHEIDYILFSTTPTTEHTGNPNEVSDTRYVTKPELQAMFEDESNSFTPW
Idi_PYCC 6858  PDSFTYLTRIHYLAPSDGLWGEHEIDYILFSTTPTTEHTGNPNEVSDTRYVTKSELQTMFEDESNSFTPW
Clustal Consensus *****:*****:*****.***:*****

      220     230     240     250
....|....|....|....|....|....|....|....|....|....|....|....|....|
Idi_CBS 7918  KLIARDFLFGWWDQLLARRNEKGEVDAKSLEDLSDNKVWKM
Idi_PYCC 6859  KLIARDFLFGWWDQLLARRNEKGEVDAKSLEDLSDDKVWKM
Idi_PYCC 6858  KLIARDFLFGWDELLARRNEKGEVDAKSLEYLSDDKVWKM
Clustal Consensus *****:*****:*****.***:*****

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      10      20      30      40      50      60      70
CrtYB_CBS 7918  ....|....|....|....|....|....|....|....|....|....|....|....|
CrtYB_PYCC 6859  MTALAYYQIHLIYTLPIILGLLGLLTSPILTKFDIYKISILVFIASFATTTPWDSWIIRNGAWTPYSAESGQ
CrtYB_PYCC 6858  MTALAYYQIHLIYTLPIILGLLGLLTSPILTKFDIYKISILVFIASFATTTPWDSWIIRNGAWTPYSAETGQ
Clustal Consensus  *:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****:

      80      90      100     110     120     130     140
CrtYB_CBS 7918  ...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|
CrtYB_PYCC 6859  GVLGTFDLDVPEEYAFFVIQTVITGLVYVLATRHLPLSLALPKTRSSALSALKALIPLPPIIYLFTHAPS
CrtYB_PYCC 6858  GVLGTFDLDVPEEYAFFIIQTVITGLVYVLATRHLPLSLALPKTRSSARSALKALIPLPPIIYLFTHAPS
Clustal Consensus **:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****:

      150     160     170     180     190     200     210
crtYB_CBS 7918  ...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|
CrtYB_PYCC 6859  PSPDPLVTDHYFYMRALSLITPPMLLAALSGEYAFDWRSGRAKSTIAAIMIPTVYLIWVDYVAVGQDS
CrtYB_PYCC 6858  PSPDPLVTDHYFYMRALSLITAPTMLLATLSGEYAFDWRSGRAKSTLAAITIPVYLIWVDYVAVGQES
Clustal Consensus **:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****:

      220     230     240     250     260     270     280
crtYB_CBS 7918  ...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|
CrtYB_PYCC 6859  WSINDEKIVGWRLLGVLPIEEALFLLTNLMIVLGLSACDHTQALYLLHGRTIYGKKMPPSFLITPPV
CrtYB_PYCC 6858  WSINDEKIVGWRLLGVLPIEEALFLLTNLMIVLGLSACDHTQALYLLHGRTIYGKKMPLSFPLVMPV
Clustal Consensus *****:*****:*****:*****:*****:*****:*****:*****:*****:*****:

      290     300     310     320     330     340     350
crtYB_CBS 7918  ...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|
CrtYB_PYCC 6859  LSLFFSSRPYSSQPKRDLELAVKLEKKSRSFFVASAGFPSEVRERLVGLYAFRCVTDLIDSPVSSNP
CrtYB_PYCC 6858  LSLFFSSRPYSSQPKRDLELAVKILEKKSRSFFVASAGFPCEVRERLVGLYAFRCVTDLIDSPDMSSNP
Clustal Consensus *****:*****:*****:*****:*****:*****:*****:*****:*****:*****:

      360     370     380     390     400     410     420
crtYB_CBS 7918  ...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|
CrtYB_PYCC 6859  HATIDMVSDFLTLFGPPLHPSQDKILSSPLPPSHPSRPTGMYPPLPPSLSPAELVQFLTERVPVQY
CrtYB_PYCC 6858  NDTIDMISDFLTLFGPSLHPSHRDETLSSTLLPPTHPSRPTGLYPLSPPSFTSVELQFLTKRVPVQY
Clustal Consensus : ** *:*****:***.*** *: *: :* ***.*****:***.*****:..:* ***.****:

      430     440     450     460     470     480     490
crtYB_CBS 7918  ...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|
CrtYB_PYCC 6859  HFAFRLLAKLQGLIPRYPLDELLRGYTTDLFPLSTEAVQARKTPIETTADLLDYGLCVAGSVAELLVYV
CrtYB_PYCC 6858  HFAFRLLAKLQGLIPRYPLDELLRGYTDLAFPLSTESVEARKTPIKTTADLLDYGLCVAGSVAELLVYV
Clustal Consensus *****:*****:*****:*****:*****:*****:*****:*****:*****:*****:

      500     510     520     530     540     550     560
crtYB_CBS 7918  ...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|
CrtYB_PYCC 6859  SWASAPSQVPATIEEREAVLVSREMGTALQLVNIARDIKGDATEGRFYLPPLSFFGLRDESKLAIPTDWT
CrtYB_PYCC 6858  SWASAPDQVPATIEGRETVLVSREMGSALQLVNIARDIKGDAEGRLYLPPLSFFGLREESKLAIPIDWT
Clustal Consensus ***** .*****:* **:*:*****:*****:***** ** *****:***:*** **

      570     580     590     600     610     620     630
crtYB_CBS 7918  ...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|
CrtYB_PYCC 6859  EPRPQDFDKLLSLSPSSTLSSNASSEFRFEWKTYSLPLVAYAEDLAKHSYKIDRLPTEVQAGMRAACA
CrtYB_PYCC 6858  KSRPQDFDELLSLSPASTSSSPNTSGNLRFEWKTYSLPLIAYAEDLAKHSYKIDLLPTEVRAGMRAACA
Clustal Consensus :.*****:*****:***.***: .:.* ** *****:*****:***** *****:*****

      640     650     660     670
crtYB_CBS 7918  ...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|
CrtYB_PYCC 6859  SYLLIGREIKVVWKGVDGERRTVAGWRRVRKVLVVMNGWEGQ
CrtYB_PYCC 6858  SYLLIGREIKVVWKGVDGERRTVAGWRRVQKVLVVMNGWEGQ
Clustal Consensus *****:*****:*****:*****:*****:*****:*****:*****:*****:*****:

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          10          20          30          40          50          60          70
CrtI_CBS 7918  MGKEQDQDKPTAIIVGCIGGIATAARLAKEGFQVTVFEKNDYSGGRCSLIERDGYRFDQGPSLLLLPDL
CrtI_PYCC 6859  MGKEQDQDKPTAIIVGCIGGIATAARLAKEGFQVTVFEKNDYSGGRCSLIERDGYRFDQGPSLLLLPDL
CrtI_PYCC 6858  MGKEQEONKPTAIIVGCIGGIFTAARLAKEGFQVTVFEKNDYSGGRCSLIERDGYRFDQGPSLLLLPDL
Clustal Consensus *****:*****

          80          90          100         110         120         130         140
CrtI_CBS 7918  FKQTFEDLGEKMEDWVDLIKCEPNYVCHFHEETFTLSTDMALLKREVERFEGKDGDFRFLSFIQEAHRH
CrtI_PYCC 6859  FKQTFEDLGEKMEDWVDLIKCEPNYVCHFHEETFTLSTDMALLKREVERFEGKDGDFRFLSFIQEAHRH
CrtI_PYCC 6858  FKQTYEDLGEKMEDWVDLIKCEPNYVCHFHEETFTLSTDLALLKREVERFEGKDGDFRFLSFIQEAHRH
Clustal Consensus ****:*****:*****:*****:*****:*****:*****

          150         160         170         180         190         200         210
CrtI_CBS 7918  YELAVVHVLQKNFPGFAAFLRLQFIGQILALHPFESIWTRVCRYFKTDRLRRVFSFAVMYMGQSPYSAPG
CrtI_PYCC 6859  YELAVVHVLQKNFPGFAAFLRLQFIGQILALHPFESIWTRVCRYFKTDRLRRVFSFAVMYMGQSPYSAPG
CrtI_PYCC 6858  YELAVVHVLQKNFPGFAAFLRLQFIGQILALHPFESIWTRVCRYFKTDRLRRVFSFAVMYMGQSPYSAPG
Clustal Consensus *****

          220         230         240         250         260         270         280
CrtI_CBS 7918  TYSLLQYTELTEGIWYPRGGFWQVPNTLLQIVKRNNPSAKFNFNAPVSVLLSPAKDRATGVRLESGEEH
CrtI_PYCC 6859  TYSLLQYTELTEGIWYPRGGFWQVPNTLLQIVKRNNPSAKFNFNAPVSVLLSPSKDRATGVRLESGEEH
CrtI_PYCC 6858  TYSLLQYTELTEGIWYPRGGFWQVPNTLLQIVKRNNPSAKFNFNTPVSRVLLSPAKDRAIGVRLESGEEH
Clustal Consensus *****:***:*****:*** *****

          290         300         310         320         330         340         350
CrtI_CBS 7918  HADVIVNADLVYASEHLIPDDARNKIGQLGEVKRSWWADLVGGKCLKGSCSSLSFYWSMDRIVDGLGGH
CrtI_PYCC 6859  HADVIVNADLVYASEHLIPDDARNKSGQLGEVKRSWWADLVGGKCLKGSCSSLSFYWSMDRIVDGLGGH
CrtI_PYCC 6858  YADVIVNADLVYASEHLIPDDARNKTGQLGQVKRSWWADLVGGKCLKGSCSSLSFYWSMDRIVDGLGGH
Clustal Consensus :*****

          360         370         380         390         400         410         420
CrtI_CBS 7918  NIFLAEDFKGSFDTIFEELGLPADPSFYVNVPSRIDPSAAPEGKDAIVILVPCGHIDASNPQDYKNKLVAR
CrtI_PYCC 6859  NIFLAEDFKGSFDTIFEELGLPADPSFYVNVPSRIDPSAAPEGKDAIVILVPCGHIDTNSNPQDYKNKLVAR
CrtI_PYCC 6858  NIFLAEDFKGSFDTIFEELGLPADPSFYVNVPSRIDPSAAPEGKDAIVILVPCGHINTSNPQDYKNKLVAR
Clustal Consensus *****:*****:*****

          430         440         450         460         470         480         490
CrtI_CBS 7918  ARKFVIQTLSAKLGLPDFEKMIVAEKVHDAPSWEKEFNLDGSIILGLAHNFMQVLGFRPSTRHPKYDKLF
CrtI_PYCC 6859  ARKFVIQTLSAKLGLPDFEKMIVAEKVHDAPSWEKEFNLDGSIILGLAHNFMQVLGFRPSTRHPKYDKLF
CrtI_PYCC 6858  AREFVIQTLSAKLGLPDFEKMIVAEKVHDAHSWEKEFNLDGSIILGLAHNFMQVLGFRPSTRHPKYDKLF
Clustal Consensus **:***:*****:***** *****

          500         510         520         530         540         550         560
CrtI_CBS 7918  FVGASTHPGTGVPIVLAKAKLTANQVLESFDRSPAPDPNMSLSVPYKPLKSNGTGIDSQVQLKFMDLER
CrtI_PYCC 6859  FVGASTHPGTGVPIVLAKAKLTANQVLESFNRPPAPDPMSLSVPYKPLKSKGTGIDAQVDLKPMDLER
CrtI_PYCC 6858  FVGASTHPGTGVPIVLAKAKLTANQVLESFDRPPAPDPNMSLSVPYKPLKSNGTGIDTIQLKSMDLER
Clustal Consensus *****:*****:*****:*****:*****:*****

          570         580
CrtI_CBS 7918  WVYLLVLLIGAVIARSVGVLAFL
CrtI_PYCC 6859  WVYFFMLLIGAAIARFYGVLFN
CrtI_PYCC 6858  WVYLLLVAVFVVRFIGALP-
Clustal Consensus *****:***:*** **
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F)

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      10      20      30      40      50      60      70
....|....|....|....|....|....|....|....|....|....|....|....|....|
CrtS_CBS 7918 MFILVLLTGALGLAAFSWASIAFFSLYLAPRRSSLYNLQGNHTNYFTGNFLDILSARTGEEHAKYREKY
CrtS_PYCC 6859 MSILVLLTGVLGLAAFSWAFIAFFSLYLAPRQSSLYNLQGPDHTNYFTGNFLDILSARTGEEHAKYREKY
CrtS_PYCC 6858 MSILILFTGALGLTAFFWASIAFFSLYLAPRRSSLYNLQGPDHTNFLTGNFLEILSARTGEEHAKYREKY
Clustal Consensus * **:*:**:***:** ** *****:*****:***:*****:*****

      80      90      100     110     120     130     140
....|....|....|....|....|....|....|....|....|....|....|....|....|
CrtS_CBS 7918 GSTLRFAGIAGAPVLNSTDPKVFNHVMKEAYDYPKPGMAARVLR IATGDGVVTAEGEAKRHRRIIMIPSL
CrtS_PYCC 6859 GSTLRFAGIAGT PVLNSTDPKVFNHVMKEAYDYPKPGMAARVLR IATGDGVVTAEGEAKRHRRIIMIPSL
CrtS_PYCC 6858 GSTLRFAGIAGMPVLNSTDPKVFNHVMKEAYDYPKPGMAARVLR IATGDGVVTAEGEAKRHRRIIMIPSL
Clustal Consensus ***** *****

      150     160     170     180     190     200     210
....|....|....|....|....|....|....|....|....|....|....|....|....|
CrtS_CBS 7918 SAQAVKSMVPIFLEKGMELVDKMMEDAAEKDMAVGESAGEKKATRLETEGVDVKDWWGRATLDVMALAGF
CrtS_PYCC 6859 SAQAVKSMVPIFLEKGMELVDKMMEDAAEKDMAVGDSAGEKKATRLETEGVDVKDWWGRATLDVMALAGF
CrtS_PYCC 6858 SAQAVKSMVPIFLEKGMELVDKMMEDAAEKDMTVGESIGEKKVTRLDVEGVDVKDWWGRATLDVMALAGF
Clustal Consensus *****:***:****:**:*****

      220     230     240     250     260     270     280
....|....|....|....|....|....|....|....|....|....|....|....|....|
CrtS_CBS 7918 DYKSDSLQNKTNELYVAFVGLTDGFAPTLDSFKAIMWDFVPYFRMTKRRHEIPLTQGLAVSRRVGIELME
CrtS_PYCC 6859 DYKSDSLQNKTNELYVAFVGLTDGFAPTLDSFKAIMWDFI PFYFRMTKRRHEIPLTQGLAVSRRVGIELME
CrtS_PYCC 6858 DYKSDSLQNKFNELYVAFVGLTDGFAPTFDSAMAIMWDFI PFYFRMTKRRHEIPLTQGLAVSRRVGIELME
Clustal Consensus ***** *****:** *****:*****:*****

      290     300     310     320     330     340     350
....|....|....|....|....|....|....|....|....|....|....|....|....|
CrtS_CBS 7918 QKKQAVLGSASDQAVDKDVGQRDILSLLVRANIAANLPESQKLSDEEVLAQISNLLFAGYETSSTVLTW
CrtS_PYCC 6859 QKKQAVLDSSSDQAVDKDVGQRDILSLLVRANIAANLPESQKLSDEEVLAQISNLLFAGYETSSTVLTW
CrtS_PYCC 6858 QKKQSVLGSASDQAVDKDVEGRDILSLLVRANIAANLPESQKLSDEEVLAQISNLLFAGYETSSTVLTW
Clustal Consensus ****:*:**:*****:*****

      360     370     380     390     400     410     420
....|....|....|....|....|....|....|....|....|....|....|....|....|
CrtS_CBS 7918 MFHRLSEDKAVQDKLREEICQIDTDMPTLDELNALPYLEAFVKESLRLDPPSPYANRECLKDEDFIPLAE
CrtS_PYCC 6859 MFHRLSEDKAVQDRLEEEICQINTDTPTLDELNALPYLEAFVKESLRLDPPSPYANRECLKDEDFIPLAE
CrtS_PYCC 6858 MFHRLSEDKTQDKLREEICQIDTDMPTLDELNALPYLEAFVKESLRLDPPSPYANRECLKDEDFIPLAE
Clustal Consensus *****:***:*****:** *****:*****

      430     440     450     460     470     480     490
....|....|....|....|....|....|....|....|....|....|....|....|....|
CrtS_CBS 7918 PVIGRDGSVINEVRITKGTVMVMLPLFNINRSKFIYGEDAEFRPERWLEDVTDLSNLSIEAPYGHQASFIS
CrtS_PYCC 6859 PVIGRDGSVINEVRITKGTVMVMLPLYNINRSKFIYGEDAEFRPERWLDATDLSNLSIEAPYGHQATFIS
CrtS_PYCC 6858 PVVGRDGSIIINEVRVTKGTVMVMLPLYNINRSKYIYGEDAEFRPERWLEDTTFESFNSIEAPYGHQATFIS
Clustal Consensus **:*****:*****:*****:*****:*****:***:*:**:*****:***

      500     510     520     530     540     550
....|....|....|....|....|....|....|....|....|....|....|....|...
CrtS_CBS 7918 GPRACFGWRFAVAEMKAFLEVTLLRRVQFEP IISHPEYEHITLII SRPRIVGREKEGYQMLQVKPVE
CrtS_PYCC 6859 GPRACFGWRFAVAEMKAFLEVTLLRRVQFEP IISHPEYEHITLII SRPRIVGREKEGYQMLQVKPVE
CrtS_PYCC 6858 GPRACFGWRFAVAEMKAFLEVTLLRVEFEP IISRPEYEHITLII SRPRIVGREKEGYQMLKVPVVG
Clustal Consensus *****:*****:*****:*****:*****:****

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Figure S2. Amino acid alignments of the proteins involved in the astaxanthin biosynthetic route in *Phaffia* spp.

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      10      20      30      40      50      60      70      80      90     100
P. australis_Ste3-1 MNDALFFVFAAIALLLLVLSYCPHFRTGNIGAIALVLWCFTSNLLYFIDCLVYWNNTNLLTPVWCDIMVKIQATTQTGLAAACLCINRRLAISCSKQTS
      110      120      130      140      150      160      170      180      190     200
P. australis_Ste3-1 ATSKSRRWAFWSDMLICALAPIIVAIISYCVQSHRYNIVENFGCSGSPWMDVYAILGSGYPPMLLITVSSITYGAVAIYNFIVQRRRFQAVLQQNSSLNTC
      210      220      230      240      250      260      270      280      290     300
P. australis_Ste3-1 RFVRLIGVAGVNIIVISLLFAIRETVIAARSVYTSVSWDYIHYDFDLILTFNSAFLGEPQLWIELNLCRWLPCLASFIYFAFFGMHEDVLSYTYIWAR
      310      320      330      340      350      360      370
P. australis_Ste3-1 SQALLHAKERIFGRPPPVDPSQYPKLGTAVASPSERGSRNGMPDEEQAFPYSHMETSEKRDTSSEHPLPRIKVVVS

      10      20      30      40      50      60      70      80      90     100
P. australis_Ste3-2 MRDALFFIYSGLAIIILLIACGPHIRAGNVGAIISLMTWCLANVTYFINALIYQDTAADLTPWCDIVVKIQCAVQTGLAAACLCINRRLATISSPTQSR
      110      120      130      140      150      160      170      180      190     200
P. australis_Ste3-2 QTETSQRQAFWSDVAICLVPTALVLIIVSYCVQAHRYNIENFGCFPATWLELYAILGLFVPPVLCAGSFCGGFAIYNFLAQRFRFQAVLQQNSSLNS
      210      220      230      240      250      260      270      280      290     300
P. australis_Ste3-2 SRLRLVGVAVDMVLSLPGFYVEIHNAYTLQPTYSWADLHDNENLVKEIDQSILNAQPGSWASINLSRWMTTLAAFIYFAFFGMHEDALSFFHASIWTKI
      310      320      330      340      350      360      370      380
P. australis_Ste3-2 SAGFGYIWIIRFFGKSEPPSYDSSQLTQLGTTIASPSDQNRFCNSIKDEEAYFAYENMTGLEKSDSSLGVDKSIKIVTVNIQRTIS

      10      20      30      40      50      60      70      80      90     100
P. tasmanica_Ste3-1 MSDAVFPVFAALLLLLVLSYCPHFRTGNIGAITLVIWCFLSNFFYFVDCIVYWDTVKNLTPVWCDIMVKIQATTQTGLAAACLCINRRLAISCSKTQTN
      110      120      130      140      150      160      170      180      190     200
P. tasmanica_Ste3-1 ITSKARRRAFWSMDLICALAPVVVVVSYCIQSHRYNVIENYGCAGVPWLDTYAIIIGLYPSLLMGFISSITYGAVAIYKFVAQRRRFQAVLQQNSSLNTS
      210      220      230      240      250      260      270      280      290     300
P. tasmanica_Ste3-1 RFVRLIGVAGNIVISLLEFAIRETVLATRFRDPTVSWDYIHDDFSLVIPIDSSYLSENPQLWVELNLSRWLPCLASFIYFAFFGMHEDVLAAYTYVWMS
      310      320      330      340      350      360      370      380
P. tasmanica_Ste3-1 SEALSRTREIRLFRASFPVYDPSQYPKLGTIVASPSERVSRERNPDEEEDLPYSHMEISEKNDTEDRSSPHVTVTIEVEKVVVS

      10      20      30      40      50      60      70      80      90     100
P. tasmanica_Ste3-2 MKDVLFPVYSGFAVILLMACGPHVRAGNVGAIISLMTWCLANITYFINALIYQDTAENLTPWCDIVVKIQCAVQTGLAAACLCINRRLATISSPTRSR
      110      120      130      140      150      160      170      180      190     200
P. tasmanica_Ste3-2 QTETSQRQAFWSDIAICLVPTTLVLIIVSYCVQAHRYNIENFGCFPATWLELYAILGLYIPVLCACSFPGGFAIYNFLAQRFRFQAVLQQNSSALNS
      210      220      230      240      250      260      270      280      290     300
P. tasmanica_Ste3-2 SRFLRLIGVAVDMVLSLPGFYVEIHNTRNLQPTYSWADIHENFGLVKEIDLSVLNESDWSVDSLRSWMTTLAAFIYFAFFGMHEDALLFYASIWTKI
      310      320      330      340      350      360      370      380
P. tasmanica_Ste3-2 SAIFSYPWMRTSKMSEPPSYDSSQLTQLGTTVASADLERFCNTIKDEEAYFAYENMIGSEKSGSDMGVDKIVTVTKIEKTIS

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Figure S3. Predicted proteins of the pheromone receptor genes of *P. australis* and *P. tasmanica*. The transmembrane domains of each sequence are highlighted in blue.


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      10      20      30      40      50      60      70      80      90     100
P. australis_Hd1 MESFPA[SDLSAPLDSLVDKFLNSI]RAGI[FVEISQIYDAFAEERRKAR]NEGLLT[FEYQEEI]SAS[VGFLSTLAS]CMNNIPEDKTFQTSVIGILNSANNIPE
      110     120     130     140     150     160     170     180     190     200
P. australis_Hd1 VCPFRFLPSPLNTLPKPKPDSERSMRPRT[EH]PSSFRHLRDFWFI[VH]LDHPYPS[AEQEELALAKN]LTKNSVNLWFNNMRR[RS]GWMDFVIRTHALNNQNRMKEL
      210     220     230     240     250     260     270     280     290     300
P. australis_Hd1 [V]LHRS[LP]AVEQ[SH]PEL[P]E[LRQQLDR]IQD[VH]D[E]KGGHDKVRDMMAGALDYRESSGVTVVEIGRFPDKNKEVENDTTKTDSSSDLYQASSATKEAQHWLD
      310     320     330     340     350     360     370     380     390     400
P. australis_Hd1 PYLTSTSGLVGLPSVPLSNRP[TKSSKRSFSDHVP]HVAASLDVPSVNYHQLINFPNRPDQNR[EGGM]THQFPVPTHAYYPTYPQLQKPLPLLGPIFYQSSF
      410     420     430     440     450     460     470     480     490     500
P. australis_Hd1 NSQFPAYDLN[TSRAQAWL]P[PH]VVDLSGGPN[HQR]SVSP[LSRAK]STG[PSL]SITTT[PS]IRSSAN[ESAGNELAA][KLEALRIKKEAL]KKEK[EQLR]AEAAE
      ....
P. australis_Hd1 [LGEV]FDC

      10      20      30      40      50      60      70      80      90     100
P. australis_Hd2 MNSLSKIPQMSVGLGVDFSDLDL[LLTSKEFTIED]LYLPVPTS[CETLEEL]GTPHT[LARNLGA]LYLSRAFALRELSL[LQ]FDTAFFADRTFLLDANS[LK]KV
      110     120     130     140     150     160     170     180     190     200
P. australis_Hd2 FKGLLKATL[EH]RYSVELSHHQ[ET]TIQLAGVWTSDD[EQ]TPVSV[RRSSFT]KNTIDT[LQALYD]LNOYPN[PVELKTI]AVK[VGLQPKQI]RAW[EQ]NRRNR[RS]PAC
      210     220     230     240     250     260     270     280     290     300
P. australis_Hd2 [SQK]KTFMSLKRK[IAASDLN]LMTVHKRRS[RG]TAS[FENEQ]EDQSVPSRLGSPISLQTEKASIVPDTQGR[LKACCP]SVADLFDTF[SN]DQDASTPWSTIISDGP
      310     320     330     340     350     360     370     380     390     400
P. australis_Hd2 SIYASFEQVPQ[IESS]LPPA[IFEPAD]IMSVQIADGSSNVSNKSFSSHPVYTPALN[LNETTK]THPVDWRMVF[AKSN]SRSLAPRFEEVGAQLNS[KMR]RGIKNV
      410
P. australis_Hd2 [L]IVSPIT[T]TER

      10      20      30      40      50      60      70      80      90     100
P. tasmanica_Hd1 MESYF[PSDLSARLDSLVEKFLNPI]AGV[FV]DLSQIYDAFAEERRK[AW]S[EG]LLT[FE]YQEEI[SASV]GFLSTLAS[CM]TNTPDENTDF[CTT]VIGI[LND]ANNASE
      110     120     130     140     150     160     170     180     190     200
P. tasmanica_Hd1 ICPPRH[LT]LPSN[TL]P[KAD]TGRVMPR[PT]EH[PSSFRHLRDFWFI]V[H]LDHPYPS[AEQEELALAKN]LTKNSVNLWFNNMRR[RS]GWMDFVIRTHAVNNQNR[M]REL
      210     220     230     240     250     260     270     280     290     300
P. tasmanica_Hd1 VLLHRS[LP]ASERSHPEL[P]E[LRQQLDR]IQD[VH]D[E]KGGHDKVRDMMW[TALE]YKDSFEGTADRTQ[SL]E[KRKEK]GKGT[TR]SDFSSDLYKKSFTTKD[VH]PWIP
      310     320     330     340     350     360     370     380     390     400
P. tasmanica_Hd1 YPAPASGLIGYPPSVL[NRPV]QNSKRSFSEDDSYVAAPIDAVSDYHQLMSLNGPNQ[HEG]SLHTHQLP[AY]HYPTYPQLRN[PL]FMLGPTSYHSSD
      410     420     430     440     450     460     470     480     490     500
P. tasmanica_Hd1 P[Q]FPAYDLNASTRAQ[TW]LSSNPA[GV]LGGPKV[QR]SVSP[LSRAK]PVLSSASSTTT[PS]SRSSAN[ESAGNELAA][KLEALRIKKEAL]KKEK[EQLR]VEAAEAL
      ....
P. tasmanica_Hd1 [GEV]FDC

      10      20      30      40      50      60      70      80      90     100
P. tasmanica_Hd2 MNSLPKPPQK[ST]GPGVDFSDDRGAPSSSEFATEDL[LD]VPM[SICETLEEL]GTPHT[LARNLGA]LYLSK[ASALRELSLM]QDAAPPA[ERST]LLETNSL[LK]KV
      110     120     130     140     150     160     170     180     190     200
P. tasmanica_Hd2 FKGLLKATL[EH]RYSMEL[THY]QELI[IQ]LAGVWTSDD[EQ]P[SV]TV[RRSSFT]KNTIDT[LQALYD]LNOYPN[PVELKTI]AAR[VGLQPKQI]RAW[EQ]NRRNR[RS]PAC
      210     220     230     240     250     260     270     280     290     300
P. tasmanica_Hd2 [P]HKKALKTSTRATAASHL[KIDIV]KRKSP[SRT]S[IE]TETKDEGVPSRLGSPISPQTNRISSV[QP]QERPRDGHSSVAN[FETS]PKKQDSSALWLVSSDRS
      310     320     330     340     350     360     370     380
P. tasmanica_Hd2 STYPNFEGPPQIGSSLHFSTPEADL[MNV]RLAEDPFDLRNKSTSSHPVFTPVFGSNEIMDIDP[MNWR]MIFATPNSRTVAPGS[RKV]GAQ

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Key: Homeodomain Coiled-coil Nuclear localization signal Alpha-helix

Figure S4. Predicted proteins of the homeodomain transcription factor genes of *P. australis* and *P. tasmanica*. The secondary organization is highlighted.