**Online Resource 4** Supplementary Tables and Figures

**Genetic diversity within late-summer run and half-pounder steelhead (*Oncorhynchus mykiss*) in the Rogue River, Oregon**

David I Dayan[1*], Steve Mazur[3], Laura J Green[3], Andrew J Wells[3], Marc A Johnson[2], Daniel J Van Dyke[4], Peter A Samarin[4], Ryan D Battleson[4], Kathleen G O'Malley[1]

[1] State Fisheries Genomics Laboratory, Coastal Oregon Marine Experiment Station, Department of Fisheries, Wildlife and Conservation Sciences, Hatfield Marine Science Center, Oregon State University, Newport, OR, USA
[2] Native Fish Conservation and Recovery, Oregon Department of Fish and Wildlife, Salem, OR, USA
[3] Oregon Department of Fish and Wildlife, Gold Beach, OR, USA
[4] Rogue Watershed District, Oregon Department of Fish and Wildlife, Central Point, OR, USA

* Corresponding author, email: david.dayan@oregonstate.edu, ORCID ID: 0000-0001-5001-4062

## Supplemental Tables

**Table S1** Observed *vs.* Expected heterozygosity for neutral and migration timing datasets among groups. Collections drawn from multiple years are combined

|  | Winter | | Early Summer | | Late Summer | | Half Pounder | |
|---|---|---|---|---|---|---|---|---|
|  | Ho | He | Ho | He | Ho | He | Ho | He |
| **Neutral Dataset** | 0.305 | 0.311 | 0.301 | 0.304 | 0.301 | 0.308 | 0.299 | 0.309 |
| **Migration Timing Dataset** | 0.102 | 0.096 | 0.010 | 0.009 | 0.387 | 0.355 | 0.266 | 0.357 |

**Table S2** Mean admixture proportions and standard deviation for the four groups analyzed with STRUCTURE using $k = 3$. Cluster 1 appears as purple, 2 as blue-green, and 3 as yellow (in order from top to bottom) in the $k = 3$ row of Fig. 2

|  | Cluster 1 | Cluster 2 | Cluster 3 |
|---|---|---|---|
| Late Summer | 0.37 ± 0.18 | 0.33 ± 0.21 | 0.30 ± 0.16 |
| Half Pounder | 0.34 ± 0.17 | 0.32 ± 0.21 | 0.34 ± 0.18 |
| Early Summer | 0.32 ± 0.17 | 0.17 ± 0.09 | 0.51 ± 0.18 |
| Winter | 0.41 ± 0.18 | 0.18 ± 0.08 | 0.42 ± 0.18 |

**Table S3** Mean admixture proportions and standard deviation for the four groups analyzed with STRUCTURE using $k = 4$. Cluster 1 appears as purple, 2 as blue, 3 as green, and 4 as yellow (in order top to bottom) in the $k = 3$ row of Fig. 2

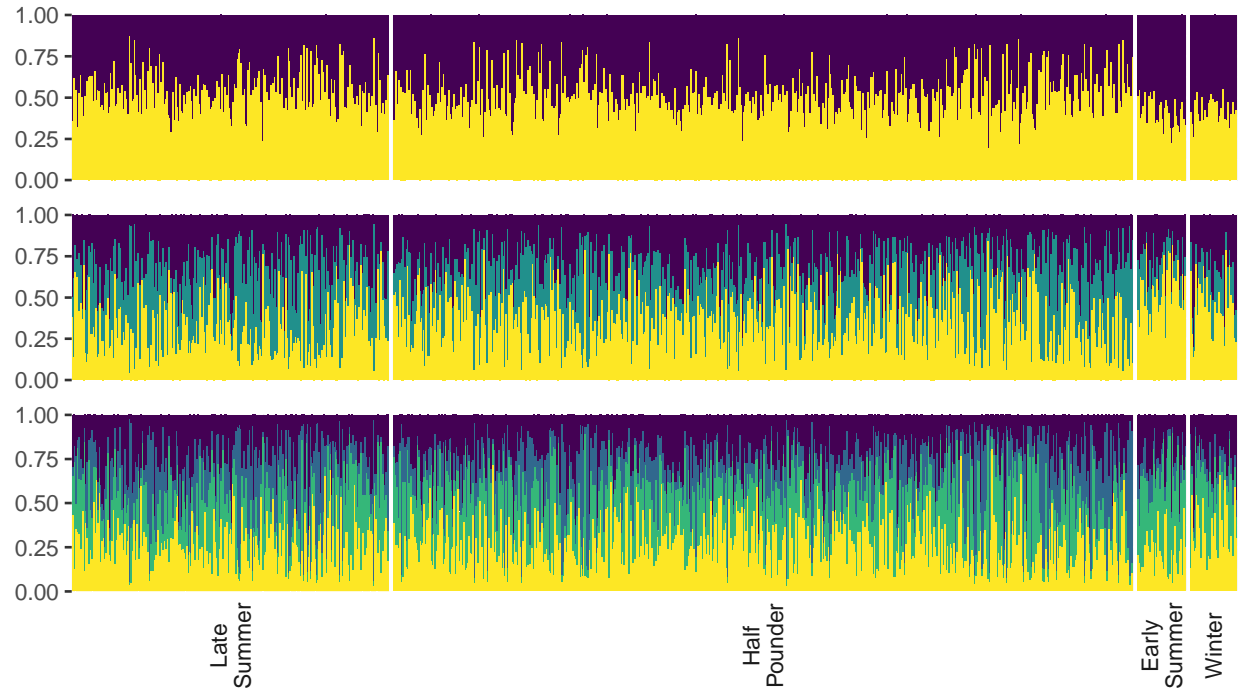|  | Cluster 1 | Cluster 2 | Cluster 3 | Cluster 4 |
|---|---|---|---|---|
| Late Summer | 0.27 ± 0.16 | 0.25 ± 0.23 | 0.22 ± 0.17 | 0.26 ± 0.13 |
| Half Pounder | 0.25 ± 0.15 | 0.24 ± 0.24 | 0.25 ± 0.20 | 0.26 ± 0.14 |
| Early Summer | 0.27 ± 0.17 | 0.09 ± 0.06 | 0.42 ± 0.24 | 0.21 ± 0.12 |
| Winter | 0.29 ± 0.16 | 0.09 ± 0.05 | 0.31 ± 0.20 | 0.31 ± 0.15 |

**Fig. S1** Admixture proportions from STRUCTURE for $k = 2 - 4$ for each of the four groups. Collections drawn from multiple years are combined

**a**

Early−Summer
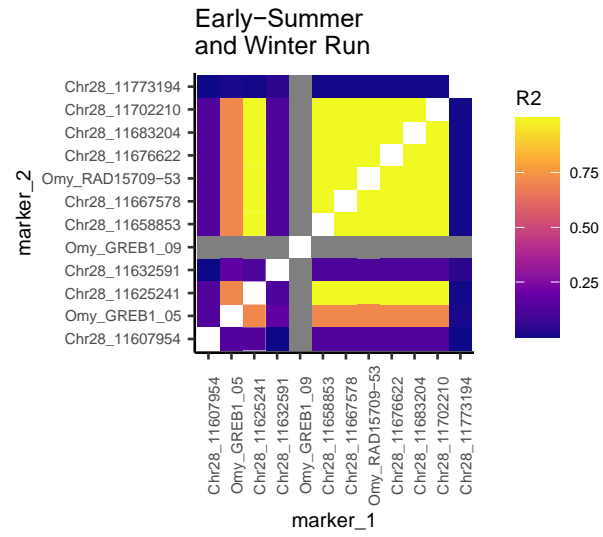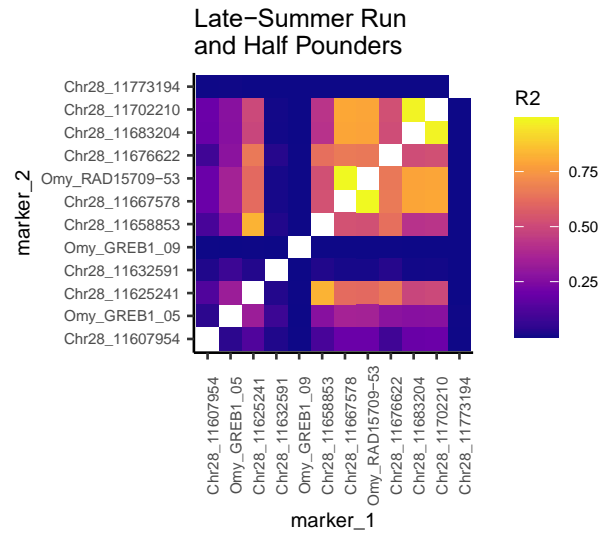and Winter Run

**b**

Late−Summer Run
and Half Pounders

**Fig. S2** Linkage disequilibrium ($r^2$) among migration timing markers in (a) early-summer and winter runs, (b) late-summer run and half pounders
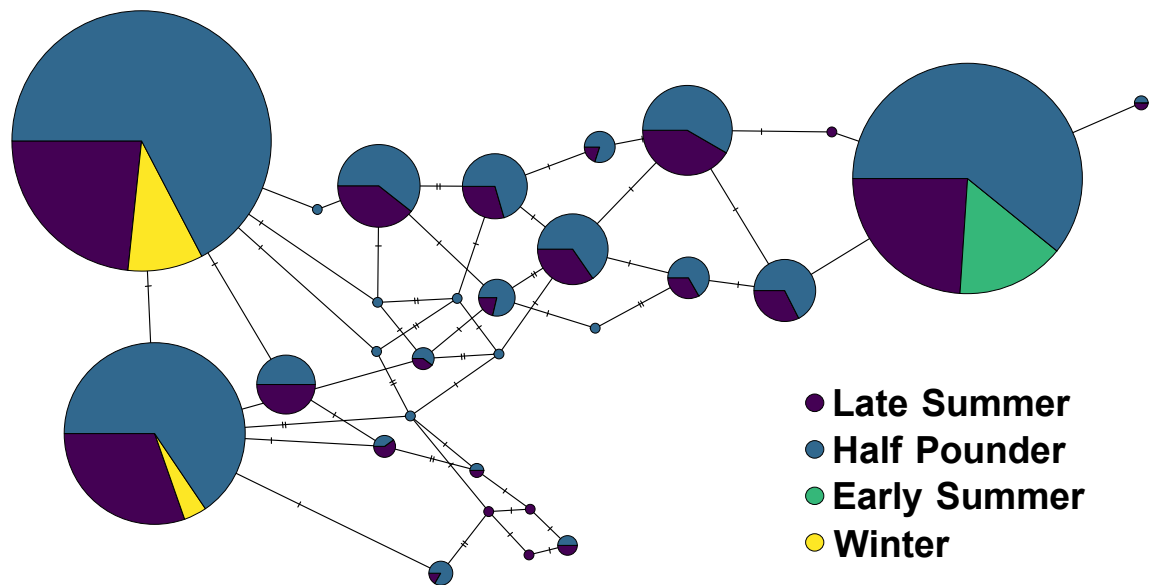
**Fig. S3** Haplotype network. Each node represents a unique haplotype observed in the dataset. Colors within nodes represent proportion of each group with that haplotype. Edges represent the inferred minimum spanning tree connecting haplotypes. Collections drawn from multiple years are combined