Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/24 00:47:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927004.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_SRR927004 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927004_1.fastq.gz SRR927004_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 24 00:47:21 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927004.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	24,977,928
Mapped reads	24,576,413 / 98.39%
Unmapped reads	401,515 / 1.61%
Mapped paired reads	24,576,413 / 98.39%
Mapped reads, first in pair	12,315,544 / 49.31%
Mapped reads, second in pair	12,260,869 / 49.09%
Mapped reads, both in pair	24,327,208 / 97.39%
Mapped reads, singletons	249,205 / 1%
Secondary alignments	0
Supplementary alignments	358,951 / 1.44%
Read min/max/mean length	30 / 101 / 101.59
Duplicated reads (estimated)	1,724,842 / 6.91%
Duplication rate	5.57%
Clipped reads	7,070,952 / 28.31%

2.2. ACGT Content

Number/percentage of A's	667,738,352 / 28.97%
Number/percentage of C's	448,491,875 / 19.46%
Number/percentage of T's	678,157,879 / 29.42%
Number/percentage of G's	510,151,760 / 22.13%
Number/percentage of N's	259,654 / 0.01%

GC Percentage	41.59%

2.3. Coverage

Mean	0.7451
Standard Deviation	2.7995

2.4. Mapping Quality

Mean Mapping Quality	53.43

2.5. Insert size

Mean	147,488.88
Standard Deviation	3,755,817.86
P25/Median/P75	157 / 202 / 269

2.6. Mismatches and indels

General error rate	0.93%
Mismatches	20,824,025
Insertions	387,482
Mapped reads with at least one insertion	1.55%
Deletions	1,247,015
Mapped reads with at least one deletion	4.94%
Homopolymer indels	53.14%

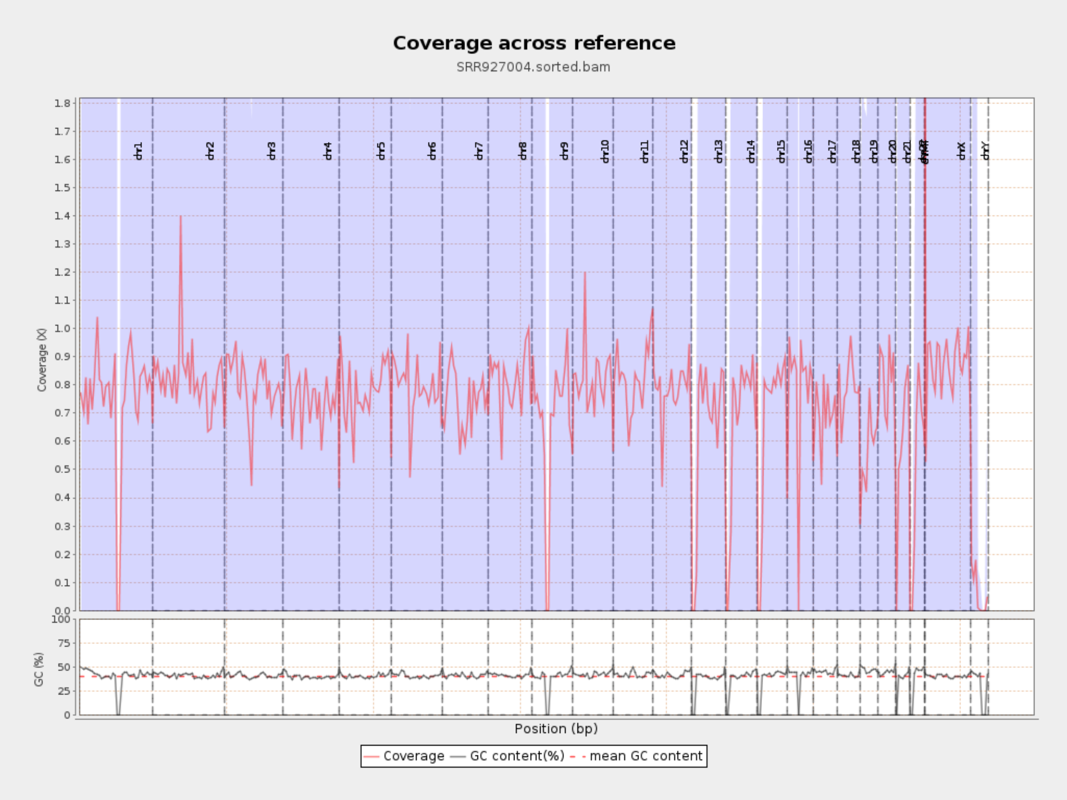
2.7. Chromosome stats

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

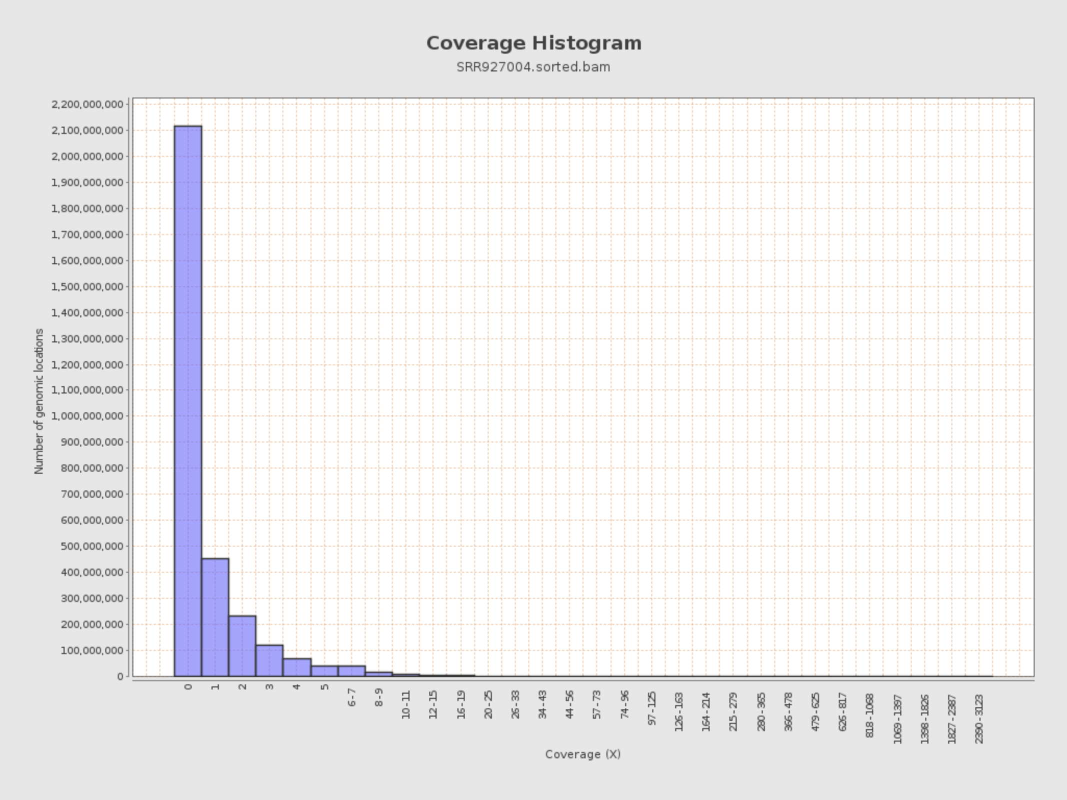
		bases	coverage	deviation
chr1	249250621	187756643	0.7533	3.8207
chr2	243199373	202063168	0.8309	4.6265
chr3	198022430	157424873	0.795	1.5999
chr4	191154276	144308832	0.7549	2.0087
chr5	180915260	140958428	0.7791	1.5718
chr6	171115067	136830530	0.7996	2.4731
chr7	159138663	118516438	0.7447	2.4005
chr8	146364022	119994541	0.8198	1.8426
chr9	141213431	94498413	0.6692	3.3726
chr10	135534747	112314654	0.8287	5.3242
chr11	135006516	110340611	0.8173	2.6778
chr12	133851895	104186286	0.7784	1.6199
chr13	115169878	73271183	0.6362	1.4287
chr14	107349540	69982695	0.6519	1.5012
chr15	102531392	67858238	0.6618	1.5238
chr16	90354753	69261853	0.7666	3.2424
chr17	81195210	55971509	0.6893	1.9888
chr18	78077248	63077940	0.8079	3.0876
chr19	59128983	33509723	0.5667	2.3709
chr20	63025520	51154704	0.8117	1.7387
chr21	48129895	29131931	0.6053	2.3277
chr22	51304566	25568690	0.4984	1.3713
chrMT	16571	86032	5.1917	5.0699
chrX	155270560	134913282	0.8689	1.934

chrY	59373566	3597562	0.0606	1.9471

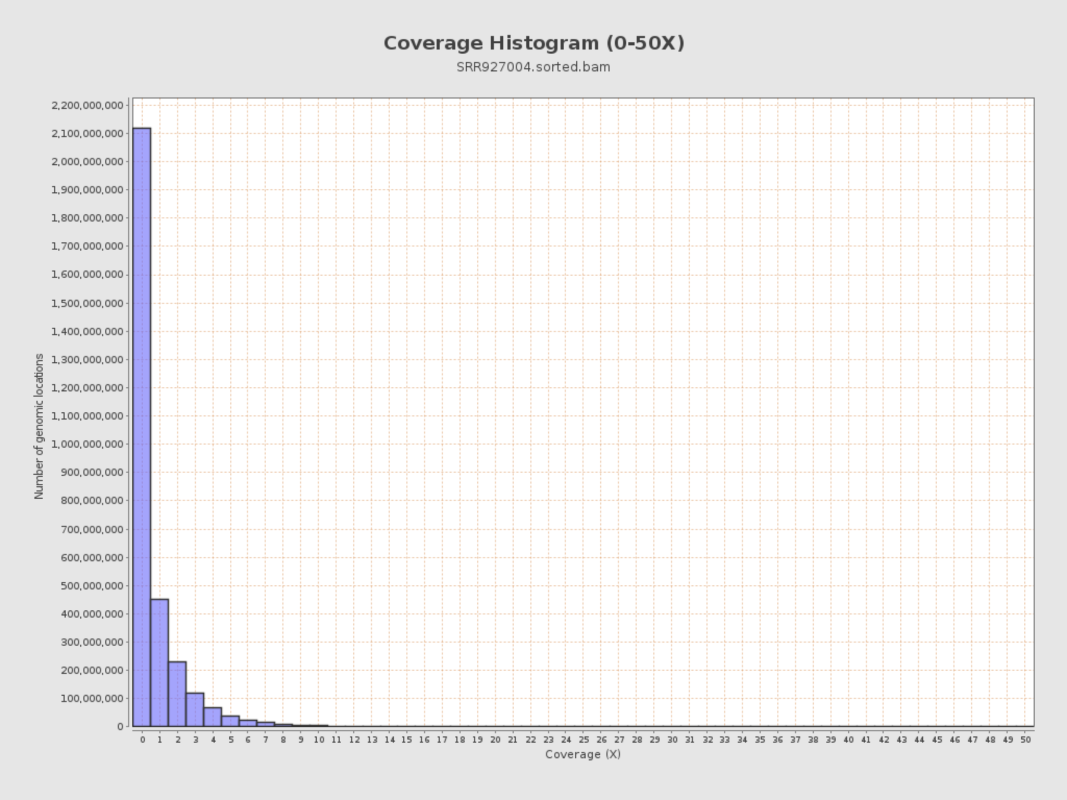
3. Results : Coverage across reference



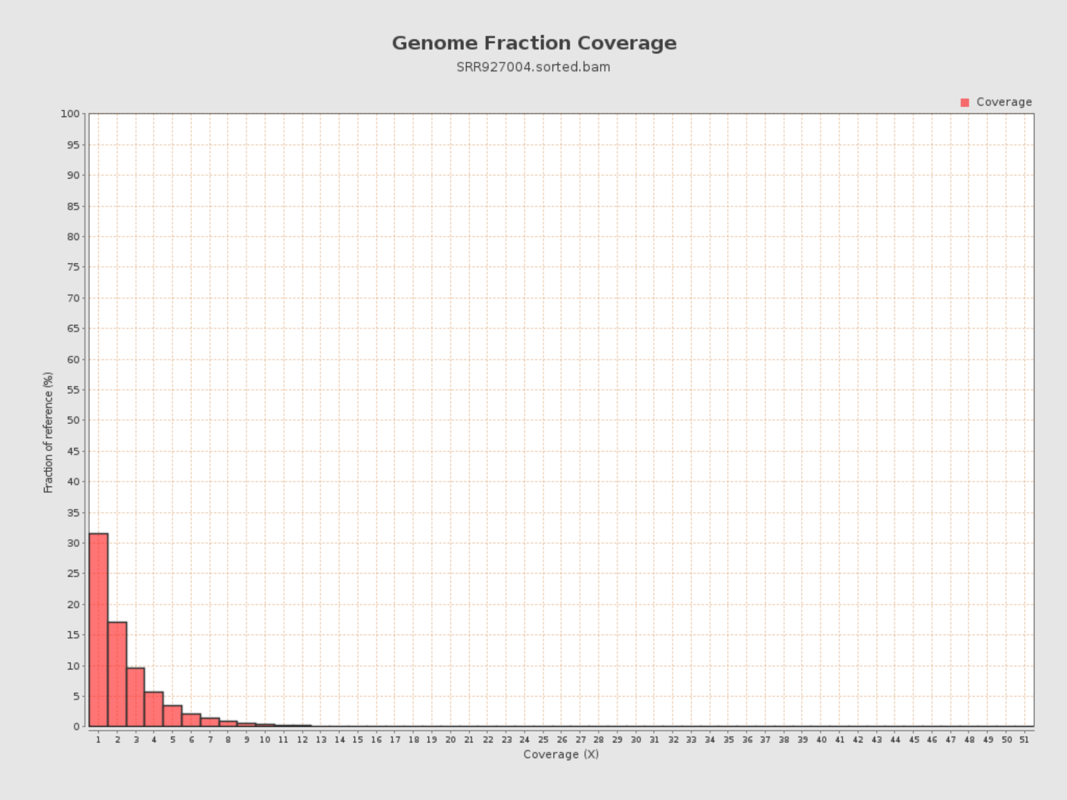
4. Results : Coverage Histogram



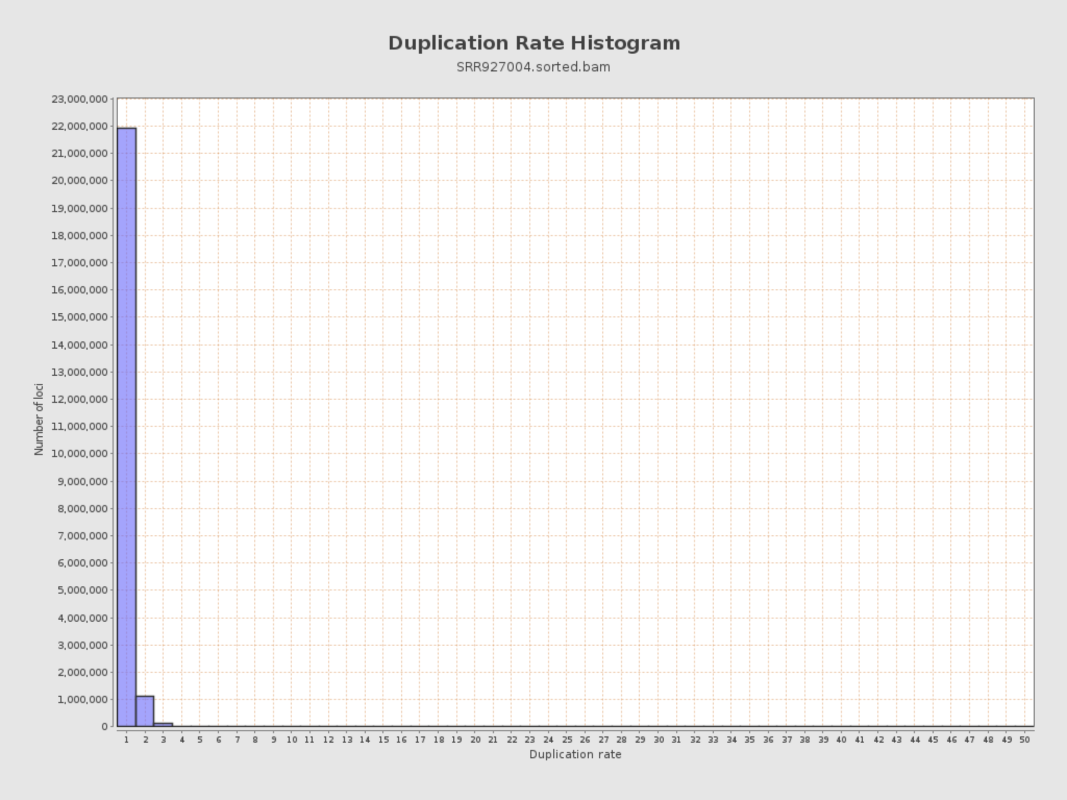
5. Results : Coverage Histogram (0-50X)



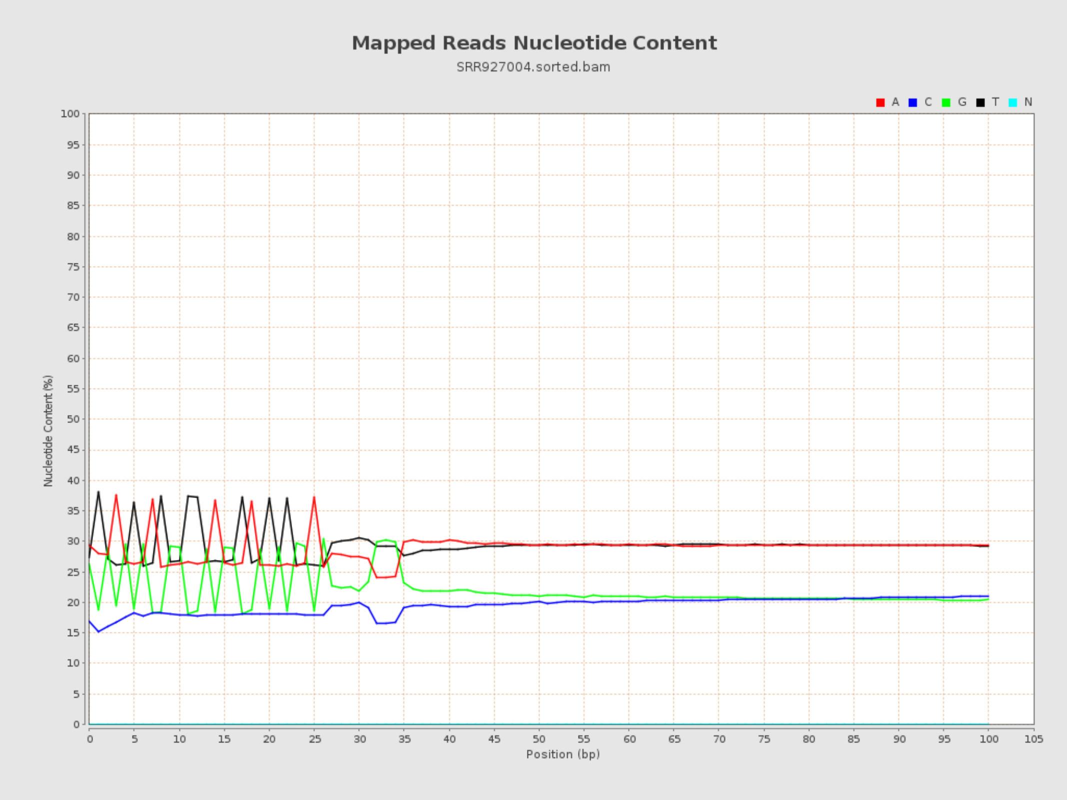
6. Results : Genome Fraction Coverage



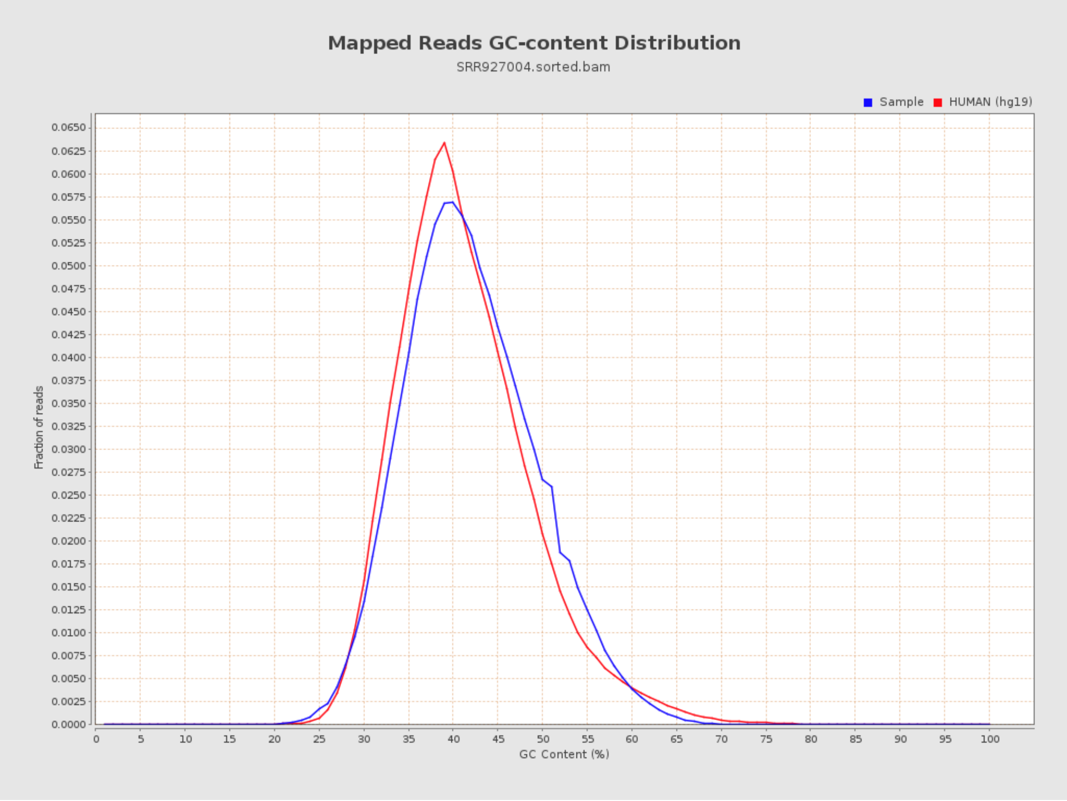
7. Results : Duplication Rate Histogram



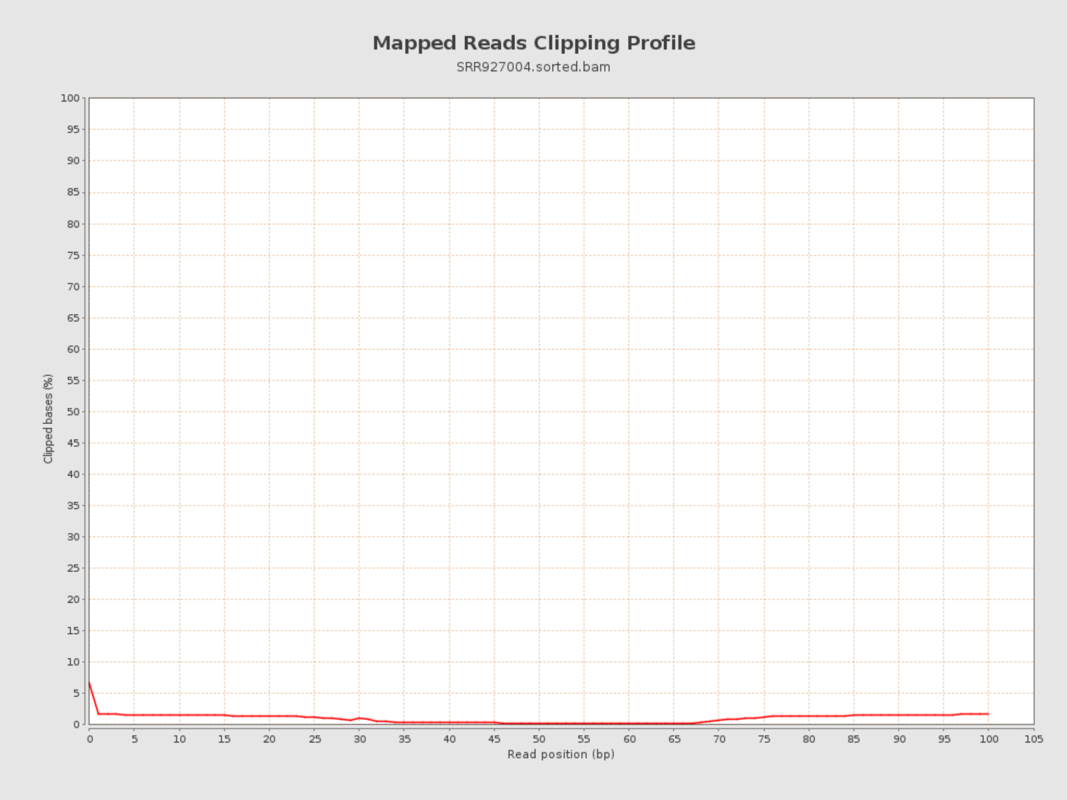
8. Results : Mapped Reads Nucleotide Content



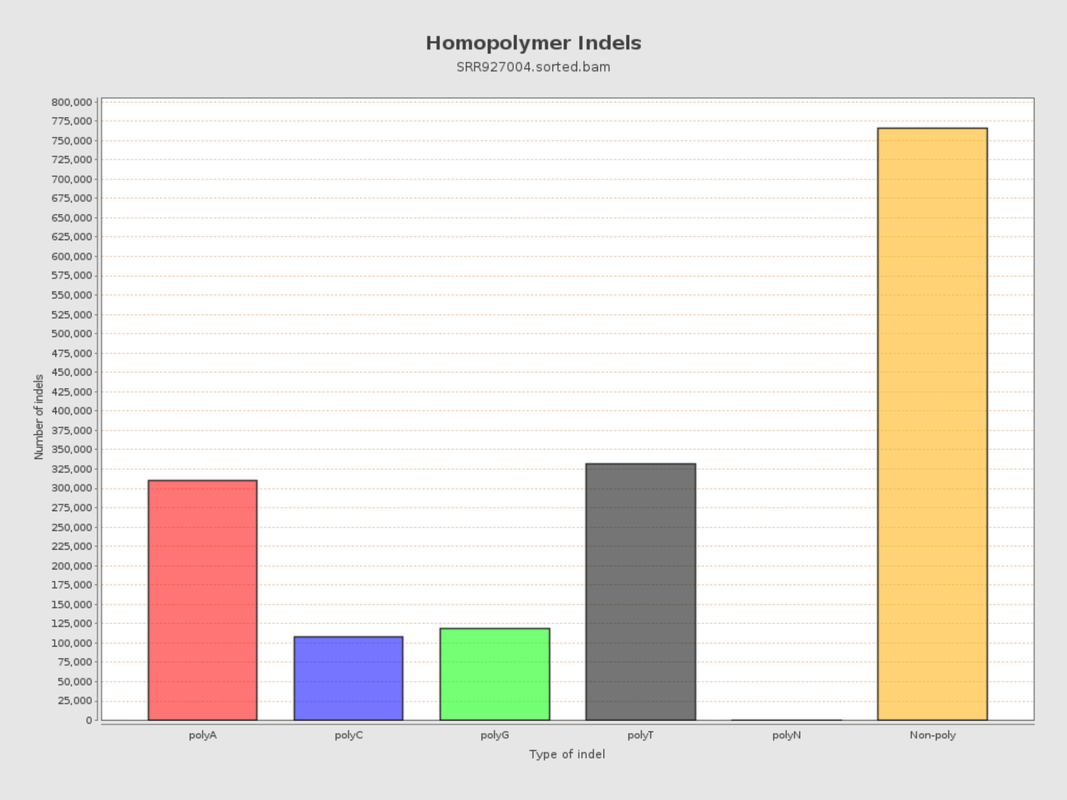
9. Results : Mapped Reads GC-content Distribution



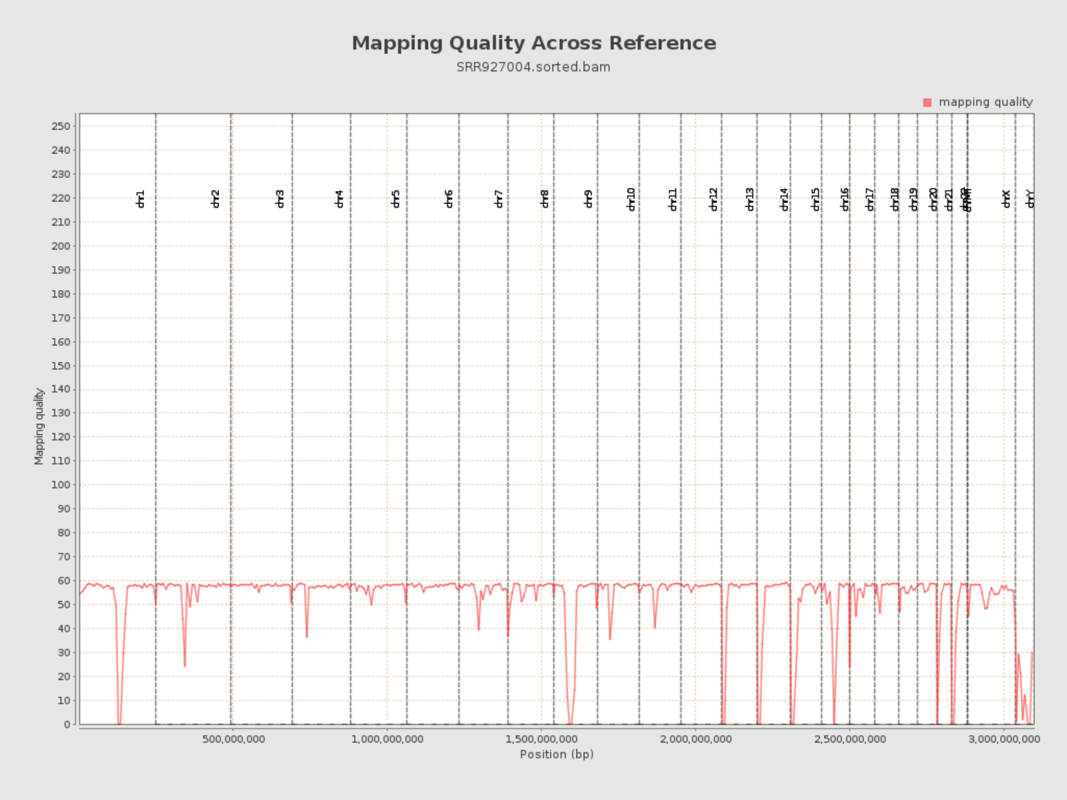
10. Results : Mapped Reads Clipping Profile



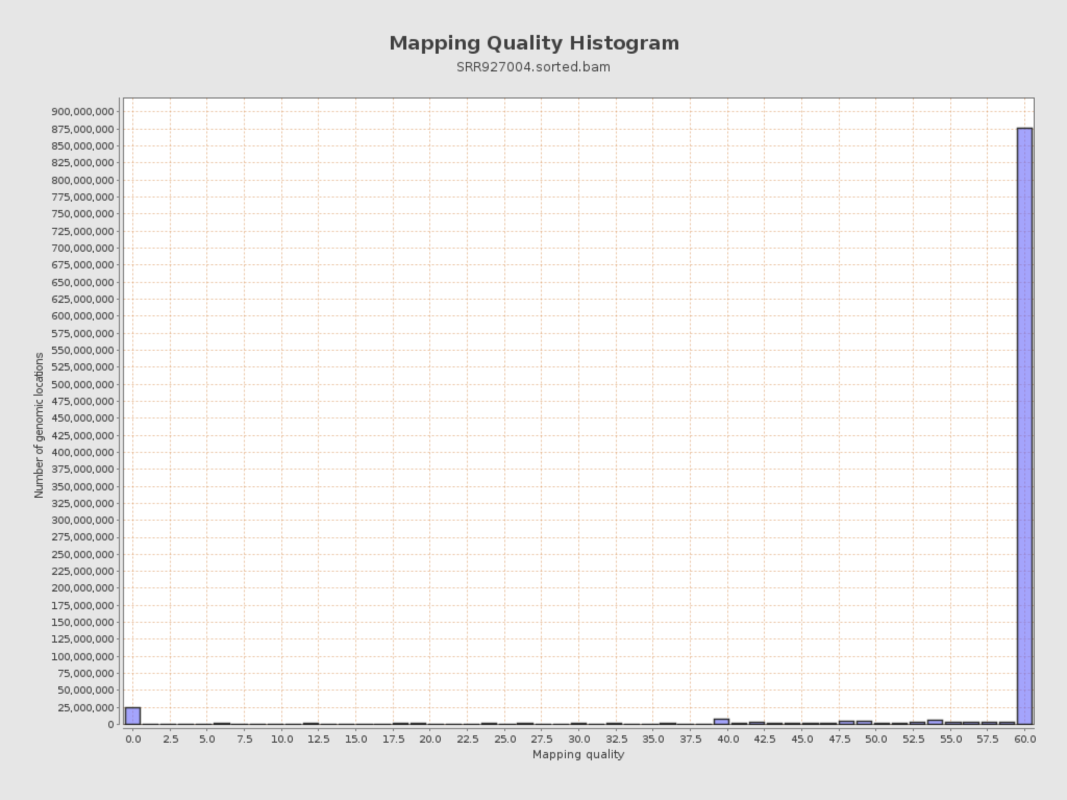
11. Results : Homopolymer Indels



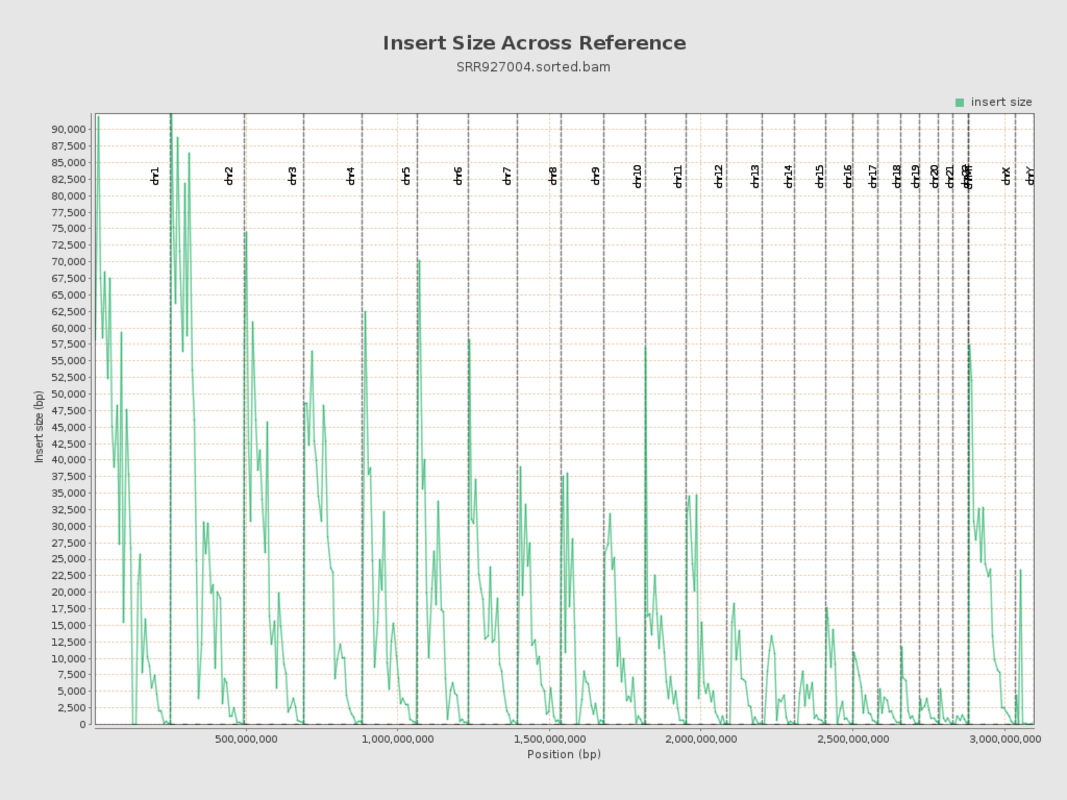
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram