Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/20 15:59:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504590.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_SRR504590 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504590_1.fastq.gz SRR504590_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 20 15:59:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504590.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	363,688,574
Mapped reads	347,718,484 / 95.61%
Unmapped reads	15,970,090 / 4.39%
Mapped paired reads	347,718,484 / 95.61%
Mapped reads, first in pair	174,054,463 / 47.86%
Mapped reads, second in pair	173,664,021 / 47.75%
Mapped reads, both in pair	344,943,020 / 94.85%
Mapped reads, singletons	2,775,464 / 0.76%
Secondary alignments	0
Supplementary alignments	987,185 / 0.27%
Read min/max/mean length	30 / 100 / 100.11
Duplicated reads (estimated)	76,408,158 / 21.01%
Duplication rate	18.01%
Clipped reads	54,639,266 / 15.02%

2.2. ACGT Content

Number/percentage of A's	9,488,271,772 / 28.42%
Number/percentage of C's	7,162,295,392 / 21.45%
Number/percentage of T's	9,393,272,106 / 28.13%
Number/percentage of G's	7,340,564,168 / 21.98%
Number/percentage of N's	7,061,436 / 0.02%

GC Percentage	43.43%

2.3. Coverage

Mean	10.7899
Standard Deviation	94.9609

2.4. Mapping Quality

Mean Mapping Quality	53.37

2.5. Insert size

Mean	33,081.16
Standard Deviation	1,723,007.36
P25/Median/P75	132 / 188 / 246

2.6. Mismatches and indels

General error rate	0.59%
Mismatches	187,017,767
Insertions	3,372,155
Mapped reads with at least one insertion	0.93%
Deletions	4,147,652
Mapped reads with at least one deletion	1.15%
Homopolymer indels	40.41%

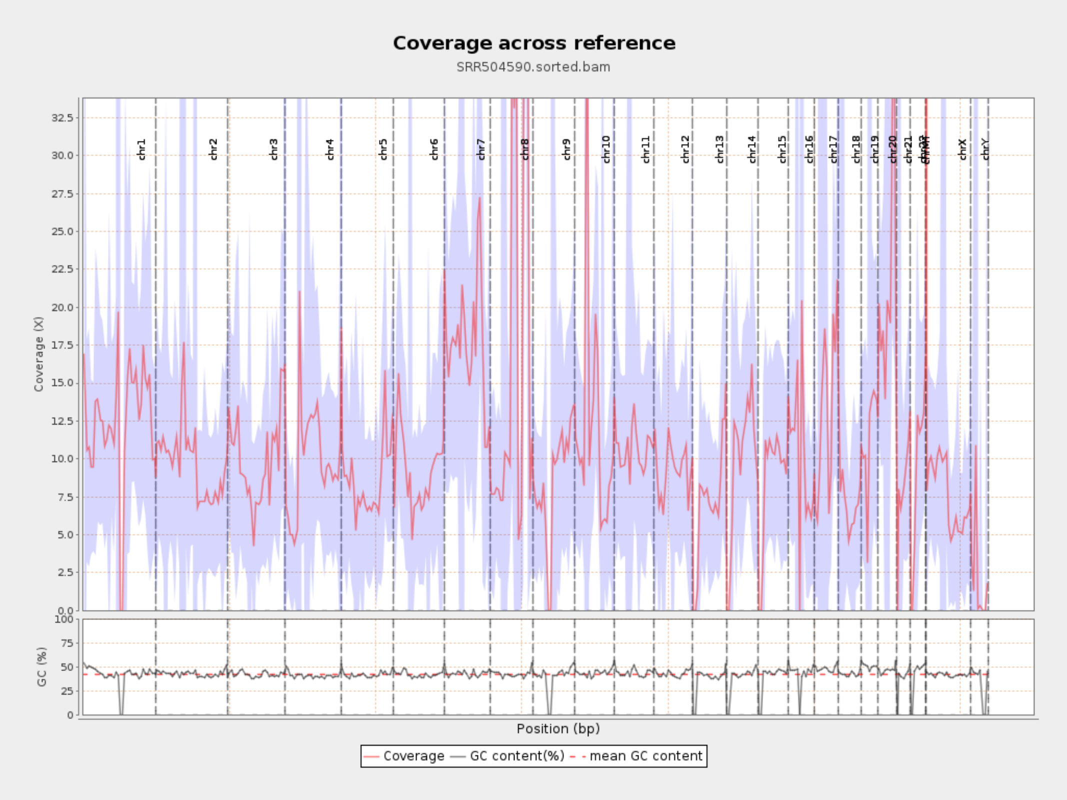
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

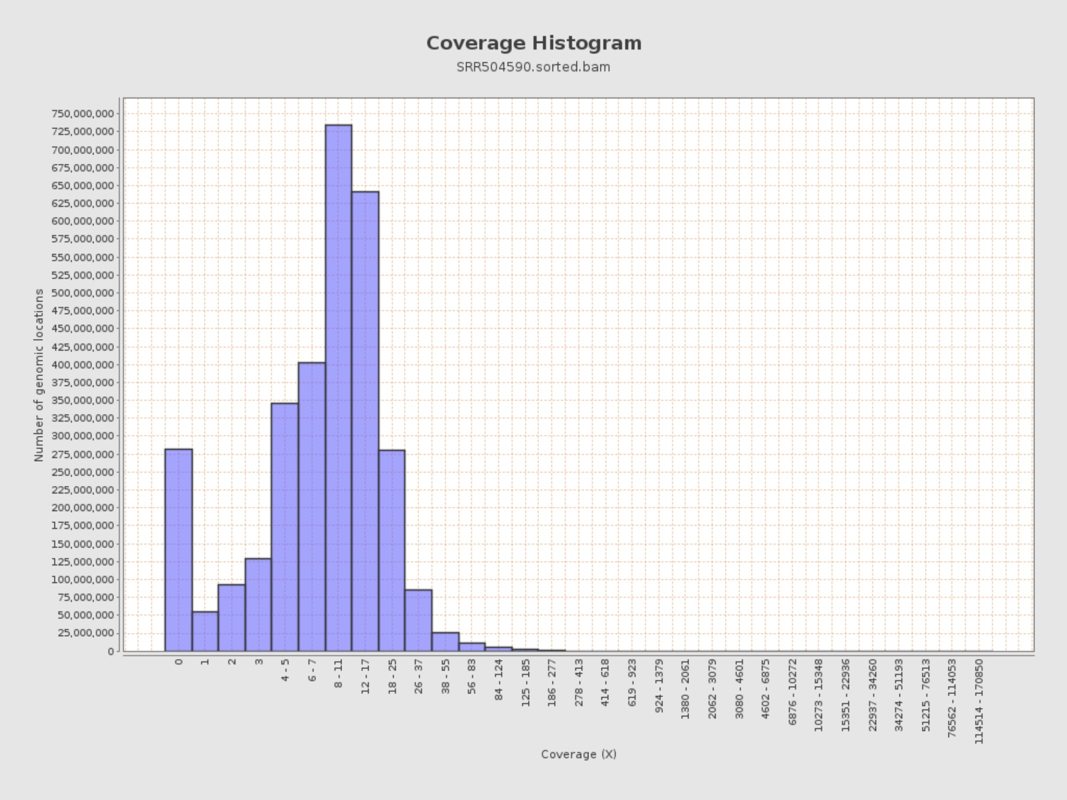
		bases	coverage	deviation
chr1	249250621	3104872351	12.4568	172.1016
chr2	243199373	2359596988	9.7023	57.3547
chr3	198022430	1975854377	9.9779	16.527
chr4	191154276	1893796907	9.9072	113.8021
chr5	180915260	1577315545	8.7185	10.3614
chr6	171115067	1565242831	9.1473	22.4536
chr7	159138663	2816941083	17.7012	136.7559
chr8	146364022	2936509401	20.0631	66.9605
chr9	141213431	1203856182	8.5251	60.3867
chr10	135534747	1625964934	11.9967	257.3845
chr11	135006516	1435268221	10.6311	38.7087
chr12	133851895	1248641291	9.3285	8.7471
chr13	115169878	811314860	7.0445	6.3933
chr14	107349540	1083472702	10.0929	9.4449
chr15	102531392	872430828	8.5089	7.1731
chr16	90354753	927726120	10.2676	73.3474
chr17	81195210	1035731934	12.7561	44.6978
chr18	78077248	569599566	7.2953	93.948
chr19	59128983	667398928	11.2872	89.4337
chr20	63025520	1404389301	22.2829	29.0661
chr21	48129895	401161640	8.335	40.6056
chr22	51304566	450069775	8.7725	9.4385
chrMT	16571	119702612	7,223.6203	1,539.4691
chrX	155270560	1187200676	7.646	18.612

chrY	59373566	128122955	2.1579	115.6934

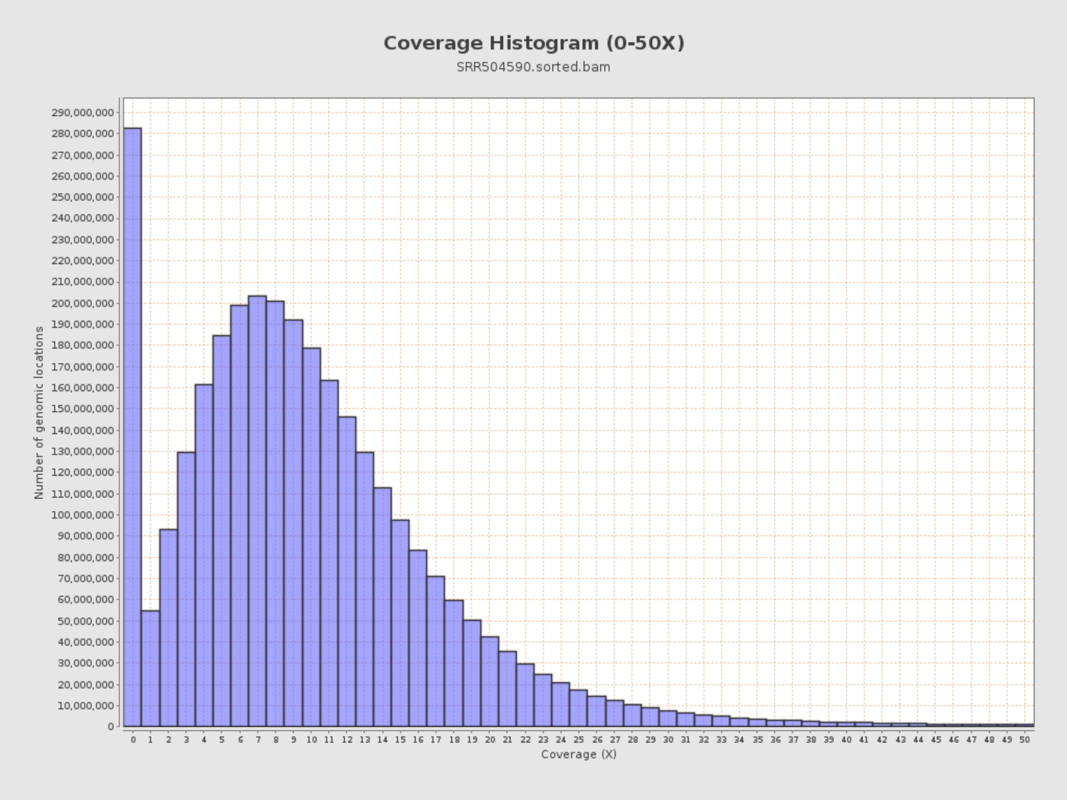
3. Results : Coverage across reference



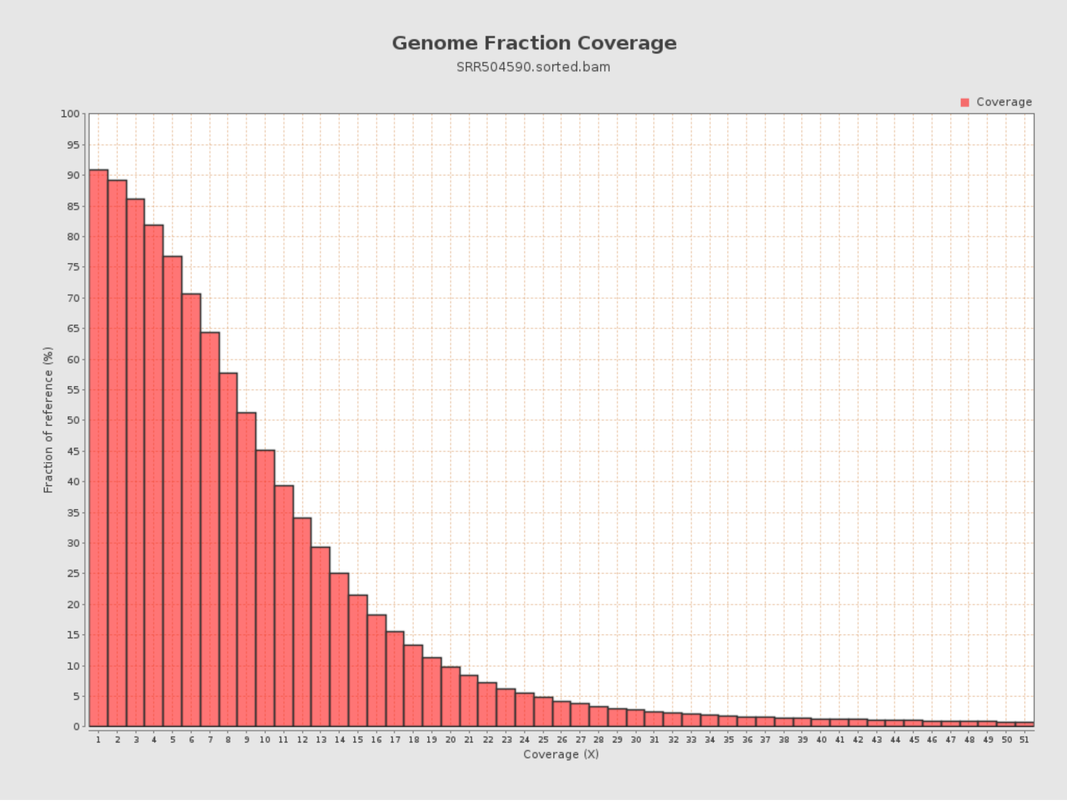
4. Results : Coverage Histogram



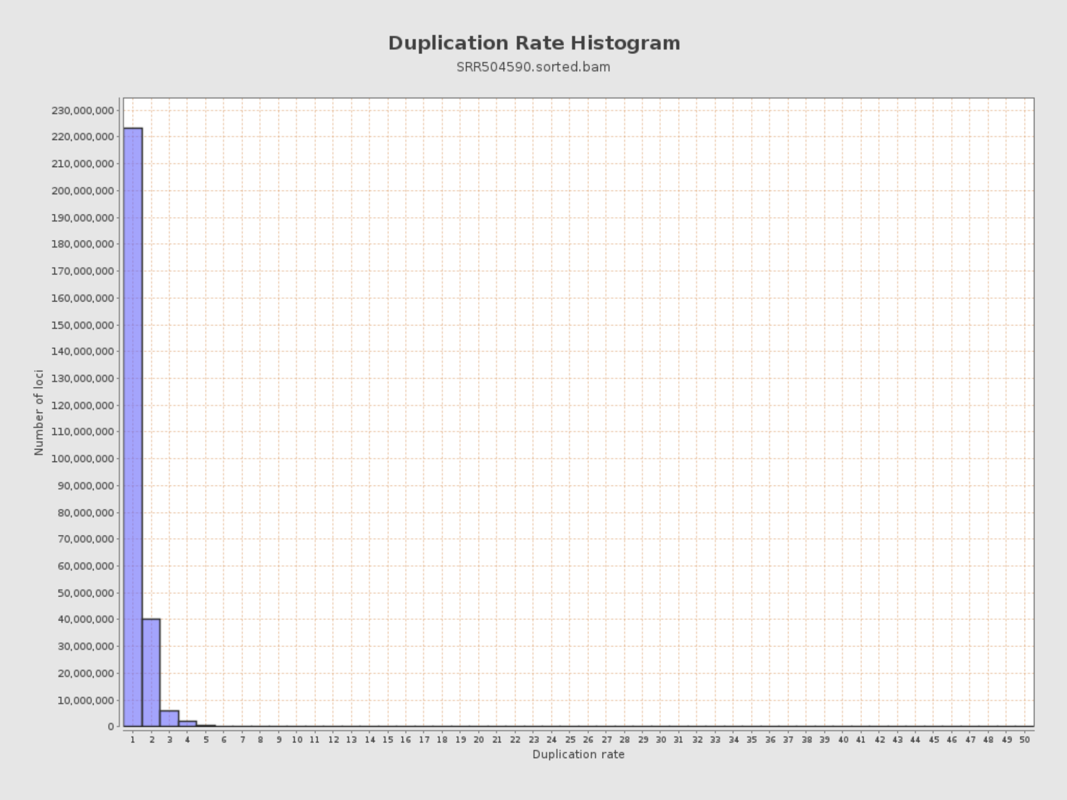
5. Results : Coverage Histogram (0-50X)



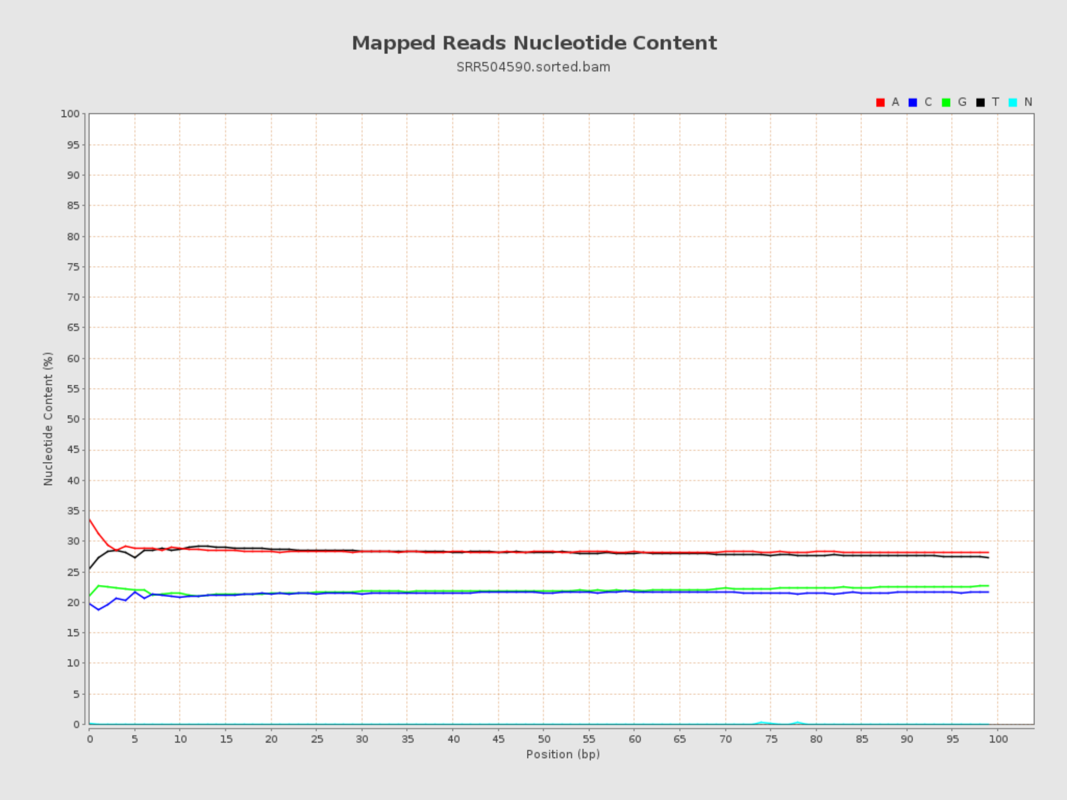
6. Results : Genome Fraction Coverage



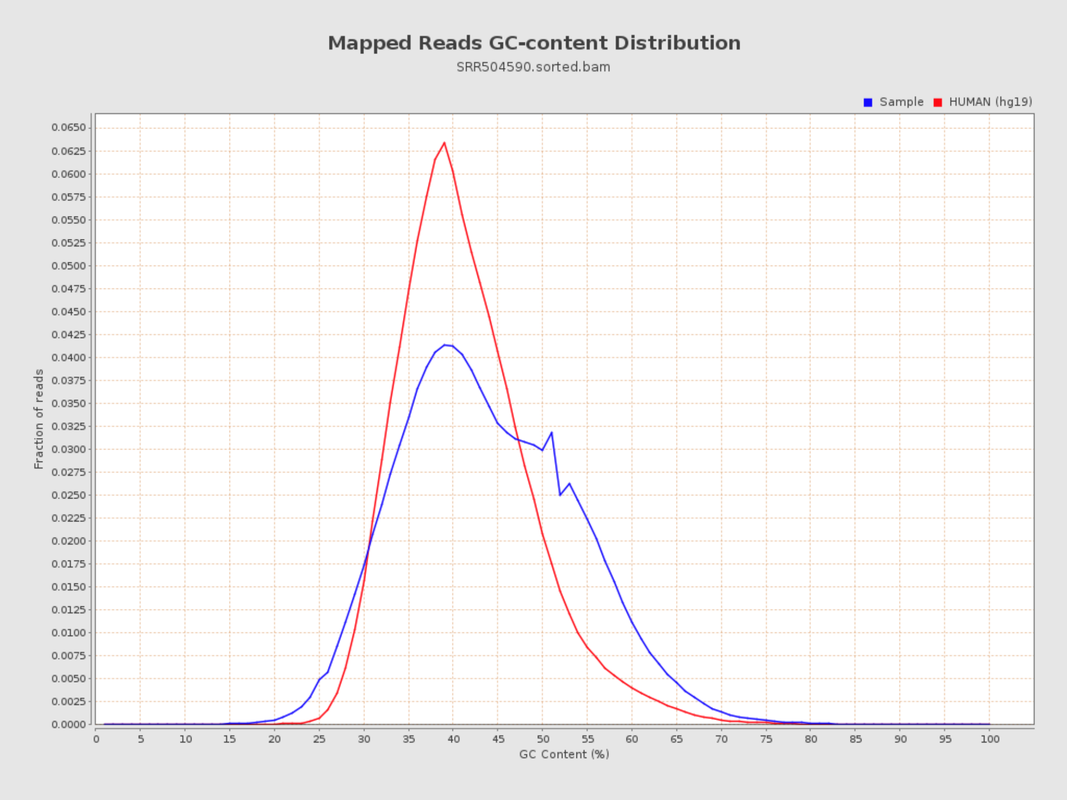
7. Results : Duplication Rate Histogram



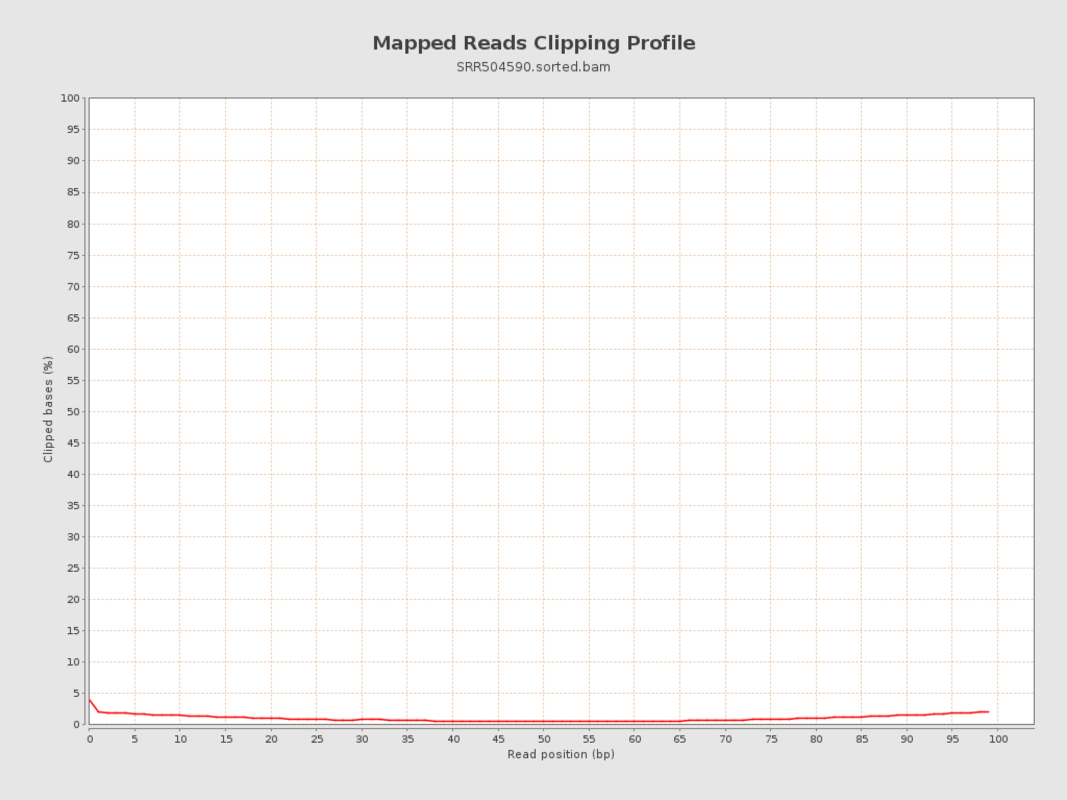
8. Results : Mapped Reads Nucleotide Content



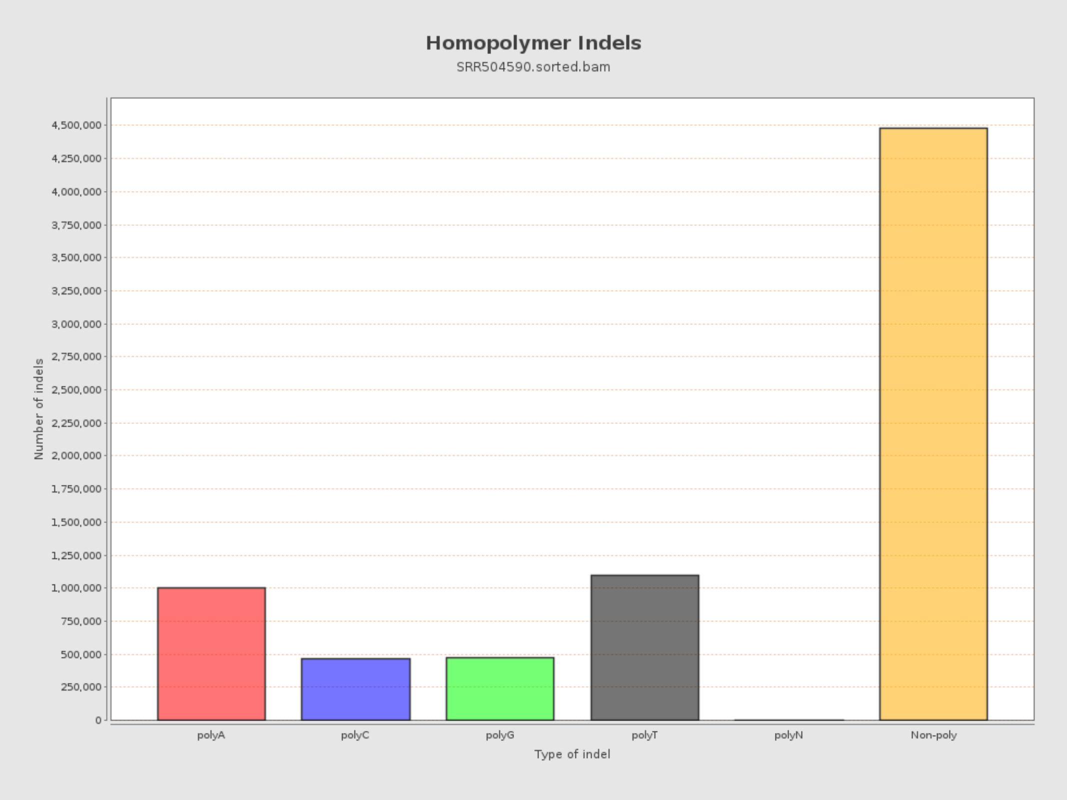
9. Results : Mapped Reads GC-content Distribution



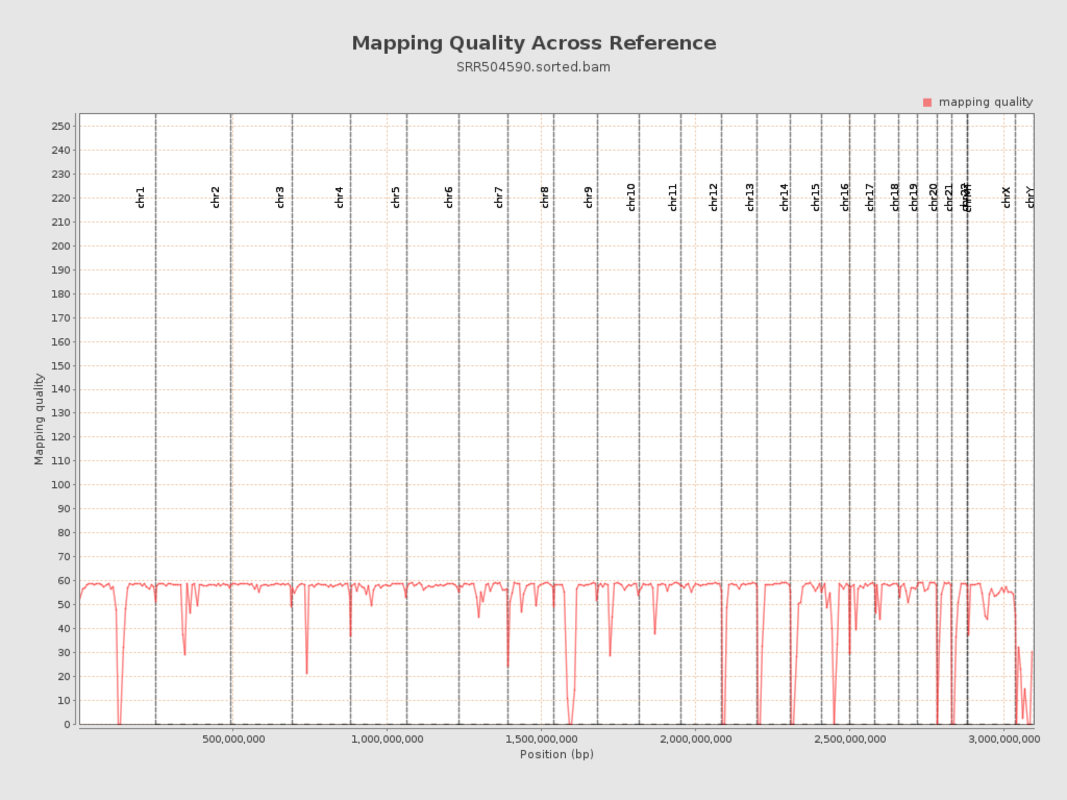
10. Results : Mapped Reads Clipping Profile



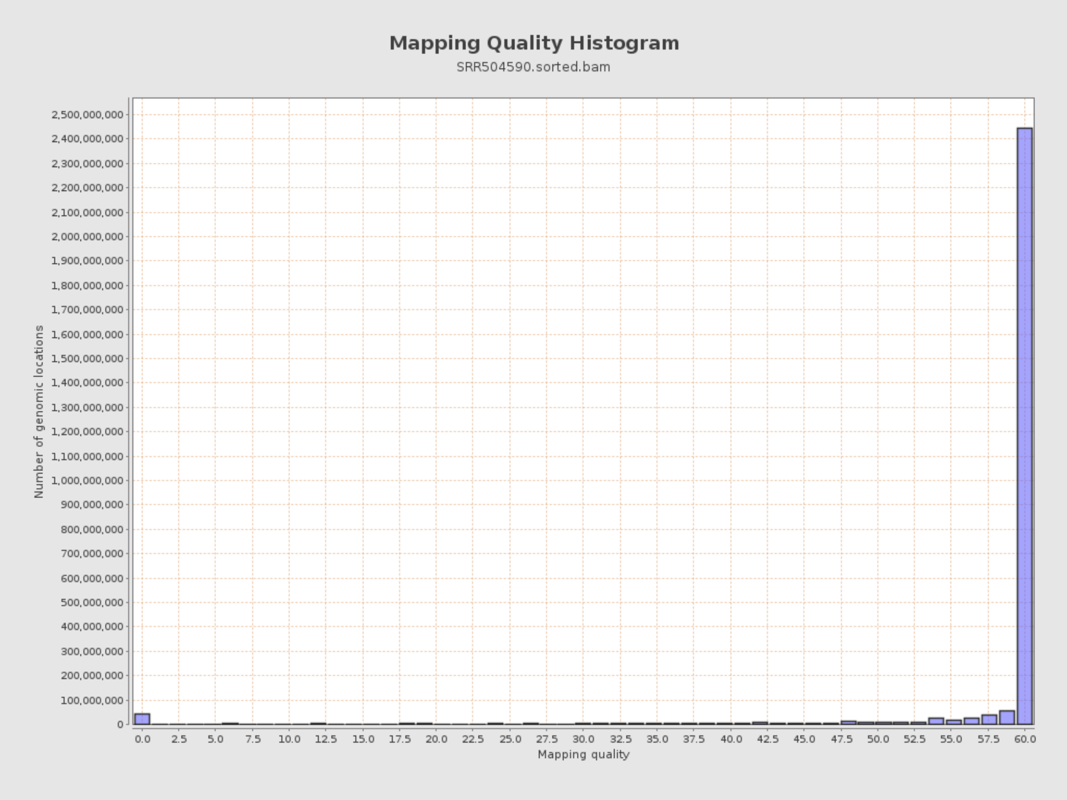
11. Results : Homopolymer Indels



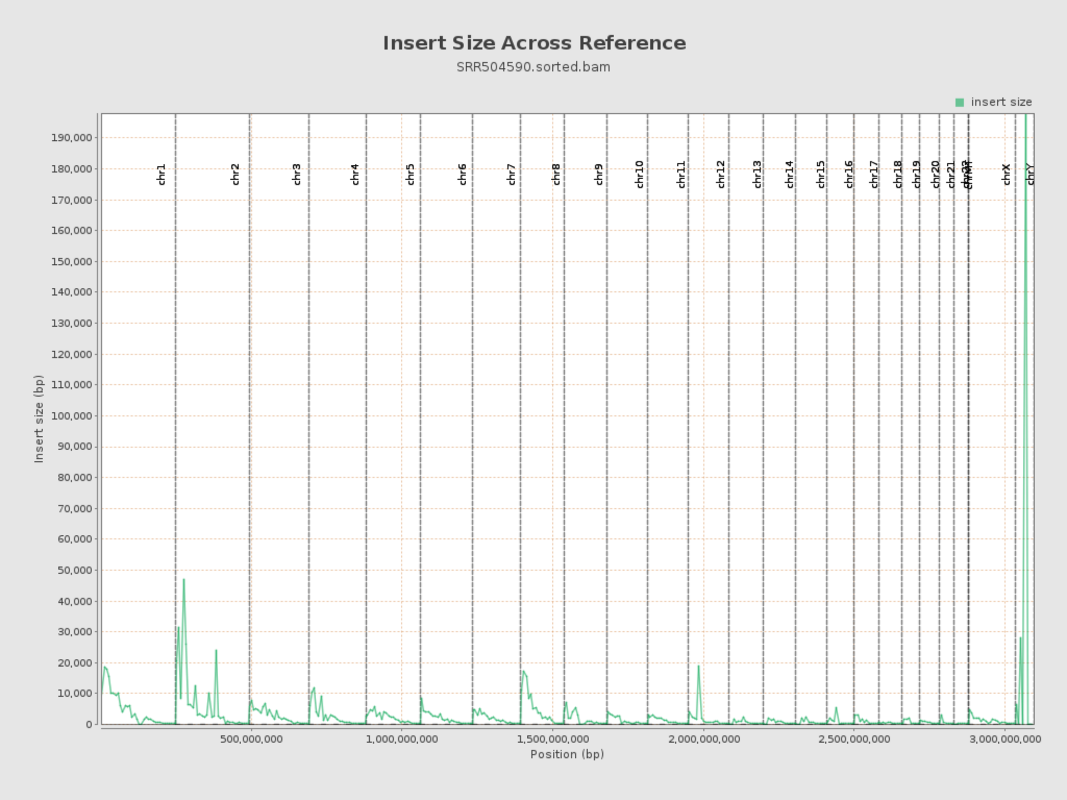
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram