

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/05 01:12:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174047.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_SRR10174047 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174047_1.fastq.gz SRR10174047_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Sep 05 01:12:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174047.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,310,928
Mapped reads	5,173,257 / 97.41%
Unmapped reads	137,671 / 2.59%
Mapped paired reads	5,173,257 / 97.41%
Mapped reads, first in pair	2,586,453 / 48.7%
Mapped reads, second in pair	2,586,804 / 48.71%
Mapped reads, both in pair	5,077,244 / 95.6%
Mapped reads, singletons	96,013 / 1.81%
Secondary alignments	0
Supplementary alignments	492,281 / 9.27%
Read min/max/mean length	30 / 133 / 128.08
Duplicated reads (estimated)	3,904,400 / 73.52%
Duplication rate	64.88%
Clipped reads	1,990,174 / 37.47%

2.2. ACGT Content

Number/percentage of A's	183,872,064 / 29.99%
Number/percentage of C's	120,550,002 / 19.66%
Number/percentage of T's	183,759,184 / 29.97%
Number/percentage of G's	124,965,346 / 20.38%
Number/percentage of N's	6,990 / 0%

GC Percentage	40.04%
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2.3. Coverage

Mean	0.1982
Standard Deviation	2.8478

2.4. Mapping Quality

Mean Mapping Quality	52.85
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2.5. Insert size

Mean	915,521.38
Standard Deviation	8,949,734.36
P25/Median/P75	147 / 203 / 289

2.6. Mismatches and indels

General error rate	1%
Mismatches	5,993,566
Insertions	61,278
Mapped reads with at least one insertion	1.15%
Deletions	130,177
Mapped reads with at least one deletion	2.45%
Homopolymer indels	43.27%

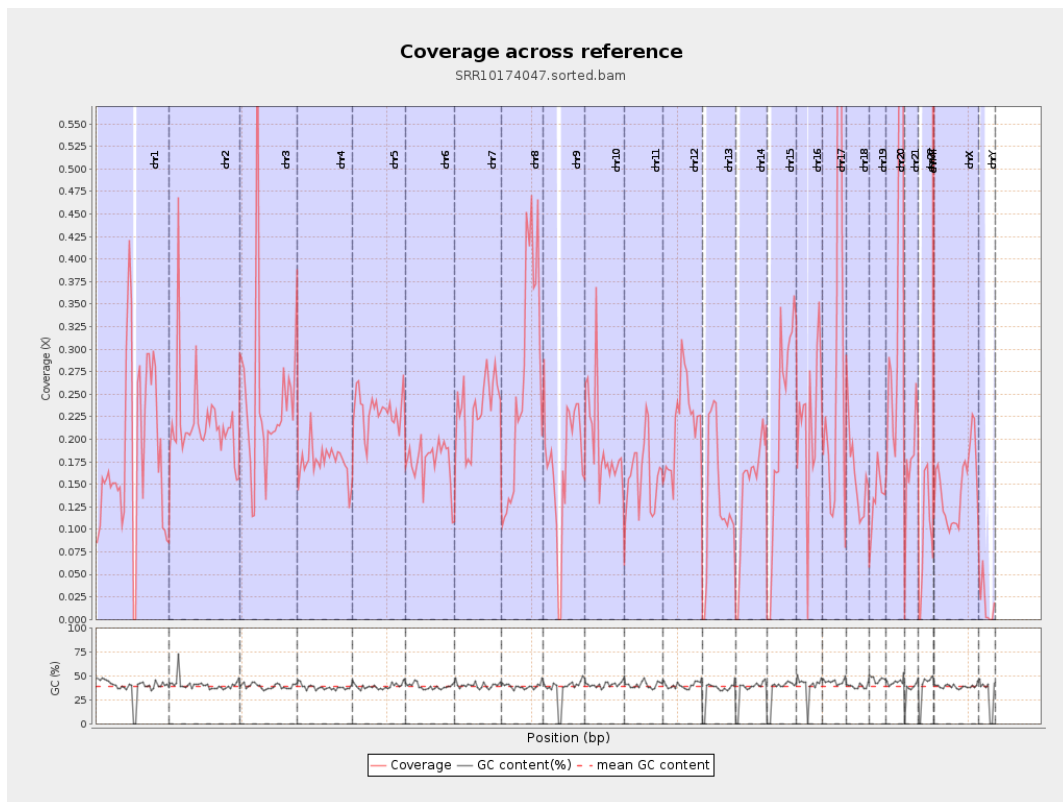
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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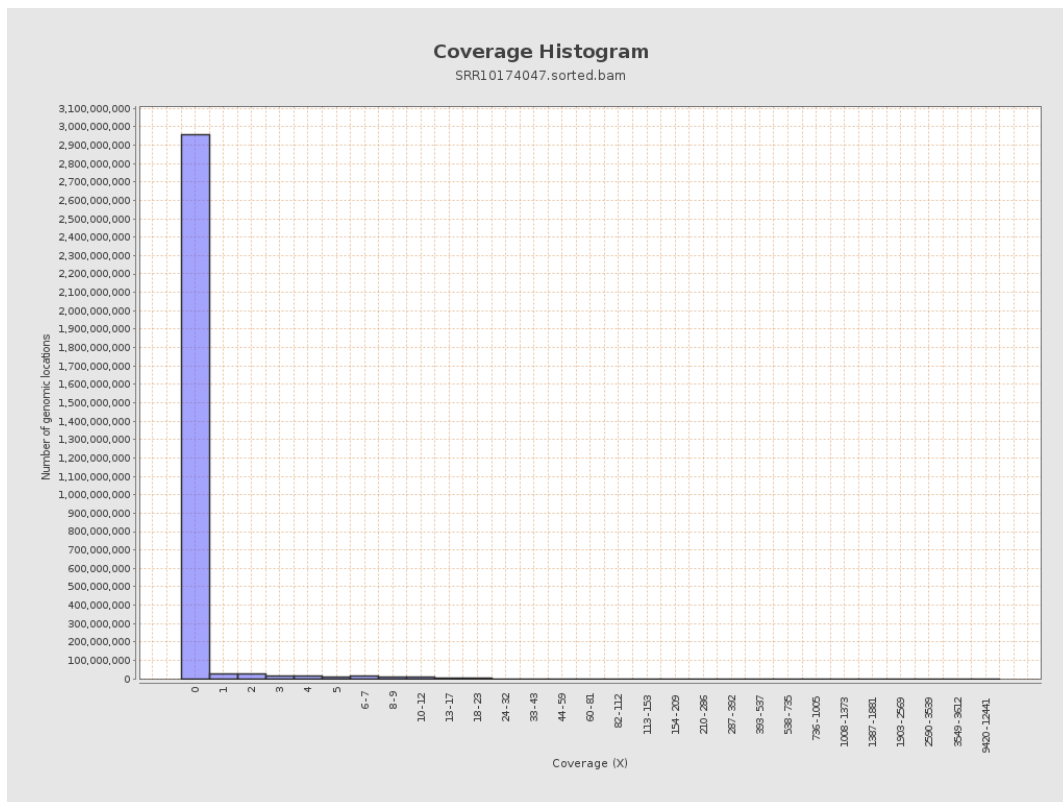
		bases	coverage	deviation
chr1	249250621	45390031	0.1821	1.785
chr2	243199373	52941330	0.2177	8.7141
chr3	198022430	47453518	0.2396	1.3724
chr4	191154276	33400115	0.1747	1.2883
chr5	180915260	41859419	0.2314	1.3219
chr6	171115067	29976383	0.1752	1.2952
chr7	159138663	37519938	0.2358	1.7688
chr8	146364022	38455416	0.2627	1.9214
chr9	141213431	23887041	0.1692	1.3882
chr10	135534747	26431301	0.195	2.3815
chr11	135006516	21579768	0.1598	1.1247
chr12	133851895	29046485	0.217	1.2799
chr13	115169878	15050688	0.1307	0.9981
chr14	107349540	15682477	0.1461	1.0516
chr15	102531392	22150875	0.216	1.2726
chr16	90354753	20119325	0.2227	1.6916
chr17	81195210	25063485	0.3087	1.694
chr18	78077248	12603445	0.1614	2.042
chr19	59128983	8098529	0.137	1.4177
chr20	63025520	28562921	0.4532	2.0615
chr21	48129895	8415263	0.1748	1.2113
chr22	51304566	4723607	0.0921	0.8085
chrMT	16571	1266265	76.4145	66.6483
chrX	155270560	22754660	0.1465	1.0504

chrY	59373566	1033154	0.0174	0.6007
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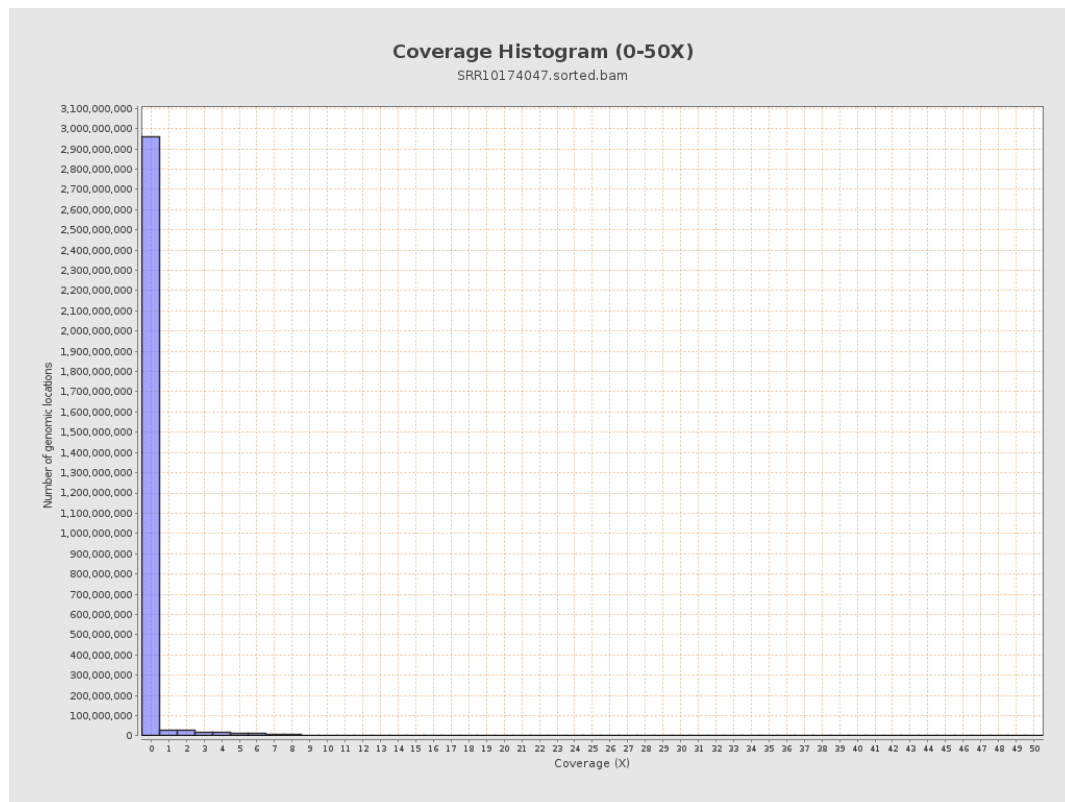
3. Results : Coverage across reference



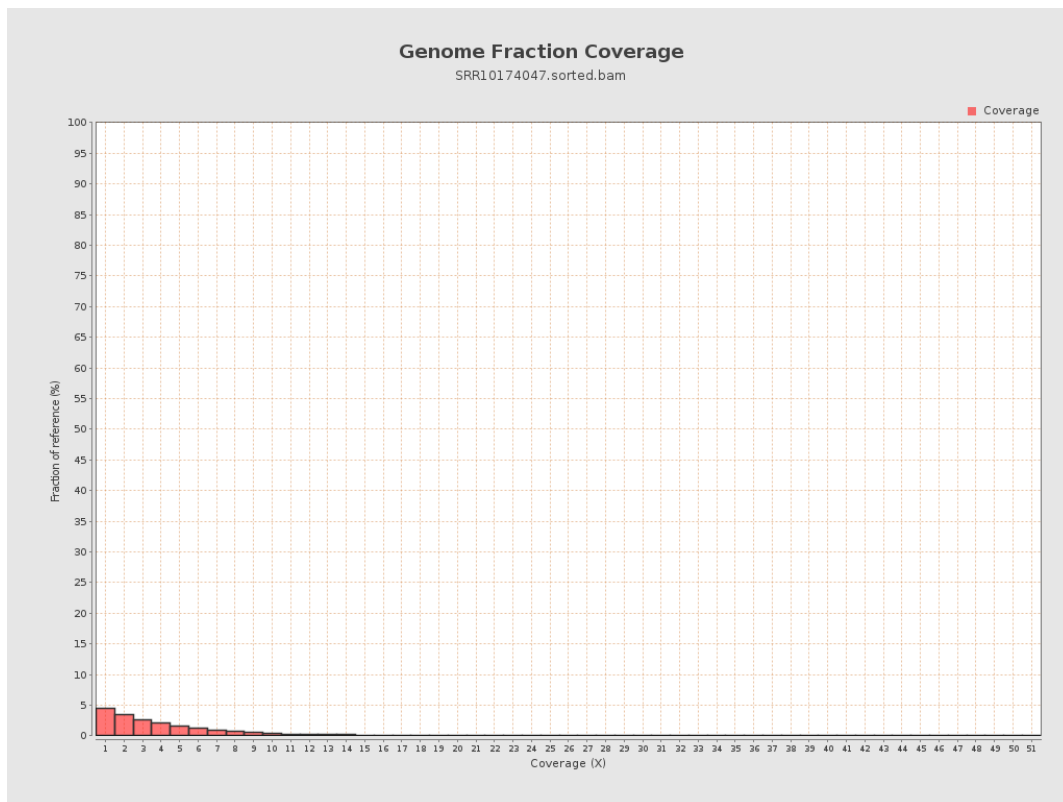
4. Results : Coverage Histogram



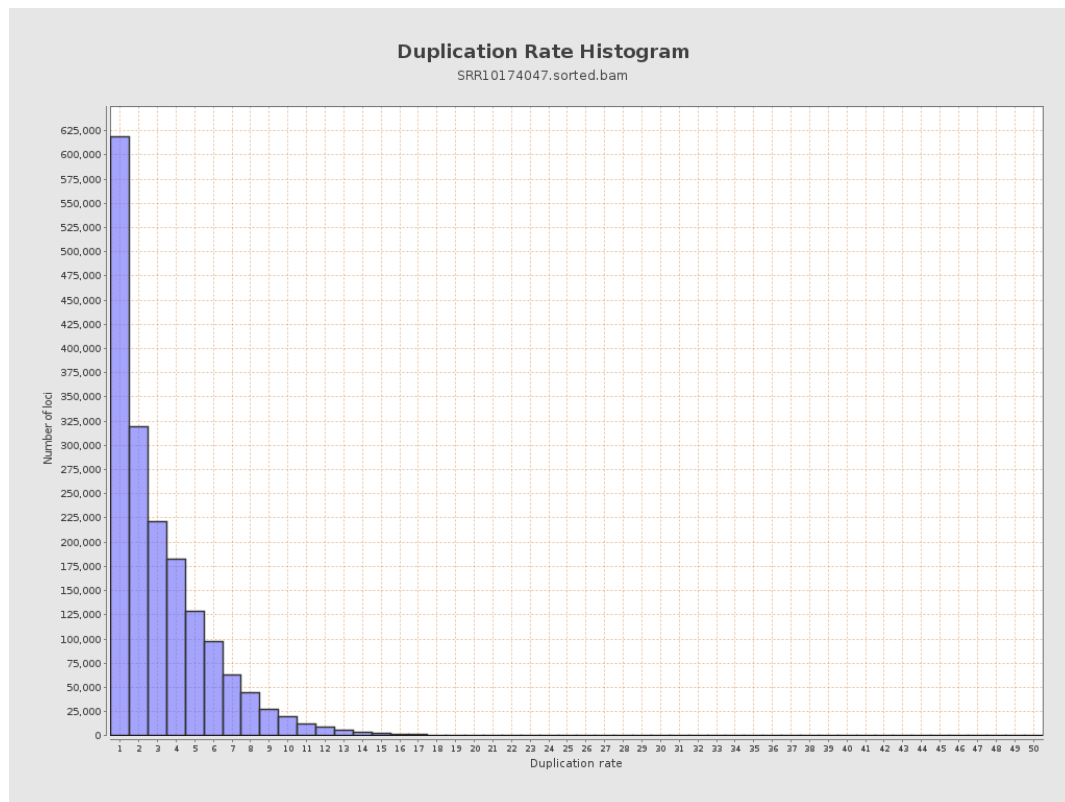
5. Results : Coverage Histogram (0-50X)



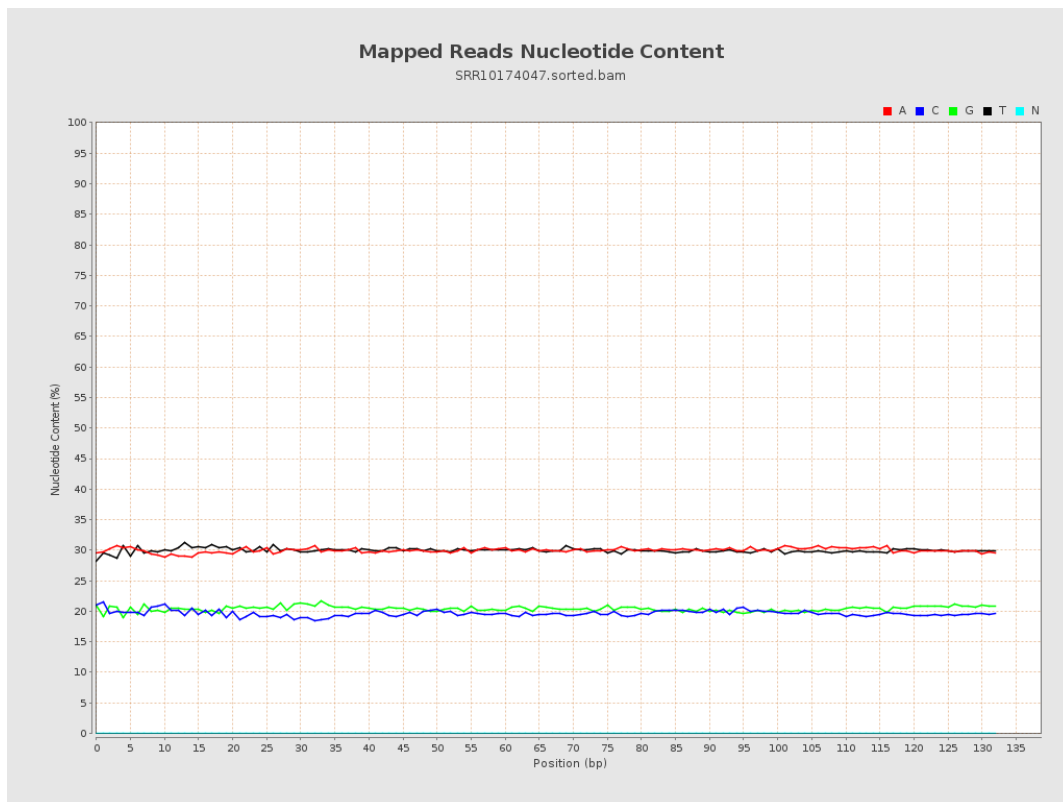
6. Results : Genome Fraction Coverage



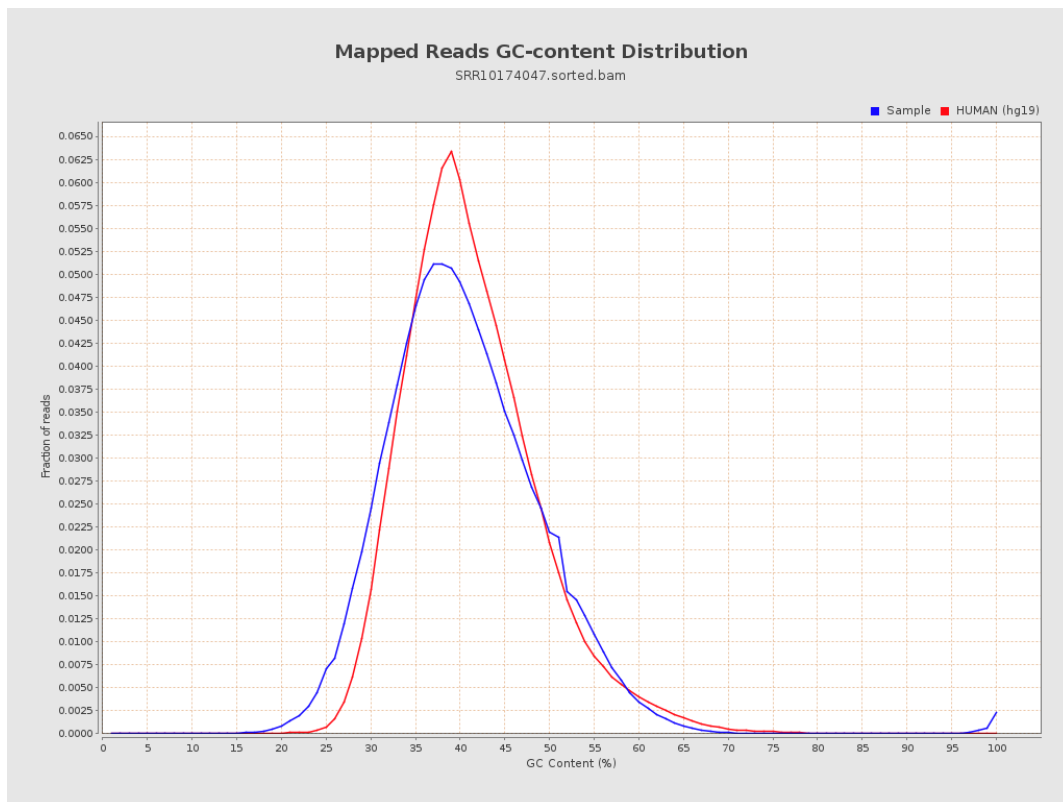
7. Results : Duplication Rate Histogram



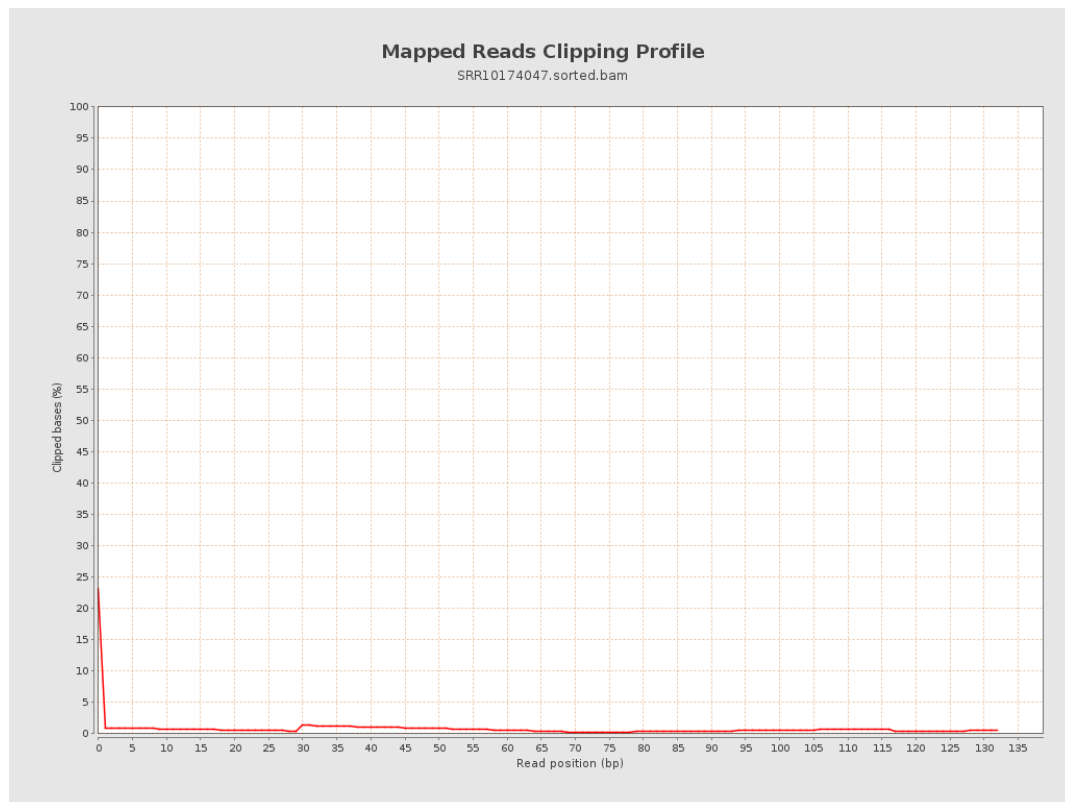
8. Results : Mapped Reads Nucleotide Content



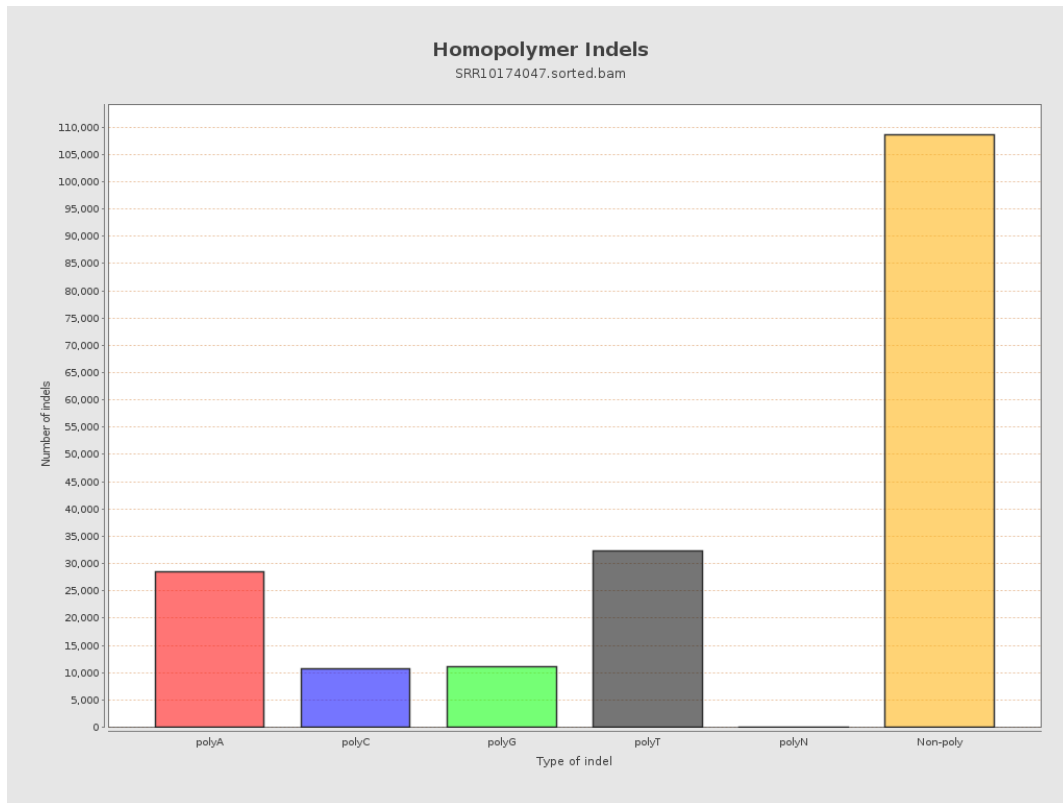
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



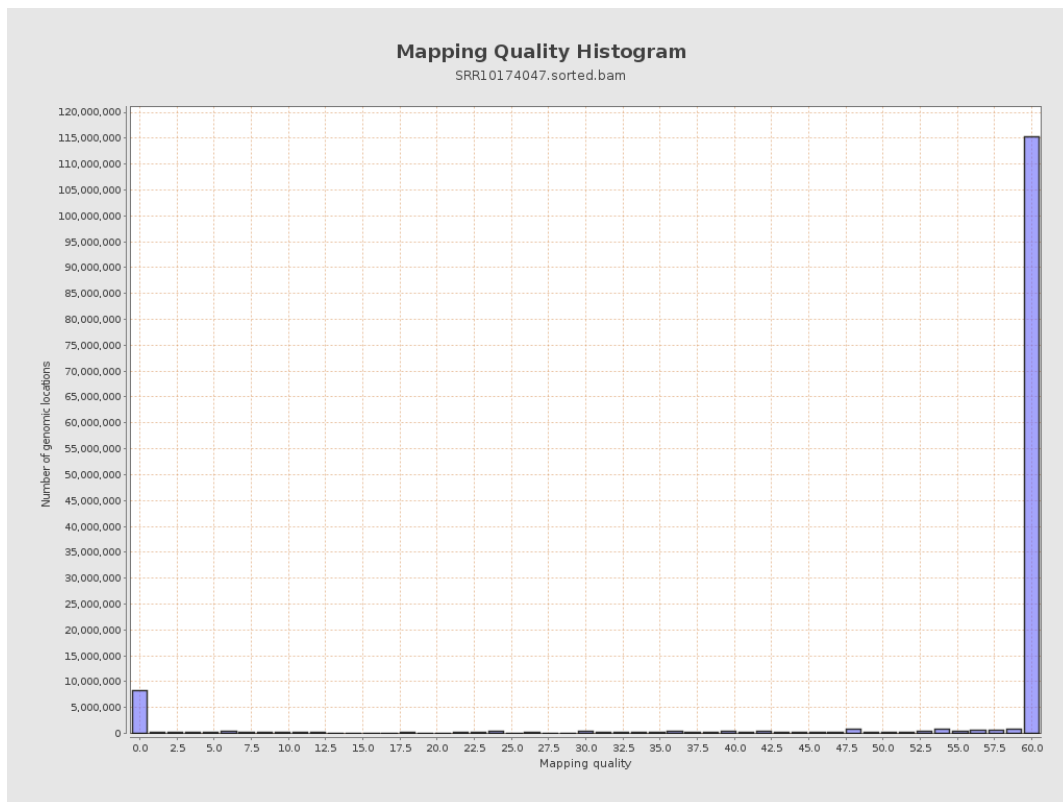
11. Results : Homopolymer Indels



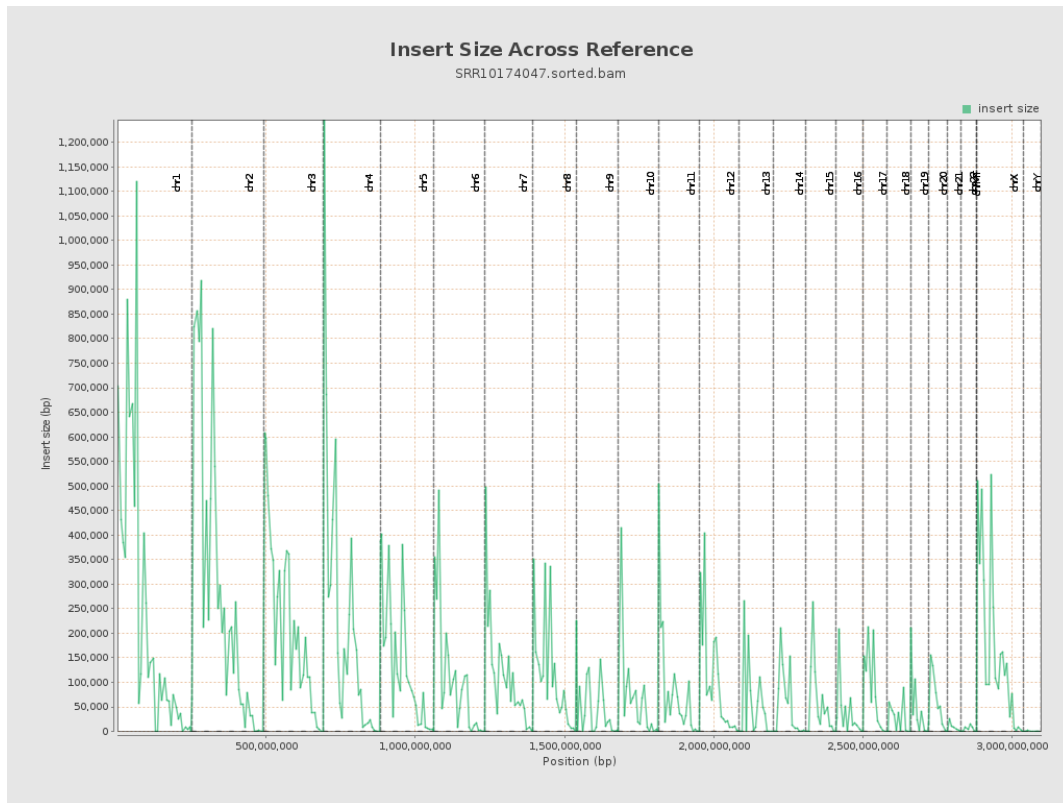
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

