SARS-COV-2 VARIANTS IN RISK ASSESSMENT POSITION AS OF 23 March 2021 PHE

Last horizon scan	Signals currently under monitoring and investigation	Variants under investigation	Variants of concern
Cluster detection 19-03-2021 Mutation Scan 23-03-2021 International Scan 23-03-2021 Signals investigated at last scan: 2 New genomes in last 24 hr period: 1699 Note: Signals of individual mutations and new clusters excluded until defined variant identified	B.1.429 (California)	VUI-21JAN-01 P.2 (Brazil)	VOC-20DEC-01 B.1.1.7 (UK)
	B.1.526 (New York)	VUI-21FEB-01 A.23.1 with E484K (UK) focus Liverpool	VOC-20DEC-02 B.1.351 (South Africa)
	B.1.1.7 with S494P (UK)	VUI-21FEB-03 B.1.525	VOC-21JAN-02 P.1 (Japan ex Brazil)
	A.27 (France)	VUI-21FEB-04 B1.1.318 (England)	VOC-21FEB-02 B.1.1.7 with E484K (UK) focus Bristol/SW.
		VUI-21MAR-01 B.1.324.1 with E484K (UK)	
		VUI-21MAR-02 P.3 (Philippines)	

VOC/VUI GENOMIC CASE DEFINITIONS

As of 16/03/2021

		Confirmed	Probable	HR-LQG
VOC-20DEC-02	B.1.351	**All lineage defining changes called** as alternate bases.	**AT LEAST 4 lineage defining changes** called as alternate base and all other positions either N or mixed base OR at least 5 of the 9 non-synonymous changes (indicated by * in the table).	**Fewer than 4 positions** are called but at least one is called as alternate (variant) base AND all other defining positions reported as N (unknown) or mixed bases OR fewer than 5 of the 9 required positions are called as alternate base, fewer then 5 lineage defining positions are called as wildtype and all other positions are called as N or mixed base.
VUI-21JAN-01	P.2	**All lineage defining changes called** as alternate base OR 6 of 7 changes called as alternate base AND remaining position either N or mixed bases.	N/A	**Fewer than 6 positions** are called but at least one is called as alternate (variant) base AND all other defining positions reported as N (unknown) or mixed bases.
VOC-21JAN-02	P.1	**All lineage defining changes called** as alternate bases.	**AT LEAST 5 lineage defining changes** called as alternate base AND all other positions either N or mixed bases.	**Fewer than 5 positions** are called but at least one is called as alternate (variant) base AND all other defining positions reported as N (unknown) or mixed bases.

VOC-20DEC-02

gene	amino_acid	actual_nucleotide	note
S Gene	L18F	21614C>T	not lineage defining
	D80A*	21801A>C	
	D215G*	22206A>G	
	R246I	22299G>T	not lineage defining
	K417N*	22813G>T	not lineage defining
	E484K*	23012G>A	
	N501Y*	23063A>T	
	A701V*	23664C>T	
ORF1ab	*T265I*	*1059C>T*	*nsp2T85I*
	*K1655N**	*5230G>T*	*nsp3K837N*
	K3353R	*10323A>G*	*nsp5K90R*
ORF3a	*Q57H*	*25563G>T*	
	S171L	*25904C>T*	
E Gene	*P71L**	*26456C>T*	
N Gene	*T205I**	*28887C>T*	

VUI-21JAN-01

gene	amino_acid	actual_nucleotide	note
	-	100>T	not included in definition due to masking
orf1ab	L3468V	10667T>G	nsp5:L205V
	-	11824C>T	nsp6:I248I
	-	12964A>G	nsp9:G93G; not lineage defining
S Gene	E484K	23012G>A	
orf8	F120F	28253C>T	
N Gene	A119S	28628G>T	
	M234I	28975G>T	
	-	29754>T	not included in definition due to masking

VOC-21JAN-02

gene	amino_acid	actual_nucleotide	note
orf1ab	-	733T>C	
	-	2749C>T	
	S1188L	3828C>T	nsp3:S370L
	K1795Q	5648A>C	nsp3:K977Q
	-	11288_96del	
	-	12778C>T	
	-	13860C>T	
	E5665D	17259G>T	nsp13:E341D
S Gene	L18F	21614C>T	
	T20N	21621C>A	
	P26S	21638C>T	
	D138Y	21974G>T	
	R190S	22132G>T	Not present in entire clade
	K417T	22812A>C	
	E484K	23012G>A	
	N501Y	23063A>T	
	H655Y	23525C>T	
	T1027I	24642C>T	
orf8	E92K	28167G>A	
	-	28263insAACA	
N Gene	P80R	28512C>G	
	-	28877A>T	
	-	28878G>C	

N.B. Rows in red are not lineage defining but have been acquired by a subset of isolates within the lineage and those with a * are included in the nine variants included in the "probable" genomic definition.

VOC/VUI GENOMIC CASE DEFINITIONS

As of 16/03/2021

		Confirmed	Probable	HR-LQG
VUI-21FEB-01	A.23.1+E484K	**All lineage defining changes called** as alternate bases.	**AT LEAST 5 lineage defining changes** called as alternate base and all other positions either N or mixed base	**Fewer than 5 positions** are called but at least one is called as alternate (variant) base AND all other defining positions reported as N (unknown) or mixed bases.
VOC-21FEB-02	B.1.1.7+E484K	**All lineage defining changes called** as alternate bases.	N/A	**Probable or Confirmed VOC202012/01 and Fewer than 4 positions** are called but at least one is called as alternate (variant) base AND all other defining positions reported as N (unknown) or mixed bases.
VUI-21FEB-03	B.1.525	**All lineage defining changes called** as alternate bases.	**AT LEAST 5 lineage defining changes** called as alternate base AND all other positions either N or mixed bases.	**Fewer than 5 positions** are called but at least one is called as alternate (variant) base AND all other defining positions reported as N (unknown) or mixed bases.

VUI-21FEB-01

gene	amino_acid	actual_nucleotide	note
orf1ab	L1559F	4940C>T	nsp3:L741F
	M3655I	11230G>T	nsp6:M86I
	L3667F	11266G>T	nsp6:L98F
	M3752I	11521G>T	nsp6:M183I
S Gene	R102I	21867G>T	
	F157L	22033C>A	
	V367F	22661G>T	
	E484K	23012G>A	
	Q613H	23401G>T	
	P681R	23604C>G	
orf8	L84S	28144T>C	
N Gene	E92K	28167G>A	
	S202N	28878G>A	

VOC-21FEB-02

gene	amino_acid	actual_nucleotide	note
orf1ab	L730F	2453C>T	nsp2:L550F
	-	7843C>T	nsp3:N1708N
S Gene	E484K	23012G>A	
M Gene	-	27092C>T	
N Gene	A173V	28791C>T	
	A398T	29465G>A	

VUI-21FEB-03

gene	amino_acid	actual_nucleotide	note
orf1ab	-	1498C>T	
	-	1807A>G	
	-	2659G>A	
	T2007I	6285C>T	
	-	8593T>C	
	-	9565C>T	
	3675_7del	11288_96del	nsp6:106_8del
	P4715S	144407C>T	nsp12:P323S
	-	18171C>T	
	-	20724A>G	
S Gene	Q52R	21717A>G	
	A67V	21762C>T	
	69_70del	21765_70del	
	144del	21991_3del	
	E484K	23012G>A	
	Q677H	23593G>C	
	F888L	24224T>C	
	-	24748C>T	
E Gene	L21F	26305C>T	
M Gene	I82T	26767T>C	
orf6	2del	27205_7del	
N Gene	2_3del	28278_80del	
	A12G	28308C>G	
	-	28699A>G	
	-	29543G>T	

N.B. Rows in red are not lineage defining but have been acquired by a subset of isolates within the lineage and those with a * are included in the nine variants included in the “probable” genomic definition.

VOC/VUI GENOMIC CASE DEFINITIONS

As of 16/03/2021

	Confirmed	Probable	HR-LQG
VUI-21FEB-04 B.1.318	**All lineage defining changes called** as alternate bases.	**AT LEAST 5 lineage defining changes** called as alternate base and all other positions either N or mixed base.	**Fewer than 5 positions** are called but at least one is called as alternate (variant) base AND all other defining positions reported as N (unknown) or mixed bases.

VUI-21FEB-04

Gene	Amino Acid	Nucleotide	Note
orf1ab	E378V	3852A>T	nsp3:E378V
	-	3961C>T	
	K2511N	7798G>T	nsp3K1693N
	T2936I	9072C>T	nsp4:T173I
	A3209V	9891C>T	nsp4:A446V
	T3284I	10116C>T	nsp5:T21I
	3675_7del	11288_96del	nsp6:106_8del
	V6672M	20578G>A	nsp15:V320M
S	T95I	21846C>T	
	144del	21991_3del	
	E484K	23012G>A	
	-	23287T>C	
	P681H	23604C>A	
	D796H	23948G>C	
	-	24382C>T	
	-	25276C>A	
M	I82T	26767T>C	
orf8	1_3del	27894_901del	
	E106*	28209G>T	
-	-	28271A>G	
N	A208_A209delinsG	28896_8del	

N.B. Rows in red are not lineage defining but have been acquired by a subset of isolates within the lineage and those with a * are included in the nine variants included in the “probable” genomic definition.

VOC/VUI GENOMIC CASE DEFINITIONS

As of 16/03/2021

		Confirmed	Probable	HR-LQG
VUI-21MAR-01	B.1.324.1 + E484K	**All lineage defining changes called** as alternate bases.	N/A	**Fewer than 8 positions** are called but at least one is called as alternate (variant) base AND all other defining positions reported as N (unknown) or mixed bases.
VUI-21MAR-02	P.3	**All lineage defining changes called** as alternate bases.	**AT LEAST 7 lineage defining changes** called as alternate base and all other positions either N or mixed base	**Fewer than 7 positions** are called but at least one is called as alternate (variant) base AND all other defining positions reported as N (unknown) or mixed bases.

VUI-21MAR-01

Gene	Amino Acid	Nucleotide	Note
orf1ab	G894S	2945G>A	nsp3: G76S
	-	8704T>C	from wider lineage
		8986C>T	
	-	13617G>A	from wider lineage
	G5530C	16852G>T	nsp13: G206C
S	-	22388C>T	
	E484K	23012G>A	
orf8	10_21del	27922_56del	
-	-	28272A>T	from wider lineage

VUI-21MAR-02

Gene	Amino Acid	Nucleotide	Note
orf1ab	D736G	4926A>G	
	-	7564C>A	
	L438P	9867T>C	
	D112E	11308C>A	
	-	12049C>T	
	L71F	12053C>T	
	A368V	17339C>T	
S	141_3del	21981_9del	
	E484K	23012G>A	
	N501Y	23063A>T	
	P681H	23604C>A	
	-	23341T>C	
	-	24187T>A	
	E1092K-	24836G>A	
	H1101Y	24863C>T	
	H1101Y	24863C>T	
	V1176F	25088G>T	
orf8	K2Q	27897A>C	

N.B. Rows in red are not lineage defining but have been acquired by a subset of isolates within the lineage and those with a * are included in the nine variants included in the “probable” genomic definition.

E484K GENOMIC CASE DEFINITION

As of 14/02/2021

Confirmed:
All required nucleotide changes (23012G>A) are called as alternate base and all other nucleotides in the codon are wild type (23013 & 23014)

Probable:
All required nucleotide changes (23012G>A) are called as alternate base and at least one other nucleotide in the codon is called as N or mixed base (23013 & 23014)

Low Quality:
All required nucleotide changes (23012G>A) are called as N or mixed base and all other nucleotides in the codon are wild type, N or mixed base (23013 & 23014)

Definition	Codon
Wildtype	GAA
Confirmed	AAA
Probable	ANN
Low_qc	NAA/NNN

N.B. High rish LQG definition to be discussed