

## Report: SeqDEAS

Date: 2023-10-22

**Experiment:** Cardiomyopathies in Children

**Reference Genome:** Human Genome hg38

**gtf Annotation:** hg38

### 1. Trimming

Method/ Tool: PoreChop

Parameter: none

### 2. Data Processing

Method/ Tool: Seqkit

Parameter: -m 100 (Minimum length)

### 3. Alignment

Method/ Tool: DeSALT

Parameter: -s 2 (Seed step), -l 14 (Seeding l-mer), -x ont1d (Read type)

### 4. Post-Processing

Method/ Tool: Samtools

Parameter: none

### 5. Isoform Detection

Method/ Tool: FLAIR

Parameter: FLAIR-correct, FLAIR-quantify -quality 4

### 6. Statistical Analysis

Method/ Tool: ZO-transformed, Bonferroni-corrected Beta Regression

Parameter: Significance niveau: 0.05