Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 15:41:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084816.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_SRR3084816 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084816.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 15:41:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084816.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,958,253
Mapped reads	1,812,445 / 92.55%
Unmapped reads	145,808 / 7.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,948 / 0.92%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	70,523 / 3.6%
Duplication rate	3.44%
Clipped reads	715,466 / 36.54%

2.2. ACGT Content

Number/percentage of A's	34,712,445 / 28.22%
Number/percentage of C's	22,297,904 / 18.13%
Number/percentage of T's	39,603,854 / 32.2%
Number/percentage of G's	26,353,329 / 21.43%
Number/percentage of N's	17,473 / 0.01%
GC Percentage	39.56%

2.3. Coverage

Mean	0.0397

Standard Deviation	0.2673

2.4. Mapping Quality

Mean Mapping Quality	46.62

2.5. Mismatches and indels

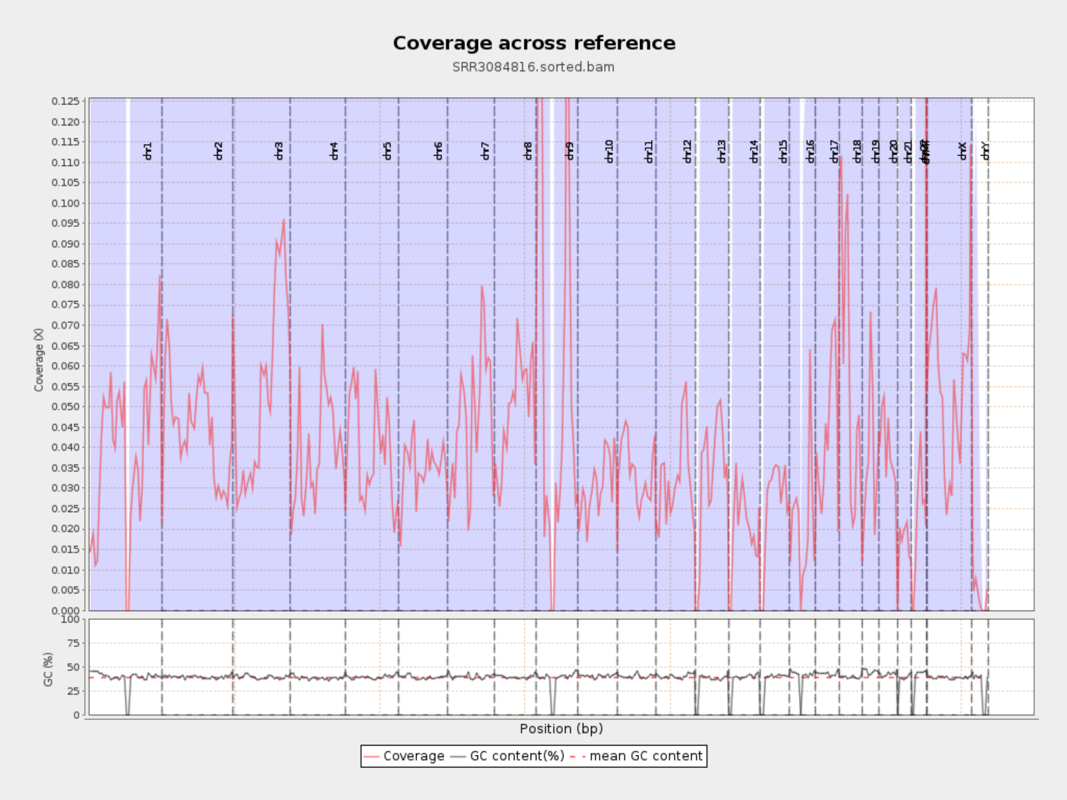
General error rate	0.79%
Mismatches	948,892
Insertions	9,950
Mapped reads with at least one insertion	0.55%
Deletions	28,809
Mapped reads with at least one deletion	1.58%
Homopolymer indels	49.34%

2.6. Chromosome stats

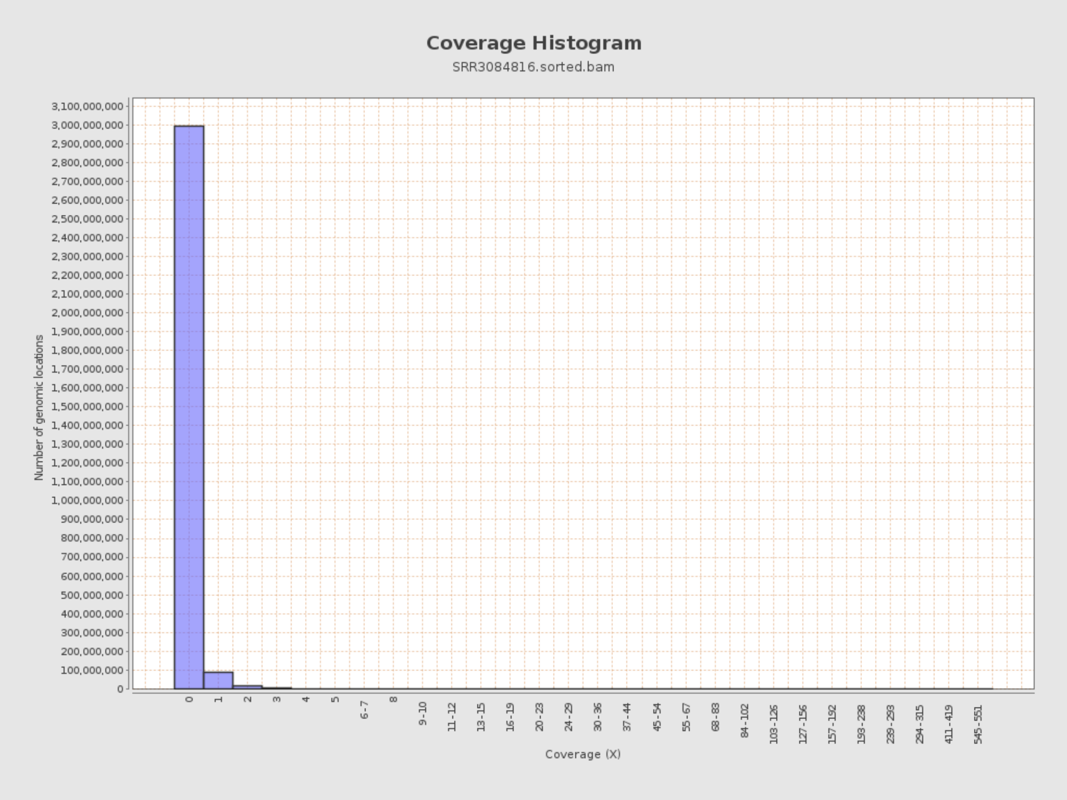
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10003418	0.0401	0.3427
chr2	243199373	10868175	0.0447	0.3603
chr3	198022430	10760866	0.0543	0.2702
chr4	191154276	7508884	0.0393	0.2298
chr5	180915260	7154488	0.0395	0.2313
chr6	171115067	5954376	0.0348	0.2272
chr7	159138663	7517424	0.0472	0.2921

chr8	146364022	7228625	0.0494	0.3166
chr9	141213431	9028880	0.0639	0.3283
chr10	135534747	4123924	0.0304	0.2069
chr11	135006516	4600121	0.0341	0.2441
chr12	133851895	4354291	0.0325	0.2086
chr13	115169878	3746043	0.0325	0.2095
chr14	107349540	2090661	0.0195	0.1631
chr15	102531392	2652431	0.0259	0.192
chr16	90354753	1977828	0.0219	0.1756
chr17	81195210	3595454	0.0443	0.247
chr18	78077248	4612930	0.0591	0.3906
chr19	59128983	2259283	0.0382	0.2678
chr20	63025520	2490488	0.0395	0.231
chr21	48129895	772578	0.0161	0.1493
chr22	51304566	1088366	0.0212	0.1666
chrMT	16571	12752	0.7695	0.9295
chrX	155270560	8389673	0.054	0.2766
chrY	59373566	240258	0.004	0.0764

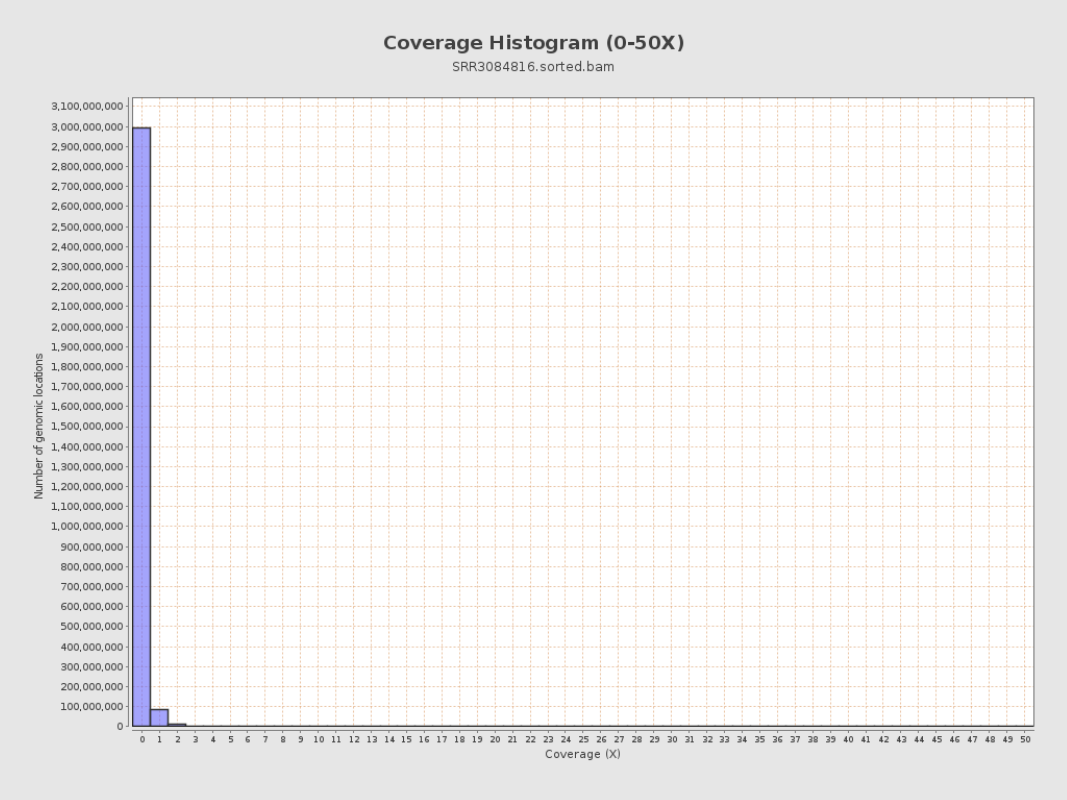
3. Results : Coverage across reference



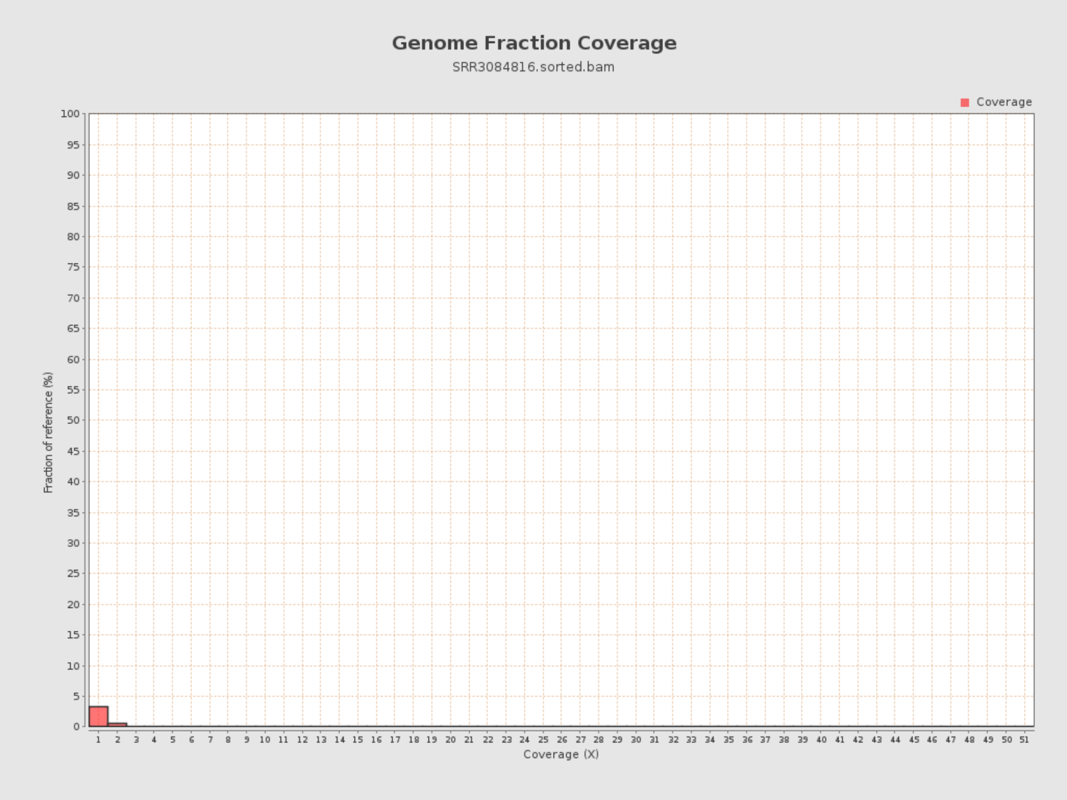
4. Results : Coverage Histogram



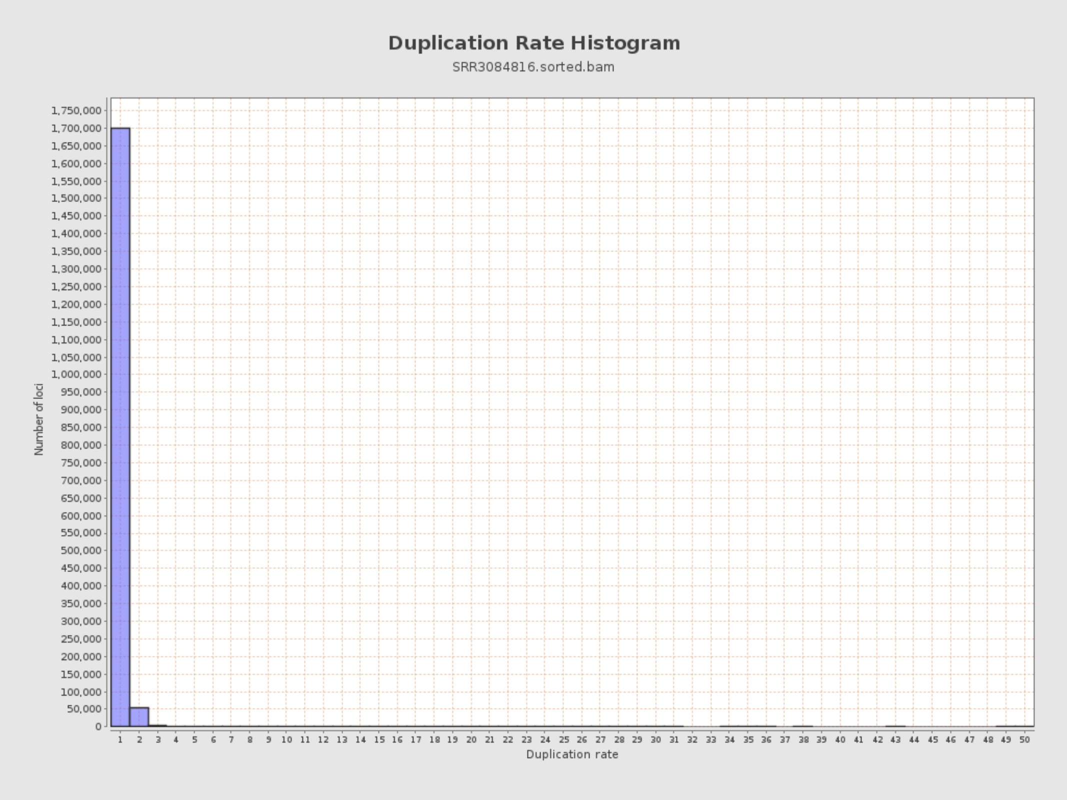
5. Results : Coverage Histogram (0-50X)



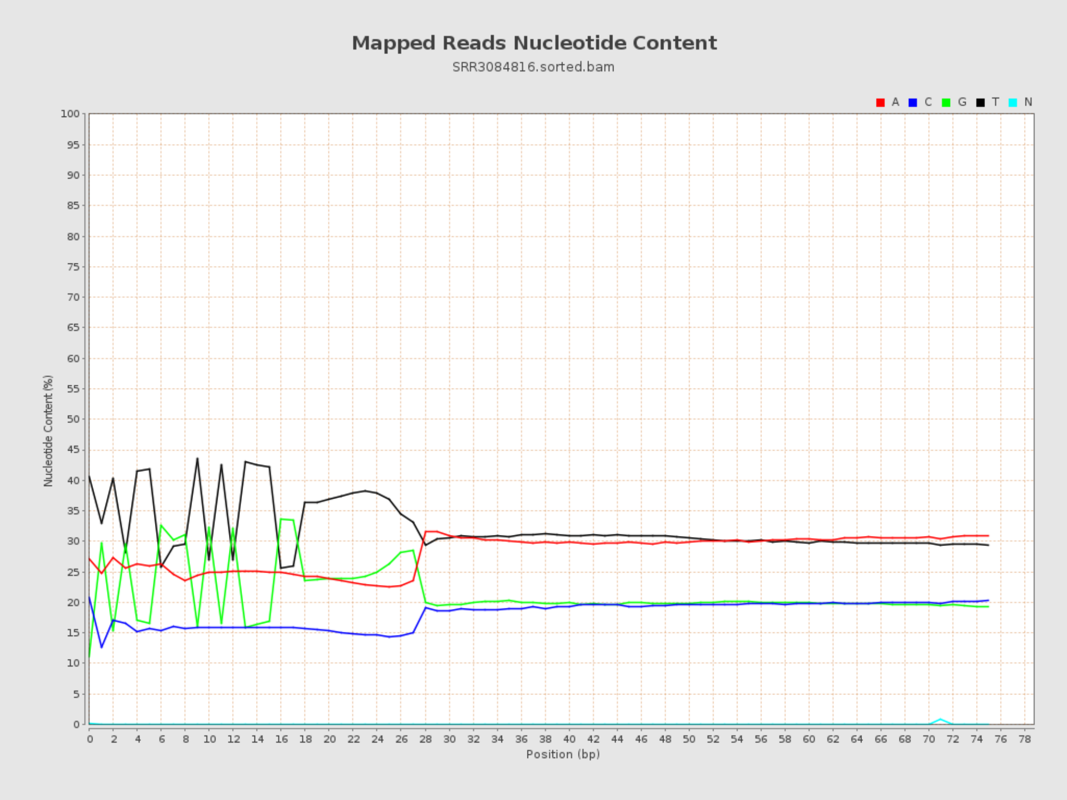
6. Results : Genome Fraction Coverage



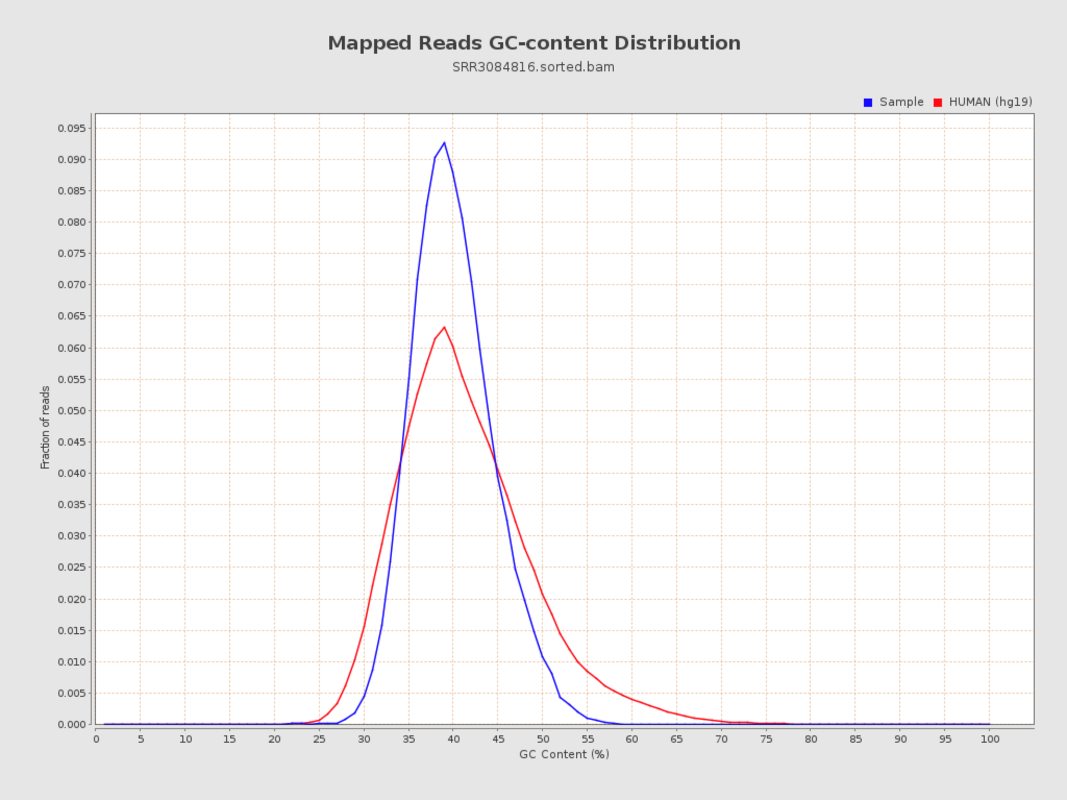
7. Results : Duplication Rate Histogram



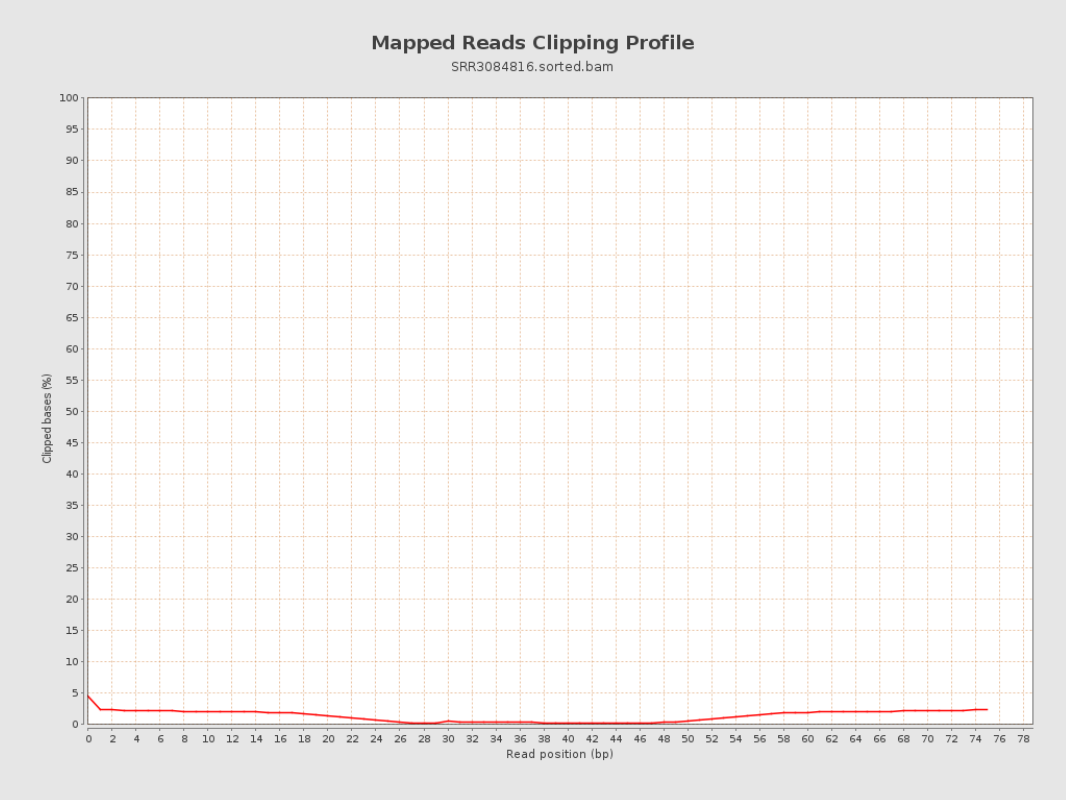
8. Results : Mapped Reads Nucleotide Content



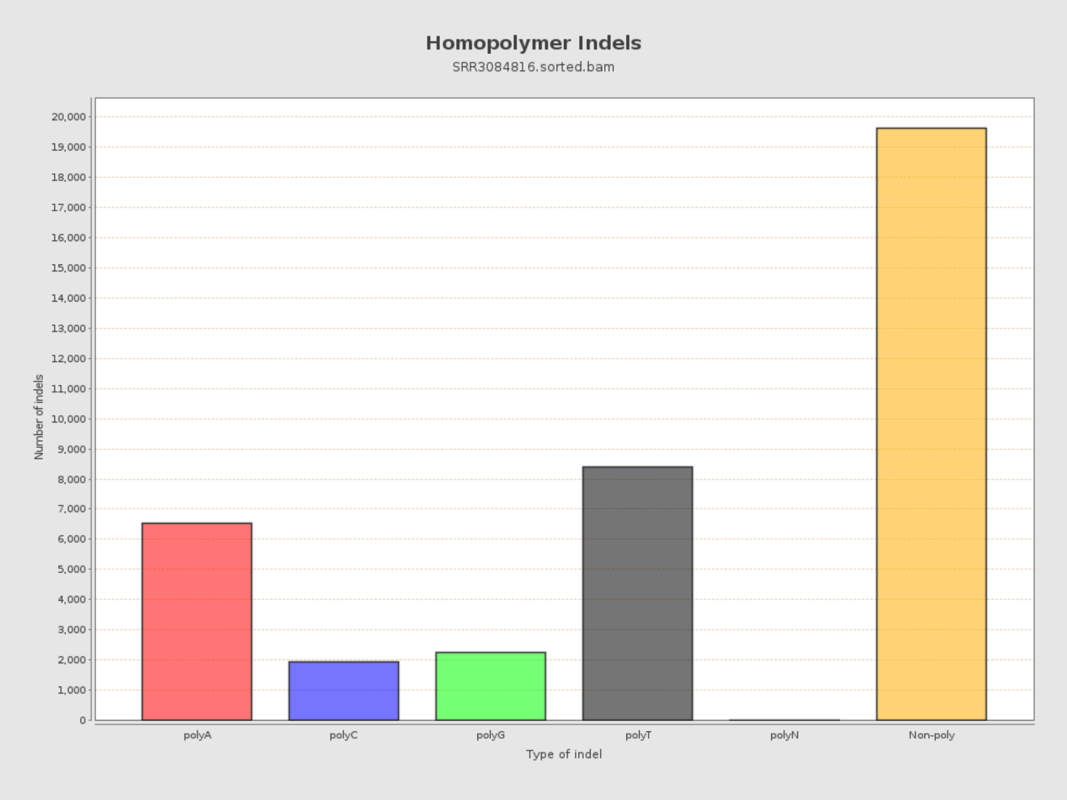
9. Results : Mapped Reads GC-content Distribution



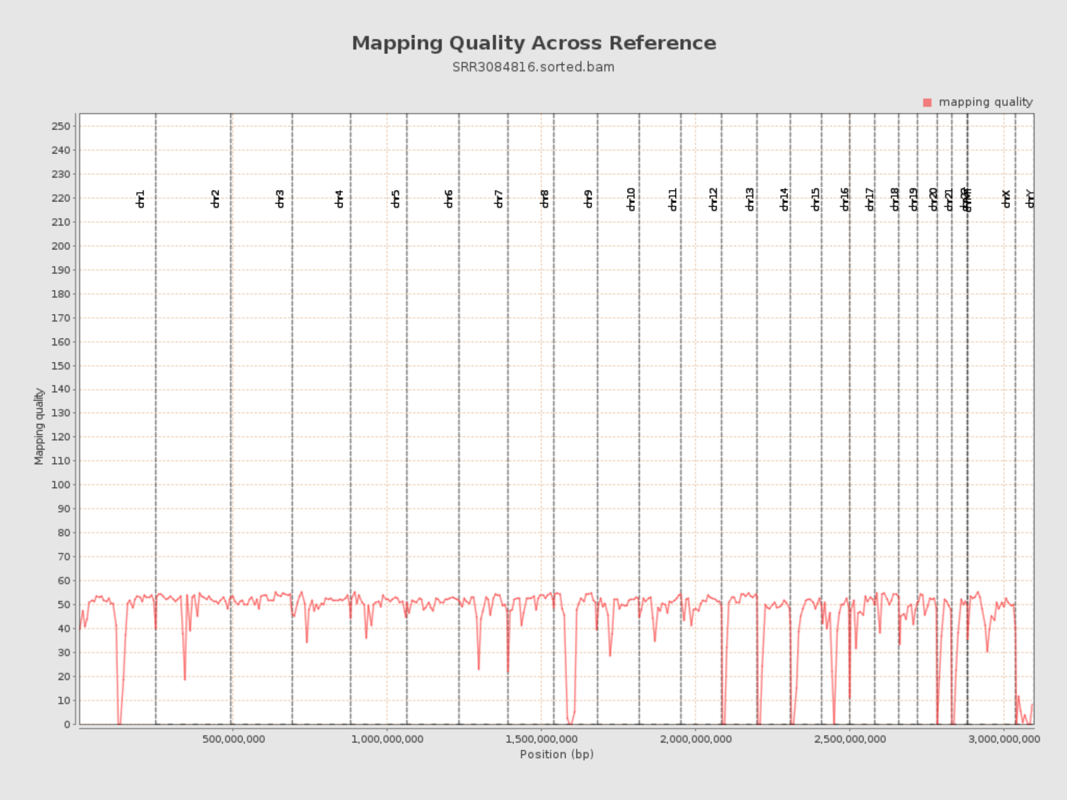
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram