

**Table S7.** Estimates of population genetic indices among 40 populations of the *Populus koreana* based on each of the 11 nSSR loci.

| Locus         | $N_a$ | $N_e$ | $H_e$ | $H_o$ | $F_{IS}$ | $F_{ST}$ | $N_m$ | $F_{null}$ |
|---------------|-------|-------|-------|-------|----------|----------|-------|------------|
| GCPM-1260     | 3.825 | 2.551 | 0.579 | 0.622 | -0.075   | 0.145    | 1.469 | 0.053      |
| GCPM-1063     | 5.525 | 3.697 | 0.704 | 0.660 | 0.062    | 0.123    | 1.781 | 0.096      |
| PeuSSR-186    | 2.625 | 1.359 | 0.207 | 0.130 | 0.371    | 0.112    | 1.977 | 0.312      |
| PeuSSR-48175  | 5.675 | 3.354 | 0.658 | 0.578 | 0.121    | 0.180    | 1.139 | 0.149      |
| PeuSSR-56336  | 2.975 | 2.152 | 0.503 | 0.465 | 0.075    | 0.176    | 1.169 | 0.150      |
| PeuSSR-83115  | 8.025 | 5.302 | 0.779 | 0.799 | -0.025   | 0.116    | 1.914 | 0.054      |
| PeuSSR-98348  | 6.325 | 4.287 | 0.730 | 0.580 | 0.206    | 0.115    | 1.915 | 0.173      |
| PeuSSR-135862 | 2.950 | 2.095 | 0.493 | 0.526 | -0.066   | 0.149    | 1.428 | 0.057      |
| PeuSSR-149476 | 5.275 | 3.398 | 0.678 | 0.468 | 0.310    | 0.141    | 1.524 | 0.252      |
| PeuSSR-172575 | 3.800 | 2.683 | 0.604 | 0.605 | -0.002   | 0.104    | 2.147 | 0.049      |
| PeuSSR-185039 | 2.625 | 1.596 | 0.326 | 0.223 | 0.317    | 0.290    | 0.613 | 0.355      |
| Mean          | 4.511 | 2.952 | 0.569 | 0.514 | 0.118    | 0.150    | 1.552 | 0.154      |

*Abbreviations:*  $N_a$ , no. of different alleles;  $N_e$ , no. of effective alleles;  $H_e$ , expected heterozygosity;  $H_o$ , observed heterozygosity;  $F_{IS}$ , inbreeding coefficient at the population level;  $F_{ST}$ , the proportion of differentiation among populations;  $N_m$ , gene flow,  $N_m \approx [(1/ F_{ST})-1]/4$ ;  $F_{null}$ , null allele frequency.