

**Table S1. SNPs Fixed Between *C. variegatus* (generalist) and *C. desquamator* (scale-eater).**  
Asterisks (\*) show SNPs in gene regions (bold) annotated for skeletal system effects.

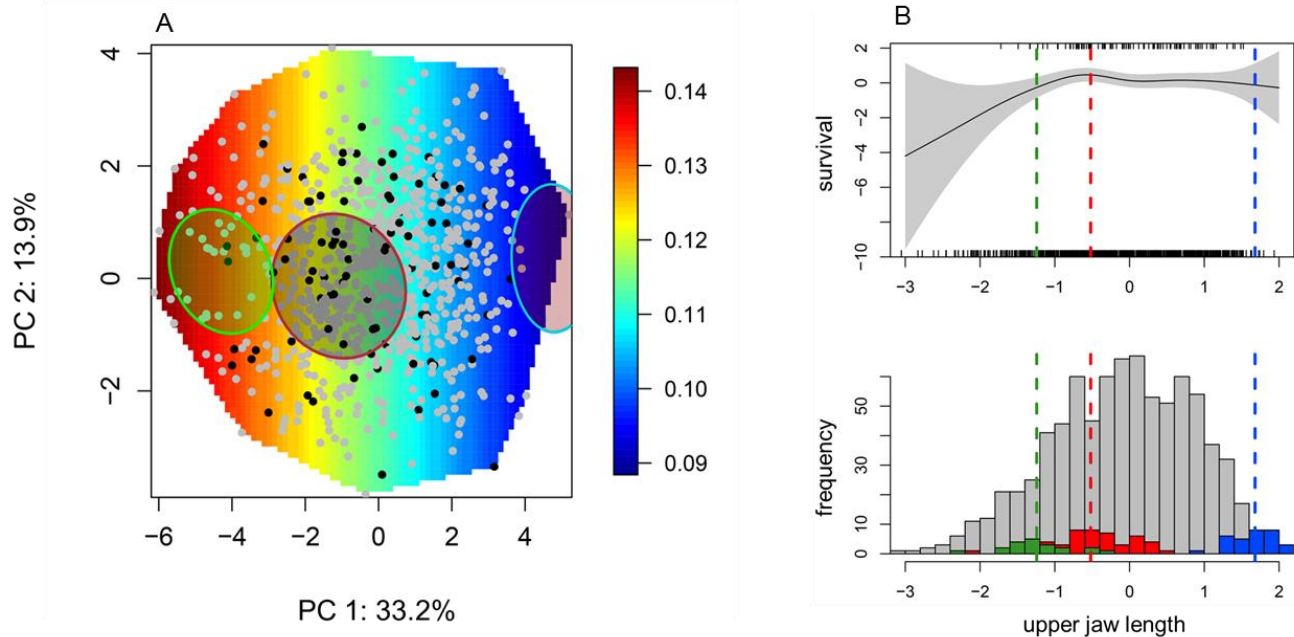
SNP	Scaffold	Median PIP	PIP percentile	Median $\beta$	<i>P</i>	GENE
1	KL652900.1	0.00245	0.988	0.617581	5.36E-10	NA
2	KL653356.1	0.00205	0.966	0.458927	2.59E-09	NA
3	KL652510.1	0.002	0.961	0.460259	1.53E-09	NA
4	KL653712.1	0.0019	0.950	0.121984	1.07E-05	FAM49B
5	KL652554.1	0.00185	0.941	0.302317	2.43E-09	PIGR
6	KL653302.1	0.0016	0.888	0.136604	4.36E-10	MAGI3
7	KL653302.1	0.0016	0.888	0.136604	8.26E-10	MAGI3
8	KL653302.1	0.0016	0.888	0.136604	1.67E-08	MAGI3
9	KL652758.1	0.0013	0.778	0.128798	4.87E-06	FBXO32
10	KL652758.1	0.0013	0.778	0.128798	4.87E-06	FBXO32
11	KL652583.1	0.0012	0.729	0.018276	0.01289	EIF2B3
12	KL652583.1	0.00115	0.698	0.01545	0.02878	EIF2B3
13	KL652584.1	0.0011	0.674	-0.047672	1.14E-09	LINGO1
14	KL652584.1	0.0011	0.674	-0.047672	2.31E-09	LINGO1
15*	KL652632.1	0.001	0.614	0.126082	3.08E-09	<b>CABP2</b>
16*	KL652632.1	0.001	0.614	0.126082	1.17E-08	<b>CABP2</b>
17*	KL653422.1	9.00E-04	0.551	-0.030165	0.0811	<b>COL11A1</b>
18*	KL653422.1	9.00E-04	0.551	-0.030165	0.0811	<b>COL11A1</b>
19*	KL653422.1	9.00E-04	0.551	-0.030165	0.0811	<b>COL11A1</b>
20*	KL653422.1	9.00E-04	0.551	-0.030165	0.128	<b>COL11A1</b>
21	KL652603.1	0.00065	0.386	0.005032	0.000628	MEF2C
22	KL652585.1	6.00E-04	0.362	0.021429	9.90E-08	FAM172A

**Table S2.** Top 20 SNPs associated with jaw size after correcting for population structure in PLINK with the top two principle components. None reach our Bonferroni corrected level of significance ( $P < 4.0 \times 10^{-9}$ ).

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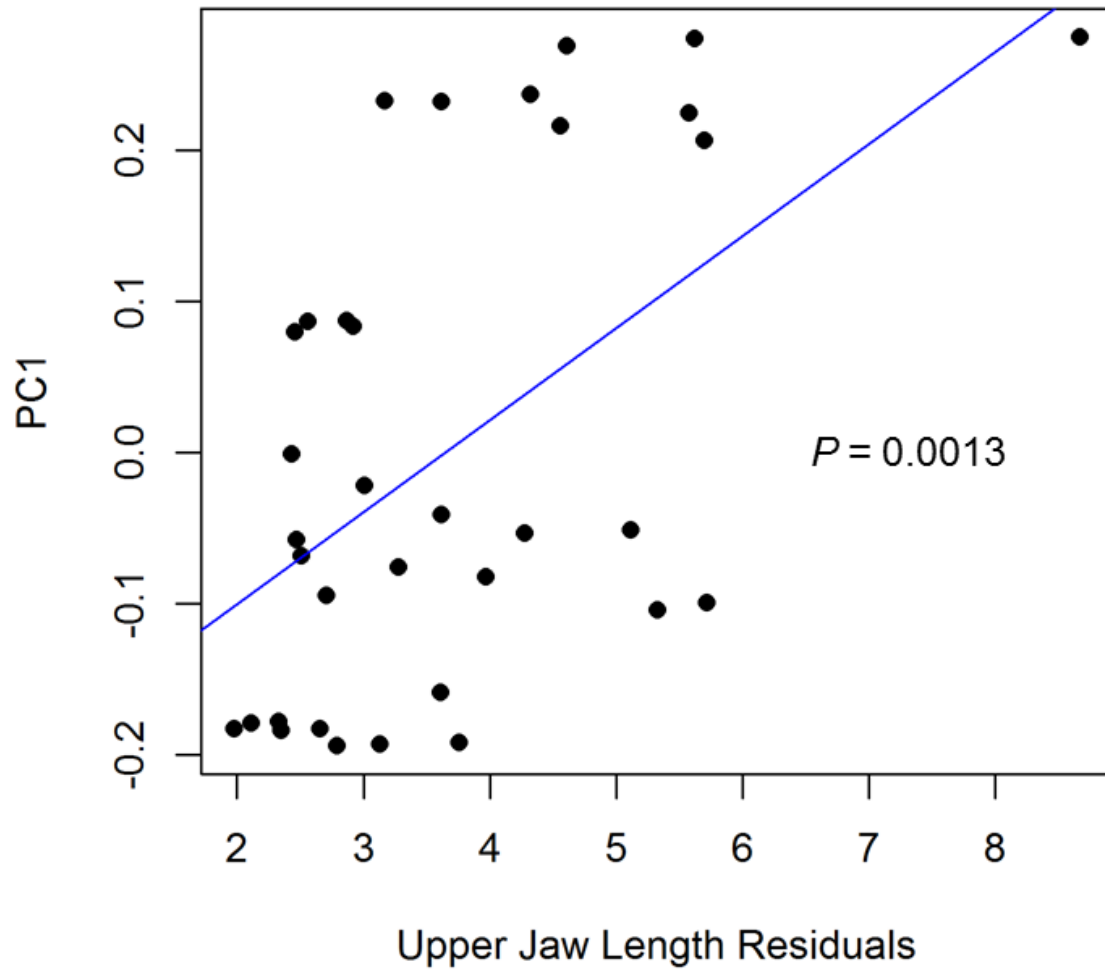
<b>SNP</b>	<b>Scaffold</b>	<b>Beta</b>	<b>P</b>
1	KL653294.1	-6.432	6.83E-07
2	KL653071.1	-6.403	7.36E-07
3	KL653414.1	6.393	7.57E-07
4	KL653264.1	6.37	8.03E-07
5	KL652620.1	6.534	9.31E-07
6	KL653172.1	6.368	9.58E-07
7	KL652789.1	6.217	1.20E-06
8	KL653414.1	6.158	1.40E-06
9	KL653049.1	6.207	1.45E-06
10	KL652731.1	6.179	1.55E-06
11	KL652573.1	6.013	2.04E-06
12	KL652868.1	-6.137	2.05E-06
13	KL653566.1	6.188	2.15E-06
14	KL652753.1	5.973	2.27E-06
15	KL652694.1	-6.08	2.36E-06
16	KL652841.1	5.955	2.38E-06
17	KL652723.1	-5.931	2.54E-06
18	KL653042.1	6.035	2.65E-06
19	KL652694.1	-5.966	2.69E-06
20	JPKM01108474.1	5.891	2.82E-06

Fig S1.



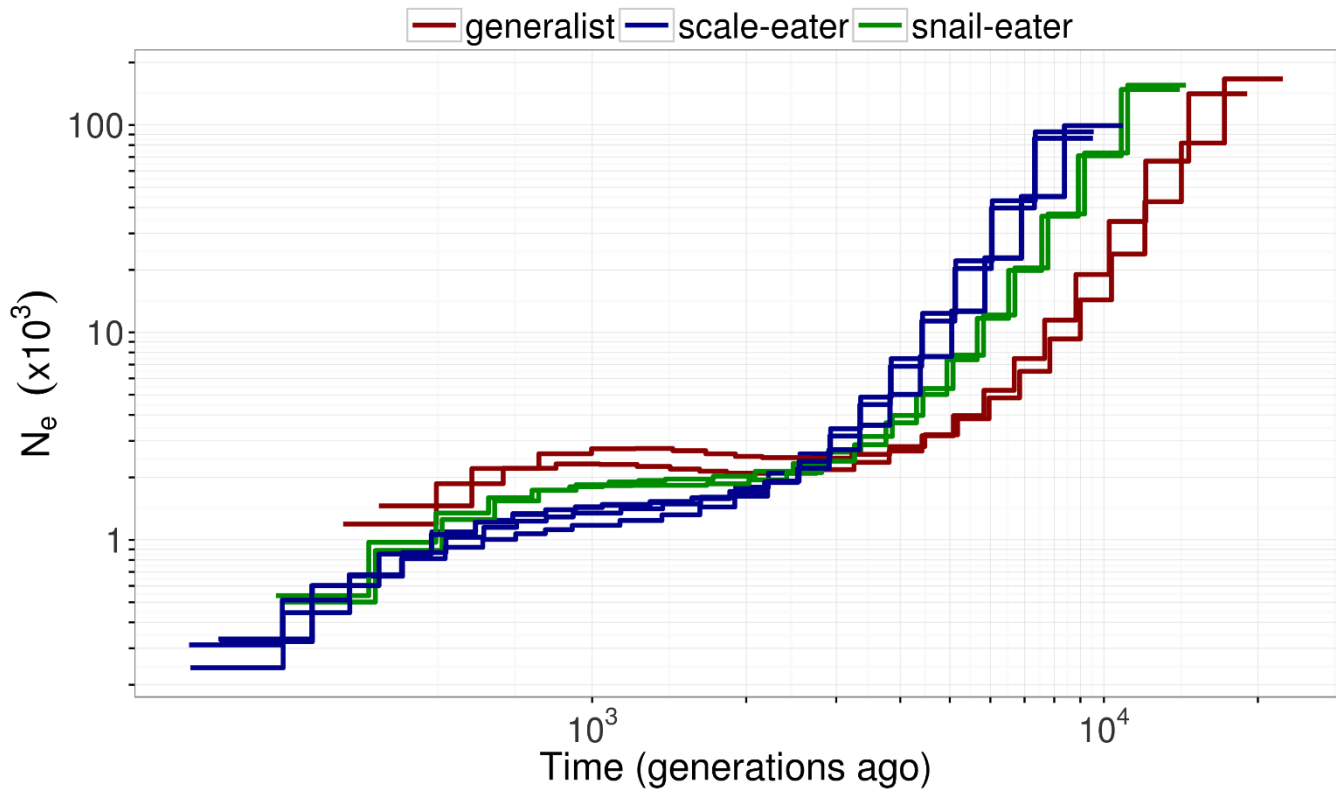
**Figure S1. Larger phenotypic distance between *C. desquamator* (scale-eater) and *C. variegatus* (generalist).** *C. variegatus* (red), *C. desquamator* (blue), and *C. brontotheroides* (green) from each lake population were crossed in every direction to produce F<sub>2</sub> hybrids which were left for three months in an enclosure on San Salvador. Heat colors correspond to survival probability (with blue being low and red being high). A) F<sub>2</sub> hybrid survivors (grey dots) and deaths (black dots) plotted against principal components together explaining 47% of the variation across measurements for 16 morphological traits. Phenotypes for all lab-raised purebred species are represented by 95% confidence ellipses. The phenotypic distance is greater between *C. desquamator* and *C. variegatus* (red and blue) than *C. brontotheroides* and *C. variegatus* (red and green). B) Smoothing splines with 95% shaded confidence regions show survival probability (upper panel) and histograms (lower panel) show the distribution of upper jaw lengths within the F<sub>2</sub> hybrid population relative to parental trait ranges. Rug plots indicate jaw lengths of F<sub>2</sub> hybrid survivors (upper axis) and deaths (lower axis). Dashed lines show mean jaw length for each species (modified from Martin 2016a).

Fig. S2



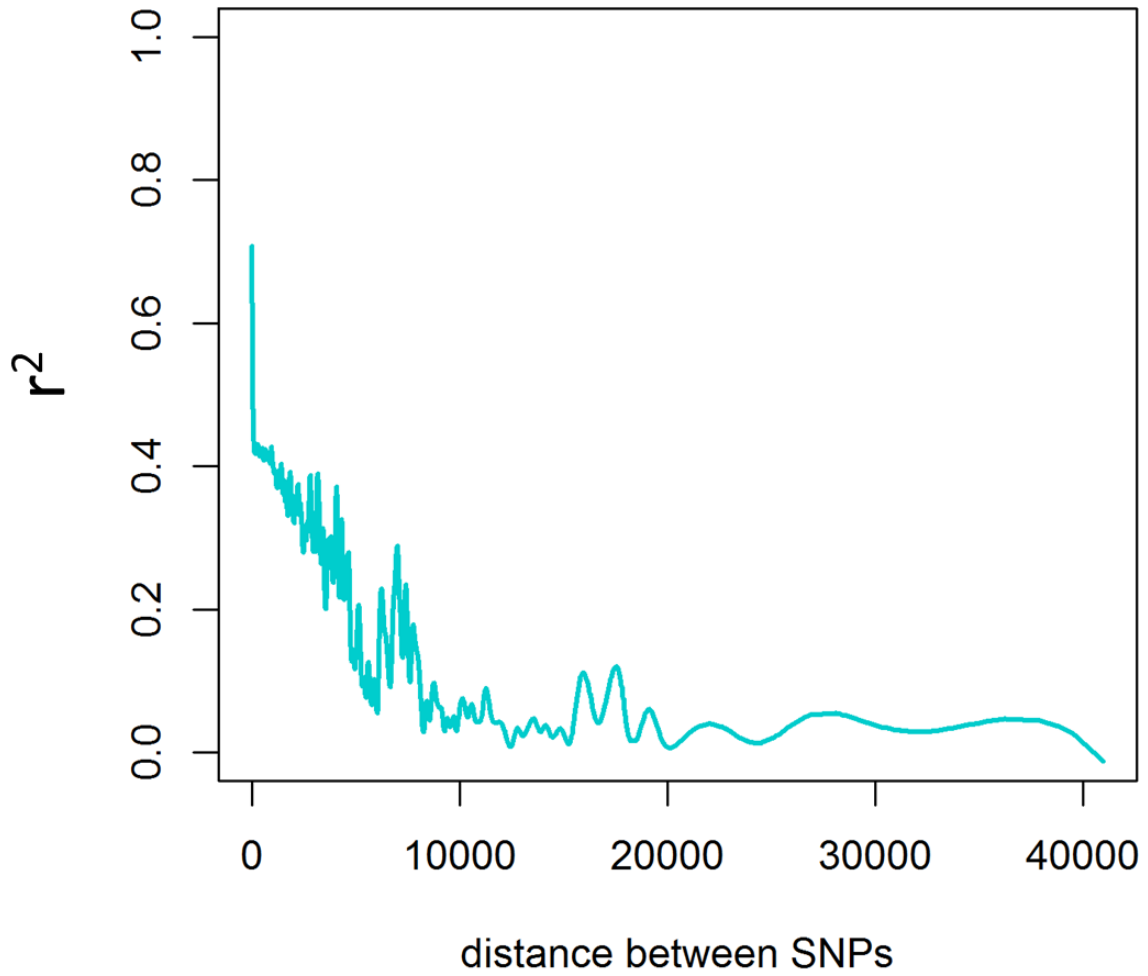
**Figure S2. Principal Component 1 Correlated with Jaw Length.** Jaw measurements were log transformed and regressed against log-transformed body length. We fit a log-transformed trait by log-transformed body length linear regression and plot the residuals versus the top principal component that explains 5.45% of the variation in our genomic dataset. The correlation between jaw size and PC1 is significant ( $P = 0.0013$ ).

Fig. S3



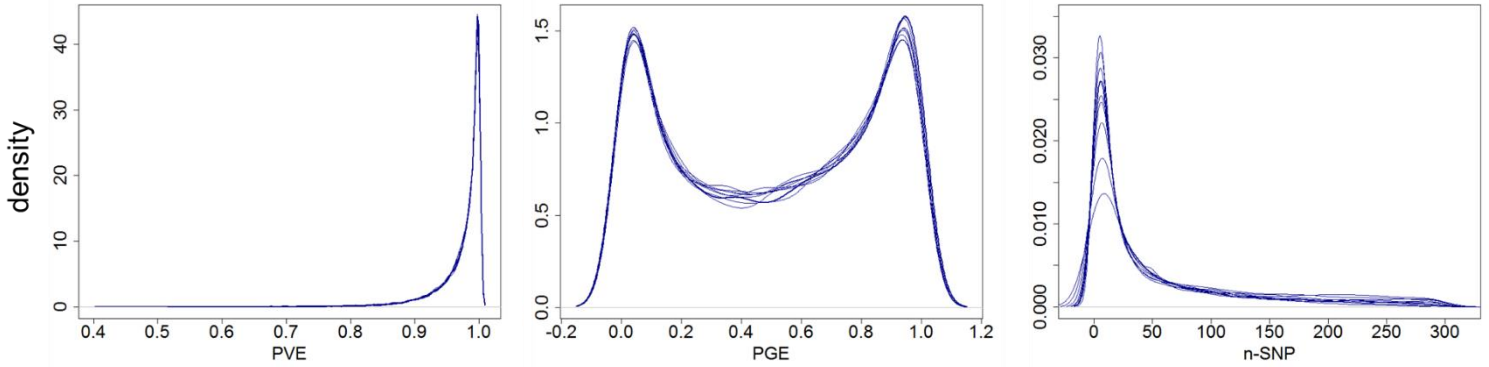
**Figure S3. Ancestral Population Size of San Salvador Pupfish Species.** Historical effective population sizes estimated by the Multiple Sequentially Markovian Coalescent (MSMC) for *C. variegatus* (red), *C. desquamator* (blue) and *C. brontotheroides* (green) using a six-month generation time and mutation rate estimated for cichlids ( $6.6 \times 10^{-8}$  mutations per site per year: Recknagel et al. 2013).

Fig. S4



**Figure S4.** Decay of linkage disequilibrium ( $r^2$ ) across a 4.5 Mb scaffold.

Fig. S5



**Figure S5.** Posterior density distributions for hyperparameters obtained from GEMMA's Bayesian sparse linear mixed model describing A) the proportion of variance in phenotypes explained by every SNP (PVE), B) the proportion of phenotypic variation explained by SNPs of large effect (PGE), and C) the number of large effect SNPs required to explain PGE (nSNP). Individual lines represent ten independent MCMC runs.