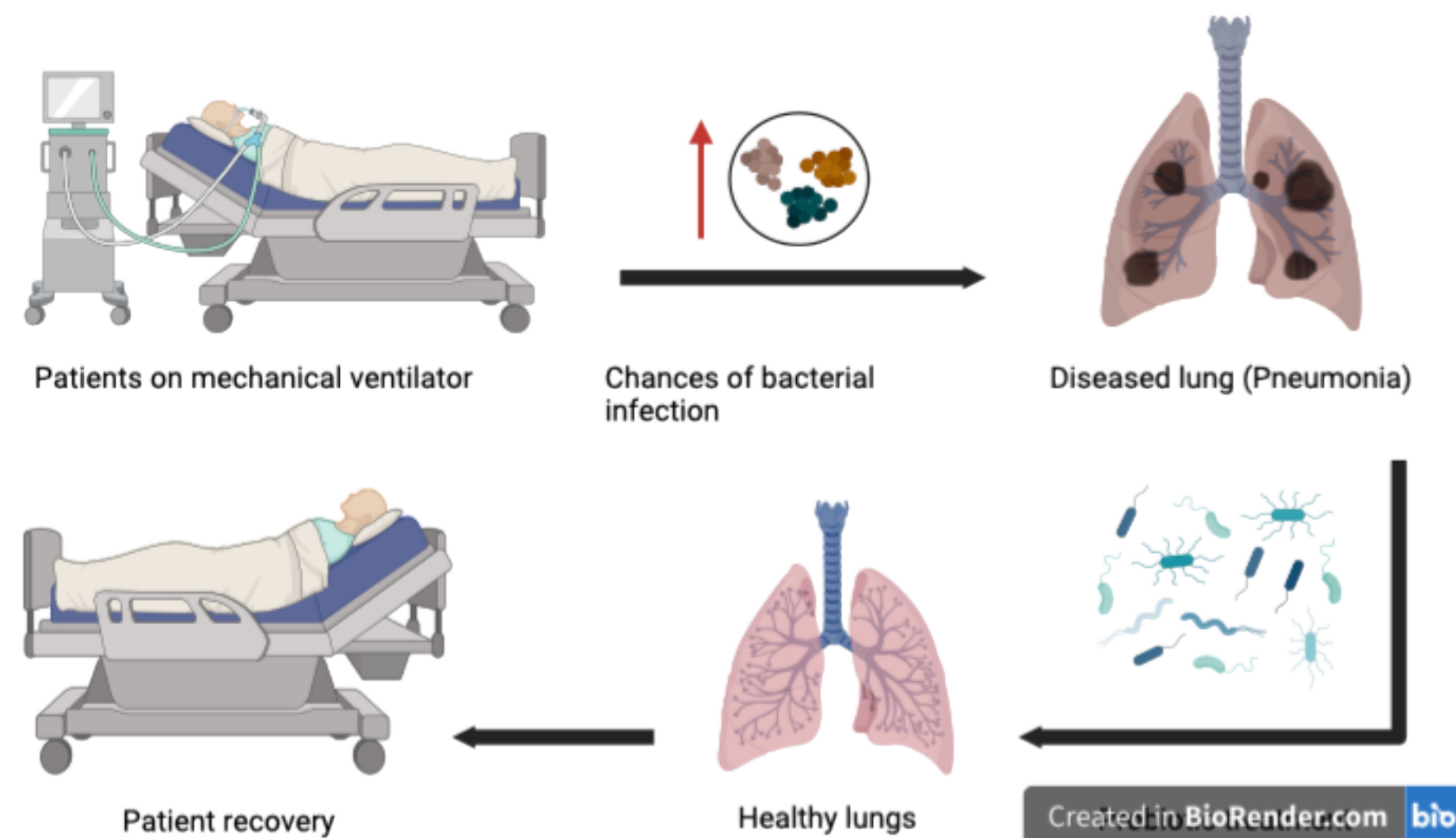


Probiotics in the clinical course in patients with critical care illness to modulate gut microbiota composition



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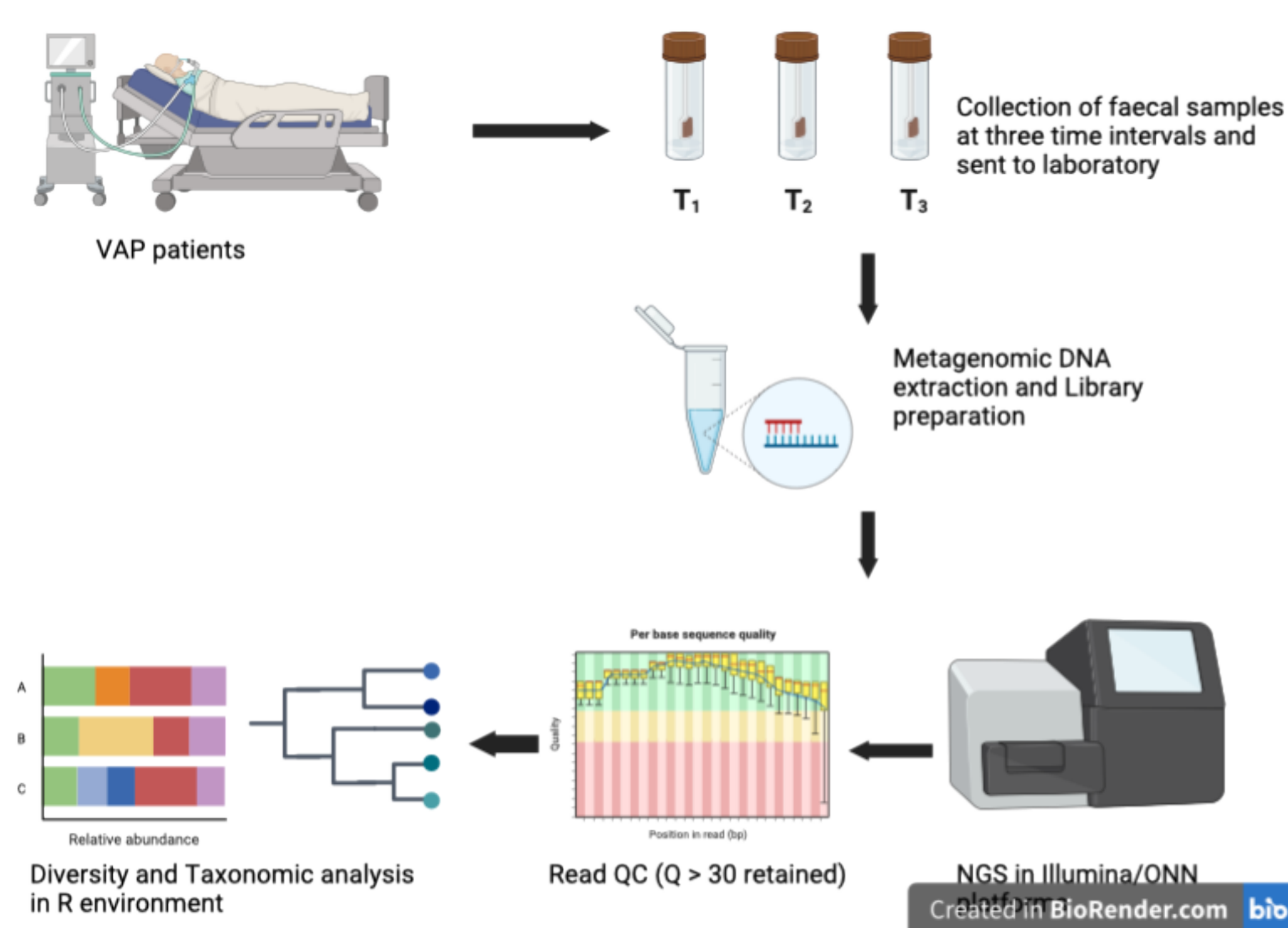
INTRODUCTION



Ventilator-Associated Pneumonia (VAP) is a nosocomial infection that affects patients who rely on mechanical ventilation, which increases patient morbidity and mortality and increases overall treatment cost. Through this prospective observational study we aim to investigate the effects of probiotics VAP and its relationship with clinical outcomes in mechanically ventilated patients.

METHODS

- Cohort Size (n) = 169, Included = 86, Excluded = 83
- VSL#3®: 112.5 billion CFU/cap
- Dose of 6 capsule/day
- Subject completed the study ; 22 (probiotics treated) and 13 (control)
- Faecal samples were collected at three intervals



- Sequence done in Illumina MiSeq and Oxford nanopore platform
- Sequence QC by FastQ
- Taxonomy assigned using SILVA138.1 and Kraken2
- Diversity analysis in vegan and phyloseq packages

RESULTS and DISCUSSION

Highlights

- Differences in alpha diversity of gut microbiota between probiotic-treated and non-treated groups were not statistically significant
- Longitudinal analysis of commensal and pathogenic taxa at three different time-points revealed no significant differences in abundance among taxa in first two time-points
- Significant increase of *Streptococcus* observed in probiotic treated group at T₃ (p=0.03)
- At species level analysis, *Lactobacillus paracasei* and *Streptococcus thermophilus* (contained in VSL#3®) were significantly higher in probiotic-treated group
- *L. paracasei* was higher overall in probiotic group, whereas sequential increase of *S. thermophilus* with

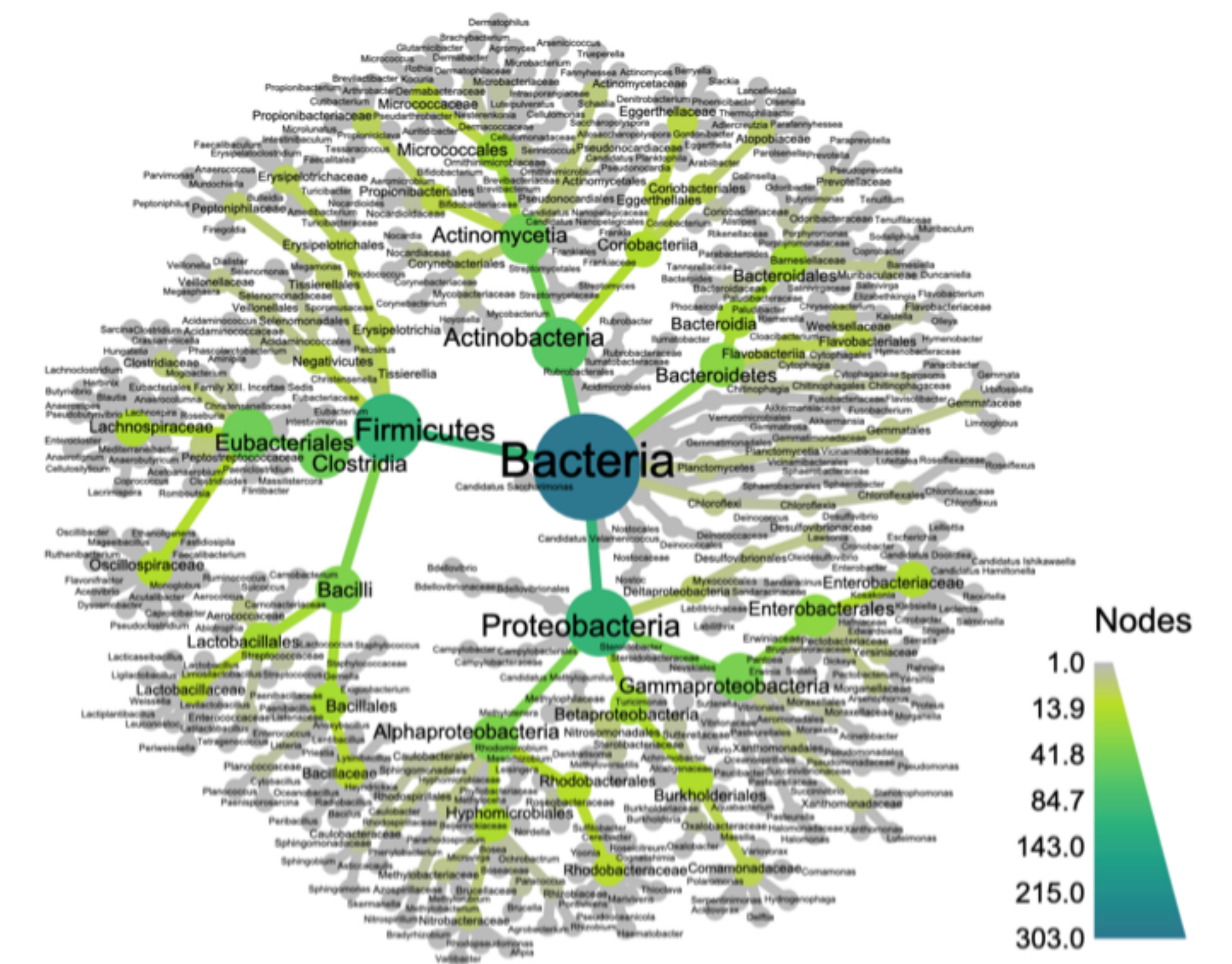


Figure 1 Taxa tree depicting the organization of identified taxa from phylum through genus level for nanopore reads. On the lower right-hand side is the color scale, the color intensity of the nodes represents the abundances of taxa.

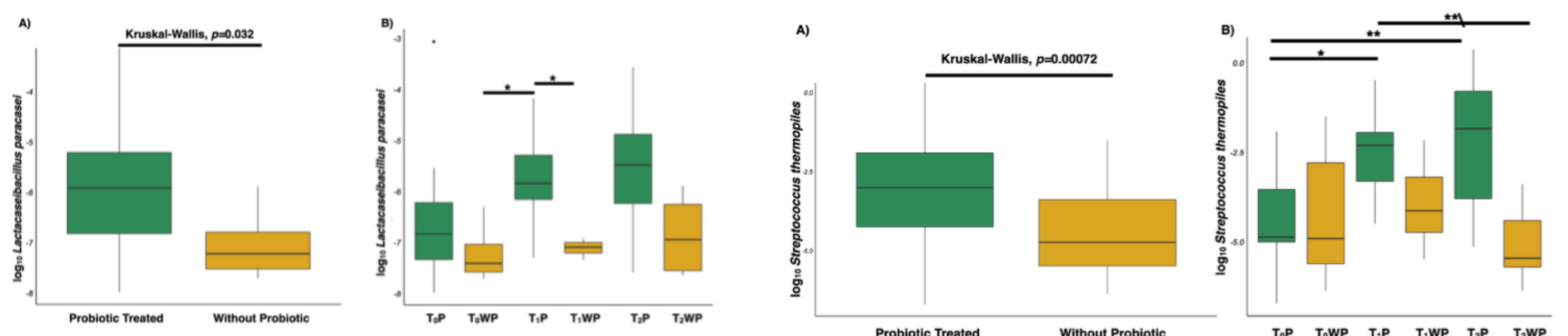


Figure 2: Probiotic treated group shows a significant increase in *Lactobacillus paracasei* at all three timepoints, demonstrating a clear contrast to the unchanging levels in the control group (*<0.01).

Figure 3: Probiotic treated group shows a significant increase in *Streptococcus thermophilus* at all three timepoints, demonstrating a clear contrast to the unchanging levels in the control group(*<0.05, **<0.01).

CONCLUSIONS

- Elevated abundance of *Lactobacillus paracasei* and *Streptococcus thermophilus* (contained in VSL#3®) observed in the probiotic-treated group
- Higher overall abundance of *L. paracasei* in the probiotic group
- Sequential increase of *S. thermophilus* with progression of probiotic dose
- Results suggest probiotic treatment may result in favorable alterations in gut microbiome composition
- No significant benefit observed in decreasing incidence of ventilator acquired pneumonia, reducing length of hospital stay.
- Further investigation into optimal dosages and frequencies of probiotics required to enhance clinical outcomes

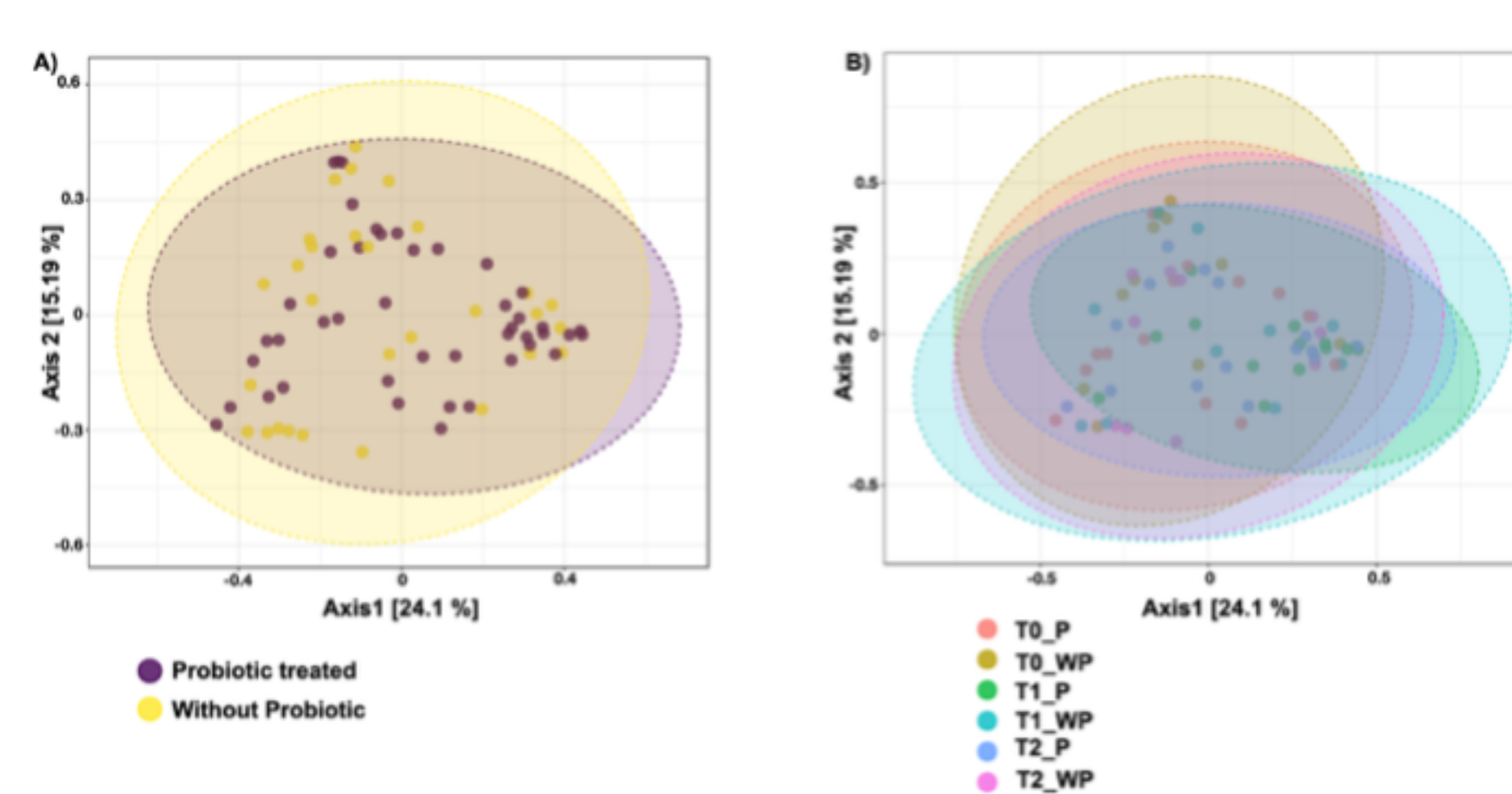


Figure 4: Principal coordinate analysis plot (PcoA) of the gut microbiome. Each dot represents a particular sample, which is color coded based on the time points. A) Between probiotic treated and without probiotic B) Between the time-points of probiotic treatment .

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