

Table S1. List of bacteria significantly enriched in the NALB group vs. the SWM group. This list of bacteria was used in downstream network analyses to track the oxalate microbial network in each group, over time.

| <b>Lowest Assigned Taxonomy</b> | <b>Taxonomic Level</b> | <b>No. of OTUs</b> | <b>Log2 Fold Change</b> | <b>FDR</b>   |
|---------------------------------|------------------------|--------------------|-------------------------|--------------|
| Bacteroides                     | Genus                  | 144                | 0.61-3.84               | <0.001-0.044 |
| Clostridiales                   | Order                  | 46                 | 0.84-2.28               | <0.001-0.031 |
| S24-7                           | Family                 | 34                 | 0.82-2.83               | <0.001-0.049 |
| Lachnospiraceae                 | Family                 | 31                 | 0.84-2.69               | <0.001-0.044 |
| Ruminococcaceae                 | Family                 | 20                 | 0.64-2.93               | <0.001-0.047 |
| Parabacteroides                 | Genus                  | 19                 | 0.8-1.79                | <0.001-0.048 |
| Erysipelotrichaceae             | Family                 | 12                 | 0.82-2.53               | <0.001-0.035 |
| Oscillospira                    | Genus                  | 12                 | 0.87-1.3                | <0.001-0.048 |
| Rikenellaceae                   | Family                 | 12                 | 0.76-2.03               | <0.001-0.049 |
| Proteus                         | Genus                  | 10                 | 0.95-1.65               | <0.001-0.041 |
| Coprococcus                     | Genus                  | 8                  | 0.88-1.68               | <0.001-0.034 |
| Ruminococcus                    | Genus                  | 8                  | 0.86-2.15               | <0.001-0.04  |
| Unassigned                      | NA                     | 7                  | 0.82-2.92               | <0.001-0.043 |
| Sporosarcina                    | Genus                  | 6                  | 0.84-2.08               | <0.001-0.047 |
| Bacillus                        | Genus                  | 5                  | 0.87-1.02               | 0.021-0.041  |
| Butyricimonas                   | Genus                  | 4                  | 1.16-2.64               | <0.001-0.011 |
| RF32                            | Order                  | 4                  | 1.1-1.85                | <0.001-0.02  |
| Clostridiaceae                  | Family                 | 3                  | 0.85-1.95               | <0.001-0.04  |
| Lactobacillus                   | Genus                  | 3                  | 0.99-2.38               | <0.001-0.03  |
| Acinetobacter                   | Genus                  | 2                  | 1.11-1.12               | 0.016        |
| AF12                            | Genus                  | 2                  | 2.46-2.48               | <0.001       |
| Alphaproteobacteria             | Class                  | 2                  | 3.2-3.53                | <0.001       |
| Bacteroidales                   | Order                  | 2                  | 1.23-2.37               | <0.001-0.007 |
| Burkholderiales                 | Order                  | 2                  | 1.28-4.92               | <0.001       |
| Candidatus Arthromitus          | Genus                  | 2                  | 1.01-1.02               | 0.025-0.026  |
| Clostridium                     | Genus                  | 2                  | 0.91-1.48               | <0.001-0.03  |
| Coprobacillus                   | Genus                  | 2                  | 3.69-3.79               | <0.001       |
| Corynebacterium                 | Genus                  | 2                  | 0.91-1.08               | 0.027        |
| Dehalobacterium                 | Genus                  | 2                  | 0.72-0.74               | 0.016-0.019  |
| Enterobacteriaceae              | Family                 | 2                  | 1.23                    | 0.008-0.009  |
| Facklamia                       | Genus                  | 2                  | 0.94-1.38               | 0.002-0.033  |
| Helicobacteraceae               | Family                 | 2                  | 1.06-3.24               | <0.001-0.01  |
| Lactobacillales                 | Order                  | 2                  | 1.5-2.16                | <0.001       |
| RF39                            | Order                  | 2                  | 1.54-1.85               | <0.001       |
| Rikenella                       | Genus                  | 2                  | 3.48-3.49               | <0.001       |
| Stenotrophomonas                | Genus                  | 2                  | 1.63-1.7                | <0.001       |
| YS2                             | Order                  | 2                  | 1.08-1.14               | 0.009-0.013  |

|                   |        |   |      |        |
|-------------------|--------|---|------|--------|
| Adlercreutzia     | Genus  | 1 | 0.91 | 0.036  |
| Akkermansia       | Genus  | 1 | 1.15 | <0.001 |
| Bacillaceae       | Family | 1 | 1.44 | 0.004  |
| Bacillales        | Order  | 1 | 2.82 | <0.001 |
| Bilophila         | Genus  | 1 | 2.79 | <0.001 |
| Carnobacteriaceae | Family | 1 | 1.18 | 0.01   |
| Dorea             | Genus  | 1 | 0.95 | 0.028  |
| Enterococcaceae   | Family | 1 | 1.14 | 0.007  |
| RF16              | Family | 1 | 1.63 | <0.001 |
| Granulicatella    | Genus  | 1 | 1.9  | <0.001 |
| Helicobacter      | Genus  | 1 | 3.25 | <0.001 |
| Morganella        | Genus  | 1 | 2.08 | <0.001 |
| Sutterella        | Genus  | 1 | 5.03 | <0.001 |
| Vagococcus        | Genus  | 1 | 1.37 | <0.001 |

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