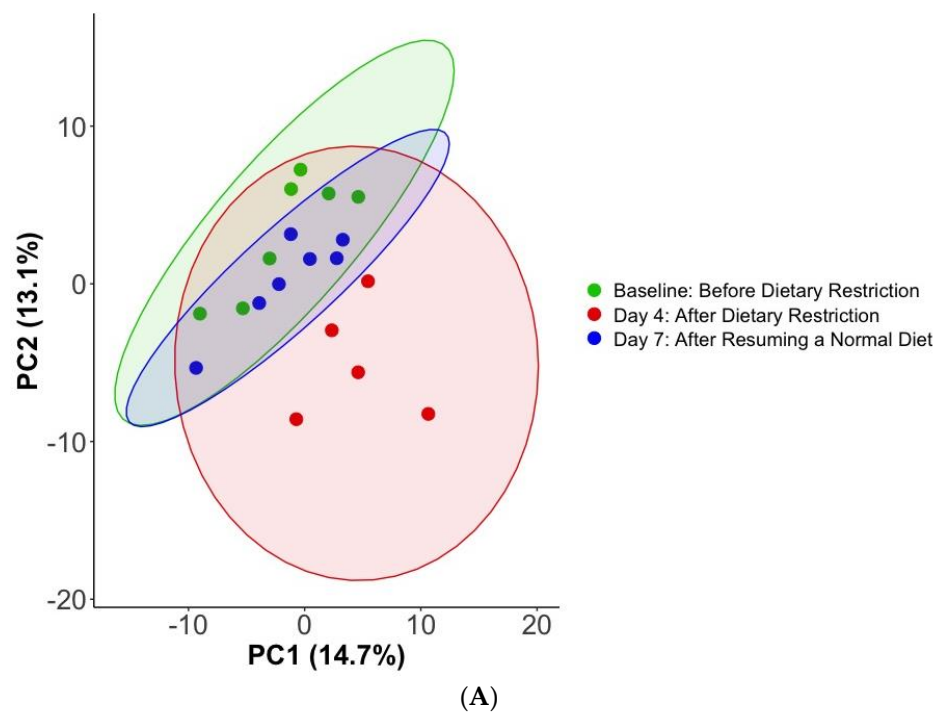


Figure S1. All enriched canonical pathways on day 7 compared to baseline.



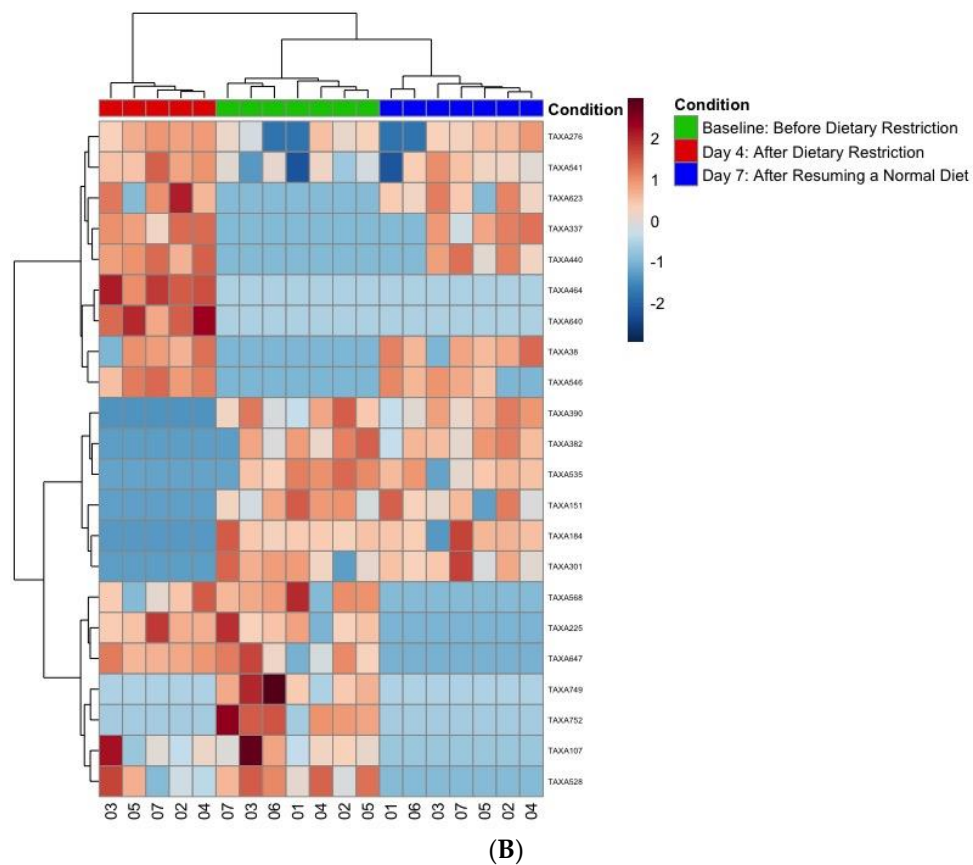


Figure S2. Principal component analysis and heatmap of species abundance after prevalence filtering. (A) PCA; (B) Heatmap.

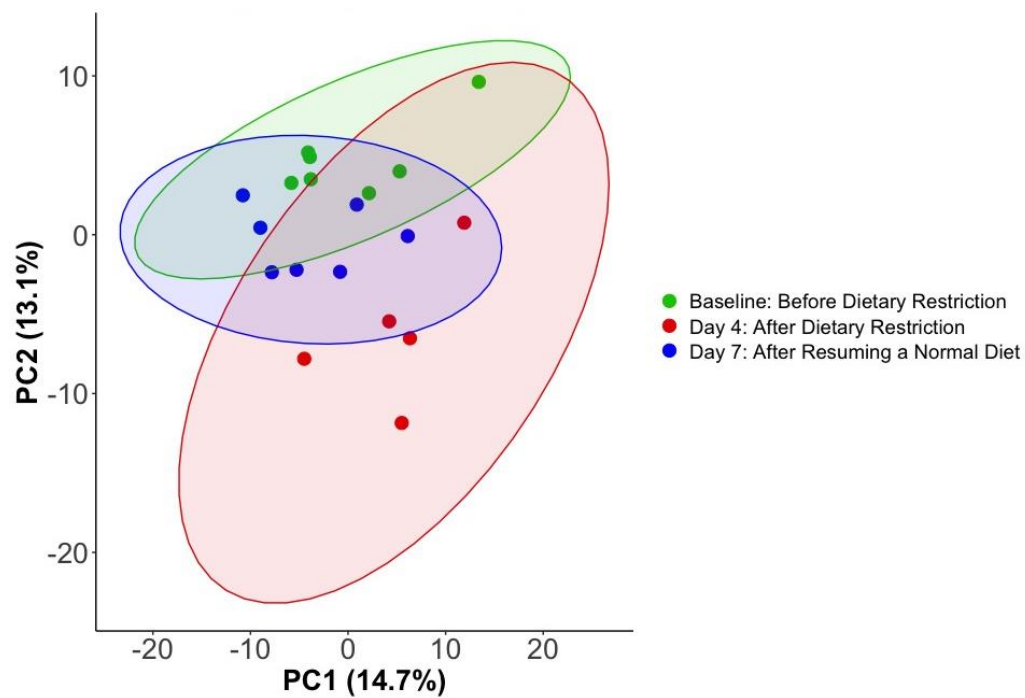


Figure S3. Principal component analysis of metabolic pathway changes after prevalence filtering.

Table S1. The top 20 differentially expressed genes for each condition compared to baseline. Genes are ordered from the most upregulated (rows 1–10) to the most downregulated (rows 11–20). The log-fold change of each gene is displayed in the “LogFC” column.

| Row ID | Day 2 Genes | | Day 4 Genes | | Day 7 Genes | |
|--------|-------------|-------|-------------|-------|-------------|-------|
| | Gene ID | LogFC | Gene ID | LogFC | Gene ID | LogFC |
| 1 | ZC4H2 | 0.83 | HSPA1B | 0.72 | ARID5B | 0.68 |
| 2 | FAM135A | 0.67 | KCNQ5 | 0.60 | NLRC5 | 0.67 |
| 3 | STX18-AS1 | 0.64 | HIBADH | 0.54 | STX18-AS1 | 0.65 |
| 4 | NLRC5 | 0.63 | CHCHD3 | 0.54 | FAM135A | 0.62 |
| 5 | ALG9 | 0.59 | HSPA1A | 0.52 | RALGAPA2 | 0.62 |
| 6 | LINC01422 | 0.59 | FAM135A | 0.51 | STK38L | 0.60 |
| 7 | KCNQ5 | 0.55 | SRGAP2 | 0.51 | MMS22L | 0.60 |
| 8 | CD84 | 0.53 | PCCB | 0.51 | AL359232.1 | 0.58 |
| 9 | ZNF519 | 0.53 | HDAC9 | 0.51 | IFI44L | 0.57 |
| 10 | IFNG-AS1 | 0.51 | STX6 | 0.49 | ORC5 | 0.57 |
| 11 | BTG2 | −0.87 | ZFP36 | −0.74 | ARRDC3 | −0.86 |
| 12 | NFKBIA | −0.83 | ID1 | −0.69 | RSRC2 | −0.70 |
| 13 | ZFP36 | −0.80 | ACSL3 | −0.69 | ERCC1 | −0.63 |
| 14 | SLC7A5 | −0.79 | SLC7A5 | −0.67 | AL021918.5 | −0.61 |
| 15 | PIK3IP1 | −0.74 | DCTN4 | −0.66 | CEP19 | −0.55 |
| 16 | GADD45B | −0.73 | SMAD7 | −0.66 | DCTN4 | −0.54 |
| 17 | FOS | −0.73 | PRKX | −0.64 | RPAP2 | −0.54 |
| 18 | IER5 | −0.73 | PMAIP1 | −0.64 | MMP24OS | −0.53 |
| 19 | AC020916.1 | −0.71 | PDE4B | −0.64 | NDUFB1 | −0.52 |
| 20 | KDM6B | −0.67 | NFKBIA | −0.62 | EFCAB2 | −0.52 |