Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 00:03:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083617.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_SRR3083617 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083617.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 00:03:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083617.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,109,897
Mapped reads	1,883,622 / 89.28%
Unmapped reads	226,275 / 10.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,069 / 0.81%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	103,484 / 4.9%
Duplication rate	4.32%
Clipped reads	902,081 / 42.75%

2.2. ACGT Content

Number/percentage of A's	32,839,791 / 26.5%
Number/percentage of C's	23,051,039 / 18.6%
Number/percentage of T's	38,998,987 / 31.47%
Number/percentage of G's	29,033,539 / 23.43%
Number/percentage of N's	5,581 / 0%
GC Percentage	42.03%

2.3. Coverage

Mean	0.04

Standard Deviation	0.4116

2.4. Mapping Quality

Mean Mapping Quality	44.79

2.5. Mismatches and indels

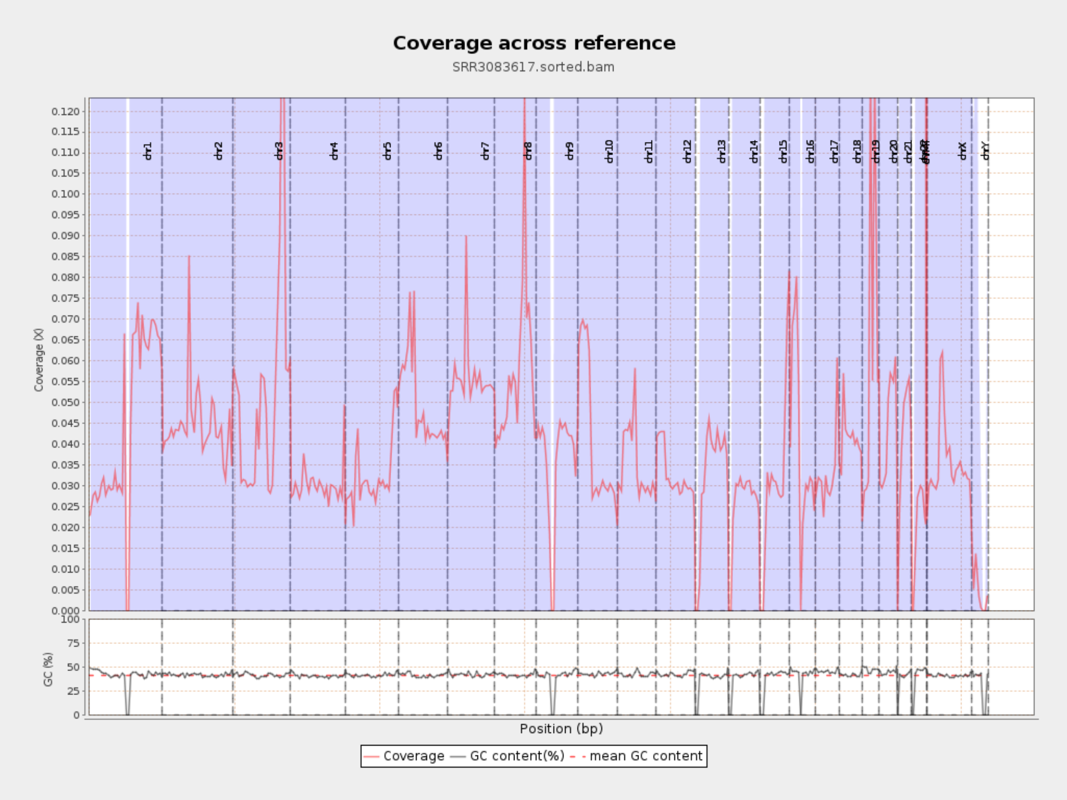
General error rate	0.74%
Mismatches	901,249
Insertions	9,301
Mapped reads with at least one insertion	0.49%
Deletions	28,018
Mapped reads with at least one deletion	1.47%
Homopolymer indels	47.09%

2.6. Chromosome stats

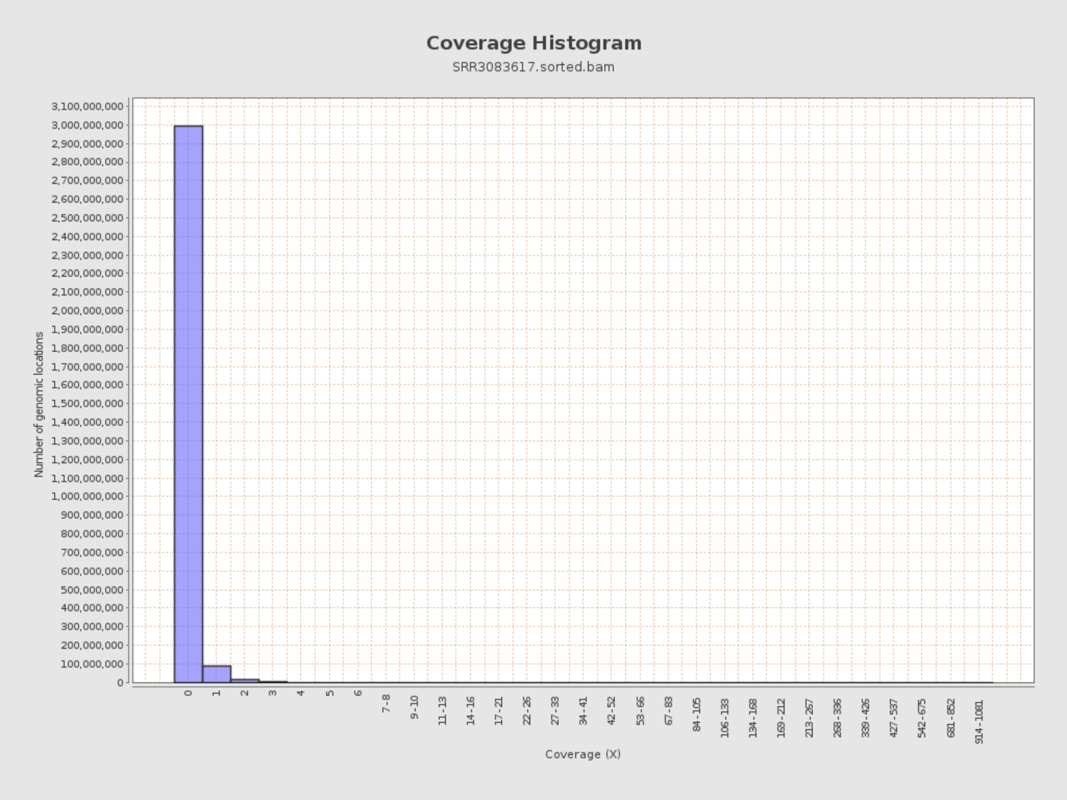
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11014300	0.0442	0.7954
chr2	243199373	10851788	0.0446	0.5712
chr3	198022430	10354468	0.0523	0.2704
chr4	191154276	5769506	0.0302	0.2154
chr5	180915260	5891326	0.0326	0.2109
chr6	171115067	8532876	0.0499	0.3501
chr7	159138663	8924637	0.0561	0.6853

chr8	146364022	8420152	0.0575	0.3947
chr9	141213431	5002109	0.0354	0.3108
chr10	135534747	5634713	0.0416	0.3151
chr11	135006516	4706224	0.0349	0.3214
chr12	133851895	4361147	0.0326	0.2122
chr13	115169878	3696180	0.0321	0.2088
chr14	107349540	2699657	0.0251	0.1977
chr15	102531392	3145480	0.0307	0.2307
chr16	90354753	3633295	0.0402	0.2509
chr17	81195210	2734895	0.0337	0.2313
chr18	78077248	3255395	0.0417	0.6182
chr19	59128983	3770978	0.0638	0.5469
chr20	63025520	2769399	0.0439	0.253
chr21	48129895	1951232	0.0405	0.2429
chr22	51304566	988279	0.0193	0.1598
chrMT	16571	38116	2.3002	2.1719
chrX	155270560	5563970	0.0358	0.2396
chrY	59373566	264439	0.0045	0.1019

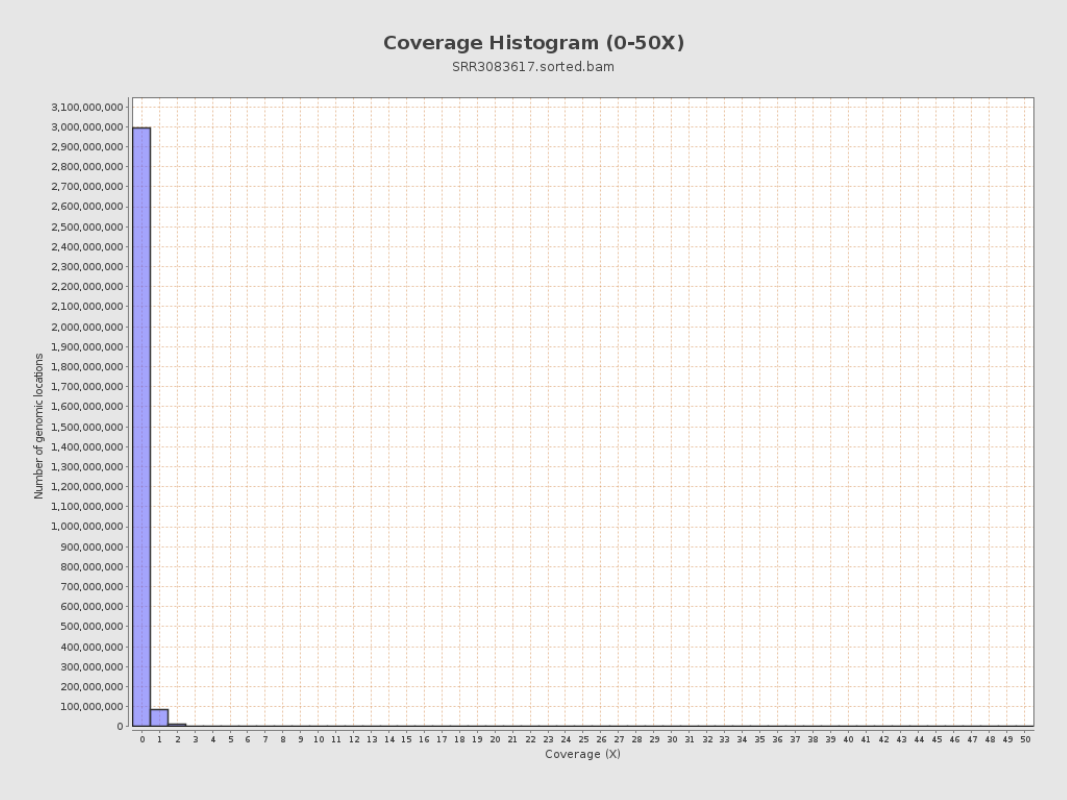
3. Results : Coverage across reference



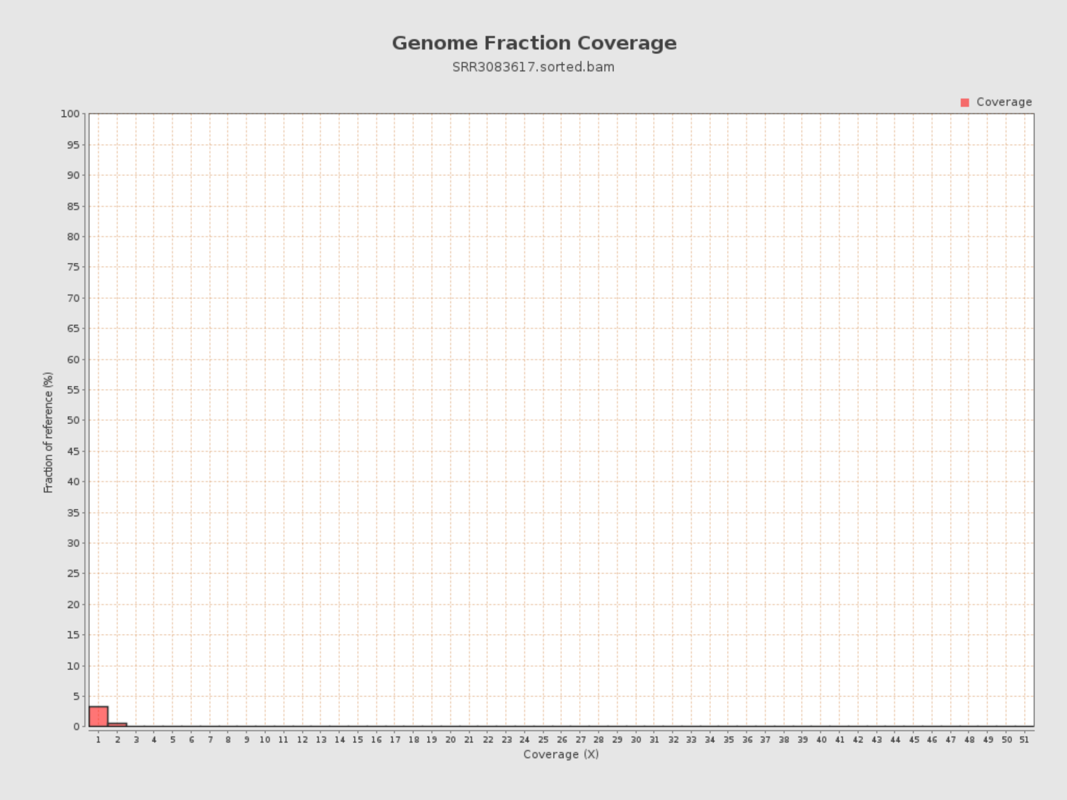
4. Results : Coverage Histogram



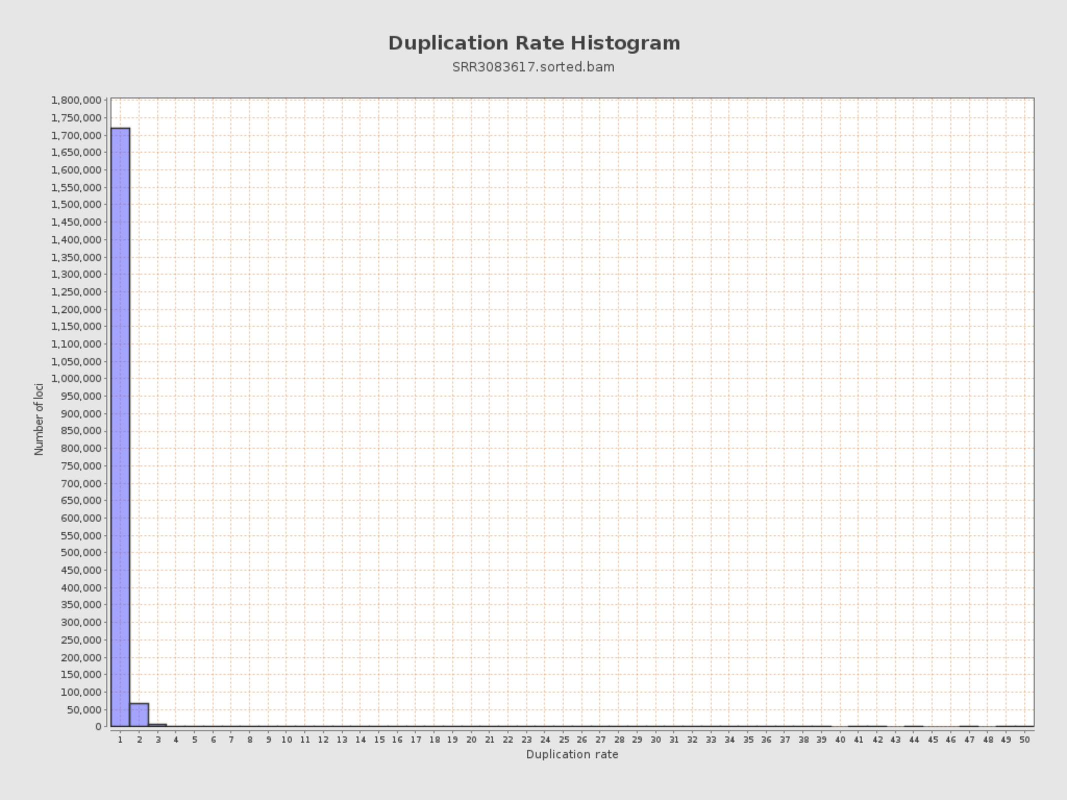
5. Results : Coverage Histogram (0-50X)



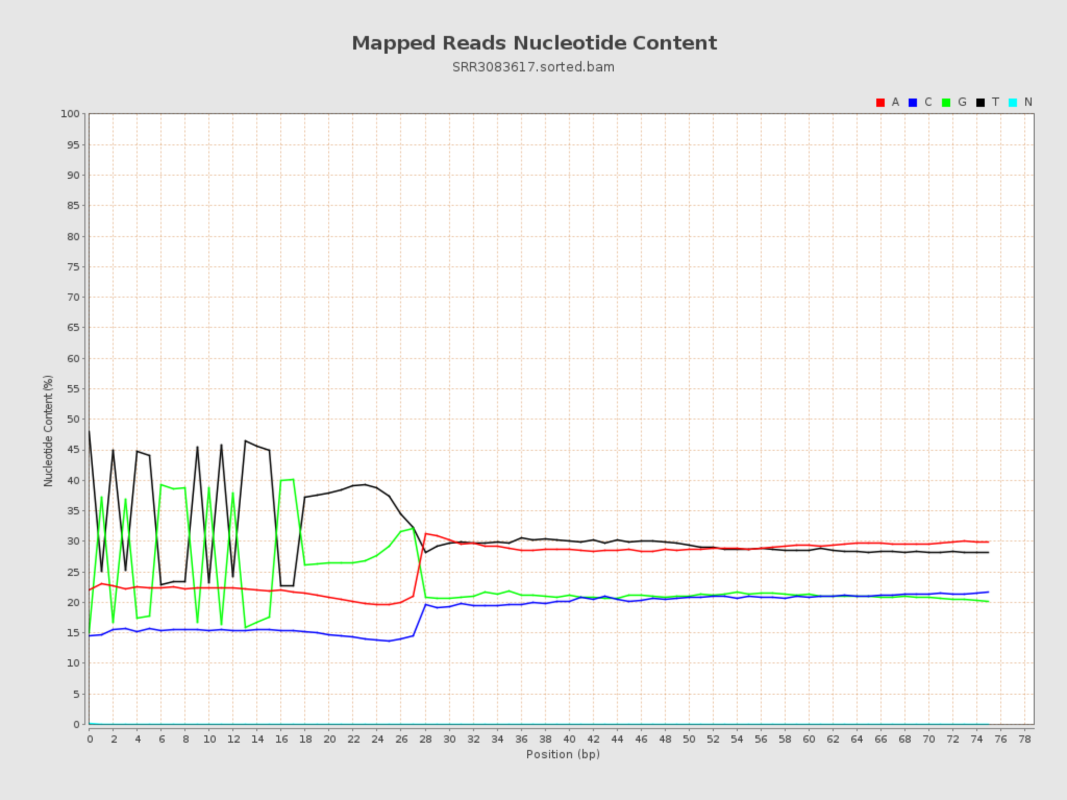
6. Results : Genome Fraction Coverage



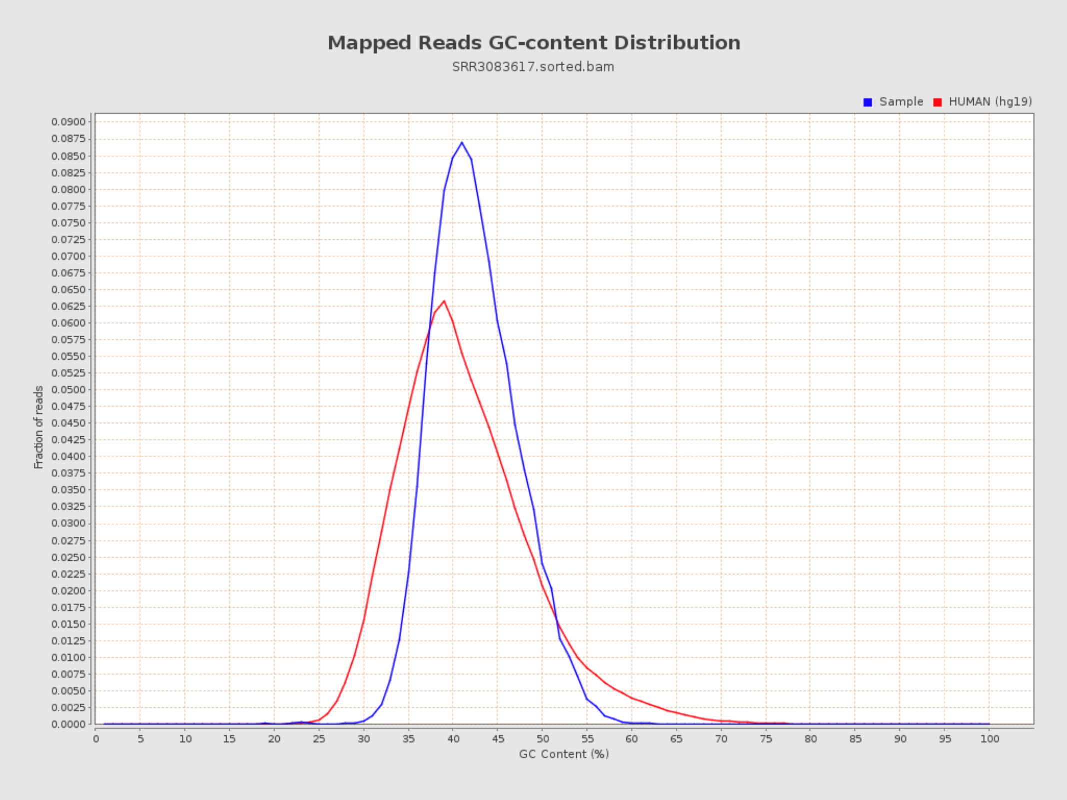
7. Results : Duplication Rate Histogram



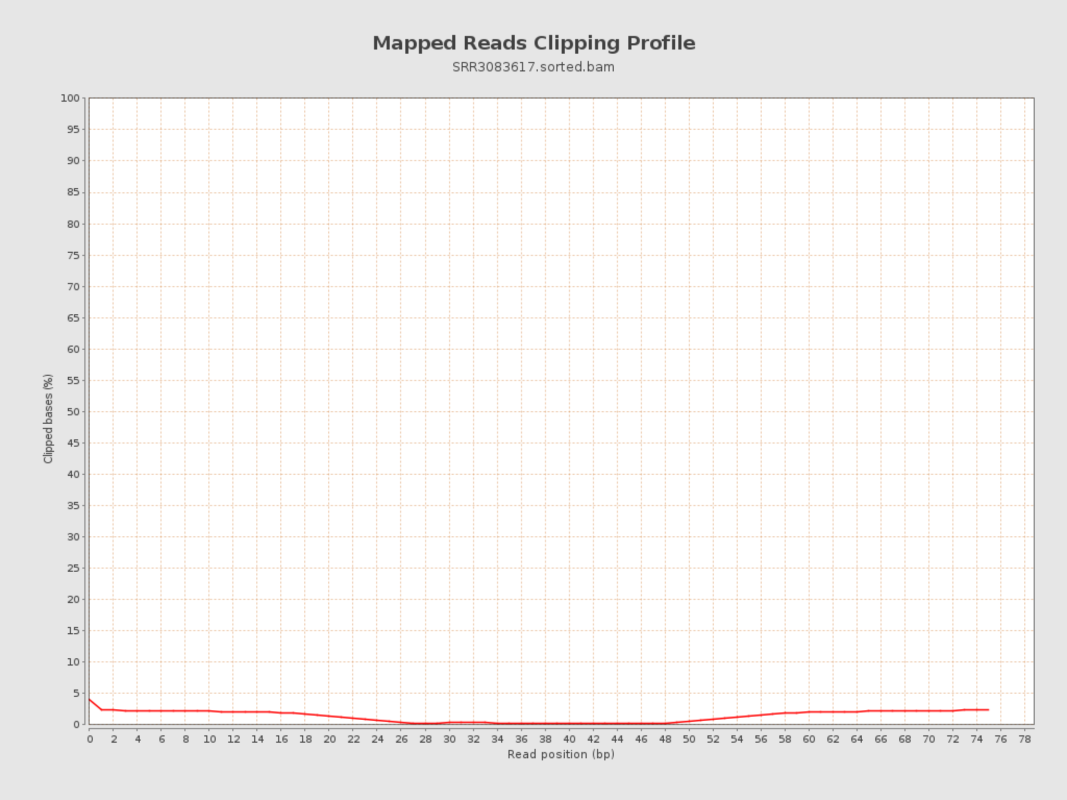
8. Results : Mapped Reads Nucleotide Content



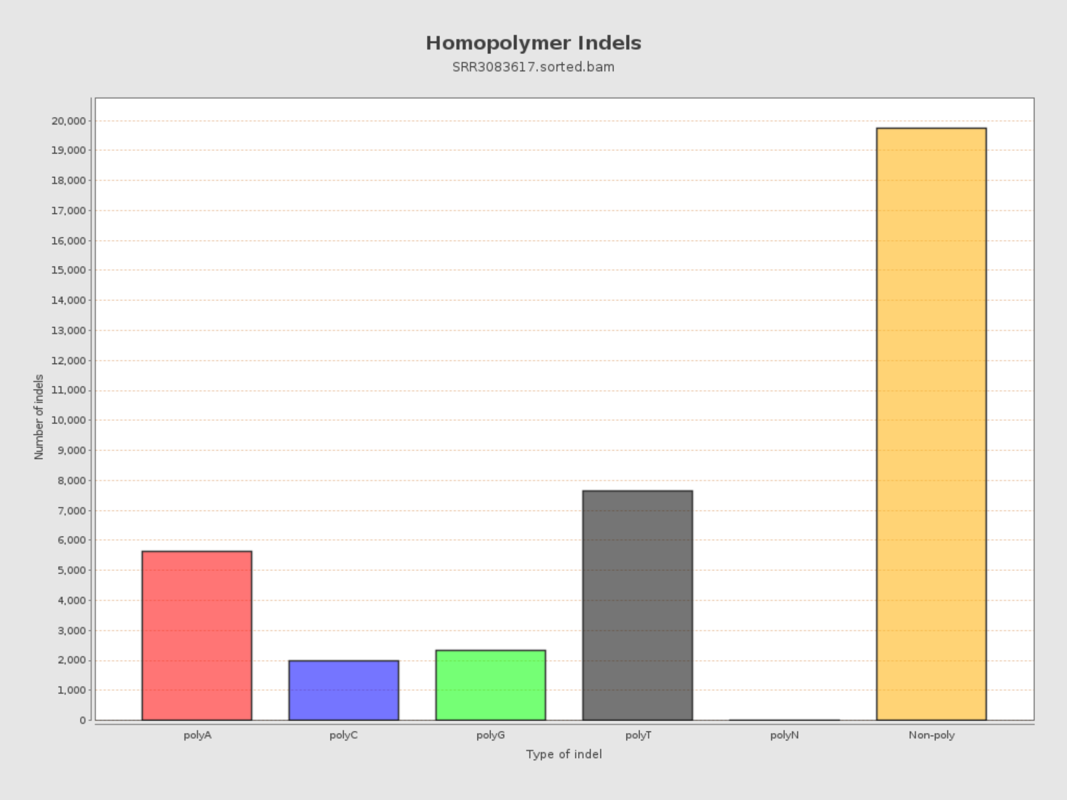
9. Results : Mapped Reads GC-content Distribution



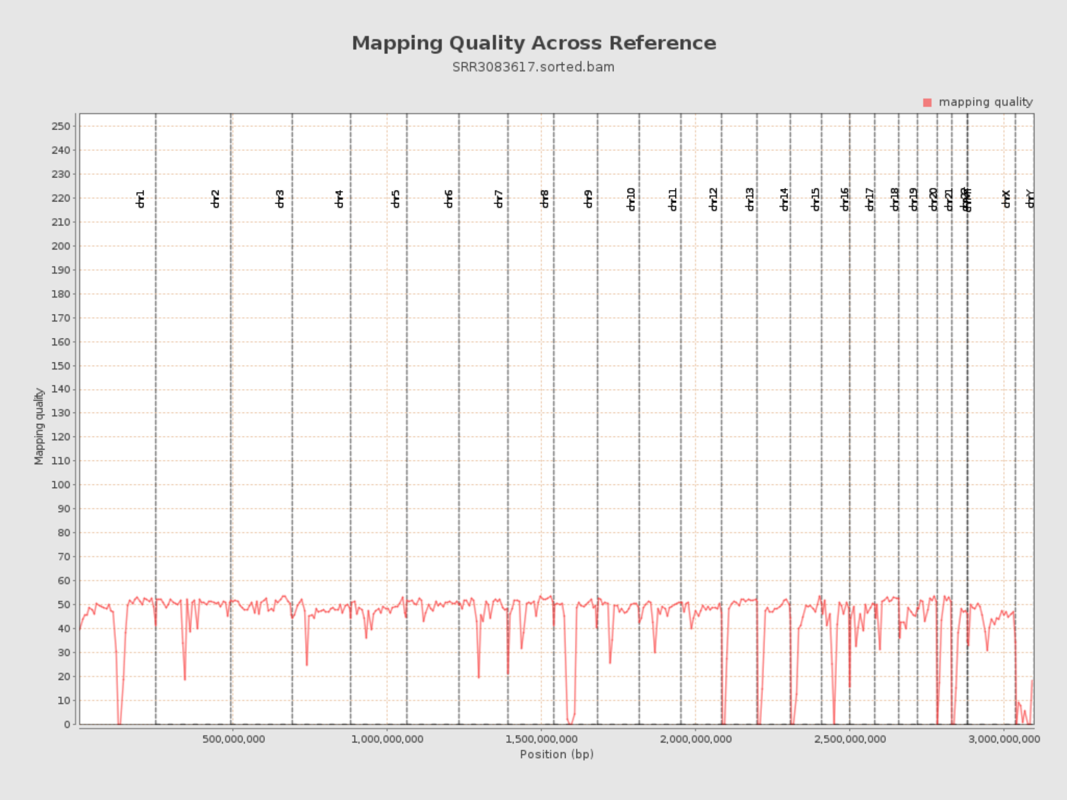
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram