Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/01 06:56:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472803.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_SRR3472803 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472803.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 01 06:56:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472803.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,985,399
Mapped reads	2,300,973 / 77.07%
Unmapped reads	684,426 / 22.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,966 / 0.67%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	121,593 / 4.07%
Duplication rate	3.91%
Clipped reads	1,322,512 / 44.3%

2.2. ACGT Content

Number/percentage of A's	39,262,315 / 26.89%
Number/percentage of C's	28,956,117 / 19.83%
Number/percentage of T's	43,251,853 / 29.62%
Number/percentage of G's	34,528,811 / 23.65%
Number/percentage of N's	3,455 / 0%
GC Percentage	43.48%

2.3. Coverage

Mean	0.0472

Standard Deviation	0.3623

2.4. Mapping Quality

Mean Mapping Quality	43.2

2.5. Mismatches and indels

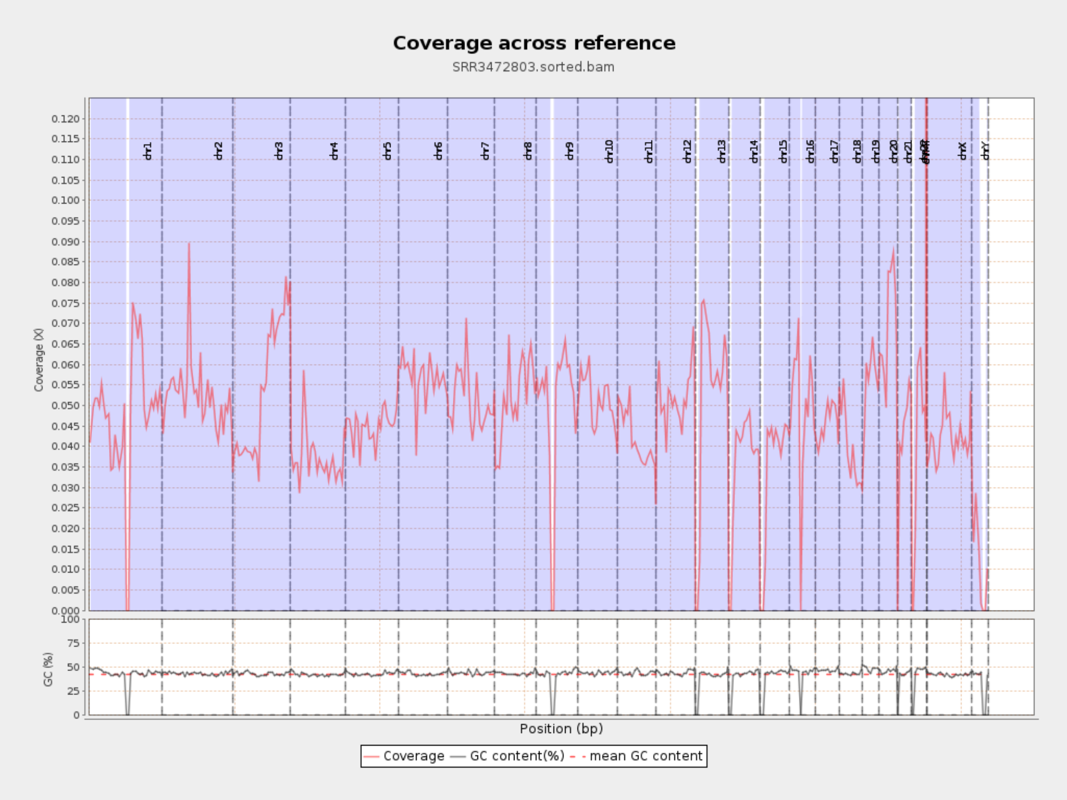
General error rate	0.92%
Mismatches	1,322,295
Insertions	11,475
Mapped reads with at least one insertion	0.49%
Deletions	35,992
Mapped reads with at least one deletion	1.55%
Homopolymer indels	45.71%

2.6. Chromosome stats

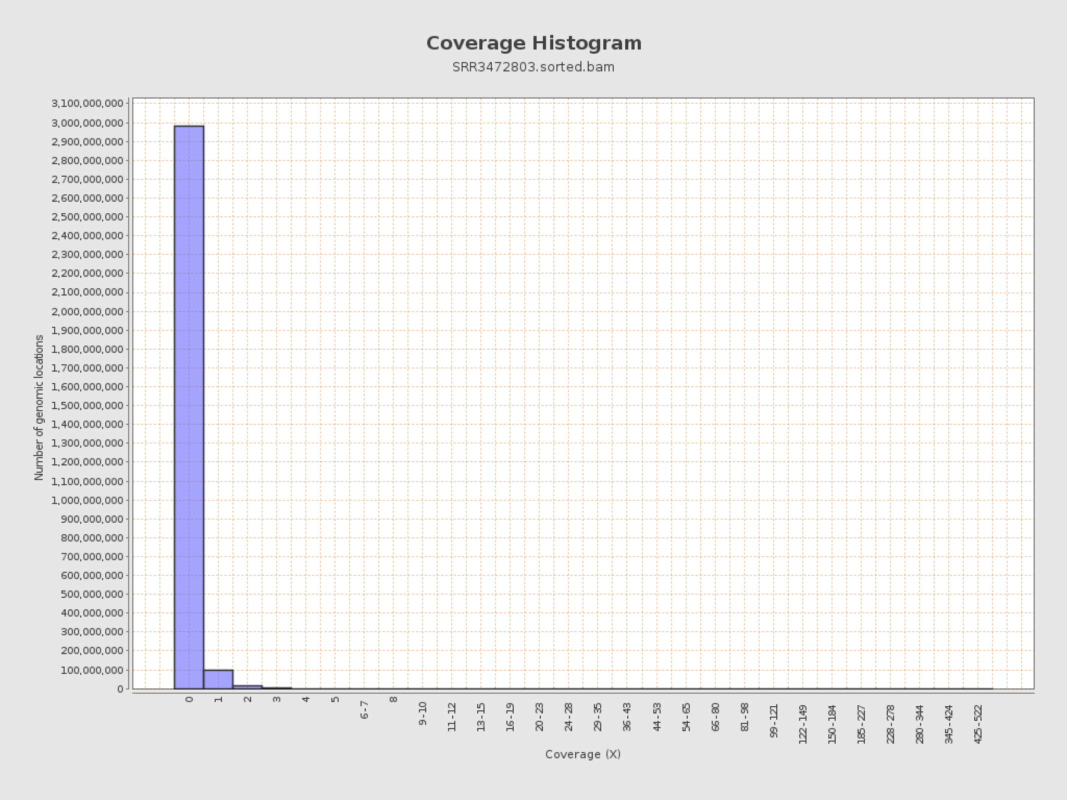
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11840222	0.0475	0.4396
chr2	243199373	12827114	0.0527	0.4812
chr3	198022430	10550639	0.0533	0.285
chr4	191154276	7037507	0.0368	0.2614
chr5	180915260	8114265	0.0449	0.2655
chr6	171115067	9723239	0.0568	0.3235
chr7	159138663	8147170	0.0512	0.4965

chr8	146364022	7544099	0.0515	0.3496
chr9	141213431	6961148	0.0493	0.3977
chr10	135534747	6986521	0.0515	0.3481
chr11	135006516	5652676	0.0419	0.3934
chr12	133851895	6955249	0.052	0.292
chr13	115169878	6038189	0.0524	0.2909
chr14	107349540	3823674	0.0356	0.2802
chr15	102531392	3520658	0.0343	0.253
chr16	90354753	4457677	0.0493	0.3048
chr17	81195210	3710995	0.0457	0.29
chr18	78077248	3121373	0.04	0.6532
chr19	59128983	3307382	0.0559	0.3767
chr20	63025520	4419342	0.0701	0.3432
chr21	48129895	2046837	0.0425	0.2906
chr22	51304566	1943205	0.0379	0.251
chrMT	16571	143401	8.6537	6.2252
chrX	155270560	6520237	0.042	0.2987
chrY	59373566	675094	0.0114	0.1642

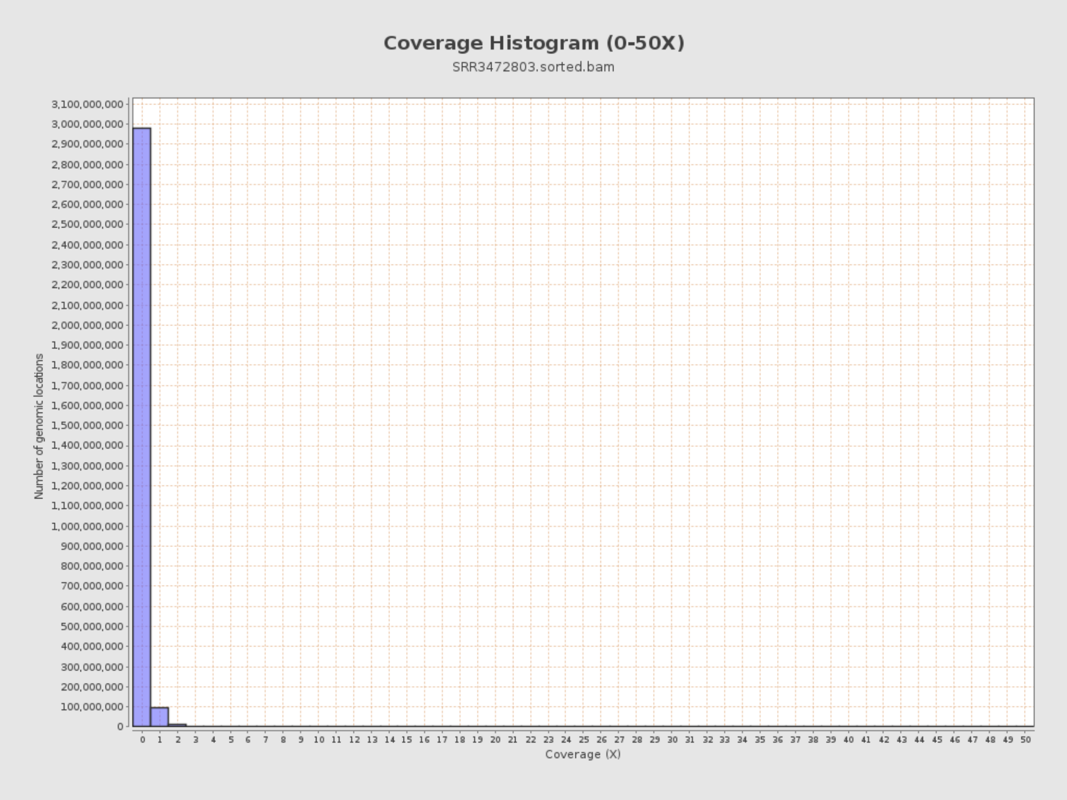
3. Results : Coverage across reference



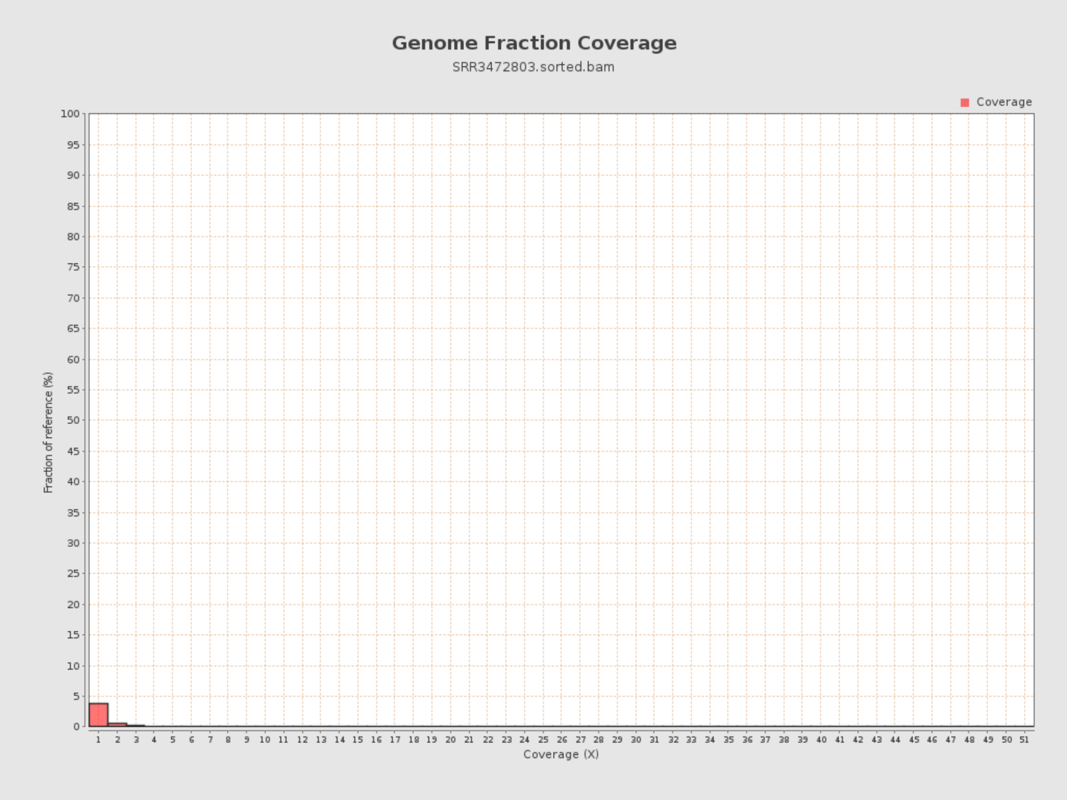
4. Results : Coverage Histogram



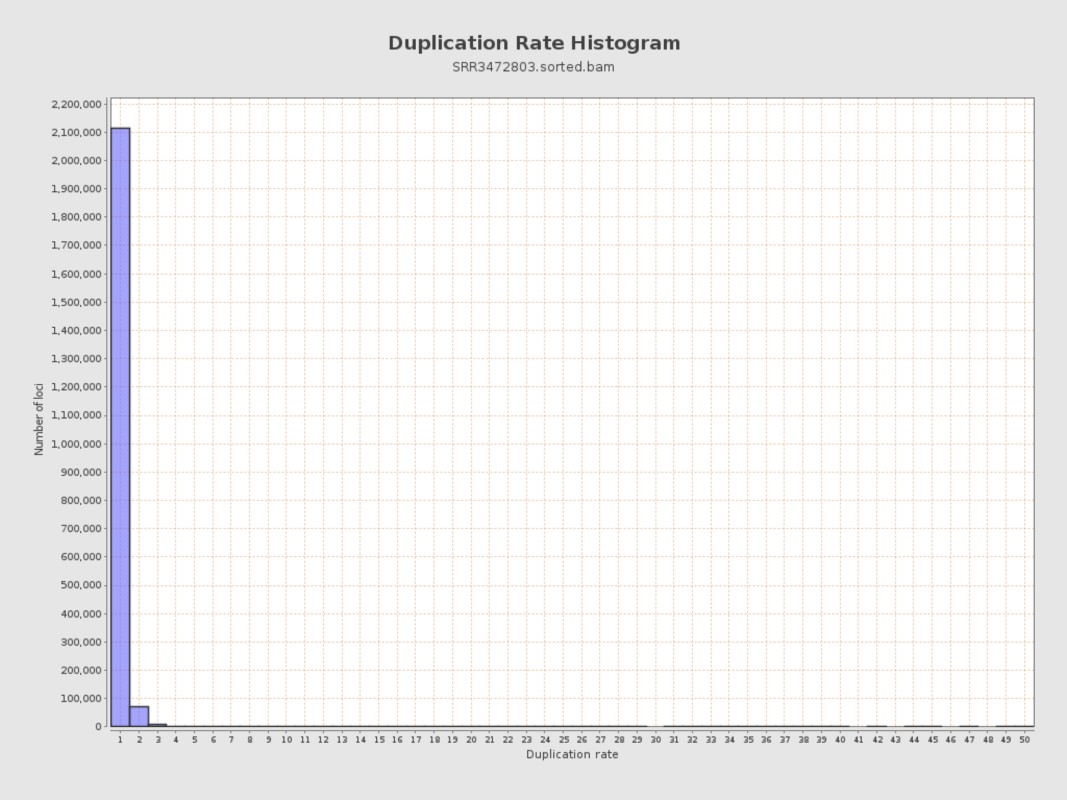
5. Results : Coverage Histogram (0-50X)



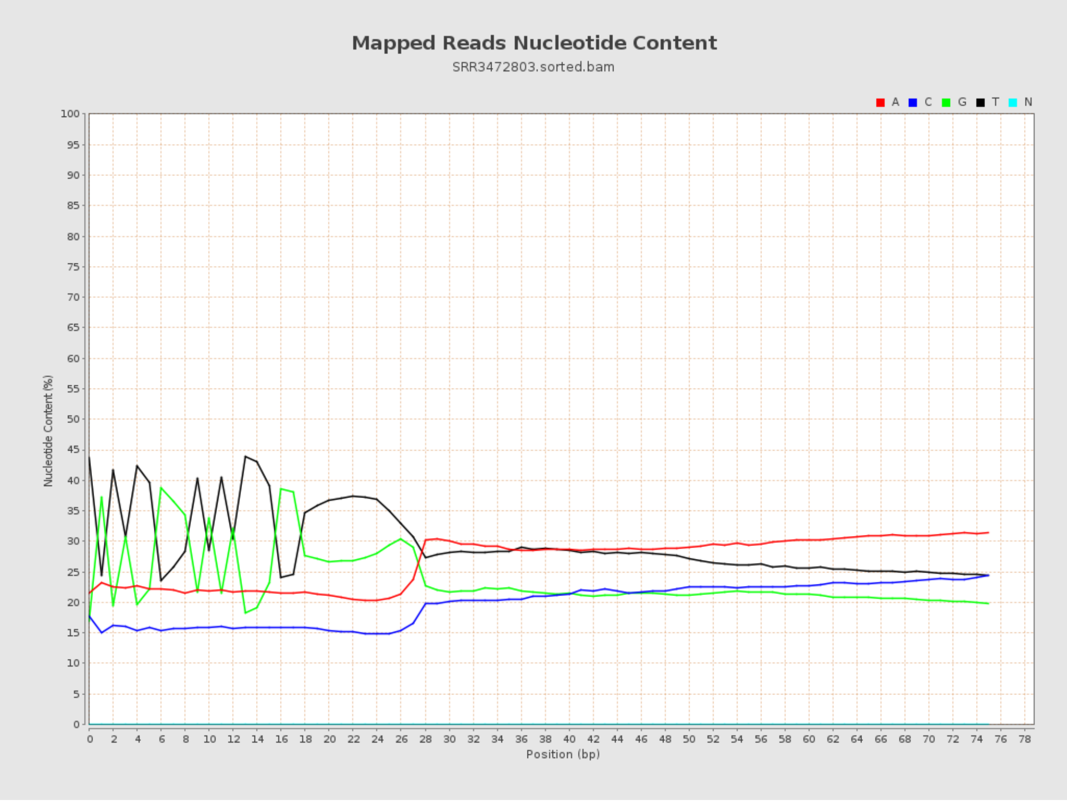
6. Results : Genome Fraction Coverage



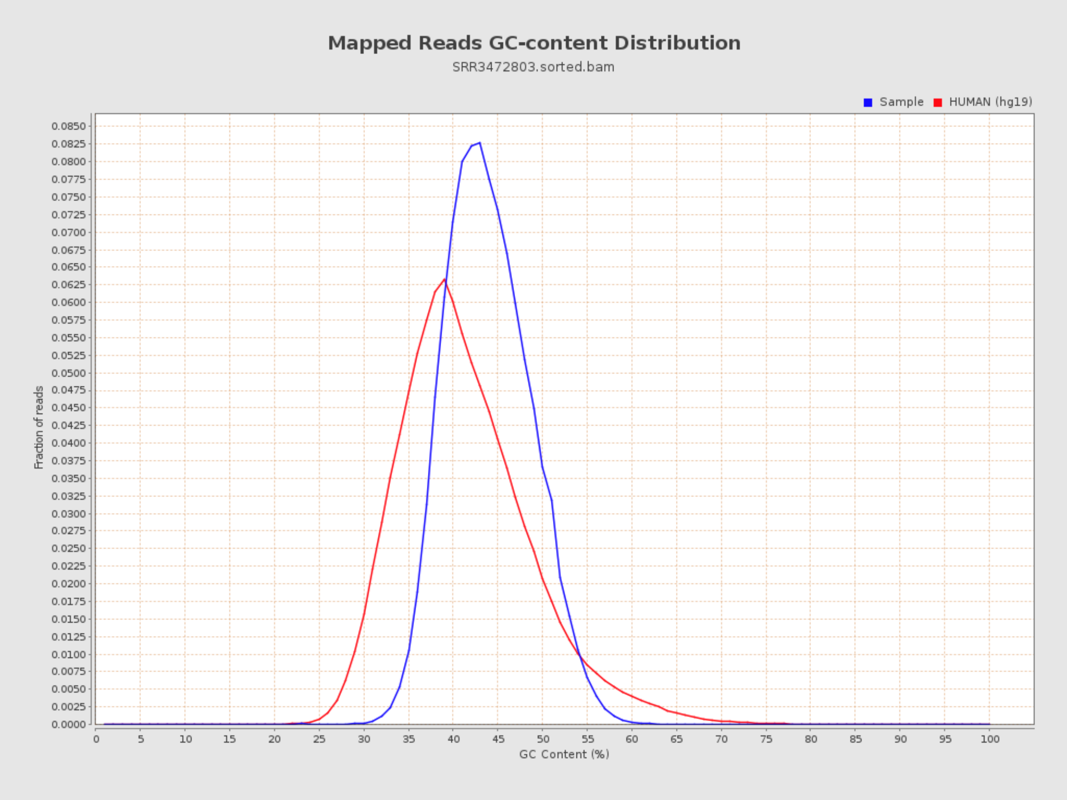
7. Results : Duplication Rate Histogram



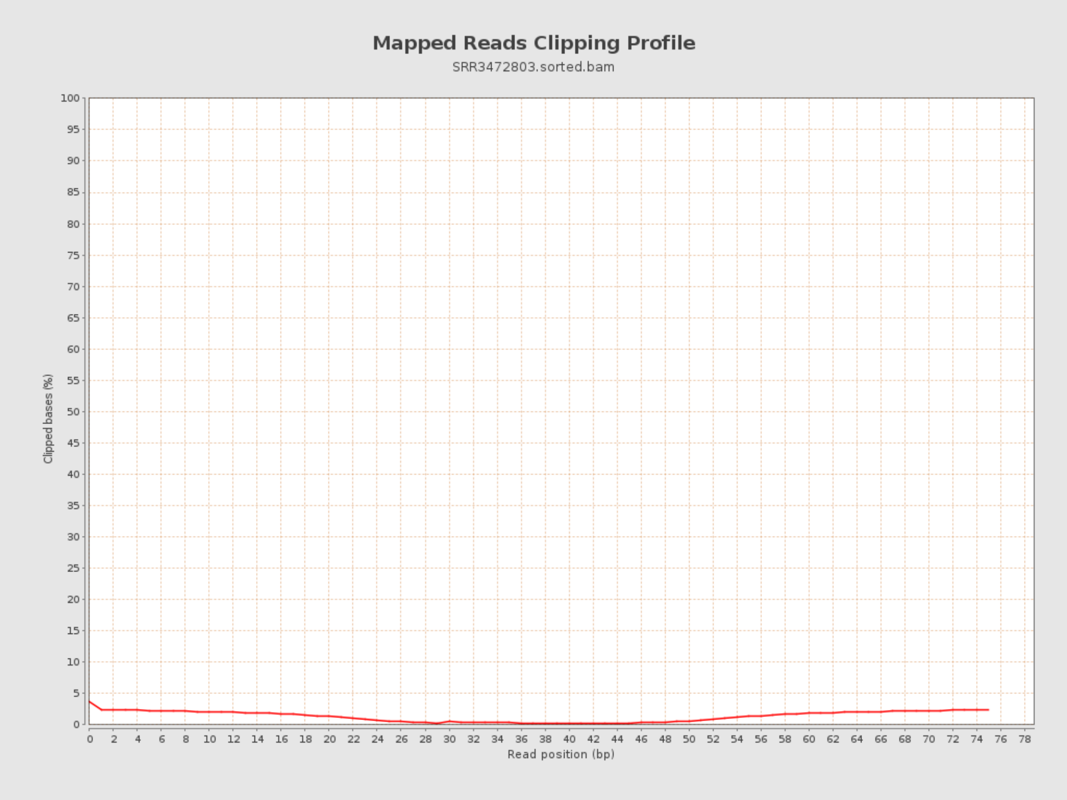
8. Results : Mapped Reads Nucleotide Content



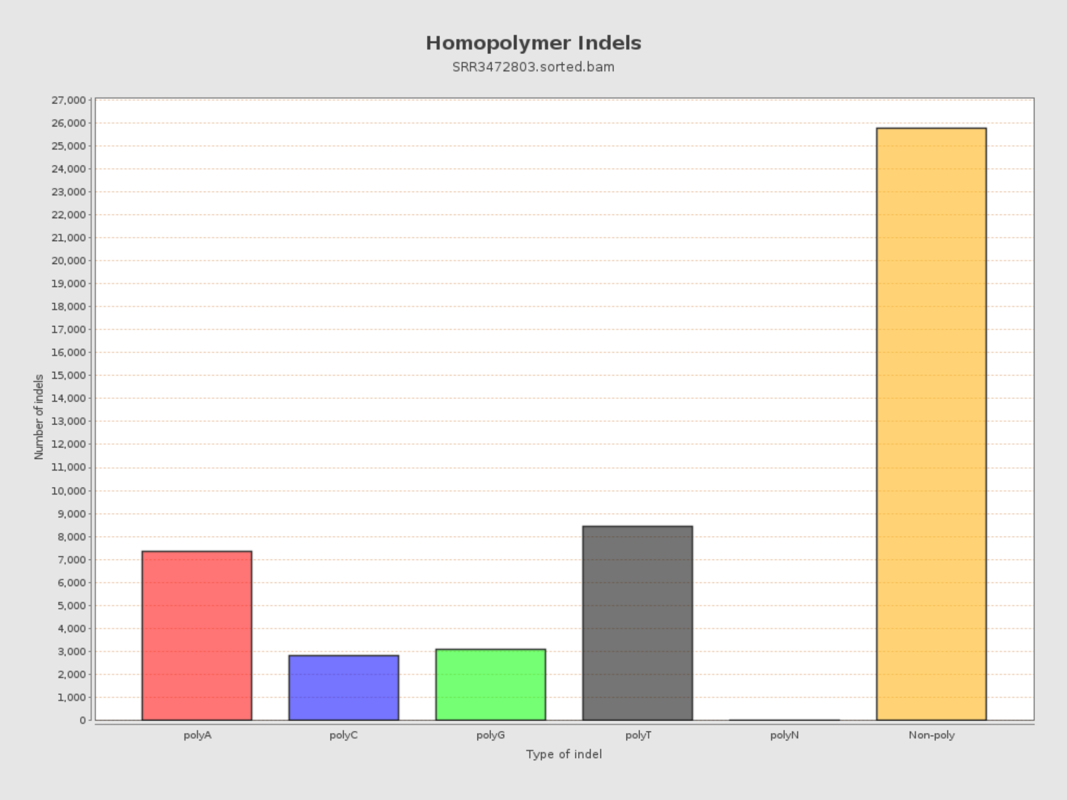
9. Results : Mapped Reads GC-content Distribution



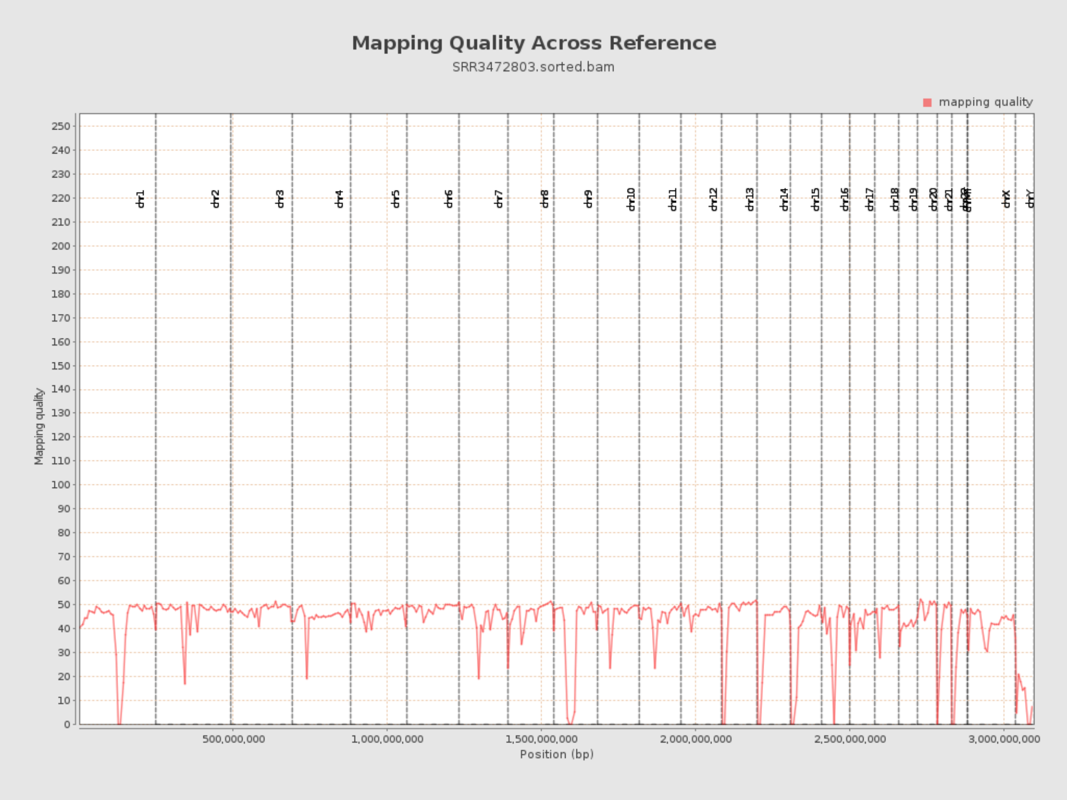
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram