Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 15:26:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082480.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_SRR3082480 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082480.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 15:26:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082480.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,693,385
Mapped reads	1,493,815 / 88.21%
Unmapped reads	199,570 / 11.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,637 / 0.69%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	44,831 / 2.65%
Duplication rate	2.38%
Clipped reads	615,887 / 36.37%

2.2. ACGT Content

Number/percentage of A's	29,111,247 / 28.66%
Number/percentage of C's	19,120,701 / 18.82%
Number/percentage of T's	30,866,300 / 30.38%
Number/percentage of G's	22,484,206 / 22.13%
Number/percentage of N's	2,022 / 0%
GC Percentage	40.96%

2.3. Coverage

Mean	0.0328

Standard Deviation	0.2822

2.4. Mapping Quality

Mean Mapping Quality	46.14

2.5. Mismatches and indels

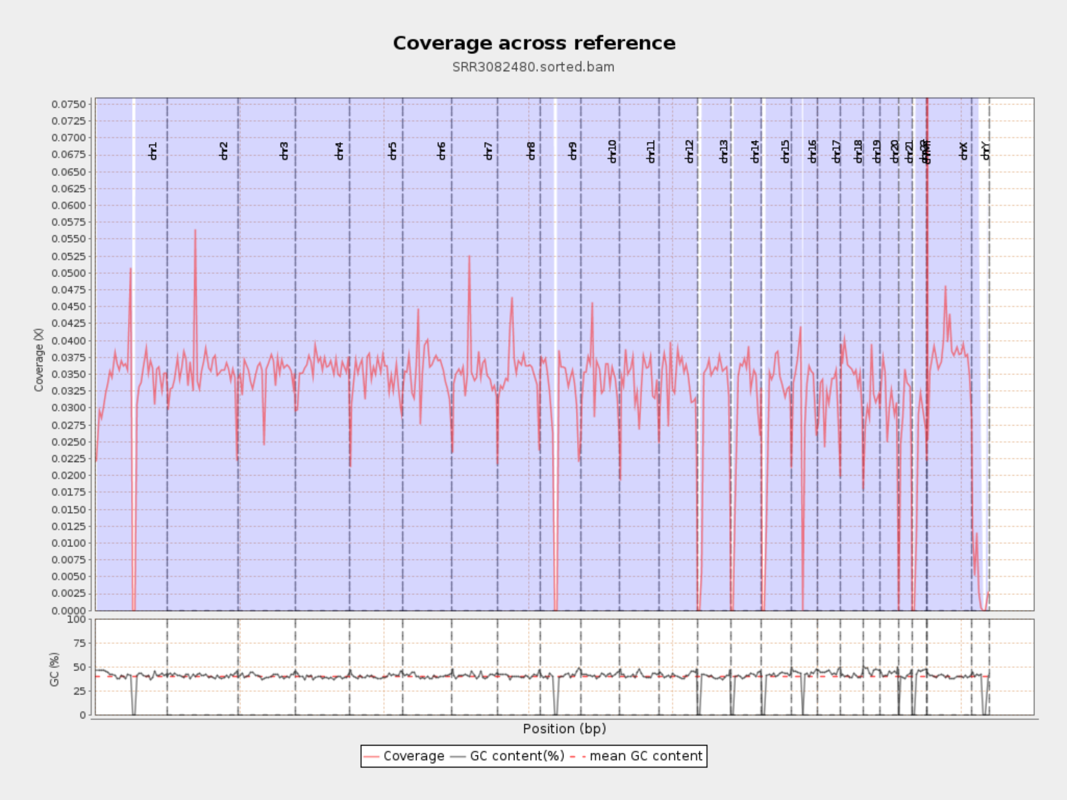
General error rate	0.85%
Mismatches	850,703
Insertions	8,203
Mapped reads with at least one insertion	0.54%
Deletions	21,750
Mapped reads with at least one deletion	1.44%
Homopolymer indels	47.03%

2.6. Chromosome stats

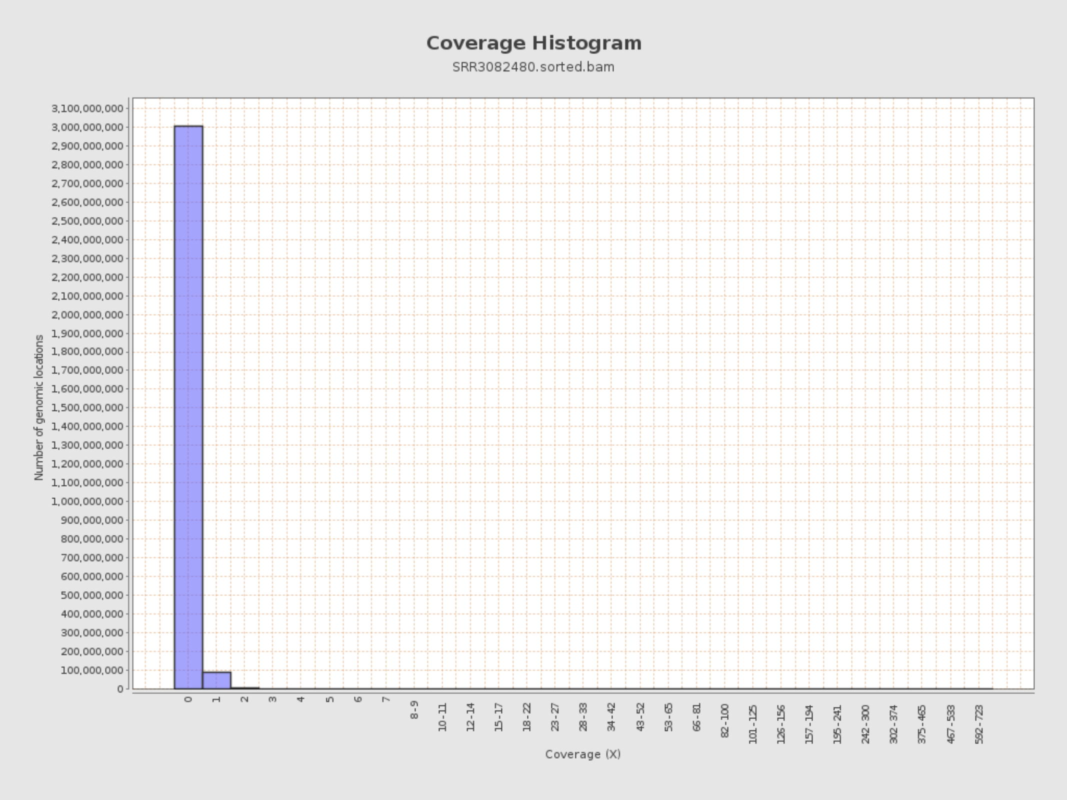
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8086960	0.0324	0.4554
chr2	243199373	8693866	0.0357	0.3257
chr3	198022430	6954985	0.0351	0.2015
chr4	191154276	6853543	0.0359	0.2071
chr5	180915260	6312307	0.0349	0.2017
chr6	171115067	6069305	0.0355	0.226
chr7	159138663	5613020	0.0353	0.339

chr8	146364022	5213793	0.0356	0.4752
chr9	141213431	4248536	0.0301	0.2576
chr10	135534747	4709799	0.0347	0.2603
chr11	135006516	4577133	0.0339	0.2381
chr12	133851895	4576823	0.0342	0.2009
chr13	115169878	3392679	0.0295	0.1842
chr14	107349540	3079213	0.0287	0.1896
chr15	102531392	2869408	0.028	0.1804
chr16	90354753	2761435	0.0306	0.2035
chr17	81195210	2516531	0.031	0.1984
chr18	78077248	2787093	0.0357	0.4305
chr19	59128983	1822137	0.0308	0.3617
chr20	63025520	1945388	0.0309	0.1911
chr21	48129895	1328659	0.0276	0.1847
chr22	51304566	1043737	0.0203	0.1528
chrMT	16571	22543	1.3604	1.3888
chrX	155270560	5904613	0.038	0.2244
chrY	59373566	236319	0.004	0.0889

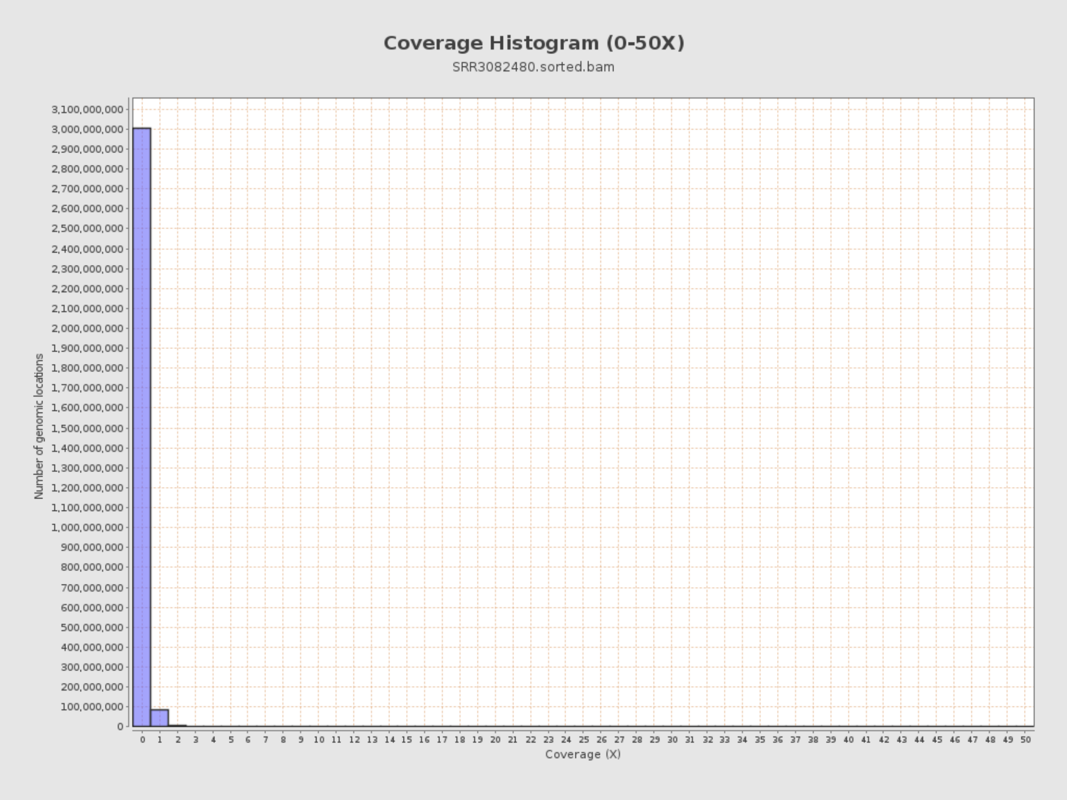
3. Results : Coverage across reference



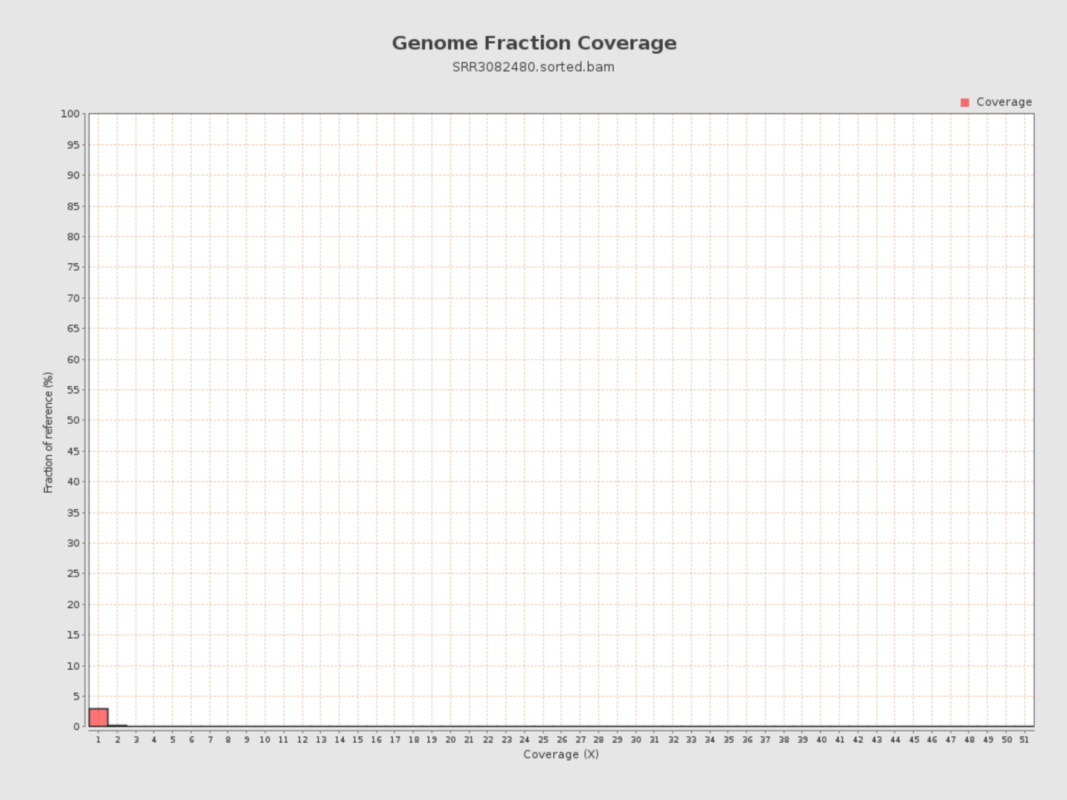
4. Results : Coverage Histogram



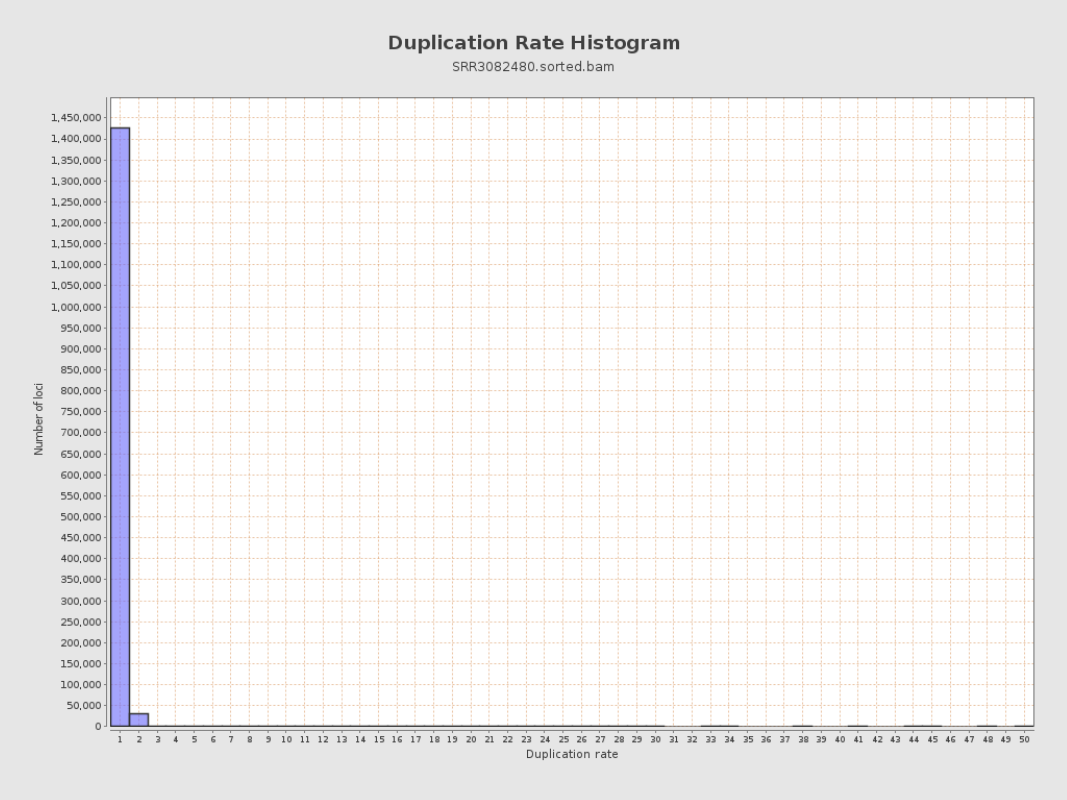
5. Results : Coverage Histogram (0-50X)



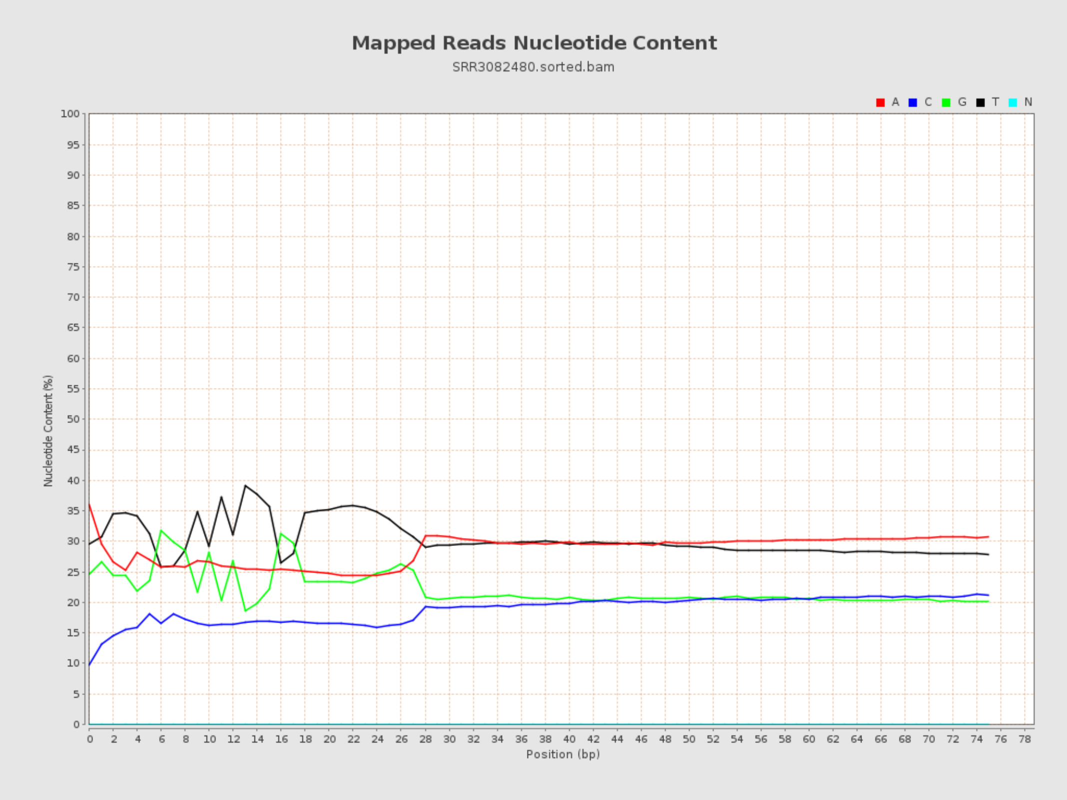
6. Results : Genome Fraction Coverage



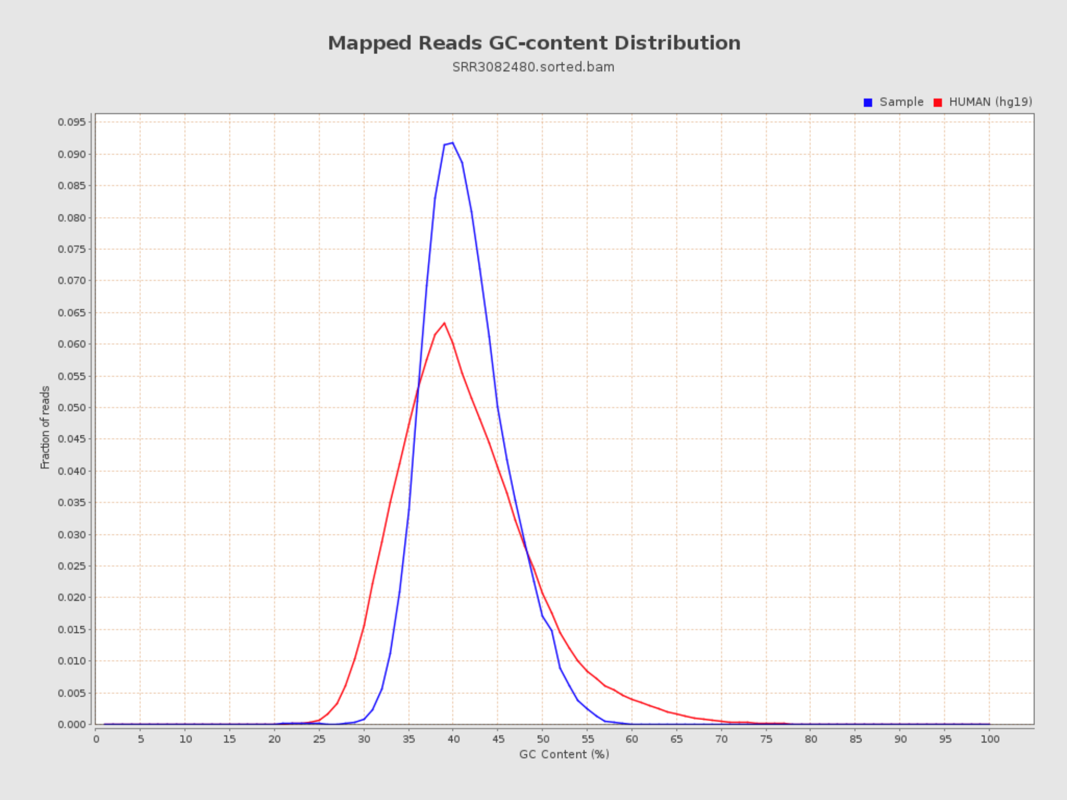
7. Results : Duplication Rate Histogram



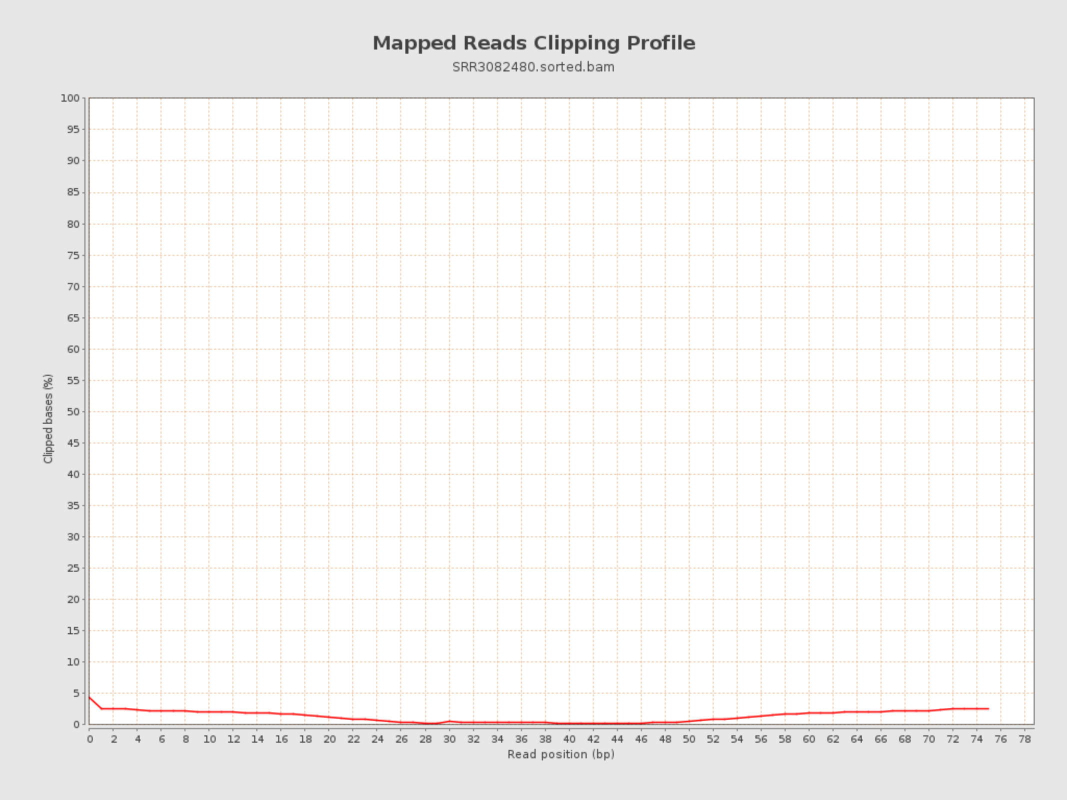
8. Results : Mapped Reads Nucleotide Content



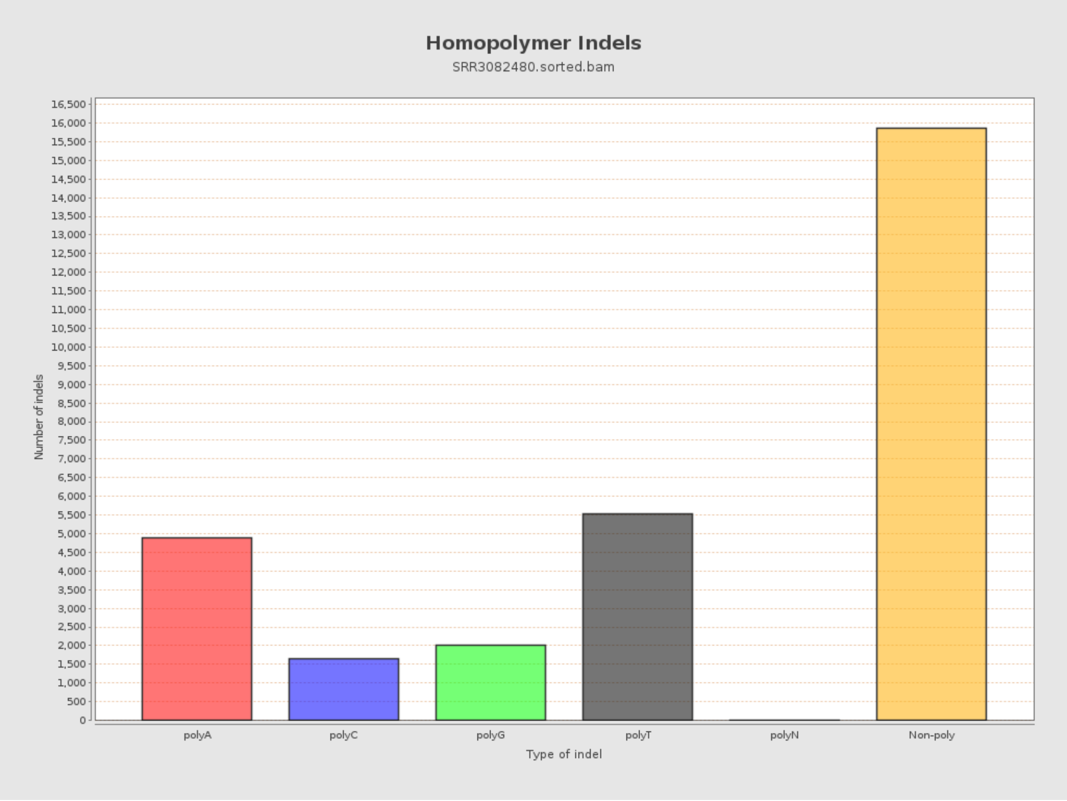
9. Results : Mapped Reads GC-content Distribution



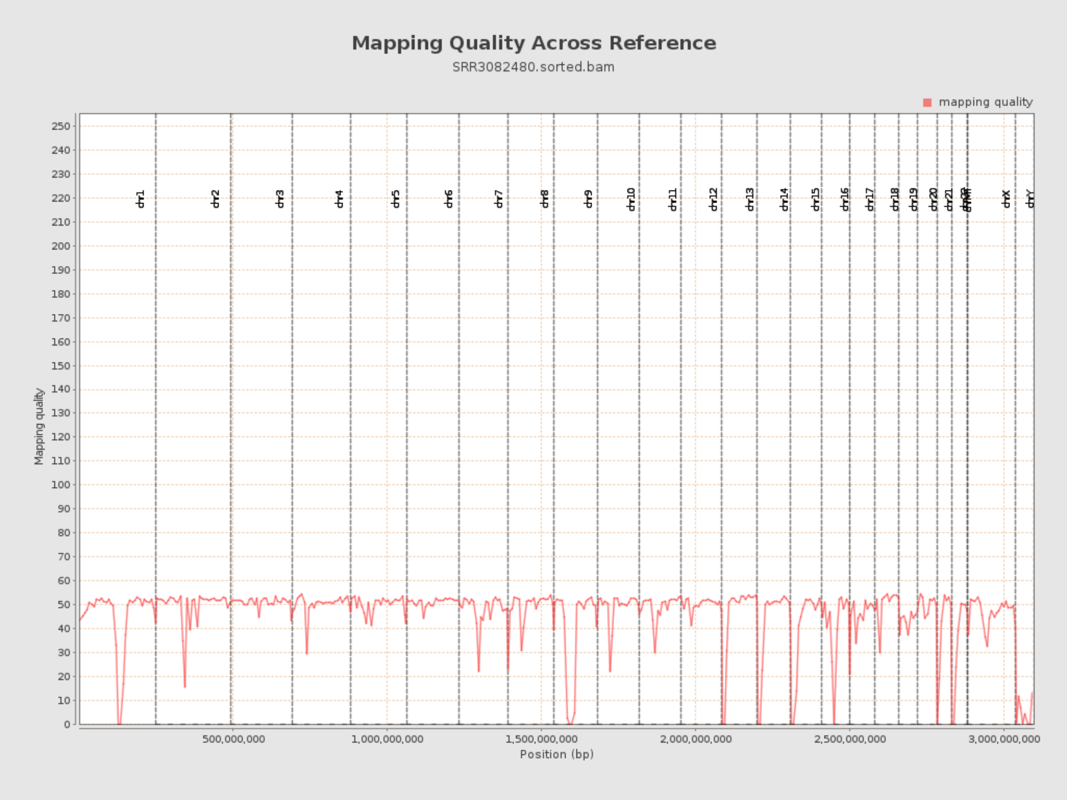
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram