

## Electronic Supplementary Material

### Monitoring Neutralization Property Change of Evolving Hantaan and Seoul Viruses with A Novel Pseudovirus-Based Assay

Tingting Ning<sup>1</sup> • Ling Wang<sup>2</sup> • Shuo Liu<sup>1</sup> • Jian Ma<sup>1</sup> • Jianhui Nie<sup>1</sup> • Weijin Huang<sup>1</sup> • Xuguang Li<sup>3</sup> • Yuhua Li<sup>2</sup>✉ • Youchun Wang<sup>1</sup>✉

1. Division of HIV/AIDS and Sexually Transmitted Virus Vaccines, National Institutes for Food and Drug Control (NIFDC), Beijing 102629, China
2. Division of Arboviruses Vaccine, National Institutes for Food and Drug Control (NIFDC), Beijing 102629, China
3. Centre for Biologics Evaluation, Biologics and Genetic Therapies Directorate, Health Canada, Ottawa, On K2J 4X9, Canada

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**Table S1** Genbank numbers of the 56 mutants of HTNV glycoprotein and PCR primers used for making the 56 point mutation constructs. The upper one is the forward primer and the lower one is the reverse primer.

No.	variation	Structure element	Frequency (%)	Genbank sequence number	PCR primers
1	V16A <sup>a</sup>	-, Gn	43.96	ALL25319.1	5'-ATGGCTTCCCTGGTGTGGCCCGCTCTCACCTCAGGAATGTCTA-3' 5'-TAGACATTCCTGAGGGTGAGAGCGGGCCACACCAGGGAAGCCAT-3'
2	K26R <sup>b</sup>	β1, Gn	1.65	ACN60122.1	5'-AGGAATGTCTACGATATGAGAATTGAATGTCCCCATA-3' 5'-TATGGGGACATTCAATTCTCATATCGTAGACATTCCT-3'
3	G37E <sup>a</sup>	-, Gn	83.52	BAZ96166.1	5'-ATACCGTCAGCTTCGGCGAAAACCTCCGTGATTGGATAT-3' 5'-ATATCCAATCACGGAGTTTTTCGCCGAAGCTGACGGTAT-3'
4	P48R <sup>b</sup>	-, Gn	1.65	AGC97006.1	5'-ATATGTGGAGCTCCCCAGAGTGCCTCTCGCCGATACCGCTCAGAT-3' 5'-ATCTGAGCGGTATCGGCGAGAGGCACTCTGGGGAGCTCCACATAT-3'
5	V49M <sup>ab</sup>	β2, Gn	80.77	AGC97031.1	5'-ATTGGATATGTGGAGCTCCCCCTATGCCTCTCGCCGATACCGCTCAGATGGT-3' 5'-ACCATCTGAGCGGTATCGGCGAGAGGCATAGGGGGGAGCTCCACATATCCAAT-3'
6	T54I <sup>b</sup>	α1, Gn	1.65	AAL36997.1	5'-ATATGTGGAGCTCCCCCTGTGCCTCTCGCCGATATCGCTCAGATGGTCCCGAGTCCAGCTGTT-3' 5'-AACAGCTGGACTCGGGGACCATCTGAGCGATATCGGCGAGAGGCACAGGGGGGAGCTCCACATAT-3'
7	A55T <sup>b</sup>	-, Gn	12.09	AAK66741.1	5'-ATATGTGGAGCTCCCCCTGTGCCTCTCGCCGATACACACAGATGGTCCCGAGTCCAGCTGTTCCATGGATAA-3' 5'-TTATCCATGGAACAGCTGGACTCGGGGACCATCTGTGTGGTATCGGCGAGAGGCACAGGGGGGAGCTCCACATAT-3'
8	A55I <sup>b</sup>	-, Gn	6.04	ACA61215.1	5'-TATGTGGAGCTCCCCCTGTGCCTCTCGCCGATACCATTCAGATGGTCCCGAGTCCAGCTGTTCCATGGATAA-3' 5'-TTATCCATGGAACAGCTGGACTCGGGGACCATCTGAATGGTATCGGCGAGAGGCACAGGGGGGAGCTCCACATA-3'
9	M57L <sup>b</sup>	-, Gn	35.16	ANK77979.1	5'-AGTCCCCCTGTGCCTCTCGCCGATACCGCTCAGCTGGTCCCGAGTCCAGCTGTTCCATGGATAAACCACAGT-3' 5'-ACTGGTGGTTATCCATGGAACAGCTGGACTCGGGGACCAGCTGAGCGGTATCGGCGAGAGGCACAGGGGGGAGCT-3'
10	V58M <sup>b</sup>	-, Gn	1.65	AKO63083.1	5'-AGTCCCCCTGTGCCTCTCGCCGATACCGCTCAGATGATGCCCGAGTCCAGCTGTTCCATGGATAA-3' 5'-TTATCCATGGAACAGCTGGACTCGGGCATCATCTGAGCGGTATCGGCGAGAGGCACAGGGGGGAGCT-3'
11	S64N <sup>b</sup>	-, Gn	25.27	AAA79712.1	5'-ATACCGCTCAGATGGTCCCGAGTCCAGCTGTAACATGGATAAACCACAGTCCCTGAACACCATCACCAAG-3' 5'-CTTGGTGATGGTGTTCAGGGACTGGTGGTTATCCATGTTACAGCTGGACTCGGGGACCATCTGAGCGGTAT-3'
12	I74V <sup>b</sup>	β4, Gn	4.95	AKO63082.1	5'-ATAACCACCAGTCCCTGAACACCGTCAACCAAGTATAACCCAGGTGAGCTGGAGGGGAAA-3' 5'-TTTCCCCTCCAGCTCACCTGGGTATACTTGGTGACGGTGTTCAGGGACTGGTGGTTAT-3'
13	I74A <sup>b</sup>	β5, Gn	1.65	ABS83844.1	5'-ATAACCACCAGTCCCTGAACACCGCCACCAAGTATAACCCAGGTGAGCTGGAGGGGAAA-3' 5'-TTTCCCCTCCAGCTCACCTGGGTATACTTGGTGGCGGTGTTCAGGGACTGGTGGTTAT-3'
14	T75A <sup>b</sup>	β4, Gn	6.59	ALA20821.1	5'-ATAACCACCAGTCCCTGAACACCATCGCCAAGTATAACCCAGGTGAGCTGGAGGGGAAA-3' 5'-TTTCCCCTCCAGCTCACCTGGGTATACTTGGCGATGGTGTTCAGGGACTGGTGGTTAT-3'
15	Y77H <sup>b</sup>	β4, Gn	1.1	ACA61213.1	5'-ATAACCACCAGTCCCTGAACACCATCACCAAGCATAACCCAGGTGAGCTGGAGGGGAAA-3' 5'-TTTCCCCTCCAGCTCACCTGGGTATGCTTGGTGTGGTGTTCAGGGACTGGTGGTTAT-3'
16	V80I <sup>b</sup>	β4, Gn	6.59	ACA61212.1	5'-AACACCATCACCAAGTATAACCCAGATTAGCTGGAGGGGAAAGGCTGACCAGA-3' 5'-TCTGGTCAGCCTTTCCCCTCCAGCTAATCTGGGTATACTTGGTGATGGTGT-3'
17	S81I <sup>b</sup>	β4, Gn	9.34	AFS64897.1	5'-AACACCATCACCAAGTATAACCCAGGTGATCTGGAGGGGAAAGGCTGACCAGA-3' 5'-TCTGGTCAGCCTTTCCCCTCCAGATCACCTGGGTATACTTGGTGATGGTGT-3'
18	S81T <sup>b</sup>	β4, Gn	2.2	BAK08371.1	5'-AACACCATCACCAAGTATAACCCAGGTGACCTGGAGGGGAAAGGCTGACCAGA-3' 5'-TCTGGTCAGCCTTTCCCCTCCAGGTACCTGGGTATACTTGGTGATGGTGT-3'

19	G84K <sup>b</sup>	β4, Gn	3.85	AKO63083.1	5'-AAGTATACCCAGGTGAGCTGGAGGAAGAAGGCTGACCAGAGCCAGAGCAGCCAAAA-3' 5'-TTTTGGCTGCTCTGGCTCTGGTCAGCCTTCTTCCTCCAGCTCACCTGGGTATACTT-3'
20	G84R <sup>b</sup>	β4, Gn	1.65	ANK77984.1	5'-AAGTATACCCAGGTGAGCTGGAGGAGAAAGGCTGACCAGAGCCAGAGCAGCCAAAA-3' 5'-TTTTGGCTGCTCTGGCTCTGGTCAGCCTTCTTCCTCCAGCTCACCTGGGTATACTT-3'
21	D87G <sup>b</sup>	-, Gn	1.1	ABS83836.1	5'-AAGTATACCCAGGTGAGCTGGAGGGGAAAGGCTGGCCAGAGCCAGAGCAGCCAAAA-3' 5'-TTTTGGCTGCTCTGGCTCTGGCCAGCCTTCCCTCCAGCTCACCTGGGTATACTT-3'
22	Q88P <sup>b</sup>	-, Gn	4.95	AIL25231.1	5'-AGCTGGAGGGGAAAGGCTGACCCTAGCCAGAGCAGCCAAAAACA-3' 5'-TGTTTTGGCTGCTCTGGCTAGGGTCAGCCTTCCCTCCAGCT-3'
23	Q88H <sup>b</sup>	-, Gn	1.1	AAC63438.1	5'-AGCTGGAGGGGAAAGGCTGACCATAGCCAGAGCAGCCAAAAACA-3' 5'-TGTTTTGGCTGCTCTGGCTATGGTCAGCCTTCCCTCCAGCT-3'
24	S89A <sup>b</sup>	-, Gn	33.52	BAA82617.1	5'-TGAGCTGGAGGGGAAAGGCTGACCAGGCTCAGAGCAGCCAAAACAGCTTTGAAA-3' 5'-TTTCAAAGCTGTTTTGGCTGCTCTGAGCCTGGTCAGCCTTCCCTCCAGCTCA-3'
25	S89G <sup>b</sup>	-, Gn	4.95	AIL25231.1	5'-TGAGCTGGAGGGGAAAGGCTGACCAGGGCCAGAGCAGCCAAAACAGCTTTGAAA-3' 5'-TTTCAAAGCTGTTTTGGCTGCTCTGGCCCTGGTCAGCCTTCCCTCCAGCTCA-3'
26	S91A <sup>b</sup>	-, Gn	25.82	AGC97133.1	5'-AAAGGCTGACCAGAGCCAGGCTAGCCAAAACAGCTTTGAAAACCGTGAGCA-3' 5'-TGCTCACGGTTTTCAAAGCTGTTTTGGCTAGCCTGGCTCTGGTCAGCCTTT-3'
27	V126I <sup>a</sup>	β6, cGn	78.57	BAZ96167.1	5'-AGAGCTACAGGTCCAGGAAGTCCATCACCTGCTATGACCTGTCTGTAACAGCACCTA-3' 5'-TAGGTGCTGTTACAGGACAGGTACATAGCAGGTGATGGACTTCTGGACCTGTAGCTCT-3'
28	C234Y <sup>c</sup>	-, Gn	0.55	AAA03156.1	5'-TCCTTCGAGTCCACCTACAACGACACAGAAAAT-3' 5'-ATTTTCTGTGTCGTTGTAGGTGGACTCGAAGGA-3'
29	A254S <sup>b</sup>	-, Gn	4.95	ABD28178.1	5'-TCTGTATTGTGGGAGGCAACTCCAGCCCCATCTACGTCCCCACCCTCGACGAC-3' 5'-GTCGTCGAGGGTGGGGACGTAGATGGGGCTGGAGTTGCCTCCCACAATACAGA-3'
30	I256W <sup>b</sup>	β15, Gn	5.49	ABU51324.1	5'-ATTGTGGGAGGCAACTCCGCTCCCTGGTACGTCCCCACCCTCGACGACTT-3' 5'-AAGTCGTGAGGGTGGGGACGTACCAGGGAGCGGAGTTGCCTCCCACAAT-3'
31	T271S <sup>a</sup>	α6, Gn	40.11	AGC97134.1	5'-ACTTCAGATCCATGGAGGCTTTCAGCGGCATTTTTAGGTCCCCTCACGGAGA-3' 5'-TCTCCGTGAGGGGACCTAAAAATGCCGCTGAAAGCCTCCATGGATCTGAAGT-3'
32	H282R <sup>c</sup>	-, Gn	0.55	AAG10043.1	5'-CCTCACGGAGAGGACAGAGACCTGGCCGGCGAG-3' 5'-CTCGCCGGCCAGGTCTCTGTCTCCTCCGTGAGG-3'
33	Y316F <sup>a</sup>	β17, Gn	40.66	AMX23679.1	5'-AGCGACACCCTGAGGCTGATTGCTTTTAGCGGCATTCCCAGCTACAGCTCCCTCAGCATT-3' 5'-AATGCTGAGGGAGCTGTAGCTGGGAATGCCGCTAAAAGCAATCAGCCTCAGGGTGTGCGCT-3'
34	G318S <sup>c</sup>	β17, Gn	1.65	ABS83838.1	5'-CTGATTGCTTATAGCTCTATTCCCAGCTACAGC-3' 5'-GCTGTAGCTGGGAATAGAGCTATAAGCAATCAG-3'
35	I359M <sup>a</sup>	β22, Gn	41.76	BAZ96167.1	5'-AACTGCGACAAGTCCGCCATCCCCCTCATGTGGACCGGCATGATCGAT-3' 5'-ATCGATCATGCCGGTCCACATGAGGGGGATGGCGGACTTGTGCGAGTT-3'
36	V373I <sup>a</sup>	-, Gn	69.78	BAZ96166.1	5'-ATCTGCCCGGATACTATGAGGCCATTCACCCTGTACAGTGTCT-3' 5'-AGAACACTGTACAAGGGTGAATGGCCTCATAGTATCCGGGCAGAT-3'
37	F460I <sup>c</sup>	-, Gn	0.55	AFS64897.1	5'-ACAATTACCTCCCTGATTAGCCTGTGCTGGA-3' 5'-TCCAGGCAGCAGGCTAATCAGGGAGGTAATTGT-3'
38	F479S <sup>c</sup>	-, Gn	0.55	AFS64897.1	5'-CTGTGCGTGCCCGGCTCTCATGGATGGGCTACA-3' 5'-TGTAGCCCATCCATGAGAGCCGGGCACGCACAG-3'
39	V508I <sup>a</sup>	-, Gn	68.68	AFS64896.1	5'-ATCACATTTCATCCTGACCATTCTGAAGTTTATCGCCAACATCTTTCATACATCCAAT-3' 5'-ATTGGATGTATGAAAAGATGTTGGCGATAAACTTCAGAATGGTCAGGATGATGAATGTGAT-3'

40	F809S <sup>c</sup>	βE0, Gc	0.55	AFS64897.1	5'-AGAGTGTGTGTGCAGTCTGGCGAGGAAAACCTC-3' 5'-GAGGTTTTCCCTCGCCAGACTGCACACACTCT-3'
41	N813H <sup>b</sup>	βF0, Gc	2.2	ARO49440.1	5'-TGTGTGCAGTTCGGCGAGGAACACCTCTGTAAGATCATCGACATGAATGA-3' 5'-TCATTTCATGTCGATGATCTTACAGAGGTGTTCTCGCCGAACTGCACACA-3'
42	K816I <sup>b</sup>	βF0, Gc	1.65	ACA61214.1	5'-AGTGTGTGTGCAGTTCGGCGAGGAAAACCTCTGTATTATCATCGACATGAATGACTGCTTCGTCTCCAGGCAT-3' 5'-ATGCCTGGAGACGAAGCAGTCATTATGTCGATGATAATACAGAGGTTTTCTCGCCGAACTGCACACACT-3'
43	I817V <sup>b</sup>	βF0, Gc	31.87	ACA61213.1	5'-AGTGTGTGTGCAGTTCGGCGAGGAAAACCTCTGTAAGGTCATCGACATGAATGACTGCTTCGTCTCCAGGCAT-3' 5'-ATGCCTGGAGACGAAGCAGTCATTATGTCGATGACCTTACAGAGGTTTTCTCGCCGAACTGCACACACT-3'
44	I817T <sup>b</sup>	βF0, Gc	1.1	BAA86849.1	5'-TTCGGCGAGGAAAACCTCTGTAAGATCACCGACATGAATGACTGCTTCGTCTCCAGGCAT-3' 5'-ATGCCTGGAGACGAAGCAGTCATTATGTCGGTGATCTTACAGAGGTTTTCTCGCCGAA-3'
45	I818V <sup>b</sup>	βF0, Gc	1.1	ANK77957.1	5'-TTCGGCGAGGAAAACCTCTGTAAGATCGTCGACATGAATGACTGCTTCGTCTCCAGGCAT-3' 5'-ATGCCTGGAGACGAAGCAGTCATTATGTCGACGATCTTACAGAGGTTTTCTCGCCGAA-3'
46	N821D <sup>bc</sup>	βG0, Gc	1.1	ABS83844.1	5'-AAAACCTCTGTAAGATCATCGACATGGATGACTGCTTCGTCTCCAGGCATGTGAAGGT-3' 5'-ACCTTCACATGCCTGGAGACGAAGCAGTCATCCATGTCGATGATCTTACAGAGGTTTT-3'
47	F892S <sup>bc</sup>	βi, Gc	1.1	AAC63438.1	5'-AAAGGCTTCCTGTGTCCCGAGTTCCTCCGGCAGCTCCAGAAAGAAGTGTAACCTTCGCTACCACCCCTATCTGCGAGT-3' 5'-ACTCGCAGATAGGGGTGGTAGCGAAGTTACTTCTTCTGGAGCTGCCGGGAACTCGGGACACAGGAAGCCTTT-3'
48	E905G <sup>b</sup>	βj, Gc	1.65	ABS83840.1	5'-AAGTGTAACCTTCGCTACCACCCCTATCTGCGGATACGATGGCAACATGGTGAGCGGTATAA-3' 5'-TTATAGCCGCTCACCATGTTGCCATCGTATCCGCAGATAGGGGTGGTAGCGAAGTTACTT-3'
49	M918L <sup>b</sup>	-, Gc	1.1	AEW43002.1	5'-AACATGGTGAGCGGCTATAAGAAGGTGCTGGCCACCATCGACAGCTTTCAAAAGCTTAAATACCAGCA-3' 5'-TGCTGGTATTAAGCTTTGAAAAGCTGTGCGATGGTGGCCAGCACCTTCTTATAGCCGCTCACCATGTT-3'
50	F934S <sup>c</sup>	βk, Gc	0.55	AEW43002.1	5'-ACCAGCACCATGCATTCTACCGACGAGAGAATC-3' 5'-GATTCTCTCGTCGGTAGAATGCATGGTGCTGGT-3'
51	E940K <sup>c</sup>	VI, Gc	0.55	ACN60122.1	5'-ACCGACGAGAGAATCAAGTGGAAAGACCCCGAC-3' 5'-GTCGGGGTCTTTCCACTTGATTTCTCTCGTCGGT-3'
52	P944R <sup>c</sup>	-, Gc	0.55	AFS64897.1	5'-ATCGAGTGGAAAAGACAGAGACGGCATGCTGAGG-3' 5'-CCTCAGCATGCCGTCTCTGTCTTTCCACTCGAT-3'
53	V1077E <sup>c</sup>	stem, Gc	3.82	BAA00280.1	5'-ATCGAGAATAGCAAAGAATACGACGATGGCGCT-3' 5'-AGCGCCATCGTCGTATTCTTTGCTATTCTCGAT-3'
54	F1091S <sup>c</sup>	stem, Gc	0.55	AFS64897.1	5'-GGCATCAAGTGCTGGTCTGTGAAGTCCGGCGAA-3' 5'-TTCGCCGGACTTCACAGACCAGCACTTGATGCC-3'
55	K1093T <sup>c</sup>	stem, Gc	0.55	AAK27683.2	5'-AAGTGTGGTTCGTGACTTCCGGCGAATGGATT-3' 5'-AATCCATTTCGCCGGAAGTCACGAACCAGCACTT-3'
56	G1104V <sup>c</sup>	stem, Gc	0.55	AGC96991.1	5'-AGCGGCATCTTCTCCGTTAATTGGATTGCTCTG-3' 5'-CAGGACAATCCAATTAACGGAGAAGATGCCGCT-3'

“a” refers to the hot substitution;

“b” refers to epitope-related substitution;

“c” refers to prediction-related substitution;

“-”, variants who are not located on the secondary structures.

**Table S2.** Genbank numbers of the 51 mutants of SEOV glycoprotein and PCR primers used for making the 51 point mutation constructs. The upper one is the forward primer while the lower one is the reverse primer.

Number	variation	Structure element	Frequency (%)	Genbank sequence number	PCR primers
1	R24K <sup>b</sup>	β1, Gn	10.08	ADE34591.1	5'TGAAGAACGTGTTTCGATATGAAGATCCAGTGCCCCCATTCCGTGAAAT-3' 5'-ATTTACACGGAATGGGGGCACTGGATCTTCATATCGAACACGTTCTCA-3'
2	Q26R <sup>b</sup>	β1, Gn	1.68	AIS71980.1	5'-AACGTGTTTCGATATGAGAATCAGGTGCCCCCATTCCGTGAAATTTGG-3' 5'-CCAAATTTACGGAATGGGGGCACCTGATTCTCATATCGAACACGTT-3'
3	K32N <sup>a</sup>	-, Gn	86.55	AEX56249.1	5'-GAATCCAGTGCCCCCATTCCGTGAACTTTGGCGAGACAAGCGTGA-3' 5'-TCACGCTTGTCTCGCCAAAAGTTCACGGAATGGGGGCACTGGATTC-3'
4	S48P <sup>b</sup>	β2, Gn	6.72	ACO37156.1	5'-ATACACCGAGCTCCCCCTCTCCCTCTGCAGGAGGCTGAGCAGCTCGT-3' 5'-ACGAGCTGCTCAGCCTCTGCAGAGGGAGAGGGGGAGCTCGGTGTAT-3'
5	A52S <sup>b</sup>	α1, Gn	1.68	ADE34589.1	5'-TCTCAGCCTGCAGGAGTCTGAGCAGCTCGTGCCCCGAAA-3' 5'-TTTCGGGCACGAGCTGCTCAGACTCCTGCAGGCTGAGA-3'
6	I79V <sup>b</sup>	β4, Gn	9.24	ADE34587.1	5'-AATAAGCTGACCAAAGTGGTCTGGAGGAAGAAGGCCAAC-3' 5'-GTTGGCCTTCTCCTCCAGACCACTTTGGTCAGTTATT-3'
7	R81Q <sup>b</sup>	β4, Gn	5.88	AIS71976.1	5'-ACCAAAGTGATCTGGCAGAAGAAGGCCAACCAAG-3' 5'-CTTGGTTGGCCTTCTTCTGCCAGATCACTTTGGT-3'
8	K82R <sup>b</sup>	β4, Gn	1.68	ADE34593.1	5'-CTGACCAAAGTGATCTGGAGGAGGAAGGCCAACCAAGAGT-3' 5'-ACTCTTGGTTGGCCTTCTCCTCCAGATCACTTTGGTCAG-3'
9	S88L <sup>b</sup>	-, Gn	2.52	AAG28741.1	5'-AAGAAGGCCAACCAAGAGCTCGCTAATCAGAATTCC-3' 5'-GGAATTCTGATTAGCGAGCTCTTGGTTGGCCTTCTT-3'
10	L96V <sup>a</sup>	β5, Gn	92.44	AIS71978.1	5'-TCAGAAATCCTTTGAGGTTCATGGAGTCCGAGGTGTCCTTTAAG-3' 5'-CTTAAAGGACACCTCGGACTCCATGACCTCAAAGGAATTCTGA-3'
11	M97V <sup>a</sup>	β5, Gn	70.59	AIS71978.1	5'-AATTCCTTTGAGCTCGTGGAGTCCGAGGTGTCCTTTAAGG-3' 5'-CCTTAAAGGACACCTCGGACTCCACGAGCTCAAAGGAATT-3'
12	V164I <sup>b</sup>	β9, Gn	93.28	ADE34588.1	5'-CTCGGACCCTACAGGATCCAAGTGGTGTATGAGAGAACCTA-3' 5'-TAGGTTCTCTCATACACCACTTGGATCCTGTAGGGTCCGAG-3'
13	P186H <sup>c</sup>	β11, Gn	1.68	ADE34595.1	5'-GGAAAATGCTTCGTGCATGATAAAGCCGTCGTG-3' 5'-CACGACGGCTTTATCATGCACGAAGCATTTTCC-3'
14	Y199C <sup>c</sup>	-, Gn	0.84	BAA86852.1	5'-CTCAAGAGGGGAATGTGTGCCATCGCCTCCATC-3' 5'-GATGGAGGCGATGGCACACATCCCCTTTGAG-3'
15	T327A <sup>a</sup>	-, Gn	86.55	AFS64912.1	5'-CTCCACCAGCATCCTGGCTGCCAGCGAGGACGGCAGATTC-3' 5'-GAATCTGCCGTCCTCGTGGCAGCCAGGATGCTGGTGGAG-3'
16	N409I <sup>c</sup>	-, Gn	1.68	AAZ86070.1	5'-CTGGTGTCAAACAGATTAGGTTTCAGGGCCGCC-3' 5'-GGCGGCCCTGAACCTAATCTGTTTGGACACCAG-3'
17	G448A <sup>c</sup>	-, Gn	1.68	SPP28729.1	5'-AAAACCCTCGTGATCGCTCAGTGTATCTATAACC-3' 5'-GGTATAGATACACTGAGCGATCACGAGGGTTTT-3'
18	Y452I <sup>c</sup>	-, Gn	1.68	SPP28729.1	5'-ATCGGACAGTGTATCATTACCATCACATCCCTC-3' 5'-GAGGGATGTGATGGTAATGATACACTGTCCGAT-3'
19	T455Q <sup>c</sup>	-, Gn	1.68	SPP28729.1	5'-TGATCTATAACCAATCCCTCTTTTCCCTG-3' 5'-CAGGGAAAAGAGGGATTGGATGGTATAGATACA-3'

20	S456V <sup>c</sup>	-, Gn	1.68	SPP28729.1	5'-ATCTATACCATCACAGTTCTCTTTCCCTGCTG-3' 5'-CAGCAGGGAAAAGAGAACTGTGATGGTATAGAT-3'
21	P462Q <sup>c</sup>	-, Gn	1.68	SPP28729.1	5'-CTCTTTTCCCTGCTGCAAGGCGTGGCCATTCC-3' 5'-GGAATGGGCCACGCCTTGCAGCAGGGAAAAGAG-3'
22	H466F <sup>c</sup>	-, Gn	1.68	SPP28729.1	5'-CTGCCTGGCGTGGCCATTTCCATCGCCATTGAA-3' 5'-TTC AATGGCGATGAAAATGGCCACGCCAGGCAG-3'
23	T669R <sup>c</sup>	-, Gc	1.68	SPP28729.1	5'-TCCGTCCCCATGCACAGAGACCTGGAGCTCGAT-3' 5'-ATCGAGCTCCAGGTCTCTGTGCATGGGGACGGA-3'
24	D670N <sup>c</sup>	-, Gc	0.84		5'-GTCCCCATGCACACCAACCTGGAGCTCGATTTC-3' 5'-GAAATCGAGCTCCAGGTTGGTGTGCATGGGGAC-3'
25	R682K <sup>a</sup>	-, Gc	86.55	AIS71976.1	5'-AGCCTGCCCTCCTCCTCCAAGTACACCTATAAGAGGCACCTCACAAAT-3' 5'-ATTTGTGAGGTGCCTCTTATAGGTGTAAGTGGAGGAGGAGGGCAGGCT-3'
26	H750Y <sup>b</sup>	βc, Gc	1.68	ADE34590.1	5'-GCACACCGCCAAGTGCTACTTCGAGAAGGACTACGA-3' 5'-TCGTAGTCCTTCTCGAAGTAGCACTTGGCGGTGTGC-3'
27	F792L <sup>c</sup>	βe, Gc	0.84	AIS91796.1	5'-CCCCTCGGCACCGCCTTGAAAATCATCTCCGTC-3' 5'-GACGGAGATGATTTTCAAGGCGGTGCCGACGGG-3'
28	Y811H <sup>b</sup>	βF0, Gc	2.52	SPP17880.1	5'-AGTTCGGAGAAGAGCACCTGTGCAAAAACAATTG-3' 5'-CAATTGTTTTGCACAGGTGCTCTTCTCCGAAC-3'
29	L812F <sup>b</sup>	βF0, Gc	1.68	AKZ66275.1	5'-AGTTCGGAGAAGAGTACTTCTGCAAAAACAATTGACATG-3' 5'-CATGTCAATTGTTTTGCAGAAGTACTTCTTCCGAAC-3'
30	I882S <sup>b</sup>	-, Gc	2.52	AAC63441.1	5'-AAGGACAAGCCCTTTAGCTGCCCGAGTCCCTGGCCAATTCAG-3' 5'-CTGAATTGGCCAGGGAACCTCGGGCAGCTAAAGGGCTTGTCTT-3'
31	C883R <sup>b</sup>	-, Gc	0.84	AFS64903.1	5'-AAGGACAAGCCCTTTATCAGACCCGAGTTCCTGGCCAATTCA-3' 5'-TGAATTGGCCAGGGAACCTCGGGTCTGATAAAGGGCTTGTCTT-3'
32	P887A <sup>b</sup>	-, Gc	0.84	AAF09195.1	5'-TATCTGCCCGAGTTCGCTGGCCAATTCAGAAAGAAATGC-3' 5'-GCATTCTTTCTGAATTGGCCAGCGAAGTTCGGGGCAGATA-3'
33	K893T <sup>b</sup>	βi, Gc	1.68	ADE34589.1	5'-TGGCCAATTCAGAAAGACATGCAACTTCGCCACCACACCCGTC-3' 5'-GACGGGTGTGGTGGCGAAGTTGCATGCTTCTTGAATTGGCCA-3'
34	T899S <sup>b</sup>	-, Gc	0.84	AFS64902.1	5'-AAATGCAACTTCGCCACCTCTCCCGTCTGCGAGTACGACGGA-3' 5'-TCCGTCTACTCGCAGACGGGAGAGGTGGCGAAGTTGCATT-3'
35	V901I <sup>b</sup>	βj, Gc	9.24	ADE34587.1	5'-AACTTCGCCACCACACCCATCTGCGAGTACGACGGA-3' 5'-TCCGTCTACTCGCAGATGGGTGTGGTGGCGAAGTT-3'
36	E903G <sup>b</sup>	βj, Gc	0.84	AFS64903.1	5'-ACCACACCCGTCTGCGGATACGACGGAAATATC-3' 5'-GATATTTCCGTCGTATCCGCAGACGGGTGTGGT-3'
37	I908V <sup>b</sup>	-, Gc	6.72	ADE34591.1	5'-CGAGTACGACGGAAAATGTCATCAGCGGATACAAGAA-3' 5'-TTCTTGTATCCGCTGATGACATTTCCGTCGTAATCG-3'
38	I908T <sup>b</sup>	-, Gc	0.84	AQR58376.1	5'-CGAGTACGACGGAAAATACCATCAGCGGATACAAGAA-3' 5'-TTCTTGTATCCGCTGATGGTATTTCCGTCGTAATCG-3'
39	I909F <sup>b</sup>	-, Gc	1.68	ADE34590.1	5'-CGAGTACGACGGAAAATATCTCAGCGGATACAAGAA-3' 5'-TTCTTGTATCCGCTGAAGATATTTCCGTCGTAATCG-3'
40	V915F <sup>b</sup>	-, Gc	1.68	ADE34590.1	5'-ATCAGCGGATACAAGAAATCCTGGCCACCATCGACTCCTTC-3' 5'-GAAGGAGTTCGATGGTGGCCAGGAATTTCTTGTATCCGCTGAT-3'
41	A917E <sup>bc</sup>	-, Gc	0.84	AAF09195.1	5'-ATACAAGAAAAGTCTGGAGACCATCGACTCCTTCCAGT-3' 5'-ACTGGAAGGAGTTCGATGGTCTCCAGGACTTTCTTGTAT-3'
42	I952V <sup>b</sup>	βI0, Gc	1.68	ADE34587.1	5'-TGCTGAGGGACCACATCAACGTCTCATCAGCAAGGACAT-3' 5'-ATGTCCTTGCTGATGACGACGTTGATGTGGTCCCTCAGCA-3'

43	V953I <sup>b</sup>	β11, Gc	2.52	AJG06109.1	5'-GACCACATCAACATTATCATCAGCAAGGACATCG-3' 5'-CGATGTCCTTGCTGATGATAATGTTGATGTGGTC-3'
44	I954V <sup>b</sup>	β12, Gc	0.84	ACO37156.1	5'-ACCACATCAACATTGTCTGTCAGCAAGGACATCGATTTTCGAG-3' 5'-CTCGAAATCGATGTCCTTGCTGACGACAATGTTGATGTGGT-3'
45	I958V <sup>b</sup>	-, Gc	0.84	ACO37156.1	5'-ATTGTCATCAGCAAGGACGTCGATTTTCGAGAACCTGGC 5'-GCCAGGTTCTCGAAATCGACGTCCTTGCTGATGACAAT-3'
46	I958T <sup>b</sup>	-, Gc	0.84	AIS71981.1	5'-ATTGTCATCAGCAAGGACACCGATTTTCGAGAACCTGGC-3' 5'-GCCAGGTTCTCGAAATCGGTGTCCTTGCTGATGACAAT-3'
47	N966S <sup>c</sup>	-, Gc	0.84	AAG28741.1	5'-GAGAACCTGGCCGAGTCTCCCTGTAAGGTCCGGC-3' 5'-GCCGACCTTACAGGGAGACTCGCCAGGTTCTC-3'
48	P999L <sup>c</sup>	-, Gc	0.84		5'-TCCCTGACAGAGTGCTTGACCTTCCTGACCTCC-3' 5'-GGAGGTCAGGAAGGTCAAGCACTCTGTCAGGGA-3'
49	R1006K <sup>a</sup>	βC, Gc	90.76	AGB05596.1	5'-TACCTTCCTGACCTCCATTAAGCTTGCGACATGGCTATC-3' 5'-GATAGCCATGTTCGCAAGCTTTAATGGAGGTCAGGAAGGTA-3'
50	C1049W <sup>c</sup>	-, Gc	0.84	AAL66175.1	5'-TGTCACGGCAAGGAGTGGTCCCTGACAGGCCTG-3' 5'-CAGGCCTGTCAGGGACCACTCCTTGCCGTGACA-3'
51	L1051S <sup>a</sup>	-, Gc	84.03	AGB05596.1	5'-ACGGCAAGGAGTGCTCCAGCACAGGCCTGCAGGCTTCCGCTCCTCAT-3' 5'-ATGAGGAGCGGAAGCCTGCAGGCCTGTGCTGGAGCACTCCTTGCCGT-3'

“a” refers to the hot substitution;

“b” refers to epitope-related substitution;

“c” refers to prediction-related substitution;

“-”, variants who are not located on the secondary structure.