Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/24 14:58:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504609.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_SRR504609 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504609_1.fastq.gz SRR504609_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 24 14:58:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504609.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	434,871,932
Mapped reads	289,771,002 / 66.63%
Unmapped reads	145,100,930 / 33.37%
Mapped paired reads	289,771,002 / 66.63%
Mapped reads, first in pair	145,061,853 / 33.36%
Mapped reads, second in pair	144,709,149 / 33.28%
Mapped reads, both in pair	288,156,098 / 66.26%
Mapped reads, singletons	1,614,904 / 0.37%
Secondary alignments	0
Supplementary alignments	1,831,032 / 0.42%
Read min/max/mean length	30 / 100 / 100.17
Duplicated reads (estimated)	74,779,805 / 17.2%
Duplication rate	22.48%
Clipped reads	14,279,453 / 3.28%

2.2. ACGT Content

Number/percentage of A's	7,429,398,026 / 25.82%
Number/percentage of C's	6,893,439,253 / 23.96%
Number/percentage of T's	7,478,871,126 / 25.99%
Number/percentage of G's	6,964,954,146 / 24.21%
Number/percentage of N's	5,492,079 / 0.02%

GC Percentage	48.17%

2.3. Coverage

Mean	9.2966
Standard Deviation	23.89

2.4. Mapping Quality

Mean Mapping Quality	53.78

2.5. Insert size

Mean	24,279.48
Standard Deviation	1,506,321.31
P25/Median/P75	173 / 207 / 264

2.6. Mismatches and indels

General error rate	0.5%
Mismatches	140,340,491
Insertions	2,138,659
Mapped reads with at least one insertion	0.72%
Deletions	2,817,301
Mapped reads with at least one deletion	0.94%
Homopolymer indels	39.95%

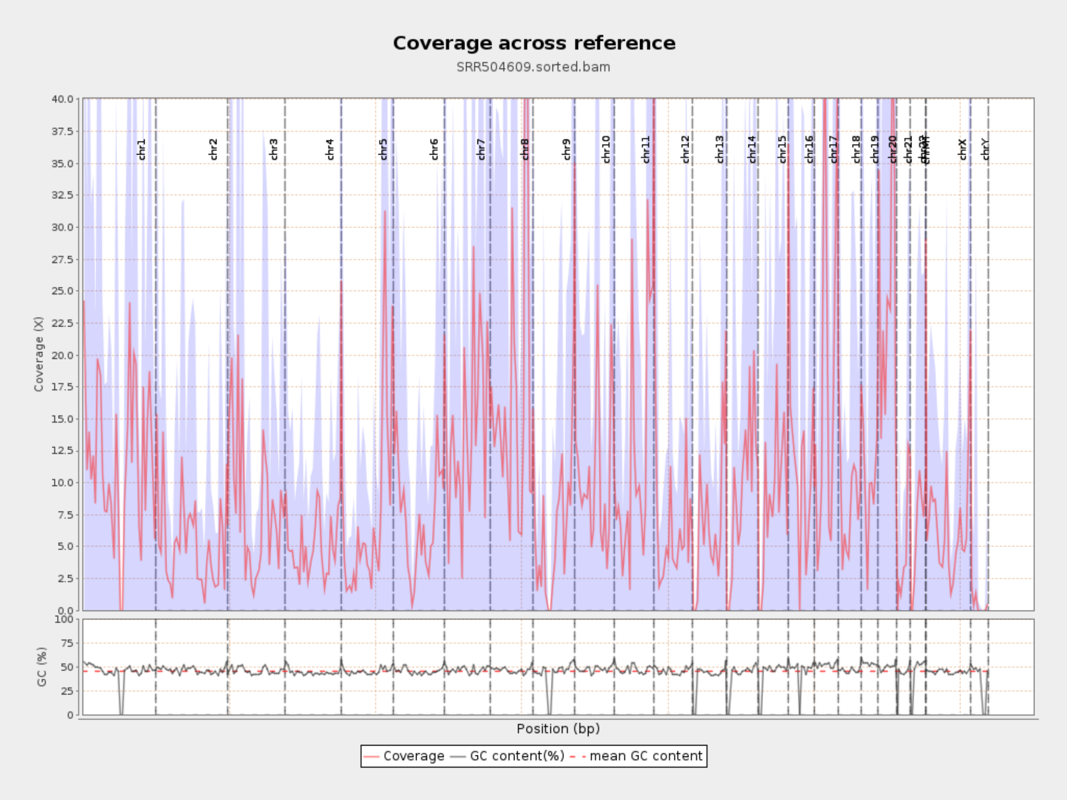
2.7. Chromosome stats

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

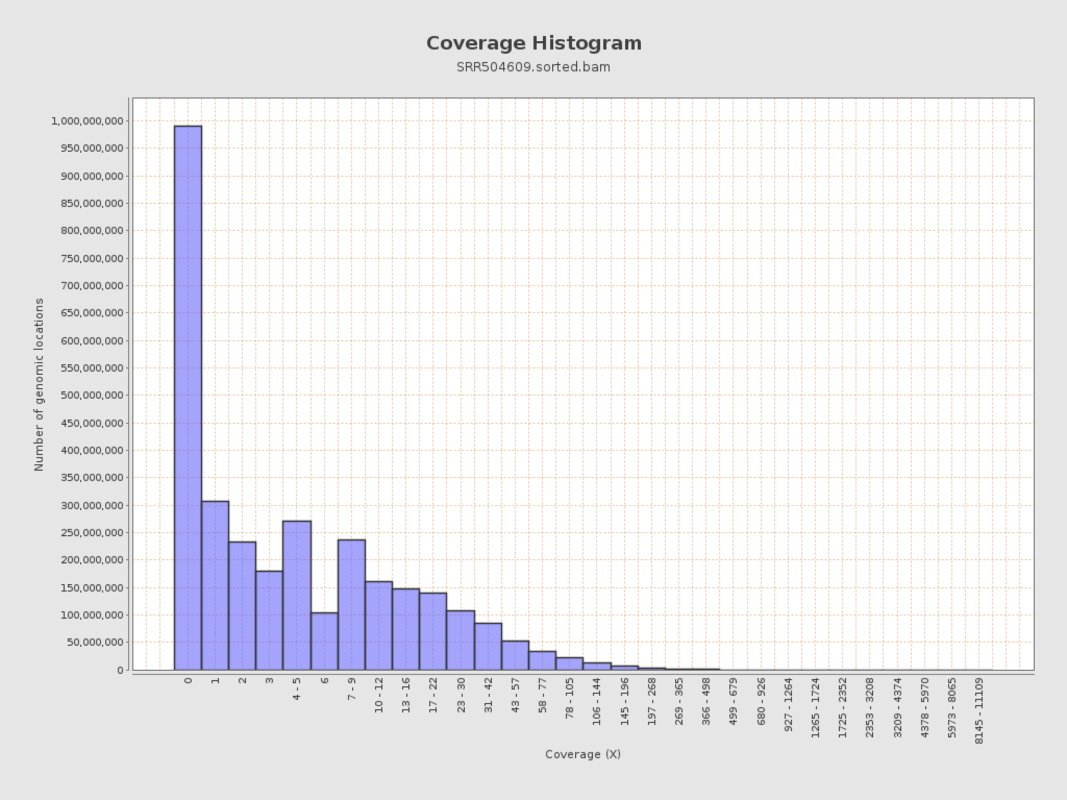
		bases	coverage	deviation
chr1	249250621	2916280186	11.7002	23.2985
chr2	243199373	1284790927	5.2829	13.2812
chr3	198022430	1626467511	8.2136	22.2727
chr4	191154276	970871084	5.079	9.6404
chr5	180915260	1402767605	7.7537	22.1406
chr6	171115067	1220555323	7.133	13.8341
chr7	159138663	2303051143	14.472	26.7372
chr8	146364022	2594174010	17.7241	42.2588
chr9	141213431	878439176	6.2206	17.3755
chr10	135534747	1414383415	10.4356	21.5852
chr11	135006516	1621928999	12.0137	27.5878
chr12	133851895	868432633	6.488	16.0324
chr13	115169878	786998215	6.8334	15.2367
chr14	107349540	1019839272	9.5002	19.0263
chr15	102531392	877926037	8.5625	17.8424
chr16	90354753	1073642103	11.8825	26.8129
chr17	81195210	1397607290	17.2129	55.4031
chr18	78077248	657696891	8.4237	24.2317
chr19	59128983	604445123	10.2225	21.9155
chr20	63025520	1633305793	25.915	46.2371
chr21	48129895	239724287	4.9808	12.9067
chr22	51304566	316172915	6.1627	15.8866
chrMT	16571	481899	29.0809	12.6413
chrX	155270560	1041865210	6.71	12.5506

chrY	59373566	27617091	0.4651	10.7076

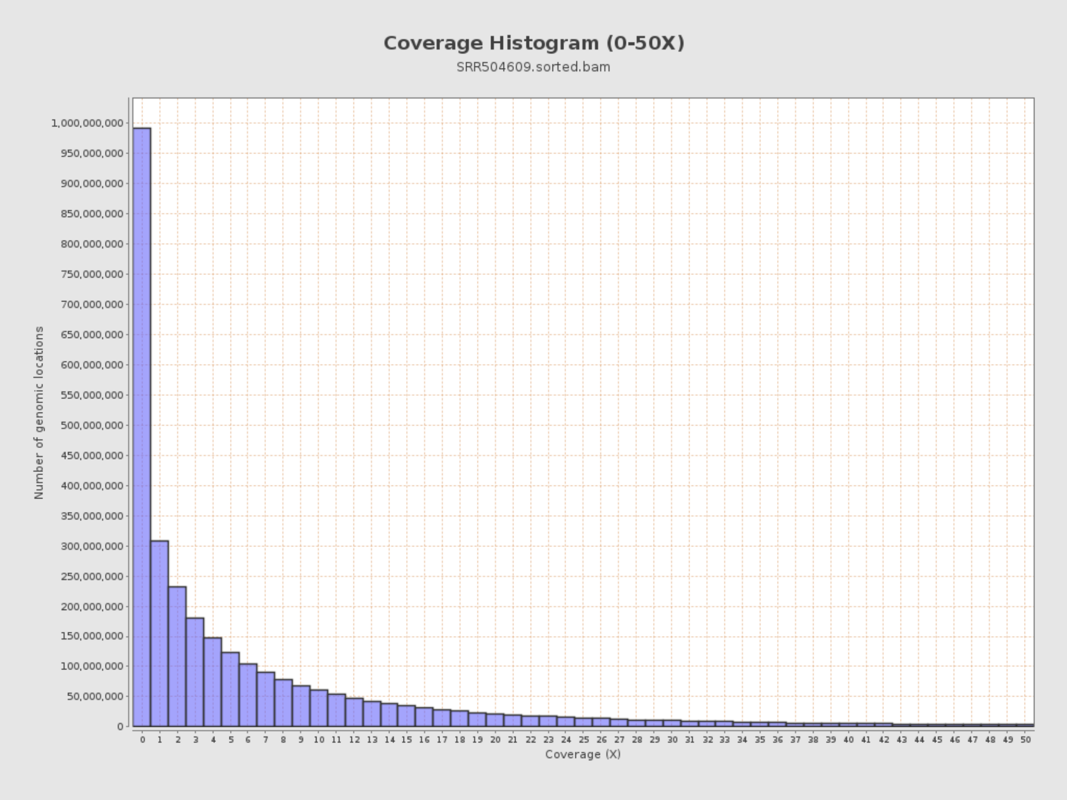
3. Results : Coverage across reference



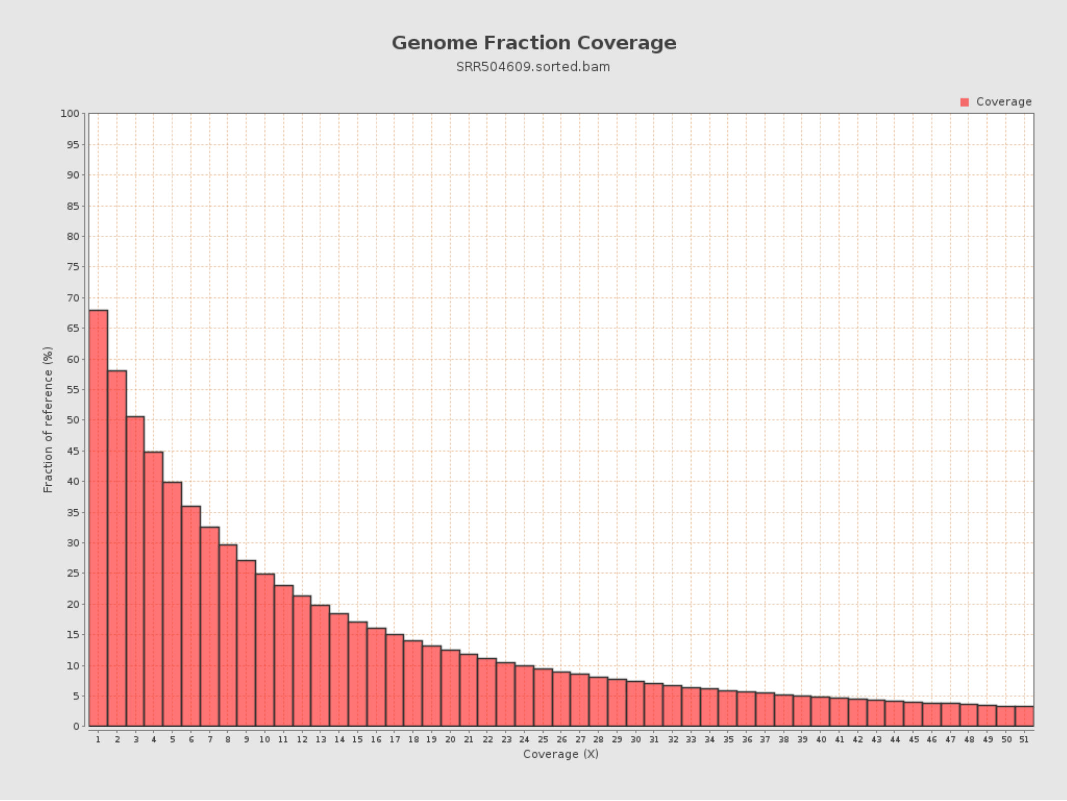
4. Results : Coverage Histogram



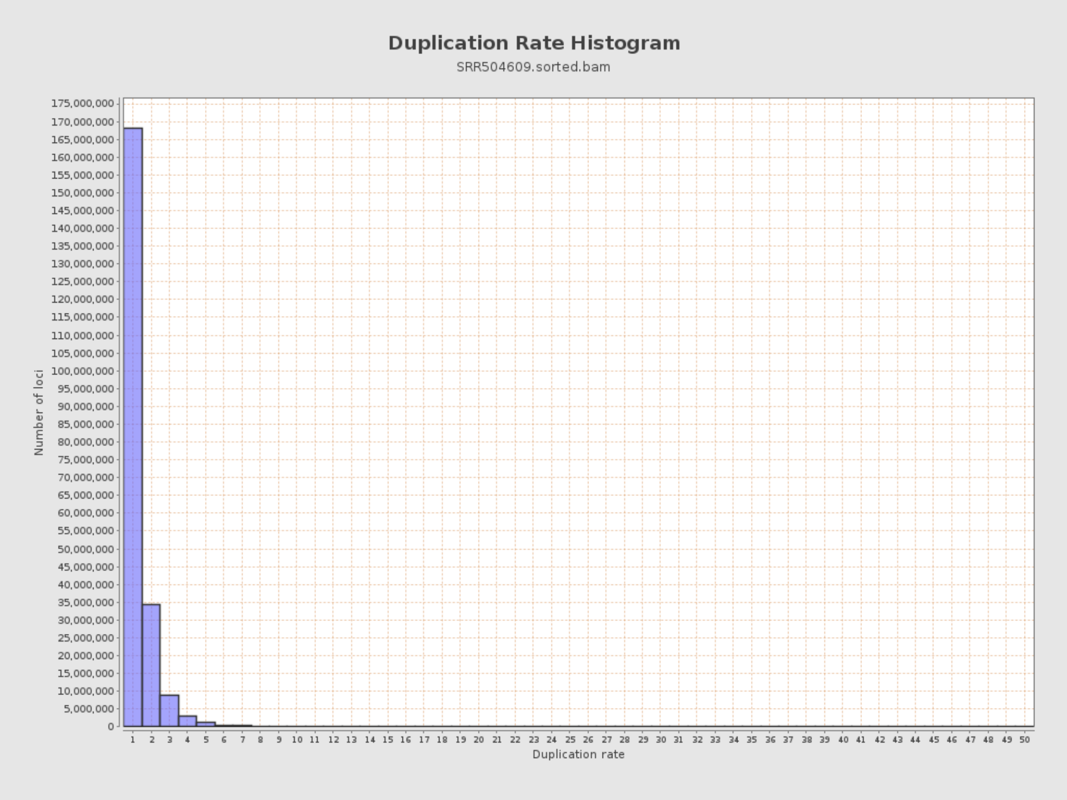
5. Results : Coverage Histogram (0-50X)



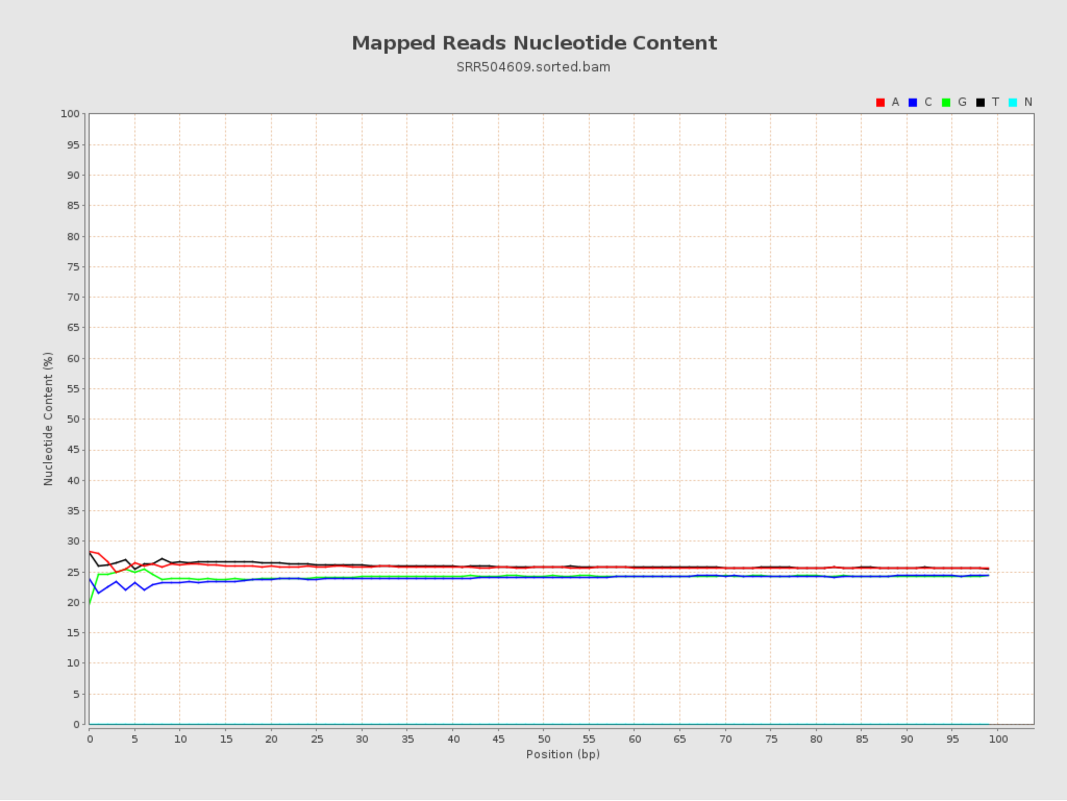
6. Results : Genome Fraction Coverage



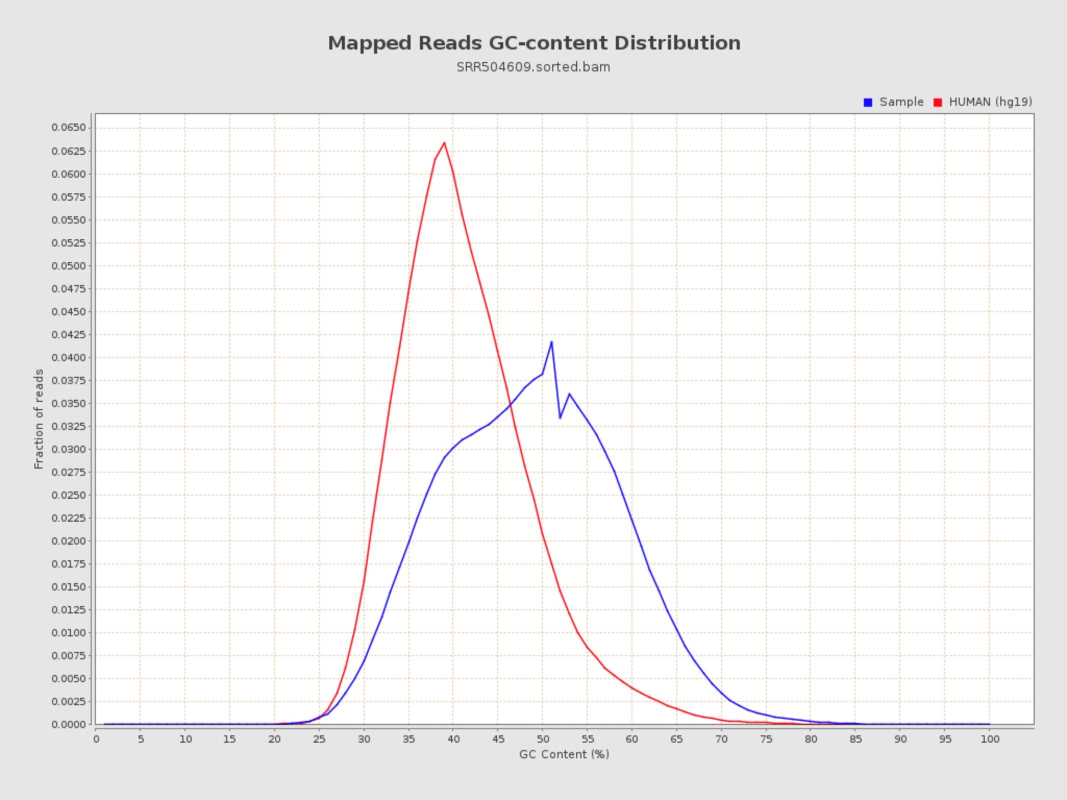
7. Results : Duplication Rate Histogram



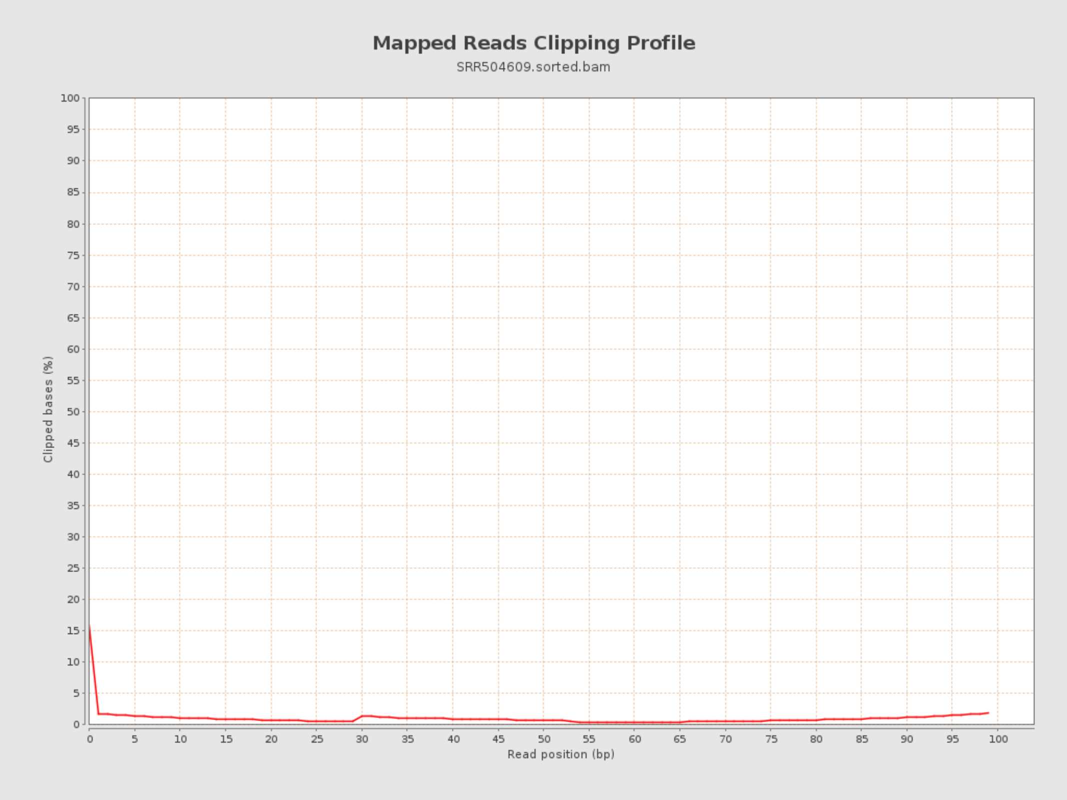
8. Results : Mapped Reads Nucleotide Content



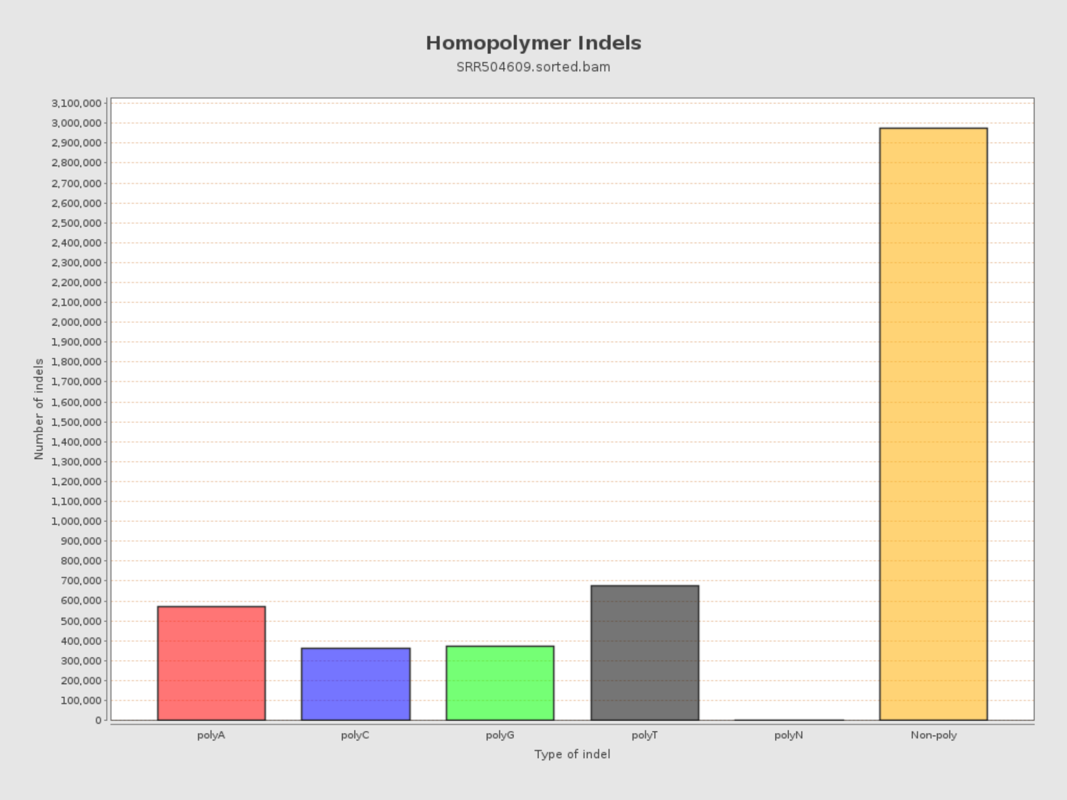
9. Results : Mapped Reads GC-content Distribution



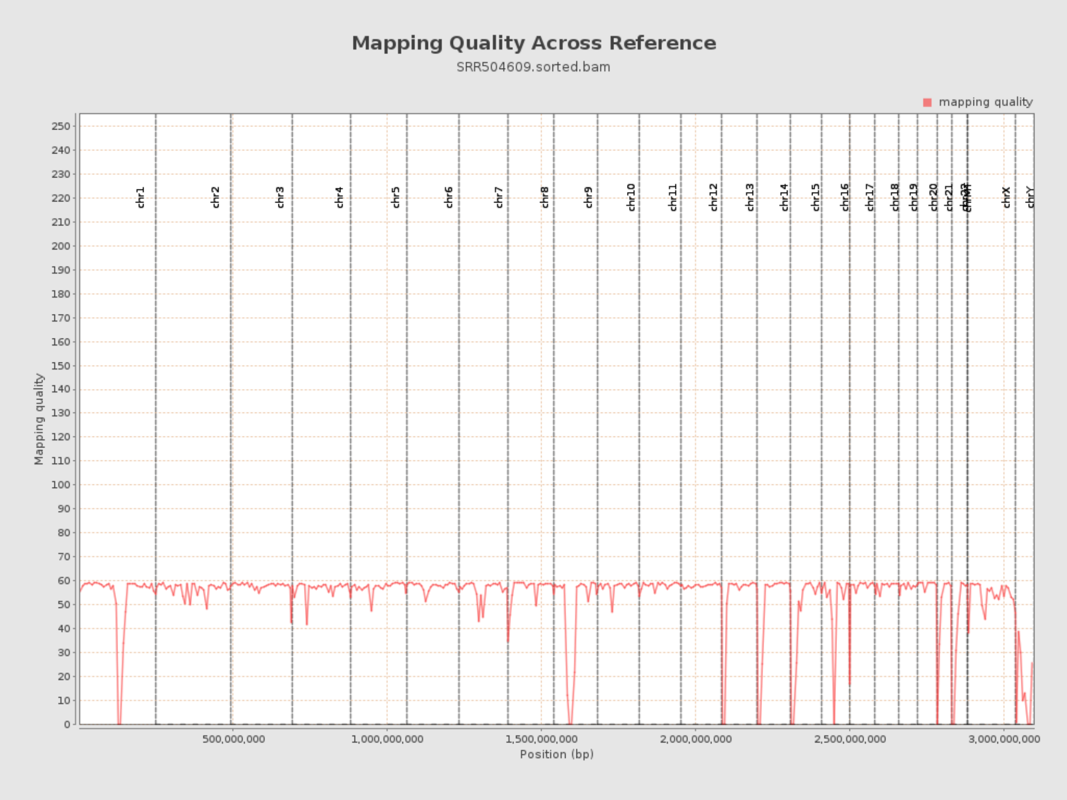
10. Results : Mapped Reads Clipping Profile



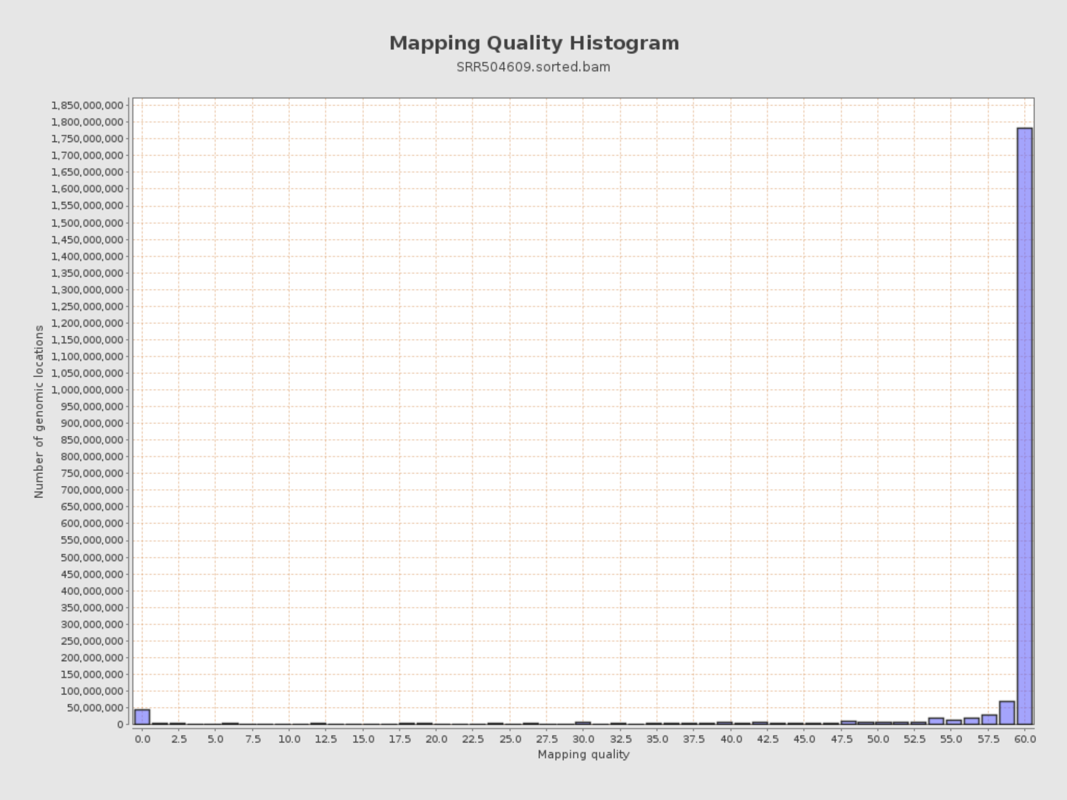
11. Results : Homopolymer Indels



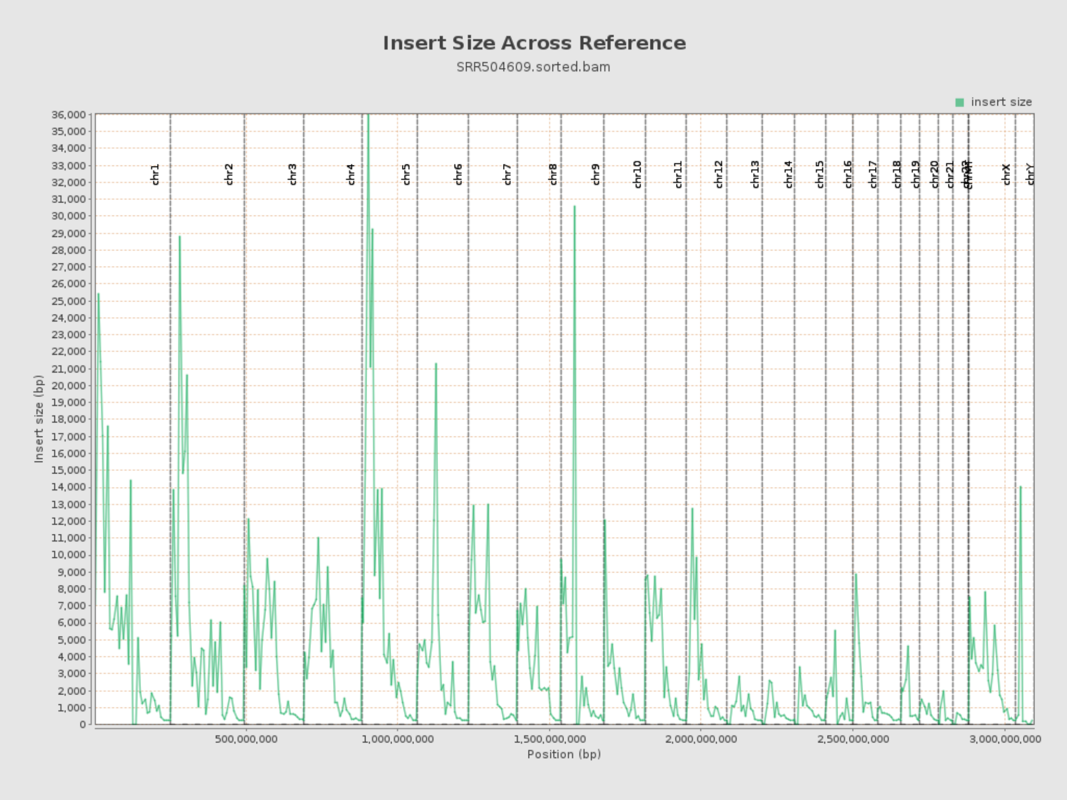
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram