Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 11:20:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084364.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_SRR3084364 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084364.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 11:20:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084364.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,600,088
Mapped reads	2,344,431 / 90.17%
Unmapped reads	255,657 / 9.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,499 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	94,623 / 3.64%
Duplication rate	3.39%
Clipped reads	1,006,987 / 38.73%

2.2. ACGT Content

Number/percentage of A's	43,229,636 / 27.4%
Number/percentage of C's	30,693,511 / 19.45%
Number/percentage of T's	48,385,156 / 30.66%
Number/percentage of G's	35,270,874 / 22.35%
Number/percentage of N's	207,206 / 0.13%
GC Percentage	41.81%

2.3. Coverage

Mean	0.051

Standard Deviation	0.3485

2.4. Mapping Quality

Mean Mapping Quality	46.01

2.5. Mismatches and indels

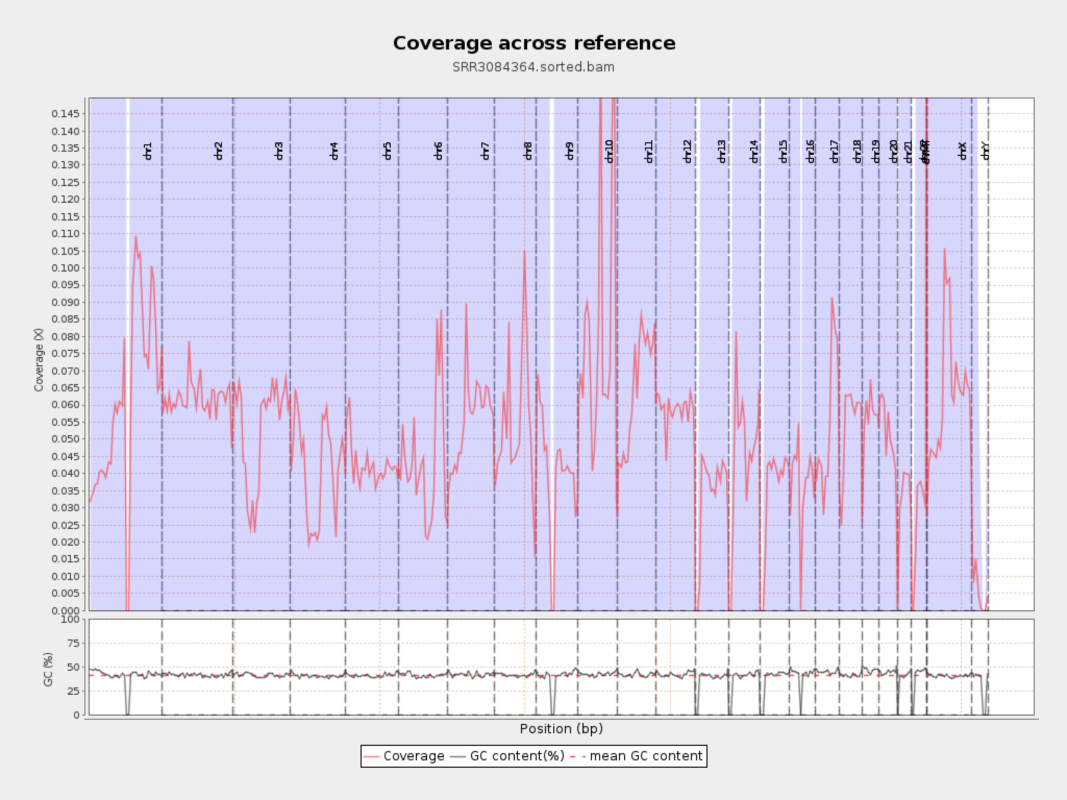
General error rate	1.01%
Mismatches	1,574,752
Insertions	10,679
Mapped reads with at least one insertion	0.45%
Deletions	30,166
Mapped reads with at least one deletion	1.27%
Homopolymer indels	46.96%

2.6. Chromosome stats

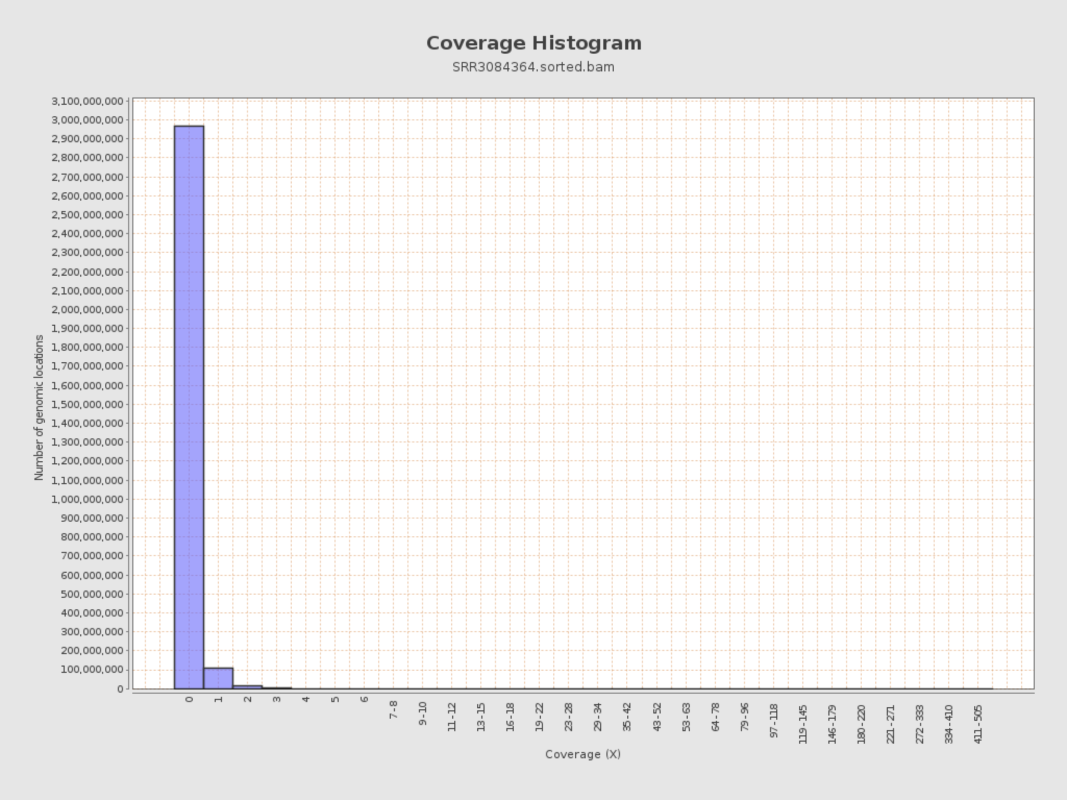
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15196512	0.061	0.5378
chr2	243199373	15080708	0.062	0.3968
chr3	198022430	10525176	0.0532	0.2703
chr4	191154276	7947431	0.0416	0.2438
chr5	180915260	7708830	0.0426	0.2398
chr6	171115067	7466412	0.0436	0.274
chr7	159138663	8945825	0.0562	0.5632

chr8	146364022	7939134	0.0542	0.336
chr9	141213431	5664491	0.0401	0.2848
chr10	135534747	11241653	0.0829	0.4548
chr11	135006516	8701287	0.0645	0.3478
chr12	133851895	7839206	0.0586	0.2828
chr13	115169878	3816511	0.0331	0.211
chr14	107349540	4742255	0.0442	0.2501
chr15	102531392	3487359	0.034	0.2176
chr16	90354753	3355187	0.0371	0.2462
chr17	81195210	4438818	0.0547	0.2956
chr18	78077248	4224950	0.0541	0.4667
chr19	59128983	3355453	0.0567	0.4206
chr20	63025520	3254869	0.0516	0.2677
chr21	48129895	1557501	0.0324	0.218
chr22	51304566	1262106	0.0246	0.1808
chrMT	16571	6408	0.3867	0.6978
chrX	155270560	9755070	0.0628	0.3252
chrY	59373566	326075	0.0055	0.1102

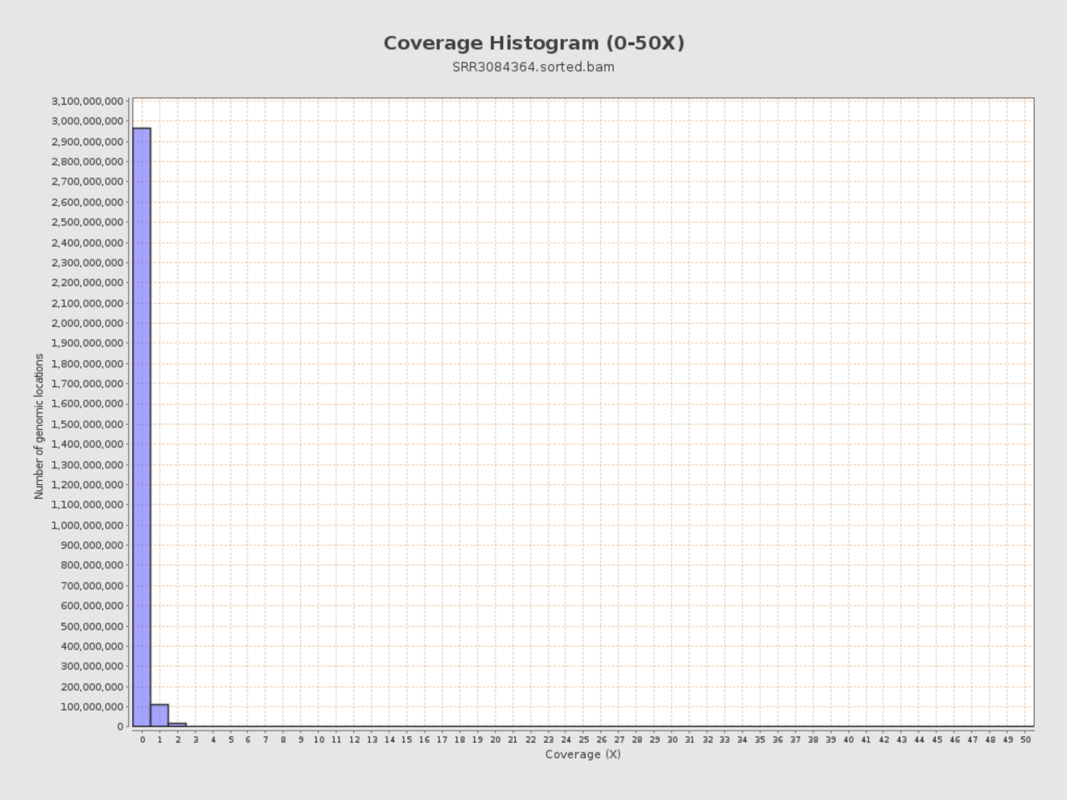
3. Results : Coverage across reference



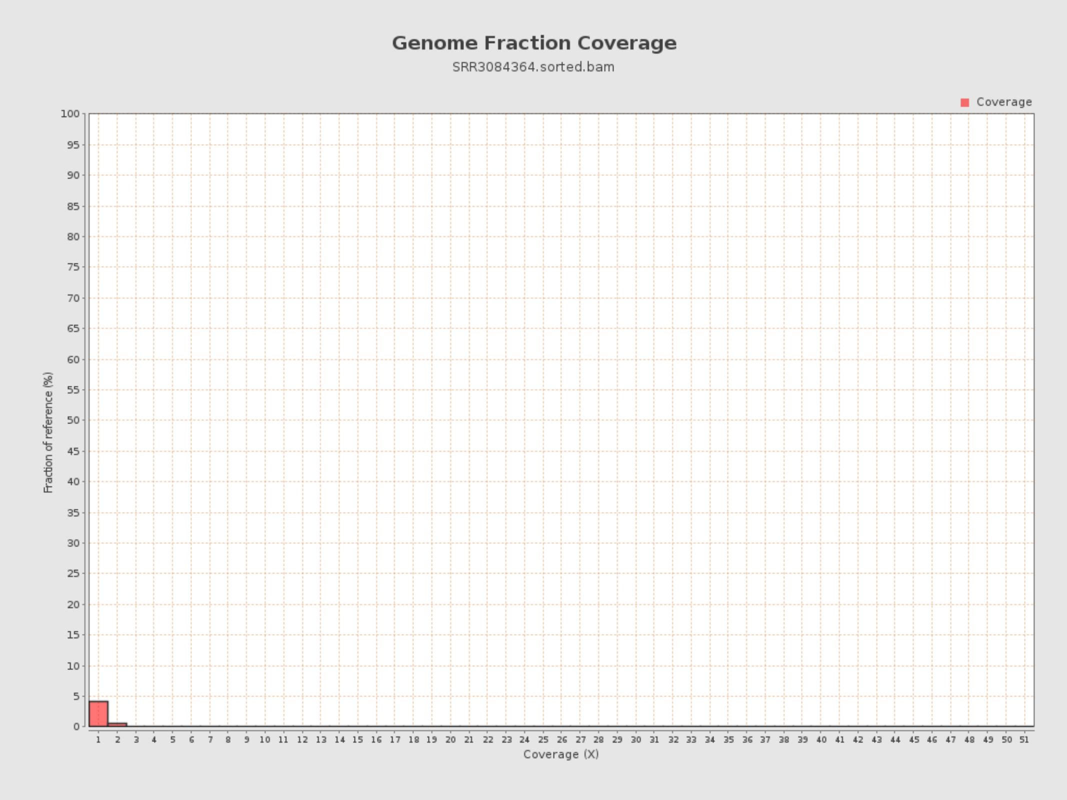
4. Results : Coverage Histogram



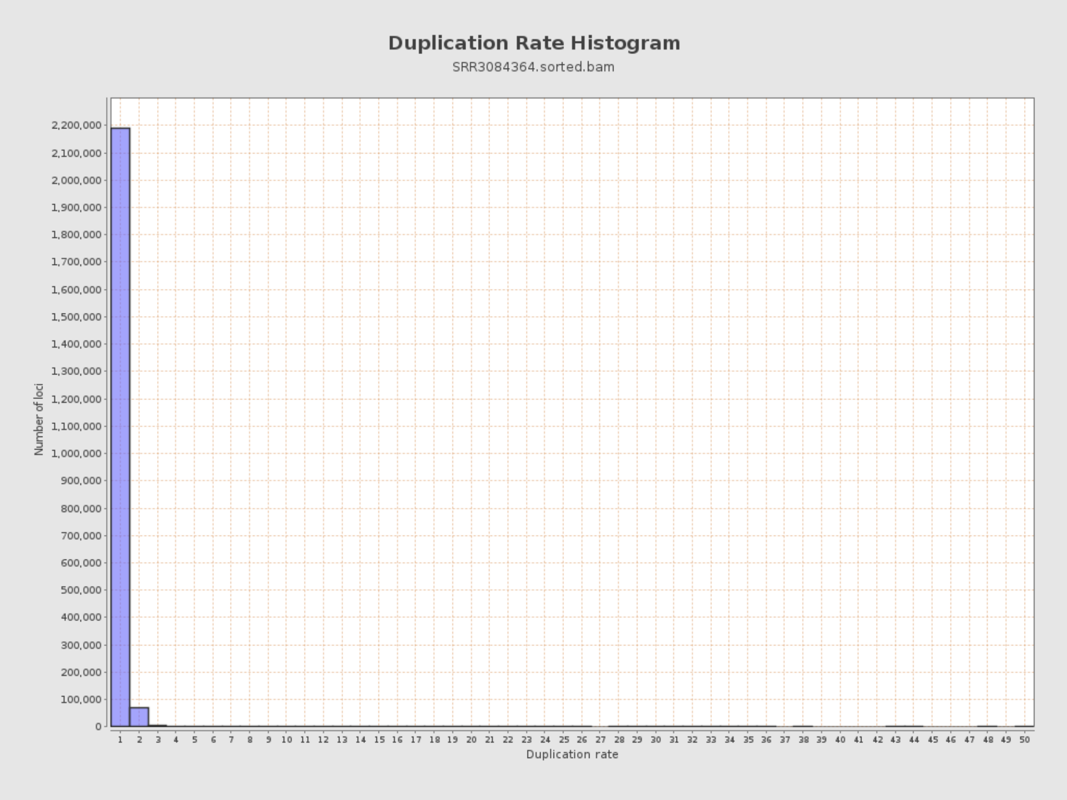
5. Results : Coverage Histogram (0-50X)



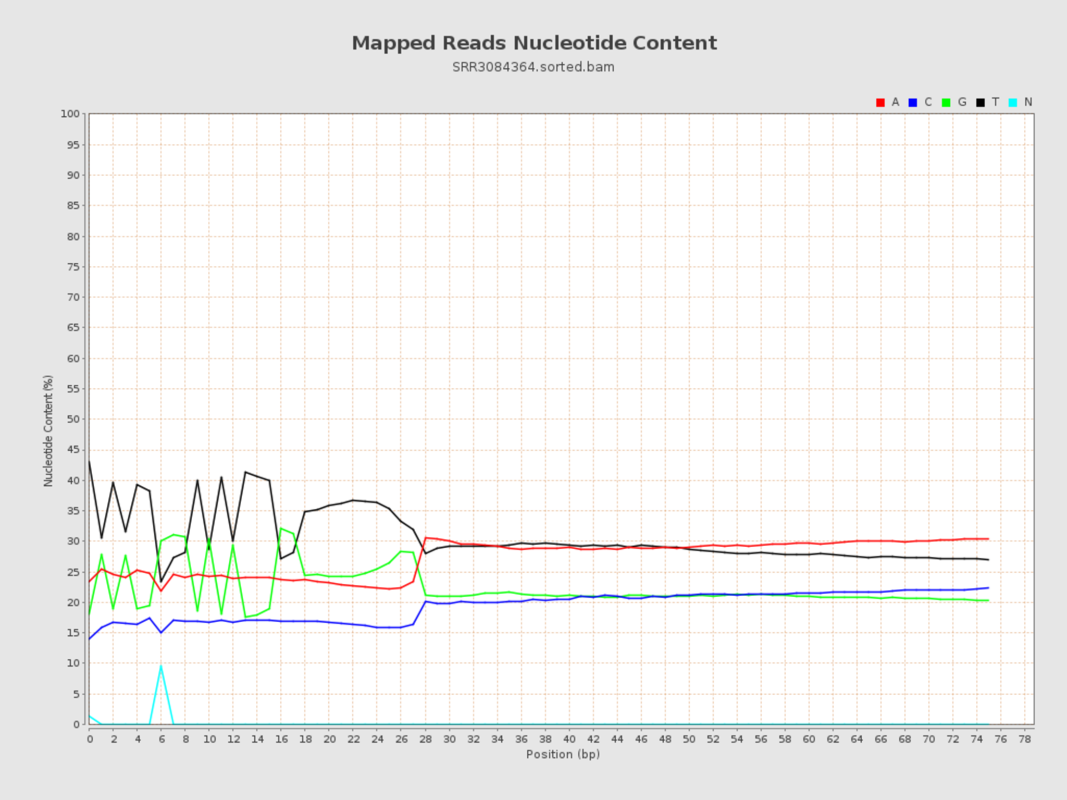
6. Results : Genome Fraction Coverage



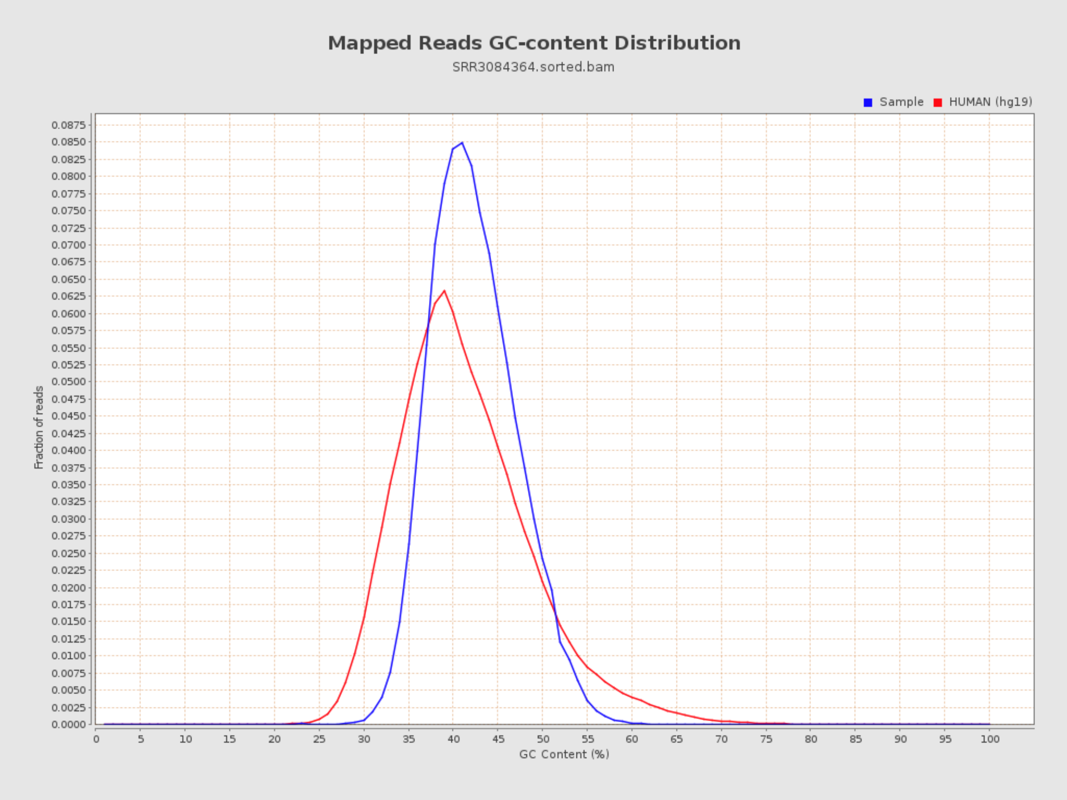
7. Results : Duplication Rate Histogram



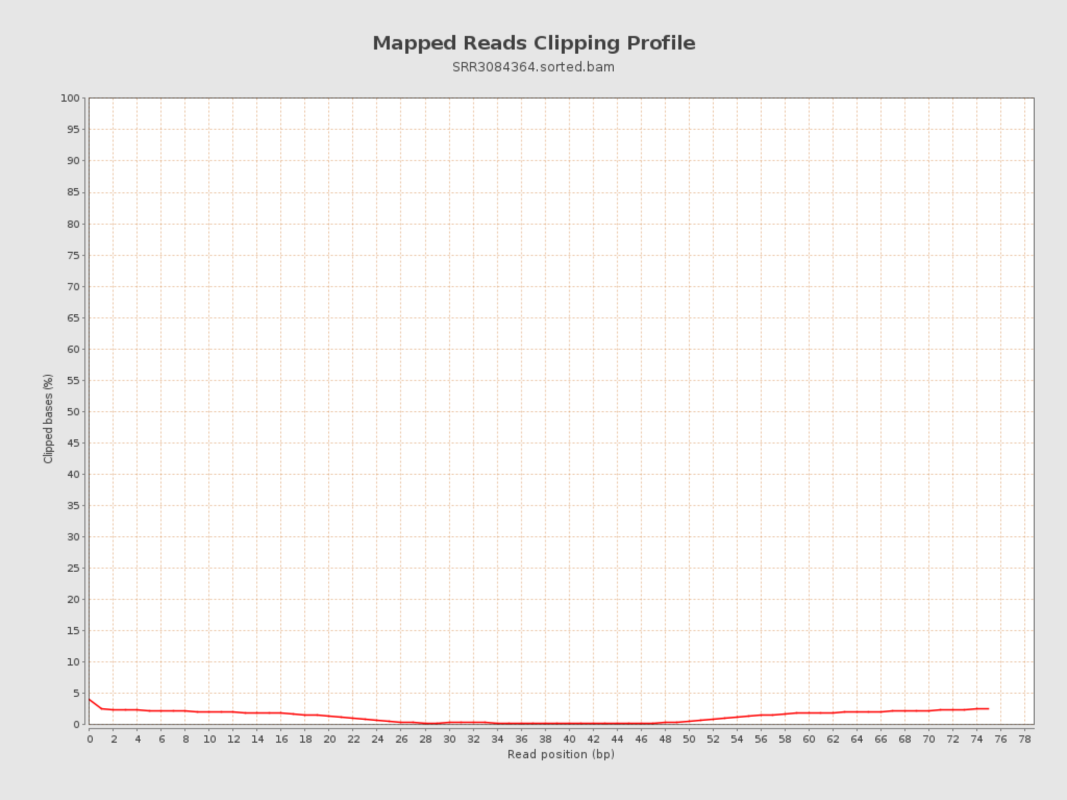
8. Results : Mapped Reads Nucleotide Content



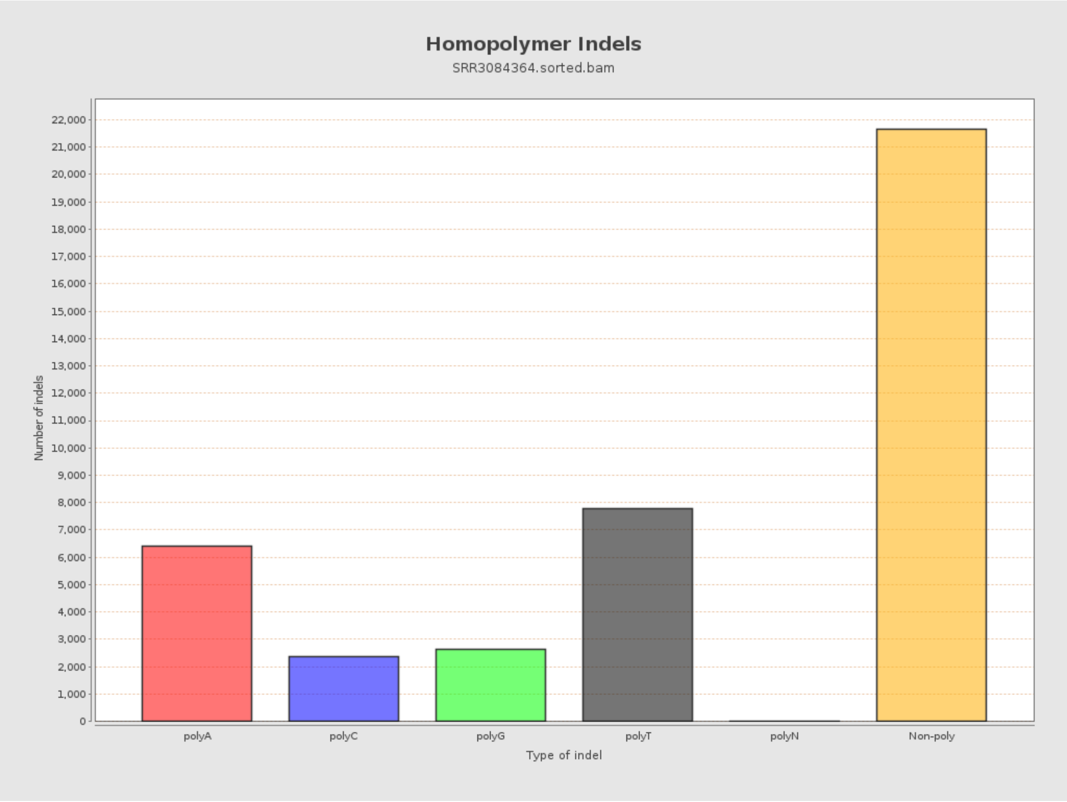
9. Results : Mapped Reads GC-content Distribution



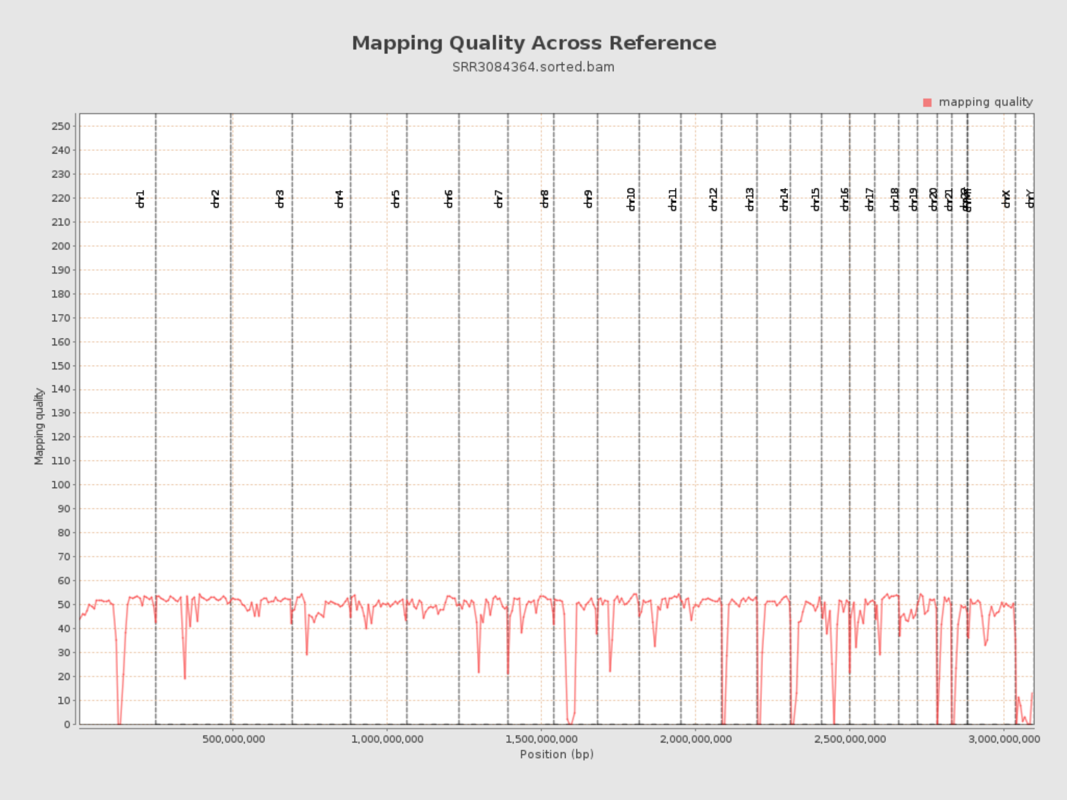
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram