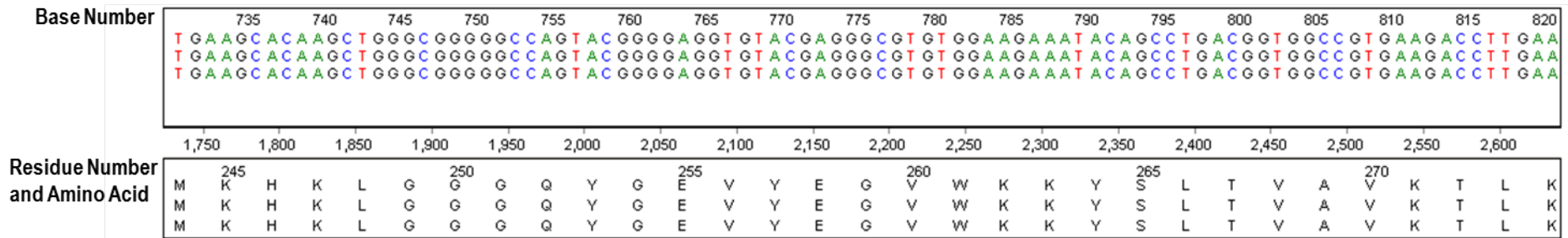
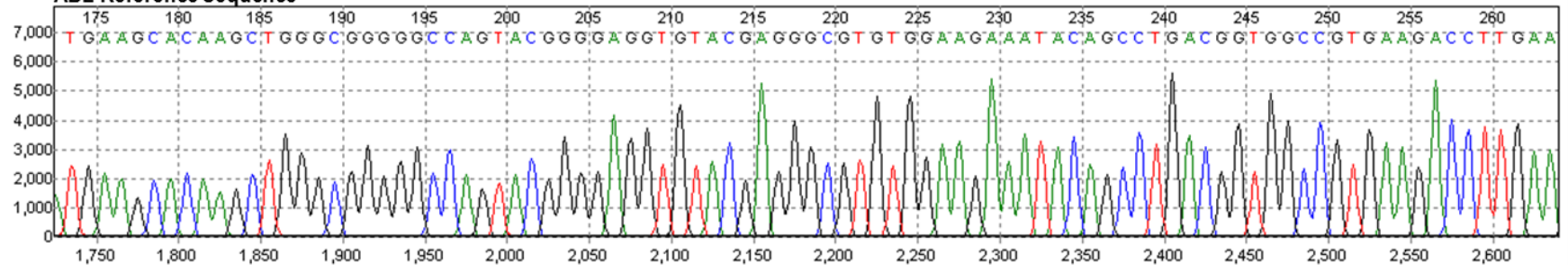


S1 Appendix: K562 nilotinib resistance intermediates do not harbour any Bcr-Abl kinase domain mutations

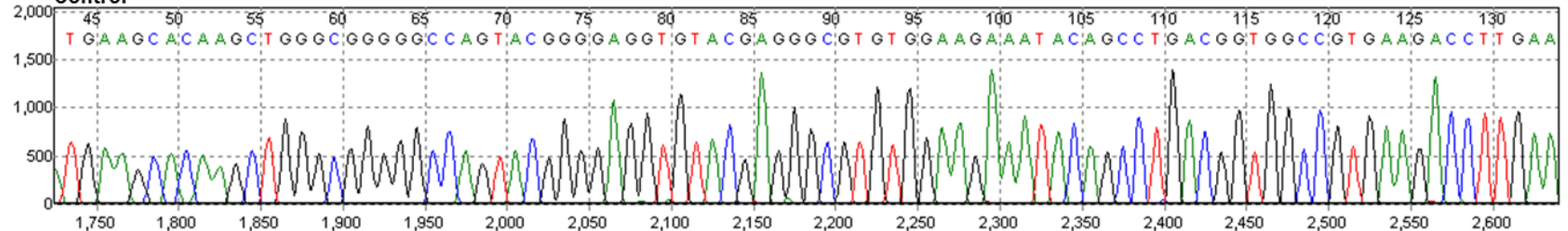
DNA sequencing of the Bcr-Abl kinase domain of K562 control cells and nilotinib resistance intermediates was conducted and compared with the GenBank ABL reference sequence. Data demonstrate that neither the control cells nor any of the resistance intermediates contain mutations. Data were analysed using Mutation Surveyor Version 3.24 with each peak representing a DNA base (A=Adenine; C=Cytosine; G=Guanine; or T=Thymine) in the 5'-3' direction of the ABL sequence. The base number for both the reference sequence and the sequences of interest are indicated. The amino acid and corresponding residue number are also indicated. The amino acid sequences exactly match the reference sequence with no kinase domain mutations present. NIL=nilotinib



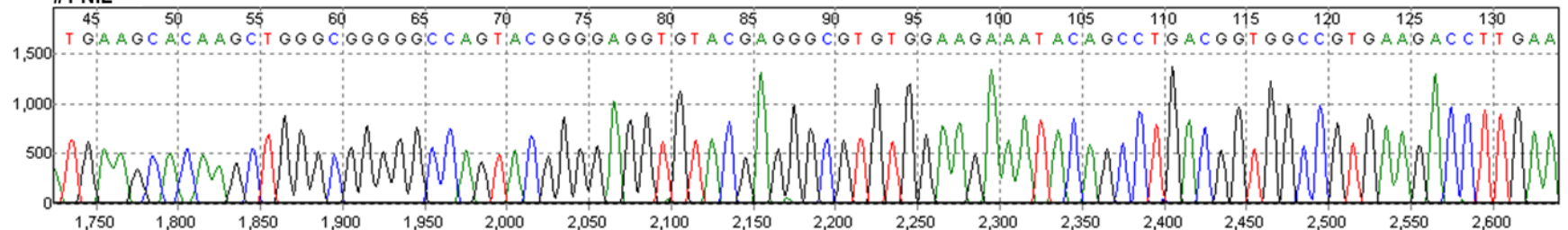
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Control



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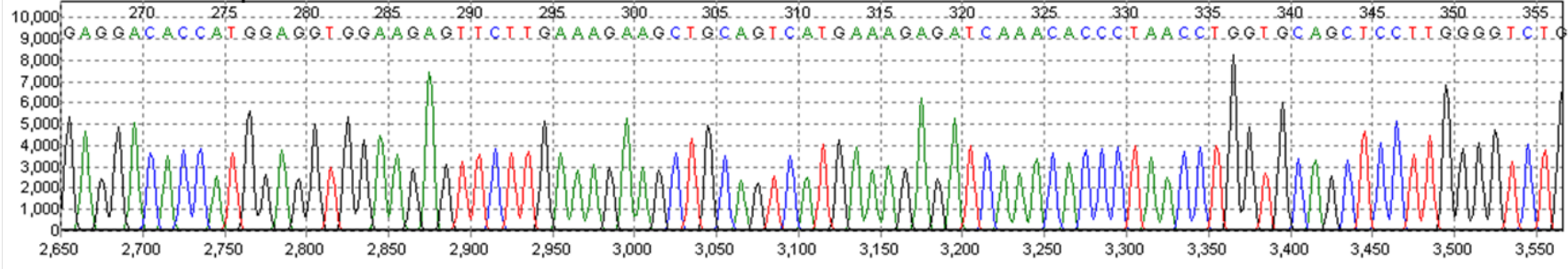


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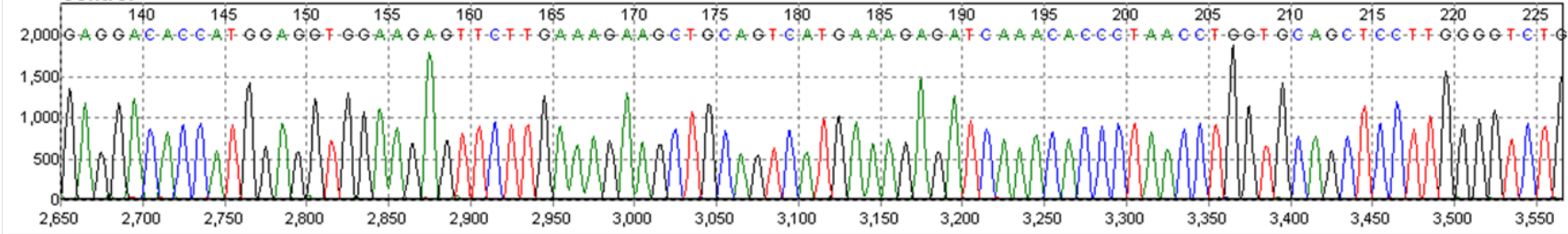
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275 280 285 290 295 300 305
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 E D T M E V E E F L K E A A V M K E I K H P N L V Q L L G V C
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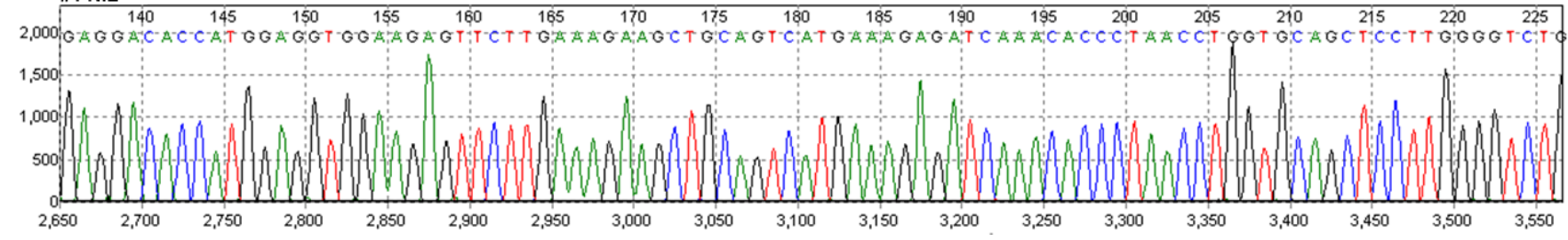
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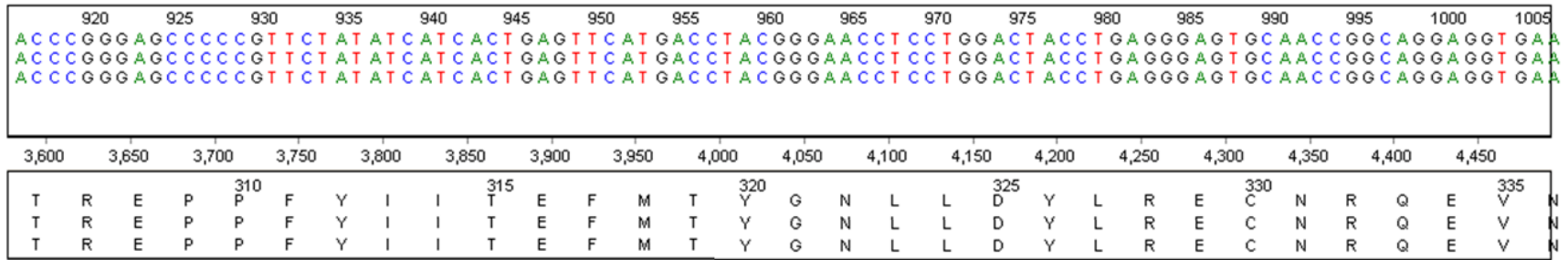


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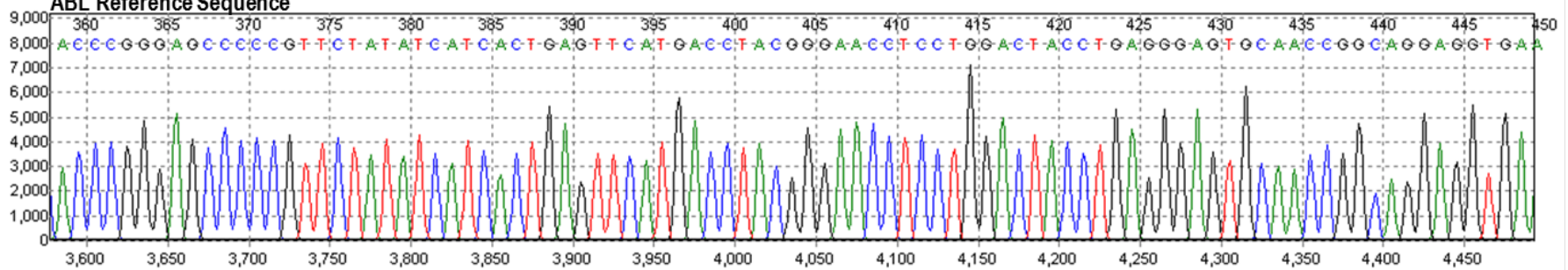


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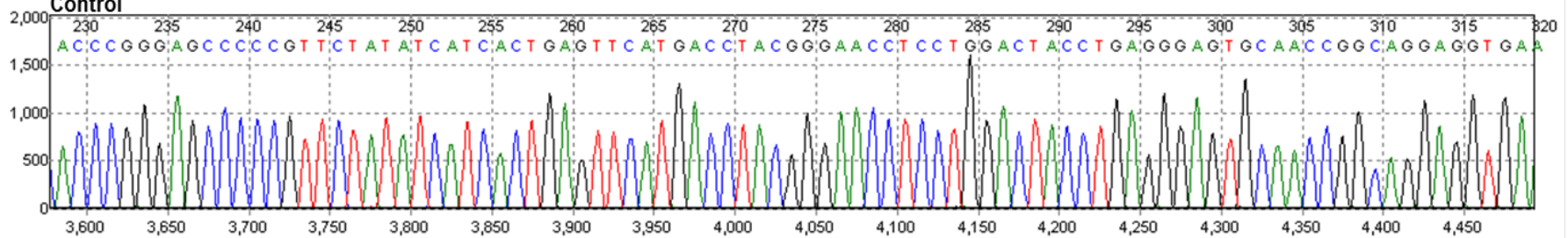




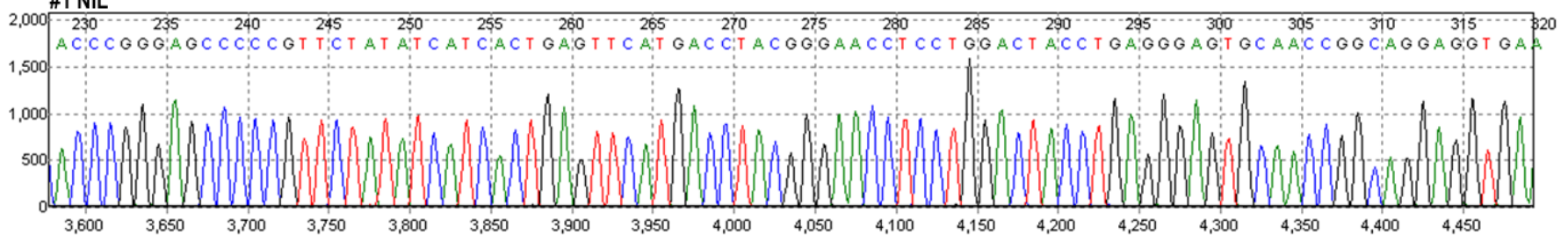
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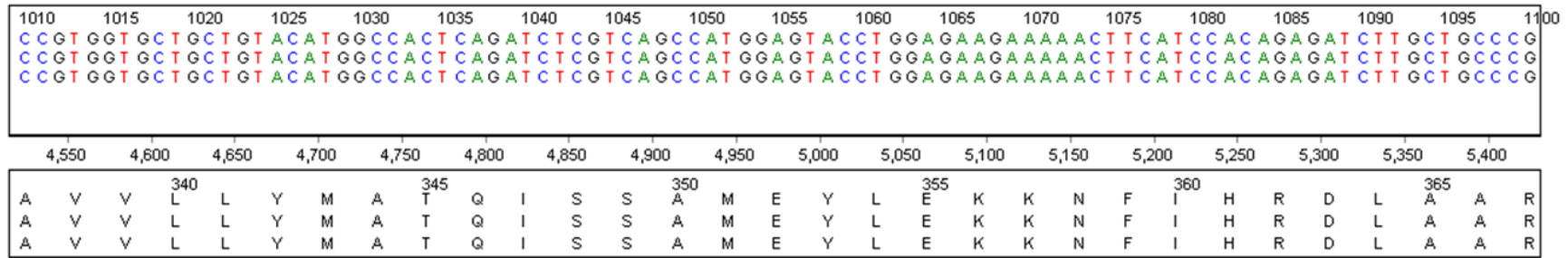


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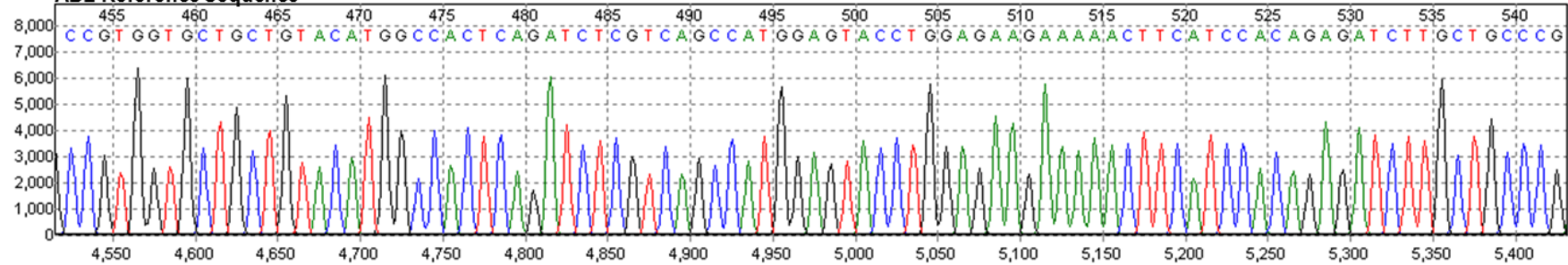


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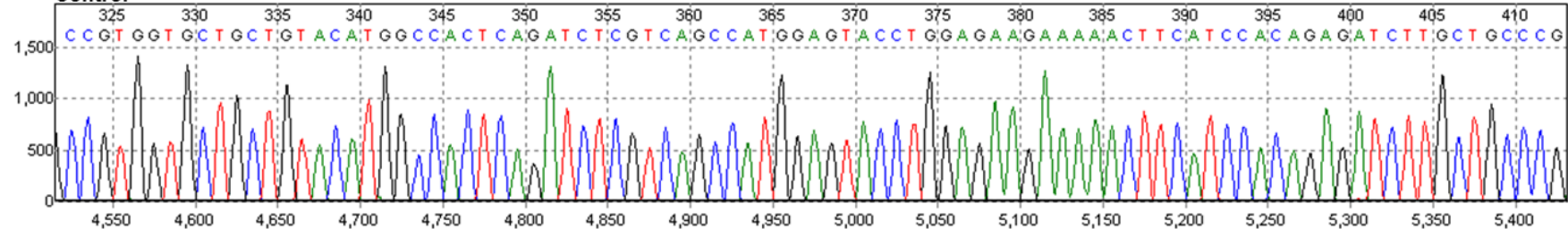




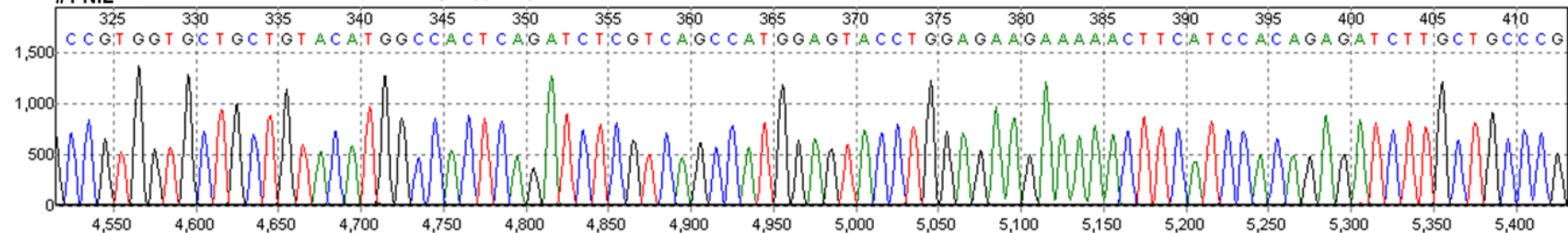
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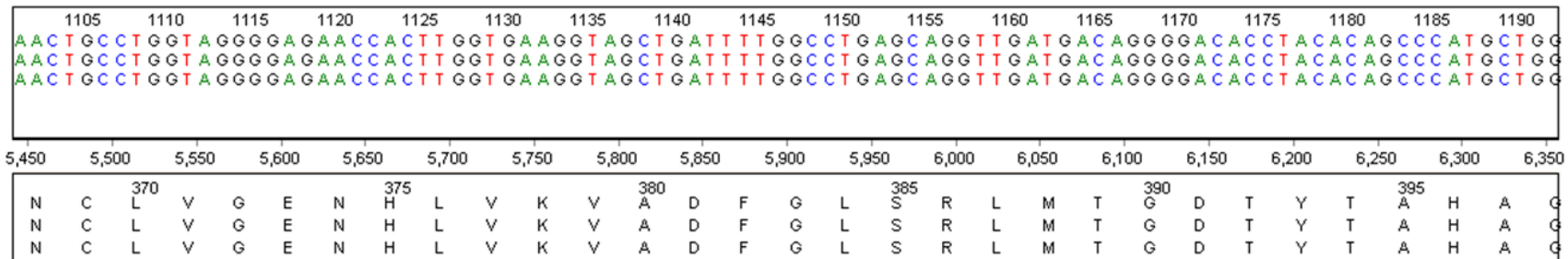


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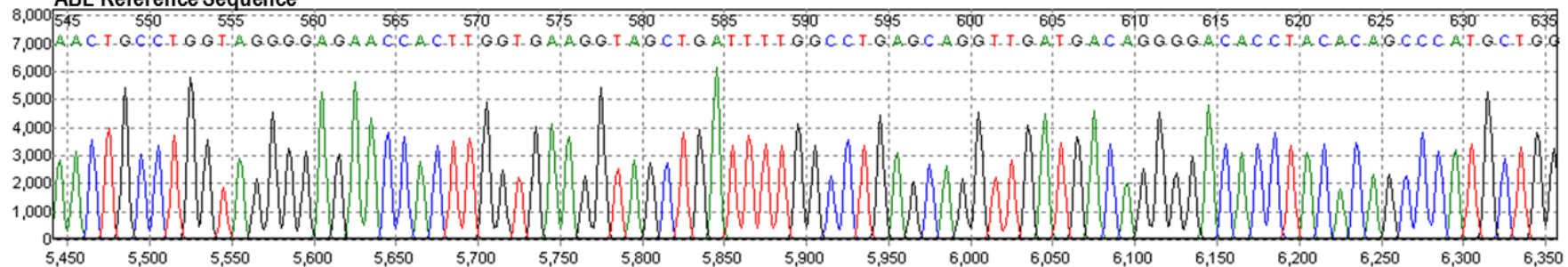


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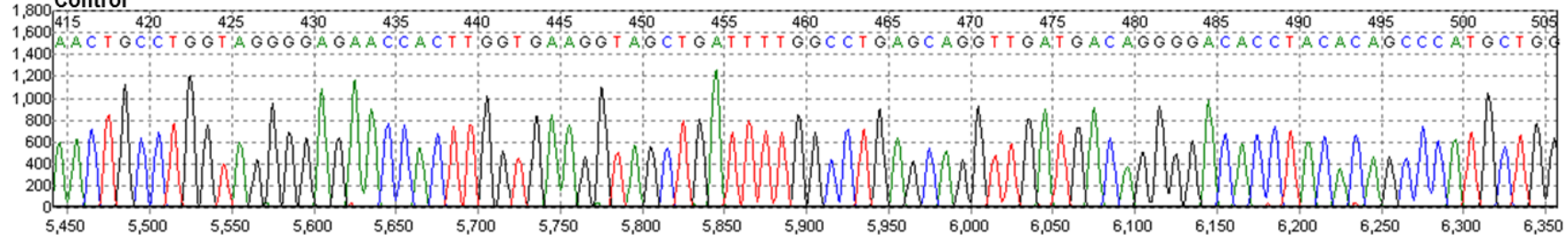




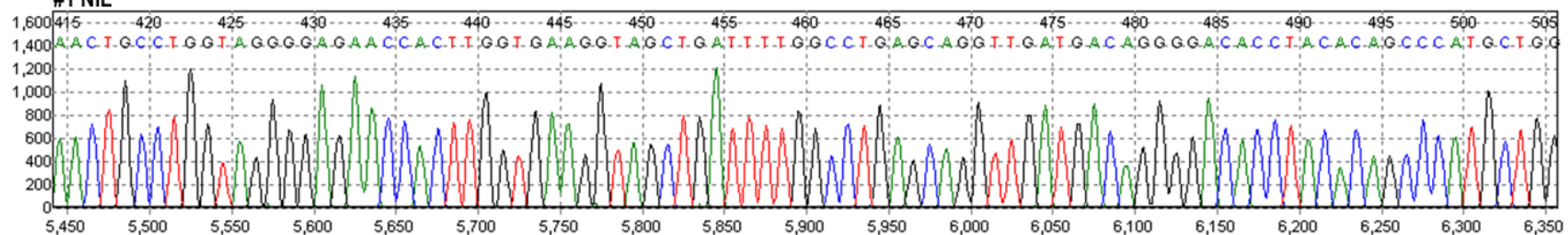
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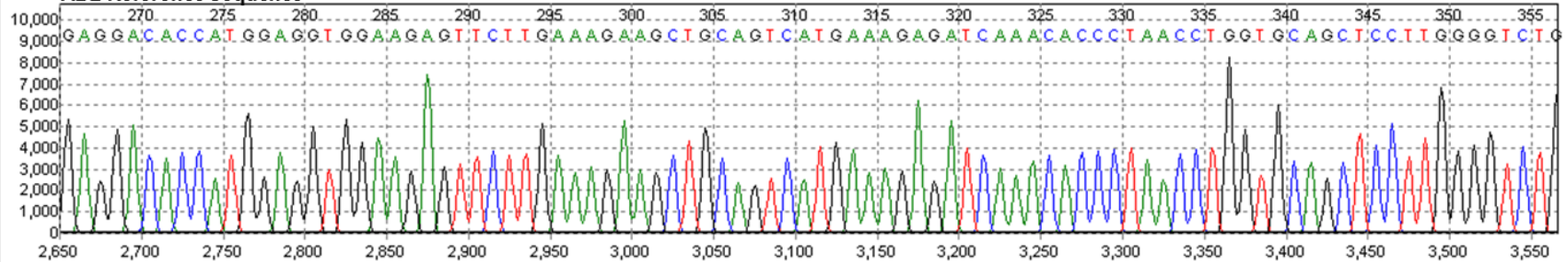


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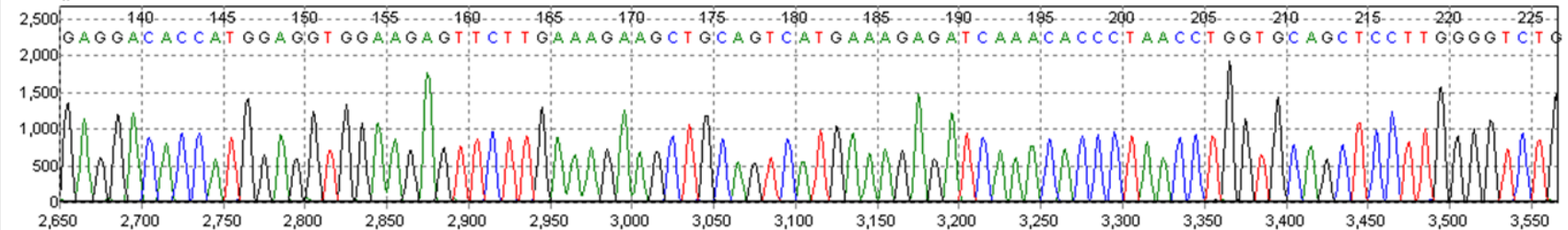
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E	D	T	M	E	V	E	E	F	L	K	E	A	A	V	M	K	E	I	K	H	P	N	L	V	Q	L	L	G	V	C						
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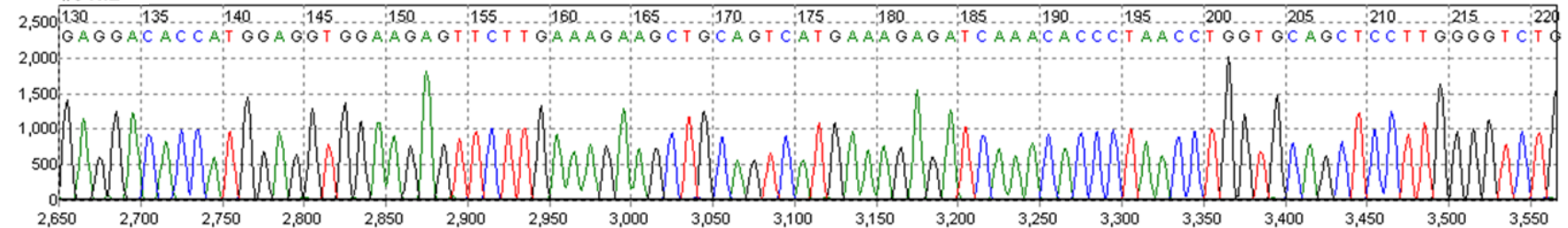
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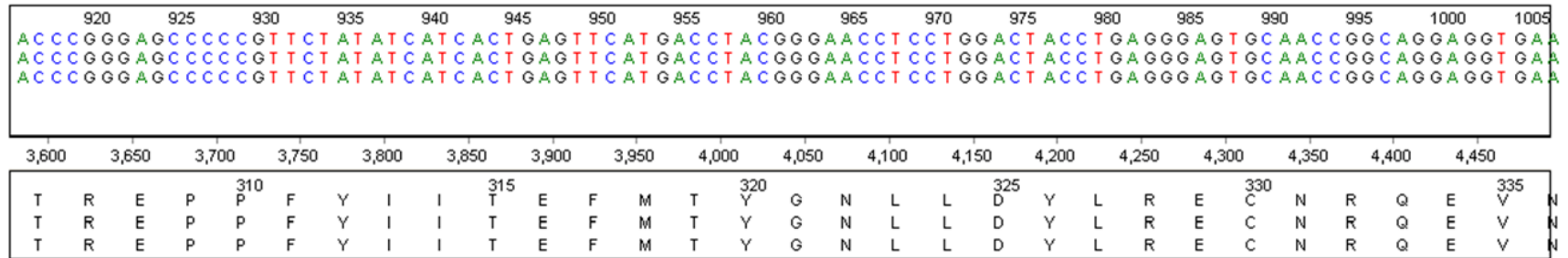


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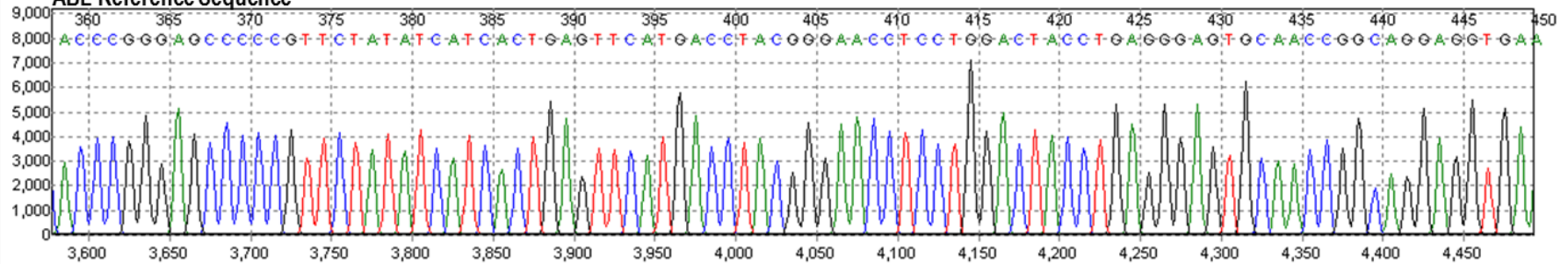


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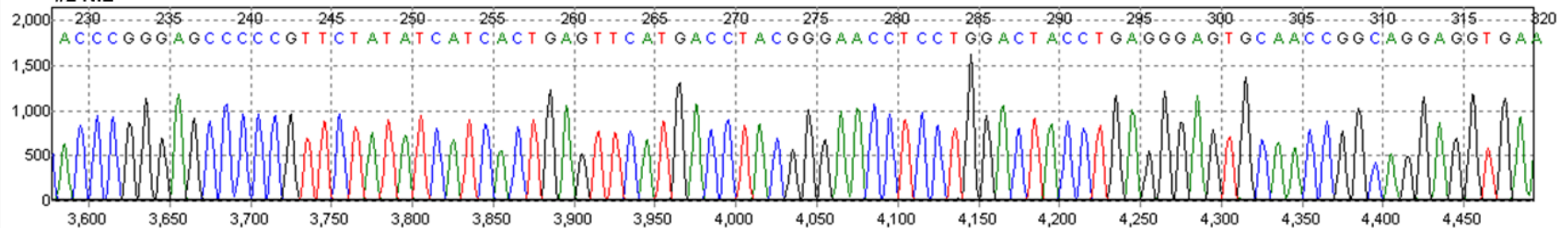




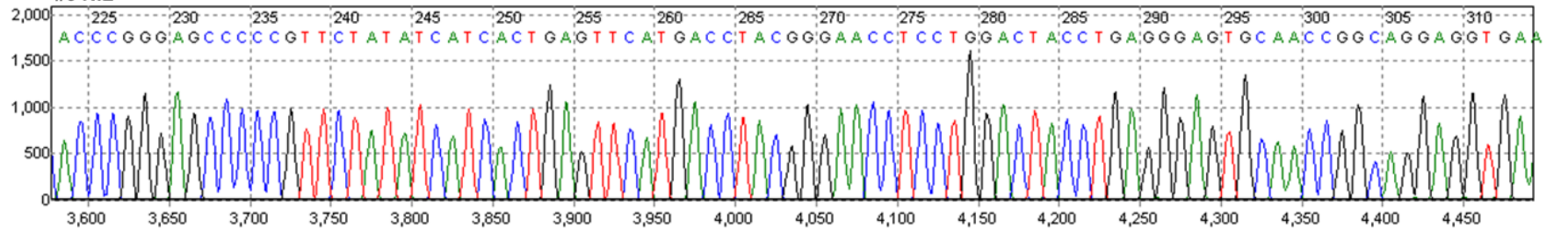
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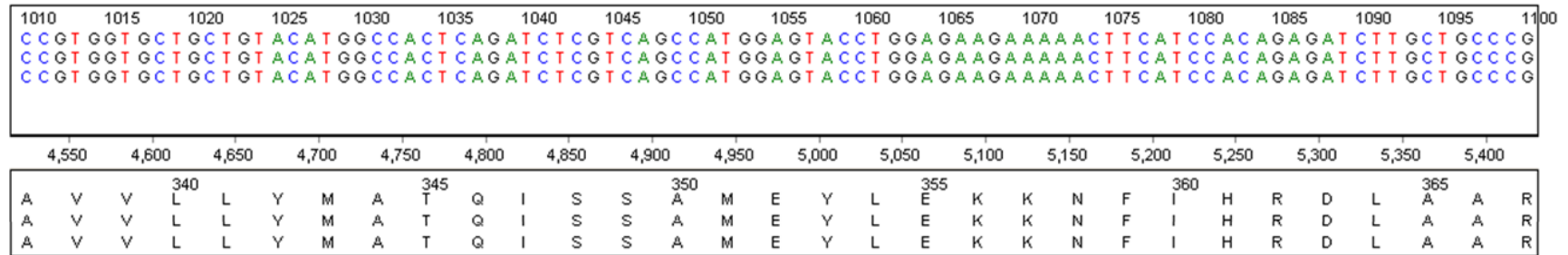


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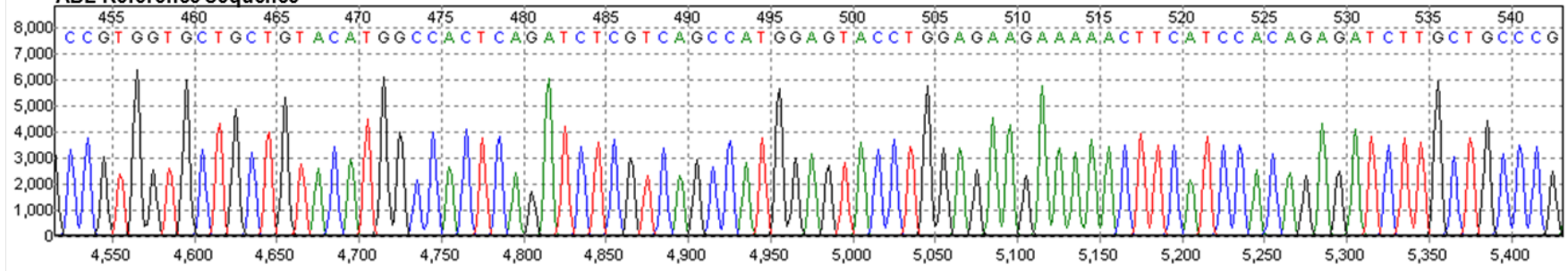


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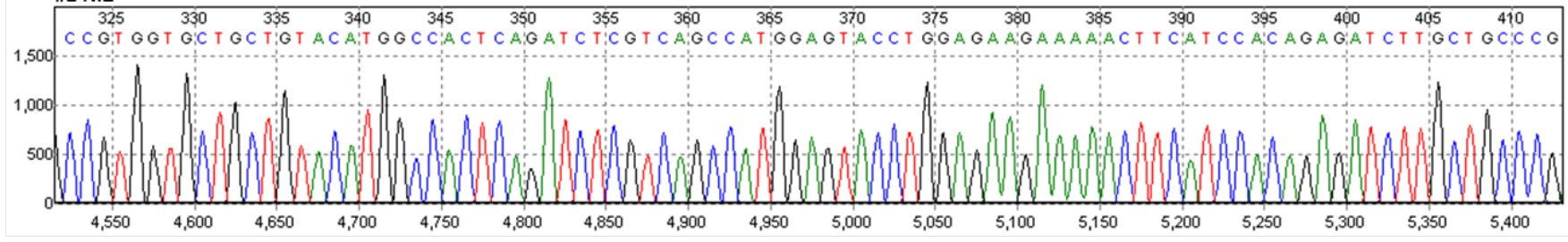




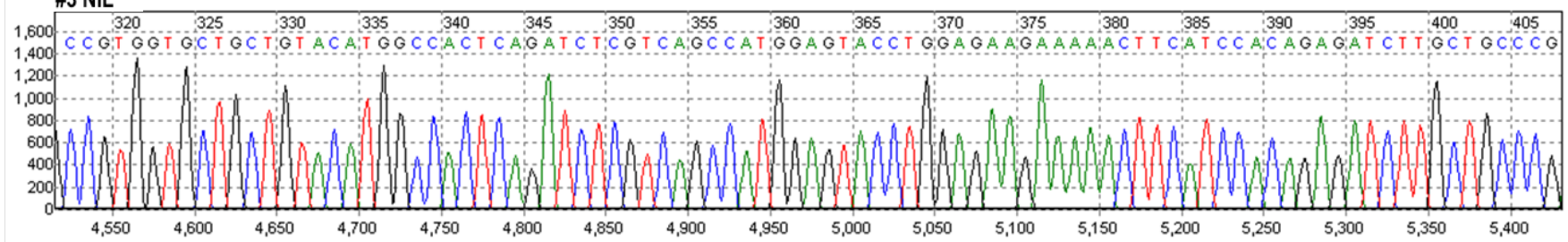
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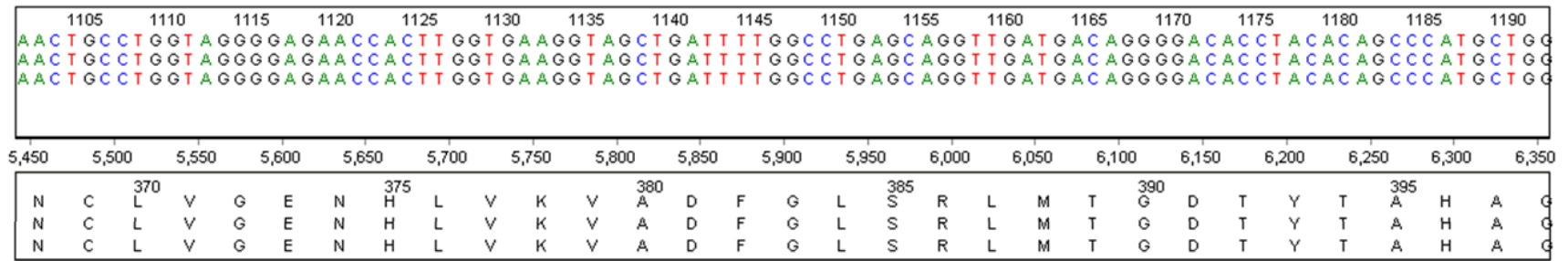


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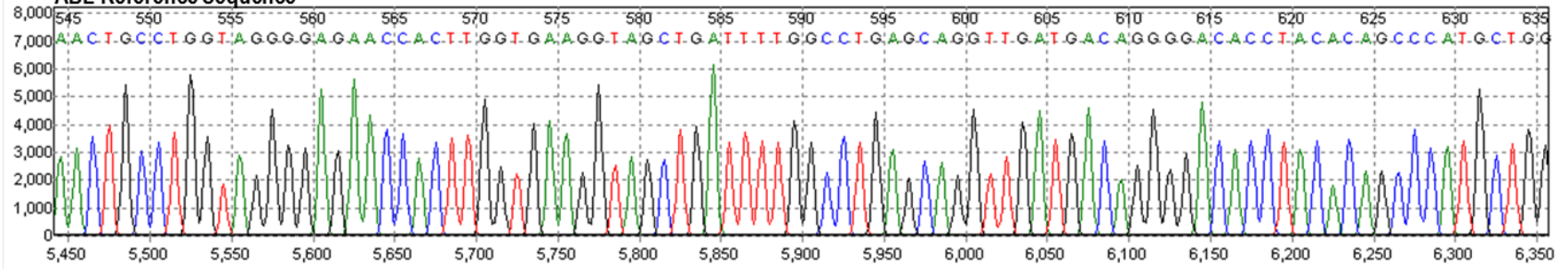


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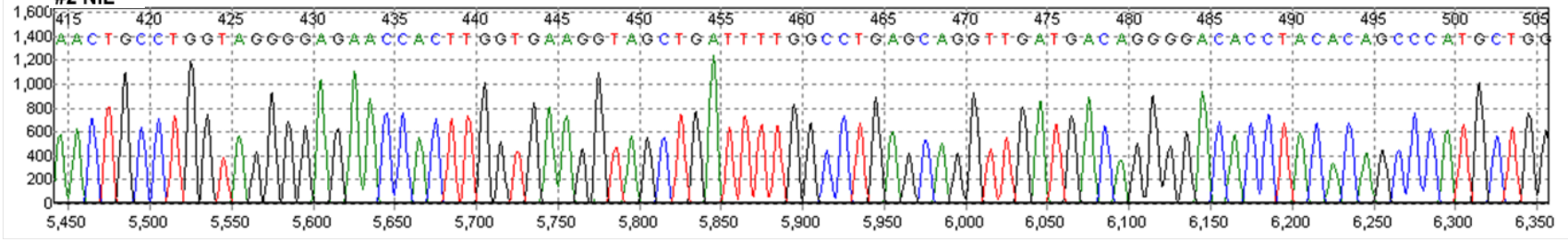




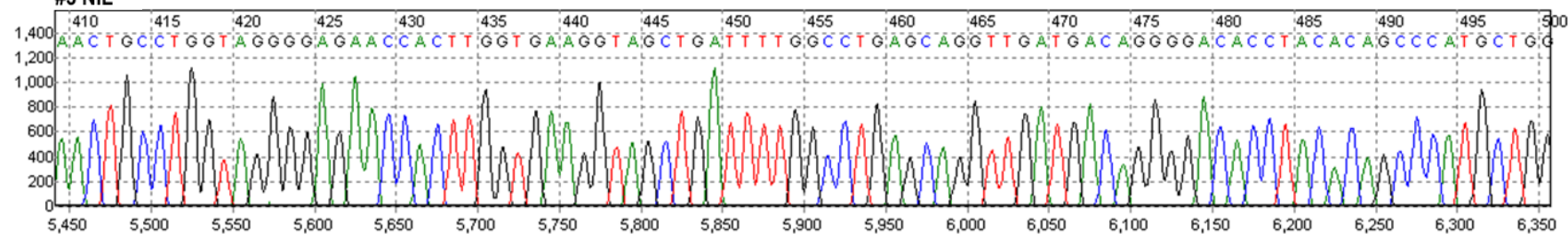
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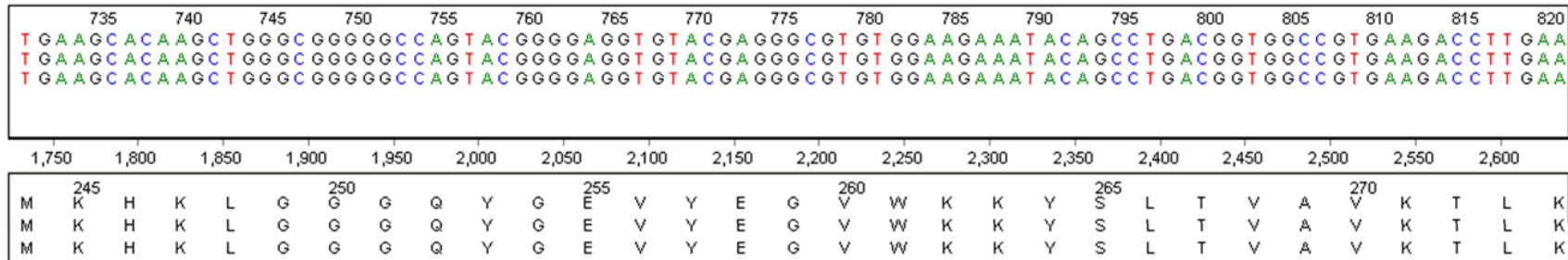


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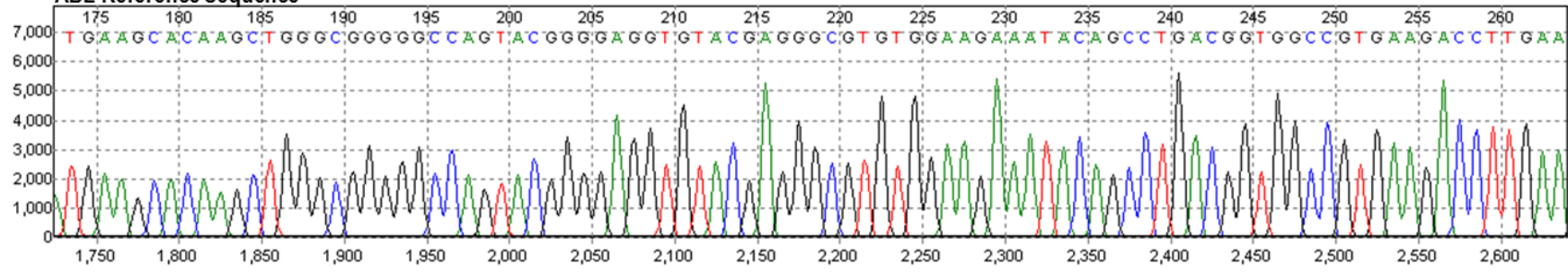


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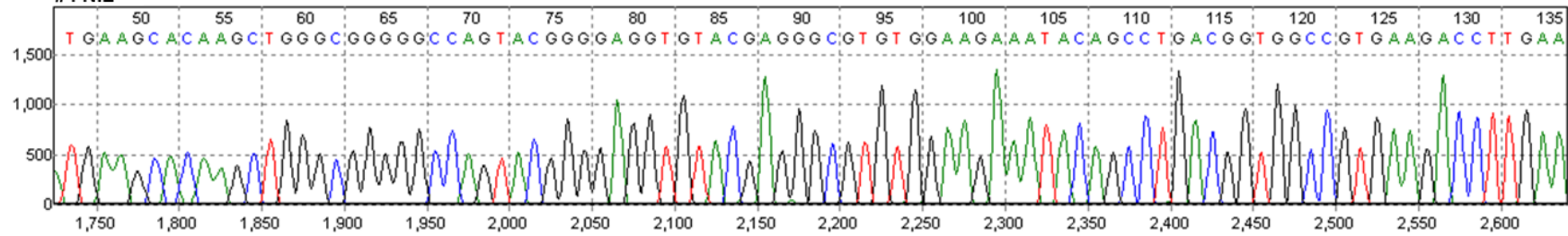




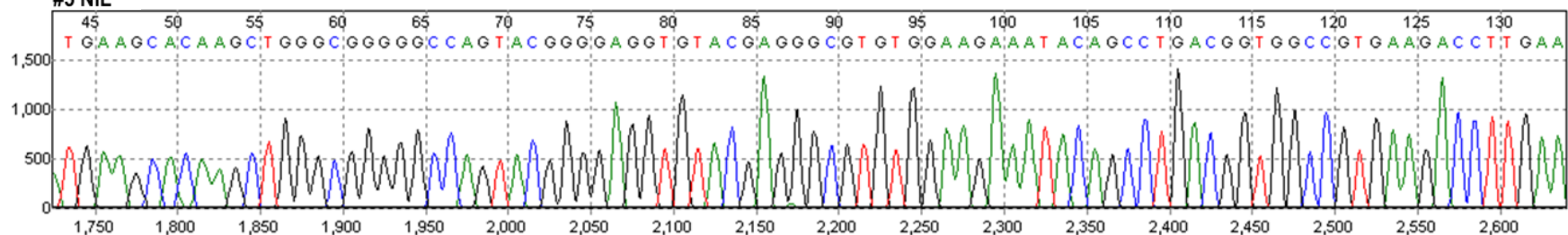
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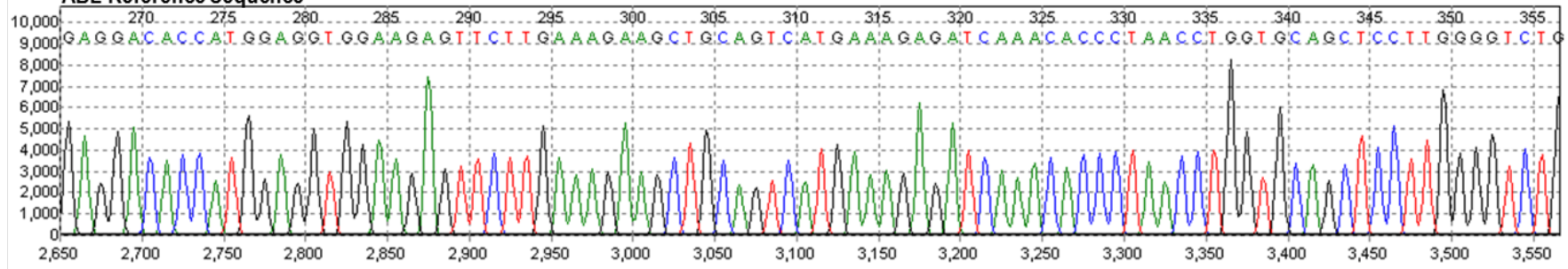


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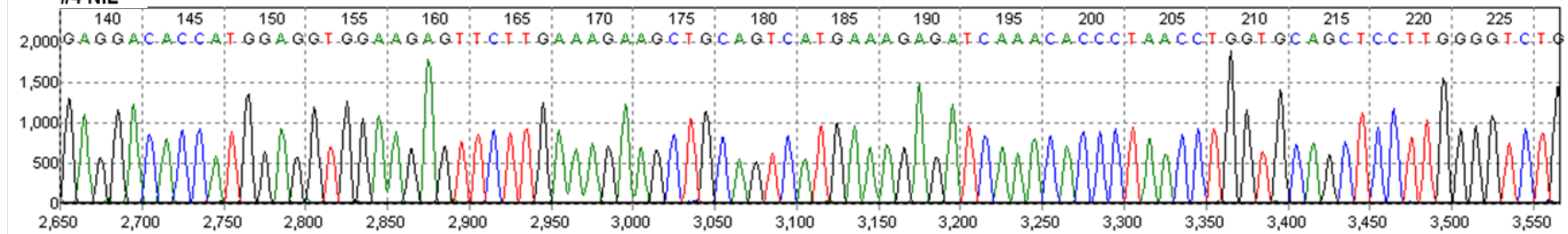
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275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355
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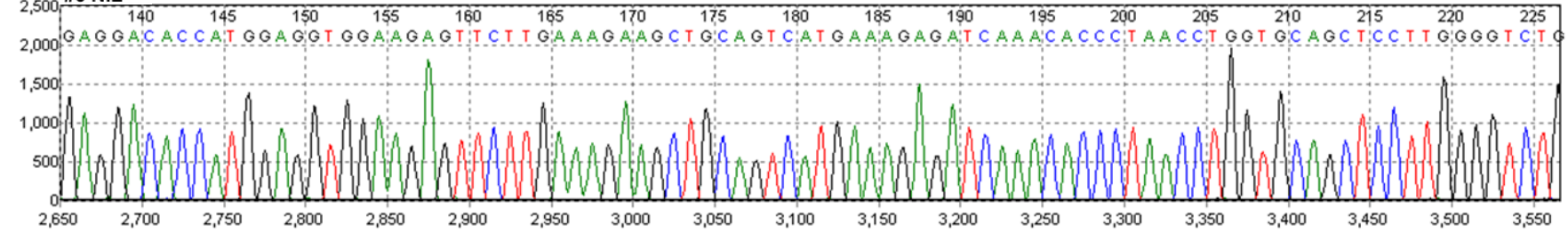
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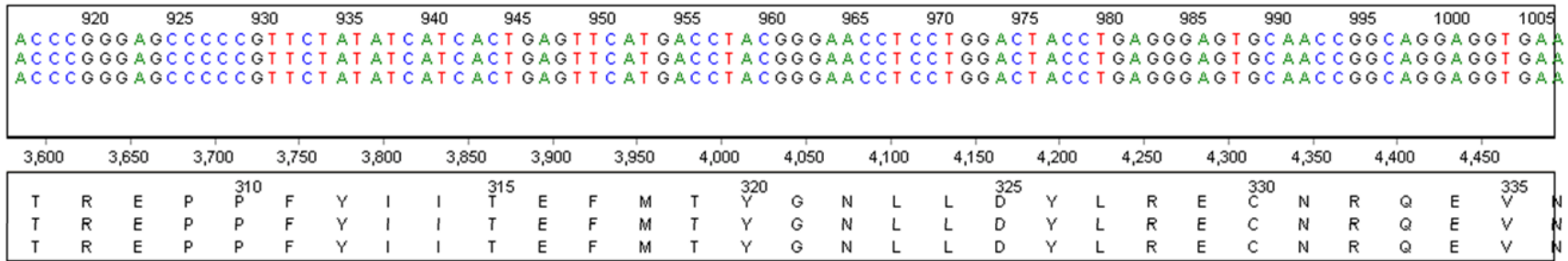


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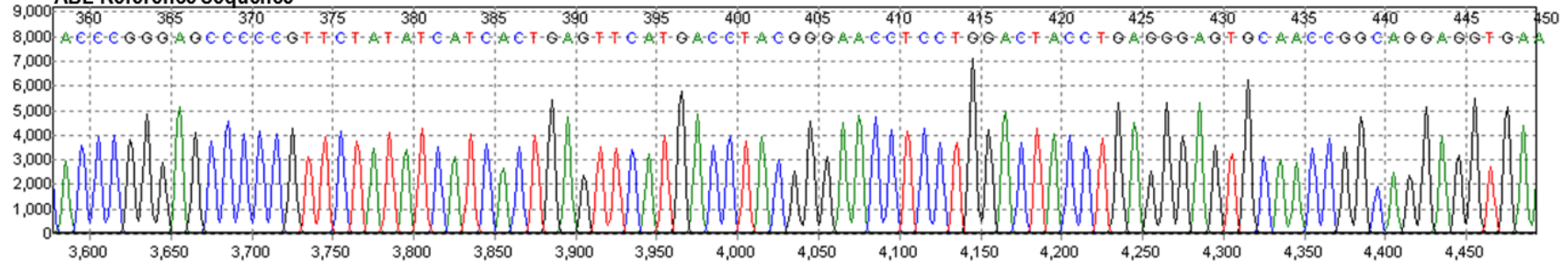


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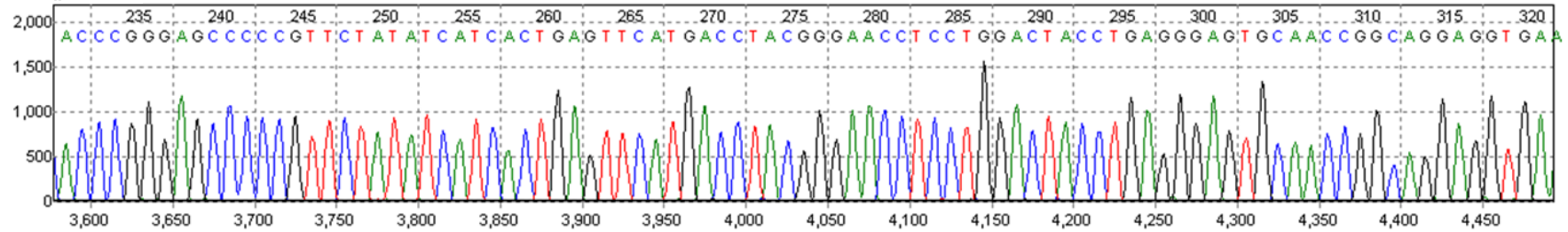




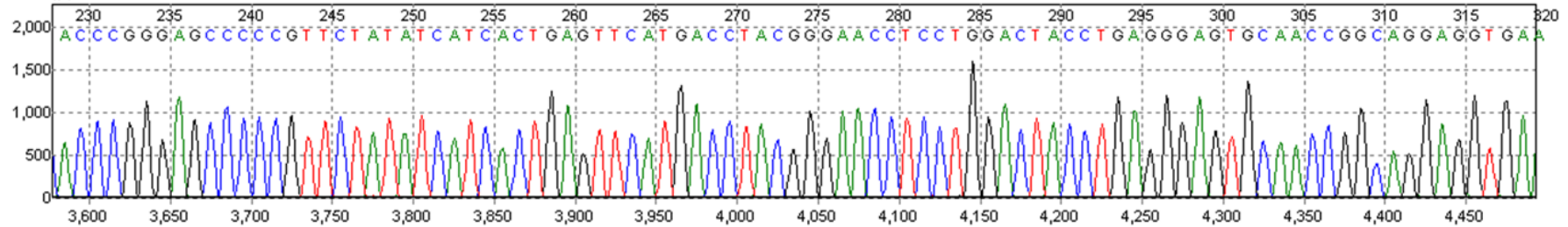
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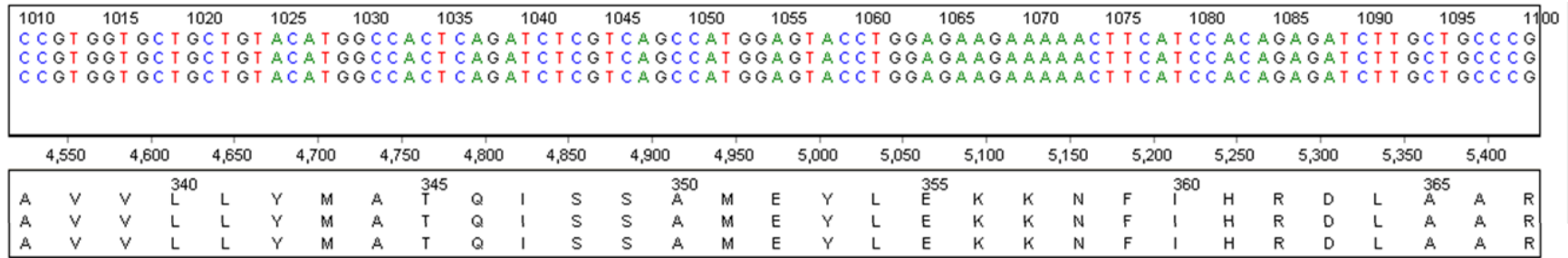


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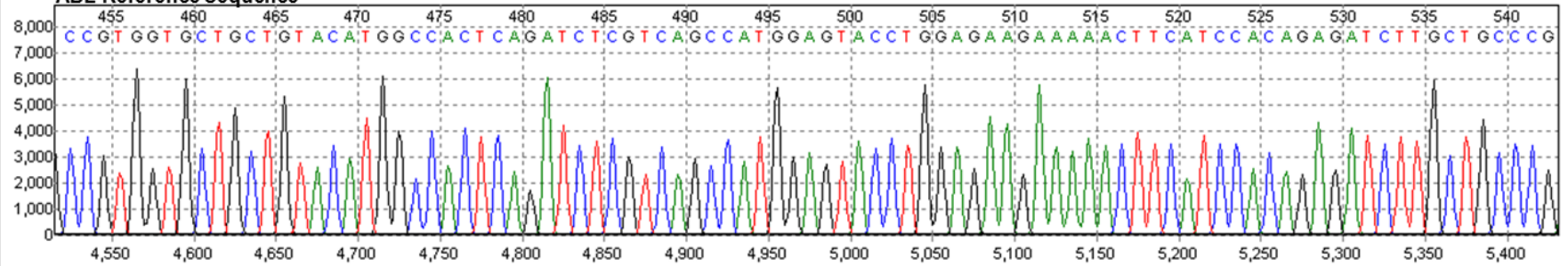


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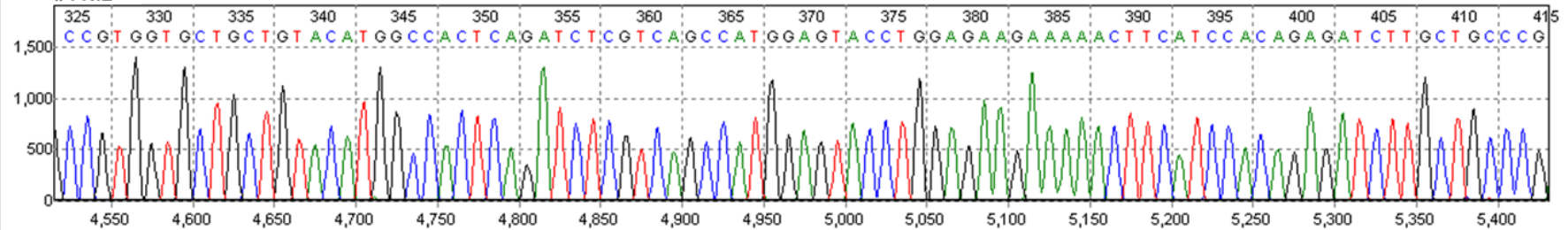




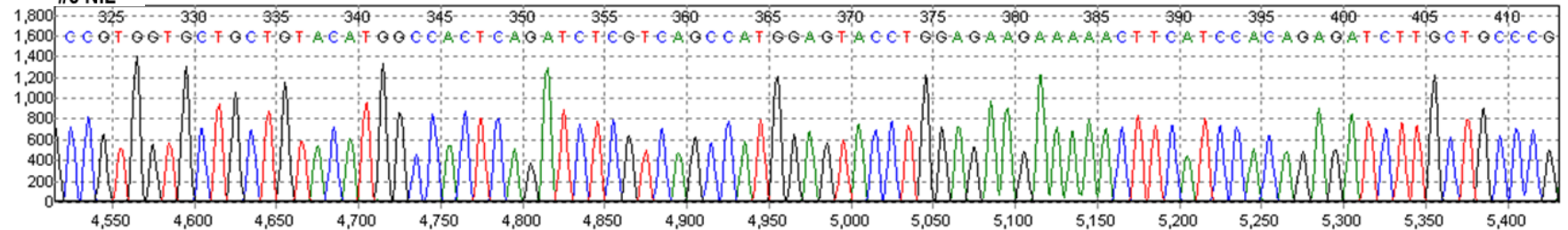
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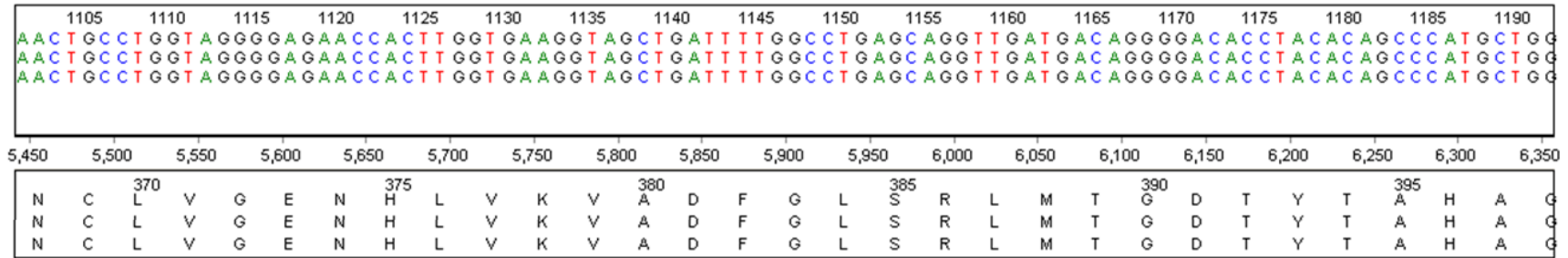


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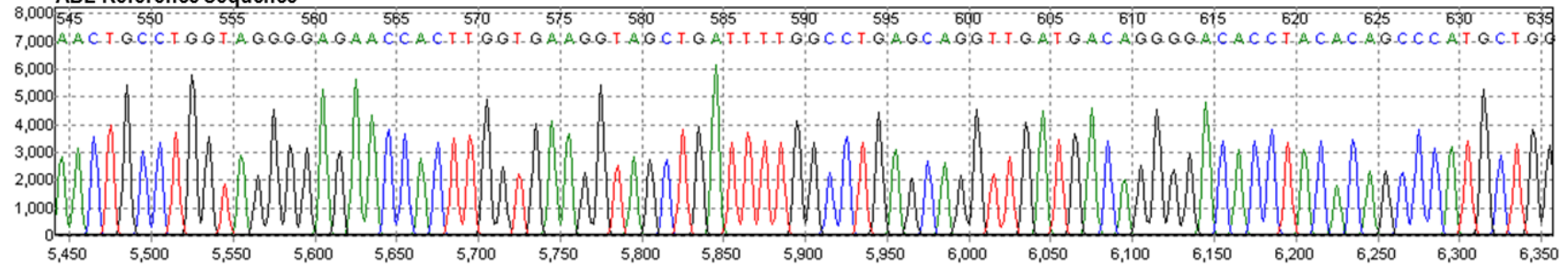


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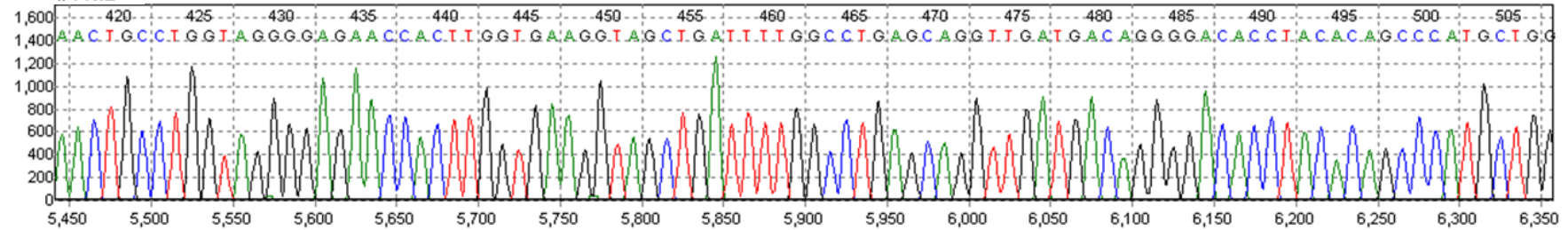




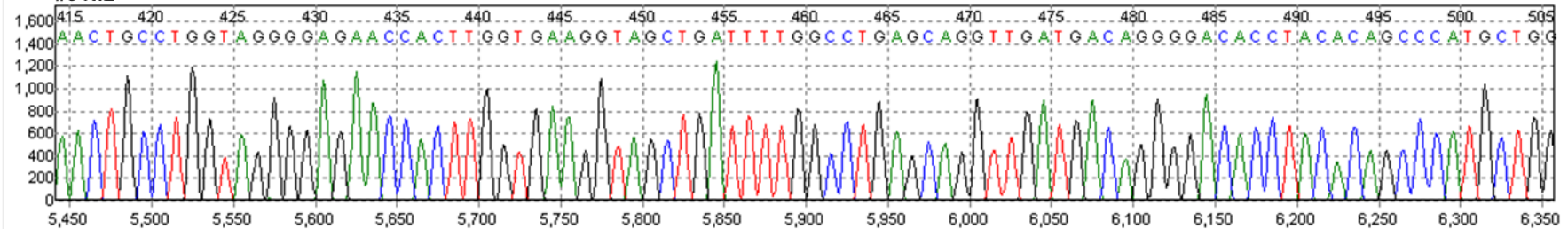
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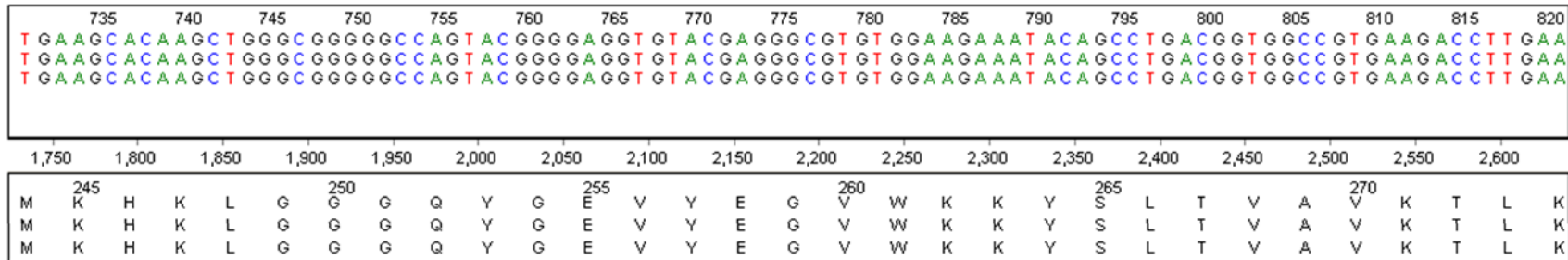


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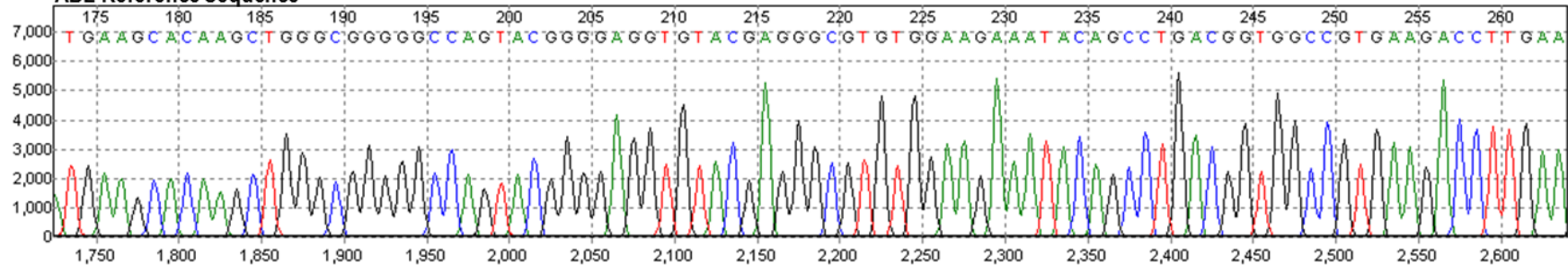


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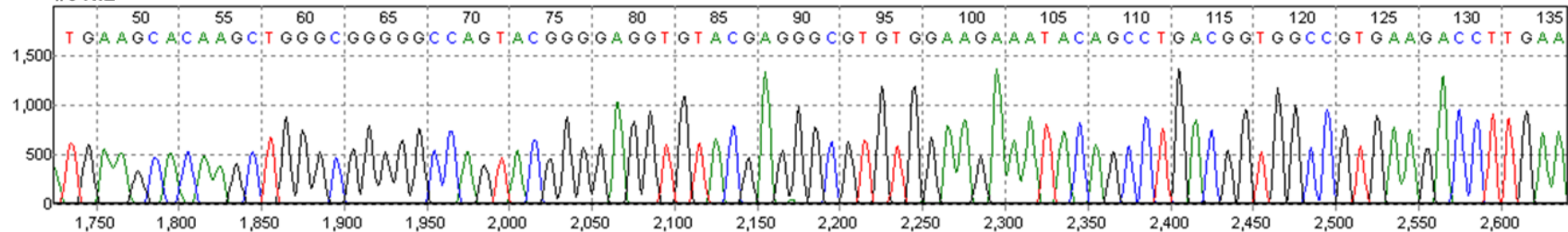




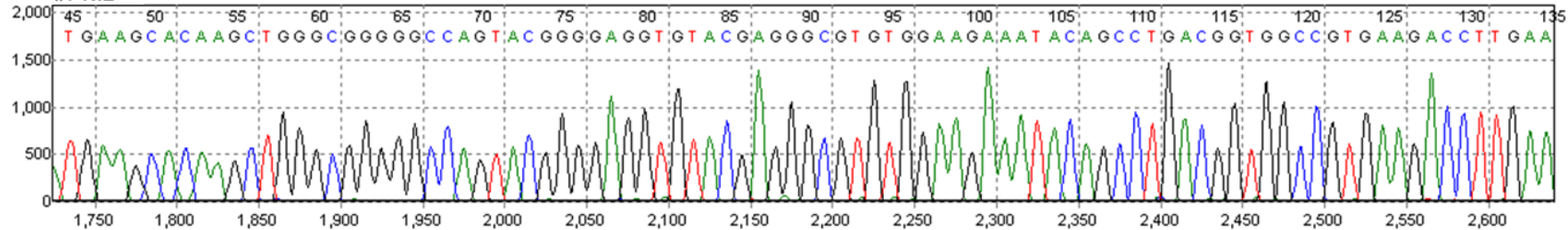
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#6 NIL



#7 NIL

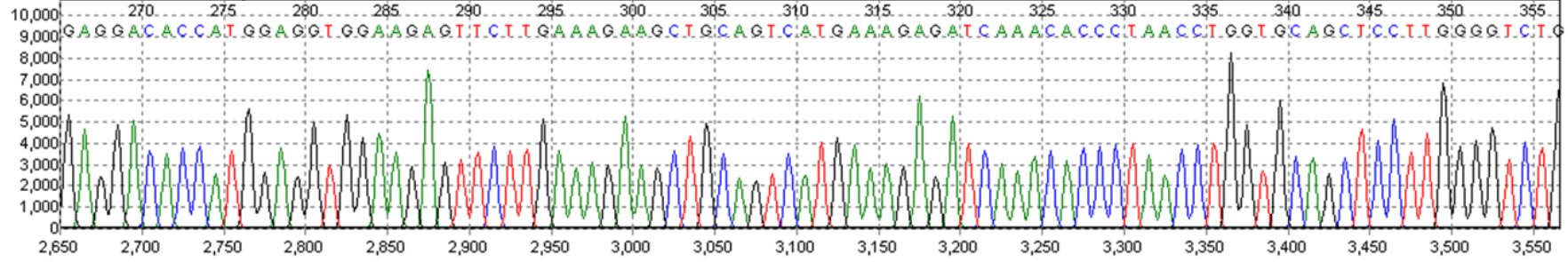


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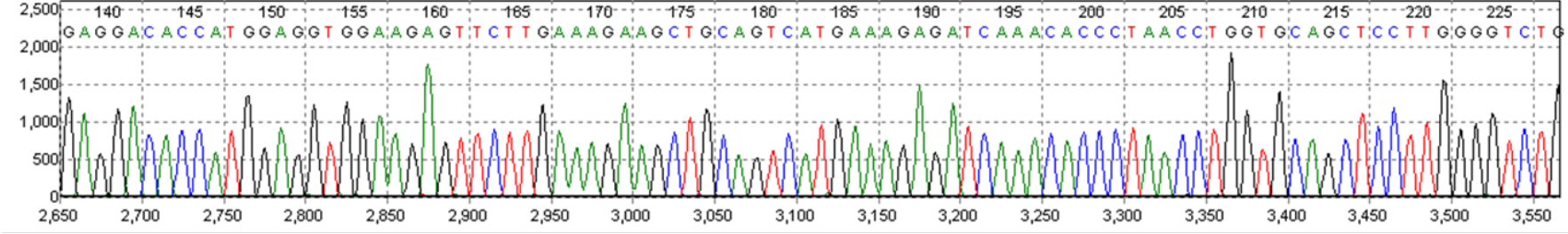
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 E D T M E V E E F L K E A A V M K E I K H P N L V Q L L G V C
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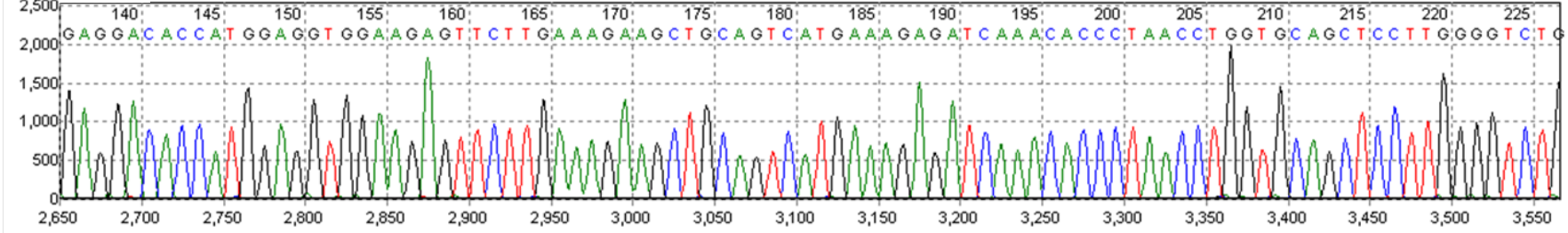
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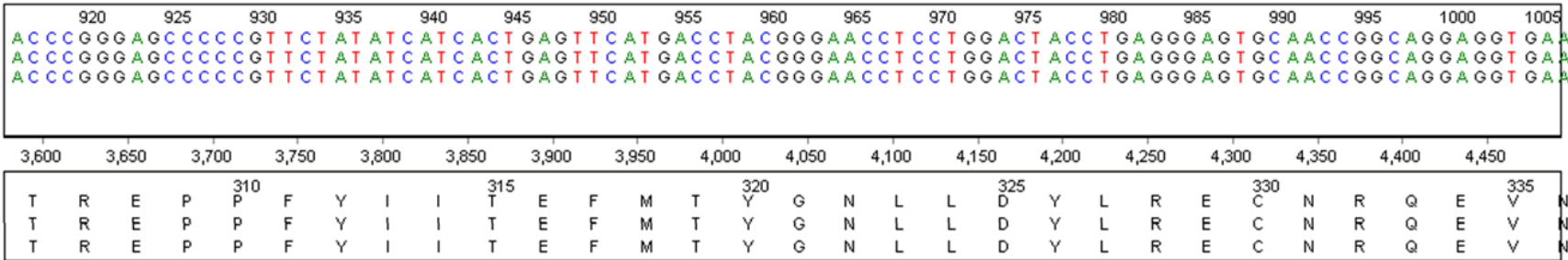


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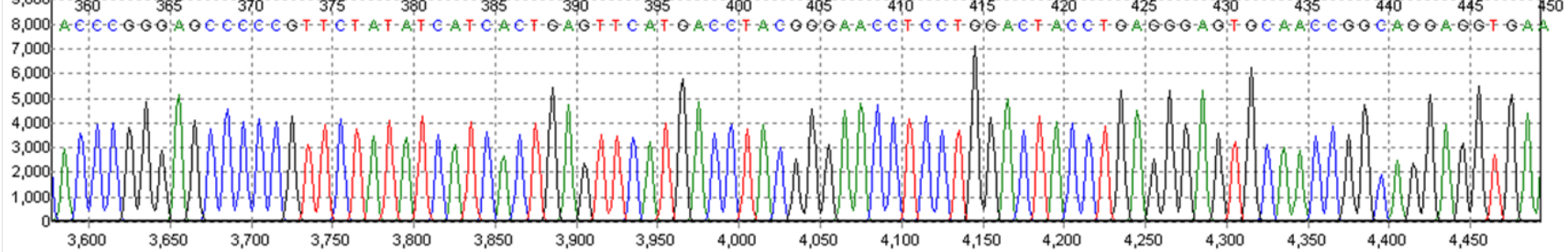


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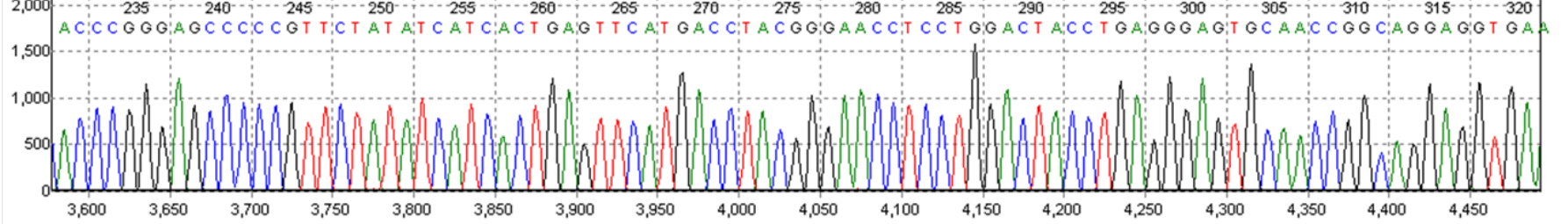




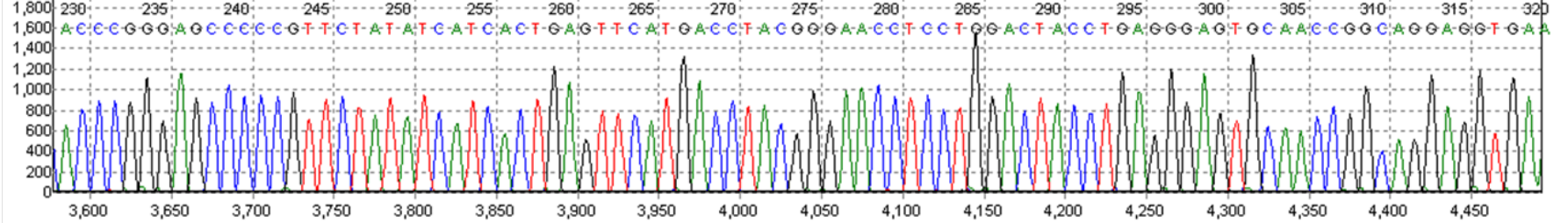
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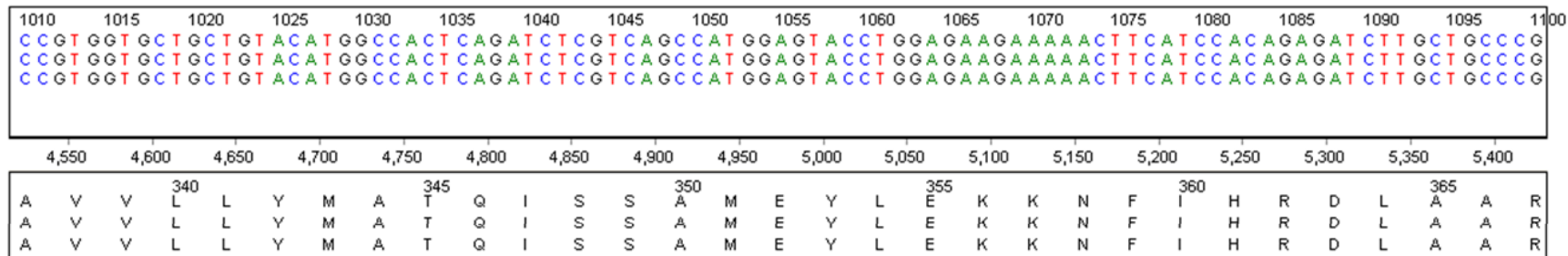


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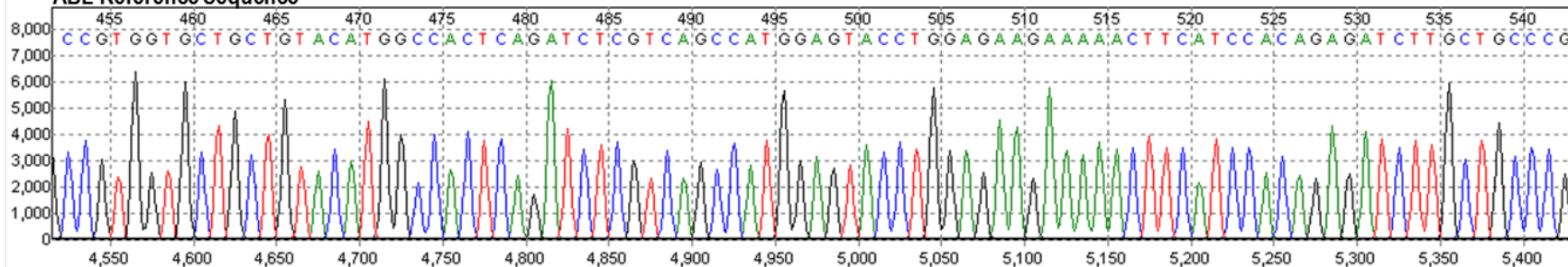


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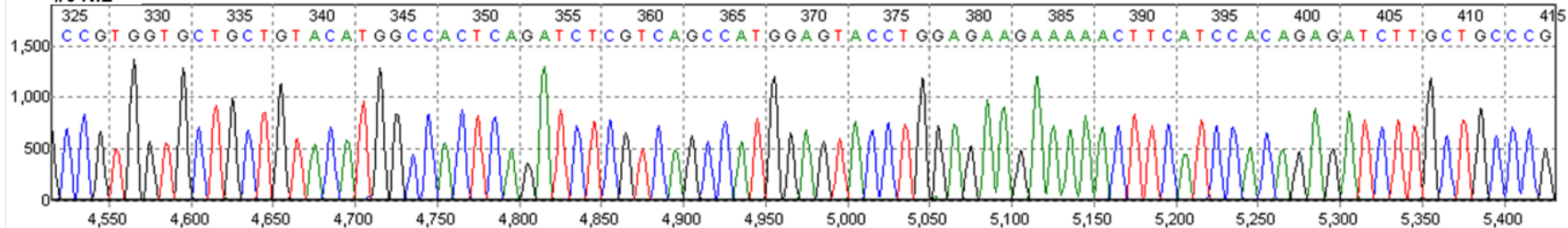




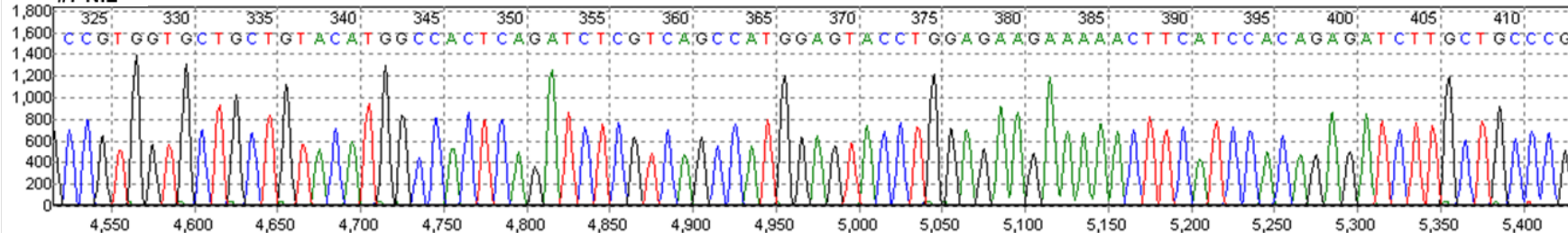
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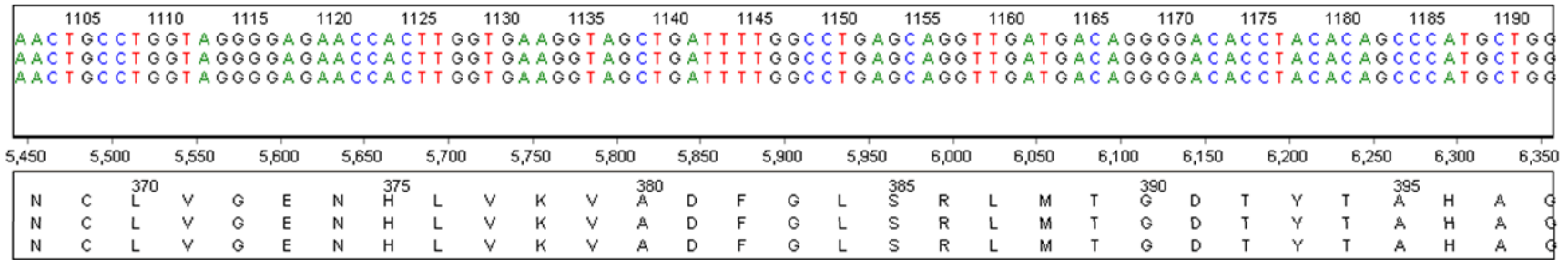


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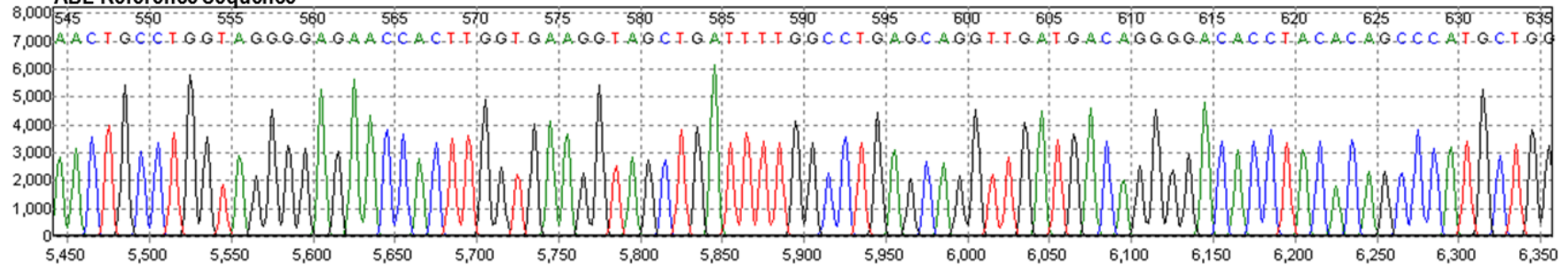


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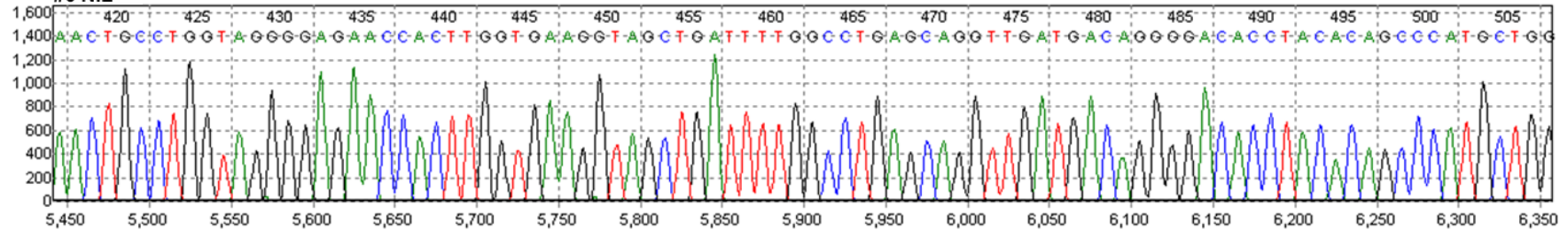




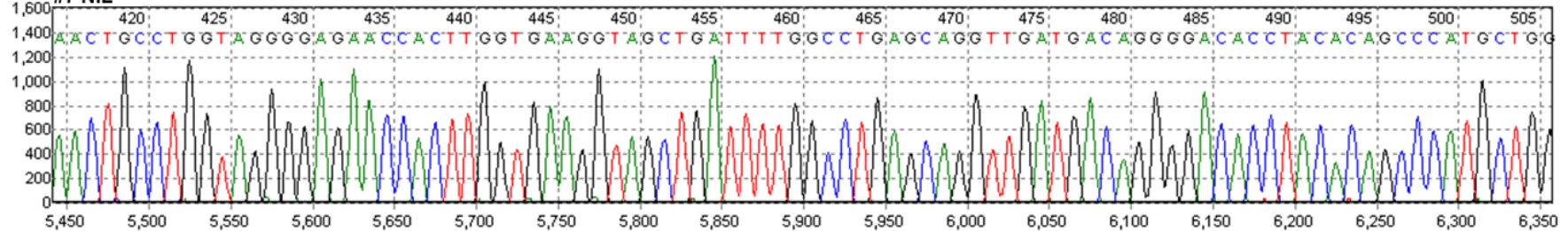
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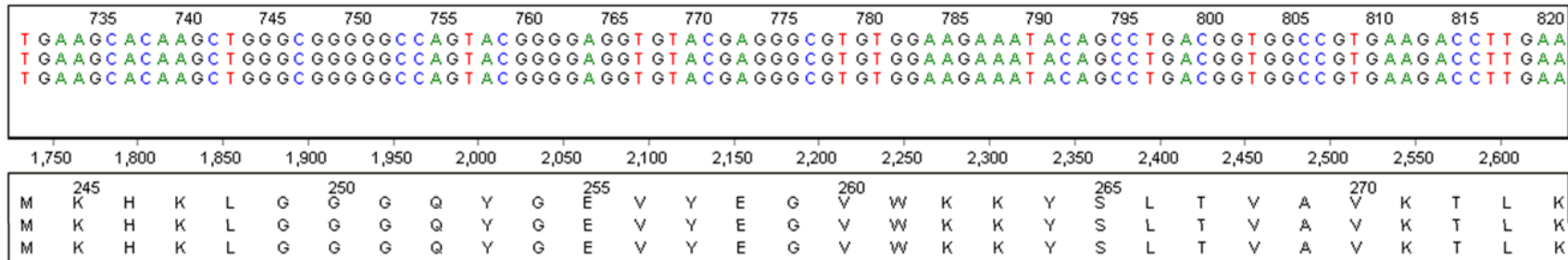


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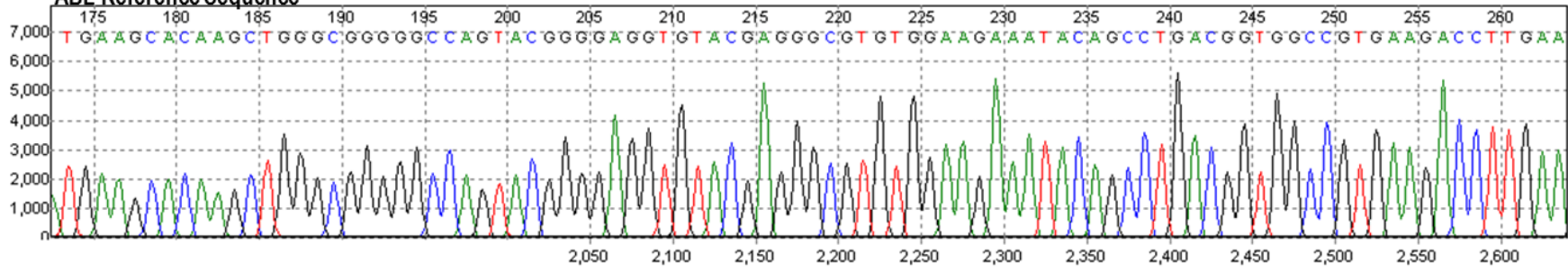


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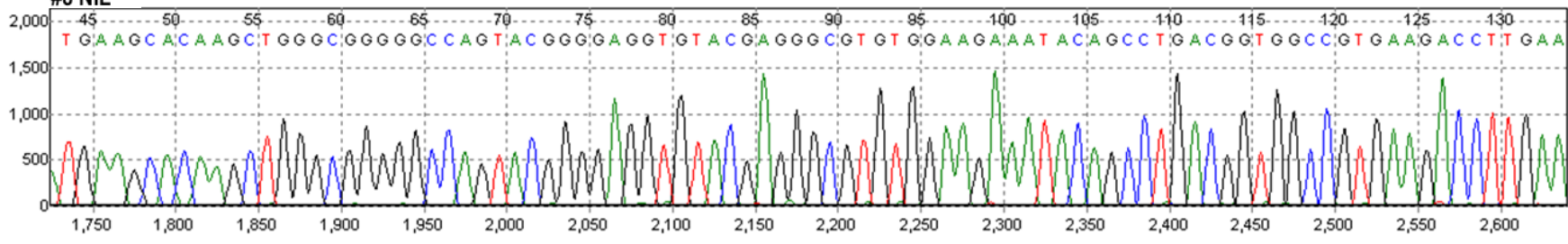




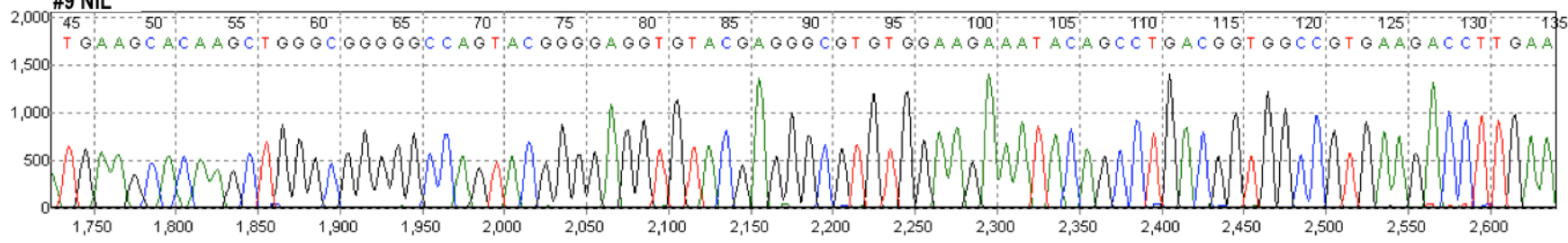
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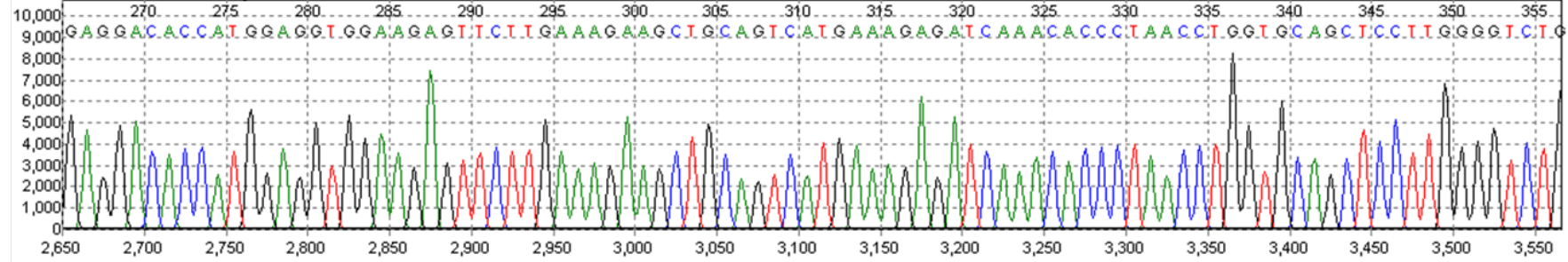


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 G A G G A C A C C A T G G A G G T G G A A G A G T T C T T G A A A G A A G C T G C A G T C A T G A A A G A G A T C A A A C A C C C T A A C C T G G T G C A G C T C C T T G G G G T C T G
 G A G G A C A C C A T G G A G G T G G A A G A G T T C T T G A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

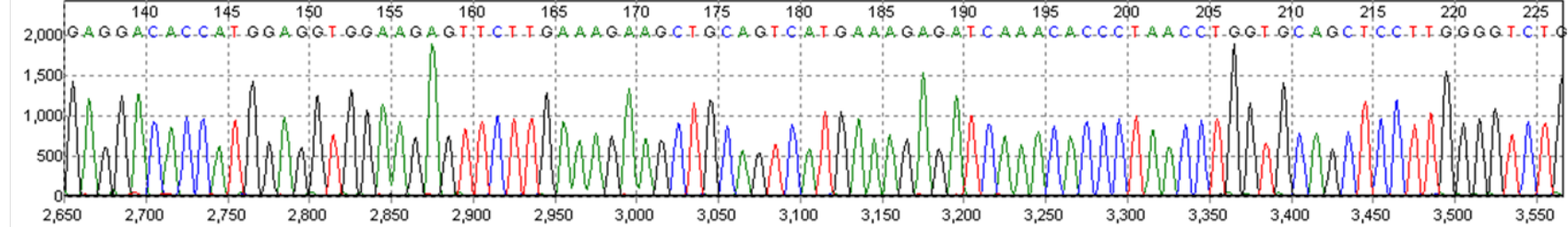
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275 280 285 290 295 300 305
 E D T M E V E E F L K E A A V M K E I K H P N L V Q L L G V C
 E D T M E V E E F L K E A A V M K E I K H P N L V Q L L G V C
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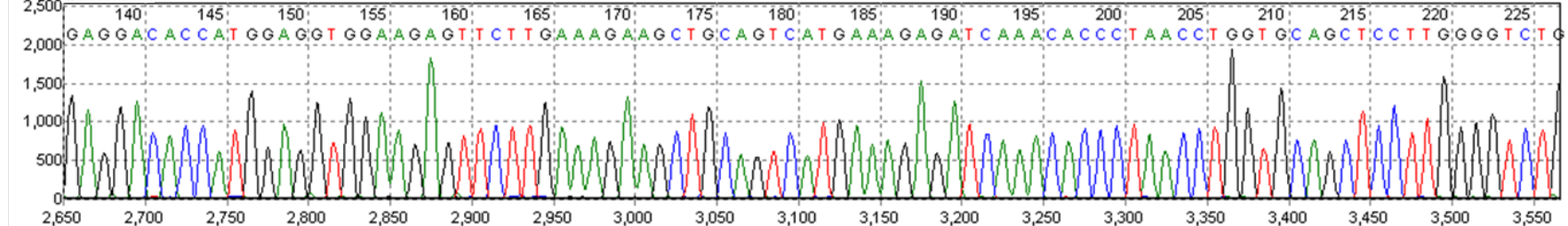
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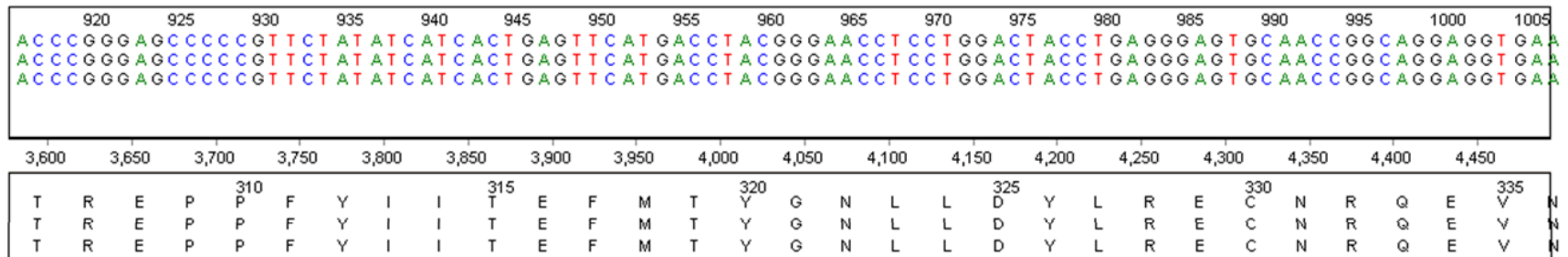


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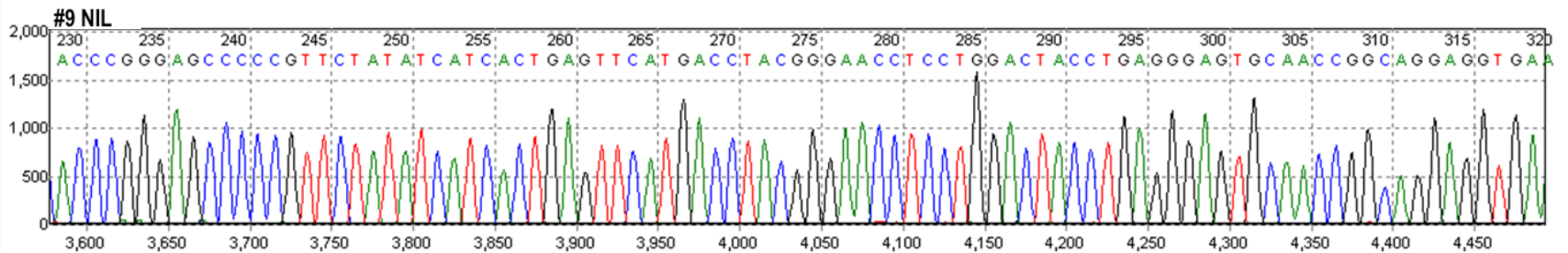
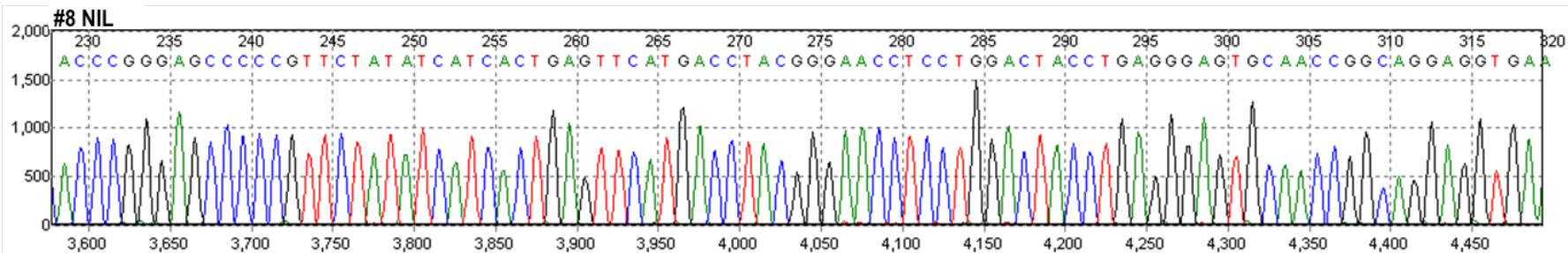
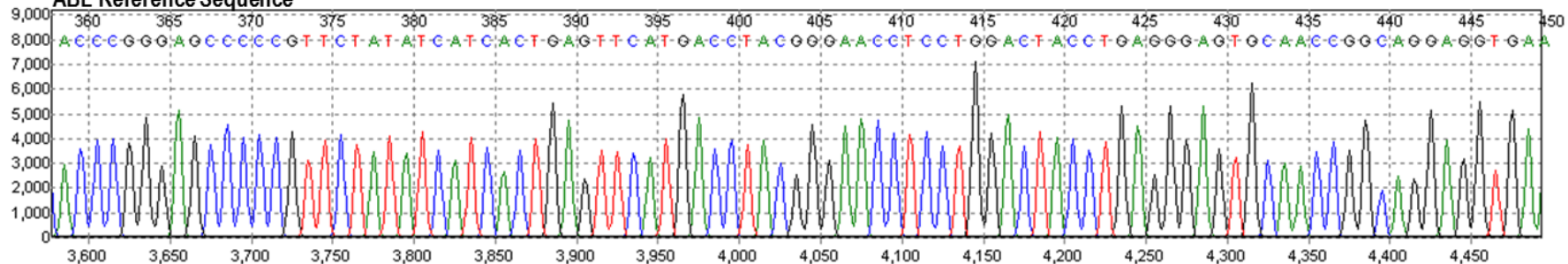


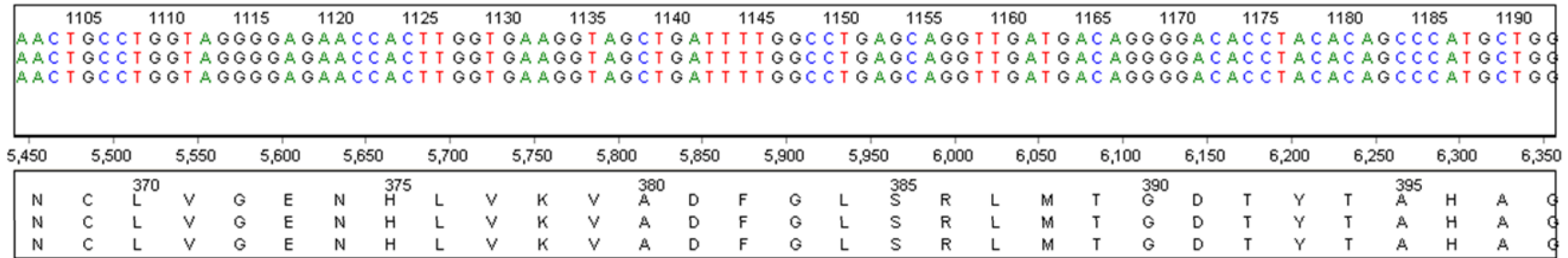
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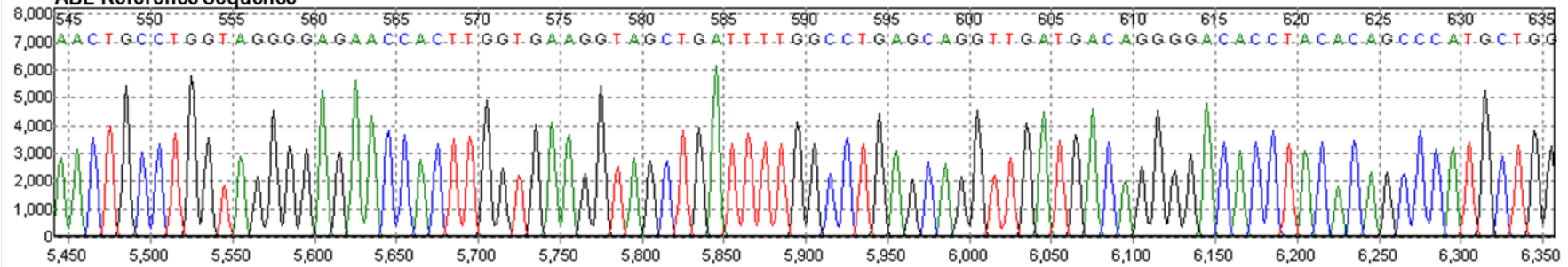


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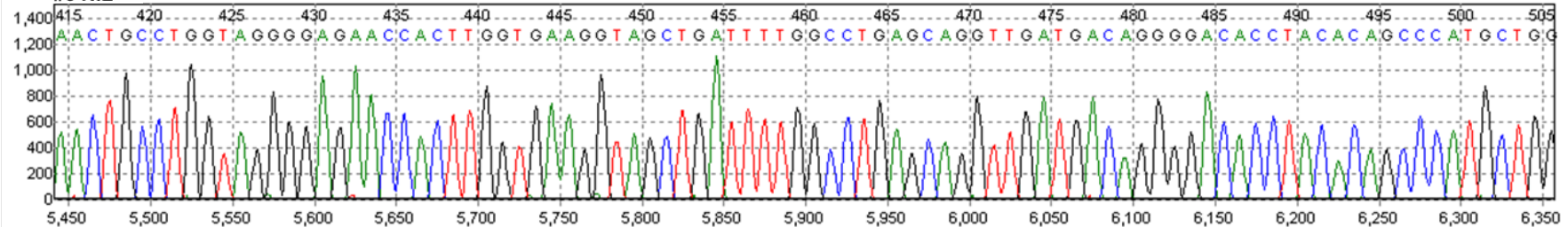




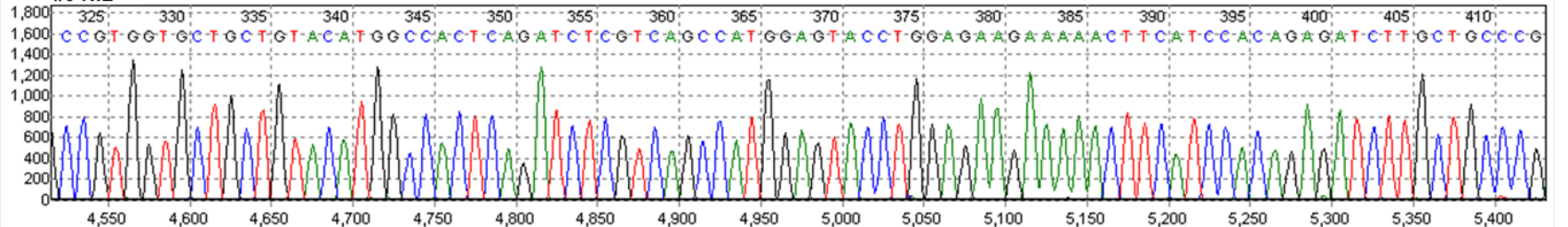
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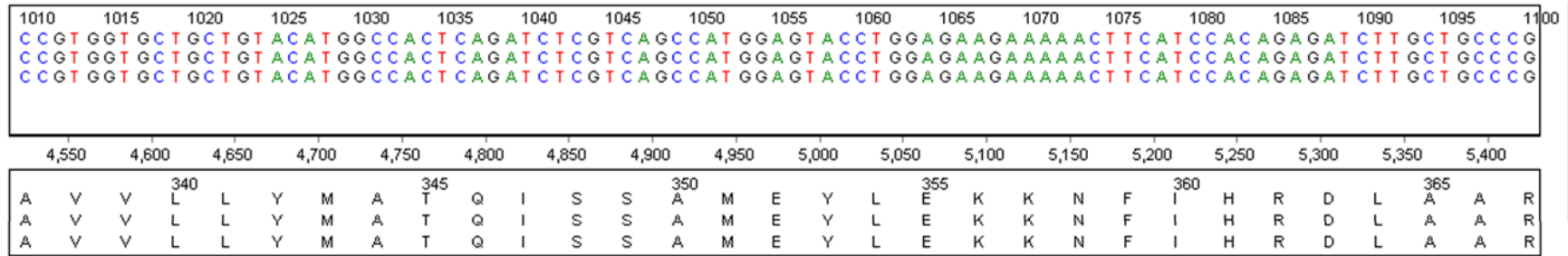


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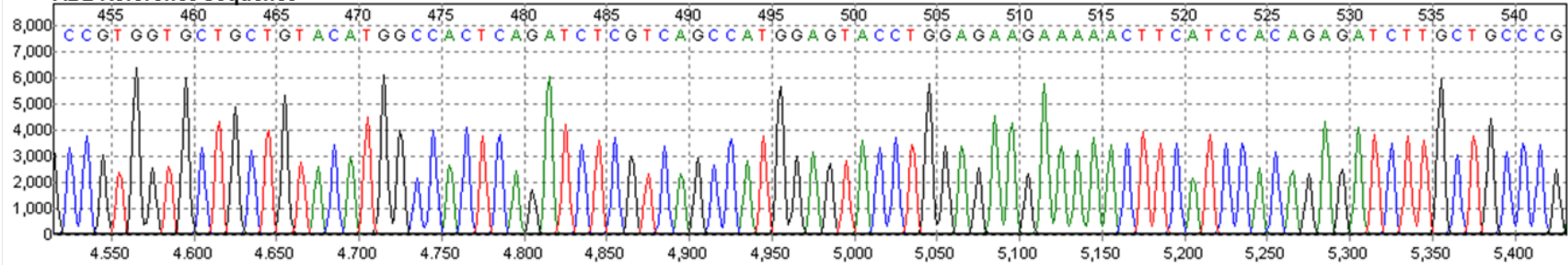


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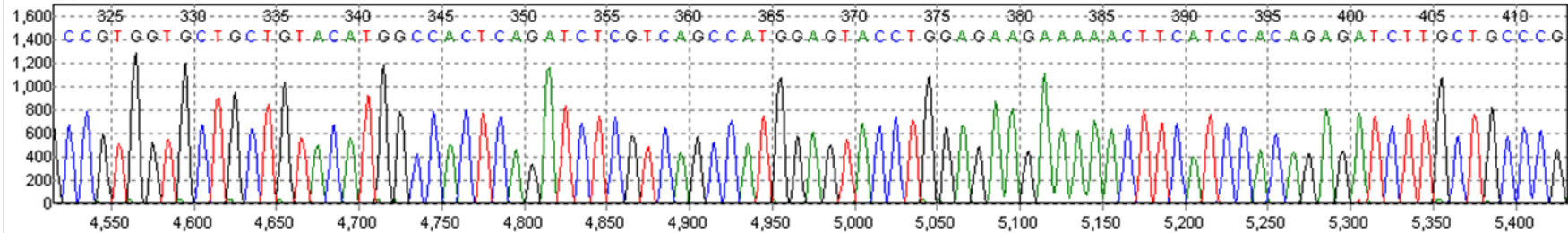




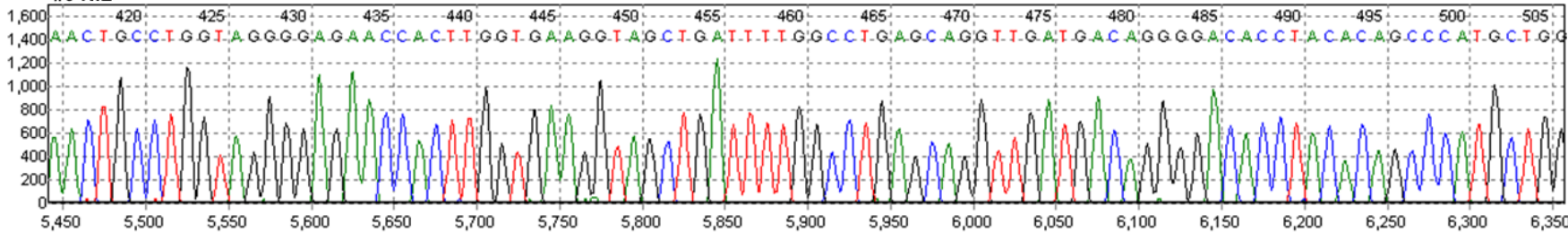
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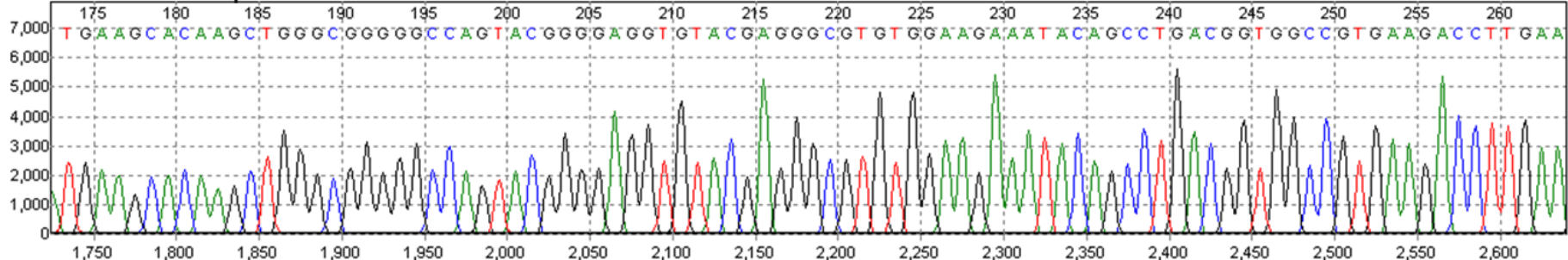
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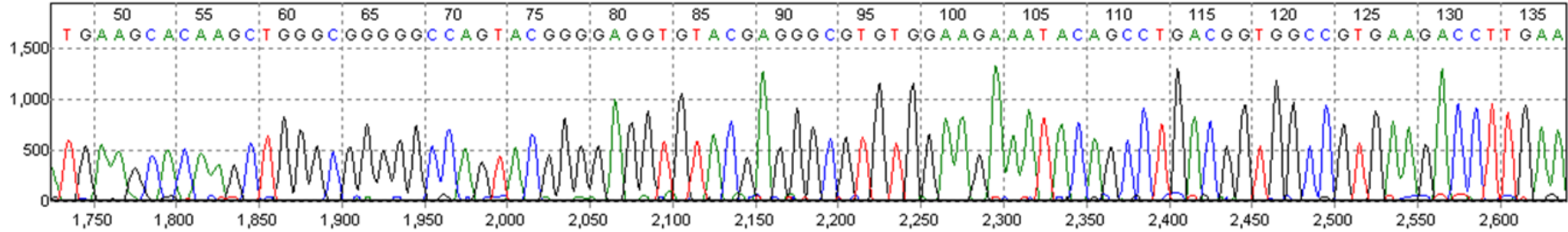
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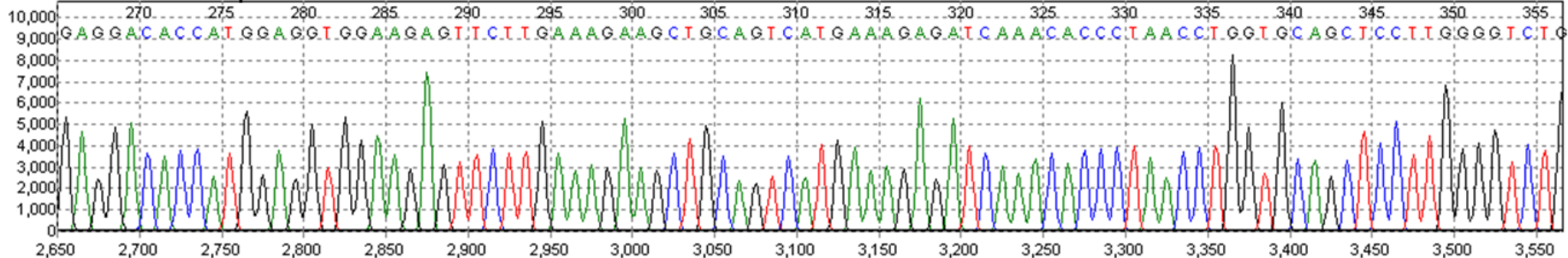


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 G A G G A C A C C A T G G A G G T G G A A G A G T T C T T G A A A G A A G C T G C A G T C A T G A A A G A G A T C A A A C A C C C T A A C C T G G T G C A G C T C C T T G G G G T C T G
 G A G G A C A C C A T G G A G G T G G A A G A G T T C T T G A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

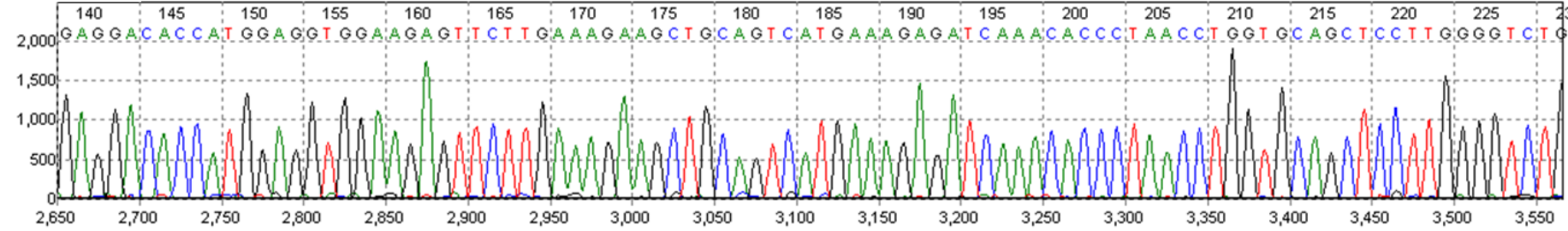
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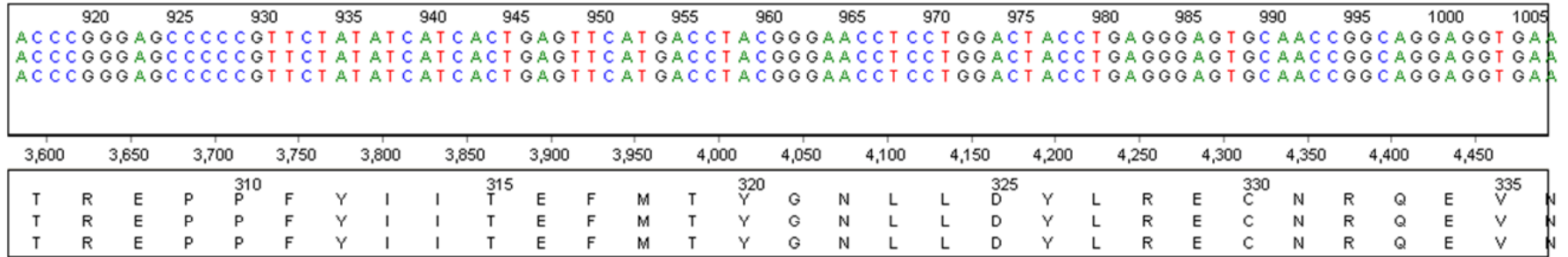
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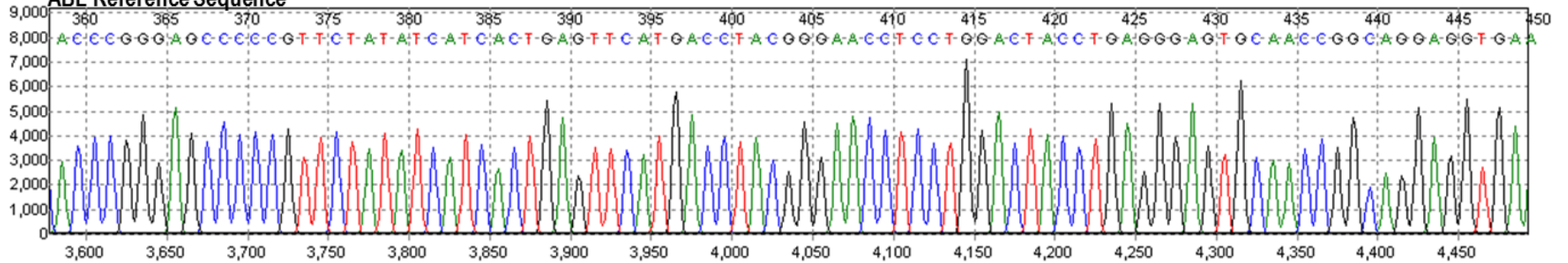


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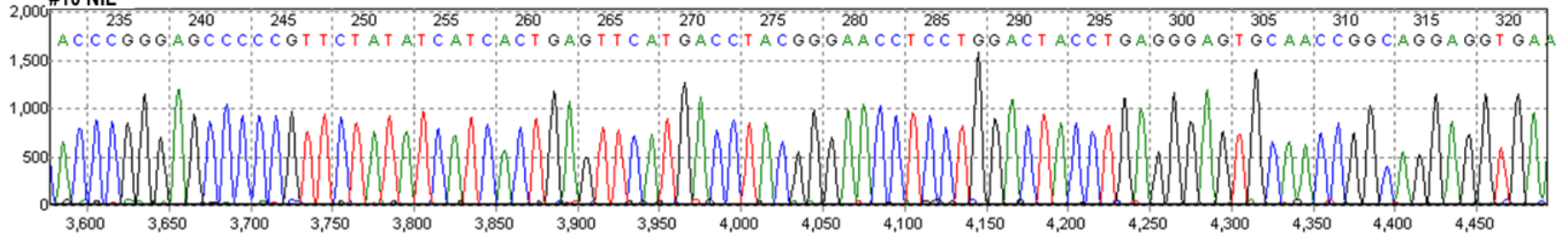


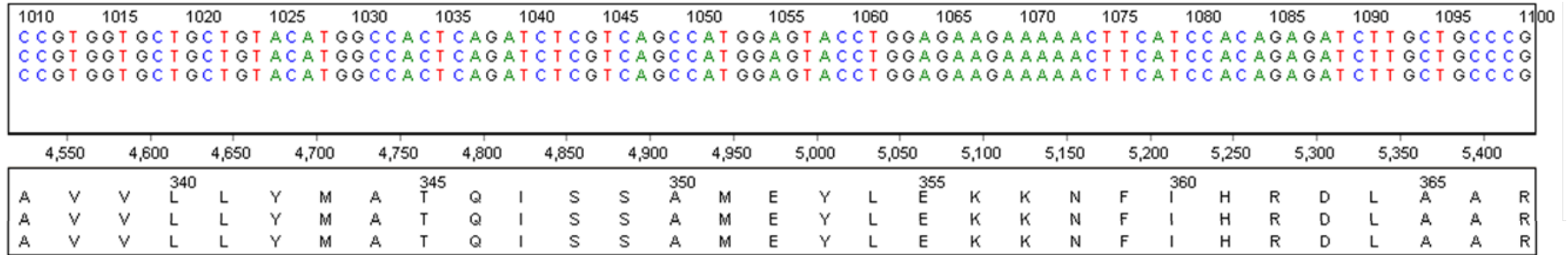


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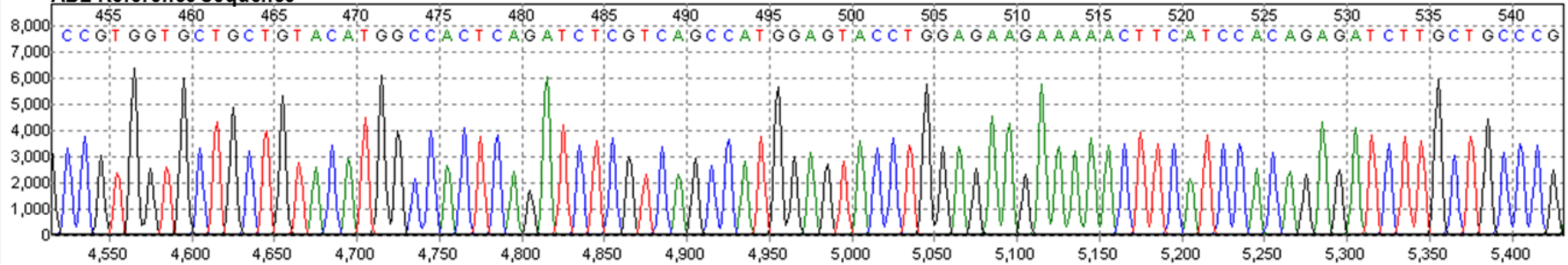


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ABL Reference Sequence



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