

Report: SeqDEAS

Date:

Experiment: _____

Reference Genome: _____

gtf Annotation: _____

1. Trimming

Method/ Tool: _____

Parameter: _____

2. Data Processing

Method/ Tool: _____

Parameter: _____

3. Alignment

Method/ Tool: _____

Parameter: _____

4. Post-Processing

Method/ Tool: _____

Parameter: _____

5. Isoform Detection

Method/ Tool: _____

Parameter: _____

6. Statistical Analysis

Method/ Tool: _____

Parameter: _____