Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 20:26:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084964.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_SRR3084964 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084964.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 20:26:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084964.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,639,103
Mapped reads	2,370,750 / 89.83%
Unmapped reads	268,353 / 10.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,587 / 0.89%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	110,723 / 4.2%
Duplication rate	3.31%
Clipped reads	1,111,414 / 42.11%

2.2. ACGT Content

Number/percentage of A's	43,912,910 / 27.91%
Number/percentage of C's	29,135,103 / 18.52%
Number/percentage of T's	49,264,347 / 31.31%
Number/percentage of G's	35,015,482 / 22.25%
Number/percentage of N's	20,906 / 0.01%
GC Percentage	40.77%

2.3. Coverage

Mean	0.0508

Standard Deviation	0.501

2.4. Mapping Quality

Mean Mapping Quality	45.1

2.5. Mismatches and indels

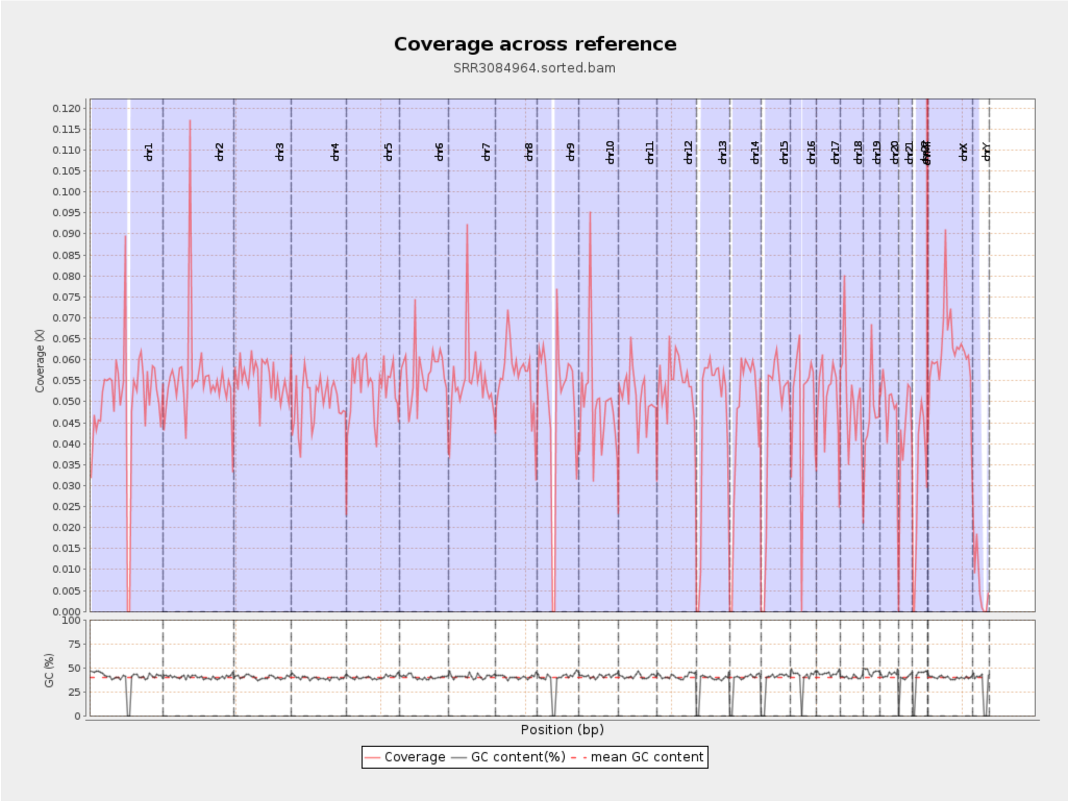
General error rate	0.87%
Mismatches	1,344,387
Insertions	12,632
Mapped reads with at least one insertion	0.53%
Deletions	36,736
Mapped reads with at least one deletion	1.53%
Homopolymer indels	46%

2.6. Chromosome stats

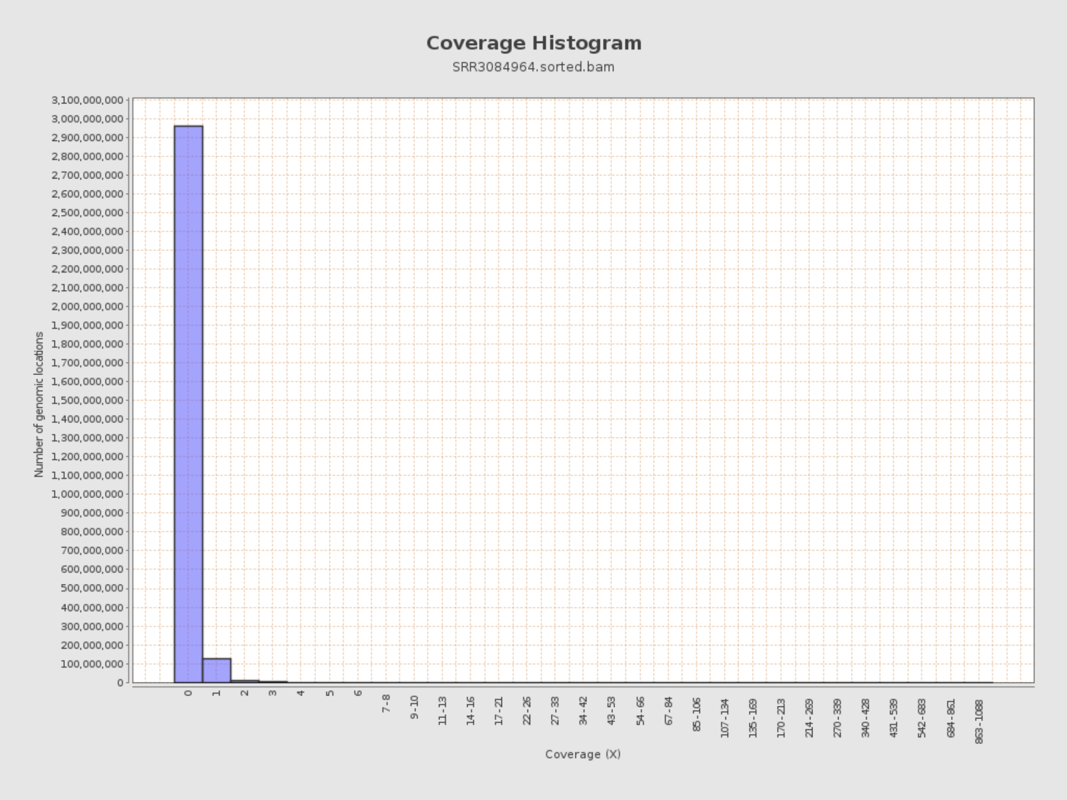
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12416162	0.0498	0.8879
chr2	243199373	13504254	0.0555	0.6215
chr3	198022430	10974029	0.0554	0.2695
chr4	191154276	9545714	0.0499	0.261
chr5	180915260	9719776	0.0537	0.2625
chr6	171115067	9668795	0.0565	0.4178
chr7	159138663	8796957	0.0553	0.5077

chr8	146364022	8164875	0.0558	0.6731
chr9	141213431	7016274	0.0497	0.5299
chr10	135534747	6725069	0.0496	0.548
chr11	135006516	6848662	0.0507	0.4321
chr12	133851895	7297875	0.0545	0.2785
chr13	115169878	5234135	0.0454	0.234
chr14	107349540	4874933	0.0454	0.297
chr15	102531392	4578685	0.0447	0.2396
chr16	90354753	4483245	0.0496	0.3229
chr17	81195210	4101059	0.0505	0.3105
chr18	78077248	4031142	0.0516	1.0845
chr19	59128983	2787736	0.0471	0.7352
chr20	63025520	3086454	0.049	0.262
chr21	48129895	1960651	0.0407	0.2602
chr22	51304566	1549891	0.0302	0.1898
chrMT	16571	27776	1.6762	1.7161
chrX	155270560	9627527	0.062	0.3605
chrY	59373566	386262	0.0065	0.1274

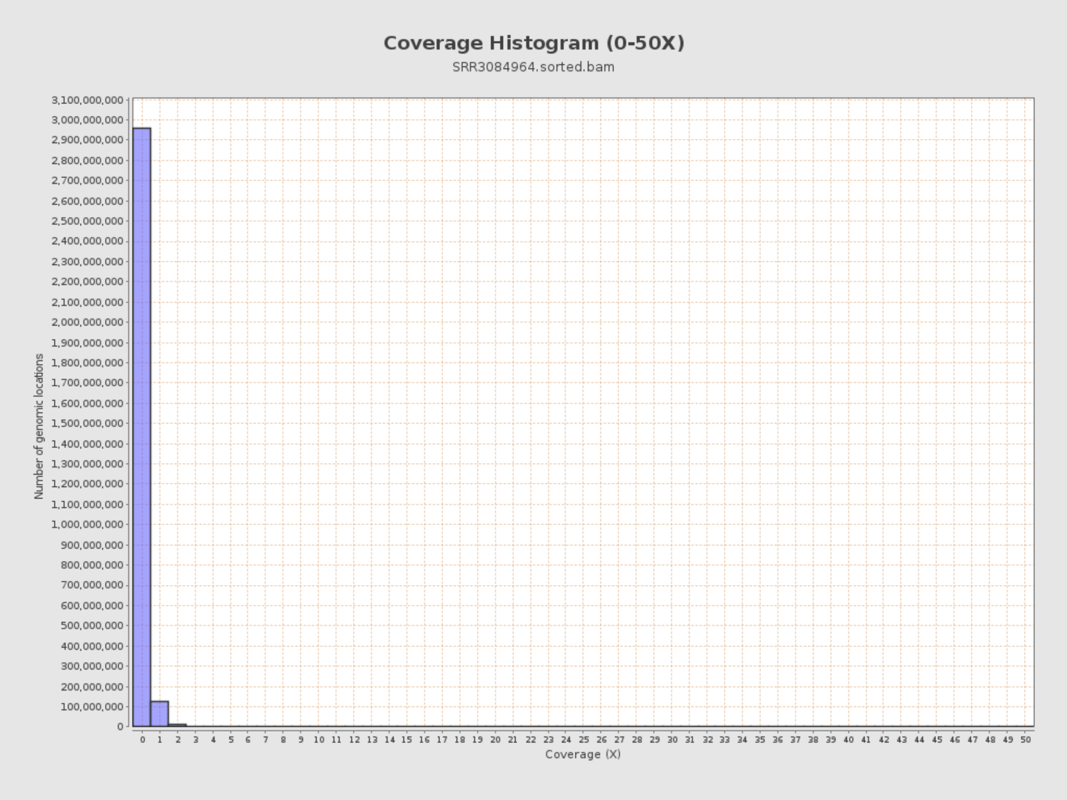
3. Results : Coverage across reference



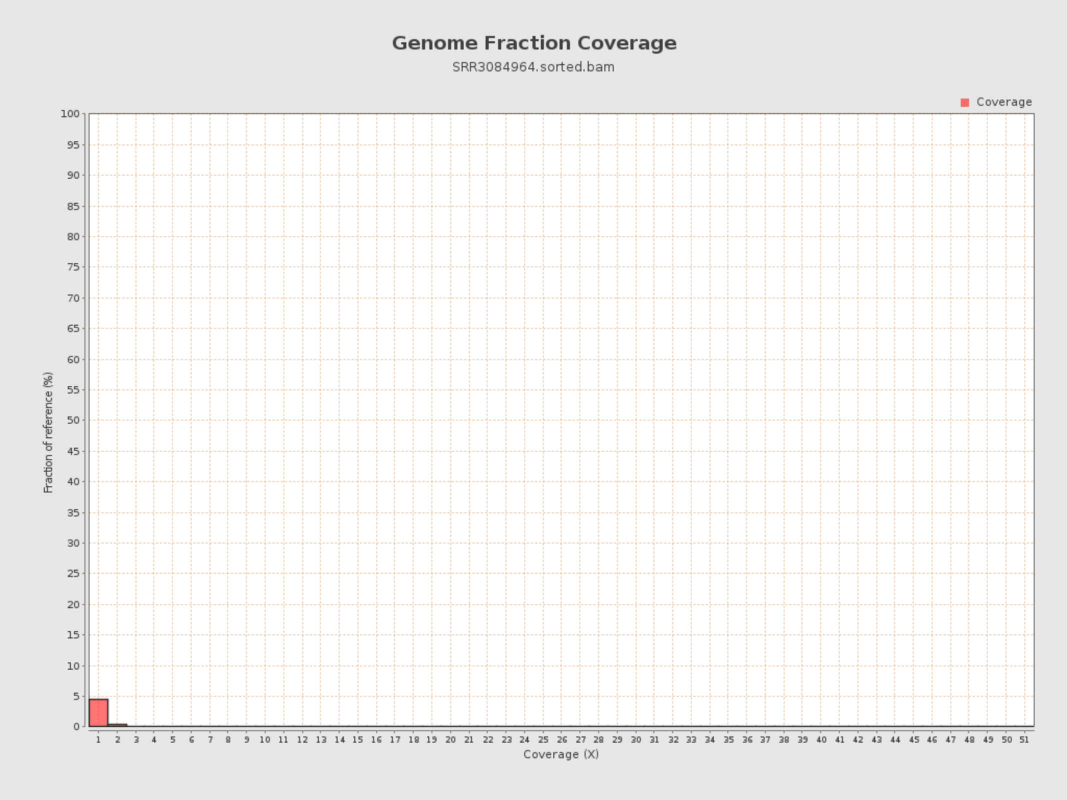
4. Results : Coverage Histogram



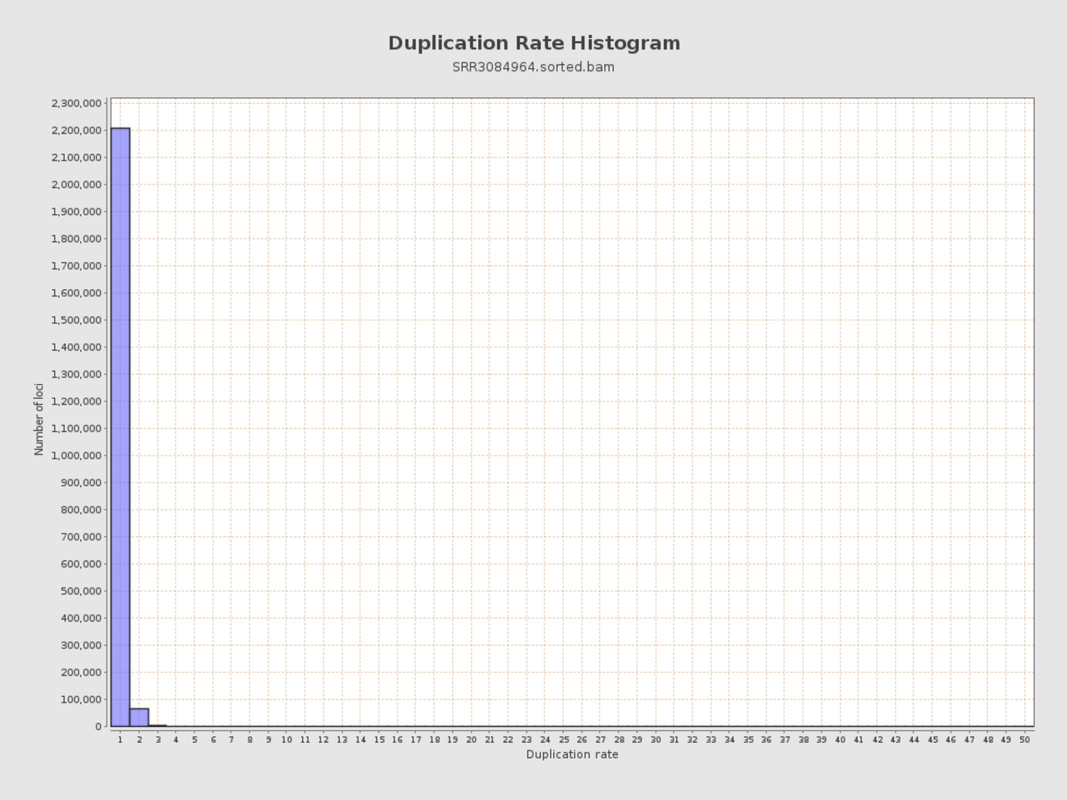
5. Results : Coverage Histogram (0-50X)



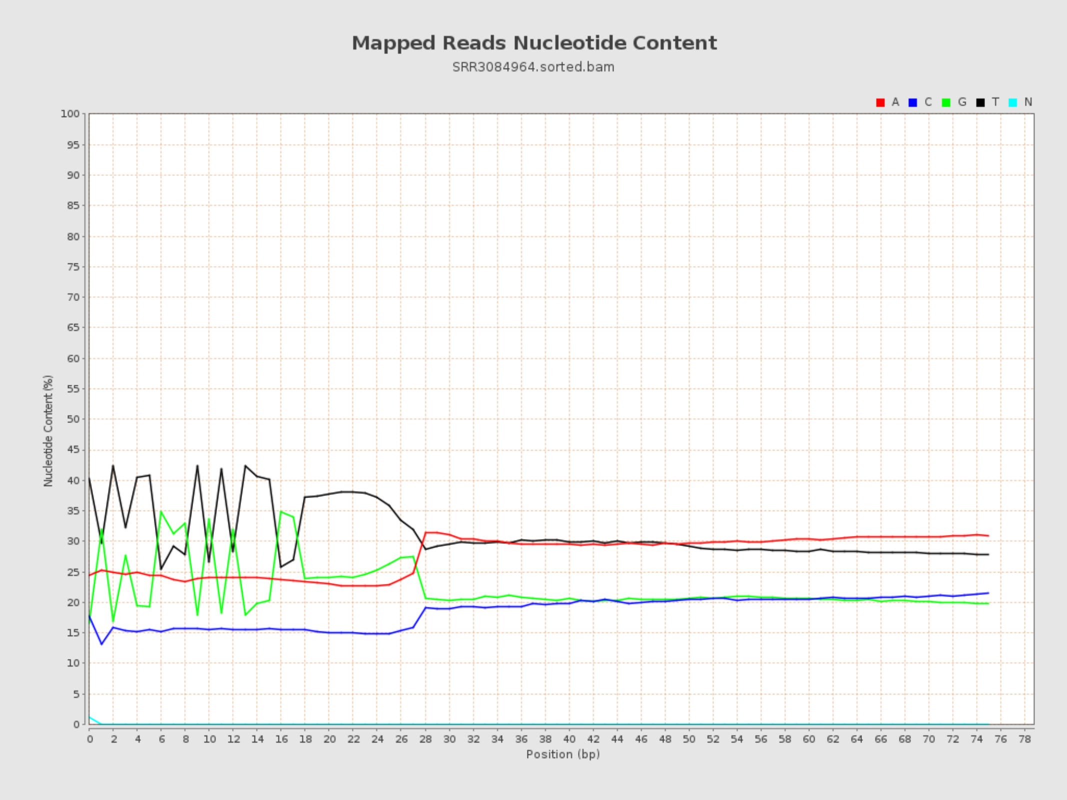
6. Results : Genome Fraction Coverage



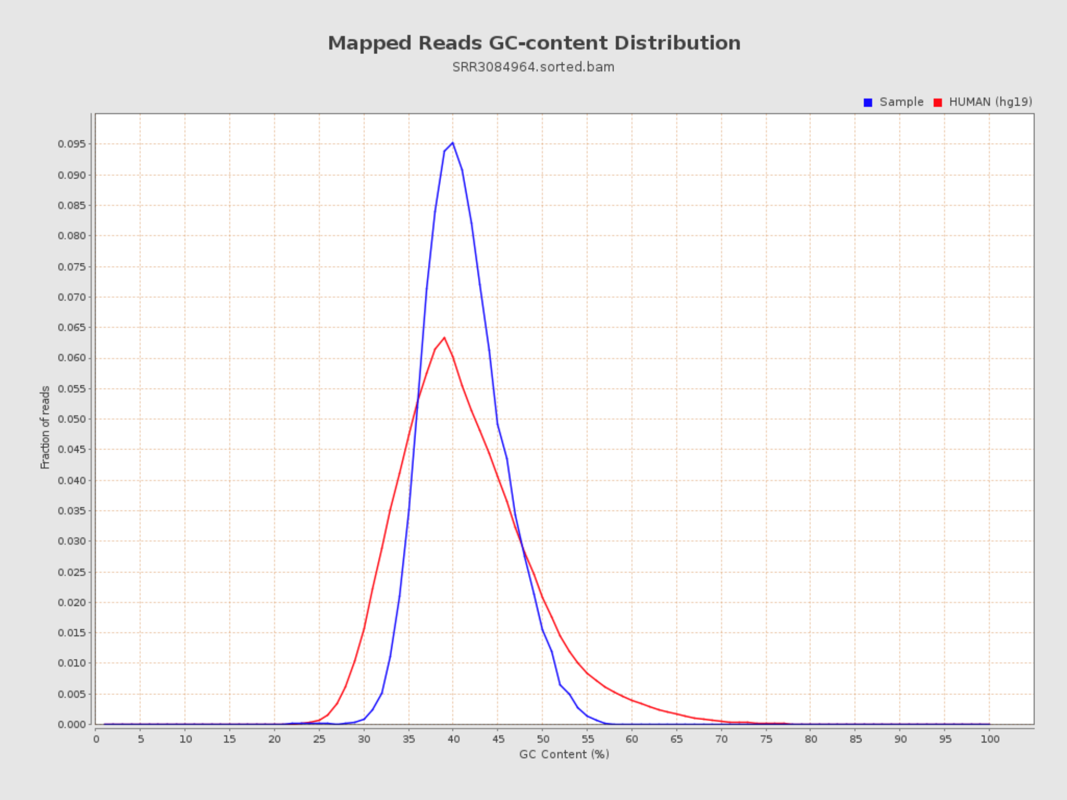
7. Results : Duplication Rate Histogram



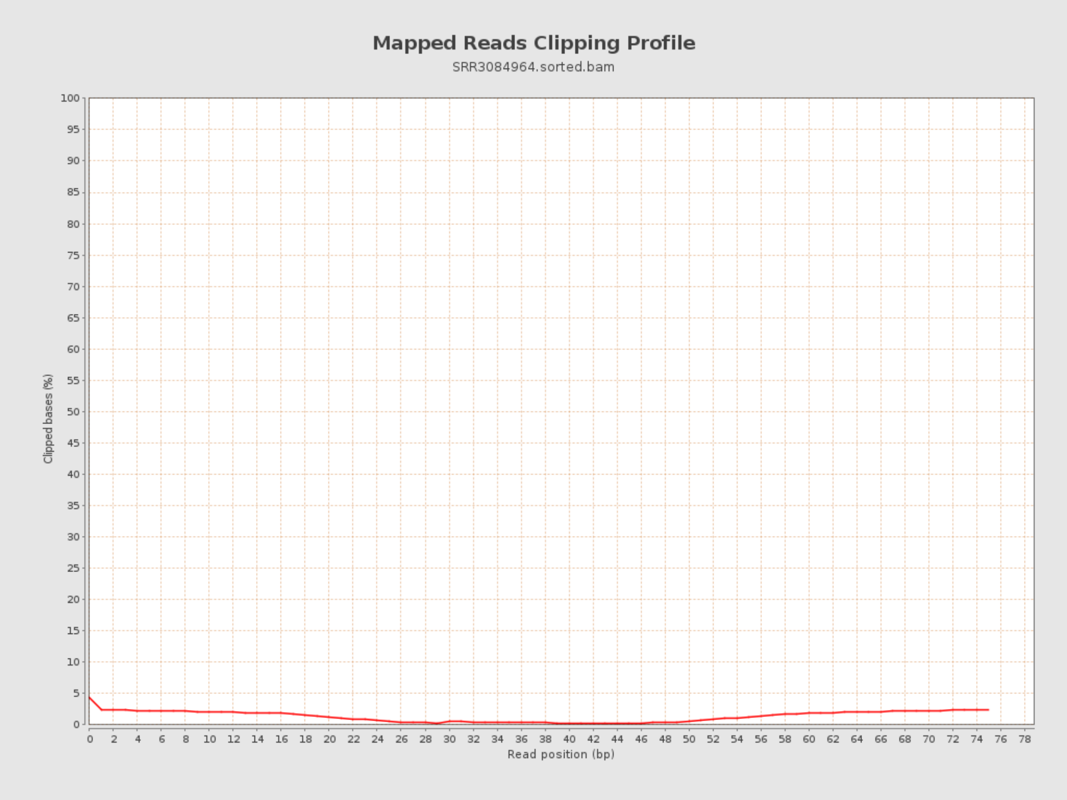
8. Results : Mapped Reads Nucleotide Content



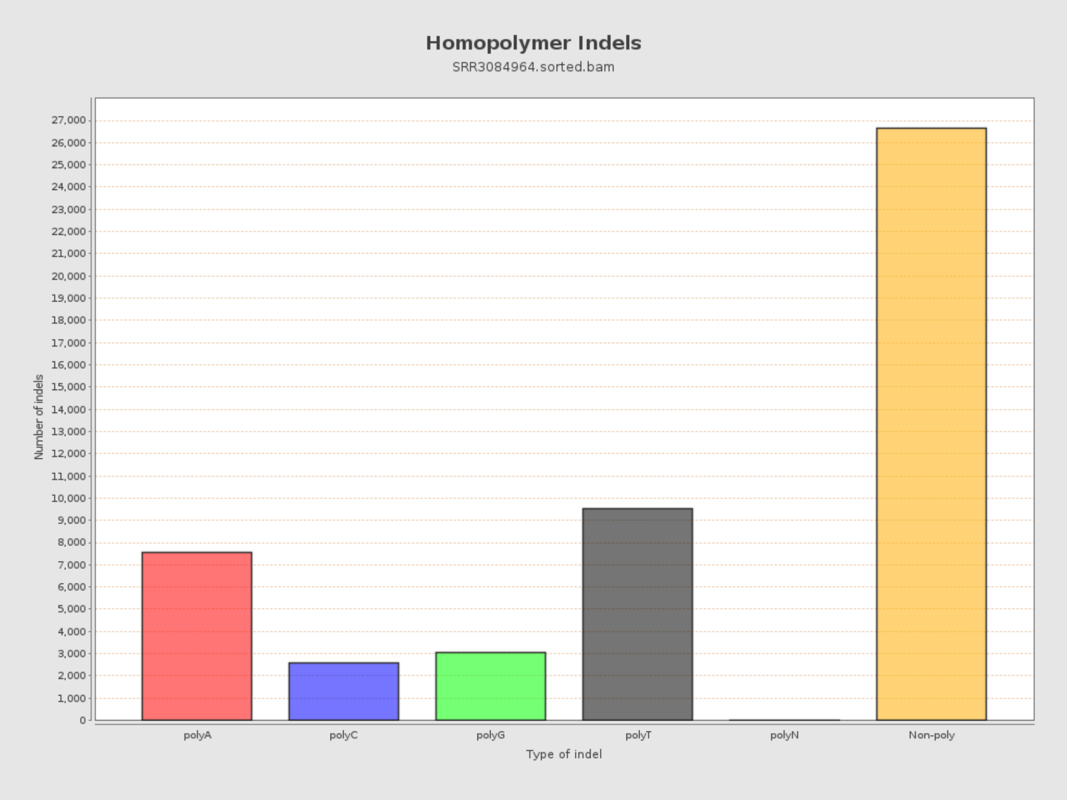
9. Results : Mapped Reads GC-content Distribution



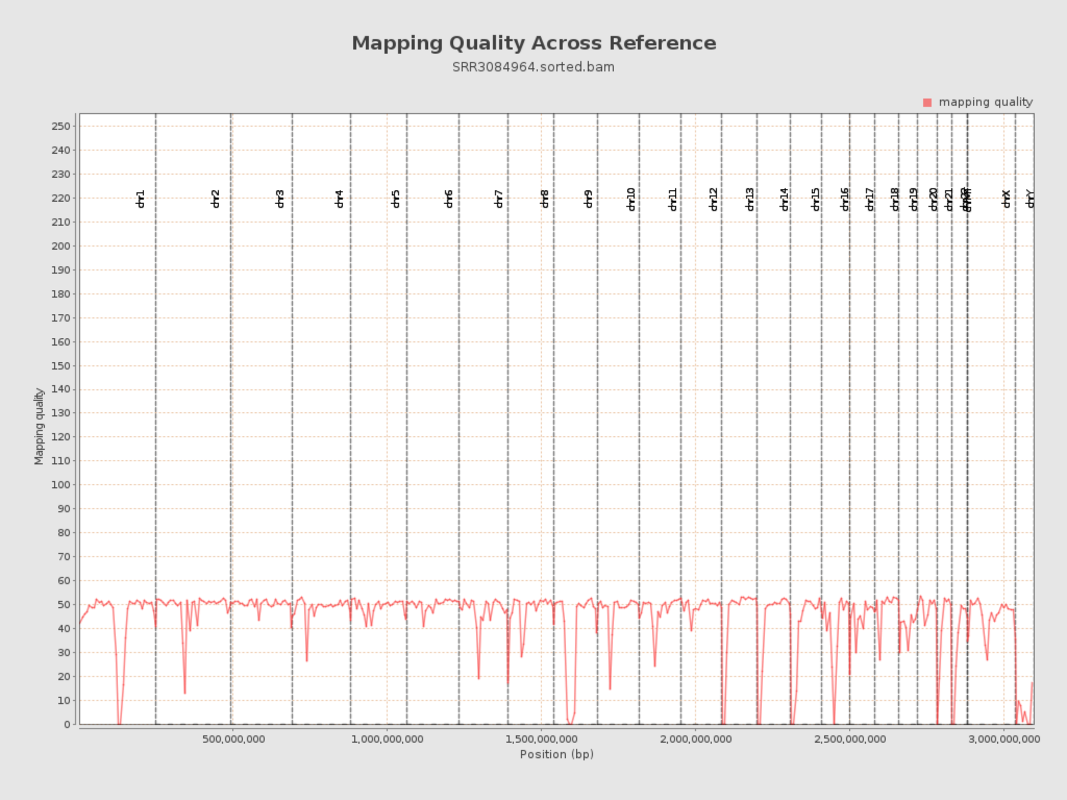
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram