Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 21:48:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082967.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_SRR3082967 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082967.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 21:48:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082967.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,391,281
Mapped reads	2,895,130 / 85.37%
Unmapped reads	496,151 / 14.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,465 / 0.51%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	162,230 / 4.78%
Duplication rate	4.18%
Clipped reads	1,143,624 / 33.72%

2.2. ACGT Content

Number/percentage of A's	55,895,742 / 28.41%
Number/percentage of C's	35,552,763 / 18.07%
Number/percentage of T's	64,308,893 / 32.68%
Number/percentage of G's	40,989,175 / 20.83%
Number/percentage of N's	19,556 / 0.01%
GC Percentage	38.9%

2.3. Coverage

Mean	0.0636

Standard Deviation	0.6441

2.4. Mapping Quality

Mean Mapping Quality	47.27

2.5. Mismatches and indels

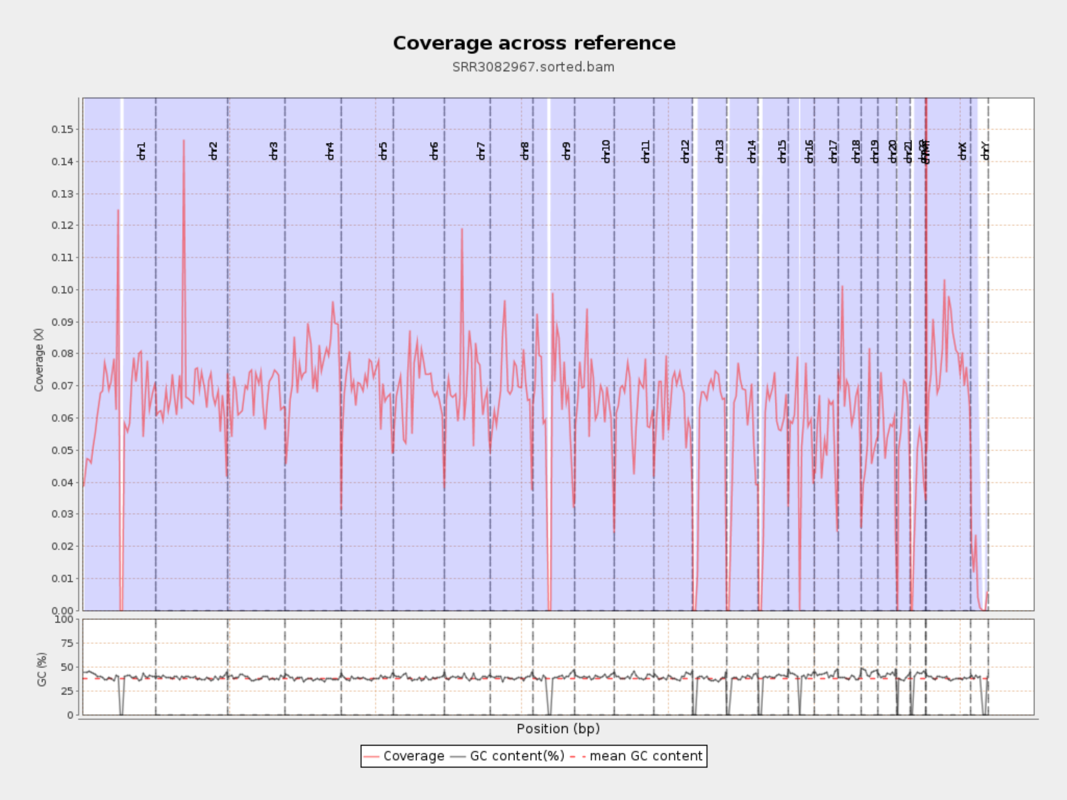
General error rate	0.94%
Mismatches	1,812,090
Insertions	16,922
Mapped reads with at least one insertion	0.58%
Deletions	50,375
Mapped reads with at least one deletion	1.72%
Homopolymer indels	46.83%

2.6. Chromosome stats

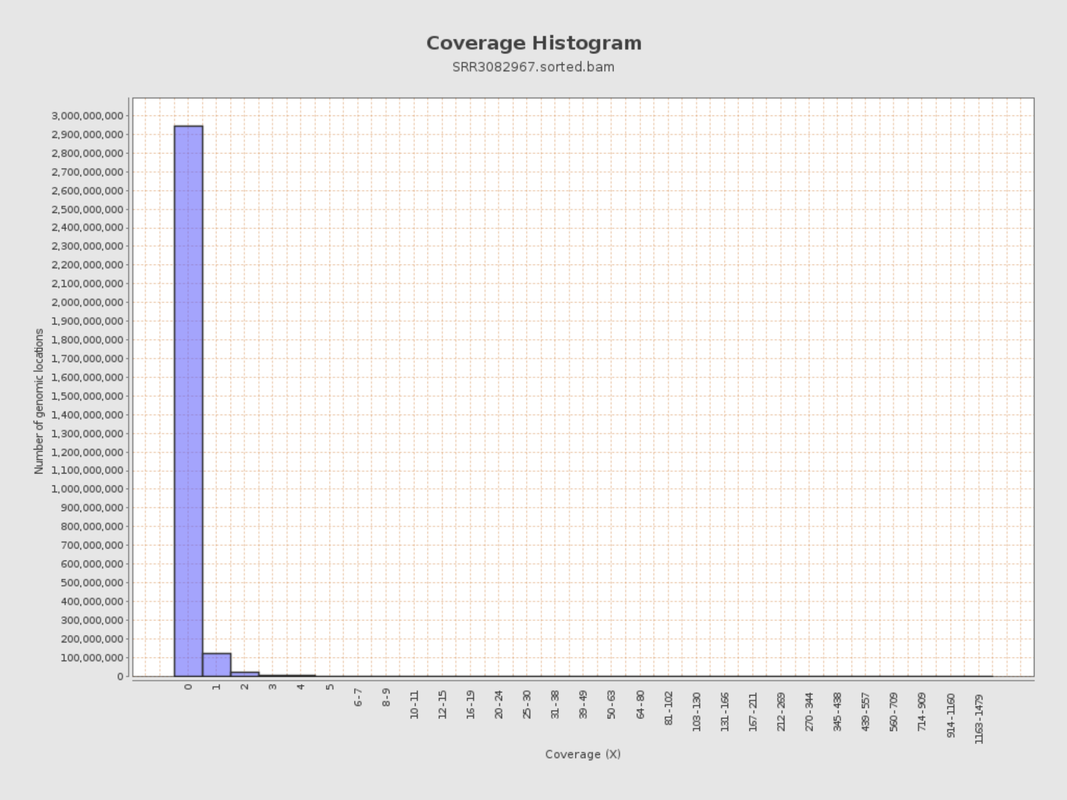
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15558126	0.0624	1.2891
chr2	243199373	16697310	0.0687	0.7064
chr3	198022430	13437529	0.0679	0.3294
chr4	191154276	14565637	0.0762	0.3575
chr5	180915260	12460245	0.0689	0.3357
chr6	171115067	11882166	0.0694	0.4156
chr7	159138663	11116407	0.0699	0.776

chr8	146364022	10105627	0.069	0.9508
chr9	141213431	8931051	0.0632	0.6827
chr10	135534747	9039886	0.0667	0.4467
chr11	135006516	8649968	0.0641	0.4838
chr12	133851895	8598252	0.0642	0.3349
chr13	115169878	6542552	0.0568	0.2977
chr14	107349540	5763932	0.0537	0.3549
chr15	102531392	5287600	0.0516	0.283
chr16	90354753	4834905	0.0535	0.3955
chr17	81195210	4341500	0.0535	0.3665
chr18	78077248	5410498	0.0693	1.3832
chr19	59128983	3012970	0.051	0.7732
chr20	63025520	3607633	0.0572	0.3201
chr21	48129895	2609076	0.0542	0.3434
chr22	51304566	1787458	0.0348	0.227
chrMT	16571	20627	1.2448	1.4589
chrX	155270560	12125137	0.0781	0.4123
chrY	59373566	467449	0.0079	0.1876

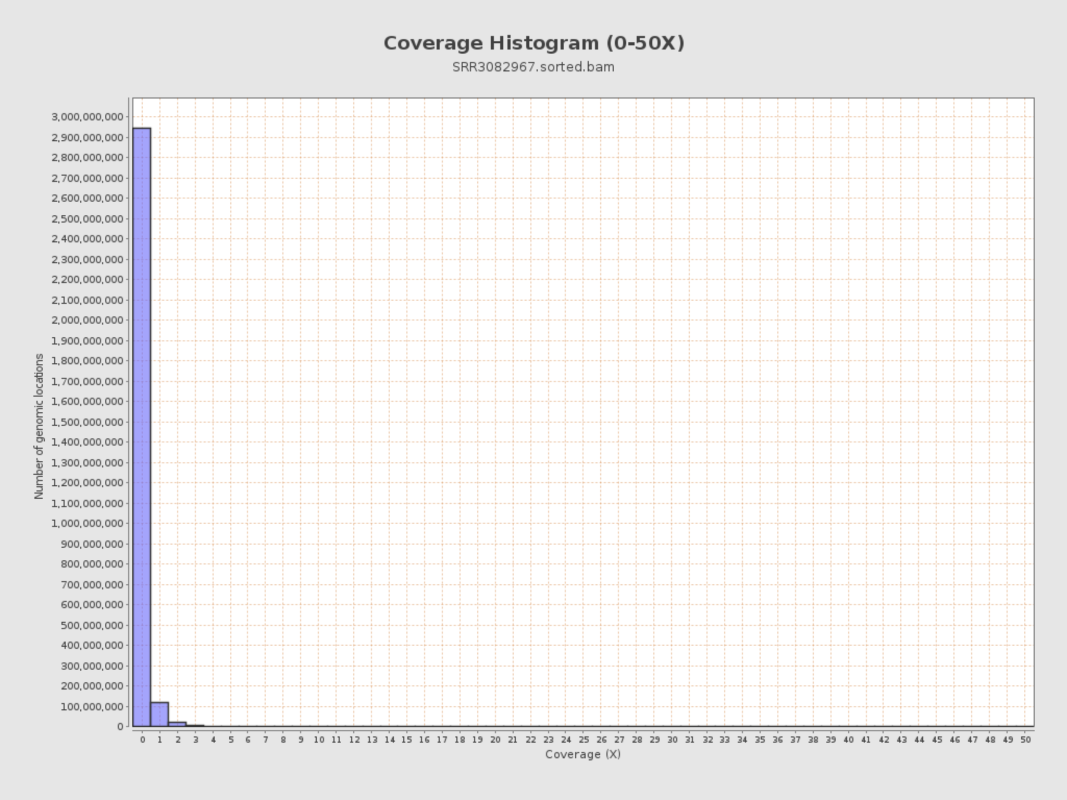
3. Results : Coverage across reference



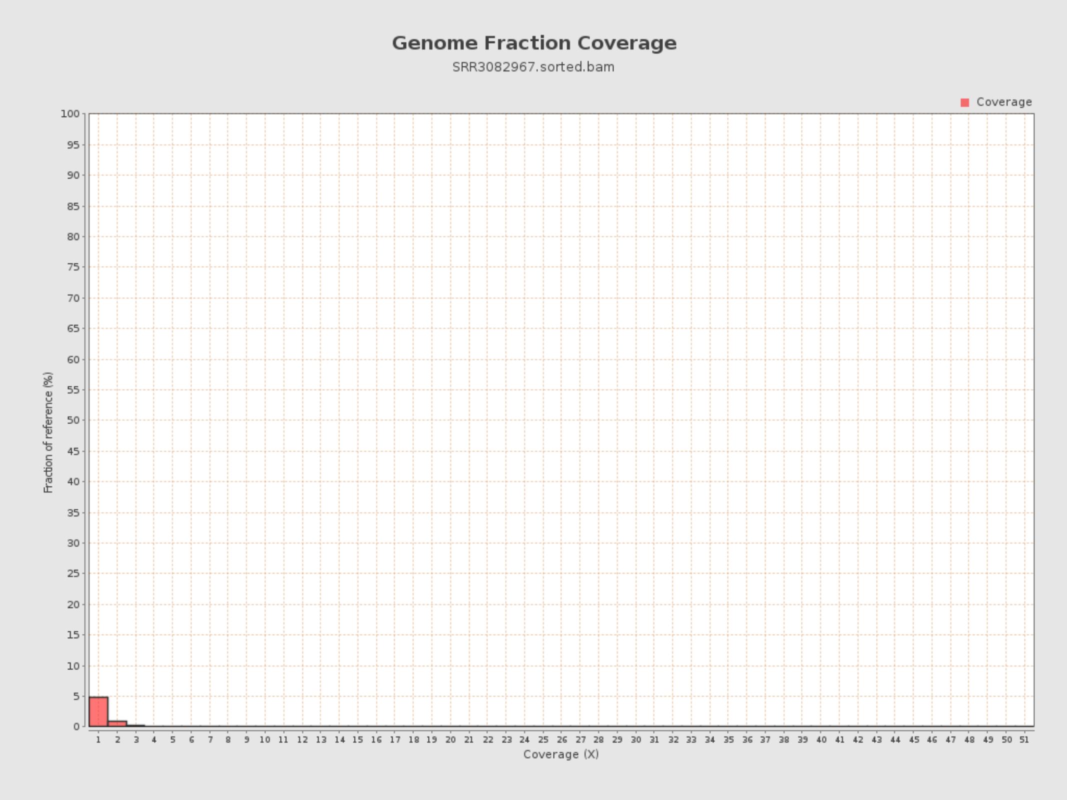
4. Results : Coverage Histogram



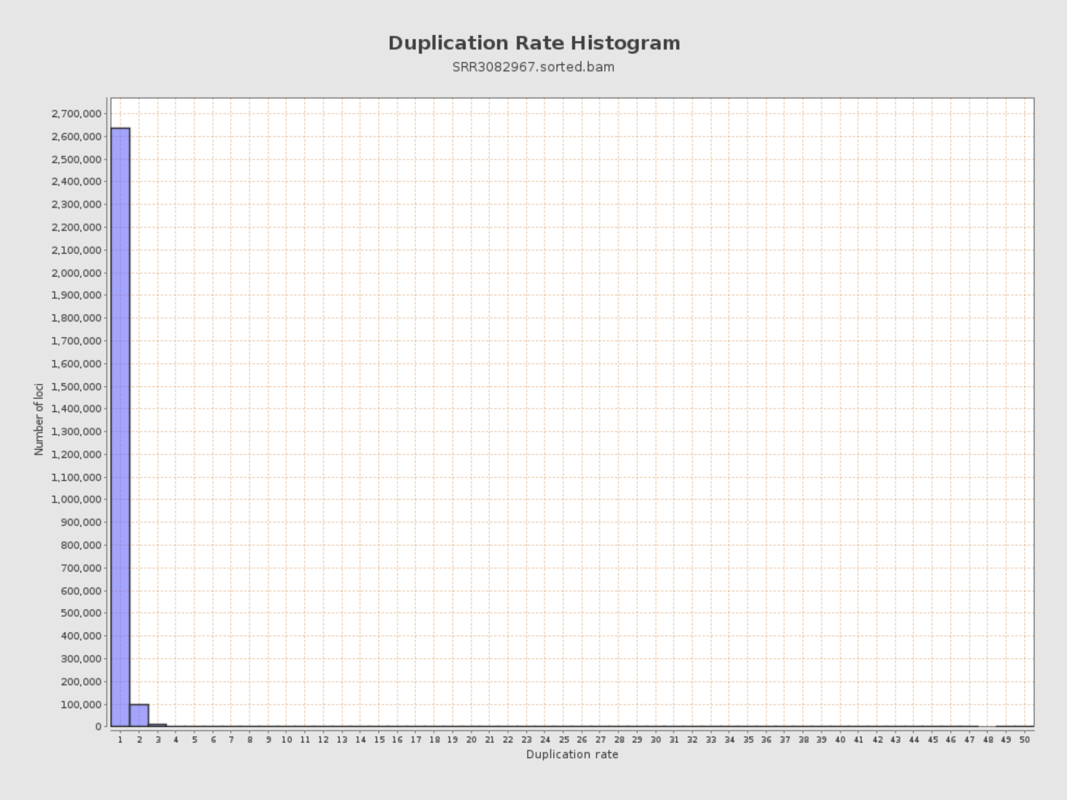
5. Results : Coverage Histogram (0-50X)



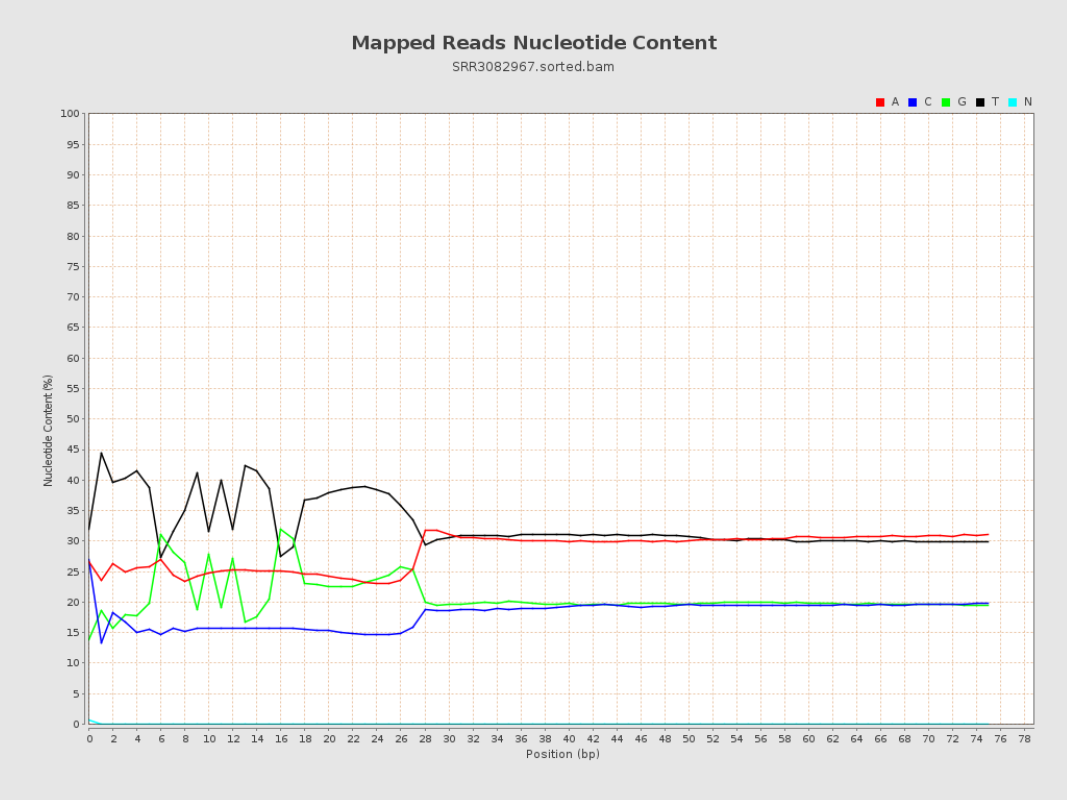
6. Results : Genome Fraction Coverage



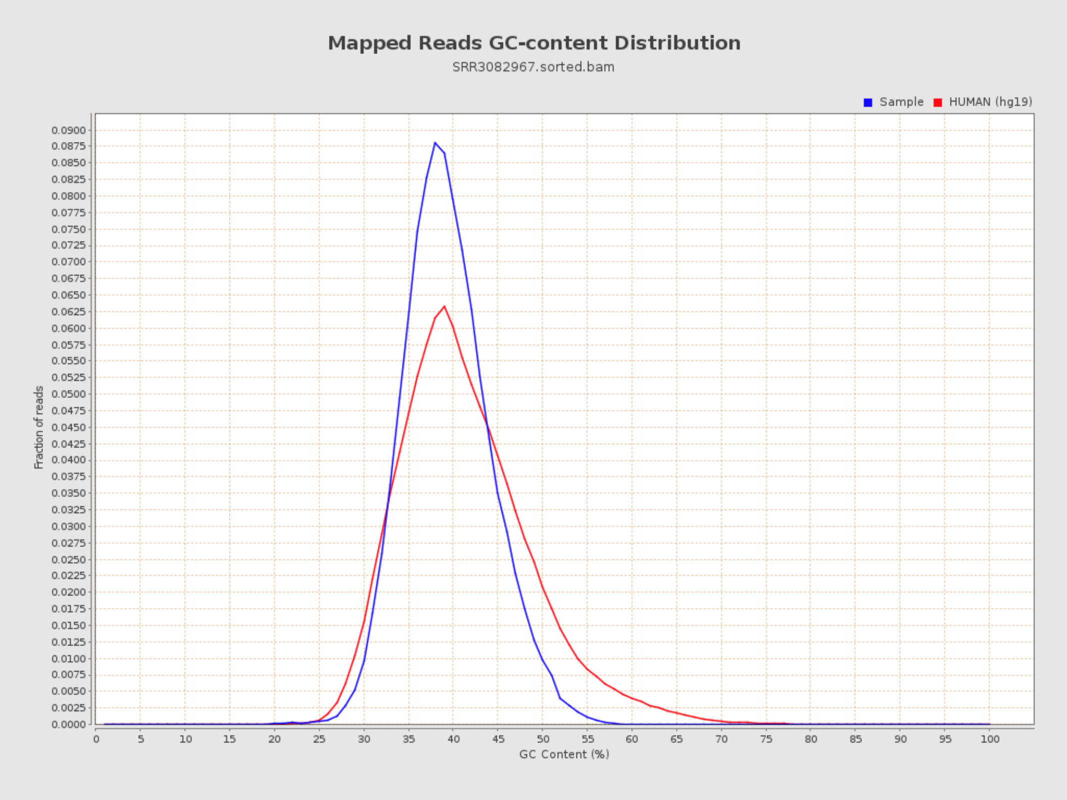
7. Results : Duplication Rate Histogram



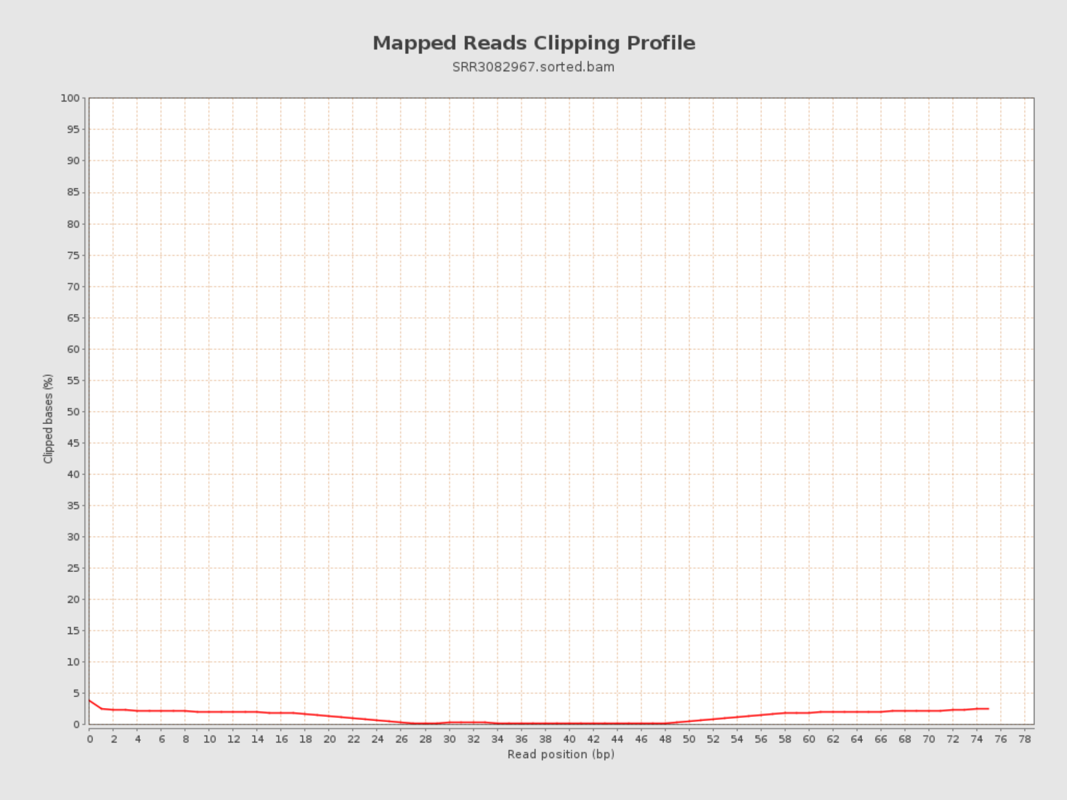
8. Results : Mapped Reads Nucleotide Content



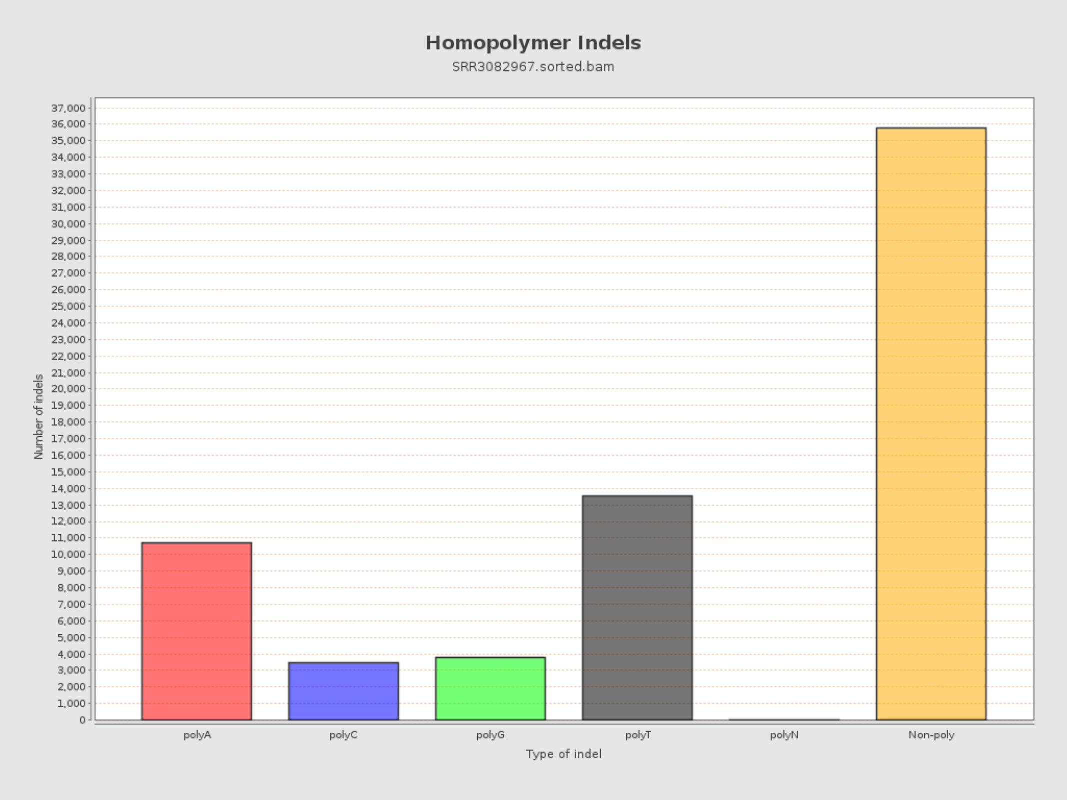
9. Results : Mapped Reads GC-content Distribution



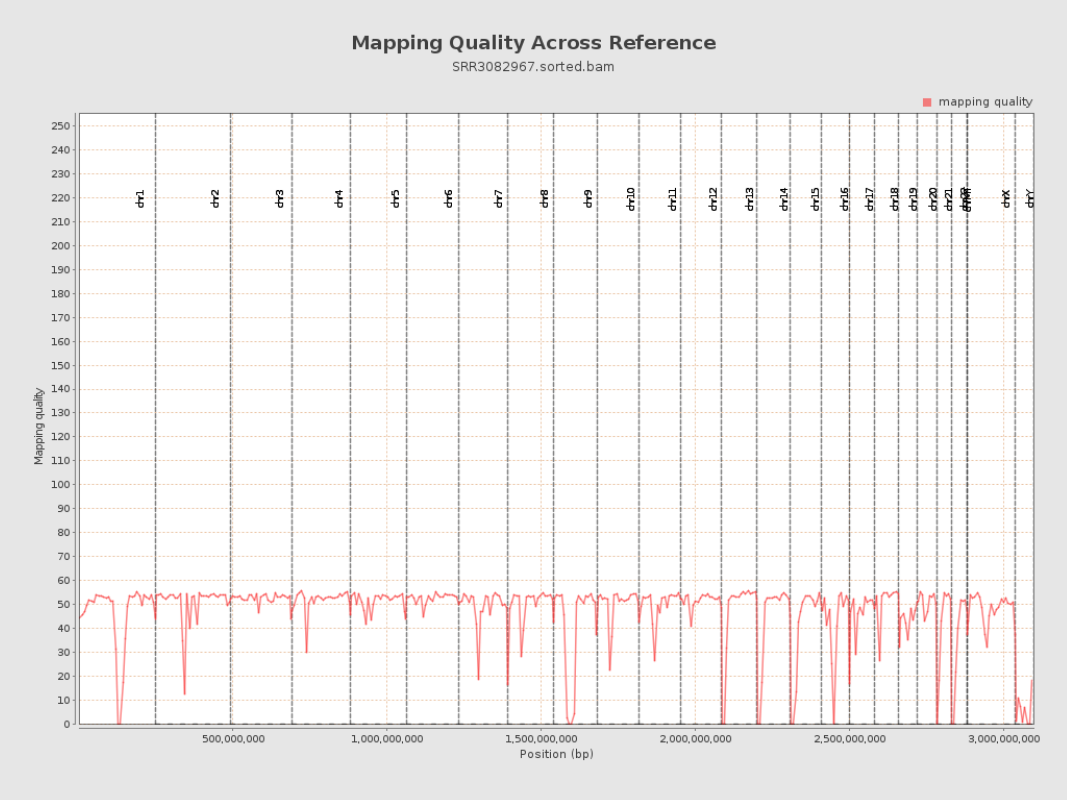
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram