Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/01 09:06:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472830.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_SRR3472830 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472830.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 01 09:06:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472830.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,529,789
Mapped reads	2,192,559 / 86.67%
Unmapped reads	337,230 / 13.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,677 / 0.9%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	65,363 / 2.58%
Duplication rate	2.09%
Clipped reads	1,145,181 / 45.27%

2.2. ACGT Content

Number/percentage of A's	38,409,067 / 27.02%
Number/percentage of C's	28,555,682 / 20.09%
Number/percentage of T's	42,052,340 / 29.58%
Number/percentage of G's	33,131,213 / 23.31%
Number/percentage of N's	3,302 / 0%
GC Percentage	43.4%

2.3. Coverage

Mean	0.0459

Standard Deviation	0.3544

2.4. Mapping Quality

Mean Mapping Quality	43.73

2.5. Mismatches and indels

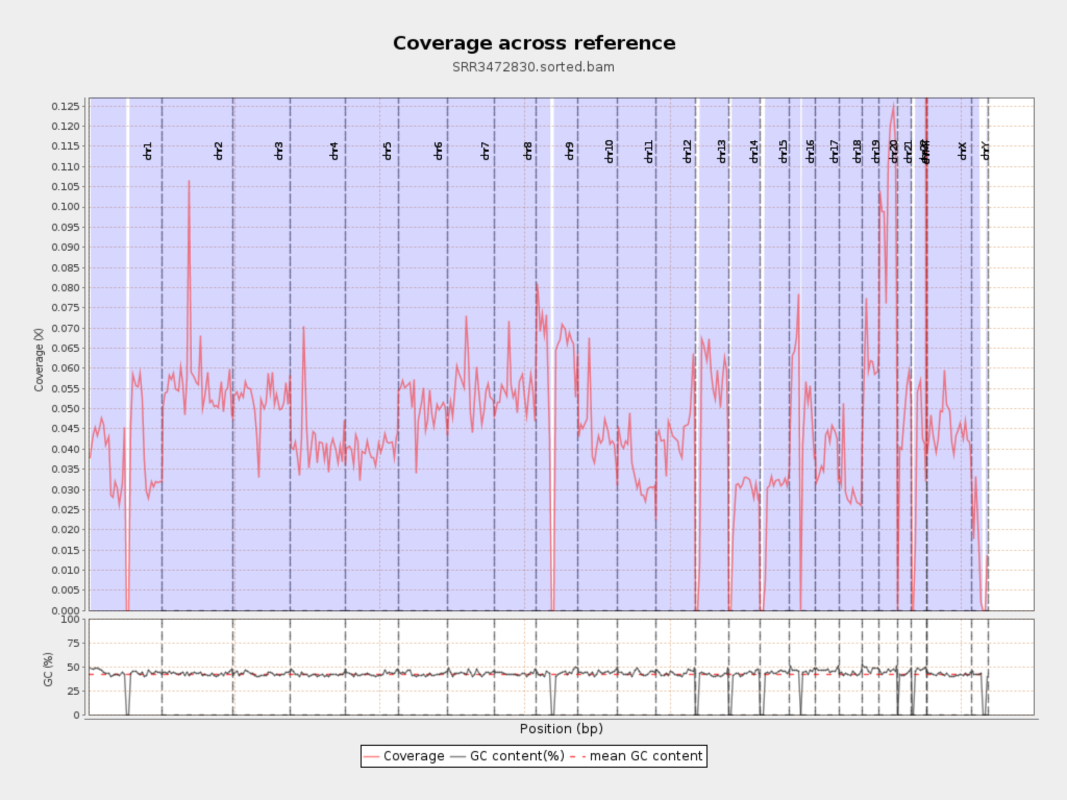
General error rate	0.88%
Mismatches	1,223,263
Insertions	11,502
Mapped reads with at least one insertion	0.52%
Deletions	32,937
Mapped reads with at least one deletion	1.48%
Homopolymer indels	44.68%

2.6. Chromosome stats

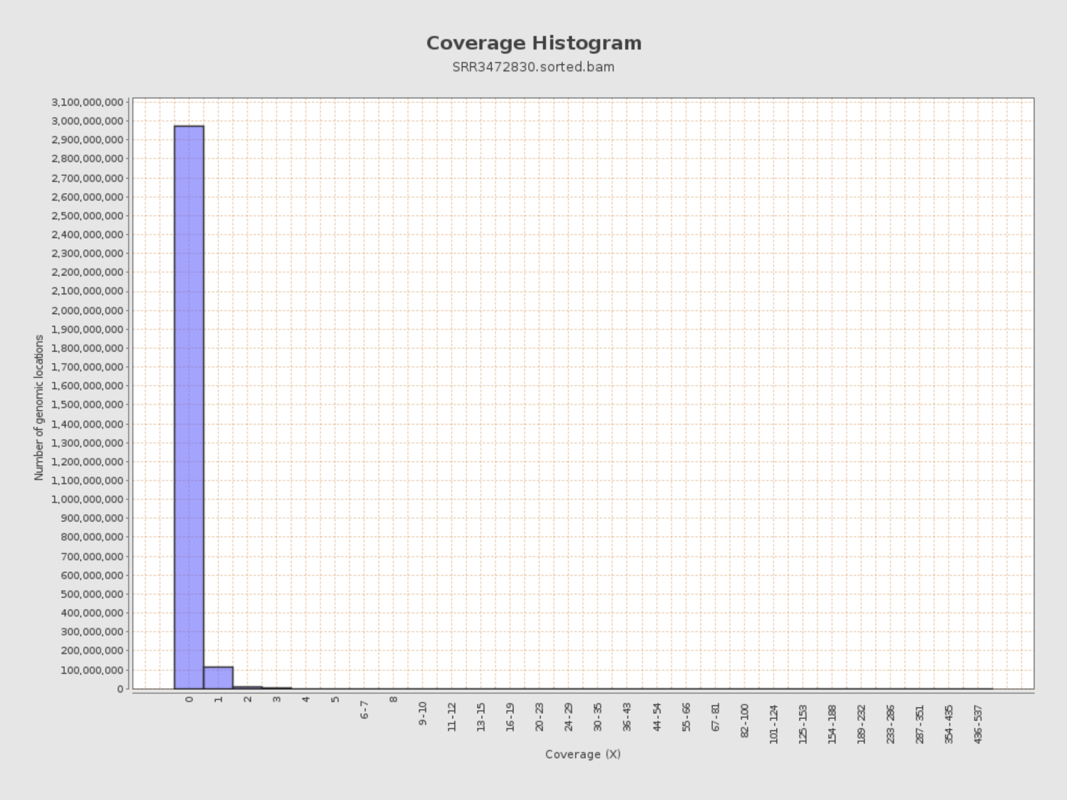
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9302524	0.0373	0.4329
chr2	243199373	13792393	0.0567	0.5496
chr3	198022430	10304307	0.052	0.252
chr4	191154276	7893125	0.0413	0.2632
chr5	180915260	7221059	0.0399	0.222
chr6	171115067	8703111	0.0509	0.2701
chr7	159138663	8656377	0.0544	0.4456

chr8	146364022	7938403	0.0542	0.3533
chr9	141213431	8381935	0.0594	0.4269
chr10	135534747	5969370	0.044	0.3418
chr11	135006516	4724963	0.035	0.3278
chr12	133851895	5957247	0.0445	0.2443
chr13	115169878	5729857	0.0498	0.2558
chr14	107349540	2802317	0.0261	0.223
chr15	102531392	2606793	0.0254	0.1935
chr16	90354753	4600752	0.0509	0.2829
chr17	81195210	3203597	0.0395	0.2417
chr18	78077248	2392713	0.0306	0.6999
chr19	59128983	3642030	0.0616	0.379
chr20	63025520	6597750	0.1047	0.3801
chr21	48129895	2133550	0.0443	0.2758
chr22	51304566	1699004	0.0331	0.2102
chrMT	16571	187737	11.3292	7.0825
chrX	155270560	6998355	0.0451	0.27
chrY	59373566	771019	0.013	0.1911

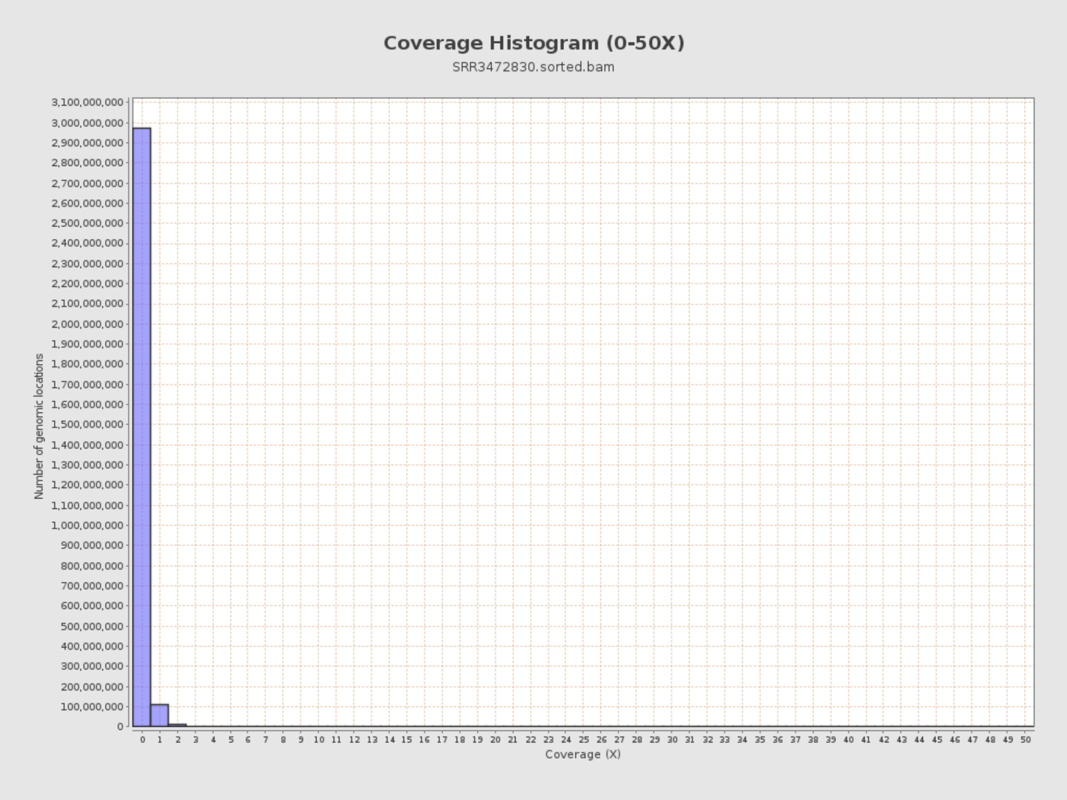
3. Results : Coverage across reference



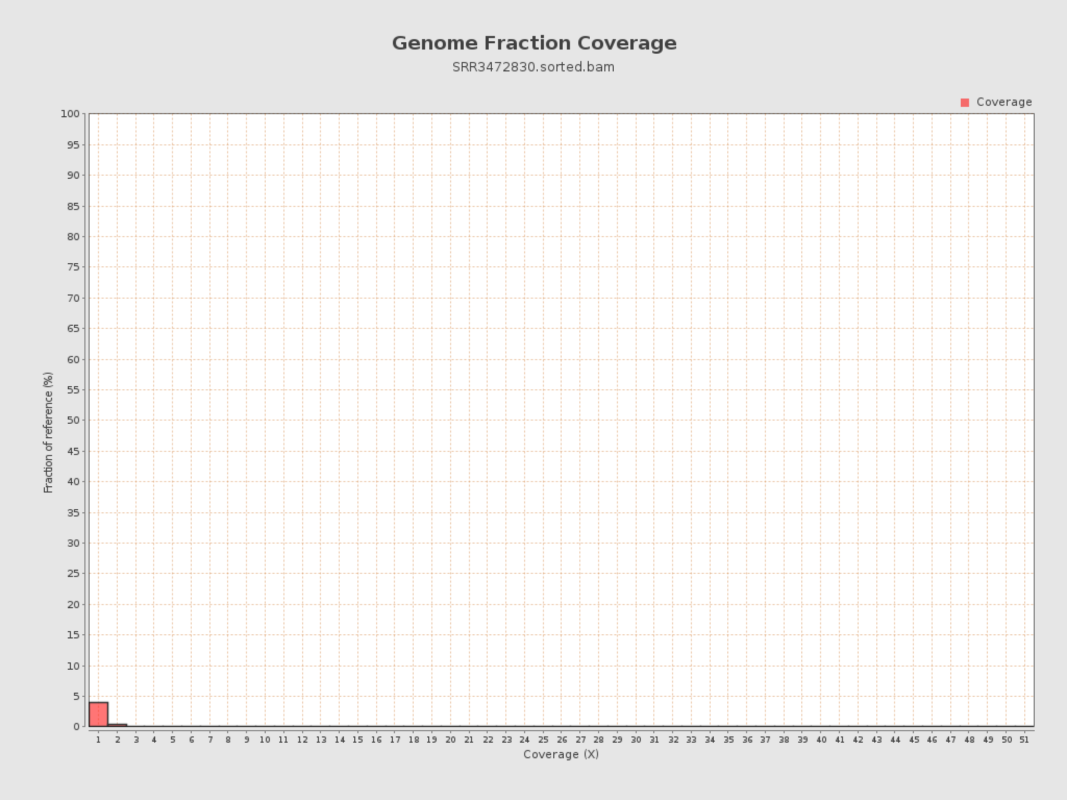
4. Results : Coverage Histogram



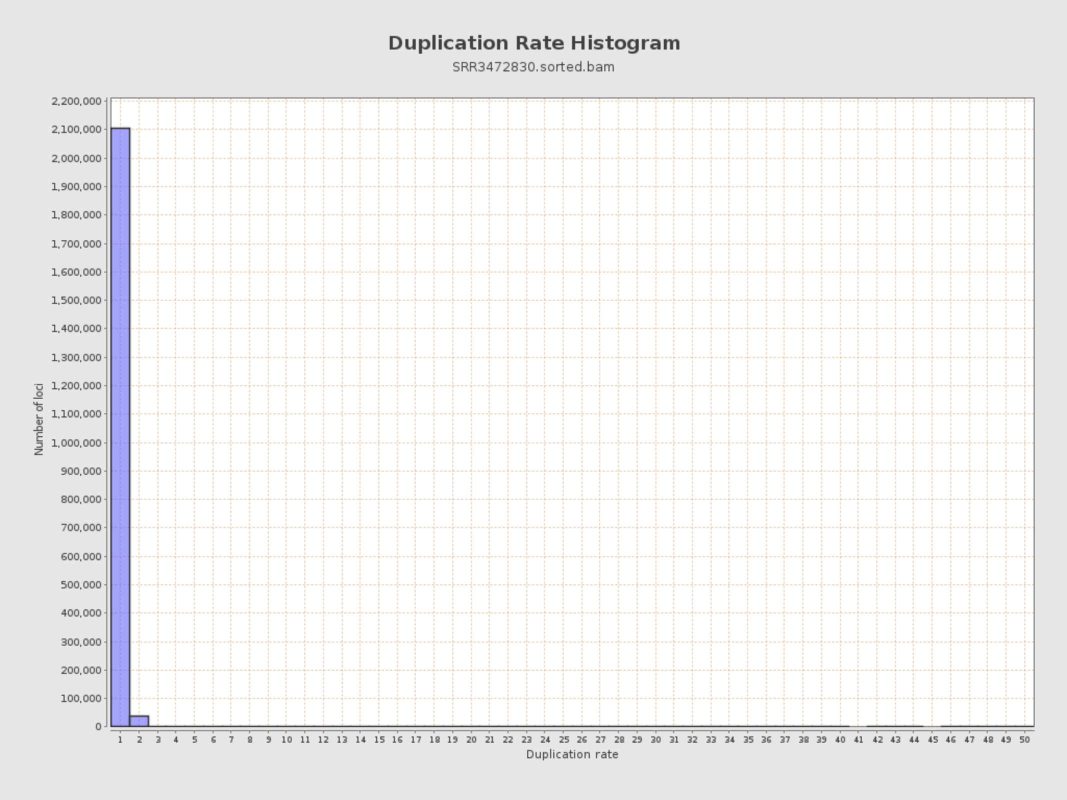
5. Results : Coverage Histogram (0-50X)



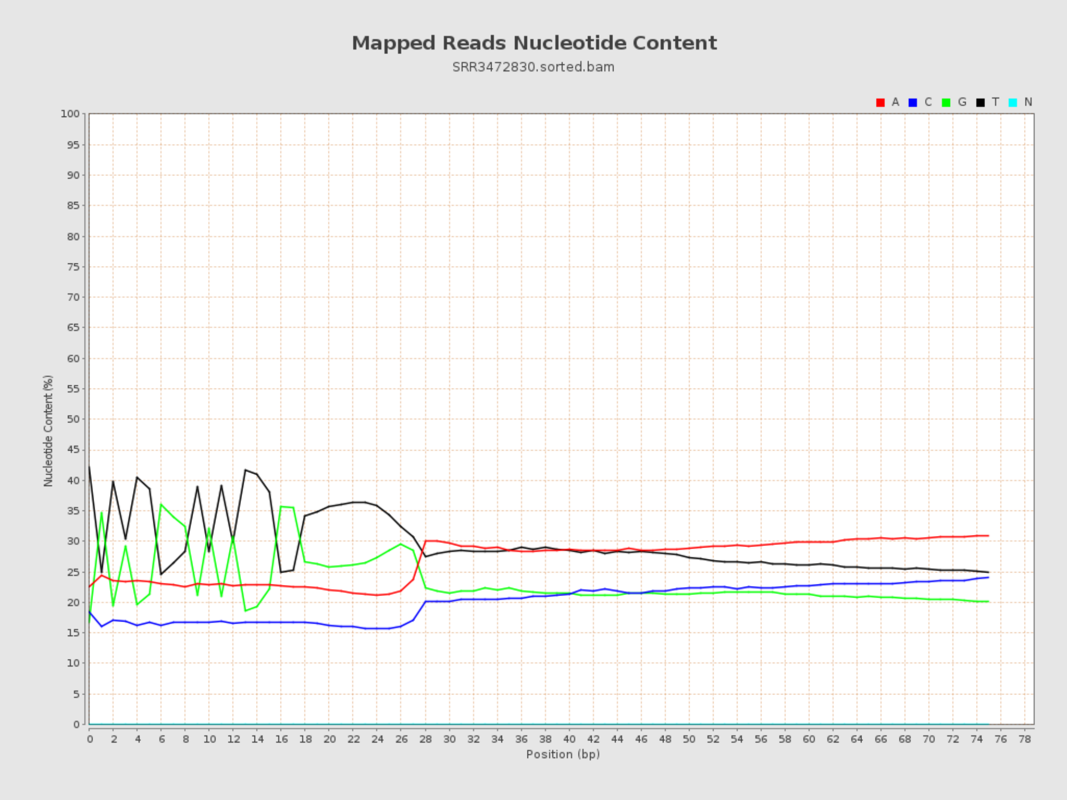
6. Results : Genome Fraction Coverage



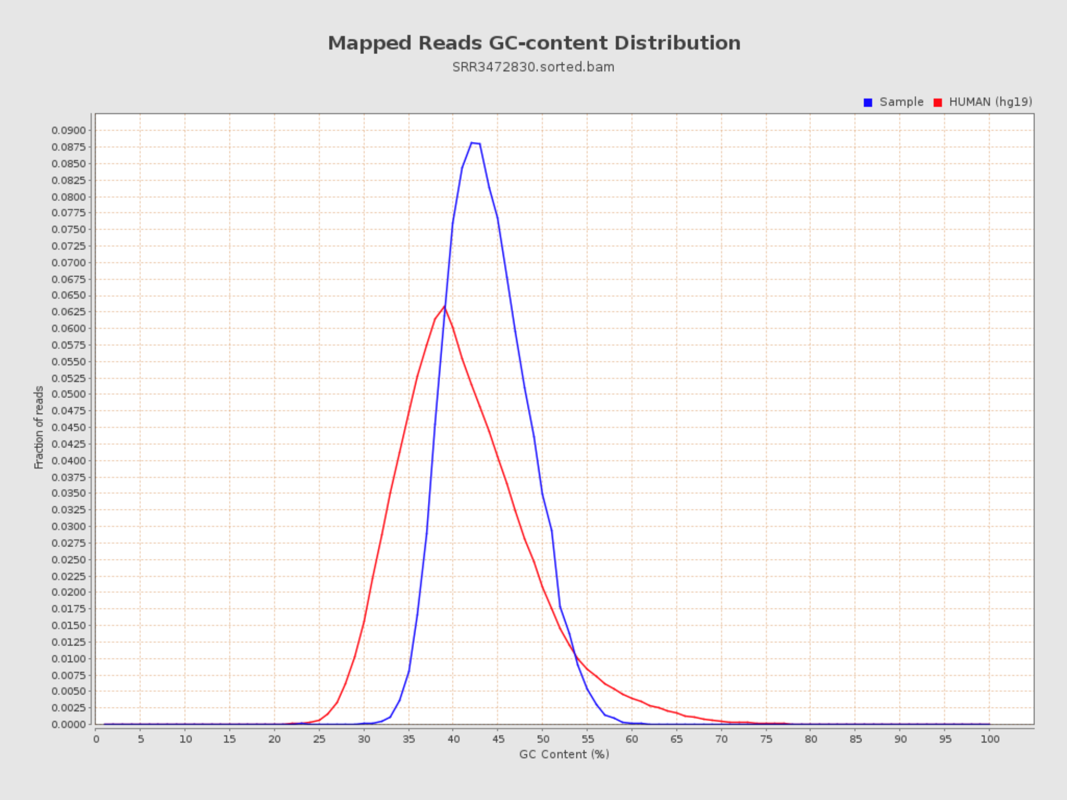
7. Results : Duplication Rate Histogram



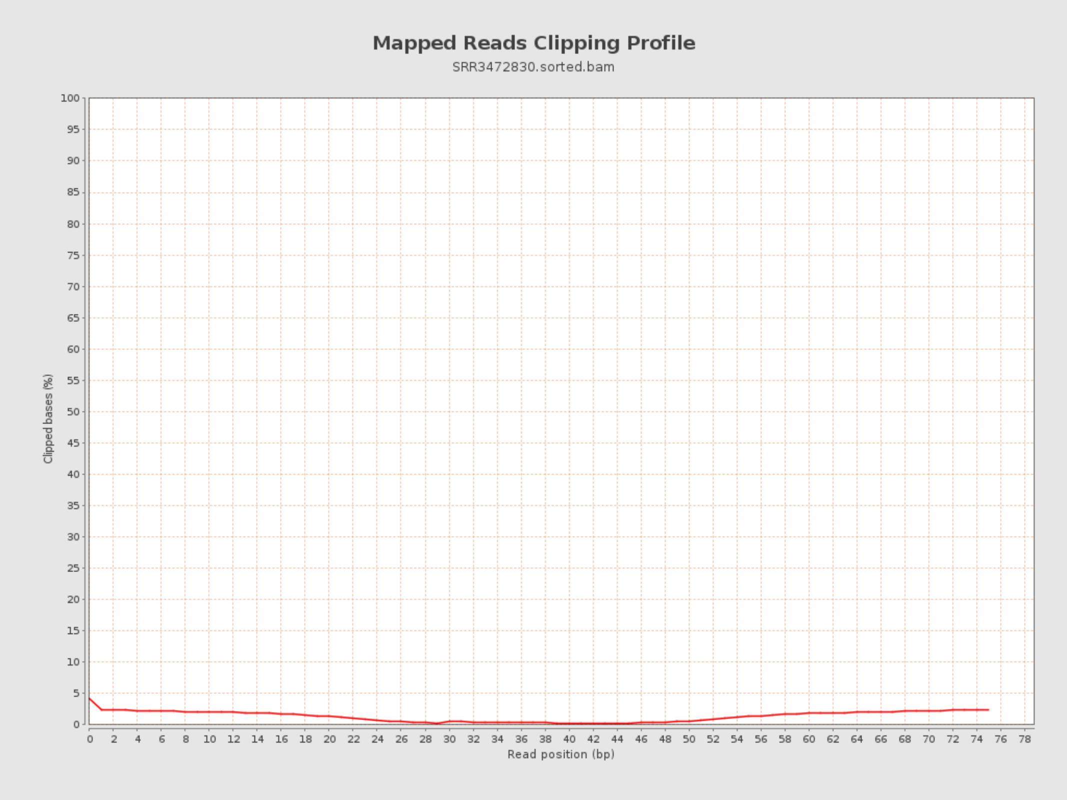
8. Results : Mapped Reads Nucleotide Content



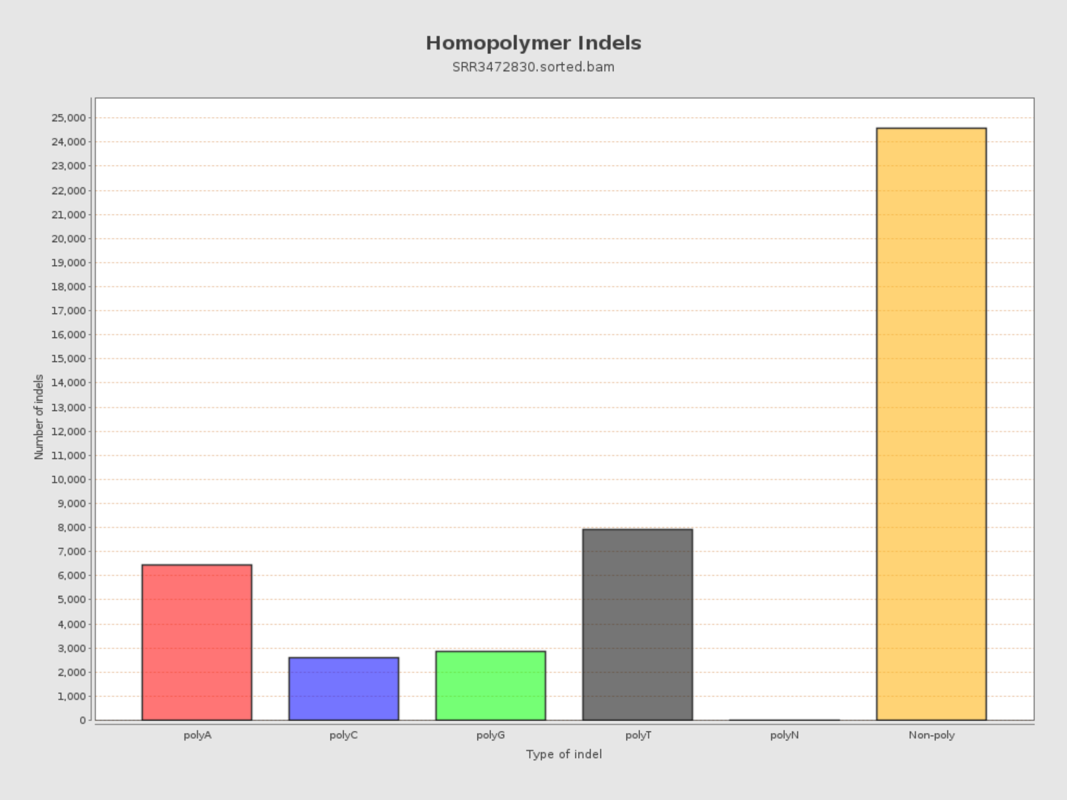
9. Results : Mapped Reads GC-content Distribution



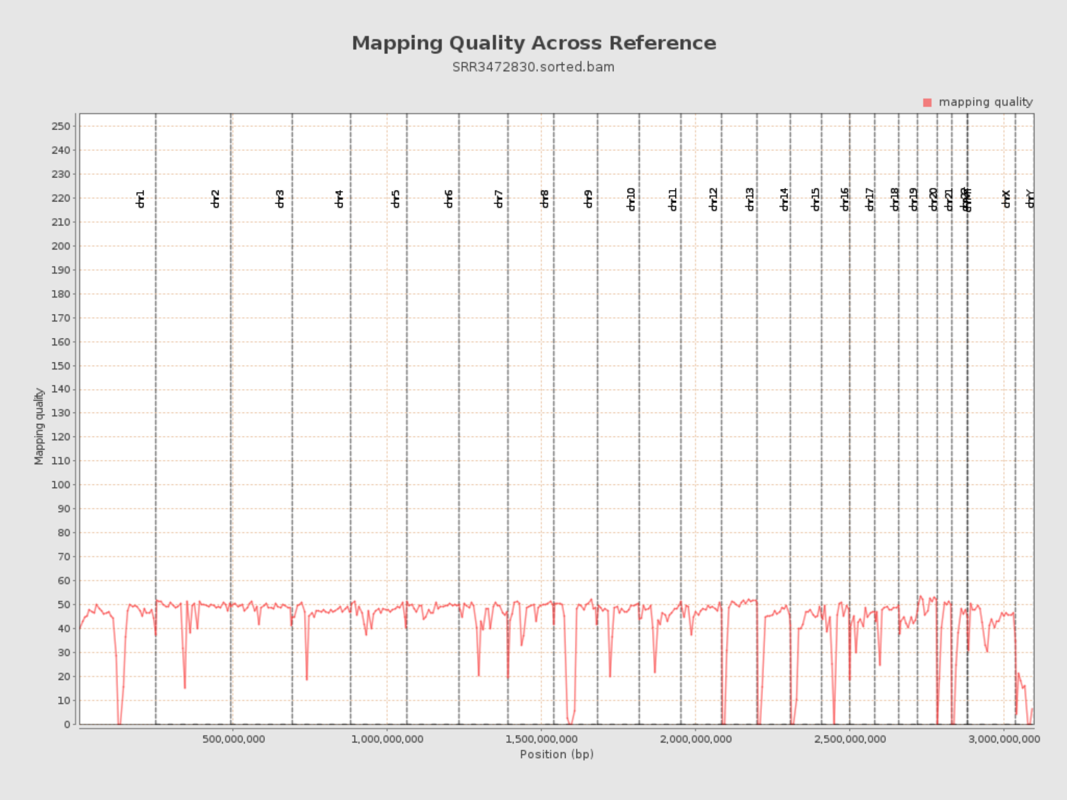
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram