



LGC Genomics GmbH  
Ostendstraße 25  
12459 Berlin  
Germany  
Tel: +49 (0)30 5304 2200  
Fax: +49 (0)30 5304 2201  
Email: [genomics@lgcgroup.com](mailto:genomics@lgcgroup.com)  
Web: [www.lgcgroup.com/genomics](http://www.lgcgroup.com/genomics)

## Project 11410AA-NGS948 data delivery, 23 Oct 2017:

Samples: 3  
Sequencing amount: 20 million read pairs  
Sequencing type: 300 bp paired-end read (Illumina MiSeq V3)

### Delivery contents:

- 'RAW': raw sequencing data after basecalling in compressed FASTQ format
- 'AdapterClipped': compressed FASTQ files containing sequencing adapter clipped reads

FastQC reports (<https://www.bioinformatics.babraham.ac.uk/projects/fastqc/>), containing read quality metrics, are stored along with the FASTQ files.

### Data analysis overview:

- Demultiplexing of all libraries for each sequencing lane using the Illumina bcl2fastq 1.8.4 software (folder 'RAW'):
  - 1 or 2 mismatches or Ns were allowed in the barcode read when the barcode distances between all libraries on the lane allowed for it
- Clipping of sequencing adapter remnants from all raw reads (folder 'AdapterClipped'):
  - reads with final length < 20 bases were discarded
- Creation of FastQC reports for all FASTQ files
- Generation of read\_counts.xlsx, containing all read counts for all samples at a glance

If you have any questions related to your data or some steps of the data analysis, do not hesitate to contact me directly:

**Email:** [marie.weissenborn@lgcgroup.com](mailto:marie.weissenborn@lgcgroup.com)

**Tel.:** +49 (0)30 5304 2202