Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/01 07:35:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472811.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_SRR3472811 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472811.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 01 07:35:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472811.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,622,902
Mapped reads	2,188,324 / 83.43%
Unmapped reads	434,578 / 16.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,716 / 0.79%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	79,424 / 3.03%
Duplication rate	2.68%
Clipped reads	1,228,132 / 46.82%

2.2. ACGT Content

Number/percentage of A's	37,458,703 / 26.85%
Number/percentage of C's	28,037,447 / 20.1%
Number/percentage of T's	41,110,560 / 29.47%
Number/percentage of G's	32,888,519 / 23.58%
Number/percentage of N's	2,579 / 0%
GC Percentage	43.68%

2.3. Coverage

Mean	0.0451

Standard Deviation	0.3392

2.4. Mapping Quality

Mean Mapping Quality	43.53

2.5. Mismatches and indels

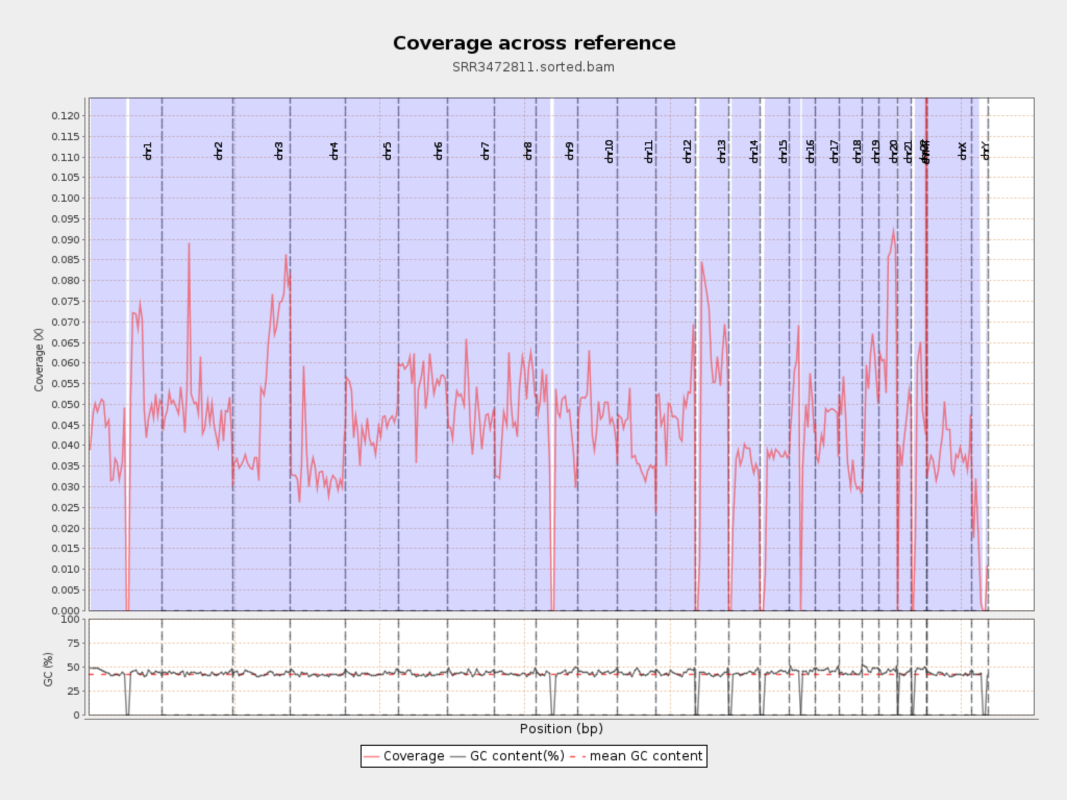
General error rate	0.88%
Mismatches	1,210,670
Insertions	10,963
Mapped reads with at least one insertion	0.5%
Deletions	32,142
Mapped reads with at least one deletion	1.45%
Homopolymer indels	45.14%

2.6. Chromosome stats

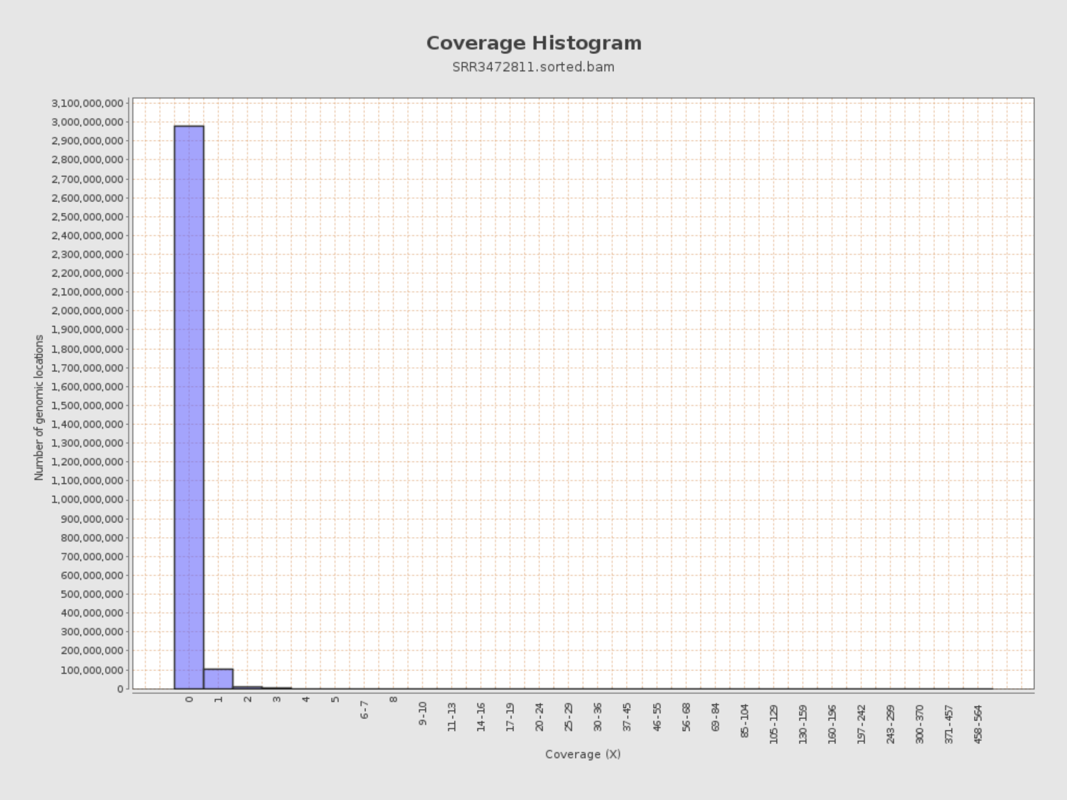
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11497906	0.0461	0.3999
chr2	243199373	12073271	0.0496	0.4832
chr3	198022430	10506005	0.0531	0.2642
chr4	191154276	6430595	0.0336	0.2394
chr5	180915260	8167508	0.0451	0.2447
chr6	171115067	9599538	0.0561	0.2962
chr7	159138663	7639554	0.048	0.4295

chr8	146364022	7188538	0.0491	0.3328
chr9	141213431	5969262	0.0423	0.3756
chr10	135534747	6537168	0.0482	0.3285
chr11	135006516	5280060	0.0391	0.354
chr12	133851895	6571396	0.0491	0.2628
chr13	115169878	6399251	0.0556	0.2773
chr14	107349540	3323724	0.031	0.2359
chr15	102531392	3112234	0.0304	0.2209
chr16	90354753	4252150	0.0471	0.281
chr17	81195210	3606927	0.0444	0.2639
chr18	78077248	2996182	0.0384	0.6833
chr19	59128983	3251432	0.055	0.3398
chr20	63025520	4632404	0.0735	0.3343
chr21	48129895	1922002	0.0399	0.2692
chr22	51304566	1911965	0.0373	0.234
chrMT	16571	73141	4.4138	3.799
chrX	155270560	5902776	0.038	0.2647
chrY	59373566	711059	0.012	0.1675

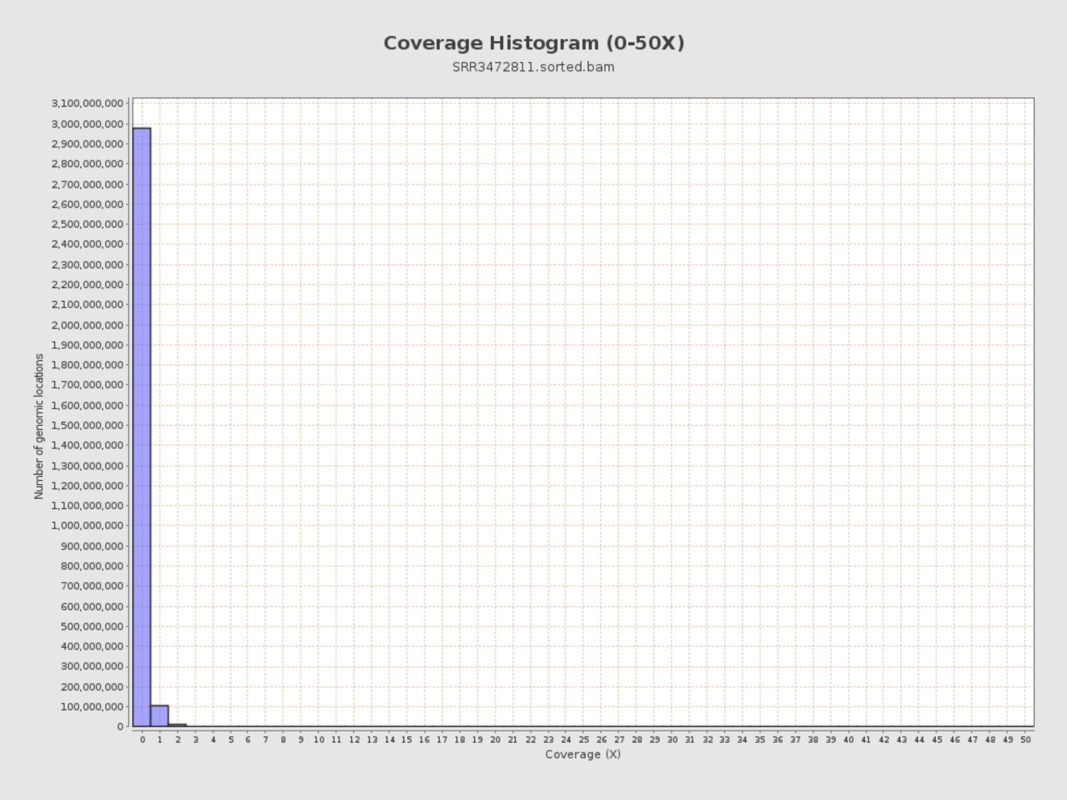
3. Results : Coverage across reference



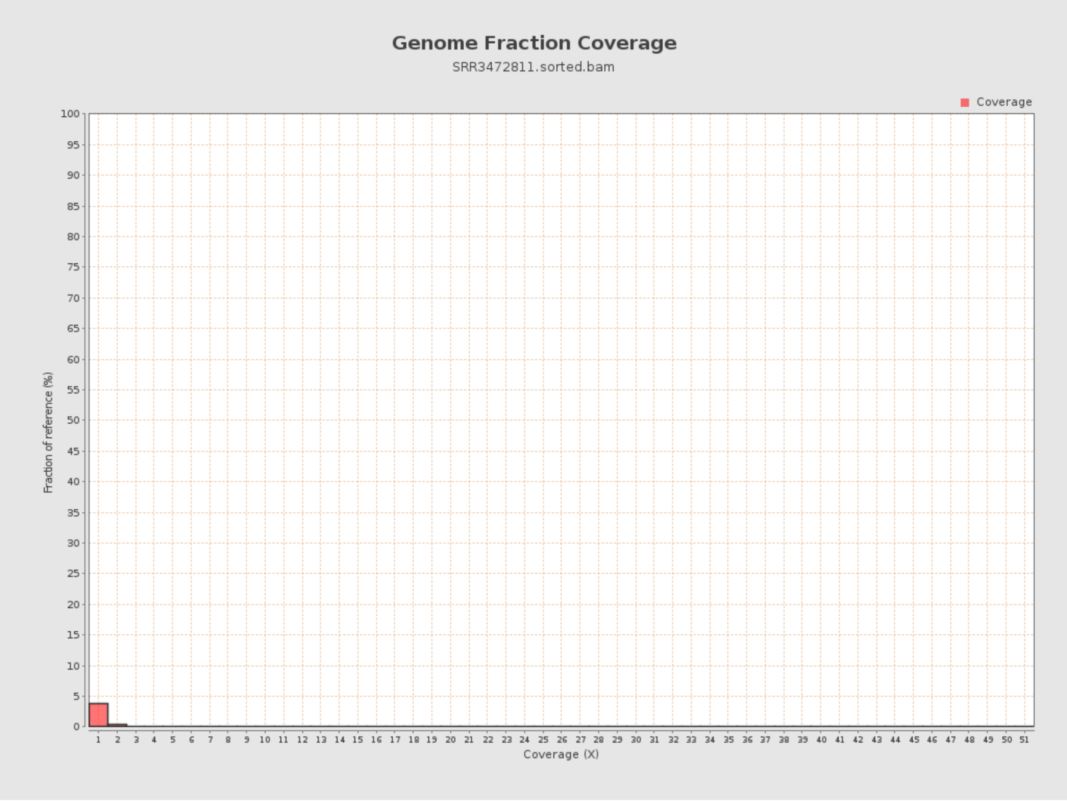
4. Results : Coverage Histogram



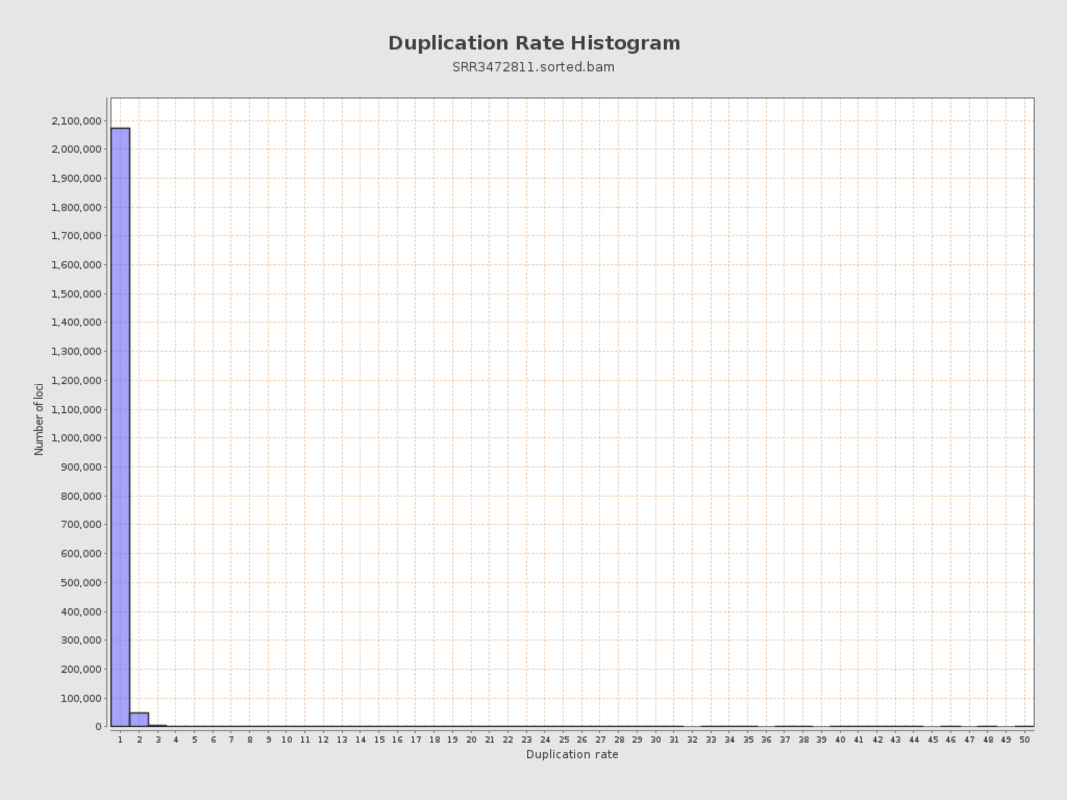
5. Results : Coverage Histogram (0-50X)



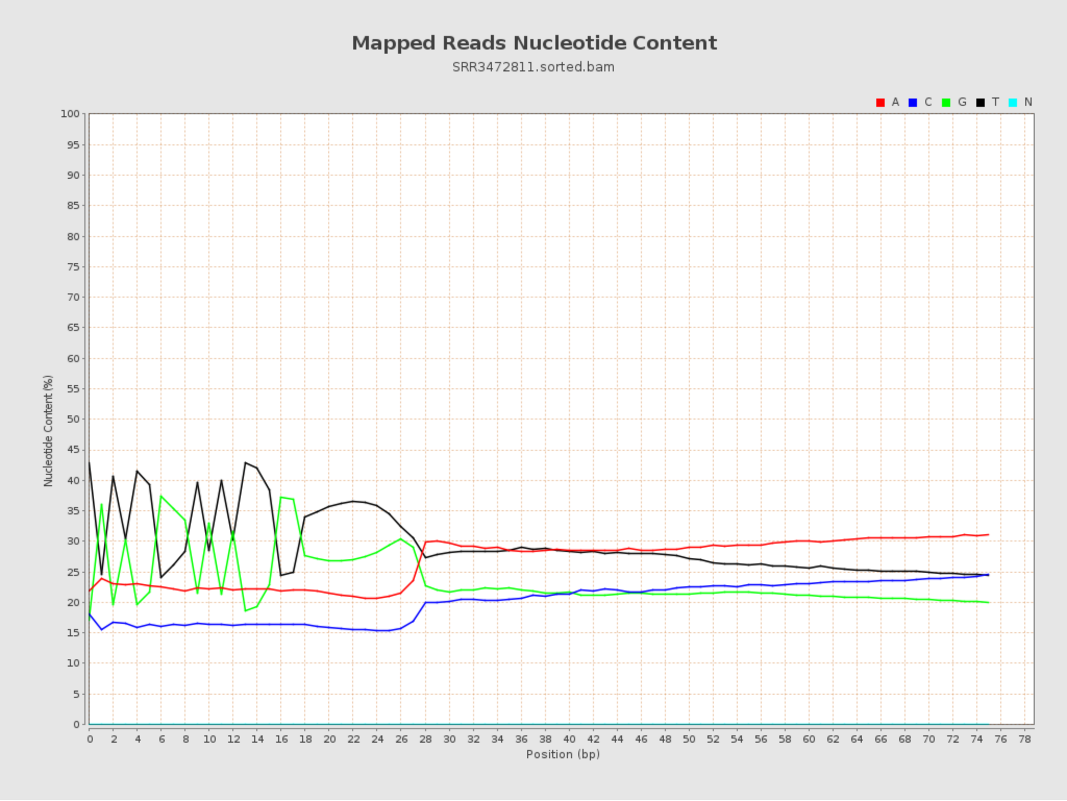
6. Results : Genome Fraction Coverage



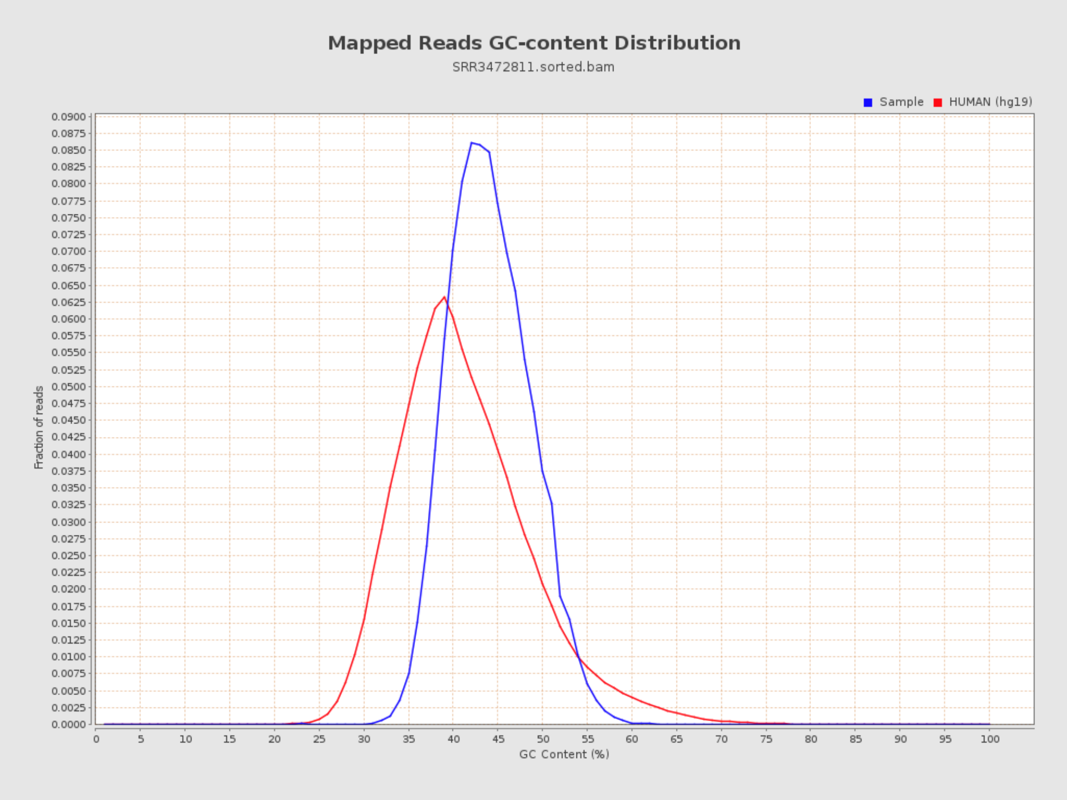
7. Results : Duplication Rate Histogram



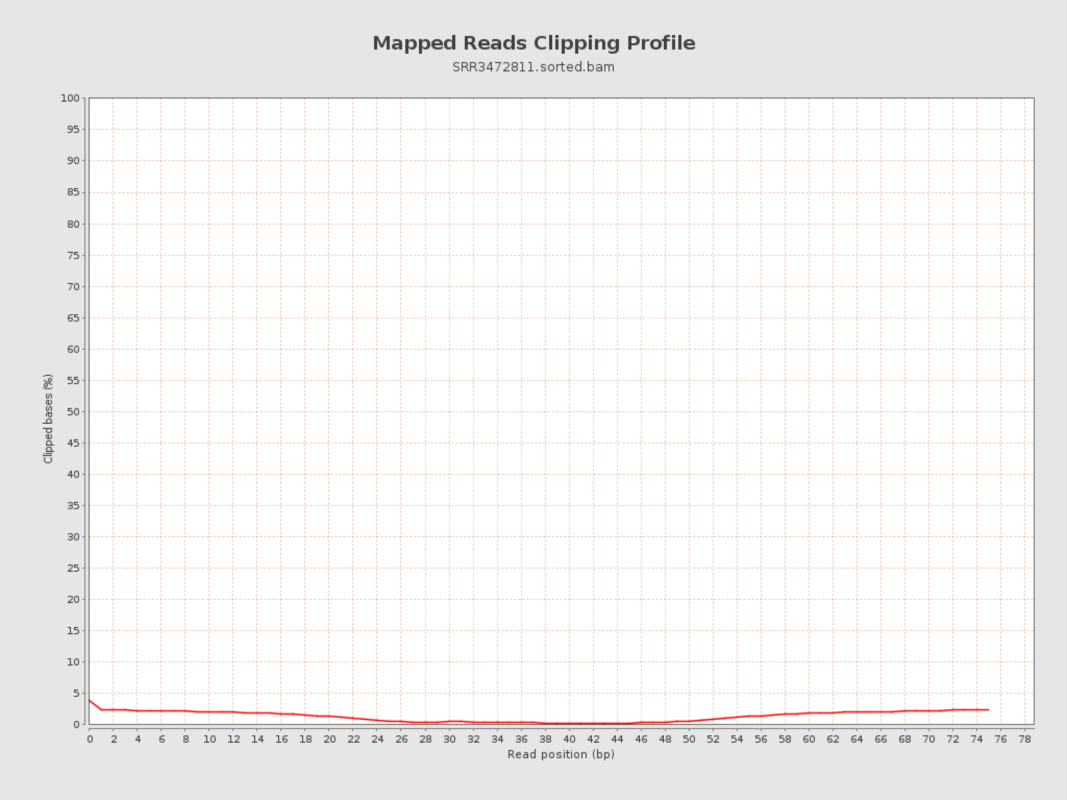
8. Results : Mapped Reads Nucleotide Content



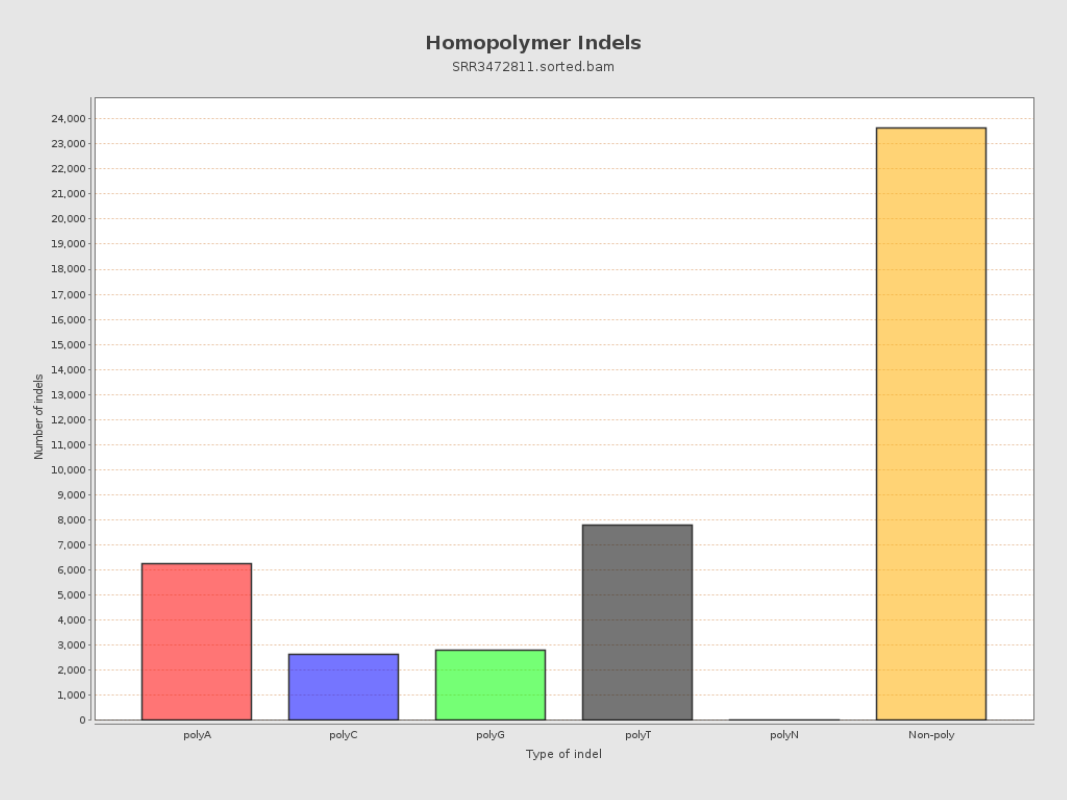
9. Results : Mapped Reads GC-content Distribution



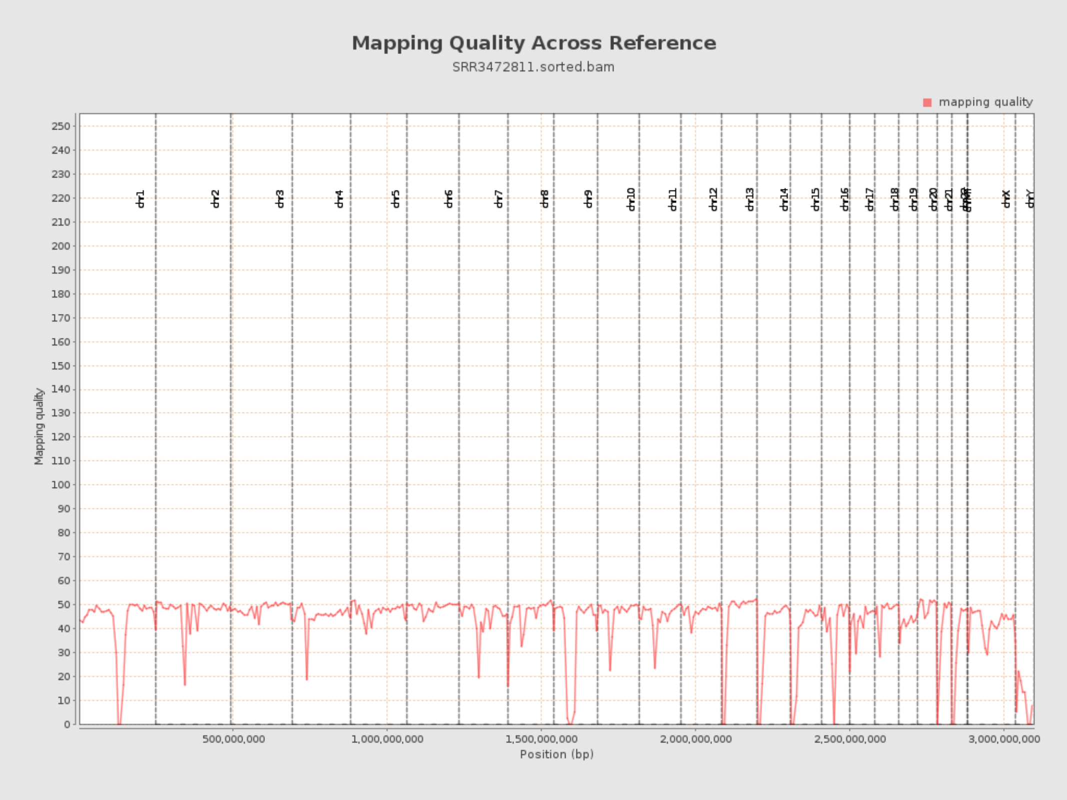
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram