Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/24 00:25:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927003.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_SRR927003 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927003_1.fastq.gz SRR927003_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 24 00:25:46 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927003.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,462,630
Mapped reads	11,189,064 / 97.61%
Unmapped reads	273,566 / 2.39%
Mapped paired reads	11,189,064 / 97.61%
Mapped reads, first in pair	5,600,980 / 48.86%
Mapped reads, second in pair	5,588,084 / 48.75%
Mapped reads, both in pair	11,020,302 / 96.14%
Mapped reads, singletons	168,762 / 1.47%
Secondary alignments	0
Supplementary alignments	312,733 / 2.73%
Read min/max/mean length	30 / 101 / 102.13
Duplicated reads (estimated)	640,169 / 5.58%
Duplication rate	4.61%
Clipped reads	4,601,510 / 40.14%

2.2. ACGT Content

Number/percentage of A's	293,873,858 / 28.77%
Number/percentage of C's	197,297,987 / 19.32%
Number/percentage of T's	298,785,647 / 29.25%
Number/percentage of G's	231,275,281 / 22.64%
Number/percentage of N's	193,108 / 0.02%

GC Percentage	41.96%

2.3. Coverage

Mean	0.3302
Standard Deviation	1.4211

2.4. Mapping Quality

Mean Mapping Quality	52.71

2.5. Insert size

Mean	291,047.07
Standard Deviation	5,237,572.19
P25/Median/P75	142 / 185 / 249

2.6. Mismatches and indels

General error rate	0.98%
Mismatches	9,749,872
Insertions	176,689
Mapped reads with at least one insertion	1.55%
Deletions	534,744
Mapped reads with at least one deletion	4.66%
Homopolymer indels	52.08%

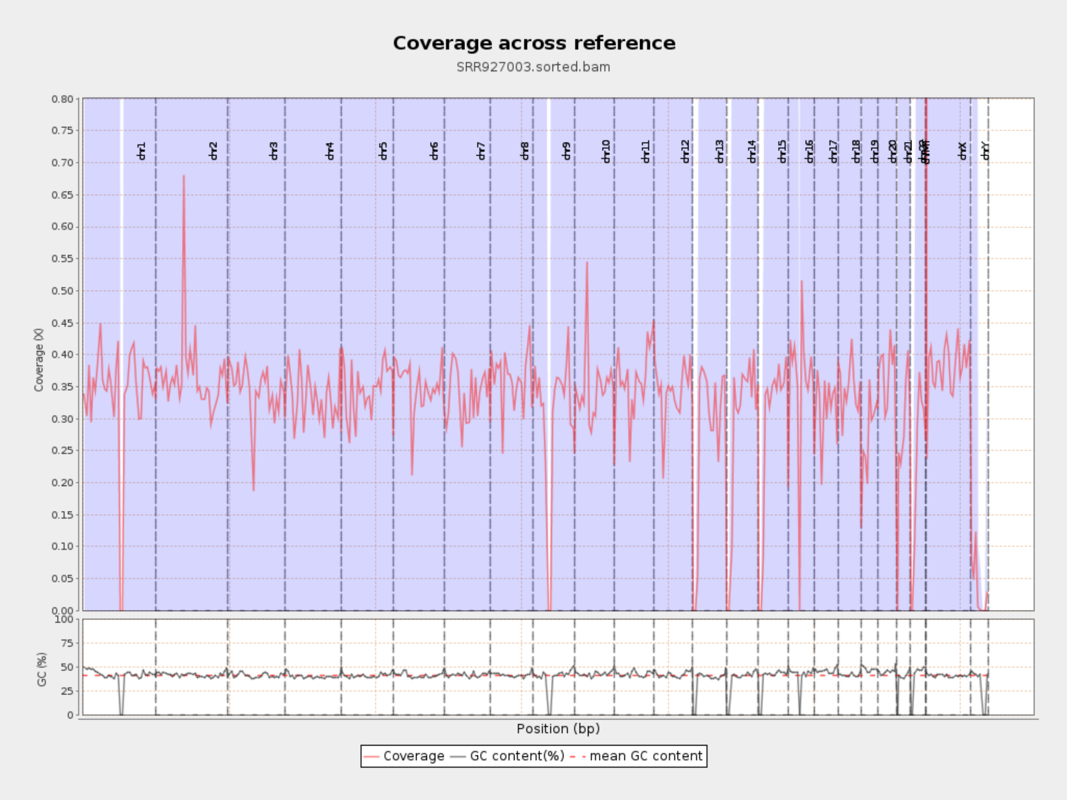
2.7. Chromosome stats

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

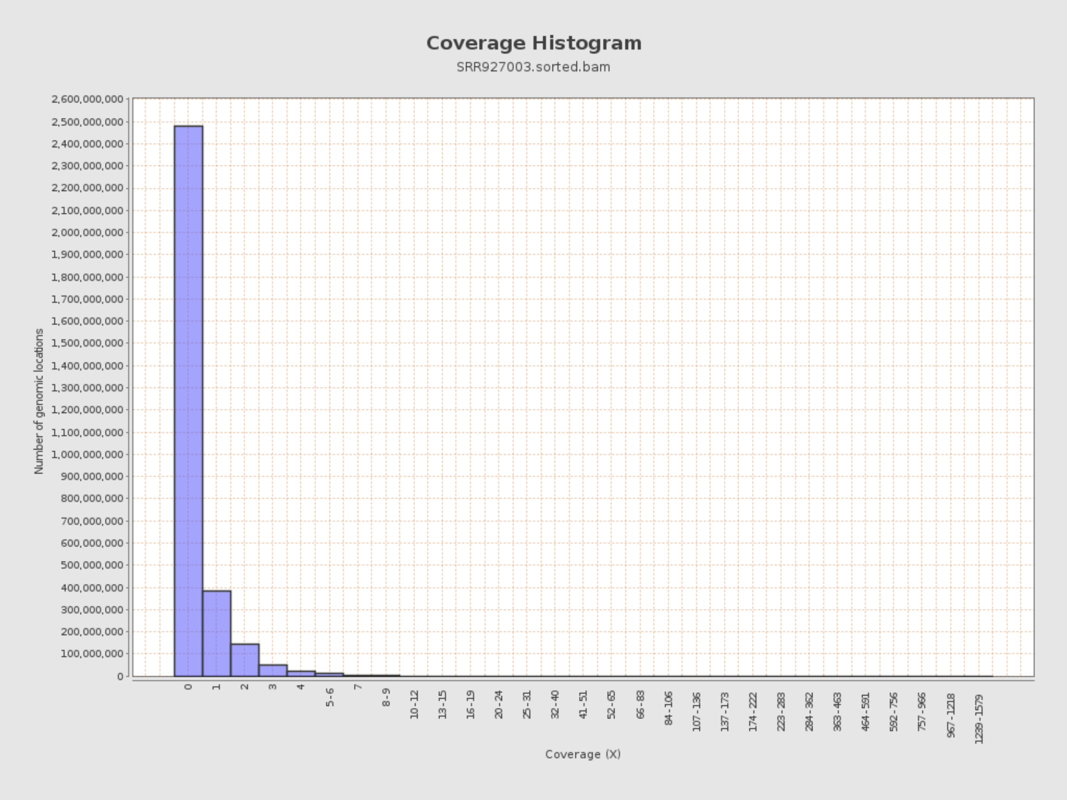
		bases	coverage	deviation
chr1	249250621	84324201	0.3383	1.9162
chr2	243199373	89531449	0.3681	2.4128
chr3	198022430	67818233	0.3425	0.8341
chr4	191154276	64101984	0.3353	1.1603
chr5	180915260	62872306	0.3475	0.8397
chr6	171115067	60009611	0.3507	0.9981
chr7	159138663	53734091	0.3377	1.0885
chr8	146364022	53116559	0.3629	0.9967
chr9	141213431	42627270	0.3019	1.6596
chr10	135534747	47020373	0.3469	2.5924
chr11	135006516	48539187	0.3595	1.1222
chr12	133851895	46172387	0.345	0.8559
chr13	115169878	31787870	0.276	0.7452
chr14	107349540	30956725	0.2884	0.7818
chr15	102531392	29145859	0.2843	0.7711
chr16	90354753	31594294	0.3497	1.8339
chr17	81195210	25978497	0.32	1.0418
chr18	78077248	27066846	0.3467	1.6955
chr19	59128983	16342500	0.2764	1.2782
chr20	63025520	23552749	0.3737	0.9239
chr21	48129895	13252815	0.2754	1.131
chr22	51304566	11358632	0.2214	0.697
chrMT	16571	219957	13.2736	12.2505
chrX	155270560	59061848	0.3804	0.9865

chrY	59373566	2023871	0.0341	1.4021

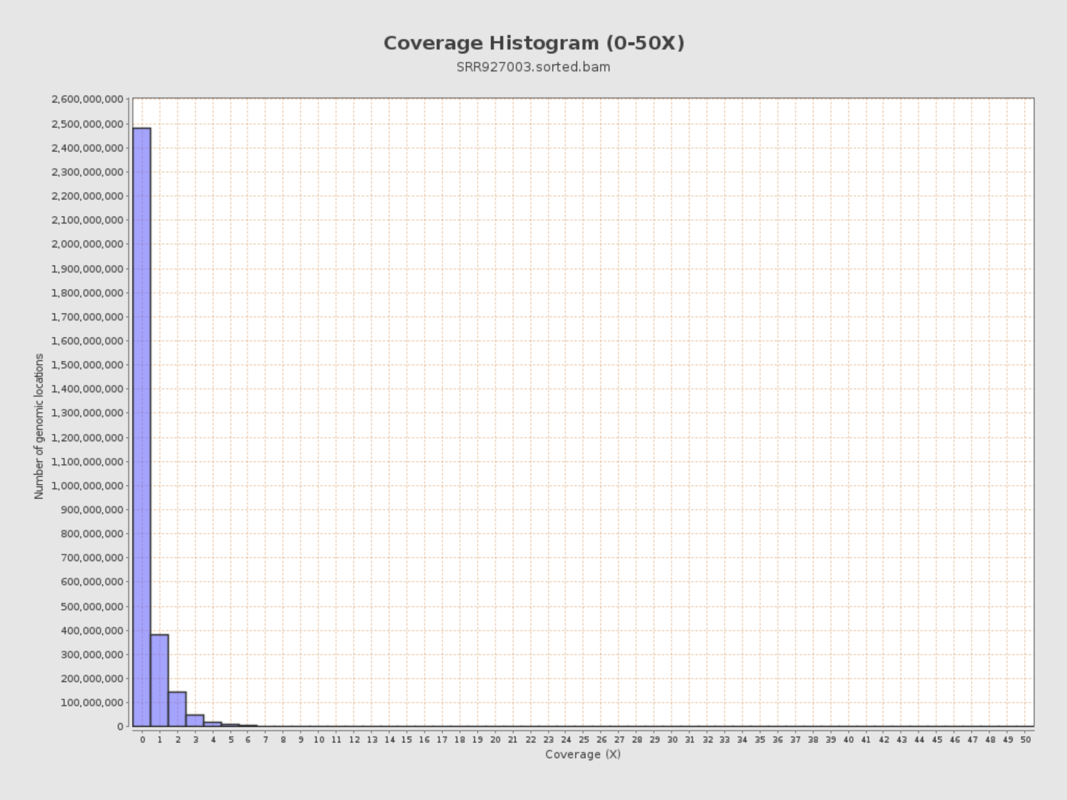
3. Results : Coverage across reference



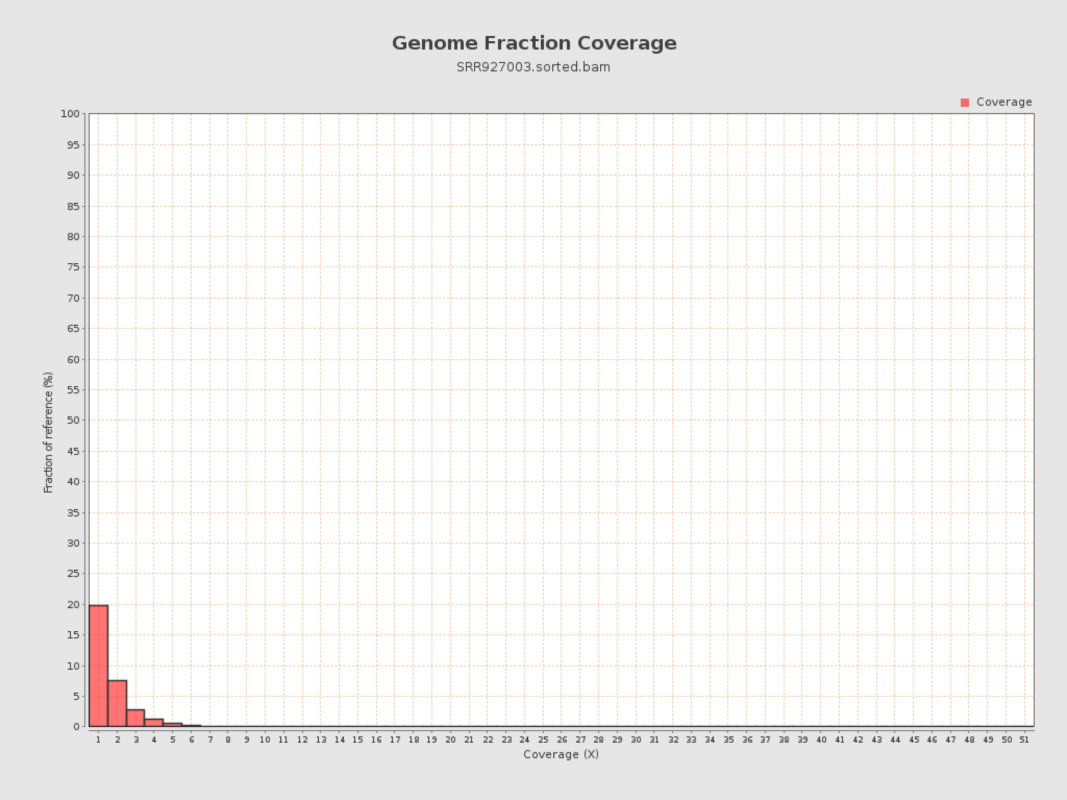
4. Results : Coverage Histogram



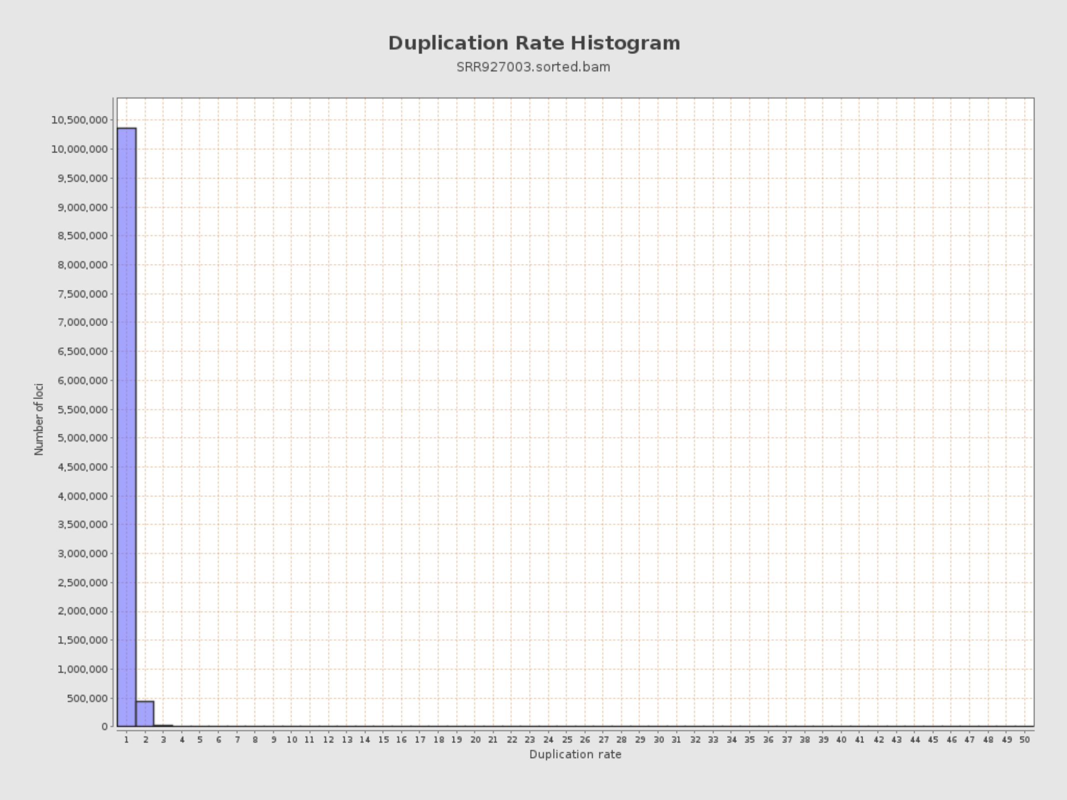
5. Results : Coverage Histogram (0-50X)



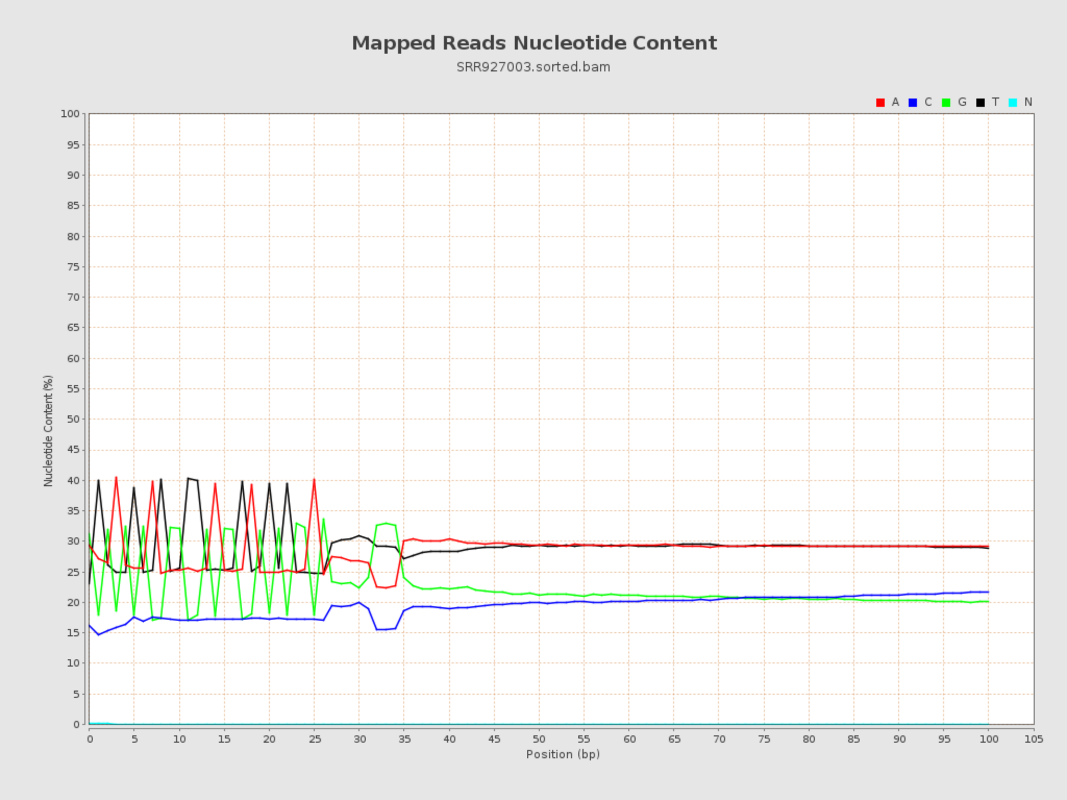
6. Results : Genome Fraction Coverage



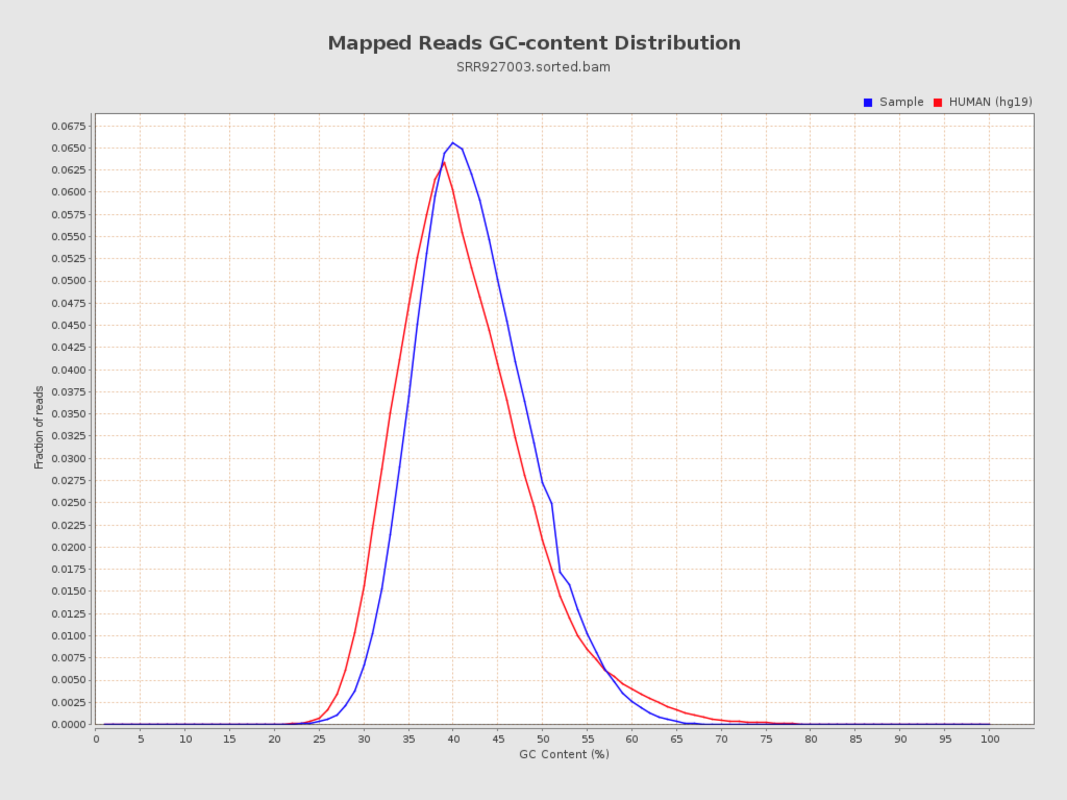
7. Results : Duplication Rate Histogram



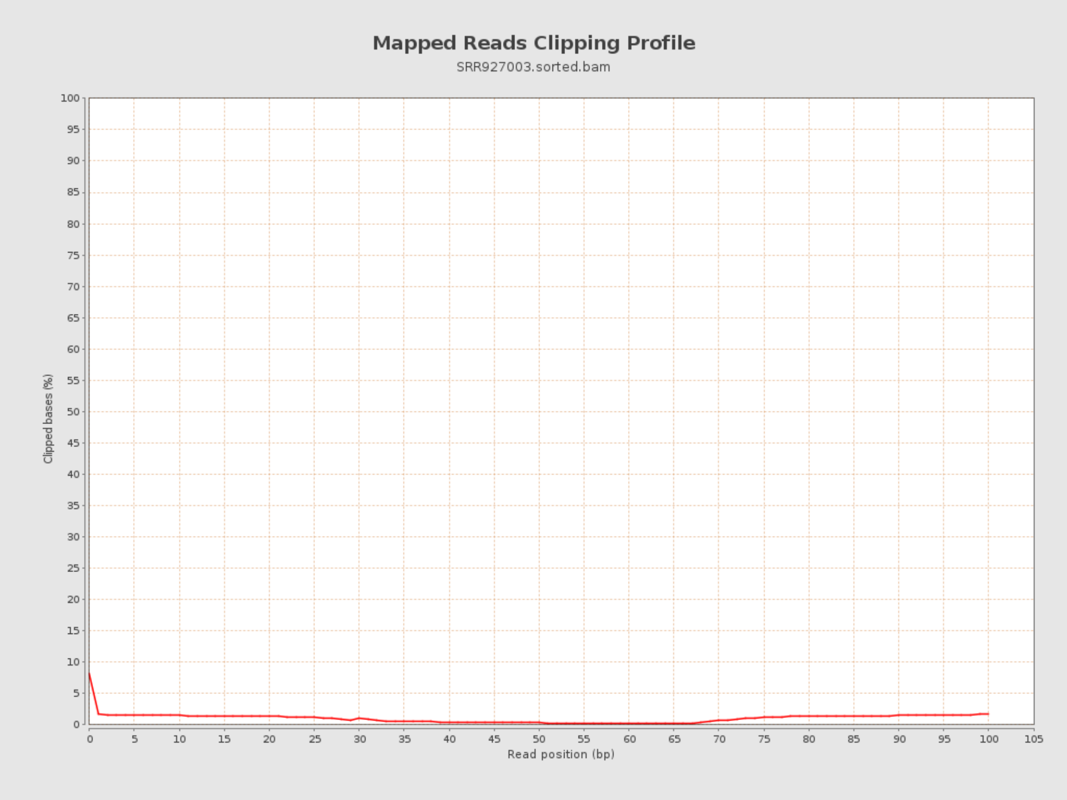
8. Results : Mapped Reads Nucleotide Content



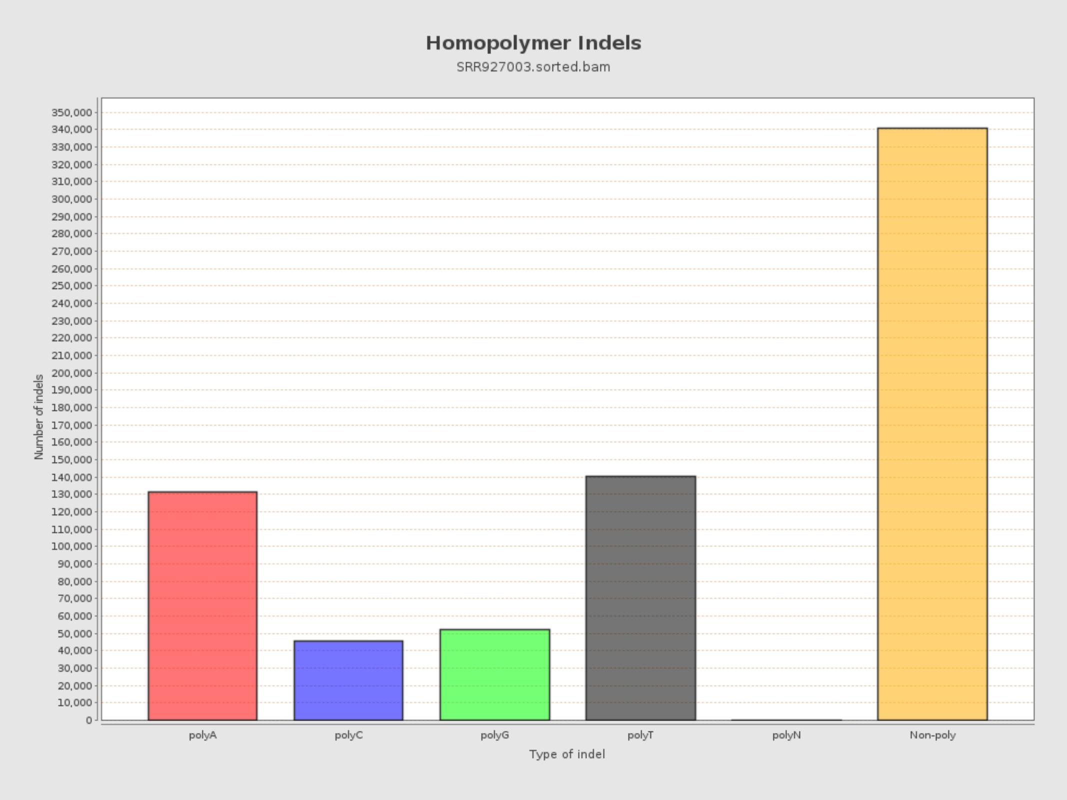
9. Results : Mapped Reads GC-content Distribution



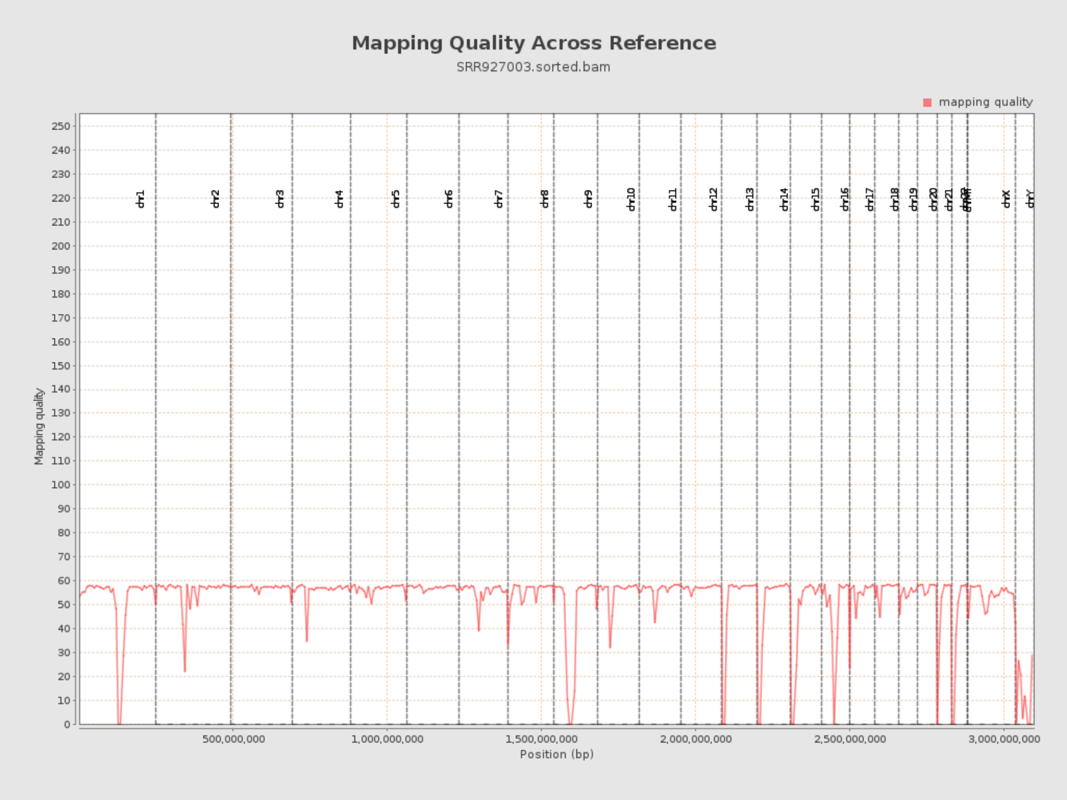
10. Results : Mapped Reads Clipping Profile



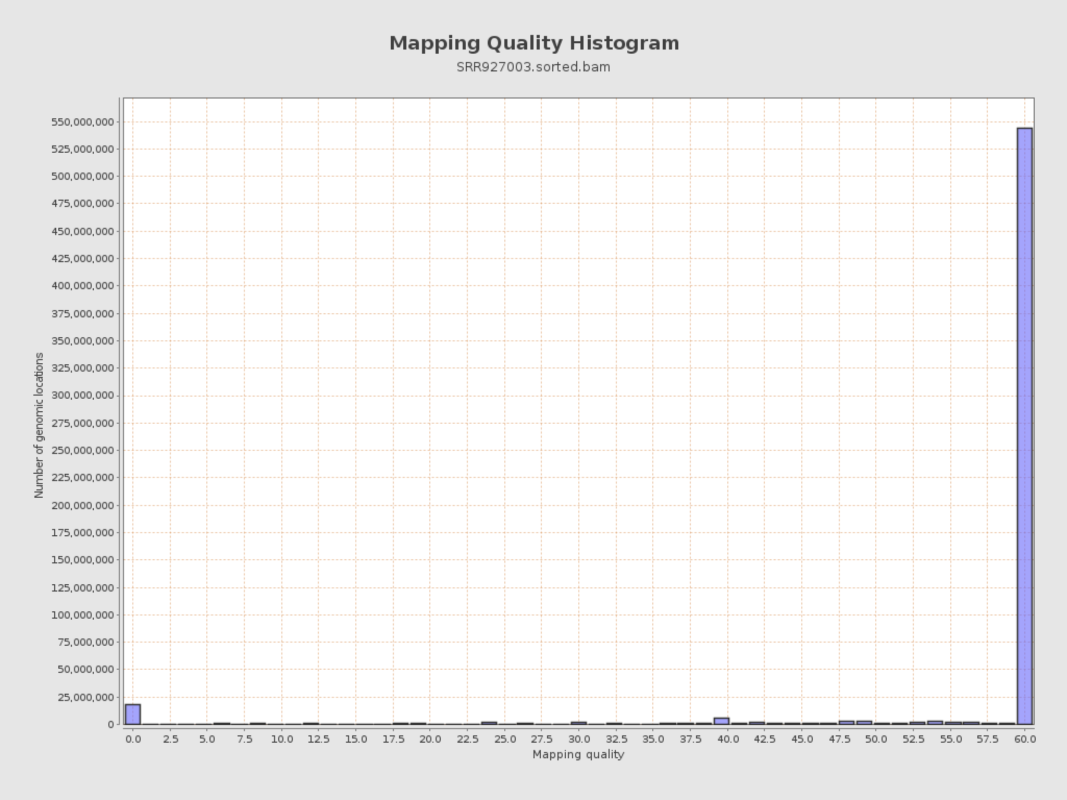
11. Results : Homopolymer Indels



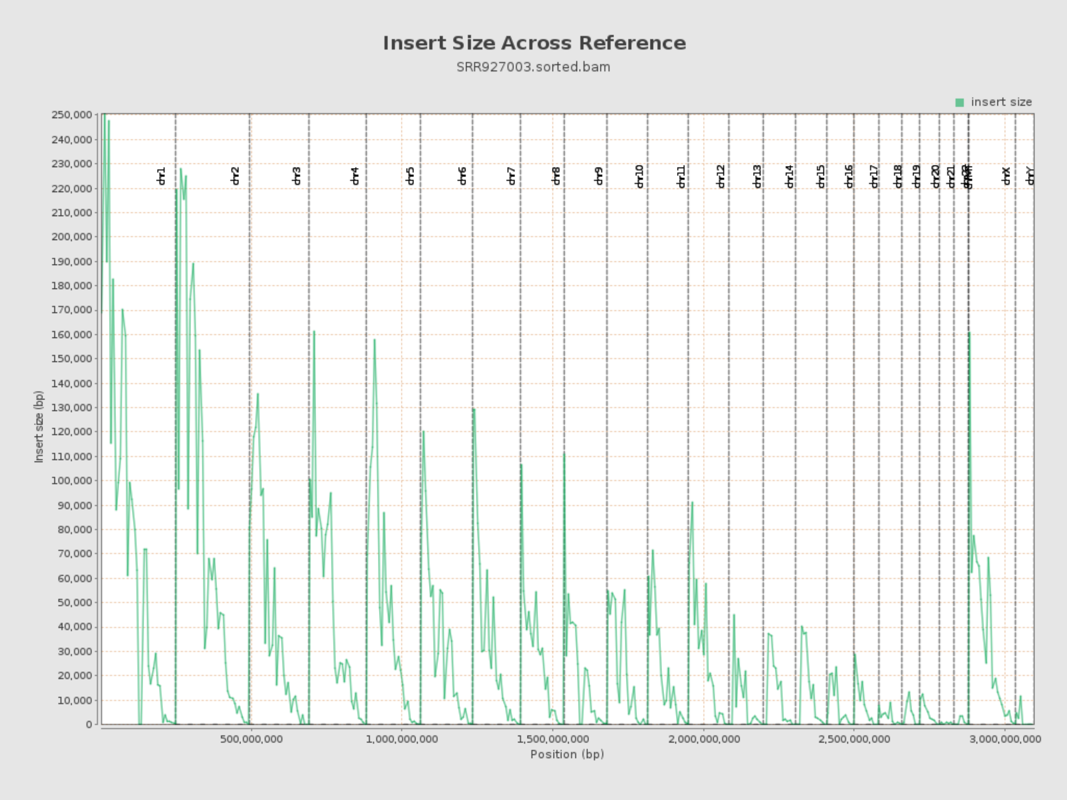
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram