Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 16:20:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819024.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_SRR1819024 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819024.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 16:20:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819024.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,762,259
Mapped reads	1,634,210 / 92.73%
Unmapped reads	128,049 / 7.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,178 / 1.43%
Read min/max/mean length	30 / 101 / 101.55
Duplicated reads (estimated)	604,505 / 34.3%
Duplication rate	29.17%
Clipped reads	1,642,589 / 93.21%

2.2. ACGT Content

Number/percentage of A's	42,579,017 / 28.16%
Number/percentage of C's	31,152,622 / 20.6%
Number/percentage of T's	44,255,790 / 29.27%
Number/percentage of G's	33,226,010 / 21.97%
Number/percentage of N's	6,765 / 0%
GC Percentage	42.57%

2.3. Coverage

Mean	0.0489

Standard Deviation	0.5861

2.4. Mapping Quality

Mean Mapping Quality	49.21

2.5. Mismatches and indels

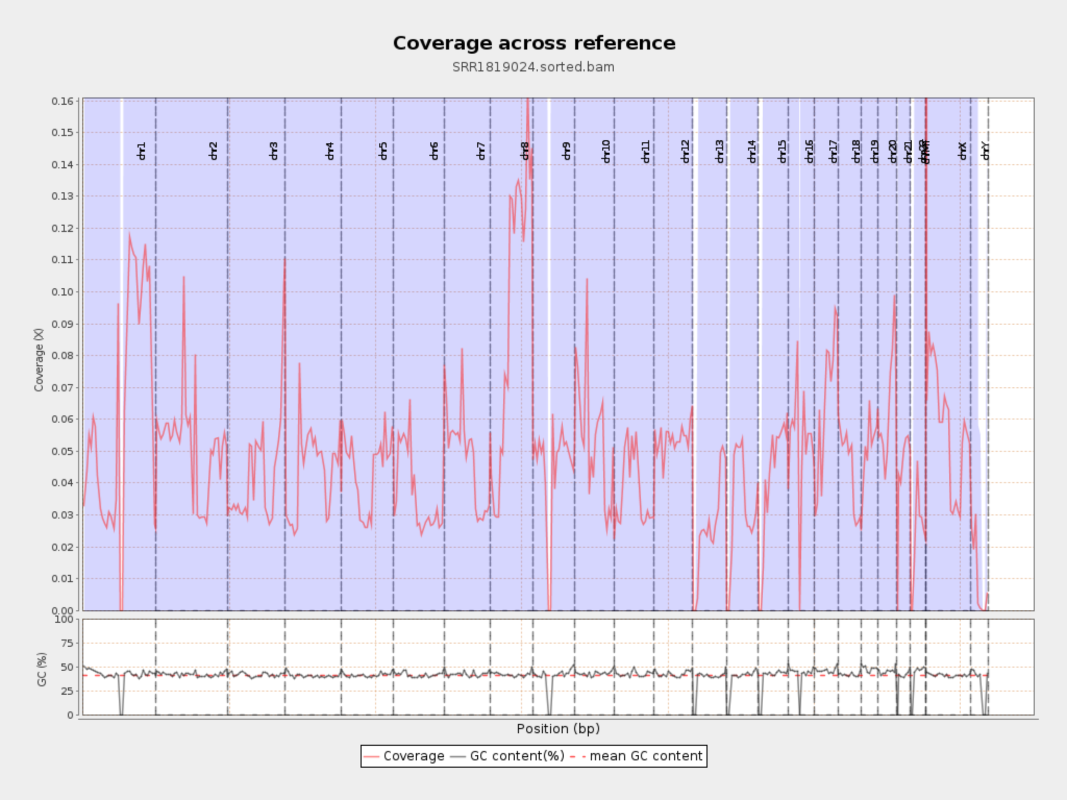
General error rate	0.66%
Mismatches	944,396
Insertions	25,877
Mapped reads with at least one insertion	1.54%
Deletions	49,886
Mapped reads with at least one deletion	2.98%
Homopolymer indels	41.37%

2.6. Chromosome stats

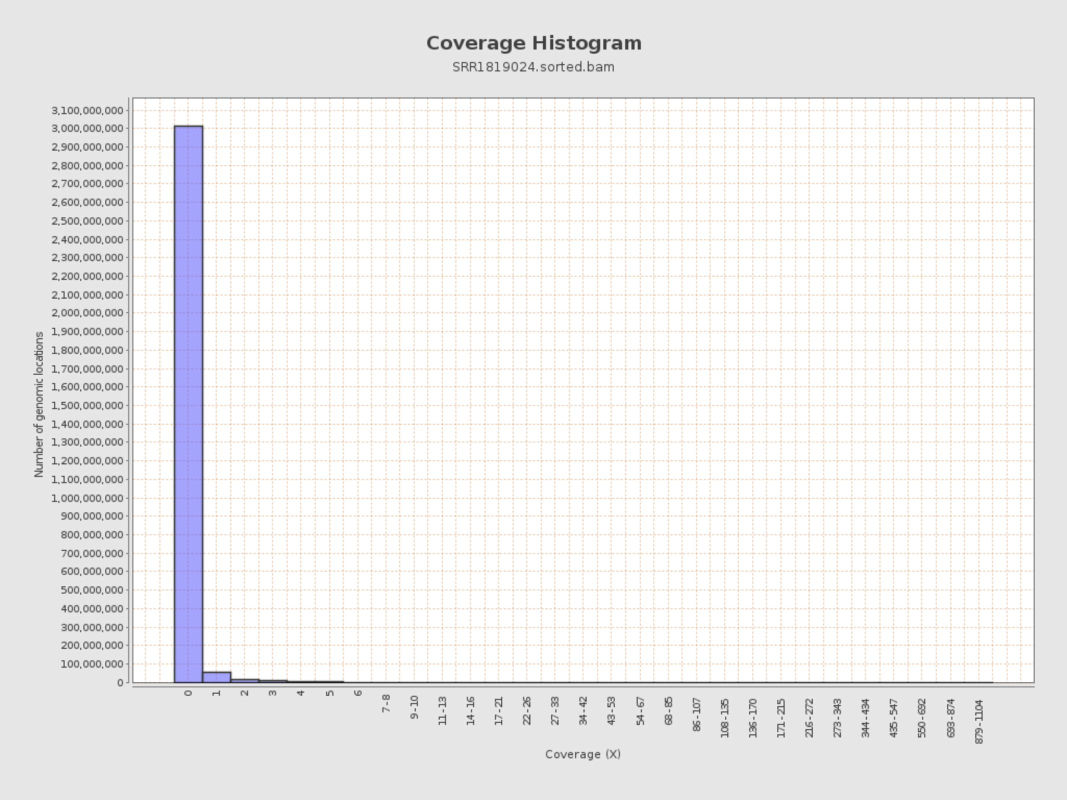
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15523586	0.0623	1.0413
chr2	243199373	12651082	0.052	0.857
chr3	198022430	8520493	0.043	0.3475
chr4	191154276	8405611	0.044	0.4196
chr5	180915260	8049556	0.0445	0.3614
chr6	171115067	6297476	0.0368	0.3777
chr7	159138663	7704782	0.0484	0.6556

chr8	146364022	14101237	0.0963	0.5764
chr9	141213431	6291935	0.0446	0.5267
chr10	135534747	7300384	0.0539	0.7394
chr11	135006516	5100639	0.0378	0.3591
chr12	133851895	7217927	0.0539	0.4041
chr13	115169878	3048478	0.0265	0.27
chr14	107349540	3457057	0.0322	0.3212
chr15	102531392	4100199	0.04	0.3363
chr16	90354753	4694535	0.052	0.7071
chr17	81195210	5281752	0.0651	0.4926
chr18	78077248	3481712	0.0446	0.5702
chr19	59128983	3056042	0.0517	0.785
chr20	63025520	4097310	0.065	0.4593
chr21	48129895	2126349	0.0442	0.3819
chr22	51304566	1177476	0.023	0.2847
chrMT	16571	65212	3.9353	3.6353
chrX	155270560	8980229	0.0578	0.438
chrY	59373566	583575	0.0098	0.664

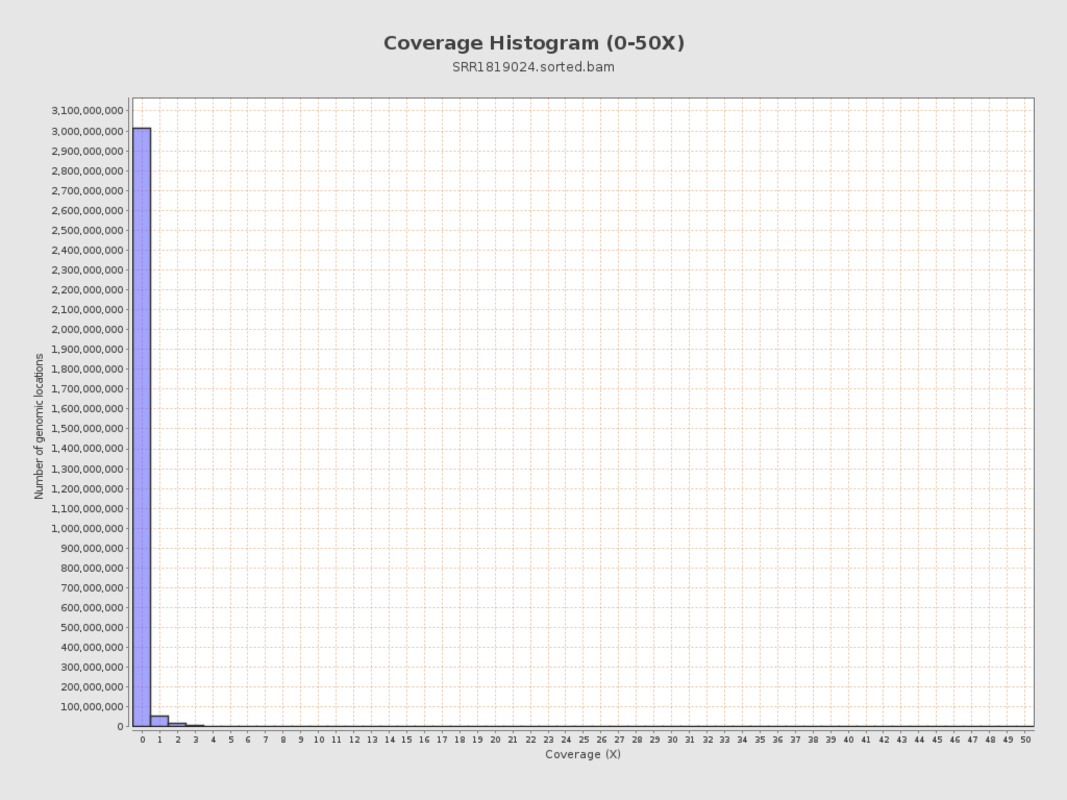
3. Results : Coverage across reference



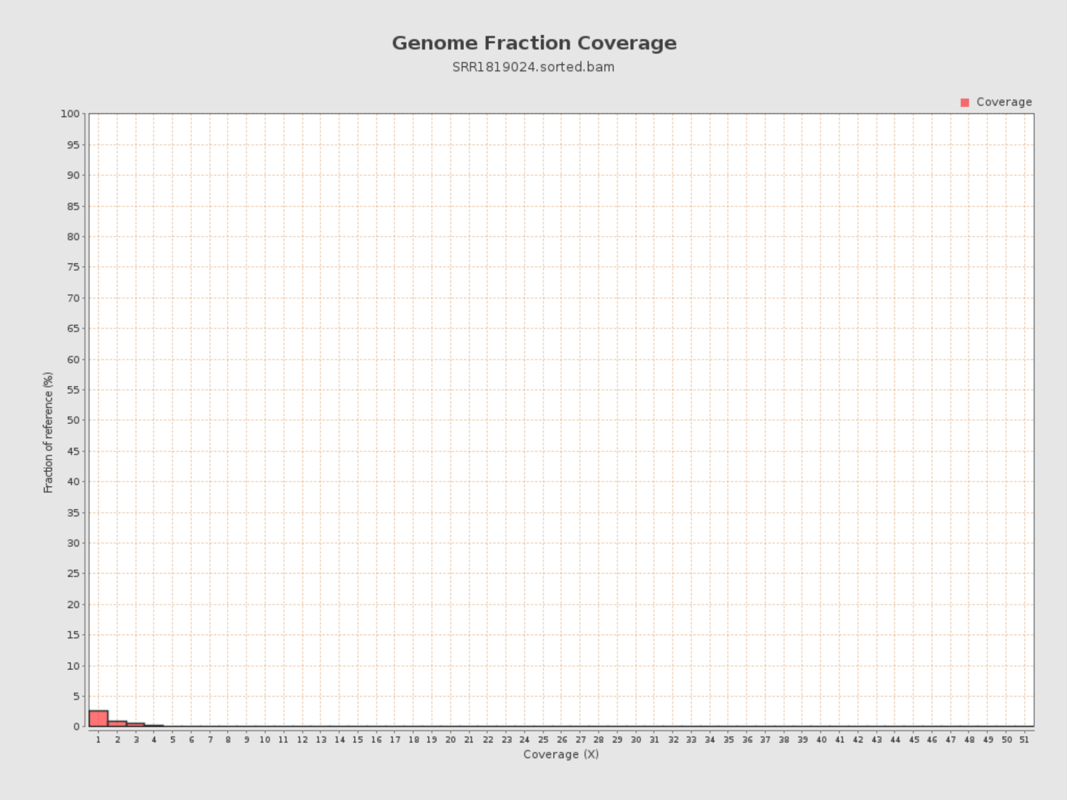
4. Results : Coverage Histogram



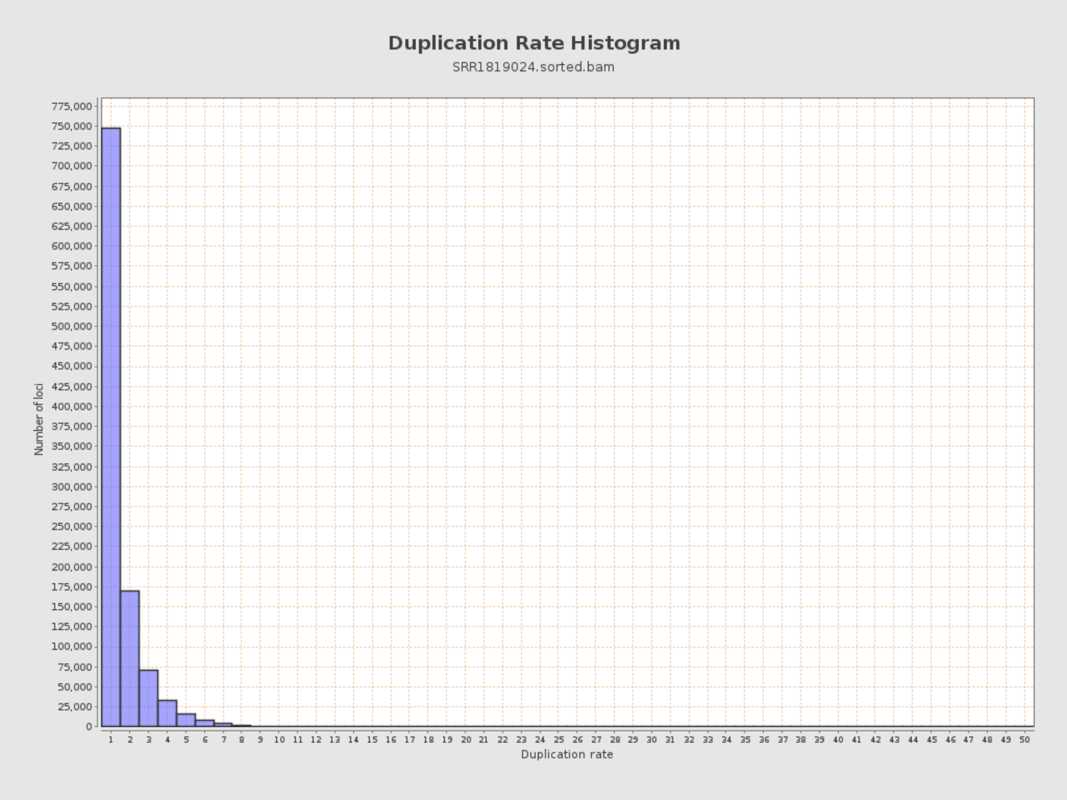
5. Results : Coverage Histogram (0-50X)



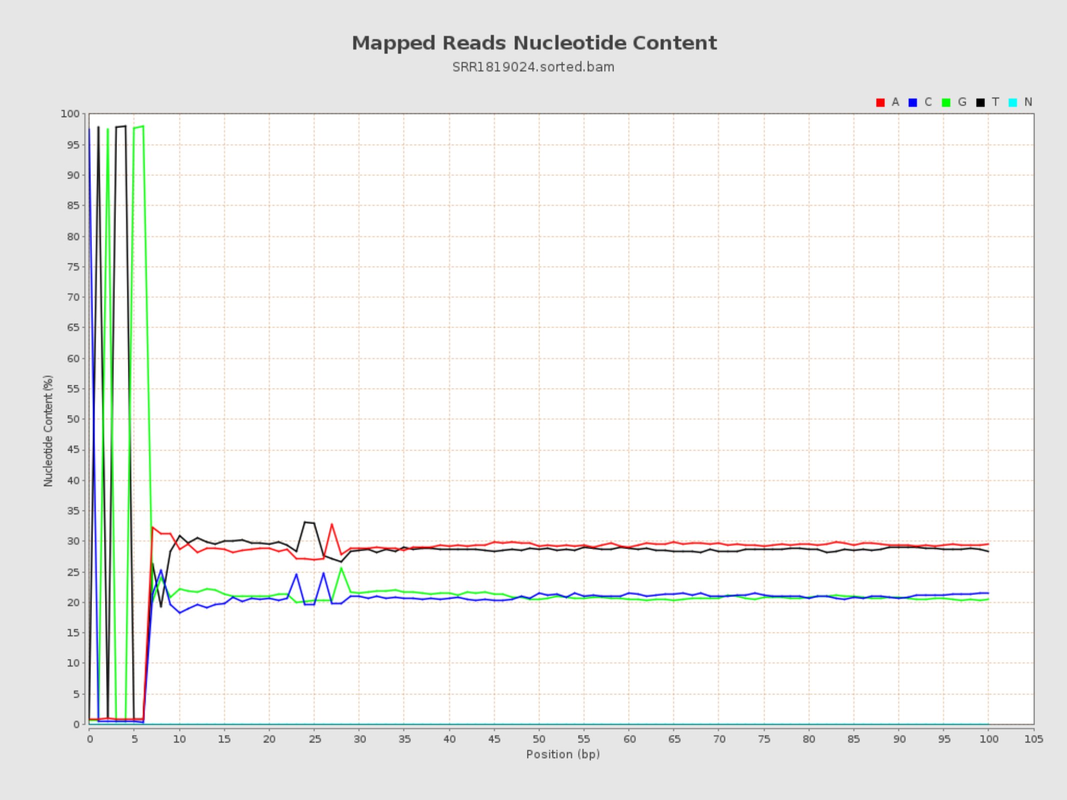
6. Results : Genome Fraction Coverage



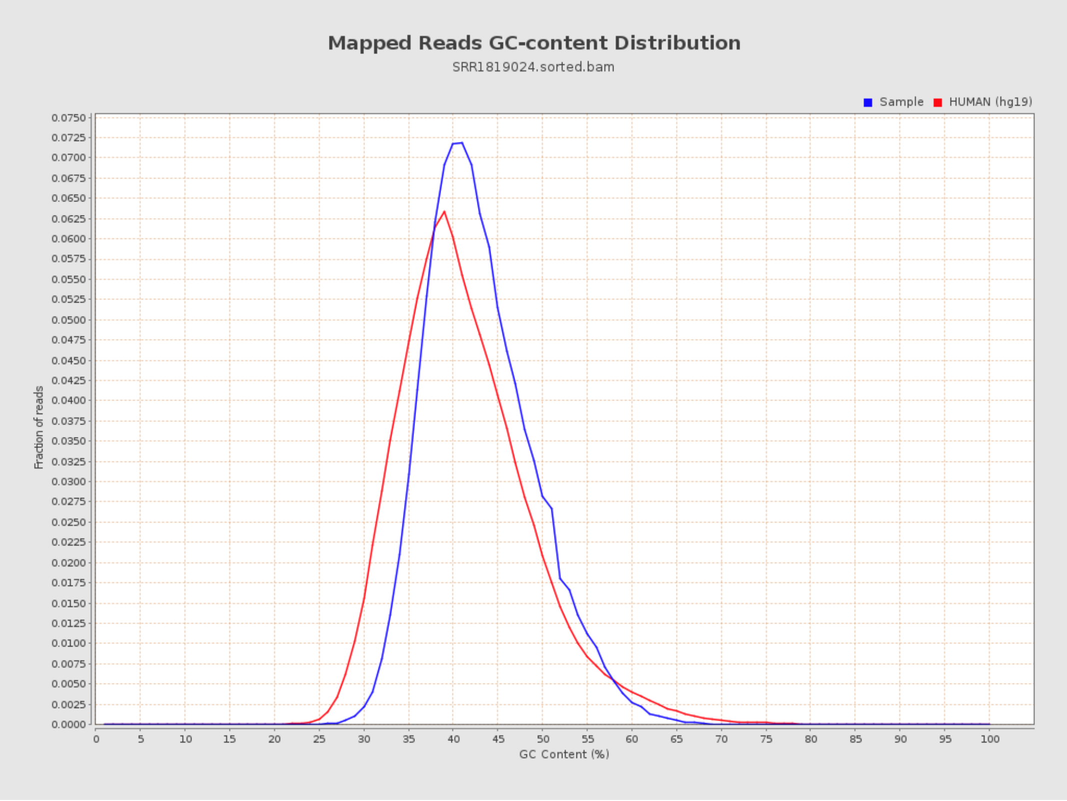
7. Results : Duplication Rate Histogram



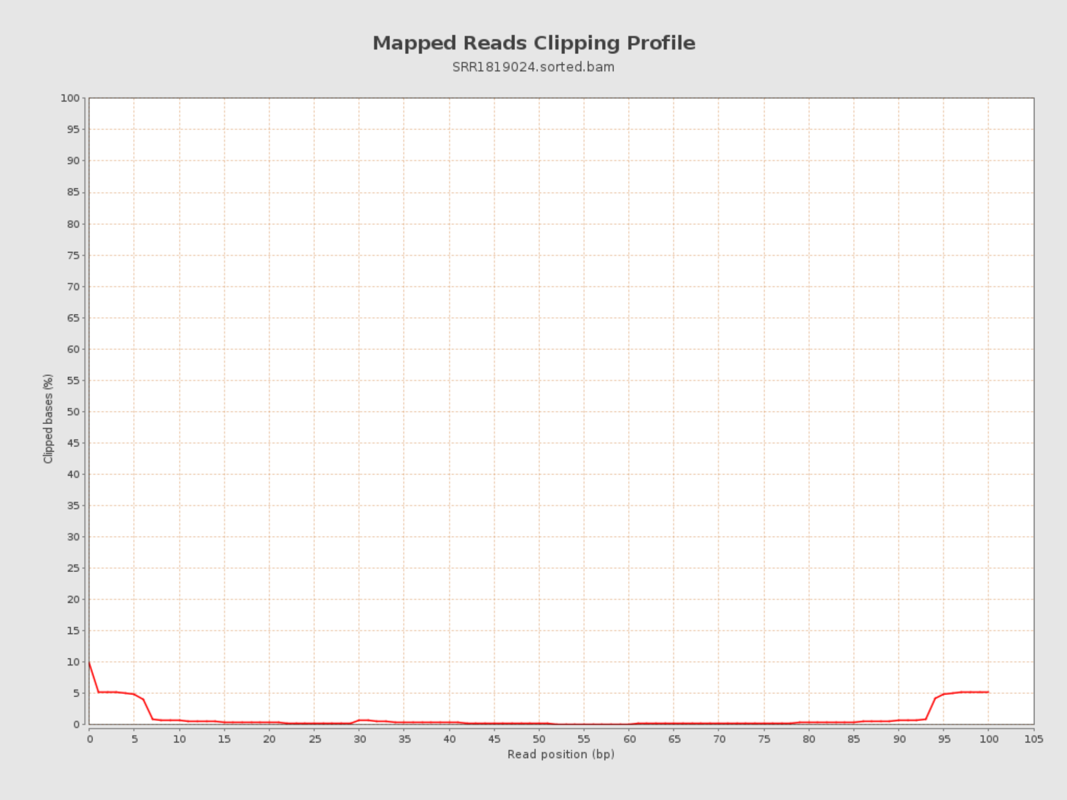
8. Results : Mapped Reads Nucleotide Content



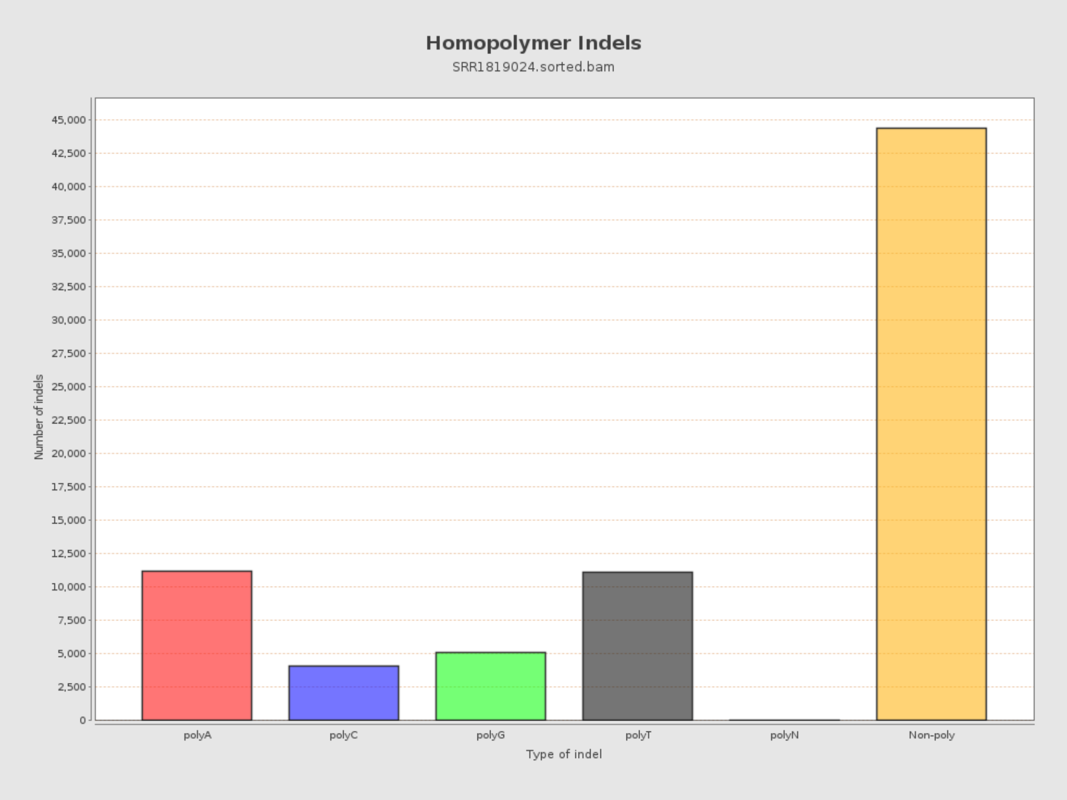
9. Results : Mapped Reads GC-content Distribution



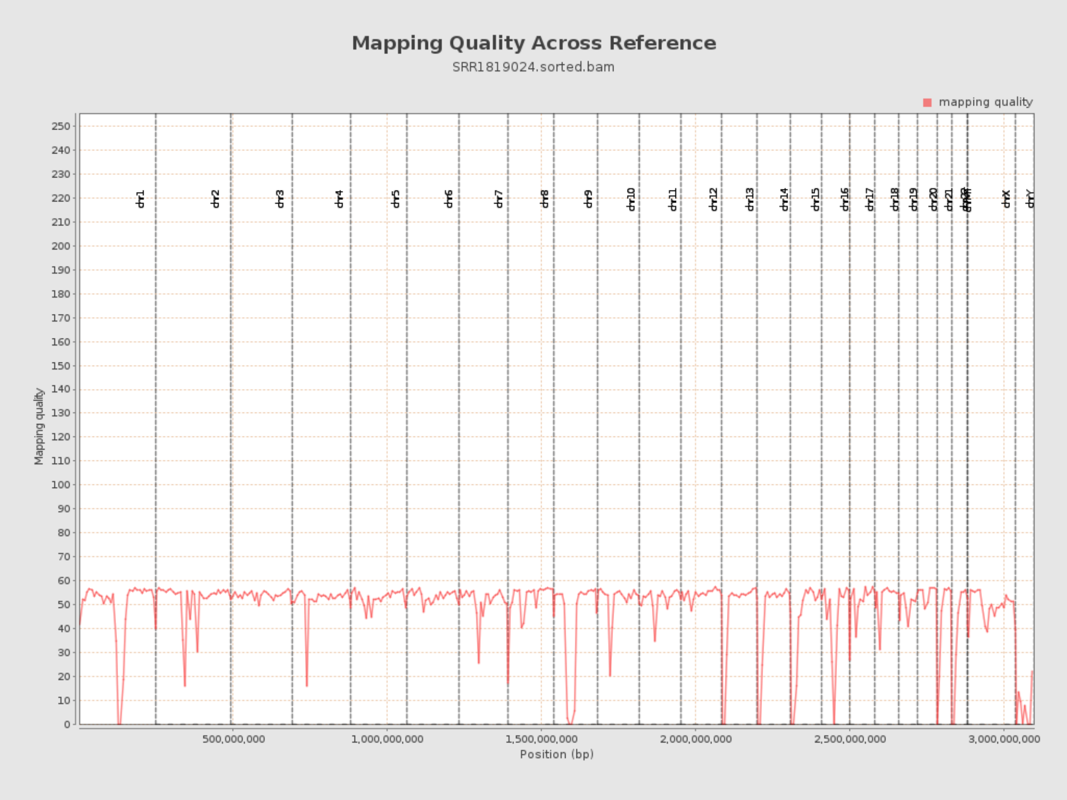
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram