Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 12:11:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818971.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_SRR1818971 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818971.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 12:11:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818971.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,911,341
Mapped reads	2,827,837 / 97.13%
Unmapped reads	83,504 / 2.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	42,479 / 1.46%
Read min/max/mean length	30 / 101 / 101.56
Duplicated reads (estimated)	1,542,175 / 52.97%
Duplication rate	45.15%
Clipped reads	2,850,788 / 97.92%

2.2. ACGT Content

Number/percentage of A's	75,439,188 / 28.82%
Number/percentage of C's	55,945,302 / 21.38%
Number/percentage of T's	76,936,417 / 29.4%
Number/percentage of G's	53,381,324 / 20.4%
Number/percentage of N's	13,270 / 0.01%
GC Percentage	41.77%

2.3. Coverage

Mean	0.0846

Standard Deviation	0.9688

2.4. Mapping Quality

Mean Mapping Quality	49.08

2.5. Mismatches and indels

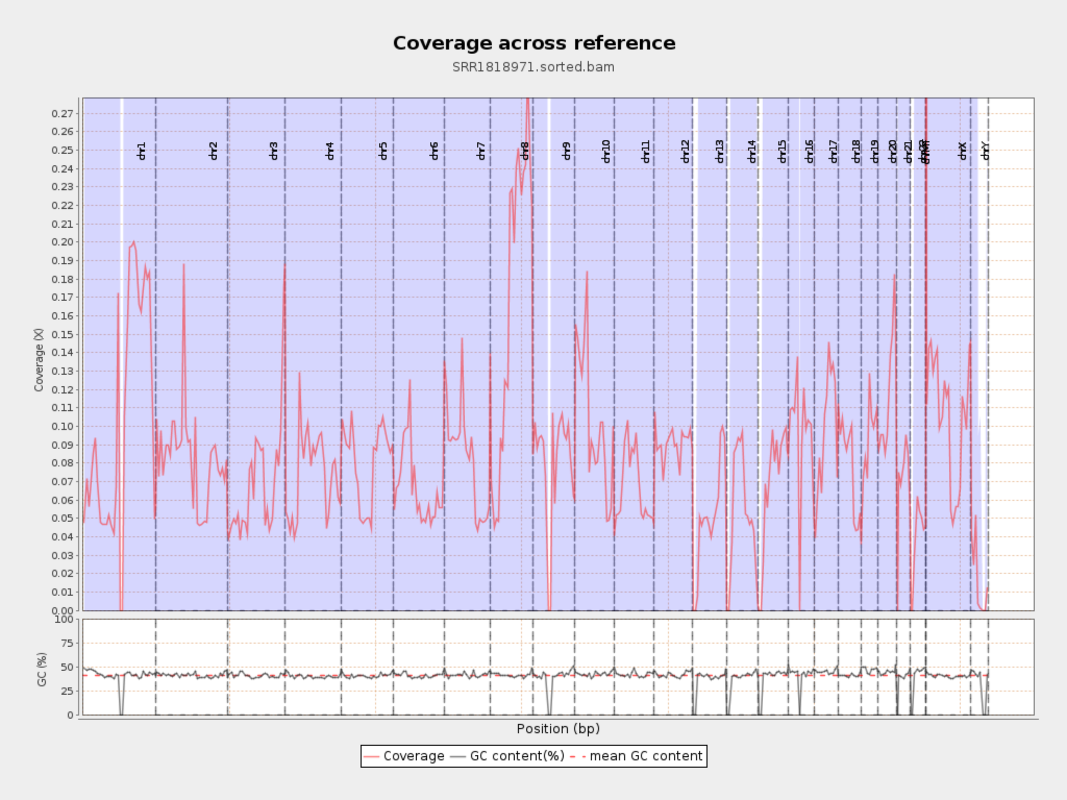
General error rate	0.66%
Mismatches	1,644,073
Insertions	39,612
Mapped reads with at least one insertion	1.36%
Deletions	82,667
Mapped reads with at least one deletion	2.87%
Homopolymer indels	42.27%

2.6. Chromosome stats

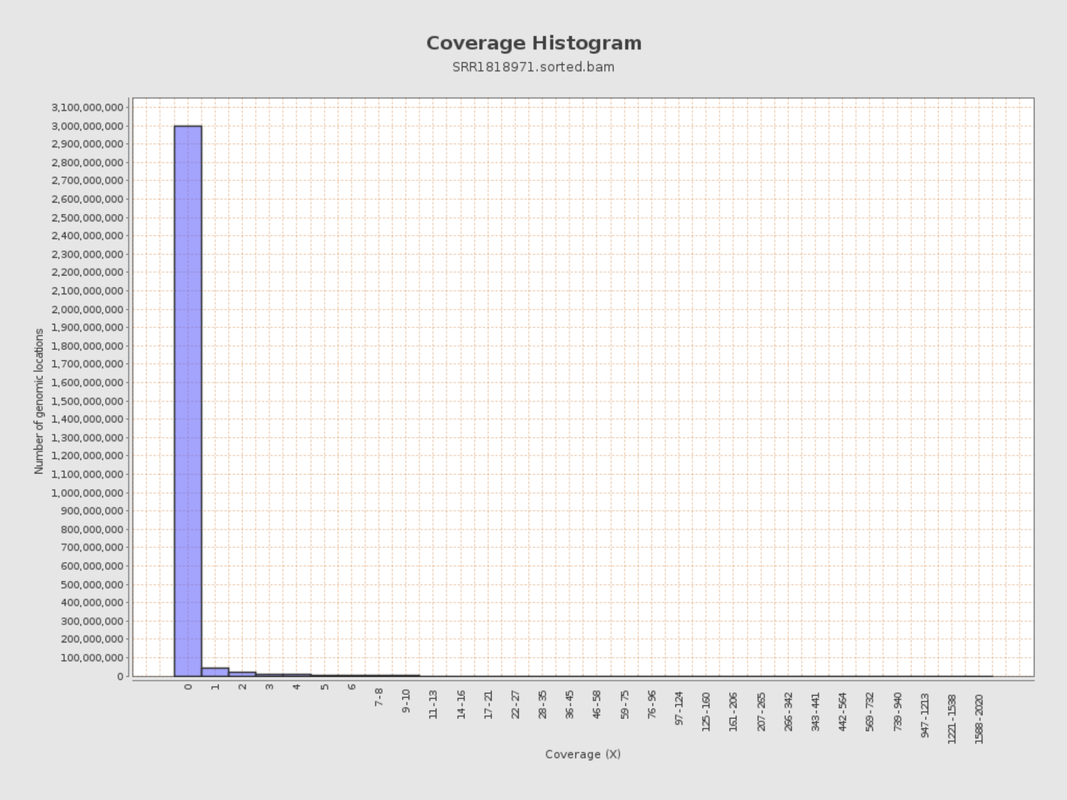
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	25872262	0.1038	1.7954
chr2	243199373	20261973	0.0833	1.1357
chr3	198022430	13562895	0.0685	0.5593
chr4	191154276	14136832	0.074	0.6679
chr5	180915260	14646652	0.081	0.6178
chr6	171115067	11450989	0.0669	0.6768
chr7	159138663	13161517	0.0827	1.2675

chr8	146364022	25046254	0.1711	1.0004
chr9	141213431	11285765	0.0799	0.9291
chr10	135534747	13903628	0.1026	1.1175
chr11	135006516	9068052	0.0672	0.6757
chr12	133851895	12209712	0.0912	0.6694
chr13	115169878	5889686	0.0511	0.4837
chr14	107349540	5881978	0.0548	0.5134
chr15	102531392	6879792	0.0671	0.5562
chr16	90354753	8482144	0.0939	0.9234
chr17	81195210	8064696	0.0993	0.7821
chr18	78077248	6145617	0.0787	1.1016
chr19	59128983	5467477	0.0925	1.6321
chr20	63025520	7531304	0.1195	0.8228
chr21	48129895	3387554	0.0704	0.6317
chr22	51304566	1946696	0.0379	0.4555
chrMT	16571	63649	3.841	4.8853
chrX	155270560	16576532	0.1068	0.8059
chrY	59373566	942376	0.0159	0.7822

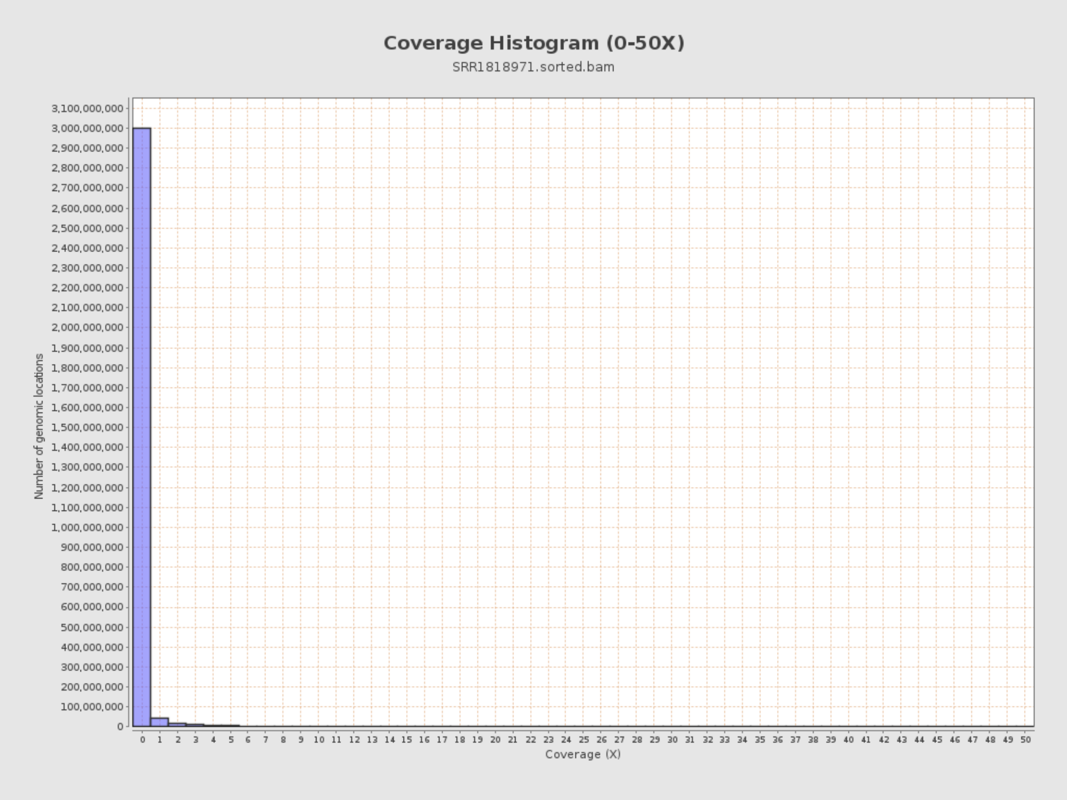
3. Results : Coverage across reference



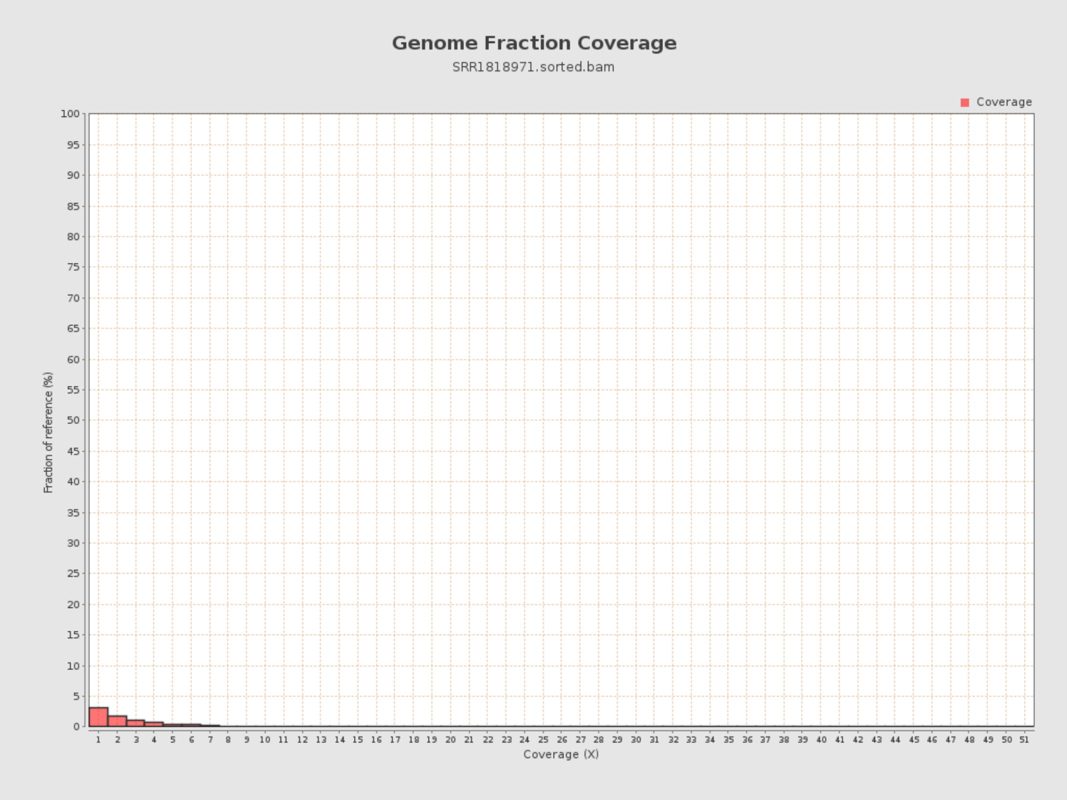
4. Results : Coverage Histogram



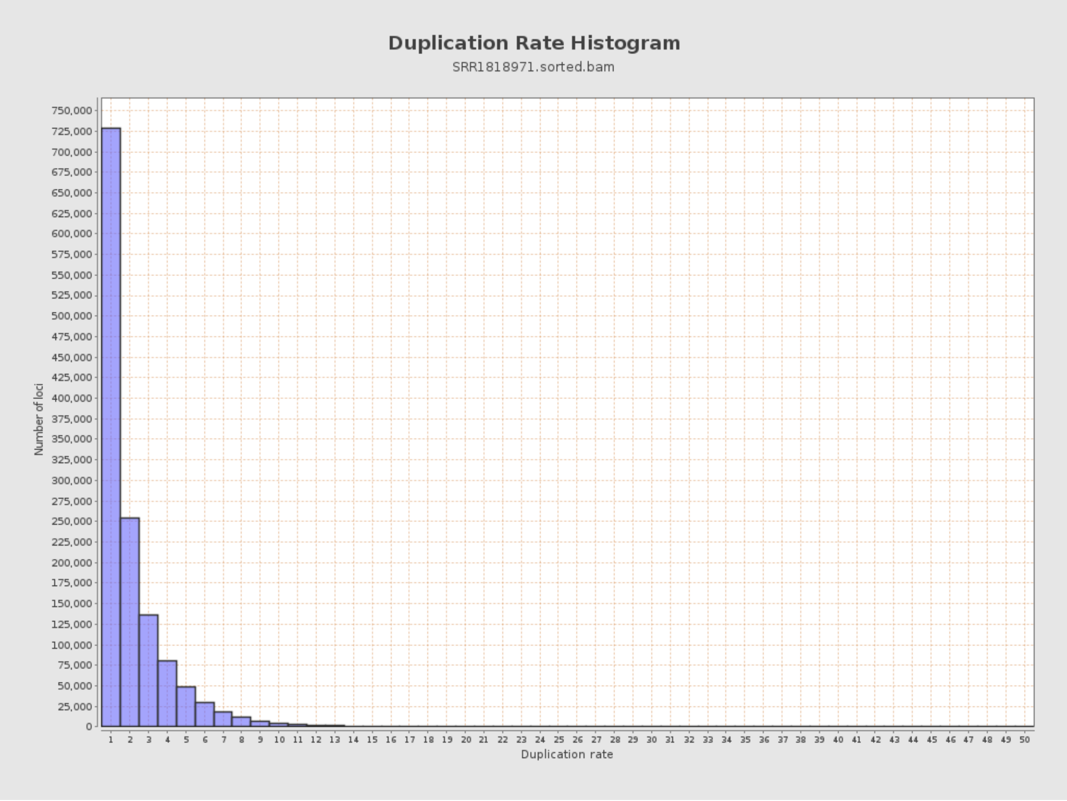
5. Results : Coverage Histogram (0-50X)



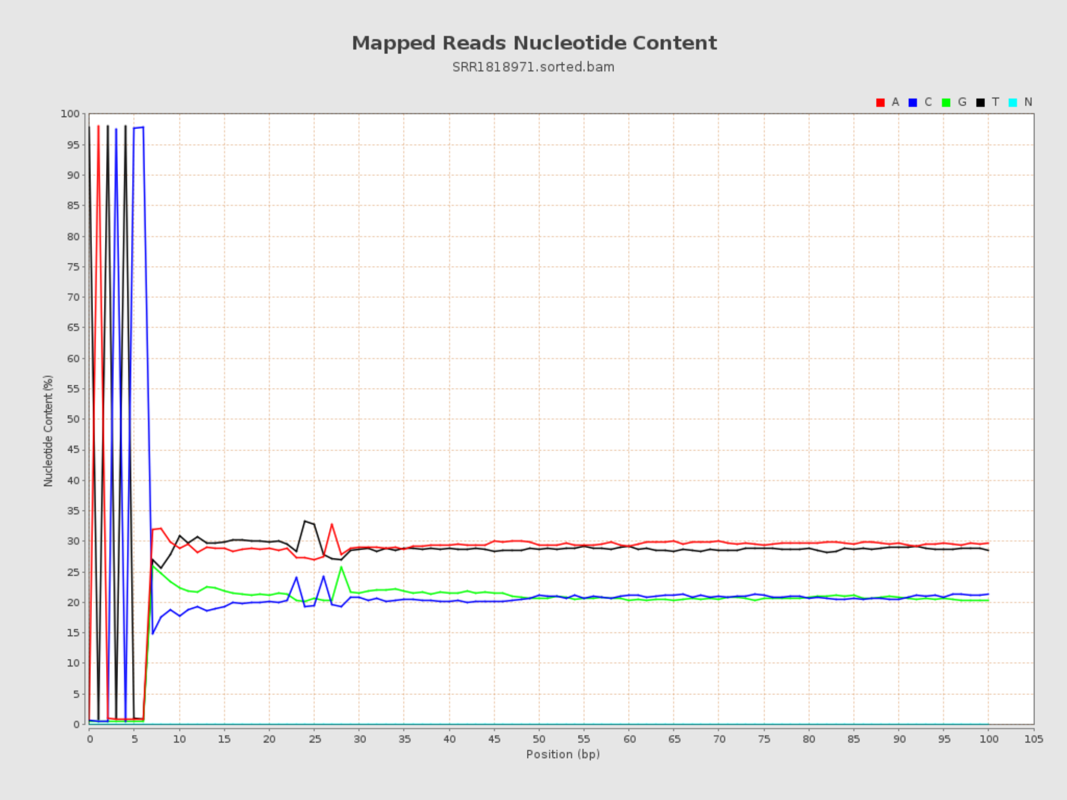
6. Results : Genome Fraction Coverage



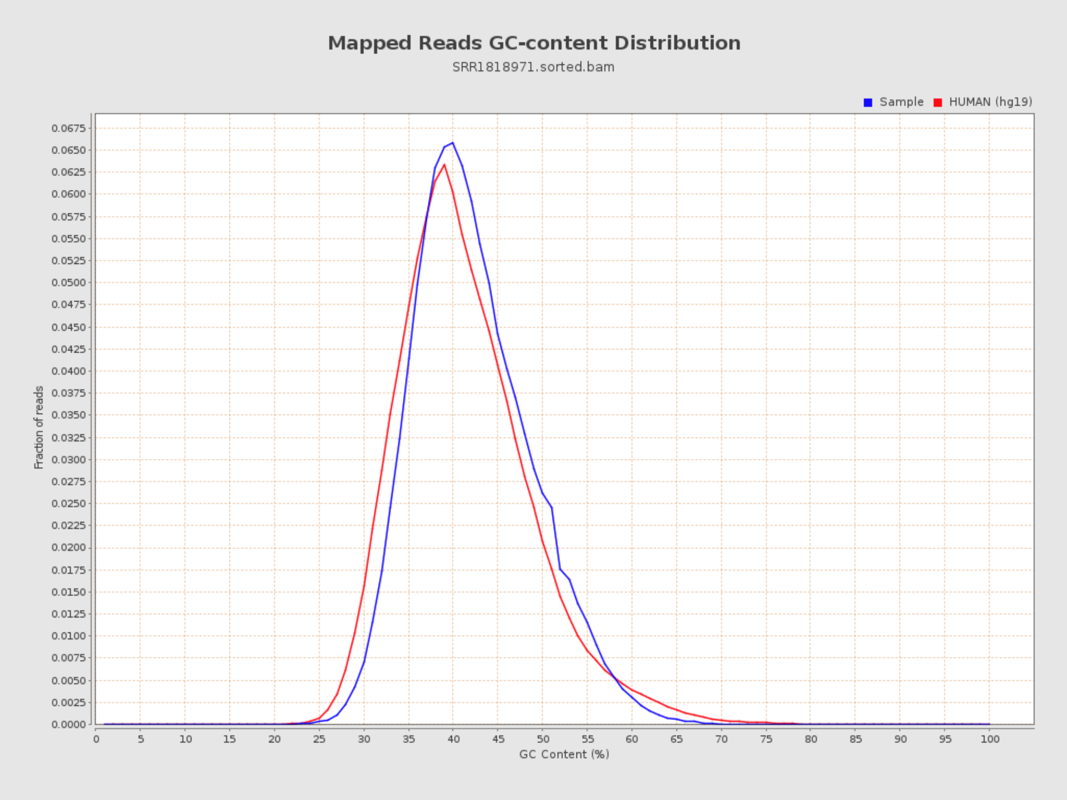
7. Results : Duplication Rate Histogram



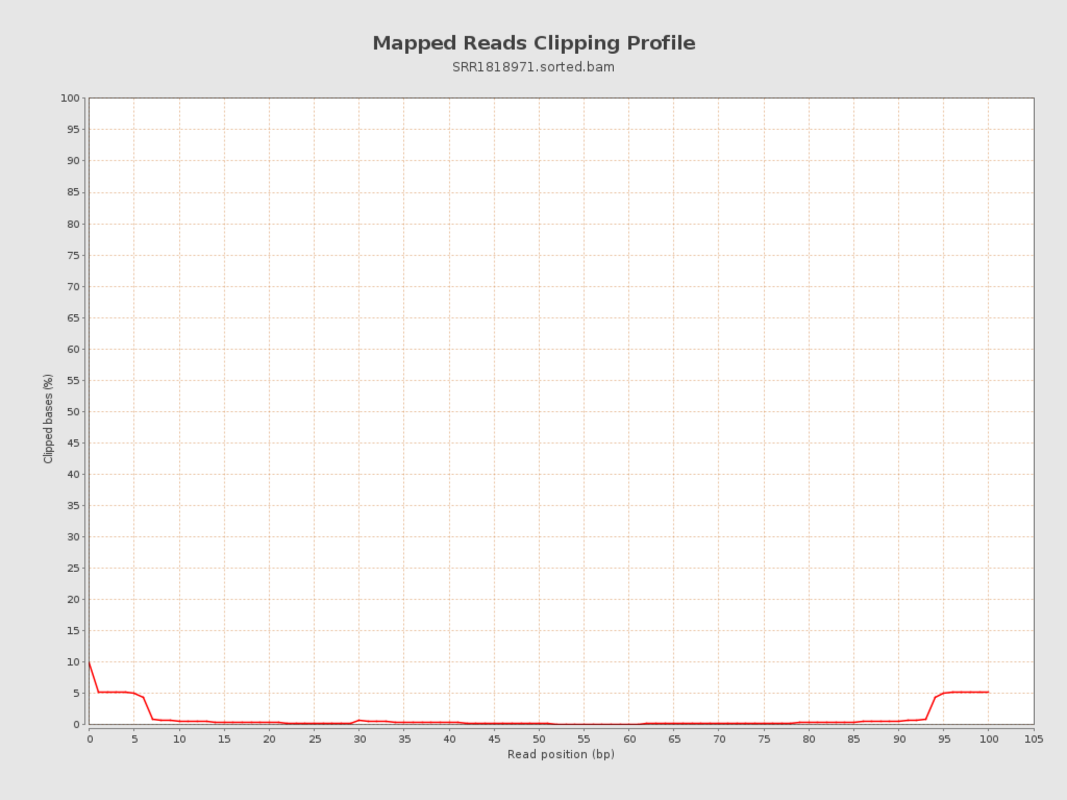
8. Results : Mapped Reads Nucleotide Content



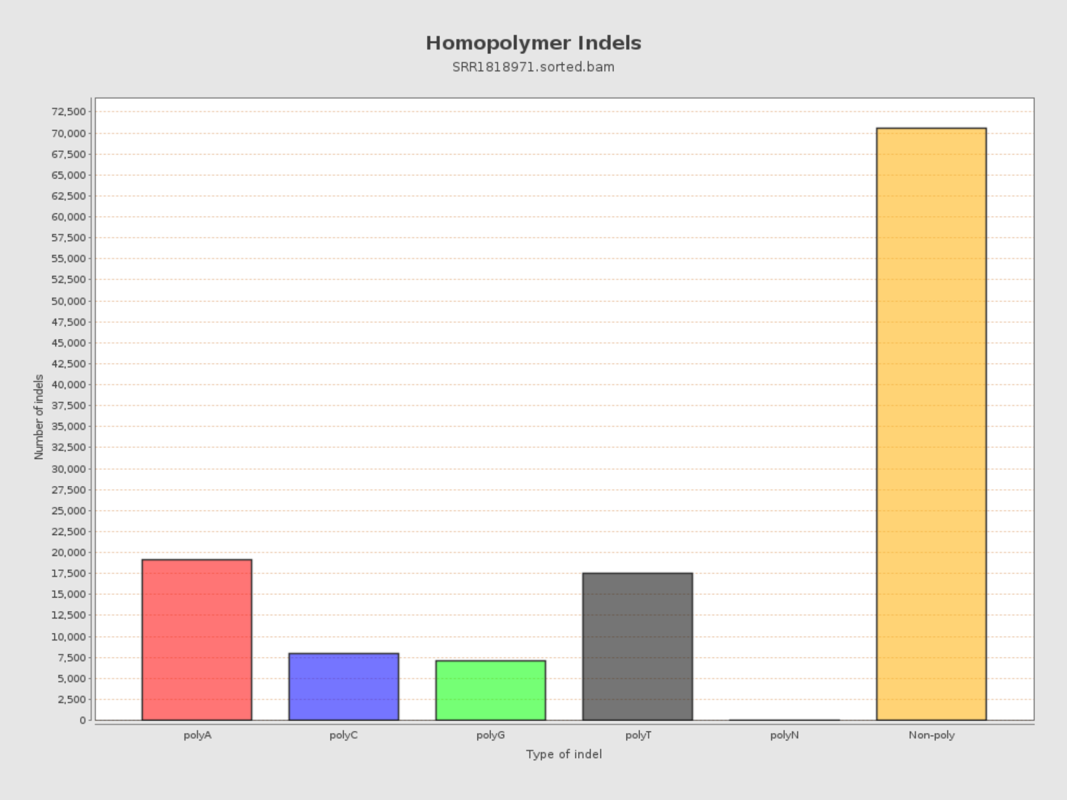
9. Results : Mapped Reads GC-content Distribution



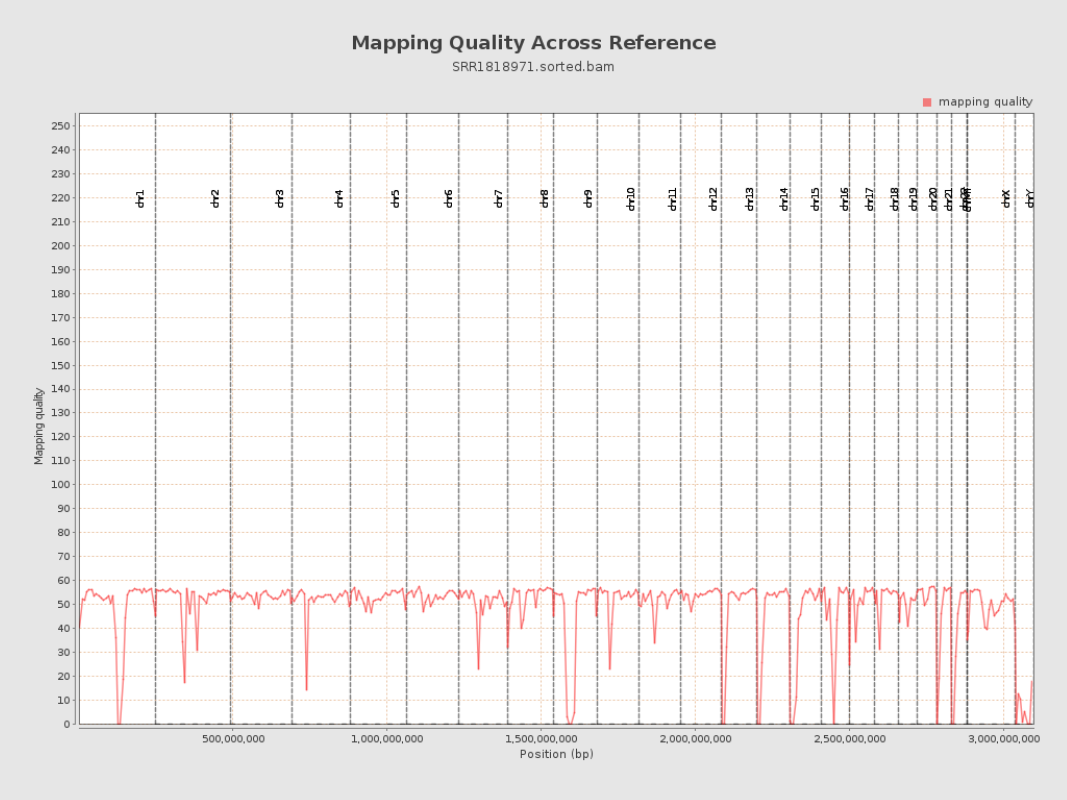
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram