



Data Article

Data on gut metagenomes of the patients with alcoholic dependence syndrome and alcoholic liver cirrhosis



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ABSTRACT

Alcoholism is associated with significant changes in gut microbiota composition. Metagenomic sequencing allows to assess the altered abundance levels of bacterial taxa and genes in a culture-independent way. We collected 99 stool samples from the patients with alcoholic dependence syndrome ($n=72$) and alcoholic liver cirrhosis ($n=27$). Each of the samples was surveyed

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