**SUPPLEMENTAL MATERIALS**

**Differences in the microbial composition of hemodialysis patients treated with and without β-blockers**

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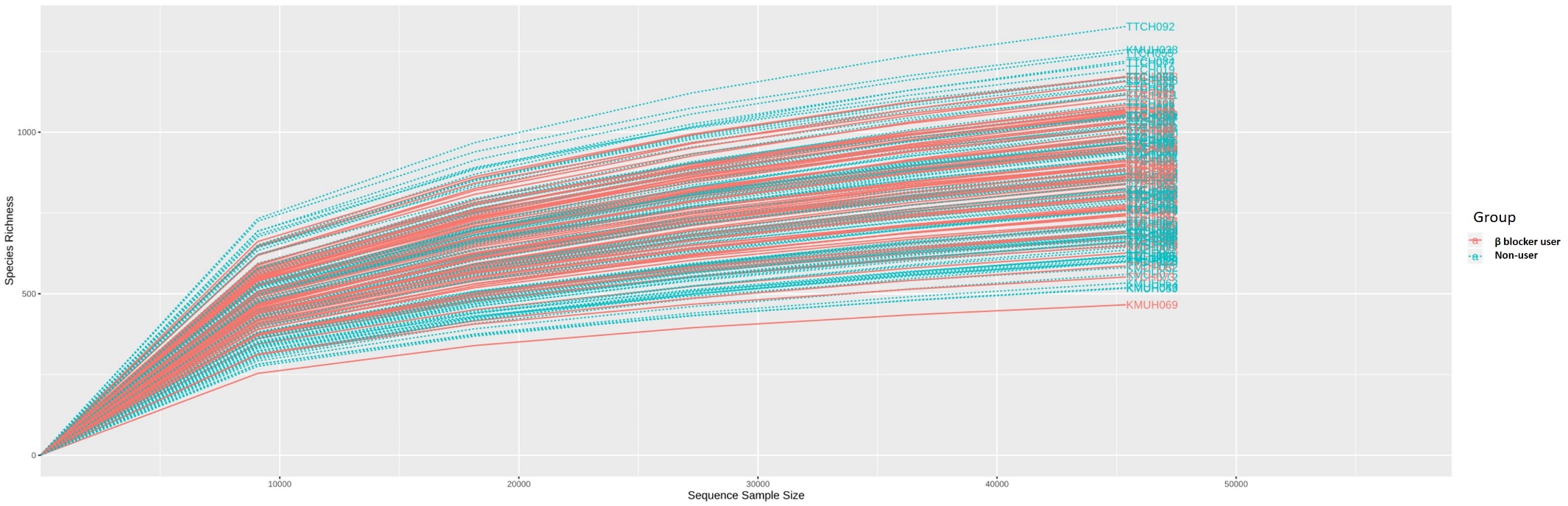
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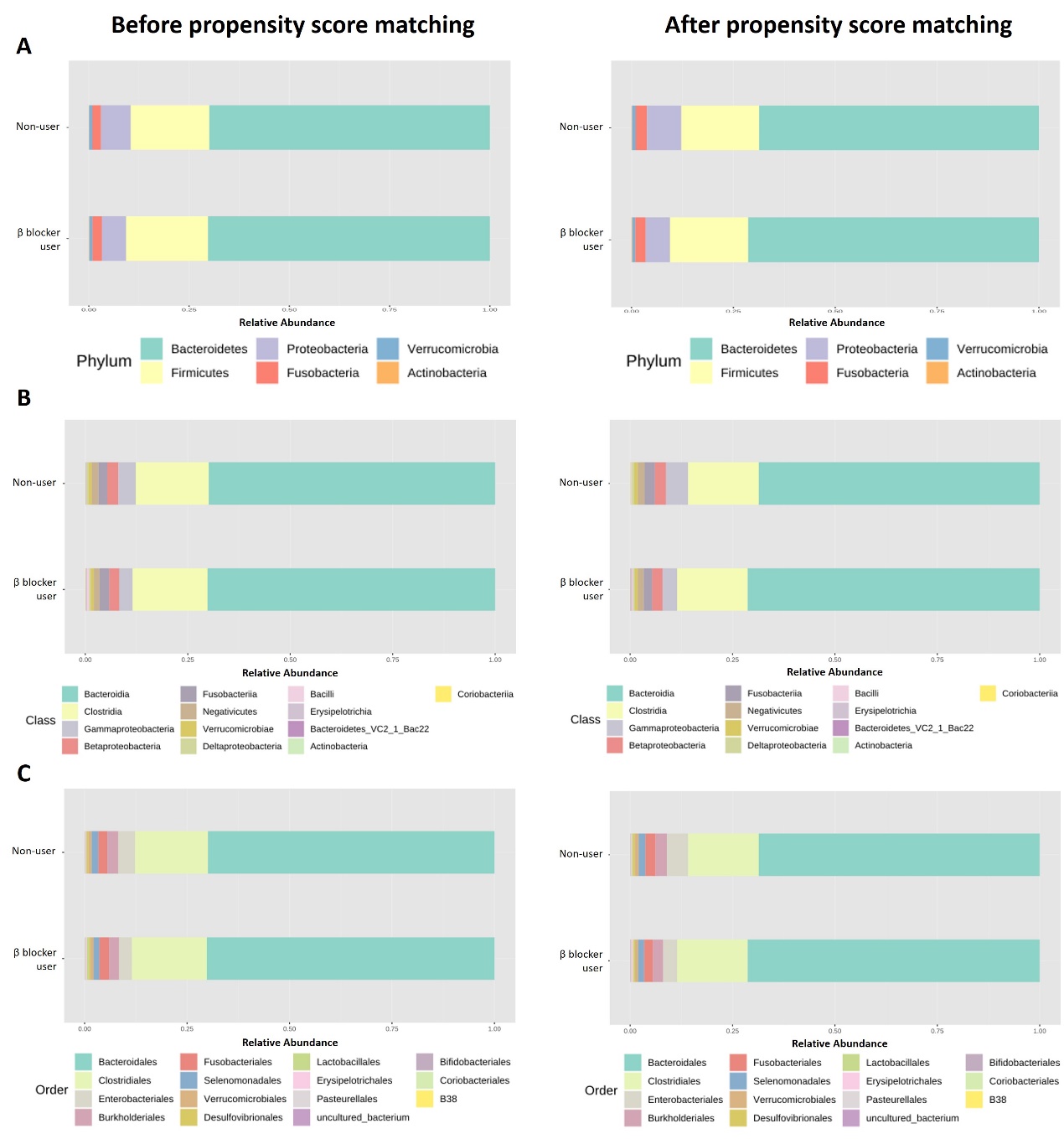
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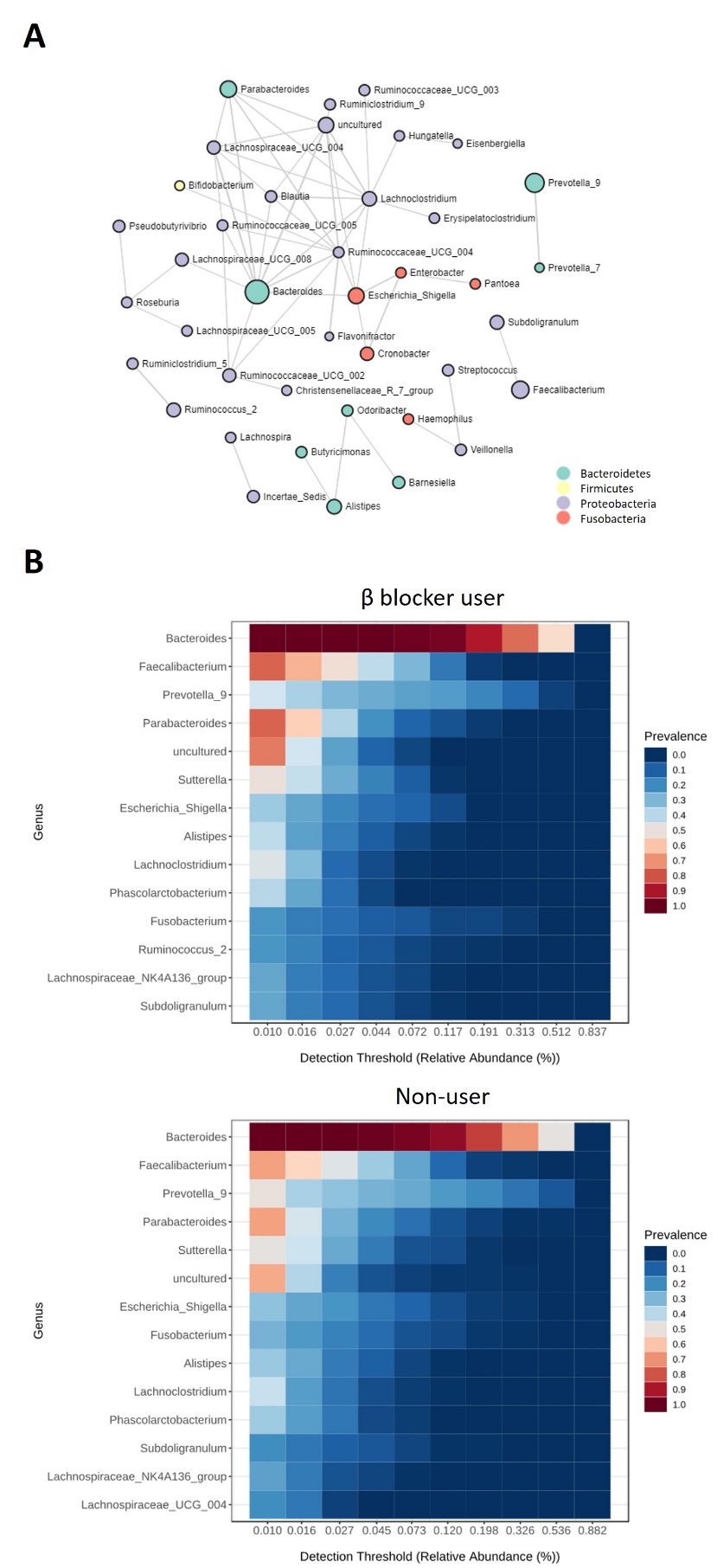
**Figure S1.** Rarefaction curves of the number of OTUs versus the sequencing effort per sample in the full cohort.



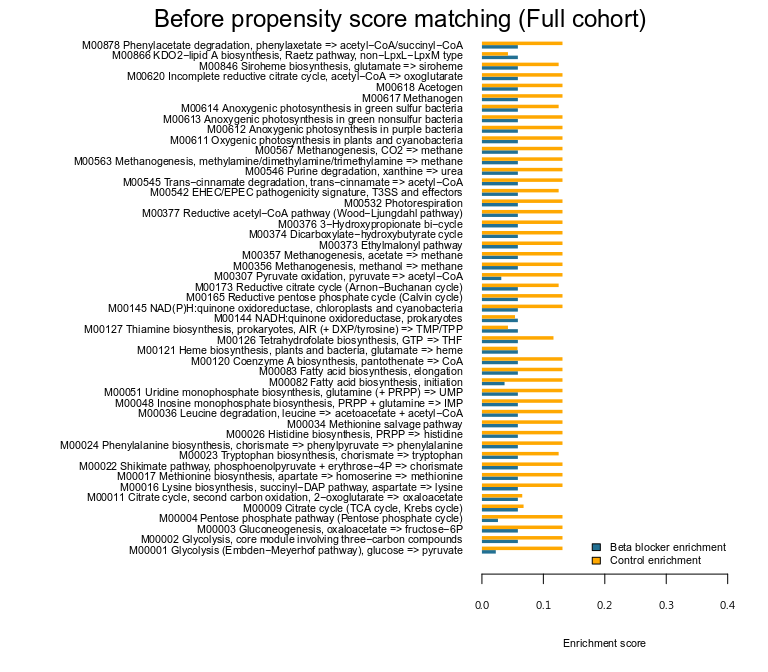
**Figure S2.** The relative abundance percentage of intestinal microbiota between β-blocker users and non-users in the full cohort and propensity score matching cohort. (A) Phylum level (B) Class level (C) Order level.



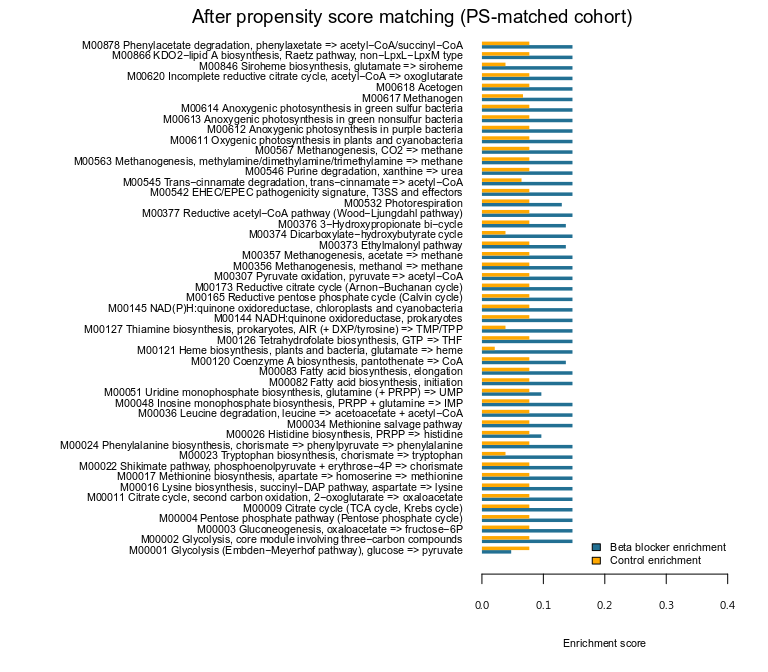
**Figure S3.** Core microbiome analysis in hemodialysis patients with and without β-blocker used. (A) SparCC correlation analysis (genus level using 100 SparCC permutations, 0.35 correlation threshold, and 0.05 *p*-value threshold) in all hemodialysis patients with and without β-blocker used (B) Relative abundance and sample prevalence of bacterial genus in β-blocker users and non-users.



**Figure S4.** Enrichment analysis for predictive Kyoto Encyclopedia of Genes and Genomes (KEGG) metabolic modules between β-blocker users and non-users in full (before propensity score matching) cohort. No significant KEGG enriched pathways were observed (all *p*-value > 0.05).



**Figure S5.** Enrichment analysis for predictive Kyoto Encyclopedia of Genes and Genomes (KEGG) metabolic modules between β-blocker users and non-users in propensity score-matched cohort. No significant KEGG enriched pathways were observed (all *p*-value > 0.05).



**Table S1.** Summary table of significant genus difference in hemodialysis patients with and without β-blocker treatment in zero-inflated Gaussian fit model

|  |  |  |
| --- | --- | --- |
| **Genus** | **Zero-inflated Gaussian fit method** | |
|  | **Before propensity score matching** | **After propensity score matching** |
|  | ***p*-value** | ***p*-value** |
| Prevotella\_2 | 0.192 | 0.004 |
| **Prevotellaceae NK3B31 group** | **0.030** | **0.005** |
| Subdoligranulum | 0.400 | 0.011 |
| **Flavonifractor** | **0.044** | **0.015** |
| **Tyzzerella** | **0.049** | **0.024** |
| Streptococcus | 0.073 | 0.037 |
| Ruminococcaceae UCG-005 | 0.283 | 0.039 |
| Faecalibacterium | 0.501 | 0.044 |
| Christensenellaceae R7 group | 0.473 | 0.063 |
| Ruminococcaceae UCG-003 | 0.791 | 0.069 |
| Enterobacter | 0.599 | 0.070 |
| Lachnospiraceae UCG-004 | 0.641 | 0.091 |
| Ruminiclostridium 9 | 0.044 | 0.093 |
| Ruminococcaceae UCG-004 | 0.016 | 0.100 |
| Lachnospiraceae UCG-005 | 0.236 | 0.115 |
| Pantoea | 0.711 | 0.140 |
| Anaerotruncus | 0.031 | 0.144 |
| Intestinibacter | 0.496 | 0.148 |
| Eubacterium ventriosum group | 0.488 | 0.187 |
| Erysipelatoclostridium | 0.271 | 0.200 |
| Ruminiclostridium 6 | 0.204 | 0.210 |
| Collinsella | 0.748 | 0.210 |
| Lachnoclostridium | 0.850 | 0.232 |
| Bacteroides | 0.282 | 0.232 |
| Prevotella 9 | 0.796 | 0.244 |
| uncultured | 0.117 | 0.252 |
| Eubacterium coprostanoligenes group | 0.765 | 0.252 |
| Cronobacter | 0.810 | 0.254 |
| Roseburia | 0.303 | 0.274 |
| Lachnospiraceae NC2004 group | 0.573 | 0.311 |
| Ruminiclostridium | 0.314 | 0.312 |
| Eubacterium hallii group | 0.111 | 0.316 |
| Butyricimonas | 0.448 | 0.344 |
| Eisenbergiella | 0.080 | 0.351 |
| Barnesiella | 0.554 | 0.358 |
| Clostridium sensu stricto 1 | 0.778 | 0.375 |
| Lachnospiraceae UCG-010 | 0.778 | 0.382 |
| Phascolarctobacterium | 0.926 | 0.385 |
| Ruminiclostridium 5 | 0.043 | 0.397 |
| Akkermansia | 0.169 | 0.399 |
| Bifidobacterium | 0.651 | 0.422 |
| Haemophilus | 0.534 | 0.444 |
| Lachnospira | 0.613 | 0.446 |
| Fusicatenibacter | 0.887 | 0.460 |
| Sutterella | 0.991 | 0.460 |
| Megamonas | 0.957 | 0.483 |
| Lactonifactor | 0.385 | 0.488 |
| Dorea | 0.897 | 0.551 |
| Desulfovibrio | 0.087 | 0.555 |
| Parabacteroides | 0.194 | 0.573 |
| Pseudobutyrivibrio | 0.910 | 0.577 |
| Odoribacter | 0.761 | 0.577 |
| Intestinimonas | 0.096 | 0.581 |
| Lachnospiraceae NK4A136 group | 0.819 | 0.644 |
| Hungatella | 0.288 | 0.644 |
| Eubacterium ruminantium group | 0.457 | 0.645 |
| Eubacterium oxidoreducens group | 0.651 | 0.658 |
| Bilophila | 0.750 | 0.682 |
| Lachnospiraceae UCG-008 | 0.618 | 0.694 |
| Prevotella 7 | 0.804 | 0.694 |
| Paraprevotella | 0.869 | 0.709 |
| uncultured bacterium | 0.849 | 0.723 |
| Erysipelotrichaceae UCG-003 | 0.739 | 0.822 |
| Escherichia Shigella | 0.915 | 0.838 |
| Parasutterella | 0.326 | 0.858 |
| Fusobacterium | 0.990 | 0.872 |
| Incertae Sedis | 0.959 | 0.874 |
| Veillonella | 0.522 | 0.888 |
| Blautia | 0.829 | 0.894 |
| Ruminococcus 2 | 0.145 | 0.896 |
| Oscillospira | 0.523 | 0.913 |
| Alistipes | 0.650 | 0.921 |
| Ruminococcaceae UCG-013 | 0.745 | 0.925 |
| Ruminococcaceae UCG-002 | 0.388 | 0.928 |
| Anaerostipes | 0.581 | 0.938 |
| Ruminococcus 1 | 0.876 | 0.958 |
| Ruminococcaceae NK4A214 group | 0.498 | 0.979 |
| Family XIII AD3011 group | 0.018 | - |
| Lachnospiraceae ND3007 group | 0.464 | - |