Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 16:32:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084833.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_SRR3084833 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084833.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 16:32:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084833.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,762,351
Mapped reads	1,596,472 / 90.59%
Unmapped reads	165,879 / 9.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,109 / 1.2%
Read min/max/mean length	30 / 76 / 76.42
Duplicated reads (estimated)	54,135 / 3.07%
Duplication rate	2.13%
Clipped reads	739,834 / 41.98%

2.2. ACGT Content

Number/percentage of A's	29,644,307 / 27.92%
Number/percentage of C's	20,817,178 / 19.61%
Number/percentage of T's	31,405,889 / 29.58%
Number/percentage of G's	24,289,169 / 22.88%
Number/percentage of N's	14,583 / 0.01%
GC Percentage	42.48%

2.3. Coverage

Mean	0.0343

Standard Deviation	0.3997

2.4. Mapping Quality

Mean Mapping Quality	42.99

2.5. Mismatches and indels

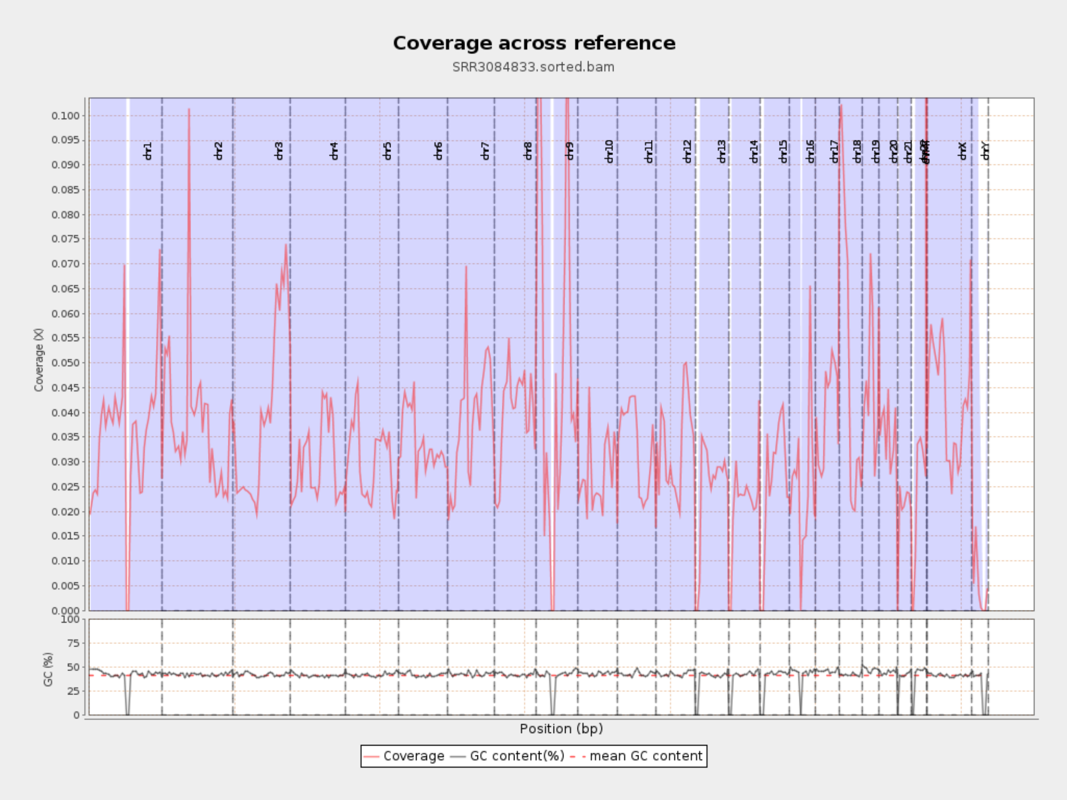
General error rate	0.84%
Mismatches	872,083
Insertions	9,448
Mapped reads with at least one insertion	0.58%
Deletions	22,125
Mapped reads with at least one deletion	1.37%
Homopolymer indels	43.09%

2.6. Chromosome stats

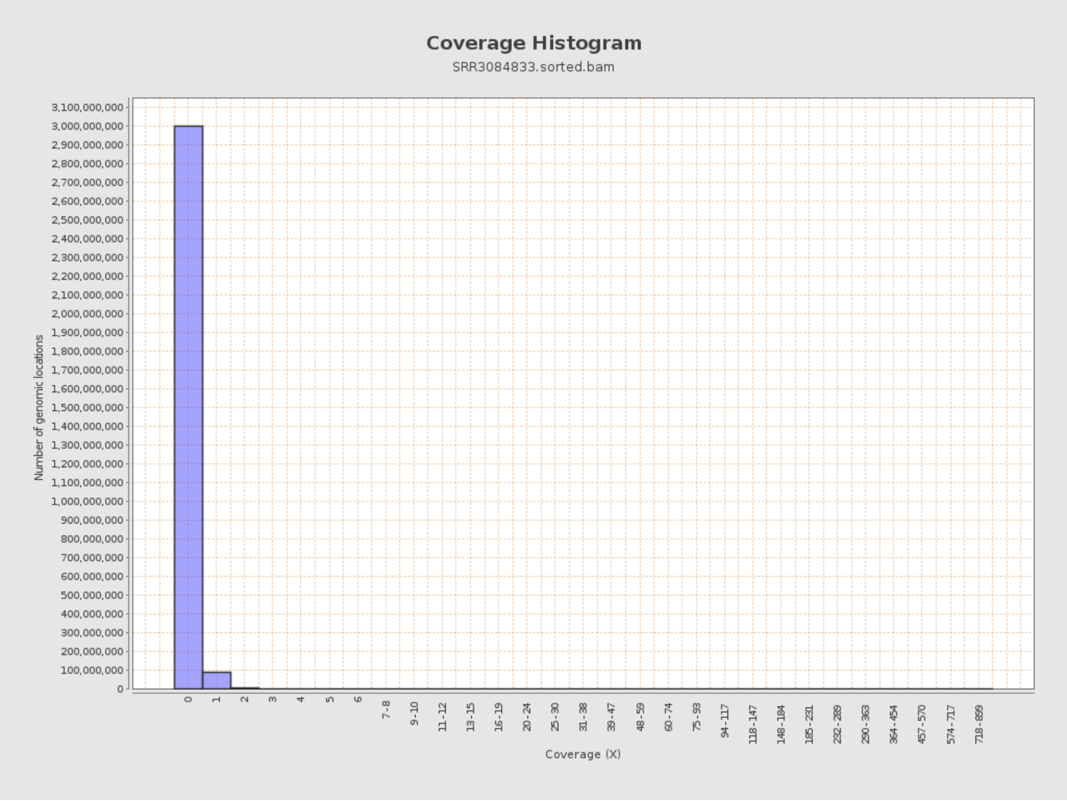
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8919959	0.0358	0.7752
chr2	243199373	9234964	0.038	0.5702
chr3	198022430	7884987	0.0398	0.2131
chr4	191154276	5704033	0.0298	0.1936
chr5	180915260	5489747	0.0303	0.1959
chr6	171115067	5807622	0.0339	0.2127
chr7	159138663	6147836	0.0386	0.457

chr8	146364022	5788527	0.0395	0.3842
chr9	141213431	7098962	0.0503	0.4504
chr10	135534747	3694093	0.0273	0.2646
chr11	135006516	4460034	0.033	0.3729
chr12	133851895	4454539	0.0333	0.2014
chr13	115169878	2817156	0.0245	0.1639
chr14	107349540	2193883	0.0204	0.2029
chr15	102531392	2695516	0.0263	0.1811
chr16	90354753	2341320	0.0259	0.2217
chr17	81195210	3325890	0.041	0.2539
chr18	78077248	4056881	0.052	0.8917
chr19	59128983	2728949	0.0462	0.5086
chr20	63025520	2265705	0.0359	0.218
chr21	48129895	981003	0.0204	0.1774
chr22	51304566	1146218	0.0223	0.1568
chrMT	16571	46778	2.8229	2.329
chrX	155270560	6619307	0.0426	0.2746
chrY	59373566	304805	0.0051	0.1724

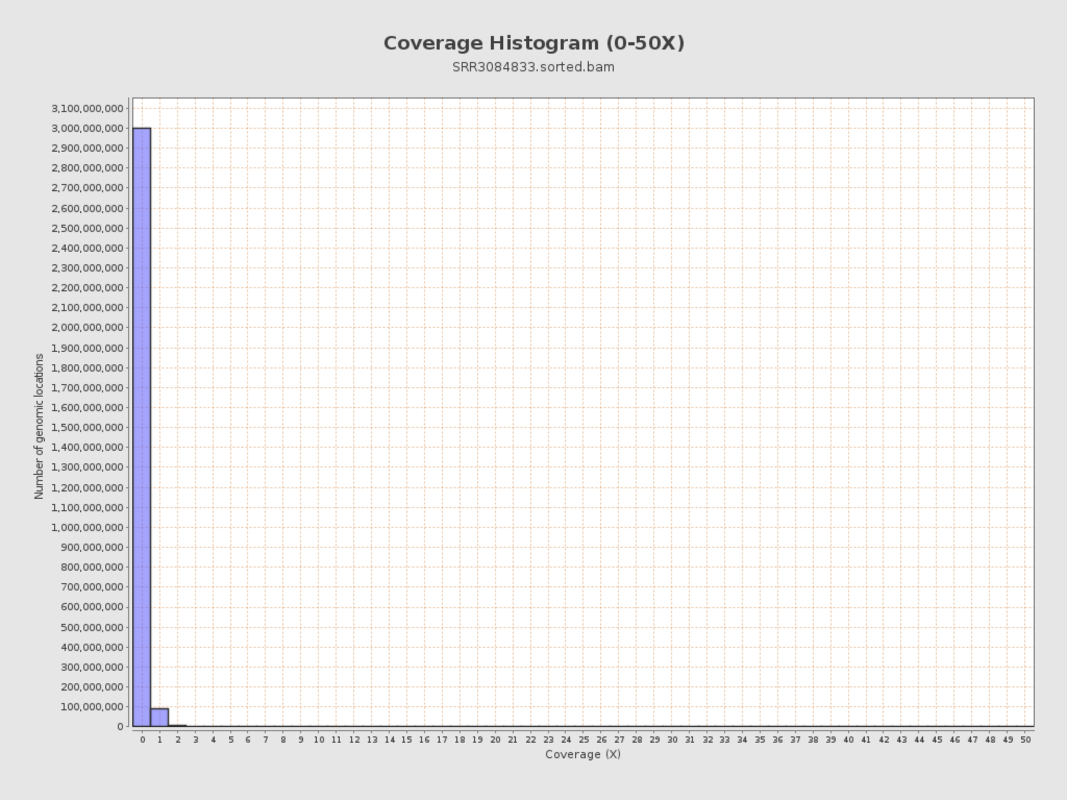
3. Results : Coverage across reference



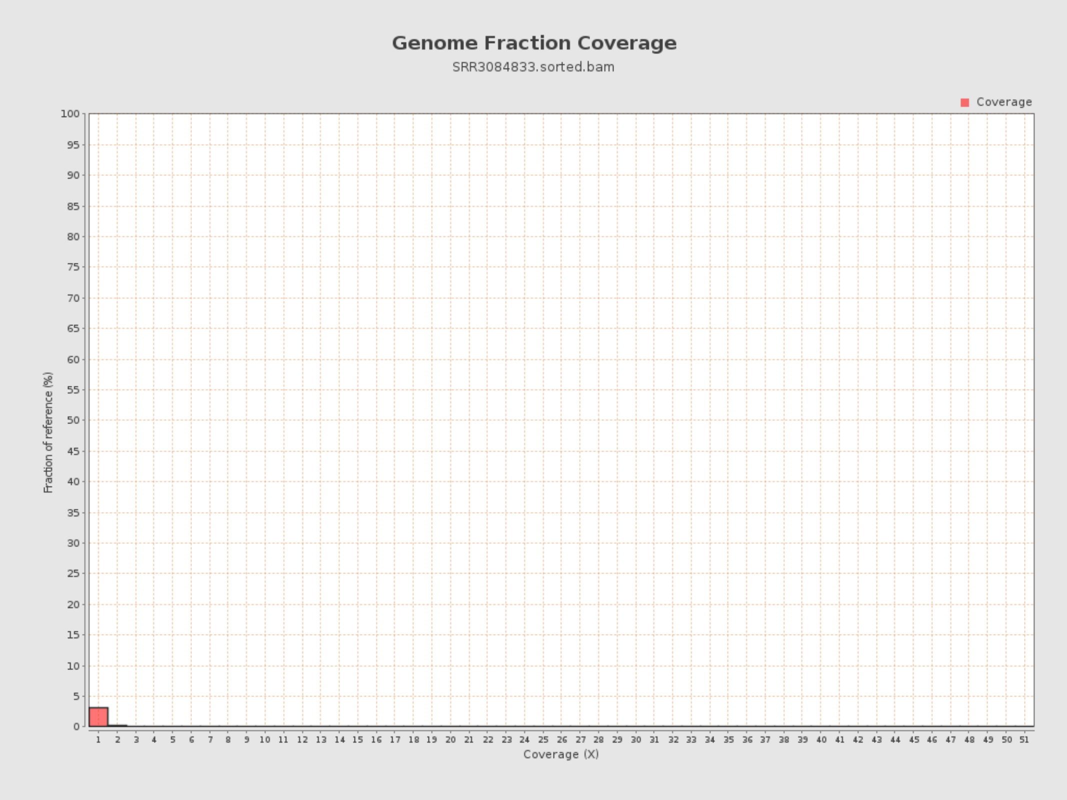
4. Results : Coverage Histogram



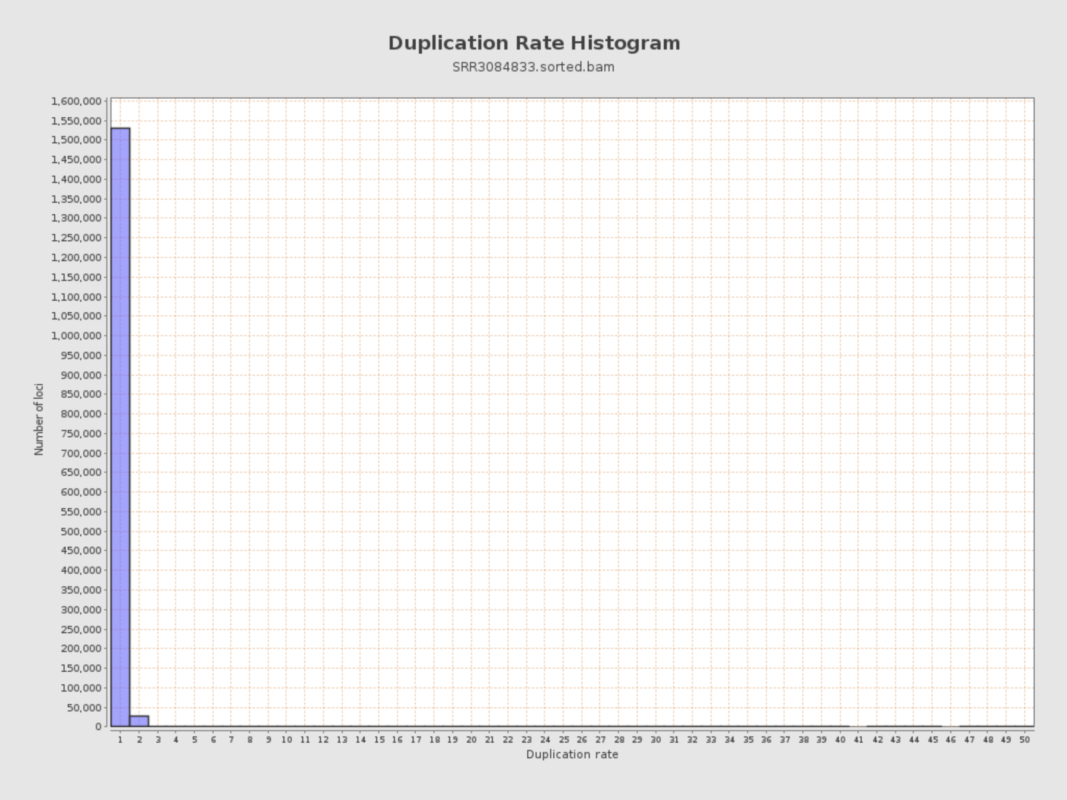
5. Results : Coverage Histogram (0-50X)



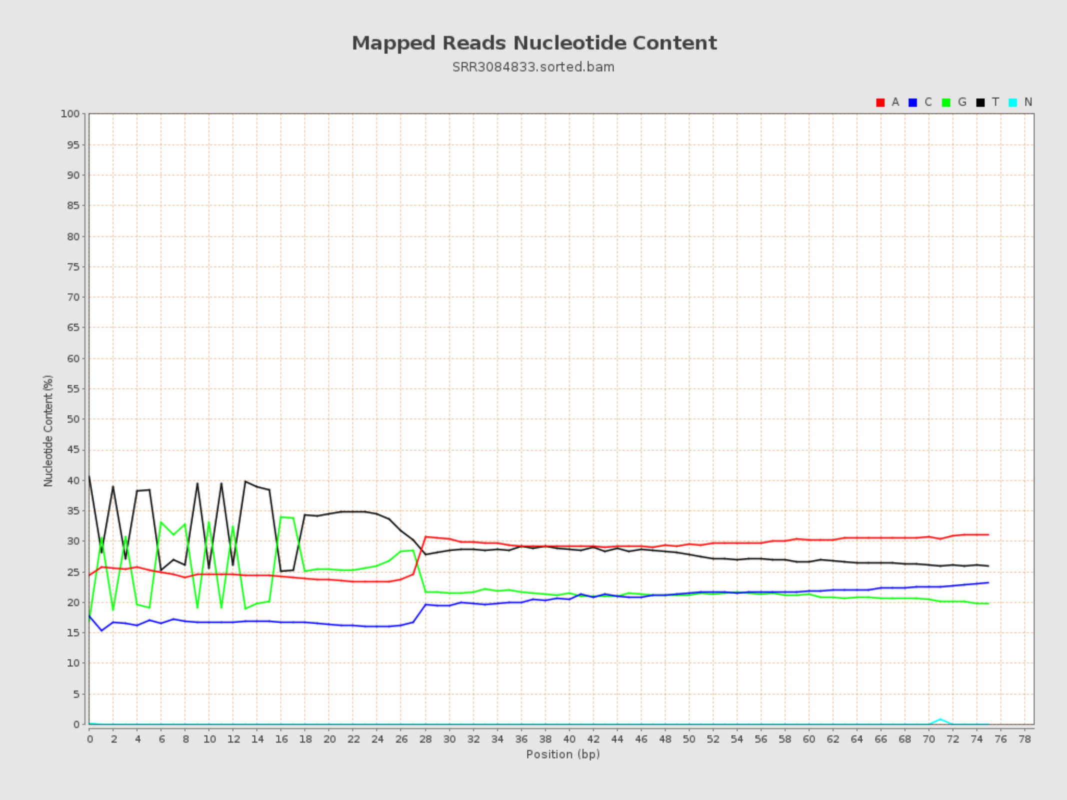
6. Results : Genome Fraction Coverage



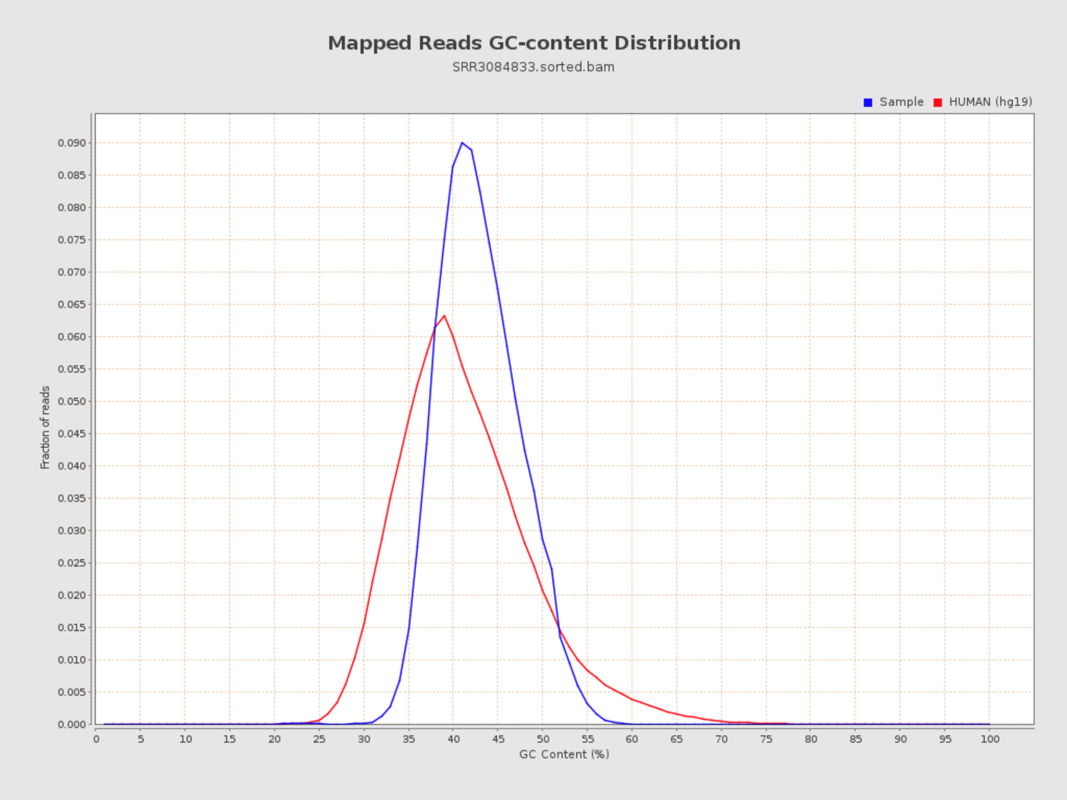
7. Results : Duplication Rate Histogram



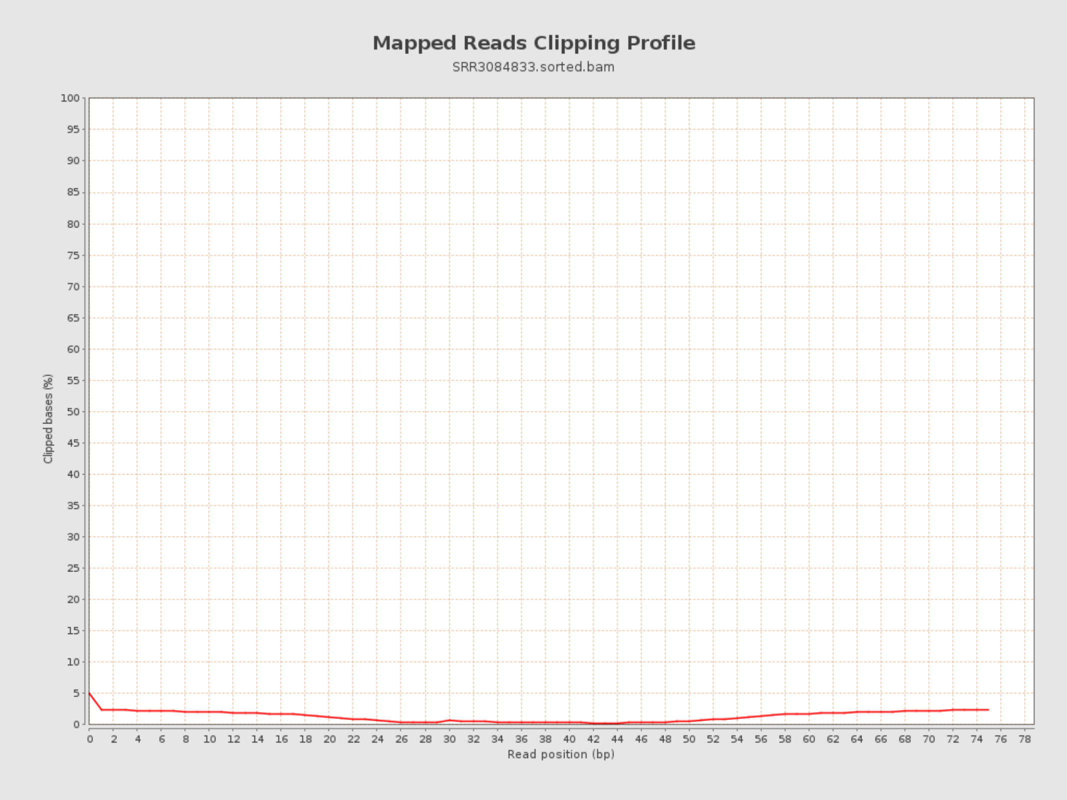
8. Results : Mapped Reads Nucleotide Content



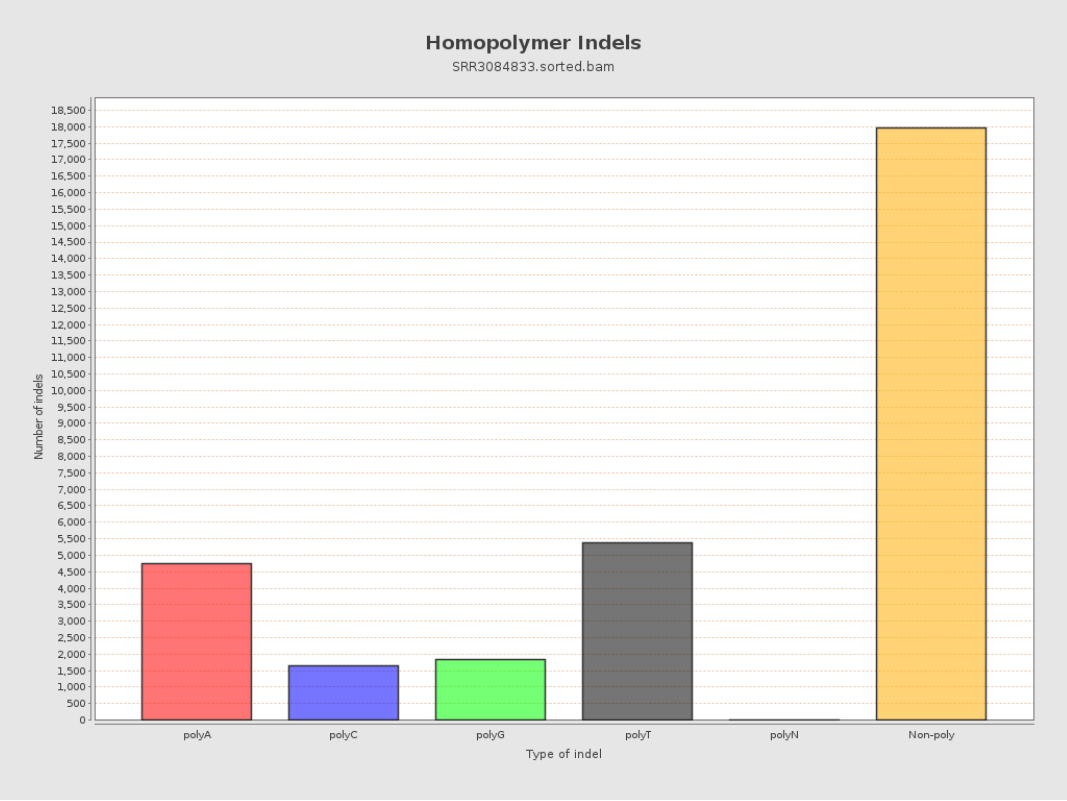
9. Results : Mapped Reads GC-content Distribution



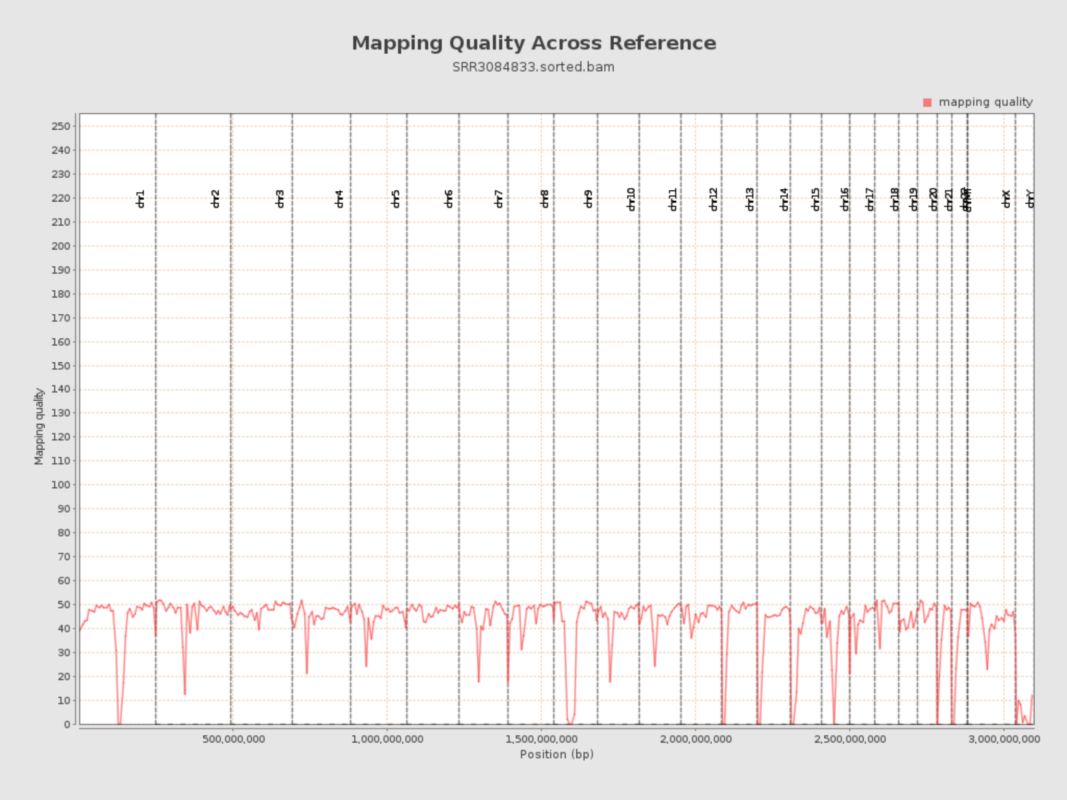
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram