

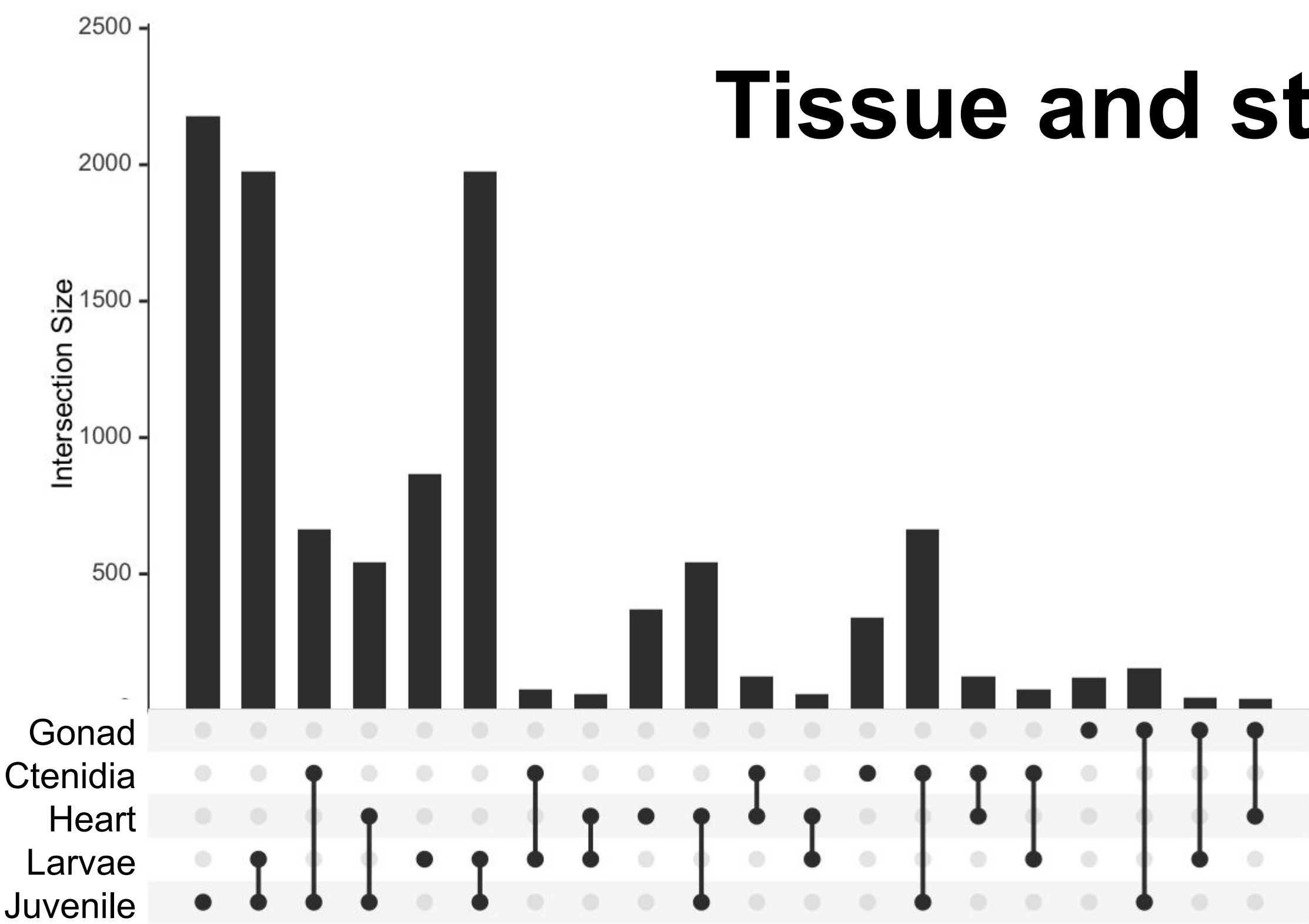
Genomic Resources for the Pacific Geoduck (*Panopea generosa*)

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Summary

- The Pacific Geoduck genome has been sequenced and assembled
- Deep coverage tissue specific transcriptomes are available
- Single-cell RNA-seq efforts provide new insight into developmental trajectories

Tissue and stage specific transcriptomes

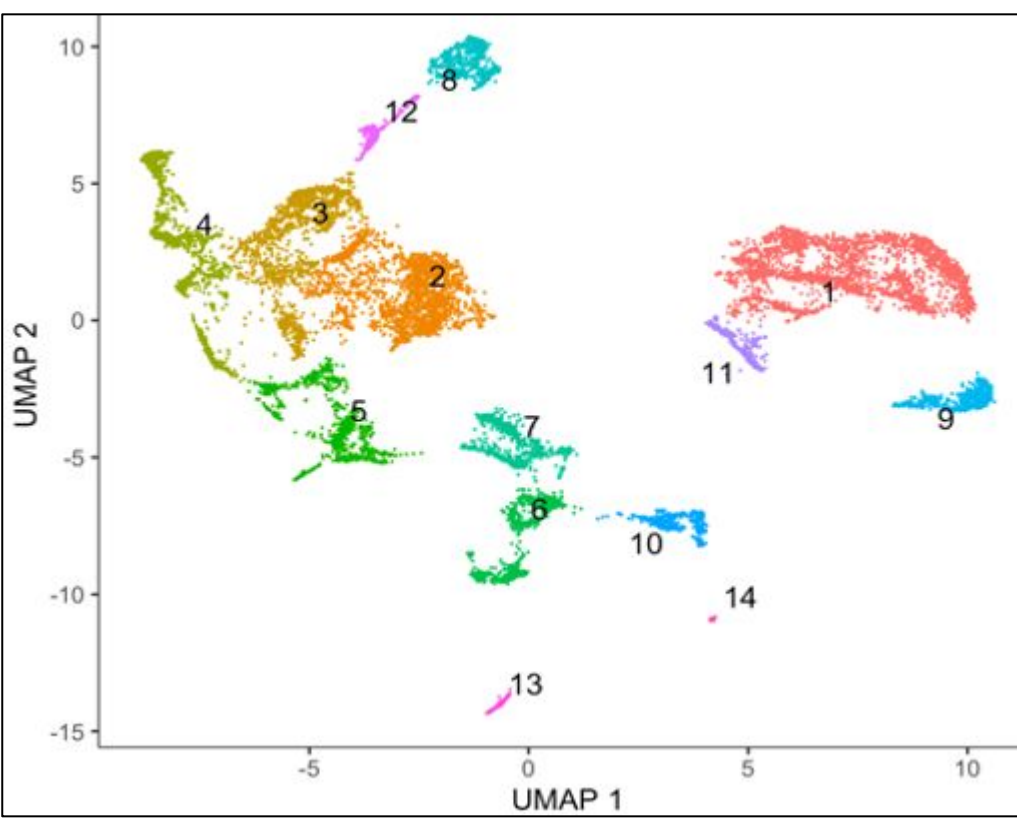


Gene-set Descriptor	Number of Genes
Ctenidia Unique	340
Gonad Unique	119
Heart Unique	371
Juvenile Unique	2180
Larvae Unique	868
Express in all libraries	11294

Comparative Genomics

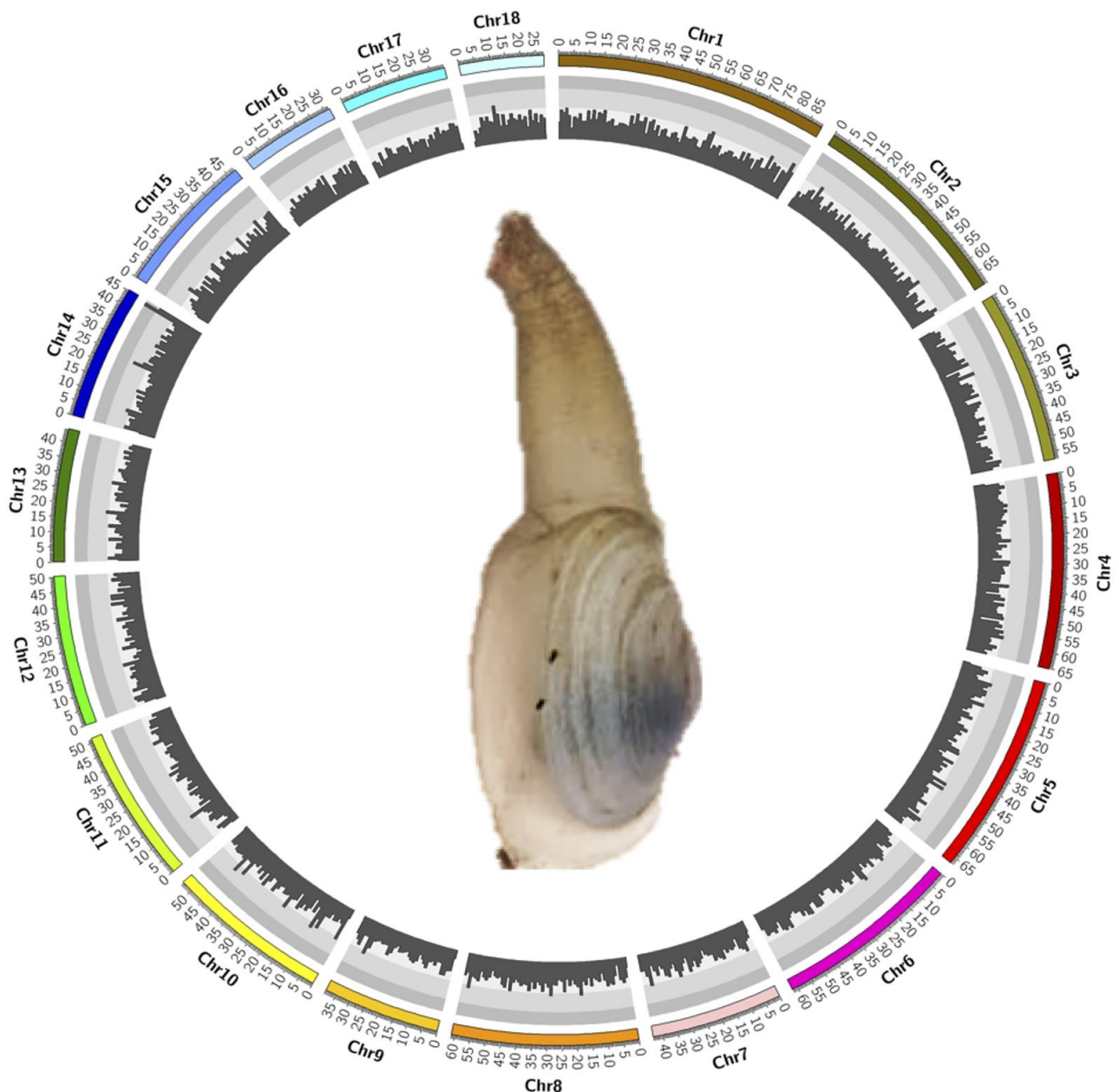
Species	GenBank Assembly Accession	Genome size (Mbp)	Chromosomes	Number of Genes	GC content (%)	Reference
<i>P. generosa</i>	GCA_902825435.1	942	18	34,947	33.78	(Putnam et al. 2023)
<i>R. philippinarum</i>	GCA_009026015.1	1230	19	27,652	32.26	(Mun et al. 2017)
<i>C. virginica</i>	GCA_002022765.4	685	11	38,826	34.82	(Gómez-Chiarri et al. 2015)
<i>C. gigas</i>	GCA_902806645.1	648	10	38,296	33.50	(Zhang et al. 2012)

Single-Cell RNA-seq



Single-cell sequencing has been carried out on 17 hpf embryos with distinct cell cluster identified based on expression (above). Cell group 4 patterns suggest association with gonad development. Top marker genes for group 4 are listed and corresponding expression in tissue libraries (below).

Cell Group 4 Top Markers					
gene_id	gene_ID	ctenidia	heart	gonad	larvae juvenile
PGEN_00g199430	G2/mitotic-specific cyclin-B	28	0	56	76 30
PGEN_00g070070	inner centromere protein	3	0	2	9 7
PGEN_00g089980	G2/mitotic-specific cyclin-A	6	0	9	63 21
PGEN_00g259100	histone-lysine N-methyltransferase NSD2	7	4	10	8 8
PGEN_00g054930	sperm-specific protein PHI-2B/PHI-3	0	0	50	8 0
PGEN_00g068740	dentin sialophosphoprotein-like	2	21	3	25 3
PGEN_00g078980	homeobox protein CDX-1	0	0	3	38 2
PGEN_00g330580	lymphocyte-specific helicase	2	0	2	4 4
PGEN_00g120520	putative UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase LOC100288842	2	0	2	3 2
PGEN_00g281640	metal-response element-binding transcription factor 2-like	3	1	1	3 4



Geoduck genome representation with chromosome name on the outermost track, followed by chromosome position in kilobase pairs (kbp), color bars indicating each chromosome, and gene density (genes/kbp) on the innermost track.

Genome Statistics

Genome	Total scaffold length (bp)	942,353,201
	Scaffold N50 (bp)	57,743,597
	GC content, N excluded (%)	33.78
Genes	Number of genes	34,947
	Mean gene length (bp)	201
	Mean coding region length (bp)	201
Exons	Mean number of exons per gene	6.78
	Mean length (bp)	201
	Total length (Mbp)	47
Introns	Genes with introns (%)	72.04
	Mean length (bp)	2185
	Total length (Mbp)	338

Support

Access to data, papers, and poster
github.com/RobertsLab/poster-geoduck-NSA-2023

