Figure S1: Differential abundance analysis at the genera level using LefSe for all patients from baseline (Time 0) to 6 months (Time 6) post-surgery (n=28).

Only the top 10 significant results ($p<0.05$) are presented.

NA = Sequences that were assigned at a higher taxonomic level (kingdom, phylum, class, order, family) but were not assigned to a specific genus.

