Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 01:03:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819119.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_SRR1819119 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819119.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 01:03:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819119.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,658,912
Mapped reads	5,212,661 / 92.11%
Unmapped reads	446,251 / 7.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,228 / 0.43%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	656,771 / 11.61%
Duplication rate	8.7%
Clipped reads	5,232,820 / 92.47%

2.2. ACGT Content

Number/percentage of A's	73,738,014 / 24.01%
Number/percentage of C's	60,846,147 / 19.81%
Number/percentage of T's	95,051,421 / 30.95%
Number/percentage of G's	77,470,662 / 25.23%
Number/percentage of N's	4,520 / 0%
GC Percentage	45.04%

2.3. Coverage

Mean	0.0992

Standard Deviation	0.8382

2.4. Mapping Quality

Mean Mapping Quality	45.34

2.5. Mismatches and indels

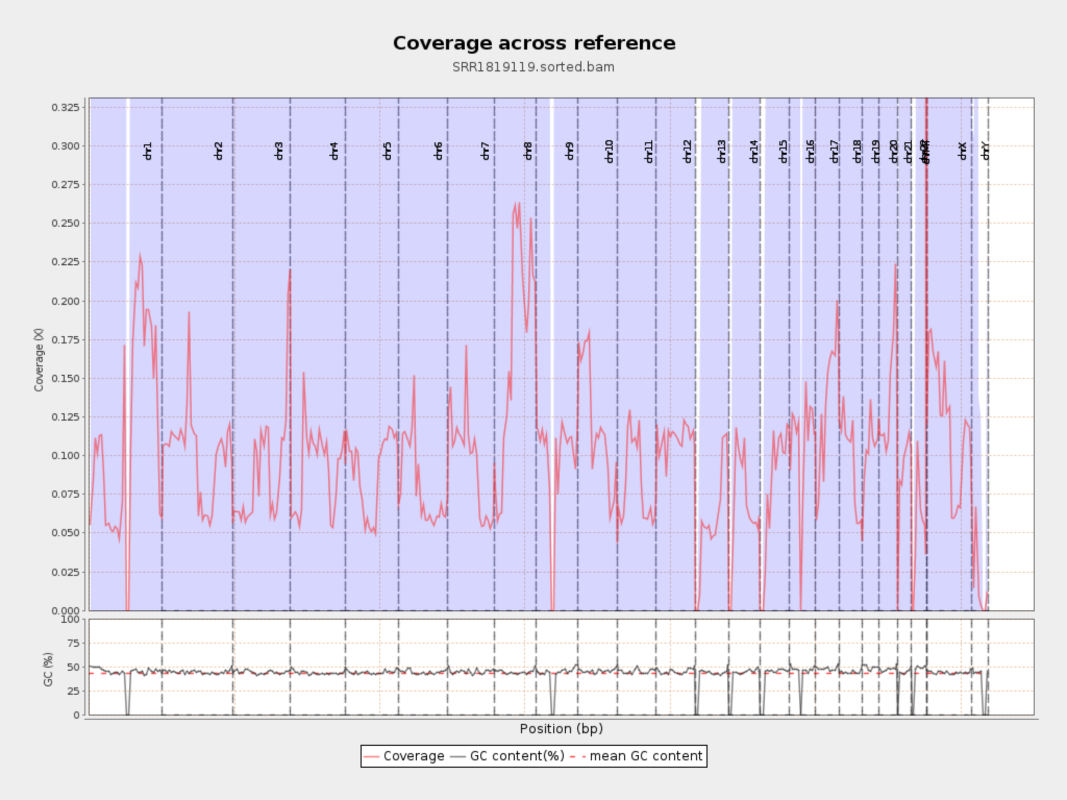
General error rate	0.51%
Mismatches	1,542,909
Insertions	16,661
Mapped reads with at least one insertion	0.32%
Deletions	56,570
Mapped reads with at least one deletion	1.08%
Homopolymer indels	44.32%

2.6. Chromosome stats

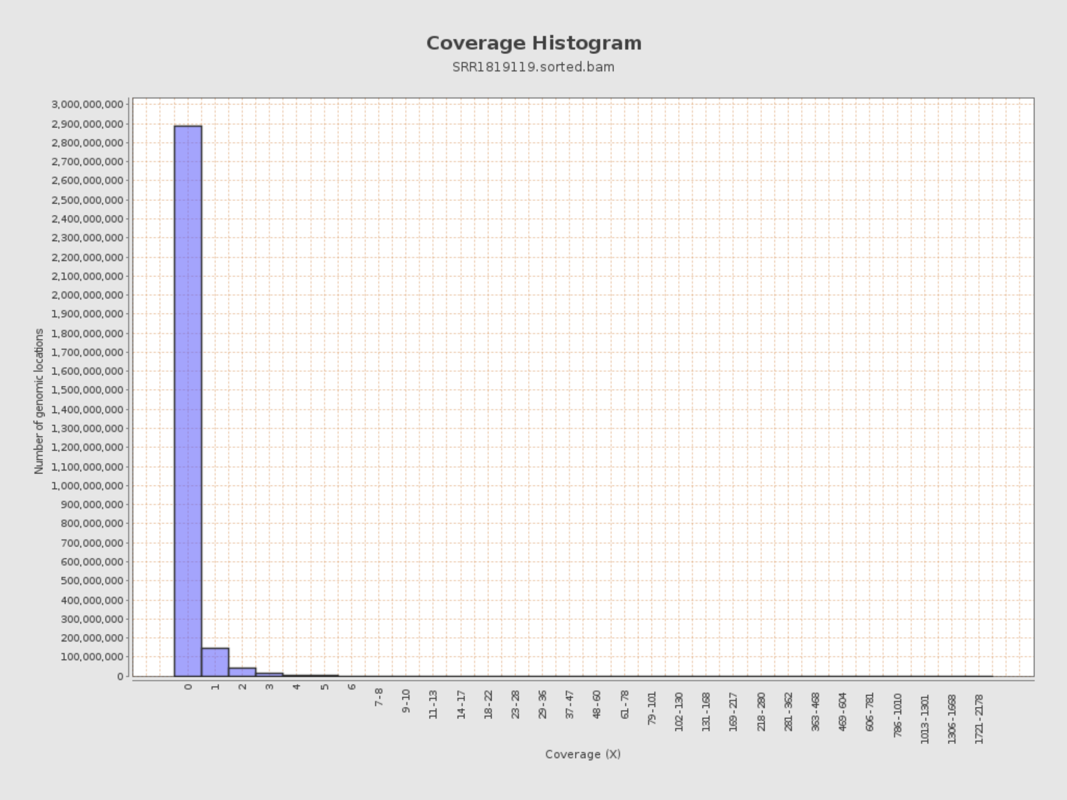
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	28661218	0.115	1.6586
chr2	243199373	24706053	0.1016	1.0129
chr3	198022430	17528466	0.0885	0.4185
chr4	191154276	17518497	0.0916	0.5828
chr5	180915260	16385076	0.0906	0.4293
chr6	171115067	13709197	0.0801	0.5835
chr7	159138663	15394306	0.0967	1.0808

chr8	146364022	25304542	0.1729	0.9395
chr9	141213431	13332031	0.0944	0.7236
chr10	135534747	16458788	0.1214	0.8304
chr11	135006516	11050784	0.0819	0.8004
chr12	133851895	14939582	0.1116	0.476
chr13	115169878	6702459	0.0582	0.3431
chr14	107349540	7191214	0.067	0.3841
chr15	102531392	8032646	0.0783	0.4012
chr16	90354753	9699991	0.1074	0.5164
chr17	81195210	10959124	0.135	0.5964
chr18	78077248	7630941	0.0977	1.4557
chr19	59128983	6238684	0.1055	1.0873
chr20	63025520	8933385	0.1417	0.5508
chr21	48129895	4280273	0.0889	0.5415
chr22	51304566	2569034	0.0501	0.3122
chrMT	16571	73343	4.426	3.9417
chrX	155270560	18844593	0.1214	0.5979
chrY	59373566	1060727	0.0179	0.557

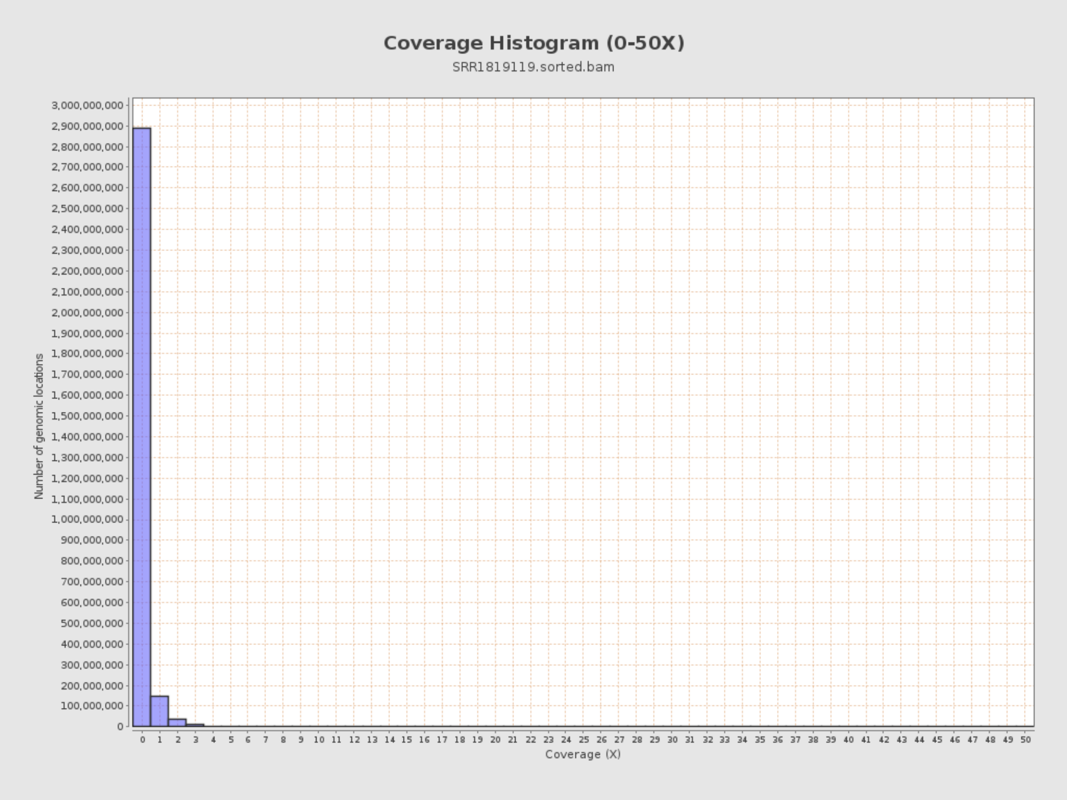
3. Results : Coverage across reference



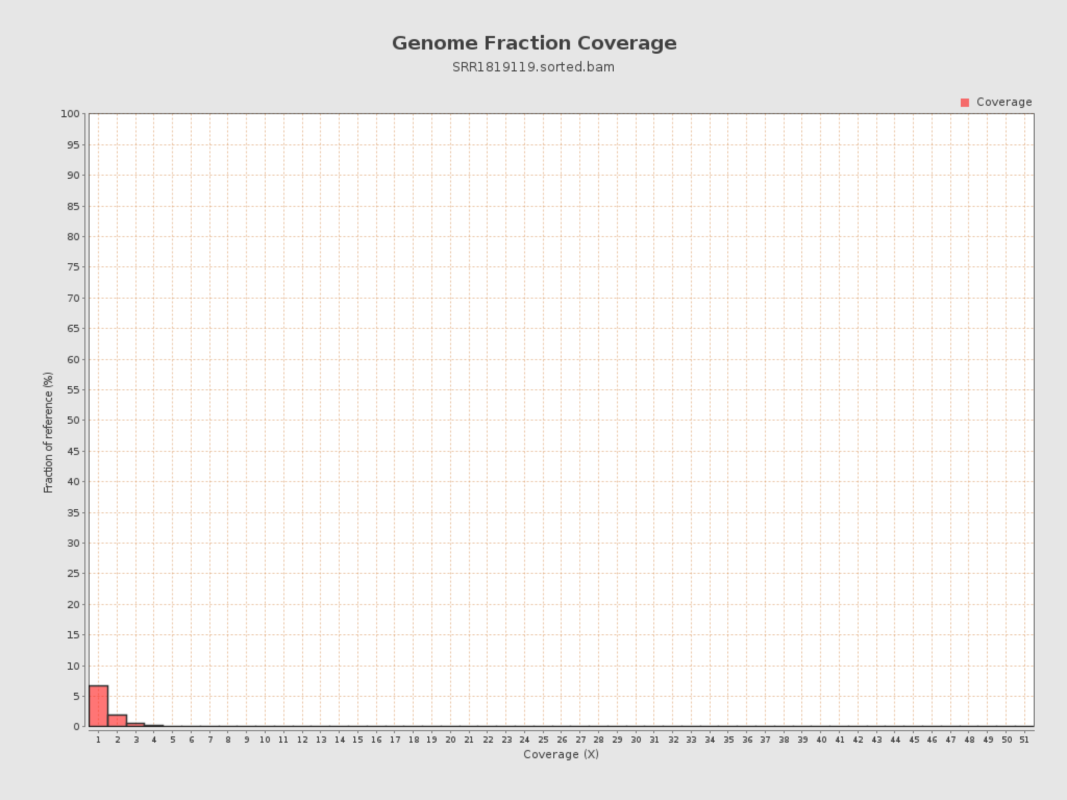
4. Results : Coverage Histogram



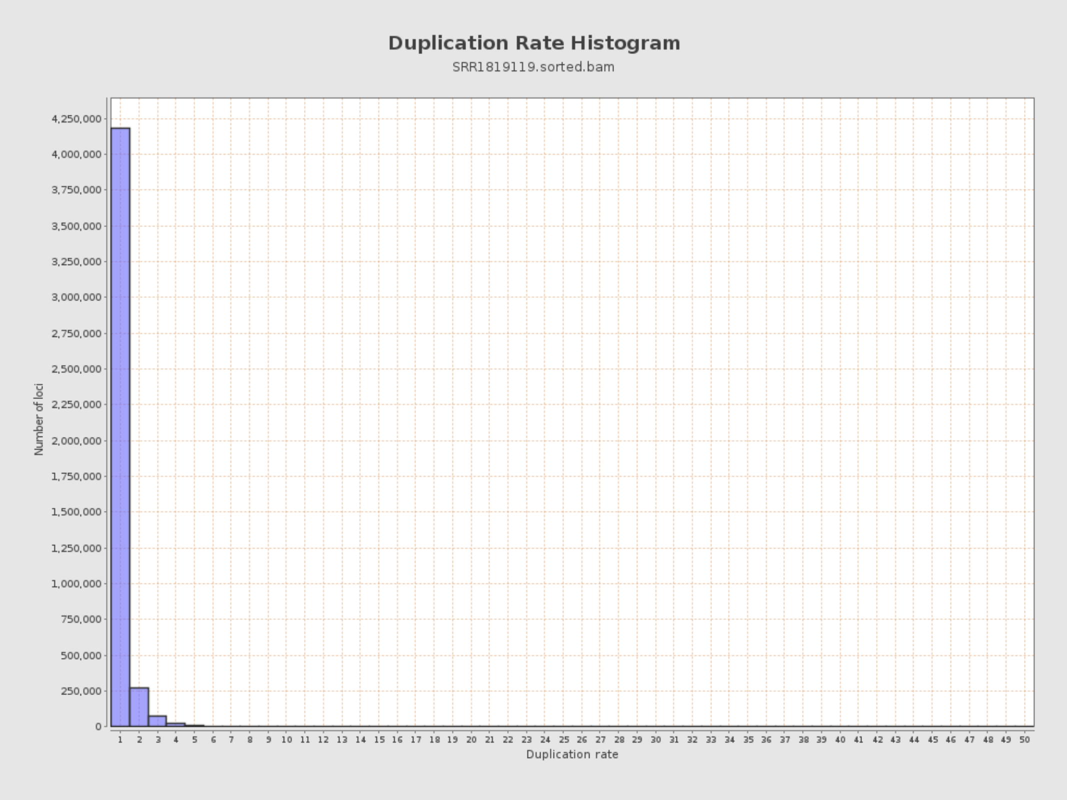
5. Results : Coverage Histogram (0-50X)



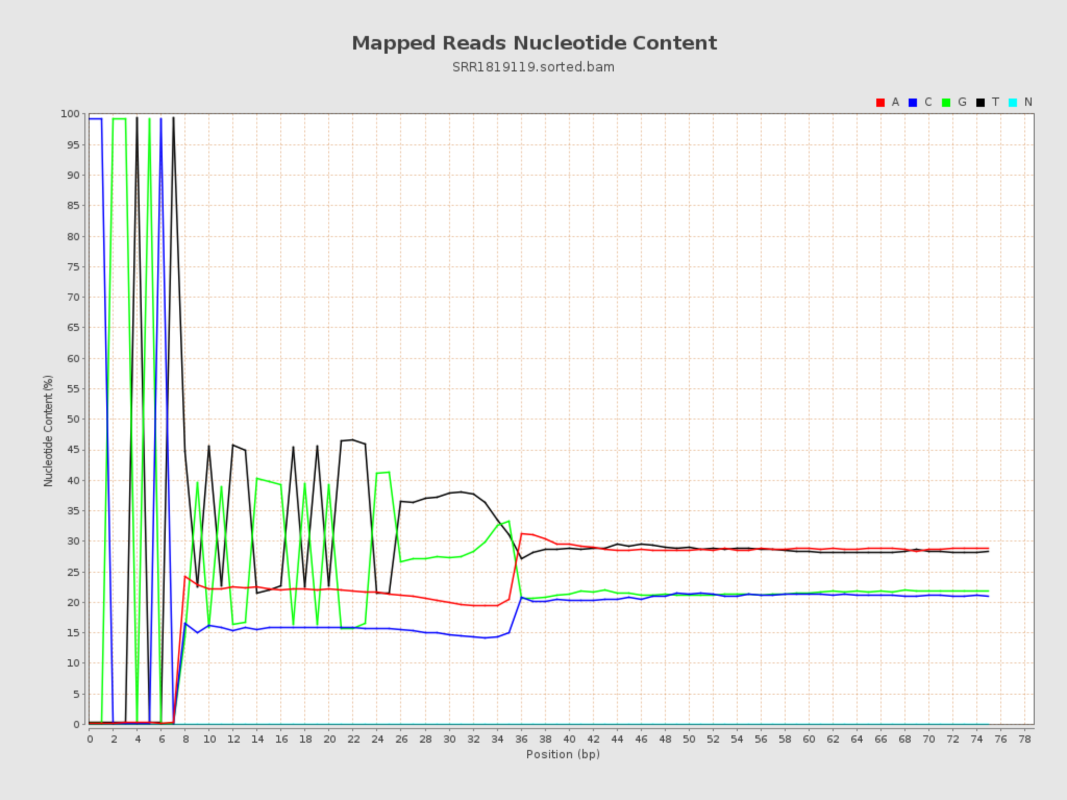
6. Results : Genome Fraction Coverage



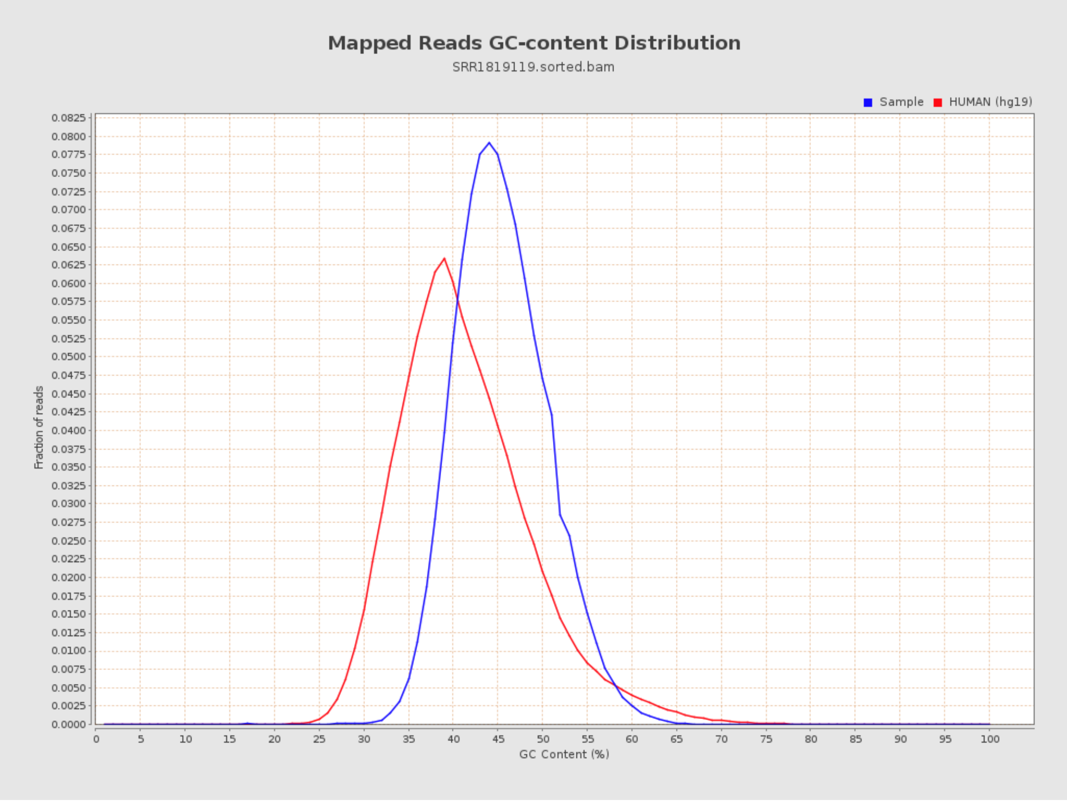
7. Results : Duplication Rate Histogram



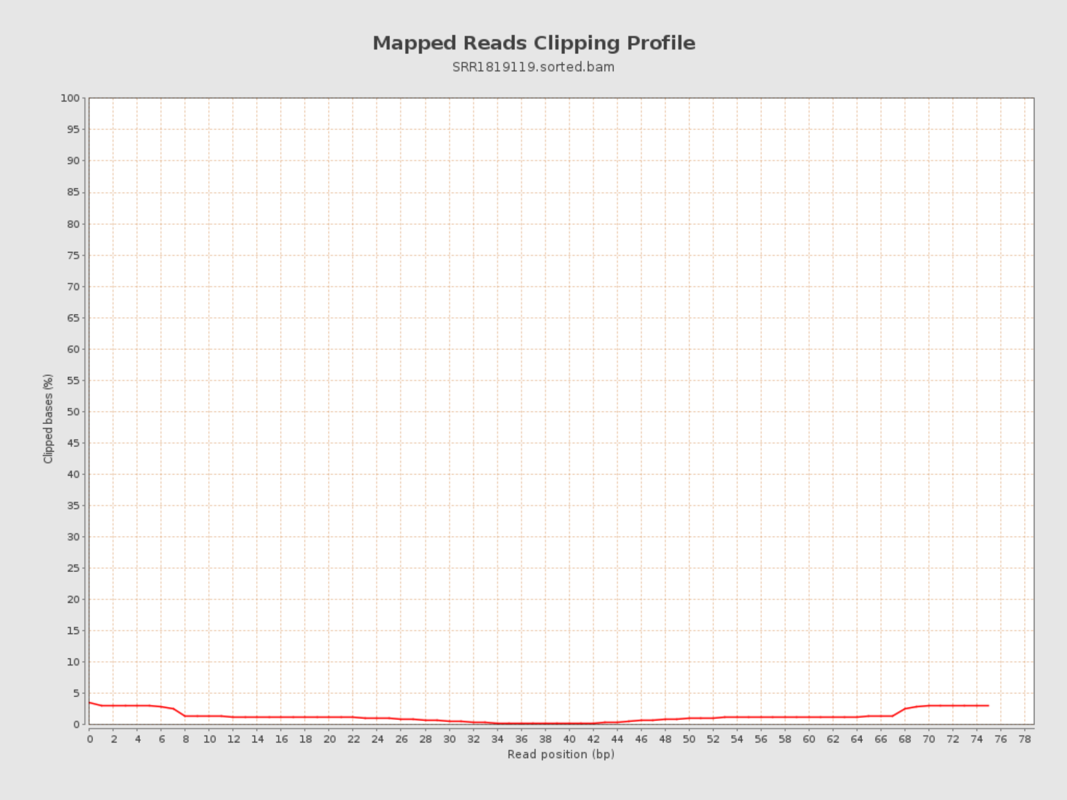
8. Results : Mapped Reads Nucleotide Content



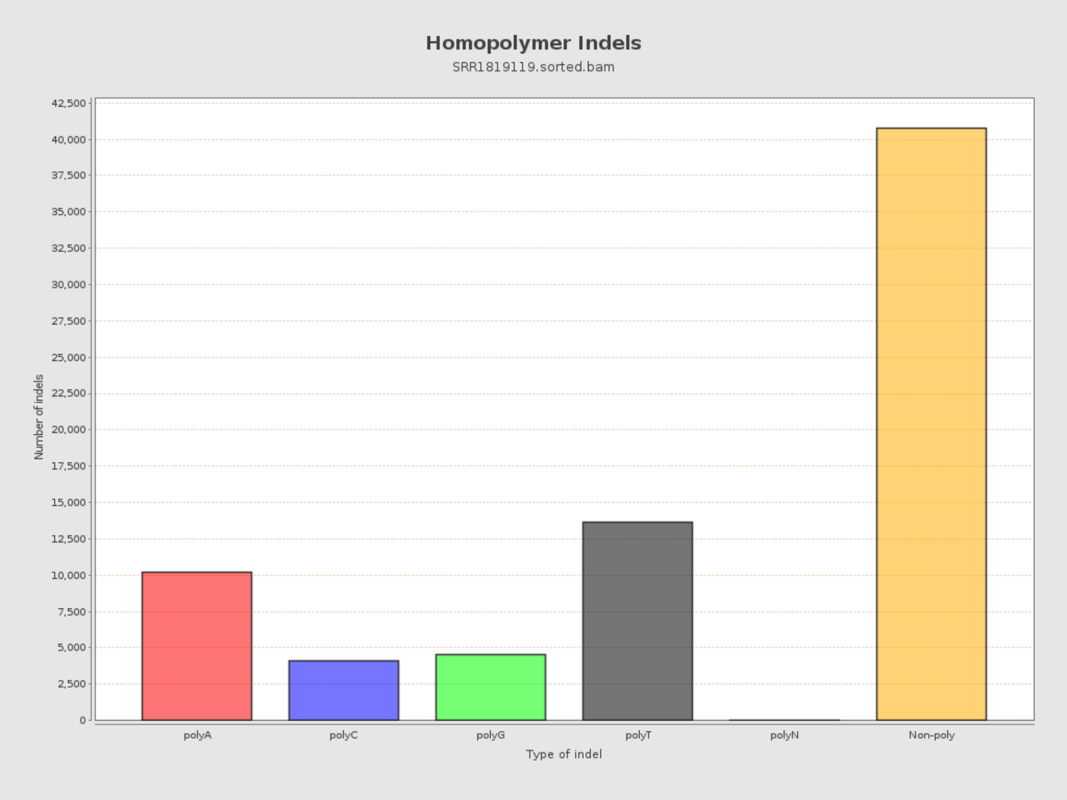
9. Results : Mapped Reads GC-content Distribution



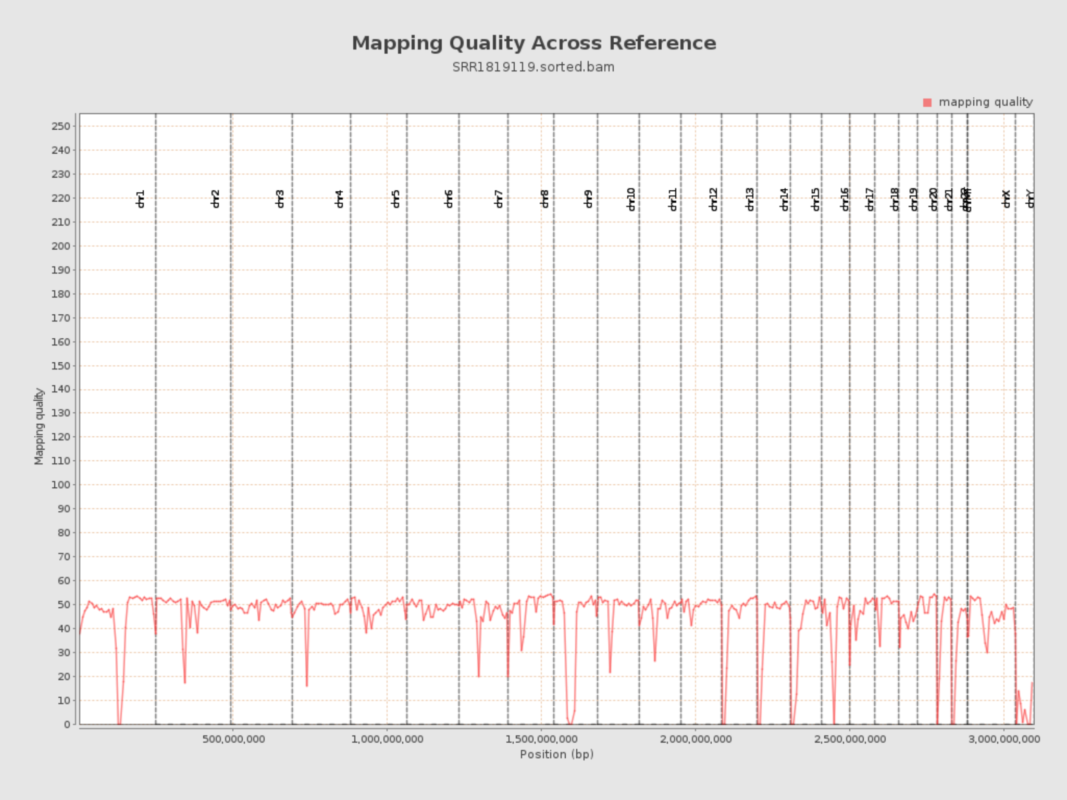
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram