Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 08:33:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975203.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_SRR975203 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975203_1.fastq.gz SRR975203_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 08:32:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975203.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,960,846
Mapped reads	2,926,411 / 98.84%
Unmapped reads	34,435 / 1.16%
Mapped paired reads	2,926,411 / 98.84%
Mapped reads, first in pair	1,464,862 / 49.47%
Mapped reads, second in pair	1,461,549 / 49.36%
Mapped reads, both in pair	2,916,584 / 98.51%
Mapped reads, singletons	9,827 / 0.33%
Secondary alignments	0
Supplementary alignments	39,889 / 1.35%
Read min/max/mean length	30 / 151 / 151.65
Duplicated reads (estimated)	503,165 / 16.99%
Duplication rate	14.69%
Clipped reads	2,126,206 / 71.81%

2.2. ACGT Content

Number/percentage of A's	119,805,229 / 29.83%
Number/percentage of C's	79,517,610 / 19.8%
Number/percentage of T's	119,550,381 / 29.77%
Number/percentage of G's	82,705,640 / 20.59%
Number/percentage of N's	24,754 / 0.01%

GC Percentage	40.39%

2.3. Coverage

Mean	0.1298
Standard Deviation	2.2972

2.4. Mapping Quality

Mean Mapping Quality	53.38

2.5. Insert size

Mean	83,537.66
Standard Deviation	2,772,142.93
P25/Median/P75	141 / 175 / 223

2.6. Mismatches and indels

General error rate	1.19%
Mismatches	4,557,045
Insertions	88,490
Mapped reads with at least one insertion	2.85%
Deletions	149,040
Mapped reads with at least one deletion	4.88%
Homopolymer indels	44.78%

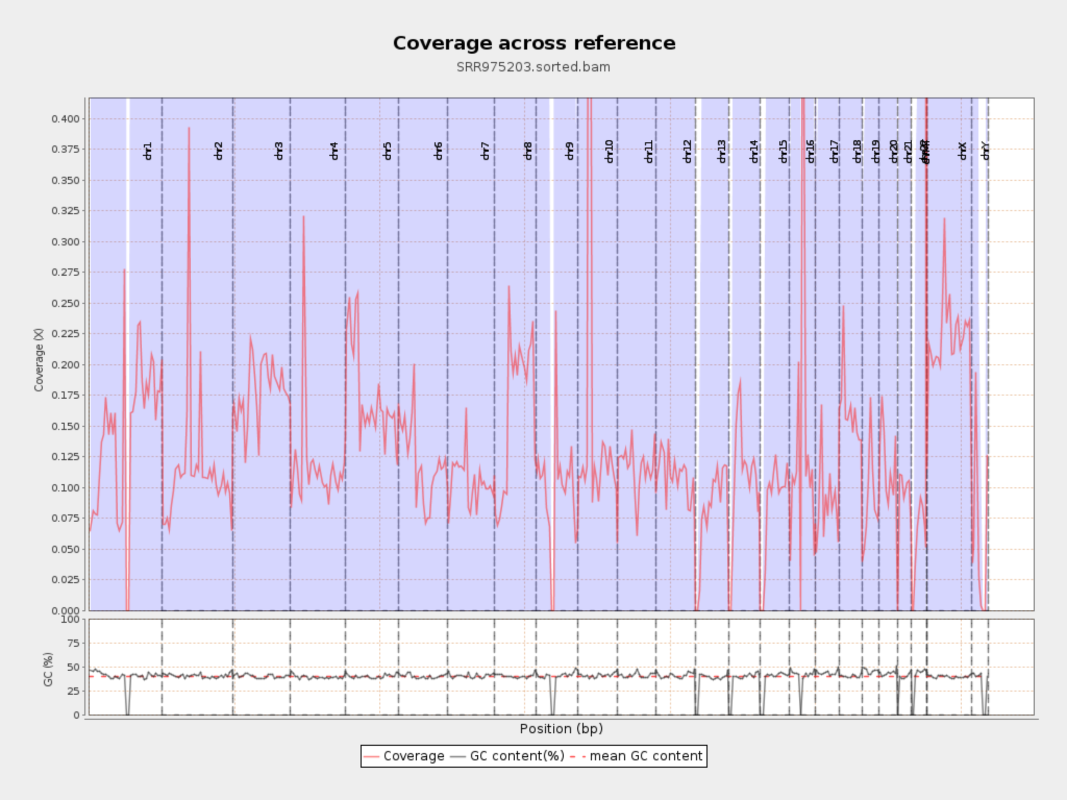
2.7. Chromosome stats

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

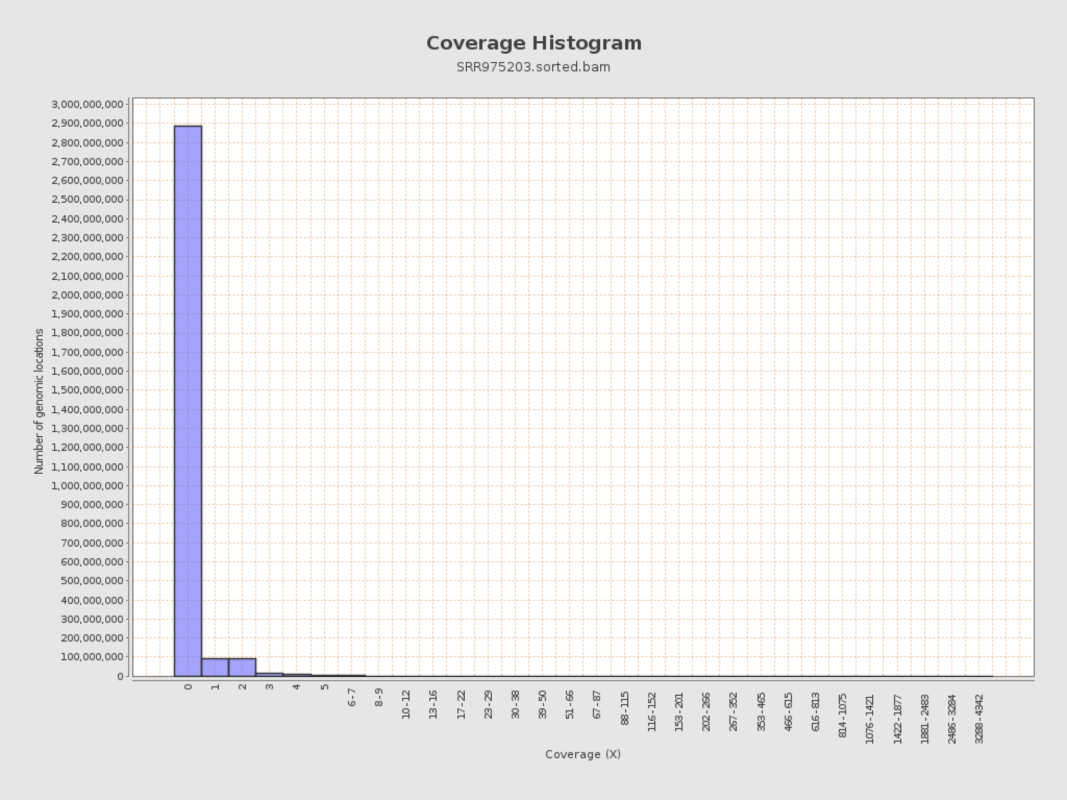
		bases	coverage	deviation
chr1	249250621	35590561	0.1428	2.2321
chr2	243199373	28165421	0.1158	1.9899
chr3	198022430	35452877	0.179	0.7484
chr4	191154276	22357625	0.117	1.4268
chr5	180915260	31737954	0.1754	0.6381
chr6	171115067	20661596	0.1207	0.8933
chr7	159138663	16763992	0.1053	1.11
chr8	146364022	24360070	0.1664	0.9151
chr9	141213431	13926955	0.0986	2.7046
chr10	135534747	22276259	0.1644	8.3195
chr11	135006516	15545316	0.1151	0.9877
chr12	133851895	14720598	0.11	0.4925
chr13	115169878	9294645	0.0807	0.4113
chr14	107349540	11418587	0.1064	0.5116
chr15	102531392	8679109	0.0846	0.4238
chr16	90354753	12895310	0.1427	3.2362
chr17	81195210	7050313	0.0868	1.6209
chr18	78077248	12795229	0.1639	2.6679
chr19	59128983	5481713	0.0927	1.1224
chr20	63025520	7545796	0.1197	0.7099
chr21	48129895	4359301	0.0906	0.869
chr22	51304566	2841122	0.0554	0.3581
chrMT	16571	148742	8.976	6.5805
chrX	155270560	34523119	0.2223	0.941

chrY	59373566	3323605	0.056	2.7525

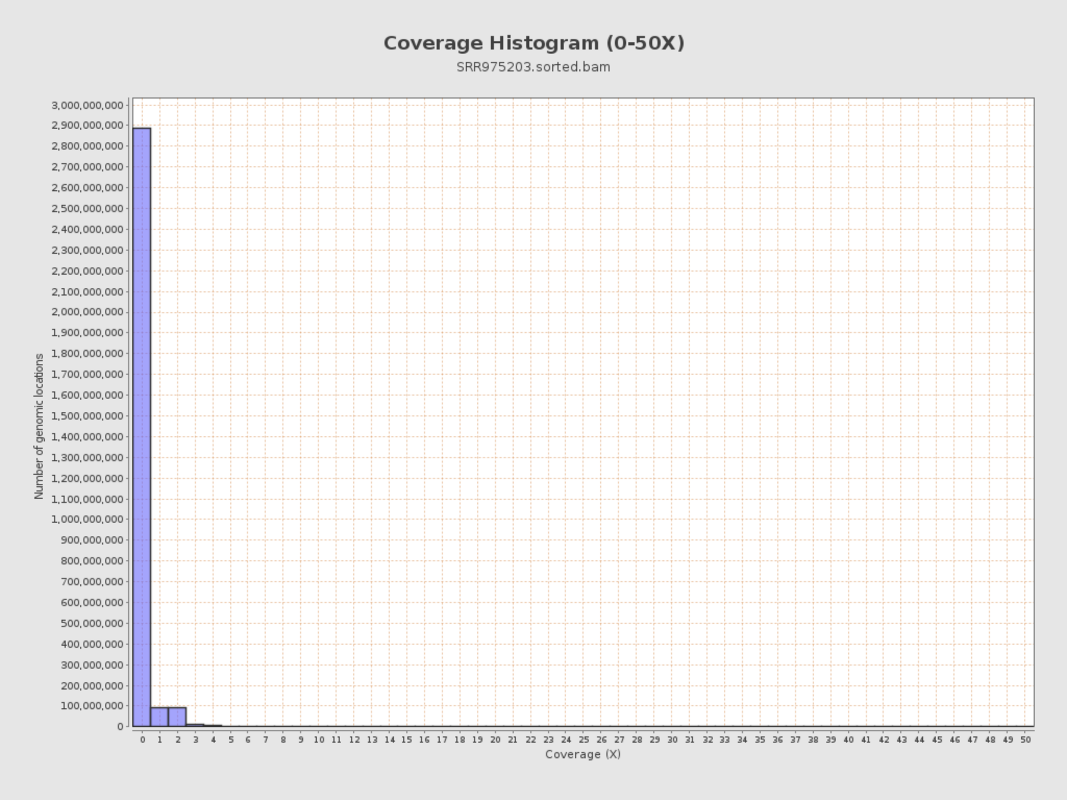
3. Results : Coverage across reference



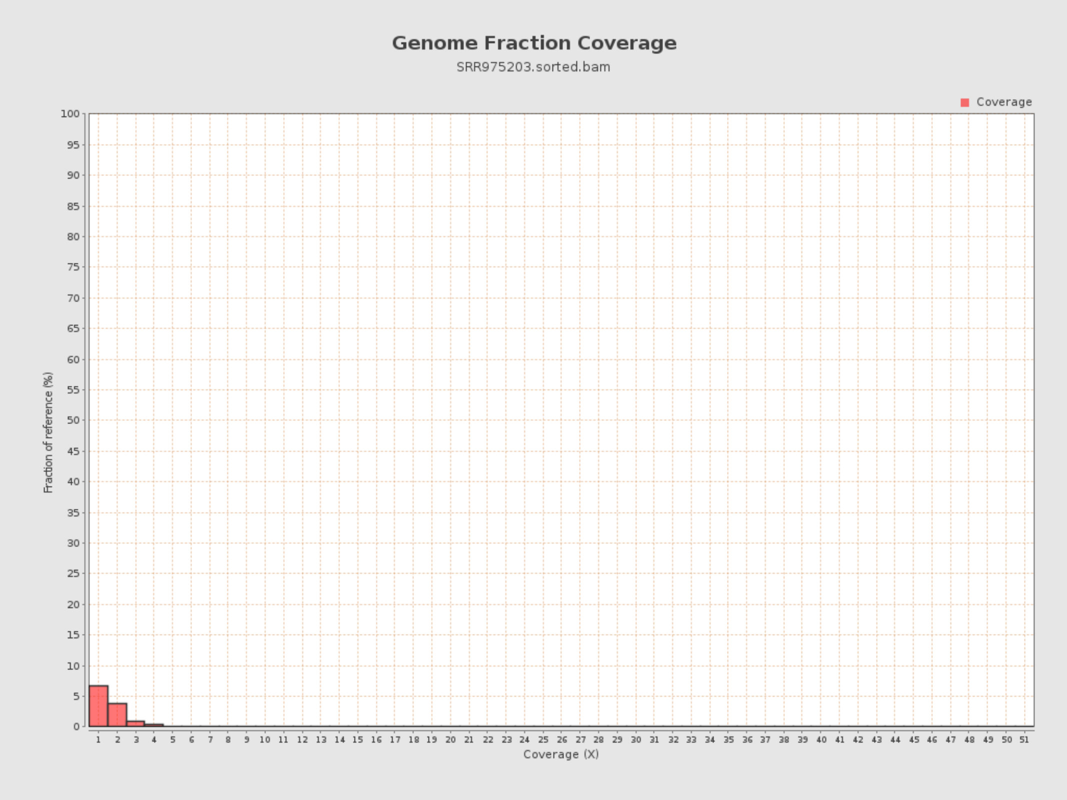
4. Results : Coverage Histogram



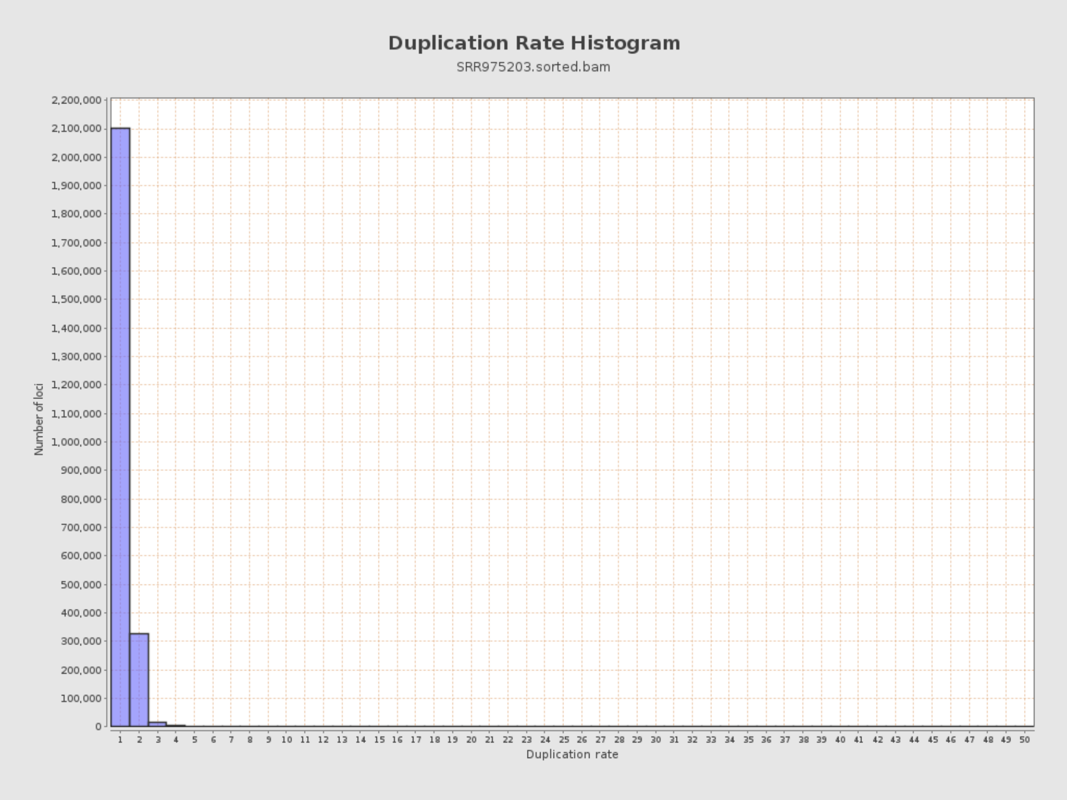
5. Results : Coverage Histogram (0-50X)



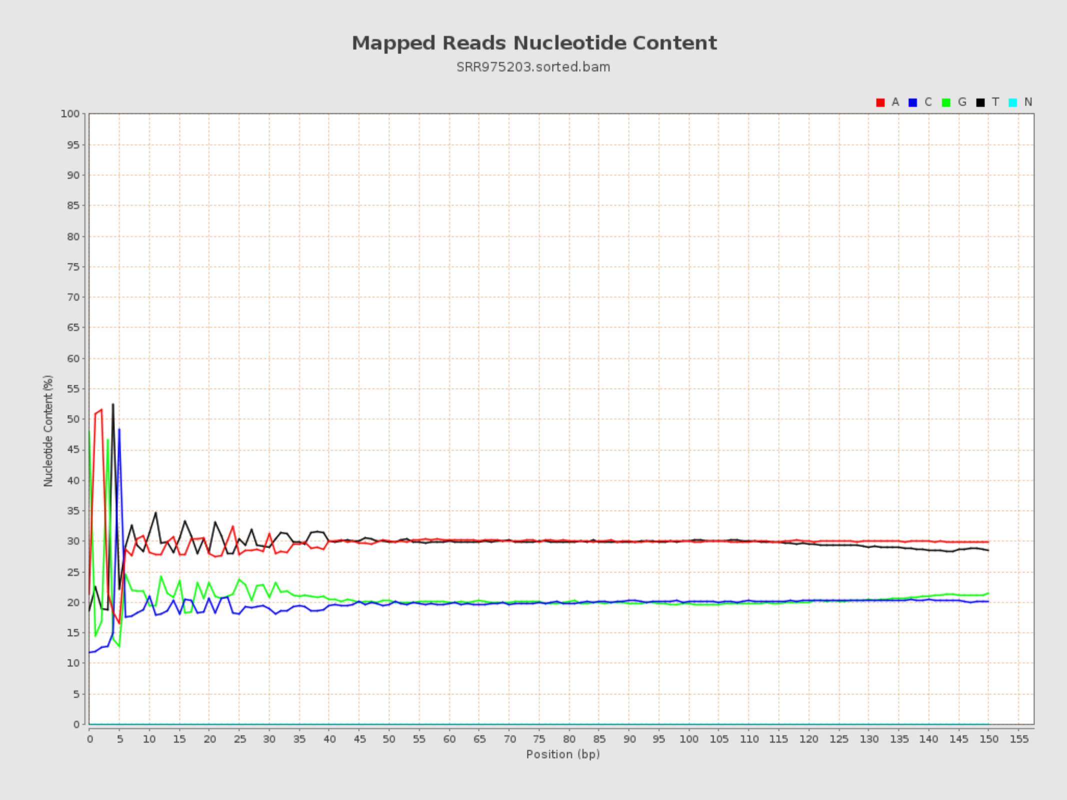
6. Results : Genome Fraction Coverage



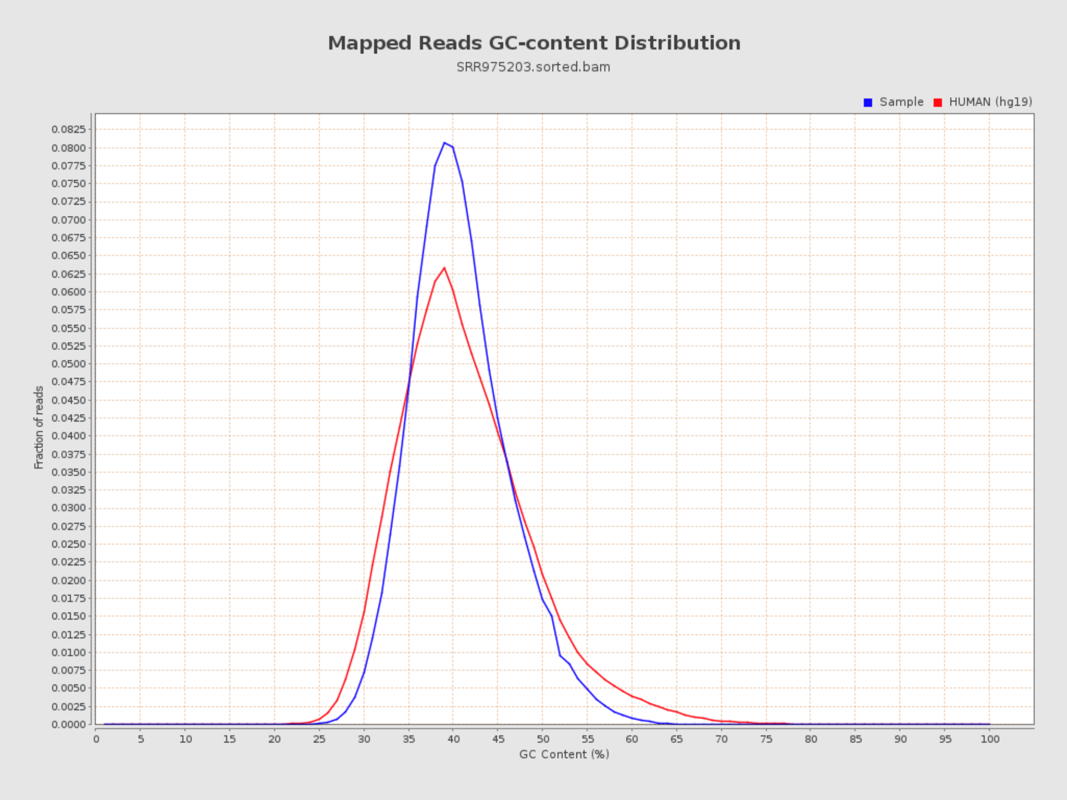
7. Results : Duplication Rate Histogram



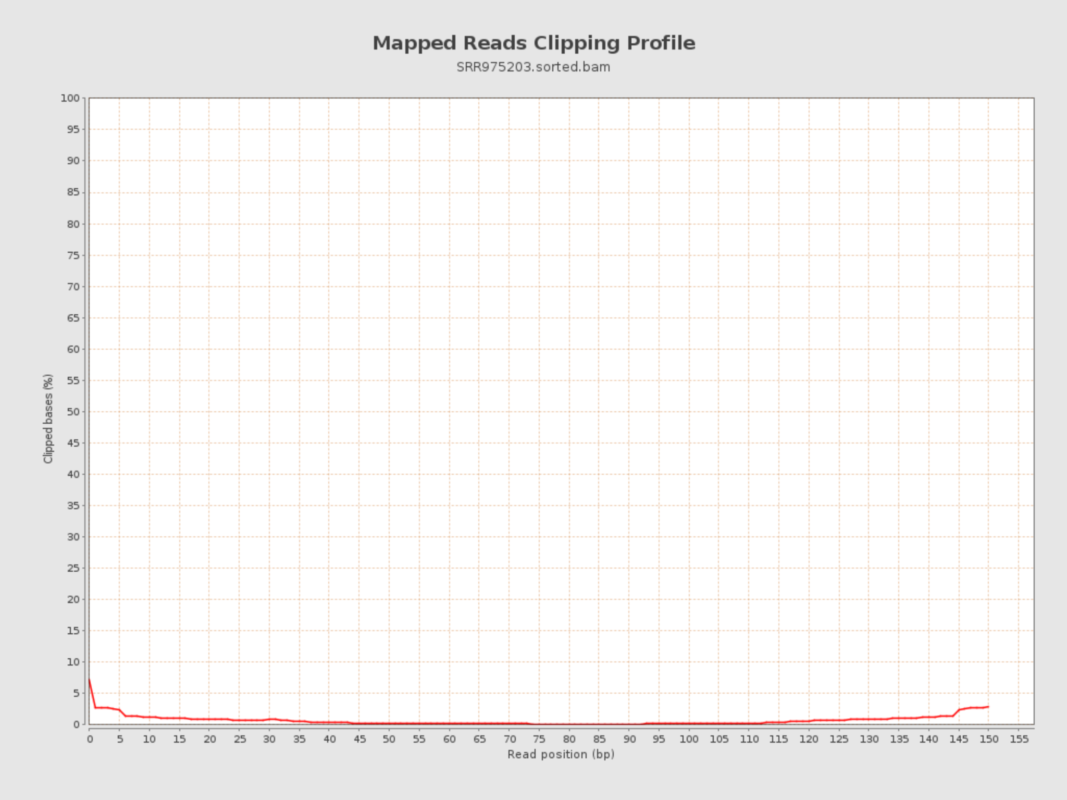
8. Results : Mapped Reads Nucleotide Content



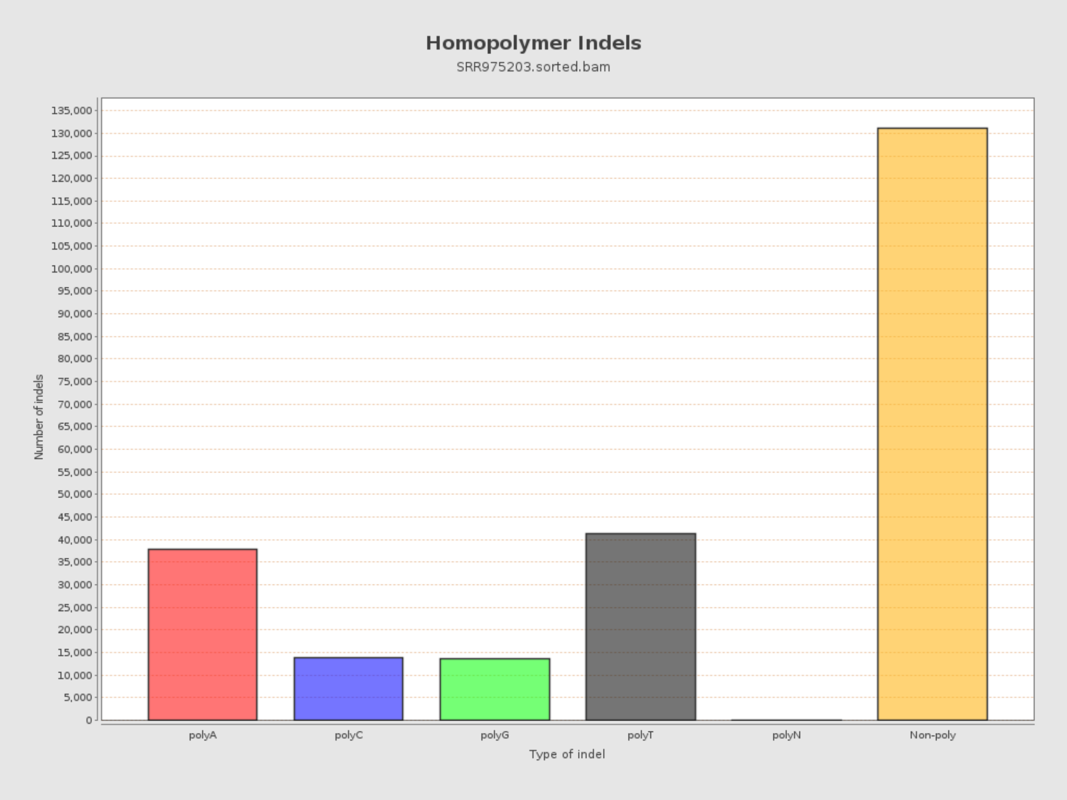
9. Results : Mapped Reads GC-content Distribution



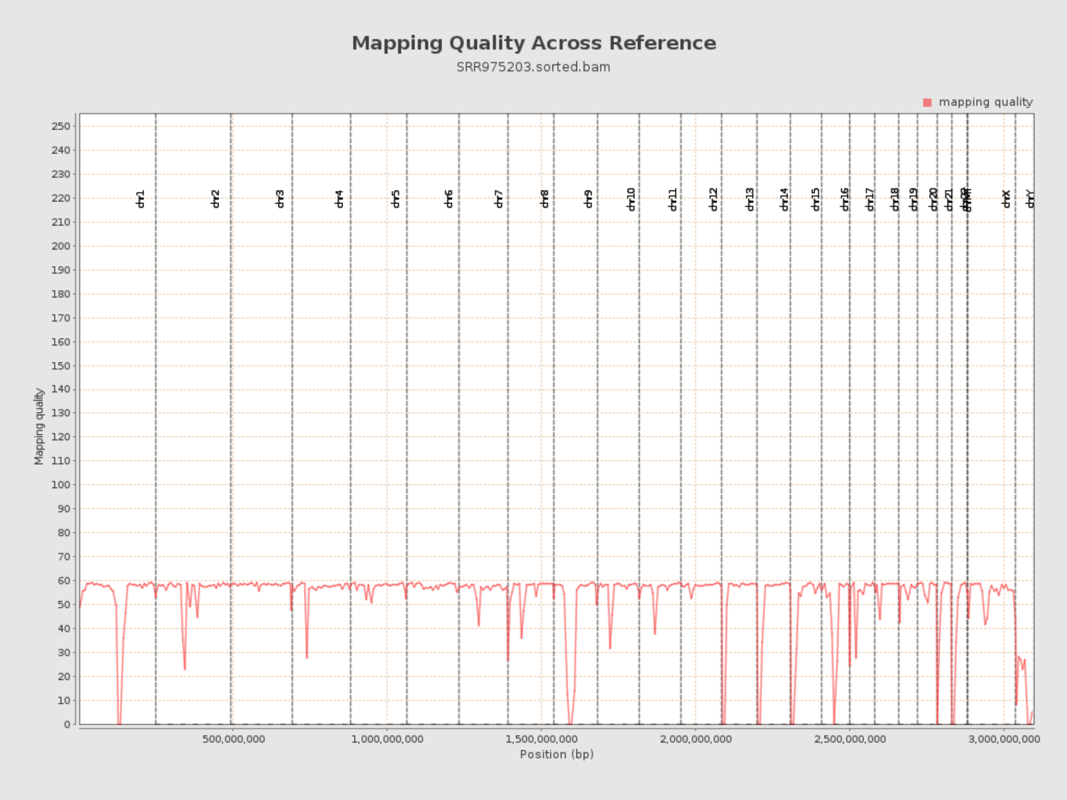
10. Results : Mapped Reads Clipping Profile



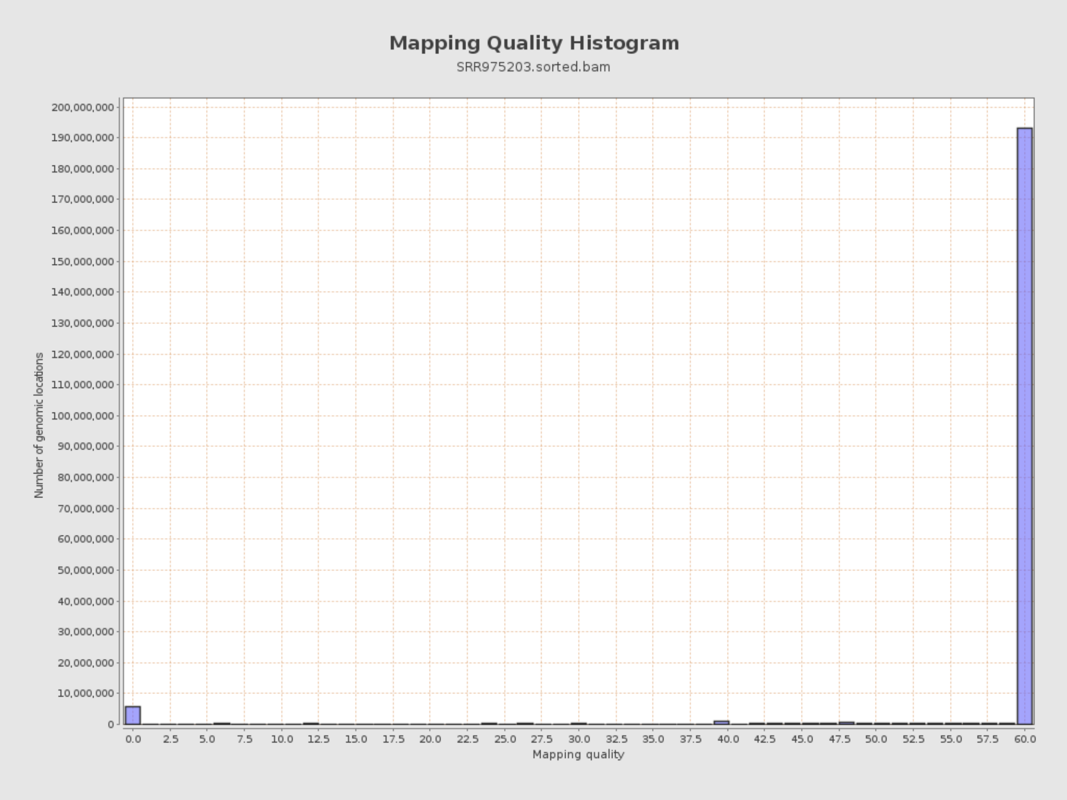
11. Results : Homopolymer Indels



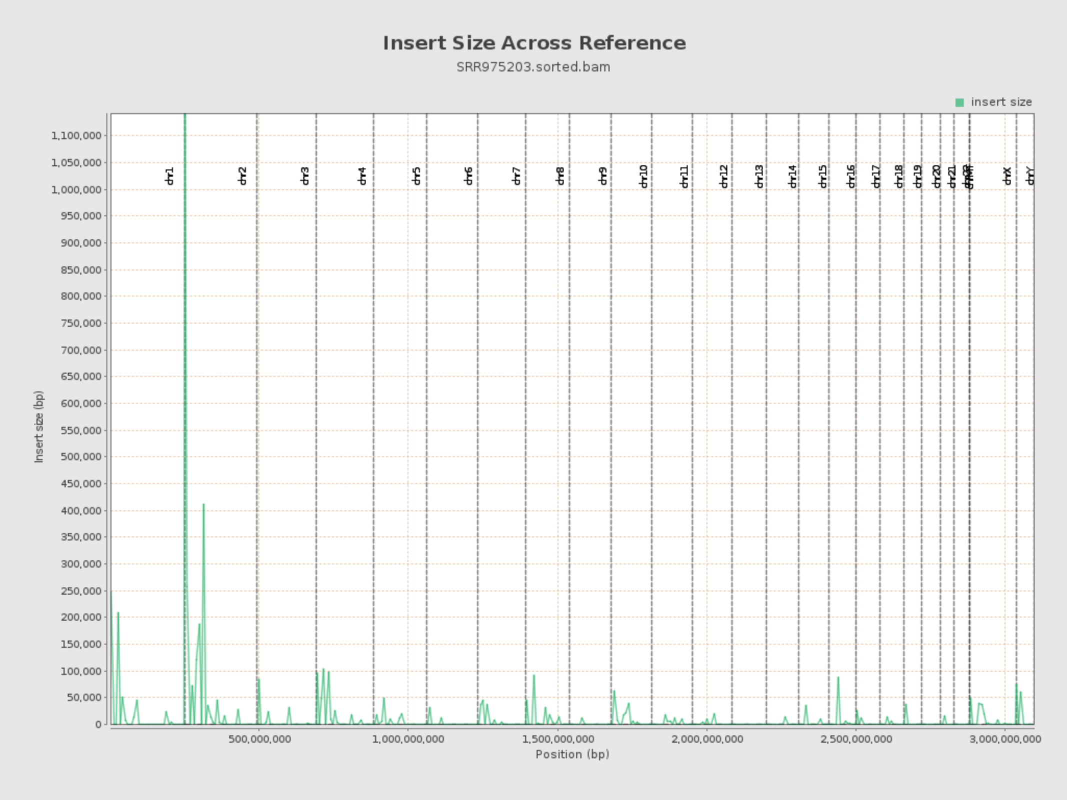
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram