

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 07:11:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124933.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_SRR3124933 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124933_1.fastq.gz SRR3124933_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 07:11:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124933.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,641,396
Mapped reads	4,590,694 / 98.91%
Unmapped reads	50,702 / 1.09%
Mapped paired reads	4,590,694 / 98.91%
Mapped reads, first in pair	2,298,538 / 49.52%
Mapped reads, second in pair	2,292,156 / 49.39%
Mapped reads, both in pair	4,574,210 / 98.55%
Mapped reads, singletons	16,484 / 0.36%
Secondary alignments	0
Supplementary alignments	26,261 / 0.57%
Read min/max/mean length	30 / 101 / 101.22
Duplicated reads (estimated)	336,409 / 7.25%
Duplication rate	5.3%
Clipped reads	1,923,855 / 41.45%

2.2. ACGT Content

Number/percentage of A's	111,500,054 / 27.39%
Number/percentage of C's	81,175,221 / 19.94%
Number/percentage of T's	117,294,046 / 28.81%
Number/percentage of G's	96,789,395 / 23.77%
Number/percentage of N's	397,515 / 0.1%

GC Percentage	43.71%
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2.3. Coverage

Mean	0.1316
Standard Deviation	1.0627

2.4. Mapping Quality

Mean Mapping Quality	52.98
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2.5. Insert size

Mean	47,102.76
Standard Deviation	2,058,843.41
P25/Median/P75	140 / 189 / 265

2.6. Mismatches and indels

General error rate	0.89%
Mismatches	3,492,232
Insertions	58,187
Mapped reads with at least one insertion	1.23%
Deletions	143,522
Mapped reads with at least one deletion	3.06%
Homopolymer indels	47%

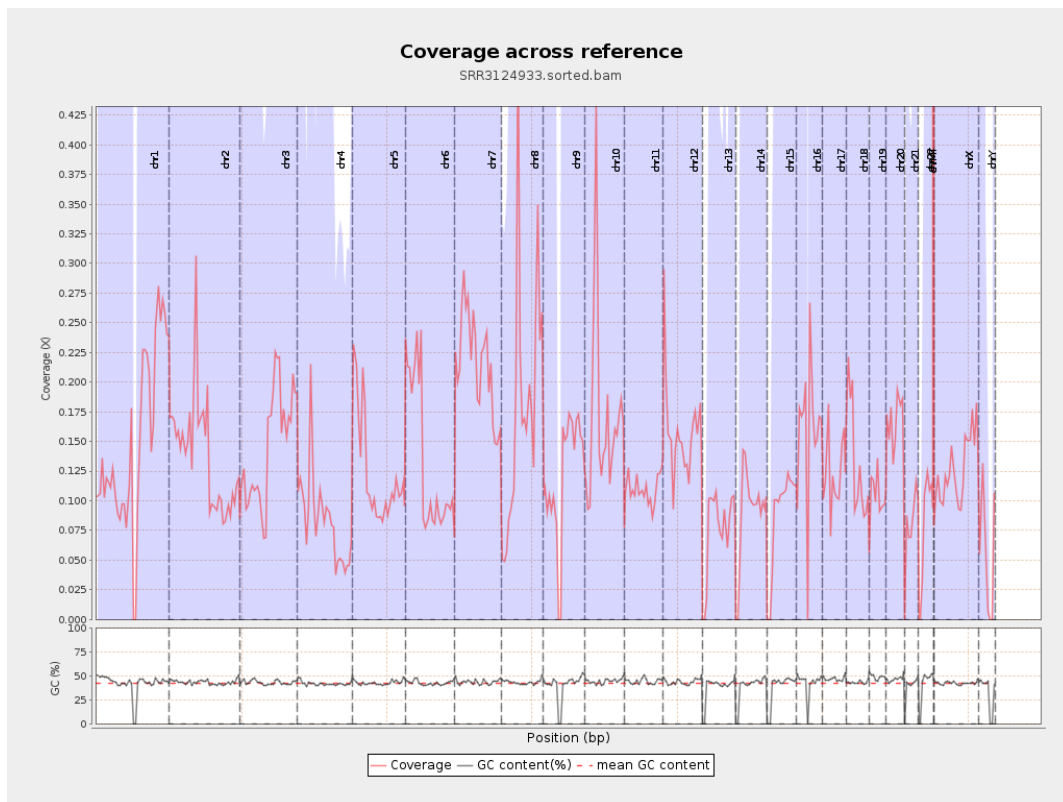
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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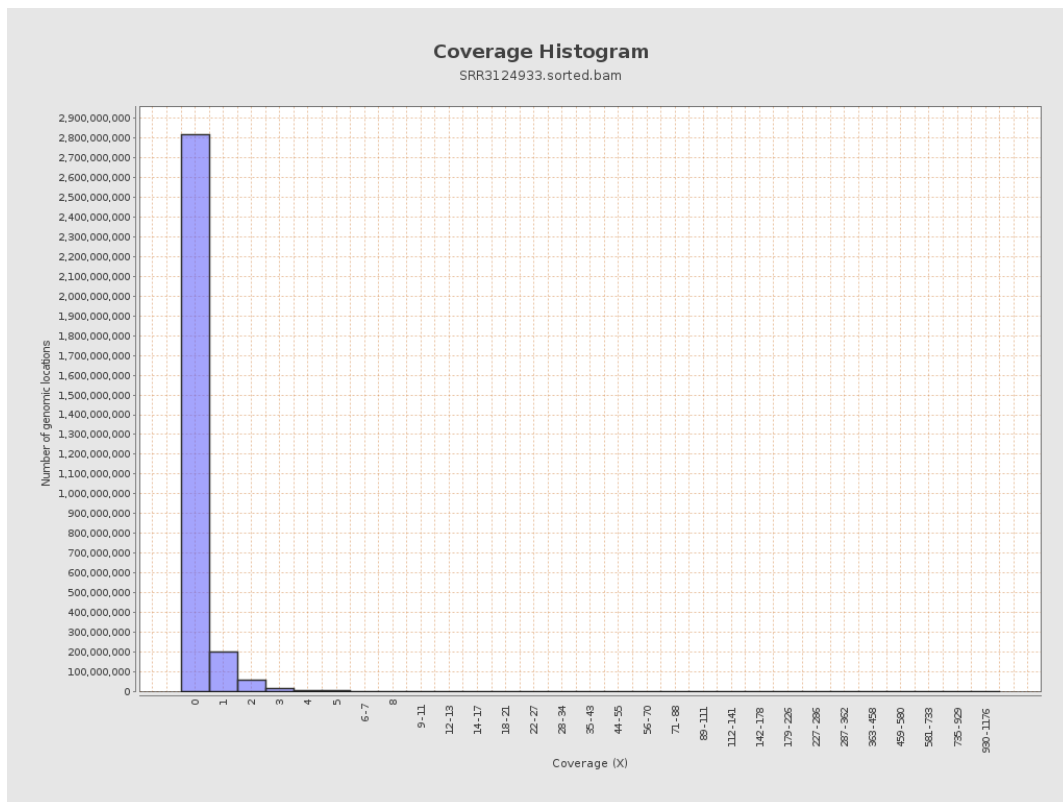
		bases	coverage	deviation
chr1	249250621	37110565	0.1489	1.2794
chr2	243199373	33808868	0.139	1.4
chr3	198022430	28598741	0.1444	0.4986
chr4	191154276	15841454	0.0829	0.814
chr5	180915260	22240311	0.1229	0.4732
chr6	171115067	22953237	0.1341	0.8907
chr7	159138663	34381741	0.216	1.7479
chr8	146364022	26582224	0.1816	0.6894
chr9	141213431	17087194	0.121	1.2033
chr10	135534747	22923453	0.1691	2.2358
chr11	135006516	14691471	0.1088	0.7134
chr12	133851895	21166097	0.1581	0.5311
chr13	115169878	8701211	0.0756	0.3506
chr14	107349540	9665915	0.09	0.4216
chr15	102531392	9081344	0.0886	0.3916
chr16	90354753	14457597	0.16	1.2689
chr17	81195210	9872137	0.1216	1.3681
chr18	78077248	10481464	0.1342	1.2716
chr19	59128983	6235196	0.1055	0.9607
chr20	63025520	10458834	0.1659	0.5779
chr21	48129895	3896221	0.081	0.5046
chr22	51304566	3950037	0.077	0.3834
chrMT	16571	415379	25.0666	12.9954
chrX	155270560	19577831	0.1261	0.5798

chrY	59373566	3226653	0.0543	1.1411
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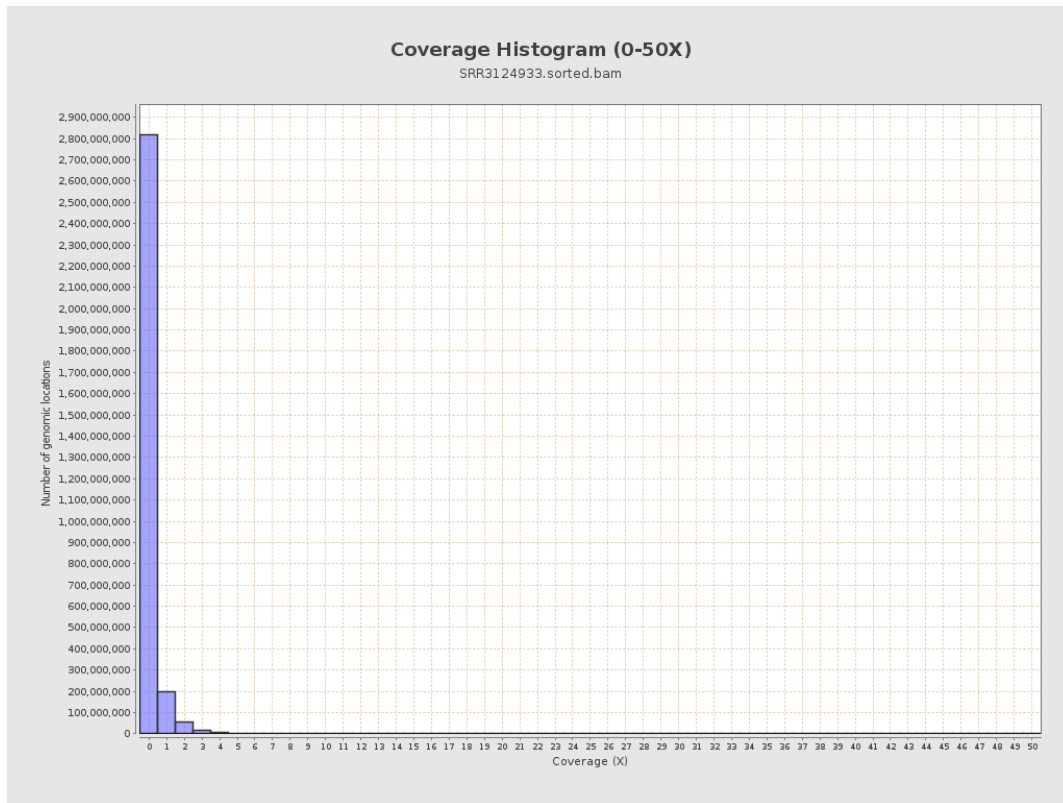
3. Results : Coverage across reference



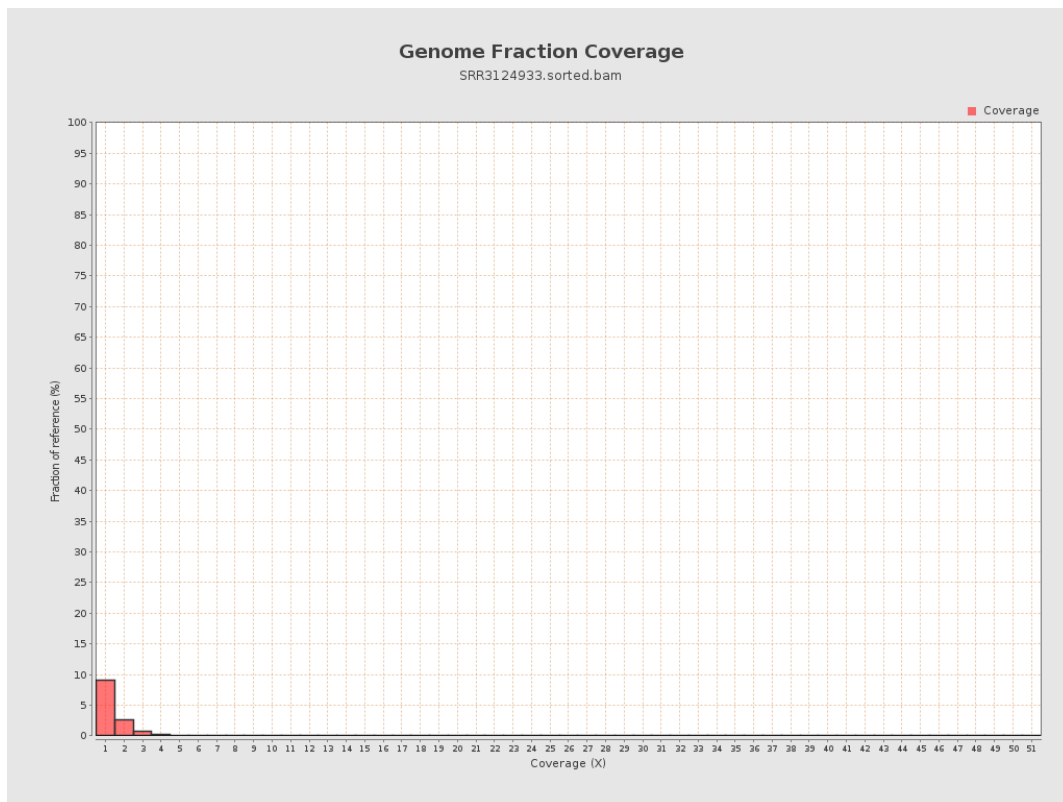
4. Results : Coverage Histogram



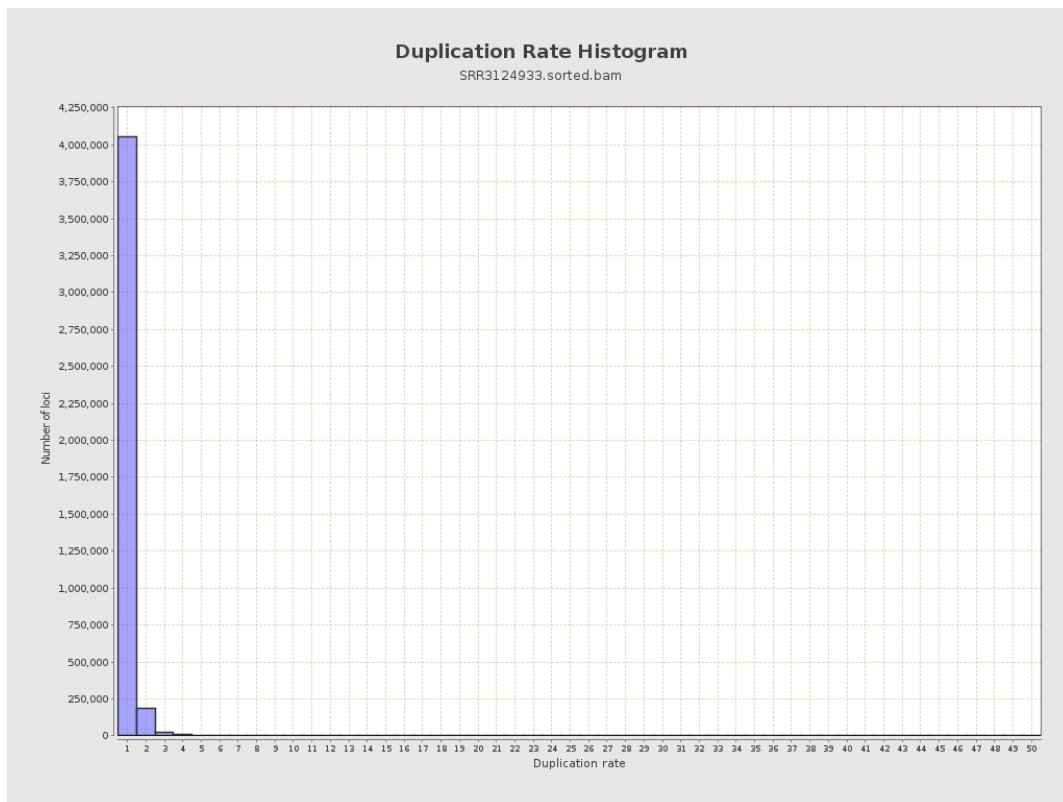
5. Results : Coverage Histogram (0-50X)



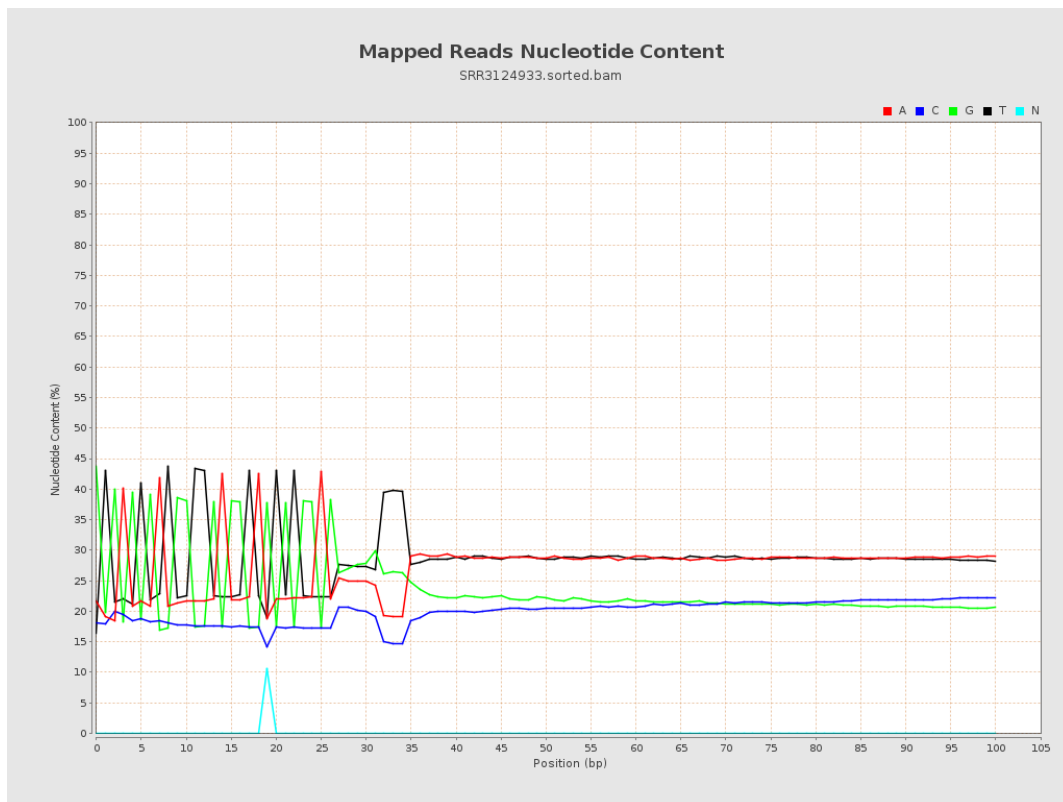
6. Results : Genome Fraction Coverage



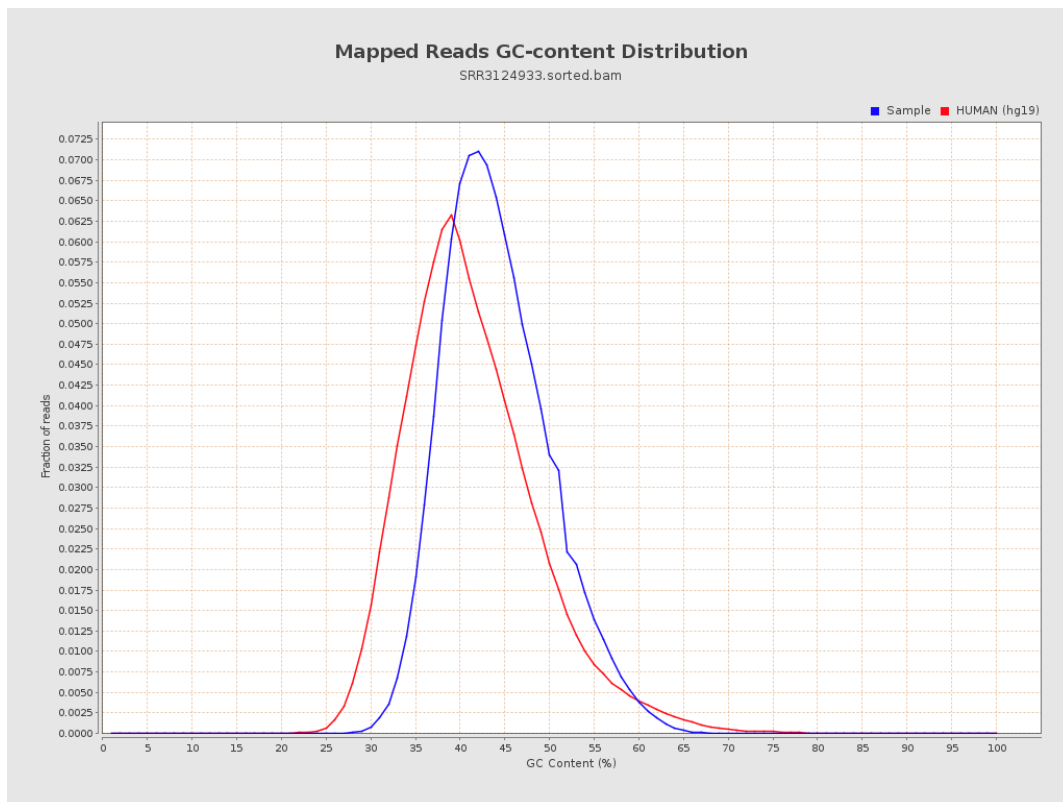
7. Results : Duplication Rate Histogram



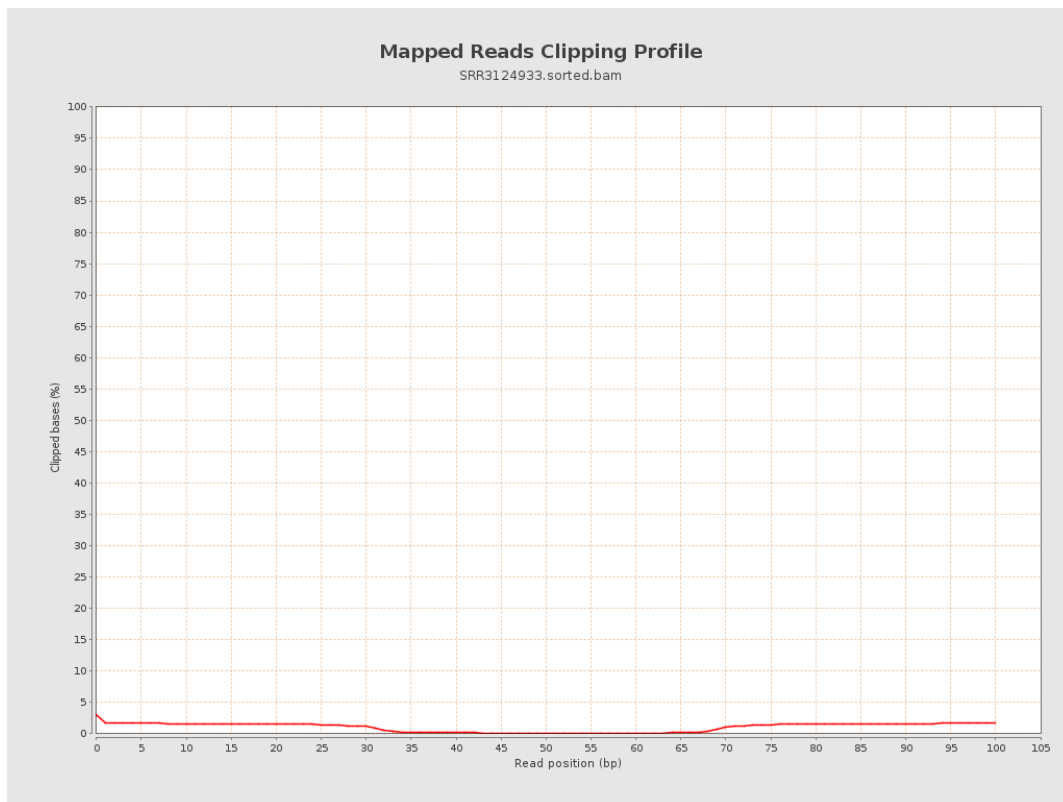
8. Results : Mapped Reads Nucleotide Content



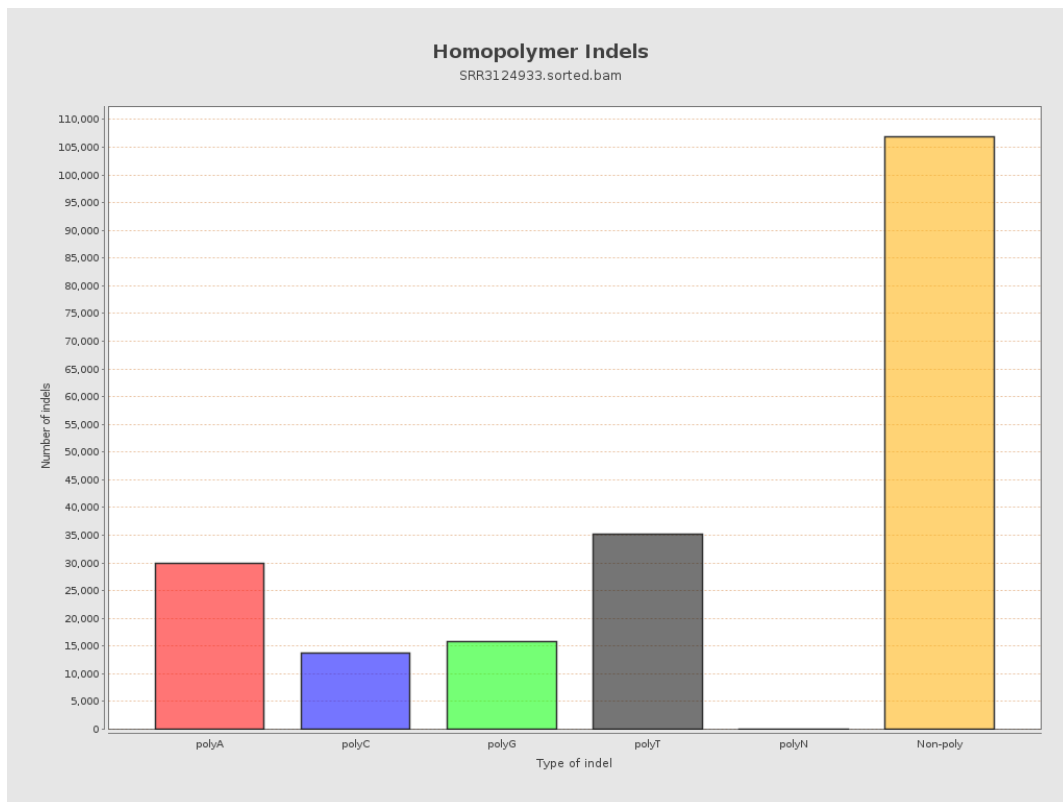
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



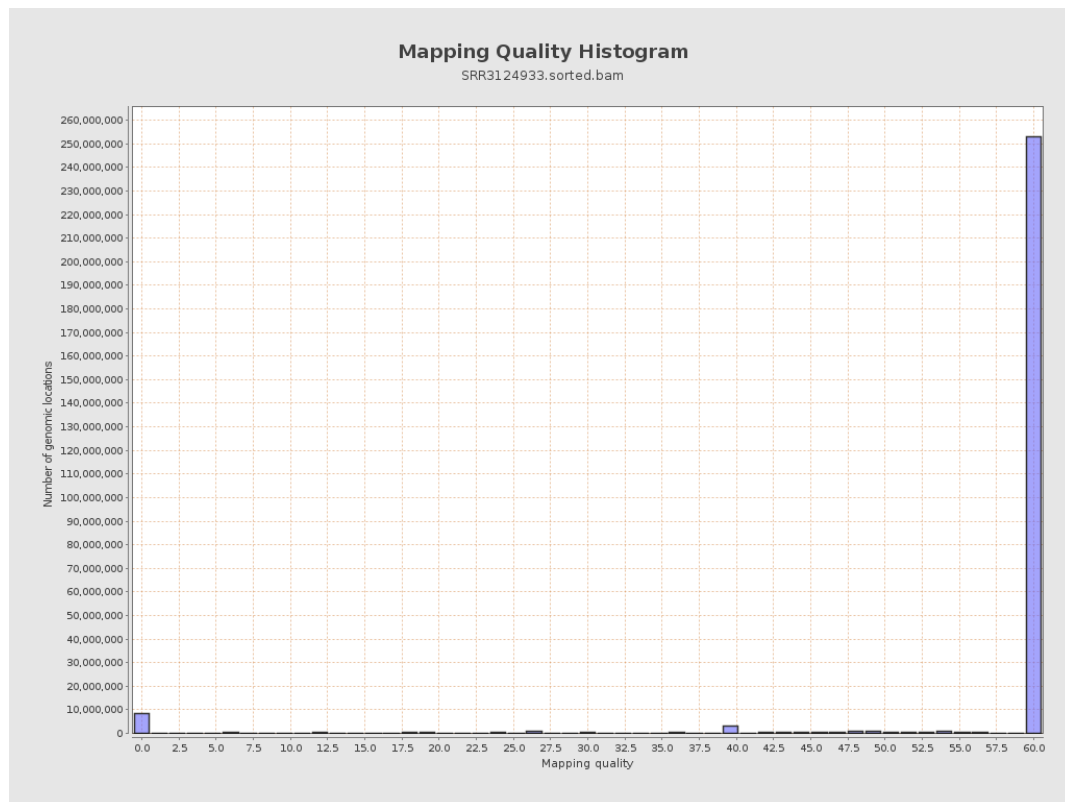
11. Results : Homopolymer Indels



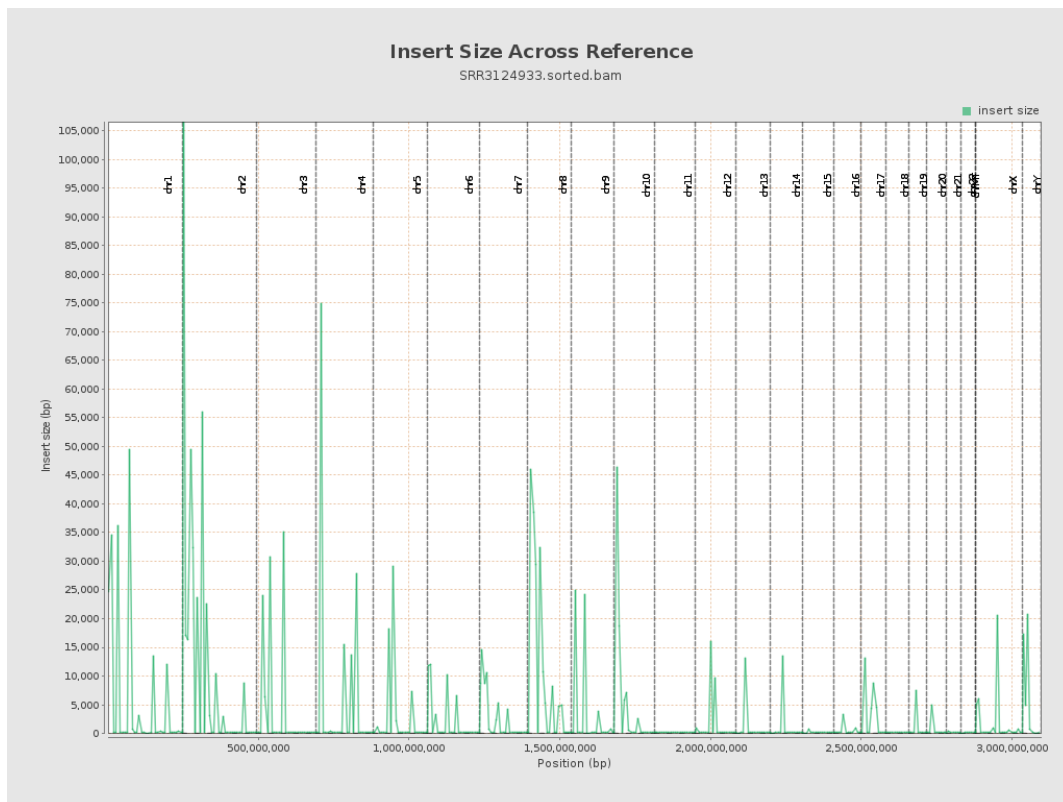
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

