

Lastal_AlignmentStat

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2018-09-04

#Genome Alignment Summary This report presents genome alignment stats for for **/Users/bhanson/Documents/Data/Sc**

The reference used for the genome alignment is:

/Users/bhanson/Documents/Data/Scripts/Scripts/Pipelines/Lastal_MinION_GeneticElement/Example/A

Summary stats for this alignment are:

Number of sequences aligned to reference: 19,199

The number of aligned bases, insertions, and deletions is: 152,741,368

- This sums the number of matched and mismatched bases, plus detected insertions and deletions

The number of insertions is: 9,212,706

- As percent: 6.031572

The number of deletions is: 8,953,274

- As percent: 5.861722

The number of mismatches is: 9,542,394

- As percent: 6.2474198

#Overall Accuracy rate The overall accuracy is: 81.8592861%

#Match/Mismatch Profile

##**Table 1** - Match/Mismatch Matrix

| | Ref_A | Ref_C | Ref_G | Ref_T |
|--------|------------|------------|------------|------------|
| Read_A | 30,774,914 | 808,176.5 | 806,004 | 781,628.7 |
| Read_C | 783,236.5 | 31,757,030 | 811,113.5 | 779,305.1 |
| Read_G | 779,514.3 | 812,533 | 31,768,343 | 782,945.6 |
| Read_T | 783,109.8 | 806,212.6 | 808,614.8 | 30,733,162 |

##**Table 2** - Match/Mismatch Percent Matrix | | Ref_A | Ref_C | Ref_G | Ref_T | :-----|:-----
 ---|:-----|:-----|:-----| Read_A | 92.9172534 | 2.3641984 | 2.3571451 | 2.3630551 Read_C
 | 2.3647891 | 92.9004053 | 2.372088 | 2.3560304 Read_G | 2.3535509 | 2.3769429 | 92.9059866 | 2.3670364
 Read_T | 2.3644066 | 2.3584535 | 2.3647803 | 92.913878

##Transitions vs transversions

Probability a mismatch is a transition: 2.356295

Probability a mismatch is a transversion: 2.3671621