Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/24 02:49:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927009.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_SRR927009 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927009_1.fastq.gz SRR927009_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 24 02:49:16 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927009.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	22,971,152
Mapped reads	22,367,101 / 97.37%
Unmapped reads	604,051 / 2.63%
Mapped paired reads	22,367,101 / 97.37%
Mapped reads, first in pair	11,198,766 / 48.75%
Mapped reads, second in pair	11,168,335 / 48.62%
Mapped reads, both in pair	21,975,406 / 95.67%
Mapped reads, singletons	391,695 / 1.71%
Secondary alignments	0
Supplementary alignments	379,982 / 1.65%
Read min/max/mean length	30 / 101 / 101.69
Duplicated reads (estimated)	1,742,691 / 7.59%
Duplication rate	6.12%
Clipped reads	7,711,902 / 33.57%

2.2. ACGT Content

Number/percentage of A's	601,404,170 / 29.17%
Number/percentage of C's	388,694,270 / 18.85%
Number/percentage of T's	614,223,490 / 29.79%
Number/percentage of G's	457,186,912 / 22.17%
Number/percentage of N's	386,107 / 0.02%

GC Percentage	41.02%

2.3. Coverage

Mean	0.6666
Standard Deviation	2.6336

2.4. Mapping Quality

Mean Mapping Quality	51.82

2.5. Insert size

Mean	213,721.11
Standard Deviation	4,508,361.68
P25/Median/P75	191 / 247 / 316

2.6. Mismatches and indels

General error rate	1.02%
Mismatches	20,428,814
Insertions	352,142
Mapped reads with at least one insertion	1.55%
Deletions	1,130,831
Mapped reads with at least one deletion	4.92%
Homopolymer indels	53.07%

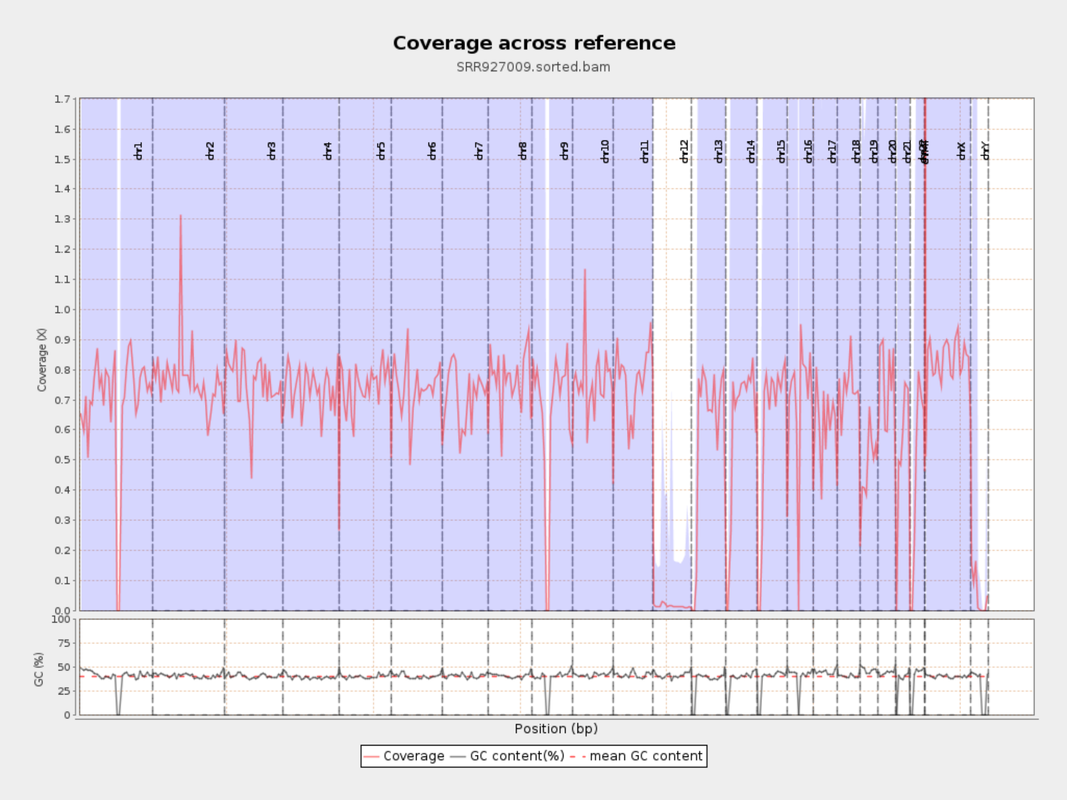
2.7. Chromosome stats

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

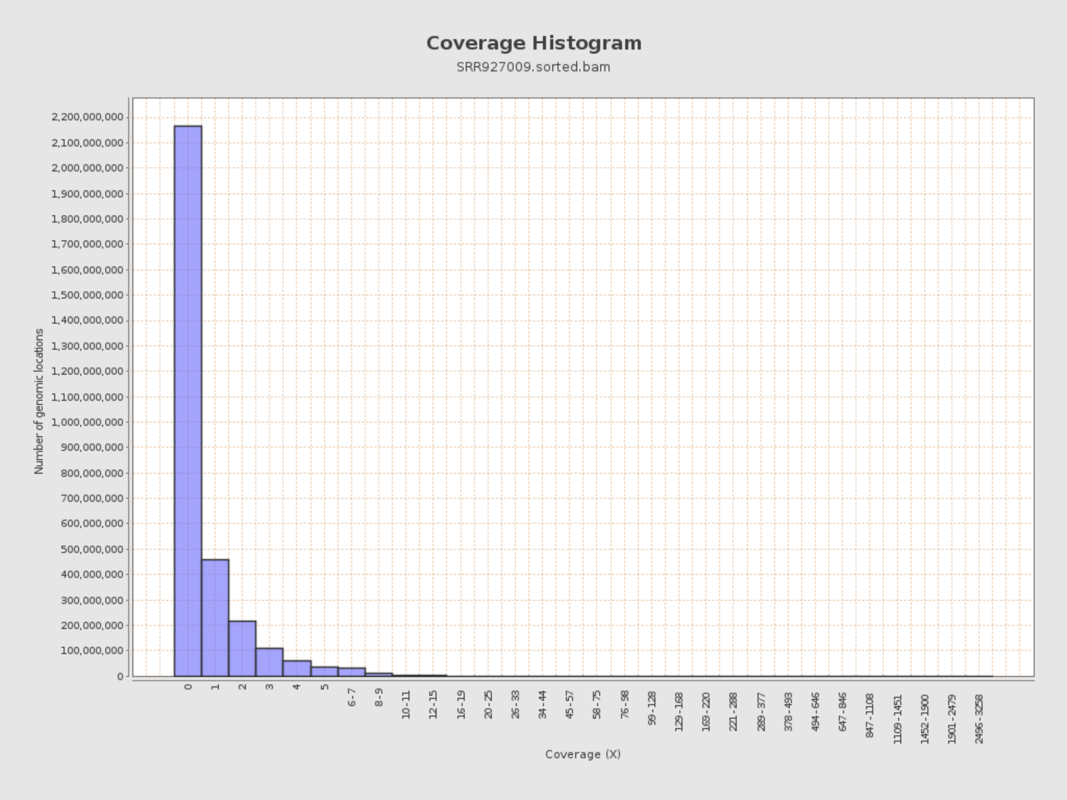
		bases	coverage	deviation
chr1	249250621	173207728	0.6949	3.6874
chr2	243199373	187275851	0.7701	4.2149
chr3	198022430	149962841	0.7573	1.4957
chr4	191154276	141270850	0.739	1.8899
chr5	180915260	134963664	0.746	1.4824
chr6	171115067	127556102	0.7454	2.445
chr7	159138663	113173448	0.7112	2.2328
chr8	146364022	113278708	0.774	1.7549
chr9	141213431	91077433	0.645	3.1921
chr10	135534747	104051333	0.7677	5.128
chr11	135006516	102756714	0.7611	2.3962
chr12	133851895	1976793	0.0148	0.3057
chr13	115169878	68598868	0.5956	1.3237
chr14	107349540	65237494	0.6077	1.3896
chr15	102531392	62299462	0.6076	1.3931
chr16	90354753	61277785	0.6782	3.2701
chr17	81195210	49938618	0.615	1.6895
chr18	78077248	57969391	0.7425	3.0682
chr19	59128983	28726245	0.4858	2.4764
chr20	63025520	46985769	0.7455	1.5937
chr21	48129895	26310520	0.5467	2.1291
chr22	51304566	23745731	0.4628	1.2396
chrMT	16571	536696	32.3877	23.44
chrX	155270560	128068175	0.8248	1.8212

chrY	59373566	3253278	0.0548	1.7264

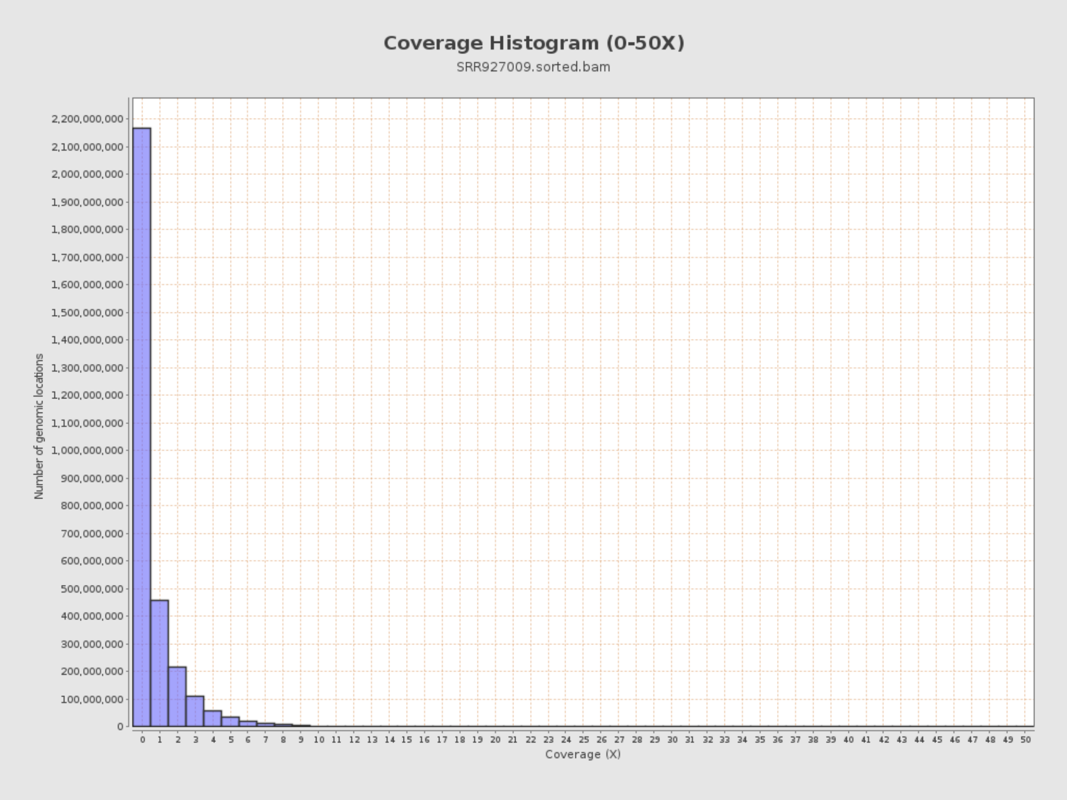
3. Results : Coverage across reference



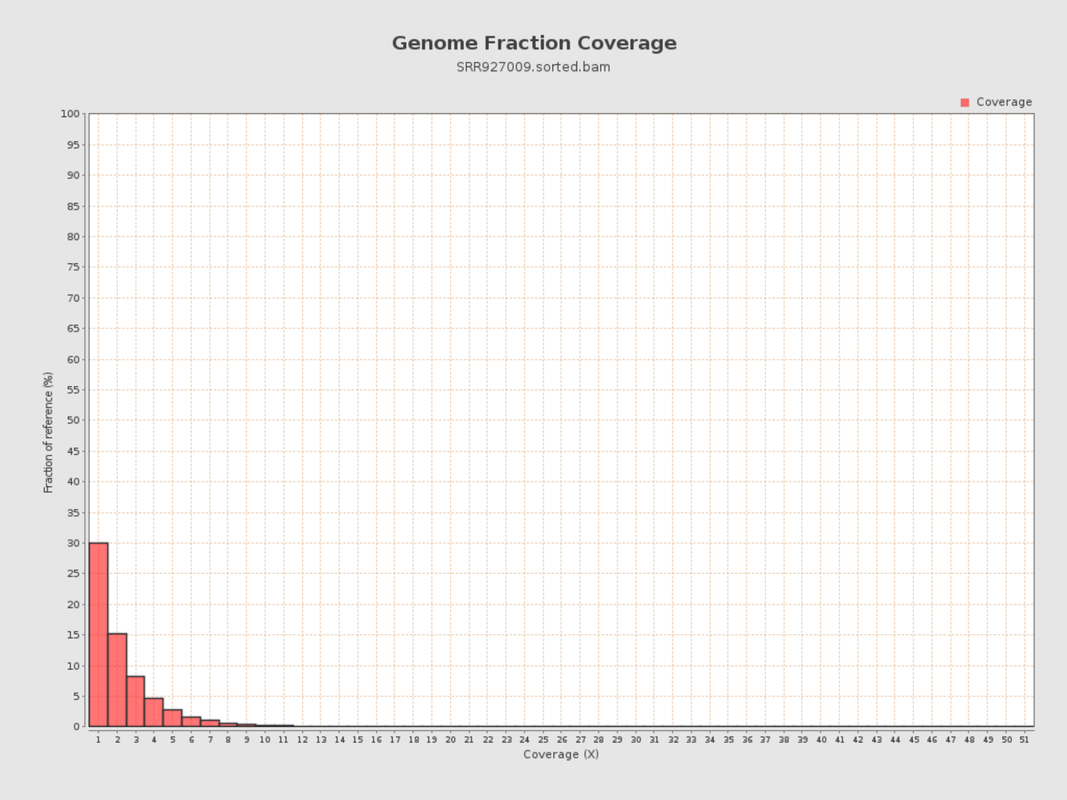
4. Results : Coverage Histogram



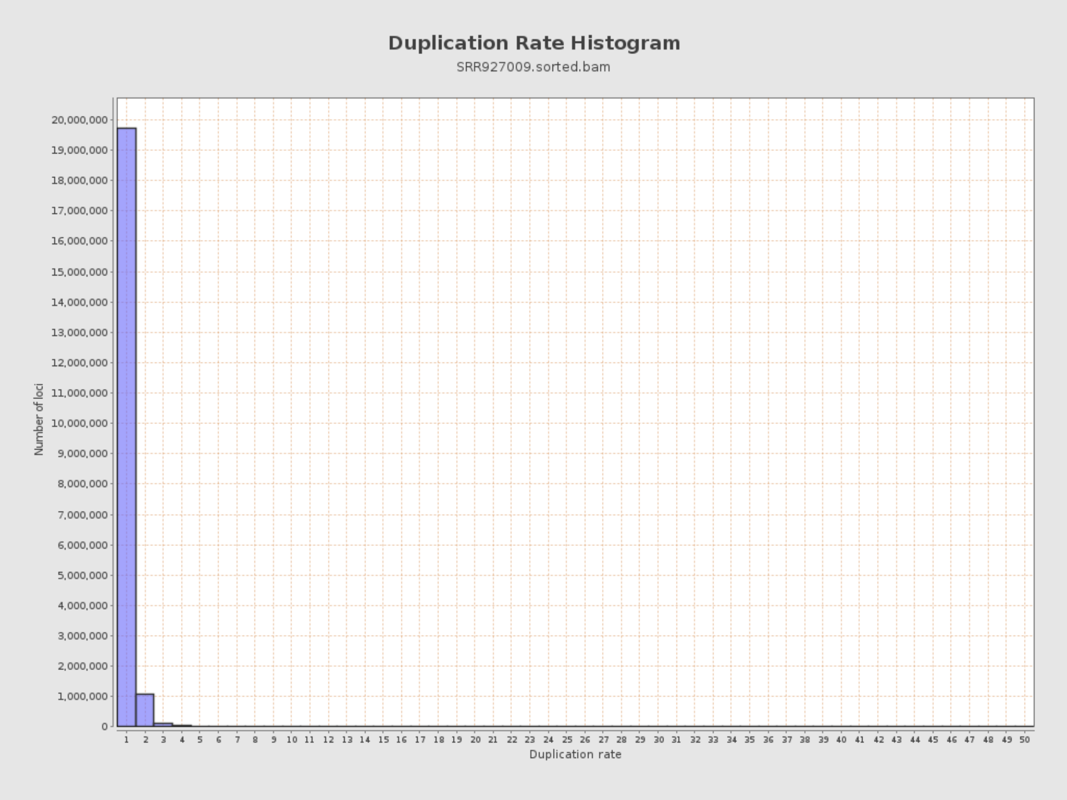
5. Results : Coverage Histogram (0-50X)



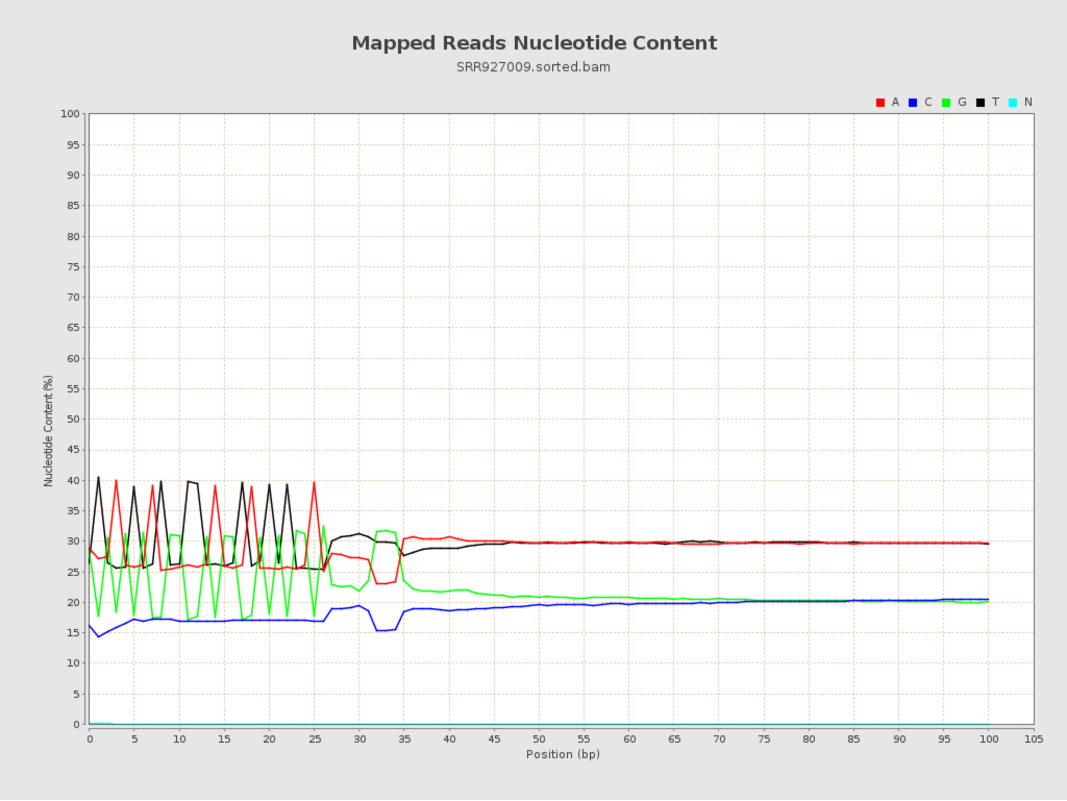
6. Results : Genome Fraction Coverage



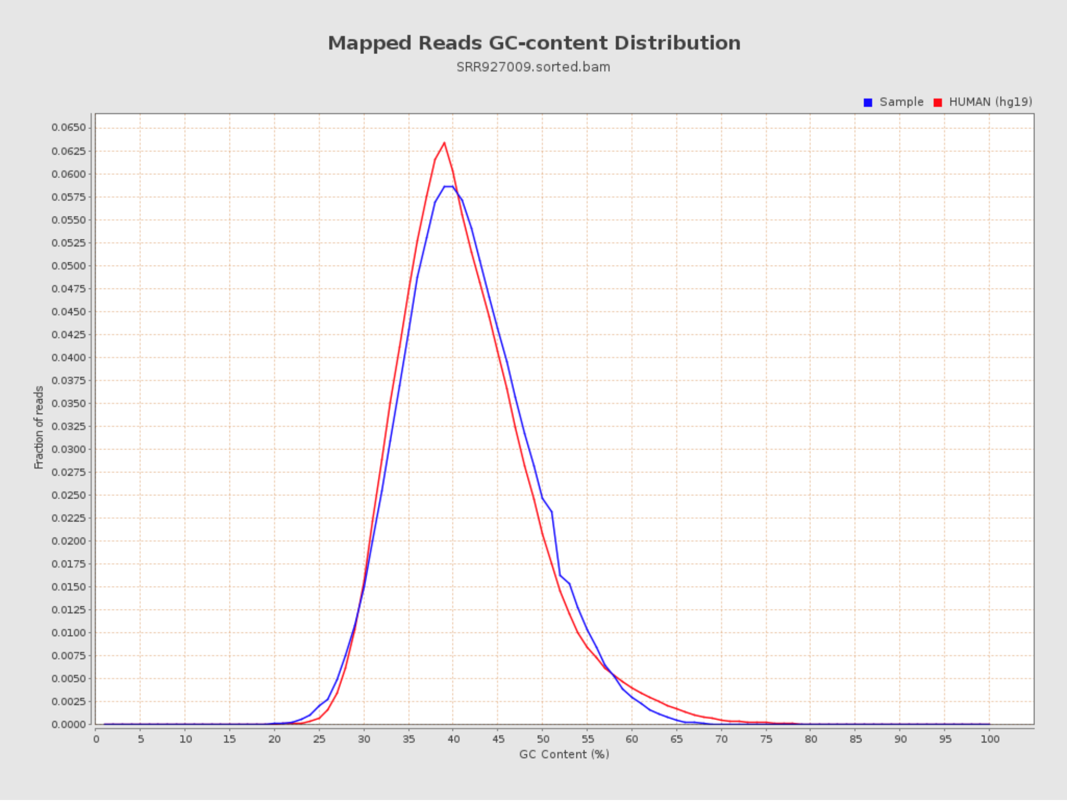
7. Results : Duplication Rate Histogram



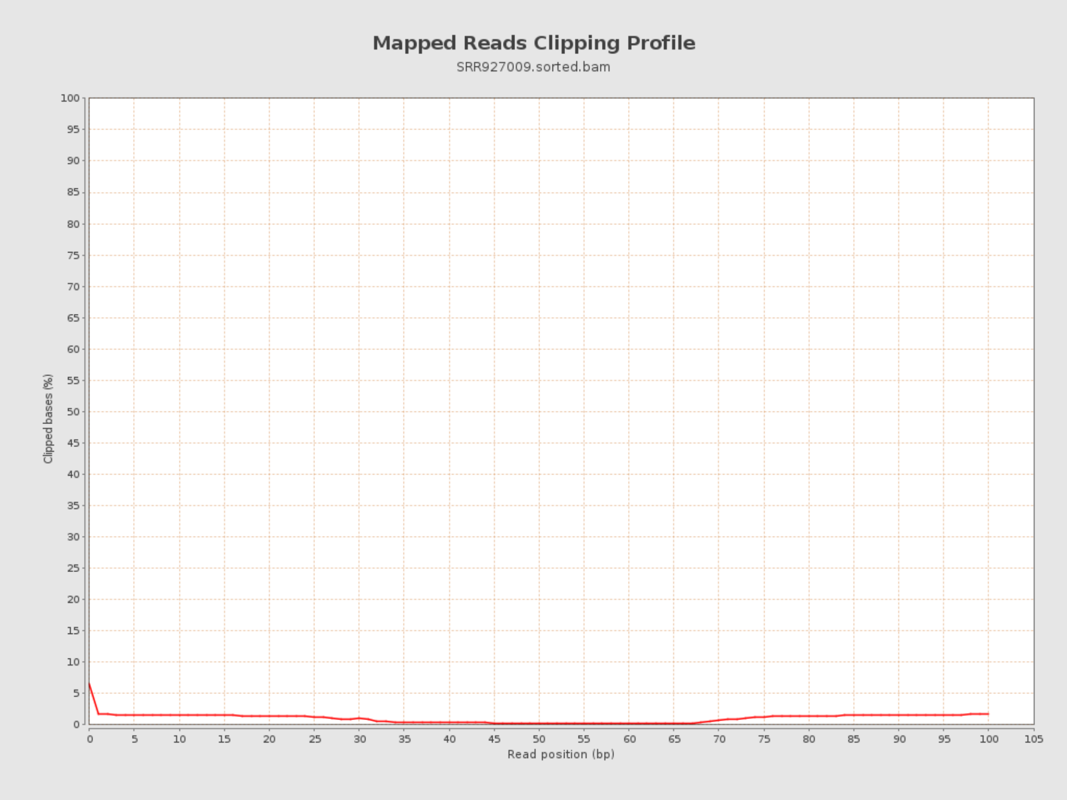
8. Results : Mapped Reads Nucleotide Content



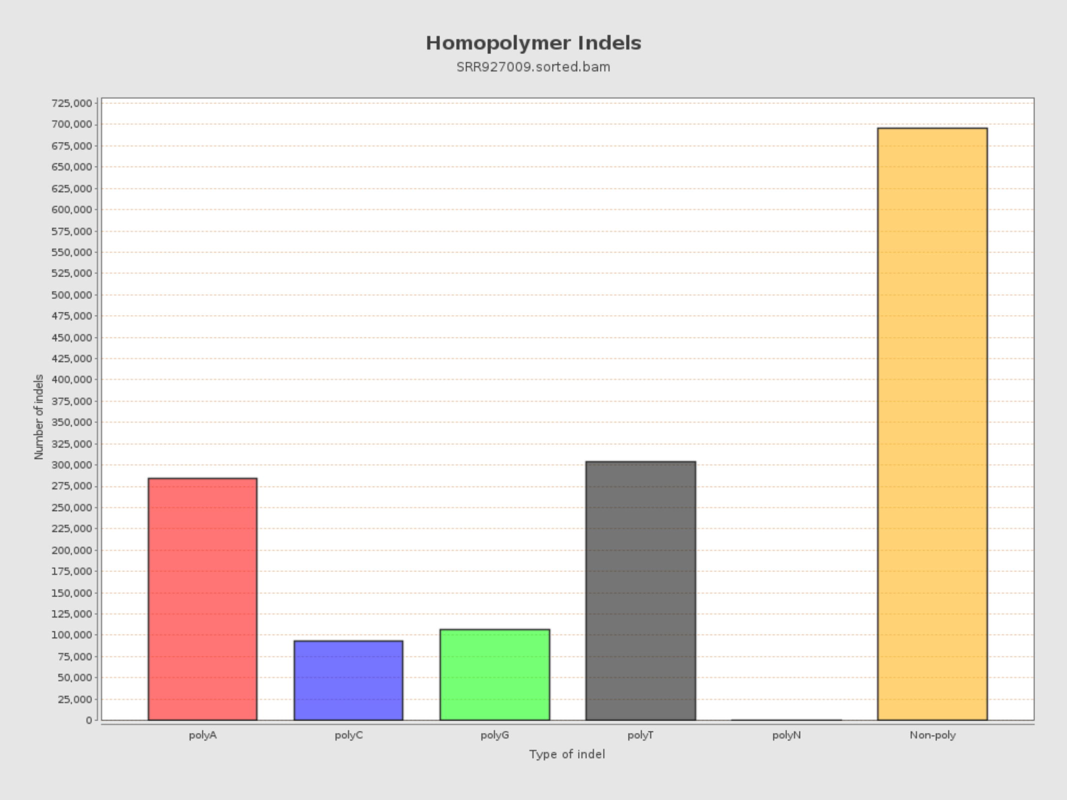
9. Results : Mapped Reads GC-content Distribution



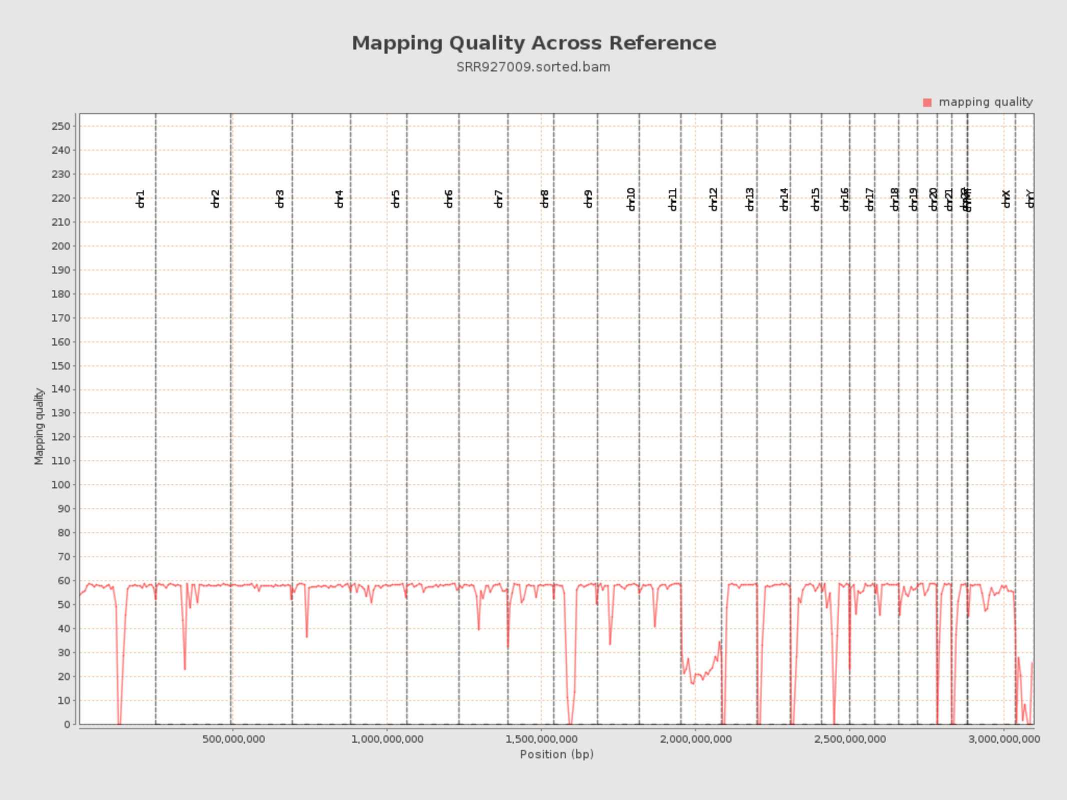
10. Results : Mapped Reads Clipping Profile



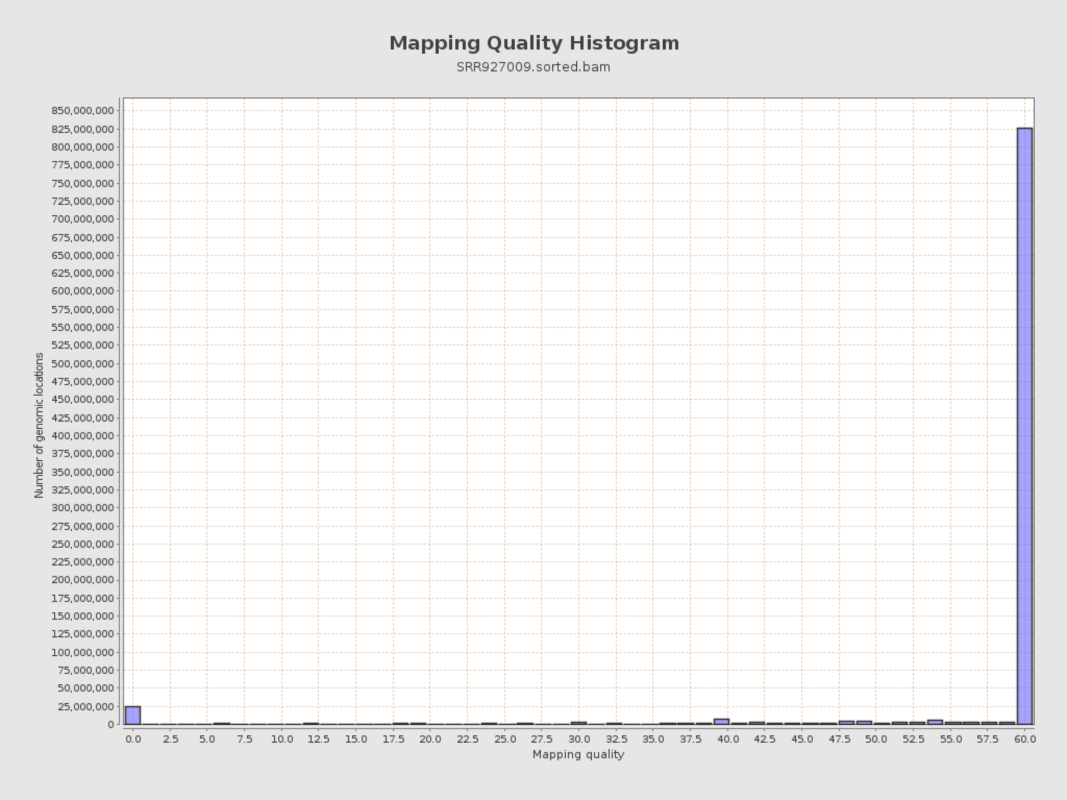
11. Results : Homopolymer Indels



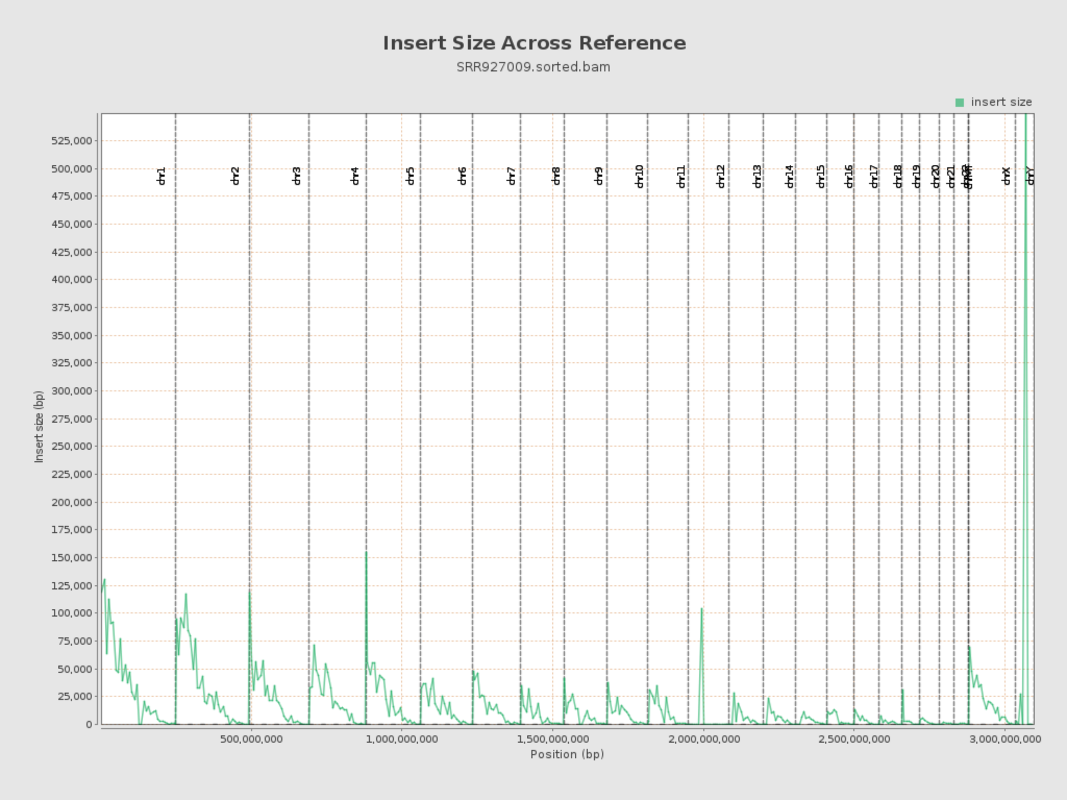
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram