# Data Repository Crohn’s disease project AG Chang

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## **Data abstract**

We have investigated a Crohn’s disease (CD) cohort by our multi-parameter microbiota flow cytometry approach to characterise the microbiota on single-cell level for attributes of the disease. The microbiota is isolated from stool samples and stained according to the published protocol for (a) host immunoglobulins IgA1, IgA2, IgM, IgG and (b) agglutinin binding to mannose, galactose or N-Acetyl-glucosamine surface sugar moities. For all samples we also determined the microbiome composition by 16S rRNA (V3-V4) sequencing on the illumina MiSeq plattform. We provide the raw .fcs and FASTQ files of 64 CD patients distributed into two cohorts (55 inddividuals in cohort 1, 19 individuals in cohort 2). Cohort 2 has two samples for two timepoints.

For comparison we additionally analysed 55 healthy donors.

All .fcs files were generated on BD Influx®.

The metadata is collected in the provided meta.csv.

The staining parameters are summarized in provided panel.csv.

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