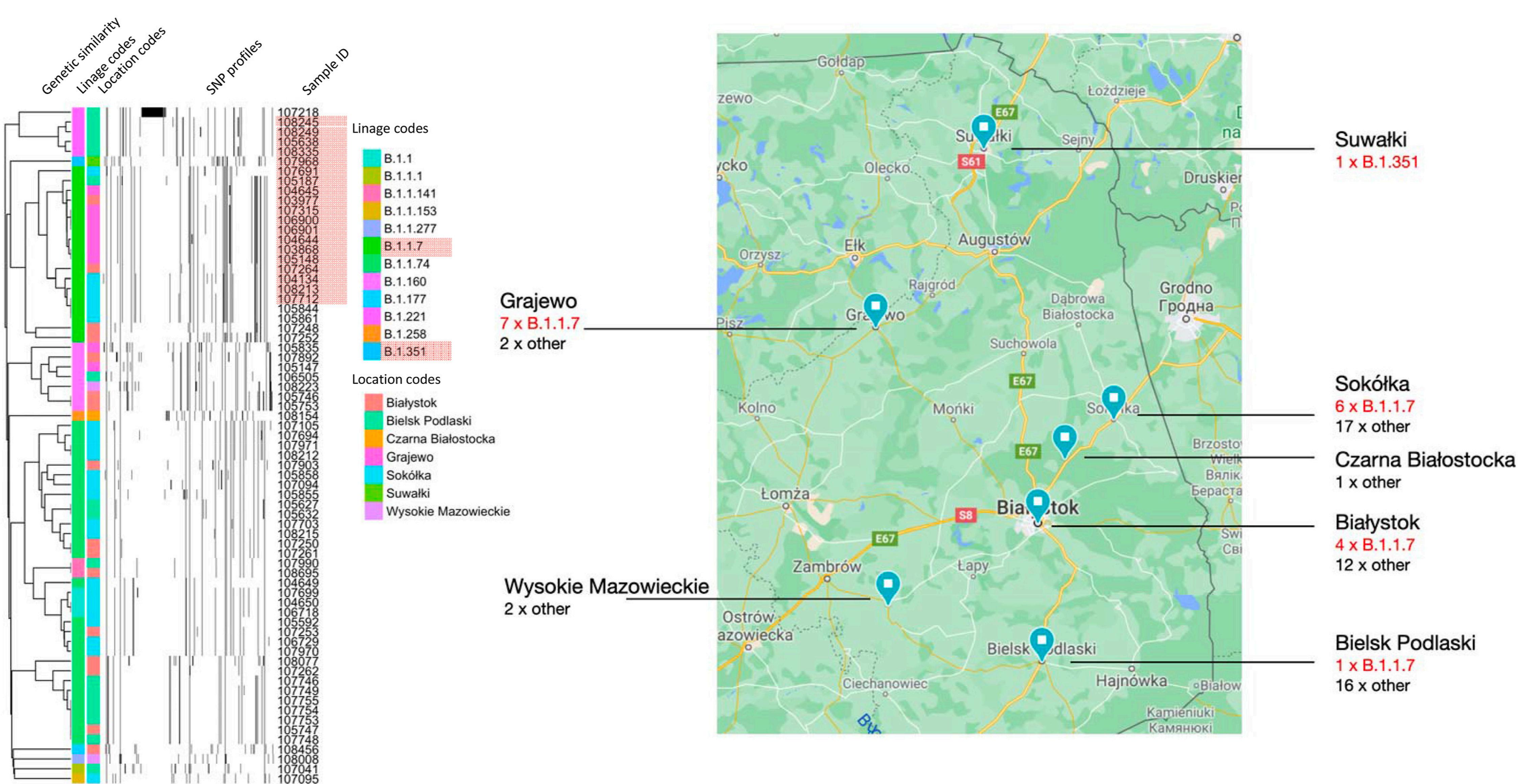


Zmienność genetyczna wirusa SARS-CoV-2 w populacji polskiej i światowej ze szczególnym uwzględnieniem sekwencji białka S

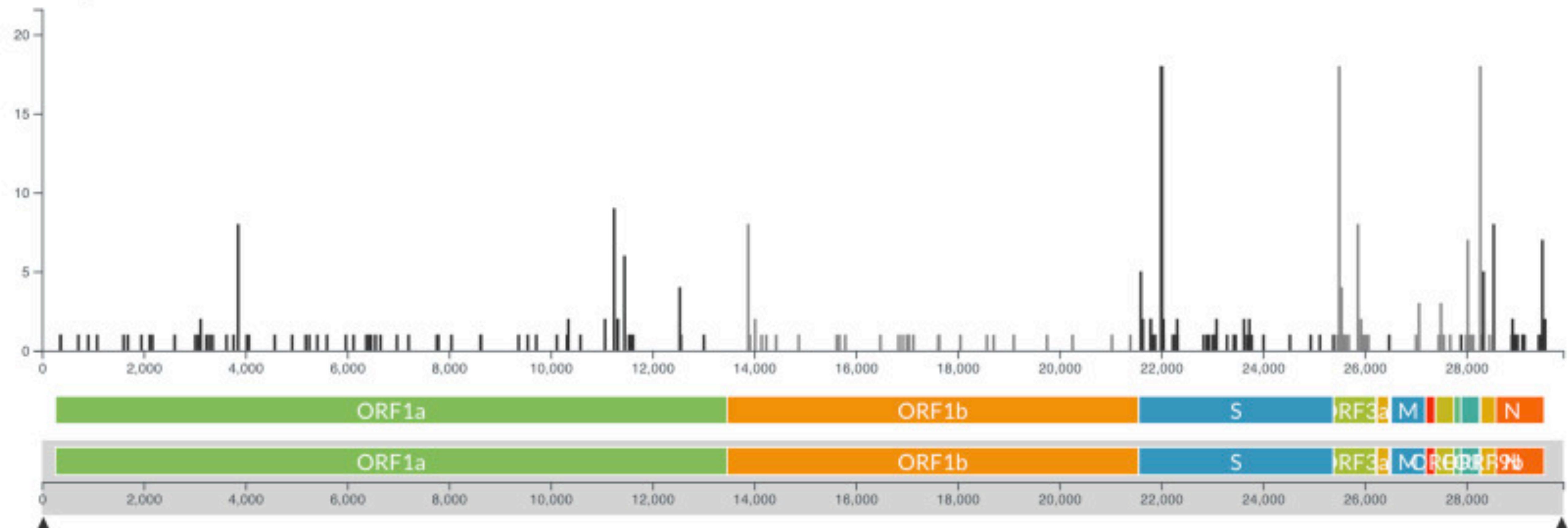
Etap 2, Zadanie 1: „Analiza bioinformatyczna surowych danych z sekwencjonowania genomów wirusa SARS-CoV-2 uzyskanych w technologii NGS oraz danych zewnętrznych zimportowanych ze światowych baz genomowych SARS-CoV-2”



The first SARS-CoV-2 genetic variants of concern (VOC) in Poland: The concept of a comprehensive approach to monitoring and surveillance of emerging variants

B

Diversity



The first SARS-CoV-2 genetic variants of concern (VOC) in Poland: The concept of a comprehensive approach to monitoring and surveillance of emerging variants

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Search

Accession ID Virus name complete high coverage
 Location Poland Host low coverage excl w/Patient status
 Collection to Submission to collection date compl
 Clade all Lineage Substitutions Variants Reset Fulltext ▲

<input type="checkbox"/>	Virus name	Passage de	Accession ID	Collection da	Submission D	i	Length	Host	monitor.mi2.ai/2021-06-08/united_kingdom/
<input type="checkbox"/>	hCoV-19/Poland/30-USAFSAM-S3061/2021	Original	EPI_ISL_2450440	2021-05-07	2021-06-08	<i>i</i>	29,783	Hum	
<input type="checkbox"/>	hCoV-19/Poland/PZH-LUM-1294/2021	Original	EPI_ISL_2449006	2021-05-22	2021-06-08	<i>i</i>	29,732	Hum	
<input type="checkbox"/>	hCoV-19/Poland/PZH-LUM-1293/2021	Original	EPI_ISL_2449005	2021-05-22	2021-06-08	<i>i</i>	29,734	Hum	
<input type="checkbox"/>	hCoV-19/Poland/PZH-LUM-1292/2021	Original	EPI_ISL_2449004	2021-05-21	2021-06-08	<i>i</i>	29,723	Hum	Data: 2021-06-08 ▾ Państwo: Europe / United Kingdom ▾
<input type="checkbox"/>	hCoV-19/Poland/PZH-LUM-1291/2021	Original	EPI_ISL_2449003	2021-05-18	2021-06-08	<i>i</i>	29,734	Hum	
<input type="checkbox"/>	hCoV-19/Poland/PZH-LUM-1290/2021	Original	EPI_ISL_2449002	2021-05-18	2021-06-08	<i>i</i>	29,732	Hum	
<input type="checkbox"/>	hCoV-19/Poland/PZH-LUM-1289/2021	Original	EPI_ISL_2449001	2021-05-18	2021-06-08	<i>i</i>	29,718	Hum	
<input type="checkbox"/>	hCoV-19/Poland/PZH-LUM-1288/2021	Original	EPI_ISL_2449000	2021-05-14	2021-06-08	<i>i</i>	29,719	Hum	
<input type="checkbox"/>	hCoV-19/Poland/PZH-LUM-1287/2021	Original	EPI_ISL_2448999	2021-05-14	2021-06-08	<i>i</i>	29,725	Hum	
<input type="checkbox"/>	hCoV-19/Poland/PZH-LUM-1286/2021	Original	EPI_ISL_2448998	2021-05-18	2021-06-08	<i>i</i>	29,732	Hum	
<input type="checkbox"/>	hCoV-19/Poland/PZH-LUM-1285/2021	Original	EPI_ISL_2448997	2021-05-18	2021-06-08	<i>i</i>	29,722	Hum	
<input type="checkbox"/>	hCoV-19/Poland/PZH-LUM-1284/2021	Original	EPI_ISL_2448996	2021-05-18	2021-06-08	<i>i</i>	29,734	Hum	
<input type="checkbox"/>	hCoV-19/Poland/PZH-LUM-1282/2021	Original	EPI_ISL_2448995	2021-05-22	2021-06-08	<i>i</i>	29,722	Hum	
<input type="checkbox"/>	hCoV-19/Poland/PZH-LUM-1281/2021	Original	EPI_ISL_2448994	2021-05-20	2021-06-08	<i>i</i>	29,725	Hum	
<input checked="" type="checkbox"/>	hCoV-19/Poland/PZH-LUM-1280/2021	Original	EPI_ISL_2448993	2021-05-20	2021-06-08	<i>i</i>	29,737	Hum	
<input type="checkbox"/>	hCoV-19/Poland/PZH-LUM-1279/2021	Original	EPI_ISL_2448992	2021-05-20	2021-06-08	<i>i</i>	29,730	Hum	
<input type="checkbox"/>	hCoV-19/Poland/PZH-LUM-1277/2021	Original	EPI_ISL_2448991	2021-05-18	2021-06-08	<i>i</i>	29,731	Hum	

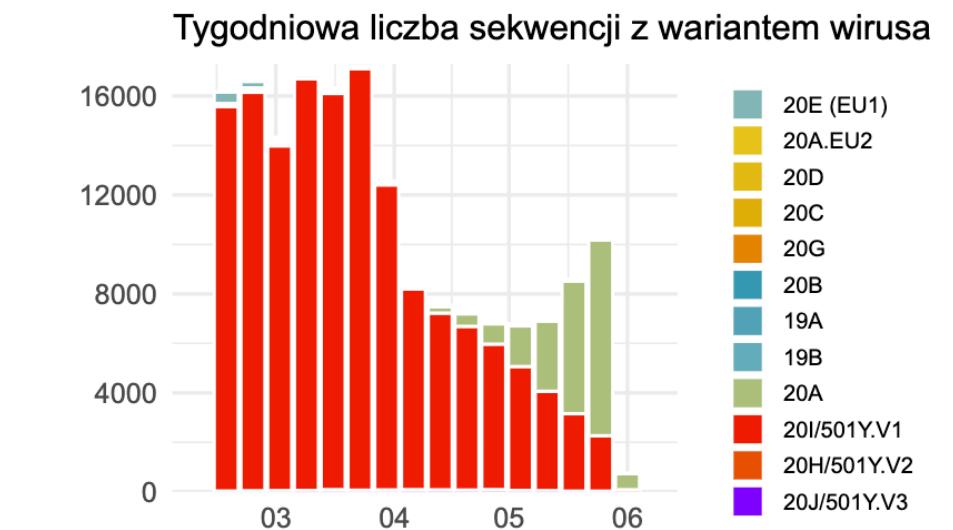
Total: 14,929 viruses << < 1 2 3 4 5 > >> S

Total: 1,894,271 viruses

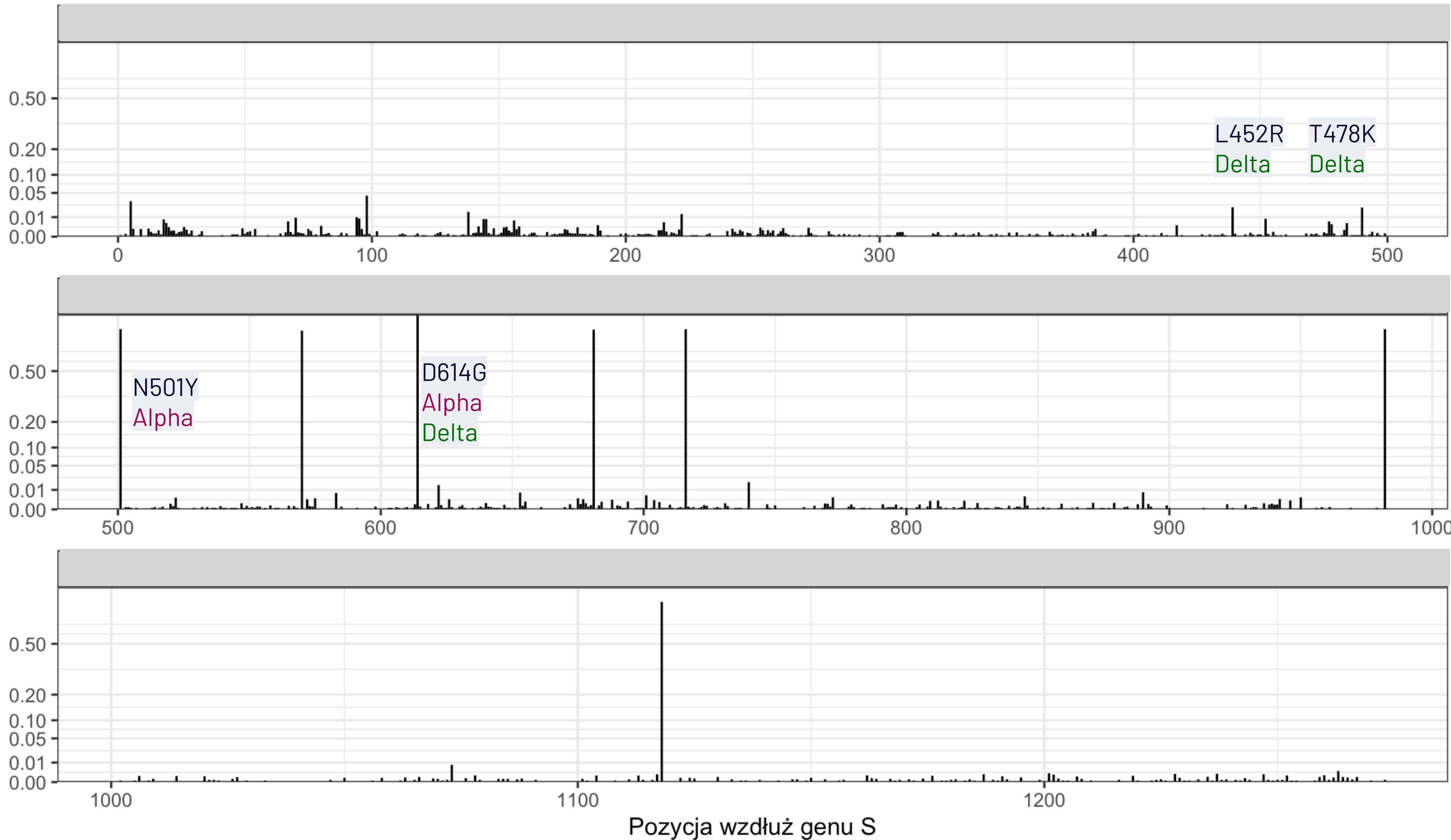
Na dzień 2021-06-08 w bazie GISAID dla wybranego państwa są 441886 sekwencje SARS-CoV-2.

Maksymalna data pobrania dla próbek z bazy GISAID: 2021-06-03.

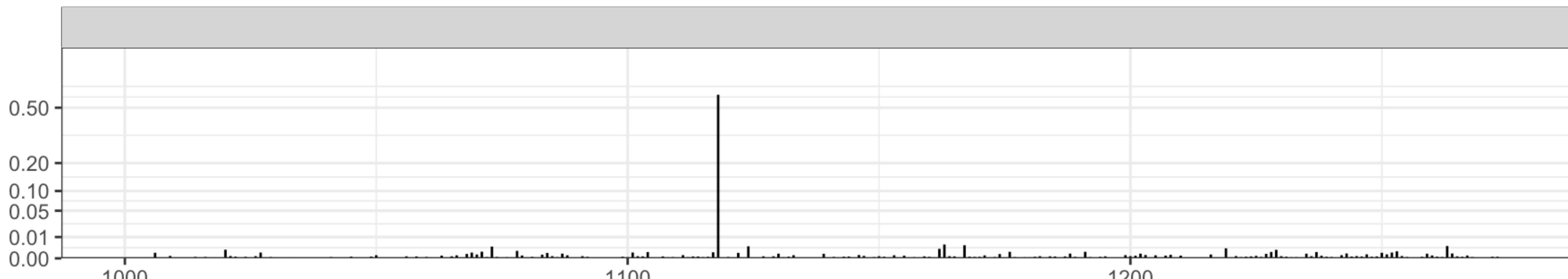
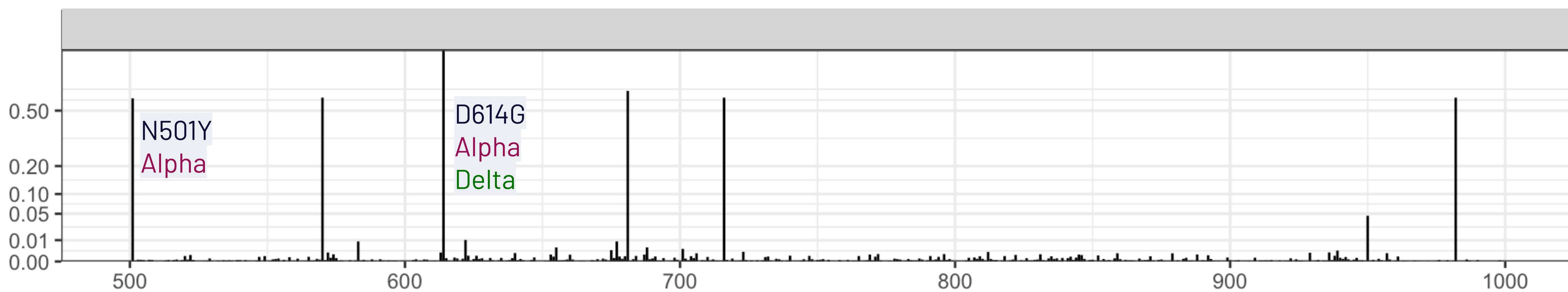
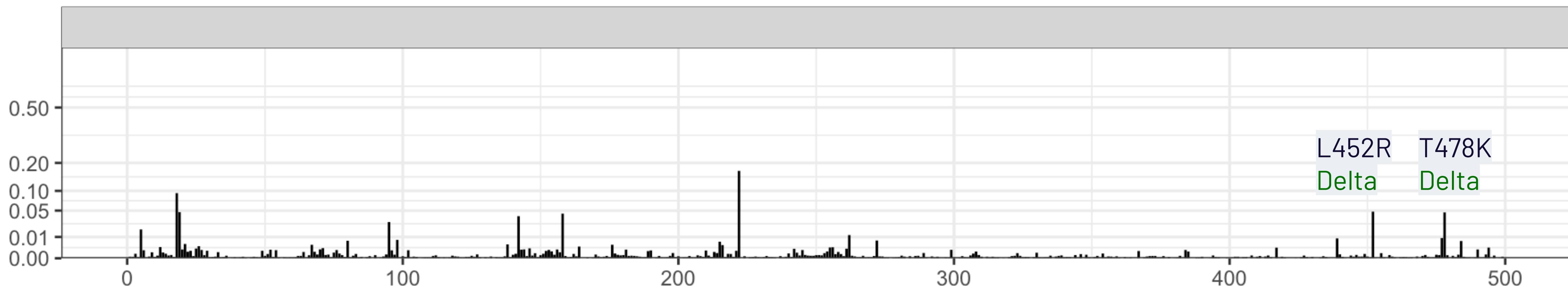
Liczba (lewy panel) i udział (prawy panel) wariantów wirusa oznaczone z bazy GISAID. Dane prezentowane w agregacji tygodniowej. Wyniki dla ostatnich 3 miesięcy.



Częstości mutacji w 14 tys sekwencji z Polski

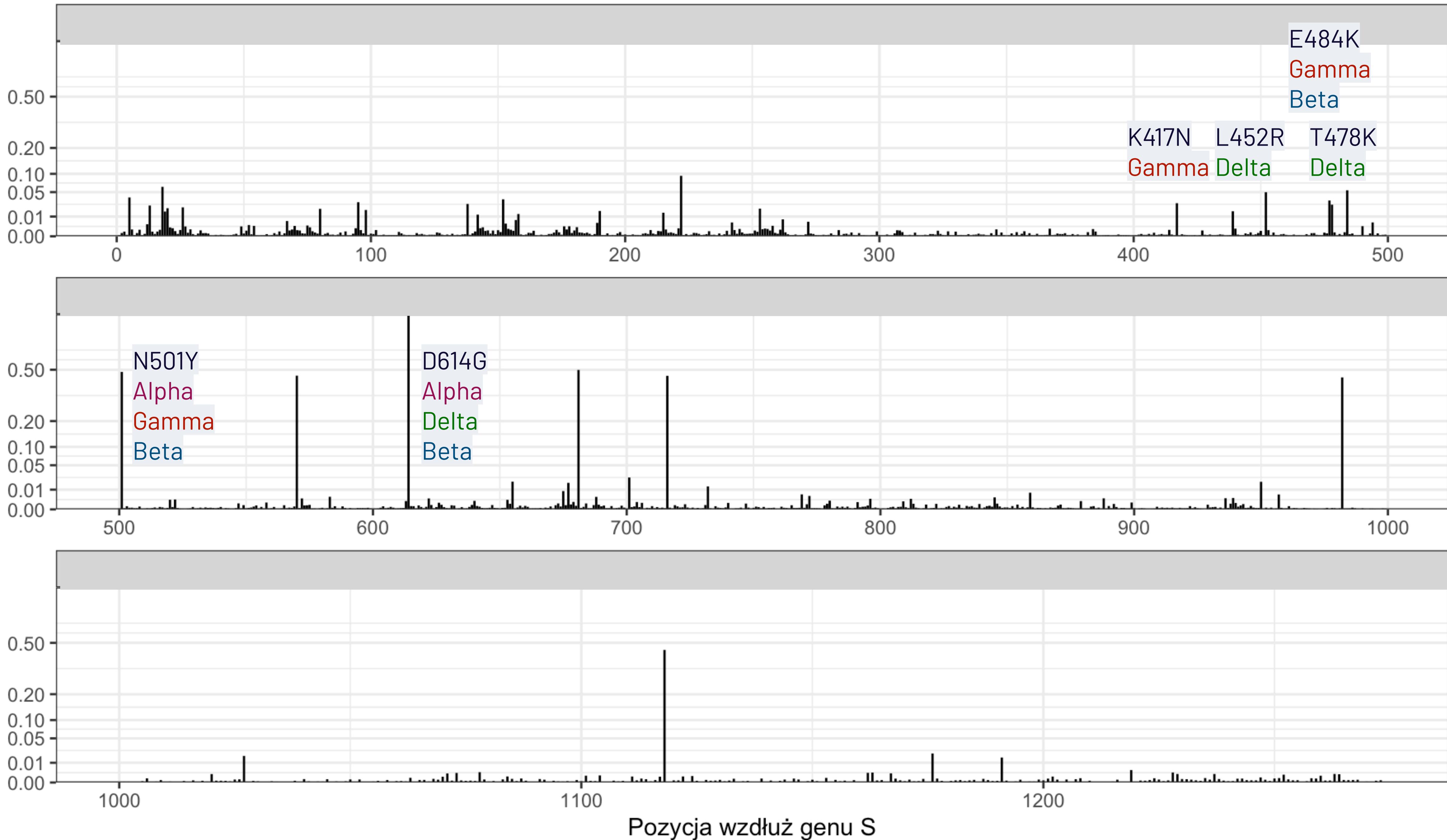


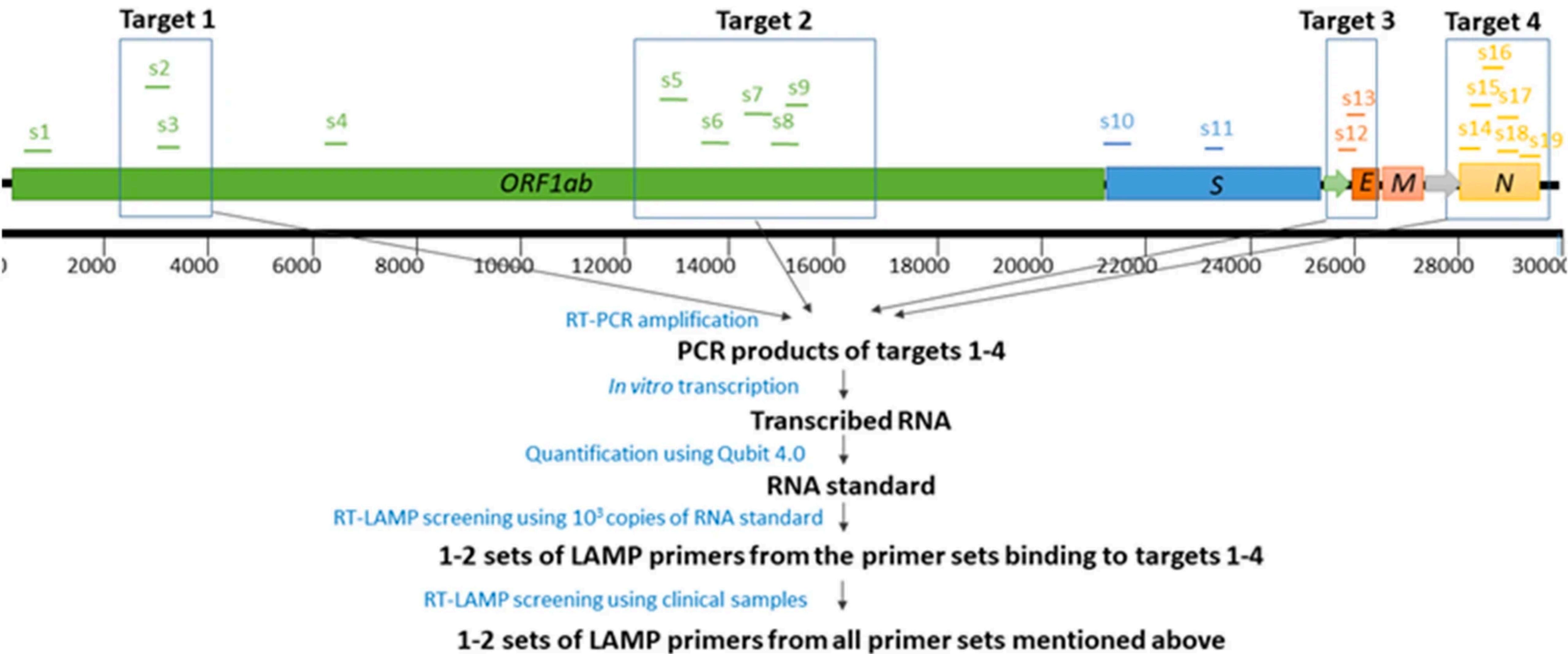
Częstości mutacji w 350 tys sekwencji z Anglii



Pozycja wzdłuż genu S

Częstości mutacji w 1.8 miliona sekwencji z całego świata





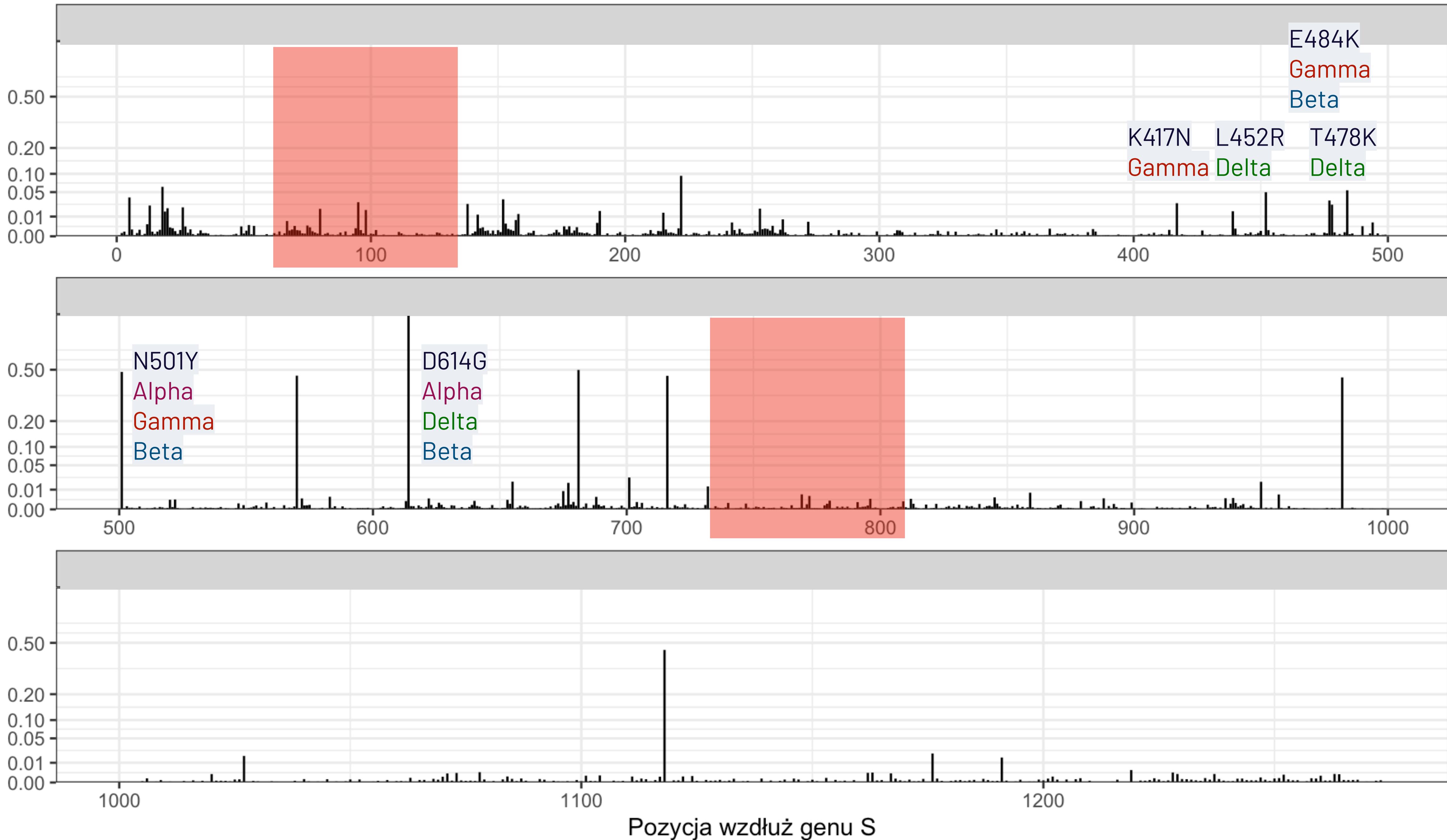
Comparative evaluation of 19 reverse transcription loop-mediated isothermal amplification assays for detection of SARS-CoV-2

Primer sets	Primer name	Primer sequence (5'-3')	Target gene	Genomic location (nt)	Sensitivity (or LOD)
S10	F3	CTGACAAAGTTTCAGATCCTCAG	S	21,678–21,886	NA
	B3	AGTACCAAAAAATCCAGCCTCTT			
	FIP	TCCCAGAGACATGTATGCATGGAATCAACTCAGGACTTGTTCTTACC			
	BIP	TGGTACTAAGAGGTTGATAACCTGTTAGACTTCTCAGTGGAAAGCA			
	LF	CCAAGTAACATTGGAAAAGAAA			
	LB	GTCCTACCATTAAATGATGGTGT			
S11	F3	TCTATTGCCATACCCACAA	S	23,693–23,937	200 copies/25 µL reaction
	B3	GGTGTGTTGAAATTGTTGAC			
	FIP	CATTCAAGTTGAATCACCAACAAATGTGTGTTACCACAGAAATTCTACC			
	BIP	GTTGCAATATGGCAGTTTGACATTGGGTGTTTGCTTGT			
	LF	ACTGATGTCTGGTCATAGACACT			
	LB	TAAACCGTGCTTAACGGAAATGC			

Comparative evaluation of 19 reverse transcription loop-mediated isothermal amplification assays for detection of SARS-CoV-2

296 CGCTAGTTATCAGACTCAGACTAATTCTCCTCGGCGGGCACGTAGTGTAGCTAGTCATCCATTGCCTACACTATGT
297 CACTTGGTGCAGAAAATTCAAGTTGCTTAACACTCTAATAAC **TCTATTGCCATACCCACAA** ATTTACTATTAGTGTACCA
298 GAAATTCTACCAGTGTCTATGACCAAGACATCAGTAGATTGTACAATGTACATTGTGGTATTCAA
299 TCTTTGTTGCAATATGGCAGTTTGACACAATTAAACCGTGCTTAACGGAAATAGCTGTTGAACAAGACAAAAACA
300 CCCAAGAAGTTTGACAAAGTCAAACAAATTACAAAACACCACCAATTAAAGATTGGTGGTTAACCAA
301 ATATTACCAGATCCATCAAAACCAAGCAAGAGGTCAATTATTGAAGATCTACTTTCAACAAAGTGACACTGCAGATGC
302 TGGCTTCATCAAACAATATGGTATTGCCTTGGTATTGCTGCTAGAGACCTCATTGTGCACAAAAGTTAACGGCC
303 TTACTGTTGCCACCTTGCTCACAGATGAAATGATTGCTCAATACACTTCTGCACTGTTAGCGGGTACAATCACTCT
304 GGTTGGACCTTGGTGCAGGTGCTGCATTACAAATACCATTGCTATGCAAATGGCTTATAGGTTAATGGTATTGGAGT
305 TACACAGAATGTTCTATGAGAACCAAAAAATTGATTGCCAACCAATTAAATAGTGTATTGGCAAAATTCAAGACTCAC
306 TTTCTCCACAGCAAGTGCACTTGGAAAATTCAAGATGTGGTCAACCAAAATGCACAAGCTTAAACACGCTTAA
307 CAACCTAGCTCCAATTGGTCAATTCAAGTGTAAATGATATCCTTACGTCTTGACAAAGTTGAGGCTGAAGT
308 GCAAATTGATAGGTTGATCACAGGCAGACTCAAAGTTGCAGACATATGTGACTCAACAAATTAAATTAGAGCTGAGAAA
309 TCAGAGCTCTGCTAATCTGCTGCTACTAAAATGTCAGAGTGTGACTTGGACAATCAAAAGAGTTGATTGGATTGG
310 AAGGGCTATCATCTTATGTCCTTCCCTCAGTCAGCACCTCATGGTAGTCTTGACATTGACTTATGTCCTGCACA
311 AGAAAAAGAACCTCACAACTGCTCCTGCCATTGTCATGATGGAAAAGCACACTTCCCTCGTAAGGTGTTCAA
312 ATGGCACACACTGGTTGTAACACAAAGGAATTGGTATGAACCACAAATCATTACTACAGACAACACATTGTCGGT
313 AACTGTGATGTTGTAATAGGAATTGTCAACACACAGTTATGATCCTTGCAACCTGAATTAGACTCATTCAAGGAGGA
314 GTTAGATAAAATTAAAGAACATACATCACCAAGATGTTGATTAGGTGACATCTCTGGCATTAAATGCTCAGTTGTA
315 ACATTCAAAAAGAAATTGACCGCCTCAATGAGGTTGCCAAGAACATTAAATGAATCTCTCATCGATCTCCAAGAACATTGG
316 AAGTATGAGCAGTATATAAAATGCCATGGTACATTGGCTAGGTTTATAGCTGGCTTGCCATAGTAATGGTGAC
317 AATTATGCTTGCTGTATGACCAAGTTGCTGTAGTTGCTCAAGGGCTGTTCTGGATCCTGCTGCAAATTGATG
318 AAGACGACTCTGAGCCAGTGCTCAAAGGAGTCAAATTACATTACACATAAACGAACCTATGGATTGTTATGAGAAC
319 TCACAATTGGAACTGTAACTTGAAGCAAGGTGAAATCAAGGATGCTACTCCTCAGATTGTCGCGCTACTGCAACG
320 ATACCGATAACAAGCCTCACTCCCTTGGATTGGCTTATTGTTGGCGTTGCACTTGTGCTTTTCAAGCGCTTCAA

Częstości mutacji w 1.8 miliona sekwencji z całego świata



Sequence

Preferences

Set_Fixed

Core_Primers

Loop_Primers

Results

Resources

LAMP Core Primer Selection

Target DNA	TTTCACACGT	GGTGT	TTATT	ACCCTGACAA	AGTTTCAGA	TCCTCAGTTT	TACATTCAAC	TCAGGACTTG	TTCTTACCTT	TCTTTCCA	TGTTACTTGG	TTCCATGCTA	TACATGTCTC	TGGGACCAAT	GGTACTAAGA	GGTTTGATAA
(Complement)	aaagtgtgcaccacaaaataatggactgttcaaaagtct	aggagtcaaaatgttaagttg	agtcctgaac	aagaatggaa	agaaaagg	ttaaaatgtacagag	accctgg	ttaccatgattct	ccaaactatt							
ID dG(dimer)	1	11	21	31	41	51	61	71	81	91	101	111	121	131	141	
○ [11]	-2.16	[11]	GTGTTTATT	ACCCTGACAAAGT	TCAGA	TCCTCAGTTT	TACATT			agaaaagg	ttaaaatgtacagag	accctgg	ttaccatgattct	ccaaactatt		
○ [79]	-2.18							[79]	TCTTACCTT	TCTTTCCA	TGT	GG	TTCCATGCTA	TACATGTCT		ctccaaactatt
○ [101]	-2.27										[101]	GTCTC	TGGGACCAAT	GGTACTAAGA	GGTTTGATAA	
○ [28]	-2.36		[28]	TGACAAAGTTTCAGA	TCCTCAGTTT	TACATTCAAC	TCAGGAC			agtt	ttaaaatgtacagag	accctgg	ttaccatgattct	ccaaactatt		
○ [57]	-2.46						[57]	TCAAC	TCAGGACTTG	TTCTT	CTT	TCTTTCCA	TGTTACTTGG		gagaccctgg	ttaccatgattct

 Generate Loop Primers

 Get Selected Primers

ID:11 dimer dG: -2.16

	5' pos	3' pos	len	Tm	5' dG	3' dG	% GC	(required oligos are orange)
F3	12	33	22	55.93	-4.32	-4.16	36	GTGTTTATTACCCTGACAAAGT
B3	192	216	25	55.80	-4.69	-4.27	32	CCTCTTATTATGTTAGACTCTCAA
FIP			47					TGGAACCAAGTAACATTGAAAAGA TCAGATCCTCAGTTTACATT
BIP			46					GCTATACATGTCTCTGGACCAAT GGAAGCAAATAAACACCATCA
F2	36	57	22	55.18	-4.15	-4.06	36	TCAGATCCTCAGTTTACATT
F1c	81	105	25	60.98	-5.02	-3.52	36	TGGAACCAAGTAACATTGAAAAGA
B2	169	190	22	57.12	-5.70	-4.91	36	GGAAGCAAATAAACACCATCA
B1c	107	130	24	61.82	-3.55	-4.55	46	GCTATACATGTCTCTGGACCAAT

Utrwalone mutacje w poszczególnych wariantach

