Supplementary material for

***Comparative genomics highlight the importance of lineage-specific gene families in evolutionary divergence of the coral genus, Montipora***

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**Supplementary Table**

**Supplementary Table S1.** Summary of comparison of KEGG metabolic pathways among acroporid genomes. MCR indicates the module completion ratio, calculated by GenoMaple.

**Supplementary Table S2.** IDs of gene families common to *Montipora* and *Astreopora* or restricted to *Montipora*, that are expressed during three life stages (planula larvae, metamorphosed larvae, and recruits).

**Supplementary Table S3.** IDs of gene families common to three genera (*Montipora*, *Acropora* and *Astreopora*) or common to *Montipora* and *Acropora*, that are expressed during three life stages (planula larvae, metamorphosed larvae, and recruits).

**Supplementary Table S4.** Summary of gene families significantly (Fisher’s exact test: *p* < 0.05) expanded in the *Montipora* genome compared to those of *Acropora* or *Astreopora*.

**Supplementary Table S5.** Summary of samples used for RNA-seq.

**Supplementary Table S6.** Summary of publicly available RNA-seq samples that were included for gene prediction in *Montipora* and *Astreopora*.

**Supplementary Table S7.** Summary of RNA-seq samples used for comparative transcriptomic analyses.

**Supplementary Figure**

**Supplementary Figure S1.** Summary of gene predictions for *M. cactus*, *M. efflorescens*, and *Astreopora myriophthalma*.

**Supplementary Data**

**Supplementary Data S1.** Result of orthologous clustering in Acroporidae genomes using Orthofinder.

**Supplementary Data S2.** Summary of retained scaffolds after genome assembly curation for *Montipora cactus* and *M. efflorescens*.

**Supplementary Data S3.** Gene models for *M. cactus* in GTF format.

**Supplementary Data S4.** Gene models for *M. efflorescens* in GTF format.

**Supplementary Data S5.** Gene models for *Astreopora myriophthalma* in GTF format.