Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/23 23:28:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927001.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_SRR927001 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927001_1.fastq.gz SRR927001_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 23 23:28:44 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927001.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	31,343,678
Mapped reads	30,854,178 / 98.44%
Unmapped reads	489,500 / 1.56%
Mapped paired reads	30,854,178 / 98.44%
Mapped reads, first in pair	15,468,538 / 49.35%
Mapped reads, second in pair	15,385,640 / 49.09%
Mapped reads, both in pair	30,550,508 / 97.47%
Mapped reads, singletons	303,670 / 0.97%
Secondary alignments	0
Supplementary alignments	335,118 / 1.07%
Read min/max/mean length	30 / 101 / 101.44
Duplicated reads (estimated)	2,601,928 / 8.3%
Duplication rate	6.52%
Clipped reads	8,839,574 / 28.2%

2.2. ACGT Content

Number/percentage of A's	828,330,206 / 28.7%
Number/percentage of C's	568,206,830 / 19.69%
Number/percentage of T's	842,143,377 / 29.18%
Number/percentage of G's	647,245,497 / 22.43%
Number/percentage of N's	322,211 / 0.01%

GC Percentage	42.11%

2.3. Coverage

Mean	0.9331
Standard Deviation	3.8513

2.4. Mapping Quality

Mean Mapping Quality	52.59

2.5. Insert size

Mean	101,428.66
Standard Deviation	3,092,767.94
P25/Median/P75	151 / 195 / 260

2.6. Mismatches and indels

General error rate	0.94%
Mismatches	26,399,187
Insertions	477,662
Mapped reads with at least one insertion	1.52%
Deletions	1,546,278
Mapped reads with at least one deletion	4.88%
Homopolymer indels	52.99%

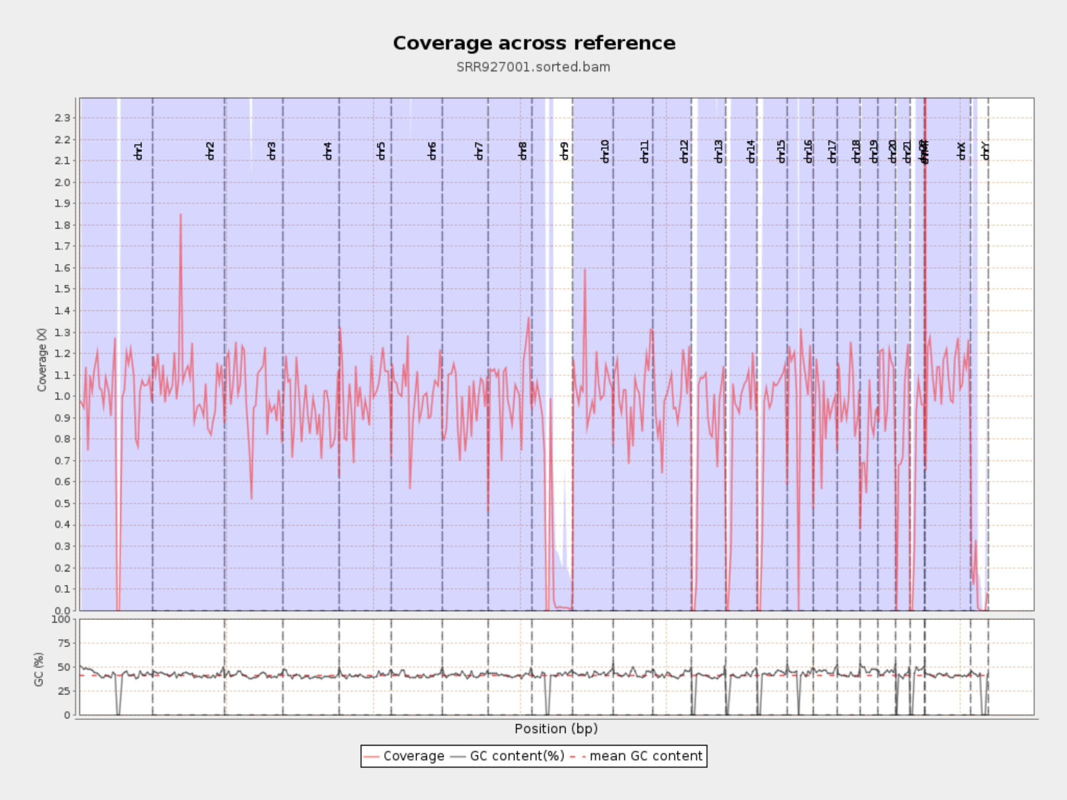
2.7. Chromosome stats

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

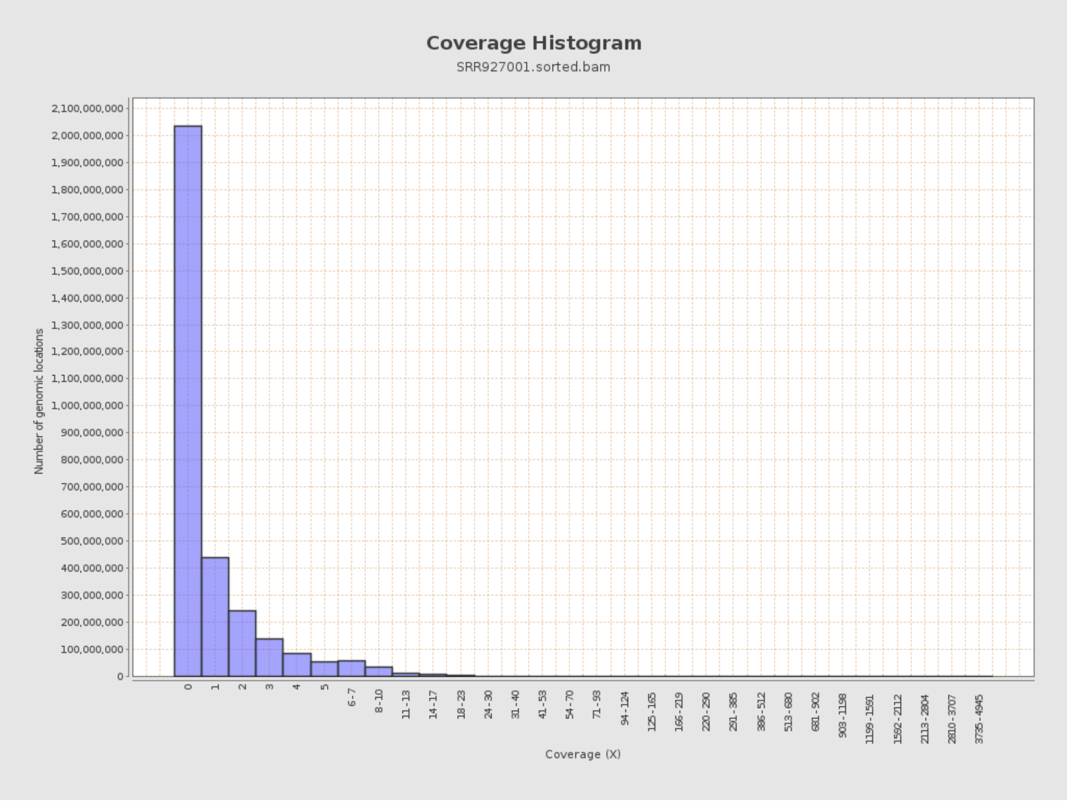
		bases	**coverage**	**deviation**
chr1	249250621	243178676	0.9756	5.8063
chr2	243199373	259147551	1.0656	6.2631
chr3	198022430	200322755	1.0116	1.9914
chr4	191154276	179174569	0.9373	3.4495
chr5	180915260	183098708	1.0121	1.9583
chr6	171115067	174039919	1.0171	3.4375
chr7	159138663	152782935	0.9601	2.7907
chr8	146364022	153219881	1.0468	2.4162
chr9	141213431	54284471	0.3844	4.8767
chr10	135534747	144007000	1.0625	6.3905
chr11	135006516	136896622	1.014	3.4178
chr12	133851895	132775260	0.992	2.0126
chr13	115169878	93355344	0.8106	1.7711
chr14	107349540	90091240	0.8392	1.8871
chr15	102531392	85989064	0.8387	1.8933
chr16	90354753	91346680	1.011	4.3161
chr17	81195210	74464019	0.9171	2.5966
chr18	78077248	78601842	1.0067	5.4436
chr19	59128983	46631083	0.7886	3.6169
chr20	63025520	66634305	1.0573	2.2952
chr21	48129895	38167130	0.793	3.1096
chr22	51304566	33942626	0.6616	1.7127
chrMT	16571	313523	18.92	17.1561
chrX	155270560	170717921	1.0995	2.4436

chrY	59373566	5261784	0.0886	3.3416

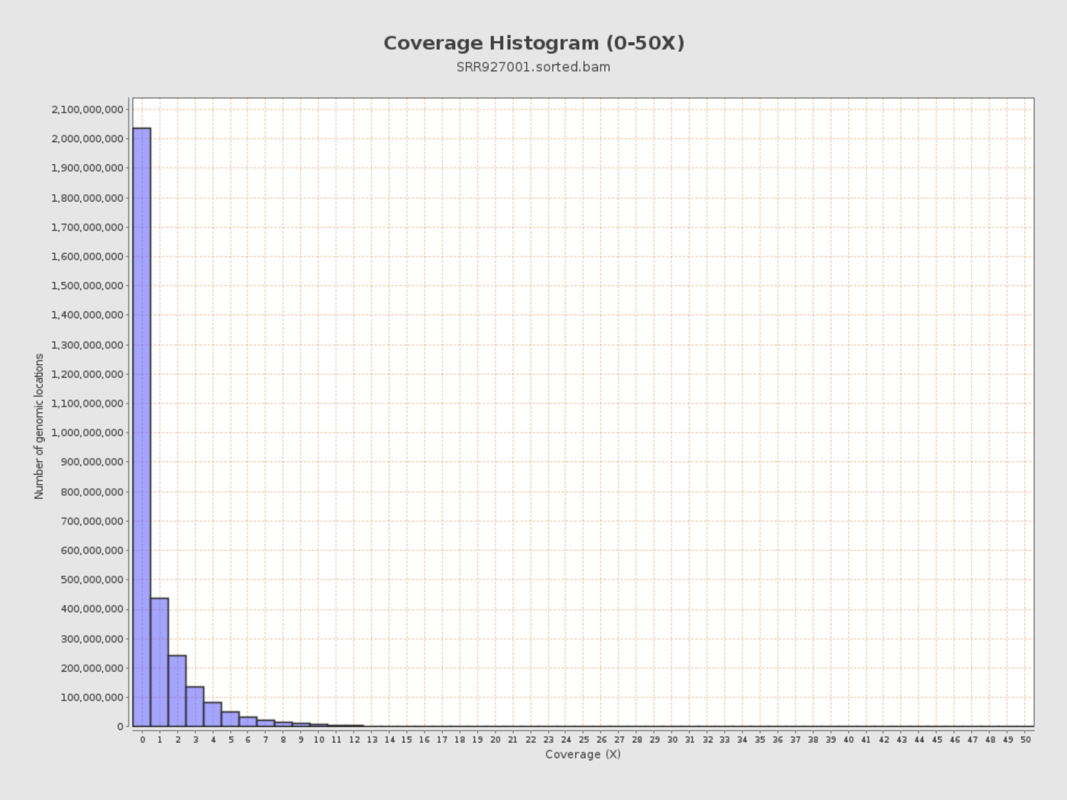
3. Results : Coverage across reference



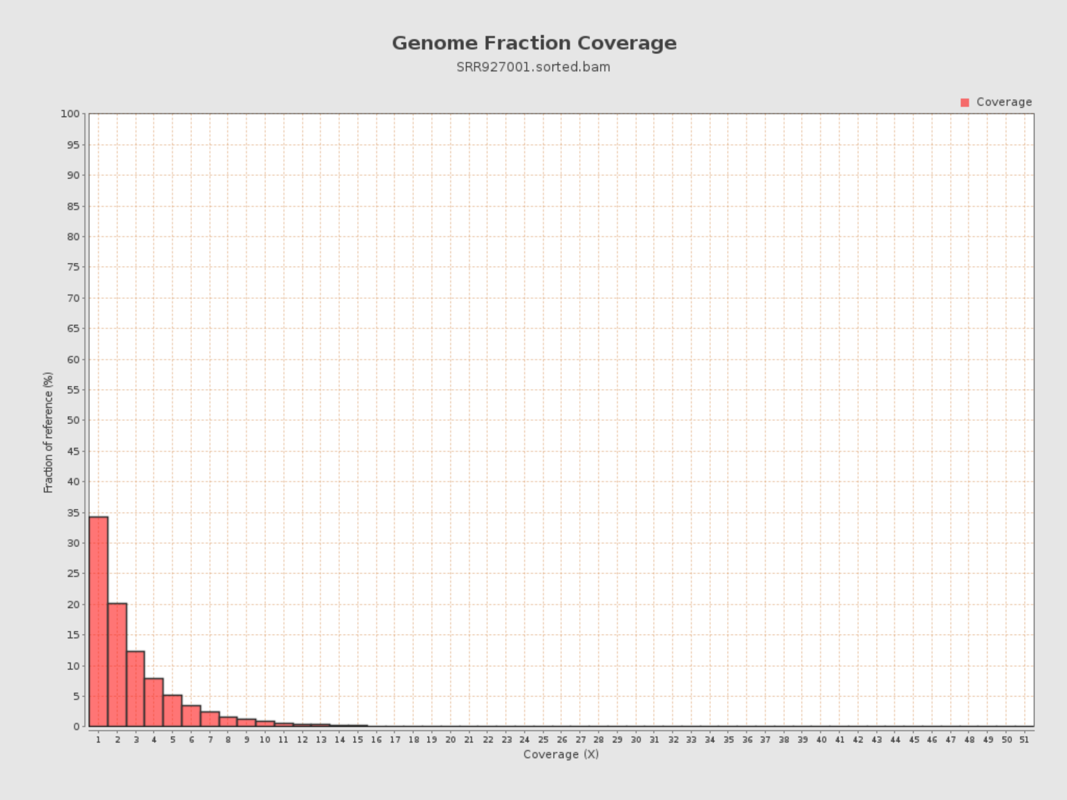
4. Results : Coverage Histogram



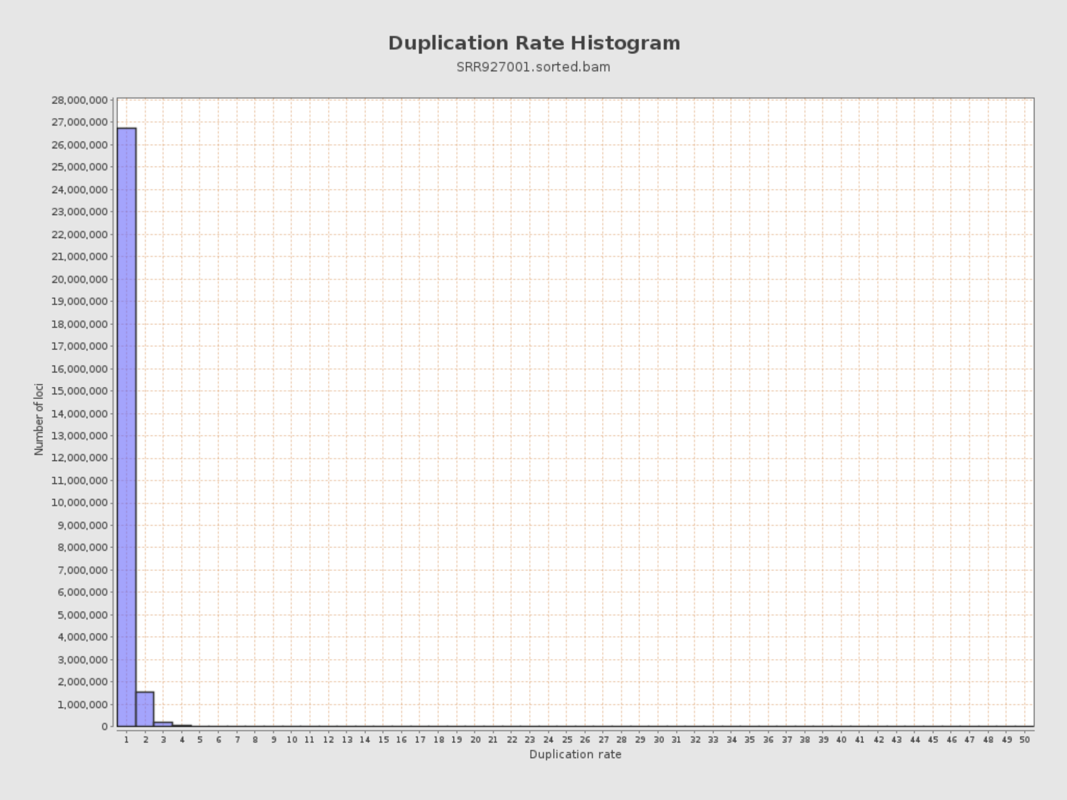
5. Results : Coverage Histogram (0-50X)



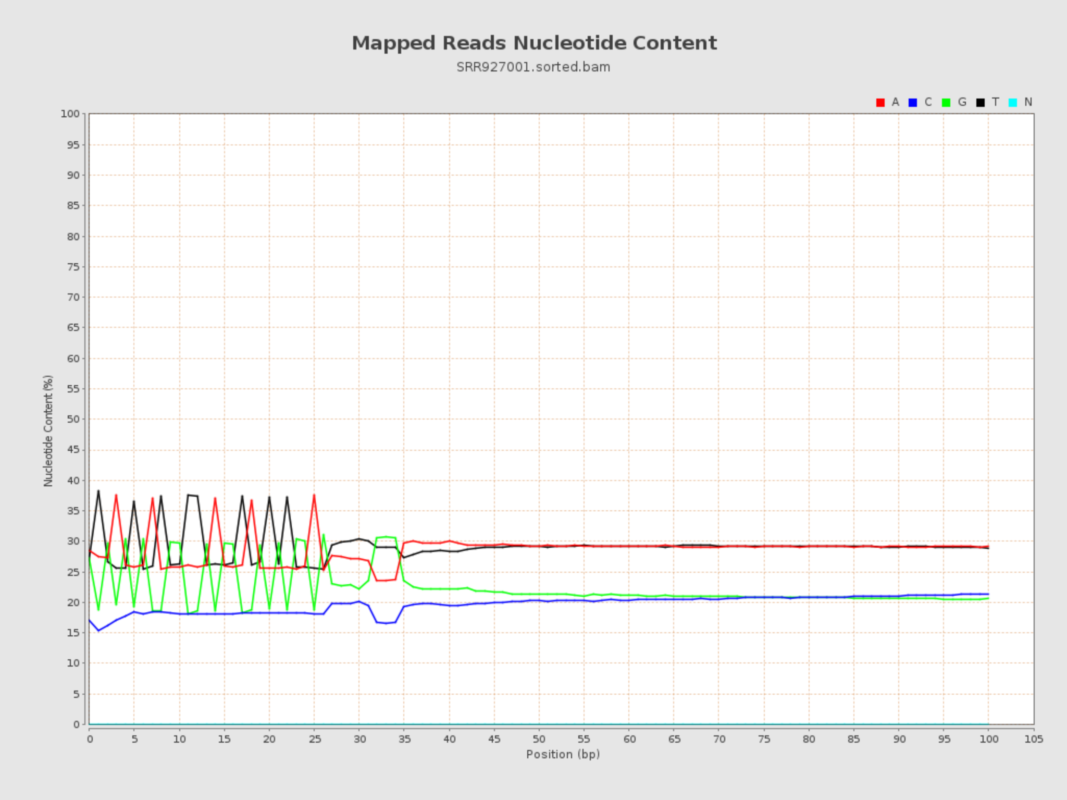
6. Results : Genome Fraction Coverage



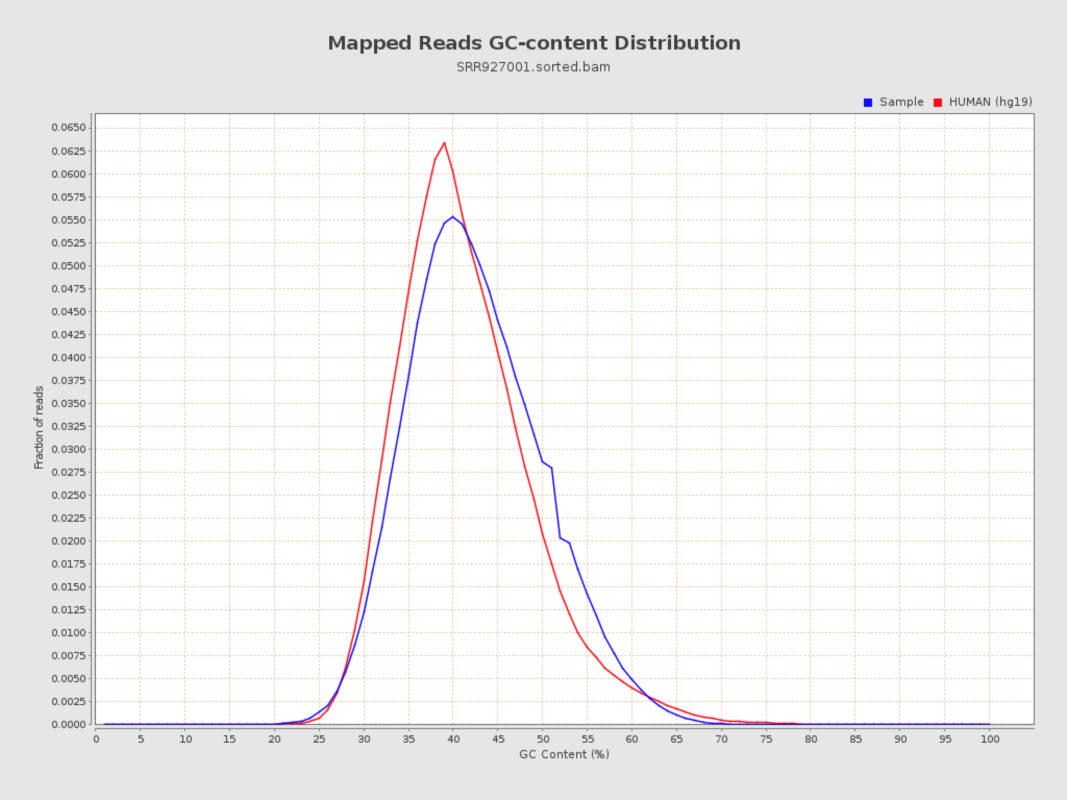
7. Results : Duplication Rate Histogram



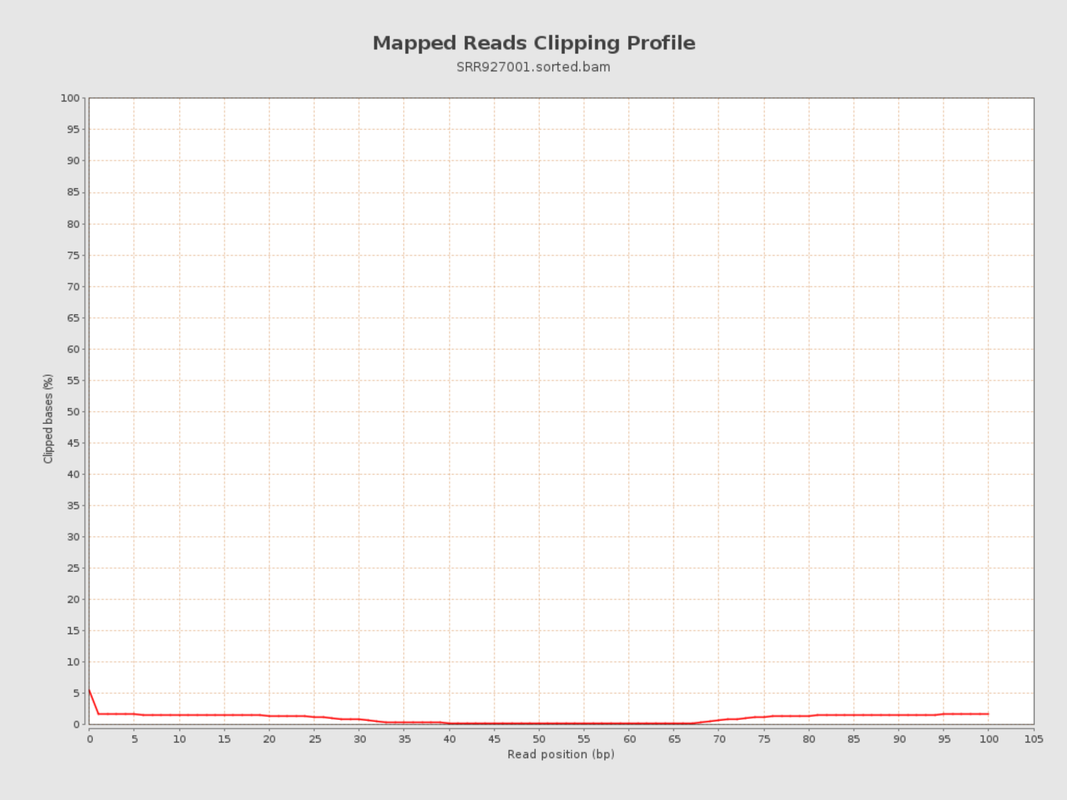
8. Results : Mapped Reads Nucleotide Content



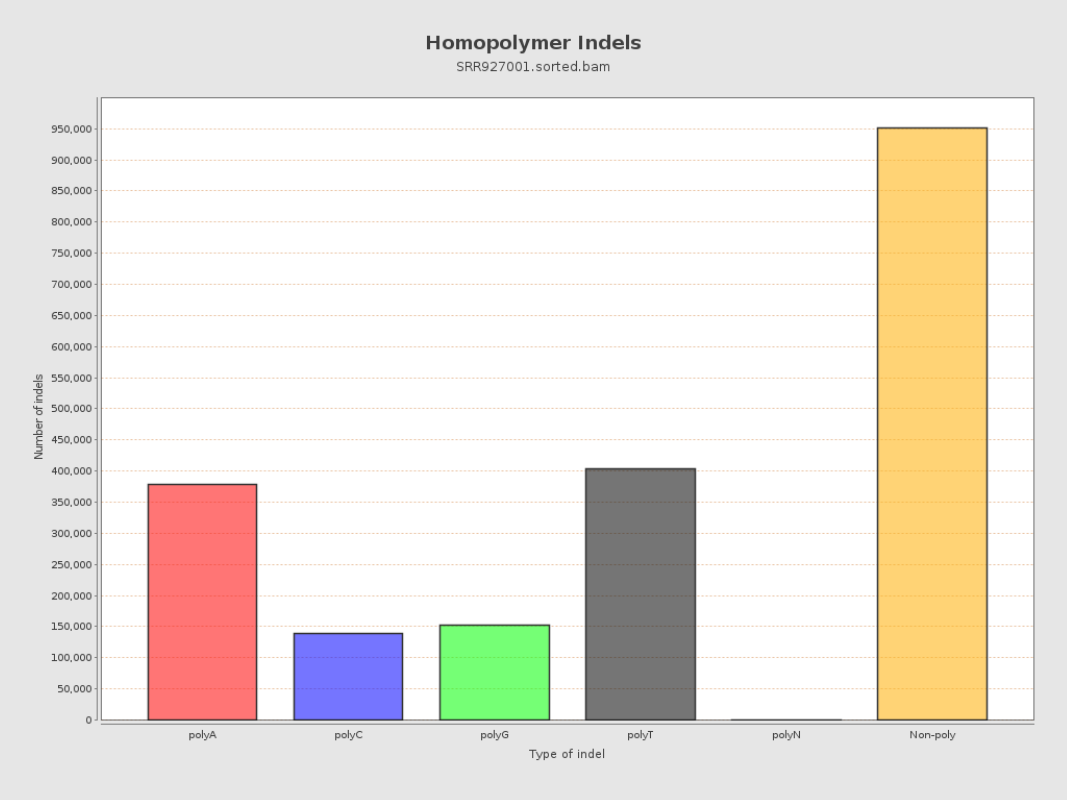
9. Results : Mapped Reads GC-content Distribution



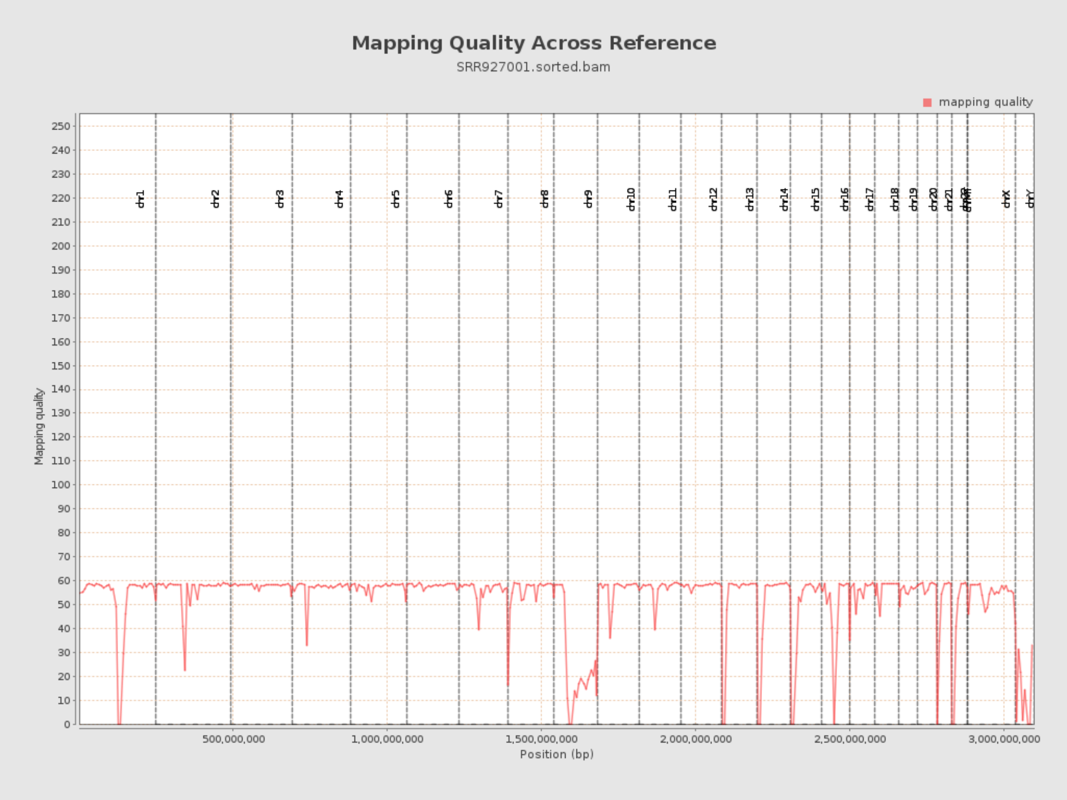
10. Results : Mapped Reads Clipping Profile



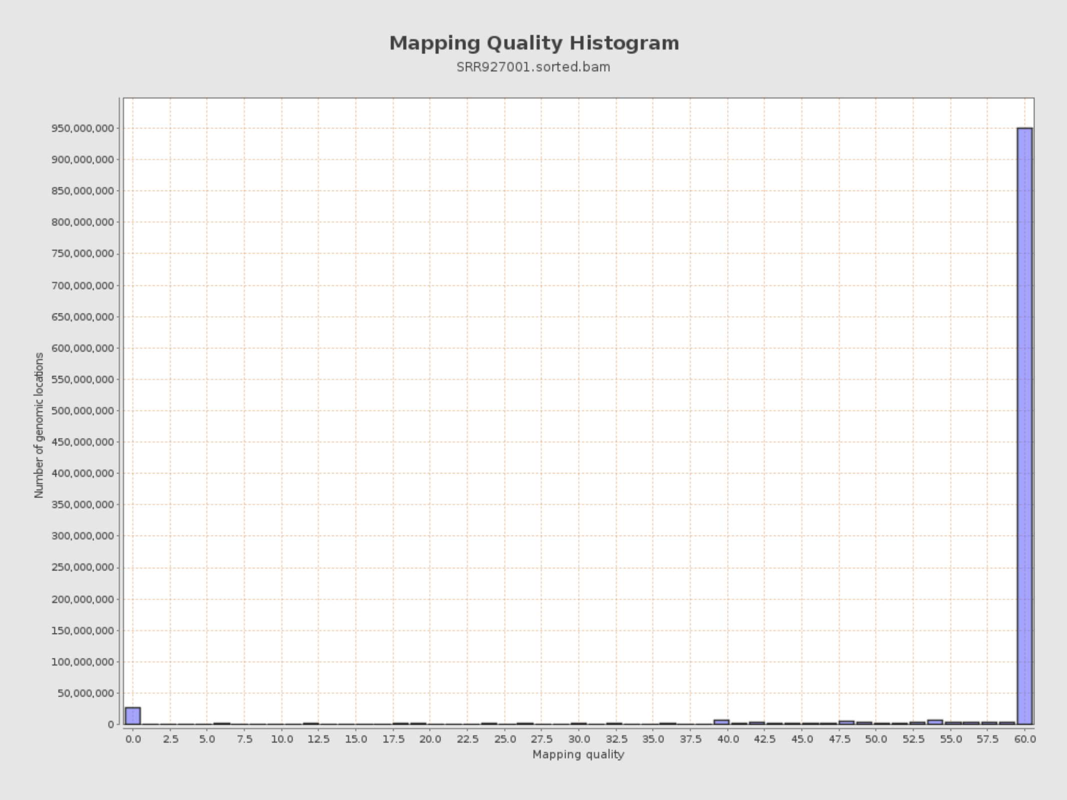
11. Results : Homopolymer Indels



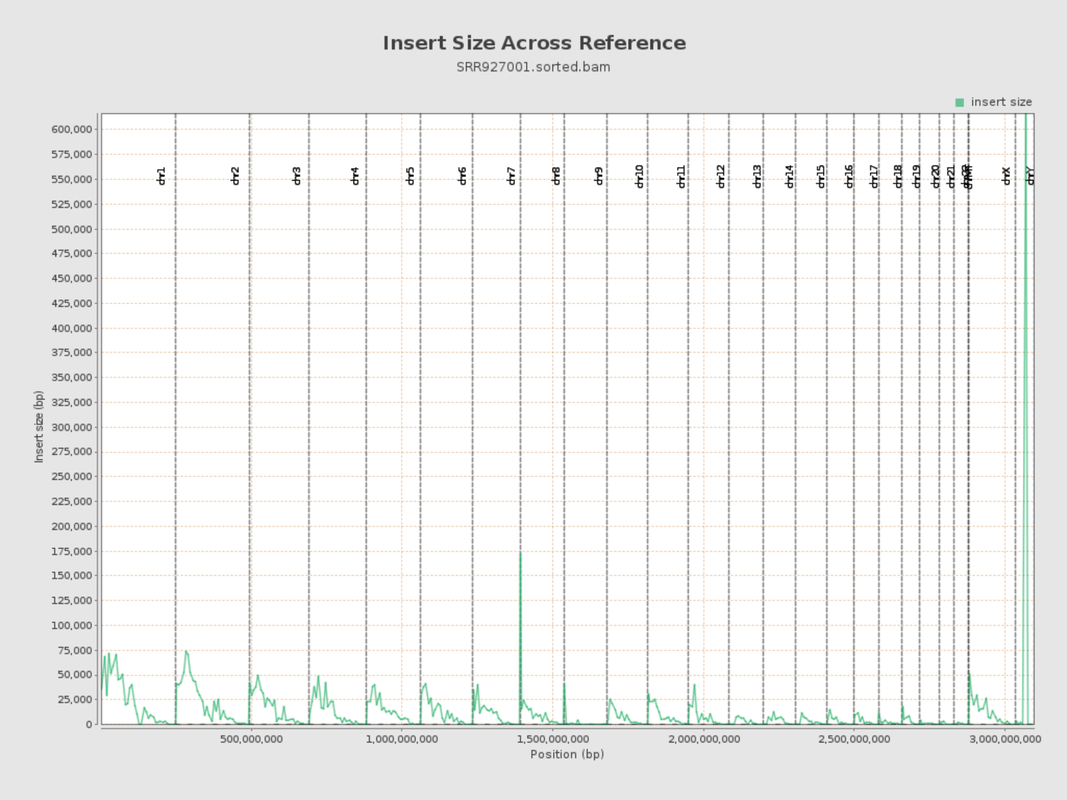
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram