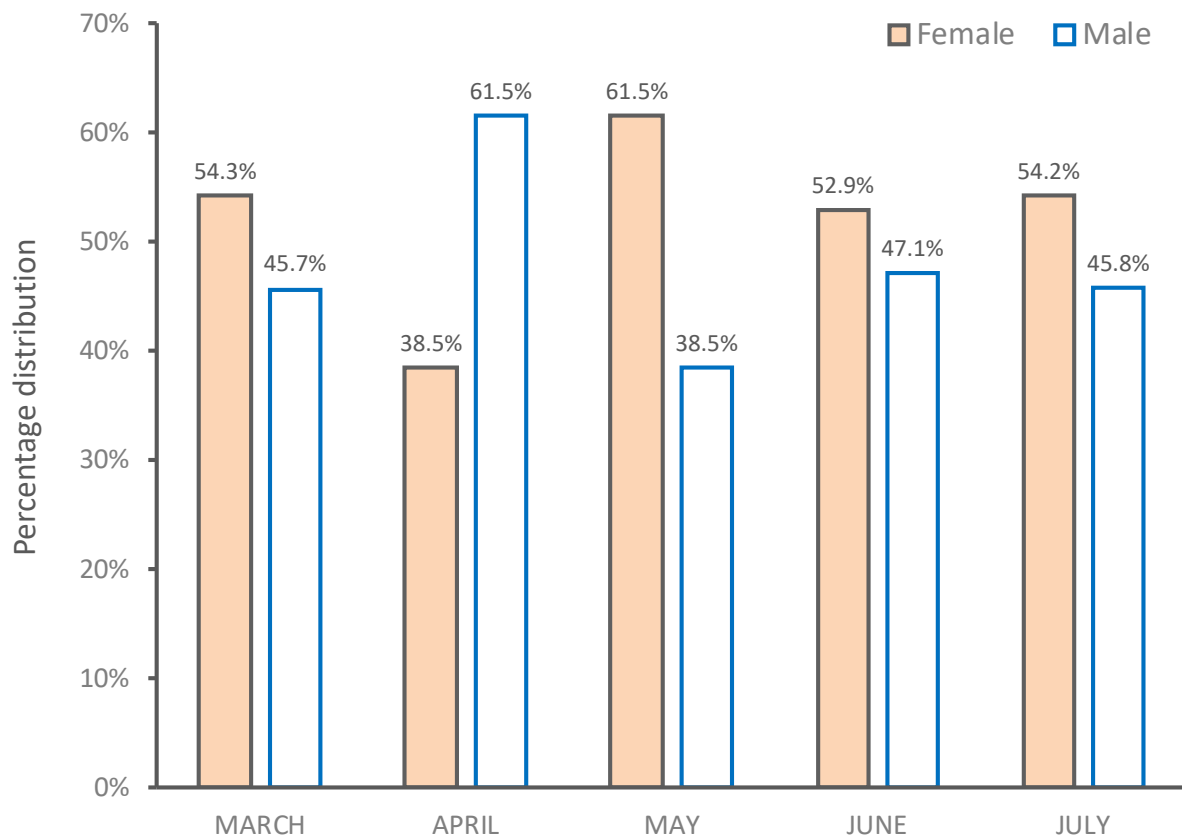


Supplementary Material S1

<b>Supplementary material 1. List of mutations related to the particular variants that can be identified by using 14 different TaqMan SARS-CoV-2 mutation panel assays</b>							
<b>Country of Origin</b>	<b>Variants</b>	<b>Presence of Mutation</b>					
South Africa	B.1.351/ (Beta)	E484K	D614G	A701V	N501Y	L242_244L	K417N
UK	B.1.1.7 //(Alpha)	E484K*	D614G	delH69V70	Q27stop		N501Y
India	B.1.617.1/ (Kappa)	E484Q	D614G	L452R	P681R		
India	B.1.617.2/ (Delta)	T478K	D614G	L452R	P681R		
India	B.1.617.3	E484Q		L452R	P681R		
India	B.1.617.2 / (Delta plus)	T478K	D614G	L452R	P681R		K417N
UK/ Nigeria	B.1.525/ (Eta)	E484K	D614G	delH69V70			
Japan/ Brazil	P.1/B.1.1.28/ (Gamma)	E484K	D614G	K417T	N501Y	T20N	
US-CA	B.1.427/ B.1.429/ (Epsilon)	L452R	D614G				
US-NY	B.1.526 / (Iota)	E484K*	D614G	A701V*	L452R*		

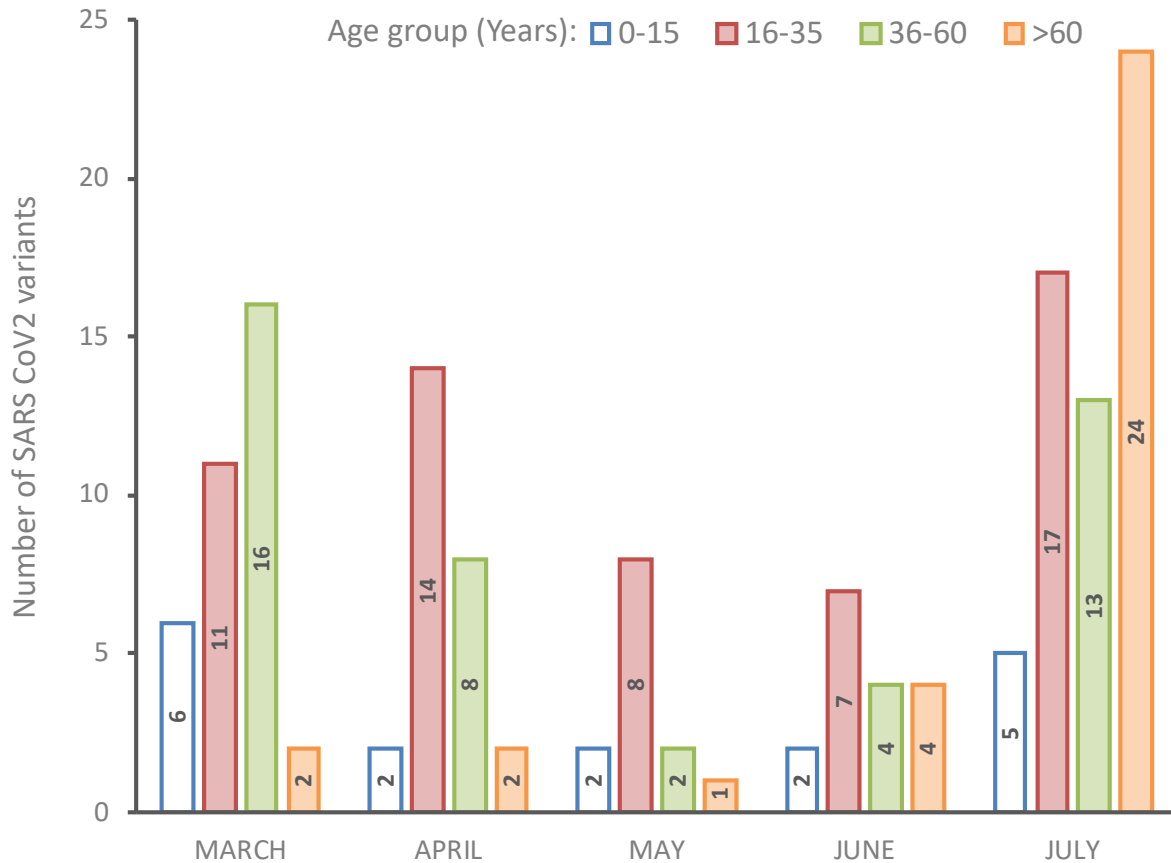
\* Present in some strains

## Supplementary Material S2



Supplementary material S2. Distribution of SARS CoV2 variants between male and female  
SARS-CoV-2 variants were 72 (48%) from male and 78 (52%) from female. Male were 45.7%, 61.5%, 38.5%, 47.1% and 45.8% from March to July, respectively. Female were 54.3%, 38.5%, 61.5%, 52.9% and 54.2% from March to July, respectively. There was no significant difference between SARS-CoV-2 variants cases from male and female in March to July.

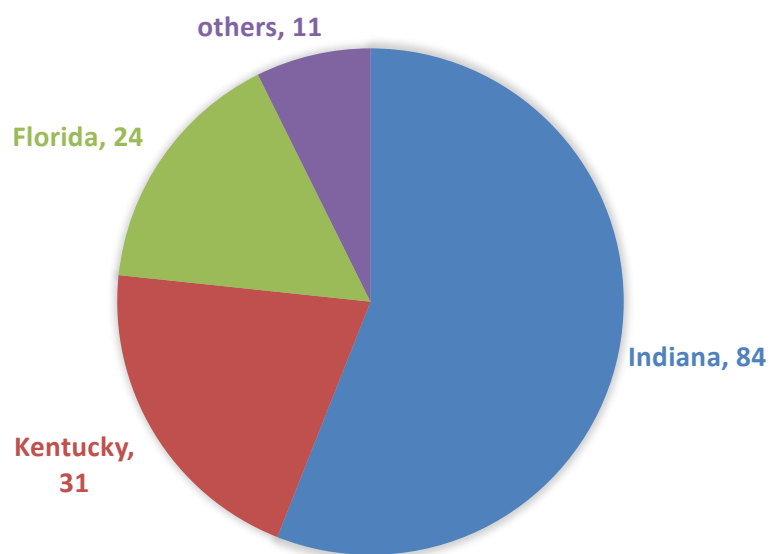
### Supplementary Material S3



#### Supplementary material S3. Age-wise distribution of SARS CoV2 variants.

The number of SARS-CoV-2 variants was significantly higher in 16-35 age group than 0-15 and >60 ( $p < 0.05$ ) but no significant difference with age group 36-60. Cases of SARS-CoV-2 variants are significantly lower in age group 0-15 than other all age groups. The number of SARS-CoV-2 variants was significantly higher with 6 (35.3%) in March than other month having 2 (11.8%) in age group 0-15 ( $p < 0.05$ ). From age group 16-35, SARS-CoV-2 variants cases were significantly higher with 17(29.8%) in July than June with 7(12.2%) ( $p < 0.05$ ). Among age group 36-60, SARS-CoV-2 variants cases were significantly higher in March with 16 (37.2%) than in May with 2 (4.6%) and from age group > 60 years, significantly higher in July with 24 (72.7%) than all other months ( $p < 0.05$ ).

Supplementary Material S4



Supplementary material S4. Frequency of SARS CoV2 variants based on locations. Among total SARS-CoV-2 variants identified, 84 (56%) were from Indiana, 31 (20.7%) from Kentucky, 24 (16%) from Florida and 11(7.3%) from other states.

Supplementary Material S5

<b>Supplementary material S5. Concordance of genotyping with sequencing</b>			
<b>Mutation present</b>			
<b>Sample</b>	<b>Genotypic analysis</b>	<b>Sequencing result</b>	<b>Strain type</b>
1	L452R, D614G	L452R, D614G	B.1.526 (Iota)
2	D614G, L452R, P681R, T478K	D614G, L452R, P681R, T478K	B.1.617.2 (Delta)
3	D614G, L452R, P681R, T478K	D614G, L452R, P681R, T478K	B.1.617.2 (Delta)
4	D614G, N501Y, delH69V70, Q27stop	D614G, N501Y, delH69V70, Q27stop	B.1.1.7 (Alpha)
5	L452R, D614G	L452R, D614G	B.1.526 (Iota)
6	D614G, L452R, P681R, T478K	D614G, L452R, P681R, T478K	B.1.617.2 (Delta)
7	D614G, L452R, P681R, T478K	D614G, L452R, P681R, T478K	B.1.617.2 (Delta)
8	D614G, L452R, P681R, T478K	D614G, L452R, P681R, T478K	B.1.617.2 (Delta)
9	D614G, N501Y, delH69V70, Q27stop	D614G, N501Y, delH69V70, Q27stop	B.1.1.7 (Alpha)

Supplementary material S5. Genotyping result has similar mutations that were detected by sequencing data. The genotypic analysis revealed B.1.617.2 (Delta), B.1.1.7 (Alpha) and B.1.526 (Iota) variants based on the mutation allele present in the spike proteins, and is concordant with the variants identified by the sequencing.