Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/25 02:29:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927057.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_SRR927057 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927057_1.fastq.gz SRR927057_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 25 02:29:20 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927057.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	23,881,674
Mapped reads	23,228,573 / 97.27%
Unmapped reads	653,101 / 2.73%
Mapped paired reads	23,228,573 / 97.27%
Mapped reads, first in pair	11,653,899 / 48.8%
Mapped reads, second in pair	11,574,674 / 48.47%
Mapped reads, both in pair	22,869,218 / 95.76%
Mapped reads, singletons	359,355 / 1.5%
Secondary alignments	0
Supplementary alignments	477,066 / 2%
Read min/max/mean length	30 / 101 / 101.83
Duplicated reads (estimated)	1,746,281 / 7.31%
Duplication rate	5.79%
Clipped reads	10,426,151 / 43.66%

2.2. ACGT Content

Number/percentage of A's	606,224,421 / 28.73%
Number/percentage of C's	408,080,491 / 19.34%
Number/percentage of T's	619,003,199 / 29.34%
Number/percentage of G's	476,455,090 / 22.58%
Number/percentage of N's	318,988 / 0.02%

GC Percentage	41.92%

2.3. Coverage

Mean	0.6821
Standard Deviation	2.8827

2.4. Mapping Quality

Mean Mapping Quality	52.91

2.5. Insert size

Mean	221,363.11
Standard Deviation	4,586,722.25
P25/Median/P75	141 / 183 / 245

2.6. Mismatches and indels

General error rate	1.06%
Mismatches	21,685,161
Insertions	343,742
Mapped reads with at least one insertion	1.45%
Deletions	1,006,566
Mapped reads with at least one deletion	4.22%
Homopolymer indels	51.45%

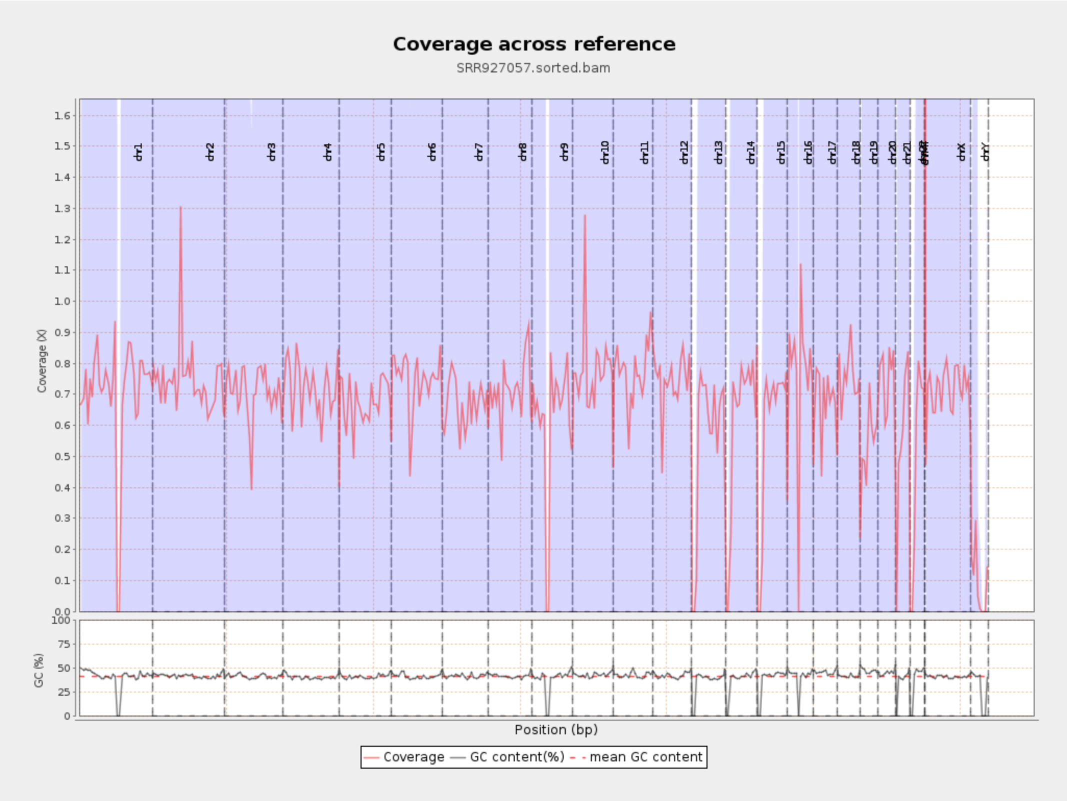
2.7. Chromosome stats

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

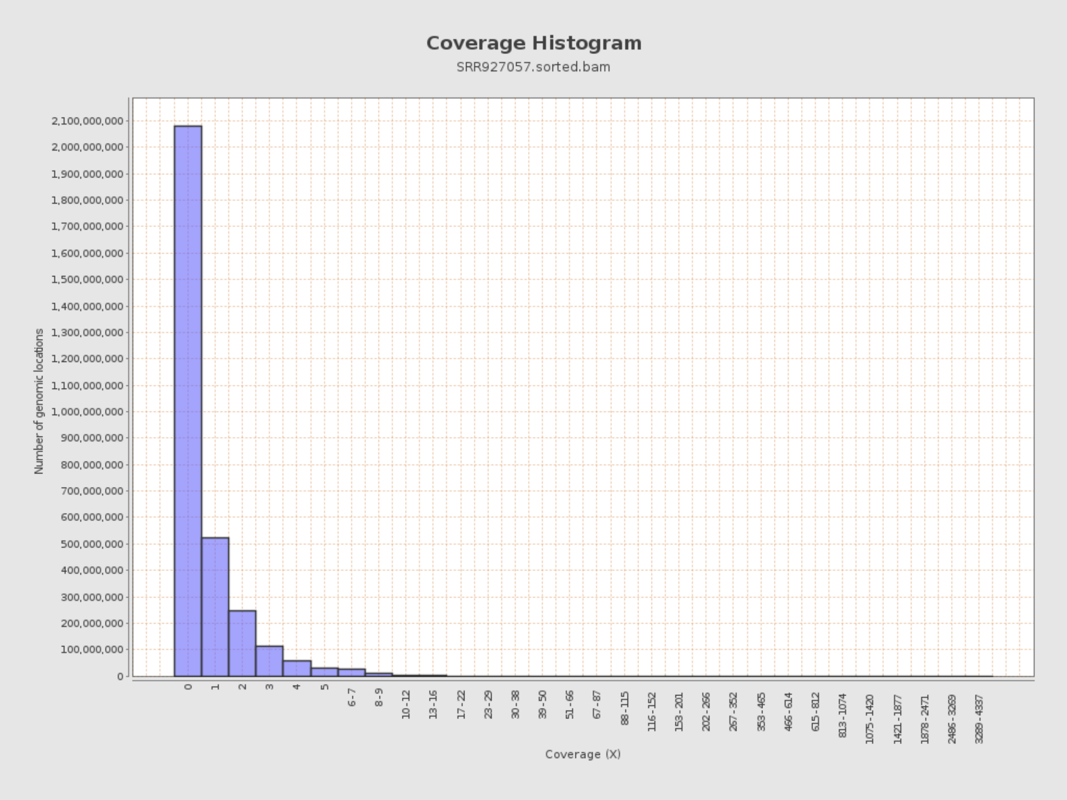
		bases	coverage	deviation
chr1	249250621	175668704	0.7048	4.569
chr2	243199373	182570420	0.7507	4.264
chr3	198022430	139722481	0.7056	1.3927
chr4	191154276	137969352	0.7218	2.3787
chr5	180915260	122223157	0.6756	1.3267
chr6	171115067	128535484	0.7512	1.534
chr7	159138663	106494184	0.6692	2.1686
chr8	146364022	105392019	0.7201	1.7801
chr9	141213431	85795383	0.6076	3.782
chr10	135534747	106781472	0.7879	5.6686
chr11	135006516	103644532	0.7677	2.3467
chr12	133851895	99692469	0.7448	1.4401
chr13	115169878	64016708	0.5558	1.2093
chr14	107349540	64661427	0.6023	1.3612
chr15	102531392	58655235	0.5721	1.2614
chr16	90354753	67103417	0.7427	3.7982
chr17	81195210	54496654	0.6712	2.36
chr18	78077248	59933175	0.7676	3.9003
chr19	59128983	31817419	0.5381	2.5374
chr20	63025520	46719313	0.7413	1.545
chr21	48129895	27638446	0.5742	1.9738
chr22	51304566	25169760	0.4906	1.2436
chrMT	16571	319709	19.2933	10.8259
chrX	155270560	110872355	0.7141	1.6544

chrY	59373566	5665359	0.0954	3.0858

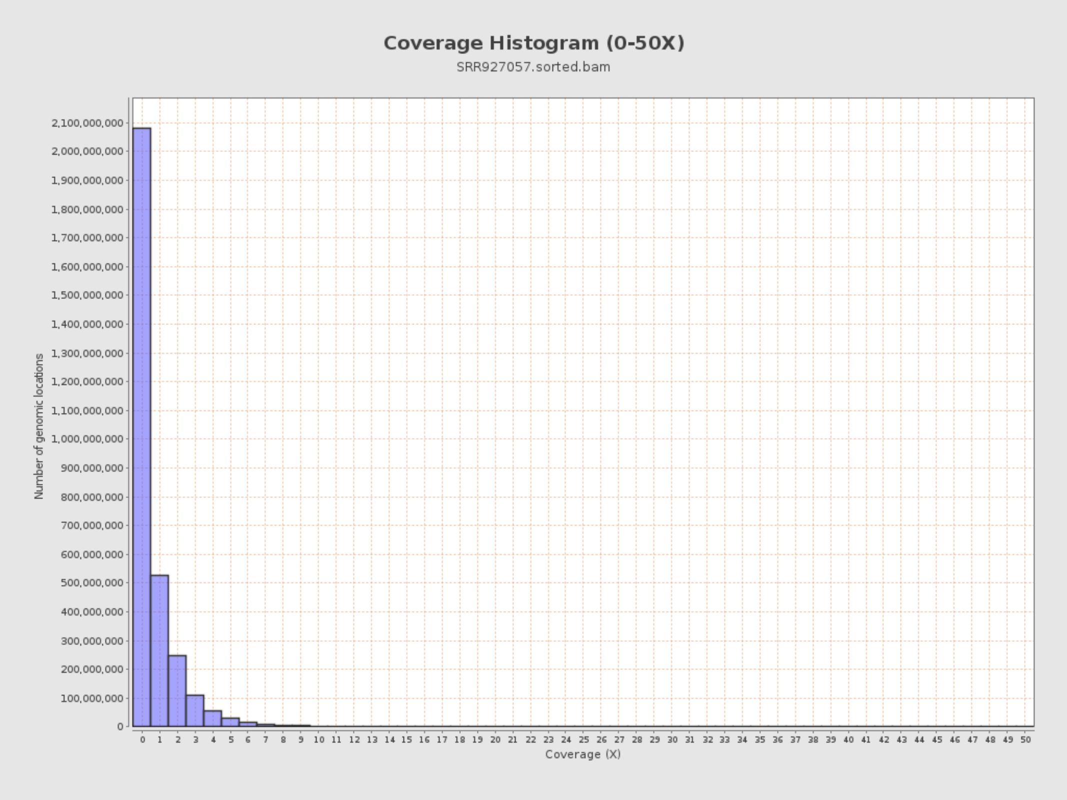
3. Results : Coverage across reference



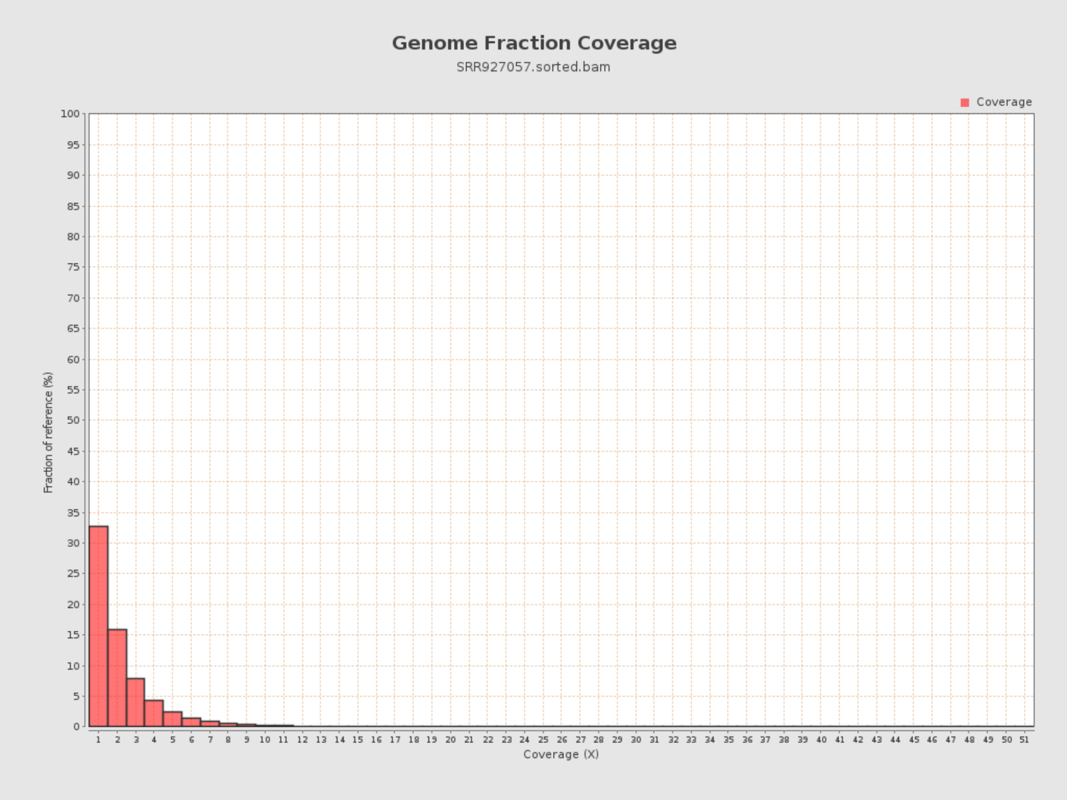
4. Results : Coverage Histogram



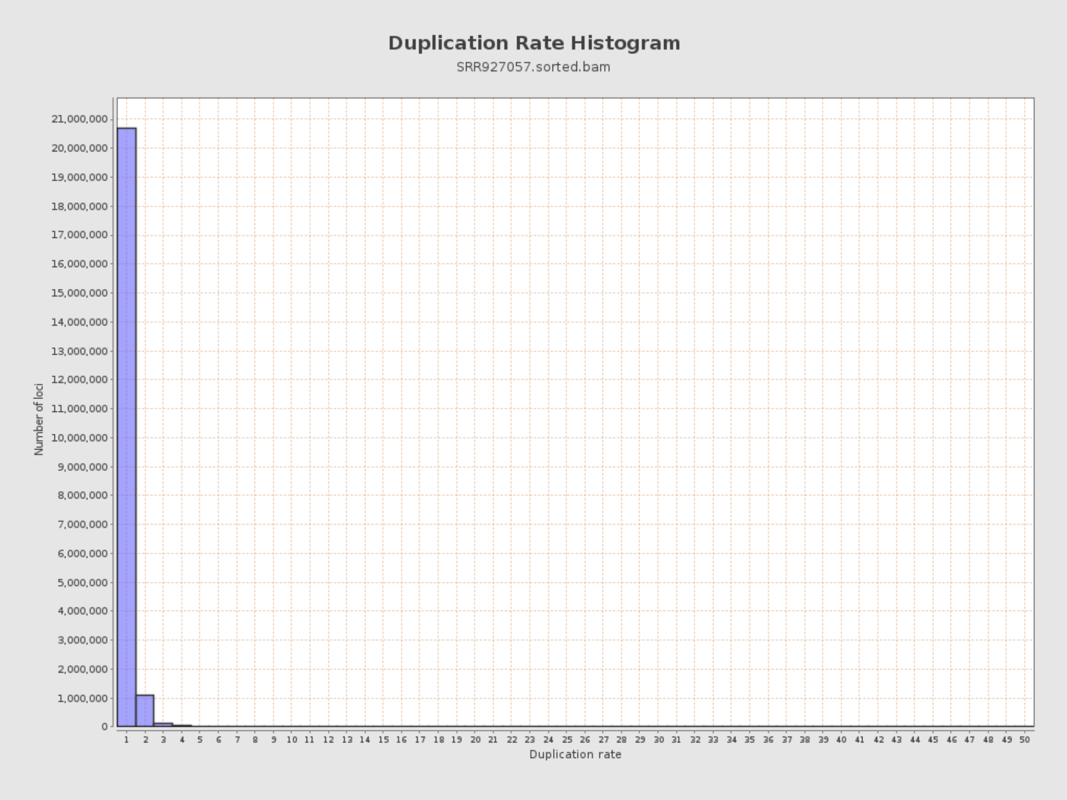
5. Results : Coverage Histogram (0-50X)



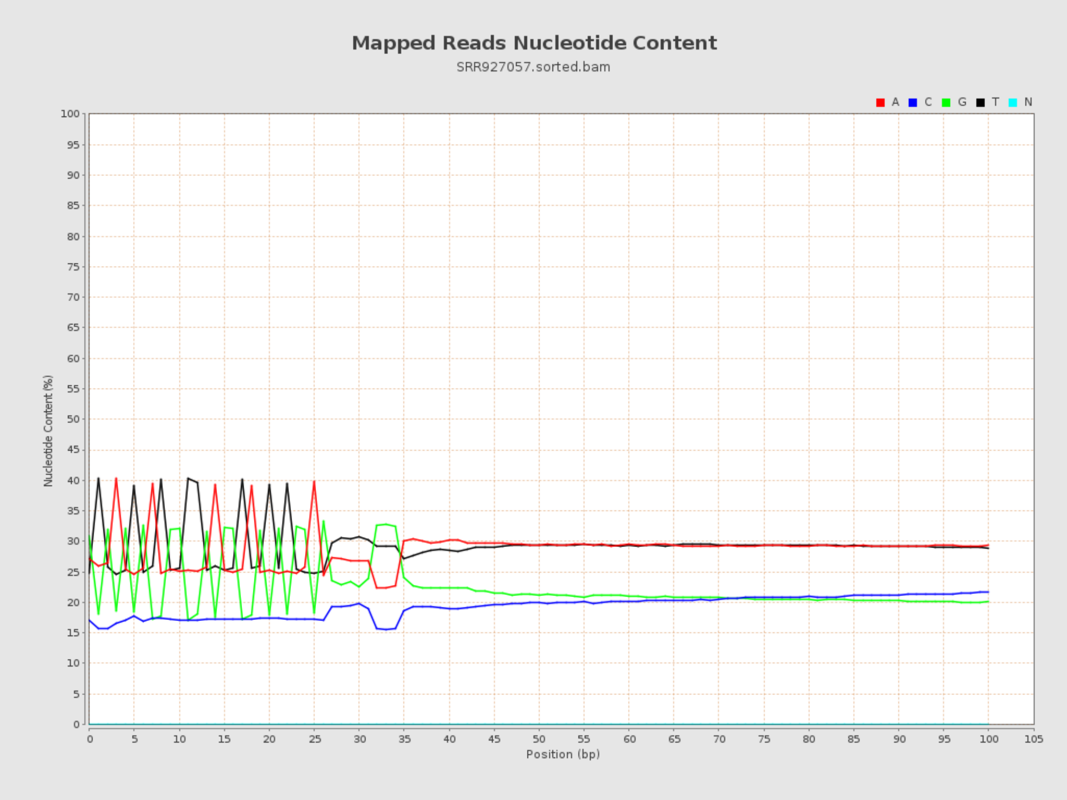
6. Results : Genome Fraction Coverage



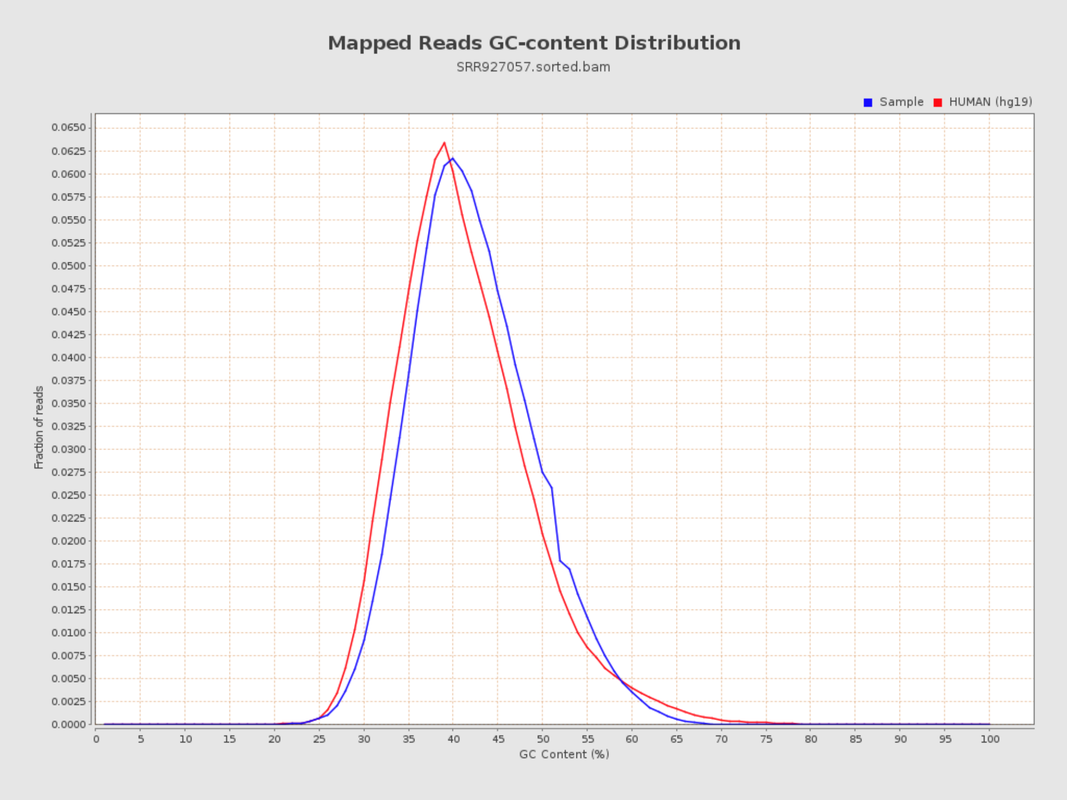
7. Results : Duplication Rate Histogram



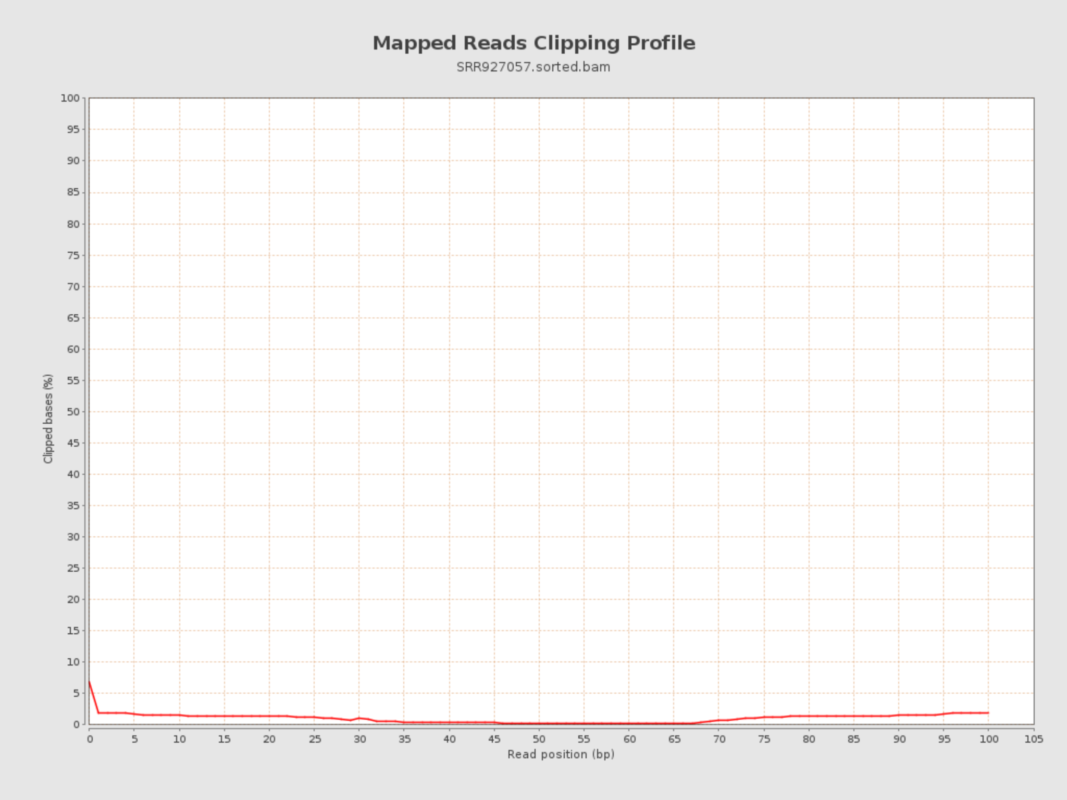
8. Results : Mapped Reads Nucleotide Content



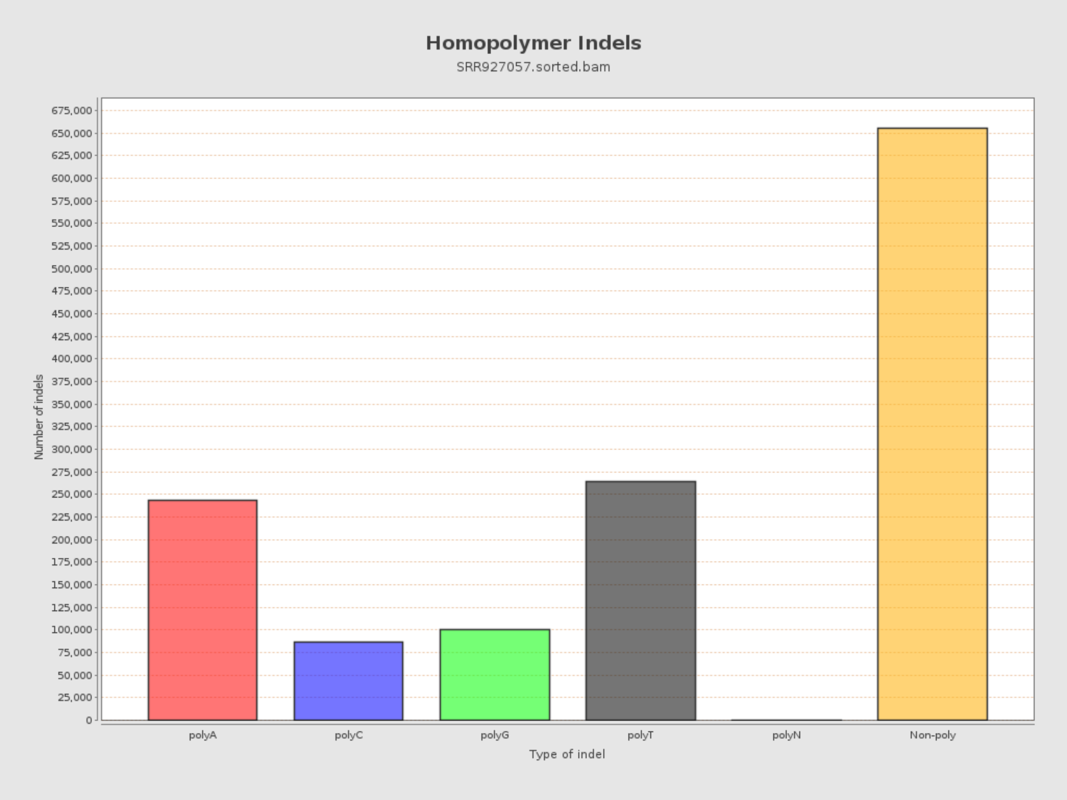
9. Results : Mapped Reads GC-content Distribution



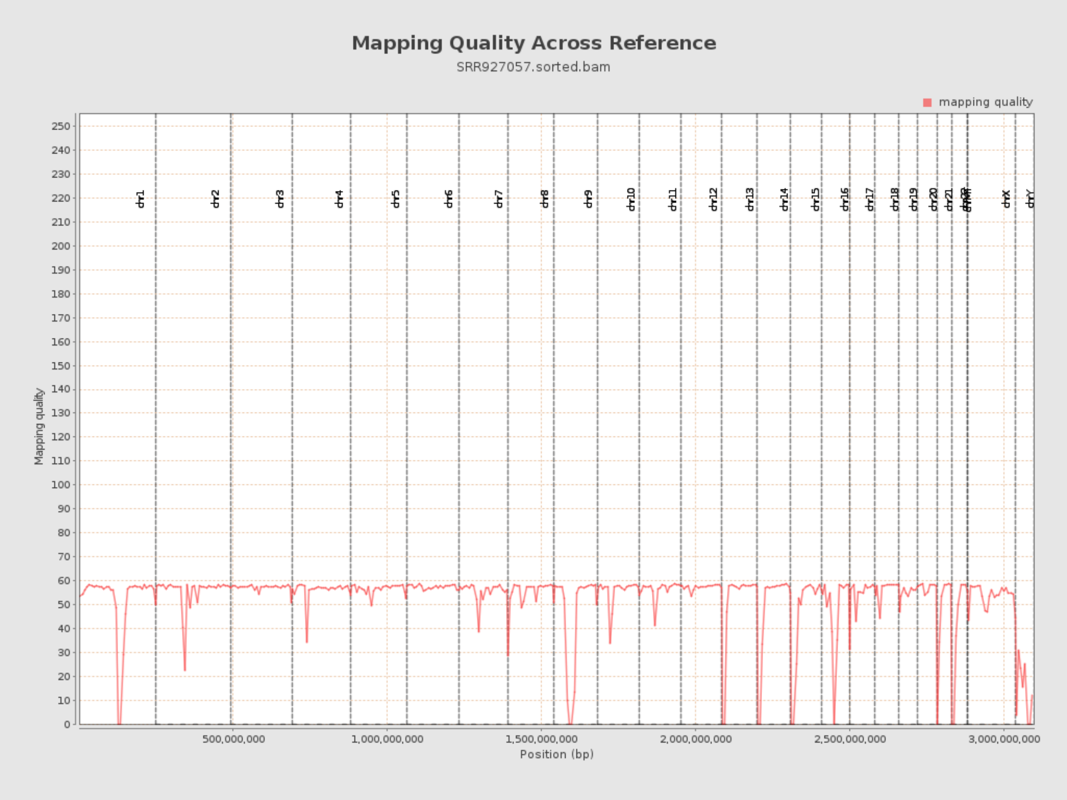
10. Results : Mapped Reads Clipping Profile



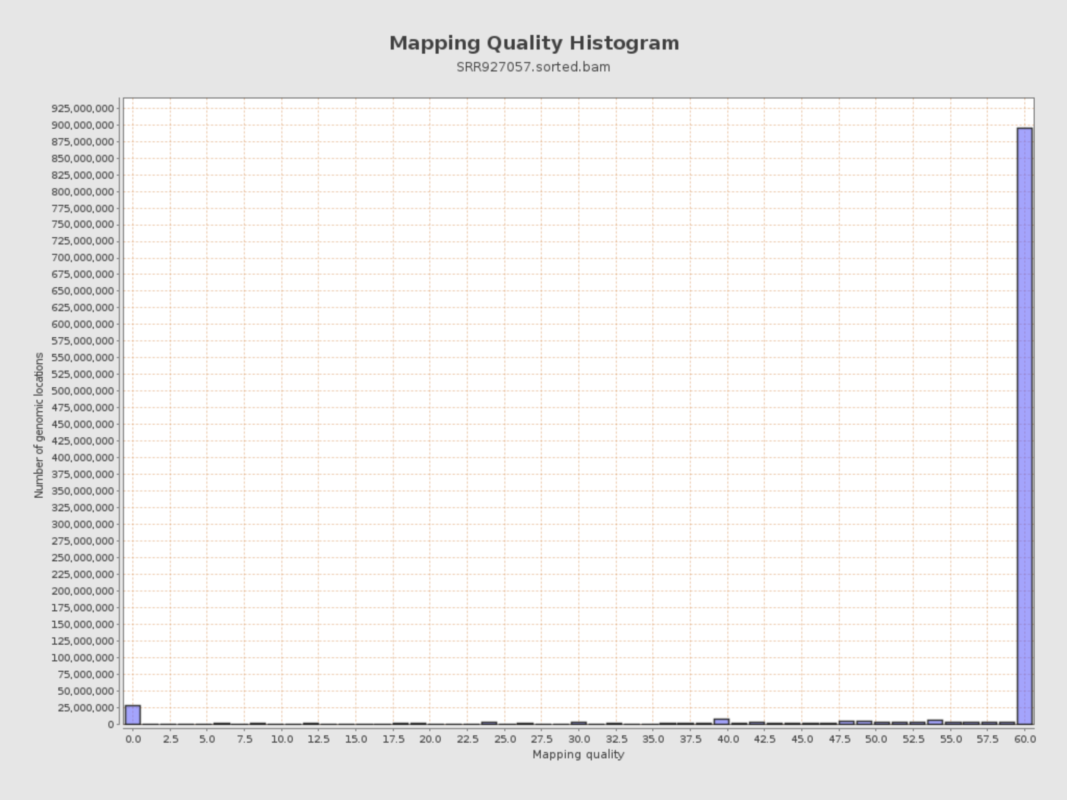
11. Results : Homopolymer Indels



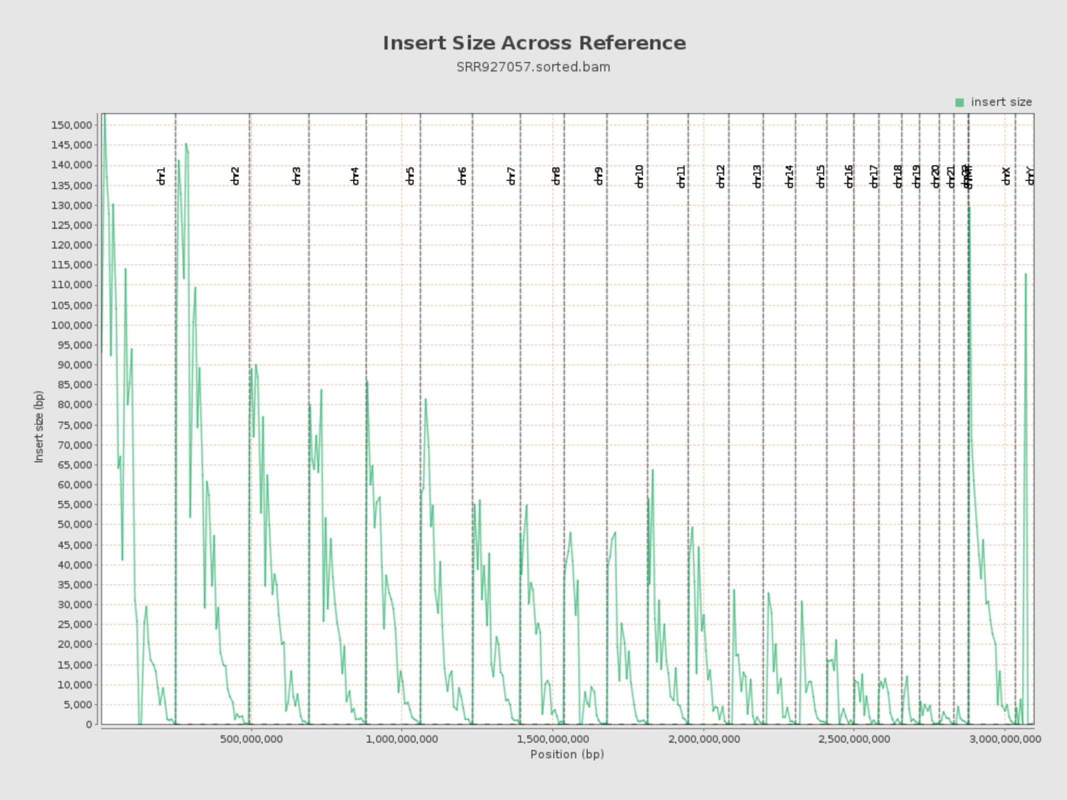
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram