Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/04 18:25:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR960892.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_SRR960892 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR960892_1.fastq.gz SRR960892_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jan 04 18:25:22 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR960892.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	221,864,044
Mapped reads	218,000,068 / 98.26%
Unmapped reads	3,863,976 / 1.74%
Mapped paired reads	218,000,068 / 98.26%
Mapped reads, first in pair	109,234,779 / 49.24%
Mapped reads, second in pair	108,765,289 / 49.02%
Mapped reads, both in pair	216,826,398 / 97.73%
Mapped reads, singletons	1,173,670 / 0.53%
Secondary alignments	0
Supplementary alignments	387,457 / 0.17%
Read min/max/mean length	30 / 101 / 101.07
Duplicated reads (estimated)	31,220,960 / 14.07%
Duplication rate	9.63%
Clipped reads	30,166,568 / 13.6%

2.2. ACGT Content

Number/percentage of A's	6,550,621,950 / 30.55%
Number/percentage of C's	4,175,004,617 / 19.47%
Number/percentage of T's	6,539,363,396 / 30.5%
Number/percentage of G's	4,174,094,355 / 19.47%
Number/percentage of N's	470,034 / 0%

GC Percentage	38.94%

2.3. Coverage

Mean	6.9276
Standard Deviation	94.1734

2.4. Mapping Quality

Mean Mapping Quality	53.64

2.5. Insert size

Mean	15,329.65
Standard Deviation	1,161,794.43
P25/Median/P75	136 / 163 / 192

2.6. Mismatches and indels

General error rate	1.19%
Mismatches	249,442,492
Insertions	2,569,261
Mapped reads with at least one insertion	1.15%
Deletions	2,708,700
Mapped reads with at least one deletion	1.2%
Homopolymer indels	40.81%

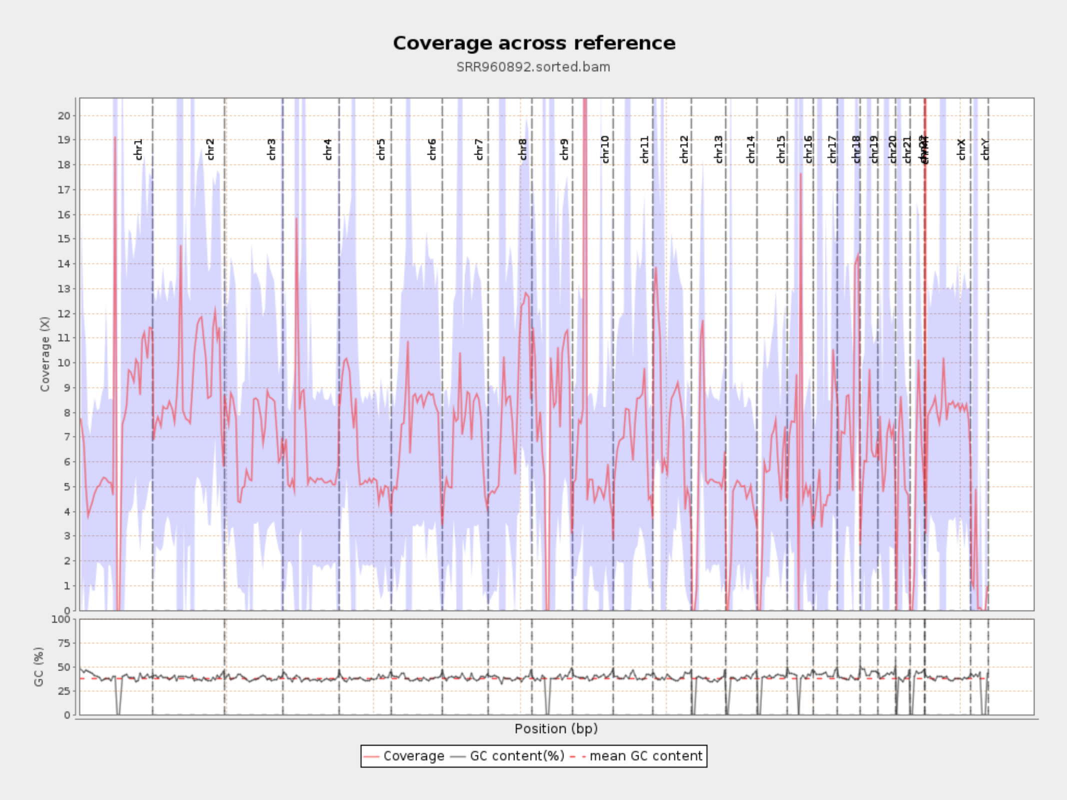
2.7. Chromosome stats

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

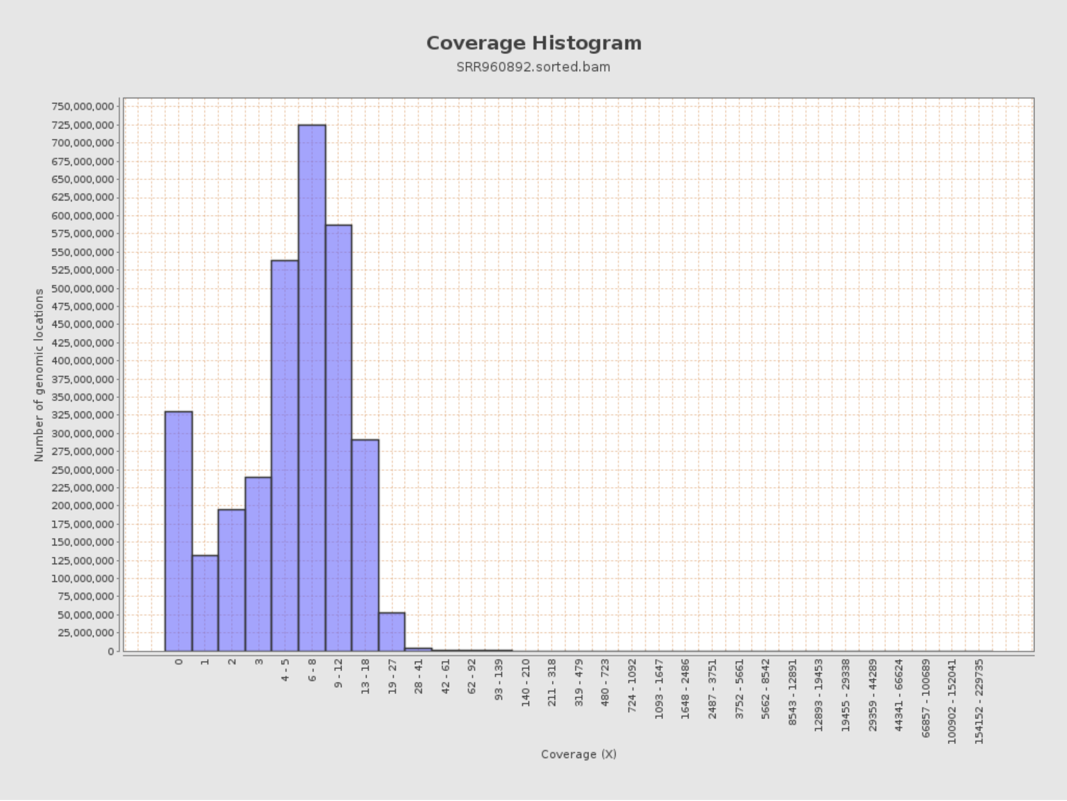
		bases	coverage	deviation
chr1	249250621	1818900523	7.2975	234.3821
chr2	243199373	2253322160	9.2653	50.2792
chr3	198022430	1408537471	7.113	14.1943
chr4	191154276	1193827167	6.2454	76.6684
chr5	180915260	1158664602	6.4045	8.1347
chr6	171115067	1313519967	7.6762	27.4165
chr7	159138663	1111084893	6.9819	58.9373
chr8	146364022	1225833923	8.3752	95.4808
chr9	141213431	1085763025	7.6888	76.7302
chr10	135534747	953786289	7.0372	221.3907
chr11	135006516	949847514	7.0356	36.4634
chr12	133851895	1083737232	8.0965	7.8688
chr13	115169878	602760900	5.2337	4.686
chr14	107349540	426393513	3.972	6.8225
chr15	102531392	524206378	5.1126	4.581
chr16	90354753	581729049	6.4383	85.2815
chr17	81195210	458585467	5.6479	24.2702
chr18	78077248	676402521	8.6632	80.1695
chr19	59128983	373864196	6.3229	102.6641
chr20	63025520	415414940	6.5912	22.1985
chr21	48129895	268381466	5.5762	30.9667
chr22	51304566	247454606	4.8232	6.163
chrMT	16571	8444813	509.614	106.5172
chrX	155270560	1245270558	8.02	25.6844

chrY	59373566	60118631	1.0125	66.3364

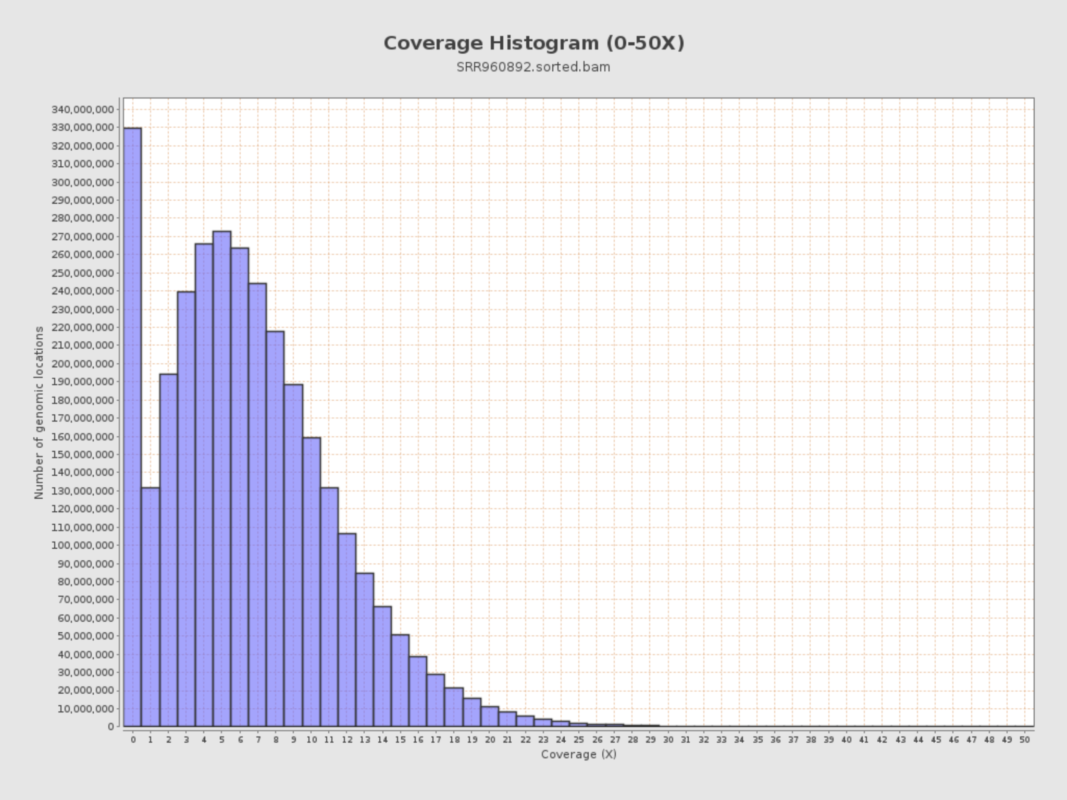
3. Results : Coverage across reference



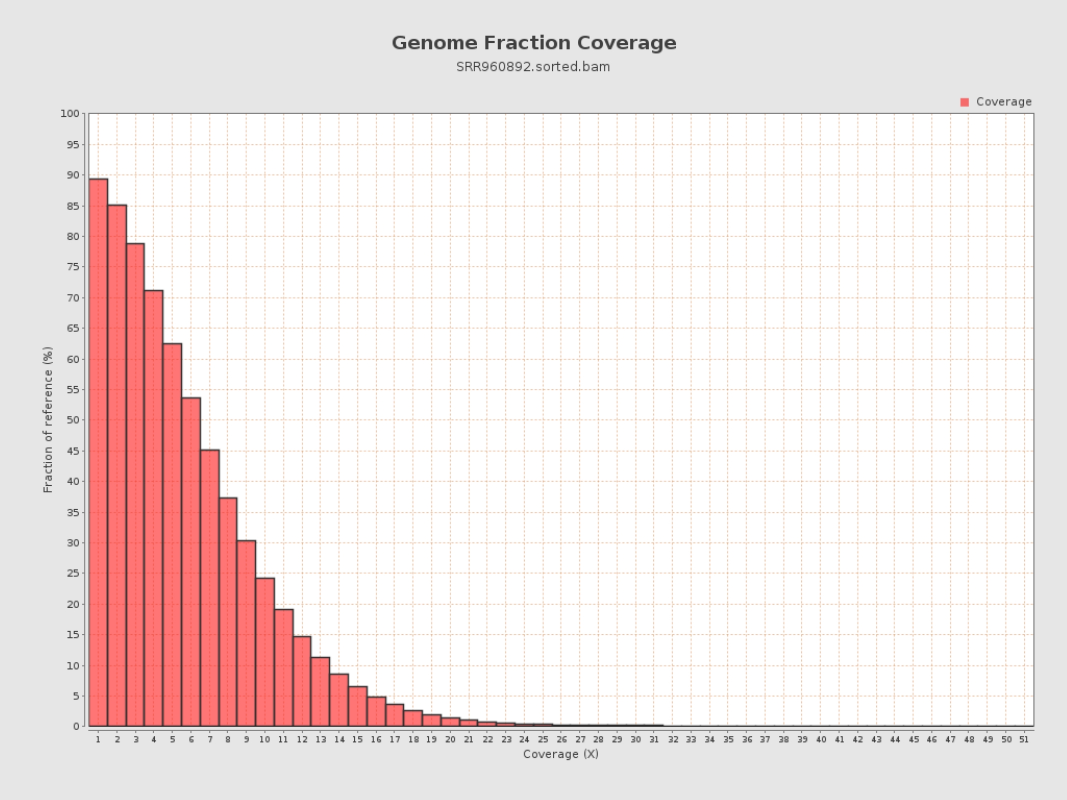
4. Results : Coverage Histogram



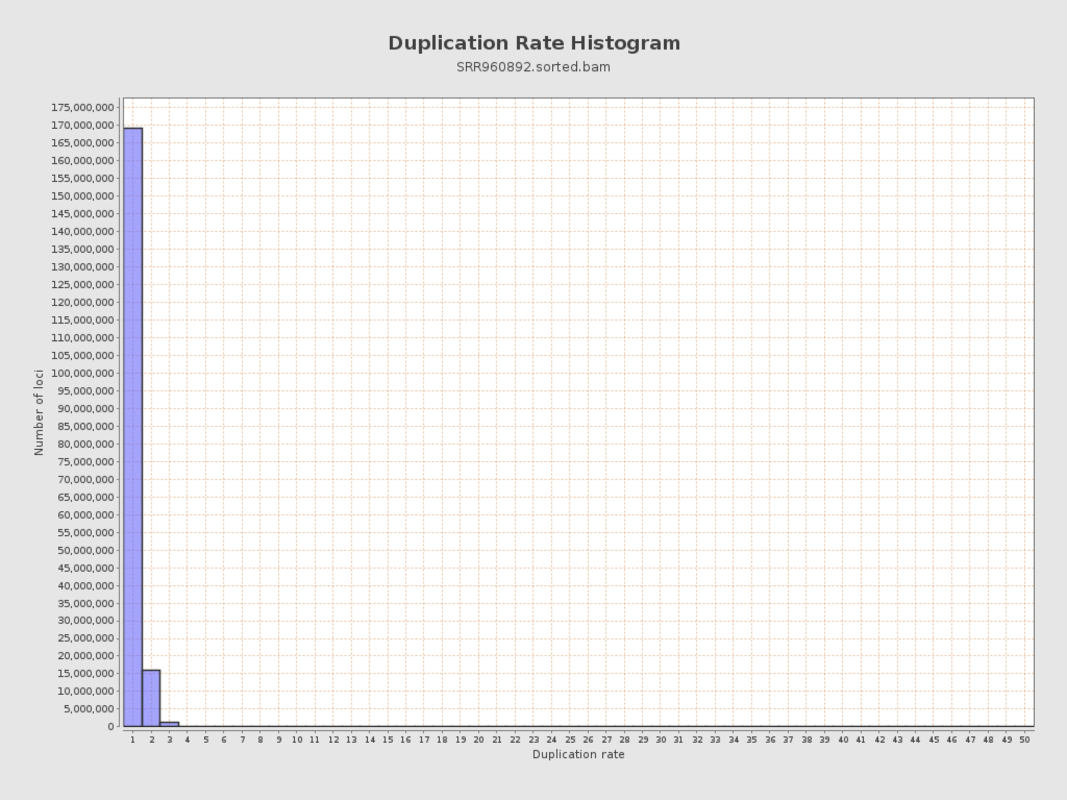
5. Results : Coverage Histogram (0-50X)



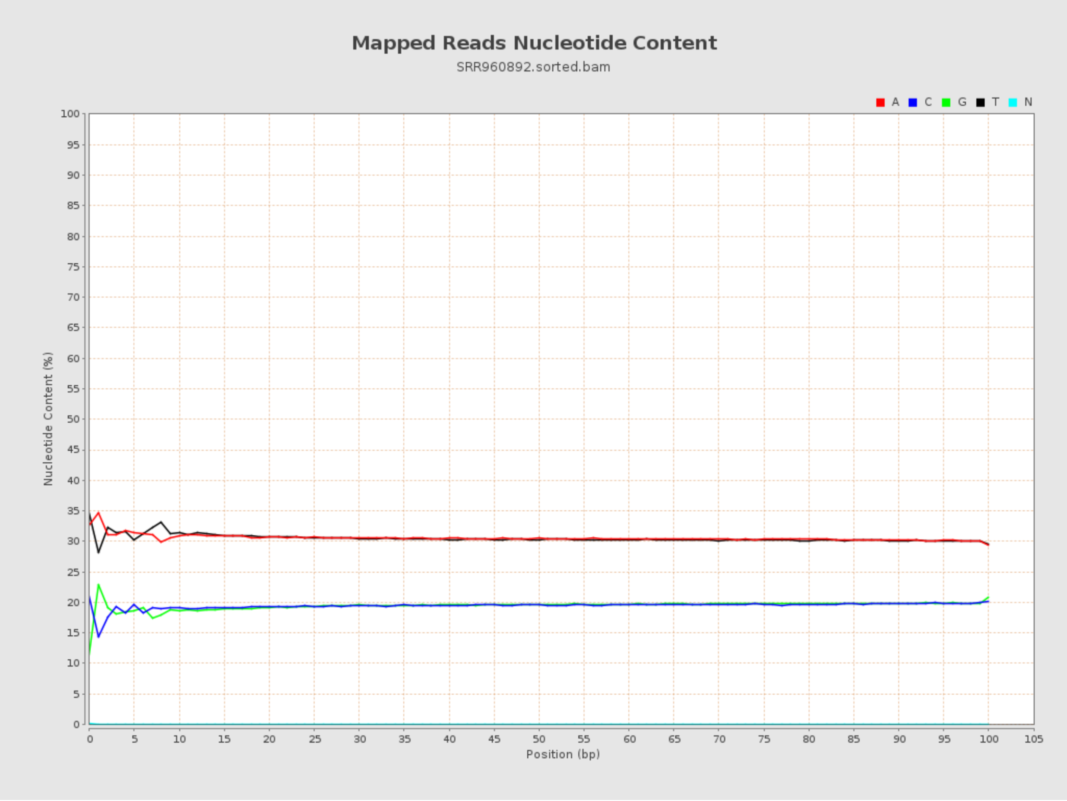
6. Results : Genome Fraction Coverage



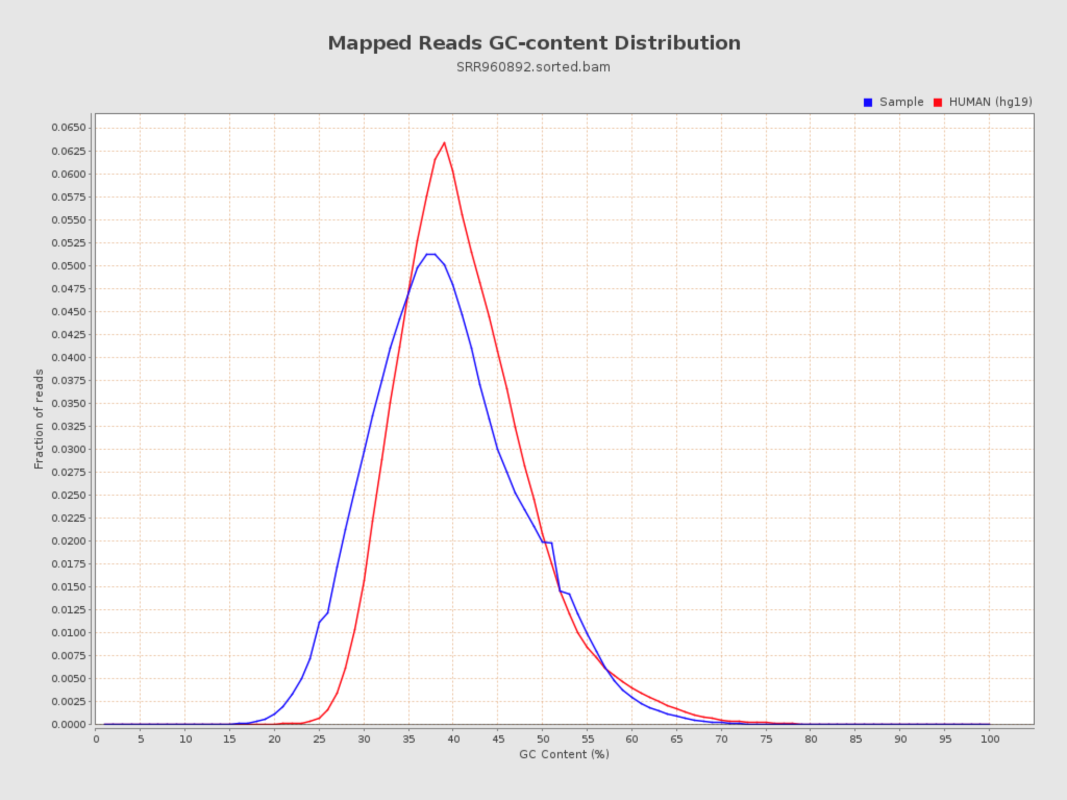
7. Results : Duplication Rate Histogram



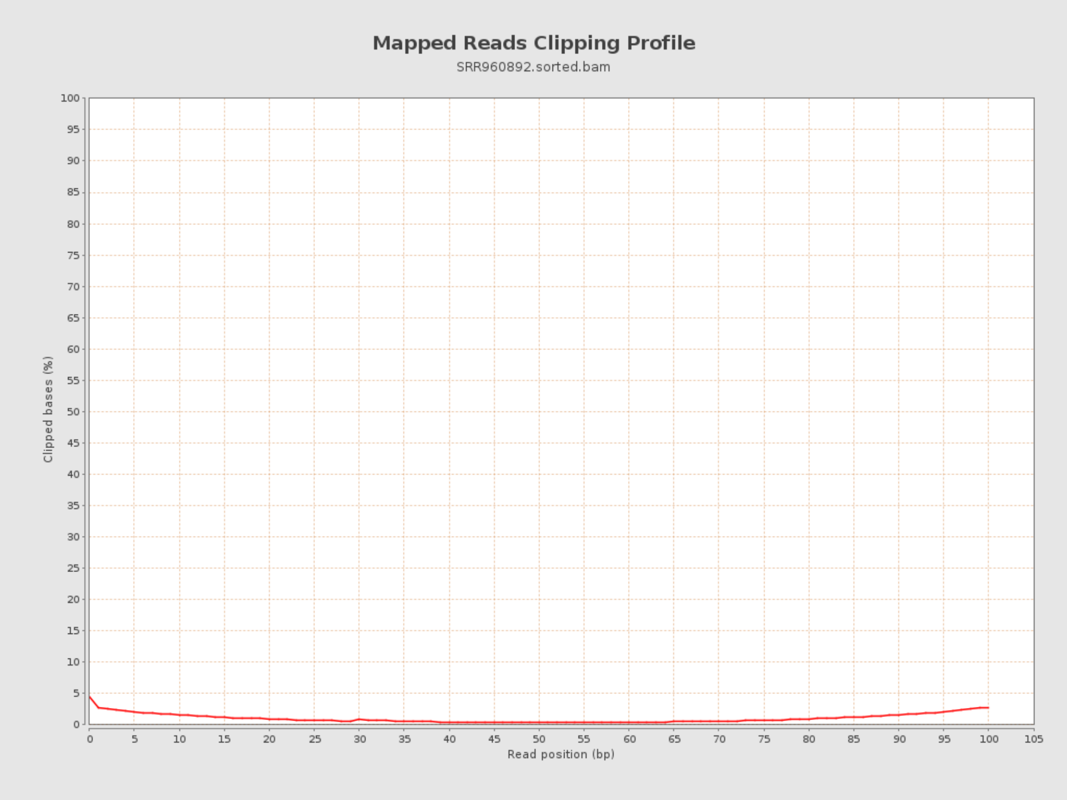
8. Results : Mapped Reads Nucleotide Content



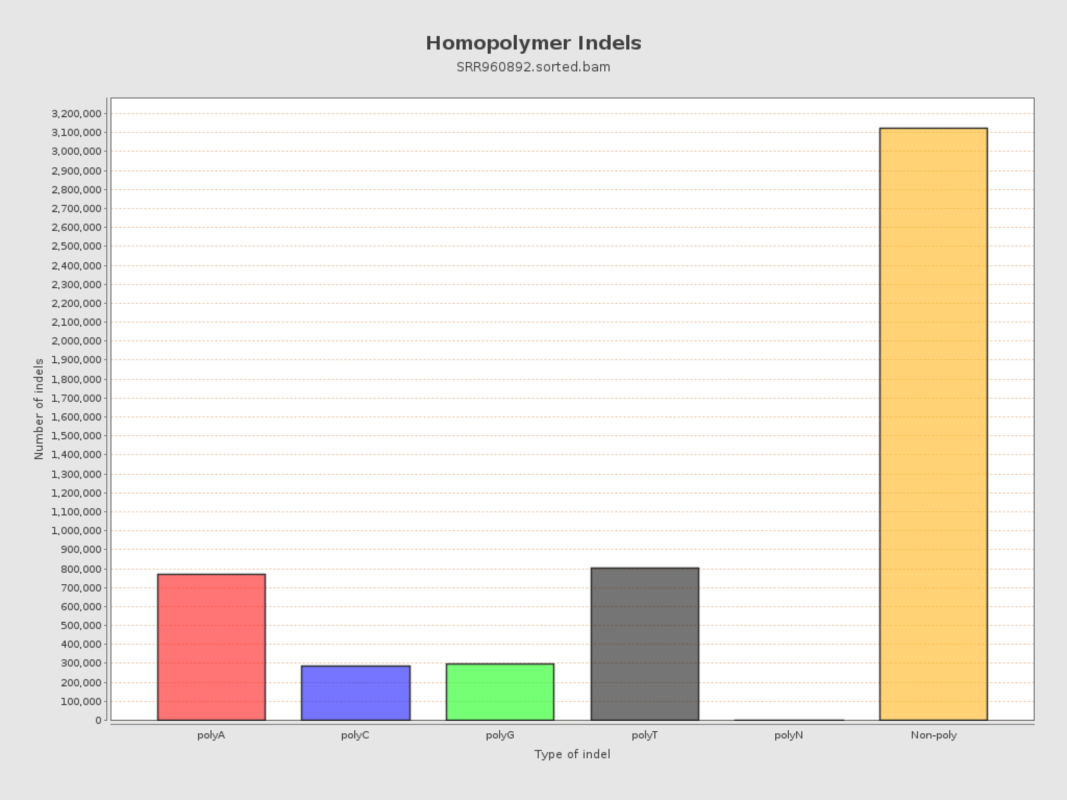
9. Results : Mapped Reads GC-content Distribution



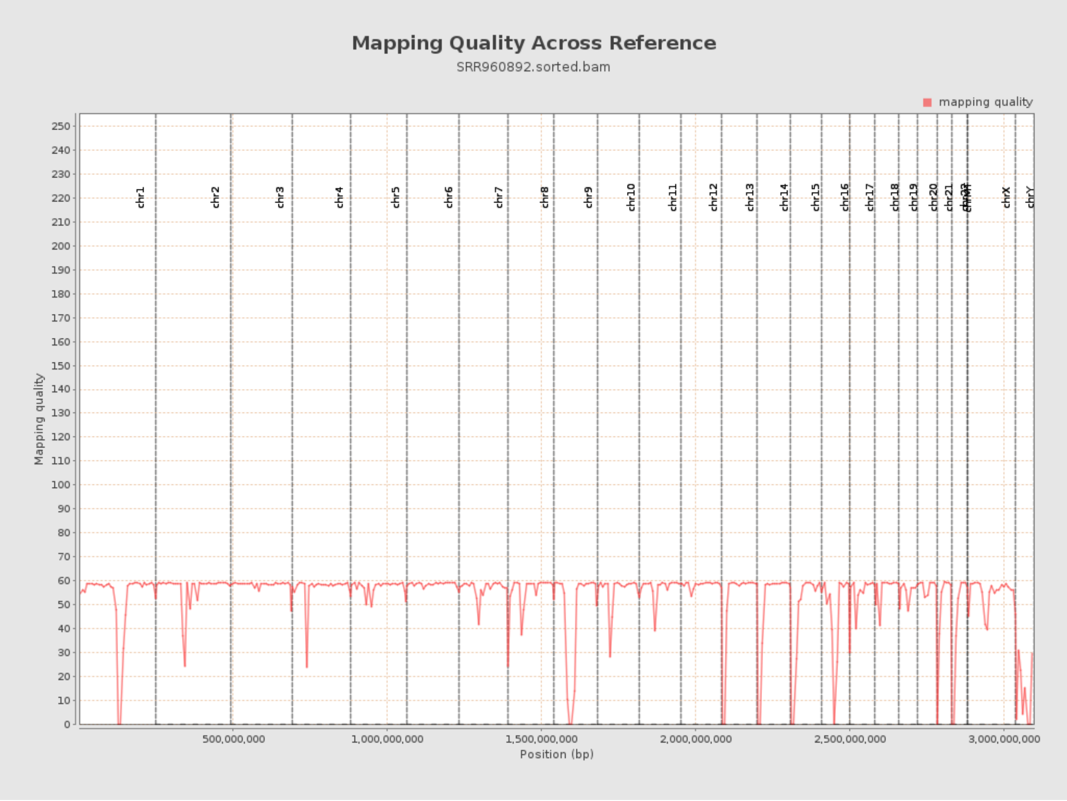
10. Results : Mapped Reads Clipping Profile



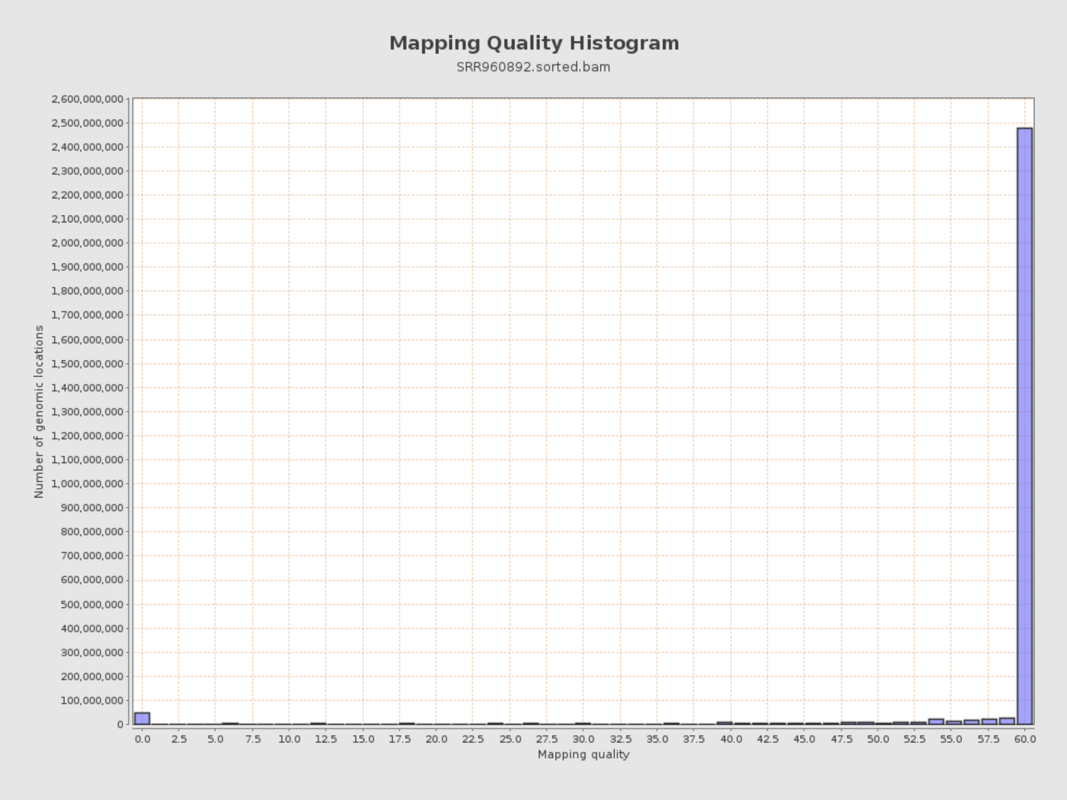
11. Results : Homopolymer Indels



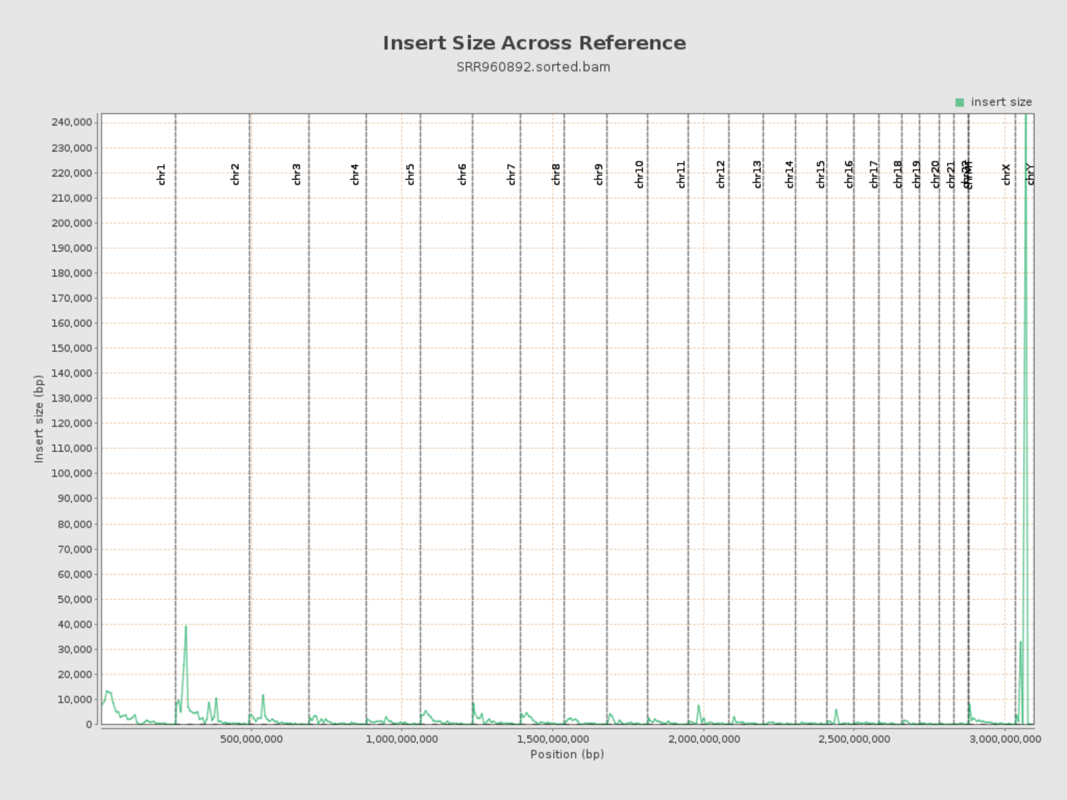
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram