**Supplementary Figure 1. Diversity analysis of gut metagenomes from adult melanoma patients receive immune checkpoint inhibitor therapy.** Multidimensional scaling (MDS) plot with weighted UniFrac distances comparing immune checkpoint inhibitor therapy (ICT) responders (marked in magenta) versus those with progressive disease (marked in blue) for (A) all ICT, (B) IN only, and (C) P only. Metagenomic shotgun sequencing data was generated from fecal samples collected from melanoma patients prior to ICT and taxonomic abundance was determined using MetaPhlAn IN, ipilimumab and nivolumab. P, pembrolizumab.

A
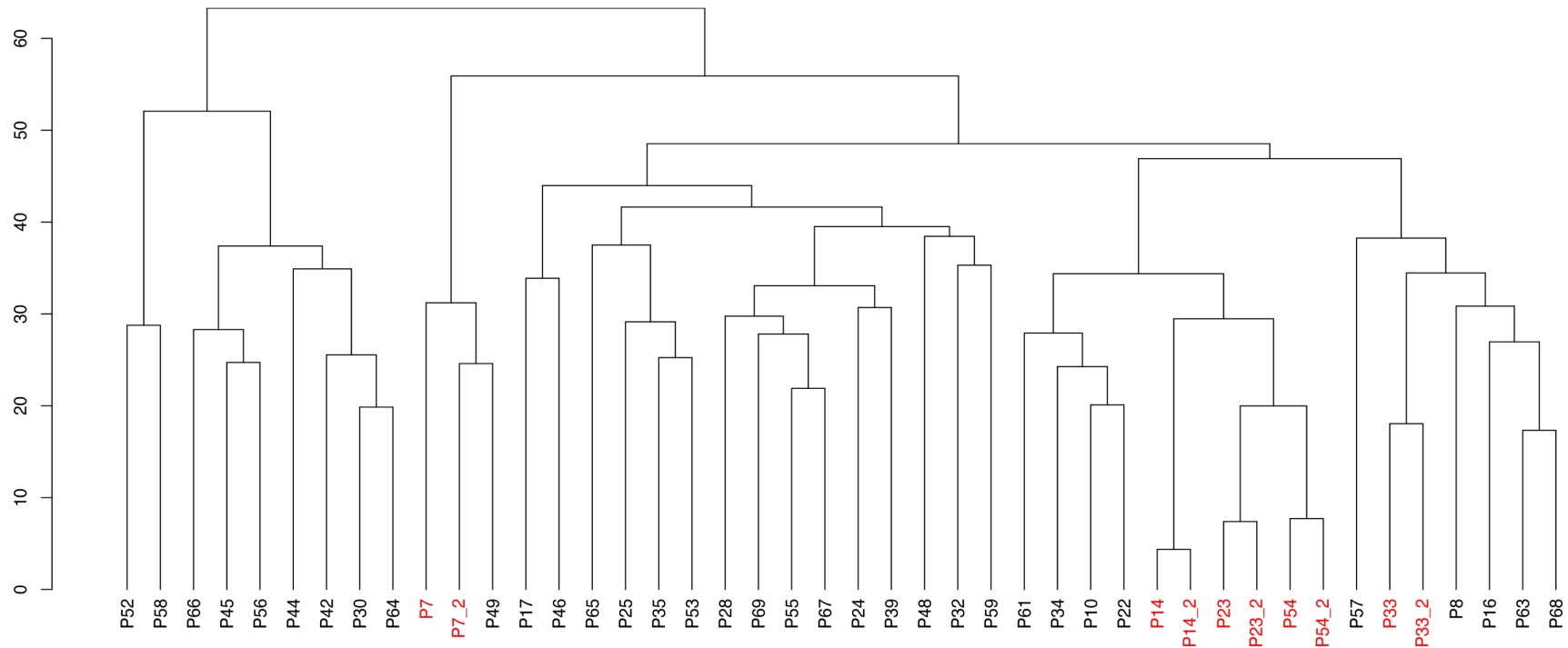
B
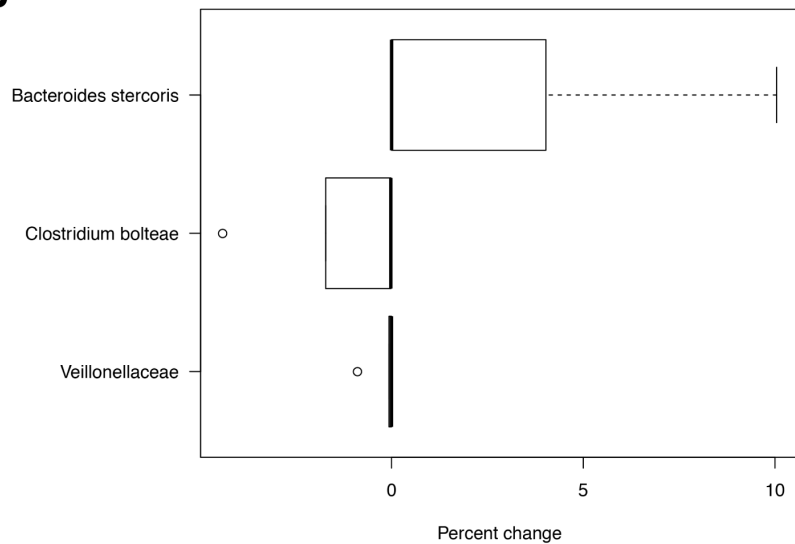
Supplemental Figure 2. Comparison of gut microbiota taxonomic composition in repeat fecal specimens in adult melanoma patients receiving ICT therapy. Five adult melanoma patients (P7, P14, P23, P54, and P33) had repeat fecal specimens collected within one month of initiation of ICT. Metagenomic shotgun sequencing data was generated from fecal samples collected from melanoma patients receiving ICT and taxonomic abundance was determined using MetaPhlAn. (A) Hierarchical clustering of species abundances shown as dendrogram plots with paired samples marked in red. (B) Specific bacteria taxa noted to have increased (*Bacteroides stercoris*, p=0.063) or decreased (*Clostridium boltae*, p=0.063; *Veillonellaceae*, p=0.063) abundance in the repeat sample. Statistical analysis by Wilcoxan-signed-rank test.