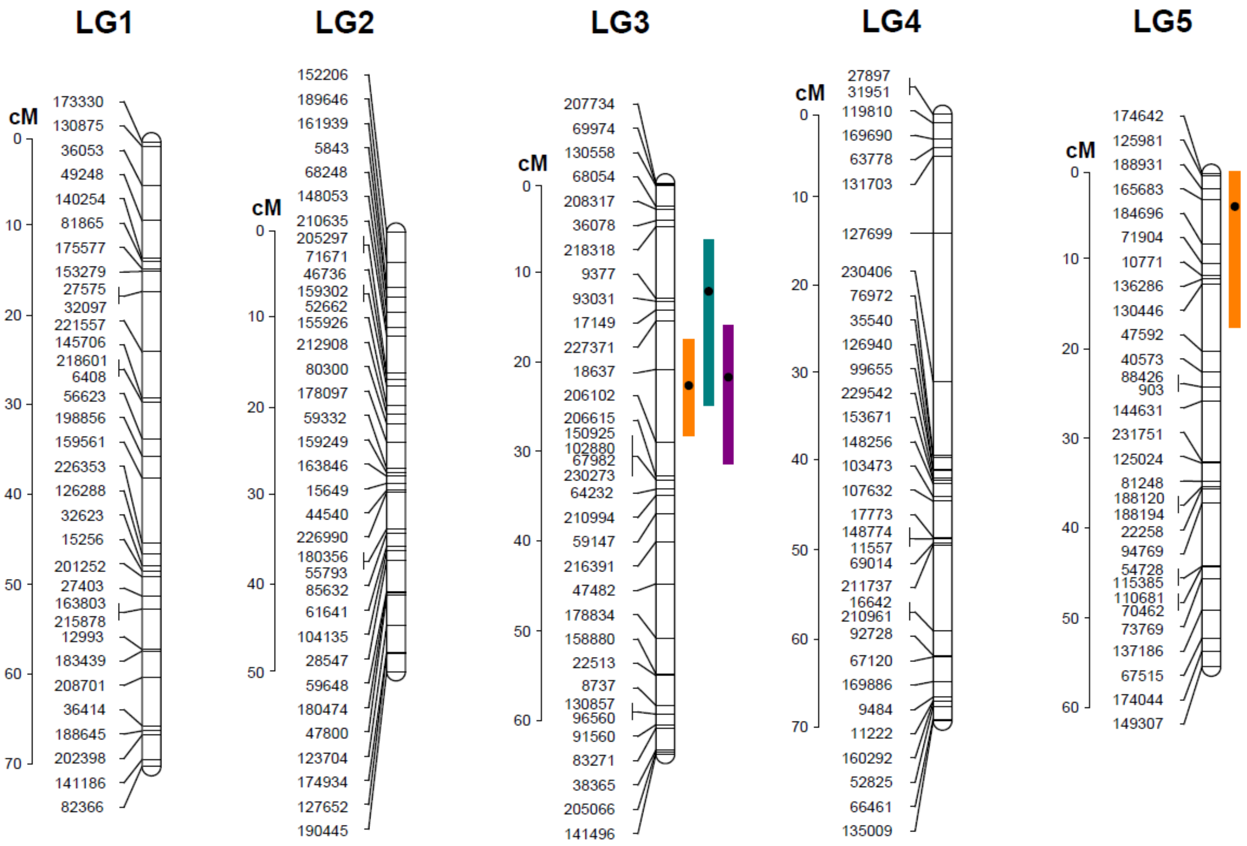
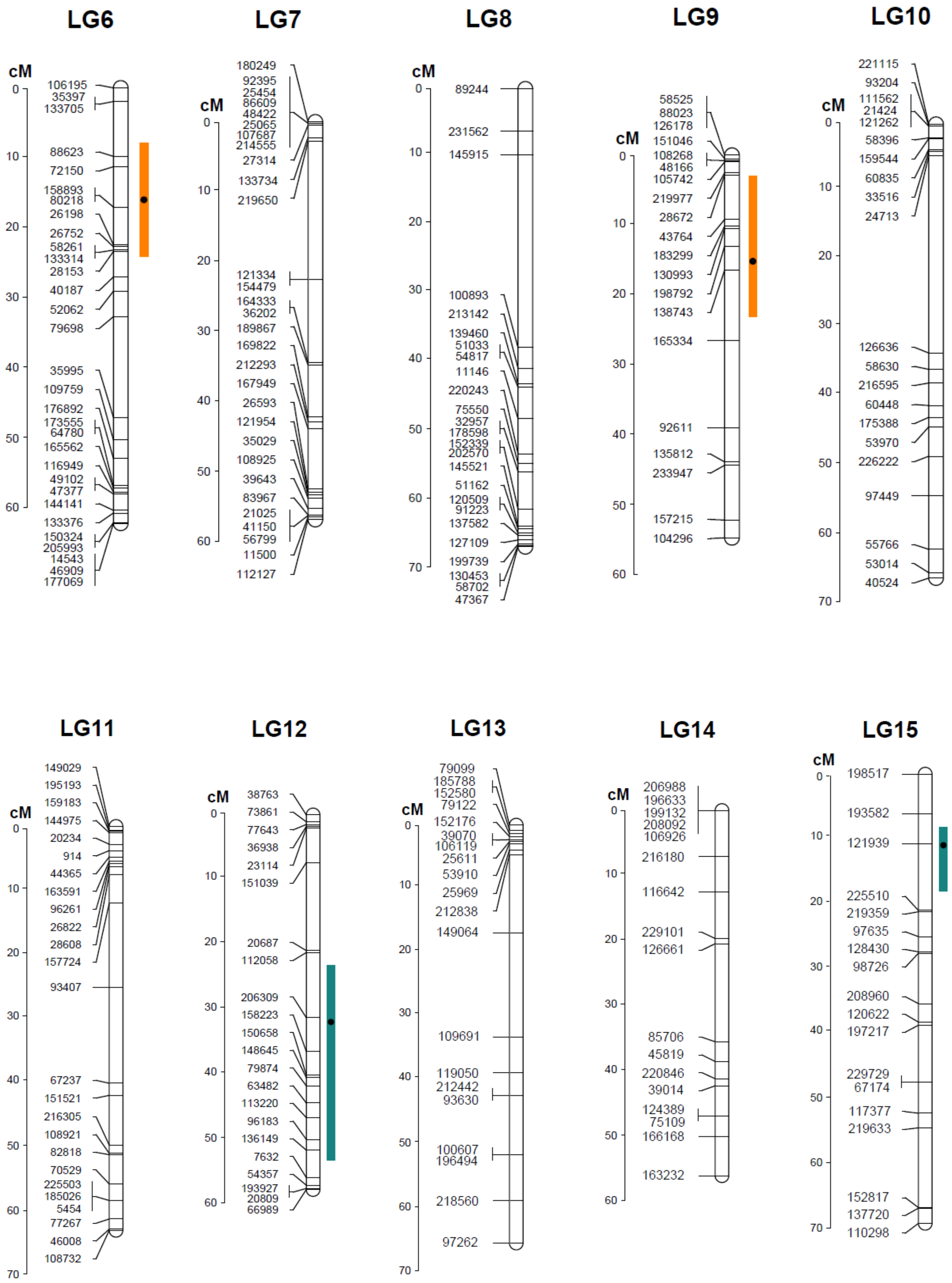
Supplementary Figures

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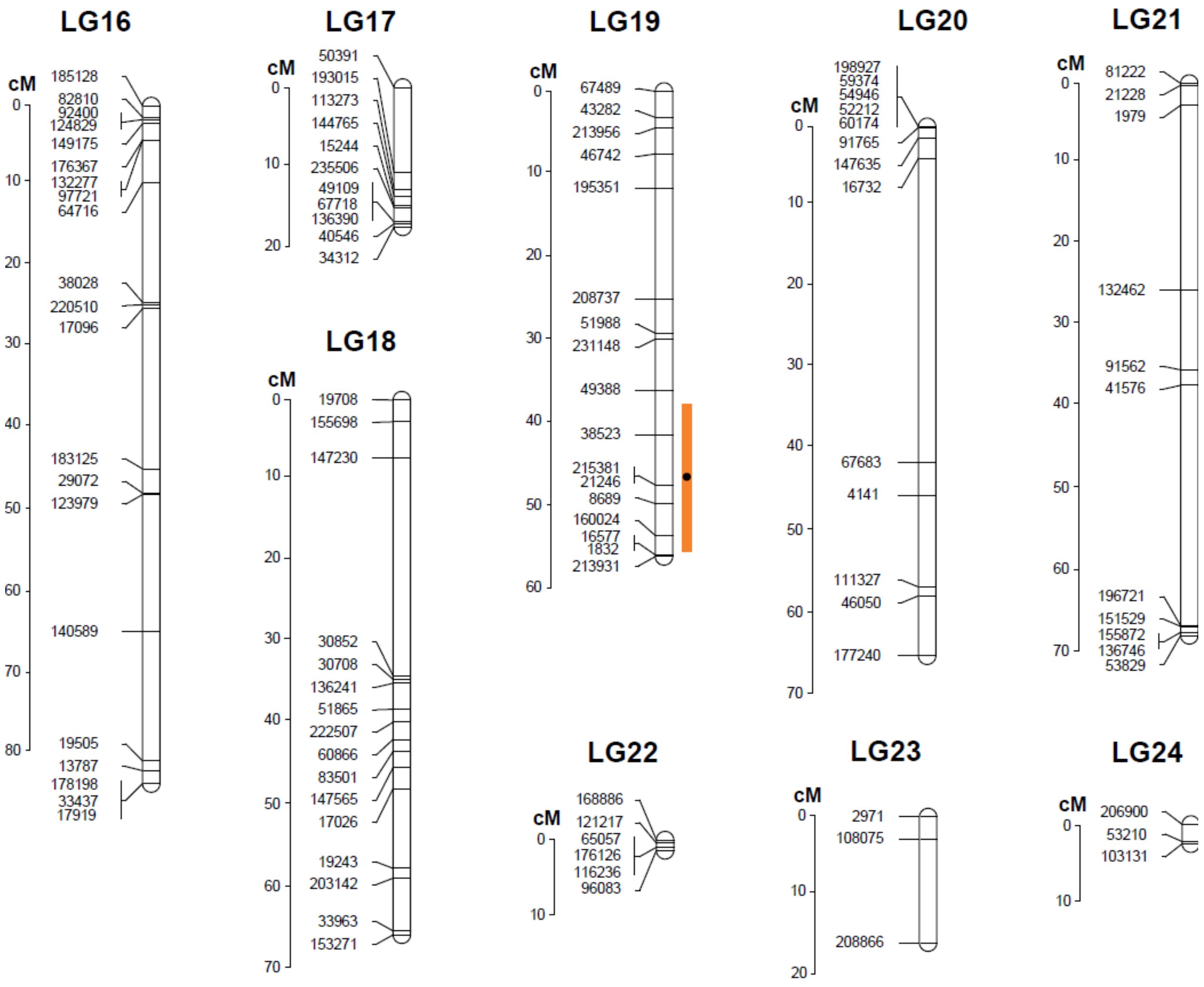
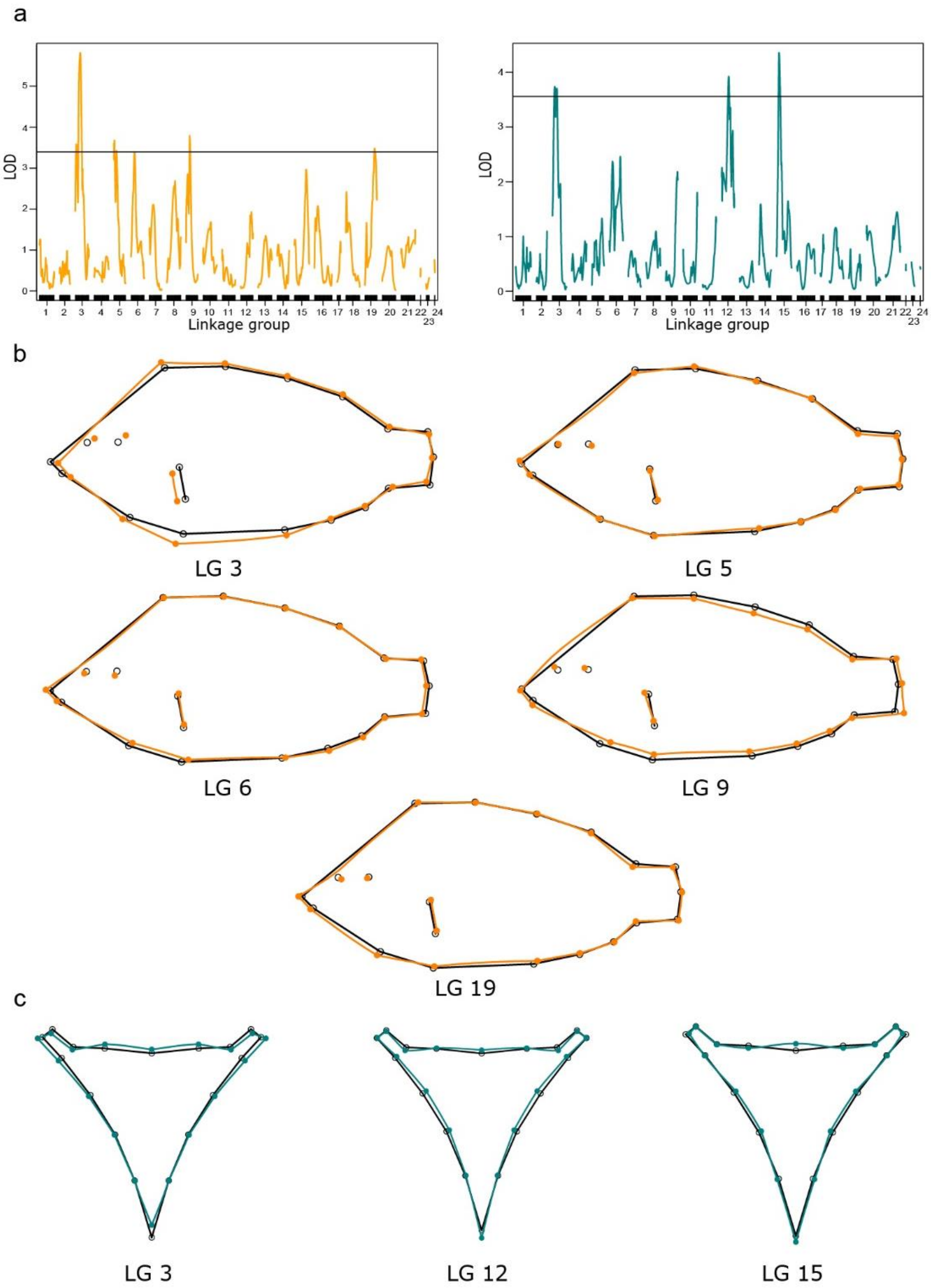
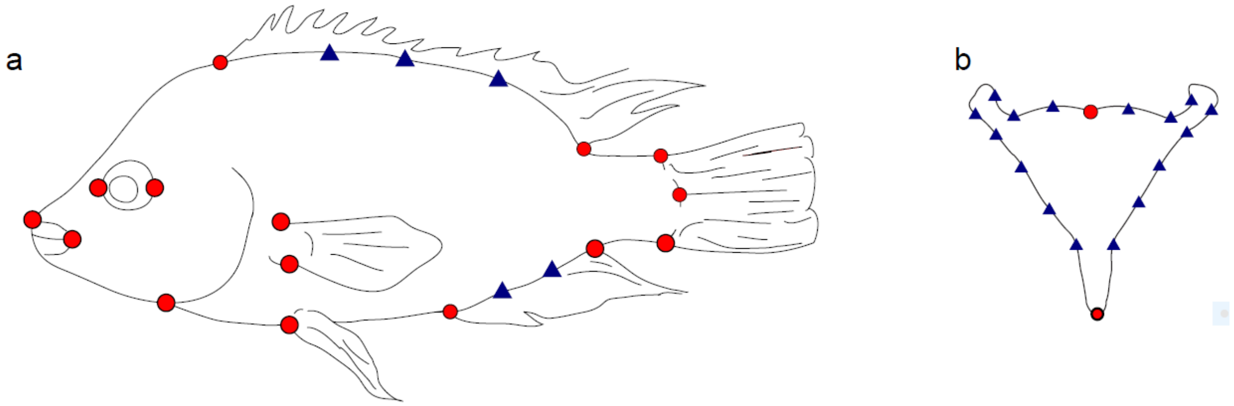


Supplementary Figure 1 | Linkage map and QTL location. Linkage groups (LG) obtained with an F2 mapping design (*A. astorquii* x *A. zaliosus*). Recombination map distances are indicated with a scale in centiMorgan (cM) on the left of each LG. Marker IDs, as numbered by the Stacks software, are given on the left of the LGs with lines pointing their position. Colored bars on the right of the LGs (when present) indicate the Bayesian confidence interval for the QTL position: orange bars, body shape; green bars, pharyngeal jaw shape; violet bar, covariation of body shape and pharyngeal jaw shape. Black dots on the colored bars indicate the position at which the highest LOD score of the QTL is found (see Supplementary Table 1 for details).

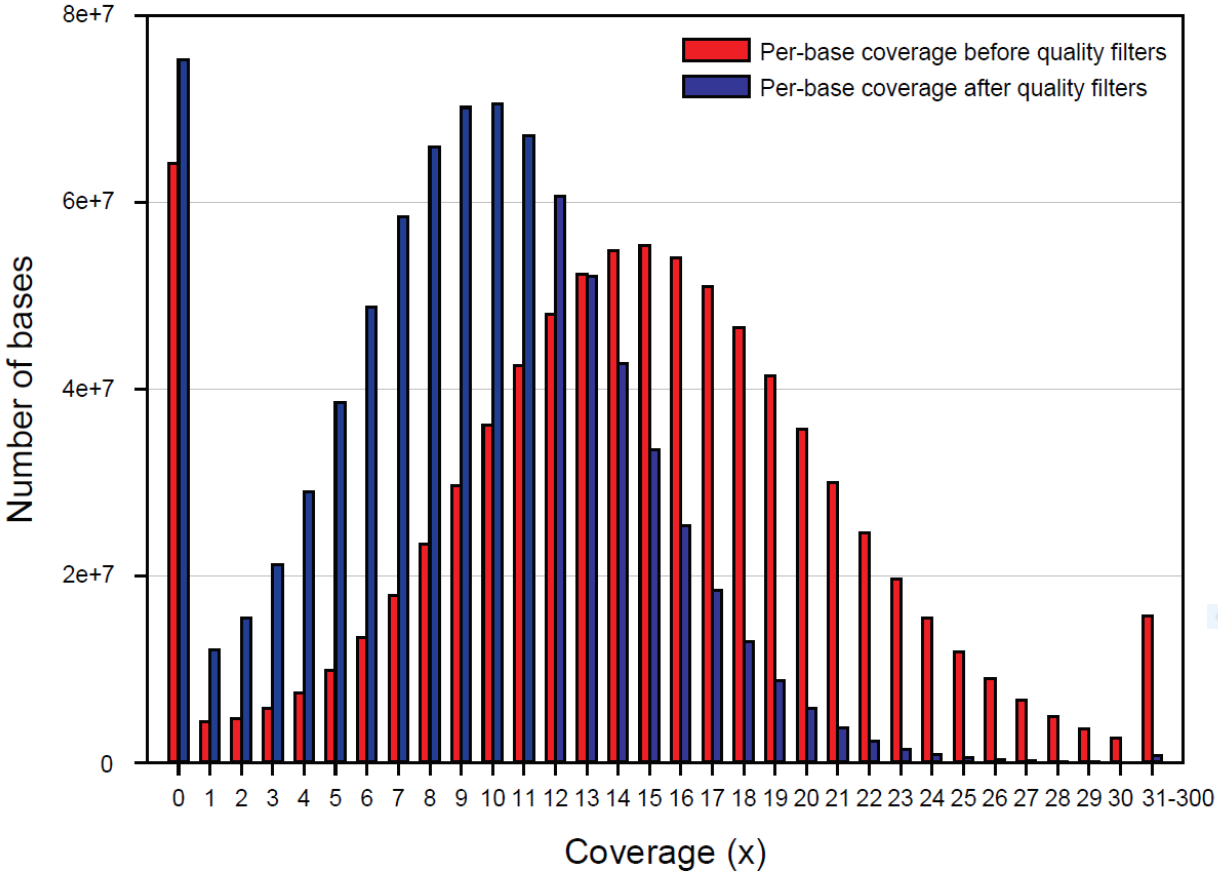


Supplementary Figure 2 | LOD score profiles and additive genetic effect of QTL. (**a**) LOD scores at each position in each linkage group (left, body shape; right, pharyngeal jaw shape). The horizontal line identifies the genome-wide significance threshold obtained through permutations

(LOD=3.39 for body shape, LOD=3.56 for pharyngeal jaw shape). (**b)** Additive genetic effect at each QTL for body shape. (**c**) Additive genetic effect at each QTL for pharyngeal jaw shape. Effects are depicted as shape change (colored wireframe) relative to a common starting shape (black wireframe). Within each trait, effects are scaled in the same way so that higher difference between the colored and the black wireframes correspond to higher effect sizes.



Supplementary Figure 3 | Configuration of points used in the geometric morphometric analyses of shape. Points in red have been treated as landmarks, blue triangles represent semilandmarks. (**a**) Body. (**b**) Lower pharyngeal jaw.



Supplementary Figure 4 | Coverage distribution of the PoolSeq dataset. The bar plot shows the per-base coverage distribution along the Midas genome of the two species pools combined. The grouped red and blue bars indicate the coverage before and after the quality filters applied (see Methods for details).

Supplementary Tables

Trait	LG	LOD score	Bayesian credible interval (cM)	Additive effect (SS)	Additive effect (%)	Additive effect (LOD)	Dominant effect (SS)	Dominant effect (%)	Dominant effect (LOD)
Body shape	3	5.8184	18-23-28	0.0047	3.86	10.83	0.0024	1.96	0.07
Body shape	5	3.6775	0-3-17	0.0019	1.52	5.9	0.0023	1.91	0.27
Body shape	6	3.3903	8-17.4-23.2	0.0025	2	2.95	0.0026	2.1	1.35
Body shape	9	3.7923	4-16.8-23	0.0038	3.07	5.43	0.0029	2.33	0.47
Body shape	19	3.4841	38-47-56	0.002	1.64	4.73	0.002	1.62	0.48
Pharyngeal jaw shape	3	3.7369	6-11-24	0.0048	4.08	3.19	0.0035	3	1.51
Pharyngeal jaw shape	12	3.9260	24-33-54	0.0034	2.92	2.78	0.0064	5.47	2.03
Pharyngeal jaw shape	15	4.3561	9-11-18	0.0031	2.62	3.77	0.0026	2.2	1.61
Shape covariation	3	5.5507	16-22-31	0.0064	8.56	6.81	0.0011	1.5	0.14

Supplementary Table 1 | Position and effect of QTL of body shape, pharyngeal jaw shape and their covariation. Summary of the QTL significant at the permutational genome-wide threshold. LOD scores are provided for the peak at the center of the Bayesian credible interval. Permutational-derived LOD significance thresholds are 3.39 for body shape, 3.56 for pharyngeal jaw shape and 3.52 for their covariation. The Bayesian credible interval is provided in centiMorgan in the form “lower extreme-center-upper extreme”. QTL effects are expressed as sum of squares and as percentage of the total Procrustes sum of squares in the mapping population.