Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/25 09:56:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504612.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_SRR504612 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504612_1.fastq.gz SRR504612_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 25 09:56:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504612.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	480,339,368
Mapped reads	319,404,949 / 66.5%
Unmapped reads	160,934,419 / 33.5%
Mapped paired reads	319,404,949 / 66.5%
Mapped reads, first in pair	159,908,356 / 33.29%
Mapped reads, second in pair	159,496,593 / 33.2%
Mapped reads, both in pair	317,171,248 / 66.03%
Mapped reads, singletons	2,233,701 / 0.47%
Secondary alignments	0
Supplementary alignments	2,028,887 / 0.42%
Read min/max/mean length	30 / 100 / 100.17
Duplicated reads (estimated)	87,978,846 / 18.32%
Duplication rate	23.93%
Clipped reads	15,688,914 / 3.27%

2.2. ACGT Content

Number/percentage of A's	8,193,551,307 / 25.84%
Number/percentage of C's	7,580,177,588 / 23.9%
Number/percentage of T's	8,235,947,334 / 25.97%
Number/percentage of G's	7,678,282,912 / 24.21%
Number/percentage of N's	23,562,787 / 0.07%

GC Percentage	48.12%

2.3. Coverage

Mean	10.2464
Standard Deviation	26.4252

2.4. Mapping Quality

Mean Mapping Quality	53.75

2.5. Insert size

Mean	25,812.88
Standard Deviation	1,552,207.62
P25/Median/P75	173 / 207 / 264

2.6. Mismatches and indels

General error rate	0.61%
Mismatches	186,698,086
Insertions	2,356,042
Mapped reads with at least one insertion	0.72%
Deletions	3,141,382
Mapped reads with at least one deletion	0.95%
Homopolymer indels	40.01%

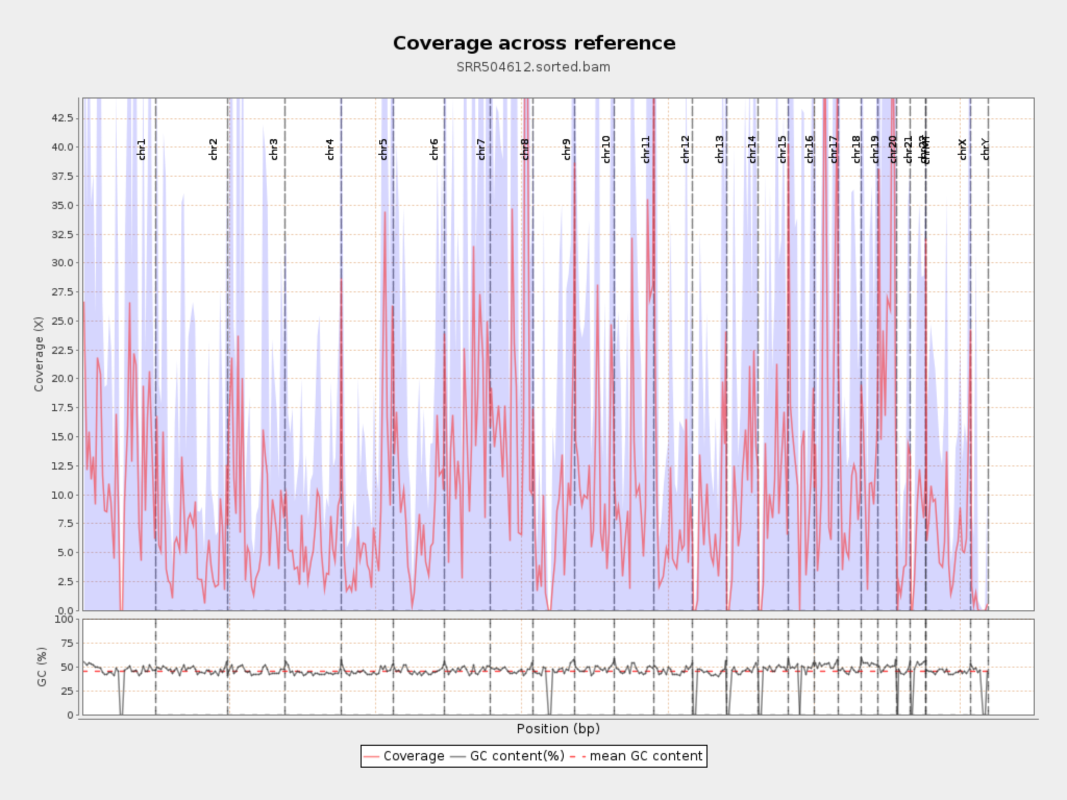
2.7. Chromosome stats

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

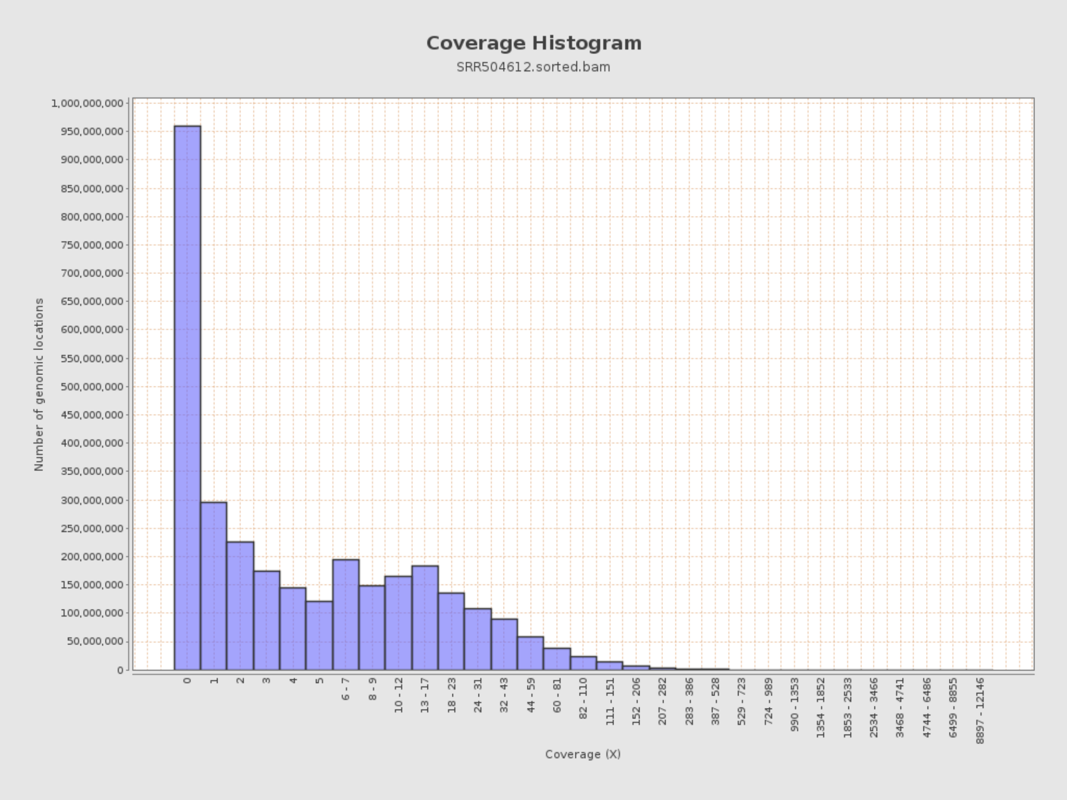
		bases	coverage	deviation
chr1	249250621	3217191190	12.9075	25.7545
chr2	243199373	1417243673	5.8275	15.6338
chr3	198022430	1791658182	9.0478	24.558
chr4	191154276	1069675410	5.5959	10.6322
chr5	180915260	1546597180	8.5487	24.4734
chr6	171115067	1343805484	7.8532	15.2584
chr7	159138663	2538105466	15.949	29.4972
chr8	146364022	2856507769	19.5165	46.8013
chr9	141213431	967788543	6.8534	19.0714
chr10	135534747	1559929233	11.5094	23.8245
chr11	135006516	1787852272	13.2427	30.4237
chr12	133851895	956579982	7.1466	17.9066
chr13	115169878	866970449	7.5278	16.8146
chr14	107349540	1123987164	10.4703	20.944
chr15	102531392	966791728	9.4292	19.6468
chr16	90354753	1184284052	13.107	29.6197
chr17	81195210	1540978445	18.9787	61.3159
chr18	78077248	724453450	9.2787	26.4205
chr19	59128983	667166775	11.2832	24.1748
chr20	63025520	1801164316	28.5783	51.0108
chr21	48129895	264044934	5.4861	14.154
chr22	51304566	348481180	6.7924	17.5205
chrMT	16571	532298	32.1223	14.6649
chrX	155270560	1147557812	7.3907	13.8604

chrY	59373566	30287161	0.5101	11.7163

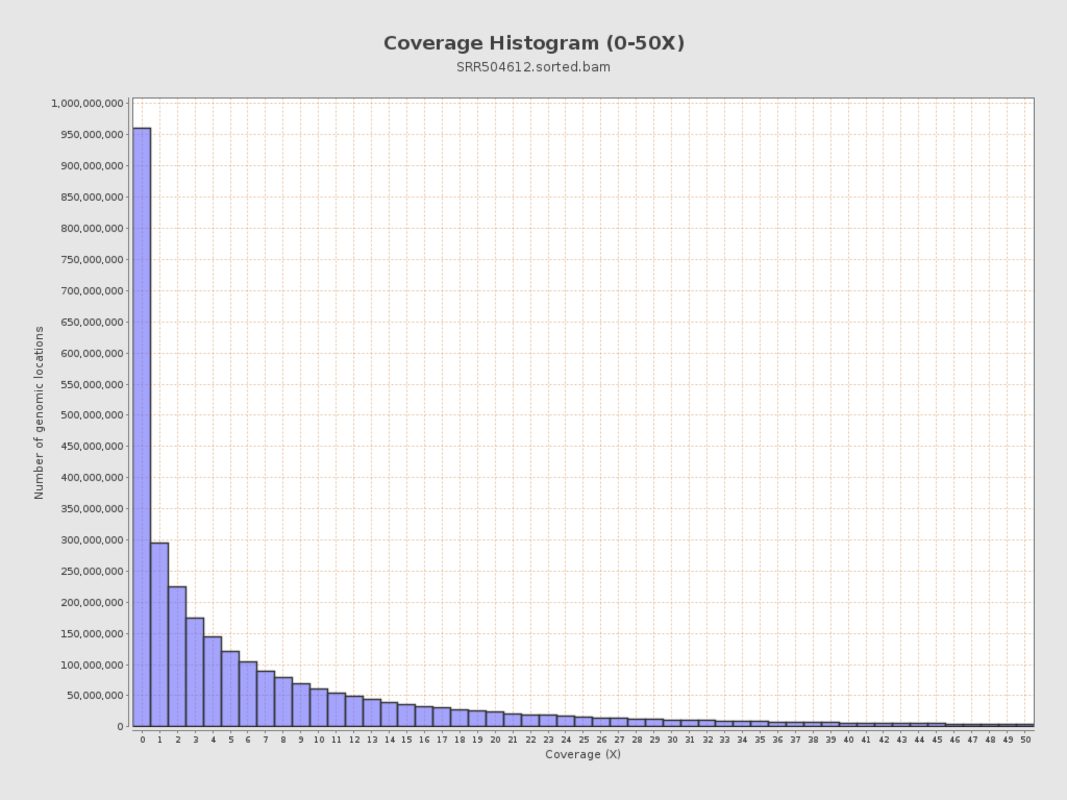
3. Results : Coverage across reference



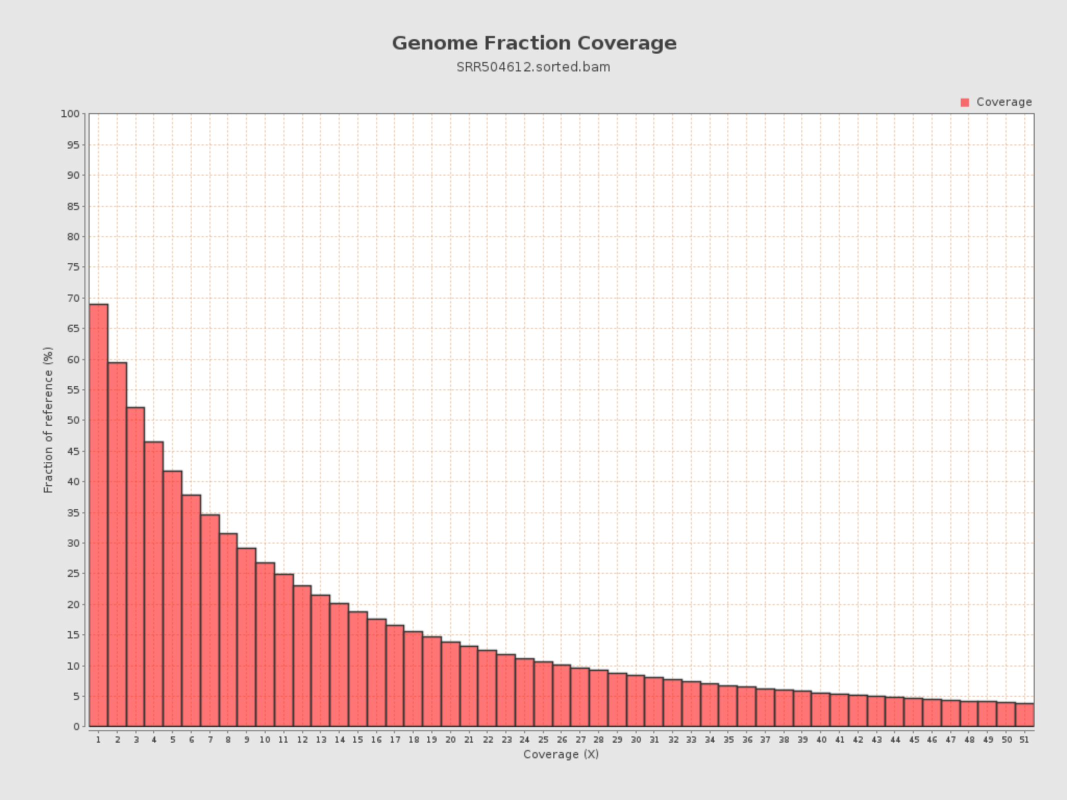
4. Results : Coverage Histogram



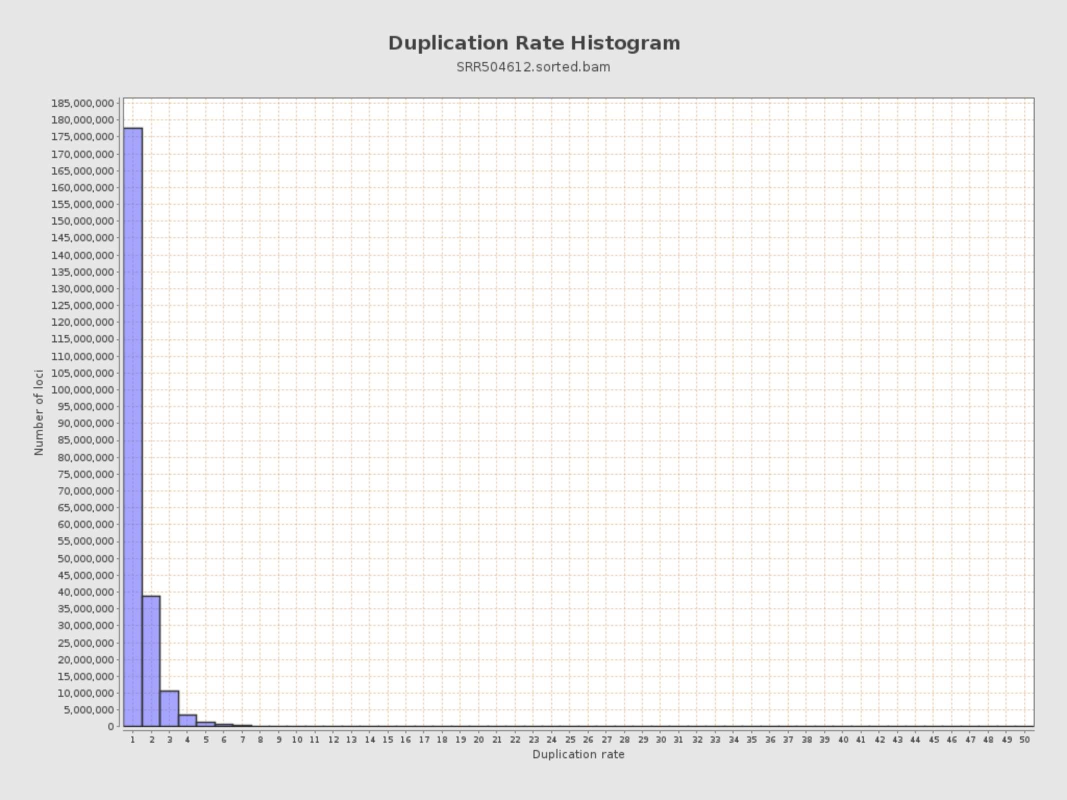
5. Results : Coverage Histogram (0-50X)



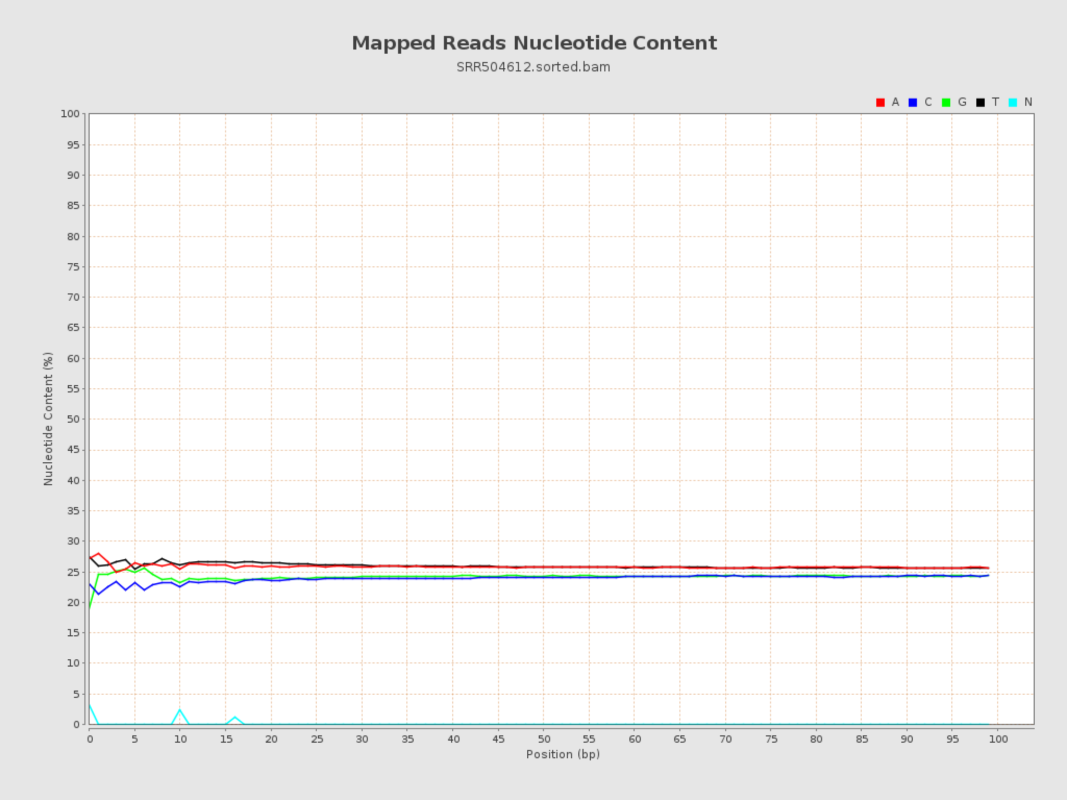
6. Results : Genome Fraction Coverage



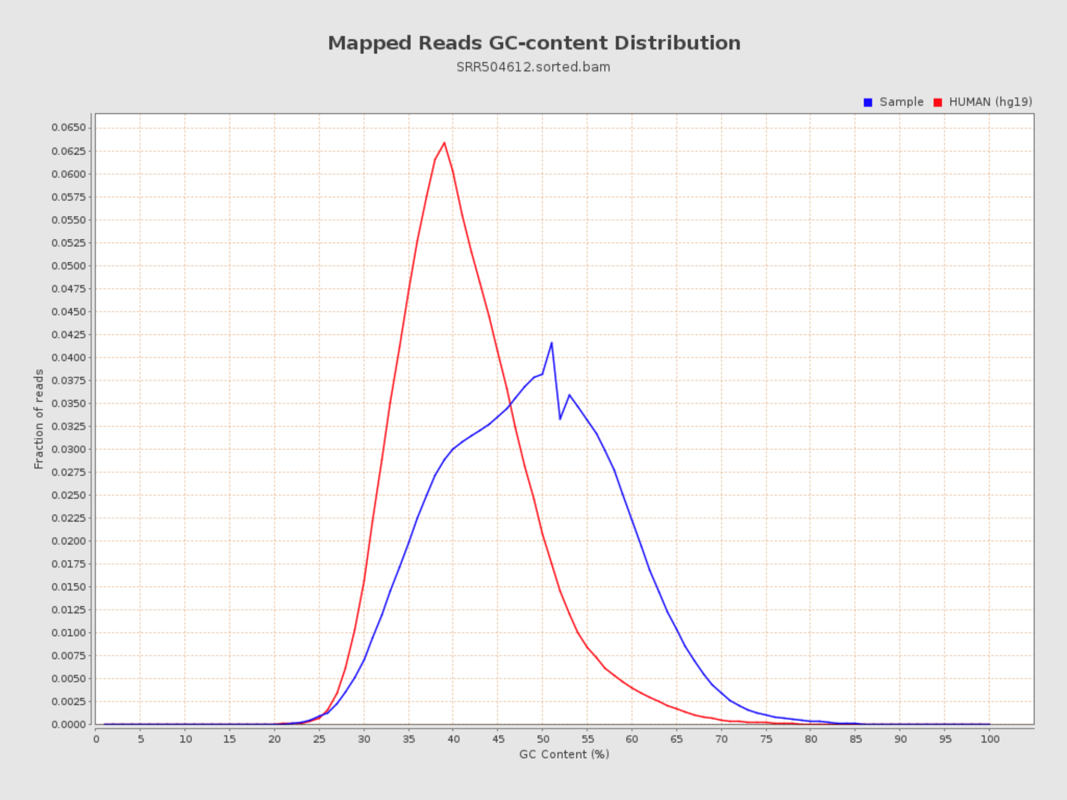
7. Results : Duplication Rate Histogram



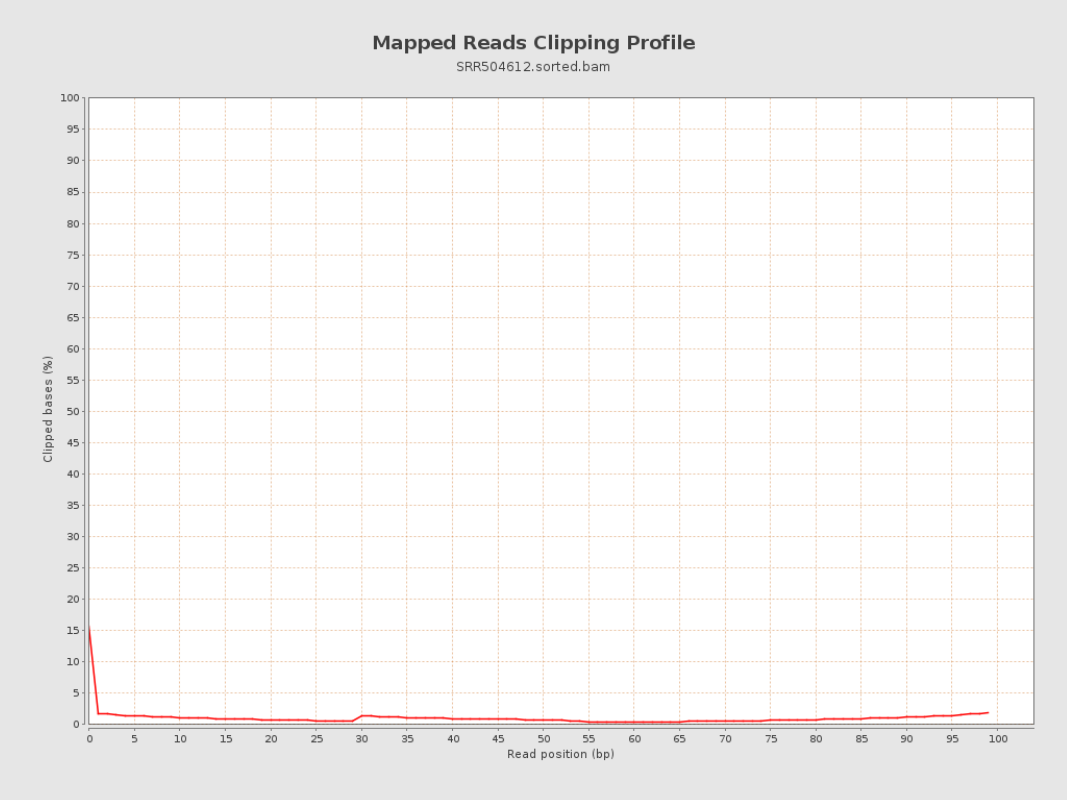
8. Results : Mapped Reads Nucleotide Content



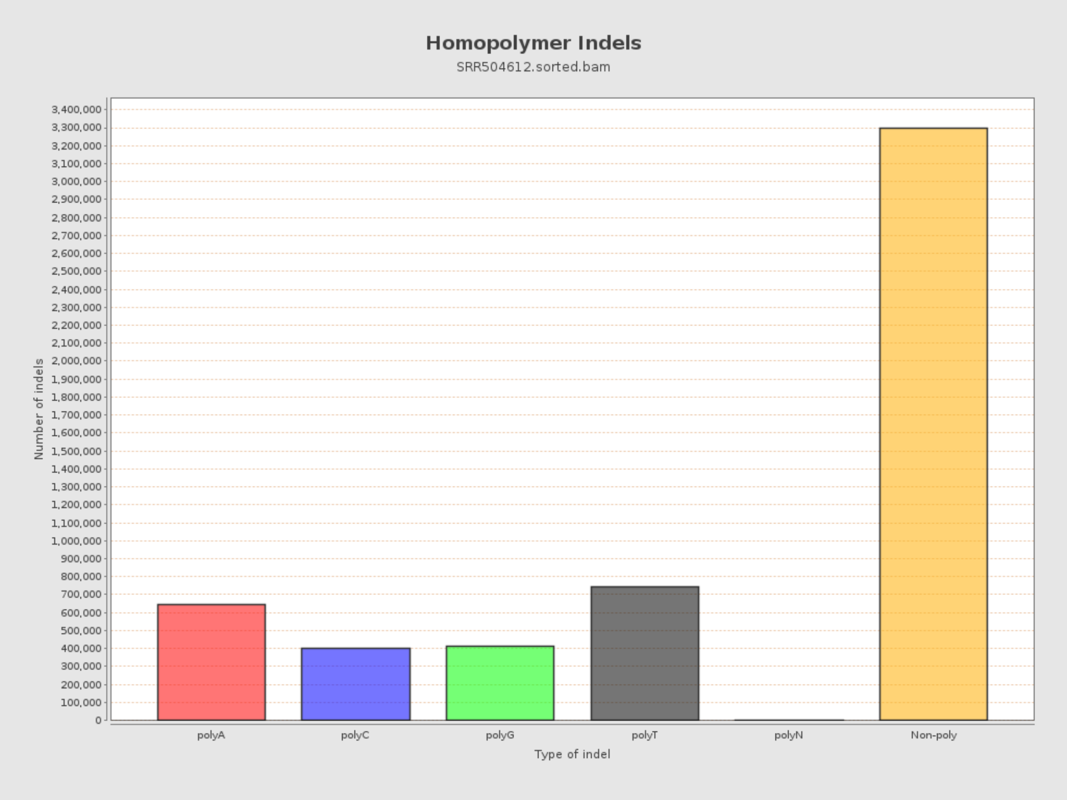
9. Results : Mapped Reads GC-content Distribution



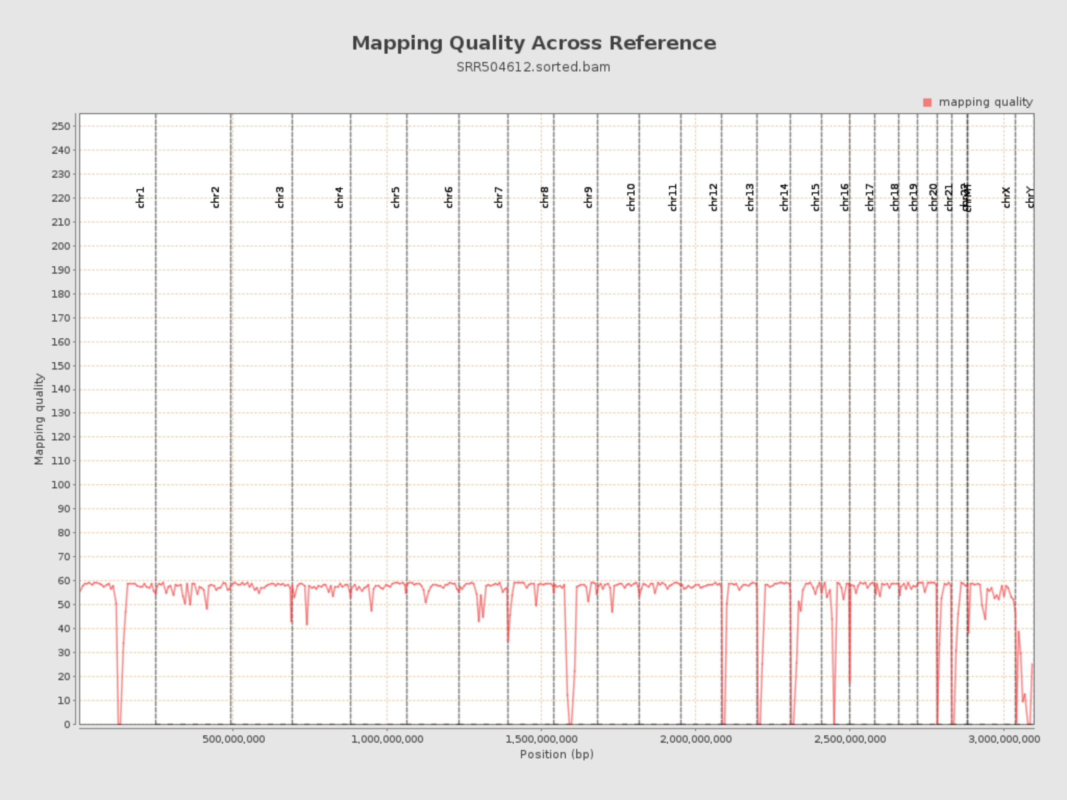
10. Results : Mapped Reads Clipping Profile



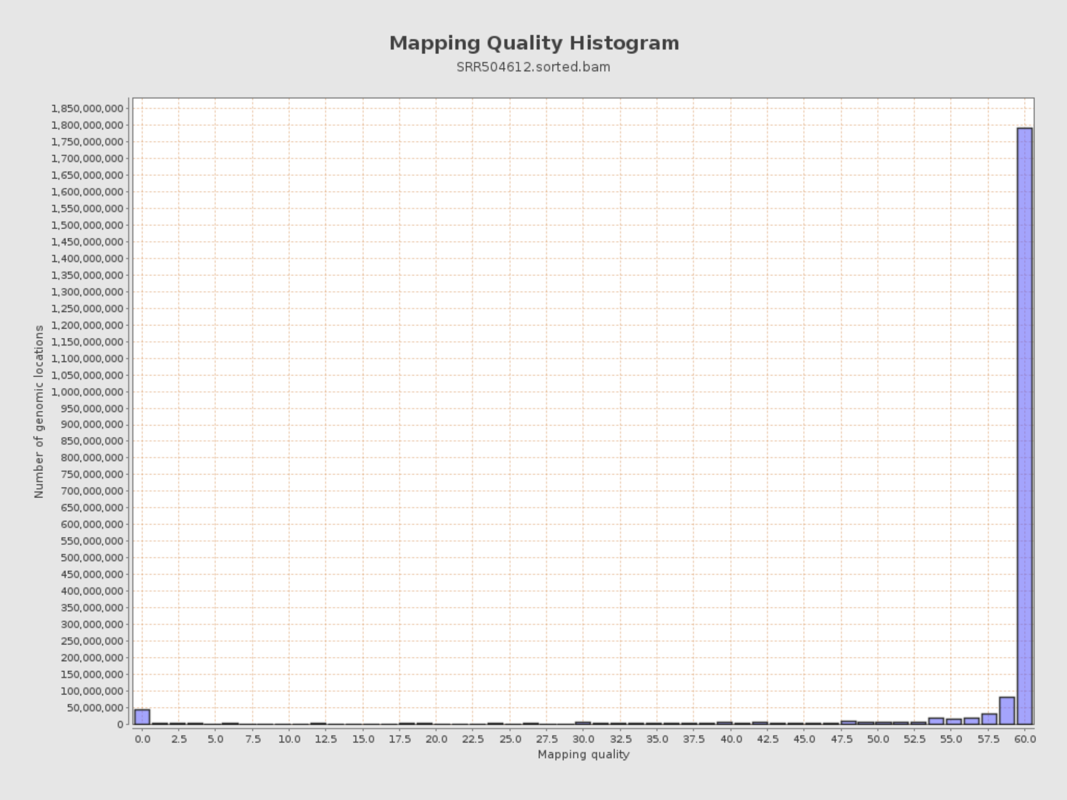
11. Results : Homopolymer Indels



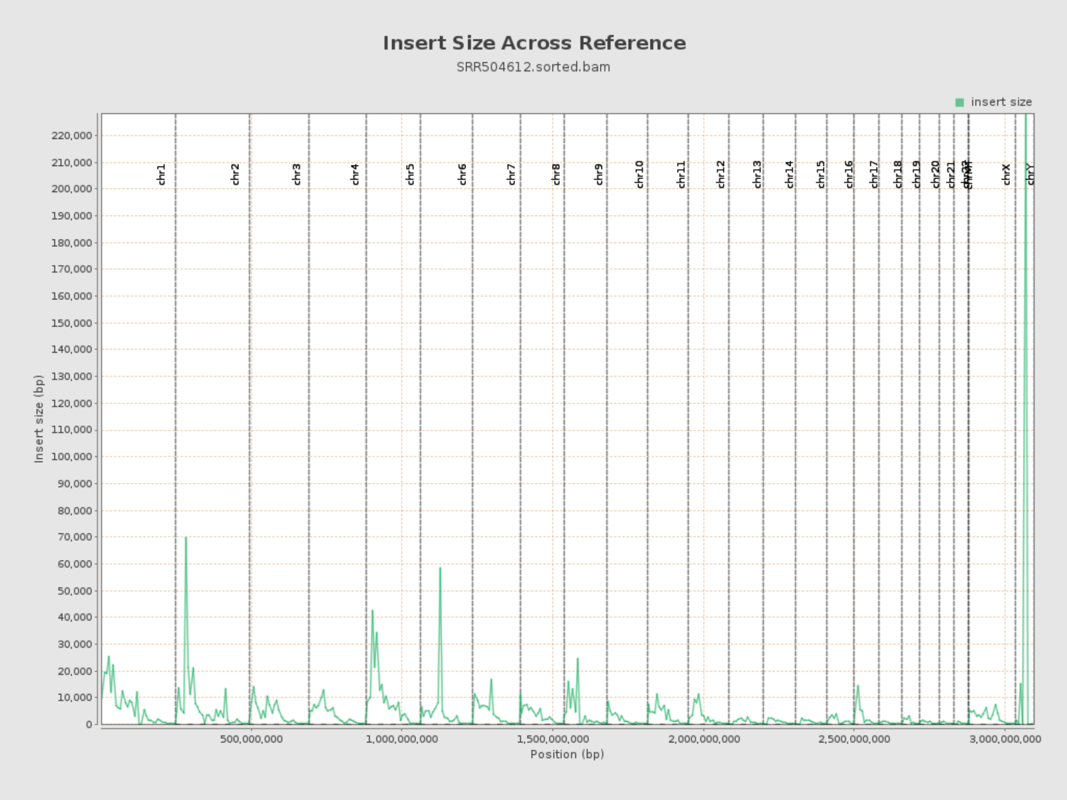
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram