



Figure S1. Pictures of native Korean Sapsaree dogs with different hair length phenotypes. In the picture, from left to right, are long- and short-haired Sapsaree dogs. Pictures were from the Korean Sapsaree foundation (<http://eng.sapsaree.org/>).







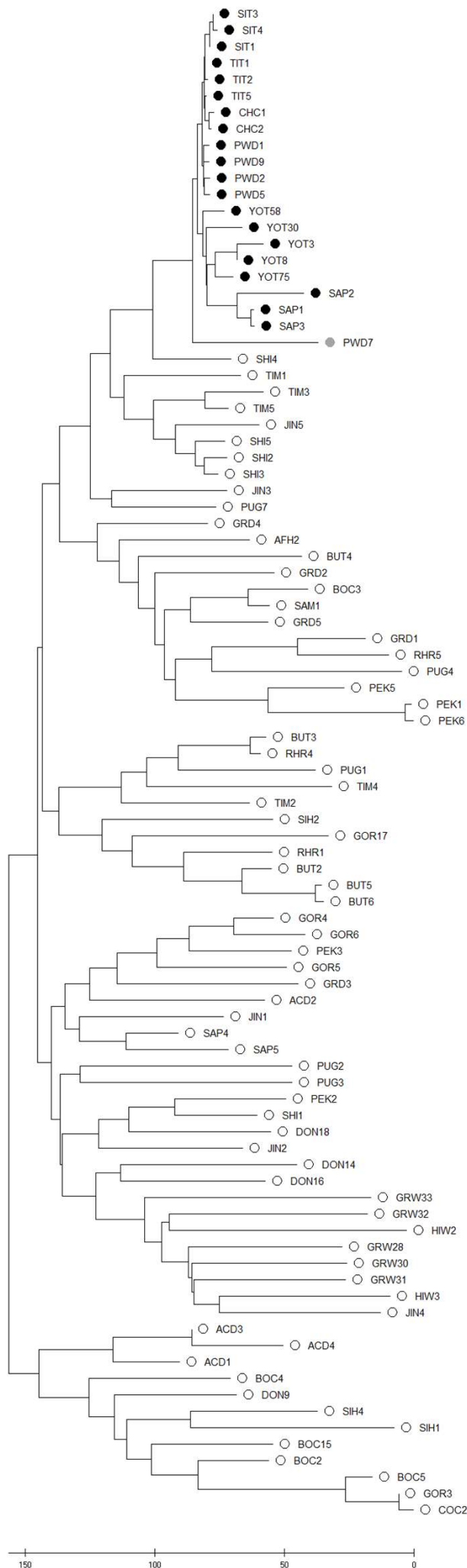


Figure S4. Neighbor-joining tree constructed using the CFA13:8,530,000–8,730,000 bp region of 92 dogs belonging to 24 dog breeds with various hair length phenotypes. Branch length was measured based on the number of nucleotide differences in the CFA13:8,530,000–8,730,000 bp region of each individual. Individuals homozygous for *RSP02* 3' UTR insertion are indicated by black circles, and those without insertion are indicated by white circles. Gray circles indicate individuals heterozygous for the insertion. GOR (Golden Retriever), ACD (Australian Cattle Dog), AFH (Afghan Hound), YOT (Yorkshire Terrier), BOC (Border Collie), BUT (Bull Terrier), GRD (Great Dane), CHC (Chinese Crested), COC (Chow Chow), PWD (Portuguese Water Dog), RHR (Rhodesian Ridgeback), SIH (Siberian Husky), SAM (Samoyed), DON (Donggyengi), GRW (Grey Wolf), HIW (Himalayan Wolf), JIN (Jindo), PEK (Pekingese), PUG (Pug), SAP (Sapsaree), SHI (Shiba), SIT (Shih Tzu), TIM (Tibetan Mastiff), TIT (Tibetan Terrier).





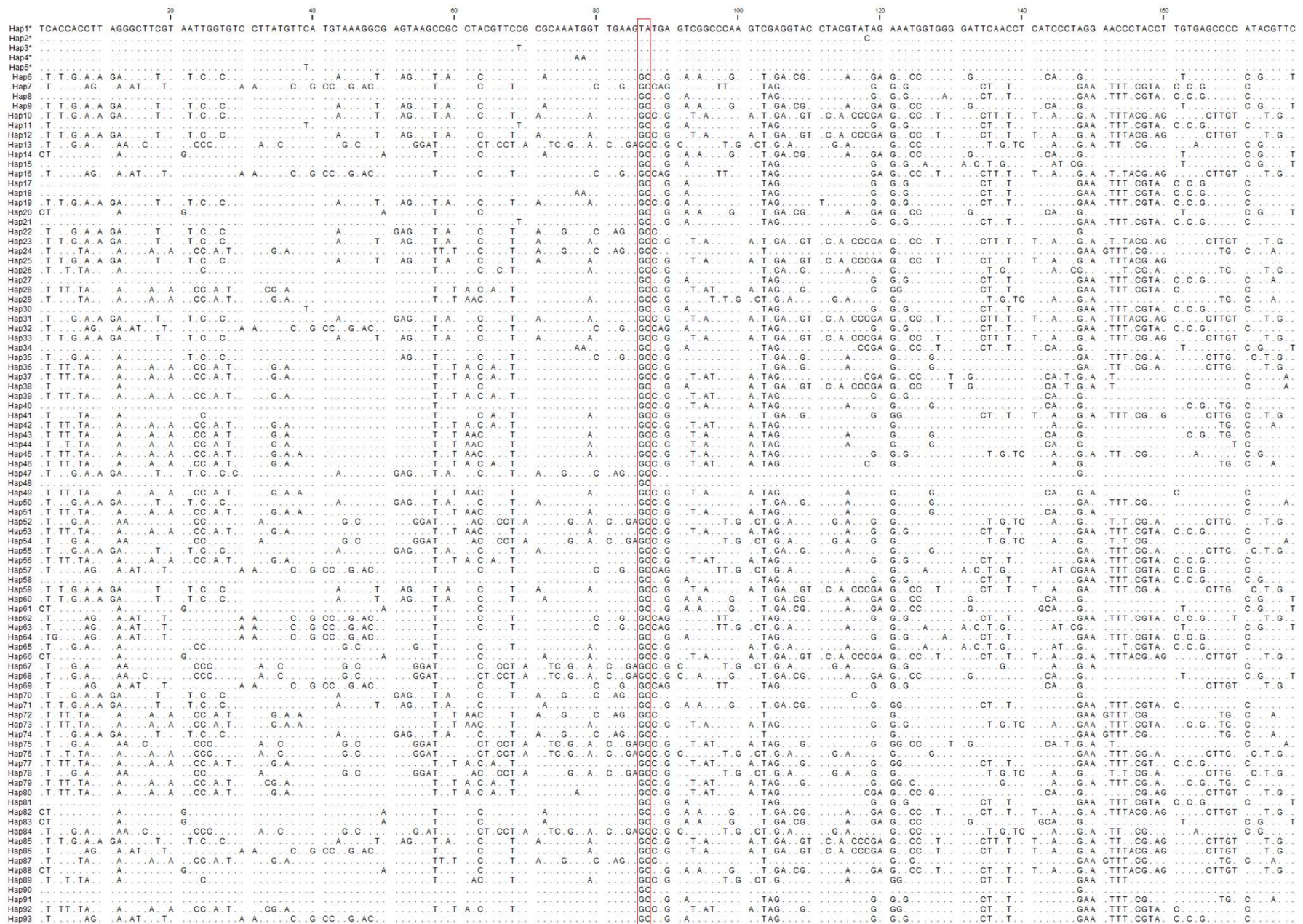


Figure S6. Result of multiple sequence alignment using 93 haplotype sequences of the *RSPO2* 3' UTR selective sweep region. The first five haplotypes are associated with the *RSPO2*-repeat allele. SNPs identical to those of Hap1 are replaced by dots, and SNPs specific to the insertion-related haplotypes are indicated in a red box.

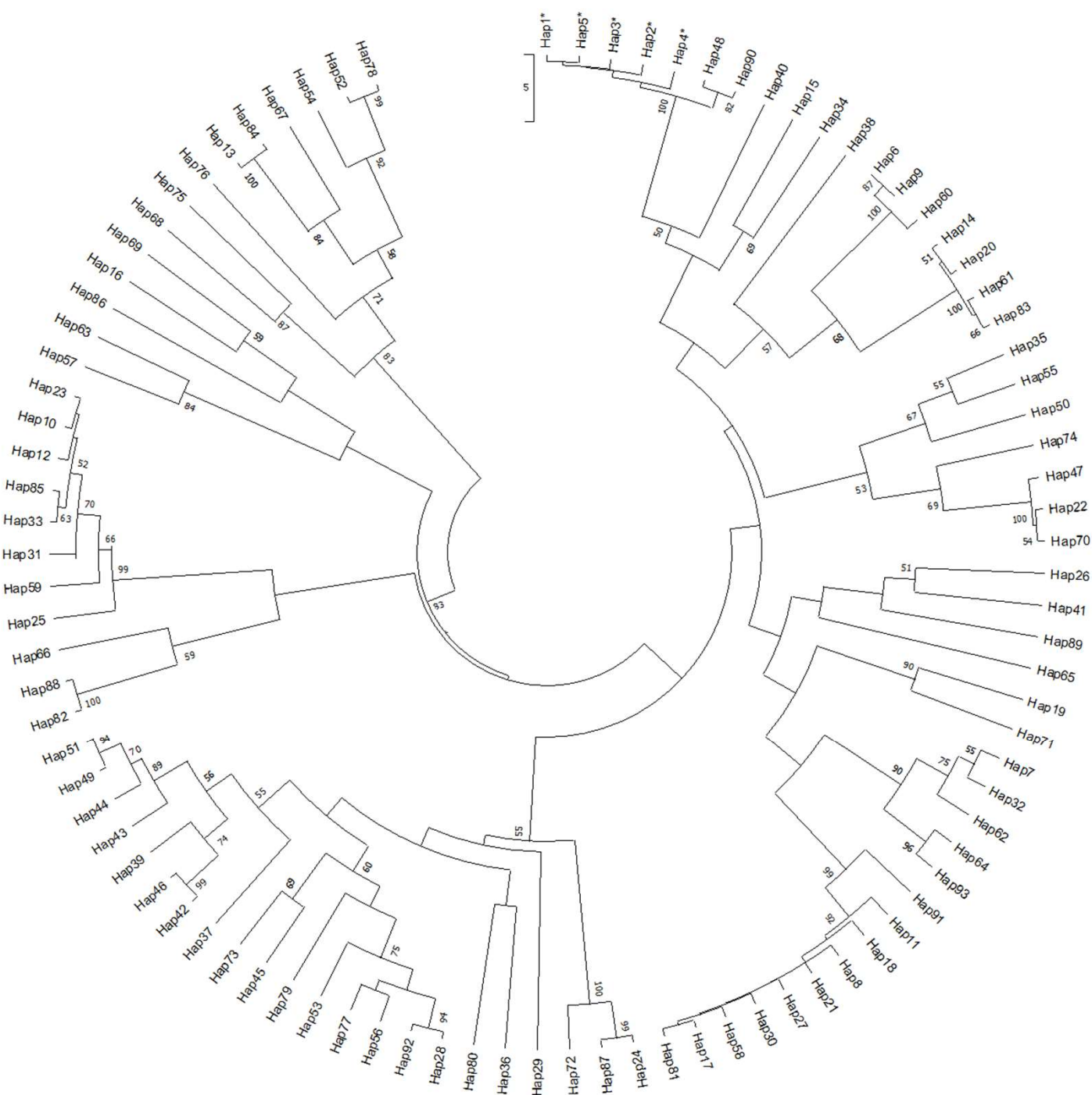


Figure S7. Phylogenetic relationships among the haplotypes of the haplotype block 20 region. A consensus UPGMA tree was created from the pairwise comparisons of 178 SNP markers present in 93 haplotypes with 1,000 bootstrapping replications. Branch length was determined using pairwise nucleotide difference. The 5 haplotypes associated with insertion are marked with asterisks.