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| **Supplemental Table 3. Genus level genome scale metabolic network reconstructions** | | | | |
| **Genus** | **Average Model Size**  (average of number of reactions in member-species reconstructions) | **Number of species-level models included in each genus** | **Average Network Overlap Within genus**  (average number of shared reactions, normalized by average network size) | **Average Fraction of Unique Reactions**  (what fraction of a given species’ network is unique within its genus, normalized by average network size) |
| Akkermansia | 818 | 1 | 1 | 1 |
| Barnesiella | 898 | 2 | 0.9621 | 0.0379 |
| Blautia | 980.9 | 10 | 0.8751 | 0.0093 |
| Clostridium\_difficile | 999.5 | 2 | 0.9735 | 0.0265 |
| Coprobacillus | 910.3 | 3 | 0.9821 | 0.0092 |
| Enterobacteriaceae | 1335.5 | 10 | 0.8738 | 0.0054 |
| Enterococcus | 916.4 | 10 | 0.8865 | 0.0143 |
| Lachnospiraceae | 966 | 10 | 0.85 | 0.0175 |
| Mollicutes | 485.2 | 10 | 0.8233 | 0.0268 |