**Figure 1. The gut microbiota composition and function were significantly different between healthy controls and anorexia patients prior to and following clinical renourishment.** Boxplots showing BMI in healthy controls (HC), anorexia patients before clinical renourishment (T1), and anorexia patients following clinical renourishment (T2) for both the UNC and Denver cohorts (A), the Denver cohort (B), and the UNC cohort (C). Scatter plots showing Principal Coordinates Analysis for taxonomies (D-F) and metabolic pathways (G-J). Ordination plots are shown for both the UNC and Denver cohorts (D and G), the Denver cohort (E and H), and the UNC cohort (F and J). For each ordination plot, p and R2 values from PERMANOA test are shown. Boxplots next to each ordination plot show the first and second axes (MDS1 and MDS2) for HC, T1, and T2 patients. Statistical test: unpaired t-test for HC versus T1 and HC versus T2, paired t-test for T1 versus T2.

**Extended Figure 1. BMI, fat mass, and diversity of the metabolic pathways in patients with anorexia nervosa were significantly impacted by clinical renourishment yet remained distinct to non-AN controls.** (A) Boxplot showing BMI in healthy controls (HC), anorexia patients before clinical renourishment (T1), and anorexia patients following clinical renourishment (T2) at the Denver and UNC sites. t-test \*\*\* adjusted p < 0.05. (B-H) Boxplots showing fat measurements by Dual energy x-ray absorptiometry (DXA) and bioelectric impedance analysis (BIA) at the UNC site. (I-K) Boxplot showing Shannon diversity index for taxonomies at both the UNC and Denver sites (I), the Denver site (J), and the UNC site (K). (L-N) Boxplot showing Shannon diversity index for metabolic pathways at both the UNC and Denver sites (L), the Denver site (M), and the UNC site (N). Statistical tests: unpaired t-test for HC versus T1 and HC versus T2, paired t-test for T1 versus T2.

**Supplemental Figure 1.** **The gut microbiota composition for severely low BMI patients at UNC was not different from the healthy gut microbiome**. Principal coordinates analysis for UNC patients with BMI lower than 15 (n=12). p and R2 values from PERMANOA test are shown.

**Figure 2.** **Clinical renourishment of patients with anorexia nervosa was associated with specific changes in metabolic pathways in the intestinal microbiota, while the gut microbiota composition was not affected by clinical renourishment.** Heatmaps showing the adjusted log10 p-values from t-tests comparing the log10 normalized counts of taxonomies (A) and relative abundances of metabolic pathways (B) between healthy controls (HC) and anorexia patients before clinical renourishment (T1), and anorexia patients following clinical renourishment (T2). Heatmaps show the most 50 abundant species or metabolic pathways that were significantly different between healthy controls and anorexia patients. P-values are adjusted using the Benjamini-Hochberg procedure.

**Extended Figure 2.** **The gut microbiota composition which was distinct between healthy controls and anorexia patients was not significantly affected by clinical renourishment.** Boxplots showing the abundances of most significant taxa from the heatmap (Figure 2A) that were significantly different between healthy controls and anorexia patients.

**Extended Figure 3.** **Metabolic pathways in the gut microbiome were significantly affected by clinical renourishment yet remained distinct to healthy controls.** Boxplots showing the abundances of most significant metabolic pathways from the heatmap (Figure 2B) that were significantly different between healthy controls and anorexia patients.

**Figure 3. A similar and robust pattern of dysbiosis in the gut microbiome was observed at the UNC and Denver sites**. Scatter plots showing the unadjusted log10 p-values from t-test comparing the log10 normalized counts of genera (A-C) and relative abundances of metabolic pathways (D-F) in healthy controls versus anorexia patients prior to clinical renourishment (HC versus T1), healthy controls versus anorexia patients following clinical renourishment (HC versus T2), and anorexia patients prior to versus following clinical renourishment (T1 vs T2) at the UNC and Denver sites. In the case of HC versus T1 or HC versus T2 comparisons, positive or negative log10 p-values indicate that the mean abundance of the genera or metabolic pathways were greater or smaller in HC compared to T1 or T2, respectively. In the case of T1 and T2 comparison, positive or negative log10 p-values indicate that the mean abundance of genera or metabolic pathways were greater or smaller in T1 compared to T2, respectively.

**Figure 4. The gut microbiome composition prior to clinical renourishment is associated with weight gain in patients with AN with markedly low BMIs.** (A) Heatmap showing the adjusted log10 p-vales from mixed linear models with log10 normalized counts of species prior to clinical renourishment as dependent variable, BMI change per day as a fixed effect, and the site as a random effect. Positive and negative p-values indicate positive and negative associations between abundances of species and BMI change per day, respectively. The Heatmap shows the most 50 abundant species that were significantly associated with BMI change per day at the Denver site. (B) Boxplots showing the abundances of the most significant taxa that were positively or negatively associated with BMI change per day in the heatmap (A). P-values are adjusted using the Benjamini-Hochberg procedure.