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Stock Composition and Ocean Spatial Distribution Inference from California Recreational Chinook Salmon Fisheries Using Genetic Stock Identification

William H. Satterthwaite

Javier Ciancio

Eric D. Crandall

California State University, Monterey Bay, ecrandall@csumb.edu

Melodie L. Palmer-Zwahlen

Allen M. Grover

See next page for additional authors

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Authors

William H. Satterthwaite, Javier Ciancio, Eric D. Crandall, Melodie L. Palmer-Zwahlen, Allen M. Grover, Michael R. O'Farrell, Eric C. Anderson, Michael S. Mohr, and John Carlos Garza

1 **Stock composition and ocean spatial distribution inference from California recreational**
2 **Chinook salmon fisheries using Genetic Stock Identification**

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4 William H. Satterthwaite¹

5 Javier Ciancio^{2,3}

6 Eric Crandall^{2,4}

7 Melodie L. Palmer-Zwahlen⁵

8 Allen M. Grover^{5,6}

9 Michael R. O'Farrell¹

10 Eric C. Anderson¹

11 Michael S. Mohr¹

12 John Carlos Garza¹

13

14 ¹Fisheries Ecology Division, Southwest Fisheries Science Center

15 National Marine Fisheries Service, NOAA

16 110 Shaffer Rd, Santa Cruz, CA 95060 USA

17

18 ²Institute of Marine Sciences

19 University of California, Santa Cruz

20 1156 High Street

21 Santa Cruz, CA 95064 USA

22

23 ³Present address:

24 Centro Nacional Patagónico-CONICET

25 Bvd. Brown 2915

26 U9120ACD Puerto Madryn Argentina

27

28 ⁴Present address:

29 Division of Science and Environmental Policy

30 California State University, Monterey Bay

31 100 Campus Center, Seaside, CA 93955 USA

32

33 ⁵Marine Region, Ocean Salmon Project

34 California Department of Fish and Wildlife

35 5355 Skylane Blvd Suite B

36 Santa Rosa, California 95403, USA

37

38 ⁶Present address:

39 Institute of Marine Sciences

40 University of California, Santa Cruz

41 1156 High Street

42 Santa Cruz, CA 95064 USA

43

44 Corresponding author: William Satterthwaite, +1 (831) 420-3997, will.satterthwaite@noaa.gov

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48

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50 Collected the data: MPZ, AG, JC

51 Analyzed the data: WS, EC, JC, EA, MO

52 Wrote the paper: WS, EC, MO, MM, JCG

53 Revised the paper: all

54 Designed the study / framed hypotheses: WS, EC, MO, MM, JCG, MPZ, AG

55 **Abstract**

56 We apply genetic stock identification (GSI) data and models of the catch and sampling process
57 to describe spatial and temporal patterns in the stock composition and stock-specific catch-per-
58 unit-effort (CPUE) of both tagged and untagged stocks encountered in California recreational
59 ocean Chinook salmon fisheries during the period 1998-2002. Spatial and temporal distributions
60 inferred from GSI sampling of stocks with tagged hatchery components were broadly consistent
61 with those previously inferred from studies of tag recoveries alone, while GSI provided
62 additional insight into untagged stocks of conservation concern. The catch in all times and areas
63 was dominated (typically $\geq 90\%$) by the “Central Valley Fall” genetic reporting group, which is
64 comprised primarily of Sacramento River fall run Chinook. Other contributing stocks were more
65 spread out in space and time with the exception of Central Valley winter run Chinook, which
66 were rarely encountered by boats fishing in port areas north of Point Reyes. Localized stock-
67 specific CPUE appeared to increase near a stock’s respective natal river while decreasing in
68 other port areas at the time of adult return to freshwater for spawning. We describe methods for
69 quantifying uncertainty in stock proportions, stock-specific catch, and determining the statistical
70 support for proposed management boundaries hypothesized to represent “break points” in the
71 spatial distributions for stocks of concern, and find at most equivocal support for a proposed
72 delineation line at Point Reyes in north-central California.

73

74 **1. Introduction**

75 Ocean salmon fisheries on the west coast of North America are generally mixed-stock
76 fisheries, in that fish harvested in any given area usually come from multiple source rivers
77 (Winans et al. 2001, Weitkamp and Neely 2002, Weitkamp 2010). While some stocks are usually

78 relatively abundant and productive, their harvest is often constrained to protect less abundant or
79 weaker stocks, including those managed under the U.S. Endangered Species Act (ESA) as
80 “threatened” or “endangered” (Pacific Fishery Management Council [PFMC] 2012, 2013). The
81 goal of “weak stock management,” as practiced for these mixed-stock ocean salmon fisheries, is
82 to maximize overall harvest opportunity while simultaneously meeting conservation benchmarks
83 for all managed stocks. The primary tools used in California for implementing weak stock
84 management are 1) allowing fishing only in specific times and areas (i.e., time-area fisheries) to
85 minimize impacts on weak stocks and/or 2) establishing catch quotas. Currently, spatial
86 management of salmon fisheries off the coast of California is accomplished primarily through
87 seasonal openings of fisheries at relatively broad spatial scales, corresponding to the ocean areas
88 delineated in Figure 1, based on an understanding of stock-specific spatial distributions informed
89 by tag recoveries from stocks of interest or their proxies.

90 Until recently, managers have relied almost entirely on coded-wire tags (CWTs)
91 recovered from harvested fish to obtain information on stock-specific harvest (Nandor et al.
92 2010). CWTs provide brood year, hatchery/stock of origin, and other pertinent information
93 related to its respective release-group. In tandem with CWT recoveries from the escapement and
94 in-river harvest, this allows cohort reconstructions (Hilborn and Walters 1992, Goldwasser et al.
95 2001, Mohr 2006) that are used to estimate demographic parameters and stock/age-specific
96 ocean exploitation rates. These stock/age-specific exploitation rates serve as the basis for the
97 management of almost all west coast ocean salmon fisheries (PFMC 2012), with some untagged
98 natural or less abundant stocks managed on the basis of tagged “proxy” stocks. Since CWTs are
99 almost exclusively deployed on hatchery-origin fish, the suitability of this approach relies on the
100 assumption that tagged proxy stocks act similarly to the untagged stocks of interest, which can be

101 comprised of natural-origin fish from nearby watersheds as well as the natural-origin component
102 of stocks with hatchery supplementation. Thus, CWT-based management may not include direct
103 information on the harvest of some stocks or stock components of interest.

104 Genetic stock identification (GSI) has the potential to identify any individual fish to its
105 population of origin. Currently, genetic assignments are typically reported at the level of reliably
106 distinguishable “reporting groups” in the genetic reference database (i.e., the baseline). Many
107 genetic reporting groups, however, are composed of multiple genetically-similar populations
108 (Seeb et al. 2007, Clemento et al. 2014), and reporting group boundaries do not always coincide
109 with managed stocks, some of which may not themselves coincide with biological populations.
110 Nevertheless, for convenience, we use the terms “stock” and “reporting group” interchangeably
111 hereafter. Worldwide, GSI has been applied to multiple management problems in salmon
112 fisheries, including monitoring and responding to stock composition in terminal fisheries or other
113 geographically-restricted harvest situations (Beacham et al. 1987, Shaklee et al. 1999, Parken et
114 al. 2008, Griffiths et al. 2010, Ensing et al. 2013), evaluating the suitability of proxies for
115 untagged stocks (Bernard et al. 2014, Satterthwaite et al. 2014), estimating the stock composition
116 of escapement (Hess et al. 2014), determining the composition of discarded bycatch (Wilmot et
117 al. 1998), determining the source of introduced populations (Di Prinzio et al. in press), and
118 determining the composition of mixed-stock Atlantic salmon fisheries (Koljonen et al. 2005,
119 Koljonen et al. 2006, Gauthier-Ouellet et al. 2009). However, GSI has not been as widely applied
120 in management as some have envisioned (Waples et al. 2008) and applications to open-ocean
121 fisheries managed primarily with time-area regulations have been limited (Winans et al. 2001,
122 Crozier et al. 2004, Satterthwaite et al. 2014). Nevertheless, GSI has the potential to inform time-
123 area management, potentially at a finer scale than is currently practiced, especially when capture

124 locations associated with individual fish are also recorded (Bellinger et al. in review). Even at
125 the coarser spatial scale considered in current time-area management models, GSI has the
126 potential to provide important information on the relative fishery exposure of untagged stocks for
127 which direct distributional information is not available from CWT data.

128 To implement weak stock management using either time-area management or quotas,
129 information regarding stock-specific spatial distributions is important. Understanding where and
130 when certain stocks are more (less) prevalent and large (small) contributors to the fishery allows
131 structuring of fisheries such that abundant stocks are targeted and impacts to weak stocks are
132 limited.

133 We used GSI to analyze the stock composition of California recreational salmon fisheries
134 between 1998 and 2002 and to define the contributions of individual Chinook salmon
135 (*Oncorhynchus tshawytscha*) stocks to these fisheries. Because recreational fisheries tend to be
136 confined to a relatively small geographic area near their respective home port of landing, harvest
137 is likely to reflect the local area stock composition. We estimate the spatial and temporal
138 distribution of multiple stocks, some of which already have distributional information available
139 from CWT data and some of which are untagged. We present results as both stock proportions
140 (e.g. Winans et al. 2001, Crozier et al. 2004, Tucker et al. 2009) and stock-specific CPUE (Sato
141 et al. 2009, Satterthwaite et al. 2014, Bellinger et al. in review) to infer local stock mixtures and
142 relative stock abundance, respectively. We then show how a model of stock-specific CPUE,
143 accounting for the uncertainty introduced by genetic assignment, sampling, and process error,
144 can be used to test for a hypothesized break point in stock distributions that might serve as a new
145 delineation line between management areas. Finally, we evaluate the consistency of results
146 obtained from GSI sampling with those previously obtained from CWT proxy stocks. These data

147 offer a relatively unique opportunity to draw inference about the contribution of particular
148 Chinook salmon stocks to these fisheries, as well as to define stock-specific ocean distribution on
149 a relatively small scale.

150

151 **2. Materials and Methods**

152 *2.1. Study System*

153 Ocean salmon fisheries off the coast of California harvest a mix of Chinook salmon
154 stocks (retention of coho [*O. kisutch*] is not currently permitted, and contacts with other
155 salmonids in this area are minimal). Both commercial and recreational fisheries are substantial,
156 with recreational fisheries generally contributing about a third of the total California ocean
157 harvest, although they have made up as much as 58% of the catch in recent years (PFMC 2013).
158 Since the mid-1990s, four “major port management areas” have been used by the Pacific Fishery
159 Management Council (PFMC) when structuring ocean fisheries in California: 1) Klamath
160 Management Zone (KC) area - Oregon/California border to Horse Mountain, 2) Fort Bragg (FB)
161 area – Horse Mountain to Point Arena, 3) San Francisco (SF) area – Point Arena to Pigeon Point,
162 and 4) Monterey (MO) area – Pigeon Point to U.S./Mexico border (Figure 1). Each major port
163 area is comprised of several minor ports where fishery monitoring is conducted. Fisheries are
164 predominantly managed on the basis of time-area closures and minimum legal size limits
165 (typically 20 or 24 inches total length for recreational fisheries, larger for commercial fisheries),
166 although quotas occasionally apply to the commercial catch in the two northern management
167 areas.

168 Our analysis focuses on six genetic “reporting groups” (Seeb et al. 2007, Clemento et al.
169 2014) of management or conservation relevance in this region: 1) “Central Valley Fall” consists

170 of Sacramento River fall run, San Joaquin River fall run, Sacramento River late fall run, and
171 Feather River Hatchery spring run. Sacramento River fall run is far more abundant than other
172 stocks in this reporting group, is typically dominated by hatchery-produced fish (Barnett-Johnson
173 et al. 2007, Kormos et al. 2012, Palmer-Zwahlen and Kormos 2013), and makes up a large
174 proportion of the catch in California and Southern Oregon in most years (PFMC 2013). Late fall
175 run fish also have a hatchery component and may have a more southerly ocean distribution than
176 fall run fish (Satterthwaite et al. 2013). San Joaquin River fall run fish are much less abundant
177 than Sacramento River fall run (Carlson and Satterthwaite 2011; Kormos et al. 2012; Palmer-
178 Zwahlen and Kormos 2013) and are also supplemented by hatchery production. Feather River
179 Hatchery spring run are highly introgressed with Feather River Hatchery fall run and thus cannot
180 be distinguished with GSI (Clemento et al. 2014). All of these components are supplemented by
181 hatcheries with marking and tagging programs. 2) “Central Valley Spring” consists of naturally
182 produced spring run fish primarily from Deer, Mill, Butte, Battle and Clear creeks. Feather River
183 Hatchery spring run (marked and tagged) are excluded from the genetic reporting group but
184 included in the Central Valley spring run evolutionarily significant unit (ESU), which is listed
185 under the United States Endangered Species Act (ESA) as threatened (Lindley et al. 2004). There
186 is no hatchery production in the Central Valley Spring reporting group, although there have been
187 brief and relatively small-scale efforts to tag natural-origin smolts. 3) “Central Valley Winter”
188 consists of a mix of naturally spawned and conservation hatchery produced winter run fish from
189 the upper Sacramento River basin and this ESU is ESA-listed as endangered (Lindley et al.
190 2004). Winter run fish have also been inferred to have a more southerly distribution than fall run
191 fish on the basis of ocean fishery recoveries of CWT deployed by an ongoing hatchery program
192 (O’Farrell et al. 2012a, Satterthwaite et al. 2013). 4) “Klamath River” consists of predominantly

193 Klamath-Trinity Basin fall run Chinook but includes the genetically similar spring run as well
194 (Williams et al. 2013). Both the fall and spring runs from this reporting group are supplemented
195 by hatchery production with marking and tagging programs, with the fall run typically much
196 more abundant than spring run and a substantial contributor to ocean and river fisheries (PFMC
197 2013). 5) “California Coast” corresponds to California Coastal Chinook ESU, which is ESA-
198 listed as threatened and consists of coastal fall run stocks between the Klamath River (exclusive)
199 and the Russian River (inclusive). Some of these watersheds formerly contained spring run
200 stocks as well, but they have been extirpated (Bjorkstedt et al. 2005, Spence et al. 2008). Since
201 there is currently no hatchery production or tagging of fish from this ESU (a small number of
202 tags were released by a since-discontinued hatchery program), the ocean harvest rate of age-4
203 Klamath River fall run Chinook is used as a management proxy (O’Farrell et al. 2012b). Using
204 GSI data collected by the commercial fishery, Satterthwaite et al. (2014) found generally similar
205 spatial patterns in CPUE of Klamath River and California Coast fish in spring and early summer
206 with some divergence apparent in the late summer and fall. 6) “Rogue River” consists of a
207 composite of natural-origin fall run fish and hatchery-origin spring run fish with a tagging
208 program (Seeb et al. 2007).

209

210 *2.2. Data collection and genotyping*

211 During 1998-2002, the California Department of Fish and Wildlife (CDFW) collected
212 approximately 23,000 fin clips during the routine dockside sampling of private skiffs and
213 charterboats in the California recreational Chinook ocean salmon fishery. Sampling occurred at
214 approximately 20 fishing ports located between the Oregon-California border and Point
215 Conception (Figure 1) and fin clips were stored in ethanol and frozen prior to DNA extraction.

216 The amount of fishing effort (angler-days) and catch (retained Chinook salmon from any stock)
217 corresponding to the number of sampled recreational trips from which genetic samples were
218 taken was tracked and compiled separately for each month/major port area/year combination
219 (stratum), except that Bodega Bay (BB) was analyzed separately from the rest of the SF
220 management area, which we termed Golden Gate (GG), due to a hypothesized change in stock-
221 specific local density occurring at Point Reyes. In addition, data from the Klamath Management
222 Zone was separated into Crescent City (CR) and Eureka (EU), since these subareas are sampled
223 and reported separately in PFMC salmon documents. Since the CDFW samples approximately
224 20% of all salmon landings, and thus only a subset of fishing trips was sampled for genetic
225 analyses, these catch and effort values are less than those reported in PFMC documents (e.g.,
226 PFMC 2013) for the recreational fishery as a whole. The smaller values used here allow for
227 direct calculation of CPUE from catch estimates made using our dataset since effort and total
228 catch are measured for the same subset of the fishery.

229 Budgetary and staffing constraints only allowed the genotyping of approximately one half of
230 the samples. Selection of tissues for genotyping was done using stratified random sampling, with
231 complete sampling of small strata. If less than 111 tissue samples were collected within a
232 stratum, all tissue samples from that stratum were genotyped. For strata with larger collections,
233 110 tissue samples were selected at random for genotyping. For this subsampling, FB, BB, GG,
234 and MO (Figure 1; Table 1) were each treated as distinct areas, while CR and EU were treated as
235 a single area.

236 Genomic DNA was extracted from each fin clip with DNeasy 96 extraction kits using a
237 BioRobot 3000 (Qiagen Inc.). DNA extractions were diluted 1:2 and 1.25 μ l of this dilution was
238 added to a pre-amplification PCR containing 2.5 μ l PCR master mix (Qiagen) and unlabeled

239 primer pairs from each of the 96 SNP loci used in Clemento et al. (2014), each with a final
240 concentration of 0.05 μ M. Reaction products were diluted ~6:1 and added to 2.5 μ l of PCR
241 master mix and 0.25U AmpliTaq Gold DNA polymerase (Applied Biosystems) following the
242 manufacturer's protocols. These were then mixed with 96 TaqMan assays (Applied Biosystems),
243 on 96.96 Dynamic Arrays (Fluidigm Corporation) using the Fluidigm IFC Controllers to create
244 9,216 individual PCR reactions that were thermal cycled on a Fluidigm FC1™ thermal cycler,
245 with products imaged on an EP1 Reader. Genotypes were called and the data compiled using the
246 Fluidigm SNP Genotyping Analysis software. During this scoring process, the relative
247 fluorescence of alternate assays at each locus was visualized as a scatterplot for 96 individuals.
248 Individual points that fell outside of clusters diagnostic of either the heterozygote or alternate
249 homozygote genotypes were considered to have poor data quality (due to poor sample condition
250 or laboratory error) and left uncalled for that locus (Clemento et al. 2011). Individual genotypes
251 with more than 5 uncalled loci were excluded from later analyses as described below.

252

253 *2.3. Genetic Stock Identification*

254 The resultant 96-locus genotypes were used to determine the most probable reporting group
255 of origin using the software *gsi_sim* (Anderson et al. 2008). This program uses established
256 genetic stock identification (GSI) methods (Smouse 1990, Rannala and Mountain 1997) to
257 compare each genotype to allele frequencies estimated for previously-sampled, distinct
258 populations included in the "reference baseline" (Clemento et al. 2014). In our case the baseline
259 consists of 68 North American Chinook salmon populations plus California coho (which are
260 occasionally mistaken for Chinook salmon). Because some populations cannot be reliably
261 discriminated on the basis of these 96 loci, the populations are grouped into 38 reporting groups

262 (37 Chinook groups, plus coho) that can be reliably differentiated. This baseline is focused on
263 California and Oregon stocks but includes populations from as far north as Alaska and is
264 expected to include representatives of every stock likely to be encountered in fisheries off the
265 coast of California.

266 The `gsi_sim` program jointly estimates the mixing proportions---the unknown proportions of
267 fish from each population or reporting group in the baseline present in the stratum being
268 analyzed---and each individual's posterior probabilities of group membership. These individual
269 posterior probabilities are influenced by the mixing proportions estimated from the sample in
270 which the fish was analyzed, and thus the level at which data are stratified or aggregated could
271 influence the individual fish assignments. We therefore evaluated the effect of aggregating our
272 data over different temporal and spatial strata, by comparing individual assignments in the 1998
273 season under five different levels of aggregation against CWT data that were available for 121
274 fish from that season. Going from coarsest to finest, the five levels of aggregation were: (1) a
275 single stratum of all fish from all times and locations, (2) calendar month by area/subarea (Figure
276 1), (3) calendar month by sampling port, (4) 3-week sliding window by area and (5) 3-week
277 sliding window by sampling port. The results showed very little difference among these five
278 levels of aggregation (concordance between GSI and CWT in 119 of 121 fish for all 5 levels of
279 aggregation) so we used a 3-week sliding window and management area prior because it was the
280 finest resolution that still yielded sample sizes greater than 20 for most strata.

281 The baseline includes genotypes from coho salmon, which are fixed for a single allele at
282 nearly all 96 of the loci, allowing us to identify and remove from analysis a relatively small
283 number of mis-identified salmon that had been retained by fishermen. The exclusion probability
284 for the multilocus SNP genotypes was $p < 10^{-20}$ for unrelated individuals, and identical

285 genotypes therefore represent the same fish which was inadvertently sampled more than once.
286 All but the first instance of an identical genotype was removed from the analysis. Finally, we
287 removed genotypes with low-confidence assignments from the analysis. Low confidence was
288 due to poor data quality (individual heterozygosity [iHZ] < 0.16 or > 0.56, indicating allelic
289 dropout or sample contamination, respectively) or high uncertainty in reporting group
290 assignment as indicated by the log of a fish's genotype probability falling more than three
291 standard-deviations from the log-genotype probability expected in the population to which the
292 fish was assigned and posterior probability of reporting group membership (see below) < 0.9 or
293 data missing from more than 5 loci (see Clemento et al. 2014 for further details about these
294 criteria). Following removal of these genotypes, we plotted stock-specific catch for each year-
295 month-area combination both proportionally and scaled as catch per unit effort.

296

297 *2.4. Stock-specific catch and distribution model*

298 We assumed that stock-specific CPUE served as a proxy of local density. Estimates were
299 made separately each month to encompass the effects of seasonal fish movements, but we
300 combined information across years, assuming additive effects of area and year on log-CPUE
301 (constant multiplicative effects on CPUE) as in Satterthwaite et al. (2013). That is, for each
302 reporting group r in each month m , the mean catch rate (λ) for an assumed negative binomial
303 process was modeled as

304

$$305 \lambda_{rmyx} = e^{\beta_{rm} + \gamma_{rmy} + \rho_{rmx}} \quad (1)$$

306

307 where y indexes years, x indexes fishing areas, β_{rm} is the (stock- and month-specific) intercept, γ
 308 is the year effect, and ρ is the area effect. Thus year effects were assumed to scale monthly
 309 stock-specific CPUE up or down uniformly through space (i.e., an effect of cohort strength), with
 310 the scaling of relative CPUE across space constant through time. For identifiability, $e^{\beta_{rm}}$ is the
 311 estimate for stock r in month m in GG in 1998, with $\rho_{GG} = \gamma_{1998} = 0$.

312 We accounted for stochasticity in the catch and sampling process, as well as genetic
 313 assignment uncertainty, as in Satterthwaite et al. (2014), except that, since we had multiple years
 314 of data for a particular month/area combination, we modeled overdispersion relative to a Poisson
 315 catch process by using a negative binomial distribution (Mangel 2006, Satterthwaite et al. 2013).
 316 Briefly, given f units of fishing effort expended in a given area and month/year (subscripts
 317 suppressed), the expected mean for the total catch of fish from a particular stock, C_r , is the
 318 product of effort and stock-specific mean catch rate, λ_r :

$$320 \quad C_r \sim \text{NegativeBinomial}(\text{mean} = f\lambda_r, \text{dispersion} = k) \quad (2)$$

321
 322 and thus $p(C_r, \lambda_r, k, f)$ is given by the probability density function of a negative binomial
 323 distribution. By Bayes' theorem,

$$325 \quad p(\lambda_r, k | C_r, f) = \frac{p(\lambda_r, k) p(C_r | \lambda_r, k, f)}{p(C_r, f)} \quad (3)$$

326
 327 and since $p(C_r, f)$ is a constant with respect to λ_r and k it can be neglected in sampling the
 328 posterior distributions of β , γ , and ρ (the constituents of λ_r , see equation 1) and k via Markov
 329 Chain Monte Carlo (MCMC; Gelman et al. 2004) sampling methods. For the constituents of λ_r ,

330 we assumed independent log-uniform prior distributions allowing for lambda values as low as
 331 10^{-87} and as high as 100 (which is well beyond the bounds of the data), while our uniform prior
 332 on k allowed values as low as 0.2 (highly overdispersed, even lower values were excluded
 333 because they led to convergence problems) and as high as 1000 (essentially equivalent to a
 334 Poisson).

335 Since only a subset of the catch corresponding to trips from which samples were collected
 336 was genotyped, and assignments to reporting groups are uncertain, C_r is not known with
 337 certainty. Given n fish successfully genotyped, the vector \mathbf{n} of the number of such fish assigning
 338 to each reporting group n_r is the sum of multinomial random vectors, each of a single trial with
 339 cell probabilities given by \mathbf{g}_i , the vector of posterior probabilities that fish i originated from each
 340 of the R total possible reporting groups (g_{ri}), expressed as:

341

$$342 \{n_1, n_2, \dots, n_R\} \sim \sum_{i=1}^n \text{Multinomial}(trials = 1, p = \{g_{1i}, g_{2i}, \dots, g_{Ri}\}). \quad (4)$$

343

344 Given C total fish caught over all of the sampled trips (of which n were genotyped and u were
 345 not, $C=n+u$), the total number of fish from each reporting group C_r is the sum of n_r genotyped
 346 fish from that stock and u_r un-genotyped fish from that stock, with the composition of \mathbf{u}
 347 depending on the unknown proportion of the sample consisting of each stock π_r . In the course of
 348 the MCMC, we simulated realized values of the vector of stock proportions $\boldsymbol{\pi}$ from their
 349 posterior distribution given the currently drawn values of n_r (from equation 4) and a unit
 350 information Dirichlet prior, expressed as

351

$$352 \{\pi_1, \pi_2, \dots, \pi_R\} \sim \text{Dirichlet}\left(n_1 + \frac{1}{R}, n_2 + \frac{1}{R}, \dots, n_R + \frac{1}{R}\right). \quad (5)$$

353

354 We then drew u_r from a multinomial distribution with values for $\boldsymbol{\pi}$ drawn via equation (5),

355 expressed as

356

357 $\{u_1, u_2, \dots, u_R\} \sim \text{Multinomial}(trials = u, p = \{\pi_1, \pi_2, \dots, \pi_R\})$ (6)

358

359 and calculated C_r as the sum of n_r and u_r , which we used to update k and the components of λ_r

360 via MCMC with equation (3) giving the target density.

361

362 We thus have several options for quantifying uncertainty in metrics of stock-specific catch. We can quantify uncertainty in the composition of the genotyped sample by examining the

363 posterior distribution of n_r/n , we can quantify uncertainty in the catch composition (including

364 ungenotyped catch) using the posterior distribution of C_r/C , we can describe uncertainty in the

365 stock composition of the source population being sampled using the posterior distribution for π_r ,

366 and we can quantify uncertainty in stock-specific catch using the posterior distribution of C_r .

367 Similarly, we can quantify uncertainty in stock-specific CPUE using the posterior distribution for

368 λ_r . See the Discussion (sections 4.1 and 4.2) for guidance on quantifying uncertainty when no

369 fish assigning to the stock of interest are recovered from the genotyped sample. We examined the

370 importance of accounting for assignment error by comparing our posterior credible intervals of

371 catch proportions to confidence intervals calculated assuming hypergeometric sampling with

372 known stock identities in a set of illustrative examples varying in sample size and stock

373 proportion.

374

375 *2.5. Hypothesis testing*

376 We evaluated the strength of evidence for a delineation in stock-specific local density at
377 Point Reyes by comparing estimates of stock-specific CPUE for sampled recreational trips out of
378 GG (San Francisco, Sausalito, Berkeley, Emeryville, and Princeton/Half Moon Bay,
379 corresponding primarily to fishing south of Point Reyes) against trips out of BB (Bodega Bay,
380 corresponding primarily to fishing north of Point Reyes). For each stock/month, we used the
381 MCMC chains generated as described above to establish the posterior distribution of the ratio
382 between stock specific catch rates in the southern (GG) versus northern (BB) portions of the SF
383 management area:

384

$$385 \quad D_{rm} = \frac{\exp(\rho_{r,m,x=GG})}{\exp(\rho_{r,m,x=BB})} \quad (7)$$

386

387 We used the quantiles of this chain to determine whether credible intervals on this ratio were
388 entirely above or below 1.0 and used the posterior median as a point estimate of how much the
389 distribution of a particular stock within the current SF management area (our GG and BB areas
390 combined) was skewed south of Point Reyes ($D > 1$) or north of it ($D < 1$).

391 Note that if catch of fish assigning to a particular stock was zero or very low in the southern
392 portion of the SF area (GG), this ratio will be near 0 and the MCMC sampler will typically
393 converge. However, if assigned catch is near zero in the northern portion, the ratio will approach
394 infinity and cause convergence problems. It is thus informative to inspect cases of poor
395 convergence to determine whether assigned catch was near zero in both areas or only the
396 northern portion of the SF management area (BB).

397 We considered there to be strong support for a change in stock distributions around the Point
398 Reyes boundary if the median GG/BB ratio was > 2 (for GG) or < 0.5 (for BB), AND the

399 lower/upper bound of the 95% credible interval was 0.1 more/less than 1. We considered there to
400 be moderate support for such a difference if the lower/upper bound of the credible interval was
401 0.1 more/less than 1. We considered there to be weak support for a difference if the lower/upper
402 bound of the credible interval was 0.01 more/less than 1, or if zero fish plausibly assigning to the
403 applicable stock were sampled in one of the two areas (GG or BB).

404 All MCMC chains were “burned in” for at least 5,000 iterations and run for at least 25,000
405 iterations in the retained chain. Additional burn-in iterations were performed if a Geweke (1992)
406 diagnostic on the posterior chain for the ratio returned a $|z| > 2.0$ when comparing the first 10% to
407 the last 50% of the retained chain, and additional iterations were performed if a Raftery and
408 Lewis (1995) diagnostic indicated that the retained chain was not sufficient to identify the 0.025
409 quantiles to an accuracy of ± 0.02 with probability of at least 0.95, with diagnostics implemented
410 using the R (R Core Team 2013) package “coda” (Plummer et al. 2006).

411

412 **3. Results**

413 We successfully genotyped 10,278 fish that were sampled during the five-year 1998-2002
414 period, representing between 1 – 12% of the total recreational landings in these areas each month
415 (Table 1; month/area strata with landings < 15 are excluded from this range). Of these fish, 189
416 were genetically identified as coho salmon and removed from further analysis. An additional 406
417 genotypes were removed from the dataset for poor data quality and 41 were removed due to high
418 uncertainty in group assignment, leaving a total of 9,642 genotypes for further analysis. To
419 assess whether the fish removed due to low-confidence assignments were not representative of
420 all the fish genotyped, we compared the maximum a-posteriori assignments of the 41 fish
421 removed due to high uncertainty in reporting group assignments to those of all 9,642 fish that

422 were not removed. There was no significant difference in the distribution of assigned reporting
423 units amongst the two groups (χ^2 test, $p > 0.25$, by simulation). For all years combined, our
424 genetic assignments were concordant with coded-wire tag data for 292 out of 298 cases (Table
425 2), indicating a discordance rate of 2.0% between GSI and CWT.

426

427 *3.1. Stock Proportions and Stock-Specific Total Catch*

428 Stock proportions were dominated by fish from the Central Valley Fall reporting group for
429 nearly all times and areas for which data were available, with the exception of CR during August
430 and September, which, in some years, showed a high proportion of Klamath River fish (Figure
431 2). However, it should be noted that the sample size for CR during these exceptional years was
432 small (<35 fish per stratum). In the interest of legibility, Figure 2 does not reflect uncertainty in
433 the individual stock proportion estimates, but uncertainty in both proportions and catch are
434 addressed in section 4.1 of the Discussion.

435

436 *3.2. Spatial and Temporal Variability in Stock-Specific CPUE*

437 Other than the Central Valley Fall group, all stocks were caught at less than 0.5 fish per
438 angler-day in all time-area combinations, and catch rates above 1.0 fish per angler-day were rare
439 even for Central Valley Fall (Figure 3). These fisheries had a bag limit of two fish per angler
440 day, which may cause the relationship between local abundance and CPUE to be concave down
441 at high density. At the same time, the relationship may be concave up at low density if higher
442 abundances make it easier for fishermen to cue in on dense aggregations. As a result it is unclear
443 whether we are likely to be overestimating or underestimating differences in fish densities
444 among management areas.

445 The location of highest CPUE for Central Valley Fall fish tended to vary across months: it
446 was typically highest in southern areas in April and May, with a more even north-south
447 distribution in June and July, and with relatively low CPUE in the north in August and
448 September. Similarly, CPUE of Klamath River fish was highest near EU and CR (located just
449 south and north of the Klamath River mouth, respectively), and was often zero or near zero in
450 southern ports during August and September. Instances of nonzero CPUE were also more spread
451 out earlier in the year.

452 There was no consistent time-area combination for the highest within-year CPUE of Central
453 Valley Fall fish. While the highest CPUE was observed in July for all years except 2002, the
454 location of highest CPUE varied among GG, BB, and FB. In 2002, CPUE of Central Valley Fall
455 fish was highest in GG for all months except April (FB) and September (CR). In the interest of
456 legibility, Figure 3 does not reflect uncertainty in the individual stock-specific CPUEs, but
457 factors contributing to uncertainty in CPUE are addressed in section 4.2 of the Discussion, and
458 section 3.3 describes inference about statistical support for differences in CPUE.

459

460 *3.3. Changes in Stock-Specific CPUE Across Point Reyes*

461 Fish assigned to the Central Valley Winter reporting group were never sampled north of FB
462 and very rarely sampled north of Point Reyes. Thus in most months there appeared to be support
463 for a hypothesized difference in local density of winter run fish north (i.e., BB) and south (i.e.,
464 GG) of Point Reyes (Table 3), although the small number of winter run fish sampled limit the
465 strength of conclusions that we can draw. There appeared to be strong support for higher CPUE
466 of Central Valley Spring fish in BB during June but higher CPUE in GG during September.
467 There was strong support for higher Central Valley Fall CPUE in GG during May but not in

468 other months. There was strong support for higher CPUE of California Coast fish in BB during
469 April, contrasted with weak support for higher CPUE of California Coast fish in GG during May.
470 There was weak support for higher CPUE of Klamath River fish in GG in May, but strong
471 support for higher CPUE in BB during July and weak support for higher CPUE in BB during
472 September. There was moderate support for higher CPUE of Rogue River fish in GG during
473 April, and weak support for the same pattern in June and September.

474

475 **4. Discussion**

476 Genetic stock identification methods provided the ability to estimate spatial and temporal
477 variation in stock proportions and stock-specific CPUE for a suite of untagged and partially
478 tagged stocks of conservation concern, including untagged California Coast and Central Valley
479 Spring stocks (both listed as threatened) and the partially tagged Central Valley Winter stock,
480 and to evaluate the consistency of observed patterns with previous assumptions or inferences
481 made from tagged proxy stocks. It also allowed analysis of partially tagged stocks (Central
482 Valley Fall, Klamath River, Central Valley Winter, Rogue River) and comparison of these
483 observed patterns to those determined in previous studies utilizing just the tagged components of
484 these stocks. These results allowed for a relatively comprehensive characterization of the stocks
485 that contributed to the California recreational ocean salmon fishery during the five year study
486 period.

487 The 298 fish with known stock of origin provided via CWT suggested a discordance rate
488 of 2.0% (6/298), similar to the 1.05% rate reported by Clemento et al. (2014, 11/1052, $\chi^2 = 1.75$,
489 $p > 0.18$) for a fishery sample that allowed substantially more comparisons due to a large
490 increase in the Central Valley Fall CWT tagging rate starting in brood year 2007 (Buttars 2012).

491 Discordant assignments were too rare to identify particularly problematic stocks with high
492 confidence, although apparent misassignments either to or from the Rogue River stock made up
493 33% of discordant results in this study despite the overall small proportion of Rogue River fish.
494 Similarly, Clemento et al. (2014) reported only a 45% GSI~CWT agreement rate for Rogue
495 River, noting that Rogue River fish are genetically similar to fish from the Klamath River and
496 North California / South Oregon Coast reporting groups.

497

498 *4.1. Stock Proportions*

499 Stock proportions did not vary in any consistent way across years, with the proportion of
500 Central Valley Fall fish consistently high relative to all other reporting groups including Klamath
501 River. While Klamath River and other non-Central Valley Fall stocks often contribute to
502 fisheries in the northern areas of California, even constituting the majority of the catch on
503 occasion, the same was not observed for the southern areas. In all years, months, and areas
504 considered here, areas south of FB rarely had substantial contributions from stocks originating
505 outside of the Central Valley. However, a separate study showed that in 2007, a year of
506 unusually low Sacramento River fall Chinook abundance, fish assigning to the Central Valley
507 Fall reporting group made up only 71% of a sample of 340 fish collected from the MO
508 recreational fishery (Lindley et al. 2009). During this study, the average proportion of Central
509 Valley Fall fish in the MO fishery was 92% among all months and years.

510 Uncertainty in stock proportion estimates depends primarily on the sample size and the
511 magnitude of stock proportions, with smaller relative error as sample sizes increase or stock
512 proportions increase (Allen-Moran et al. 2013). Additionally, if the interest is in composition of
513 the catch per se (sampled without replacement) as opposed to the source population from which

514 the catch was sampled (generally large enough to consider as sampled with replacement),
515 uncertainty decreases for a given sample size when that sample size makes up an increasing
516 fraction of the total catch. Thus for illustrative purposes we present uncertainty calculations for
517 two sampling strata: MO in July 1999 which had a relatively large sample size that constituted
518 approximately 20% of the total harvest (the target sampling rate for the current CWT program),
519 and CR in September 2001 which had a small sample size but nevertheless genotyped
520 approximately 40% of the total harvest for that stratum.

521 For CR in September of 2001, 29 total fish were harvested by sampled trips, of which 12
522 fish were successfully genotyped. Of these 12 fish, 7 assigned with high probability to Central
523 Valley Fall, 4 assigned with high probability to Klamath River, and 1 indeterminate fish assigned
524 with moderate probability to either Klamath River or Rogue River (but almost certainly one of
525 those two). Resultant 95% credible intervals on the proportion of catch from each reporting
526 group were 0.34-0.76 Central Valley Fall, 0.21-0.59 Klamath River, and 0.0-0.10 Rogue River.
527 Assuming all assignments were certain and that the indeterminate fish assigned to Rogue River,
528 the methods described in Allen-Moran et al. (2013) applying a normal approximation to a
529 hypergeometric sampling model yield approximate 95% confidence intervals of 0.37-0.80 for
530 Central Valley Fall, 0.20-0.63 for Klamath River (assuming the indeterminate fish was Klamath
531 River, otherwise the bounds drop to 0.13-0.54), and 0-0.20 for Rogue River. These differences
532 appear to result largely from propagating the uncertainty associated with assignment error, but in
533 part because the normal approximation employed by Allen-Moran et al. (2013) breaks down with
534 small numbers of fish, and because our method explicitly accounts for the simultaneous
535 estimation of multiple proportions. An exact solution implemented via the "Sprop" function in R
536 package "samplingbook" (Manitz et al. 2013) yields confidence intervals of 0.31-0.83 for Central

537 Valley Fall, 0.17-0.69 for Klamath River (or 0.14-0.62 if the indeterminate fish is of Rogue
538 River origin), and 0.03-0.34 for Rogue River (assuming the indeterminate fish is of Rogue River
539 origin).

540 For MO in July 1999, 574 total fish were harvested by sampled trips, of which 108 were
541 successfully genotyped. 102 assigned with high probability to Central Valley Fall, 4 assigned
542 with essential certainty to Central Valley Winter, and 2 fish assigned to Rogue River with high
543 probability. Resultant 95% credible intervals on the proportion of catch from each reporting
544 group were 0.88-0.97 Central Valley Fall, 0.01-0.07 Central Valley Winter, and 0.0-0.05 Rogue
545 River. Assuming all assignments were certain, the methods described in Allen-Moran et al.
546 (2013) applying a normal approximation to a hypergeometric sampling model yield approximate
547 95% confidence intervals of 0.91-0.98 Central Valley Fall (0.89-0.98 using exact method), 0.01-
548 0.07 Central Valley Winter (0.01-0.09 using exact method), and 0-0.04 Rogue River (0.004-0.06
549 using exact method). Thus in this case accounting for assignment error causes relatively little
550 change in the estimated uncertainty.

551 These results suggest that future GSI sampling programs should employ larger sample
552 sizes (and/or sample a large fraction of the catch) if confident inference about rare stocks is
553 desired. In general, the sample size required scales inversely with the target proportion (i.e. a
554 proportion half as small requires twice the sample size) and with the square of the desired
555 precision (i.e. halving the standard error requires quadrupling the sample size, Allen-Moran et al.
556 2013).

557 Uncertainty in stock-specific catch is similar to uncertainty in catch stock proportions
558 when total catch is assumed known, as was the case in this study. The MCMC sampler we

559 developed could be readily expanded to account for uncertainty in total catch by integrating over
560 the plausible range of variability in the number of ungenotyped fish u .

561 A related concern is the detection of rare stocks. For detection of stocks present in the
562 sampled ocean area, the sampled fish can be treated as taken with replacement and modeled
563 using a binomial, such that the probability of sampling at least one fish (Q_1) with a sample of
564 size n given stock proportion p is:

565

$$566 \quad Q_1 = 1 - (1 - p)^n \quad (8)$$

567

568 And the required sample size to achieve a specified probability of detection is:

569

$$570 \quad n = \frac{\log(1 - Q_1)}{\log(1 - p)} \quad (9)$$

571

572 When determining the presence of a stock in the catch (totaling C), sampling is
573 without replacement and modeled as a hypergeometric process:

574

$$575 \quad Q_1 = 1 - \frac{\binom{C(1-p)}{n}}{\binom{C}{n}} \quad (10)$$

576

577 And the required sample size is approximately (see Allen-Moran et al. 2013 for an exact
578 solution):

579

580
$$n = \left(1 - (1 - Q_1)^{\frac{1}{Cp}}\right) \left(C - \frac{Cp - 1}{2}\right) \quad (11)$$

581

582 Equations 8 and 10 suggest a way of quantifying uncertainty about rare stock presence,
583 given no recoveries of that stock in a sample. Subtracting the relevant equation from 1.0 yields
584 the probability of obtaining 0 recoveries from a stock, given it is present at proportion p ; and this
585 can serve as a likelihood function for determining the probability of any value of p , given 0
586 observed recoveries and some prior on p , in a Bayesian framework. The prior merits careful
587 consideration and one might want to consider an approach that shares information across space
588 and/or time, such that an observation of 0 recoveries for a particular stock is considered stronger
589 evidence for absence if the same stock has been consistently undetected in adjacent areas and/or
590 the same area at different times.

591

592 *4.2. Spatial and Temporal Variability in Stock-Specific CPUE*

593 Consistent with earlier studies of CWT recoveries, Central Valley Winter fish appear
594 most concentrated in the south (O'Farrell et al. 2012a, Satterthwaite et al. 2013) and are almost
595 never recovered from samples north of the SF management area. Central Valley Fall fish appear
596 to concentrate in the Gulf of the Farallones, near the mouth of the Central Valley river network
597 in the fall, with CPUE in northern areas dropping at the time adult spawners return to the Central
598 Valley, as previously inferred from CWT (Satterthwaite et al. 2013). These results suggest that
599 inferences based on tagged hatchery fish from these stocks are representative of the hatchery plus
600 natural origin composite, at least in terms of coarse scale spatial distribution (see also Weitkamp
601 and Neely 2002, Weitkamp 2010). However, since Central Valley Fall appears dominated by

602 hatchery-origin fish (Barnett Johnson et al. 2007, Kormos et al. 2012, Palmer-Zwahlen and
603 Kormos 2013), little difference between hatchery-origin fish and the composite would be
604 expected even if natural-origin fish differed in their distribution. Still, the Central Valley Winter
605 composite is primarily natural-origin (Winship et al. 2014), suggesting that the tagged hatchery
606 fish are similar in distribution to their natural-origin counterparts. Despite considerable variation
607 in the reconstructed abundance of Sacramento fall run Chinook salmon over these years
608 (O'Farrell et al. 2013), peak CPUE of Central Valley Fall fish was between 1.0 and 1.5 fish per
609 angler day in all years, with limited predictability in when and where the peak CPUE occurred.

610 In August and September of most years, CPUE of the untagged California Coast stock
611 was highest in Fort Bragg while CPUE of Klamath River fish was highest in Eureka and
612 Crescent City, similar to the pattern found by Satterthwaite et al. (2014) using commercial data
613 collected in 2011 and 2012 and consistent with the results in NMFS (2000) derived from CWT
614 recovery data from a since-discontinued hatchery program. Thus the potential for these stocks to
615 diverge in their spatial distribution, likely to the mouths of their natal rivers in the fall, appears to
616 be supported for an extended time period and across fishery sectors. The reinforcement of this
617 result supplied by this study is particularly relevant because an upper limit to the expected age-4
618 Klamath River fall run harvest rate is used to constrain the ocean fisheries for the purpose of
619 protecting the California Coast stock (O'Farrell et al. 2012b).

620 The apparent, but weak, tendency for higher CPUE of Rogue River fish in GG than BB
621 was unexpected since the Rogue River is the northernmost source river among the stocks
622 analyzed. Given all of the factors besides stock that can influence CPUE (e.g. weather
623 conditions, nonrandom spatial sampling by fishermen), these patterns in CPUE should not be
624 over-interpreted as reflective of absolute spatial distributions, but they are reflective of spatial

625 patterns of overlap with fisheries, which may be more relevant from a management perspective
626 than absolute spatial distribution.

627 Uncertainty in CPUE is affected by the same considerations as stock proportions and
628 catch (described in section 4.1) and also by the amount of fishing effort, with uncertainty
629 decreasing as fishing effort increases (Satterthwaite et al. 2013). Because Equation 3 has a
630 nonzero value for positive λ_r even when $C_r=0$, the posterior distribution for λ_r calculated using
631 our methods will always account for the possibility that a stock was present (had some nonzero
632 probability of being caught) even if it was not sampled, becoming more confident at ruling out
633 all but very low probability of presence as fishing effort increases. As with stock proportions,
634 careful consideration should be given to prior specification and/or sharing information across
635 space or time when making inference about rarely sampled stocks.

636 An additional challenge in interpreting either stock proportions or stock-specific CPUE
637 results from this study are the effects of minimum size limits in the fishery. Since fish sampled in
638 this study were not aged, and there is not detailed information on size-at-age available for all of
639 the stocks studied here, we were unable to adjust catch on the basis of stock-specific expected
640 proportions of fish that are legal size (Satterthwaite et al. 2013) and thus underestimating
641 contacts with stocks of fish with smaller body size such as Central Valley Winter, for which age-
642 3 fish (those most commonly encountered in the fishery) have mean total lengths growing from
643 approximately 21 to 28 inches over the course of the fishing season with a standard deviation of
644 about 2 inches (O'Farrell et al. 2012a). In addition, the minimum size limit in effect varied both
645 spatially and temporally throughout the study period, ranging from 20 to 24 inches total length.
646 It was also common for the minimum size limit in the KC to be less than the limit in effect for
647 the southern areas, especially during the spring fisheries.

648

649 *4.3. Suitability of Point Reyes as a Management Delineation Line*

650 This study yielded limited support for using Point Reyes as an additional management
651 delineation line. Although marginal statistical support was found for changes in local CPUE for
652 some stocks, these differences were not found consistently for all months. The most consistent
653 pattern was found for Central Valley Winter fish, which were almost never sampled north of
654 Point Reyes, but contact rates with Central Valley Winter fish tend to be low in GG as well, and
655 without more intensive sampling it is difficult to quantify how much lower CPUE of Central
656 Valley Winter fish might be in BB versus GG. A general decrease in CPUE moving north would
657 be expected based on previous results (O'Farrell et al. 2012a, Satterthwaite et al. 2013), but these
658 studies also reported occasional winter run fish even further north than BB. Only 1% of all
659 Central Valley Winter CWTs recovered in California ocean recreational fisheries have been
660 taken north of BB.

661

662 *4.4. Fishery Implications*

663 The consistently high proportions of Central Valley Fall fish in all times and areas
664 demonstrate how vitally important this stock is to California recreational fisheries. Central
665 Valley Fall abundance was relatively high during the study period, yet a rapid decline a few
666 years after the end of the study period culminated in the lowest recorded abundance of this stock
667 (Lindley et al. 2009) and the closure of nearly all ocean salmon fisheries in California and
668 Oregon during 2008 and 2009. While other stocks, such as the Klamath River and Central
669 Valley Winter, have more frequently constrained California ocean salmon fishing opportunity,
670 the much lower relative CPUE of other contributing stocks demonstrates that the abundance of

671 the Central Valley Fall stock is the primary driver of the recreational fishery in terms of catch per
672 angler day and suggests that fishery success would not be buffered by these stocks during times
673 of low Central Valley Fall abundance.

674

675 *4.5. Utility of Approach*

676 The ability of GSI to produce stock proportion estimates could be useful in forecasting
677 impacts of quota fisheries, which are currently rare in California but are more frequently
678 employed in other areas. However, because the observed proportions of the stocks of greatest
679 conservation concern (e.g., Central Valley Winter, California Coastal) were quite small, large
680 sample sizes would be required to estimate these proportions with precision or to be confident
681 that a sample not containing any fish from the stock of interest equates to a very low proportion
682 of that stock existing in the ocean fishery being sampled (Allen-Moran et al. 2013).

683 Understanding the full impacts of the ocean fisheries would also require increased spatial
684 coverage since many of these stocks are also harvested in appreciable numbers in fisheries off
685 the coast of Oregon (Satterthwaite et al. 2013). Representative sampling of both commercial and
686 recreational fisheries would need to occur simultaneously to get a complete picture of tagged and
687 untagged stock distribution by time and area; however, because the current management
688 framework does not directly limit impacts on untagged stocks, it is not immediately clear how
689 such information could be used.

690 The documentation of spatio-temporal variation in stock-specific CPUE is largely
691 consistent with previous inferences from CWT recoveries. This suggests that the common
692 practice of extrapolating from tagged proxy stocks to untagged surrogates can be appropriate in
693 at least some cases, although the total number of comparisons made to test this assumption is still

694 limited, and the Central Valley Fall case may not be very informative given the predominance of
695 hatchery-origin fish in the aggregate stock. New insights into the spatial distribution of untagged
696 stocks is somewhat limited by their rarity. The CPUE of Central Valley Spring fish was so
697 consistently low that differences between strata with low CPUE and strata with zero catch are
698 generally statistically indistinguishable (Satterthwaite et al. 2013). This is a general problem
699 with inference about rare stocks, regardless of the type of tag employed, and reiterates the need
700 for large sample sizes (Allen-Moran et al. 2013) when rare stocks are of interest. An additional
701 complication in interpreting our estimates of stock proportions or CPUE is that these estimates
702 are not age-specific. Thus, the collection and analysis of supplemental age data (e.g., scale aging,
703 Kormos et al. 2010) is necessary to gain information on the strength of specific cohorts and to
704 conform with the current age-specific harvest management goals in place for many of these
705 stocks (PFMC 2012).

706

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716

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923 **Figure Captions**

924

925 Figure 1. Map of California salmon fishery management areas (KC, FB, SF, MO), sub-areas
926 defined in this paper (CR, EU, BB, GG), sampled ports, and natal rivers of major Chinook
927 salmon populations.

928

929 Figure 2. Chinook salmon stock proportions by year, month, and area. Numbers below bars
930 indicate the number of Chinook salmon successfully genotyped. Blank bars indicate no data (due
931 either to fishery closure or lack of samples collected). (color required)

932

933 Figure 3. Stock-specific CPUE (fish per angler-day) for sampled fish. Blank bars indicate no data
934 (due either to fishery closure or lack of samples collected). (color required)

935

Table 1

Table 1. California ocean recreational fishery Chinook salmon landings: total fish landed for the period 1998-2002 compared to the number of Chinook salmon analyzed. Landing data provided by CDFW. Blank cells indicate fishery closures.

		Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov
CR	Genotyped				86	105	106	136	49		
	Landed				4,458	13,113	6,177	14,712	3,852		
	Prop. Genotyped				0.02	0.01	0.02	0.01	0.01		
EU	Genotyped				199	405	229	321	87		
	Landed				4,458	13,113	6,177	14,712	3,852		
	Prop. Genotyped				0.04	0.03	0.04	0.02	0.02		
FB	Genotyped	2	82	252	363	410	373	375	172	2	1
	Landed	14	664	3,712	9,923	21,441	32,684	21,599	2,621	6	2
	Prop. Genotyped	0.14	0.12	0.07	0.04	0.02	0.01	0.02	0.07	0.33	0.50
BB	Genotyped		9	87	80	152	176	106	100	32	3
	Landed		9	3,955	5,312	13,042	49,639	11,347	7,287	569	14
	Prop. Genotyped		1.00	0.02	0.02	0.01	0.004	0.01	0.01	0.06	0.21
SF	Genotyped		7	434	362	371	346	398	350	298	123
	Landed		779	20,232	32,170	48,162	66,104	46,101	21,311	14,001	3,184
	Prop. Genotyped		0.01	0.02	0.01	0.01	0.005	0.01	0.02	0.02	0.04
MO	Genotyped		234	443	436	423	468	327	122		
	Landed		7,371	86,439	36,806	30,186	28,693	5,100	1,847		
	Prop. Genotyped		0.03	0.01	0.01	0.01	0.01	0.02	0.06	0.07	

Table 2. Concordance between CWT and GSI assignments to stock of origin. The "Concordant CWT" column gives the number of CWT'd fish for which the GSI stock assignment matched the reporting group corresponding to the CWT release code, while the "Discordant CWT" column lists the other stocks from which CWT were recovered, and how often, for fish assigning to a given reporting group.

Reporting group	Concordant CWT	Discordant CWT
Central Valley Spring	1	none
Central Valley Fall	281	Klamath River (1), Upper Columbia Summer/Fall (1)
Klamath River	4	Rogue River (1), Central Valley Fall (2)
Rogue River	3	Central Valley Fall (1)
Mid Oregon Coast	1	none
Mid Columbia River Tule	1	none
Snake River Fall	1	none

Table 3. Stocks with significantly greater CPUE south of Pt. Reyes (GG) or north of Pt. Reyes (BB). ++ indicates that the median GG/BB ratio is > 2 (for GG) or < 0.5 (for BB), AND the lower/upper bound of the 95% credible interval is 0.1 more/less than 1. A + indicates that the lower/upper bound of the credible interval is 0.1 more/less than 1. If there is no additional mark, but an area is reported, the lower/upper bound of the credible interval is 0.01 above/below 1, or zero fish plausibly assigning to the applicable stock were genotyped in either GG or BB. Blank cells showed little or no evidence of a difference.

	April	May	June	July	August	September
Rogue R.	GG+		GG			GG
Klamath R.		GG		BB++		BB
CA Coast	BB++	GG				
CV Fall		GG++				
CV Spring			BB++			GG++
CV Winter	GG	GG	GG		GG	GG

Figure 1

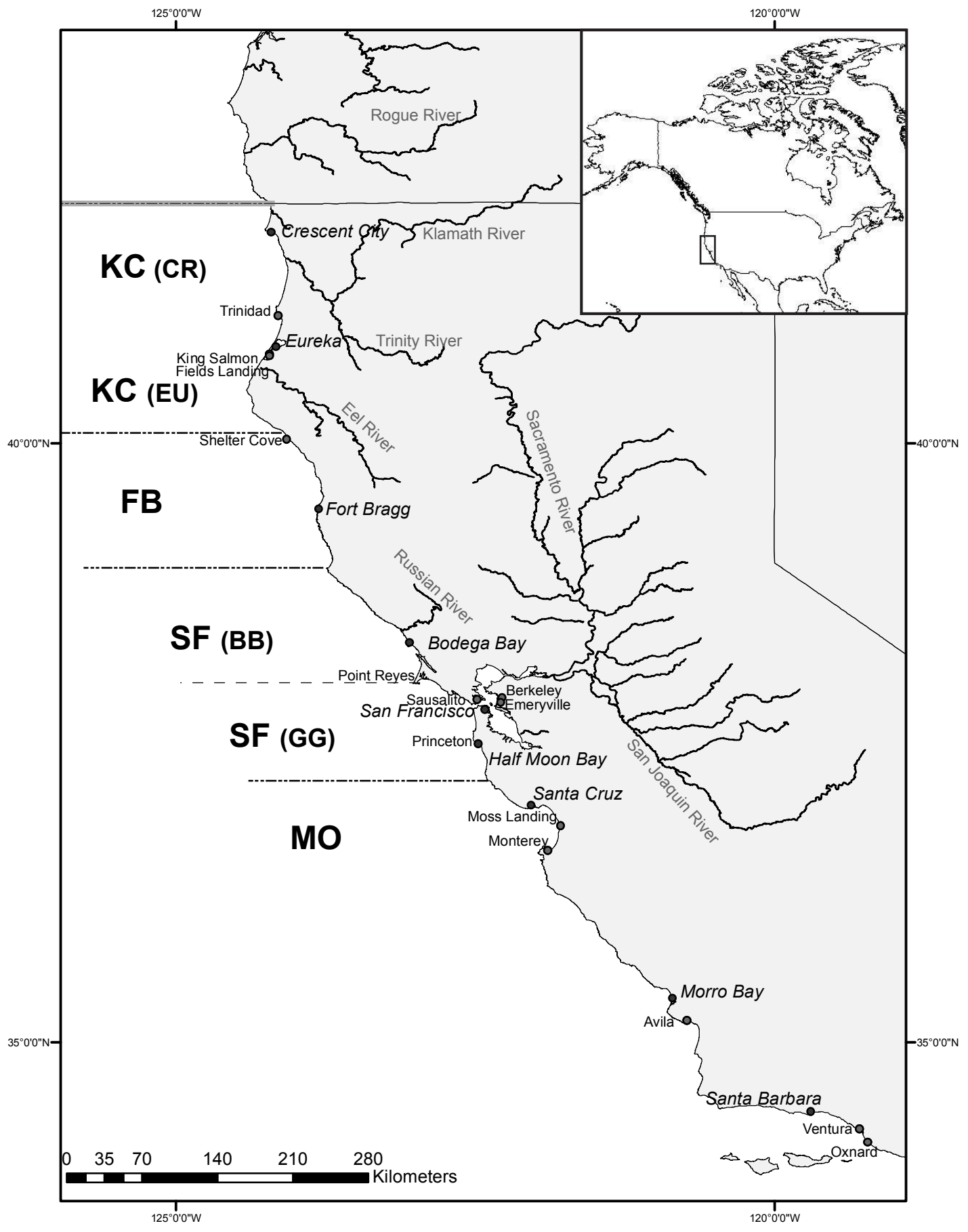


Figure 2

April

May

June

July

August

September

1998

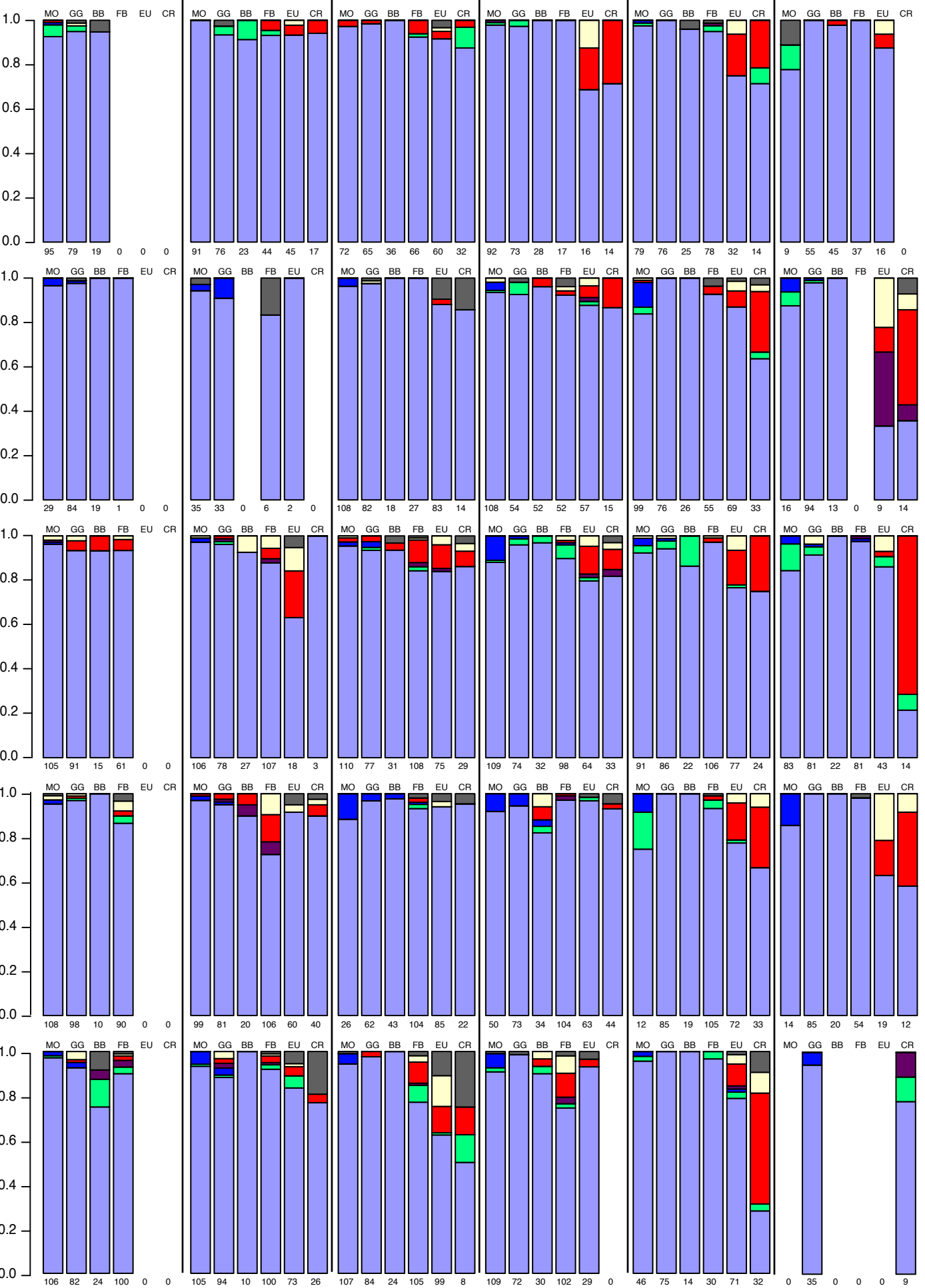
1999

2000

2001

2002

Stock Proportion



- Central Valley Fall
- California Coast
- Other Reporting Unit
- Central Valley Spring
- Klamath
- Rogue
- Central Valley Winter

Figure 3