Description of Additional Supplementary Files

**Supplementary Data 1.** Fecal samples and acute leukemia patients included in this study.

**Supplementary Data 2.** Prevalence and abundance of genera included in the analysis of human samples.

**Supplementary Data 3.** Correlation between the changes in the fecal levels of MRE in patients and the changes in the levels of genera or OTUs.

**Supplementary Data 4.** List of L. rhamnosus strains and ANI values.

**Supplementary Data 5.** Taxa that discriminate untreated mice from mice that were allowed to recover from antibiotic treatment.

**Supplementary Data 6.** Significantly different taxa between mice treated with antibiotics that received or not Lactobacillus.

**Supplementary Data 7.** Significantly different taxa between mice treated with antibiotics that received or not Lactobacillus identified by using sequencing data that has been normalized with 16S rRNA qPCR.

**Supplementary Data 8.** Correlation between the relative abundance of taxa and MRKP in mice.

**Supplementary Data 9.** Significantly different taxa between mice treated with antibiotics that received or not the Clostridiales cocktail.

**Supplementary Data 10.** Significantly different metabolites between mice treated with antibiotics that received or not Lactobacillus.

**Supplementary Data 11.** Correlation between the relative abundance of taxa and butyrate, serine, threonine or glucose in mice.

**Supplementary Data 12.** Correlations between the relative abundance of taxa, butyrate and Lactobacillus levels in patients.

**Supplementary Data 13.** Characteristics of the patients included in this study.

**Supplementary Data 14.** Tables containing the Omic processed data used in this study.