Supplementary Information Guide

1) **Octopus Genome Supplementary Notes**

Supplementary Notes.pdf

This document contains Supplementary Notes 1-12. (PDF, 8.4MB)

2) **Supplementary Video 1: *Octopus bimaculoides*: Adaptive coloration**

SV1.mp4

The ability to camouflage is present throughout the animal kingdom, but cephalopods uniquely achieve adaptive coloration. Three different structures in the skin contribute to the color of an octopus: chromatophores, iridophores, and leucophores. The reflectin family of proteins reversibly regulates iridescence. Muscles in the skin allow octopuses to alter texture and disrupt the visual boundaries of the body. Most importantly, this complex behavior happens very quickly, allowing octopuses to change their appearance almost instantaneously. The *O. bimaculoides* genome and transcriptome is reported by Albertin and Simakov et al. Credit: Z. Yan Wang, C. Ragsdale, J. Reynolds, and Schadenfreude the octopus. (mp4 video, 37.9MB)

3) **Supplementary Video 2: *Octopus bimaculoides*: Arms and Suckers**

SV2.mp4

Octopuses are perhaps most easily recognized by their eight appendages. The arms are strong muscular hydrostats, each covered with hundreds of suckers that allow octopuses to exert powerful suction forces. The flexibility and strength of octopus arms is a unique morphological innovation in the animal kingdom. The *O. bimaculoides* genome and transcriptome is reported by Albertin and Simakov et al. Credit: Z. Yan Wang, C. Ragsdale, J. Reynolds, and Schadenfreude the octopus. (mp4 video, 37.7MB)

4) **Metazoan C2H2 superfamily tree**

C2H2.pdf

Approximate maximum likelihood tree of metazoan C2H2-ZNFs. The tree was built using a near-complete subset of transcriptome-confirmed C2H2-ZNF sequences (1,452/1,790) from octopus (dark blue), 539 from human (red), 388 from mouse (pink), 159 from zebrafish (purple), 7 from *A. queenslandica* (yellow), 88 from *A. californica* (aqua), 24 from *C. intestinalis* (dark purple), 65 from *S. kowalevskii* (violet), 44 from *T. castaneum* (orange), 39 from *N. vectensis* (mustard), 87 from *L. gigantea* (teal), and 72 from *C. teleta* (green). (PDF, 476KB)

5) **Metazoan GPCR superfamily tree**

GPCR.pdf

Approximate maximum likelihood tree of bilaterian GPCRs. The tree was built using the 329 GPCR sequences from octopus (dark blue), 185 from human (red), 160 from mouse (pink), 226 from zebrafish (magenta), 204 from *S. kowalevskii* (purple), 125 from *L. gigantea* (aqua), 258 from *C. teleta* (green), and 87 from *A. californica* (grey-blue). For clarity, only a subset of vertebrate olfactory receptors were used. The octopus Class A rhodopsins are centered around 7 o'clock. (PDF, 235KB)

6) **TE Load and Tissue Expression**
TeLoadAndTissueExpression.xlsx

Genes with tissue-specfic expression and high levels of TE content in the 5kb up- and down-stream regions. Normalized expression levels for each tissue are provided. (Excel, 595KB)

7) **Cephalopod Novelties**
CephalopodNovelties.xlsx

Cephalopod novel gene families. First column contains URLs to the clusters with additional information. (Excel, 128 KB)

8) **Micro-synteny**
Microsynteny.xlsx

Detected micro-synteny including inference whether the synteny block was present in the most recent common ancestor (MRCA) of bilaterians (bilMRCA). Each line decodes one block per species, with connecting blocks listed in column 4. (Excel, 454KB)