Dear Dr. X,

Please find uploaded the manuscript entitled “*Microbiota: are you sick?*” By Jose M. Marti *et al*., for your kind consideration for publication as a Letter in Nature.

As you must know, there is general assent on the need for methodologies that can help to unravel the increasing amount of –*omic* information being generated on microbial diversity. In this paper, we use newly available methods to examine the dynamic association between gut microbiota and human health. We reveal how a universal fluctuation scaling law, which describes the temporal variability of the system, is able to distinguish healthy from sick microbiota. We provide a mechanistic explanation based on the statistical theory of errors, which predicts two distinguishable phases of the gut microbiome. Data analyzed in this work show that a noise induced phase transition corresponds to the route leading to disease. A complete software framework, ComplexCruncher, and a web platform, ComplexCruncher Web Portal, have been engineered so that users can implement this technology from a web browser and develop their own database. The universal law and the mechanistic model proposed here can be applied to virtually any temporal (or spatial) set of high throughput genetic data in environmental, industrial and medical metagenomes.

We hope you will find our work as promising as we do and consider it suitable for publication in Nature.

Sincerely yours,

Amparo Latorre, Andres Moya & Carlos Peña Garay