Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/05 14:13:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR960899.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_SRR960899 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR960899_1.fastq.gz SRR960899_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Jan 05 14:13:54 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR960899.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	67,927,788
Mapped reads	66,818,198 / 98.37%
Unmapped reads	1,109,590 / 1.63%
Mapped paired reads	66,818,198 / 98.37%
Mapped reads, first in pair	33,448,910 / 49.24%
Mapped reads, second in pair	33,369,288 / 49.12%
Mapped reads, both in pair	66,551,788 / 97.97%
Mapped reads, singletons	266,410 / 0.39%
Secondary alignments	0
Supplementary alignments	167,043 / 0.25%
Read min/max/mean length	30 / 101 / 101.1
Duplicated reads (estimated)	4,953,727 / 7.29%
Duplication rate	3.58%
Clipped reads	6,985,711 / 10.28%

2.2. ACGT Content

Number/percentage of A's	1,941,354,510 / 29.45%
Number/percentage of C's	1,351,386,388 / 20.5%
Number/percentage of T's	1,931,508,193 / 29.3%
Number/percentage of G's	1,367,958,868 / 20.75%
Number/percentage of N's	244,085 / 0%

GC Percentage	41.25%

2.3. Coverage

Mean	2.1302
Standard Deviation	23.1212

2.4. Mapping Quality

Mean Mapping Quality	53.63

2.5. Insert size

Mean	23,520.86
Standard Deviation	1,440,565.09
P25/Median/P75	137 / 148 / 158

2.6. Mismatches and indels

General error rate	0.66%
Mismatches	41,510,908
Insertions	727,909
Mapped reads with at least one insertion	1.05%
Deletions	805,832
Mapped reads with at least one deletion	1.16%
Homopolymer indels	41.7%

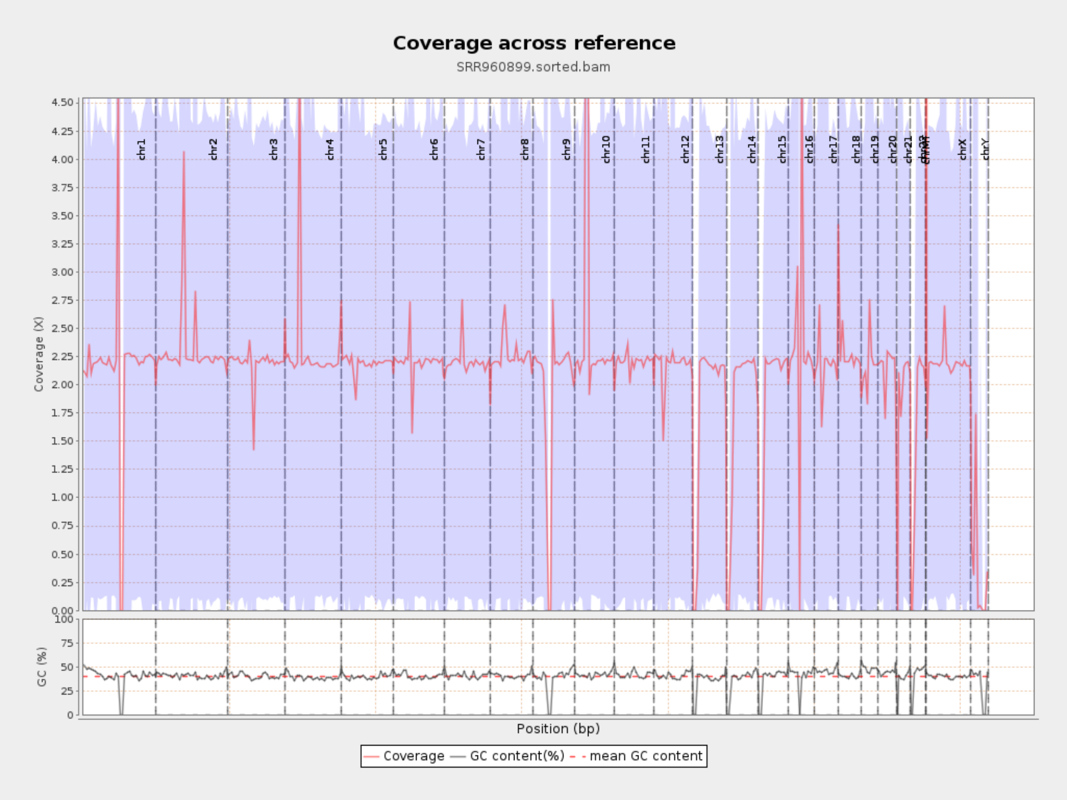
2.7. Chromosome stats

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

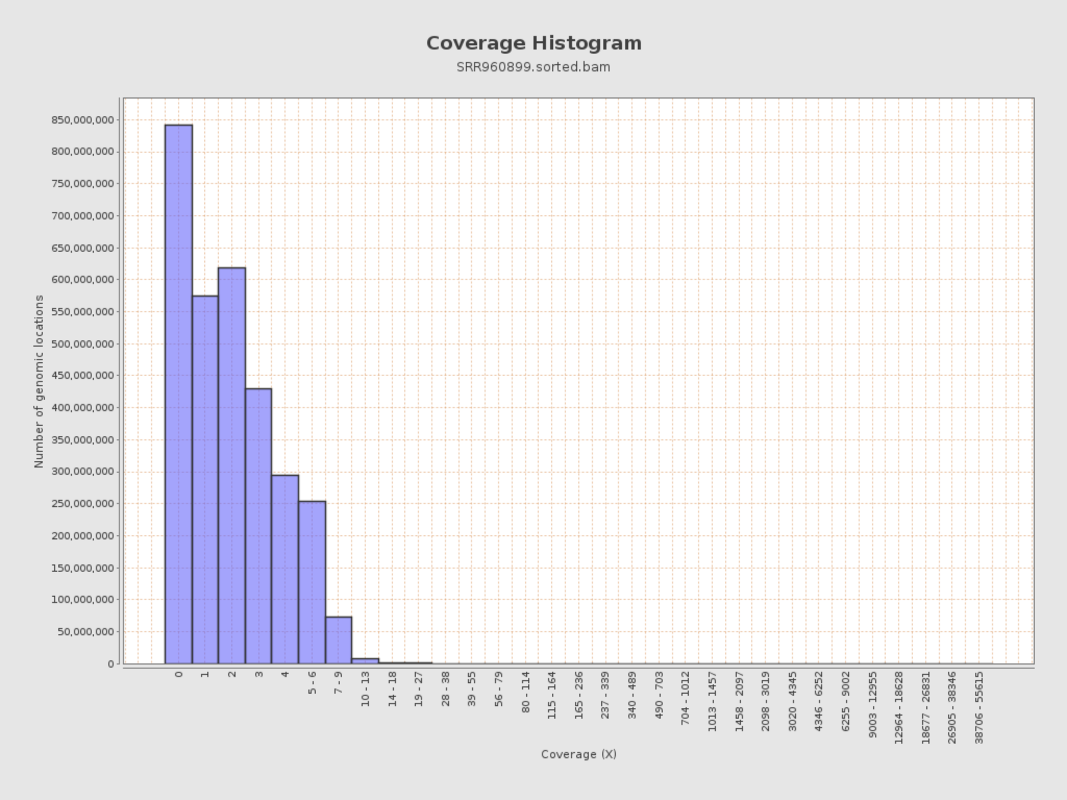
		bases	coverage	deviation
chr1	249250621	537135263	2.155	55.4001
chr2	243199373	564919856	2.3229	14.5926
chr3	198022430	433900219	2.1912	4.9258
chr4	191154276	443368574	2.3194	20.2328
chr5	180915260	395682608	2.1871	2.7763
chr6	171115067	376966340	2.203	6.9372
chr7	159138663	351791613	2.2106	14.3184
chr8	146364022	331344176	2.2638	23.7391
chr9	141213431	275291224	1.9495	19.9617
chr10	135534747	343418457	2.5338	52.5605
chr11	135006516	297202127	2.2014	9.3047
chr12	133851895	291465314	2.1775	5.479
chr13	115169878	208996587	1.8147	1.977
chr14	107349540	194309671	1.8101	2.5279
chr15	102531392	183215566	1.7869	2.0003
chr16	90354753	210740228	2.3324	21.5328
chr17	81195210	176989489	2.1798	8.843
chr18	78077248	179812652	2.303	24.0066
chr19	59128983	128773016	2.1778	26.9077
chr20	63025520	135887750	2.1561	7.68
chr21	48129895	90628314	1.883	10.0843
chr22	51304566	77355345	1.5078	2.2426
chrMT	16571	5106268	308.1448	48.9884
chrX	155270560	338164589	2.1779	7.2634

chrY	59373566	22032144	0.3711	21.4832

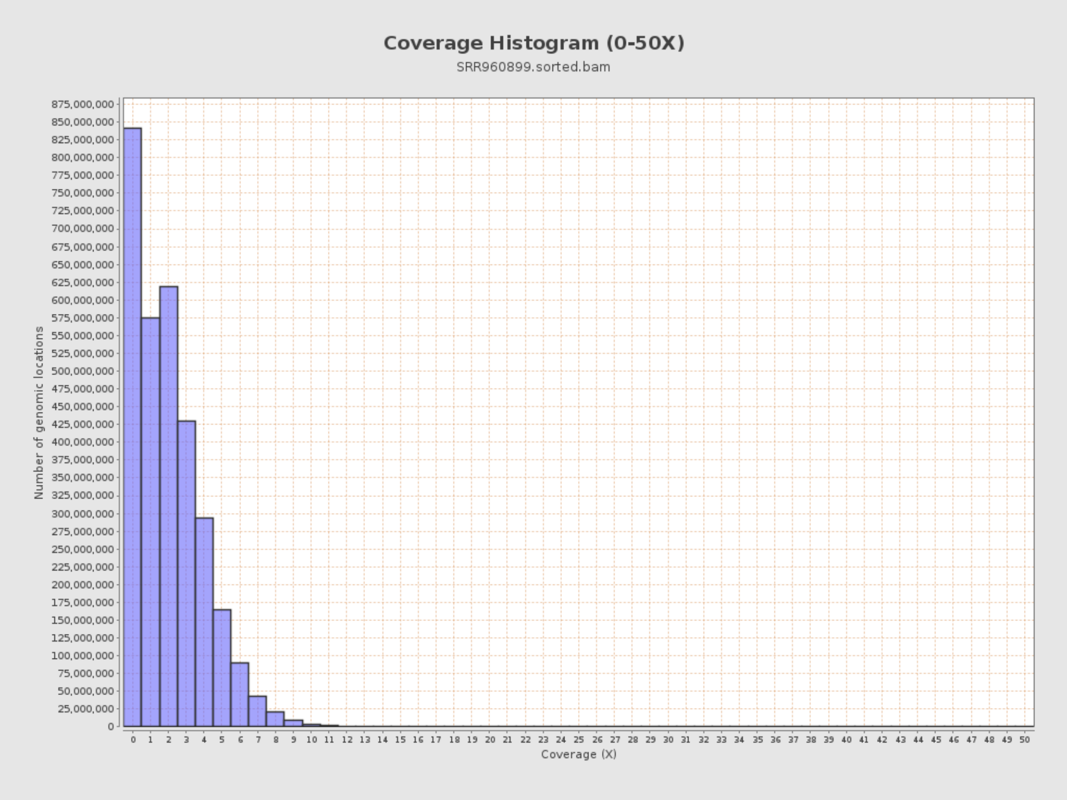
3. Results : Coverage across reference



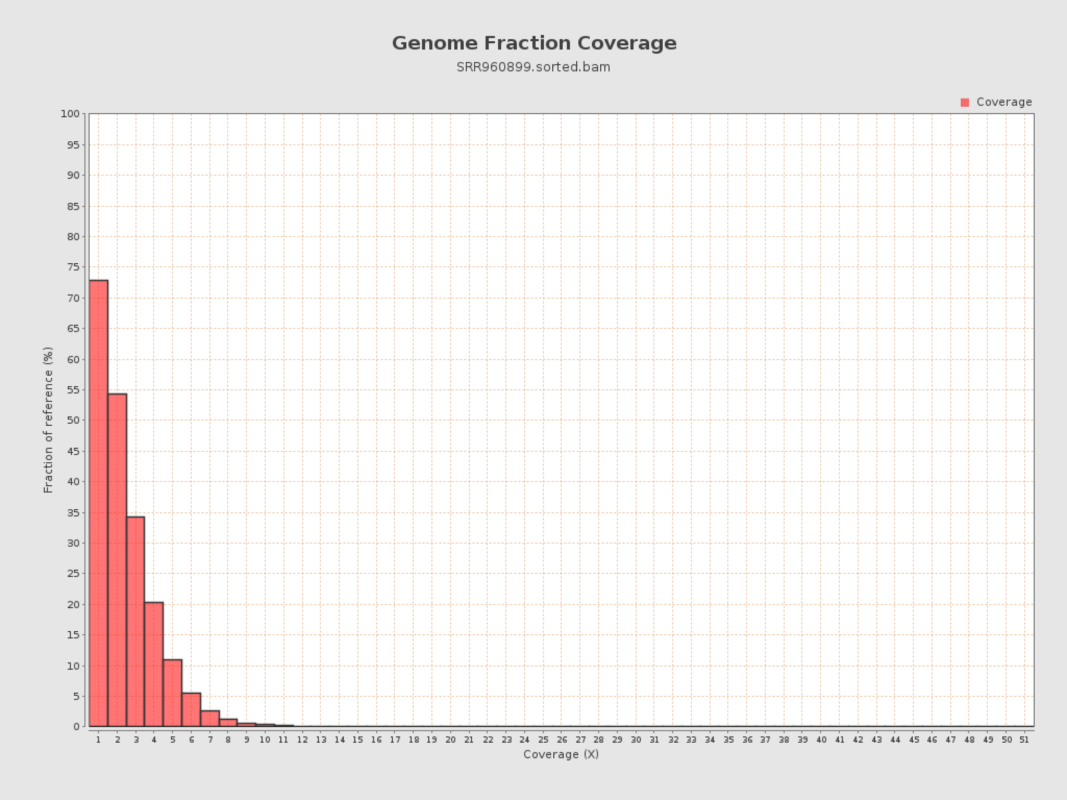
4. Results : Coverage Histogram



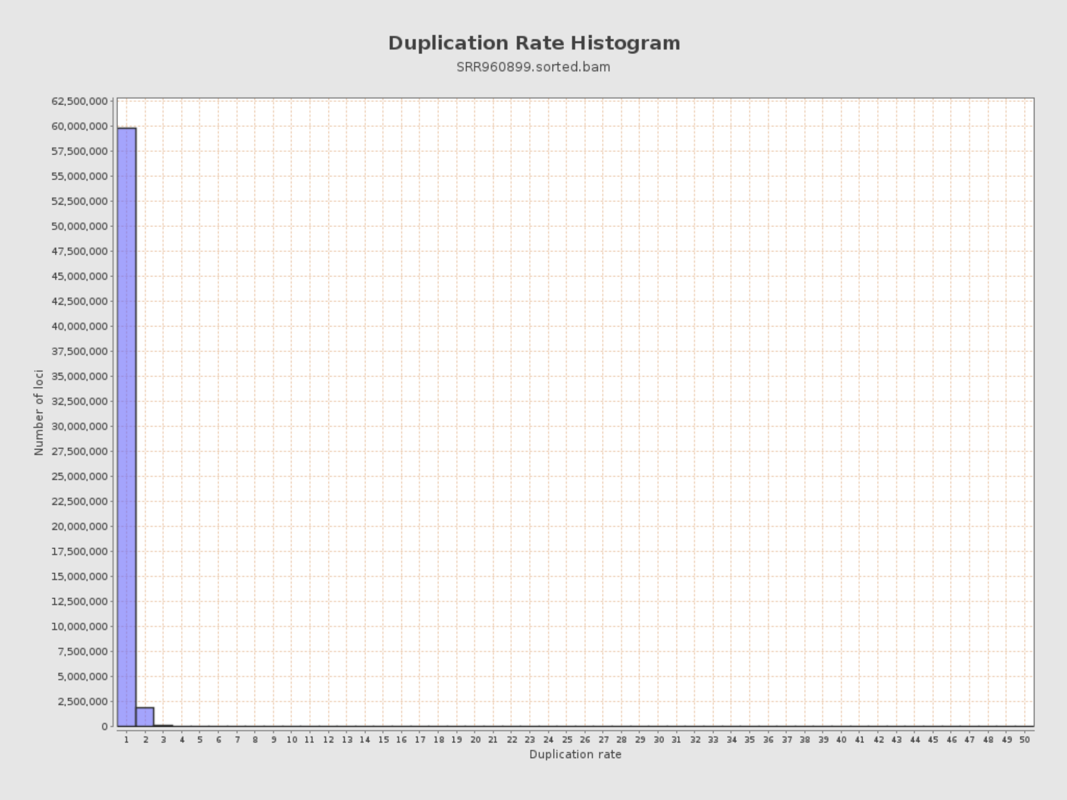
5. Results : Coverage Histogram (0-50X)



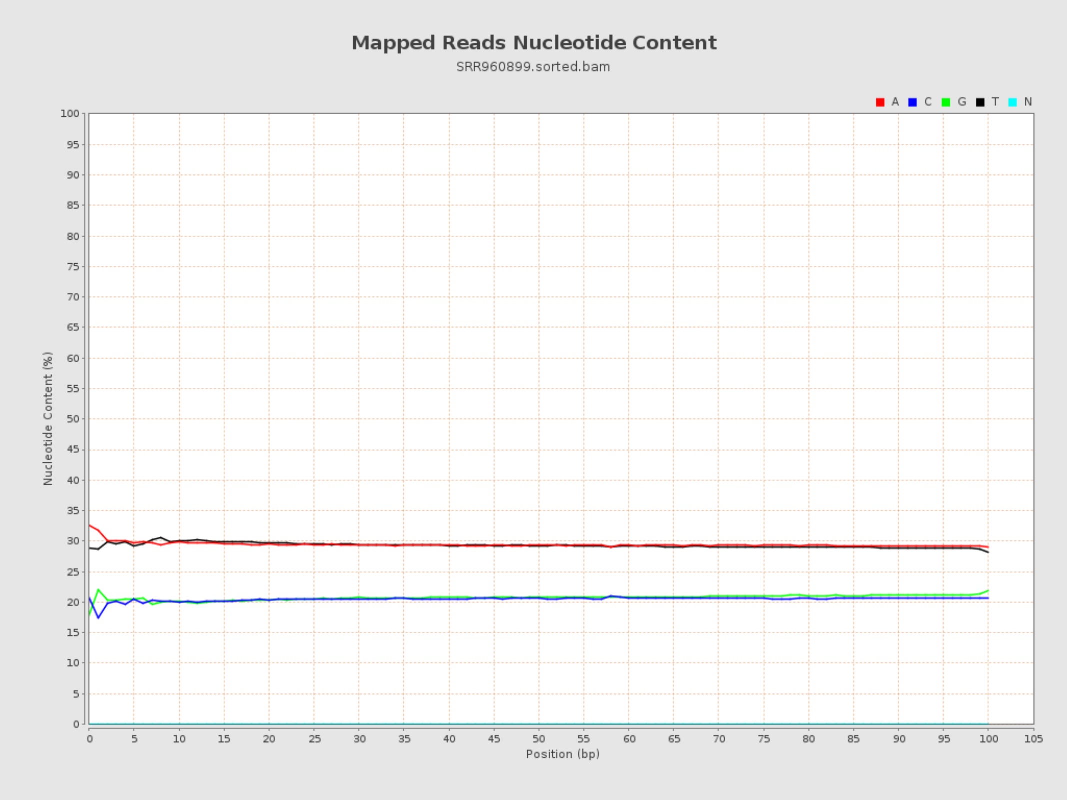
6. Results : Genome Fraction Coverage



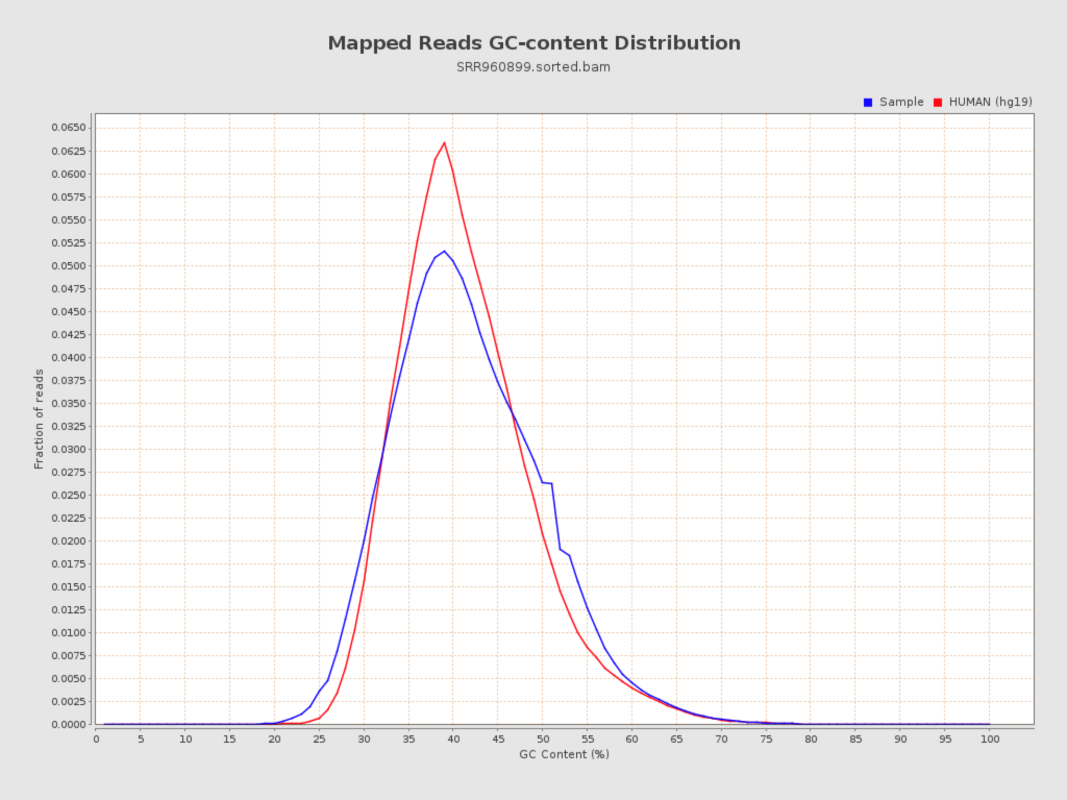
7. Results : Duplication Rate Histogram



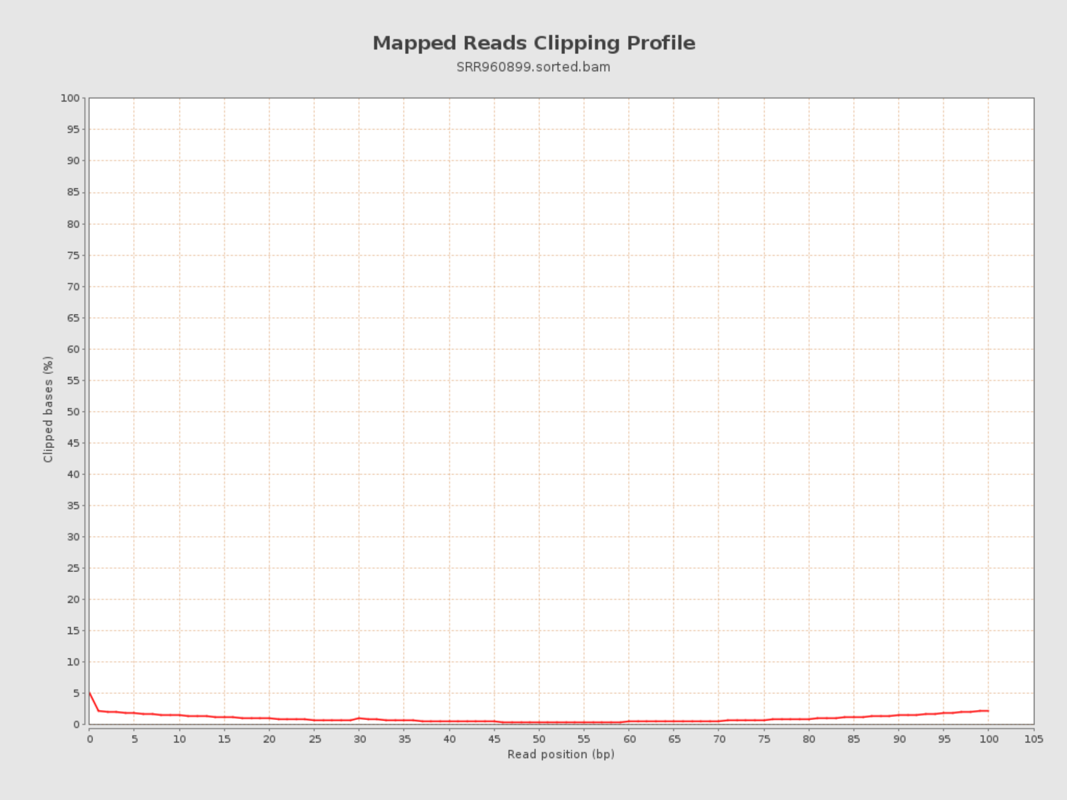
8. Results : Mapped Reads Nucleotide Content



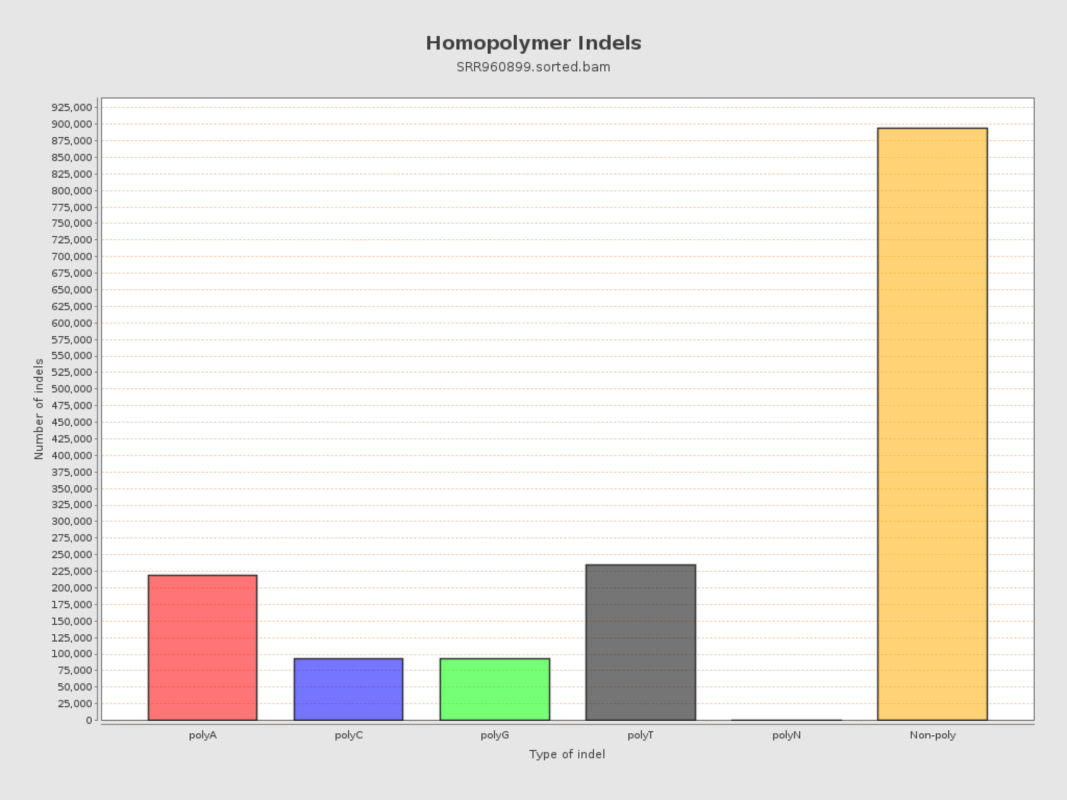
9. Results : Mapped Reads GC-content Distribution



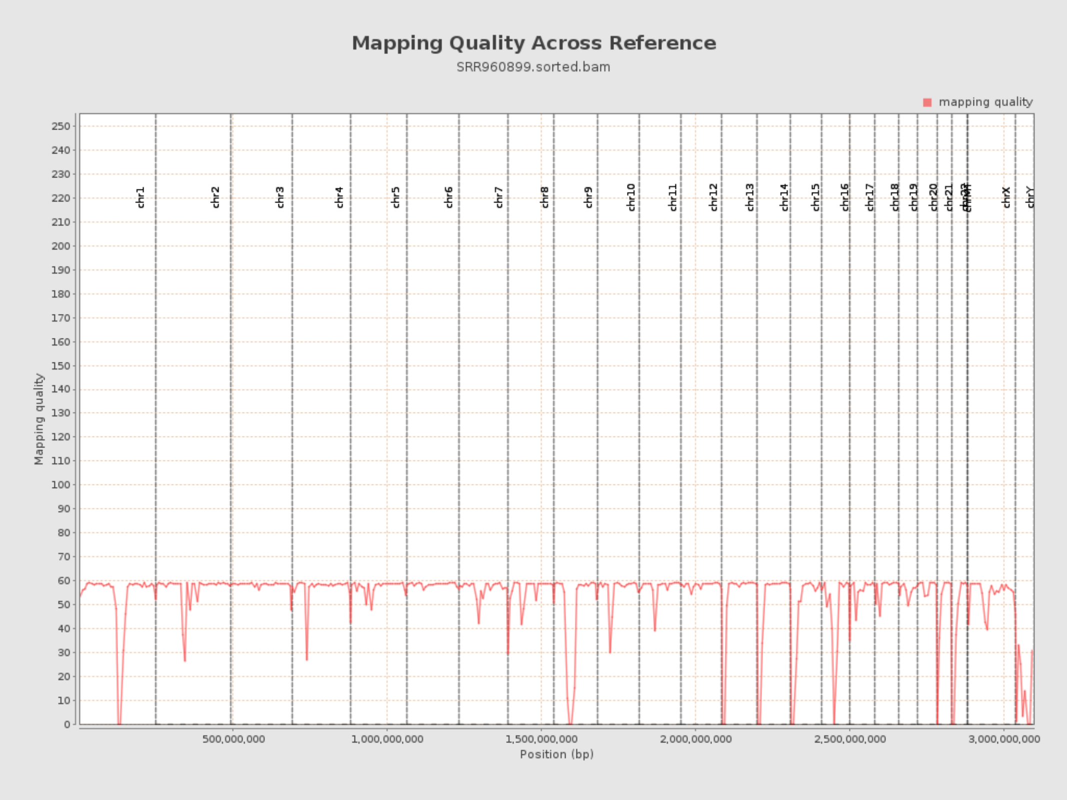
10. Results : Mapped Reads Clipping Profile



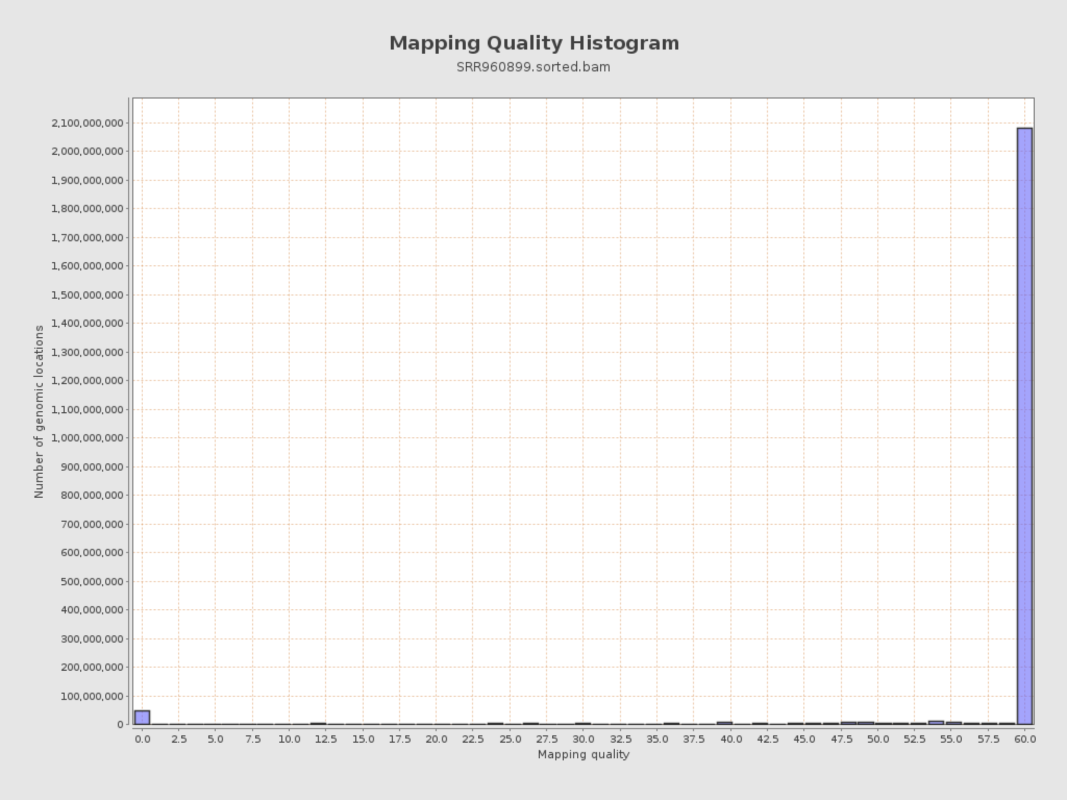
11. Results : Homopolymer Indels



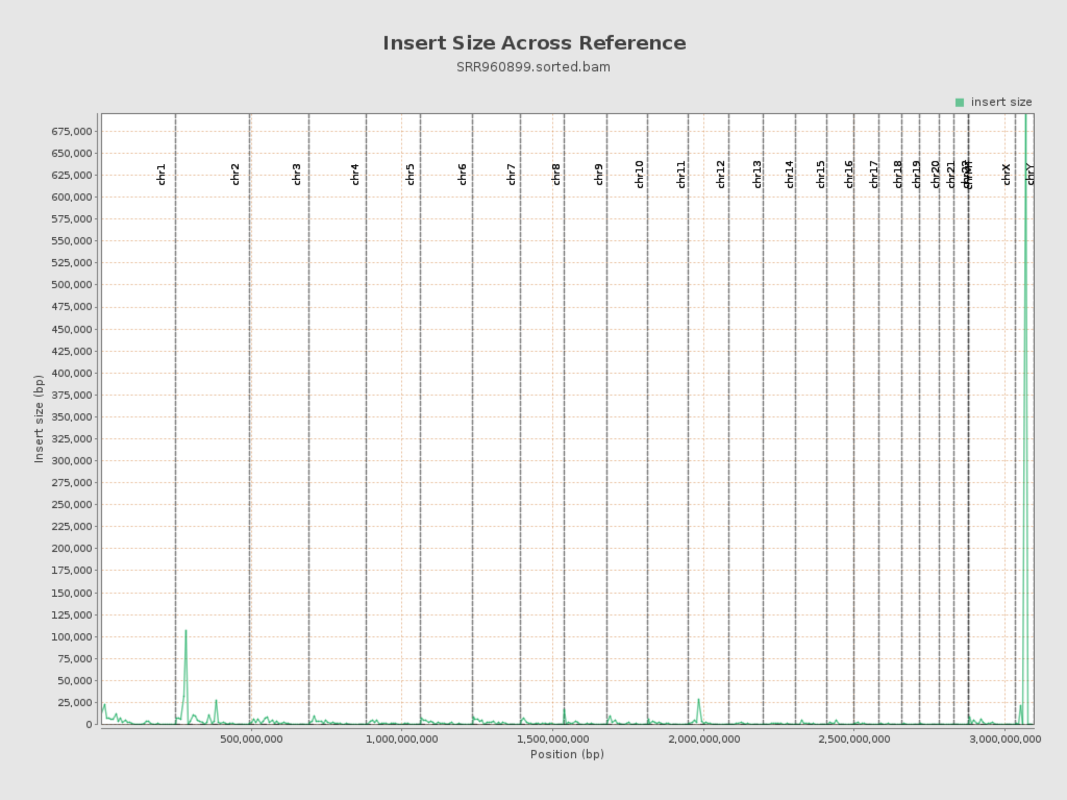
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram