Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 12:41:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084764.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_SRR3084764 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084764.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 12:41:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084764.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,940,828
Mapped reads	1,781,096 / 91.77%
Unmapped reads	159,732 / 8.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,048 / 0.72%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	66,228 / 3.41%
Duplication rate	2.83%
Clipped reads	661,594 / 34.09%

2.2. ACGT Content

Number/percentage of A's	34,727,347 / 28.46%
Number/percentage of C's	22,690,877 / 18.6%
Number/percentage of T's	38,356,908 / 31.44%
Number/percentage of G's	26,178,159 / 21.46%
Number/percentage of N's	49,346 / 0.04%
GC Percentage	40.06%

2.3. Coverage

Mean	0.0394

Standard Deviation	0.3456

2.4. Mapping Quality

Mean Mapping Quality	47.48

2.5. Mismatches and indels

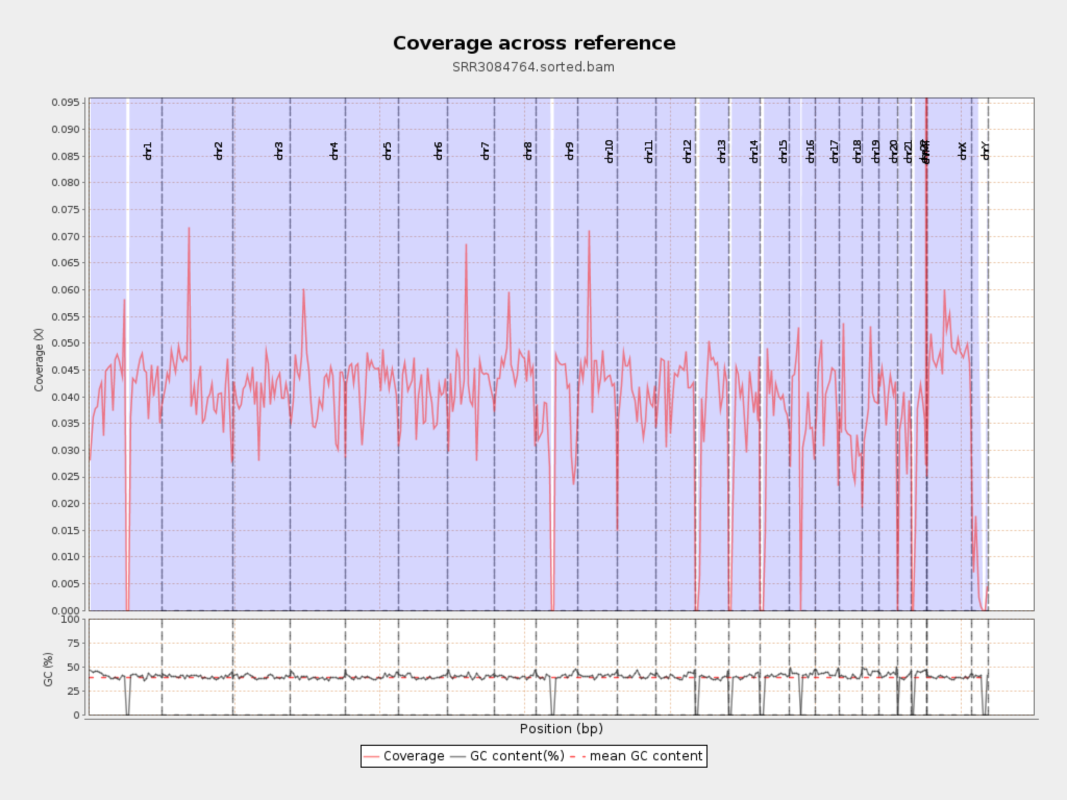
General error rate	0.9%
Mismatches	1,081,212
Insertions	10,185
Mapped reads with at least one insertion	0.57%
Deletions	32,736
Mapped reads with at least one deletion	1.82%
Homopolymer indels	47.62%

2.6. Chromosome stats

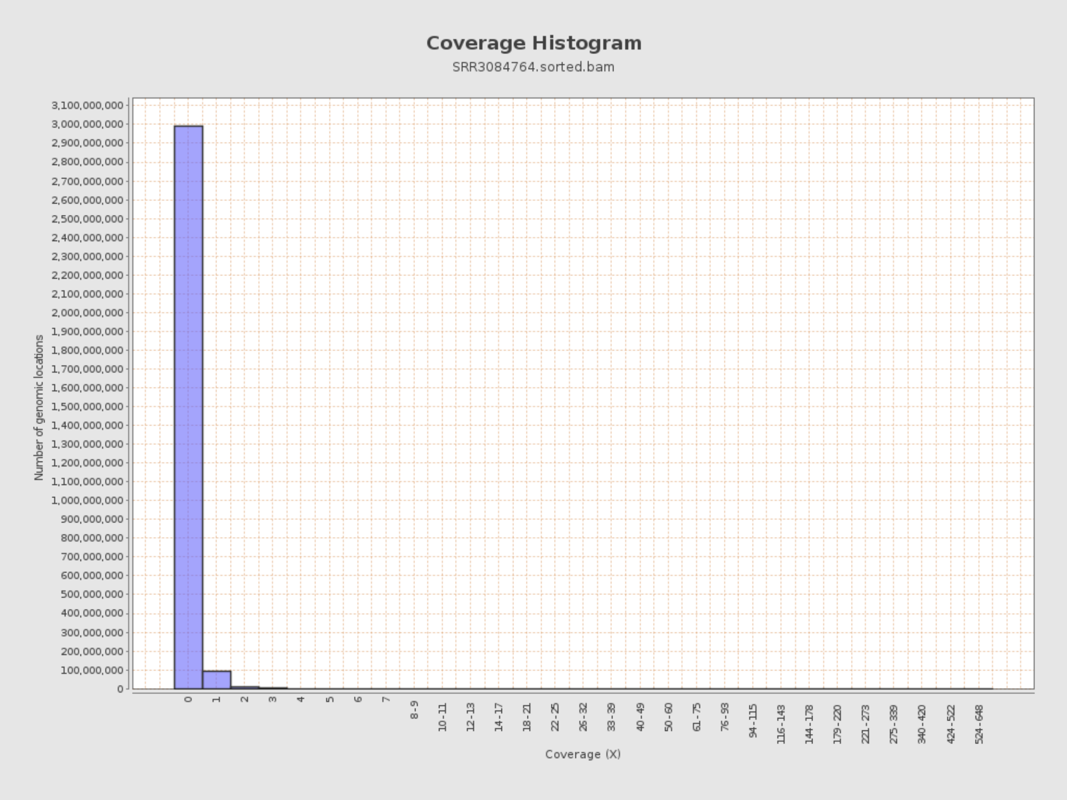
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9916030	0.0398	0.5499
chr2	243199373	10389161	0.0427	0.3971
chr3	198022430	8105259	0.0409	0.2247
chr4	191154276	8003063	0.0419	0.2454
chr5	180915260	7857105	0.0434	0.2322
chr6	171115067	6819128	0.0399	0.2617
chr7	159138663	6833971	0.0429	0.4597

chr8	146364022	6643361	0.0454	0.433
chr9	141213431	4715469	0.0334	0.3382
chr10	135534747	6119604	0.0452	0.3555
chr11	135006516	5383542	0.0399	0.3081
chr12	133851895	5632682	0.0421	0.2307
chr13	115169878	4111837	0.0357	0.2093
chr14	107349540	3585643	0.0334	0.2234
chr15	102531392	3363896	0.0328	0.2039
chr16	90354753	3167827	0.0351	0.2422
chr17	81195210	3282605	0.0404	0.2614
chr18	78077248	2589101	0.0332	0.7434
chr19	59128983	2287803	0.0387	0.4104
chr20	63025520	2557238	0.0406	0.2341
chr21	48129895	1521685	0.0316	0.2188
chr22	51304566	1365334	0.0266	0.1789
chrMT	16571	9142	0.5517	0.7876
chrX	155270560	7478231	0.0482	0.2713
chrY	59373566	317664	0.0054	0.1398

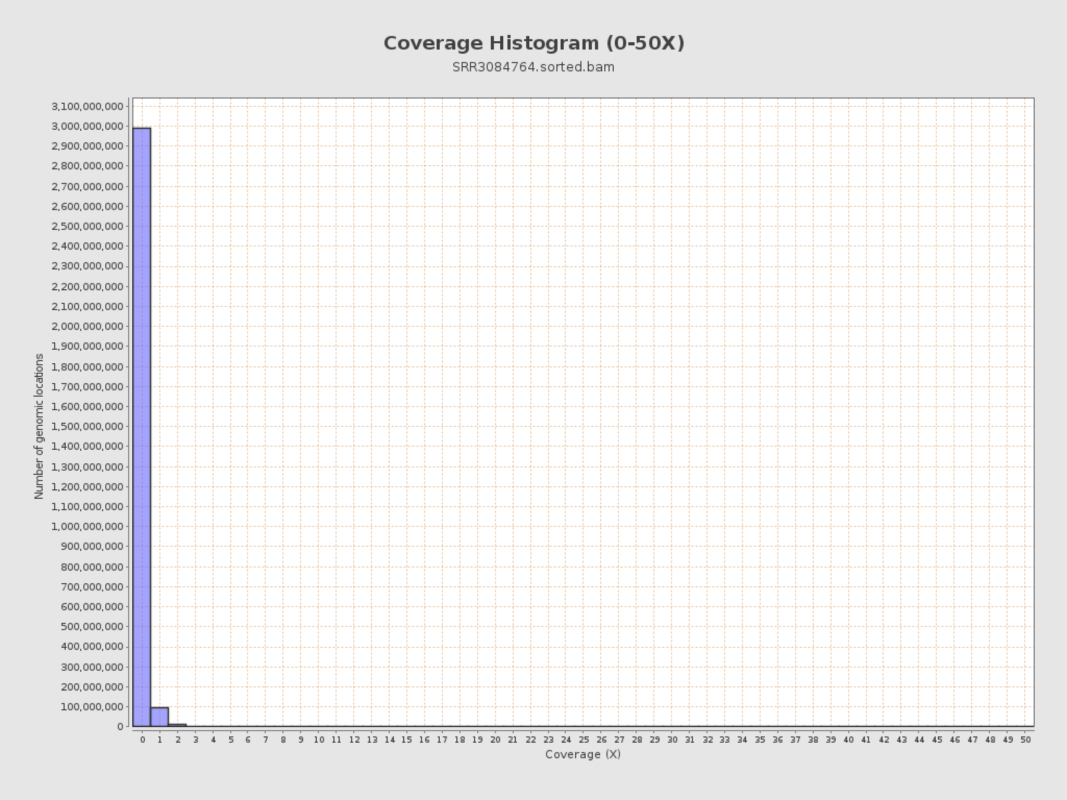
3. Results : Coverage across reference



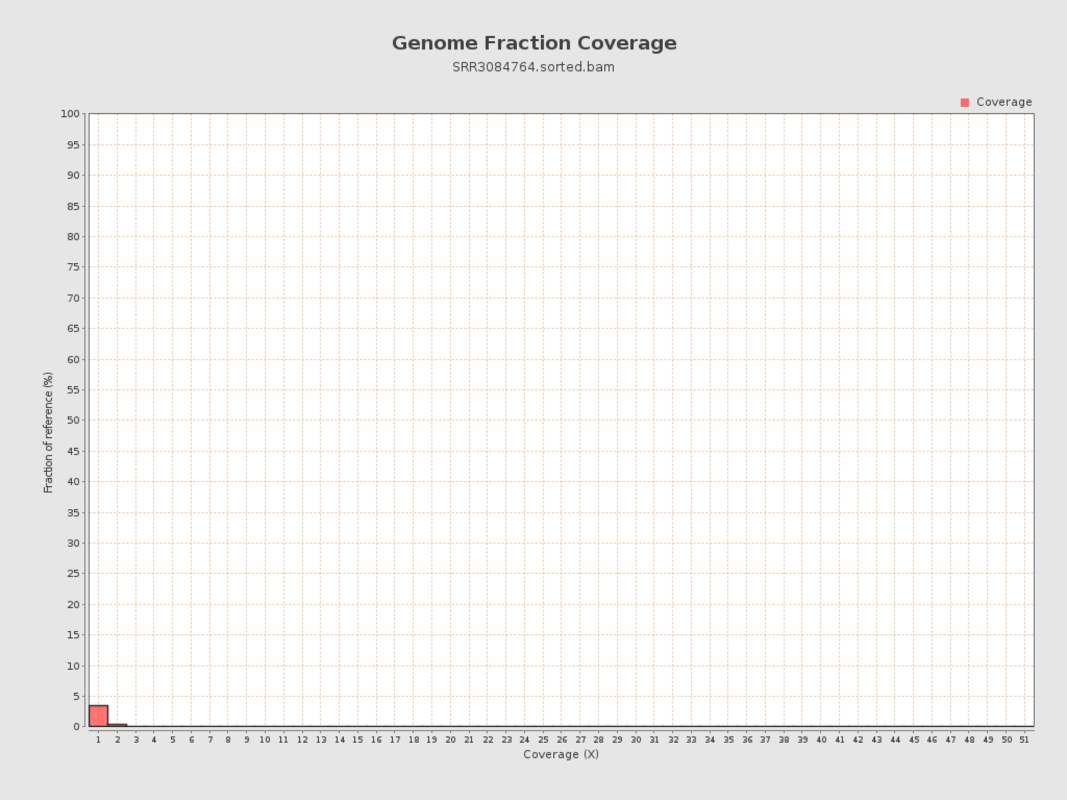
4. Results : Coverage Histogram



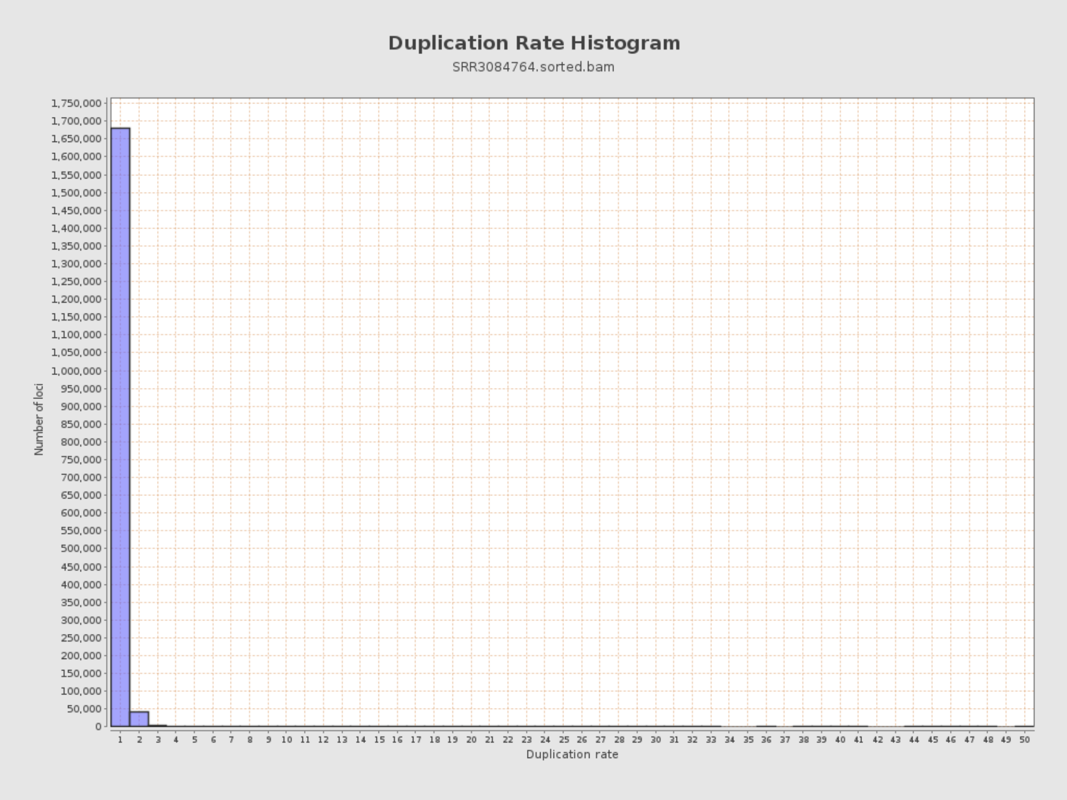
5. Results : Coverage Histogram (0-50X)



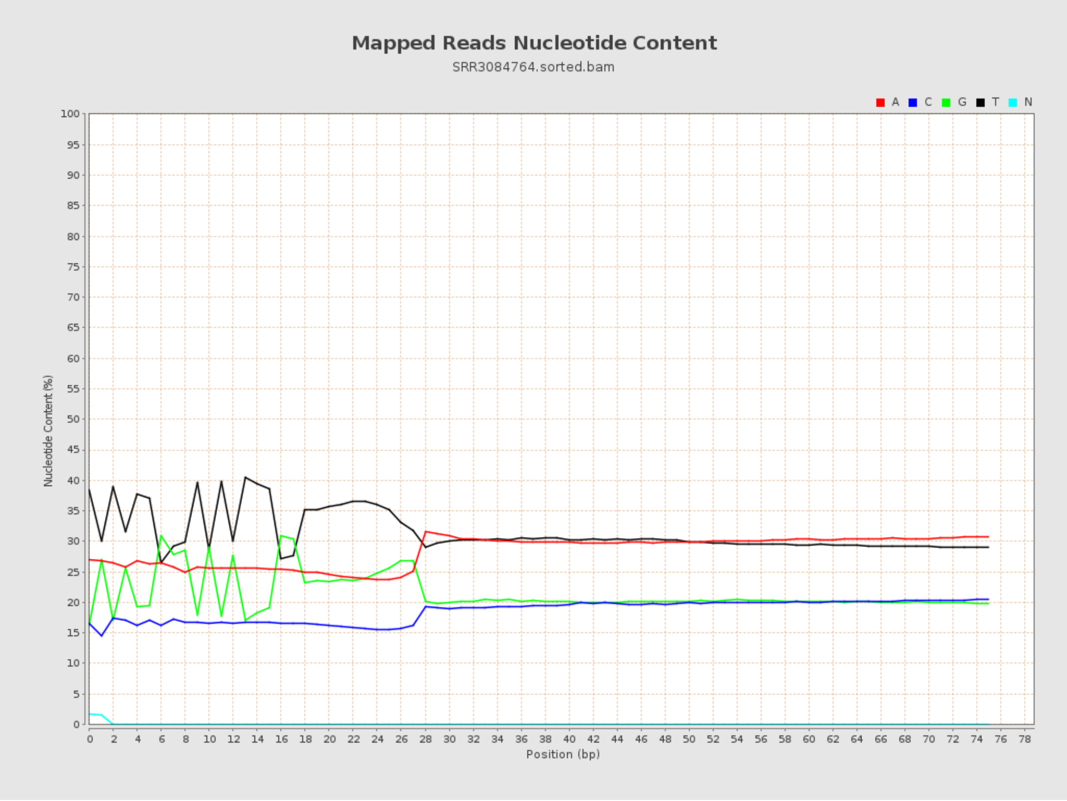
6. Results : Genome Fraction Coverage



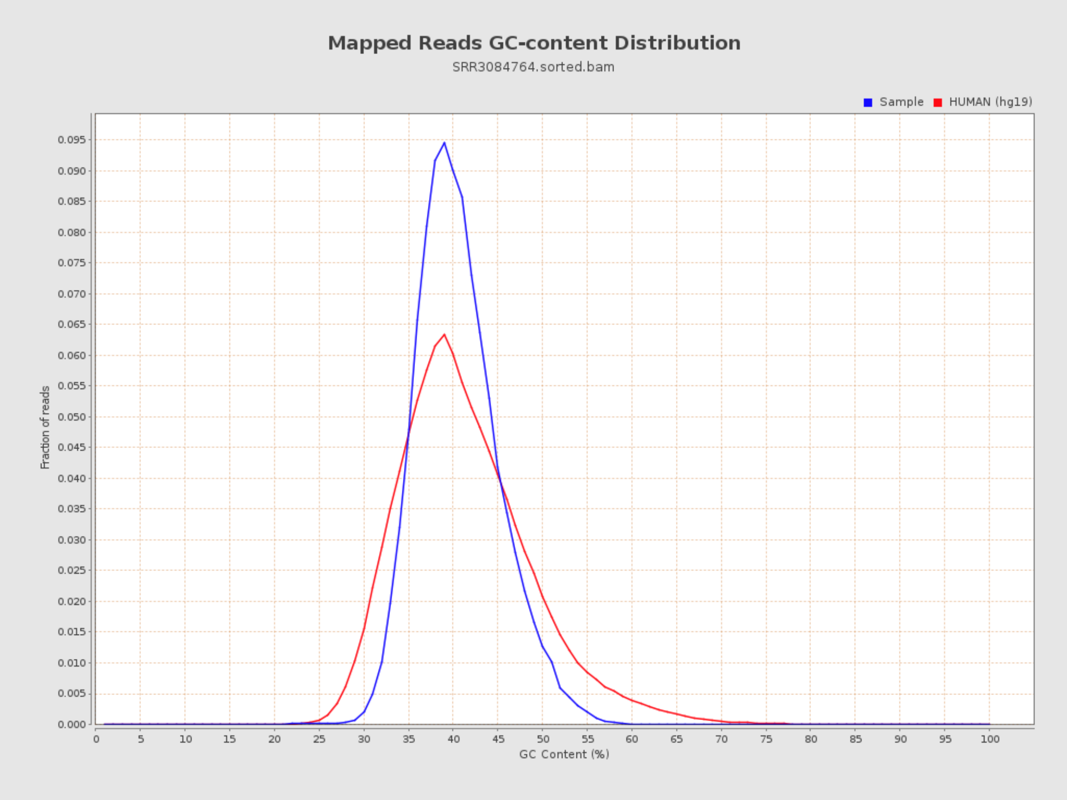
7. Results : Duplication Rate Histogram



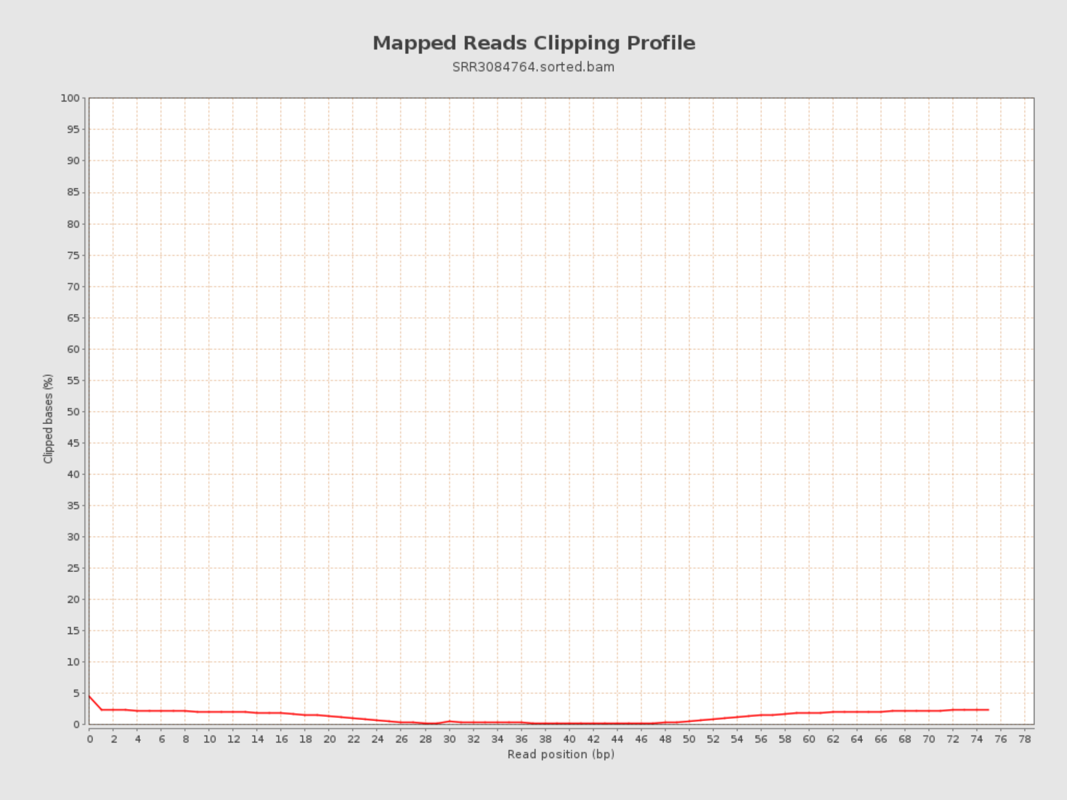
8. Results : Mapped Reads Nucleotide Content



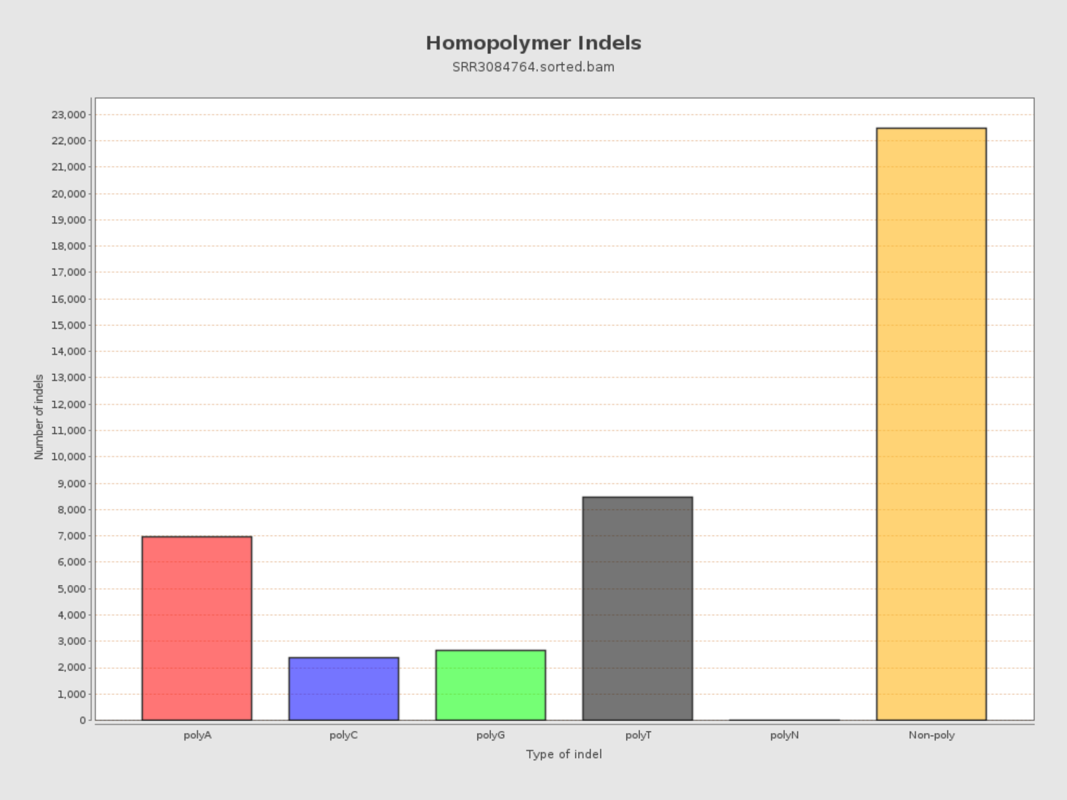
9. Results : Mapped Reads GC-content Distribution



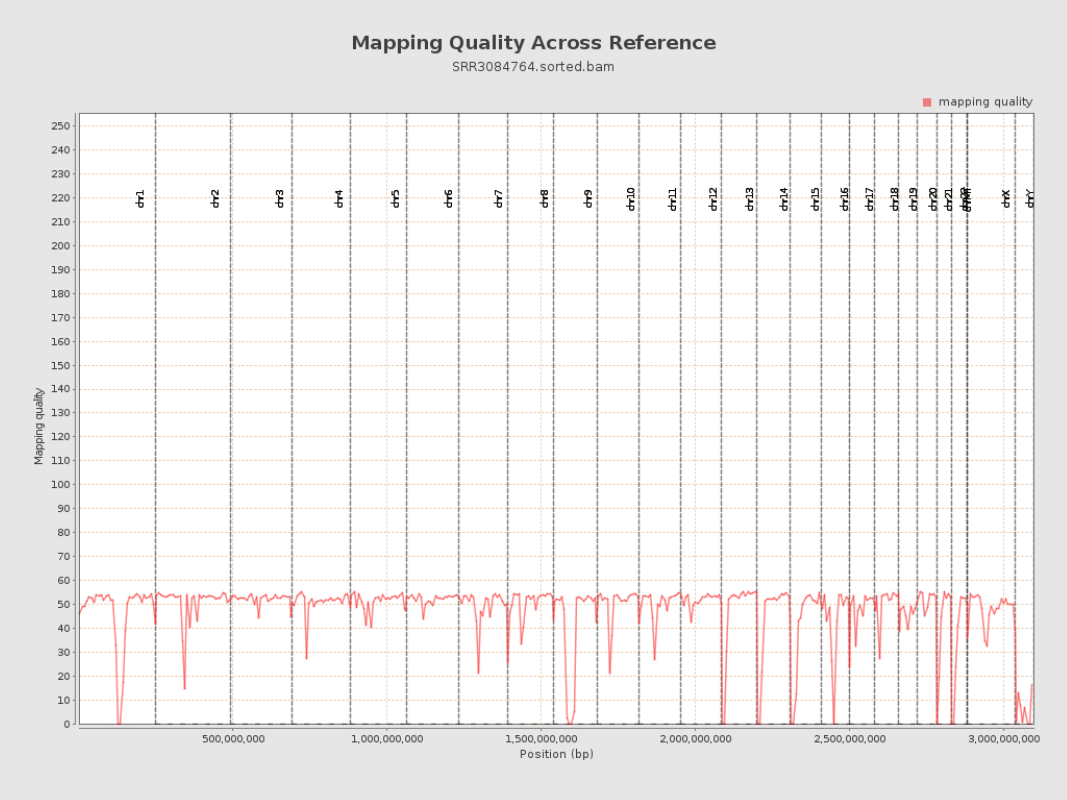
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram