## **History for:**

## RNA-Seq Analysis log

RNA-Seq Analysis 2.7

29 Jun 2023 17:00:46

Version: CLC Genomics Server 23.0.4

Modified by: fito

Reference type Genome annotated with genes and transcripts
Reference sequence S\_lycopersicum\_chromosomes.4.00 (Genome)
Gene track S\_lycopersicum\_chromosomes.4.00 (Gene)
mRNA track S\_lycopersicum\_chromosomes.4.00 (mRNA)

Yes

Enable handling of spike-in controls Do not use spike-in controls

Mismatch cost 2 3 Insertion cost Deletion cost 3 Length fraction 1.0 Similarity fraction 0.98 Global alignment No Auto-detect paired distances Yes Strand specific Reverse Library type Bulk Maximum number of hits for a read 1 Count paired reads as two No

Ignore broken pairs Yes

Expression value Unique counts

Calculate expression for genes

without transcripts

Minimum read count fusion gene 5

table

Create reads track Yes
Create report Yes
Create fusion gene table No
Create list of unmapped reads

Comments: Originates from:

i=	AM24_1_1 (paired, trimmed pairs)
XX.	S_lycopersicum_chromosomes.4.00 (Genome)
<b>⇒</b> :	S_lycopersicum_chromosomes.4.00 (Gene)
<b>⇒</b> :	S_lycopersicum_chromosomes.4.00 (mRNA)