Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/01 08:50:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472827.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_SRR3472827 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472827.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 01 08:50:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472827.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,000,000
Mapped reads	3,439,317 / 85.98%
Unmapped reads	560,683 / 14.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,239 / 0.61%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	112,208 / 2.81%
Duplication rate	2.32%
Clipped reads	1,709,354 / 42.73%

2.2. ACGT Content

Number/percentage of A's	60,800,145 / 27.07%
Number/percentage of C's	44,147,814 / 19.66%
Number/percentage of T's	67,497,249 / 30.05%
Number/percentage of G's	52,154,541 / 23.22%
Number/percentage of N's	4,080 / 0%
GC Percentage	42.88%

2.3. Coverage

Mean	0.0726

Standard Deviation	0.4829

2.4. Mapping Quality

Mean Mapping Quality	44.8

2.5. Mismatches and indels

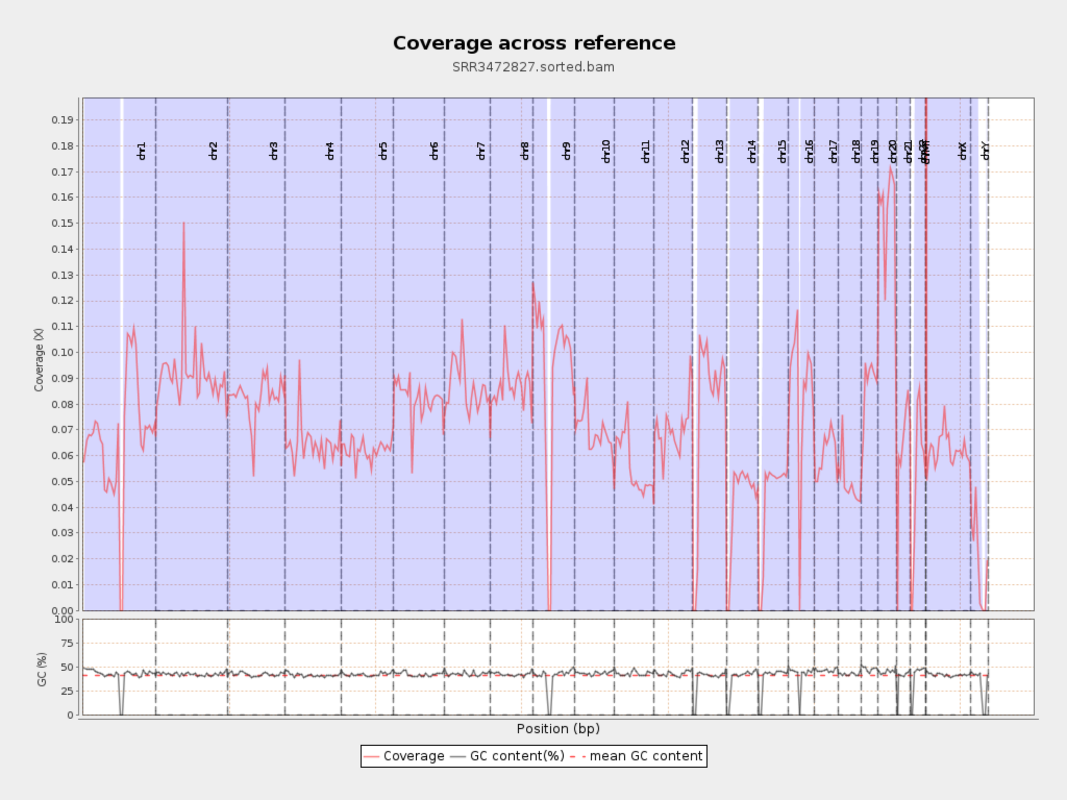
General error rate	0.84%
Mismatches	1,844,543
Insertions	17,500
Mapped reads with at least one insertion	0.5%
Deletions	51,797
Mapped reads with at least one deletion	1.49%
Homopolymer indels	45.3%

2.6. Chromosome stats

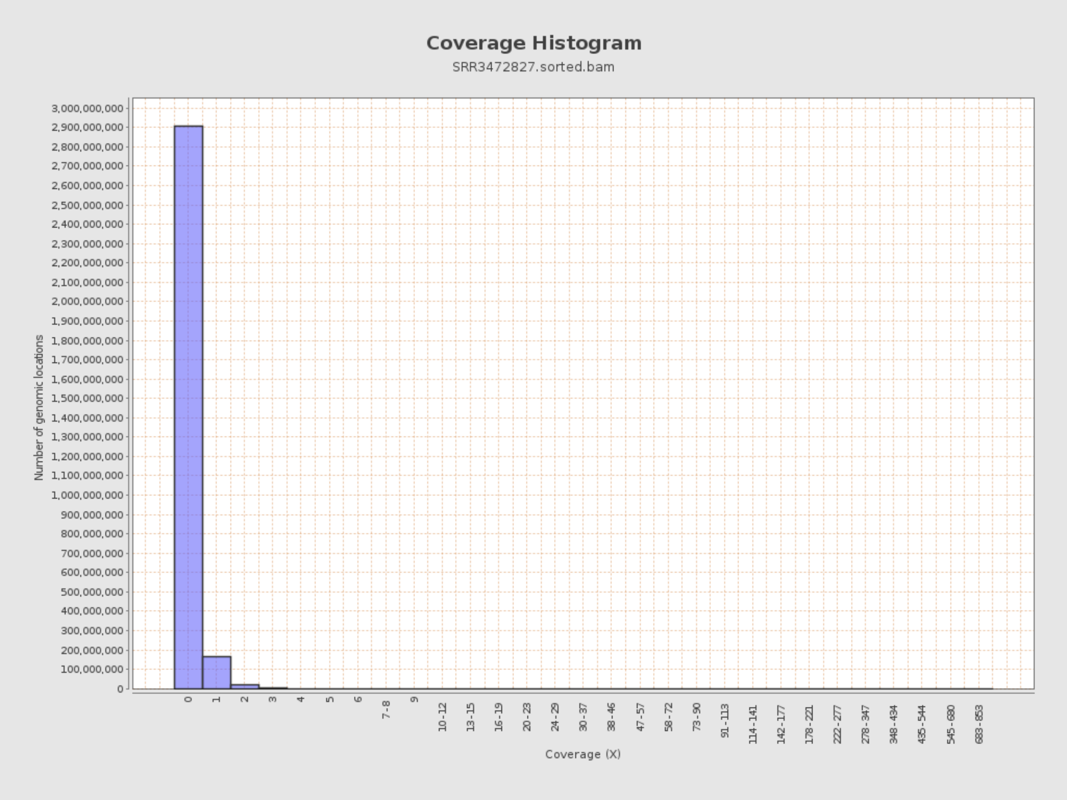
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16589743	0.0666	0.6074
chr2	243199373	22317179	0.0918	0.7371
chr3	198022430	16277100	0.0822	0.323
chr4	191154276	12403205	0.0649	0.3318
chr5	180915260	11291668	0.0624	0.2856
chr6	171115067	14004751	0.0818	0.3691
chr7	159138663	13835251	0.0869	0.6555

chr8	146364022	12700290	0.0868	0.4914
chr9	141213431	13041124	0.0924	0.5865
chr10	135534747	9424600	0.0695	0.4243
chr11	135006516	7518724	0.0557	0.4633
chr12	133851895	9456778	0.0707	0.3158
chr13	115169878	9019417	0.0783	0.3321
chr14	107349540	4584066	0.0427	0.3096
chr15	102531392	4298023	0.0419	0.2619
chr16	90354753	7512396	0.0831	0.3802
chr17	81195210	4956563	0.061	0.3157
chr18	78077248	3870014	0.0496	1.0167
chr19	59128983	5158608	0.0872	0.4916
chr20	63025520	9775154	0.1551	0.4823
chr21	48129895	3063338	0.0636	0.3556
chr22	51304566	2579109	0.0503	0.2719
chrMT	16571	243471	14.6926	10.3474
chrX	155270560	9659145	0.0622	0.3428
chrY	59373566	1116085	0.0188	0.2398

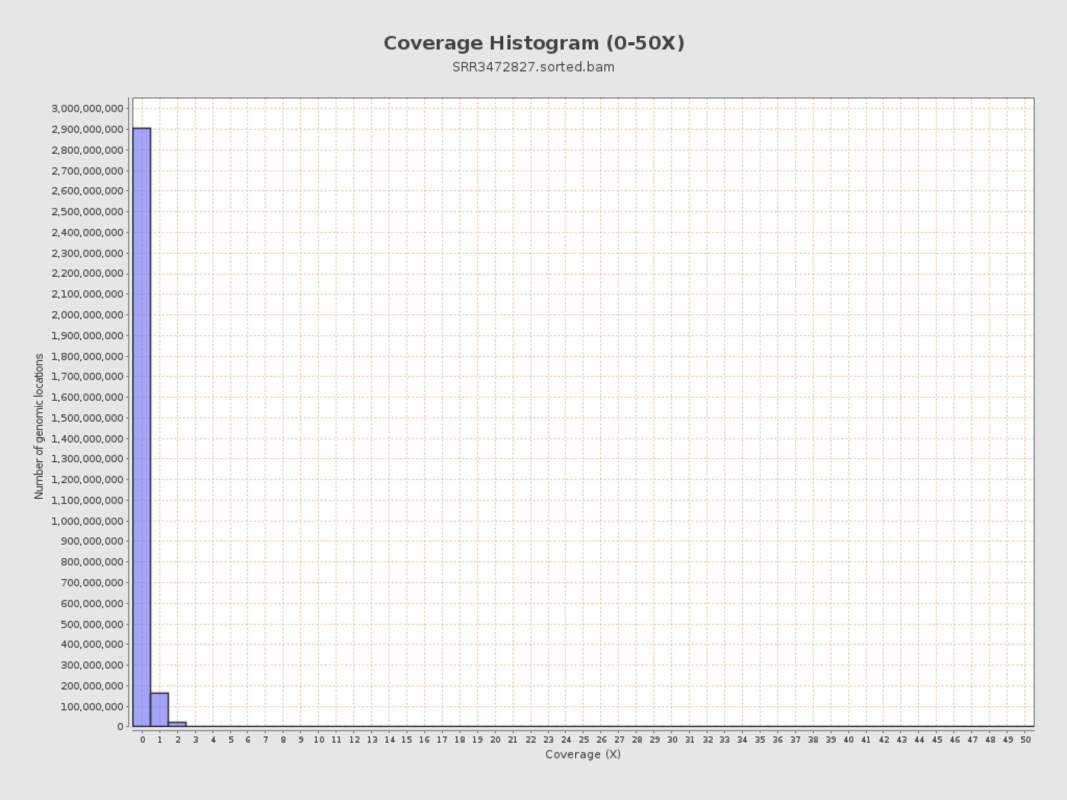
3. Results : Coverage across reference



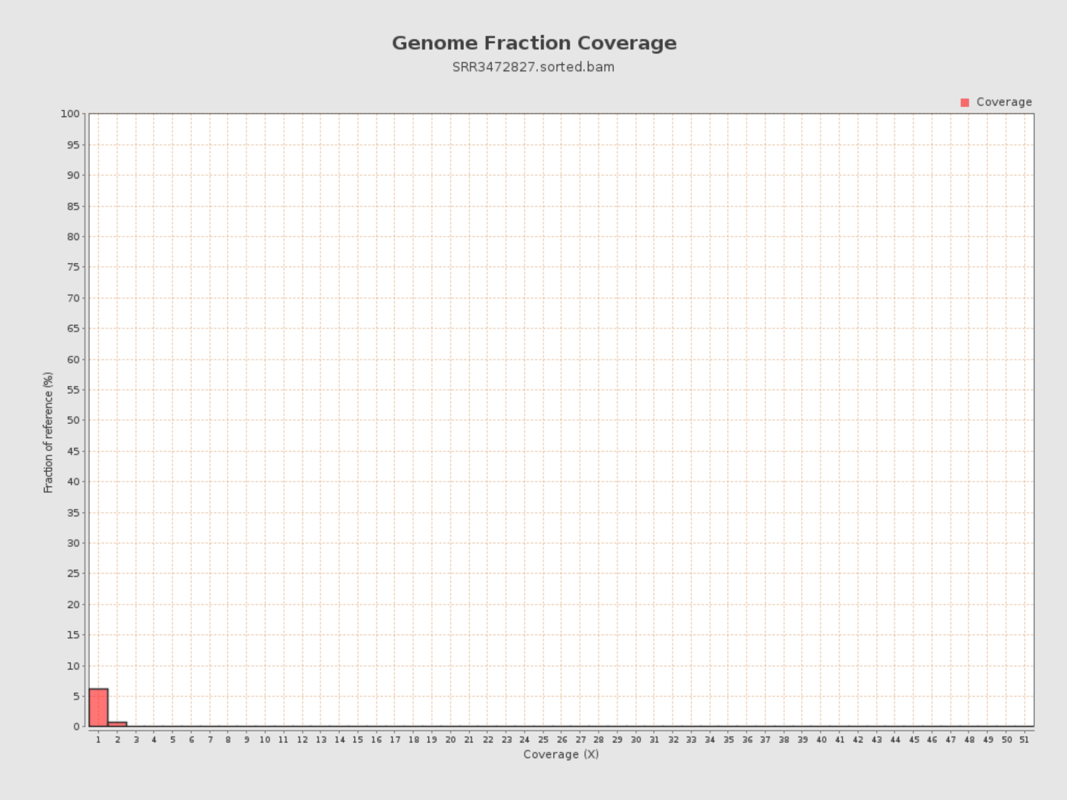
4. Results : Coverage Histogram



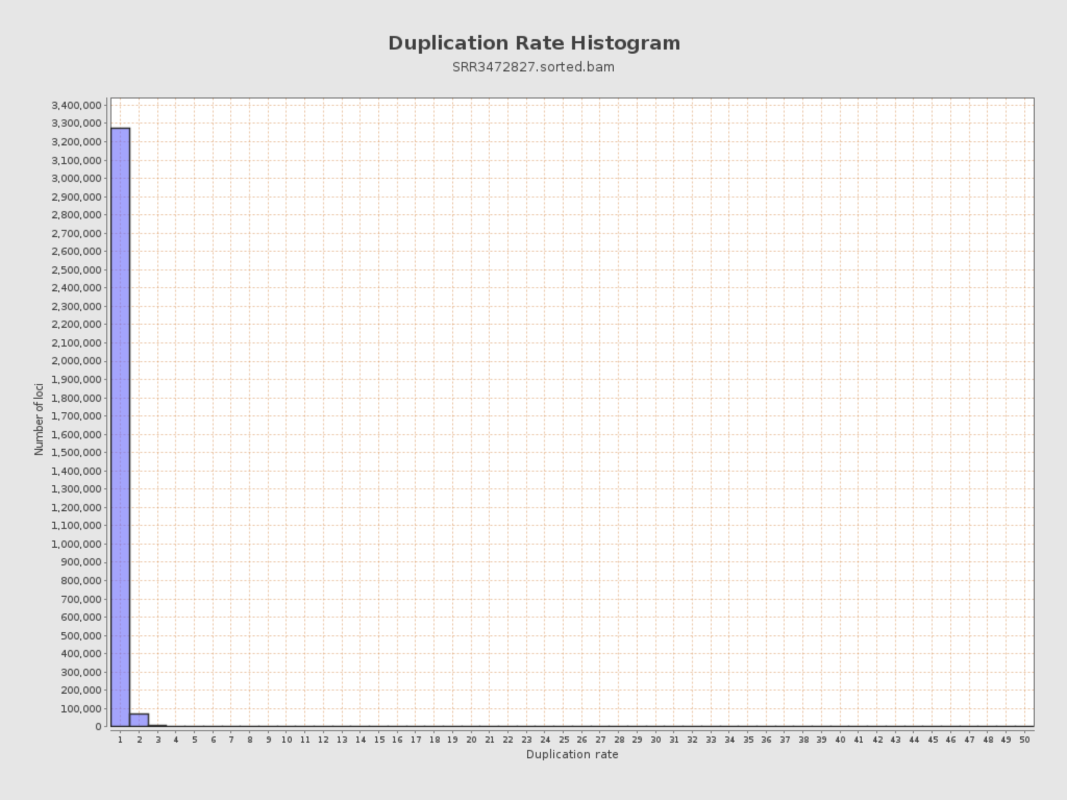
5. Results : Coverage Histogram (0-50X)



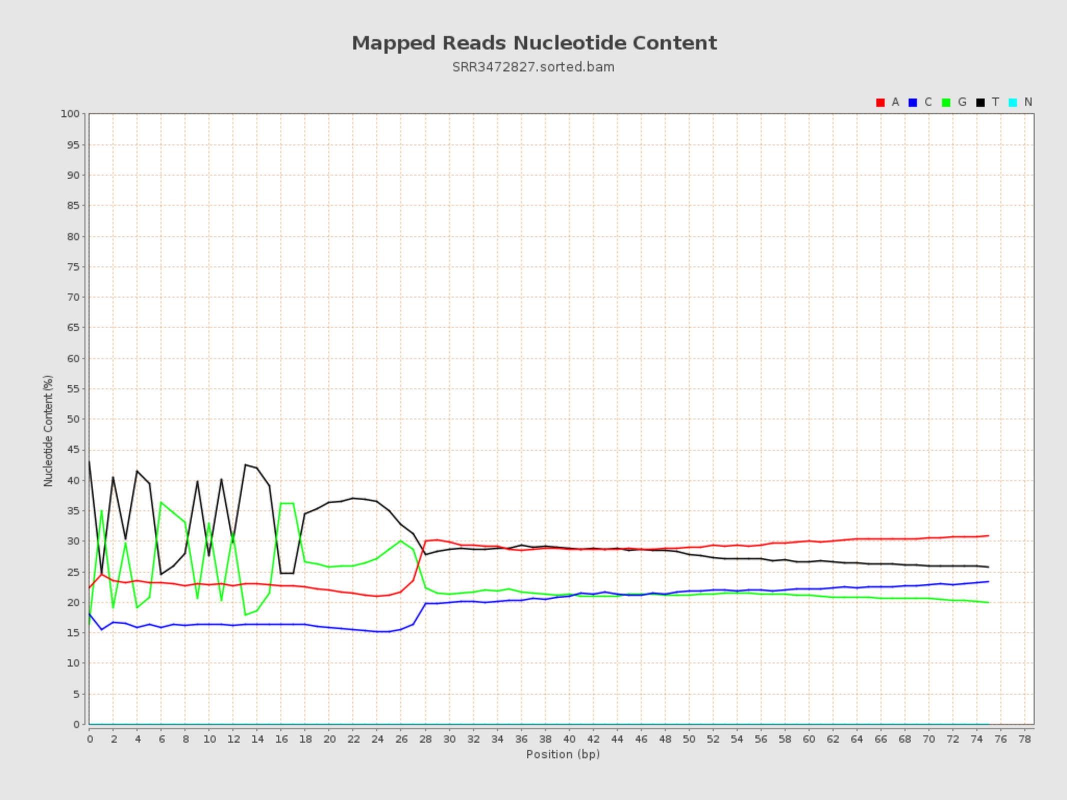
6. Results : Genome Fraction Coverage



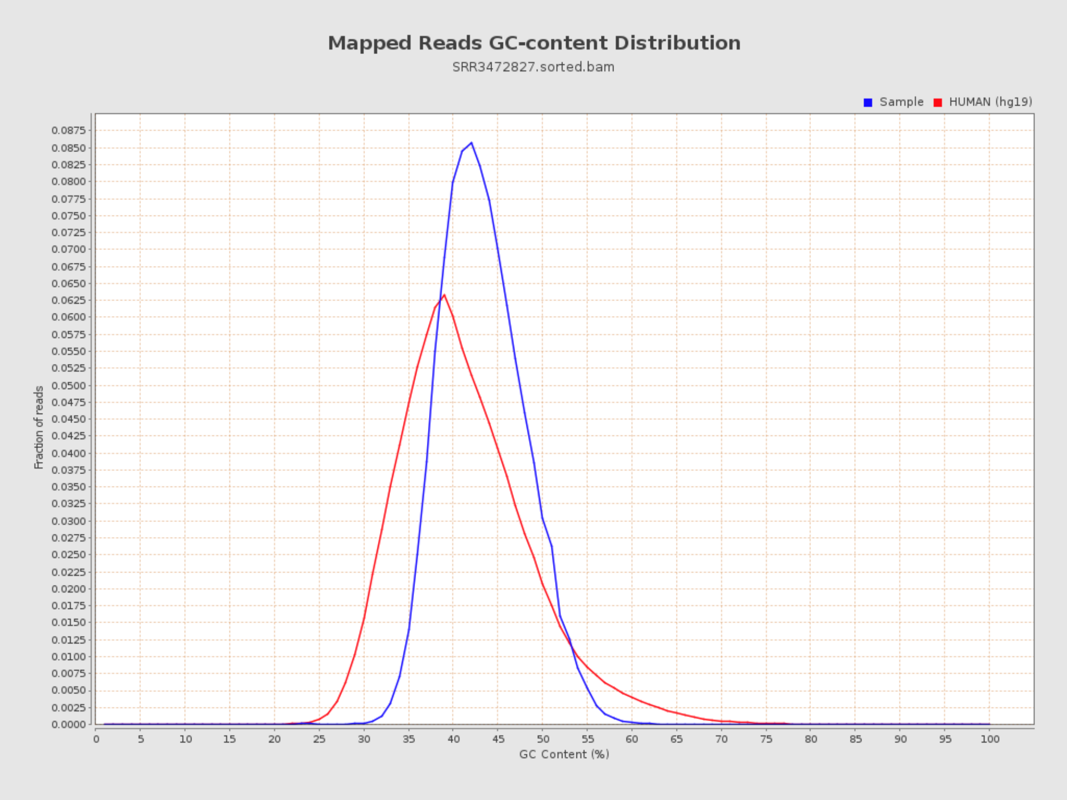
7. Results : Duplication Rate Histogram



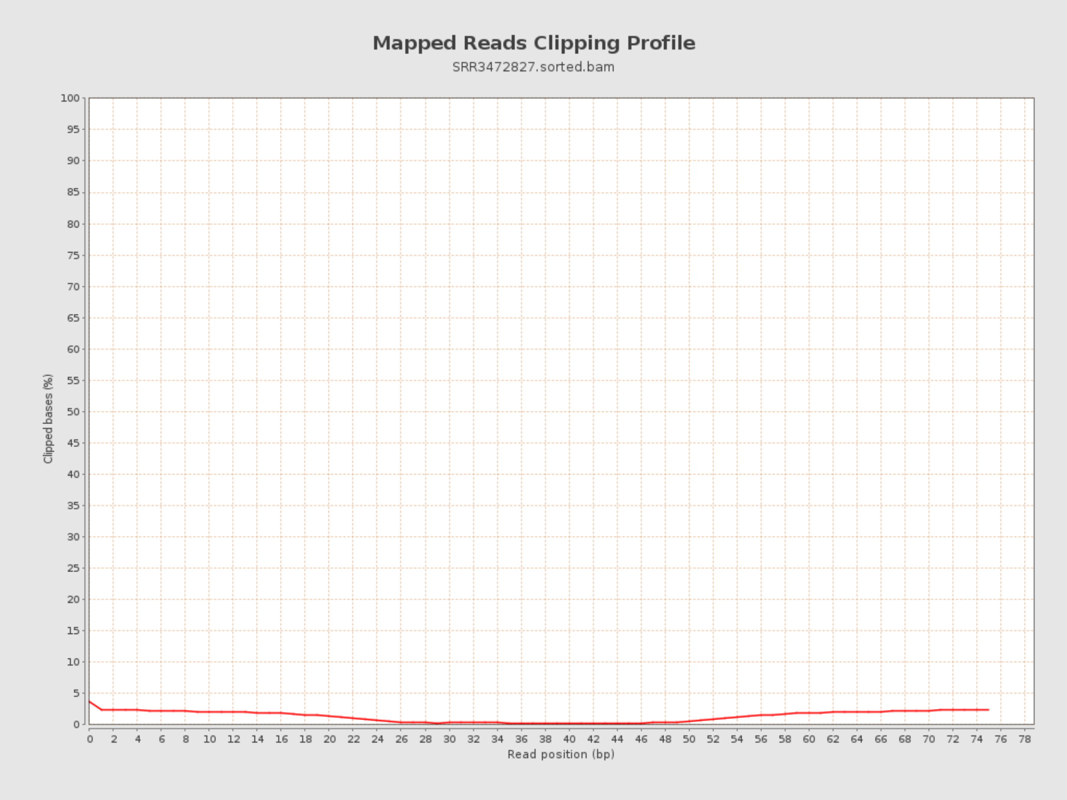
8. Results : Mapped Reads Nucleotide Content



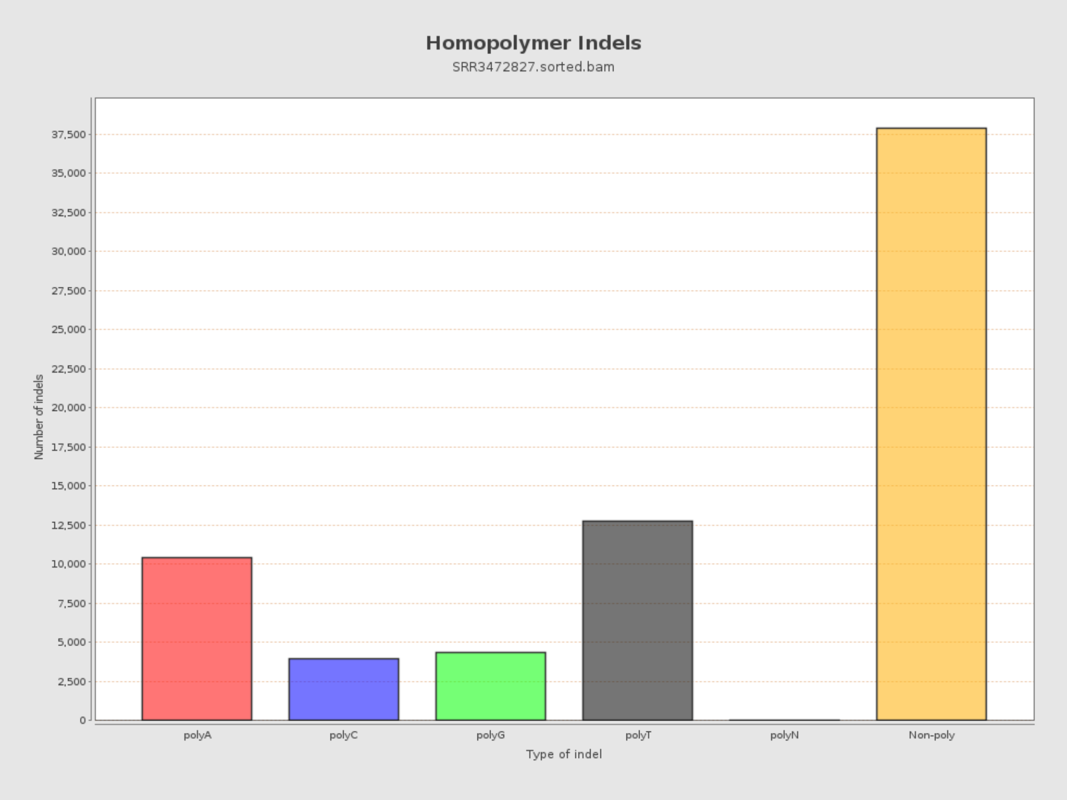
9. Results : Mapped Reads GC-content Distribution



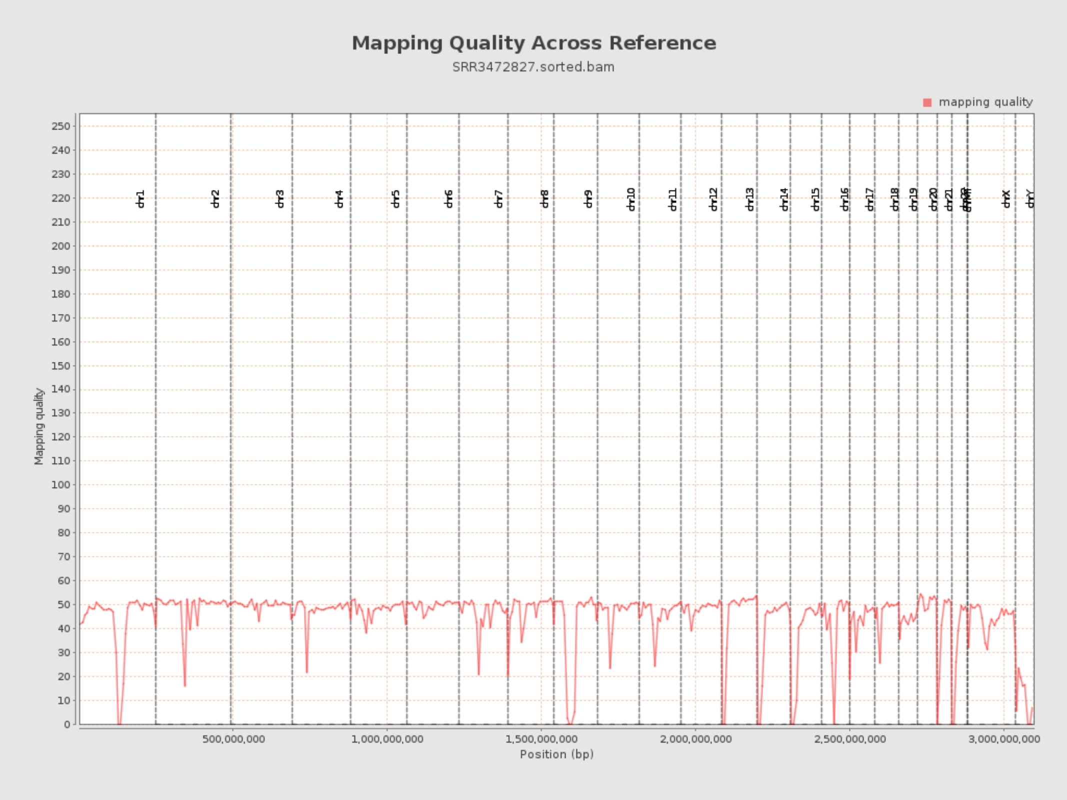
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram