Mapping Reads to Reference

331126 + 0 in total (QC−passed reads + QC−failed reads)

0 + 0 duplicates

328217 + 0 mapped (99.12%:−nan%)

331126 + 0 paired in sequencing

165563 + 0 read1

165563 + 0 read2

325972 + 0 properly paired (98.44%:−nan%)

326568 + 0 with itself and mate mapped

1649 + 0 singletons (0.50%:−nan%)

0 + 0 with mate mapped to a different chr

0 + 0 with mate mapped to a different chr (mapQ>=5)