Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/05 09:45:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR960897.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_SRR960897 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR960897_1.fastq.gz SRR960897_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Jan 05 09:45:49 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR960897.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	217,957,998
Mapped reads	214,530,156 / 98.43%
Unmapped reads	3,427,842 / 1.57%
Mapped paired reads	214,530,156 / 98.43%
Mapped reads, first in pair	107,475,627 / 49.31%
Mapped reads, second in pair	107,054,529 / 49.12%
Mapped reads, both in pair	213,397,106 / 97.91%
Mapped reads, singletons	1,133,050 / 0.52%
Secondary alignments	0
Supplementary alignments	386,707 / 0.18%
Read min/max/mean length	30 / 101 / 101.07
Duplicated reads (estimated)	30,591,989 / 14.04%
Duplication rate	9.53%
Clipped reads	29,197,301 / 13.4%

2.2. ACGT Content

Number/percentage of A's	6,460,033,116 / 30.62%
Number/percentage of C's	4,095,425,718 / 19.41%
Number/percentage of T's	6,451,515,212 / 30.58%
Number/percentage of G's	4,090,195,793 / 19.39%
Number/percentage of N's	1,110,278 / 0.01%

GC Percentage	38.8%

2.3. Coverage

Mean	6.8174
Standard Deviation	93.4595

2.4. Mapping Quality

Mean Mapping Quality	53.64

2.5. Insert size

Mean	15,709.9
Standard Deviation	1,177,054.56
P25/Median/P75	136 / 164 / 192

2.6. Mismatches and indels

General error rate	1.19%
Mismatches	245,283,909
Insertions	2,492,040
Mapped reads with at least one insertion	1.13%
Deletions	2,630,625
Mapped reads with at least one deletion	1.19%
Homopolymer indels	40.79%

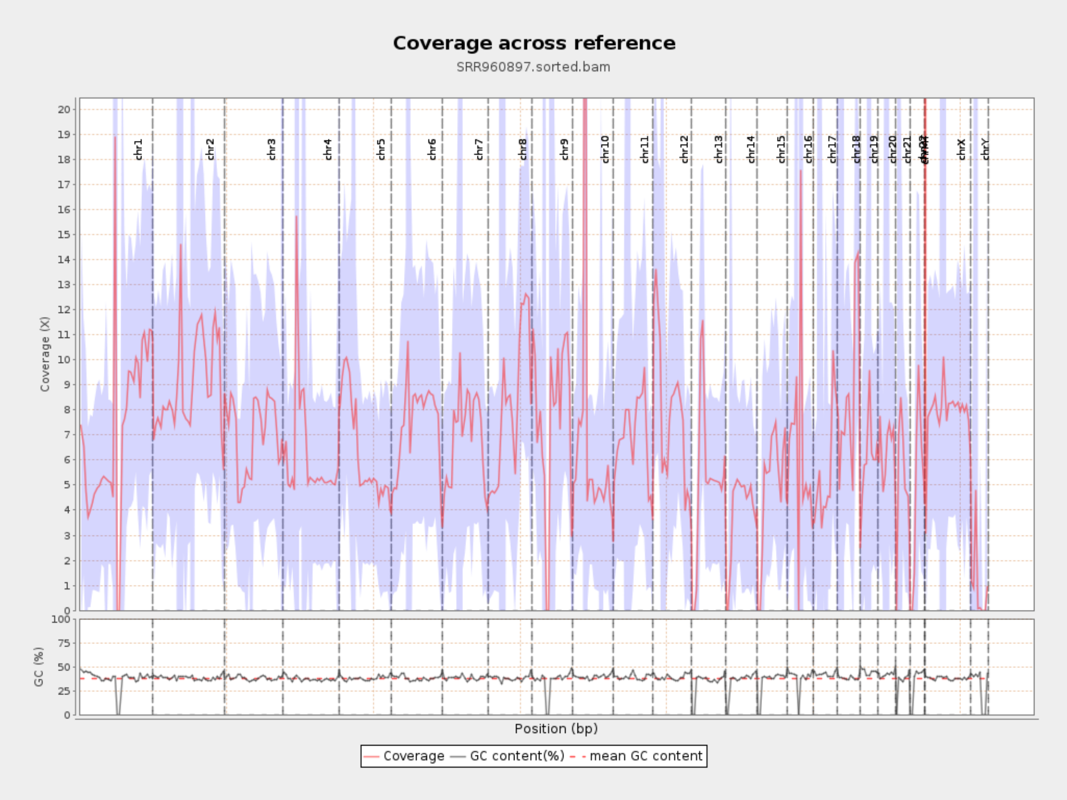
2.7. Chromosome stats

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

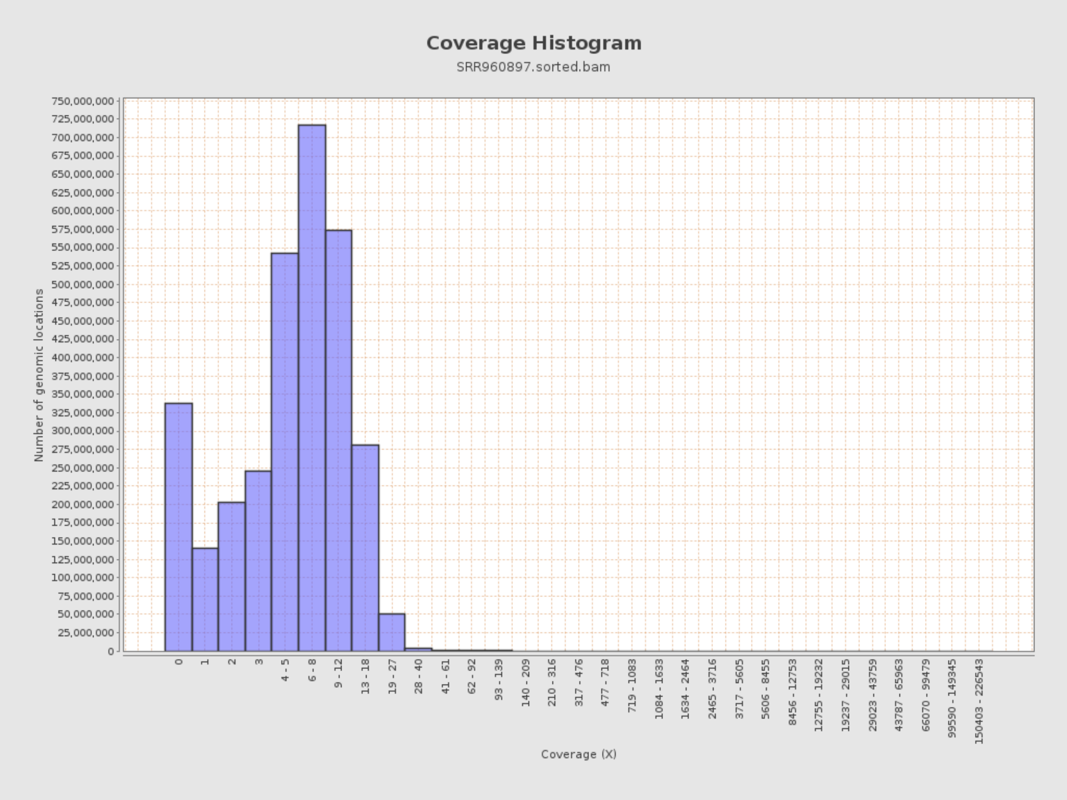
		bases	coverage	deviation
chr1	249250621	1786346123	7.1669	231.6491
chr2	243199373	2220494290	9.1303	49.8394
chr3	198022430	1389846534	7.0186	14.0484
chr4	191154276	1179593475	6.1709	76.3653
chr5	180915260	1142405921	6.3146	8.0709
chr6	171115067	1294461593	7.5649	27.1865
chr7	159138663	1095052258	6.8811	58.7072
chr8	146364022	1207936109	8.253	96.6917
chr9	141213431	1067833034	7.5618	76.5921
chr10	135534747	939147900	6.9292	220.2716
chr11	135006516	934765383	6.9239	36.277
chr12	133851895	1066897335	7.9707	7.7603
chr13	115169878	593927250	5.157	4.6392
chr14	107349540	419396122	3.9068	6.8171
chr15	102531392	513980303	5.0129	4.5577
chr16	90354753	570716463	6.3164	85.1211
chr17	81195210	445982252	5.4927	23.9031
chr18	78077248	667193894	8.5453	79.9975
chr19	59128983	362606763	6.1325	101.3142
chr20	63025520	406303834	6.4467	22.1575
chr21	48129895	263940540	5.4839	30.3369
chr22	51304566	239413303	4.6665	6.0937
chrMT	16571	8239237	497.2082	107.5335
chrX	155270560	1229018039	7.9153	25.3885

chrY	59373566	58951288	0.9929	65.689

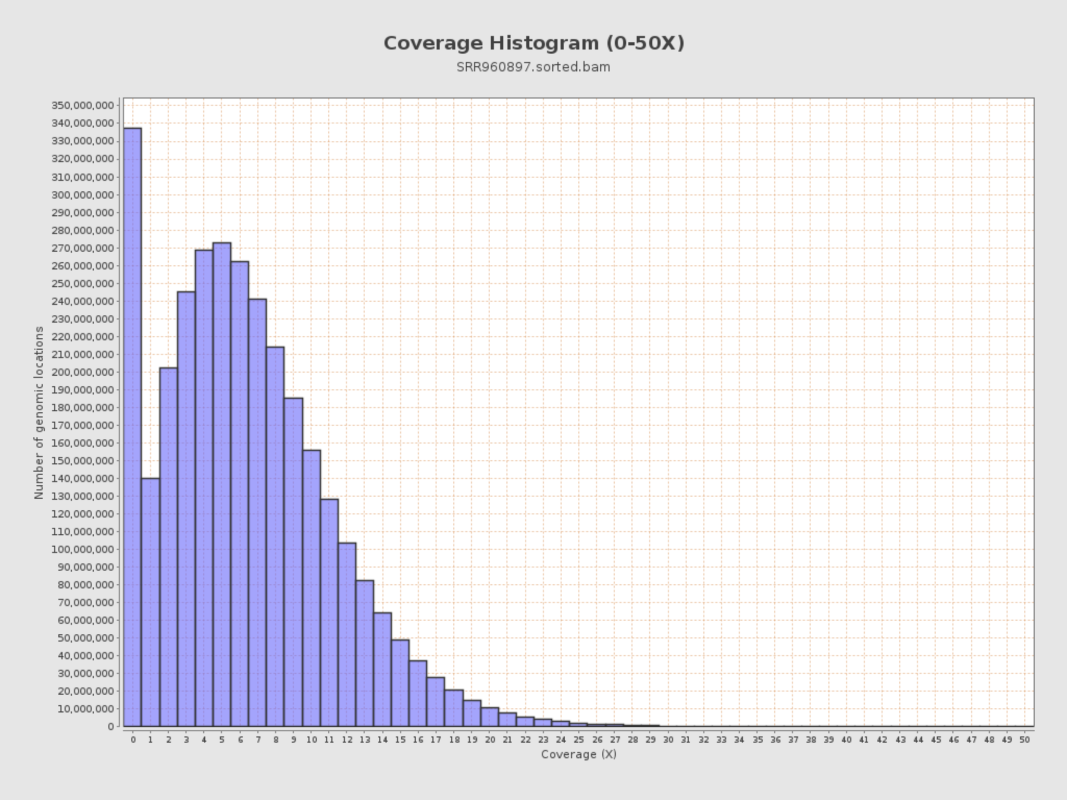
3. Results : Coverage across reference



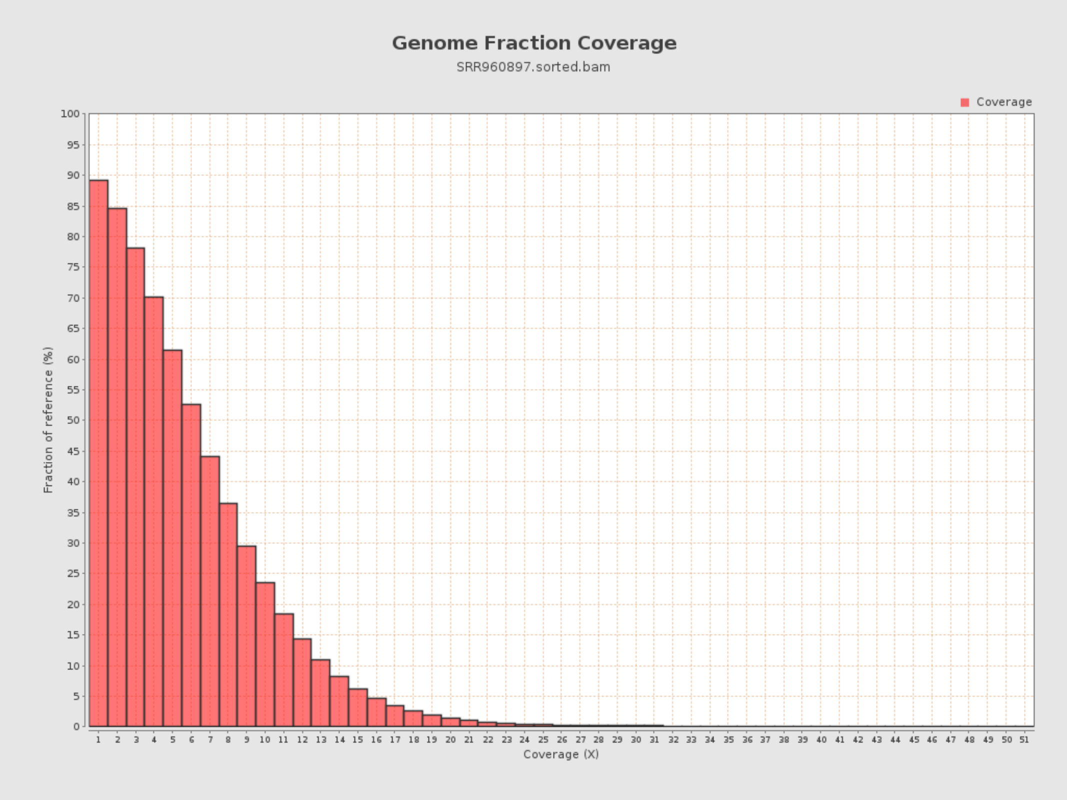
4. Results : Coverage Histogram



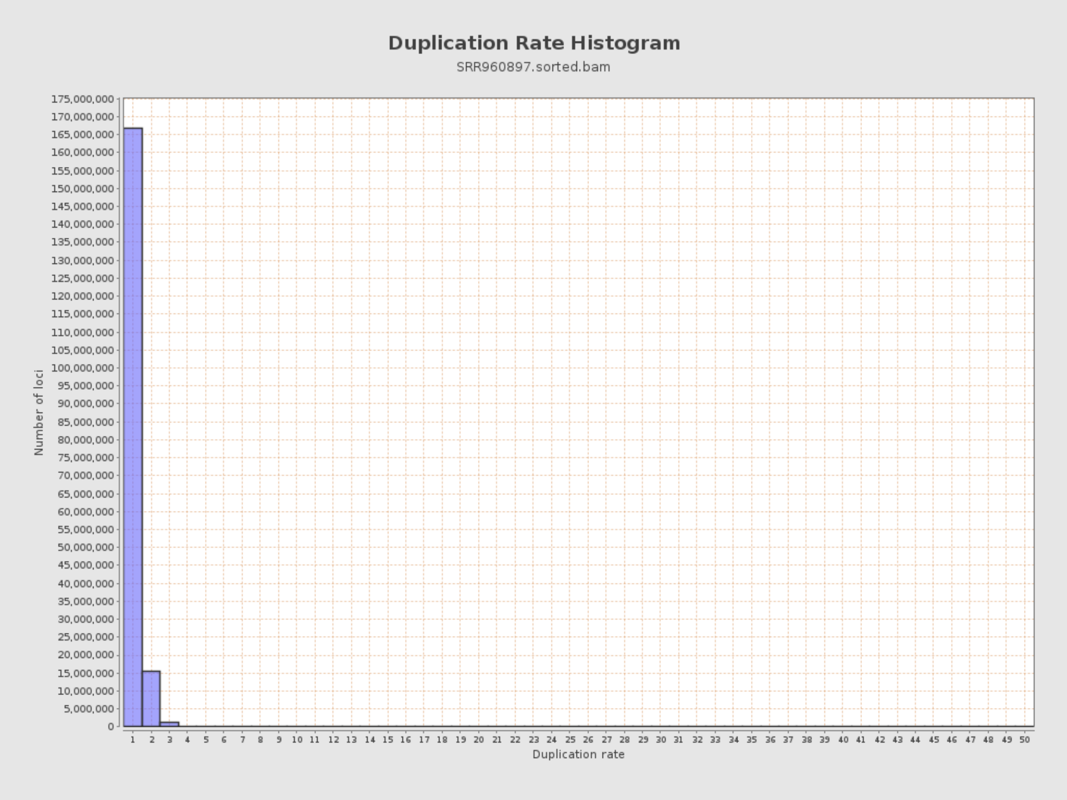
5. Results : Coverage Histogram (0-50X)



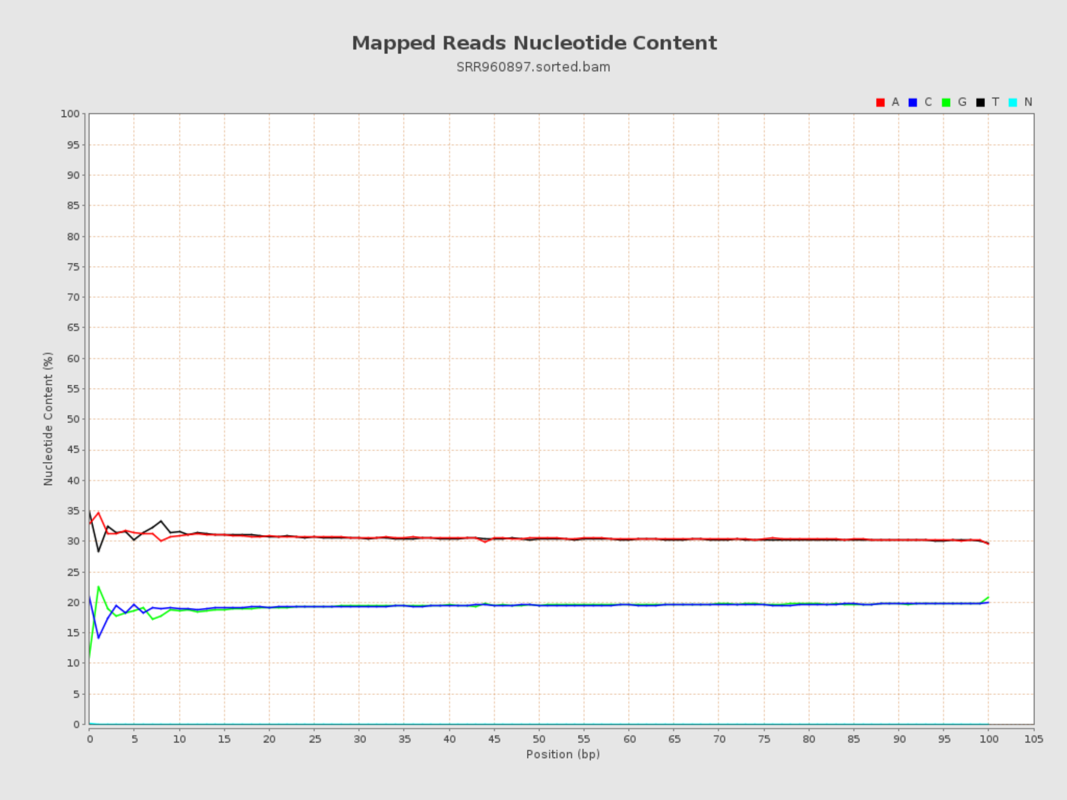
6. Results : Genome Fraction Coverage



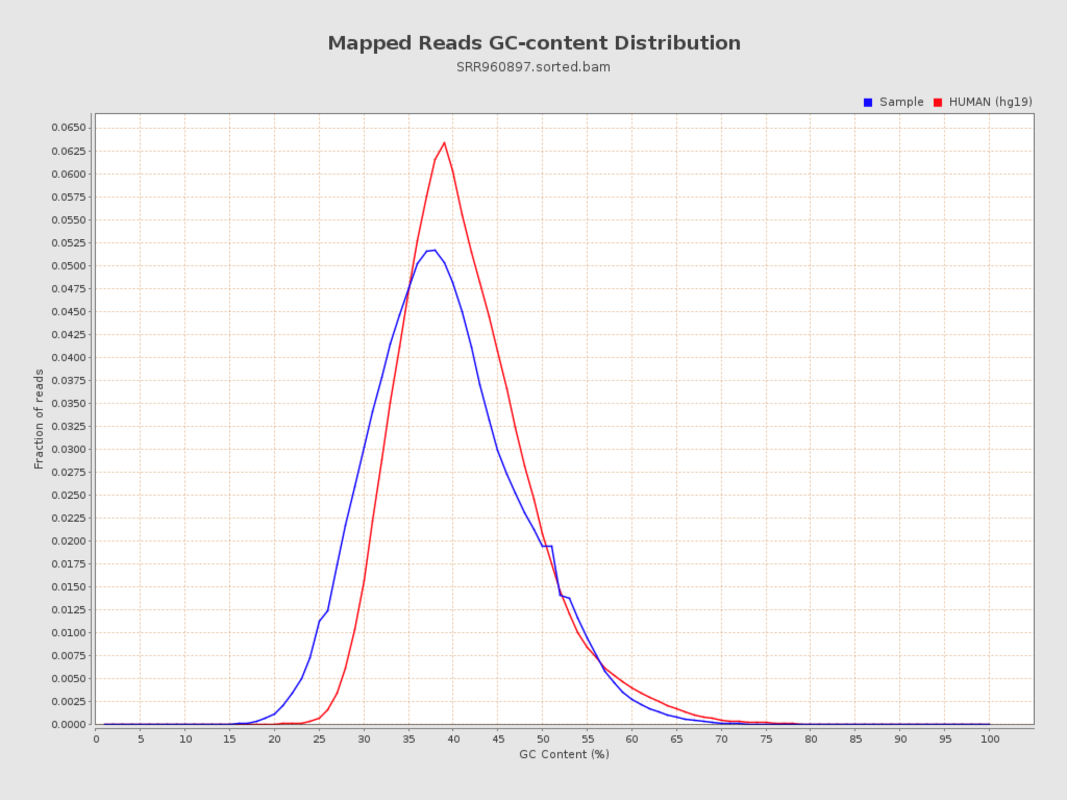
7. Results : Duplication Rate Histogram



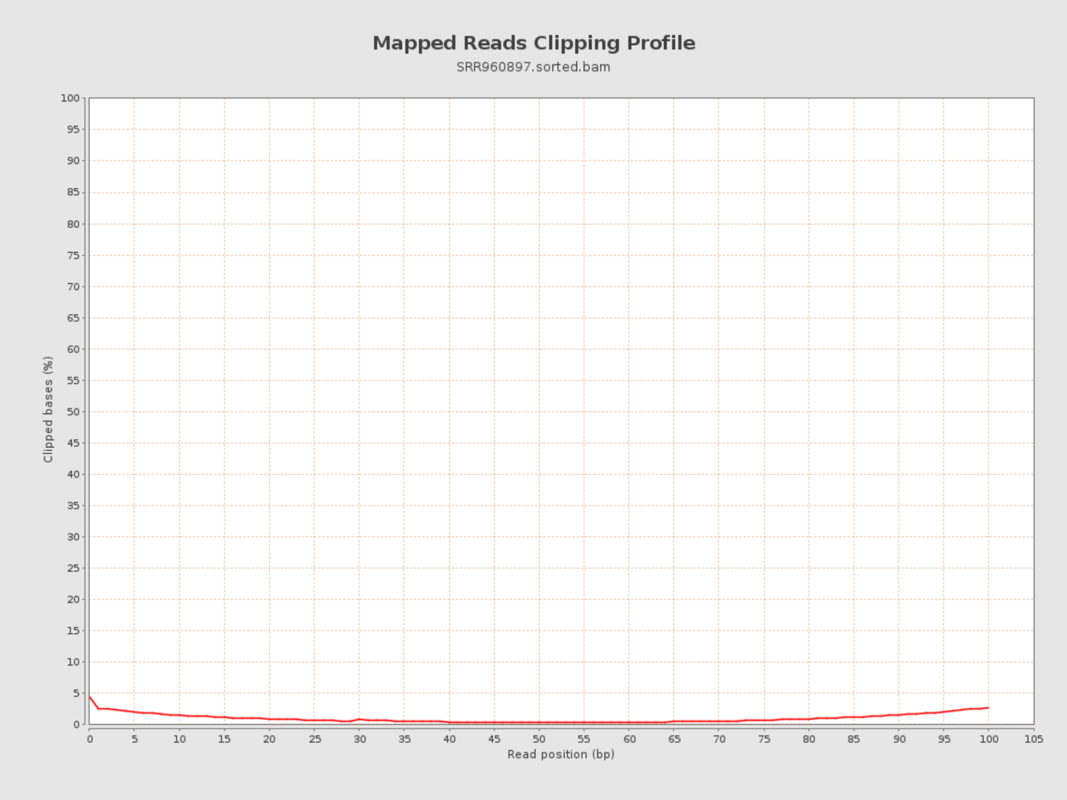
8. Results : Mapped Reads Nucleotide Content



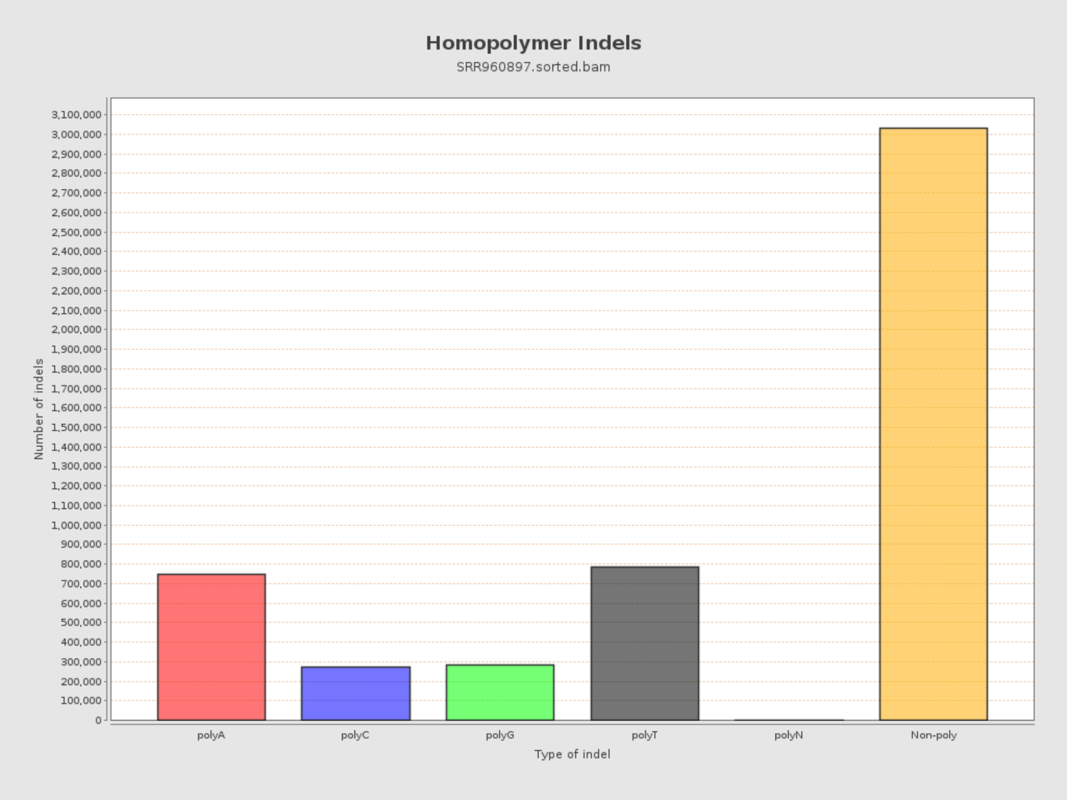
9. Results : Mapped Reads GC-content Distribution



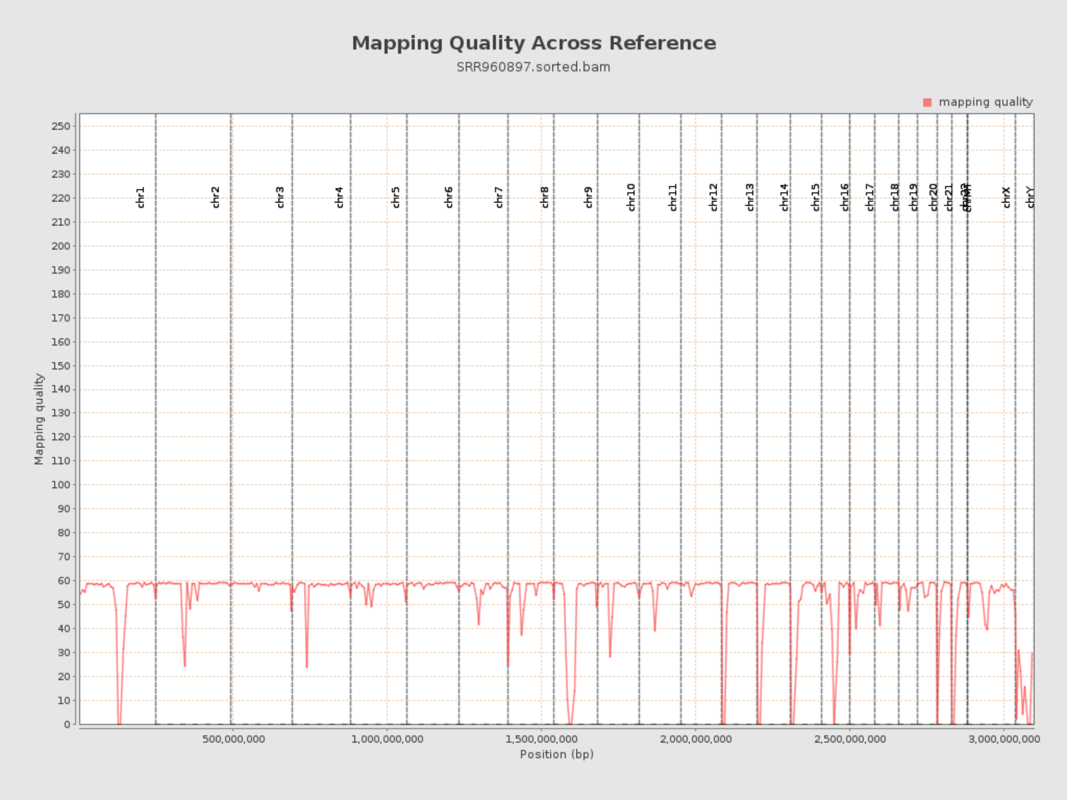
10. Results : Mapped Reads Clipping Profile



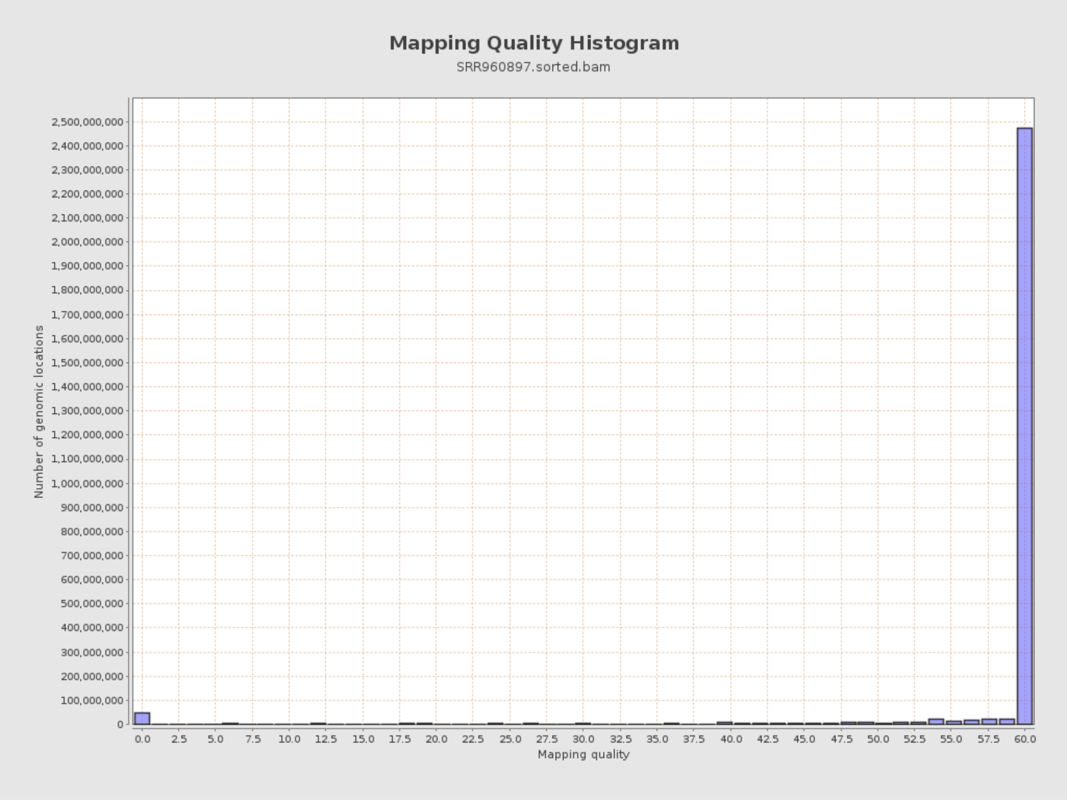
11. Results : Homopolymer Indels



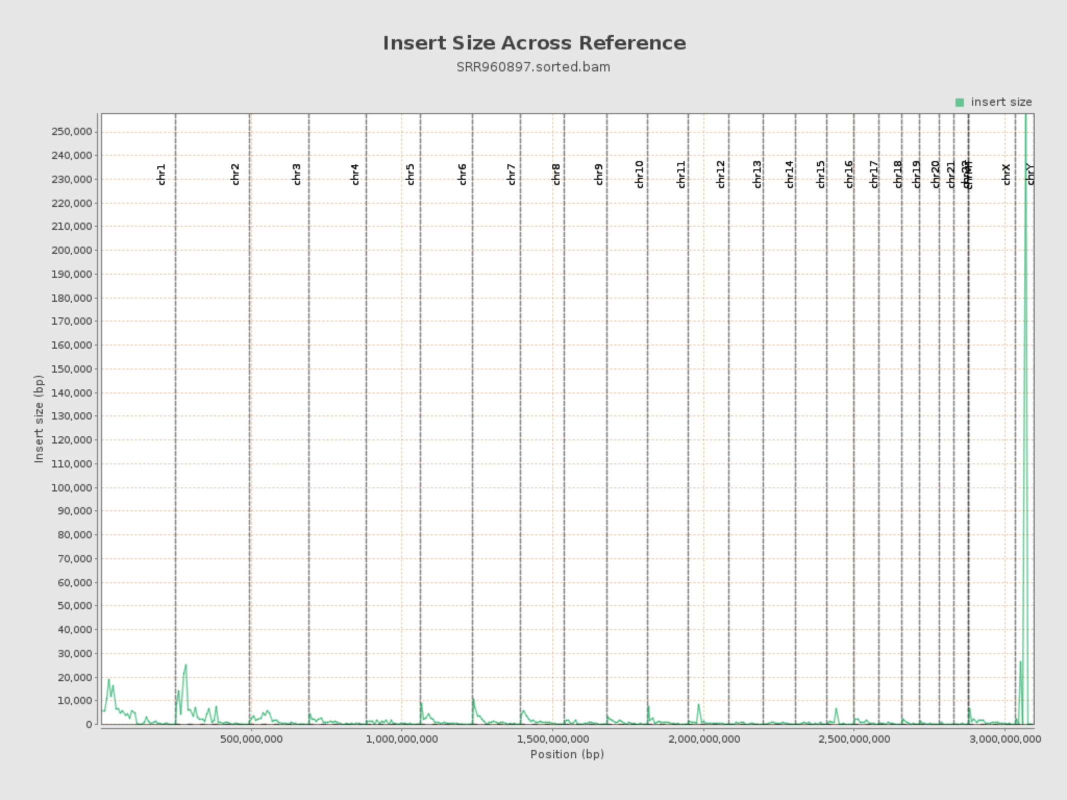
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram