Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 19:45:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084900.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_SRR3084900 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084900.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 19:45:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084900.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,349,216
Mapped reads	2,093,399 / 89.11%
Unmapped reads	255,817 / 10.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,822 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	109,550 / 4.66%
Duplication rate	4.47%
Clipped reads	840,368 / 35.77%

2.2. ACGT Content

Number/percentage of A's	40,184,119 / 28.37%
Number/percentage of C's	25,633,019 / 18.09%
Number/percentage of T's	45,591,699 / 32.18%
Number/percentage of G's	30,229,504 / 21.34%
Number/percentage of N's	21,945 / 0.02%
GC Percentage	39.43%

2.3. Coverage

Mean	0.0458

Standard Deviation	0.3781

2.4. Mapping Quality

Mean Mapping Quality	47.15

2.5. Mismatches and indels

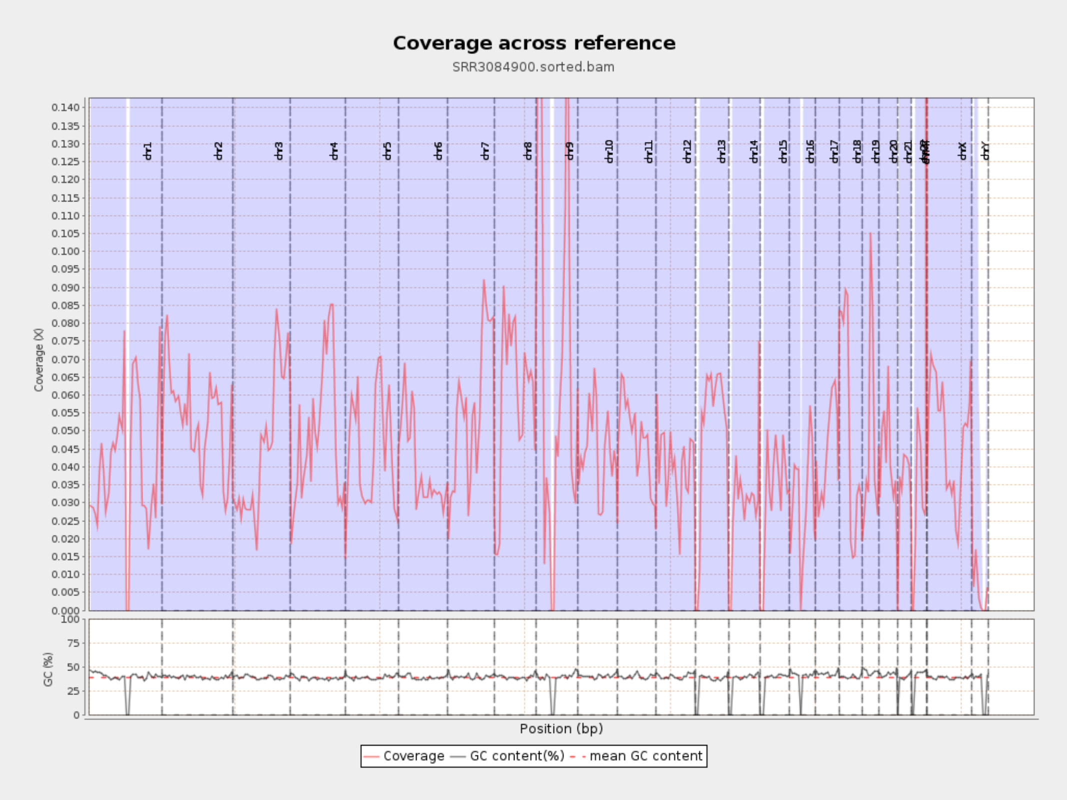
General error rate	0.84%
Mismatches	1,164,528
Insertions	10,998
Mapped reads with at least one insertion	0.52%
Deletions	31,376
Mapped reads with at least one deletion	1.48%
Homopolymer indels	48.65%

2.6. Chromosome stats

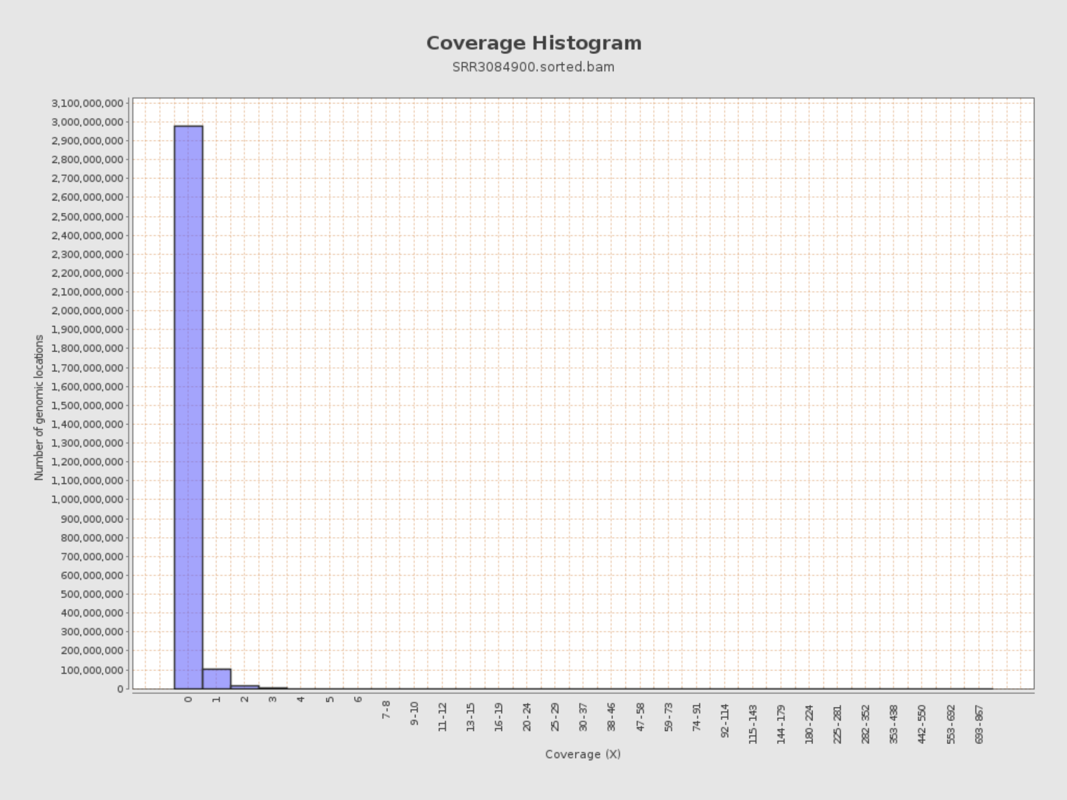
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10079296	0.0404	0.7881
chr2	243199373	13101682	0.0539	0.3796
chr3	198022430	8920309	0.045	0.241
chr4	191154276	9348786	0.0489	0.2571
chr5	180915260	8175905	0.0452	0.249
chr6	171115067	6878522	0.0402	0.2357
chr7	159138663	9029706	0.0567	0.3346

chr8	146364022	8715529	0.0595	0.5328
chr9	141213431	10489126	0.0743	0.3941
chr10	135534747	5994104	0.0442	0.2914
chr11	135006516	6424794	0.0476	0.3036
chr12	133851895	5359249	0.04	0.2276
chr13	115169878	5711013	0.0496	0.2528
chr14	107349540	2995065	0.0279	0.1984
chr15	102531392	3314290	0.0323	0.2052
chr16	90354753	2842426	0.0315	0.2223
chr17	81195210	3659123	0.0451	0.257
chr18	78077248	3986320	0.0511	0.6569
chr19	59128983	2852518	0.0482	0.4503
chr20	63025520	2758406	0.0438	0.248
chr21	48129895	1663584	0.0346	0.2196
chr22	51304566	1426542	0.0278	0.1877
chrMT	16571	209469	12.6407	6.4873
chrX	155270560	7452572	0.048	0.2719
chrY	59373566	326557	0.0055	0.1303

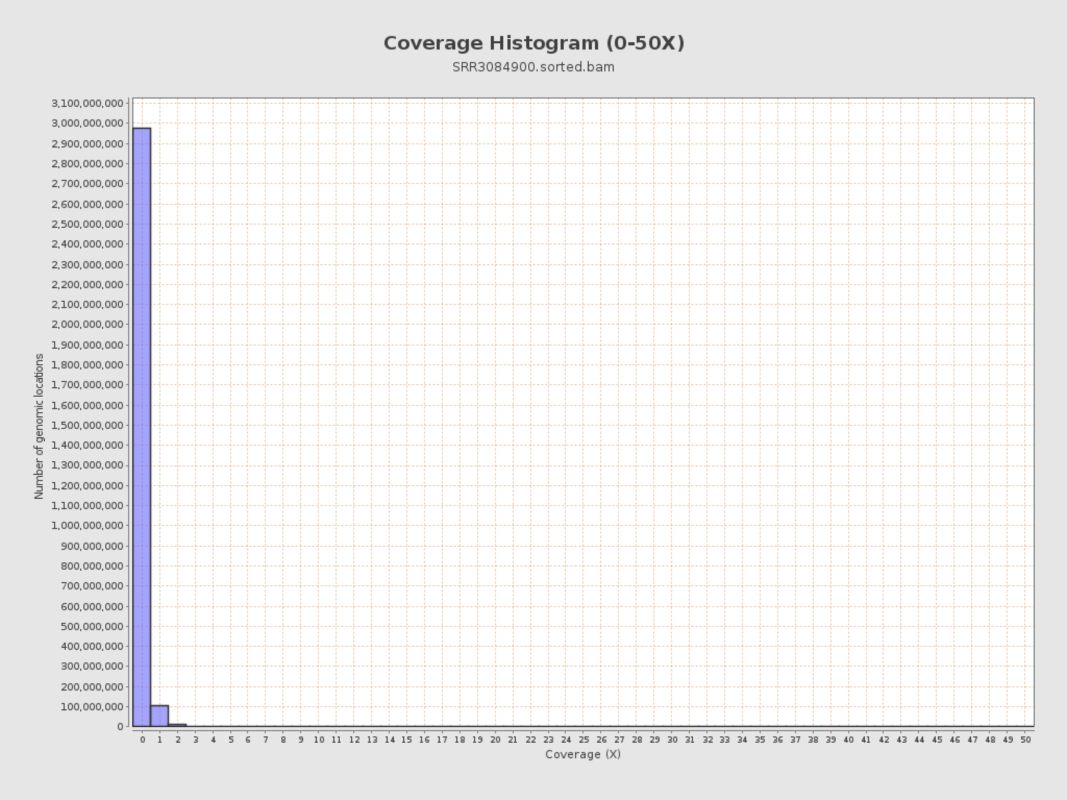
3. Results : Coverage across reference



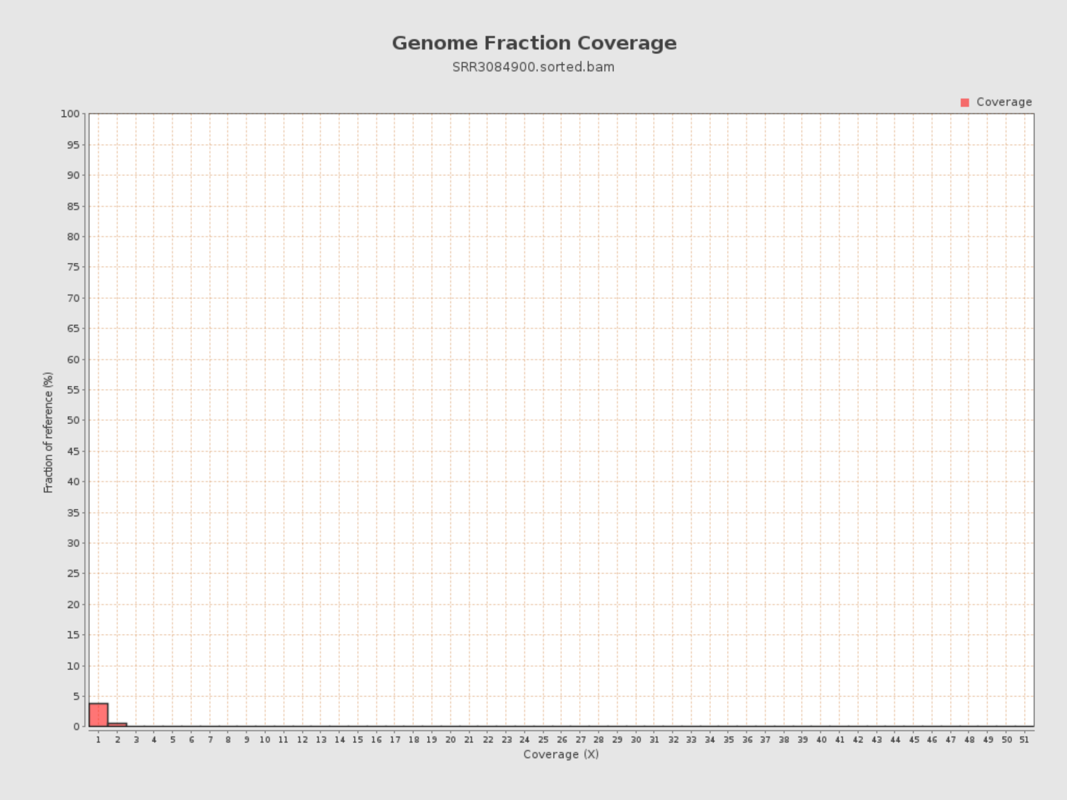
4. Results : Coverage Histogram



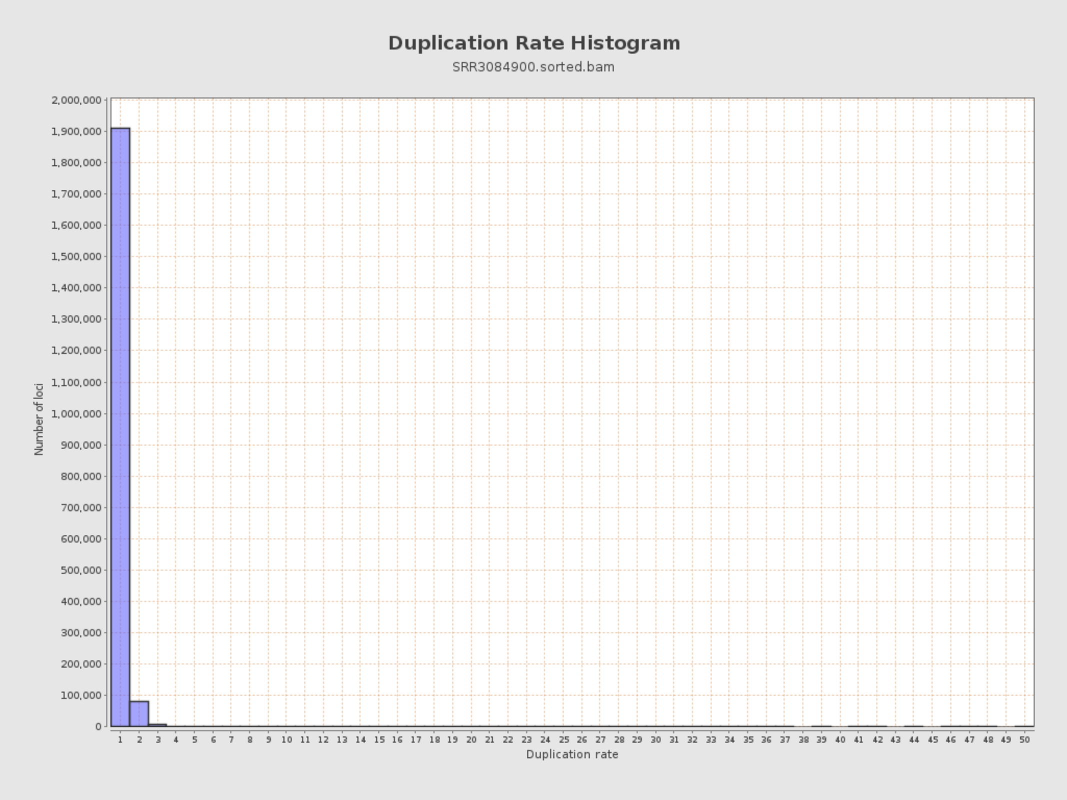
5. Results : Coverage Histogram (0-50X)



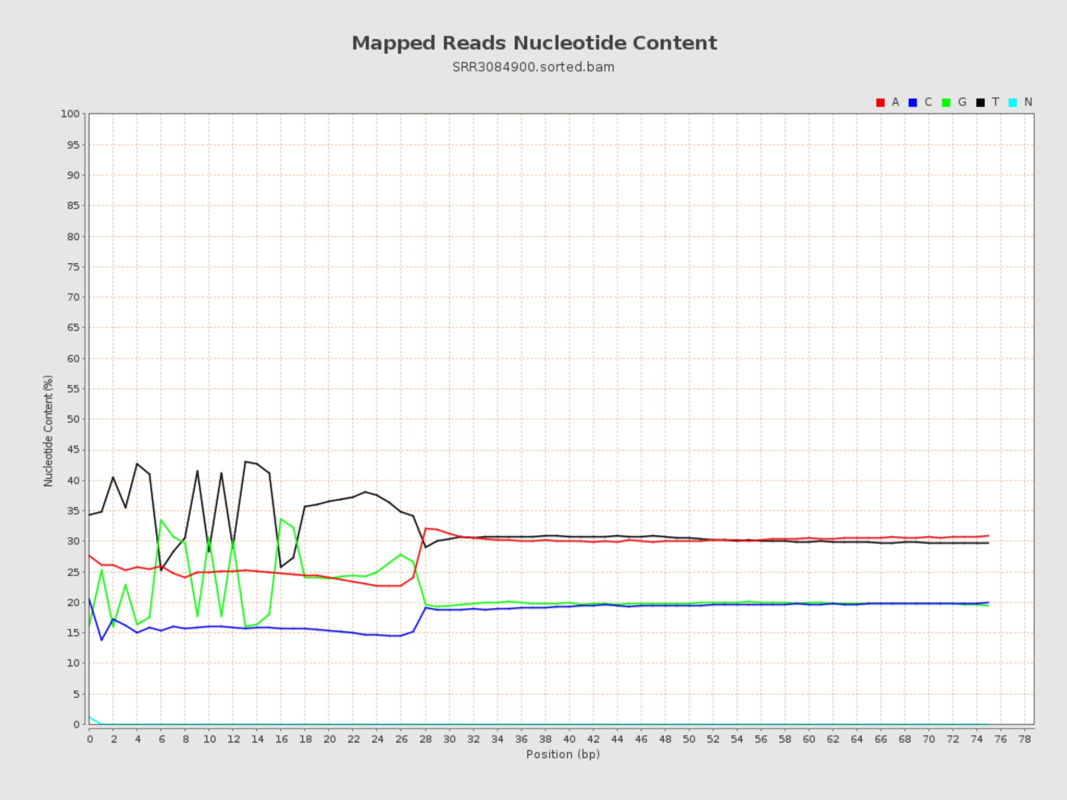
6. Results : Genome Fraction Coverage



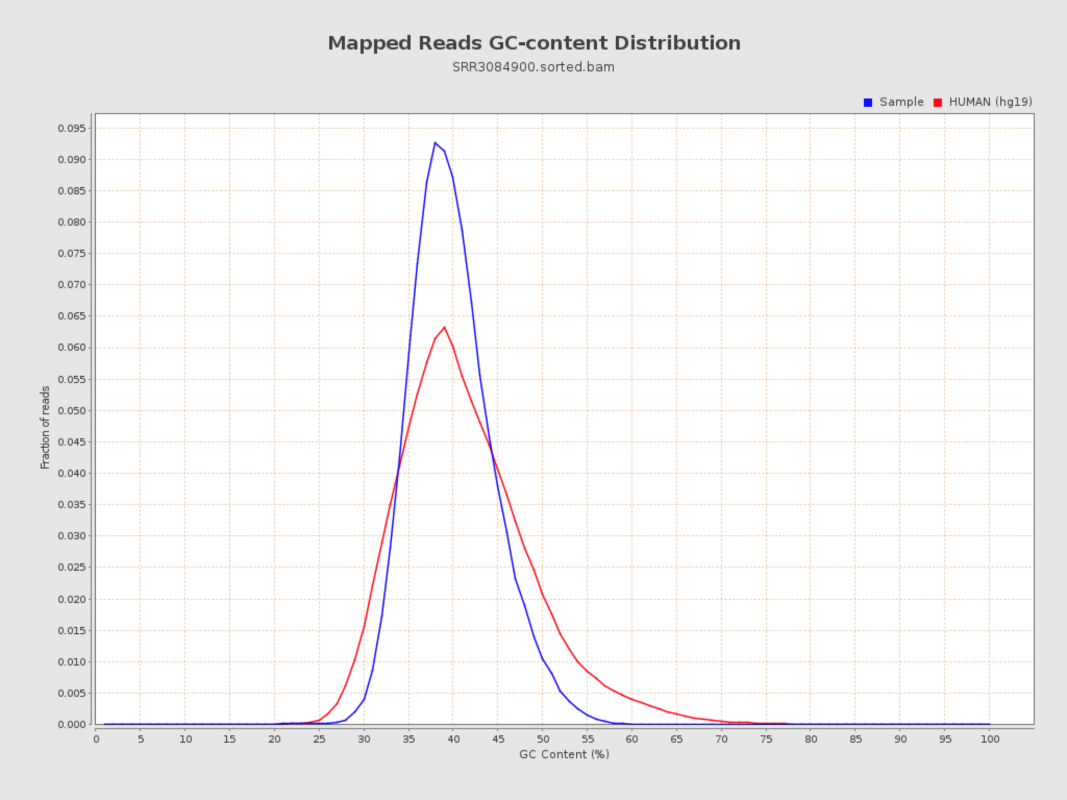
7. Results : Duplication Rate Histogram



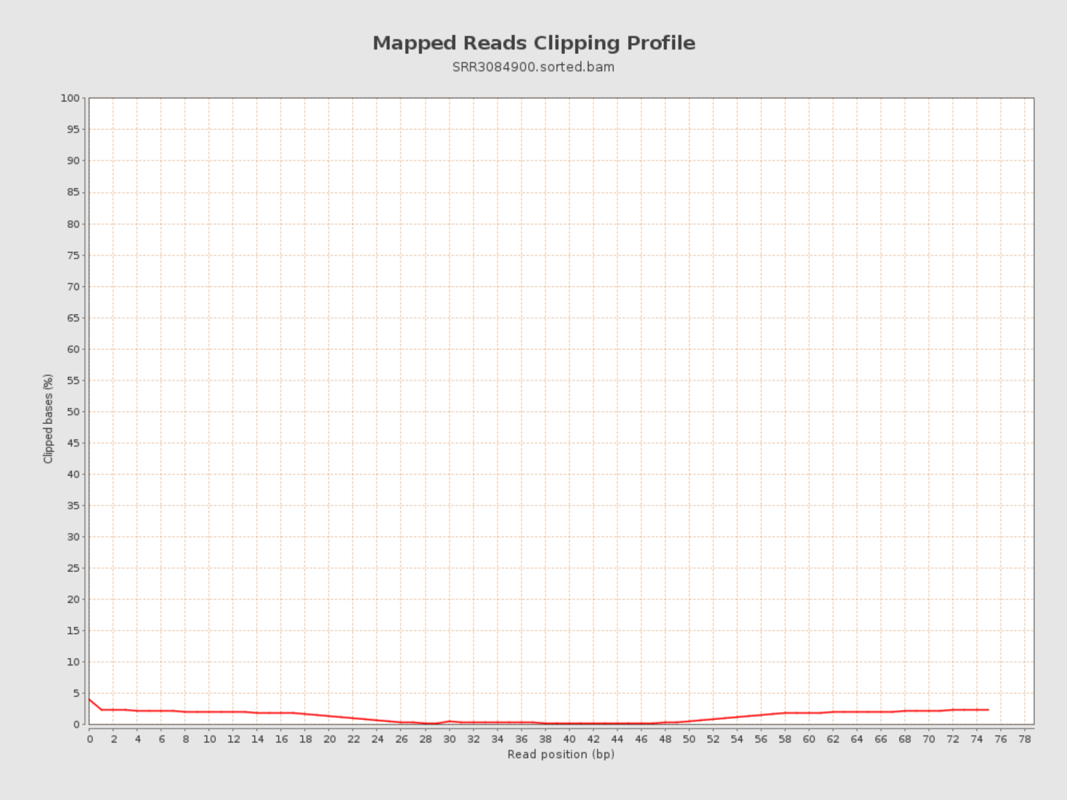
8. Results : Mapped Reads Nucleotide Content



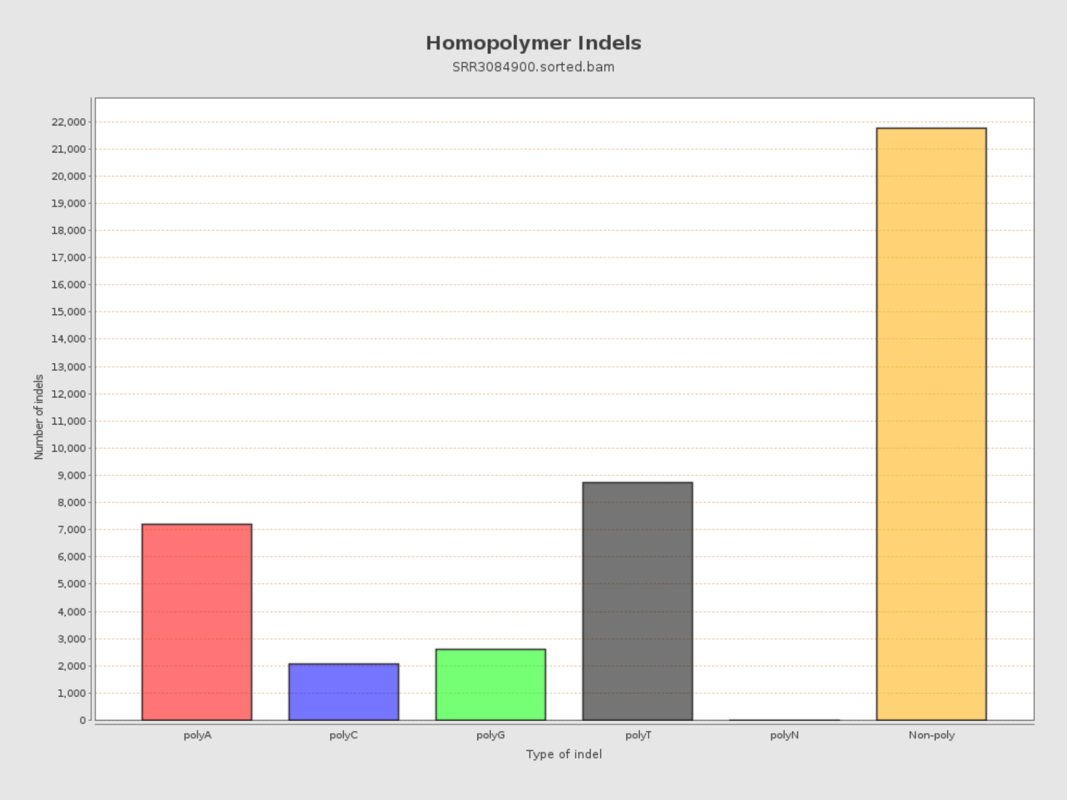
9. Results : Mapped Reads GC-content Distribution



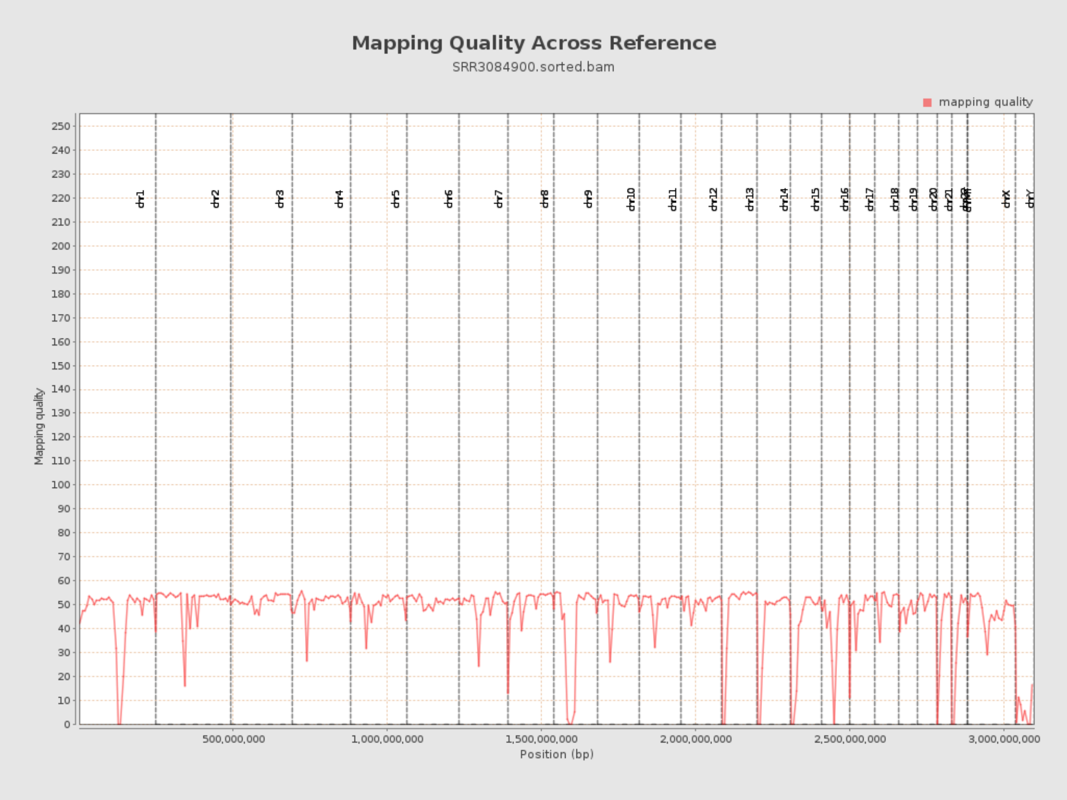
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram