

Table S9. The statistics of cpDNA genetic diversity for each population of *Populus koreana*.

Region/Pop	N_{cpDNA}	H_d	P_i	H_{ap}
The Greater Khingan				
1	15	0.876	0.0018	H1(5) H2(1) H3(3)H4(1) H5(1) H6(1)
2	13	0.603	0.0012	H1(8) H7(1) H8(3)
3	8	0.893	0.00093	H1(2) H8(2) H9(1) H10(2)
4	9	0.972	0.00202	H8(2) H11(1) H12(1) H13(1)
5	10	0.933	0.00186	H1(3) H3(1) H7(1) H8(1) H14(1)
6	10	0.978	0.00362	H1(1) H3(2) H15(1) H16(1) H17(1)
7	7	0.952	0.00534	H1(2) H18(1)
8	4	0	0.00183	H4(1)
9	10	0.844	0.00075	H1(2) H3(3) H4(1) H8(3) H19(1)
Southern Heilongjiang				
10	19	0	0	H1(19)
11	7	0	0	H1(7)
12	3	0	0	H1(3)
13	7	0.286	0.00016	H1(6) H20(1)
14	8	0.929	0.00145	H1(2) H4(1) H8(2)
15	10	0.844	0.00332	H1(1) H3(2) H17(1) H19(3) H21(1)
16	8	0	0	H1(8)
17	10	0.844	0.0014	H1(5) H3(2) H19(1)
18	10	0.756	0.00157	H1(5) H4(2) H8(1) H22(1)
19	9	0.978	0.00351	H1(1) H4(1) H8(2) H18(1) H23(1)
20	4	0.5	0.00029	H1(3) H8(1)
The Changbai Mountains				
21	10	0.905	0.00077	H1(2) H3(1) H4(1) H8(2) H24(1)
22	7	0	0	H1(7)
23	8	0.806	0.00236	H1(4) H4(1) H8(2)
24	14	0.275	0.00016	H1(12) H25(1)
25	9	0.694	0.00051	H1(5) H3(1) H4(1) H8(2)
26	9	0.556	0.00061	H3(6) H4(2) H26(1)
27	14	0.143	0.00008	H1(13) H25(1)
28	9	0	0	H1(9)
29	12	0.409	0.00024	H1(9) H27(3)
30	11	0.182	0.00011	H1(10) H8(1)
31	10	0.867	0.0021	H1(4) H3(1) H4(1) H8(1)
32	8	0.893	0.00165	H1(1) H3(3) H28(1) H29(1) H30(1)
33	9	0.978	0.02169	H4(2) H8(1) H31(1) H32(1)
Hebei Province				
34	15	0.886	0.00376	H8(1) H16(1) H17(3) H33(4) H34(3) H35(1)
The Korean Peninsula				
35	7	1	0.00402	H1(1) H19(1) H20(1)
36	14	0.901	0.0024	H1(3) H4(1) H8(4) H19(1) H36(1) H37(1) H38(1) H39(1) H40(1)
37	13	0.936	0.00169	H1(3) H3(1) H8(2) H19(2) H40(1) H41(1)
38	12	0.939	0.00169	H1(3) H4(1) H19(1) H24(1) H39(2)
39	11	0.8	0.00101	H1(5) H3(2) H4(1) H8(1) H40(1)
40	15	0.952	0.00151	H1(1) H3(3) H8(1) H19(2) H32(1) H38(1) H40(2) H42(1)
Mean	9.95	0.65775	0.0019352	-

Abbreviations: N_{cpDNA} , sample size analyzed for chloroplast DNA; H_d , haplotype diversity; P_i , nucleotide diversity; H_{ap} , haplotype. Bold fonts indicate private haplotype