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Review of the Inner Bay of Fundy Atlantic Salmon (*Salmo salar*) Monitoring Activities Associated with the Live Gene Bank

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Foreword

This series documents the scientific basis for the evaluation of aquatic resources and ecosystems in Canada. As such, it addresses the issues of the day in the time frames required and the documents it contains are not intended as definitive statements on the subjects addressed but rather as progress reports on ongoing investigations.

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TABLE OF CONTENTS

LIST OF ABBREVIATIONS.....	V
ABSTRACT.....	IV
1.0 INTRODUCTION.....	1
1.1 INNER BAY OF FUNDY ATLANTIC SALMON ECOLOGY	1
1.2 INNER BAY OF FUNDY ATLANTIC SALMON STATUS.....	1
1.3 REVIEW OBJECTIVES.....	2
2.0 MATERIALS AND METHODS.....	3
2.1 LIVE GENE BANK.....	3
2.1.1 Collections and Distributions	3
2.1.2 Genetic Analysis.....	4
2.2 SMOLT ASSESSMENT	4
2.2.1 Big Salmon River.....	5
2.2.2 Stewiacke River.....	6
2.2.3 Gaspereau River	6
2.3 ADULT ASSESSMENT	7
2.3.1 Big Salmon River.....	7
2.3.2 Gaspereau River	8
2.4 LIVE GENE BANK SURVIVAL	8
2.4.1 Freshwater Survival Estimates	9
2.4.2 Marine Survival Estimates	9
2.5 PROJECTS.....	9
2.5.1 2010-2016 Crossbreeding Experiment in the Petitcodiac River	9
2.5.2 Electrofishing Surveys	10
2.5.3 Statistical Analysis.....	12
3.0 RESULTS	13
3.1 LIVE GENE BANK.....	13
3.1.1 Collections.....	13
3.2 SMOLT ASSESSMENT	13
3.2.1 Big Salmon River.....	13
3.2.2 Stewiacke River.....	16
3.2.3 Gaspereau River	17
3.3 ADULT ASSESSMENT	18
3.3.1 Big Salmon River.....	18
3.3.2 Gaspereau River	20
3.4 LIVE GENE BANK SURVIVAL	22
3.4.1 Freshwater Survival Estimates	22
3.4.2 Marine Survival Estimates	22
3.5 PROJECTS.....	23

3.5.1 Petitcodiac River Crossbreeding Experiment.....	23
3.5.2 Stewiacke River Electrofishing Surveys.....	24
3.5.3 Broadscale Electrofishing Survey Results	26
4.0 CONCLUSIONS.....	28
4.1 CONCLUSION FROM LGB PROGRAM RELEASES	28
4.2 CONCLUSIONS ON THE OVERALL STOCK STATUS	30
4.3 OTHER POINTS FOR CONSIDERATION	31
5.0 ACKNOWLEDGEMENTS	31
6.0 REFERENCES	32
7.0 TABLES	36
8.0 FIGURES.....	68
9.0 APPENDICES.....	103

LIST OF ABBREVIATIONS

1SW: one sea winter	DNA: deoxyribonucleic acid	LGB _{PG} : Live Gene Bank pre-grilse
2SW: two sea winter	DU: Designatable Unit	Lgth: length
3SW: three sea winter	Eff.: efficiency	Loc.: location
A: angling	EQU: equalized	LoP: Long Pool
ABL: Aquatic Biotechnology Laboratory	EU: European	LP: Lodge Pool
Ad.: adipose	F: female	M: mark
Ad: adult	FC: fin clip	M: male
AE: aquaculture escapee	FFFN: Fort Folly First Nations	m: metres
Age _R : river age	FFHR: Fort Folly Habitat Restoration	MB: Mast Brow
Age _S : sea age	FL: fork length	MBF: Mactaquac Biodiversity Facility
ANOVA: Analysis of Variance	FMP: fish management practice	Meth.: method
AP: Amateur Pool	GAK: Gaspereau River	MLC: mid-lower caudal
BB: Bonnell Brook	GB: Gravelly Bar	MM: month
BD: blue dye	GPS: Global Positioning System	Morts.: mortalities
BF: Biodiversity Facility	H/AC: hatchery adipose-clip stray	MP: Miller Pool
BP: bypass	HSD: Honest Significant Difference	MSW: multi-sea winter
BSR: Big Salmon River	IBoF: Inner Bay of Fundy	MUC: mid-upper caudal
Capt.: capture	JD: Julian day	N/A: data not available
Cat.: category	Juv: juvenile	NB: New Brunswick
CBF: Coldbrook Biodiversity Facility	KP: King Pool	NBDERD: New Brunswick Department of Energy and Resource Development
CER: conservation egg requirement	L: large	NC: not collected
cm: centimetres	LC: lower caudal	NMB: New Minas Basin
Colc.: Colchester	LGB: Live Gene Bank	NS: Nova Scotia
COSEWIC: Committee on the Status of Endangered Wildlife in Canada	LGB _{FRY} : Live Gene Bank fry	NSH: Nashwaak River
CP: Catt Pool	LGB _{PARR} : Live Gene Bank parr	NSPI: Nova Scotia Power Inc.
Cumb.: Cumberland County	LGB _{PS} : Live Gene Bank pre-smolt	OBoF: Outer Bay of Fundy
DD: day		Obs.: observed
DFO: Fisheries and Oceans Canada		PIT: passive integrated transponder
		PP: Picture Pool

Prop.: proportion	Se: seine	Tiss. Samp.: tissue sample
R: recapture	SJR: Saint John River	TN: tangle net
RB: Rody Bar	Smolt _{LGB} : Live Gene Bank origin smolt	TOB: Tobique River
Rec.: record	Smolt _{WILD} : wild origin smolt	ToR: Terms of Reference
Recap.: recapture	SP: Smith Pool	U or Unk.: unknown
Rel: release	Sp: spawned	UPGMA: Unweighted Pair Group with Arithmetic Mean
RP: Rody Pool	SPERA: Strategic Program for Ecosystem- Based Research and Advice	W: wild
RST: rotary screw trap	ST: streamer tag	WB: Walker Brow
S: small	STW: Stewiacke River	WD: Walton Dam
SAR: Science Advisory Report	Temp.: temperature	WP: Whirl Pool
SARA: <i>Species-At-Risk Act</i>		YOY: young of year

ABSTRACT

This document is a synopsis of the Inner Bay of Fundy (IBoF) Designatable Unit (DU) Atlantic Salmon monitoring activities, undertaken from 2001 to 2016, associated with the Live Gene Bank (LGB) Program. All of the assessment activities heavily incorporate genetic analyses to evaluate the success of the LGB in preventing the extirpation of this endangered salmon population. Over the last 15 years, the activities have included and/or continue to include: 2 updated electrofishing surveys for juvenile salmon (2013 and 2014), annual smolt abundance estimates from the Big Salmon and Gaspereau rivers, annual adult abundance estimates to the Big Salmon River, annual counts of adult salmon returning to the Gaspereau River at White Rock Dam, a summary of annual LGB collections and distribution, and an assessment of a crossbreeding experiment in the Pollet River, a tributary of the Petitcodiac River.

In 2003, an assessment of the status of the IBoF Atlantic Salmon discussed severe declines in the population since the 1970s. A review of all the aforementioned assessment activities indicates that the pattern persists to this day. The genetic analyses discussed within this document and more in-depth in the accompanying documents (O'Reilly et al. 2018; Harvie et al. 2018) also reveal the dwindling presence of true IBoF origin salmon outside the envelop of the Live Gene Bank supportive rearing program.

1.0 INTRODUCTION

1.1 INNER BAY OF FUNDY ATLANTIC SALMON ECOLOGY

Inner Bay of Fundy (IBoF) Atlantic Salmon (*Salmo salar*), like most salmon populations, have a unique lifecycle that helps them adapt to the freshwater and marine environments. As such, mature IBoF Atlantic Salmon return to their natal rivers from May to November to spawn. The young develop and emerge from the redds (gravel nest pits) in May or June and grow as parr feeding on invertebrate drift (COSEWIC 2006). Wild produced parr eventually smoltify after 2 to 4 years and emigrate to the ocean where they grow to maturity. The IBoF Atlantic Salmon return to their natal rivers after 1 year at sea to spawn as grilse [also referred to as one-sea-winter (1SW) or small (<63cm) salmon] or after 2 and 3 years spent at sea [also referred to as multi-sea-winter (MSW) or large (≥63cm) salmon]. The IBoF salmon are considered unique in that survival after spawning is relatively high, they have a high incidence of repeat spawning (typically consecutively), a high proportion of individuals mature as grilse with a greater proportion of females than males, and it is postulated that they have a localized marine migration (COSEWIC 2006).

1.2 INNER BAY OF FUNDY ATLANTIC SALMON STATUS

The Committee on the Status of Endangered Wildlife in Canada (COSEWIC) considers the IBoF population as a unique Designatable Unit (DU) based on genetic (Verspoor et al. 2002), phylogeographic, local selection, life history, behavioural and demographic evidence (COSEWIC 2001; Amiro 2003). The IBoF Atlantic Salmon DU range consists of all rivers draining into the Bay of Fundy starting with the Pereaux River [Nova Scotia (NS)] and extending around the Bay to the Mispic River [New Brunswick (NB)]. Although this region contains many rivers, note that only 50 rivers are depicted in Figure 1 as per the Recovery Strategy (DFO 2010). Of the 50 listed rivers, historically, it is thought that salmon only inhabited 32 of these rivers based on archived data and reported recreational catches (Amiro 2003; COSEWIC 2006). However, recent evidence suggests that another ten rivers have reported salmon production (DFO 2008). During the broadscale electrofishing surveys completed in 2000, 2002, 2003, and 2014, all or a majority of the remaining eight rivers were also assessed (Gibson et al. 2003a, 2004, and this document). The IBoF river stocks have been in decline since the 1980s (Gibson and Amiro 2003; Gibson et al. 2003b; DFO 2008) and have known periods of low abundance throughout their history (Amiro and Jefferson 1996). These rivers were closed to salmon fisheries in 1989 based on Big Salmon and Stewiacke rivers in-season assessments and have remained closed to all fishing since 1990 (Amiro and Jefferson 1996).

COSEWIC designated the IBoF Atlantic Salmon as 'endangered' in May 2001 (COSEWIC 2001), and later re-examined and confirmed this status in 2006 (COSEWIC 2006) and again in 2010 (COSEWIC 2010) as the population has declined to less than 200 individuals from the 40,000 individuals estimated earlier in the 20th century (Amiro 2003). In June 2003, the DU was further listed under the Canadian *Species at Risk Act* (SARA) (Flanagan et al. 2006). This listing under SARA, section 37, requires competent ministers to develop a Recovery Strategy for the Inner Bay of Fundy Atlantic Salmon, and this document was finalized in April 2010 (DFO 2010). Within the Recovery Strategy, Critical Freshwater Habitat essential to the persistence of the IBoF salmon population was identified and is comprised of 10 rivers that contained residual native populations: Big Salmon, Upper Salmon, Point Wolfe, Economy, Portapique, Great Village, Folly, Debert, Stewiacke, and Gaspereau rivers (DFO 2010). Since the completion of the Recovery Strategy, the important marine and estuarine habitat for IBoF salmon has also been identified (DFO 2013).

The primary activity being undertaken to prevent the extirpation of salmon within this DU is Live Gene Banking (LGB), a modified captive breeding and rearing program specifically designed to minimize the loss of genetic diversity and aid in the recovery of the population (O'Reilly and Doyle 2007; DFO 2008). The program involves: the captive rearing of wild-exposed broodstock, deoxyribonucleic acid (DNA)-based selective mating strategies to maximize genetic variability, early stocking of progeny to prolong exposure to natural selection in freshwater rivers and, finally, collection of parr/smolt to renew the broodstock 'pool' (Goff et al. 2001). Initiated in 1998 with the collection of parr (Marshall et al. 1999), the Mactaquac Biodiversity Facility (MBF) continues to maintain the Big Salmon River LGB program, whereas the Coldbrook Biodiversity Facility (CBF) (and prior to closure in 2013, the Mersey Biodiversity Facility) facilitated the Nova Scotia LGB program with the Stewiacke River and, in 1999, added the Gaspereau River program (Gibson et al. 2004).

The Recovery Strategy (DFO 2010) outlines performance indicators which:

“... are an important component of the recovery evaluation for the IBoF Salmon populations. A review of progress towards a recovery goal should be completed within 5 years and in every subsequent five-year period to: 1) gauge the extent that recovery activities are successful in contributing to the stated recovery goal for the species; 2) measure the extent to which progress has been made towards the achievement of each of the objectives; and 3) provide feedback on what changes are required to improve effectiveness.”

1.3 REVIEW OBJECTIVES

This research document was requested by Fisheries and Oceans Canada (DFO), Maritimes Region, Science Branch, to evaluate and summarize the IBoF DU assessment or monitoring activities that have been carried out by DFO Science with respect to the LGB program evaluation. This review, in conjunction with two other research documents addressing LGB-associated genetics (O'Reilly et al. 2018; Harvie et al. 2018), will direct the development of a 5-year plan for the LGB program. Specifically, this document examines the assessment of the LGB program and will support the development of a Science Advisory Report (SAR) for the Review of the IBoF Atlantic Salmon Science Associated with the Live Gene Bank (DFO 2018). This document addresses the Terms of Reference [ToR] Item 4 (status of IBoF salmon and evaluate the different release strategies of the LGB program) in Appendix 1 to support the development of the SAR.

The IBoF salmon population has historically been assessed using data from two index rivers: the Big Salmon River in New Brunswick and the Stewiacke River in Nova Scotia, supplemented with recreational catch and effort data prior to fisheries closure, electrofishing data, as well as adult fish counts on the Upper Salmon River (NB) and Gaspereau River (NS) (DFO 2008). This document will continue to focus on DFO-led efforts in the Big Salmon, Stewiacke, and Gaspereau rivers, as well as include the data collected during the cross-breeding experiment in the Petitcodiac River system and special electrofishing surveys (Stewiacke River and IBoF Broadscale). The objective of this review is to update and summarize the latest monitoring and assessment efforts in order to evaluate the current status of the IBoF population as it relates to the LGB program and assess its progress in achieving the recovery goals.

2.0 MATERIALS AND METHODS

2.1 LIVE GENE BANK

2.1.1 Collections and Distributions

Release strategies (i.e., distributions) have evolved over the lifetime of the LGB based on adaptive program management decisions directed by assessment and genetic results. Progeny from the pedigreed matings are released into tributaries of LGB program-related rivers as unfed fry, feeding fry, parr, smolts, pre-grilse or adults.

In the LGB or non-supplementation part of the IBoF salmon conservation program, previously obtained subsets of offspring from each family are digitally imaged, enumerated, and variance in family size minimized through a process termed “equalization”. The individuals who are retained and released into their respective LGB in-river habitats [i.e., Big Salmon River (BSR) fry are released into Bonnell Brook, while Stewiacke (STW) River fry are distributed to Pembroke River] through the process of equalization are known as the equalized (EQU) collections. The targeted number of EQU releases for individual families is determined by (a) the total number of potential EQU releases (across all families), expected freshwater survival, and broodstock requirements (numbers of candidate spawners needed in future spawning activities), and (b) the extent of reduction in variance in family size associated with different equalization regimes (different target numbers to equalize to). By equalizing the number of juveniles released into their respective LGB river, it (a) minimizes (but doesn’t eliminate) domestication selection associated with the rearing of salmon in the hatchery environment from fertilization to release, (b) increases the number of families recovered from the wild, (c) minimizes variance in family size overall, decreasing expected rates of loss of genetic variation and accumulation of inbreeding, (d) exposes LGB salmon (eventual parents) to native wild river conditions, potentially benefitting offspring via epigenetic or maternal egg provisioning effects, and (e) provides the potential for natural selection from release to collection at Age-1 or Age-2, possibly minimizing genetic changes associated with domestication at this later juvenile stage.

The juveniles will grow into Age-1 parr (and residual Age-2 parr) in the wild (termed wild-exposed salmon) until the following year when teams return to each respective LGB wild-exposed site to electrofish for juveniles, return them to their respective Biodiversity Facility (BF) for sampling, tagging, genetic analysis, growth to maturity, and possible selection into subsequent mating plans.

A small number of eggs from each family are also withheld at each BF for complete rearing in captivity. This group, known as the ‘captive F1 group’, are a safety measure in the event wild-exposed fish cannot be collected due to weather-events or logistical reasons. This strategy guarantees the number of families remaining in the population is maintained regardless of natural events.

Smolts are also collected from the Rotary Screw Trap (RST, aka. smolt wheel) operated on the Big Salmon River and the downstream bypasses at the White Rock Dam on the Gaspereau River. These fish are transported to their respective BFs, sampled, tagged, genetically analysed, grown to maturity, and possibly selected for mating plans. Collection at the smolt stage increases time of exposure in the wild (i.e., potentially decreasing domestication) and parents. However, it does not allow for as much family recovery, as initial family inputs from the generalized LGB or supplementation releases are not equalized [e.g., offspring from large females (high-fecundity) will ‘dilute’ smaller families, as well as offspring from the few remaining anadromous parents]. During the first season of the Stewiacke River RST smolt assessment

project (2014), smolts were transported to the CBF, genetically analysed to possibly capture offspring of wild Stewiacke adults and for inclusion into the LGB.

Anadromous returns are also collected from the trap in the White Rock Dam pool-and-weir fishway on the Gaspereau River. These adults are all transported to the CBF for possible inclusion in the Gaspereau River LGB mating plan.

All mature adults that will not be spawned in the LGB mating plans, termed non-targeted adults, are released into the wild prior to spawning (i.e., an alternative release strategy) to increase LGB inputs into 'receiver' rivers. Adult releases have been, and in some cases are, released based on their priority designation (e.g., low priority equals a well-represented family within existing LGBs). For example, Stewiacke River non-targeted low-priority adults were released into the Salmon River [Colchester (Colc.)] and non-targeted Gaspereau adults were previously distributed to the Cornwallis River, but are currently released in the St. Croix River, NS.

2.1.2 Genetic Analysis

The LGB programs involve multiple generations of captive-reared adults with various rearing histories (i.e., wild exposed to full captivity) and subsequent release strategies (e.g., juveniles, kelts, or mature adult releases). The long-term management of these populations could affect the persistence and adaptability of these fish upon their return to the wild environment (O'Reilly and Doyle 2007). In order to investigate some of the effects of the LGB program on survivability of released salmon in the supported river systems, tissue samples are collected from each individual either retained at the BF for LGB or sampled by electrofishing.

Results of genotyping assays from DNA-extracted tissue samples are submitted to the DFO Genetics Unit for analyses. Genotype information is then used to help biologists address several questions important to managers, including estimation of the proportion of adult returns produced by the LGB program vs residual wild salmon populations and/or strays, assessment of spawning success of LGB-origin juvenile releases returning as adults (and/or direct LGB-origin adult releases), assessment of the spawning success of wild returning adults, estimation of relatedness for broodstock selection and spawning (pairing of male and female parents) purposes, and for carrying out research into possible effects of inbreeding^{1,2}, outbreeding domestication selection³, heterosis⁴, Mean Kinship, etc., on possible indicators of offspring fitness in the wild.

2.2 SMOLT ASSESSMENT

To facilitate the annual collection of smolts for the LGB program, annual smolt assessment programs were initiated on the Big Salmon, Gaspereau, and, more recently, Stewiacke rivers to

¹ Inbreeding: the mating between relatives; or an increase in the mating between relatives beyond that which would be expected to occur through chance alone; or the increase in the co-occurrence of alleles that are identical-by-descent within an individual relative to some reference point (usually individuals in the parent generation).

² Inbreeding depression: a reduction in trait performance (e.g., survival) associated with a given level of inbreeding.

³ Domestication selection: adaptation to captive conditions (simple but less accurate) or genetic change associated with the different selective regimes experienced by an individual in the hatchery environment relative to that which he/she would have experienced in the wild.

⁴ Heterosis: An increase in offspring performance resulting from the combining of genetic material from genetically divergent populations (or less similar populations).

estimate smolt abundance by origin (LGB versus wild). This smolt monitoring data is used to assess in-river and marine survival for the progeny of the LGB program and any remnant wild adult spawners. Whenever mark-recapture data were available, it was incorporated into a Bayesian estimate procedure described by Gazey and Staley (1986) to determine the most probable estimate (the mode) of population size and a binomial distribution was assumed for random sampling error.

2.2.1 Big Salmon River

Emigrating smolts are captured on the Big Salmon River using a RST (Flanagan et al. 2006) that is annually (since 2001) installed near the mouth of the river in Amateur Pool (N45.42240°, W-65.40984°; Table 1, Figure 2).

The objective of the installation is to both estimate annual smolt abundance and collect non-adipose-clipped smolts to be integrated into the LGB at the MBF. Smolt and parr releases from the LGB program were easily discernable from wild or LGB fry releases by the absence of the adipose fin (small fleshy fin anterior to the caudal fin). Whether non-adipose clipped smolt are wild- (produced in-river) or LGB-origin (released as fry) was determined using genetic information.

All smolts sent to the MBF for inclusion in the LGB are tissue sampled for genetic analysis and, in some years, portions of non-retained smolts were tissue sampled.

A proportion of the smolts caught daily in the RST are marked and released three kilometers upriver in order to calculate the RST capture efficiency. Counts of recaptures from these 'recycled smolts' are used to estimate annual smolt abundance. When possible, both non-adipose-clipped and adipose-clipped smolts were marked and recycled upriver. A chi-square test was completed to test for differences in the proportions of wild/LGB_{FRY} origin versus LGB_{PARR} in the original capture and subsequent recapture collections. Mark-recapture data were combined for these two groups unless results from the chi-square test indicated significantly different recapture efficiencies between the wild/LGB_{FRY} origin and LGB_{PARR} origin smolts.

Sampling occurs daily when the RST is set to capture (i.e., drum lowered into the water flow). Typically, the RST is fished daily (seven days a week); however, some exceptions apply where the program was reduced, operating for only part of the week (discussed below). The operation consists of:

1. triaging by species, smolt origin [i.e., adipose-clipped (parr release) or non-adipose-clipped], and smolt 'fate' (e.g., LGB collection, recycling, release),
2. measuring and recording fish species, length, weight, and origin, and
3. sampling and tagging to collect scale and/or tissue samples, inserting a Passive Integrated Transponder (PIT) tag (started in 2004), or marking the individual with a fin clip, and photographing for morphometric measurements.

During 2012 to 2014, the RST only operated 5 days per week, from Sunday evening until Friday morning. In 2013 and 2014, a portion of the smolts were marked and recycled upriver on Monday through Thursday mornings, in order to estimate the RST efficiency during that time. No smolts were recycled upriver in 2012 to estimate smolt abundance during the periods when the RST was fishing. Instead, mean RST efficiency (10.8%) observed from 2001 until 2011 was used in smolt abundance and fishing effort coefficient calculations (Table 1). A fishing effort coefficient (number of days RST operated/total number of days in migration monitoring period) was used to adjust the 5 day abundance estimate to a total season smolt abundance estimate

in these three seasons. The fishing effort coefficients used were 0.68 (2012), 0.74 (2013) and 0.74 (2014).

Genetic analysis (or parentage assignment) of tissue samples randomly collected from outgoing non-adipose-clipped smolts, in combination with assessment data, provides smolt abundance estimates by either LGB-origin ($smolt_{LGB}$) or wild-origin ($smolt_{WILD}$). The non-adipose-clipped smolts that did not assign to parents of the LGB program are grouped as $smolt_{WILD}$ and would include: a) progeny from the remnant wild population, b) LGB-origin returning adults and adults released specifically between 2003 and 2005, c) mature male parr, d) strays from other nearby rivers, and/or e) aquaculture escapes.

2.2.2 Stewiacke River

In 2014, an RST operation was re-established in the Stewiacke River where a smolt assessment had not been undertaken since 2008 (S. O'Neil pers. comm.; unpublished data). Sampling protocols were similar to the Big Salmon River program. Due to logistical interruptions (e.g., flooding, wheel tampering, change in location), an estimate of smolt abundance cannot be derived for the 2014 cohort, but biological characteristics were collected and the majority of the smolts were transferred to the CBF for possible inclusion into the LGB. The RST was situated below the Little River confluence (N45.162362°, W-63.286669°; Figure 3). The RST was installed and monitored in 2015 and 2016 but, again, a reliable smolt abundance estimate could not be derived due to low catches and low efficiency. None of the smolt captured were retained for possible inclusion into the LGB program.

2.2.3 Gaspereau River

The Gaspereau River is a hydroelectric controlled watershed comprised of the Black and Gaspereau river systems with five generating stations (Amiro and Jefferson 1996) (Figure 4). The river is managed by Nova Scotia Power Inc. (NSPI) through their Fish Management Practice (FMP) program and is separated into 6 separate management areas where habitat protection and/or fish passage is administered according to a specific target species (Meade 2000). Downstream fish passage is provided for smolts via 3 surface bypass structures that contain assessment traps, which are typically monitored (smolts enumerated) between April 15th to May 31st, although dates are adjusted to the smolt 'emigration window' based on water temperatures and seasonal flows. Sampling has occurred at this site since 2002 (DFO-MAR-2012-07 2012-Notice of Permit from Species at Risk) where smolts are enumerated and finally transferred to the CBF for tagging (PIT tag), tissue sampling, measurements, and inclusion into the Gaspereau River LGB program. Either marked LGB-origin smolts (released upriver of White Rock Dam) or wild-produced (i.e., non-adipose-clipped or unmarked) smolts (captured in bypasses and recycled upriver of White Rock Dam) have been used since 2007 (except in 2011) to evaluate the capture efficiencies of the three bypasses and estimate smolt abundance. In 2014, due to the trap failure in Bypass Pass (BP) #1 the smolt abundance estimate was derived using the combined efficiencies of BP #2 and BP #3 observed in 2016. Since 2014, smolts have been processed at time-of-capture to obtain biological characteristics (i.e., length, presence of fin clips, scale and tissue samples).

Genetic analysis (or parentage assignment) of tissue samples randomly collected from outgoing non-adipose-clipped smolts in combination with assessment data provide smolt abundance estimates by origin [LGB juvenile releases **and/or adult spawners (non-targeted LGB or anadromous returns)**]. The non-adipose-clipped smolts that did not assign to the parents of the LGB program are categorized as p progeny of adult spawners, and include progeny of the remnant wild salmon and a small number of mature LGB adult salmon released upriver of White Rock Dam to spawn naturally. Since 2008, all of the LGB fall parr releases have been marked

with an adipose fin clip, making it possible to estimate smolt output separately for the LGB unfed fry and fall parr emigrating as smolts starting in 2011.

2.3 ADULT ASSESSMENT

Evaluation of the status of Atlantic Salmon in the Maritimes Region is based on abundance monitoring for a number of index populations. For most index populations, status is evaluated using a comparison of the estimated egg deposition (calculated from the estimated abundance and biological characteristics of returning adult salmon) relative to a reference point known as the Conservation Egg Requirement (CER). The river-specific CER is based on an egg deposition of 2.4 eggs/m² (Elson 1975; CAFSAC 1991) multiplied by the amount of accessible fluvial rearing habitat that is of suitable gradient (Amiro 1993). An egg deposition of 2.4 eggs/m² is considered a limit reference point in the context of DFO's Precautionary Approach Framework (DFO 2009; DFO 2012; Gibson and Claytor 2012) for DFO's Maritimes Region (DFO 2017). The two index rivers monitored for adult abundance within the IBoF DU are the Big Salmon (NB) and the Gaspereau (NS) rivers, both of which are supported by LGB releases.

2.3.1 Big Salmon River

The most recent returning adult population estimate for the Big Salmon River was last reported by Gibson et al. (2008). Adult abundance estimates have continued annually using similar methods, including an early season diver count of salmon holding in the largest pools in August, a mid-season count which usually occurs in September of the same pools enumerated during the August survey followed by a seining/marketing activity of captured adults, and finally a 3-section swim survey in October. The length of the mainstem that contains the majority of the holding pools is divided into 3 sections, and teams of 2 to 4 divers swim adjacently through each section in order to visually cover the whole stream width (Figure 2). The Upper section is approximately 5 km in length starting at Walton Dam Pool and finishing at Walker Brow Pool, with a total of seven index holding pools, which are pools that annually contain returning adult salmon and can be relied upon for an accurate abundance estimate if assessment practices need to be reduced, throughout the section. The Middle section is approximately 4 km in length starting at Walker Brow pool and ending at the electrofishing site #22 (downstream of Mary Pitcher Falls; Figure 2; Jones et al. 2006), and includes a few established pools and various long run/riffle sections. Finally, the Lower section is approximately 2.7 km starting at Miller pool and finishing at Amateur pool with 14 index pools in total. Typically, during the early September count, the pools holding schools of adults, which can be efficiently seined, are identified, and then these pools are seined, captured salmon are marked, and then released for identification or recapture in the late-season diver swim. If sufficient numbers of salmon are tagged, an abundance estimate is generated (i.e., 2007 and 2010). If not, a single census mark-recapture value (0.57 from Gibson et al. 2004) is applied to the largest observed count for that season. A good representative sample of returning adults was not captured through seining activities in every year, therefore the annual adult abundance estimates were divided into small and large spawners based on the diver observations (i.e., ratio of small to large).

Egg deposition estimates were determined using annual small and large adult abundance estimates, data on biological characteristics (**small salmon**: annual data was used, if available; if not available, mean values from the time-series were used; **large salmon**: mean values from the time-series were used), as well as a length-fecundity relationship established for Atlantic Salmon from the Stewiacke River (Amiro and MacNeil 1986). To estimate the total egg contribution from the non-targeted LGB adults released into the Big Salmon River from 2003 to 2005, a length-fecundity relationship (eggs = 337.93e^(0.0436Xfork length)) developed from

captive-reared salmon maintained at the MBF for the regular broodstock was used (Jones et al. 2006).

From 1996 to 2005, prior to freeze-up, 2 sections, collectively representing approximately 45% of the headwater reaches of the Big Salmon River and considered to be prime spawning habitat, were surveyed for the presence of redds by New Brunswick Department of Energy and Resource Development (NBDERD) staff (Gibson et al. 2003b; Jones et al. 2006). A survey was not completed in 2003 because of poor visibility, a result of high water conditions (Gibson et al. 2004). The annual count estimates were not corrected for the area covered (i.e., estimates are not representative of spawning habitat for the whole river and do not account for unsurveyed habitat) and were used as another indication of spawning escapement. Since 2006, these spawning areas have been periodically surveyed by DFO Science staff and other collaborators, but are dependent on crew availability and water conditions. Since 2006, redd counts were completed in Section B on six occasions, while only twice in Section A (Figure 2). Section A was initially used for redd surveys, as it contained prime spawning habitat for returning adult salmon. However, after observing that few to no redds were present in the upper reaches of the river, Section B was assessed and noted that it had a higher prevalence of redds. Thus, redd surveys were conducted in Section B from hereon in.

2.3.2 Gaspereau River

Adult salmon ascending the Gaspereau River encounter several migration barriers (Figure 4), although both upstream and downstream passage exists at the White Rock Hydro Station, Lanes Mills (Gaspereau Lake), and at Aylesford Lake (Meade 2000). The restoration and enhancement program for the Gaspereau River was reinstated in 1992, when adult salmon were either seined or angled in the White Rock Headpond and transported to the CBF (Amiro and Jefferson 1996). Since 1995, salmon have been enumerated at the White Rock Dam, which now includes an assessment trap after retrofitting in 2002. Individuals caught in the trap were held for incorporation into the Gaspereau LGB program (Meade 2000; DFO-MAR-2012-07 2012; DFO 2007).

Emigrating kelts are also captured and enumerated in the downstream bypasses, although only during the smolt migration period. Scale and tissue samples, sex, and lengths are obtained from the broodstock collected at the fishway and a PIT tag is injected for individual identification.

Egg deposition of sea-run releases is calculated using the length-fecundity curve, where the number of eggs = $446.54 * e^{(0.0362 * \text{Fork Length})}$ (Cutting et al. 1987), and was derived from the LaHave River adults. The length-fecundity curve (eggs = $309.8 * e^{(0.045 * \text{Fork Length})}$) for the Gaspereau River captive-reared adult releases was developed based on a 2006 egg count of 14 females broodstock ranging from 44 to 85 cm in length (B. Lenentine, DFO Science, unpublished data).

In 2014, divers swam an approximate 2.2 km section of the Gaspereau River below the White Rock facility to determine if adult salmon were being delayed by inefficiencies in upstream fish passage provisions. However, no salmon were observed, which could have been the result of very poor visibility.

2.4 LIVE GENE BANK SURVIVAL

Assessing both freshwater and marine survival of LGB progeny was identified as a key component in the Recovery Strategy for IBoF salmon and DFO's adaptive management approach for the LGB program. Evaluation of two different LGB release strategies (either releases as unfed fry or fall parr) has been possible on the Big Salmon River because of ongoing collaborative smolt and adult assessment projects in conjunction with genetic analysis

or parentage assignment work. The collection of scale samples from out-migrating non-adipose-clipped smolts since 2014 has provided some preliminary survival estimates for the unfed fry released above White Rock Dam on the Gaspereau River.

2.4.1 Freshwater Survival Estimates

Since 2001, LGB-origin unfed fry and/or fall parr have been released into the Big Salmon River. In this report, survival of LGB origin juveniles released in 2001 to 2012 in native river habitat is estimated. The LGB-related survival rates are calculated using the annual smolt abundance estimates combined with the age data interpreted from scale samples, as well as the genetic analysis information from non-adipose-clipped and adipose-clipped smolts (when available) for the Big Salmon River. To a lesser extent, freshwater survival rates have also been derived for the Pollet and Gaspereau rivers

2.4.2 Marine Survival Estimates

Annual smolt and adult abundance estimates on the Big Salmon River, combined with the age determination and genetic analysis from scale and tissue samples collected from returning adults, respectively, provides the best available data on LGB smolt-to-adult survival by release strategy (released as unfed fry, fall parr, or smolt). For the purpose of determining the marine survival of wild (i.e., smolt produced from 'wild' adult spawners) and LGB-origin smolts, returning adult salmon have been captured on the Big Salmon River, biological characteristics (e.g., length, sex, presence of fin clips/fin erosion) recorded, and scale and tissue samples taken. Returning adults missing an adipose fin were presumed to be from LGB parr/smolt releases, which were later confirmed using DNA fingerprint information and parentage analyses, where offspring were tested against spawned pairs of male and female salmon (also referred to as LGB crosses).

Returning adults with an intact adipose fin, but assigning to LGB crosses using DNA fingerprint information, were identified as LGB-origin salmon that were released at the unfed fry stage. Returning adults exhibiting an adipose fin that either: a) assigned to previously sampled and genotyped returning adults via single-parent parentage analysis, or b) failed to assign to any known LGB cross, were identified as wild origin (wild-produced) and quite possibly from adult salmon not captured and tissue sampled during regular assessment activities. Adults that fail to assign to any genotyped candidate parent are potential offspring of non-genotyped mature male parr and non-captured, non-genotyped returning adults, but may also be strays from nearby rivers or aquaculture escapes.

Due to the release of unclipped fall parr in 2006 and 2007 it was difficult to compare smolt-to-adult survival rates for the two release strategies on the Gaspereau River. The combined smolt-to-adult return rate information (origins include LGB juvenile releases and 'wild' adult spawners) is presented for the Gaspereau River using the annual smolt abundance estimates from 2007 to 2015 and small and large returns to the White Rock fishway from 2008 to 2016.

2.5 PROJECTS

2.5.1 2010-2016 Crossbreeding Experiment in the Petitcodiac River

The Petitcodiac River is thought to have produced 20% of the IBoF population prior to the causeway being built in the late 1960s. The combination of the causeway construction with ineffective upstream and downstream fish passage and high marine mortality effectively extirpated the salmon population from this large watershed. The opening of the Petitcodiac River causeway gates in 2010 removed the fish passage problem in the system. This potentially

high quality habitat, unoccupied by residual wild or LGB salmon, presented an opportunity to assess possible benefits of outbreeding, at the sub-basin scale [Chignecto Bay vs New Minas Basin (NMB)], on offspring performance in the wild. Multiple crosses between salmon from various pairs of IBoF river populations [i.e., Stewiacke and Gaspereau from the New Minas Basin, and Point Wolfe and Big Salmon rivers from the Chignecto Bay] were carried out at the biodiversity facilities. In 2011 and 2012, 337,622 and 37,246 unfed fry, respectively, were then released into the Pollet River tributary of the Petitcodiac River. This research was conducted both to determine whether any specific cross types exhibited higher juvenile survival (to the smolt stage) in this particular river, and to assess whether outbred (between river or basin crosses) survived better than within-river crosses at sea. Since 2013, the Fort Folly Habitat Restoration (FFHR) group have evaluated the survival of the fry releases from various crosses with the tissue sampling of smolt captured in fyke nets and a RST operated on the Pollet River (Figure 5). In 2013, a proportion of the smolts caught were marked and recycled to determine RST catch efficiency and generate a smolt abundance estimate. In 2014, an upstream fyke net was installed to catch and mark smolts to determine the efficiency of the RST. Biological characteristics (e.g., length, weight, scale and tissue samples) were collected from each salmon captured and all other fish species were enumerated prior to release in both years.

In late September 2014, a three-section swim survey was conducted in the Pollet River to note the presence of small salmon returning from the 2010 fry releases (Figure 5). The Upper section was approximately 5.3 km in length from the base of Gibson Falls to the Highway 895 Bridge. The Middle section was approximately 2.9 km in length and included a diver count of salmon holding in Salmon Hole, Liberty Hole, Babcock Brook and Beautiful Camp pools. The Lower section was approximately 4.3 km and included salmon counts in River Glade and Farm House pools (Figure 5). The presence of other species and juvenile salmon was noted throughout the survey. On a separate date, two divers also assessed a section above Gibson Falls, as salmon can ascend the falls under certain water conditions (e.g., high water levels). The survey was repeated in 2015 and 2016 to note the return of either small or large salmon from the 2011 or 2012 fry releases.

Parentage analyses were conducted using the process of exclusion on the smolt samples collected in 2013. The offspring genotypes were compared with those of known candidate parent pairs and single parents over an average of 12 loci in common between the parents and offspring. The process of Mendelian inheritance requires that, at each locus, an offspring must share one allele with one parent and the other allele with its other parent. Any parent that does not meet this criterion, allowing for a small percentage of genotyping errors, is therefore excluded as a match. Parents were assigned to an offspring when the exclusion process reduced the number of candidate parents to a single pair of known crosses.

2.5.2 Electrofishing Surveys

Two electrofishing surveys designed to address specific objectives (described below, see sections 2.5.2.1 and 2.5.2.2) were conducted in 2013 and 2014, using backpack electrofishing units (either Smith-Root LR-24 or 12B series) by crews of two to four people. The surveys were open sites (spot checks only) using a previously established catchability coefficient (by Bayes method) of 34.7% (Jones et al. 2004). The data collected included: area fished, shock time, other species identification and count, habitat details and photos, Global Positioning System (GPS) coordinates, water and air temperature. The captured salmon were measured and weighed, as well as scale (from the parr only) and tissue sampled.

Electrofishing is also used as a method to collect juvenile salmon for inclusion in the Big Salmon River (Bonnell Brook) and Stewiacke River (Pembroke River) LGB programs yearly.

2.5.2.1 2013 Stewiacke River Survey

An extensive electrofishing survey was conducted between August 20th and September 11th, 2013, throughout the Stewiacke River (Figure 3). The goals of the survey were: 1) to calculate the salmon densities in the various tributaries, 2) to investigate if wild spawning is occurring, and 3) to determine the contribution of LGB spawners (i.e., as returning adults) to the salmon population within the Stewiacke River. A total of 40 sites were electrofished, of which 11 were historical reference sites previously sampled for monitoring trends in juvenile abundance (Amiro and Jefferson 1996; Gibson and Amiro 2003).

A similar parentage analyses previously described for the Petitcodiac Crossbreeding experiment was conducted on juvenile salmon captured during the Stewiacke River electrofishing survey. However, during the Stewiacke River parentage analyses, only 10 loci were used compared with 12 in the Petitcodiac Crossbreeding study. Furthermore, a grandparentage analysis was completed on the Stewiacke River fish and is a similar process to the parentage analyses, whereby, at each locus, the offspring must share one allele with either one of its maternal grandparents and the other allele with either one of its paternal grandparents.

2.5.2.2 2014 Broadscale Electrofishing Survey

In order to evaluate the recent status of juvenile abundance in non-LGB supported IBoF rivers, an extensive electrofishing assessment was completed in 2014. A repetition of the last broadscale survey (Gibson et al. 2003a) was not feasible due to costly genetic analysis, thus the goal in 2014 was adapted to investigate the presence or absence of juvenile salmon in primarily non-LGB supported rivers, i.e., no juveniles had been stocked in the rivers for at least four years. These rivers were prioritized as High, Medium, or Low Priority Rivers, where:

- High Priority = juveniles found in last survey. No LGB stocking;
- Medium Priority = no juveniles found in last survey. No LGB stocking; and
- Low Priority = LGB adult stocking only. Investigate success of natural spawning.

A total of 38 rivers were included in the survey, although four rivers could not be assessed due to time constraints (Goose Creek) or lack of accessible salmon habitat (Tantramar, Habitant, and Pereaux rivers) (Figure 6).

A total of 85 sites were electrofished between August 11 and October 2, 2014. The majority of the sites were chosen based on the previous surveys (2000, 2002, and 2004); however, the number of sites per river was reduced and only sections of accessible prime salmon habitat were electrofished.

All sites were single-pass assessments using an estimated catchability coefficient value of 34.7% (Jones et al. 2004) to estimate the total number of salmon at each site. All salmon caught were measured, weighed, and tissue sampled. Scale sampling was completed exclusively on parr (i.e., no fry or young of year [YOY]). Subsets of collections of other species were measured for length and weight at each site (i.e., American Eel). Measurements relating to the river and equipment were also recorded, such as length, width, and depth of the stream at the sampled site, water and air temperature as well as electrofishing unit settings and shocking time. The Irish, Demoiselle, Maccan, Carters, and Kennetcook rivers were further sampled to include weights and lengths of all other fish species captured in order to calculate total fish biomass and assess fish community changes over time, which can be indicators of a rivers health. The fish biomass data was collected with the intention of being included in a Strategic Program for

Ecosystem-Based Research and Advice (SPERA) project that will be developing eco-region benchmarks of fish productivity in freshwater⁵ (Randall et al. 2017).

Genetic analyses were completed by the DFO Population Ecology Division, Salmon Section, Genetics Unit and included;

1. parentage analysis,
2. standard allele frequency and distance-based assignment tests,
3. structure genomic assignment tests,
4. private allele analyses,
5. spatial and temporal F_{ST} analyses,
6. temporal analyses of within population variation,
7. population temporal factorial correspondence analyses,
8. population temporal phylogenetic tree analyses, and
9. individual phylogenetic analyses.

Results presented in this document will focus on the summary of the parentage analysis for the juveniles captured in the Salmon River (Colchester; LGB-supported river with the release of mature adults), as well as an overview of the assignment of the other juveniles caught in the survey to IBoF, Outer Bay of Fundy (OBoF), or other sources as well as the results of the individual phylogenetic analysis. The genetic results of the juveniles captured from the Black River, in particular, are not included, as well as some of the other samples as they are extensively reviewed in O'Reilly et al. (2018).

2.5.3 Statistical Analysis

The biological (phenotypic and genetic) characteristics were analysed and graphical outputs were completed in R Version 3.3.3 (2017-03-06) - "Another Canoe" (© 2017 The R Foundation for Statistical Computing). Biological characteristics were scrutinized using Analyses of Variance (ANOVAs) to assess differences in length and age amongst the three origins of smolts (e.g., wild, LGB_{FRY}, and LGB_{PARR}) caught in the Big Salmon River, and amongst wild or LGB_{FRY} releases for the Pollet, Stewiacke, and Gaspereau rivers. A two-way ANOVA was used to investigate differences in emigration day amongst each origin and throughout the time series. If overall tests were significant, Tukey Honest Significant Difference (HSD) *post-hoc* tests were completed to investigate which pairs of groups differed significantly (Field 2012). Difference in sex proportions amongst wild and LGB_{FRY} Big Salmon River smolts were assessed using a logistic regression, as this nominal-scale variable will not follow a normal distribution (Zar 2010). The logistic regression was fit in R with the general linear model procedure, including the binomial family argument initially investigating the significance of the interaction of smolt origin and years of sampling. The interaction was not significant, therefore the final regression used investigated the significance of each variable independently. Remaining graphical outputs and statistical analyses were completed in Microsoft Excel 2016 (© Microsoft 2018).

⁵ More details available in the DFO report [Development of Eco-region Benchmarks of Fish Productivity in Freshwaters: Incorporating Habitat, Water Temperature, Nutrients, and Flow as Primary Drivers of Productivity of Fishes that Support Commercial, Aboriginal, and Recreational Fisheries](#).

3.0 RESULTS

3.1 LIVE GENE BANK

3.1.1 Collections

The collections of wild exposed juveniles, either parr or smolt, and adults are the foundation of the LGB programs in both New Brunswick and Nova Scotia. Salmon were collected as either parr via electrofishing, smolts from RSTs or a downstream bypass facility, and adults via a fishway trap. These salmon were transferred to the Biodiversity Facilities for inclusion into their respective LGBs. A summary of all the LGB collections (from 2001 to 2016) is in Appendix 2.

3.1.2 Distributions

For the most part, the salmon collected were reared to maturity and selected based on genotype for inclusion into the pedigreed mating plans. Non-targeted mature adult salmon [and in some cases immature adult salmon] were released into tributaries as a secondary conservation measure (e.g., low priority genetics, increase wild exposure prior to spawning). Release of immature salmon beyond the smolt stage (i.e., pre-grilse) is not common but can occur due to facility capacity limitations. Genotyped, post-spawned kelts are also released following LGB spawning events into a designated IBoF river, if they are no longer required for the LGB program. Offspring from the LGB spawning activities were also distributed either in the tributary of origin or in several 'receiver' rivers within the vicinity of the 'donor' river.

Appendix 3 and 4 outline the annual distributions by stock from both MBF and CBF. The distribution tables reflect the changes in release strategies, which have evolved over the lifetime of the LGB programs based on evaluation of success for each salmon stage. For interpretation of the smolt assessment results by origin, the distributions for the Big Salmon (Table 2) and Gaspereau (Table 3) rivers are presented to indicate years and numbers of adipose-clipped releases.

3.2 SMOLT ASSESSMENT

3.2.1 Big Salmon River

This section adds to and complements some of the previously published smolt abundance estimates and genetic analysis results by Flanagan et al. (2006) and biological characteristic comparisons between smolts of different origins from the 2003 smolt class (de Mestral et al. 2013).

3.2.1.1 Smolt Abundance Estimates by Origin (LGB vs 'Wild' Produced)

Since 2001, with the exception of years 2012 to 2014 when the RST was only fished five days per week, total smolt abundance was determined using mark-recapture procedures based on the smolt catches, marked and recycled smolts, and recaptures at the RST during the entire smolt migration period (Table 1). The 2001 to 2005 data has been previously reported in Flanagan et al. (2006).

In 2012, a total of 888 smolts were captured during the 5-day per week operation. Applying the mean RST efficiency (10.8%) from 2001 to 2011 to the catch, the smolt abundance estimate for this time was 8,258 fish (Table 4). The majority of the smolts ($n = 884$) were captured from May 1st until May 25th and the RST was operational for 17 of the 25 days (or 68%). Using the fishing effort coefficient (0.68) to adjust for a 5-day abundance estimate and to account for non-fished days, produced a smolt estimate of 12,144 fish in 2012. In 2013, 29 of the 287 marked smolts were recaptured and when applied to the 5-day per week schedule and a catch of 813

fish, this generated a smolt abundance estimate of 8,035 for the 31 days of operation. The estimate for the entire smolt migration was 10,886 fish in 2013 (Table 4). Using the same approach for 2014, the smolt catch of 415 fish [mark (M) = 120; recaptures (R) = 15; fishing effort coefficient 0.74] generated an abundance estimate of 4,513 fish.

In all other years, once the RST was installed, it operated continuously, except during rare occasions when the drum had to be lifted for safety reasons, such as predicted high water events (Table 1). This near continuous operation allowed for daily enumeration, marking, and recycling to estimate smolt abundance for the entire migration period. For example, in 2016, a total of 1,328 unmarked wild- or LGB-origin smolts were captured during the six weeks of operation at the Big Salmon River. The first smolt was captured on May 3rd, while 50% of the total catch had occurred by May 15th. Three hundred and eighty-four smolts were marked with a 3 mm dermal punch in the caudal fin [mid-upper caudal (MUC) punch] and then released at Hearst Lodge. Seventy-one (71) of the marked smolts were recaptured in the RST at Amateur Pool, resulting in an overall efficiency of 18.5% (Table 1). This mark-recapture data generated a most probable Bayesian estimate of 7,180 (2.5 and 97.5 percentiles: 5,860 – 9,240) smolts (Table 5).

Smolt estimates since 2001 have varied from the lowest emigration of 4,295 smolts in 2002 to the highest, 17,355 smolts in 2006 (Table 5; Figure 7). The 2016 estimate represents: 1) a decrease of 26% from 2015, 2) a 15% decrease in the 5-year mean, 3) the seventh lowest estimated total since smolt assessments commenced in 2001, and 4) only 36% of average smolt production estimates from the late 1960s and early 1970s (Ritter 1989).

Genetic analysis (or parentage assignment) of tissue samples randomly collected from outgoing non-adipose-clipped smolts in combination with assessment data provided smolt abundance estimates by origin (LGB unfed fry releases or adult spawners). All outgoing adipose-clipped smolts can be attributed to either fall or spring parr releases (Table 2).

The results of parentage assignment data for the analysed smolt indicate that, on average, from 2003 to 2016, about 50.6% of the non-adipose-clipped smolts originated from the LGB unfed fry releases (Table 6). The greatest contribution from the LGB fry releases (79.9%) was the 2016 smolt class, whereas the smallest percentage (33.1%) occurred in 2014 and was likely attributed to the low number (97,209) of unfed fry released in 2012 (Table 2; Figure 8). Applying these percentages to the non-adipose-clipped smolt abundance estimates provides the annual smolt production estimates from the unfed fry release program (Table 5). The mean annual smolt production from the adult spawners between 2003 and 2016 has been 4,729 fish (ranging from 1,230 to 8,401). Over that same time period, the mean annual smolt production from the in-river LGB unfed fry releases has been 4,646 fish (ranging from 1,482 to 8,954) (Table 5). Excluding the few fish (n = 40) observed in 2014, the annual smolt production from the adipose-clipped LGB fall and spring parr releases on the Big Salmon River has ranged from 1,050 to 8,940 with an annual mean of 4,034 fish (Table 7). Successful spawning of a portion of the 112 LGB adults released in 2003 to 2005 was determined by the genetic analysis of the non-adipose-clipped smolts sampled from 2006 to 2008. Thirty-two of the 505 smolts were assigned to at least one parent from the LGB adult releases (Table 6; Figure 8).

3.2.1.2 Biological Characteristics

The annual mean length of wild/LGB_{FRY} smolts (age classes combined, genetic origin not considered) sampled during the spring RST operations has ranged from 14.6 cm (2009) to 16.0 cm (2001) since monitoring began in 2001 (Figure 9). The mean length of wild/LGB_{FRY} or non-adipose-clipped smolts sampled on the Big Salmon River in 2016 was 15.9 cm, the second highest value since 2001 and 0.3 cm longer than the smolts sampled in 2015. The mean length

increase likely reflects the larger proportion of Age-3 smolts in 2016 compared with earlier or 'younger' emigrating smolts observed in 2015 (Figure 9).

The age distribution has fluctuated over the past 15 years, although the Big Salmon River smolt runs remain primarily Age-2 dominant (Figure 10). In 2016, analyses of scale samples ($n = 485$) collected from wild/LGB_{FRY} smolts in the Big Salmon River indicated that 58.8% were Age-2, which is the second lowest Age-2 proportion recorded in the time period. The remainder was Age-3 smolts (40%) and a few smolts were Age-4 (1.2%) in 2016. Age-2 smolts have comprised 70% or more of the total non-adipose-clipped smolts sampled in all but three years since 2001: 2011 (52.4%), 2012 (62.9%), and 2016 (58.8%).

3.2.1.3 Genetic Considerations

One of the goals of a recovery stocking strategy is that released fish have similar biological characteristics to the native fish. The actual origin of the sampled emigrating smolts identified as wild/LGB_{FRY}-origin has been differentiated through genetic analysis since 2004; therefore, this aforementioned group can be separated into wild- and LGB_{FRY}-origin. The LGB_{PARR} group is identified by a lack of adipose fin (clipped prior to release in the wild).

Origin-Specific Length at Age

From 2004 to 2015, the average length for Age-2 smolts was: 15.2 cm (range: 14.5 – 16.0 cm) for the wild-origin smolts (or from adult spawners), 14.7 cm (range: 13.9 – 15.5 cm) for smolts released as unfed fry (LGB_{FRY}), and 14.2 cm (range: 12.0 – 17.2 cm) for the smolts released as parr (LGB_{PARR}) (Figure 11). The length of Age-2 smolts released as unfed fry versus wild-produced fry (wild) was not significantly different ($p = 0.097$), although both groups were significantly longer than the LGB_{PARR} group ($p < 0.001$).

From 2004 to 2015 (2004 to 2013 for LGB_{PARR}), the average length of Age-3 smolts was: 16.7 cm (range: 15.9 – 18.0 cm) for wild-origin smolts, 15.6 cm (range: 14.8 – 16.9 cm) for the LGB_{FRY} smolts, and 15.3 cm (range: 14.2 – 19.0 cm) for the LGB_{PARR} smolts (Figure 11). The length of Age-3 wild was significantly longer than LGB_{FRY} ($p < 0.001$), as well as the LGB_{PARR} ($p < 0.001$). The LGB_{FRY} are also significantly longer than the age-3 LGB_{PARR} group ($p = 0.007$).

Origin-Specific Age Proportion

From 2004 to 2015, the average percentage of Age-2 wild-origin sampled smolts was 78.5% (range: 64.0 – 94.4%) and Age-3 wild smolts was 20.5% (range: 3.7 – 35.1%) with only a few Age-1 (0.2%, range: 0 – 0.9%) and Age-4 (0.8%, range: 0 – 4.7%) smolts (Figure 12). The Age-1 smolts were likely unclipped LGB_{PARR} releases and not wild produced. During the same years, the average percentage of Age-2 LGB_{FRY} sampled smolts was 72.1% (range: 39.2 - 95.3%) and Age-3 LGB_{FRY} smolts was 26.9% (range: 4.2 – 60.8%) with only a few Age-1 (0.8%, range: 0 – 3.8%) and Age-4 (0.2%, range: 0 – 1.9%) smolts. Between 2001 and 2014, the average percentage of Age-1 LGB_{PARR} sampled smolts was 30.7%, where the LGB_{PARR} were released the previous fall as 0+ fall fingerlings. Age-2 LGB_{PARR} sampled smolts was 58.4% and Age-3 LGB_{PARR} smolts was 10.8% with only a few Age-4 smolts (0.1%, range: 0 – 0.6%). The age proportions were not significantly different ($p > 0.05$) amongst the smolt origin, except for Age-1 parr, which were significantly higher than both the wild smolts ($p < 0.001$) and LGB_{FRY} smolts ($p = 0.002$).

Wild vs LGB_{FRY} Smolt Sex Proportion

The sex of wild/LGB_{FRY} origin smolt that died either in the field or later at Mactaquac was determined through necropsy, while the sex of smolt that were transferred to Mactaquac and survived was determined from secondary sex characteristics at maturity and/or spawning records.

The smolts were PIT tagged at the RST so they can be identified throughout their lifetime in captivity. Since obtaining sex data was not based on random sampling, but rather ‘opportunistic’ sampling (i.e., mortality or sexual maturation of kept LGB smolts), the percentages given may not be representative of the BSR smolt run in a given year. Smolts were collected throughout the entire emigration period and sex information was available for 48% of the LGB-collected smolts.

From 2004 to 2015, the average percentage of female wild-origin sampled smolts was 57.0% (range: 27.3 – 69.2%) and male wild smolts was 43.0% (range: 30.8 – 72.7%) (Figure 13). During the same time period, the average percentage of female LGB_{FRY} sampled smolts was 59.9% (range: 44.0 – 75.0%) and male LGB_{FRY} smolts was 40.1% (range: 25.0 – 56.0%) (Figure 13). The sex proportions were not significantly different ($p > 0.05$) between the smolt origins throughout the years (origin*year; $p > 0.05$), although there was significant variation in sex balance throughout the sampling period ($p = 0.0003$).

Wild, LGB_{FRY}, and LGB_{PARR} Smolt Migration Timing

There was a significant difference in the average emigration day of wild, LGB_{FRY}, and LGB_{PARR} smolts ($p < 0.001$), where 50% (median) of the ‘wild’ smolts (either from residual wild populations or produced from adult spawners) emigrated sooner [Julian Day (JD) 136 or May 16th] than the LGB_{FRY} (JD 140 or May 20th) and lastly the LGB_{PARR} (JD 145 or May 25th; Figure 14). The trend of wild smolts emigrating earlier than their LGB counterparts was consistently observed throughout the 12 years of available data.

3.2.2 Stewiacke River

3.2.2.1 Smolt Count

Estimation of the number of non-adipose-clipped and adipose-clipped smolts emigrating from the Stewiacke River has been attempted since 2014 using mark-recapture techniques, but a late RST installation in 2014 and then the recovery of very few ‘recycled smolts’ in 2015 or 2016 has hindered the ability to generate a reliable smolt abundance estimate during the first three seasons of operation.

3.2.2.2 Biological Characteristics

Length at Age

The annual mean length of wild/LGB_{FRY} smolts (age classes combined, genetic origin not considered) sampled during the spring RST operations since 2014 was 14.1 cm, ranging from 13.2 cm (2015) to 15.1 cm (2016). Once the samples were partitioned into age classes, the average length was 14.0 cm (range: 13.2 – 15.0 cm) for the Age-2 wild- or LGB_{FRY}-origin and 14.6 cm (range: 14.1 – 15.5 cm) for the Age-3 wild- or LGB_{FRY}-origin (Figure 15). The sample sizes for the Stewiacke River smolt run were much smaller than the Gaspereau and Big Salmon river smolts and extremely low for the Age-3 smolt class ($n = 12$).

Age Proportions

The age distribution of smolt has remained consistent over the past three years of sampling where it is primarily Age-2 dominant (Figure 16). The analysis of scale samples ($n = 267$) collected from wild/LGB_{FRY} smolts in the Stewiacke River indicated that, on average, 92.0% (range: 85.7 – 95.8%) were Age-2. The remainder were Age-3 smolts (6.7%; range: 1.7 - 14.3%) and a few smolts were Age-1 (1.3%; range: 0 – 4.0%). The Age-1 smolts were likely unclipped LGB_{PARR} releases and not wild produced.

Migration Timing

Differences in yearly emigration timing could not be investigated as the RST operation has not been consistent over the three years of operation (e.g., wheel inoperable at various times, flooding events).

3.2.3 Gaspereau River

3.2.3.1 Smolt Estimates

The number of non-adipose-clipped and adipose-clipped smolts emigrating from the Gaspereau River, upriver of the White Rock Dam, has been estimated from 2007 to 2016, with the exception of 2011, using mark-recapture techniques. In 2011, the efficiency of the 3 bypass collection facilities was not assessed, as no marked smolts were released upriver of White Rock Dam. In 2011, mean efficiency (42.7%) of the 3 bypasses from 2001 to 2016 was applied to the combined bypass catch (n = 2,441) for an estimated smolt abundance of 5,719 fish in 2011 (Table 8). For an unknown period of the 2014 smolt monitoring season, the wooden floor of the assessment trap within BP #1 had holes in it and therefore failed to retain all captured smolts in that season. None of the 28 marked smolts were recaptured in any of the 3 bypasses, thus the overall efficiency was unknown in 2014. Since the overall smolt catch in BP #1 was not reflective of the actual number of smolt utilizing BP #1, using the overall mean efficiency was not appropriate in 2014. The smolt abundance in 2014 was 1,174 fish, estimated by applying the overall efficiency of 9.54% (R = 50, M = 524) of BP #2 and BP #3 as determined in 2016 (Appendices 5a and 5b) to the total catch (n = 112) observed in BP #2 and BP #3 in 2014 (Table 8). Since 2007, the total number of smolts emigrating from upriver of White Rock Dam on the Gaspereau River has ranged between 1,174 and 7,354 fish and averages about 4,200 smolts annually.

3.2.3.2 Smolt Origin

Genetic analysis (or parentage assignment) of tissue samples randomly collected from outgoing non-adipose-clipped smolts in combination with assessment data provide smolt abundance estimates by origin [i.e., LGB juvenile releases or 'wild' produced fish from adult spawners (either from previous ungenotyped LGB releases or residual wild populations)]. Since 2011, all emigrating adipose-clipped smolts can be attributed to fall parr releases (Table 3).

The results of the parentage assignment for the smolts analysed indicate that, on average, about 58.5% of the non-adipose-clipped smolts originated from the juvenile releases within the LGB program (Table 9). More specifically, from 2011 to 2016, about 68.1% of the non-adipose-clipped smolts originated from the unfed fry releases. Applying the genetic analysis results to the smolt abundance estimates for the non-adipose-clipped smolts (Table 8) shows the annual contributions from the adult spawners [either residual wild populations or progeny produced from LGB adult releases (genotyped or ungenotyped)] and LGB juveniles to the smolt production upriver of White Rock Dam on the Gaspereau River since 2007 (Table 10).

3.2.3.3 Biological Characteristics

Gaspereau, Stewiacke and Big Salmon Rivers Smolt Length Comparison

A sampling program for smolts was initiated on the Gaspereau River in 2014. In most years prior to 2014, biological characteristics of smolts caught in the bypasses were not collected at the time of capture, as these data were primarily collected for the LGB program, thus minimal handling was ensured with efforts to reduce fish stress and mortality. Since multi-year biological and genetic information is not available, the length of the Gaspereau River 'wild'-origin or LGB unfed fry smolts (2016) was compared to the length of the Stewiacke River (2014 to 2016) and

of the BSR smolts (2016) for their respective origins (Figure 17). Gaspereau River smolts are significantly larger [average fork length (FL): 18.2 cm; $p < 0.001$] than Big Salmon River smolts (average FL: 15.9 cm; $p < 0.001$), which are significantly larger than Stewiacke River smolts (average FL: 13.7 cm; $p < 0.001$).

Wild/LGB_{FRY}-Origin Smolt Age Proportions

From 2014 to 2016, the average percentage of Age-2 wild- or LGB_{FRY}-origin sampled smolts was 76.5% (range: 65.3 – 83.3%) and Age-3 wild or LGB_{FRY} smolts was 21.9% (range: 15.4 - 34.7%) with only a few Age-4 (1.5%, range: 0 – 3.8%) smolts (Figure 18).

Wild/LGB_{FRY}-Origin Smolt Migration Timing

The emigration timing was only investigated for the wild- or LGB_{FRY}- origin smolts as per availability of data for 2011 through 2016. The median emigration day (50% of the whole run) of the wild- or LGB_{FRY}- origin smolts was JD 131 or May 11th, although there is significance difference amongst the years ($p < 0.001$; range: JD 126 [May 6th] – JD 142 [May 22nd]) (Figure 19).

3.3 ADULT ASSESSMENT

3.3.1 Big Salmon River

Approximately 280 small salmon and 420 large salmon are required to achieve the CER of 2.2 million eggs established for the Big Salmon River by Marshall et al. (1992).

3.3.1.1 Annual Counts, Abundance Estimates and Redd Surveys

Annual Counts

Since the last detailed assessment of the adult returns to the Big Salmon River (Jones et al. 2006), sufficient mark-recapture data were only available from the adult surveys completed in 2007 and 2010. The Bayesian estimate procedure was applied to these data to estimate total adult abundance for those years. In 2007, 14 small and one large salmon were marked with small blue carlin tags on September 6th and 10th. During a diver survey of the upper, middle, and lower sections of the river on October 10th, 28 fish were observed including nine of the 15 marked salmon. Mark-recapture data were incorporated into the Bayesian estimate procedure and this analysis indicated an adult abundance estimate of 47 fish (2.5 and 97.5 percentiles: 31 – 108) (Figure 20). Using the ratio of small-to-large salmon observed during the October swim, the 47 fish can be apportioned into 44 small and three large salmon (Table 11; Appendix 6). In 2010, a total of 23 salmon were tagged with external acoustic transmitters on either: July 7th, July 29th, August 10th, September 14th or September 15th. On October 12, 2010, divers surveyed the upper, middle, and lower sections of the river and 19 salmon were observed including five of the 23 salmon previously tagged. These data generated a most probable Bayesian estimate of 87 adult returns (2.5 and 97.5 percentiles: 53 - 343) (Figure 20). Using the proportions of small and large salmon observed on the dive survey from September 13th, the 87 fish separate into 78 small and nine large salmon (Table 11; Appendix 6).

Abundance Estimates

In all other years, the adult abundance estimate was generated by applying the derived observation rate of 0.57 (Gibson et al. 2004) to the largest observed count for that year (Table 11; Appendix 6). As an example, in 2016, three separate diver counts were conducted. During the August survey, 6 small and 2 large salmon were observed. During the September assessment, the count increased to eight small and three large salmon and then dropped to 2 small and 2 large on the three section swim on October 18th (Table 11). Applying the derived

observation rate (0.57) to the 11 fish observed on September 7th suggests that 19 adult salmon returned to spawn in 2016 (Figure 21). Based on the small-to-large salmon ratio observed during the September pool count (largest count of the 3 surveys), the 19 fish were divided into 14 small and 5 large salmon (Table 11; Appendix 6). Since 2003, the first year in which small salmon returns from the LGB program were expected, adult abundance estimates have averaged 46 fish, ranging from 16 (2004) to 118 (2011) (Table 11; Figure 21). Interestingly, in 2014, based on genetics and interpretation of scale samples it was estimated that 33 of the total returns (n = 49) likely originated from the non-targeted wild exposed 'pre-grilse' released in spring of 2014 (Table 11).

Redd Surveys

In 1996 and 1997, an average of 33.5% of the total redds were counted in Section A; in 1998 and 1999, the average was 16.5%; in 2000, only 3% of the total was observed in Section A. Since 2008, the redd counts for Section B of the Big Salmon River headwaters have been quite variable ranging from 8 to 83 total redds observed (Table 12). Some of the highest Section B counts in the time-series were observed between 2008 and 2010. For those years that data is available (n = 10), total redd count in Section B correlates with the total adult abundance estimates (p = 0.02; Figure 22). Redd counts up to 2005 were reported by Jones et al. (2006).

3.3.1.2 Egg Deposition Estimates and Biological Characteristics

No mortalities or losses were reported (i.e., illegal harvests), thus small and large salmon return estimates were used to evaluate the annual egg depositions since 2000. The biological data (i.e., sex ratio and mean length) collected since 2000 was used to calculate the annual egg deposition estimates, although sufficient samples for each size category were not obtained each year. For those years with less than six fish (per size group), the mean data for the time-series was used. For small salmon, the minimum sample size was collected for 10 of the 17 years, while there were no years in which at least 6 large salmon were captured and subsequently sampled for biological characteristics (Table 13; Appendix 7, 8).

Based on the length-fecundity relationship [eggs = $431.3^{(0.0368 \times \text{fork length})}$] from Amiro and MacNeill (1986), and using the mean sex ratio and female length (2000 to 2016), the egg deposition estimates in 2016 were 27,598 eggs for the small and 23,012 eggs for the large salmon returns (Table 13). Combined, this represents 2.3% of the CER for the Big Salmon River in 2016. Since 2000, the annual egg deposition estimates on the Big Salmon River have been below 10% of the CER in 15 of the 17 years assessed and averaging about 5% over the time series (Figure 23). Based on the length-fecundity relationship for captive-reared adults (Jones et al. 2006) and using the annual sex ratio and mean length (female) data, the egg deposition estimates from 2003 to 2005 for the non-targeted LGB adult releases ranged from 138,814 to 283,646 (Table 13). Estimated egg depositions from these LGB adults released in the headwaters of the Big Salmon River more than doubled overall estimated egg depositions in those years (Figure 23).

3.3.1.3 Adult Origin

From 2003 to 2016 (no adults were sampled in 2004, 2012 and 2013), 176 small salmon have been captured (either by net or angling) and tissue sampled on the Big Salmon River (Table 14). Based on parentage analysis of the small salmon sampled, 44 of 176 samples⁶ processed can be attributed to LGB releases. Thirty-three (33) were released as unfed fry, while

⁶ These numbers have been updated since the LGB review meeting to include the genetic results of the 2016 adults as well as an update for the 2015 adults.

the remaining 11 were returns released as adipose-clipped fall parr. Another 30 small salmon were progeny of previously sampled adult returns. Two (2) adipose-clipped small salmon did not assign to the Big Salmon River LGB program and, therefore, were likely hatchery-origin strays from a nearby river (Table 14). The number of small salmon sampled annually has averaged about 25%, but it varied between zero and 66% of the total abundance estimates (Table 14). Taking the annual proportion of the total actual returns (small and large salmon) into account and adjusting the genetic results to the total small salmon returns, the actual returns since 2005 breakdown is as follows: 89 LGB fry releases, 22 LGB parr releases, 95 repeat spawner adult returns and 3 adipose-clipped strays (Table 15). From 2005 to 2016, when LGB-origin small salmon were expected based on previous LGB releases and sampled on the Big Salmon River, progeny of LGB fry and parr releases represented 24% of the total small salmon returns (Table 15). From the samples of large salmon analyzed (n = 28), another 3 adults can be assigned to the LGB (2 fry and 1 parr) and another adipose-clipped stray was observed (Table 16). Given the small number of samples, no attempt was made to apply the genetic results to the total large salmon returns.

An analysis of 154 scale samples collected from wild- or unknown-origin small and large salmon captured on the Big Salmon River from 2000 to 2016, indicate that the majority of returning adults continue to mature after one sea-winter, but repeat spawners are much less prevalent (11.5%) than during the late 1960s and 1970s (Jessop 1986; Amiro 2003). Only 3 large salmon matured as maiden two sea winter (2SW) salmon (Table 17). Similar to the historical samples summarized by Amiro (2003), there was a high percentage (60.8%) of females among the 1SW salmon sampled since 2000. The data collected from the 45 small and large LGB salmon during the more recent time period indicated similar results (93.3% 1SW of which 59.5% were females) as wild- or unknown-origin salmon (Table 17).

3.3.2 Gaspereau River

The area above White Rock and below Lane Mills (including Trout River) represents 86% of available salmon habitat in the Gaspereau River system. The required egg deposition for this 332,500 m² of habitat is 798,216 eggs in order to reach conservation requirements (Gibson et al. 2008). The available habitat and conservation target estimates exclude the habitat above Lanes Mills, as the current management arrangement limits salmon to downstream of Lanes Mills to avoid turbine mortality in other areas of the watershed (Gibson et al. 2008).

3.3.2.1 Annual Adult Counts by Origin

Adult returns to the Gaspereau River are monitored by counting the small and large salmon captured in a pool and weir fishway designed to bypass the White Rock Dam. This document provides an update of the counts since 2007 (Gibson et al. 2008). In 2016, 5 small salmon were captured in the fishway trap, transported to CBF and incorporated into the LGB program. The mean count over the past decade has been 7 fish ranging from 2 to 16, and recent annual counts remain amongst the lowest in the time-series (Table 18; Figure 24). Since the LGB program was initiated on the Gaspereau River, adult returns captured in the fishway have been tissue sampled to determine origin of returns. Based on the genetic analysis, and for those years when LGB-origin adults were expected, most of the returning adults assign via parentage analysis to LGB salmon either from artificial spawning in the LGB program or through natural spawning of LGB adult releases in the Gaspereau River and are, therefore, LGB in origin. Salmon that do not assign to LGB parents are assumed to be either from the residual wild

population or ungenotyped LGB adult releases in the Gaspereau River. From 2005 to 2016⁷, 71.2% of the small and 72.7% of the large returns were progeny of LGB releases (adult) (Table 18). Of the remaining adults, the majority either do not assign to any parents in the parentage database or were not tissue sampled (classified as unknown), though several did match LGB post-spawned adult kelts released upriver of White Rock Dam.

3.3.2.2 Egg Deposition Estimate

Every year since 2002, all salmon returns captured in the White Rock Dam fishway have been transported to the CBF for possible inclusion into the LGB program (Gibson et al. 2004 for salmon returns prior to 2004; post-2004 returns are reported in this document). In most years, the small and large adult returns were used as broodstock, although in some years (i.e., 2011, 2015) some of the returning adults were transported from CBF and released to the Gaspereau River upriver of White Rock Dam to spawn naturally. Spawning escapement from 1997 to 2001 was estimated by Gibson et al. (2004). No spawners were released above White Rock from 2002 until 2005 and egg deposition for those years since 2006 was estimated when either anadromous returns, any 'retired' repeat spawning broodstock (no longer used in the LGB program), and/or any non-targeted LGB adults from the Gaspereau LGB program were released to spawn naturally. No mortalities or losses were reported (i.e., illegal harvests); thus, no adjustments were made to account for loss. If available, the biological data (i.e., sex and length) from the individual fish handled and released upriver was used to estimate egg deposition. In the case of the non-targeted LGB adults, a sub-sample of the total number of fish released was used. Using the length-fecundity curve $\text{eggs} = 446.54 * e^{(0.0362 * \text{Fork Length})}$ (Cutting et al. 1987) for anadromous spawners and the length-fecundity curve ($\text{eggs} = 309.8 * e^{(0.045 * \text{Fork Length})}$) for LGB adult releases, the egg deposition estimates since 2006 have ranged from 33,821 to 513,649 eggs for the three groups of spawners combined (Figure 25). Since 2006, egg depositions from anadromous returns have never exceeded 80,000 eggs or 10% of the CER. In 2006, 2007, and 2012, the estimated eggs from the non-targeted LGB adults released above White Rock Dam have been close to the CER (Figure 25). Since 2000, considering the potential eggs from all returning anadromous adults, the egg deposition estimates on the Gaspereau River, upriver of White Rock Dam have been below 10% of the CER in 15 of the 17 years assessed (Figure 25).

3.3.2.3 Biological Characteristics

An analysis of 125 scale samples collected from wild- or unknown-origin small and large salmon captured on the Gaspereau River from 2001 to 2016, indicate about 60% were maiden 1SW, 36% maiden 2SW and 3% repeat spawning salmon (Table 19). Scale analysis of the LGB and hatchery-origin small and large salmon were very similar (63% 1SW; 33% 2SW 3% repeat spawners) to the wild-origin fish with the addition of one 3SW salmon. Given that Amiro (2003) reported tag returns from non-maturing 1SW Gaspereau River salmon in distant fisheries, the higher proportion of maiden 2SW salmon in the Gaspereau River population compared to the Big Salmon River is not unexpected (Table 19). Amiro (2003) did not report on historical biological characteristics from this population, but Amiro and Jefferson (1996) summarized the biological data for 30 adult returns collected for broodstock in 1995. The age structure from the 125 fish analyzed since 2001 was similar to those samples from 1995, and there were similarities between the LGB-origin and wild-origin returns. One notable difference was the low proportion (i.e., 11.9%) of females in the LGB-origin small salmon group when compared to the

⁷ These numbers have been updated since the LGB review meeting to include the genetic results of the 2015 and 2016 adults.

recent (71.4%) and historical (69%; Amiro and Jefferson 1996) wild-origin small salmon returns (Table 19).

3.4 LIVE GENE BANK SURVIVAL

3.4.1 Freshwater Survival Estimates

3.4.1.1 Big Salmon River

Combining the annual smolt estimates by origin, genetic analysis results, and age data (Tables 5 and 7), the survival from release to the smolt stage for the LGB fry and parr releases on the Big Salmon River was determined. Summing the number of Age-2, Age-3 and Age-4 smolts across multiple classes (a three-year period), and the total smolt production from the unfed fry releases has ranged from 1,971 to 7,766 fish (Table 20). The percentage of released unfed fry surviving to the smolt stage has ranged from 1.0 to 2.5% with a 1.8% mean survival rate over the time series (release year: 2001 to 2012) (Table 20; Figure 26). Similarly, total smolt output by release year can be calculated for the adipose fin-clipped juveniles, primarily released as Age-0+ fall fingerlings. The age of smoltification has changed over the time-series (a smaller proportion smoltifying as Age-1 since 2005; Figure 12) with the total smolt production estimates ranging from 1,067 to 9,755 fish (Table 21) from 2001 until 2011. Mean survival to the smolt stage for the LGB progeny released as parr over the time series has been 6.6% (ranging from 2.5 to 10.6%) (Figure 26). Egg to smolt survival estimates for the LGB adults released from 2003 to 2005 are calculated using the egg deposition estimates (Table 13) and annual smolt estimates by origin, genetic analysis results, and age data (Tables 5 and 6). The mean annual egg to smolt survival rate was 0.42% with values that ranged from 0.18 to 0.90% (Table 22).

3.4.1.2 Gaspereau River

A time series of freshwater survival rates for unfed fry and parr releases to smolt stage on the Gaspereau is being developed. Non-adipose fin-clipped parr released in 2007 meant that it is not possible to partition smolts by release strategy until 2011, i.e., Age-3 smolts migrating in 2010 could be either from unfed fry or parr releases in 2007. The available survival rate estimates for unfed fry are presented in Table 23. Age breakdown from the smolt assessment activities has generated preliminary estimates ranging from 0.5% to 2.1%. Interestingly, the highest survival rate is a minimum estimate for the 182,750 unfed fry released, as it is for the Age-2 smolts only (Table 23). Ageing the 2011, 2012, and 2013 scale samples collected from post-smolts at CBF would add an additional 3 years to this time series. Another point of interest is the fact that the Age-2 and Age-3 smolts produced from the 2013 releases resulted in a 1.3% survival estimate. These were in competition with the progeny from the LGB adults released in 2012 that produced one of the highest egg deposition estimates since 1997 (Figure 25).

3.4.2 Marine Survival Estimates

3.4.2.1 Big Salmon River

The annual small salmon abundance estimates from the Big Salmon River (Table 15) from 2002 to 2016 combined with the smolt abundance estimates (Tables 5 and 7) from 2001 to 2015 were used to determine the annual smolt-to-small salmon return rates (Table 24). Combining smolts and small salmon produced from wild spawners, LGB fry, and LGB parr, the smolt-to-small salmon return rate has averaged 0.32% ranging from (0.05% to 0.69%) over the time series (Figure 27). The mean smolt-to-small salmon return rate for the smolts that originated from LGB unfed fry is 0.20% or one small salmon return for every 477 smolts emigrating and ranged from zero to 0.40% (Table 24). This is about 3 times better than the mean return rate for LGB parr of 0.06% or one small salmon return for every 1,718 smolts (Figure 27).

3.4.2.2 Gaspereau River

The annual smolt abundance estimates from the Gaspereau River upriver of White Rock Dam (Table 8 and 10) from 2007 to 2015 combined with the small salmon returns to the fishway (Table 18) from 2008 to 2016 were used to determine the annual smolt-to-small salmon return rates (Table 25). Combining smolts and small salmon by origin, the mean smolt-to-small salmon return rate has averaged 0.18% while ranging from 0% to 0.43% over the time series (Figure 28). With the addition of the large salmon returns the following year, the mean value increases to 0.25% and ranging from (0% to 0.64%). There were no small or large returns from the approximately 2,000 smolts that emigrated in 2012 (Table 9; Figure 28). It is important to note that smolt-to-adult survival rates would be considered a minimum estimate as generally more than half (i.e., bypass efficiencies; Table 8) of the emigrating smolts above White Rock Dam are exposed to the negative impacts (i.e., acute turbine mortality, delayed mortality) during migration through turbines. In fact, smolts utilizing the surface downstream bypasses have been observed to suffer from significant scale loss, which could also negatively affect survival in the marine environment.

3.5 PROJECTS

3.5.1 Petitcodiac River Crossbreeding Experiment

3.5.1.1 Smolt Estimates

A total of 164 smolts were captured in the Pollet River RST from April 30 until June 21, 2013, of which 70 smolts were marked with a caudal punch and recycled upriver to estimate the efficiency of the RST. Six (6) of the 70 smolts were recaptured and provide the basis for the smolt abundance estimate of 1,925 (2.5 and 97.5 percentiles: 1,100 – 6,125). In 2014, the RST was operated from May 8th until June 9th and captured a total of 294 smolts. A total of 27 smolts were captured in fyke-nets operated upriver of the RST (near River Glade, New Brunswick; Figure 5)—all captured smolts were marked and released. A total of 5 marked smolts were captured in the RST to generate a smolt abundance estimate of 1,600 fish (2.5 and 97.5 percentiles: 875 – 6,000). In 2015, only 25 smolts were captured in the RST, which meant a mark-recapture estimate was not possible. A smolt abundance estimate of 190 fish was calculated using the mean capture efficiency (0.1345) from the previous two seasons. Fyke-net catches near the RST site were 10 and 31 in 2013 and 2014, respectively, but this data was not used for the smolt abundance estimates.

3.5.1.2 Smolt Origin and Age

In 2010, there were about 120 crosses between fish from the Nova Scotia (NS) Live Gene Bank program at CBF and about 30 crosses of Big Salmon River LGB fish at MBF for the crossbreeding experiment. About 73% of the unfed fry released into the Pollet River in 2011 were from the NS crosses. In 2011, all crosses were conducted from the New Brunswick (NB) Big Salmon River and Point Wolfe River LGB programs, as salmon from the NS LGB program were not available. Genetic analysis or parentage assignment conducted on the tissue samples collected from the Age-2 smolts captured in 2013 (n = 161) indicated that 46% of the smolts originated from the Big Salmon River LGB crosses (Table 26). No genetic analysis has been completed on the tissue samples collected from smolts captured in 2014 (n = 325) or 2015 (n = 25). Parentage analysis would determine the origin (which cross) of the smolts and these tissue samples are currently archived at the Aquatic Biotechnology Laboratory (ABL).

The smolt age breakdown by smolt class is dependent on the numbers of unfed fry released annually. The results for the 2013, 2014, and 2015 smolt classes are presented in Figure 29.

3.5.1.3 In-river Survival of LGB Releases

Unfed fry-to-smolt survival for the 337,622 (combination NS and Big Salmon River LGB crosses) unfed fry released in 2011 was estimated to be 0.6% (Table 27). Based on the genetic analysis of the 2013 smolts, the unfed fry-to-smolt (Age-2) survival for the Big Salmon River crosses (0.92%) was 2.3 times better than the survival for the NS crosses (0.40%) (Table 27). In comparison, the unfed fry-to-smolt survival for Big Salmon River LGB fish released into the Big Salmon River was 1.2% for the Age-2 smolts and 1.3% when combining all age classes (Table 20). The survival of the 2012 unfed fry ($n = 37,246$) to the smolt stage from the crossbreeding experiment was 3.9% (Table 27), which was double that observed from unfed fry released in the Big Salmon River that same year (Table 20).

3.5.1.4 Biological Characteristics

Mean length for the out-migrating smolt (all age classes combined) for all three years (2013, 2014, and 2015) was greater than 16 cm (Figure 30). The largest annual mean length (> 18 cm) that was observed in 2015 was reflective of the higher proportion of Age-3 smolts sampled in comparison to 2013 and 2014.

Based on river-specific data, smolts from the Gaspereau River were longer than smolts on the Big Salmon River, which are longer than Stewiacke River smolts (Figure 17). Not much is known about the size of smolts from the North Minas Basin stocks. The overall mean length of smolts sampled from the different crosses was very similar to that observed from river-specific data despite similar rearing conditions (Figure 31).

3.5.1.5 Annual Adult Counts

In 2014, four sections of the Pollet River (Figure 5) were surveyed by divers on September 29th and 30th. These sections surveyed included more than 20 km of habitat and contain the known major holding pools within the river. One small salmon was observed in the lower section. Visibility was considered to be good to very good. Given that only one salmon was observed, no seining or mark and recapture activities were warranted. These same sections of the Pollet River were surveyed by divers on October 7 and October 9, 2015, and September 29, 2016. In 2015, 2 small salmon were observed in the upper section, while in 2016, 1 small salmon was observed in the middle section and 1 large salmon was observed in the upper section. In addition to these surveys organized by DFO Science staff, 2 Fort Folly First Nation (FFFN) divers conducted a survey of the upper section on August 25, 2015, and observed 4 small salmon holding in the pool just below Gordon Falls (upper section). Again, as few fish were observed, no seining or sampling activities were conducted to investigate whether any of these returns were progeny of the cross breeding experiment.

3.5.2 Stewiacke River Electrofishing Surveys

3.5.2.1 Survey Results

The objective of the survey was to investigate the presence of non-LGB salmon in relation to stocking activities. The bulk of the fish intercepted were expected to be stocked juveniles from LGB crosses (CBF), but areas identified and targeted could contain juveniles from natural/wild spawning adults. For example, the upper mainstem Stewiacke was above any of the stocking sites, although some juveniles could have migrated upstream from the lower sites and the Little River, which had never been stocked with juveniles, as well as other headwater areas of multiple tributaries (e.g., Goshen, Rutherford, Newton, Putnam brooks). A total of 40 sites in 11 tributaries and two mainstem sections were surveyed. A total of 234 fry and 168 parr were collected, tissue sampled, and 379 juveniles were transferred to the CBF.

The summary and analysis results are presented in Appendices 9 and 10, Figures 32 and 33, and Tables 28-30.

3.5.2.2 Genetic Analysis

A total of 401 tissue samples were collected from juvenile salmon in 2013 and submitted to the ABL at the Bedford Institute of Oceanography (BIO/DFO) in Dartmouth, Nova Scotia. The Genetics Unit analyzed the results from genotyping assays. Three (3) of the samples exhibited genetic characteristics of hybrids/trout, 2 samples exhibited triploidy (aquaculture strain), and 3 samples failed to be analyzed. There was a very high concordance between juvenile ages based on either scale data or parentage assignment (cross year) results (97%). Furthermore, 8 of the 10 non-concordant ages involved juveniles of Age 0+ and these results were based on length, rather than scale or parentage age (all 8 from Goshen Brook).

Parentage analysis assigned 345 juveniles to parent pairs or single parents, leaving 48 juveniles with 1 or both parents undetermined. After 2 additional loci were added, grandparentage analyses were carried out allowing the putative identification of a large percentage of these remaining juveniles; 34 assigned to 1 set of maternal and paternal grandparents and are very likely grand offspring of LGB salmon, and a further 13 assigned to either the maternal or paternal grandparents and are probably partially descended from LGB salmon (these individuals 2 parents and 1 of their grandparents are unknown).

Figure 32 displays the overall results of the parentage and grandparentage analyses (see Appendix 10 for detailed results). The LGB offspring release group is defined as the electrofished juveniles that were LGB juvenile releases, essentially captured salmon directly released from CBF. Pembroke River and the Stewiacke mainstem had the highest concentrations of LGB releases, as these are near the juvenile release sites.

The female adult release category identifies the juveniles produced by females released as adults from the LGB program. All adult female releases were found to have spawned in the upper reaches of the main stem and in the Big/Little Branch with male parr (released as juveniles from the LGB program) and one adult male angled on the Stewiacke River (this adult male was also released as a juvenile from the LGB program, out-migrated as a smolt, survived at sea, and returned to successfully reproduce in the Stewiacke River).

The female juvenile release group identifies the electrofished juveniles produced by females released as juveniles through the LGB program and that spawned as adults (i.e., sea-run returns). The male parents were predominately mature parr that reproduced at Age-1 or Age-2, with the exception of two males that spawned either as old (Age-3) parr or 1SW adults, and all were released as juveniles via the LGB program. These spawnings were much more spread out geographically than those of the female adult releases. It is important to note that in Goshen Brook, one of the females may have spawned two years in a row, given the ages of her three offspring.

The female wild offspring of two Salmon River (Colchester) parent category identifies an interesting case, where the female parent is the wild-spawned offspring of two adult salmon actually released into the Salmon River. She spawned as an adult with a LGB-released male parr and her offspring were only sampled from one mainstem site.

The next category, female unknown, identifies an undetermined female parent spawning with a LGB-released male parr, and the last group, both sexes unknown, identifies the one electrofished juvenile that assigned ambiguously to multiple parents.

Tables 28 – 30 summarize the data from the perspective of the electrofished juveniles and the spawners.

3.5.3 Broadscale Electrofishing Survey Results

3.5.3.1 Survey Results

All rivers outlined in the methodologies were electrofished except: Goose Creek (NB), Tantramar River (NB), Habitant River (NS), and Pereaux River (NS). These were omitted from the survey due to either access issues (i.e., Goose Creek – steep cliffs) or lack of suitable habitat (i.e., low water levels or dry riverbed at time of survey). Salmon presence was only detected in 7 of the 34 rivers surveyed: Mispéc River (NB), Mosher River (NB), Black River (NB), Irish River (NB), Salmon River (Colchester; NS), Portapique River (NS), and the Great Village River (NS).

The summary and analysis results are presented in Table 31 and Appendix 11, and the density comparison (Figure 35) to the historical surveys are depicted in Figure 34.

The highest prevalence of salmon was observed in the North Chignecto portion of the IBoF, in proximity to the Saint John River (OBoF DU) (Table 31; Figure 35). The Irish River had salmon in only 1 of the 4 sites electrofished, where 4 Age-2+ parr were caught [FL range: 14.3 - 15.3 cm], fewer than the 2000 (2 of 2 sites) and 2002 (3 of 3 sites) studies. In 2014, 1 juvenile salmon was captured in the Mosher River, compared with 1 Age-2 parr (FL: 15.4 cm) that was captured at the 1 site surveyed on the Mosher River in 2002, whereas no salmon were found in 2000 (1 site) (Figure 34). The Mispéc River site (1) had 6 Age-1 parr (FL: 12.2 – 14.3 cm), whereas the previous surveys found a few salmon in 2000 (2 sites) and none in 2002. The Black River had the highest densities in the IBoF non-supported rivers where 37 parr, 4 Age-2 (FL: 13.9 – 21.9 cm) and 33 Age-1 (FL: 10.1 – 15.2 cm) and 2 fry (FL: 7.1 – 7.8 cm) were captured in both sites surveyed. Again historically, salmon were found in both 2000 (one site) and 2002 (three sites).

Salmon presence was also observed in a few rivers of the North Minas Basin. The Portapique River had 3 Age-1 parr in 2 of the 4 sites (FL range: 14.8 – 16.6cm), where only a few salmon were found in 2000 (2 sites), none in 2002 (7 sites), and again none in 2003 (2 sites). The Portapique River is the only river in Nova Scotia that has never been supported by LGB where salmon were found. The survey on the Great Village River only found 1 parr in 1 of the 4 sites; age was not clear, but either Age-1 or Age-2 was expected (FL: 16.3 cm). The Great Village River is technically a LGB supported river, although only spent adults (2012), fall parr (2010), and fry (2011) were distributed recently. The 1 parr found, given its age, could not be a product of either of these distributions. Prior to 2004, this river did not receive progeny from the LGB, but low densities of salmon were found in both 2000 (2 sites), 2002 (6 sites), and 2003 (2 sites) (Figure 34).

Salmon River (Colchester) was electrofished to evaluate the spawning success of the non-targeted adults released into this tributary, as there was very little evidence that previous adult releases had successfully spawned (Gibson et al. 2004). Recent spawning has been successful over the years, as several year classes were detected throughout the system, whereas no fish had been detected in 2000 (2 sites) or 2002 (3 sites). Salmon were detected in 3 of 3 sites, including 4 Age-2 parr, (FL range: 11.6 – 13.4 cm), 39 Age-1 parr, (FL range: 9.2 – 13.4 cm), and 2 fry (FL range: 5.5 – 5.6 cm). Non-targeted LGB adult releases to the Salmon River (Colchester) that likely contributed to these juveniles include; 235 (2011), 362 (2012), and 221 (2013) (Appendix 4).

All fish were tissue sampled to investigate origin, i.e., identifying if these fish were from Inner Bay origin, strays from other DUs, or aquaculture escapee progeny (see next section).

3.5.3.2 Genetic Analysis

Investigations into the origins of juveniles captured in the 2014 Broadscale Electrofishing survey involved several genetic analyses, some of which are complicated by the multitude of possible sources of unknown salmon in the area.

These sources of introgression from non-IBoF sources could include (O'Reilly et al. 2018):

1. the Outer Bay of Fundy (OBoF) DU stocks, specifically the Saint John River (SJR), which empties into the Bay of Fundy a few tens of kilometers distant from the most Southeast rivers of the Chignecto Bay, including the Big Salmon River (see Figure 36);
2. escaped aquaculture or farm salmon (of local or SJR in origin) from southwest NB sites; and
3. escaped European-origin farm salmon from both Canadian and United States sites in the Gulf of Maine and Cobscook Bay.

Parentage assignment results of the juveniles captured in the electrofishing survey indicate that 40 of the 45 individuals obtained from the Salmon River (Colchester) were produced by the wild-spawning of Stewiacke LGB adult releases into the Salmon River in October 2012 (LGB supported river, adult release program). For 13 of these, both parents were adult releases; for 1 fry, the male parent was the adult release (2013), spawning with an unknown female; for the other 26, the female parent was the adult release and the male was unknown, possibly a mature parr or ungenotyped adult release. The female adult releases often spawned with more than 1 known (genotyped) male adult release and/or unknown males (mature male parr, non-genotyped adult releases, or possibly, wild returning males). The parentage of the remaining 5 Salmon River juveniles could not be determined (1 had too few loci to discriminate between multiple candidate parents).

Parentage could not be determined for juveniles collected on non-LGB-supported IBoF rivers (i.e., Mispec, Black, Mosher, Irish, Portapique, and Great Village). To assess whether these fish were progeny from LGB parents who strayed from the Big Salmon and Stewiacke river programs, they were tested against Stewiacke and Big Salmon rivers adult releases from 2011 to 2013. Alternatively, the genotypes of the juveniles were analyzed using Colony, a program to cluster individuals into most-likely half-sib and full-sib groups, and it appeared that about 8 females and 29 males were involved as parents to the Black River juveniles; 1 female and 3 males for the Irish River; 3 females and 6 males for the Mispec River; and 2 females and 2 males for the Portapique River. Three of these juveniles had too few loci to be useful. Numbers of parents are uncertain due to such small sibling groups.

Investigations into the possible origins of these juveniles continued using individual genetic assignment methods. Since earlier baseline sample collections were not available from most of the rivers recently surveyed (e.g., the Black, Mispec, etc.), samples were tested against the original five baseline collections discussed earlier [i.e., Nashwaak River (OBoF), Tobique River (OBoF), Stewiacke River (IBoF), Big Salmon River (IBoF), and Gaspereau (IBoF)]. Tests were carried out using three likelihood- (Frequency, Bayesian and Distance) and three probability-based (Frequency, Bayesian and Distance) approaches (see O'Reilly et al. 2018 for further information on methodology used) (Table 32).

Under the likelihood-based methods, approximately 50 to 60% of the samples assigned to the IBoF, primarily to the Stewiacke River baseline sample, and the remainder to the OBoF, predominantly to the Nashwaak River baseline sample (Table 32). These aggregate results in part reflect the 'heavy' proportion of juveniles collected from the Salmon River (Colchester) of the Minas Basin (eastern IBoF and distant to the SJR) in this combined set of samples. Approximately 70% of the samples collected were from the Salmon River (Colchester) and were

already identified through parentage analysis as progeny of adult salmon releases from the Stewiacke River LGB program. The likelihood-based method supported the results as 80 to 86% of the samples assigned to the Stewiacke River baseline (Table 33). The other 'large' numbers of samples collected were from the Black River (western IBoF and second most peripheral to SJR). A modest proportion of samples (up to 29%) collected from the Black River assigned either to Big Salmon River or Stewiacke River baseline, depending on the specific likelihood method employed, but the majority, approximately 53 to 79% of all individuals tested, were more likely to cross assign to the OBoF (Table 34).

Microsatellite genotype information was also used to estimate Nei's $D_{(A)}$ genetic distance between pairs of individuals, and this was used to construct unweighted pair group with arithmetic mean (UPGMA) phylogenetic trees of electrofished juveniles in the context of 20 representatives from each of the 5 baseline sample collections (Figures 37-39).

Results of these phylogenetic analyses were variable. Individual juveniles from the electrofishing survey obtained from a given river were shown to cluster with IBoF sources (Big Salmon River and/or Stewiacke River baselines), but also with OBoF sources (Nashwaak River and/or Tobique River baselines). For example, one of three individuals collected from the Portapique River clustered closely with Nashwaak River and then Tobique River baseline samples, but the other two individuals group with Stewiacke River, Gaspereau River, and then Big Salmon River baseline samples.

Another genetic evaluation discussed in O'Reilly et al. (2018) is the European (EU) analysis.

“Short variants of alleles are present and common in many wild populations surveyed from the European continent, and in suspect European farm escapes collected from rivers in and around the IBoF, many of which exhibit markers for EU ancestry at other loci. Therefore, short alleles at each of these four loci (SSsp1605 alleles 220-224 bp; SSsp2215 alleles 118 to 134 bp, SSsp1G7 alleles 130 to 162 bp, and Ssa202 alleles 239-251 bp) are considered to be short EU type alleles, and these four loci are considered to be informative for Continent Of Origin.”

The salmon that exhibited the presence of these European type alleles (Ssa 202-247, SSsp 1605-224) are identified in each of the phylogenetic trees (Figures 37-39). For more detailed information on the EU ancestry fish and respective genetics, see O'Reilly et al. (2018).

In Figures 37 to 39 is also reported the presence of short microsatellite alleles, potential markers for European farm ancestry (discussed in detail in O'Reilly et al. 2018), in juveniles captured in the electrofishing surveys. Short European-type alleles were observed in several individuals collected from the Black, Mispic and Mosher Rivers, three of the most peripheral Chignecto Bay rivers, the mouths of which are geographically closest to the Cobscook Bay, where marine net pen rearing of US farm salmon in the area is concentrated (DFO 1999). European genetic material was prevalent in Maine farm salmon broodstock (Baum 1998), and it is a possible source of these alleles.

4.0 CONCLUSIONS

4.1 CONCLUSION FROM LGB PROGRAM RELEASES

Since the LGB program was initiated on the Big Salmon River, about 24% of the anadromous returns have assigned to the LGB program once the adult assessment results and genetic analysis were considered. Genetic results from the parentage analysis of adult salmon captured at the fishway on the Gaspereau River, from 2005 until 2016, suggests that the majority (71% of

small and 73% of large salmon) of the anadromous returns to White Rock Dam are the direct result of the LGB program.

A summary of the comparative biological characteristics between 'wild' (i.e., unknown origin of adult spawners) and LGB-origin anadromous returns to the Big Salmon and Gaspereau rivers, indicated mostly similar results between the groups, in terms of size distribution, age distribution, and sex ratio. One (1) discernible difference noted was the lower proportion of females in the LGB-origin 1SW salmon group relative to that observed for comparable wild-origin Gaspereau River salmon. The study by Amiro (2003) reported tag returns from non-maturing 1SW Gaspereau River salmon in distant fisheries (i.e., increases in female migration distances and years-at-sea results in fewer 1SW mature females, as observed in other salmon DUs). Comparing the biological characteristics of salmon collected on the Big Salmon River since 2000 to the data collected in 1960s and 1970s (Amiro 2003) indicated similarities in age at first maturity (1SW salmon), proportion female, and size at age, but a much lower incidence of repeat spawners in the more recent time period.

The juvenile production by the LGB and supplementation program on the Big Salmon River has increased the smolt production by 2 to 3 times that of the anadromous adult spawners, which, on average, translates into an additional 8,500 smolts annually. The biological characteristics, in-river survival and marine survival of the 2 main release strategies (i.e., LGB fry and LGB parr) continue to differ over the time period. The in-river survival of LGB parr from the time of release to the smolt stage is about 3 times greater than that of the LGB unfed fry releases, 6.6% versus 1.8%, although smolts that result from the unfed fry releases are more comparable biologically (i.e., run-timing, size-at-age, age distribution) to the smolts produced from the anadromous spawners. Similar to the research presented by de Mestral et al. (2013) on emigrating Big Salmon River smolts in 2003, captive-origin groups (i.e., both LGB fry and parr released juveniles) had a delayed median migration day (by approximately 4 to 9 days) than their wild counterparts. This trend was observed throughout the 12 years of smolt assessment on the Big Salmon River. The established release sites for the captive groups are found throughout the catchment and not in geographic isolation from the observed natural spawning areas (Figure 2); therefore, migration distance should not favor the wild migrants. As discussed by de Mestral et al. (2013), there is likely a heritable component to migration timing, and the timing of out-migration likely evolved to synchronize or match optimal marine conditions for maximum post-smolt survival.

The migration timing delay of LBG fry, and especially parr, is a deviation from wild populations, which has been consistent over the last decade. The 4 to 9 day delay could be a hindrance to re-establishing salmon populations in the Big Salmon River if it truly decreases marine survival. Comparisons between LGB-origin smolt reared in captivity for varying lengths of time (released at the fry versus parr stage) provide insight into the possible effects of captive rearing on subsequent marine survival. The mean smolt-to-small salmon return rate for Big Salmon River smolts originating as LGB-origin fry is 0.20% (or approximately one small salmon return for every 477 emigrating smolts), whereas the mean return rate for LGB-origin smolts released as parr is approximately three times lower (Table 24 and Figure 27).

Most of the results on the effects of the various release strategies (and duration of captive rearing) involves fry and parr release stages. The release of mature non-targeted adults has been, and continues to be, a common support strategy in other watersheds within the IBoF and is utilized in other DUs. Again, the Big Salmon River focusses on juvenile release programs; however, the river did receive mature adults in 2003, 2004 and 2005. Genetic analysis determined that a portion of the 112 non-targeted LGB adults released into the Big Salmon River between 2003 and 2005 successfully spawned as they produced out-migrating smolts (Table 6). The estimated egg contribution from the released LGB adults, assuming all released

females successfully spawned, was 2 to 3 times that of the anadromous spawners in those same years yet, when considering progeny from all adult spawners (excluding those assigned to LGB fry), only about 11% of the smolts assign to those released LGB adults. There was no evidence that these LGB adults produced recruits from the parentage analysis of the 51 returning fish sampled between 2007 and 2009. Collectively, these results indicate that the spawning success of captive-reared adults in native river habitat may be quite variable, and further research into the efficacy of this release strategy (and how to improve its efficiency) is warranted.

The results of the cross breeding experiment in the Pollet River indicated that the unfed fry releases in 2011 from the Big Salmon River crosses survived about 2.3 times better to the smolt stage than the unfed fry released from the combined NS LGB program outcrosses. Interestingly, despite being reared in similar environmental conditions from fertilization to release, the early juvenile growth rates of the Age-2 smolts appeared to be influenced by their river-of-origin and potential genetic differences between stocks. The smolt progeny of Stewiacke River x Stewiacke River crosses were the smallest, smolts that originated from Gaspereau River x Gaspereau River crosses largest, while smolts from Big Salmon River x Big Salmon River crosses were intermediate in size, which generally corresponds with the river-specific data collected from 2014 to 2016 (Figure 17).

4.2 CONCLUSIONS ON THE OVERALL STOCK STATUS

Despite contributions from between 16 and 118 anadromous spawners, as well as substantial juvenile releases from the LGB program that resulted in smolt outputs in the vicinity of 15,000 fish annually, the Big Salmon River continues to remain well below CER (mean CER 5%: ranging from 1.5 to 12.1%), and this appears to be due to poor marine survival.

The smolt-to-small salmon return rate from the combined group of wild spawners, LGB fry, and LGB parr has averaged 0.32% from 2002 to 2016 (Table 24; Figure 27) or about 3 small salmon for every 1,000 smolt emigrating. This also suggests that poor marine survival continues to limit population viability and constrains the recovery of IBoF salmon, as reported earlier by Gibson et al. (2008). As a comparison, the return rates to the Big Salmon River in the late 1960s and early 1970s was about 60 small salmon returning for every 1,000 smolts produced (Ritter 1989). The smolt to adult return rates observed on the Gaspereau River since 2007 are also very poor and below historic levels, as are other nearby distant migrating populations (Outer Bay of Fundy and Southern Uplands; DFO 2017).

The first broadscale electrofishing surveys of juvenile Atlantic Salmon in IBoF rivers were done in 2000, 2002, and 2003. The interest for an updated survey of juveniles in the IBoF stemmed from a need for IBoF Recovery Program review updates. Both the directed Stewiacke River electrofishing survey (2013) and the broadscale IBoF electrofishing survey (2014) were designed to investigate the return and spawning success of sea run spawners into rivers of both LGB-supported [Stewiacke in 2013 and Salmon River (Colchester) in 2014] and, most importantly, currently unsupported rivers (33 IBoF rivers). The genetic analysis of the juveniles caught in the Stewiacke River survey detected the presence of 2 'unknown' female spawners. These unknowns are suspected wild spawners but could also be from ungenotyped LGB salmon (LGB adult releases) in the system.

The minimal presence of juveniles in the 33 unsupported rivers surveyed, the finding that most juveniles recently sampled from the Stewiacke River system are either direct descendants of LGB crosses or LGB adult releases, and results suggesting that many juveniles sampled from peripheral Chignecto Bay rivers are probably not inner Bay in origin, are consistent with the overall finding that few truly wild, native sea-run adults returned to spawn in the IBoF in recent

years. However, a small number (generally several dozen) adult salmon enter the BSR in most years, a large proportion of which appear to be native, either produced directly by LGB crosses or (predominantly) by previous anadromous adult returns and mature male parr.

Given that juvenile salmon are no longer present or, if present, are at extremely low densities in the non-LGB supported rivers, these results substantiate the findings of Gibson et al. (2008) that IBoF salmon would likely be extirpated without the LGB program.

4.3 OTHER POINTS FOR CONSIDERATION

The Great Village River and the Portapique River are two of ten rivers identified as Critical Freshwater Habitat essential to the persistence of IBoF salmon, and they were known to have residual native populations. These were the only two rivers from the Critical Habitat list surveyed in 2014 where juveniles were collected in both, albeit in dismal numbers (i.e., one fish from the Great Village River and three from the Portapique River).

Both likelihood- and probability-based tests assigned these juveniles to, primarily, an OBoF baseline sample collection; if not of local origin, they do not contribute to the maintenance of inner Bay of Fundy genetic characteristics. Moreover, these were also the only two rivers in the Minas Basin where salmon were captured [excluding the Salmon River (Colchester)] in the broadscale electrofishing survey in 2014.

Another issue observed during the large-scale electrofishing surveys, which likely affects the presence of salmon in several IBoF rivers, is habitat connectivity/fish passage. Low marine survival plus other estuarine/freshwater impacts compounded by delayed and/or hindered migration both into and out of rivers is equating to unsurmountable odds for this endangered population. Fish passage issues are tangible impacts, which largely can and should be addressed throughout a substantial part of this DU.

This document, as well as several other recently published studies, describe some of the effects of captive breeding and rearing on IBoF salmon trait characteristics and/or performance in the wild (Harvie et al. 2018, Clarke 2014; Wilke et al. 2014; de Mestral et al. 2013) and provides insight into the likely expected efficacy of different management strategies (including stage of release) in increasing juvenile abundance and the number of returning anadromous Atlantic Salmon. Future conservation efforts for this DU should consider adaptation to captivity and small population size effects on fitness in the wild, include strong monitoring and research components, and be based on adaptive management, the ultimate goal of which would be to increase the likelihood of restoring Atlantic Salmon to rivers and streams of the Inner Bay of Fundy.

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7.0 TABLES

Table 1. A summary of the Big Salmon River rotary screw trap (RST) operation in Amateur Pool from 2001 to 2016. "Temp." = temperature, "LGB" = Live Gene Bank produced fish, "FC" = fin clip, "BD" = blue dye, "LC" = Lower caudal fin, "MUC/MLC" = mid-upper caudal/mid-lower caudal fin clips/punch, "ST" = streamer tag, "Recap." = recaptured, "Eff." = efficiency, "Morts." = mortalities, "N/A" = smolts were not recycled in that given year.

Year	RST Timing				RST Catches		RST Efficiency from Smolt Recycles					LGB		
	Install Date	Temp. (°C)	1 st Smolt Catch Date	RST Removal Date	Wild/LGB _{FRY}	LGB _{PARR}	Total # Smolts	Total # Recycled Smolts	Type Mark Applied	Total # RST Fish Recap.	RST Eff.	Total # LGB Smolts	PIT Tags	Morts.
2001	May 9	7.0	May 10	June 21	692	1	693	377	BD (LC), ST, FC (LC)	22	5.8%	0	0	26
2002	Apr 29	3.0	May 3	June 19	439	207	646	118	BD (LC)	13	11.0%	0	0	6
2003	May 6	8.0	May 8	June 17	1,071	458	1,529	1,301	ST	133	10.2%	204	0	9
2004	May 3	8.5	May 4	June 29	361	156	517	271	ST	28	10.3%	130	49	2
2005	May 3	5.0	May 4	June 27	444	429	873	603	ST	63	10.4%	77	77	7
2006	Apr 28	9.5	Apr. 29	June 15	900	725	1,625	1,192	ST	115	9.6%	198	197	4
2007	May 1	6.0	May 4	June 20	1,104	1,145	2,249	1,599	ST FC	303	18.9%	342	51	8
2008	May 1	5.0	May 2	June 15	1,007	203	1,210	895	ST	85	9.5%	194	187	2
2009	Apr 16	4.0	Apr. 27	June 23	1,128	450	1,578	901	ST	84	9.3%	242	242	7
2010	Apr 26	8.9	Apr. 29	June 22	1,474	853	2,427	1,780	ST	222	12.5%	300	300	4
2011	Apr 26	6.8	May 4	June 16	1,069	310	1,379	1,081	ST, MUC	114	10.5%	204	200	1

Year	RST Timing				RST Catches			RST Efficiency from Smolt Recycles				LGB		
	Install Date	Temp. (°C)	1 st Smolt Catch Date	RST Removal Date	Wild/LGB _{FRY}	LGB _{PARR}	Total # Smolts	Total # Recycled Smolts	Type Mark Applied	Total # RST Fish Recap.	RST Eff.	Total # LGB Smolts	PIT Tags	Morts.
2012 ¹	Apr 30	4.0	May 1	June 6	755	133	888	N/A	N/A	N/A	N/A	203	199	4
2013 ¹	Apr 30	11.0	May 1	June 19	735	78	813	287	MUC	29	10.14%	302	302	10
2014 ¹	May 6	6.0	May 7	June 26	411	4	415	120	MUC	15	14.2%	149	149	9
2015	May 12	6.5	May 13	June 26	1,013	0	1,013	498	MUC	52	10.4%	395	395	10
2016	Apr 28	7.5	May 3	June 14	1,328	0	1,328	384	MUC/MLC	71	18.5%	395	395	24

¹ RST operated from Sunday night to Friday morning in these years.

Table 2. Numbers of Live Gene Bank (LGB) unmarked (non-adipose-clipped) and marked (adipose clipped or garment tagged) juvenile salmon distributed to the Big Salmon River from 2001 to 2016.

Year	Fry (0+)	Parr (0+)		Parr (1+)		Smolt (1 year)		Smolt (2 year)	
	Unmarked	Unmarked	Adipose Clipped	Adipose Clipped	Tagged	Unmarked	Adipose Clipped	Unmarked	Adipose Clipped
2001	185,523	0	77,718	0	0	0	0	0	0
2002	138,682	0	34,062	0	0	0	19,725	0	0
2003	296,818	0	54,000	21,025	0	0	13,360	0	0
2004	369,109	0	90,843	7,009	0	0	11,663	0	0
2005	258,873	0	69,862	892	0	0	1,295	0	0
2006	413,413	0	72,556	665	0	0	1,413	50	0
2007	370,605	0	87,088	0	0	0	0	0	0
2008	265,126	0	87,786	0	0	0	0	0	0
2009	177,971	0	56,984	0	0	0	1,243	0	829
2010	200,378	0	43,140	0	0	382	0	1,695	0
2011	401,486	3,137	12,000	13	0	102	0	330	0
2012	97,209	50	0	0	0	0	0	0	0
2013	341,995	0	0	0	0	0	0	0	0
2014	255,386	0	0	0	0	0	0	0	0
2015	302,307	0	0	0	0	0	0	259	0
2016	404,398	0	0	0	0	0	0	0	0
Total	4,479,279	3,187	686,039	28,926	0	382	43,384	2,025	829

Table 3. Preliminary numbers of Live Gene Bank (LGB) non-adipose-clipped and adipose-clipped juvenile salmon distributed to the Gaspereau River upriver of the White Rock Dam from 2001 to 2016.

Year	Non-Adipose-Clipped					Adipose-Clipped			
	Unfed Fry (0+)	6 Week Post-Feeding Fry (0+)	Fall Parr (0+)	Spring Parr (1+)	Smolt (1 Year)	Fall Parr (0+)	Spring Parr (1+)	Smolt (1 Year)	Smolt (2 Year)
2001	0	0	0	0	0	31,404	0	2,172	0
2002	0	4,033	0	0	0	0	0	0	0
2003	0	0	0	0	0	18,105	18,600	9,372	0
2004	0	0	0	0	0	5,878	0	0	0
2005	76,980	18,997	0	0	0	9,000	0	0	0
2006	46,666	0	37,501	0	6,480	0	0	0	0
2007	280,000	0	19,662	189	0	0	0	0	1,034
2008	275,000	0	0	0	3,302	23,628	0	0	0
2009	117,700	0	0	0	0	22,023	0	0	0
2010	86,511	0	0	0	0	20,003	0	0	0
2011	221,000	0	0	0	0	0	0	0	0
2012	220,000	0	0	0	0	0	0	300	0
2013	191,700	0	0	0	0	0	0	0	0
2014	182,750	0	0	0	0	0	0	0	0
2015	153,000	0	0	0	0	0	0	0	0
2016	188,187	0	0	0	0	0	0	0	0

Table 4. Full season smolt abundance estimates calculated using the total number of smolts caught, marked (and recycled) and recaptured as well as sampling effort for the years the rotary screw trap (RST) was operated on a five day • week⁻¹ schedule (2012-2014) during the smolt migration period on the Big Salmon River. "N/A" = fish were not recycled in a given year.

Year	Total Catch	Total Marks	Total Recaps	RST Efficiency	5 day • week ⁻¹ Smolt Abundance	Days Fished	Total Days of Migration Period	Proportion of Migration Period	Smolt Abundance Estimate Season
2012	888	N/A	N/A	*10.8%	8,258	17	25	0.68	12,144
2013	813	287	29	10.1%	8,035	31	42	0.74	10,886
2014	415	120	15	14.2%	3,325	28	38	0.74	4,513

* Mean RST Efficiency used (Table 1).

Table 5. Annual abundance estimates for Big Salmon River-emigrating non-adipose clipped smolts [either Live Gene Bank (LGB) or wild-origin] by age from 2001 until 2016. “ - ” = assessment data not available, “N/A” = assessment completed, emigrating smolt data not available for given age class.

Year	Abundance Estimate	% LGB _{FRY}	Non-Adipose Clipped Smolts							Adult Spawners				Live Gene Bank - Unfed Fry			
			Abundance by Age				Proportions by Age			Abundance by Age				Abundance by Age			
			Age-2	Age-3	Age-4	Total	Age-2	Age-3	Age-4	Age-2	Age-3	Age-4	Total	Age-2	Age-3	Age-4	Total
2001	5,290	N/A	160	8	1	169	0.95	0.05	0.01	5,008	250	31	5,290	N/A	N/A	N/A	-
2002	4,295	N/A	59	21	1	81	0.73	0.26	0.01	3,128	1,114	53	4,295	N/A	N/A	N/A	-
2003	9,200	44.7%	194	23	2	219	0.89	0.11	0.01	4,510	966	84	5,560	3,640	N/A	N/A	3,640
2004	5,970	50.8%	90	38	0	128	0.70	0.30	0.00	2,063	871	0	2,934	2,134	901	N/A	3,036
2005	4,550	73.0%	86	24	1	111	0.77	0.22	0.01	953	266	11	1,230	2,572	718	30	3,320
2006	17,355	51.6%	196	75	9	280	0.70	0.27	0.03	5,880	2,250	270	8,401	6,268	2,399	288	8,954
2007	6,400	36.9%	271	83	2	356	0.76	0.23	0.01	3,073	941	23	4,037	1,799	551	13	2,363
2008	10,750	36.4%	162	34	1	197	0.82	0.17	0.01	5,626	1,181	35	6,841	3,215	675	20	3,909
2009	11,960	54.9%	210	33	0	243	0.86	0.14	0.00	4,660	732	0	5,392	5,676	892	0	6,568
2010	12,620	43.3%	253	76	3	332	0.76	0.23	0.01	5,453	1,638	65	7,156	4,164	1,251	49	5,464
2011	10,135	44.8%	119	107	1	227	0.52	0.47	0.00	2,931	2,636	25	5,592	2,382	2,142	20	4,543
2012	11,120	38.1%	117	67	0	184	0.64	0.36	0.00	4,376	2,506	0	6,881	2,695	1,543	0	4,239
2013	9,840	54.4%	264	30	0	294	0.90	0.10	0.00	4,032	458	0	4,490	4,804	546	0	5,350
2014	4,470	33.1%	144	25	2	171	0.84	0.15	0.01	2,517	437	35	2,988	1,248	217	17	1,482
2015	9,690	66.4%	364	42	1	407	0.89	0.10	0.00	2,911	336	8	3,255	5,755	664	16	6,435
2016	7,180	79.9% ¹	310	170	5	485	0.64	0.35	0.01	922	506	15	1,443	3,667	2,011	59	5,737
Mean (2003 to 2016)		50.6%	-	-	-	-	0.73	0.23	0.01	-	-	-	4,729	-	-	-	4,646

¹ Percentage updated since the LGB review meeting based on genetic data.

Table 6. Parentage analysis of Big Salmon River non-adipose clipped smolts [either Live Gene Bank (LGB) or wild-origin] from 2003 to 2016. Other parents include: research, LGB unknown sire or dam, Point Wolfe LGB adult or unfed fry release “-” = assessment data not available. N/A = not applicable.

Year	Adult Spawners					Total	% Unfed Fry	% LGB Adult
	Live Gene Bank		Wild Adults					
	Unfed Fry (0+)	Adult	Other Parents ¹	Previous Adult Return	Unknown Parents			
2003	92	0	0	0	114	206	44.7%	N/A
2004	60	0	0	0	58	118	50.8%	N/A
2005	54	0	0	1	19	74	73.0%	N/A
2006	97	11	1	16	63	188	51.6%	5.9%
2007	48	10	1	9	62	130	36.9%	7.7%
2008	68	11	2	57	49	187	36.4%	5.9%
2009	134	1	12	38	59	244	54.9%	0.4%
2010	113	0	36	42	70	261	43.3%	N/A
2011	91	0	4	48	60	203	44.8%	N/A
2012	77	0	1	49	75	202	38.1%	N/A
2013	112	0	0	35	59	206	54.4%	N/A
2014	59	0	4	28	87	178	33.1%	N/A
2015	261	0	11	23	98	393	66.4%	N/A
2016 ¹	163	0	1	7	33	204	79.9%	N/A
Mean	-	-	-	-	-	-	50.6%	-

¹ Numbers updated since the LGB review meeting based on genetic data.

Table 7. Annual abundance estimates for Big Salmon River-emigrating adipose-clipped smolts by age from 2001 until 2014. “ - ” = assessment data not available, “N/A” = assessment completed, emigrating smolt data not available for given age class.

Year	Abundance Estimate	Adipose-Clipped Smolts										Live Gene Bank Fall Fingerling ^{1,2}				
		Abundance by Age					Proportions by Age					Abundance by Age				
		Age-1	Age-2	Age-3	Age-4	Total	Age-1	Age-2	Age-3	Age-4	Total	Age-1	Age-2	Age-3	Age-4	Total
2002	2,035	42	N/A	N/A	N/A	42	1.00	N/A	N/A	N/A	1.0	2,035	N/A	N/A	N/A	2,035
2003	6,120	90	22	N/A	N/A	112	0.80	0.20	N/A	N/A	1.0	4,918	1,202	N/A	N/A	6,120
2004	1,690	43	8	0	N/A	51	0.84	0.16	0.00	N/A	1.0	1,425	265	0	N/A	1,690
2005	4,175	76	30	2	0	108	0.70	0.28	0.02	0.00	1.0	2,938	1,160	77	0	4,175
2006	8,940	20	108	27	1	156	0.13	0.69	0.17	0.01	1.0	1,146	6,189	1,547	57	8,940
2007	5,855	19	180	24	1	224	0.08	0.80	0.11	0.00	1.0	497	4,705	627	26	5,855
2008	2,110	14	25	3	0	42	0.33	0.60	0.07	0.00	1.0	703	1,256	151	0	2,110
2009	4,755	15	82	2	0	99	0.15	0.83	0.02	0.00	1.0	720	3,938	96	0	4,755
2010	6,840	12	161	13	0	186	0.06	0.87	0.07	0.00	1.0	441	5,921	478	0	6,840
2011	2,940	4	46	22	0	72	0.06	0.64	0.31	0.00	1.0	163	1,878	898	0	2,940
2012	1,900	2	24	1	0	27	0.07	0.89	0.04	0.00	1.0	141	1,689	70	0	1,900
2013	1,050	2	18	1	0	21	0.10	0.86	0.05	0.00	1.0	100	900	50	0	1,050
2014	40	0	1	2	0	3	0.00	0.33	0.67	0.00	1.0	0	13	27	0	40
Mean (2003 to 2014)	-	-	-	-	-	-	0.28	0.59	0.14	0.00	-	-	-	-	-	4,034

¹ Includes contribution from spring parr releases in 2003 to 2005 (Table 2).

² Mean excludes the 2014 estimate.

Table 8. Bypass catch, mark-recapture estimate, bypass efficiency estimate, and smolt abundance estimate (non-adipose clipped and adipose clipped) available data on the Gaspereau River from 2002 to 2016. “-” = assessment data not available, “N/A” = fish were not marked in the given year, “Unknown” = no mark-recapture experimental data.

Year	Bypass 1, 2 and 3 Catch			Marks	Recaps	Bypass 1, 2 and 3 Efficiency	Total	Abundance Estimate						
	Non-Adipose Clipped	Adipose-Clipped	Total					Non-Adipose Clipped	Adipose-Clipped					
									Fall Parr	Smolt	Unk. ¹	95% CL's		
2002	219	1,354	1,57	1,500	² 606	40.4%	3,973	542	-	-	3,431	3,718	4,091	
2003	180	2,074	2,25	1,500	² 446	29.7%	7,581	605	-	-	6,976	7,088	8,140	
2004	-	-	2,34	-	-	-	-	-	-	-	-	-	-	
2005	-	-	440	-	-	-	-	-	-	-	-	-	-	
2006	-	-	324	-	-	-	-	-	-	-	-	-	-	
2007	1,743	600	2,34	1,033	² 599	58.0%	4,040	3,005	-	1,035	-	3,780	4,340	³
2008	734	2,201	2,93	3,300	² 2,201	66.7%	4,400	1,100	-	3,300	-	4,312	4,496	³
2009	1,019	1,245	2,26	264	⁴ 106	40.2%	5,635	2,536	3,099	-	-	4,750	6,910	³
2010	605	1,662	2,26	55	⁴ 17	30.9%	7,354	1,963	5,391	-	-	5,017	13,135	³
2011	1,317	1,124	2,44	N/A	-	-	5,719	3,085	⁵ 2,634	-	-	N/A	N/A	
2012	591	373	964	300	² 147	49.0%	1,968	1,207	461	300	-	1,712	2,312	³
2013	1,502	-	1,50	48	⁴ 24	50.0%	3,000	3,000	-	-	-	2,150	4,900	³
2014	212	-	212	28	⁴ -	Unknown ⁶	1,174	1,174	⁷ -	-	-	N/A	N/A	
2015	541	-	541	139	⁴ 23	16.5%	3,268	3,268	-	-	-	2,350	5,325	³
2016	2,366	-	2,36	524	⁴ 238	45.4%	5,212	5,212	-	-	-	4,640	5,920	³

¹ Abundance estimate includes smolts from LGB parr and LGB smolt releases.

² LGB-origin smolts released upriver of White Rock Dam to determine efficiencies of the bypasses.

³ 2.5-97.5 percentiles.

⁴ Non-adipose-clipped wild origin smolts marked, recycled and released upriver of White Rock Dam to determine efficiencies of the bypasses.

⁵ Smolt abundance estimate was determined by dividing total bypass catch by the mean bypass efficiency (42.7%).

⁶ Near the end of the smolt migration period it was noticed that wooden floor of bypass #1 was rotten and smolts were passing the assessment facility unaccounted for.

⁷ Smolt abundance estimate was determined by dividing bypass 2 and bypass 3 catch by the combined bypass 2 and bypass 3 efficiency (9.54%) determined in 2016 (see Appendix 5a,b).

Table 9. Parentage analysis summary for Gaspereau River non-adipose clipped smolts from 2003 to 2016. “-” = assessment data not available, N/A = not applicable.

Year	LGB Release ¹		Wild or LGB Adult ²	Total	% Adult	% Juvenile
	Juvenile	Unfed Fry	Adult Spawners			
2003	2	-	49	51	96.1%	3.9%
2004	2	-	88	90	97.8%	2.2%
2005	27	-	107	134	79.9%	20.1%
2006	167	-	6	173	3.5%	96.5%
2007	124	-	3	127	2.4%	97.6%
2008	153	-	10	163	6.1%	93.9%
2009	45	-	61	106	57.5%	42.5%
2010	127	-	108	235	46.0%	54.0%
2011	N/A	45	104	149	69.8%	30.2%
2012	N/A	103	97	200	48.5%	51.5%
2013 ³	N/A	207	17	224	7.6%	92.4%
2014	N/A	119	19	138	13.8%	86.2%
2015	N/A	125	82	207	39.6%	60.4%
2016 ³	N/A	177	25	202	12.4%	87.6%
Mean	-	-	-	-	41.5%	58.5%

¹ Wild exposed in the genetics database.

² Wild produced in the genetics database.

³ Numbers updated since the LGB review meeting based on genetic data.

Table 10. Smolt abundance estimates by origin for Gaspereau River-emigrating salmon from 2007 to 2016. “-” = data not available, “N/A” = assessment completed, no analysis available

Year	Non-Adipose Clipped		Adipose-Clipped		Total Smolts
	Adult Spawner	LGB Juvenile Release	LGB Fall Parr Release	LGB Smolt Release	
2007	71	2,934	¹ 0	1,035	4,040
2008	67	1,033	¹ 0	3,300	4,400
2009	1,459	1,077	¹ 3,099	0	5,635
2010	902	1,061	¹ 5,391	0	7,354
2011	2,153	932	² 2,634	0	5,719
2012	585	622	² 461	300	1,968
2013 ³	228	2,772	² 0	0	3,000
2014	162	1,012	² 0	0	1,174
2015	1,295	1,973	² 0	0	3,268
2016 ³	645	4,567	² 0	0	5,212

¹ Combination of unfed fry/6 week post-feeding fry/unclipped fall parr releases.

² Unfed fry releases only.

³ Numbers updated since the LGB review meeting based on genetic data.

Table 11. Big Salmon River adult Atlantic Salmon counts by stream-side observation and dive surveys from 1988 to 2016. Data sources and spawning escapement estimates (1988 to 2003) are also provided and can be found in Gibson et al. 2004. **Bold date** = count for specified year, "N/A" = assessment not completed for given year, "-" = assessment data not available, References for counts or estimates from 1988 to 2005 (see Jones et al. 2006).

Year	Date	Count Technique	Count	Estimated Spawners		
				Small	Large	Total
1988	Fall	Diver	300-400 fish ¹¹	-	-	350
1989	Fall	Diver	975 fish ¹¹	-	-	975
1990	Oct. 18	Diver	¹ 64 small / 169 large	-	-	235
1991	Aug. 16	Diver	49 small / 115 large	-	-	-
1991	Sept. 12, 17	Diver	² 105 small/151 large	-	-	300
1992	Aug. 21	Visual		-	-	-
1992	Sept. 29	Diver	150 fish (45% small)	-	-	150
1993	Aug. 27	Visual	165 fish (69% small)	-	-	300
1994	Sept. 27	Visual	³ 225 fish (60% small)	-	-	225
1995	Aug. 22	Visual	⁴ 10 small / 23 large	-	-	-
1995	Sept. 26	Visual	^{4,5,8} 18 small / 53 large	-	-	110
1996	-	Visual	⁶ 100-150 fish ¹¹	-	-	125
1997	-	Visual	50 fish ¹¹	-	-	50
1998	-	Visual	25-50 fish ¹¹	-	-	38
1999	N/A	N/A	N/A	N/A	N/A	N/A
2000	Oct. 16-18	Diver	^{7,8} 23 small / 5 large	34	7	41
2001	Oct. 22, 23	Diver	^{7,8} 12 small / 8 large	18	12	30
2002	Aug. 27, Sept. 3	Diver	^{7,8} 16 small / 5 large	24	7	31
2003	Oct. 2	Diver	⁹ 10 small / 2 large	18	3	21
2004	Oct. 20	Diver	¹⁰ 4 small / 5 large	7	9	16
2005	Sept. 7, 8, 14	Diver	^{7,10} 23 small / 11 large	41	19	60
2006	Aug. 30 , Oct. 11	Diver	^{7,10} 34 small / 10 large	60	17	77
2007	Aug. 1, Sept. 5, Oct. 10	Diver	^{7,12} 26 small / 2 large	44	3	47
2008	July 15, Sept. 15, Oct. 8	Diver	^{7,10} 20 small / 8 large	35	14	49
2009	Aug. 5 , Sept. 3, Oct. 21	Diver	^{7,10} 20 small / 1 large	35	2	37
2010	July 6, Sept. 13 , Oct. 12	Diver	^{7,12} 44 small / 5 large	78	9	87
2011	July 27 , Sept. 7, Oct. 13	Diver	^{7,10} 63 small / 4 large	111	7	118
2012	July 23 , Sept. 12, Oct. 25	Diver	^{7,10} 6 small / 3 large	11	5	16
2013	Aug 8, Sept. 9 , Oct. 19	Diver	^{7,10} 4 small / 2 large	7	4	11
2014	Aug 7, Sept. 8, 9, Oct. 21	Diver	^{10,13} 26 small / 2 large	46	3	49
2015	Aug 11, Sept. 16 , Oct. 20	Diver	^{7,10} 16 small / 2 large	28	4	32
2016	Aug 8, Sept. 7 , Oct. 18	Diver	¹⁰ 8 small / 3 large	14	5	19

¹ High water (count is a minimum estimate); ² Complete river surveyed, except one pool; ³ Diver observations on Oct. 19 indicated escapements could have been less than 225; ⁴ 15 pools surveyed representing 74% of the total river based on the 1991 complete river survey; ⁵ Streamside survey on Oct. 19 indicated no new fish in the river; ⁶ Counts were hindered by high water, estimated number is based on two partial surveys and a count for Catt and Rody pools; ⁷ counts for each survey can be found in Appendix 4; ⁸ Adjusted counts = counts / (proportion of river surveyed / (estimated observation rate) – based on calculation by Amiro and Jefferson (1996); ⁹ Mark recapture estimate (Gibson et al. 2004); ¹⁰ Borrowed observation rate (0.57) from 2003 survey (Gibson et al. 2004); ¹¹ Unknown size composition; ¹² total estimate is derived from Bayesian model; and ¹³ the small salmon estimate includes 33 LGB returns that were released as pre-grilse in 2014.

Table 12. Summary of Big Salmon River redds counted from 1996 to 2016. Sections surveyed are located in the headwaters as indicated on Figure 2. "N/A" = assessment not completed, " - " = assessment data not available.

Year	Survey Date	Section A ¹			Section B ²			Number of Redds Observed		
		Small	Large	Total	Small	Large	Total	Small	Large	Total
1996	Nov. 6	20	14	34	15	47	62	35	61	96
1997	Nov. 6	3	4	7	4	11	15	7	15	22
1998	Nov. 6	2	4	6	9	21	30	11	25	36
1999	Nov. 5	6	2	8	18	24	42	24	26	50
2000	Nov. 7	2	0	2	22	39	61	24	39	63
2001	Nov. 13	4	1	5	6	26	32	10	27	37
2002	Nov. 8	5	2	7	4	32	36	9	34	43
2003	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
2004	Nov. 10	0	0	0	13	30	43	13	30	43
2005	Nov. 8	-	-	-	-	-	-	14	56	70
2006	⁴ N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
2007	⁴ N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
2008	Oct. 23	-	-	-	50	14	64	50	14	64
2009	Nov. 9	8	2	10	59	24	83	67	26	93
2010	Nov. 3	0	0	0	69	4	73	69	4	73
2011	⁴ N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
2012	Nov. 13	-	-	-	32	5	37	-	-	-
2013	Nov. 14	-	-	-	6	2	8	-	-	-
2014	⁴ N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
2015	⁴ N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
2016	Nov. 9	-	-	-	11	0	11	-	-	-

¹ Section A is from the Anderson Brook pipe downstream to the Schoales Dam bridge (2.4 km).

² Section B is from the old trail access point downstream to the dead water just upstream of the King pool (2.0 km). A more detailed description of each section is in Jones et al. 2006.

³ The low count in the upper section in the 2000 survey may be a reflection of restricted access due to beaver dams.

⁴ Redd surveys not completed for these years due to limited resources, poor stream conditions, etc.

Table 13. Counts, biological characteristics, and estimated number of eggs for small and large salmon returning to the Big Salmon River and LGB adults released to the Big Salmon River, as well as overall percent egg conservation requirement from 2000 to 2016. "CER" = conservation egg requirement, " - " = assessment data not available.

Year	Small Salmon Returns						Large Salmon Returns					Total Eggs	% CER	
	Mean Female Length	Fecundity	Proportion Female	Spawner Count	Small Eggs		Mean Female Length	Fecundity	Proportion Female	Spawner Count	Large Eggs			
2000	53.0	3,033	0.300	34	30,937		-	-	-	7	32,217	1	63,154	2.9%
2001	-	-	-	18	35,483	1	-	-	-	12	55,229	1	90,712	4.1%
2002	-	-	-	24	47,310	1	-	-	-	7	32,217	1	79,527	3.6%
2003	55.1	3,276	0.333	18	19,637		-	-	-	3	13,808	1	33,445	1.5%
2004	-	-	-	7	13,799	1	-	-	-	9	41,422	1	55,221	2.5%
2005	54.8	3,240	0.294	41	39,055		-	-	-	19	87,446	1	126,501	5.8%
2006	56.5	3,446	0.471	60	97,384		-	-	-	17	78,241	1	175,625	8.0%
2007	54.7	3,231	0.643	44	91,412		-	-	-	3	13,808	1	105,220	4.8%
2008	55.7	3,355	0.696	35	81,728		-	-	-	14	64,434	1	146,162	6.6%
2009	57.2	3,540	0.556	35	68,889		-	-	-	2	9,205	1	78,094	3.5%
2010	55.7	3,349	0.711	78	185,729		-	-	-	9	41,422	1	227,151	10.3%
2011	54.7	3,229	0.652	111	233,690		-	-	-	7	32,217	1	265,907	12.1%
2012	-	-	-	11	21,684	1	-	-	-	5	23,012	1	44,696	2.0%
2013	-	-	-	7	13,799	1	-	-	-	4	18,410	1	32,209	1.5%
2014	-	-	-	13	25,627	1,2	-	-	-	3	13,808	1	39,435	1.8%
2015	56.3	3,424	0.769	28	73,726		-	-	-	4	18,410	1	92,136	4.2%
2016	-	-	-	14	27,598	1	-	-	-	5	23,012	1	50,610	2.3%
Mean³	55.4	3,313	0.595	-	-		70.4	5,753	0.800	-	-		-	-
	Small Salmon LGB Releases						Large Salmon LGB Releases							
2003	-	-	-	-	-		78.7	10,448	1.000	15	156,720		156,720	7.1%
2004	-	-	-	-	-		79.2	10,678	1.000	13	138,814		138,814	6.3%
2005	47.8	2,716	0.686	35	65,184		65.0	5,749	0.776	49	218,462		283,646	12.9%

¹ Time-series mean values (small or large salmon treated separately) applied to spawner count to calculate eggs in that year.

² The 33 LGB pre-grilse were excluded from the estimated egg calculation.

³ Mean values are calculated using all fish sampled from 2000 to 2016 (see Appendix 7).

Table 14. Summary of the Big Salmon River small salmon parentage analysis results for individuals sampled from 2000 to 2016. "N/A" = parental analysis is not applicable as no returning adults of this category were expected for that year, " - " = assessment data not available.

Year	# Tissue Sampled	Live Genk Bank Origin		Adult Spawners			Small Salmon Escapement	Proportion of Total Return Sampled
		Unfed Fry	Fall Parr (Adipose-Clipped)	Progeny of Wild Adult Returns (Genetically Analyzed)	Adipose-Clipped Stray	Unknown		
2000	0	N/A	N/A	N/A	N/A	0	34	0.00
2001	0	N/A	N/A	N/A	N/A	0	18	0.00
2002	0	N/A	N/A	N/A	N/A	0	24	0.00
2003	6	N/A	1	1	N/A	0	18	0.33
2004	0	-	-	N/A	-	-	7	0.00
2005	19	2	0	N/A	0	17	41	0.46
2006	17	2	1	2	N/A	0	60	0.28
2007	14	5	2	2	0	5	44	0.32
2008	23	4	1	3	0	15	35	0.66
2009	9	1	0	3	0	5	35	0.26
2010	45	9	6	11	2	19	78	0.58
2011	23	4	0	11	0	8	111	0.21
2012	0	-	-	-	-	-	11	0.00
2013	0	-	-	-	-	-	7	0.00
2014	3	0	0	0	0	3	13	0.23
2015 ³	13	3	0	0	0	10	28	0.46
2016 ³	4	3	0	0	0	1	14	0.29
Totals	176	33	11	30	2	102	-	-

¹ This LGB return could be from the spring smolt release in 2005 or fall parr release in 2004 (age 1.1).

² Age-2: 1 – confirmed by genetics that the individual is from the 2002 spawning class, thus a fall parr release.

³ Numbers updated since the LGB review based on genetic data

Table 15. Estimated Big Salmon River small salmon returns by origin based on the parentage analysis from 2000 to 2016. "N/A" = parental analysis is not applicable as no returning adults of this category were expected for that year, " - " = assessment data not available.

Year	Live Genk Bank Origin		Adult Spawners		
	Unfed Fry	Fall Parr (Adipose-Clipped)	Progeny of Wild Adult Returns (Genetically Analyzed)	Adipose-Clipped Stray	Unknown
2000	N/A	N/A	N/A	N/A	34
2001	N/A	N/A	N/A	N/A	18
2002	N/A	N/A	N/A	N/A	24
2003	N/A	3	N/A	0	15
2004	-	-	N/A	-	-
2005	4	0	N/A	0	37
2006	7	4	N/A	0	49
2007	16	6	6	0	16
2008	6	2	5	0	23
2009	4	0	12	0	19
2010	16	10	19	3	33
2011	19	0	53	0	39
2012	-	-	-	-	-
2013	-	-	-	-	-
2014	0	0	0	0	13
2015 ¹	6	0	0	0	22
2016 ¹	11	0	0	0	3
Totals 2005 to 2016	89	22	95	3	254
% of Total	19.2%	4.8%	20.5%	0.6%	54.9%

¹ Estimates updated since the LGB review based on genetic data.

Table 16. Summary of the Big Salmon River large salmon parentage analysis results from 2000 to 2016. "N/A" = parental analysis is not applicable as no returning adults of this category were expected for that year, " - " = assessment data not available.

Year	# Sampled	Live Genk Bank Origin		Adult Spawners			Large Salmon Escapement	Proportion of Total Return Sampled
		Unfed Fry	Fall Parr (Adipose-Clipped)	Progeny of Wild Adult Returns (Genetically Analyzed)	Adipose-Clipped Strays	Unknown		
2000	0	N/A	N/A	N/A	N/A	0	7	0.00
2001	0	N/A	N/A	N/A	N/A	0	12	0.00
2002	0	N/A	N/A	N/A	N/A	0	7	0.00
2003	1	N/A	0	N/A	0	1	3	0.33
2004	0	-	-	N/A	-	-	9	0.00
2005	4	0	0	N/A	0	4	19	0.21
2006	3	0	0	N/A	0	3	17	0.18
2007	2	0	0	N/A	0	2	3	0.67
2008	2	1	0	0	0	1	14	0.14
2009	4	0	1	0	1	3	2	2.00
2010	4	0	0	0	0	4	9	0.44
2011	0	-	-	-	-	-	7	0.00
2012	0	-	-	-	-	-	5	0.00
2013	0	-	-	-	-	-	4	0.00
2014	1	1	0	0	0	0	3	0.33
2015	0	-	-	-	-	-	4	0.00
2016	0	-	-	-	-	-	5	0.00
Totals	21	2	1	0	1	18	-	-

Table 17. Summary of a) Live Gene Bank (LGB) origin and b) wild or unknown origin small and large adult salmon returns by total age after smoltification between 2000 and 2016 (n = 197 scale samples; see Appendix 8 for individual data). "Unknown" = data not known, "–" = assessment data not available, N/A = not applicable.

Total Years After Smoltification	Spawning History			Individual Count	Mean Female Length (cm)	Mean Fecundity (# of Eggs)	% Female	% Sample	
	1 st	2 nd	3 rd						
a) Live Gene Bank Origin									
Small Salmon									
1	0	N/A	N/A	¹	42	54.9	3,252	59.5%	93.3%
Large Salmon									
2	0	N/A	N/A	²	1	80.0	8,191	100.0%	2.2%
2	1	N/A	N/A	³	1	-	-	0.0%	2.2%
3	2	N/A	N/A	³	1	80.0	8,191	100.0%	2.2%
b) Wild or Unknown Origin									
Small Salmon									
1	0	N/A	N/A	¹	132	55.6	3,337	60.8%	85.7%
2	1	N/A	N/A	³	3	62.0	4,223	66.7%	1.9%
Large Salmon									
1	0	N/A	N/A	¹	3	-	-	0.0%	1.9%
2	1	N/A	N/A	³	9	65.1	4,734	62.5%	5.8%
3	1	2	N/A	³	3	69.6	5,586	100.0%	1.9%
4	1	2	3	³	2	75.0	6,814	100.0%	1.3%
2	0	N/A	N/A	²	1	73.5	6,449	100.0%	0.6%
3	2	N/A	N/A	³	1	-	-	Unknown	0.6%

¹ Maiden 1SW salmon.

² Maiden 2SW salmon.

³ Repeat spawner.

Table 18. Summary of small and large Atlantic Salmon returns captured at the White Rock Dam fishway on the Gaspereau River from 2001 to 2016. "Unknown" = unknown origin, either origin could not be determined by parentage analysis or tissue sample were not collected. "LGB" = returns from Live Gene Bank program – confirmed by genetic analysis, "Hatchery" = hatchery returns prior to the LGB program, and "Wild" = wild-origin from previous adult spawners, "–" = assessment data not available, N/A = not applicable.

Year	Small Salmon					Large Salmon					Grand Total
	Hatchery	LGB	Wild	Unknown	Total	Hatchery	LGB	Wild	Unknown	Total	
1995	29	N/A	33	0	62	0	N/A	19	0	19	81
1996	75	N/A	41	0	116	29	N/A	33	0	62	178
1997	30	N/A	12	0	83	7	N/A	12	0	19	102
1998	62	N/A	8	0	78	12	N/A	9	0	21	99
1999	0	N/A	3	0	3	13	N/A	25	0	38	41
2000	35	N/A	5	0	56	13	N/A	7	0	20	76
2001	11	N/A	12	0	23	13	N/A	20	0	33	56
2002	2	N/A	8	0	10	4	N/A	0	0	4	14
2003	3	N/A	3	0	6	0	N/A	2	0	2	8
2004	6	N/A	5	7	18	1	N/A	0	0	1	19
2005	N/A	2	0	0	2	0	N/A	0	0	0	2
2006	N/A	2	1	0	3	N/A	1	0	0	1	4
2007	N/A	0	0	3	3	N/A	0	0	0	0	3
2008	N/A	11	0	1	12	N/A	4	0	0	4	16
2009	N/A	4	0	0	4	N/A	0	0	1	1	5
2010	N/A	2	1	3	6	N/A	3	0	0	3	9
2011	N/A	5	0	3	8	N/A	4	0	1	5	13
2012	N/A	1	0	1	2	N/A	1	0	0	1	3
2013	N/A	0	0	0	0	N/A	0	0	1	2	2
2014	N/A	2	0	0	2	N/A	0	0	0	0	2
2015 ¹	N/A	5	0	0	5	N/A	3	0	2	5	10
2016 ¹	N/A	3	0	2	5	N/A	0	0	0	0	5
TOTALS SINCE LGB PROGRAM INITIATED (2005 TO 2016)											
Total	22	37	30	20	109	18	16	23	5	62	171
% Total	N/A	71.2%	3.8%	25.0%	N/A	N/A	72.7%	4.5%	22.7%	N/A	N/A

¹ Numbers updated since the LGB review based on genetic data.

Table 19. Summary of a) Live Gene Bank (LGB) origin and b) wild or unknown origin small and large salmon by total age after smoltification, spawning history, mean length (cm), fecundity (number of eggs), percent female, and percentage of salmon in the Gaspereau River. Values were determined from 125 aged scale samples collected from wild, hatchery and LGB-origin adult returns captured in the White Rock Dam fishway from 2001 to 2016. “ – ” = assessment data not available, N/A = not applicable.

Total Years After Smoltification	Spawning History			Individual Count	Mean Female Length (cm)	Mean Fecundity (# of Eggs)	% Female	% Sample	
	1 st	2 nd	3 rd						
a) Live Gene Bank or Hatchery Origin									
Small Salmon									
1	0	N/A	N/A	¹	42	53.6	3,100	11.9%	62.7%
Large Salmon									
2	0	N/A	N/A	²	22	70.3	5,732	86.4%	32.8%
3	0	N/A	N/A	³	1	N/A	N/A	0.0%	1.5%
3	1	N/A	N/A	⁴	2	N/A	N/A	0.0%	3.0%
b) Wild or Unknown Origin									
Small Salmon									
1	0	N/A	N/A	¹	35	53.6	3,100	71.4%	60.3%
Large Salmon									
2	0	N/A	N/A	²	21	68.6	5,385	95.2%	36.2%
3	1	N/A	N/A	⁴	2	75.0	6,814	50.0%	3.4%

¹ Maiden 1SW salmon.

² Maiden 2SW salmon.

³ Maiden 3SW salmon.

⁴ Repeat spawner.

Table 20. Estimated survival of released Big Salmon River Live Gene Bank unfed fry to the smolt stage from 2001 to 2016. “ - “ = assessment data not available.

Release Year (yy)	Number Released	Smolt Abundance Estimate			Total Smolt Output	Percent Survival to Smolt Stage			
		(Age-2) (yy + 2)	(Age-3) (yy + 3)	(Age-4) (yy + 4)		Age-2	Age-3	Age-4	Total
2001	185,523	3,640	901	30	4,571	2.0%	0.5%	0.0%	2.5%
2002	138,682	2,134	718	288	3,140	1.5%	0.5%	0.2%	2.3%
2003	296,818	2,572	2,399	13	4,984	0.9%	0.8%	0.0%	1.7%
2004	369,109	6,268	551	20	6,839	1.7%	0.1%	0.0%	1.9%
2005	258,873	1,799	675	0	2,474	0.7%	0.3%	0.0%	1.0%
2006	413,413	3,215	892	49	4,156	0.8%	0.2%	0.0%	1.0%
2007	370,605	5,676	1,251	20	6,947	1.5%	0.3%	0.0%	1.9%
2008	265,126	4,164	2,142	0	6,305	1.6%	0.8%	0.0%	2.4%
2009	177,971	2,382	1,543	0	3,925	1.3%	0.9%	0.0%	2.2%
2010	200,378	2,695	546	17	3,259	1.3%	0.3%	0.0%	1.6%
2011	401,486	4,804	217	16	5,036	1.2%	0.1%	0.0%	1.3%
2012	97,209	1,248	664	59	1,971	1.3%	0.7%	0.1%	2.0%
2013	341,995	5,755	2,011	-	7,766	1.7%	0.6%	-	2.3%+
2014	255,386	3,667	-	-	3,667	1.4%	-	-	-
2015	302,307	-	-	-	-	-	-	-	-
2016	404,398	-	-	-	-	-	-	-	-
Mean	-	3,573	1,116	43	4,646	1.4%	0.5%	0.0%	1.8%

Table 21. Estimated survival of released Big Salmon River Live Gene Bank parr (fall and spring releases) to the smolt stage from 2001 to 2012. “ – “ = assessment data not available.

Release Year (yy)	# Released	Spring Parr Released (yy + 1)	Smolt Abundance Estimate				Total Smolt Output	Percent Survival to Smolt Stage				
			(Age-1) (yy + 1)	(Age-2) (yy + 2)	(Age-3) (yy + 3)	(Age-4) (yy + 4)		Age-1	Age-2	Age-3	Age-4	Total
2001	77,718	0	2,035	1,202	0	0	3,237	2.6%	1.5%	0.0%	0.0%	4.2%
2002	34,062	21,025	4,918	265	77	57	5,318	8.9%	0.5%	0.1%	0.1%	9.7%
2003	54,000	7,009	1,425	1,160	1,547	26	4,158	2.3%	1.9%	2.5%	0.0%	6.8%
2004	90,843	892	2,938	6,189	627	0	9,755	3.2%	6.7%	0.7%	0.0%	10.6%
2005	69,862	665	1,146	4,705	151	0	6,002	1.6%	6.7%	0.2%	0.0%	8.5%
2006	72,556	0	497	1,256	96	0	1,849	0.7%	1.7%	0.1%	0.0%	2.5%
2007	87,088	0	703	3,938	478	0	5,120	0.8%	4.5%	0.5%	0.0%	5.9%
2008	87,786	0	720	5,921	898	0	7,539	0.8%	6.7%	1.0%	0.0%	8.6%
2009	56,984	0	441	1,878	70	0	2,390	0.8%	3.3%	0.1%	0.0%	4.2%
2010	43,140	0	163	1,689	50	0	1,902	0.4%	3.9%	0.1%	0.0%	4.4%
2011	15,137 ¹	0	141	900	27	0	1,067	0.9%	5.9%	0.2%	0.0%	7.1%
2012	50	0	100	13	0	0	113	-	-	-	-	-
Mean	-	-	-	-	-	-	-	2.1%	4.0%	0.5%	0.0%	6.6%

1 3,137 were unmarked – so these are minimum estimates for this release group.

Table 22. Estimated egg-to-smolt survival from LGB adults released in Big Salmon River from 2003 to 2005. “ – “ = assessment data not available

Release Year (yy)	Estimated Eggs	Smolt Abundance Estimate				Total Smolt Output	Percent Survival to Smolt Stage				
		(Age-1) (yy + 1)	(Age-2) (yy + 2)	(Age-3) (yy + 3)	(Age-4) (yy + 4)		Age-1	Age-2	Age-3	Age-4	Total
2003	156,720	-	1,015	345	57	1,418	-	0.65%	0.22%	0.04%	0.90%
2004	138,814	-	148	115	0	263	-	0.11%	0.08%	0.00%	0.19%
2005	283,646	-	460	49	0	509	-	0.16%	0.02%	0.00%	0.18%
Mean							-	0.31%	0.11%	0.01%	0.42%

Table 23. Preliminary estimated survival of Gaspereau River Live Gene Bank (LGB) unfed fry to the smolt stage from 2010 to 2014.
 “-” = assessment data not available, “N/A” = unaged post-smolt sample data collected for the LGB from 2011 to 2013 that is not yet available.

Release Year (yy)	Marked	# Released	Smolt Abundance Estimate				Total Smolt Output	Percent Survival to Smolt Stage				
			(Age-1) (yy + 1)	(Age-2) (yy + 2)	(Age-3) (yy + 3)	(Age-4) (yy + 4)		Age-1	Age-2	Age-3	Age-4	Total
2001	Unmarked	-	-	-	-	-	-	-	-	-	-	-
2002	Unmarked	4,033	-	-	-	-	-	-	-	-	-	-
2003	Unmarked	-	-	-	-	-	-	-	-	-	-	-
2004	Unmarked	-	-	-	-	-	-	-	-	-	-	-
2005	Unmarked	95,977	-	-	-	-	-	-	-	-	-	-
2006	Unmarked	46,666	-	-	-	-	-	-	-	-	-	-
2007	Unmarked	280,000	-	-	-	N/A	-	-	-	-	-	-
2008	Unmarked	275,000	-	-	N/A	N/A	-	-	-	-	-	-
2009	Unmarked	117,700	-	N/A	N/A	N/A	-	-	N/A	N/A	N/A	N/A
2010	Unmarked	86,511	-	N/A	N/A	8	8	-	N/A	N/A	0.0%	N/A
2011	Unmarked	221,000	-	N/A	311	44	355	-	N/A	0.1%	0.0%	N/A
2012	Unmarked	220,000	-	694	292	36	1,021	-	0.3%	0.1%	0.0%	0.5%
2013	Unmarked	191,700	-	1,637	720	-	2,357	-	0.9%	0.4%	-	1.3%
2014	Unmarked	182,750	-	3,812	-	-	3,812	-	2.1%	-	-	2.1%
2015	Unmarked	153,000	-	-	-	-	-	-	-	-	-	-
2016	Unmarked	188,187	-	-	-	-	-	-	-	-	-	-
Mean	-	-	-	-	-	-	-	-	1.1%	0.2%	0.0%	1.3%

Table 24. Estimated smolt-to-small salmon return rates for Big Salmon River Live Gene Bank (LGB) origin fry and parr, as well as adult spawners. N/A =not applicable, “ - “ = assessment data not available.

Smolt Year	LGB Smolt Release	Combined			Smolt-to-Small Salmon Return Rate by Origin			% Combined ¹
		LGB Unfed Fry	LGB Parr	Adult Spawners	LGB Unfed Fry	LGB Parr	Adult Spawners	
2001	-	-	-	5,290	N/A	N/A	0.45%	0.45%
2002	19,725	-	2,035	4,295	N/A	0.15%	0.35%	0.28%
2003	13,650	3,640	6,120	5,560	-	-	-	0.05%
2004	11,663	3,036	1,691	2,934	0.13%	0.00%	1.26%	0.54%
2005	1,296	3,320	4,175	1,230	0.21%	0.10%	3.98%	0.69%
2006	1,413	8,954	8,940	8,401	0.18%	0.07%	0.26%	0.17%
2007	-	2,363	5,855	4,037	0.25%	0.03%	0.69%	0.29%
2008	-	3,909	2,110	6,841	0.10%	0.00%	0.45%	0.27%
2009	2,072	6,568	4,756	5,392	0.24%	0.21%	0.96%	0.47%
2010	2,077	5,464	6,840	7,156	0.35%	0.00%	1.29%	0.57%
2011	432	4,543	2,939	5,592	-	-	-	0.08%
2012	-	4,239	1,900	6,881	-	-	-	0.05%
2013	-	5,350	1,050	4,490	0.00%	0.00%	0.29%	0.12%
2014	-	1,482	40	2,988	0.40%	0.00%	0.74%	0.62%
2015	-	6,435	-	3,255	0.17%	NA	0.09%	0.14%
2016	-	5,737	-	1,443	-	-	-	-
Mean (2004 to 2010)		-	-	-	0.21%	0.06%	1.27%	0.43%
Mean (2001 to 2015)		-	-	-	0.20%	0.06%	0.90%	0.32%

¹ Combined excludes LGB smolt releases.

Table 25. Estimated smolt-to-small and large salmon return rates for Gaspereau River Live Gene Bank (LGB) origin fry and parr, as well as adult spawners. “ - ” = assessment data not available.

Smolt Year	LGB Smolt Release	LGB Unfed Fry	LGB Parr	Adult Spawners	% Small	% Small + Large
2007	1,035	2,934 ¹	-	71	0.40%	0.43%
2008	3,300	1,033 ¹	-	67	0.36%	0.64%
2009	-	1,077 ¹	3,099	1,459	0.11%	0.21%
2010	-	1,061 ¹	5,391	902	0.10%	0.12%
2011	-	932	2,634	2,153	0.02%	0.05%
2012	300	622	461	585	0.00%	0.00%
2013	-	2,772	-	228	0.07%	0.23%
2014	-	1,012	-	162	0.43%	0.43%
2015	-	1,973	-	1,295	0.15%	-
2016	-	4,567	-	645	-	-
Mean	-	-	-	-	0.18%	0.25%

¹ Includes some non-adipose-clipped fall parr.

Table 26. Parentage assignment results from age-2 smolt sampled on the Pollet River in 2013. "BSR" = Big Salmon River Live Gene Bank, "GAK" = Gaspereau River Live Gene Bank, "NMB" = New Minas Basin Live Gene Bank, "STW" = Stewiacke River Live Gene Bank.

Crosses	Age-2 Smolt Genetic Analysis	Age-2 Smolt Abundance
BSR x BSR	74	833
GAK x GAK	27	304
GAK x NMB	16	180
GAK x STW	31	349
NMB x NMB	7	23
STW x NMB	7	79
STW x STW	4	45
BSR x BSR	0.460	833
Nova Scotia Crosses	0.540	980
Total	161	1813

Table 27. Estimated survival of Live Gene Bank released unfed fry to the smolt stage on the Pollet River. “ - ” = assessment data not available.

Release Year (yy)	# Released	Smolt Abundance Estimate			Total Smolt Output	Percent Survival to Smolt Stage			
		(Age-2) (yy + 2)	(Age-3) (yy + 3)	(Age-4) (yy + 4)		Age-2	Age-3	Age-4	Total
2002	56,159	-	-	-	-	-	-	-	-
2003	0	-	-	-	-	-	-	-	-
2004	0	-	-	-	-	-	-	-	-
2005	120,094	-	-	-	-	-	-	-	-
2006	0	-	-	-	-	-	-	-	-
2007	0	-	-	-	-	-	-	-	-
2008	0	-	-	-	-	-	-	-	-
2009	63,550	-	-	112	112	-	-	0.2%	-
2010	0	-	0	0	-	-	-	-	-
2011	337,622	1,813	280	0	2,093	0.5%	0.1%	0.0%	0.6%
2012	37,246	1,320	129	-	1,450	3.5%	0.3%	0.0%	3.9%
2013	0	61	-	-	61	-	-	-	-
2014	0	-	-	-	-	-	-	-	-
2015	0	-	-	-	-	-	-	-	-
2016	50,000	-	-	-	-	-	-	-	-
Mean	-	-	-	-	-	2.0%	0.2%	0.1%	2.3%

Table 28. Summary statistics for the estimated densities (number per 100 m²) of Stewiacke River Atlantic Salmon fry and parr via electrofishing surveys during 2013. "LGB" = whether (Y) or not (N) the river received Live Gene Bank juvenile salmon since 2009 Note: the majority of electrofishing sites were upstream of distribution sites, " - " = assessment data not available.

Tributary	LGB	# of Sites	Age-0 Parr (Fry)					Age-1 and Older Parr				
			Mean	Standard Deviation	Minimum	Maximum	Median	Mean	Standard Deviation	Minimum	Maximum	Median
Big/Little Branch	Y	5	2.62	1.99	0.80	5.70	2.80	3.00	1.35	1.70	4.90	3.30
Blackie Brook	Y	1	0.00	-	0.00	0.00	-	1.70	-	1.70	1.70	-
Cox Brook	Y	1	0.00	-	0.00	0.00	-	0.50	-	0.50	0.50	-
Fall Brook	Y	1	0.00	-	0.00	0.00	-	0.00	-	0.00	0.00	-
Goshen Brook	Y	2	7.50	10.61	0.00	15.00	7.5	4.90	6.93	0.00	9.80	4.9
Little River	N	7	0.00	-	0.00	0.00	0.00	0.30	0.79	0.00	2.10	0.00
Mainstem I	N	5	0.00	-	0.00	0.00	0.00	1.34	0.84	0.00	2.10	1.60
Mainstem II	Y	7	6.13	8.12	0.00	23.50	4.00	3.81	2.70	1.00	7.30	2.70
Newton Brook	Y	3	0.00	-	0.00	0.00	0.00	4.70	5.88	0.00	11.30	2.80
Pembroke Brook	Y	2	51.45	24.82	33.90	69.00	51.45	0.85	0.07	0.80	0.90	0.85
Putnam Brook	Y	1	0.00	-	0.00	0.00	-	2.80	-	2.80	2.80	-
Rutherford Brook	Y	4	0.10	0.20	0.00	0.40	0.00	6.78	7.73	2.00	18.30	3.40
Sutherland Brook	Y	1	0.00	-	0.00	0.00	-	0.00	-	0.00	0.00	-

Table 29. The 2013 Stewiacke River juvenile parentage and grandparentage analyses.

Category	Age			
	0+	1+	2+	3+/4+
LGB crosses (direct capture of released juveniles)	217	46	53	3
Female adult release + Male parr releases (spawned and angles as adult)	0	13	0	0
Female adult release + Male juvenile release (spawned as parr)	0	21	0	0
Female adult release + undetermined Male	0	4	0	0
Female fry release (spawned as adult) + Male fry release (spawned as adult)	0	2	0	0
Female fry release (spawned as adult) + Male juvenile release (spawned as parr- 2 males from same parents)	0	3	6	5
Female fry release (spawned as adult) + undetermined Male	0	1	7	0
Female parr/smolt release (spawned as adult) + Male juvenile release (spawned as parr- 2 males from same parent)	0	1	0	3
Female wild offspring of 2 Salmon River adult releases (spawned as adult) + Male juvenile release (spawned as parr)	0	6	0	0
Undetermined Female + Male juvenile release (spawned as parr)	0	0	0	1
Both parents undetermined	0	0	1	0

Table 30. The number of parents contributing to produced juveniles, by gender and parental types, for all sites combined.

Category	Female Parent	Male Parent
LGB crosses	217	211
Wild spawning – Stewiacke Adult Release	6	0
Wild spawning – Parr/smolt releases spawning as adult	2	1
Wild spawning – Fry release spawning as adult	6	2
Wild spawning – Juvenile release spawning as parr	0	24
Wild spawning – Wild spawned offspring of 2 Salmon River adult releases	1	0
Parent as yet undetermined ¹	2	9
Total (detected and potential) wild-spawning parents	17	36

¹ Estimates of female and male parents are based on kinship analysis results.

Table 31. Estimated densities (number per 100m²) of Atlantic Salmon fry and parr from electrofishing surveys on IBoF rivers during 2014. **Bold** rivers = salmon juvenile densities > zero (0), "Std. Dev." = standard deviation, "Min." = minimum density, "Max." = maximum density

River	Priority	# of Sites	Age-0 Parr (Fry)					Age-1 and Older Parr				
			Mean	Std. Dev.	Min.	Max.	Median	Mean	Std. Dev.	Min.	Max.	Median
Apple River	Medium	3	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Avon River	Medium	2	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bains Brook	High	3	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bass River	Medium	4	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Black River	High	2	0.35	0.07	0.30	0.40	0.35	7.20	7.07	2.20	12.20	7.2
Carters Brook	Medium	2	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chiganois River	Low	3	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Crooked Creek	High	1	0.00	-	0.00	0.00	0.00	0.00	-	0.00	0.00	0.00
Demoiselle Creek	High	2	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Diligent River	Medium	1	0.00	-	0.00	0.00	0.00	0.00	-	0.00	0.00	0.00
Emerson Creek	Medium	2	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Gardner Creek	High	2	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Great Village River	Low	4	0.00	0.00	0.00	0.00	0.00	0.20	0.40	0.00	0.80	0.00
Halfway River	Medium	2	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Harrington River	High	4	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Irish River	High	4	0.00	0.00	0.00	0.00	0.00	0.28	0.55	0.00	1.10	0.00
Kennetcook River	High	3	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Little Salmon River	High	1	0.00	-	0.00	0.00	0.00	0.00	-	0.00	0.00	0.00
Maccan River	High	4	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Memramcook River	Medium	3	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Mispec River	High	1	0.40	-	0.40	0.40	-	2.10	-	2.10	2.10	-
Moose River	Medium	1	0.00	-	0.00	0.00	0.00	0.00	-	0.00	0.00	0.00
Mosher River	Medium	1	0.00	-	0.00	0.00	0.00	0.50	-	0.50	0.50	-
North River (Colc.)	High	6	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
North River (Cumb.)	Medium	1	0.00	-	0.00	0.00	0.00	0.00	-	0.00	0.00	0.00
Parrsboro River	High	2	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Portapique River	High	4	0.00	0.00	0.00	0.00	0.00	0.45	0.66	0.00	1.40	0.2
Quiddy River	Medium	2	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Ramshead	Medium	1	0.00	-	0.00	0.00	0.00	0.00	-	0.00	0.00	0.00
River Hebert	High	3	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Salmon River (Colc.)	Low	3	0.50	0.87	0.00	1.50	0.00	8.27	3.70	4.50	11.90	8.4
Shepody	Medium	1	0.00	-	0.00	0.00	0.00	0.00	-	0.00	0.00	0.00
Shubenacadie River	High	5	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
St. Croix River	High	2	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Table 32. Summary results of likelihood- and probability-based individual assignment analyses, testing salmon electrofished from assorted Inner Bay of Fundy (IBoF) rivers during the 2014 IBoF Broadscale survey against baseline sample collections. “BSR” = Big Salmon River, “STW” = Stewiacke River, “GAK” = Gaspereau River, “NSH” = Nashwaak River, “TOB” = Tobique River, “IBoF” = Inner Bay of Fundy, “OBoF” = Outer Bay of Fundy, “-” = assessment data not available

River Assignment Method		BSR	STW	GAK	NSH	TOB	Total	IBoF	OBoF	Total	
Likelihood	Frequency	Number	11.00	40.00	3.00	29.00	14.00	97.00	54.00	43.00	97.00
		Percent	11.34	41.24	3.09	29.90	14.43	100.00	55.67	44.33	100.00
		Total	97.00	97.00	97.00	97.00	97.00	-	97.00	97.00	-
	Bayesian	Number	6.00	42.00	0.00	30.00	19.00	97.00	48.00	49.00	97.00
		Percent	6.19	43.30	0.00	30.93	19.59	100.00	49.48	50.52	100.00
		Total	97.00	97.00	97.00	97.00	97.00	-	97.00	97.00	-
	Distance	Number	7.00	49.00	2.00	20.00	19.00	97.00	58.00	39.00	97.00
		Percent	7.22	50.52	2.06	20.62	19.59	100.00	59.79	40.21	100.00
		Total	97.00	97.00	97.00	97.00	97.00	-	97.00	97.00	-
Probability	Frequency	Number	6.00	18.00	0.00	53.00	20.00	97.00	24.00	73.00	97.00
		Percent	6.19	18.56	0.00	54.64	20.62	100.00	24.74	75.26	100.00
		Total	97.00	97.00	97.00	97.00	97.00	-	97.00	97.00	-
	Bayesian	Number	0.00	20.00	0.00	64.00	13.00	97.00	20.00	77.00	97.00
		Percent	0.00	20.62	0.00	65.98	13.40	100.00	20.62	79.38	100.00
		Total	97.00	97.00	97.00	97.00	97.00	-	97.00	97.00	-
	Distance	Number	1.00	25.00	0.00	65.00	6.00	97.00	26.00	71.00	97.00
		Percent	1.03	25.77	0.00	67.01	6.19	100.00	26.80	73.20	100.00
		Total	97.00	97.00	97.00	97.00	97.00	-	97.00	97.00	-

Table 33. Summary results of likelihood- and probability-based individual assignment analyses, testing salmon collected from the Salmon River (Colchester) during the 2014 Inner Bay of Fundy (IBoF) Broadscale electrofishing survey against baseline sample collections. . “BSR” = Big Salmon River, “STW” = Stewiacke River, “GAK” = Gaspereau River, “NSH” = Nashwaak River, “TOB” = Tobique River, “IBoF” = Inner Bay of Fundy, “OBoF” = Outer Bay of Fundy, “-” = assessment data not available.

River Assignment Method		BSR	STW	GAK	NSH	TOB	Total	IBoF	OBoF	Total	
Likelihood	Frequency	Number	4.00	35.00	0.00	2.00	3.00	44.00	39.00	5.00	44.00
		Percent	9.09	79.55	0.00	4.55	6.82	100.00	88.64	11.36	100.00
		Total	44.00	44.00	44.00	44.00	44.00	-	44.00	44.00	-
	Bayesian	Number	2.00	35.00	0.00	3.00	4.00	44.00	37.00	7.00	44.00
		Percent	4.55	79.55	0.00	6.82	9.09	100.00	84.09	15.91	100.00
		Total	44.00	44.00	44.00	44.00	44.00	-	44.00	44.00	-
	Distance	Number	0.00	38.00	0.00	3.00	3.00	44.00	38.00	6.00	44.00
		Percent	0.00	86.36	0.00	6.82	6.82	100.00	86.36	13.64	100.00
		Total	44.00	44.00	44.00	44.00	44.00	-	44.00	44.00	-
Probability	Frequency	Number	2.00	17.00	0.00	17.00	8.00	44.00	19.00	25.00	44.00
		Percent	4.55	38.64	0.00	38.64	18.18	100.00	43.18	56.82	100.00
		Total	44.00	44.00	44.00	44.00	44.00	-	44.00	44.00	-
	Bayesian	Number	0.00	19.00	0.00	21.00	4.00	44.00	19.00	25.00	44.00
		Percent	0.00	43.18	0.00	47.73	9.09	100.00	43.18	56.82	100.00
		Total	44.00	44.00	44.00	44.00	44.00	-	44.00	44.00	-
	Distance	Number	1.00	23.00	0.00	18.00	2.00	44.00	24.00	20.00	44.00
		Percent	2.27	52.27	0.00	40.91	4.55	100.00	54.55	45.45	100.00
		Total	44.00	44.00	44.00	44.00	44.00	-	44.00	44.00	-

Table 34. Summary results of likelihood- and probability-based individual assignment analyses, testing salmon electrofished from the Black River during the 2014 Inner Bay of Fundy (IBoF) Broadscale electrofishing survey against baseline sample collections using different Likelihood- and Probability-based methods. "BSR" = Big Salmon River, "STW" = Stewiacke River, "GAK" = Gaspereau River, "NSH" = Nashwaak River, "TOB" = Tobique River, "IBoF" = Inner Bay of Fundy, "OBoF" = Outer Bay of Fundy, " - " = assessment data not available.

River Assignment Method		BSR	STW	GAK	NSH	TOB	Total	IBoF	OBoF	Total	
Likelihood	Frequency	Number	11.00	0.00	3.00	24.00	0.00	38.00	14.00	24.00	38.00
		Percent	28.95	0.00	7.89	63.16	0.00	100.00	36.84	63.16	100.00
		Total	38.00	38.00	38.00	38.00	38.00	-	38.00	38.00	-
	Bayesian	Number	6.00	2.00	0.00	30.00	0.00	38.00	8.00	30.00	38.00
		Percent	15.79	5.26	0.00	78.95	0.00	100.00	21.05	78.95	100.00
		Total	38.00	38.00	38.00	38.00	38.00	-	38.00	38.00	-
	Distance	Number	7.00	9.00	2.00	20.00	0.00	38.00	18.00	20.00	38.00
		Percent	18.42	23.68	5.26	52.63	0.00	100.00	47.37	52.63	100.00
		Total	38.00	38.00	38.00	38.00	38.00	-	38.00	38.00	-
Probability	Frequency	Number	6.00	0.00	0.00	32.00	0.00	38.00	6.00	32.00	38.00
		Percent	15.79	0.00	0.00	84.21	0.00	100.00	15.79	84.21	100.00
		Total	38.00	38.00	38.00	38.00	38.00	-	38.00	38.00	-
	Bayesian	Number	0.00	0.00	0.00	38.00	0.00	38.00	0.00	38.00	38.00
		Percent	0.00	0.00	0.00	100.00	0.00	100.00	0.00	100.00	100.00
		Total	38.00	38.00	38.00	38.00	38.00	-	38.00	38.00	-
	Distance	Number	1.00	0.00	0.00	37.00	0.00	38.00	1.00	37.00	38.00
		Percent	2.63	0.00	0.00	97.37	0.00	100.00	2.63	97.37	100.00
		Total	38.00	38.00	38.00	38.00	38.00	-	38.00	38.00	-

8.0 FIGURES

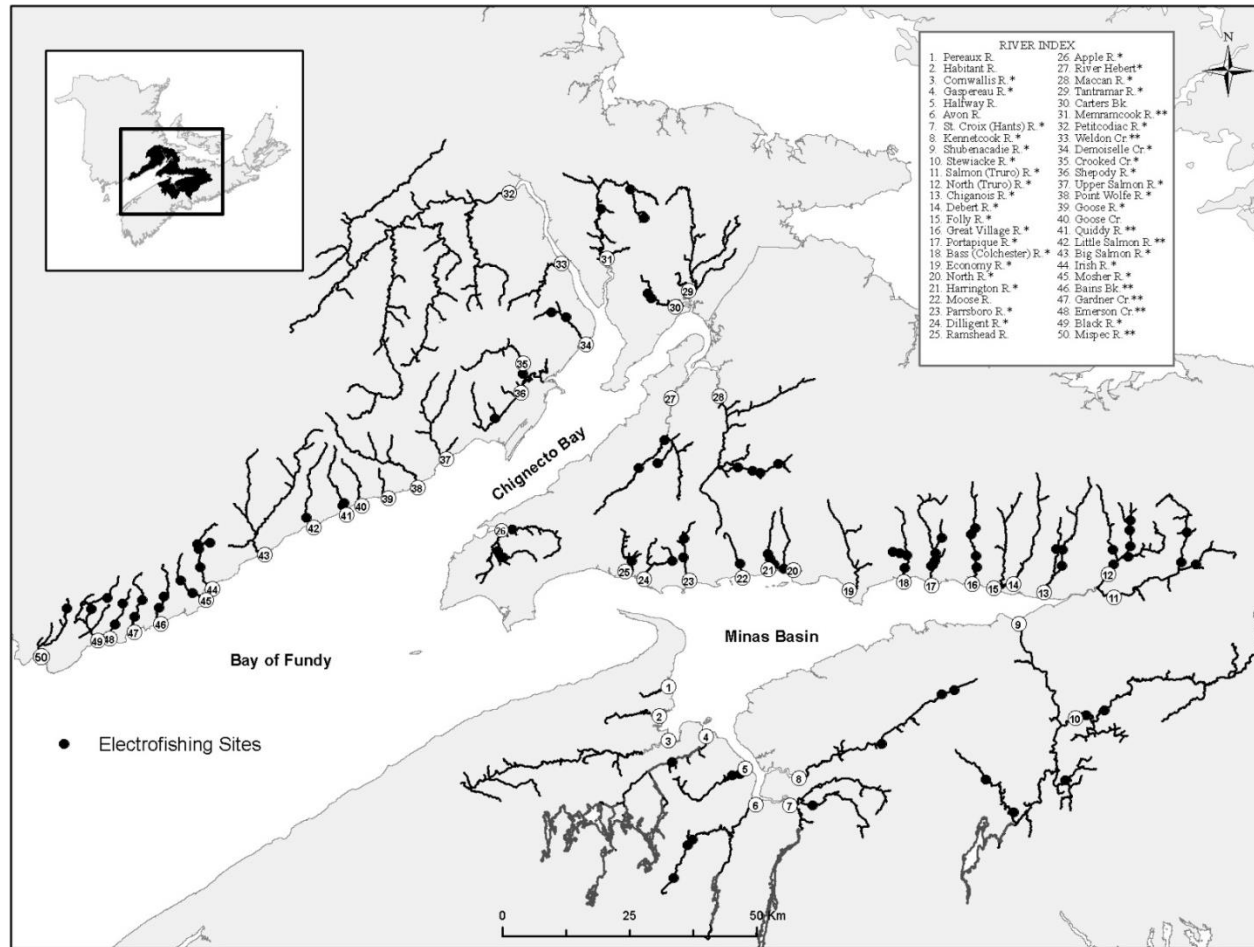


Figure 1. The locations of the Inner Bay of Fundy (IBoF) Atlantic Salmon designatable unit (DU) and the fifty (50) IBoF rivers in the Recovery Strategy (DFO 2010). The rivers marked with an asterisk (*) supported self-sustaining Atlantic Salmon populations, as suggested by recreational catch and historical electrofishing data. The double asterisk (**) identified rivers are reported to have produced salmon.

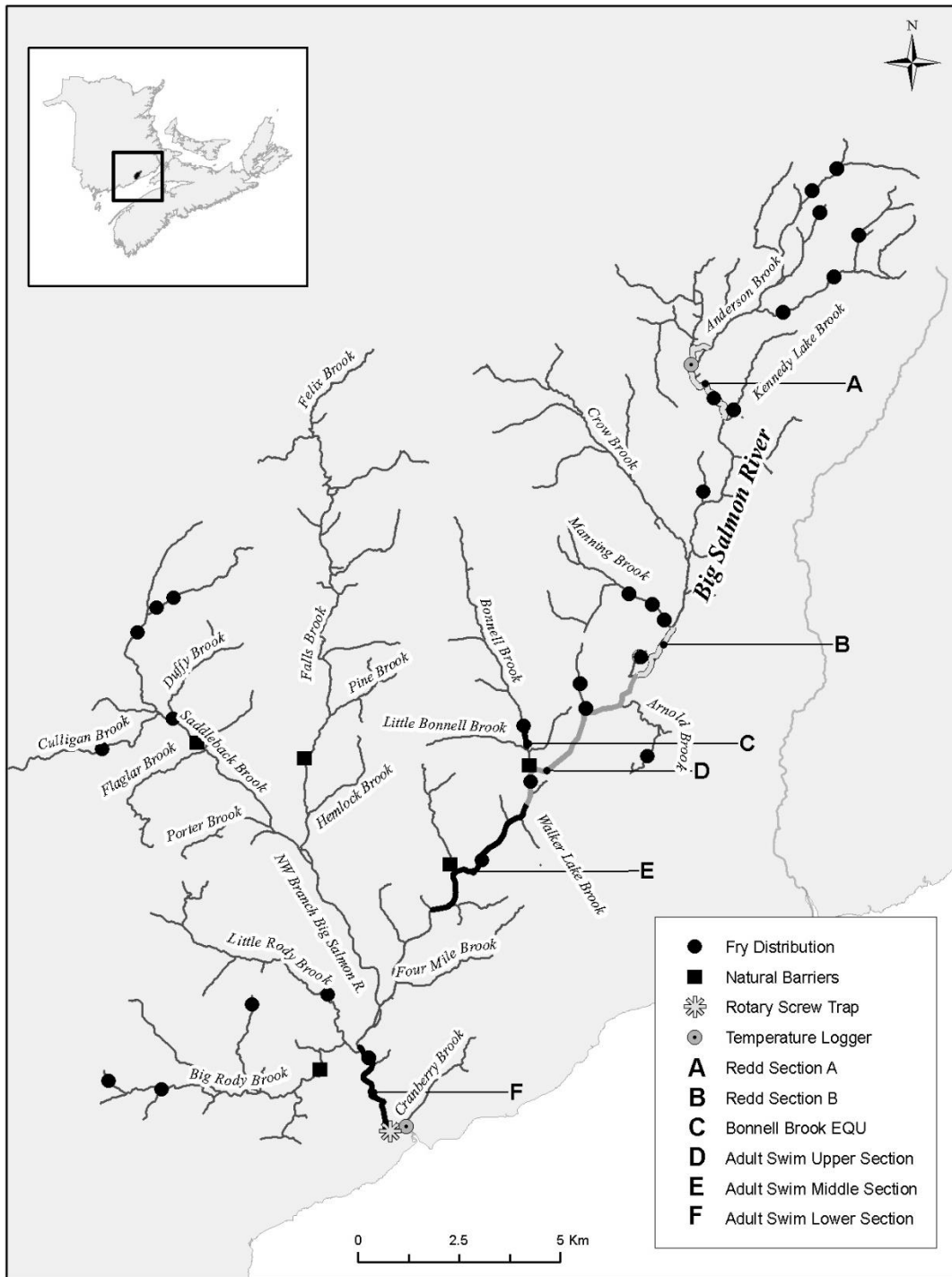


Figure 2. Map of assessment efforts on the Big Salmon River, New Brunswick (NB) showing locations of fry distribution sites [general (solid black circle) and equalized (EQU; bold C, solid black line)], natural barriers (solid black square), rotary screw trap operations (grey asterisk), temperature loggers (solid grey circle with solid black inner circle), adult swim surveys [upper (bold D, solid grey line), middle (bold E, solid black line), lower (bold F, solid black line)] and redd surveys [section A (bold A, solid light grey line with black outline) and section B (bold B, solid light grey line with black outline)].

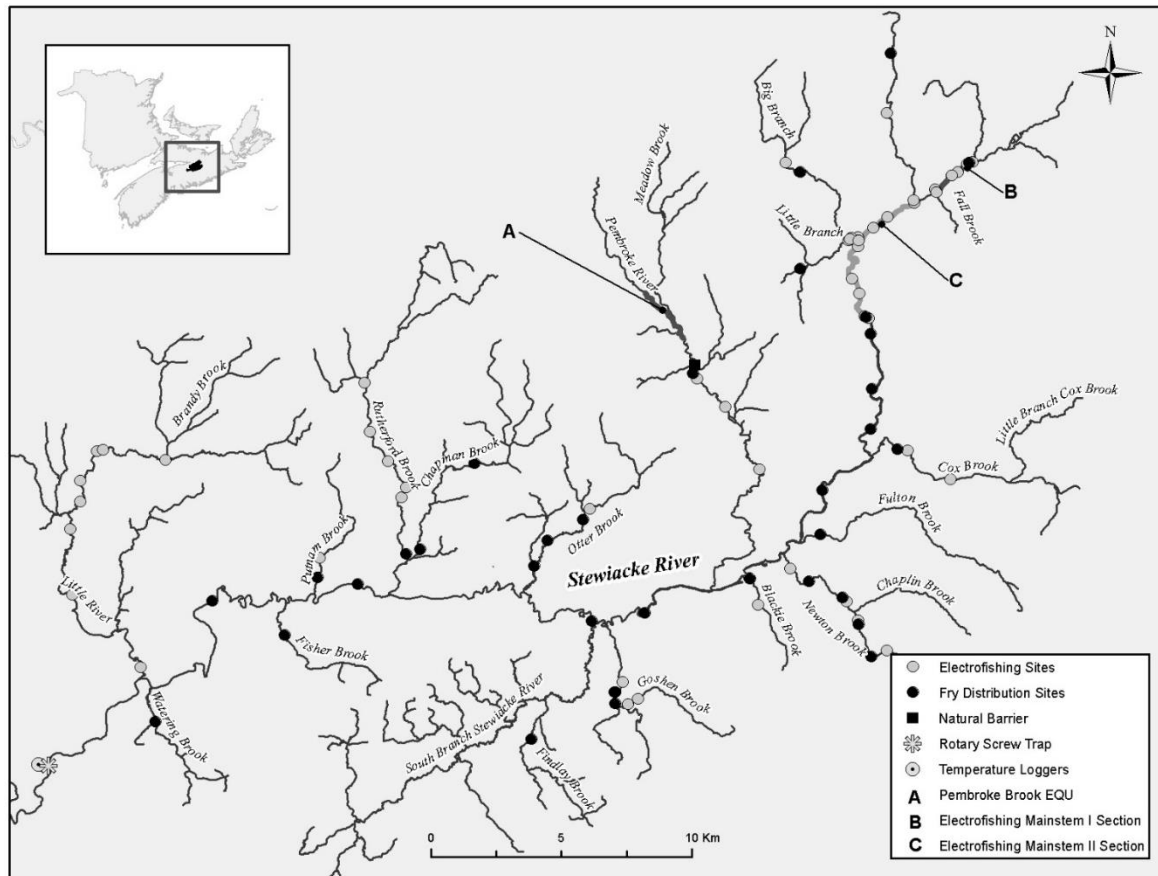


Figure 3. Map of assessment efforts on the Stewiacke River, Nova Scotia (NS) showing locations of fry distribution sites [general (solid black circle) and equalized (EQU; bold A, solid black line), natural barriers (solid black square), temperature loggers (solid grey circle with solid black inner circle), rotary screw trap operations (grey asterisk), and electrofishing sites (solid grey circle)] and surveys [section I (bold B, dark grey line) and section II (bold C, light grey line)].

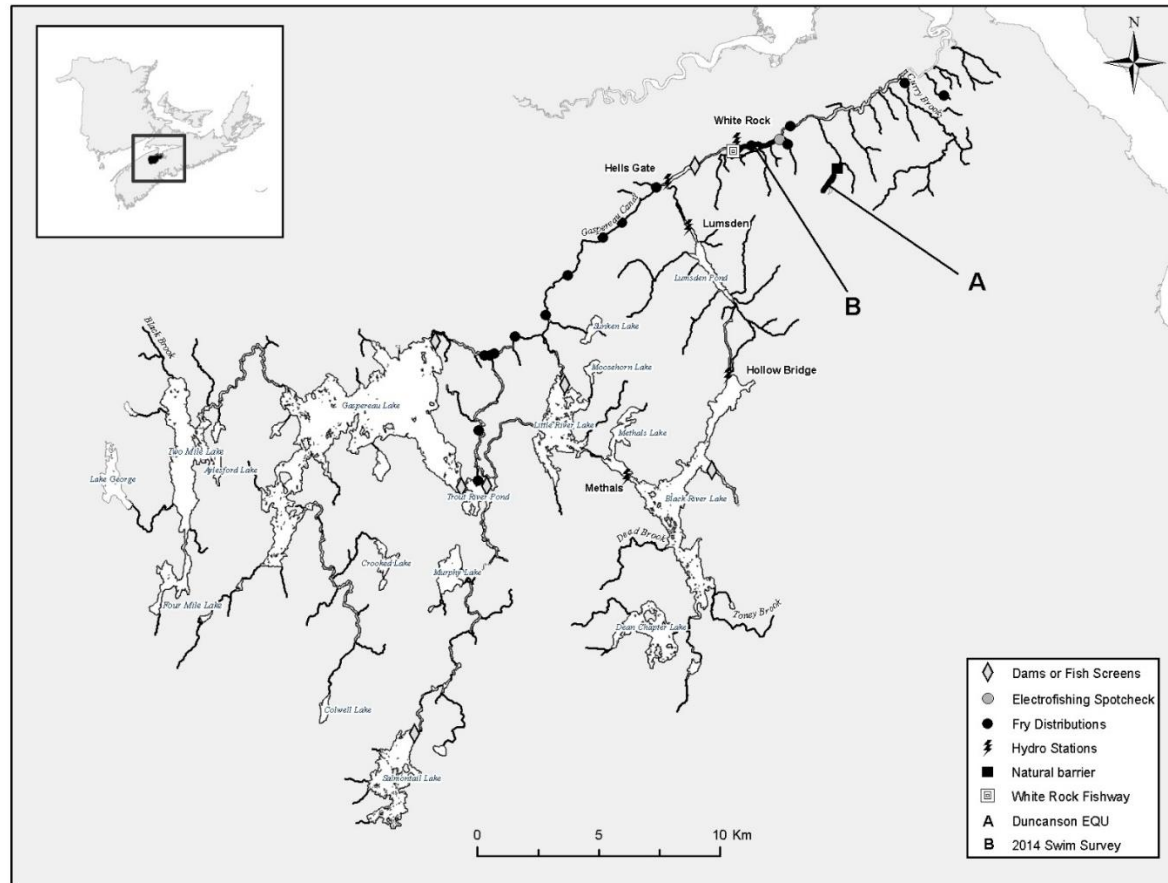


Figure 4. Map of assessment efforts on the Gaspereau River, Nova Scotia (NS) showing locations of hydroelectric landmarks [dams/fish screen (white diamond), hydro station (black zigzag), and White Rock fishway (grey square)], fry distribution sites [general distribution (solid black circle) and equalized (EQU; bold A, solid black line)], natural barriers (solid black square), temperature loggers (solid grey circle with solid inner black circle), electrofishing sites (solid grey circle), adult swim survey (bold B, solid black line).

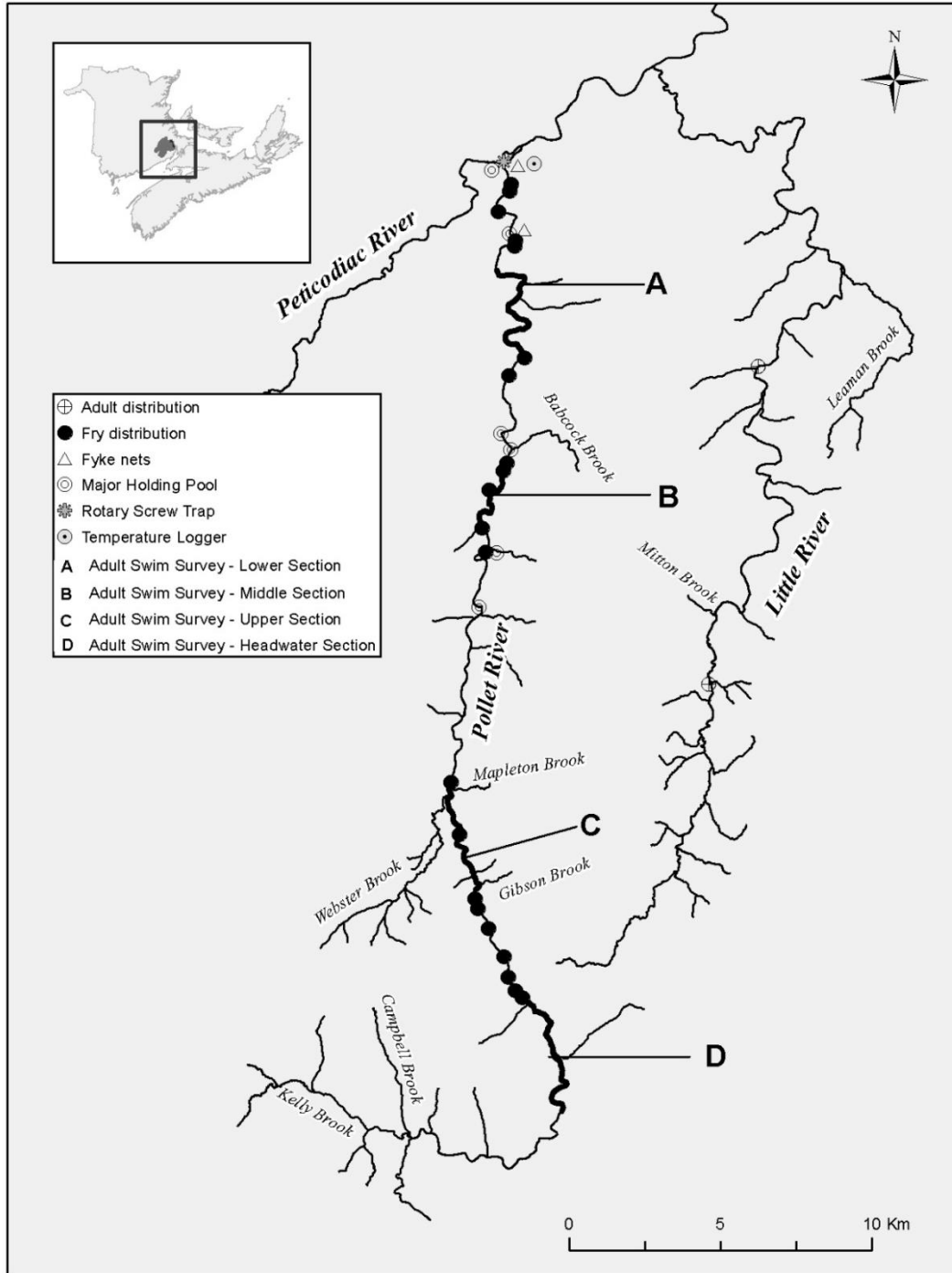


Figure 5. Map of assessment efforts on the Pollet River and Little River (Petitcodiac River watershed), New Brunswick (NB) showing locations of fry (solid black circle) and adult (solid white circle with black cross) distribution sites, fyke net (solid white triangle) and rotary screw trap operations (grey asterisk), temperature loggers (solid grey circle with solid inner black circle), and adult swim surveys [upper (bold A, solid black line), middle (bold B, solid black line), lower (bold C, solid black line), headwater sections (bold D, solid black line)].

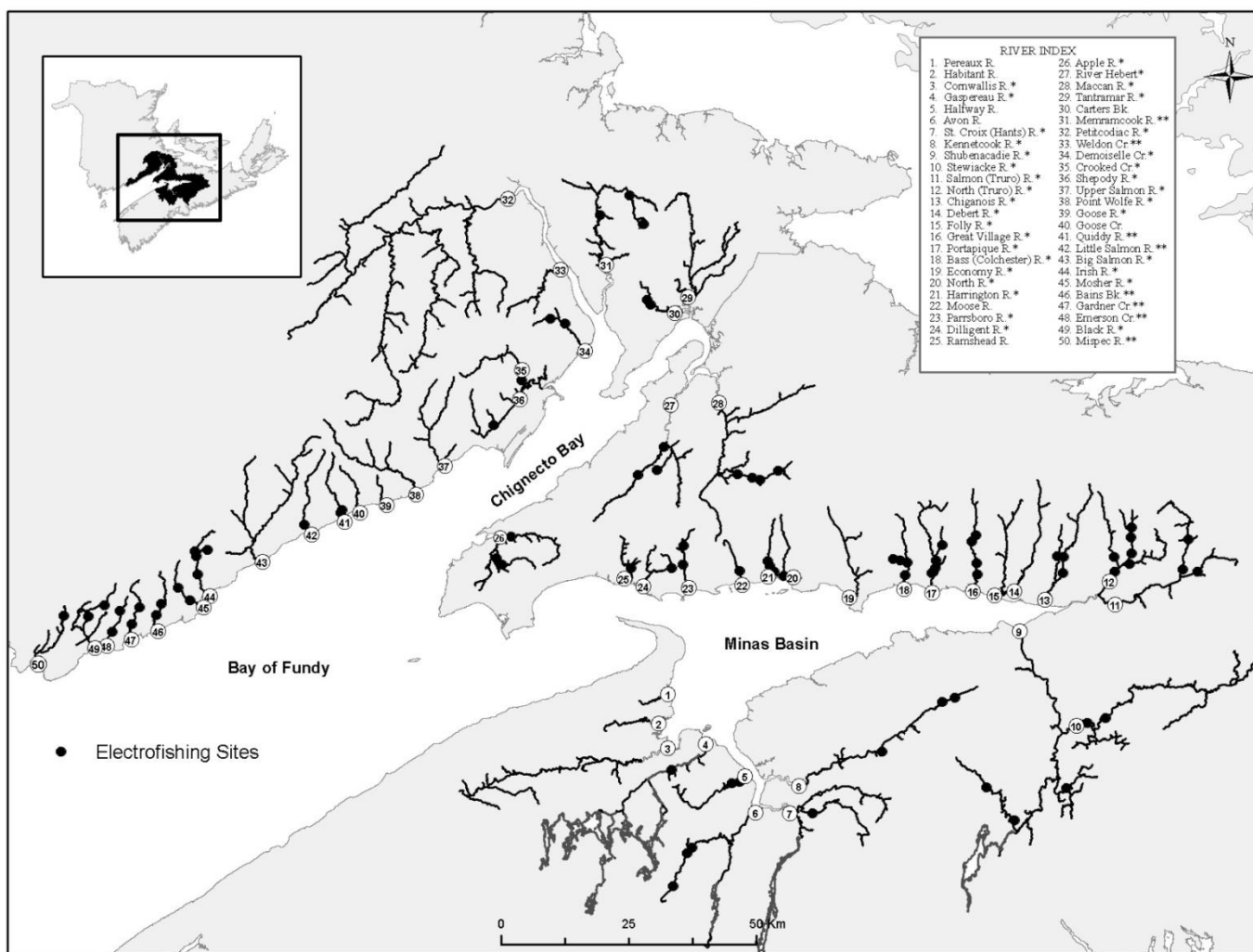


Figure 6. Map of the sites sampled via electrofishing surveys (solid black circles) on Inner Bay of Fundy (IBoF) rivers where salmon have historically been observed during the IBoF Broadscale Electrofishing survey in 2014. The rivers marked with an asterisk (*) supported self-sustaining Atlantic Salmon populations, as suggested by recreational catch and historical electrofishing data. The double asterisk (**) identified rivers are reported to have produced salmon.

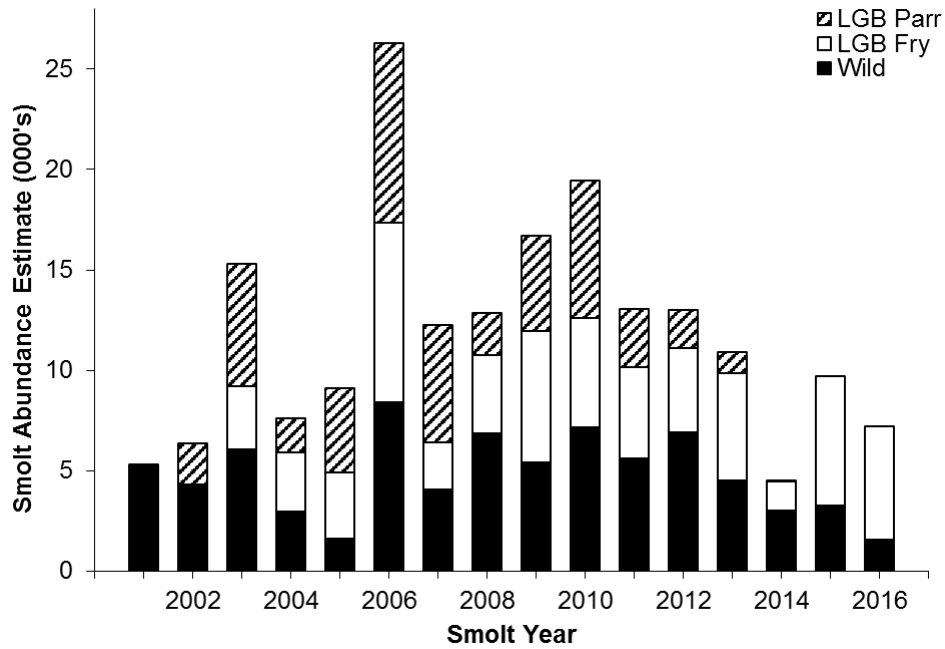


Figure 7. Estimates of Big Salmon River smolt abundance (000's) by origin from 2001 to 2016.

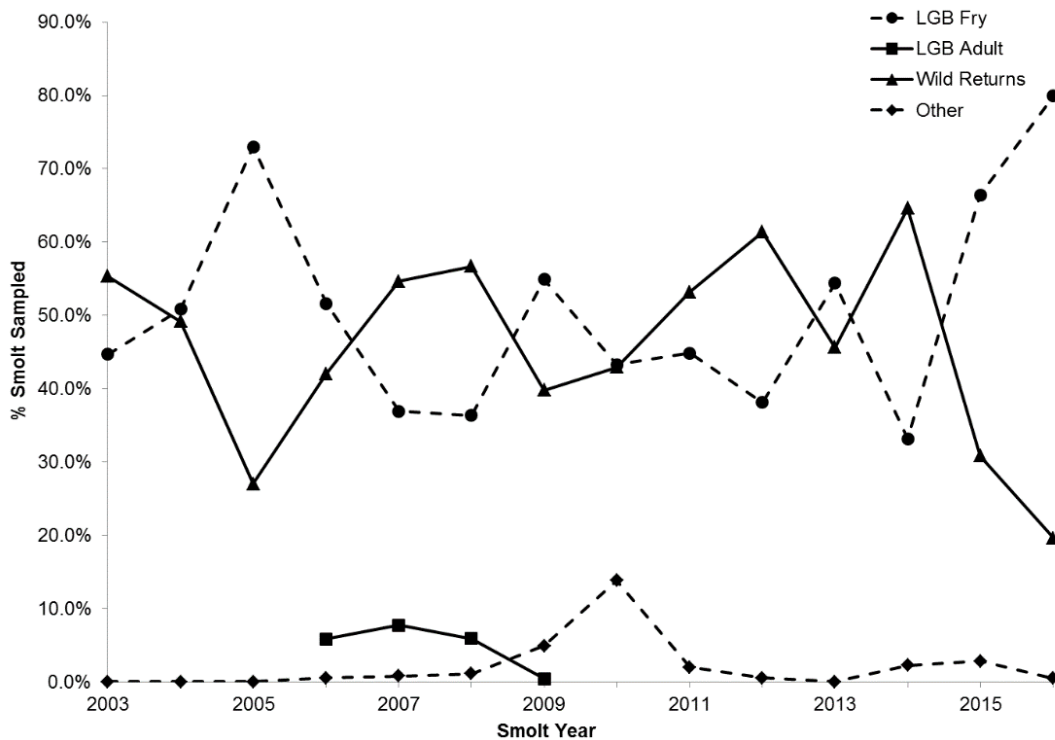


Figure 8. Genetic parentage analysis to determine origin of the Big Salmon River-emigrating non-adipose clipped smolts sampled from 2003 to 2016. 'Wild returns' are a combination of those smolts that assign to previous adult returns (i.e., sampled during assessment activities) and those that do not assign to any parents in the Live Gene Bank database.

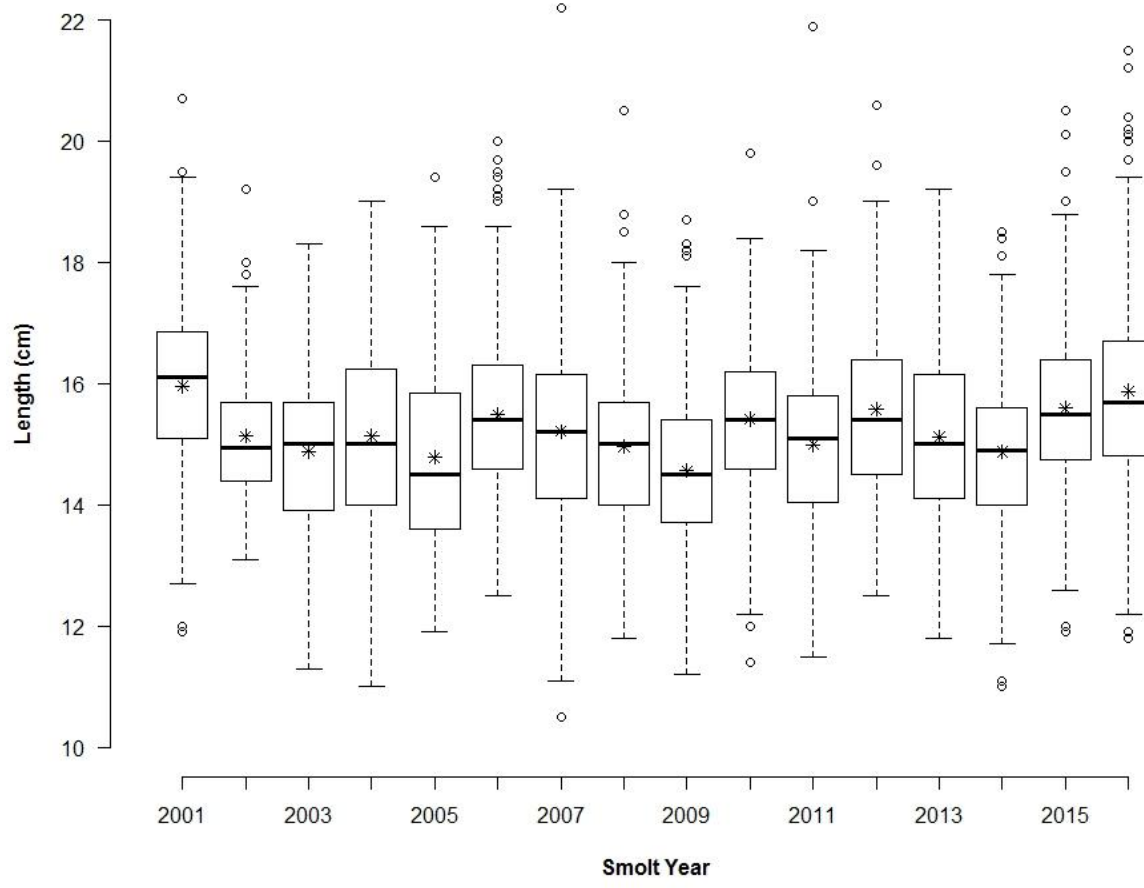


Figure 9. Box plot summarizing the variation in wild/LGB_{FRY} smolt lengths measured at the Big Salmon River Rotary Screw Trap from 2001 to 2016, showing the median and the 25th and 75th percentiles. Error bars represent the 10th and 90th percentiles, with outliers denoted as circles. The black asterisk represents the mean.

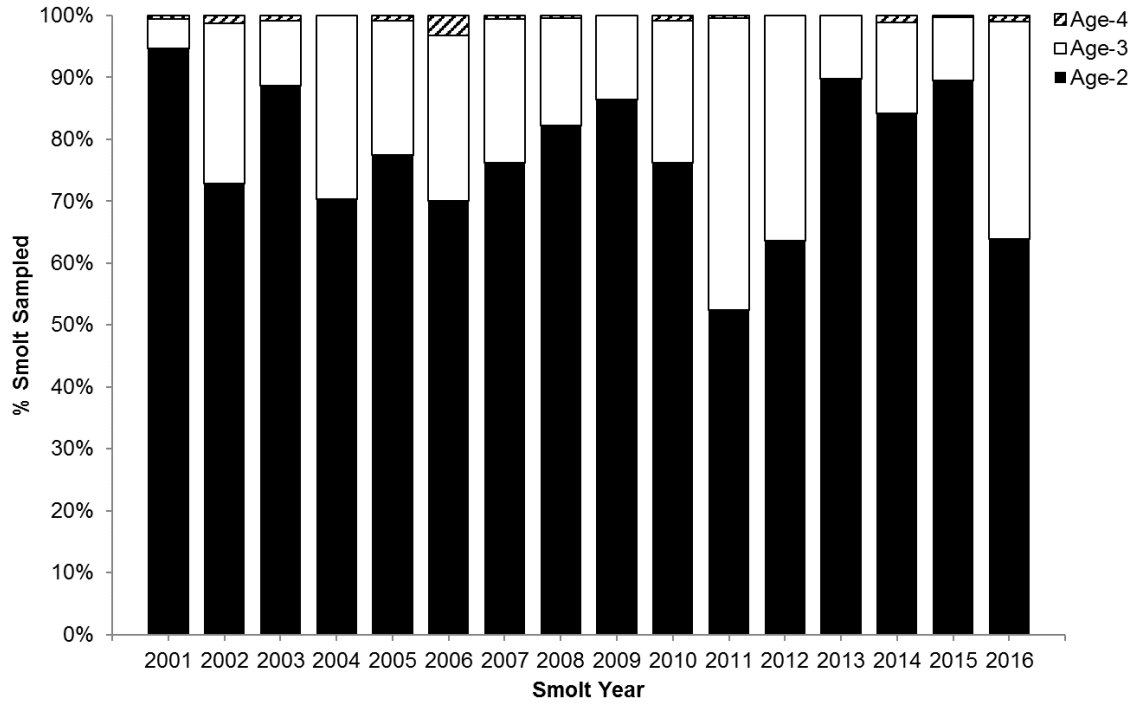


Figure 10. Big Salmon River wild and/or Live Gene Bank fry-origin smolt age proportions as determined by scale analysis from 2001 to 2016. Scale sampling at the Big Salmon River includes all smolt collected for the LGB (wild/LGB_{FRY} origin), as well as a proportion of LGB_{PARR}.

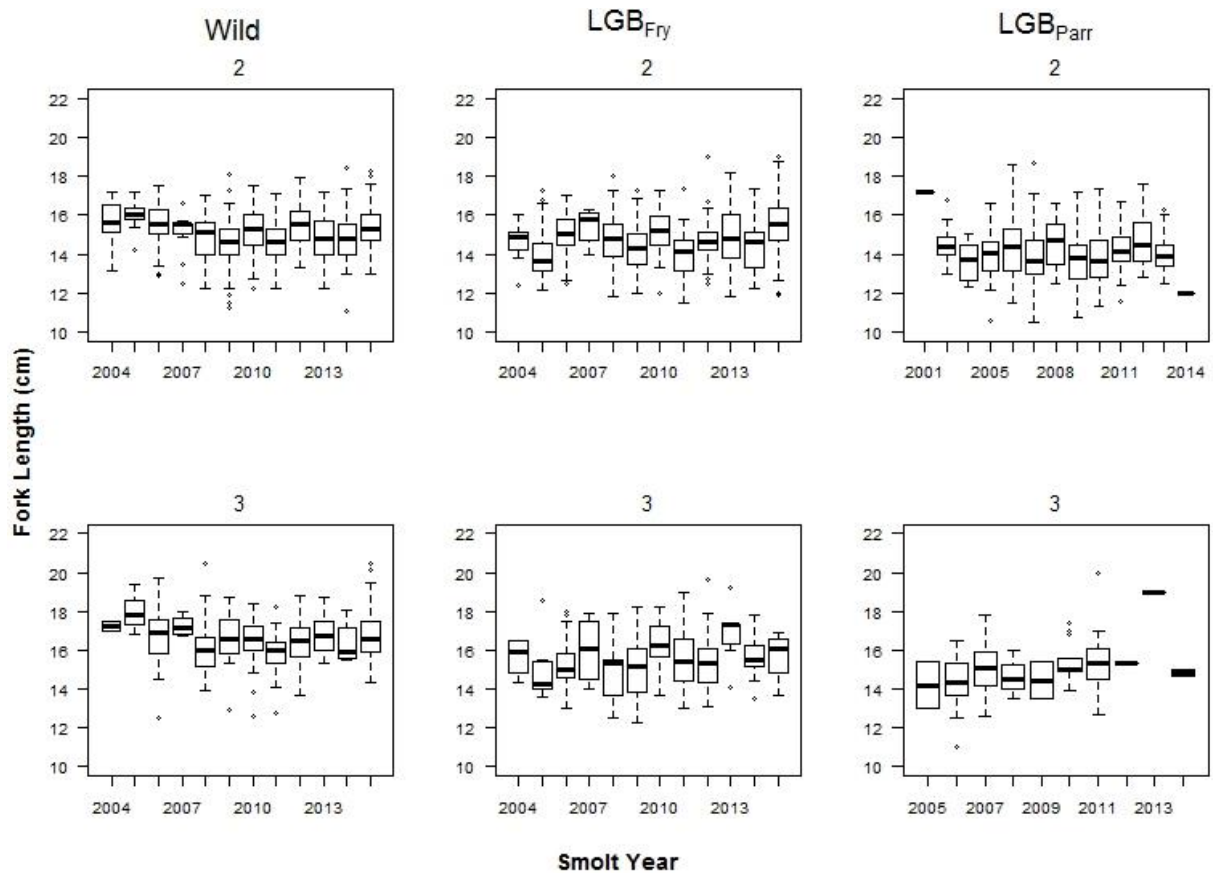


Figure 11. Length boxplot of Big Salmon River wild, LGB_{Fry} and LGB_{Parr} smolt by age class from 2001 or 2004 to 2015, as determined by scale analysis.

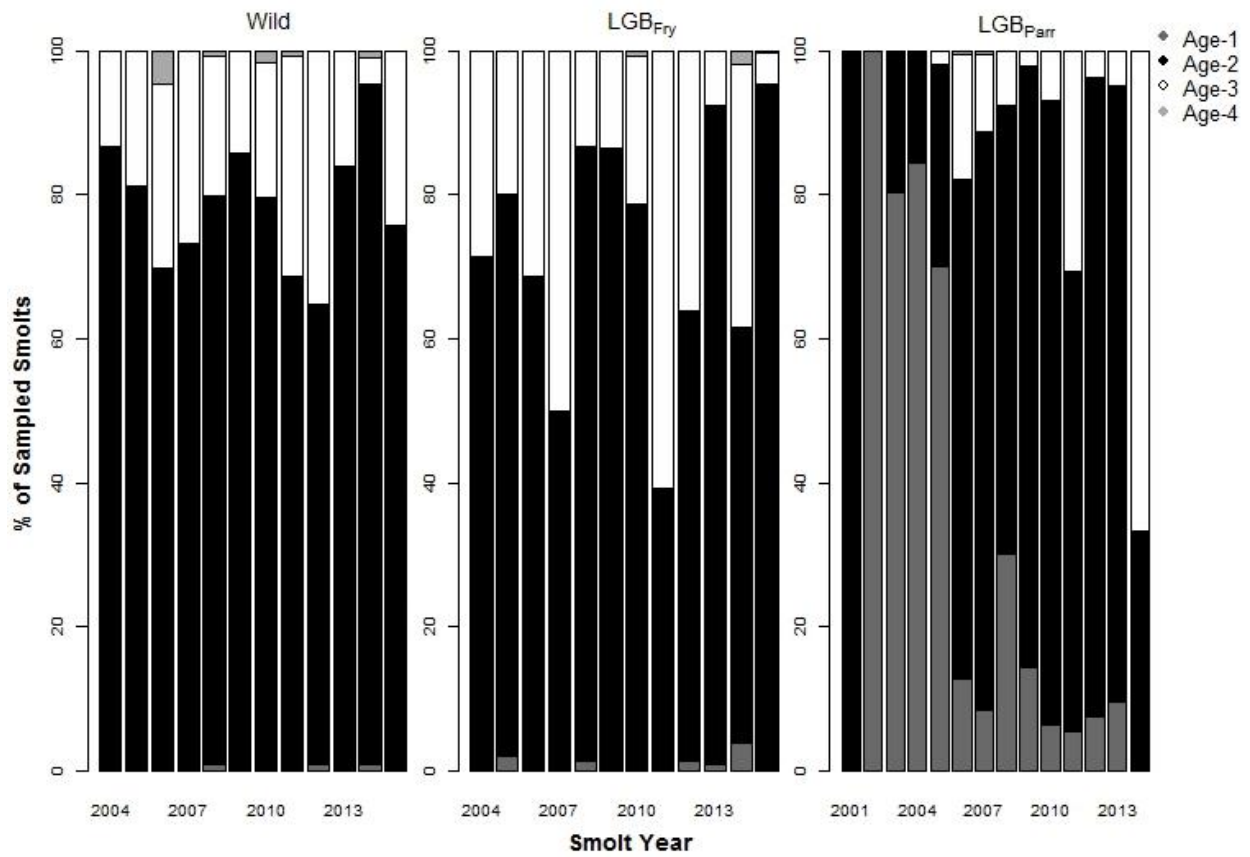


Figure 12. Summary of the age proportions of Big Salmon River wild, LGB_{FRY} and LGB_{PARR} smolt as determined by scale analysis. The Age-1 wild and LGB_{FRY} smolts were likely unclipped LGB_{PARR} releases and not wild produced.

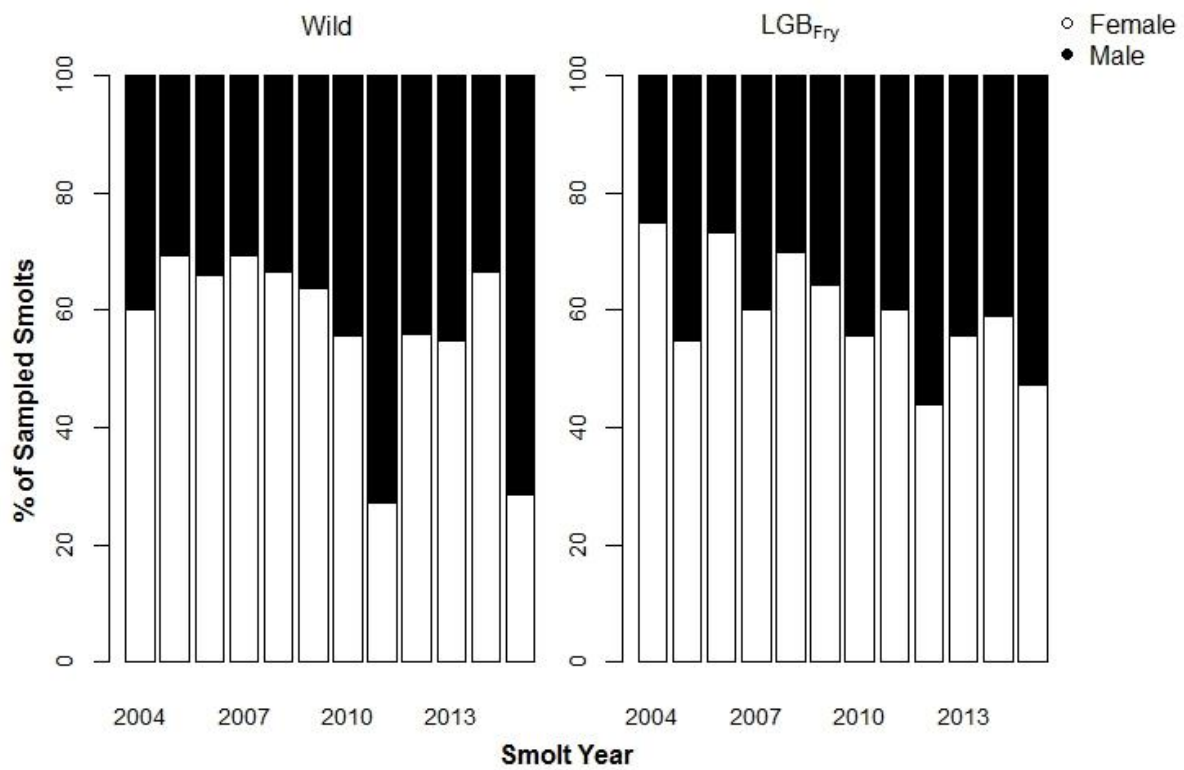


Figure 13. Summary of the Big Salmon River wild and LGB_{Fry} smolt sex proportions from 2004 to 2015.

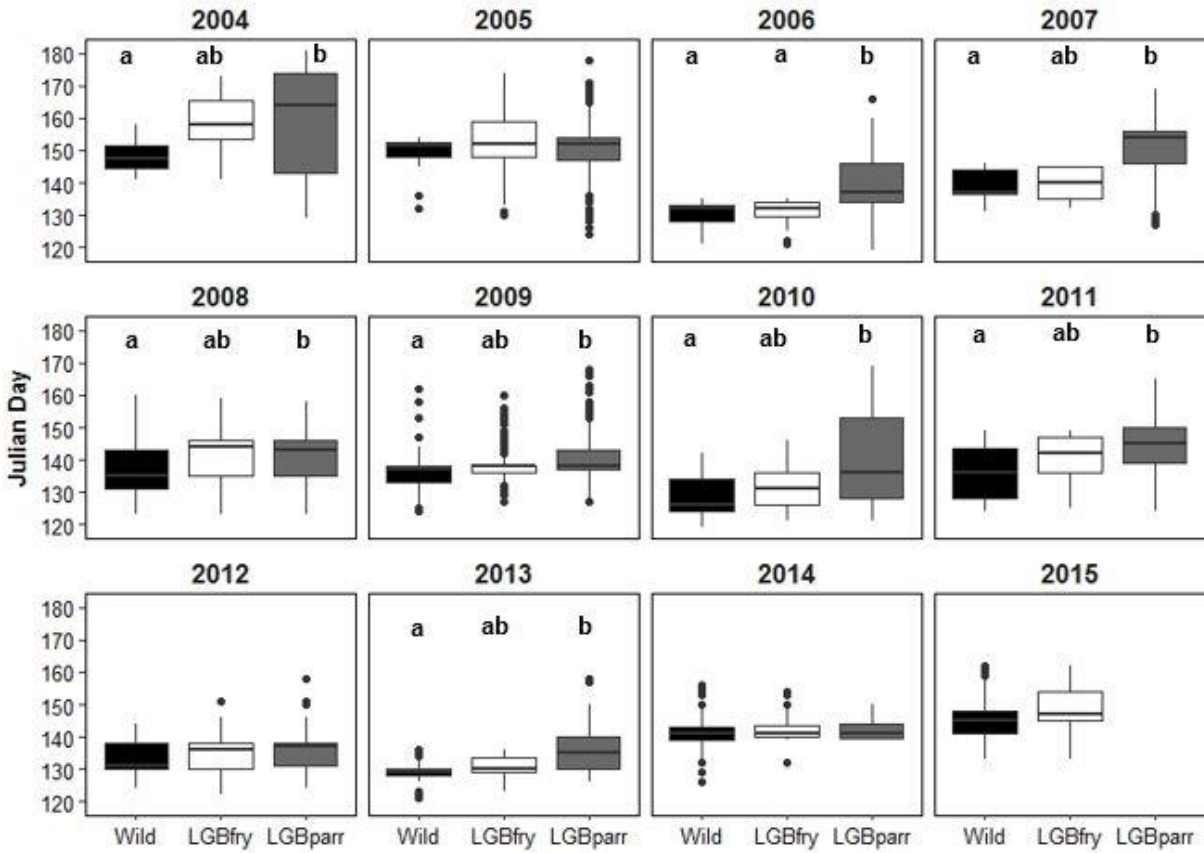


Figure 14. Summary of the Big Salmon River smolt emigration trend, for each available year, comparing the wild (black), LGB_{FRY} (white), and LGB_{PARR} (grey) origin smolt. Letters denote which groups are significantly different.

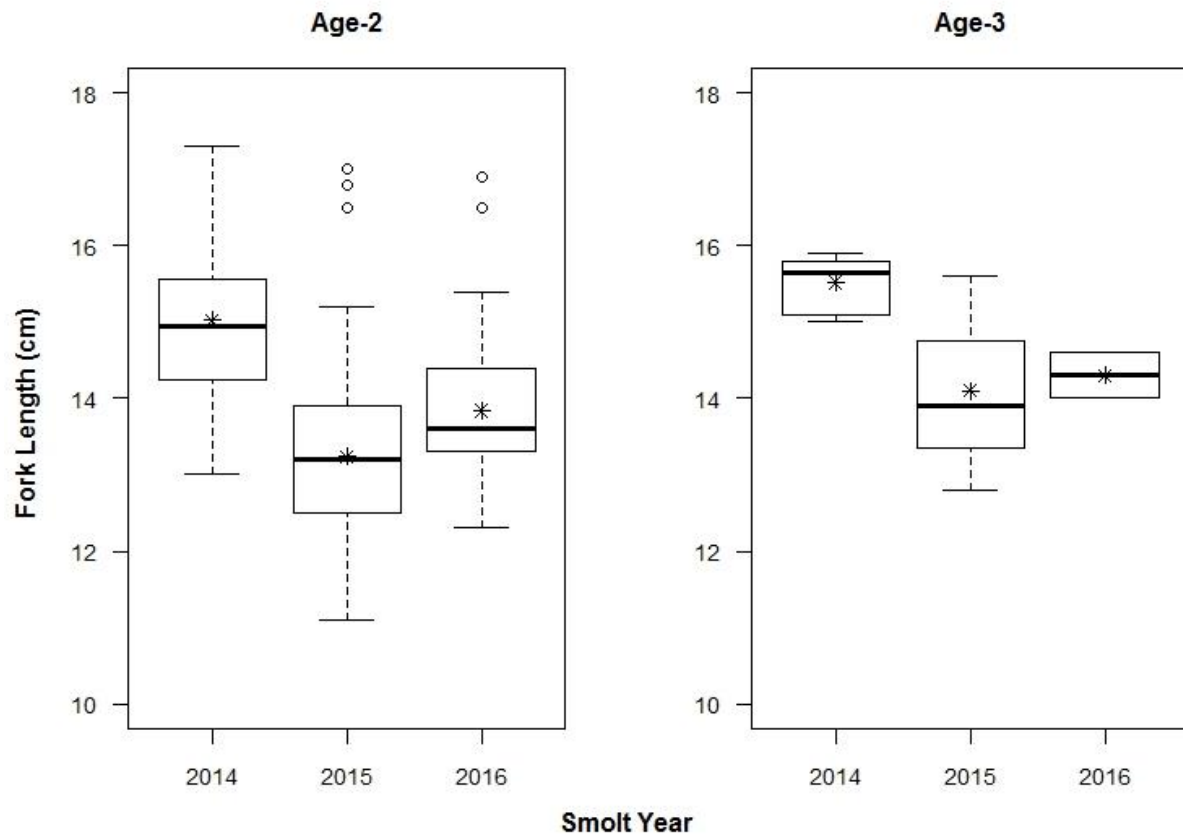


Figure 15. Length boxplot of Stewiacke River wild or LGB_{FRY} origin smolt by age class from 2014 to 2016, as determined by scale analysis. Sample sizes available for the Age-3 category were minimal ($n = 12$).

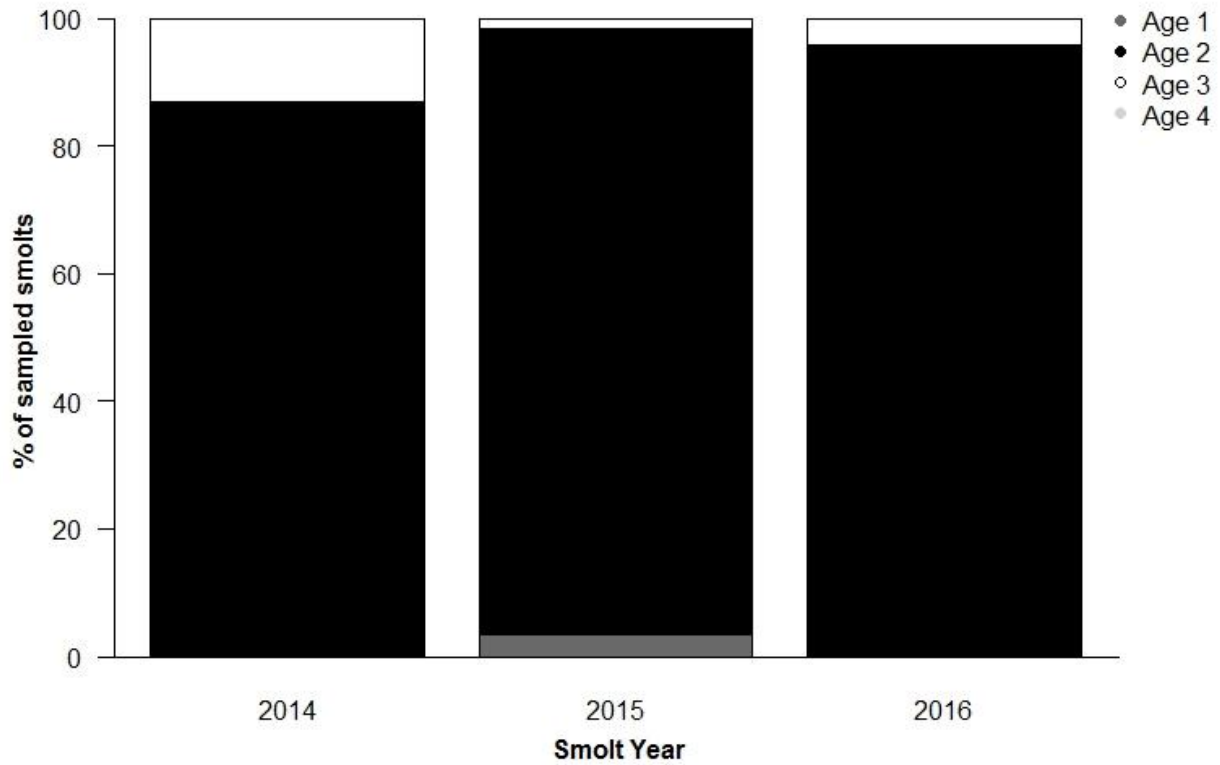


Figure 16. Summary of the sampled Stewiacke River wild or LGB_{FRY} smolt age proportions as determined by scale analysis, from 2014 to 2016. The Age-1 smolts were likely unclipped LGB_{PARR} releases and not wild produced.

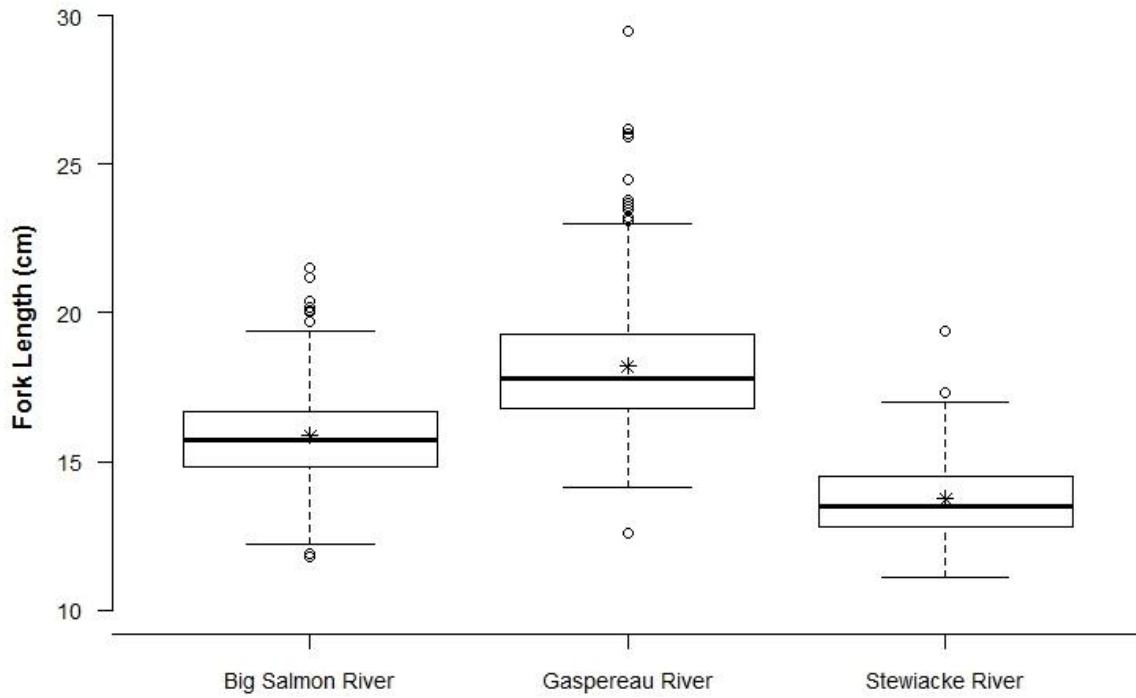


Figure 17. Boxplot of the wild- or LGB unfed fry-origin smolt lengths among the Gaspereau (2016), Big Salmon (2016), and Stewiacke (2014-2016) rivers. Black asterixes represent mean smolt length for each river.

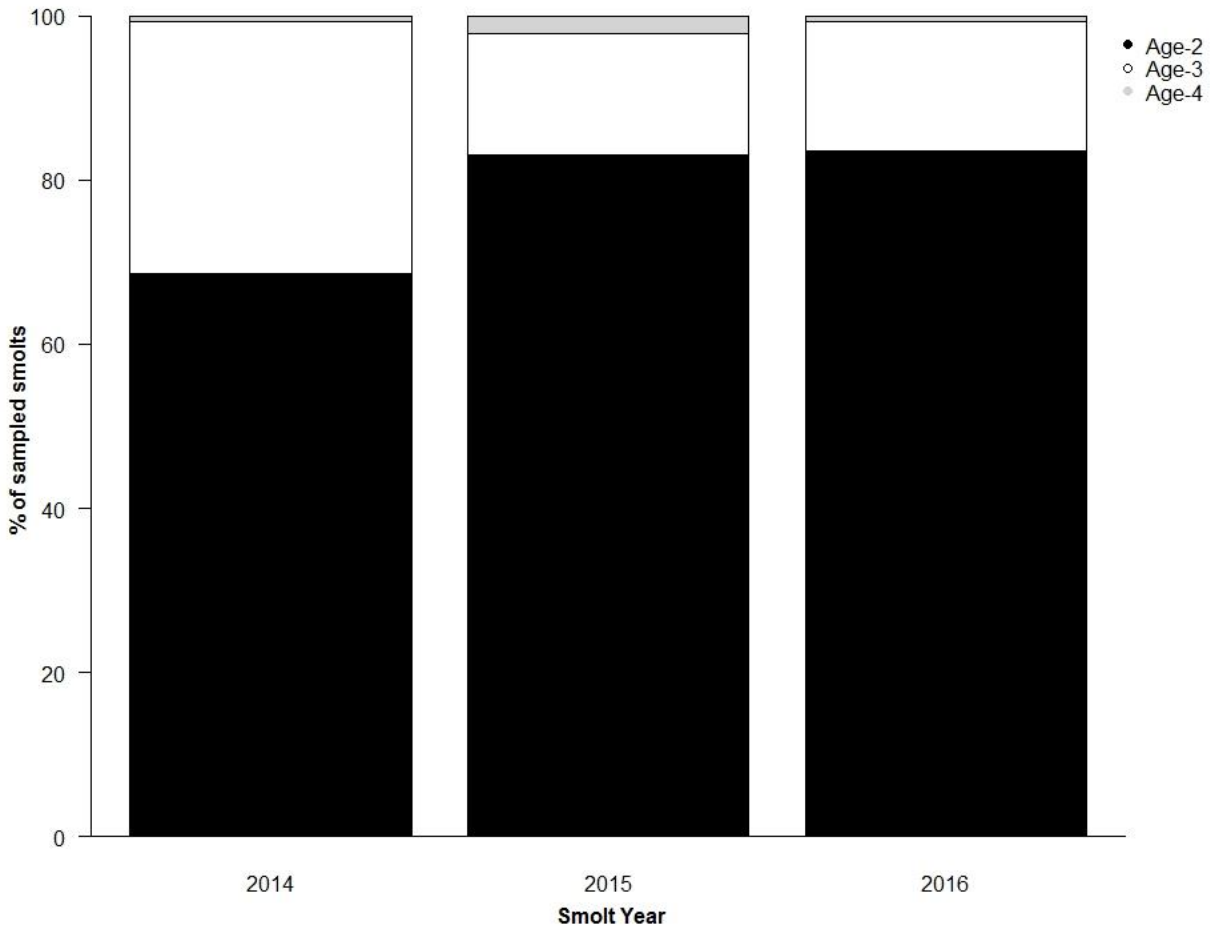


Figure 18. Summary of the age proportions for sampled Gaspereau River wild-or LGB_{FRY}-origin smolt, as determined by scale analysis, from 2014 to 2016.

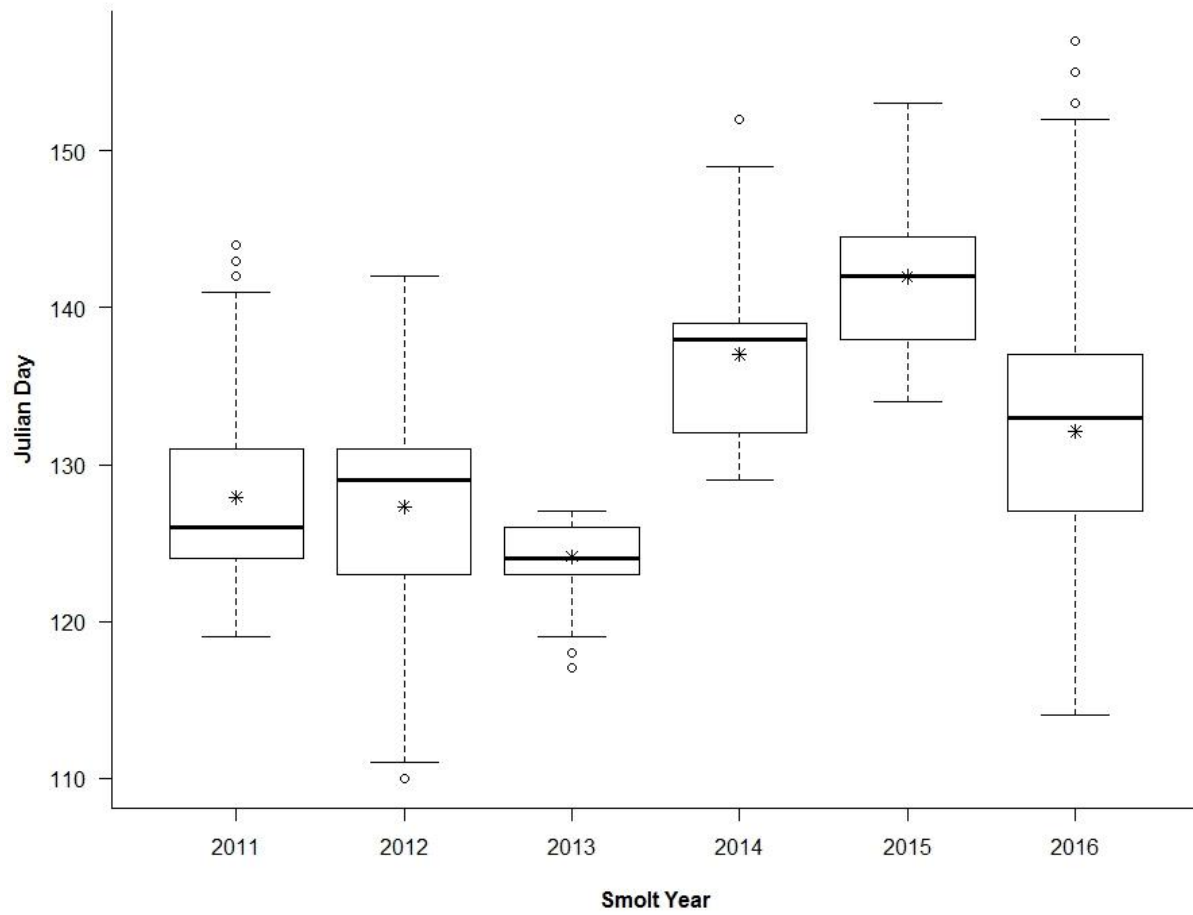


Figure 19. Boxplot of the Gaspereau River wild-or LGB_{FRY}-origin smolts emigration pattern from 2011 to 2016. Black asterisks represent mean emigration date.

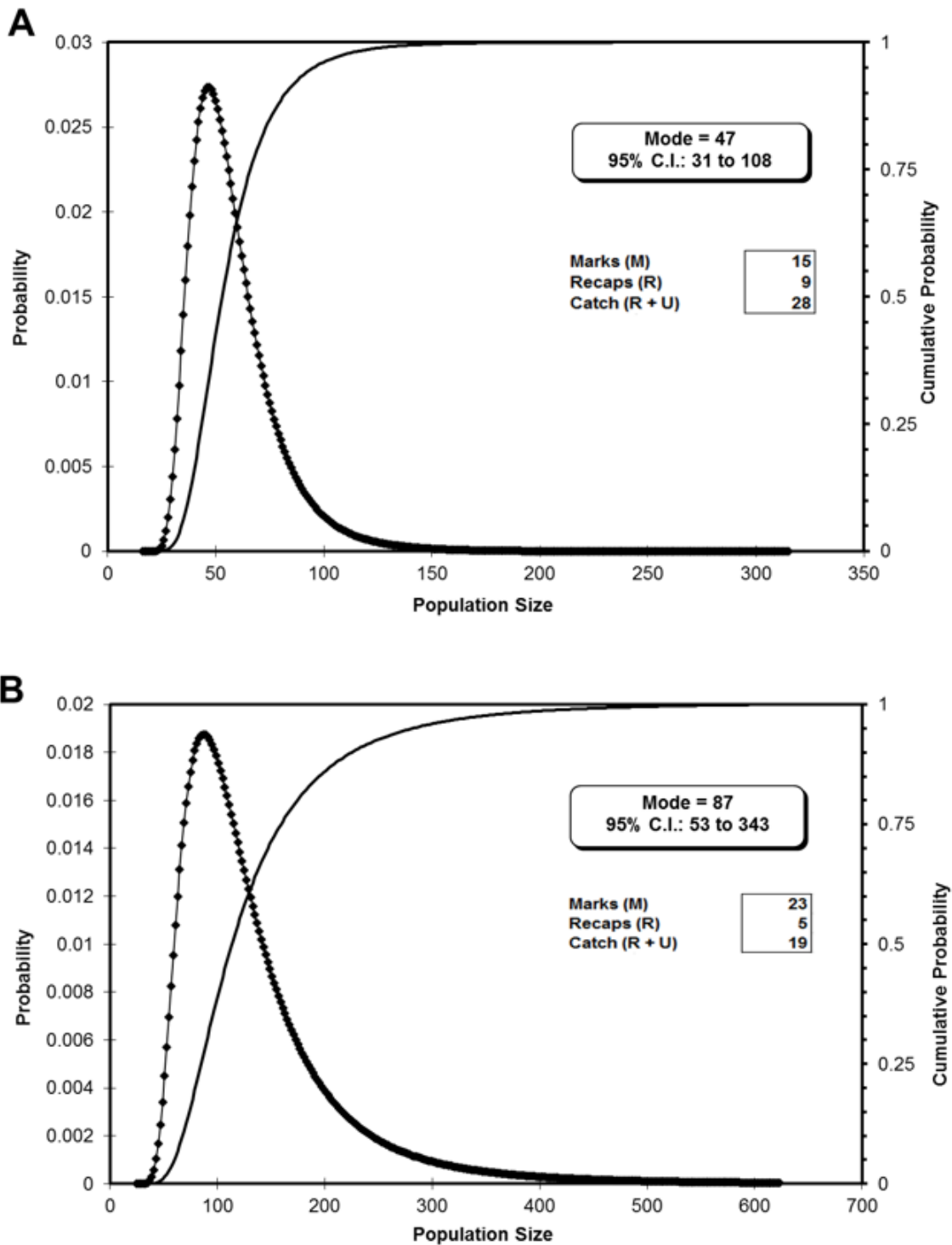


Figure 20. Probability density (solid line with solid black circles) and cumulative probability (solid black line) of a Bayesian analysis based on an adjusted Peterson estimate from mark-recapture data, for the number of total (small and large combined) salmon returning to Big Salmon River in a) 2007 and b) 2010.

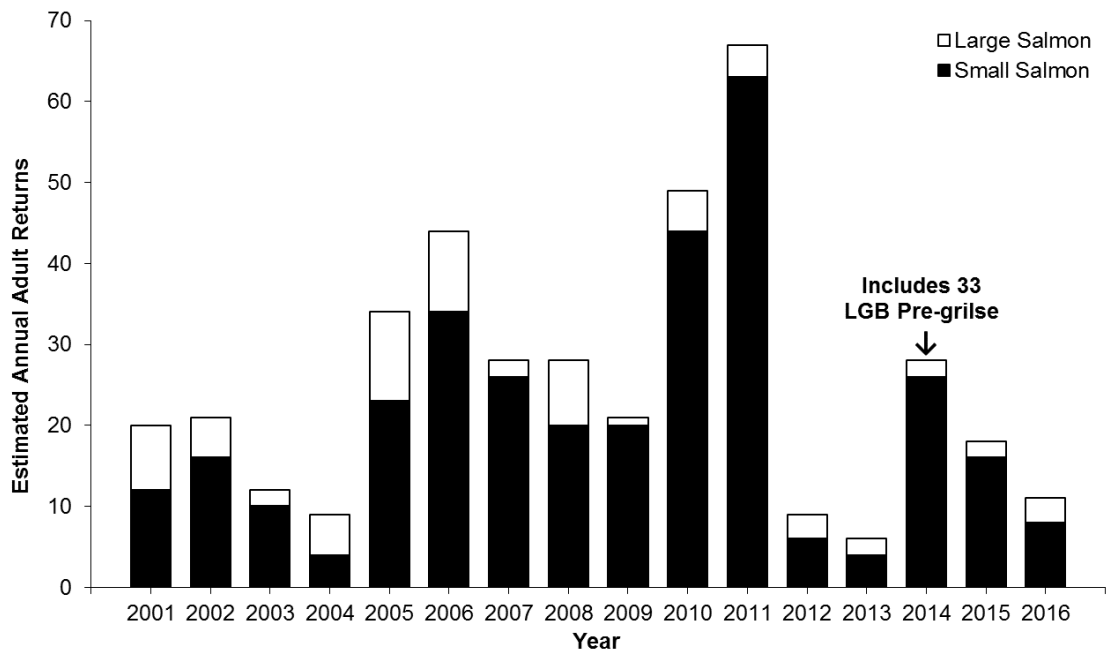


Figure 21. Estimated Big Salmon River small (solid white) and large (solid black) adult salmon returns from 2001 to 2016.

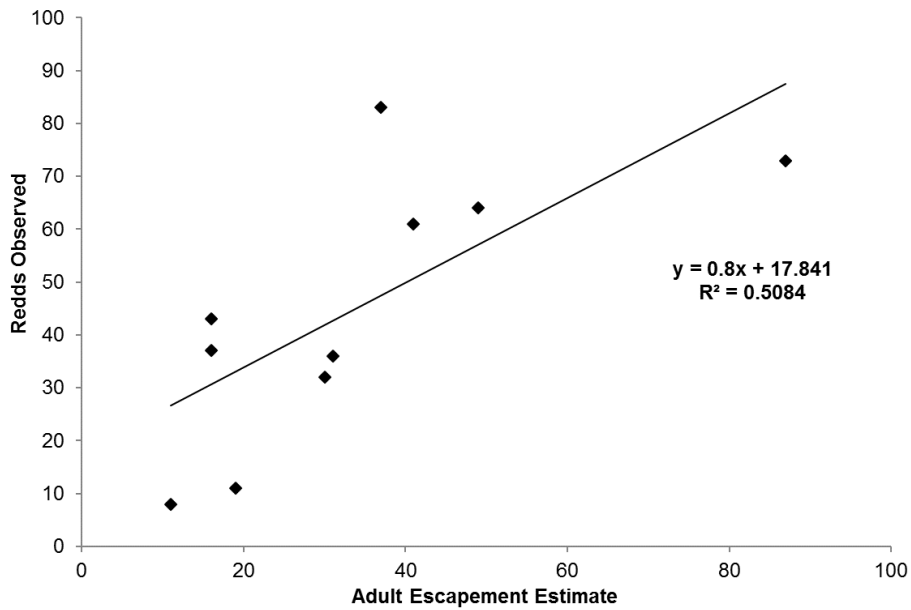


Figure 22. Relationship between total redds observed during the Big Salmon River redd survey (section B; from Manning to King pools) and total adult escapement abundance estimate from 2000 to 2016 (when assessment data is available).

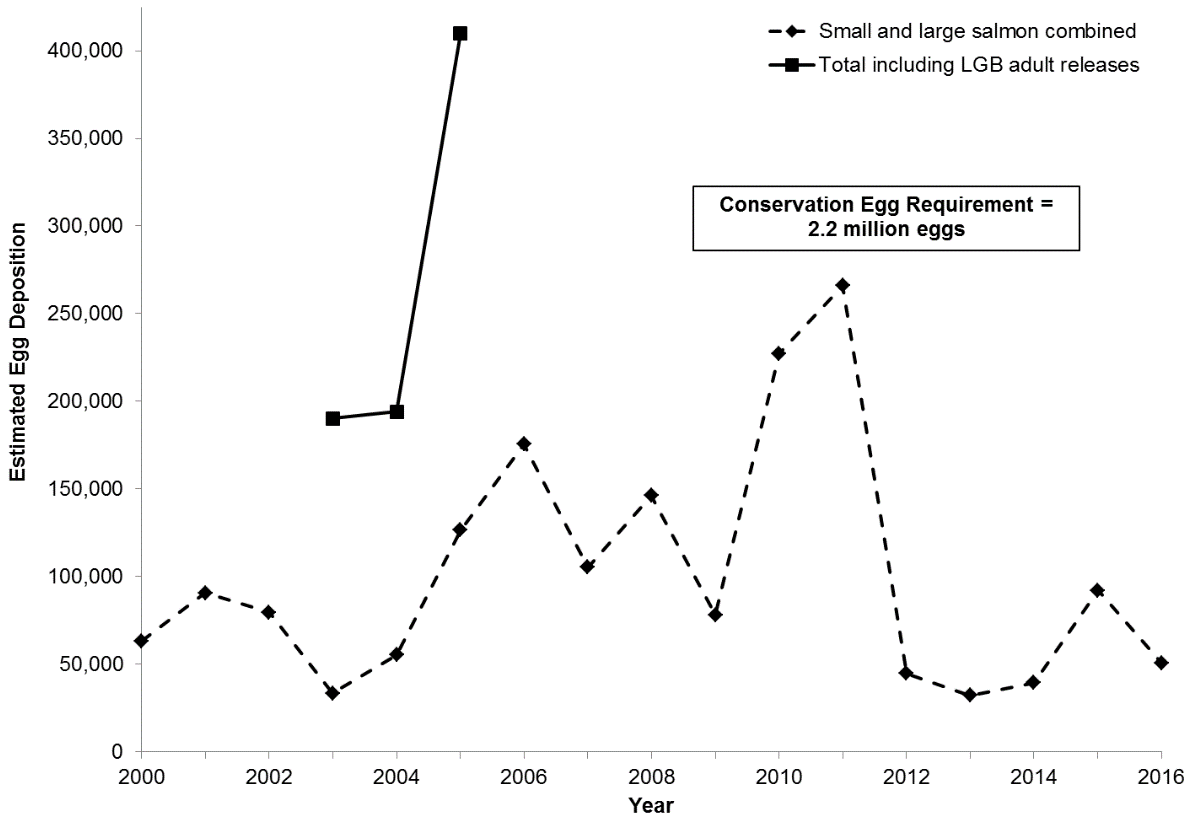


Figure 23. Estimated egg deposition on the Big Salmon River from 2000 to 2016.

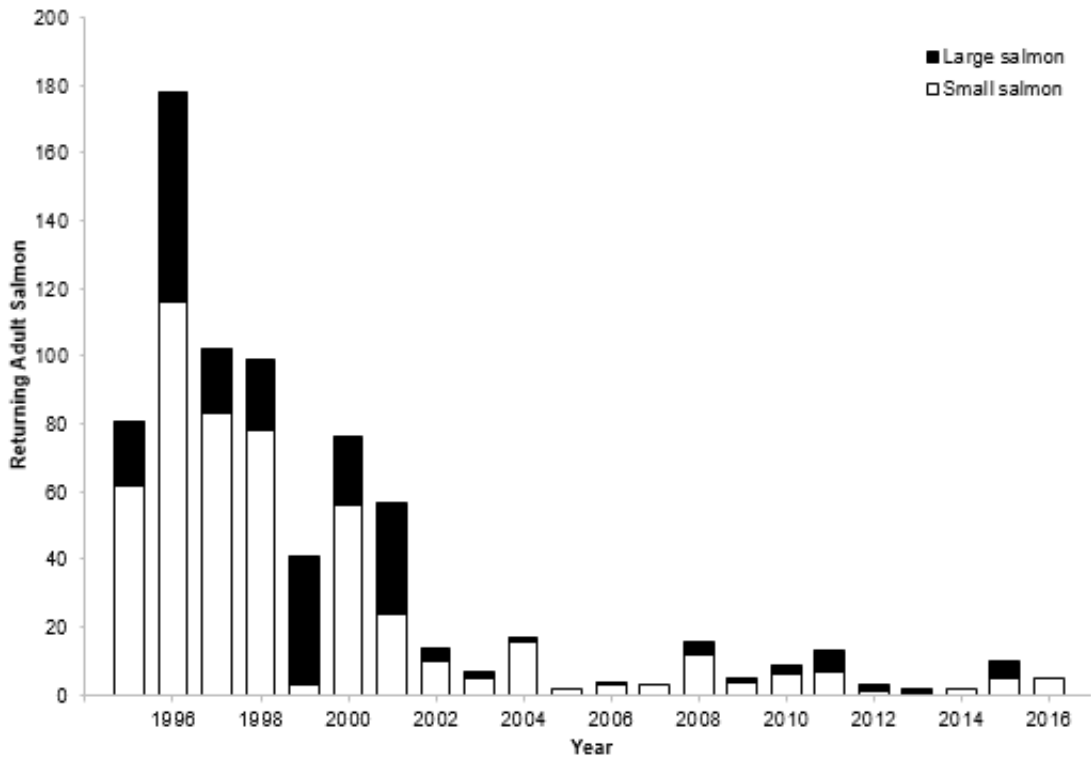


Figure 24. Gaspereau River small and large salmon counts to the White Rock Dam fishway from 1995 to 2016.

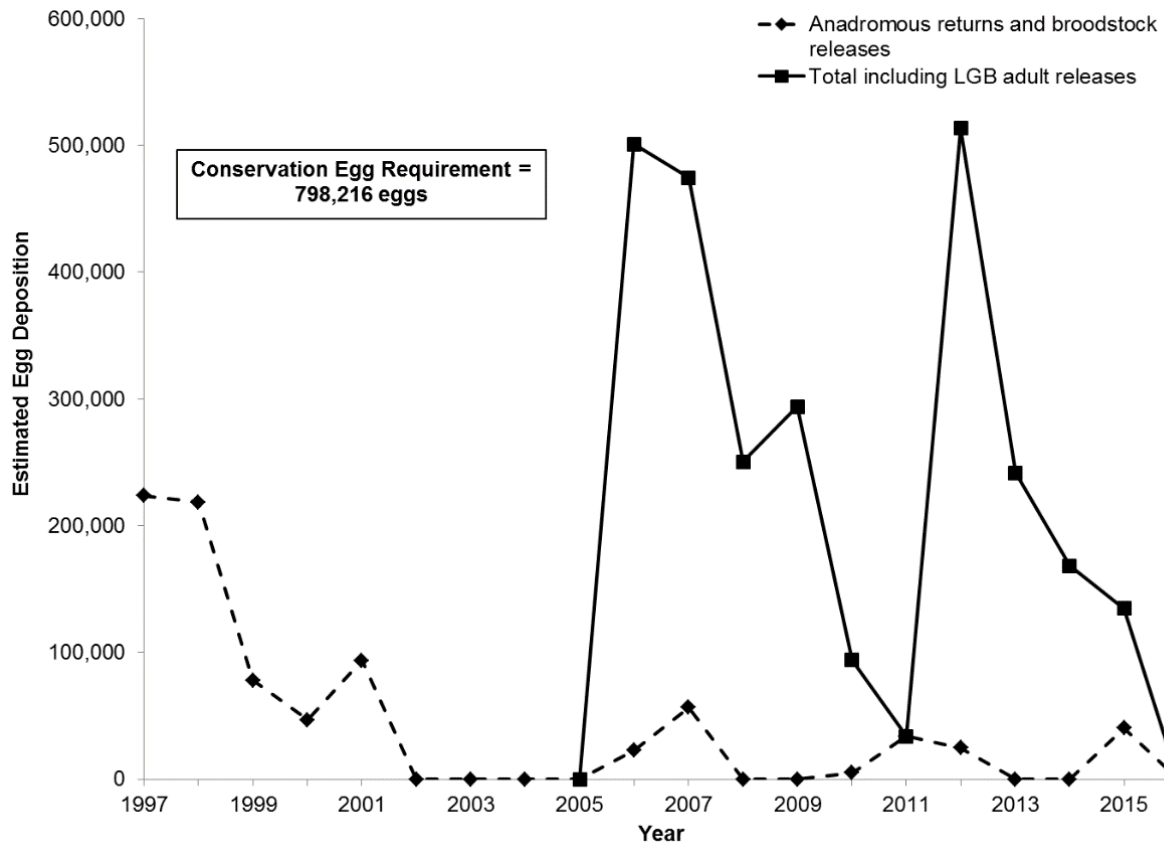


Figure 25. Estimated Gaspereau River salmon egg deposition with contributions from anadromous returns, surplus anadromous broodstock and non-targeted Live Gene Bank adults released upriver of the White Rock Dam from 1997 to 2016.

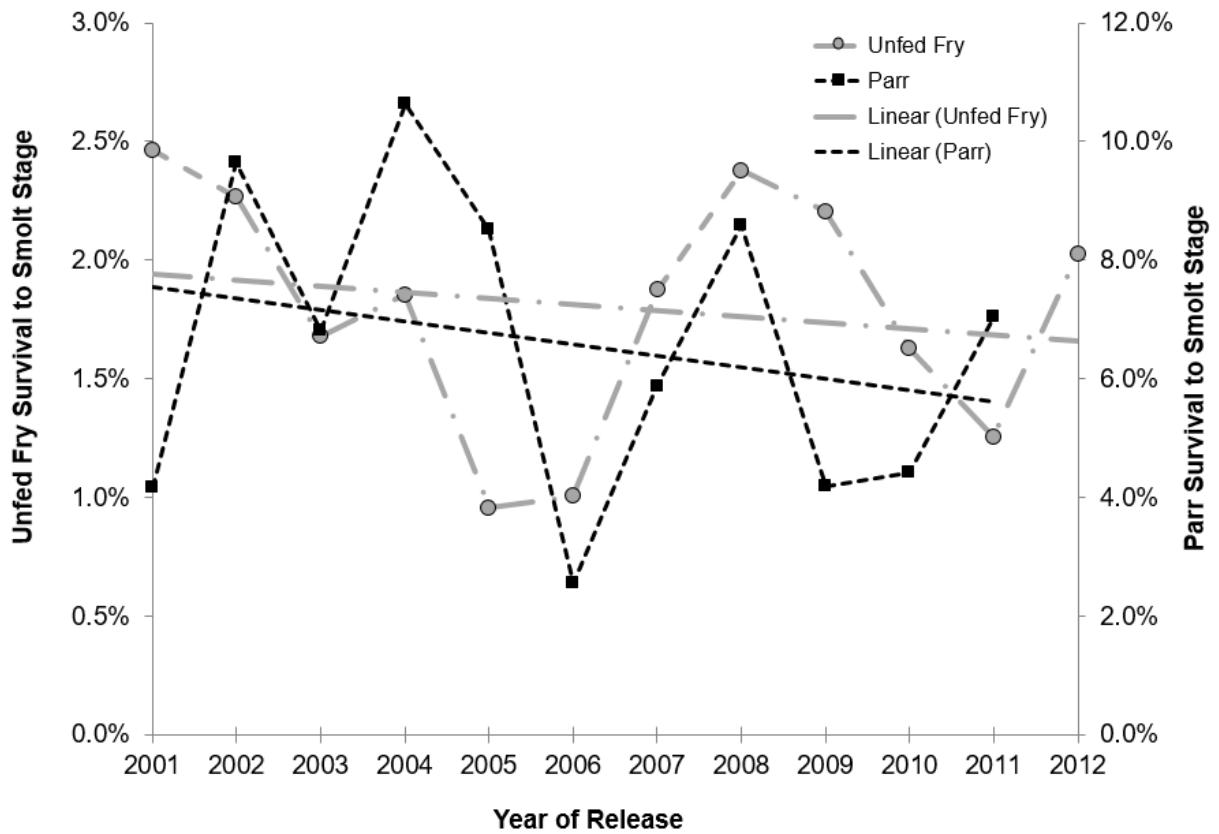


Figure 26. Big Salmon River Live Gene Bank unfed fry and parr releases with percent survival to the smolt stage from 2001 to 2016.

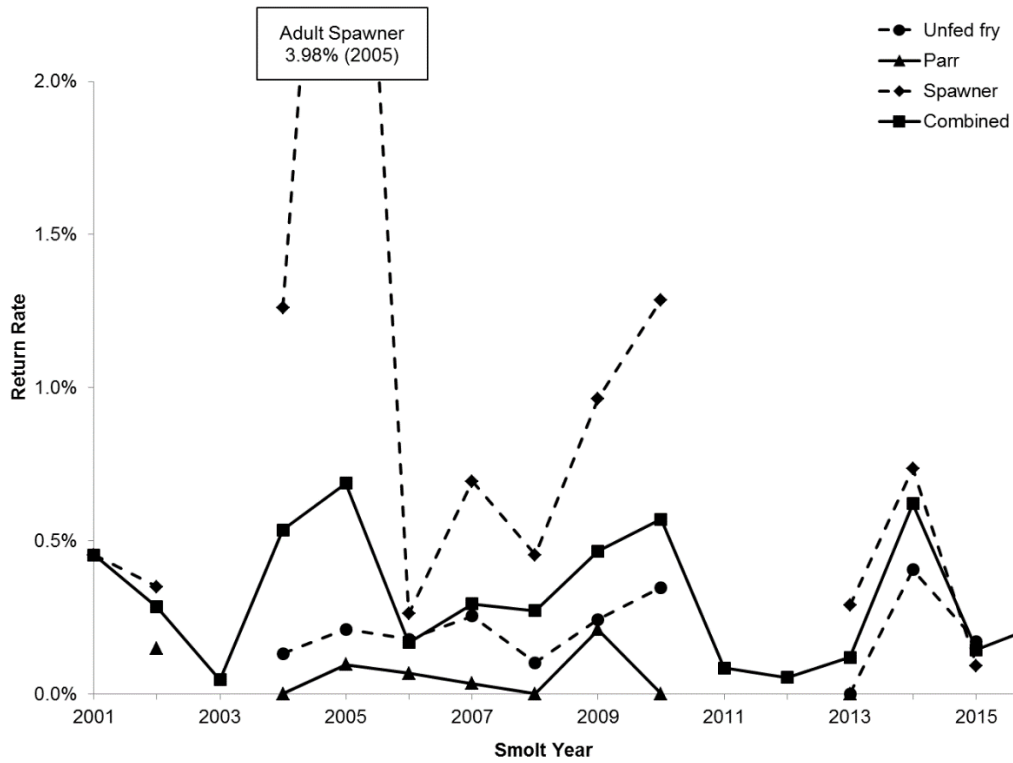


Figure 27. Big Salmon River smolt-to-small salmon return rates from 2001 to 2016.

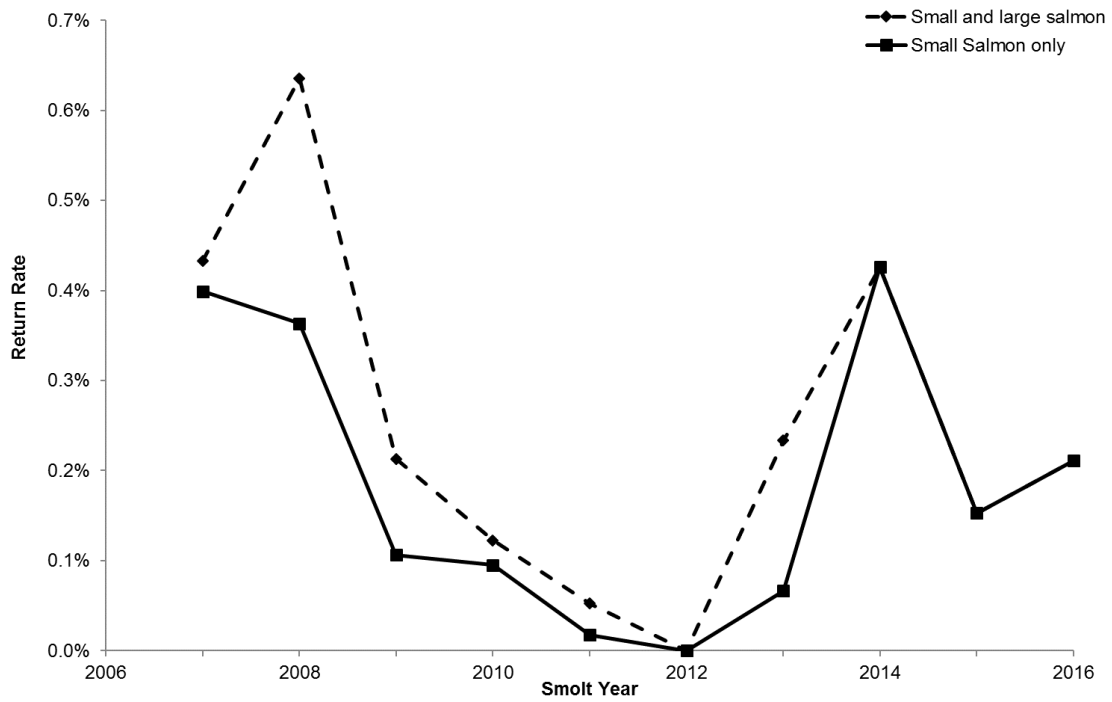


Figure 28. Gaspereau River smolt-to-adult return rates from 2007 to 2016.

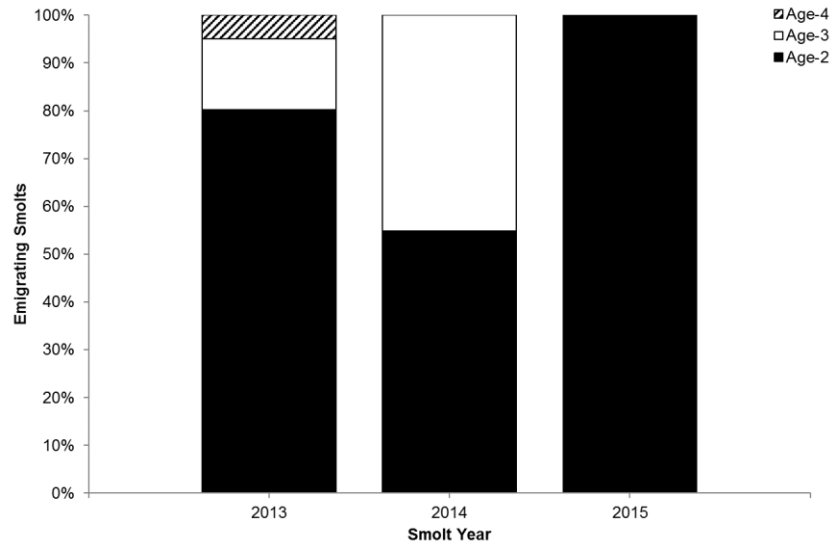


Figure 29. Percentages of various aged Pollet River Live Gene Bank fry-origin emigrating smolts from 2013 to 2015.

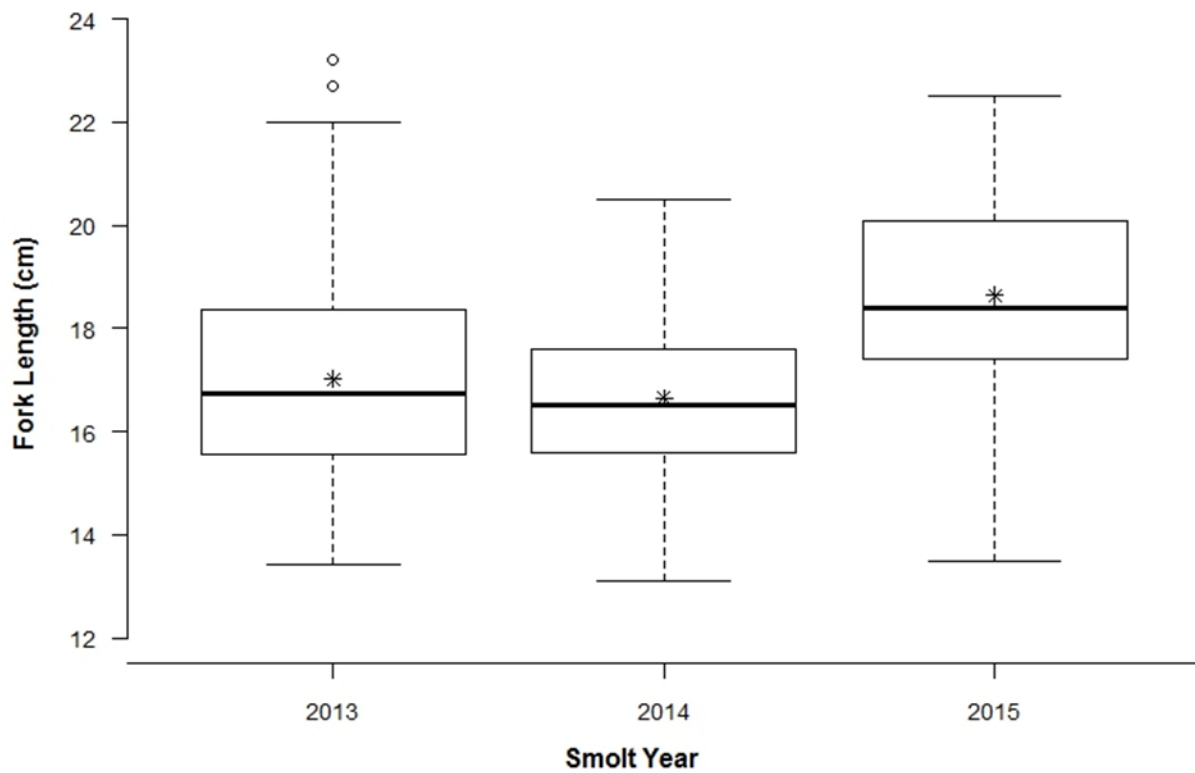


Figure 30. Summary of LGB smolts fork length data collected during assessment projects on the Pollet River from 2013 to 2015. Plots show the median and the 25th and 75th percentiles. Error bars represent the 10th and 90th percentiles, with outliers denoted as circles. The black asterisk represents the mean.

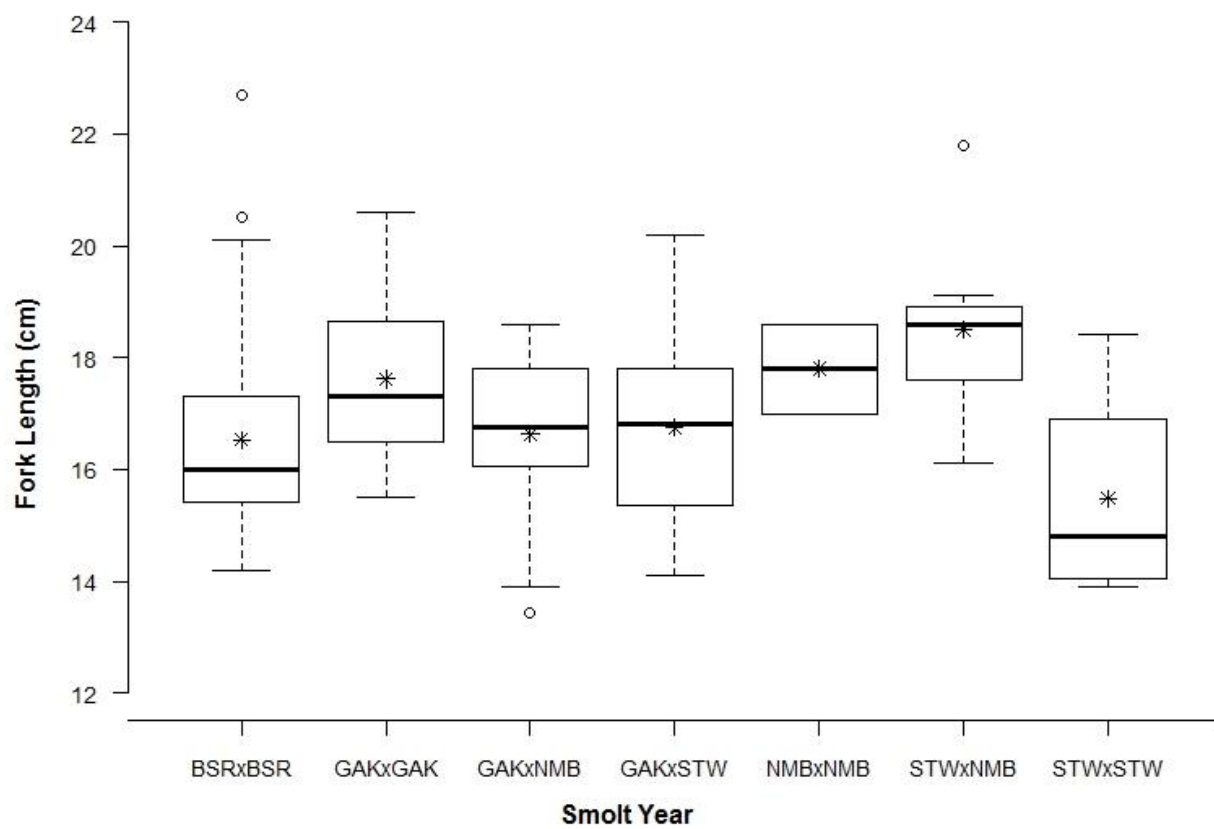


Figure 31. Summary of Age-2 LGB smolt fork length data by origin (cross) sampled during assessment projects on the Pollet River in 2013. Plots show the median and the 25th and 75th percentiles. Error bars represent the 10th and 90th percentiles, with outliers denoted as circles. The black asterisk represents the mean.

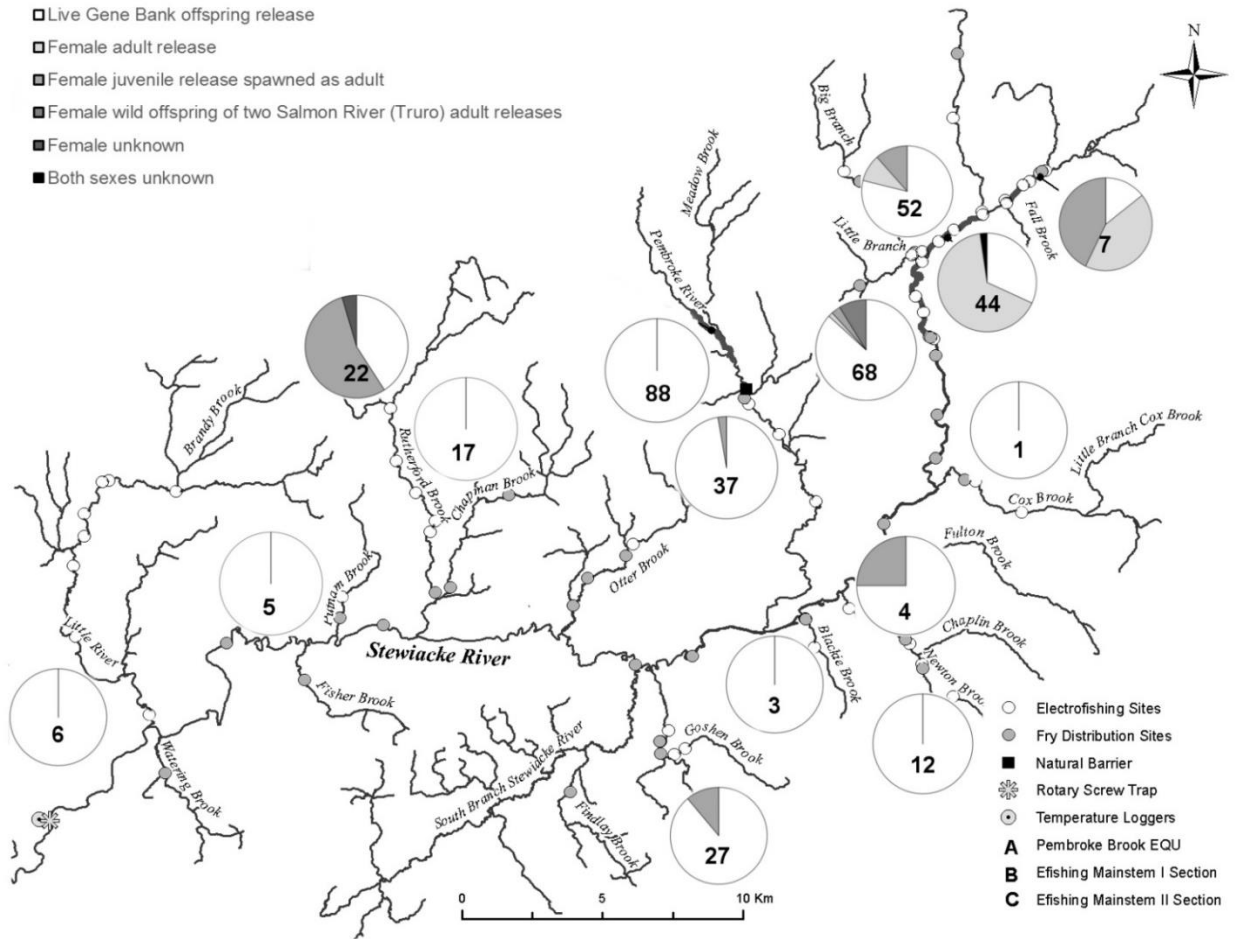


Figure 32. Final parentage results of captured juveniles during the Stewiacke River electrofishing survey in 2013. "EQU" = equalized LGB fry releases

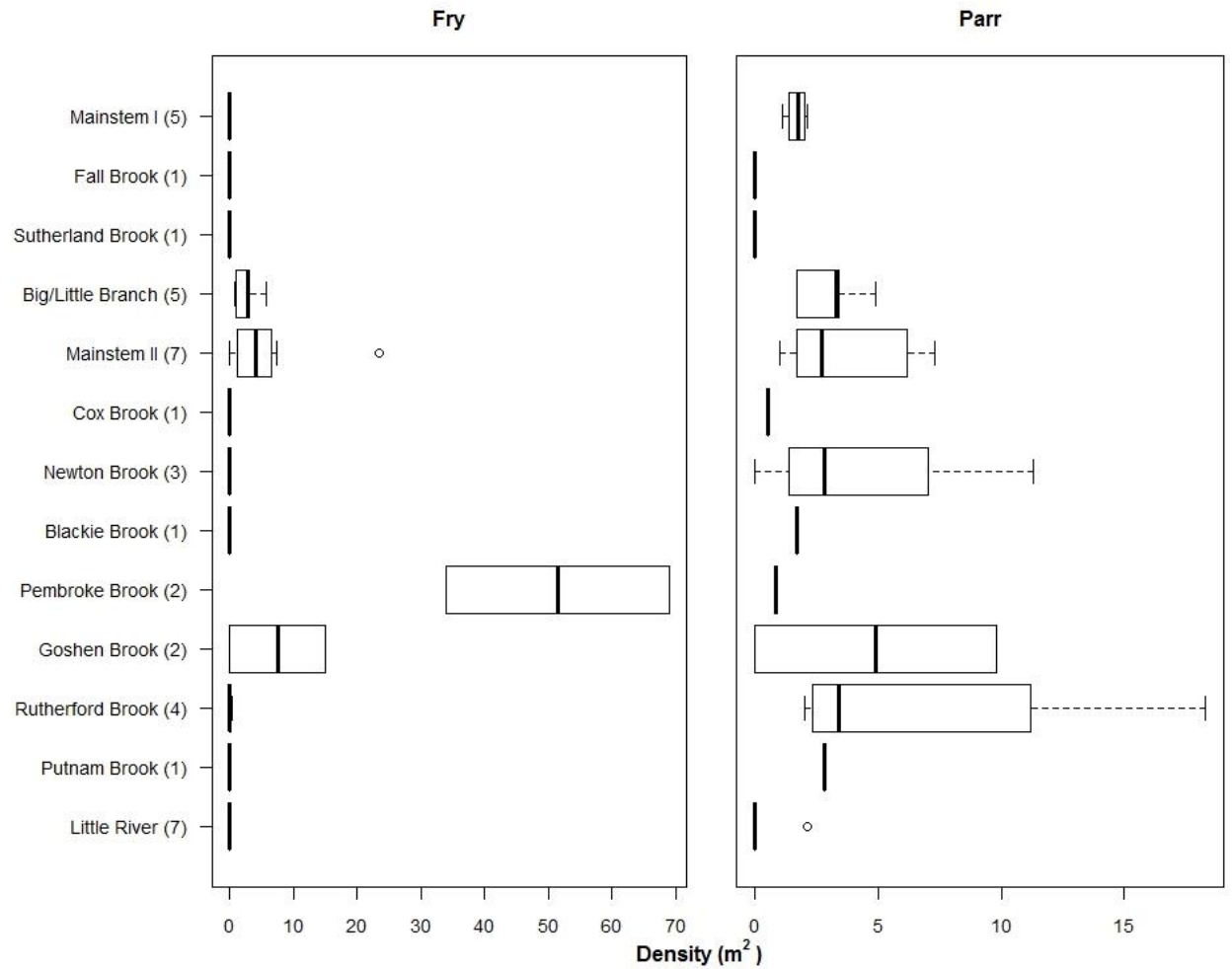


Figure 33. Densities of Stewiacke River Atlantic Salmon fry (left) and parr (right) based on an electrofishing survey completed in 2013. The numbers in (#) represent the number of sites electrofished per tributary or section of mainstem. The black rectangle represents the median density and the whiskers depict the minimum and maximum densities observed.

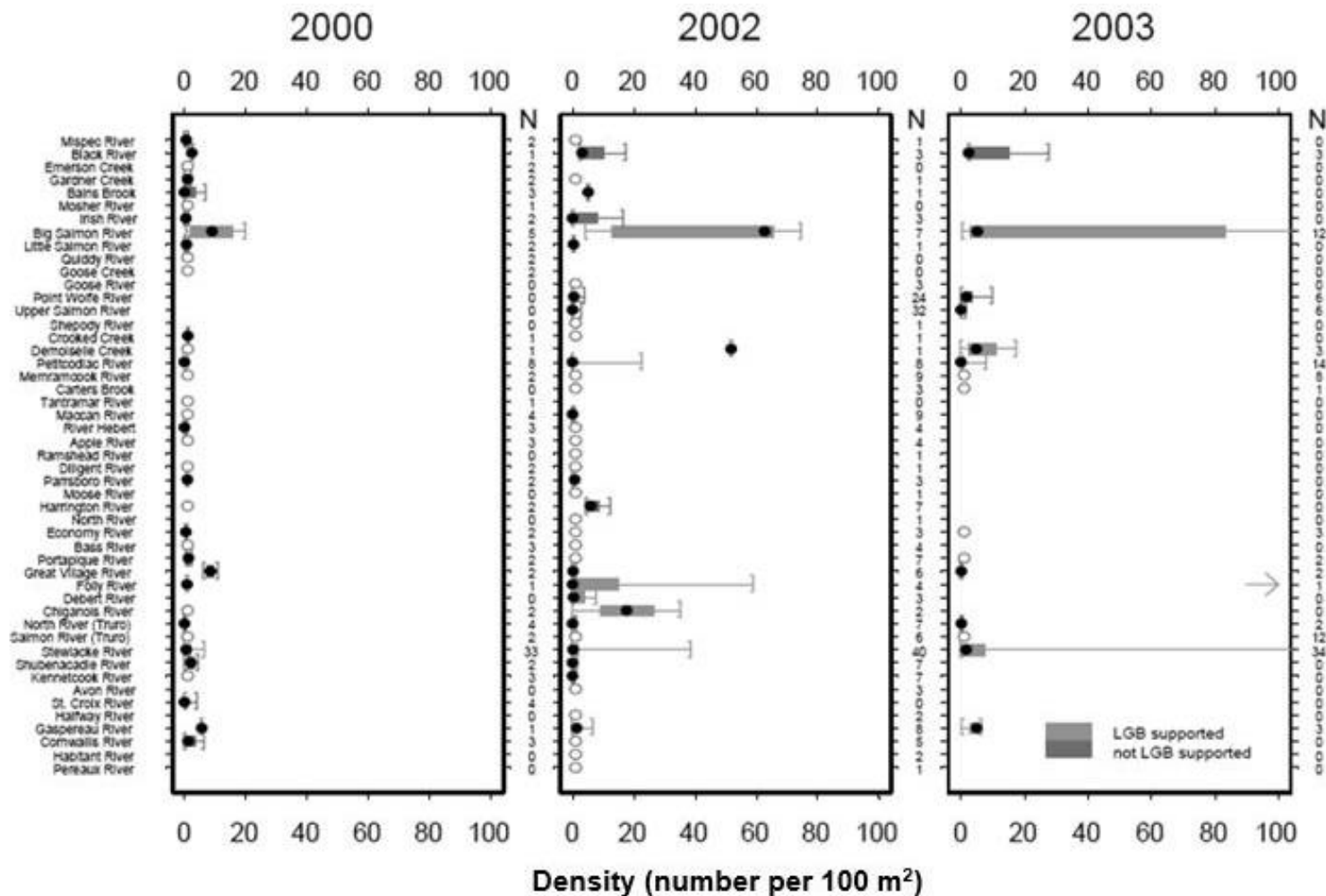


Figure 34. Densities of juvenile Atlantic Salmon in inner Bay of Fundy rivers based on electrofishing during 2000, 2002 and 2003 (Gibson et al. 2004). The column “N” represents the number of sites electrofished each year in each river. The black dot represents the median density. The whiskers depict the minimum and maximum densities observed each year. LGB supported rivers are in light grey and non-supported in dark grey. Rivers with blank spaces were not electrofished.

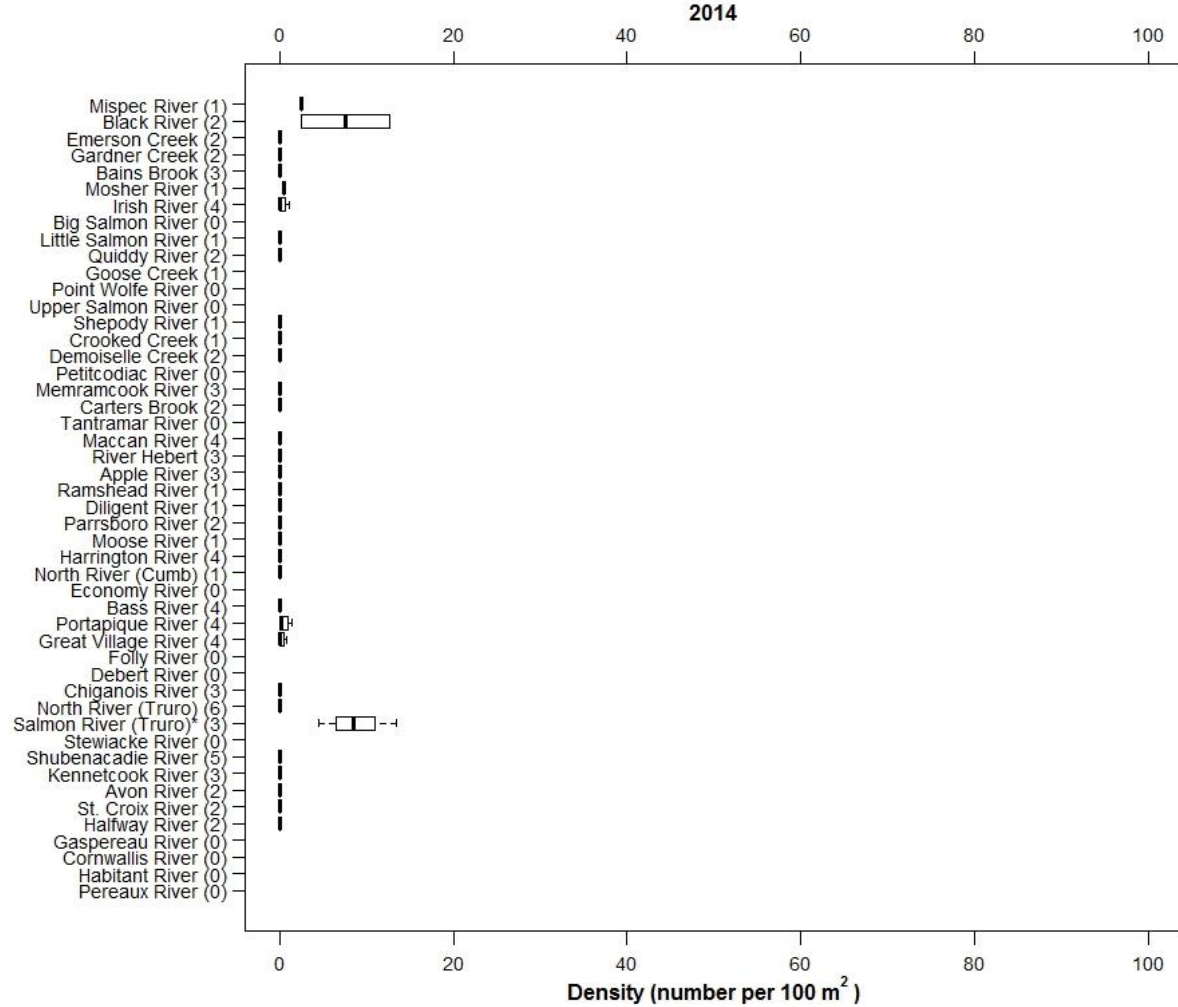


Figure 35. Densities of juvenile Atlantic Salmon in inner Bay of Fundy rivers based on electrofishing during 2014. The numbers in (#) represents the number of sites electrofished each year in each river. The black rectangle represents the median density. The whiskers depict the minimum and maximum densities observed each year. LGB supported rivers are depicted with an *. Rivers with blank spaces were not electrofished. Note: the 2014 update is on a smaller density scale to observe the lower densities.

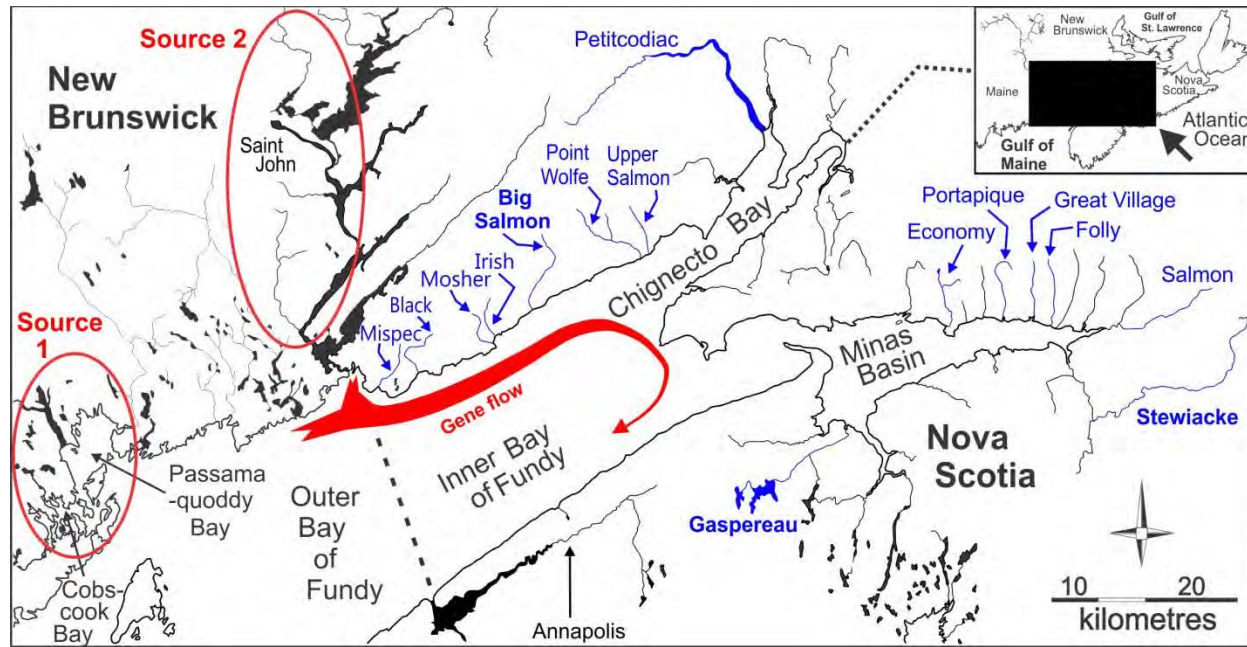


Figure 36. Hypothesized primary sources of gene flow from non-native sources into the inner Bay of Fundy, including aquaculture salmon from concentrations of net pen sites in the Passamaquoddy and Cobscook Bay areas (Source 1) and wild and hatchery origin salmon from the large Saint John River (Source 2). Arrow width reflects possible magnitude of gene flow into river populations of the inner Bay of Fundy.

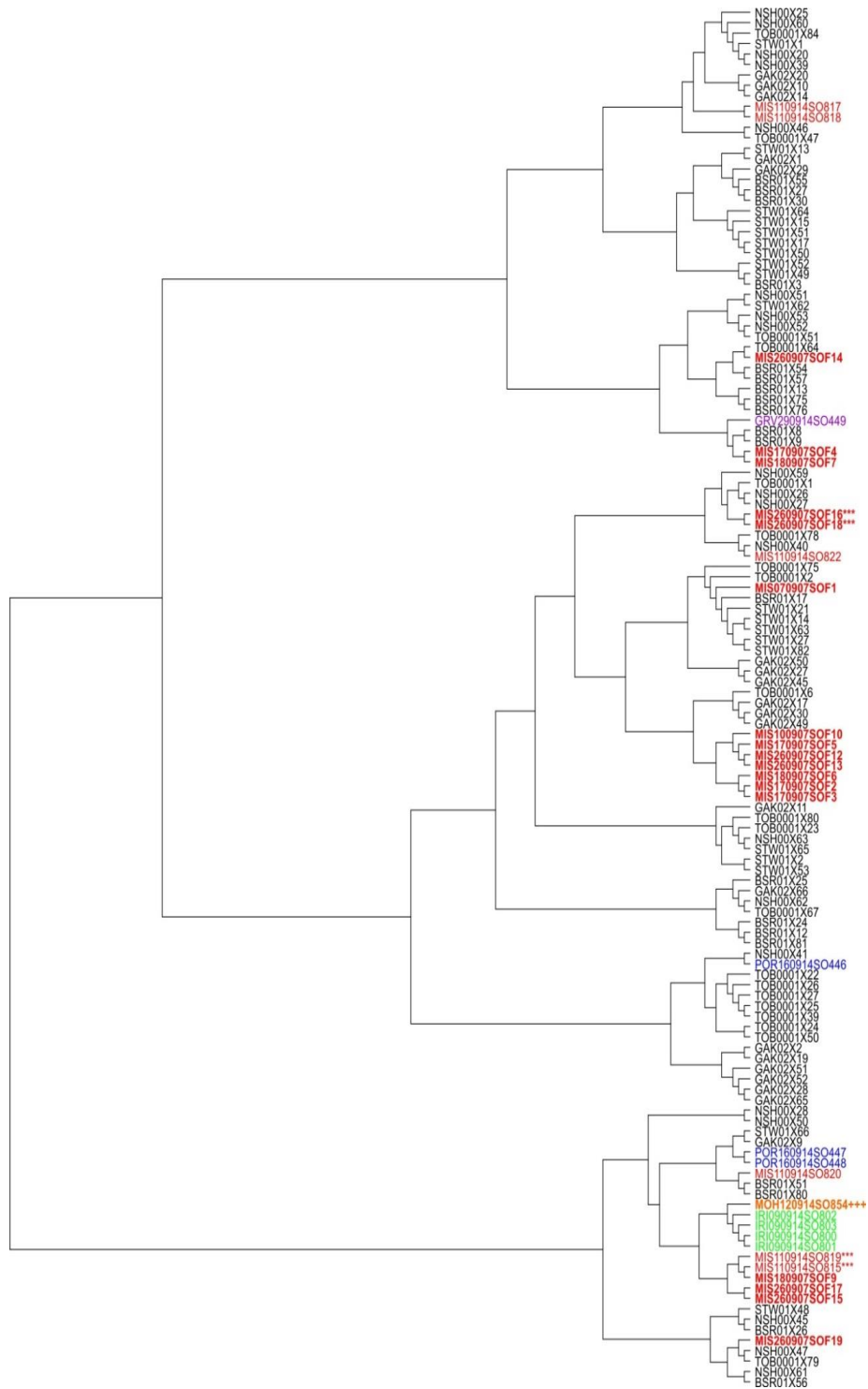


Figure 37. Microsatellite-based UPGMA phylogeny of individual juvenile Atlantic Salmon collected on the Mispec (red), Portapique (blue), Irish (green), Mosher (orange), and Great Village (magenta) rivers in 2014 along with 20 individuals from each of five reference collections (BSR01X [Big Salmon River], STW01X [Stewiacke River], NSH00X [Nashwaak River], TOB0001X [Tobique River], and GAK02X [Gaspereau River]). **Bold** denotes samples collected in 2007, *** indicates the presence of Ssa202-247 alleles, and +++ 1605-224 alleles.

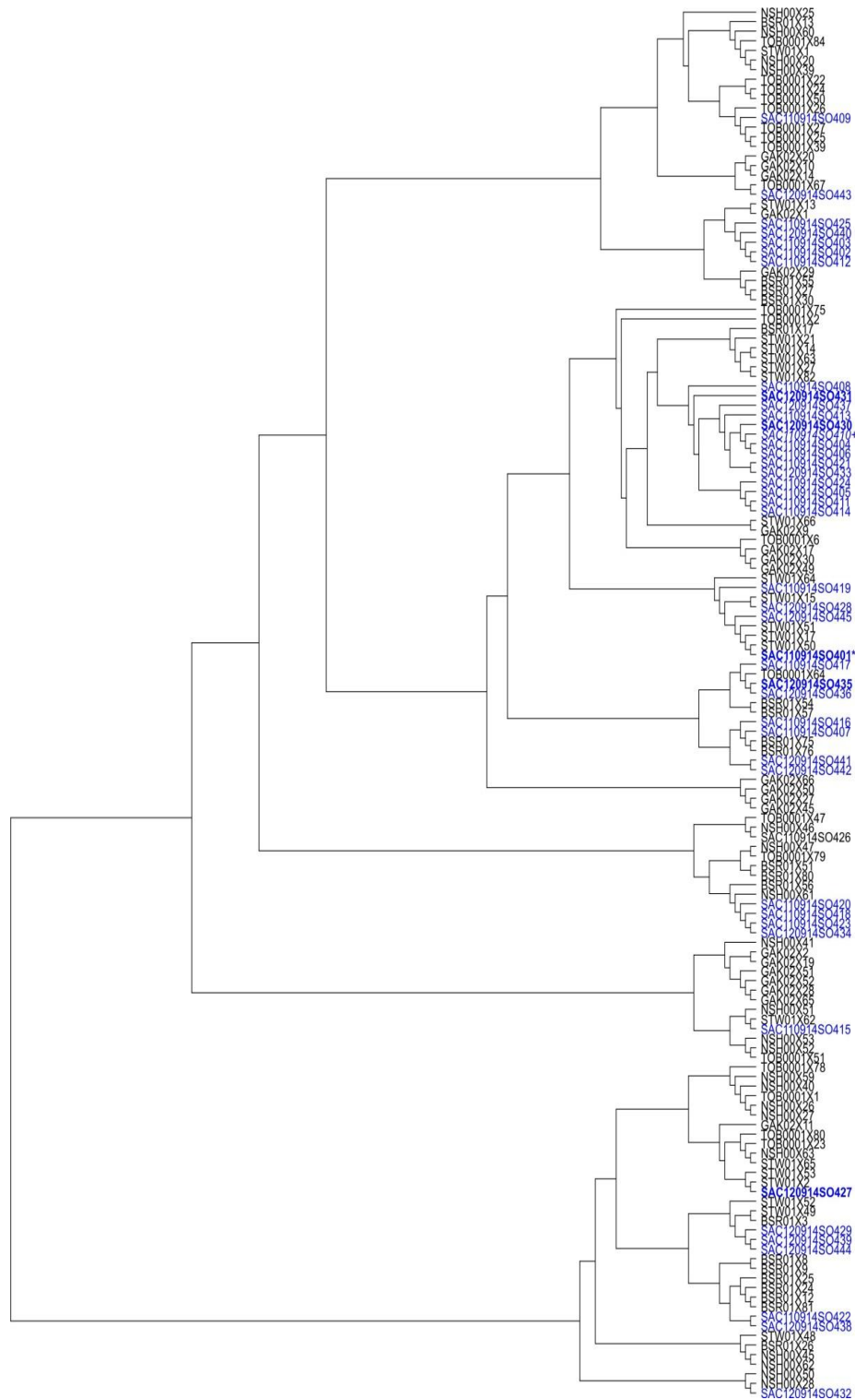


Figure 38. Microsatellite-based UPGMA phylogeny of individual juvenile Atlantic Salmon collected on the Black River (with Code BLK110914) in 2014 along with 20 individuals from each of five reference collections (BSR01X, STW01X, NSH00X, TOB001X, and GAK02X). Red font denotes samples exhibiting an Ssa202-247 allele, and orange denotes one or more 1605 alleles shifted 2 base pairs relative to the common variant found in NA salmon.

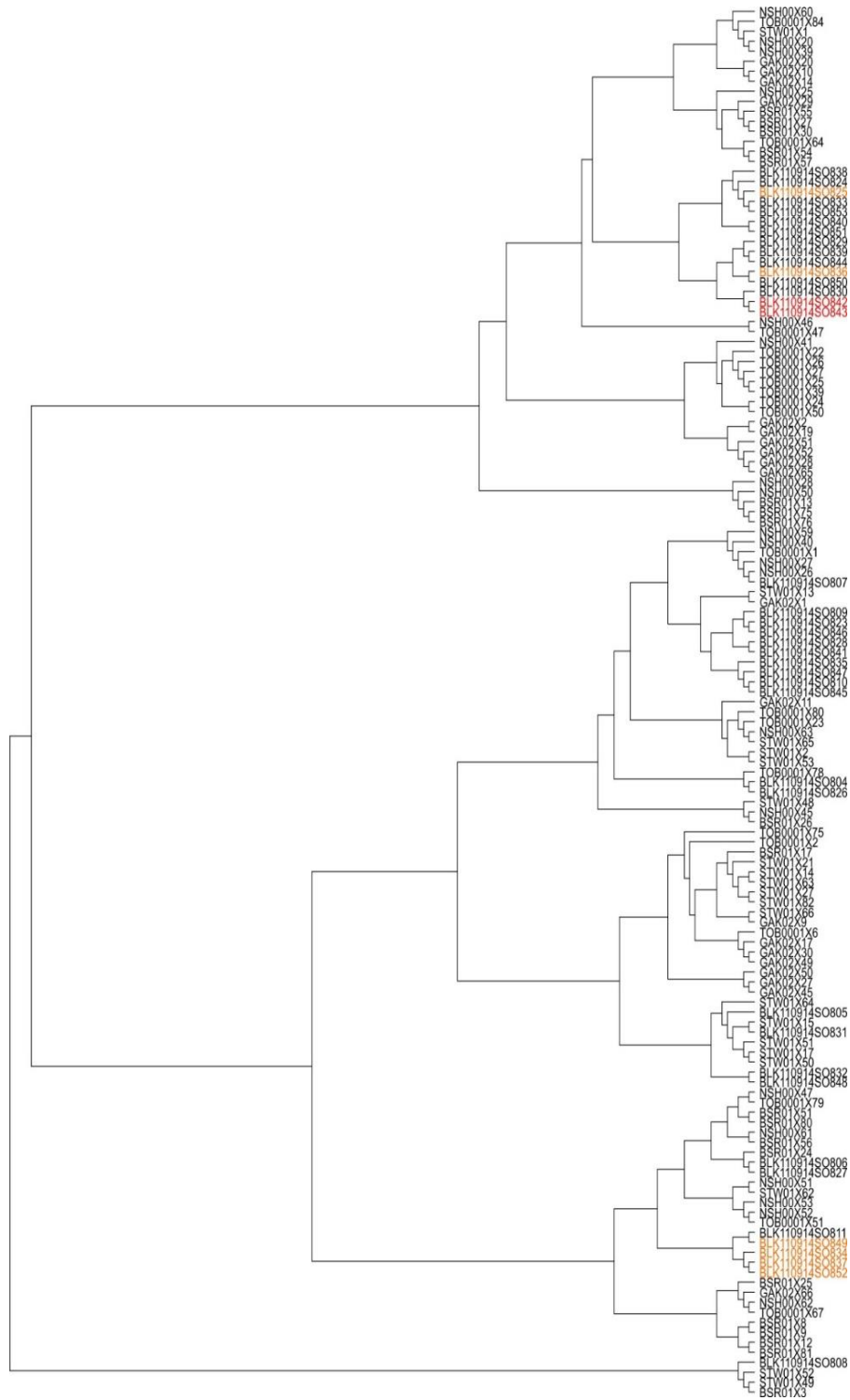


Figure 39. Microsatellite-based UPGMA phylogeny of individual juvenile Atlantic Salmon collected on the Black River (with Code BLK110914) in 2014 along with 20 individuals from each of five reference collections (BSR01X, STW01X, NSH00X, TOB0001X, and GAK02X). Red font denotes samples exhibiting an Ssa202 -247 allele, and orange denotes one or more 1605 alleles shifted 2 base pairs relative to the common variant found in NA salmon.

9.0 APPENDICES

Appendix 1. Terms of Reference.

Review of the Inner Bay of Fundy Atlantic Salmon Science Associated with the Live Gene Bank

Regional Advisory Process - Maritimes Region

June 13 - 16, 2017

Dartmouth, Nova Scotia

Chairperson: Kent Smedbol

Context

The Committee on the Status of Endangered Wildlife in Canada (COSEWIC) identified the inner Bay of Fundy (IBoF) Atlantic Salmon assemblage as a Designatable Unit (DU) and assessed this population as Endangered in May 2001 (COSEWIC 2006). Furthermore, this population was included as Endangered on Schedule 1 of the Species at Risk Act (SARA) when the Act was passed in 2002. In 1998, prior to listing under SARA, population trends observed in several rivers of the Inner Bay of Fundy prompted the collections of juveniles to be reared in the Biodiversity Facilities in the Maritimes Region (Mactaquac, Mersey, and Coldbrook biodiversity facilities) effectively initiating the present-day Live Gene Bank (LGB) programs. The objective of the LGB program is to use captive breeding and rearing technologies to conserve genetic characteristics of IBoF Salmon and maintain populations until recovery can occur (DFO 2008a). In 2008, the Recovery Potential Assessment (RPA) forecasted that this population would be extinct without the support of the LGB program (DFO 2008b; Gibson et al. 2008).

Several evaluations have been conducted to assess the scientific merit of the Live Gene Bank program. In 2004, a review was done for the Director General of Fisheries, Environment and Biodiversity Science. In 2006, COSEWIC contracted a review of the status and assessment of the IBoF Salmon population, which resulted in COSEWIC confirming the previous assessment of endangered and, in 2008, an RPA was completed for IBoF Salmon to support recovery planning under SARA. In 2008, DFO Science also struck a national working group that produced a Science Advisory Report evaluating the contribution of captive breeding facilities to biodiversity conservation. Additionally, since its inception, yearly updates and summaries of ongoing assessment activities and genetic analyses have helped, and continue to help, adaptively manage the LGB program and guide the IBoF Salmon program through the Planning Group and Recovery Teams (DFO 2010).

However, a comprehensive analysis and review of the LGB program on the recovery of the IBoF population does not exist for the three-generation (15 years) lifetime of the program. Therefore, DFO Maritimes Science requested the evaluation of IBoF Salmon science with respect to all LGB activities. The intent of this review is to provide an assessment of the LGB program following three generations (i.e., 15 years) of IBoF Salmon population restoration and maintenance as population recovery has yet to occur. This review will direct the development of an updated 5-year plan for the LGB program.

Objectives

The purpose for this meeting is to evaluate the contribution of the LGB program in achieving two key objectives [or key aspects of the recovery goal, as described in the Recovery Strategy]: 1) to conserve the genetic characteristics of IBoF Salmon and 2) to help re-establish self-sustaining populations of IBoF Salmon [or maintain populations until recovery can occur].

More specifically, the objectives of the meeting are to:

- evaluate the success of conserving genetic characteristics of the IBoF Salmon population across three generations of captive breeding and rearing;
- investigate the origins and levels of inbreeding in IBoF Salmon;
- evaluate the effects of the overall program (multiple generations of captive breeding and rearing), and specific management strategies employed within, on fitness-related traits in IBoF Salmon; and
- assess the status of Atlantic Salmon in the IBoF DU based on DFO information, and where possible, evaluate the different release strategies of the LGB program.

In addition, the meeting will also report recent findings of possible introgression of non-native wild and aquaculture genetic material into IBoF populations, a new potential threat to the conservation of IBoF genetic characteristics.

Expected Publications

- Research Documents (3)
- Proceedings
- Science Advisory Report

Participation

- DFO Science
- DFO Species at Risk Management Division
- DFO Fisheries & Aquaculture Management
- Parks Canada Agency- Fundy National Park
- Aboriginal Organizations and First Nations
- NGOs
- Technical expert reviewers

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Appendix 2. Summary of Live Gene Bank collections from 2001 to 2016. The Big Salmon River collections are housed at the Mactaquac Biodiversity Facility, whereas the collections from the Stewiacke and Gaspereau rivers are transported and maintained at the Coldbrook Biodiversity Facility. "EQU" = equalized distributions, "–" = assessment data not available.

	Big Salmon River		Stewiacke River		Gaspereau River		
	EQU Parr	Smolt	EQU Parr	Smolt	Smolt	Small Adult	Large Adult
2001	311	0	219	0	0	36	21
2002	454	0	0	0	0	3	11
2003	442	204	0	0	0	2	5
2004	303	130	293 ¹	0	0	1	10
2005	215	77	156	0	0	0	0
2006	250	198	191	146	0	1	1
2007	170	342	152	157	0	1	0
2008	261	194	148	101	0	16	3
2009	122	242	165	150	0	1	0
2010	448	300	158	155	0	8	1
2011	403	204	375	23	1303	3	10
2012	634	203	455	5	588	3	1
2013	472	302	437	0	234	3	0
2014	413	149	531	74	300	3	0
2015	587	395	495	0	219	5	6
2016	549	395	515	0	520	5	6

¹ Included 21 fry.

Appendix 3. Summary of the Mactaquac Live Gene Bank distributions from 2001 to 2016. This excludes distributions to Fundy National Park rivers. "MSW" = multi-sea winter spawners, " - " = assessment data not available.

Distribution River	Year	Unfed Fry	Fall Parr (0+)	Spring Parr (1+)	Smolt (1 yr.)	Smolt (2 yr.)	Pre-Grilse	Grilse	MSW Spawners
Big Salmon	2001	185,523	77,718	-	-	-	-	-	-
	2002	138,682	34,062	-	19,725	-	-	-	-
	2003	296,818	54,000	21,025	13,650	-	-	-	15 ¹
	2004	369,109	90,843	7,009	11,663	-	-	-	13 ¹
	2005	258,873	69,862	892	1,295	-	-	28	56
	2006	413,413	72,556	665	1,413	50	-	-	-
	2007	370,605	87,088	-	-	-	-	-	-
	2008	265,126	87,786	-	-	-	-	-	-
	2009	177,971	56,984	-	1,243	829	-	-	-
	2010	200,378	43,140	-	382	1,695	-	-	-
	2011	401,486	15,137	13	102	330	-	-	-
	2012	97,209	50	-	-	-	1,270	-	-
	2013	341,995	-	-	-	-	1,012	-	-
	2014	255,386	-	-	-	-	288	-	-
	2015	302,307	-	-	-	259	-	-	-
	2016	404,398	-	-	-	-	-	-	-
Petitcodiac									
Pollet River	2002	56,159	-	-	-	-	-	-	-
	2005	120,094	-	-	-	-	-	-	-
	2008	-	-	-	-	-	-	3	4
	2009	63,550	-	-	-	-	-	-	-
	2011	337,622	-	-	-	-	-	-	-
	2012	37,246	-	-	-	-	-	-	-
	2015	-	-	-	-	-	-	204	-
	2016	50,000	-	-	-	-	-	-	-
Little River	2002	-	-	-	-	-	-	-	53
	2003	-	-	-	-	-	549	-	-
	2012	-	-	-	-	-	-	340	549
	2013	-	-	-	-	-	-	330	7
	2014	-	-	-	-	-	-	403	160
	2015	-	-	-	-	-	-	733	56
	2016	-	-	-	-	-	-	355	-

Distribution River	Year	Unfed Fry	Fall Parr (0+)	Spring Parr (1+)	Smolt (1 yr.)	Smolt (2 yr.)	Pre-Grilse	Grilse	MSW Spawners
Demoiselle	2001	16,222	-	-	-	-	-	-	-
	2002	10,080	-	1,078	-	-	-	-	-
Weldon Creek	2004	130,197	-	-	-	-	-	-	-
Black River	2004	53,482	-	-	-	-	-	-	49
	2005	17,915	-	-	-	-	-	-	28

¹ Females

Appendix 4. Preliminary summary of Nova Scotia (cumulative for Coldbrook and Mersey Biodiversity facilities) Live Gene Bank distributions from 2001 to 2016. Detail on origin (e.g., wild, wild-exposed) for released spawners in egg deposition tables. “ - ” = assessment data not available.

Distribution River	River of Origin	Year	Unfed Fry	6-week Fry	Fall Parr (0+)	Spring Parr (1+)	Smolt (1 yr.)	Smolt (2 yr.)	Adult Spawners
Stewiacke River	Stewiacke	2001	12,700	29,400	34,000	-	-	-	-
	Stewiacke	2002	24,000	42,000	88,300	-	6,000	-	-
	Stewiacke	2003	34,700	-	27,000	-	17,600	-	-
	Stewiacke	2004	13,900	10,000	2,800	-	7,400	-	737
	Stewiacke	2005	150,400	158,100	178,100	-	4,500	1,290	-
	Stewiacke	2006	156,000	45,000	35,000	-	9,000	-	44
	Stewiacke	2007	197,500	120,000	120,000	-	10,000	1,000	112
	Stewiacke	2008	135,000	99,000	75,000	-	10,000	1,450	-
	Stewiacke	2009	70,000	60,000	42,000	-	10,000	350	-
	Stewiacke	2010	112,000	65,000	50,000	6,000	10,000	700	-
	Stewiacke	2011	166,800	-	64,000	-	10,000	-	396
	Stewiacke	2012	157,000	-	36,000	-	10,000	-	125
	Stewiacke	2013	260,400	-	437	-	-	-	212
	Stewiacke	2014	242,050	-	-	170	-	30	270
	Stewiacke	2015	244,000	-	-	-	-	150	870
	Stewiacke	2016	253,371	-	-	-	-	93	702
Chiganois River	Stewiacke	2002	24,000	27,000	37,000	-	-	-	-
	Stewiacke	2003	42,600	46,500	32,900	-	-	-	-
	Stewiacke	2004	-	-	-	-	8,150	-	-
	Stewiacke	2005	15,100	-	15,900	-	-	-	-
	Stewiacke	2006	-	37,000	-	-	-	-	-
	Stewiacke	2008	16,000	640	5,000	-	-	-	130
	Stewiacke	2009	16,000	-	3,000	-	-	-	-
	Stewiacke	2010	51,000	-	-	-	-	-	-
Debert River	Stewiacke	2002	10,000	27,000	45,500	-	-	-	-
	Stewiacke	2003	49,800	34,000	47,800	-	-	-	-
	Stewiacke	2004	9,100	-	-	-	8,150	-	-
	Stewiacke	2005	43,000	16,000	-	-	-	-	-
	Stewiacke	2006	20,000	-	40,000	-	5,000	-	-
	Stewiacke	2007	37,500	-	25,000	-	-	-	138
	Stewiacke	2009	16,000	-	21,000	-	-	-	-
	Stewiacke	2010	10,000	-	18,500	-	-	-	30
	Stewiacke	2011	37,000	-	41,300	-	-	-	92
	Stewiacke	2012	45,000	15,000	42,600	-	-	-	169
	Stewiacke	2014	113,550	-	-	-	-	-	-

Distribution River	River of Origin	Year	Unfed Fry	6-week Fry	Fall Parr (0+)	Spring Parr (1+)	Smolt (1 yr.)	Smolt (2 yr.)	Adult Spawners
	Stewiacke	2015	43,800	-	-	-	-	-	-
	Stewiacke	2016	13,784	-	-	-	-	-	-
Folly River	Stewiacke	2002	32,000	27,000	24,500	-	-	-	-
	Stewiacke	2003	9,700	35,000	43,700	-	-	-	-
	Stewiacke	2004	13,000	9,100	-	-	4,640	-	-
	Stewiacke	2005	15,100	35,600	16,000	-	-	-	-
	Stewiacke	2006	20,000	-	50,000	-	5,000	-	-
	Stewiacke	2007	37,500	-	25,000	-	-	-	71
	Stewiacke	2008	38,000	-	4,000	-	-	-	40
	Stewiacke	2009	16,000	-	21,000	-	-	-	-
	Stewiacke	2010	22,500	-	18,500	-	-	-	30
	Stewiacke	2011	37,000	-	30,000	-	-	-	-
	Stewiacke	2012	45,250	-	37,700	-	-	-	-
	Stewiacke	2013	15,000	-	-	-	-	-	-
	Stewiacke	2014	96,950	-	-	-	-	-	-
	Stewiacke	2015	41,975	-	-	-	-	-	-
	Stewiacke	2016	55,136	-	-	-	-	-	-
Great Village River	Stewiacke	2004	300	-	-	-	24,810	-	-
	Great Village	2005	-	-	8,000	-	-	-	-
	?	2007	16,000	-	-	-	-	-	461
	Stewiacke	2008	-	-	-	-	-	-	109
	Stewiacke	2010	-	-	45,000	-	-	-	-
	Stewiacke	2011	30,000	-	-	-	-	-	-
	Stewiacke	2012	-	-	-	-	-	-	49
Economy River	Economy	2004	600	-	-	-	-	-	-
	Economy	2006	34,000	-	24,000	-	-	-	-
	Economy	2007	10,000	-	2,500	-	-	-	-
	Stewiacke	2010	-	-	800	-	-	-	280
	Stewiacke	2011	-	-	12,500	-	99	-	294
	Stewiacke	2012	-	-	-	-	-	-	156
Salmon River (Colchester)	Stewiacke	2002	-	-	-	-	-	-	190
	Stewiacke	2003	-	-	-	-	-	-	132
	Stewiacke	2005	-	-	200	-	-	-	116
	Stewiacke	2006	15,000	-	16,500	-	-	-	281
	Stewiacke	2007	12,500	-	-	-	-	-	428
	Stewiacke	2008	-	-	-	-	-	-	253
	Stewiacke	2009	-	-	-	-	-	-	-

Distribution River	River of Origin	Year	Unfed Fry	6-week Fry	Fall Parr (0+)	Spring Parr (1+)	Smolt (1 yr.)	Smolt (2 yr.)	Adult Spawners
	Stewiacke	2010	25,000	-	-	-	-	-	316
	Stewiacke	2011	-	-	-	3,000	-	-	235
	Stewiacke	2012	-	-	-	-	-	-	362
	Stewiacke	2013	-	-	-	-	-	-	221
	Stewiacke	2014	-	-	-	-	-	-	256
	Stewiacke	2016	189,530	-	-	-	-	-	59
Gaspereau River	Gaspereau	2001	-	-	42,700	-	10,900	-	-
	Gaspereau	2002	-	7,400	-	-	16,500	-	-
	Gaspereau	2003	-	-	21,700	18,600	27,400	-	-
	Gaspereau	2004	-	-	8,400	-	11,500	-	-
	Gaspereau	2005	77,000	19,000	18,000	-	1,700	-	-
	Gaspereau	2006	70,000	-	45,000	-	6,500	-	251
	Gaspereau	2007	400,000	-	46,000	190	10,000	1,030	276
	Gaspereau	2008	350,000	-	54,000	-	10,000	750	362
	Gaspereau	2009	160,000	-	48,800	-	12,000	-	-
	Gaspereau	2010	100,000	42,000	20,000	-	10,000	750	69
	Gaspereau	2011	248,500	-	13,500	-	7,600	-	163
	Gaspereau	2012	232,500	-	22,100	-	3,200	-	236
	Gaspereau	2013	302,600	1,100	-	-	-	-	282
	Gaspereau	2014	245,150	-	-	-	-	-	130
	Gaspereau	2015	151,500	-	-	-	-	-	293
	Gaspereau	2016	219,075	-	-	-	-	-	178
Bass River	Stewiacke	2008	320,000	-	-	-	-	-	-
Cornwallis River	Gaspereau	2005	-	-	-	-	-	2,700	-
	Gaspereau	2006	-	-	-	-	-	633	-
	Gaspereau	2010	-	-	68,000	71	-	344	68
	Gaspereau	2011	-	-	23,000	-	-	-	387
	Gaspereau	2012	15,500	-	20,300	-	-	-	216
	Gaspereau	2013	-	-	1,182	-	-	-	109
	Gaspereau	2014	143,100	-	-	-	-	-	203
	Gaspereau	2015	-	-	-	-	-	-	138
St. Croix River	Gaspereau	2014	-	-	-	-	-	-	349
	Gaspereau	2015	76,000	-	-	-	-	-	437
	Gaspereau	2016	115,830	-	-	-	-	-	350

Appendix 5a. Daily unmarked smolt (wild and LGB_{FRY} combined) captures at the Gaspereau River White Rock Dam surface downstream bypasses in 2016. "MM" = month, "DD" = day, "N/A" = sampling not completed on these days.

MM	DD	Bypass 1 Sampling		Bypass 2 and 3 Sampling		Recapture Totals			
		Catch	Marked and Recycled	Bypass 2 Catch	Bypass 3 Catch	BP1	BP2	BP3	Total
Apr.	22	0	0	0	0	0	0	0	0
Apr.	23	1	1	0	0	0	0	0	0
Apr.	24	3	1	0	0	0	0	0	0
Apr.	25	6	4	1	0	0	0	0	0
Apr.	26	10	6	8	8	0	0	0	0
Apr.	27	14	8	2	5	0	0	0	0
Apr.	28	9	6	4	5	1	0	0	1
Apr.	29	11	6	0	0	1	0	1	2
Apr.	30	21	12	1	4	3	0	1	4
May	1	20	12	18	15	2	0	3	5
May	2	26	15	14	20	3	1	2	6
May	3	12	7	34	12	0	0	1	1
May	4	63	25	112	46	3	4	3	10
May	5	36	21	26	48	0	0	2	2
May	6	36	22	13	39	9	1	1	11
May	7	101	24	5	32	6	0	1	7
May	8	68	25	0	7	2	0	0	2
May	9	67	25	0	24	3	0	0	3
May	10	42	25	11	10	2	1	0	3
May	11	74	25	38	11	4	2	0	6
May	12	155	25	19	35	18	1	2	21
May	13	54	25	8	19	7	0	1	8
May	14	131	25	6	40	15	2	0	17
May	15	87	25	3	38	11	0	3	14
May	16	75	25	12	39	12	0	2	14
May	17	63	25	8	22	9	0	3	12
May	18	23	14	5	24	10	0	0	10
May	19	36	22	8	27	10	2	1	13
May	20	31	17	4	24	8	1	5	14
May	21	38	23	7	21	18	0	1	19
May	22	13	8	3	21	2	0	1	3
May	23	13	8	4	12	6	0	0	6
May	24	9	5	2	15	9	0	1	10
May	25	6	4	N/A	N/A	5	0	0	5
May	26	4	3	N/A	N/A	3	0	0	3
May	27	2	0	N/A	N/A	0	0	0	0
May	28	1	0	N/A	N/A	2	0	0	2
May	29	1	0	N/A	N/A	1	0	0	1
May	30	1	0	N/A	N/A	0	0	0	0
May	31	1	0	N/A	N/A	0	0	0	0
June	1	1	0	N/A	N/A	1	0	0	1
June	2	0	0	N/A	N/A	0	0	0	0
June	3	1	0	N/A	N/A	0	0	0	0
June	4	0	0	N/A	N/A	0	0	0	0
June	5	1	0	N/A	N/A	2	0	0	2
Total		1,367	524	376	623	188	15	35	238

Appendix 5b. Smolt recapture efficiencies for each of the Gaspereau River White Rock Dam surface downstream bypasses in 2016.

Bypass	Marks	Recaps	Efficiency
Recycled (All Bypasses)	524	238	45.42%
Recycled (Bypass 1)	524	188	35.88%
Recycled (Bypass 2)	524	15	2.86%
Recycled (Bypass 3)	524	35	6.68%

Appendix 6. Counts of Big Salmon River small and large adult Atlantic Salmon by dive surveys and abundance estimates from 2000 to 2016. Counts outlined were used to split total abundance estimate into small and large salmon. “-” = assessment data not available.

Year	Pool Count						Abundance Estimate	
	July/August		September		October		Small	Large
	Small	Large	Small	Large	Small	Large		
2000	-	-	-	-	23	5	34	7
2001	-	-	-	-	12	8	18	12
2002	-	-	16	5	-	-	24	7
2003	-	-	-	-	10	2	18	3
2004	-	-	-	-	4	5	7	9
2005	-	-	23	11	-	-	41	19
2006	34	10	-	-	3	0	60	17
2007	16	2	27	7	26	2	44	3
2008	5	0	19	0	20	8	35	14
2009	20	1	8	2	5	2	35	2
2010	18	1	44	5	-	-	78	9
2011	63	4	42	10	50	3	111	7
2012	6	3	2	2	0	1	11	5
2013	0	2	4	2	2	2	7	4
2014	20	2	36	2	26	2	46	3
2015	13	3	16	2	6	0	28	4
2016	6	2	8	3	2	2	14	5

Appendix 7. Summary of the Big Salmon River small and large salmon biological characteristics collected from 2000 to 2016. "Prop." = proportion, "–" = assessment data not available.

Year	Small					Large					Total Salmon	Prop. Small Sampled
	Total	Male Count	Female Count	Female Mean Length	Prop. Female	Total	Male Count	Female Count	Female Mean Length	Prop. Female		
2000	10	7	3	53.0	0.300	1	-	1	73.5	1.00	11	0.909
2001	0	-	-	-	-	0	-	-	-	-	0	-
2002	2	-	2	53.5	1.000	3	2	1	70.4	0.33	5	0.400
2003	6	4	2	55.1	0.333	1	-	1	65.7	1.00	7	0.857
2004	0	-	-	-	-	1	-	1	80.4	1.00	1	0.000
2005	17	12	5	54.8	0.294	2	-	2	64.0	1.00	19	0.895
2006	17	9	8	56.5	0.471	3	1	2	66.0	0.67	20	0.850
2007	14	5	9	54.7	0.643	0	-	-	-	-	14	1.000
2008	23	7	16	55.7	0.696	1	-	1	80.0	1.00	24	0.958
2009	9	4	5	57.2	0.556	4	1	3	69.0	0.75	13	0.692
2010	45	13	32	55.7	0.711	2	-	2	72.5	1.00	47	0.957
2011	23	8	15	54.7	0.652	0	-	-	-	-	23	1.000
2012	0	-	-	-	-	0	-	-	-	-	0	-
2013	0	-	-	-	-	0	-	-	-	-	0	-
2014	3	-	3	53.7	1.000	1	-	1	80.0	1.00	4	0.750
2015	13	3	10	56.3	0.769	0	-	-	-	-	13	1.000
2016	3	3	-	-	0.000	1	-	1	64.3	1.00	4	0.750
Total	185	75	110	55.4	0.595	20	4	16	70.4	0.80	205	0.902

Appendix 8. Individual Big Salmon River adult salmon biological characteristic data collected from 2000 to 2016. "Rec." = record, "Capt." = capture, "Loc." = location, "WD" = Walton Dam, "WB" = Walker Brow, "GB" = Gravelly Bar, "LoP" = Long Pool, "RB" = Rody Bar, "CP" = Catt Pool, "MB" = Mast Brow, "LP" = Lodge Pool, "WP" = Whirl Pool, "PP" = Picture Pool, "SP" = Smith Pool, "KP" = King Pool, "AP" = Amateur Pool, "RP" = Rody Pool, "MP" = Miller Pool, "Meth." = method, "S" = seine, "TN" = tangle net, "A" = angling, "MM" = month, "DD" = day, "Cat." = category, "S" = small, "L" = large, "Lgth" = length, "Obs." = observed, "M" = male, "F" = female, "U" = unknown sex, "Ad." = adipose, "W" = wild, "LGB_P" = Live Gene Bank parr, "LGB_F" = Live Gene Bank fry, "LGB_{PS}" = Live Gene Bank pre-smolt, "LGB_{PG}" = Live Gene Bank pre-grilse, "AE" = aquaculture escapee, "H/AC" = hatchery adipose-clip stray, "Tiss. Samp." = tissue sample, "Age_R" = river age in years, "Age_S" = sea age in years, "?" = unknown age data, "-" = assessment data not available.

Rec. #	Capt. Loc.	Capt. Meth.	Year	MM	DD	Cat.	Lgth (cm)	Obs. Sex	Ad. Fin Clip	Origin	Tiss. Samp.	Age _R	Age _S	Spawning Marks		
														1 st	2 nd	3 rd
1	WD	Se/TN	2000	Oct.	16	S	56.5	M	-	W	Y	3	1	-	-	-
2	WD	Se/TN	2000	Oct.	16	S	55.0	M	-	W	Y	?	1	-	-	-
3	WD	Se/TN	2000	Oct.	16	S	58.5	M	-	W	Y	2	1	-	-	-
4	WD	Se/TN	2000	Oct.	16	S	58.0	M	-	W	Y	2	1	-	-	-
5	WD	Se/TN	2000	Oct.	16	L	73.5	F	-	W	Y	2	2	-	-	-
6	WB	Se/TN	2000	Oct.	17	S	53.5	M	-	W	Y	2	1	-	-	-
7	WB	Se/TN	2000	Oct.	17	S	55.5	F	-	W	Y	2	1	-	-	-
8	GB	Se/TN	2000	Oct.	17	S	55.5	F	-	W	Y	3	1	-	-	-
9	GB	Se/TN	2000	Oct.	17	S	57.5	M	-	W	Y	2	1	-	-	-
10	LoP	Se/TN	2000	Oct.	18	S	55.0	M	N	W	Y	3	1	-	-	-
11	LoP	Se/TN	2000	Oct.	18	S	48.0	F	N	W	Y	2	1	-	-	-
12	RB	Se/TN	2002	Sept.	18	L	70.4	F	N	W	Y	2	3	1	2	-
13	RB	Se/TN	2002	Sept.	18	S	52.6	F	N	W	Y	2	1	-	-	-
14	CP	Se/TN	2002	Sept.	18	S	54.3	F	N	W	Y	2	1	-	-	-
15	CP	Se/TN	2002	Sept.	18	L	67.8	M	N	W	Y	?	2	1	-	-
16	CP	Se/TN	2002	Sept.	18	L	67.7	M	N	W	Y	3	2	1	-	-
17	R	Se/TN	2003	Sept.	9	S	61.5	M	N	W	N	-	-	-	-	-
18	R	Se/TN	2003	Sept.	9	S	53.7	M	Y	LGB _{PARR}	Y	1	1	-	-	-
19	R	Se/TN	2003	Sept.	9	L	65.7	F	N	W	Y	2	2	1	-	-
20	R	Se/TN	2003	Sept.	9	S	50.0	M	N	W	Y	2	1	-	-	-
21	R	Se/TN	2003	Sept.	9	S	56.5	M	N	W	Y	2	1	-	-	-
22	R	Se/TN	2003	Sept.	9	S	55.0	F	N	W	Y	2	1	-	-	-
23	R	Se/TN	2003	Sept.	9	S	55.2	F	N	W	Y	3	1	-	-	-
24	WD	Se/TN	2004	Sept.	15	L	80.4	F	N	W	N?	-	-	-	-	-
25	WD	Se/TN	2005	Aug.	5	L	68.0	U	N	W	Y	2	2	1	-	-
26	WD	Se/TN	2005	Aug.	5	S	54.0	U	N	W	Y	2	1	-	-	-
27	WD	Se/TN	2005	Aug.	5	S	62.0	U	N	W	Y	3	1	-	-	-
28	WD	Se/TN	2005	Aug.	5	L	85.0	U	N	W	Y	2	3	2	-	-
29	MB	Se/TN	2005	Sept.	8	S	57.0	F	N	W	Y	2	1	-	-	-

Rec. #	Capt. Loc.	Capt. Meth.	Year	MM	DD	Cat.	Lgth (cm)	Obs. Sex	Ad. Fin Clip	Origin	Tiss. Samp.	Age _R	Age _S	Spawning Marks		
														1 st	2 nd	3 rd
30	MB	Se/TN	2005	Sept.	8	L	64.0	M	N	W	Y	3	1	-	-	-
31	MB	Se/TN	2005	Sept.	8	S	58.0	M	N	W	Y	?	1	-	-	-
32	MB	Se/TN	2005	Sept.	8	S	56.5	F	N	W	Y	2	1	-	-	-
33	MB	Se/TN	2005	Sept.	8	S	58.0	M	N	W	Y	2	1	-	-	-
34	MB	Se/TN	2005	Sept.	8	S	55.5	M	N	W	Y	2	1	-	-	-
35	MB	Se/TN	2005	Sept.	8	S	60.5	M	N	W	Y	3	1	-	-	-
36	WD	Se/TN	2005	Sept.	8	L	65.5	F	N	W	Y	2	2	1	-	-
37	WD	Se/TN	2005	Sept.	8	S	62.5	M	N	W	Y	3	1	-	-	-
38	WD	Se/TN	2005	Sept.	8	S	56.5	F	N	W	Y	3	1	-	-	-
39	CP	Se/TN	2005	Sept.	14	S	55.5	M	N	W	Y	3	1	-	-	-
40	CP	Se/TN	2005	Sept.	14	S	61.5	M	N	W	Y	2	1	-	-	-
41	CP	Se/TN	2005	Sept.	14	L	63.5	M	N	W	Y	2	1	-	-	-
42	CP	Se/TN	2005	Sept.	14	S	50.5	F	N	LGB _{FRY}	Y	3	1	-	-	-
43	CP	Se/TN	2005	Sept.	14	S	62.5	F	N	W	Y	2	2	1	-	-
44	CP	Se/TN	2005	Sept.	14	S	59.0	M	N	W	Y	?	1	-	-	-
45	CP	Se/TN	2005	Sept.	14	S	53.5	F	N	W	Y	2	1	-	-	-
46	CP	Se/TN	2005	Sept.	14	S	61.5	M	N	W	Y	3	1	-	-	-
47	CP	Se/TN	2005	Sept.	14	S	51.0	M	N	LGB _{FRY}	Y	?	1	-	-	-
48	WD	Se/TN	2006	Aug.	31	L	68.5	F	N	W	Y	2	3	1	2	-
49	WD	Se/TN	2006	Aug.	31	S	51.5	M	N	LGB _{FRY}	Y	2	1	-	-	-
50	WD	Se/TN	2006	Aug.	31	L	65.0	M	N	W	Y	3	1	-	-	-
51	WD	Se/TN	2006	Aug.	31	S	57.5	F	N	W	Y	2	1	-	-	-
52	WD	Se/TN	2006	Aug.	31	S	57.4	M	N	W	Y	2	1	-	-	-
53	WD	Se/TN	2006	Aug.	31	S	51.2	F	Y	LGB _{PARR}	Y	2	1	-	-	-
54	WD	Se/TN	2006	Aug.	31	L	68.5	M	N	W	Y	2	2	1	-	-
55	WD	Se/TN	2006	Aug.	31	S	61.0	F	N	W	Y	3	1	-	-	-
56	WD	Se/TN	2006	Aug.	31	L	63.5	F	N	W	Y	2	2	1	-	-
57	WD	Se/TN	2006	Aug.	31	S	57.7	F	N	W	Y	2	1	-	-	-
58	WD	Se/TN	2006	Aug.	31	S	60.4	M	N	W	Y	2	1	-	-	-
59	WB	Se/TN	2006	Sept.	6	S	58.1	M	N	W	Y	2	1	-	-	-
60	WB	Se/TN	2006	Sept.	6	S	54.6	F	N	LGB _{FRY}	Y	2	1	-	-	-
61	WB	Se/TN	2006	Sept.	6	S	58.0	M	N	W	Y	2	1	-	-	-
62	WB	Se/TN	2006	Sept.	6	S	53.5	M	N	W	Y	4	1	-	-	-
63	WB	Se/TN	2006	Sept.	6	S	60.0	M	N	W	Y	2	1	-	-	-
64	WB	Se/TN	2006	Sept.	6	S	60.5	M	N	W	Y	3	1	-	-	-
65	R	Se/TN	2006	Sept.	7	S	56.8	F	N	W	Y	2	1	-	-	-
66	R	Se/TN	2006	Sept.	7	S	54.6	F	N	W	Y	2	1	-	-	-
67	R	Se/TN	2006	Sept.	7	S	58.4	F	N	W	Y	2	1	-	-	-

Rec. #	Capt. Loc.	Capt. Meth.	Year	MM	DD	Cat.	Lgth (cm)	Obs. Sex	Ad. Fin Clip	Origin	Tiss. Samp.	Age _R	Age _S	Spawning Marks		
														1 st	2 nd	3 rd
68	R	Se/TN	2007	Sept.	6	S	55.5	F	N	W	Y	2	1	-	-	-
69	R	Se/TN	2007	Sept.	6	S	53.5	F	Y	LGB _{PARR}	Y	2	1	-	-	-
70	R	Se/TN	2007	Sept.	6	S	57.0	M	N	LGB _{FRY}	Y	2	1	-	-	-
71	R	Se/TN	2007	Sept.	6	S	57.0	F	N	W	Y	?	?	-	-	-
72	R	Se/TN	2007	Sept.	6	S	56.5	F	Y	LGB _{PARR}	Y	2	1	-	-	-
73	R	Se/TN	2007	Sept.	6	S	50.5	M	N	W	Y	?	1	-	-	-
74	R	Se/TN	2007	Sept.	6	S	52.0	M	N	LGB _{FRY}	Y	3	1	-	-	-
75	LP	Se/TN	2007	Sept.	6	S	52.0	F	N	LGB _{FRY}	Y	2	1	-	-	-
76	WB	Se/TN	2007	Sept.	10	S	50.5	F	N	LGB _{FRY}	Y	2	1	-	-	-
77	WB	Se/TN	2007	Sept.	10	S	55.0	F	N	W	Y	2	1	-	-	-
78	WB	Se/TN	2007	Sept.	10	S	59.5	M	N	W	Y	2	1	-	-	-
79	WB	Se/TN	2007	Sept.	10	S	55.5	F	N	LGB _{FRY}	Y	2	1	-	-	-
80	WB	Se/TN	2007	Sept.	10	S	59.5	M	N	W	Y	2	1	-	-	-
82	MB	Se/TN	2007	Sept.	10	S	57.0	F	N	W	Y	2	1	-	-	-
83	WP	A	2007	Nov.	19	L	-	F	N	W	Y	3	4	1	2	3
84	WD	Se/TN	2008	Sept.	16	S	60.0	M	N	W	Y	2	1	-	-	-
85	WD	Se/TN	2008	Sept.	16	S	54.3	F	N	W	Y	2	1	-	-	-
86	WD	Se/TN	2008	Sept.	16	S	62.5	M	N	W	Y	2	1	-	-	-
87	WD	Se/TN	2008	Sept.	16	S	56.3	F	N	W	Y	2	1	-	-	-
88	WD	Se/TN	2008	Sept.	16	S	52.5	F	N	W	Y	3	1	-	-	-
89	WD	Se/TN	2008	Sept.	16	S	62.0	M	N	W	Y	2	1	-	-	-
90	WD	Se/TN	2008	Sept.	16	S	56.6	F	N	W	Y	2	1	-	-	-
91	WD	Se/TN	2008	Sept.	16	S	61.9	F	N	W	Y	2	1	-	-	-
92	WD	Se/TN	2008	Sept.	16	S	59.3	F	N	W	Y	2	1	-	-	-
93	WD	Se/TN	2008	Sept.	16	S	57.8	F	N	W	Y	2	1	-	-	-
94	WD	Se/TN	2008	Sept.	16	S	54.0	F	N	W	Y	2	1	-	-	-
95	GB	Se/TN	2008	Sept.	17	L	80.0	F	N	LGB _{FRY}	Y	2	2	-	-	-
96	GB	Se/TN	2008	Sept.	17	S	53.2	F	N	W	Y	2	1	-	-	-
97	GB	Se/TN	2008	Sept.	17	S	53.5	F	N	LGB _{FRY}	Y	3	1	-	-	-
98	GB	Se/TN	2008	Sept.	17	S	59.5	M	N	LGB _{FRY}	Y	3	1	-	-	-
99	GB	Se/TN	2008	Sept.	17	S	.	F	N	W	Y	2	1	-	-	-
100	R	Se/TN	2008	Oct.	8	S	57.8	F	N	W	Y	2	1	-	-	-
101	PP	A	2008	Nov.	19	S	51.0	F	Y	LGB _{PARR}	Y	2	1	-	-	-
102	SP	A	2008	Nov.	20	S	54.5	F	N	LGB _{FRY}	Y	2	1	-	-	-
103	SP	A	2008	Nov.	24	S	59.0	F	N	LGB _{FRY}	Y	2	1	-	-	-
104	WP	A	2008	Nov.	25	S	54.5	F	N	W	Y	2	1	-	-	-
105	PP	A	2008	Nov.	27	S	58.5	M	N	W	Y	2	1	-	-	-
106	SP	A	2008	Nov.	27	S	56.0	M	N	W	Y	3	1	-	-	-

Rec. #	Capt. Loc.	Capt. Meth.	Year	MM	DD	Cat.	Lgth (cm)	Obs. Sex	Ad. Fin Clip	Origin	Tiss. Samp.	Age _R	Age _S	Spawning Marks		
														1 st	2 nd	3 rd
107	SP	A	2008	Nov.	28	S	52.0	M	N	W	Y	2	1	-	-	-
108	KP	A	2009	Apr.	28	S	58.5	F	N	W	Y			-	-	-
110	WB	Se/TN	2009	Sept.	10	L	66.5	F	N	W	Y	2	2	1	-	-
112	WB	Se/TN	2009	Sept.	10	S	56.5	M	N	W	Y	2	1	-	-	-
113	KP	A	2009	Nov.	20	S	60.0	M	Y	LGB _{PARR}	Y	2	2	1	-	-
114	AP	A	2009	Nov.	19	S	58.0	M	N	W	Y	2	1	-	-	-
115	PP	A	2009	Nov.	20	S	57.5	F	N	W	Y	?	1	-	-	-
116	WP	A	2009	Nov.	21	S	56.5	F	N	W	Y	2	1	-	-	-
118	AP	A	2009	Nov.	24	S	54.0	M	N	W	Y	2	1	-	-	-
119	CP	A	2009	Nov.	26	S	52.5	F	N	W	Y	2	1	-	-	-
120	KP	A	2009	Dec.	1	S	61.0	F	N	W	Y	3	1	-	-	-
121	KP	A	2009	Dec.	1	S	60.0	M	N	LGB _{FRY}	Y	2	1	-	-	-
122	KP	A	2009	Dec.	1	S	61.5	F	N	W	Y	2	2	1	-	-
123	CP	Se/TN	2010	July	7	L	75.0	F	N	W	Y	2	4	1	2	3
124	CP	Se/TN	2010	July	7	S	57.3	F	N	LGB _{FRY}	Y	2	1	-	-	-
125	CP	Se/TN	2010	July	7	S	54.6	F	N	W	Y	3	1	-	-	-
126	CP	Se/TN	2010	July	7	S	56.8	F	N	LGB _{FRY}	Y	2	1	-	-	-
127	RP	Se/TN	2010	July	29	S	57.6	F	Y	LGB _{PARR}	Y	1	1	-	-	-
128	RP	Se/TN	2010	July	29	S	59.6	M	N	W	Y	2	1	-	-	-
129	RP	Se/TN	2010	July	29	S	56.7	F	Y	LGB _{PARR}	Y	2	1	-	-	-
130	RP	Se/TN	2010	Aug.	10	S	59.6	M	Y	LGB _{PARR}	y	2	1	-	-	-
131	RP	Se/TN	2010	Aug.	10	S	58.7	F	N	LGB _{FRY}	Y	2	1	-	-	-
132	MP	Se/TN	2010	Aug.	10	S	55.0	F	N	W	Y	2	1	-	-	-
133	CP	Se/TN	2010	Sept.	14	S	61.5	F	N	LGB _{FRY}	Y	2	1	-	-	-
134	CP	Se/TN	2010	Sept.	14	S	61.0	M	N	W	Y	2	1	-	-	-
135	CP	Se/TN	2010	Sept.	14	S	59.0	F	N	W	Y	2	1	-	-	-
137	CP	Se/TN	2010	Sept.	14	S	56.5	M	Y	LGB _{PARR}	Y	2	1	-	-	-
138	CP	Se/TN	2010	Sept.	14	S	53.5	F	N	W	Y	2	1	-	-	-
140	CP	Se/TN	2010	Sept.	14	S	58.5	M	Y	LGB _{PARR}	Y	2	1	-	-	-
141	CP	Se/TN	2010	Sept.	14	S	54.0	F	N	W	Y	2	1	-	-	-
142	CP	Se/TN	2010	Sept.	14	S	52.0	F	N	LGB _{FRY}	Y	2	1	-	-	-
143	CP	Se/TN	2010	Sept.	14	S	53.0	F	N	W	Y	2	1	-	-	-
144	CP	Se/TN	2010	Sept.	14	S	60.5	F	N	W	Y	2	1	-	-	-
145	CP	Se/TN	2010	Sept.	14	S	54.5	F	N	W	Y	2	1	-	-	-
146	CP	Se/TN	2010	Sept.	14	S	55.5	F	N	W	Y	2	1	-	-	-
148	WB	Se/TN	2010	Sept.	15	S	52.5	F	N	LGB _{FRY}	Y	2	1	-	-	-
149	WB	Se/TN	2010	Sept.	15	S	55.5	M	N	W	Y	2	1	-	-	-
150	WB	Se/TN	2010	Sept.	15	L	70.0	F	N	W	Y	2	3	1	2	-

Rec. #	Capt. Loc.	Capt. Meth.	Year	MM	DD	Cat.	Lgth (cm)	Obs. Sex	Ad. Fin Clip	Origin	Tiss. Samp.	Age _R	Age _S	Spawning Marks 1 st	2 nd	3 rd
151	WB	Se/TN	2010	Sept.	15	S	55.0	M	N	W	Y	2	1	-	-	-
152	WB	Se/TN	2010	Sept.	15	S	59.0	F	N	W	Y	2	1	-	-	-
153	WB	Se/TN	2010	Sept.	15	S	51.5	F	N	W	Y	2	1	-	-	-
154	WB	Se/TN	2010	Sept.	15	S	55.0	F	N	W	Y	2	1	-	-	-
155	WB	Se/TN	2010	Sept.	15	S	57.5	M	N	W	Y	?	?	-	-	-
156	WB	Se/TN	2010	Sept.	15	S	57.0	M	N	LGB _{FRY}	Y	3	1	-	-	-
157	WB	Se/TN	2010	Sept.	15	S	52.0	F	N	W	Y	2	1	-	-	-
158	WB	Se/TN	2010	Sept.	15	S	53.0	F	N	W	Y	2	1	-	-	-
159	WB	Se/TN	2010	Sept.	15	S	56.5	F	N	W	Y	2	1	-	-	-
160	WB	Se/TN	2010	Sept.	15	S	54.5	F	N	W	Y	2	1	-	-	-
161	WB	Se/TN	2010	Sept.	15	S	57.0	M	N	W	Y	2	1	-	-	-
162	WB	Se/TN	2010	Sept.	15	S	55.0	F	N	W	Y	?	?	-	-	-
165	LP	A	2010	Nov.	15	S	55.5	M	N	W	Y	3	1	-	-	-
168	AP	A	2010	Nov.	16	S	55.5	F	N	W	Y	2	1	-	-	-
171	WP	A	2010	Nov.	17	S	55.0	F	Y	LGB _{PARR}	Y	1	1	-	-	-
172	RP	A	2010	Nov.	19	S	60.5	M	N	LGB _{FRY}	Y	3	1	-	-	-
174	LP	A	2010	Nov.	19	S	56.0	F	N	LGB _{FRY}	Y	2	1	-	-	-
178	KP	A	2010	Nov.	26	S	55.5	F	N	W	Y	2	1	-	-	-
179	KP	A	2010	Nov.	26	S	57.0	F	N	W	Y	2	1	-	-	-
180	KP	A	2010	Nov.	26	S	56.0	F	N	W	Y	2	1	-	-	-
183	RP	Se/TN	2011	Sept.	8	S	51.6	F	N	W	Y	2	1	-	-	-
186	RP	Se/TN	2011	Sept.	8	S	60.3	M	N	LGB _{FRY}	Y	3	1	-	-	-
187	RP	Se/TN	2011	Sept.	8	S	61.6	M	N	W	Y	3	1	-	-	-
188	WD	Se/TN	2011	Sept.	9	S	53.5	F	N	W	Y	2	1	-	-	-
189	WD	Se/TN	2011	Sept.	9	S	58.0	F	N	W	Y	2	1	-	-	-
190	WD	Se/TN	2011	Sept.	9	S	58.0	F	N	W	Y	2	1	-	-	-
191	WD	Se/TN	2011	Sept.	9	S	54.0	M	N	W	Y	2	1	-	-	-
192	MB	Se/TN	2011	Sept.	9	S	56.3	M	N	W	Y	3	1	-	-	-
193	MB	Se/TN	2011	Sept.	9	S	54.0	F	N	W	Y	2	1	-	-	-
194	RP	A	2011	Nov.	9	S	53.0	F	N	W	Y	2	1	-	-	-
195	RP	A	2011	Nov.	9	S	55.5	F	N	LGB _{FRY}	Y	2	1	-	-	-
196	RP	A	2011	Nov.	9	S	54.5	F	N	LGB _{FRY}	Y	2	1	-	-	-
197	LP	A	2011	Nov.	10	S	56.5	F	N	W	Y	?	1	-	-	-
198	CP	A	2011	Nov.	10	S	55.0	F	N	W	Y	2	1	-	-	-
199	MP	A	2011	Nov.	10	S	55.5	F	N	W	Y	2	1	-	-	-
203	LP	A	2011	Nov.	18	S	53.5	F	N	W	Y	2	1	-	-	-
204	CP	A	2011	Nov.	18	S	61.0	M	N	LGB _{FRY}	Y	2	1	-	-	-
205	AP	A	2011	Nov.	21	S	58.5	M	N	W	Y	3	1	-	-	-

Rec. #	Capt. Loc.	Capt. Meth.	Year	MM	DD	Cat.	Lgth (cm)	Obs. Sex	Ad. Fin Clip	Origin	Tiss. Samp.	Age _R	Age _S	Spawning Marks 1 st	2 nd	3 rd
206	WP	A	2011	Nov.	21	S	52.5	F	N	W	Y	2	1	-	-	-
208	LoP	A	2011	Nov.	21	S	57.5	F	N	W	Y	2	1	-	-	-
209	AP	A	2011	Nov.	29	S	62.0	M	N	W	Y	2	1	-	-	-
210	WP	A	2011	Nov.	29	S	59.5	M	N	W	Y	?	1	-	-	-
211	WP	A	2011	Nov.	29	S	52.0	F	N	W	Y	2	1	-	-	-
222	MP	Se/TN	2014	Sept.	9		80.0	F	N	LGB _{FRY}	Y	2	3	2	-	-
228	WD	Se/TN	2014	Sept.	9	S	53.1	F	N	W	Y	2	1	-	-	-
231	WD	Se/TN	2014	Sept.	9	S	52.3	F	N	W	Y	2	1	-	-	-
232	WD	Se/TN	2014	Sept.	9	S	55.6	F	N	W	Y	?	?	-	-	-
234	MP	Se/TN	2015	Sept.	17	S	53.5	F	N	W	Y		1	-	-	-
236	MP	Se/TN	2015	Sept.	17	S	60.0	F	N	W	Y	2	1	-	-	-
238	RP	Se/TN	2015	Sept.	17	S	55.0	F	N	W	Y	2	1	-	-	-
239	RP	Se/TN	2015	Sept.	17	S	56.5	F	N	W	Y	2	1	-	-	-
240	RP	Se/TN	2015	Sept.	17	S	51.5	M	N	W	Y		1	-	-	-
241	RP	Se/TN	2015	Sept.	17	S	55.0	F	N	LGB _{FRY}	Y	2	1	-	-	-
242	WD	Se/TN	2015	Sept.	18	S	58.5	F	N	W	Y	2	1	-	-	-
243	WD	Se/TN	2015	Sept.	18	S	60.5	F	N	W	Y	2	1	-	-	-
244	MB	Se/TN	2015	Sept.	18	S	60.0	F	N	W	Y	2	1	-	-	-
245	MB	Se/TN	2015	Sept.	18	S	56.5	M	N	W	Y	2	1	-	-	-
246	MB	Se/TN	2015	Sept.	18	S	52.5	F	N	W	Y	2	1	-	-	-
247	MP	Se/TN	2016	Oct.	4	L	64.3	F	N	W	Y	2	2	1	-	-
248	MP	Se/TN	2016	Oct.	4	S	54.7	M	N	LGB _{FRY}	Y	2	1	-	-	-
249	MP	Se/TN	2016	Oct.	4	S	59.9	M	N	LGB _{FRY}	Y	2	1	-	-	-
250	MP	Se/TN	2016	Oct.	4	S	53.6	M	N	LGB _{FRY}	Y	2	1	-	-	-
163	LoP	A	2010	Nov.	9	S	52.5	F	No	RECAP	RECAP	2	1	-	-	-
175	RP	A	2010	Nov.	19	S	54.5	F	No	RECAP	RECAP	-	-	-	-	-
173	LP	A	2010	Nov.	19	S	59.0	F	No	RECAP	RECAP	2	1	-	-	-
139	CP	Se/TN	2010	Sept.	14	S	60.5	M	No	RECAP	RECAP	2	1	-	-	-
200	MP	A	2011	Nov.	10	S	60.5	M	No	RECAP	RECAP	3	1	-	-	-
207	WP	A	2011	Nov.	21	S	60.5	M	No	RECAP	RECAP	-	-	-	-	-
166	LP	A	2010	Nov.	15	L	72.0	M	No	RECAP	RECAP	-	-	-	-	-
181	AP	A	2010	Dec.	15	L	73.0	F	No	RECAP	RECAP	-	-	-	-	-
RECAP	AP	A	2008	Nov.	20	L	80.5	F	No	RECAP	RECAP	-	-	-	-	-
201	MP	A	2011	Nov.	10	L	<50	F	No	RECAP	RECAP	-	-	-	-	-
117	LP	A	2009	Nov.	24	S	33.0	M	Yes	LGB _{PS}	Y	2	-	-	-	-
109	RP	A	2009	Sept.	8	S	37.0	U	Yes	LGB _{PS}	Y	2	-	-	-	-
185	RP	Se/TN	2011	Sept.	8	S	39.3	M	Yes	LGB _{PS}	Y	2	-	-	-	-
184	RP	Se/TN	2011	Sept.	8	S	39.9	un	Yes	LGB _{PS}	Y	2	-	-	-	-

Rec. #	Capt. Loc.	Capt. Meth.	Year	MM	DD	Cat.	Lgth (cm)	Obs. Sex	Ad. Fin Clip	Origin	Tiss. Samp.	Age _R	Age _S	Spawning Marks		
														1 st	2 nd	3 rd
202	MP	A	2011	Nov.	10	L	<35	M	Yes	LGB _{PS}	N	-	-	-	-	-
170	AP	A	2010	Nov.	16	L	70.5	F	No	AE	Y	1	1	-	-	-
136	CP	Se/TN	2010	Sept.	14	L	72.0	F	No	AE	Y	1	1	-	-	-
177	AP	A	2010	Nov.	22	L	73.0	F	No	AE	Y	1	1	-	-	-
81	MB	Se/TN	2007	Sept.	10	L	85.0	F	No	AE	Y	1	2	-	-	-
164	LP	A	2010	Nov.	15	L	>72	F	No	AE	Y	1	1	-	-	-
167	RP	A	2010	Nov.	15	L	>74	F	No	AE	Y	1	1	-	-	-
176	AP	A	2010	Nov.	22	L	>75	F	No	AE	Y	1	1	-	-	-
182	RP	A	2010	Dec.	15	L	>75	F	No	AE	N	-	-	-	-	-
169	SP	A	2010	Nov.	16	S	57.5	M	Yes	H/AC	Y	1	1	-	-	-
147	CP	Se/TN	2010	Sept.	14	S	58.0	F	Yes	H/AC	Y	1	1	-	-	-
111	WB	Se/TN	2009	Sept.	10	S	79.0	F	Yes	H/AC	Y	2	2	-	-	-
224	MP	Se/TN	2014	Sept.	9	S	43.9	F	Yes	LGB _{PG}	Y	2	1	-	-	-
221	RP	M	2014	Sept.	8	S	45.0	F	Yes	LGB _{PG}	Y	2	1	-	-	-
218	RP	Se/TN	2014	Sept.	8	S	46.9	M	Yes	LGB _{PG}	Y	1	1	-	-	-
226	MP	Se/TN	2014	Sept.	9	S	48.4	F	Yes	LGB _{PG}	Y	2	1	-	-	-
214	RP	Se/TN	2014	Sept.	8	S	48.6	F	Yes	LGB _{PG}	Y	2	1	-	-	-
220	RP	Se/TN	2014	Sept.	8	S	48.7	F	Yes	LGB _{PG}	Y	2	1	-	-	-
225	MP	Se/TN	2014	Sept.	9	S	49.6	M	Yes	LGB _{PG}	Y	1	1	-	-	-
217	RP	Se/TN	2014	Sept.	8	S	49.9	M	Yes	LGB _{PG}	Y	2	1	-	-	-
227	MP	Se/TN	2014	Sept.	9	S	49.9	M	Yes	LGB _{PG}	Y	2	1	-	-	-
215	RP	Se/TN	2014	Sept.	8	S	51.3	F	Yes	LGB _{PG}	Y	2	1	-	-	-
233	WD	Se/TN	2014	Sept.	9	S	51.4	M	Yes	LGB _{PG}	Y	1	1	-	-	-
237	MP	Se/TN	2015	Sept.	17	S	51.5	F	Yes	LGB _{PG}	Y	2	2	1	-	-
219	RP	Se/TN	2014	Sept.	8	S	51.6	M	Yes	LGB _{PG}	Y	?	1	-	-	-
212	RP	Se/TN	2014	Sept.	8	S	51.9	F	Yes	LGB _{PG}	Y	2	1	-	-	-
223	MP	Se/TN	2014	Sept.	9	S	53.6	M	Yes	LGB _{PG}	Y	2	1	-	-	-
230	WD	Se/TN	2014	Sept.	9	S	53.6	M	Yes	LGB _{PG}	Y	3	1	-	-	-
216	RP	Se/TN	2014	Sept.	8	S	55.3	F	Yes	LGB _{PG}	Y	2	1	-	-	-
213	RP	Se/TN	2014	Sept.	8	S	56.6	M	Yes	LGB _{PG}	Y	2	1	-	-	-
229	WD	Se/TN	2014	Sept.	9	S	56.8	M	Yes	LGB _{PG}	Y	2	1	-	-	-
235	MP	Se/TN	2015	Sept.	17	S	62.5	M	Yes	LGB _{PG}	Y	2	2	1	-	-

Appendix 9. Summary of electrofishing survey on the Stewiacke River during 2013.

Tributary	Latitude	Longitude	Area (m ²)	MM	DD	Shock Time (sec)	Atlantic Salmon	American Eel	Brook Trout	Brown Trout	White Sucker	Blacknose Dace	Common Shiner	Creek Chub	Lake Chub	Lamprey
Little River	45.24363	63.27689	701	8	21	650	0	81	0	1	1	1	0	0	7	1
	45.25326	63.27189	377	8	21	446	0	53	4	2	11	8	0	2	20	1
	45.26760	63.23023	329	8	21	931	0	58	4	0	0	0	0	0	2	0
	45.26049	63.27196	770	8	21	1,036	0	41	0	2	6	1	0	0	26	0
	45.27068	63.26373	980	8	22	985	0	58	8	1	16	13	1	0	34	0
	45.27099	63.26072	710	8	23	693	0	62	7	0	6	6	0	0	2	0
	45.19624	63.24228	829	8	30	1,343	6	45	0	0	5	3	0	1	0	0
Putnam Brook	45.22740	63.15577	425	9	10	1,456	5	10	11	4	0	0	0	0	0	0
Rutherford Brook	45.29445	63.13309	344	8	22	472	22	10	2	8	6	7	0	0	1	2
Mainstem I	45.25831	63.11263	222	8	22	595	2	22	0	1	1	1	0	0	5	0
	45.25483	63.11493	781	9	10	1,325	12	22	0	4	2	8	1	0	0	0
	45.26733	63.12178	455	9	10	1,217	3	7	0	4	0	2	0	0	3	1
	45.37046	62.83668	273	8	26	1,810	1	15	9	0	10	42	0	6	13	1
	45.37075	62.83559	153	8	26	315	0	0	10	0	6	6	0	0	4	0
	45.36980	62.83830	470	8	26	710	3	4	8	1	15	16	0	0	16	1
	45.36710	62.84290	146	8	26	479	1	2	1	2	7	39	1	0	2	0
Fall Brook	45.36115	62.85447	381	8	26	886	2	8	7	2	8	16	0	0	4	0
Mainstem II	45.36070	62.85340	287	8	26	538	0	9	5	2	0	13	0	0	2	0
Sutherland Brook	45.31649	62.88727	538	8	20	1,753	16	5	0	2	7	3	0	0	32	0
	45.35630	62.86416	315	8	26	583	2	2	4	2	4	15	0	0	0	0
	45.35158	62.87730	800	8	27	1,050	20	13	2	10	7	60	1	0	2	0
	45.34783	62.88440	488	8	27	1,030	14	8	2	17	5	29	0	0	2	0
	45.34144	62.89201	500	8	28	1,061	9	5	4	3	0	4	7	0	16	0
	45.31726	62.88857	392	9	11	740	39	1	0	1	0	3	0	0	3	0
	45.32490	62.89158	437	9	11	1,001	15	2	0	1	1	9	0	0	4	0
Big/Little Branch	45.35646	62.86481	569	8	26	704	0	2	18	0	0	3	0	0	4	0
Big/Little Branch	45.34455	62.89191	652	8	27	1,302	24	5	14	3	1	9	0	0	27	0
	45.34433	62.89518	694	8	27	1,111	6	4	8	5	1	2	1	0	23	0
	45.34344	62.89638	363	9	11	808	3	0	4	2	0	5	1	0	0	0

Tributary	Latitude	Longitude	Area (m ²)	MM	DD	Shock Time (sec)	Atlantic Salmon	American Eel	Brook Trout	Brown Trout	White Sucker	Blacknose Dace	Common Shiner	Creek Chub	Lake Chub	Lamprey
	45.34365	62.89613	410	9	11	633	9	3	1	0	1	0	0	0	5	0
Cox Brook	45.34283	62.89149	610	8	28	937	13	2	13	9	0	9	0	0	12	0
	45.27096	62.86789	563	8	28	1,976	1	31	0	20	9	4	0	0	0	0
Newton Brook	45.20205	62.87794	400	8	30	963	0	5	19	31	0	0	0	0	0	0
	45.21252	62.89203	309	8	30	1,241	12	6	17	10 7	0	0	0	0	0	0
	45.23051	62.92527	435	8	30	1,440	4	9	0	51	0	0	0	0	0	0
Goshen Brook	45.18121	63.00188	286	9	6	919	0	0	10	22	0	0	0	0	0	0
	45.18375	63.00443	326	9	6	816	28	0	7	38	0	0	0	0	0	0
Blackie Brook	45.22726	62.94517	544	9	6	1,701	3	2	5	30	1	0	0	0	0	0
Pembroke Brook	45.28610	62.95680	364	9	9	950	88	4	0	2	0	1	0	0	0	0
	45.26461	62.94009	325	9	9	860	39	3	0	6	0	0	1	0	0	0

Appendix 10. Detailed summary of the genetic parental analysis for the Stewiacke River Atlantic Salmon juveniles sampled during the electrofishing survey in 2013. "LGB" = Live Gene Bank, "F" = female, "M" = male, "Ad" = adult, "Rel" = release, "Juv" = juvenile, "Sp" = spawned, "U" = unknown.

Site	Live Gene Bank Offspring Release				Female Adult Release			Female Juvenile Release Spawned as Adult			
	2012 LGB Cross (0+ Fry)	2011 LGB Cross (1+ Parr)	2010 LGB Cross (2+ Parr)	2009/8 LGB Cross (3+/4+ Parr)	2 F Ad Rel + 1 M Ad Angled (Parr Rel)	5 F Ad Rel + 8 M Juv Rel Sp as Parr	2 F Ad Rel + M U	2 F Fry Rel + 2 M Fry Rel Sp as Ad (4.0/3.1)	6 F Fry Rel + 11 M Juv Rel Sp as Parr	2 F Fry Rel + 4 M U	2 F Parr/Smolt Rel + 3 M Juv Rel Sp as Parr
Big/Little Branch	23	5	13	0	4	1	0	0	5	1	0
Blackie Brook	0	0	3	0	0	0	0	0	0	0	0
Cox Brook	0	0	1	0	0	0	0	0	0	0	0
Goshen Brook	8	14	2	0	0	0	0	1	2	0	0
Little River	0	6	0	0	0	0	0	0	0	0	0
Mainstem I	0	0	0	1	2	1	0	0	0	0	3
Mainstem II (Lower)	52	1	6	0	0	0	1	1	1	0	0
Mainstem II (Upper)	10	1	3	0	7	19	3	0	0	0	0
Newton Brook (Upper)	0	0	12	0	0	0	0	0	0	0	0
Newton Brook (Lower)	0	1	2	0	0	0	0	0	0	0	1
Pembroke Brook (Lower)	36	0	0	0	0	0	0	0	1	0	0
Pembroke Brook (Upper)	87	0	1	0	0	0	0	0	0	0	0
Putnam Brook	0	0	5	0	0	0	0	0	0	0	0
Rutherford Brook (Lower)	1	15	0	1	0	0	0	0	0	0	0
Rutherford Brook (Upper)	0	3	5	1	0	0	0	0	5	7	0

Appendix 10 (continued). Detailed summary of the genetic parental analysis of the Stewiacke River Atlantic Salmon juveniles sampled during the electrofishing survey in 2013. "LGB" = Live Gene Bank, "F" = female, "M" = male, "Ad" = adult, "Rel" = release, "Juv" = juvenile, "Sp" = spawned, "U" = unknown.

Site	Female Wild Offspring of Two Salmon River (Colc.) Adult Releases 1 F Sp as Ad + 1 M Juv Rel Sp as Parr	Female Unknown 1 F U + 1 M Juv Rel Sp as Parr	Both Sexes Unknown	Total
Big/Little Branch	0	0	0	52
Blackie Brook	0	0	0	3
Cox Brook	0	0	0	1
Goshen Brook	0	0	0	27
Little River	0	0	0	6
Mainstem I	0	0	0	7
Mainstem II (Lower)	6	0	0	68
Mainstem II (Upper)	0	0	1	44
Newton Brook (Upper)	0	0	0	12
Newton Brook (Lower)	0	0	0	4
Pembroke Brook (Lower)	0	0	0	37
Pembroke Brook (Upper)	0	0	0	88
Putnam Brook	0	0	0	5
Rutherford Brook (Lower)	0	0	0	17
Rutherford Brook (Upper)	0	1	0	22

Appendix 11. Summary of the Inner Bay of Fundy (IBoF) non-LGB supported rivers broadscale electrofishing survey in 2014. "NC" = not collected, "–" = assessment data not available.

River and Tributary	Latitude	Longitude	Area (m ²)	Month	Day	Shock Time (sec)	Atlantic Salmon	American Eel	Brook Trout	Brown Trout	Rainbow Trout	Blacknose Dace	Common Shiner	Chub sp.	Creek Chub	Lake Chub	Golden Shiner	Slimy Sculpin	Stickleback sp.	White Sucker
Apple River																				
South Branch	45.43459	64.80157	597	Aug.	14	859	0	5	4	0	0	0	0	0	0	0	0	0	0	0
East Apple River	45.47207	64.76703	528	Aug.	14	714	0	15	0	0	0	0	0	0	0	0	0	0	0	0
Fowler Brook	45.42253	64.78960	388	Aug.	14	608	0	8	3	0	0	0	0	0	0	0	0	0	0	0
Avon River																				
Mainstem	45.06509	64.35705		Data Lost			-	-	-	-	-	-	-	-	-	-	-	-	-	-
	44.92738	64.30700		Data Lost			-	-	-	-	-	-	-	-	-	-	-	-	-	-
Bains Brook																				
Mainstem	45.31463	65.65050	1,026	Sept.	10	NC	0	10	8	0	0	0	0	0	0	0	0	0	0	0
	45.33479	65.63924	774	Sept.	9	NC	0	0	40	0	0	0	0	0	0	0	0	0	0	0
	45.36522	65.59565	803	Sept.	9	NC	0	17	24	0	0	6	0	0	0	0	0	0	0	0
Bass River																				
West Branch	45.44330	63.80592	324	Sept.	15	613	0	2	22	0	0	0	0	0	0	0	0	0	0	0
Mainstem	45.43862	63.77189	343	Sept.	15	680	0	17	8	0	0	0	0	0	0	0	0	0	0	0
	45.41560	63.77910	242	Sept.	15	661	0	11	18	0	0	0	0	0	0	0	0	0	0	0
West Branch (left branch only)	45.44199	63.79212	224	Sept.	15	300	0	3	23	0	0	0	0	0	0	0	0	0	0	0
Black River																				
Mainstem	45.32923	65.78213	1,053	Sept.	11	NC	9	0	30	0	0	67	0	0	0	0	0	0	2	2
	45.30600	65.84844	706	Sept.	11	NC	31	3	23	0	0	43	0	0	0	0	0	0	0	0
Carters Brook																				
Mainstem	45.88854	64.42525	465	Aug.	26	NC	0	23	37	0	0	0	0	0	0	0	0	0	0	17
	45.89520	64.43434	520	Aug.	26	NC	0	9	34	0	0	0	0	0	0	0	0	0	0	0
Chiganois River																				
Mainstem	45.45024	63.38034	3,499	Sept.	17	762	0	11	0	0	0	32	0	0	0	0	0	0	0	0
	45.42324	63.38363	346	Sept.	17	698	0	22	0	0	0	48	0	0	0	0	0	0	0	2
Staples Brook	45.45180	63.39568	220	Sept.	17	517	0	6	3	0	0	90	0	0	0	0	0	0	0	2
Crooked Creek																				
Mainstem	45.74894	64.74883	265	Aug.	29	671	0	0	0	0	6	0	0	0	0	0	0	8	0	0

River and Tributary	Latitude	Longitude	Area (m ²)	Month	Day	Shock Time (sec)	Atlantic Salmon	American Eel	Brook Trout	Brown Trout	Rainbow Trout	Blacknose Dace	Common Shiner	Chub sp.	Creek Chub	Lake Chub	Golden Shiner	Slimy Sculpin	Stickleback sp.	White Sucker
Demoiselle Creek																				
Mainstem	45.85990	64.67908	266	Sept.	8	500	0	1	2	0	0	0	0	0	0	0	0	0	0	0
	45.85088	64.64117	275	Sept.	8	502	0	1	1	0	0	0	0	0	0	0	0	0	2	0
Diligent River																				
Mainstem	45.42256	64.36476	675	Aug.	27	NC	0	0	136	0	0	0	0	0	0	0	0	0	2	0
Emerson Creek																				
Mainstem	45.28294	65.76090	606	Sept.	12	NC	0	13	28	0	0	0	0	0	0	0	0	0	0	0
	45.31913	65.74081	679	Sept.	12	NC	0	8	58	0	0	3	0	0	0	0	0	0	0	0
Gardner Creek																				
Mainstem	45.32820	65.69418	599	Sept.	10	NC	0	14	36	0	0	46	0	0	0	0	0	0	0	0
	45.29777	65.71078	790	Sept.	10	NC	0	30	6	0	0	142	0	0	0	0	0	0	0	0
Great Village River																				
Rockland Brook	45.47686	63.60912	373	Sept.	29	624	1	1	3	0	0	7	0	0	0	0	0	0	0	0
Mainstem	45.41845	63.59699	411	Sept.	29	455	0	5	0	0	0	18	0	0	0	0	0	0	0	0
	45.47606	63.61209	264	Sept.	29	614	0	0	3	0	0	11	0	0	0	0	0	0	0	0
	45.43802	63.59924	716	Sept.	29	532	0	0	2	0	0	19	0	0	0	1	0	0	0	0
Halfway River																				
Mainstem	45.04378	64.19210	409	Sept.	30	403	0	28	0	0	0	0	0	0	0	7	0	0	0	0
	45.04552	64.19325	139	Sept.	30	528	0	60	0	0	0	0	0	0	0	21	0	0	0	6
Harrington River																				
Mainstem	45.42046	64.10896	832	Sept.	5	1,051	0	19	21	0	0	0	0	0	0	0	0	0	0	0
	45.41808	64.10583	578	Sept.	5	598	0	6	5	0	0	0	0	0	0	0	0	0	0	0
	45.42315	64.11196	352	Sept.	5	922	0	5	28	0	0	0	0	0	0	0	0	0	0	0
	45.42472	64.11400	565	Sept.	5	798	0	7	21	0	0	0	0	0	0	0	0	0	0	0
River Hebert																				
Atkinson Brook	45.59673	64.40435	515	Aug.	11	718	0	2	9	0	0	10	0	0	0	0	0	0	0	0
Kelley River	45.58803	64.45027	1,120	Aug.	11	892	0	19	0	0	0	18	0	0	0	0	0	0	0	3
	45.63815	64.38543	1,504	Aug.	11	1,262	0	14	0	0	0	2	0	0	2	0	0	0	0	1
Irish River																				
Mainstem	45.38956	65.54916	1,060	Sept.	8	NC	0	5	18	0	0	0	0	0	0	0	0	0	0	0
	45.42110	65.55462	1,053	Sept.	9	NC	4	7	9	0	0	0	0	0	0	0	0	0	0	0
	45.42987	65.55790	938	Sept.	9	NC	0	16	29	0	0	0	0	0	0	0	0	0	0	0
	45.43333	65.52777	468	Sept.	9	NC	0	0	68	0	0	0	0	0	0	0	0	0	0	0

River and Tributary	Latitude	Longitude	Area (m ²)	Month	Day	Shock Time (sec)	Atlantic Salmon	American Eel	Brook Trout	Brown Trout	Rainbow Trout	Blacknose Dace	Common Shiner	Chub sp.	Creek Chub	Lake Chub	Golden Shiner	Slimy Sculpin	Stickleback sp.	White Sucker
Kennetcook River																				
Mainstem	45.19263	63.68098	139	Oct.	2	888	0	28	0	0	0	0	0	0	0	0	0	0	0	24
	45.19948	63.65333	200	Oct.	2	428	0	5	3	0	0	0	0	0	2	0	0	0	0	4
	45.10323	63.82896	99	Oct.	2	463	0	6	3	0	0	0	0	0	0	1	0	0	0	2
Little Salmon River																				
Mainstem	45.48247	65.28703	643	Sept.	26	811	0	14	4	0	0	1	0	0	0	0	0	0	0	0
Maccan River																				
Southampton Branch	45.58143	64.14194	731	Aug.	13	955	0	20	0	25	0	2	0	0	0	0	0	0	0	0
	45.59800	64.10033	620	Aug.	13	1,088	0	12	0	45	0	0	0	0	0	0	0	0	0	0
	45.58559	64.16409	966	Aug.	13	1,070	0	23	0	17	0	11	0	0	0	0	1	0	0	0
	45.59111	64.20248	714	Aug.	13	967	0	23	0	3	0	16	0	0	0	0	0	0	0	0
Memramcook River																				
Mainstem	46.07115	64.44757	464	Aug.	29	574	0	4	0	0	0	7	11	0	0	0	0	0	0	0
	46.08087	64.48880	842	Aug.	29	888	0	14	0	0	0	10	1	0	0	0	0	0	0	3
Stoney Creek	46.04451	64.55714	816	Aug.	26	NC	0	9	1	0	0	40	2	2	0	0	0	0	0	7
Mispec River																				
Mainstem	45.30883	65.88228	814	Sept.	11	NC	7	0	0	0	20	97	0	2	0	0	0	0	0	2
Moose River																				
Mainstem	45.42019	64.19186	625	Aug.	27	NC	0	25	8	0	0	30	0	0	0	0	0	0	0	0
Mosher River																				
Mainstem	45.34343	65.56667	608	Sept.	12	NC	1	3	45	0	0	0	0	0	0	0	0	0	0	0
North River (Cumberland)																				
Mainstem	45.41413	64.08330	264	Sept.	15	623	0	17	6	0	0	0	0	0	0	0	0	0	0	0
North River (Colchester)																				
Mainstem	45.45555	63.21200	511	Sept.	12	891	0	26	0	0	0	88	0	0	0	0	0	0	0	0
	45.49606	63.21195	201	Sept.	10	748	0	41	1	4	0	74	0	0	0	0	0	0	0	0
	45.42582	63.25380	1,107	Sept.	10	912	0	22	0	0	0	56	0	0	0	0	0	0	0	0
West Brook	45.45203	63.25413	213	Sept.	12	436	0	10	0	0	0	30	0	0	0	0	0	0	0	0
Middle Branch	45.49569	63.21304	318	Sept.	10	752	0	5	4	1	0	76	0	0	0	0	0	0	0	0
South Branch	45.43875	63.21774	421	Sept.	10	697	0	12	0	0	0	195	0	0	0	0	0	0	0	0
Parrsboro River																				
Jeffers Brook	45.46241	64.33446	1,140	Aug.	27	NC	0	10	45	0	0	0	0	0	0	0	0	0	0	0

River and Tributary	Latitude	Longitude	Area (m ²)	Month	Day	Shock Time (sec)	Atlantic Salmon	American Eel	Brook Trout	Brown Trout	Rainbow Trout	Blacknose Dace	Common Shiner	Chub sp.	Creek Chub	Lake Chub	Golden Shiner	Slimy Sculpin	Stickleback sp.	White Sucker
Farrells Brook	45.42822	64.33739	591	Aug.	27	NC	0	115	3	0	0	1	0	1	0	0	0	0	0	5
Portapique River																				
Matheson Brook	45.47001	63.68596	185	Sept.	16	729	0	1	83	0	0	0	0	0	0	0	0	0	0	0
Cook Brook	45.42110	63.71075	202	Sept.	16	622	0	12	7	0	0	26	0	0	0	0	0	0	0	0
Mainstem	45.42919	63.70335	430	Sept.	16	813	2	14	5	0	0	3	0	0	0	0	0	0	0	0
	45.44238	63.69924	708	Sept.	16	1,176	1	18	5	0	0	25	0	0	0	0	0	0	0	0
Quiddy River																				
Mainstem	45.50633	65.19368	720	Aug.	11	505	0	3	3	0	0	0	0	0	0	0	0	0	0	0
	45.50741	65.19347	394	Aug.	11	502	0	5	0	0	0	1	0	0	0	0	0	0	0	0
Ramshead River																				
Mainstem	45.42133	64.46361	405	Aug.	27	NC	0	4	10	0	0	0	0	0	0	0	0	0	0	0
Salmon River (Colchester)																				
Black Brook	45.42462	63.04550	638	Sept.	11	1,038	1 6	11	0	0	0	125	0	4	0	0	0	0	0	11
Mainstem	45.42870	63.08070	546	Sept.	11	1,010	1 0	33	0	0	0	94	0	0	0	0	0	0	0	3
	45.48134	63.06982	411	Sept.	12	1,004	1 9	21	0	0	0	88	0	0	0	0	0	0	0	6
Shepody River																				
Mainstem	45.66974	64.81747	209	Aug.	29	506	0	0	6	0	4	0	0	0	0	0	0	151	0	0
Shubenacadie River																				
Mainstem	45.06839	63.54396	285	Oct.	2	511	0	3	1	0	0	34	0	0	9	0	0	0	0	0
	45.12460	63.29201	377	Sept.	18	673	0	26	0	0	0	0	6	0	27	0	0	0	0	0
	45.04087	63.37418	379	Oct.	2	769	0	32	21	0	0	0	0	0	10	0	0	0	0	0
	45.13311	63.24889	638	Oct.	1	719	0	40	5	0	0	0	2	0	21	0	0	0	0	5
	44.98299	63.50102	630	Oct.	2	717	0	38	0	0	0	0	0	0	0	0	0	0	0	0
St. Croix River																				
Meander River	45.03176	63.88314				Data lost	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	44.99410	64.00175				Data lost	-	-	-	-	-	-	-	-	-	-	-	-	-	-