

Supplementary Table 3: Inter-Sequencing run precision: Variant identification concordance across three different library preparation and sequencing runs.

Accession	ACSQ-2 (Rep-1)				ACSQ-3 (Rep-2)				ACSQ-4 (Rep-3)				Concordance
	Median Coverage-R1	Coverage >= 30x-R1	Pango Lineage	WHO label	Median Coverage-R2	Coverage >= 30xR-2	Pango Lineage	WHO label	Median Coverage-3	Coverage >= 30x-R3	Pango Lineage	WHO label	
ACSQ1-3	345	86.06%	AY.3	Delta (B.1.617.2-like)	120	80.09%	AY.3	Delta (B.1.617.2-like)	149	84.77%	AY.82	Delta (B.1.617.2-like)	YES
ACSQ1-7	2289	99.78%	AY.25	Delta (B.1.617.2-like)	364	99.33%	AY.25	Delta (B.1.617.2-like)	444	98.70%	AY.25	Delta (B.1.617.2-like)	YES
ACSQ1-2	797	99.01%	AY.3	Delta (B.1.617.2-like)	338	98.92%	AY.3	Delta (B.1.617.2-like)	418	98.34%	AY.3	Delta (B.1.617.2-like)	YES
ACSQ2-14	547	92.60%	AY.3	Delta (B.1.617.2-like)	226	92.85%	AY.3	Delta (B.1.617.2-like)	241	94.21%	AY.3	Delta (B.1.617.2-like)	YES
ACSQ2-20	757	99.59%	AY.39.1	Delta (B.1.617.2-like)	310	99.39%	AY.39.1	Delta (B.1.617.2-like)	383	99.01%	AY.39.1	Delta (B.1.617.2-like)	YES
ACSQ2-17	633	95.39%	AY.103	Delta (B.1.617.2-like)	265	95.65%	AY.103	Delta (B.1.617.2-like)	298	97.21%	AY.103	Delta (B.1.617.2-like)	YES
ACSQ4-1	1286	98.32%	B.1.1.529	Omicron (B.1.1.529-like)	1363	99.15%	B.1.1.529	Omicron (B.1.1.529-like)	1209	97.54%	B.1.1.529	Omicron (B.1.1.529-like)	YES
ACSQ4-85	1131	96.64%	B.1.1.529	Omicron (B.1.1.529-like)	1201	97.10%	B.1.1.529	Omicron (B.1.1.529-like)	1308	96.61%	B.1.1.529	Omicron (B.1.1.529-like)	YES
ACSQ4-2	867	92.42%	B.1.1.529	Omicron (B.1.1.529-like)	1130	94.96%	B.1.1.529	Omicron (B.1.1.529-like)	900	95.46%	B.1.1.529	Omicron (B.1.1.529-like)	YES