Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 00:06:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819104.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_SRR1819104 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819104.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 00:06:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819104.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,836,667
Mapped reads	2,560,018 / 90.25%
Unmapped reads	276,649 / 9.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,595 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	136,967 / 4.83%
Duplication rate	3.97%
Clipped reads	2,564,106 / 90.39%

2.2. ACGT Content

Number/percentage of A's	37,097,032 / 25.28%
Number/percentage of C's	26,996,958 / 18.39%
Number/percentage of T's	47,684,803 / 32.49%
Number/percentage of G's	34,992,145 / 23.84%
Number/percentage of N's	2,043 / 0%
GC Percentage	42.23%

2.3. Coverage

Mean	0.0474

Standard Deviation	0.389

2.4. Mapping Quality

Mean Mapping Quality	44.22

2.5. Mismatches and indels

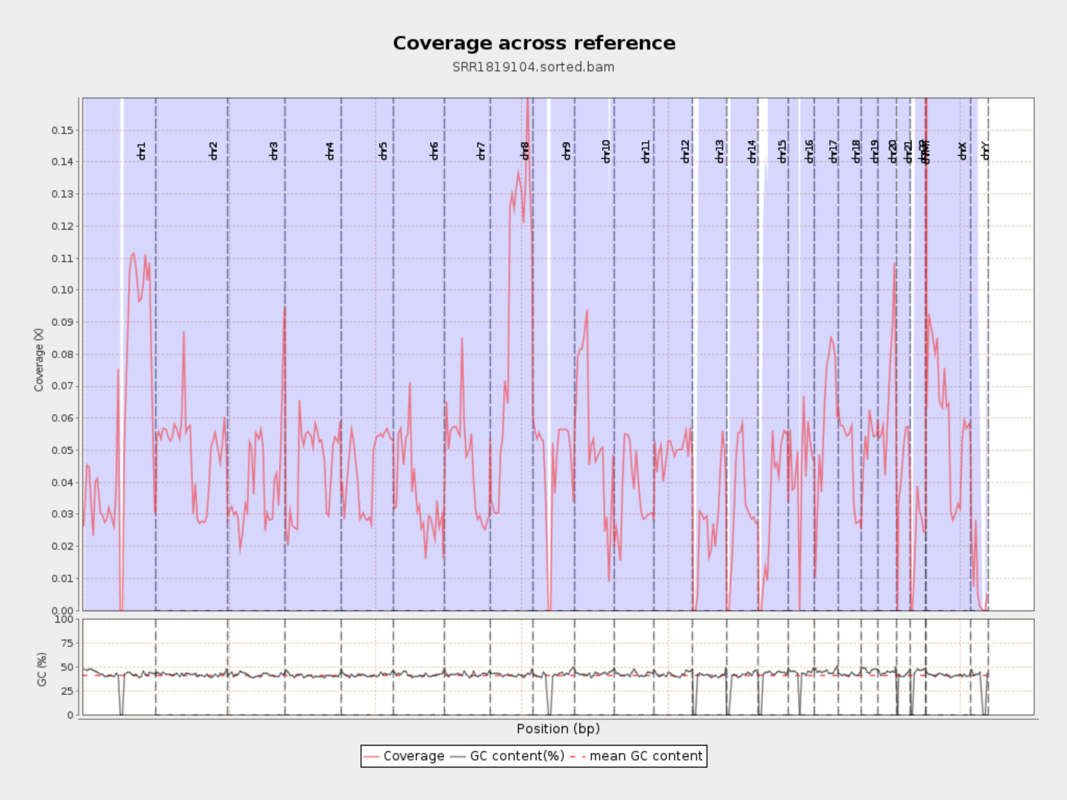
General error rate	0.52%
Mismatches	749,787
Insertions	9,998
Mapped reads with at least one insertion	0.39%
Deletions	26,968
Mapped reads with at least one deletion	1.05%
Homopolymer indels	42.84%

2.6. Chromosome stats

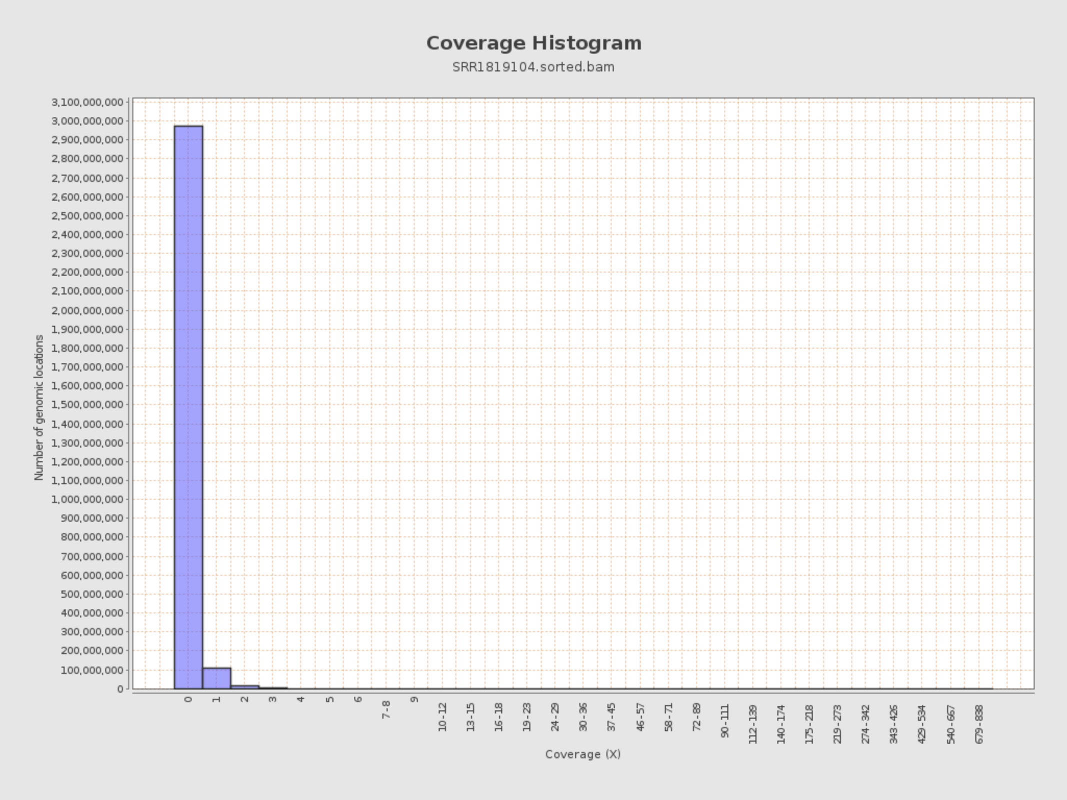
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14407834	0.0578	0.6392
chr2	243199373	12082324	0.0497	0.5097
chr3	198022430	7868658	0.0397	0.2352
chr4	191154276	8646870	0.0452	0.2906
chr5	180915260	7979107	0.0441	0.2443
chr6	171115067	6269486	0.0366	0.3102
chr7	159138663	7388320	0.0464	0.55

chr8	146364022	13959411	0.0954	0.4386
chr9	141213431	6404564	0.0454	0.3543
chr10	135534747	7311053	0.0539	0.4181
chr11	135006516	4807074	0.0356	0.3601
chr12	133851895	6719878	0.0502	0.2622
chr13	115169878	3092616	0.0269	0.1916
chr14	107349540	3457948	0.0322	0.2125
chr15	102531392	3316943	0.0324	0.2339
chr16	90354753	3999040	0.0443	0.2707
chr17	81195210	4870692	0.06	0.2985
chr18	78077248	3666983	0.047	0.6269
chr19	59128983	3106085	0.0525	0.4654
chr20	63025520	4326444	0.0686	0.3087
chr21	48129895	2061095	0.0428	0.262
chr22	51304566	1105108	0.0215	0.1696
chrMT	16571	115034	6.9419	4.3122
chrX	155270560	9372660	0.0604	0.334
chrY	59373566	482179	0.0081	0.2172

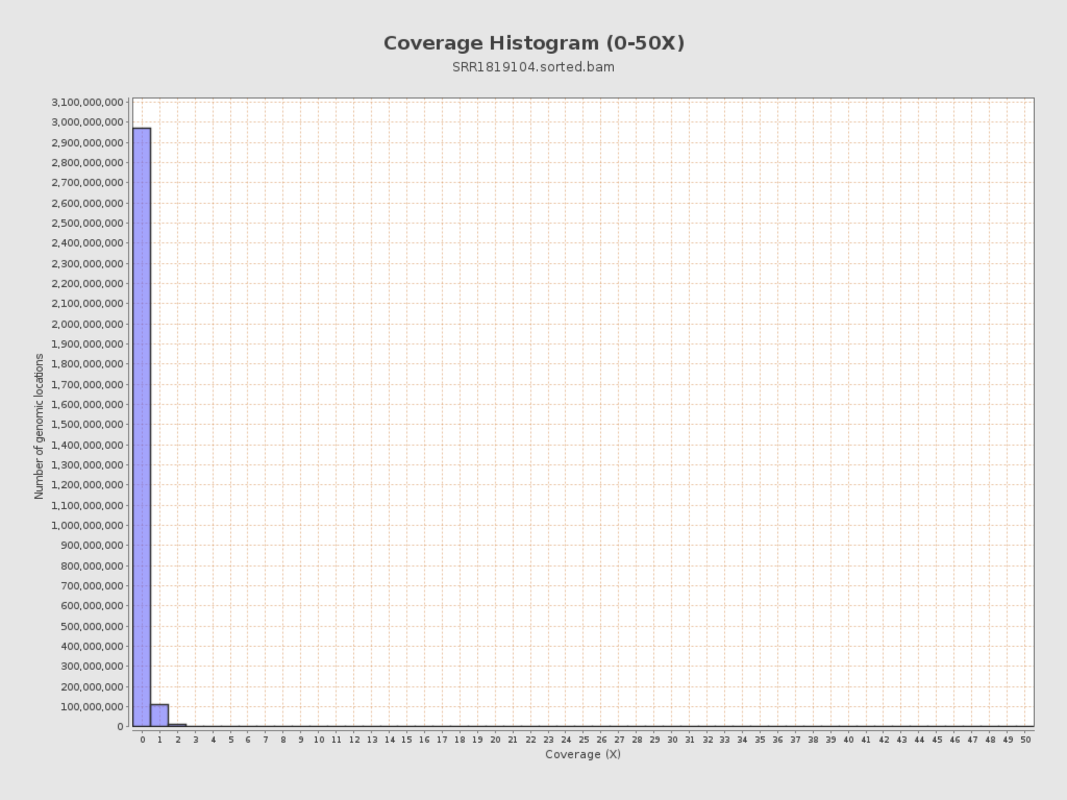
3. Results : Coverage across reference



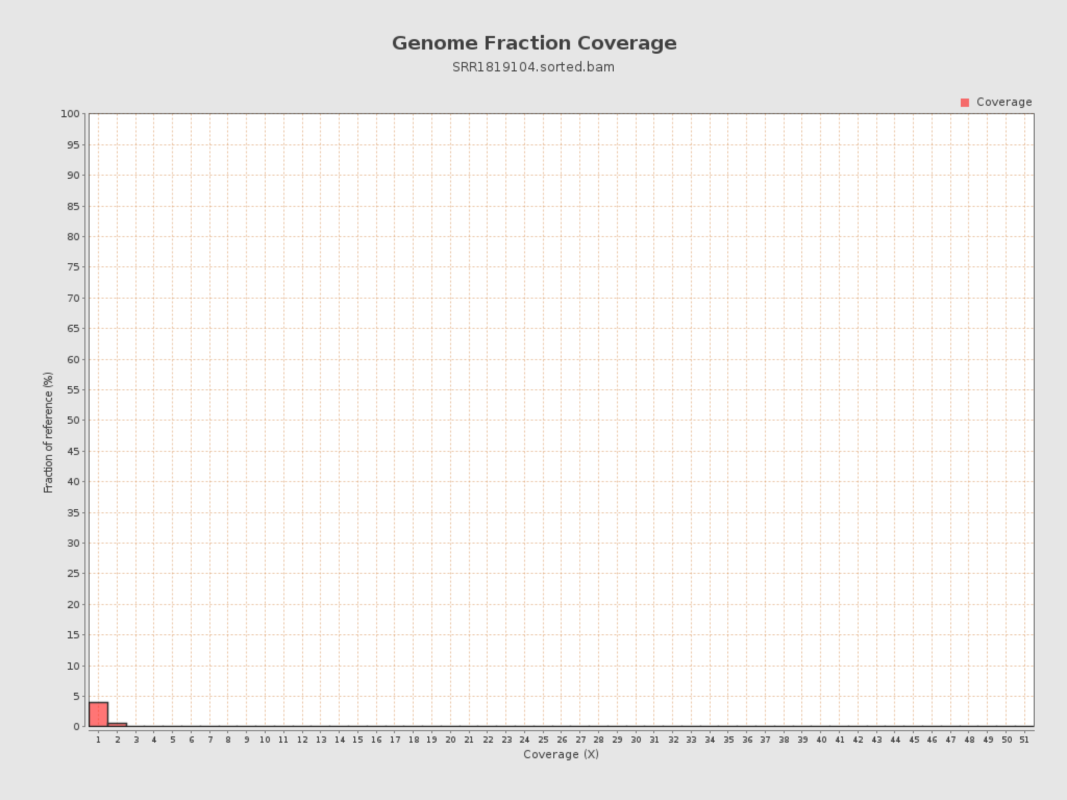
4. Results : Coverage Histogram



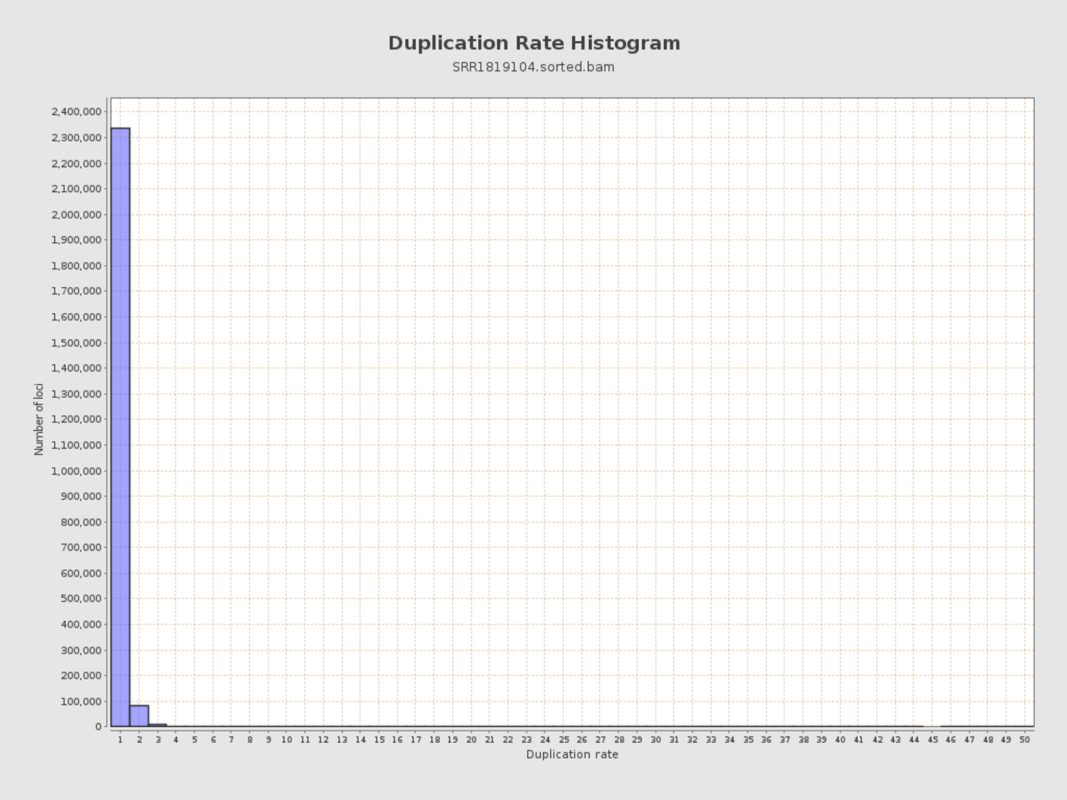
5. Results : Coverage Histogram (0-50X)



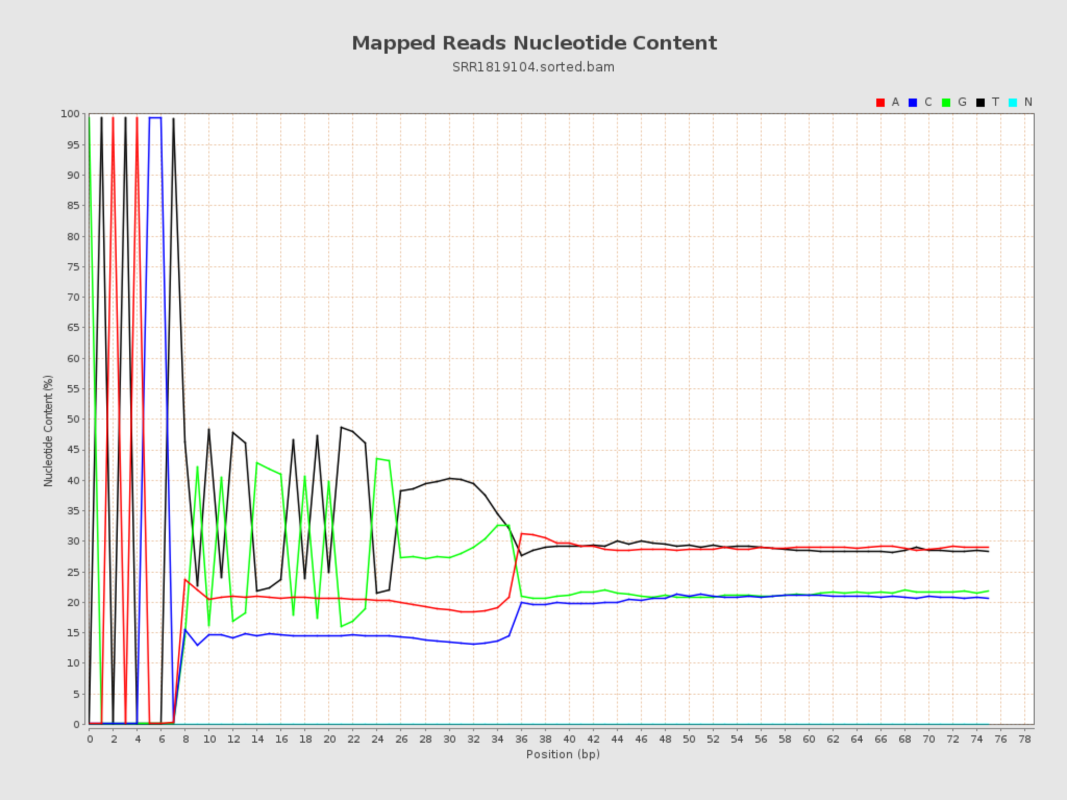
6. Results : Genome Fraction Coverage



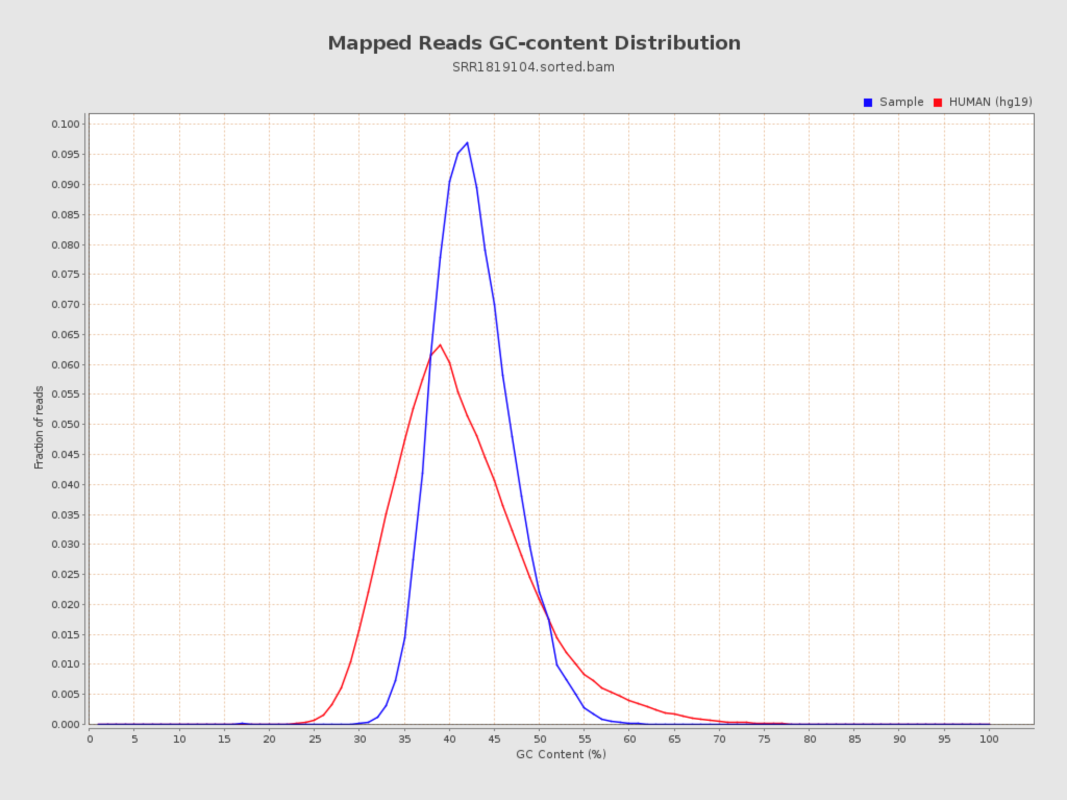
7. Results : Duplication Rate Histogram



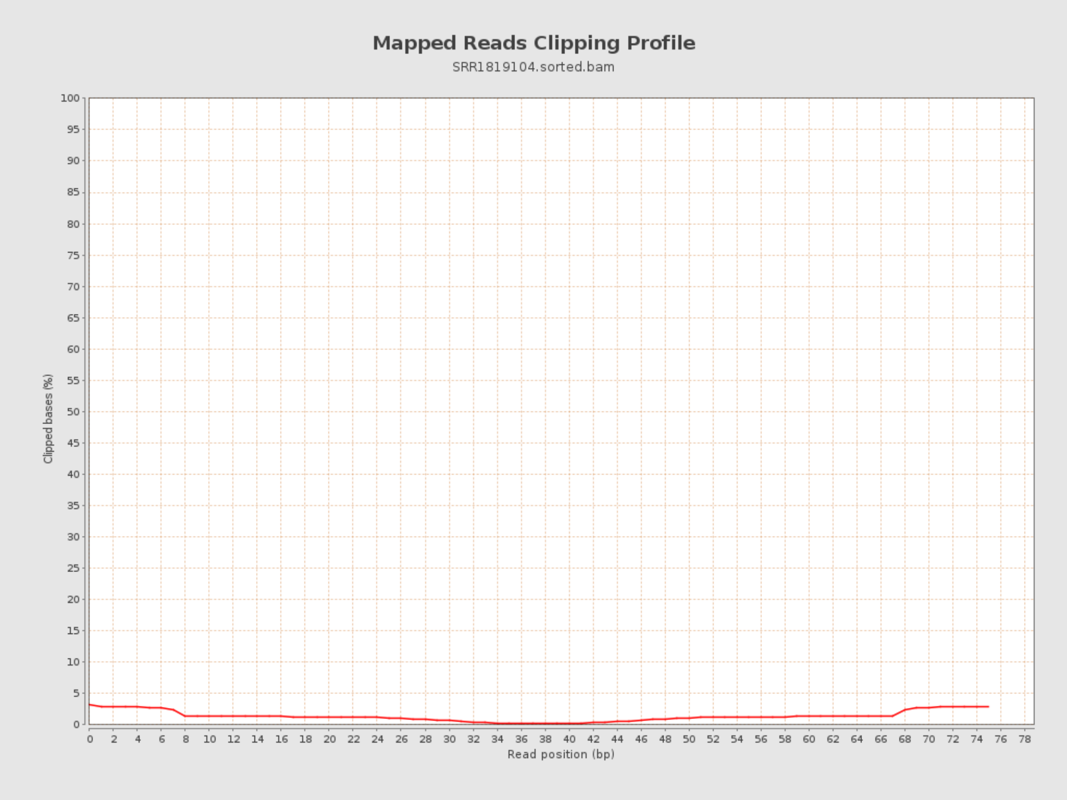
8. Results : Mapped Reads Nucleotide Content



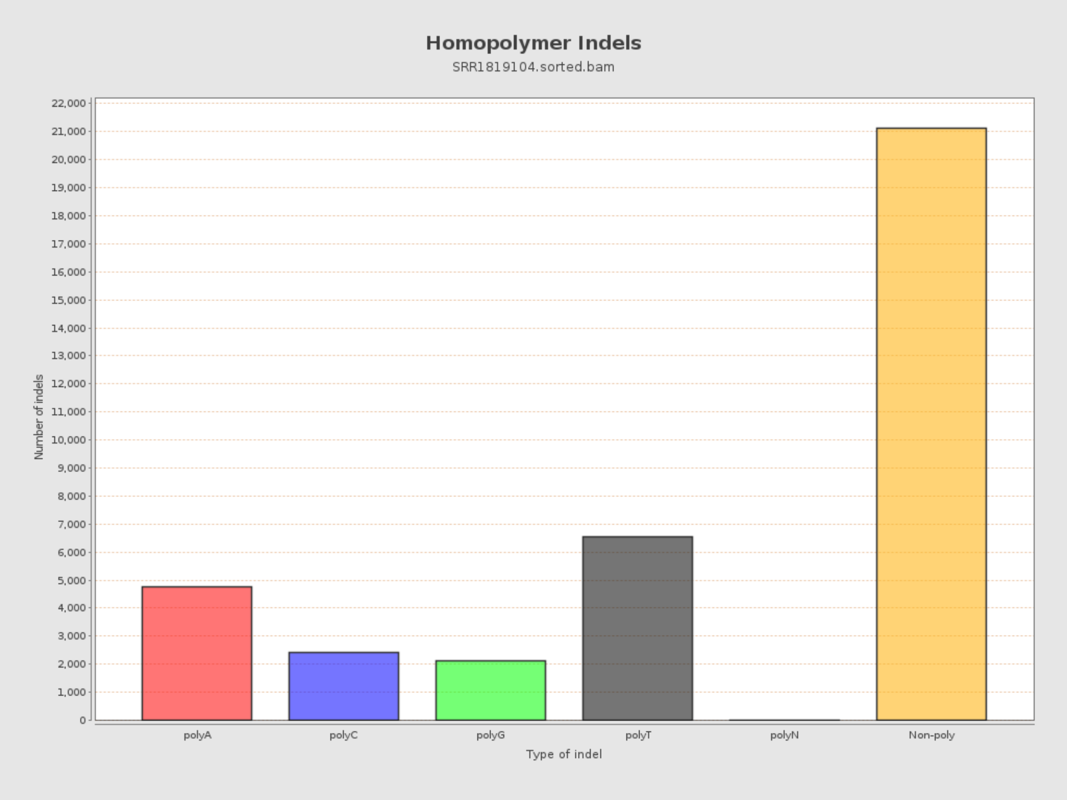
9. Results : Mapped Reads GC-content Distribution



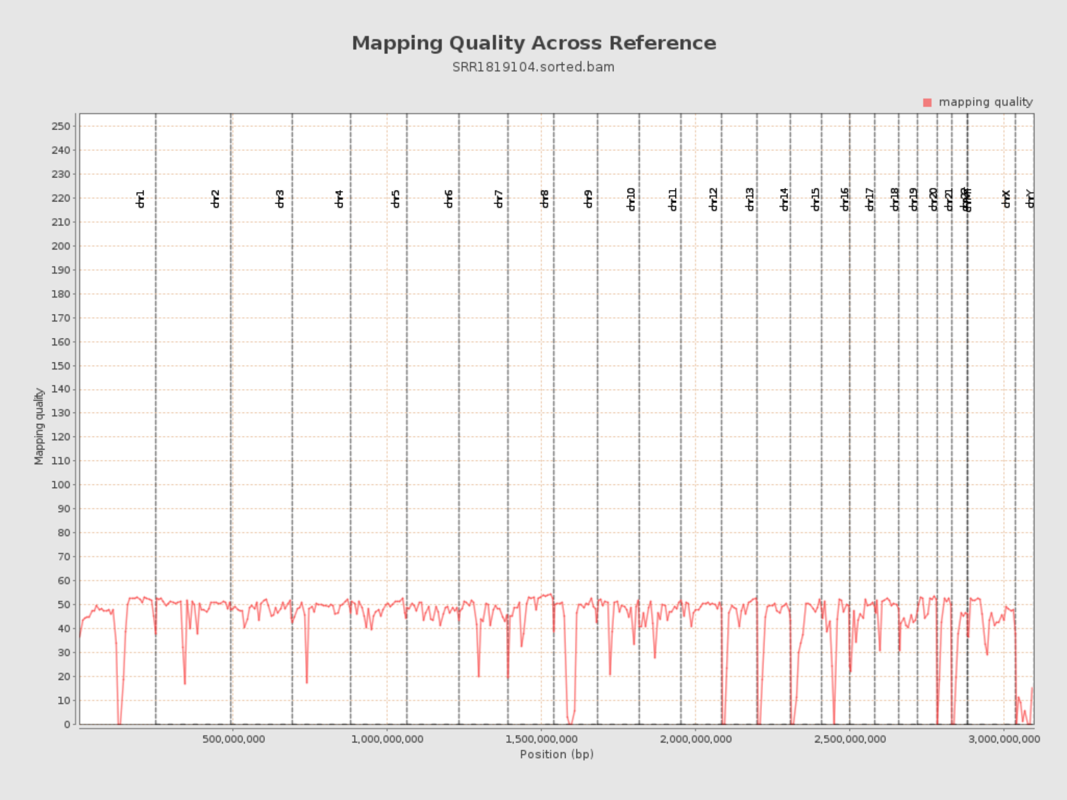
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram