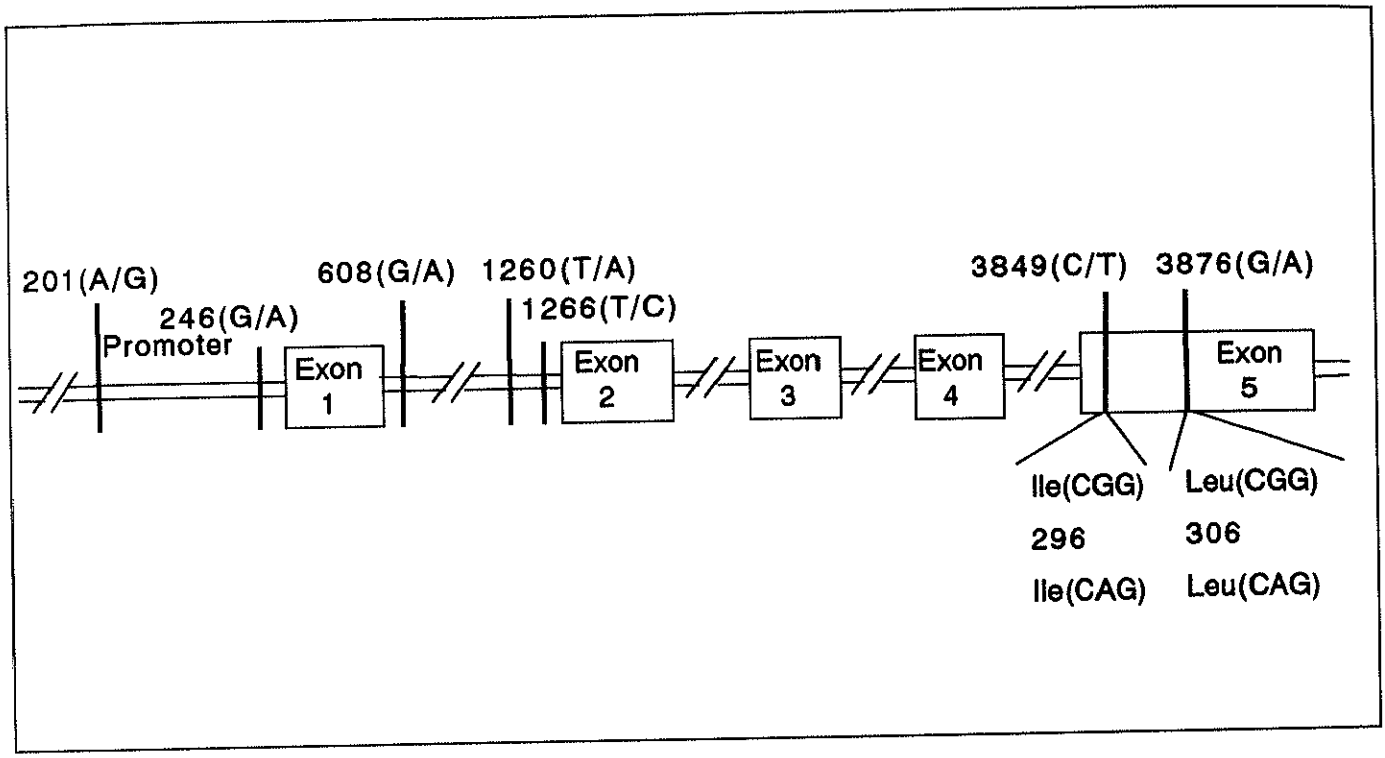

Fig. 1. Genetic polymorphisms in the promoter and coding regions of the CCK-A receptor gene. Exons are shown as boxes. Introns and the promoter region are shown as double lines. Positions of nucleotide substitutions of polymorphic sites are given over the figure. Amino acid changes by nucleotide substitutions and their numbers of the amino acid residues are indicated under exon 5.

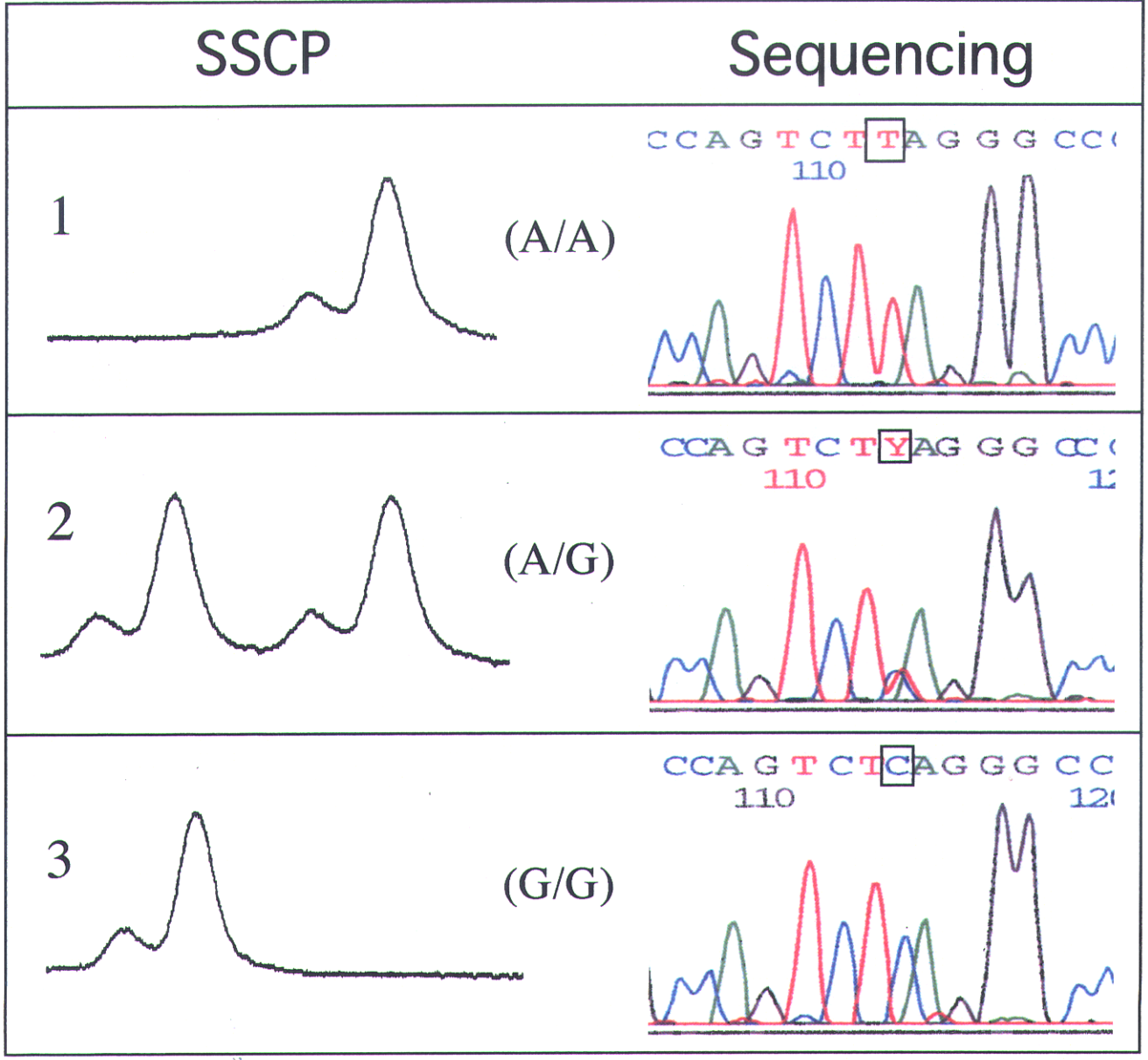

Fig. 2: SSCP patterns of PCR products and PCR direct sequences corresponding to the 201A→G nucleotide substitution in the promoter region of the CCK-AR gene. Nucleotide sequences were determined by using reverse primer. Sample 1, 2, 3 indicate homozygous genotype of the A allele (A/A), heterozygous genotype (A/G), and homozygous genotype of the G allele (G/G), respectively.

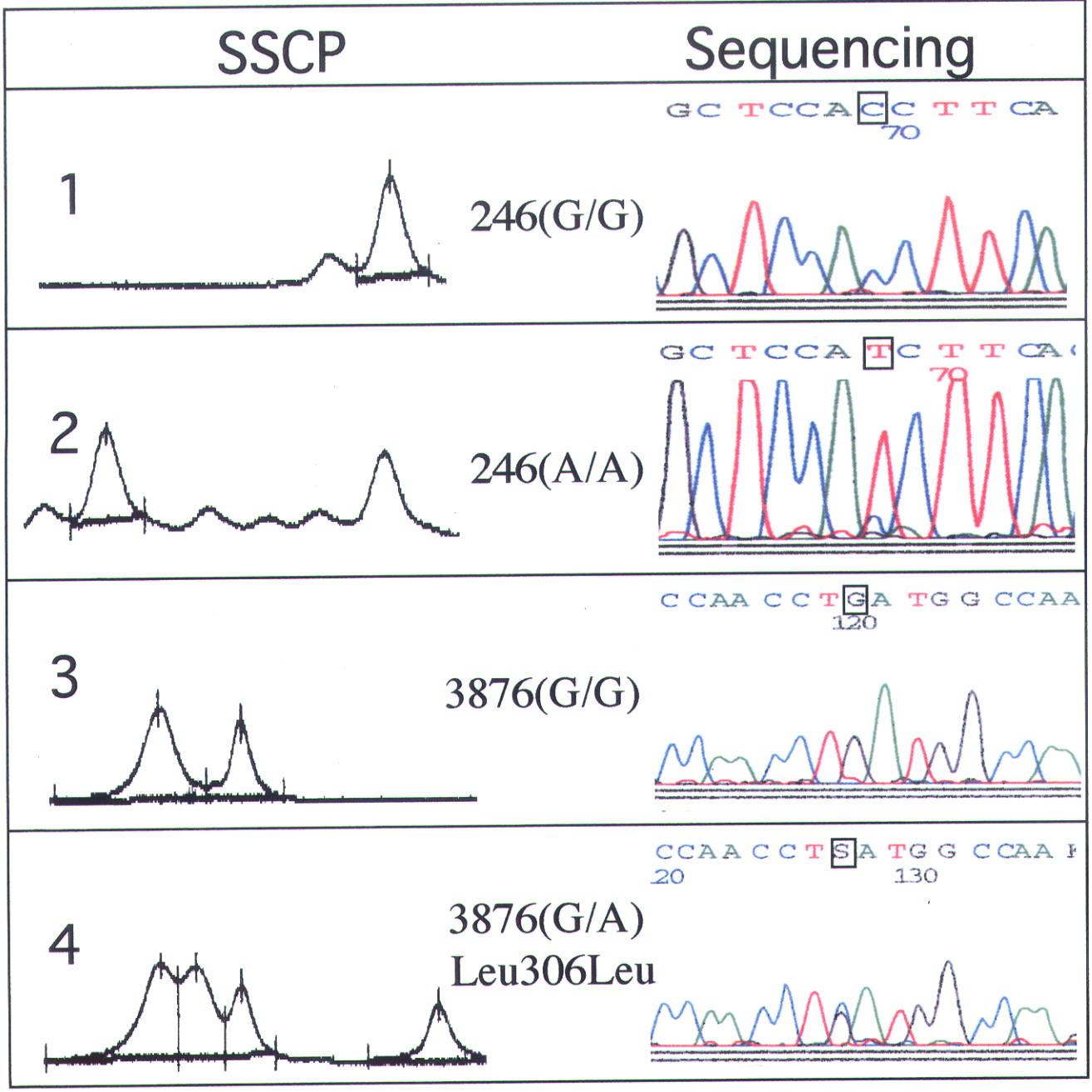

Fig. 3: SSCP patterns of PCR products and PCR direct sequences corresponding to the 246(G/A) nucleotide substitution in the promoter region (sample 1, 2), and a silent mutation in exon 5 (Leu306Leu; sample 3, 4) of the CCK-AR gene. Sample 1, 3 indicate wild types, and 2, 4 indicate variants of each locus. Nucleotide sequences of variants for 3876(G/A) were determined by using forward primer. The nucleotide substitution for 246(G/A) was determined by using reverse primer.

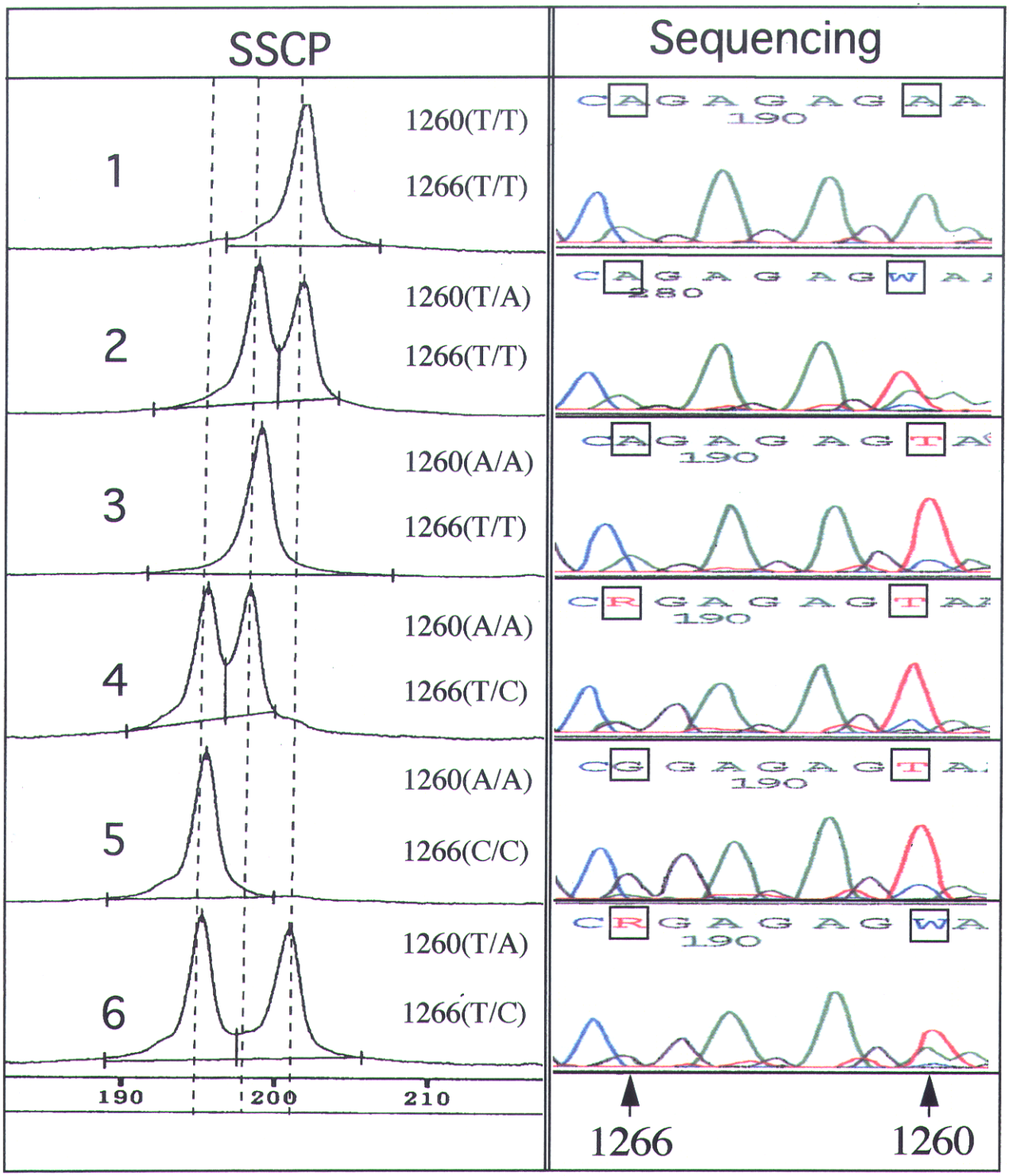

Fig. 4: Six SSCP patterns of PCR products and PCR direct sequences corresponding to the 1260T→A and 1266T→C nucleotide substitution in intron 1 of the CCK-AR gene. All of the nucleotide sequences were determined by using reverse primer. Sample 1-6 indicate each genotypes in both 1260 and 1266 locus.

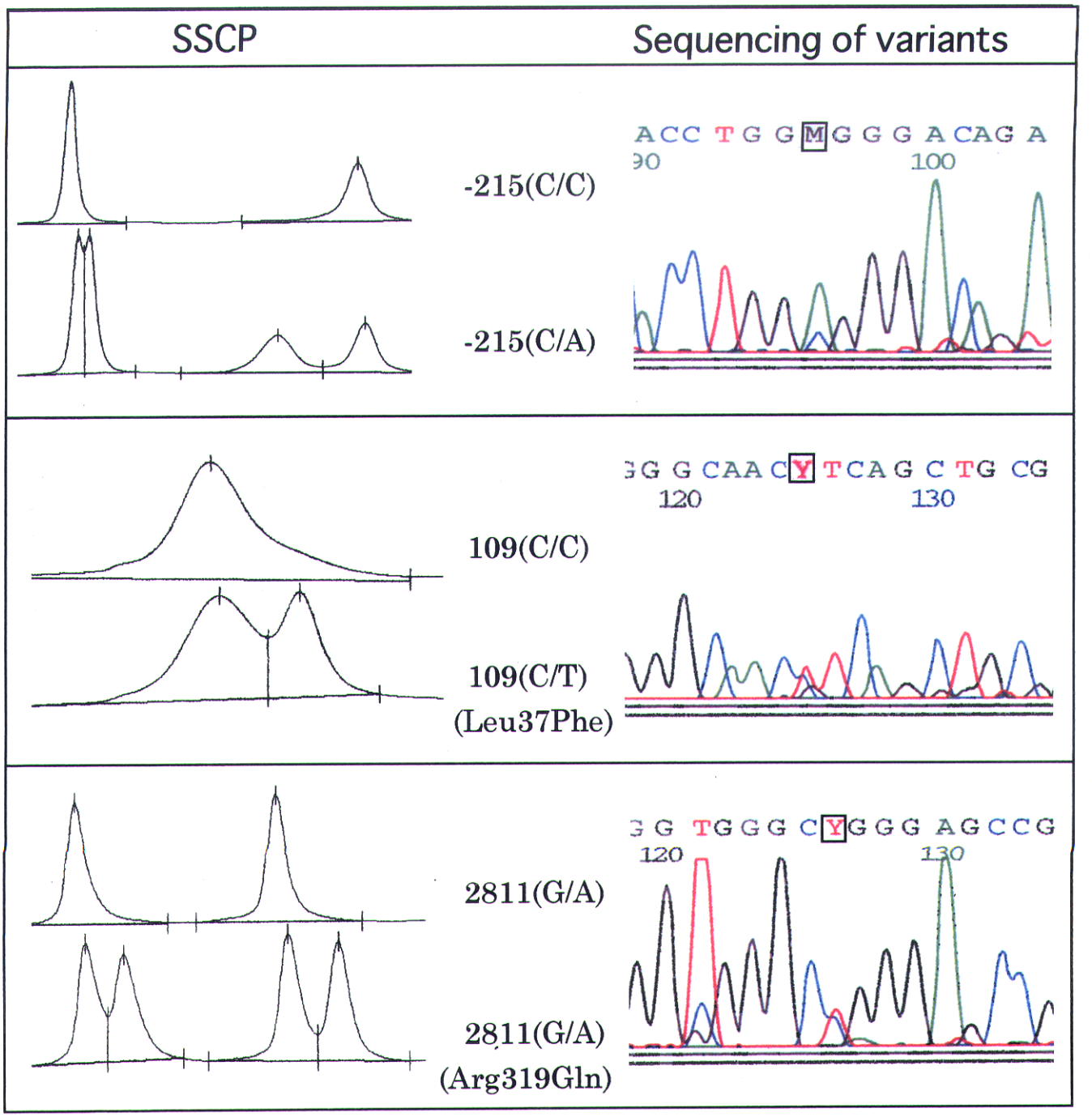

Fig.5: SSCP patterns of PCR products and PCR direct sequences corresponding to the -215(C/A) nucleotide substitution in the promoter region, a missense mutation in exon 1 (Leu37Phe) , and in exon 5 (Arg319Gln) of the CCK-BR gene. Upper columns of SSCP pattern indicate wild types, and lower columns indicate variants. Nucleotide sequences of variants for 109(C/T) and 2811(G/A) were determined by using forward primer. The nucleotide substitution for -215(C/A) was determined by using reverse primer.

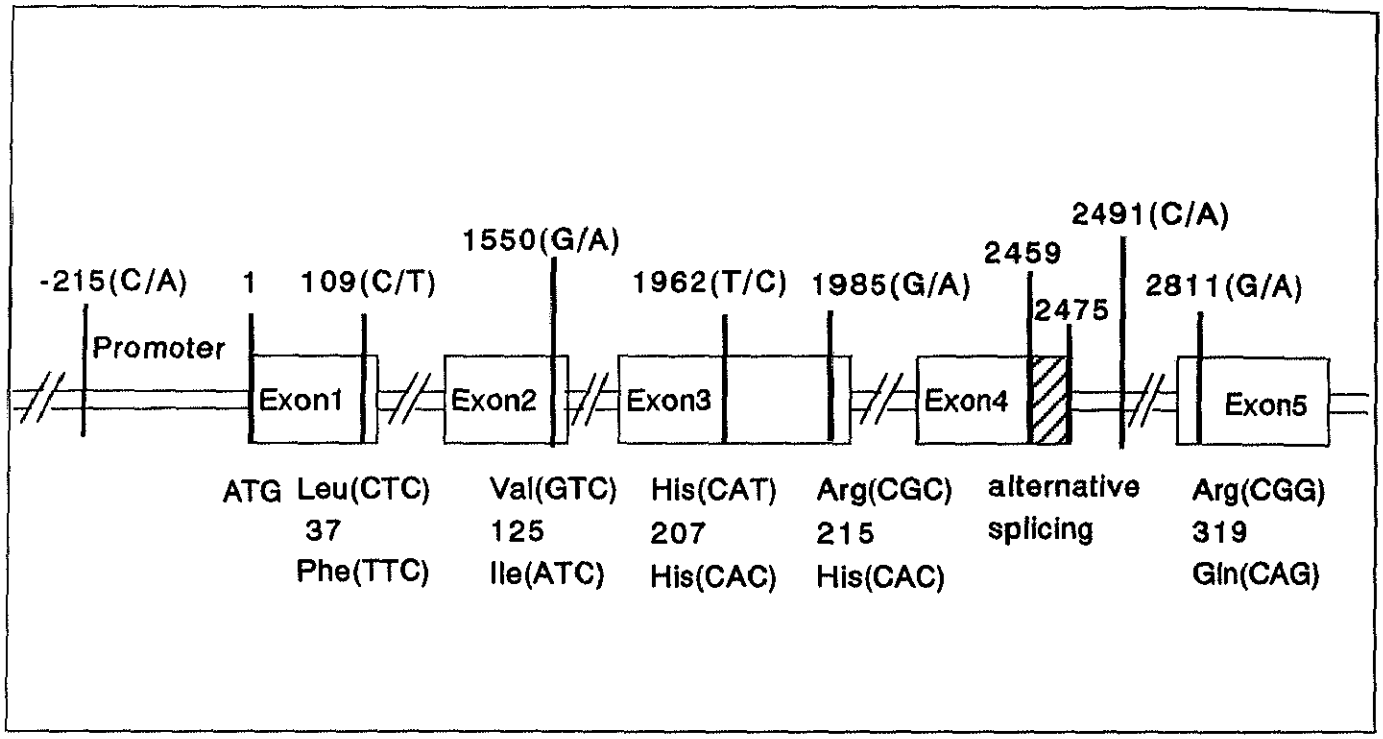

Fig. 6. Genetic polymorphisms in the promoter and coding regions of the CCK-B receptor gene. Exons are shown as boxes. Introns and the promoter region are shown as double lines. Positions of nucleotide substitutions of polymorphic sites are given over the figure. Amino acid changes by nucleotide substitutions and the numbers of the amino acid residues are indicated under the exons.

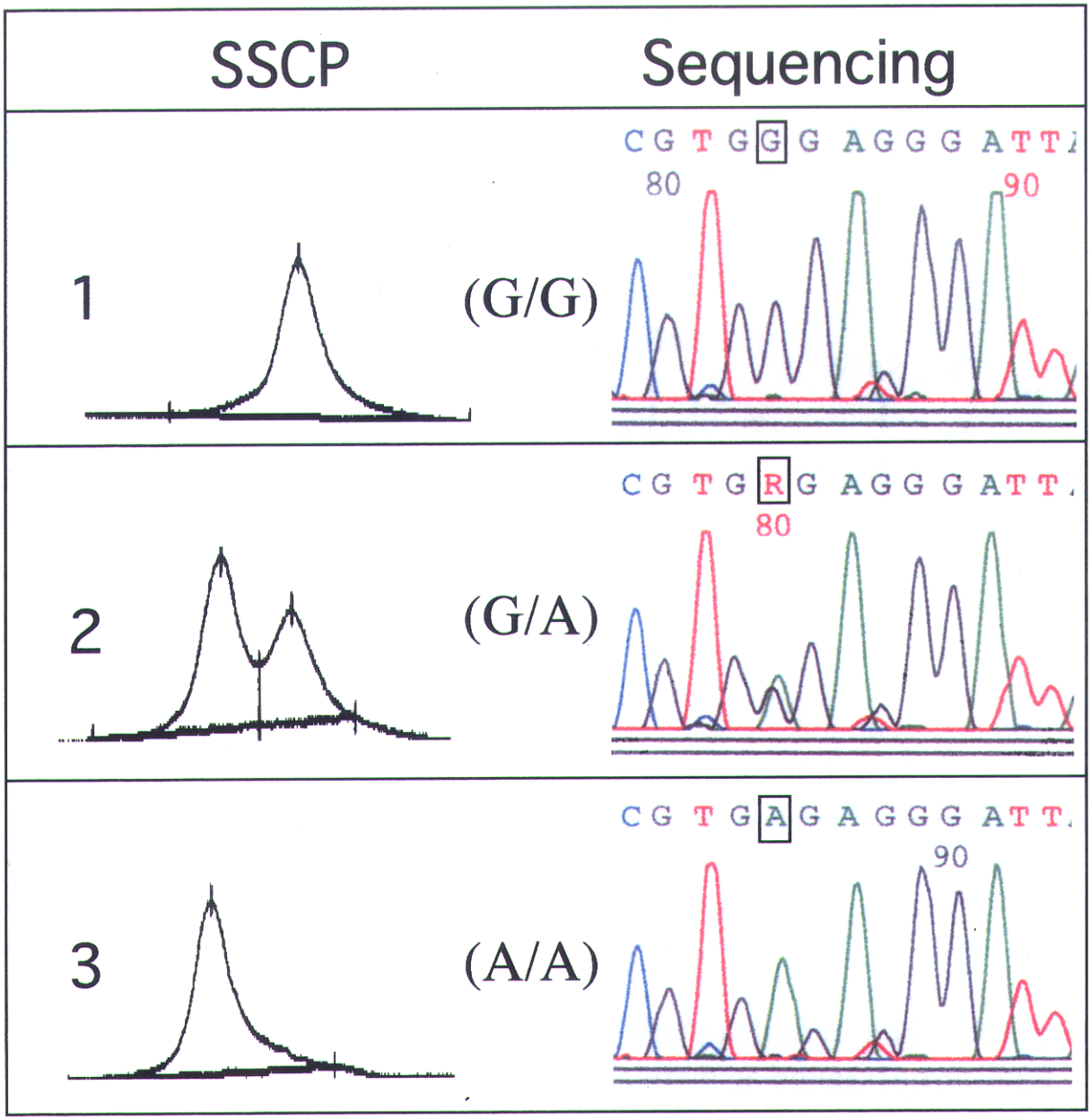

Fig. 7: SSCP patterns of PCR products and PCR direct sequences corresponding to the -196G → A nucleotide substitution of the promoter region of the CCK gene. Nucleotide sequences were determined by using forward primer. Sample 1, 2, 3 indicate homozygous genotype of the G allele (G/G), heterozygous genotype (G/A), and homozygous genotype of the A allele (A/A), respectively.

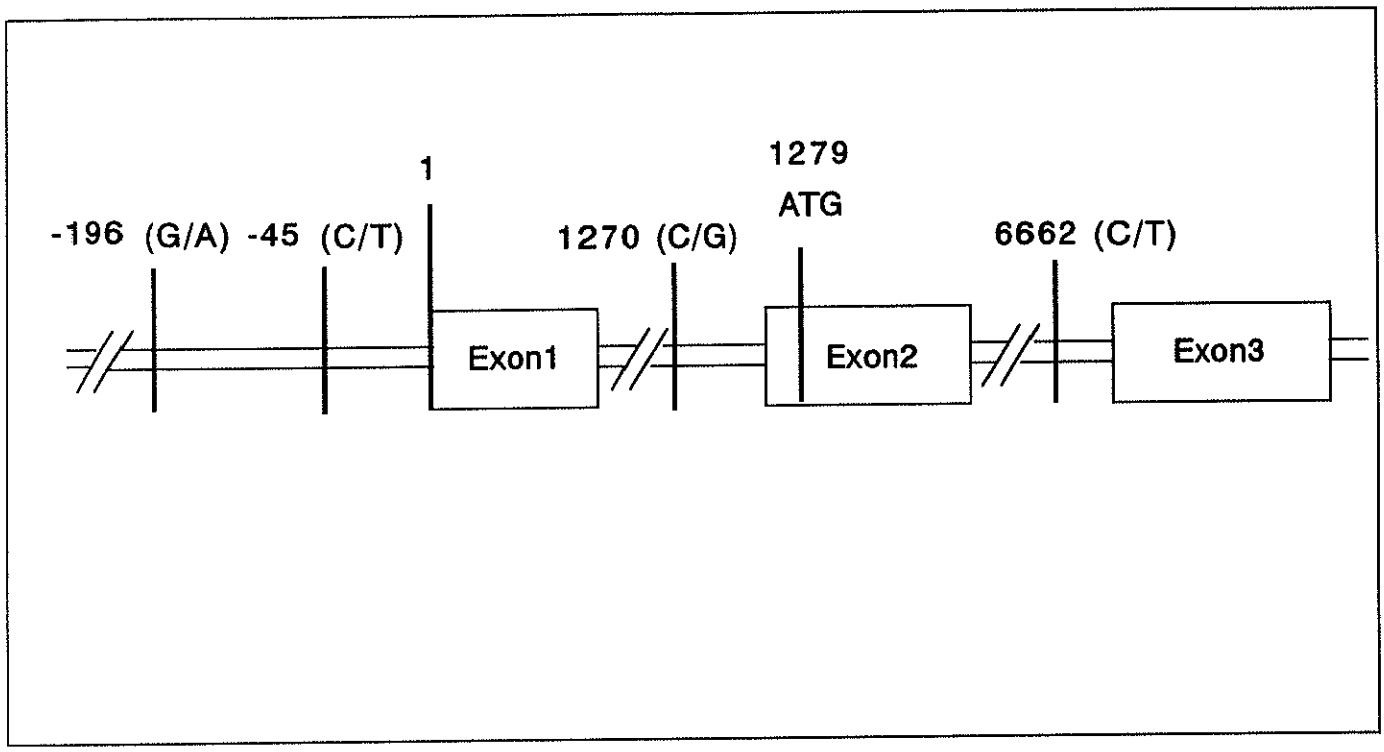

Fig. 8. Genetic polymorphisms in the promoter and coding regions of the CCK gene. Exons are shown as boxes. Introns and the promoter region are shown as double lines. Positions of nucleotide substitutions of polymorphic sites are given over the figure.