Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 11:45:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975209.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_SRR975209 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975209_1.fastq.gz SRR975209_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 11:45:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975209.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,066,336
Mapped reads	6,993,094 / 98.96%
Unmapped reads	73,242 / 1.04%
Mapped paired reads	6,993,094 / 98.96%
Mapped reads, first in pair	3,501,450 / 49.55%
Mapped reads, second in pair	3,491,644 / 49.41%
Mapped reads, both in pair	6,966,808 / 98.59%
Mapped reads, singletons	26,286 / 0.37%
Secondary alignments	0
Supplementary alignments	99,743 / 1.41%
Read min/max/mean length	30 / 151 / 151.7
Duplicated reads (estimated)	1,532,010 / 21.68%
Duplication rate	17.66%
Clipped reads	5,033,122 / 71.23%

2.2. ACGT Content

Number/percentage of A's	285,289,923 / 29.78%
Number/percentage of C's	189,239,812 / 19.75%
Number/percentage of T's	287,705,541 / 30.03%
Number/percentage of G's	195,704,048 / 20.43%
Number/percentage of N's	102,714 / 0.01%

GC Percentage	40.18%

2.3. Coverage

Mean	0.3097
Standard Deviation	5.504

2.4. Mapping Quality

Mean Mapping Quality	53.39

2.5. Insert size

Mean	79,683.61
Standard Deviation	2,681,202.25
P25/Median/P75	143 / 177 / 226

2.6. Mismatches and indels

General error rate	1.27%
Mismatches	11,586,132
Insertions	205,010
Mapped reads with at least one insertion	2.78%
Deletions	348,471
Mapped reads with at least one deletion	4.79%
Homopolymer indels	45.42%

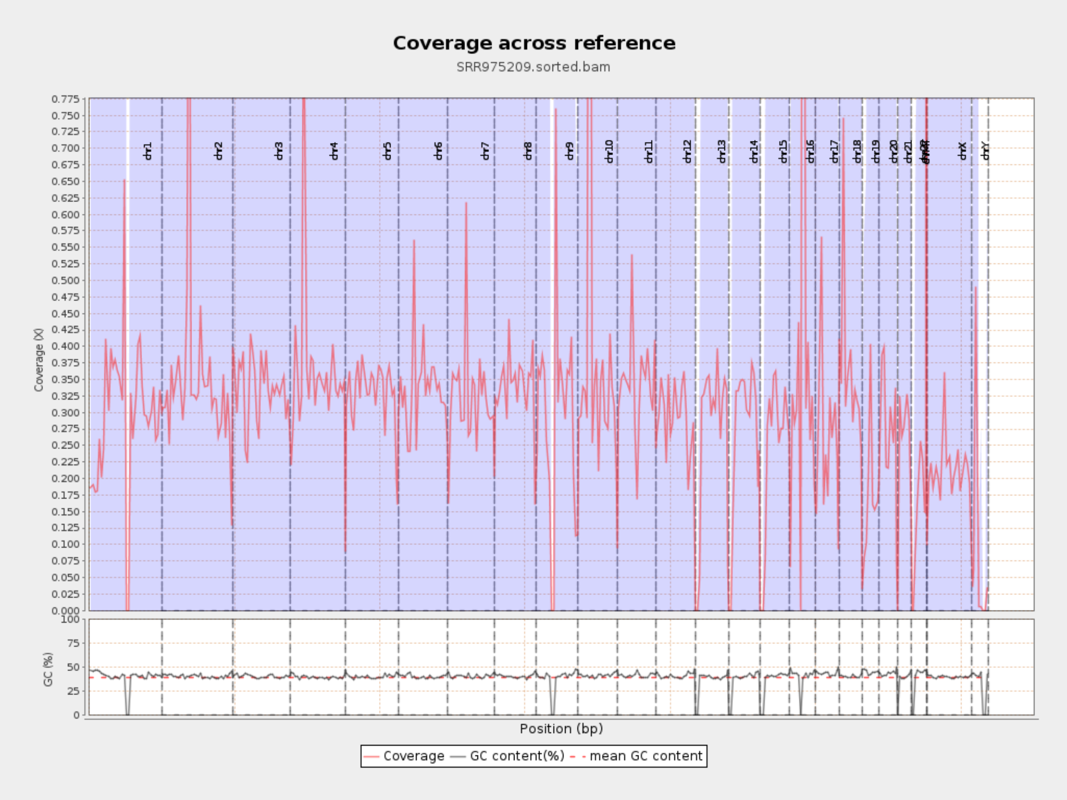
2.7. Chromosome stats

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

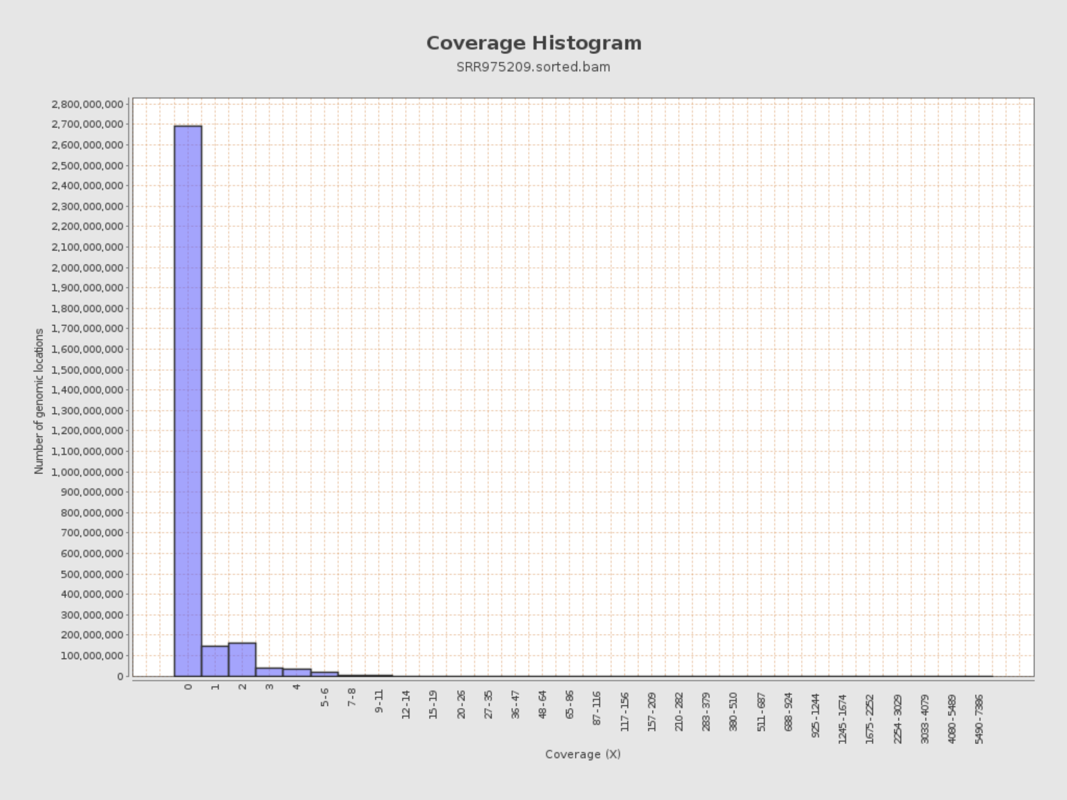
		bases	coverage	deviation
chr1	249250621	73478783	0.2948	5.4946
chr2	243199373	87125977	0.3582	5.7755
chr3	198022430	66776062	0.3372	1.1539
chr4	191154276	69984775	0.3661	3.9624
chr5	180915260	59575059	0.3293	1.0355
chr6	171115067	57662578	0.337	2.7149
chr7	159138663	52215993	0.3281	5.2834
chr8	146364022	49785566	0.3401	1.7884
chr9	141213431	42689105	0.3023	9.4683
chr10	135534747	56439528	0.4164	14.7079
chr11	135006516	45842745	0.3396	4.1732
chr12	133851895	38961991	0.2911	0.9595
chr13	115169878	31044796	0.2696	0.881
chr14	107349540	28896213	0.2692	1.0122
chr15	102531392	24954364	0.2434	0.8461
chr16	90354753	37448305	0.4145	10.2161
chr17	81195210	21228746	0.2615	5.1781
chr18	78077248	28881570	0.3699	9.4599
chr19	59128983	10368508	0.1754	3.0287
chr20	63025520	18097941	0.2872	1.5568
chr21	48129895	12186276	0.2532	2.2947
chr22	51304566	7216207	0.1407	0.6705
chrMT	16571	65435	3.9488	3.2519
chrX	155270560	33027654	0.2127	1.54

chrY	59373566	4809126	0.081	8.0413

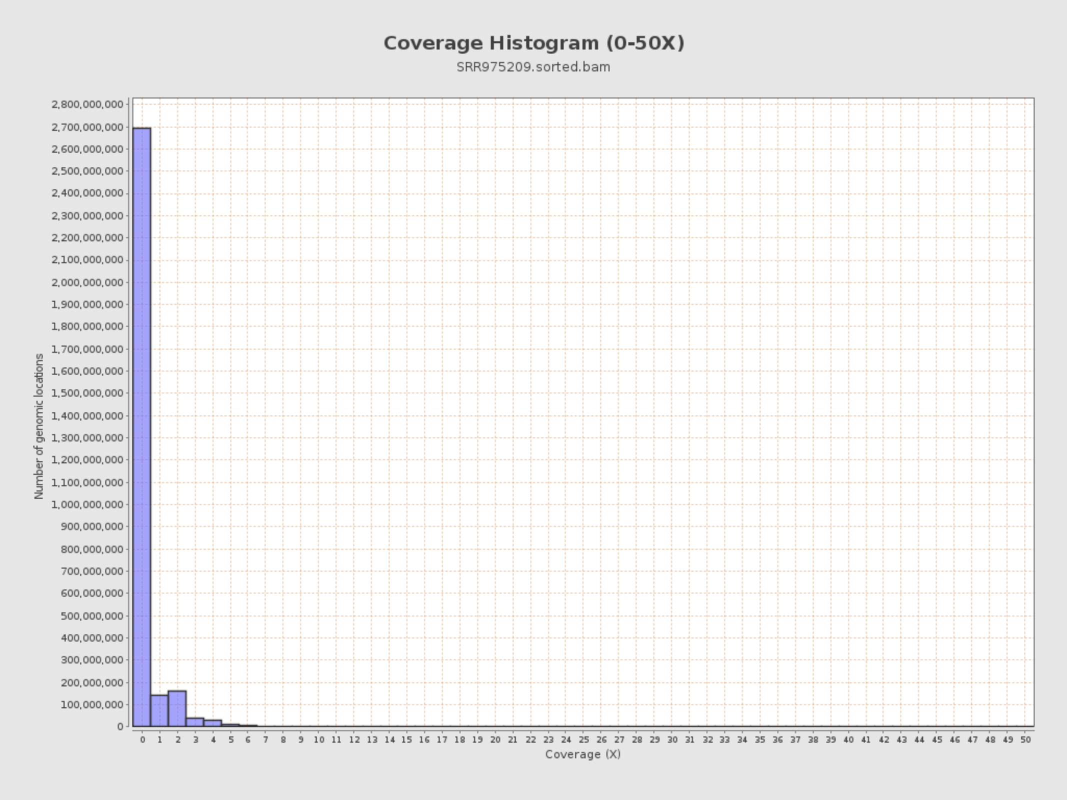
3. Results : Coverage across reference



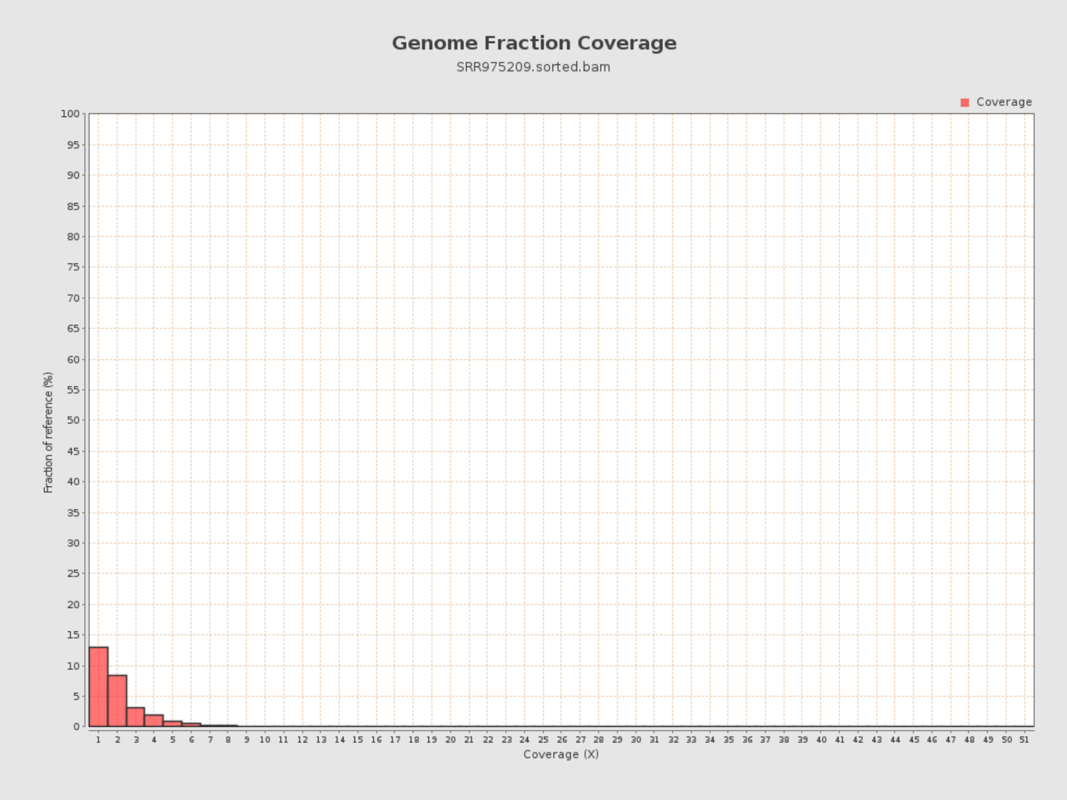
4. Results : Coverage Histogram



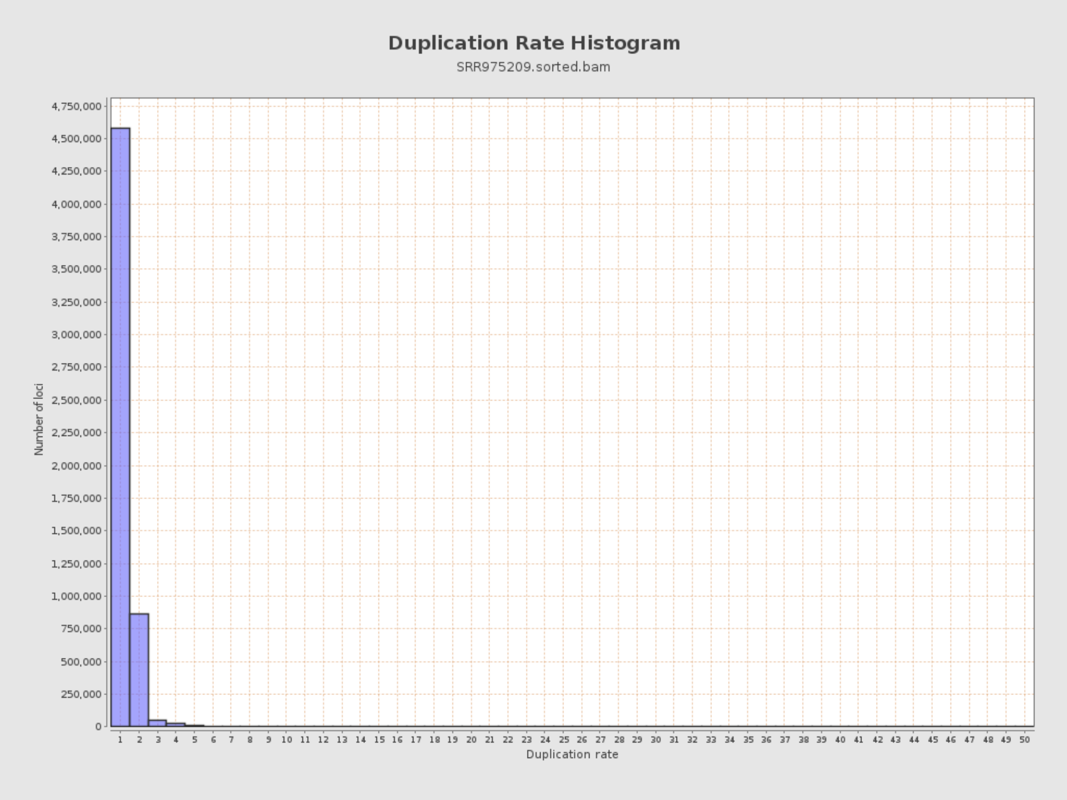
5. Results : Coverage Histogram (0-50X)



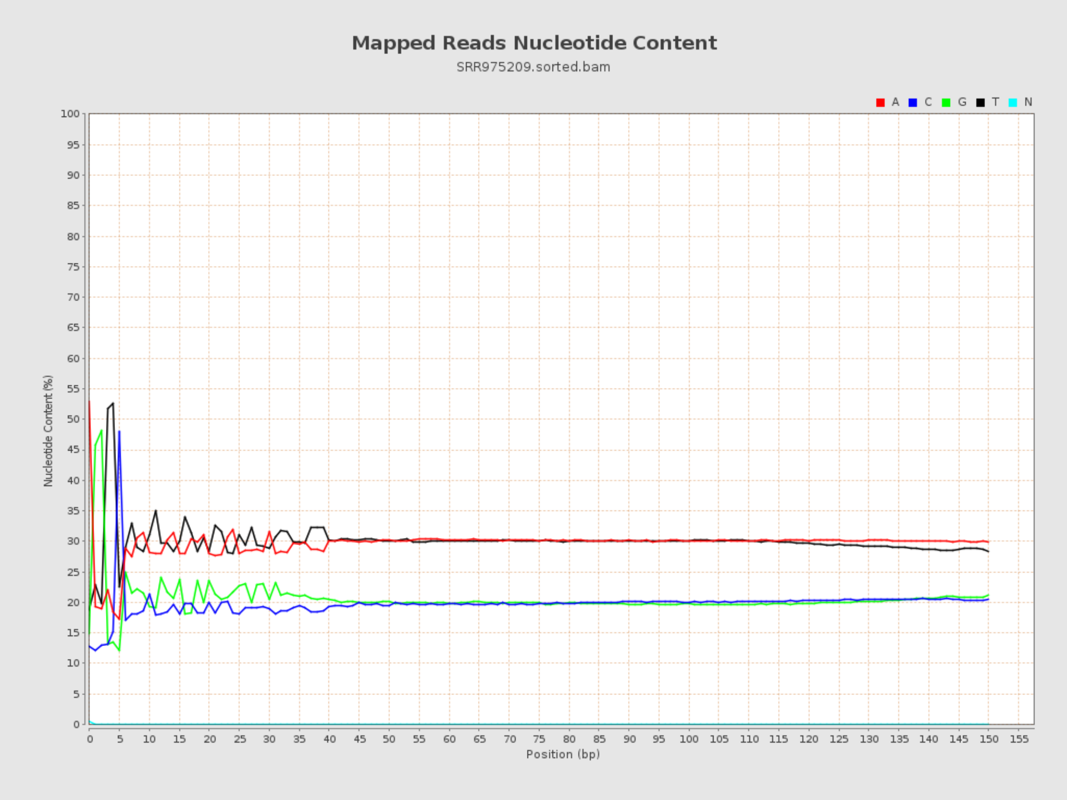
6. Results : Genome Fraction Coverage



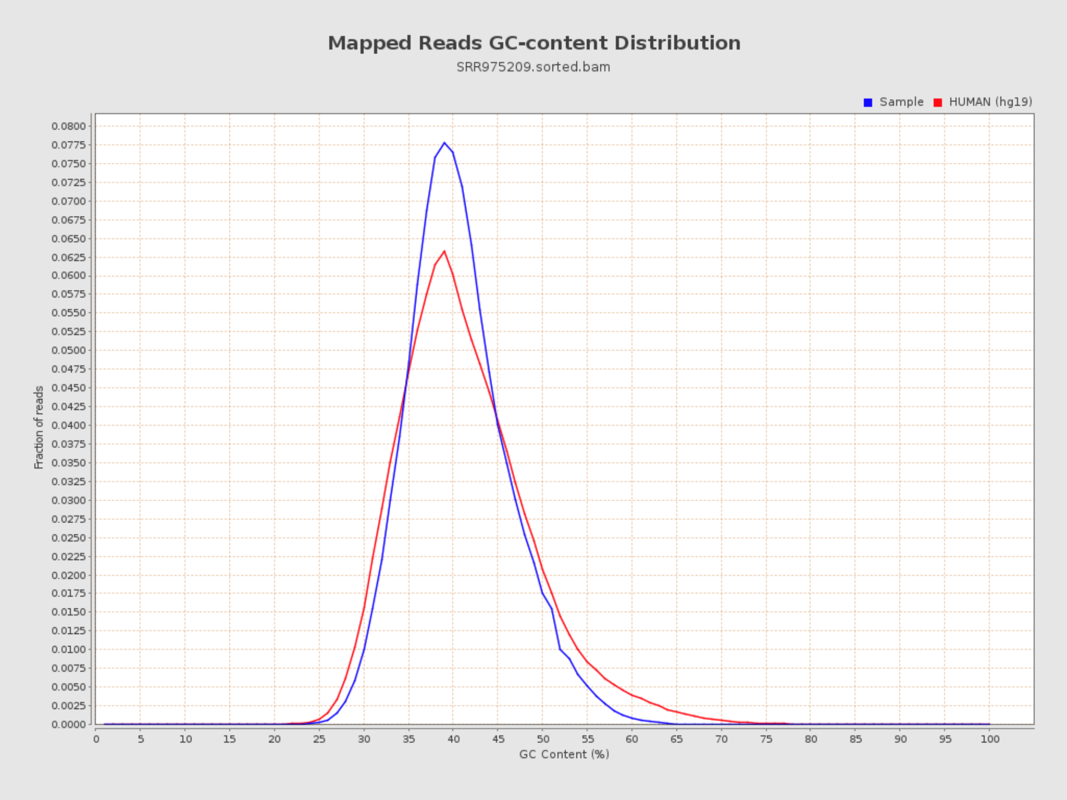
7. Results : Duplication Rate Histogram



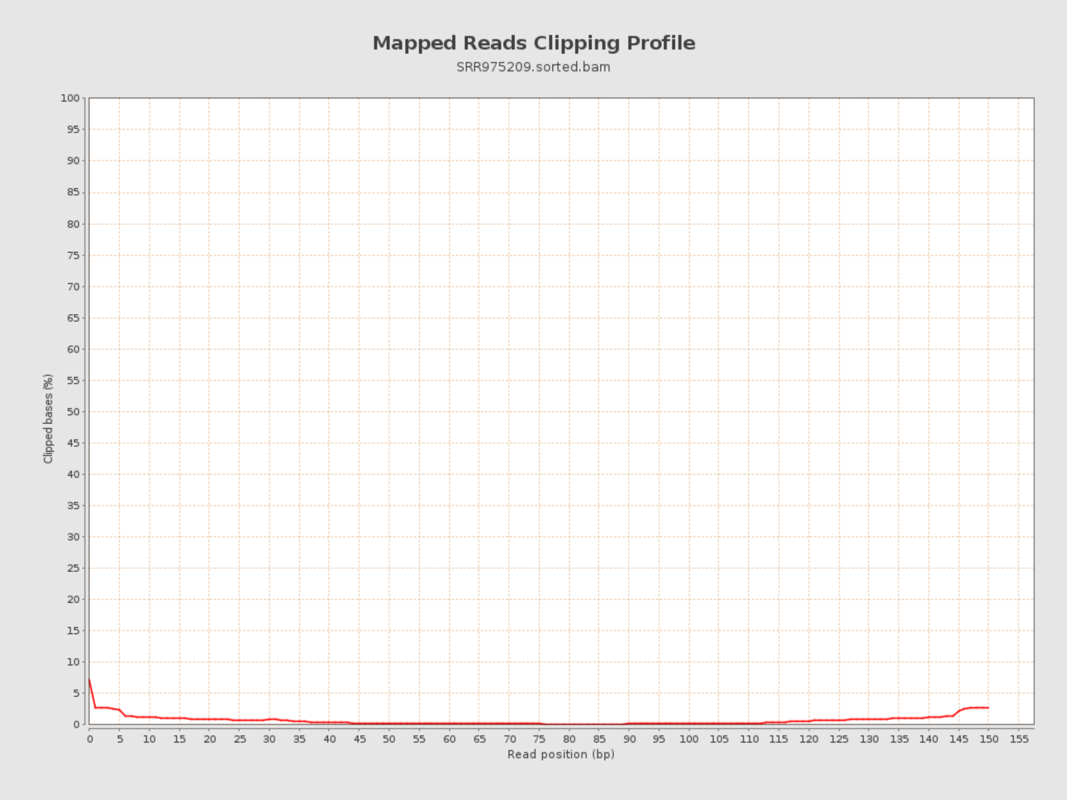
8. Results : Mapped Reads Nucleotide Content



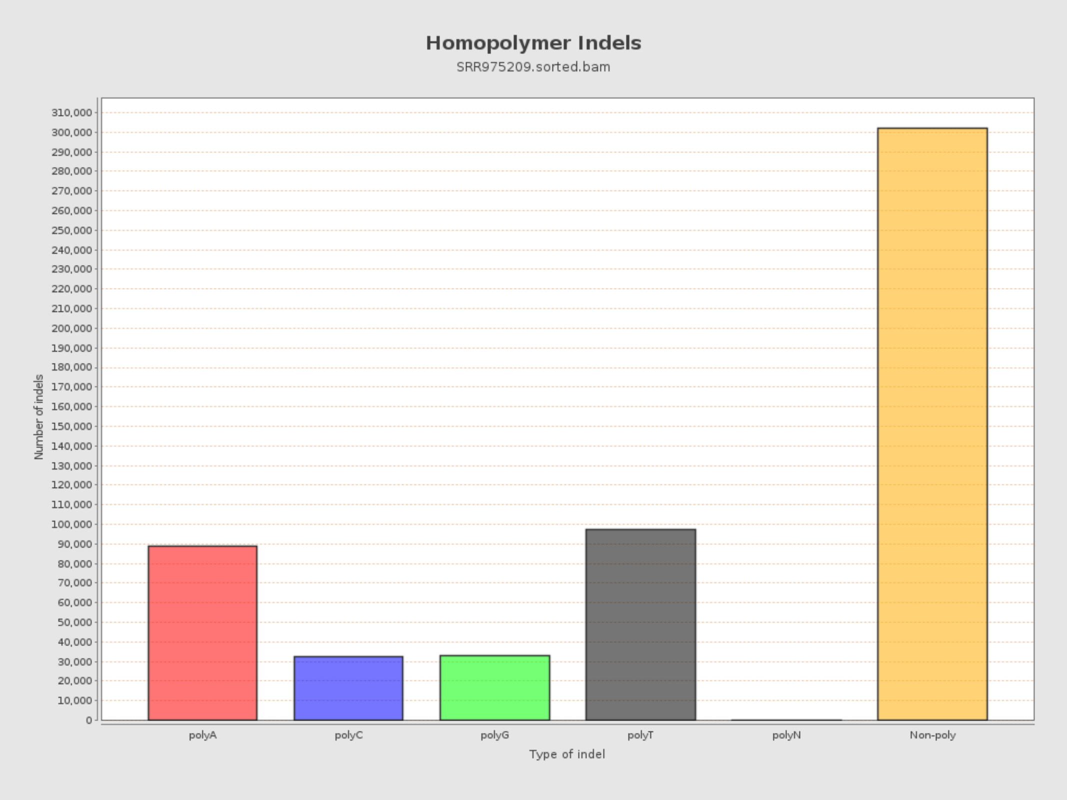
9. Results : Mapped Reads GC-content Distribution



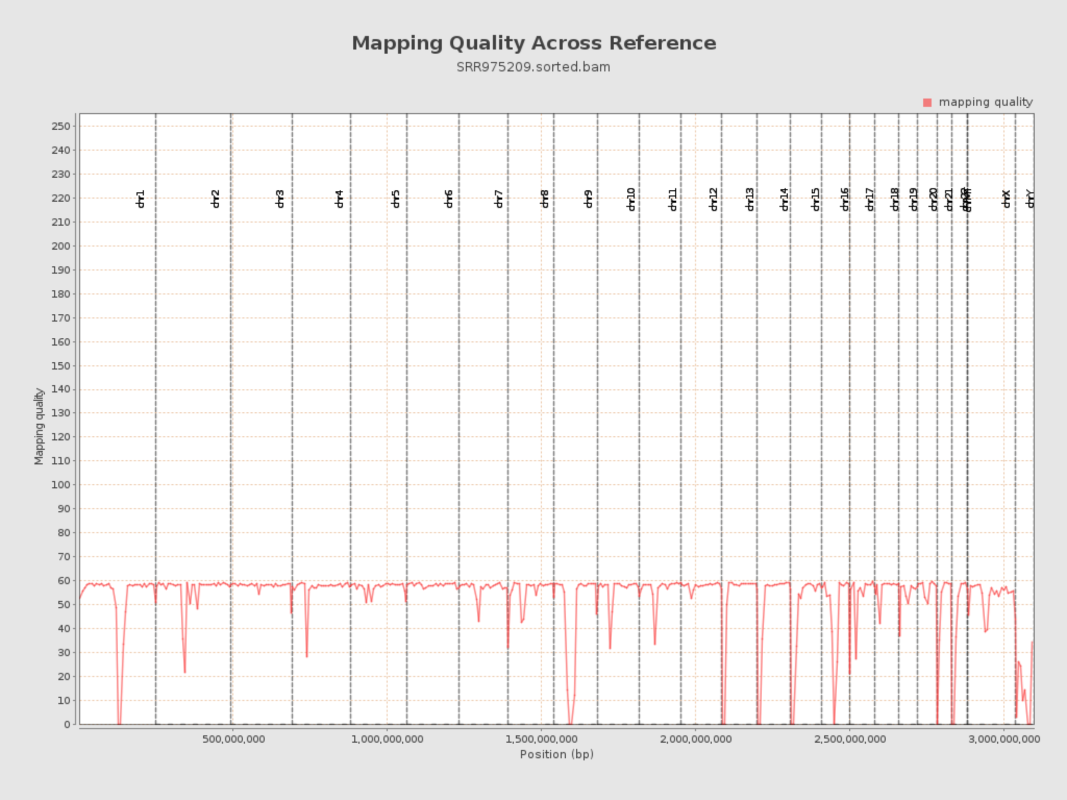
10. Results : Mapped Reads Clipping Profile



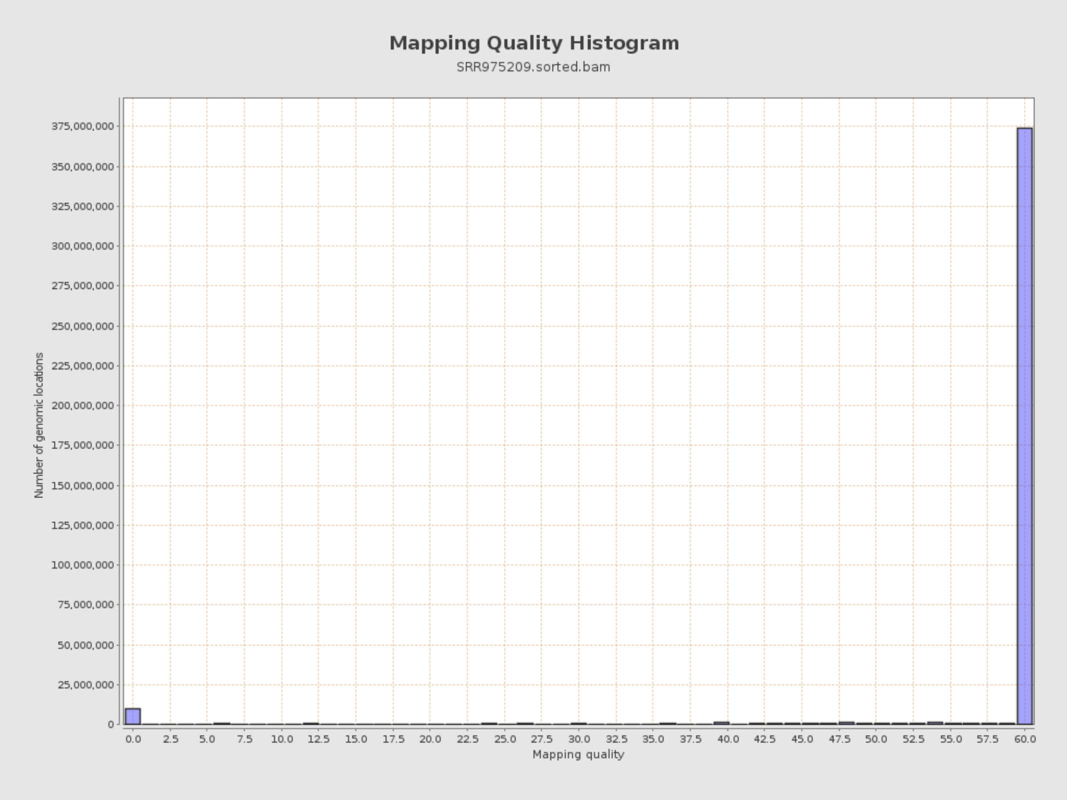
11. Results : Homopolymer Indels



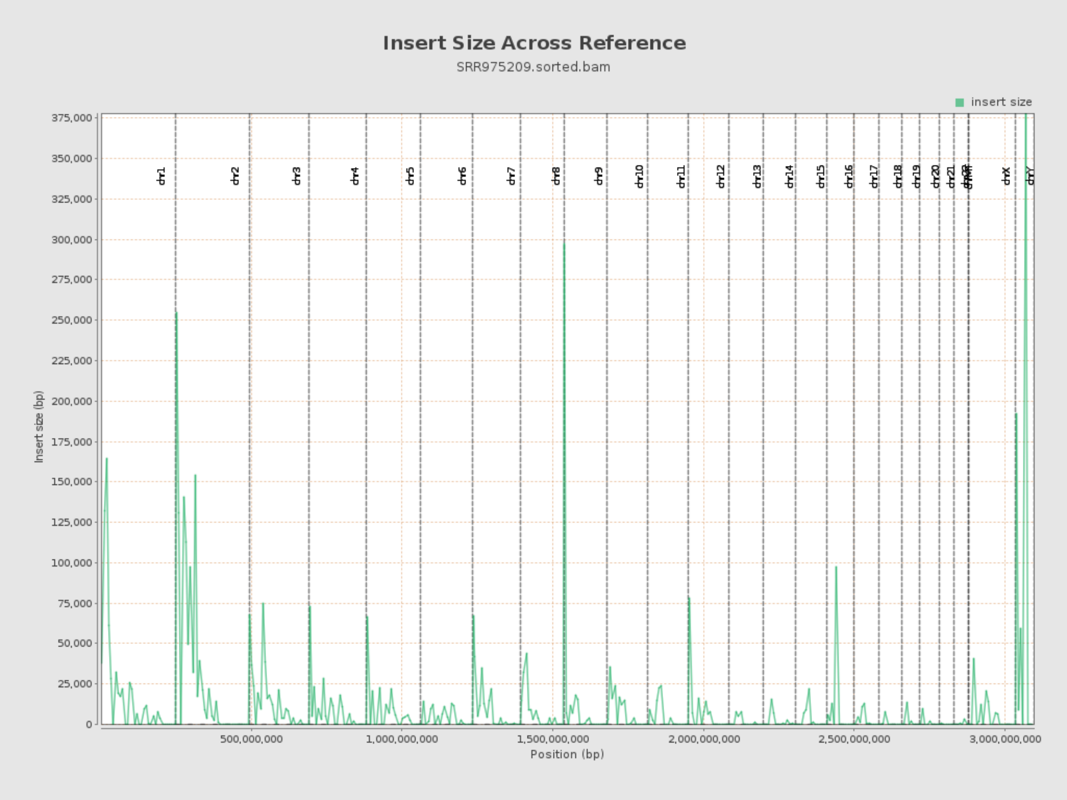
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference


Insert Size Across Reference

SRR975209.sorted.bam

15. Results : Insert Size Histogram