Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/01 08:06:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472817.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_SRR3472817 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472817.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 01 08:06:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472817.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,696,196
Mapped reads	2,168,976 / 80.45%
Unmapped reads	527,220 / 19.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,575 / 0.39%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	124,063 / 4.6%
Duplication rate	4.6%
Clipped reads	1,218,771 / 45.2%

2.2. ACGT Content

Number/percentage of A's	36,383,107 / 26.3%
Number/percentage of C's	26,711,257 / 19.31%
Number/percentage of T's	42,443,698 / 30.68%
Number/percentage of G's	32,790,729 / 23.7%
Number/percentage of N's	2,573 / 0%
GC Percentage	43.01%

2.3. Coverage

Mean	0.0447

Standard Deviation	0.3488

2.4. Mapping Quality

Mean Mapping Quality	44.47

2.5. Mismatches and indels

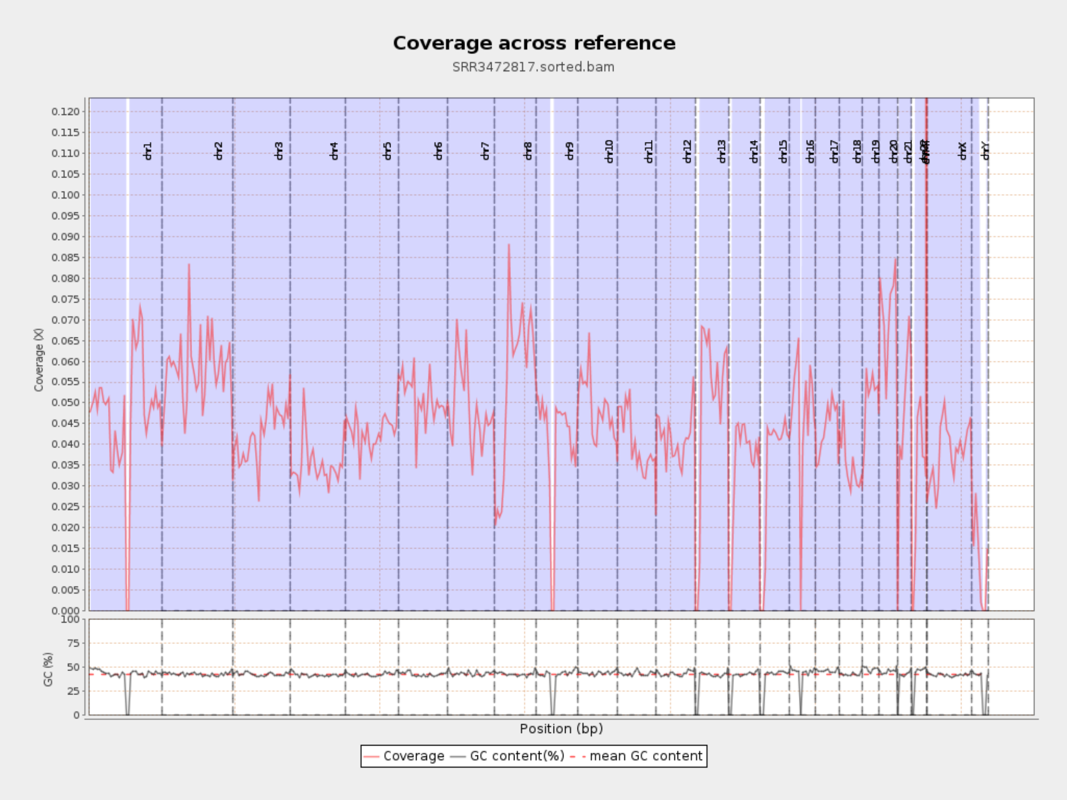
General error rate	0.88%
Mismatches	1,201,877
Insertions	10,060
Mapped reads with at least one insertion	0.46%
Deletions	33,702
Mapped reads with at least one deletion	1.54%
Homopolymer indels	46.75%

2.6. Chromosome stats

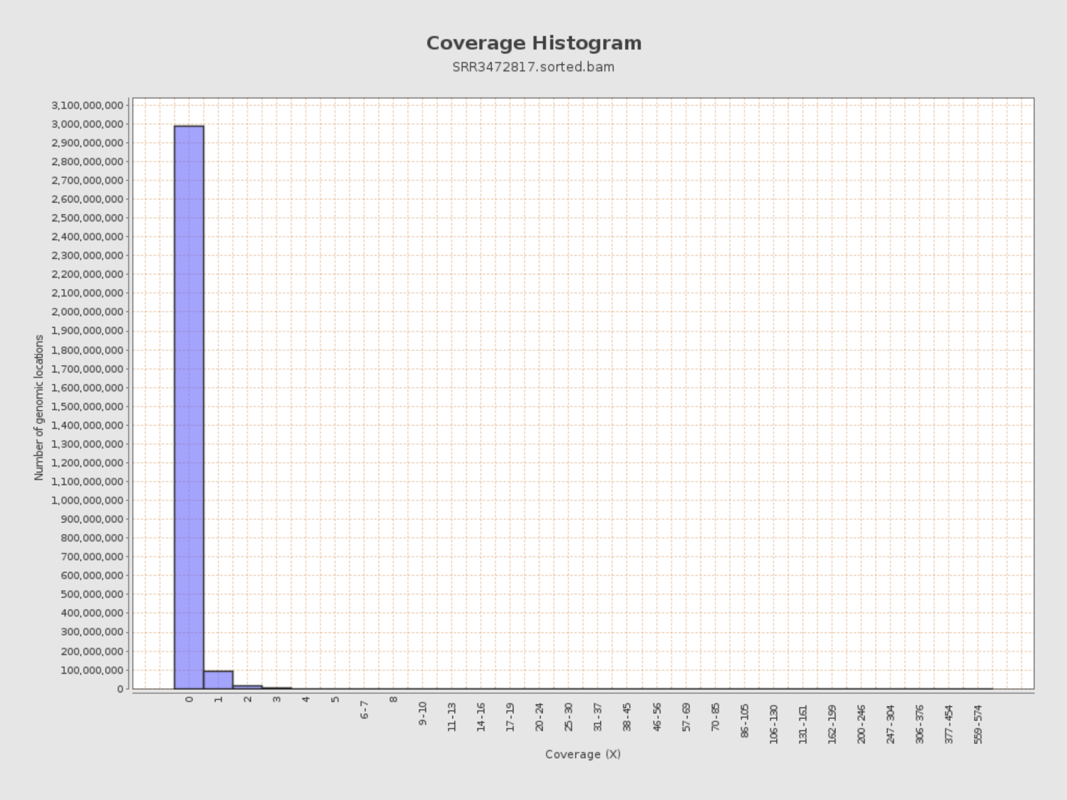
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11729291	0.0471	0.436
chr2	243199373	14194241	0.0584	0.48
chr3	198022430	8446517	0.0427	0.2514
chr4	191154276	6701213	0.0351	0.2454
chr5	180915260	7760944	0.0429	0.2534
chr6	171115067	8747182	0.0511	0.3125
chr7	159138663	7779694	0.0489	0.4688

chr8	146364022	8122261	0.0555	0.3739
chr9	141213431	5603543	0.0397	0.3588
chr10	135534747	6632219	0.0489	0.3432
chr11	135006516	5456040	0.0404	0.3782
chr12	133851895	5569757	0.0416	0.254
chr13	115169878	5706393	0.0495	0.279
chr14	107349540	3663296	0.0341	0.2465
chr15	102531392	3524822	0.0344	0.2386
chr16	90354753	4315124	0.0478	0.2854
chr17	81195210	3561924	0.0439	0.2814
chr18	78077248	2762723	0.0354	0.6119
chr19	59128983	3025972	0.0512	0.368
chr20	63025520	4513816	0.0716	0.3416
chr21	48129895	2273959	0.0472	0.2936
chr22	51304566	1509664	0.0294	0.2182
chrMT	16571	223780	13.5043	8.8699
chrX	155270560	5901608	0.038	0.2661
chrY	59373566	665013	0.0112	0.1592

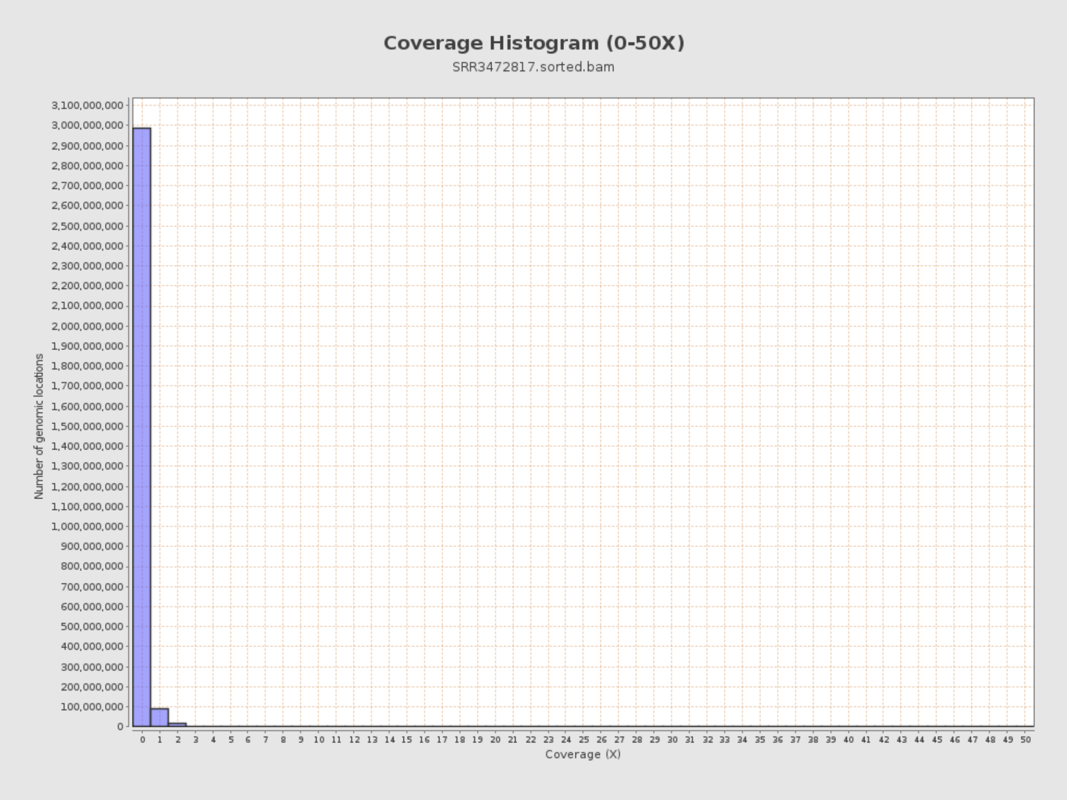
3. Results : Coverage across reference



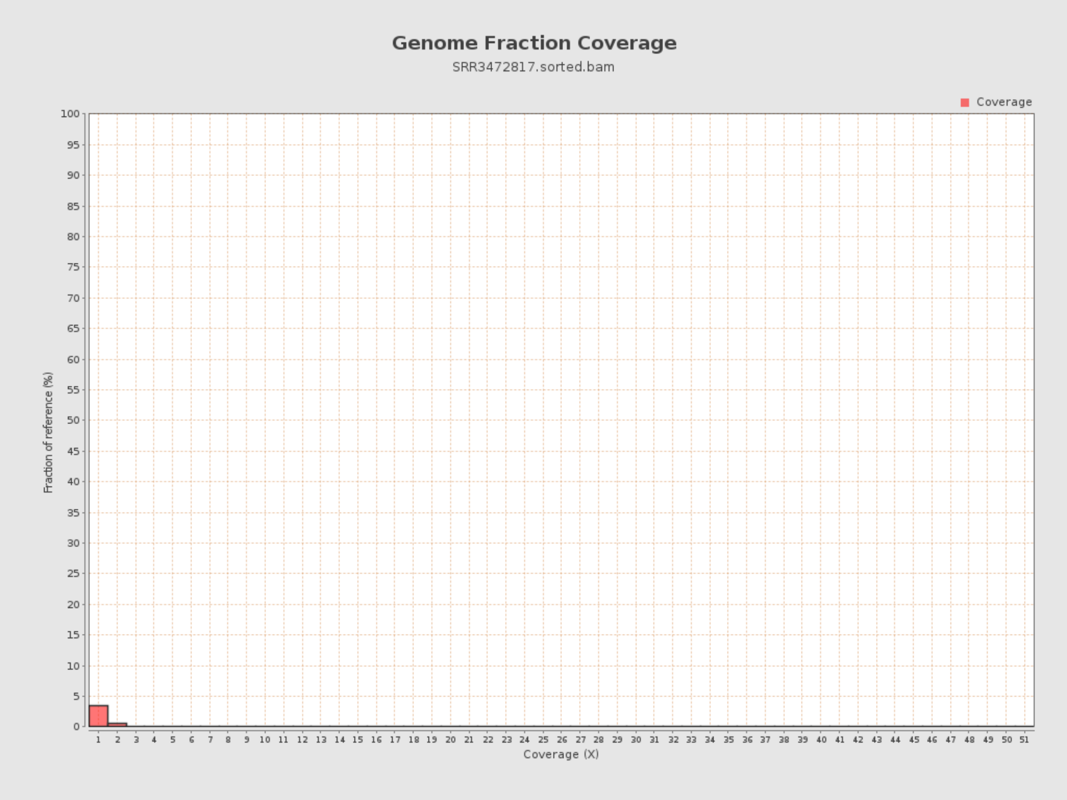
4. Results : Coverage Histogram



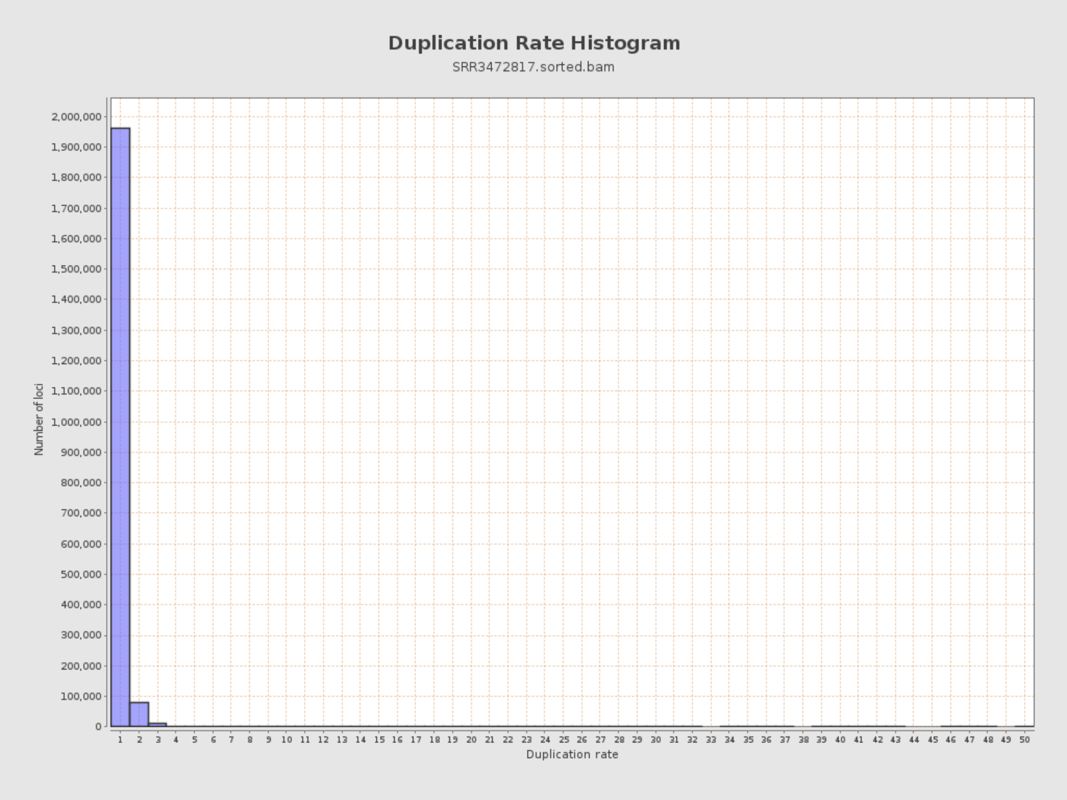
5. Results : Coverage Histogram (0-50X)



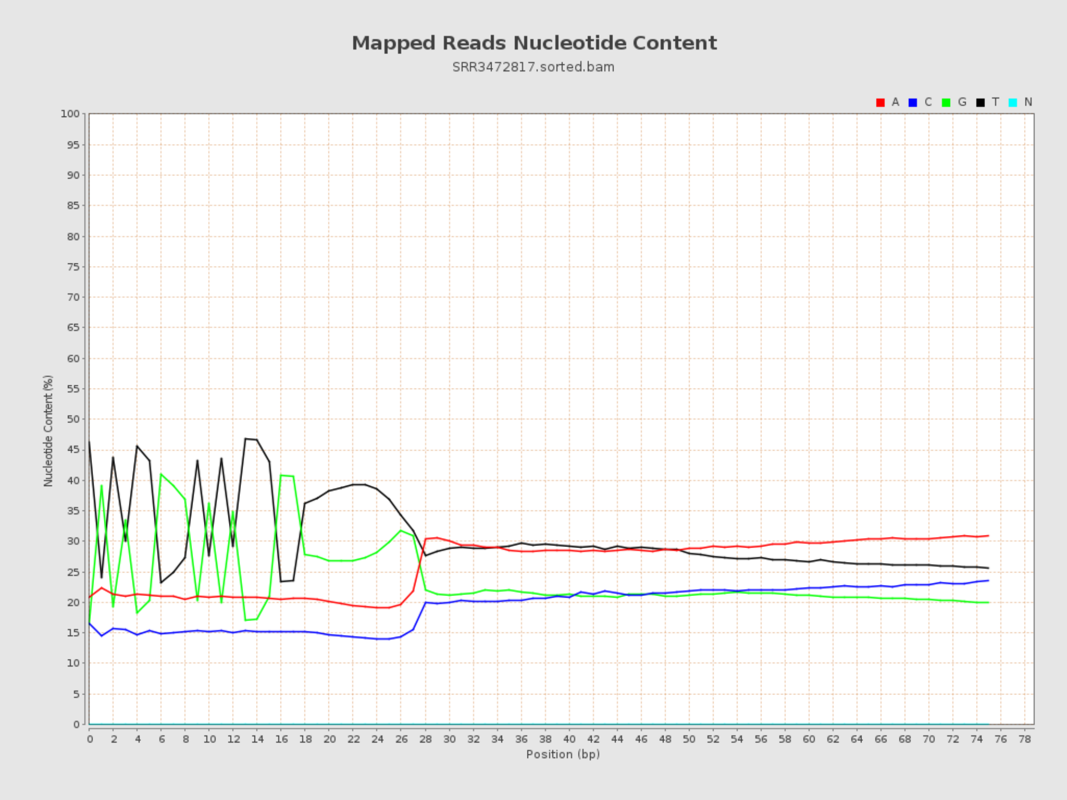
6. Results : Genome Fraction Coverage



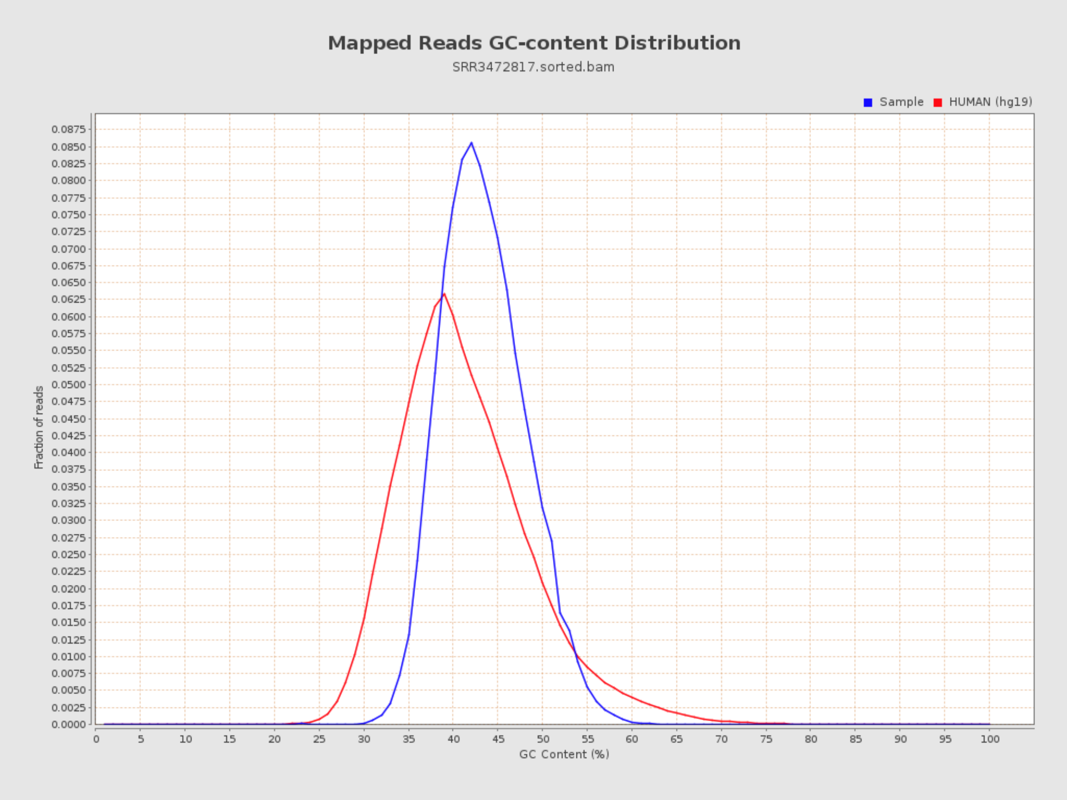
7. Results : Duplication Rate Histogram



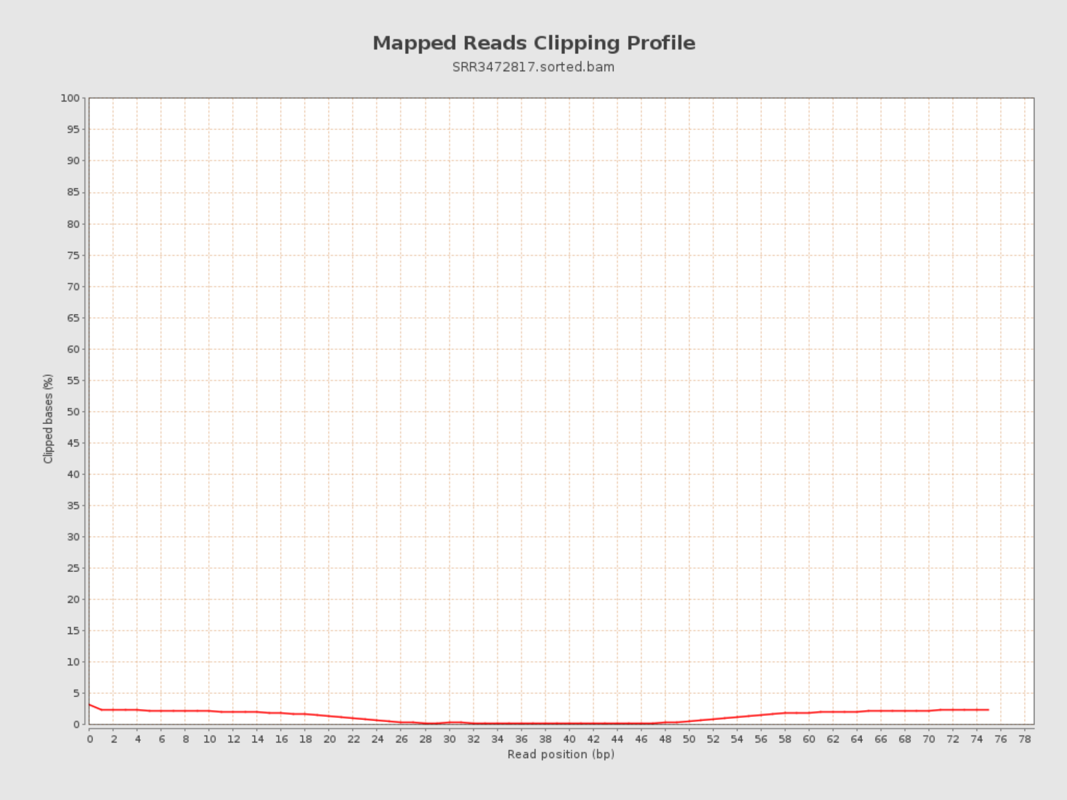
8. Results : Mapped Reads Nucleotide Content



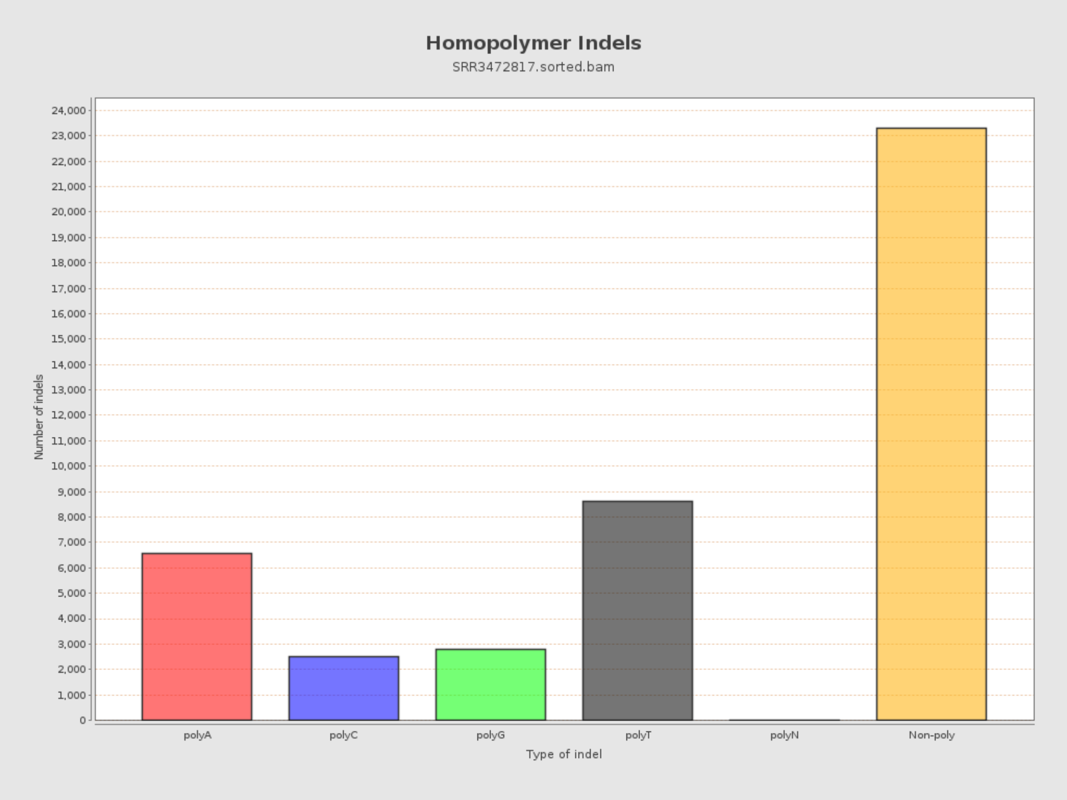
9. Results : Mapped Reads GC-content Distribution



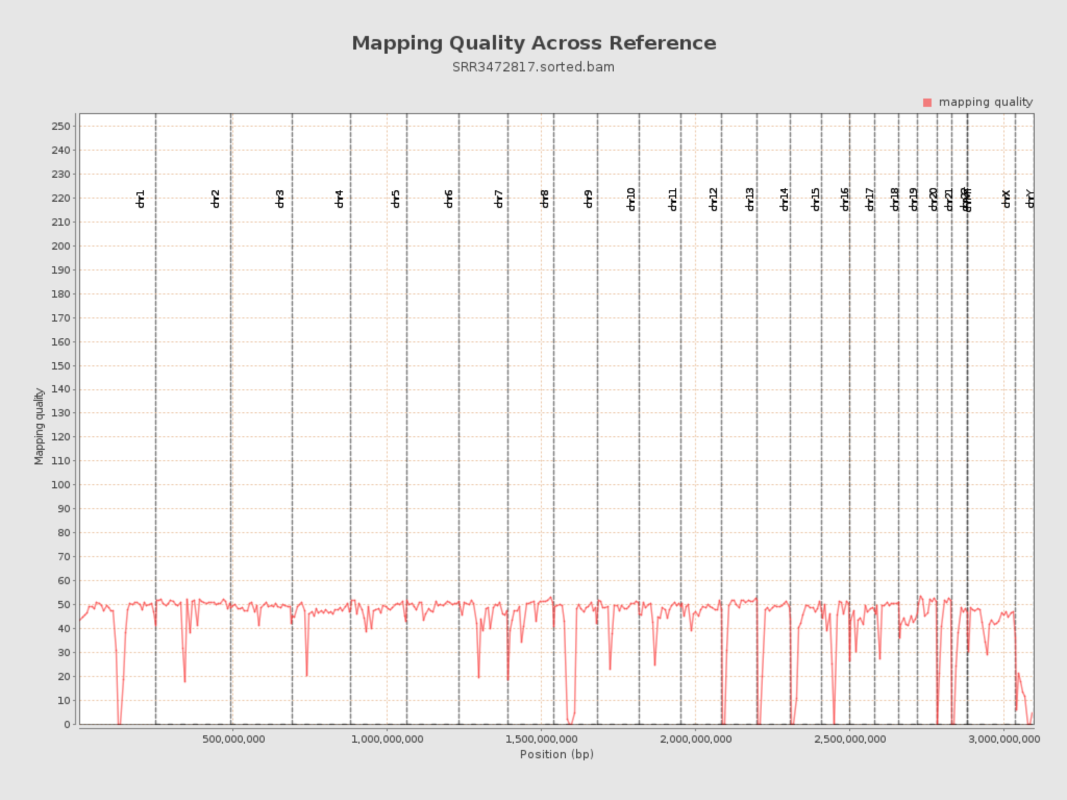
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram