Background The circulating free DNA (cfDNA) originating mostly from the abnormal cell apoptosis, necrosis or netosis contains sequences of microorganisms encountered previously by the patients. Therefore, it may be a source of information about past infections and may become a tool to evaluate human microbiome in relation to specific diseases. The aim of the study was to identify bacterial sequences in cfDNA of patients with different types of glomerulopathies.

Methods Blood samples from 9 patients with lupus nephritis (LN), 5 with IgA nephropathy, 4 with membranous nephropathy and 3 healthy controls were collected once. cfDNA was isolated (QIAmp, Qiagen) and quantified (Thermo Fisher Scientific, Waltham). Sequencing libraries were constructed, and quality checked (KAPA-Roche, Basel). Samples were sequenced on NextSeq 550 (Illumina, San Diego), before a multi-step bioanalysis.

Results Bacterial sequences represented 0.031% of the cfDNA. The most frequent bacterial genera in the cfDNA of patients with glomerulopathies included: Escherichia, Streptococcus, Klebsiella, Brevundimonas and Moraxella and they varied between the studied patient groups. The cluster of four LN and one MN patients had distinctive bacterial cfDNA pattern which was observed on the species, family, order, class and phylum level.

Conclusions Bacterial sequences in cfDNA of patients with lupus nephritis differ from patients with IgA nephropathy and membranous nephropathy. Validation in a larger patient population is warranted.