**Supplementary Table S1. Differential Abundant Genera Identified Among Groups**

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| --- | --- | --- | --- | --- | --- | --- |
| **Genus** | **Healthy Control** | **Benign GYN** | **EM I–II** | **EM III–IV** | **q value** | **Trend** |
| *Prevotella* | 0.042 | 0.048 | 0.057 | 0.064 | 0.013 | ↑ |
| *Blautia* | 0.065 | 0.058 | 0.045 | 0.032 | 0.021 | ↓ |
| *Subdoligranulum* | 0.054 | 0.049 | 0.039 | 0.030 | 0.026 | ↓ |
| *Ruminococcus* | 0.059 | 0.052 | 0.041 | 0.036 | 0.030 | ↓ |
| *Bacteroides* | 0.061 | 0.058 | 0.056 | 0.054 | 0.057 | ↓ |

This table presents genus-level taxa whose relative abundances differed significantly among the four participant groups: healthy controls, patients with benign gynecologic conditions, early-stage endometriosis (stage I–II), and advanced-stage endometriosis (stage III–IV). Data are shown as mean relative abundance per group. Statistical comparisons were performed using the Kruskal–Wallis test followed by Benjamini–Hochberg false discovery rate (FDR) correction. Only genera with q values < 0.06 are included. Arrows indicate the overall direction of abundance change with increasing disease severity.