Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/24 02:11:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927007.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_SRR927007 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927007_1.fastq.gz SRR927007_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 24 02:11:01 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927007.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	25,960,678
Mapped reads	25,287,029 / 97.41%
Unmapped reads	673,649 / 2.59%
Mapped paired reads	25,287,029 / 97.41%
Mapped reads, first in pair	12,680,316 / 48.84%
Mapped reads, second in pair	12,606,713 / 48.56%
Mapped reads, both in pair	24,858,616 / 95.75%
Mapped reads, singletons	428,413 / 1.65%
Secondary alignments	0
Supplementary alignments	1,065,206 / 4.1%
Read min/max/mean length	30 / 101 / 102.71
Duplicated reads (estimated)	2,407,001 / 9.27%
Duplication rate	7.49%
Clipped reads	12,385,084 / 47.71%

2.2. ACGT Content

Number/percentage of A's	652,065,289 / 28.67%
Number/percentage of C's	433,898,156 / 19.08%
Number/percentage of T's	669,621,168 / 29.44%
Number/percentage of G's	518,344,757 / 22.79%
Number/percentage of N's	426,791 / 0.02%

GC Percentage	41.87%

2.3. Coverage

Mean	0.7353
Standard Deviation	2.6703

2.4. Mapping Quality

Mean Mapping Quality	52.3

2.5. Insert size

Mean	472,277.23
Standard Deviation	6,726,848.32
P25/Median/P75	138 / 182 / 247

2.6. Mismatches and indels

General error rate	0.98%
Mismatches	21,642,384
Insertions	405,602
Mapped reads with at least one insertion	1.57%
Deletions	1,214,936
Mapped reads with at least one deletion	4.68%
Homopolymer indels	51.67%

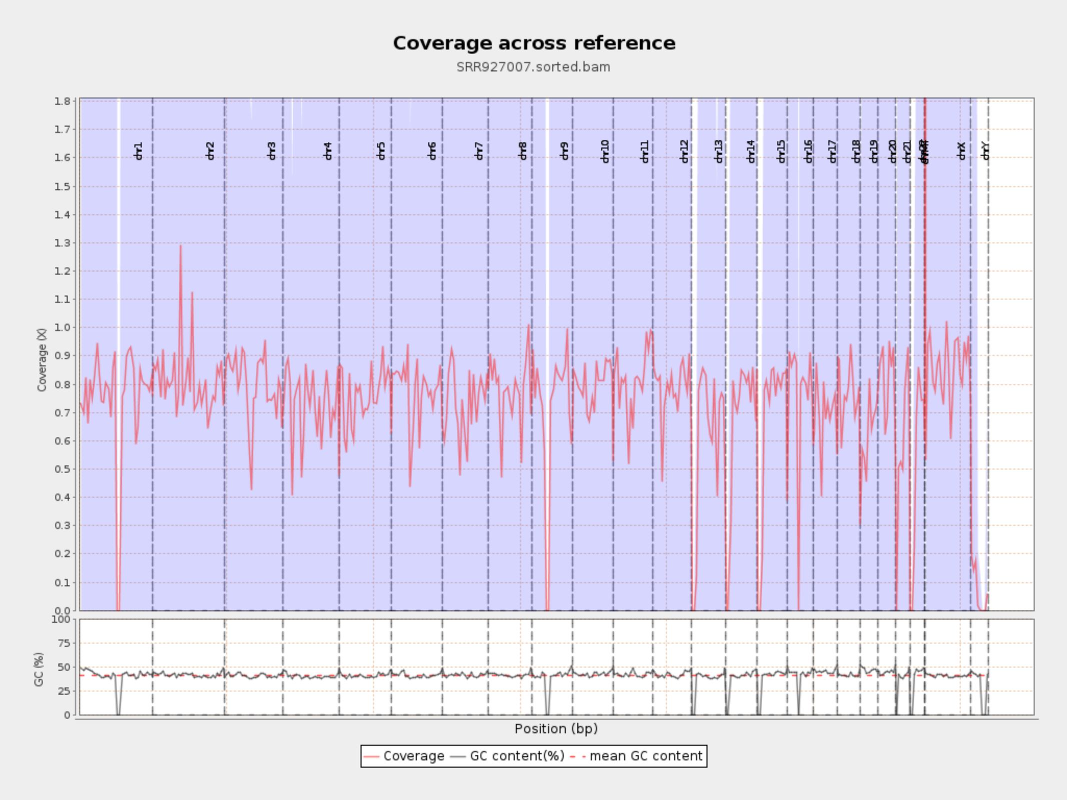
2.7. Chromosome stats

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

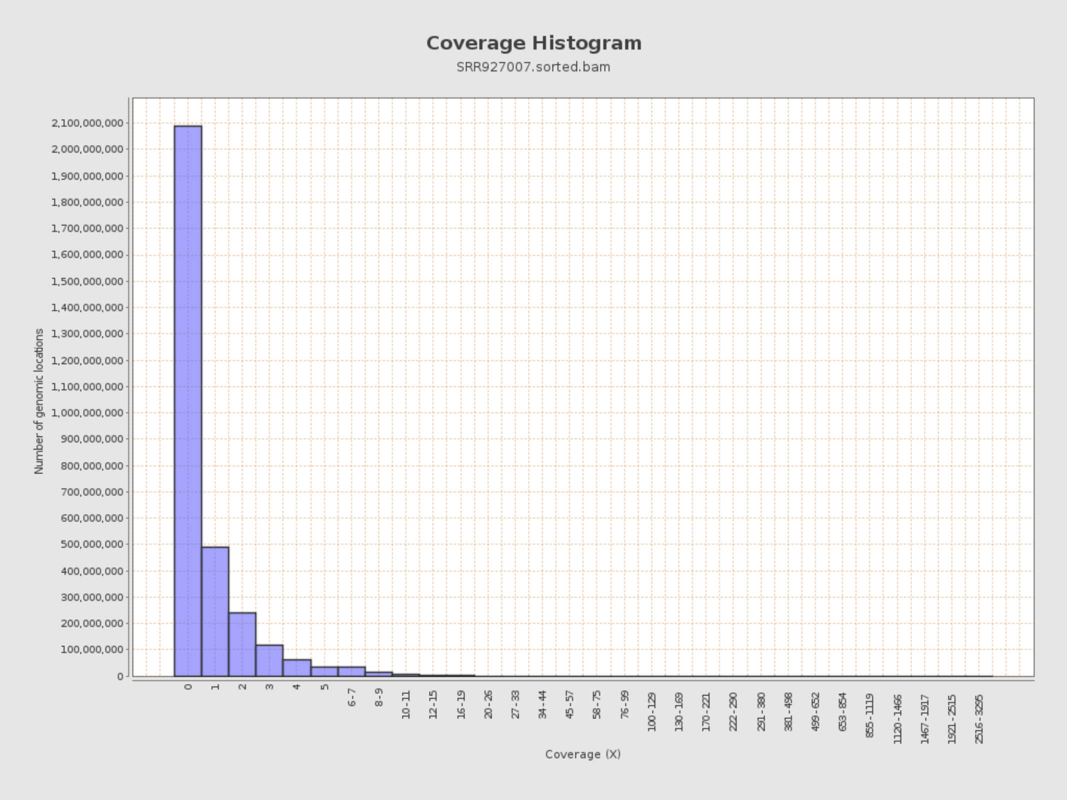
		bases	coverage	deviation
chr1	249250621	185825728	0.7455	3.6472
chr2	243199373	198908887	0.8179	5.0842
chr3	198022430	158326524	0.7995	1.5953
chr4	191154276	139442548	0.7295	1.9422
chr5	180915260	137617558	0.7607	1.5694
chr6	171115067	133733387	0.7815	2.3835
chr7	159138663	115956559	0.7287	1.9114
chr8	146364022	113774209	0.7773	1.7809
chr9	141213431	98803608	0.6997	3.1827
chr10	135534747	109071004	0.8047	3.2418
chr11	135006516	109236830	0.8091	2.4775
chr12	133851895	104934595	0.784	1.634
chr13	115169878	69083844	0.5998	1.3733
chr14	107349540	69726804	0.6495	1.5415
chr15	102531392	66474667	0.6483	1.4856
chr16	90354753	67075498	0.7424	3.3507
chr17	81195210	56058117	0.6904	1.6411
chr18	78077248	60879084	0.7797	3.0075
chr19	59128983	36621622	0.6194	2.4058
chr20	63025520	51703893	0.8204	1.7585
chr21	48129895	28569135	0.5936	2.4938
chr22	51304566	26440497	0.5154	1.4904
chrMT	16571	1612965	97.3366	81.1249
chrX	155270560	132142405	0.851	1.8259

chrY	59373566	4128442	0.0695	2.3633

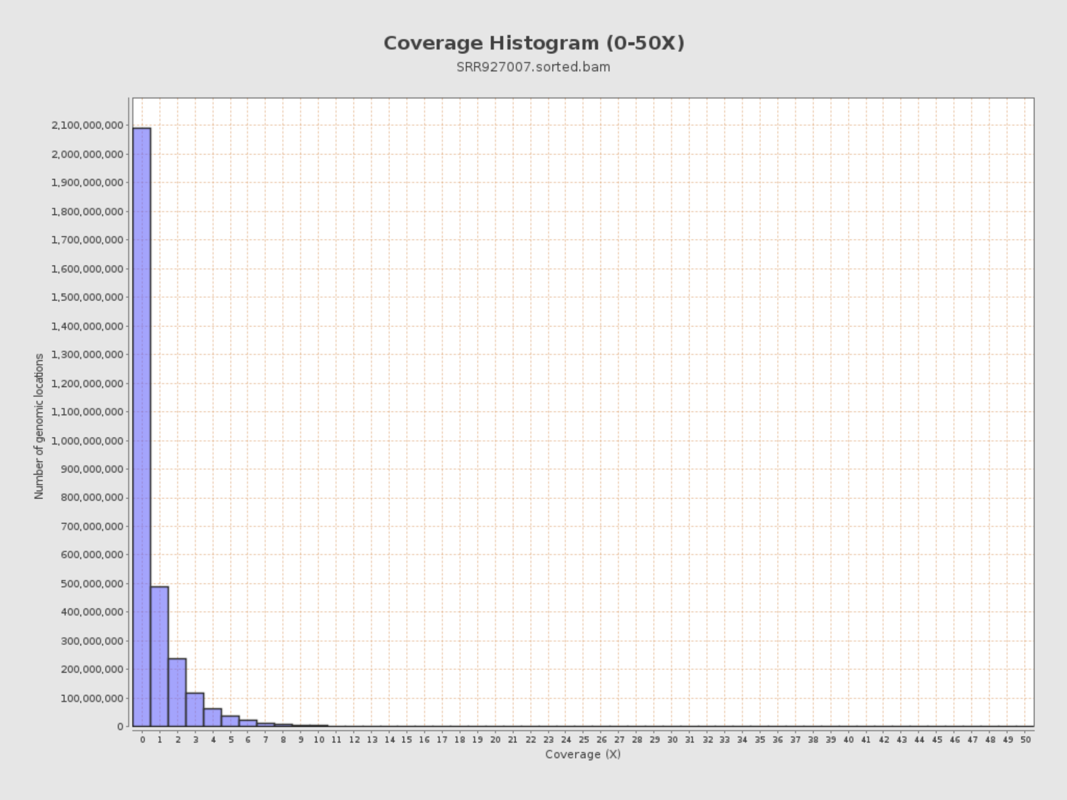
3. Results : Coverage across reference



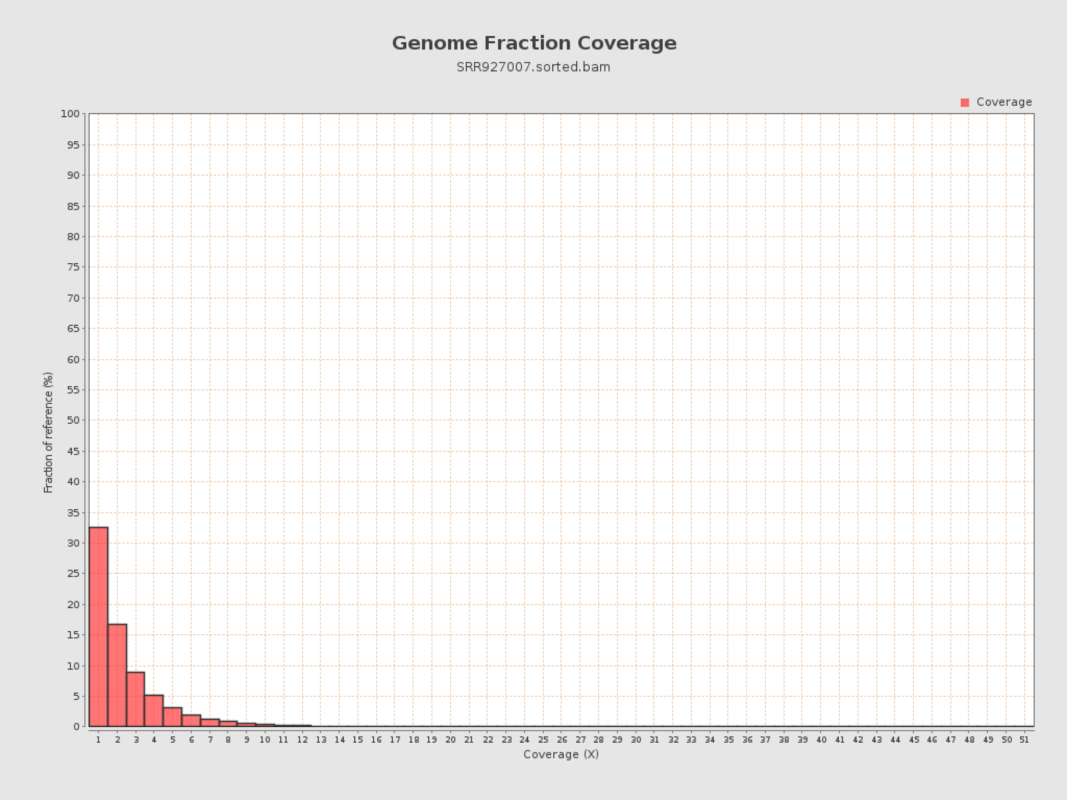
4. Results : Coverage Histogram



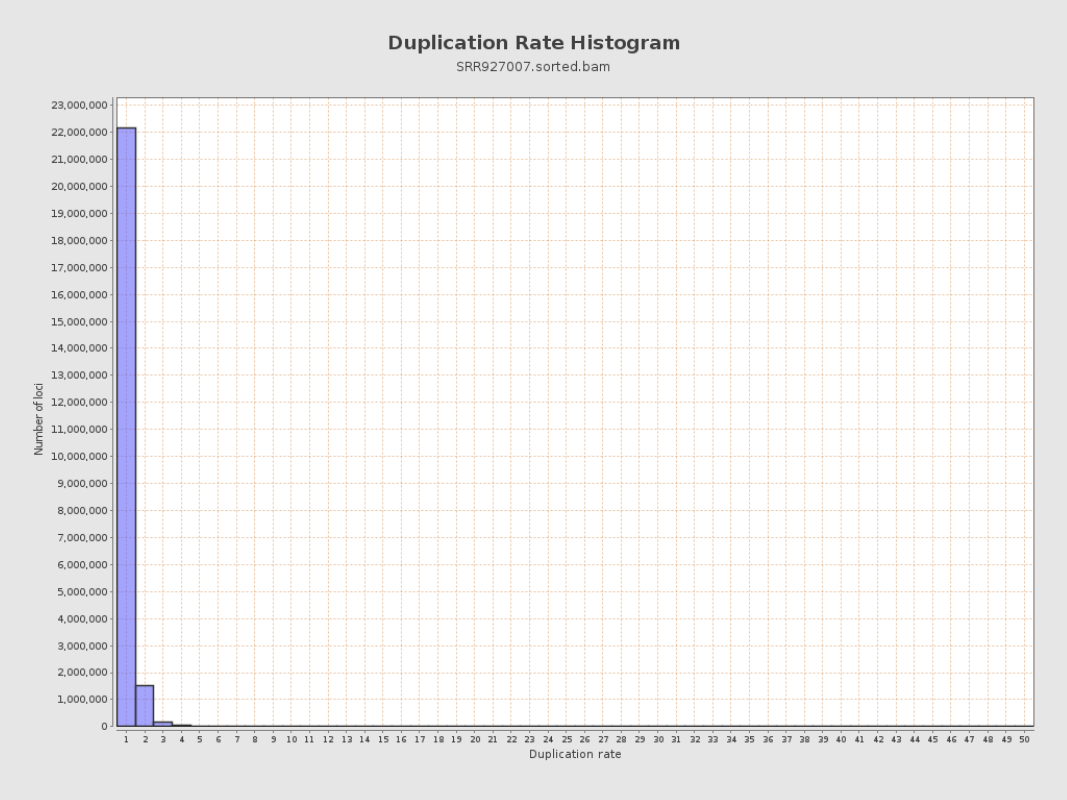
5. Results : Coverage Histogram (0-50X)



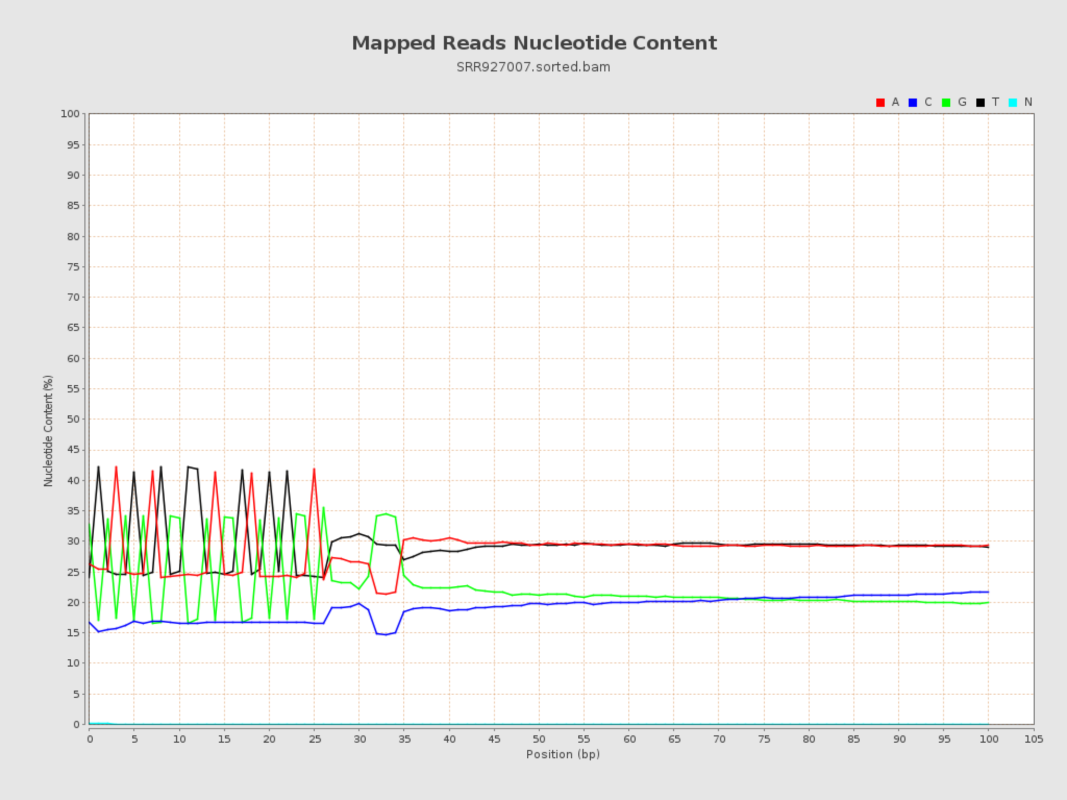
6. Results : Genome Fraction Coverage



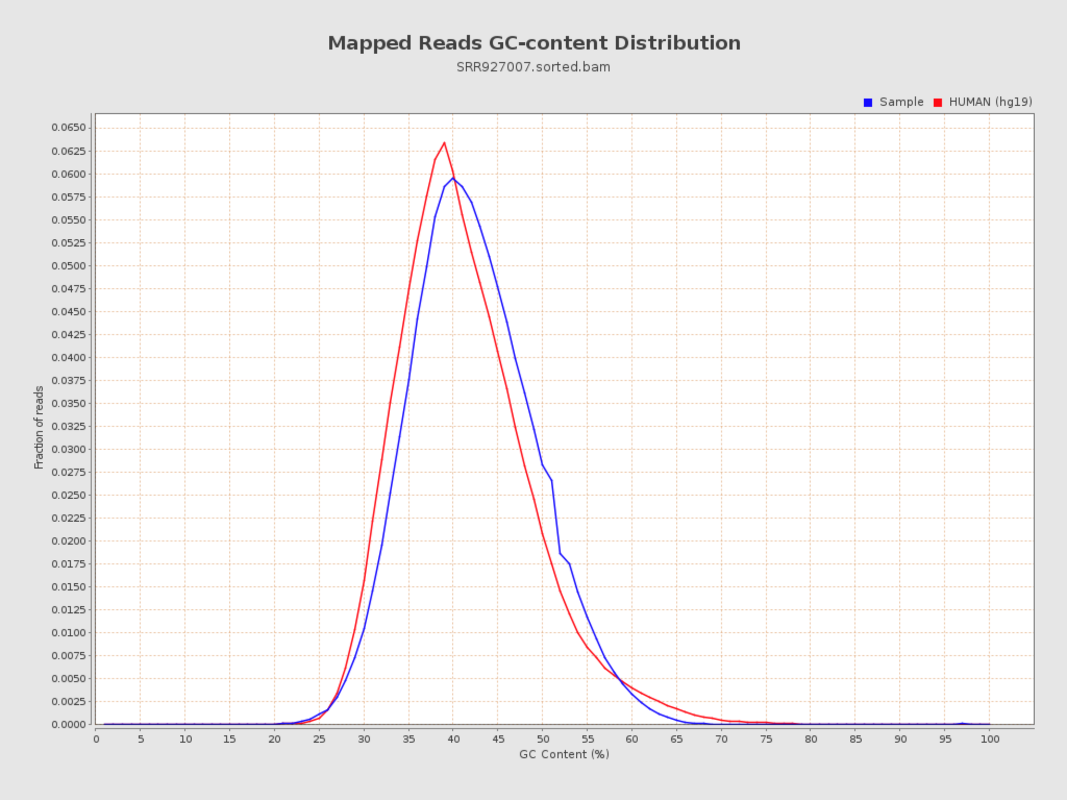
7. Results : Duplication Rate Histogram



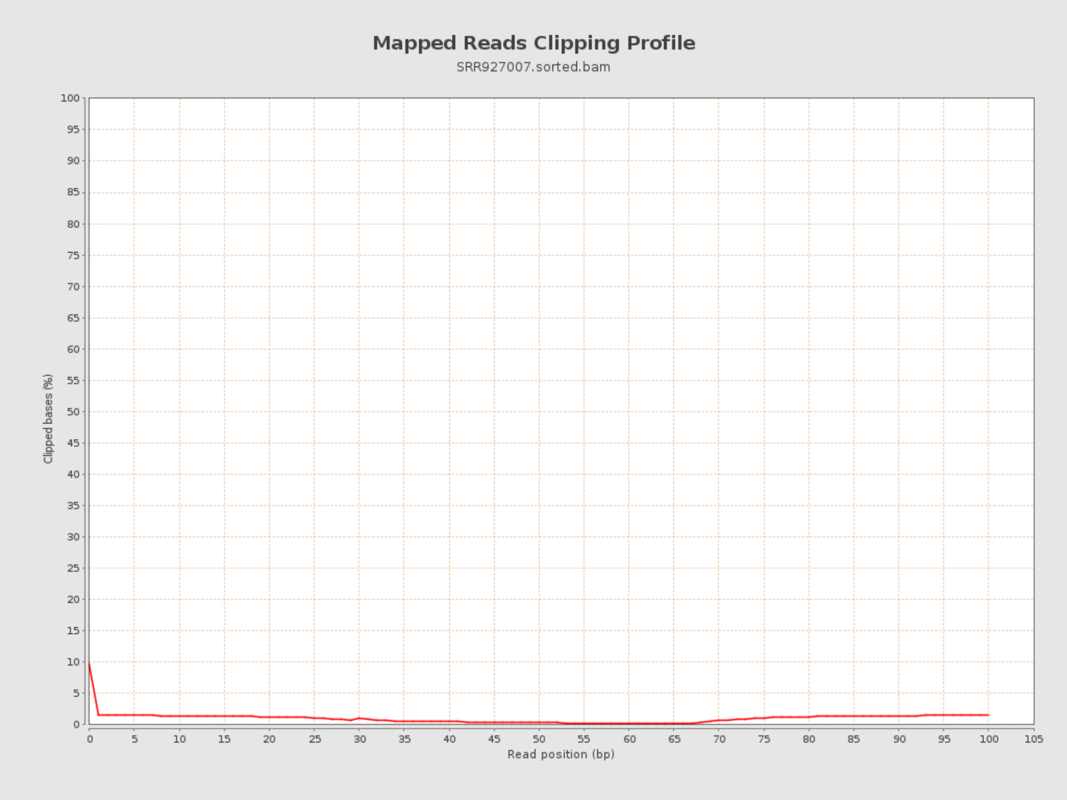
8. Results : Mapped Reads Nucleotide Content



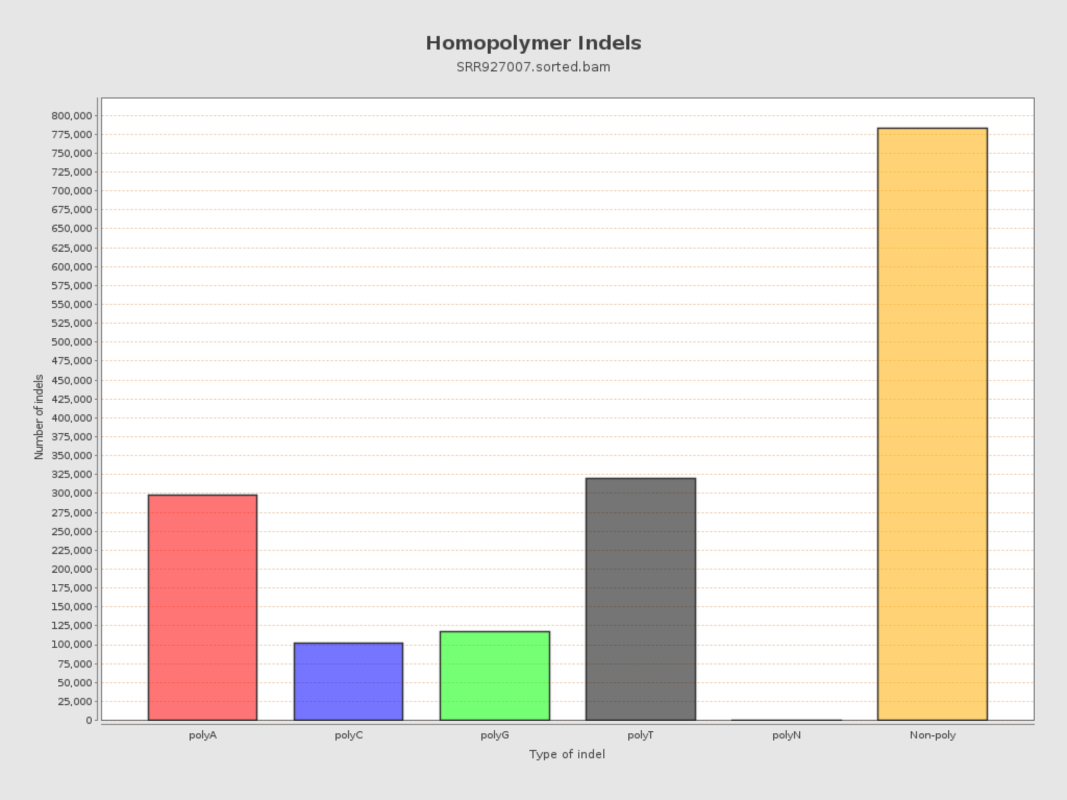
9. Results : Mapped Reads GC-content Distribution



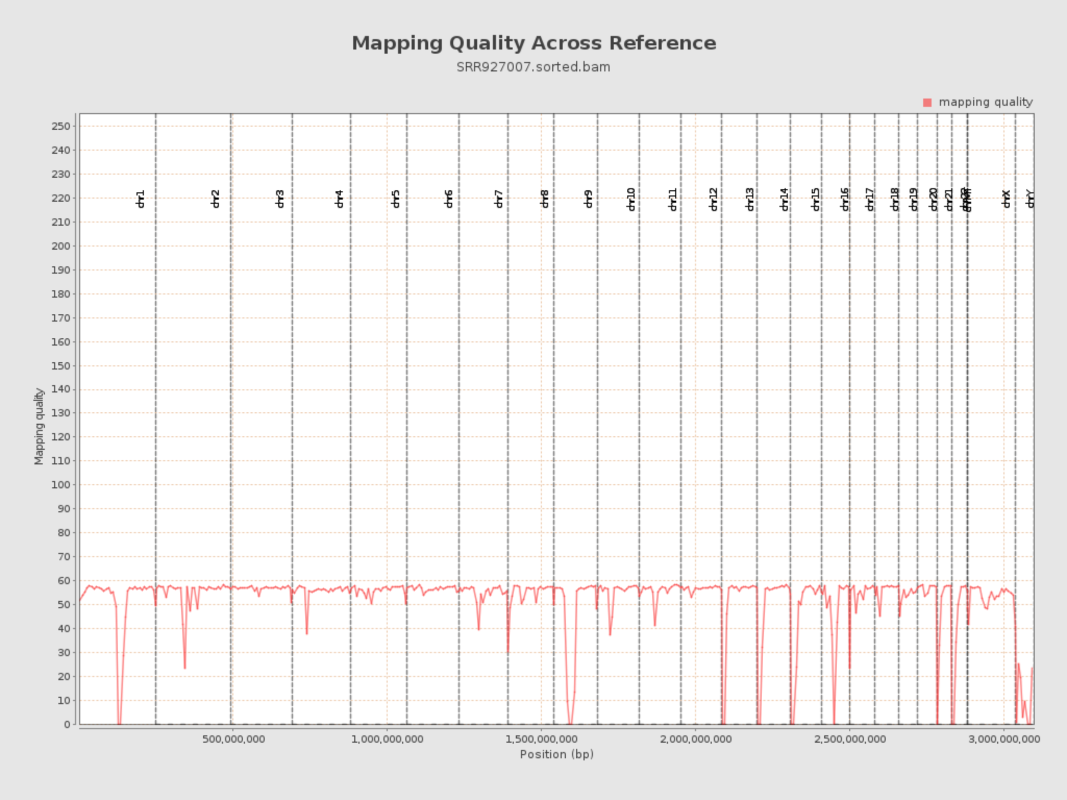
10. Results : Mapped Reads Clipping Profile



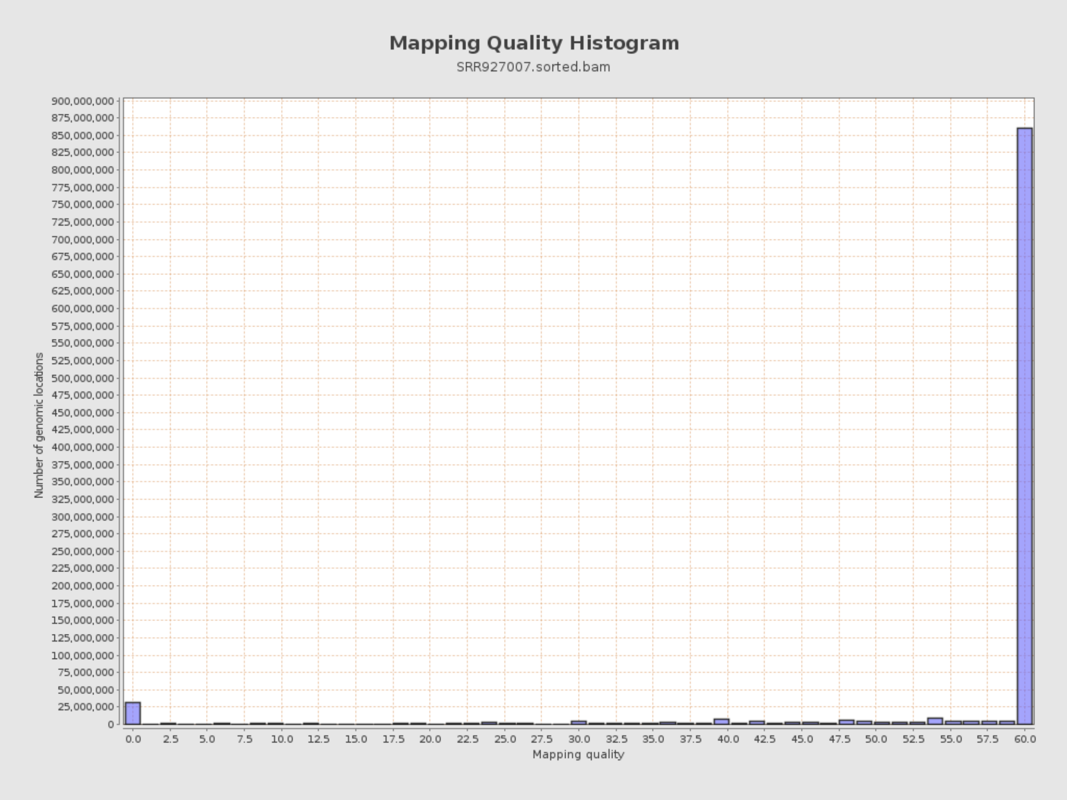
11. Results : Homopolymer Indels



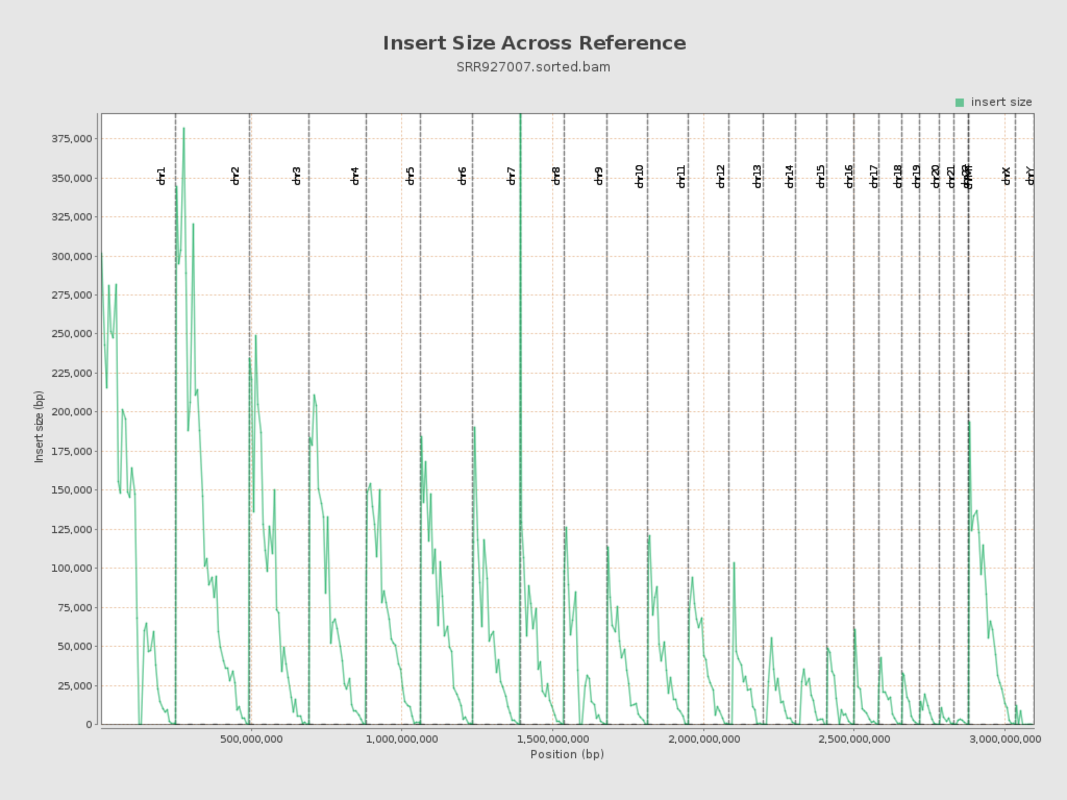
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram