Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/05 00:21:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR960894.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_SRR960894 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR960894_1.fastq.gz SRR960894_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Jan 05 00:21:31 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR960894.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	225,779,896
Mapped reads	221,957,500 / 98.31%
Unmapped reads	3,822,396 / 1.69%
Mapped paired reads	221,957,500 / 98.31%
Mapped reads, first in pair	111,249,241 / 49.27%
Mapped reads, second in pair	110,708,259 / 49.03%
Mapped reads, both in pair	220,654,844 / 97.73%
Mapped reads, singletons	1,302,656 / 0.58%
Secondary alignments	0
Supplementary alignments	386,955 / 0.17%
Read min/max/mean length	30 / 101 / 101.07
Duplicated reads (estimated)	31,812,806 / 14.09%
Duplication rate	9.69%
Clipped reads	33,743,659 / 14.95%

2.2. ACGT Content

Number/percentage of A's	6,637,539,993 / 30.5%
Number/percentage of C's	4,251,674,028 / 19.53%
Number/percentage of T's	6,626,426,066 / 30.44%
Number/percentage of G's	4,248,612,887 / 19.52%
Number/percentage of N's	1,237,001 / 0.01%

GC Percentage	39.05%

2.3. Coverage

Mean	7.0329
Standard Deviation	94.3266

2.4. Mapping Quality

Mean Mapping Quality	53.63

2.5. Insert size

Mean	15,558.7
Standard Deviation	1,168,827.24
P25/Median/P75	136 / 164 / 192

2.6. Mismatches and indels

General error rate	1.26%
Mismatches	267,965,045
Insertions	2,605,884
Mapped reads with at least one insertion	1.14%
Deletions	2,761,078
Mapped reads with at least one deletion	1.21%
Homopolymer indels	40.66%

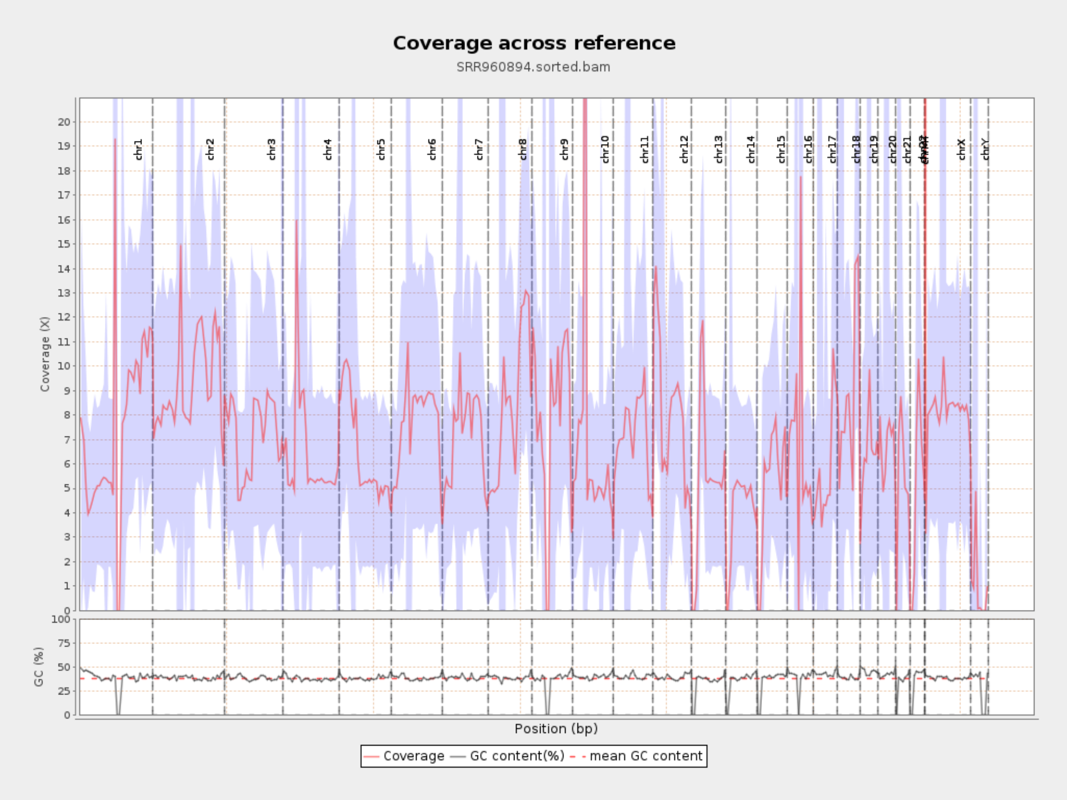
2.7. Chromosome stats

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

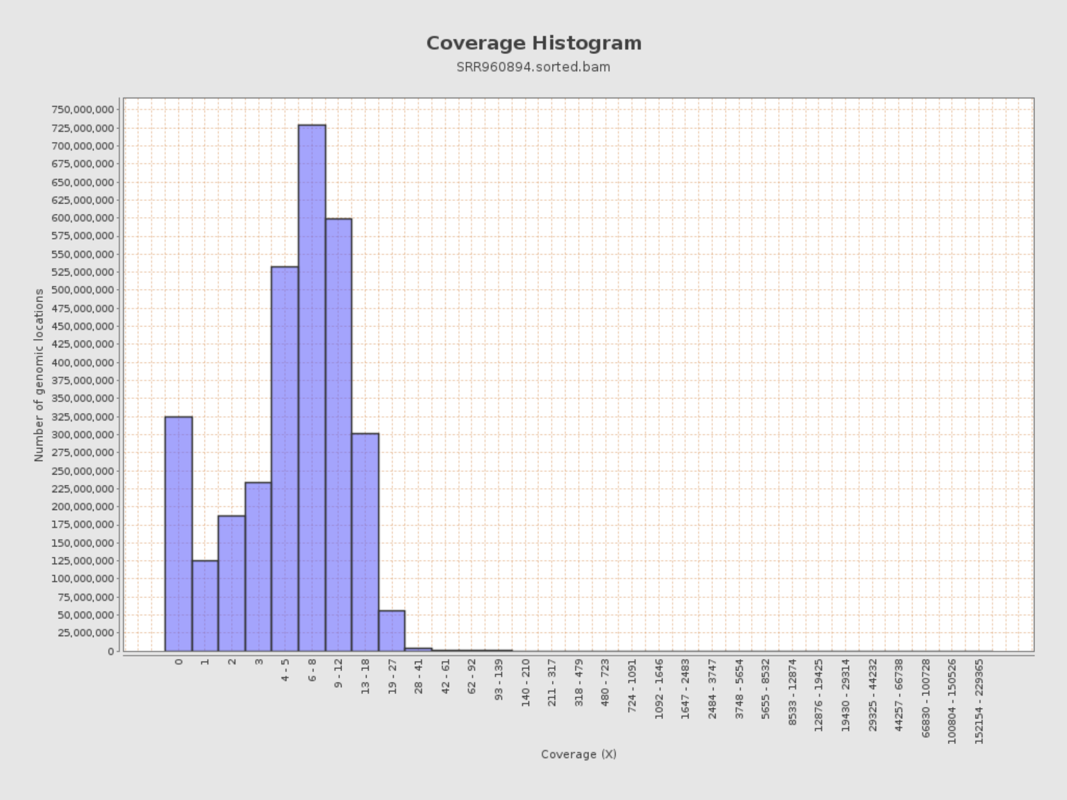
		bases	coverage	deviation
chr1	249250621	1847093395	7.4106	235.5681
chr2	243199373	2285406747	9.3973	50.4504
chr3	198022430	1428790115	7.2153	13.8245
chr4	191154276	1210096679	6.3305	76.1754
chr5	180915260	1174553294	6.4923	8.2861
chr6	171115067	1332644297	7.788	27.6656
chr7	159138663	1129011851	7.0945	59.8974
chr8	146364022	1242492211	8.4891	93.5569
chr9	141213431	1102964245	7.8106	76.8098
chr10	135534747	965494428	7.1236	220.9827
chr11	135006516	966130887	7.1562	36.9712
chr12	133851895	1100588789	8.2224	7.8835
chr13	115169878	611239423	5.3073	4.7192
chr14	107349540	432665262	4.0304	6.8546
chr15	102531392	533519651	5.2035	4.631
chr16	90354753	591795153	6.5497	85.524
chr17	81195210	467284186	5.7551	24.4741
chr18	78077248	686345676	8.7906	80.7844
chr19	59128983	382315277	6.4658	103.1558
chr20	63025520	423709446	6.7228	22.2695
chr21	48129895	271901296	5.6493	30.7775
chr22	51304566	253056884	4.9324	6.2241
chrMT	16571	8717123	526.0469	109.319
chrX	155270560	1263686446	8.1386	26.0693

chrY	59373566	60339002	1.0163	65.1894

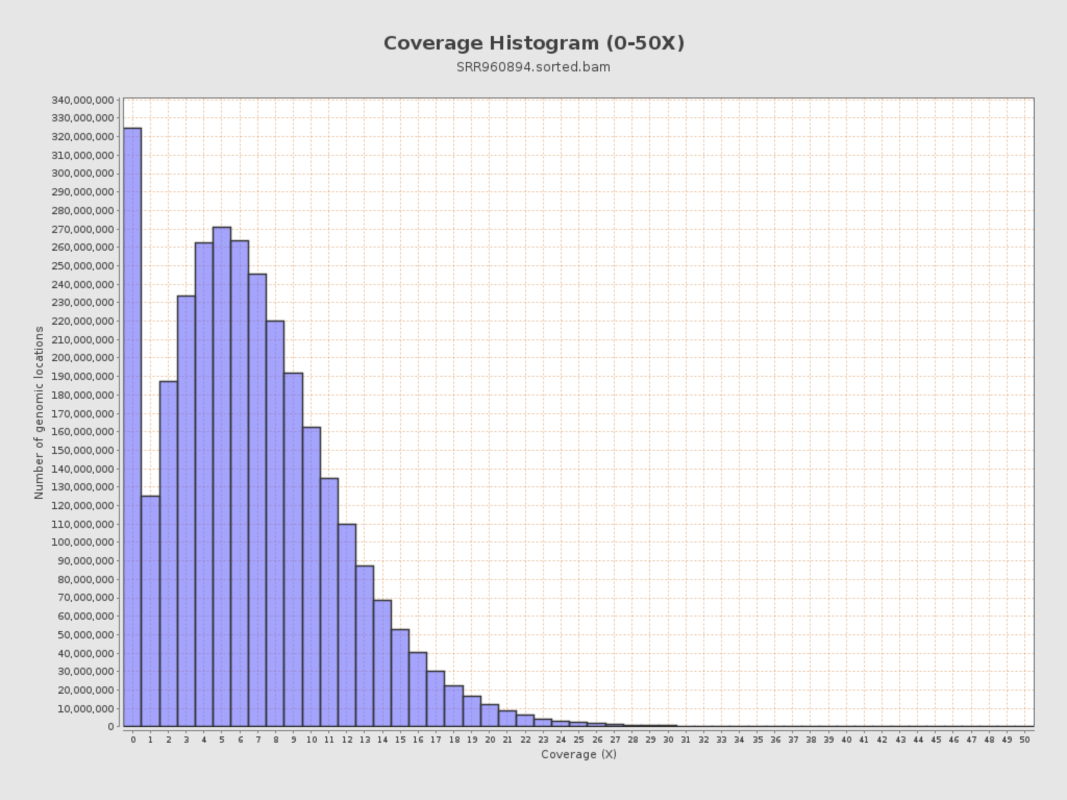
3. Results : Coverage across reference



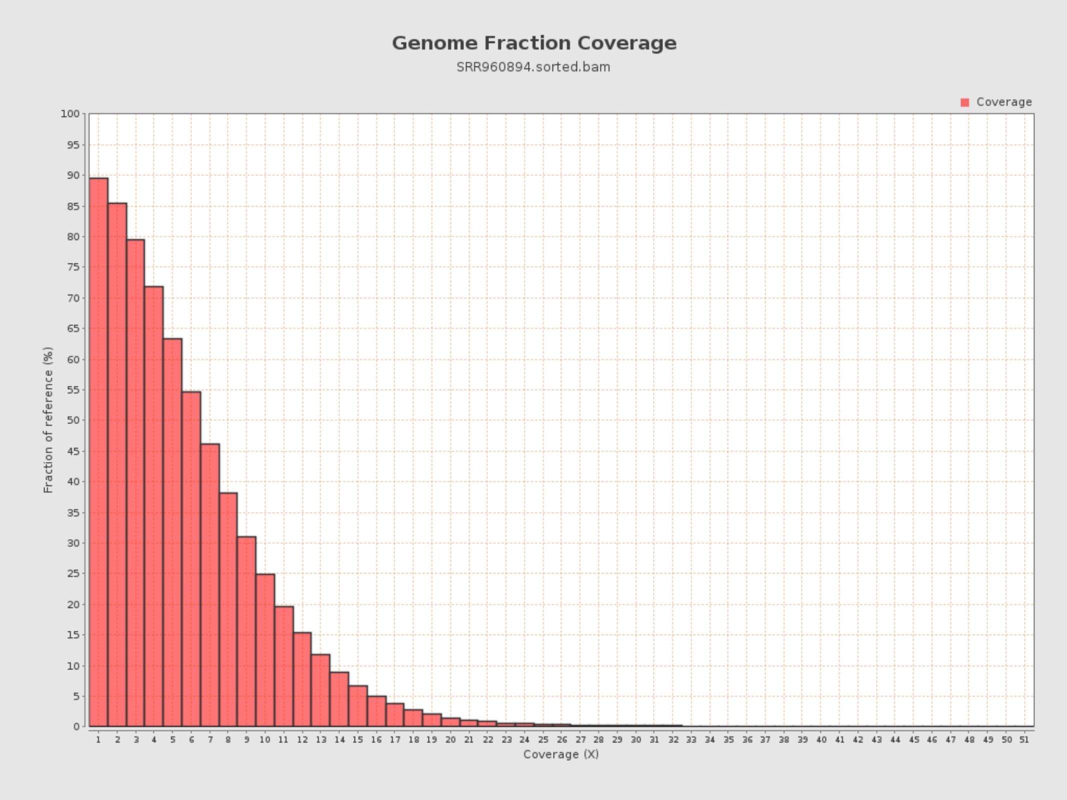
4. Results : Coverage Histogram



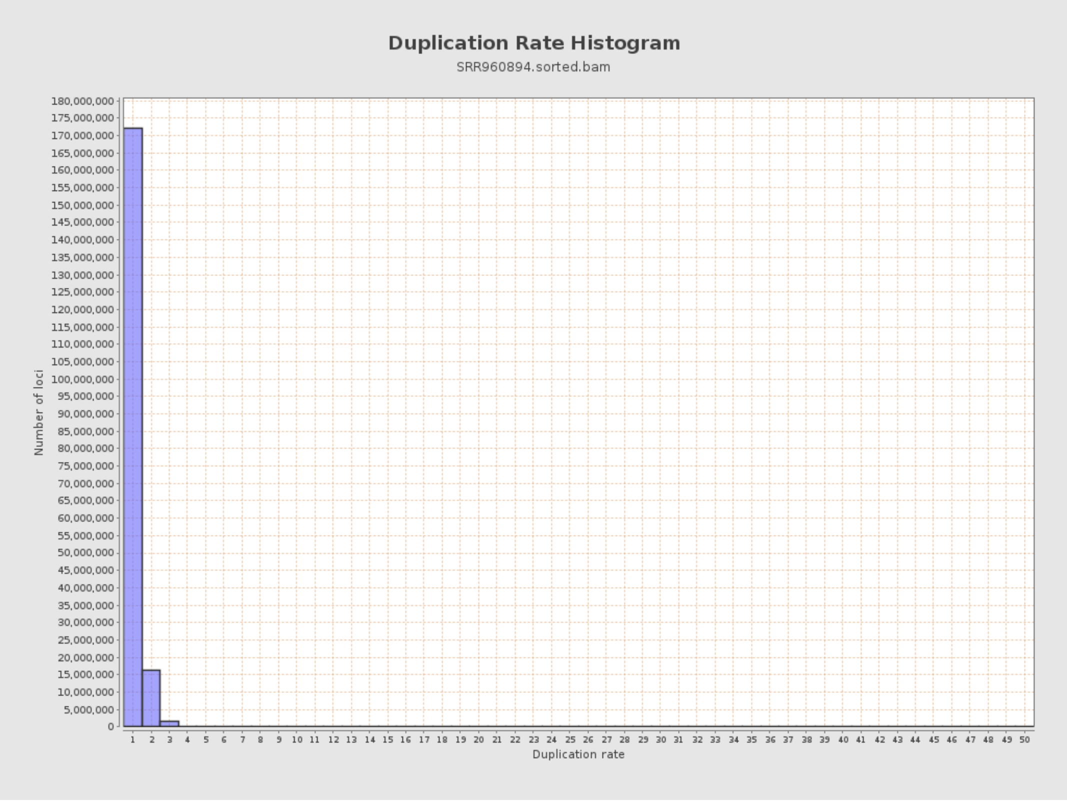
5. Results : Coverage Histogram (0-50X)



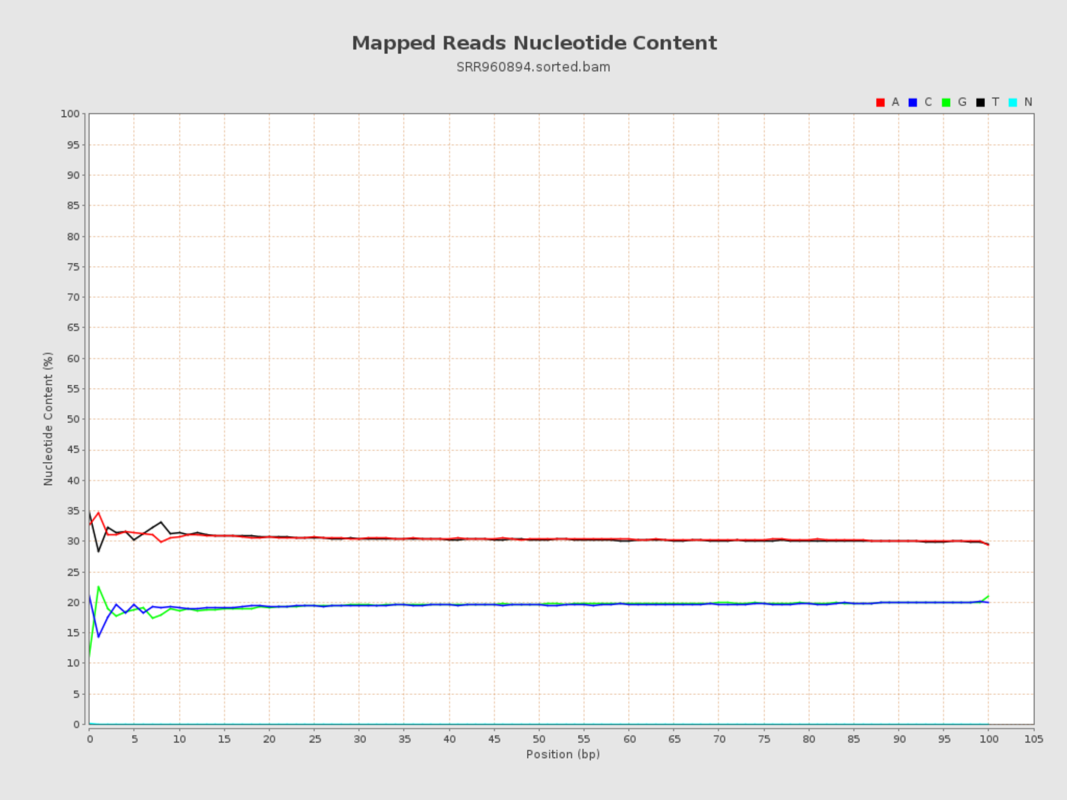
6. Results : Genome Fraction Coverage



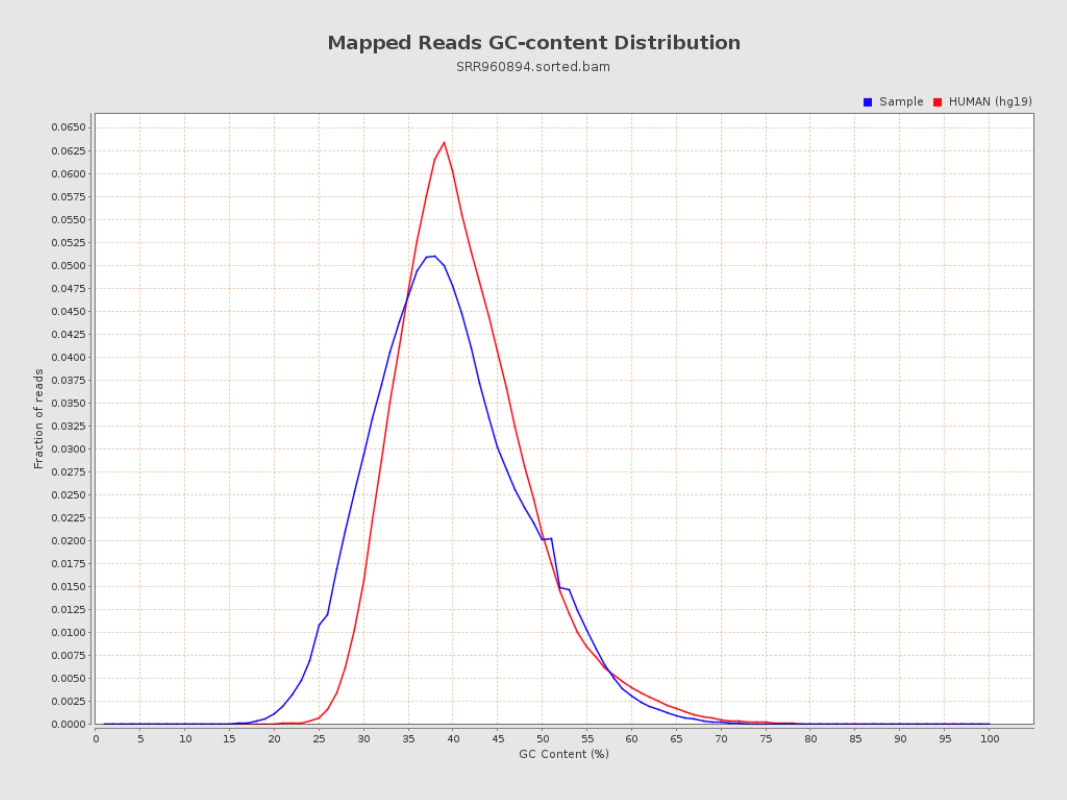
7. Results : Duplication Rate Histogram



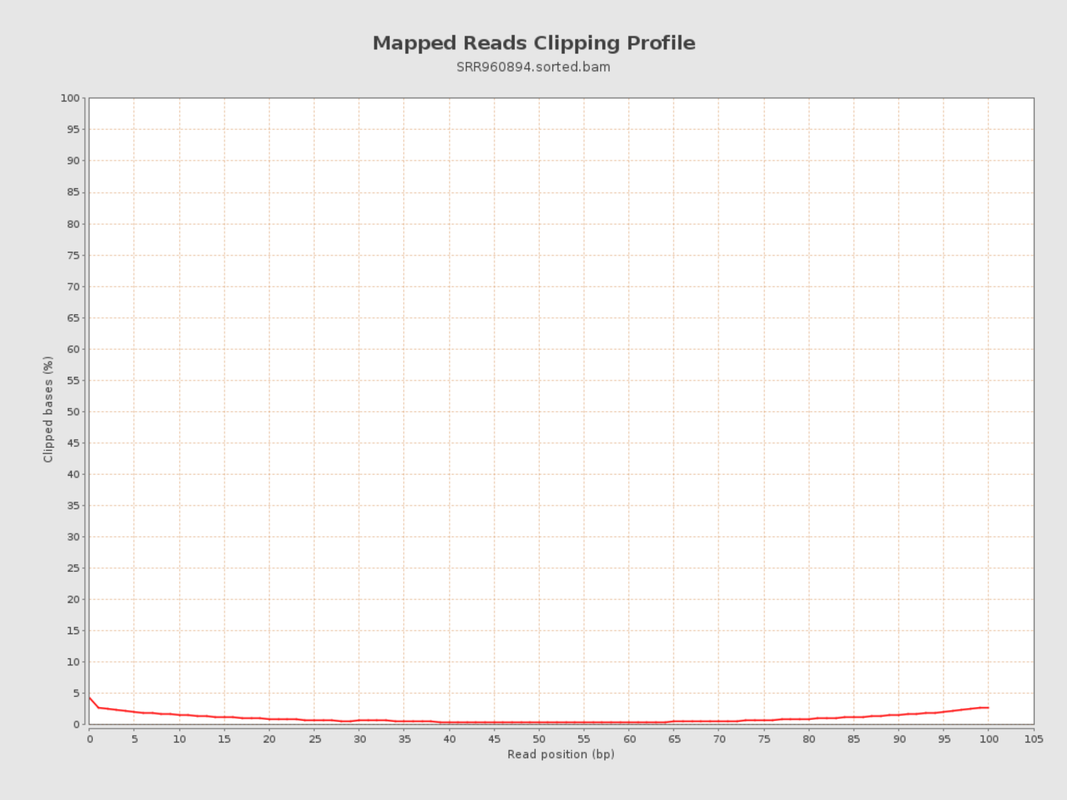
8. Results : Mapped Reads Nucleotide Content



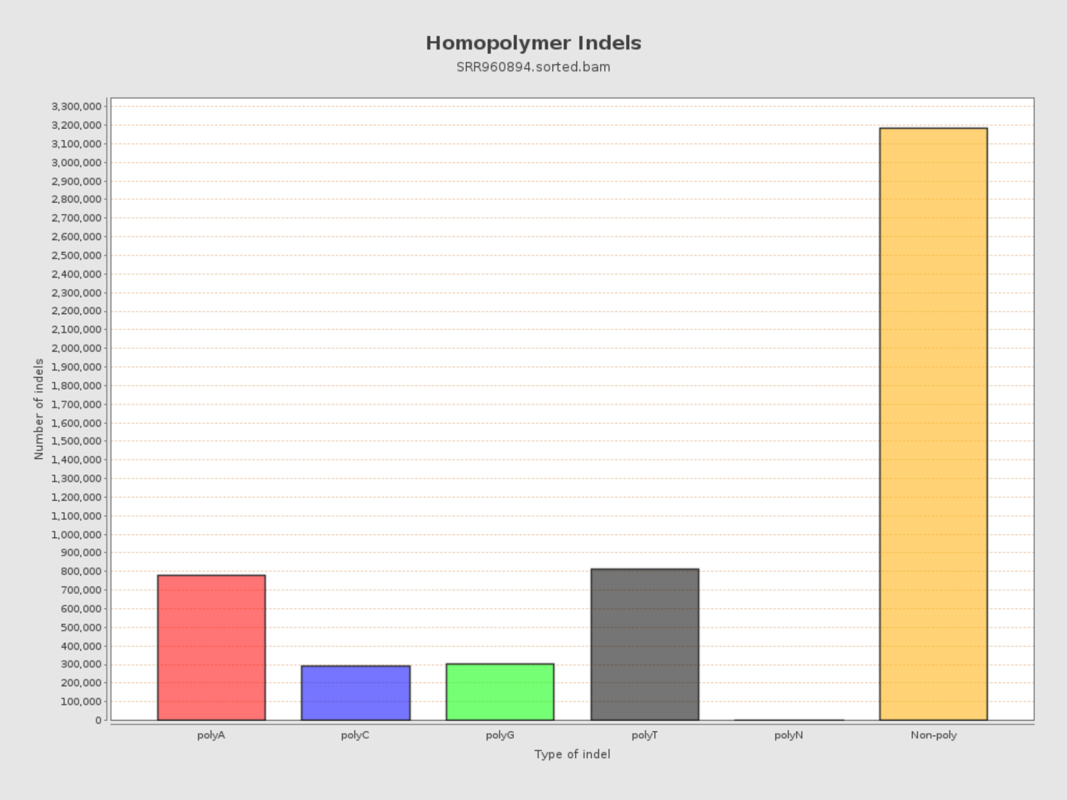
9. Results : Mapped Reads GC-content Distribution



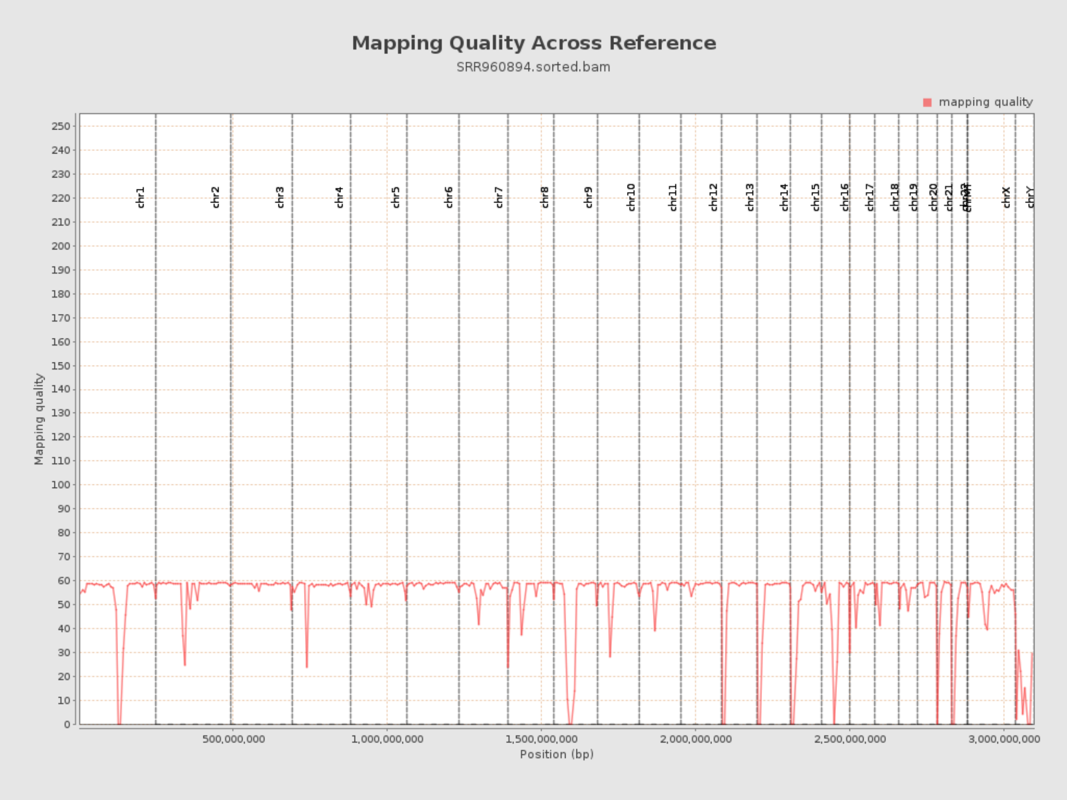
10. Results : Mapped Reads Clipping Profile



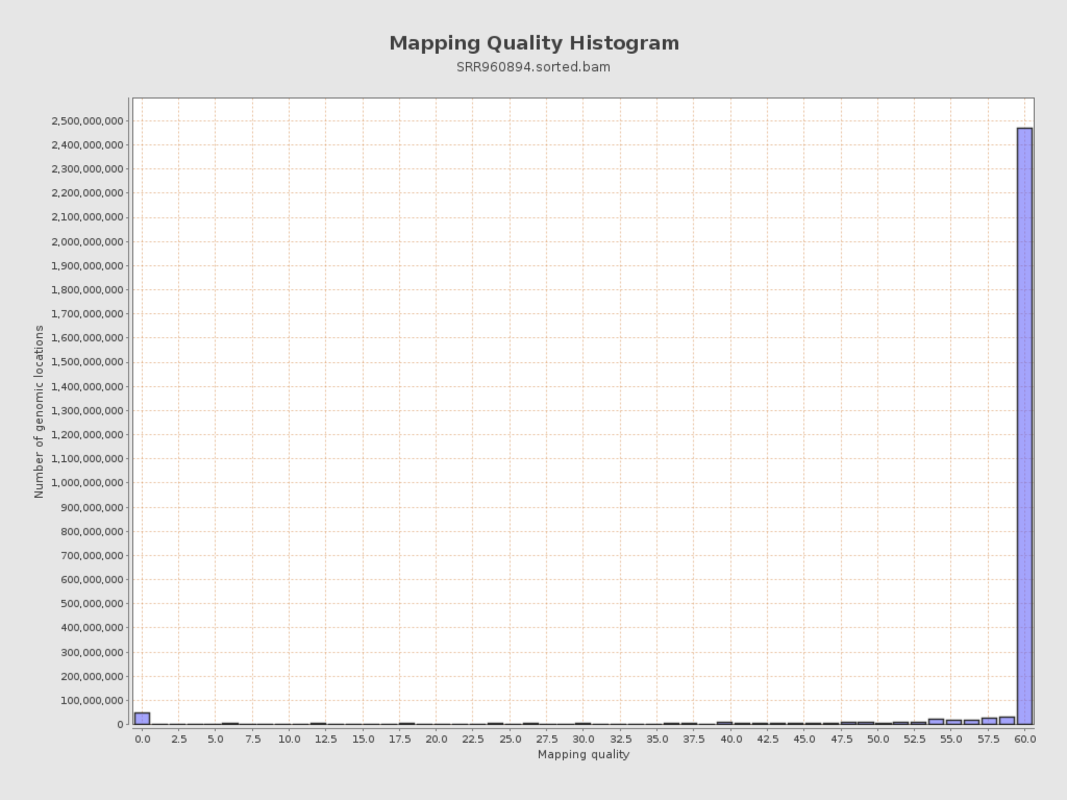
11. Results : Homopolymer Indels



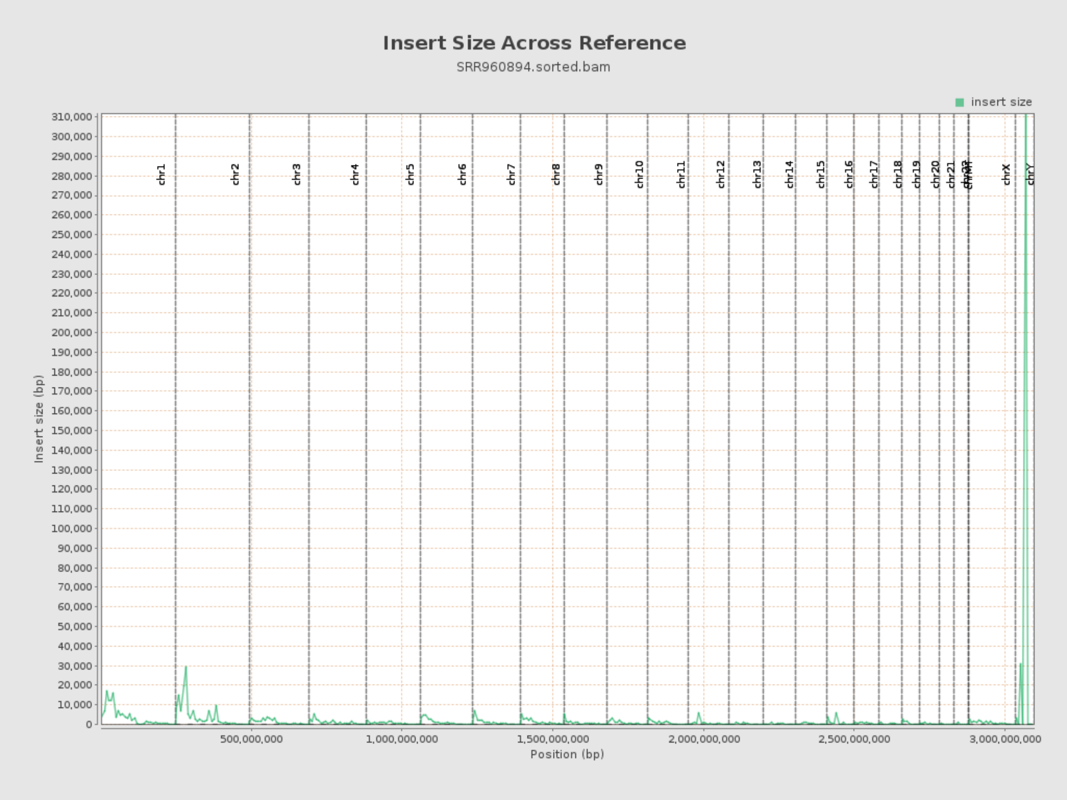
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram