Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/05 06:28:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR960896.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_SRR960896 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR960896_1.fastq.gz SRR960896_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Jan 05 06:28:58 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR960896.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	220,574,048
Mapped reads	216,936,532 / 98.35%
Unmapped reads	3,637,516 / 1.65%
Mapped paired reads	216,936,532 / 98.35%
Mapped reads, first in pair	108,688,833 / 49.28%
Mapped reads, second in pair	108,247,699 / 49.08%
Mapped reads, both in pair	215,787,550 / 97.83%
Mapped reads, singletons	1,148,982 / 0.52%
Secondary alignments	0
Supplementary alignments	386,691 / 0.18%
Read min/max/mean length	30 / 101 / 101.07
Duplicated reads (estimated)	31,016,325 / 14.06%
Duplication rate	9.59%
Clipped reads	30,202,919 / 13.69%

2.2. ACGT Content

Number/percentage of A's	6,522,657,771 / 30.57%
Number/percentage of C's	4,151,499,762 / 19.46%
Number/percentage of T's	6,512,879,993 / 30.53%
Number/percentage of G's	4,146,432,200 / 19.44%
Number/percentage of N's	1,069,494 / 0.01%

GC Percentage	38.89%

2.3. Coverage

Mean	6.8937
Standard Deviation	93.7841

2.4. Mapping Quality

Mean Mapping Quality	53.64

2.5. Insert size

Mean	15,327.21
Standard Deviation	1,160,599.81
P25/Median/P75	136 / 163 / 192

2.6. Mismatches and indels

General error rate	1.2%
Mismatches	249,615,334
Insertions	2,542,394
Mapped reads with at least one insertion	1.14%
Deletions	2,693,868
Mapped reads with at least one deletion	1.2%
Homopolymer indels	40.79%

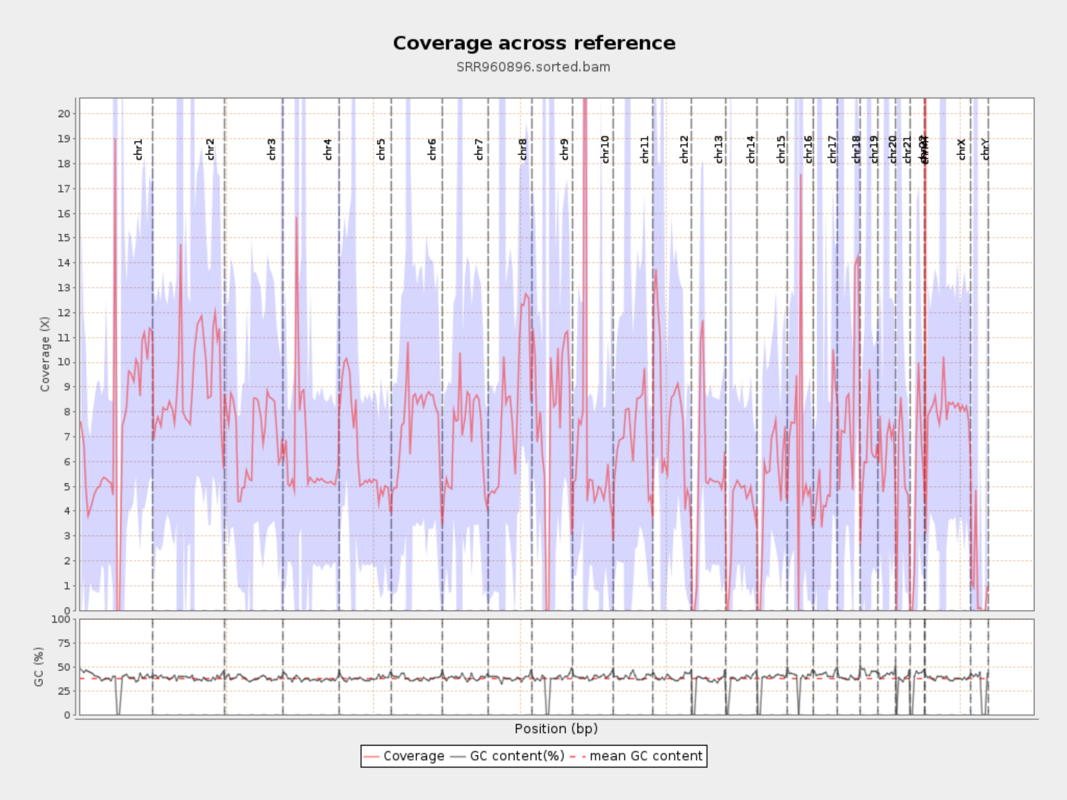
2.7. Chromosome stats

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

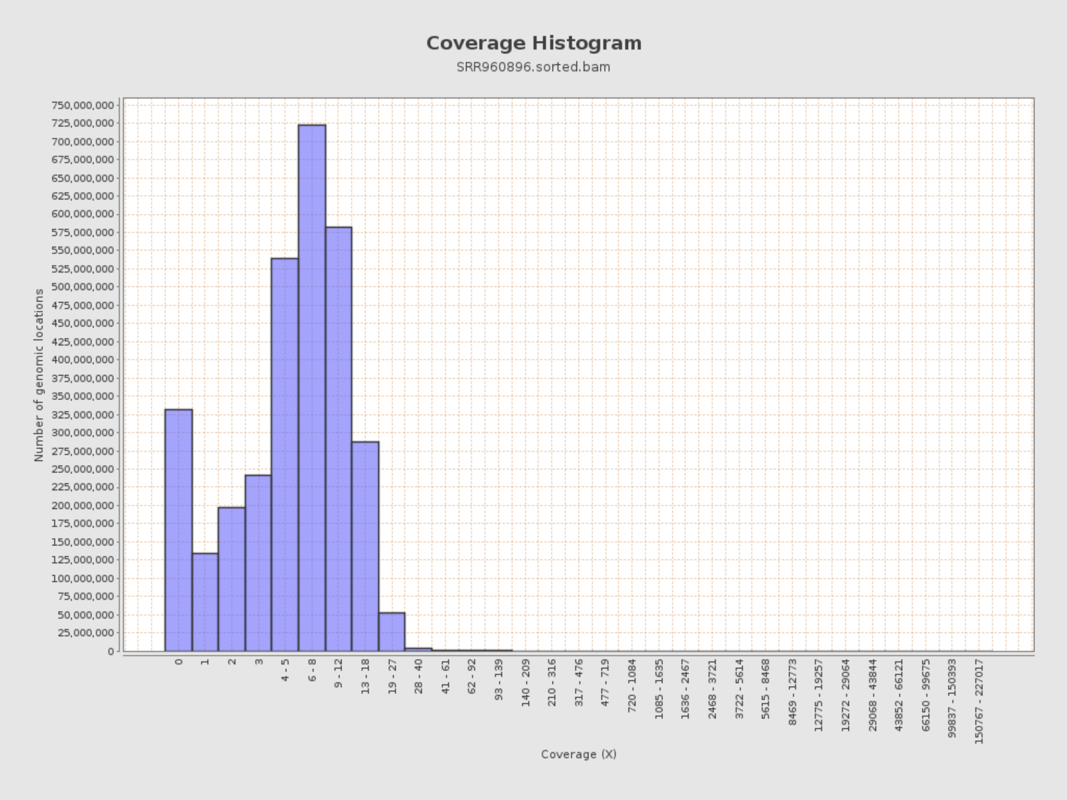
		bases	**coverage**	**deviation**
chr1	249250621	1807670681	7.2524	232.6866
chr2	243199373	2243580863	9.2253	50.2365
chr3	198022430	1403923181	7.0897	13.9051
chr4	191154276	1189771478	6.2241	76.765
chr5	180915260	1153883847	6.378	8.1768
chr6	171115067	1307326337	7.64	27.2861
chr7	159138663	1105346714	6.9458	58.8905
chr8	146364022	1219518313	8.3321	95.8446
chr9	141213431	1080710642	7.653	76.3595
chr10	135534747	949283871	7.004	220.9501
chr11	135006516	945828485	7.0058	36.4231
chr12	133851895	1077539139	8.0502	7.8041
chr13	115169878	599999775	5.2097	4.6781
chr14	107349540	423751800	3.9474	6.8104
chr15	102531392	521192608	5.0832	4.5756
chr16	90354753	578176779	6.399	85.1116
chr17	81195210	454703956	5.6001	24.1498
chr18	78077248	673701387	8.6287	80.5001
chr19	59128983	370715425	6.2696	102.7919
chr20	63025520	412484260	6.5447	22.4062
chr21	48129895	267011908	5.5477	30.8916
chr22	51304566	244971600	4.7748	6.1688
chrMT	16571	8422732	508.2815	110.9284
chrX	155270560	1241598283	7.9964	25.4891

chrY	59373566	59682110	1.0052	65.8357

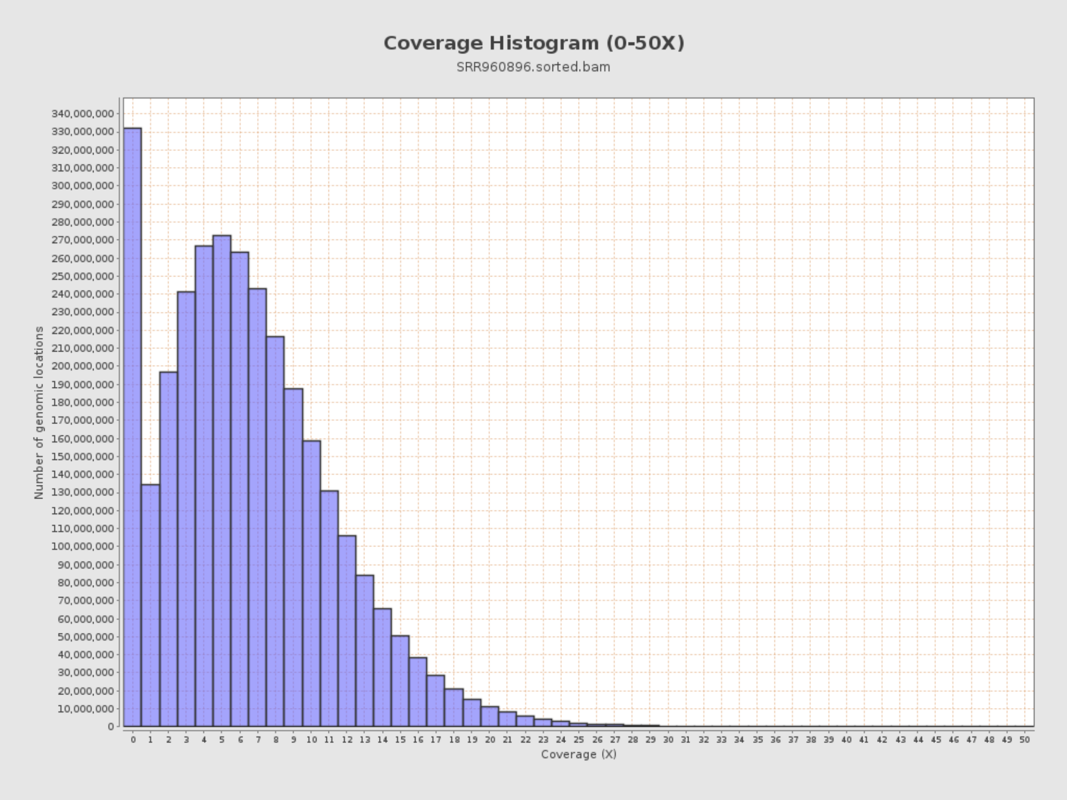
3. Results : Coverage across reference



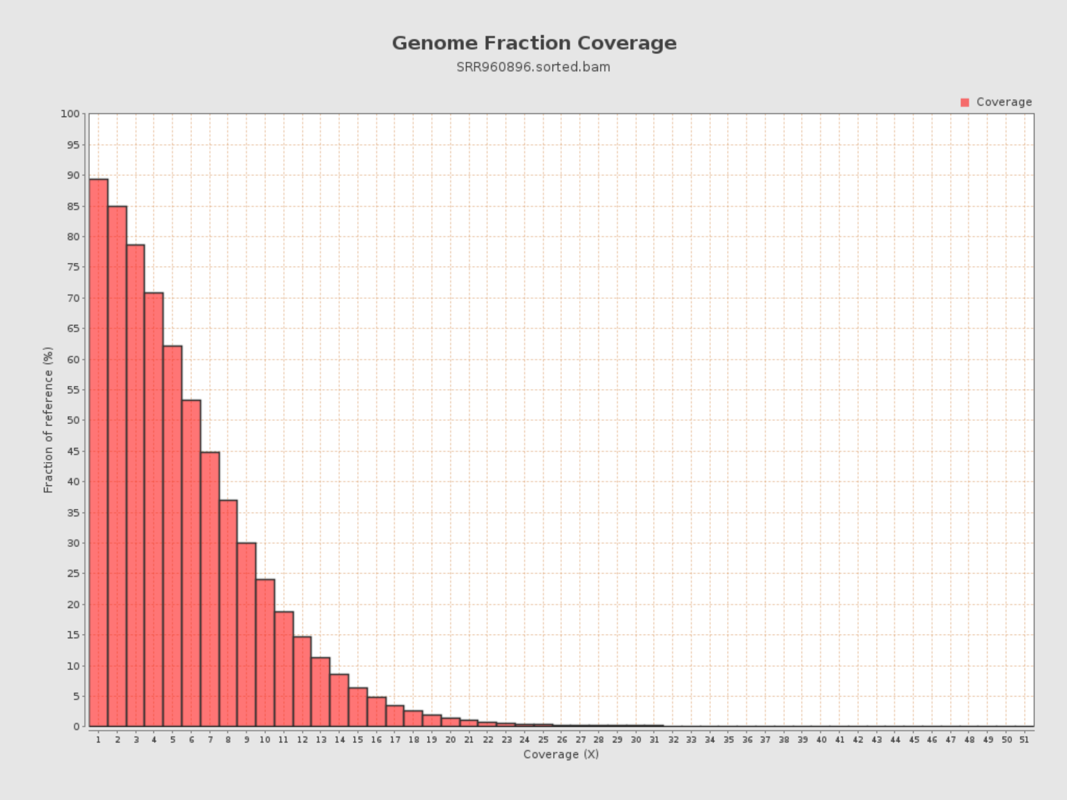
4. Results : Coverage Histogram



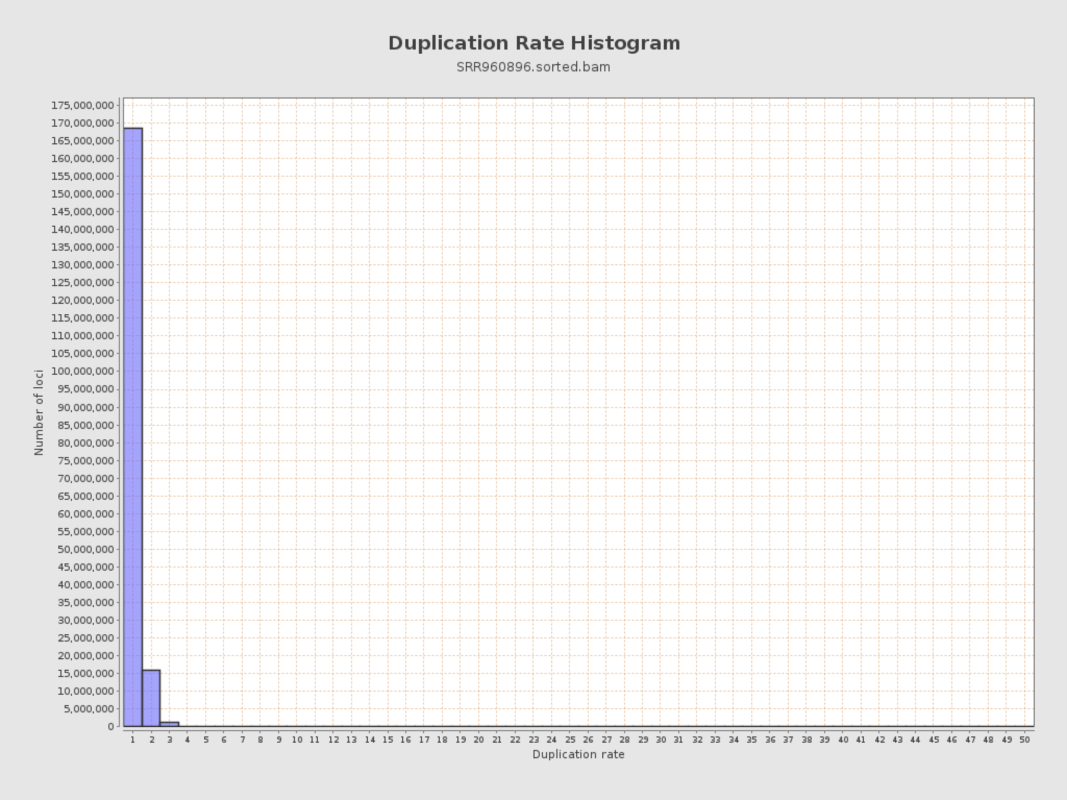
5. Results : Coverage Histogram (0-50X)



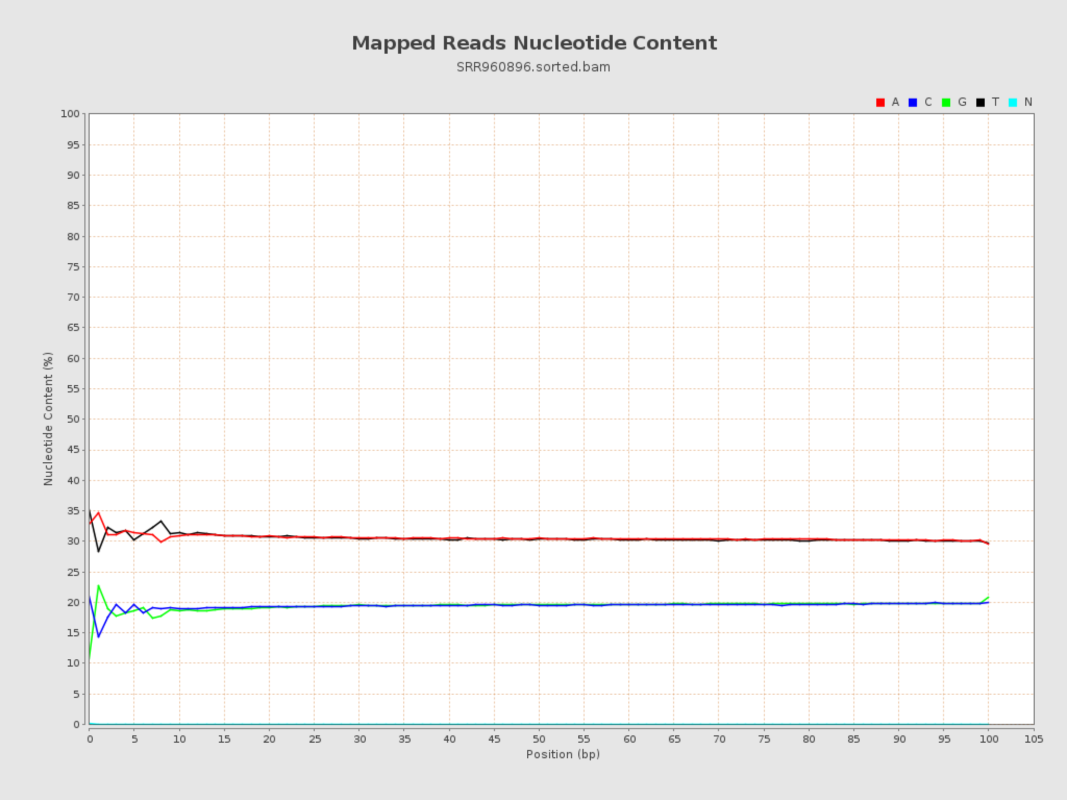
6. Results : Genome Fraction Coverage



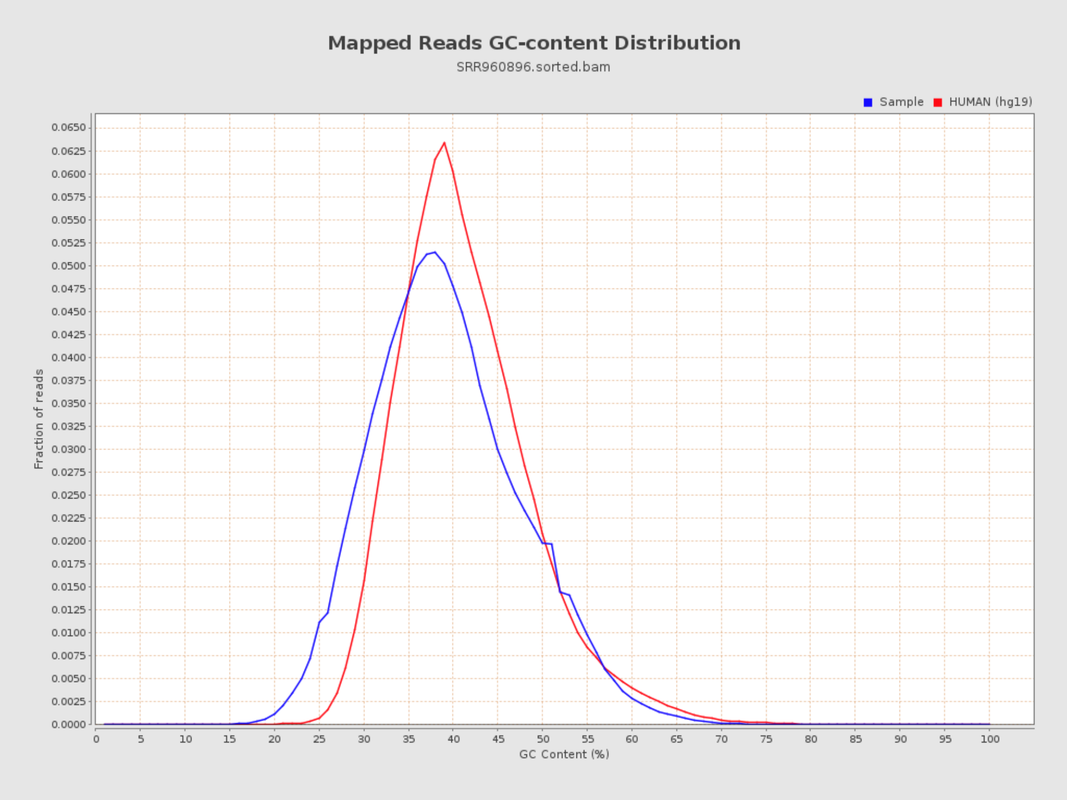
7. Results : Duplication Rate Histogram



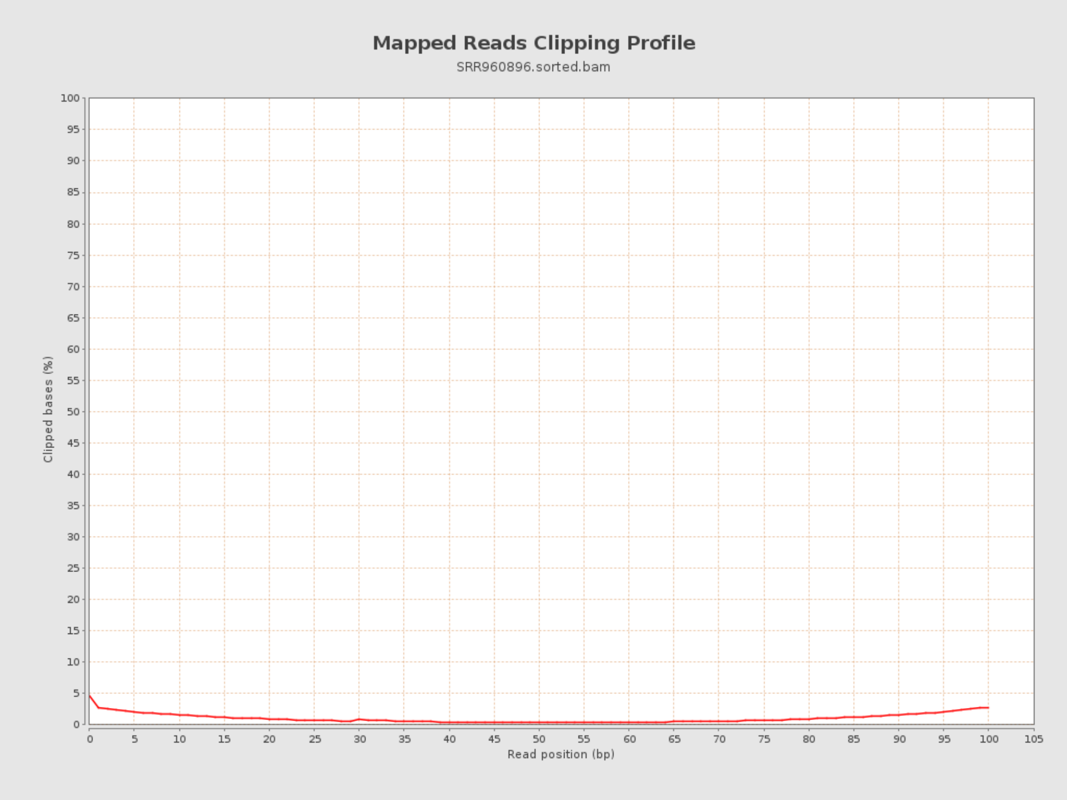
8. Results : Mapped Reads Nucleotide Content



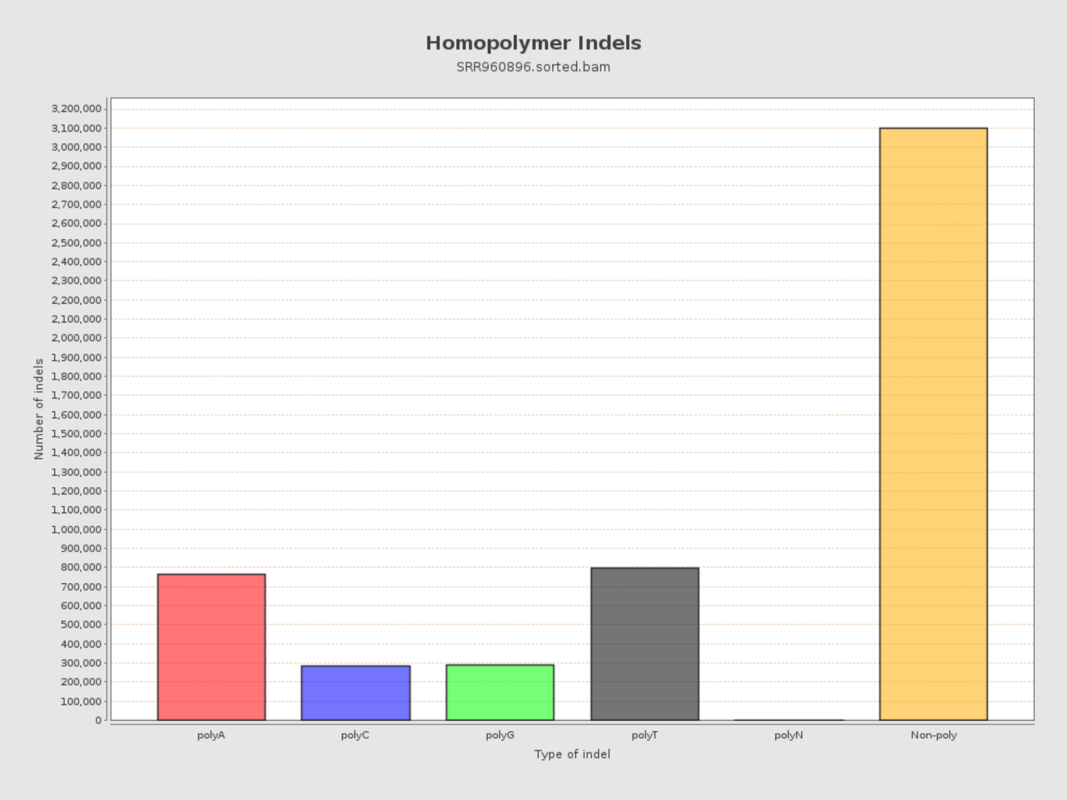
9. Results : Mapped Reads GC-content Distribution



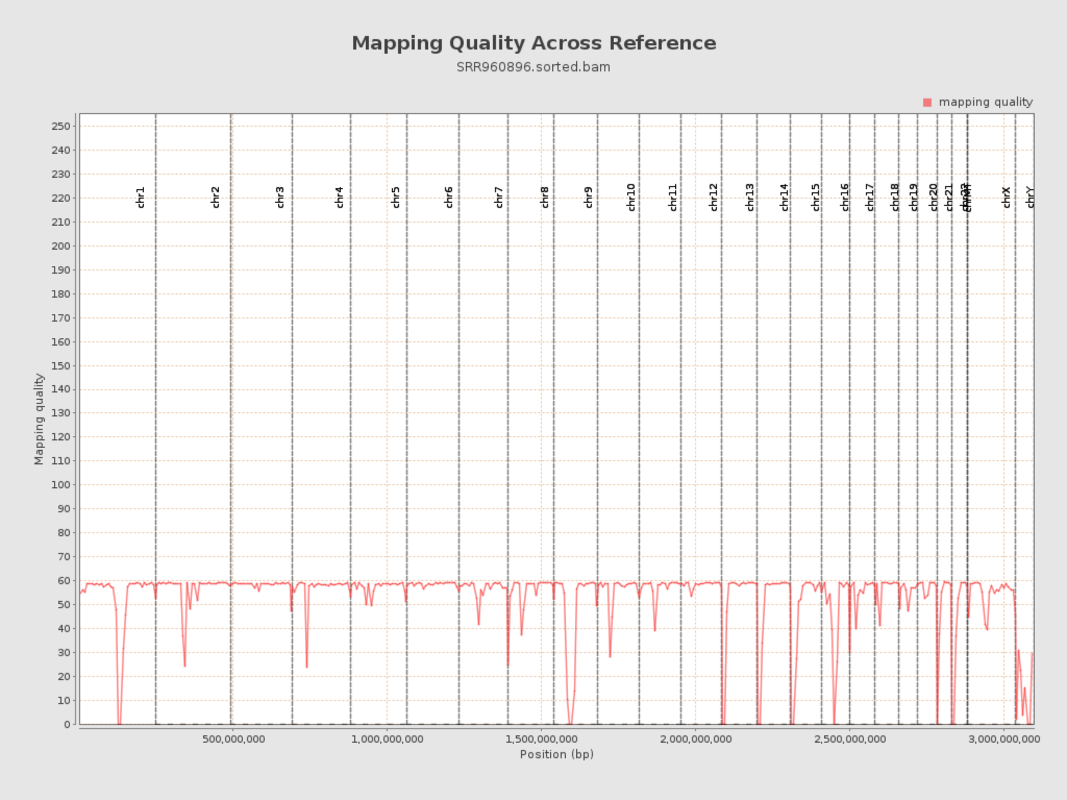
10. Results : Mapped Reads Clipping Profile



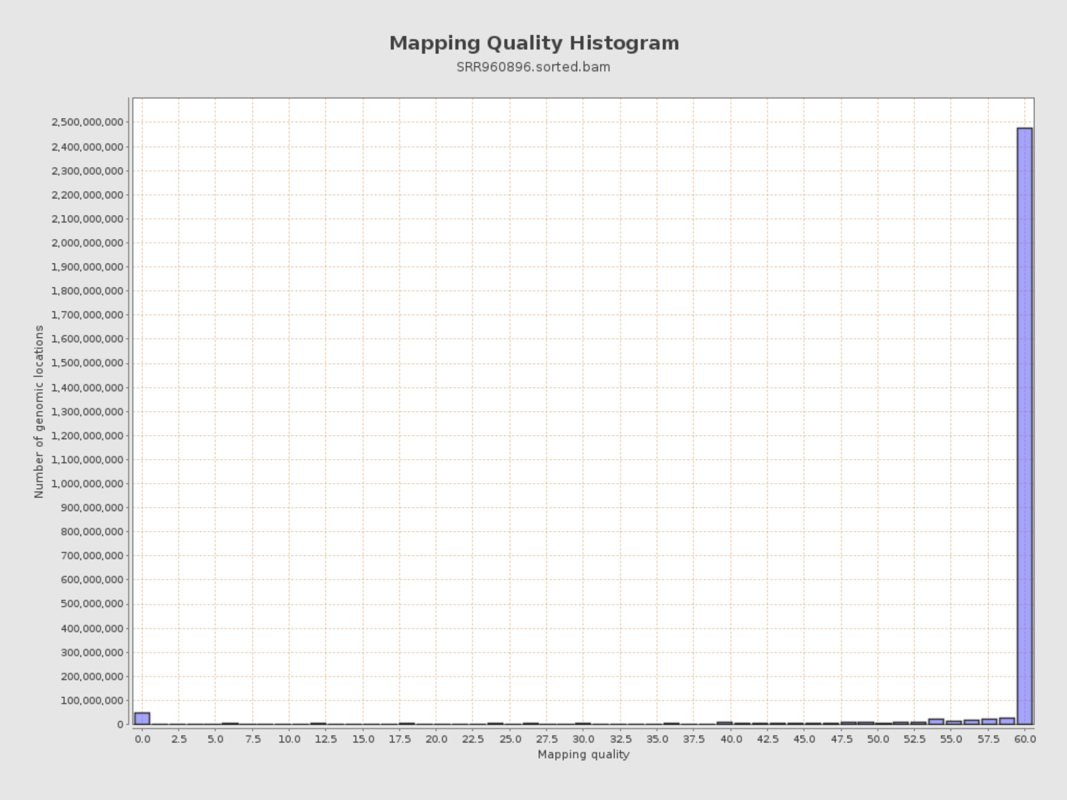
11. Results : Homopolymer Indels



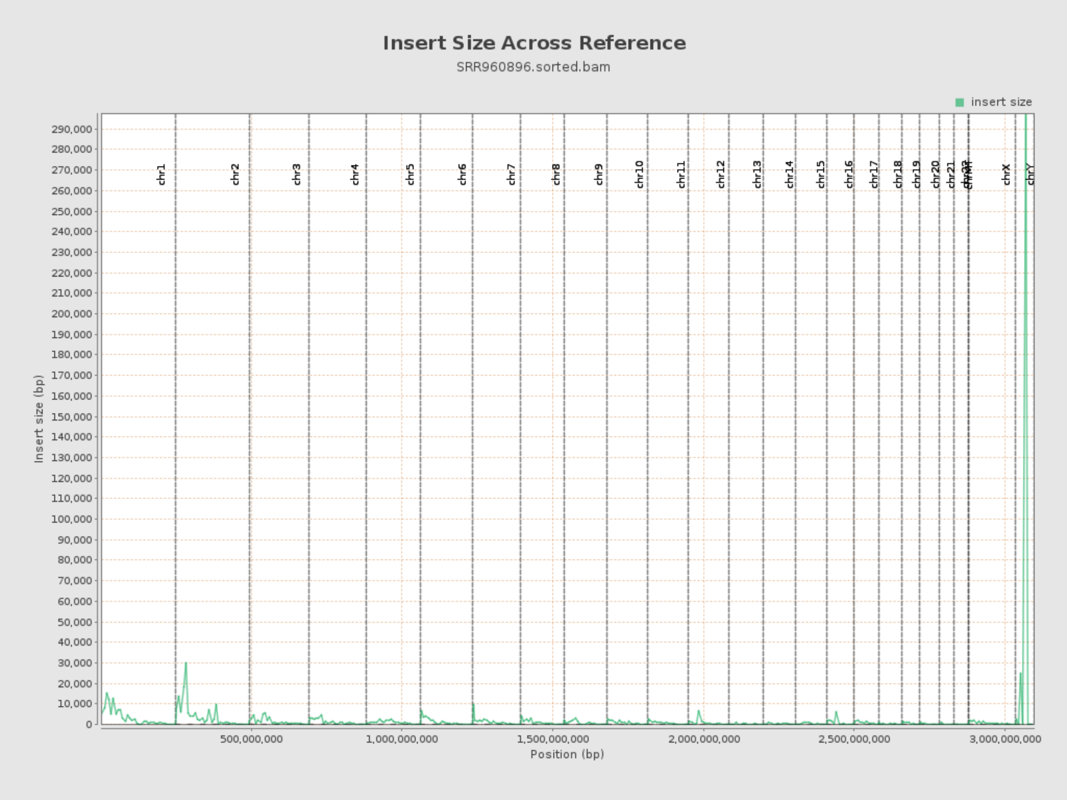
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram