Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/22 20:35:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926927.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_SRR926927 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926927_1.fastq.gz SRR926927_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 22 20:35:46 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926927.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,408,376
Mapped reads	10,486,669 / 91.92%
Unmapped reads	921,707 / 8.08%
Mapped paired reads	10,486,669 / 91.92%
Mapped reads, first in pair	5,258,282 / 46.09%
Mapped reads, second in pair	5,228,387 / 45.83%
Mapped reads, both in pair	10,289,024 / 90.19%
Mapped reads, singletons	197,645 / 1.73%
Secondary alignments	0
Supplementary alignments	319,232 / 2.8%
Read min/max/mean length	30 / 101 / 102.16
Duplicated reads (estimated)	638,780 / 5.6%
Duplication rate	4.99%
Clipped reads	4,844,283 / 42.46%

2.2. ACGT Content

Number/percentage of A's	268,052,339 / 28.43%
Number/percentage of C's	182,126,584 / 19.32%
Number/percentage of T's	273,416,176 / 29%
Number/percentage of G's	219,096,552 / 23.24%
Number/percentage of N's	180,169 / 0.02%

GC Percentage	42.55%

2.3. Coverage

Mean	0.3048
Standard Deviation	1.288

2.4. Mapping Quality

Mean Mapping Quality	52.58

2.5. Insert size

Mean	320,639.3
Standard Deviation	5,558,799.19
P25/Median/P75	139 / 184 / 254

2.6. Mismatches and indels

General error rate	0.99%
Mismatches	9,012,815
Insertions	160,006
Mapped reads with at least one insertion	1.5%
Deletions	498,802
Mapped reads with at least one deletion	4.63%
Homopolymer indels	51.92%

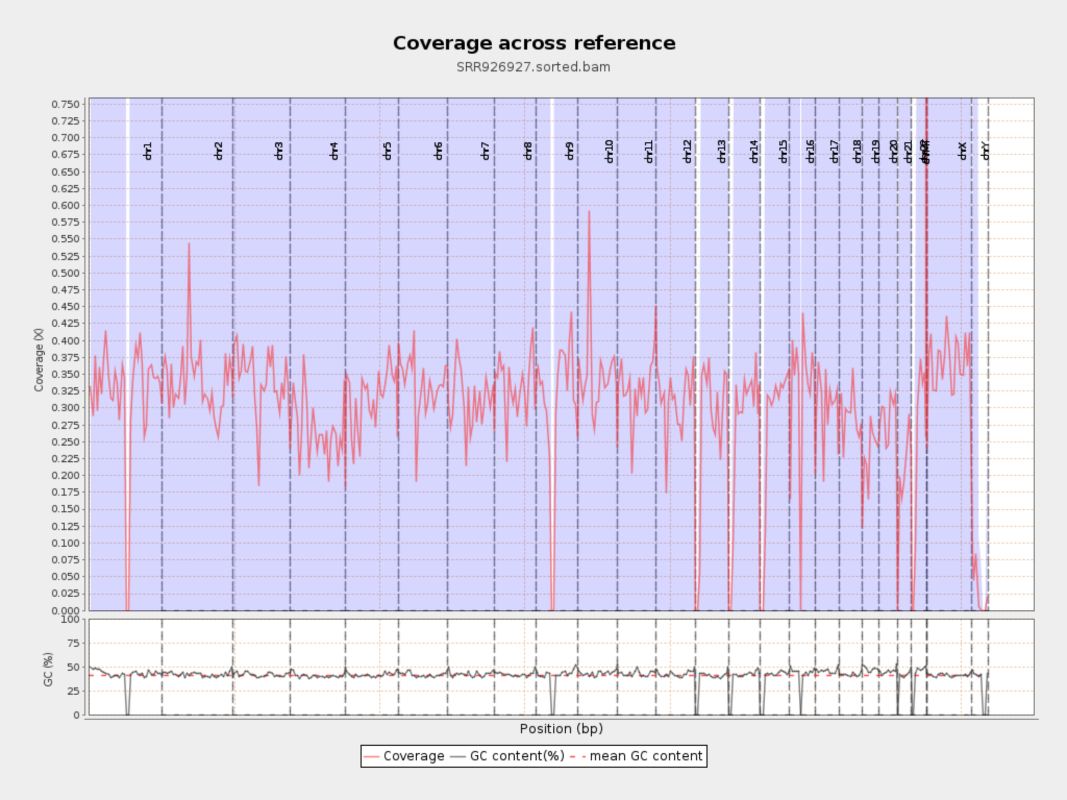
2.7. Chromosome stats

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

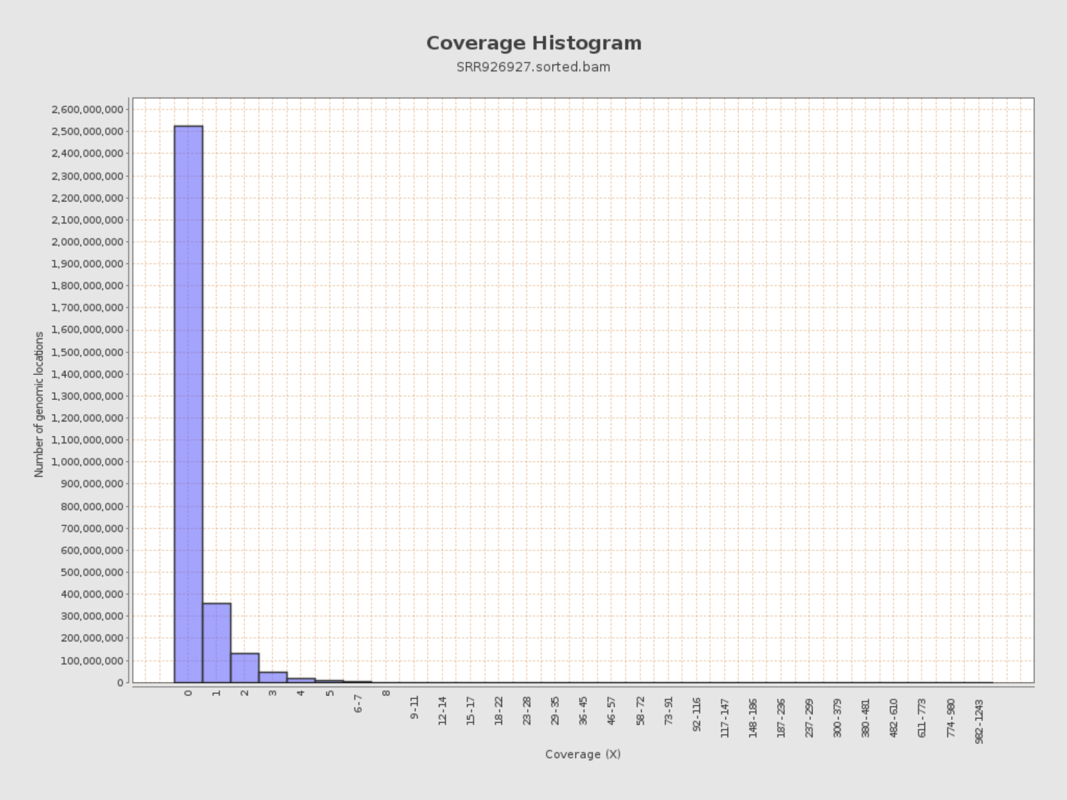
		bases	**coverage**	**deviation**
chr1	249250621	79474025	0.3189	1.225
chr2	243199373	82698035	0.34	1.974
chr3	198022430	67689382	0.3418	0.8494
chr4	191154276	51028129	0.2669	1.2561
chr5	180915260	56878620	0.3144	0.7957
chr6	171115067	57400077	0.3354	1.4739
chr7	159138663	49657645	0.312	0.9839
chr8	146364022	48887743	0.334	0.9137
chr9	141213431	42714600	0.3025	1.4191
chr10	135534747	47509592	0.3505	2.7985
chr11	135006516	44062533	0.3264	1.113
chr12	133851895	41568242	0.3106	0.8318
chr13	115169878	30270990	0.2628	0.733
chr14	107349540	28334915	0.264	0.7494
chr15	102531392	27114525	0.2645	0.7527
chr16	90354753	29375212	0.3251	1.5632
chr17	81195210	24667434	0.3038	0.9245
chr18	78077248	22665503	0.2903	1.4131
chr19	59128983	13705969	0.2318	0.9706
chr20	63025520	18012266	0.2858	0.8211
chr21	48129895	9608346	0.1996	0.9856
chr22	51304566	11766798	0.2294	0.7157
chrMT	16571	57635	3.4781	3.4662
chrX	155270560	56793885	0.3658	0.9318

chrY	59373566	1656118	0.0279	1.0051

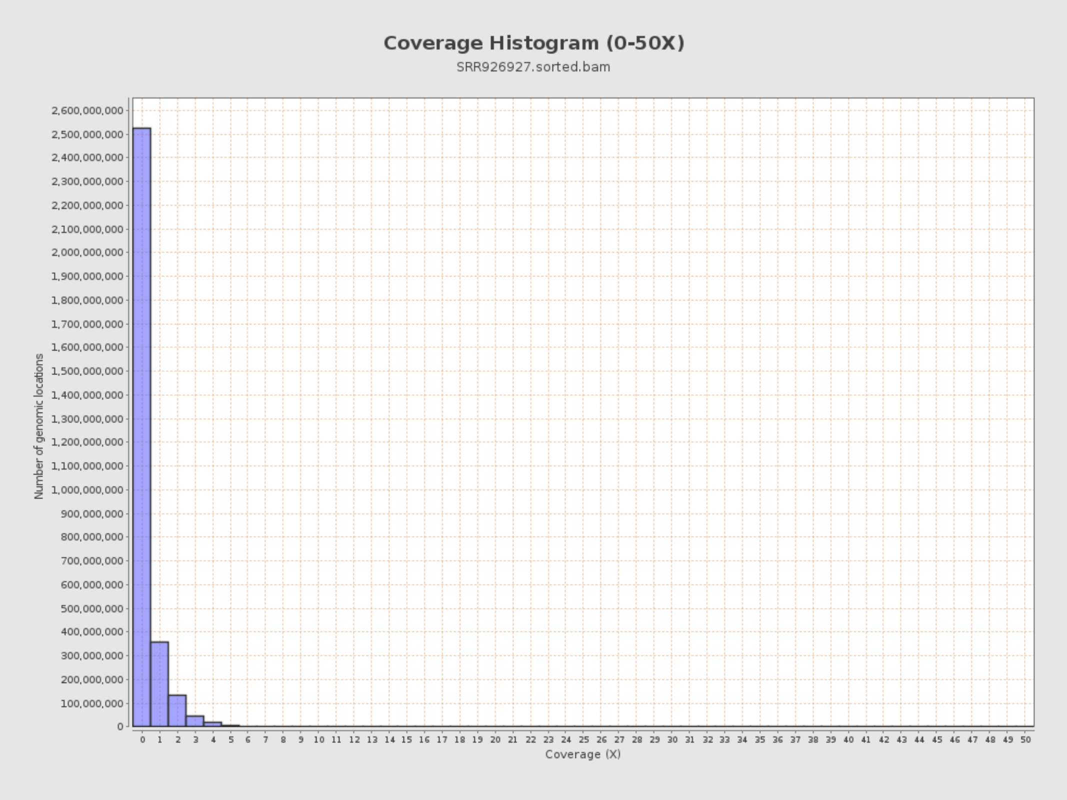
3. Results : Coverage across reference



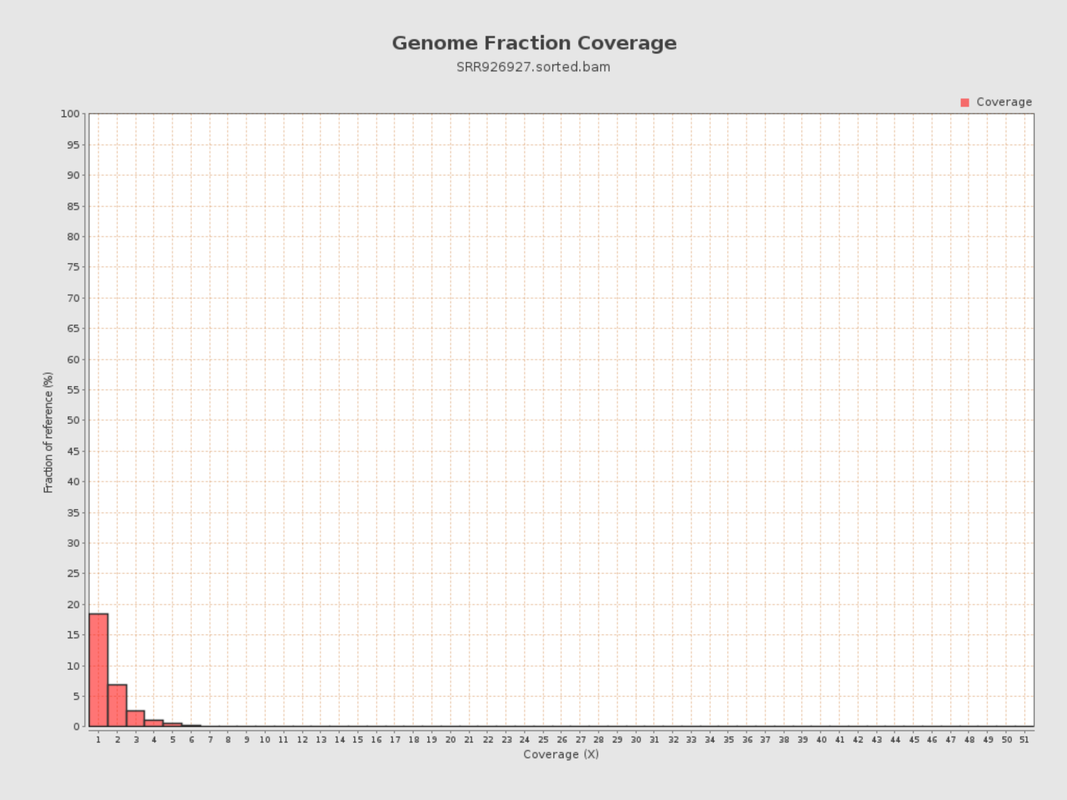
4. Results : Coverage Histogram



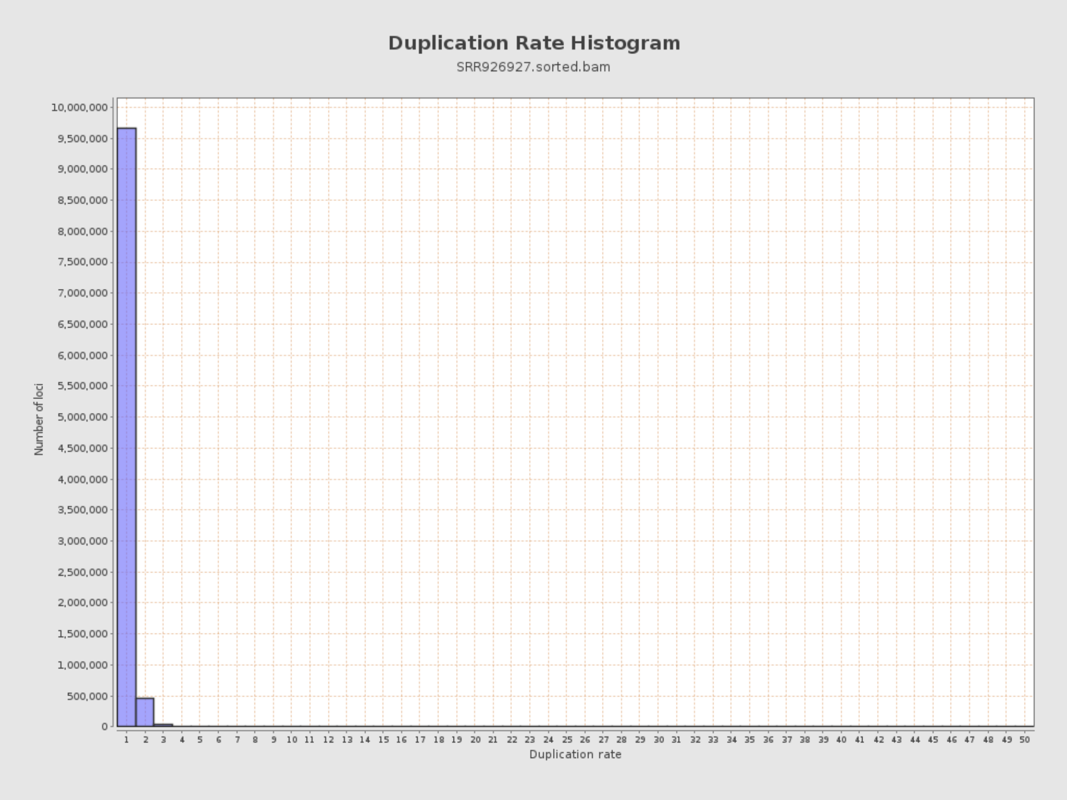
5. Results : Coverage Histogram (0-50X)



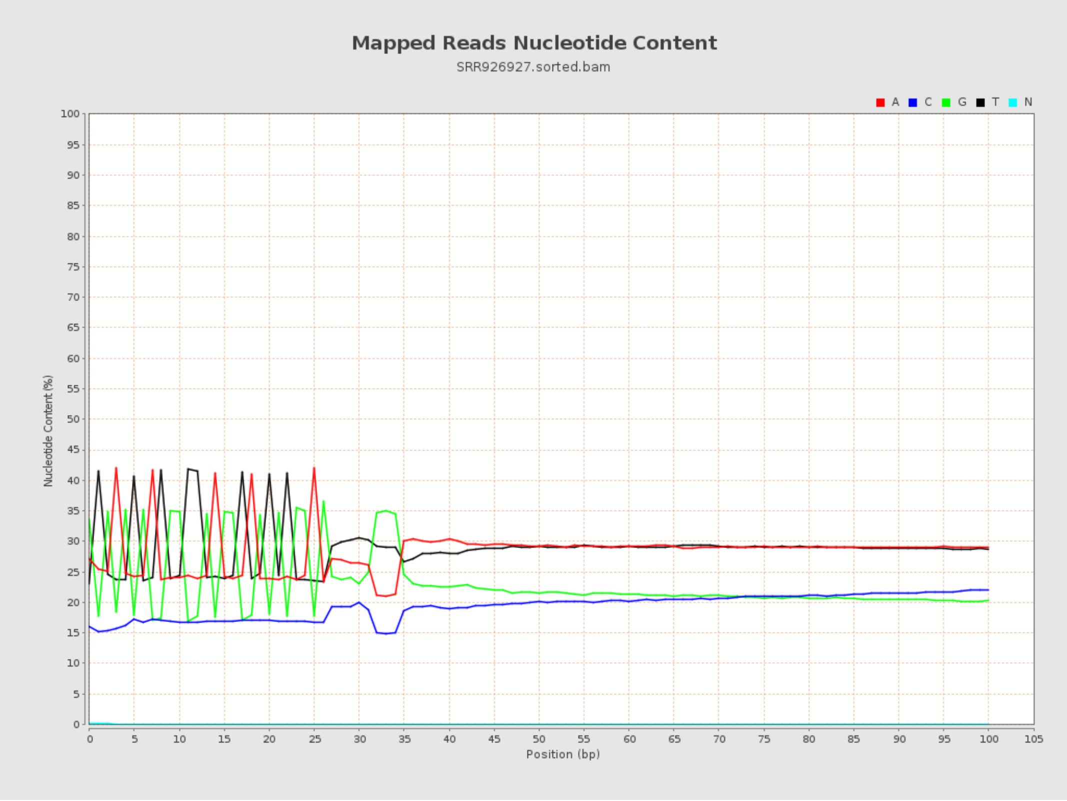
6. Results : Genome Fraction Coverage



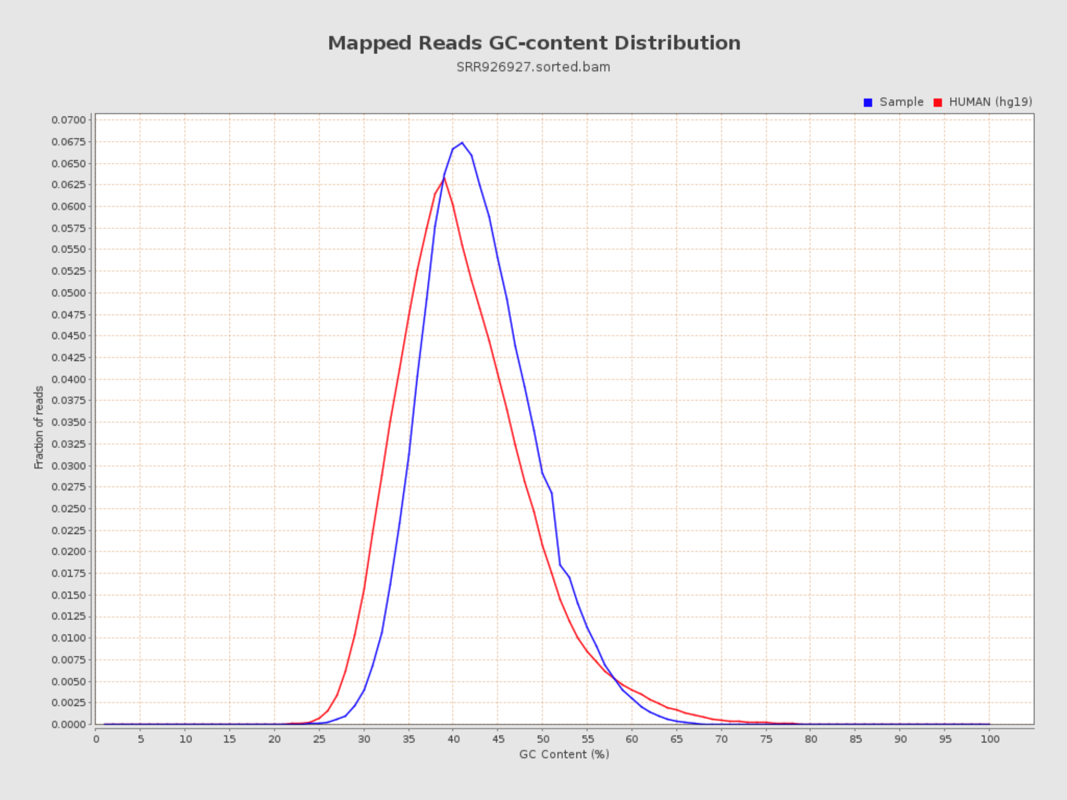
7. Results : Duplication Rate Histogram



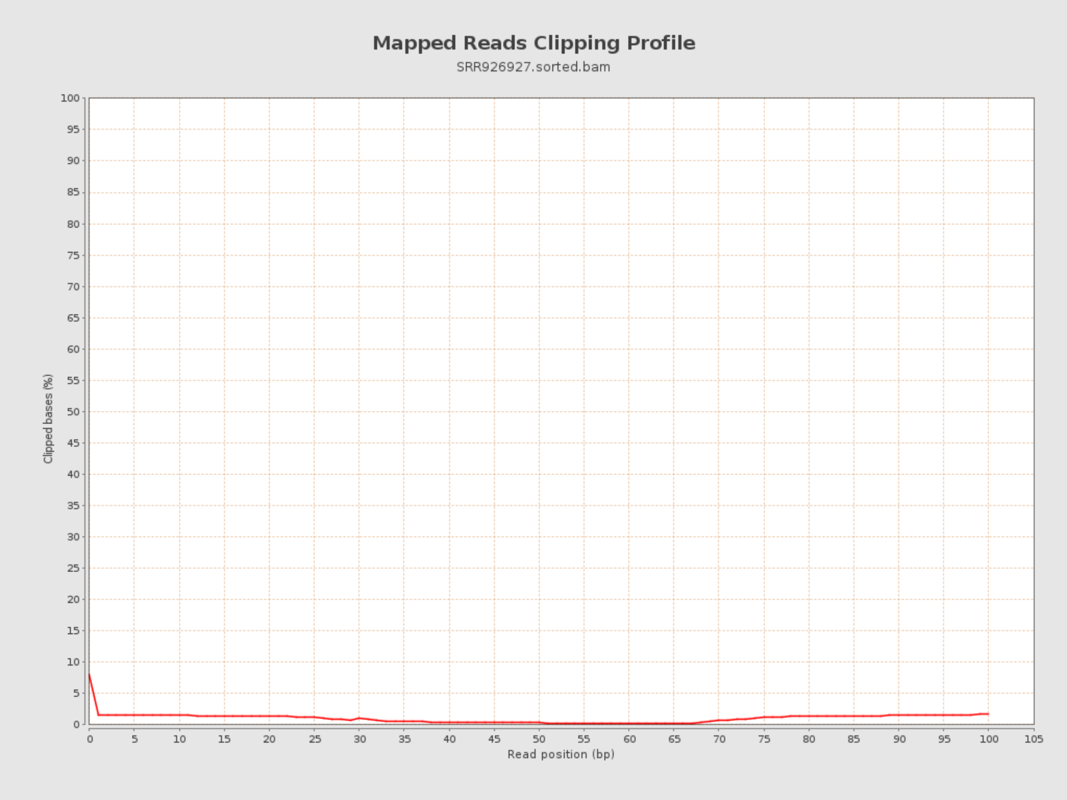
8. Results : Mapped Reads Nucleotide Content



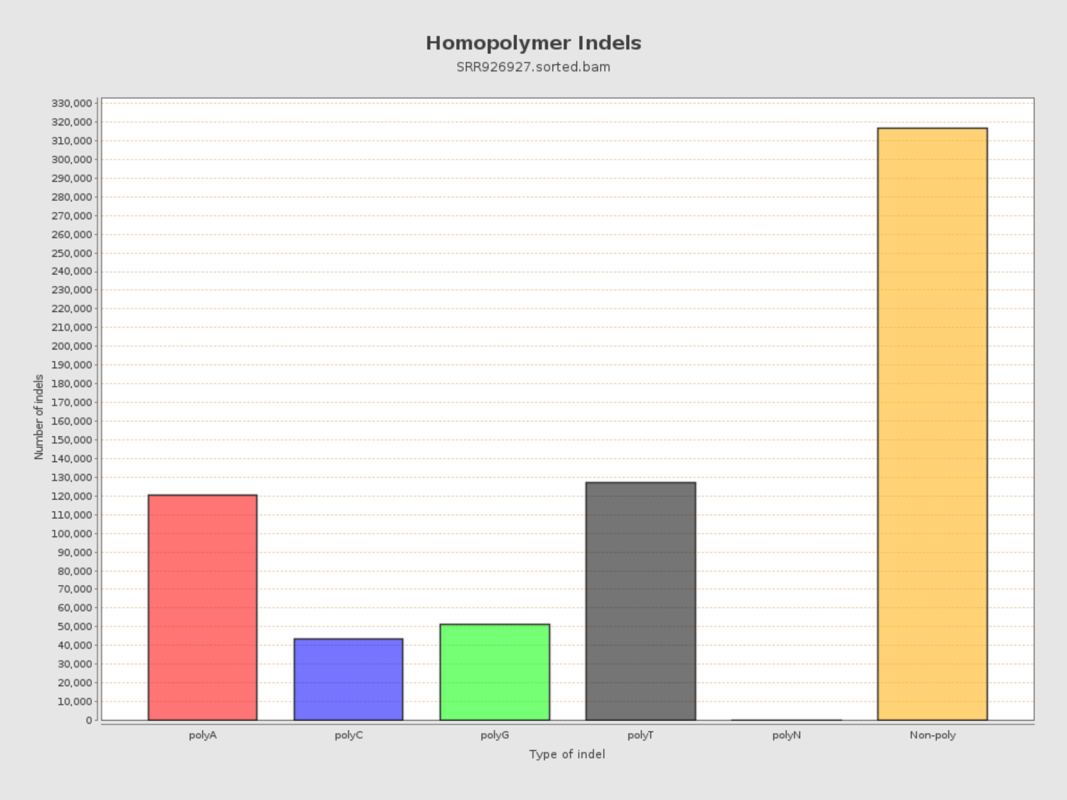
9. Results : Mapped Reads GC-content Distribution



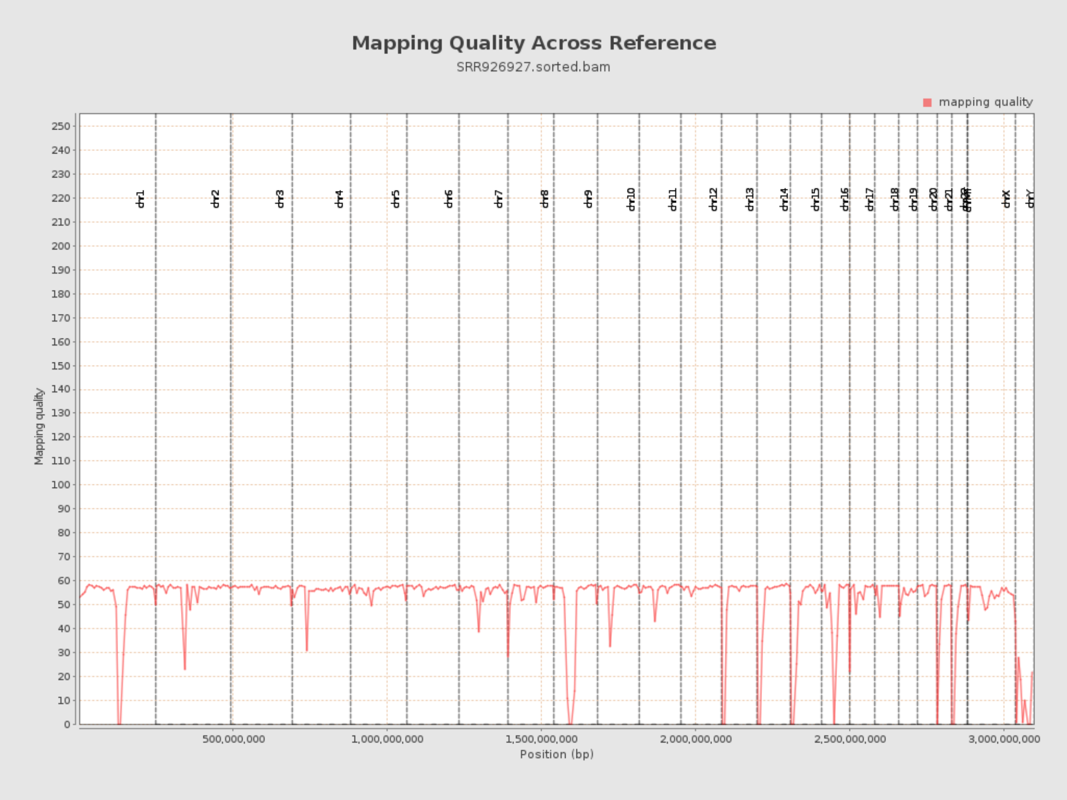
10. Results : Mapped Reads Clipping Profile



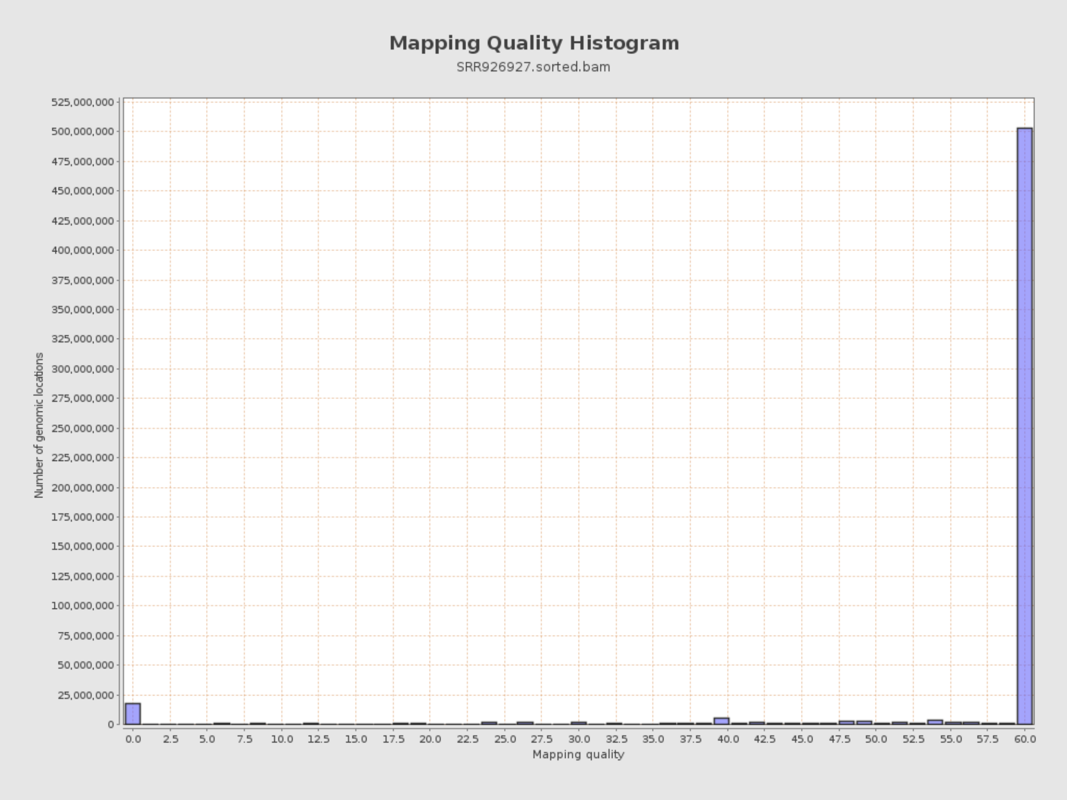
11. Results : Homopolymer Indels



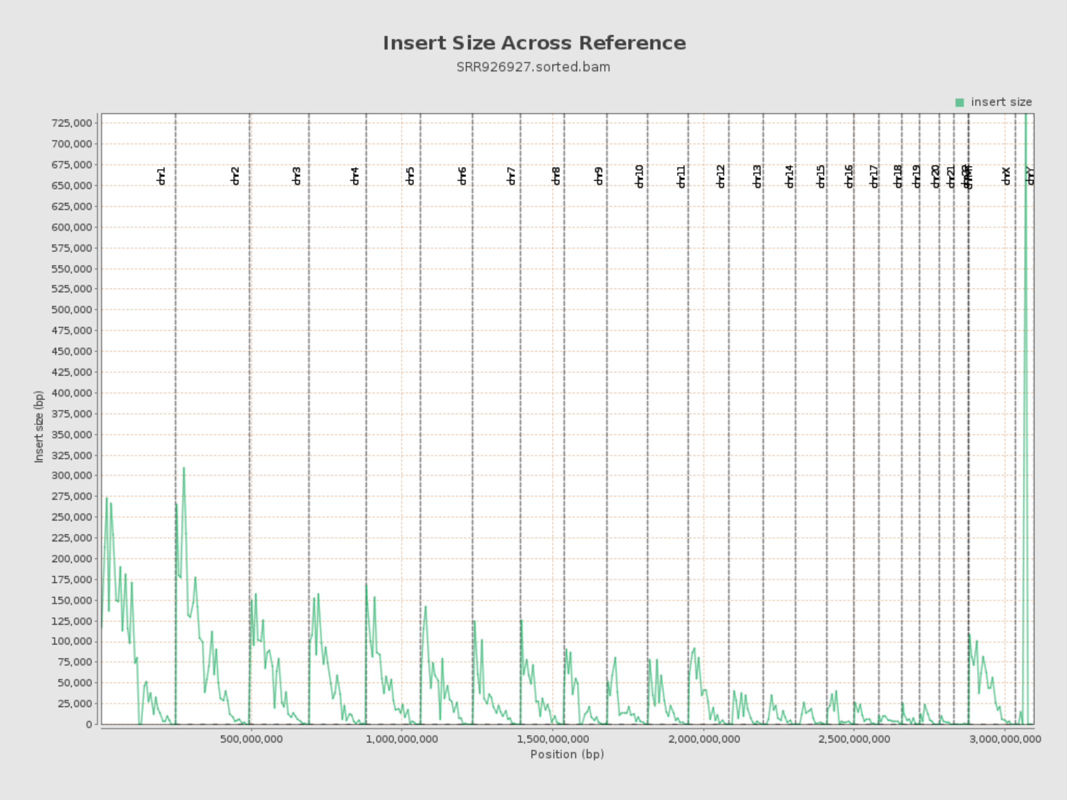
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram