Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 23:18:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819096.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_SRR1819096 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819096.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 23:17:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819096.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,825,254
Mapped reads	3,506,543 / 91.67%
Unmapped reads	318,711 / 8.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,670 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	503,079 / 13.15%
Duplication rate	9.49%
Clipped reads	3,510,169 / 91.76%

2.2. ACGT Content

Number/percentage of A's	53,618,060 / 25.87%
Number/percentage of C's	36,018,903 / 17.38%
Number/percentage of T's	65,852,925 / 31.78%
Number/percentage of G's	51,747,057 / 24.97%
Number/percentage of N's	2,952 / 0%
GC Percentage	42.35%

2.3. Coverage

Mean	0.067

Standard Deviation	0.6067

2.4. Mapping Quality

Mean Mapping Quality	45.48

2.5. Mismatches and indels

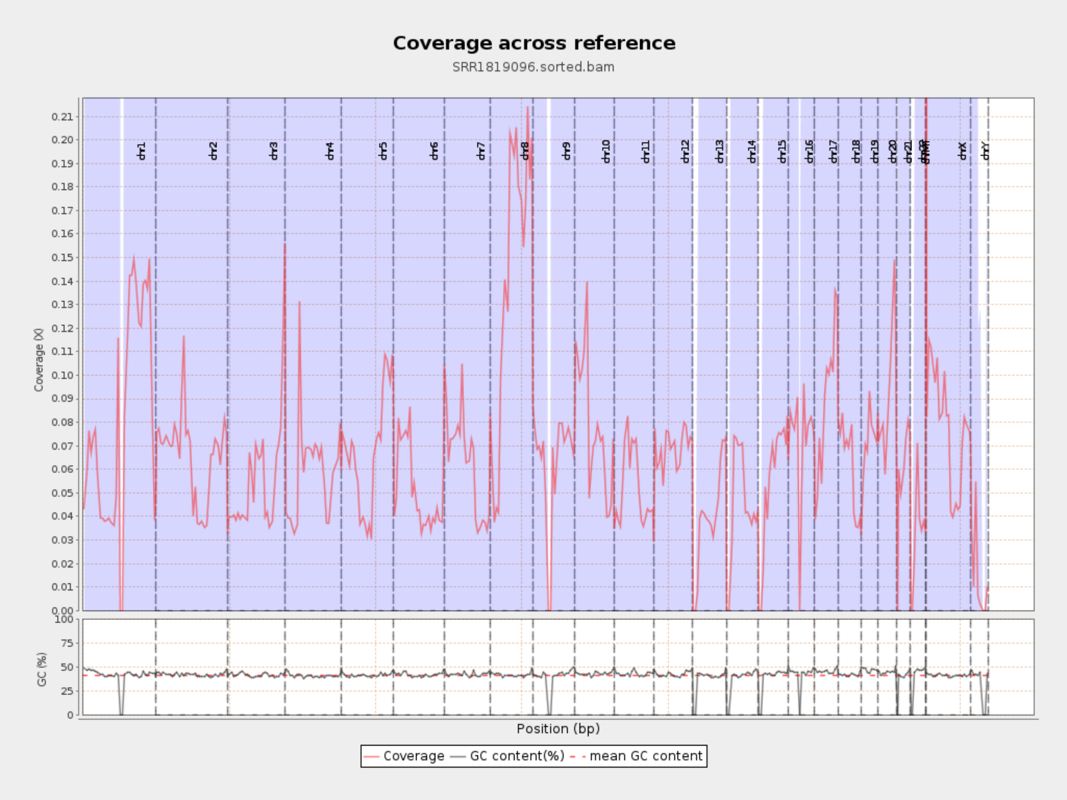
General error rate	0.51%
Mismatches	1,029,376
Insertions	15,449
Mapped reads with at least one insertion	0.44%
Deletions	37,004
Mapped reads with at least one deletion	1.05%
Homopolymer indels	43.12%

2.6. Chromosome stats

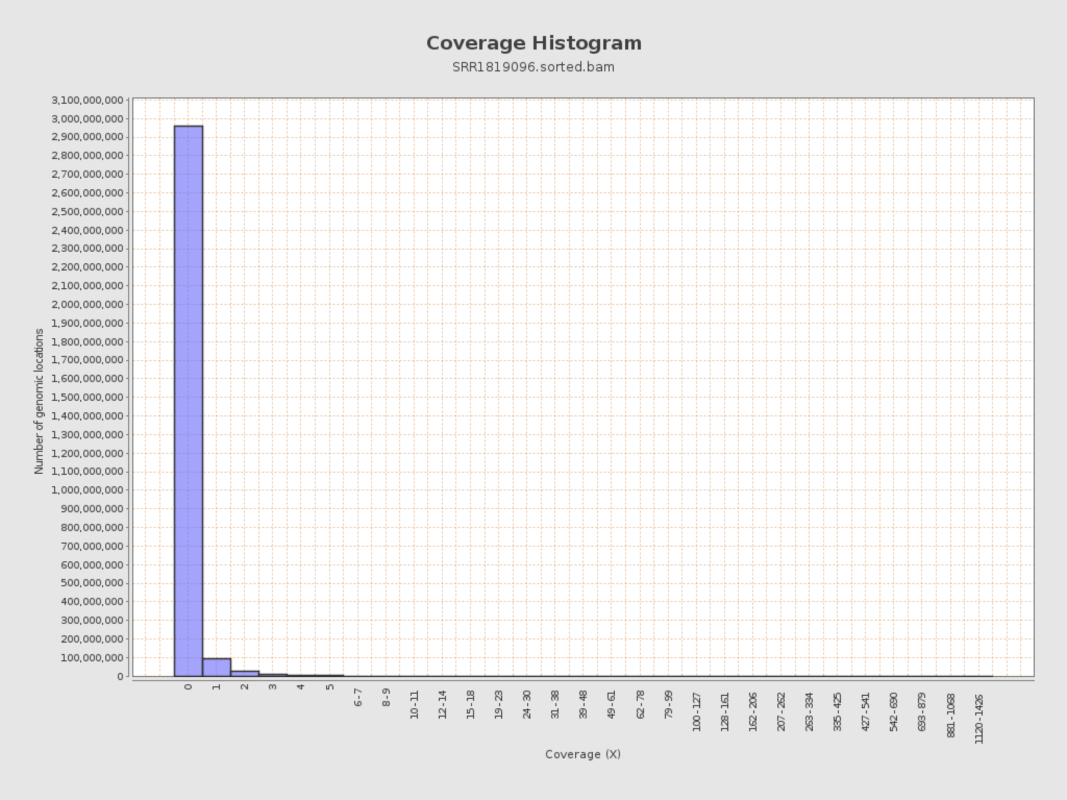
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20082896	0.0806	1.1322
chr2	243199373	16117581	0.0663	0.6973
chr3	198022430	10879023	0.0549	0.3355
chr4	191154276	11273996	0.059	0.508
chr5	180915260	12257174	0.0678	0.3769
chr6	171115067	8741019	0.0511	0.394
chr7	159138663	10008162	0.0629	0.6579

chr8	146364022	21200834	0.1449	0.8847
chr9	141213431	8733373	0.0618	0.4779
chr10	135534747	10532789	0.0777	0.7292
chr11	135006516	7031882	0.0521	0.499
chr12	133851895	9303111	0.0695	0.3839
chr13	115169878	4556359	0.0396	0.2872
chr14	107349540	4893881	0.0456	0.3134
chr15	102531392	5412438	0.0528	0.3262
chr16	90354753	6443702	0.0713	0.4296
chr17	81195210	7133727	0.0879	0.4665
chr18	78077248	4818096	0.0617	0.9135
chr19	59128983	4250136	0.0719	0.7236
chr20	63025520	5984249	0.0949	0.4675
chr21	48129895	2878747	0.0598	0.4786
chr22	51304566	1636992	0.0319	0.2552
chrMT	16571	118175	7.1314	5.6801
chrX	155270560	12185281	0.0785	0.443
chrY	59373566	827539	0.0139	0.4816

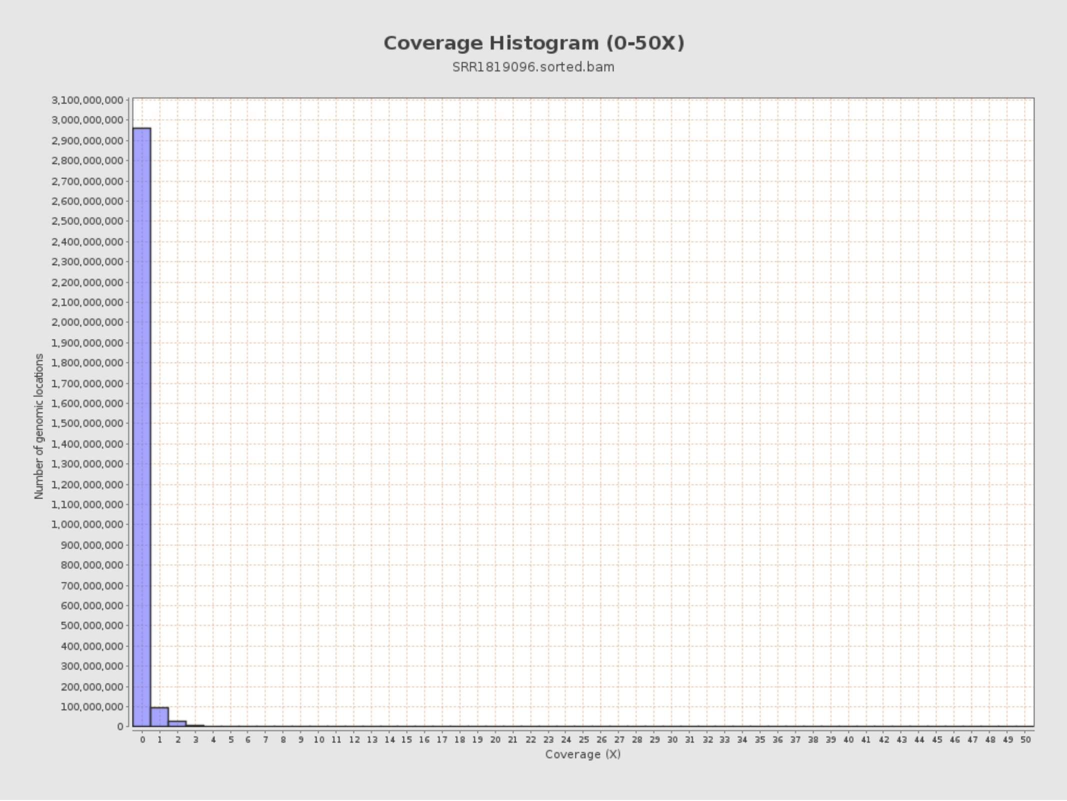
3. Results : Coverage across reference



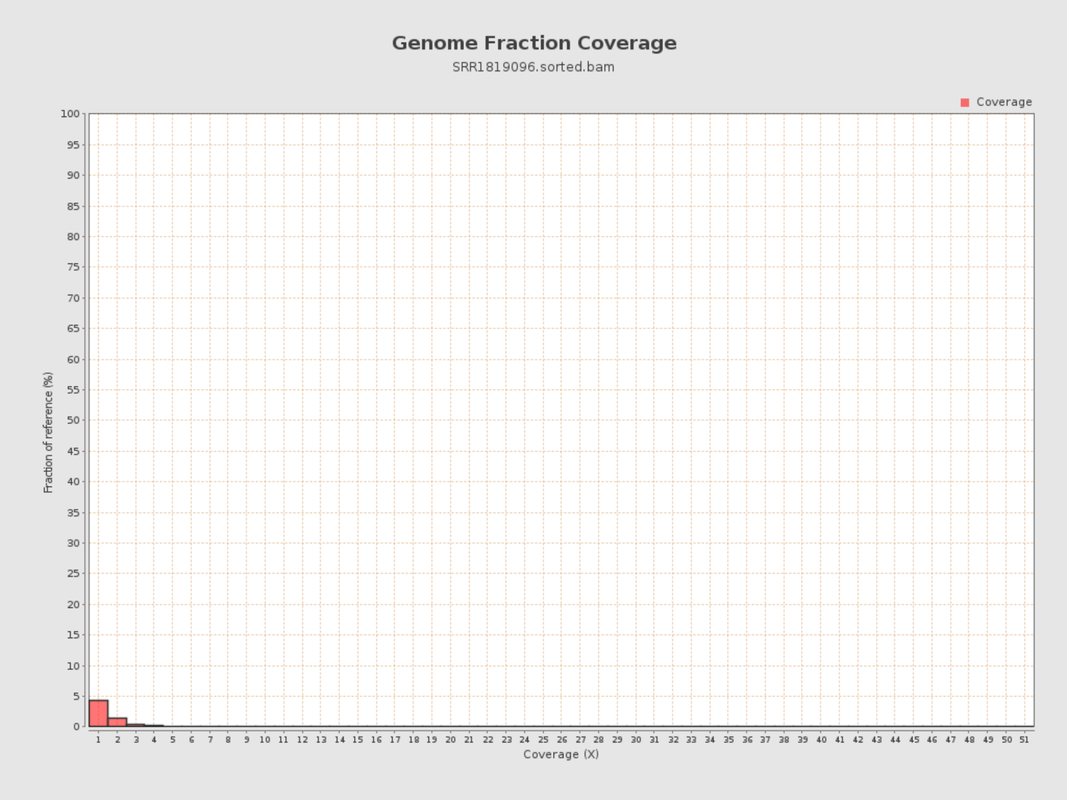
4. Results : Coverage Histogram



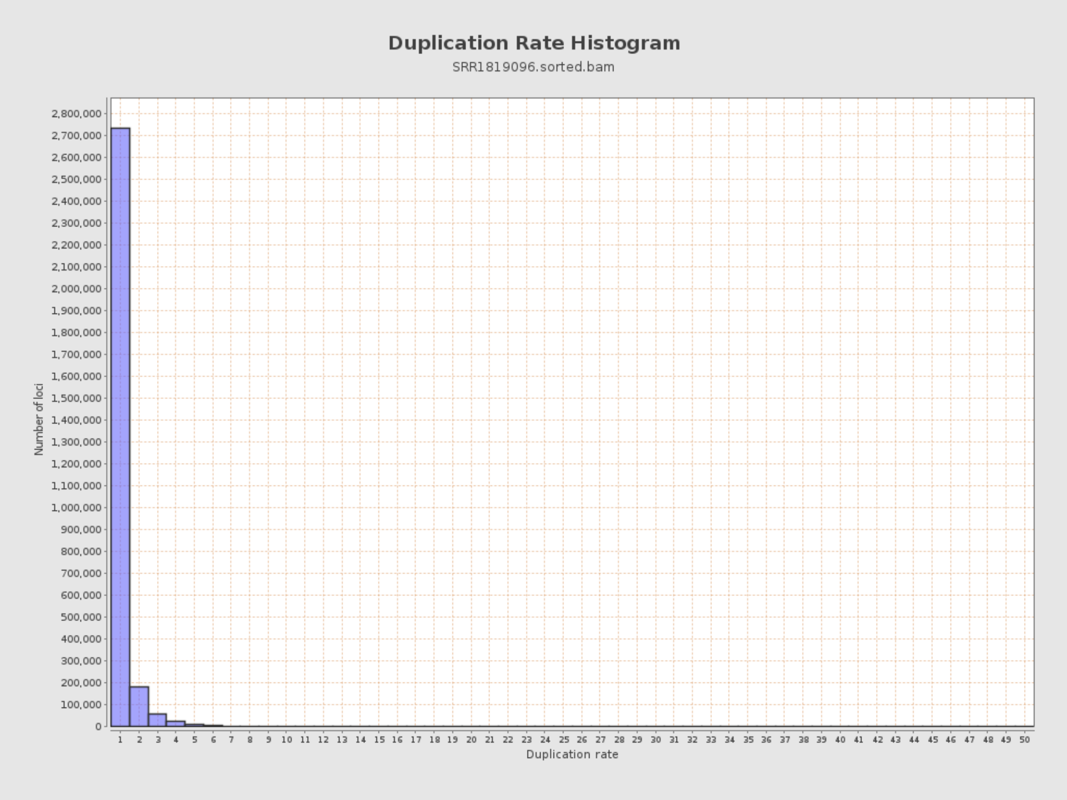
5. Results : Coverage Histogram (0-50X)



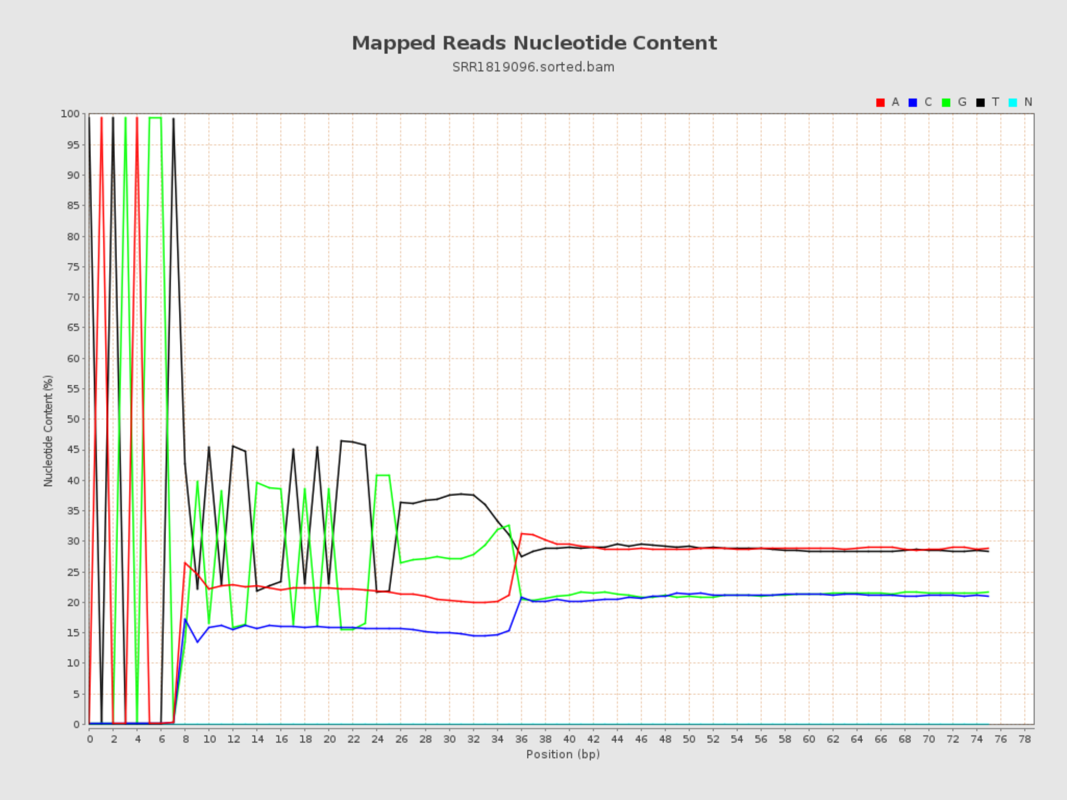
6. Results : Genome Fraction Coverage



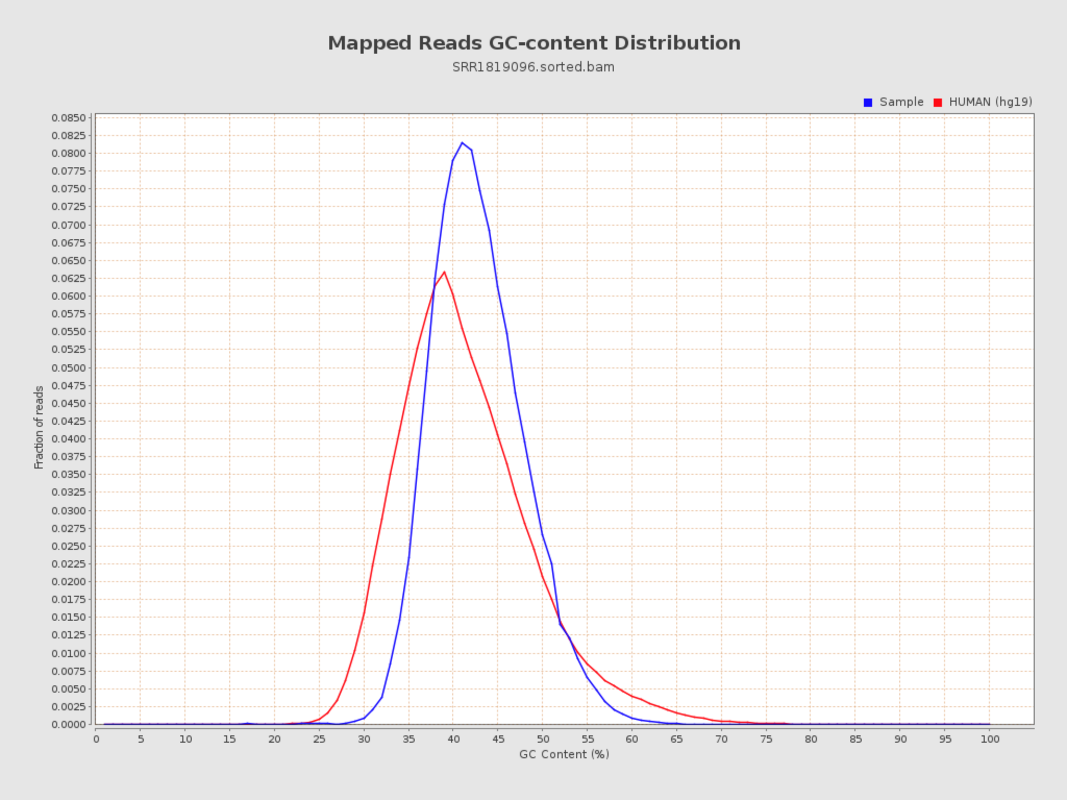
7. Results : Duplication Rate Histogram



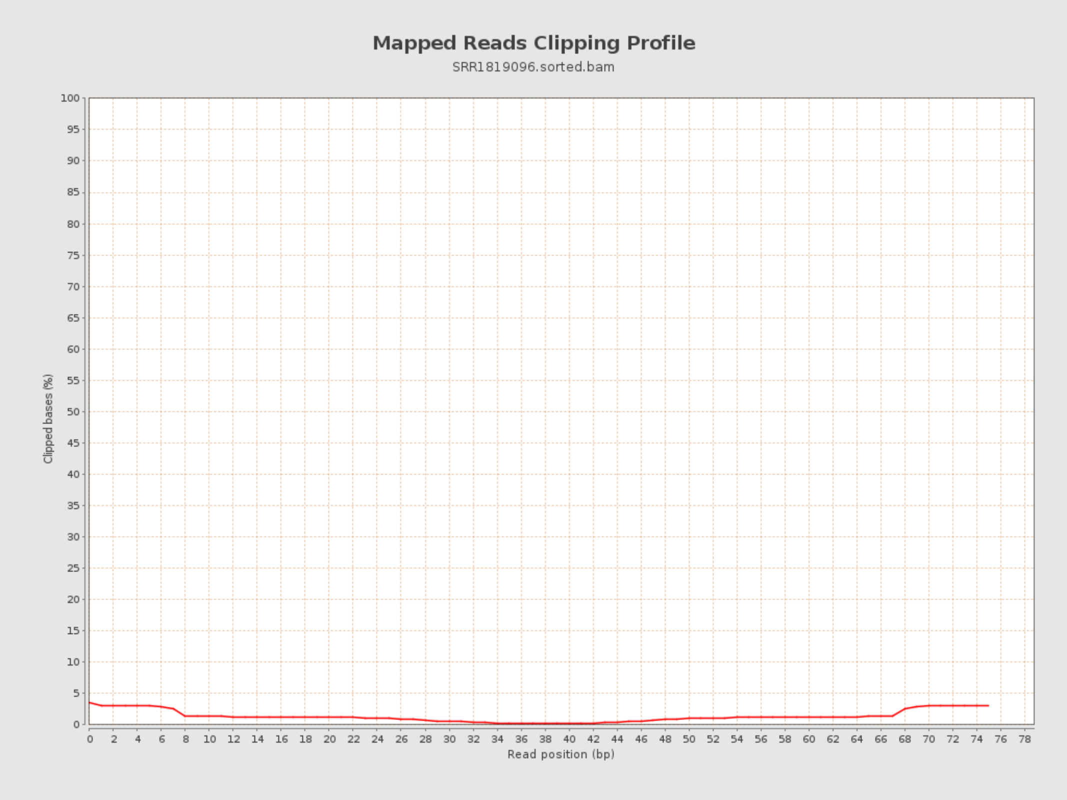
8. Results : Mapped Reads Nucleotide Content



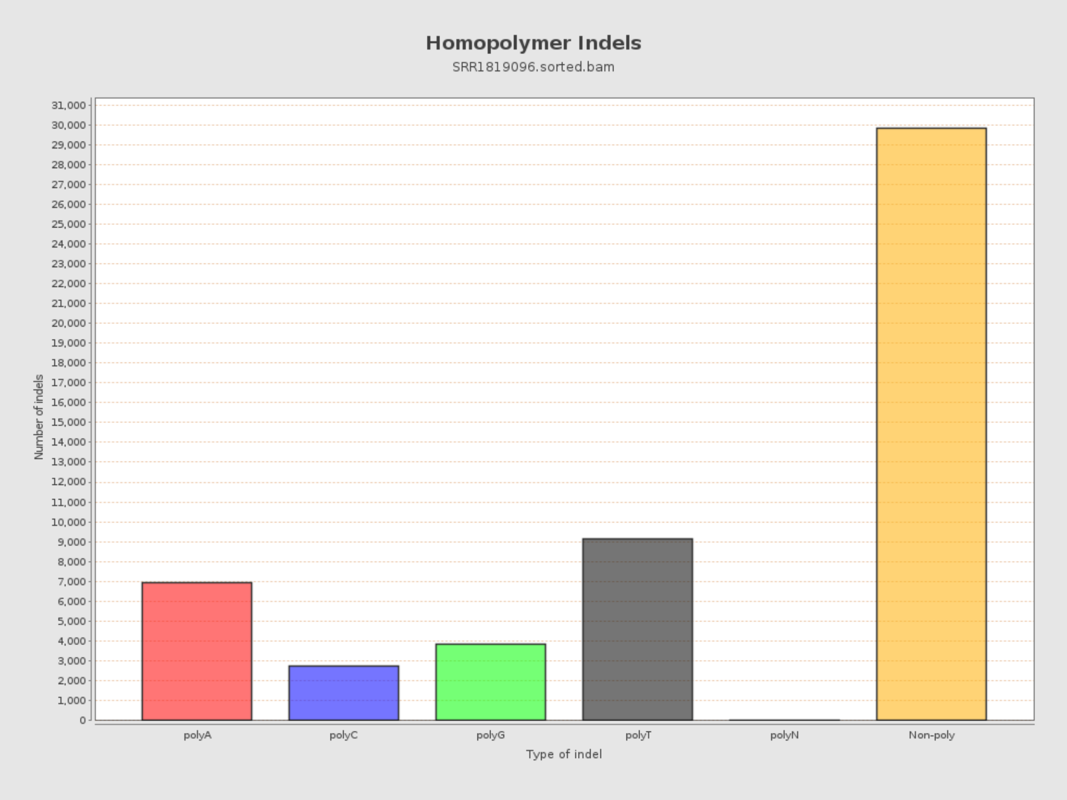
9. Results : Mapped Reads GC-content Distribution



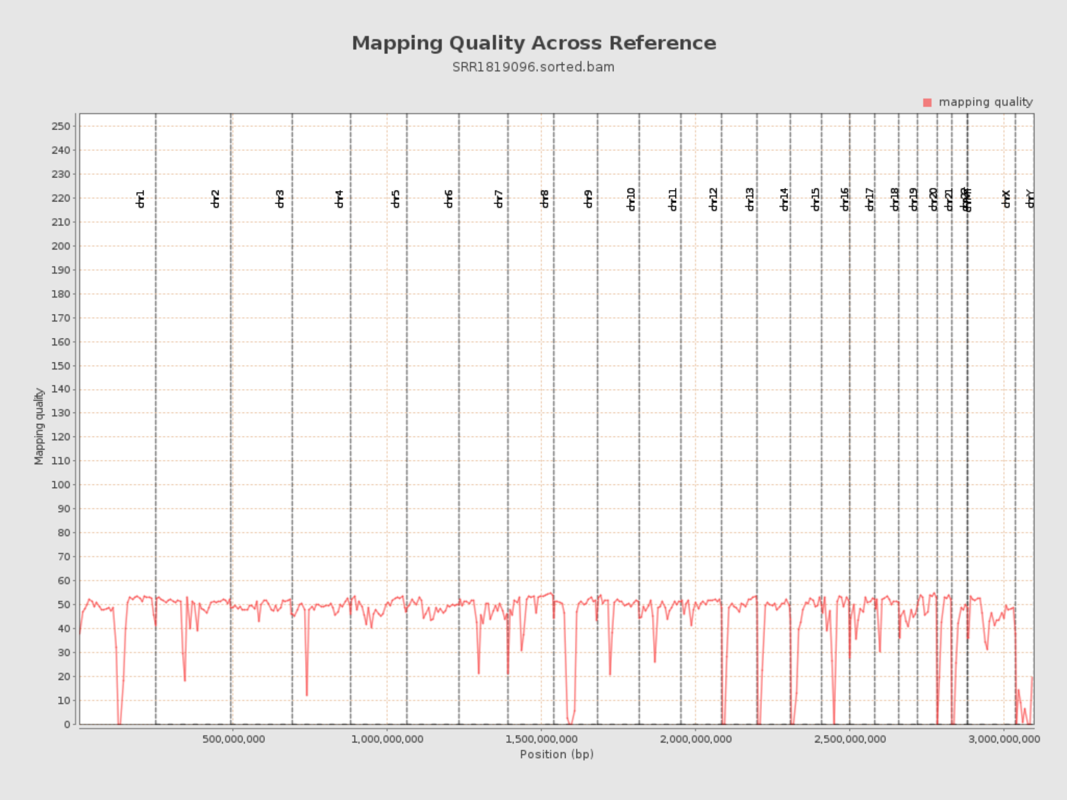
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram