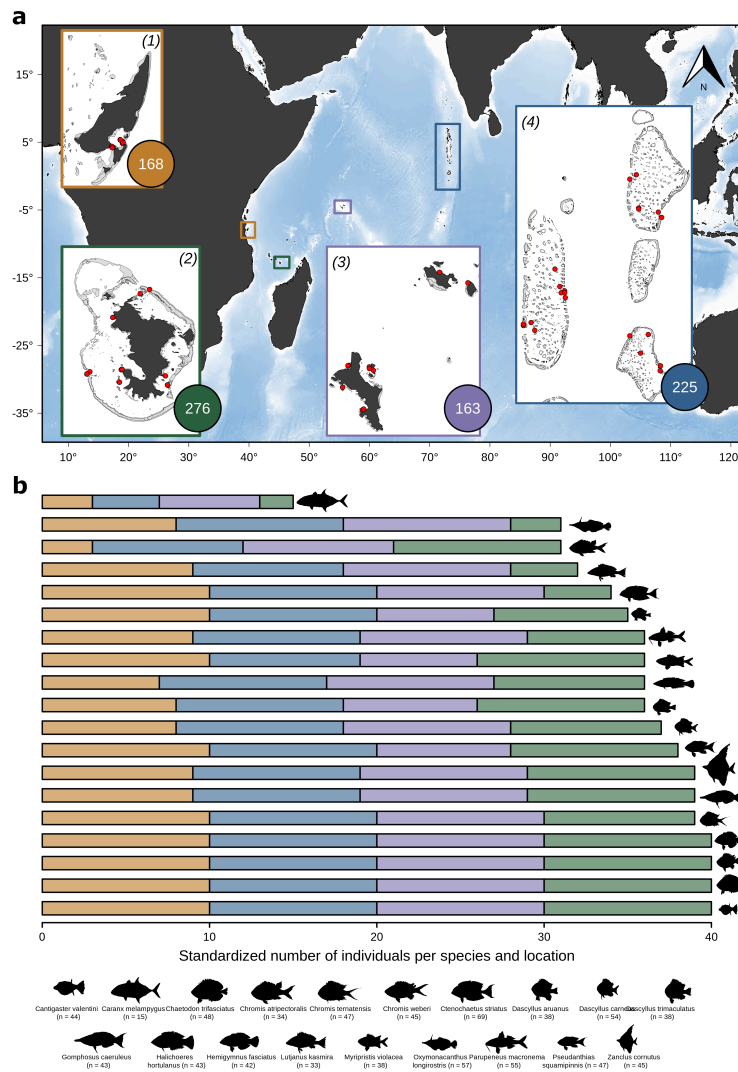


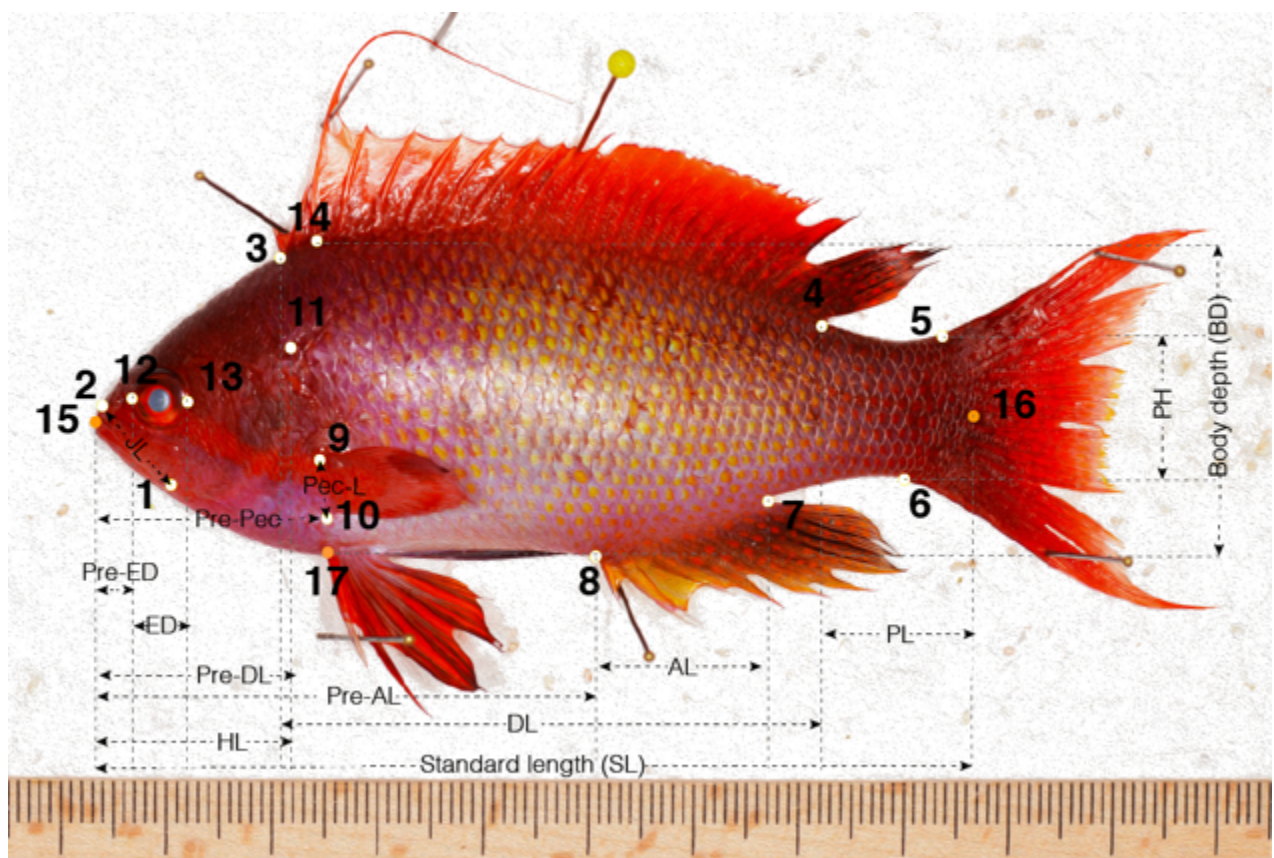
# Supplementary Information

## Continuity in morphological disparity in tropical reef fishes across evolutionary scales

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4 **Supplementary Figure 1. Geographic location of the sampling sites in the Western Indian Ocean, where the intraspecific morphological data and the genetic data were collected.** (a)  
5 **Map of the sampling locations in the Western Indian Ocean: Mafia Island (Tanzania; 1), Mayotte**  
6 **Island (France island in Comorian archipelago; 2), the islands of Mahe, Praslin and La Digue**  
7 **(Seychelles; 3), and three central atolls of the Maldives, namely Kaafu North, Alif Alif, and Vaavu**  
8 **(Republic of Maldives; 4). The circled values on each small map indicate the number of species**  
9 **sampled at each location, and the red points mark the positions of the sampling sites at each location**  
10 **sampled at each location, and the red points mark the positions of the sampling sites at each location**  
11 **for the individuals considered in the genetic data set.** (b) **Standardized number of individuals**  
12 **selected for the genetic analyses, separated by species and location.**



14 **Supplementary Figure 2. Morphometric data collection on tropical reef fishes.** The  
 15 interspecific data set was constructed based on 1061 individual species (10 families) gathered from<sup>1</sup>  
 16 and characterized by 14 available landmarks on the fish body (white dots). The intraspecific data  
 17 set included 1111 individuals belonging to 17 species (embedded in the same 10 families); it was  
 18 constructed based on the same 14 body landmarks plus 3 additional ones (orange dots). The  
 19 intraspecific data set included only species belonging to families included in the interspecific data  
 20 set. Landmarks around the head area are related to feeding mechanics, while the remaining ones are  
 21 related to locomotion mechanics. Here, a male *Pseudanthias squamipinnis* (sea goldie, Serranidae)  
 22 sample is shown as an example. For species with strong sexual dimorphism (e.g., *Pseudanthias*  
 23 *squamipinnis*), only male specimens were included in the morphological trait analysis. All the  
 24 morphological measurement terms are defined in the Supplementary Table 7.

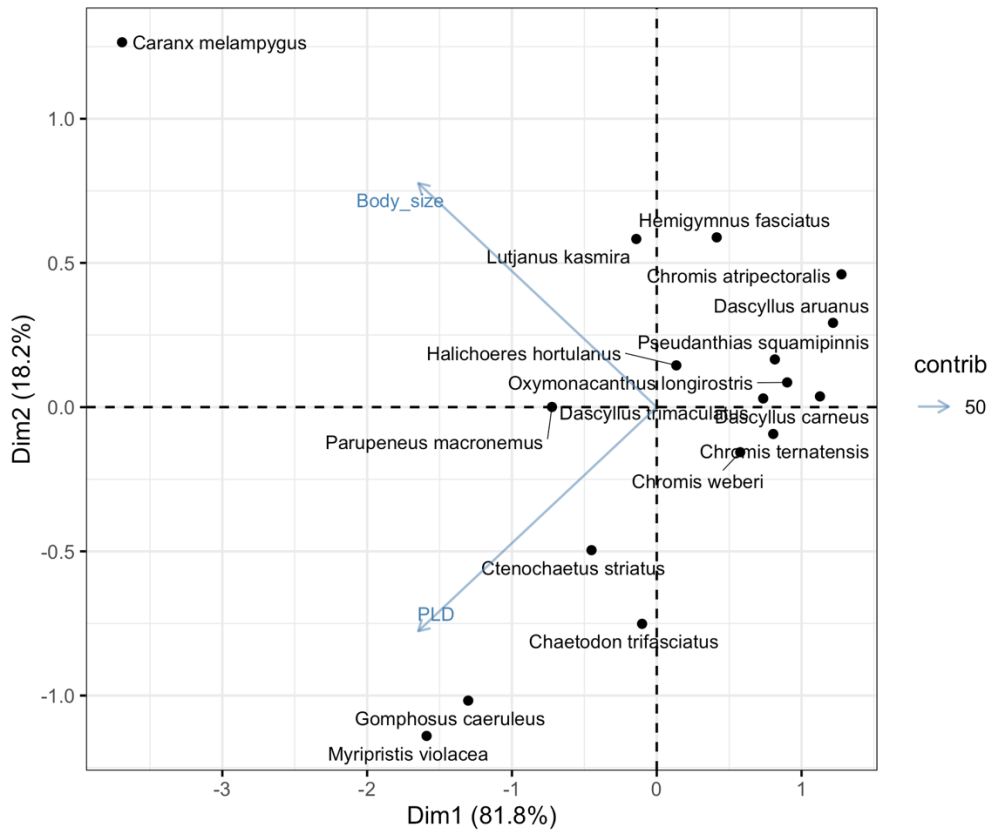


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Reference:

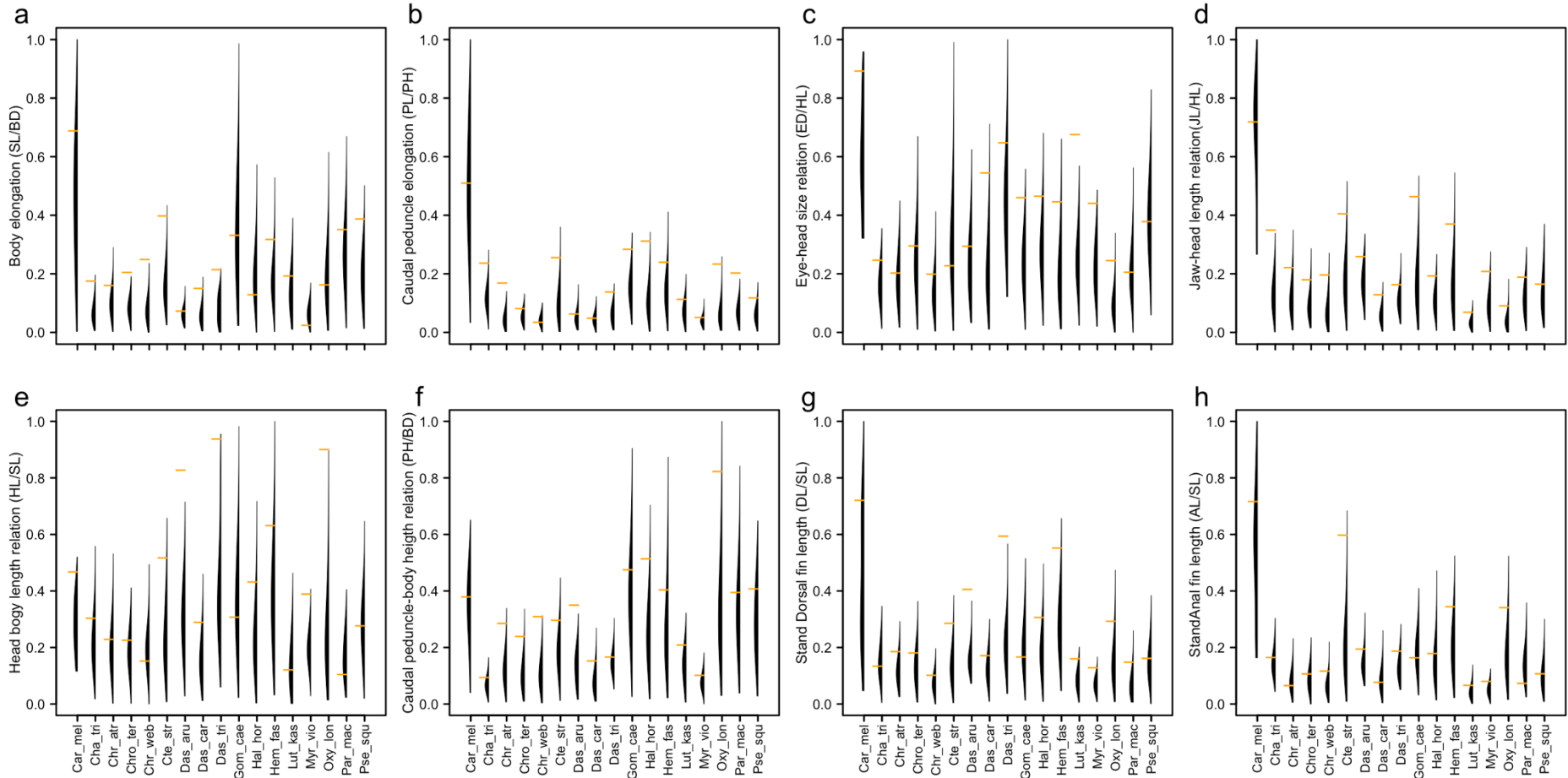
1. Claverie, T. & Wainwright, P. C. A Morphospace for Reef Fishes: Elongation Is the Dominant Axis of Body Shape Evolution. PLoS One 9, e112732 (2014).

30 **Supplementary Figure 3. Principal component analysis (PCA) based on body size and**  
 31 **pelagic larval duration (PLD) for the 17 selected Western Indian Ocean fish species.**

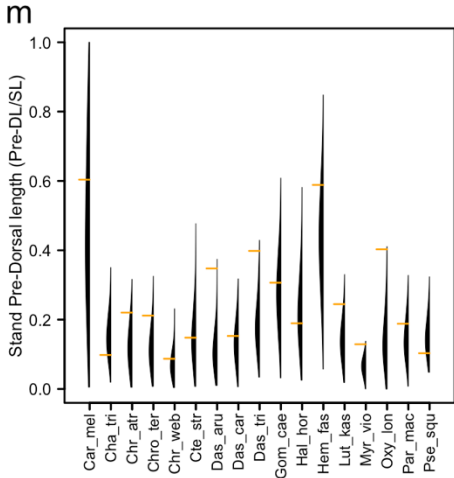
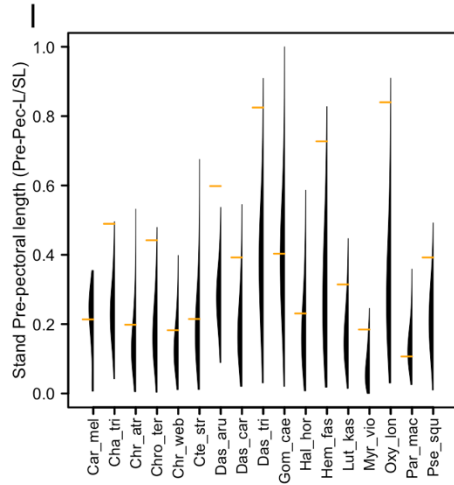
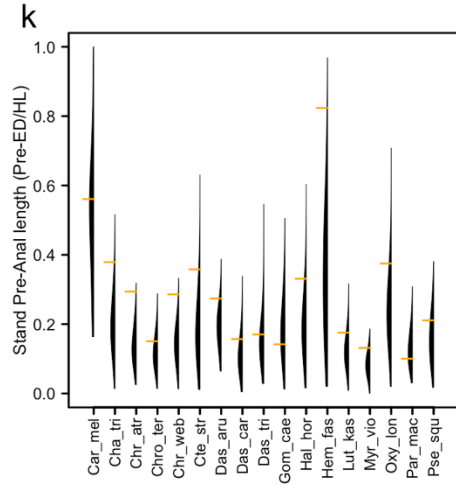
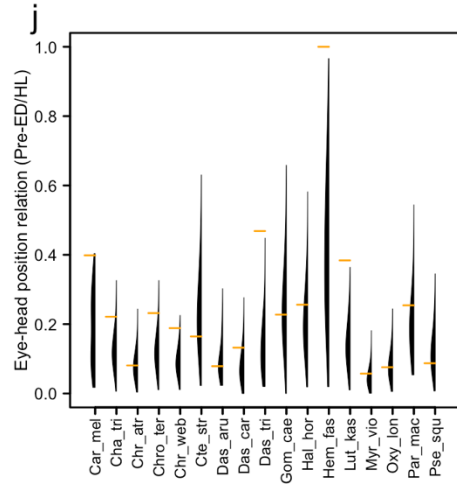
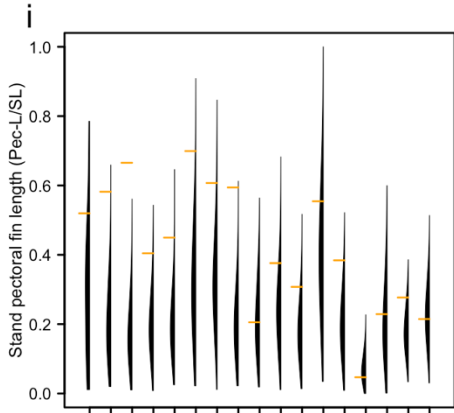


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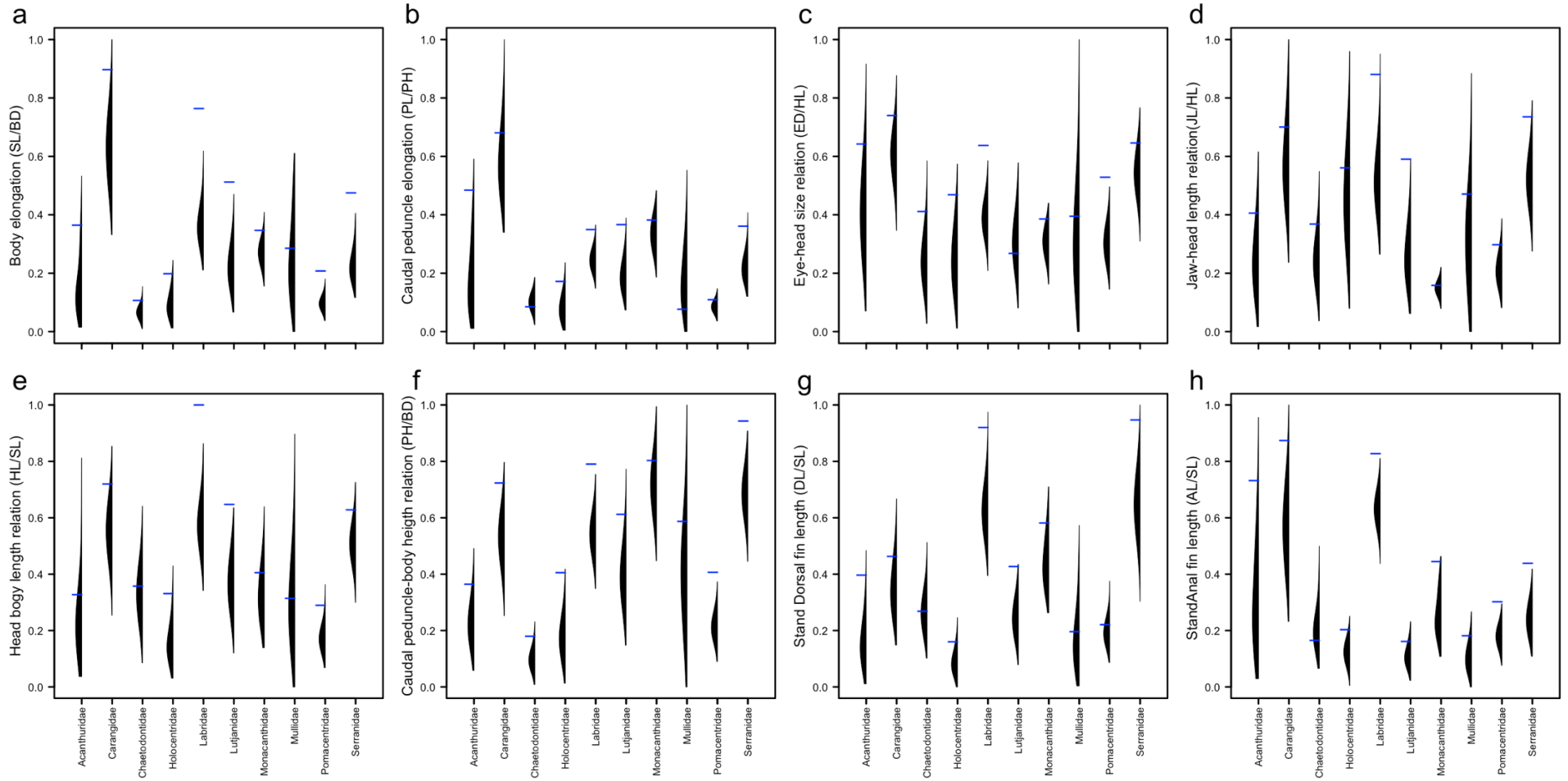
33 **Supplementary Figure 4. Illustration of the morphological trait disparity (mtD) in tropical reef fishes at the intraspecific level.** Each plot  
 34 represents the morphological trait disparity for all the studied species: the black shaded areas represent the expected morphological variability  
 35 under null models (999 randomizations), whereas the orange segments represent the values observed in our data set.



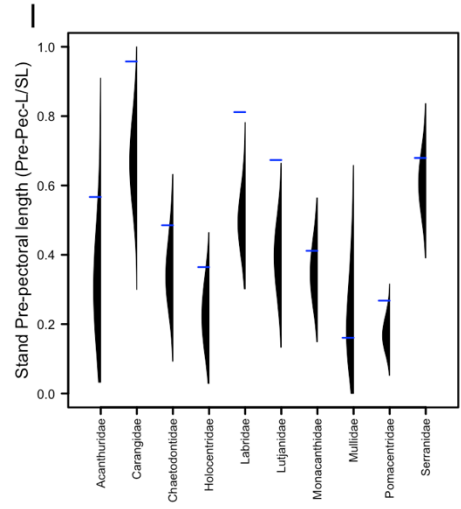
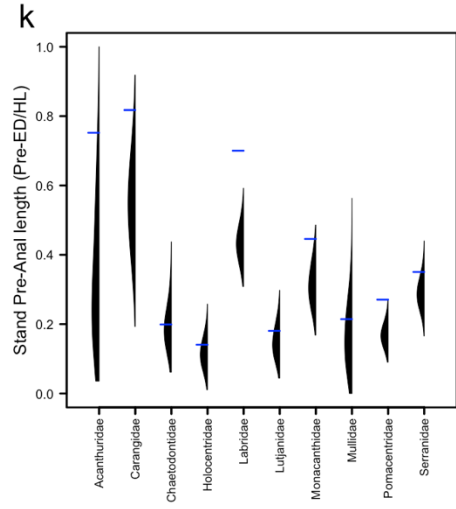
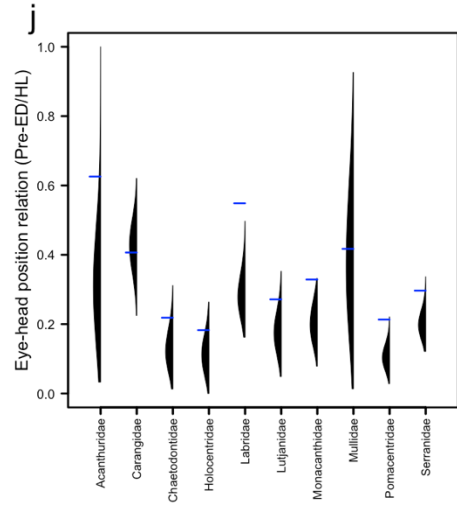
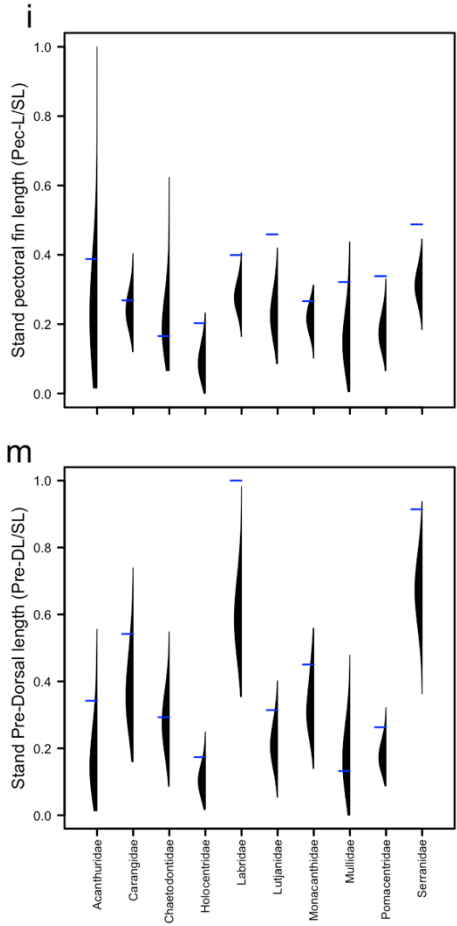
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39 **Supplementary Figure 5. Illustration of the morphological trait disparity (mtD) in tropical reef fishes at the interspecific level.** Each plot  
 40 represents the morphological trait disparity for all the studied families: the black shaded areas represent the expected morphological variability  
 41 under null models (999 randomizations), whereas the blue segments represent the values observed in our data set.

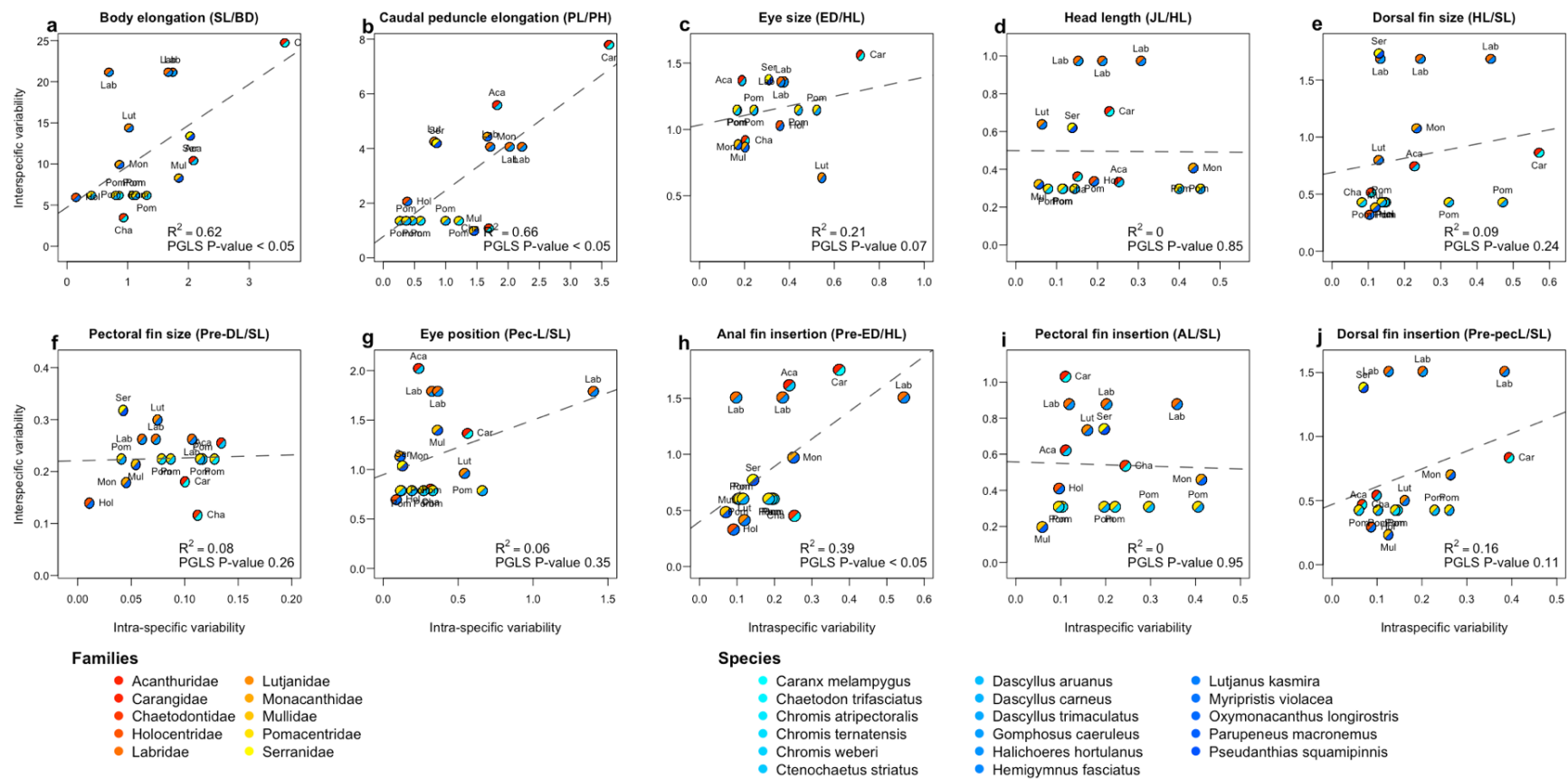


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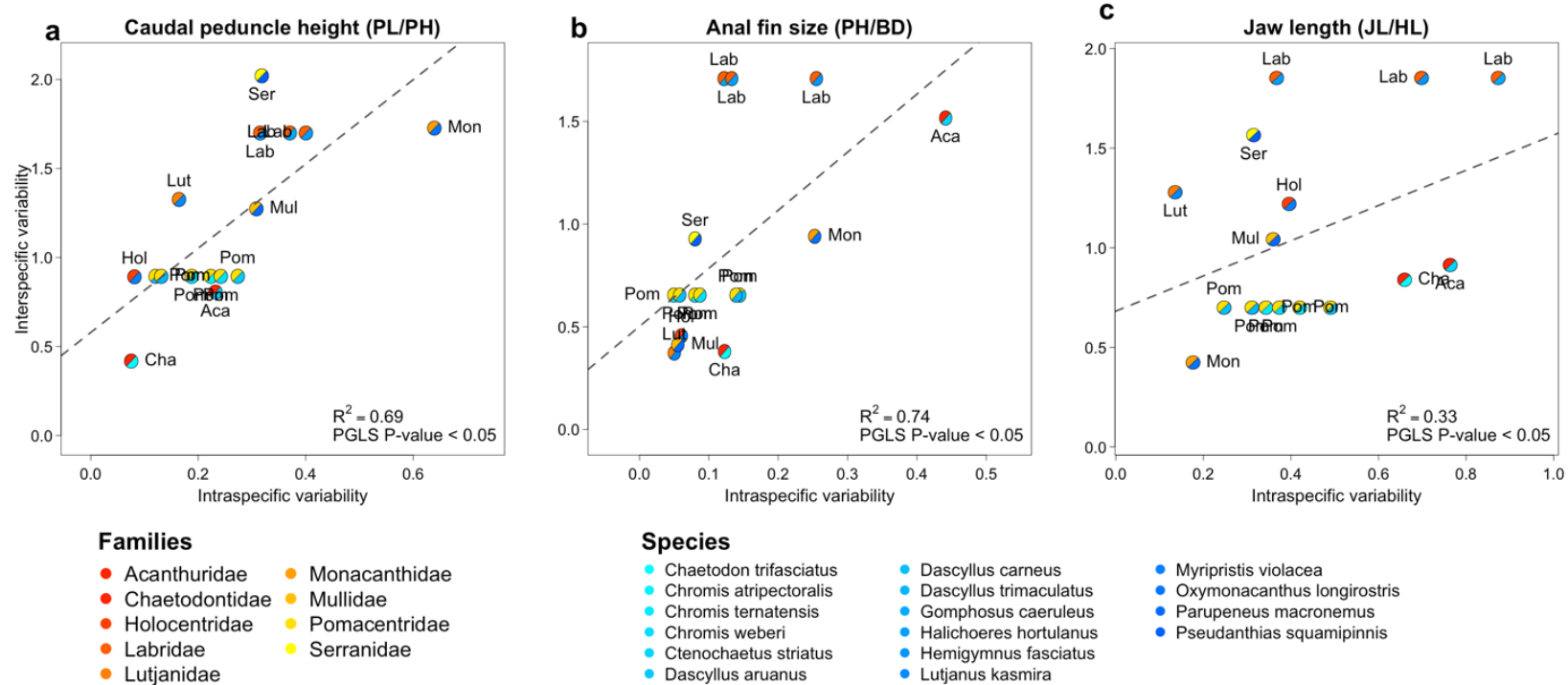
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46 **Supplementary Figure 6. Intra- and interspecific morphological trait disparity (mtD) relationships for fish traits.** Phylogenetic generalized  
 47 least squares (PGLS) controlled relationships between the intra- and interspecific mtD in tropical reef fishes for (a) body elongation, relative (b)  
 48 caudal peduncle elongation, (c) eye size, (d) head length, (e) dorsal fin size, (f) pectoral fin size, (g) eye position, (h) anal fin insertion, (i) pectoral  
 49 fin insertion, and (j) dorsal fin insertion. The dashed line represents the Ordinary Least Square regression between intra- and interspecific  
 50 morphological variability. The reported P-values in each panel corresponds to the significance of the relation accounting for phylogenetical  
 51 relationship between species (PGLS: phylogenetic generalized least-squares). Each symbol contains two colors, one corresponding to the  
 52 intraspecific data set and the other to the interspecific data set.

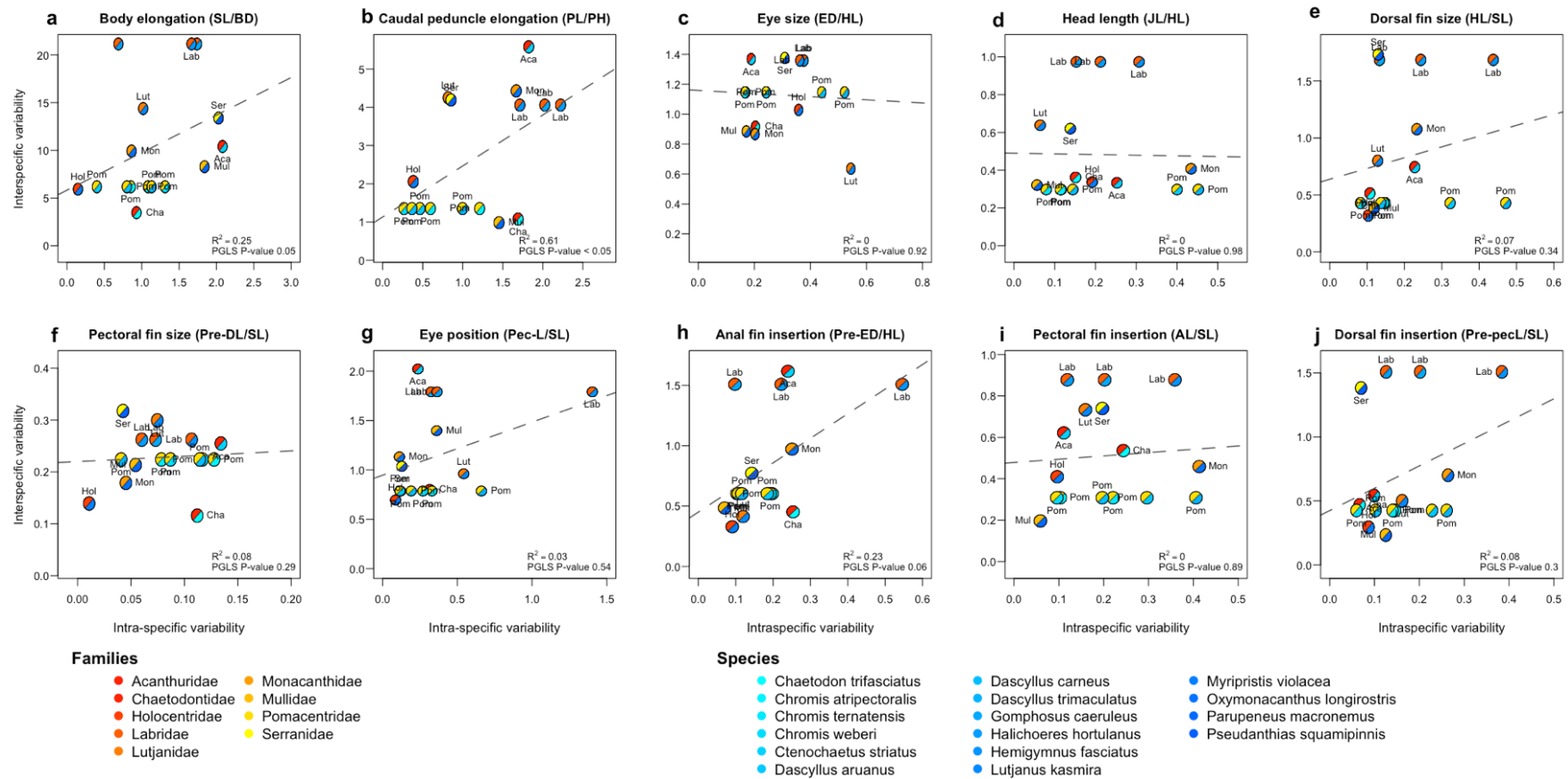




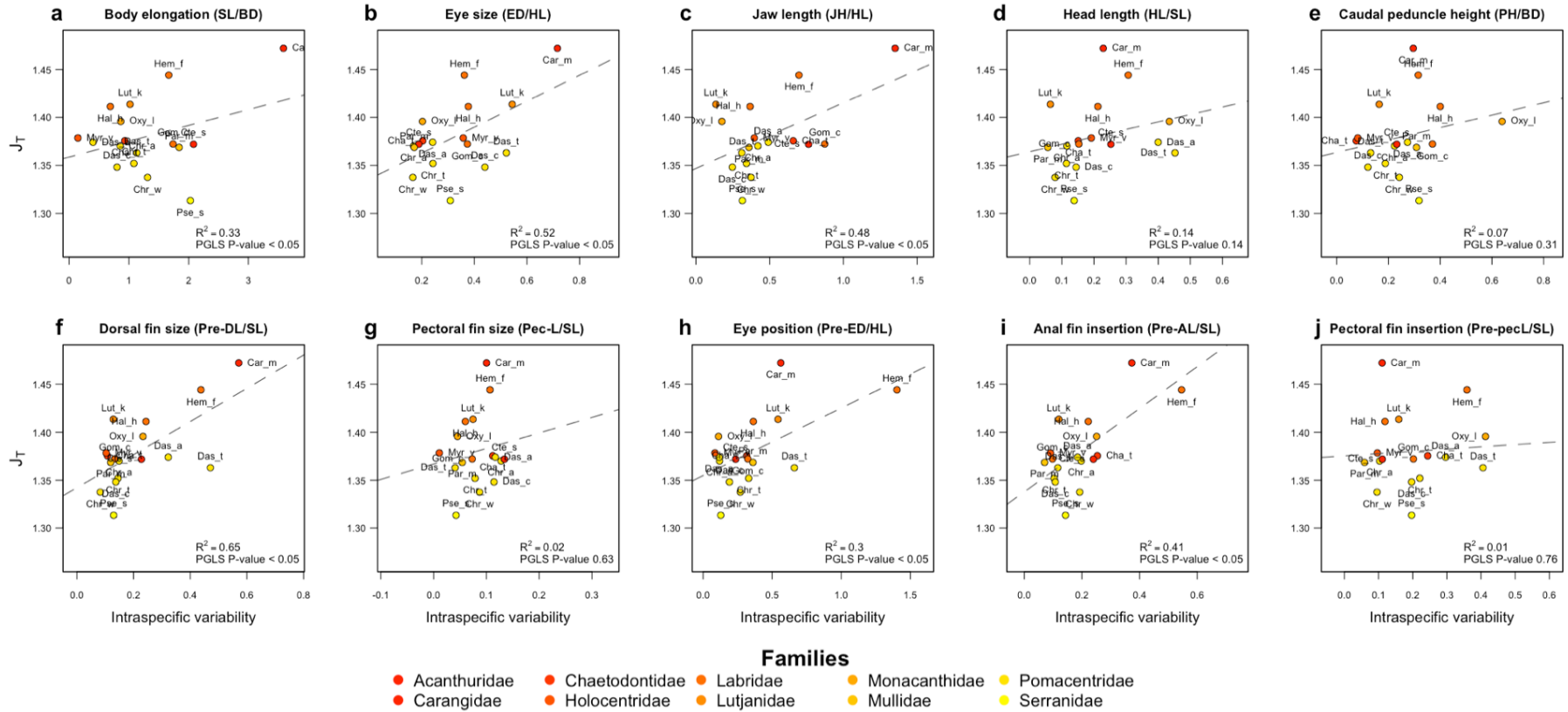
54 **Supplementary Figure 7. Relationships between the intraspecific and interspecific morphological disparity in tropical reef fishes when**  
 55 **excluding the Carangid fish species (*Caranx melampyngus*).** Relationships between intraspecific and interspecific variability for (a) caudal  
 56 peduncle height (PL: caudal peduncle length, PH: caudal peduncle height); (b) anal fin length (AL: anal fin length) and (c) Jaw-head length  
 57 relationship (JL: jaw length, HL: head length). The dashed line represents the Ordinary Least Square regression between intra- and interspecific  
 58 morphological variability. The reported P-values in each panel corresponds to the significance of the relation accounting for phylogenetical  
 59 relationship between species (PGLS: phylogenetic generalized least-squares). Each symbol contains two colors, one corresponding to the  
 60 intraspecific data set and the other to the interspecific data set.



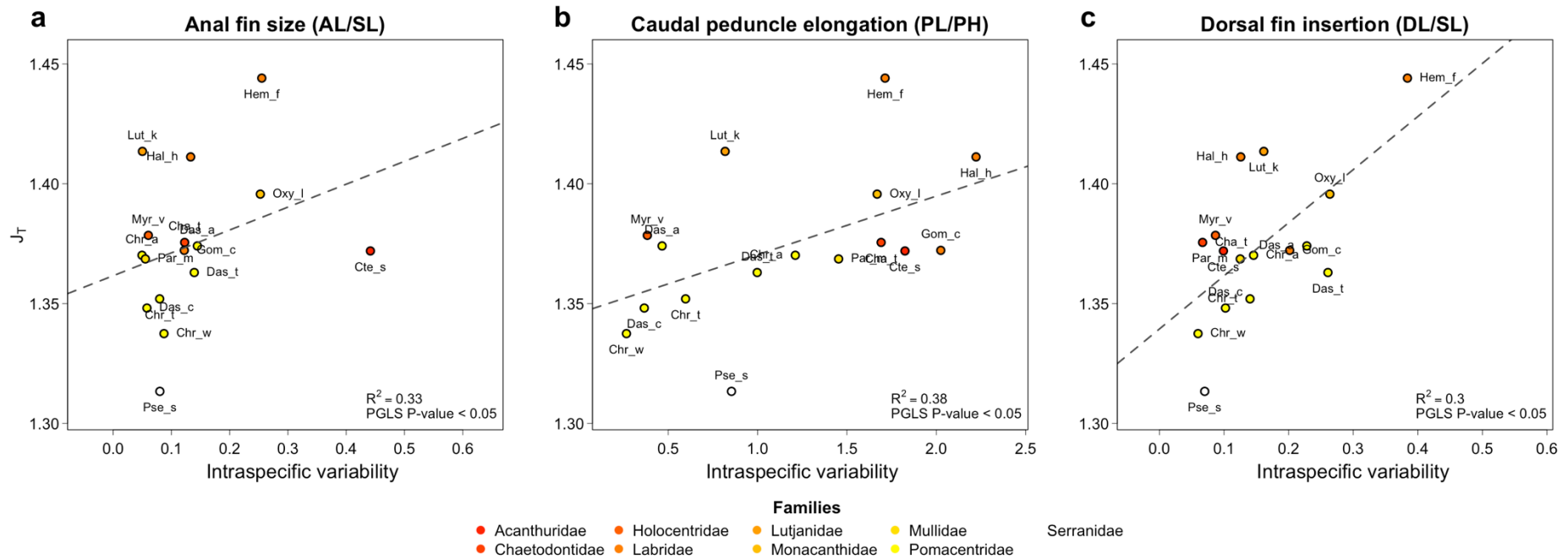
62 **Supplementary Figure 8. Intra- and interspecific morphological trait disparity (mtD) relationships for fish traits when excluding the**  
 63 **Carangid fish species (*Caranx melampyus*).** Phylogenetic generalized least squares (PGLS) controlled relationships between the intra- and  
 64 interspecific mtD in tropical reef fishes for for (a) body elongation, relative (b) caudal peduncle elongation, (c) eye size, (d) head length, (e) dorsal  
 65 fin size, (f) pectoral fin size, (g) eye position, (h) anal fin insertion, (i) pectoral fin insertion, and (j) dorsal fin insertion. The dashed line represents  
 66 the Ordinary Least Square regression between intra- and interspecific morphological variability. The reported P-values in each panel correspond  
 67 to the significance of the relation accounting for the phylogenetic relationship between species (PGLS: phylogenetic generalized least-squares).  
 68 Each symbol contains two colors, one corresponding to the intraspecific data set and the other to the interspecific data set.



70 **Supplementary Figure 9. Intraspecific morphological trait disparity (mtD) and genetic diversity ( $J_T$ ) relationships for fish traits.**  
 71 Phylogenetic generalized least squares (PGLS) controlled relationships between the intraspecific mtD and the overall genetic diversity ( $J_T$ ) for the  
 72 relative (a) body elongation, (b) eye size, (c) jaw length, (d) head length, (e) caudal peduncle height, (f) dorsal fin size, (g) pectoral fin size, (h)  
 73 eye position, (i) anal fin insertion, (h) eye position, (i) anal fin insertion and (j) pectoral fin insertion. The dashed line represents the Ordinary Least  
 74 Square regression between total genetic diversity ( $J_T$ ) and intraspecific morphological disparity. The reported P-values in each panel corresponds  
 75 to the significance of the relation accounting for phylogenetical relationship between species (PGLS: phylogenetic generalized least-squares)  
 76 Points are colored according to the interspecific data set, while labels indicate the intraspecific data set.

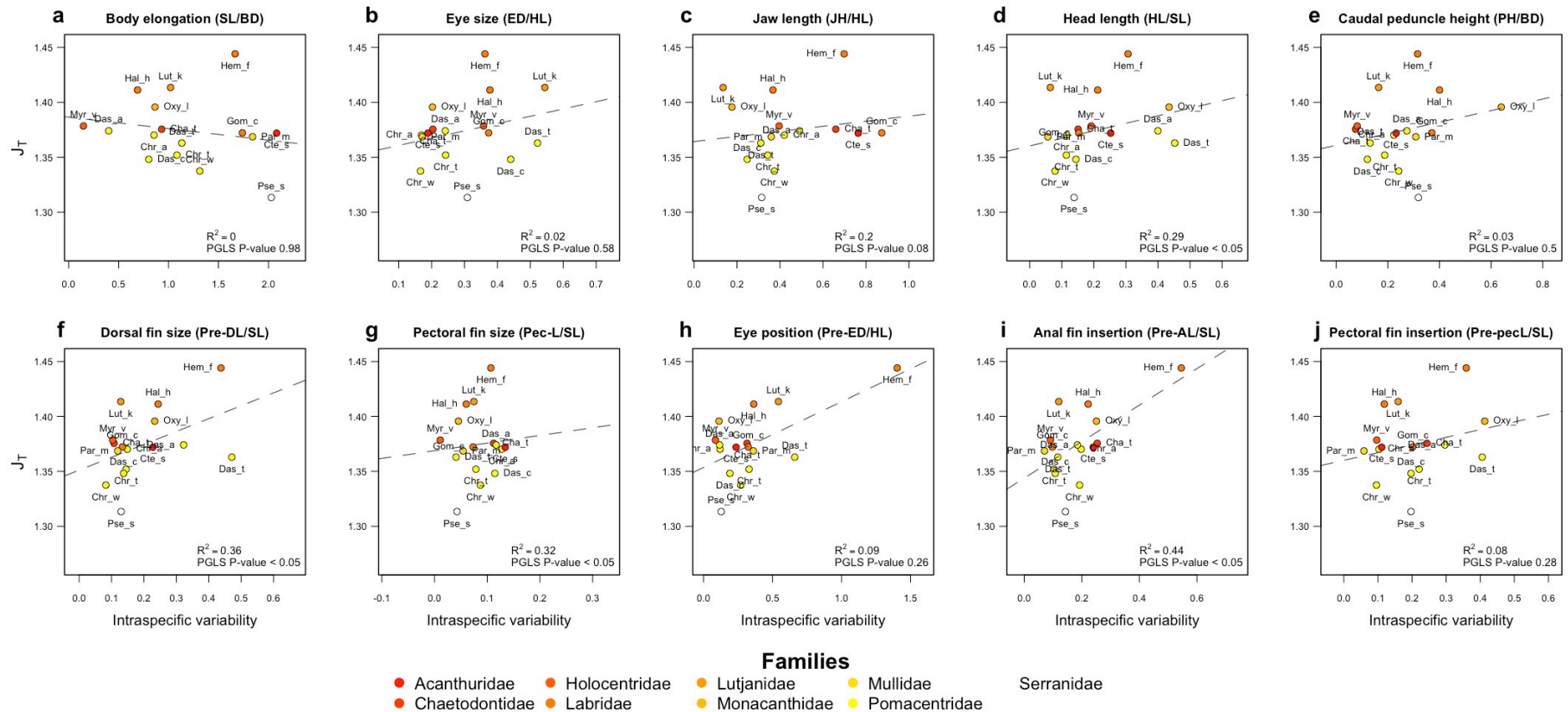


78 **Supplementary Figure 10. Relationships between the total intraspecific genetic diversity ( $J_T$ ) and the morphological trait variation for 16**  
 79 **tropical reef fish species when excluding the Carangid fish species, namely *Caranx melampyus*.** Phylogenetic generalized least squares  
 80 (PGLS) relationships between total intraspecific genetic diversity of the Western Indian Ocean and the variability in (a) relative anal fin size (AL:  
 81 anal fin length; SL: standard length), (b) caudal peduncle elongation (PL: caudal peduncle length; PH: caudal peduncle height), and (c) the dorsal  
 82 fin insertion (DL: dorsal fin length). The dashed line represents the Ordinary Least Square regression between total genetic diversity ( $J_T$ ) and  
 83 intraspecific morphological disparity. The reported P-values in each panel corresponds to the significance of the relation accounting for  
 84 phylogenetical relationship between species (PGLS: phylogenetic generalized least-squares). Points are colored according to the interspecific data  
 85 set, while labels indicate the intraspecific data set

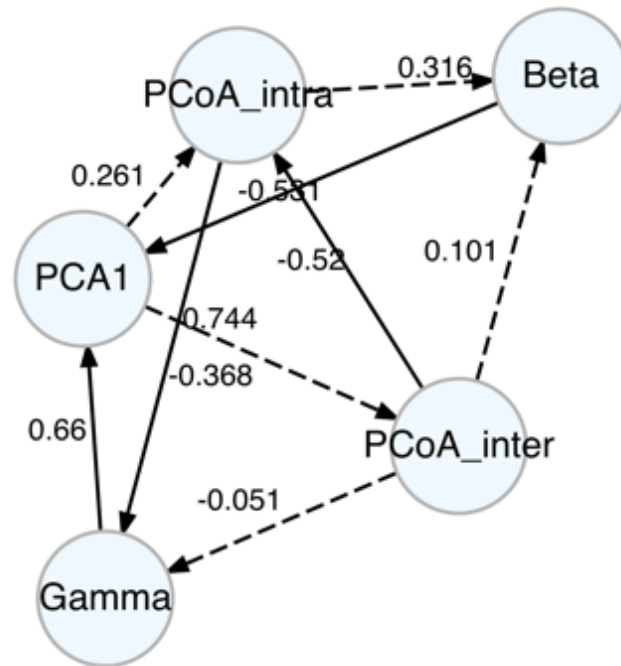


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87 **Supplementary Figure 11. Intraspecific morphological trait disparity (mtD) and genetic diversity ( $J_T$ ) relationships for 16 tropical reef**  
 88 **fish species when excluding the Carangid fish species, namely *Caranx melampyus*.** Phylogenetic generalized least squares (PGLS) controlled  
 89 relationships between the intraspecific mtD and the overall genetic diversity ( $J_T$ ) for the relative (a) body elongation, (b) eye size, (c) jaw length,  
 90 (d) head length, (e) caudal peduncle height, (f) dorsal fin size, (g) pectoral fin size, (h) eye position, (i) anal fin insertion, (j) pectoral fin insertion,  
 91 and (j) dorsal fin insertion. The dashed line represents the Ordinary Least Square regression between total genetic diversity ( $J_T$ ) and intraspecific  
 92 morphological disparity. Points are colored according to the interspecific data set, while labels indicate the intraspecific data set.



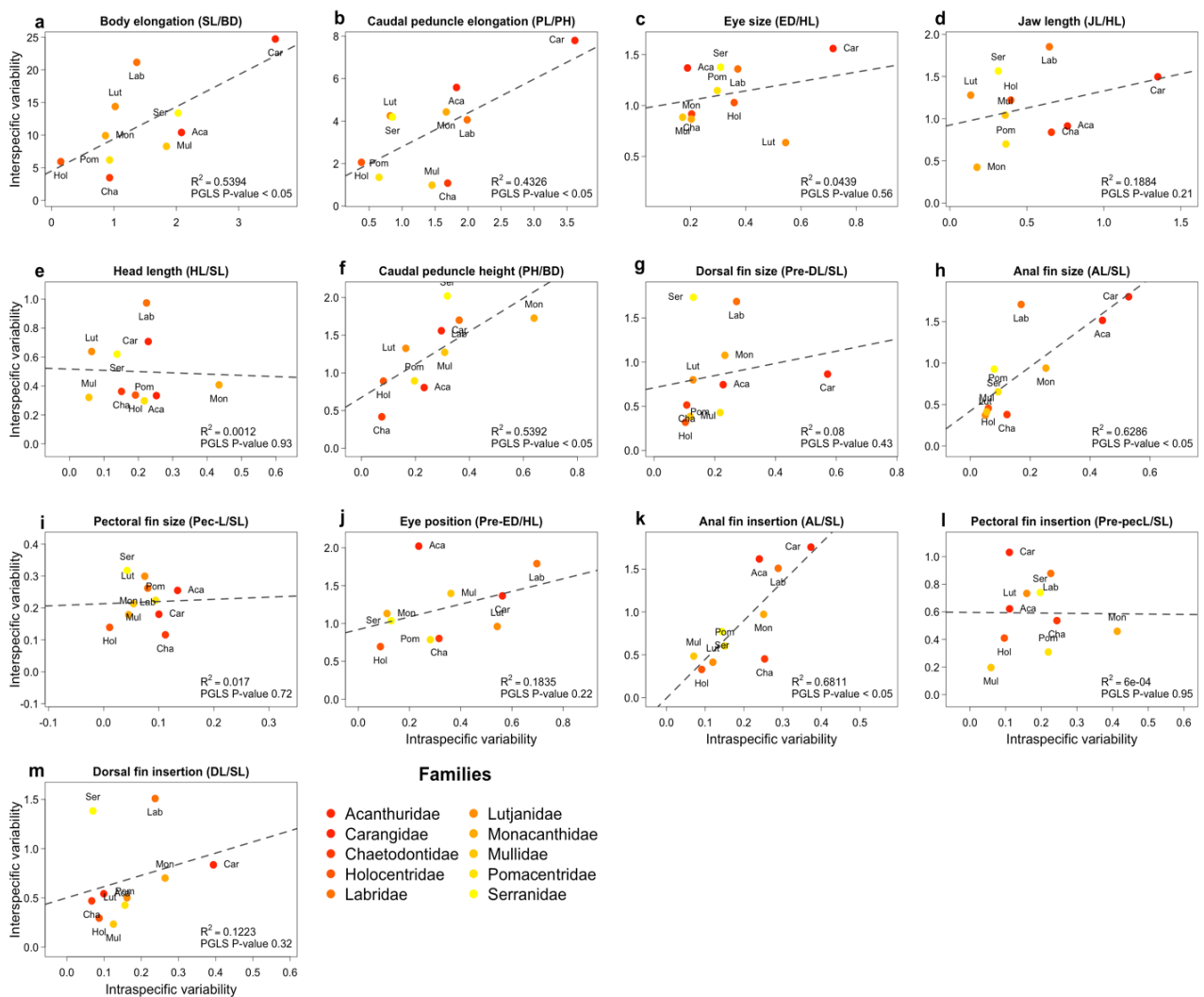
94 **Supplementary Figure 12. Structural equation model (SEM) linking genetic**  
95 **diversity and morphological trait (mtD) disparity.** SEM with dispersal trait BS (body  
96 size) and PLD (pelagic larval duration) included in a principal component analysis  
97 (PCA) axis and linked to  $\gamma$  diversity (Gamma) and  $\beta$  diversity (Beta). The relationships  
98 between the diversity components and intraspecific (PCoA\_intra) and interspecific  
99 (PCoA\_inter) trait disparity are also shown.



100  
101

102 **Supplementary Figure 13. Intra- and interspecific morphological trait disparity**  
 103 **(mtD) relationships for fish traits by averaging the traits variability by fish family.**  
 104 Phylogenetic generalized least squares (PGLS) controlled relationships between the  
 105 intra- and interspecific mtD in tropical reef fishes for (a) body elongation, relative (b)  
 106 caudal peduncle elongation, (c) eye size, (d) jaw length, (e) head length, (f) caudal  
 107 peduncle height, (g) dorsal fin size, (h) anal fin size, (i) pectoral fin size, (j) eye position,  
 108 (k) anal fin insertion, (l) pectoral fin insertion, and (m) dorsal fin insertion. The dashed  
 109 line represents the Ordinary Least Square regression between intra- and interspecific  
 110 morphological variability. The reported P-values in each panel corresponds to the  
 111 significance of the relation accounting for phylogenetical relationship between species  
 112 (PGLS: phylogenetic generalized least-squares). Each symbol contains two colors, one  
 113 corresponding to the intraspecific data set and the other to the interspecific data set.

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116

117 **Supplementary Table 1. Ecological trait information for the 17 tropical reef fish species**  
 118 **of the intraspecific data set.** PLD: pelagic larval duration (days). Home range was coded as  
 119 narrow for species with a restricted home range and wide for highly mobile species<sup>1</sup>. Diet was  
 120 retrieved from Fishbase<sup>2</sup> and recoded according to the predominant diet composition, where  
 121 PK stands for *plankton*, IS for *sessile invertebrates*, IM for *mobile benthic invertebrates*, OM  
 122 for *omnivores*, and FC for *piscivores* (see Methods for details).

123

Family	Genus species	PLD (days)	Home range	Diet
Carangidae	<i>Caranx melampyus</i>	57.6	wide	FC
Chaetodontidae	<i>Chaetodon trifasciatus</i>	43	narrow	IS
Pomacentridae	<i>Chromis atripectoralis</i>	19	narrow	PK
Pomacentridae	<i>Chromis ternatensis</i>	28.5	narrow	PK
Pomacentridae	<i>Chromis weberi</i>	31.2	narrow	PK
Acanthuridae	<i>Ctenochaetus striatus</i>	43.87	narrow	OM
Pomacentridae	<i>Dascyllus aruanus</i>	21.1	narrow	PK
Pomacentridae	<i>Dascyllus carneus</i>	24.3	narrow	PK
Pomacentridae	<i>Dascyllus trimaculatus</i>	28	narrow	PK
Labridae	<i>Gomphosus caeruleus</i>	56.6	wide	IM
Labridae	<i>Halichoeres hortulanus</i>	32.5	wide	IM
Labridae	<i>Hemigymnus fasciatus</i>	25.8	wide	IM
Lutjanidae	<i>Lutjanus kasmira</i>	31	wide	IM
Holocentridae	<i>Myripristis violacea</i>	60.4	wide	PK
Monacanthidae	<i>Oxymonacanthus longirostris</i>	25.95	narrow	IS
Mullidae	<i>Parupeneus macronemus</i>	41.8	wide	IM
Serranidae	<i>Pseudanthias squamipinnis</i>	26	narrow	PK

124



125 **Supplementary Table 2. The intraspecific data set (n = 1111 individuals, 17 species, 10 families).** Specimens constituting this data set were  
 126 collected in four regions of the Western Indian Ocean during 2016–2017. The table includes taxonomic information and the number of individuals  
 127 sampled per population (i.e., Maldives, Mayotte Island, Seychelles and Mafia Island).

Family	Genus species	Number of individuals (n)				Total
		Maldives	Mayotte	Seychelles	Mafia	
Carangidae	<i>Caranx melampyngus</i>	3	0	2	3	8
Chaetodontidae	<i>Chaetodon trifasciatus</i>	18	32	10	11	71
Pomacentridae	<i>Chromis atripectoralis</i>	15	53	14	9	91
Pomacentridae	<i>Chromis ternatensis</i>	15	47	11	10	83
Pomacentridae	<i>Chromis weberi</i>	18	71	15	11	115
Acanthuridae	<i>Ctenochaetus striatus</i>	26	40	6	12	84
Pomacentridae	<i>Dascyllus aruanus</i>	15	7	9	11	42
Pomacentridae	<i>Dascyllus carneus</i>	30	82	9	8	129
Pomacentridae	<i>Dascyllus trimaculatus</i>	11	7	9	11	38
Labridae	<i>Gomphosus caeruleus</i>	24	24	10	10	68
Labridae	<i>Halichoeres hortulanus</i>	28	33	10	10	81
Labridae	<i>Hemigymnus fasciatus</i>	11	12	11	6	40
Lutjanidae	<i>Lutjanus kasmira</i>	9	11	4	10	34
Holocentridae	<i>Myripristis violacea</i>	10	9	13	10	42
Monacanthidae	<i>Oxymonacanthus longirostris</i>	12	44	3	8	67
Mullidae	<i>Parupeneus macronemus</i>	23	23	9	11	66
Serranidae	<i>Pseudanthias squamipinnis</i>	19	8	11	14	52
						1111

128

129 **Supplementary Table 3. Fish body landmarks and derived morphological traits.**

130 This table describes each biometric (a) measure and (b) ratio used in our analyses. To  
 131 replace missing points in the interspecific (i.e., above species level) data set, the two  
 132 most extreme points on the x axis were used as a measure of standard length (i.e.,  
 133 Landmark A; LMA: 15, Landmark B; LMB: 16), while the two most extreme points on  
 134 the y axis were used as a measure of body depth (i.e., LM 14, 17). The linear distance  
 135 measures (a; L1; L2) were converted into ratios (b; L1/L2) to serve as components of  
 136 body, head and fin shapes. As with the procrustes-aligned body landmarks, the use of  
 137 ratios reduces the chance that the analysis is dominated by a single variable, e.g., body  
 138 size.

Type	Body part	LMA	LMB	Code	Biometric description
(a) Length	Head	2	1	JL - measure	Jaw length
		15	12	Pre-ED - measure	Pre ocular distance
		12	13	ED - measure	Eye diameter
		15	11	HL - measure	Head length
	Body	14	17	BD - measure	Body depth
		15	16	SL - measure	Standard length
		4	16	PL - measure	Caudal peduncle length
		4	7	PH - measure	Caudal peduncle height
	Fin	15	8	Pre-AL - measure	Anal fin anterior insertion
		8	7	AL - measure	Anal fin length
		15	3	Pre-DL - measure	Dorsal fin anterior insertion
		3	4	DL - measure	Dorsal fin length
		15	9	Pre-Pec-L - measure	Pectoral fin anterior insertion
		9	10	Pec-L - measure	Base of the pectoral fin length
	Type	Body part	L1	L2	Code
(b) Ratio	Head	JL	HL	JL	Jaw-head-length relationship
		Pre-ED	HL	Pre-ED	Eye-head-position relationship
		ED	HL	ED	Eye-head-size relationship
		HL	SL	HL	Head-body-length relationship
	Body	SL	BD	Bod-Elo	Body elongation
		PL	PH	Ped-Elo	Caudal peduncle elongation
		PH	BD	Ped-H	Caudal-peduncle-body-height relationship
	Fin	Pre-AL	SL	Pre-AL	Pre-anal length standardized by standard length
		AL	SL	AL	Anal fin length standardized by standard length
		Pre-DL	SL	Pre-DL	Pre-dorsal fin length standardized by standard length
		DL	SL	DL	Dorsal fin length standardized by standard length
		Pre-Pec-L	SL	Pre-Pec-L	Pre-pectoral fin length standardized by standard length
		Pec-L	SL	Pec-L	Pectoral fin length standardized by standard length

139

140 **Supplementary Table 4. Population sample size and single nucleotide polymorphisms (SNP) data on 17 tropical reef fish species.** The table  
141 includes information on the total sampling success per sampling sites (MF: Mafia Island; MV: Maldives; MY: Mayotte Island; SC: Seychelles),  
142 as well as the number of raw SNPs and filtered SNPs used in the downstream analyses (see genotyping in Methods). To compute genetic diversity  
143 metrics across the 17 species, the SNP data had to be down-sampled to the lowest common number of filtered SNPs and number of individuals  
144 per population standardized over 999 randomizations (see genotyping and computation of genetic diversity metrics in Methods).

Genus species	Species code	Total sampling						Standardized resampling 999×				
		MF	MV	MY	SC	Total SNPs	Filtered SNPs	MF	MV	MY	SC	Resampled SNPs
<i>Caranx melampygus</i>	Car_m	3	4	6	2	107395	15431	3	4	6	2	4479
<i>Chaetodon trifasciatus</i>	Cha_t	11	12	15	10	327595	20950	10	10	10	10	4479
<i>Chromis atripectoralis</i>	Chr_a	3	9	9	13	1255718	7225	3	9	9	10	4479
<i>Chromis ternatensis</i>	Chr_t	10	14	14	9	873075	17369	10	10	10	9	4479
<i>Chromis weberi</i>	Chr_w	10	10	13	12	926904	14370	10	10	10	10	4479
<i>Ctenochaetus striatus</i>	Cte_s	10	15	40	4	697607	9664	10	10	10	4	4479
<i>Dascyllus aruanus</i>	Das_a	11	12	7	8	986800	22105	10	10	7	8	4479
<i>Dascyllus carneus</i>	Das_c	8	17	20	9	1086702	16260	8	10	10	9	4479
<i>Dascyllus trimaculatus</i>	Das_t	8	12	8	10	682522	38934	8	10	8	10	4479
<i>Gomphosus caeruleus</i>	Gom_c	9	12	12	10	854088	6253	9	10	10	10	4479
<i>Halichoeres hortulanus</i>	Hal_h	7	14	13	9	242929	18934	7	10	10	9	4479
<i>Hemigymnus fasciatus</i>	Hem_f	10	11	11	10	229050	15606	10	10	10	10	4479
<i>Lutjanus kasmira</i>	Lut_k	9	9	11	4	806613	7420	9	9	10	4	4479
<i>Myripristis violacea</i>	Myr_v	10	9	7	12	463771	14890	10	9	7	10	4479
<i>Oxymonacanthus longirostris</i>	Oxy_l	8	11	35	3	111506	9679	8	10	10	3	4479
<i>Parupeneus macronema</i>	Par_m	9	17	22	7	635207	7432	9	10	10	7	4479
<i>Pseudanthias squamipinnis</i>	Pse_s	13	15	8	11	696705	4479	10	10	8	10	4479

145 **Supplementary Table 5. The interspecific data set (n = 1061 species, 10 families).** Specimens constituting this data set were extracted from <sup>3</sup>.  
 146 The table includes taxonomic information and the number of species within each genus for the 10 tropical reef fish families that are also found in  
 147 the intraspecific data set.

Genus	n	Family	Genus	n	Family	Genus	n	Family	Genus	n	Family	Genus	n	Family	
<i>Acanthurus</i>	29	Acanthuridae	<i>Myripristis</i>	17	Holocentridae	<i>Pseudocoris</i>	4	Labridae	<i>Stephanolepis</i>	1	Monacanthidae	<i>Cromileptes</i>	1	Serranidae	
<i>Ctenochaetus</i>	8		<i>Neoniphon</i>	4		<i>Pseudodax</i>	1		<i>Thamnaconus</i>	3		<i>Dermatolepis</i>	1		
<i>Naso</i>	12		<i>Ostichthys</i>	5		<i>Pseudojuloides</i>	7		<i>Mulloidichthys</i>	2		Mullidae	<i>Diploprion</i>		2
<i>Paracanthurus</i>	1		<i>Plectrypops</i>	1		<i>Pseudolabrus</i>	8		<i>Parupeneus</i>	20	<i>Epinephelus</i>		55		
<i>Prionurus</i>	3		<i>Pristilepis</i>	1		<i>Pteragogus</i>	7		<i>Upeneichthys</i>	1	<i>Gracila</i>		1		
<i>Zebrasoma</i>	6		<i>Sargocentron</i>	24		<i>Stethojulis</i>	7		<i>Suezichthys</i>	2	<i>Upeneus</i>	1	<i>Grammistes</i>		1
<i>Alectis</i>	2		<i>Ammolabrus</i>	1		<i>Thalassoma</i>	17		<i>Abudefduf</i>	13	<i>Grammistops</i>	1	<i>Holanthias</i>		8
<i>Alepes</i>	5	<i>Anampses</i>	12	<i>Wetmorella</i>	2	<i>Acanthochromis</i>	1	<i>Hypoplectrodes</i>	2	<i>Luzonichthys</i>	10				
<i>Atule</i>	1	<i>Bodianus</i>	15	<i>Xiphocheilus</i>	1	<i>Amblyglyphidodon</i>	4	<i>Liopropoma</i>	3	<i>Nemanthias</i>	1				
<i>Carangoides</i>	12	<i>Cheilinus</i>	7	<i>Xyrichtys</i>	11	<i>Amblypomacentrus</i>	2	<i>Luzonichthys</i>	3	<i>Plectranthias</i>	11				
<i>Caranx</i>	6	<i>Cheilio</i>	1	<i>Aphareus</i>	2	<i>Amphiprion</i>	21	<i>Nemanthias</i>	1	<i>Plectropomus</i>	7				
<i>Decapterus</i>	3	<i>Choerodon</i>	15	<i>Aprion</i>	1	<i>Cheiloprion</i>	1	<i>Plectranthias</i>	11	<i>Pogonoperca</i>	1				
<i>Elagatis</i>	1	<i>Cirrhitlabrus</i>	25	<i>Aprion</i>	1	<i>Chromis</i>	53	<i>Plectropomus</i>	7	<i>Pseudanthias</i>	43				
<i>Gnathanodon</i>	1	<i>Conniella</i>	1	<i>Etelis</i>	2	<i>Chrysiptera</i>	23	<i>Pseudogramma</i>	6	<i>Rabaulichthys</i>	1				
<i>Megalaspis</i>	1	<i>Coris</i>	16	<i>Lipocheilus</i>	1	<i>Dascyllus</i>	9	<i>Rabaulichthys</i>	1	<i>Rainfordia</i>	1				
<i>Parastromateus</i>	1	<i>Cymolutes</i>	3	<i>Lutjanus</i>	35	<i>Dischistodus</i>	5	<i>Rainfordia</i>	1	<i>Sacura</i>	2				
<i>Pseudocaranx</i>	2	<i>Diproctacanthus</i>	1	<i>Macolor</i>	1	<i>Hemiglyphidodon</i>	1	<i>Serranocirrhitus</i>	1	<i>Suttonia</i>	1				
<i>Scomberoides</i>	3	<i>Epibulus</i>	2	<i>Paracaesio</i>	4	<i>Lepidozygus</i>	1	<i>Suttonia</i>	1	<i>Trachypoma</i>	1				
<i>Selar</i>	1	<i>Gomphosus</i>	2	<i>Pinjalo</i>	2	<i>Neoglyphidodon</i>	8	<i>Trachypoma</i>	1	<i>Variola</i>	2				
<i>Selaroides</i>	1	<i>Halichoeres</i>	44	<i>Pristipomoides</i>	8	<i>Neopomacentrus</i>	12								
<i>Seriola</i>	3	<i>Hemigymnus</i>	2	<i>Symphoricichthys</i>	1	<i>Parma</i>	2								
<i>Seriolina</i>	1	<i>Hologymnosus</i>	3	<i>Symphorus</i>	1	<i>Plectroglyphidodon</i>	9								
<i>Trachinotus</i>	6	<i>Labrichthys</i>	1	<i>Acreichthys</i>	1	<i>Pomacentrus</i>	34								
<i>Trachurus</i>	1	<i>Labroides</i>	5	<i>Aluterus</i>	1	<i>Pomacentrus</i>	3								
<i>Ulua</i>	1	<i>Labropsis</i>	6	<i>Amanes</i>	1	<i>Premnas</i>	1								
<i>Amphichaetodon</i>	2	<i>Larabicus</i>	1	<i>Brachaluteres</i>	1	<i>Pristotis</i>	2								
<i>Chaetodon</i>	73	<i>Leptojulius</i>	4	<i>Cantherhines</i>	7	<i>Stegastes</i>	11								
<i>Chelmon</i>	3	<i>Macropharyngodon</i>	8	<i>Meuschenia</i>	1	<i>Acanthistius</i>	1								
<i>Chelmonops</i>	1	<i>Novaculichthys</i>	4	<i>Monacanthus</i>	2	<i>Monacanthus</i>	1								
<i>Coradion</i>	3	<i>Oxycheilinus</i>	7	<i>Oxymonacanthus</i>	2	<i>Anyperodon</i>	1								
<i>Forcipiger</i>	2	<i>Paracheilinus</i>	8	<i>Paraluteres</i>	1	<i>Aporops</i>	1								
<i>Hemitaurichthys</i>	3	<i>Parajulis</i>	1	<i>Paramonacanthus</i>	3	<i>Aulacocephalus</i>	1								
<i>Heniochus</i>	7	<i>Polylepion</i>	1	<i>Pervagor</i>	8	<i>Belonoperca</i>	2								
<i>Parachaetodon</i>	1	<i>Pseudocheilinos</i>	1	<i>Pseudalutarius</i>	1	<i>Caprodon</i>	2								
<i>Prognathodes</i>	1	<i>Pseudocheilinus</i>	4	<i>Pseudomonacanthus</i>	1	<i>Cephalopholis</i>	18								
												<b>Total species</b>	<b>1061</b>		

148 **Supplementary Table 6.** Values of multiplicative and additive partitioning frameworks of  
149 genetic diversity. To quantify the different  $\bar{\alpha}$ ,  $\beta$  and  $\gamma$  components we used the partitioning for  
150 true diversities proposed by <sup>4</sup> and applied to genetic data, expressed as follows:  $J_T = J_S \times J_{ST}$ ,  
151 where  $J_S$  represents the within-population genetic component ( $\bar{\alpha}$ ),  $J_{ST}$  represents the between-  
152 population ( $\beta$ ) component, and  $J_T$  represents the overall genetic diversity ( $\gamma$ ). All of these  
153 metrics were calculated for each species and each of the  $999 \times 4479$  SNP data sets.  
154

Genus species	$J_T$ ( $\gamma$ )	$J_S$ ( $\bar{\alpha}$ )	$J_{ST}$ ( $\beta$ )
<i>Canthigaster valentini</i>	1.3785	1.3743	1.0030
<i>Caranx melampygus</i>	1.4721	1.4739	1.0000
<i>Chaetodon trifasciatus</i>	1.3755	1.3735	1.0015
<i>Chromis atripectoralis</i>	1.3702	1.3655	1.0034
<i>Chromis ternatensis</i>	1.3520	1.3459	1.0045
<i>Chromis weberi</i>	1.3375	1.3317	1.0043
<i>Ctenochaetus striatus</i>	1.3720	1.3717	1.0002
<i>Dascyllus aruanus</i>	1.3741	1.3654	1.0064
<i>Dascyllus carneus</i>	1.3482	1.3466	1.0011
<i>Dascyllus trimaculatus</i>	1.3630	1.3615	1.0011
<i>Gomphosus caeruleus</i>	1.3722	1.3716	1.0004
<i>Halichoeres hortulanus</i>	1.4112	1.4097	1.0011
<i>Hemigymnus fasciatus</i>	1.4441	1.4241	1.0140
<i>Lutjanus kasmira</i>	1.4135	1.4131	1.0003
<i>Myripristis violacea</i>	1.3785	1.3783	1.0001
<i>Oxymonacanthus longirostris</i>	1.3957	1.3782	1.0127
<i>Parupeneus macronemus</i>	1.3686	1.3625	1.0045
<i>Pseudanthias squamipinnis</i>	1.3134	1.3099	1.0026

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