Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 19:56:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084903.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_SRR3084903 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084903.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 19:56:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084903.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,436,641
Mapped reads	2,190,293 / 89.89%
Unmapped reads	246,348 / 10.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,751 / 0.69%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	111,512 / 4.58%
Duplication rate	4.41%
Clipped reads	834,196 / 34.24%

2.2. ACGT Content

Number/percentage of A's	42,854,844 / 28.69%
Number/percentage of C's	27,030,544 / 18.09%
Number/percentage of T's	48,163,908 / 32.24%
Number/percentage of G's	31,319,700 / 20.96%
Number/percentage of N's	23,107 / 0.02%
GC Percentage	39.06%

2.3. Coverage

Mean	0.0483

Standard Deviation	0.3452

2.4. Mapping Quality

Mean Mapping Quality	47.4

2.5. Mismatches and indels

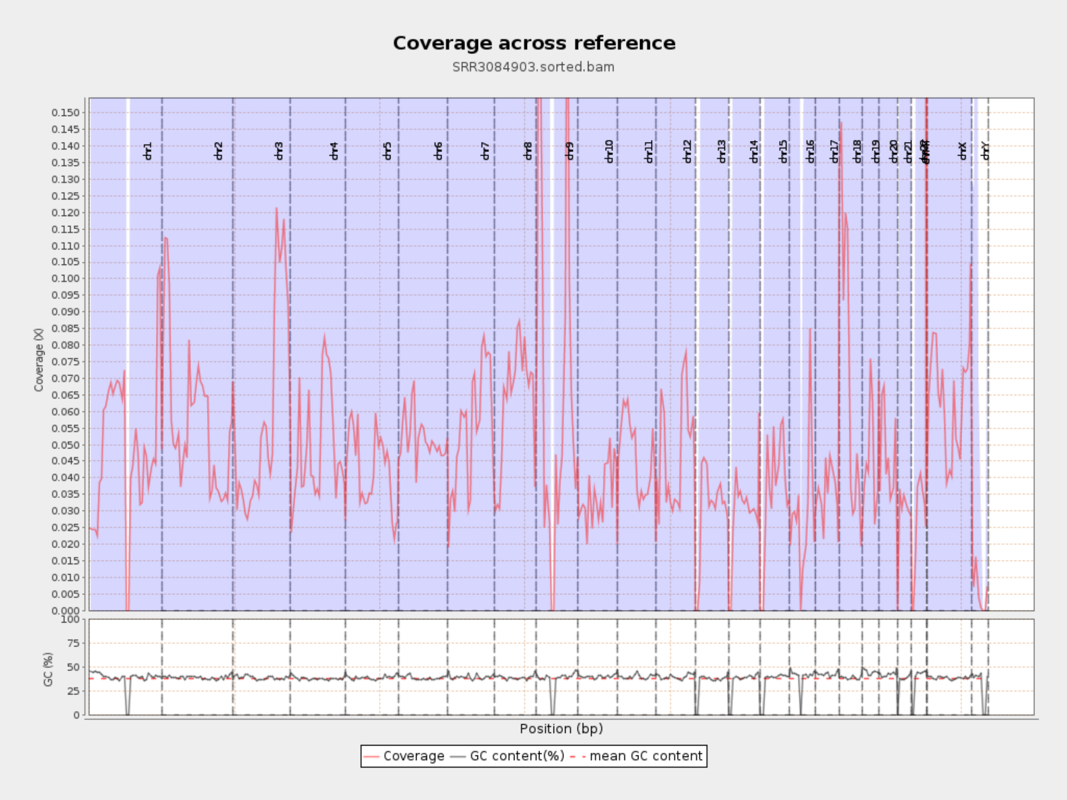
General error rate	0.83%
Mismatches	1,214,600
Insertions	11,339
Mapped reads with at least one insertion	0.51%
Deletions	32,403
Mapped reads with at least one deletion	1.47%
Homopolymer indels	48.73%

2.6. Chromosome stats

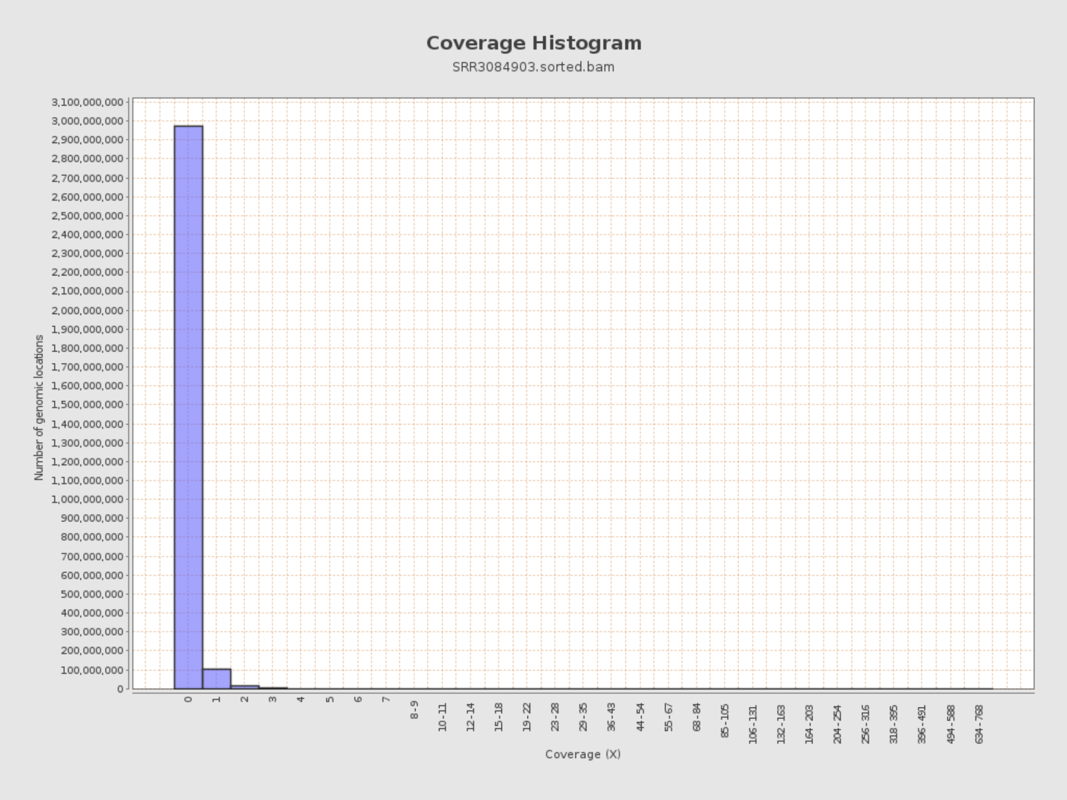
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12148313	0.0487	0.5034
chr2	243199373	13923253	0.0573	0.4055
chr3	198022430	11724203	0.0592	0.2809
chr4	191154276	9438576	0.0494	0.2578
chr5	180915260	7732619	0.0427	0.24
chr6	171115067	8876403	0.0519	0.2723
chr7	159138663	8793893	0.0553	0.3701

chr8	146364022	9273291	0.0634	0.5809
chr9	141213431	9814759	0.0695	0.3877
chr10	135534747	4718967	0.0348	0.2632
chr11	135006516	6242593	0.0462	0.2958
chr12	133851895	6380689	0.0477	0.2523
chr13	115169878	3462567	0.0301	0.1983
chr14	107349540	3029086	0.0282	0.1982
chr15	102531392	3711334	0.0362	0.2183
chr16	90354753	2709179	0.03	0.2143
chr17	81195210	2909170	0.0358	0.2292
chr18	78077248	5658342	0.0725	0.6089
chr19	59128983	2733024	0.0462	0.3426
chr20	63025520	3000827	0.0476	0.2556
chr21	48129895	1403095	0.0292	0.2074
chr22	51304566	1299363	0.0253	0.1807
chrMT	16571	360813	21.7738	11.0631
chrX	155270560	9775277	0.063	0.3101
chrY	59373566	328733	0.0055	0.1341

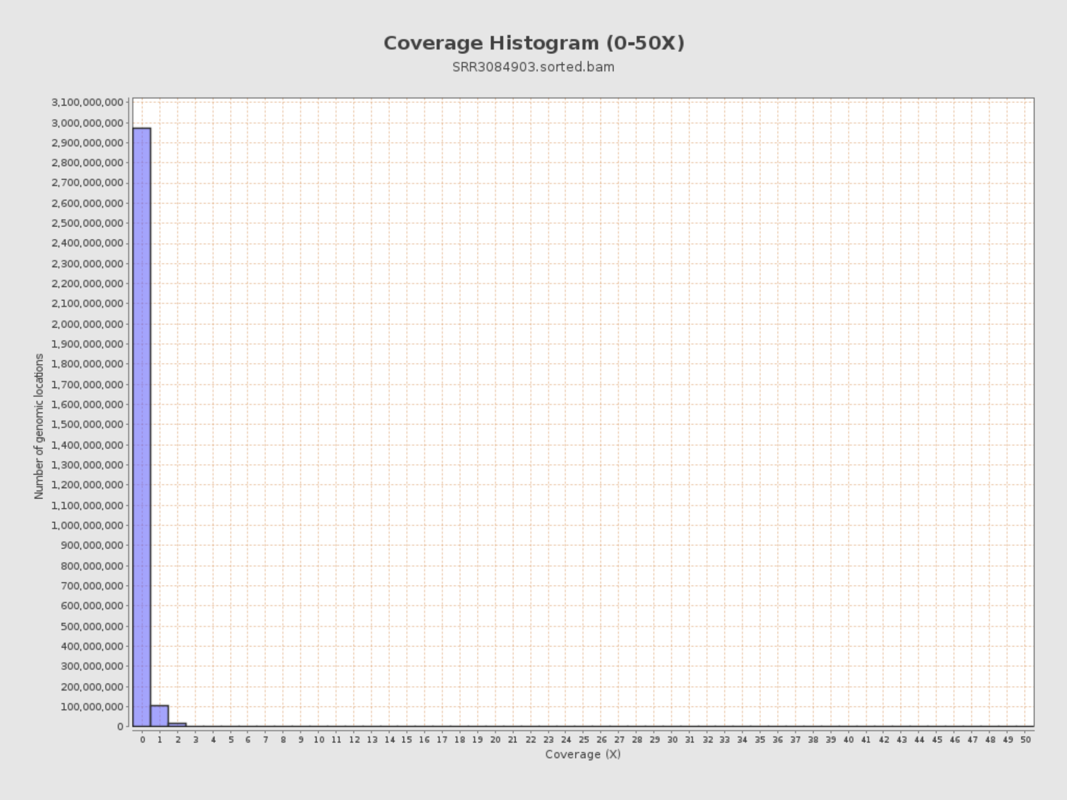
3. Results : Coverage across reference



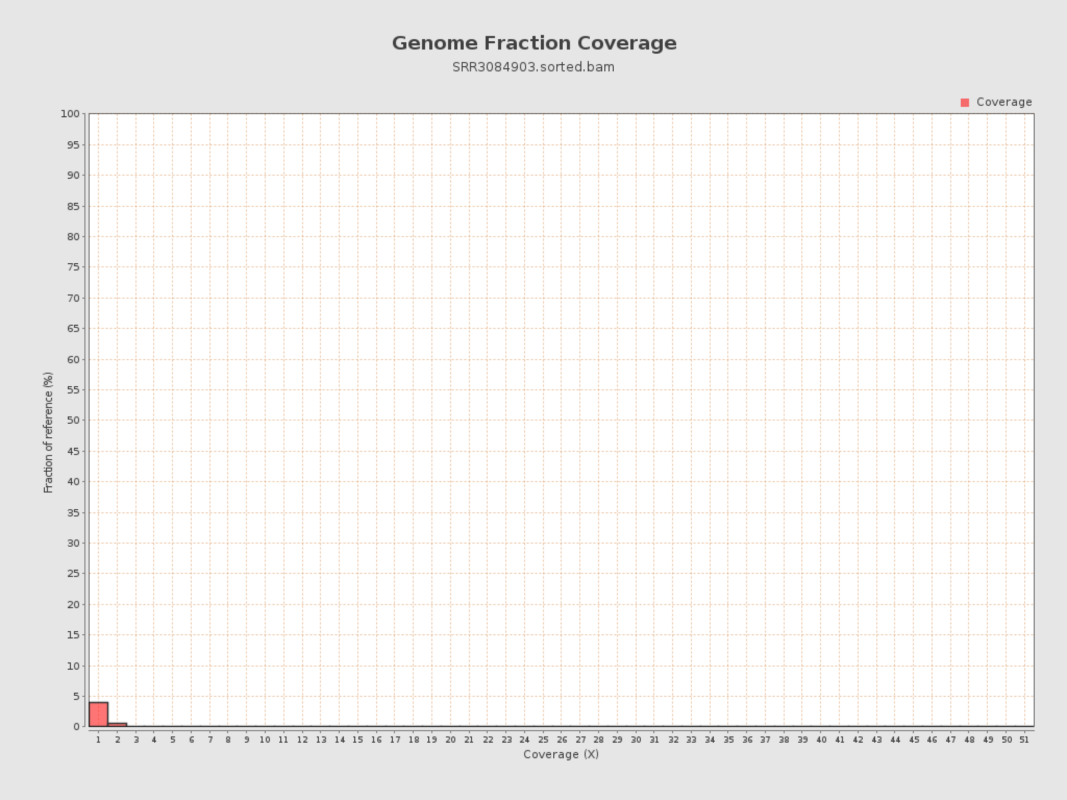
4. Results : Coverage Histogram



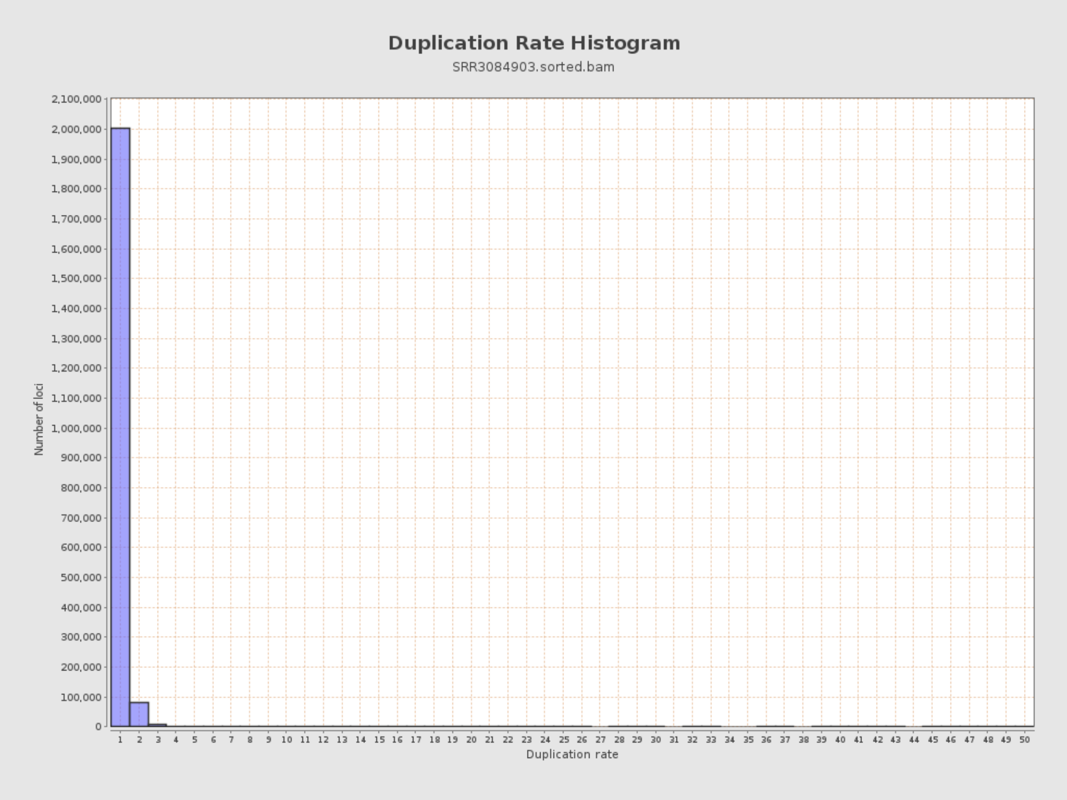
5. Results : Coverage Histogram (0-50X)



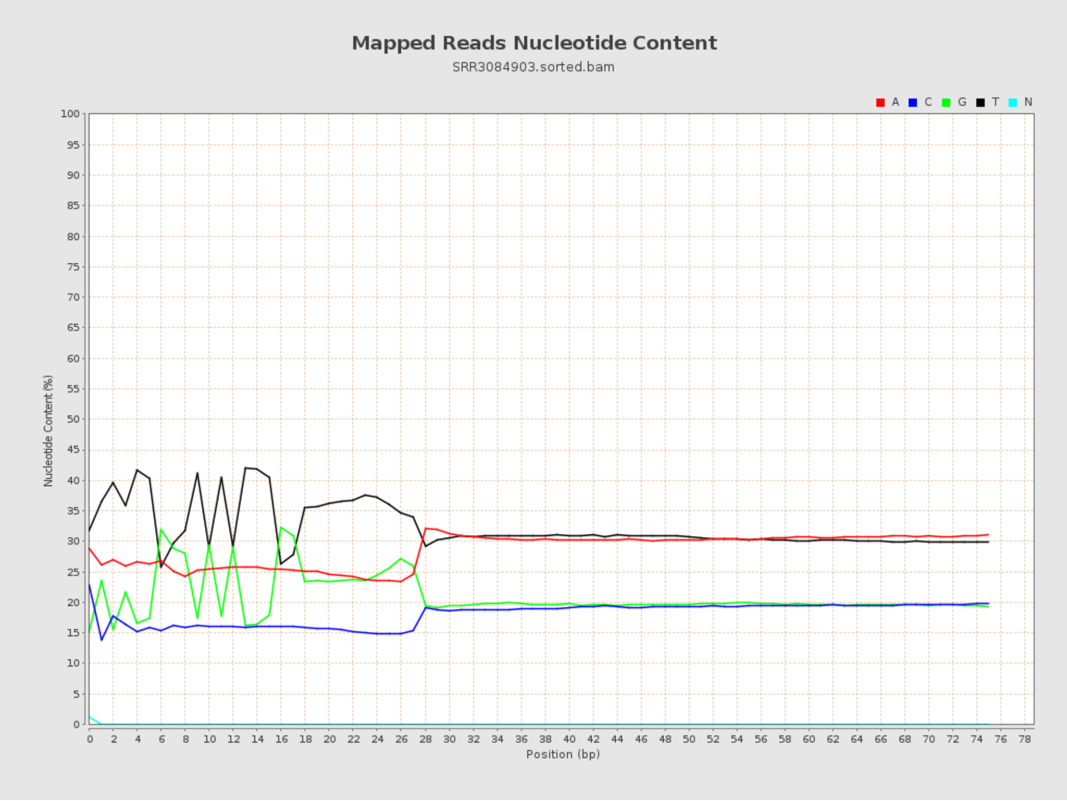
6. Results : Genome Fraction Coverage



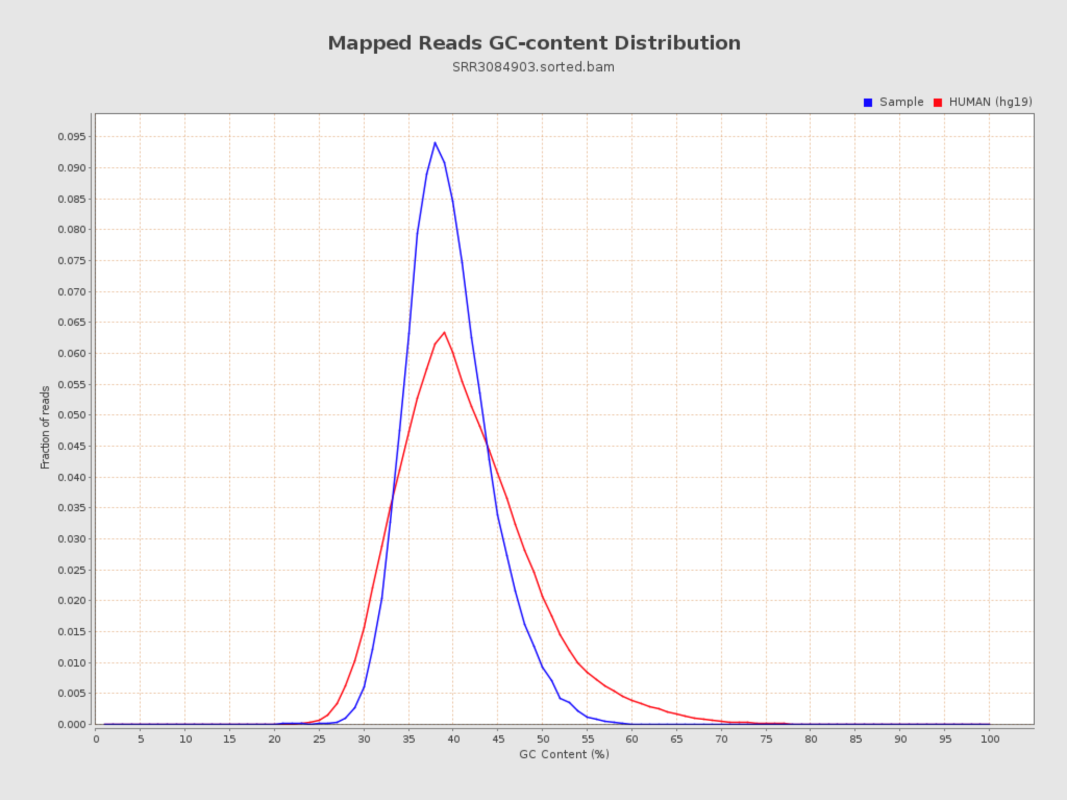
7. Results : Duplication Rate Histogram



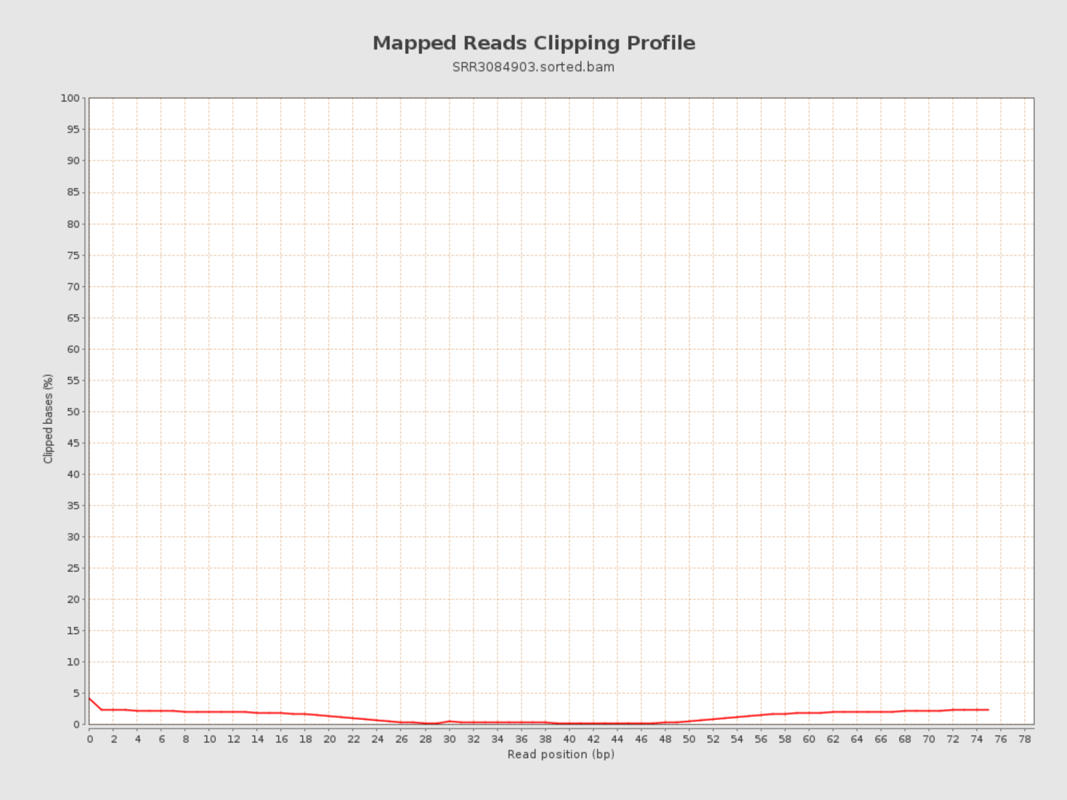
8. Results : Mapped Reads Nucleotide Content



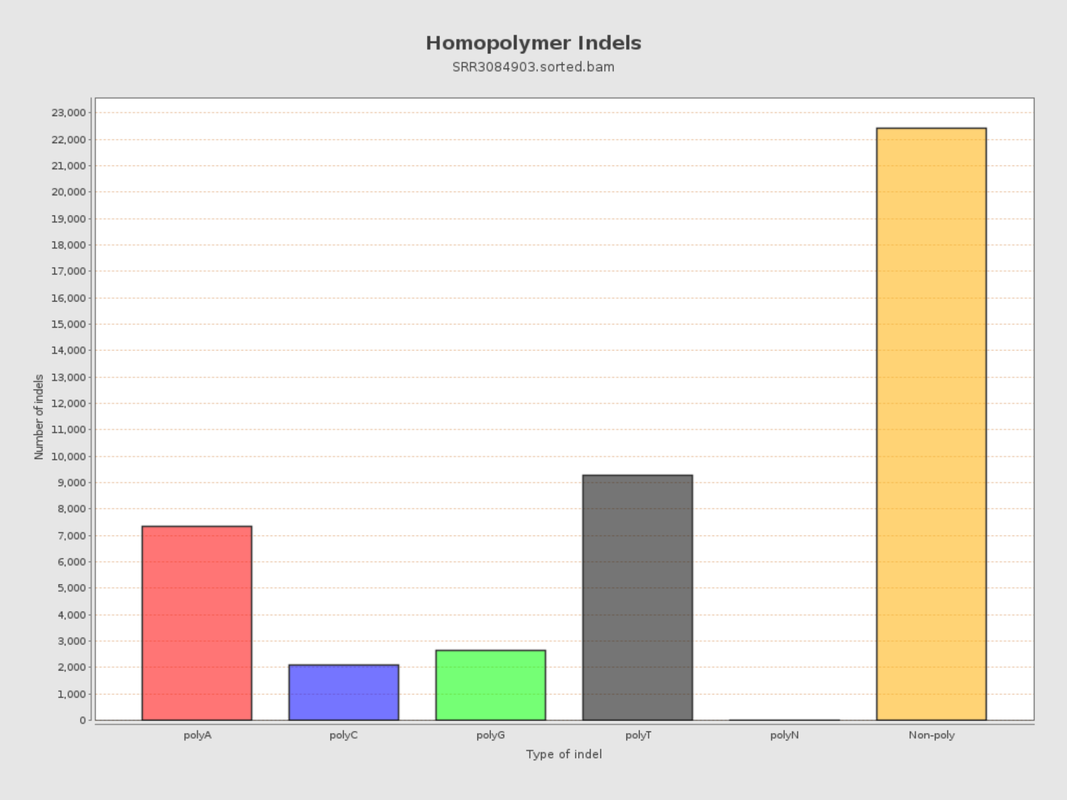
9. Results : Mapped Reads GC-content Distribution



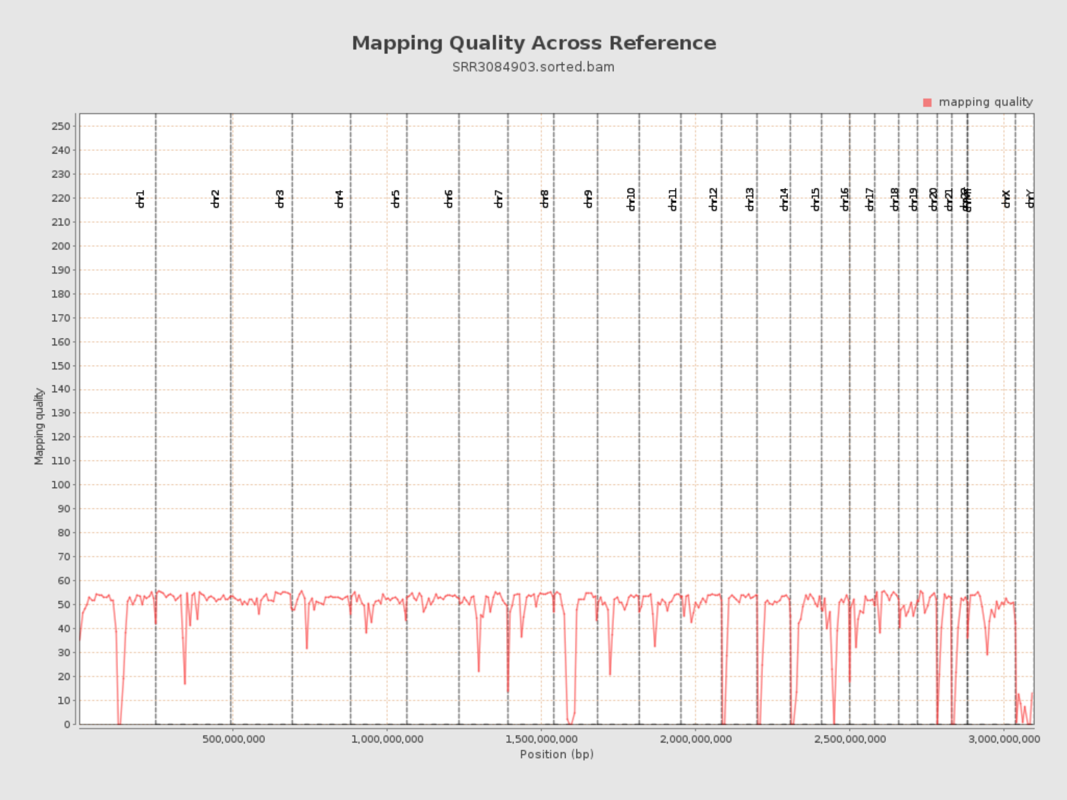
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram