Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/07 15:50:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR960921.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_SRR960921 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR960921_1.fastq.gz SRR960921_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Jan 07 15:50:14 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR960921.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	228,796,776
Mapped reads	223,960,439 / 97.89%
Unmapped reads	4,836,337 / 2.11%
Mapped paired reads	223,960,439 / 97.89%
Mapped reads, first in pair	112,481,271 / 49.16%
Mapped reads, second in pair	111,479,168 / 48.72%
Mapped reads, both in pair	221,950,264 / 97.01%
Mapped reads, singletons	2,010,175 / 0.88%
Secondary alignments	0
Supplementary alignments	462,616 / 0.2%
Read min/max/mean length	30 / 101 / 101.08
Duplicated reads (estimated)	37,938,690 / 16.58%
Duplication rate	12.18%
Clipped reads	41,273,171 / 18.04%

2.2. ACGT Content

Number/percentage of A's	6,687,775,074 / 30.63%
Number/percentage of C's	4,240,038,224 / 19.42%
Number/percentage of T's	6,686,034,067 / 30.62%
Number/percentage of G's	4,217,518,770 / 19.32%
Number/percentage of N's	1,937,289 / 0.01%

GC Percentage	38.74%

2.3. Coverage

Mean	7.0548
Standard Deviation	104.3531

2.4. Mapping Quality

Mean Mapping Quality	53.57

2.5. Insert size

Mean	18,993.36
Standard Deviation	1,278,761.04
P25/Median/P75	155 / 183 / 213

2.6. Mismatches and indels

General error rate	1.49%
Mismatches	319,248,044
Insertions	2,653,208
Mapped reads with at least one insertion	1.16%
Deletions	2,922,453
Mapped reads with at least one deletion	1.27%
Homopolymer indels	40.15%

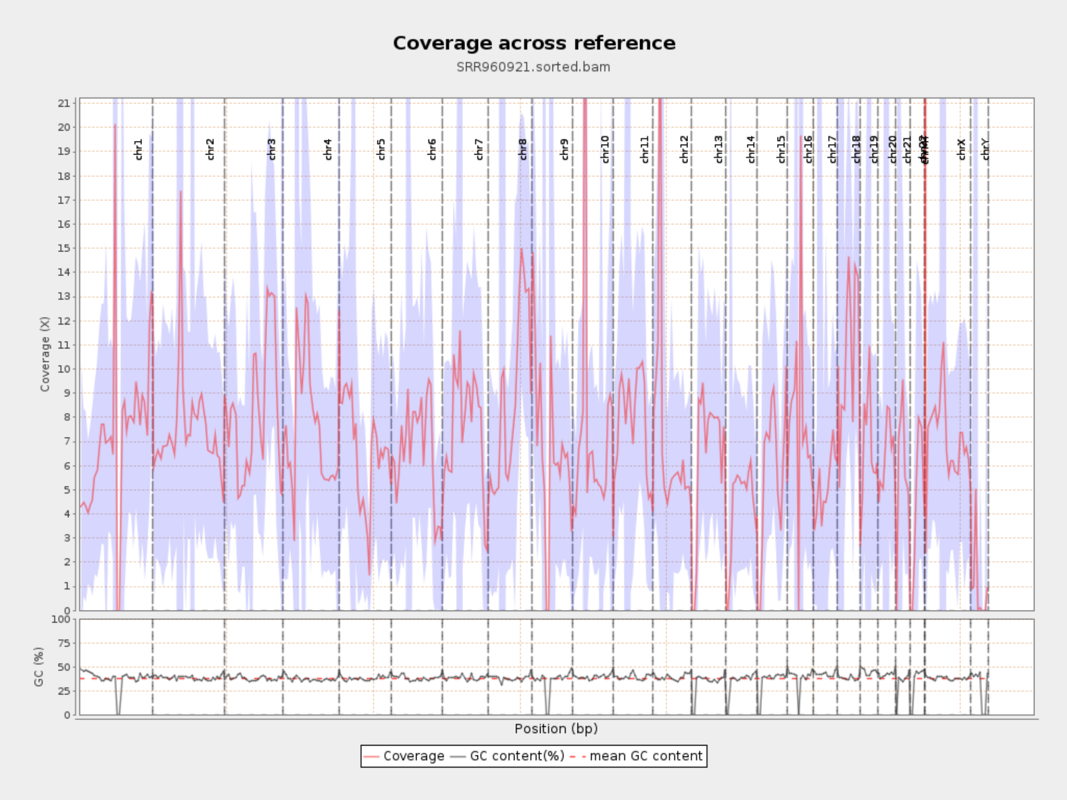
2.7. Chromosome stats

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

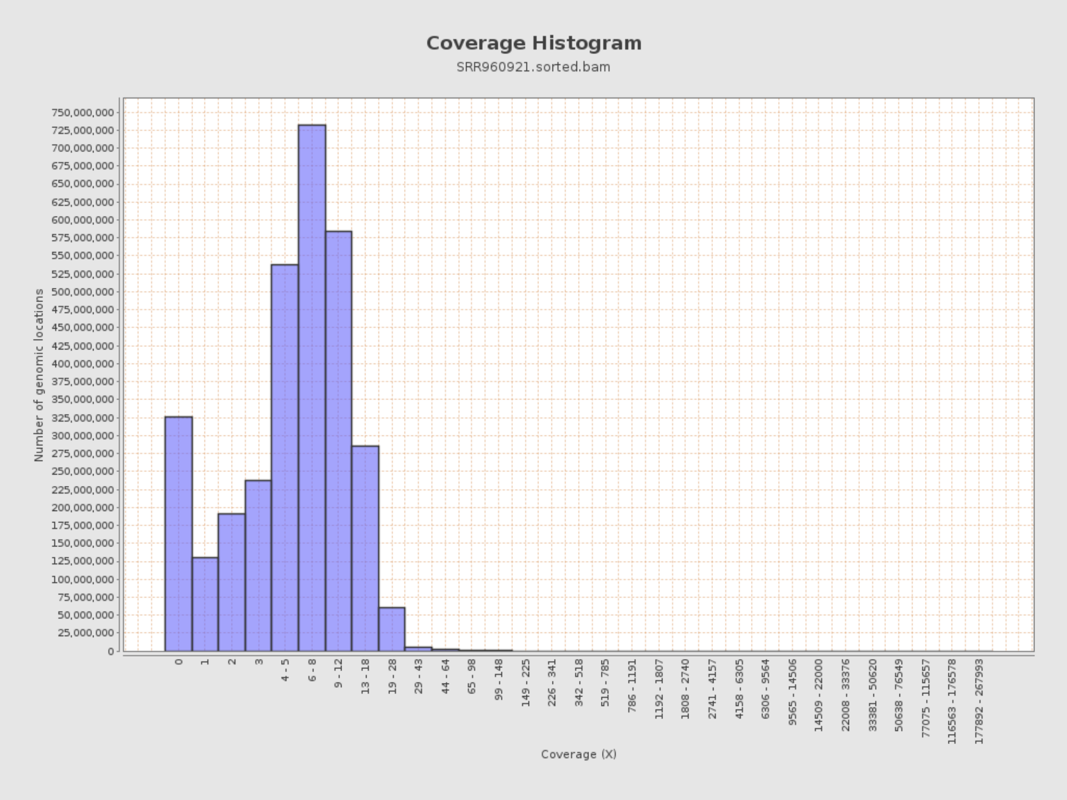
		bases	coverage	deviation
chr1	249250621	1812775361	7.2729	276.7079
chr2	243199373	1839847835	7.5652	55.4326
chr3	198022430	1625989396	8.2111	9.6309
chr4	191154276	1443573233	7.5519	56.1562
chr5	180915260	1188078727	6.567	9.4564
chr6	171115067	1149143751	6.7156	27.3128
chr7	159138663	1201505326	7.5501	69.0999
chr8	146364022	1281979072	8.7588	134.4109
chr9	141213431	932171865	6.6012	98.3932
chr10	135534747	1039357184	7.6686	199.3276
chr11	135006516	1064395031	7.884	43.5367
chr12	133851895	988086947	7.3819	11.7021
chr13	115169878	755101413	6.5564	4.8931
chr14	107349540	464966176	4.3313	7.4591
chr15	102531392	587404369	5.729	5.1834
chr16	90354753	715513795	7.9189	86.0381
chr17	81195210	414826357	5.109	25.8331
chr18	78077248	839146018	10.7476	101.1834
chr19	59128983	401959369	6.798	116.2008
chr20	63025520	408929692	6.4883	18.7048
chr21	48129895	291444561	6.0554	22.6186
chr22	51304566	223463841	4.3556	5.7045
chrMT	16571	4917358	296.7448	57.0943
chrX	155270560	1105448957	7.1195	29.354

chrY	59373566	59582453	1.0035	52.1594

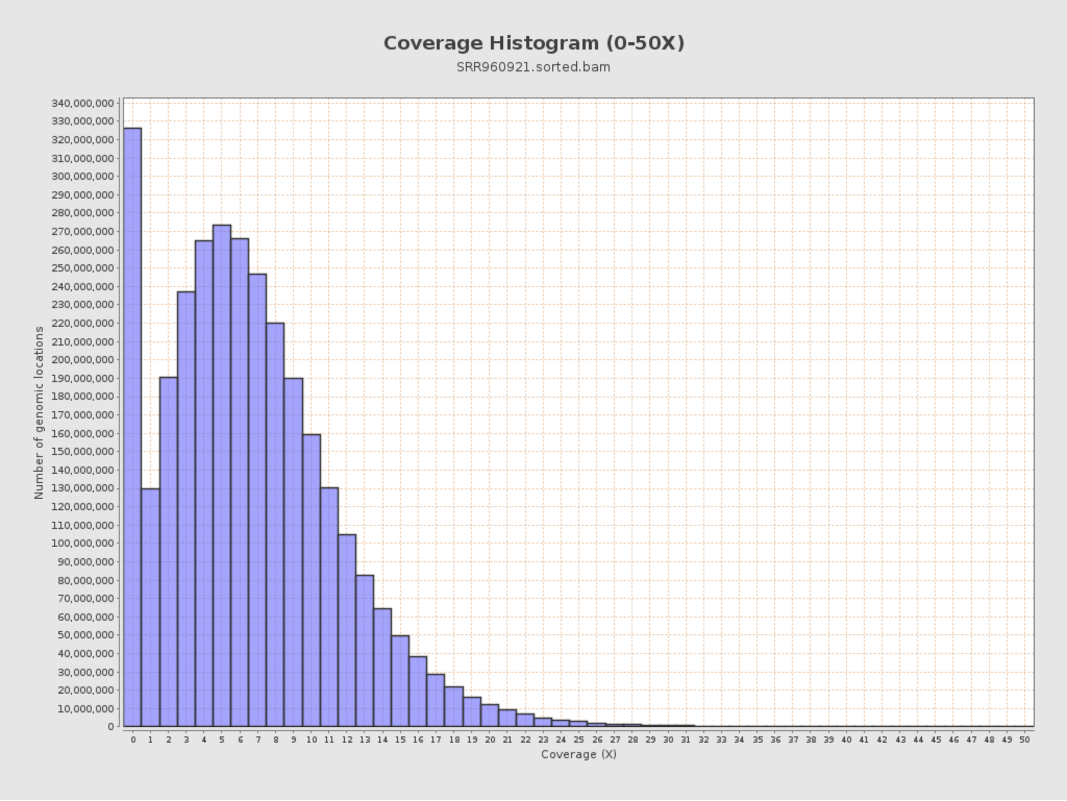
3. Results : Coverage across reference



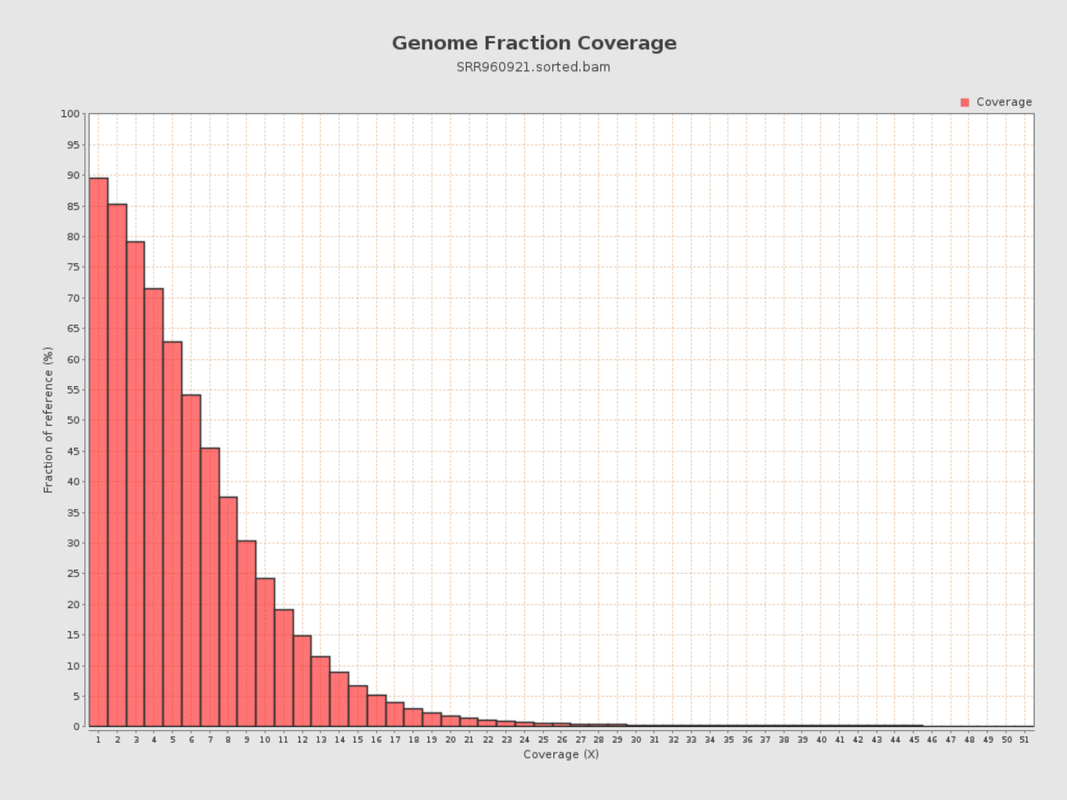
4. Results : Coverage Histogram



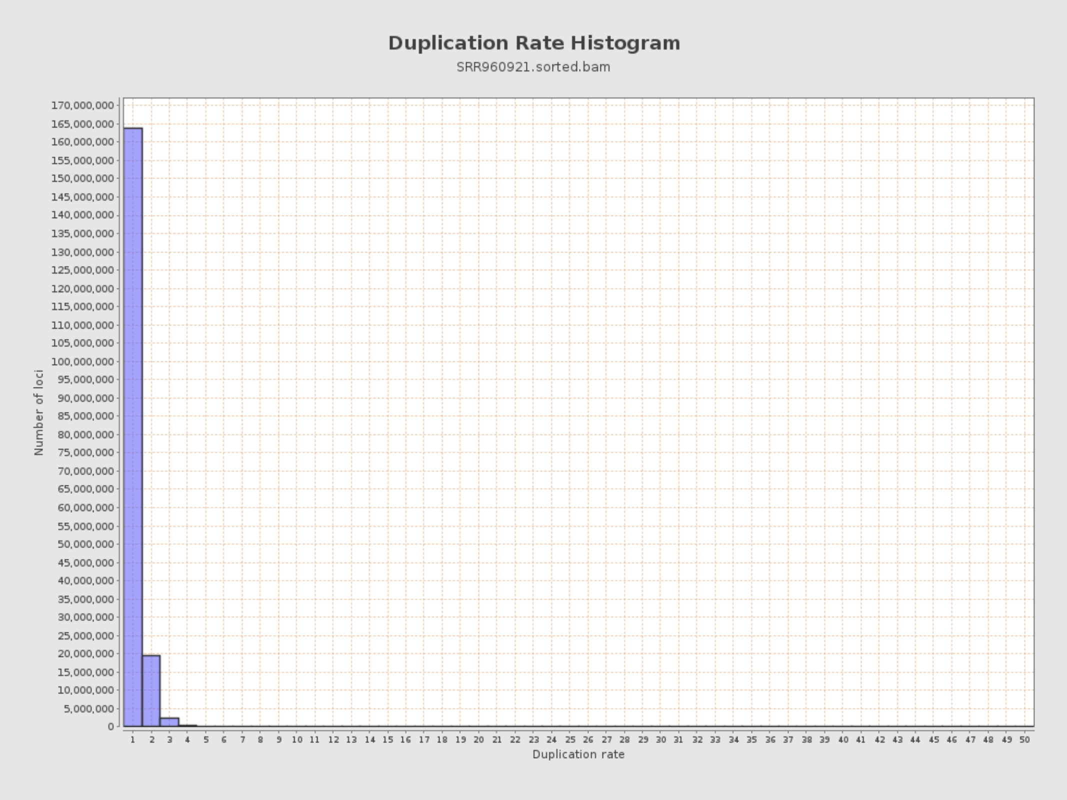
5. Results : Coverage Histogram (0-50X)



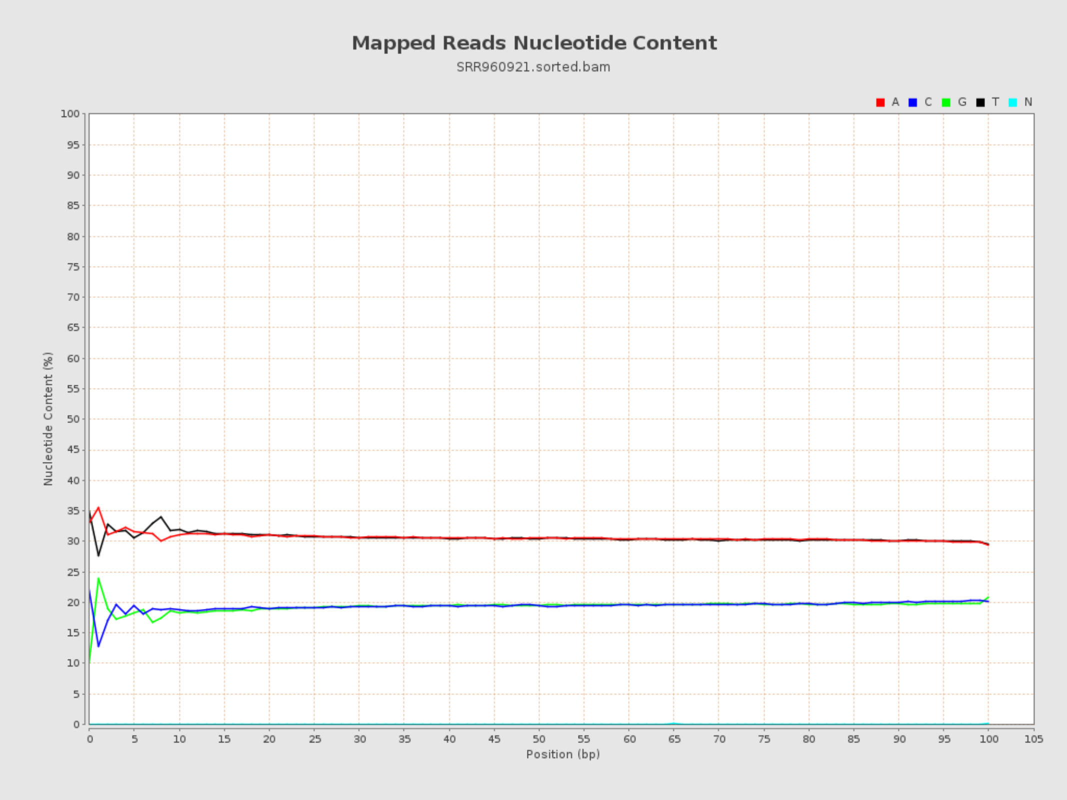
6. Results : Genome Fraction Coverage



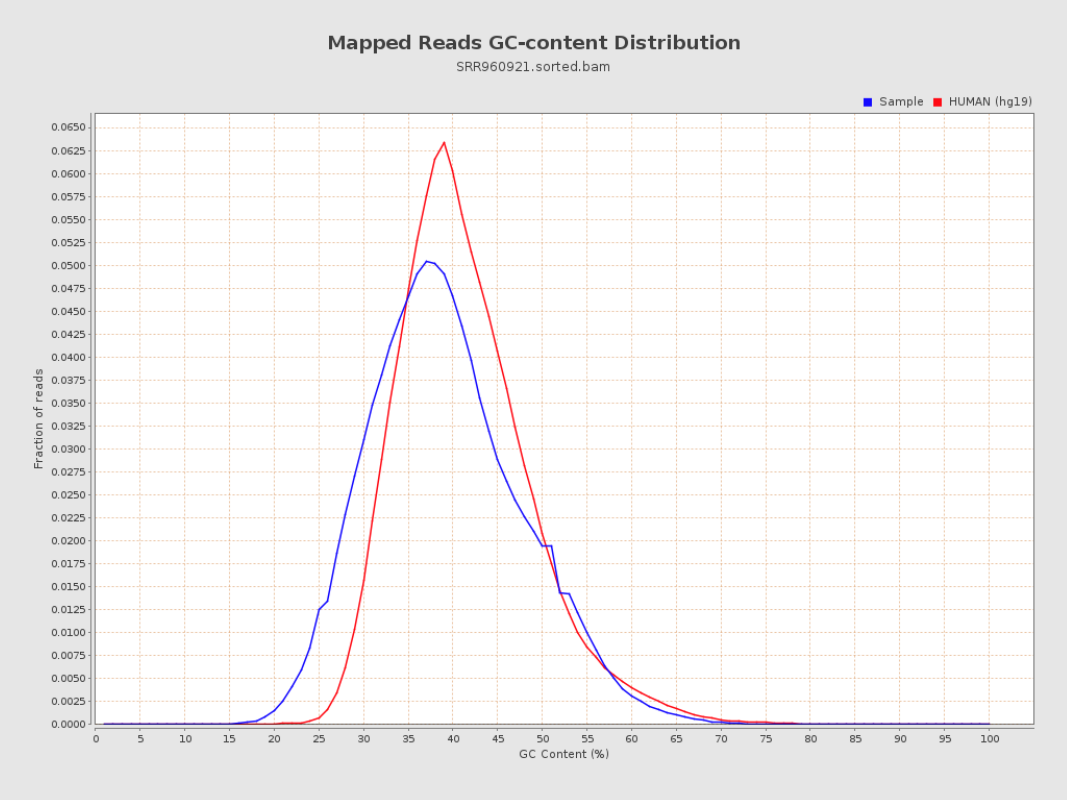
7. Results : Duplication Rate Histogram



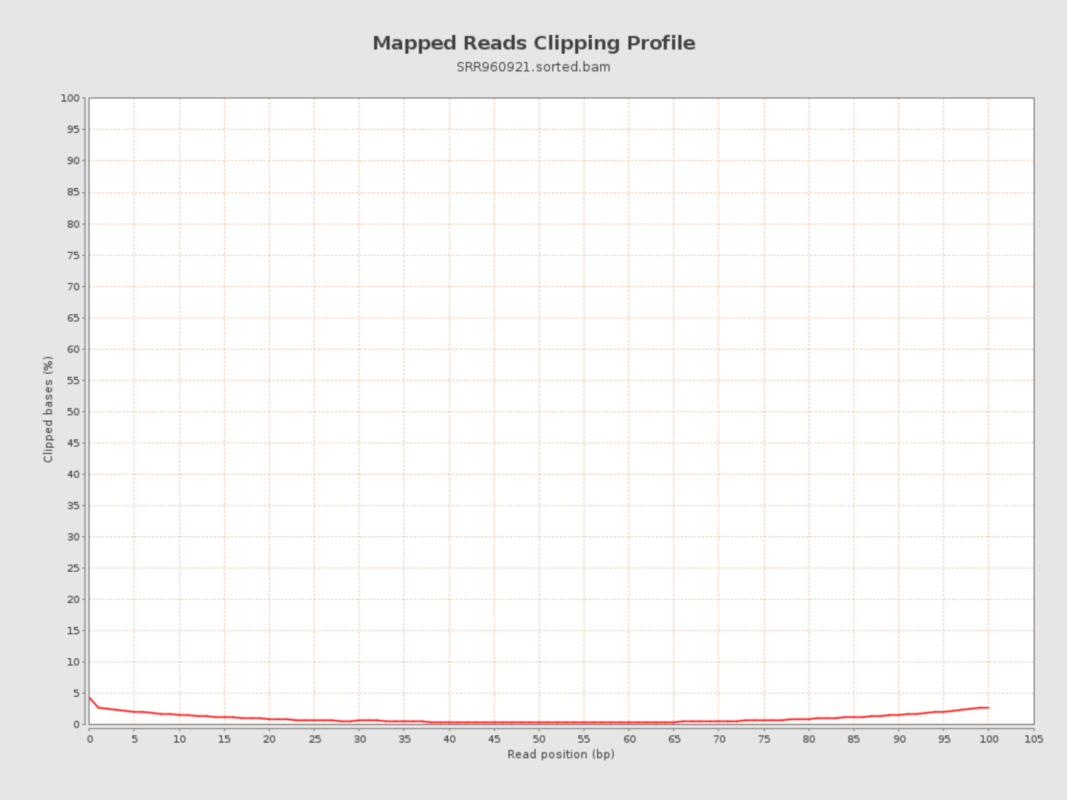
8. Results : Mapped Reads Nucleotide Content



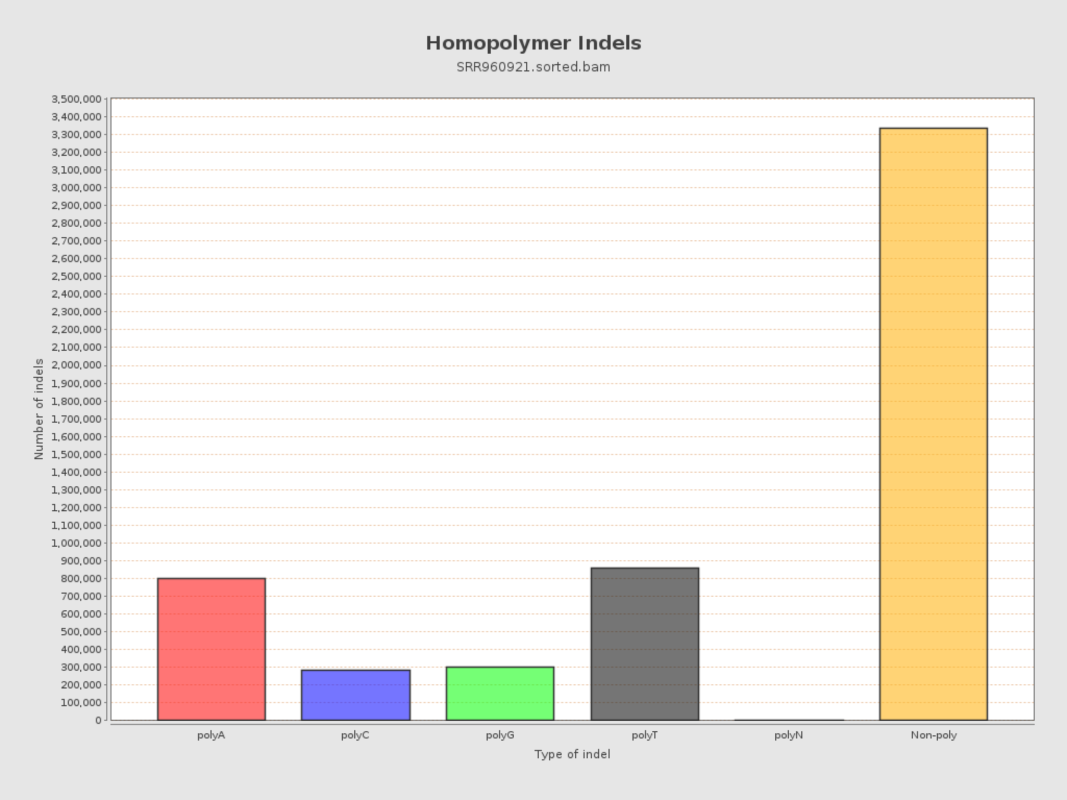
9. Results : Mapped Reads GC-content Distribution



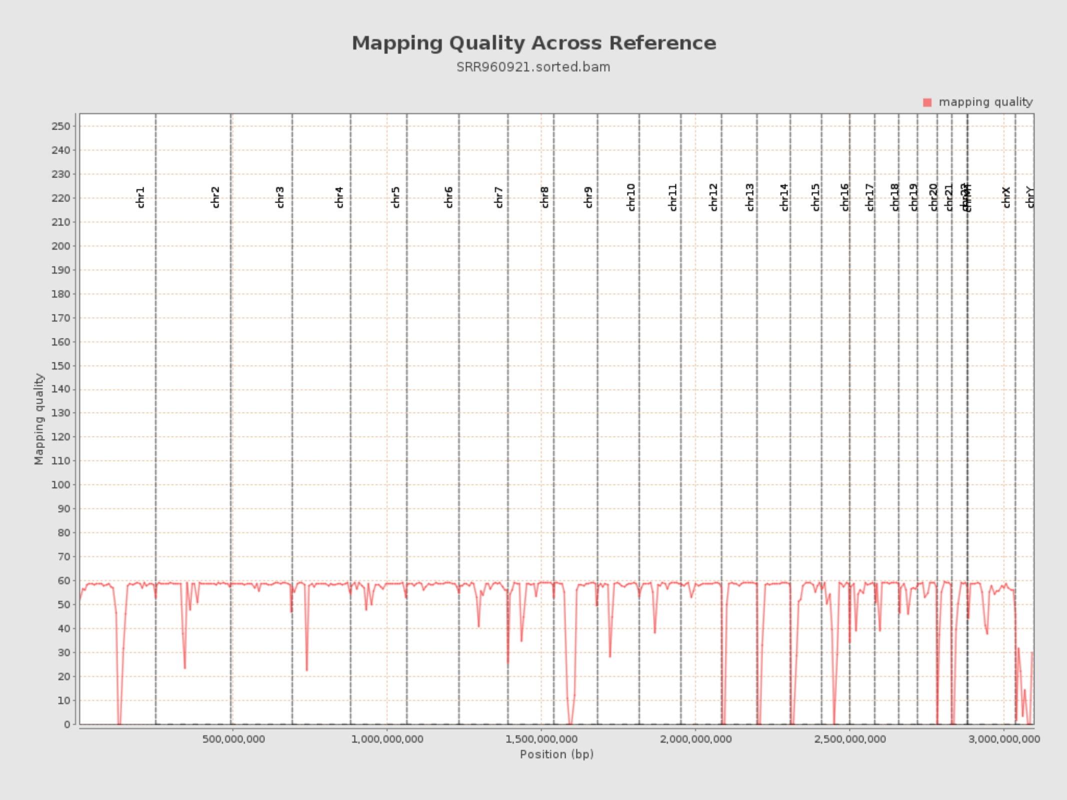
10. Results : Mapped Reads Clipping Profile



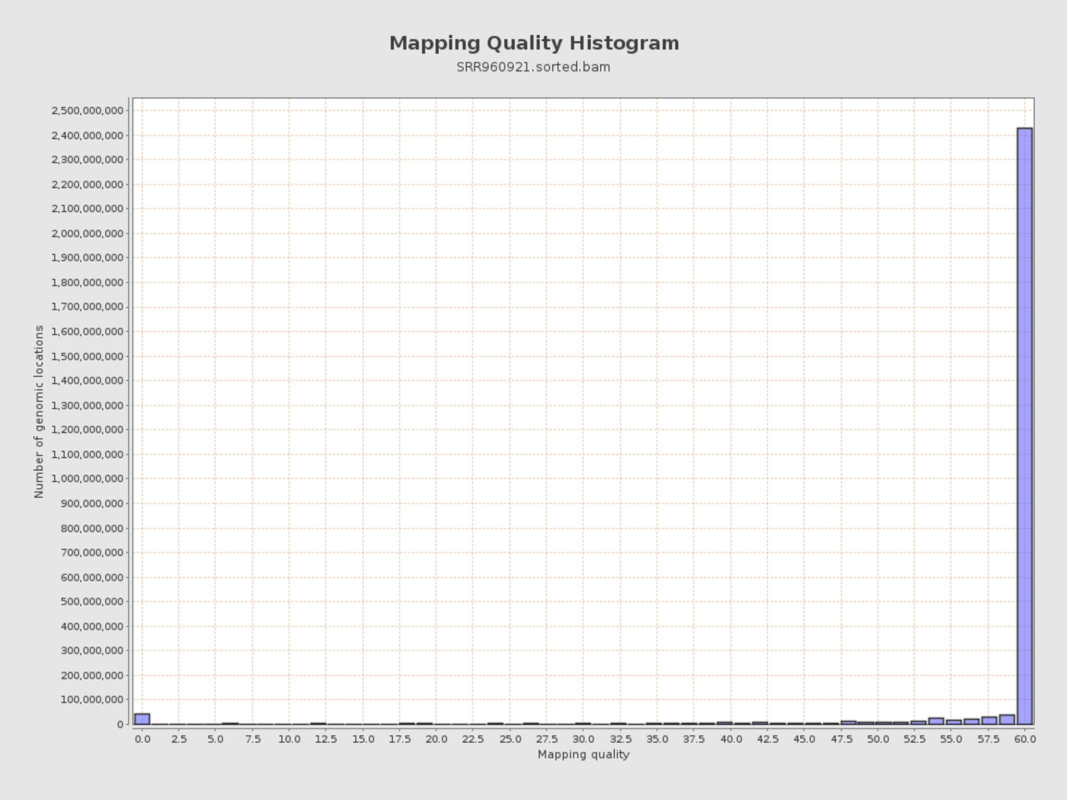
11. Results : Homopolymer Indels



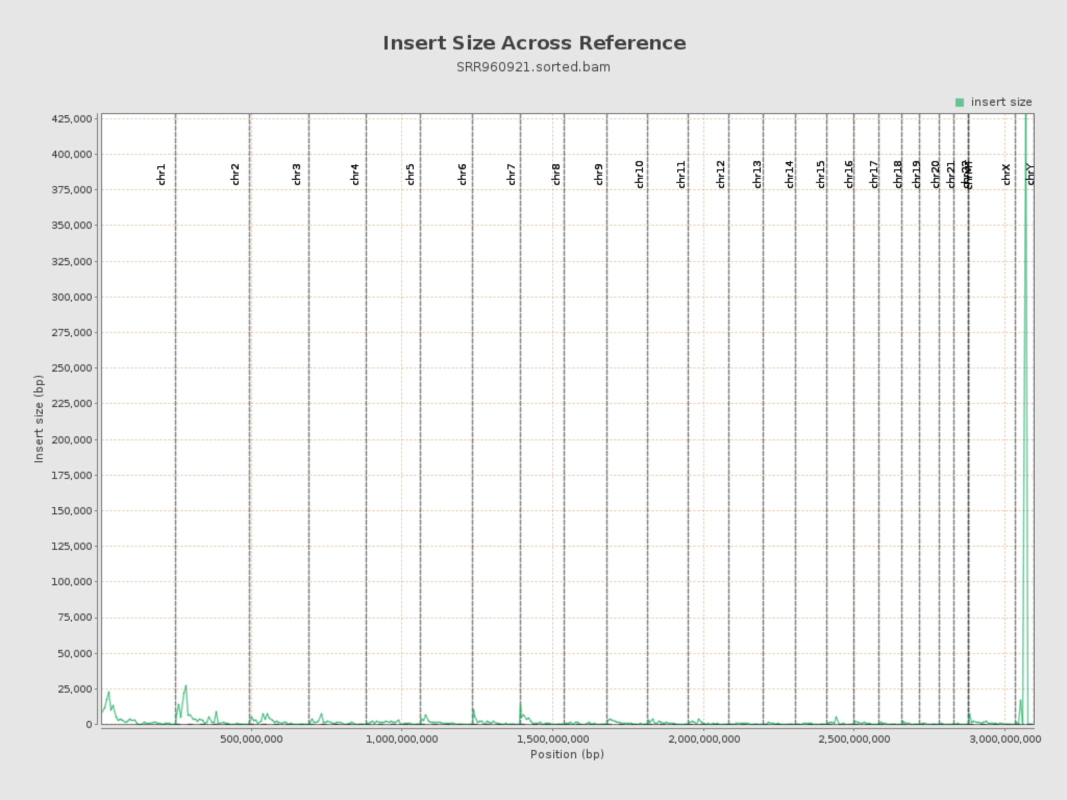
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram