SUPPLEMENTARY TABLE 1. SARS-CoV-2 Variant Classifications and Definitions*

Classification	Definition	Possible Attributes	Potential Public Health Actions
Variant of Interest (VOI)	A SARS-CoV-2 variant with specific genetic markers that have been associated with changes to receptor binding, reduced neutralization by antibodies generated against previous infection or vaccination, reduced efficacy of treatments, potential diagnostic impact, or predicted increase in transmissibility or disease severity.	• Specific genetic markers that are predicted to affect transmission, diagnostics, therapeutics, or immune escape • Evidence that it is the cause of an increased proportion of cases or unique outbreak clusters • Limited prevalence or expansion in the US or in other countries	• Enhanced sequence surveillance • Enhanced laboratory characterization, or epidemiological investigations to assess how easily the virus spreads to others, the severity of disease, the efficacy of therapeutics and whether currently authorized vaccines offer protection
Variant of Concern (VOC)	A SARS-CoV-2 variant for which there is evidence of an increase in transmissibility, more severe disease (e.g., increased hospitalizations or deaths), significant reduction in neutralization by antibodies generated during previous infection or vaccination, reduced effectiveness of treatments or vaccines, or diagnostic detection failures.	In addition to the above possible attributes of a VOI: • Evidence of impact on diagnostics, treatments, or vaccines • Widespread interference with diagnostic test targets • Evidence of substantially decreased susceptibility to one or more class of therapies • Evidence of significant decreased neutralization by antibodies generated during previous infection or vaccination • Evidence of reduced vaccine-induced protection from severe disease • Evidence of increased transmissibility • Evidence of increased disease severity	• Notification to WHO under the International Health Regulations • Reporting to CDC • Local or regional efforts to control spread, • Increased testing • Research to determine the effectiveness of vaccines and treatments against the variant • Based on the characteristics of the variant, additional considerations may include the development of new diagnostics or the modification of vaccines or treatments
Variant of High Consequence (VOHC)	A variant of high consequence has clear evidence that prevention measures or medical countermeasures have	In addition to the above possible attributes of a VOI or VOC:	• Notification to WHO under the International Health Regulations, reporting to CDC

	significantly reduced effectiveness relative to previously circulating variants.	- Impact on medical countermeasures - Demonstrated failure of diagnostics - Evidence to suggest a significant reduction in vaccine effectiveness, a disproportionately high number of vaccine breakthrough cases, or very low vaccine-induced protection against severe disease - Significantly reduced susceptibility to multiple Emergency Use Authorization (EUA) or approved therapeutics - More severe clinical disease and increased hospitalizations	- Announcement of strategies to prevent or contain transmission - Recommendations to update treatments and vaccines

*Further information on this variant classification scheme can be found at https://www.cdc.gov/coronavirus/2019-ncov/cases-updates/variant-surveillance/variant-info.html

SUPPLEMENTARY TABLE 2. Number of SARS-CoV-2 sequences and unweighted proportions of B.1.1.7 and P.1 by United States jurisdiction, with corresponding weighted regional estimates and 95% Confidence Intervals for the United States and by U.S. Health and Human Services (HHS) Region*, for the 2-week period ending April 24, 2021

U.S. HHS Region	U.S. Jurisdiction	Total positive SARS-CoV-2 RT-PCR test results reported to CDC, n	SARS-CoV-2 sequences reported to or generated by CDC, n[†]	% of reported SARS-CoV-2 RT-PCR tests with a sequence available[†]	Unweighted % of sequences classified as variant		Weighted[§] % of all estimated SARS-CoV-2 infections attributable to variant (95% CI)	
					B.1.1.7	P.1	B.1.1.7	P.1
Region	All Jurisdictions	807,024	25,000	3.1	62.7	6.5	66.0 (62.0–69.8)	5.0 (3.3–7.5)
1	Connecticut	12,164	519	4.3	57.0	1.5	50.9 (43.4–58.3)	6.5 (2.0–19.0)
	Massachusetts	21,129	3,165	15.0	50.9	11.5		
	Maine	3,880	119	3.1	32.8	2.5		
	New Hampshire	3,475	339	9.8	43.1	4.7		
	Rhode Island	3,795	436	11.5	45.0	5.7		
	Vermont	1,789	179	10.0	72.6	0.6		
2	New Jersey	46,298	1,046	2.3	49.2	2.6	54.5 (36.6–71.4)	3.1 (1.4–6.5)
	New York	79,347	626	0.8	52.9	3.4		
	Puerto Rico	10,329	119	1.2	71.4	1.7		
	Virgin Islands	41	0	0.0	0.0	0.0		
3	District of Columbia	1,864	56	3.0	66.1	0.0	66.5 (61.0–71.6)	1.6 (0.7–3.3)
	Delaware	4,655	56	1.2	69.6	0.0		
	Maryland	27,880	446	1.6	69.3	0.4		
	Pennsylvania	51,001	1,539	3.0	62.6	1.8		
	Virginia	15,523	410	2.6	71.2	2.7		
	West Virginia	5,421	257	4.7	62.6	0.0		
4	Alabama	4,665	48	1.0	79.2	2.1	70.5 (64.8–75.5)	4.9 (2.5–9.6)
	Florida	91,476	3,164	3.5	68.7	8.1		
	Georgia	11,416	460	4.0	81.3	3.0		
	Kentucky	5,753	156	2.7	73.7	3.2		
	Mississippi	874	26	3.0	69.2	0.0		
	North Carolina	23,555	816	3.5	61.6	1.7		
	South Carolina	9,419	84	0.9	57.1	3.6		
	Tennessee	11,477	309	2.7	80.3	3.2		
5	Illinois	36,934	1,438	3.9	59.3	22.5	73.1 (59.7–83.3)	7.7 (1.6–30.8)
	Indiana	13,184	540	4.1	69.4	9.3		
	Michigan	64,126	1,878	2.9	80.8	2.2		
	Minnesota	36,092	545	1.5	76.9	1.3		
	Ohio	19,709	407	2.1	75.4	3.2		
	Wisconsin	10,848	278	2.6	65.1	5.4		
6	Arkansas	1,242	38	3.1	52.6	21.1	74.1 (70.6–77.2)	4.6 (3.3–6.2)
	Louisiana	4,132	99	2.4	69.7	7.1		
	New Mexico	1,600	98	6.1	67.3	0.0		
	Oklahoma	2,445	39	1.6	82.1	0.0		
	Texas	42,282	1,031	2.4	74.6	4.9		
7	Iowa	5,427	42	0.8	64.3	9.5	72.4 (59.7–82.3)	7.0 (1.3–29.4)
	Kansas	2,933	69	2.4	63.8	13.0		
	Missouri	7,484	128	1.7	75.0	3.9		
	Nebraska	4,063	40	1.0	77.5	2.5		
8	Colorado	19,239	646	3.4	61.9	4.6	56.8 (45.9–67.0)	3.8 (1.9–7.5)

	Montana	1,557	18	1.2	55.6	5.6		
	North Dakota	1,063	13	1.2	23.1	0.0		
	South Dakota	1,949	16	0.8	68.8	6.3		
	Utah	4,512	63	1.4	50.8	0.0		
	Wyoming	600	19	3.2	57.9	0.0		
9	Arizona	10,076	179	1.8	63.7	5.0	57.7 (48.9–66.0)	6.9 (3.6–12.9)
	California	32,892	2,429	7.4	53.1	8.7		
	Guam	63	64	101.6	100.0	0.0		
	Hawaii	1,218	10	0.8	40.0	0.0		
	Marshall Islands	0	0	0.0	0.0	0.0		
	Northern Mariana Islands	0	0	0.0	0.0	0.0		
	Nevada	4,812	143	3.0	59.4	2.8		
10	Alaska	2,718	5	0.2	20.0	0.0	52.3 (38.5–65.8)	5.0 (2.7–8.9)
	Idaho	2,119	24	1.1	45.8	0.0		
	Oregon	8,966	190	2.1	41.6	4.2		
	Washington	15,513	136	0.9	55.9	7.4		

Abbreviations: CI = Confidence Interval; HHS = Health and Human Services.

*https://www.hhs.gov/about/agencies/iea/regional-offices/index.html

[†] Sequences reflect those generated by or reported to CDC through NS3 and contract labs, and do not include the >5000 sequences a week produced by public health laboratories and other U.S. institutions, which are not integrated into CDC's genomic surveillance currently (https://covid.cdc.gov/covid-data-tracker/#published-covid-sequences).

[§]Weights for generating regional and national estimates are calculated for 1-week intervals