



Figure S2 Genotype calling from marine and freshwater read counts

Reads were assumed to be independent and have a 1% error rate. M=marine allele, F=freshwater allele. The FF/MF and MF/MM genotypes indicate that there is a >95% probability that the genotype is not the third possible genotype, but that there is not a >95% certainty for any single genotype call. These genotypes were frequently called for bins that spanned recombination breakpoints.