

Table S2. Grouping of Omicron sub-variants based on the mutations, key features, and percentage of mutations in the N-terminal domain.

| Group Number | Sub-variant(s) | Key Features | Percentage of Mutations Carried |
|--------------|---|---|---------------------------------|
| 1 | BQ.1.1, BA.2, BA.2.12.1 | Similar to groups 2 and 3; distinctive sites show no mutations: K147, W152, F157, I210. | 11.5% |
| 2 | BA.2.75.1, BA.2.75.5 | Similar to groups 1 and 3; distinctive sites are G142, and G257X. | 26.9% |
| 3 | BL.1, BA.2.75.3, BA.2.75.4, BA.2.75.6, BA.2.75.7 | Similar to groups 1 and 2. | 30.8% |
| 4 | BM.1, BA.4, BA.4.1.10, BA.4.6, BA.4.7, BA.5, 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 | Distinctive mutation from BA.5.1.18 is T19I. | 100% |
| - | BA.5.1.18 | Similar to group 4; distinctive mutation T19X. | 100% |
| 5 | BU.1, BW.1 | Shares residues 19-143 and 213 with groups 6, 7 and 8. | 100% |
| 6 | BM.1.1, BM.4.1, BR.2 | Similar to groups 7 and 8; distinctive mutations T19I and Y144E. | 96.2% |
| - | BA.2.75.8 | Similar to group 6; distinctive mutation T19X. | 96.2% |

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| 7 | BR.1, CA.1, BM.2, BN.1 | Similar to groups 6 and 8; distinctive mutation Y144X. | 96.2% |
| - | BM.1.1.1 | Similar to group 7; distinctive mutation Y144G. | 96.2% |
| 8 | BQ.1, BA.2.3.20, BA.2.10 | Similar to groups 6 and 7; distinctive mutation Y144K. | 96.2% |
| 9 | BJ.1, XBB | Share the same mutations in positions 19-95. | 92.3% |
| - | BS.1 | | 100% |
| - | BA.2.10.4 | | 100% |
| - | BA.1 | Only two mutations A67V, and T95I. | 7.7% |
| - | BA.1.1 | Unique mutations H69L, and L212I. | 30.7% |
| - | BA.2.75 | Unique mutations H69L, V70I, G142X, V143X, and L212I. | 34.6% |
| - | BA.2.75.2 | Mutations shared with other variants. | 15.4% |
| - | BF.7 | Mutations shared with other variants. | 7.7% |

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| - | BM.4.1.1 | Mutations shared with other variants. | 26.9% |
| - | BY.1 | Mutations shared with other variants. | 92.3% |