Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/23 05:57:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926964.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_SRR926964 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926964_1.fastq.gz SRR926964_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 23 05:57:05 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926964.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	29,991,400
Mapped reads	29,293,339 / 97.67%
Unmapped reads	698,061 / 2.33%
Mapped paired reads	29,293,339 / 97.67%
Mapped reads, first in pair	14,706,827 / 49.04%
Mapped reads, second in pair	14,586,512 / 48.64%
Mapped reads, both in pair	28,911,844 / 96.4%
Mapped reads, singletons	381,495 / 1.27%
Secondary alignments	0
Supplementary alignments	737,748 / 2.46%
Read min/max/mean length	30 / 101 / 102.02
Duplicated reads (estimated)	2,353,440 / 7.85%
Duplication rate	6.3%
Clipped reads	9,313,093 / 31.05%

2.2. ACGT Content

Number/percentage of A's	796,327,191 / 29%
Number/percentage of C's	537,115,752 / 19.56%
Number/percentage of T's	804,675,523 / 29.3%
Number/percentage of G's	607,597,633 / 22.13%
Number/percentage of N's	191,104 / 0.01%

GC Percentage	41.69%

2.3. Coverage

Mean	0.8877
Standard Deviation	3.2139

2.4. Mapping Quality

Mean Mapping Quality	53.16

2.5. Insert size

Mean	256,720.65
Standard Deviation	4,929,722.76
P25/Median/P75	150 / 195 / 263

2.6. Mismatches and indels

General error rate	1.01%
Mismatches	27,017,359
Insertions	478,624
Mapped reads with at least one insertion	1.61%
Deletions	1,495,543
Mapped reads with at least one deletion	4.97%
Homopolymer indels	52.65%

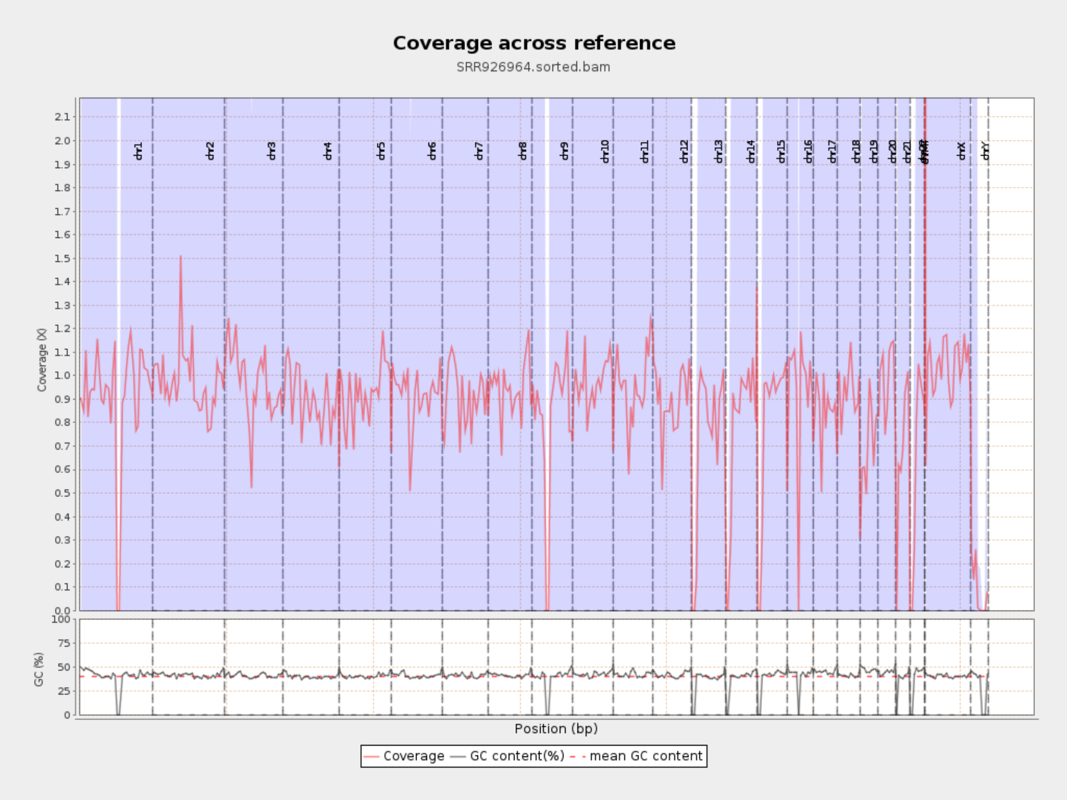
2.7. Chromosome stats

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

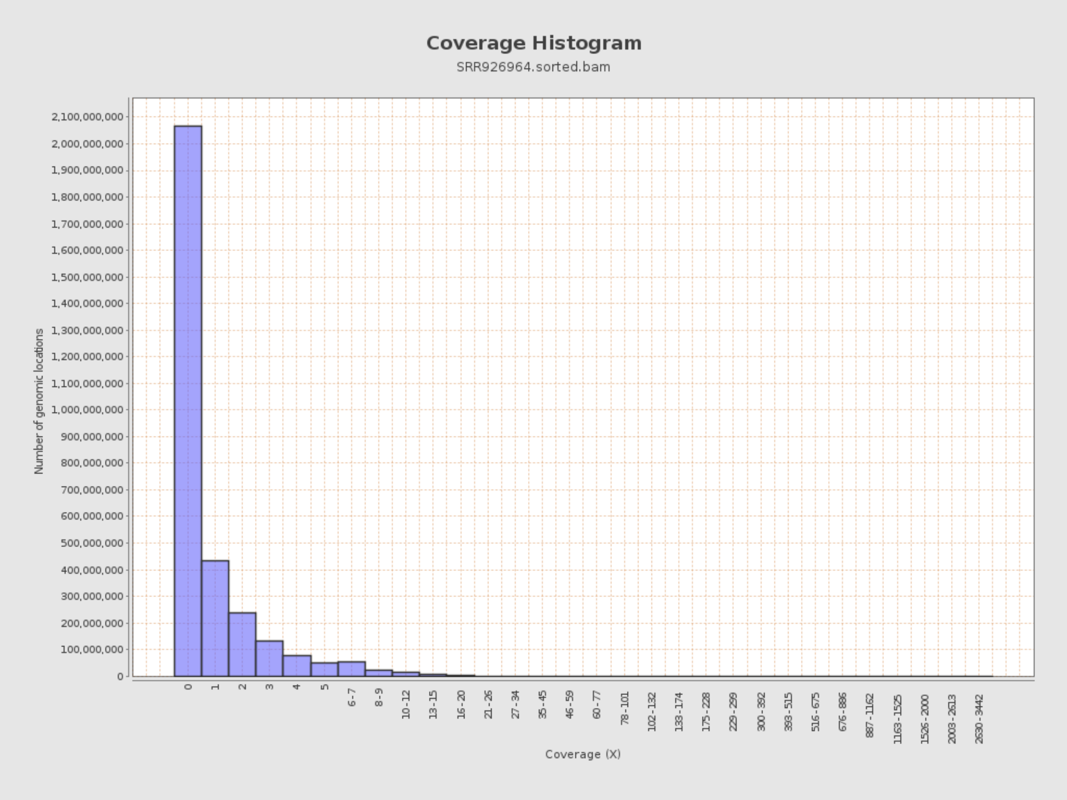
		bases	coverage	deviation
chr1	249250621	227598327	0.9131	4.1862
chr2	243199373	238604779	0.9811	5.149
chr3	198022430	192639451	0.9728	1.9538
chr4	191154276	172550267	0.9027	2.747
chr5	180915260	167752779	0.9272	1.8906
chr6	171115067	158193439	0.9245	2.4316
chr7	159138663	145159762	0.9122	2.655
chr8	146364022	138822725	0.9485	2.2738
chr9	141213431	114505839	0.8109	4.0168
chr10	135534747	132034070	0.9742	4.1967
chr11	135006516	128738330	0.9536	2.947
chr12	133851895	120286809	0.8987	2.093
chr13	115169878	84935078	0.7375	1.7122
chr14	107349540	82408507	0.7677	1.796
chr15	102531392	80693079	0.787	1.8515
chr16	90354753	82549613	0.9136	4.2783
chr17	81195210	68157482	0.8394	3.2691
chr18	78077248	74209864	0.9505	4.6474
chr19	59128983	41270954	0.698	2.5791
chr20	63025520	62127876	0.9858	2.1828
chr21	48129895	33515311	0.6964	2.4371
chr22	51304566	32410646	0.6317	1.7126
chrMT	16571	3930654	237.2008	155.4595
chrX	155270560	159919555	1.0299	2.3026

chrY	59373566	5040184	0.0849	2.6491

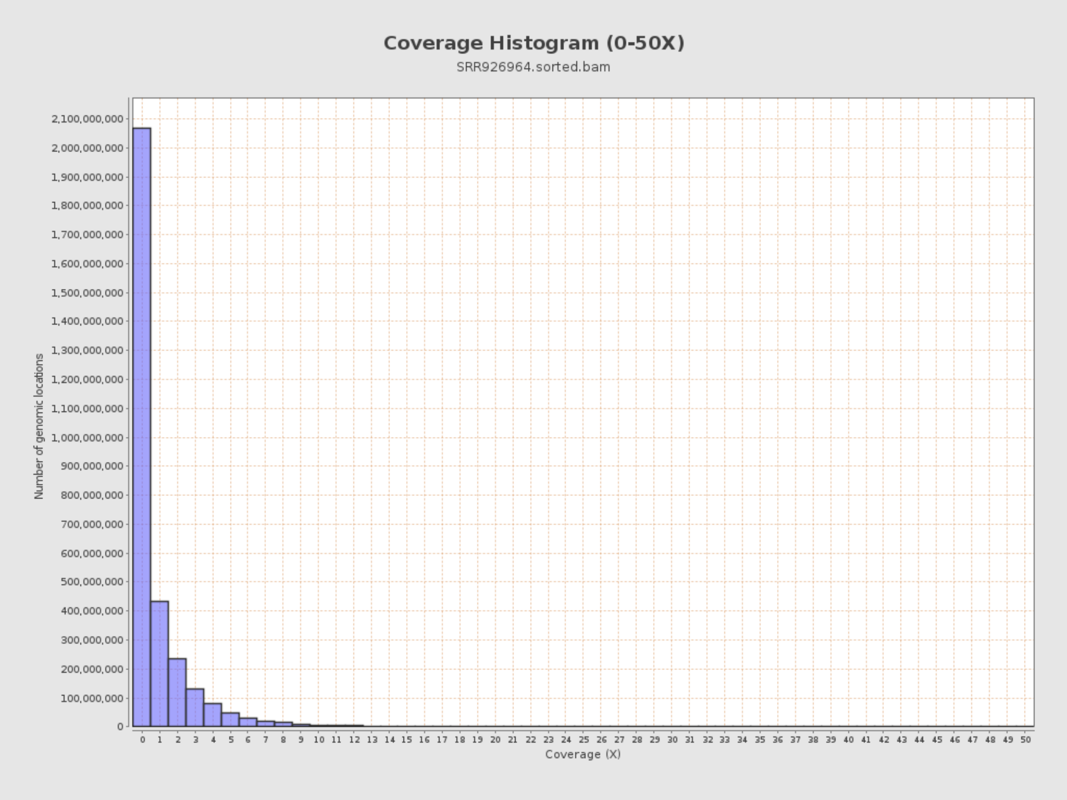
3. Results : Coverage across reference



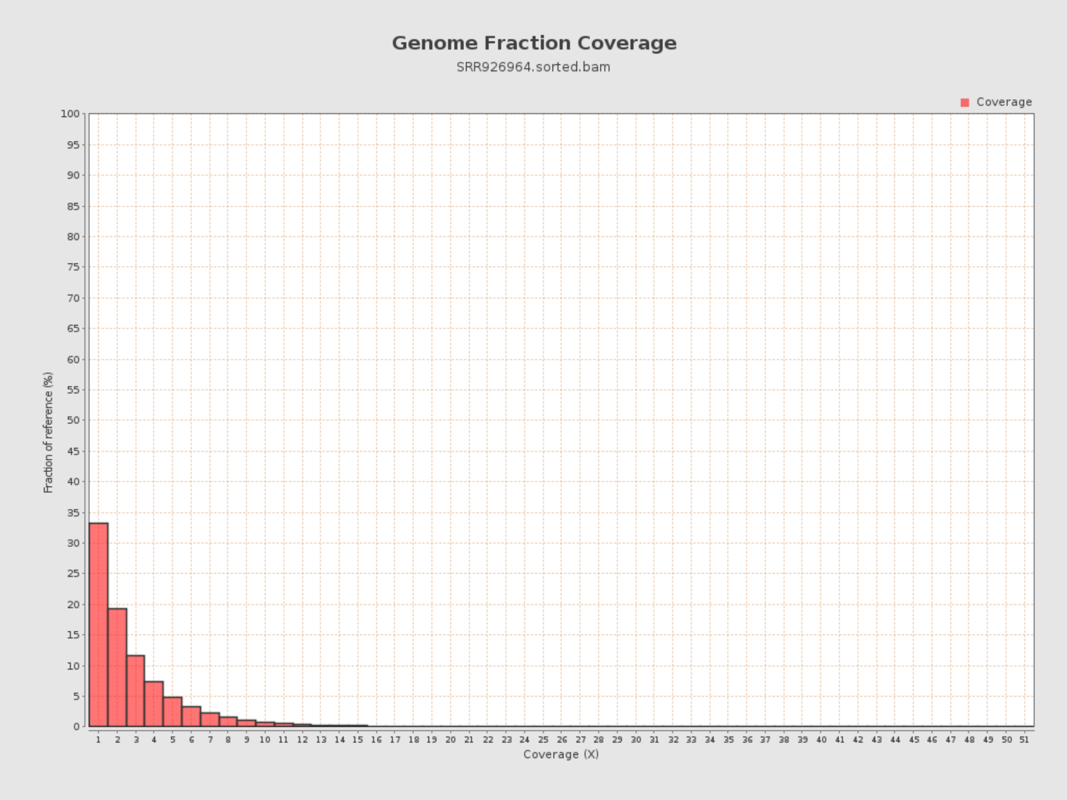
4. Results : Coverage Histogram



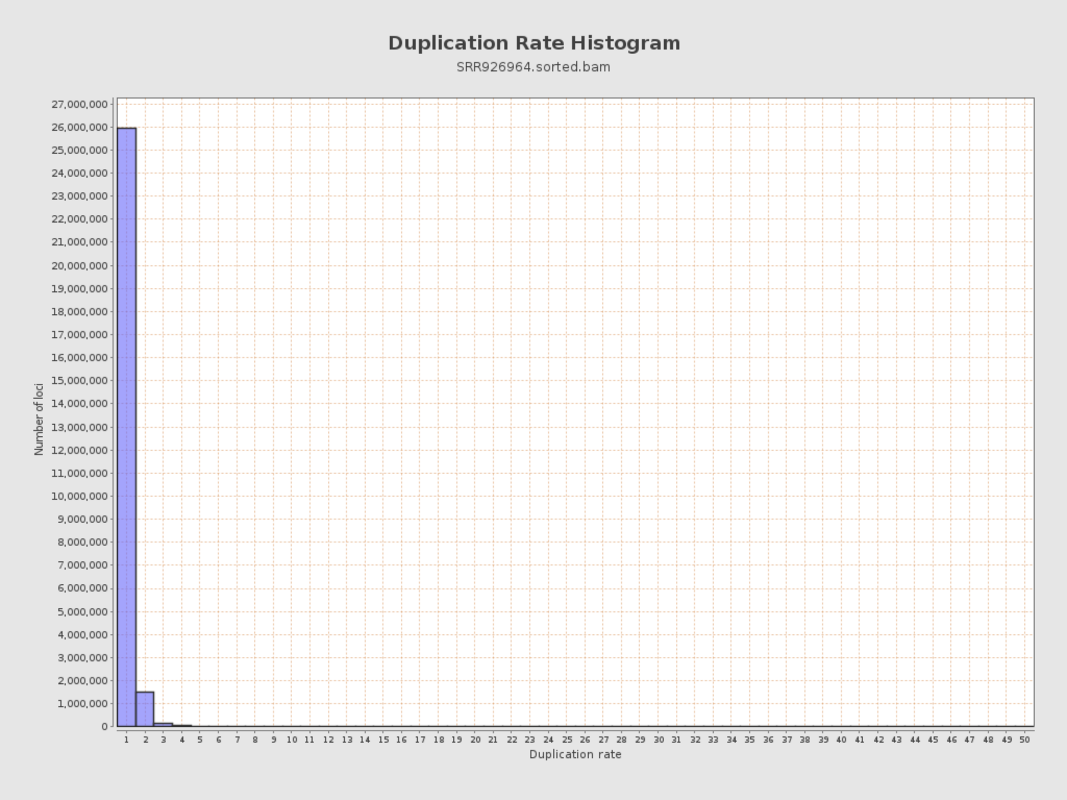
5. Results : Coverage Histogram (0-50X)



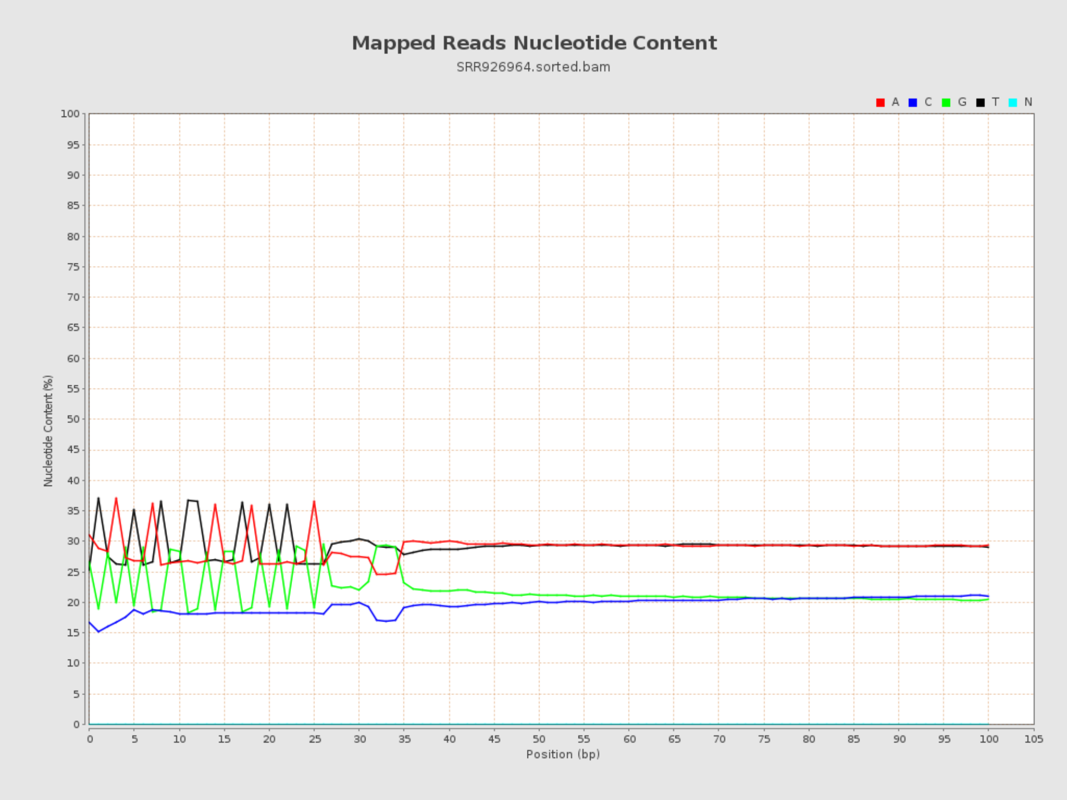
6. Results : Genome Fraction Coverage



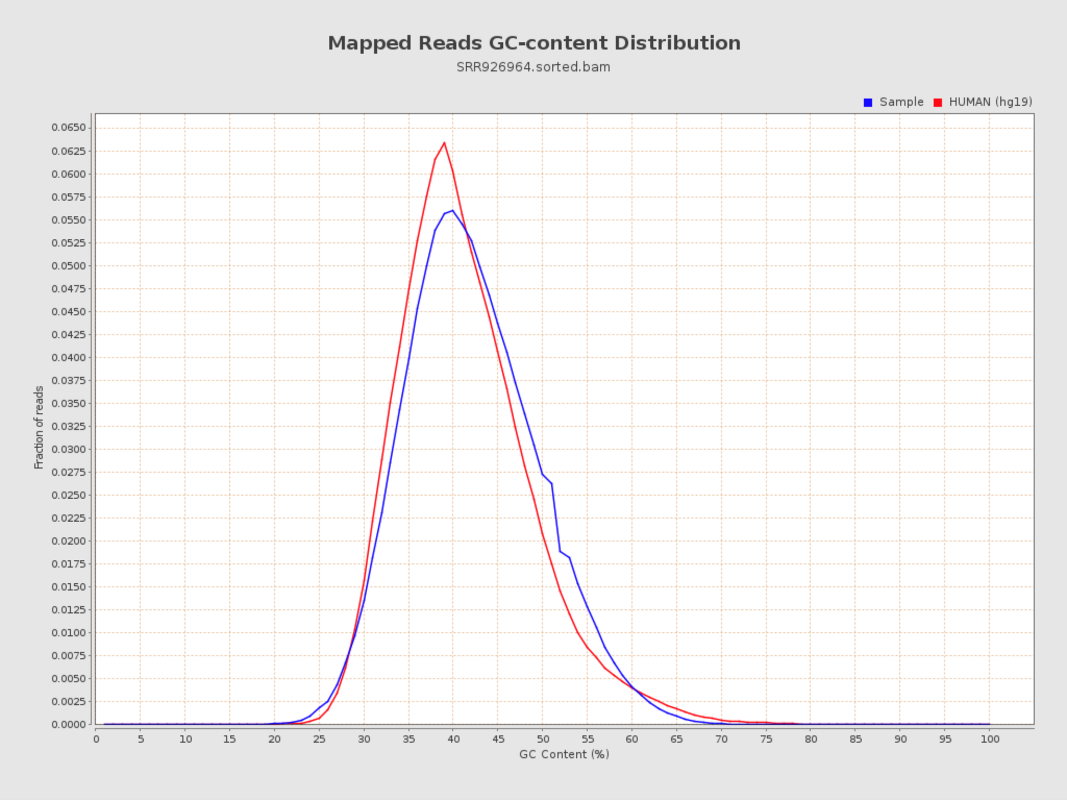
7. Results : Duplication Rate Histogram



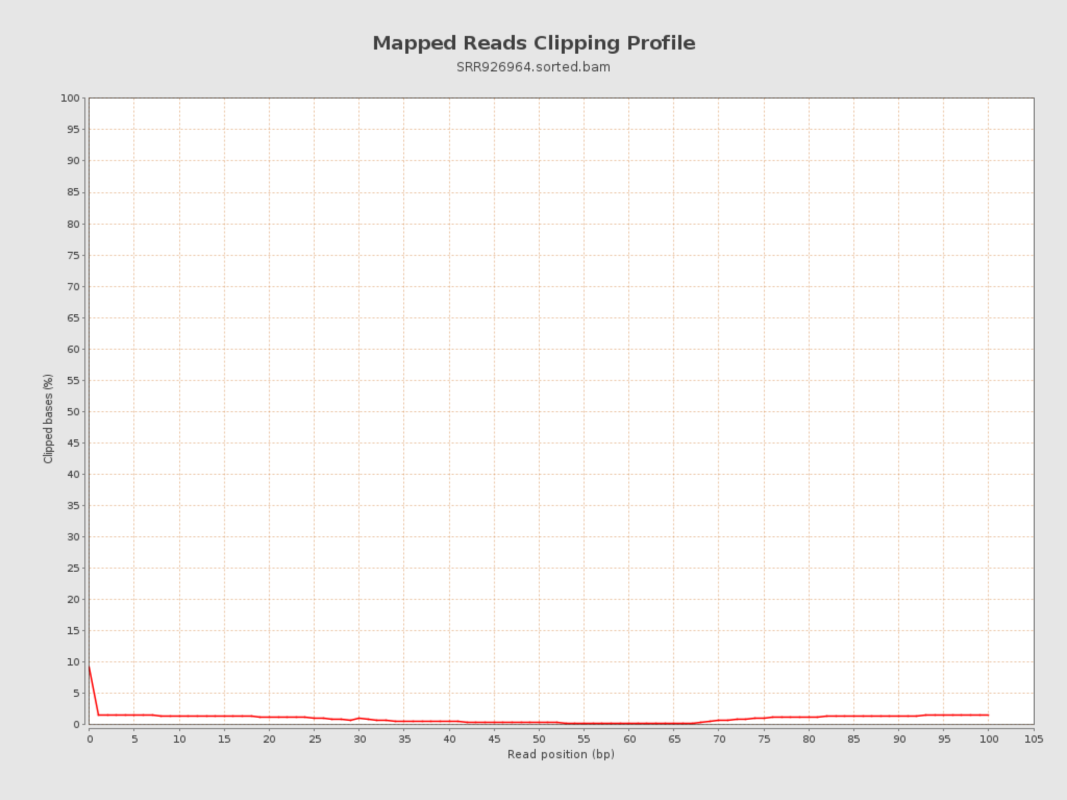
8. Results : Mapped Reads Nucleotide Content



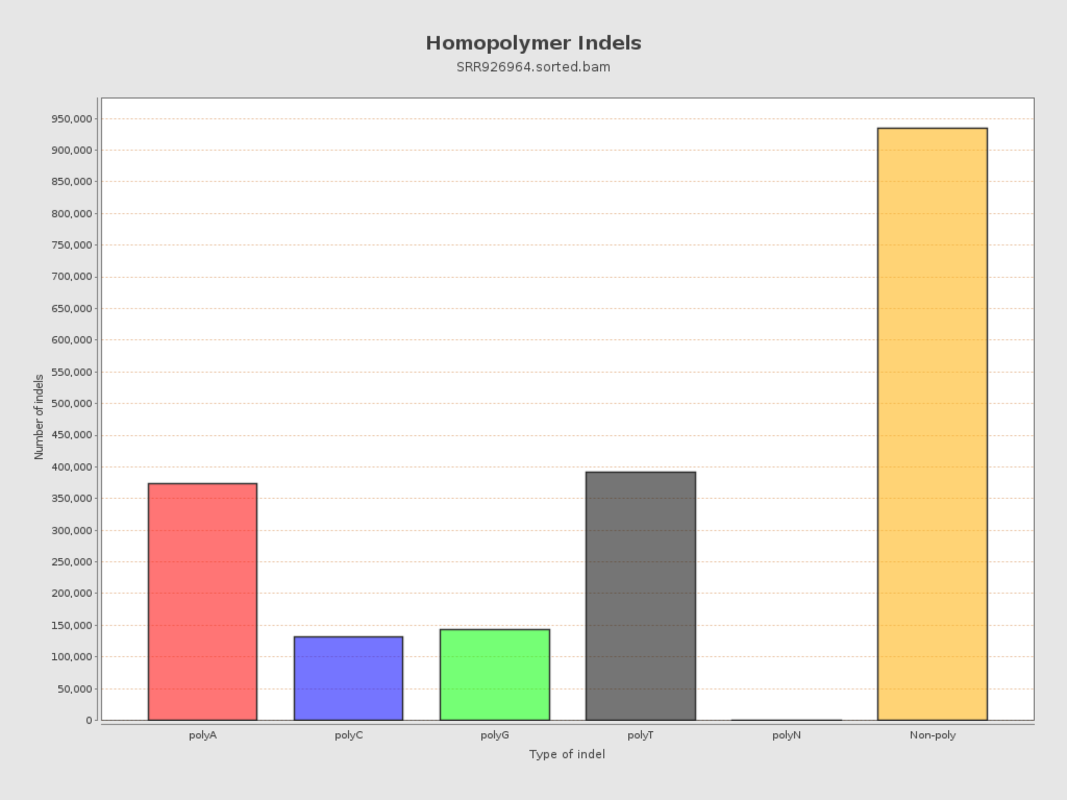
9. Results : Mapped Reads GC-content Distribution



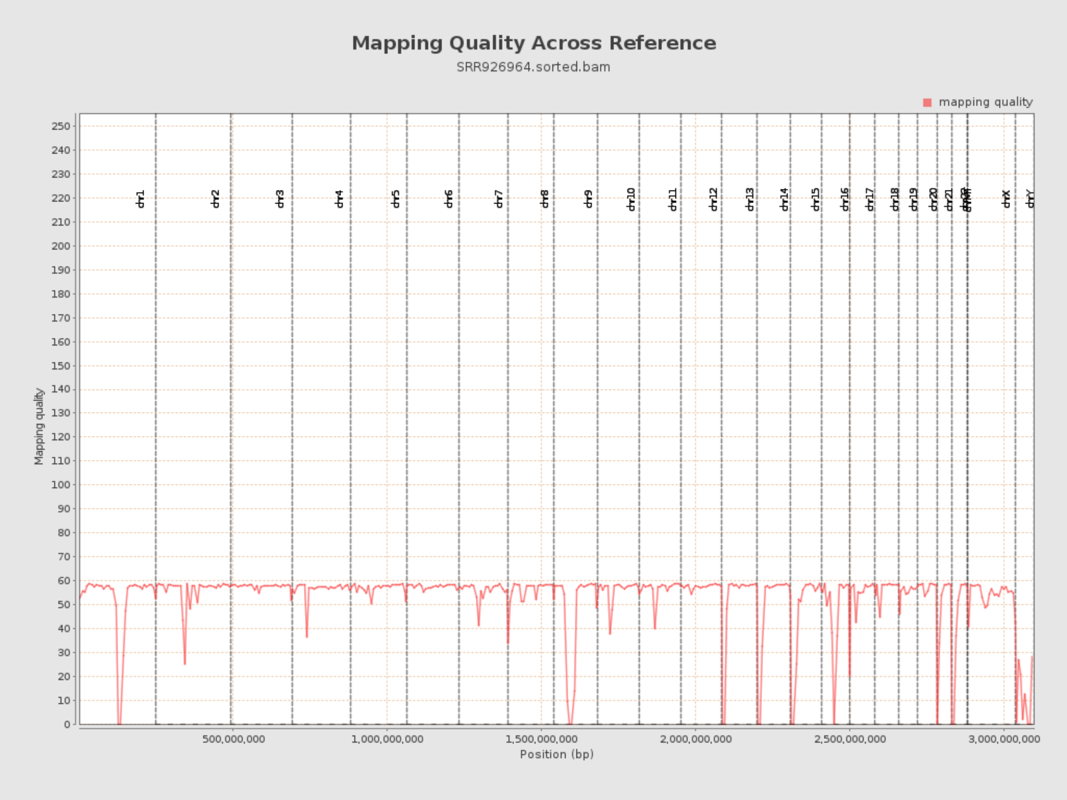
10. Results : Mapped Reads Clipping Profile



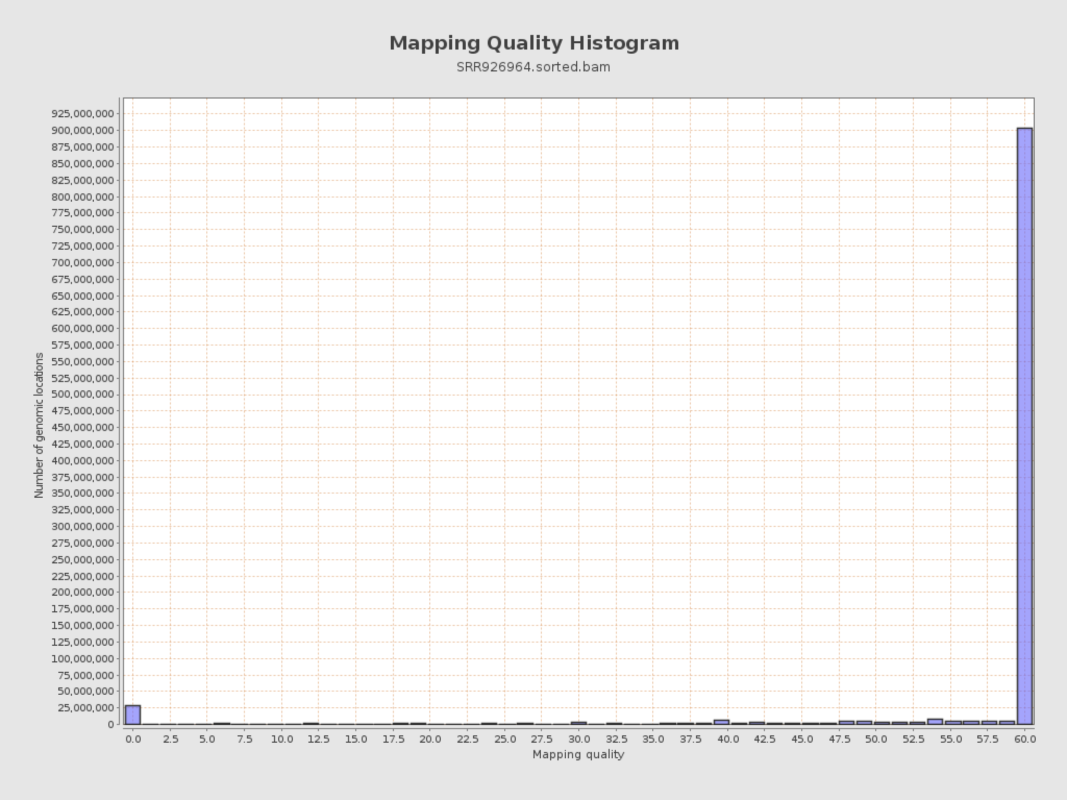
11. Results : Homopolymer Indels



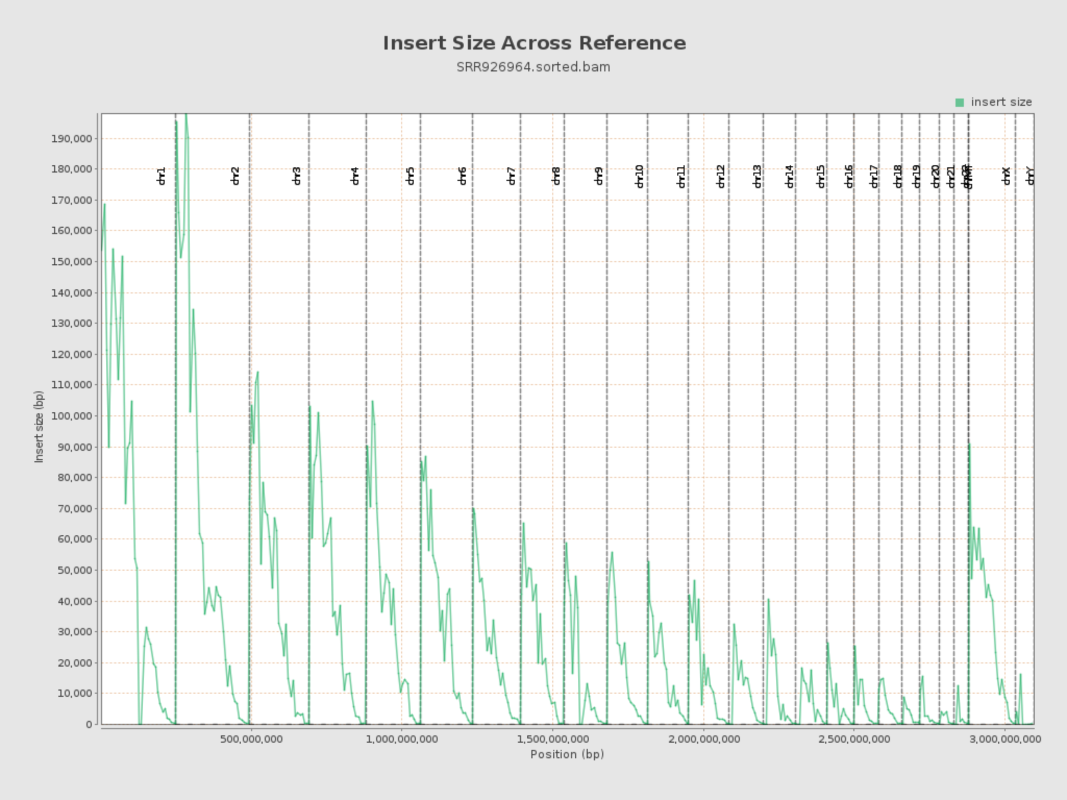
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram