Table S1. Sampling locations, sample size (n), average observed heterozygosity (*H*o), gene diversity (*H*s), inbreeding coefficient (*F*is), and proportion of loci with significant linkage disequilibria (P < 0.05; %LD) by population.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Population | n | Latitude | Longitude | Ho | Hs | Fis | LD |
| BBR | 8 | 45.37986 | -122.41015 | 0.171 | 0.168 | 0.015 | 0.050 |
| BPPI | 7 | 45.37919 | -122.40415 | 0.092 | 0.129 | 0.282 | 0.052 |
| CBR | 6 | 45.39243 | -122.49561 | 0.139 | 0.266 | 0.376 | 0.092 |
| CC | 6 | 45.35845 | -122.48145 | 0.111 | 0.311 | 0.513 | 0.109 |
| CLB | 7 | 45.37249 | -122.60039 | 0.094 | 0.134 | 0.297 | 0.033 |
| CPS | 10 | 45.37861 | -122.57660 | 0.076 | 0.046 | -0.415 | 0.004 |
| CRP | 12 | 45.37874 | -122.58533 | 0.089 | 0.102 | 0.272 | 0.036 |
| DBR | 12 | 45.37320 | -122.60605 | 0.153 | 0.244 | 0.312 | 0.129 |
| FMR | 9 | 45.31748 | -122.43463 | 0.127 | 0.190 | 0.383 | 0.109 |
| FPT | 12 | 45.33974 | -122.43922 | 0.146 | 0.202 | 0.292 | 0.104 |
| HD | 7 | 45.31340 | -122.37220 | 0.149 | 0.152 | 0.172 | 0.066 |
| MBB | 8 | 45.37794 | -122.60950 | 0.133 | 0.071 | -0.889 | 0.008 |
| MEP | 11 | 45.37716 | -122.61611 | 0.133 | 0.214 | 0.303 | 0.101 |
| MLB | 7 | 45.29860 | -122.36108 | 0.142 | 0.295 | 0.447 | 0.130 |
| MOST | 4 | 45.48172 | -122.65471 | 0.099 | 0.260 | 0.509 | 0.052 |
| MRS | 6 | 45.29014 | -122.36169 | 0.171 | 0.090 | -0.819 | 0.007 |
| MSR | 10 | 45.35858 | -122.46577 | 0.219 | 0.239 | 0.075 | 0.087 |
| MTT | 9 | 45.42118 | -122.55317 | 0.109 | 0.088 | 0.007 | 0.020 |
| MUB | 6 | 45.31162 | -122.38004 | 0.201 | 0.213 | 0.025 | 0.039 |
| OBBT | 3 | 45.48150 | -122.65171 | 0.099 | 0.197 | 0.362 | 0.001 |
| RSP | 11 | 45.39648 | -122.56226 | 0.205 | 0.282 | 0.251 | 0.158 |
| SED | 7 | 45.38149 | -122.49701 | 0.111 | 0.157 | 0.383 | 0.149 |