

A petri dish held by a gloved hand, showing a bacterial culture with numerous small, yellowish, circular colonies arranged in a grid pattern. The colonies are on a light-colored agar surface. The petri dish is held at an angle, showing the top and side. The background is blurred, showing a laboratory setting with a blue glove and a white surface.

## Restriction Site Analysis of SARS-CoV-2 Demonstrates the signature of a synthetic virus

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**The likelihood SARS-CoV-2 is a natural sarbecovirus is less than one in a billion based on this analysis**

Steven Quay, MD, PhD, FCAP  
14 Nov 2021

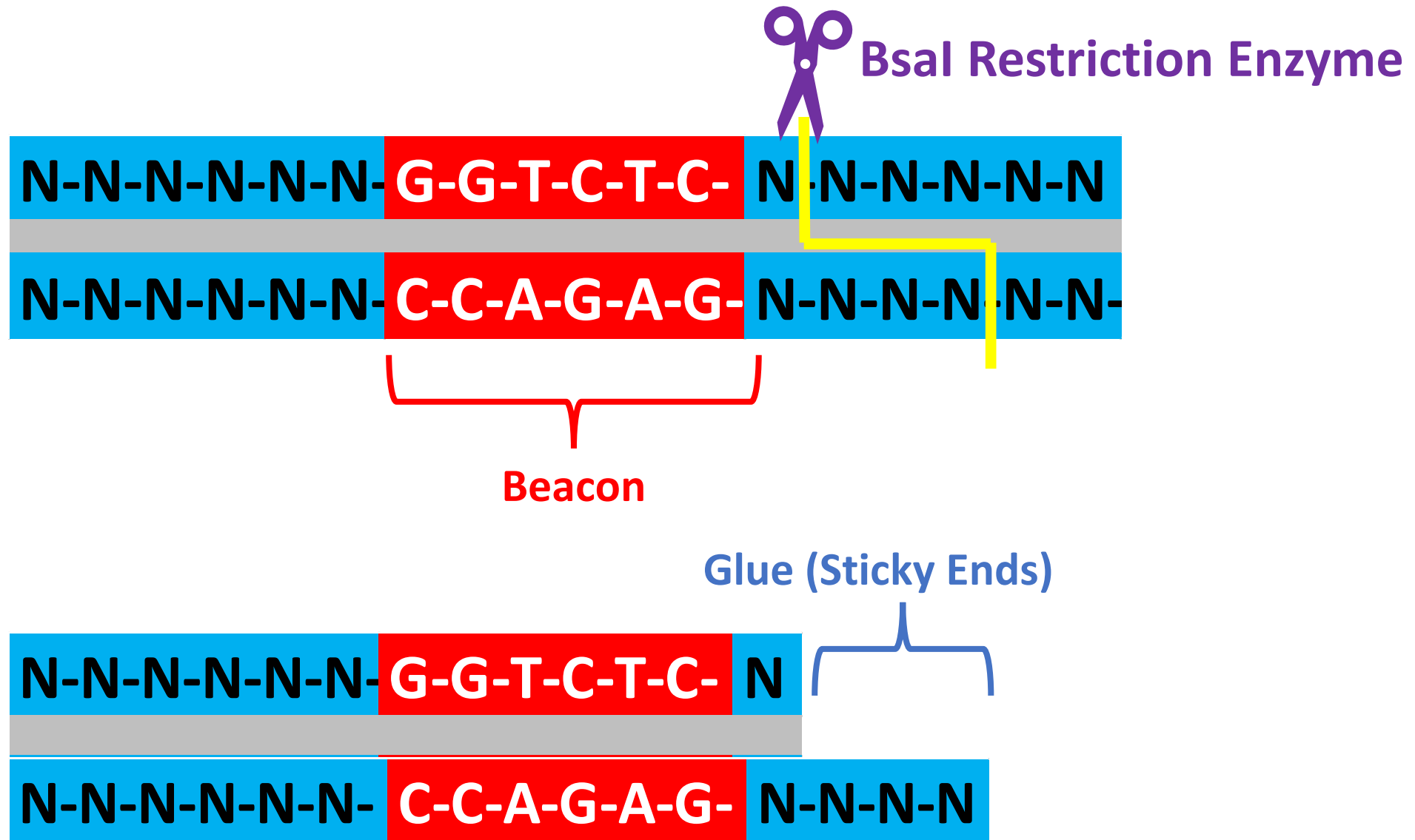


# Introduction

- **Two hypotheses of the origin of SARS-CoV-2 exist:**
  - A spillover from an animal host somewhere outside a laboratory
  - A laboratory-related accident
- Finding features within the genome to address these hypotheses would advance the investigation without requiring the cooperation of third-parties
- Previous analyses of the unprecedented, first ever furin cleavage site in a sarbecovirus and the exceptional pre-adaption of the receptor binding domain to human ACE2 have been challenged because they provide an evolutionary advantage to the virus and, no matter how seemingly unnatural, as supporting a natural process
- Here I perform an analysis of the number, location, genome pattern, and sequences of two restriction sites, BsaI and BsmBI, that helps distinguish natural viruses from synthetic viruses
  - These two Type IIC restriction enzymes are the workhorses of synthetic coronavirus research and part of Baric's "No See 'Em" technology
  - An advantage of this analytical approach is that, in synthetic biology, the manipulation of these small, six nt sequences is the foundation of reverse genetics but their small size and random location within a genome, unrelated to genes, makes it extremely unlikely that they could provide an evolutionary advantage
- **Finding multiple patterns within SARS-CoV-2's genome to be both a) consistent with man-made chimeric virus genomes and b) demonstrably extremely inconsistent with all observed natural sarbecovirus genomes, this could greatly advance the investigation of COVID-19's origins."**

# How Do Restriction Enzymes Work?

## The Beacon and Glue of Synthetic Biology



# SARS1 Assembly Process: I

- Top: Human Urbani strain with three natural BglII sites noted (in black)
- Bottom: Synthetic assembly uses three human-designed BglII sites (red), two BglII sites (black), with BglII (1577) extinguished

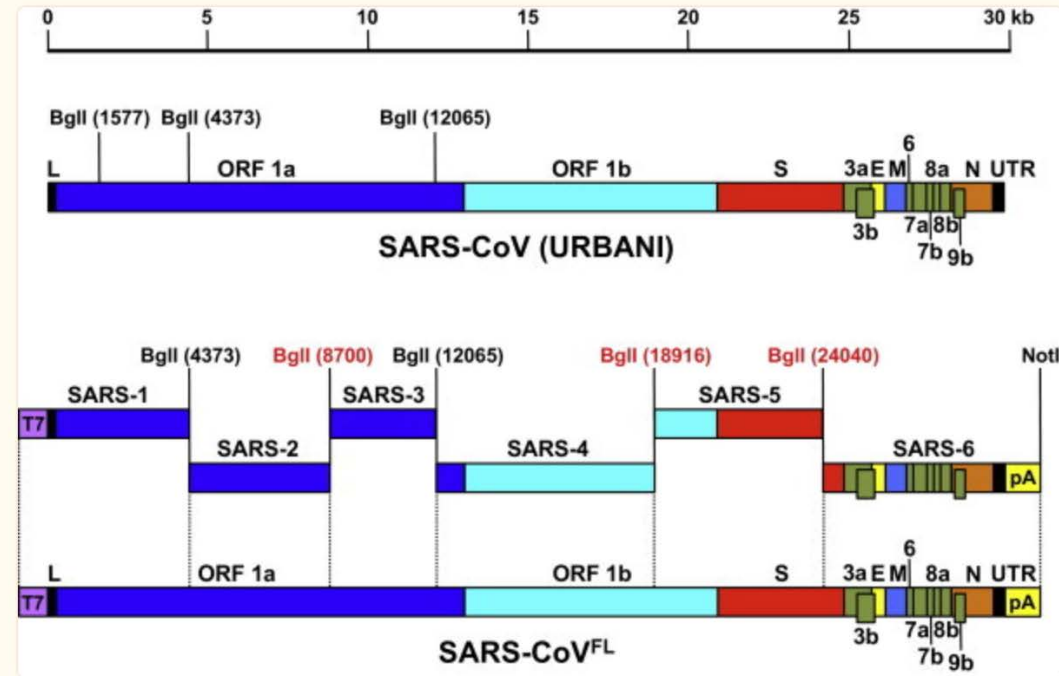


Fig. 2

Systematic assembly of a SARS-CoV full-length cDNA clone by in vitro ligation. A full-length cDNA of the SARS-CoV Urbani strain (SARS-CoV<sup>FL</sup>) was assembled by in vitro ligation of six contiguous cDNA fragments (SARS-1 to SARS-6) spanning the entire viral genome, which were flanked by native (in black) or engineered (in red) unique BglII restriction endonuclease sites. The assembled full-length cDNA contained a T7 RNA polymerase promoter (T7) at the 5' end and a poly(A) tail (pA) at the 3' end, allowing for in vitro transcription of full-length, capped polyadenylated transcripts. The viral genes and relevant restriction sites are indicated.

Figure adapted from [Yount et al. \(2003\)](#).

## Reverse genetics with a full-length infectious cDNA of severe acute respiratory syndrome coronavirus

Boyd Yount<sup>\*1</sup>, Kristopher M. Curtis<sup>\*1</sup>, Elizabeth A. Fritz<sup>2</sup>, Lisa E. Hensley<sup>4</sup>, Peter B. Jahrling<sup>4</sup>, Erik Prentice<sup>5</sup>, Mark R. Denison<sup>5</sup>, Thomas W. Geisbert<sup>4</sup>, and Ralph S. Baric<sup>\*3</sup>

# SARS1 Assembly Process: II

- Actual changes to create restriction sites:
- 4,419: Natural restriction site used without change
- 8,749, 12,133, 24,088: Synthetic restriction site created with a single nt change (small letter t or g)
- 18,966: Sometimes 4 nt changes are needed to give restriction site and preserve amino acid code

B SARS Junctions	
SARS A/B Junction	GCCATAATGGC <sup>4,419</sup> CGGTATTACCG
SARS B/C Junction*	GCCAGCGTGGC <sup>t 8,749</sup> CGGTCGCACCG
SARS C/D Junction	GCCCAAGAGGC <sup>g 12,113</sup> CGGGTTCTCCG
SARS D/E Junction*	GCCCTCCTGGC <sup>at g t 18,966</sup> CGGGAGGACCG
SARS E/F Junction*	GCCTACACGGC <sup>t 24,088</sup> CGGATGTGCCG

# “Spike substitution strategy.”



中国科学院武汉病毒研究所  
WUHAN INSTITUTE OF VIROLOGY, CAS



“The original fragments E and F were shortened to leave spike gene as an independent fragment. The new fragments were designated as Es and Fs.

**BsaI** or **BsmBI** sites were introduced into the junctions of Es/Spike and Spike/Fs.

Then any spike could be substituted into the genome of SARSr-CoV WIV1 through this strategy.”

-Ben Hu, Peter Daszak, Zhengli-Li Shi

Note (right) that the Es restriction site is on the sense strand and the Fs restriction site is on the anti-sense strand. That rotational symmetry is the basis for the elimination of the designed restriction sites after ligation in the final clone.

The ‘No See ‘Em’ technique

PLoS Pathog. 2017 Nov; 13(11): e1006698.

Published online 2017 Nov 30. doi: [10.1371/journal.ppat.1006698](https://doi.org/10.1371/journal.ppat.1006698)

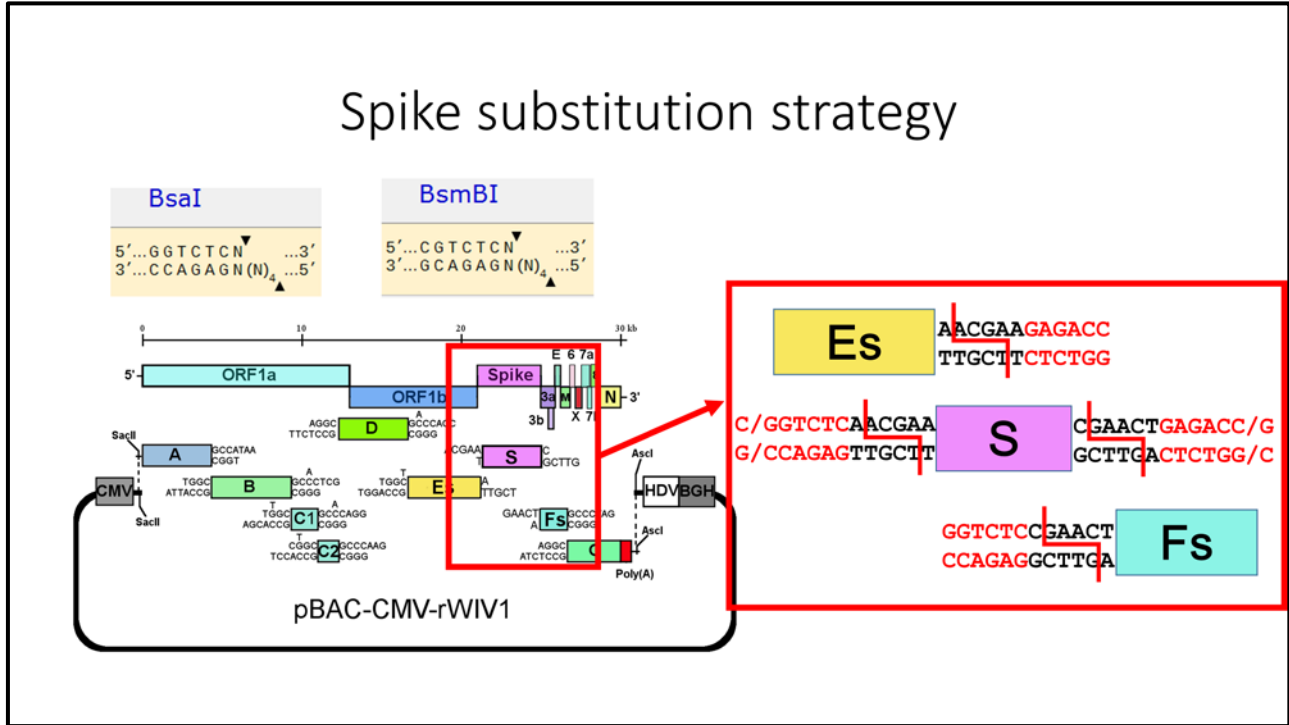
PMCID: PMC5708621

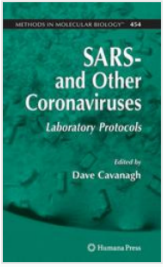
PMID: [29190287](https://pubmed.ncbi.nlm.nih.gov/29190287/)

Discovery of a rich gene pool of bat SARS-related coronaviruses provides new insights into the origin of SARS coronavirus

Ben Hu, Data curation, Formal analysis, Investigation, Validation, Visualization, Writing – original draft,<sup>#1</sup> Lei-Ping Zeng, Investigation, Methodology,<sup>#1</sup> Xing-Lou Yang, Investigation, Resources,<sup>#1</sup> Xing-Yi Ge, Formal analysis, Resources,<sup>1</sup> Wei Zhang, Investigation,<sup>1</sup> Bei Li, Investigation,<sup>1</sup> Jia-Zheng Xie, Investigation,<sup>1</sup> Xu-Rui Shen, Investigation,<sup>1</sup> Yun-Zhi Zhang, Resources,<sup>2,3</sup> Ning Wang, Investigation,<sup>1</sup> Dong-Sheng Luo, Investigation, Resources,<sup>1</sup> Xiao-Shuang Zheng, Investigation,<sup>1</sup> Mei-Niang Wang, Resources,<sup>1</sup> Peter Daszak, Funding acquisition, Writing – review & editing,<sup>4</sup> Lin-Fa Wang, Conceptualization, Funding acquisition, Writing – review & editing,<sup>5</sup> Jie Cui, Conceptualization, Formal analysis, Funding acquisition, Software, Writing – review & editing,<sup>1,7</sup> and Zheng-Li Shi, Conceptualization, Funding acquisition, Methodology, Project administration, Supervision, Visualization, Writing – review & editing<sup>1,7</sup>

Christian Drosten, Editor





[SARS- and Other Coronaviruses](#) pp 293-315 | [Cite as](#)

## Systematic Assembly and Genetic Manipulation of the Mouse Hepatitis Virus A59 Genome

Authors

[Authors and affiliations](#)

Eric F. Donaldson, Amy C. Sims, Ralph S. Baric

Protocol

First Online: 01 August 2008



Citations



Downloads

Part of the [Methods in Molecular Biology](#) book series (MIMB, volume 454)

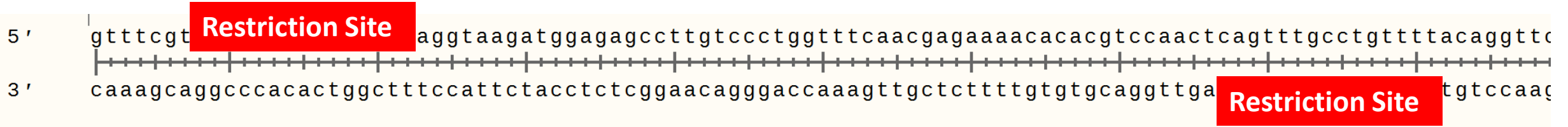
### Abstract

We have developed a DNA assembly platform that utilizes the nonspecific, highly variable sequence signatures of type II restriction enzymes to assemble a full-length molecular clone of murine hepatitis coronavirus (MHV) strain A59. The approach also allows changes to be engineered into a DNA fragment by designing primers that incorporate the restriction site and the mutations of interest. By adding the type II restriction site in the proper orientation, subsequent digestion removes the restriction site and leaves a sticky end comprising the mutation of interest ready to ligate to a second fragment generated in parallel as its complement. In this chapter, we discuss the details of the method to assemble a full-length infectious clone of MHV and then engineer a specific mutation into the clone to demonstrate the power of this unique site-directed “No See’m” mutagenesis approach.

# The ‘No See ‘Em’ Gene Manipulation Assembly Platform

While it is true this technique hides the ligation seams in the finished synthetic virus, having access to potential precursor viruses, fragments or families of related sarbecoviruses allows the assembly path to be observed by the absence of certain genetic features.

**August 2008**

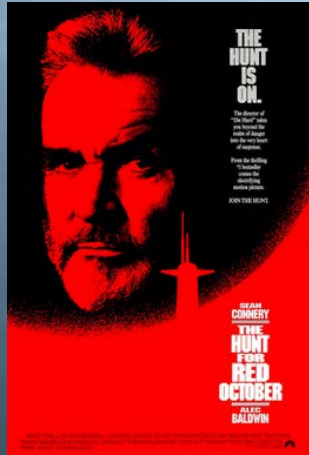


Signature of 'No See 'Em' Synthetic Assembly in Precursor:

Addition of Symmetrical Restriction Sites on 5' (Positive Sense) and 3' (Negative Sense) Strands

Removal of Native Restriction Sites Where Needed





In the movie, The Hunt for Red October, the submarine was so quiet it was undetectable...

Until it was realized that it made less noise than the natural background.

Looking for a “hole in the ocean,” the absence of a sonar signal, made it detectable.

# Hypothesis: Can “holes in the genome” with respect to restriction sites provide a signature of synthetic assembly of a virus?

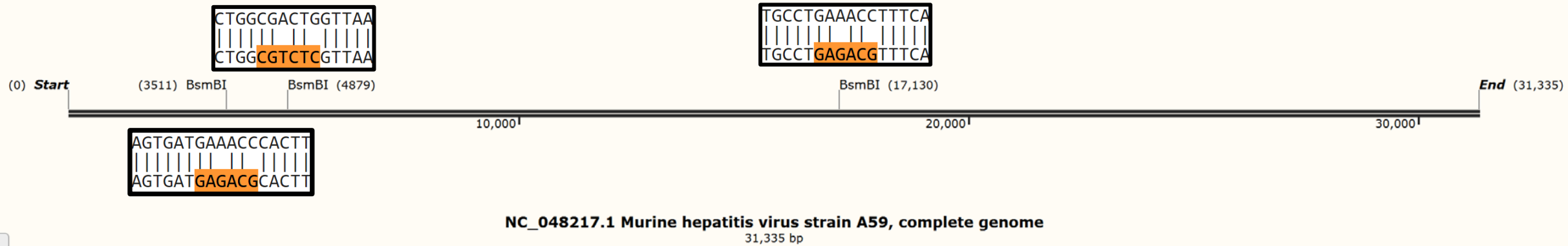
- How many of these two restriction sites are expected to be found in natural sarbecoviruses?
  - Any given hexamer sequence will occur every 4096 nts or 7.3/30k genome
  - Given the G:C bias of these sequences and a 40% G:C content of SARS-CoV-2, it should occur every 6944 or 4.3/30k genome
  - Therefore, a combined total of between 8.6 and 14.6 BsmBI and BsaI restriction sites per genome is predicted

## BsaI



## Esp3I-BsmB1





## Example of Synthetic Biology Workflow

- Destruction of native BsmBI restriction sites by the introduction of point mutations is often the first step in the laboratory synthetic biology workflow and reverse genetics of coronaviruses



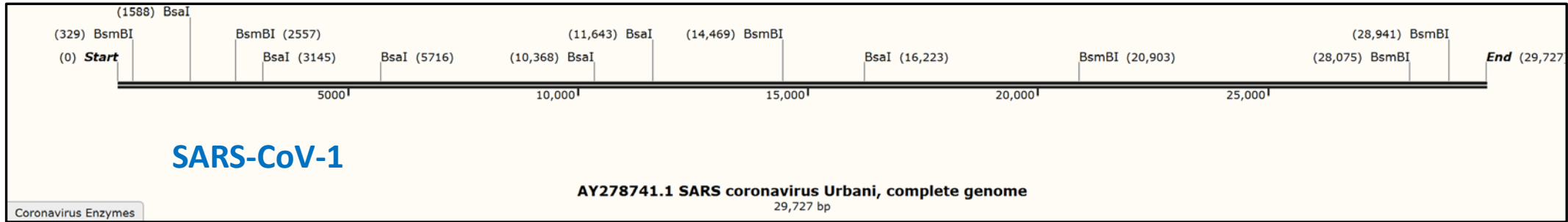
- Here, three native BsmBI restriction sites (above) are removed by making two 3<sup>rd</sup> position in the codon, synonymous substitutions, yielding a synthetic virus with no remaining BsmBI restriction sites (below)



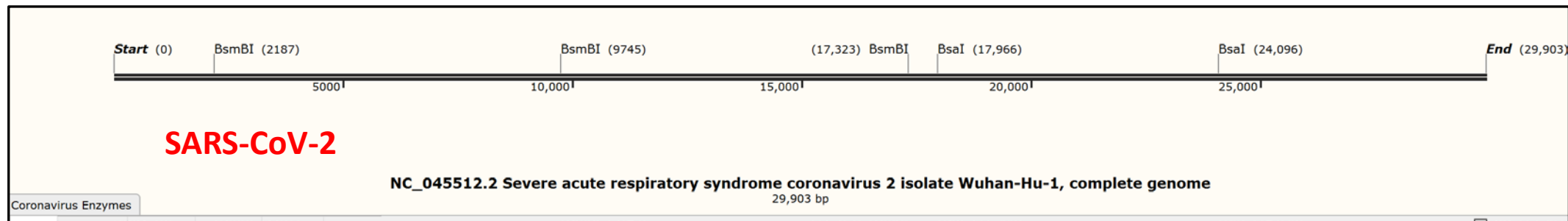
Donaldson E.F., Sims A.C., Baric R.S. (2008) Systematic Assembly and Genetic Manipulation of the Mouse Hepatitis Virus A59 Genome. In: Cavanagh D. (eds) SARS- and Other Coronaviruses. Methods in Molecular Biology (Methods and Protocols), vol 454. Humana Press, Totowa, NJ. [https://doi.org/10.1007/978-1-59745-181-9\\_21](https://doi.org/10.1007/978-1-59745-181-9_21)

# SARS-CoV-1, SARS-CoV-2, and related viruses are different

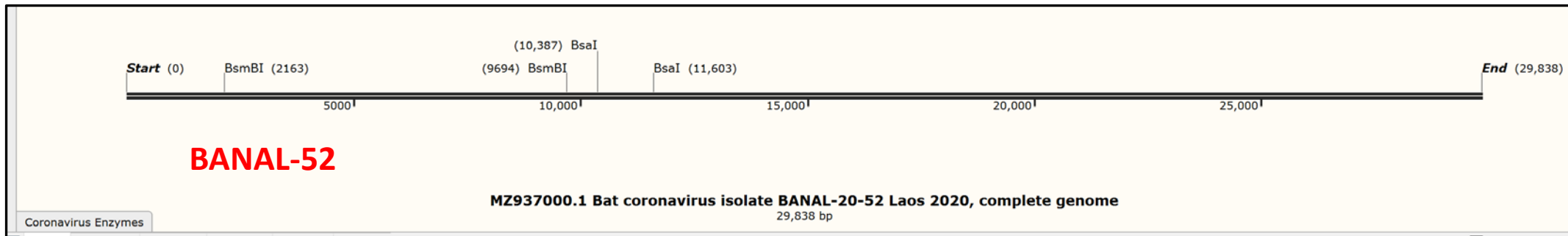
## Restriction Sites



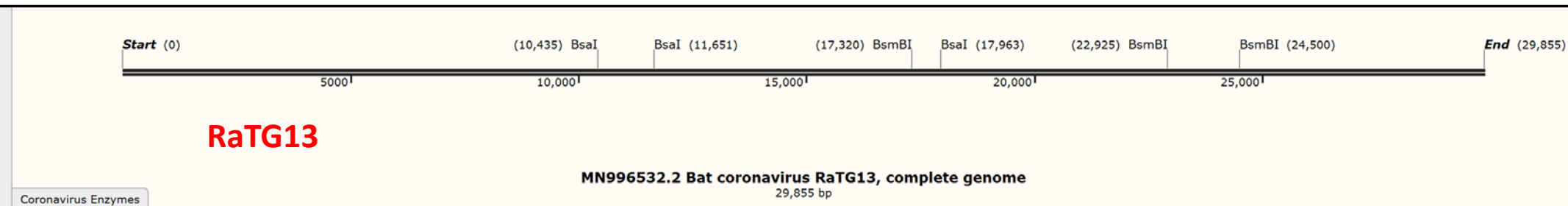
**N = 12**



**N = 5**



**N = 4**



**N = 6**

ARTICLE

<https://doi.org/10.1038/s41467-021-22905-7>

OPEN



# SARS-CoV-2 gene content and COVID-19 mutation impact by comparing 44 *Sarbecovirus* genomes

Irwin Jungreis<sup>1,2</sup>, Rachel Sealfon<sup>3</sup> & Manolis Kellis<sup>1,2</sup>

42 Sarbecoviruses from above paper in green

## Current Biology

Volume 30, Issue 11, 8 June 2020, Pages 2196–2203.e3



Report

# A Novel Bat Coronavirus Closely Related to SARS-CoV-2 Contains Natural Insertions at the S1/S2 Cleavage Site of the Spike Protein

Hong Zhou<sup>1,8</sup>, Xing Chen<sup>2,8</sup>, Tao Hu<sup>1,8</sup>, Juan Li<sup>1,8</sup>, Hao Song<sup>3</sup>, Yanran Liu<sup>1</sup>, Peihan Wang<sup>1</sup>, Di Liu<sup>4</sup>, Jing Yang<sup>5</sup>, Edward C. Holmes<sup>6</sup>, Alice C. Hughes<sup>2</sup>, Yuhai Bi<sup>5</sup>, Weifeng Shi<sup>1,7,9</sup>

16 Sarbecoviruses from above paper in red

Coronavirus Identifier	Restriction Sites				Total
	Esp3I-BsmB1		BsaI		
	Start to 15,000	15,001 to end	Start to 15,000	15,001 to end	
>KY417151_Bat_SARS_like_CoV_Rs7327	3	1	4	1	9
>KY417152_Bat_SARS_like_CoV_Rs9401	3	2	4	1	10
>KY417144_Bat_SARS_like_CoV_Rs4084	3	2	4	1	10
>KF367457_Bat_SARS_like_CoV_WIV1	3	3	4	1	11
>KU973692_UNVERIFIED_SARS_related_CoV_F46	3	1	2	3	9
>KF569996_Rhinolophus_affinis_CoV_LYRa11	3	1	3	2	9
>NC_004718_SARS_CoV_Tor2	3	3	5	1	12
>MK211376_CoV_BtRs_BetaCoV_YN2018B	3	2	4	2	11
>KJ473816_BtRs_BetaCoV_YN2013	3	3	4	2	12
>KY770858_Bat_CoV_Anlong_103	3	3	4	2	12
>FJ588686_Bat_SARS_CoV_Rs672_2006	3	1	3	3	10
>KJ473815_BtRs_BetaCoV_GX2013	4	3	3	3	13
>JX993987_Bat_CoV_Rp_Shaanxi2011	3	3	3	3	12
>KT444582_SARS_like_CoV_WIV16	2	3	4	3	12
>KY417145_Bat_SARS_like_CoV_Rf4092	3	2	4	3	12
>KY417143_Bat_SARS_like_CoV_Rs4081	2	1	4	3	10
>MK211378_CoV_BtRs_BetaCoV_YN2018D	3	2	4	3	12
>MK211377_CoV_BtRs_BetaCoV_YN2018C	3	2	4	3	12
>KY417142_Bat_SARS_like_CoV_As6526	3	1	4	3	11
>KY417147_Bat_SARS_like_CoV_Rs4237	2	2	4	3	11
>KY417148_Bat_SARS_like_CoV_Rs4247	2	2	4	3	11
>MK211375_CoV_BtRs_BetaCoV_YN2018A	3	2	4	3	12
>JX993988_Bat_CoV_Cp_Yunnan2011	3	3	5	2	13
>KJ473814_BtRs_BetaCoV_HuB2013	1	2	2	5	10
>DQ412043_Bat_SARS_CoV_Rm1	1	3	4	3	11
>KY417146_Bat_SARS_like_CoV_Rs4231	3	2	4	4	13
>KY417149_Bat_SARS_like_CoV_Rs4255	2	2	4	4	12
>KP886808_Bat_SARS_like_CoV_YNLF_31C	1	2	5	3	11
>GQ153542_Bat_SARS_CoV_HKU3_7_GQ153542	1	2	5	3	11
>DQ022305_Bat_SARS_CoV_HKU3_1	1	2	4	4	11
>GQ153547_Bat_SARS_CoV_HKU3_12_GQ153547	1	2	4	4	11
>MG772933_Bat_SARS_like_CoV_bat_SL_CoVZC45	3	2	4	5	14
>MG772934_Bat_SARS_like_CoV_bat_SL_CoVZXC2	3	2	4	5	14
>DQ071615_Bat_SARS_CoV_Rp3	4	2	4	5	15
>MK211374_CoV_BtRl_BetaCoV_SC2018	2	1	4	5	12
>KY938558_Bat_CoV_strain_16B0133	4	1	5	4	14
>KY770860_Bat_CoV_Jiyuan_84	3	2	4	5	14
>DQ412042_Bat_SARS_CoV_Rf1	2	1	5	5	13
>DQ648856_Bat_CoV_BtCoV_273_2005	2	1	5	5	13
>KJ473812_BtRf_BetaCoV_HeB2013	2	2	5	5	14
>KY352407_SARS_related_CoV_strain_BtKY72	1	1	7	4	13
>NC_014470_Bat_CoV_BM48_31_BGR_2008	2	1	5	8	16
>AY278489_SARS-CoV-1_GD01	3	3	5	1	12
>AY304486.1_Civet_SARS_CoV_SZ3	3	3	5	1	12
>AY390556_SARS-CoV-1_GZ02	3	3	5	1	12
>AY485277.1_SARS-CoV-1_Sino1-11	3	3	5	2	13
>AY508724_SARS-CoV-1_NS-1	3	3	5	1	12
>DQ084200_SARS-like_CoV_HKU3-3	1	2	4	4	11
>DQ648857_SARS-like_CoV_BtCoV/279/2005	1	2	4	3	10
>KF294457_SARS-related_bat_CoV_Longquan-140	1	2	3	5	11
>KY770859.1_SARS_CoV_Anlong-112	3	3	3	2	11
Cambodian Bat RShSTT182_EPI_ISL_852604	1	3	3	1	8
Cambodian Bat RShSTT200_EPI_ISL_852605	1	3	3	1	8
Japanese Rc-o319	4	2	3	1	10
Pangolin Guangdong 1	2	1	2	4	9
Pangolin GuangxiP2V 2017	1	2	2	3	8
RMYN02	2	1	2	3	8
Thai bat RacC203	3	1	1	2	7

# Summary of Natural Sarbecoviruses

- Two data sets were used to establish the properties of natural sarbecoviruses
  - 58 sequenced genomes from before 2020 which are documented to be sourced from nature
  - A number of published synthetic sarbecoviruses
- Natural sarbecoviruses have, on average, 11.8 restriction sites (RS) per genome (combining BsaI and BsmBI)
  - No natural virus has fewer than seven total RSs
- When dividing the genome in half, at nt 15,000, natural sarbecoviruses have a distribution of RS between the two halves in which there is never a segment without at least one of each RS
- In examining BsaI and BsmBI RSs from the 5' to 3' of the genome, no pattern or order of RSs is seen
  - They alternate in an apparent random order

# Total Number of Restriction Sites in 58 Sarbecoviruses



- Mean =  $11.4 \pm 2.1$  per genome (combined BsmBI & Bsal)
- No natural sarbecoviruses has been found with fewer than seven per genome
- Based on observed number and distribution the probabilities shown below can be calculated

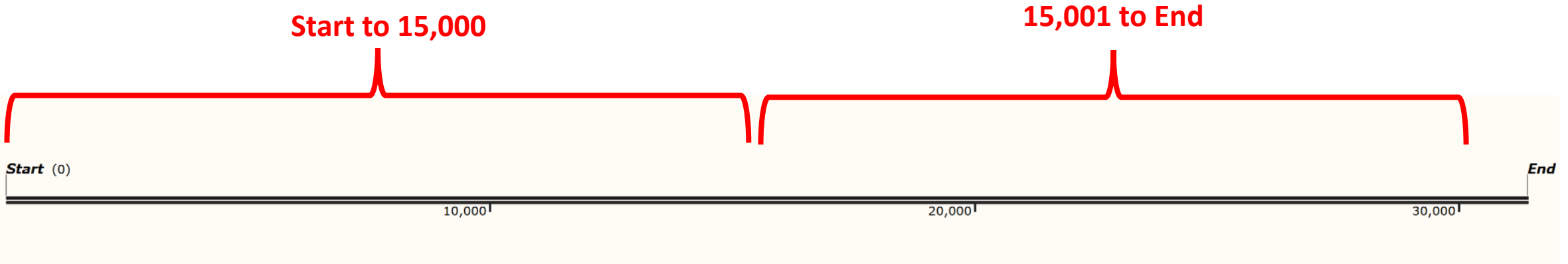
Number of sites (X)	Probability $\leq X$
$\leq 4$	0.00016
$\leq 5$	0.0009
$\leq 6$	0.004

# Summary of Synthetic Viruses & SARS-CoV-2

- **Synthetic viruses can routinely have fewer than seven total restriction, a number never before seen in a natural virus**
- **Synthetic viruses often have one or more genome segments that are missing a restriction site, a distribution never seen in natural viruses**
- **In examining Bsal and BsmBI RSs from the 5' to 3' of the genome, a pattern of segregation of restriction sites can be observed. This has never been seen in a natural virus**
- **SARS-CoV-2 has five total restriction sites, with a likelihood of 0.0009 for a natural virus**
- **SARS-CoV-2 has no Bsal sites in the first 17,320 nt with a likelihood of 0.0013 for a natural virus**
- **SARS-CoV-2 has a “segregated” RS pattern: BsmBI-BsmBI-BsmBI-Bsal-Bsal, never seen in a natural virus and with a likelihood of 0.05**
- **SARS-CoV-2 has seven RSs that differ from natural sarbecoviruses, a likelihood of 0.000014 to have occurred naturally by random mutations within the 42 nts of the RSs in a total genome of 30,000**
- **The likelihood these four features occurred together in a natural sarbecoviruses is one in greater than 1.2 billion**



# Genome Segmental Distribution of Restriction Sites in 58 Sarbecoviruses



Restriction Enzyme	Genome Section	
	Start to 15,000	15,001 to End
BsmBI	$2.4 \pm 0.9$	$2.0 \pm 0.7$
BsaI	$3.9 \pm 1.0$	$3.0 \pm 1.5$

- The 58 viruses have 232 total restriction site segments (two segments and two enzymes per virus)
- All of the 232 segments have at least two restriction sites, at least one of each enzyme
- Thus, the 95% confidence upper bound for the probability of zero restriction sites at a given region of the genome is given by the approximation (Rule of Threes) as  $3/232 = <0.013$

# Genome Distribution Pattern of Restriction Sites in 58 Sarbecoviruses

## Hypothesis:

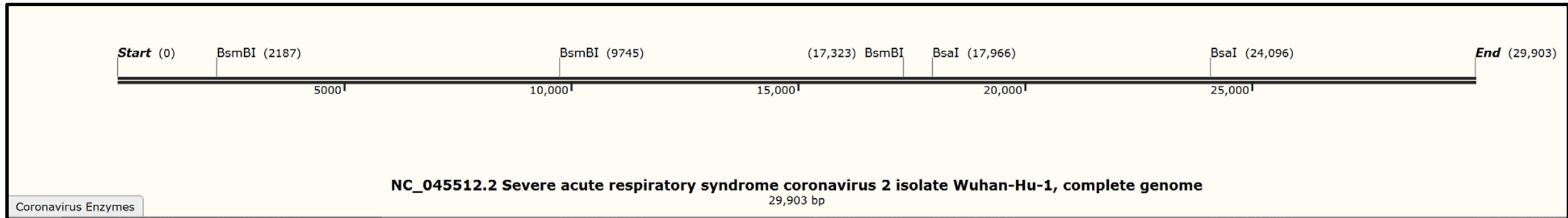
- A natural sarbecovirus will have a “random” distribution of BsmBI and BsaI restriction sites when viewing the 5' to 3' genome sequence
- A synthetic virus may display a “segregated” distribution of BsmBI and BsaI restriction sites when viewing the 5' to 3' genome sequence. This facilitates one step, unidirectional assembly of cloned segments



**Random Distribution:** (RS1)a-(RS2)b-(RS1)c-(RS2)d, where a-d equal 1-5 and RS1 and RS2 can be either BsmBI or BsaI

**Segregated Distribution:** (RS1)a-(RS2)b where a and b equal 1-5 and RS1 and RS2 can be either BsmBI or BsaI

# SARS-CoV-2 restriction sites number and pattern have never been observed in a natural sarbecovirus

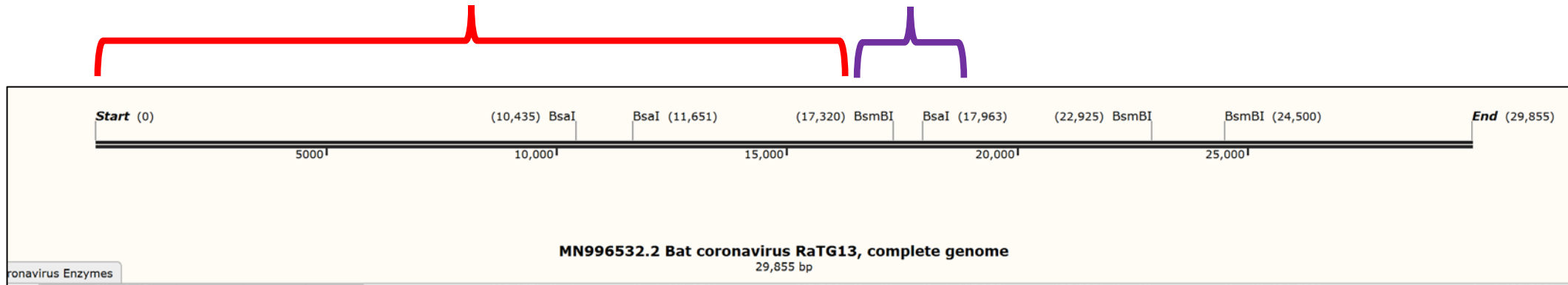


- **SARS-CoV-2 has a total of five BsaI and BsmBI restriction sites**
  - A natural sarbecovirus has never been observed with less than seven
  - The likelihood SARS-CoV-2 is not a natural virus, based on RS number, is >99.9%
- **SARS-CoV-2 has no BsaI restriction sites in the first 60% of the genome and no BsmBI restriction sites in the remaining 40% of the genome**
  - This “segregated” distribution has never been seen in a natural virus, making the likelihood SARS-CoV-2 is not a natural virus, based on this pattern, at 95%

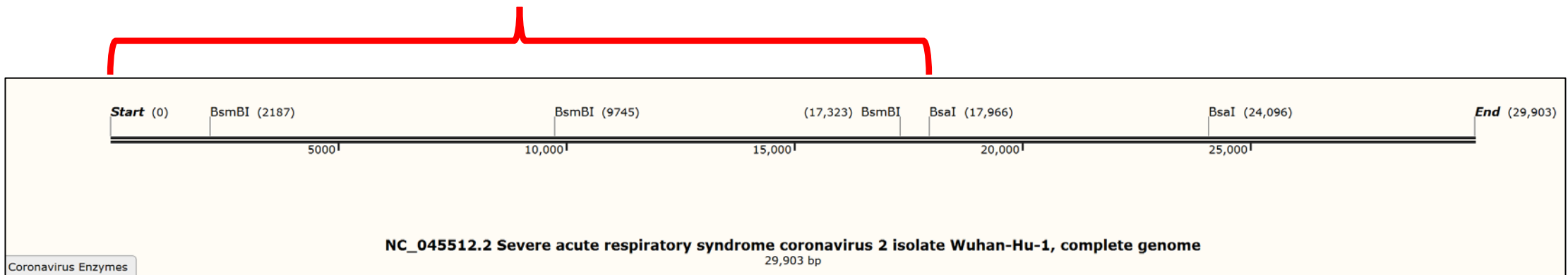
# SARS-CoV-2 and RaTG13 Share Two Restriction Sites and Have Seven Unique Sites

No BsmBI restriction sites over 58% of the entire genome has never been seen in nature and has a likelihood of being a natural virus of less than one in 500

Shared Restriction Sites



No BsaI restriction sites over 60% of the entire genome has never been seen in nature and has a likelihood of being a natural virus of less than one in 500



# What is the probability that the seven-restriction site changes between SARS-CoV-2 & RaTG13 occurred randomly?

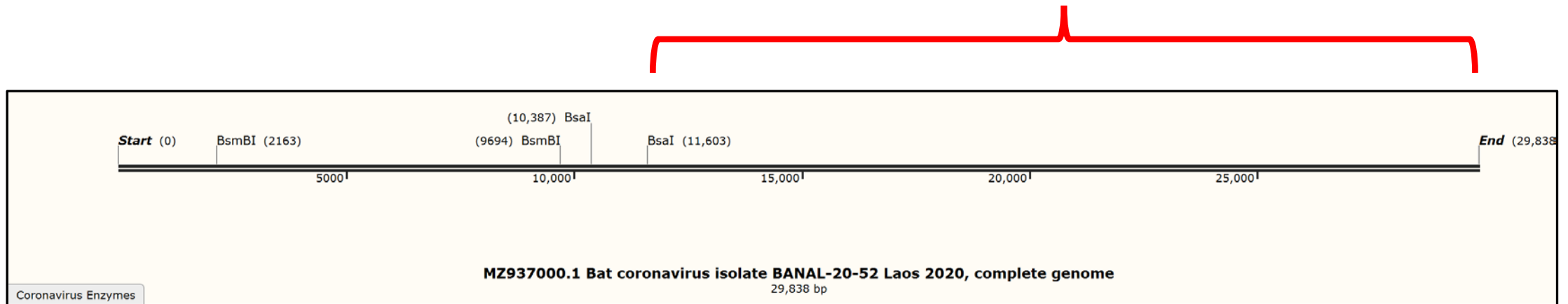
- SARS-CoV-2 has a genome of 29,903 nts
- SARS-CoV-2 and RaTG13 are 96.2% identical at the genome level
- Assumptions
  - The viruses differ by seven restriction sites of six nt each
  - Random probability of six nts being identical is  $(0.962)$  to the 6<sup>th</sup> power or 0.793
  - Probability of at least one nt difference in one restriction site is  $1.0 - 0.793 = 0.207$
  - Probability of all 7 restriction sites with at least 1 mutation is  $(0.207)$  to the 7<sup>th</sup> power =

**0.000014 or one in >72,990**

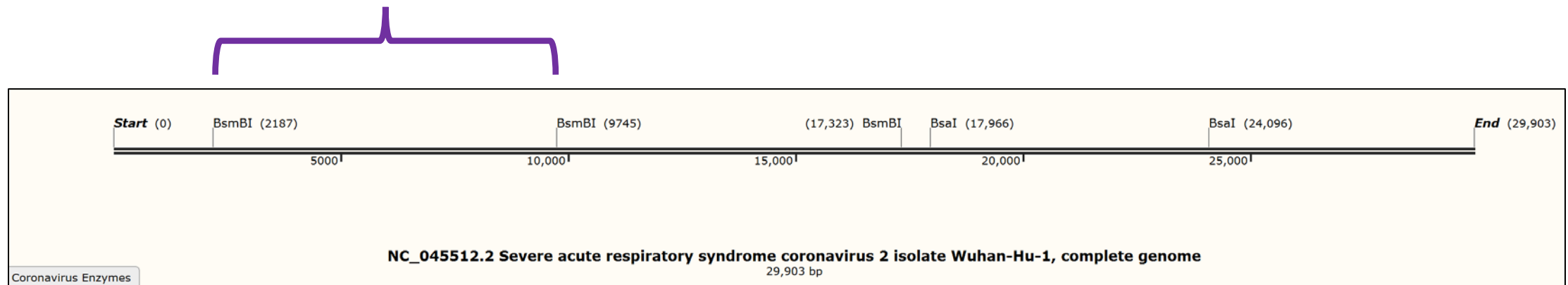
**This pattern of 7 RS changes could not have been random**

# SARS-CoV-2 and BANAL-52 Share Two Restriction Sites and Have Five Unique Sites

No BsaI or BsmBI restriction sites over 61% of the entire genome has never been seen in nature and has a likelihood of being a natural virus of less than one in 50,000



## Shared Restriction Sites



# What is the probability that the five restriction site changes between SARS-CoV-2 & BANAL-52 occurred randomly?

- SARS-CoV-2 has a genome of 29,903 nts
- SARS-CoV-2 and BANAL-52 are 96.9% identical at the genome level
- Assumptions
  - The viruses differ by five restriction sites of six nt each
  - Random probability of six nts being identical is  $(0.969)$  to the 6<sup>th</sup> power or 0.828
  - Probability of at least one nt difference in one restriction site is  $1.0 - 0.828 = 0.172$
  - Probability of all 5 restriction sites with at least 1 mutation is  $(0.172)$  to the 5<sup>th</sup> power =

**0.000151 or one in >6,600**

**This pattern of 5 RS changes could not have been random**





# SARS-CoV-2 BsmBI Restriction Site 2187

The out-of-frame GAGACG restriction site is found in only three of 58 sarbecoviruses, including SARS-CoV-2 and excluding RaTG13.

	L	E	E	K	F	K	E	G	V	E	F	L	R	D	G	W	E	I	V	K	F	I	S	T	C	A	C	E	I	V
NC_045512_SARS_CoV_2_Wuhan_Hu_1_aa	L	E	E	K	F	K	E	G	V	E	F	L	R	D	G	W	E	I	V	K	F	I	S	T	C	A	C	E	I	V
NC_045512_SARS_CoV_2_Wuhan_Hu_1	CTT	GAA	GAG	AAG	TTT	AAG	GAA	GGT	GTA	GAG	TTT	CTT	AGA	GAC	GGT	TGG	GAA	ATT	GTT	AAA	TTT	ATC	TCA	ACC	TGT	GCT	TGT	GAA	ATT	GTC
MN996532_Bat_CoV_RaTG13	CTC	GAA	GAG	AAA	TTG	AAG	GAA	GGT	GTA	GAG	TTT	CTT	AGA	GAT	GGT	TGG	GAA	ATT	GTT	AAA	TTT	ATC	TCA	ACT	TGT	GCT	TGT	GAA	ATT	GTC
MG772933_Bat_SARS_like_CoV_bat_SL_CoVZC45	CTC	GAA	GAG	AAA	TTG	AAA	GAA	GGT	ATA	GAG	TTT	CTT	AGA	GAC	GGT	TGG	GAA	ATT	GTT	AAA	TTT	ATC	TCA	ACT	TGT	GCT	TGT	GAA	ATA	GTC
MG772934_Bat_SARS_like_CoV_bat_SL_CoVZXC21	CTC	GAA	GAG	AAA	TTG	AAG	GAA	GGT	GTA	GAG	TTT	CTT	AGA	GAC	GGT	TGG	GAA	ATT	GTT	AAA	TTT	ATC	TCT	ACT	TGT	GCT	TGT	GAA	ATT	GTC
NC_004718_SARS_CoV	ATT	GAG	GCG	AAA	CTT	AGT	GCA	GGA	GTT	GAA	TTT	CTC	AAG	GAT	GCT	TGG	GAG	ATT	CTC	AAA	TTT	CTC	ATT	ACA	GGT	GTT	TTT	GAC	ATC	GTC
KT444582_SARS_like_CoV_WIV16	ATT	GAG	GCG	AAA	CTT	AGT	GCA	GGA	GTT	GAA	TTT	CTC	AAG	GAT	GCT	TGG	GAG	ATT	CTC	AAA	TTT	CTC	ATT	ACA	GGT	GTT	TTT	GAC	ATC	GTT
KY417146_Bat_SARS_like_CoV_Rs4231	ATT	GAG	GCG	AAA	CTT	AGT	GCA	GGA	GTT	GAA	TTT	CTC	AAG	GAT	GCT	TGG	GAG	ATT	CTC	AAA	TTT	CTC	ATT	ACA	GGT	GTT	TTT	GAC	ATC	GTC
MK211376_CoV_BtRs_BetaCoV_YN2018B	ATT	GAG	GCG	AAA	CTT	AGT	GCA	GGA	GTT	GAA	TTT	CTC	AAG	GAT	GCT	TGG	GAG	ATT	CTC	AAA	TTT	CTC	ATT	ACA	GGT	GTT	TTT	GAC	ATC	GTC
KY417151_Bat_SARS_like_CoV_Rs7327	ATT	GAG	GCG	AAA	TTT	AGT	GCA	GGA	GTT	GAA	TTT	CTC	AAG	GAT	GCT	TGG	GAG	ATT	CTC	AAA	TTT	CTC	ATT	ACA	GGT	GTT	TTT	GAC	ATC	GTC
KY417152_Bat_SARS_like_CoV_Rs9401	ATT	GAG	GCG	AAA	CTT	AGT	GCA	GGA	GTT	GAA	TTT	CTC	AAG	GAT	GCT	TGG	GAG	ATT	CTC	AAA	TTT	CTC	ATT	ACA	GGT	GTT	TTT	GAC	ATC	GTC
KY417144_Bat_SARS_like_CoV_Rs4084	ATT	GAG	GCG	AAA	CTT	AGT	GCA	GGA	GTT	GAA	TTT	CTC	AAG	GAT	GCT	TGG	GAG	ATT	CTC	AAA	TTT	CTC	ATT	ACA	GGT	GTT	TTT	GAC	ATC	GTC
KF367457_Bat_SARS_like_CoV_WIV1	ATT	GAG	GCG	AAA	CTT	AGT	GCA	GGA	GTT	GAA	TTT	CTC	AAG	GAT	GCT	TGG	GAG	ATT	CTC	AAA	TTT	CTC	ATT	ACA	GGT	GTT	TTT	GAC	ATC	GTC
KU973692_UNVERIFIED_SARS_related_CoV_F46	GTT	GAG	TCT	AGA	CTT	AGT	GAT	GGA	GTT	GAA	TTT	CTC	AAG	GAT	GCT	TGG	GAG	ATT	CTT	AAA	TTG	ATC	AGA	GGT	ATG	TTT	GAC	ATC	GTT	
KY417145_Bat_SARS_like_CoV_Rf4092	ATT	GAG	GCA	AAA	CTT	AGT	GCA	GGA	GTT	GAA	TTT	CTC	AAG	GAT	GCT	TGG	GAG	ATT	CTC	AAA	TTT	CTC	ATT	ACA	GGT	GTT	TTT	GAC	ATC	GTC
KJ473816_BtRs_BetaCoV_YN2013	ATT	GAG	GCA	AAA	CTT	AGT	GCA	GGA	GTT	GAA	TTT	CTT	AAG	GAT	GCT	TGG	GAG	ATC	CTC	AAA	TTT	CTC	ATT	ACA	GGT	GTT	TTT	GAC	ATC	GTC
KY770858_Bat_CoV_Anlong_103	ATT	GAG	GCA	AAA	CTT	AGT	GCA	GGA	GTT	GAA	TTT	CTC	AAG	GAT	GCT	TGG	GAG	ATT	CTC	AAA	TTT	CTC	ATT	ACA	GGT	GTT	TTT	GAC	ATC	GTC
KY417143_Bat_SARS_like_CoV_Rs4081	ATT	GAG	GCG	AAA	CTT	AGT	GCA	GGA	GTT	GAA	TTT	CTC	AAG	GAT	GCT	TGG	GAG	ATT	CTC	AAA	TTT	CTC	ATT	ACA	GGT	GTT	TTT	GAC	ATC	GTT
KY417149_Bat_SARS_like_CoV_Rs4255	ATT	GAG	GCG	AAA	CTT	AGT	GCA	GGA	GTT	GAA	TTT	CTC	AAG	GAT	GCT	TGG	GAG	ATT	CTC	AAA	TTT	CTC	ATT	ACA	GGT	GTT	TTT	GAC	ATC	GTT
MK211378_CoV_BtRs_BetaCoV_YN2018D	ATT	GAG	GCG	AAA	CTT	AGT	GCA	GGA	GTT	GAA	TTT	CTC	AAG	GAT	GCT	TGG	GAG	ATT	CTC	AAA	TTT	CTC	ATT	ACA	GGT	GTT	TTT	GAC	ATC	GTC
FJ588686_Bat_SARS_CoV_Rs672_2006	ATT	GAG	GCA	AAA	CTT	AGT	GCA	GGA	GTT	GAA	TTT	CTC	AAG	GAT	GCT	TGG	GAG	ATT	CTT	AAA	TTT	CTC	ATT	ACA	GGT	GTT	TTT	GAC	ATT	GTC
MK211377_CoV_BtRs_BetaCoV_YN2018C	ATT	GAG	GCG	AAA	CTT	AGT	GCA	GGA	GTT	GAA	TTT	CTC	AAG	GAT	GCT	TGG	GAG	ATT	CTC	AAA	TTT	CTC	ATT	ACA	GGT	GTT	TTT	GAC	ATC	GTC
KY417142_Bat_SARS_like_CoV_As6526	ATT	GAG	GCG	AAA	TTT	AGT	GCA	GGA	GTT	GAA	TTT	CTC	AAG	GAT	GCT	TGG	GAG	ATT	CTC	AAA	TTT	CTC	ATT	ACA	GGT	GTT	TTT	GAC	ATC	GTC
KY417147_Bat_SARS_like_CoV_Rs4237	ATT	GAG	GCG	AAA	CTT	AGT	GCA	GGA	GTT	GAA	TTT	CTC	AAG	GAT	GCT	TGG	GAG	ATT	CTC	AAA	TTT	CTC	ATT	ACA	GGT	GTT	TTT	GAC	ATC	GTC
KY417148_Bat_SARS_like_CoV_Rs4247	ATT	GAG	GCA	AAA	CTT	AGT	GCA	GGA	GTT	GAA	TTT	CTT	AAG	GAT	GCT	TGG	GAG	ATT	CTC	AAA	TTT	CTC	ATT	ACA	GGT	GTT	TTT	GAC	ATC	GTC
MK211375_CoV_BtRs_BetaCoV_YN2018A	ATT	GAG	GCA	AAA	CTT	AGT	GCA	GGA	GTT	GAA	TTT	CTC	AAG	GAT	GCT	TGG	GAG	ATT	CTC	AAA	TTT	CTC	ATC	ACA	GGT	GTT	TTT	GAC	ATT	GTC
DQ071615_Bat_SARS_CoV_Rp3	ATT	GAG	GCG	AAA	CTT	AGT	GCA	GGA	GTT	GAA	TTT	CTC	AAG	GAT	GCT	TGG	GAG	ATT	CTC	AAA	TTT	CTG	ATT	ACA	GGT	GTT	TTT	GAC	ATC	GTC
KP886808_Bat_SARS_like_CoV_YNLF_31C	ATT	GAG	GCG	AAA	CTT	AGT	GCA	GGA	GTT	GAA	TTT	CTC	AAG	GAT	GCT	TGG	GAG	ATT	CTC	AAA	TTT	CTT	ATT	ACA	GGT	GTG	TTT	GAC	ATC	GTC
KJ473815_BtRs_BetaCoV_GX2013	ATT	GAA	GCT	AAA	CTC	AGT	GCA	GGG	GTT	GAA	TTT	CTT	AGA	GAT	GCC	TGG	GAA	ATT	CTA	AAA	TTG	CTG	GTT	ACA	GGA	GTG	TTT	GAC	ATT	GTT
KF569996_Rhinolophus_affinis_CoV_LYRa11	GTT	GAG	TCT	AGA	CTT	AGT	GAT	GGA	ATT	GAA	TTT	CTC	AAA	GAT	GCT	TGG	GAG	ATT	CTT	AAA	TTG	ATC	AGA	GGT	GTG	TTT	GAC	ATC	GTT	
JX993988_Bat_CoV_Cp_Yunnan2011	GTT	GAG	TCT	AGA	CTT	AGT	GAT	GGA	ATT	GAA	TTT	CTC	AAG	GAT	GCT	TGG	GAG	ATT	CTT	AAA	TTG	ATC	AGG	GGT	GTG	TTT	GAC	ATC	GTT	
MK211374_CoV_BtR1_BetaCoV_SC2018	GTT	GAG	ACT	AAG	CTT	AAT	ACG	GGA	GTG	GAG	TTT	CTT	AAG	GAT	GCT	TGG	GAA	ATT	CTA	AAA	TTG	CTA	GTC	ACA	GGT	GTG	TTT	GAC	ATT	GTT
KJ473814_BtRs_BetaCoV_HuB2013	ATT	GAG	GCT	AAA	CTC	GGT	GCA	GGG	ATT	GAA	TTT	CTC	AGG	GAT	GCC	TGG	GAA	ATT	CTA	AAA	TTG	TTG	ACA	GGA	ATG	TTT	GAC	ATC	GTC	
DQ412043_Bat_SARS_CoV_Rm1	GTT	GAG	GCT	AAA	CTC	AGT	GCA	GGA	ATT	GAA	TTT	CTC	AGG	GAT	GCC	TGG	GAA	ATT	CTA	AAA	TTT	TTG	GTT	ACA	GGA	GTG	TTT	GAC	ATT	GTT
KY938558_Bat_CoV_strain_16B0133	CTT	GAG	ACT	AAG	CTT	AAT	GCA	GGA	ATA	GAG	TTT	CTC	AAG	GAT	GCT	TGG	GAA	ATT	CTT	AAA	TTG	CTA	GTT	ACA	GGT	GTG	TTT	GAC	ATT	GTT
DQ412042_Bat_SARS_CoV_Rf1	CTT	GAG	ACT	AAG	CTT	AAT	GCA	GGA	ATA	GAG	TTT	CTC	AAG	GAT	GCT	TGG	GAA	ATT	CTT	AAA	TTG	CTA	GTT	ACA	GGT	GTG	TTT	GAC	ATT	GTT
DQ648856_Bat_CoV_BtCoV_273_2005	CTT	GAG	ACT	AAG	CTT	AAT	GCA	GGA	ATA	GAG	TTT	CTC	AAG	GAT	GCT	TGG	GAA	ATT	CTT	AAA	TTG	CTA	GTT	ACA	GGT	GTG	TTT	GAC	ATT	GTT
KJ473812_BtRf_BetaCoV_HeB2013	CTT	GAG	ACT	AAG	CTT	AAT	GCA	GGA	ATA	GAG	TTT	CTC	AAG	GAT	GCT	TGG	GAA	ATT	CTT	AAA	TTG	CTA	GTT	ACA	GGT	GTG	TTT	GAC	ATT	GTT
KY770860_Bat_CoV_Jiyuan_84	CTT	GAG	ACT	AAG	CTT	AAT	GCA	GGA	ATA	GAG	TTT	CTT	AAG	GAT	GCT	TGG	GAA	ATT	CTT	AAA	TTG	CTA	GTT	ACA	GGT	GTG	TTT	GAC	ATT	GTT
JX993987_Bat_CoV_Rp_Shaanxi2011	ATT	GAG	ACT	AAG	CTT	AGT	GCA	GGA	GTT	GAA	TTT	CTT	AGG	GAT	GCC	TGG	GAA	ATT	CTT	AAA	TTG	TTG	GTT	ACA	GGA	GTG	TTT	GAC	ATC	GTT
GQ153542_Bat_SARS_CoV_HKU3_7	GTT	GAG	GCT	AAA	CTT	AGT	GCA	GGA	GTT	GAA	TTT	CTT	AGA	GAT	GCT	TGG	GAA	ATT	CTT	AAA	TTG	ATC	ACA	GGA	GTA	TTT	GAT	GTC	ATT	
DQ022305_Bat_SARS_CoV_HKU3_1	GTT	GAG	GCT	AAA	CTT	AGT	GCA	GGA	GTT	GAA	TTT	CTT	AGA	GAT	GCT	TGG	GAA	ATT	CTT	AAA	TTG	ATC	ACA	GGA	GTA	TTT	GAT	GTC	ATT	
GQ153547_Bat_SARS_CoV_HKU3_12	GTT	GAG	GCT	AAA	CTT	AGT	GCA	GGA	GTT	GAA	TTT	CTT	AGA	GAT	GCT	TGG	GAA	ATT	CTT	AAA	TTG	ATC	ACA	GGA	GTA	TTT	GAT	GTC	ATT	
KY352407_SARS_related_CoV_strain_BtKY72	CTT	GAA	AGT	CAA	TTG	CAG	AAA	GGC	GTG	AGG	TTG	CTT	AAG	GAG	GCT	TGG	CAC	ATC	TTG	CAG	TTT	CTT	GTC	ACT	GGC	GCT	TAC	ACT	ATT	GTG
NC_014470_Bat_CoV_BM48_31_BGR_2008	CTT	GAG	CAA	AAG	CTC	CAA	GGT	GGC	ATT	GAT	TTT	CTT	CGT	CAA	GCT	TGG	GGC	ATT	CTT	AAA	CTT	CTA	GTC	ACT	GGC	GCT	TAT	GTG	GTT	ATA

# SARS-CoV-2 BsmBI Restriction Site 9745

<b>RaTG13</b>	9718	TTTTTACTGGTTCTTTAGTAACTACCTAAAAAGGCGTGTAGTCTTTAATGGTGTTTCCTT	9777
<b>CoV-2</b>	9721	TTTCTATTGGTTCTTTAGTAATTACCTAAA <b>GAGACG</b> TGTAGTCTTTAATGGTGTTTCCTT	9780

**RaTG13**

**5'3' Frame 2**

tttttactggttcttttagtaactacctaaa**aaggcgt**gttagtctttaatggtgtttcc  
F Y W F F S N Y L K R R V V F N G V S

**CoV-2**

**5'3' Frame 2**

tttctattggttcttttagtaattacctaaa**gagacgt**gttagtctttaatggtgtttcc  
F Y W F F S N Y L K R R V V F N G V S

**Synonymous mutation in homologous peptide region**

# SARS-CoV-2 BsmBI Restriction Site 9745

The out-of-frame GAGACG restriction site is found in only three of 58 sarbecoviruses, including SARS-CoV-2. It is absent in RaTG13.

NC_045512_SARS_CoV_2_Wuhan_Hu_1_aa	K	H	F	Y	W	F	F	S	N	Y	L	<b>K</b>	<b>R</b>	R	V	V	F	N	G	V	S	F	S	T	F	E	E	A	A	L
NC_045512_SARS_CoV_2_Wuhan_Hu_1_AAG	CAT	TTC	TAT	TGG	TTC	TTT	AGT	AAT	TAC	CTA	AAG	AGA	CG	GTA	GTC	TTT	AAT	GGT	GTT	TCC	TTT	AGT	ACT	TTT	GAA	GAA	GCT	CGC	CTG	
MN996532_Bat_CoV_RaTG13	AAG	CAT	<b>TTT</b>	<b>TAC</b>	TGG	TTC	TTT	AGT	<b>AAC</b>	TAC	CTA	<b>AAA</b>	<b>AGG</b>	CG	GTA	GTC	TTT	AAT	GGT	GTT	TCC	TTT	AGT	ACT	TTT	GAA	GAA	GCT	CGC	<b>TTA</b>
MG772933_Bat_SARS_like_CoV_bat_SL_CoVZC45	AAG	CAT	<b>TTT</b>	TAT	TGG	TTC	TTT	AGT	<b>AAC</b>	TAC	CTA	AAG	AGA	CG	GTA	GTC	TTT	AAT	GGT	GTT	TCC	TTT	AGT	<b>ACA</b>	TTT	<b>GAG</b>	<b>GAG</b>	GCT	<b>GCA</b>	<b>TTA</b>
MG772934_Bat_SARS_like_CoV_bat_SL_CoVZXC21	AAG	CAT	<b>TTT</b>	TAT	TGG	TTC	TTT	AGT	<b>AAC</b>	TAC	CTA	AAG	AGA	CG	GTA	GTC	TTT	AAT	GGT	GTT	TCC	TTT	AGT	<b>ACA</b>	TTT	<b>GAG</b>	<b>GAG</b>	GCT	<b>GCA</b>	<b>TTA</b>
NC_004718_SARS_CoV	AAG	<b>CAC</b>	<b>TGC</b>	<b>CAT</b>	TGG	TTC	TTT	<b>AAC</b>	<b>AAC</b>	<b>TAT</b>	<b>CTT</b>	<b>AGG</b>	<b>AAA</b>	<b>AG</b>	<b>GTC</b>	ATG	TTT	AAT	<b>GGA</b>	GTT	<b>ACA</b>	TTT	AGT	<b>ACC</b>	<b>TTC</b>	<b>GAG</b>	<b>GAG</b>	GCT	<b>GCT</b>	<b>TTG</b>
KT444582_SARS_like_CoV_WIV16	AAG	<b>CAC</b>	<b>TGC</b>	<b>CAT</b>	TGG	TTC	TTT	<b>AAC</b>	<b>AAC</b>	<b>TAT</b>	<b>CTT</b>	<b>AGG</b>	<b>AAA</b>	<b>AG</b>	<b>GTC</b>	ATG	TTT	AAT	<b>GGA</b>	GTT	<b>ACA</b>	TTT	AGT	<b>ACC</b>	<b>TTC</b>	<b>GAG</b>	<b>GAG</b>	GCT	<b>GCT</b>	<b>TTG</b>
KY417146_Bat_SARS_like_CoV_Rs4231	AAG	<b>CAC</b>	<b>TGC</b>	<b>CAT</b>	TGG	TTC	TTT	<b>AAC</b>	<b>AAC</b>	<b>TAT</b>	<b>CTT</b>	<b>AGG</b>	<b>AAA</b>	<b>AG</b>	<b>GTC</b>	ATG	TTT	AAT	<b>GGA</b>	GTT	<b>ACA</b>	TTT	AGT	<b>ACC</b>	<b>TTC</b>	<b>GAG</b>	<b>GAG</b>	GCT	<b>GCT</b>	<b>TTG</b>
MK211376_CoV_BtRs_BetaCoV_YN2018B	AAG	<b>CAC</b>	<b>TGC</b>	<b>CAT</b>	TGG	TTC	TTT	<b>AAC</b>	<b>AAC</b>	<b>TAT</b>	<b>CTT</b>	<b>AGG</b>	<b>AAA</b>	<b>AG</b>	<b>GTC</b>	ATG	TTT	AAT	<b>GGA</b>	GTT	<b>ACA</b>	TTT	AGT	<b>ACC</b>	<b>TTC</b>	<b>GAG</b>	<b>GAG</b>	GCT	<b>GCT</b>	<b>TTG</b>
KY417151_Bat_SARS_like_CoV_Rs7327	AAG	<b>CAC</b>	<b>TGC</b>	<b>CAT</b>	TGG	TTC	TTT	<b>AAC</b>	<b>AAC</b>	<b>TAT</b>	<b>CTT</b>	<b>AGG</b>	<b>AAA</b>	<b>AG</b>	<b>GTC</b>	ATG	TTT	AAT	<b>GGA</b>	GTT	<b>ACA</b>	TTT	AGT	<b>ACC</b>	<b>TTC</b>	<b>GAG</b>	<b>GAG</b>	GCT	<b>GCT</b>	<b>TTG</b>
KY417152_Bat_SARS_like_CoV_Rs9401	AAG	<b>CAC</b>	<b>TGC</b>	<b>CAT</b>	TGG	TTC	TTT	<b>AAC</b>	<b>AAC</b>	<b>TAT</b>	<b>CTT</b>	<b>AGG</b>	<b>AAA</b>	<b>AG</b>	<b>GTC</b>	ATG	TTT	AAT	<b>GGA</b>	GTT	<b>ACA</b>	TTT	AGT	<b>ACC</b>	<b>TTC</b>	<b>GAG</b>	<b>GAG</b>	GCT	<b>GCT</b>	<b>TTG</b>
KY417144_Bat_SARS_like_CoV_Rs4084	AAG	<b>CAC</b>	<b>TGC</b>	<b>CAT</b>	TGG	TTC	TTT	<b>AAC</b>	<b>AAC</b>	<b>TAT</b>	<b>CTT</b>	<b>AGG</b>	<b>AAA</b>	<b>AG</b>	<b>GTC</b>	ATG	TTT	AAT	<b>GGA</b>	GTT	<b>ACA</b>	TTT	AGT	<b>ACC</b>	<b>TTC</b>	<b>GAG</b>	<b>GAG</b>	GCT	<b>GCT</b>	<b>TTG</b>
KF367457_Bat_SARS_like_CoV_WIV1	AAG	<b>CAC</b>	<b>TGC</b>	<b>CAT</b>	TGG	TTC	TTT	<b>AAC</b>	<b>AAC</b>	<b>TAT</b>	<b>CTT</b>	<b>AGG</b>	<b>AAA</b>	<b>AG</b>	<b>GTC</b>	ATG	TTT	AAT	<b>GGA</b>	GTT	<b>ACA</b>	TTT	AGT	<b>ACC</b>	<b>TTC</b>	<b>GAG</b>	<b>GAG</b>	GCT	<b>GCT</b>	<b>TTG</b>
KU973692_UNVERIFIEDED_SARS_related_CoV_F46	AAG	<b>CAC</b>	<b>TGC</b>	<b>CAT</b>	TGG	TTC	TTT	<b>AAC</b>	<b>AAC</b>	<b>TAT</b>	<b>CTT</b>	<b>AGG</b>	<b>AAA</b>	<b>AG</b>	<b>GTC</b>	ATG	TTT	AAT	<b>GGA</b>	GTT	<b>ACA</b>	<b>TTT</b>	AGT	<b>ACC</b>	<b>TTC</b>	<b>GAG</b>	<b>GAG</b>	<b>GCA</b>	<b>GCT</b>	<b>TTG</b>
KY417145_Bat_SARS_like_CoV_Rf4092	AAG	<b>CAC</b>	<b>TGC</b>	<b>CAT</b>	TGG	TTC	TTT	<b>AAC</b>	<b>AAC</b>	<b>TAT</b>	<b>CTT</b>	<b>AGG</b>	<b>AAA</b>	<b>AG</b>	<b>GTC</b>	ATG	TTT	AAT	<b>GGA</b>	GTT	<b>ACA</b>	TTT	AGT	<b>ACC</b>	<b>TTC</b>	<b>GAG</b>	<b>GAG</b>	GCT	<b>GCT</b>	<b>TTG</b>
KJ473816_BtRs_BetaCoV_YN2013	AAG	<b>CAC</b>	<b>TGC</b>	<b>CAT</b>	TGG	TTC	TTT	<b>AAC</b>	<b>AAC</b>	<b>TAT</b>	<b>CTT</b>	<b>AGG</b>	<b>AAA</b>	<b>AG</b>	<b>GTC</b>	ATG	TTT	AAT	<b>GGA</b>	GTT	<b>ACA</b>	TTT	AGT	<b>ACC</b>	<b>TTC</b>	<b>GAG</b>	<b>GAG</b>	GCT	<b>GCT</b>	<b>TTG</b>
KY770858_Bat_CoV_Anlong_103	AAG	<b>CAC</b>	<b>TTT</b>	<b>CAT</b>	TGG	TTC	TTT	<b>AAT</b>	<b>AAT</b>	<b>TAT</b>	<b>CTT</b>	<b>AGG</b>	<b>AAA</b>	<b>AG</b>	<b>GTC</b>	ATG	TTT	AAT	<b>GGA</b>	GTT	<b>ACA</b>	TTT	AGT	<b>ACC</b>	<b>TTC</b>	<b>GAG</b>	<b>GAG</b>	GCT	<b>GCT</b>	<b>TTG</b>
KY417143_Bat_SARS_like_CoV_Rs4081	AAG	<b>CAC</b>	<b>TGC</b>	<b>CAT</b>	TGG	TTC	TTT	<b>AAC</b>	<b>AAC</b>	<b>TAT</b>	<b>CTT</b>	<b>AGG</b>	<b>AAA</b>	<b>AG</b>	<b>GTC</b>	ATG	TTT	AAT	<b>GGA</b>	GTT	<b>ACA</b>	TTT	AGT	<b>ACC</b>	<b>TTC</b>	<b>GAG</b>	<b>GAG</b>	GCT	<b>GCT</b>	<b>TTG</b>
KY417149_Bat_SARS_like_CoV_Rs4255	AAG	<b>CAC</b>	<b>TGC</b>	<b>CAT</b>	TGG	TTC	TTT	<b>AAC</b>	<b>AAC</b>	<b>TAT</b>	<b>CTT</b>	<b>AGG</b>	<b>AAA</b>	<b>AG</b>	<b>GTC</b>	ATG	TTT	AAT	<b>GGA</b>	GTT	<b>ACA</b>	TTT	AGT	<b>ACC</b>	<b>TTC</b>	<b>GAG</b>	<b>GAG</b>	GCT	<b>GCT</b>	<b>TTG</b>
MK211378_CoV_BtRs_BetaCoV_YN2018D	AAG	<b>CAC</b>	<b>TGC</b>	<b>CAT</b>	TGG	TTC	TTT	<b>AAC</b>	<b>AAC</b>	<b>TAT</b>	<b>CTT</b>	<b>AGG</b>	<b>AAA</b>	<b>AG</b>	<b>GTC</b>	ATG	TTT	AAT	<b>GGA</b>	GTT	<b>ACA</b>	TTT	AGT	<b>ACC</b>	<b>TTC</b>	<b>GAG</b>	<b>GAG</b>	GCT	<b>GCT</b>	<b>TTG</b>
FJ588686_Bat_SARS_CoV_Rs672_2006	AAG	<b>CAC</b>	<b>TGC</b>	<b>CAT</b>	TGG	TTC	TTT	<b>AAC</b>	<b>AAC</b>	<b>TAT</b>	<b>CTT</b>	<b>AGG</b>	<b>AAA</b>	<b>AG</b>	<b>GTC</b>	ATG	TTT	AAT	<b>GGA</b>	GTT	<b>ACA</b>	TTT	AGT	ACT	<b>TTC</b>	<b>GAG</b>	<b>GAG</b>	GCT	<b>GCT</b>	<b>TTG</b>
MK211377_CoV_BtRs_BetaCoV_YN2018C	AAG	<b>CAC</b>	<b>TGC</b>	<b>CAT</b>	TGG	TTC	TTT	<b>AAC</b>	<b>AAC</b>	<b>TAT</b>	<b>CTT</b>	<b>AGG</b>	<b>AAA</b>	<b>AG</b>	<b>GTC</b>	ATG	TTT	AAT	<b>GGA</b>	GTT	<b>ACA</b>	TTT	AGT	<b>ACC</b>	<b>TTC</b>	<b>GAG</b>	<b>GAG</b>	GCT	<b>GCT</b>	<b>TTG</b>
KY417142_Bat_SARS_like_CoV_As6526	AAG	<b>CAC</b>	<b>TGC</b>	<b>CAT</b>	TGG	TTC	TTT	<b>AAC</b>	<b>AAC</b>	<b>TAT</b>	<b>CTT</b>	<b>AGG</b>	<b>AAA</b>	<b>AG</b>	<b>GTC</b>	ATG	TTT	AAT	<b>GGA</b>	GTT	<b>ACA</b>	TTT	AGT	<b>ACC</b>	<b>TTC</b>	<b>GAG</b>	<b>GAG</b>	GCT	<b>GCT</b>	<b>TTG</b>
KY417147_Bat_SARS_like_CoV_Rs4237	AAG	<b>CAC</b>	<b>TGC</b>	<b>CAT</b>	TGG	TTC	TTT	<b>AAC</b>	<b>AAC</b>	<b>TAT</b>	<b>CTT</b>	<b>AGG</b>	<b>AAA</b>	<b>AG</b>	<b>GTC</b>	ATG	TTT	AAT	<b>GGA</b>	GTT	<b>ACA</b>	TTT	AGT	<b>ACC</b>	<b>TTC</b>	<b>GAG</b>	<b>GAG</b>	GCT	<b>GCT</b>	<b>TTG</b>
KY417148_Bat_SARS_like_CoV_Rs4247	AAG	<b>CAC</b>	<b>TGC</b>	<b>CAT</b>	TGG	TTC	TTT	<b>AAC</b>	<b>AAC</b>	<b>TAT</b>	<b>CTT</b>	<b>AGG</b>	<b>AAA</b>	<b>AG</b>	<b>GTC</b>	ATG	TTT	AAT	<b>GGA</b>	GTT	<b>ACA</b>	TTT	AGT	<b>ACC</b>	<b>TTC</b>	<b>GAG</b>	<b>GAG</b>	GCT	<b>GCT</b>	<b>TTG</b>
MK211375_CoV_BtRs_BetaCoV_YN2018A	AAG	<b>CAC</b>	<b>TGC</b>	<b>CAT</b>	TGG	TTC	TTT	<b>AAC</b>	<b>AAC</b>	<b>TAT</b>	<b>CTT</b>	<b>AGG</b>	<b>AAA</b>	<b>AG</b>	<b>GTC</b>	ATG	TTT	AAT	<b>GGA</b>	GTT	<b>ACA</b>	TTT	AGT	<b>ACC</b>	TTT	<b>GAG</b>	<b>GAG</b>	GCT	<b>GCT</b>	<b>TTG</b>
DQ071615_Bat_SARS_CoV_Rp3	AAG	<b>CAC</b>	<b>TTT</b>	<b>CAC</b>	TGG	TTC	TTT	<b>AAT</b>	<b>AAT</b>	<b>TAT</b>	<b>CTT</b>	<b>AGG</b>	<b>AAA</b>	<b>AG</b>	<b>GTC</b>	<b>GTG</b>	TTT	AAT	<b>GGA</b>	GTT	<b>ACA</b>	TTT	AGT	<b>ACC</b>	<b>TTC</b>	<b>GAG</b>	<b>GAG</b>	GCT	<b>GCT</b>	<b>TTG</b>
KP886808_Bat_SARS_like_CoV_YNLF_31C	AAG	<b>CAC</b>	<b>TGC</b>	<b>CAT</b>	TGG	TTC	TTT	<b>AAC</b>	<b>AAC</b>	<b>TAT</b>	<b>CTT</b>	<b>AGG</b>	<b>AAA</b>	<b>AG</b>	<b>GTC</b>	ATG	TTT	AAT	<b>GGA</b>	GTT	<b>ACA</b>	TTT	AGT	<b>ACC</b>	<b>TTC</b>	<b>GAG</b>	<b>GAG</b>	GCT	<b>GCT</b>	<b>TTG</b>
KJ473815_BtRs_BetaCoV_GX2013	AAG	<b>CAC</b>	<b>TGT</b>	<b>CAC</b>	TGG	TTC	TTT	<b>AAT</b>	<b>AAT</b>	<b>TAT</b>	<b>CTT</b>	<b>AGG</b>	<b>AAA</b>	<b>AG</b>	<b>GTC</b>	ATG	TTT	AAT	<b>GGA</b>	GTT	<b>ACA</b>	<b>TTT</b>	AGT	ACT	<b>TTC</b>	GAA	GAA	GCT	<b>GCT</b>	<b>TTG</b>
KF569996_Rhinolophus_affinis_CoV_LYRa11	AAG	<b>CAC</b>	<b>TGC</b>	<b>CAC</b>	TGG	TTC	TTT	<b>AAC</b>	<b>AAC</b>	<b>TAT</b>	<b>CTT</b>	<b>AGG</b>	<b>AAA</b>	<b>AG</b>	<b>GTC</b>	ATG	TTT	AAT	<b>GGA</b>	GTT	<b>ACA</b>	TTT	<b>AGC</b>	<b>ACC</b>	TTT	<b>GAG</b>	<b>GAG</b>	<b>GCG</b>	<b>GCT</b>	<b>TTA</b>
JX993988_Bat_CoV_Cp_Yunnan2011	AAG	<b>CAC</b>	<b>TGT</b>	<b>CAT</b>	TGG	TTC	TTT	<b>AAT</b>	<b>AAT</b>	<b>TAT</b>	<b>CTT</b>	<b>AGG</b>	<b>AAA</b>	<b>AG</b>	<b>GTC</b>	ATG	TTT	AAT	<b>GGA</b>	GTT	<b>ACA</b>	<b>TTT</b>	AGT	ACT	<b>TTC</b>	GAA	GAA	GCT	<b>GCT</b>	<b>TTG</b>
MK211374_CoV_BtR1_BetaCoV_SC2018	AAG	<b>CAC</b>	<b>TGC</b>	<b>CAT</b>	TGG	TTC	TTT	<b>AGC</b>	<b>AAC</b>	<b>TAT</b>	<b>CTT</b>	<b>AGG</b>	<b>AAA</b>	<b>AG</b>	<b>GTC</b>	ATG	TTT	AAT	<b>GGA</b>	GTT	<b>ACA</b>	TTT	AGT	<b>ACC</b>	<b>TTC</b>	<b>GAG</b>	<b>GAG</b>	GCT	<b>GCT</b>	<b>TTG</b>
KJ473814_BtRs_BetaCoV_HuB2013	AAG	<b>CAC</b>	<b>TGT</b>	<b>CAT</b>	TGG	TTC	TTT	<b>AAC</b>	<b>AAC</b>	<b>TAT</b>	<b>CTT</b>	<b>AGG</b>	<b>AAA</b>	<b>AG</b>	<b>GTC</b>	ATG	TTT	AAT	<b>GGA</b>	GTT	<b>ACA</b>	<b>TTT</b>	<b>AGC</b>	<b>ACC</b>	TTT	<b>GAG</b>	<b>GAG</b>	<b>GCA</b>	<b>GCT</b>	<b>TTG</b>
DQ412043_Bat_SARS_CoV_Rm1	<b>AGG</b>	<b>CAC</b>	<b>TGT</b>	<b>CAT</b>	TGG	TTC	TTT	<b>AAT</b>	<b>AAC</b>	<b>TAT</b>	<b>CTT</b>	<b>AGG</b>	<b>AAA</b>	<b>AG</b>	<b>GTC</b>	ATG	TTT	AAT	<b>GGA</b>	GTT	<b>ACA</b>	TTT	<b>AGC</b>	<b>ACC</b>	TTT	<b>GAG</b>	<b>GAG</b>	<b>GCA</b>	<b>GCT</b>	<b>TTG</b>
KY938558_Bat_CoV_strain_16B0133	AAG	<b>CAC</b>	<b>TGC</b>	<b>CAC</b>	TGG	TTC	TTT	<b>AAT</b>	<b>AAC</b>	TAC	<b>CTT</b>	AAG	AGA	<b>AG</b>	<b>GTC</b>	ATG	TTT	AAT	<b>GGA</b>	GTT	<b>ACA</b>	TTT	<b>AGC</b>	<b>ACC</b>	TTT	<b>GAG</b>	<b>GAG</b>	GCT	<b>GCT</b>	<b>TTA</b>
DQ412042_Bat_SARS_CoV_Rf1	AAG	<b>CAC</b>	<b>TGC</b>	<b>CAC</b>	TGG	TTC	TTT	<b>AAT</b>	<b>AAC</b>	TAC	<b>CTT</b>	AAG	AGA	<b>AG</b>	<b>GTC</b>	ATG	TTT	AAT	<b>GGA</b>	GTT	<b>ACA</b>	TTT	<b>AGC</b>	<b>ACC</b>	TTT	<b>GAG</b>	<b>GAG</b>	GCT	<b>GCT</b>	<b>TTA</b>
DQ648856_Bat_CoV_BtCoV_273_2005	AAG	<b>CAC</b>	<b>TGC</b>	<b>CAC</b>	TGG	TTC	TTT	<b>AAT</b>	<b>AAC</b>	TAC	<b>CTT</b>	AAG	AGA	<b>AG</b>	<b>GTC</b>	ATG	TTT	AAT	<b>GGA</b>	GTT	<b>ACA</b>	TTT	<b>AGC</b>	<b>ACC</b>	TTT	<b>GAG</b>	<b>GAG</b>	GCT	<b>GCT</b>	<b>TTA</b>
KJ473812_BtRf_BetaCoV_HeB2013	AAG	<b>CAC</b>	<b>TGC</b>	<b>CAC</b>	TGG	TTC	TTT	<b>AAT</b>	<b>AAC</b>	TAC	<b>CTT</b>	AAG	AGA	<b>AG</b>	<b>GTC</b>	ATG	TTT	AAT	<b>GGA</b>	GTT	<b>ACA</b>	TTT	<b>AGC</b>	<b>ACC</b>	TTT	<b>GAG</b>	<b>GAG</b>	GCT	<b>GCT</b>	<b>TTA</b>
KY770860_Bat_CoV_Jiyuan_84	AAG	<b>CAC</b>	<b>TGC</b>	<b>CAC</b>	TGG	TTC	TTT	<b>AAT</b>	<b>AAC</b>	TAC	<b>CT</b>																			



# RaTG13 Bsal Restriction Site 10,435

The out-of-frame GAGACC is found in RaTG13 and 52 out of 57 of the other sarbecoviruses.

Only five of 58 viruses do NOT have this restriction site, including SARS-CoV-2.

Accession	NC_045512_SARS_CoV_2_Wuhan_Hu_1_aa	C	A	M	R	P	N	F	T	I	K	G	S	F	L	N	G	S	C	G	S	V	G	F	N	I	D	Y	D	C	V	
NC_045512_SARS_CoV_2_Wuhan_Hu_1	TGT	GCT	ATG	AGG	CCC	AAT	TTC	ACT	ATT	AAG	GGT	TCA	TTC	CTT	AAT	GGT	TCA	TGT	GGT	AGT	GTT	GGT	TTT	AAC	ATA	GAT	TAT	GAC	TGT	GTC		
MN996532_Bat_CoV_RaTG13	TGT	GCT	ATG	AGA	CCT	AAC	TTT	ACA	ATT	AAG	GGT	TCA	TTC	CTT	AAT	GGT	TCT	TGT	GGT	AGT	GTT	GGT	TTT	AAC	ATA	GAT	TAT	GAC	TGT	GTC		
MG772933_Bat_SARS_like_CoV_bat_SL_CoVZC45	TGT	GCC	ATG	AGA	CCT	AAT	TTT	ACT	ATT	AAG	GGT	TCA	TTC	CTT	AAT	GGT	TCA	TGT	GGT	AGT	GTT	GGT	TTT	AAT	ATA	GAC	TAT	GAC	TGT	GTC		
MG772934_Bat_SARS_like_CoV_bat_SL_CoVZXC21	TGT	GCC	ATG	AGA	CCT	AAT	TTT	ACT	ATT	AAG	GGT	TCA	TTC	CTT	AAT	GGT	TCA	TGT	GGT	AGT	GTT	GGT	TTT	AAT	ATA	GAC	TAT	GAC	TGT	GTC		
NC_004718_SARS_CoV	TGT	GCC	ATG	AGA	CCT	AAT	CAT	ACC	ATT	AAA	GGT	TCT	TTC	CTT	AAT	GGT	TCA	TGT	GGT	AGT	GTT	GGT	TTT	AAC	ATT	GAT	TAT	GAT	TGC	GTG		
KT444582_SARS_like_CoV_WIV16	TGT	GCC	ATG	AGA	CCT	AAC	CAT	ACC	ATT	AAA	GGT	TCT	TTC	CTT	AAT	GGT	TCA	TGT	GGT	AGT	GTT	GGT	TTT	AAC	ATT	GAT	TAT	GAT	TGC	GTG		
KY417146_Bat_SARS_like_CoV_Rs4231	TGT	GCC	ATG	AGA	CCT	AAC	CAT	ACC	ATT	AAA	GGT	TCT	TTC	CTT	AAT	GGT	TCA	TGT	GGT	AGT	GTT	GGT	TTT	AAC	ATT	GAT	TAT	GAT	TGC	GTG		
MK211376_CoV_BtRs_BetaCoV_YN2018B	TGT	GCC	ATG	AGA	CCT	AAC	CAT	ACC	ATT	AAA	GGT	TCT	TTC	CTT	AAT	GGT	TCA	TGT	GGT	AGT	GTT	GGT	TTT	AAC	ATT	GAT	TAT	GAT	TGC	GTG		
KY417151_Bat_SARS_like_CoV_Rs7327	TGT	GCC	ATG	AGA	CCT	AAC	CAT	ACC	ATT	AAA	GGT	TCT	TTC	CTT	AAT	GGT	TCA	TGT	GGT	AGT	GTT	GGT	TTT	AAC	ATT	GAT	TAT	GAT	TGC	GTG		
KY417152_Bat_SARS_like_CoV_Rs9401	TGT	GCC	ATG	AGA	CCT	AAC	CAT	ACC	ATT	AAA	GGT	TCT	TTC	CTT	AAT	GGT	TCA	TGT	GGT	AGT	GTT	GGT	TTT	AAC	ATT	GAT	TAT	GAT	TGC	GTG		
KY417144_Bat_SARS_like_CoV_Rs4084	TGT	GCC	ATG	AGA	CCT	AAC	CAT	ACC	ATT	AAA	GGT	TCT	TTC	CTT	AAT	GGT	TCA	TGT	GGT	AGT	GTT	GGT	TTT	AAC	ATT	GAT	TAT	GAT	TGC	GTG		
KF367457_Bat_SARS_like_CoV_WIV1	TGT	GCC	ATG	AGA	CCT	AAC	CAT	ACC	ATT	AAA	GGT	TCT	TTC	CTT	AAT	GGT	TCA	TGT	GGT	AGT	GTT	GGT	TTT	AAC	ATT	GAT	TAT	GAT	TGC	GTG		
KU973692_UNVERIFIEDED_SARS_related_CoV_F46	TGT	GCC	ATG	AGA	CCT	AAT	TAC	ACT	ATT	AAG	GGC	TCT	TTC	CTT	AAT	GGT	TCA	TGT	GGT	AGT	GTT	GGT	TTT	AAC	AAT	ATT	GAC	TAT	GAT	TGC	GTG	
KY417145_Bat_SARS_like_CoV_Rf4092	TGT	GCC	ATG	AGA	CCT	AAC	CAT	ACC	ATT	AAA	GGT	TCT	TTC	CTT	AAT	GGT	TCA	TGT	GGT	AGT	GTT	GGT	TTT	AAC	ATT	GAT	TAT	GAT	TGC	GTG		
KJ473816_BtRs_BetaCoV_YN2013	TGT	GCC	ATG	AGA	CCT	AAC	CAT	ACC	ATT	AAA	GGT	TCT	TTC	CTT	AAT	GGT	TCA	TGT	GGT	AGT	GTT	GGT	TTT	AAC	ATT	GAT	TAT	GAT	TGC	GTG		
KY770858_Bat_CoV_Anlong_103	TGT	GCC	ATG	AGA	CCT	AAT	CAC	ACC	ATT	AAA	GGT	TCT	TTC	CTA	AAT	GGT	TCA	TGT	GGT	AGT	GTT	GGT	TTT	AAC	ATA	GAC	TAT	GAT	TGC	GTG		
KY417143_Bat_SARS_like_CoV_Rs4081	TGT	GCC	ATG	AGA	CCT	AAC	CAT	ACC	ATT	AAA	GGT	TCT	TTC	CTT	AAT	GGT	TCA	TGT	GGT	AGT	GTT	GGT	TTT	AAC	ATT	GAT	TAT	GAT	TGC	GTG		
KY417149_Bat_SARS_like_CoV_Rs4255	TGT	GCC	ATG	AGA	CCT	AAC	CAT	ACC	ATT	AAA	GGT	TCT	TTC	CTT	AAT	GGT	TCA	TGT	GGT	AGT	GTT	GGT	TTT	AAC	ATT	GAT	TAT	GAT	TGC	GTG		
MK211378_CoV_BtRs_BetaCoV_YN2018D	TGT	GCC	ATG	AGA	CCT	AAC	CAT	ACC	ATT	AAA	GGT	TCT	TTC	CTT	AAT	GGT	TCA	TGT	GGT	AGT	GTT	GGT	TTT	AAC	ATT	GAT	TAT	GAT	TGC	GTG		
FJ588686_Bat_SARS_CoV_Rs672_2006	TGT	GCC	ATG	AGA	TCT	AAT	CAC	ACC	ATT	AAA	GGT	TCT	TTC	CTT	AAT	GGT	TCA	TGT	GGT	AGT	GTT	GGT	TTT	AAC	GTT	GAT	TAT	GAT	TGC	GTG		
MK211377_CoV_BtRs_BetaCoV_YN2018C	TGT	GCC	ATG	AGA	CCT	AAC	CAT	ACC	ATT	AAA	GGT	TCT	TTC	CTT	AAT	GGT	TCA	TGT	GGT	AGT	GTT	GGT	TTT	AAC	ATT	GAT	TAT	GAT	TGC	GTG		
KY417142_Bat_SARS_like_CoV_As6526	TGT	GCC	ATG	AGA	CCT	AAC	CAT	ACC	ATT	AAA	GGT	TCT	TTC	CTT	AAT	GGT	TCA	TGT	GGT	AGT	GTT	GGT	TTT	AAC	ATT	GAT	TAT	GAT	TGC	GTG		
KY417147_Bat_SARS_like_CoV_Rs4237	TGT	GCC	ATG	AGA	CCT	AAT	CAT	ACC	ATT	AAA	GGT	TCT	TTC	CTT	AAT	GGT	TCA	TGT	GGT	AGT	GTT	GGT	TTT	AAC	ATT	GAT	TAT	GAT	TGC	GTG		
KY417148_Bat_SARS_like_CoV_Rs4247	TGT	GCC	ATG	AGA	CCT	AAC	CAT	ACC	ATT	AAA	GGT	TCT	TTC	CTT	AAT	GGT	TCA	TGT	GGT	AGT	GTT	GGT	TTT	AAC	ATT	GAT	TAT	GAT	TGC	GTG		
MK211375_CoV_BtRs_BetaCoV_YN2018A	TGT	GCC	ATG	AGA	CCT	AAC	CAT	ACC	ATT	AAA	GGT	TCT	TTC	CTT	AAT	GGT	TCA	TGT	GGT	AGT	GTT	GGT	TTT	AAC	ATT	GAT	TAT	GAT	TGC	GTG		
DQ071615_Bat_SARS_CoV_Rp3	TGT	GCC	ATG	AGA	CCT	AAT	CAC	ACT	ATT	AAA	GGT	TCT	TTC	CTA	AAT	GGT	TCA	TGT	GGT	AGT	GTT	GGT	TTT	AAC	ATA	GAC	TAT	GAT	TGC	GTG		
KP886808_Bat_SARS_like_CoV_YNLF_31C	TGT	GCC	ATG	AGA	CCT	AAT	CAC	ACC	ATT	AAA	GGT	TCT	TTC	CTA	AAT	GGT	TCA	TGT	GGT	AGT	GTT	GGT	TTT	AAC	ATA	GAC	TAT	GAT	TGC	GTG		
KJ473815_BtRs_BetaCoV_GX2013	TGT	GCC	ATG	AGA	CCT	AAT	CAC	ACC	ATT	AAA	GGT	TCT	TTC	CTT	AAT	GGT	TCA	TGT	GGT	AGT	GTT	GGT	TTT	AAC	ATT	GAT	TAT	GAT	TGC	GTG		
KF569996_Rhinolophus_affinis_CoV_LYRa11	TGT	GCT	ATG	AGA	CCT	AAT	TAT	ACT	ATC	AAG	GGT	TCT	TTC	CTT	AAT	GGT	TCA	TGT	GGT	AGT	GTT	GGT	TTT	AAC	AAT	ATT	GAC	TAT	GAT	TGC	GTG	
JX993988_Bat_CoV_Cp_Yunnan2011	TGT	GCC	ATG	AGA	CCT	AAC	CAC	ACC	ATC	AAG	GGT	TCT	TTC	CTT	AAT	GGT	TCA	TGT	GGT	AGT	GTT	GGT	TTT	AAC	AAT	ATT	GAC	TAT	GAT	TGC	GTG	
MK211374_CoV_BtR1_BetaCoV_SC2018	TGT	GCC	ATG	AGA	CCT	AAT	CAC	ACC	ATT	AAA	GGT	TCT	TTC	CTA	AAT	GGT	TCA	TGT	GGT	AGT	GTT	GGT	TTT	AAC	AAT	ATA	GAC	TAT	GAT	TGC	GTG	
KJ473814_BtRs_BetaCoV_HuB2013	TGT	GCC	ATG	AGA	CCC	AAC	CAT	ACC	ATT	AAG	GGT	TCT	TTC	CTT	AAT	GGT	TCA	TGT	GGT	AGT	GTT	GGT	TTT	AAC	ATT	GAC	TAT	GAT	TGC	GTG		
DQ412043_Bat_SARS_CoV_Rm1	TGT	GCC	ATG	AGA	CCA	AAT	TAC	ACC	ATC	AAG	GGT	TCT	TTC	CTT	AAT	GGT	TCA	TGT	GGT	AGT	GTT	GGT	TTT	AAC	ATT	GAT	TAT	GAT	TGC	GTG		
KY938558_Bat_CoV_strain_16B0133	TGT	GCC	ATG	AGA	CCT	AAC	TAC	ACC	ATT	AAG	GGT	TCT	TTC	CTC	AAC	GGG	TCA	TGT	GGT	AGT	GTT	GGT	TTT	AAC	ATT	GAC	TAT	GAT	TGC	GTG		
DQ412042_Bat_SARS_CoV_Rf1	TGT	GCC	ATG	AGA	CCT	AAC	TAC	ACC	ATT	AAG	GGT	TCT	TTC	CTC	AAT	GGG	TCA	TGT	GGT	AGT	GTT	GGT	TTT	AAC	ATT	GAC	TAT	GAT	TGC	GTG		
DQ648856_Bat_CoV_BtCoV_273_2005	TGT	GCC	ATG	AGA	CCT	AAC	TAC	ACC	ATT	AAG	GGT	TCT	TTC	CTC	AAT	GGG	TCA	TGT	GGT	AGT	GTT	GGT	TTT	AAC	ATT	GAC	TAT	GAT	TGC	GTG		
KJ473812_BtRf_BetaCoV_HeB2013	TGT	GCC	ATG	AGA	CCT	AAC	TAC	ACC	ATT	AAG	GGT	TCT	TTC	CTC	AAT	GGG	TCA	TGT	GGT	AGT	GTT	GGT	TTT	AAC	ATT	GAC	TAT	GAT	TGC	GTG		
KY770860_Bat_CoV_Jiyuan_84	TGT	GCC	ATG	AGA	TCT	AAC	TAC	ACC	ATT	AAG	GGT	TCT	TTC	CTC	AAT	GGG	TCA	TGT	GGT	AGT	GTT	GGT	TTT	AAC	ATT	GAC	TAT	GAT	TGC	GTG		
JX993987_Bat_CoV_Rp_Shaanxi2011	TGT	GCT	ATG	AGA	CCT	AAT	CAT	ACC	ATC	AAG	GGT	TCT	TTC	CTT	AAT	GGT	TCA	TGT	GGT	AGT	GTT	GGT	TTT	AAC	ATT	GAC	TAT	GAT	TGC	GTG		
GQ153542_Bat_SARS_CoV_HKU3_7	TGT	GCC	ATG	AGA	CCT	AAT	TAC	ACC	ATT	AAG	GGT	TCC	TTC	CTT	AAT	GGT	TCA	TGT	GGT	AGT	GTT	GGT	TTT	AAC	ATT	GAT	TAT	GAT	TGC	GTG		
DQ022305_Bat_SARS_CoV_HKU3_1	TGT	GCC	ATG	AGA	CCT	AAT	CAC	ACC	ATT	AAG	GGT	TCC	TTC	CTT	AAT	GGT	TCA	TGT	GGT	AGT	GTT	GGT	TTT	AAC	ATT	GAT	TAT	GAT	TGC	GTG		
GQ153547_Bat_SARS_CoV_HKU3_12	TGT	GCC	ATG	AGA	CCT	AAT	TAC	ACC	ATT	AAG	GGT	TCC	TTC	CTT	AAT	GGT	TCA	TGT	GGT	AGT	GTT	GGT	TTT	AAC	AAT	ATT	GAT	TAT	GAT	TGC	GTG	
KY352407_SARS_related_CoV_strain_BtKY72	TGT	GCA	ATG	AGA	CCT	AAC	TTT	ACT	ATT	AAA	GGT	TCA	TTC	CTT	AAT	GGT	TCT	TGT	GGT	AGT	GTT	GGT	TTT	AAC	TTC	AAC	ATA	GAC	TAT	GAC	TGT	GTC
NC_014470_Bat_CoV_BM48_31_BGR_2008	TGT	GCA	ATG	AGG	TCC	AAC	CAC	ACT	ATT	AAG	GGT	TCA	TTC	CTT	AAT	GGT	TCT	TGT	GGT	AGT	GTT	GGT	TTT	AAC	ATT	GAC	TAT	GAC	TGC	GTG		

# RaTG13 Bsal Restriction Site 11,651

<b>RaTG13</b>	11638	TTACTTTGGTCTCTTTTGTCTTACTCAACCGTTACTTTAGACTGACTCTTGGTGTTTATGA	11697
<b>CoV-2</b>	11641	TTACTTTGGCCTCTTTTGTCTTACTCAACCGCTACTTTAGACTGACTCTTGGTGTTTATGA	11700

**RaTG13** 5'3' Frame 2  
ttactttggctctcttttgtcttactcaaccgttactttagactgactcttggtgtttat  
Y F G L F C L L N R Y F R L T L G V Y

**CoV-2** 5'3' Frame 2  
ttactttggcctctcttttgtcttactcaaccgctactttagactgactcttggtgtttat  
Y F G L F C L L N R Y F R L T L G V Y

**Synonymous mutation in homologous peptide region**

# RaTG13 Bsal Restriction Site 11,651

The in-frame GGTCTC site is found in only three of 57 sarbecoviruses, including RaTG13 but not SARS-CoV-2.

55 of 58 sarbecoviruses, including SARS-CoV-2, have this restriction site extinguished.

NC_045512_SARS_CoV_2_Wuhan_Hu_1_aa	L	V	Y	C	F	L	G	Y	F	C	T	C	Y	F	G	L	F	C	L	L	N	R	Y	F	R	L	T	L	G	V
NC_045512_SARS_CoV_2_Wuhan_Hu_1	CTA	GTT	TAT	TGT	TTC	TTA	GGC	TAT	TTT	TGT	ACT	TGT	TAC	TT	GGC	CTC	TT	TGT	TTA	CTC	AAC	CGC	TAC	TTT	AGA	CTG	ACT	CTT	GGT	GTT
MN996532_Bat_CoV_RaTG13	CTA	GTT	TAT	TGT	TTC	TTA	GGC	TAT	TTT	TGT	ACT	TGT	TAC	TT	GGT	CTC	TT	TGT	TTA	CTC	AAC	CGT	TAC	TTT	AGA	CTG	ACT	CTT	GGT	GTT
MG772933_Bat_SARS_like_CoV_bat_SL_CoVZC45	CTA	GTT	TAT	TGT	TTC	TTA	GGT	TAT	TTT	TGT	ACT	TGT	TAT	TT	GGT	CTC	TT	TGT	TTA	CTC	AAC	CGC	TAT	TTT	AGG	CTT	ACT	CTT	GGT	GTT
MG772934_Bat_SARS_like_CoV_bat_SL_CoVZXC21	CTA	GTT	TAT	TGT	TTC	TTA	GGT	TAT	TTT	TGT	ACT	TGT	TAT	TT	GGT	CTC	TT	TGT	TTA	CTC	AAC	CGC	TAT	TTT	AGG	CTT	ACT	CTT	GGT	GTT
NC_004718_SARS_CoV	CTT	GTT	TAT	TGT	TTC	TTA	GGC	TAT	TTT	TGT	TGC	TGC	TAC	TT	GGC	CTT	TT	TGT	TTA	CTC	AAC	CGT	TAC	TTT	AGG	CTT	ACT	CTT	GGT	GTT
KT444582_SARS_like_CoV_WIV16	CTT	GTT	TAT	TGT	TTC	TTA	GGC	TAT	TTT	TGT	TGC	TGC	TAT	TT	GGC	CTT	TT	TGT	TTA	CTC	AAC	CGT	TAC	TTT	AGG	CTT	ACT	CTT	GGT	GTT
KY417146_Bat_SARS_like_CoV_Rs4231	CTT	GTT	TAT	TGT	TTC	TTA	GGT	TAT	TTT	TGT	TGC	TGC	TAC	TT	GGC	CTT	TT	TGT	TTA	CTC	AAC	CGT	TAC	TTT	AGG	CTT	ACT	CTT	GGT	GTT
MK211376_CoV_BtRs_BetaCoV_YN2018B	CTT	GTT	TAT	TGT	TTC	TTA	GGC	TAT	TTT	TGT	TGC	TGC	TAT	TT	GGC	CTT	TT	TGT	TTA	CTC	AAC	CGT	TAC	TTT	AGG	CTT	ACT	CTT	GGT	GTT
KY417151_Bat_SARS_like_CoV_Rs7327	CTT	GTT	TAT	TGT	TTC	TTA	GGC	TAT	TTT	TGT	TGC	TGC	TAT	TT	GGC	CTT	TT	TGT	TTA	CTC	AAC	CGT	TAC	TTT	AGG	CTT	ACT	CTT	GGT	GTT
KY417152_Bat_SARS_like_CoV_Rs9401	CTT	GTT	TAT	TGT	TTC	TTA	GGC	TAT	TTT	TGT	TGC	TGC	TAT	TT	GGC	CTT	TT	TGT	TTA	CTC	AAC	CGT	TAC	TTT	AGG	CTT	ACT	CTT	GGT	GTT
KY417144_Bat_SARS_like_CoV_Rs4084	CTT	GTT	TAT	TGT	TTC	TTA	GGC	TAT	TTT	TGT	TGC	TGC	TAT	TT	GGC	CTT	TT	TGT	TTA	CTC	AAC	CGT	TAC	TTT	AGG	CTT	ACT	CTT	GGT	GTT
KF367457_Bat_SARS_like_CoV_WIV1	CTT	GTT	TAT	TGT	TTC	TTA	GGC	TAT	TTT	TGT	TGC	TGC	TAT	TT	GGC	CTT	TT	TGT	TTA	CTC	AAC	CGT	TAC	TTT	AGG	CTT	ACT	CTT	GGT	GTT
KU973692_UNVERIFIED_SARS_related_CoV_F46	CTT	GTT	TAT	TGT	TTC	TTA	GGC	TAT	TTT	TGT	TGC	TGC	TAT	TT	GGC	CTT	TT	TGT	TTA	CTC	AAC	CGC	TAC	TTT	AGG	CTT	ACT	CTT	GGT	GTT
KY417145_Bat_SARS_like_CoV_Rf4092	CTT	GTT	TAT	TGT	TTC	TTA	GGC	TAT	TTT	TGT	TGC	TGC	TAT	TT	GGC	CTT	TT	TGT	TTA	CTC	AAC	CGT	TAC	TTT	AGG	CTT	ACT	CTT	GGT	GTT
KJ473816_BtRs_BetaCoV_YN2013	CTT	GTT	TAT	TGT	TTC	TTA	GGC	TAT	TTT	TGT	TGC	TGC	TAT	TT	GGC	CTT	TT	TGT	TTA	CTC	AAC	CGT	TAC	TTT	AGG	CTT	ACT	CTT	GGT	GTT
KY770858_Bat_CoV_Anlong_103	CTT	GTT	TAT	TGT	TTC	TTA	GGT	TAT	TTT	TGT	TGC	TGC	TAC	TT	GGC	CTT	TT	TGT	TTA	CTC	AAC	CGT	TAC	TTT	AGG	CTT	ACT	CTT	GGT	GTT
KY417143_Bat_SARS_like_CoV_Rs4081	CTT	GTT	TAT	TGT	TTC	TTA	GGC	TAT	TTT	TGT	TGC	TGC	TAT	TT	GGC	CTT	TT	TGT	TTA	CTC	AAC	CGT	TAC	TTT	AGG	CTT	ACT	CTT	GGT	GTT
KY417149_Bat_SARS_like_CoV_Rs4255	CTT	GTT	TAT	TGT	TTC	TTA	GGC	TAT	TTT	TGT	TGC	TGC	TAT	TT	GGC	CTT	TT	TGT	TTA	CTC	AAC	CGT	TAC	TTT	AGG	CTT	ACT	CTT	GGT	GTT
MK211378_CoV_BtRs_BetaCoV_YN2018D	CTT	GTT	TAT	TGT	TTC	TTA	GGC	TAT	TTT	TGT	TGC	TGC	TAT	TT	GGC	CTT	TT	TGT	TTA	CTC	AAC	CGT	TAC	TTT	AGG	CTT	ACT	CTT	GGT	GTT
FJ588686_Bat_SARS_CoV_Rs672_2006	CTT	GTT	TAT	TGT	TTC	TTA	GGT	TAT	TTT	TGT	TGC	TGC	TAC	TT	GGC	CTT	TT	TGT	TTA	CTC	AAC	CGT	TAC	TTT	AGG	CTT	ACT	CTT	GGT	GTT
MK211377_CoV_BtRs_BetaCoV_YN2018C	CTT	GTT	TAT	TGT	TTC	TTA	GGC	TAT	TTT	TGT	TGC	TGC	TAT	TT	GGC	CTT	TT	TGT	TTA	CTC	AAC	CGT	TAC	TTT	AGG	CTT	ACT	CTT	GGT	GTT
KY417142_Bat_SARS_like_CoV_As6526	CTT	GTT	TAT	TGT	TTC	TTA	GGC	TAT	TTT	TGT	TGC	TGC	TAT	TT	GGC	CTT	TT	TGT	TTA	CTC	AAC	CGT	TAC	TTT	AGG	CTT	ACT	CTT	GGT	GTT
KY417147_Bat_SARS_like_CoV_Rs4237	CTT	GTT	TAT	TGT	TTC	TTA	GGT	TAT	TTT	TGT	TGC	TGC	TAC	TT	GGC	CTT	TT	TGT	TTA	CTC	AAC	CGT	TAC	TTT	AGG	CTT	ACT	CTT	GGT	GTT
KY417148_Bat_SARS_like_CoV_Rs4247	CTT	GTT	TAT	TGT	TTC	TTA	GGT	TAT	TTT	TGT	TGC	TGC	TAC	TT	GGC	CTT	TT	TGT	TTA	CTC	AAC	CGT	TAC	TTT	AGG	CTT	ACT	CTT	GGT	GTT
MK211375_CoV_BtRs_BetaCoV_YN2018A	CTT	GTT	TAT	TGT	TTC	TTA	GGT	TAT	TTT	TGT	TGC	TGC	TAC	TT	GGC	CTT	TT	TGT	TTA	CTC	AAC	CGT	TAC	TTT	AGG	CTT	ACT	CTT	GGT	GTT
DQ071615_Bat_SARS_CoV_Rp3	CTT	GTT	TAT	TGT	TTC	TTA	GGT	TAT	TTT	TGT	TGC	TGC	TAC	TT	GGC	CTT	TT	TGT	TTA	CTC	AAC	CGT	TAC	TTT	AGG	CTT	ACT	CTT	GGT	GTT
KP886808_Bat_SARS_like_CoV_YNLF_31C	CTT	GTT	TAT	TGT	TTC	TTA	GGC	TAT	TTT	TGT	TGC	TGC	TAC	TT	GGC	CTT	TT	TGT	TTA	CTC	AAC	CGT	TAC	TTT	AGG	CTT	ACT	CTT	GGT	GTT
KJ473815_BtRs_BetaCoV_GX2013	CTT	GTC	TAT	TGT	TTC	TTA	GGC	TAT	TTT	TGT	TGC	TGC	TAC	TT	GGC	CTT	TT	TGT	TTA	CTC	AAC	CGC	TAC	TTT	AGG	CTT	ACT	CTT	GGT	GTT
KF569996_Rhinolophus_affinis_CoV_LYRa11	CTT	GTC	TAT	TGT	TTC	TTG	GGC	TAT	TTT	TGT	TGC	TGC	TAC	TT	GGC	CTT	TT	TGT	TTA	CTC	AAC	CGC	TAC	TTT	AGA	CTT	ACT	CTT	GGT	GTT
JX993988_Bat_CoV_Cp_Yunnan2011	CTT	GTT	TAT	TGT	TTC	TTG	GGC	TAT	TTT	TGT	TGC	TGC	TAC	TT	GGT	CTT	TT	TGT	TTA	CTC	AAC	CGC	TAC	TTT	AGA	CTT	ACT	CTT	GGT	GTT
MK211374_CoV_BtR1_BetaCoV_SC2018	CTT	GTT	TAT	TGT	TTC	TTA	GGC	TAT	TTT	TGT	TGC	TGC	TAC	TT	GGC	CTT	TT	TGT	TTA	CTC	AAC	CGT	TAC	TTT	AGG	CTT	ACT	CTT	GGT	GTT
KJ473814_BtRs_BetaCoV_HuB2013	CTT	GTC	TAT	TGT	TTC	TTA	GGC	TAT	TTT	TGT	TGC	TGC	TAC	TT	GGT	CTG	TT	TGT	TTA	CTC	AAC	CGT	TAC	TTT	AGA	CTT	ACT	CTT	GGT	GTT
DQ412043_Bat_SARS_CoV_Rm1	CTT	GTC	TAT	TGT	TTC	TTA	GGC	TAT	TTT	TGT	TGC	TGC	TAC	TT	GGT	CTG	TT	TGC	TTG	CTC	AAC	CGC	TAC	TTT	AGA	CTT	ACT	CTT	GGT	GTT
KY938558_Bat_CoV_strain_16B0133	CTT	GTC	TAT	TGT	TTC	TTA	GGC	TAT	TTT	TGT	TGC	TGC	TAC	TT	GGC	CTC	TT	TGC	TTA	CTC	AAC	CGC	TAC	TTT	AGA	CTT	ACT	CTT	GGT	GTT
DQ412042_Bat_SARS_CoV_Rf1	CTT	GTC	TAT	TGT	TTC	TTA	GGC	TAT	TTT	TGT	TGC	TGC	TAC	TT	GGC	CTC	TT	TGT	TTA	CTC	AAC	CGC	TAC	TTT	AGA	CTT	ACT	CTT	GGT	GTT
DQ648856_Bat_CoV_BtCoV_273_2005	CTT	GTC	TAT	TGT	TTC	TTA	GGC	TAT	TTT	TGT	TGC	TGC	TAC	TT	GGC	CTC	TT	TGT	TTA	CTC	AAC	CGC	TAC	TTT	AGA	CTT	ACT	CTT	GGT	GTT
KJ473812_BtRf_BetaCoV_HeB2013	CTT	GTT	TAT	TGT	TTC	TTA	GGC	TAT	TTT	TGT	TGC	TGC	TAC	TT	GGC	CTC	TT	TGT	TTA	CTC	AAC	CGC	TAC	TTT	AGA	CTT	ACT	CTT	GGT	GTT
KY770860_Bat_CoV_Jiyuan_84	CTT	GTC	TAT	TGT	TTC	TTA	GGC	TAT	TTT	TGT	TGC	TGC	TAC	TT	GGC	CTT	TT	TGC	TTA	CTC	AAC	CGC	TAT	TTT	AGA	CTT	ACT	CTT	GGT	GTT
JX993987_Bat_CoV_Rp_Shaanxi2011	CTT	GTC	TAT	TGT	TTC	TTA	GGC	TAT	TTT	TGT	TGC	TGC	TAC	TT	GGT	CTT	TT	TGC	TTA	CTC	AAC	CGG	TAC	TTT	AGA	CTT	ACT	CTT	GGT	GTT
GQ153542_Bat_SARS_CoV_HKU3_7	CTT	GTC	TAT	TGT	TTC	TTA	GGC	TAT	TTT	TGT	TGC	TGC	TAC	TT	GGC	TTA	TT	TGC	TTA	CTC	AAC	CGC	TAC	TTT	AGA	CTT	ACT	CTT	GGT	GTT
DQ022305_Bat_SARS_CoV_HKU3_1	CTT	GTT	TAT	TGT	TTC	TTA	GGC	TAT	TTT	TGT	TGC	TGC	TAC	TT	GGC	TTA	TT	TGT	TTA	CTC	AAC	CGC	TAT	TTT	AGA	CTT	ACT	CTT	GGT	GTT
GQ153547_Bat_SARS_CoV_HKU3_12	CTT	GTT	TAT	TGT	TTC	TTA	GGC	TAT	TTT	TGT	TGC	TGC	TAC	TT	GGC	TTA	TT	TGT	TTA	CTC	AAC	CGC	TAT	TTT	AGA	CTT	ACT	CTT	GGT	GTT
KY352407_SARS_related_CoV_strain_BtKY72	CTT	GTC	TAT	TGT	TTC	TTA	GGC	TAT	TTT	TGT	TGC	TGC	TAT	TAT	GGC	TTT	TT	TGT	TTA	CTC	AAC	CGC	TAC	TTT	AGA	TTT	ACT	TTT	GGT	GTT
NC_014470_Bat_CoV_BM48_31_BGR_2008	CTT	GTT	TAT	TGT	TTC	TTG	GGC	TAT	TTT	TGT	TGC	TGC	TGT	TGT	GGT	CTT	TT	TGT	TTA	CTC	AAC	CGC	TAT	TTT	AGA	TTA	ACT	CTT	GGT	GTT

# RaTG13 BsmBI Restriction Site 22,925

<b>RaTG13</b>	22918	CCGTCTC	TTTAGAAAAGCTAATCTTAAACCCTTTGAGAGGGATATCTCAACTGAAATTTA	22977
<b>CoV-2</b>	22921	TAGATTGTTT	TAGGAAGTCTAATCTCAAACCTTTTGGAGAGAGATATTTCAACTGAAATCTA	22980

**RaTG13**

**5'3' Frame 2**  
c c g t c t c t t t a g a a a a g c t a a t c t t a a a c c c t t t g a g a g g g a t a t c t c a a c t g a a a t t  
R L F R K A N L K P F E R D I S T E I

**CoV-2**

**5'3' Frame 2**  
t a g a t t g t t t a g g a a g t c t a a t c t c a a a c c t t t t g a g a g a g a t a t t t c a a c t g a a a t c  
R L F R K S N L K P F E R D I S T E I

**Synonymous mutation in homologous peptide region**



# RaTG13 BsmBI Restriction Site 22,925

The in-frame CGTCTC restriction site in RaTG13 is unique among sarbecoviruses, including SARS-CoV-2.

The leucine amino acid in the restriction site is not found in 56 out of 58 sarbecoviruses.

The consensus dipeptide is RS, not RL.

	NC_045512_SARS_CoV_2_Wuhan_Hu_1_aa	Y	L	Y	R	L	F	R	K	S	N	L	K	P	F	E	R	D	I	S	T	E	I	Y	Q	A	G	S	T	P	C	
	NC_045512_SARS_CoV_2_Wuhan_Hu_1	TAC	CTG	TA	AGA	TTG	TTT	AGG	AAG	TCT	AAT	CTC	AAA	CCT	TTT	GAG	AGA	GAT	ATT	TCA	ACT	GAA	ATC	TAT	CAG	GCC	GGT	AGC	ACA	CCT	TGT	
	MN996532_Bat_CoV_RaTG13	TAT	CTT	TA	CGT	CTC	TTT	AGA	AAA	GCT	AAT	CTT	AAA	CCC	TTT	GAG	AGG	GAT	ATC	TCA	ACT	GAA	ATT	TAC	CAA	GCA	GGC	AGC	AAA	CCT	TGT	
	MG772933_Bat_SARS_like_CoV_bat_SL_CoVZC45	TAC	AGG	TC	CAT	CGT	CT	ACC	AAA	T--	---	-TG	AAA	CCA	TTT	GAA	AGA	GAT	CTT	TCC	TCA	GAC	GAG	---	---	---	---	---	---	---	---	
	MG772934_Bat_SARS_like_CoV_bat_SL_CoVZXC21	TAT	AGG	TC	CAT	CGC	CT	ACC	AAA	T--	---	-TA	AAA	CCA	TTT	GAA	AGA	GAC	CTT	TCT	TCA	GAT	GAG	---	---	---	---	---	---	---	---	
	NC_004718_SARS_CoV	TAT	AAA	TA	AGG	TAT	TT	AGA	CAT	GGC	AAG	CTT	AGG	CCC	TTT	GAG	AGA	GAC	ATA	TCT	AAT	GTG	CCT	TTG	TCC	CCT	GAT	GGC	AAA	CCT	TGC	
	KT444582_SARS_like_CoV_WIV16	TAT	AAA	TA	AGA	TCT	TC	AGA	CAT	GGC	AAG	CTT	AGG	CCT	TTT	GAG	AGA	GAT	ATT	TCT	AAT	GTG	CCT	TTG	TCT	CCT	GAT	GGC	AAA	CCT	TGT	
	KY417146_Bat_SARS_like_CoV_Rs4231	TAT	TTA	TA	AGA	TGG	TT	AGA	AGG	TCT	AAG	CTT	AAC	CCT	TAT	GAG	CGC	GAC	TTA	TCT	AAC	GAC	ATC	TAT	TCA	CCT	GGA	GGT	CAG	TCT	TGC	
	MK211376_CoV_BtRs_BetaCoV_YN2018B	TAT	AAA	TA	AGA	TCT	TC	AGA	CAT	GGC	AAG	CTT	AGG	CCC	TTT	GAG	AGA	GAC	ATT	TCT	AAT	GTG	CCT	TTG	TCC	CCT	GAT	GGC	AAA	CCA	TGT	
	KY417151_Bat_SARS_like_CoV_Rs7327	TAT	AAA	TA	AGA	TCT	TC	AGA	CAT	GGC	AAG	CTT	AGG	CCC	TTT	GAG	AGA	GAC	ATT	TCT	AAT	GTG	CCT	TTG	TCC	CCT	GAC	GGC	AAA	CCA	TGT	
	KY417152_Bat_SARS_like_CoV_Rs9401	TAT	AAA	TA	AGA	TCT	TC	AGA	CAT	GGC	AAG	CTT	AGG	CCC	TTT	GAG	AGA	GAC	ATT	TCT	AAT	GTG	CCT	TTG	TCC	CCT	GAC	GGC	AAA	CCA	TGT	
	KY417144_Bat_SARS_like_CoV_Rs4084	TAT	TTA	TA	AGA	TGG	TT	AGA	AGG	TCT	AAG	CTT	AAC	CCT	TAT	GAG	CGC	GAC	TTA	TCT	AAC	GAC	ATC	TAT	TCA	CCT	GGA	GGT	CAG	TCT	TGC	
	KF367457_Bat_SARS_like_CoV_WIV1	TAT	AAA	TA	AGA	TCT	TC	AGA	CAT	GGC	AAG	CTT	AGG	CCT	TTT	GAG	AGA	GAT	ATT	TCT	AAT	GTG	CCT	TTG	TCT	CCT	GAT	GGC	AAA	CCT	TGT	
	KU973692_UNVERIFIED_SARS_related_CoV_F46	TAT	TTT	TA	AGG	TCT	AC	CGC	TCA	AGT	AAG	CTT	AAA	CCA	TTG	GAG	CGA	GAT	CTT	TCA	TCT	GAT	GA	--	AAC	GGT	GTA	CGT	ACA	CTG	AGC	
	KY417145_Bat_SARS_like_CoV_Rf4092	TAT	TTT	TA	AGG	TCT	AC	CGC	TCA	AGT	AAG	CTT	AAA	CCA	TTG	GAG	CGA	GAT	CTT	TCA	TCT	GAT	GA	--	AAC	GGT	GTA	CGT	ACA	CTG	AGC	
	KJ473816_BtRs_BetaCoV_YN2013	TAT	TTT	TA	AGA	TCT	AT	CGC	TCC	ACC	AAA	TTA	AAG	CCA	TTT	GAG	CGT	GAT	CTT	TCT	TCT	GAC	GA	--	G	AAT	GGT	GTT	CGT	ACA	CTT	AGT
	KY770858_Bat_CoV_Anlong_103	TAT	TTT	TA	AGA	TCT	AT	CGC	TCC	ACC	AAA	TTA	AAG	CCA	TTT	GAG	CGT	GAT	CTT	TCT	TCT	GAC	GA	--	G	AAT	GGT	GTT	CGT	ACA	CTT	AGT
	KY417143_Bat_SARS_like_CoV_Rs4081	TAT	TAT	TA	AGA	TCT	TC	CGA	AAA	ACA	AAA	CTT	AAA	CCT	TTT	GAG	AGG	GAT	CTA	ACT	TCT	GAC	GA	--	AAT	GGT	GTA	CGT	ACT	CTT	AGT	
	KY417149_Bat_SARS_like_CoV_Rs4255	TAT	TAT	TA	AGA	TCC	CC	AGA	AAA	ACA	AAA	CTT	AAA	CCT	TTT	GAG	AGG	GAT	CTA	TCT	TCT	GAC	GA	--	AAT	GGT	GTA	CGT	ACT	CTT	AGT	
	MK211378_CoV_BtRs_BetaCoV_YN2018D	TAT	TAT	TA	AGA	TCC	CC	AGA	AAA	ACA	AAA	CTT	AAA	CCT	TTT	GAG	AGG	GAT	CTA	ACT	TCT	GAC	GA	--	AAT	GGT	GTA	CGT	ACT	CTT	AGT	
	FJ588686_Bat_SARS_CoV_Rs672_2006	TAT	TAT	TA	AGA	TCC	CC	AGA	AAA	ACA	AAA	CTT	AAA	CCT	TTT	GAG	AGG	GAT	CTA	ACT	TCT	GAC	GA	--	AAT	GGT	GTA	CGT	ACT	CTT	AGT	
	MK211377_CoV_BtRs_BetaCoV_YN2018C	TAT	TAT	TA	AGA	TCC	CT	AGA	AAG	ACA	AAA	CTT	AAA	CCT	TTT	GAG	AGG	GAC	CTA	TCT	TCA	GAC	GA	--	AAT	GGT	GTA	CGT	ACT	CTT	AGT	
	KY417142_Bat_SARS_like_CoV_As6526	TAT	TAT	TA	AGA	TCC	CT	AGA	AAG	ACA	AAA	CTT	AAA	CCT	TTT	GAG	AGG	GAC	CTA	TCT	TCA	GAC	GA	--	AAT	GGT	GTA	CGT	ACT	CTT	AGT	
	KY417147_Bat_SARS_like_CoV_Rs4237	TAT	TAT	TA	AGA	TCC	CC	AGA	AAA	ACA	AAA	CTT	AAA	CCT	TTT	GAG	AGG	GAT	CTA	TCT	TCT	GAC	GA	--	AAT	GGT	GTA	CGT	ACT	CTT	AGT	
	KY417148_Bat_SARS_like_CoV_Rs4247	TAT	TAT	TA	AGA	TCT	AC	CGT	AAG	ACT	AAG	CTC	AAG	CCT	TTT	GAG	AGA	GAT	CTA	TCC	TCT	GAT	GAT	GGT	AAT	GGT	GTA	TAC	ACA	CTT	AGT	
	MK211375_CoV_BtRs_BetaCoV_YN2018A	TAT	TAT	TA	AGA	TCT	AC	CGT	AAG	ACT	AAG	CTC	AAG	CCT	TTT	GAG	AGA	GAT	CTA	TCC	TCT	GAT	GAT	GGT	AAT	GGT	GTA	TAT	ACA	CTT	AGT	
	DQ071615_Bat_SARS_CoV_Rp3	TAT	TAG	TA	AGG	TCT	AC	CGG	AAG	ACT	AAA	CTT	AAA	CCT	TTT	GAG	AGA	GAC	CTT	TCT	TCT	GAT	GA	--	AAT	GGT	GTA	CGT	ACT	CTT	AGT	
	KP886808_Bat_SARS_like_CoV_YNLF_31C	TAT	TTT	TA	AGG	TCT	AT	CGT	TCC	AGT	AAA	TTA	AAA	CCG	TTT	GAG	AGA	GAC	CTG	TCA	TCA	GAA	GA	--	AAT	GGT	GCC	CGT	ACA	CTT	AGT	
	KJ473815_BtRs_BetaCoV_GX2013	TAT	TAT	TA	AGA	TCC	AT	CGC	AAG	ACT	AAA	TTA	AAG	CCT	TTT	GAG	AGA	GAT	CTG	TCT	TCC	GAT	GAT	GGT	AAT	GGT	GTA	TAC	ACA	CTT	TCA	
	KF569996_Rhinolophus_affinis_CoV_LYRa11	TAT	AAA	TA	AGA	TCT	TC	AGA	CAT	GGT	AAG	CTT	AGA	CCA	TTT	GAG	AGA	GAC	ATT	TCT	AAT	GTG	CCT	TTT	TCC	CCT	GAT	GGT	AAA	CCT	TGC	
	JX993988_Bat_CoV_Cp_Yunnan2011	TAT	TAT	TA	AGA	TCA	CT	AGA	AAG	ACT	AAG	CTT	AAA	CCT	TTT	GAG	AGA	GAC	CTG	TCT	TCT	GAT	GA	--	AAT	GGT	GTA	CGT	ACT	TTA	AGT	
	MK211374_CoV_BtR1_BetaCoV_SC2018	TAT	TAT	TA	AGG	TCT	AC	CGT	AAG	ACT	AAG	CTT	AAA	CCT	TTT	GAG	AGA	GAT	CTG	TCT	TCT	GAT	GAT	GGT	AAT	GGT	GTA	TAT	ACA	CTT	TCA	
	KJ473814_BtRs_BetaCoV_HuB2013	TAT	TAT	TA	AGG	TCC	AC	CGC	AAG	ACT	AAG	CTT	AAG	CCT	TTT	GAG	AGA	GAT	TTG	TCC	TCT	G--	---	---	---	---	---	---	---	---	---	---
	DQ412043_Bat_SARS_CoV_Rm1	TAT	TAG	TA	AGA	TCT	AC	AGA	AAG	GAA	AAA	CTC	AAA	CCT	TTT	GAG	AGG	GAT	TTG	TCA	TCT	G--	---	---	---	---	---	---	---	---	---	---
	KY938558_Bat_CoV_strain_16B0133	TAT	TTT	TA	AGG	TCC	AT	CGT	TCT	AGC	AAA	TTA	AAA	CCC	TTT	GAA	AGA	GAC	CTT	TCA	TCA	G--	---	---	---	---	---	---	---	---	---	---
	DQ412042_Bat_SARS_CoV_Rf1	TAT	TTT	TA	AGG	TCT	AT	CGC	TCT	AGC	AAA	TTA	AAA	CCC	TTT	GAA	AGA	GAC	CTT	TCA	TCA	G--	---	---	---	---	---	---	---	---	---	---
	DQ648856_Bat_CoV_BtCoV_273_2005	TAT	TTT	TA	AGG	TCT	AT	CGC	TCT	AGC	AAA	TTA	AAA	CCC	TTT	GAA	AGA	GAC	CTT	TCA	TCA	G--	---	---	---	---	---	---	---	---	---	---
	KJ473812_BtRf_BetaCoV_HeB2013	TAT	TTT	TA	AGG	TCT	AT	CGC	TCT	AGC	AAA	TTA	AAA	CCC	TTT	GAA	AGA	GAC	CTT	TCA	TCA	G--	---	---	---	---	---	---	---	---	---	---
	KY770860_Bat_CoV_Jiyuan_84	TAT	TTT	TA	AGG	TCT	AT	CGC	TCT	AGC	AAA	TTA	AAA	CCC	TTT	GAA	AGA	GAC	CTT	TCA	TCA	G--	---	---	---	---	---	---	---	---	---	---
	JX993987_Bat_CoV_Rp_Shaanxi2011	TAT	TAT	TA	AGG	TCT	CT	AGA	AAG	GAA	AAA	CTC	AAA	CCT	TTT	GAG	AGG	GAT	TTG	TCA	TCA	G--	---	---	---	---	---	---	---	---	---	---
	GQ153542_Bat_SARS_CoV_HKU3_7	TAT	TAC	TA	AGA	TCT	AT	CGC	AAG	ACT	AAG	TTA	AAG	CCT	TTT	GAG	AGA	GAT	CTG	TCT	TCT	G--	---	---	---	---	---	---	---	---	---	---
	DQ022305_Bat_SARS_CoV_HKU3_1	TAT	TAC	TA	AGA	TCT	AT	CGC	AAG	ACT	AAG	TTA	AAG	CCT	TTT	GAG	AGA	GAC	CTG	TCT	TCT	G--	---	---	---	---	---	---	---	---	---	---
	GQ153547_Bat_SARS_CoV_HKU3_12	TAT	TAC	TA	AGA	TCT	AT	CGC	AAG	ACT	AAG	TTA	AAG	CCT	TTT	GAG	AGA	GAC	CTG	TCT	TCT	G--	---	---	---	---	---	---	---	---	---	---
	KY352407_SARS_related_CoV_strain_BtKY72	TA	---	---	AGG	CTT	TT	AGA	CAT	GGG	AAG	ATC	AAA	CCT	TAT	GAA	CGC	GAT	ATT	TCC	AAT	GTC	CTT	TAT	AAT	TCA	GCT	GGT	GGT	ACG	TGT	
	NC_014470_Bat_CoV_BM48_31_BGR_2008	TTT	TTT	TA	AGG	AGA	TC	AGA	CAT	GGA	AAG	ATT	AAA	CCT	TAT	GGG	CGT	GAC	CTT	TCC	AAT	GTT	CTT	TTT	AAC	CCT	TCA	GGT	GGT	ACA	TGT	

# SARS-CoV-2 Bsal Restriction Site 24,096

<b>RaTG13</b>	24044	TTCATCAAACAATATGGTGATTGCCTTGGTGATATTGCTGCTAGGGATCTTATTTGTGCT	24103
<b>CoV-2</b>	24059	TTCATCAAACAATATGGTGATTGCCTTGGTGATATTGCTGCTA <b>GAGACC</b> TCATTTGTGCA	24118

**RaTG13**

**5'3' Frame 1**

ttcatcaaacaatatggtgattgccttggatattgctgcta**ggg**atccttatttgtgct  
F I K Q Y G D C L G D I A A R D L I C A

**CoV-2**

**5'3' Frame 1**

ttcatcaaacaatatggtgattgccttggatattgctgcta**gag**acccttatttgtgca  
F I K Q Y G D C L G D I A A R D L I C A

**Synonymous mutation in homologous peptide region**

# SARS-CoV-2 Bsal Restriction Site 24,096

The out-of-frame GAGACC  
restriction site is found in  
18 out of 57 but not  
RaTG13.

NC_045512_SARS_CoV_2_Wuhan_Hu_1_aa	L	G	D	I	A	A	R	D	I	C	A	Q	K	F	N	G	L	T	V	L	P	P	L	L	T	D	E	M	I	
NC_045512_SARS_CoV_2_Wuhan_Hu_1	CTT	GGT	GAT	ATT	GCT	GCT	AGA	GAC	CTC	ATT	TGT	GCA	CAA	AAG	TTT	AAC	GGC	CTT	ACT	GTT	TTG	CCA	CCT	TTG	CTC	ACA	GAT	GAA	ATG	ATT
MN996532_Bat_CoV_RaTG13	CTT	GGT	GAT	ATT	GCT	GCT	AGG	GAT	CTT	ATT	TGT	GCT	CAA	AAG	TTC	AAT	GGC	CTT	ACT	GTT	CTG	CCA	CCT	TTG	CTC	ACA	GAT	GAA	ATG	ATC
MG772933_Bat_SARS_like_CoV_bat_SL_CoVZC45	TTG	GGT	GGT	ATT	TCT	GCT	AGA	GAT	TGG	ATT	TGT	GCT	CAA	AAG	TTC	AAT	GGC	CTT	ACT	GTC	TTA	CCA	CCA	TTG	CTC	ACA	GAT	GAA	ATG	ATC
MG772934_Bat_SARS_like_CoV_bat_SL_CoVZXC21	TTG	GGT	GAT	ATT	TCT	GCT	AGA	GAT	TGG	ATT	TGT	GCT	CAA	AAG	TTC	AAT	GGC	CTT	ACT	GTC	TTA	CCA	CCA	TTG	CTC	ACA	GAT	GAA	ATG	ATC
NC_004718_SARS_CoV	CTA	GGT	GAT	ATT	AAT	GCT	AGA	GAT	CTC	ATT	TGT	GCG	CAG	AAG	TTC	AAT	GGC	CTT	ACA	GTG	TTG	CCA	CCT	CTG	CTC	ACT	GAT	GAT	ATG	ATT
KT444582_SARS_like_CoV_WIV16	CTA	GGT	GAT	ATT	AAT	GCT	AGA	GAT	CTC	ATT	TGT	GCG	CAG	AAG	TTC	AAT	GGC	CTT	ACA	GTG	CTG	CCA	CCT	CTG	CTC	ACT	GAT	GAT	ATG	ATT
KY417146_Bat_SARS_like_CoV_Rs4231	CTA	GGT	GAT	ATT	AAT	GCT	AGA	GAT	CTC	ATT	TGT	GCG	CAG	AAG	TTC	AAT	GGC	CTT	ACA	GTG	TTG	CCA	CCT	CTG	CTC	ACT	GAT	GAT	ATG	ATT
MK211376_CoV_BtRs_BetaCoV_YN2018B	CTA	GGT	GAT	ATT	AAT	GCT	AGA	GAT	CTC	ATT	TGT	GCG	CAG	AAG	TTC	AAT	GGC	CTT	ACA	GTG	TTG	CCA	CCT	TTG	CTC	ACT	GAT	GAT	ATG	ATT
KY417151_Bat_SARS_like_CoV_Rs7327	CTA	GGT	GAT	ATT	AAT	GCT	AGA	GAT	CTC	ATT	TGT	GCG	CAG	AAG	TTC	AAT	GGC	CTT	ACA	GTG	TTG	CCA	CCT	CTG	CTC	ACT	GAT	GAT	ATG	ATT
KY417152_Bat_SARS_like_CoV_Rs9401	CTA	GGT	GAT	ATT	AAT	GCT	AGA	GAT	CTC	ATT	TGT	GCG	CAG	AAG	TTC	AAT	GGC	CTT	ACA	GTG	TTG	CCA	CCT	CTG	CTC	ACT	GAT	GAT	ATG	ATT
KY417144_Bat_SARS_like_CoV_Rs4084	CTA	GGT	GAT	ATT	AAT	GCT	AGA	GAT	CTC	ATT	TGT	GCG	CAG	AAG	TTC	AAT	GGC	CTT	ACA	GTG	CTG	CCA	CCT	CTG	CTC	ACT	GAT	GAT	ATG	ATT
KF367457_Bat_SARS_like_CoV_WIV1	CTA	GGT	GAT	ATT	AAT	GCT	AGA	GAT	CTC	ATT	TGT	GCG	CAG	AAG	TTC	AAT	GGC	CTT	ACA	GTG	CTG	CCA	CCT	CTG	CTC	ACT	GAT	GAT	ATG	ATT
KU973692_UNVERIFIED_SARS_related_CoV_F46	CTA	GGT	GAT	ATT	AGT	GCT	AGA	GAC	CTC	ATT	TGT	GCC	CAA	AAG	TTC	AAT	GGC	CTT	ACA	GTG	CTA	CCA	CCA	TTG	CTC	ACA	GAT	GAA	ATG	ATT
KY417145_Bat_SARS_like_CoV_Rf4092	CTA	GGC	GAT	ATT	AGT	GCT	AGA	GAC	CTC	ATT	TGT	GCT	CAG	AAG	TTC	AAC	GGC	CTT	ACT	GTC	CTA	CCA	CCA	TTG	CTC	ACA	GAT	GAA	ATG	ATT
KJ473816_BtRs_BetaCoV_YN2013	CTA	GGC	GAT	ATT	AGT	GCT	AGA	GAC	CTC	ATT	TGT	GCT	CAG	AAG	TTC	AAC	GGC	CTT	ACT	GTC	CTA	CCA	CCA	TTG	CTC	ACA	GAT	GAA	ATG	ATT
KY770858_Bat_CoV_Anlong_103	CTA	GGC	GAT	ATT	AGT	GCT	AGA	GAC	CTC	ATT	TGT	GCT	CAG	AAG	TTC	AAT	GGC	CTT	ACT	GTC	CTG	CCA	CCA	TTG	CTC	ACA	GAT	GAA	ATG	ATT
KY417143_Bat_SARS_like_CoV_Rs4081	CTA	GGT	GAT	ATT	AAT	GCT	AGA	GAC	CTC	ATT	TGT	GCA	CAA	AAG	TTC	AAT	GGC	CTT	ACT	GTC	CTG	CCA	CCT	TTA	CTC	ACG	GAT	GAC	ATG	ATT
KY417149_Bat_SARS_like_CoV_Rs4255	CTA	GGT	GAT	ATT	AAT	GCT	AGA	GAC	CTC	ATT	TGT	GCA	CAA	AAG	TTC	AAT	GGC	CTT	ACT	GTC	TTG	CCA	CCT	TTA	CTC	ACG	GAT	GAC	ATG	ATT
MK211378_CoV_BtRs_BetaCoV_YN2018D	CTA	GGT	GAT	ATT	AAT	GCT	AGA	GAC	CTC	ATT	TGT	GCA	CAA	AAG	TTC	AAT	GGC	CTT	ACT	GTC	CTG	CCA	CCT	TTA	CTC	ACG	GAT	GAC	ATG	ATC
FJ588686_Bat_SARS_CoV_Rs672_2006	CTA	GGC	GAT	ATT	AGT	GCT	AGA	GAC	CTC	ATT	TGT	GCT	CAG	AAG	TTC	AAC	GGC	CTT	ACT	GTC	CTA	CCA	CCA	TTG	CTC	ACA	GAT	GAA	ATG	ATT
MK211377_CoV_BtRs_BetaCoV_YN2018C	CTA	GGT	GAT	ATT	AAT	GCT	AGA	GAC	CTC	ATT	TGT	GCA	CAA	AAG	TTC	AAT	GGC	CTT	ACT	GTC	CTT	CCA	CCT	TTA	CTC	ACA	GAC	GAC	ATG	ATT
KY417142_Bat_SARS_like_CoV_As6526	CTA	GGT	GAT	ATT	AAT	GCT	AGA	GAC	CTC	ATT	TGT	GCA	CAA	AAG	TTC	AAT	GGC	CTT	ACT	GTC	CTT	CCA	CCT	TTA	CTC	ACA	GAC	GAC	ATG	ATT
KY417147_Bat_SARS_like_CoV_Rs4237	CTA	GGT	GAT	ATT	AAT	GCT	AGA	GAC	CTC	ATT	TGT	GCA	CAA	AAG	TTC	AAT	GGC	CTT	ACT	GTC	TTG	CCA	CCT	TTA	CTC	ACG	GAT	GAC	ATG	ATT
KY417148_Bat_SARS_like_CoV_Rs4247	CTA	GGT	GAT	ATT	AAT	GCT	AGA	GAT	CTC	ATT	TGT	GCG	CAG	AAG	TTC	AAT	GGC	CTT	ACA	GTG	TTG	CCA	CCT	CTA	CTC	ACA	GAT	GAC	ATG	ATT
MK211375_CoV_BtRs_BetaCoV_YN2018A	CTA	GGT	GAT	ATT	AAT	GCT	AGA	GAC	CTC	ATT	TGT	GCA	CAA	AAG	TTC	AAT	GGC	CTT	ACT	GTC	CTT	CCA	CCT	TTA	CTC	ACA	GAT	GAC	ATG	ATT
DQ071615_Bat_SARS_CoV_Rp3	CTA	GGC	GAT	ATT	AGT	GCT	AGA	GAC	CTC	ATT	TGT	GCT	CAG	AAG	TTT	AAT	GGC	CTT	ACT	GTC	CTA	CCA	CCA	CTG	CTC	ACA	GAT	GAA	ATG	ATT
KP886808_Bat_SARS_like_CoV_YNLF_31C	TTG	GGT	GGT	ATT	AAC	GCT	AGA	GAT	CTC	ATT	TGT	GCT	CAA	AAG	TTT	AAT	GGC	CTT	ACA	GTG	CTA	CCA	CCT	TTG	CTC	ACT	GAT	GAT	ATG	ATT
KJ473815_BtRs_BetaCoV_GX2013	CTA	GGC	GAT	ATT	AGT	GCT	AGA	GAC	CTC	ATT	TGT	GCT	CAG	AAG	TTC	AAT	GGC	CTT	ACT	GTC	CTA	CCA	CCA	TTG	CTC	ACA	GAT	GAA	ATG	ATT
KF569996_Rhinolophus_affinis_CoV_LYRa11	CTA	GGC	GAT	ATT	AGT	GCT	AGA	GAC	CTC	ATT	TGT	GCG	CAA	AAG	TTT	AAT	GGC	CTT	ACT	GTC	CTT	CCA	CCT	TTG	CTC	ACT	GAC	GAA	ATG	ATT
JX993988_Bat_CoV_Cp_Yunnan2011	CTA	GGC	GAT	ATT	AGT	GCT	AGA	GAT	CTC	ATT	TGT	GCG	CAG	AAG	TTC	AAT	GGC	CTT	ACT	GTC	CTT	CCA	CCT	CTA	CTC	ACG	GAT	GAA	ATG	ATT
MK211374_CoV_BtR1_BetaCoV_SC2018	CTA	GGT	GAT	ATT	AGT	GCT	AGA	GAC	CTC	ATT	TGT	GCA	CAA	AAG	TTC	AAT	GGC	CTT	ACT	GTC	CTA	CCA	CCT	TTA	CTC	ACG	GAT	GAC	ATG	ATT
KJ473814_BtRs_BetaCoV_HuB2013	CTA	GGC	GAT	ATT	AGT	GCT	AGA	GAC	CTC	ATT	TGT	GCT	CAA	AAA	TTC	AAT	GGC	CTT	ACT	GTT	CTA	CCA	CCA	TTG	CTC	ACA	GAT	GAA	ATG	ATT
DQ412043_Bat_SARS_CoV_Rm1	CTA	GGC	GAT	ATT	AGT	GCT	AGA	GAC	CTC	ATT	TGT	GCT	CAA	AAG	TTT	AAT	GGC	CTT	ACT	GTC	CTA	CCA	CCA	TTG	CTC	ACA	GAT	GAA	ATG	ATT
KY938558_Bat_CoV_strain_16B0133	TTG	GGT	GGT	ATT	AAC	GCA	AGA	GAT	CTC	ATT	TGT	GCT	CAA	AAG	TTT	AAT	GGG	CTG	ACA	GTG	TTA	CCA	CCT	TTG	CTC	ACT	GAT	GAC	ATG	ATT
DQ412042_Bat_SARS_CoV_Rf1	CTG	GGT	GGT	ATT	AAC	GCA	AGA	GAT	CTC	ATT	TGT	GCT	CAA	AAG	TTT	AAT	GGC	CTG	ACA	GTG	TTA	CCA	CCT	TTG	CTC	ACT	GAT	GAC	ATG	ATT
DQ648856_Bat_CoV_BtCoV_273_2005	CTG	GGT	GGT	ATT	AAC	GCA	AGA	GAT	CTC	ATT	TGT	GCT	CAA	AAG	TTT	AAT	GGC	CTG	ACA	GTG	TTA	CCA	CCT	TTG	CTC	ACT	GAT	GAC	ATG	ATT
KJ473812_BtRf_BetaCoV_HeB2013	TTG	GGT	GGT	ATT	AAC	GCA	AGA	GAT	CTC	ATT	TGT	GCT	CAA	AAG	TTT	AAT	GGC	CTG	ACA	GTG	TTA	CCA	CCT	TTG	CTC	ACT	GAT	GAC	ATG	ATT
KY770860_Bat_CoV_Jiyuan_84	TTG	GGT	GGT	ATT	AAC	GCA	AGA	GAT	CTC	ATT	TGT	GCT	CAA	AAG	TTT	AAT	GGC	CTG	ACA	GTG	TTA	CCA	CCT	TTG	CTC	ACT	GAT	GAC	ATG	ATT
JX993987_Bat_CoV_Rp_Shaanxi2011	CTA	GGC	GAT	ATT	AGT	GCT	AGA	GAT	CTC	ATT	TGT	GCA	CAA	AAA	TTC	AAC	GGC	CTT	ACT	GTC	TTA	CCA	CCA	TTG	CTC	ACA	GAT	GAA	ATG	ATT
GQ153542_Bat_SARS_CoV_HKU3_7	CTA	GGT	GAT	ATT	AGT	GCT	AGA	GAC	CTC	ATT	TGT	GCC	CAG	AAG	TTC	AAT	GGC	CTT	ACT	GTC	CTA	CCA	CCA	CTG	CTC	ACA	GAT	GAC	ATG	ATT
DQ022305_Bat_SARS_CoV_HKU3_1	CTA	GGT	GAT	ATT	AGT	GCT	AGA	GAC	CTC	ATT	TGT	GCC	CAG	AAG	TTC	AAT	GGC	CTT	ACT	GTC	CTA	CCA	CCA	CTG	CTC	ACA	GAT	GAC	ATG	GTT
GQ153547_Bat_SARS_CoV_HKU3_12	CTA	GGT	GAT	ATT	AGT	GCT	AGA	GAC	CTC	ATT	TGT	GCC	CAG	AAG	TTC	AAT	GGC	CTT	ACT	GTC	CTA	CCA	CCA	CTG	CTT	ACA	GAT	GAC	ATG	ATT
KY352407_SARS_related_CoV_strain_BtKY72	TTA	GGT	GGT	ATT	AAT	GCT	AGA	GAC	CTC	ATT	TGT	GCT	CAA	AAG	TTC	AAT	GGT	CTG	ACC	GTT	TTG	CCA	CCT	TTA	CTT	ACA	GAC	GAC	ATG	ATT
NC_014470_Bat_CoV_BM48_31_BGR_2008	TTA	GGT	GGT	ATT	AAT	GCT	CGT	GAC	CTC	ATT	TGT	GCA	CAA	AAG	TTC	AAT	GGG	CTG	ACA	GTG	CTC	CCA	CCC	CTA	CTC	ACT	GAT	GAA	ATG	ATT

# RaTG13 BsmBI Restriction Site 24,500

<b>RaTG13</b>	24464	ATTTCTAGCGTGTTAAATGATATCCTTTCA <b>CGTCTC</b> GACAAAGTTGAGGCTGAAGTGCAG	24523
<b>CoV-2</b>	24479	ATTTCAAGTGTTTAAATGATATCCTTTCACGTCTTGACAAAGTTGAGGCTGAAGTGCAA	24538

**RaTG13**

5'3' Frame 1

at tt ct ag cg tg tt aa at ga ta tc ct tt ca **cg t ct c** ga ca aa ag tt ga gg ct ga ag t gc ag  
I S S V L N D I L S R L D K V E A E V Q

**CoV-2**

5'3' Frame 1

at tt ca ag tg tt tt aa at ga ta tc ct tt ca **cg t ct t** ga ca aa ag tt ga gg ct ga ag t g ca a  
I S S V L N D I L S R L D K V E A E V Q

**Synonymous mutation in homologous peptide region**



- A blast of Amplicon #1 against RaTG13 showing the Bsal restriction site in the amplicon that is changed in RaTG13
- The amplicon has a 2% overall difference from RaTG13 but within the restriction site one of six or 17% are changed

**Bat coronavirus RaTG13, complete genome**  
 Sequence ID: [MN996532.2](#) Length: 29855 Number of Matches: 1

Range 1: 669 to 1761 [GenBank](#) [Graphics](#) [Next Match](#) [Pre](#)

Score	Expect	Identities	Gaps	Strand
1897 bits(1027)	0.0	1075/1096(98%)	12/1096(1%)	Plus/Plus
Query 14	GTT-CGGCGCTGATCT-AAGTCGTTTGACTTAGGCGACGAGCTTGGCACTGATCCTTATG	71		
Sbjct 669	...A.....A.....	728		
Query 72	AAGATTTTCAAGAAAACGGAACTAAACATAGCAGTGGTGTACCCCGTATCTCATGC	131		
Sbjct 729	.....	788		
Query 132	GTGAGCTTAATGGAGGAGCATACACTCGCTATGTCGATAACAACCTTCTGTGGCCCTGATG	191		
Sbjct 789	.....	848		
Query 192	GCTACCTCTTGAGTGCATTAAGACCTTCTAGCTCGTGTGGTAAAGCTTCATGCACCT	251		
Sbjct 849	.....	908		
Query 252	TGTCGAAACAACCTGGACTTTATTGACACTAAAAGAGGTGTATACTGCTGTCGTGAACATG	311		
Sbjct 909	.....	968		
Query 312	AGCATGAGATTGCTTGGTACACGGAACGTTCTGAAAAGAGCTATGAATTGCAGACACCTT	371		
Sbjct 969	.....	1028		
Query 372	TTGAAATTAATGGCAAAGAAATTTGACACATTTAATGGGGAATGTCAAATTTTGTAT	431		
Sbjct 1029	.....	1088		
Query 432	TCCCCCTAAATCCACAATCAAGACTATTCAACCAAGGGTTGAAAAGAAAAAGCTTGATG	491		
Sbjct 1089	.....	1148		
Query 492	GCTTTATGGGTAGAATTCGATCTGCTATCCAGTTGCTTCACCAAATGAATGCAACCAAA	551		
Sbjct 1149	.....	1208		
Query 552	TGTGCCTTCAACTCTCATGAAGTGTGATCATTGTGGTGAACCTTCATGGCAGCAGCGG	611		
Sbjct 1209	.....	1268		
Query 612	ATTTTGTAAAGCCACTTGTGAATTTGTGGCACTGAAAATTTGACTAAAGAGGGTGCCA	671		
Sbjct 1269	.....	1328		
Query 672	CTACTTGTGGTTACCTACCCCAAAATGCTGTTGTCAAATTTATTGTCCAGCATGTCATA	731		
Sbjct 1329	.....	1388		
Query 732	ATCCAGAAGTAGACCTGAGCATAGTCTTGCTGAGTATCATAATGAATCTGGCTTGAAAC	791		
Sbjct 1389	.....A.....	1448		
Query 792	CCATTCTCGTAAGGGTGGTCGCACTATTACTTTTGAGGCTGTGGTCTCTATGTTG	851		
Sbjct 1449	.....G.....T.....	1508		
Query 852	GTTGCTACAATAAGTGTGCCTATTGGATTCCACGTGCTAGCGCAACATAGGTTGCAATC	911		
Sbjct 1509	.....	1568		
Query 912	ATACAGGTGTTGTTGGAG-AGGTTCTGAAGGTCTTAATGAT-ACCTTCTGAAATACTTC	969		
Sbjct 1569	.....A.....A.....T.....	1628		
Query 970	-AAAAGAGAAAGTCAACATCAATAATGTTGGTGACTTTGAACTTGATGGAAGAAGATCG-	1027		
Sbjct 1629	A.....T.....A.....A.....-.....C	1686		
Query 1028	CATTATTTGGCATCTTTTTCTGCTTCTACAA-TGCTTTTGTGAAACTGGGAAAGGTT	1086		
Sbjct 1687	.....-.....G.....T.....	1745		
Query 1087	TG-ATAATAAAA-ATT	1100		
Sbjct 1746	..G.T.....C... 1761			

- The site of the Bsal restriction site that was present in Amplicon #1 and removed in amplicon #2 is shown (purple box)

- No sarbecovirus has a restriction site at this position, suggesting this was a laboratory-designed restriction site

- The finding of a restriction site in an amplicon that is not found in nature and its removal in an overlapping amplicon is consistent with reverse genetics workflow

- A blast of Amplicon #1 identifies only RaTG13 and SARS-CoV-2, both with the GTTCTC non-restriction site sequence

Sequence ID	S	G	L	K	T	I	L	R	K	G	G	R	T	I	A	F	G	G	C	Y	F	S	Y	V	G	C	H	N	K	C	
NC_045512_SARS_CoV_2_Wuhan_Hu_1_aa	S	G	L	K	T	I	L	R	K	G	G	R	T	I	A	F	G	G	C	Y	F	S	Y	V	G	C	H	N	K	C	
NC_045512_SARS_CoV_2_Wuhan_Hu_1_TCT	GGC	TTG	AAA	ACC	ATT	CTT	CGT	AAG	GGT	GGT	CGC	ACT	ATT	GCC	TTT	GGA	GGC	TGT	G	G	TTC	TCT	TAT	GTT	GGT	TGC	CAT	AAC	AAG	TGT	
MN996532_Bat_CoV_RaTG13	TCT	GGC	TTG	AAA	CCC	ATT	CTT	CGT	AAG	GGT	GGT	CGC	ACT	ATT	GCT	TTT	GGA	GGC	TGT	G	G	TTC	TCT	TAT	GTT	GGT	TGC	TAC	AAT	AAG	TGT
MG772933_Bat_SARS_like_CoV_bat_SL_CoVZC45	TCT	GGT	TTG	AAA	ACC	GTT	CTT	CGT	AAG	GGT	GGT	CGT	ACC	ATT	GCT	TAT	GGG	GGC	TGT	G	G	TTT	GCT	TAT	GTT	GGT	TGC	TAC	AAC	AAG	TGT
MG772934_Bat_SARS_like_CoV_bat_SL_CoVZXC21	TCT	GGT	TTG	AAA	ACC	GTT	CTT	CGT	AAG	GGT	GGT	CGT	ACC	ATT	GCT	TAT	GGG	GGC	TGT	G	G	TTT	GCT	TAT	GTT	GGT	TGC	TAC	AAC	AAG	TGT
NC_004718_SARS_CoV	TCA	AAC	ATT	GAA	ACT	CGA	CTC	CGC	AAG	GGG	GGT	AGG	ACT	AGA	TGT	TTT	GGA	GGC	TGT	G	G	TTT	GCC	TAT	GTT	GGC	TGC	TAT	AAT	AAG	CGT
KT444582_SARS_like_CoV_WIV16	TCA	AAC	ATT	GAA	ACT	CGA	CTC	CGC	AAG	GGG	GGT	AGG	ACT	AGA	TGT	TTT	GGA	GGC	TGT	G	G	TTT	GCC	TAT	GTT	GGC	TGC	TAC	AAC	AAG	CGT
KY417146_Bat_SARS_like_CoV_Rs4231	TCA	AAC	ATT	GAA	ACT	CGA	CTC	CGC	AAG	GGG	GGT	AGG	ACT	AGA	TGT	TTT	GGA	GGC	TGT	G	G	TTT	GCC	TAT	GTT	GGC	TGC	TAC	AAC	AAG	CGT
MK211376_CoV_BtRs_BetaCoV_YN2018B	TCA	AAC	ATT	GAA	ACT	CGA	CTC	CGC	AAG	GGG	GGT	AGG	ACT	AGA	TGT	TTT	GGA	GGC	TGT	G	G	TTT	GCC	TAT	GTT	GGC	TGC	TAT	AAC	AAG	CGT
KY417151_Bat_SARS_like_CoV_Rs7327	TCA	AAC	ATT	GAA	ACT	CGA	CTC	CGC	AAG	GGG	GGT	AGG	ACT	AGA	TGT	TTT	GGA	GGC	TGC	G	G	TTT	GCC	TAC	GTG	GGC	TGC	TAT	AAC	AAG	CGT
KY417152_Bat_SARS_like_CoV_Rs9401	TCA	AAC	ATT	GAA	ACT	CGA	CTC	CGC	AAG	GGG	GGT	AGG	ACT	AGA	TGT	TTT	GGA	GGC	TGT	G	G	TTT	GCC	TAT	GTT	GGC	TGC	TAC	AAC	AAG	CGT
KY417144_Bat_SARS_like_CoV_Rs4084	TCA	AAC	ATT	GAA	ACT	CGA	CTC	CGC	AAG	GGG	GGT	AGG	ACT	AGA	TGT	TTT	GGA	GGC	TGT	G	G	TTT	GCC	TAT	GTT	GGC	TGC	TAC	AAC	AAG	CGT
KF367457_Bat_SARS_like_CoV_WIV1	TCA	AAC	ATT	GAA	ACT	CGA	CTC	CGC	AAA	GGG	GGT	AGG	ACT	AGA	TGT	TTT	GGA	GGC	TGT	G	G	TTT	GCC	TAT	GTT	GGC	TGC	TAC	AAC	AAG	CGT
KU973692_UNVERIFIED_SARS_related_CoV_F46	TCA	AAC	ATT	GAA	ACT	CGA	CTC	CGC	AAG	GGG	GGT	AGG	ACT	AAA	TGT	TTT	GGA	GGC	TGT	G	G	TTT	GCC	TAT	GTT	GGC	TGC	TAT	AAT	AAG	CGC
KY417145_Bat_SARS_like_CoV_Rf4092	TCA	AAC	ATT	GAA	ACT	CGA	CTC	CGC	AAG	GGG	GGT	AGG	ACT	AGA	TGT	TTT	GGA	GGC	TGT	G	G	TTT	GCC	TAT	GTT	GGC	TGC	TAC	AAC	AAG	CGT
KJ473816_BtRs_BetaCoV_YN2013	TCA	AAC	ATT	GAA	ACT	CGA	CTC	CGC	AGG	GGG	GGT	AGG	ACT	AGA	TGT	TTT	GGA	GGC	TGT	G	G	TTT	GCC	TAT	GTT	GGC	TGC	TAC	AAC	AAG	CGT
KY770858_Bat_CoV_Anlong_103	TCA	AAT	ATT	GAA	ACT	CGA	CTC	CGC	AAG	GGG	GGT	AGG	ACT	AGA	TGT	TTT	GGA	GGC	TGT	G	G	TTT	GCC	TAT	GTT	GGC	TGC	TAC	AAC	AAG	CGT
KY417143_Bat_SARS_like_CoV_Rs4081	TCA	AAC	ATT	GAA	ACT	CGA	CTC	CGC	AAG	GGG	GGT	AGG	ACT	AGA	TGT	TTT	GGA	GGC	TGT	G	G	TTT	GCC	TAT	GTT	GGC	TGC	TAC	AAC	AAG	CGT
KY417149_Bat_SARS_like_CoV_Rs4255	TCA	AAC	ATT	GAA	ACT	CGA	CTC	CGC	AAG	GGG	GGT	AGG	ACT	AGA	TGT	TTT	GGA	GGC	TGT	G	G	TTT	GCC	TAT	GTT	GGC	TGC	TAC	AAC	AAG	CGT
MK211378_CoV_BtRs_BetaCoV_YN2018D	TCA	AAC	ATT	GAA	ACT	CGA	CTC	CGC	AAG	GGG	GGT	AGG	ACT	AGA	TGT	TTT	GGA	GGC	TGT	G	G	TTT	GCC	TAT	GTT	GGC	TGC	TAT	AAC	AAG	CGT
FJ588686_Bat_SARS_CoV_Rs672_2006	TCA	AAC	ATT	GAA	ACT	CGA	CTC	CGC	AAG	GGG	GGT	AGG	ACT	AGA	TGT	TTT	GGA	GGC	TGT	G	G	TTT	GCC	TAT	GTT	GGC	TGC	TAC	AAC	AAG	CGT
MK211377_CoV_BtRs_BetaCoV_YN2018C	TCA	AAC	ATT	GAA	ACT	CGA	CTC	CGC	AAG	GGG	GGT	AGG	ACT	AGA	TGT	TTT	GGA	GGC	TGT	G	G	TTT	GCC	TAT	GTT	GGC	TGC	TAT	AAC	AAG	CGT
KY417142_Bat_SARS_like_CoV_As6526	TCA	AAC	ATT	GAA	ACT	CGA	CTC	CGC	AAG	GGG	GGT	AGG	ACT	AGA	TGT	TTT	GGA	GGC	TGC	G	G	TTT	GCC	TAT	GTT	GGC	TGC	TAT	AAC	AAG	CGT
KY417147_Bat_SARS_like_CoV_Rs4237	TCA	AAC	ATT	GAA	ACT	CGA	CTC	CGC	AAG	GGG	GGT	AGG	ACT	AGA	TGT	TTT	GGA	GGC	TGT	G	G	TTT	GCC	TAT	GTT	GGC	TGC	TAC	AAC	AAG	CGT
KY417148_Bat_SARS_like_CoV_Rs4247	TCA	AAC	ATT	GAA	ACT	CGA	CTC	CGC	AAG	GGG	GGT	AGG	ACT	AGA	TGT	TTT	GGA	GGC	TGT	G	G	TTT	GCC	TAT	GTT	GGC	TGC	TAC	AAC	AAG	CGT
MK211375_CoV_BtRs_BetaCoV_YN2018A	TCA	AAC	ATT	GAA	ACT	CGA	CTC	CGC	AAG	GGG	GGT	AGG	ACT	AGA	TGT	TTT	GGA	GGT	TGT	G	G	TTT	GCC	TAT	GTT	GGC	TGC	TAT	AAC	AAG	CGT
DQ071615_Bat_SARS_CoV_Rp3	TCA	AAC	ATT	GAA	ACT	CGA	CTC	CGC	AAG	GGG	GGT	AGG	ACT	AGA	TGT	TTT	GGA	GGC	TGT	G	G	TTT	GCC	TAT	GTT	GGC	TGC	TAT	AAC	AAG	CGT
KP886808_Bat_SARS_like_CoV_YNLF_31C	TCA	AAC	ATT	GAA	ACT	CGG	CTC	CGC	AAG	GGG	GGT	AGG	ACT	AAA	TGT	TTT	GGA	GGT	TGT	G	G	TTT	TCC	TAT	GTT	GGT	TGC	TAT	AAC	AAG	CGT
KJ473815_BtRs_BetaCoV_GX2013	TCA	AAC	ATT	GAA	ACT	CGA	CTC	CGC	AAG	GGG	GGT	AGG	ACT	AAG	TGT	TTC	GGA	GGC	TGT	G	G	TTT	TCC	TAT	GTT	GGC	TGC	TAT	AAC	AAG	CGT
KF569996_Rhinolophus_affinis_CoV_LYRa11	TCA	AAC	ATT	GAA	ACT	CGA	CTC	CGC	AAG	GGG	GGT	AGG	ACT	AAA	TGT	TTC	GGT	GGG	TGT	G	G	TTT	GCC	TAT	GTT	GGC	TGC	TAT	AAC	AAA	CGT
JX993988_Bat_CoV_Cp_Yunnan2011	TCA	AAC	ATT	GAA	ACT	CGA	CTC	CGC	AAG	GGG	GGT	AGG	ATT	AAA	TGT	TTC	GGT	GGG	TGT	G	G	TTT	GCC	TAT	GTT	GGC	TGC	TAT	AAC	AAG	CGT
MK211374_CoV_BtR1_BetaCoV_SC2018	TCA	AAT	ATT	GAA	ACT	CGA	CTC	CGC	AAG	GGG	GGT	AGG	ACT	AAA	TGT	TTT	GGA	GGT	TGC	G	G	TTT	TCC	TAT	GTG	GGC	TGC	TAT	AAC	AAG	CGT
KJ473814_BtRs_BetaCoV_HuB2013	TCA	AAC	ATT	GAA	ACT	CGA	CTC	CGC	AAG	GGG	GGT	AGG	ACT	AAA	TGT	TTT	GGG	GGC	TGT	G	G	TTT	GCC	TAT	GTT	GGC	TGC	TAT	AAC	AAG	CGT
DQ412043_Bat_SARS_CoV_Rm1	TCA	AAC	ATT	GAA	ACT	CGA	CTC	CGC	AAG	GGG	GGT	AGG	ACT	AAA	TGT	TTT	GGG	GGT	TGT	G	G	TTT	GCC	TAC	GTT	GGC	TGC	TAC	AAC	AAG	CGT
KY938558_Bat_CoV_strain_16B0133	TCA	AAT	ATT	GAA	ACT	CGA	CTC	CGC	AAG	GGG	GGT	AGG	ACT	AAA	TGT	TTT	GGA	GGC	TGT	G	G	TTT	TCC	TAT	GTT	GGC	TGC	TAT	AAC	AAG	CGT
DQ412042_Bat_SARS_CoV_Rf1	TCA	AAC	ATT	GAA	ACT	CGA	CTC	CGC	AAG	GGG	GGT	AGG	ACT	AAA	TGT	TTT	GGA	GGC	TGT	G	G	TTT	TCC	TAT	GTT	GGC	TGC	TAT	AAC	AAG	CGT
DQ648856_Bat_CoV_BtCoV_273_2005	TCA	AAC	ATT	GAA	ACT	CGA	CTC	CGC	AAG	GGG	GGT	AGG	ACT	AAA	TGT	TTT	GGA	GGC	TGT	G	G	TTT	TCC	TAT	GTT	GGC	TGC	TAT	AAC	AAG	CGT
KJ473812_BtRf_BetaCoV_HeB2013	TCA	AAC	ATT	GAA	ACT	CGA	CTC	CGC	AAG	GGG	GGT	AGG	ACT	AAA	TGT	TTT	GGA	GGC	TGT	G	G	TTT	TCC	TAT	GTT	GGC	TGC	TAT	AAC	AAG	CGT
KY770860_Bat_CoV_Jiyuan_84	TCA	AAC	ATT	GAA	ACT	CGA	CTC	CGC	AAG	GGG	GGT	AGG	ACT	AAA	TGT	TTC	GGA	GGC	TGT	G	G	TTT	TCC	TAT	GTT	GGC	TGC	TAT	AAC	AAG	CGT
JX993987_Bat_CoV_Rp_Shaanxi2011	TCA	AAC	ATT	GAA	ACT	CGA	CTC	CGC	AAG	GGG	GGT	AGG	ACT	AAA	TGT	TTT	GGA	GGC	TGT	G	G	TTT	TCC	TAT	GTT	GGC	TGC	TAC	AAC	AAG	CGC
GQ153542_Bat_SARS_CoV_HKU3_7	TCA	AAC	ATT	GAA	ACT	CGA	CTC	CGC	AAG	GGG	GGT	AGG	ACT	AAG	TGT	TTT	GGA	GGC	TGT	G	G	TTT	TCC	TAT	GTG	GGC	TGC	TAT	AAC	AAG	CGT
DQ022305_Bat_SARS_CoV_HKU3_1	TCA	AAC	ATT	GAA	ACT	CGA	CTC	CGC	AAG	GGG	GGT	AGG	ACT	AAG	TGT	TTT	GGC	GGC	TGT	G	A	TTT	TCC	TAT	GTT	GGC	TGC	TAT	AAC	AAG	CGA
GQ153547_Bat_SARS_CoV_HKU3_12	TCA	AAC	ATT	GAA	ACT	CGA	CTC	CGC	AAG	GGG	GGT	AGG	ACT	AAG	TGT	TTT	GGC	GGC	TGT	G	A	TTT	TCC	TAT	GTT	GGC	TGC	TAT	AAC	AAG	CGA
KY352407_SARS_related_CoV_strain_BtKY72	TCA	GGC	ATT	ATT	TCT	CAG	CTC	CGC	AAG	GGG	GGT	AGA	GTG	TTC	CCT	TTT	GGT	GGT	TGT	G	G	TTT	TCT	TAT	GTT	GGT	TGC	TAC	AAC	AAG	TGT
NC_014470_Bat_CoV_BM48_31_BGR_2008	TCA	AAG	ATT	GAA	ACT	CGA	CTC	CGC	AAG	GGG	GGT	AGG	ATT	AAA	TCT	TTT	GGT	GGC	TGT	G	T	TTC	TCT	TAT	GTT	GGC	TGC	TAC	AAC	AAG	CGT

# Caveats

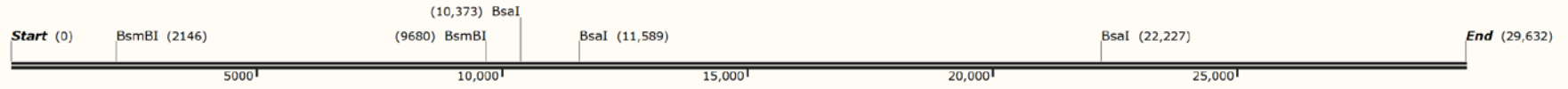
- Not seeing this pattern does not mean it is natural
- All you have to do is add back restriction sites after 'No See 'Em' technology and...poff





**BANAL-20-52 Laos 2020**  
29,838 bp

Coronavirus Enzymes



**BANAL-20-103 Laos 2020**  
29,632 bp

Coronavirus Enzymes



**BANAL-20-236 Laos 2020**  
30,024 bp

Coronavirus Enzymes



**NC\_045512.2 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome**  
29,903 bp

Coronavirus Enzymes