SeqDEAS

# Report: SeqDEAS

**Date:** 2023-10-10

**Experiment:** sfdg

**Reference Genome:** fgh

**gtf Annotation:** ghgjh

## 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