Supplemental files for:

Durland, E., DeWit, P., Langdon, C. (2021) Temporally-balanced selection during development of larval Pacific oysters (Crassostrea gigas) inherently preserves genetic diversity within offspring. Proc R Soc B. DOI: 10.1098/rspb.2020.3223

* **Supplemental figures and tables** (*Durland\_etal\_Supp\_figs\_tbls\_ESM.docx*):
	+ **Figure S1**: Example trajectories of minor allele frequency.
	+ **Figure S2**: Visualization of k-means clusters in dimensional space
	+ **Figure S3**: Locus-by-locus estimate of genotypic proportions in the fertilized egg pool
	+ **Figure S4**: Modelled estimates of temporal genotype changes for a single marker (SNP)
	+ **Figure S5**: Validation of simulation method to empirical measurements from Plough and Hedgecock (2011)
	+ **Figure S6**: Model accuracy for empirical data from Plough and Hedgecock (2011)
	+ **Figure S7**: Model accuracy for empirical data from Plough and Hedgecock (2011)
	+ **Figure S8**: Modeled residuals for spat genotype comparisons
	+ **Figure S9**: Prediction intervals of Hardy-Weinberg estimates for spat genotypes and outliers
	+ **Figure S10**: Overall change in allele frequency (day 0-22) for rare variants (MAF < 0.10)
	+ **Table S1**: Screen size and sampling number for days 0-22 of larval culture
	+ **Table S2**: ‘Goodness of fit’ for linear models on egg and spat minor allele frequencies.
	+ **Table S3**: Cross-classification of parametric tests (G,UD,BD) and cluster assignment (1-5)
	+ **Table S4**: Metadata for linkage mapping by cluster.
* **Supplementary Table S1**: Bioinformatic statistics and allele frequency data
* **Supplementary** **Figure S2**: SNPs mapped to linkage groups (all)
* **Supplementary Figure S3**: Density map of mapped markers (all)
* **Supplementary Figure S4**: Density map of mapped markers from cluster #1
* **Supplementary Figure S5**: Density map of mapped markers from cluster #2
* **Supplementary Figure S6**: Density map of mapped markers from cluster #3
* **Supplementary Figure S7**: Density map of mapped markers from cluster #4
* **Supplementary Figure S8**: Density map of mapped markers from cluster #5

References cited:

Plough, L. V., & Hedgecock, D. (2011). Quantitative trait locus analysis of stage-specific inbreeding depression in the Pacific oyster *Crassostrea gigas*. *Genetics, 189*, 1473-1486. doi:10.1534/genetics.111.131854