

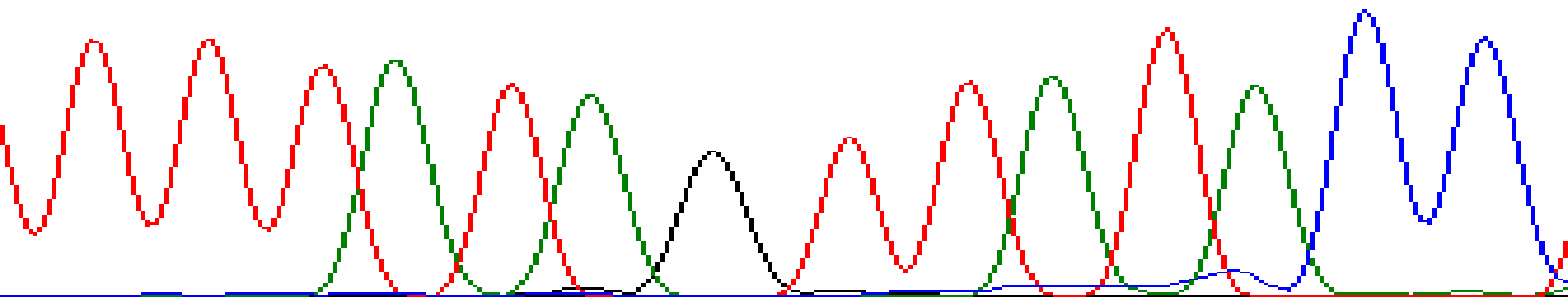
**Haag-Liautard et al.**

**Direct estimation of the mitochondrial DNA mutation rate in  
*Drosophila melanogaster***

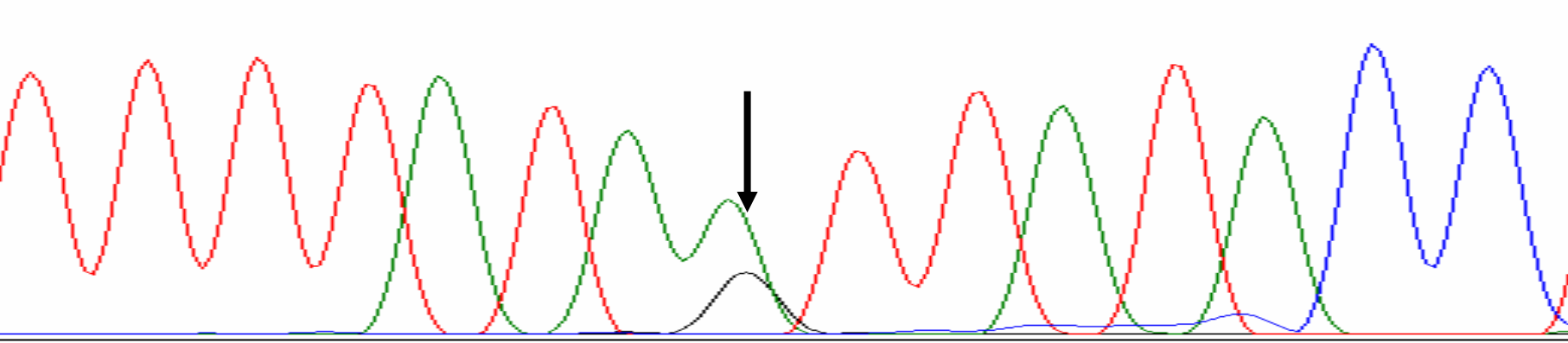
**Supplementary Material**

Position: 1,675

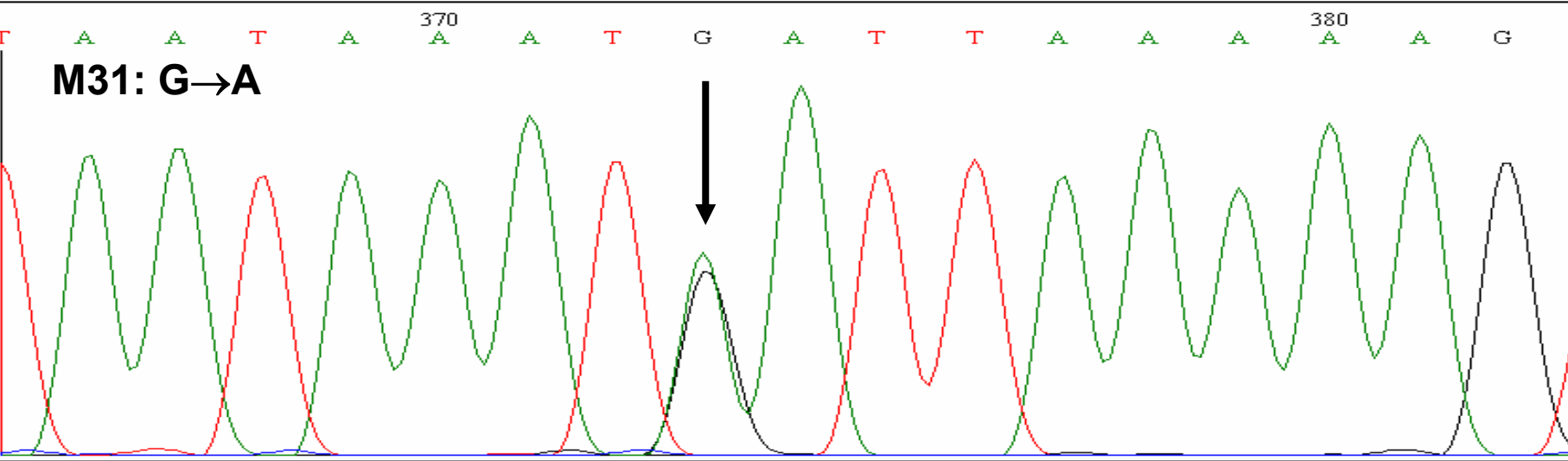
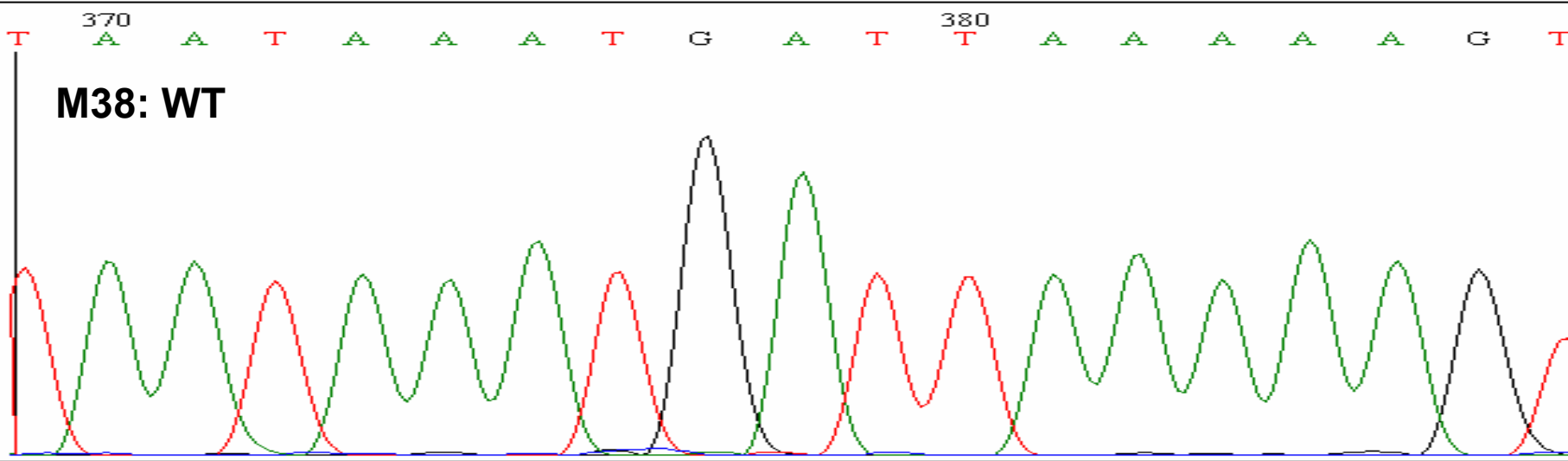
T T T A T <sup>60</sup> A G T T A T A C C  
M85: WT



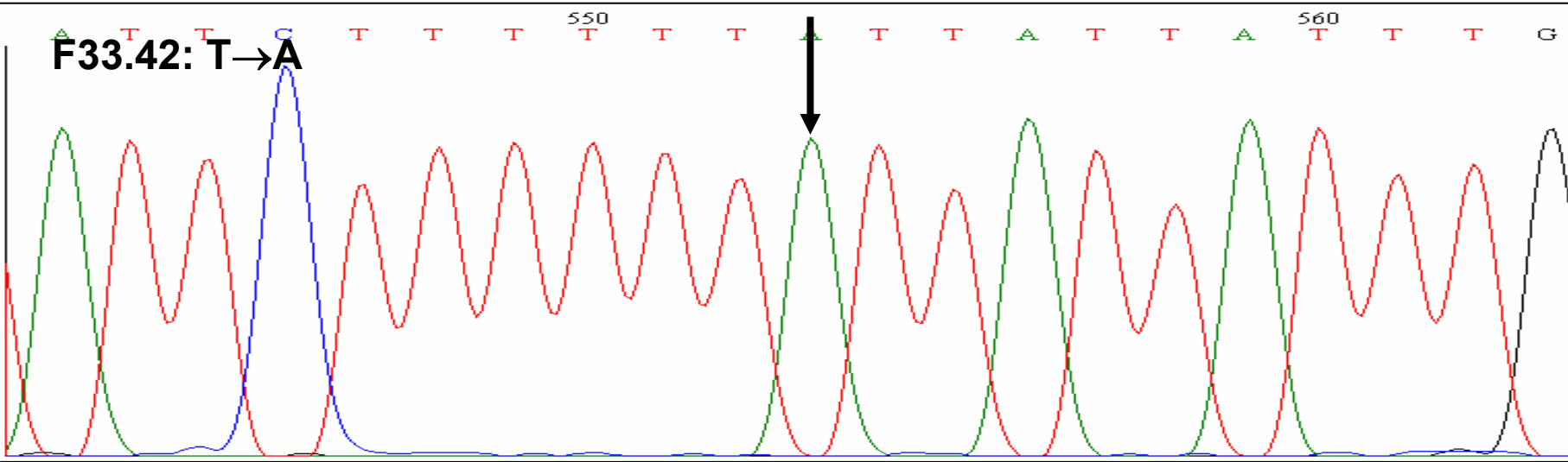
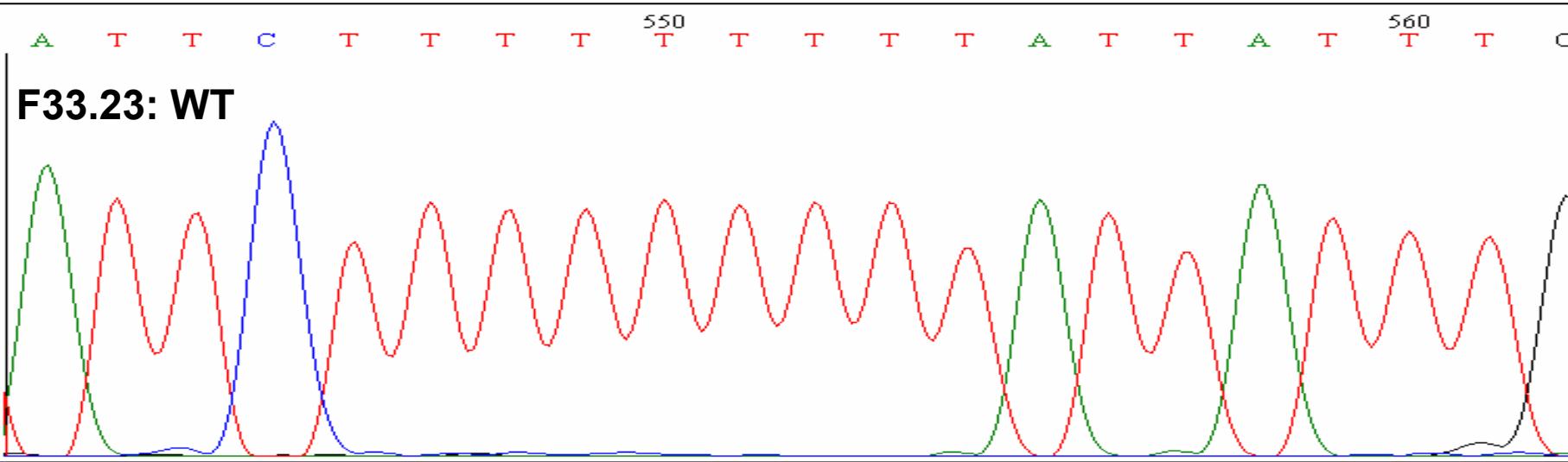
T T T T A T <sup>60</sup> A N T T A T A C C  
M79: G→A



Position: 2,693



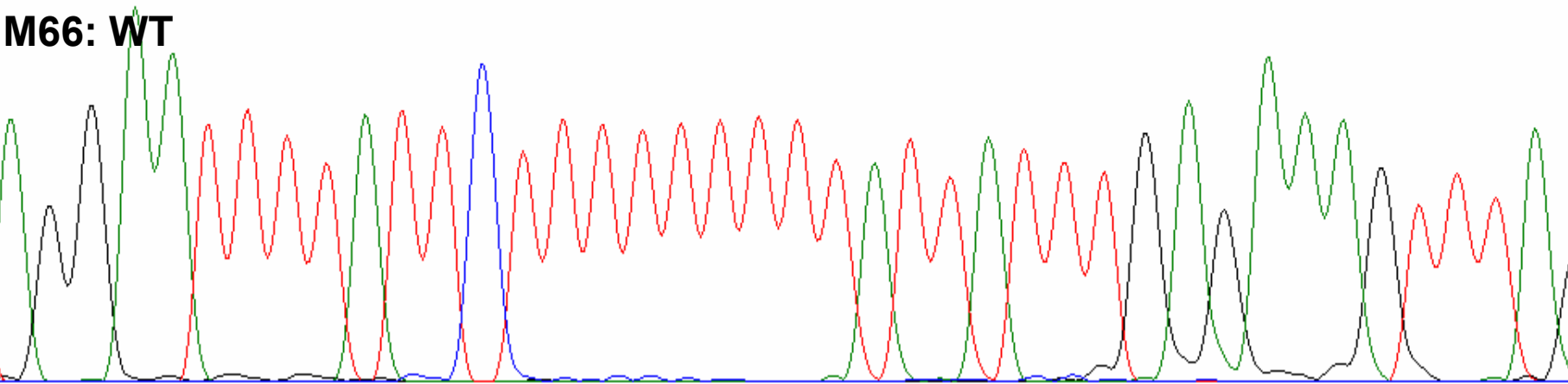
Position: 2,875



Position: 2,877

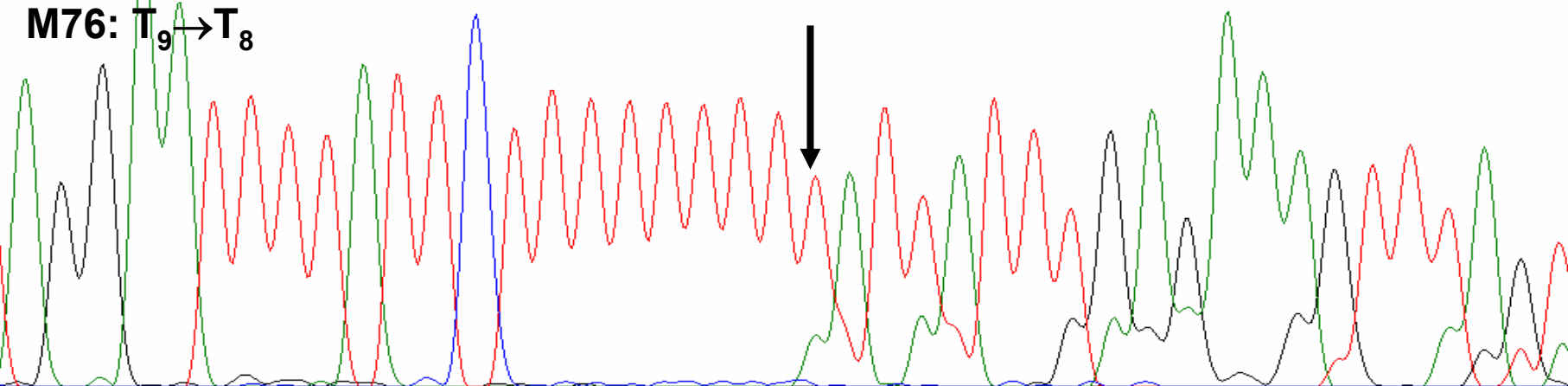
A G G A A T T T T A T T C T T T T T T T T T A T T A T T T G A G A A A G T T T A

M66: WT



A G G A A T T T T A T T C T T T T T T T T T A T T A T T N G A G A A A G T T T A G T

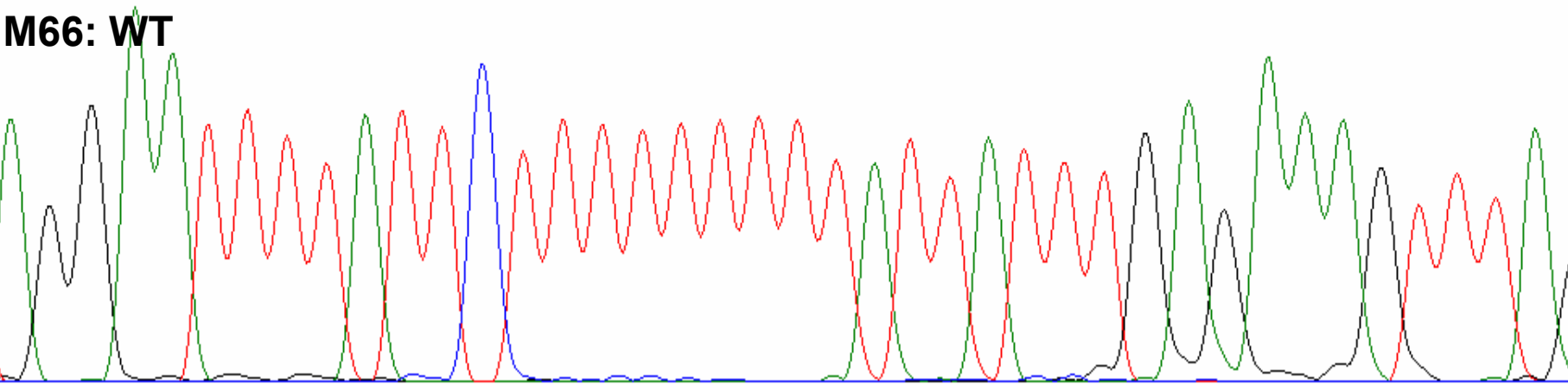
M76: T<sub>9</sub> → T<sub>8</sub>



Position: 2,877

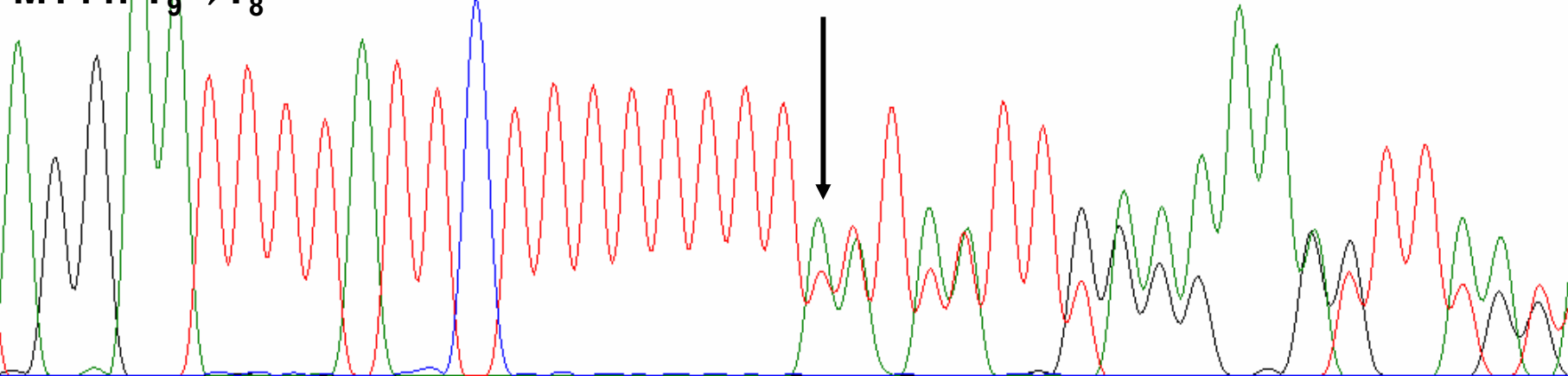
540 550 560 570  
A G G A A T T T T A T T C T T T T T T T T T A T T A T T T G A G A A A G T T T A

M66: WT

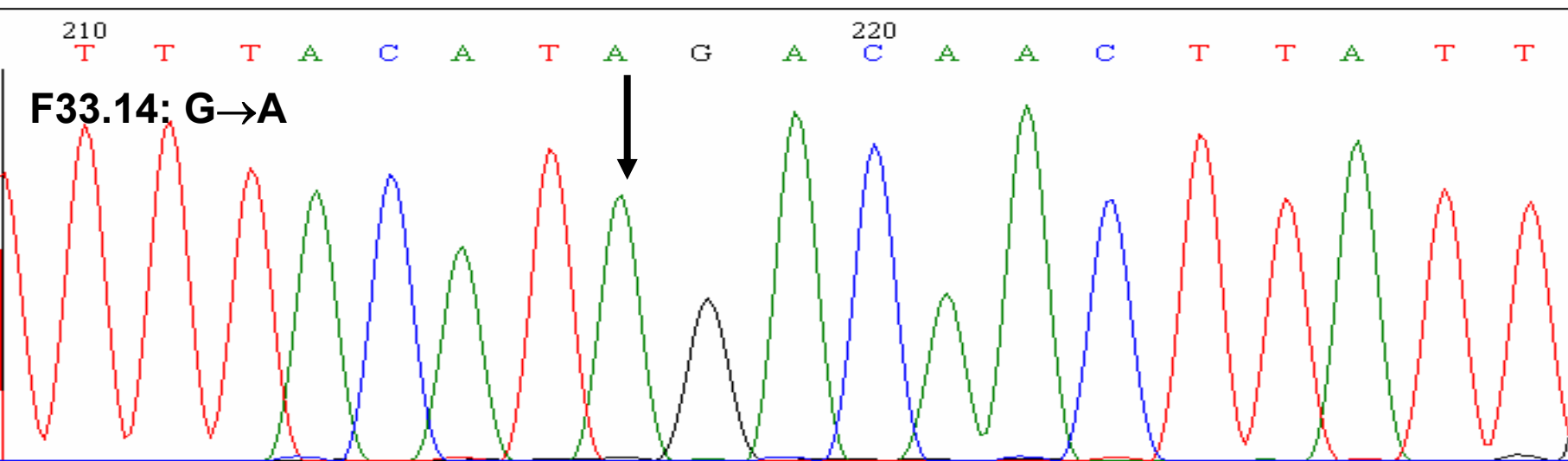
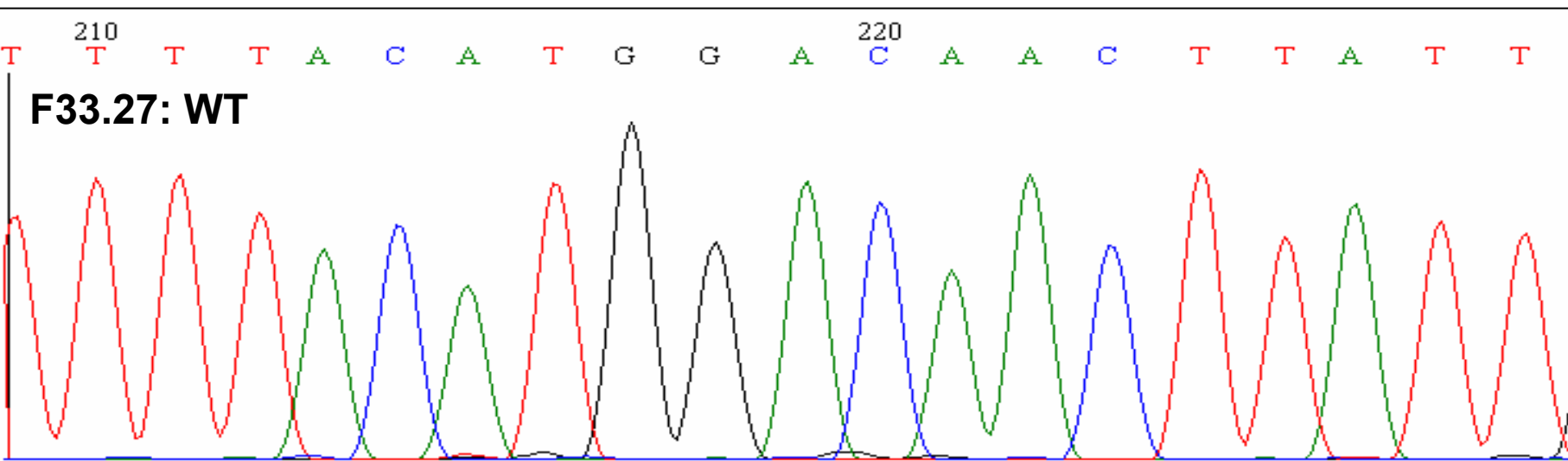


540 550 560 570  
A G G A A T T T T A T T C T T T T T T T T T A N T A N T T G G N N A A G G T T A N G

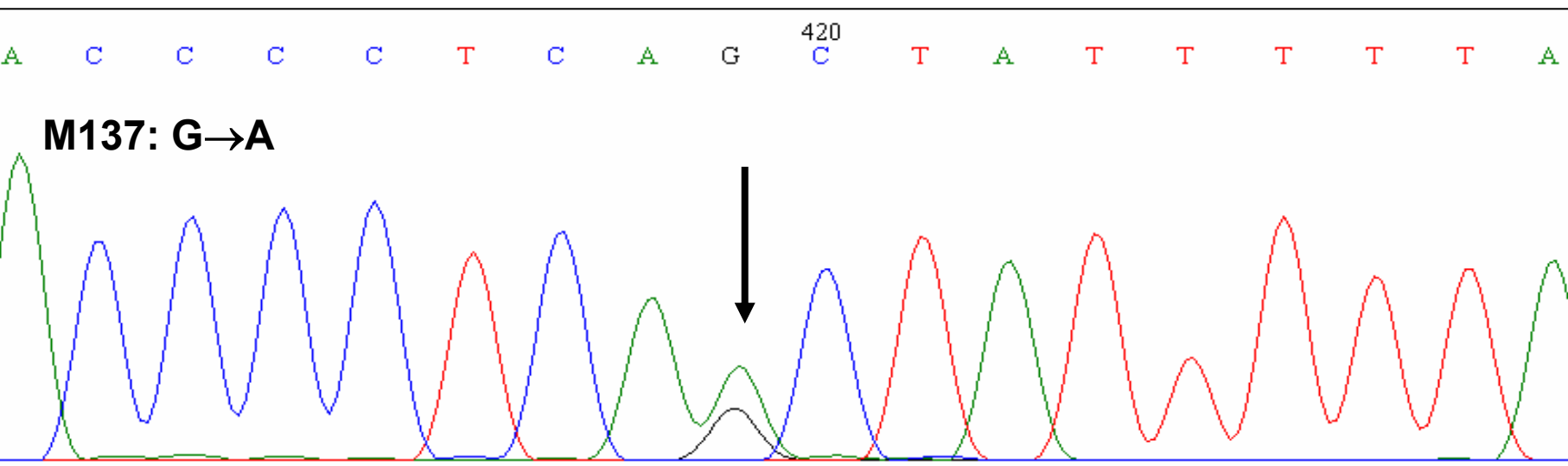
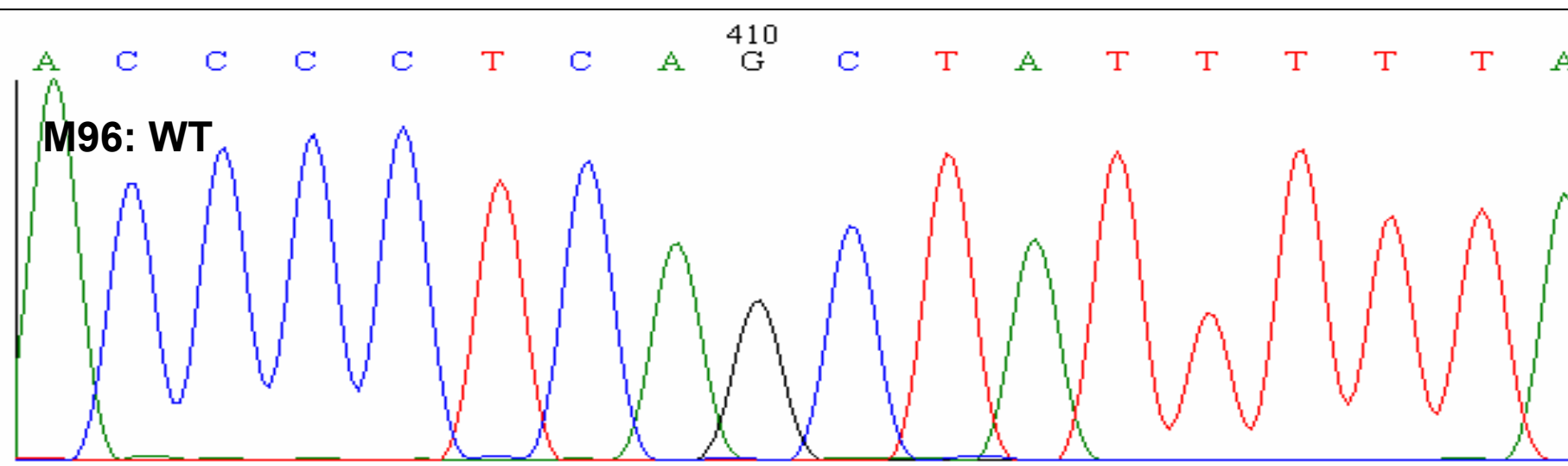
M144: T<sub>9</sub> → T<sub>8</sub>



Position: 3,254



Position: 4,098

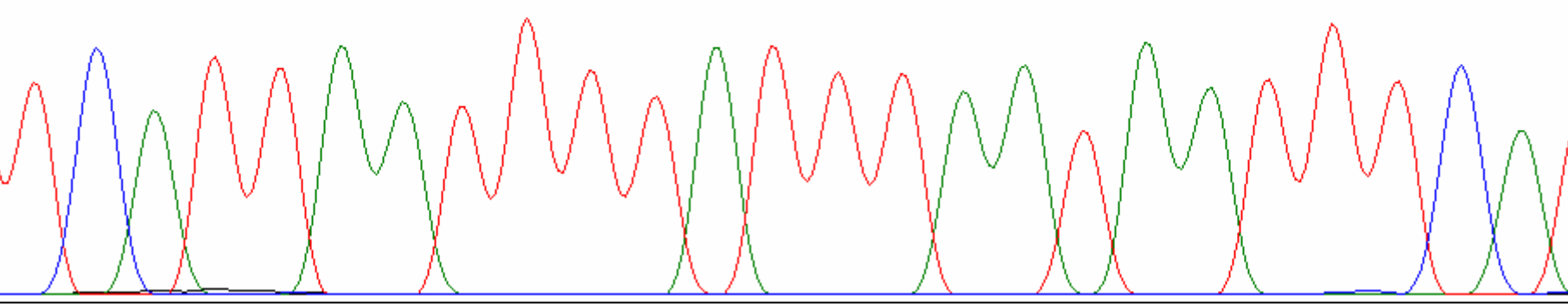




Position: 4,308

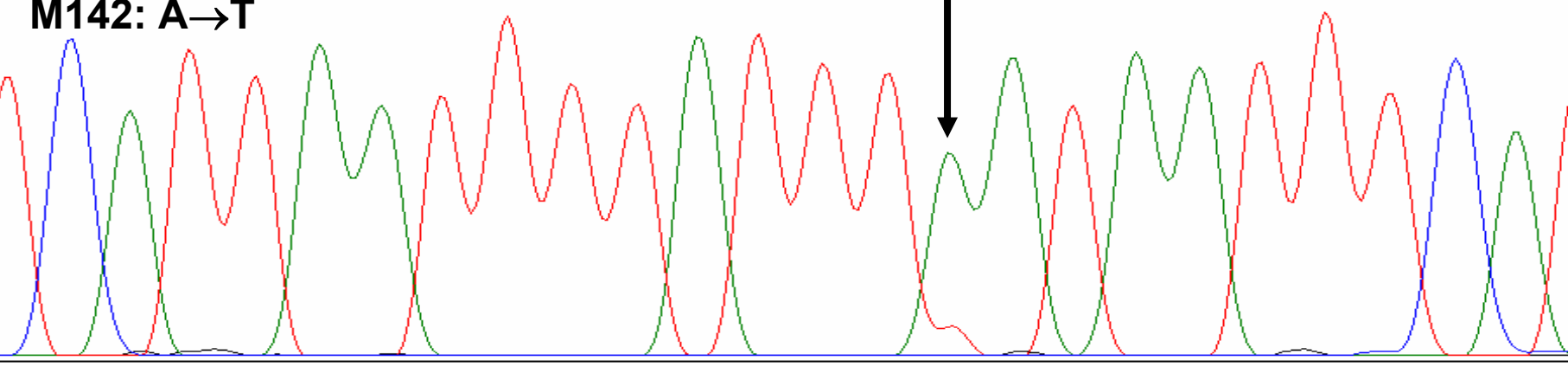
T C A T T A A T T T T A T T T A A T A A T T T C A

M159: WT



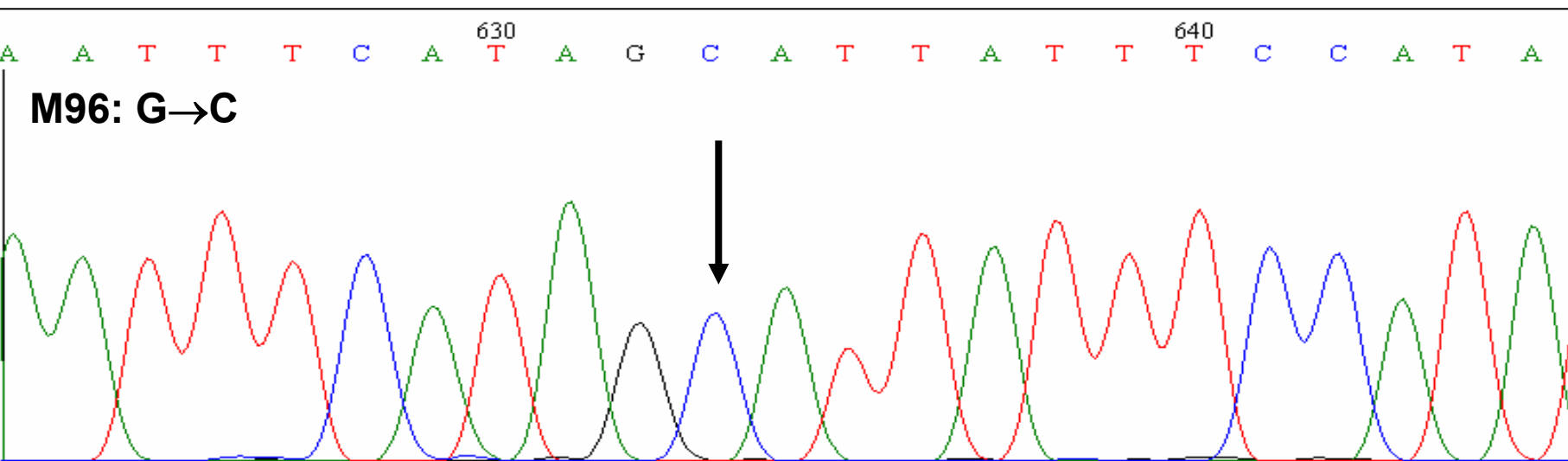
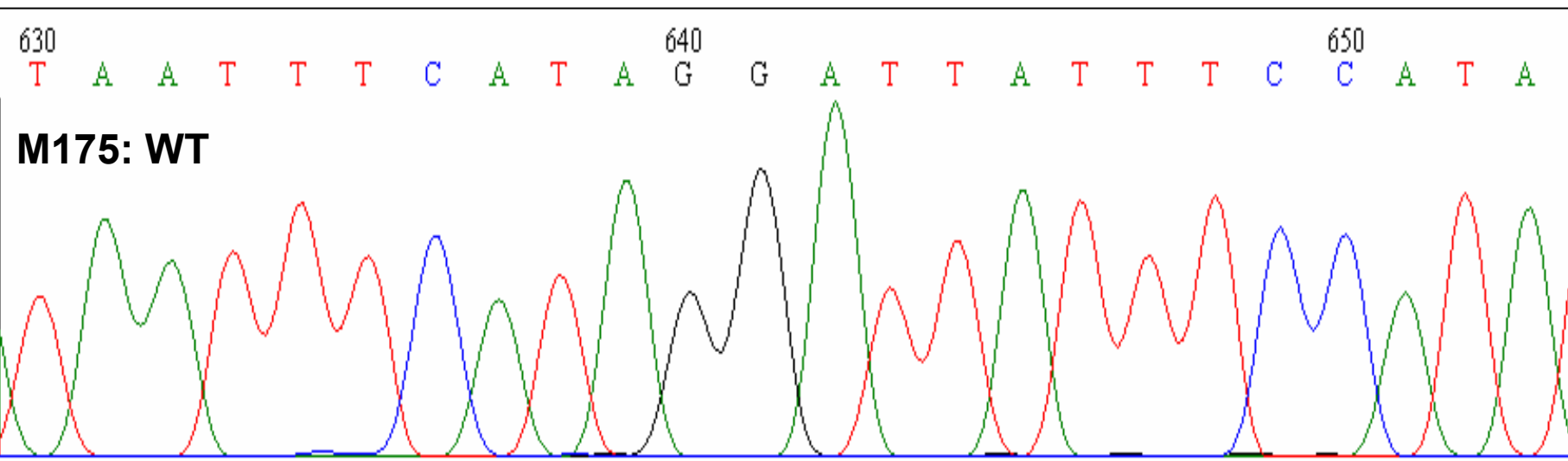
T C A T T A A T T T T A T T T A A T A A T T T C A

M142: A→T

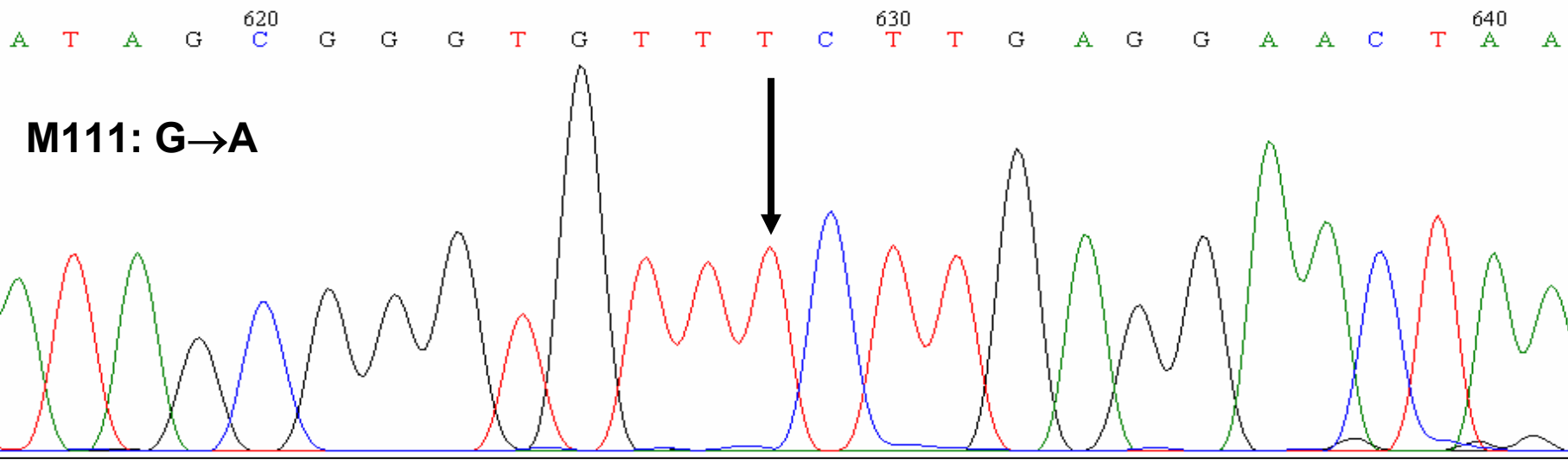
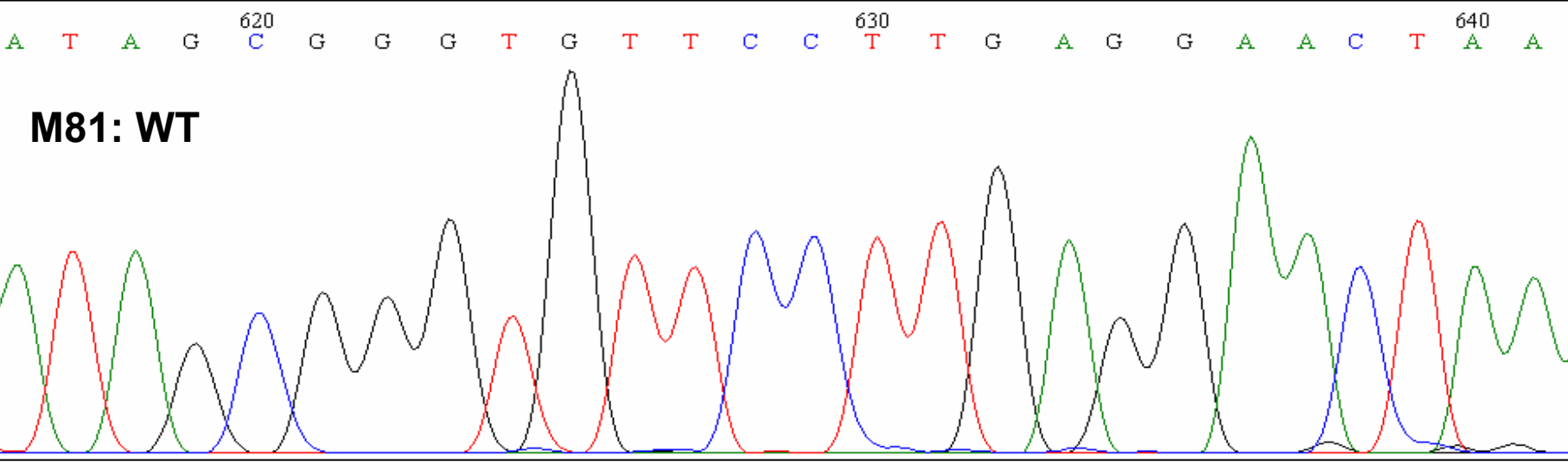


Found in two independent PCRs/sequences

Position: 4,321

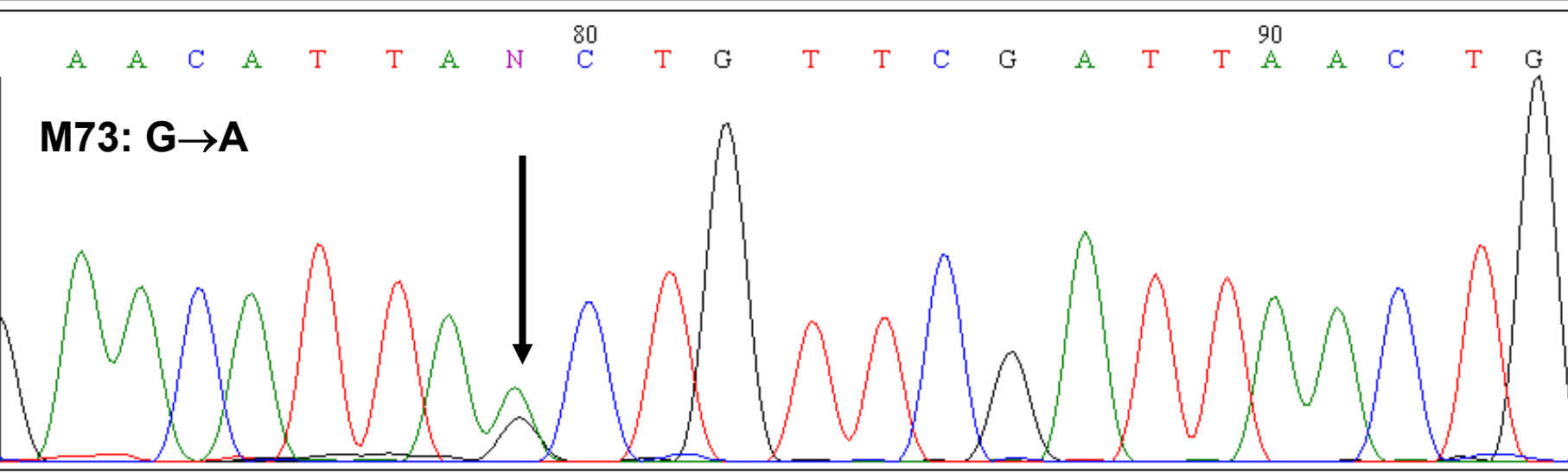
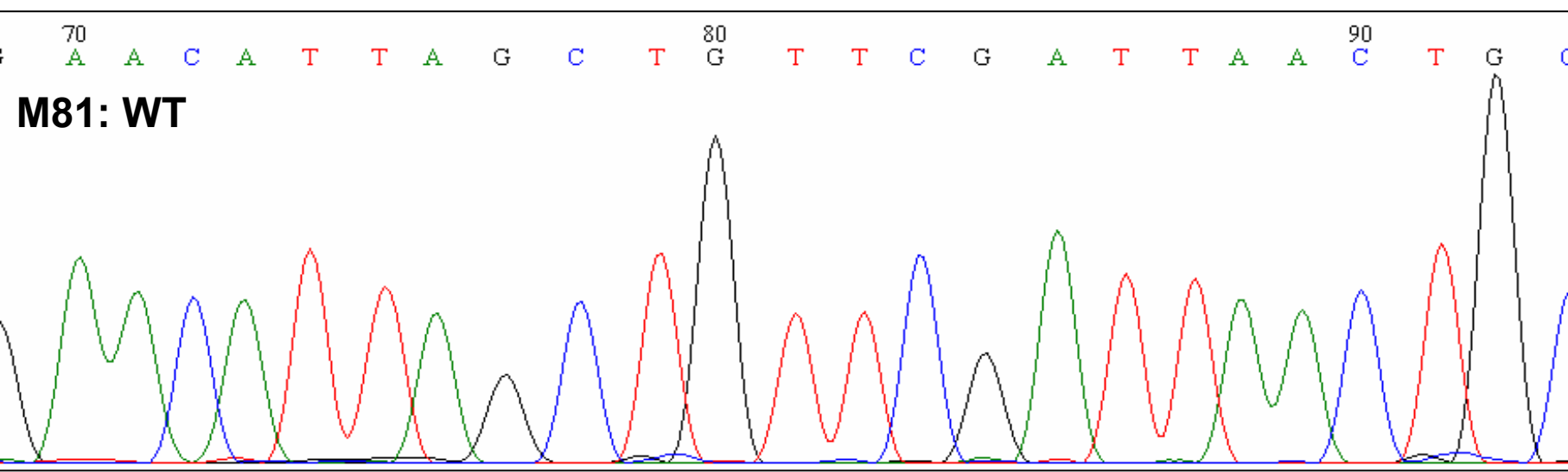


Position: 4,459

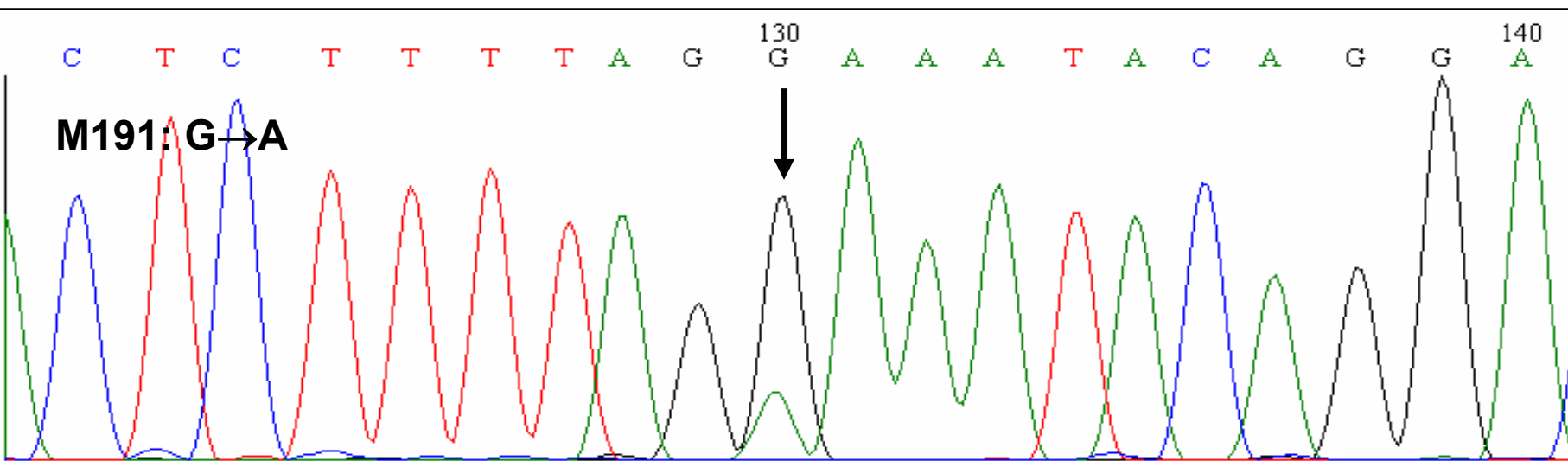
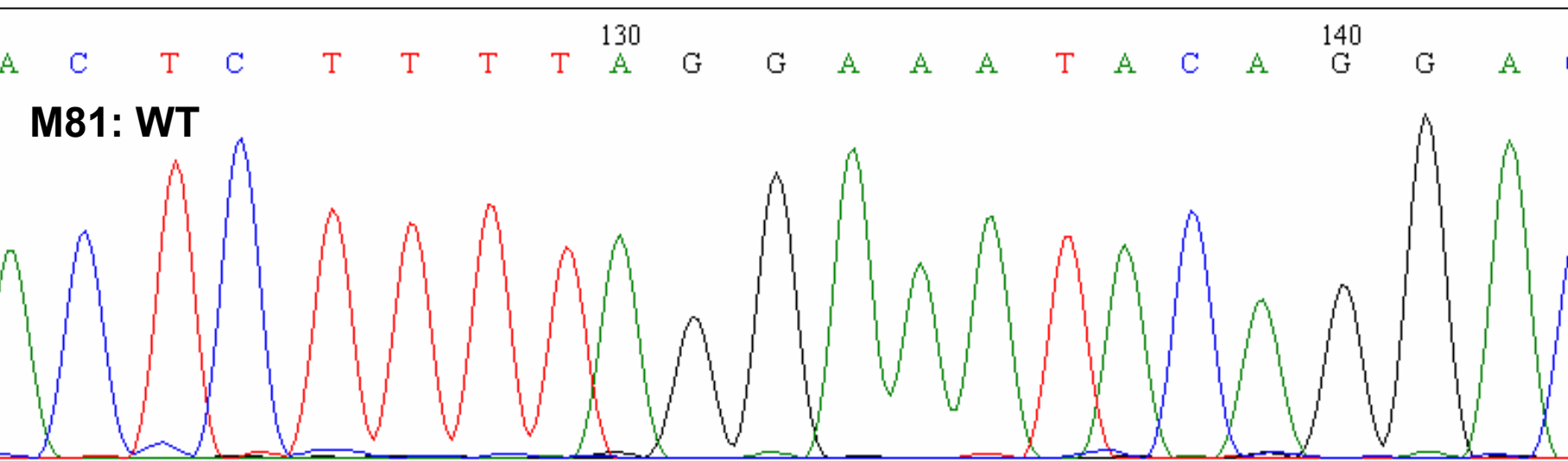


Mutation visible only on reverse sequence

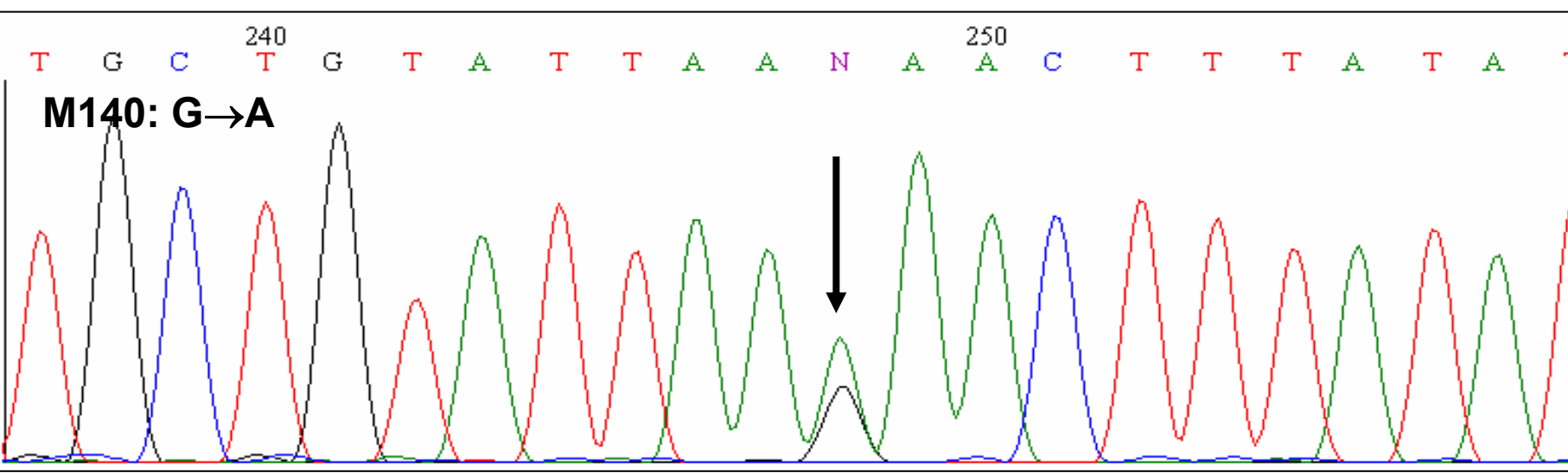
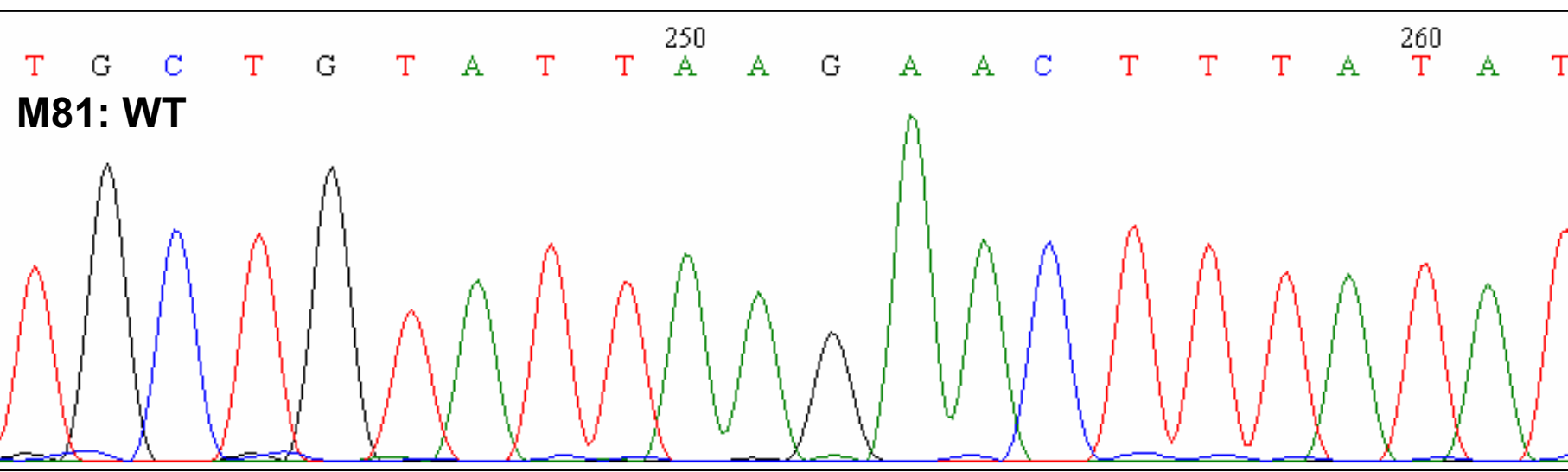
Position: 4,533



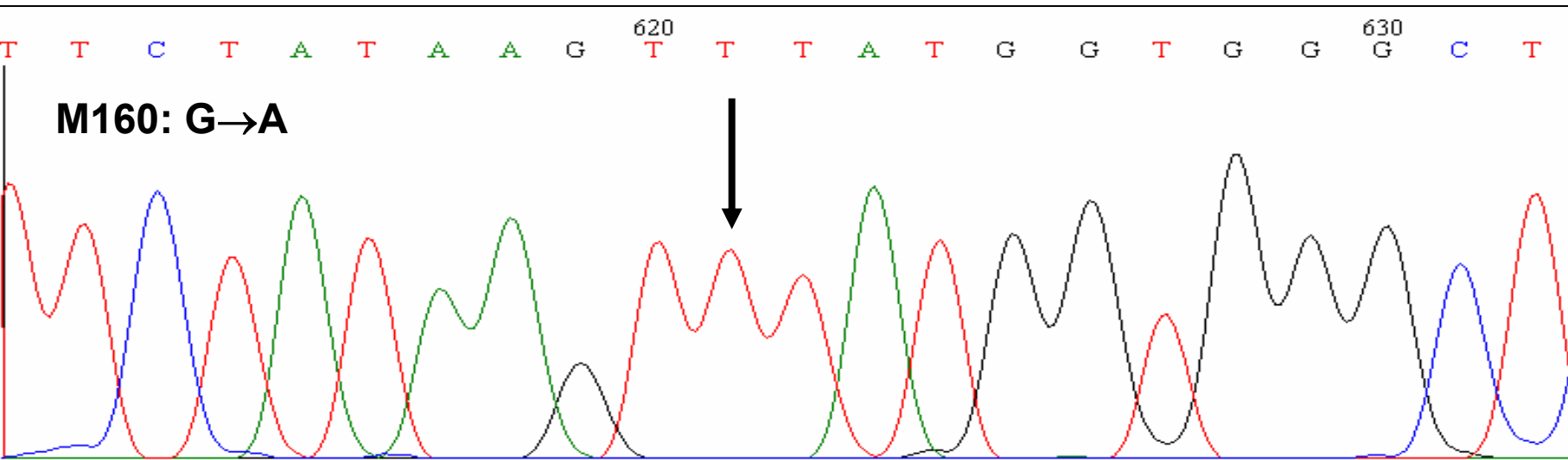
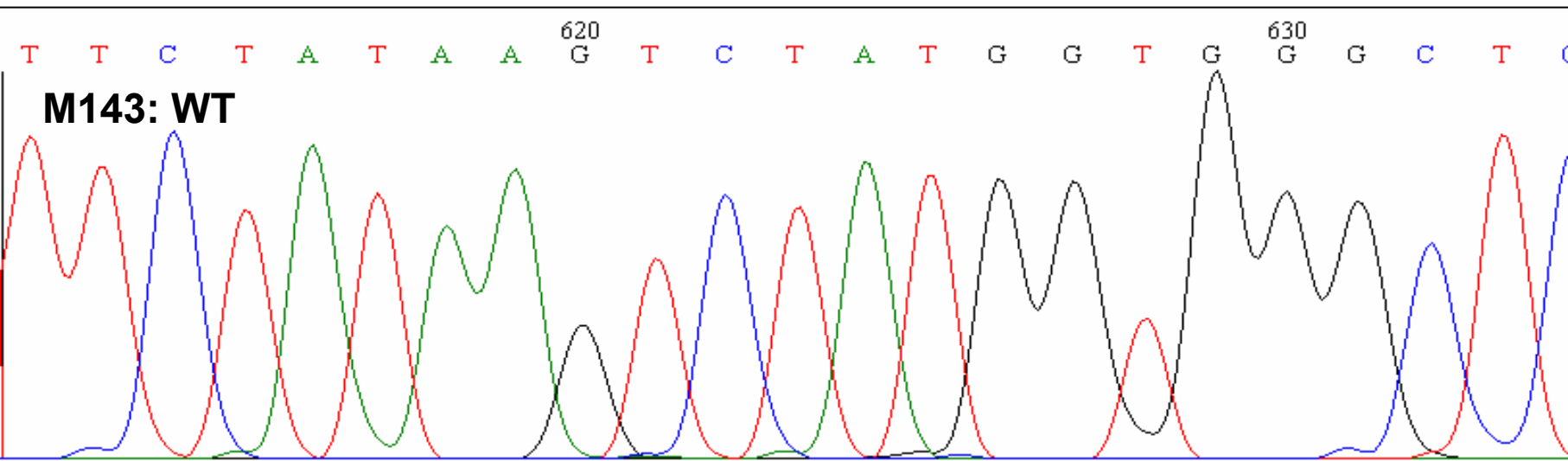
Position: 4,588



Position: 4,708

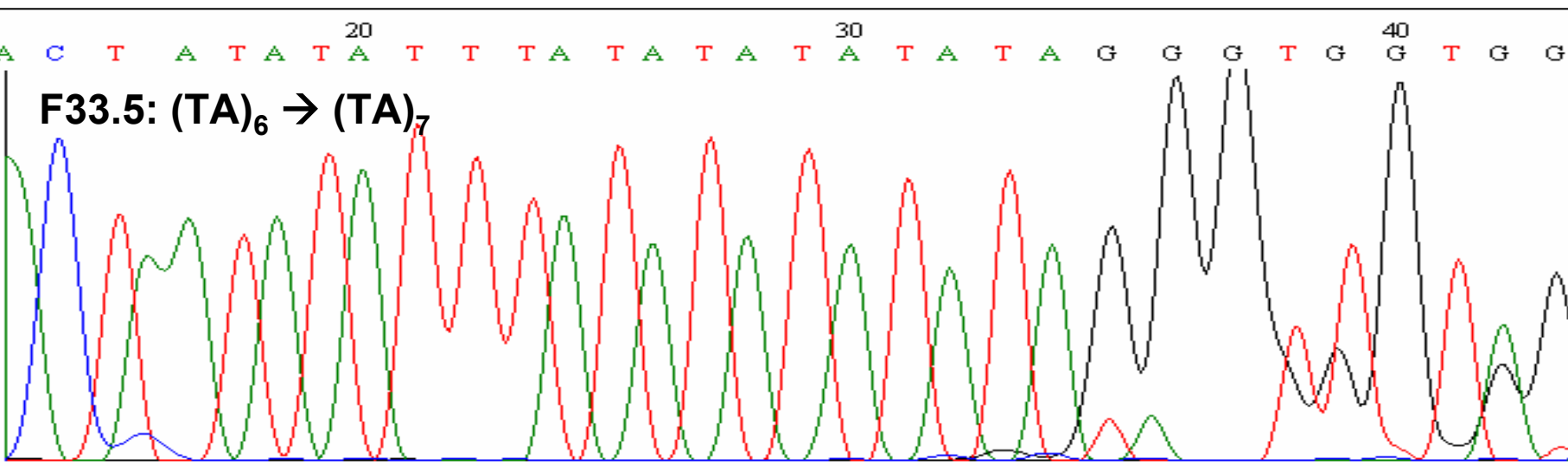
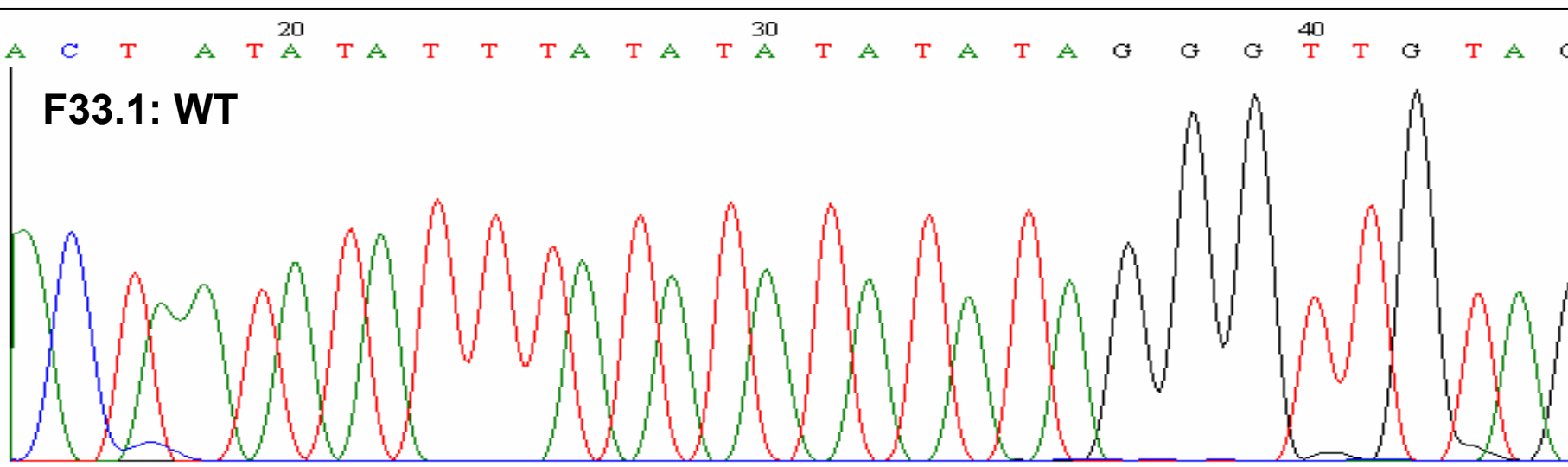


Position: 5,187



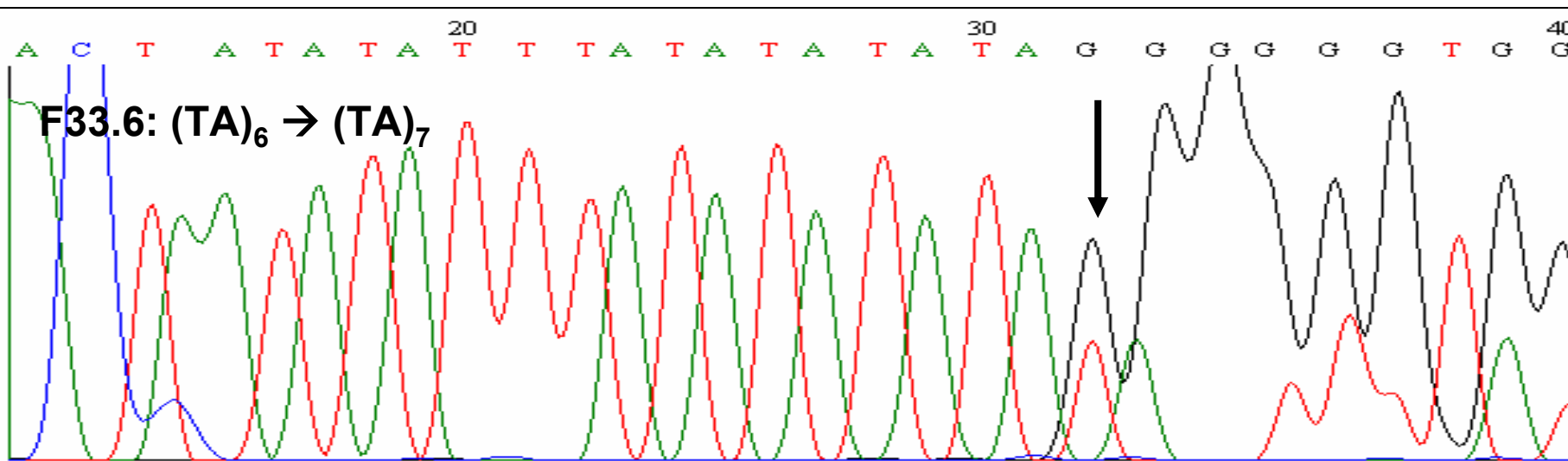
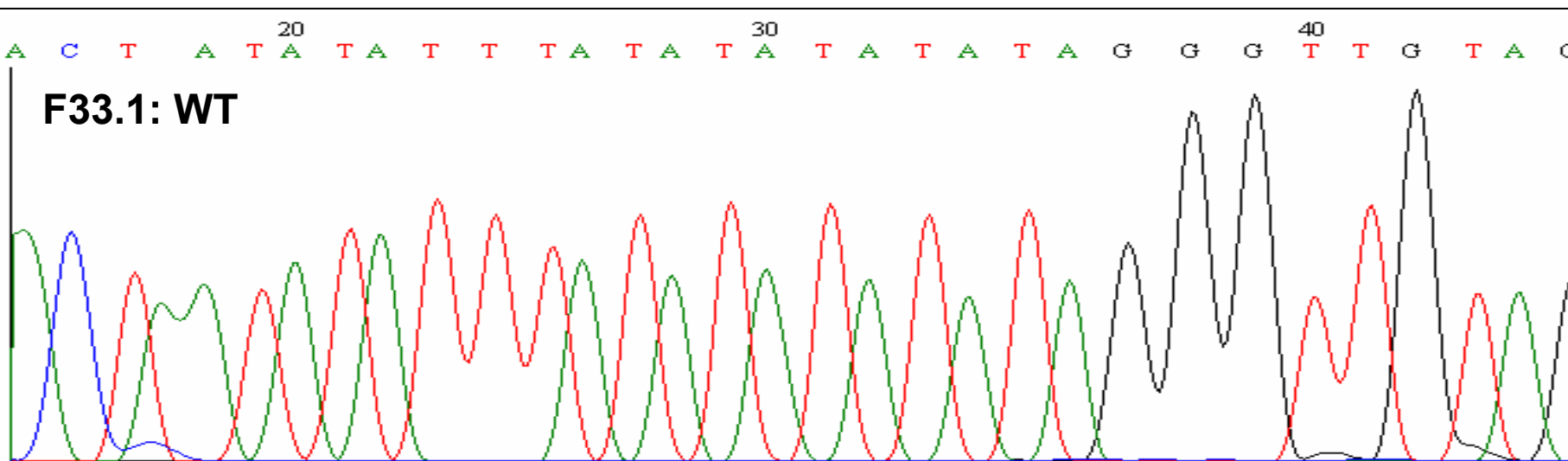
Mutation visible only on reverse sequence

Position: 5,970

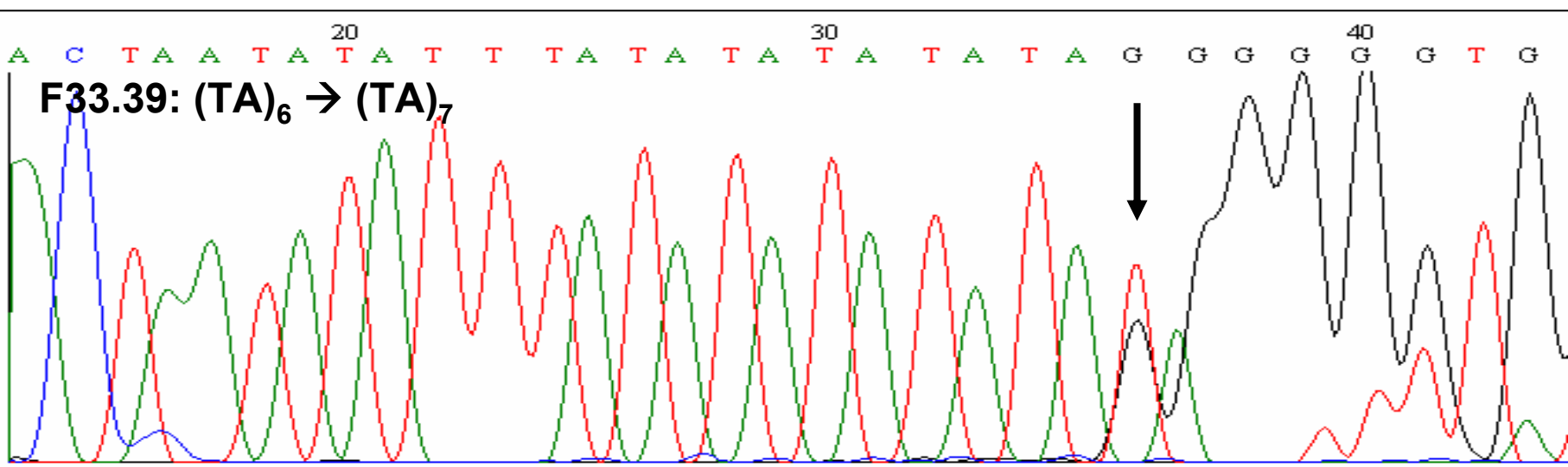
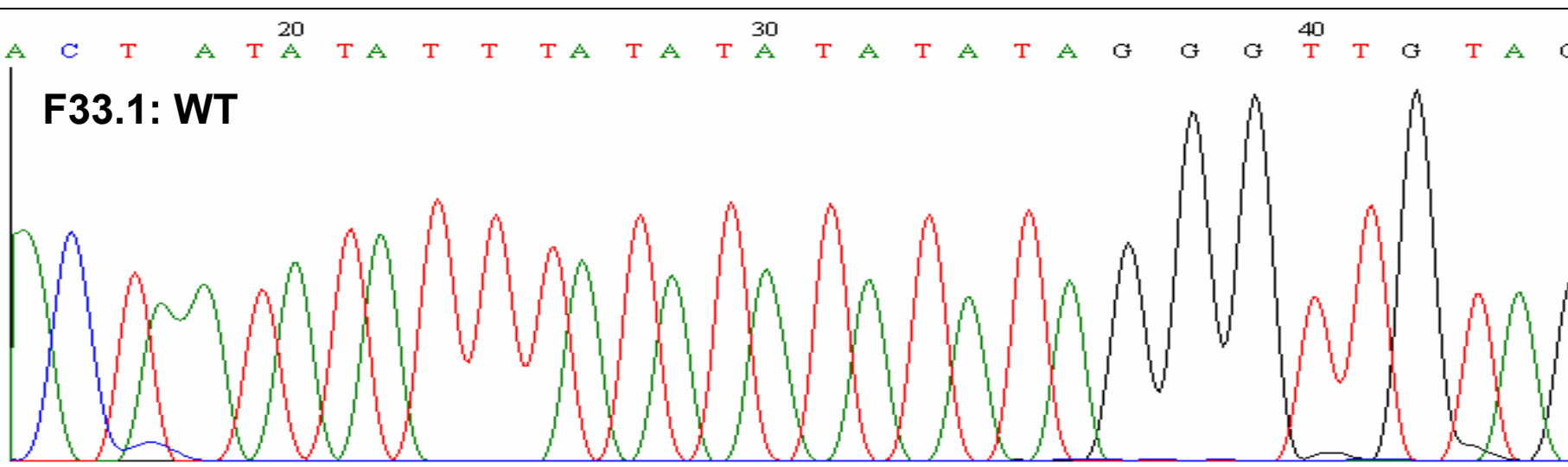




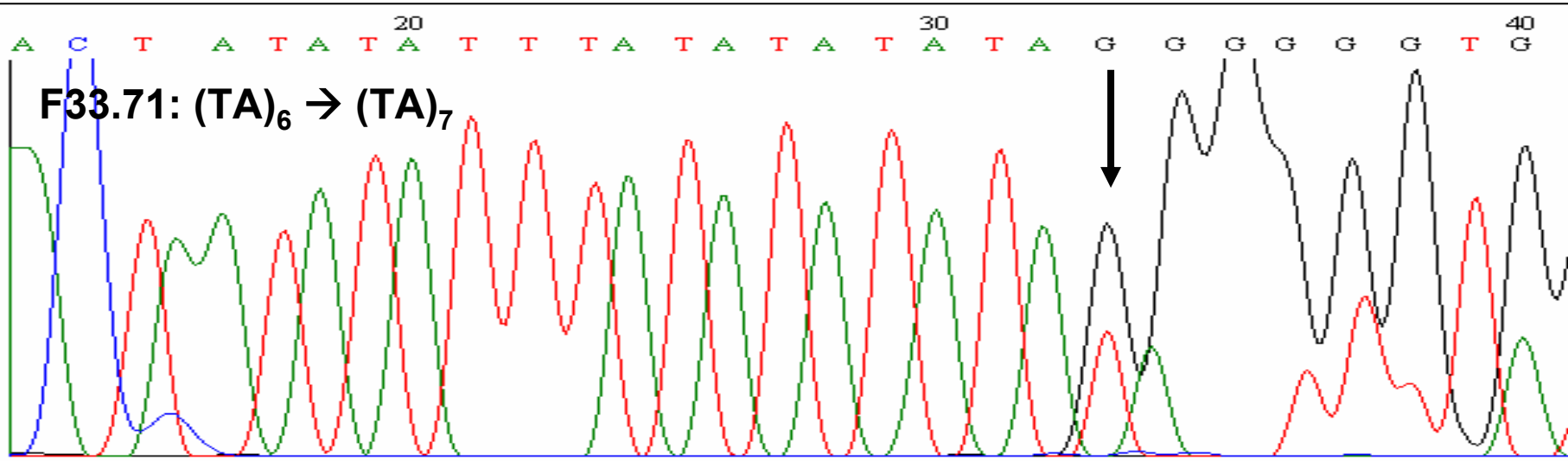
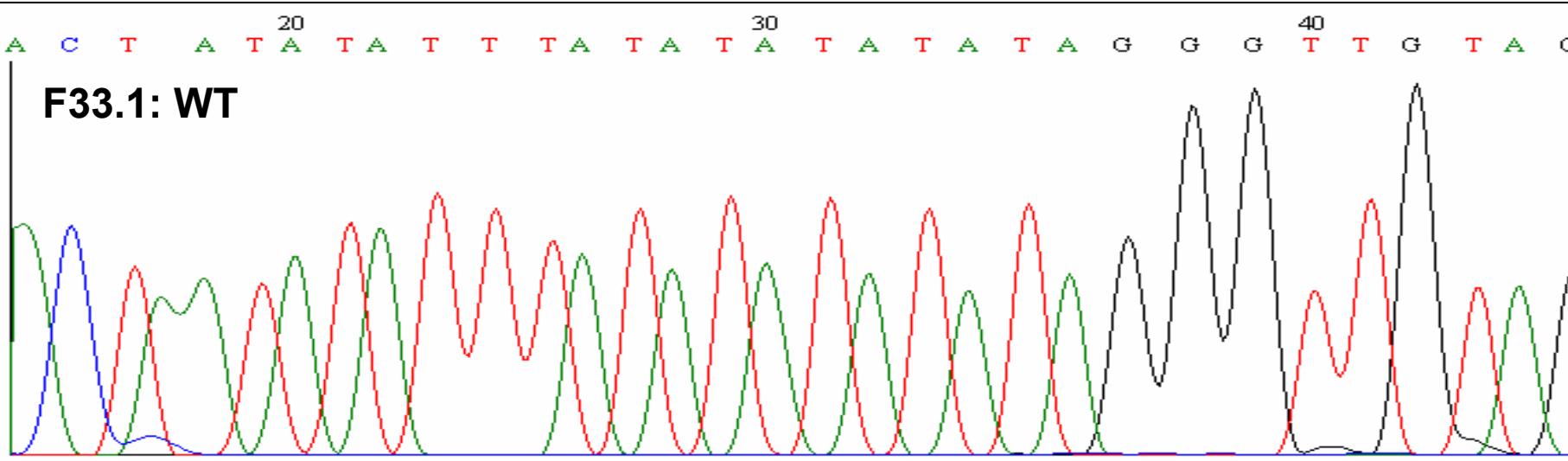
Position: 5,970



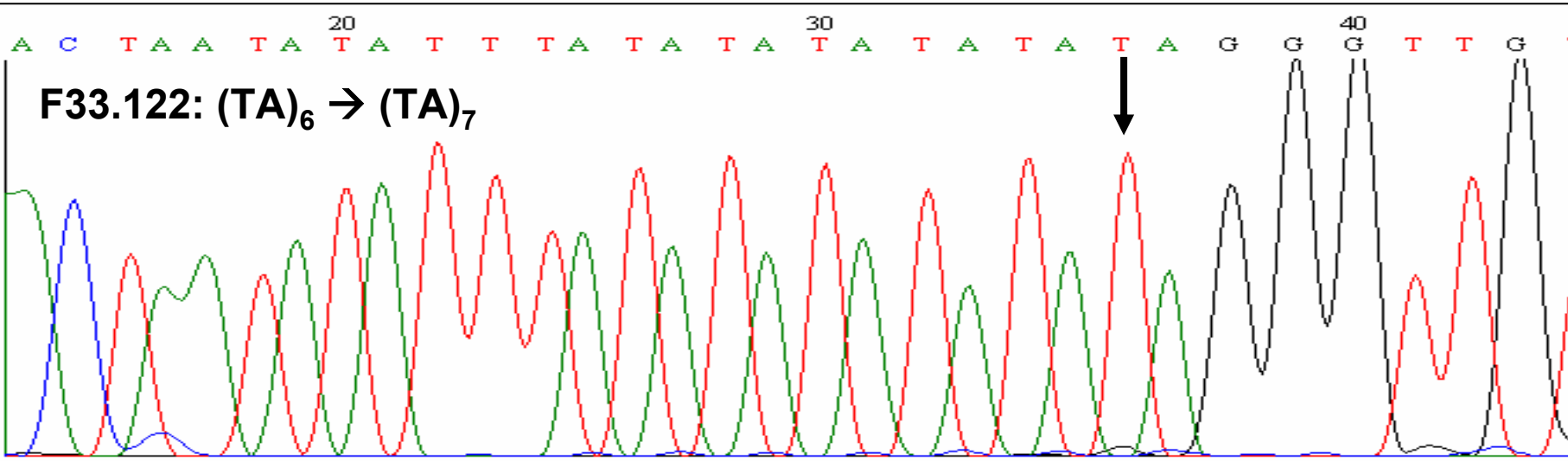
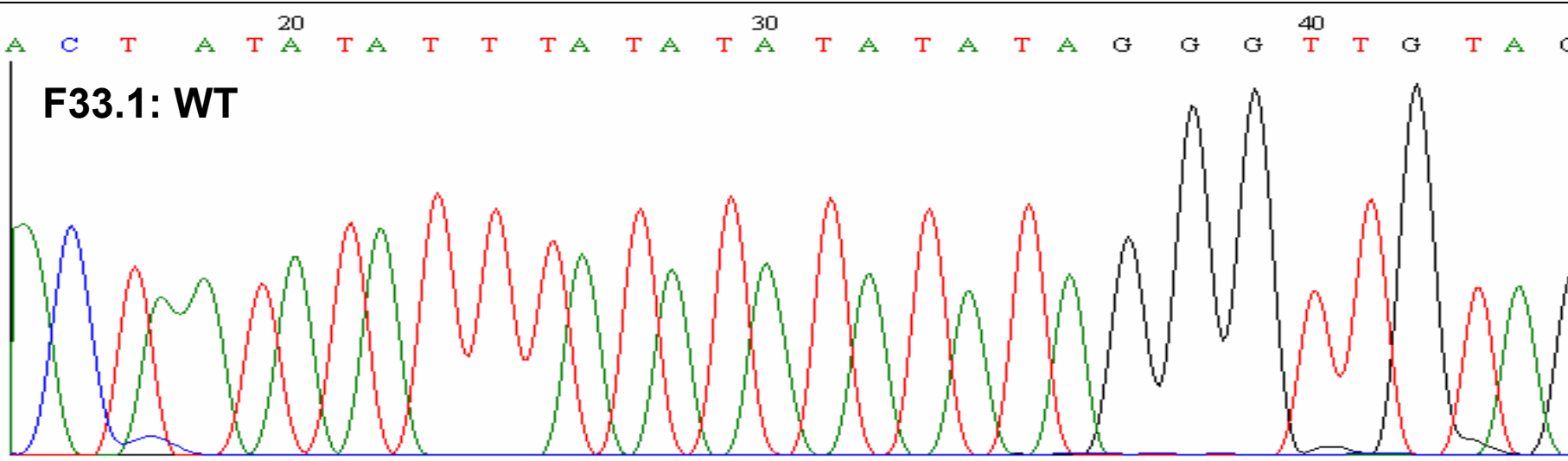
Position: 5,970



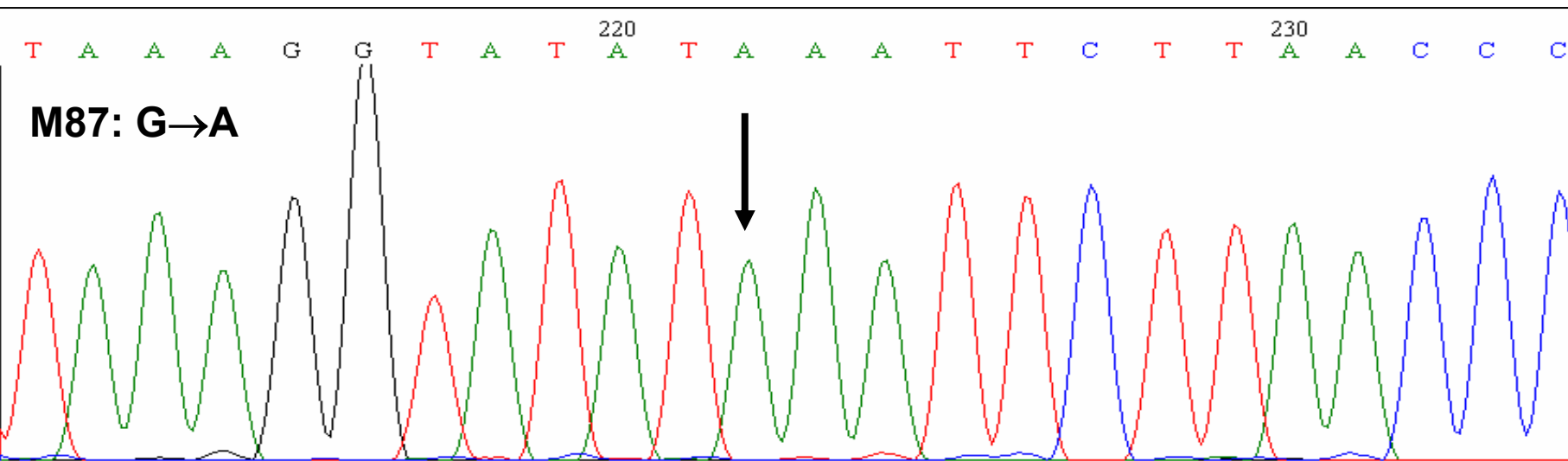
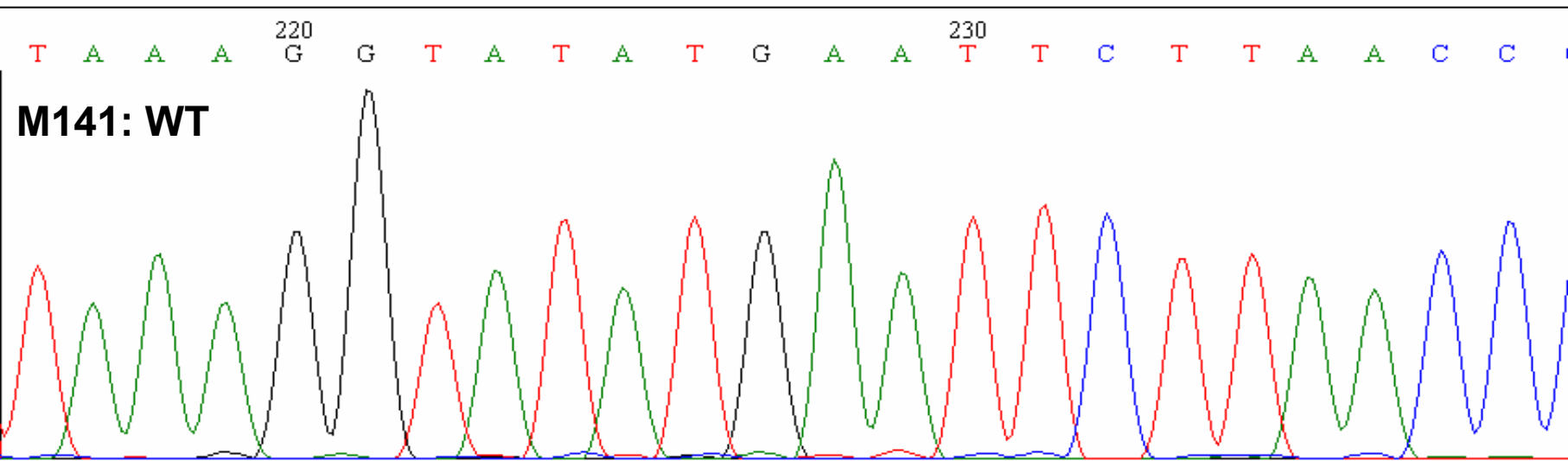
Position: 5,970



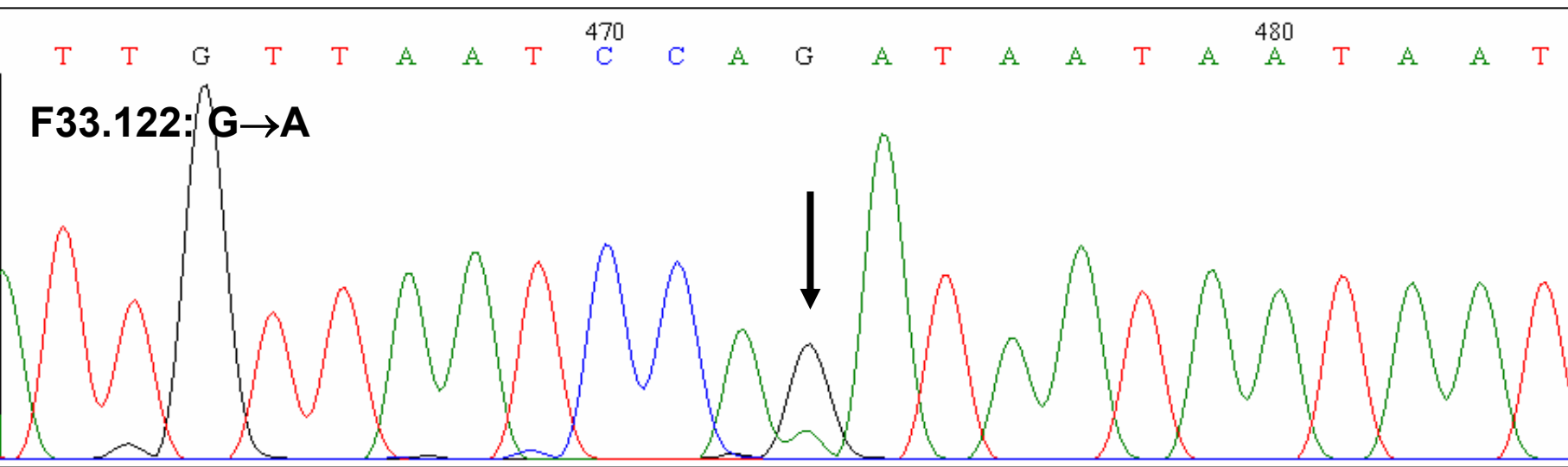
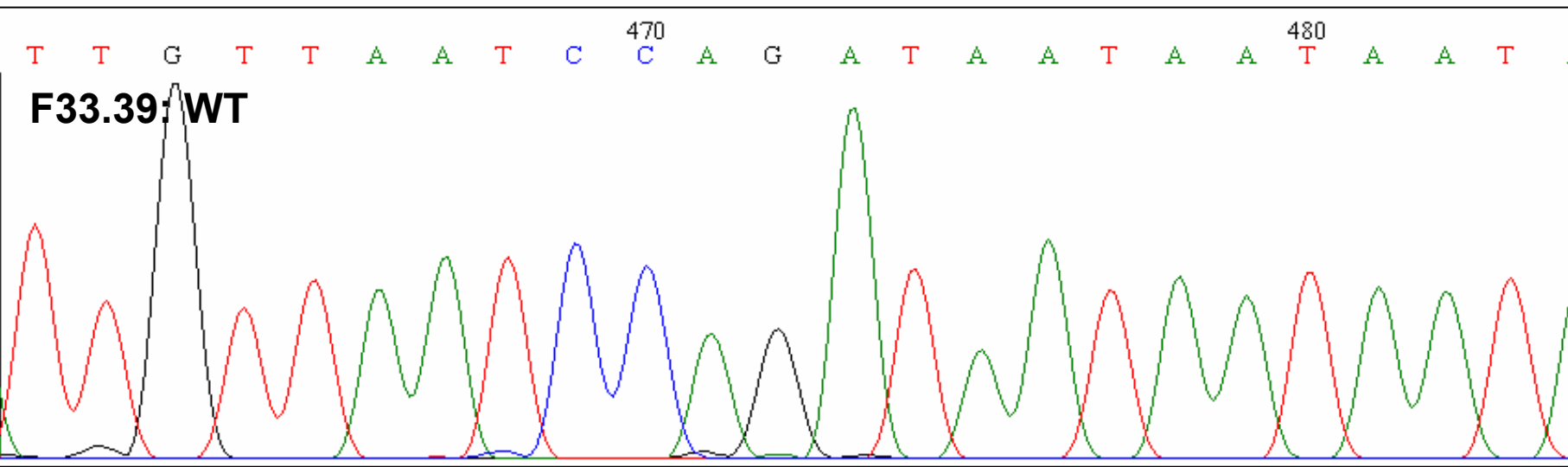
Position: 5,970



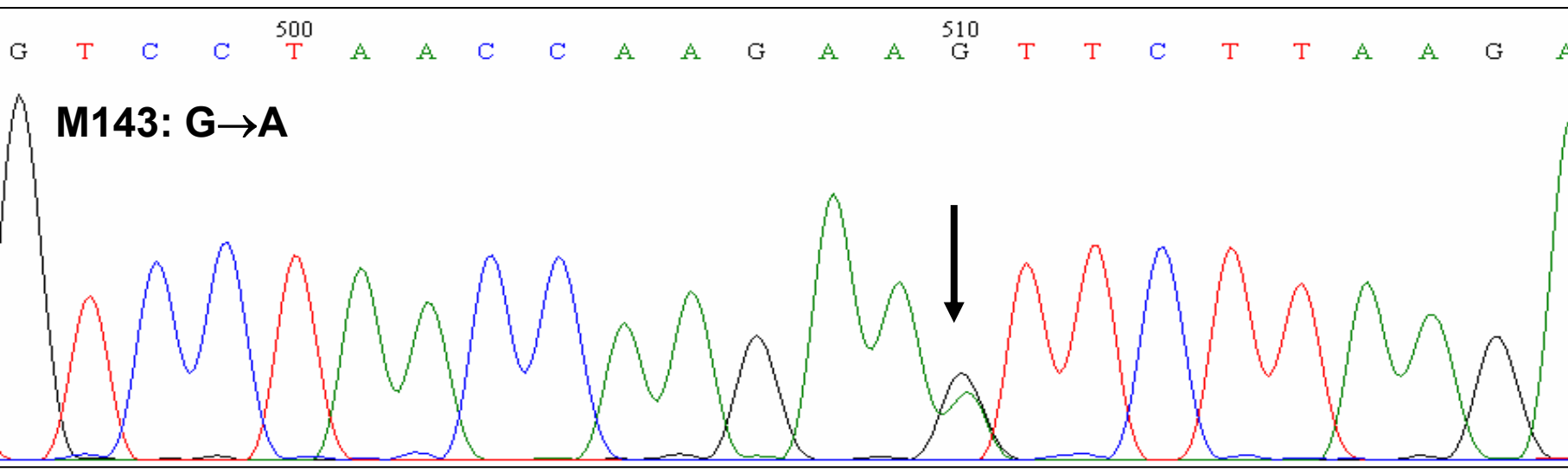
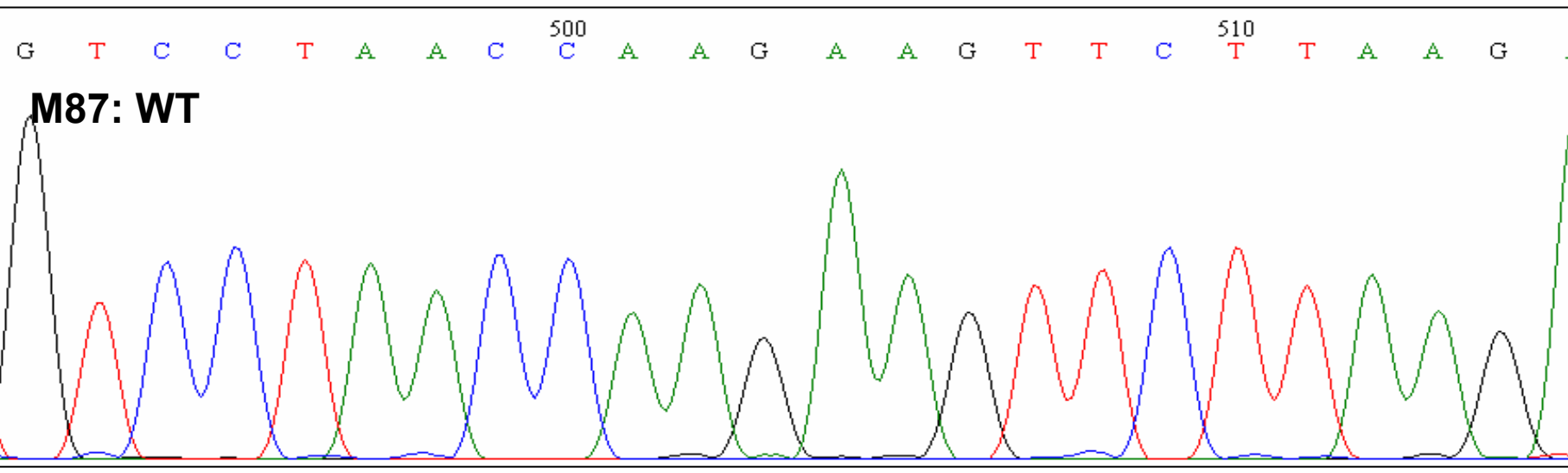
Position: 7,125



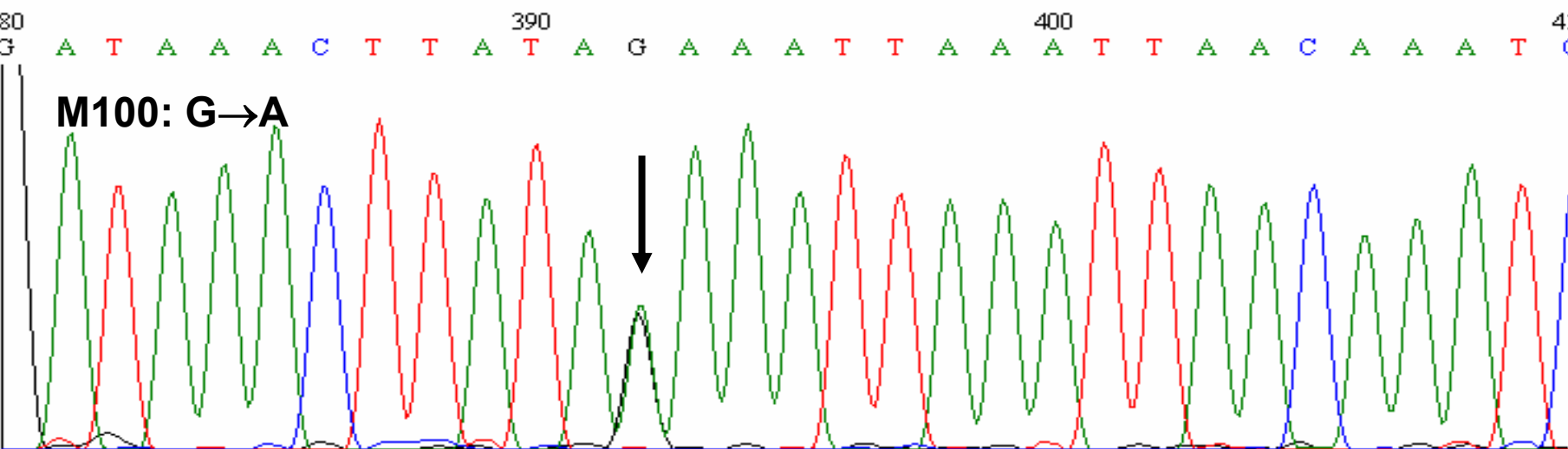
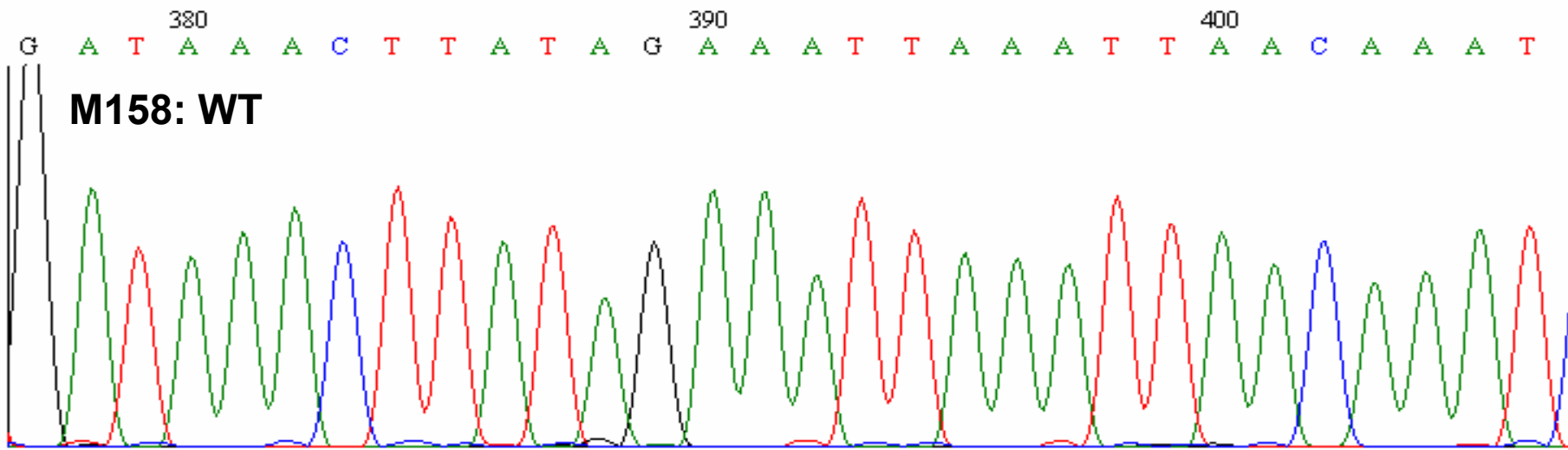
Position: 7,382



Position: 7,415

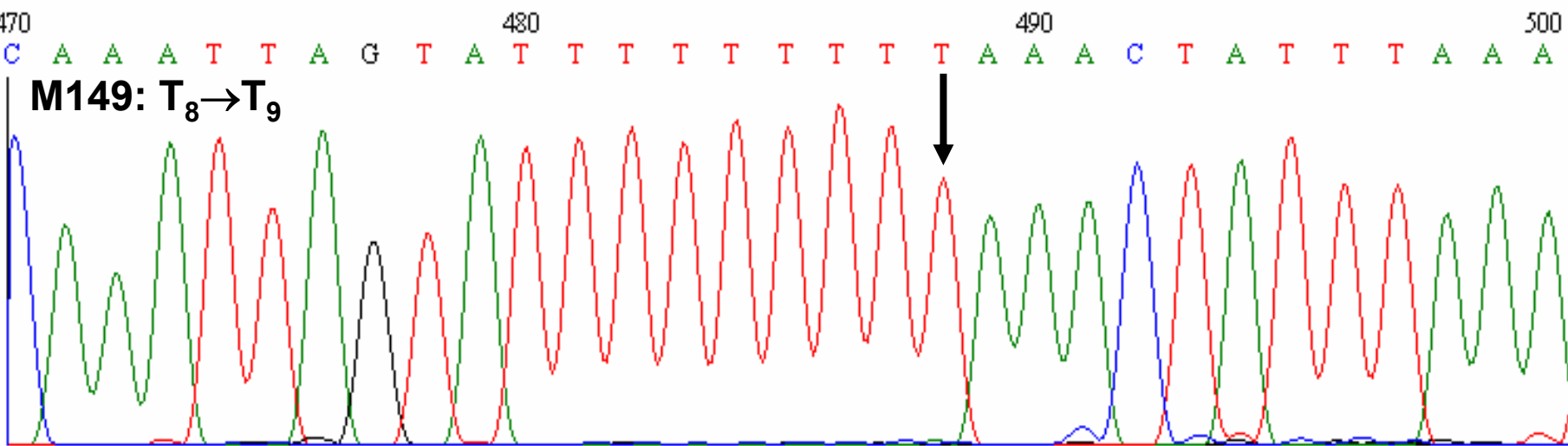
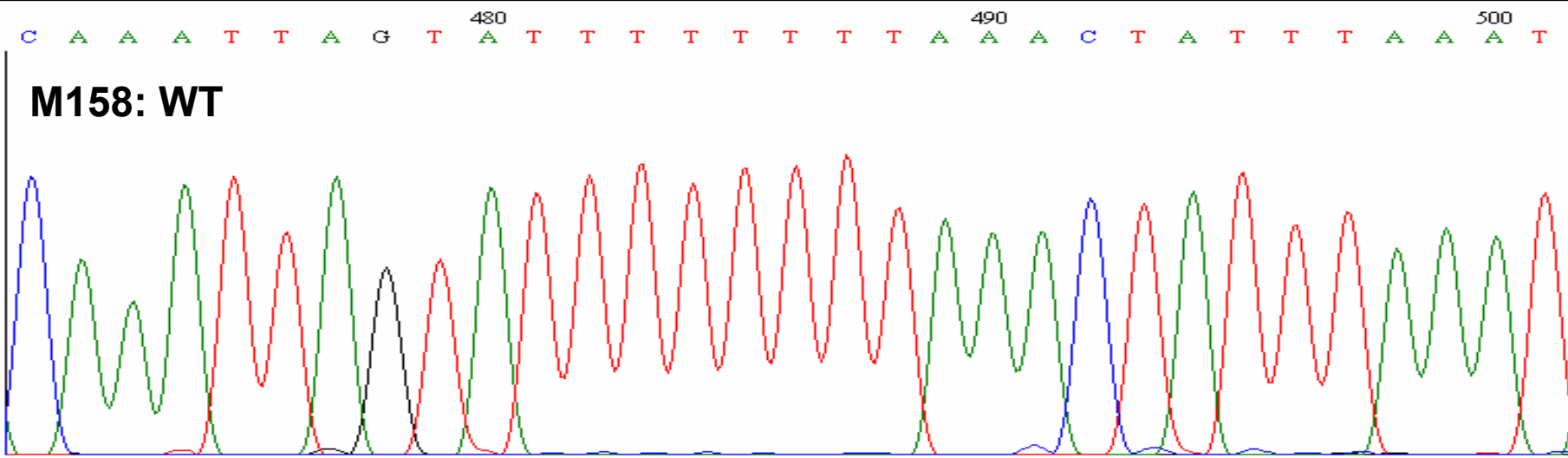


Position: 8,093

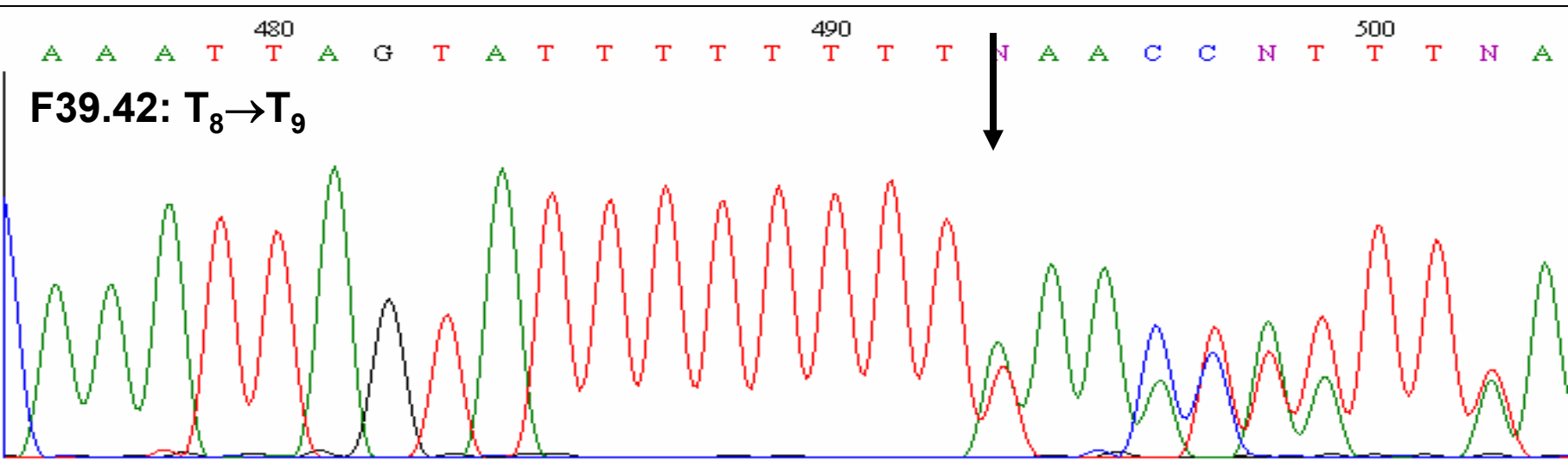
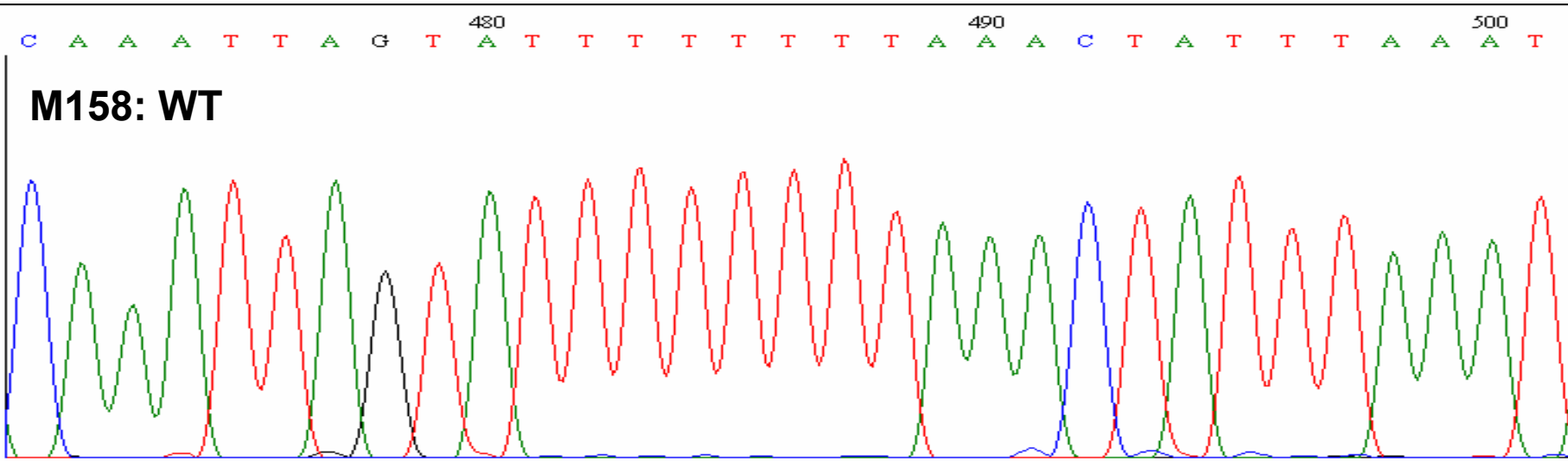




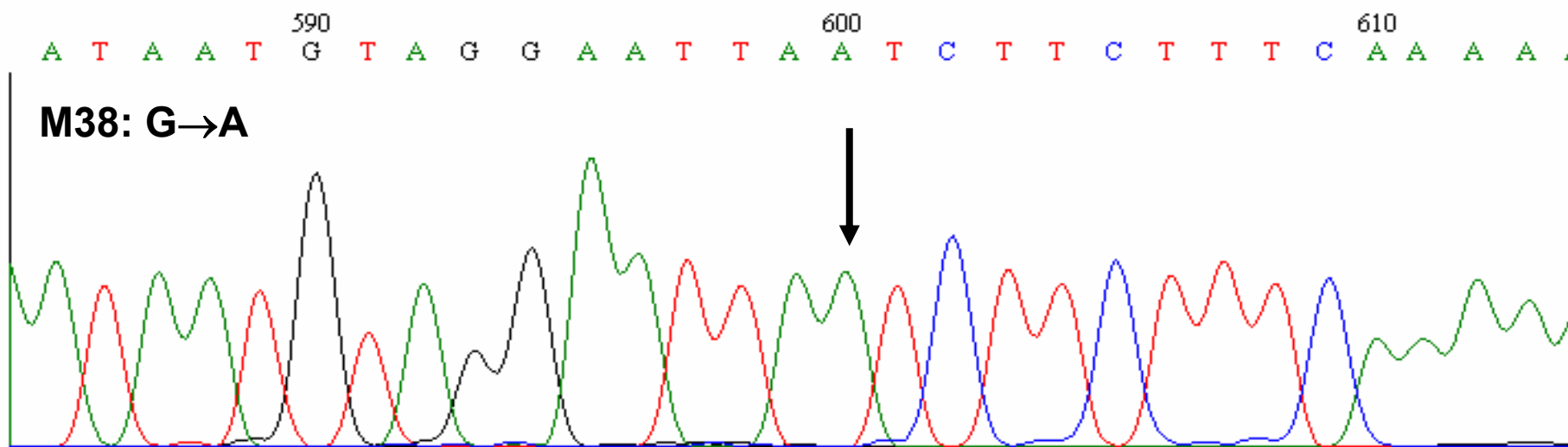
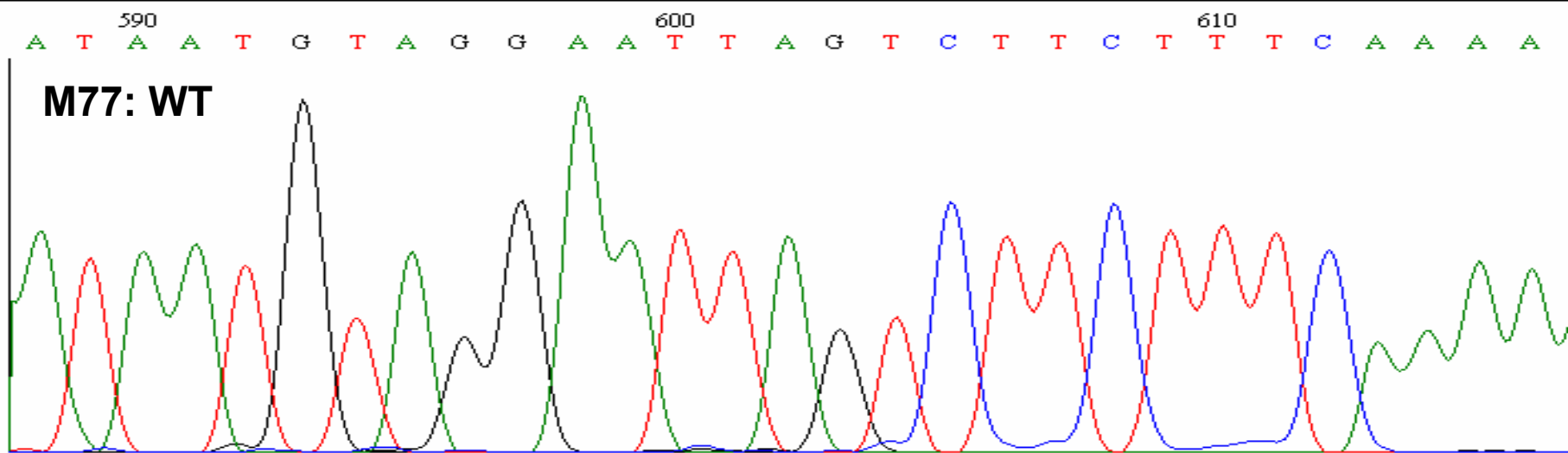
Position: 8,192



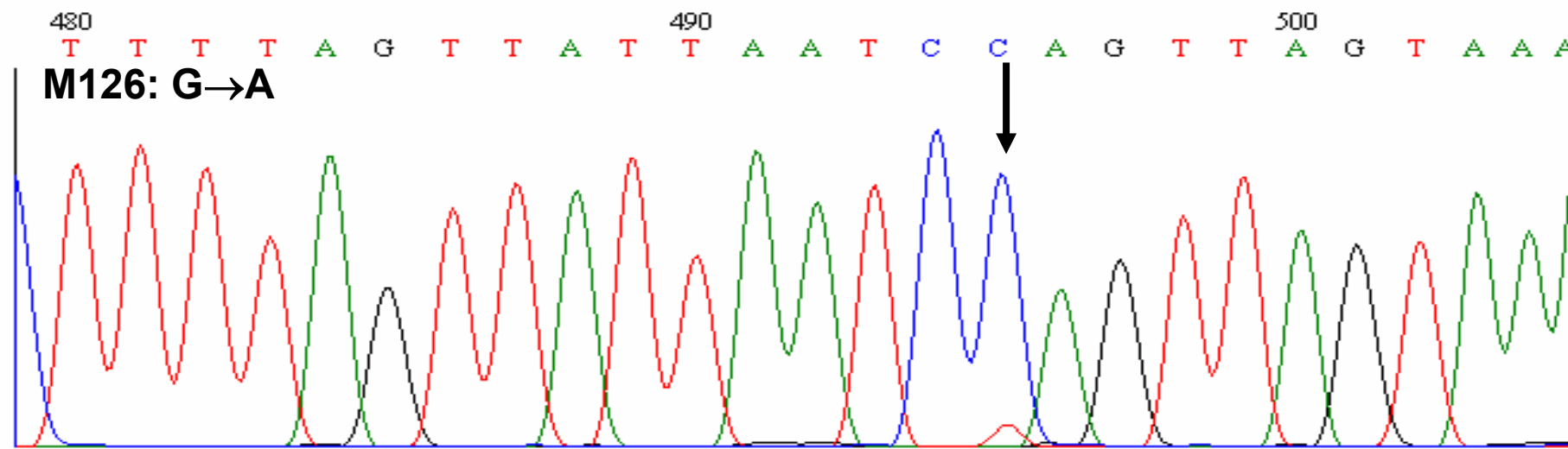
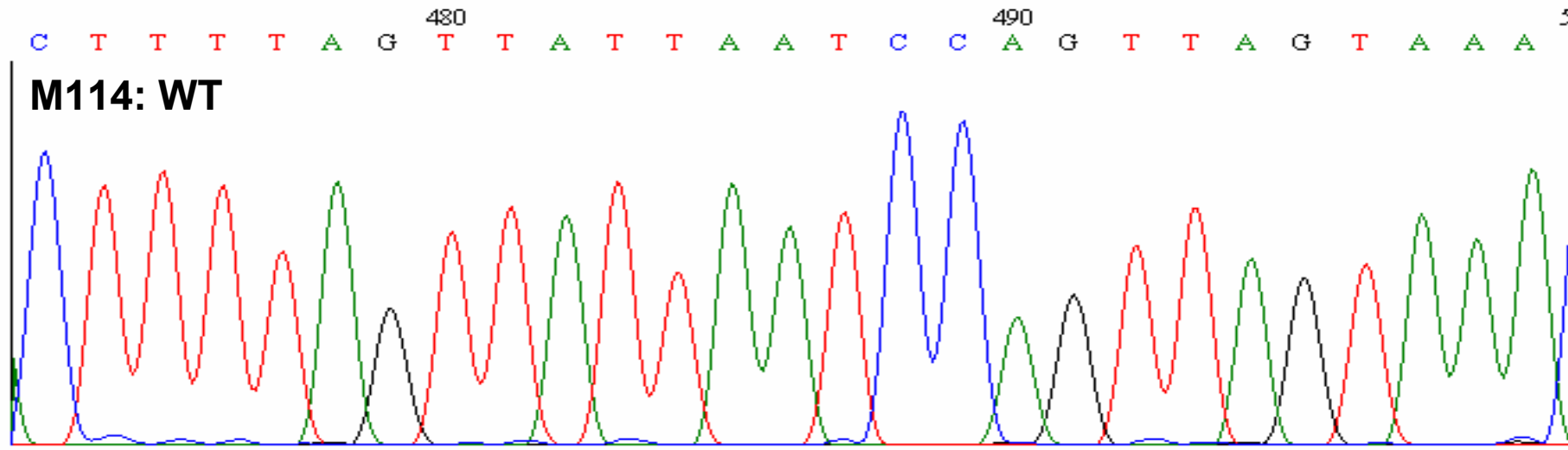
Position: 8,192



Position: 9,185

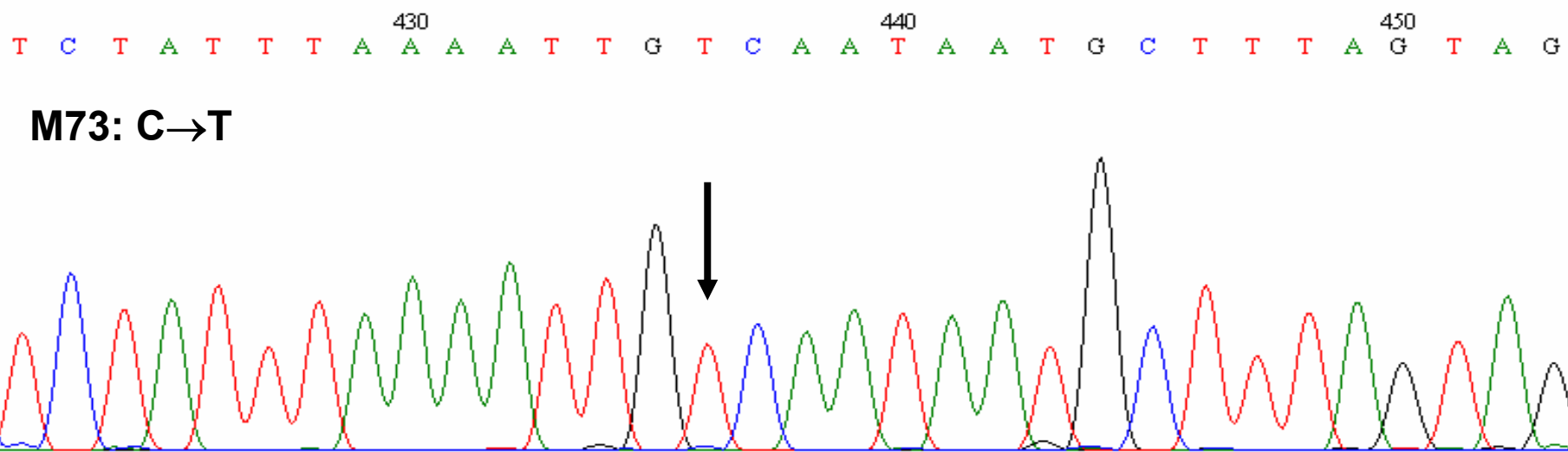
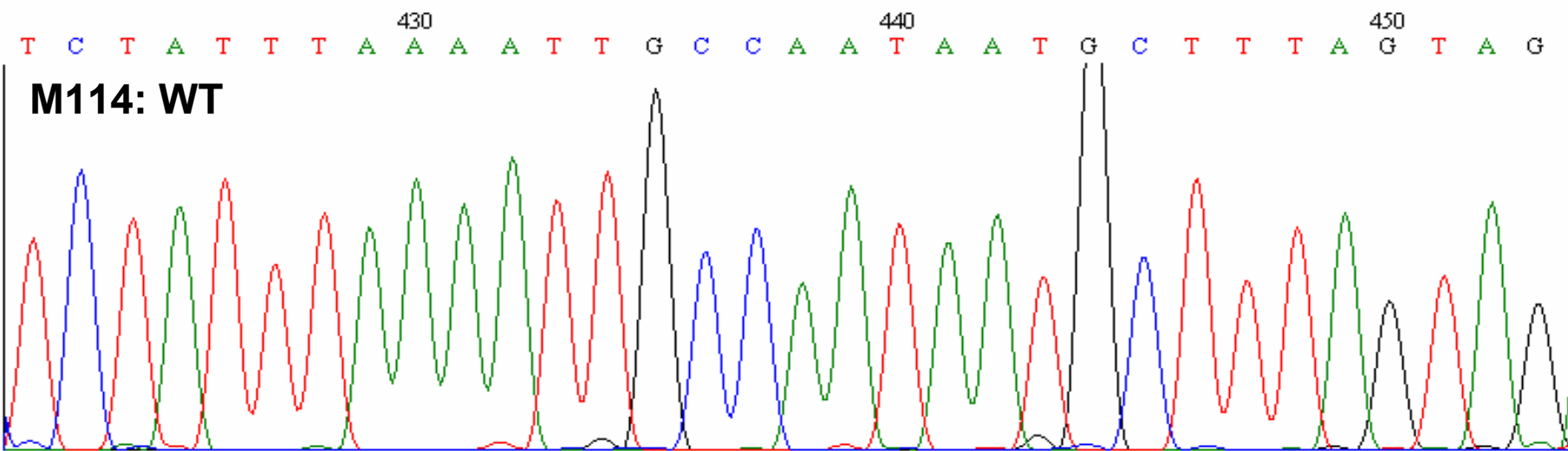


Position: 10,094

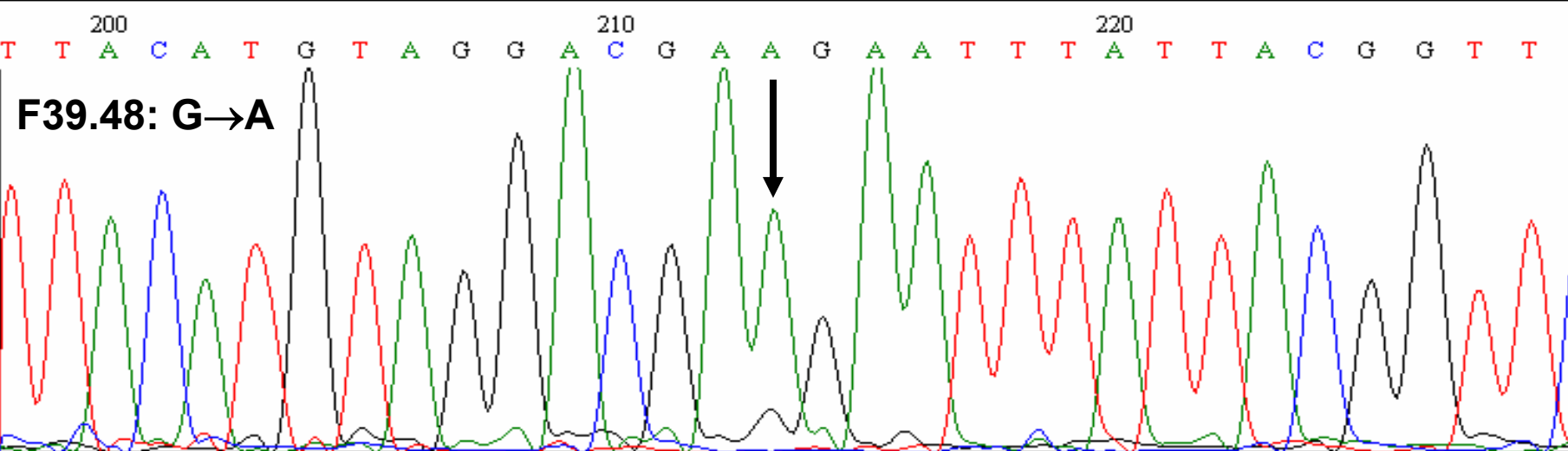
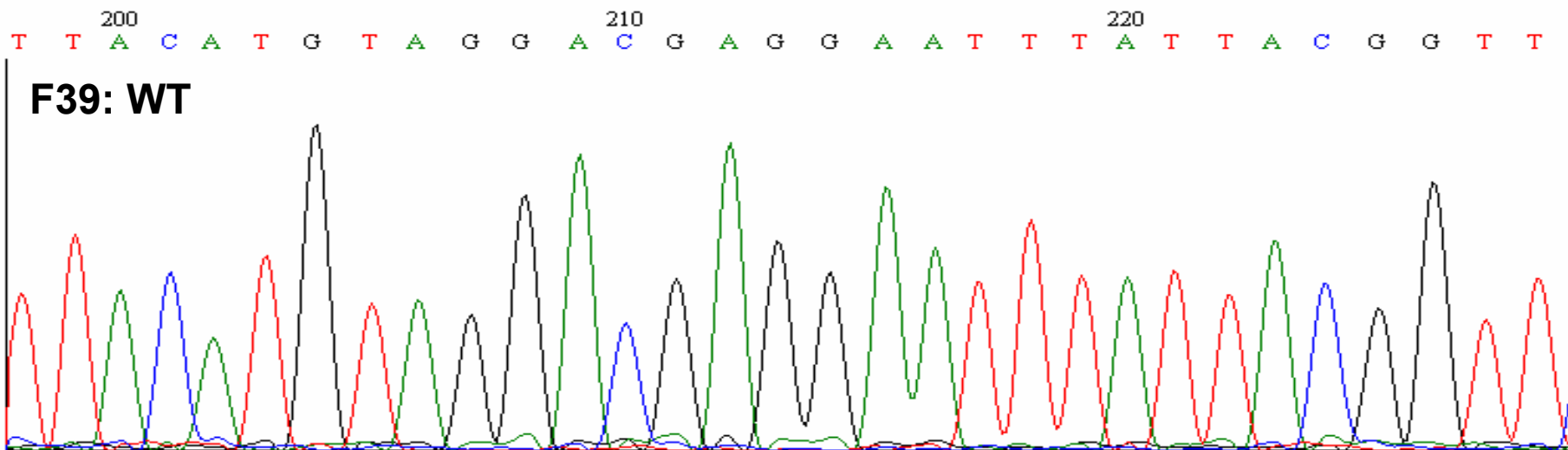


Mutation visible only on reverse sequence & observed in two independent PCRs/sequences

Position: 10,541



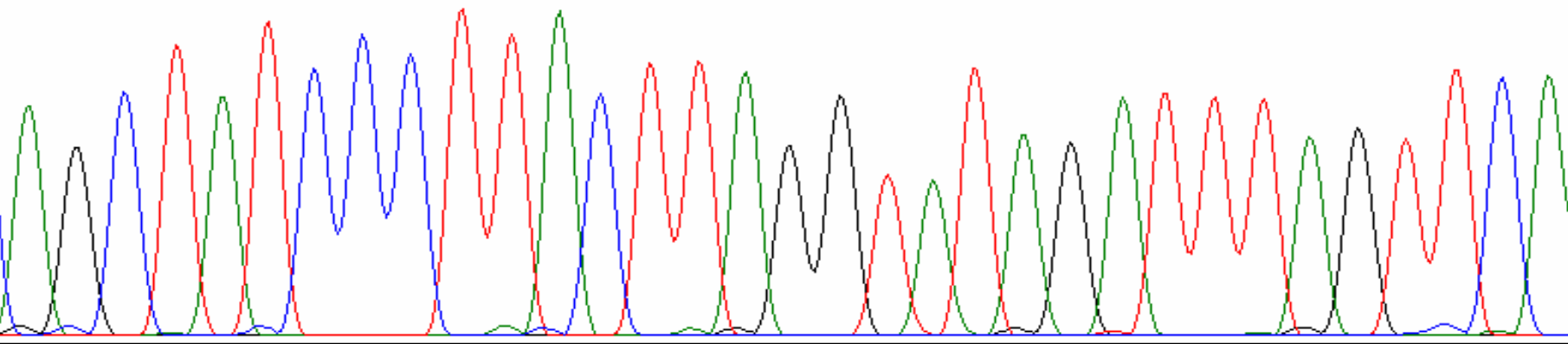
Position: 10,801 (NC)



Position: 10,970

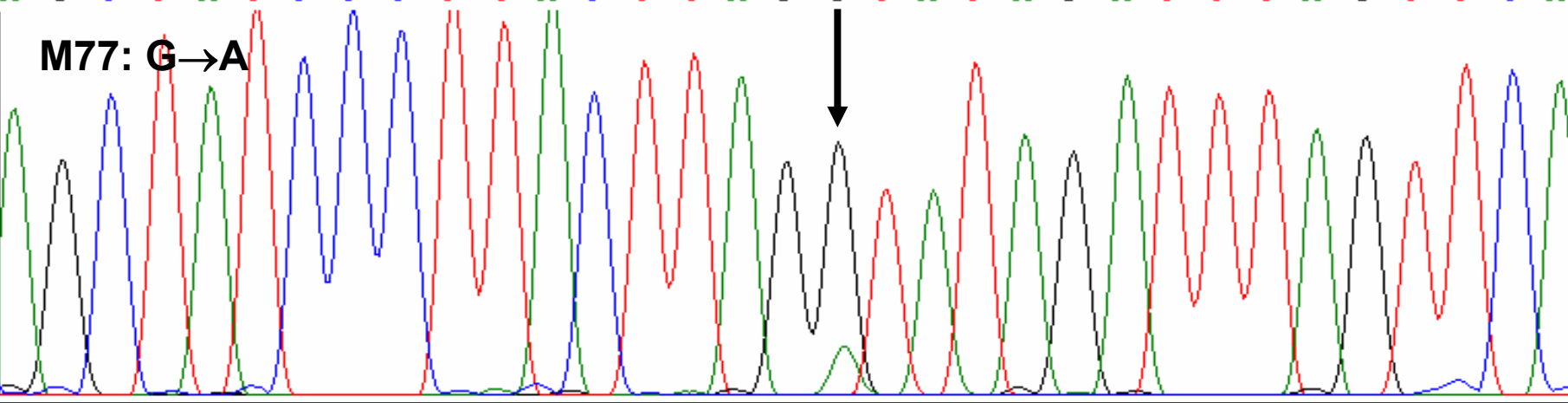
A G C T A T C C C T T A C T T A G G T A T A G A T T T A G T T C A

M38: WT

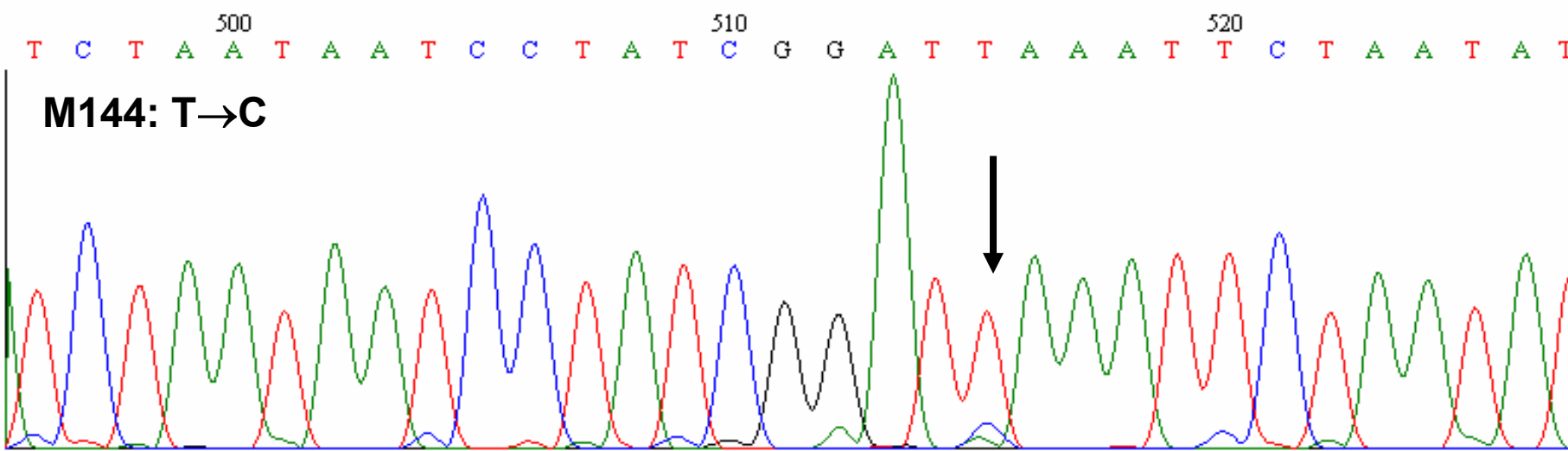
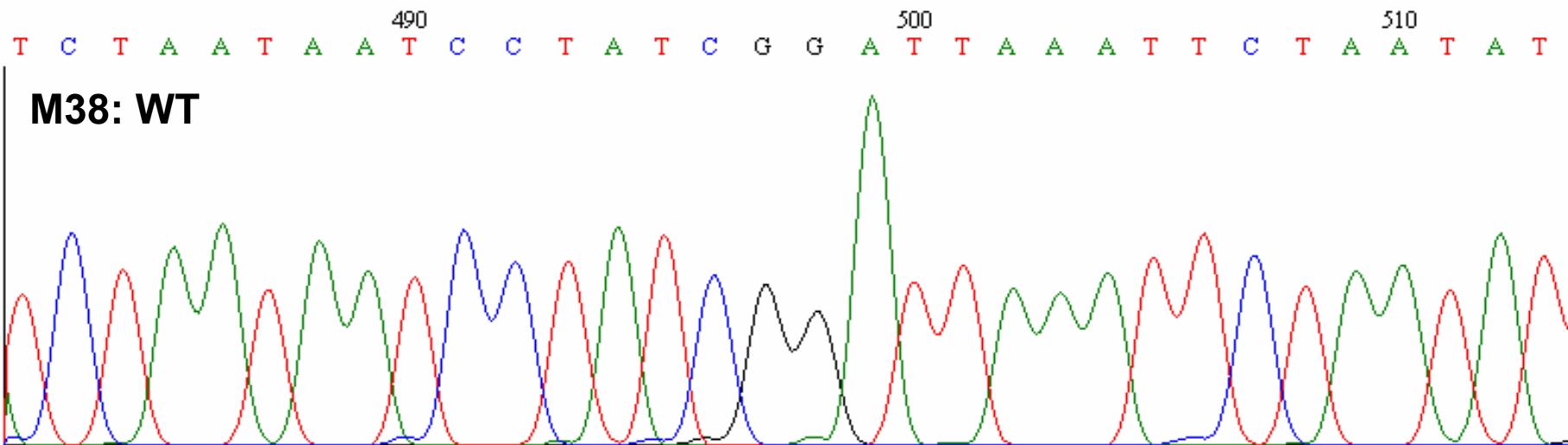


A G C T A T C C C T T A C T T A G G T A T A G A T T T A G T T C A

M77: G→A



Position: 11,132

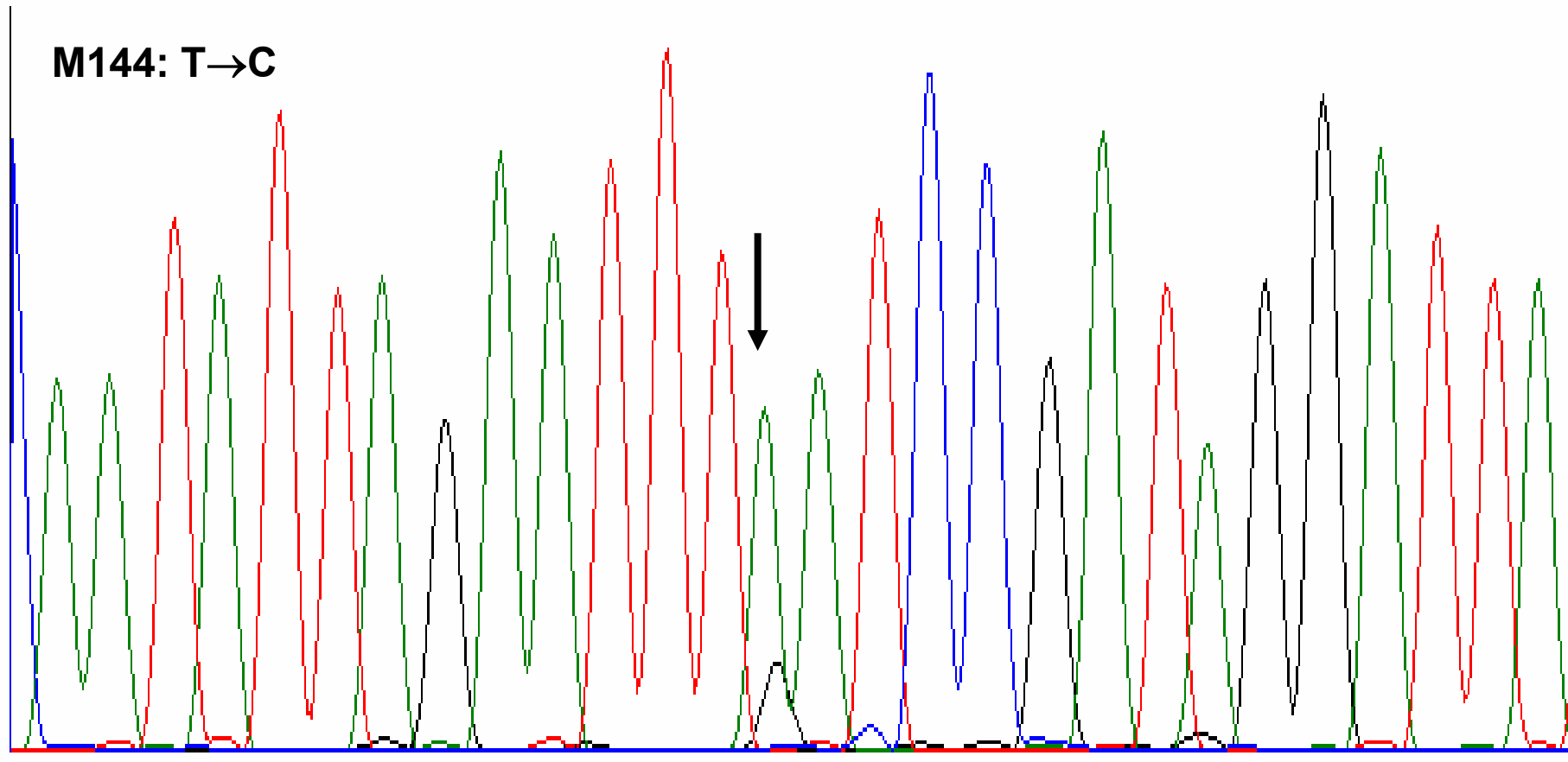




Position: 11,132

150 160  
A A T A T T A G A A T T T A A T C C G A T A G G A T T A

**M144: T→C**



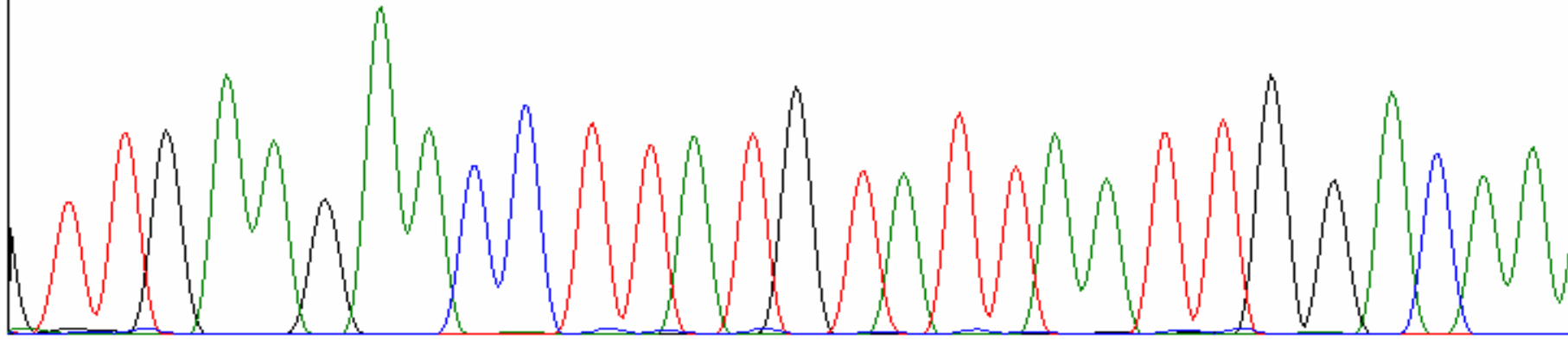
Same as previous mutation seen on reverse strand

Position: 11,542

T T G A A G A A C C T T A T G T A T T A A T T G G A C A A

80 90 100

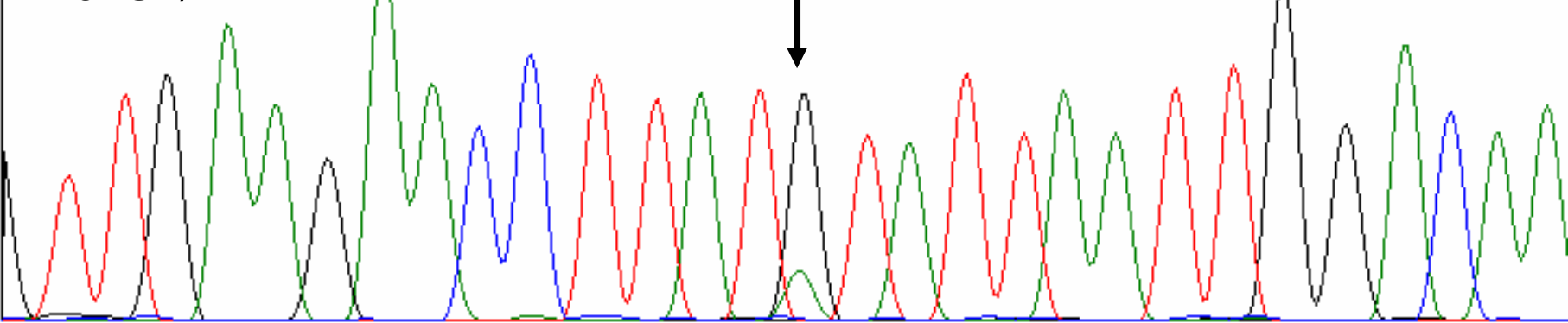
**M63: WT**



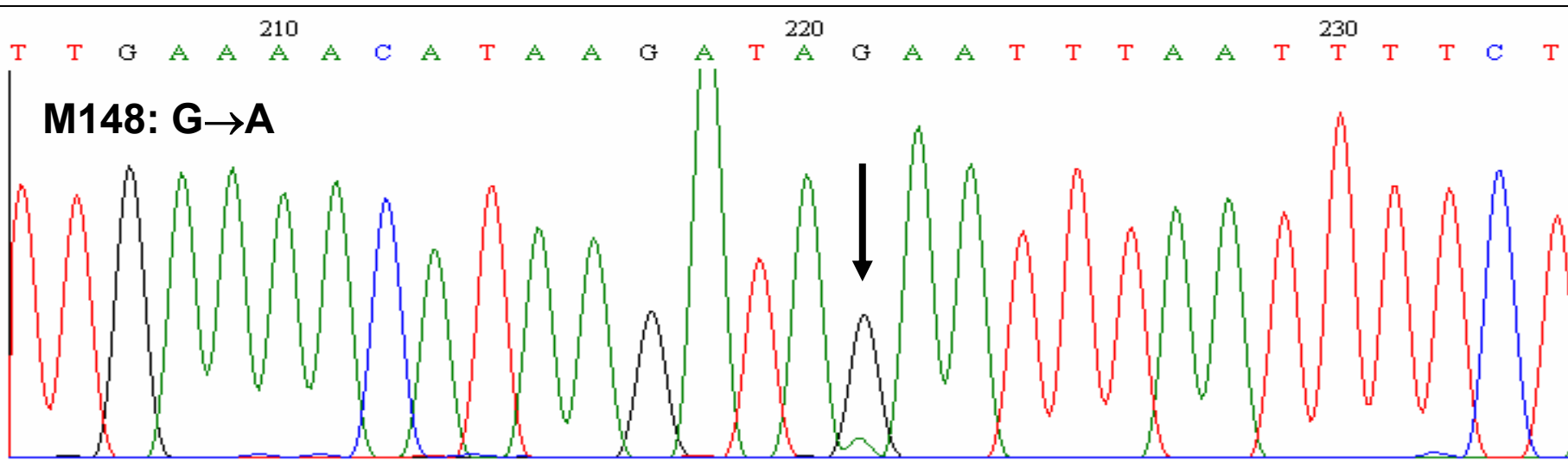
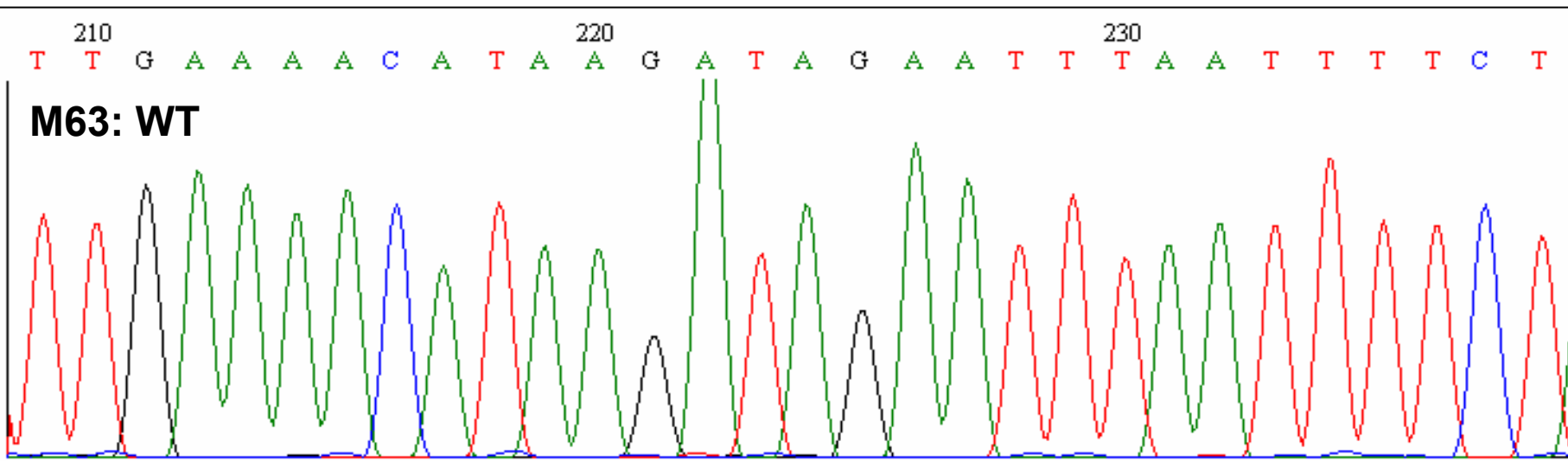
T T G A A G A A C C T T A T G T A T T A A T T G G A C A A

80 90 100

**M75: G→A**

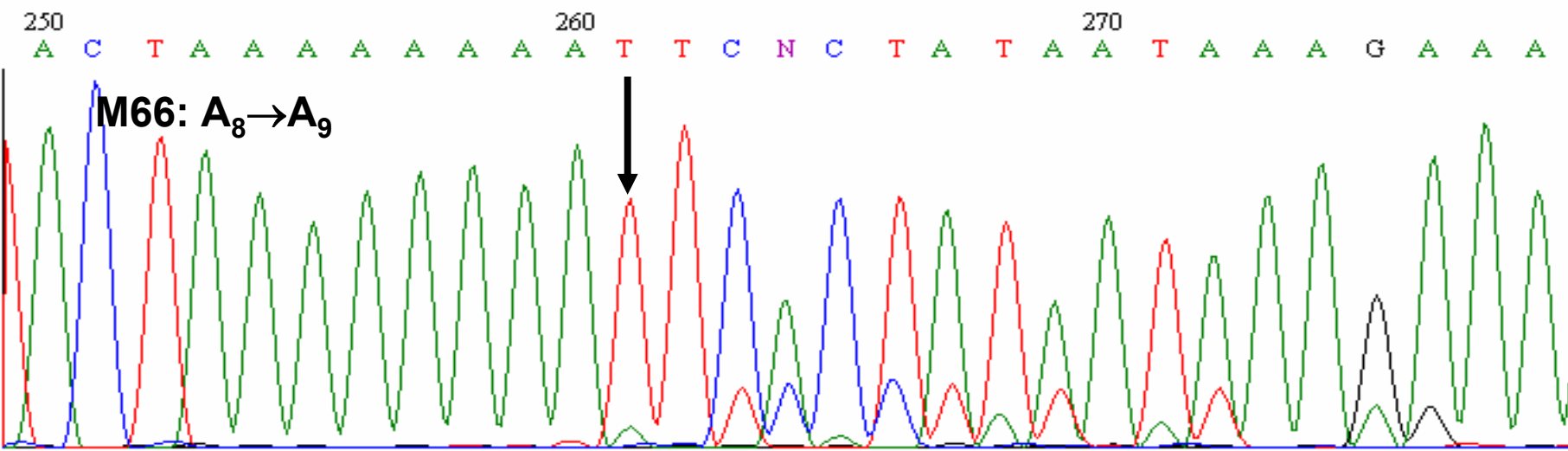
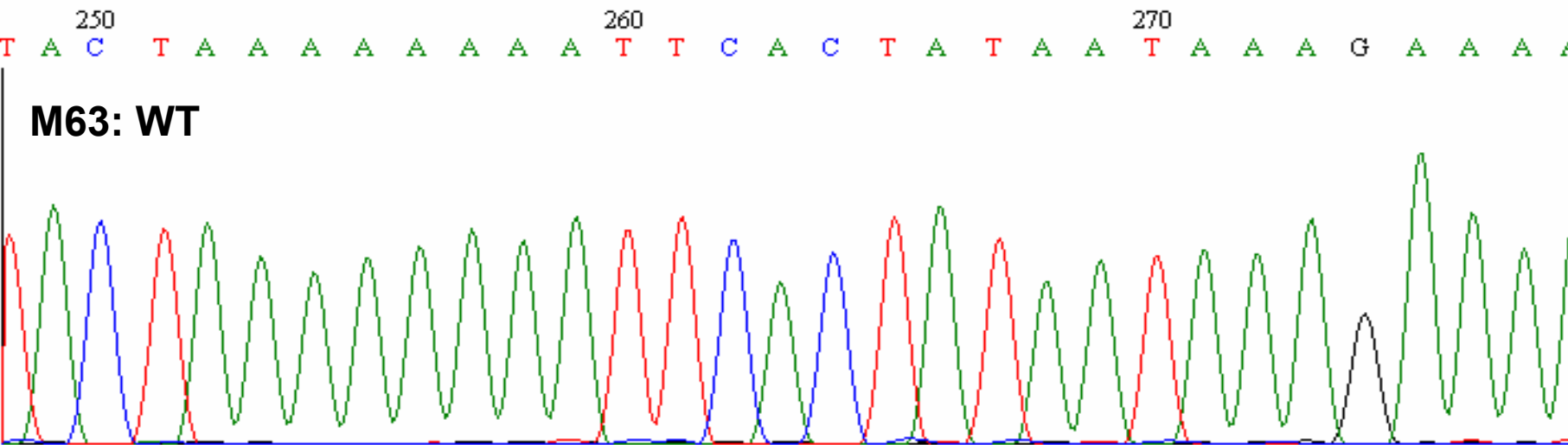


Position: 11,677

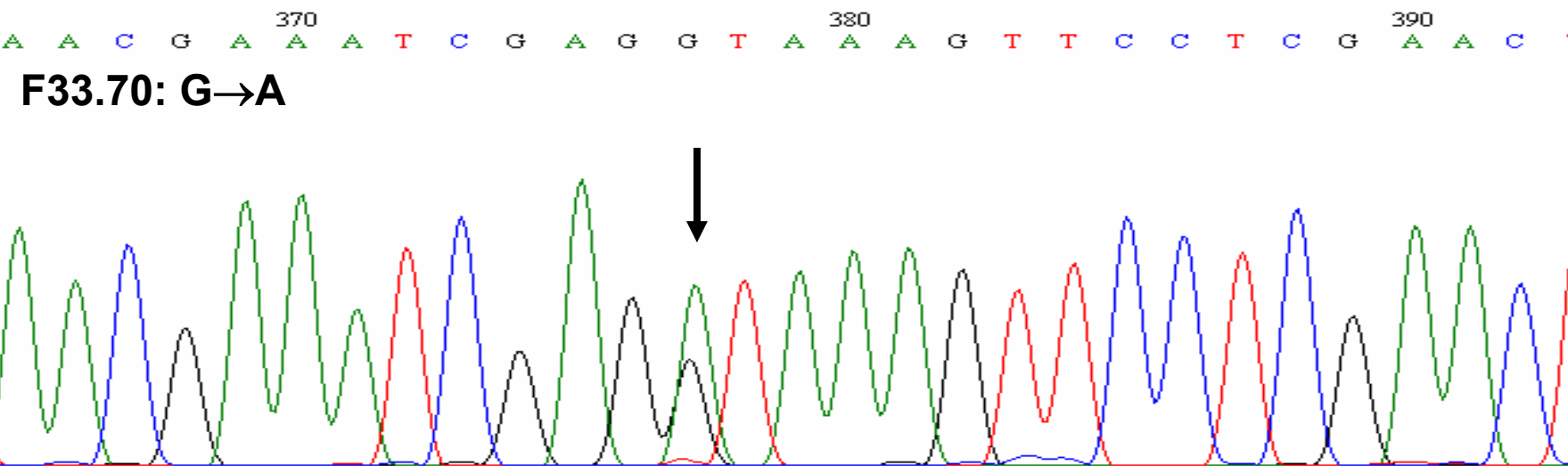
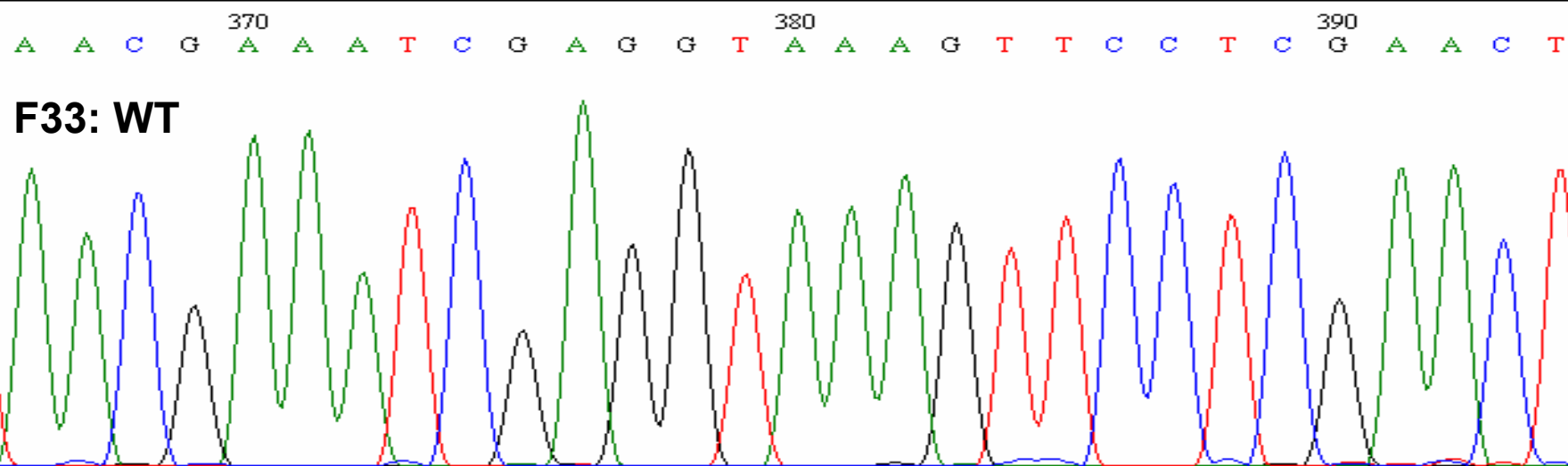


Found in two independent PCRs/sequences

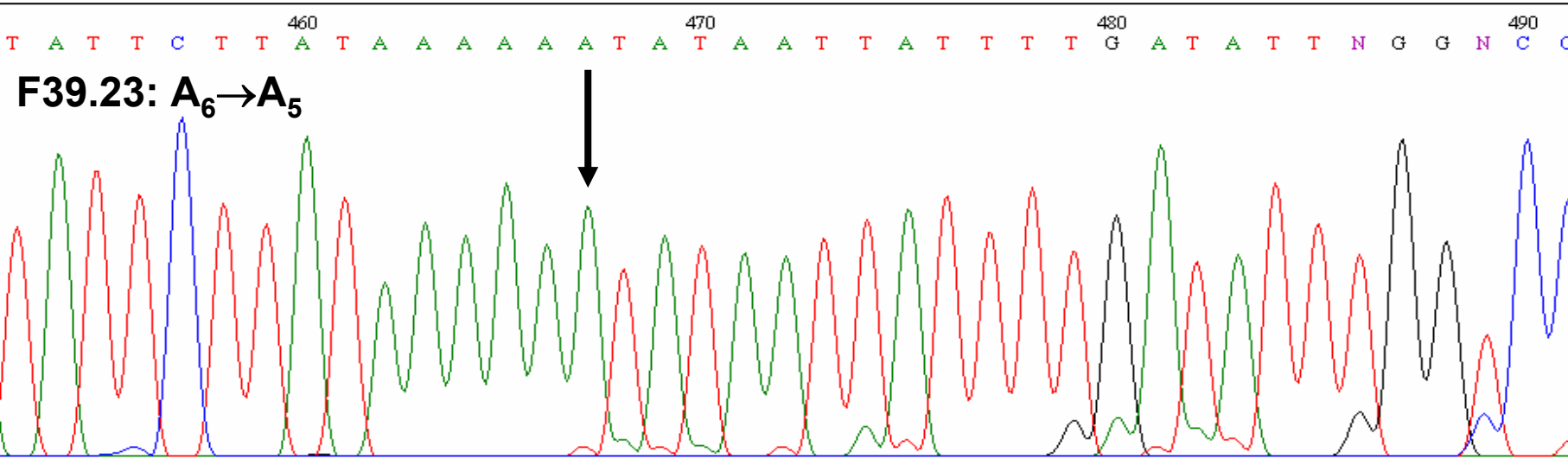
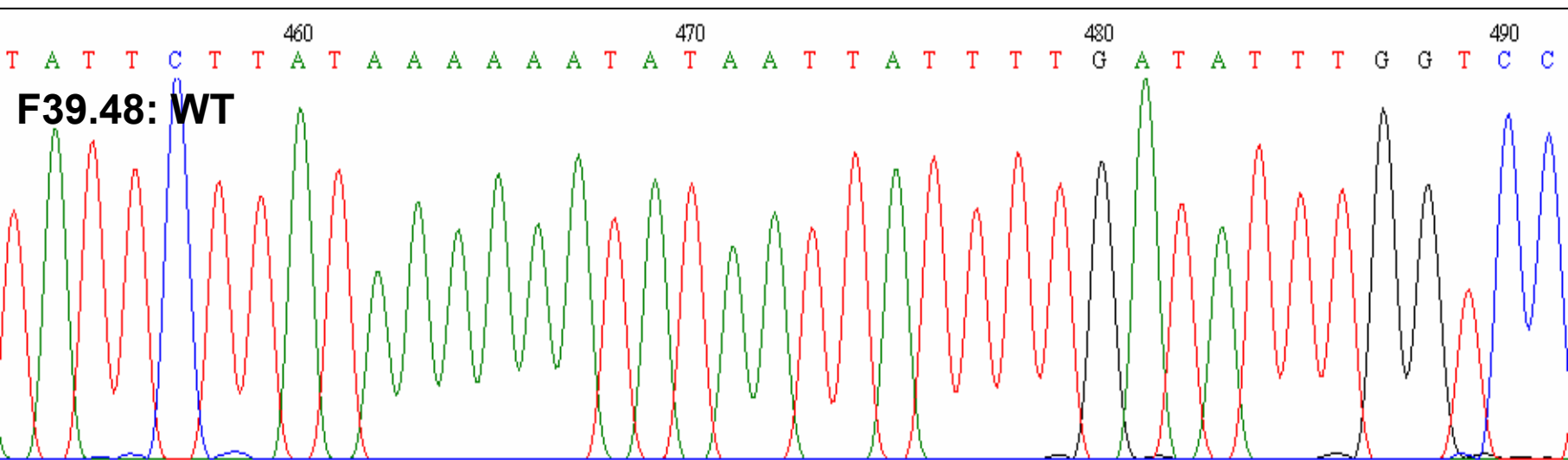
Position: 11,708



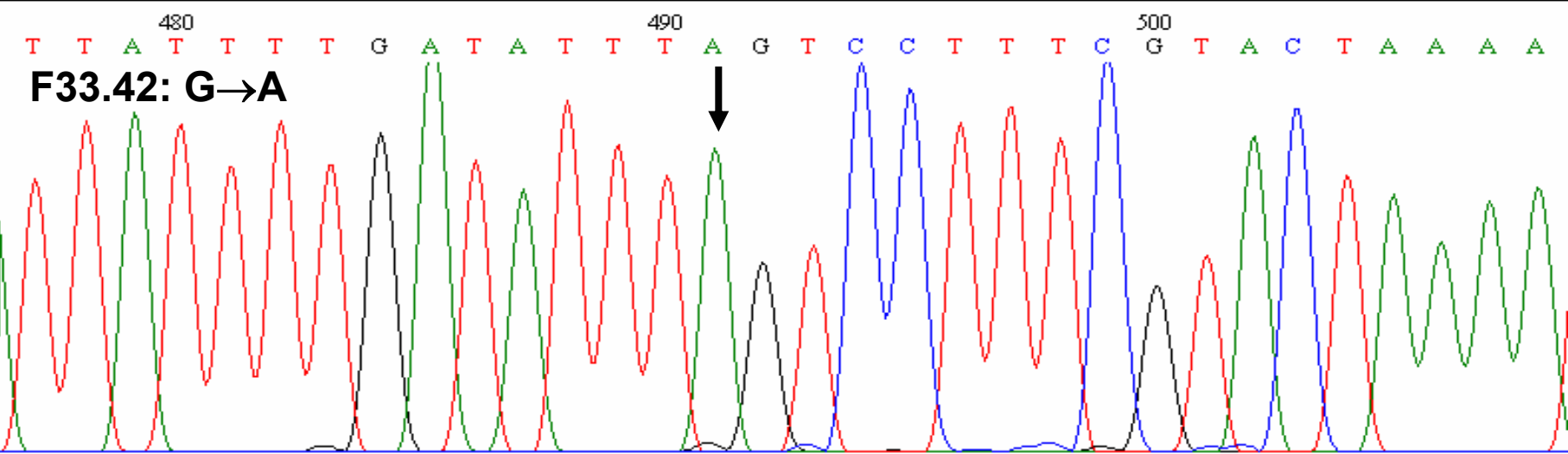
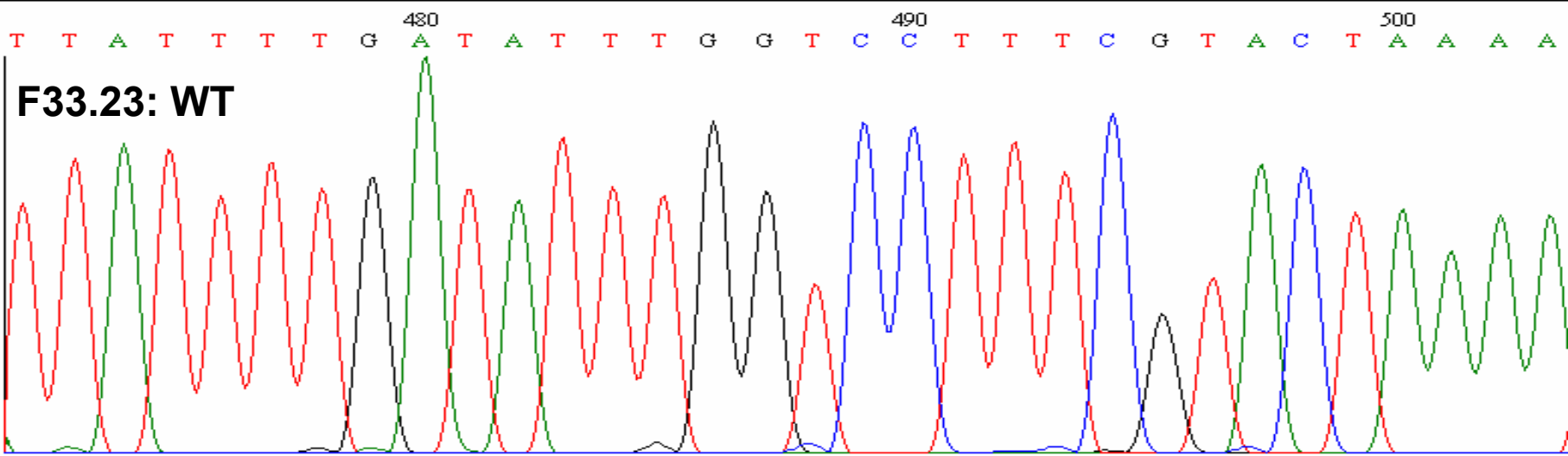
Position: 11,836



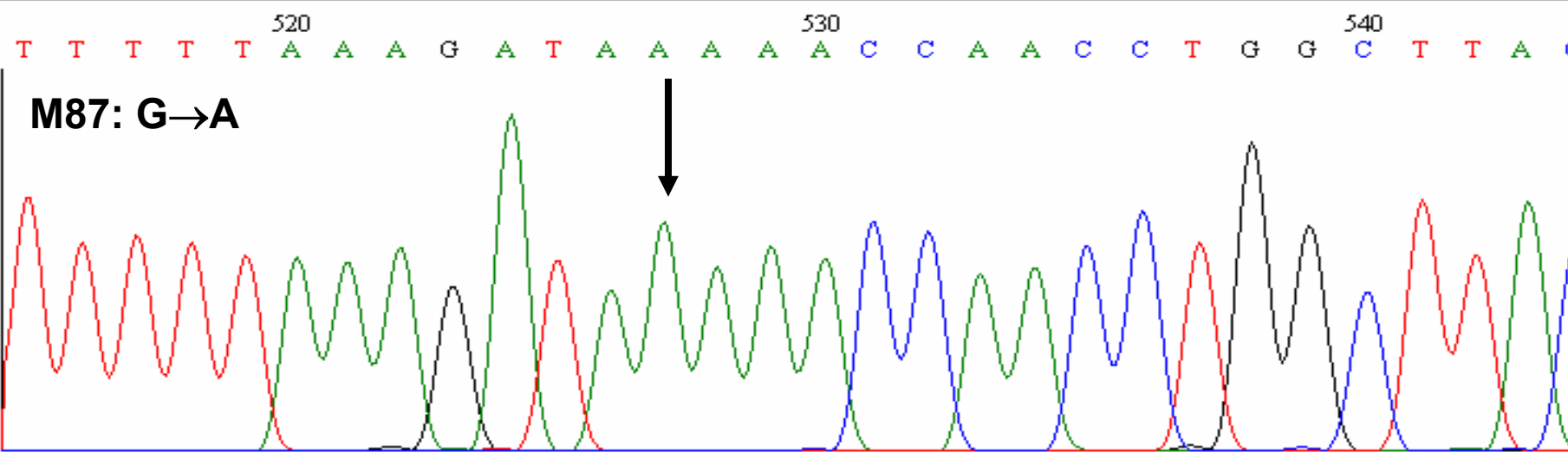
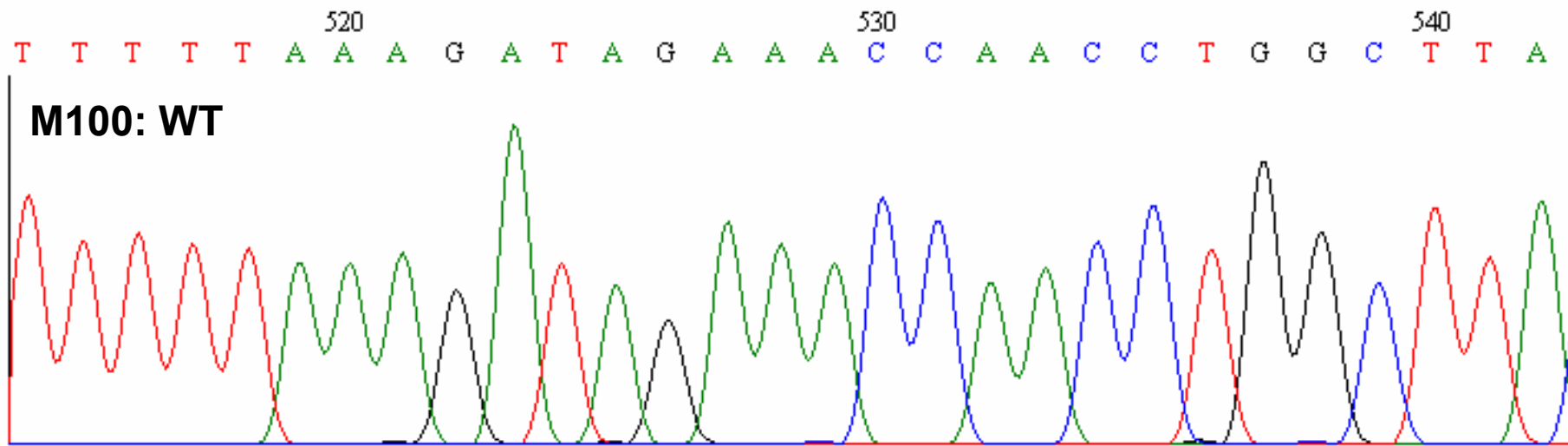
Position: 12,756



Position: 12,781

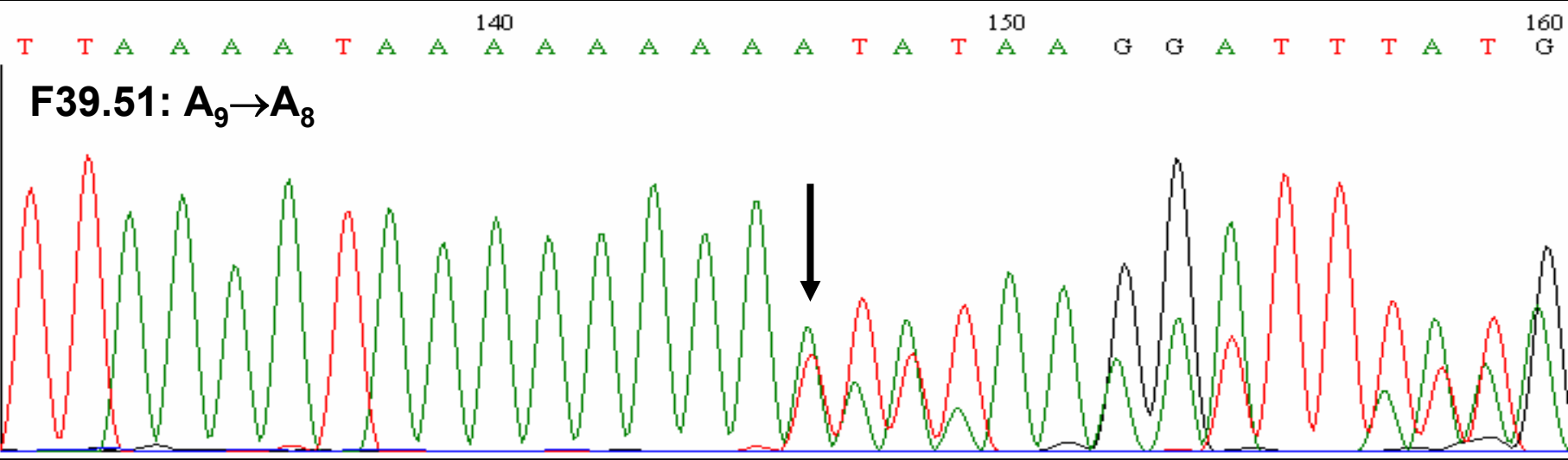
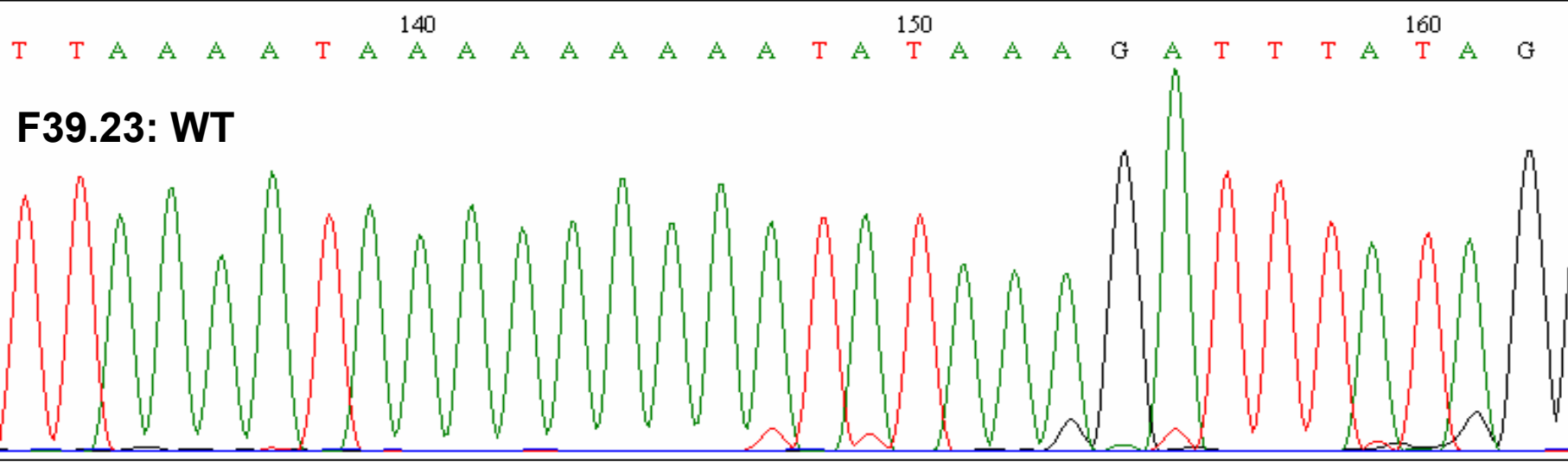


Position: 12,820

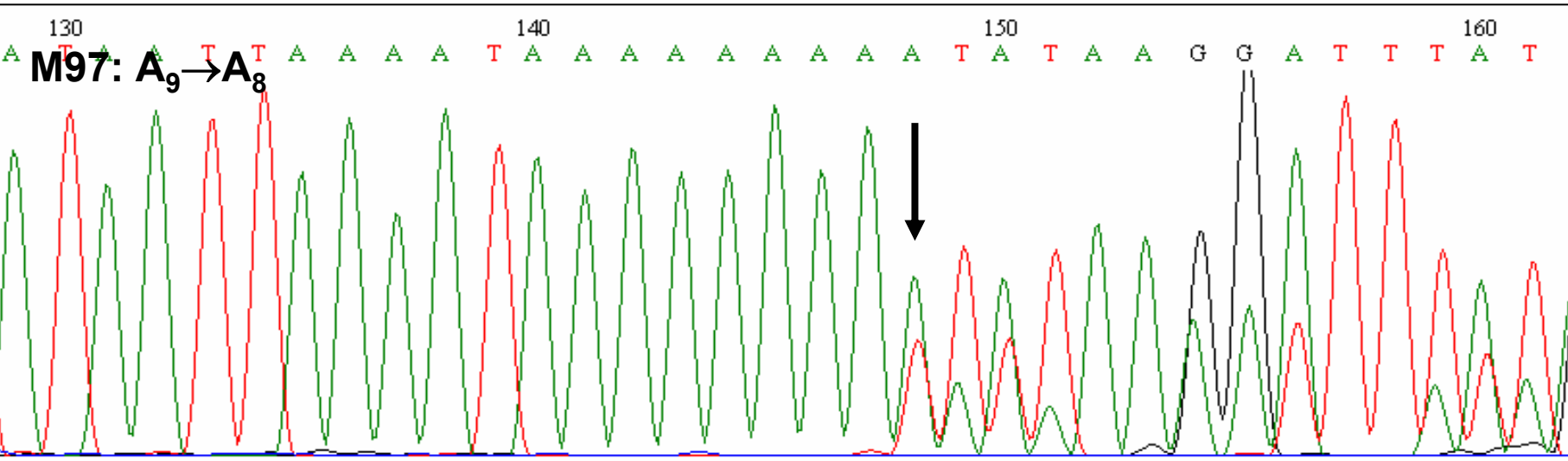
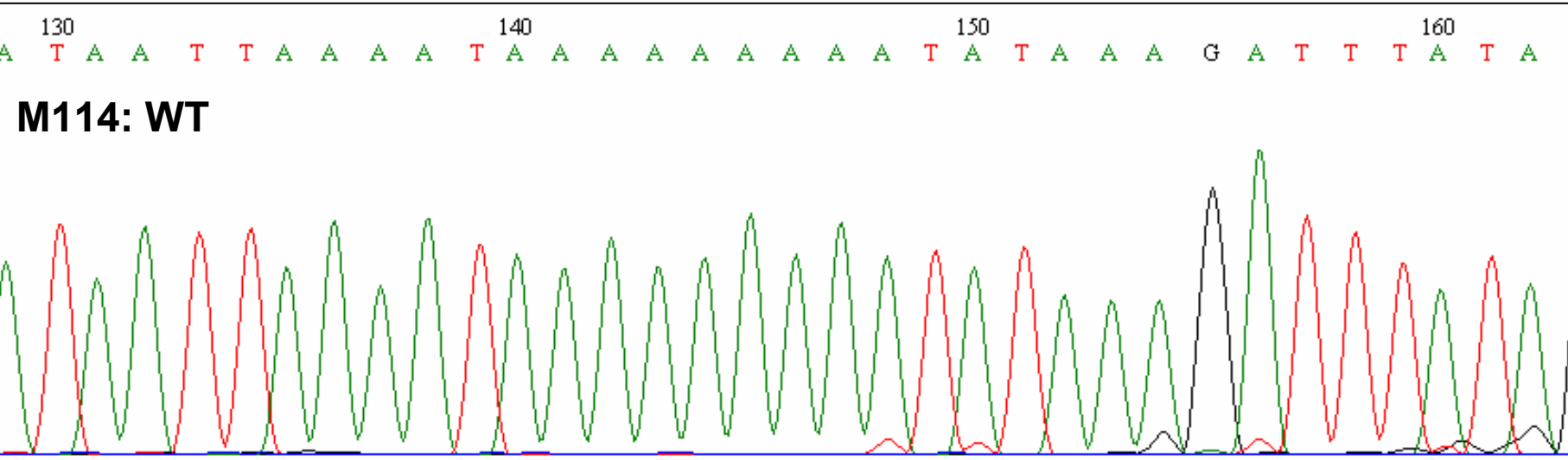




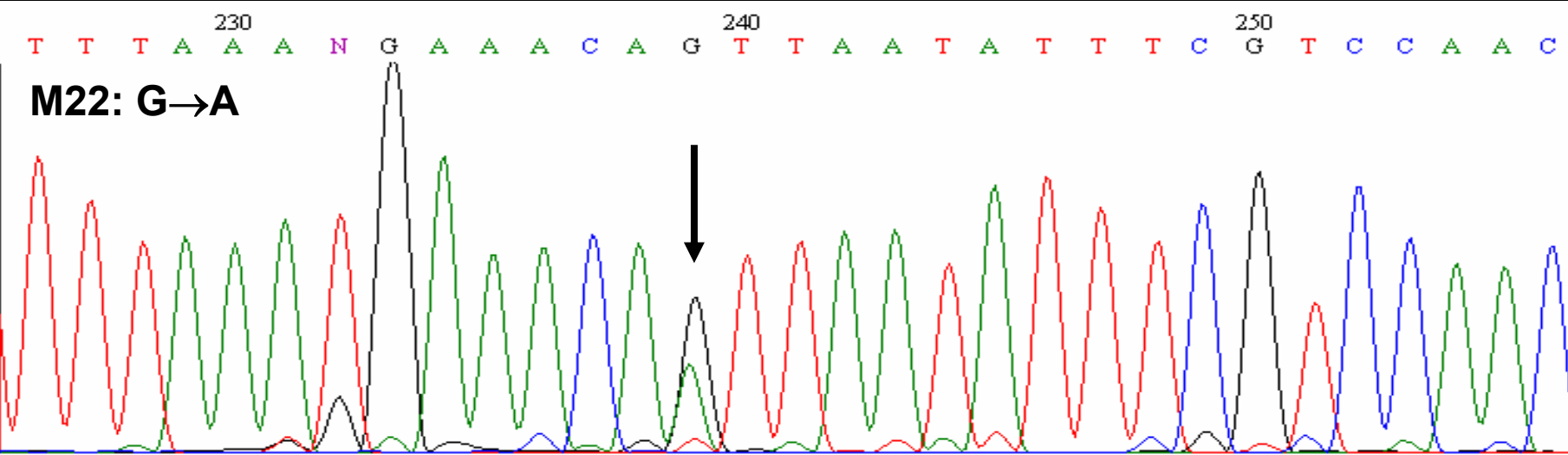
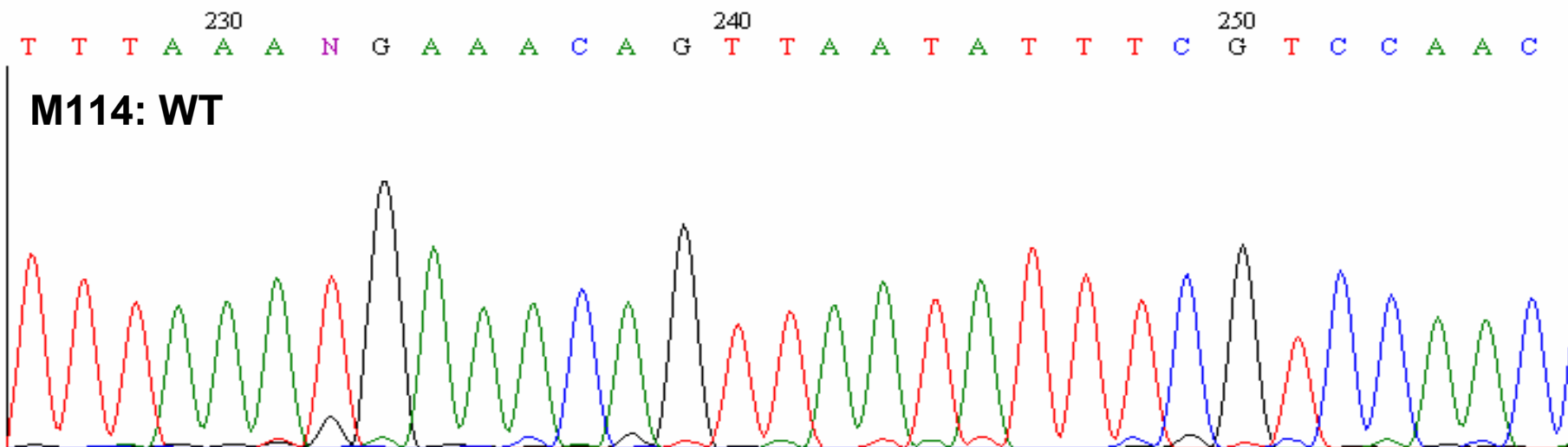
Position: 13,136



Position: 13,136



Position: 13,234



Position: 14,679

