Oikos

Appendix 1

Table A1. Gaussian mixture model classification rates. Each row represents true genotypes and the columns represent the proportion of individuals of that genotype which were assigned to each of the three genotypes: LL – low homozygote, CL - heterozygote, CC – complete homozygote. Total number of individuals in parentheses.

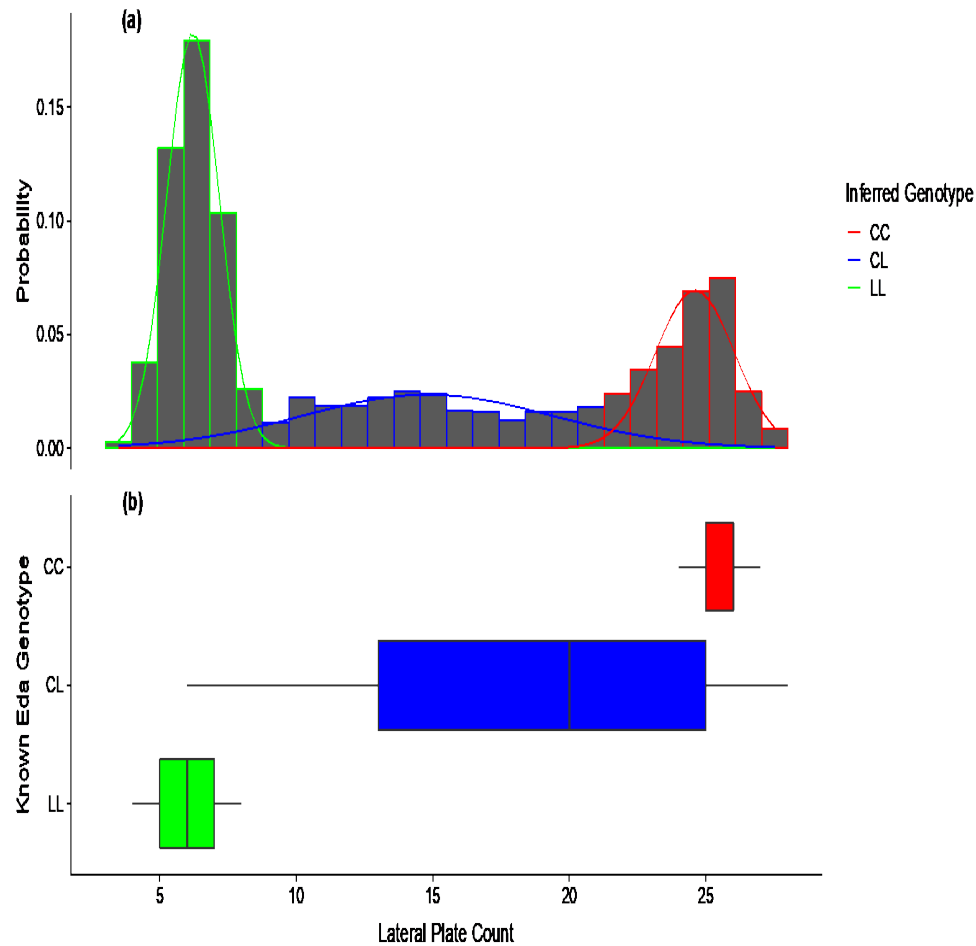|	LL	CL	CC
LL	0.932 (124)	0.023 (3)	0.045 (6)
CL	0.072 (6)	0.458 (38)	0.470 (39)
CC	0.014 (1)	0.028 (2)	0.958 (68)

Figure A1. (a) Histogram of left lateral plate counts for all fish in the study. Each box is colored by the genotype to which individuals with that plate count were assigned by the mixture model. The histogram is overlaid with the probability density functions of the posterior probability of group membership weighted by the proportion of individuals assigned to that genotype by the mixture model. (b) Box and dot plots of the distribution of plate counts for individuals of known *Eda* genotype. LL – low homozygote, CL -heterozygote, CC – complete homozygote.
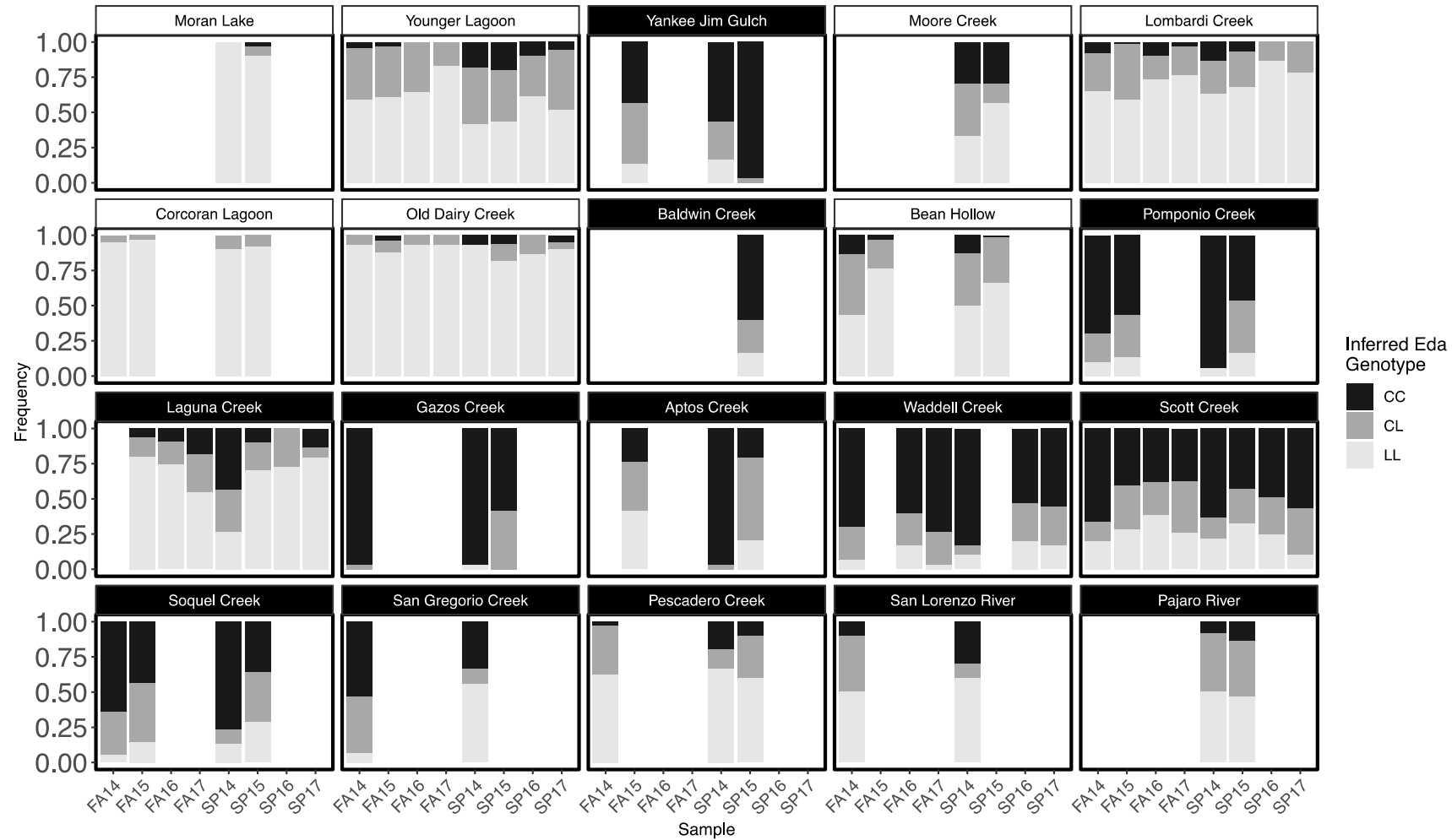
Figure A2. Time series of inferred *Eda* genotype frequencies of threespine stickleback at 20 intermittently-open estuaries from spring 2014 through fall 2017. Sites are ordered from top-left to bottom-right from smallest to largest total stream length. LL – low homozygote, CL - heterozygote, CC – complete homozygote. Sites with predators are labeled with white text on a black background, sites without predators are labeled with black text on a white background.