SARS-COV-2 VARIANTS IN RISK ASSESSMENT POSITION AS OF 10 March 2021 PHE

Last horizon scan	Signals currently under monitoring and investigation	Variants under investigation	Variants of concern
Cluster detection 09-03-2021 Mutation Scan 08-03-2021	B.1.429 (California)	VUI 202101/01 P2 (Brazil)	VOC202012/01 , B.1.1.7 (UK)
International Scan 10-03-2021 Signals investigated at last scan: 0	B.1.526 (New York)	VUI 202102/01 A.23.1 with E484K (UK) focus Liverpool	VOC202012/02 , B.1.351 (South Africa)
New genomes in last 24 hr period: 1373	B.1.1.7 with S494P (UK)	VUI 202102/03 B.1.525 (previously designated UK1188)	VOC202101/02 P1 (Japan ex Brazil)
Note: Signals of individual mutations and new clusters excluded until defined variant identified	A.27 (France)	VUI202102/04 B1.1.318 (England)	VOC 202102/02 B.1.1.7 with E484K (UK) focus Bristol/SW.
		VUI202103/01 B.1.324.1 with E484K (UK)	

VOC/VUI GENOMIC CASE DEFINITIONS

As of 16/02/2021

28263insAACA

28512C>G

28877A>T

28878G>C

P80R

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N Gene

$ S Gene \ \ \ \ \ \ \ \ \ \ \ \ \ $						Confirme	ed		Probab	le			HR-LQG	
VUI 202101/01 P.2 called as alternate base 0.6 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 or called as alternate (variant) base AND all other de positions reported as N (unknown) or mixed base 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 or called as alternate base AND all other positions either N or mixed base. Voc 202101/02 P.1 Vul 202101/01 VUl 20210/01 Fewer than 5 positions are called but at least or called as alternate base. S Gene R246 220305-T not lineage defining D215G* not lineage defining defining defining to timeage defining D215G* S Gene E484K* 220305-T mest masking mot lineage defining D11588.98660 Not present in entild mesp. 2307.C S Gene R246 222930-T not lineage defining D11588.98660 Gene R1158 230125-A mesp. 2302.C S Gene R1158 Contract of R11588.98660 Not present in entilf R1158.98660 S Gene E484K 220120-A S Gene R1158 E484K 220125-A R1158.98660 S Gene R2468 1090-T	/OC 20	2012/02	B.1.35	51	-		-	anges change positior	s called as alternations either N or mixed on-synonymous charter	te base and a l base OR at l anges (indica	ll other least 5 of	called as alter positions rep fewer than 5 alternate base	nate (variant) base orted as N (unknow of the 9 required p e, fewer then 5 line vildtype and all oth	AND all other defining m) or mixed bases OR ositions are called as age defining positions er positions are called
All lineage defining non-synonymous changes changes called as alternate base. AND all other called as alternate base. AND all other positions reported as N (unknown) or mixed base. Called as alternate bases. Ca	VUI 20	2101/01	P.2		called as alto synonymous cha	ernate base anges calle g position	e OR 6 of 7 no ed as alternate	n- ebase	N/A			called as alter	nate (variant) base	AND all other definin
Vice zoutry of zero actual nucleotide note gene amino_acid actual_nucleotide note gene amino_acid actual_nucleotide note actual_nucleotide note gene amino_acid actual_nucleotide note note actual_nucleotide in actual_nucleotide note gene amino_acid actual_nucleotide note	VOC 20	2101/02	P.1		-			anges change	s called as alternat	e base AND a	all other	called as alter	nate (variant) base	AND all other defining
gene anino_acid actual_nucleotide note gene anino_acid actual_nucleotide note actual_nucleotide note BabA* 21614C>T not lineage defining 100-T masking note - 733T>C - 733T>C BabA* 21801A>C 22206A>G not lineage defining not lineage defining 100-T msp5:12481 3828C>T nsp3:8370 K417N* 22813G>T not lineage defining not lineage defining 12864A>C nsp9:033G; not lineage defining - 1278C>T - 1278C>T K417N* 22033A>T - 12964A>G nsp9:033G; not lineage defining - 12865C>T - 1278C>T - 12865C>T -		voc	202012/02				١	/UI 202101/01		_		v	OC 202101/02	
L18F 21614C>T not lineage defining defining defining not included in definition due to masking not included in definition due to <th>gene</th> <th></th> <th></th> <th>note</th> <th></th> <th>gene</th> <th>amino_acid</th> <th>actual_nucleotide</th> <th>note</th> <th></th> <th>gene</th> <th>amino_acid</th> <th></th> <th>note</th>	gene			note		gene	amino_acid	actual_nucleotide	note		gene	amino_acid		note
S Gene R 246l 22299G>T not lineage defining not lineage defining not lineage		D80A*	21801A>C	0			-		definition due to masking		orf 1ab		2749C>T 3828C>T 5648A>C	nsp3:S370L nsp3:K977Q
def ining Integer defining Integer defining E484K* 23012G>A S Gene E484K 23012G>A T20N 21614C>T N501Y* 23063A>T off8 F120F 28253C>T T20N 2163C>T A701V* 23664C>T off8 F120F 28253C>T D138Y 21974G>T ORF1ab K1655N* 5230G>T nsp2785/ NGene A119S 28628G>T R190S 22132G>T Not present in entir K1655N* 5230G>T nsp3K837N MGene M234I 28975G>T S Gene K417T 22812A>C K3353R 10323A>G nsp5K90R - - 29754>T definition due to K417T 22812A>C S Grif 25094C>T - 29754>T definition due to masking K455Y 23625C>T E Gene P71L* 26456C>T - - 9754>T masking T1027I 24642C>T	S Gene	R246I	22299G>T	defining		orf 1ab	L3468V -	11824C>T	nsp6:I248I nsp9:G93G; not				12778C>T 13860C>T 17259G>T	nsp13:E341D
NS01Y* 23063A>T off8 F120F 28253C>T D138Y 21638C>T D138Y 21974G>T ORF1ab T265/ 1059C>T nsp2T85/ N Gene A119S 28628G>T S Gene P26S 21638C>T D138Y 21974G>T ORF1ab K1655N* 5230G>T nsp3K837N A119S 28628G>T not included in S Gene R190S 22132G>T Not present in entir ORF3a Q57H 25904C>T rsp3K837N A119S 28628G>T not included in S Gene S Gene P26S 21638C>T Not present in entir ORF3a Q57H 25904C>T - 29754>T definition due to masking S Gene P26S 21638C>T Not present in entir E Gene P71L* 26456C>T - 29754>T definition due to masking T1027I 24642C>T				defining		S Gene	E484K	23012G>A	lineage dei ining	-				
NR C00		N501Y*	23063A>T			orf 8	F120F	28253C>T		-		P26S	21638C>T	
ORF3a Q57H 25503G>T - 29754>T definition due to N501Y 23063A>T 5171L 25904C>T - 29754>T definition due to H655Y 23525C>T E Gene P71L* 26456C>T T1027I 24642C>T	ORF1ab	T265I K1655N*	1059C>T 5230G>T			N Gene					S Gene	<mark>R190S</mark> K417T	22132G>T 22812A>C	Not present in entire cl
E Gene P71L* 26456C>T T1027I 24642C>T		K3353R		nsp5K90F	2			20754~T						
	ORF3a						-	2373421						

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.

N Gene

T205I*

28887C>T

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		
	L1559F	4940C>T	nsp3:L741F		
orf 1ab	M3655I	11230G>T	nsp6:M86I		
difitab	L3667F	11266G>T	nsp6:L98F		
	M3752I	11521G>T	nsp6:M183I		
	R102I	21867G>T			
	F157L	22033C>A			
S Gene	V367F	22661G>T			
3 Gene	E484K	23012G>A			
	Q613H	23401G>T			
	P681R	23604C>G			
orf 8	L84S	28144T>C			
N Gene	E92K	28167G>A			
N Gene	S202N	28878G>A			

VOC 202102/02

gene	amino_acid	actual_nucleotid e	note
orf 1ab	L730F	2453C>T	nsp2:L550F
UITAD	-	7843C>T	nsp3:N1708N
S Gene	E484K	23012G>A	
M Gene	-	27092C>T	
N Gene	A173V	28791C>T	
N Gene	A398T	29465G>A	

VUI 202102/03 amino_acid actual_nucleotide gene note 1498C>T -1807A>G -2659G>A -T2007I 6285C>T 8593T>C orf 1ab -9565C>T 3675_7del 11288_96del nsp6:106_8del 144407C>T P4715S nsp12:P323S 18171C>T -20724A>G Q52R 21717A>G A67V 21762C>T 21765_70del 69_70del 144del 21991_3del S Gene E484K 23012G>A Q677H 23593G>C F888L 24224T>C 24748C>T . E Gene L21F 26305C>T M Gene 182T 26767T>C orf 6 2del 27205_7del 2_3del 28278_80del N Gene 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 25/02/2021

	Confirmed	Probable	HR-LQG
VUI 202102/04 B.1.318	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.

VUI202102/04

V0/202102/04					
Gene	Amino Acid	Nucleotide	Note		
	E378V	3852A>T	nsp3:E378V		
	-	3961C>T			
	K2511N	7798G>T	nsp3K1693N		
- ufd - h	T2936I	9072C>T	nsp4:T173I		
orf1ab	A3209V	9891C>T	nsp4:A446V		
	T3284I	10116C>T	nsp5:T21I		
	3675_7del	11288_96del	nsp6:106_8del		
	V6672M	20578G>A	nsp15:V320M		
	T95I	21846C>T			
	144del	21991_3del			
	E484K	23012G>A			
S	-	23287T>C			
3	P681H	23604C>A			
	D796H	23948G>C			
	-	24382C>T			
	-	25276C>A			
М	I82T	26767T>C			
orf8	1_3del	27894_901del			
0118	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.

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)

N.B. High rish LQG definition to be discussed

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