List of Figures

List of Tables

Figures

Map of sampling locations including run timing

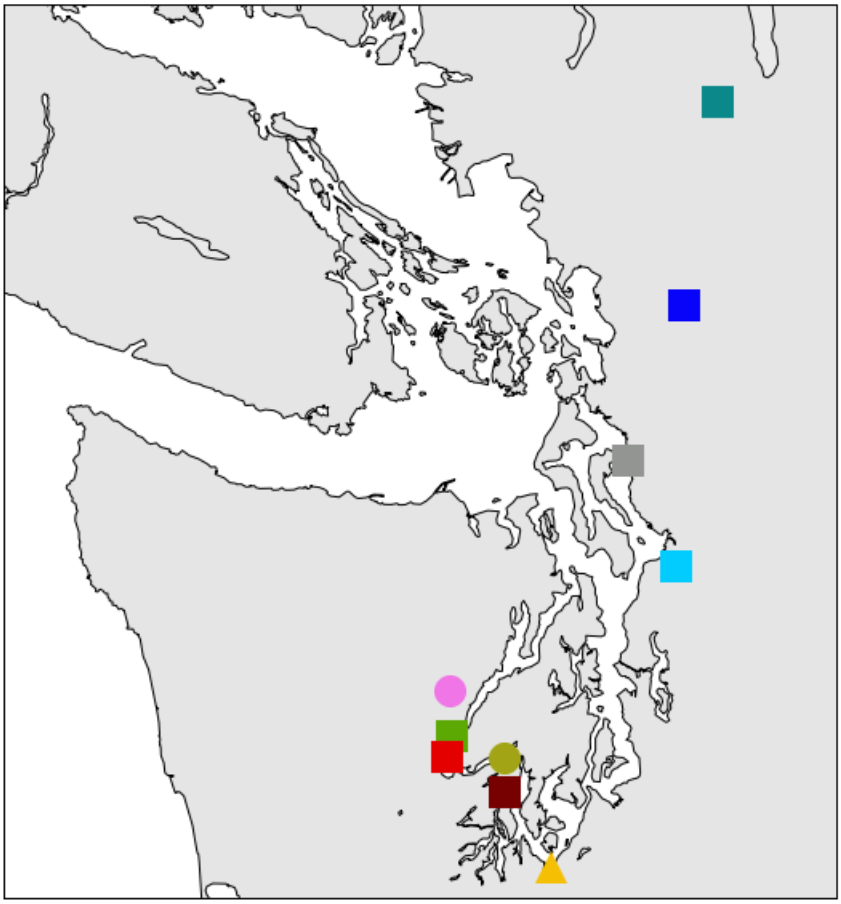

Figure 1: Collection locations and runtiming of chum salmon sampled near Puget Sound.

Linkage map

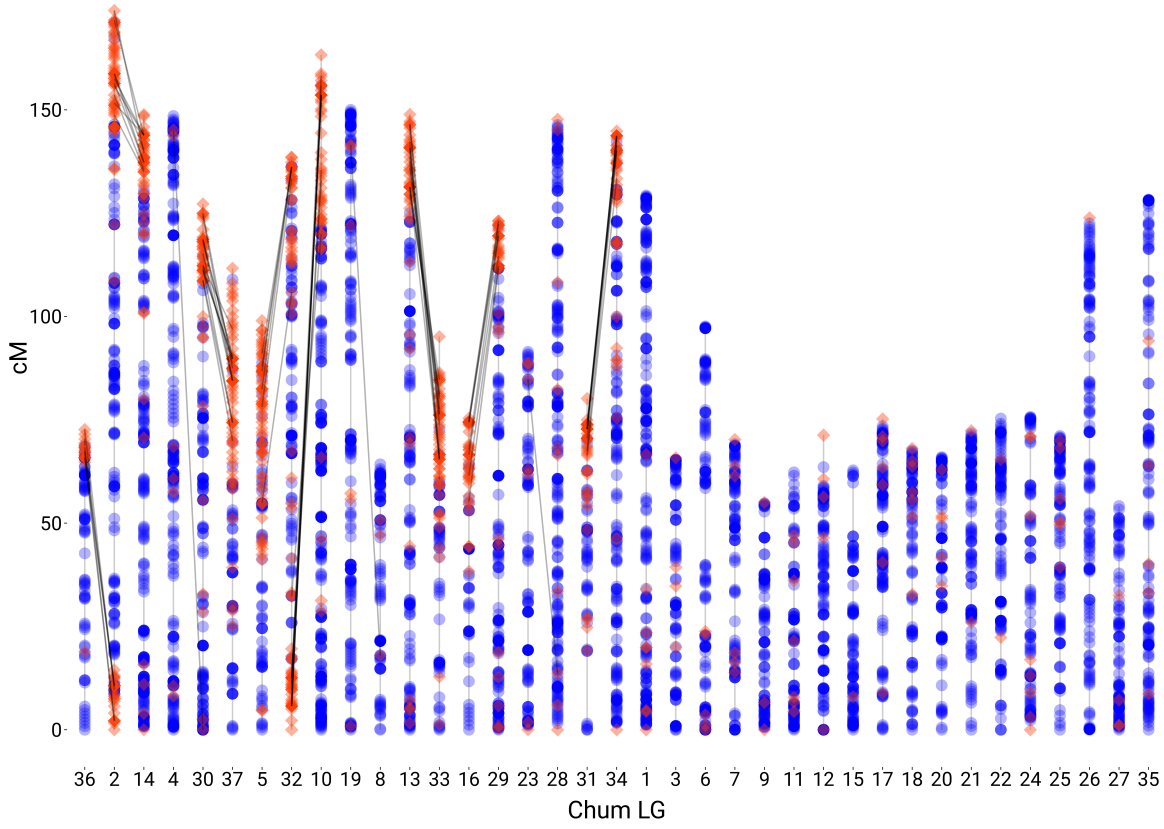

Figure 2: 37 linkage groups, likely corresponding to the 37 chromosomes in the chum salmon karyotype. Paralogous loci are shown as red diamonds, non-paralogs are blue circles. Black lines connect confounded catalog entries that have been resolved into two paralogous loci. The 16 distal concentrations of paralogs form 8 pairs of homeologous chromosomes. Notice LGs 2 and 32 have distinct ancestral relationships on each end.

Ascertainment bias

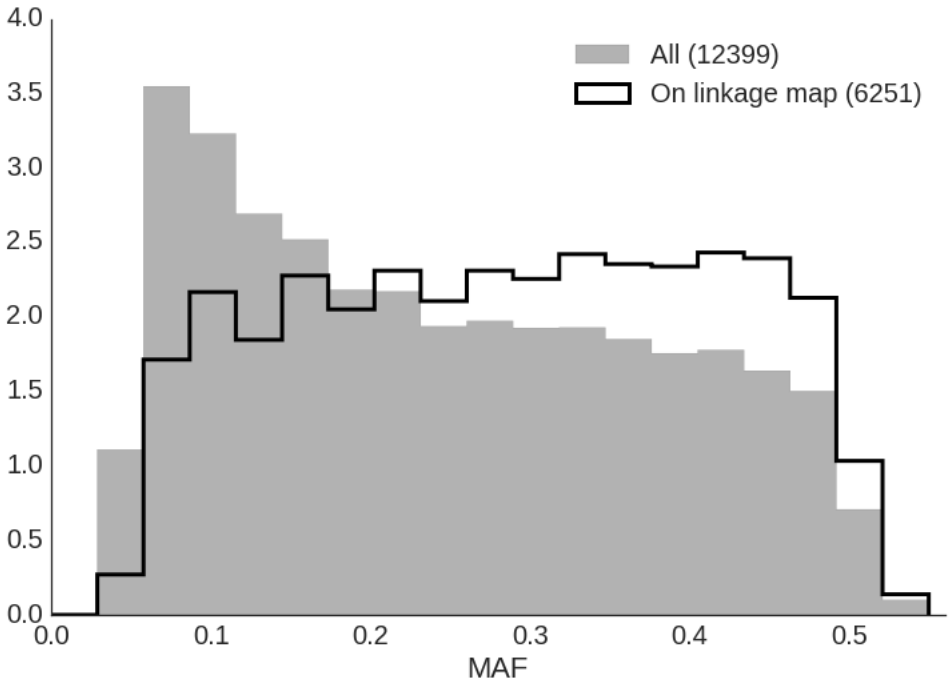

Figure 3: Folded minor allele frequency (MAF) for all loci (grey) and the subset of loci placed on the linkage map (black outline). The rightward shift in the MAF distribution shows the effect of ascertainment bias. Notice the y-axis is density-scaled to accommodate differing number of loci in each set.

Population structure

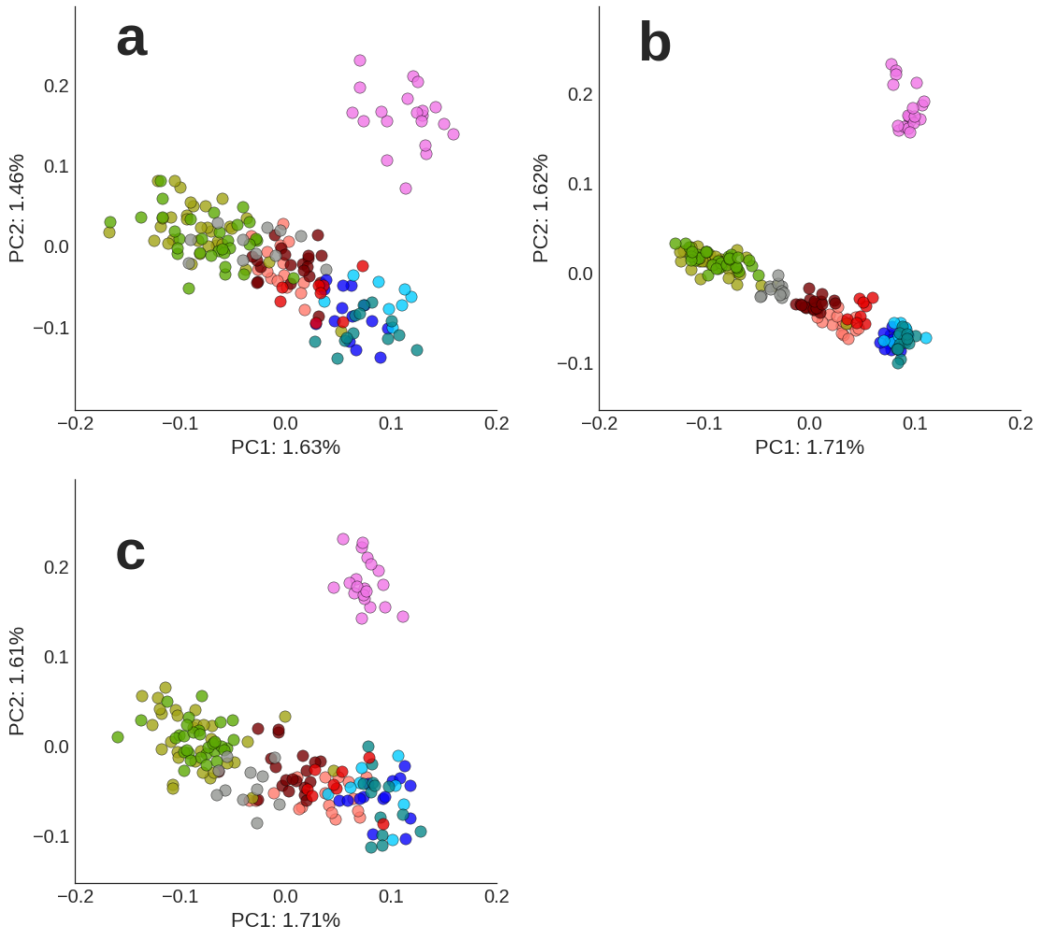

Figure 4: Population structure - Individual-based PCA from ten populations (colors) of chum salmon from Puget Sound. Population structure obtained from paralogs (a) is similar to that obtained by non-paralogs (b), especially after down-sampling to match the number of loci (c).

Manhattan plot

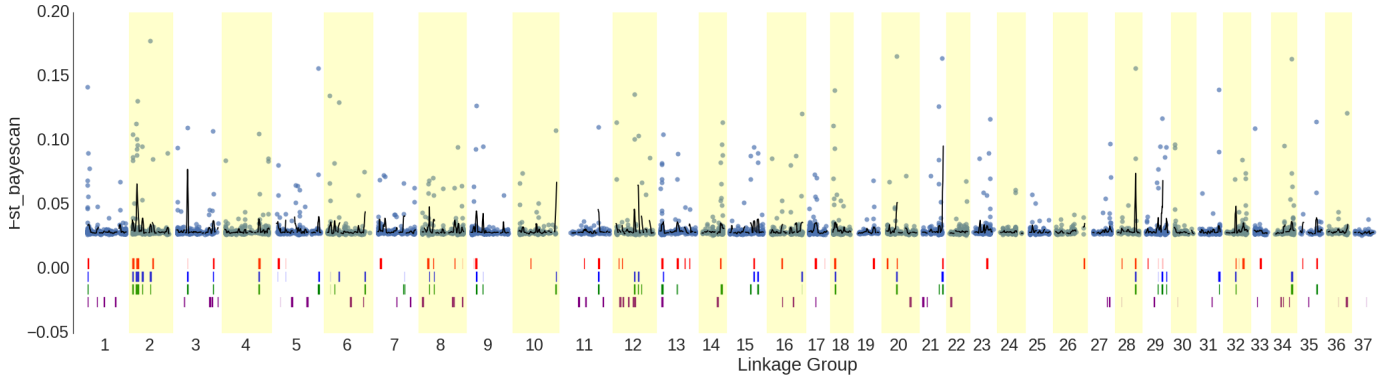

Figure 5: Manhattan plot of differentiation across the 37 linkage groups of chum salmon. Points are Bayescan Fst values for single loci. Population genetic statistics were calculated at each cM position by calculating an inverse distance-weighted average value from loci within a 5cM wide window centered on each position. Black outlines show loci selected as life history outliers in Bayescan. Black Lower shaded regions show genomic regions in the upper 99%, as determined by bootstrap permutation. Color codes for shaded regions: Red: LFMM qvalue, Blue: Bayescan qvalue, Green: Bayescan Fst, Purple: Weir Fst.

Tables

Sequencing and genotyping

Table 1: Sample sizes. usable sequences, and genotyping rates

		Aligned sequences		Genotyping rate	
Collection	n	mean	std	mean	std
Hamma Hamma	20	1,419,541	1,427,760	0.87	0.08
Lilliwaup Creek	20	2,760,125	999,141	0.98	0.01
Nisqually Kalama Creek	17	2,270,022	1,432,866	0.96	0.03
Sherwood River Fall	32	3,235,188	966,091	0.96	0.04
Sherwood River Summer	31	2,504,974	1,183,089	0.91	0.07
Skookum Creek	11	1,644,932	637,844	0.95	0.09
Snohomish River	14	1,135,085	495,888	0.94	0.07
Squakum Creek	8	999,084	650,927	0.86	0.08
Stillaguamish River	13	710,538	269,873	0.91	0.06
Hoodsport Hatchery*	8	509,422	148,391	0.85	0.08

*paired-end sequencing.

Genetic diversity

Table 2: Genetic diversity

	Heterozygosity	Ne
Hamma Hamma	0.30	339
Lilliwaup Creek	0.34	5,959
Nisqually Kalama Creek	0.32	161
Sherwood River Fall	0.33	319
Sherwood River Summer	0.31	145
Skookum Creek	0.33	1,788
Snohomish River	0.32	2,122
Squakum Creek	0.31	∞*
Stillaguamish River	0.30	1,001
Hoodsport Hatchery	0.30	∞*

*small sample size (<10)