Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 10:36:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818951.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_SRR1818951 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818951.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 10:36:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818951.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,731,536
Mapped reads	1,660,237 / 95.88%
Unmapped reads	71,299 / 4.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,000 / 1.27%
Read min/max/mean length	30 / 101 / 101.49
Duplicated reads (estimated)	585,651 / 33.82%
Duplication rate	30.08%
Clipped reads	1,673,530 / 96.65%

2.2. ACGT Content

Number/percentage of A's	44,948,605 / 29.28%
Number/percentage of C's	32,249,768 / 21.01%
Number/percentage of T's	44,358,338 / 28.9%
Number/percentage of G's	31,949,555 / 20.81%
Number/percentage of N's	6,355 / 0%
GC Percentage	41.82%

2.3. Coverage

Mean	0.0496

Standard Deviation	0.5758

2.4. Mapping Quality

Mean Mapping Quality	49.3

2.5. Mismatches and indels

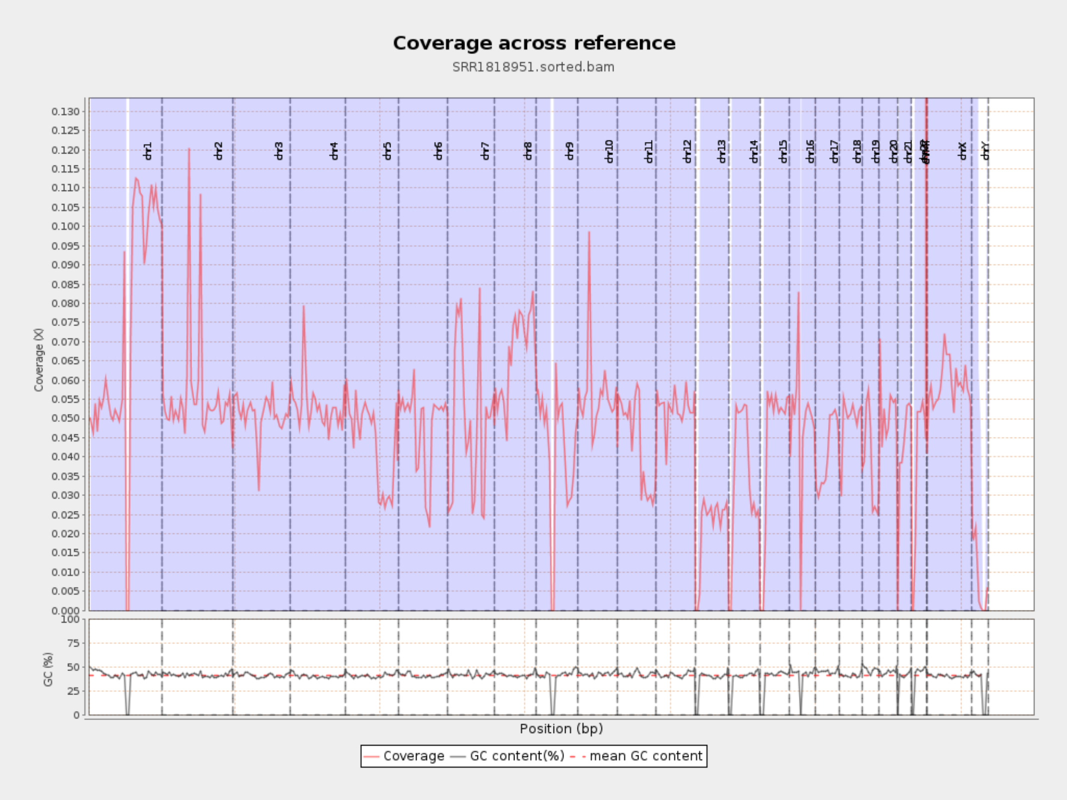
General error rate	0.68%
Mismatches	994,967
Insertions	21,801
Mapped reads with at least one insertion	1.27%
Deletions	47,935
Mapped reads with at least one deletion	2.82%
Homopolymer indels	41.69%

2.6. Chromosome stats

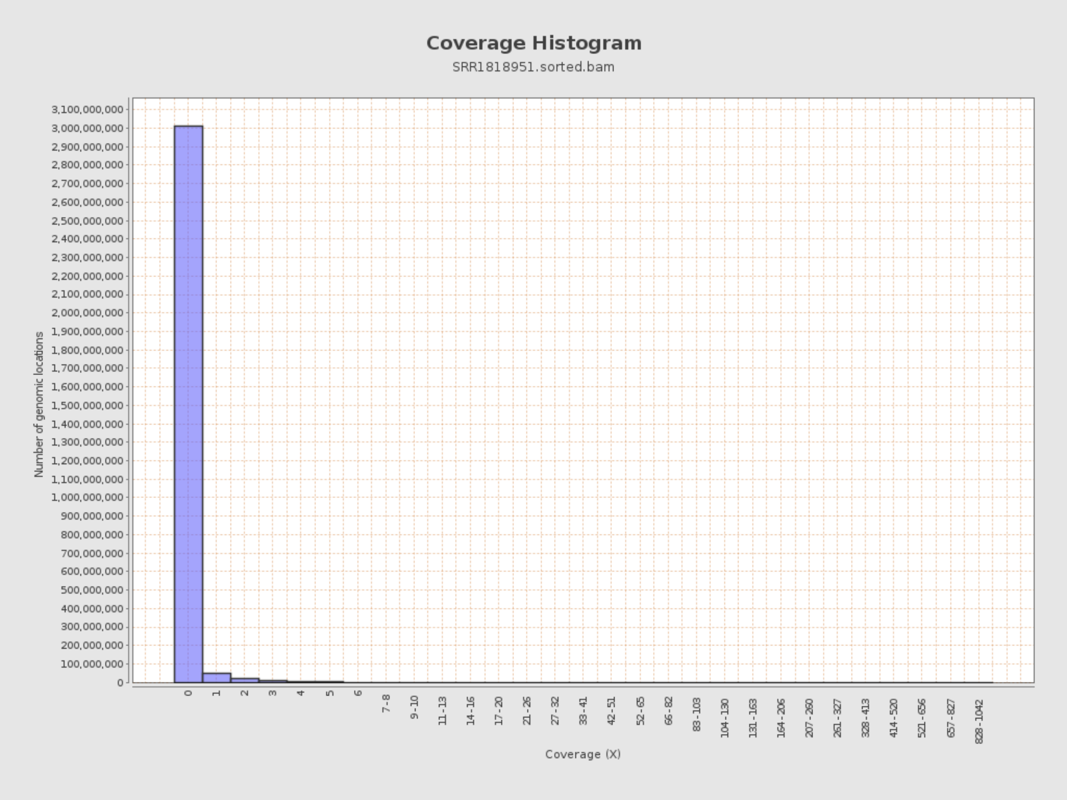
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18070071	0.0725	0.959
chr2	243199373	13777155	0.0566	0.9521
chr3	198022430	10060739	0.0508	0.367
chr4	191154276	10163386	0.0532	0.4303
chr5	180915260	7899629	0.0437	0.3559
chr6	171115067	8239558	0.0482	0.3892
chr7	159138663	7759397	0.0488	0.4446

chr8	146364022	9851648	0.0673	0.4713
chr9	141213431	5761744	0.0408	0.5714
chr10	135534747	7614691	0.0562	0.7089
chr11	135006516	5898555	0.0437	0.3803
chr12	133851895	7043913	0.0526	0.3819
chr13	115169878	2489902	0.0216	0.2357
chr14	107349540	3705738	0.0345	0.3537
chr15	102531392	4466935	0.0436	0.3463
chr16	90354753	4459292	0.0494	0.695
chr17	81195210	3329913	0.041	0.3735
chr18	78077248	3834384	0.0491	0.7402
chr19	59128983	2307325	0.039	0.7573
chr20	63025520	3278703	0.052	0.3903
chr21	48129895	2023421	0.042	0.3574
chr22	51304566	1836761	0.0358	0.3295
chrMT	16571	145838	8.8008	6.5633
chrX	155270560	9098776	0.0586	0.4948
chrY	59373566	484001	0.0082	0.6207

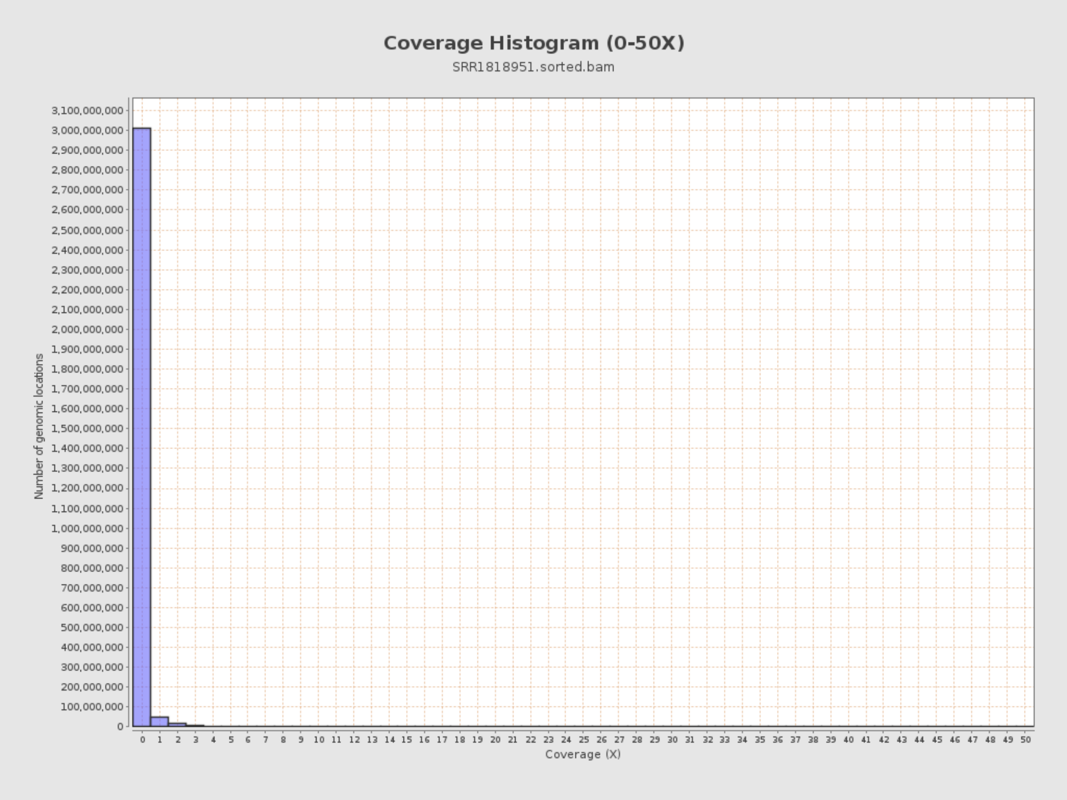
3. Results : Coverage across reference



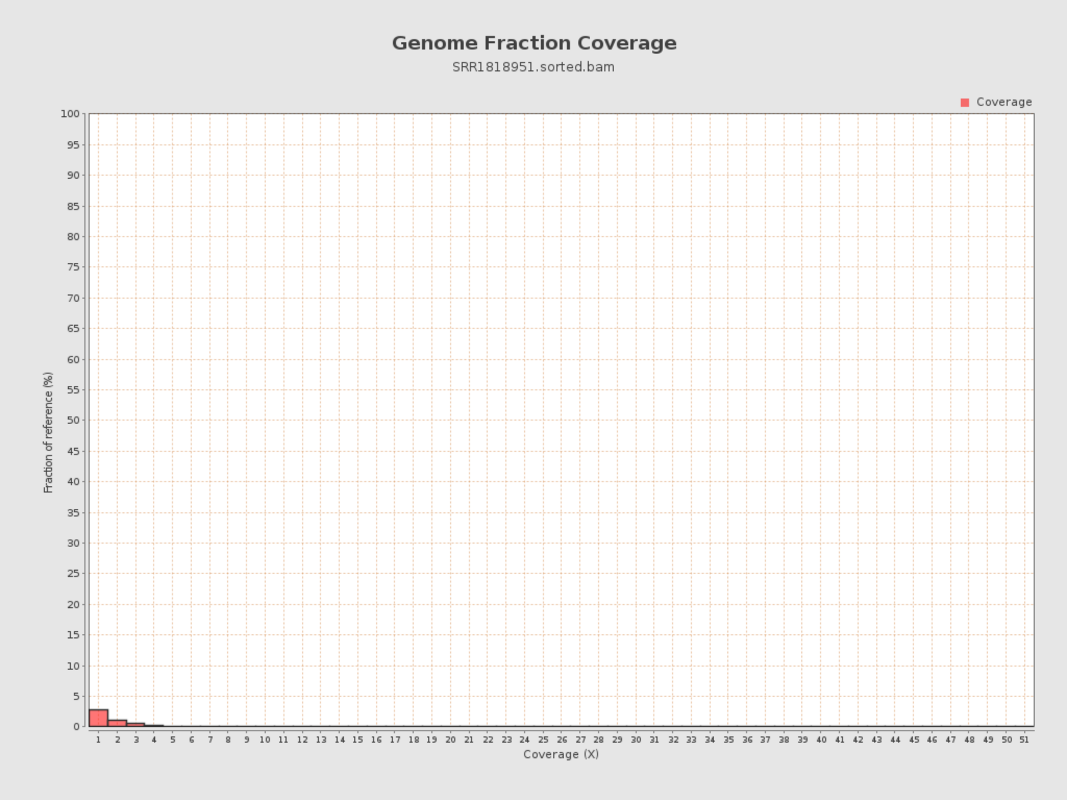
4. Results : Coverage Histogram



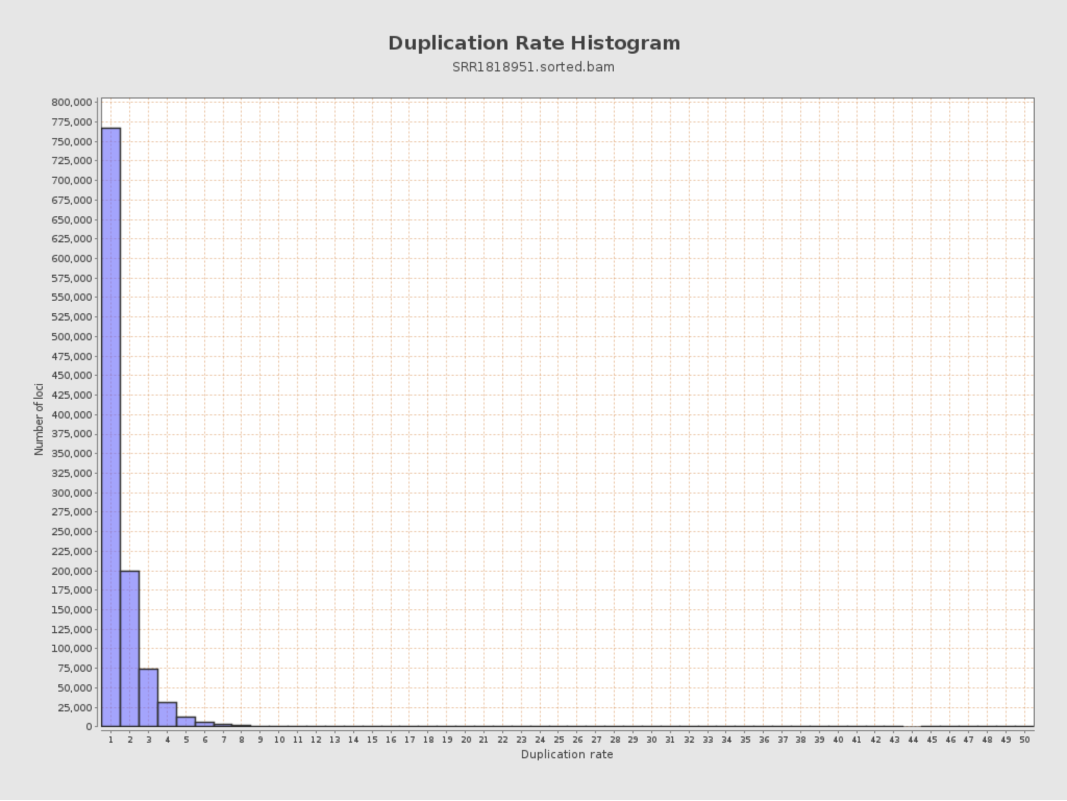
5. Results : Coverage Histogram (0-50X)



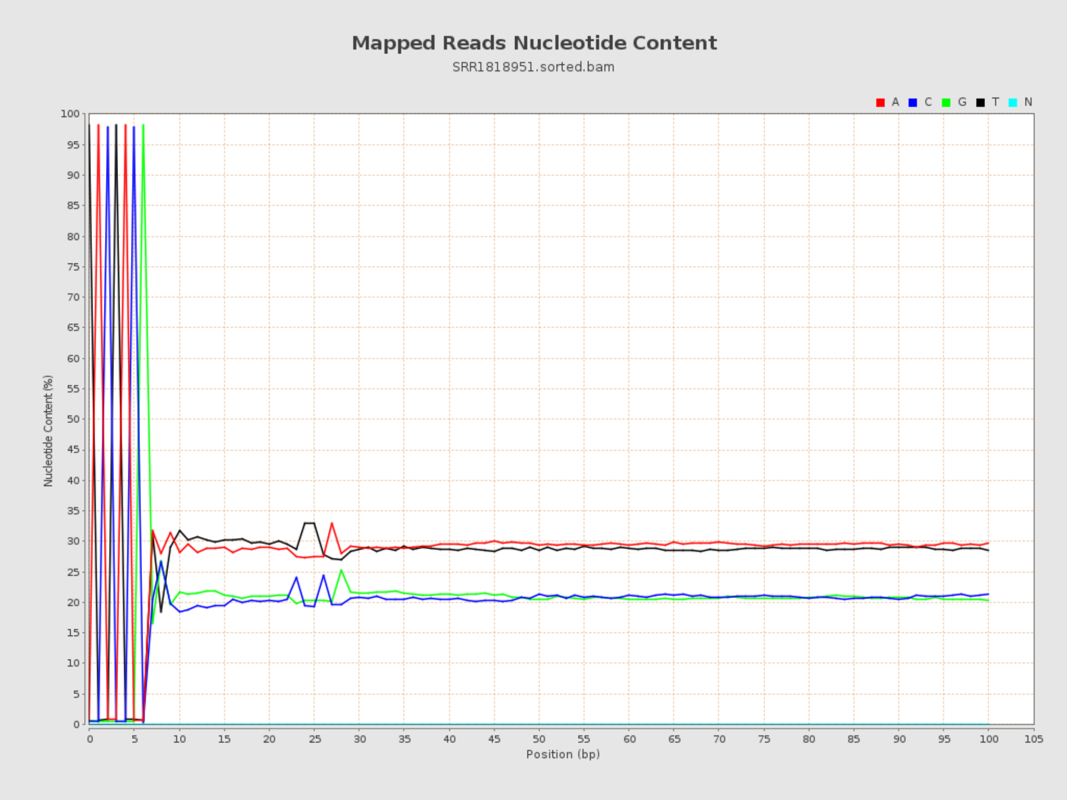
6. Results : Genome Fraction Coverage



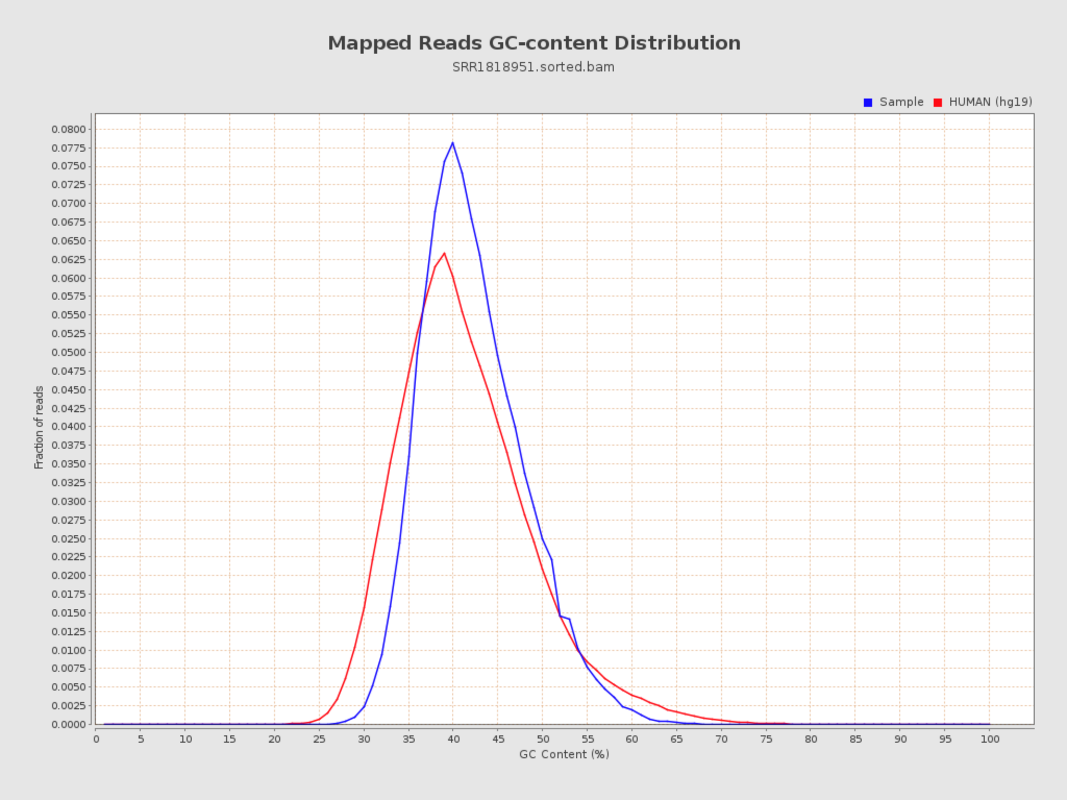
7. Results : Duplication Rate Histogram



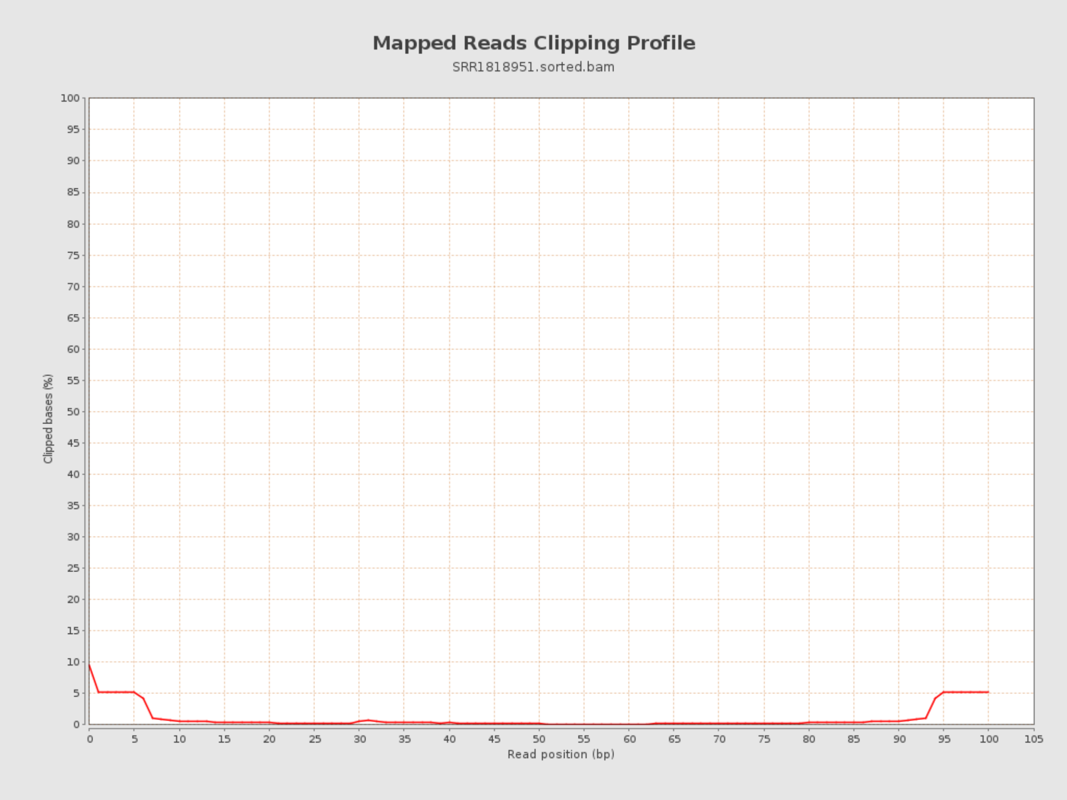
8. Results : Mapped Reads Nucleotide Content



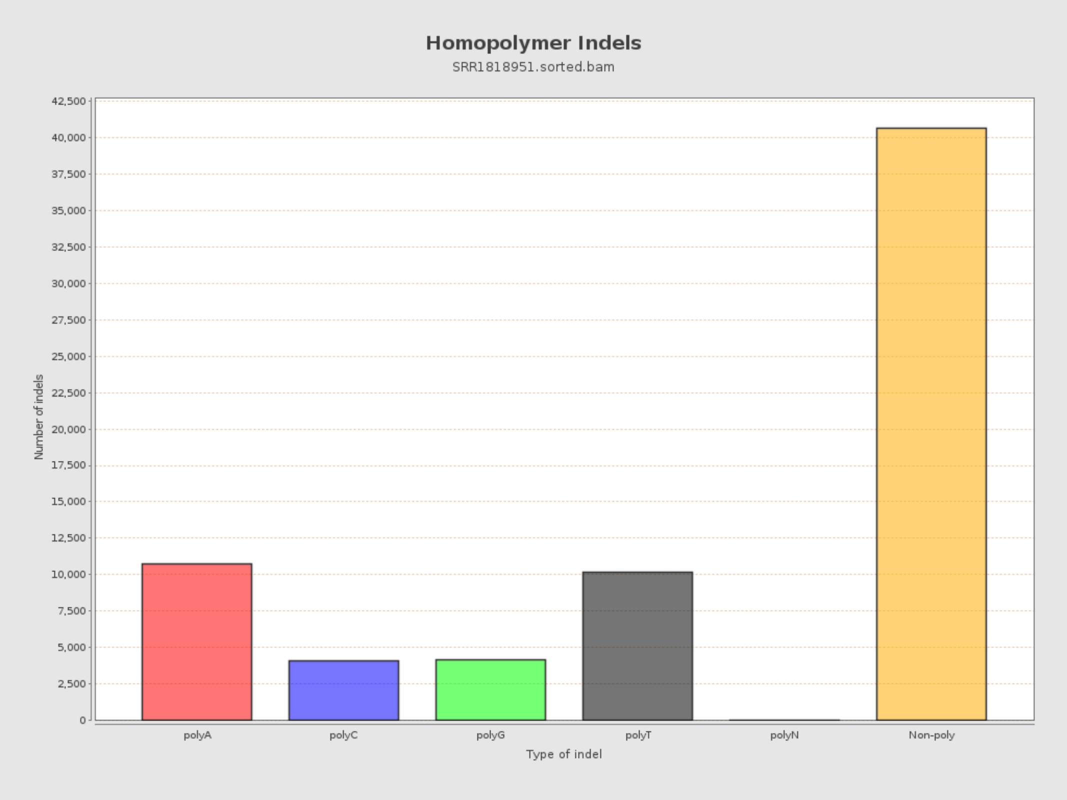
9. Results : Mapped Reads GC-content Distribution



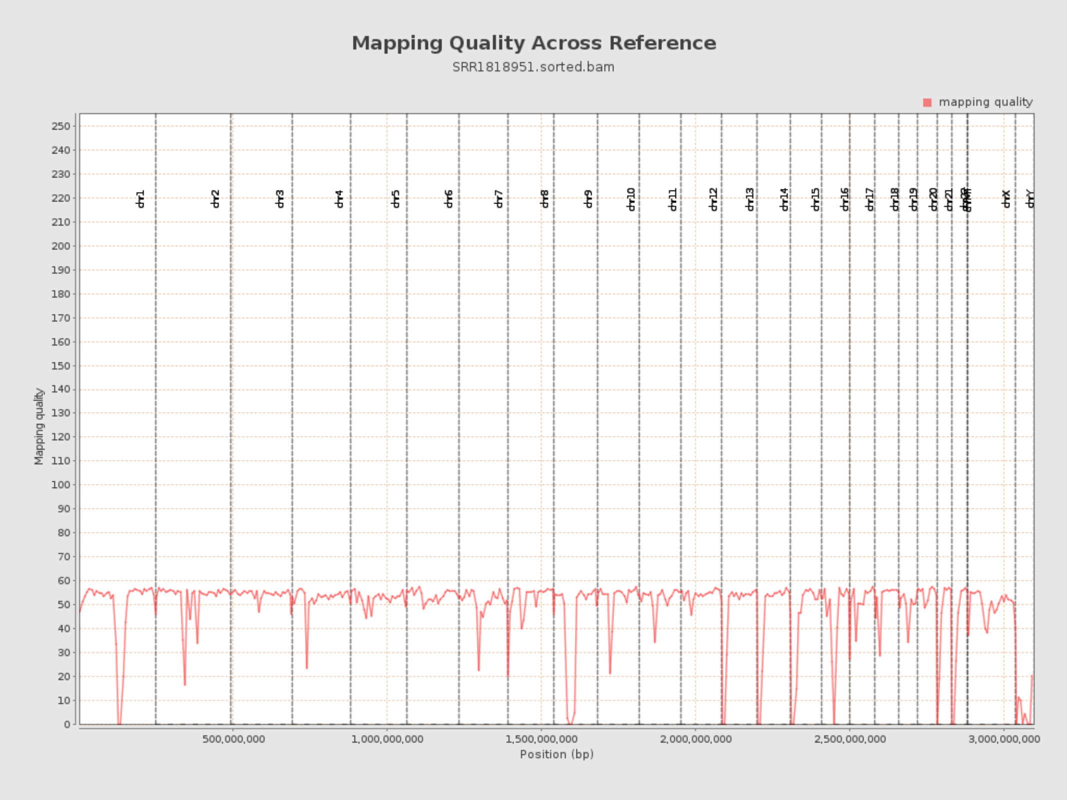
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram