

Table S3. Grouping of Omicron sub-variants based on the mutations, key features, and percentage of mutations in the RBD.

Group Number	Sub-variant(s)	Key Features	Percentage of Mutations Carried
1	BA.4, BA.4.1.10, BA.4.6, BA.4.7, BA.5, BA.5.1.18, BA.5.1.20, BA.5.2, BA.5.2.13, BA.5.3, BA.5.6, BA.5.6.2, BA.5.9, BF.11, BF.13, BM.1	Mutations shared with other variants.	100%
2	BM.1.1, BM.1.1.1, BM.4.1, BY.1, CA.1	Similar to group 3; distinctive mutation V483S.	89.3%
-	BM.2	Similar to group 2 and 3; distinctive mutation V483X.	89.3%
3	BA.2.75.8, BA.2.3.20, BR.1	Similar to group 2; distinctive mutation V483F.	89.3%
-	BR.2	Similar to group 2 and 3; distinctive mutation V483I.	89.3%
4	BU.1, BW.1	Shows mostly unique mutations when compared to other variants.	96.4%
5	BA.2.75, BA.2.75.3	Similar to BA.75.1 and BA.75.2; distinctive mutation N440K.	57.1%
-	BA.2.75.1	Similar to group 5 and BA.275.2; distinctive mutation K417N.	57.1%

-	BA.2.75.2	Similar to group 5 and BA.2.75.1.	57.1%
6	BN.1, BA.2.10	Similar to BQ.1; distinctive mutation V483F.	89.3%
-	BQ.1	Similar to group 6; distinctive site V483.	85.7%
7	XBB, BJ.1	Shows mostly unique mutations when compared to other variants.	100%
-	BA.2.10.4	Shows many unique mutations when compared to other variants.	85.7%
-	BA.2.12.1	Similar to variants BA.2.75.4 and BA.2.75.7; distinctive sites G446, L452Q, N460, F486 and Q493R.	57.1%
-	BA.2.75.4	Similar to variants BA.2.12.1 and BA.2.75.7; distinctive sites G446S, L452R, N460K, F486 and Q493.	60.7%
-	BA.2.75.5	Mutations shared with other variants.	42.9%
-	BA.2.75.6	Similar to BL.1; distinctive sites G446 and N460K.	53.6%

-	BA.2.75.7	Similar to variants BA.2.75.4 and BA.2.12.1; distinctive sites G446S, L452, N460K, F486S and Q493.	60.7%
-	BF.7	Similar to BQ.1.1; distinctive mutationsK444T and N460K.	71.4%