# **Supplementary Figures**

A graph of a diagram

Description automatically generated with medium confidence

Figure S1: The proportion of individuals that had at least one offspring (y-axis) at a given age (x-axis). Blue horizontal lines indicate the mean **PRS** values and the grey shaded area represents the confidence band associated with the mean value.

A graph of different age groups

Description automatically generated with medium confidence

Figure S2: TOP) Proportion of total population size (y-axes) for each age class (x-axes) specific to each sampling habitat (mainstem, left; tributary, right). BOTTOM) Proportion of population sampled (y-axes) for each age class (x-axes) for each sampling habitat (mainstem, left; tributary, right).

**Chart, histogram

Description automatically generated**

Figure S3: Distributions of log-likelihood ratios, generated using CKMRsim, between parent-offspring pairs (blue) and unrelated pairs (red) of Chinook salmon. Baseline samples were genotyped at 301 SNPs and 13 microsatellite loci, however only 255 SNPs were retianed for analyses. Using the available baseline samples from 2004, this CKMRsim anlsysis simulated the power of 255 SNPs plus a single multiplex of 5 microsattelite loci for valid parentage inference.

A graph of different colored lines

Description automatically generated

Figure S4: The log-likelihood ratio distribution, generated using CKMRsim, among unrelated pairs (red), half-sibling pairs (yellow), and full-sibling pairs (green) of Chinook salmon. Samples from 2020 were genotyped at 299 SNPs and 5 microsatellite loci. This CKMRsim anlsysis simulated the power of 254 SNPs plus a single multiplex of 5 microsattelite loci for valid sibship inference.

A graph of a graph of a graph of a graph of a graph of a graph of a graph of a graph of a graph of a graph of a graph of a graph of a graph of

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Figure S5: Distributions of log-likelihood ratios, generated using CKMRsim, between parent-offspring pairs (blue) and unrelated pairs (red) of Chinook salmon. The left panel displays log-likelihood distributions for these relationships using 255 SNPs, while the right panel shows the same information using 13 microsatellites.

# **Supplementary Tables**

Table S1: Input parameters for three implmentations of the parentage analysis software, COLONY. The number of Chilkat River Chinook salmon adults when using mainstem samples (implementation 2, not shown) was 295, and the Prob of dam and sire in candidates was 0.09. The number of adults when using tributary samples (implementation 3, not shown) was 306, and the Prob of dam and sire in candidates was 0.10.

|  |  |
| --- | --- |
| **Parameter** | **Implementation 1: All Adults and All Juveniles** |
| Number of adults in the sample | 583 |
| Number of offspring in the sample | 682 |
| Number of loci | 259 |
| Seed for random number generator | 1234 |
| Not updating/updating allele frequency | Updating |
| Dioecious/monoecious species | Dioecious |
| Inbreeding absent/present | Absent |
| Diploid species/haplodiploid species | Diploid |
| Polygamy/monogamy for males & females | Polygamy |
| Clone inference | No |
| Scale full sibship | Yes |
| Sibship prior | Weak |
| Unknown/known population allele frequency | Unknown |
| Number of runs | 1 |
| Length of run | Medium |
| Monitor method | Time in seconds |
| Monitor interval | Seconds |
| Version | Windows |
| Likelihood method | Full-Likelihood |
| Precision | Medium |
| Prob of Dad (and Mum) in candidates | 0.23 |

Table S2: Sample sizes of genoytped Chilkat River Chinook salmon in each sampling event and the number of individuals removed due to missing data, duplicate samples, and excessive heterozygosity. Note that duplicates found in “all adults” are due to recaptures between the mainstem and tributary sampling events.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Sample Collection** | **Genotyped** | **Missing Data** | **Duplicates** | **Excessive heterozygosity** | **Final Dataset** |
| **All adults** | 641 | 0 | 19 | 39 | 583 |
| **Mainstem Adults** | 312 | 0 | 0 | 17 | 295 |
| **Tributary Adults** | 329 | 0 | 1 | 22 | 306 |
| **Juveniles** | 700 | 10 | 1 | 7 | 682 |

Table S3 Samples sizes and locations for adult Chilkat River Chinook samples collected in 2020 with genotypes passing quality assurance steps.

|  |  |
| --- | --- |
| Sample Location | Number of Adults in Final Dataset |
| Mainstem Fishwheel (Chilkat River) | 150 |
| Mainstem Gillnet (Chilkat River | 145 |
| Kelsall (Chilkat Tributary) | 79 |
| Tahini (Chilkat Tributary) | 210 |
| Klehini (Chilkat Tributary) | 17 |

Table S4 Samples sizes and locations for juvenile Chilkat River Chinook samples collected in 2021 with genotypes passing quality assurance steps.

|  |  |
| --- | --- |
| Sample Location | Number of Juveniles in Final Dataset |
| Mainstem (Chilkat River) | 191 |
| Kelsall (Chilkat Tributary) | 247 |
| Tahini (Chilkat Tributary) | 244 |

Table S5: Key paramters and results for the dropout simulations for Chilkat River Chinook salmon.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Scenario** | **Psampling** | **Adults** | **Dropout %** | **Estimate** | **95% Range of Abundances** |
| 1 (Mainstem) | 0.18, 0.12, 0.60, 0.10 | 295 | 0 | 3,427 | 2,615 – 4,239 |
| 2 (Tributary) | 0.01, 0.34, 0.29, 0.36 | 306 | 0 | 3,283 | 2,538 – 4,028 |
| 3 (Tributary) | 0.01, 0.34, 0.29, 0.36 | 306 | 5 | 3,119 | 2,429 – 3,810 |
| 4 (Tributary) | 0.01, 0.34, 0.29, 0.36 | 306 | 10 | 2,935 | 2,306 – 3,564 |
| 5 (Tributary) | 0.01, 0.34, 0.29, 0.36 | 306 | 15 | 2,802 | 2,216 – 3,388 |
| 6 (Tributary) | 0.01, 0.34, 0.29, 0.36 | 306 | 20 | 2,600 | 2,078 – 3,123 |
| 7 (Tributary) | 0.01, 0.34, 0.29, 0.36 | 306 | 25 | 2,460 | 1,982 – 2,938 |
| 8 (Tributary) | 0.01, 0.34, 0.29, 0.36 | 306 | 30 | 2,281 | 1,855 – 2,706 |
| 9 (Tributary) | 0.01, 0.34, 0.29, 0.36 | 306 | 35 | 2,128 | 1,745 – 2,510 |
| 10 (Tributary) | 0.01, 0.34, 0.29, 0.36 | 306 | 40 | 1,978 | 1,638 – 2,319 |

# **Supplementary Material**

## **Parentage Power Analysis Methods**

We used previously collected baseline genotype data from adult Chilkat River Chinook salmon sampled in 2004 (K. Shedd & Gilk-Baumer, 2021) and the R package *CKMRsim* (Dr. Eric Anderson <https://github.com/eriqande/CKMRsim>) to evaluate the power of various combinations of genetic markers to sufficiently detect all parent-offspring relationships (false negative rate < 0.0001, for a false positive rate = 100 times the reciprocal of the number of anticipated pairwise comparisons of parents and offspring). These available baseline samples were genotyped for 301 single nucleotide polymorphism (SNP) genetic markers using Genotyping-in-Thousands by sequencing (GT-seq; Campbell et al., 2015) in combination with 13 microsatellite loci from the Genetic Analysis of Pacific Salmon (GAPS) panel (Seeb et al., 2007; Moran et al., 2013). The 301 SNP GT-seq panel was based off of the 299 SNP v3.0 GT-seq panel developed by the Columbia River Inter-tribal Fish Commission Hagerman Genetics Laboratory (Hess et al., 2014) with two additional SNPs (*Ots\_uwsnp640165* and *Ots\_uwsnp670329*) that are associated with the run timing gene GREB1L (Prince et al., 2017). We used *CKMRsim* to calculate population allele frequencies from baseline samples, simulate multi-locus genotypes for different relationships, and evaluate the statistical power of a given marker set (254 SNPs and 5 microsatellite loci) for identifying valid parentage assignments (Figure S3).

## **Parentage Power Analysis Results**

When simulating the false positive and false negative rates of parentage assignments associated with various combinations of GAPS microsatellite multiplexes in conjunction with a GT-seq SNP panel in *CKMRsim*, we determined that a single multiplex of five microsatellite loci accompanied by the SNP panel would provide ample power for valid parentage assignments. Figure 4 shows that the distribution of log-likelihood ratios for POPs versus unrelated pairs have minimal overlap, indicating adequate statistical power for differentiating between these two groups. Our evaluation of parentage panels in *CKMRsim* was based on the criteria of requiring a false positive rate that is 10 times lower than the reciprocal of the number of comparisons we made (0.1 x (641 adults x 700 parr))-1 = 2.2-5) (recommendation from Eric Anderson, author of *CKMRsim*). Using ADF&G’s baseline samples of Chilkat River Chinook salmon, we observed a simulated false positive rate of 2.34-7 and a false negative rate of 0.0006 in *CKMRsim* associated with our proposed panel.

Once the 2020 adult samples were genotyped, we re-ran the *CKMRsim* analysis to evaluate how similar the final panels performed for parentage analysis between the baseline and 2020 samples. As expected, the contemporary *CKMRsim* results indicated that the 2020 samples provided concordant statistical power for parentage inference, simulating a false positive rate of 3.98e-7 and a false negative rate of 0.0001.

# **Data Archiving/Accessibility Statement:** Data for this study are available at: <https://github.com/swrosenbaum/tGMR_simulations>

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# **Appendix**

Appendix S1: Single nucleotide polymorphism and microsatellite loci used to genotype Chilkat River Chinook salmon.

|  |  |
| --- | --- |
| Locus | Source |
| ARNT | Hess et al., 2014 |
| GTH2B-550 | Hess et al., 2014 |
| NOD1 | Hess et al., 2014 |
| Ots\_100884-287 | Hess et al., 2014 |
| Ots\_101119-381 | Hess et al., 2014 |
| Ots\_101554-407 | Hess et al., 2014 |
| Ots\_101704-143 | Hess et al., 2014 |
| Ots\_101770-82 | Hess et al., 2014 |
| Ots\_102213-210 | Hess et al., 2014 |
| Ots\_102414-395 | Hess et al., 2014 |
| Ots\_102457-132 | Hess et al., 2014 |
| Ots\_102801-308 | Hess et al., 2014 |
| Ots\_102867-609 | Hess et al., 2014 |
| Ots\_103041-52 | Hess et al., 2014 |
| Ots\_103122-180 | Hess et al., 2014 |
| Ots\_104048-194 | Hess et al., 2014 |
| Ots\_104415-88 | Hess et al., 2014 |
| Ots\_105105-613 | Hess et al., 2014 |
| Ots\_105132-200 | Hess et al., 2014 |
| Ots\_105385-421 | Hess et al., 2014 |
| Ots\_105401-325 | Hess et al., 2014 |
| Ots\_105407-117 | Hess et al., 2014 |
| Ots\_105897-124 | Hess et al., 2014 |
| Ots\_106313-729 | Hess et al., 2014 |
| Ots\_106499-70 | Hess et al., 2014 |
| Ots\_106747-239 | Hess et al., 2014 |
| Ots\_107074-284 | Hess et al., 2014 |
| Ots\_107285-93 | Hess et al., 2014 |
| Ots\_107607-315 | Hess et al., 2014 |
| Ots\_107806-821 | Hess et al., 2014 |
| Ots\_108007-208 | Hess et al., 2014 |
| Ots\_108390-329 | Hess et al., 2014 |
| Ots\_108735-302 | Hess et al., 2014 |
| Ots\_108820-336 | Hess et al., 2014 |
| Ots\_109525-816 | Hess et al., 2014 |
| Ots\_109693-392 | Hess et al., 2014 |
| Ots\_110064-383 | Hess et al., 2014 |
| Ots\_110201-363 | Hess et al., 2014 |
| Ots\_110381-164 | Hess et al., 2014 |
| Ots\_110551-64 | Hess et al., 2014 |
| Ots\_110689-218 | Hess et al., 2014 |
| Ots\_111084b-619 | Hess et al., 2014 |
| Ots\_111312-435 | Hess et al., 2014 |
| Ots\_111681-657 | Hess et al., 2014 |
| Ots\_112208-722 | Hess et al., 2014 |
| Ots\_112301-43 | Hess et al., 2014 |
| Ots\_112419-131 | Hess et al., 2014 |
| Ots\_112876-371 | Hess et al., 2014 |
| Ots\_113242-216 | Hess et al., 2014 |
| Ots\_113457-40R | Hess et al., 2014 |
| Ots\_115987-325 | Hess et al., 2014 |
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| Ots\_118205-61 | Hess et al., 2014 |
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| Ots\_122414-56 | Hess et al., 2014 |
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| Ots\_123921-111 | Hess et al., 2014 |
| Ots\_124774-477 | Hess et al., 2014 |
| Ots\_127236-62 | Hess et al., 2014 |
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| Ots\_129144-472 | Hess et al., 2014 |
| Ots\_129170-683 | Hess et al., 2014 |
| Ots\_129458-451 | Hess et al., 2014 |
| Ots\_129870-55 | Hess et al., 2014 |
| Ots\_130720-99 | Hess et al., 2014 |
| Ots\_131460-584 | Hess et al., 2014 |
| Ots\_131802-393 | Hess et al., 2014 |
| Ots\_131906-141 | Hess et al., 2014 |
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| Ots\_94903-99R | Hess et al., 2014 |
| Ots\_96222-525 | Hess et al., 2014 |
| Ots\_96500-180 | Hess et al., 2014 |
| Ots\_96899-357R | Hess et al., 2014 |
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| Ots\_97660-56 | Hess et al., 2014 |
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| Ots\_AldoB4-183 | Hess et al., 2014 |
| Ots\_arp-436 | Hess et al., 2014 |
| Ots\_AsnRS-72 | Hess et al., 2014 |
| Ots\_aspat-196 | Hess et al., 2014 |
| Ots\_CCR7 | Hess et al., 2014 |
| Ots\_CD59-2 | Hess et al., 2014 |
| Ots\_CD63 | Hess et al., 2014 |
| Ots\_cgo24-22 | Hess et al., 2014 |
| Ots\_Chin30up-211 | Hess et al., 2014 |
| Ots\_CirpA | Hess et al., 2014 |
| Ots\_cox1-241 | Hess et al., 2014 |
| Ots\_CRB211 | Hess et al., 2014 |
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| Ots\_crRAD11620-55 | Hess et al., 2014 |
| Ots\_crRAD12037-39 | Hess et al., 2014 |
| Ots\_crRAD12711-37 | Hess et al., 2014 |
| Ots\_crRAD13725-51 | Hess et al., 2014 |
| Ots\_crRAD16540-50 | Hess et al., 2014 |
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| Ots\_crRAD18937-60 | Hess et al., 2014 |
| Ots\_crRAD20262-46 | Hess et al., 2014 |
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| Ots\_crRAD33054-62 | Hess et al., 2014 |
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| Ots\_GH2 | Hess et al., 2014 |
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| Ots\_Hsp90a | Hess et al., 2014 |
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| Ots\_myo1a-384 | Hess et al., 2014 |
| Ots\_myoD-364 | Hess et al., 2014 |
| Ots\_nelfd-163 | Hess et al., 2014 |
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| Ots\_SClkF2 | Hess et al., 2014 |
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| Ots\_SL | Hess et al., 2014 |
| Ots\_slc7a2-71 | Hess et al., 2014 |
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| Ots\_TAPBP | Hess et al., 2014 |
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| Ots\_Thio | Hess et al., 2014 |
| Ots\_TLR3 | Hess et al., 2014 |
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| Ots\_u1007-124 | Hess et al., 2014 |
| Ots\_u1008-108 | Hess et al., 2014 |
| Ots\_U211 | Hess et al., 2014 |
| Ots\_U2362-227 | Hess et al., 2014 |
| Ots\_U2362-330 | Hess et al., 2014 |
| Ots\_U2446-123 | Hess et al., 2014 |
| Ots\_U2567-104 | Hess et al., 2014 |
| Ots\_U5049-250 | Hess et al., 2014 |
| Ots\_U5121-34 | Hess et al., 2014 |
| Ots\_UNKN4-150 | Hess et al., 2014 |
| Ots\_UNKN6-187 | Hess et al., 2014 |
| Ots\_USMG5-67 | Hess et al., 2014 |
| Ots\_vatf-251 | Hess et al., 2014 |
| Ots\_zn593-346 | Hess et al., 2014 |
| Ots\_zP3b | Hess et al., 2014 |
| Ots\_ZR-575 | Hess et al., 2014 |
| PGK-54 | Hess et al., 2014 |
| RAG3 | Hess et al., 2014 |
| S7-1 | Hess et al., 2014 |
| unkn526 | Hess et al., 2014 |
| Omm1080 | Seeb et al., 2007; Moran et al., 2013 |
| Ots201b | Seeb et al., 2007; Moran et al., 2013 |
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