

Supplemental table legends and figures with legends for DeLorenzo et al.

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**Table S1. Statistical significance for phenotypic measures.** Significance among each pair of *Labidochromis* parents, *Labeotropheus* parents, and their F<sub>2</sub> hybrids were assessed by ANOVA and Tukeys HSD on size-corrected, residual values. These data support significance notations in Figure 2.

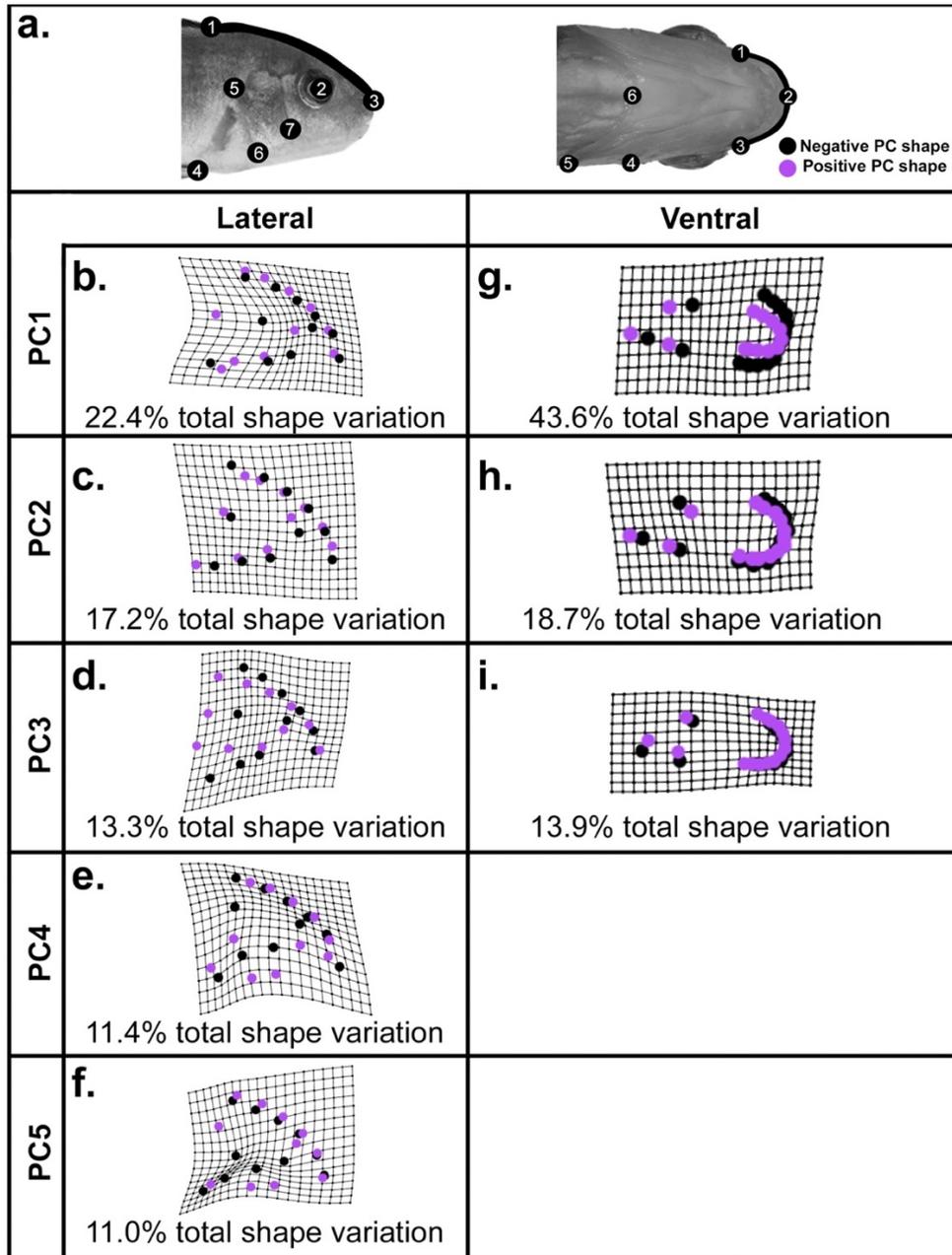
**Table S2. Correlations between all pairs of phenotypic traits in *Labidochromis* x *Labeotropheus* F<sub>2</sub> hybrids.** Calculations are for F<sub>2</sub> hybrids only. Except for correlations with standard length, all measures are size corrected. PC scores from geometric morphometric analysis were size corrected prior to assessing correlation with standard length. Values that are >0.8 or <-0.8 are in bold.

**Table S3. Details of quantitative trait loci (QTL).** For each QTL, we list cofactors used to generate models. Markers names and genetic positions in centimorgans (cM) are noted for the peak of the QTL and the upper and lower bounds of the 95% confidence interval. Marker names include the physical location on the linkage group, with names referring to the contig and nucleotide position in the *M. zebra* UMD2a assembly. LOD values, percent phenotypic variance explained by that QTL, allelic effects, and additive, dominance, and heritability calculations are for the peak marker in the QTL. QTL listed in gray text are suggestive at the 10% significance level, while those in black text meet 5% genome-wide significance based on values indicated.

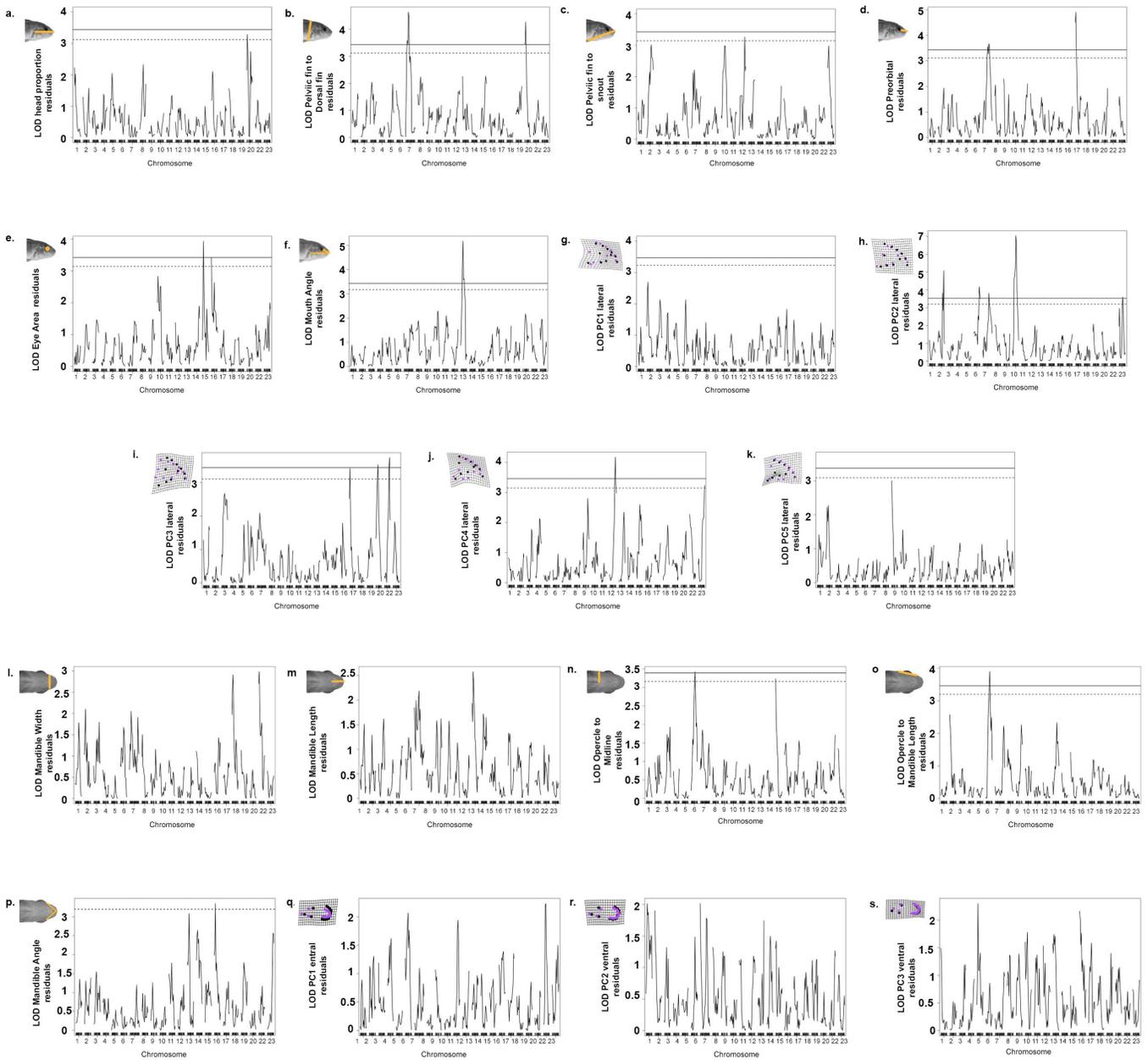
**Table S4. Candidate genes for head shape variation QTL.** For the indicated 95% confidence interval, we include candidate gene names in the *M. zebra* annotation release 104, NCBI gene ID number, and physical positions in the *M. zebra* genome UMD2a assembly.

**Table S5. Gene ontology (GO) analysis for enriched processes in candidate genes for QTL.** Over-represented biological process GO terms (p<0.05) associated with genes

in QTL intervals for each individual trait, all lateral QTL, and all ventral QTL. Each GO term includes the number of genes and NCBI Gene ID that are in the QTL interval(s) and match the category, fold enrichment, and p-value.



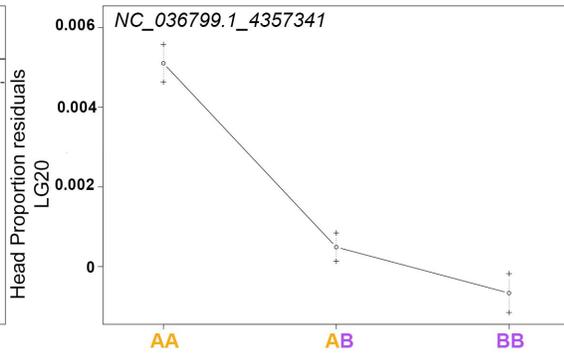
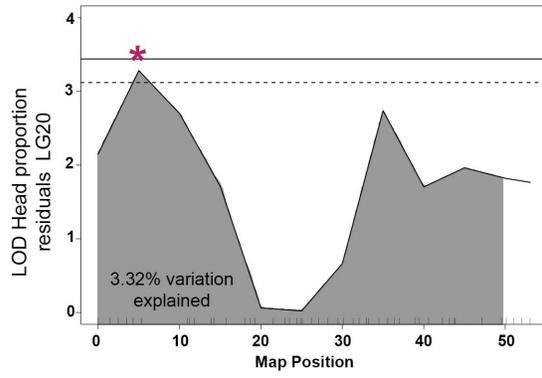
**Figure S1. Shapes indicated by PC scores following geometric morphometric analysis.** Landmarks used in analysis are as indicated in (a) and described in Figure 1. Shape illustrated by negative PC scores are in black dots and shapes for positive PC scores are in purple dots. Lateral shapes are in (b-f) and ventral analysis in (g-i) for (b, g) PC1 scores, (c, h) PC2 scores, (d, i) PC3 scores, (e) PC4 scores, and (f) PC5 scores. PC4 and PC5 scores for ventral shape did not contribute over 10% of shape variation and are thus omitted here. Total phenotypic variation explained by each PC is indicated.



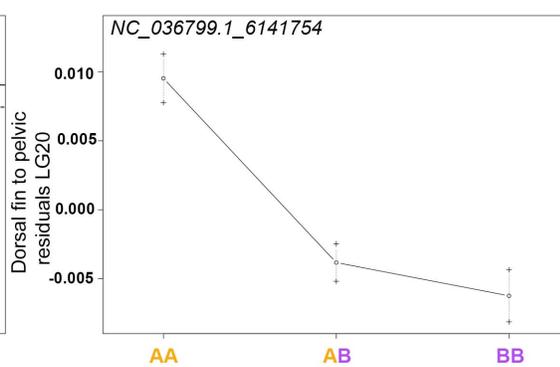
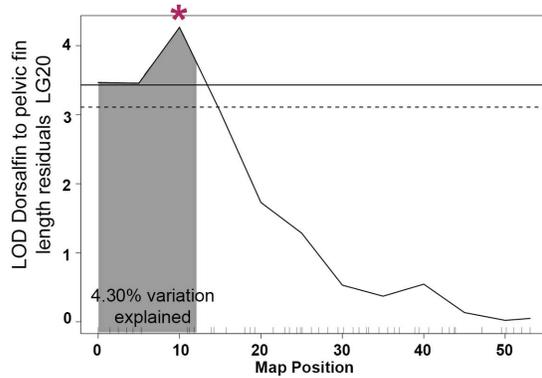
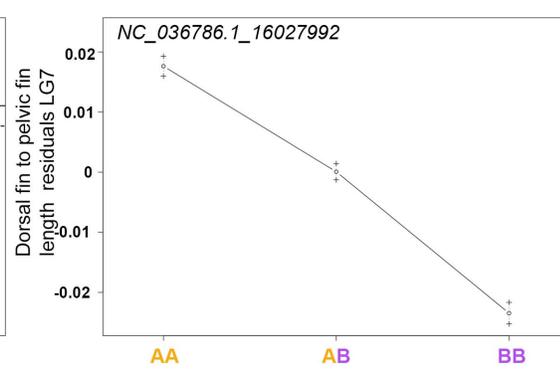
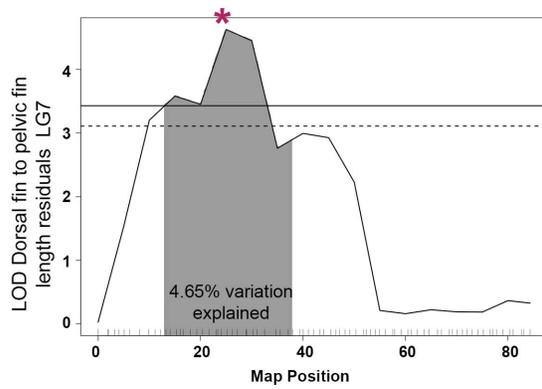
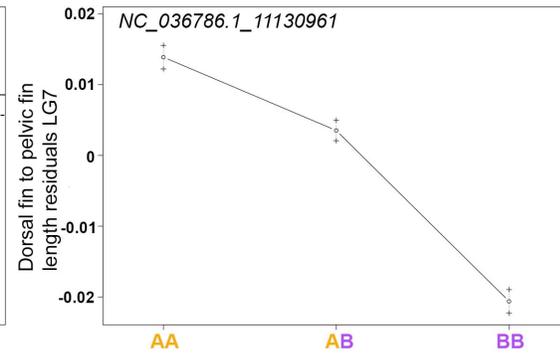
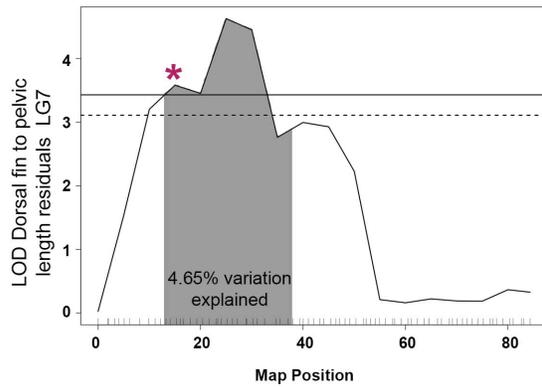
**Figure S2. Genome-wide QTL scans.** Phenotypic measures are indicated by the illustration and include **(a)** head proportion, measured as head length/standard length, **(b)** dorsal to pelvic fin length, **(c)** snout to pelvic fin length, **(d)** length of the preorbital region of the head, **(e)** eye area, **(f)** mouth angle, **(g)** PC1 lateral shape, **(h)** PC2 lateral shape, **(i)** PC3 lateral shape, **(j)** PC4 lateral shape, **(k)** PC5 lateral shape, **(l)** mandible width, **(m)** mandible length, **(n)** opercle to midline width, **(o)** length from the opercle to the mandible, **(p)** angle formed from posterior ends of the mandible to the midline, **(q)** PC1 ventral shape, **(r)** PC2 ventral shape, and **(s)** PC3 ventral shape. Genome-wide significance is indicated at the 5% (solid line) and 10% (dashed line) level. If solid and

dashed lines are not present, no QTL met these significance levels. Details of QTL scans are in Table S3. QTL scans by chromosome are in Figure S3.

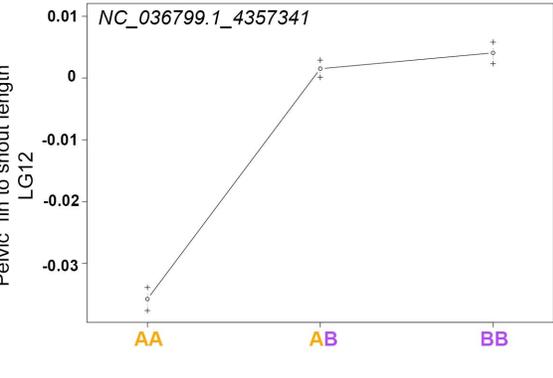
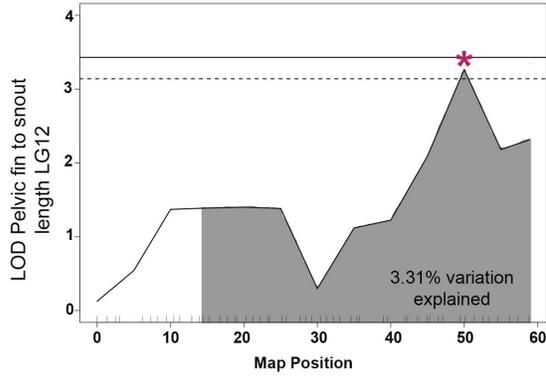
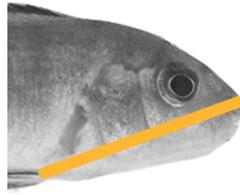
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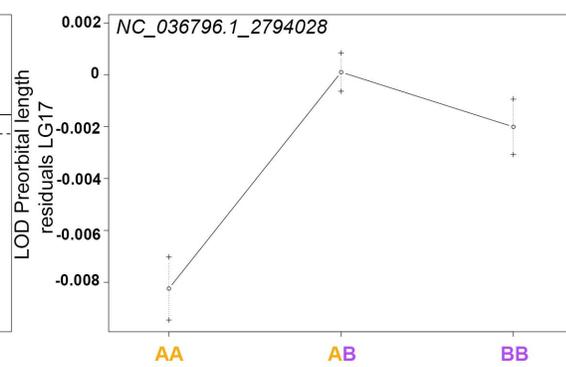
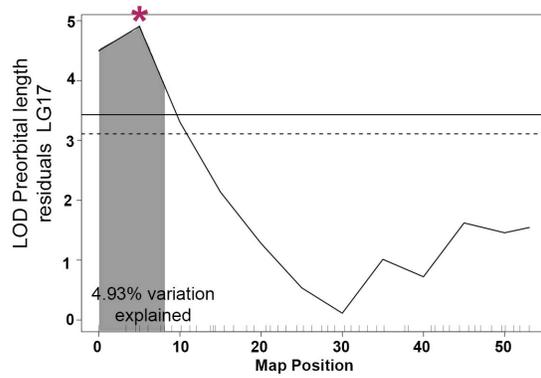
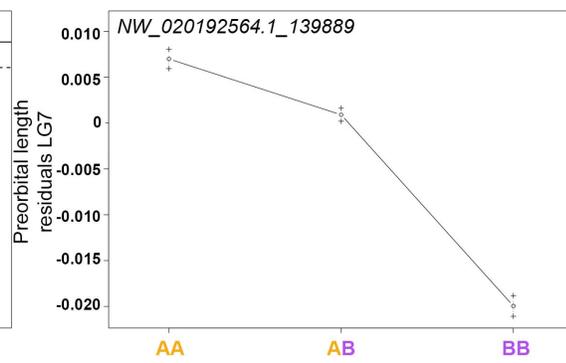
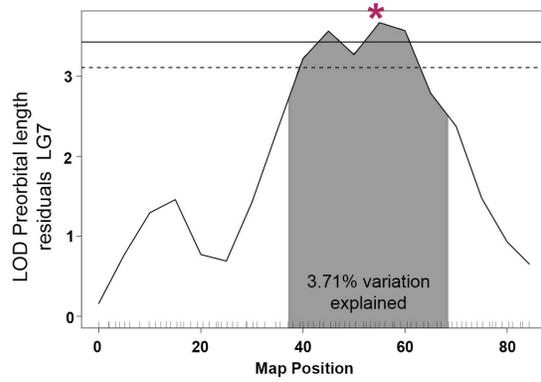
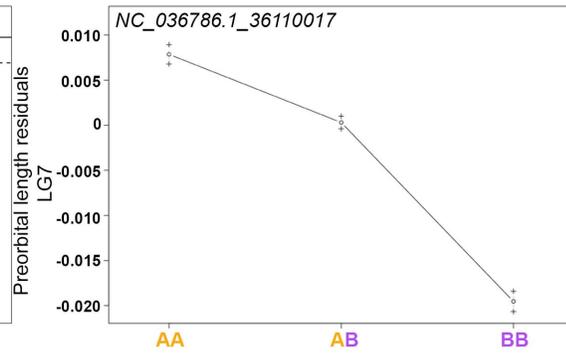
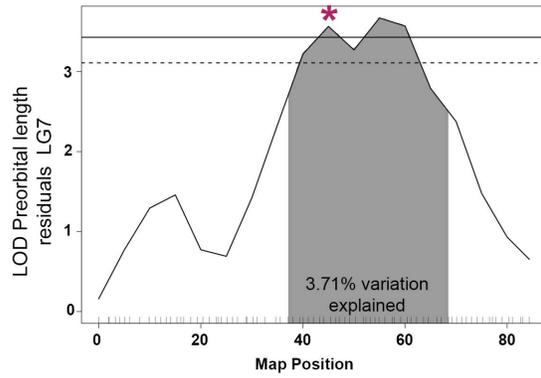
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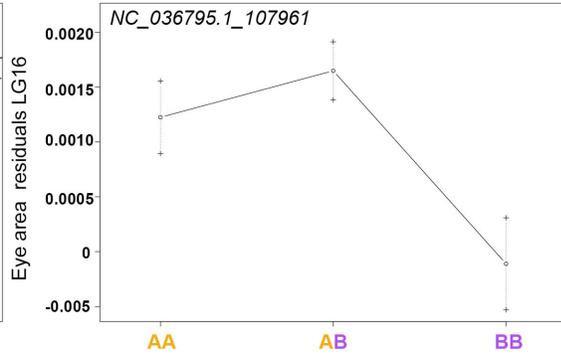
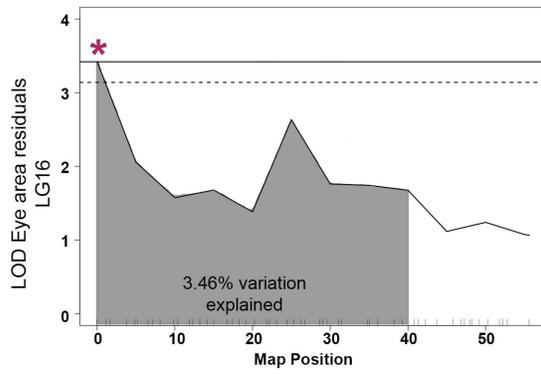
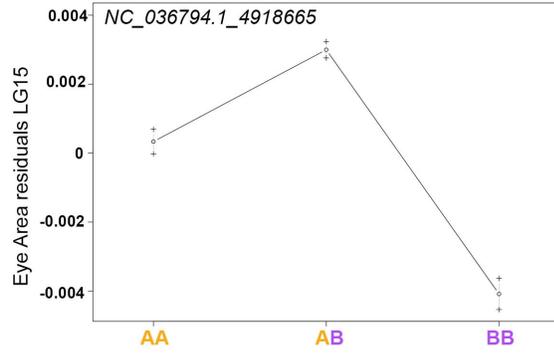
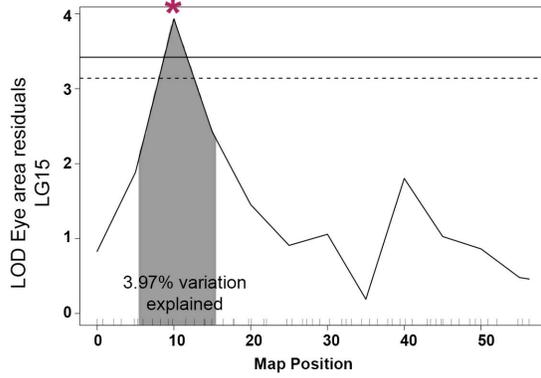
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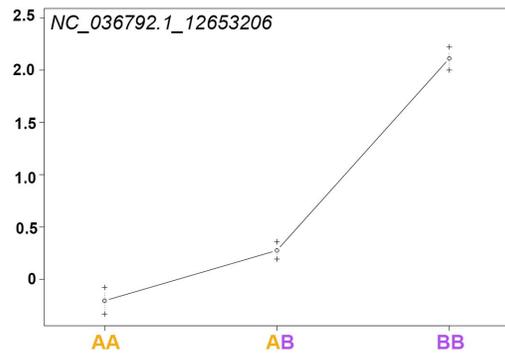
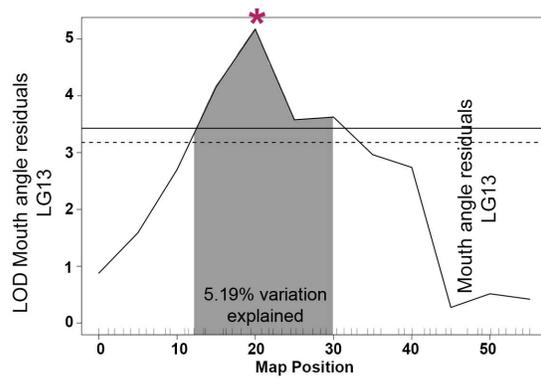
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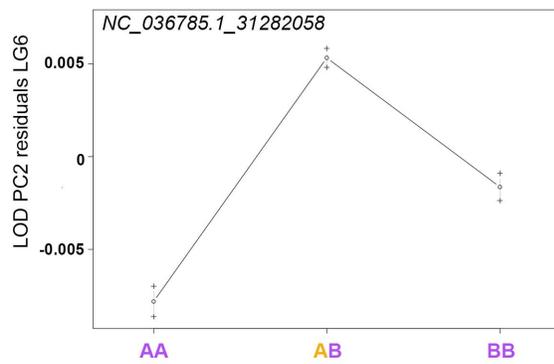
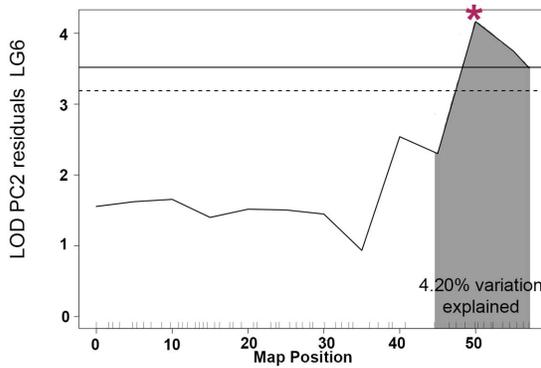
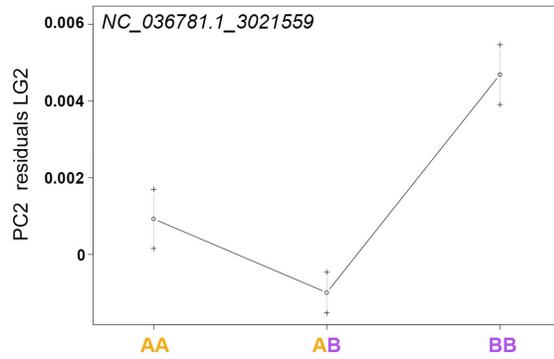
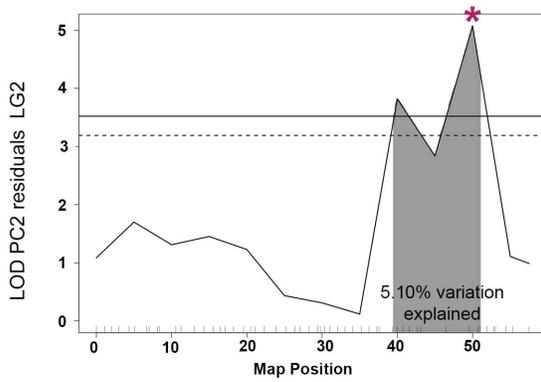
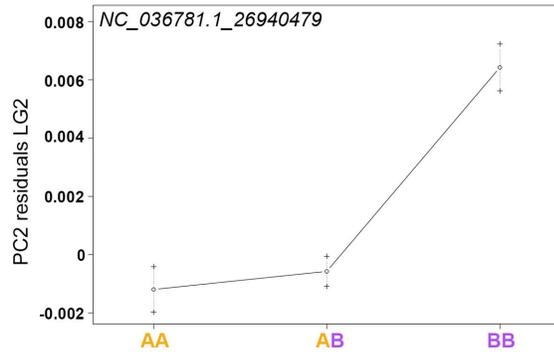
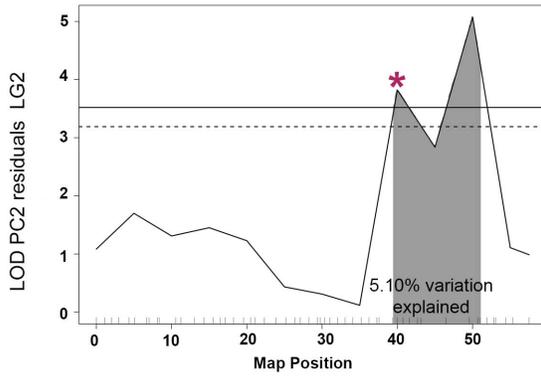
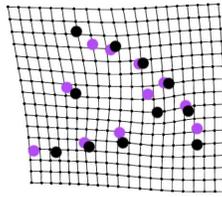
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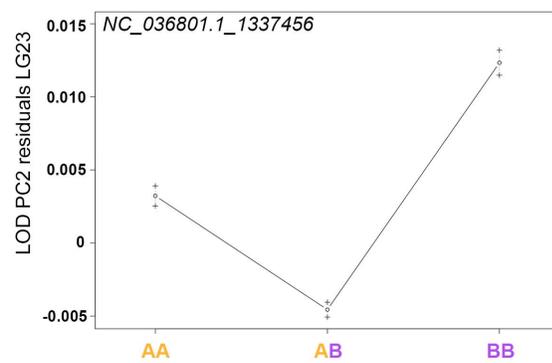
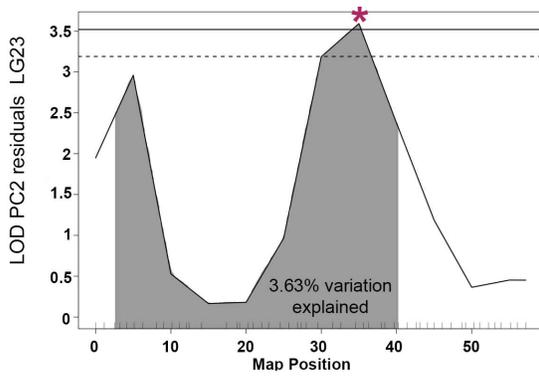
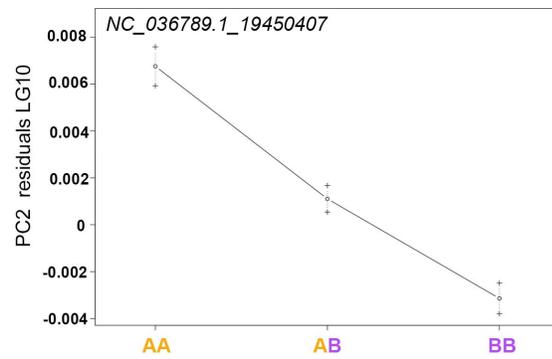
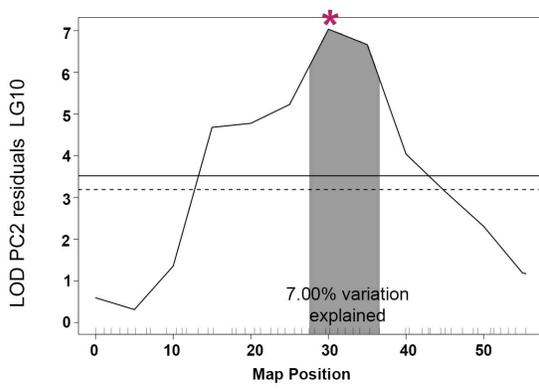
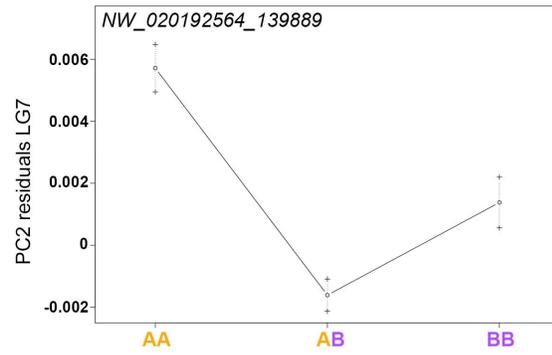
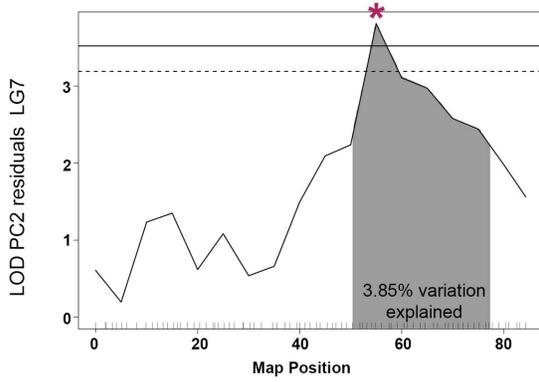
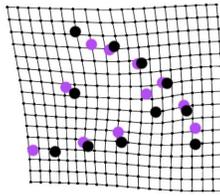
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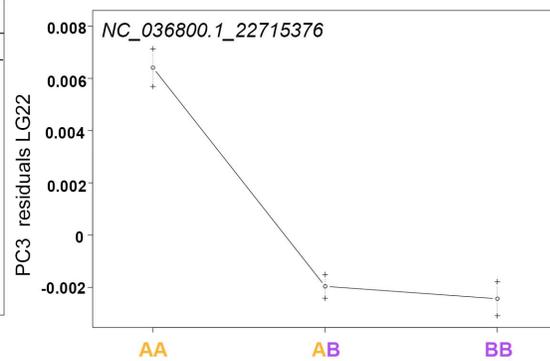
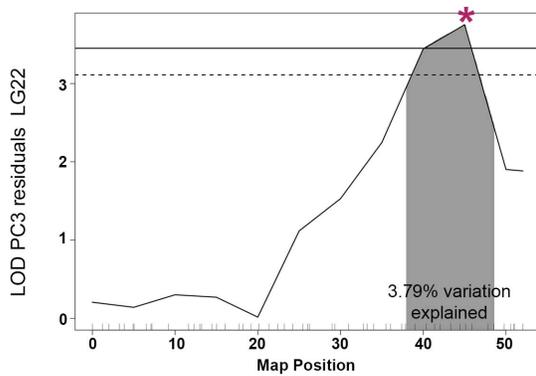
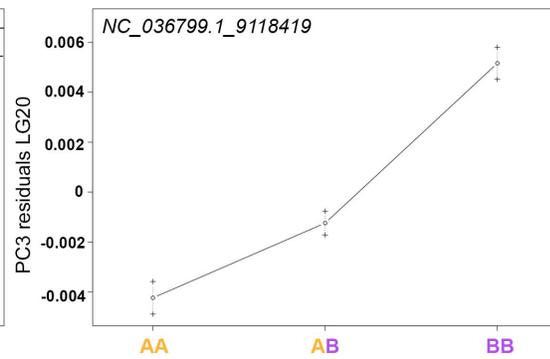
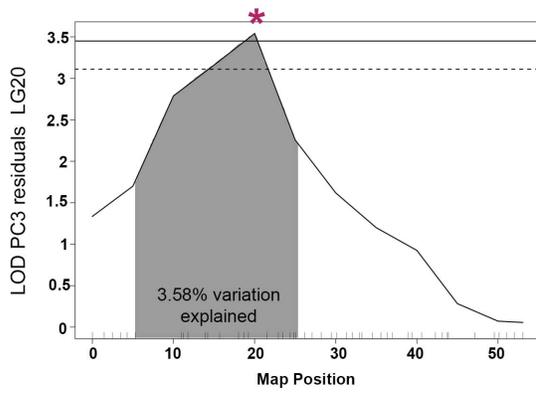
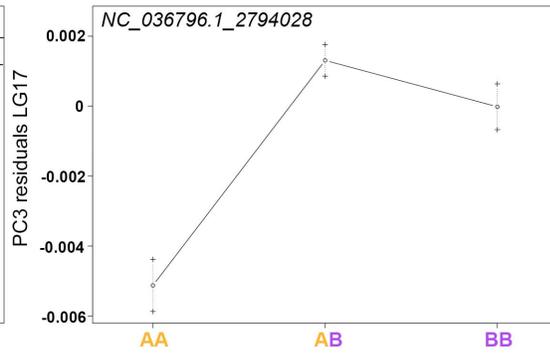
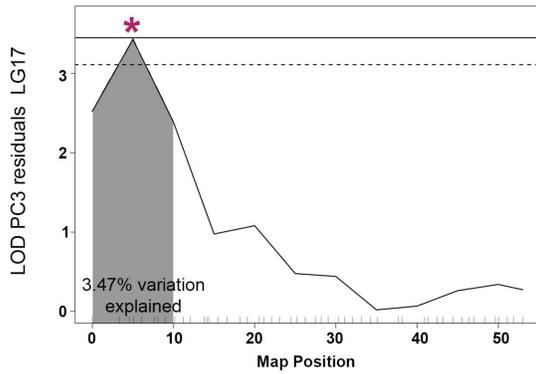
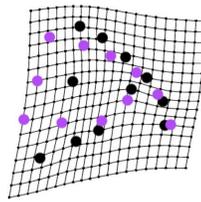
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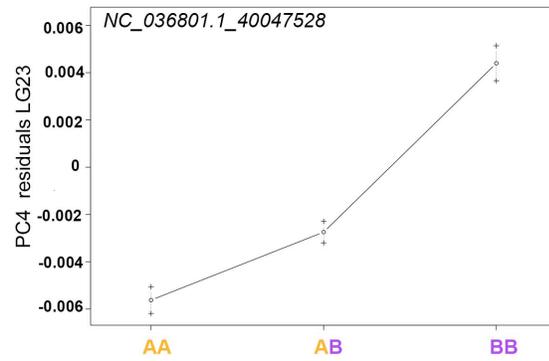
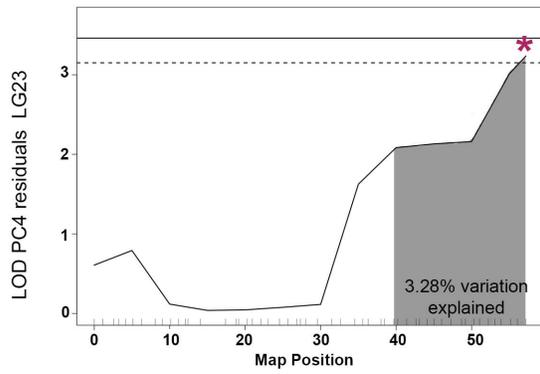
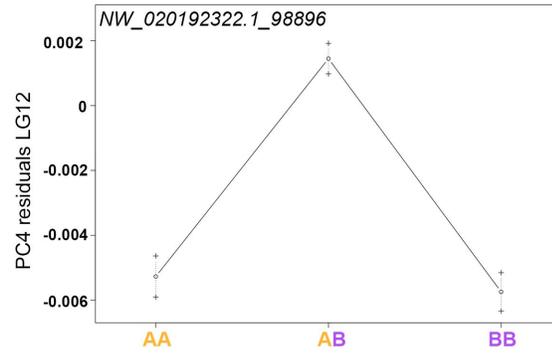
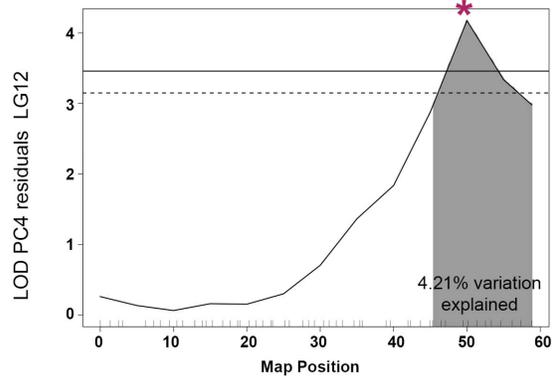
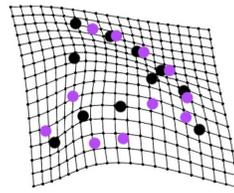
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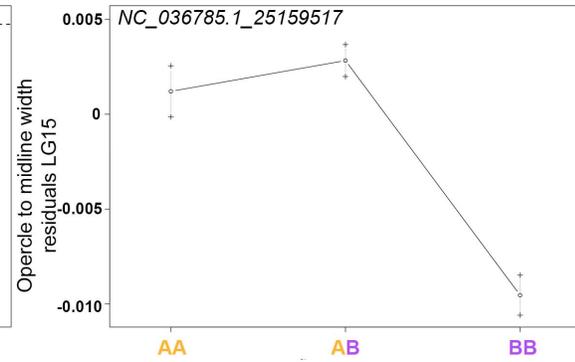
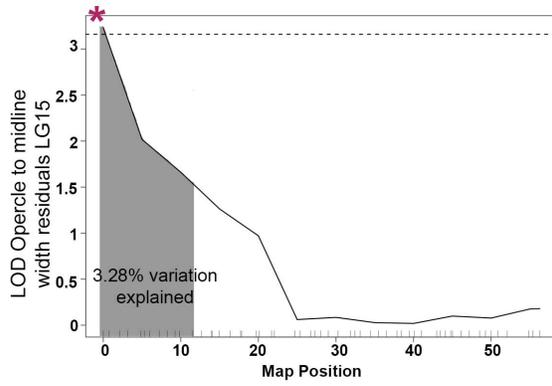
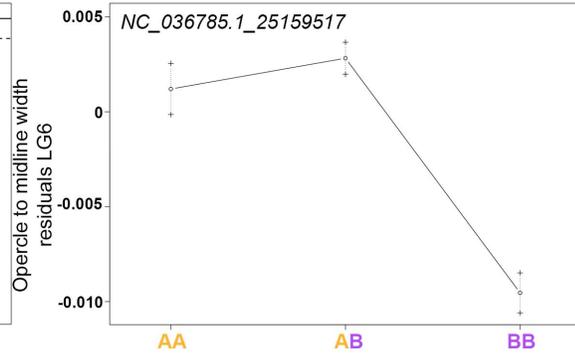
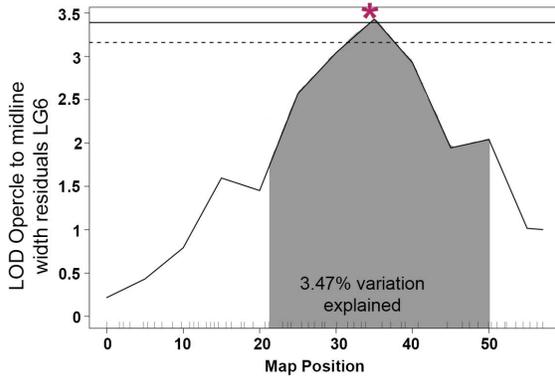
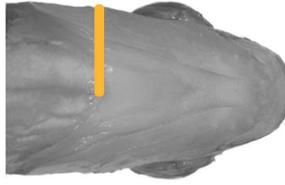
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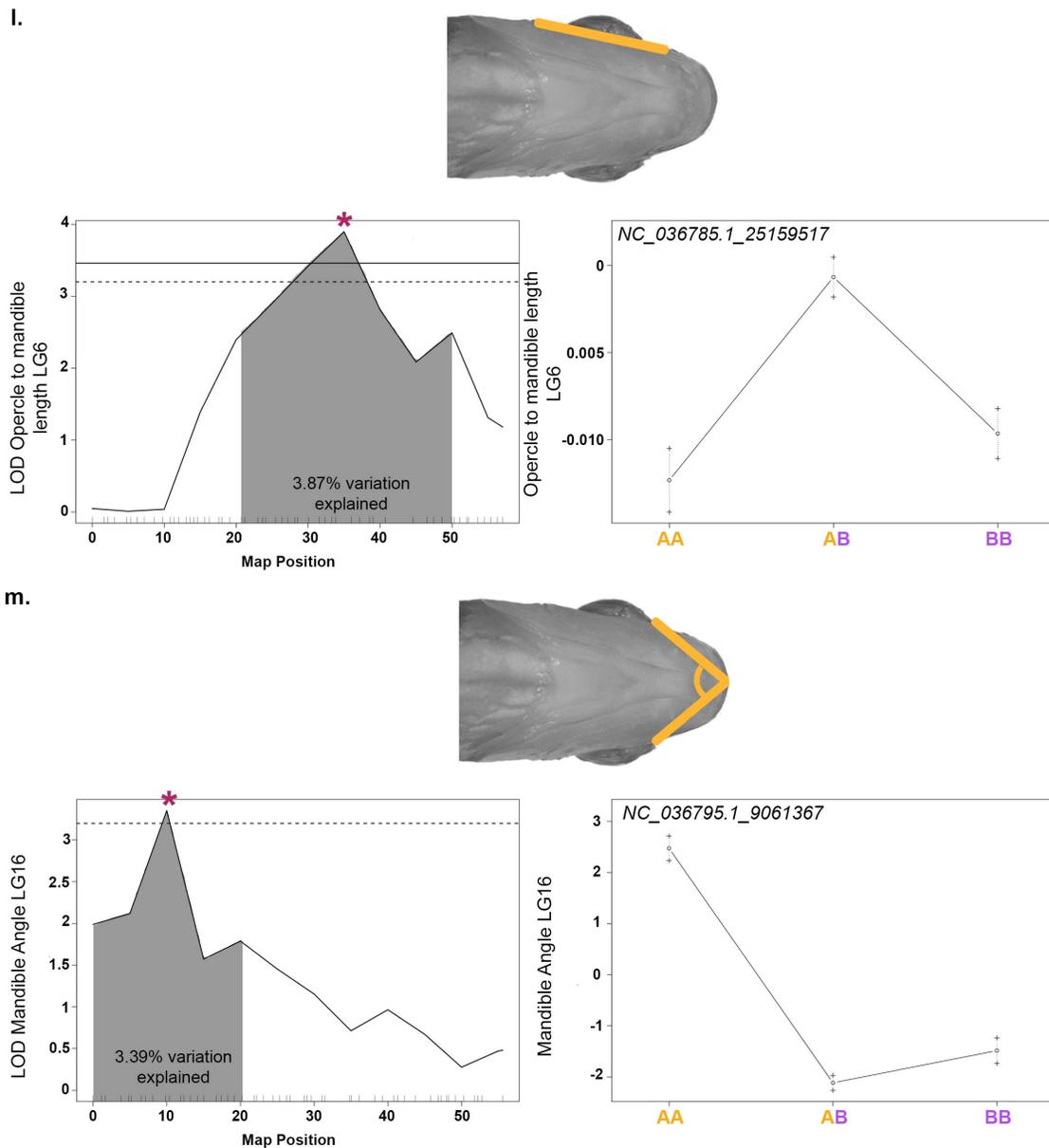


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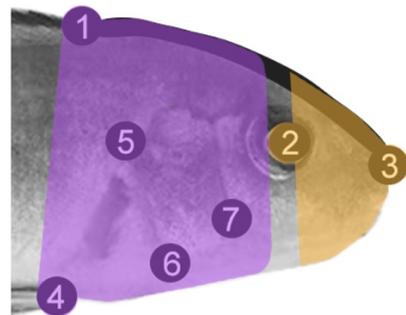
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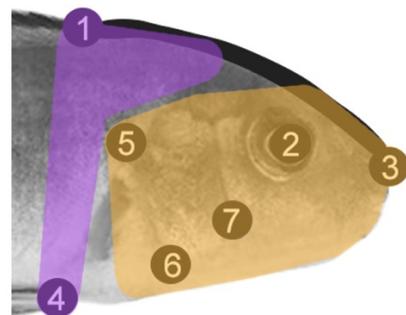


**Figure S3. QTL scans and allelic effects for QTL.** Phenotypic measures are indicated by illustration and include (a) head proportion, measured as head length/standard length, (b) dorsal to pelvic fin length, (c) snout to pelvic fin length, (d) length of the preorbital region of the head, (e) eye area, (f) mouth angle, (g-h) PC2 lateral shape, (i) PC3 lateral shape, (j) PC4 lateral shape, (k) opercle to midline width, (l) length from the opercle to the mandible, and (m) angle formed from posterior ends of the mandible to the midline. PC1 lateral shape, PC5 lateral shape, mandible width, mandible length, PC1 ventral shape, PC2 ventral shape, and PC3 ventral shape are not included in this figure as there were not any significant or suggestive QTL for these traits. 95% confidence interval for QTL is indicated by shading, percent of total phenotypic variation

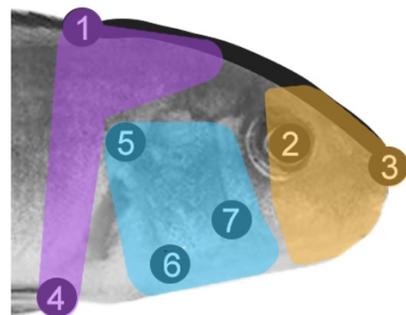
explained by QTL is reported, and genome-wide significance is shown at the 5% (solid line) and 10% (dashed line) level. Details of QTL scan are in Table S3 and genome-wide visuals are in Figure S2. Allelic effects are shown for the position indicated by \*. The A allele was inherited from the *Labidochromis* granddam and the B allele from the *Labeotropheus* grandsire.



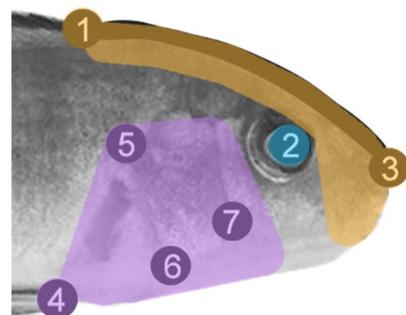
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p=0.881



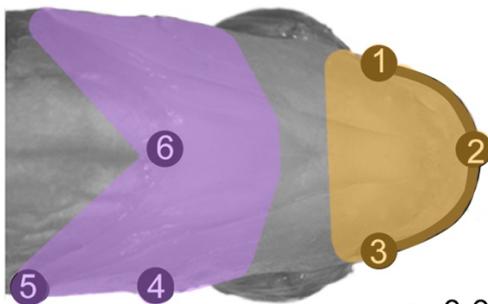
neural crest derived,  
mesoderm derived p=0.743



anterior neural crest, posterior  
neural crest, mesoderm p=0.976



feeding, vision,  
respiration p=0.273



p=0.0508  
pre-orbital, post-orbital  
anterior neural crest, posterior neural crest  
feeding, respiration

**Figure S4. Analysis of modularity.** Landmarks included in various *a priori* models are color coded with descriptions underneath the picture. For ventral shape, note that all three models have the same grouping of landmarks and thus cannot be distinguished.