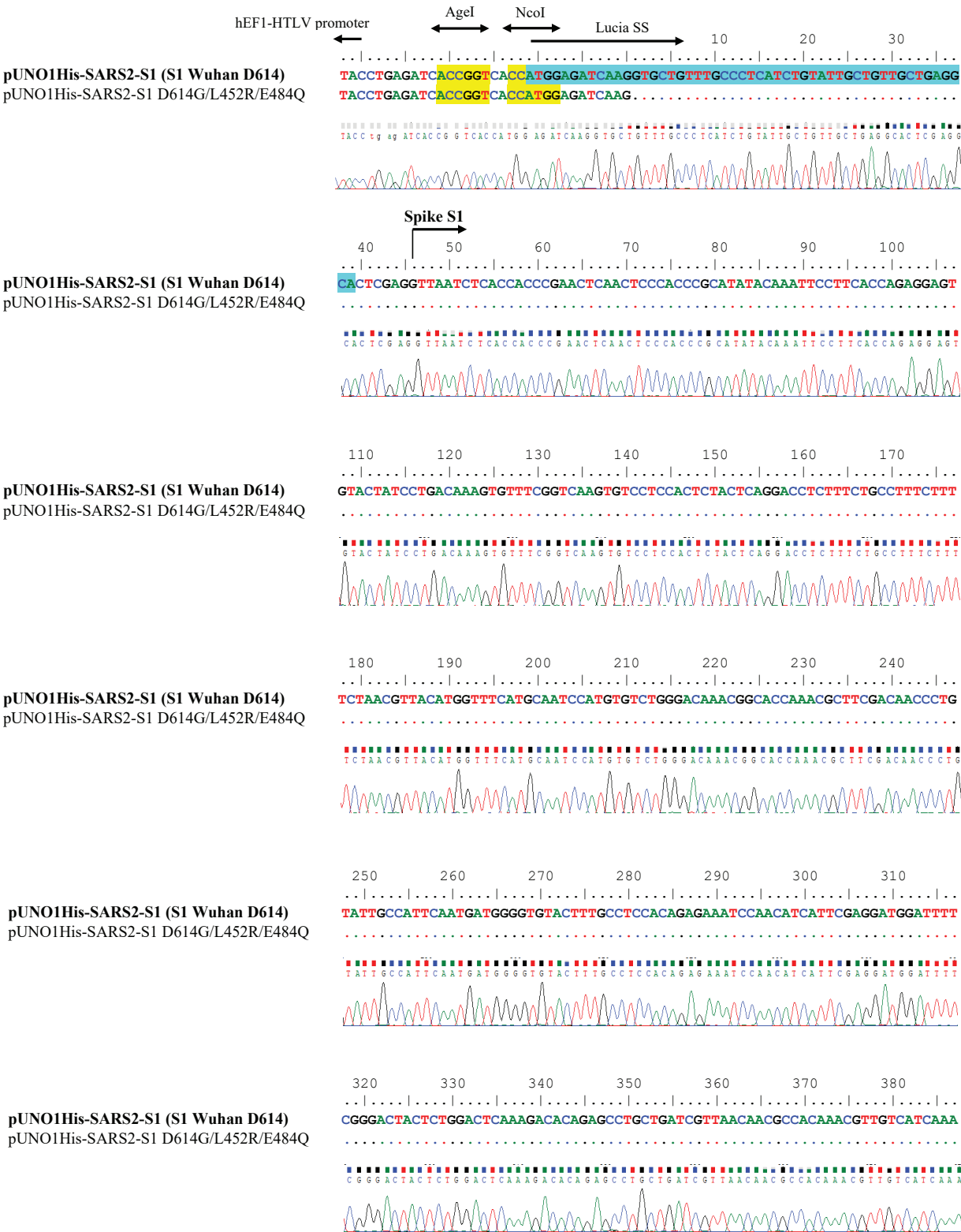
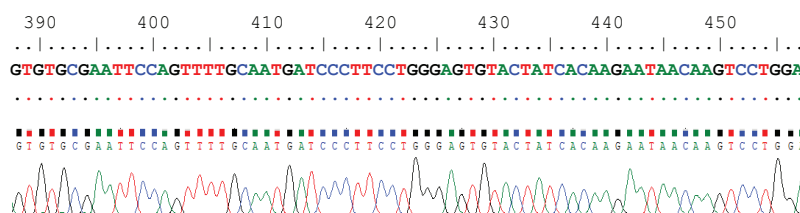


Supplementary 1.

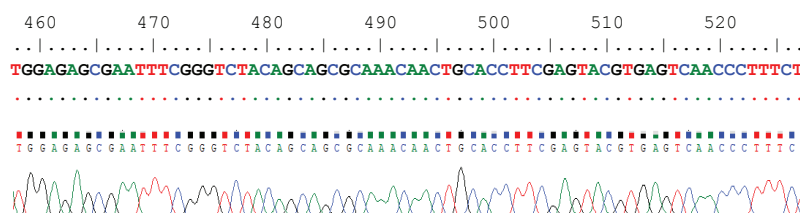
Nucleotide alignment of codon-optimized mutated pUNO1His-SARS2-S1 D614G/L452R/E484Q against the original plasmid.



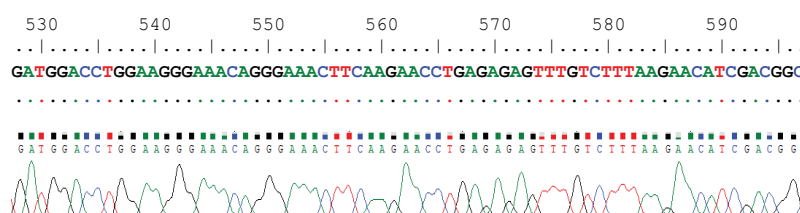
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pUNO1His-SARS2-S1 D614G/L452R/E484Q



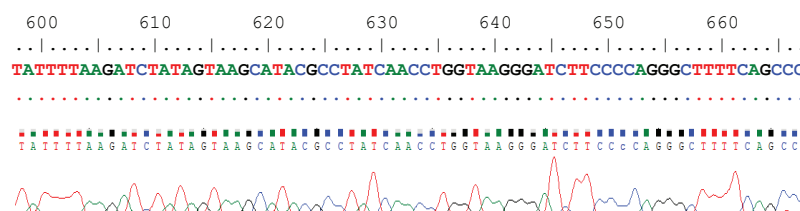
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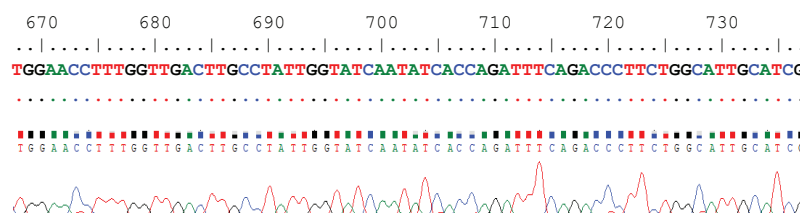
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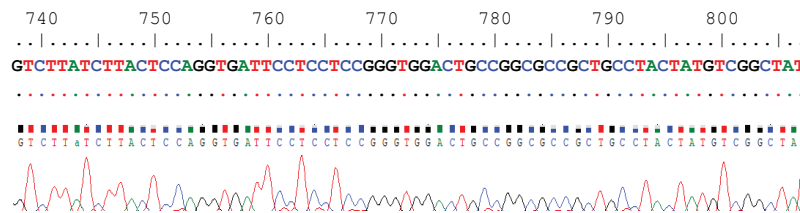
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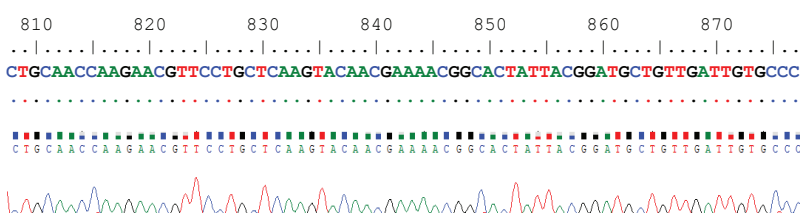
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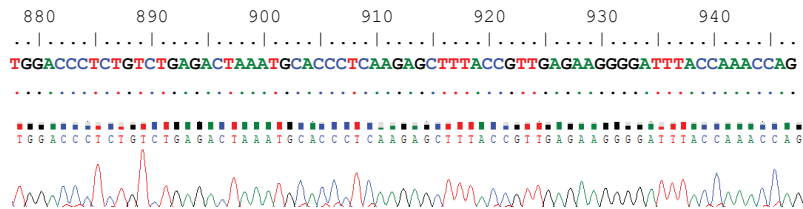
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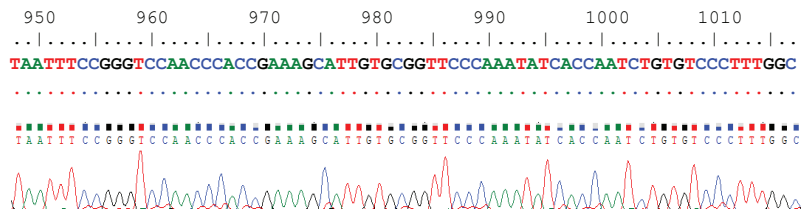
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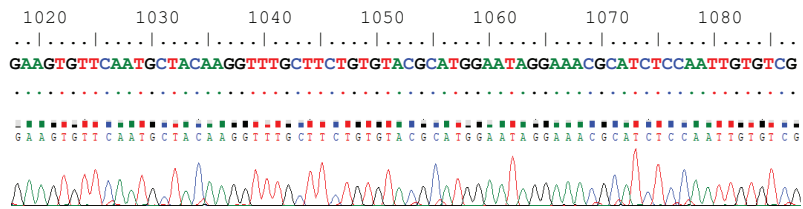
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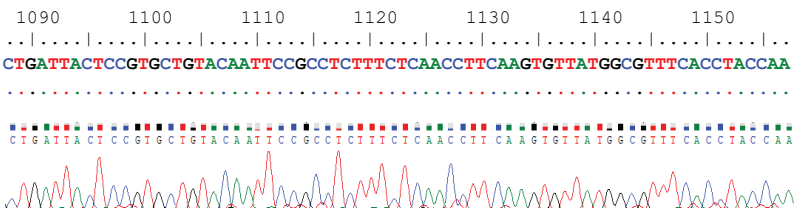
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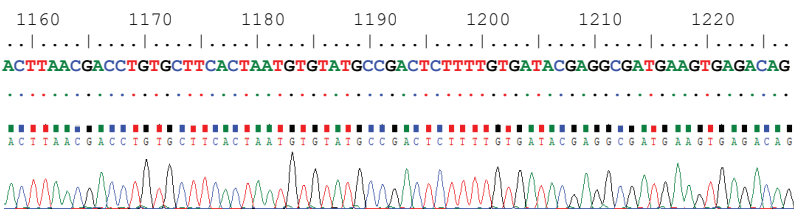
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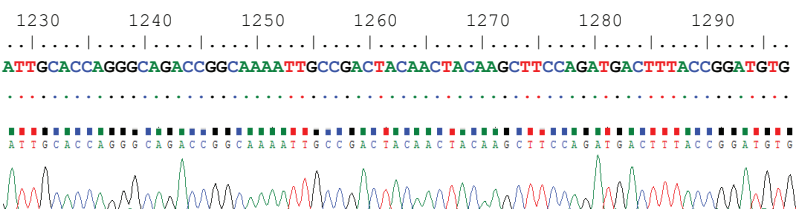
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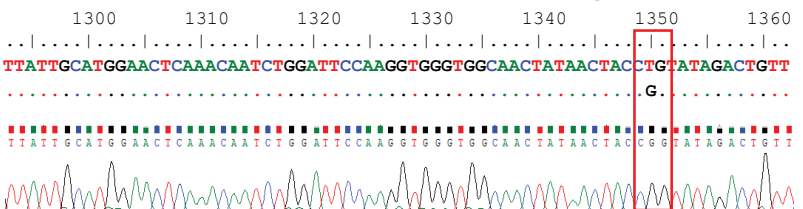
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pUNO1His-SARS2-S1 D614G/L452R/E484Q



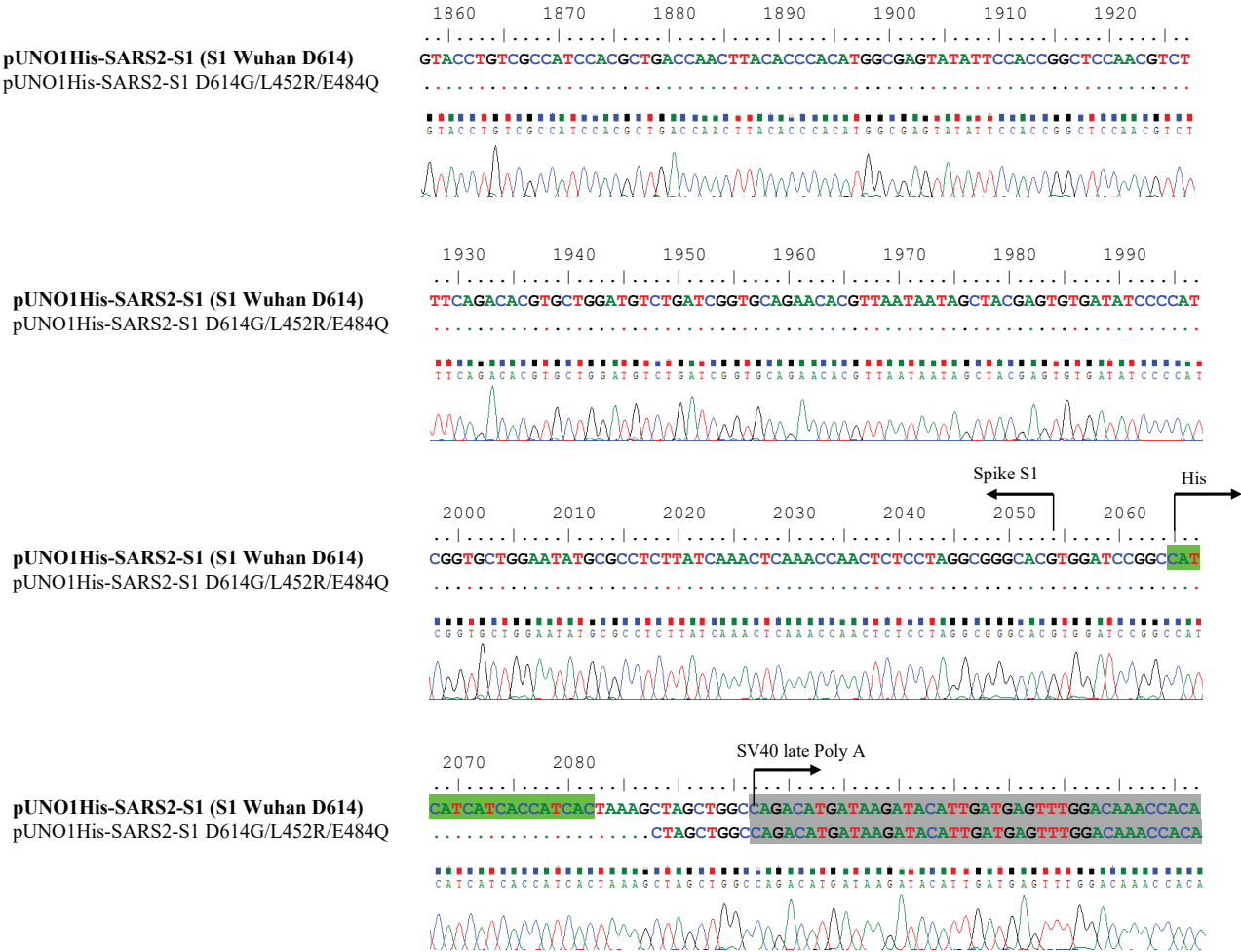
pUNO1His-SARS2-S1 (S1 Wuhan D614)
pUNO1His-SARS2-S1 D614G/L452R/E484Q



pUNO1His-SARS2-S1 (S1 Wuhan D614)
pUNO1His-SARS2-S1 D614G/L452R/E484Q







DNA sequence alignment of commercially available pUNO1His-SARS2-S1 (S1 Wuhan D614) and mutated pUNO1His-SARS2-S1 D614G/L452R/E484Q generated by site-directed mutagenesis. The alignment was performed using the ClustalW multiple alignment. A sequence chromatogram of mutated pUNO1His-SARS2-S1 D614G/L452R/E484Q was included. A red box indicates the mutation site. The hEF1-HTLV promoter, Lucia SS and SV40 late poly A were identified in mutated plasmid 5' and 3'-ends sequence, validated the original plasmid pUNO1His-SARS2-S1 (S1 Wuhan D614).