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Supplemental information

Longitudinal study across SARS-CoV-2 variants

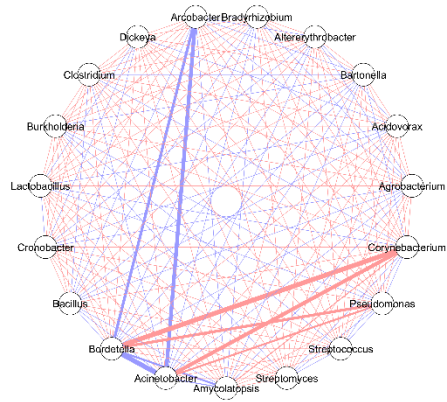
identifies transcriptionally active microbes

(TAMs) associated with Delta severity

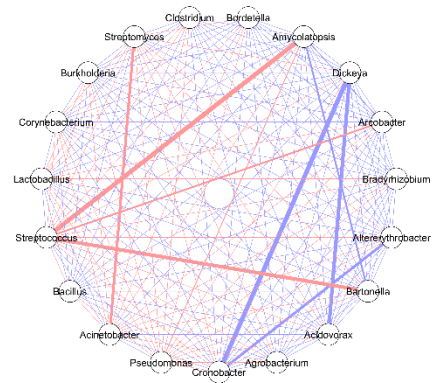
Priti Devi, Pallawi Kumari, Aanchal Yadav, Bansidhar Tarai, Sandeep Budhiraja, Uzma Shamim, and Rajesh Pandey

Supplementary Figure S1

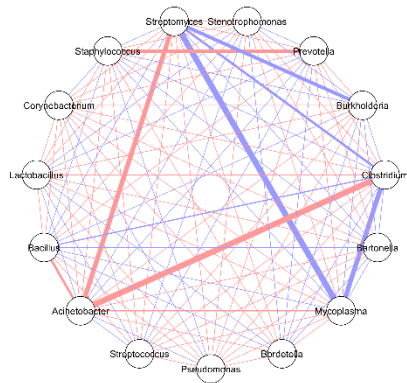
(i)



(ii)



(iii)



(iv)

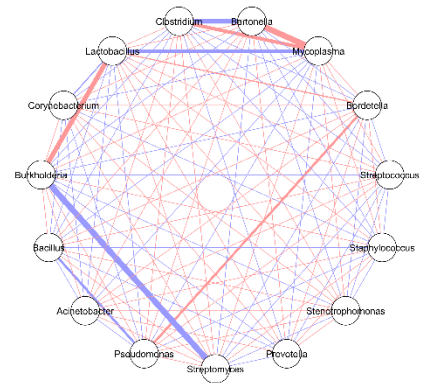


Figure S1: Visualization of co-occurrence network based on spearman correlation analysis between the different genera across different groups. Related to Figure 2. Specific interactions between the different genera of i) Pre-VOC, ii) VOCs, iii) Delta, iv) Omicron wherein the edges represent the strength of correlation and their colours shows positive and negative as blue and red, respectively.

Supplementary Figure S2

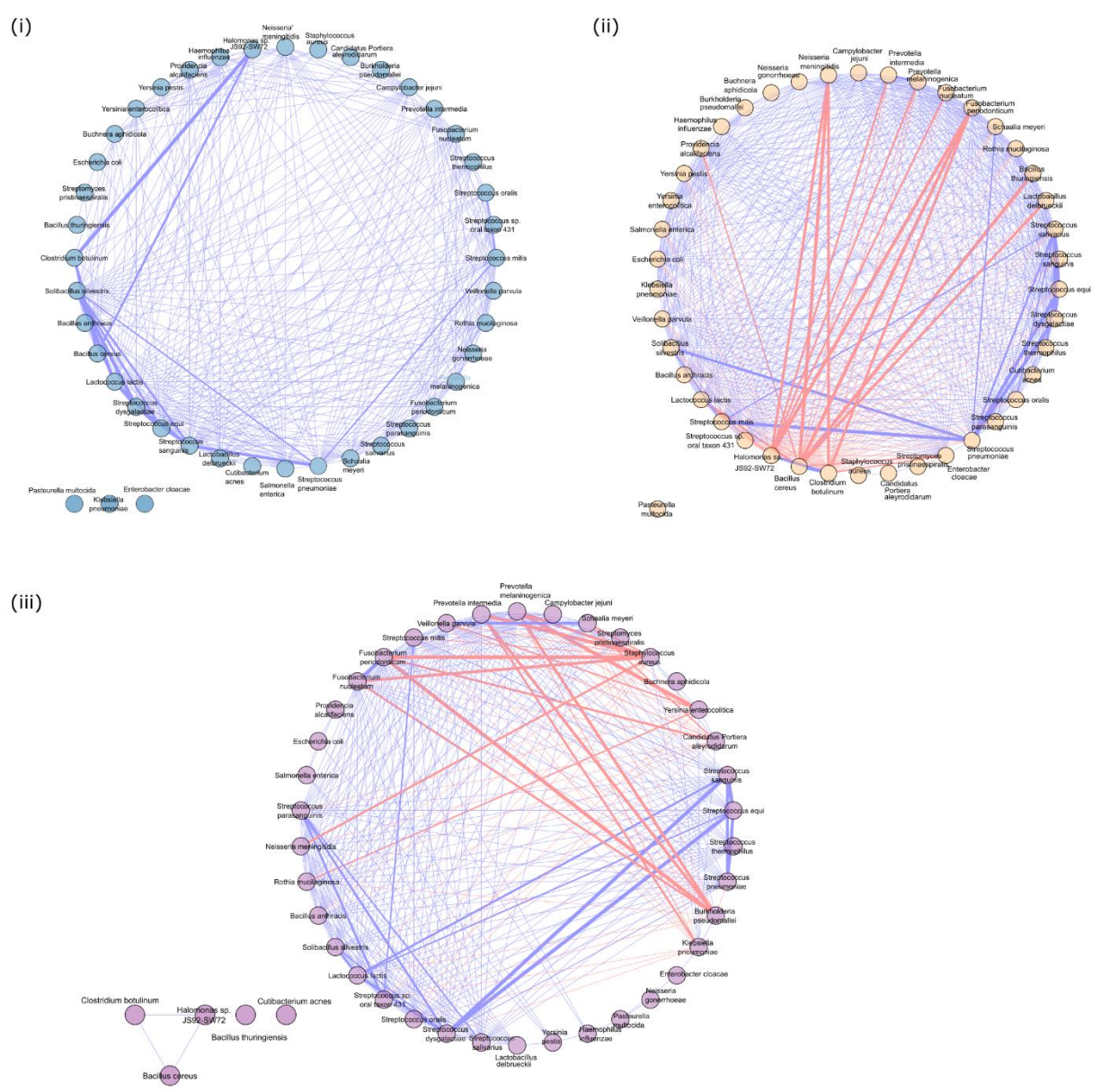


Figure S2: Visualization of co-occurrence network based on spearman correlation analysis between the core bacterial species across different groups shows significant ($p < 0.05$, $r > \pm 0.6$) specific interaction. Related to Figure 3A. i) Pre-VOC, ii) Delta, iii) Omicron wherein the edges represent the strength of correlation and their colors shows positive and negative as blue and red, respectively.

Supplementary Figure S3

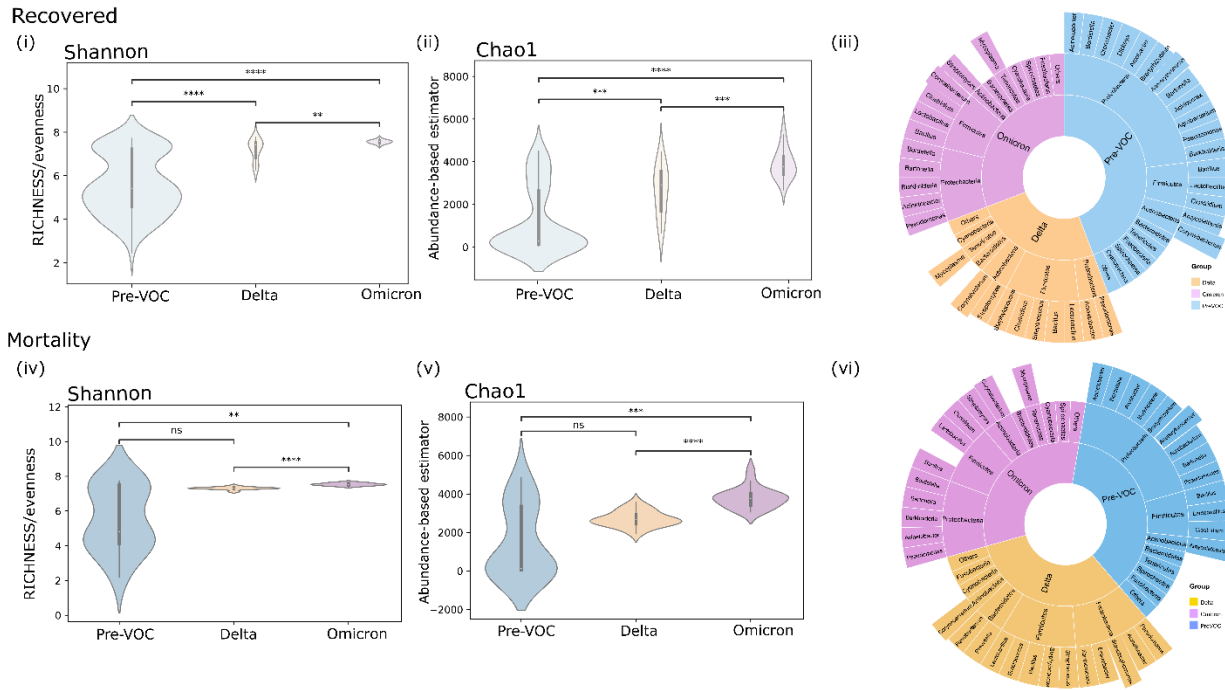


Figure S3: Figure illustrating the alpha diversity and abundance profile of phyla and genera for recovered and mortality sub-groups of Pre-VOC, Delta and Omicron. Related to Figure 5: i) Shannon (Richness), (ii) Chao-1 (Abundance-based estimator) with *p-values* calculated by the Kruskal Wallis test, (iii) Visualization of percent relative abundance proportion of phyla and genera identified in recovered subgroup: iv) Shannon (Richness), (v) Chao-1 (Abundance-based estimator) with *p-values* calculated by the Kruskal Wallis test, (vi) Visualization of percent relative abundance proportion of phyla and genera identified in mortality subgroup of Pre-VOC, Delta and Omicron.