Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/05 15:26:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR960900.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_SRR960900 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR960900_1.fastq.gz SRR960900_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Jan 05 15:26:01 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR960900.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	98,516,884
Mapped reads	97,000,271 / 98.46%
Unmapped reads	1,516,613 / 1.54%
Mapped paired reads	97,000,271 / 98.46%
Mapped reads, first in pair	48,579,712 / 49.31%
Mapped reads, second in pair	48,420,559 / 49.15%
Mapped reads, both in pair	96,597,270 / 98.05%
Mapped reads, singletons	403,001 / 0.41%
Secondary alignments	0
Supplementary alignments	236,637 / 0.24%
Read min/max/mean length	30 / 101 / 101.1
Duplicated reads (estimated)	7,901,197 / 8.02%
Duplication rate	4.1%
Clipped reads	10,161,309 / 10.31%

2.2. ACGT Content

Number/percentage of A's	2,824,481,552 / 29.51%
Number/percentage of C's	1,956,390,807 / 20.44%
Number/percentage of T's	2,811,633,695 / 29.37%
Number/percentage of G's	1,979,170,691 / 20.68%
Number/percentage of N's	212,986 / 0%

GC Percentage	41.12%

2.3. Coverage

Mean	3.0929
Standard Deviation	33.765

2.4. Mapping Quality

Mean Mapping Quality	53.63

2.5. Insert size

Mean	23,449.71
Standard Deviation	1,438,946.7
P25/Median/P75	137 / 148 / 158

2.6. Mismatches and indels

General error rate	0.68%
Mismatches	61,896,460
Insertions	1,048,484
Mapped reads with at least one insertion	1.04%
Deletions	1,152,571
Mapped reads with at least one deletion	1.15%
Homopolymer indels	41.57%

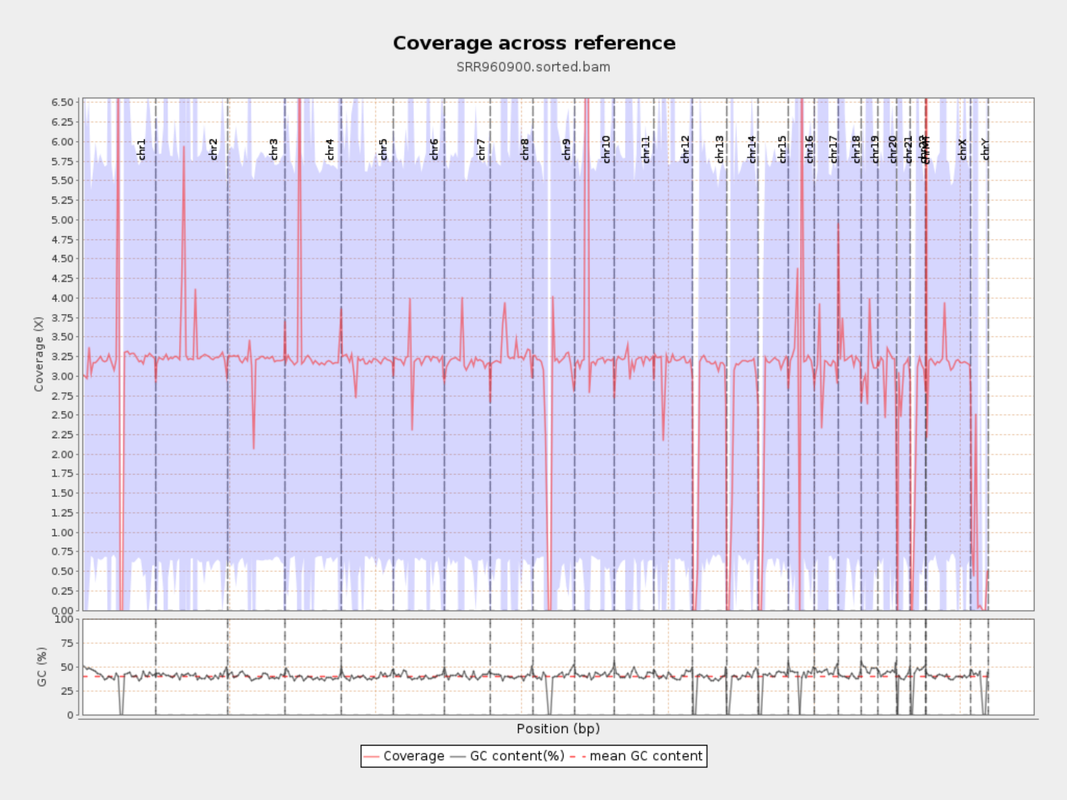
2.7. Chromosome stats

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

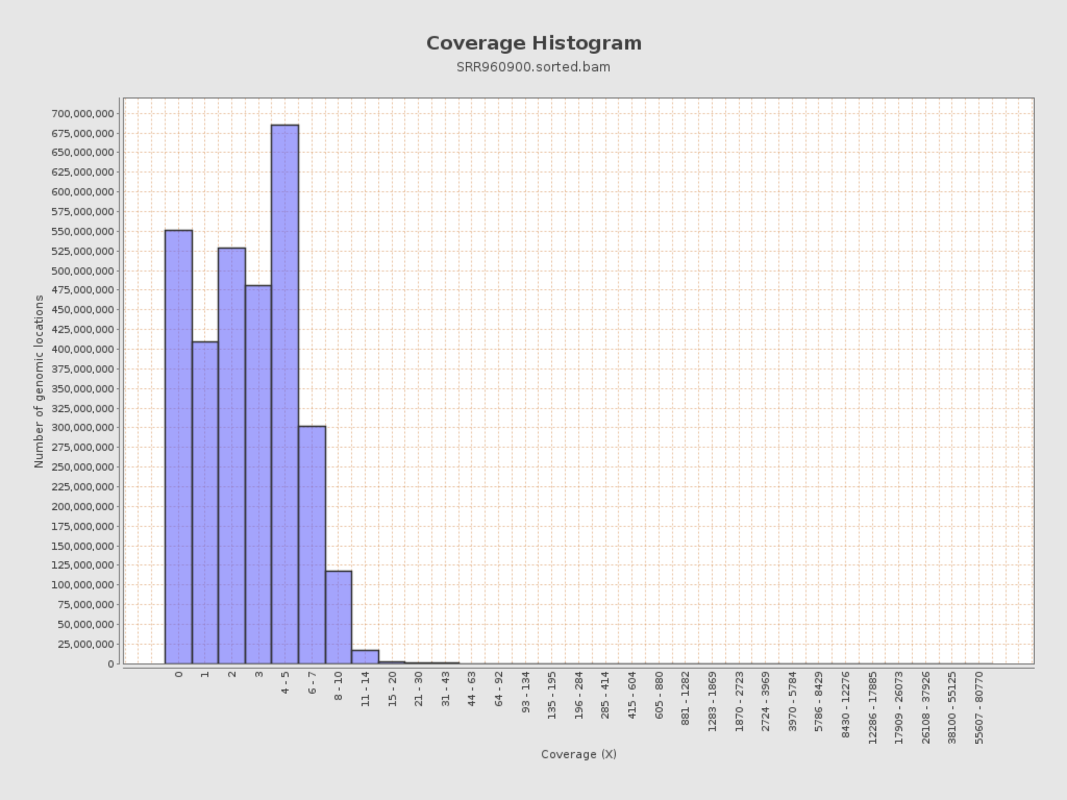
		bases	coverage	deviation
chr1	249250621	778952147	3.1252	80.8424
chr2	243199373	821183789	3.3766	21.33
chr3	198022430	631733476	3.1902	6.7312
chr4	191154276	645187666	3.3752	29.3845
chr5	180915260	575841051	3.1829	3.7475
chr6	171115067	548869831	3.2076	10.0276
chr7	159138663	510772427	3.2096	20.8066
chr8	146364022	481903698	3.2925	34.4615
chr9	141213431	399496665	2.829	29.2228
chr10	135534747	499275930	3.6837	77.3895
chr11	135006516	431124429	3.1934	13.5823
chr12	133851895	422454670	3.1561	4.6085
chr13	115169878	304251277	2.6418	2.5097
chr14	107349540	282421589	2.6309	3.3985
chr15	102531392	265461302	2.5891	2.5569
chr16	90354753	304511647	3.3702	31.4882
chr17	81195210	254466188	3.134	12.7816
chr18	78077248	261110338	3.3443	35.1557
chr19	59128983	184550109	3.1211	39.5359
chr20	63025520	196721883	3.1213	11.4424
chr21	48129895	131139683	2.7247	14.7752
chr22	51304566	111286038	2.1691	3.0275
chrMT	16571	7379473	445.3245	66.6664
chrX	155270560	492798540	3.1738	10.4559

chrY	59373566	31923214	0.5377	31.4078

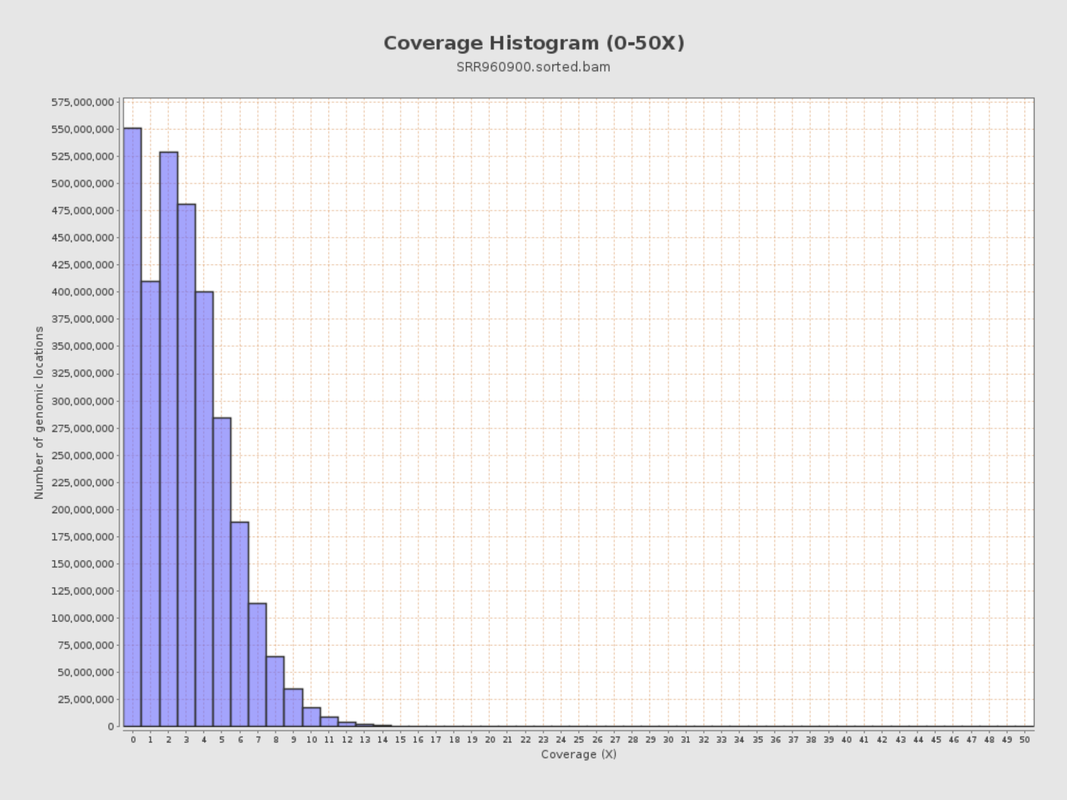
3. Results : Coverage across reference



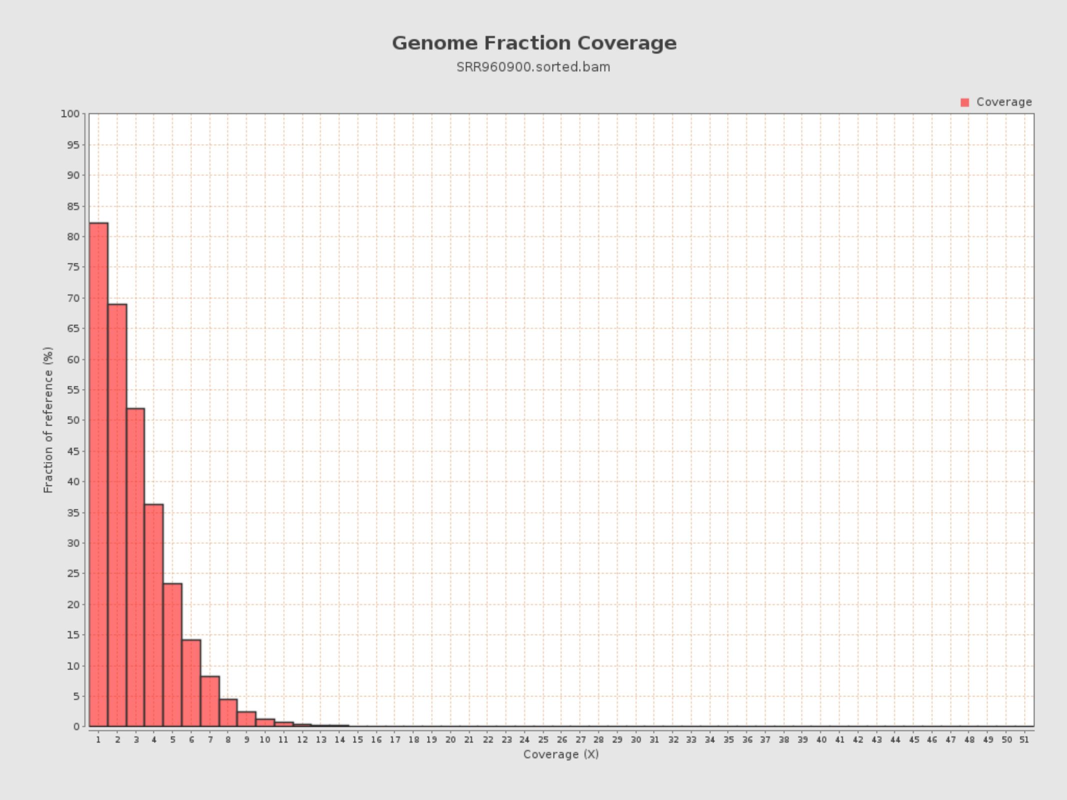
4. Results : Coverage Histogram



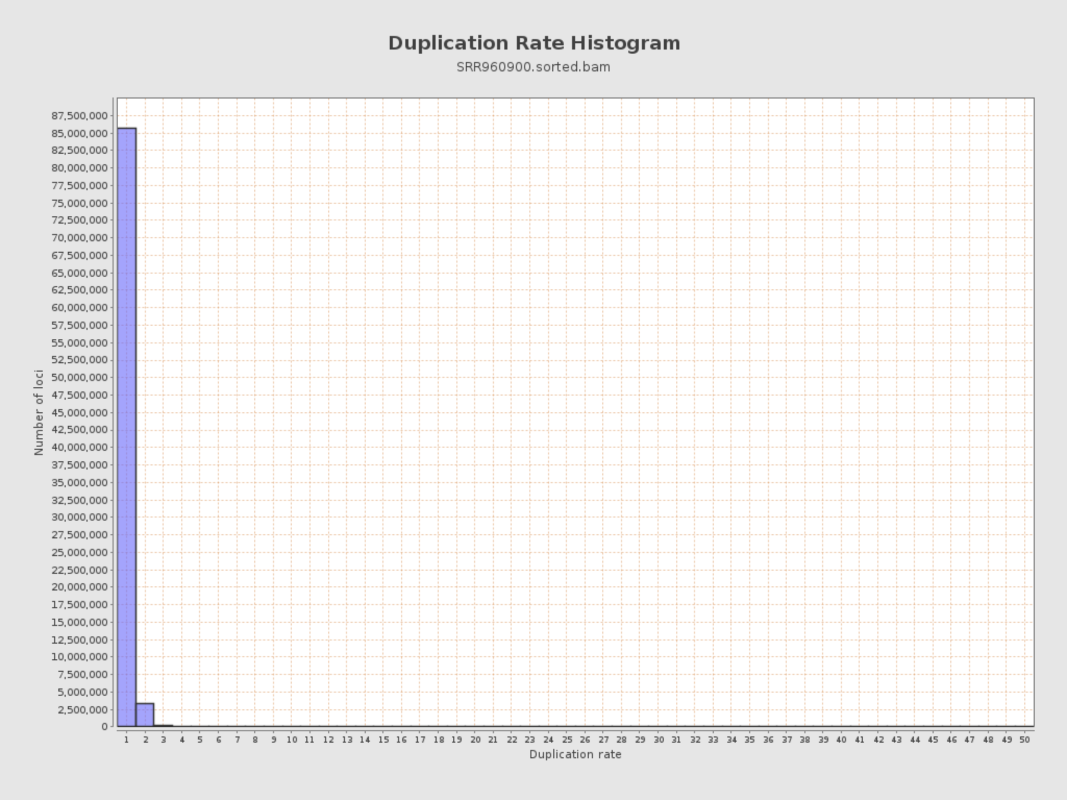
5. Results : Coverage Histogram (0-50X)



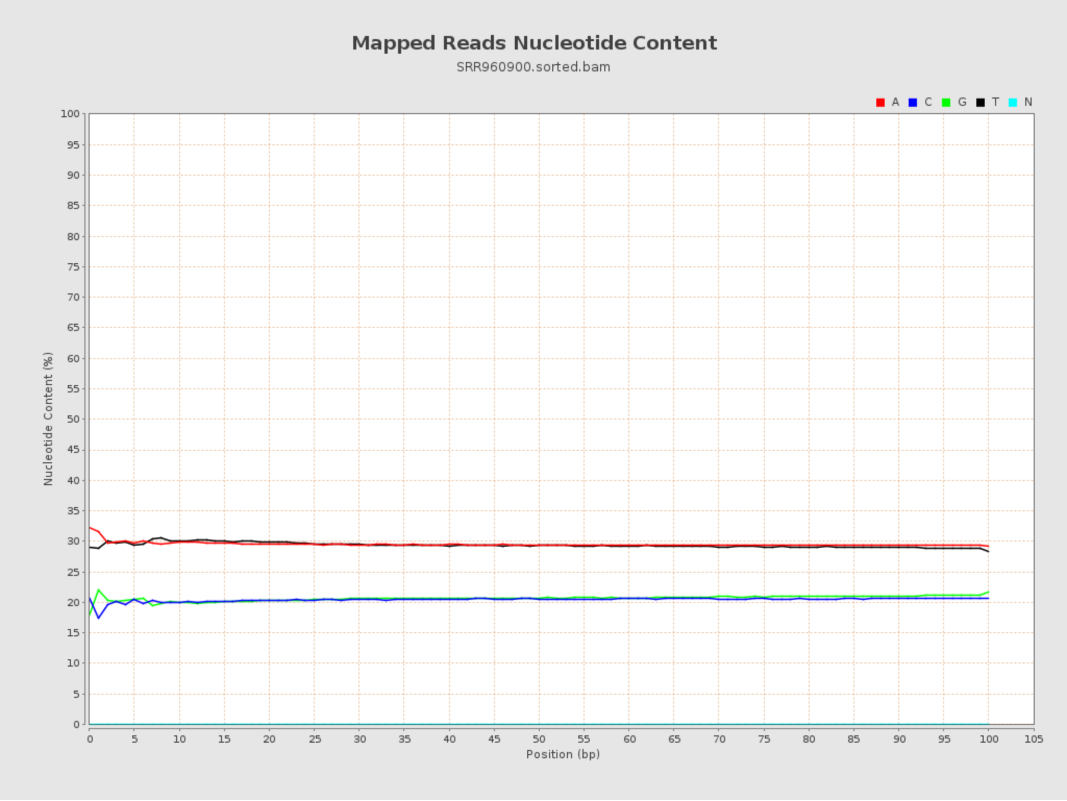
6. Results : Genome Fraction Coverage



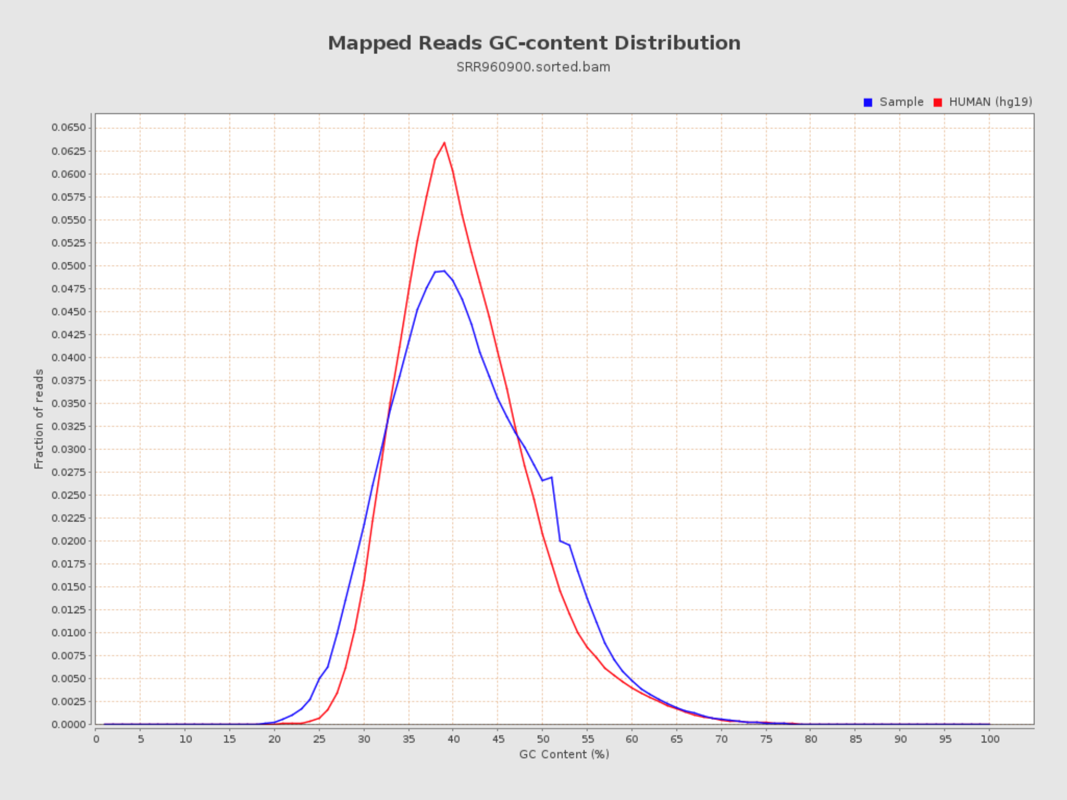
7. Results : Duplication Rate Histogram



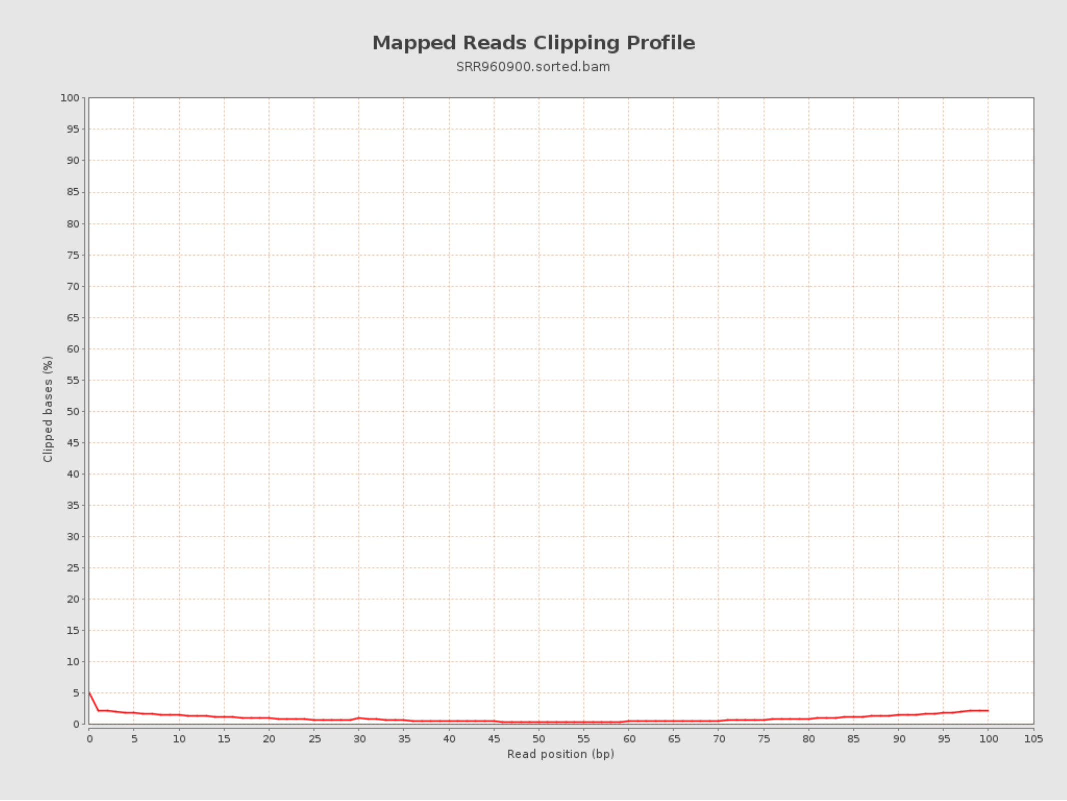
8. Results : Mapped Reads Nucleotide Content



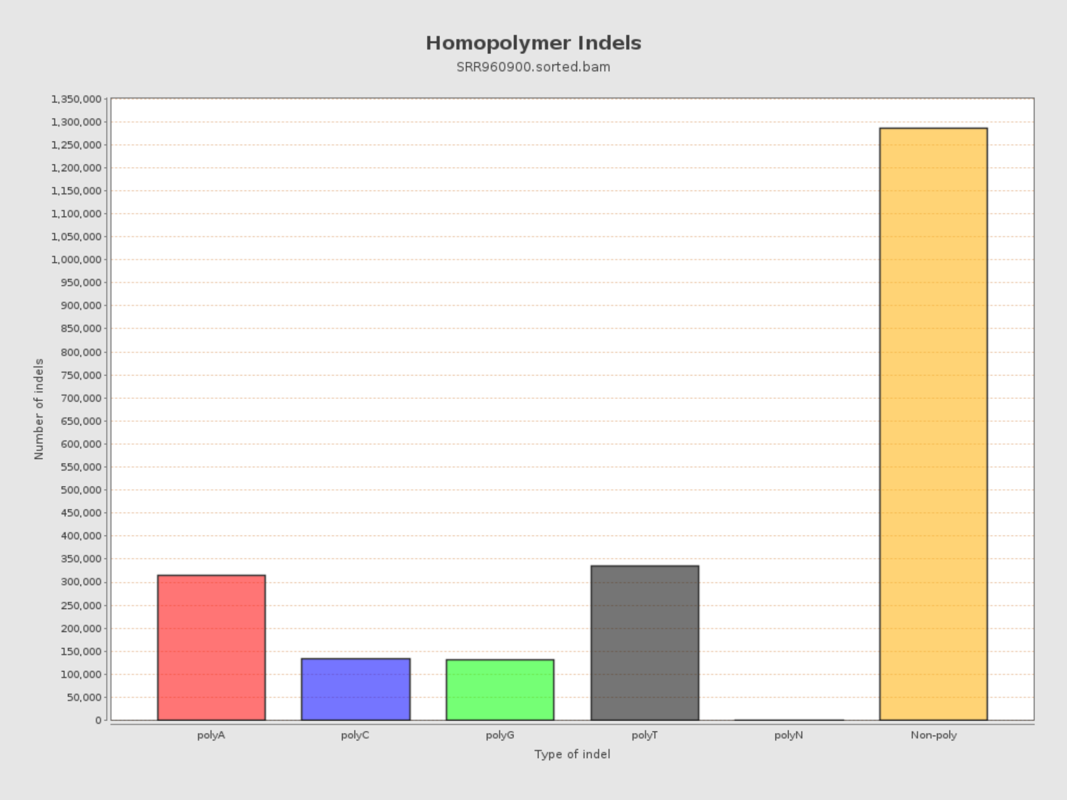
9. Results : Mapped Reads GC-content Distribution



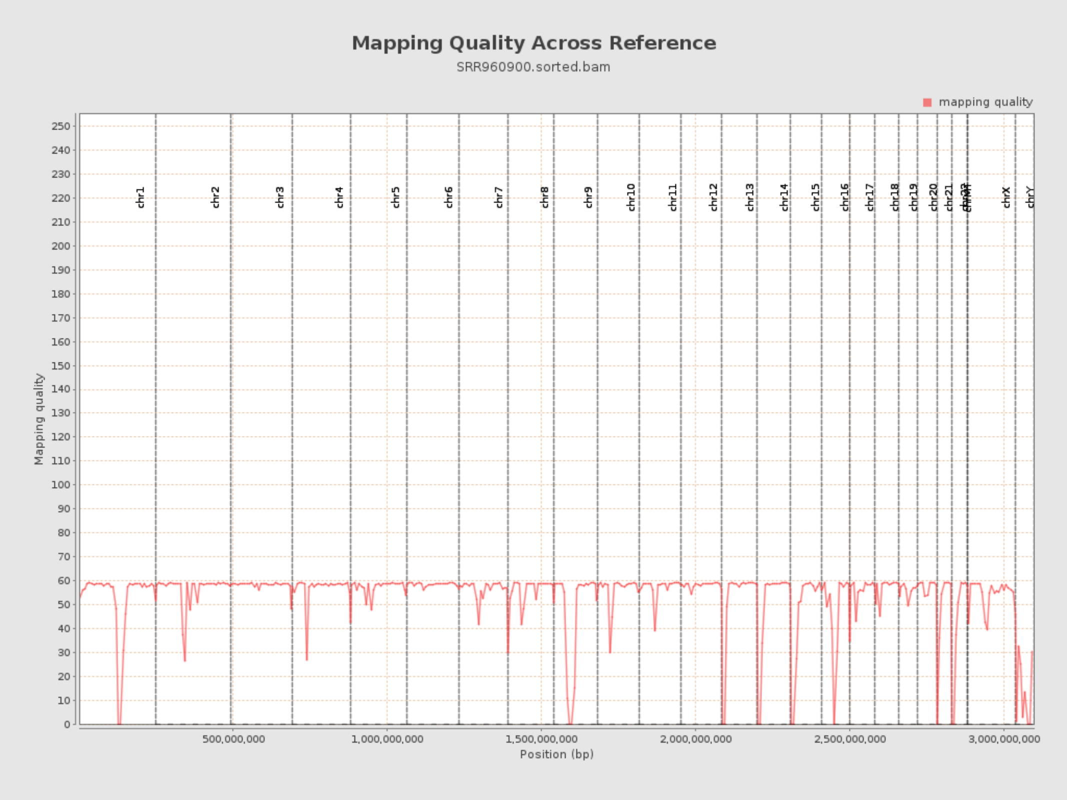
10. Results : Mapped Reads Clipping Profile



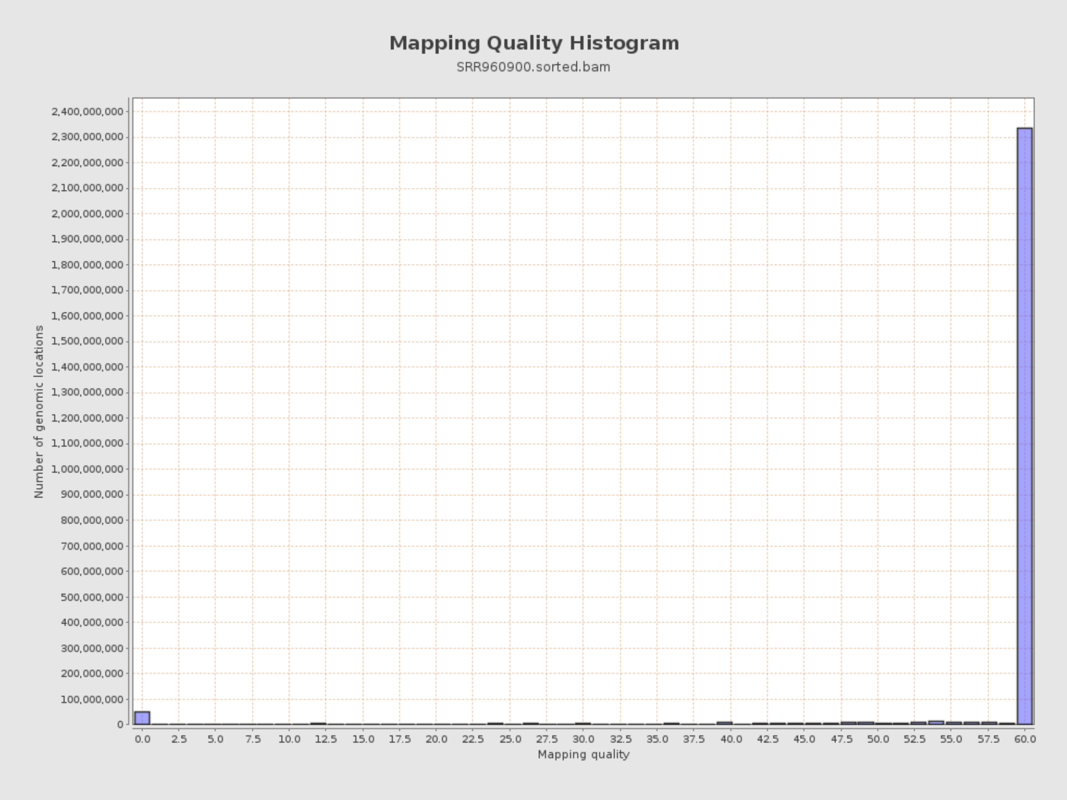
11. Results : Homopolymer Indels



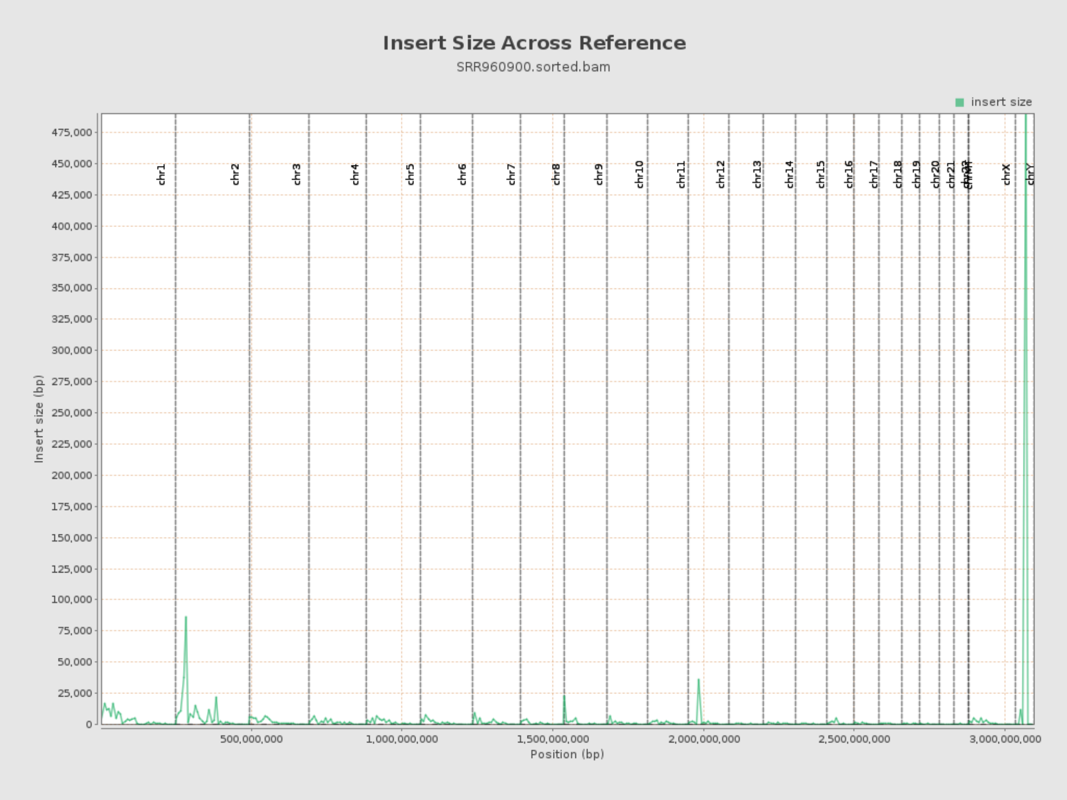
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram