

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/05 01:30:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174050.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_SRR10174050 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174050_1.fastq.gz SRR10174050_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Sep 05 01:30:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174050.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,591,860
Mapped reads	2,532,914 / 97.73%
Unmapped reads	58,946 / 2.27%
Mapped paired reads	2,532,914 / 97.73%
Mapped reads, first in pair	1,267,586 / 48.91%
Mapped reads, second in pair	1,265,328 / 48.82%
Mapped reads, both in pair	2,494,450 / 96.24%
Mapped reads, singletons	38,464 / 1.48%
Secondary alignments	0
Supplementary alignments	244,634 / 9.44%
Read min/max/mean length	30 / 133 / 128.01
Duplicated reads (estimated)	1,939,614 / 74.83%
Duplication rate	64.37%
Clipped reads	974,824 / 37.61%

2.2. ACGT Content

Number/percentage of A's	90,177,355 / 30.04%
Number/percentage of C's	59,098,031 / 19.68%
Number/percentage of T's	89,899,869 / 29.94%
Number/percentage of G's	61,054,482 / 20.34%
Number/percentage of N's	3,562 / 0%

GC Percentage	40.02%
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2.3. Coverage

Mean	0.097
Standard Deviation	1.5515

2.4. Mapping Quality

Mean Mapping Quality	52.68
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2.5. Insert size

Mean	930,367.68
Standard Deviation	9,121,437.98
P25/Median/P75	146 / 203 / 292

2.6. Mismatches and indels

General error rate	1.04%
Mismatches	3,045,562
Insertions	30,476
Mapped reads with at least one insertion	1.17%
Deletions	67,107
Mapped reads with at least one deletion	2.58%
Homopolymer indels	43.46%

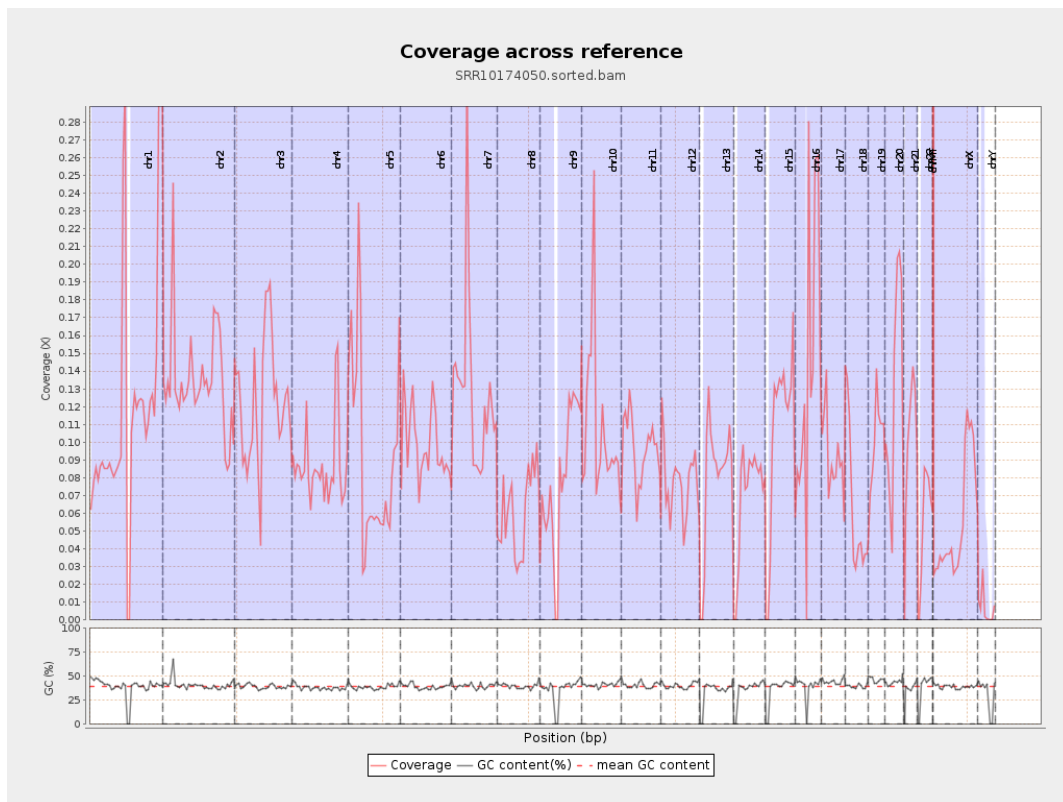
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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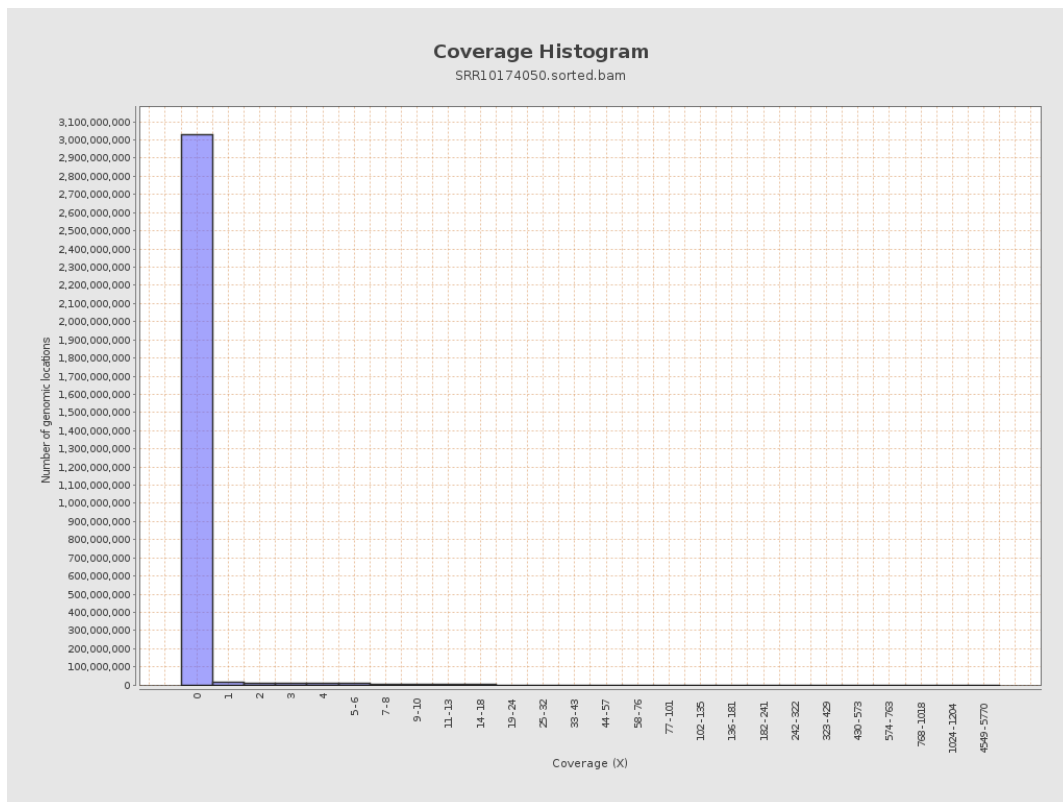
		bases	coverage	deviation
chr1	249250621	30257255	0.1214	1.4205
chr2	243199373	32767281	0.1347	4.129
chr3	198022430	24157878	0.122	1.0001
chr4	191154276	16639116	0.087	0.8893
chr5	180915260	16828754	0.093	0.8575
chr6	171115067	16980842	0.0992	0.9207
chr7	159138663	20279207	0.1274	1.5029
chr8	146364022	8899492	0.0608	0.8
chr9	141213431	11246366	0.0796	0.9365
chr10	135534747	14412396	0.1063	1.552
chr11	135006516	13004532	0.0963	0.8783
chr12	133851895	10524059	0.0786	0.8037
chr13	115169878	9193541	0.0798	0.8014
chr14	107349540	7517842	0.07	0.7491
chr15	102531392	10679949	0.1042	0.9097
chr16	90354753	12562019	0.139	1.4389
chr17	81195210	7561044	0.0931	0.9013
chr18	78077248	4867072	0.0623	1.1941
chr19	59128983	5949633	0.1006	1.3752
chr20	63025520	8230535	0.1306	1.0034
chr21	48129895	4772039	0.0991	0.9042
chr22	51304566	2774719	0.0541	0.6303
chrMT	16571	1375138	82.9846	66.78
chrX	155270560	8522418	0.0549	0.6561

chrY	59373566	399461	0.0067	0.3088
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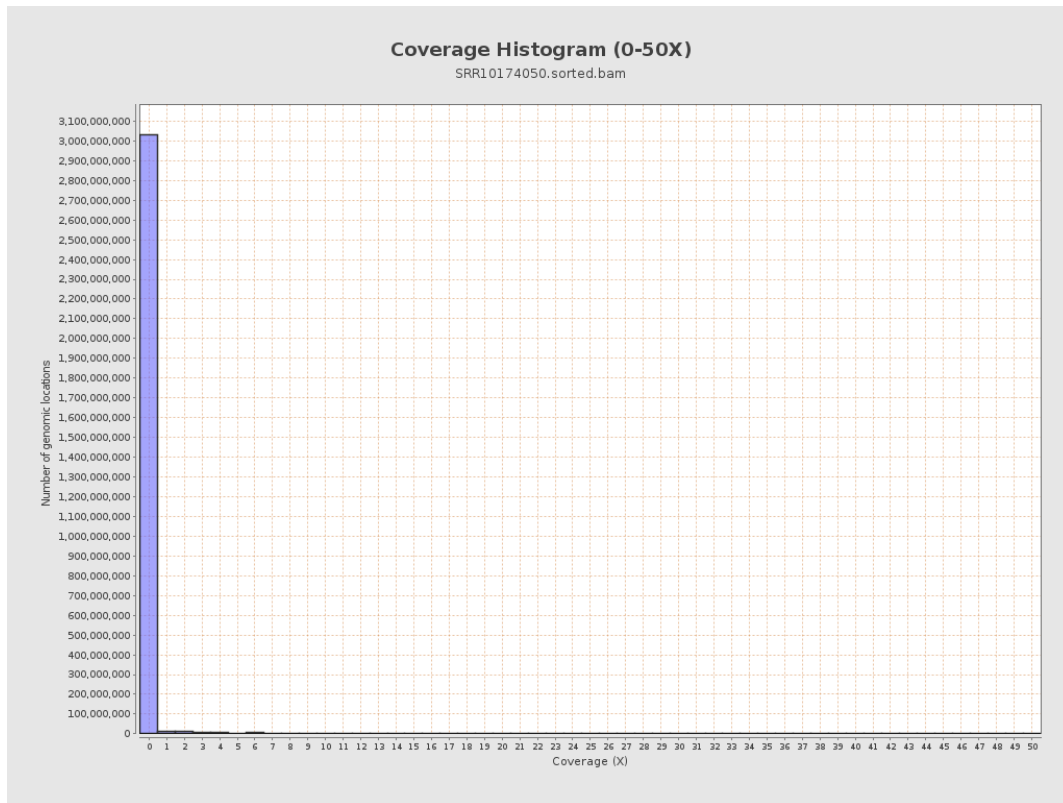
3. Results : Coverage across reference



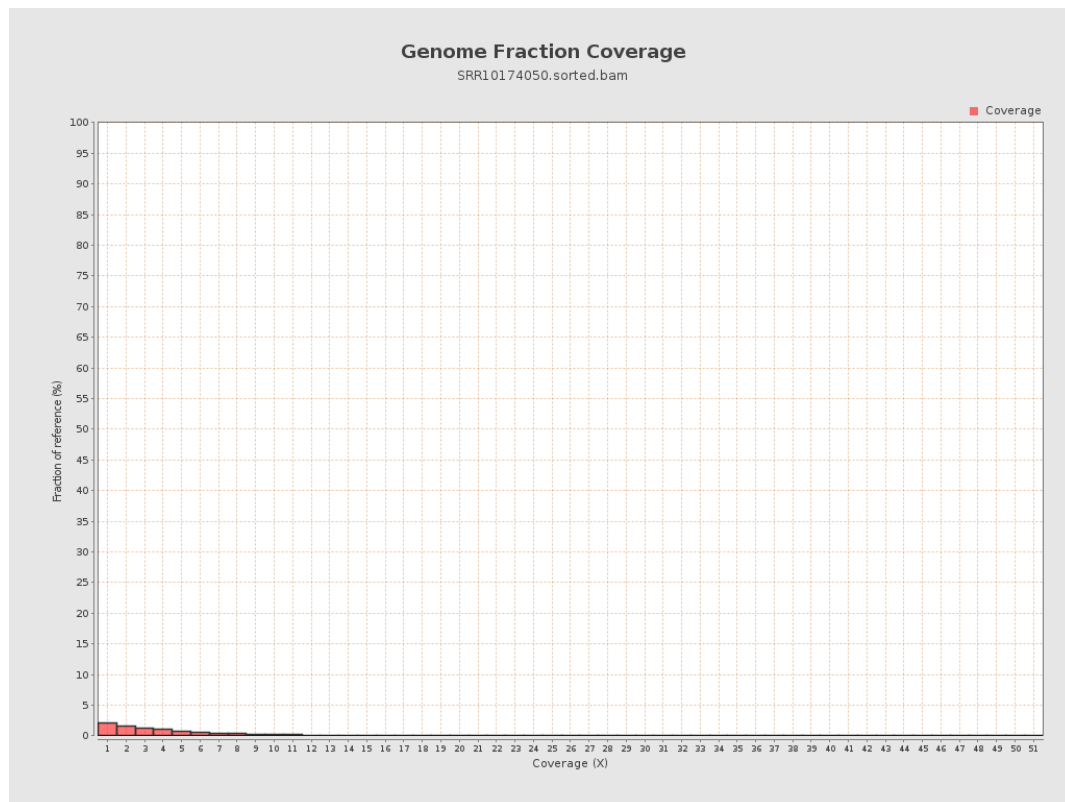
4. Results : Coverage Histogram



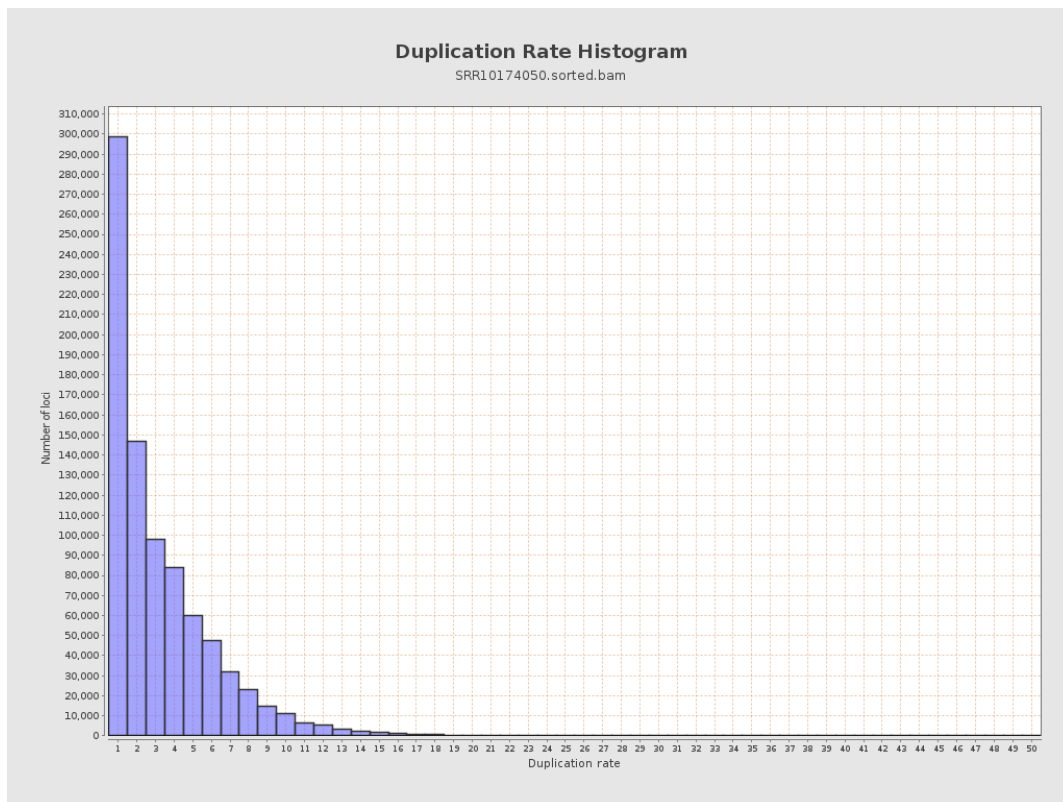
5. Results : Coverage Histogram (0-50X)



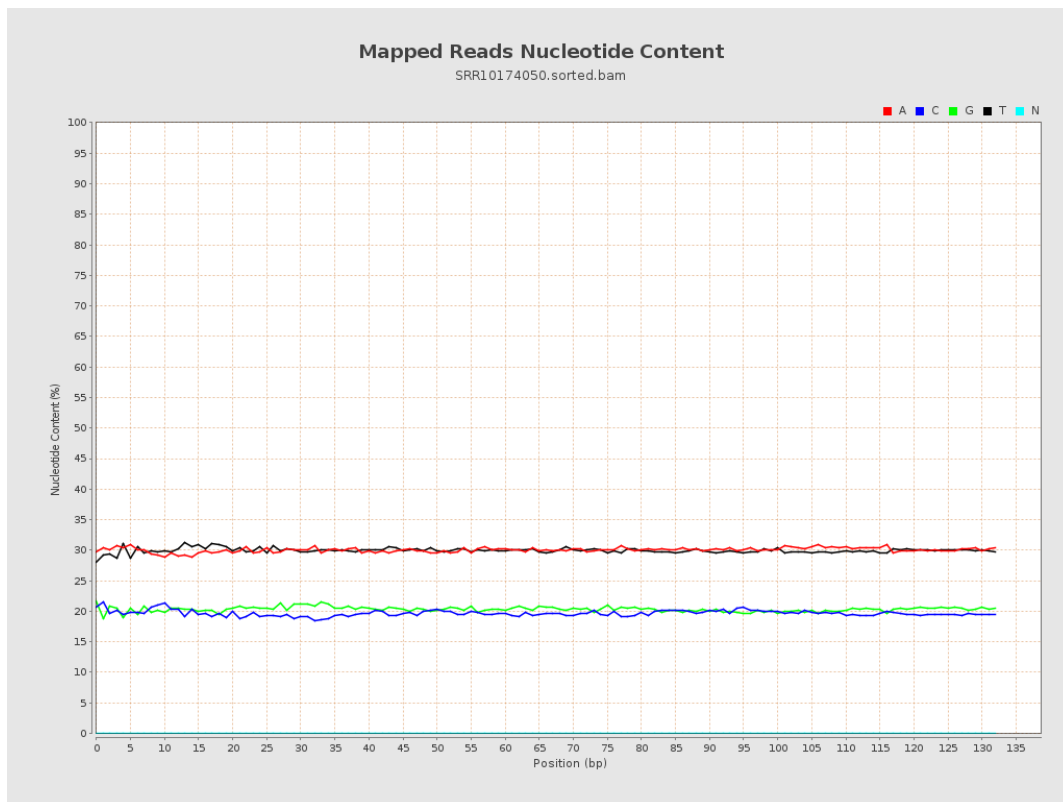
6. Results : Genome Fraction Coverage



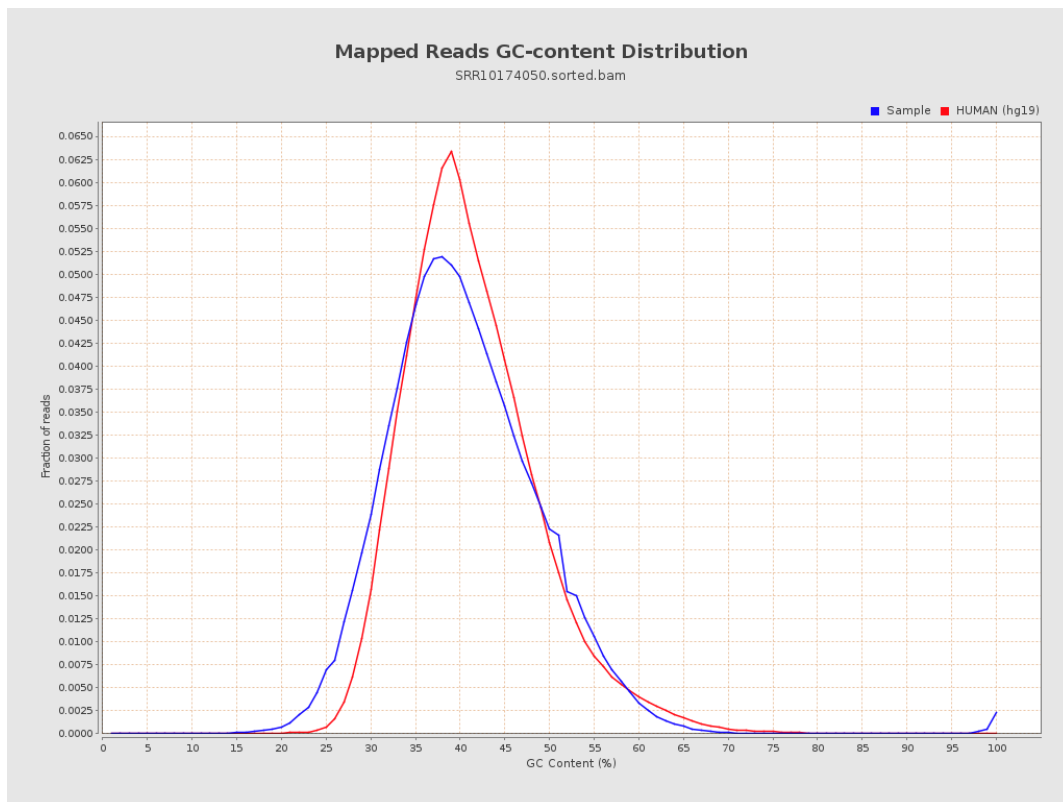
7. Results : Duplication Rate Histogram



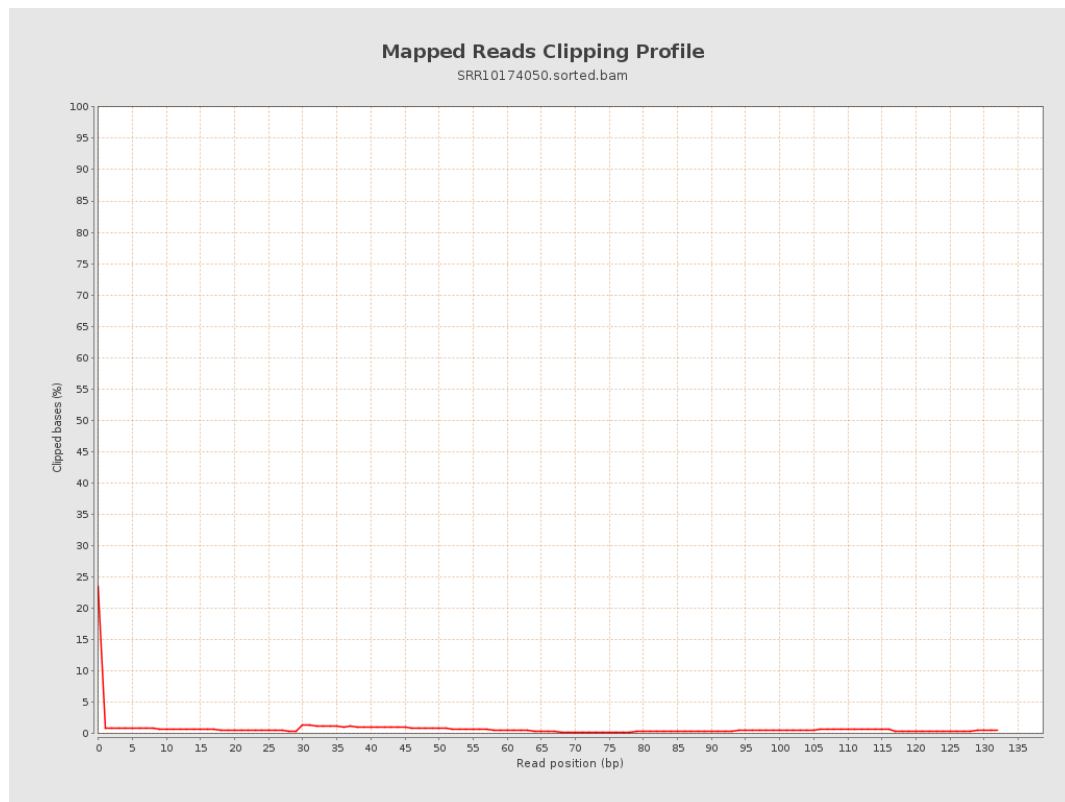
8. Results : Mapped Reads Nucleotide Content



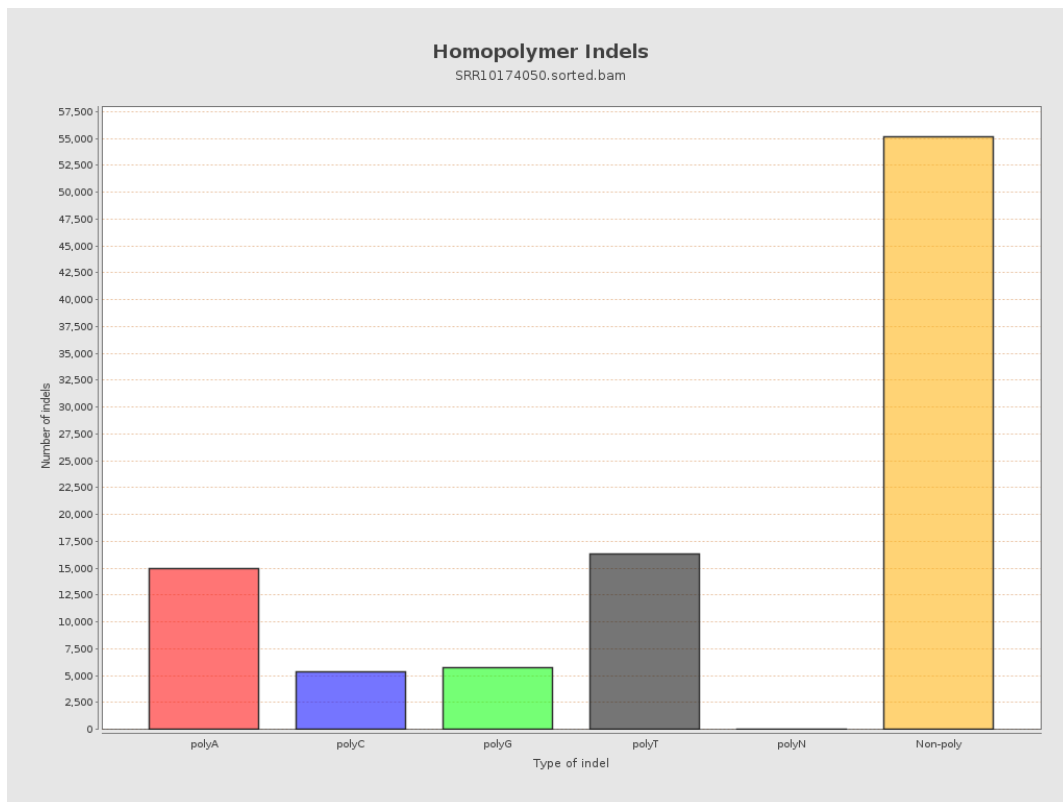
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



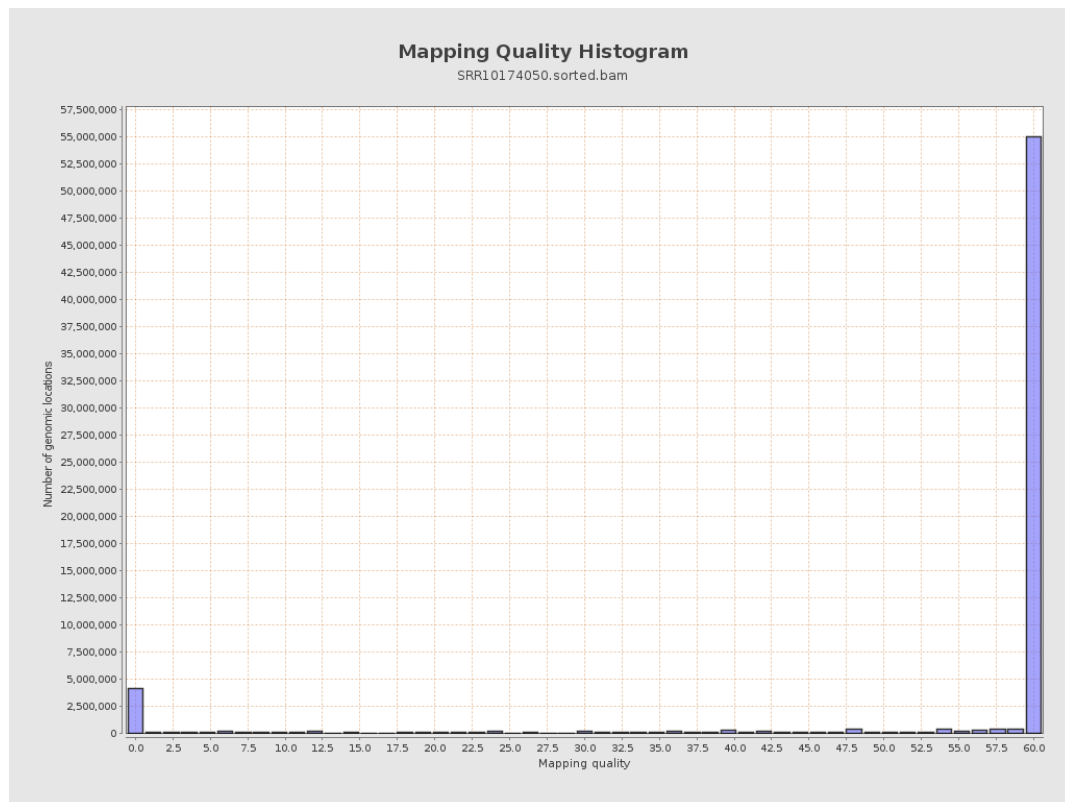
11. Results : Homopolymer Indels



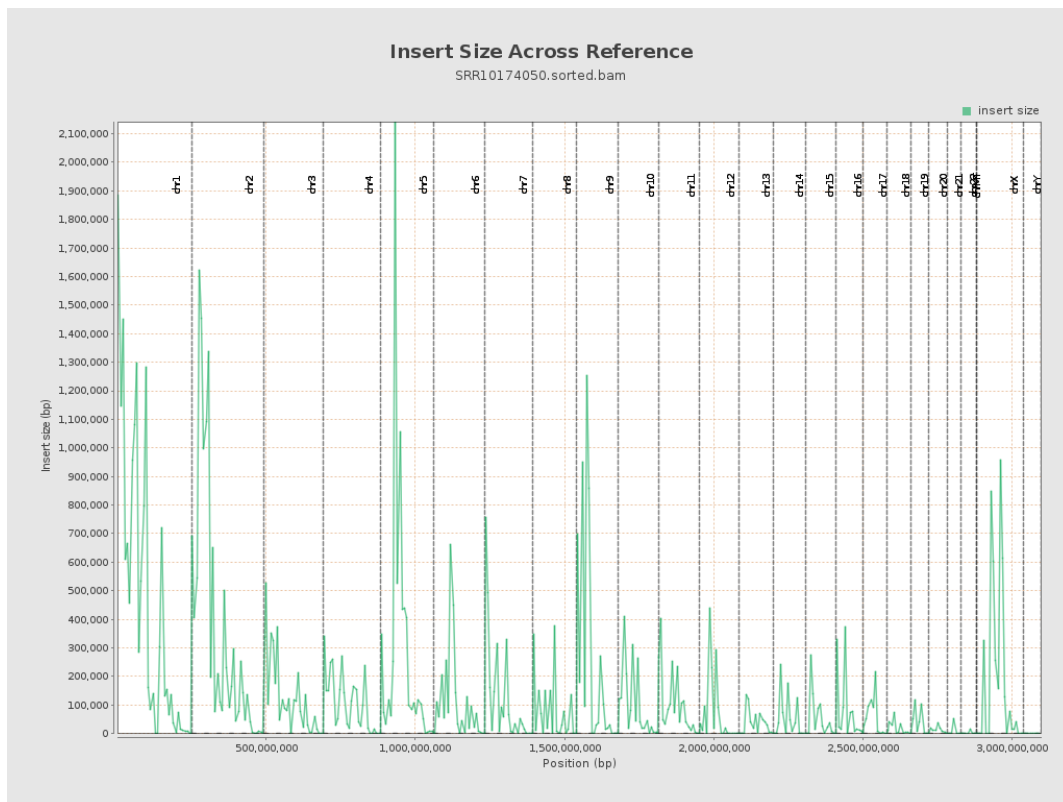
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

