Chapter 2 – Genome assembly of *Hypomesus transpacificus* (delta smelt)

Abstract

Background

Methods

* Tissue collection
* Isolation of high molecular weight genomics DNA extraction
* Library prep and sequencing
  + Linked-read
  + Long-read
  + Hi-C
* Post sequencing quality control
* Assembly
  + Long-read sequencing assembly to create Draft Assembly A using ipa
  + Scaffolding Draft Assembly A with linked-reads to produce Draft Assembly B using Scaff10X
  + Incorporation of hi-c sequencing data with Draft Assembly B to produce Draft Assembly C using SALSA2
  + Anchoring Draft Assembly C scaffolds into chromosomes using chromonomer to produce a chromosome-level Final Assembly
  + Genome assembly statistics
  + Cytogenetic analysis

Results

Discussion