

The supplementary files uploaded with this manuscript contain both raw data and analysis output to recapitulate all results and figures in this study. The contents of each data file are described below.

TranscriptCounts.csv – Transcript count data for all coastal and lagoon mussels reared in either benign or stressful pH conditions. Each row corresponds to a gene, while each column corresponds to the observed transcript count for each individual at that gene.

CountsID.csv – Identifying information for the individuals in the transcript counts matrix. Specifically, each row contains pertinent information for corresponding column of the transcript counts file, including source population and treatment information.

SupplementaryFile1.csv – File containing gene expression data for the coastal population's response to stressful pH conditions. Columns correspond to: reference contig ID (as identified in reference transcriptome provided by Moreira *et al.* 2015), transcript ID (corresponding to row number of counts matrix), \log_2 -fold change, and raw p-value for each gene.

SupplementaryFile2.csv – File containing gene expression data for the lagoon population's response to stressful pH conditions. Columns correspond to: reference contig ID (as identified in reference transcriptome provided by Moreira *et al.* 2015), transcript ID (corresponding to row number of counts matrix), \log_2 -fold change, and raw p-value for each gene.

SupplementaryFile3.csv – File containing gene expression data for population differentiation in the benign pH treatment. Columns correspond to: reference contig ID (as identified in reference transcriptome provided by Moreira *et al.* 2015), transcript ID (corresponding to row number of counts matrix), \log_2 -fold change, and raw p-value for each gene

SupplementaryFile4.csv – File containing gene expression data for population differentiation in the stressful pH treatment. Columns correspond to: reference contig ID (as identified in reference transcriptome provided by Moreira *et al.* 2015), transcript ID (corresponding to row number of counts matrix), \log_2 -fold change, and raw p-value for each gene

SupplementaryFile5.csv – File containing oceanographic data from autonomous sensing of the coastal habitat.

SupplementaryFile6.csv – File containing oceanographic data from autonomous sensing of the lagoon habitat.