Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 20:50:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084970.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_SRR3084970 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084970.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 20:50:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084970.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,639,858
Mapped reads	2,395,471 / 90.74%
Unmapped reads	244,387 / 9.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,529 / 0.97%
Read min/max/mean length	30 / 76 / 76.34
Duplicated reads (estimated)	88,620 / 3.36%
Duplication rate	2.39%
Clipped reads	980,575 / 37.14%

2.2. ACGT Content

Number/percentage of A's	47,403,041 / 29.12%
Number/percentage of C's	30,179,296 / 18.54%
Number/percentage of T's	50,564,781 / 31.06%
Number/percentage of G's	34,627,872 / 21.27%
Number/percentage of N's	22,607 / 0.01%
GC Percentage	39.81%

2.3. Coverage

Mean	0.0526

Standard Deviation	0.5654

2.4. Mapping Quality

Mean Mapping Quality	46.17

2.5. Mismatches and indels

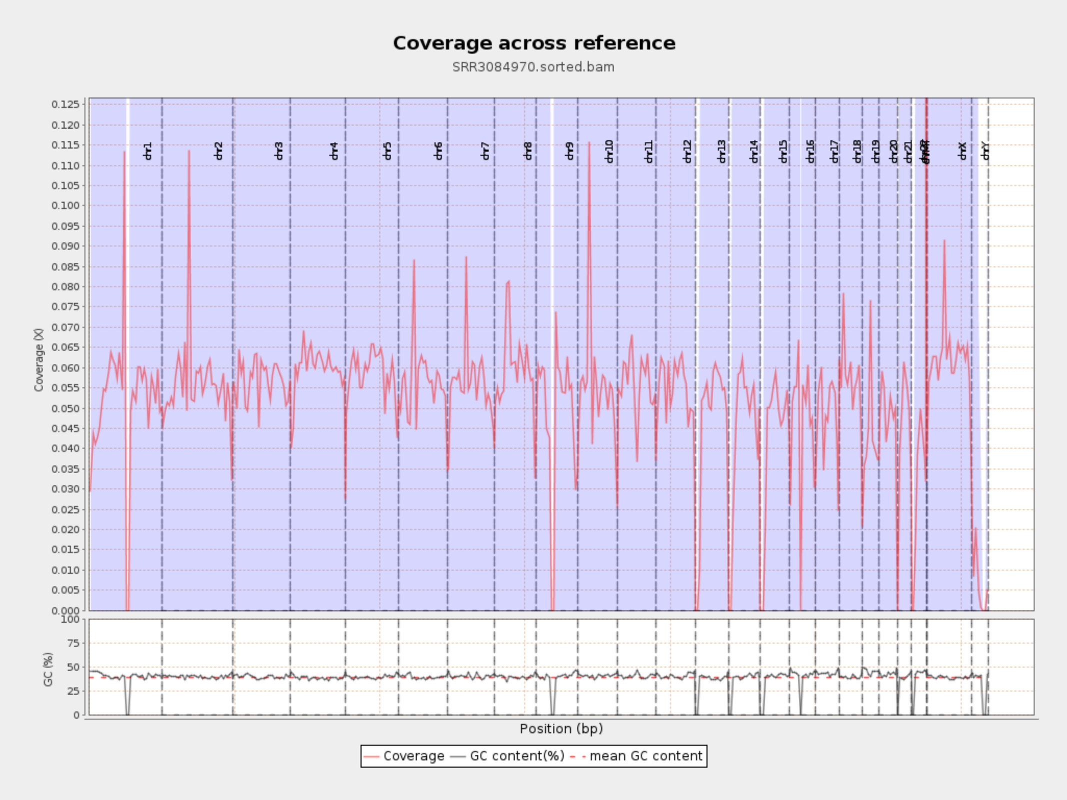
General error rate	0.87%
Mismatches	1,392,770
Insertions	13,856
Mapped reads with at least one insertion	0.57%
Deletions	38,764
Mapped reads with at least one deletion	1.6%
Homopolymer indels	46.81%

2.6. Chromosome stats

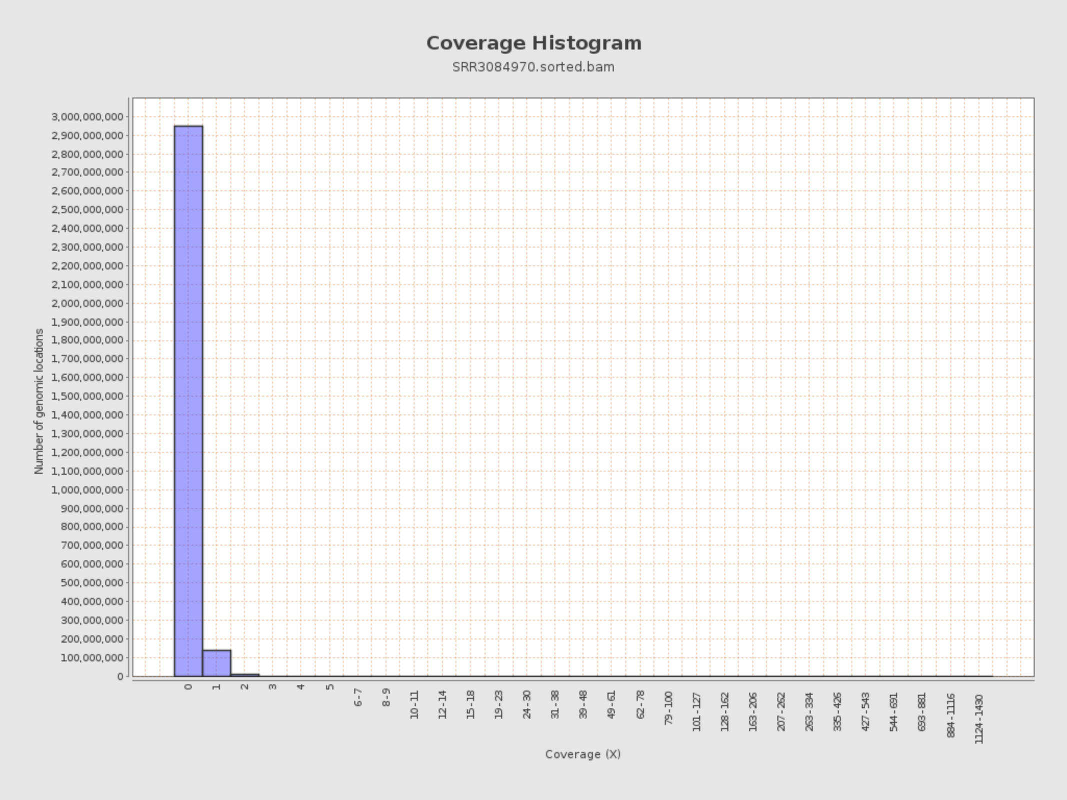
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12957815	0.052	1.2159
chr2	243199373	13741292	0.0565	0.5686
chr3	198022430	11259608	0.0569	0.265
chr4	191154276	11418422	0.0597	0.2748
chr5	180915260	10620441	0.0587	0.2636
chr6	171115067	9697993	0.0567	0.3917
chr7	159138663	9035696	0.0568	0.4828

chr8	146364022	8688390	0.0594	0.9232
chr9	141213431	6840108	0.0484	0.4799
chr10	135534747	7646535	0.0564	0.6307
chr11	135006516	7504060	0.0556	0.497
chr12	133851895	7337306	0.0548	0.2623
chr13	115169878	5213883	0.0453	0.2252
chr14	107349540	4697667	0.0438	0.265
chr15	102531392	4260317	0.0416	0.2211
chr16	90354753	4171031	0.0462	0.3217
chr17	81195210	3864920	0.0476	0.3078
chr18	78077248	4540247	0.0582	1.0031
chr19	59128983	2572491	0.0435	0.8405
chr20	63025520	3073243	0.0488	0.2609
chr21	48129895	2128484	0.0442	0.255
chr22	51304566	1507508	0.0294	0.1819
chrMT	16571	40858	2.4656	2.1973
chrX	155270560	9654733	0.0622	0.3398
chrY	59373566	387996	0.0065	0.1436

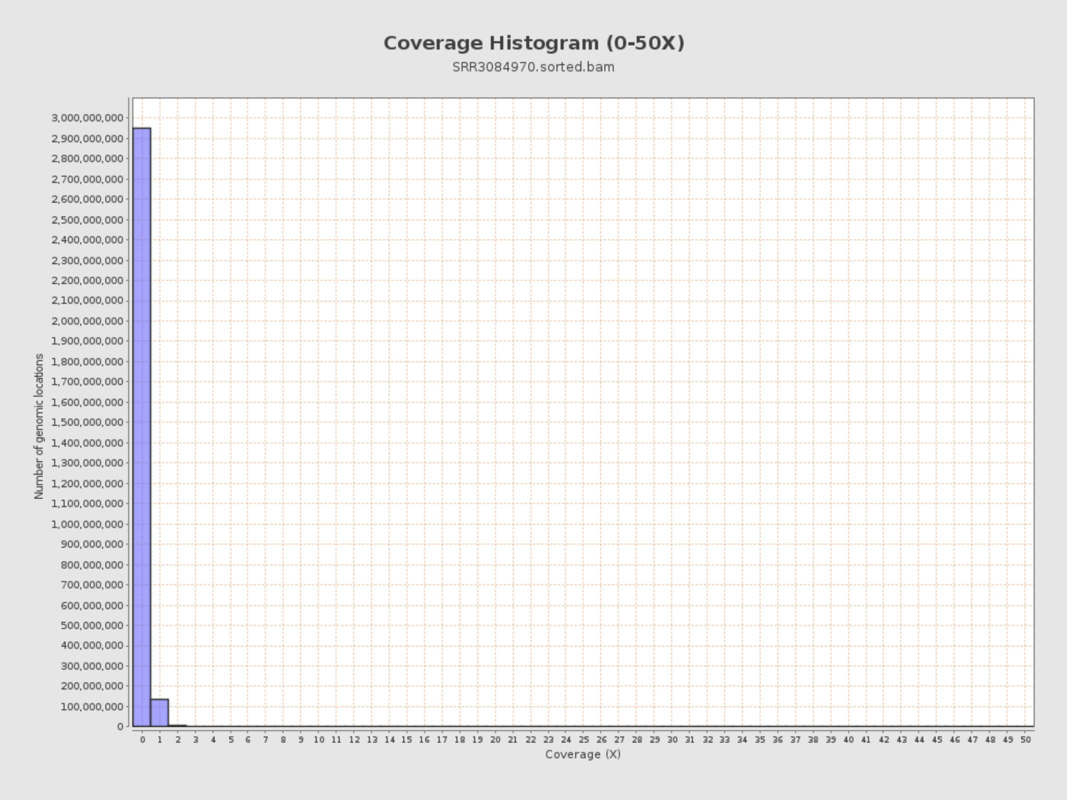
3. Results : Coverage across reference



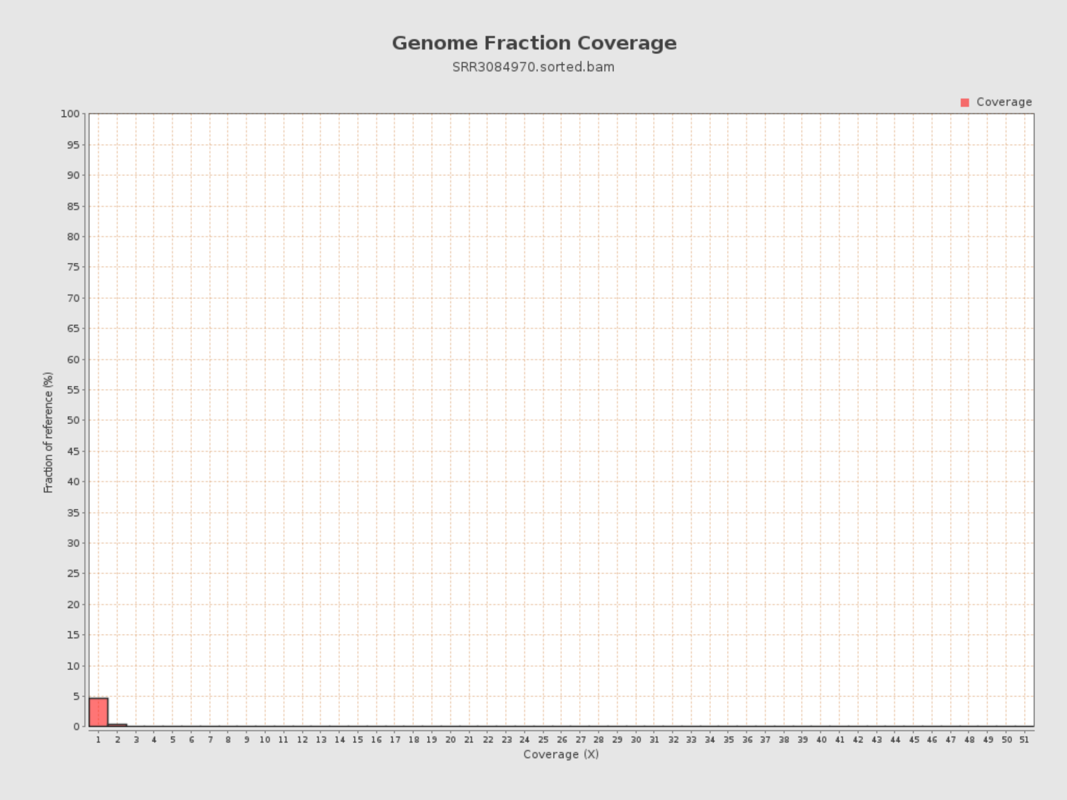
4. Results : Coverage Histogram



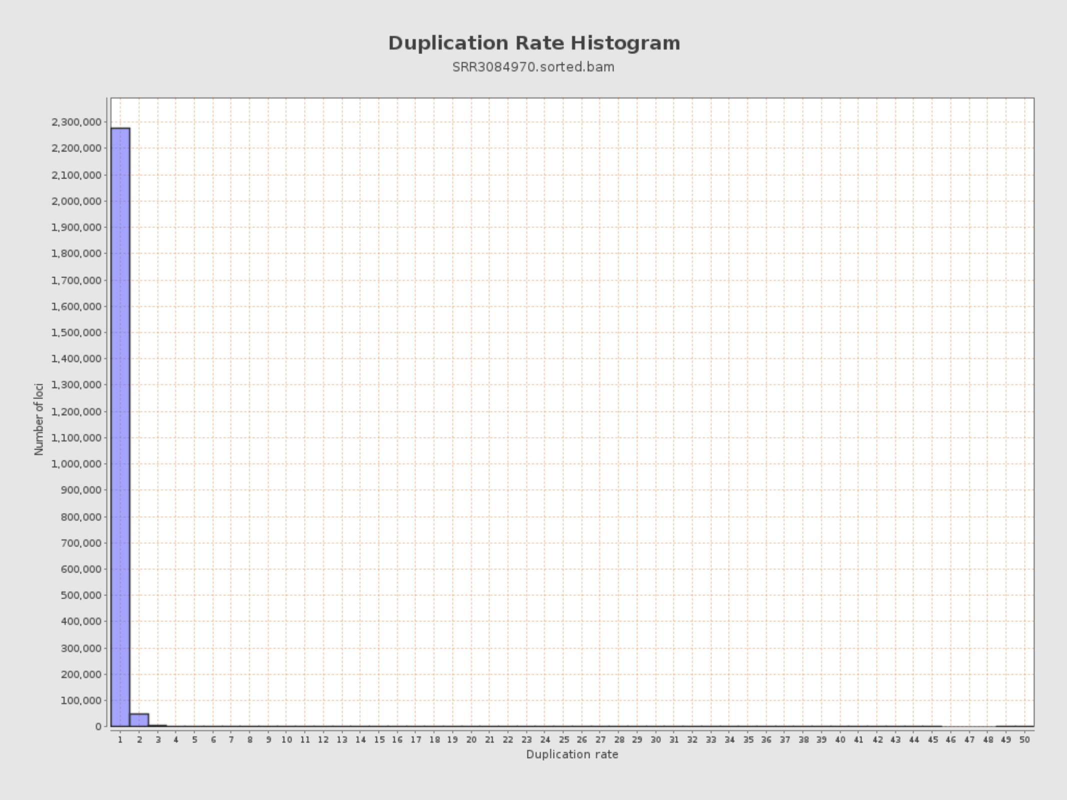
5. Results : Coverage Histogram (0-50X)



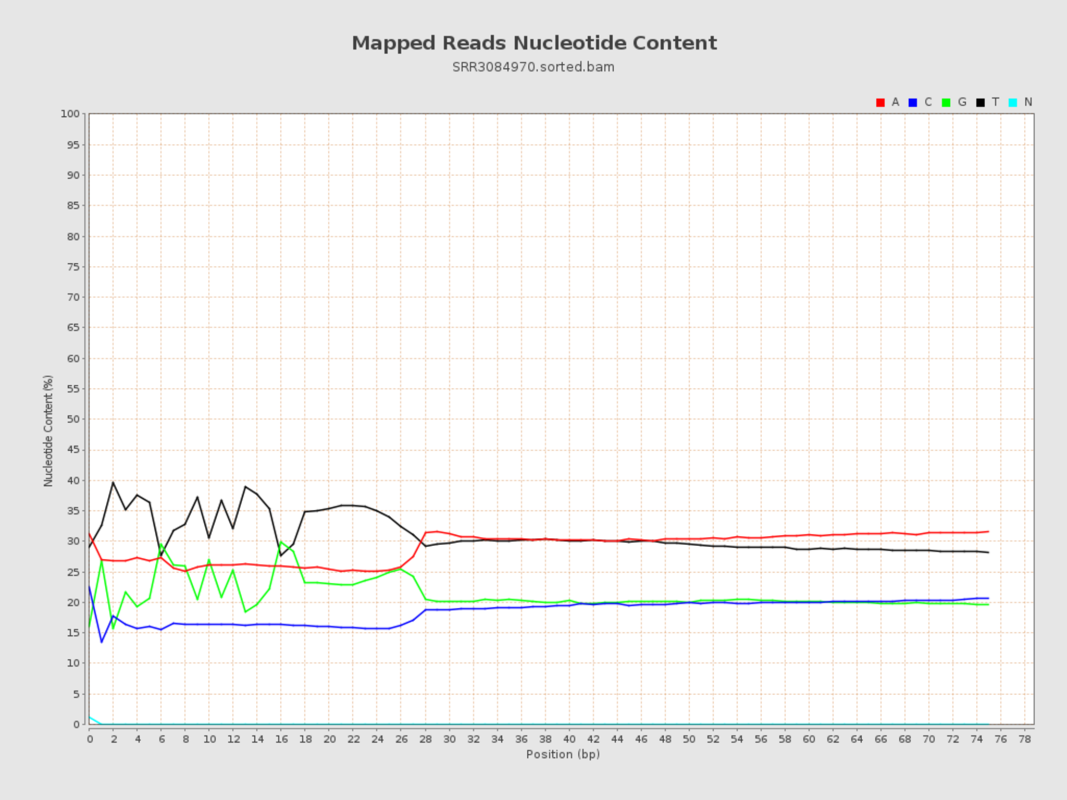
6. Results : Genome Fraction Coverage



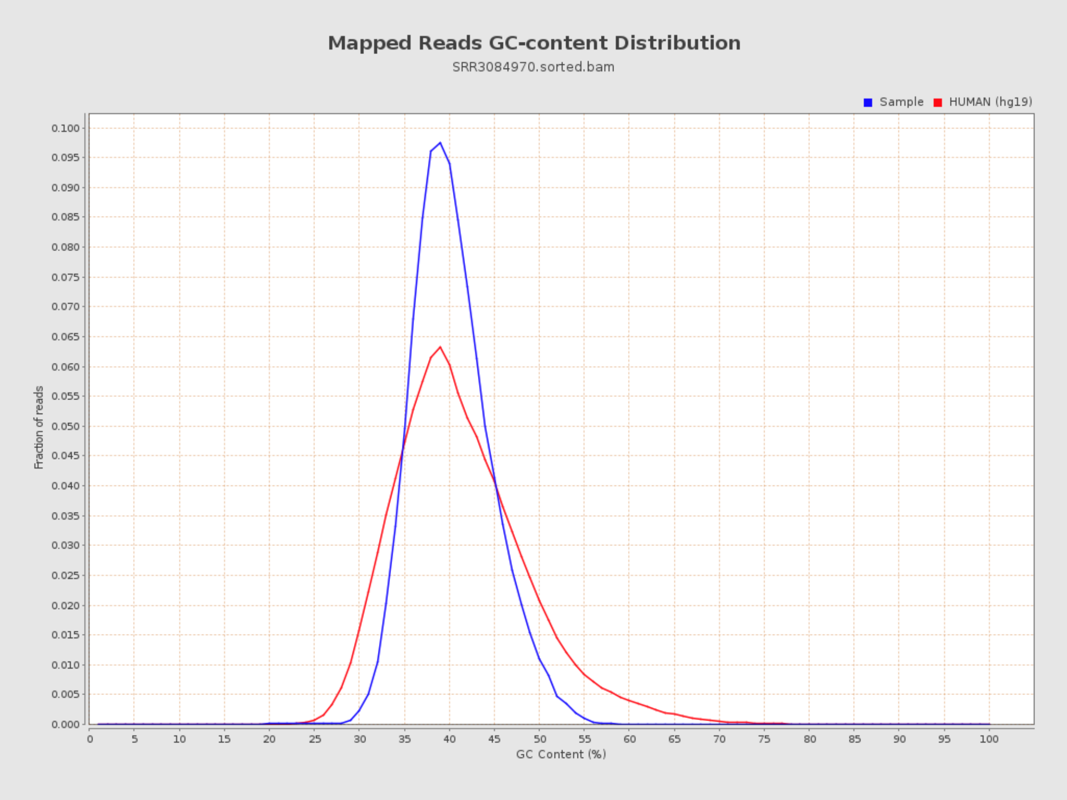
7. Results : Duplication Rate Histogram



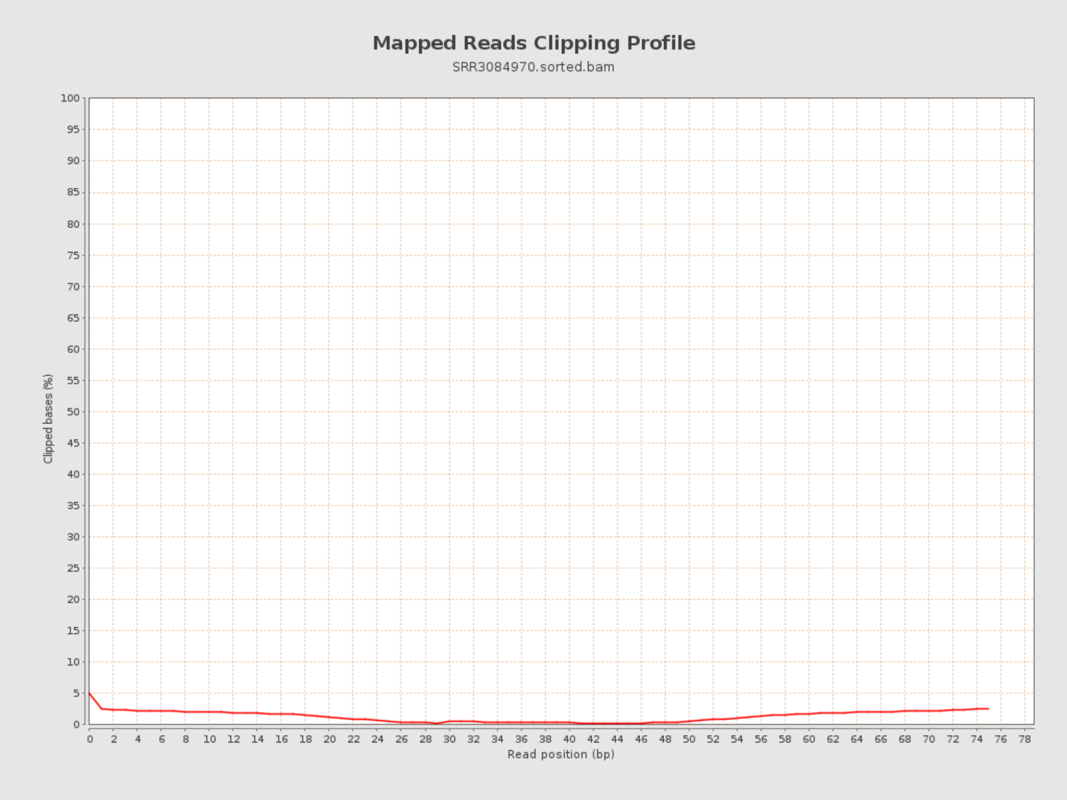
8. Results : Mapped Reads Nucleotide Content



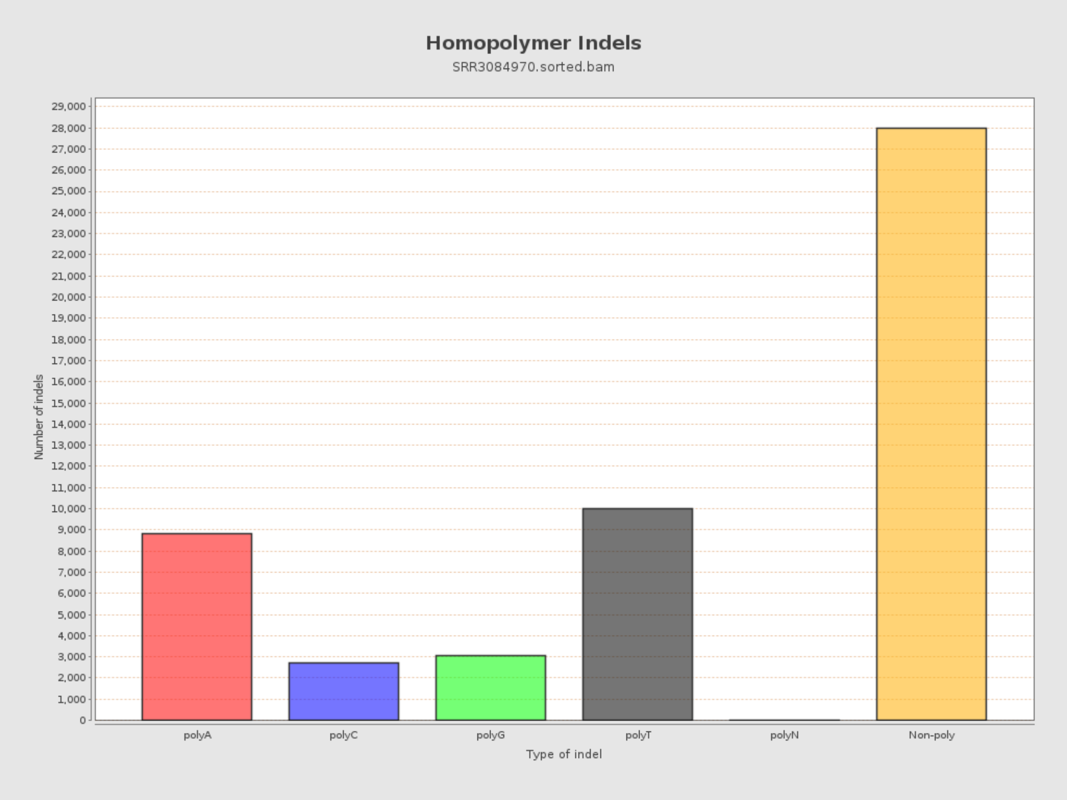
9. Results : Mapped Reads GC-content Distribution



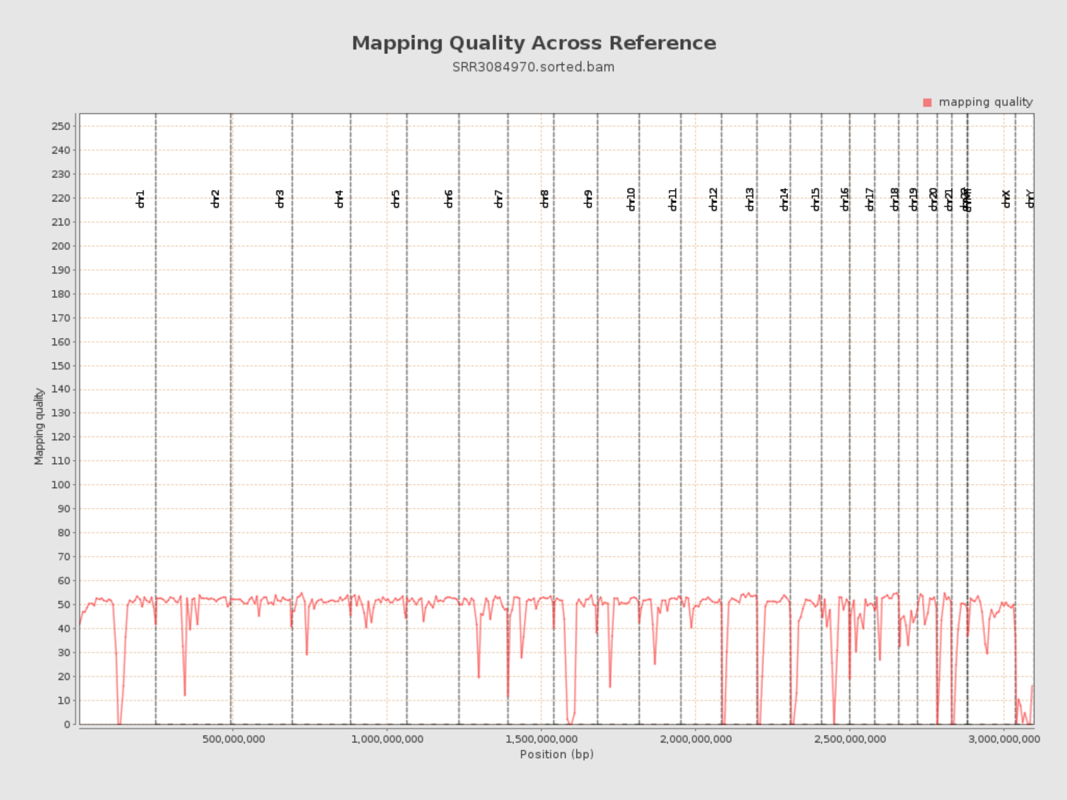
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram