SARS-COV-2 VARIANTS IN RISK ASSESSMENT POSITION AS OF 17 FEBRUARY 2021 PHE

Last horizon scan	Signals currently under monitoring and investigation	Signals escalating to Variant Technical Group	Variants under investigation	Variants escalating to NERVTAG	Variants of concern
Cluster detection 16-02-2021 **Mutation Scan** 17-02-2021 **International Scan** 17-02-2021 **Signals investigated at last scan**: 2 Note: Signals of individual mutations and new clusters excluded until defined variant identified	**B.1.429 (California)**		**VUI 202101/01** P2 (Brazil)		**VOC202012/01**, B.1.1.7 (UK)
	B.1.526 (New York)		**VUI 202102/01** A.23.1 with E484K (UK) focus Liverpool		**VOC202012/02**, B.1.351 (South Africa)
			VUI 202102/03 B.1.525 (previously designated UK1188)		**VOC202101/02** P1 (Japan ex Brazil)
					VOC 202102/02 B.1.1.7 with E484K (UK) focus Bristol/SW.

VOC/VUI GENOMIC CASE DEFINITIONS

As of 16/02/2021

		Confirmed	Probable	HR-LQG
VOC 202012/02	B.1.351	**All lineage defining non-synonymous changes called** as alternate bases.	**AT LEAST 4 lineage defining non-synonymous 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 202101/01	P.2	**All lineage defining non-synonymous changes called** as alternate base OR 6 of 7 non-synonymous 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 202101/02	P.1	**All lineage defining non-synonymous changes called** as alternate bases.	**AT LEAST 5 lineage defining non-synonymous 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 202012/02

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 202101/01

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 202101/02

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 14/02/2021

		Confirmed	Probable	HR-LQG
VUI 202102/01	A.23.1+E484K	**All lineage defining non-synonymous changes called** as alternate bases.	**AT LEAST 5 lineage defining non-synonymous 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 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 202102/02	B.1.1.7+E484K	**All lineage defining non-synonymous 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 202102/03	B.1.525	**All lineage defining non-synonymous changes called** as alternate bases.	**AT LEAST 5 lineage defining non-synonymous 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 202102/01

gene	amino_acid	actual_nucleotide	note
orf 1ab	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	
orf 8	L84S	28144T>C	
N Gene	E92K	28167G>A	
	S202N	28878G>A	

VOC 202102/02

gene	amino_acid	actual_nucleotide	note
orf 1ab	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 202102/03

gene	amino_acid	actual_nucleotide	note
orf 1ab	-	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	
orf 6	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.

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