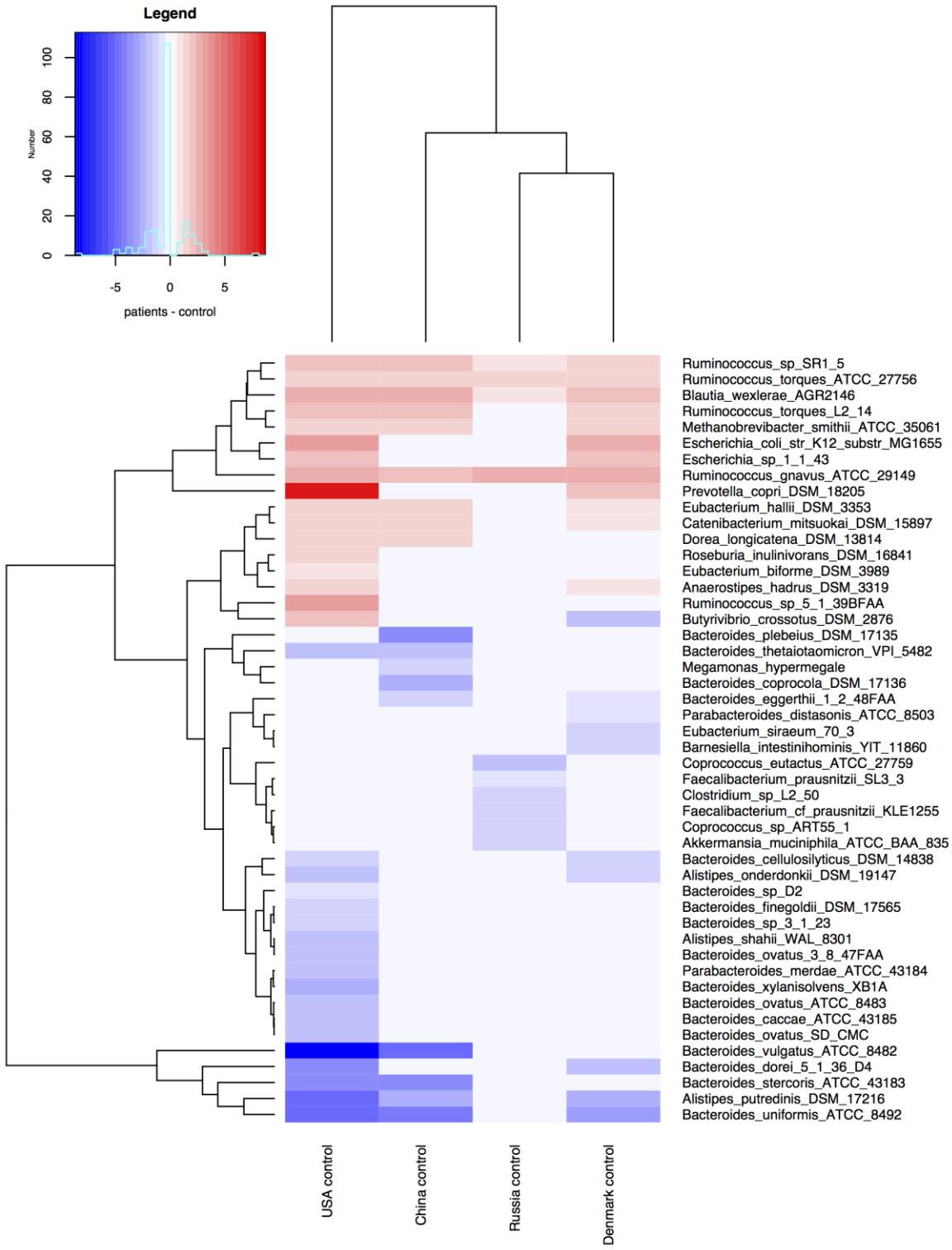
SUPPLEMENT 1

Dubinkina V.B., Tyakht A.V., Ilina E.N., Ischenko D.S., Kovarsky B.A., Yarygin K.S., Pavlenko A.V., Popenko A.S., Alexeev D.G., Taraskina A.E., Nasyrova R.F., Krupitski E.M., Skorodumova L.O., Larin A.K., Kostryukova E.S., Govorun V.M., Metagenomic analysis of taxonomic and functional changes in gut microbiota of patients with alcoholic dependence syndrome, Biomeditsinskaya khimiya, 2015, vol: 61(6), 742-749. DOI: 10.18097/PBMC20156106742



Heatmap representing the difference between the relative abundance of bacterial species that are significantly increased or decreased in the gut metagenomes of ADS patients in comparison with at least one of the control groups. Clusterings was performed by the hierarchical method based on Euclidian distance matrix. Only the species with significantly varying abundance values ($p \leq 0.05$) and the difference between the group mean values more than 1% are represented.