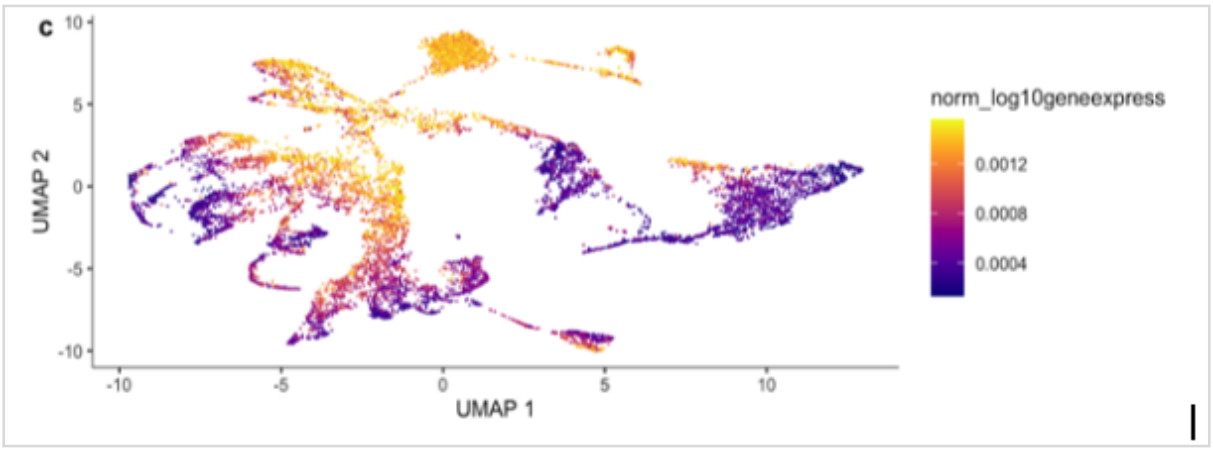
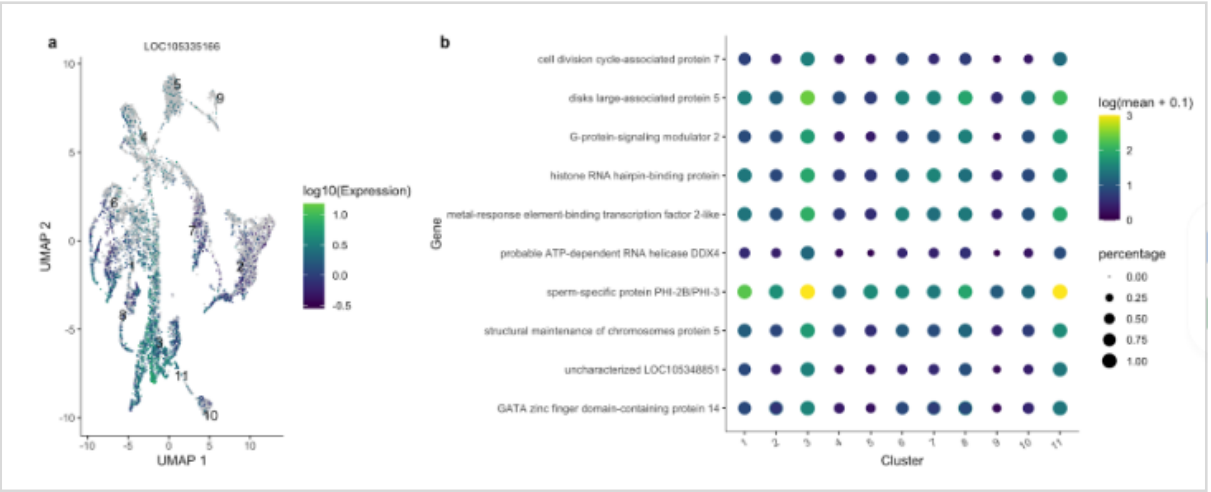
Enhancing sustainability of shellfish aquaculture through streamlined maturation control

Progress Report - Year 2

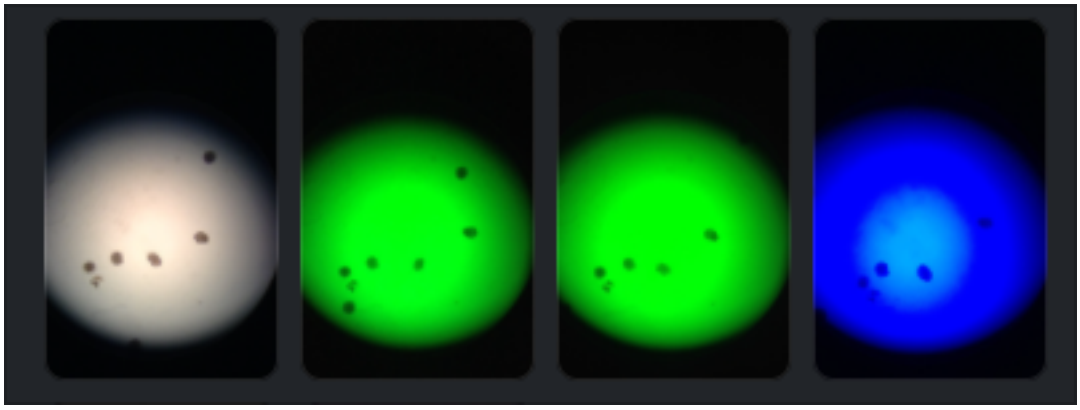
This year we have spent considerable effort on objective 1, *Characterize genomic processes involved in germ cell specification in Pacific oysters*, and have initiated activity on objective 2, *Optimize delivery techniques of custom gene-regulating molecules to oyster embryos*. Specifically in relation to objective 1, we have sequenced and functionally characterized oyster cells at cleavage and blastula stages. A primary means by which single cell RNA sequencing data is visualized is via Uniform Manifold Approximation and Projection (UMAP) which is essentially a visual representation of single cell gene expression patterns clustered based on expression characteristics. Below is a UMAP representation of all cells sequenced colored based on number of genes, a representation of developmental age.



A primary end goal for the gene expression characterization of early oyster embryos is to identify targets that could be leveraged for reproduction maturation control. To this end, Figure 2 represents an indication of cells likely to be germ cell progenitors based on expression of vasa (a). Based on this, cluster 3 represents a cohort of cells likely destined to become gonad cells and Figure 2b provides expression information for the top 10 'marker genes' of cluster 3.



Over the past year we have initiated activity on objective 2 with upgrading a microscope and confirming successful visualization (and documentation) of oyster larvae under fluorescence.



With a full characterization of genomic processes associated with germ cell specification completed, year 2 activity will focus on a replication of the single cell experiment and determining the best approach for introducing gene-regulatory molecules to oyster embryos.