Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/01 10:04:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472839.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_SRR3472839 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472839.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 01 10:04:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472839.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,981,744
Mapped reads	2,537,307 / 85.09%
Unmapped reads	444,437 / 14.91%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,485 / 0.65%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	79,603 / 2.67%
Duplication rate	2.45%
Clipped reads	1,302,672 / 43.69%

2.2. ACGT Content

Number/percentage of A's	44,388,961 / 26.93%
Number/percentage of C's	32,649,201 / 19.81%
Number/percentage of T's	49,031,951 / 29.75%
Number/percentage of G's	38,734,229 / 23.5%
Number/percentage of N's	3,847 / 0%
GC Percentage	43.31%

2.3. Coverage

Mean	0.0533

Standard Deviation	0.3469

2.4. Mapping Quality

Mean Mapping Quality	43.99

2.5. Mismatches and indels

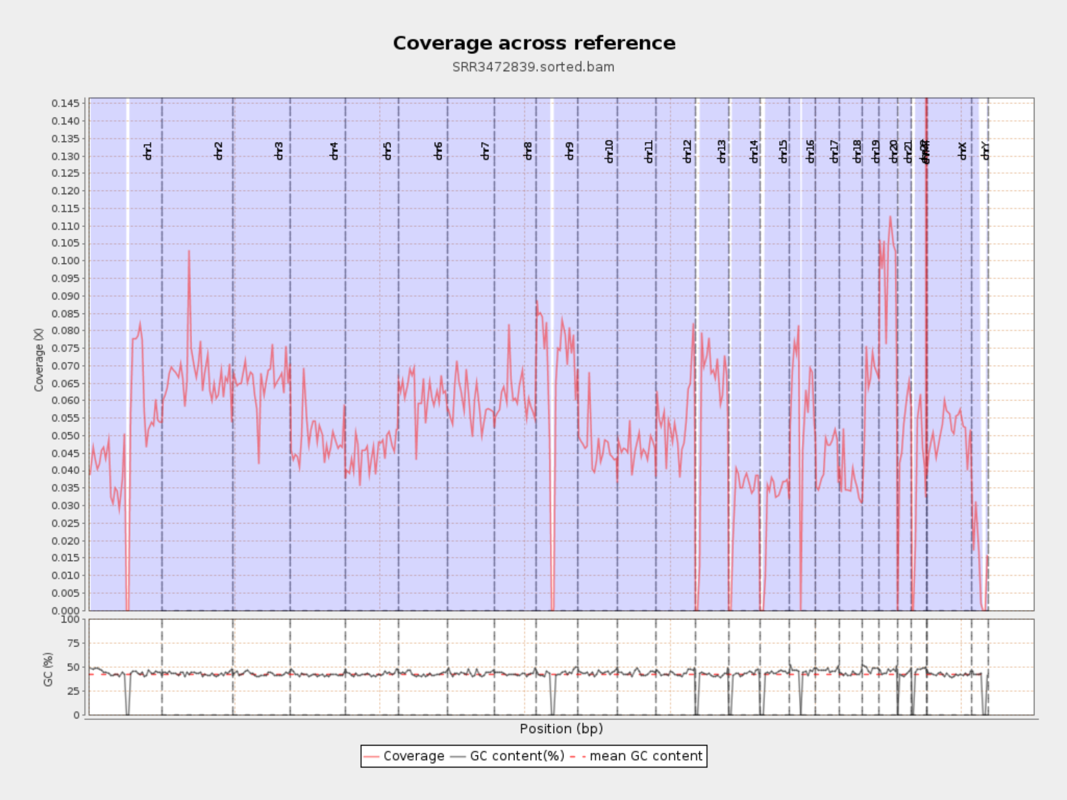
General error rate	0.86%
Mismatches	1,394,676
Insertions	12,495
Mapped reads with at least one insertion	0.49%
Deletions	34,982
Mapped reads with at least one deletion	1.36%
Homopolymer indels	45.29%

2.6. Chromosome stats

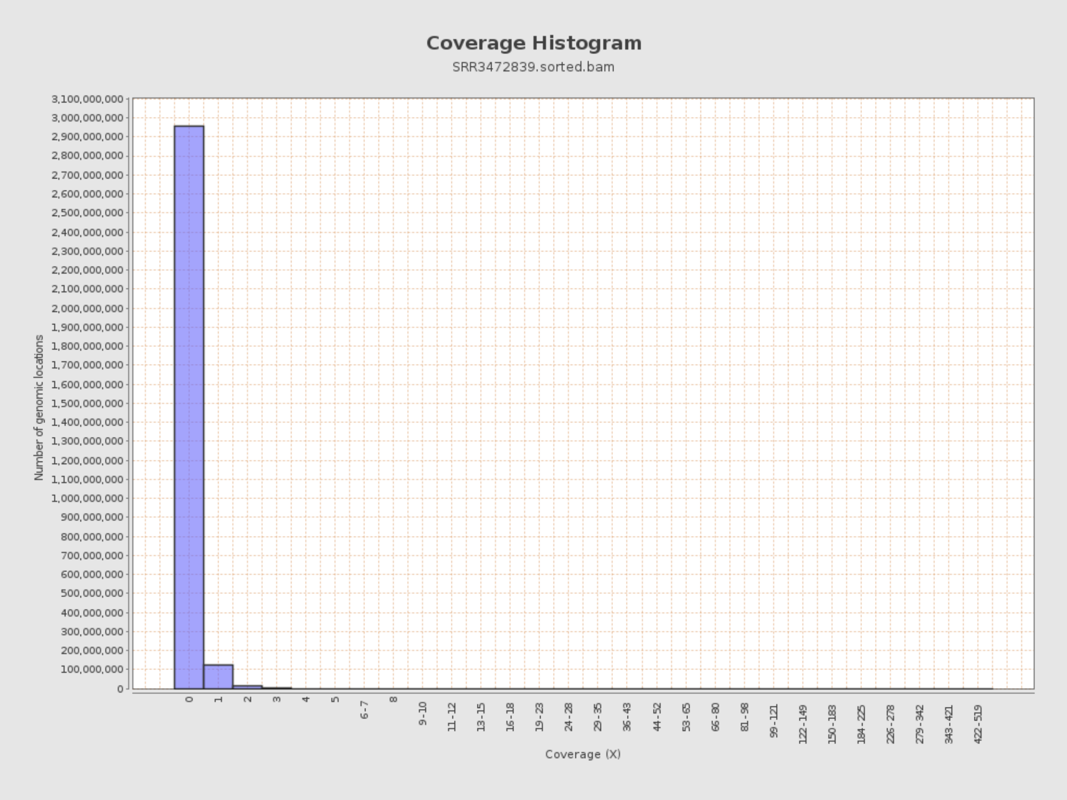
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11907432	0.0478	0.4364
chr2	243199373	16397381	0.0674	0.5026
chr3	198022430	12986346	0.0656	0.2892
chr4	191154276	9406811	0.0492	0.2752
chr5	180915260	8178987	0.0452	0.2395
chr6	171115067	10600933	0.062	0.3036
chr7	159138663	9402154	0.0591	0.3835

chr8	146364022	8962648	0.0612	0.372
chr9	141213431	9445406	0.0669	0.397
chr10	135534747	6323762	0.0467	0.335
chr11	135006516	6263295	0.0464	0.3286
chr12	133851895	7289027	0.0545	0.2697
chr13	115169878	6681141	0.058	0.281
chr14	107349540	3354730	0.0313	0.2306
chr15	102531392	2925065	0.0285	0.2055
chr16	90354753	5361343	0.0593	0.3027
chr17	81195210	3543539	0.0436	0.2491
chr18	78077248	2886901	0.037	0.6258
chr19	59128983	3817334	0.0646	0.3802
chr20	63025520	6281304	0.0997	0.3743
chr21	48129895	2359261	0.049	0.2835
chr22	51304566	1785805	0.0348	0.2224
chrMT	16571	21023	1.2687	1.4494
chrX	155270560	7918900	0.051	0.277
chrY	59373566	770307	0.013	0.1721

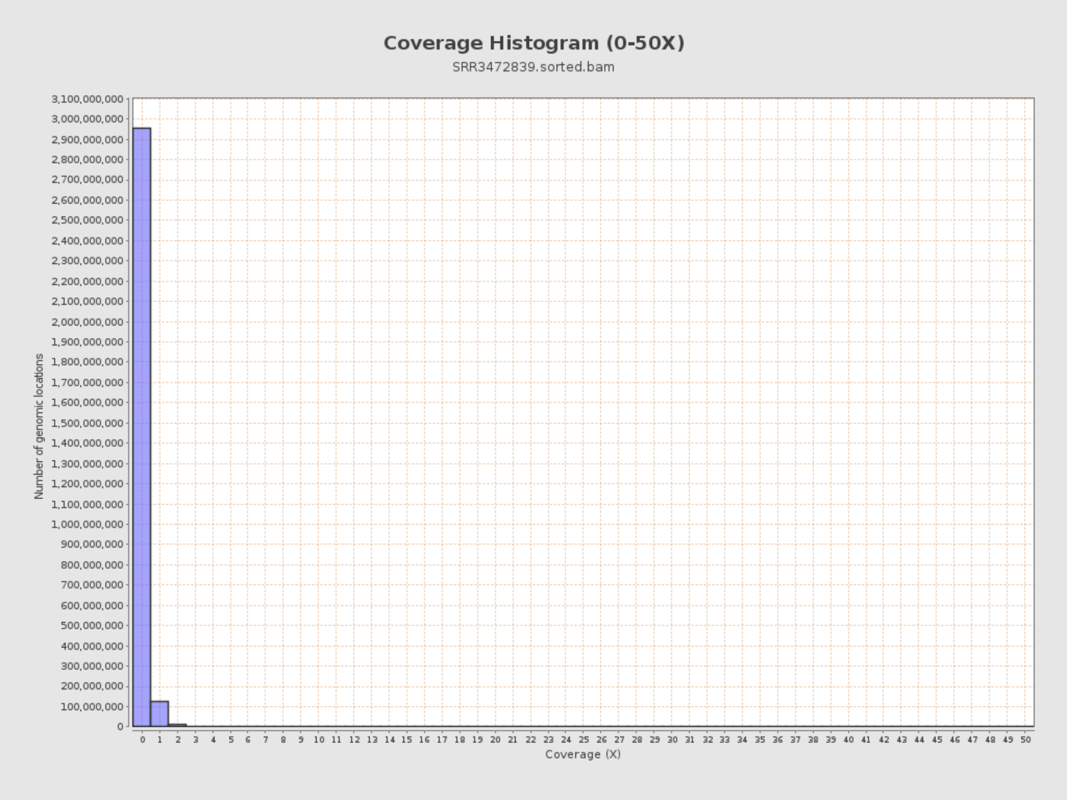
3. Results : Coverage across reference



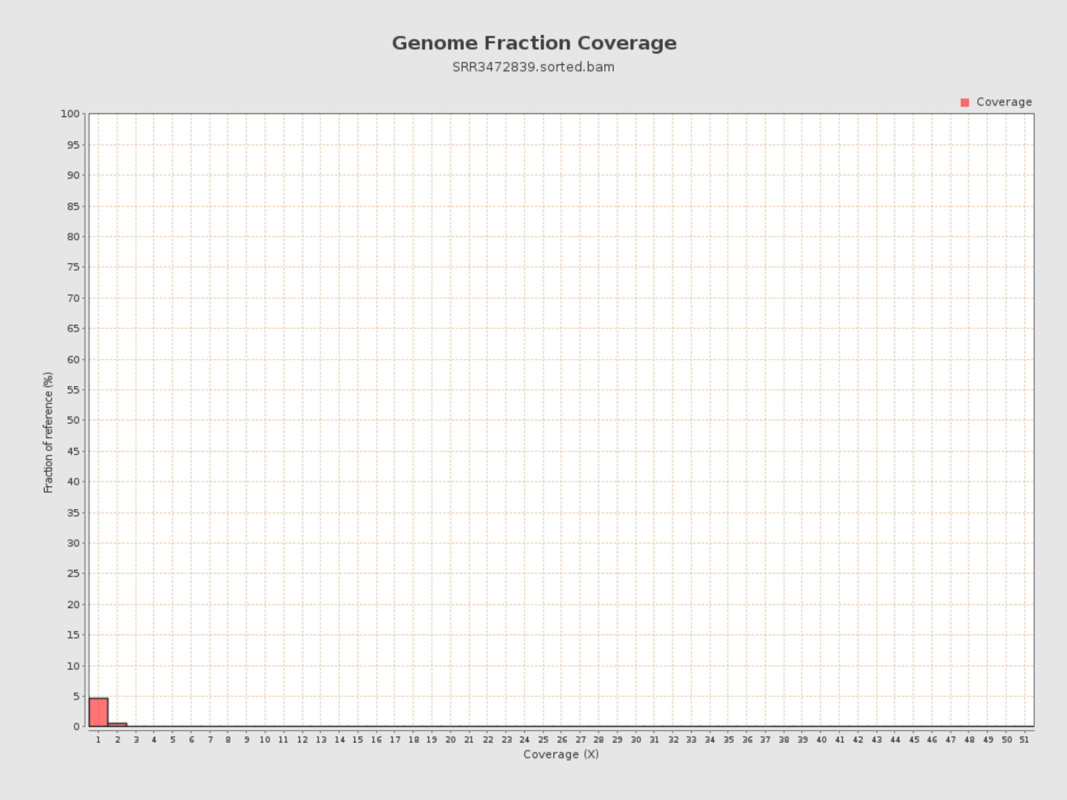
4. Results : Coverage Histogram



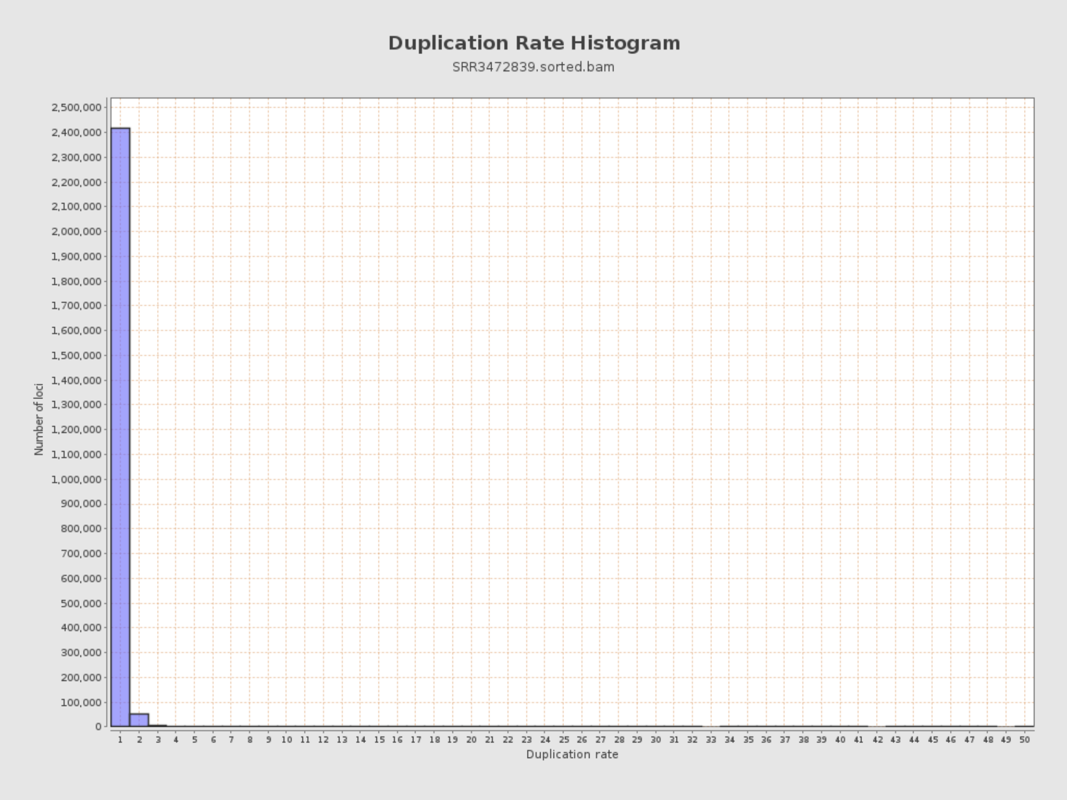
5. Results : Coverage Histogram (0-50X)



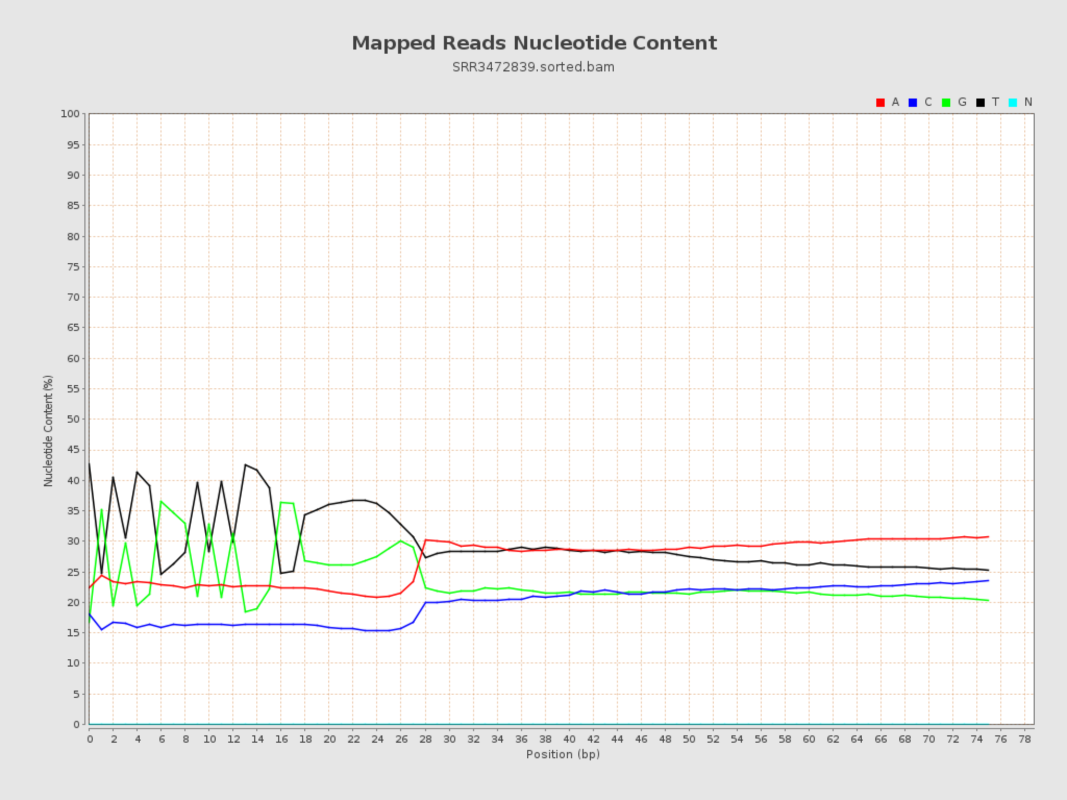
6. Results : Genome Fraction Coverage



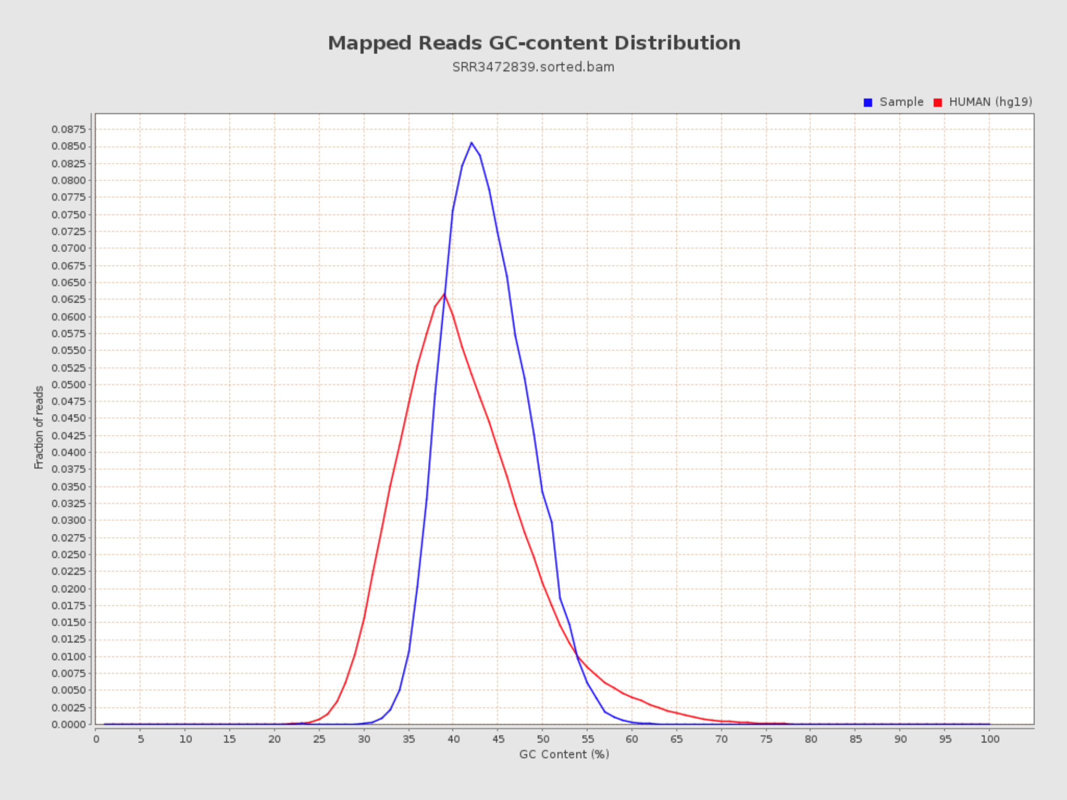
7. Results : Duplication Rate Histogram



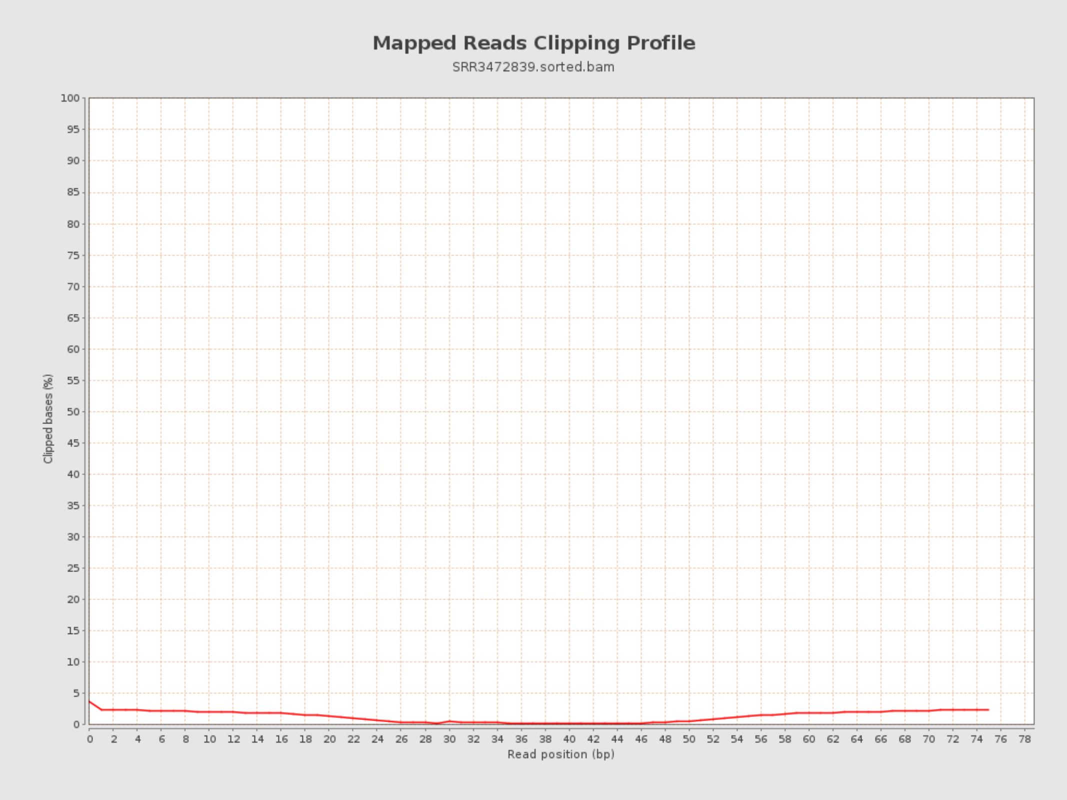
8. Results : Mapped Reads Nucleotide Content



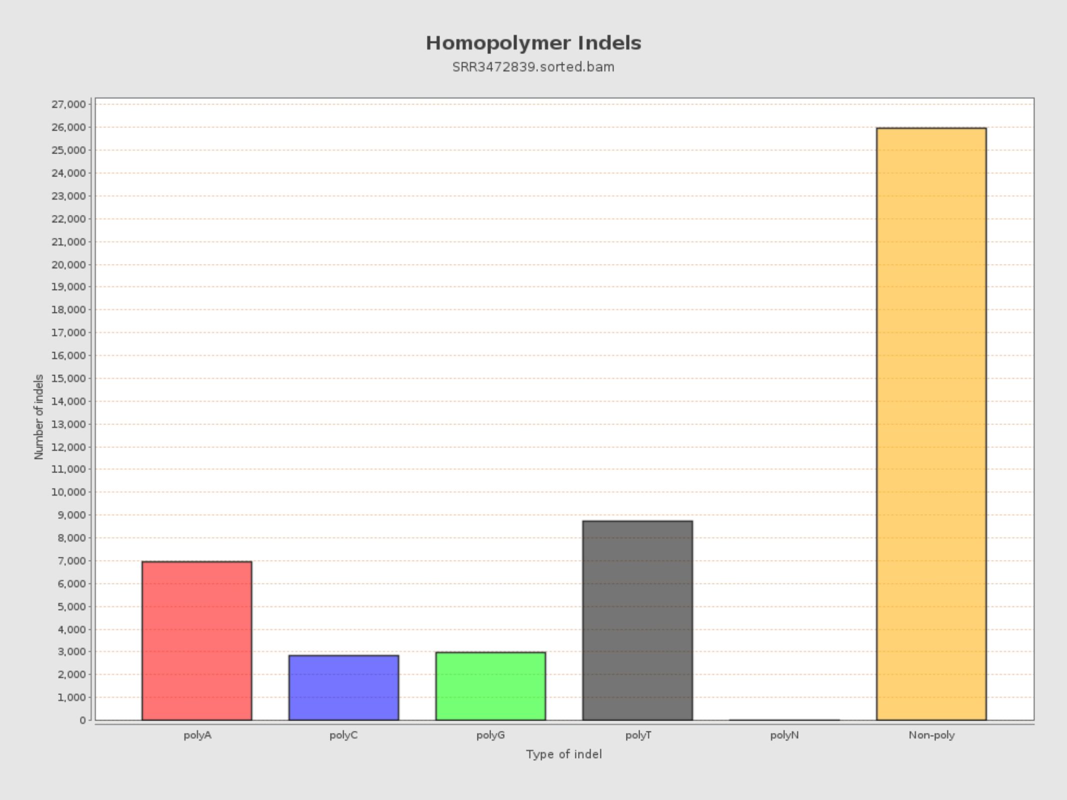
9. Results : Mapped Reads GC-content Distribution



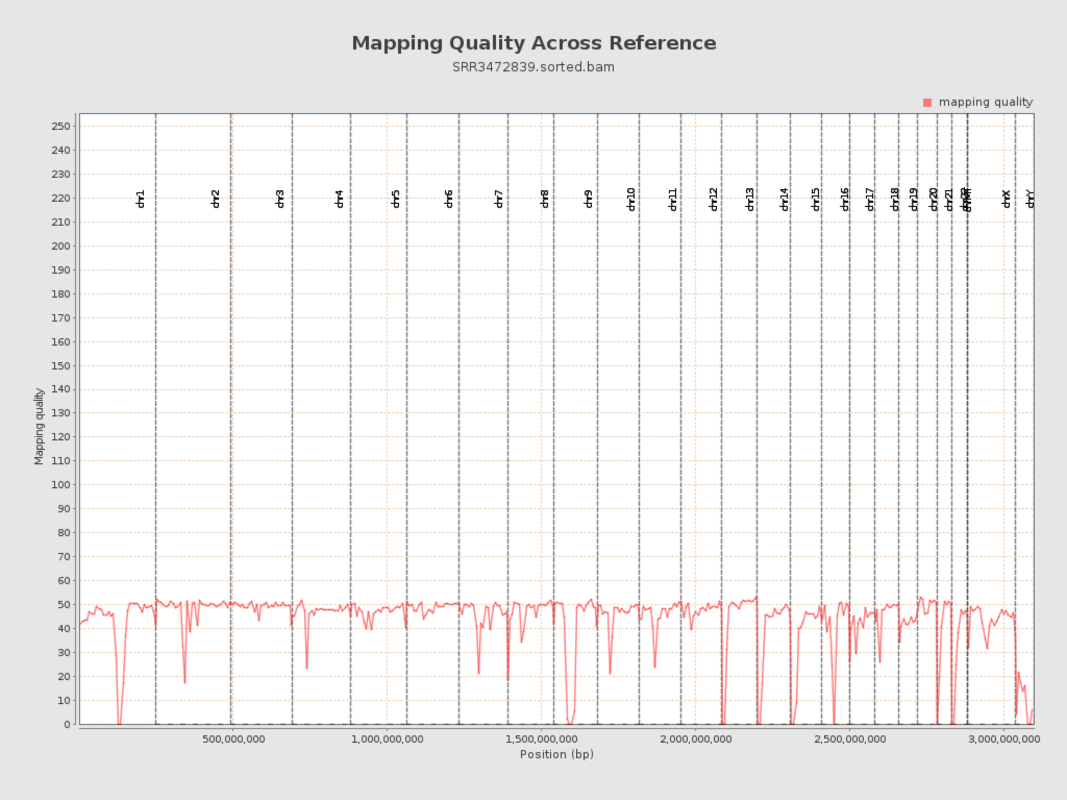
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram