

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 19:35:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174003.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR10174003 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174003_1.fastq.gz SRR10174003_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 19:35:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174003.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,577,328
Mapped reads	4,457,508 / 97.38%
Unmapped reads	119,820 / 2.62%
Mapped paired reads	4,457,508 / 97.38%
Mapped reads, first in pair	2,231,278 / 48.75%
Mapped reads, second in pair	2,226,230 / 48.64%
Mapped reads, both in pair	4,380,228 / 95.69%
Mapped reads, singletons	77,280 / 1.69%
Secondary alignments	0
Supplementary alignments	447,298 / 9.77%
Read min/max/mean length	30 / 133 / 128.03
Duplicated reads (estimated)	3,405,144 / 74.39%
Duplication rate	63.78%
Clipped reads	1,820,885 / 39.78%

2.2. ACGT Content

Number/percentage of A's	158,874,913 / 30.22%
Number/percentage of C's	102,205,691 / 19.44%
Number/percentage of T's	158,507,603 / 30.15%
Number/percentage of G's	106,075,204 / 20.18%
Number/percentage of N's	5,737 / 0%

GC Percentage	39.62%
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2.3. Coverage

Mean	0.1699
Standard Deviation	2.5648

2.4. Mapping Quality

Mean Mapping Quality	52.95
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2.5. Insert size

Mean	1,063,770.24
Standard Deviation	9,682,241.19
P25/Median/P75	144 / 202 / 290

2.6. Mismatches and indels

General error rate	1.08%
Mismatches	5,517,940
Insertions	61,989
Mapped reads with at least one insertion	1.34%
Deletions	121,881
Mapped reads with at least one deletion	2.66%
Homopolymer indels	42.77%

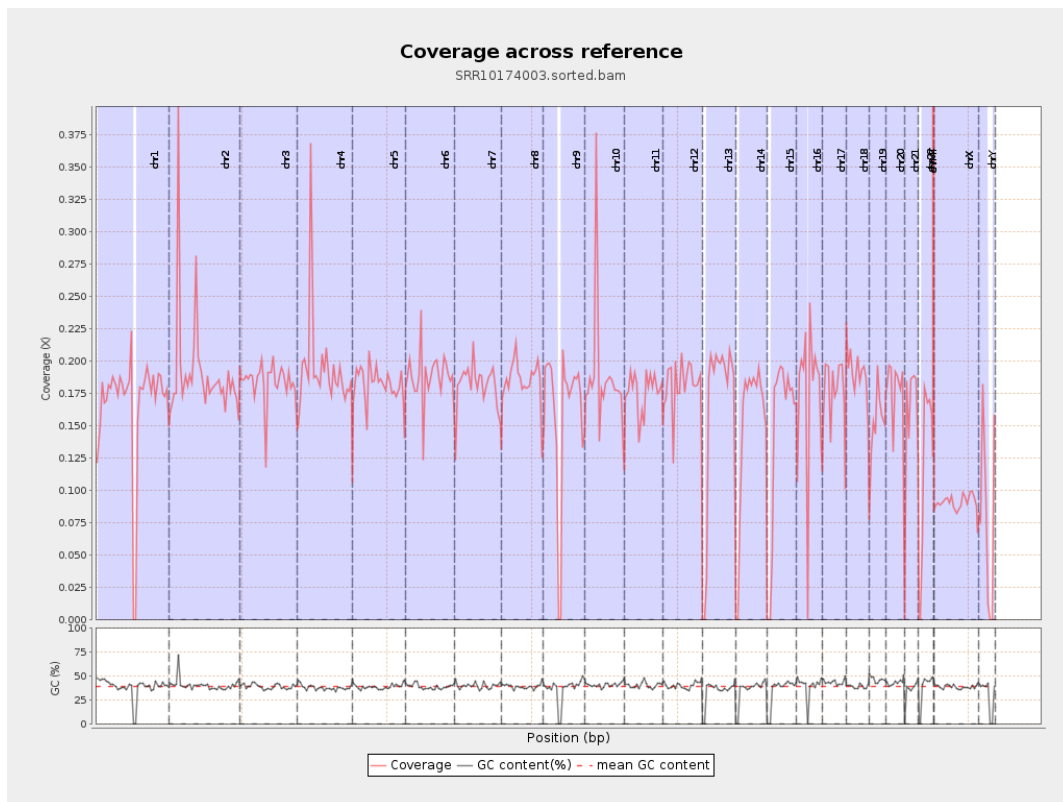
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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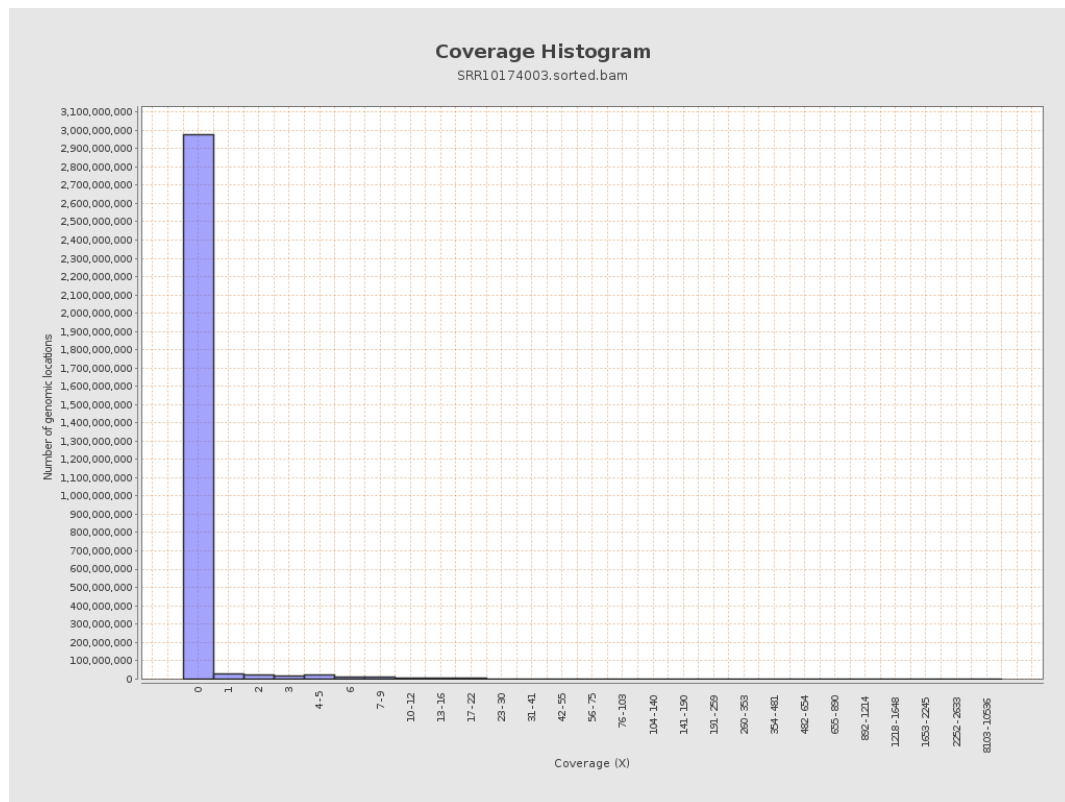
		bases	coverage	deviation
chr1	249250621	41555922	0.1667	1.8178
chr2	243199373	46334705	0.1905	7.4266
chr3	198022430	36400314	0.1838	1.2158
chr4	191154276	36841104	0.1927	1.8837
chr5	180915260	32881256	0.1817	1.2104
chr6	171115067	32111353	0.1877	1.401
chr7	159138663	29025007	0.1824	1.6384
chr8	146364022	27043764	0.1848	2.2555
chr9	141213431	22649115	0.1604	1.6734
chr10	135534747	25327811	0.1869	2.1239
chr11	135006516	23713277	0.1756	1.2189
chr12	133851895	24236089	0.1811	1.2115
chr13	115169878	18750046	0.1628	1.1568
chr14	107349540	16008982	0.1491	1.1031
chr15	102531392	14992106	0.1462	1.0644
chr16	90354753	15670935	0.1734	1.46
chr17	81195210	14197088	0.1749	1.3279
chr18	78077248	14926769	0.1912	2.5122
chr19	59128983	9108292	0.154	1.4226
chr20	63025520	11156735	0.177	1.269
chr21	48129895	7461993	0.155	1.5605
chr22	51304566	5940383	0.1158	1.0485
chrMT	16571	1073739	64.7963	49.3856
chrX	155270560	14094504	0.0908	0.8469

chrY	59373566	4473536	0.0753	1.4913
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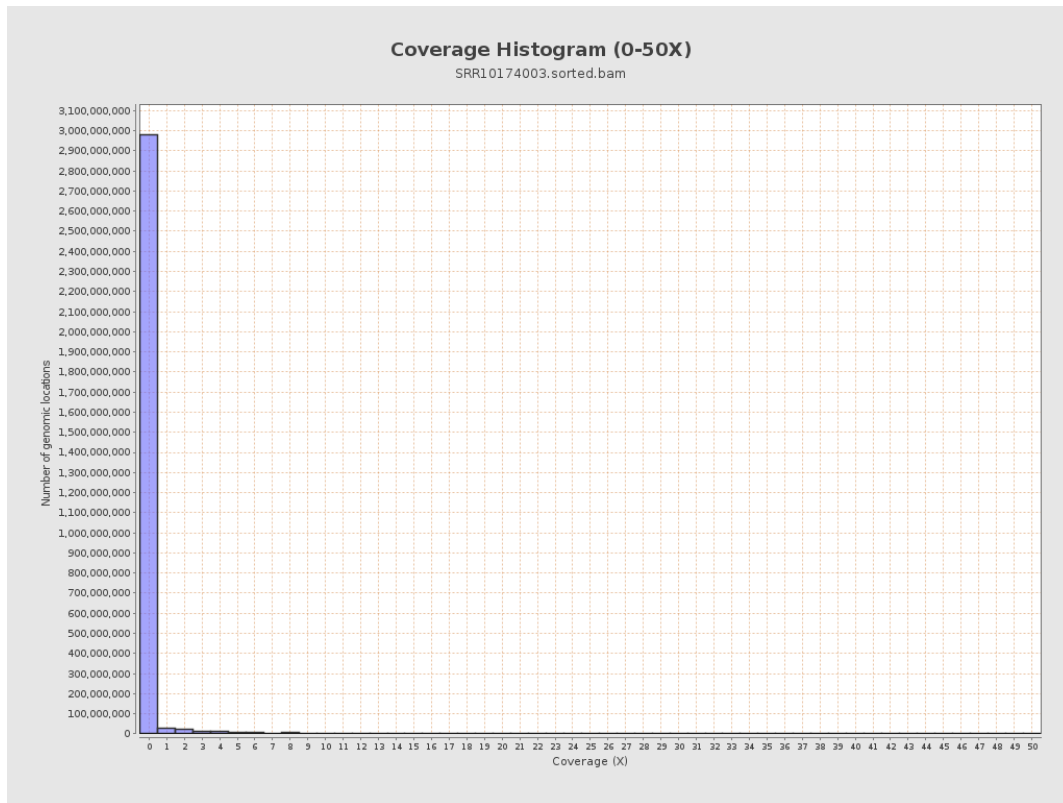
3. Results : Coverage across reference



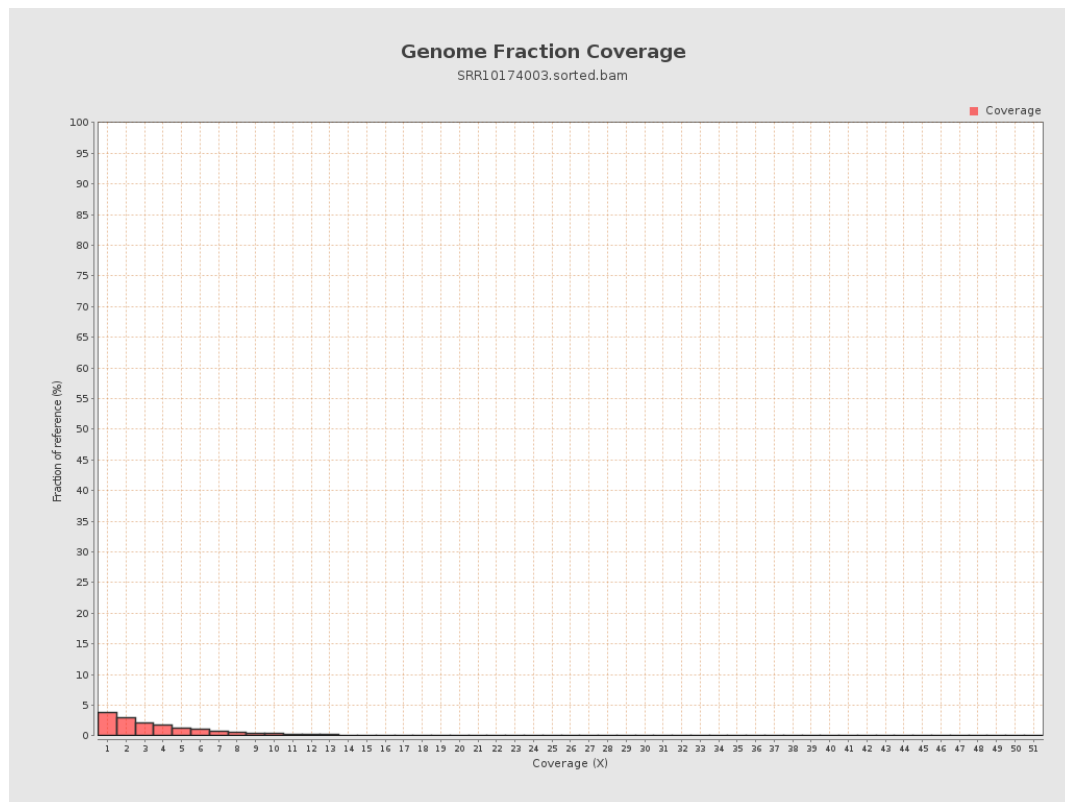
4. Results : Coverage Histogram



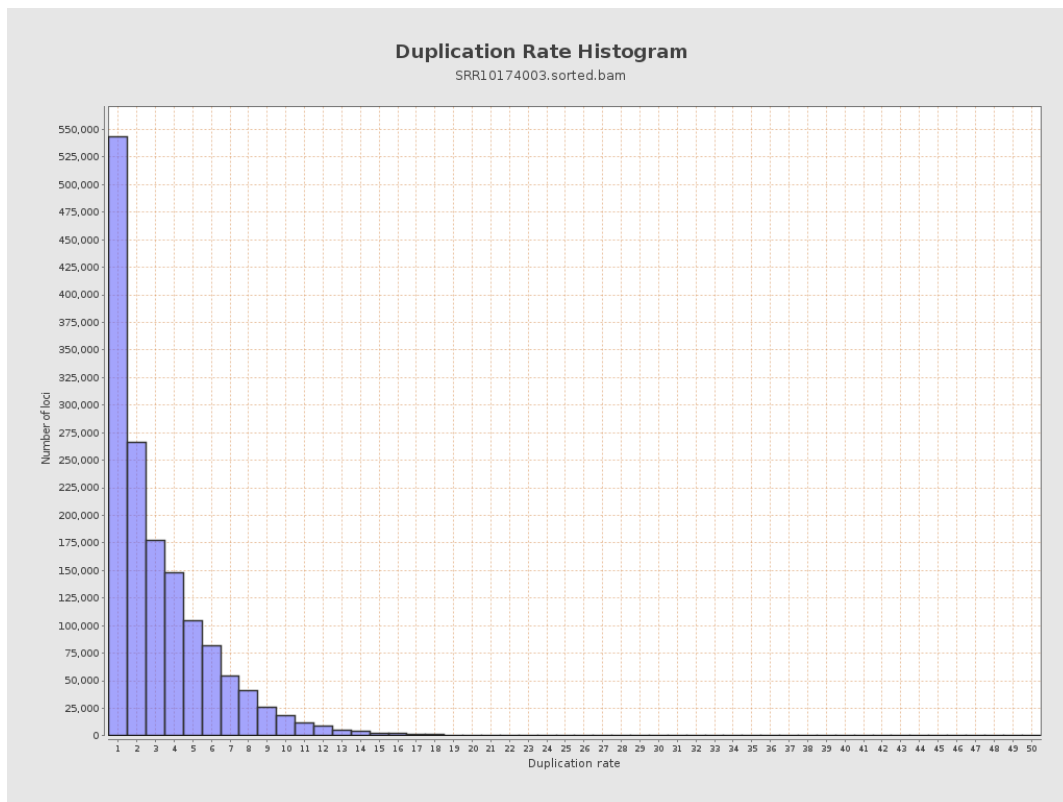
5. Results : Coverage Histogram (0-50X)



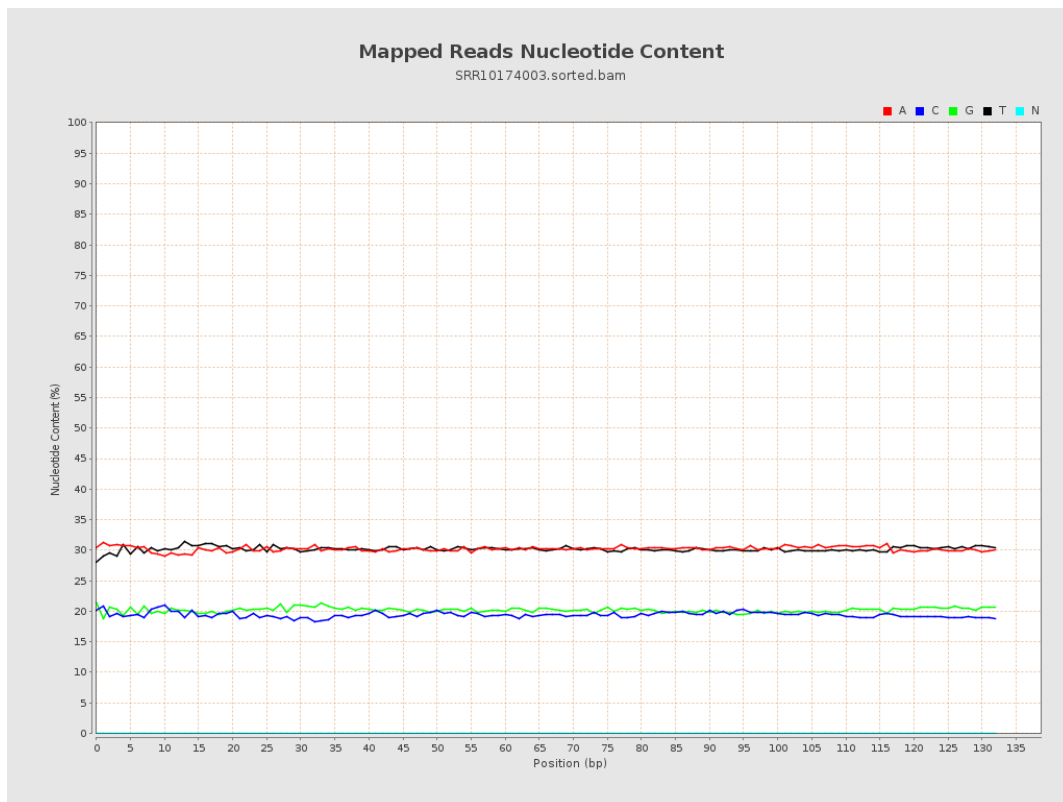
6. Results : Genome Fraction Coverage



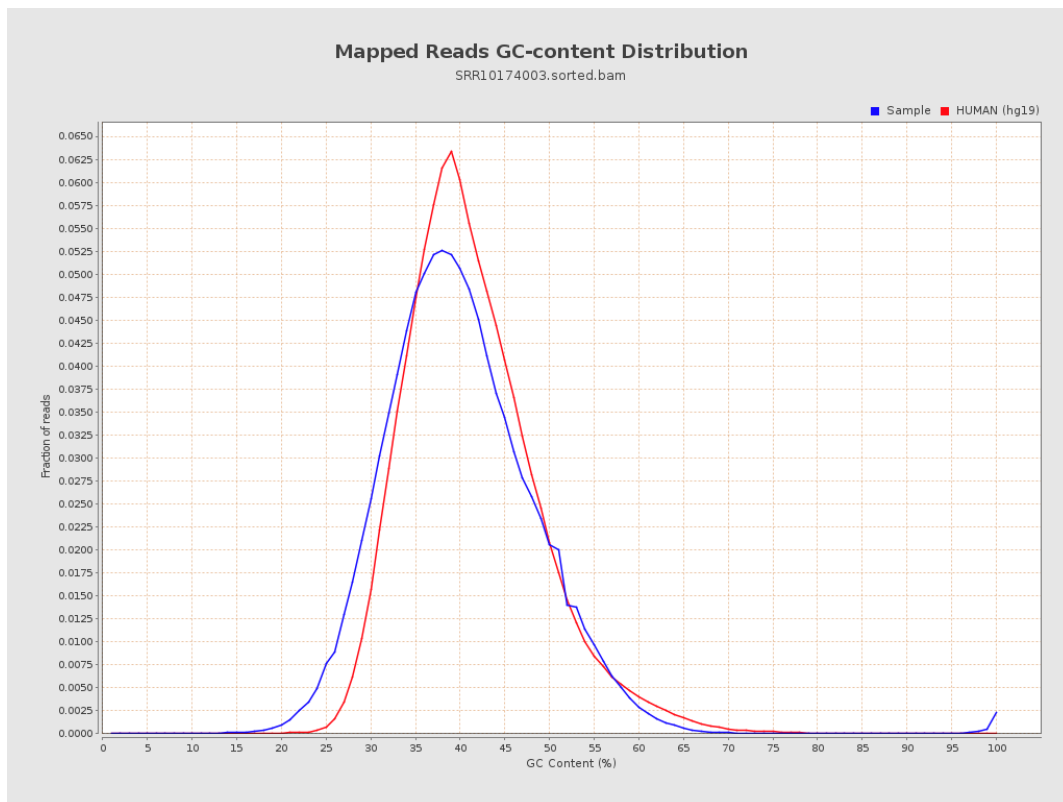
7. Results : Duplication Rate Histogram



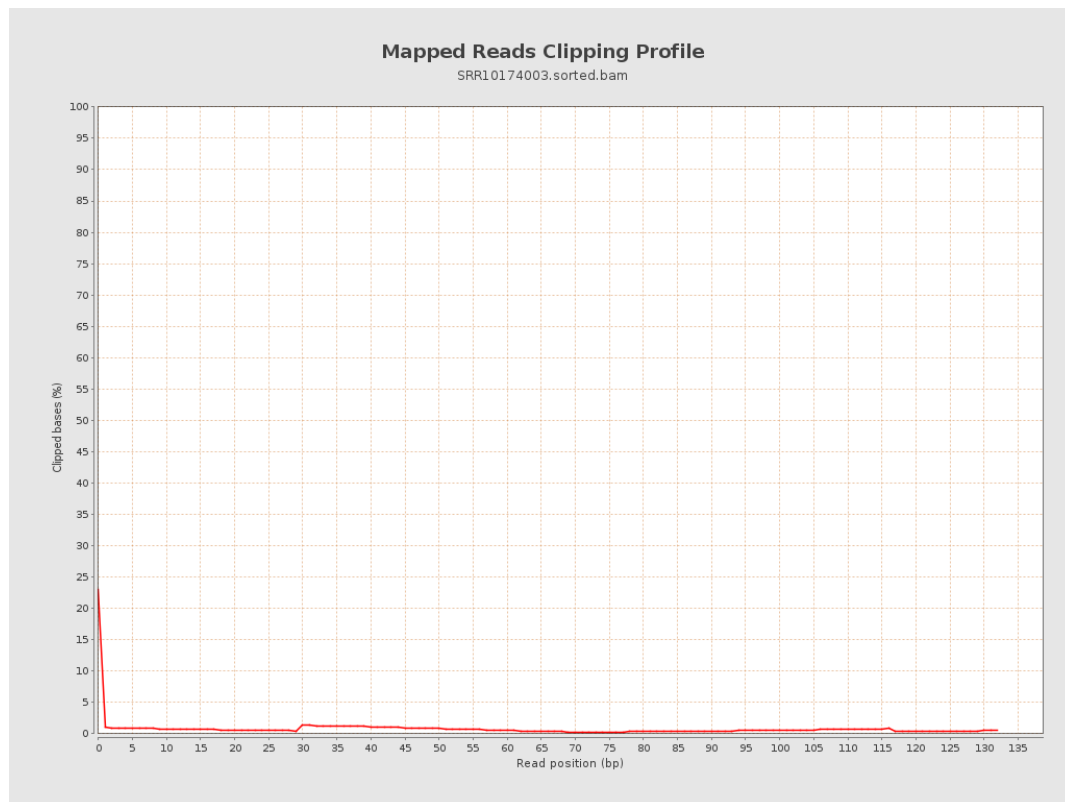
8. Results : Mapped Reads Nucleotide Content



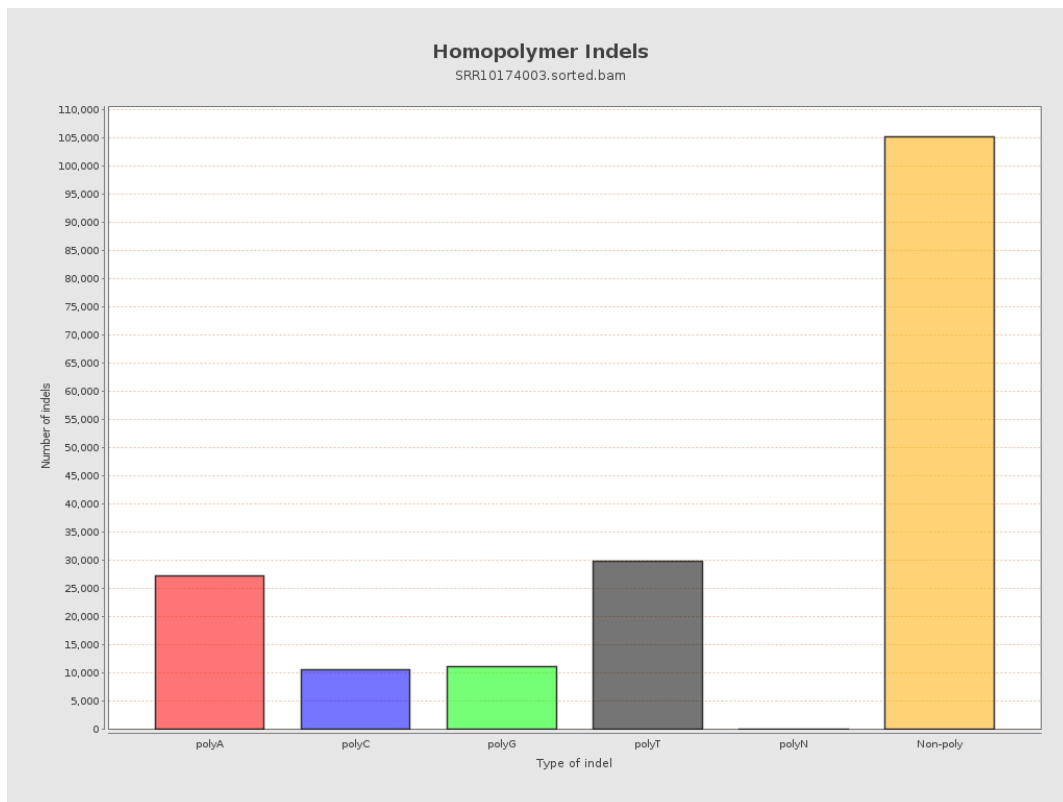
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



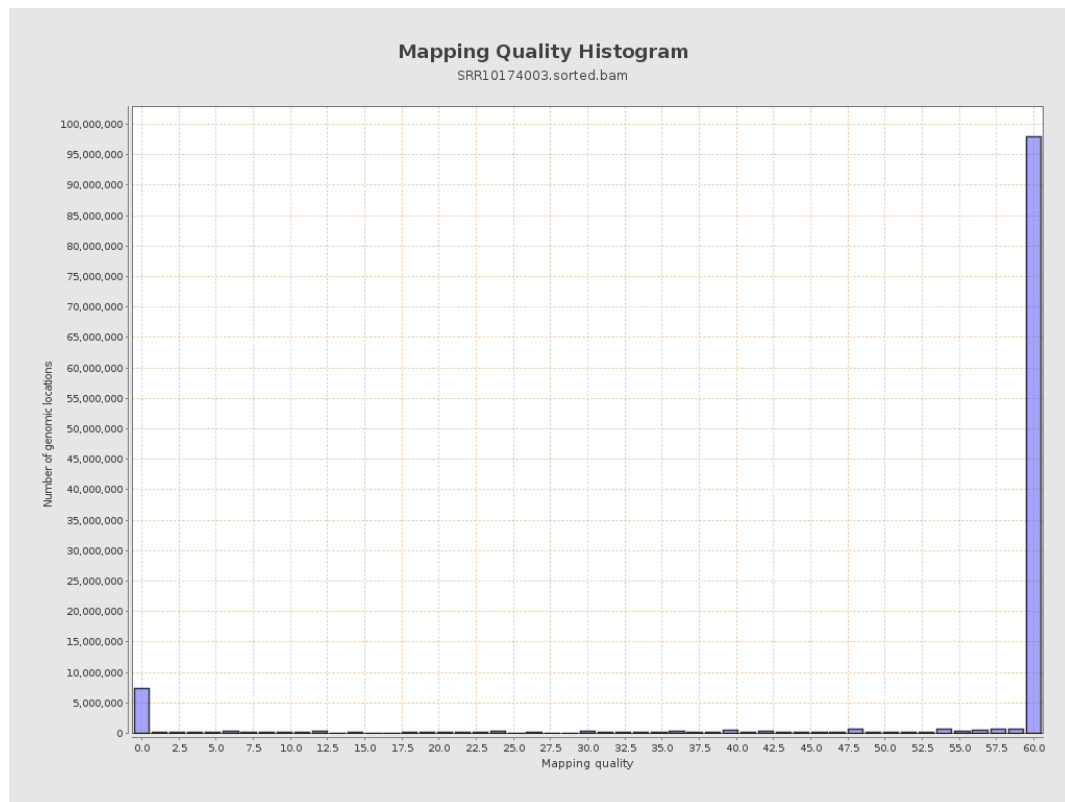
11. Results : Homopolymer Indels



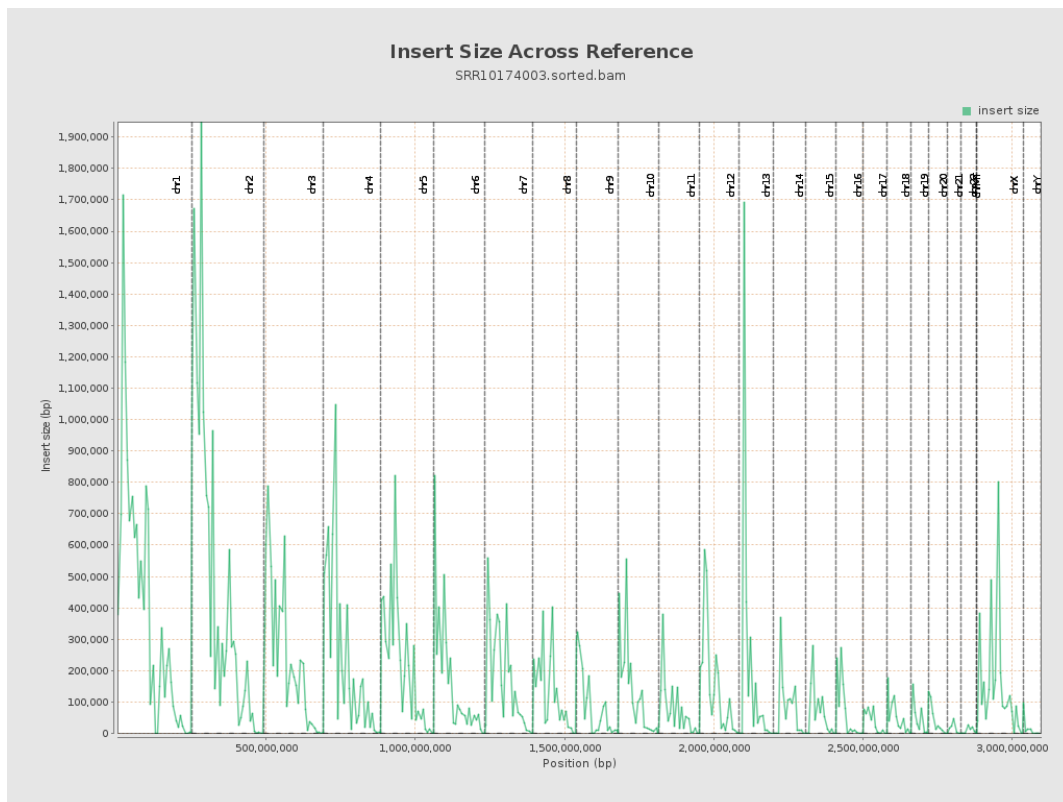
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

