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Name

Reads

Mapped

Unique

Unique 0mm

Unique 1mm

Unique 2mm

Unique 3+mm

Unique w/ Indel

Non-Unique

Non-Unique 0mm

Non-Unique 1mm

Non-Unique 2mm

Non-Unique 3+mm

Non-Unique w/ Indel

No-Match

Key for the statistics tables:

Post-Filter = reads that passed the base-caller's quality filter

Failed = reads that failed the base-caller's quality filter

Unique = reads that mapped to a single position in the genome

Non-Unique = reads that mapped to more than one position

No-Match = reads that did not map anywhere

0mm = zero mismatches (perfect match to the genome)

1mm = one mismatching base

2mm = two mismatching bases

3+mm = three or more mismatching bases

w/Indel = alignment contains an insertion or deletion