Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 20:38:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084967.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_SRR3084967 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084967.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 20:38:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084967.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,611,932
Mapped reads	2,343,309 / 89.72%
Unmapped reads	268,623 / 10.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,025 / 0.84%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	100,904 / 3.86%
Duplication rate	3.06%
Clipped reads	1,137,245 / 43.54%

2.2. ACGT Content

Number/percentage of A's	43,030,244 / 27.78%
Number/percentage of C's	29,401,534 / 18.98%
Number/percentage of T's	47,445,921 / 30.63%
Number/percentage of G's	34,981,291 / 22.59%
Number/percentage of N's	20,332 / 0.01%
GC Percentage	41.57%

2.3. Coverage

Mean	0.05

Standard Deviation	0.5118

2.4. Mapping Quality

Mean Mapping Quality	44.51

2.5. Mismatches and indels

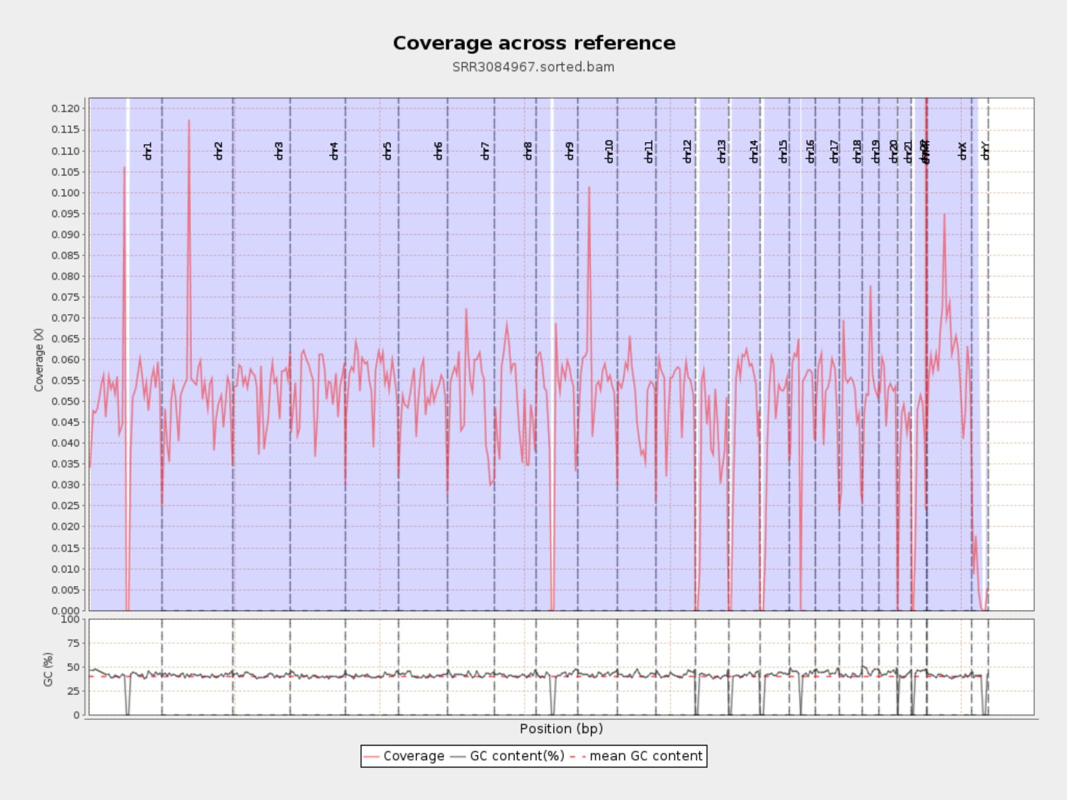
General error rate	0.87%
Mismatches	1,331,375
Insertions	12,310
Mapped reads with at least one insertion	0.52%
Deletions	36,128
Mapped reads with at least one deletion	1.53%
Homopolymer indels	45.75%

2.6. Chromosome stats

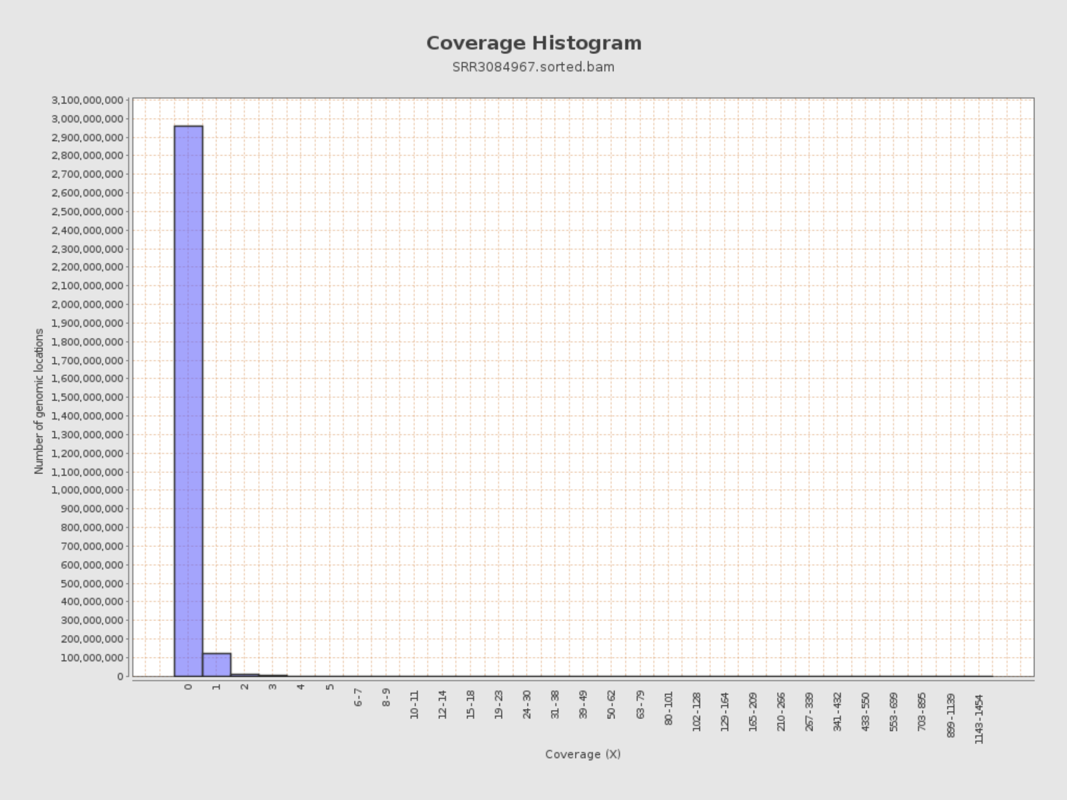
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12415924	0.0498	1.1262
chr2	243199373	12664250	0.0521	0.6332
chr3	198022430	10514528	0.0531	0.2613
chr4	191154276	10188691	0.0533	0.2643
chr5	180915260	10167292	0.0562	0.2666
chr6	171115067	8679005	0.0507	0.3336
chr7	159138663	8270852	0.052	0.4082

chr8	146364022	7232502	0.0494	0.5545
chr9	141213431	6886155	0.0488	0.47
chr10	135534747	7679066	0.0567	0.5171
chr11	135006516	6827879	0.0506	0.4683
chr12	133851895	7100884	0.0531	0.2611
chr13	115169878	4254815	0.0369	0.2116
chr14	107349540	5082480	0.0473	0.2696
chr15	102531392	4292337	0.0419	0.231
chr16	90354753	4614882	0.0511	0.3013
chr17	81195210	4256703	0.0524	0.3051
chr18	78077248	3813193	0.0488	0.9067
chr19	59128983	3200236	0.0541	0.7316
chr20	63025520	3295098	0.0523	0.2689
chr21	48129895	1901118	0.0395	0.2377
chr22	51304566	1637047	0.0319	0.1965
chrMT	16571	14407	0.8694	1.0274
chrX	155270560	9561907	0.0616	0.361
chrY	59373566	385898	0.0065	0.1217

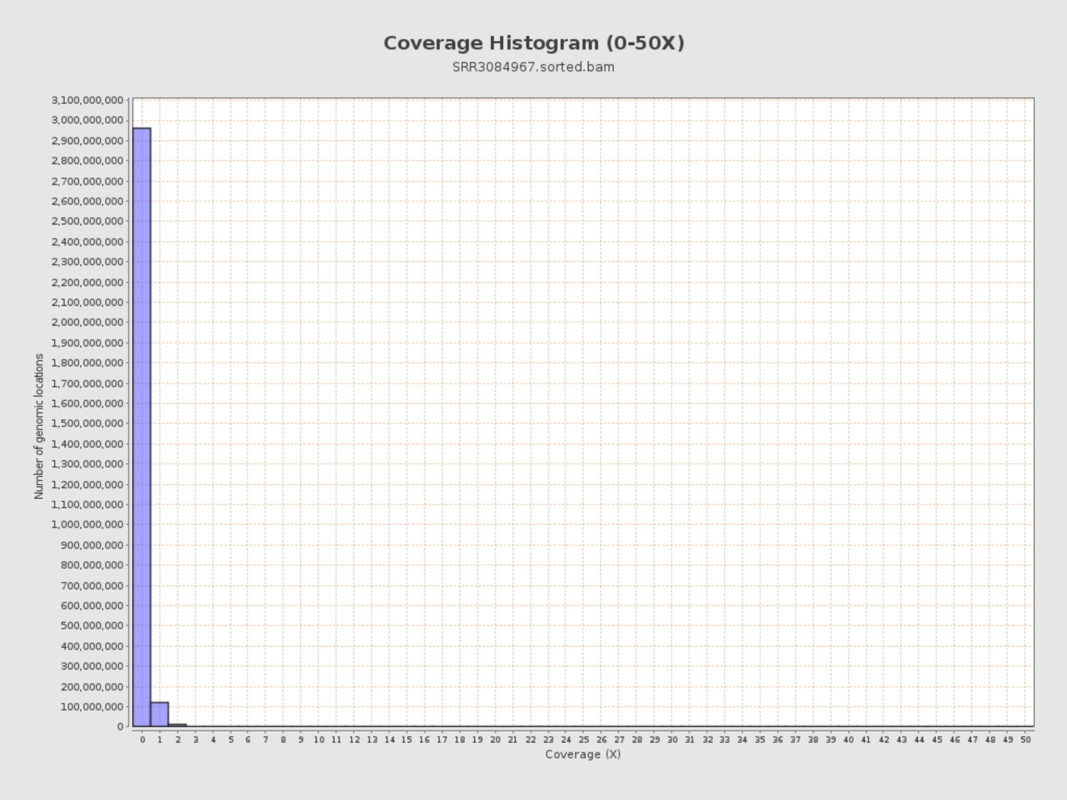
3. Results : Coverage across reference



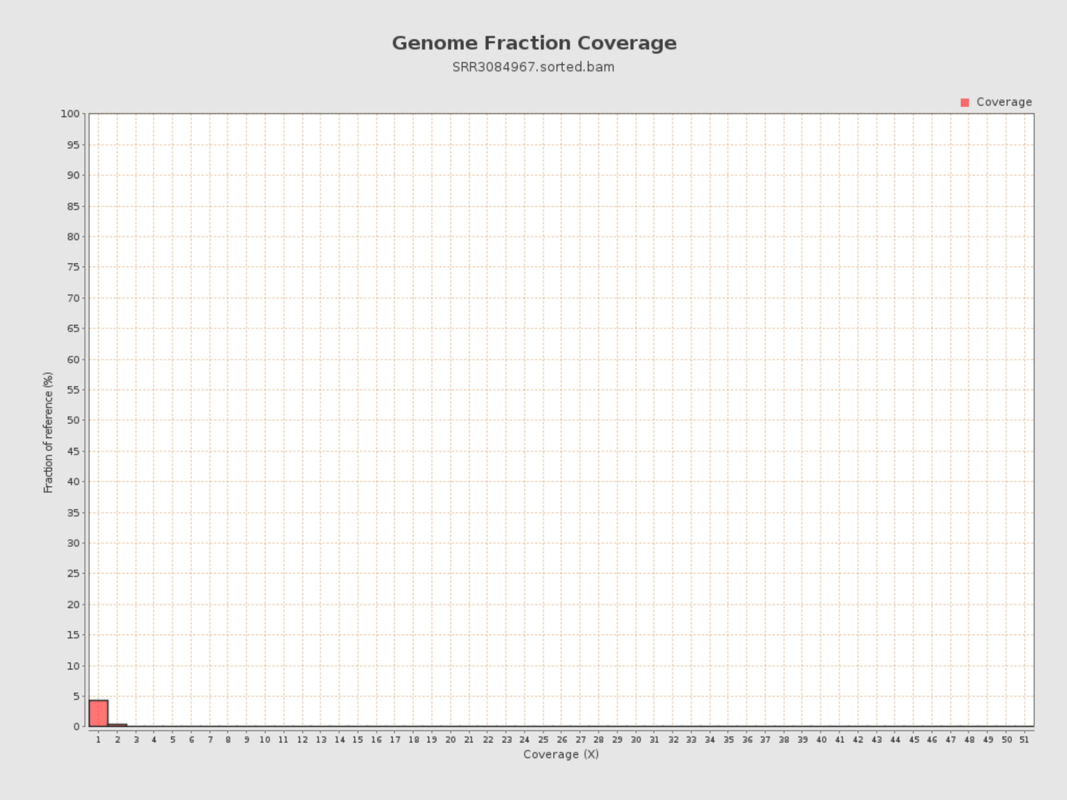
4. Results : Coverage Histogram



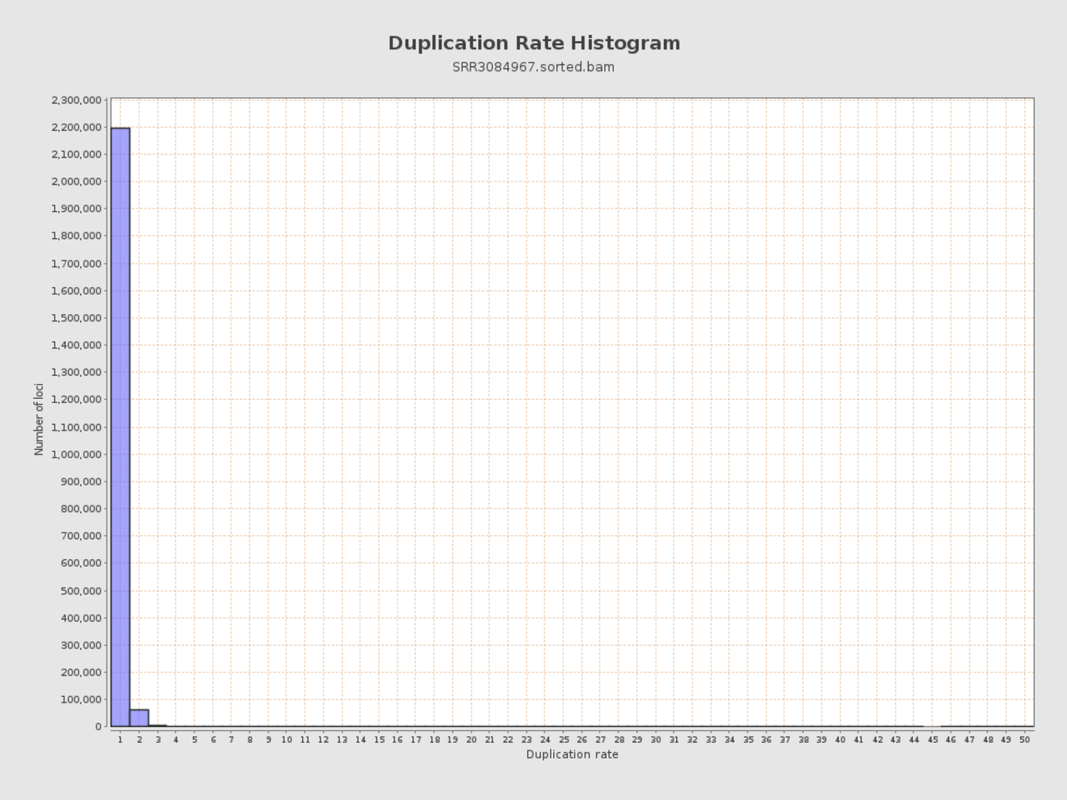
5. Results : Coverage Histogram (0-50X)



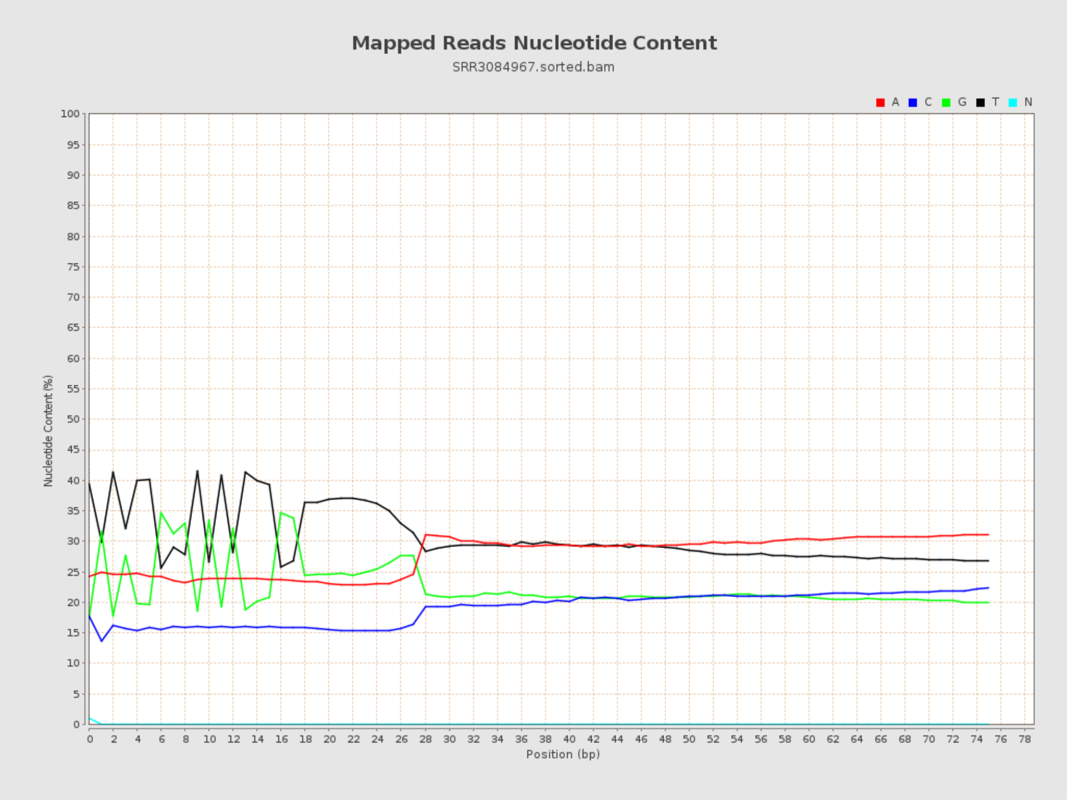
6. Results : Genome Fraction Coverage



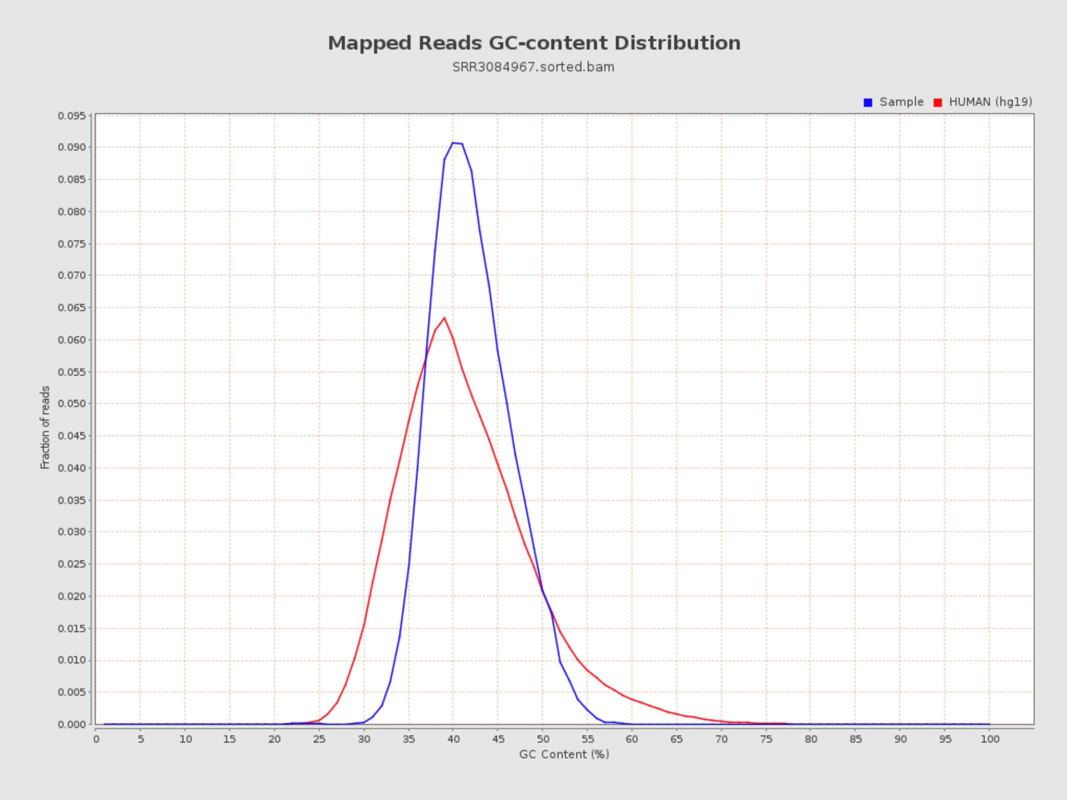
7. Results : Duplication Rate Histogram



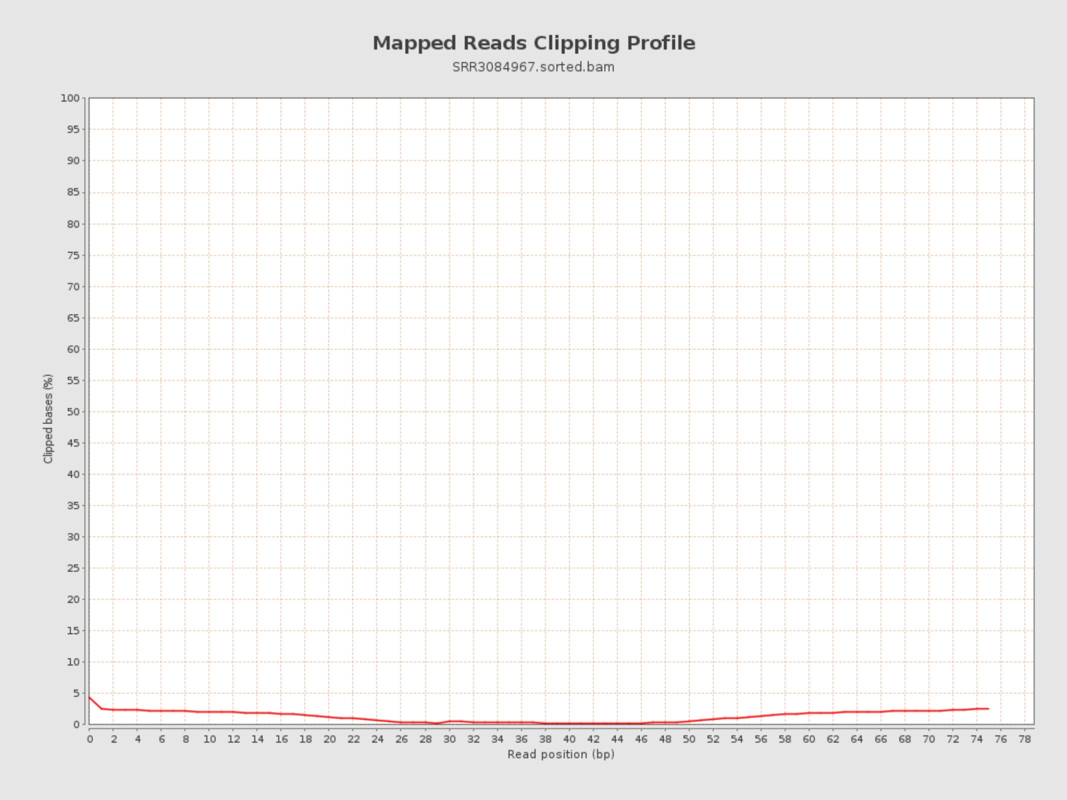
8. Results : Mapped Reads Nucleotide Content



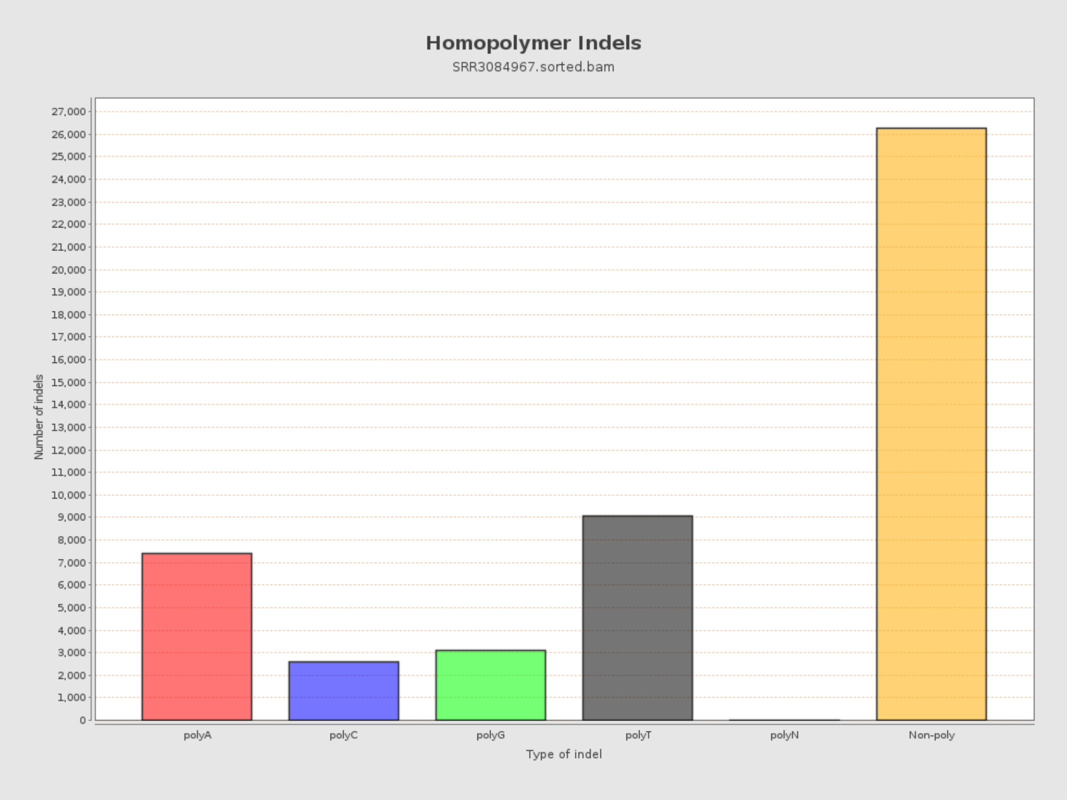
9. Results : Mapped Reads GC-content Distribution



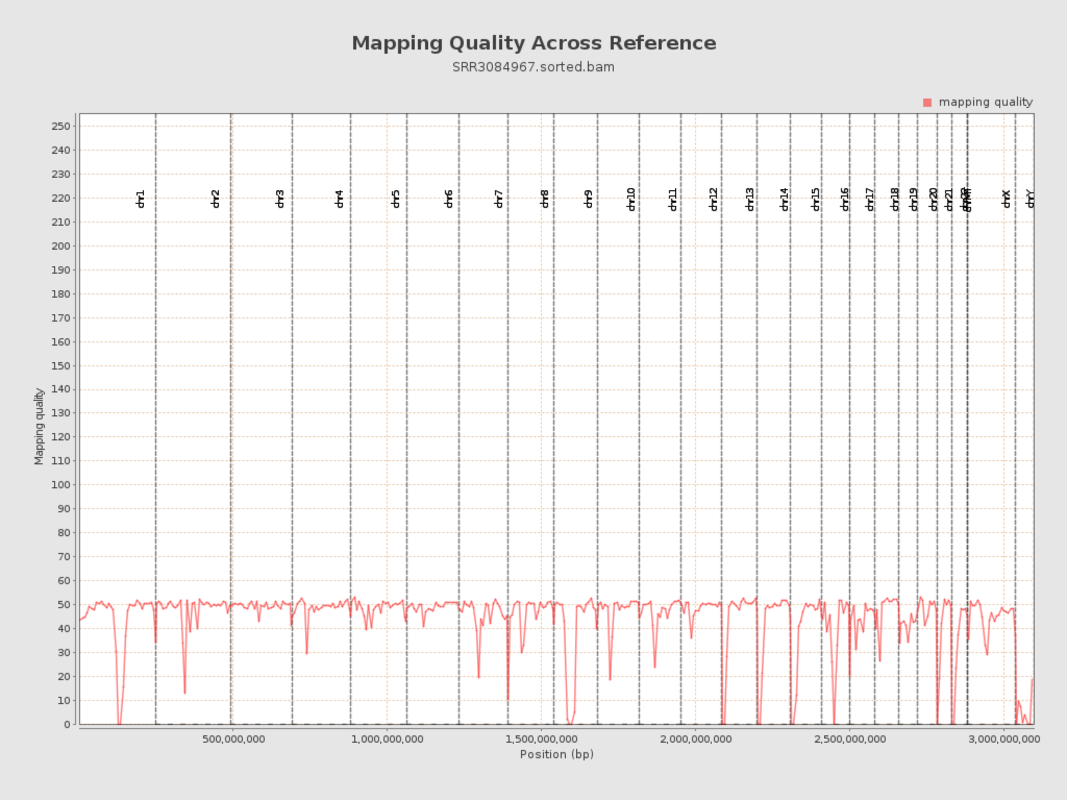
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram