

Supplementary Information

Stable Species Boundaries Despite Ten Million Years of Hybridization in Tropical Eels

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1 Supplementary Notes

Supplementary Note 1: Contrasting patterns of within-species genomic variation.

Our extensive sampling scheme of tropical eels permitted detailed analyses of genomic variation within *A. marmorata*, *A. megastoma* and *A. obscura*, as we sampled each of the three species at multiple sites throughout their geographic distribution (Fig. 1a; Supplementary Table 1). These analyses were based on a dataset of 155,896 RAD-sequencing derived single-nucleotide polymorphisms (SNPs), partitioned according to species and subsequently filtered to exclude invariant sites (minor allele count > 2) and missing data (> 20%; Supplementary Figure 1). Using these partitioned datasets, principal-component analysis (PCA) of genomic variation was performed with smartPCA in EIGENSOFT v.6.0.1 (Patterson *et al.* 2006), including the function “lsqproject” to account for missing data. For *A. marmorata*, PCA separated four populations present in the western Indian Ocean (South Africa, Reunion, Mayotte), in Indonesia (Java), the South China Sea (Philippines and Taiwan), and the western South Pacific (Bougainville Island, Solomon Islands, Vanuatu, New Caledonia, Samoa, and American Samoa). The latter three, however, were only discernible on the second principal-component axis (explaining 2.2% of genetic variation), along which the individuals from Java appeared intermediate between those from the western Indian Ocean and the western South Pacific (Supplementary Figure 4a). Our results are thus consistent with divergence among Indian and Pacific ocean populations (Ishikawa *et al.* 2004; Minegishi *et al.* 2008; Watanabe *et al.* 2008; Gagnaire *et al.* 2011) and with the region of Java representing a contact zone between those populations (Gagnaire *et al.* 2011). Conversely, no population structure was detected in either *A. megastoma* or *A. obscura* (Supplementary Figures 4c-f), supporting the hypothesized single spawning area for the two species in the western South Pacific (Schabetsberger *et al.* 2015, 2016).

Supplementary Note 2: Double-digest restriction-site associated DNA (ddRAD) sequencing.

Following Peterson *et al.* (2012), 20 units of EcoRI-HF (New England Biolabs) and 20 units of MspI (New England Biolabs) were used to digest 400 ng of genomic DNA per sample in a 37 °C incubation for 8 hours. Digests were purified with homemade paramagnetic carboxyl-modified beads (Sera-Mag, Fisher Scientific; Rohland & Reich 2012). Moreover, samples were randomly placed in PCR plates, ensuring a wide coverage of geographic sampling locations per plate during library preparation. T4 DNA ligase (New England Biolabs) was applied to ligate 100 ng of each digested DNA fragment to a EcoRI-specific P1 adapter that contained a 5-bp barcode and the MspI-specific P2 adapter in room temperature, followed by an enzyme heat-kill at 65 °C for 10 min. Twenty-four unique barcodes were used so that the ligated DNA fragments from 24 individuals could be pooled (according to one index) to form a single ddRAD-seq library. Ligations were cleaned with homemade paramagnetic carboxyl-modified beads. Fragments in the range of 300-400 bp were selected using AMPure XP beads (Agilent Technologies) and were subsequently amplified by 12 rounds of PCR with the following conditions: 98 °C for 60 s; 12 cycles of 98 °C for 10 s, 60 °C for 30 s, 72 °C for 30 s; 72 °C for 10 min using Q5[®] High Fidelity polymerase (New England Biolabs), and the Illumina sequencing primers (PCR Primer 1 and Index added PCR Primer 2; four unique 6-bp multiplexing indices were used). In total, six separate PCR reactions of the same index were amplified, pooled

and cleaned with homemade paramagnetic carboxyl-modified beads. Library quality was assessed on a TapeStation 2200 (Agilent Technologies) to confirm fragment recovery on the selected range and was quantified using a Qubit Fluorometer 2.0. To avoid index-hopping (Kircher *et al.* 2012; Sinha *et al.* 2018), none of the samples shared both the P1 barcode and the multiplexing index in a given sequencing run. In total, 20 libraries, each containing 24 barcodes, were sent to Macrogen (Korea) for 100 bp paired-end Illumina HiSeq 4000 sequencing.

Supplementary Note 3: The reliability of published age estimates for the genus *Anguilla*.

We time calibrated the species tree of tropical eels according to age estimates reported by Jacobsen *et al.* (2014) on the basis of mitochondrial genomes. In their study, Jacobsen *et al.* (2014) used the earliest fossil records of the family Anguillidae, *Eoanguilla leptoptera* from Monte Bolca, Italy (Patterson 1993; Carnevale *et al.* 2014), to constrain the divergence between Anguillidae and Serpenteridae to 55-50 Ma. Given that the age of the Monte Bolca deposits is 49.4-49.1 Ma (Benton *et al.* 2015; Matschiner *et al.* 2017), it is indeed likely that Anguillidae originated before 50 Ma. However, since fossils do not directly constrain maximum ages, the upper boundary of 55 Ma was arbitrarily specified by Jacobsen *et al.* (2014), and the divergence times estimated in their study would likely be underestimated if Anguillidae in fact originated earlier than 55 Ma. Nevertheless, we consider the timeline proposed by Jacobsen *et al.* (2014) plausible for the following reasons: (i) According to this timeline, European and American anguillid species (*A. anguilla* and *A. rostrata*) diverged from Indo-Pacific members of the genus around 10.8 Ma, which is consistent with the Messinian age (7.2-5.3 Ma) of the earliest fossils of the genus, known from the Gessoso Solifera Formation in Northern Italy (Dela Pierre *et al.* 2011); (ii) the timeline is consistent with those of two other recent studies based on genome-wide data (Musilova *et al.* 2019) and a massive taxon set (Rabosky *et al.* 2018), as the most recent common ancestor of *A. anguilla* and *A. japonica* (the only species pair included in all three studies) was estimated at 13.8 Ma in Jacobsen *et al.* (2014), at 12.4 Ma in Musilova *et al.* (2019), and at 12.9 Ma in Rabosky *et al.* (2018).

Supplementary Note 4: Assessing the robustness of divergence-time estimates.

To test how robust the divergence-time estimates are to alternative phylogenetic positions of *A. interioris*, SNAPP analyses were repeated separately with two fixed topologies in which *A. interioris* is either the sister of *A. bicolor* and *A. obscura* or the sister to the clade formed by *A. marmorata*, *A. luzonensis*, *A. bicolor*, and *A. obscura*. Furthermore, to test the robustness of divergence-time estimates to introgression involving *A. luzonensis* and *A. interioris*, the analyses were repeated after excluding these two species.

Additionally, we compiled a multi-locus phylogenetic dataset based on genome assemblies of the five species *A. anguilla*, *A. japonica*, *A. marmorata*, *A. obscura*, and *A. megastoma* to estimate divergence times among *Anguilla* species independently of the timeline of Jacobsen *et al.* (2014). Of these five species, genome assemblies of *A. anguilla* (NCBI accession GCA_000695075; Henkel *et al.* 2012a) and *A. japonica* (NCBI accession GCA_000470695; Henkel *et al.* 2012b) were included in the large-scale phylogenomic analysis of Musilova *et al.* (2019), in which their divergence was

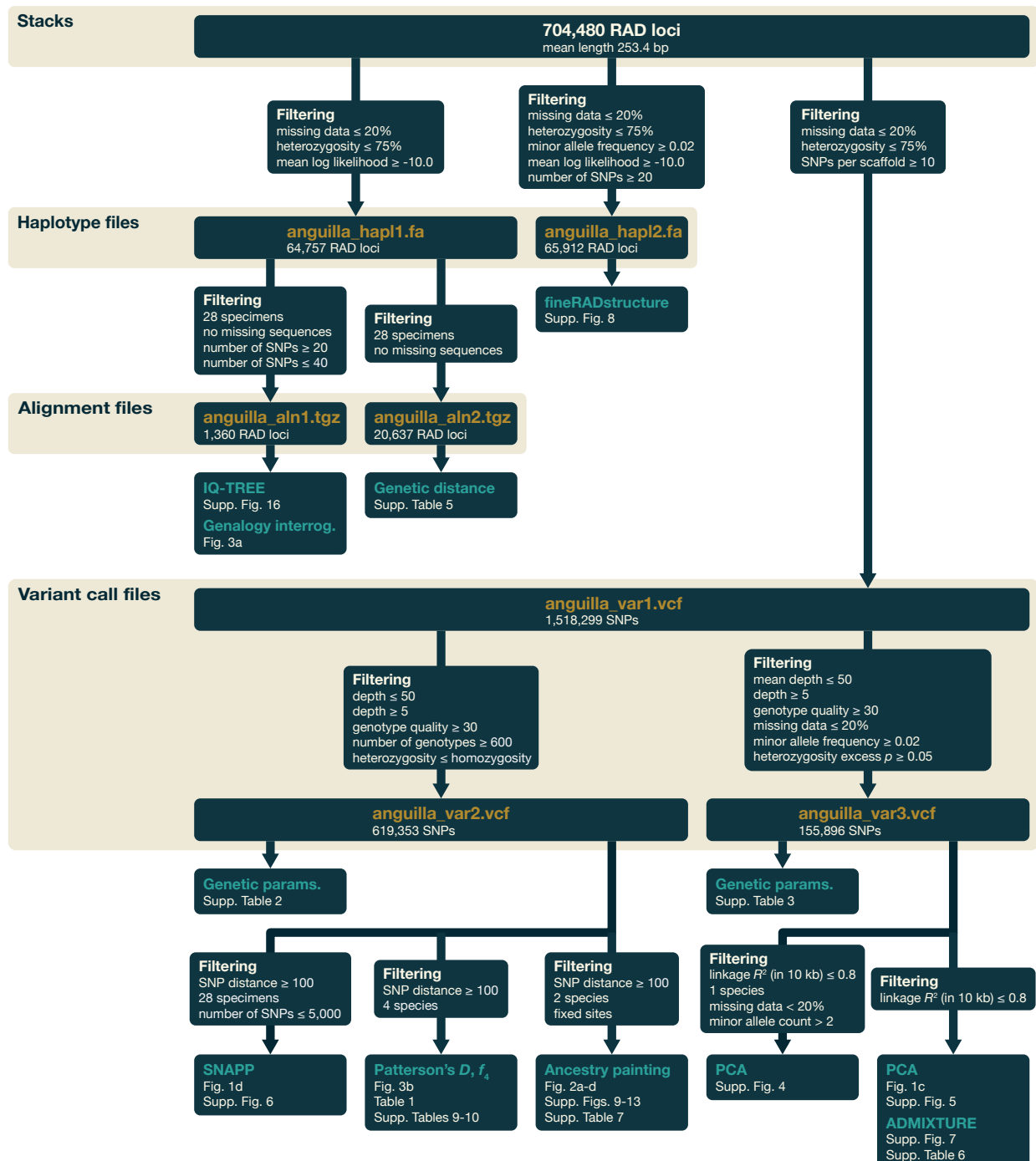
estimated at around 12.37 Ma. We thus extracted ortholog sequences, corresponding to the loci used in Musilova *et al.* (2019), from the three new genome assemblies of *A. marmorata*, *A. obscura*, and *A. megastoma* (Supplementary Table 5), and aligned these jointly with those of *A. anguilla* and *A. japonica*. Alignments were then filtered according to the protocol of Musilova *et al.* (2019), excluding 10 of the 113 genes used in Musilova *et al.* (2019) due to missing sequences. Alignments for the remaining 103 nuclear genes were concatenated and split into two separate partitions for first- and second-codon positions; third-codon positions were excluded. Together, these two partitions included 92,530 bp with 0.07% missing data. The concatenated alignment was used for phylogenetic analyses with the software BEAST 2, time calibrating the phylogeny according to the timeline estimated by Musilova *et al.* (2019). Specifically, we used 12.37 Ma, the estimated age for the divergence of *A. anguilla* and *A. japonica*, as a constraint on the age of the most recent common ancestor of the five *Anguilla* species, after initial analyses suggested an position of *A. anguilla* outside of a clade formed by the other four species. The model used in this analysis included a GTR substitution-rate matrix (Tavaré 1986), gamma-distributed among-site rate variation, a strict molecular clock, and the Yule process of species diversification (Yule 1925). The BEAST 2 analysis was performed with 10 million MCMC iterations. Convergence was again assessed with Tracer, and the posterior tree distribution was summarized in an MCC tree generated with TreeAnnotator.

As another alternative to the divergence-time estimates of Jacobsen *et al.* (2014), we also implemented age constraints according to the timeline of Rabosky *et al.* (2018). The large-scale time-calibrated phylogeny of Rabosky *et al.* (2018), based on molecular data for 11,638 ray-finned fishes and 139 fossil constraints, includes 20 species and subspecies of the genus *Anguilla* and places the earliest divergence within the genus, the separation of *A. australis*, at 21.57 Ma. As the genus was mostly (82%) represented by mitochondrial sequences in the dataset of Rabosky *et al.* (2018), we extracted homologous mitochondrial sequences from the new genome assemblies of *A. marmorata*, *A. megastoma*, and *A. obscura* (Supplementary Table 5) using BLAST, and integrated these sequences with the mitochondrial data for *Anguilla* compiled by Rabosky *et al.* (2018). This integrated mitochondrial dataset was concatenated into a single alignment and used again for phylogenetic inference with BEAST 2. According to the phylogeny of Rabosky *et al.* (2018), *A. australis* was constrained to be the outgroup of the other *Anguilla* species and the divergence of *A. australis* was fixed at 21.57 Ma. The model used in this analysis was identical to that used for nuclear data, except that the GTR substitution-rate matrix was replaced with an HKY matrix (Hasegawa *et al.* 1985) because some GTR rate parameters appeared unidentifiable in preliminary analyses. The BEAST 2 analysis was again performed for 10 million MCMC iterations, convergence was assessed with Tracer, and a MCC summary tree was generated with TreeAnnotator.

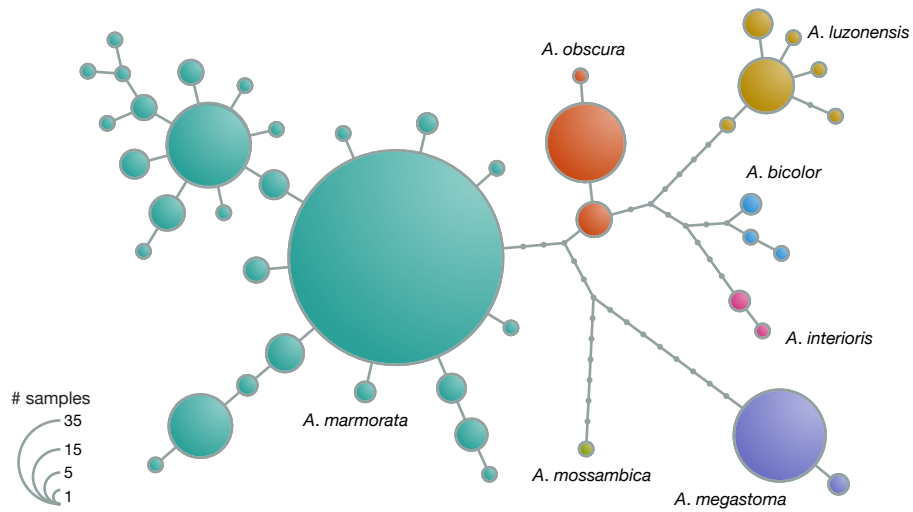
2 Supplementary Figures

Supplementary Figure 1: Molecular datasets used in this study.

Flow chart illustrating how RAD sequencing data was filtered and used for various analyses. File names are shown in yellow and analyses are highlighted in cyan.

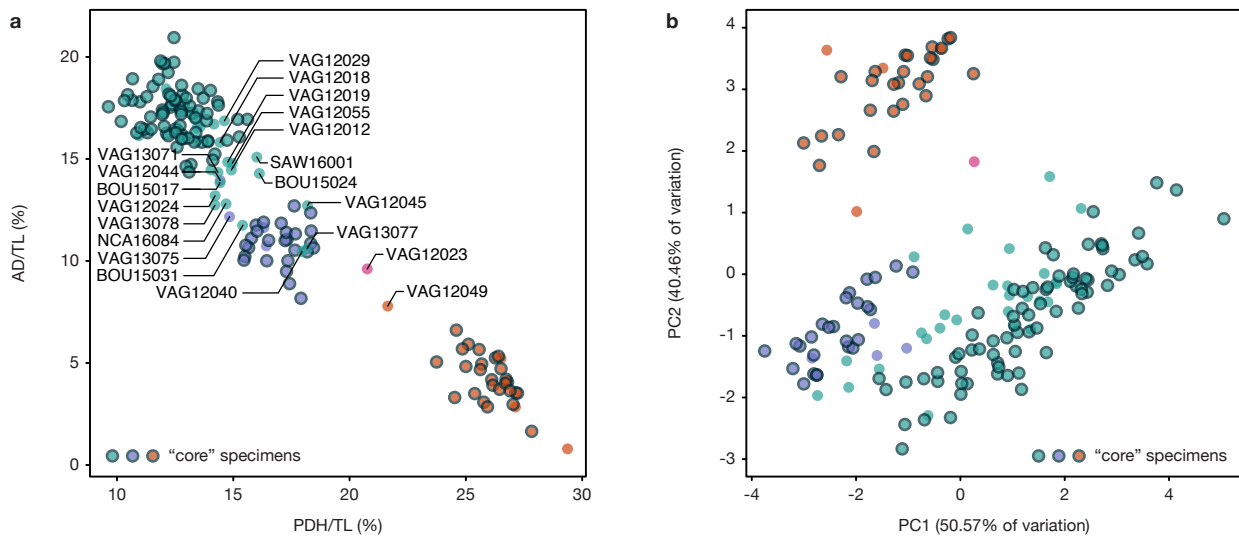


Supplementary Figure 2: Haplotype-genealogy graph based on mitochondrial sequences. Graph generated with the software Fitchi v.1.1.4 (Matschiner 2016) for two concatenated RAD loci mapping to positions 10630-10720 and 12015-12105 of the *Anguilla japonica* mitochondrial genome (NCBI accession CM002536). The genealogy of mitochondrial sequences for all 456 individuals was produced using RAxML v. 8.2.11 (Stamatakis 2014) with the GTRCAT model of sequence evolution.

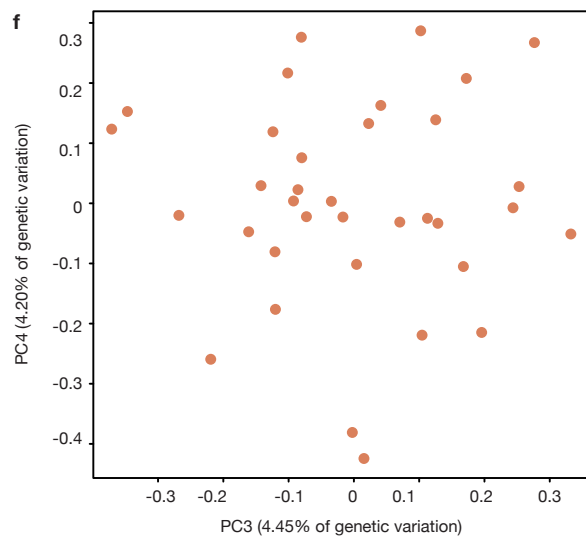
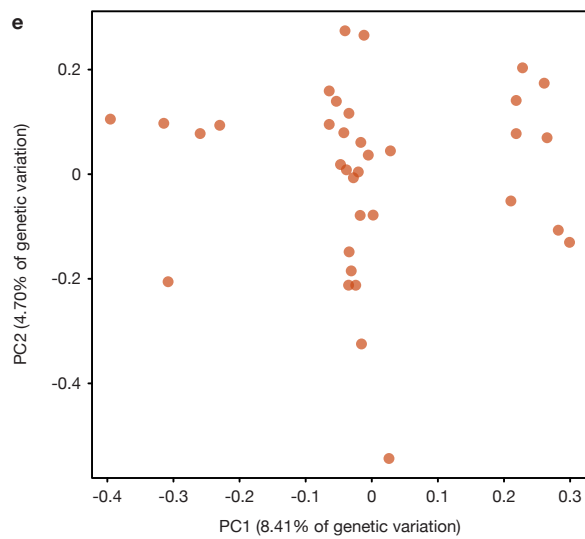
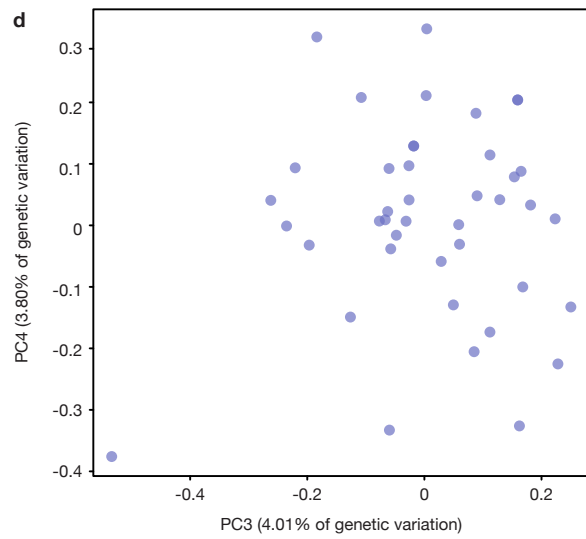
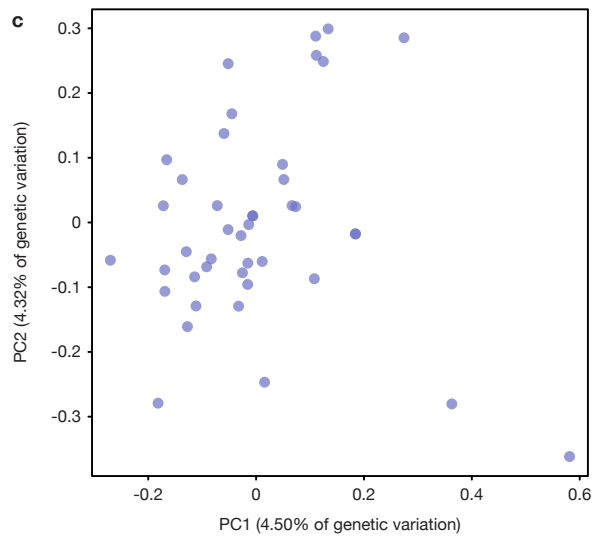
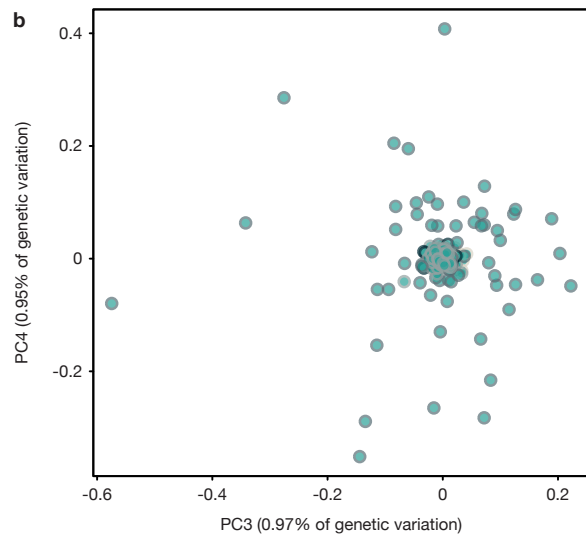
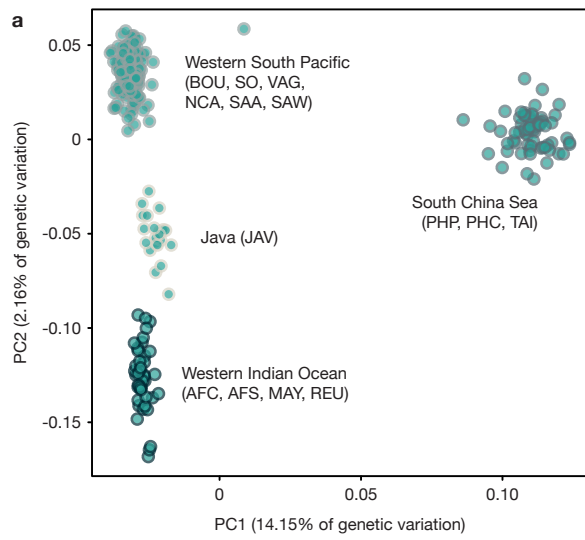


Supplementary Figure 3: Morphological variation among tropical eel species.

a) Following Watanabe *et al.* (2009), the predorsal length without the head (PDH) and the distance between the dorsal fin and the anus (AD) were measured for 161 individuals available for morphological analyses ($100 \times A. marmorata$, $30 \times A. megastoma$, $30 \times A. obscura$, and $1 \times A. interioris$) and standardized by terminal length (TL). Color code is identical to Supplementary Figure 2. Individuals selected as putatively unadmixed “core” group representatives of *A. marmorata*, *A. megastoma*, and *A. obscura* are marked with dark gray outlines. Specimen IDs (see Supplementary Table 1) are given for putative hybrids and one representative of *A. interioris*. b) First and second principal components of morphological variation. “Core” individuals were selected according to clusters shown in this plot.

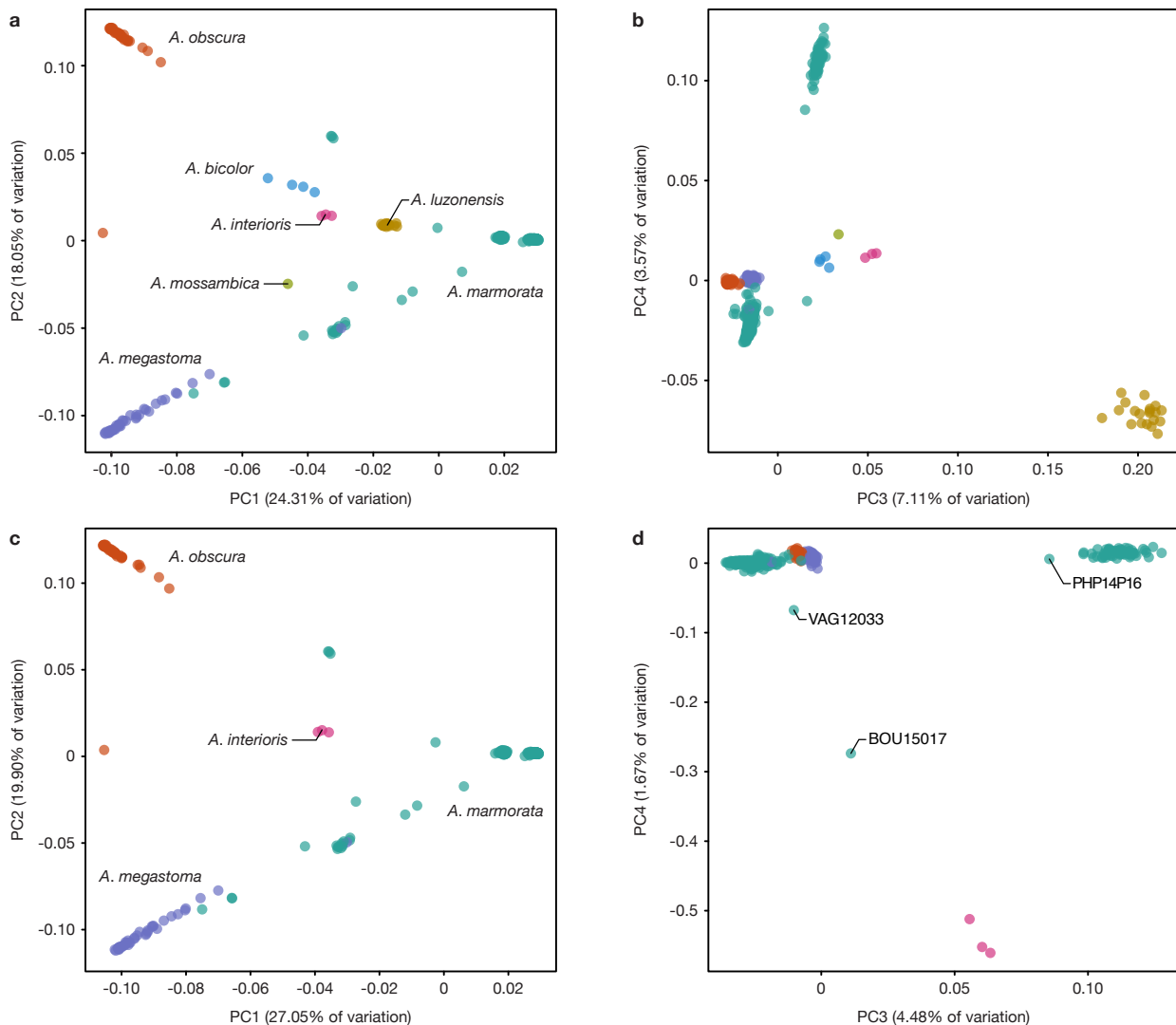
**Supplementary Figure 4 (next page):** Genomic variation within tropical eel species.

a-b) Comparison of first and second (a), and third and fourth (b), principal components of genomic variation in *A. marmorata*. c-d) Comparison of first and second (c), and third and fourth (d), principal components of genomic variation in *A. megastoma*. e-f) Comparison of first and second (e), and third and fourth (f), principal components of genomic variation in *A. obscura*. Putative between-species hybrids (see Supplementary Table 7) were excluded from this analysis. Stroke color indicates geographic origin as specified in Supplementary Figure 3.



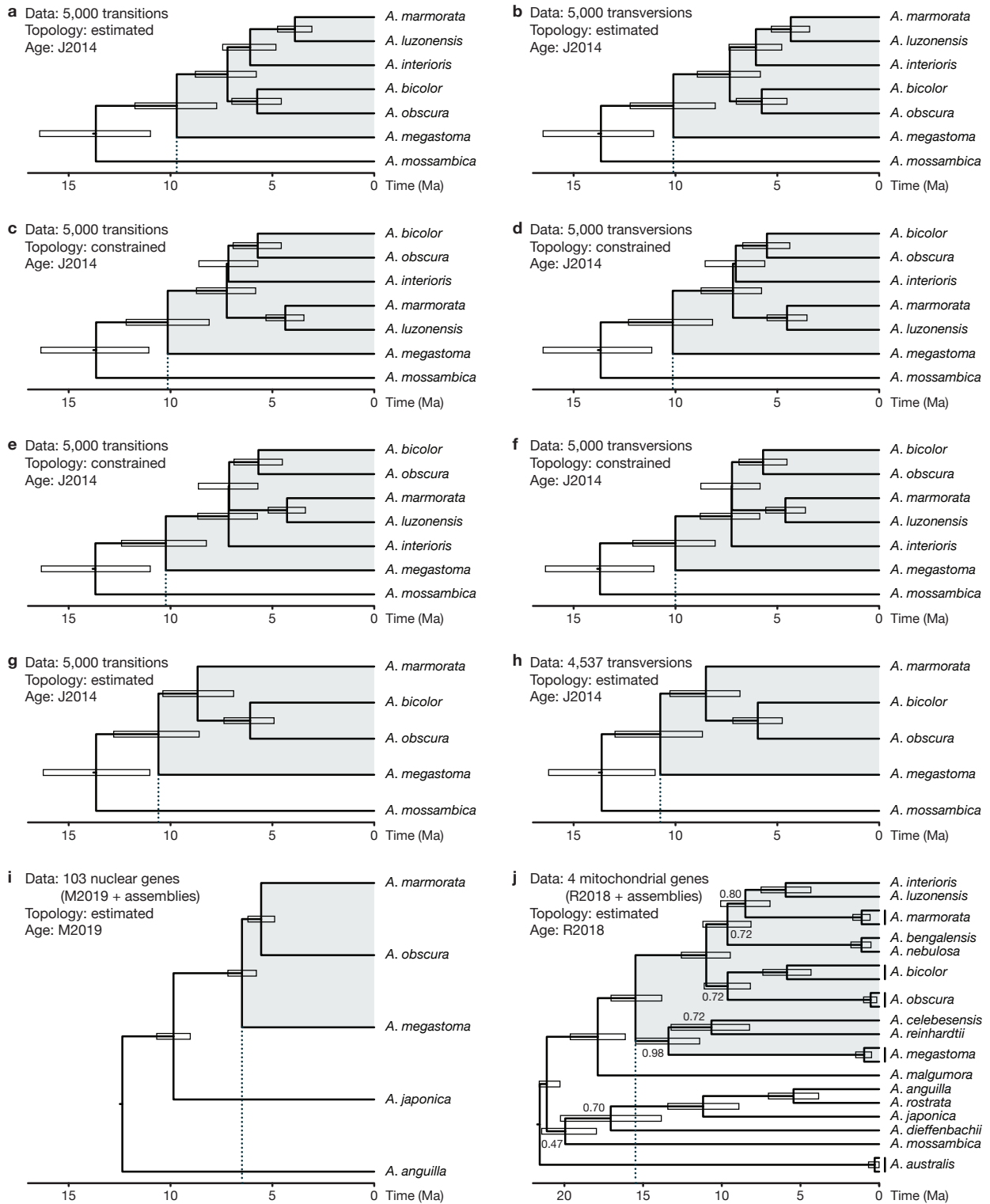
Supplementary Figure 5: Genomic variation among tropical eel species.

a) First and second principal components of genomic variation among the seven species *A. marmorata* (cyan), *A. luzonensis* (brown), *A. megastoma* (purple), *A. obscura* (red), *A. bicolor* (blue), *A. interioris* (magenta), and *A. mossambica* (green). b) Third and fourth principal components of genomic variation among the seven species. c) First and second principal components of genomic variation, focusing on the four species *marmorata* (cyan), *A. megastoma* (purple), *A. obscura* (red), and *A. interioris* (magenta). d) Third and fourth principal components of genomic variation, for the same four species as in c). The two individuals VAG12033 and PHP14P16 are characterized by a large proportion of missing data (see Supplementary Table 1), which might explain their outlier positions.



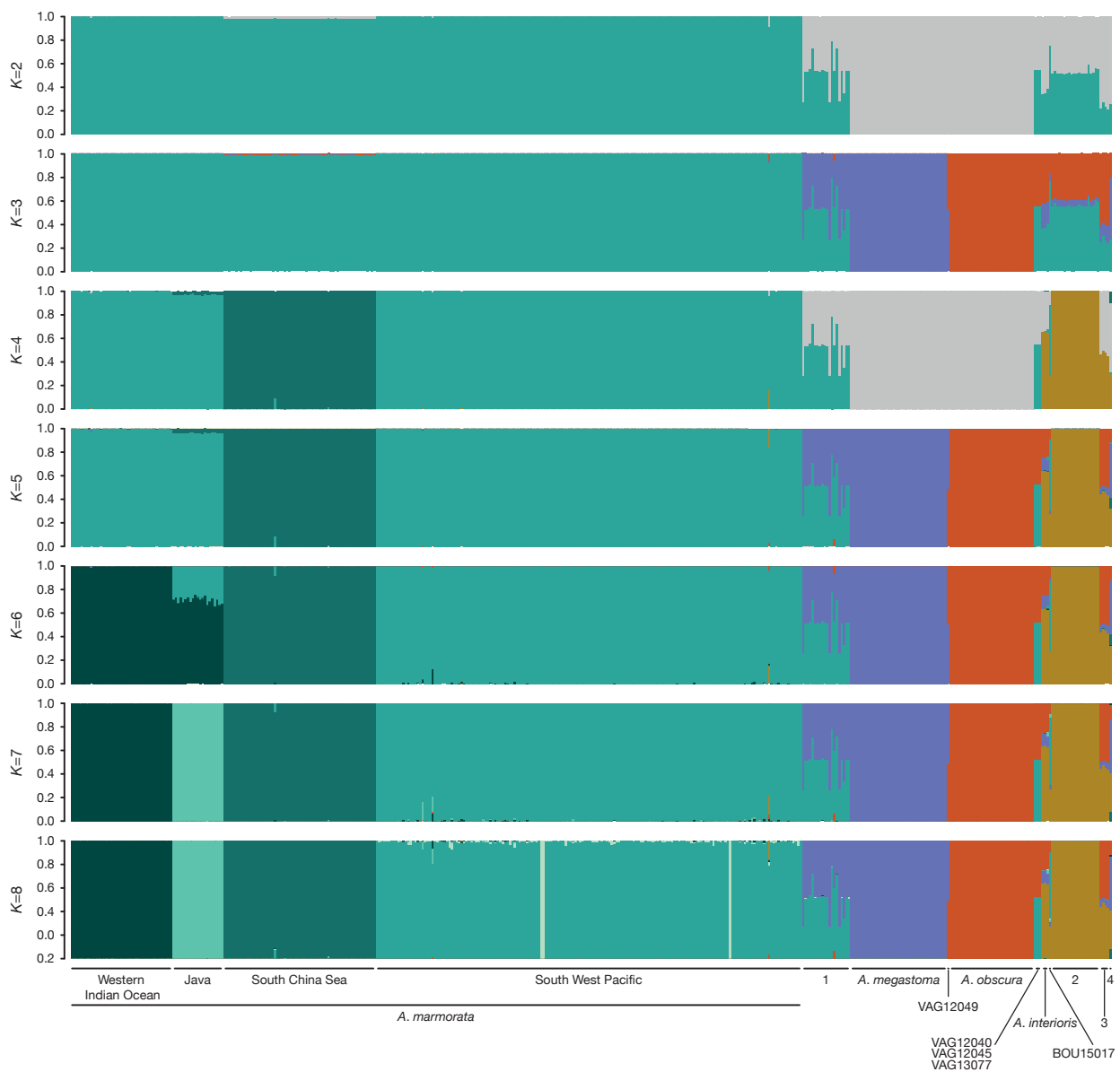
Supplementary Figure 6 (next page): Divergence times of tropical eel species.

a-b) Maximum-clade-credibility (MCC) summary trees of SNAPP analyses with 5,000 transition or transversion sites, respectively, without topology constraints and a single age constraint on the root divergence according to Jacobsen *et al.* (2014) (J2014). The gray area marks the group of species for which we find evidence of past and ongoing hybridization, and the dotted line indicates the crown age of this group. c-d) As a-b), but with a topology constraint on the position of *A. interioris* as the sister species to a clade combining *A. bicolor* and *A. obscura*; this position is supported by maximum-likelihood inference with IQ-TREE (Supplementary Figure 17). e-f) As a-b), but with a topology constraint on the position of *A. interioris* as the outgroup to a clade formed by *A. bicolor*, *A. obscura*, *A. marmorata*, and *A. luzonensis*; this position is supported by genealogy interrogation (Fig. 3a). g-h) As a-b), but excluding the two species *A. luzonensis* and *A. interioris* due to their strong signals of ancient hybridization. i) MCC tree of a BEAST analysis with 103 nuclear genes. Sequences of these genes from *A. anguilla* and *A. japonica* were included in Musilova *et al.* (2019) (M2019) and were here complemented with orthologs extracted from the new genome assemblies of *A. marmorata*, *A. megastoma*, and *A. obscura*. A single age constraint on the root was used for calibration according to Musilova *et al.* (2019). j) MCC tree of a BEAST analysis with four mitochondrial genes that were used in Rabosky *et al.* (2018) (R2018). The dataset of Rabosky *et al.* (2018) was here complemented with orthologs from the three new genome assemblies (*A. marmorata*, *A. megastoma*, and *A. obscura*), and a single age constraint on the root was used according to Rabosky *et al.* (2018). Note that the timescale in j) differs from a-i). Unless specified, all nodes received full Bayesian support.



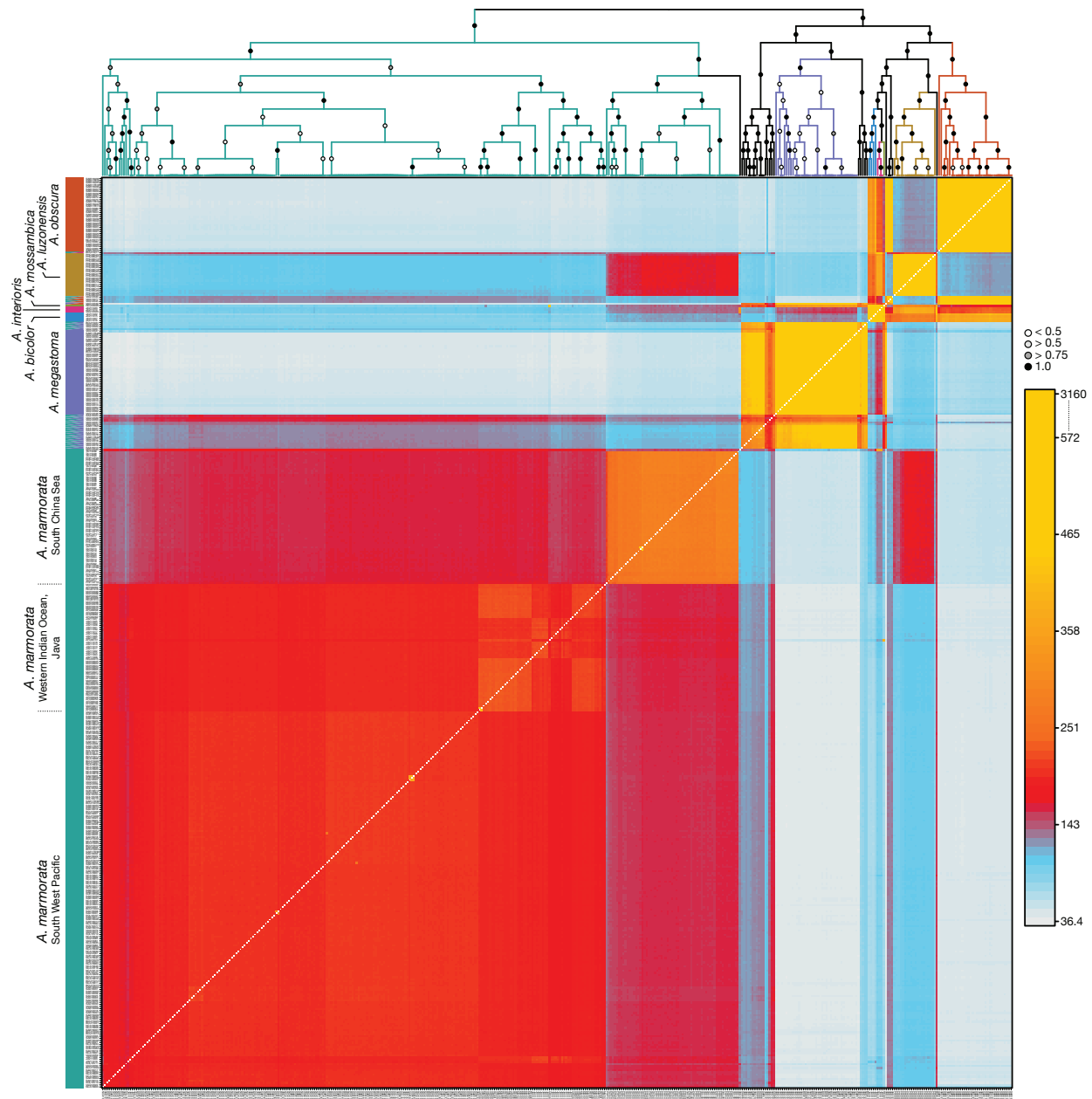
Supplementary Figure 7: Maximum-likelihood ancestry inference.

Ancestry proportions displayed in bars per individual were inferred for the models $K = 1$ to $K = 8$ based on 117,638 variable sites using the software ADMIXTURE (Alexander *et al.* 2009). The inset shows the cross-validation (CV) error for five replicates per model. For *A. marmorata*, individuals are labeled according to geographic origin: Indian Ocean (sampling locations AFC, AFS, MAY, REU), Java, South China Sea (PHP, PHC, TAI), and Pacific (BOU, NCA, SAA, SAW, SO, VAG). Label 1 marks 20 individuals that appear admixed between *A. marmorata* and *A. megastoma*: BOU15031, SAA16011, SAA16012, SAA16013, SAA16024, SAA16027, SAW17B27, SAW17B49, VAG12012, VAG12018, VAG12019, VAG12024, VAG12029, VAG12037, VAG12044, VAG12053, VAG12055, VAG13071, VAG13078, and VAG13087. Labels 2-4 indicate species *A. luzonensis* (2), *A. bicolor* (3), and *A. mossambica* (4).

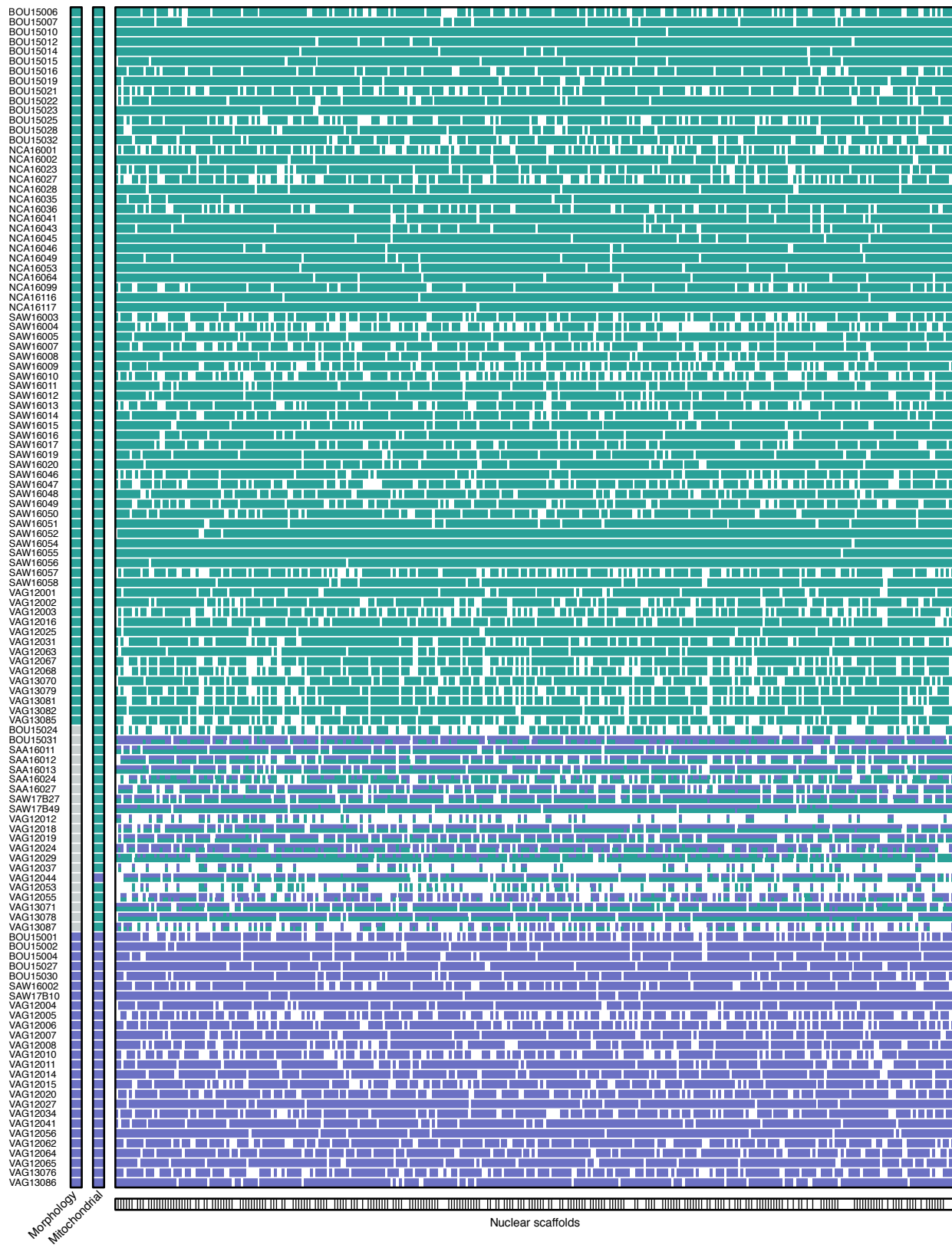


Supplementary Figure 8: Individual coancestry based on haplotype similarity.

Coancestry was investigated based on RAD loci with fineRADstructure (Malinsky *et al.* 2018). Heatmap colors indicate numbers of RAD loci with estimated shared coancestry. Individuals are listed on both axes in the same order, clustered according to the tree shown on top of the heatmap (Lawson *et al.* 2012). Note that even though *A. luzonensis* appears to have more shared coancestry with the South China Sea population of *A. marmorata* than with other populations, introgression between *A. luzonensis* and the South China Sea population of *A. marmorata* is not supported by D and f_4 statistics (Supplementary Table 10).

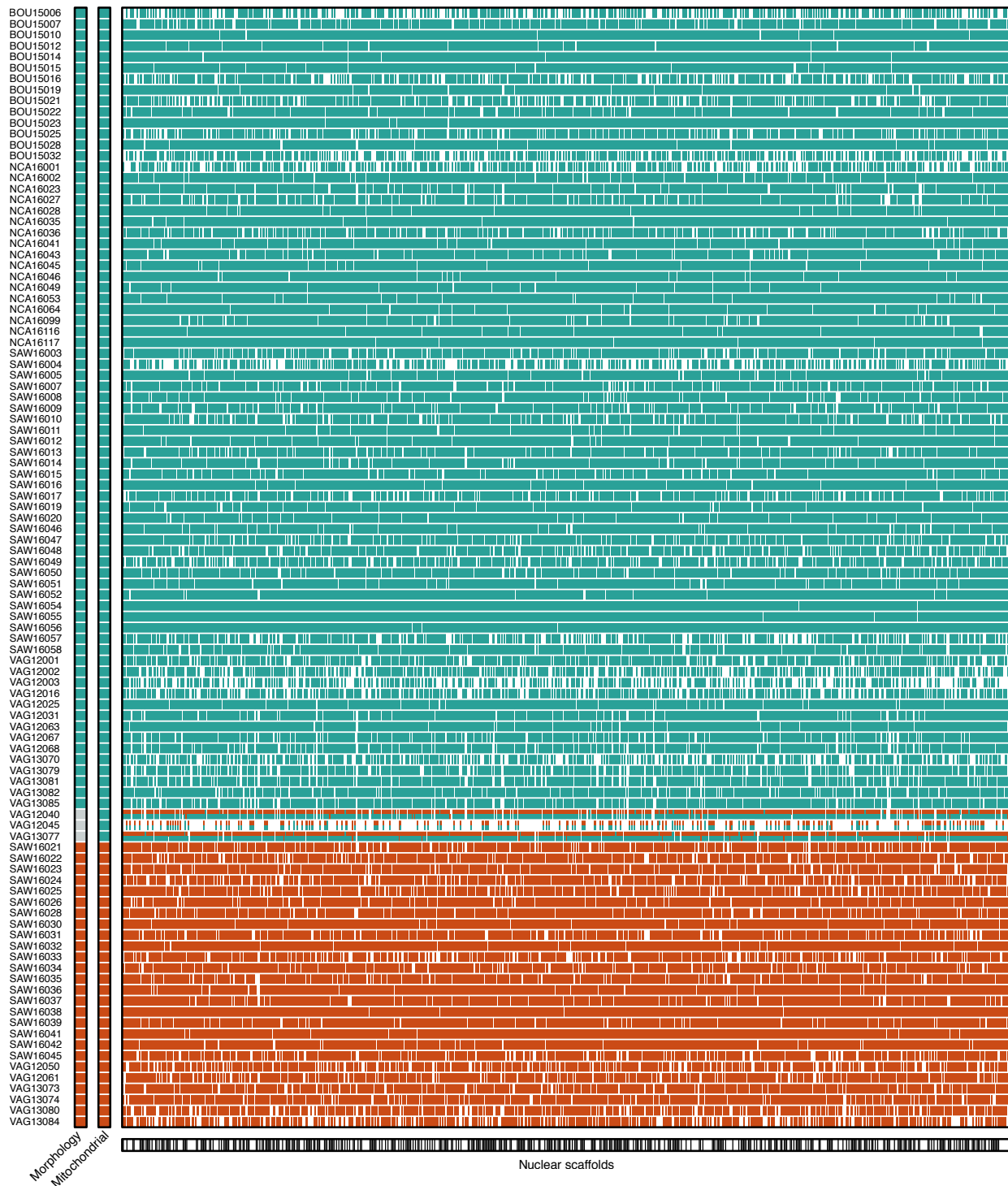


Supplementary Figure 9 (next page): Ancestry painting for *A. marmorata* and *A. megastoma*. Ancestry painting for 73 “core” *A. marmorata* individuals, 26 “core” *A. megastoma* individuals, and 20 recent hybrids between the two species. In addition, one *A. marmorata* individual (BOU15024) was included because it was initially assumed to be a hybrid based on morphological measurements (Supplementary Figure 3a); this assumption is not supported by the ancestry painting shown here. Horizontal bars indicate the genotypes at each of 302 sites fixed between the two parental species. White color indicates missing data. Heterozygous genotypes are shown with the top half in each bar matching the second parental species and vice versa. Light gray cells in the morphology column indicate individuals not classified into any of the “core” groups. The species’ color code is identical to Supplementary Figures 1-4.



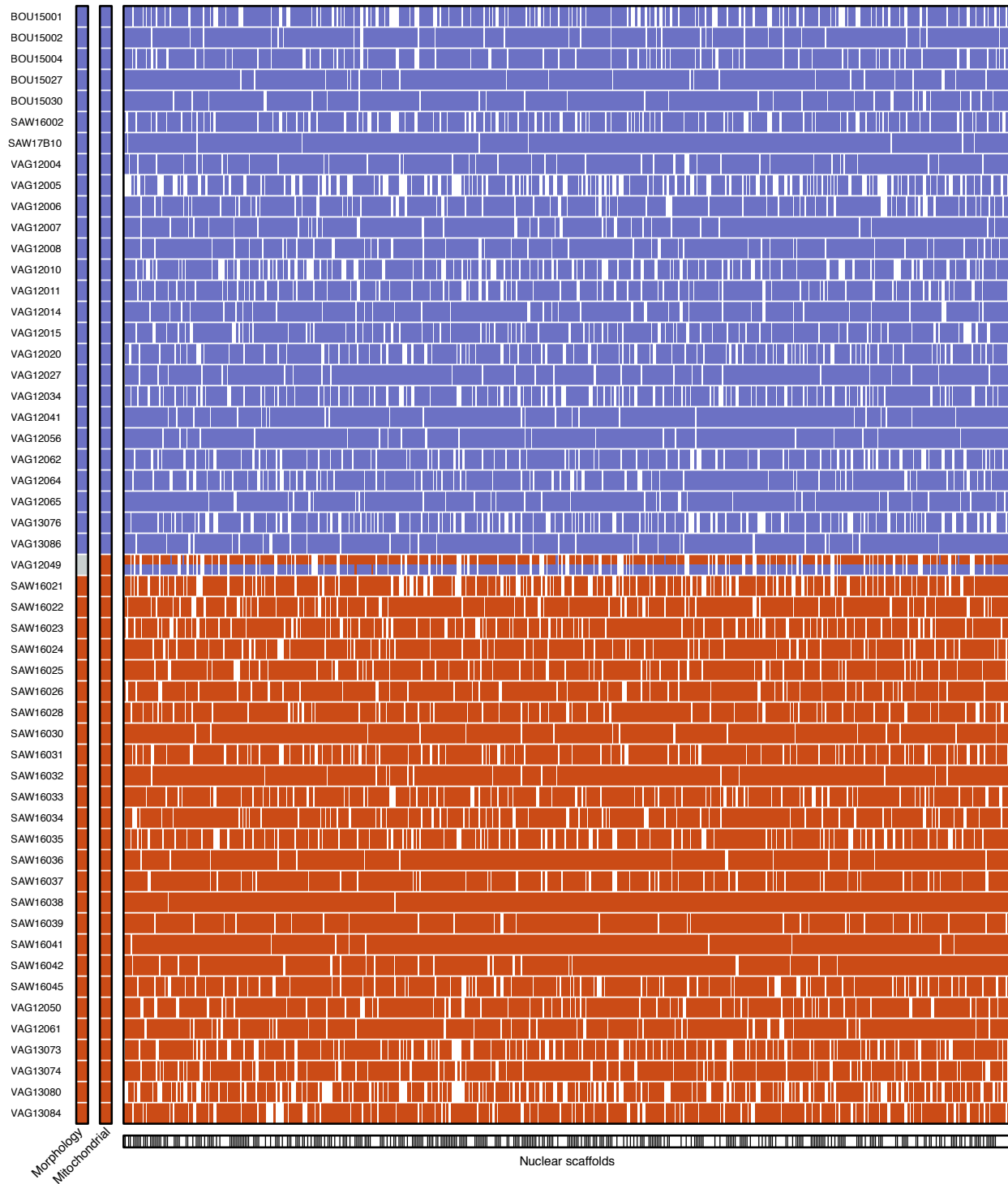
Supplementary Figure 10: Ancestry painting for *A. marmorata* and *A. obscura*.

Ancestry painting as in Supplementary Figure 9, but for 73 “core” *A. marmorata* individuals, 26 “core” *A. obscura* individuals, and 3 recent hybrids between the two species. Horizontal bars indicate the genotypes at each of 742 sites fixed between the two parental species.



Supplementary Figure 11: Ancestry painting for *A. megastoma* and *A. obscura*.

Ancestry painting as in Supplementary Figure 9, but for 26 “core” *A. megastoma* individuals, 26 “core” *A. obscura* individuals, and 1 recent hybrid between the two species. Horizontal bars indicate the genotypes at each of 525 sites fixed between the two parental species.



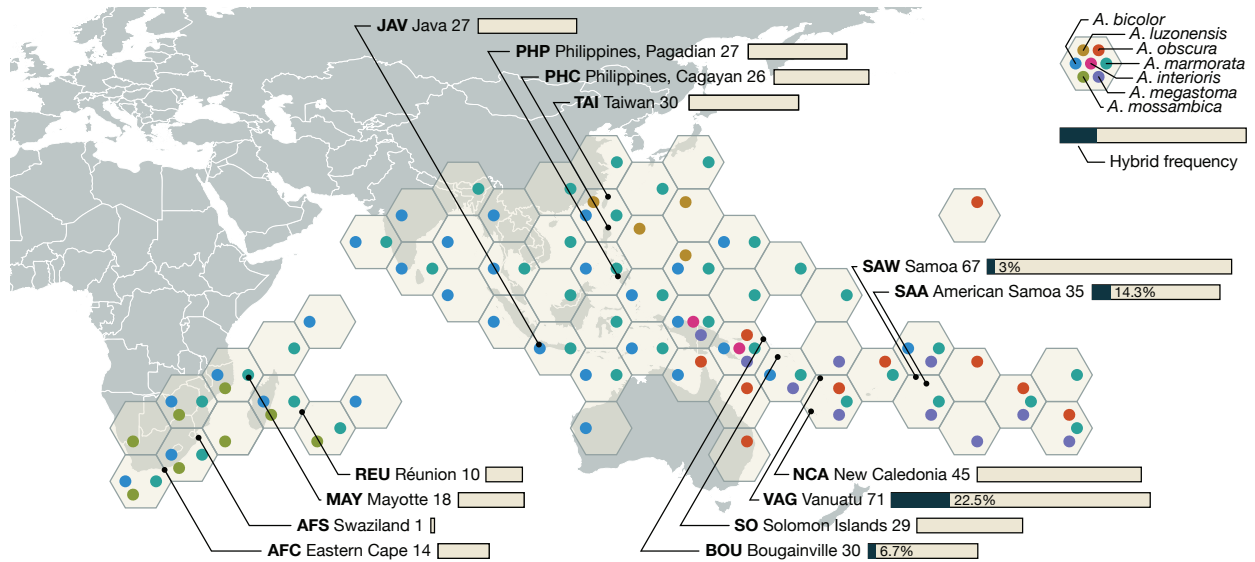
Supplementary Figure 12: Ancestry painting for *A. marmorata* and *A. interioris*.

Ancestry painting as in Supplementary Figure 9, but for 73 “core” *A. marmorata* individuals, 3 *A. interioris* individuals, and 1 recent hybrid between the two species. Horizontal bars indicate the genotypes at each of 429 sites fixed between the two parental species.



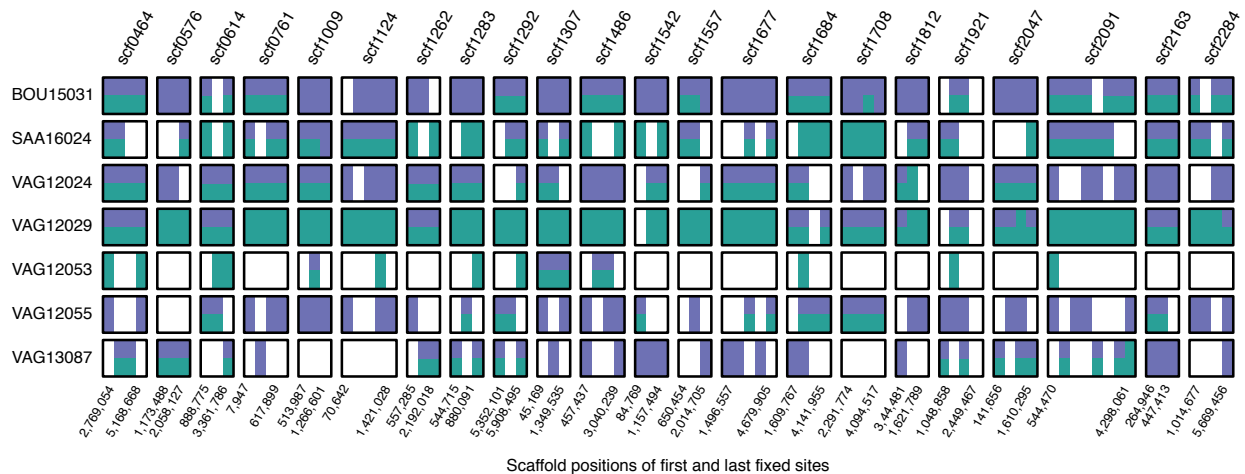
Supplementary Figure 13: Hybrid frequencies per sampling location.

Horizontal bars indicate the numbers of individuals collected at 14 sampling locations, counting only those with sufficient sequence quality that were used in genomic analyses. Hybrid frequencies are shown as black proportions of these bars.



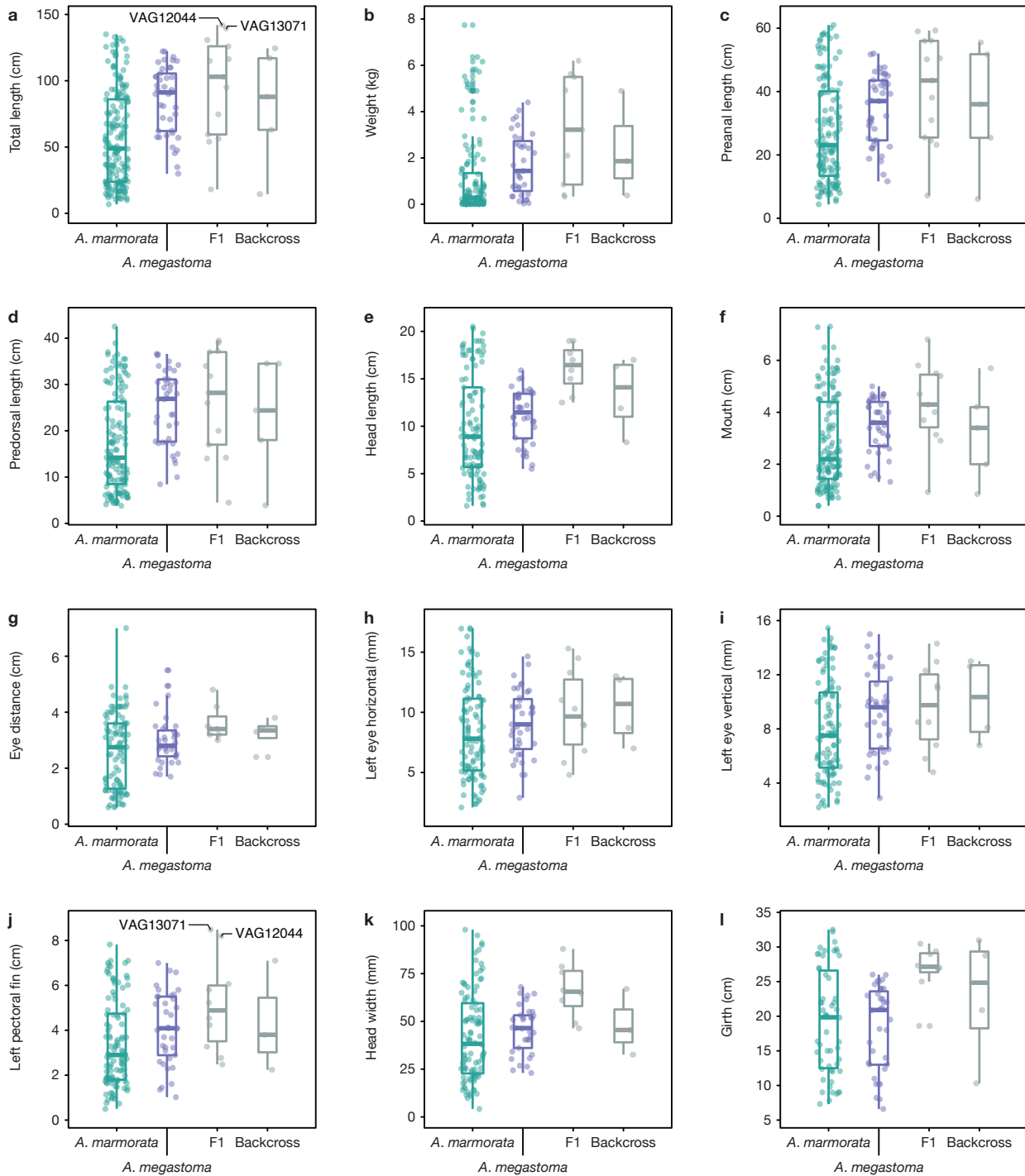
Supplementary Figure 14: Ancestry painting of long scaffolds for backcrossed hybrids between *A. marmorata* and *A. megastoma*.

Information shown here is a part of that presented in Supplementary Figure 9, focusing only on backcrossed hybrids and their genotypes on scaffolds with at least three fixed sites. Scaffold IDs are given on top and the positions of the first and last of the sites fixed on this scaffold are given below the ancestry painting. A single change from heterozygous to homozygous states or vice versa occurs six times among the seven individuals and two such changes on the same scaffold occur twice. With a mean distance of 1,708,024 bp and a maximum distance of 4,654,779 bp between the first and the last of the sites assessed on these 22 scaffolds, recombination breakpoints therefore appeared to be rare.

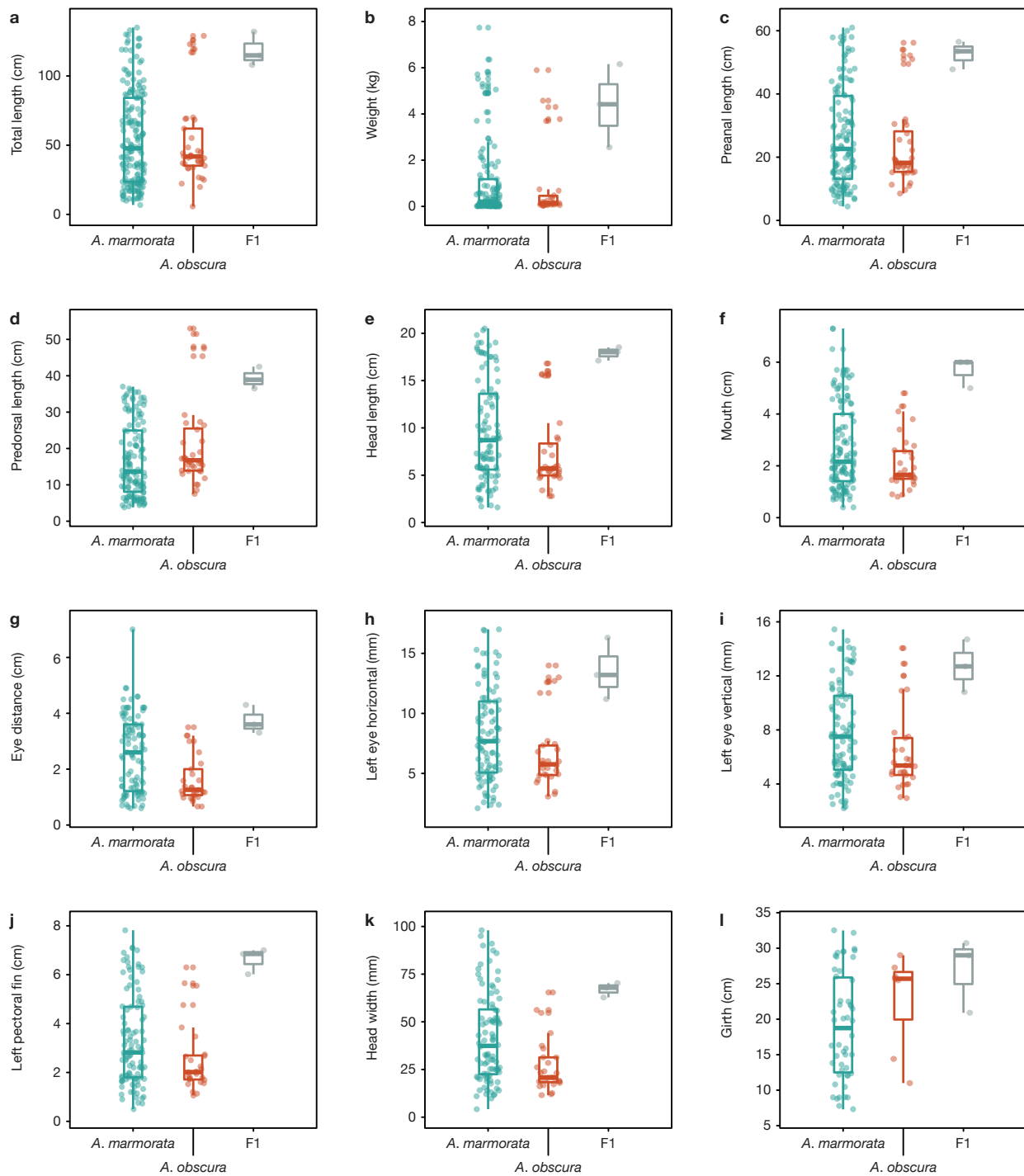


Supplementary Figure 15: Morphology of F1 and backcrossed hybrids between *A. marmorata* and *A. megastoma*.

Morphological measurements followed Watanabe *et al.* (2009). Labels indicate hybrids with transgressive phenotypes.

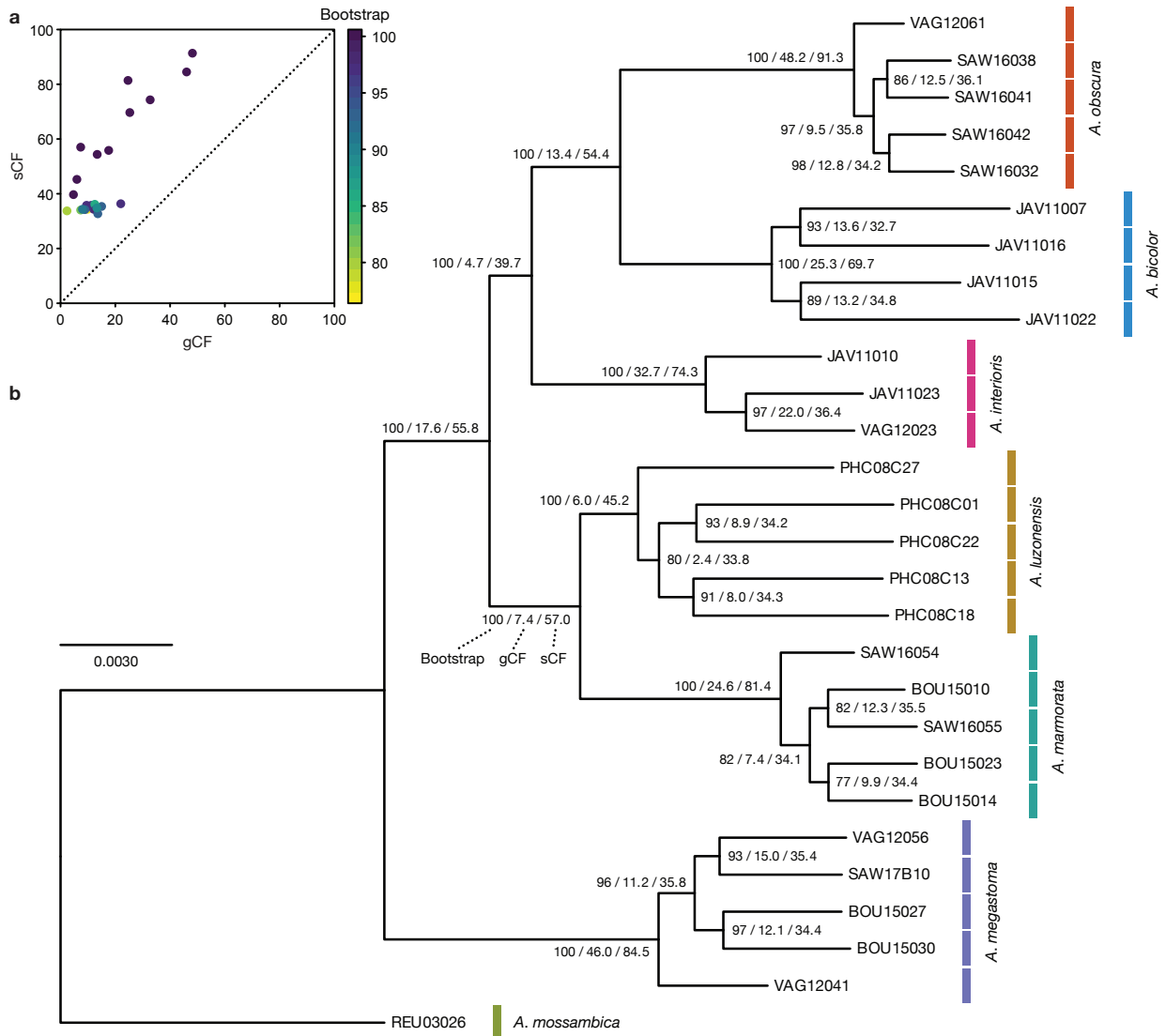


Supplementary Figure 16: Morphology of F1 hybrids between *A. marmorata* and *A. obscura*. Morphological measurements followed Watanabe *et al.* (2009).



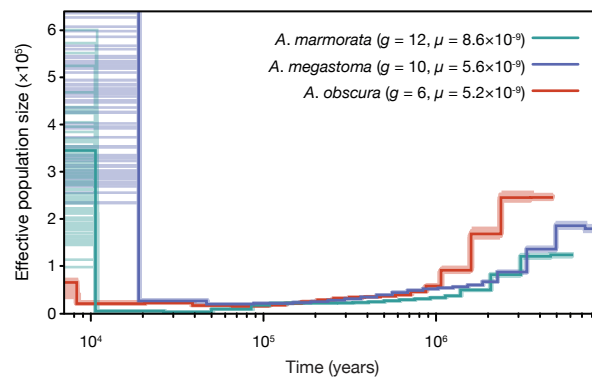
Supplementary Figure 17: Maximum-likelihood phylogenetic inference.

Phylogeny reconstructed with IQ-TREE (Nguyen *et al.* 2015) from 1,360 concatenated RAD loci without missing sequences and 20-40 variable sites per locus. Node labels indicate bootstrap support as well as per-locus (gCF) and per-site (sCF) concordance factors (Minh *et al.* 2018). For *A. marmorata*, *A. megastoma*, *A. luzonensis*, and *A. obscura*, only the five individuals with the lowest amount of missing data were used.



Supplementary Figure 18: Estimates of effective population size based on WGS data.

Changes in effective population size (N_e ; vertical axis) over time (the last 1 myr; horizontal axis) estimated using the pairwise sequential Markovian coalescent (PSMC). The PSMC was applied to WGS data of one individual for each of the three species *A. marmorata*, *A. megastoma*, and *A. obscura*. Estimates were based on assumed generation times (g) between 6 and 12 years and mutation rates (μ) between 5.2 and 8.6×10^{-9} mutations/site/generation. Semi-transparent colored lines correspond to 100 bootstrap replicates. For visualization purposes, the range of contemporary N_e values is truncated for *A. megastoma*; the maximum bootstrap value is $N_e = 2.0 \times 10^6$. Note that the apparent bottleneck pattern seen in all three species could be an artifact as it is expected even without actual population-size decline when parts of the genome are affected by introgression (Nielsen & Beaumont 2009).



3 Supplementary Tables

Supplementary Table 1: Sampled specimens.

Underlined specimens were included in the “core” group of individuals for *A. marmorata*, *A. megastoma*, and *A. obscura*, based on morphological measurements characteristic for the species. Species assignment is based on mitochondrial sequence data, and additionally on morphological measurements when these were available. Solomon Islands sampling sites SOK (Kolombangara), SOL (Kolombangara), SON (Nggatokae), SOR (Ranonga), and SOV (Vangunu) are jointly labeled “SO” in Figure 1, Supplementary Figure 4a, and descriptions in the text. The availability of morphological information is indicated in the morphology column. Unless specified otherwise, all specimens for which morphology information was available were included in morphological principal component analysis. ¹specimen removed due to read number below 600,000; ²specimen not included in morphological principal component analysis even though morphological information is available.

Specimen ID	Species	Site	Lat.	Lon.	Date	# reads	Morphology
AFC09022	<i>A. marmorata</i>	AFC	-33.615	25.667	2009/03/22	6,776,718	partial
AFC09027	<i>A. marmorata</i>	AFC	-33.615	25.667	2009/03/22	4,634,730	partial
AFC09028	<i>A. marmorata</i>	AFC	-33.615	25.667	2009/03/22	4,693,084	partial
AFC09038	<i>A. marmorata</i>	AFC	-33.615	25.667	2009/03/22	2,400,252	partial
AFC09040	<i>A. marmorata</i>	AFC	-33.615	25.667	2009/03/22	4,033,770	partial
AFC09042	<i>A. marmorata</i>	AFC	-33.615	25.667	2009/03/22	6,358,602	partial
AFC09046	<i>A. marmorata</i>	AFC	-33.615	25.667	2009/03/22	5,043,994	partial
AFC09050	<i>A. marmorata</i>	AFC	-33.615	25.667	2009/03/22	3,329,484	partial
AFC09131	<i>A. marmorata</i>	AFC	-33.046	26.662	2009/04/13	8,918,104	partial
AFC09136	<i>A. marmorata</i>	AFC	-33.046	26.662	2009/04/13	4,789,220	partial
AFC09169	<i>A. marmorata</i>	AFC	-33.615	25.667	2009/03/22	183,024 ¹	partial
AFC09192	<i>A. marmorata</i>	AFC	-33.615	25.667	2009/03/22	6,797,310	partial
AFC09250	<i>A. marmorata</i>	AFC	-33.615	25.667	2009/03/22	8,638,656	partial
AFC09269	<i>A. marmorata</i>	AFC	-33.615	25.667	2009/03/22	1,300,408	partial
AFC09282	<i>A. marmorata</i>	AFC	-33.615	25.667	2009/03/22	1,999,244	partial
AFS03068	<i>A. marmorata</i>	AFS	-26.713	31.979	2003/06/10	2,945,220	no
<u>BOU15001</u>	<i>A. megastoma</i>	BOU	-6.080	155.227	2015/04/04	10,524,168	yes
<u>BOU15002</u>	<i>A. megastoma</i>	BOU	-6.080	155.227	2015/04/04	8,753,268	yes
BOU15003	<i>A. megastoma</i>	BOU	-6.080	155.227	2015/04/04	12,765,510	yes
<u>BOU15004</u>	<i>A. megastoma</i>	BOU	-6.080	155.227	2015/04/04	8,763,996	yes
BOU15005	<i>A. megastoma</i>	BOU	-6.080	155.227	2015/04/05	6,346,666	yes ²
<u>BOU15006</u>	<i>A. marmorata</i>	BOU	-5.982	155.365	2015/04/09	9,606,592	yes
<u>BOU15007</u>	<i>A. marmorata</i>	BOU	-5.982	155.365	2015/04/09	7,034,622	yes
BOU15009	<i>A. marmorata</i>	BOU	-5.982	155.365	2015/04/10	14,488,768	yes
<u>BOU15010</u>	<i>A. marmorata</i>	BOU	-5.982	155.365	2015/04/10	6,070,202	yes
BOU15011	<i>A. marmorata</i>	BOU	-5.982	155.365	2015/04/10	12,244,134	yes
<u>BOU15012</u>	<i>A. marmorata</i>	BOU	-5.982	155.365	2015/04/10	3,809,812	yes
BOU15013	<i>A. marmorata</i>	BOU	-5.982	155.365	2015/04/10	2,920,434	yes ²
<u>BOU15014</u>	<i>A. marmorata</i>	BOU	-5.982	155.365	2015/04/10	4,069,002	yes
<u>BOU15015</u>	<i>A. marmorata</i>	BOU	-5.982	155.365	2015/04/10	4,142,280	yes
<u>BOU15016</u>	<i>A. marmorata</i>	BOU	-5.982	155.365	2015/04/10	8,406,776	yes

Supplementary Table 1 (continued)

Specimen ID	Species	Site	Lat.	Lon.	Date	# reads	Morphology
BOU15017	<i>A. marmorata</i>	BOU	-5.982	155.365	2015/04/11	6,477,100	yes
BOU15018	<i>A. marmorata</i>	BOU	-5.982	155.365	2015/04/12	16,346,782	yes
BOU15019	<i>A. marmorata</i>	BOU	-5.982	155.365	2015/04/12	3,438,714	yes
BOU15020	<i>A. marmorata</i>	BOU	-5.982	155.365	2015/04/12	4,981,164	yes
BOU15021	<i>A. marmorata</i>	BOU	-5.982	155.365	2015/04/12	1,490,284	yes
BOU15022	<i>A. marmorata</i>	BOU	-5.982	155.365	2015/04/13	2,212,684	yes
BOU15023	<i>A. marmorata</i>	BOU	-5.982	155.365	2015/04/13	4,800,140	yes
BOU15024	<i>A. marmorata</i>	BOU	-5.982	155.365	2015/04/12	12,316,926	yes
BOU15025	<i>A. marmorata</i>	BOU	-5.982	155.365	2015/04/14	1,569,478	yes
BOU15027	<i>A. megastoma</i>	BOU	-5.982	155.365	2015/04/14	4,104,044	yes
BOU15028	<i>A. marmorata</i>	BOU	-5.982	155.365	2015/04/14	3,353,376	yes
BOU15029	<i>A. marmorata</i>	BOU	-5.982	155.365	2015/04/14	715,048	yes
BOU15030	<i>A. megastoma</i>	BOU	-5.982	155.365	2015/04/14	2,705,922	yes
BOU15031	<i>A. marmorata</i>	BOU	-5.982	155.365	2015/04/14	4,074,020	yes
BOU15032	<i>A. marmorata</i>	BOU	-5.982	155.365	2015/04/12	8,950,896	yes
JAV11001	<i>A. marmorata</i>	JAV	-7.031	106.543	2011/06/NA	1,911,324	no
JAV11002	<i>A. marmorata</i>	JAV	-7.031	106.543	2011/06/NA	7,555,770	no
JAV11003	<i>A. marmorata</i>	JAV	-7.031	106.543	2011/06/NA	1,090,534	no
JAV11004	<i>A. marmorata</i>	JAV	-7.031	106.543	2011/06/NA	8,046,460	no
JAV11005	<i>A. marmorata</i>	JAV	-7.031	106.543	2011/06/NA	2,310,702	no
JAV11006	<i>A. marmorata</i>	JAV	-7.031	106.543	2011/06/NA	2,258,760	no
JAV11007	<i>A. bicolor</i>	JAV	-7.031	106.543	2011/06/NA	2,688,928	no
JAV11008	<i>A. marmorata</i>	JAV	-7.031	106.543	2011/06/NA	4,625,680	no
JAV11009	<i>A. marmorata</i>	JAV	-7.031	106.543	2011/06/NA	1,036,900	no
JAV11010	<i>A. interioris</i>	JAV	-7.031	106.543	2011/06/NA	6,425,584	no
JAV11011	<i>A. marmorata</i>	JAV	-7.031	106.543	2011/06/NA	11,251,146	no
JAV11012	<i>A. marmorata</i>	JAV	-7.031	106.543	2011/06/NA	6,491,164	no
JAV11013	<i>A. marmorata</i>	JAV	-7.031	106.543	2011/06/NA	5,513,280	no
JAV11014	<i>A. marmorata</i>	JAV	-7.031	106.543	2011/06/NA	9,067,812	no
JAV11015	<i>A. bicolor</i>	JAV	-7.031	106.543	2011/06/NA	1,363,586	no
JAV11016	<i>A. bicolor</i>	JAV	-7.031	106.543	2011/06/NA	2,046,036	no
JAV11017	<i>A. marmorata</i>	JAV	-7.031	106.543	2011/06/NA	1,643,646	no
JAV11018	<i>A. marmorata</i>	JAV	-7.031	106.543	2011/06/NA	7,677,132	no
JAV11019	<i>A. marmorata</i>	JAV	-7.031	106.543	2011/06/NA	738,182	no
JAV11020	<i>A. marmorata</i>	JAV	-7.031	106.543	2011/06/NA	272,336 ¹	no
JAV11021	<i>A. marmorata</i>	JAV	-7.031	106.543	2011/06/NA	4,231,276	no
JAV11022	<i>A. bicolor</i>	JAV	-7.031	106.543	2011/06/NA	11,179,098	no
JAV11023	<i>A. interioris</i>	JAV	-7.031	106.543	2011/06/NA	5,903,968	no
JAV11024	<i>A. marmorata</i>	JAV	-7.031	106.543	2011/06/NA	3,015,256	no
JAV11025	<i>A. marmorata</i>	JAV	-7.031	106.543	2011/06/NA	1,471,420	no
JAV11026	<i>A. marmorata</i>	JAV	-7.031	106.543	2011/06/NA	406,532 ¹	no
JAV11027	<i>A. marmorata</i>	JAV	-7.031	106.543	2011/06/NA	1,378,514	no
JAV11028	<i>A. marmorata</i>	JAV	-7.031	106.543	2011/06/NA	1,400,300	no
JAV11029	<i>A. marmorata</i>	JAV	-7.031	106.543	2011/06/NA	374,992 ¹	no
JAV11030	<i>A. marmorata</i>	JAV	-7.031	106.543	2011/06/NA	1,060,828	no
MAY03001	<i>A. marmorata</i>	MAY	-12.736	45.173	2003/11/09	3,635,428	no
MAY03003	<i>A. marmorata</i>	MAY	-12.736	45.173	2003/11/09	4,765,700	no

Supplementary Table 1 (continued)

Specimen ID	Species	Site	Lat.	Lon.	Date	# reads	Morphology
MAY03005	<i>A. marmorata</i>	MAY	-12.736	45.173	2003/11/09	4,158,434	no
MAY03006	<i>A. marmorata</i>	MAY	-12.736	45.173	2003/11/11	2,241,702	no
MAY03007	<i>A. marmorata</i>	MAY	-12.736	45.173	2003/11/09	1,725,756	no
MAY03009	<i>A. marmorata</i>	MAY	-12.736	45.173	2003/11/09	5,806,712	no
MAY03013	<i>A. marmorata</i>	MAY	-12.736	45.173	2003/11/09	2,181,048	no
MAY03017	<i>A. marmorata</i>	MAY	-12.736	45.173	2003/11/11	3,854,094	no
MAY03018	<i>A. marmorata</i>	MAY	-12.736	45.173	2003/11/09	2,476,808	no
MAY03019	<i>A. marmorata</i>	MAY	-12.736	45.173	2003/11/09	2,426,188	no
MAY03020	<i>A. marmorata</i>	MAY	-12.736	45.173	2003/11/09	1,422,048	no
MAY03021	<i>A. marmorata</i>	MAY	-12.736	45.173	2003/11/11	3,243,600	no
MAY03022	<i>A. marmorata</i>	MAY	-12.736	45.173	2003/11/11	4,022,620	no
MAY03023	<i>A. marmorata</i>	MAY	-12.736	45.173	2003/11/09	3,288,808	no
MAY03024	<i>A. marmorata</i>	MAY	-12.736	45.173	2003/11/11	3,669,560	no
MAY03025	<i>A. marmorata</i>	MAY	-12.736	45.173	2003/11/09	3,129,952	no
MAY03027	<i>A. marmorata</i>	MAY	-12.736	45.173	2003/11/11	2,452,074	no
MAY03028	<i>A. marmorata</i>	MAY	-12.736	45.173	2003/11/11	2,337,216	no
<u>NCA16001</u>	<i>A. marmorata</i>	NCA	-21.305	165.025	2016/07/27	1,463,126	yes
<u>NCA16002</u>	<i>A. marmorata</i>	NCA	-21.305	165.025	2016/07/27	3,965,922	yes
NCA16003	<i>A. marmorata</i>	NCA	-21.305	165.025	2016/07/27	885,746	yes
NCA16004	<i>A. marmorata</i>	NCA	-21.305	165.025	2016/07/27	3,202,396	partial
NCA16005	<i>A. marmorata</i>	NCA	-21.305	165.025	2016/07/27	3,506,424	partial
NCA16006	<i>A. marmorata</i>	NCA	-21.305	165.025	2016/07/27	6,456,506	partial
NCA16007	<i>A. marmorata</i>	NCA	-21.305	165.025	2016/07/27	4,056,230	partial
NCA16008	<i>A. marmorata</i>	NCA	-21.305	165.025	2016/07/27	2,850,918	partial
NCA16009	<i>A. marmorata</i>	NCA	-21.305	165.025	2016/07/27	4,937,224	partial
NCA16010	<i>A. marmorata</i>	NCA	-21.305	165.025	2016/07/27	4,202,782	no
NCA16011	<i>A. marmorata</i>	NCA	-21.305	165.025	2016/07/27	4,716,276	no
NCA16014	<i>A. marmorata</i>	NCA	-21.305	165.025	2016/07/27	4,179,094	partial
NCA16015	<i>A. obscura</i>	NCA	-21.305	165.025	2016/07/27	1,913,782	partial
NCA16018	<i>A. marmorata</i>	NCA	-21.302	165.029	2016/07/28	7,270,454	partial
NCA16020	<i>A. marmorata</i>	NCA	-21.302	165.029	2016/07/28	6,578,652	partial
NCA16021	<i>A. marmorata</i>	NCA	-21.302	165.029	2016/07/28	3,054,210	partial
NCA16022	<i>A. marmorata</i>	NCA	-21.302	165.029	2016/07/28	2,739,816	partial
<u>NCA16023</u>	<i>A. marmorata</i>	NCA	-21.302	165.029	2016/07/28	6,474,304	yes
NCA16024	<i>A. marmorata</i>	NCA	-21.302	165.029	2016/07/28	6,085,708	partial
NCA16025	<i>A. marmorata</i>	NCA	-21.302	165.029	2016/07/28	1,234,354	partial
<u>NCA16027</u>	<i>A. marmorata</i>	NCA	-21.302	165.029	2016/07/28	7,005,388	yes
<u>NCA16028</u>	<i>A. marmorata</i>	NCA	-21.302	165.029	2016/07/28	5,545,016	yes
NCA16030	<i>A. marmorata</i>	NCA	-21.302	165.029	2016/07/28	4,546,024	partial
NCA16031	<i>A. marmorata</i>	NCA	-20.491	164.258	2016/08/02	4,881,226	partial
NCA16034	<i>A. marmorata</i>	NCA	-20.491	164.258	2016/08/02	1,596,114	partial
<u>NCA16035</u>	<i>A. marmorata</i>	NCA	-20.491	164.258	2016/08/02	4,372,818	yes
<u>NCA16036</u>	<i>A. marmorata</i>	NCA	-20.491	164.258	2016/08/02	1,913,554	yes
NCA16039	<i>A. marmorata</i>	NCA	-20.491	164.258	2016/08/02	1,995,702	partial
<u>NCA16041</u>	<i>A. marmorata</i>	NCA	-20.491	164.258	2016/08/02	3,543,860	yes
NCA16042	<i>A. marmorata</i>	NCA	-20.491	164.258	2016/08/02	5,045,656	partial
<u>NCA16043</u>	<i>A. marmorata</i>	NCA	-20.491	164.258	2016/08/02	2,637,300	yes

Supplementary Table 1 (continued)

Specimen ID	Species	Site	Lat.	Lon.	Date	# reads	Morphology
NCA16044	<i>A. marmorata</i>	NCA	-20.491	164.258	2016/08/02	5,381,242	partial
<u>NCA16045</u>	<i>A. marmorata</i>	NCA	-20.491	164.258	2016/08/02	3,630,832	yes
<u>NCA16046</u>	<i>A. marmorata</i>	NCA	-22.111	166.423	2016/08/09	4,248,040	yes
<u>NCA16049</u>	<i>A. marmorata</i>	NCA	-22.111	166.423	2016/08/09	4,212,004	yes
<u>NCA16053</u>	<i>A. marmorata</i>	NCA	-22.136	166.367	2016/08/09	3,653,266	yes
NCA16056	<i>A. marmorata</i>	NCA	-22.136	166.367	2016/08/09	6,829,734	partial
NCA16063	<i>A. marmorata</i>	NCA	-22.136	166.367	2016/08/09	931,716	yes ²
<u>NCA16064</u>	<i>A. marmorata</i>	NCA	-22.136	166.367	2016/08/09	4,739,518	yes
NCA16084	<i>A. marmorata</i>	NCA	-21.749	166.084	2016/08/11	5,874,506	yes
<u>NCA16099</u>	<i>A. marmorata</i>	NCA	-21.749	166.084	2016/08/11	7,063,454	yes
NCA16110	<i>A. marmorata</i>	NCA	-22.035	166.208	2016/08/18	4,691,496	partial
<u>NCA16116</u>	<i>A. marmorata</i>	NCA	-22.035	166.208	2016/08/18	4,702,550	yes
<u>NCA16117</u>	<i>A. marmorata</i>	NCA	-22.035	166.208	2016/08/18	4,790,108	yes
NCA16120	<i>A. marmorata</i>	NCA	-22.038	166.220	2016/08/18	6,610,270	partial
PHC08C01	<i>A. luzonensis</i>	PHC	18.355	121.634	2008/09/08	4,385,110	no
PHC08C02	<i>A. luzonensis</i>	PHC	18.355	121.634	2008/09/08	2,067,082	no
PHC08C03	<i>A. luzonensis</i>	PHC	18.355	121.634	2008/09/08	6,693,386	no
PHC08C04	<i>A. luzonensis</i>	PHC	18.355	121.634	2008/09/08	7,107,044	no
PHC08C05	<i>A. luzonensis</i>	PHC	18.355	121.634	2008/09/08	8,824,514	no
PHC08C06	<i>A. luzonensis</i>	PHC	18.355	121.634	2008/09/08	9,469,068	no
PHC08C07	<i>A. luzonensis</i>	PHC	18.355	121.634	2008/09/08	6,707,486	no
PHC08C08	<i>A. luzonensis</i>	PHC	18.355	121.634	2008/09/08	176,638 ¹	no
PHC08C09	<i>A. luzonensis</i>	PHC	18.355	121.634	2008/09/08	6,465,580	no
PHC08C10	<i>A. marmorata</i>	PHC	18.355	121.634	2008/09/08	6,767,542	no
PHC08C11	<i>A. luzonensis</i>	PHC	18.355	121.634	2008/09/08	11,154,032	no
PHC08C12	<i>A. luzonensis</i>	PHC	18.355	121.634	2008/09/08	6,774,270	no
PHC08C13	<i>A. luzonensis</i>	PHC	18.355	121.634	2008/09/08	5,412,554	no
PHC08C15	<i>A. luzonensis</i>	PHC	18.355	121.634	2008/09/08	3,325,444	no
PHC08C16	<i>A. luzonensis</i>	PHC	18.355	121.634	2008/09/08	3,157,590	no
PHC08C17	<i>A. luzonensis</i>	PHC	18.355	121.634	2008/09/08	35,658 ¹	no
PHC08C18	<i>A. luzonensis</i>	PHC	18.355	121.634	2008/09/08	5,386,382	no
PHC08C19	<i>A. marmorata</i>	PHC	18.355	121.634	2008/09/08	301,666 ¹	no
PHC08C20	<i>A. marmorata</i>	PHC	18.355	121.634	2008/09/08	4,533,308	no
PHC08C21	<i>A. marmorata</i>	PHC	18.355	121.634	2008/09/08	50,532 ¹	no
PHC08C22	<i>A. luzonensis</i>	PHC	18.355	121.634	2008/09/08	6,089,432	no
PHC08C23	<i>A. luzonensis</i>	PHC	18.355	121.634	2008/09/08	58,386 ¹	no
PHC08C24	<i>A. luzonensis</i>	PHC	18.355	121.634	2008/09/08	778,644	no
PHC08C25	<i>A. marmorata</i>	PHC	18.355	121.634	2008/09/08	3,036,944	no
PHC08C26	<i>A. luzonensis</i>	PHC	18.355	121.634	2008/09/08	8,041,488	no
PHC08C27	<i>A. luzonensis</i>	PHC	18.355	121.634	2008/09/08	3,149,128	no
PHC08C28	<i>A. luzonensis</i>	PHC	18.355	121.634	2008/09/08	1,770,520	no
PHC08C29	<i>A. luzonensis</i>	PHC	18.355	121.634	2008/09/08	1,787,774	no
PHC08P20	<i>A. marmorata</i>	PHC	18.355	121.634	2008/09/08	3,961,354	no
PHC08P22	<i>A. marmorata</i>	PHC	18.355	121.634	2008/09/08	4,094,926	no
PHC08P23	<i>A. marmorata</i>	PHC	18.355	121.634	2008/09/08	5,894,520	no
PHP14P01	<i>A. marmorata</i>	PHP	7.835	123.509	2014/02/14	4,783,294	no
PHP14P02	<i>A. marmorata</i>	PHP	7.835	123.509	2014/02/14	5,889,742	no

Supplementary Table 1 (continued)

Specimen ID	Species	Site	Lat.	Lon.	Date	# reads	Morphology
PHP14P03	<i>A. marmorata</i>	PHP	7.835	123.509	2014/02/14	6,371,944	no
PHP14P04	<i>A. marmorata</i>	PHP	7.835	123.509	2014/02/14	4,141,222	no
PHP14P05	<i>A. marmorata</i>	PHP	7.835	123.509	2014/02/14	5,544,038	no
PHP14P06	<i>A. marmorata</i>	PHP	7.835	123.509	2014/02/14	2,983,648	no
PHP14P07	<i>A. marmorata</i>	PHP	7.835	123.509	2014/02/14	4,178,472	no
PHP14P08	<i>A. marmorata</i>	PHP	7.835	123.509	2014/02/14	3,034,380	no
PHP14P09	<i>A. marmorata</i>	PHP	7.835	123.509	2014/02/14	4,966,488	no
PHP14P10	<i>A. marmorata</i>	PHP	7.835	123.509	2014/02/14	5,286,256	no
PHP14P11	<i>A. marmorata</i>	PHP	7.835	123.509	2014/02/14	6,830,854	no
PHP14P12	<i>A. marmorata</i>	PHP	7.835	123.509	2014/02/14	3,904,972	no
PHP14P13	<i>A. marmorata</i>	PHP	7.835	123.509	2014/02/14	3,827,650	no
PHP14P14	<i>A. marmorata</i>	PHP	7.835	123.509	2014/02/14	5,505,830	no
PHP14P15	<i>A. marmorata</i>	PHP	7.835	123.509	2014/02/14	2,567,042	no
PHP14P16	<i>A. marmorata</i>	PHP	7.835	123.509	2014/02/14	770,766	no
PHP14P17	<i>A. marmorata</i>	PHP	7.835	123.509	2014/02/14	4,868,568	no
PHP14P18	<i>A. marmorata</i>	PHP	7.835	123.509	2014/02/14	4,753,592	no
PHP14P19	<i>A. marmorata</i>	PHP	7.835	123.509	2014/02/14	4,047,700	no
PHP14P21	<i>A. marmorata</i>	PHP	7.835	123.509	2014/02/14	1,969,502	no
PHP14P24	<i>A. marmorata</i>	PHP	7.835	123.509	2014/02/14	6,280,804	no
PHP14P25	<i>A. marmorata</i>	PHP	7.835	123.509	2014/02/14	6,543,116	no
PHP14P26	<i>A. marmorata</i>	PHP	7.835	123.509	2014/02/14	7,983,072	no
PHP14P27	<i>A. marmorata</i>	PHP	7.835	123.509	2014/02/14	9,373,838	no
PHP14P28	<i>A. marmorata</i>	PHP	7.835	123.509	2014/02/14	8,095,200	no
PHP14P29	<i>A. marmorata</i>	PHP	7.835	123.509	2014/02/14	6,411,040	no
PHP14P30	<i>A. marmorata</i>	PHP	7.835	123.509	2014/02/14	6,390,714	no
REU01002	<i>A. marmorata</i>	REU	-20.983	55.685	2001/02/05	3,454,510	no
REU01014	<i>A. marmorata</i>	REU	-20.983	55.685	2001/02/05	2,737,978	no
REU01016	<i>A. marmorata</i>	REU	-20.983	55.685	2001/02/05	1,923,798	no
REU03004	<i>A. marmorata</i>	REU	-20.983	55.685	2003/11/04	3,841,652	no
REU03008	<i>A. marmorata</i>	REU	-20.983	55.685	2003/11/04	3,107,032	no
REU03010	<i>A. marmorata</i>	REU	-20.912	55.630	2003/11/04	4,676,038	no
REU03011	<i>A. marmorata</i>	REU	-20.983	55.685	2003/11/04	4,215,150	no
REU03012	<i>A. marmorata</i>	REU	-20.912	55.630	2003/11/04	8,125,876	no
REU03015	<i>A. marmorata</i>	REU	-20.912	55.630	2003/11/04	3,492,136	no
REU03026	<i>A. mossambica</i>	REU	-20.912	55.630	2003/11/04	3,450,942	no
SAA16001	<i>A. marmorata</i>	SAA	-14.304	170.816	2016/08/18	7,116,822	partial
SAA16002	<i>A. marmorata</i>	SAA	-14.304	170.816	2016/08/19	7,015,912	partial
SAA16003	<i>A. marmorata</i>	SAA	-14.304	170.816	2016/08/18	3,522,172	partial
SAA16004	<i>A. marmorata</i>	SAA	-14.304	170.816	2016/08/18	3,740,088	partial
SAA16005	<i>A. marmorata</i>	SAA	-14.304	170.816	2016/08/18	18,305,104	no
SAA16006	<i>A. marmorata</i>	SAA	-14.304	170.816	2016/08/18	6,540,862	partial
SAA16007	<i>A. marmorata</i>	SAA	-14.304	170.816	2016/08/18	3,685,986	partial
SAA16008	<i>A. marmorata</i>	SAA	-14.304	170.816	2016/08/18	5,828,106	partial
SAA16009	<i>A. marmorata</i>	SAA	-14.304	170.816	2016/08/18	5,979,728	partial
SAA16010	<i>A. marmorata</i>	SAA	-14.304	170.816	2016/08/18	1,269,150	partial
SAA16011	<i>A. marmorata</i>	SAA	-14.304	170.816	2016/08/18	3,557,730	partial
SAA16012	<i>A. marmorata</i>	SAA	-14.304	170.816	2016/08/18	7,436,372	partial

Supplementary Table 1 (continued)

Specimen ID	Species	Site	Lat.	Lon.	Date	# reads	Morphology
SAA16013	<i>A. marmorata</i>	SAA	-14.304	170.816	2016/08/18	2,752,316	partial
SAA16014	<i>A. megastoma</i>	SAA	-14.332	170.793	2016/08/19	3,018,560	partial
SAA16015	<i>A. megastoma</i>	SAA	-14.332	170.793	2016/08/19	5,022,542	partial
SAA16016	<i>A. marmorata</i>	SAA	-14.332	170.793	2016/08/19	7,564,634	partial
SAA16017	<i>A. marmorata</i>	SAA	-14.332	170.793	2016/08/19	881,890	partial
SAA16018	<i>A. marmorata</i>	SAA	-14.332	170.793	2016/08/19	6,003,128	partial
SAA16019	<i>A. marmorata</i>	SAA	-14.332	170.793	2016/08/19	1,456,892	partial
SAA16020	<i>A. marmorata</i>	SAA	-14.332	170.793	2016/08/19	4,554,650	partial
SAA16021	<i>A. marmorata</i>	SAA	-14.332	170.793	2016/08/19	1,433,016	partial
SAA16022	<i>A. marmorata</i>	SAA	-14.332	170.793	2016/08/19	5,381,110	partial
SAA16023	<i>A. marmorata</i>	SAA	-14.304	170.816	2016/08/20	5,759,626	partial
SAA16024	<i>A. marmorata</i>	SAA	-14.304	170.816	2016/08/20	7,833,688	partial
SAA16025	<i>A. marmorata</i>	SAA	-14.304	170.816	2016/08/20	3,393,344	partial
SAA16026	<i>A. marmorata</i>	SAA	-14.304	170.816	2016/08/20	6,973,470	partial
SAA16027	<i>A. marmorata</i>	SAA	-14.304	170.816	2016/08/20	8,727,666	partial
SAA16028	<i>A. marmorata</i>	SAA	-14.304	170.816	2016/08/20	12,240 ¹	partial
SAA16029	<i>A. marmorata</i>	SAA	-14.304	170.816	2016/08/20	9,310,208	partial
SAA16030	<i>A. marmorata</i>	SAA	-14.304	170.816	2016/08/20	4,058,900	partial
SAA16031	<i>A. marmorata</i>	SAA	-14.304	170.816	2016/08/20	4,624,388	partial
SAA16032	<i>A. marmorata</i>	SAA	-14.304	170.816	2016/08/20	5,149,616	partial
SAA16033	<i>A. marmorata</i>	SAA	-14.304	170.816	2016/08/20	266,538 ¹	partial
SAA16034	<i>A. marmorata</i>	SAA	-14.304	170.816	2016/08/20	7,292,490	partial
SAA16035	<i>A. marmorata</i>	SAA	-14.304	170.816	2016/08/20	6,989,336	partial
SAA16036	<i>A. marmorata</i>	SAA	-14.304	170.816	2016/08/20	7,190,652	partial
SAA16037	<i>A. marmorata</i>	SAA	-14.304	170.816	2016/08/20	58,520 ¹	partial
SAA16038	<i>A. marmorata</i>	SAA	-14.304	170.816	2016/08/20	3,566,502	partial
SAW16001	<i>A. marmorata</i>	SAW	-13.836	171.765	2016/08/16	2,750,534	yes
<u>SAW16002</u>	<i>A. megastoma</i>	SAW	-13.904	171.575	2016/08/16	8,122,668	yes
<u>SAW16003</u>	<i>A. marmorata</i>	SAW	-13.874	171.651	2016/08/31	7,612,856	yes
<u>SAW16004</u>	<i>A. marmorata</i>	SAW	-13.874	171.651	2016/08/31	1,578,510	yes
<u>SAW16005</u>	<i>A. marmorata</i>	SAW	-13.874	171.651	2016/08/31	5,100,238	yes
<u>SAW16006</u>	<i>A. marmorata</i>	SAW	-13.874	171.651	2016/08/31	47,706 ¹	yes ²
<u>SAW16007</u>	<i>A. marmorata</i>	SAW	-13.874	171.651	2016/08/31	2,616,202	yes
<u>SAW16008</u>	<i>A. marmorata</i>	SAW	-13.874	171.651	2016/08/31	3,802,620	yes
<u>SAW16009</u>	<i>A. marmorata</i>	SAW	-13.874	171.651	2016/08/31	2,947,904	yes
<u>SAW16010</u>	<i>A. marmorata</i>	SAW	-13.874	171.651	2016/08/31	8,468,370	yes
<u>SAW16011</u>	<i>A. marmorata</i>	SAW	-13.874	171.651	2016/08/31	5,449,034	yes
<u>SAW16012</u>	<i>A. marmorata</i>	SAW	-13.874	171.651	2016/08/31	4,835,336	yes
<u>SAW16013</u>	<i>A. marmorata</i>	SAW	-13.874	171.651	2016/08/31	7,091,060	yes
<u>SAW16014</u>	<i>A. marmorata</i>	SAW	-13.874	171.651	2016/08/31	4,780,360	yes
<u>SAW16015</u>	<i>A. marmorata</i>	SAW	-13.874	171.651	2016/08/31	3,078,620	yes
<u>SAW16016</u>	<i>A. marmorata</i>	SAW	-13.874	171.651	2016/08/31	4,916,950	yes
<u>SAW16017</u>	<i>A. marmorata</i>	SAW	-13.874	171.651	2016/08/31	7,284,612	yes
<u>SAW16018</u>	<i>A. marmorata</i>	SAW	-13.874	171.651	2016/08/31	25,368 ¹	yes ²
<u>SAW16019</u>	<i>A. marmorata</i>	SAW	-13.874	171.651	2016/08/31	3,451,030	yes
<u>SAW16020</u>	<i>A. marmorata</i>	SAW	-13.874	171.651	2016/08/31	3,764,650	yes
<u>SAW16021</u>	<i>A. obscura</i>	SAW	-14.025	171.431	2016/09/01	8,156,690	yes

Supplementary Table 1 (continued)

Specimen ID	Species	Site	Lat.	Lon.	Date	# reads	Morphology
SAW16022	<i>A. obscura</i>	SAW	-14.025	171.431	2016/09/01	3,012,538	yes
SAW16023	<i>A. obscura</i>	SAW	-14.025	171.431	2016/09/01	4,522,382	yes
SAW16024	<i>A. obscura</i>	SAW	-14.025	171.431	2016/09/01	3,250,488	yes
SAW16025	<i>A. obscura</i>	SAW	-14.025	171.431	2016/09/01	2,821,526	yes
SAW16026	<i>A. obscura</i>	SAW	-14.025	171.431	2016/09/01	3,173,878	yes
SAW16027	<i>A. obscura</i>	SAW	-14.025	171.431	2016/09/01	2,975,754	yes ²
SAW16028	<i>A. obscura</i>	SAW	-14.025	171.431	2016/09/01	2,657,622	yes
SAW16029	<i>A. obscura</i>	SAW	-14.025	171.431	2016/09/01	399,402 ¹	yes ²
SAW16030	<i>A. obscura</i>	SAW	-14.025	171.431	2016/09/01	6,092,366	yes
SAW16031	<i>A. obscura</i>	SAW	-14.025	171.431	2016/09/01	2,508,612	yes
SAW16032	<i>A. obscura</i>	SAW	-14.025	171.431	2016/09/01	4,808,164	yes
SAW16033	<i>A. obscura</i>	SAW	-14.025	171.431	2016/09/01	6,932,430	yes
SAW16034	<i>A. obscura</i>	SAW	-14.025	171.431	2016/09/01	2,710,582	yes
SAW16035	<i>A. obscura</i>	SAW	-14.025	171.431	2016/09/01	7,565,924	yes
SAW16036	<i>A. obscura</i>	SAW	-14.025	171.431	2016/09/01	6,343,662	yes
SAW16037	<i>A. obscura</i>	SAW	-14.025	171.431	2016/09/01	7,089,804	yes
SAW16038	<i>A. obscura</i>	SAW	-14.025	171.431	2016/09/01	5,230,320	yes
SAW16039	<i>A. obscura</i>	SAW	-14.025	171.431	2016/09/01	4,170,504	yes
SAW16040	<i>A. obscura</i>	SAW	-14.025	171.431	2016/09/01	9,956,058	yes ²
SAW16041	<i>A. obscura</i>	SAW	-14.025	171.431	2016/09/01	5,220,798	yes
SAW16042	<i>A. obscura</i>	SAW	-14.025	171.431	2016/09/01	3,907,842	yes
SAW16043	<i>A. obscura</i>	SAW	-14.025	171.431	2016/09/01	451,282 ¹	yes
SAW16044	<i>A. obscura</i>	SAW	-14.025	171.431	2016/09/01	696,640	yes
SAW16045	<i>A. obscura</i>	SAW	-14.025	171.431	2016/09/01	3,211,904	yes
SAW16046	<i>A. marmorata</i>	SAW	-13.876	171.639	2016/09/01	6,048,220	yes
SAW16047	<i>A. marmorata</i>	SAW	-13.876	171.639	2016/09/02	7,660,116	yes
SAW16048	<i>A. marmorata</i>	SAW	-13.876	171.639	2016/09/02	2,626,456	yes
SAW16049	<i>A. marmorata</i>	SAW	-13.876	171.639	2016/09/02	7,328,702	yes
SAW16050	<i>A. marmorata</i>	SAW	-13.876	171.639	2016/09/02	3,279,138	yes
SAW16051	<i>A. marmorata</i>	SAW	-13.876	171.639	2016/09/02	2,574,796	yes
SAW16052	<i>A. marmorata</i>	SAW	-13.876	171.639	2016/09/02	3,483,700	yes
SAW16054	<i>A. marmorata</i>	SAW	-13.876	171.639	2016/09/02	5,107,548	yes
SAW16055	<i>A. marmorata</i>	SAW	-13.876	171.639	2016/09/02	5,252,892	yes
SAW16056	<i>A. marmorata</i>	SAW	-13.876	171.639	2016/09/02	5,137,008	yes
SAW16057	<i>A. marmorata</i>	SAW	-13.876	171.639	2016/09/02	1,370,838	yes
SAW16058	<i>A. marmorata</i>	SAW	-13.876	171.639	2016/09/02	3,511,122	yes
SAW17B02	<i>A. marmorata</i>	SAW	-13.968	171.862	2017/02/23	5,261,166	no
SAW17B10	<i>A. megastoma</i>	SAW	-13.968	171.862	2017/02/24	5,240,736	yes
SAW17B13	<i>A. megastoma</i>	SAW	-13.968	171.862	2017/02/24	5,383,126	partial
SAW17B16	<i>A. obscura</i>	SAW	-13.978	171.860	2017/02/25	4,077,174	partial
SAW17B17	<i>A. obscura</i>	SAW	-13.978	171.860	2017/02/25	5,551,346	partial
SAW17B18	<i>A. obscura</i>	SAW	-13.978	171.860	2017/02/25	5,749,306	partial
SAW17B19	<i>A. obscura</i>	SAW	-13.978	171.860	2017/02/25	7,420,046	partial
SAW17B27	<i>A. marmorata</i>	SAW	-13.968	171.862	2017/02/27	7,417,178	partial
SAW17B48	<i>A. megastoma</i>	SAW	-14.026	171.714	2017/03/01	7,218,260	partial
SAW17B49	<i>A. marmorata</i>	SAW	-14.026	171.714	2017/03/01	3,919,036	partial
SAW17B55	<i>A. megastoma</i>	SAW	-13.992	171.588	2017/03/09	4,638,202	partial

Supplementary Table 1 (continued)

Specimen ID	Species	Site	Lat.	Lon.	Date	# reads	Morphology
SAW17B56	<i>A. marmorata</i>	SAW	-13.968	171.862	2017/02/27	6,826,590	partial
SAW17B57	<i>A. marmorata</i>	SAW	-13.968	171.862	2017/02/27	3,774,558	partial
SAW17B58	<i>A. marmorata</i>	SAW	-13.968	171.862	2017/02/27	6,366,828	partial
SOK16354	<i>A. marmorata</i>	SOK	-8.060	156.973	2016/na/na	5,215,368	no
SOL16V01	<i>A. marmorata</i>	SOL	-7.832	156.715	2016/na/na	3,542,070	no
SOL16V02	<i>A. marmorata</i>	SOL	-7.832	156.715	2016/na/na	4,502,312	no
SOL16V03	<i>A. marmorata</i>	SOL	-7.861	156.696	2016/na/na	7,042,480	no
SOL16V04	<i>A. marmorata</i>	SOL	-7.861	156.696	2016/na/na	7,799,996	no
SOL16V06	<i>A. marmorata</i>	SOL	-7.861	156.696	2016/na/na	3,521,598	no
SOL16V07	<i>A. marmorata</i>	SOL	-7.861	156.696	2016/na/na	4,174,210	no
SOL16V08	<i>A. marmorata</i>	SOL	-7.861	156.696	2016/na/na	7,173,740	no
SOL16V10	<i>A. marmorata</i>	SOL	-7.861	156.696	2016/na/na	998,684	no
SOL16V11	<i>A. marmorata</i>	SOL	-7.861	156.696	2016/na/na	681,170	no
SOL16V12	<i>A. marmorata</i>	SOL	-7.861	156.696	2016/na/na	6,531,962	no
SOL16V13	<i>A. marmorata</i>	SOL	-7.861	156.696	2016/na/na	8,609,022	no
SON16364	<i>A. marmorata</i>	SON	-8.804	158.203	2016/na/na	1,516,152	no
SON16370	<i>A. marmorata</i>	SON	-8.804	158.203	2016/na/na	4,083,426	no
SON16371	<i>A. marmorata</i>	SON	-8.804	158.203	2016/na/na	2,774,878	no
SON16375	<i>A. marmorata</i>	SON	-8.764	158.004	2016/na/na	1,279,182 ¹	no
SON16376	<i>A. marmorata</i>	SON	-8.804	158.203	2016/na/na	1,854,150 ¹	no
SOR16R01	<i>A. marmorata</i>	SOR	-8.055	156.582	2016/na/na	4,643,324	no
SOR16R02	<i>A. marmorata</i>	SOR	-8.055	156.582	2016/na/na	5,046,382	no
SOR16R03	<i>A. marmorata</i>	SOR	-8.055	156.582	2016/na/na	4,317,646	no
SOR16R06	<i>A. marmorata</i>	SOR	-8.055	156.582	2016/na/na	5,291,718	no
SOR16R07	<i>A. marmorata</i>	SOR	-8.055	156.582	2016/na/na	5,497,242	no
SOR16R09	<i>A. marmorata</i>	SOR	-8.084	156.600	2016/na/na	16,663,830	no
SOR16R12	<i>A. marmorata</i>	SOR	-8.084	156.600	2016/na/na	6,932,478	no
SOR16R13	<i>A. marmorata</i>	SOR	-8.036	156.536	2016/na/na	7,161,788	no
SOR16R20	<i>A. marmorata</i>	SOR	-8.036	156.536	2016/na/na	5,295,472	no
SOR16R21	<i>A. marmorata</i>	SOR	-8.036	156.536	2016/na/na	5,314,182	no
SOR16R22	<i>A. marmorata</i>	SOR	-8.036	156.536	2016/na/na	2,375,032	no
SOR16R23	<i>A. marmorata</i>	SOR	-8.036	156.536	2016/na/na	6,237,660	no
SOV16374	<i>A. megastoma</i>	SOV	-8.817	158.189	2016/na/na	4,844,384	no
SOV16377	<i>A. marmorata</i>	SOV	-8.764	158.004	2016/na/na	5,086,458	no
TAI15001	<i>A. marmorata</i>	TAI	24.716	121.835	2015/06/05	3,759,770	no
TAI15002	<i>A. marmorata</i>	TAI	24.716	121.835	2015/06/05	2,931,064	no
TAI15003	<i>A. marmorata</i>	TAI	24.716	121.835	2015/06/05	5,276,728	no
TAI15004	<i>A. marmorata</i>	TAI	24.716	121.835	2015/06/05	3,095,594	no
TAI15005	<i>A. marmorata</i>	TAI	24.716	121.835	2015/06/05	4,486,336	no
TAI15006	<i>A. marmorata</i>	TAI	24.716	121.835	2015/06/05	4,999,952	no
TAI15007	<i>A. marmorata</i>	TAI	24.716	121.835	2015/06/05	5,063,884	no
TAI15008	<i>A. marmorata</i>	TAI	24.716	121.835	2015/06/05	4,908,062	no
TAI15009	<i>A. marmorata</i>	TAI	24.716	121.835	2015/06/05	5,224,604	no
TAI15010	<i>A. marmorata</i>	TAI	24.716	121.835	2015/06/05	4,291,306	no
TAI15011	<i>A. marmorata</i>	TAI	24.716	121.835	2015/06/05	1,850,660	no
TAI15012	<i>A. marmorata</i>	TAI	24.716	121.835	2015/06/05	4,193,860	no
TAI15013	<i>A. marmorata</i>	TAI	24.716	121.835	2015/06/05	4,946,272	no

Supplementary Table 1 (continued)

Specimen ID	Species	Site	Lat.	Lon.	Date	# reads	Morphology
TAI15014	<i>A. marmorata</i>	TAI	24.716	121.835	2015/06/05	3,472,668	no
TAI15015	<i>A. marmorata</i>	TAI	24.716	121.835	2015/06/05	2,665,630	no
TAI15016	<i>A. marmorata</i>	TAI	24.716	121.835	2015/06/05	4,922,922	no
TAI15017	<i>A. marmorata</i>	TAI	24.716	121.835	2015/06/05	4,966,356	no
TAI15018	<i>A. marmorata</i>	TAI	24.716	121.835	2015/06/05	3,745,542	no
TAI15019	<i>A. marmorata</i>	TAI	24.716	121.835	2015/06/05	4,070,564	no
TAI15020	<i>A. marmorata</i>	TAI	24.716	121.835	2015/06/05	3,253,040	no
TAI15021	<i>A. marmorata</i>	TAI	24.716	121.835	2015/06/05	4,451,956	no
TAI15022	<i>A. marmorata</i>	TAI	24.716	121.835	2015/06/05	3,582,168	no
TAI15023	<i>A. marmorata</i>	TAI	24.716	121.835	2015/06/05	5,037,786	no
TAI15024	<i>A. marmorata</i>	TAI	24.716	121.835	2015/06/05	6,443,022	no
TAI15025	<i>A. marmorata</i>	TAI	24.716	121.835	2015/06/05	5,691,686	no
TAI15026	<i>A. marmorata</i>	TAI	24.716	121.835	2015/06/05	6,249,920	no
TAI15027	<i>A. marmorata</i>	TAI	24.716	121.835	2015/06/05	6,987,072	no
TAI15028	<i>A. marmorata</i>	TAI	24.716	121.835	2015/06/05	4,543,658	no
TAI15029	<i>A. marmorata</i>	TAI	24.716	121.835	2015/06/05	5,325,064	no
TAI15030	<i>A. marmorata</i>	TAI	24.716	121.835	2015/06/05	5,234,126	no
<u>VAG12001</u>	<i>A. marmorata</i>	VAG	-14.275	167.548	2012/01/17	2,943,378	yes
<u>VAG12002</u>	<i>A. marmorata</i>	VAG	-14.275	167.548	2012/01/18	1,740,398	yes
<u>VAG12003</u>	<i>A. marmorata</i>	VAG	-14.275	167.548	2012/01/19	1,406,994	yes
<u>VAG12004</u>	<i>A. megastoma</i>	VAG	-14.275	167.548	2012/01/21	6,051,382	yes
<u>VAG12005</u>	<i>A. megastoma</i>	VAG	-14.275	167.548	2012/01/21	6,977,268	yes
<u>VAG12006</u>	<i>A. megastoma</i>	VAG	-14.275	167.548	2012/01/21	2,449,900	yes
<u>VAG12007</u>	<i>A. megastoma</i>	VAG	-14.275	167.548	2012/01/21	3,009,804	yes
<u>VAG12008</u>	<i>A. megastoma</i>	VAG	-14.275	167.548	2012/01/21	2,672,694	yes
<u>VAG12009</u>	<i>A. megastoma</i>	VAG	-14.275	167.548	2012/01/21	132,204 ¹	yes ²
<u>VAG12010</u>	<i>A. megastoma</i>	VAG	-14.275	167.548	2012/01/21	1,859,440	yes
<u>VAG12011</u>	<i>A. megastoma</i>	VAG	-14.275	167.548	2012/01/21	2,859,824	yes
<u>VAG12012</u>	<i>A. marmorata</i>	VAG	-14.275	167.548	2012/01/21	885,610	yes
<u>VAG12013</u>	<i>A. megastoma</i>	VAG	-14.275	167.548	2012/01/21	4,839,628	yes
<u>VAG12014</u>	<i>A. megastoma</i>	VAG	-14.275	167.548	2012/01/22	3,150,160	yes
<u>VAG12015</u>	<i>A. megastoma</i>	VAG	-14.275	167.548	2012/01/22	2,285,658	yes
<u>VAG12016</u>	<i>A. marmorata</i>	VAG	-14.275	167.548	2012/01/22	2,609,394	yes
<u>VAG12018</u>	<i>A. marmorata</i>	VAG	-14.275	167.548	2012/01/22	2,795,482	yes
<u>VAG12019</u>	<i>A. marmorata</i>	VAG	-14.275	167.548	2012/01/22	3,403,952	yes
<u>VAG12020</u>	<i>A. megastoma</i>	VAG	-14.275	167.548	2012/01/22	8,602,088	yes
<u>VAG12021</u>	<i>A. megastoma</i>	VAG	-14.275	167.548	2012/01/22	254,536 ¹	yes ²
<u>VAG12022</u>	<i>A. marmorata</i>	VAG	-14.275	167.548	2012/01/22	1,420,164	yes
<u>VAG12023</u>	<i>A. interioris</i>	VAG	-14.275	167.548	2012/01/23	3,310,828	yes
<u>VAG12024</u>	<i>A. marmorata</i>	VAG	-14.275	167.548	2012/01/22	2,999,122	yes
<u>VAG12025</u>	<i>A. marmorata</i>	VAG	-14.275	167.548	2012/01/22	5,478,366	yes
<u>VAG12026</u>	<i>A. marmorata</i>	VAG	-14.275	167.548	2012/01/22	219,894 ¹	yes ²
<u>VAG12027</u>	<i>A. megastoma</i>	VAG	-14.275	167.548	2012/01/22	6,337,898	yes
<u>VAG12028</u>	<i>A. marmorata</i>	VAG	-14.275	167.548	2012/01/22	260,506 ¹	yes ²
<u>VAG12029</u>	<i>A. marmorata</i>	VAG	-14.275	167.548	2012/01/24	3,218,850	yes
<u>VAG12030</u>	<i>A. marmorata</i>	VAG	-14.275	167.548	2012/01/24	818,028	yes
<u>VAG12031</u>	<i>A. marmorata</i>	VAG	-14.275	167.548	2012/01/24	6,862,982	yes

Supplementary Table 1 (continued)

Specimen ID	Species	Site	Lat.	Lon.	Date	# reads	Morphology
VAG12032	<i>A. megastoma</i>	VAG	-14.275	167.548	2012/01/24	255,918 ¹	yes ²
VAG12033	<i>A. marmorata</i>	VAG	-14.275	167.548	2012/01/24	725,846	yes ²
<u>VAG12034</u>	<i>A. megastoma</i>	VAG	-14.275	167.548	2012/01/24	8,292,228	yes
VAG12035	<i>A. marmorata</i>	VAG	-14.275	167.548	2012/01/24	528,696 ¹	yes ²
VAG12036	<i>A. marmorata</i>	VAG	-14.275	167.548	2012/01/24	11,598,732	yes
VAG12037	<i>A. marmorata</i>	VAG	-14.275	167.548	2012/01/24	2,505,822	yes ²
VAG12038	<i>A. megastoma</i>	VAG	-14.275	167.548	2012/01/24	4,382,324	partial
VAG12039	<i>A. marmorata</i>	VAG	-14.261	167.605	2012/01/28	18,191,152	yes
VAG12040	<i>A. marmorata</i>	VAG	-14.261	167.605	2012/01/31	7,749,912	yes
<u>VAG12041</u>	<i>A. megastoma</i>	VAG	-14.261	167.605	2012/01/31	3,770,604	yes
VAG12044	<i>A. megastoma</i>	VAG	-14.261	167.605	2012/02/01	4,910,168	yes
VAG12045	<i>A. marmorata</i>	VAG	-14.261	167.605	2012/02/01	18,655,124	yes
VAG12046	<i>A. megastoma</i>	VAG	-14.261	167.605	2012/02/01	2,129,488	yes ²
VAG12047	<i>A. megastoma</i>	VAG	-14.261	167.605	2012/02/01	1,262,984	yes ²
VAG12049	<i>A. obscura</i>	VAG	-14.261	167.605	2012/01/31	5,359,114	yes
<u>VAG12050</u>	<i>A. obscura</i>	VAG	-14.261	167.605	2012/02/02	2,618,778	yes
VAG12051	<i>A. megastoma</i>	VAG	-14.261	167.605	2012/02/02	8,358,494	partial
VAG12052	<i>A. marmorata</i>	VAG	-14.261	167.605	2012/02/02	11,983,860	partial
VAG12053	<i>A. marmorata</i>	VAG	-14.261	167.605	2012/02/02	3,660,386	partial
VAG12054	<i>A. marmorata</i>	VAG	-14.261	167.605	2012/02/01	494,650 ¹	yes ²
VAG12055	<i>A. marmorata</i>	VAG	-14.261	167.605	2012/02/01	6,158,622	yes
<u>VAG12056</u>	<i>A. megastoma</i>	VAG	-14.261	167.605	2012/02/01	6,352,762	yes
VAG12059	<i>A. marmorata</i>	VAG	-14.261	167.605	2012/01/31	983,610	yes
VAG12060	<i>A. obscura</i>	VAG	-14.261	167.605	2012/02/01	1,435,834	yes
<u>VAG12061</u>	<i>A. obscura</i>	VAG	-14.261	167.605	2012/02/01	3,400,270	yes
<u>VAG12062</u>	<i>A. megastoma</i>	VAG	-14.261	167.605	2012/02/02	4,258,918	yes
<u>VAG12063</u>	<i>A. marmorata</i>	VAG	-14.261	167.605	2012/02/02	5,949,864	yes
<u>VAG12064</u>	<i>A. megastoma</i>	VAG	-14.261	167.605	2012/02/02	3,143,290	yes
<u>VAG12065</u>	<i>A. megastoma</i>	VAG	-14.261	167.605	2012/02/02	3,238,970	yes
<u>VAG12067</u>	<i>A. marmorata</i>	VAG	-14.261	167.605	2012/02/01	5,545,036	yes
<u>VAG12068</u>	<i>A. marmorata</i>	VAG	-14.261	167.605	2012/02/02	7,125,294	yes
<u>VAG13070</u>	<i>A. marmorata</i>	VAG	-14.261	167.605	2013/03/01	3,508,578	yes
VAG13071	<i>A. marmorata</i>	VAG	-14.261	167.605	2013/03/01	3,910,052	yes
VAG13072	<i>A. marmorata</i>	VAG	-14.261	167.605	2013/03/22	5,860,892	yes ²
<u>VAG13073</u>	<i>A. obscura</i>	VAG	-14.261	167.605	2013/03/28	8,105,260	yes
<u>VAG13074</u>	<i>A. obscura</i>	VAG	-14.261	167.605	2013/03/28	7,979,904	yes
VAG13075	<i>A. megastoma</i>	VAG	-14.261	167.605	2013/03/27	4,794,394	yes
<u>VAG13076</u>	<i>A. megastoma</i>	VAG	-14.261	167.605	2013/03/30	3,882,404	yes
VAG13077	<i>A. marmorata</i>	VAG	-14.261	167.605	2013/03/27	6,948,582	yes
VAG13078	<i>A. marmorata</i>	VAG	-14.261	167.605	2013/03/26	6,147,476	yes
<u>VAG13079</u>	<i>A. marmorata</i>	VAG	-14.261	167.605	2013/03/26	7,965,414	yes
<u>VAG13080</u>	<i>A. obscura</i>	VAG	-14.261	167.605	2013/04/01	6,240,488	yes
<u>VAG13081</u>	<i>A. marmorata</i>	VAG	-14.261	167.605	2013/04/02	5,948,510	yes
<u>VAG13082</u>	<i>A. marmorata</i>	VAG	-14.261	167.605	2013/04/01	4,319,756	yes
VAG13083	<i>A. marmorata</i>	VAG	-14.261	167.605	2013/04/01	25,480 ¹	yes ²
<u>VAG13084</u>	<i>A. obscura</i>	VAG	-14.261	167.605	2013/04/01	2,637,702	yes
<u>VAG13085</u>	<i>A. marmorata</i>	VAG	-14.261	167.605	2013/04/02	6,013,544	yes

Supplementary Table 1 (continued)

Specimen ID	Species	Site	Lat.	Lon.	Date	# reads	Morphology
VAG13086	<i>A. megastoma</i>	VAG	-14.261	167.605	2013/04/03	3,298,274	yes
VAG13087	<i>A. marmorata</i>	VAG	-14.261	167.605	2013/04/03	1,115,480	partial

Supplementary Table 2: Per-species population-genetic parameters for tropical eel species.

Reported parameters are calculated for the dataset for phylogenetic analyses (before reducing it to maximally five individuals per species). Heterozygosity (h), nucleotide diversity (π), and population mutation rate (Θ) were calculated twice; first assuming that all missing data are invariable, and second assuming that missing data mask genotypes that are equally variable as the observed ones. For *A. marmorata*, all parameters were calculated first for all individuals jointly and then for each of four populations: WIO, western Indian Ocean (sampling sites AFC, AFC, MAY, REU); SCS, South China Sea (sampling sites PHP, PHC, TAI); WSP, western South Pacific (sampling sites BOU, SO, VAG, NCA, SAA, SAW). n , Number of individuals used in genomic analyses.

Species	n	Completeness	# variable sites	$h (\times 10^{-3})$	$\pi (\times 10^{-3})$	$\Theta (\times 10^{-3})$
<i>A. marmorata</i>	325	0.790	373,382	0.32/0.40	0.50/0.53	2.90/4.10
<i>A. marmorata</i> (WIO)	42	0.877	35,094	0.19/0.21	0.22/0.23	0.38/0.61
<i>A. marmorata</i> (Java)	21	0.599	25,187	0.14/0.24	0.26/0.28	0.32/0.82
<i>A. marmorata</i> (SCS)	63	0.877	201,746	0.53/0.61	0.69/0.70	2.04/2.65
<i>A. marmorata</i> (WSP)	199	0.765	191,935	0.30/0.39	0.44/0.46	1.60/3.23
<i>A. luzonensis</i>	20	0.737	113,858	0.72/0.98	1.12/1.19	1.47/2.53
<i>A. bicolor</i>	4	0.513	45,975	0.67/1.30	1.31/1.49	0.97/1.96
<i>A. obscura</i>	36	0.723	87,297	0.34/0.48	0.56/0.58	0.99/1.88
<i>A. interioris</i>	3	0.731	28,474	0.57/0.78	0.82/0.88	0.68/0.98
<i>A. megastoma</i>	41	0.738	127,411	0.43/0.58	0.71/0.71	1.40/2.41
<i>A. mossambica</i>	1	0.756	19,273	1.06/1.40	1.06/1.40	1.06/1.40

Supplementary Table 3: Per-species population-genetic parameters for tropical eel species.

As Supplementary Table 2, but using the dataset for population-genetic analyses.

Species	n	Completeness	# variable sites	$h (\times 10^{-3})$	$\pi (\times 10^{-3})$	$\Theta (\times 10^{-3})$
<i>A. marmorata</i>	325	0.910	146,998	0.65/0.72	0.86/0.88	1.14/1.20
<i>A. marmorata</i> (WIO)	42	0.948	46,793	0.53/0.56	0.57/0.57	0.51/0.67
<i>A. marmorata</i> (Java)	21	0.826	44,100	0.49/0.59	0.60/0.60	0.56/0.89
<i>A. marmorata</i> (SCS)	63	0.940	68,595	0.70/0.75	0.83/0.83	0.69/0.91
<i>A. marmorata</i> (WSP)	199	0.901	139,822	0.68/0.76	0.81/0.81	1.17/1.28
<i>A. luzonensis</i>	20	0.859	53,935	0.62/0.72	0.80/0.84	0.69/0.99
<i>A. bicolor</i>	4	0.721	13,436	0.23/0.31	0.34/0.37	0.28/0.43
<i>A. obscura</i>	36	0.844	60,983	0.40/0.48	0.48/0.54	0.69/0.98
<i>A. interioris</i>	3	0.877	12,487	0.27/0.30	0.32/0.34	0.30/0.35
<i>A. megastoma</i>	41	0.818	72,415	0.56/0.69	0.74/0.80	0.80/1.18
<i>A. mossambica</i>	1	0.777	2,595	0.14/0.18	0.14/0.18	0.14/0.18

Supplementary Table 4: Mean pairwise genetic distance between tropical eel species.

Genetic distances were calculated as uncorrected p-distances (the proportion of sites at which two sequences are different), based on a concatenated alignment of 20,637 RAD loci. These loci were selected to have no fully missing sequences for the maximally five individuals per species with the overall lowest proportion of missing data; only these individuals are included in the alignment. As p-distances are symmetric, species 1 and 2 are exchangeable. Rows are sorted by p-distance.

Species 1	Species 2	# pairs	Mean p-distance
<i>A. luzonensis</i>	<i>A. marmorata</i>	25	0.0053
<i>A. interioris</i>	<i>A. luzonensis</i>	15	0.0060
<i>A. bicolor</i>	<i>A. obscura</i>	20	0.0064
<i>A. interioris</i>	<i>A. marmorata</i>	15	0.0065
<i>A. bicolor</i>	<i>A. interioris</i>	12	0.0067
<i>A. interioris</i>	<i>A. obscura</i>	15	0.0067
<i>A. luzonensis</i>	<i>A. obscura</i>	25	0.0072
<i>A. bicolor</i>	<i>A. luzonensis</i>	20	0.0073
<i>A. bicolor</i>	<i>A. marmorata</i>	20	0.0076
<i>A. marmorata</i>	<i>A. obscura</i>	25	0.0076
<i>A. interioris</i>	<i>A. megastoma</i>	15	0.0079
<i>A. luzonensis</i>	<i>A. megastoma</i>	25	0.0081
<i>A. marmorata</i>	<i>A. megastoma</i>	25	0.0082
<i>A. megastoma</i>	<i>A. obscura</i>	25	0.0088
<i>A. bicolor</i>	<i>A. megastoma</i>	20	0.0090
<i>A. megastoma</i>	<i>A. mossambica</i>	5	0.0103
<i>A. interioris</i>	<i>A. mossambica</i>	3	0.0105
<i>A. luzonensis</i>	<i>A. mossambica</i>	5	0.0106
<i>A. marmorata</i>	<i>A. mossambica</i>	5	0.0107
<i>A. mossambica</i>	<i>A. obscura</i>	5	0.0113
<i>A. bicolor</i>	<i>A. mossambica</i>	4	0.0116

Supplementary Table 5: Genome assemblies.

The results of the BUSCO analysis are given in the order complete (c), complete and single copy (c+s), complete and duplicated (c+d), fragmented (f), missing (m). A total of 2,586 BUSCOs were searched for each assembly. scf., scaffold; ctg., contig.

Species	Assembly version	Assembly size	N50 scf.	N50 ctg.	—BUSCOs (c/c+s/c+d/f/m)—				
<i>A. marmorata</i>	Uncorrected	880,647,635	64,770	15,086	2,217	2,028	189	254	115
	Pilon-corrected	882,006,954	64,942	16,529	2,215	2,020	195	254	117
<i>A. megastoma</i>	Uncorrected	877,063,880	61,871	13,547	2,203	2,013	190	264	119
	Pilon-corrected	877,765,645	61,910	14,572	2,207	2,015	192	260	119
<i>A. obscura</i>	Uncorrected	881,549,187	54,844	12,017	2,161	1,977	184	307	118
	Pilon-corrected	882,390,062	54,849	12,681	2,168	1,982	186	304	114

Supplementary Table 6: Cross-validation (CV) error values of maximum-likelihood ancestry inference with ADMIXTURE.

CV errors were inferred for the models $K = 1$ to $K = 8$ based on 117,638 variable sites for five replicates (R1 to R5) per model.

Model	R1	R2	R3	R4	R5
$K = 1$	0.49028	0.49037	0.49046	0.49041	0.49040
$K = 2$	0.29901	0.29916	0.29903	0.29902	0.29913
$K = 3$	0.22883	0.22879	0.22882	0.26443	0.22880
$K = 4$	0.24704	0.19584	0.19579	0.19590	0.24694
$K = 5$	0.17819	0.17819	0.17816	0.17822	0.17820
$K = 6$	0.17491	0.17496	0.17500	0.17500	0.17488
$K = 7$	0.17614	0.17613	0.17610	0.17614	0.17380
$K = 8$	0.17508	0.17421	0.17849	0.17435	0.17487

Supplementary Table 7: Hybrid individuals.

Genomic and morphological characteristics of hybrid individuals identified via ancestry painting. Note that for backcrossed hybrids, the identity of maternal and paternal species are ambiguous because either the mother or the father is a hybrid itself; in this case, the name listed as maternal species indicates the species identity of the mitochondrial genome. h_{fixed} , heterozygosity at sites fixed between parental species; $f_{\text{m,genome}}$, proportion of genome derived from the maternal species; $f_{\text{m,morphology}}$, similarity to morphology of maternal species, relative to morphology of paternal species.

Specimen ID	Maternal species	Paternal species	Date	h_{fixed}	$f_{\text{m,genome}}$	$f_{\text{m,morphology}}$	Interpretation
BOU15031	<i>A. marmorata</i>	<i>A. megastoma</i>	04/2015	0.479	0.250	0.257	Backcross ¹
SAA16011	<i>A. marmorata</i>	<i>A. megastoma</i>	08/2016	0.974	0.506	NA	F1
SAA16012	<i>A. marmorata</i>	<i>A. megastoma</i>	08/2016	0.966	0.500	NA	F1
SAA16013	<i>A. marmorata</i>	<i>A. megastoma</i>	08/2016	0.981	0.510	NA	F1
SAA16024	<i>A. marmorata</i>	<i>A. megastoma</i>	08/2016	0.550	0.716	NA	Backcross ²
SAA16027	<i>A. marmorata</i>	<i>A. megastoma</i>	08/2016	0.956	0.500	NA	F1
SAW17B27	<i>A. marmorata</i>	<i>A. megastoma</i>	02/2017	0.972	0.506	NA	F1
SAW17B49	<i>A. marmorata</i>	<i>A. megastoma</i>	03/2017	0.969	0.512	NA	F1
VAG12012	<i>A. marmorata</i>	<i>A. megastoma</i>	01/2012	0.971	0.515	0.524	F1
VAG12018	<i>A. marmorata</i>	<i>A. megastoma</i>	01/2012	0.977	0.500	0.685	F1
VAG12019	<i>A. marmorata</i>	<i>A. megastoma</i>	01/2012	0.975	0.508	0.572	F1
VAG12024	<i>A. marmorata</i>	<i>A. megastoma</i>	01/2012	0.510	0.263	0.504	Backcross ¹
VAG12029	<i>A. marmorata</i>	<i>A. megastoma</i>	01/2012	0.459	0.767	0.746	Backcross ²
VAG12037	<i>A. marmorata</i>	<i>A. megastoma</i>	01/2012	0.817	0.575	NA	F1
VAG12044	<i>A. megastoma</i>	<i>A. marmorata</i>	02/2012	0.973	0.514	0.537	F1
VAG12053	<i>A. marmorata</i>	<i>A. megastoma</i>	02/2012	0.542	0.705	NA	Backcross ²
VAG12055	<i>A. marmorata</i>	<i>A. megastoma</i>	02/2012	0.460	0.250	0.545	Backcross ¹
VAG13071	<i>A. marmorata</i>	<i>A. megastoma</i>	03/2013	0.954	0.512	0.580	F1
VAG13078	<i>A. marmorata</i>	<i>A. megastoma</i>	03/2013	0.972	0.500	0.470	F1
VAG13087	<i>A. marmorata</i>	<i>A. megastoma</i>	04/2013	0.584	0.324	NA	Backcross ¹
VAG12040	<i>A. marmorata</i>	<i>A. obscura</i>	02/2012	0.951	0.507	0.540	F1
VAG12045	<i>A. marmorata</i>	<i>A. obscura</i>	02/2012	0.899	0.510	0.618	F1
VAG13077	<i>A. marmorata</i>	<i>A. obscura</i>	03/2013	0.957	0.500	0.537	F1
VAG12049	<i>A. obscura</i>	<i>A. megastoma</i>	01/2012	0.977	0.506	0.512	F1
BOU15017	<i>A. marmorata</i>	<i>A. interioris</i>	04/2015	0.939	0.520	0.666	F1

¹The mitochondrial genome of *A. marmorata* and the $f_{\text{m,genome}}$ around 0.25 indicate that the mother of the mother of this individual was an *A. marmorata* but all other grandparents were *A. megastoma*.

²The mitochondrial genome of *A. marmorata* and the $f_{\text{m,genome}}$ around 0.75 indicate that one of the grandparents of this individual, but not the mother of the mother, was an *A. megastoma* and all other grandparents were *A. marmorata*.

Supplementary Table 8: Frequency of hybrids at sampling sites.

n_t , number of sampled specimens; n_g , number of individuals used in genomic analyses, excluding those with low sequence quality.

Site	Location	Country	n_t	n_g	# hybrids	Frequency (%)
AFC	Eastern Cape	South Africa	15	14	0	0
AFS	Lubombo	Swaziland	1	1	0	0
MAY	Mayotte	France	18	18	0	0
REU	Réunion	France	10	10	0	0
JAV	Java	Indonesia	30	27	0	0
PHP	Pagadian	Philippines	27	27	0	0
PHC	Cagayan	Philippines	31	26	0	0
TAI	Yilan County	Taiwan	30	30	0	0
BOU	Bougainville	Papua New Guinea	30	30	2	6.7
SOK	Kolombangara	Solomon Islands	1	1	0	0
SOL	Vella Lavella	Solomon Islands	11	11	0	0
SON	Nggatokae	Solomon Islands	5	3	0	0
SOR	Ranongga	Solomon Islands	12	12	0	0
SOV	Vangunu	Solomon Islands	2	2	0	0
VAG	Gaua	Vanuatu	79	71	16	22.5
NCA	New Caledonia	France	45	45	0	0
SAW	Upolu	Samoa	71	67	2	3.0
SAA	Tutuila	American Samoa	38	35	5	14.3
Total			456	430	25	5.8

Supplementary Table 9: Introgression statistics for species quartets.

All species quartets compatible with the inferred species tree were tested. Quartet comparisons are sorted by D values. mar, *A. marmorata*; luz, *A. luzonensis*; int, *A. interioris*; obs, *A. obscura*; bic, *A. bicolor*; meg, *A. megastoma*; mos, *A. mossambica*; ang, *A. anguilla*; n , number of informative sites; C_{BBAA} , number of “BBAA” sites; C_{ABBA} , number of “ABBA” sites; C_{BABA} , number of “BABA” sites; D , Patterson’s D statistic (Green *et al.* 2010; Durand *et al.* 2011); f_4 , the f_4 statistic (Reich *et al.* 2009); p , p value for $f_4 = 0$ assessed through simulations with the F4 program (Meyer *et al.* 2017). The comparison reported in the last table row is based on WGS reads of a single individual of *A. obscura*, *A. marmorata*, and *A. megastoma*, aligned to the available reference-genome assembly of *A. anguilla* (Jansen *et al.* 2017).

P1	P2	P3	Outgroup	n	C_{BBAA}	C_{ABBA}	C_{BABA}	D	f_4	p
mar	luz	int	mos	10,290	273.1	182.7	77.1	0.406	-0.0070	0.000
mar	luz	int	meg	13,396	335.9	207.6	98.2	0.358	-0.0054	0.000
mar	luz	obs	meg	15,689	412.1	186.6	93.0	0.334	-0.0043	0.000
mar	luz	obs	mos	12,054	358.2	162.7	83.7	0.321	-0.0048	0.000
mar	bic	int	mos	7,772	100.9	266.3	138.4	0.316	-0.0109	0.000
mar	luz	bic	mos	11,542	311.9	158.1	82.8	0.313	-0.0052	0.000
mar	bic	int	meg	9,680	136.6	295.3	168.6	0.273	-0.0077	0.000
mar	luz	bic	meg	14,793	360.6	168.2	103.4	0.239	-0.0035	0.000
mar	obs	int	meg	10,208	137.3	307.9	197.8	0.218	-0.0051	0.000
mar	obs	int	mos	8,068	106.3	268.6	173.1	0.216	-0.0086	0.000
obs	bic	mar	meg	11,372	653.6	104.7	71.2	0.191	-0.0025	0.002
obs	bic	int	mos	8,304	373.7	123.8	84.1	0.191	-0.0030	0.005
obs	bic	int	meg	10,444	471.0	125.7	86.6	0.184	-0.0026	0.003
obs	bic	mar	mos	9,068	555.9	98.8	68.3	0.182	-0.0016	0.078
obs	bic	luz	mos	12,557	487.2	113.4	80.0	0.173	-0.0022	0.008
mar	int	meg	mos	9,951	482.4	96.4	72.7	0.140	-0.0023	0.026
obs	bic	luz	meg	16,064	582.5	108.7	82.5	0.137	-0.0015	0.017
mar	luz	meg	mos	13,129	677.0	69.0	52.9	0.133	-0.0008	0.201
luz	mar	bic	int	14,675	392.7	105.4	84.5	0.110	-0.0011	0.106
luz	bic	int	meg	14,246	133.6	228.4	191.0	0.089	-0.0015	0.062
luz	int	meg	mos	13,632	550.4	82.4	70.2	0.080	-0.0007	0.192
luz	bic	int	mos	11,133	111.4	197.5	168.3	0.080	-0.0022	0.042
mar	bic	meg	mos	11,134	441.3	110.9	95.0	0.077	-0.0003	0.430
luz	mar	obs	int	15,500	417.8	111.7	96.5	0.073	-0.0003	0.406
mar	obs	meg	mos	11,647	458.9	126.1	110.0	0.068	-0.0009	0.241
bic	obs	mar	int	11,303	520.4	80.0	73.0	0.046	-0.0007	0.261
obs	bic	meg	mos	11,761	813.0	64.7	59.5	0.042	-0.0002	0.447
bic	obs	luz	int	15,856	526.5	78.1	72.1	0.040	-0.0010	0.141
obs	int	meg	mos	11,017	557.5	96.2	90.8	0.029	-0.0011	0.137
luz	bic	meg	mos	14,602	480.2	97.0	93.1	0.020	0.0002	0.416
luz	obs	int	meg	15,143	144.2	227.1	221.7	0.012	0.0005	0.300
bic	int	meg	mos	10,451	535.3	84.0	82.0	0.012	-0.0007	0.213
luz	obs	meg	mos	15,405	507.8	107.9	106.2	0.008	-0.0001	0.461
luz	obs	int	mos	11,638	107.7	197.6	198.7	-0.003	-0.0007	0.303
obs	luz	meg	mos	15,405	507.8	106.2	107.9	-0.008	0.0001	0.463
int	bic	meg	mos	10,451	535.3	82.0	84.0	-0.012	0.0007	0.227

Supplementary Table 9 (continued)

P1	P2	P3	Outgroup	n	C_{BBAA}	C_{ABBA}	C_{BABA}	D	f_4	p
bic	luz	meg	mos	14,602	480.2	93.1	97.0	-0.020	-0.0002	0.420
int	obs	meg	mos	11,017	557.5	90.8	96.2	-0.029	0.0011	0.164
obs	bic	luz	int	15,856	526.5	72.1	78.1	-0.040	0.0010	0.141
bic	obs	meg	mos	11,761	813.0	59.5	64.7	-0.042	0.0002	0.420
obs	bic	mar	int	11,303	520.4	73.0	80.0	-0.046	0.0007	0.263
obs	mar	meg	mos	11,647	458.9	110.0	126.1	-0.068	0.0009	0.232
mar	luz	obs	int	15,500	417.8	96.5	111.7	-0.073	0.0003	0.384
bic	mar	meg	mos	11,134	441.3	95.0	110.9	-0.077	0.0003	0.403
int	luz	meg	mos	13,632	550.4	70.2	82.4	-0.080	0.0007	0.193
mar	luz	bic	int	14,675	392.7	84.5	105.4	-0.110	0.0011	0.119
luz	mar	meg	mos	14,059	690.1	53.8	69.0	-0.124	0.0008	0.183
bic	obs	luz	meg	16,064	582.5	82.5	108.7	-0.137	0.0015	0.013
int	mar	meg	mos	9,951	482.4	72.7	96.4	-0.140	0.0023	0.025
bic	obs	luz	mos	12,557	487.2	80.0	113.4	-0.173	0.0022	0.009
bic	obs	mar	mos	9,068	555.9	68.3	98.8	-0.182	0.0016	0.074
bic	obs	int	meg	10,444	471.0	86.6	125.7	-0.184	0.0026	0.006
bic	obs	mar	meg	11,372	653.6	71.2	104.7	-0.191	0.0025	0.002
bic	obs	int	mos	8,304	373.7	84.1	123.8	-0.191	0.0030	0.006
luz	mar	bic	meg	14,793	360.6	103.4	168.2	-0.239	0.0035	0.000
luz	mar	bic	mos	11,542	311.9	82.8	158.1	-0.313	0.0052	0.000
luz	mar	obs	mos	12,054	358.2	83.7	162.7	-0.321	0.0048	0.000
luz	mar	obs	meg	15,689	412.1	93.0	186.6	-0.334	0.0043	0.000
luz	mar	int	meg	13,396	335.9	98.2	207.6	-0.358	0.0054	0.000
luz	mar	int	mos	10,290	273.1	77.1	182.7	-0.406	0.0070	0.000
obs	mar	meg	ang	23,165,451	1638567.0	596786.0	587910.0	0.007	—	—

Supplementary Table 10: Introgression statistics for quartets of species and *A. marmorata* populations.

As Supplementary Table 9, but for comparisons involving individual *A. marmorata* populations. Only a single quartet involving *A. marmorata* appeared significant in Supplementary Table 9 and was tested further with separate populations. In addition, the possibility of different degrees of introgression between *A. luzonensis* and the four *A. marmorata* populations was explored because *A. luzonensis* appeared to share more coancestry with the South China Sea population of *A. marmorata* than with other populations in the fineRADstructure analysis (Supplementary Figure 8). O, Outgroup; WIO, western Indian Ocean (sampling sites AFC, AFC, MAY, REU); SCS, South China Sea (sampling sites PHP, PHC, TAI); WSP, western South Pacific (sampling sites BOU, SO, VAG, NCA, SAA, SAW).

P1	P2	P3	O	<i>n</i>	C_{BBAA}	C_{ABBA}	C_{BABA}	D	f_4	p
obs	bic	mar (WIO)	meg	11,104	653.0	105.5	71.5	0.192	-0.0016	0.042
obs	bic	mar (WIO)	mos	8,869	555.0	98.8	68.8	0.179	-0.0016	0.099
obs	bic	mar (Java)	meg	13,543	681.5	103.2	70.2	0.191	-0.0031	0.000
obs	bic	mar (Java)	mos	8,297	508.0	89.2	62.1	0.179	-0.0025	0.008
obs	bic	mar (SCS)	meg	10,794	632.5	97.2	68.1	0.176	-0.0029	0.000
obs	bic	mar (SCS)	mos	13,340	557.4	98.6	68.7	0.179	-0.0014	0.079
obs	bic	mar (WSP)	meg	16,834	656.1	100.0	70.8	0.171	-0.0015	0.025
obs	bic	mar (WSP)	mos	11,181	559.9	99.8	68.6	0.186	-0.0020	0.048
mar (WIO)	mar (Java)	luz	meg	12,097	864.9	23.7	28.0	-0.083	0.0002	0.319
mar (WIO)	mar (Java)	luz	mos	9,190	627.4	21.8	24.7	-0.063	0.0004	0.350
mar (WIO)	mar (SCS)	luz	meg	18,097	735.4	48.7	63.9	-0.135	0.0006	0.256
mar (WIO)	mar (SCS)	luz	mos	13,755	538.9	43.0	49.9	-0.074	0.0005	0.329
mar (WIO)	mar (WSP)	luz	meg	15,210	842.0	27.2	78.1	-0.483	0.0033	0.025
mar (WIO)	mar (WSP)	luz	mos	12,015	612.6	26.2	41.9	-0.232	0.0012	0.238
mar (WSP)	mar (WIO)	luz	meg	15,210	842.0	78.1	27.2	0.483	-0.0033	0.023 ¹
mar (WSP)	mar (WIO)	luz	mos	12,015	612.6	41.9	26.2	0.232	-0.0012	0.218
mar (WSP)	mar (Java)	luz	meg	15,119	831.1	76.9	30.4	0.434	-0.0034	0.021 ¹
mar (WSP)	mar (Java)	luz	mos	11,976	605.8	41.6	28.7	0.183	-0.0010	0.253
mar (WSP)	mar (SCS)	luz	meg	20,938	704.2	101.3	65.7	0.213	-0.0017	0.098
mar (WSP)	mar (SCS)	luz	mos	16,383	517.6	62.6	53.7	0.076	-0.0003	0.361

¹Note that the support for introgression between *A. luzonensis* and the *A. marmorata* populations from the western Indian Ocean and Java is not robust to outgroup choice and no longer significant after correcting for multiple tests.

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