

**Post Emergence Egg Collection and Genetic
Analyses from Chinook Salmon Redds in the San
Joaquin River Restoration Area**

2025 Monitoring and Analysis Report



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Photo credit: Bureau of Reclamation

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Self-Certification of Peer Review

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I certify that, to my best knowledge, these individuals are qualified to review this work, and that they have peer reviewed this report.

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1.0 Introduction

Efforts to re-establish populations of spring-run Chinook Salmon (*Oncorhynchus tshawytscha*) to the San Joaquin River Restoration Area (Restoration Area) are ongoing. The Restoration Area includes the river downstream of Friant Dam, near Fresno, California and extends downstream to its confluence with the Merced River. Salmon in the Restoration Area face challenges across all life stages ([SJRRP] San Joaquin River Restoration Program 2010). Annual monitoring efforts, including redd surveys to identify total spawning salmon and the resulting constructed redds (Ellsworth et al. 2025), and juvenile salmon monitoring, via rotary screw traps (Hutcherson et al. 2025), are intended to evaluate Chinook Salmon at these life stages.

One of the issues confounding the ability to determine factors contributing to the survival of juvenile salmon from the spawning grounds in Reach 1 of the Restoration Area has been the ability to ascribe individual redds to the adults constructing them. During juvenile salmon monitoring efforts, where downstream moving juvenile Chinook Salmon are captured in rotary screw traps, typically from November–May, tissue samples are collected and later genetically evaluated (Hutcherson et al. 2023; 2024). One facet of these analyses is to determine the parental genotypes of sampled juveniles. Coupled with production estimates at rotary screw traps, downstream of spawning grounds, and combined with survival estimates of marked fry released close to spawning grounds near Friant Dam, biologists can estimate family group size, with respect to maternal genotype. However, redds are frequently clustered at regularly recurring sites from Friant Dam downstream to the first rotary screw trap at Owl Hollow (Demarest et al. 2022; 2023). What is unclear is how redd distribution, proximity to the nearest collection point for juveniles, metrics pertaining to parentage (e.g., fish size, time of capture/release, brood year), or specific in-river conditions at the site of redd construction contribute to the success of individual redds.

Described herein is a novel approach to determine if viable genetic information could be collected from eggs remaining in Chinook Salmon redds post-emergence. While other methods exist for collecting such information (e.g., salmon fry can be collected during emergence from redds; eggs may be collected via hydraulic pumping [Berejikian et al. 2011]), the intent was to collect viable genetic material to ascribe parental genotypes to specific redds while limiting anthropogenic impacts to redds during active juvenile emergence. Parental genotypes are often ascribed to juveniles from tissue samples collected during rotary screw trap monitoring efforts (Hutcherson et al. 2025). The ability to pinpoint their origin to specific redds would help better understand their survival in the Restoration Area. If successful, this approach could also help better define how juvenile salmon are faring when compared to those criteria listed in Fisheries Framework ([SJRRP] 2018) and how river and redd-specific conditions (e.g., temperature, flow, gravel composition, hyporheic conditions) impact survival.

The initial goal of the egg collection effort described herein was to collect unhatched eggs from individual redds, following emergence. The second goal was submitting these eggs for genetic analyses to determine if sufficient viable genetic material was available to determine parentage. To provide a control for which to compare those eggs collected in-river, personnel at the California Department of Fish and Wildlife (CDFW) Salmon Conservation and Research Facility (SCARF) provided eggs at regularly scheduled intervals, from controlled hatchery settings, to further evaluate

genetic viability from unhatched eggs post-fertilization. Based on our review of the available scientific literature, these approaches have not been attempted.

1.1 Objectives

This study design was intended to help determine whether unhatched eggs collected from salmon redds following the emergence of viable fry had viable genetic material. Since unknown river conditions could have affected these results, salmon eggs were also provided by the SCARF to evaluate whether more controlled settings might yield more genetically viable tissues (*see* [Collection Methods](#)). Eggs from the SCARF were provided at regular intervals to help determine when unfertilized or no longer developing eggs ceased to provide sufficient genetic material after fertilization. If viable genetic information can be determined from eggs collected in-river, then juveniles captured during rotary screw trap monitoring efforts may be ascribed to specific redds identified in the spawning grounds. This would help to further determine how redd distributions or site-specific features contribute to juvenile salmon survival and further refine egg-to-fry survival/fry-to-smolt survival. The following are the target objectives of this study:

- 1) Determine whether eggs collected at regular intervals from a controlled hatchery setting have viable genetic material.
- 2) Determine if eggs collected from in-river redds, post-emergence, have viable DNA for genetic analyses.
- 3) If Objective 2 is feasible, identify maternal genotypes of eggs collected from individual redds.

2.0 Materials and Methods

2.1 Schedule and Location

For the hatchery-controlled setting, eggs were provided by CDFW staff from the SCARF at nominal 20-, 40-, and 60-day intervals post-spawning from a single batch (Lot 10, Cross 103). These collection efforts were completed October–December 2024.

In-river collection efforts followed incubation and emergence of redds found in the Restoration Area. Initial redd detections were provided from staff working on Redd and Carcass surveys during late summer and fall 2024. The emergence period was determined by accumulated thermal units (ATUs), calculated from the initial detection of each redd. Accumulated thermal units were calculated from the cumulative total of daily water temperatures (daily average) from the date of initial redd detection—for example, 10 days with a daily average of 10°C would be 100 ATUs. The ATUs at the end of emergence were based upon emergence studies from the 2020–21 seasons—the average of these was 1,170 ATUs (Demarest et al. 2021; 2023). To ensure emergence had largely

completed, collection efforts were tentatively scheduled for 1,150–1,200 ATUs following initial redd discovery. These efforts were completed December 2024–January 2025.

Initially, up to six redds in the area between Friant Dam (River mile [RM] 267.5) and Lost Lake Recreation Area (RM 264.5) were proposed for egg recovery. Redd selection was based on proximity to other redds—preference was given to those redds separated by several meters from its closest neighboring redd. This allowed personnel to follow the process outlined in the following, “Collection Methods” section, with minimal disturbance to other redds. During Chinook Salmon redd and carcass surveys, redd locations were demarcated with GPS coordinates and flagged on the adjacent shoreline with flagging noting the bearing and distance to each respective redd. This information assisted staff in locating redds selected for excavation.

2.2 Collection Methods

Two preservation approaches were used to evaluate the genetic integrity of collected eggs: (1) desiccation and (2) storage in DNA/RNA Shield™ (Zymo Research, Irvine, California), a product meant to preserve nucleic acids and inactivate pathogens (Figure 1). Eggs slated for desiccation were flattened between filter paper and subsequently dried for 24 h at 68 °C (100° F). Eggs preserved in DNA/RNA Shield™ were placed in a 2 mL vial pre-filled with the solution and stored at room temperature until submitted for genetic analyses. A label accompanied each vial or on each tissue envelope identifying the redd ID and date of collection. For both those samples collected from the river as well as those supplied by the hatchery, eggs were evenly split among the two preservation methods.

Regarding the samples collected in-river: the initial proposal called for collecting eggs at varying levels of degradation, termed (1) near-fully and (2) partially degraded; however, during the collection period, differing levels of degradation were not observed, and so these levels were not assigned (Figure 2). A minimum of 12 eggs were collected from each redd during each sampling event. At the conclusion of all redd sampling events, tissues were submitted to the Southwest Fisheries Science Center, Santa Cruz Laboratory (NOAA Fisheries).

Eggs at CDFW’s SCARF were incubated in MariSource vertical stack incubators (Legends Brands, Inc., Burlington, Washington) using a recirculation system. The recirculation system used an 80-micron micro-screen drum filter, UV sterilization, a fluidized bed drum filter, and a water chilling unit. Temperature was initially maintained at 11°C (52°F) and increased to 13°C (55°F) when eggs entered the eyed stage. Prior to entering the eyed stage, eggs were treated with 1,700 ppm hydrogen peroxide or 1,750 ppm formalin to prevent fungal growth. Eggs from CDFW’s SCARF were collected from a single fertilization event (Lot 10, Cross 103). During cleaning events at the three scheduled intervals (20-, 40-, and 60-days post-fertilization), unviable eggs, determined by their opaque and undeveloped appearance were removed from the batch. A total of 12 eggs were removed at each event, of which 6 were desiccated and 6 stored in DNA/RNA Shield™.



Figure 1.—Biologist recording the relevant data (e.g., date of collection, redd ID number) and recovering salmon eggs from net that was placed downstream of a redd before excavation. A subsample of recovered eggs was either preserved via desiccation or storage in a DNA-stabilizing solution. Photo credit: Bureau of Reclamation.

For those eggs collected from the San Joaquin River, the egg pocket of selected redds was excavated to collect unhatched eggs. Staff positioned a 1.2-m square lift net, with 3mm knotless mesh 1 m downstream of the sampled redd to catch dislodged eggs. The bottom margin of the net was placed perpendicular to the flow and flush to the substrate. The net was oriented in an upward sloping direction, from up- to downstream, to capture any dislodged eggs. While one or more staff held the net in place, another individual removed substrate from the egg pocket area of the constructed redd to dislodge any remaining eggs. Periodically, excavation ceased, and the catch net lifted to determine whether eggs were flushed downstream. Any accumulated eggs were collected following the described methods.

Substrate was initially removed by hand. Personnel proceeded slowly in case there were actively emerging salmon. If no fry were initially found, additional tools were used to ease excavation (e.g.,

shovels, trowels). If more than three fry were recovered while collecting eggs, sampling ceased for that collection event, and staff returned later, permitting the remaining fish to emerge and move downstream. If excavation ceased during the first period because of actively emerging fry, the remaining excavation was completed upon the second visit. Dislodged fry were collected for genetic analyses (up to three fish per redd; additional ones beyond the initial three were released downstream)—fry were collected to provide a method for corroborating the genetic information from eggs collected from the same redd. Excavation proceeded until reaching a depth of 30 cm (Evenson 2001; Oldenburg et al. 2009) or the targeted number of eggs were collected.



Figure 2.—Salmon eggs recovered from a redd after excavation. Note the relatively uniform cloudy appearance of the eggs. Photo credit: Bureau of Reclamation.

2.3 Analyses

The Southwest Fisheries Science Center (Santa Cruz, California) received egg samples collected from the San Joaquin River and from hatchery production at the SCARF. Samples from fry were also included as a control. The experimental design included whole and partial eggs stored in DNA/RNA Shield™ buffer, as well as whole and partial eggs that were desiccated directly upon collection. The overall goal was to examine the potential impact of these various collection methods on our ability to generate quality genotypes.

DNA was extracted from a total of 89 samples using DNeasy Blood and Tissue Kits (Qiagen Inc., Venlo, Netherlands) according to manufacturer’s recommended protocols and genotyped them with

our standard panel of 195 Chinook salmon genetic markers. Then assessed were the total and mean number of reads per sample, where reads are the number of redundant sequences at a locus that lend support to a specific genotype call.

Results of genetic analyses were generically qualified as “great,” “fine,” or “bad.” These categories denoted whether samples had nearly complete genetic data, likely had sufficient data for genetic inference, or were unsuitable for genotyping, respectively.

3.0 Results

As was detected for the two fry samples (121724_1 and 121724_2; [Appendix A](#)), high-quality samples are expected to yield mean numbers of reads in the hundreds per locus, providing high confidence in genotyping results. Generally, genotyping results for the egg samples were not good, with some notable exceptions ([Appendix B](#)). Of the six samples collected on Day 18 of incubation at the SCARF (October 25, 2024) and stored in DNA/RNA Shield™, five were suitable to collect genetic information. Four of the desiccated samples from Day 18 were suitable for genetic evaluation. None of the samples from Day 44 were suitable to collect genetic information; however, three desiccated samples from Day 60 yielded high read numbers, sufficient for genetic inference ([Table 1](#)).

Table 1.—Genetic results of eggs submitted from the Salmon Conservation and Research Facility (California Department of Fish and Wildlife) at various intervals. “Great” indicates samples had almost complete genetic data; “fine” indicated samples were probably sufficient for genetic inference; “bad” indicated the samples genotyped poorly.

Days Post Spawn:	Preservation Method:	Total Samples:	Proportion "Great":	Proportion "Fine":	Proportion "Bad":
18	DNA Shield	6	33%	50%	17%
18	Desiccation	6	33%	33%	33%
44	DNA Shield	6	0%	0%	100%
44	Desiccation	6	0%	0%	100%
60	DNA Shield	6	0%	0%	100%
60	Desiccation	6	50%	0%	50%

Though six redds were proposed for excavation, only four met the necessary criteria and were accessible—many of the other redds were in water too deep to use the sample collection gear. Of those four, eggs were recovered from only two redds. Of the remaining two, one produced no eggs during excavation attempts; the location of last one was no longer apparent in the river and excavation was not attempted because of the lack of any identifiable features and uncertainty regarding the egg pocket location.

Initial samples were collected from redd NR07 on December 17, 2024; however, during excavation more than three fry were observed in the collection net. Two were collected for genetic analyses, and the excavation ceased. Since fry were recovered during the December 17 collection event, no additional excavations were attempted that trip, permitting fry potentially remaining in other redds to emerge without disturbance. Staff returned early January 2025 to complete the redd excavations. Regardless of the date of collection, all eggs recovered from the redds were unsuitable for genotyping (Table 2). Fry submitted for analysis, from the December 2024 event, were categorized as “great” regarding the total loci reads (Appendix A).

Table 2.—Genetic results of eggs submitted for analysis. “Great” indicates samples had almost complete genetic data; “fine” indicated samples were probably sufficient for genetic inference; “bad” indicated the samples genotyped poorly.

Redd ID#:	Collection Date:	Preservation Method:	Total Samples:	Total Whole Eggs:	Prop. "Great":	Prop. "Fine":	Prop. "Bad":
NR07	17-Dec-24	DNA Shield	6	6	0%	0%	100%
NR07	17-Dec-24	Desiccation	6	6	0%	0%	100%
NR07	7-Jan-25	DNA Shield	6	4	0%	0%	100%
NR07	7-Jan-25	Desiccation	8	6	0%	0%	100%
NR12	10-Jan-25	DNA Shield	12	8	0%	0%	100%
NR12	10-Jan-25	Desiccation	12	8	0%	0%	100%

4.0 Discussion

Collecting viable genetic material from unhatched eggs remaining in redds post-emergence will not be a practical method to ascribe parental genotypes to redds in the San Joaquin River. None of the collected samples yielded sufficient DNA for reliable analyses. Even when eggs were collected under controlled hatchery conditions, and within the incubation period, only a limited proportion were considered adequate for genotyping.

Recovering eggs from redds post-emergence was more difficult than originally anticipated. While redds were identified during the surveys concurrent with the spawning period, they were not always readily identifiable, even when standing in-river with a tablet and satellite imagery to verify the redd location. Without being able to see the features of the redd, visible during and shortly after its construction, attempting to locate the redd pocket proved impractical.

Downstream survival for juvenile salmon in the Restoration Area falls short of the objectives in the Fisheries Framework ([SJRRP] 2018; Hutcherson et al. 2023; 2024; 2025). Likewise, estimates of redd production also fall below those criteria; however, for which reason may be limiting the success of juvenile salmon in these upstream areas of the Restoration Area is not certain. There is some

value in ascribing redds to specific parentage, to determine whether there are site-specific reasons why redds may have limited success regarding juvenile survival, or whether it is simply a function of the distance to the downstream capture location. Further exploration of methods to identify redd—parental genotyping may be merited if downstream juvenile survival does not increase with other restoration efforts.

5.0 References

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Hutcherson, J., Z. Sutphin, J. Giannetta, M. Grill, J.C. Garza, and A. Clemento. 2023. *Juvenile spring-run Chinook Salmon production, survival, and emigration in the San Joaquin River Restoration Area: 2019–20 monitoring and analysis report*. Bureau of Reclamation, Denver Technical Service Center, Denver, Colorado, 46 pp.

6.0 Appendix A: Genetic Results of Egg and Fry Samples Collected From Chinook Salmon Redds

Table 3.—Genetic results of egg and fry samples collected from Chinook Salmon (*Oncorhynchus tshawytscha*) redds in the San Joaquin River Restoration Area December 2024–January 2025. Green indicates sample had good genotyping; yellow indicates genetic inferences could be made; red indicates genotyping was unsuitable.

Date:	Life Stage:	Redd:	Sample #:	Preservation Method:	Comments:	Sample ID:	Sum Reads—All Loci:	Avg. Reads Across Loci:
12/17/24	Fry	NR07	1	Desiccation	Smolt index 2	121724_1	32701	160.30
12/17/24	Fry	NR07	2	Desiccation	Smolt index 2	121724_2	40180	196.96
12/17/24	Egg	NR07	3	DNA Shield	None	121724_3	190	0.93
12/17/24	Egg	NR07	4	DNA Shield	None	121724_4	239	1.17
12/17/24	Egg	NR07	5	DNA Shield	None	121724_5	168	0.82
12/17/24	Egg	NR07	6	DNA Shield	None	121724_6	197	0.97
12/17/24	Egg	NR07	7	DNA Shield	None	121724_7	245	1.20
12/17/24	Egg	NR07	8	DNA Shield	None	121724_8	232	1.14
12/17/24	Egg	NR07	9	Desiccation	None	121724_9	274	1.34
12/17/24	Egg	NR07	10	Desiccation	None	121724_10	174	0.85
12/17/24	Egg	NR07	11	Desiccation	None	121724_11	171	0.84
12/17/24	Egg	NR07	12	Desiccation	None	121724_12	151	0.74
12/17/24	Egg	NR07	13	Desiccation	None	121724_13	207	1.01
12/17/24	Egg	NR07	14	Desiccation	None	121724_14	139	0.68
1/7/25	Egg	NR07	1	DNA Shield	Whole egg	010725_1	187	0.92
1/7/25	Egg	NR07	2	DNA Shield	Whole egg	010725_2	201	0.99
1/7/25	Egg	NR07	3	DNA Shield	Whole egg	010725_3	193	0.95
1/7/25	Egg	NR07	4	DNA Shield	Whole egg	010725_4	199	0.98
1/7/25	Egg	NR07	5	DNA Shield	Partial egg	010725_5	219	1.07
1/7/25	Egg	NR07	6	DNA Shield	Partial egg	010725_6	250	1.23
1/7/25	Egg	NR07	7	Desiccation	Whole egg	010725_7	288	1.41

Date:	Life Stage:	Redd:	Sample #:	Preservation Method:	Comments:	Sample ID:	Sum Reads— All Loci:	Avg. Reads Across Loci:
1/7/25	Egg	NR07	8	Desiccation	Whole egg	010725_8	134	0.66
1/7/25	Egg	NR07	9	Desiccation	Whole egg	010725_9	375	1.84
1/7/25	Egg	NR07	10	Desiccation	Whole egg	010725_10	229	1.12
1/7/25	Egg	NR07	11	Desiccation	Whole egg	010725_11	180	0.88
1/7/25	Egg	NR07	12	Desiccation	Whole egg	010725_12	214	1.05
1/7/25	Egg	NR07	13	Desiccation	Partial egg	010725_13	173	0.85
1/7/25	Egg	NR07	14	Desiccation	Partial egg	010725_14	201	0.99
1/10/25	Egg	NR12	1	DNA Shield	Whole egg	011025_1	216	1.06
1/10/25	Egg	NR12	2	DNA Shield	Whole egg	011025_2	277	1.36
1/10/25	Egg	NR12	3	DNA Shield	Whole egg	011025_3	186	0.91
1/10/25	Egg	NR12	4	DNA Shield	Whole egg	011025_4	121	0.59
1/10/25	Egg	NR12	5	DNA Shield	Whole egg	011025_5	206	1.01
1/10/25	Egg	NR12	6	DNA Shield	Whole egg	011025_6	198	0.97
1/10/25	Egg	NR12	7	DNA Shield	Whole egg	011025_7	171	0.84
1/10/25	Egg	NR12	8	DNA Shield	Whole egg	011025_8	161	0.79
1/10/25	Egg	NR12	9	DNA Shield	Partial egg	011025_9	179	0.88
1/10/25	Egg	NR12	10	DNA Shield	Partial egg	011025_10	306	1.50
1/10/25	Egg	NR12	11	DNA Shield	Partial egg	011025_11	184	0.90
1/10/25	Egg	NR12	12	DNA Shield	Partial egg	011025_12	149	0.73
1/10/25	Egg	NR12	13	Desiccation	Whole egg	011025_13	205	1.00
1/10/25	Egg	NR12	14	Desiccation	Whole egg	011025_14	188	0.92
1/10/25	Egg	NR12	15	Desiccation	Whole egg	011025_15	240	1.18
1/10/25	Egg	NR12	16	Desiccation	Whole egg	011025_16	298	1.46
1/10/25	Egg	NR12	17	Desiccation	Whole egg	011025_17	281	1.38
1/10/25	Egg	NR12	18	Desiccation	Whole egg	011025_18	151	0.74

Date:	Life Stage:	Reed:	Sample #:	Preservation Method:	Comments:	Sample ID:	Sum Reads— All Loci:	Avg. Reads Across Loci:
1/10/25	Egg	NR12	19	Desiccation	Whole egg	011025_19	289	1.42
1/10/25	Egg	NR12	20	Desiccation	Whole egg	011025_20	285	1.40
1/10/25	Egg	NR12	21	Desiccation	Partial egg	011025_21	305	1.50
1/10/25	Egg	NR12	22	Desiccation	Partial egg	011025_22	300	1.47
1/10/25	Egg	NR12	23	Desiccation	Partial egg	011025_23	19	0.19
1/10/25	Egg	NR12	24	Desiccation	Partial egg	011025_24	21	0.21

7.0 Appendix B: Genetic Results of Eggs Provided from the Salmon Conservation and Research Facility (California Department of Fish and Wildlife)

Table 4.—Genetic results of egg samples provided by the California Department of Fish and Wildlife, from the Salmon Conservation and Research Facility, collected from Chinook Salmon (*Oncorhynchus tshawytscha*; Lot 10, Cross 103) at intervals from the time of fertilization. Green indicates sample had good genotyping; yellow indicates genetic inferences could be made; red indicates genotyping was unsuitable.

Date:	Life Stage:	Sample #:	Days Post Fertilization:	Preservation Method:	Sample ID:	Sum Reads—All Loci:	Avg. Reads Across Loci:
10/25/24	Egg	1	18	DNA Shield	102524_1	2022	9.91
10/25/24	Egg	2	18	DNA Shield	102524_2	346	1.70
10/25/24	Egg	3	18	DNA Shield	102524_3	6638	32.54
10/25/24	Egg	4	18	DNA Shield	102524_4	3654	17.91
10/25/24	Egg	5	18	DNA Shield	102524_5	18058	88.52
10/25/24	Egg	6	18	DNA Shield	102524_6	1825	8.95
10/25/24	Egg	7	18	Desiccation	102524_7	18833	192.17
10/25/24	Egg	8	18	Desiccation	102524_8	16	0.16
10/25/24	Egg	9	18	Desiccation	102524_9	5	0.05
10/25/24	Egg	10	18	Desiccation	102524_10	1917	19.56
10/25/24	Egg	11	18	Desiccation	102524_11	1112	11.35
10/25/24	Egg	12	18	Desiccation	102524_12	41935	427.91
11/20/24	Egg	13	44	DNA Shield	112025_13	194	0.95
11/20/24	Egg	14	44	DNA Shield	112025_14	200	0.98
11/20/24	Egg	15	44	DNA Shield	112025_15	179	0.88
11/20/24	Egg	16	44	DNA Shield	112025_16	165	0.81
11/20/24	Egg	17	44	DNA Shield	112025_17	196	0.96
11/20/24	Egg	18	44	DNA Shield	112025_18	179	0.88
11/20/24	Egg	19	44	Desiccation	112025_19	6	0.06
11/20/24	Egg	20	44	Desiccation	112025_20	1	0.01
11/20/24	Egg	21	44	Desiccation	112025_21	6	0.06
11/20/24	Egg	22	44	Desiccation	112025_22	4	0.04
11/20/24	Egg	23	44	Desiccation	112025_23	2	0.02
11/20/24	Egg	24	44	Desiccation	112025_24	12	0.12
12/6/24	Egg	25	60	DNA Shield	120625_25	287	1.41
12/6/24	Egg	26	60	DNA Shield	120625_26	172	0.84
12/6/24	Egg	27	60	DNA Shield	120625_27	175	0.86
12/6/24	Egg	28	60	DNA Shield	120625_28	167	0.82

Date:	Life Stage:	Sample #:	Days Post Fertilization:	Preservation Method:	Sample ID:	Sum Reads—All Loci:	Avg. Reads Across Loci:
12/6/24	Egg	29	60	DNA Shield	120625_29	223	1.09
12/6/24	Egg	30	60	DNA Shield	120625_30	136	0.67
12/6/24	Egg	31	60	Desiccation	120625_31	3	0.03
12/6/24	Egg	32	60	Desiccation	120625_32	7	0.07
12/6/24	Egg	33	60	Desiccation	120625_33	3	0.03
12/6/24	Egg	34	60	Desiccation	120625_34	58886	600.88
12/6/24	Egg	35	60	Desiccation	120625_35	44293	451.97
12/6/24	Egg	36	60	Desiccation	120625_36	49922	509.41