

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 10:51:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124963.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_SRR3124963 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124963_1.fastq.gz SRR3124963_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 10:51:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124963.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,723,048
Mapped reads	2,640,831 / 96.98%
Unmapped reads	82,217 / 3.02%
Mapped paired reads	2,640,831 / 96.98%
Mapped reads, first in pair	1,329,718 / 48.83%
Mapped reads, second in pair	1,311,113 / 48.15%
Mapped reads, both in pair	2,615,924 / 96.07%
Mapped reads, singletons	24,907 / 0.91%
Secondary alignments	0
Supplementary alignments	72,221 / 2.65%
Read min/max/mean length	30 / 151 / 152.27
Duplicated reads (estimated)	502,944 / 18.47%
Duplication rate	14.83%
Clipped reads	1,839,656 / 67.56%

2.2. ACGT Content

Number/percentage of A's	97,025,547 / 28.92%
Number/percentage of C's	65,919,794 / 19.65%
Number/percentage of T's	99,320,406 / 29.61%
Number/percentage of G's	73,174,895 / 21.81%
Number/percentage of N's	2,491 / 0%

GC Percentage	41.47%
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2.3. Coverage

Mean	0.1085
Standard Deviation	1.9586

2.4. Mapping Quality

Mean Mapping Quality	53.36
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2.5. Insert size

Mean	91,781.51
Standard Deviation	2,821,931.28
P25/Median/P75	132 / 178 / 247

2.6. Mismatches and indels

General error rate	1.32%
Mismatches	4,102,322
Insertions	94,571
Mapped reads with at least one insertion	3.26%
Deletions	174,411
Mapped reads with at least one deletion	6.25%
Homopolymer indels	43.65%

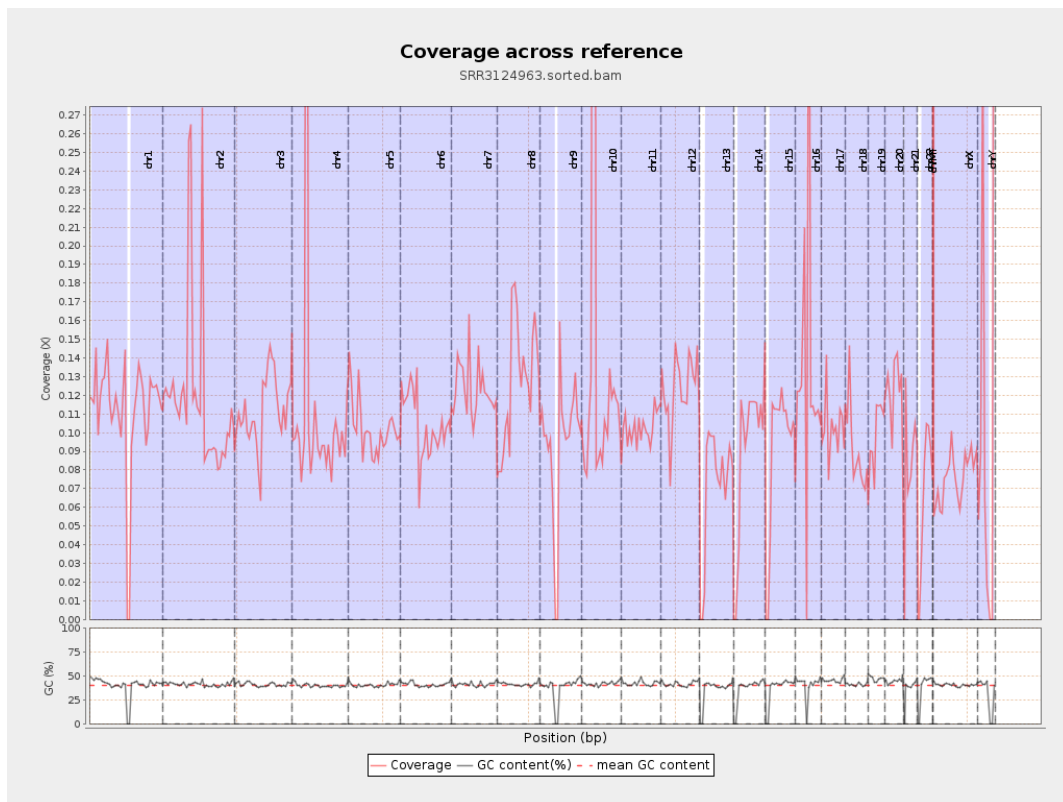
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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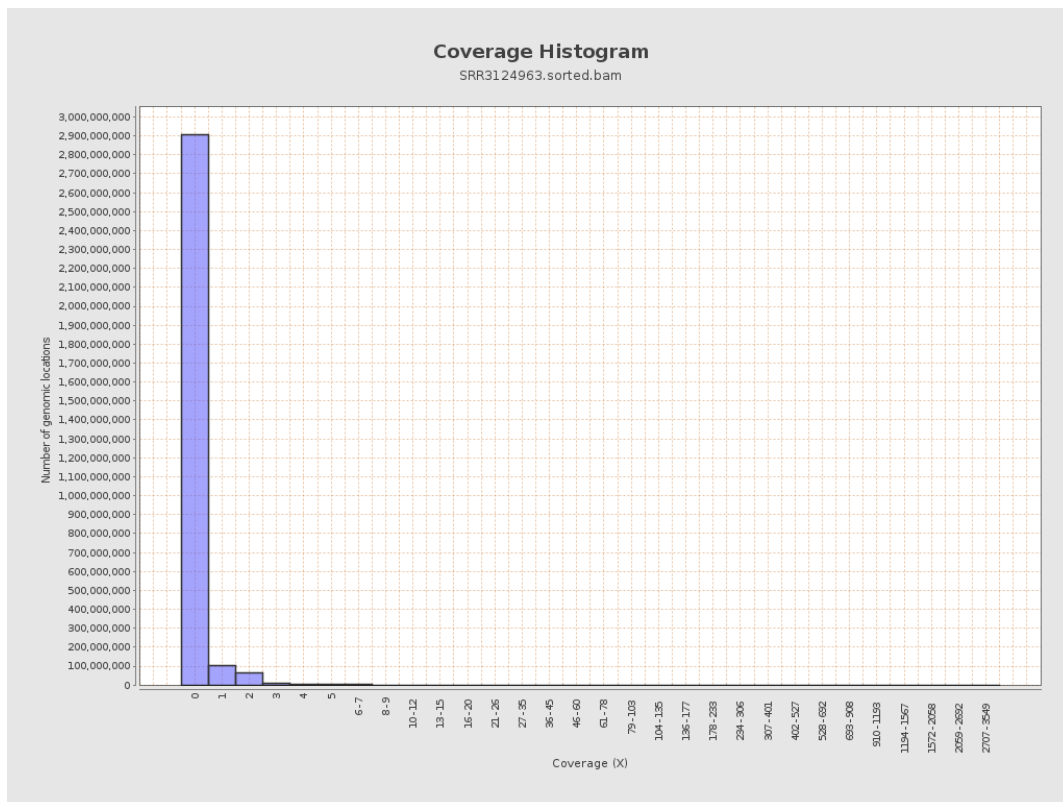
		bases	coverage	deviation
chr1	249250621	27913558	0.112	0.8849
chr2	243199373	29280962	0.1204	2.4759
chr3	198022430	22112587	0.1117	0.5079
chr4	191154276	22112851	0.1157	3.3318
chr5	180915260	18497916	0.1022	0.4973
chr6	171115067	17805519	0.1041	0.5959
chr7	159138663	19633279	0.1234	1.0363
chr8	146364022	18795957	0.1284	0.5974
chr9	141213431	13374047	0.0947	1.5311
chr10	135534747	19503839	0.1439	5.9325
chr11	135006516	13822620	0.1024	0.6899
chr12	133851895	16667021	0.1245	0.5151
chr13	115169878	8216474	0.0713	0.3805
chr14	107349540	9760418	0.0909	0.5037
chr15	102531392	9213344	0.0899	0.4348
chr16	90354753	12532023	0.1387	2.6231
chr17	81195210	8336857	0.1027	0.9594
chr18	78077248	7108688	0.091	1.4864
chr19	59128983	5867929	0.0992	0.6357
chr20	63025520	7742851	0.1229	1.2216
chr21	48129895	4115973	0.0855	1.5908
chr22	51304566	3369480	0.0657	0.4343
chrMT	16571	177510	10.7121	7.0436
chrX	155270560	11837026	0.0762	0.4778

chrY	59373566	8053318	0.1356	4.618
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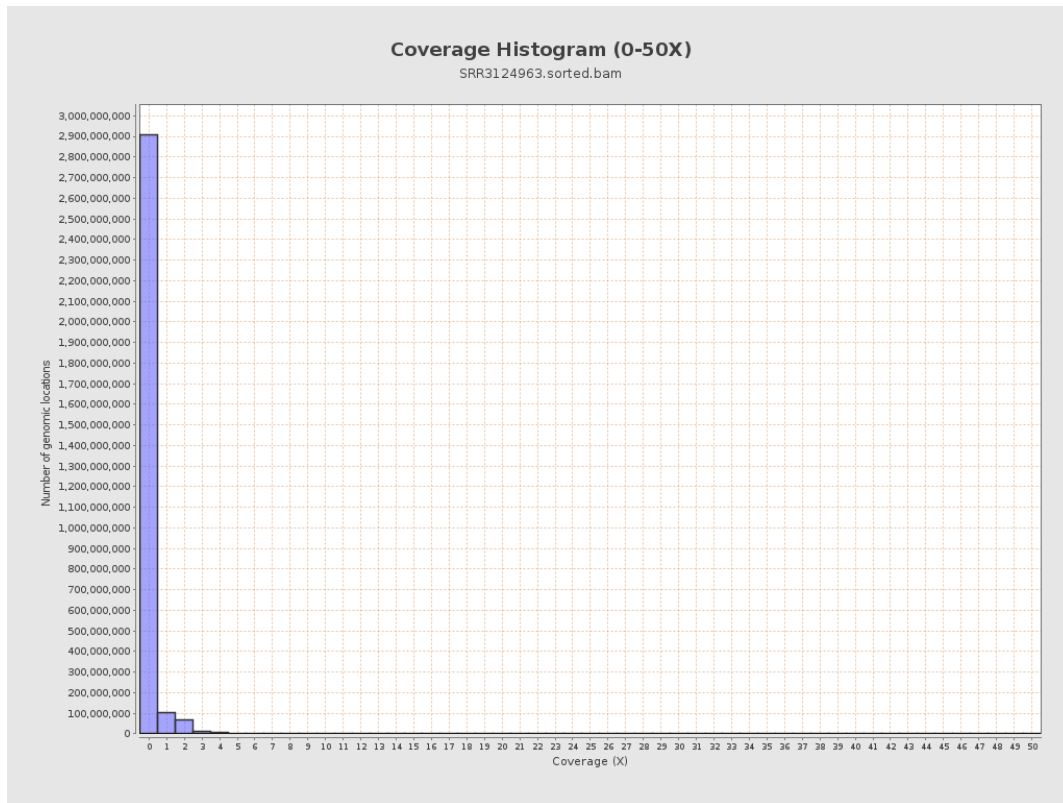
3. Results : Coverage across reference



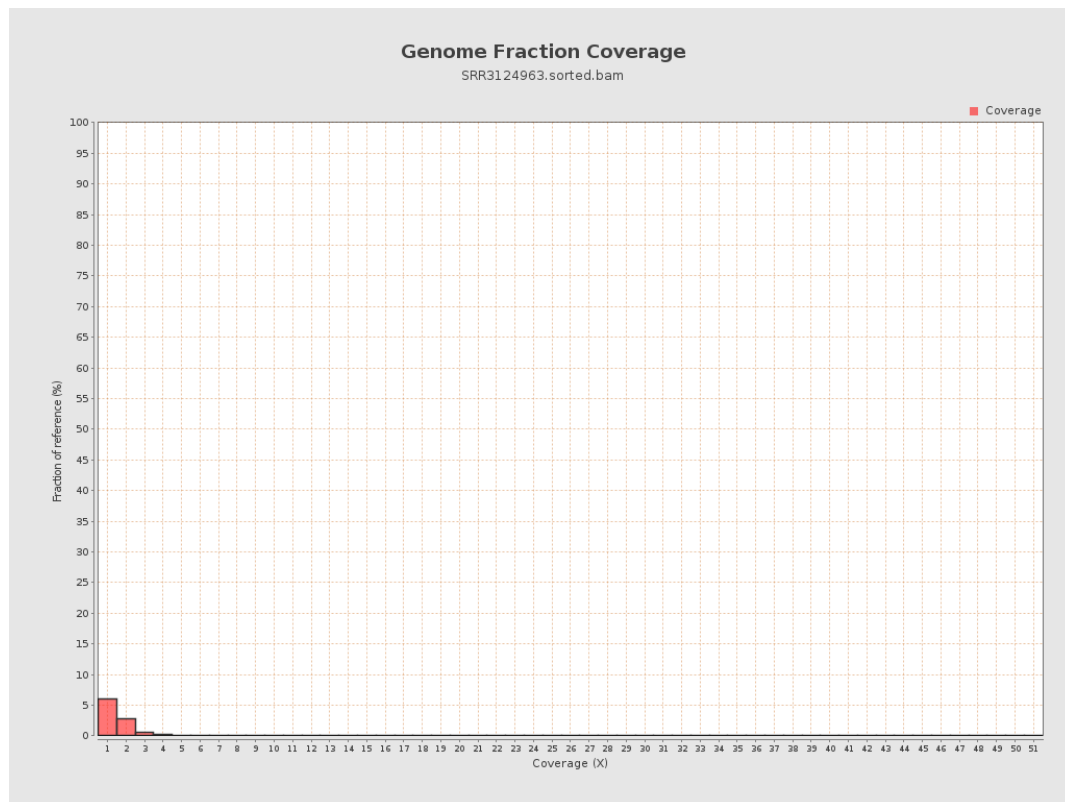
4. Results : Coverage Histogram



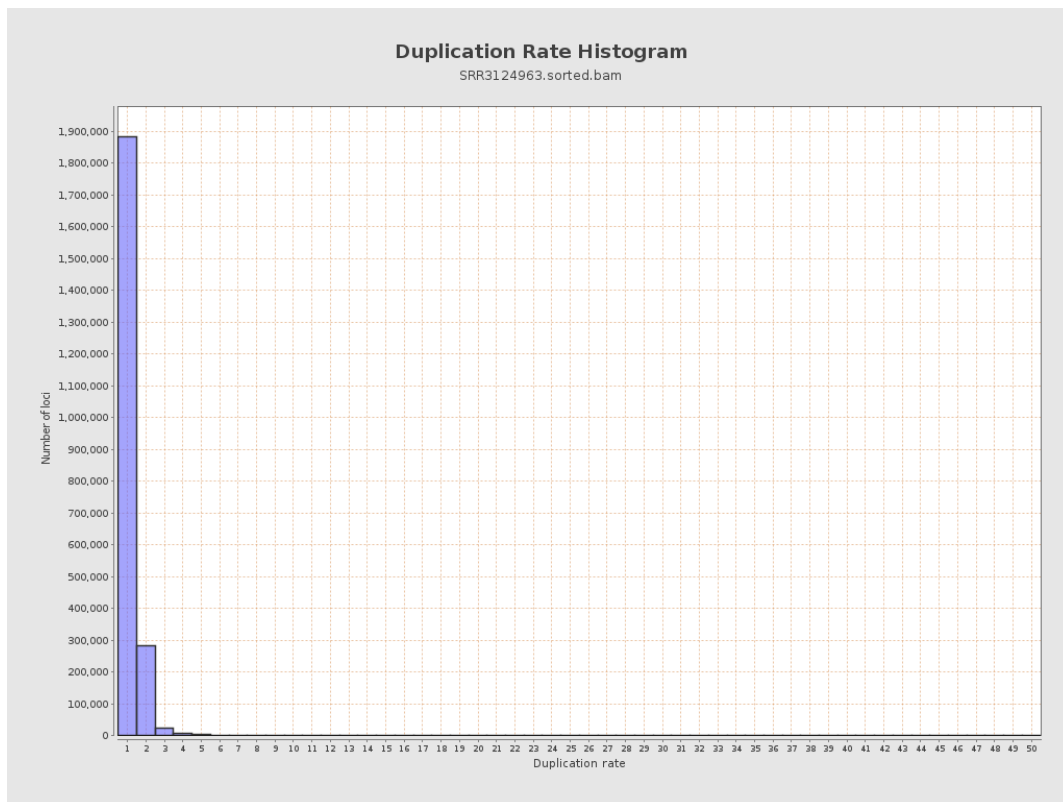
5. Results : Coverage Histogram (0-50X)



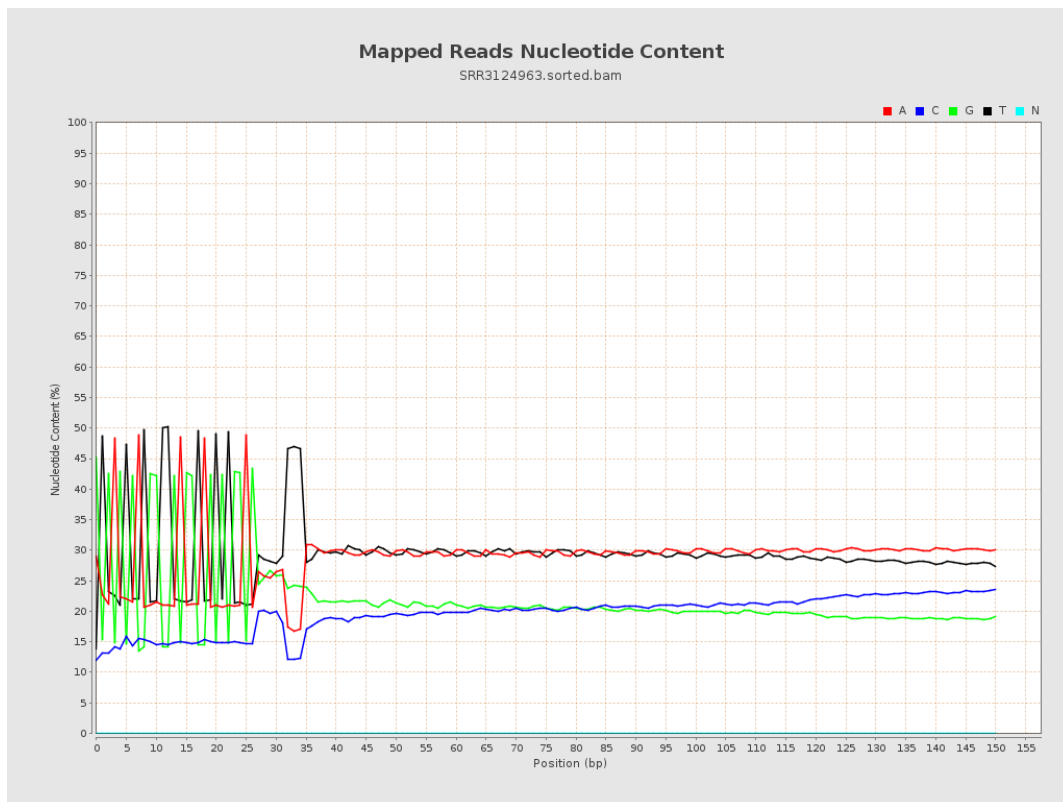
6. Results : Genome Fraction Coverage



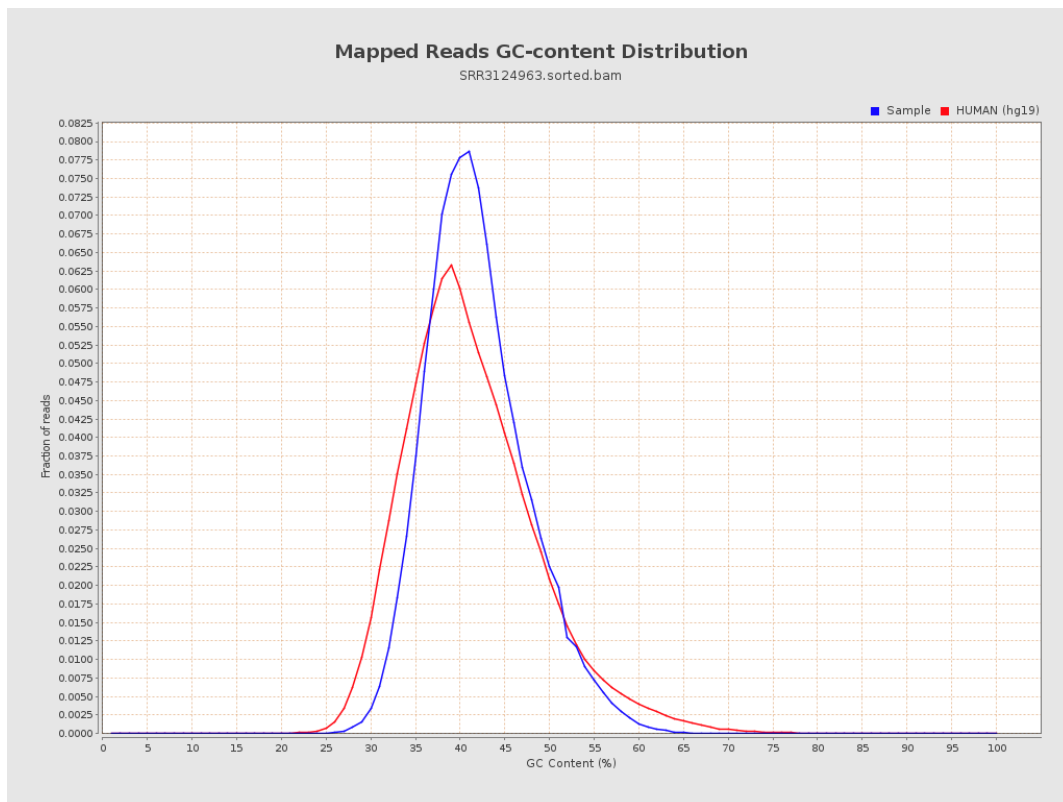
7. Results : Duplication Rate Histogram



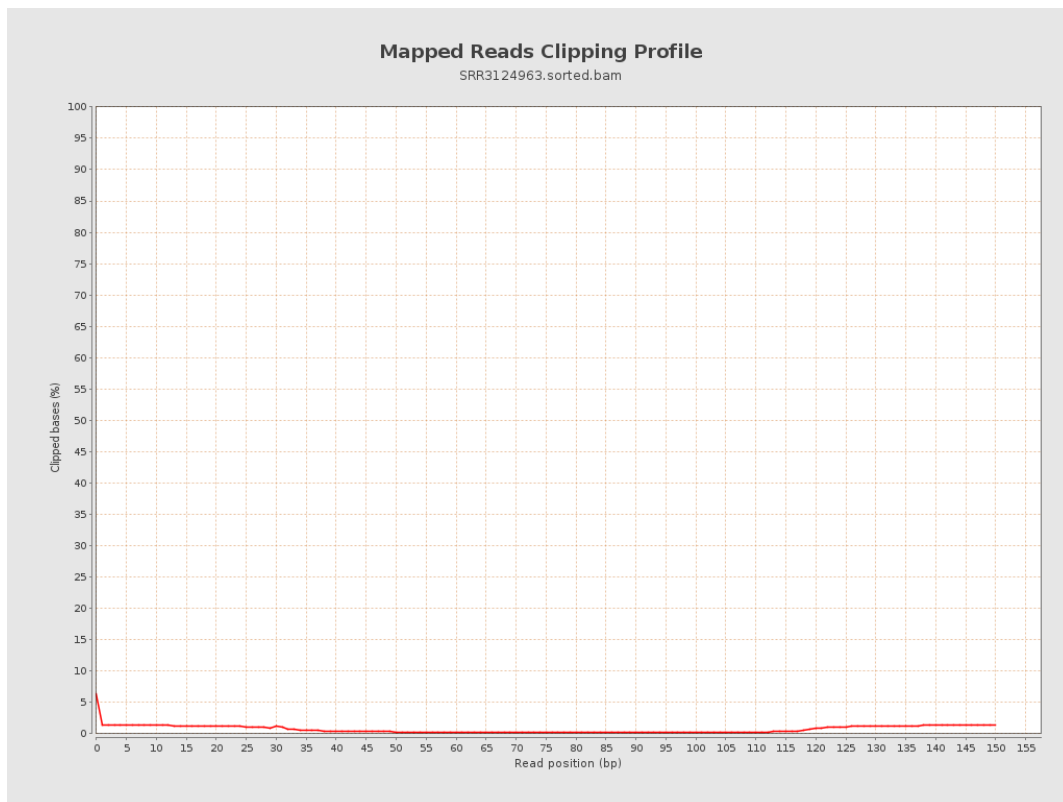
8. Results : Mapped Reads Nucleotide Content



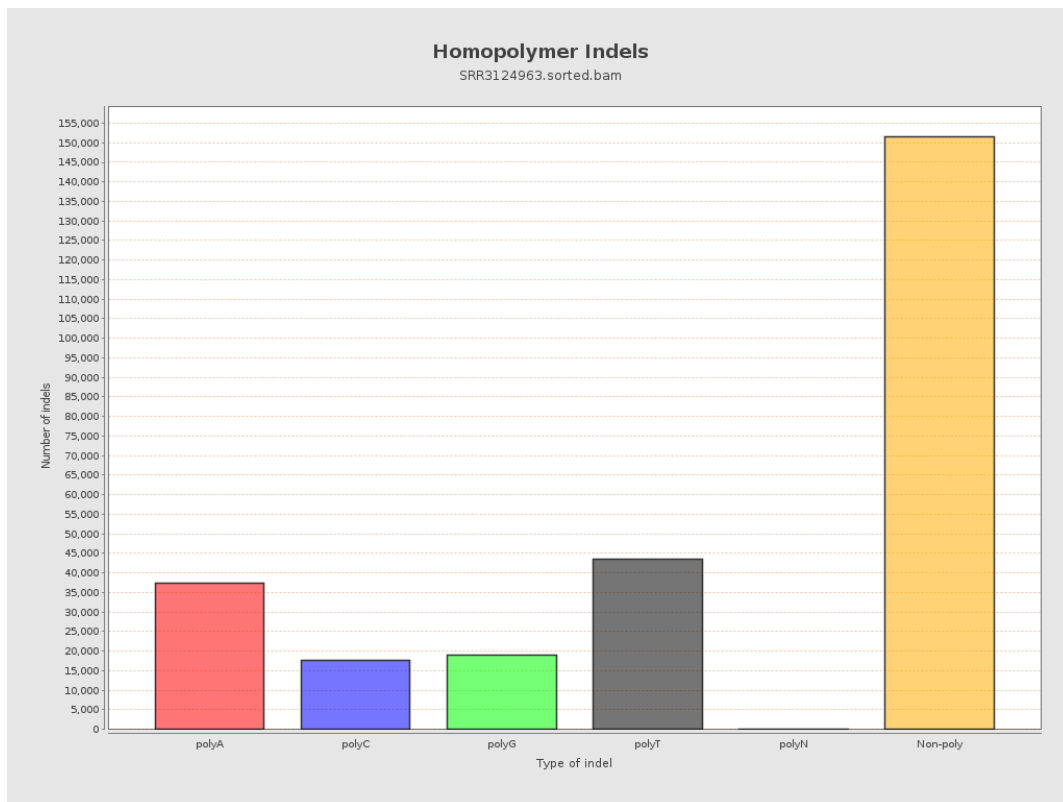
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



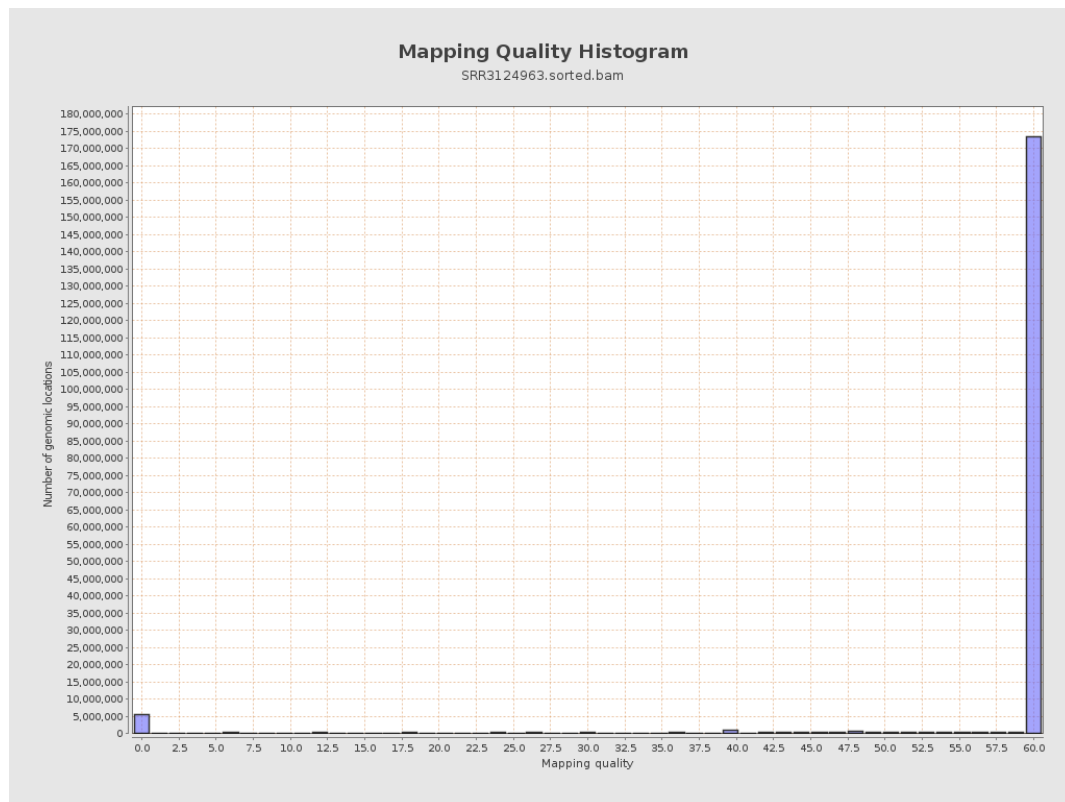
11. Results : Homopolymer Indels



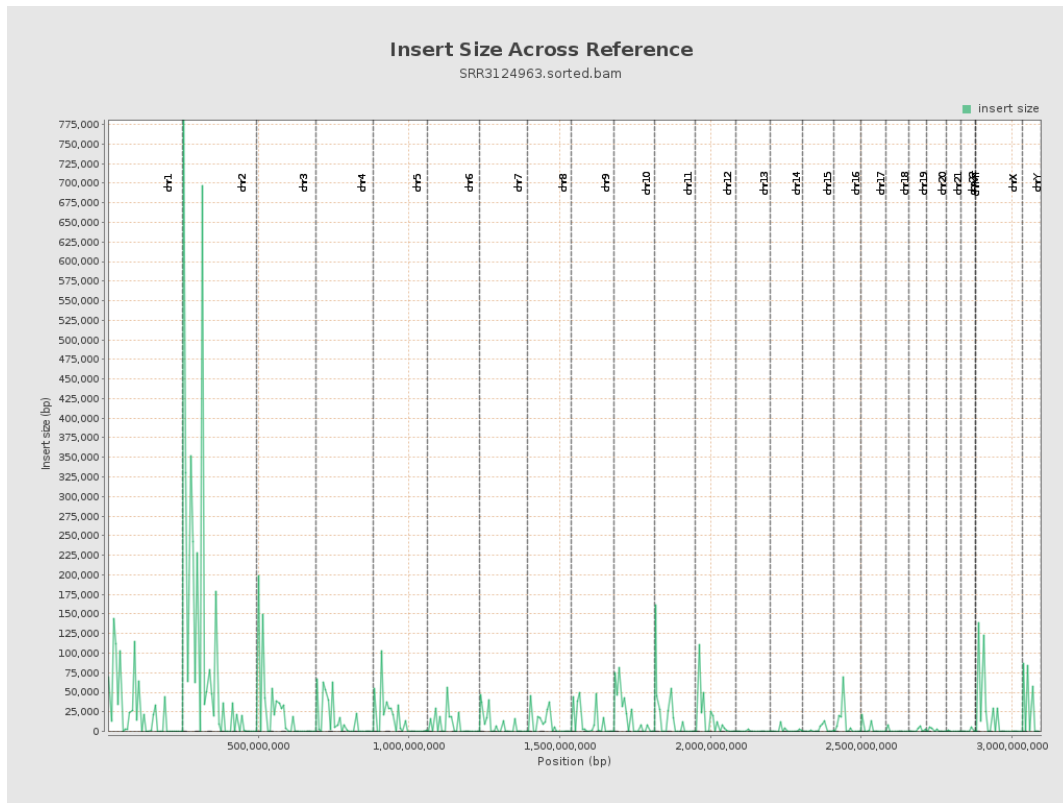
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

