

Electronic Supplementary Information

ALDH and CYP amino acid sequences were aligned in MUSCLE (Edgar, 2004) before importing into MEGA5 (Tamura, 2011). Alignments were viewed in MEGA5 and edited manually where necessary. Phylogeny was inferred using Maximum Likelihood method, using the Jones-Taylor-Thornton (JTT) model, with 1000 bootstrap replicates. For Figs. S1 & S2, branches present in less than 50% of bootstrap replicates were collapsed.

For ALDH analysis, sequences previously used by Soberia *et al*, 2010 (Ref. 14) were included and names maintained. Additionally sequences from:

Gemmata obscuriglobus (accession ZP_02730696),
Singulosphaera acidiphila (accession: ZP_09565902),
Planctomyces maris (accession ZP_01851832),
Planctomyces limnophilus (accession: YP_003629897),
Blastopirellula marina (accession ZP_01091754),
Rhodopirellula baltica (accession NP_869285),
Rhodopirellula baltica (accession: EGF24028) ,
Singulisphaera acidiphila (accession ZP_09568612),
Pirellula staleyi (accession YP_003370928),
Isosphaera pallida (accession YP_004178423),
Planctomyces brasiliensis (accession YP_004269788),
Cyanothece sp. PCC7942 (accession: YP_002379008),
Cyanothece sp. PCC7822 (accession YP_003890169),
Cyanothece sp. ATCC 51142 (accession: YP_001804643),
Cyanothece sp. CCY0110 (accession ZP_01726360),
Crocospaera watsonii WH 8501 (accession: ZP_00518574),
Crocospaera watsonii WH0003 (accession EHJ10116),
Microcoleus chthonoplastes PCC 7420 (accession ZP_05023575),
Cyanothece sp. PCC 8802 (accession: YP_003137302),
Trichodesmium erythraeum IMS101(accession YP_722268),
Moorea producta (accession ZP_08426871),
Lyngbya sp. PCC 8106 (accession ZP_01618896),
Chlorella variabilis (accession EFN6007),
Aureococcus anophagefferens (accession EGB03958),
Phaeodactylum tricornutum (accession XP_002185692),
Micromonas sp. (accession RCC299) and
Micromonas pusilla CCMP1545 were included in the alignment.

For CYP analysis, sequences previously used by Albalat & Canestro, 2009 (Ref. 5) were included and names maintained. Additionally sequences from:

Microcystis aeruginosa PCC 7806 (accession: CAO90869.1),
Microcystis aeruginosa PCC 9808 (accession: CCI27101.1),
Microcystis aeruginosa PCC 9806 (accession: CCI14887.1),
Microcystis aeruginosa PCC 9432 (accession: CCH92366.1),
Microcystis sp. T1-4 (accession: ZP 10227922.1),
Microcystis aeruginosa PCC 7941 (accession: CCI06746.1),
Microcystis aeruginosa PCC 9443 (accession: CCI03806.1),
Microcystis aeruginosa PCC 9807 (accession: CCI18751.1),
Microcystis aeruginosa NIES-843 (accession: YP 001659897.1),
Microcystis aeruginosa PCC 9701 (accession: CCI37737.1),
Microcystis aeruginosa PCC 9717 (accession: CCH97559.1),
Cyanothece sp. PCC 7424 (accession: YP 002377960.1),
Lyngbya sp. PCC 8106 (accession: ZP 01619745.1),
Oscillatoria sp. PCC 6506 (accession: ZP 07110250.1),
Nodularia spumigena CCY9414 (accession: ZP 01628555.1),
Microcoleus chthonoplastes PCC 7420 (accession: ZP 05027138.1),
Microcoleus vaginatus FGP-2 (accession: ZP 08494833.1),
Cyanothece sp. CCY0110 (accession: ZP 01730375.1),
Cyanothece sp. PCC 7425 (accession: YP 002483142.1),

Moorea producta (accession: ZP 08427236.1),
Fischerella sp. JSC-11 (accession: ZP 08985447.1),
Acaryochloris marina MBIC11017 (accession: YP 001519436.1),
Synechococcus sp. PCC 7002 (accession: YP 001733214.1),
Acaryochloris sp. CCME 5410 (accession: ZP 09250262.1),
Synechococcus sp. PCC 7335 (accession: ZP 05038129.1),
Synechocystis sp. PCC 6803 (accession: NP 442426.1),
Synechococcus sp. PCC 7335 (accession: ZP 05039471.1),
Trichodesmium erythraeum IMS101 (accession: YP 724423.1),
Acaryochloris marina MBIC11017 (accession: YP 001521335.1),
Cyanothece sp. PCC 7822 (accession: YP 003888546.1),
Microcoleus chthonoplastes PCC 7420 (accession: ZP 05029948.1),
Nostoc punctiforme PCC 73102 (accession: YP 001867927.1),
Cyanothece sp. ATCC 51142 (accession: YP 001805142.1),
Cyanothece sp. CCY0110 (accession: ZP 01732300.1),
Trichodesmium erythraeum IMS101 (accession: YP 722428.1),
Plesiocystis pacifica SIR-1 (accession: ZP 01909216.1),
Stigmatella aurantiaca DW4/3-1 (accession: ZP 01464395.1),
Herpetosiphon aurantiacus DSM 785 (accession: YP 001546879.1),
Prochlorococcus marinus sp MIT 9313 (accession: NP 895392.1),
Prochlorococcus marinus sp. MIT 9303 (accession: YP 001016373.1),
Nostoc punctiforme PCC 73102 (accession: YP 001867865.1),
Synechococcus sp. WH 8016 (accession: ZP 08955188.1),
Synechococcus sp. RS9916 (accession: ZP 01472377.1),
Cyanobium sp. PCC 7001 (accession: ZP 05046414.1),
Synechococcus sp. WH 5701 (accession: ZP 01086392.1),
Synechococcus sp. WH8102 (accession: NP 897501.1),
Synechococcus sp. CB0101 (accession: ZP 07973546.1),
Synechococcus sp. RCC307 (accession: YP 001227362.1),
Synechococcus sp. CC9605 (accession: YP 381833.1) and
Synechococcus sp. CB0205 (accession: ZP 07970771.1) were included in the alignment.

References

Edgar, R. C. (2004). MUSCLE: multiple sequence alignment with high accessionuracy and high throughput. *Nucleic acids research*, 32(accession: 5), 1792–7. doi: 10.1093/nar/gkh340

Tamura, K., Peterson, D., Peterson, N., Stecher, G., Nei, M., & Kumar, S. (2011). MEGA5: molecular evolutionary genetics analysis using maximum likelihood, evolutionary distance, and maximum parsimony methods. *Molecular Biology and Evolution*, 28(accession: 10), 2731–9. doi: 10.1093/molbev/msr121

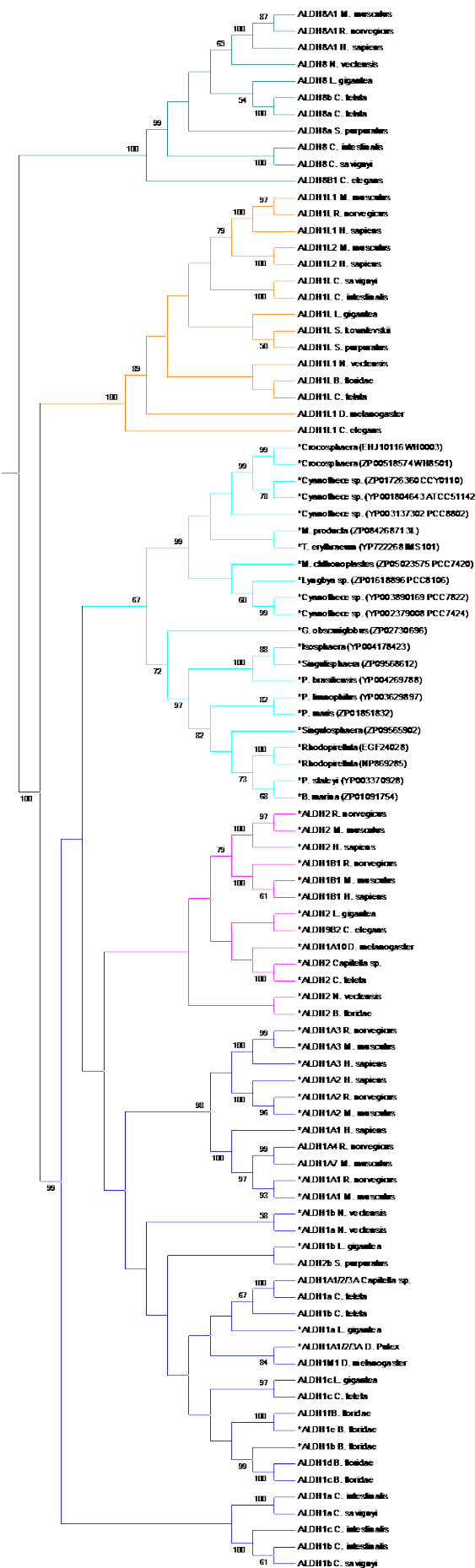


Figure 1

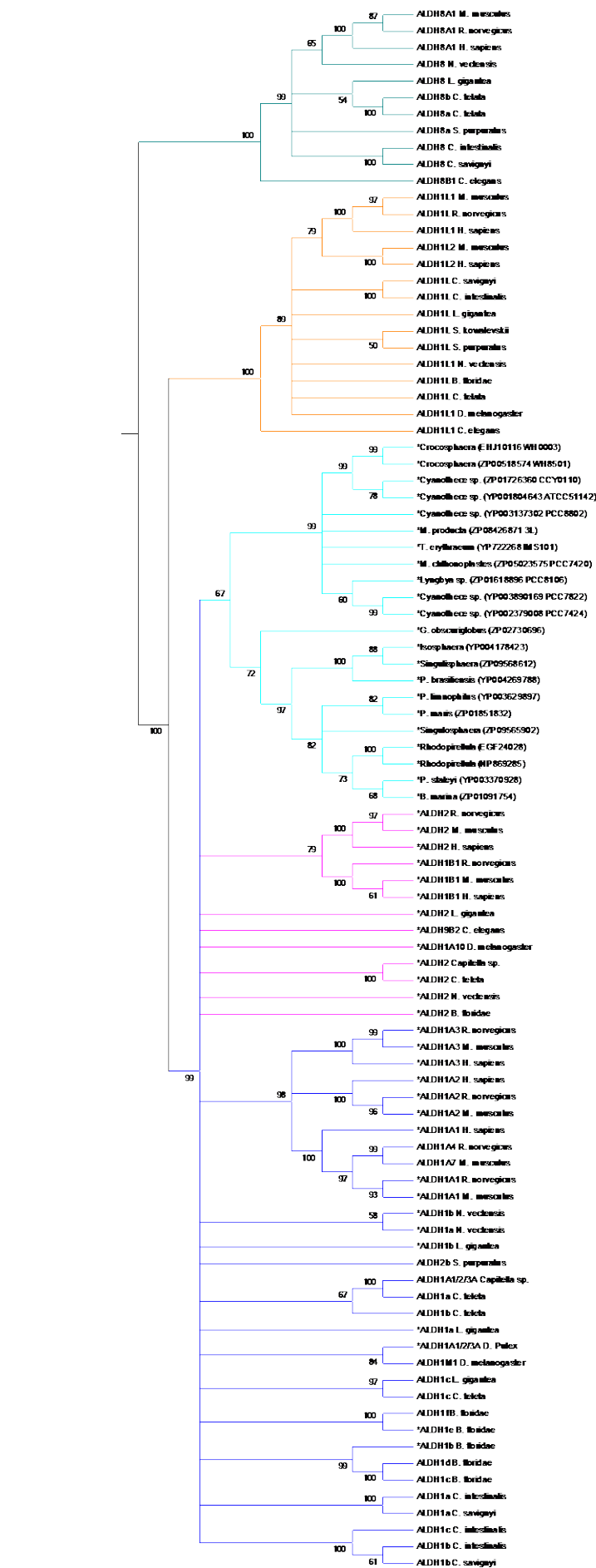


Figure S1

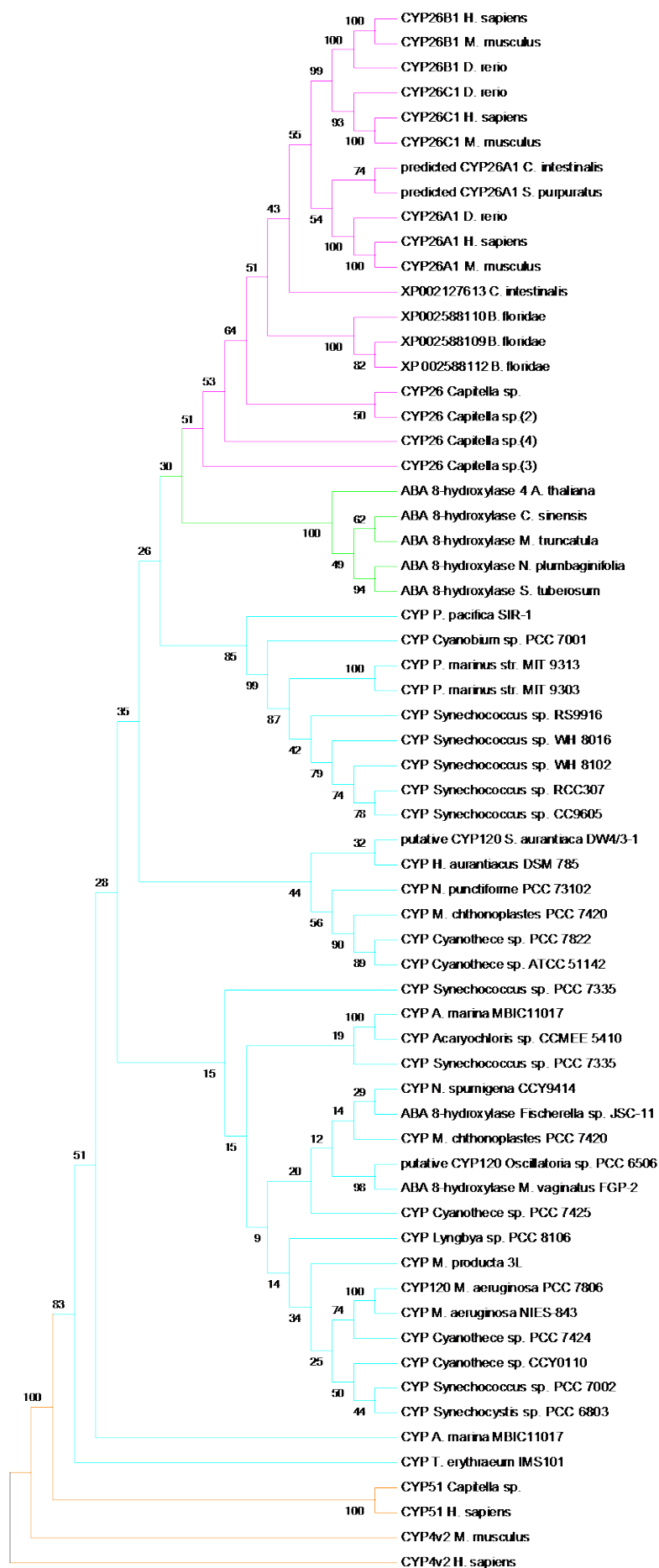


Figure 2

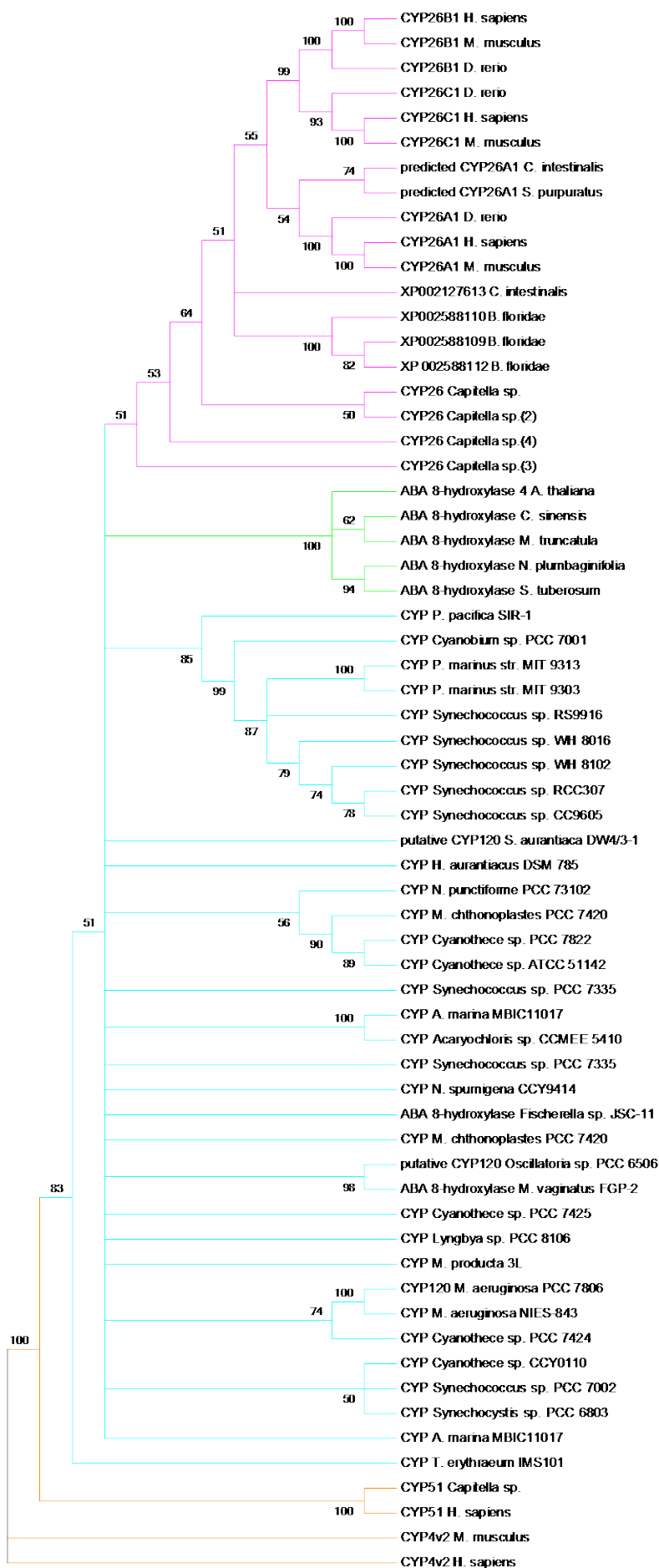


Figure S2