Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/01 09:35:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472835.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_SRR3472835 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472835.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 01 09:35:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472835.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,393,210
Mapped reads	2,784,994 / 82.08%
Unmapped reads	608,216 / 17.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,971 / 0.62%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	97,472 / 2.87%
Duplication rate	2.61%
Clipped reads	1,437,281 / 42.36%

2.2. ACGT Content

Number/percentage of A's	48,393,395 / 26.77%
Number/percentage of C's	35,988,894 / 19.9%
Number/percentage of T's	53,999,640 / 29.87%
Number/percentage of G's	42,421,067 / 23.46%
Number/percentage of N's	4,640 / 0%
GC Percentage	43.37%

2.3. Coverage

Mean	0.0584

Standard Deviation	0.4153

2.4. Mapping Quality

Mean Mapping Quality	44.44

2.5. Mismatches and indels

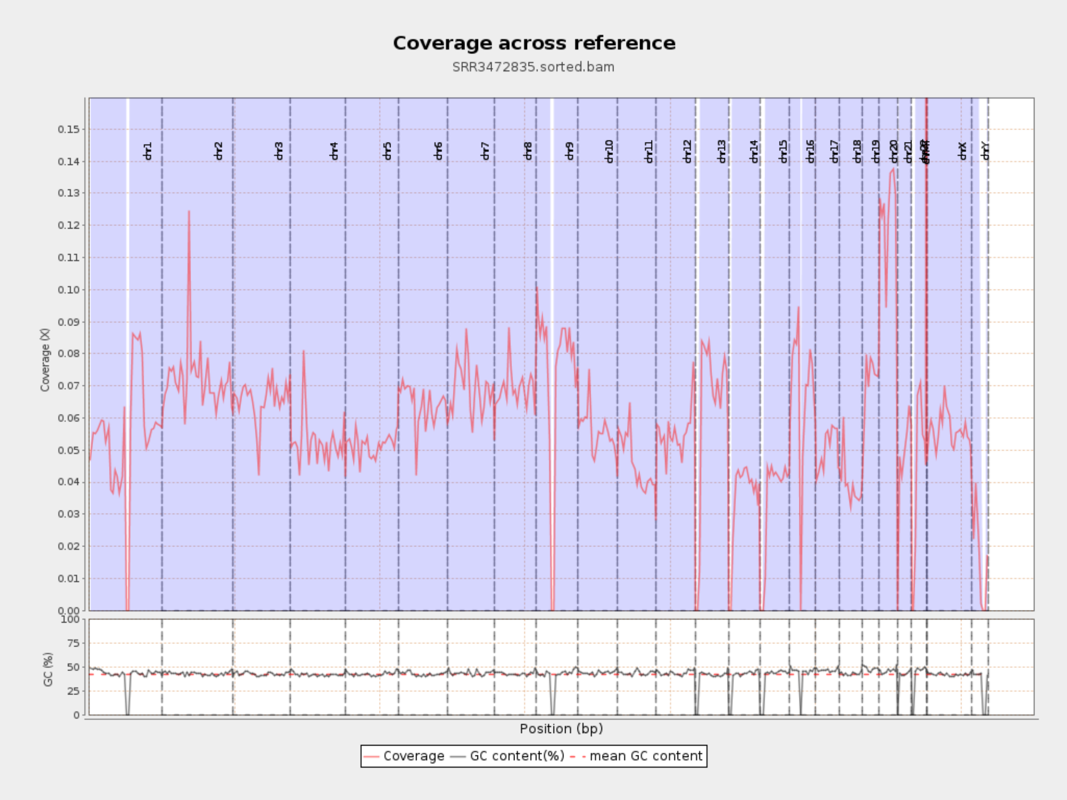
General error rate	0.86%
Mismatches	1,534,388
Insertions	13,763
Mapped reads with at least one insertion	0.49%
Deletions	39,742
Mapped reads with at least one deletion	1.41%
Homopolymer indels	44.45%

2.6. Chromosome stats

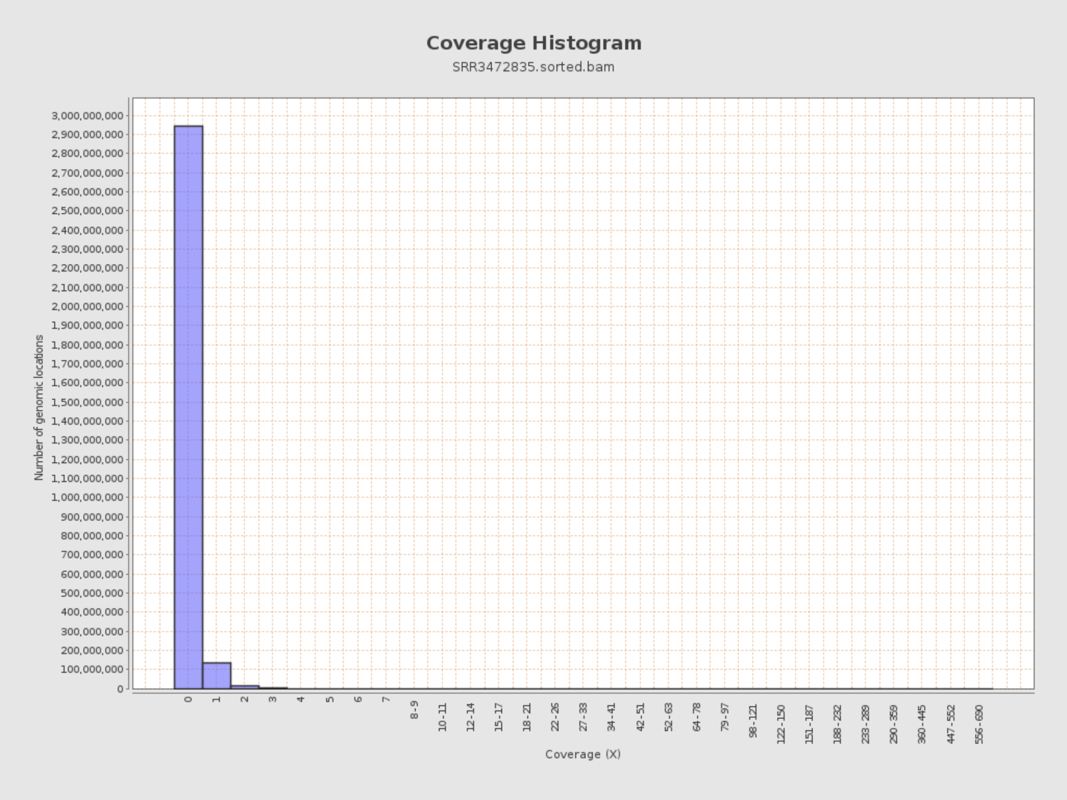
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13493357	0.0541	0.5894
chr2	243199373	17633641	0.0725	0.6305
chr3	198022430	12955759	0.0654	0.29
chr4	191154276	10019009	0.0524	0.2959
chr5	180915260	9308336	0.0515	0.26
chr6	171115067	10988147	0.0642	0.3178
chr7	159138663	11049205	0.0694	0.5217

chr8	146364022	10131768	0.0692	0.4078
chr9	141213431	10326326	0.0731	0.4815
chr10	135534747	7576145	0.0559	0.3692
chr11	135006516	6169911	0.0457	0.4146
chr12	133851895	7450246	0.0557	0.2778
chr13	115169878	7167759	0.0622	0.2946
chr14	107349540	3684883	0.0343	0.2532
chr15	102531392	3502777	0.0342	0.2279
chr16	90354753	6142966	0.068	0.3331
chr17	81195210	4098882	0.0505	0.282
chr18	78077248	3084153	0.0395	0.7757
chr19	59128983	4222020	0.0714	0.4477
chr20	63025520	7746117	0.1229	0.4275
chr21	48129895	2271080	0.0472	0.3067
chr22	51304566	2145586	0.0418	0.2552
chrMT	16571	20906	1.2616	1.2665
chrX	155270560	8740347	0.0563	0.3135
chrY	59373566	949225	0.016	0.2013

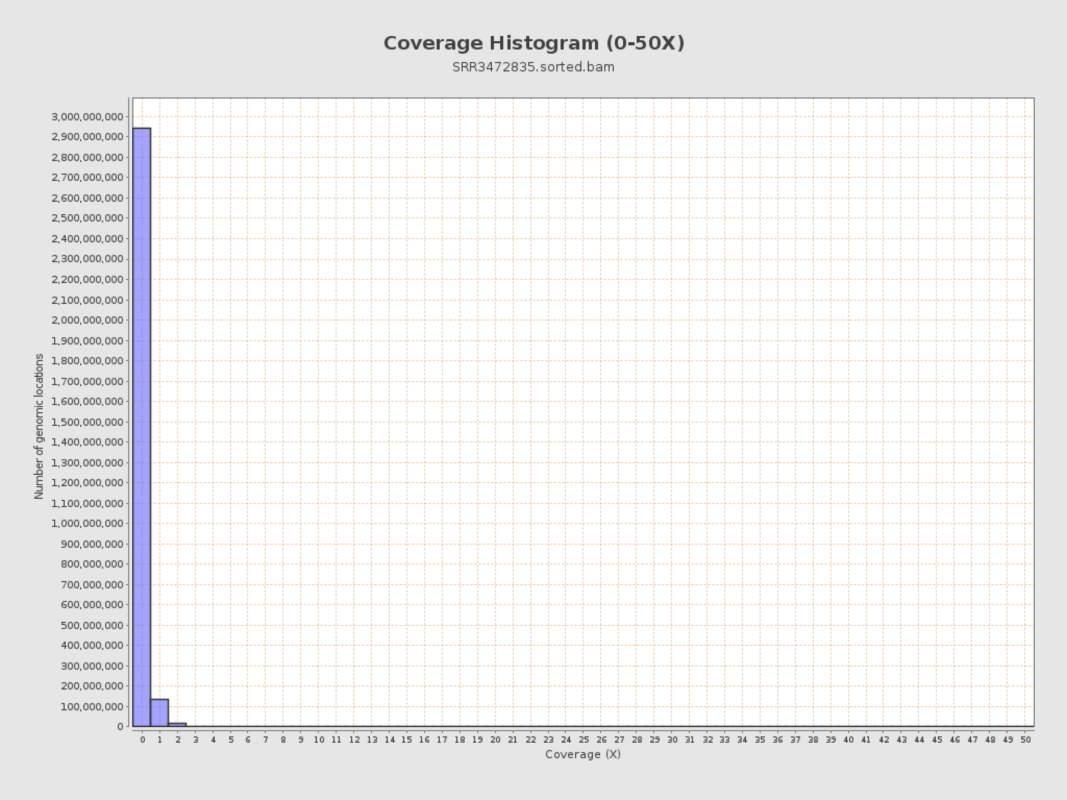
3. Results : Coverage across reference



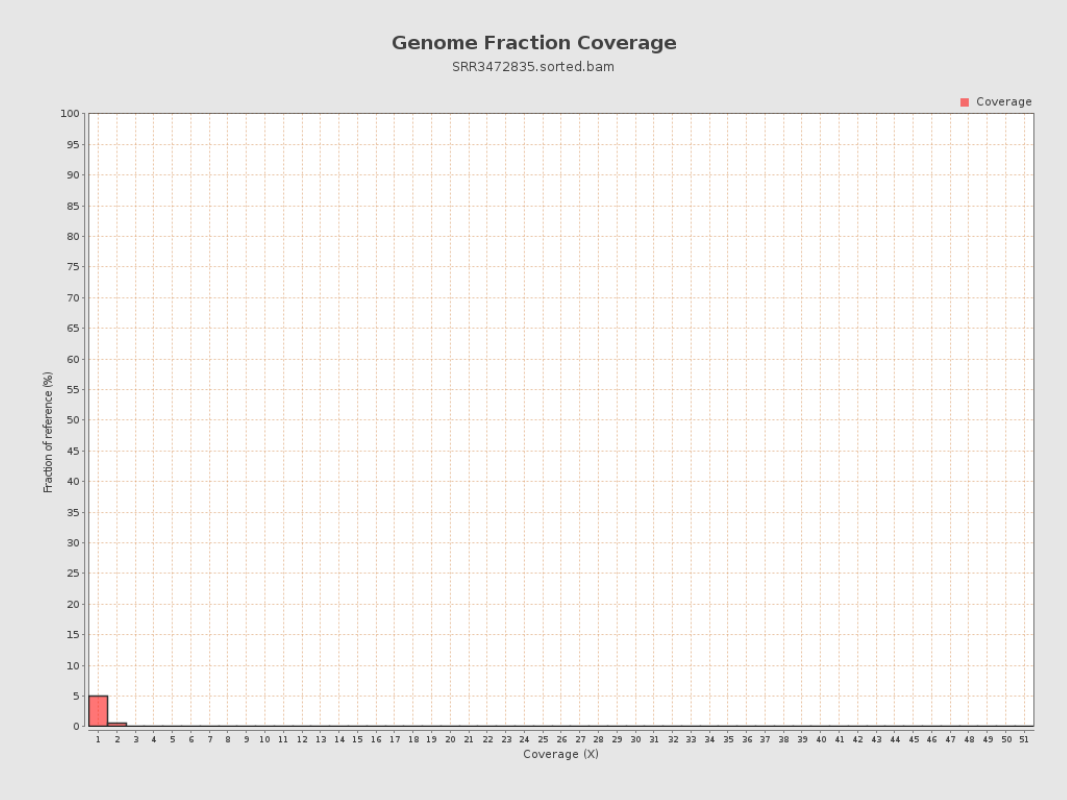
4. Results : Coverage Histogram



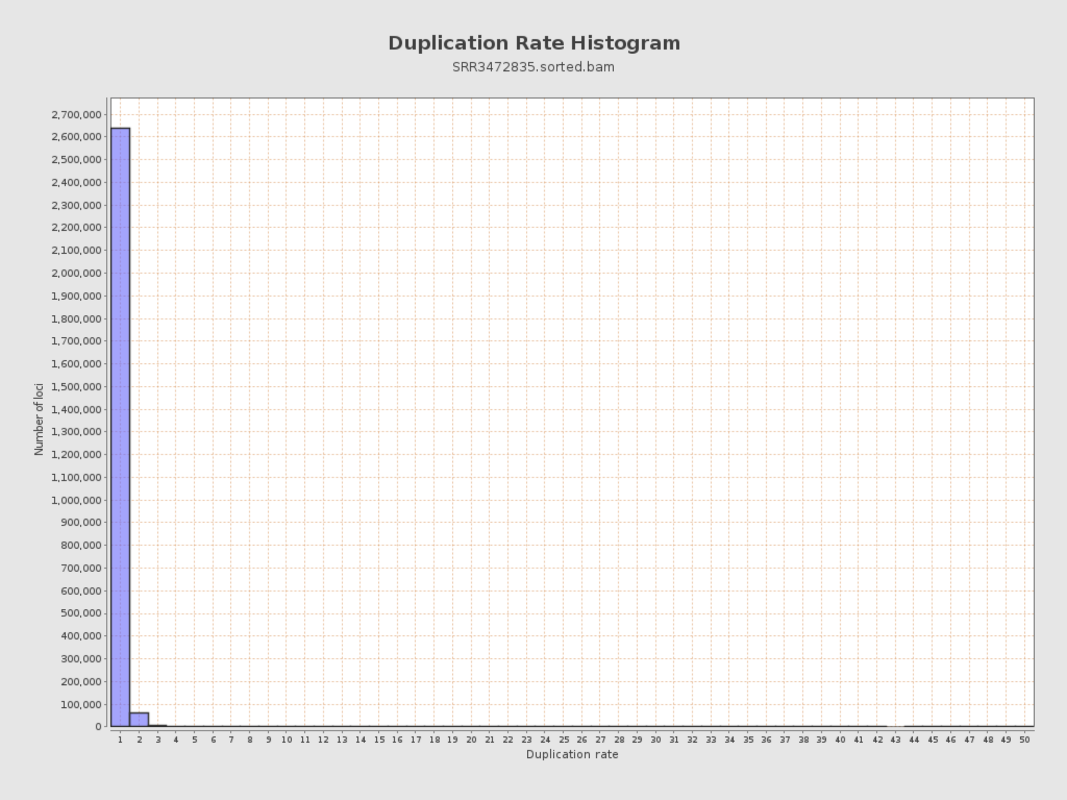
5. Results : Coverage Histogram (0-50X)



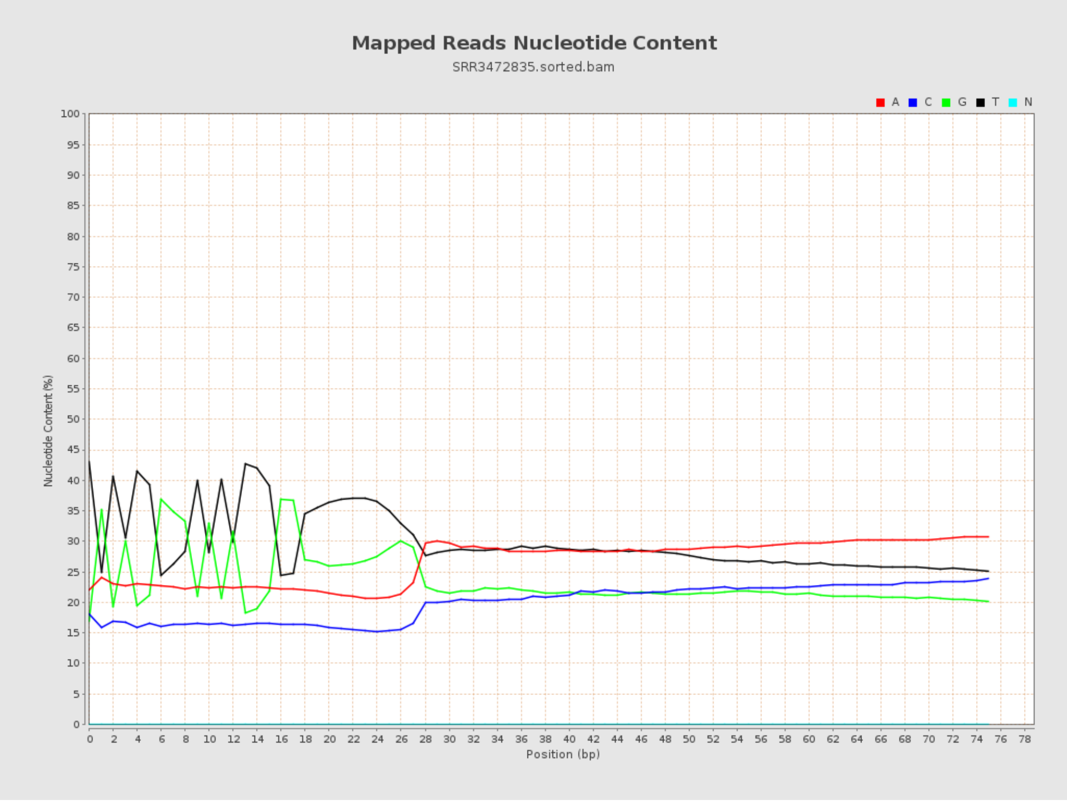
6. Results : Genome Fraction Coverage



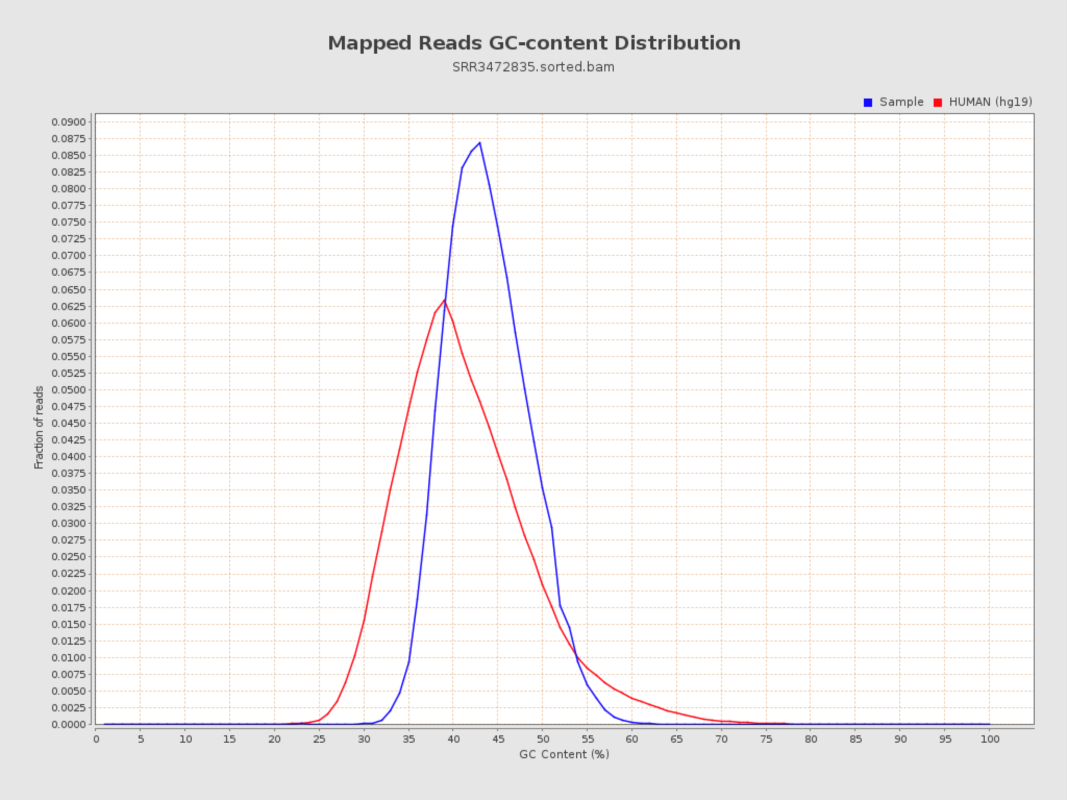
7. Results : Duplication Rate Histogram



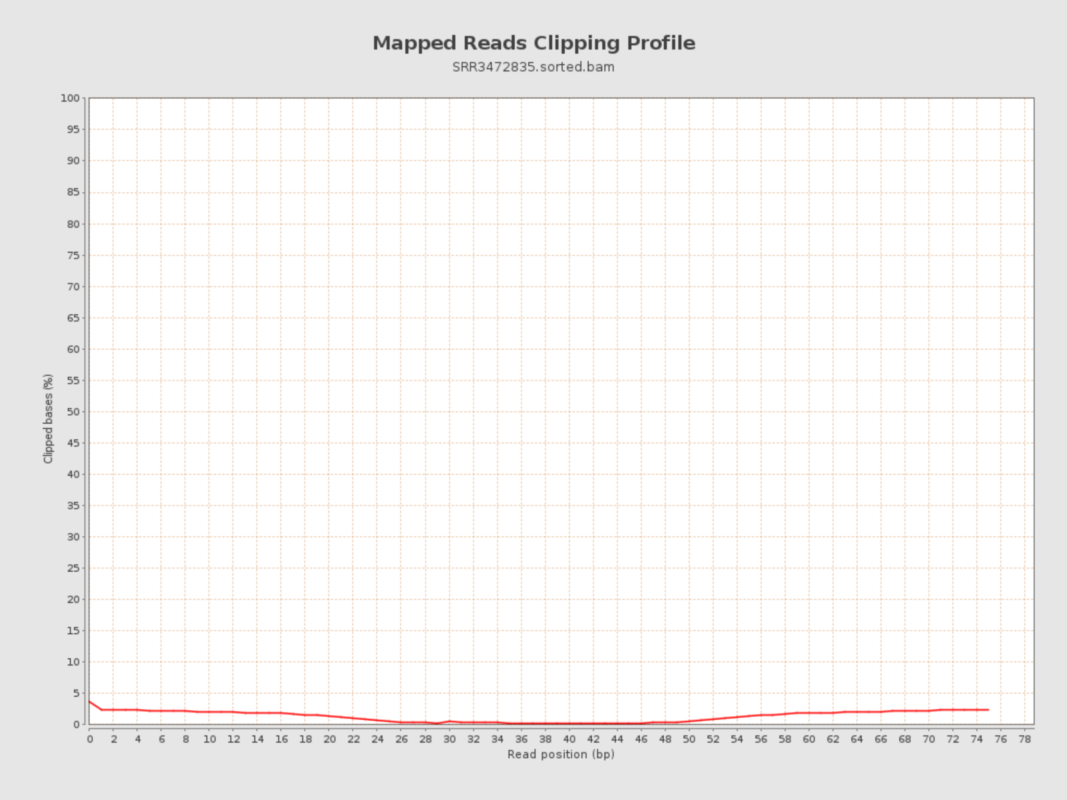
8. Results : Mapped Reads Nucleotide Content



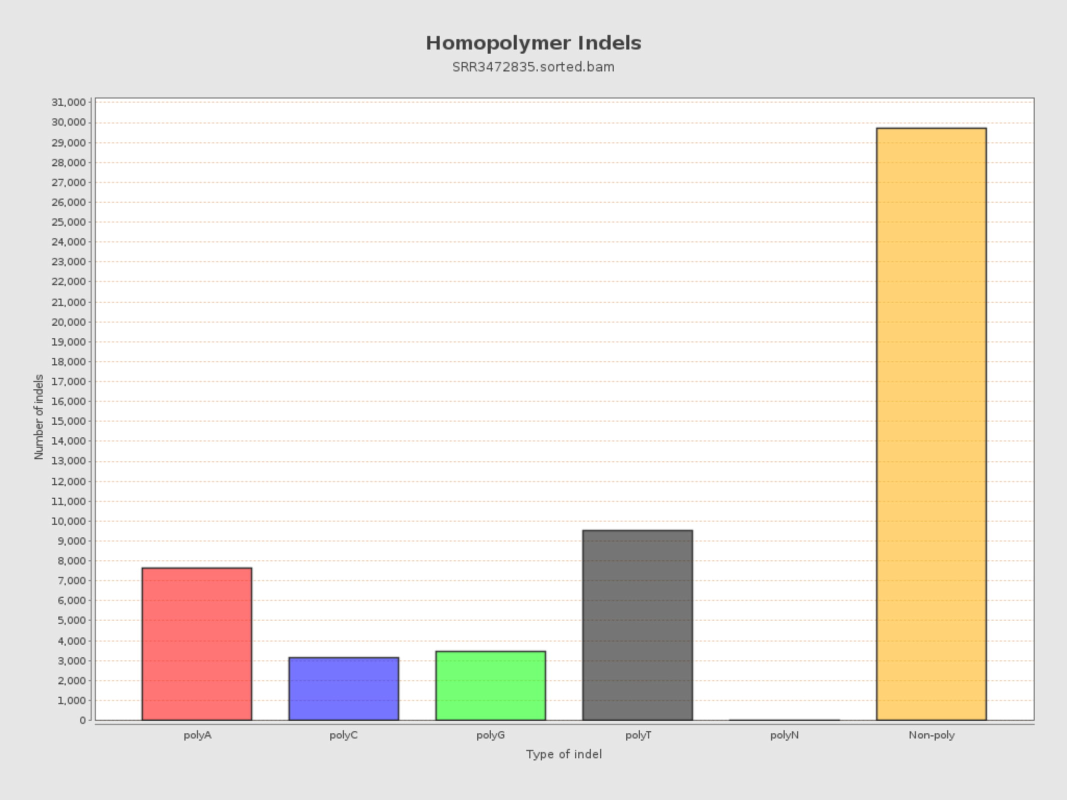
9. Results : Mapped Reads GC-content Distribution



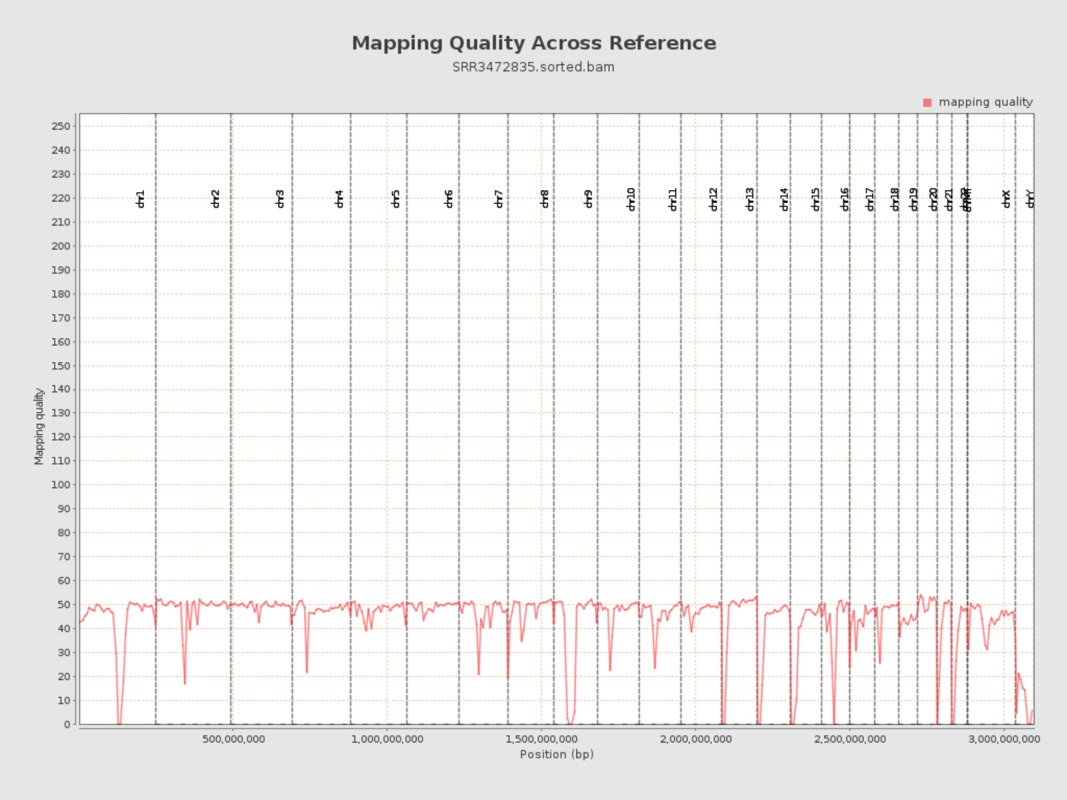
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram