Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 09:53:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081918.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_SRR3081918 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081918.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 09:53:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081918.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,870,559
Mapped reads	1,723,394 / 92.13%
Unmapped reads	147,165 / 7.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,661 / 0.73%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	56,811 / 3.04%
Duplication rate	2.29%
Clipped reads	724,840 / 38.75%

2.2. ACGT Content

Number/percentage of A's	32,448,530 / 27.85%
Number/percentage of C's	22,242,276 / 19.09%
Number/percentage of T's	35,630,377 / 30.58%
Number/percentage of G's	26,205,976 / 22.49%
Number/percentage of N's	1,304 / 0%
GC Percentage	41.58%

2.3. Coverage

Mean	0.0377

Standard Deviation	0.3639

2.4. Mapping Quality

Mean Mapping Quality	44.41

2.5. Mismatches and indels

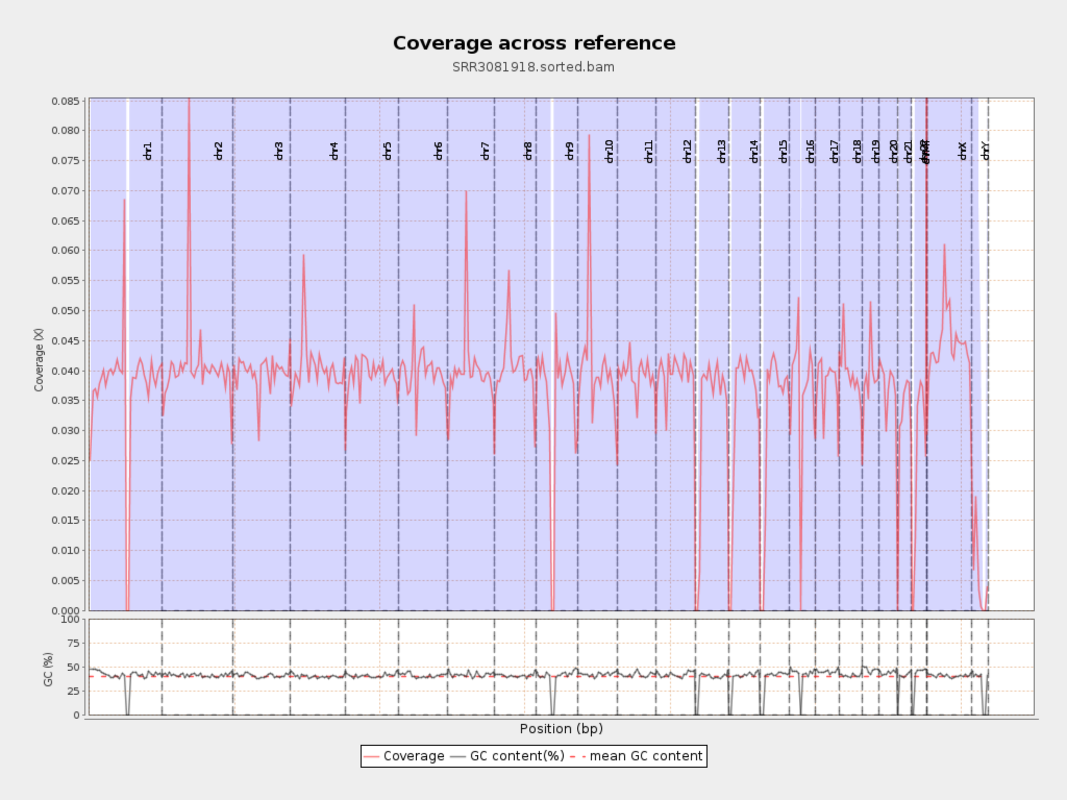
General error rate	0.88%
Mismatches	1,008,445
Insertions	9,849
Mapped reads with at least one insertion	0.57%
Deletions	27,017
Mapped reads with at least one deletion	1.55%
Homopolymer indels	45.86%

2.6. Chromosome stats

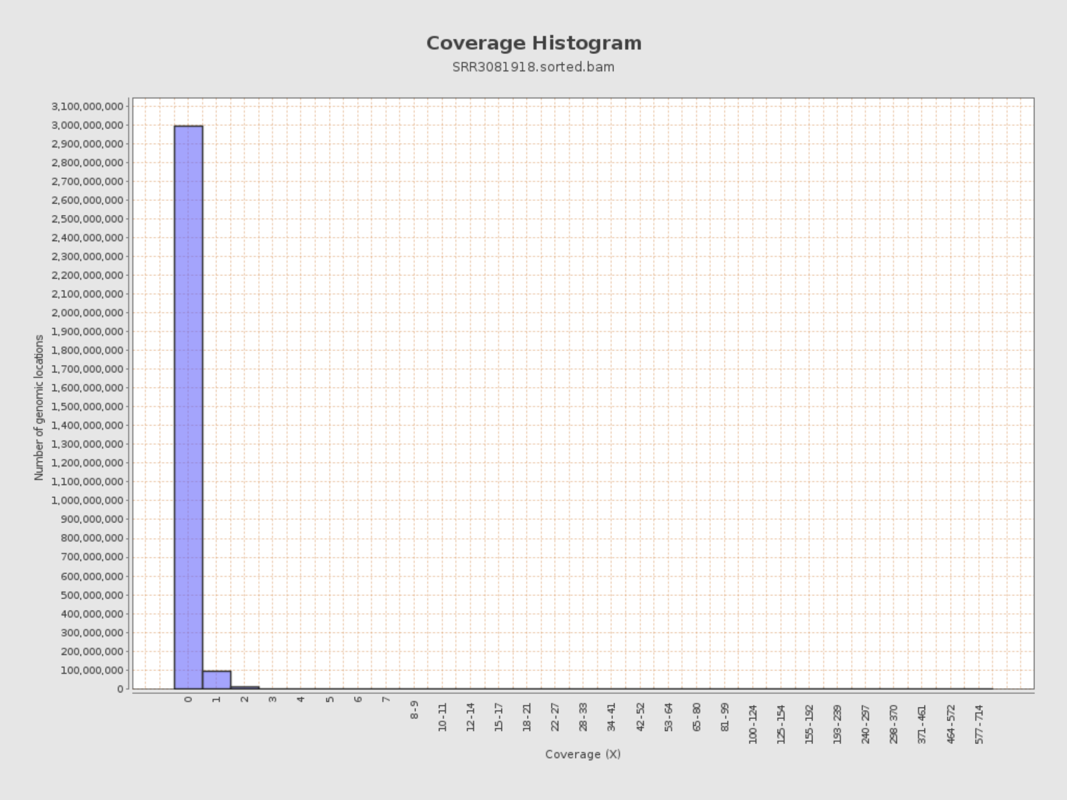
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9250872	0.0371	0.6447
chr2	243199373	9988778	0.0411	0.4674
chr3	198022430	7830816	0.0395	0.22
chr4	191154276	7727745	0.0404	0.2503
chr5	180915260	7135768	0.0394	0.2173
chr6	171115067	6792234	0.0397	0.2527
chr7	159138663	6454584	0.0406	0.502

chr8	146364022	5924201	0.0405	0.3965
chr9	141213431	4910718	0.0348	0.346
chr10	135534747	5528866	0.0408	0.3966
chr11	135006516	5271841	0.039	0.3101
chr12	133851895	5271963	0.0394	0.2182
chr13	115169878	3669666	0.0319	0.1934
chr14	107349540	3514557	0.0327	0.2207
chr15	102531392	3254097	0.0317	0.1992
chr16	90354753	3289546	0.0364	0.249
chr17	81195210	3041374	0.0375	0.2343
chr18	78077248	3115952	0.0399	0.6634
chr19	59128983	2321813	0.0393	0.4968
chr20	63025520	2328497	0.0369	0.2214
chr21	48129895	1493328	0.031	0.2159
chr22	51304566	1235973	0.0241	0.1693
chrMT	16571	1955	0.118	0.3383
chrX	155270560	6880995	0.0443	0.2616
chrY	59373566	337391	0.0057	0.1568

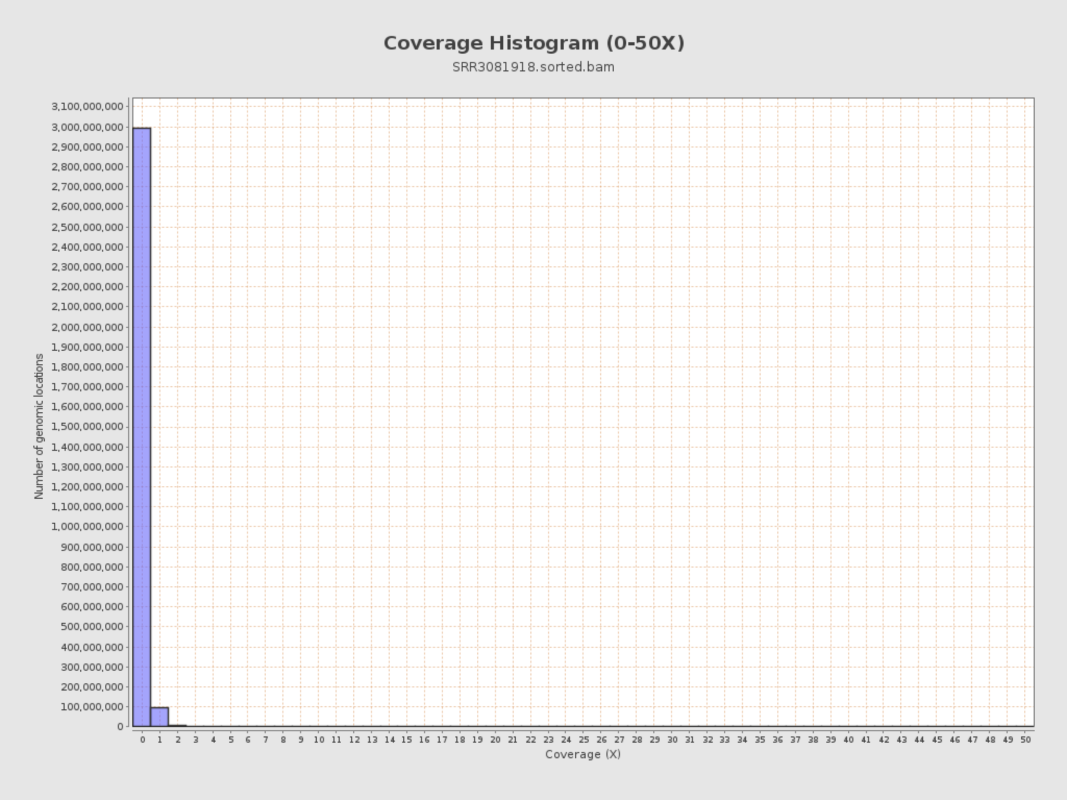
3. Results : Coverage across reference



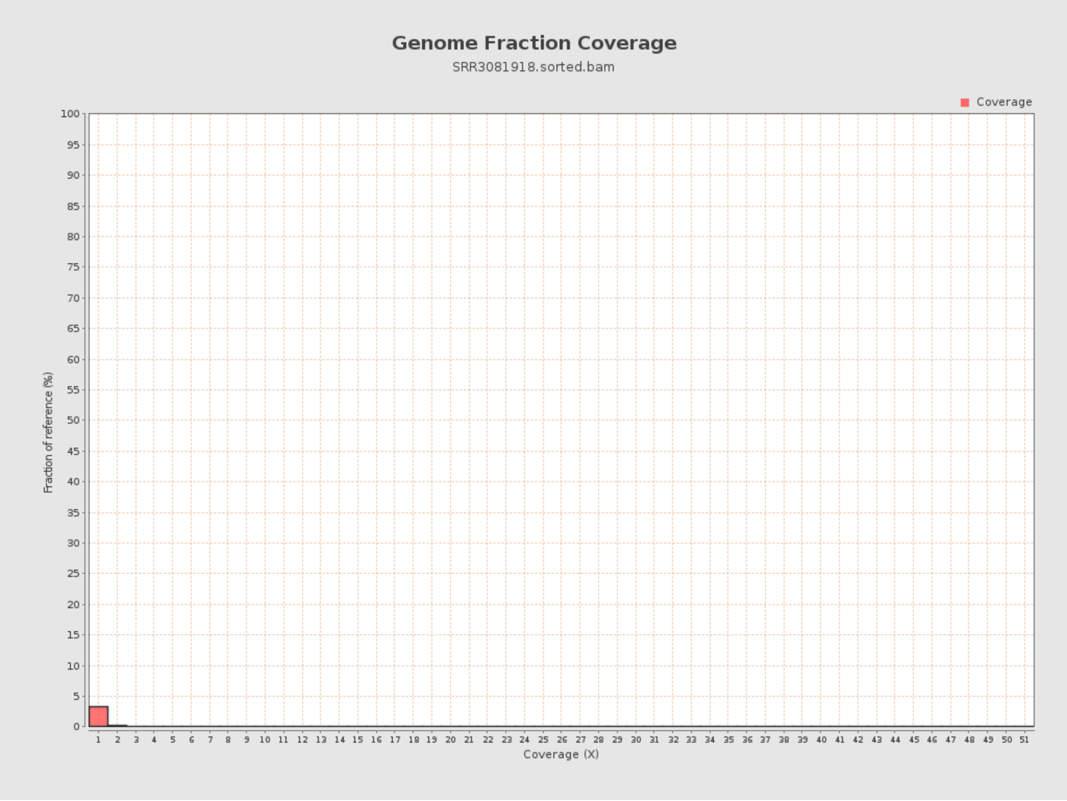
4. Results : Coverage Histogram



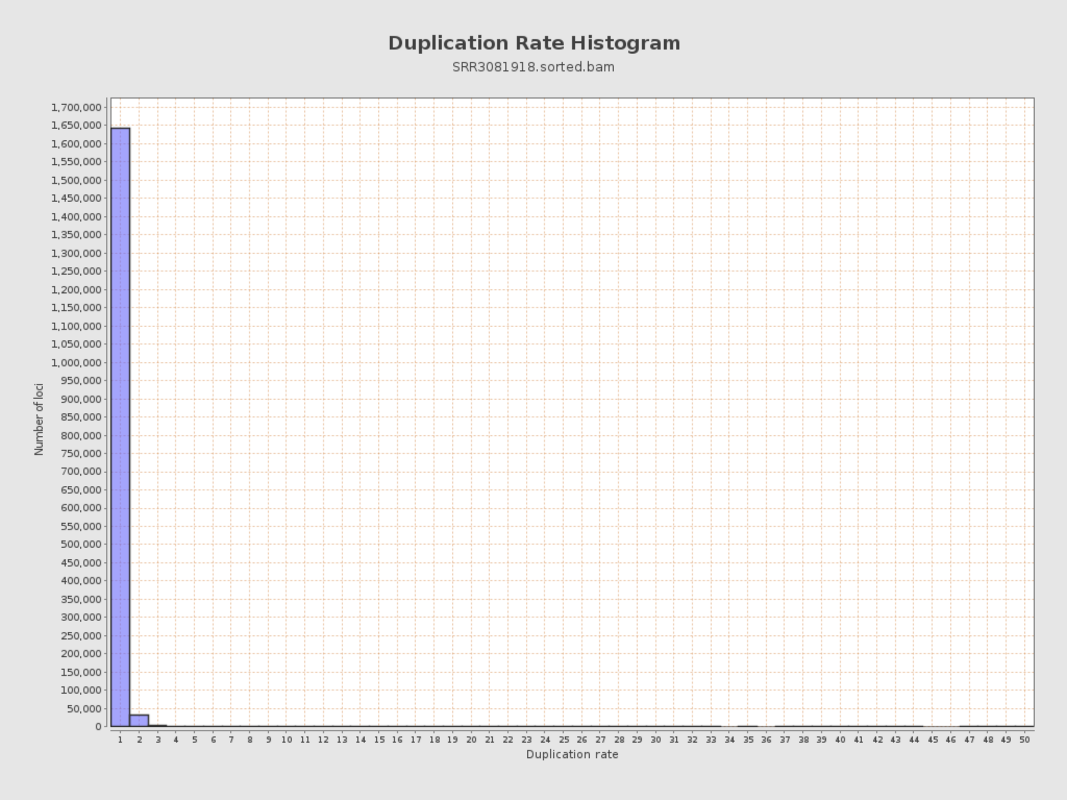
5. Results : Coverage Histogram (0-50X)



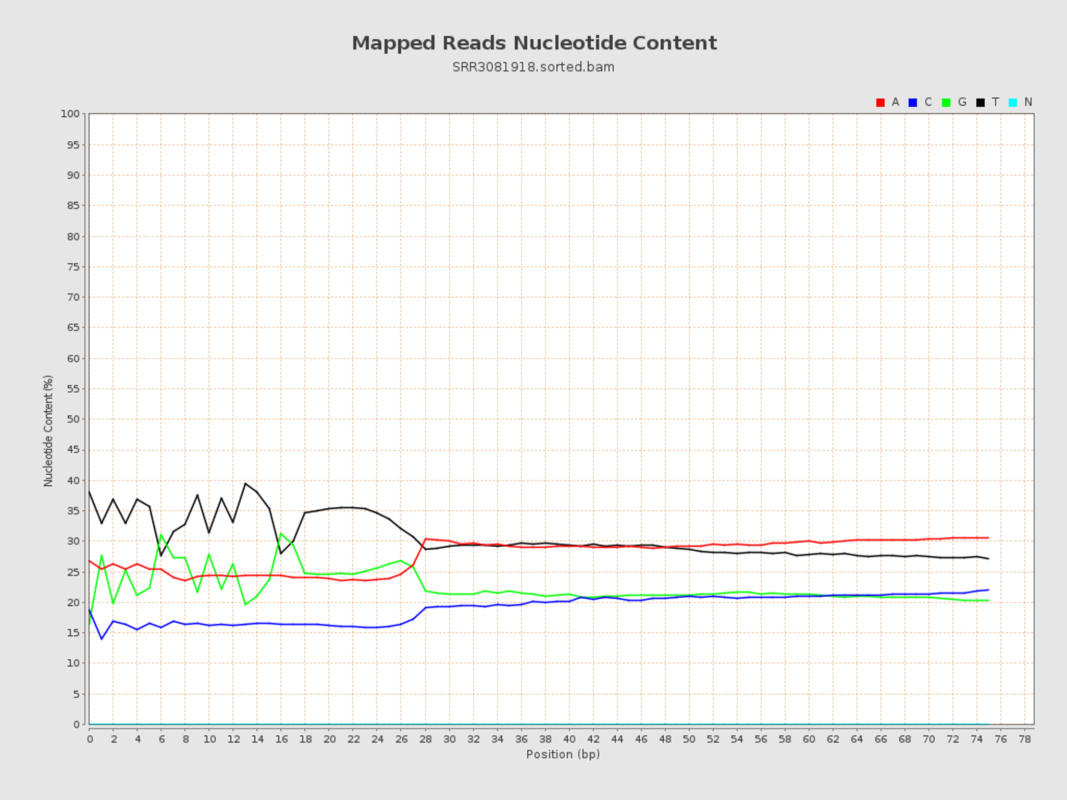
6. Results : Genome Fraction Coverage



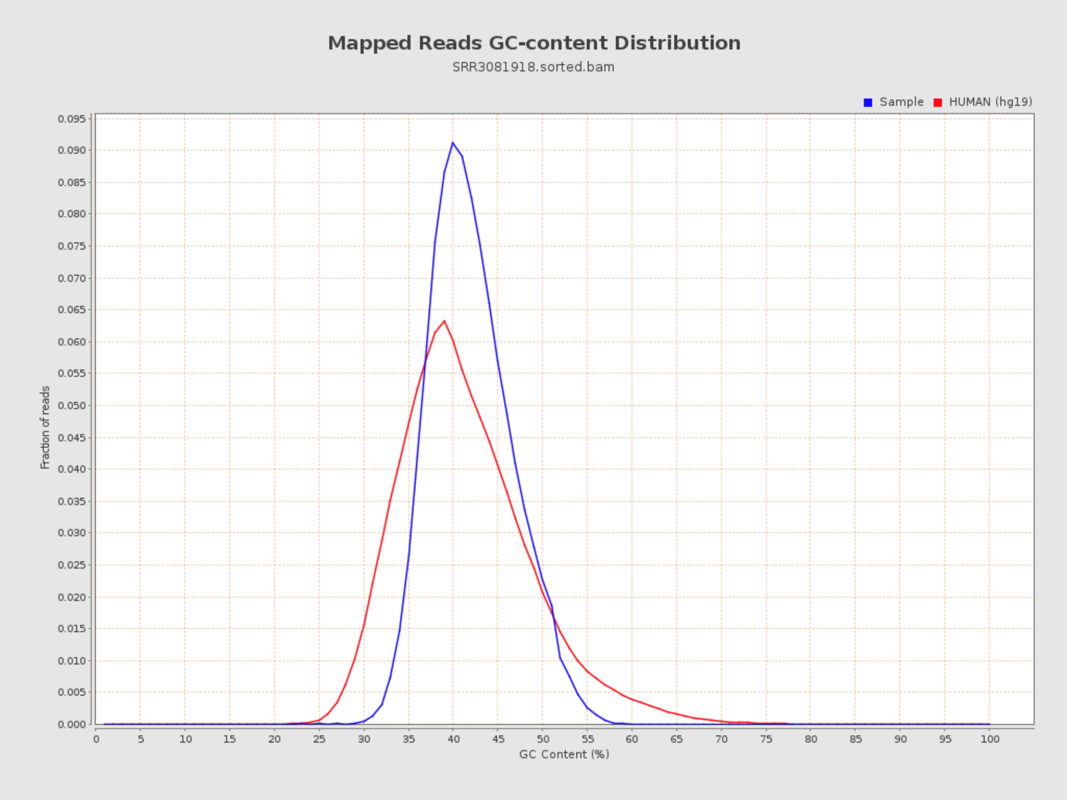
7. Results : Duplication Rate Histogram



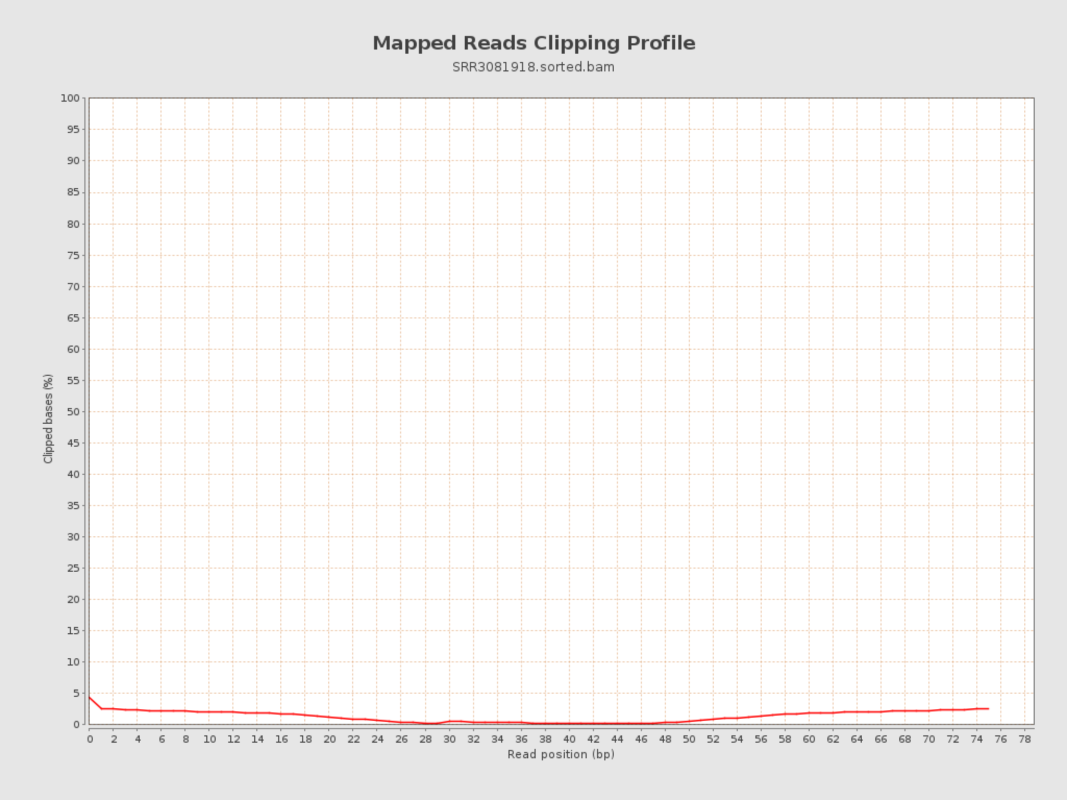
8. Results : Mapped Reads Nucleotide Content



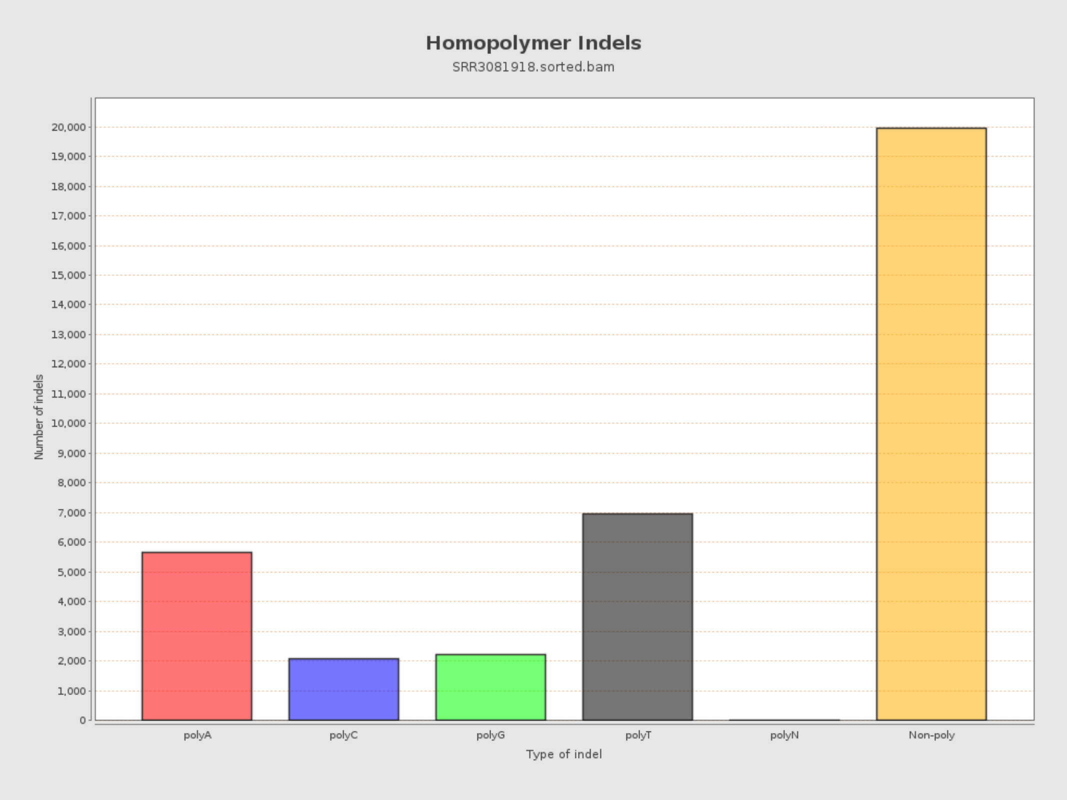
9. Results : Mapped Reads GC-content Distribution



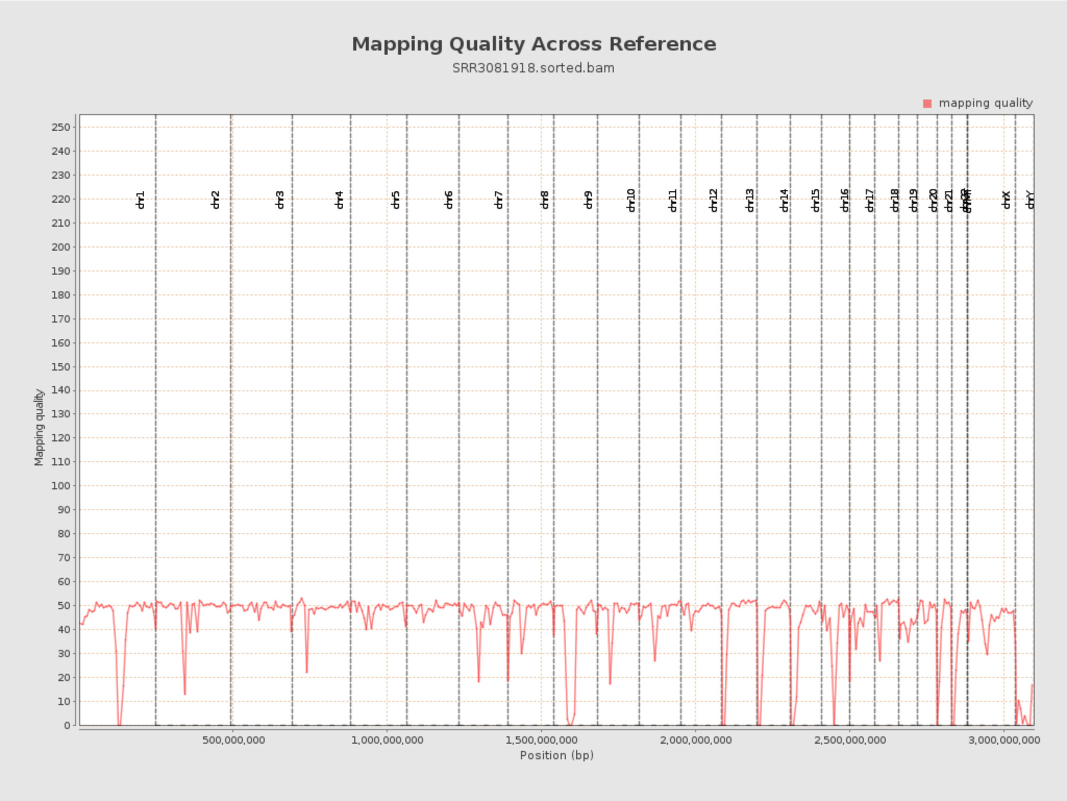
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram