Table S9.

Basin	Location	N	A/L	A/E	L/L	L/E	E/L	E/E
Siletz	Siletz	158	0.01	0.11	0.49	0.00	0.00	0.36
Klamath	Klamath estuary	496	0.03	0.02	0.38	0.00	0.13	0.40
Klamath	Klamath - Iron Gate H.	449	0.04	0.00	0.70	0.00	0.22	0.00
Klamath	Salmon R.	38	0.03	0.03	0.12	0.19	0.19	0.45
Klamath	Trinity H.	190	0.02	0.04	0.40	0.04	0.18	0.30
Eel	EelVAfl	41	0.00	0.00	0.94	0.00	0.04	0.00
Russian	RussianWSH	46	0.00	0.00	1.00	0.00	0.00	0.00
Sac./San Jo.	Butte Ck.	98	0.00	0.18	0.20	0.01	0.01	0.60
Sac./San Jo.	Battle Ck. L.F.	44	0.00	0.00	1.00	0.00	0.00	0.00
Sac./San Jo.	Feather R. H.	83	0.00	0.14	0.16	0.04	0.00	0.65
Sac./San Jo.	Keswick_WR	125	0.00	0.04	0.04	0.05	0.00	0.87

Frequencies of haplotypes recombinant/non-recombinant between the distal and RoSA region in collections from California and Oregon. L = late-migrating; E = early-migrating; A = ambiguous; 'Sac/San Jo.' = Sacramento/San Joaquin Rivers Basin; 'R.' = River; 'H.' = Hatchery; 'L.F.' = Late Fall; 'Ck.' = Creek; 'Klamath estuary' = Chinook salmon sampled in the Yurok Tribal fishery at the mouth of the Klamath River; 'EelVAfl' = Eel River Van Arsdale fish counting station; 'Keswick_WR' = Winter run Chinook salmon collected at Keswick Dam. The numbers are sums of the PHASE-estimated frequencies of the 13-SNP haplotypes with an estimated frequency > 0.01 (see Supplementary Methods). Consequently, rows do not sum exactly to 1.0.