**Supplementary Materials Note S1**

DNA from the same individual (Anne - SAMN19838403) used to generate the *Mytilus edulis* PEIMed assembly (GCA_019925275.1) was used to generate a PacBio HiFi library. The introgression of *Mytilus trossolus* or *M. galloprovincialis* was ruled out using 12 SNPs previously used to distinguish the member of the *Mytilus* species complex [1]. Sequencing was carried out by the Biotechnology Center and the University of Wisconsin – Madison. In total, 4 flow cells were used to generate the data with the Sequel2 sequencer. Calling of the CSS reads was done by the native PacBio software used by Sequel2. A total of 8,417,094 CSS reads were generated, resulting in coverage ~20X (Genome Size 1.65 Gb). Tissue samples from the same individual were also sent to Dovetail Genomics (Scotts Valley, CA). Dovetail extracted intact nuclei from muscle samples and constructed Omni-C proximity ligation libraries. Omni-C libraries were sequenced using a NovaSeq sequencer (Illumina, San Diego, CA).

We produced a primary/alternative phased assembly as well as haplotype-specific contigs using HiFiasm with the integration of the proximity ligation reads to improve phasing [2]. Putative contaminant sequences from other organisms were removed using blobtools2 [3] (Figure 1). The majority of contigs retained after filtering were putative molluscan sequences. Omni-C reads were mapped to the primary assembly using BWA [4]. The Arima genomics pipeline was used to map and process the mapped reads for scaffolding GitHub - ArimaGenomics/mapping_pipeline: Mapping pipeline for data generated using Arima-HiC). The primary assembly was scaffolded using SALSA2 [5,6] and pin_hic [7]. Metrics for all assemblies can be found in table 1. All scaffolded assemblies had 14 major scaffolds that putatively represent the *M. edulis* chromosomes. The pin_hic assembly had better contiguity than the one produced by SALSA2 (data now shown). Therefore, the pin_hic assembly was used for downstream analysis.

Table 1. Contiguity and completeness metrics for all contig- and scaffold-level assemblies.

| Statistics | Contigs | | | | Scaffolds | |
|---|---|---|---|---|---|---|
| | HiFiasm - Primary | HiFiasm - Alternative | HiFiasm - Hap1 | HiFiasm - Hap2 | PEIMed | HiFiasm - Primary + Pins |
| # of Contigs | 670 | 23318 | 905 | 735 | 9686 | 670 |
| # of Scaffolds | NA | NA | NA | NA | 1119 | 347 |
| Total Length (Gb) | 1.64 | 1.36 | 1.33 | 1.35 | 1.65 | 1.64 |
| Longest Contig (Mb) | 84.40 | 1.30 | 24.77 | 22.05 | 143.80 | 225.00 |
| N50 (Mb) | 16.64 | 0.20 | 6.22 | 6.70 | 116.50 | 105.88 |
| L50 | 30 | 1807 | 67 | 70 | 7 | 6 |
| L90 | 118 | 13911 | 226 | 225 | 13 | 14 |
| GC (%) | 32.42 | 32.43 | 32.42 | 32.39 | 32.20 | 32.36 |
| Complete BUSCOS (%) | 95.05 | NA | 93.73 | 94.06 | 90.43 | 95.05 |
| Fragmented BUSCOS (%) | 0.33 | NA | 0.66 | 1.98 | 2.31 | 0.33 |
| Missing BUSCOS (%) | 4.62 | NA | 5.61 | 3.96 | 7.26 | 4.62 |
| Merqry (C%, CV) | 83.59, 50.2 | NA | 99.0, 50.1* | 99.0, 50.1* | 83.6, 30 | 83.50, 50.2 |

*Combined Haplotypes

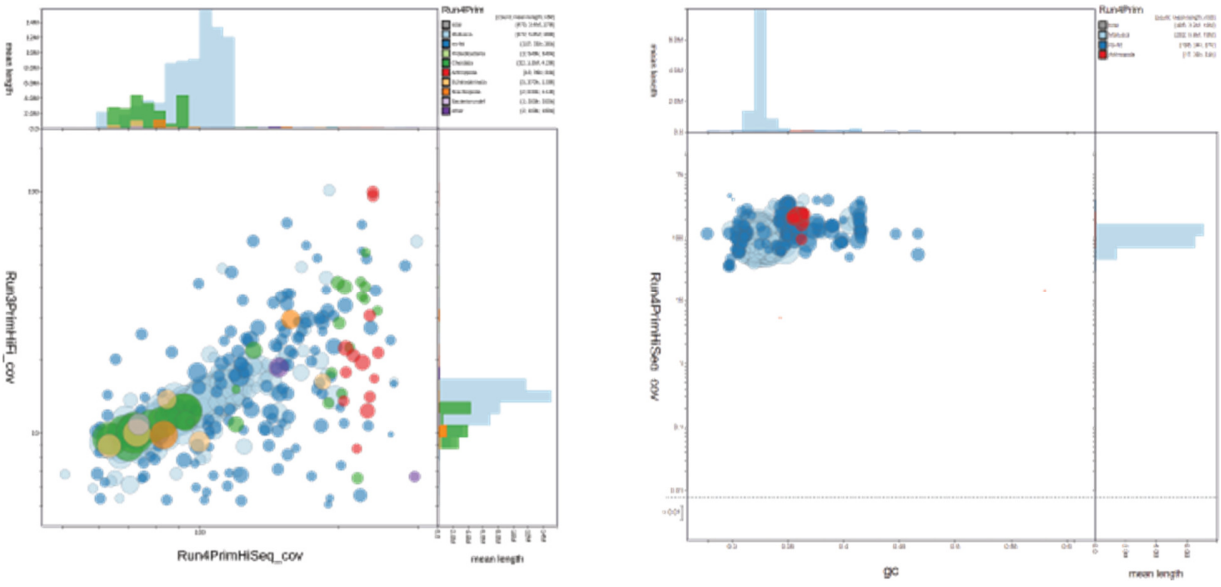


Figure 1. Blobtools2 plots before and after filtering.