Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 23:46:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819098.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_SRR1819098 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819098.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 23:46:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819098.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	993,943
Mapped reads	904,626 / 91.01%
Unmapped reads	89,317 / 8.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,636 / 0.37%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	23,715 / 2.39%
Duplication rate	1.92%
Clipped reads	905,788 / 91.13%

2.2. ACGT Content

Number/percentage of A's	13,591,609 / 25.65%
Number/percentage of C's	10,461,319 / 19.74%
Number/percentage of T's	16,419,410 / 30.98%
Number/percentage of G's	12,518,694 / 23.62%
Number/percentage of N's	711 / 0%
GC Percentage	43.37%

2.3. Coverage

Mean	0.0171

Standard Deviation	0.1832

2.4. Mapping Quality

Mean Mapping Quality	44.85

2.5. Mismatches and indels

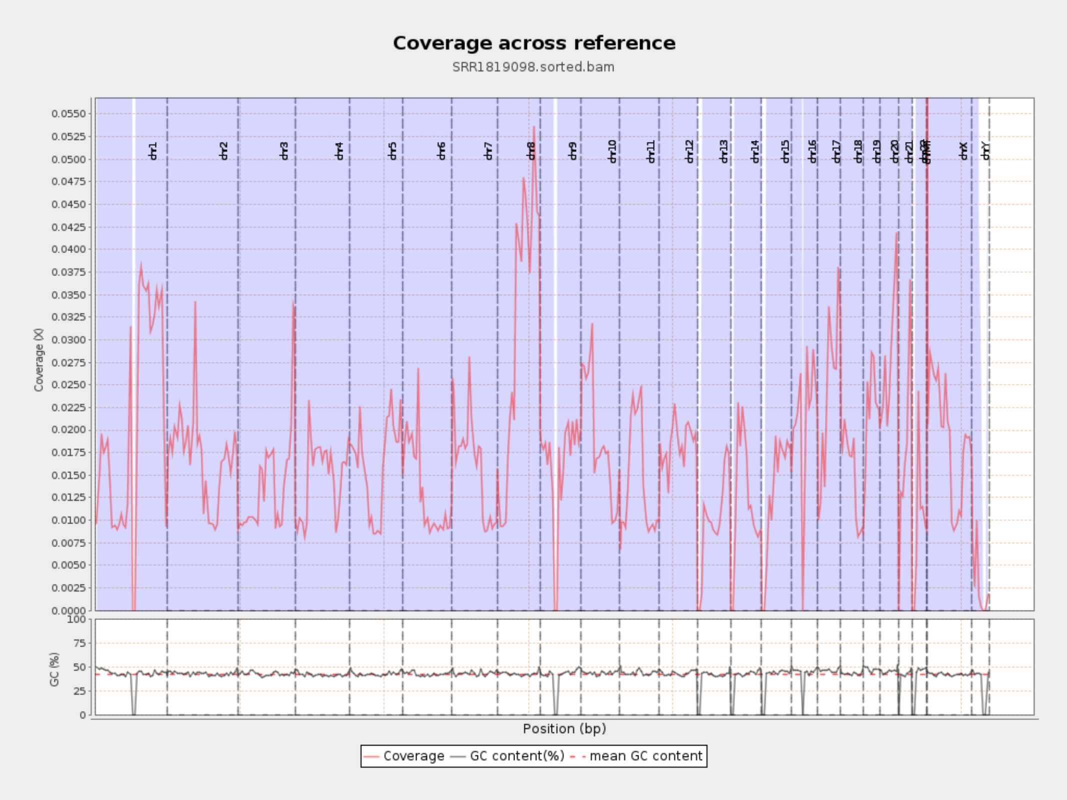
General error rate	0.53%
Mismatches	273,528
Insertions	3,769
Mapped reads with at least one insertion	0.41%
Deletions	10,093
Mapped reads with at least one deletion	1.11%
Homopolymer indels	40.79%

2.6. Chromosome stats

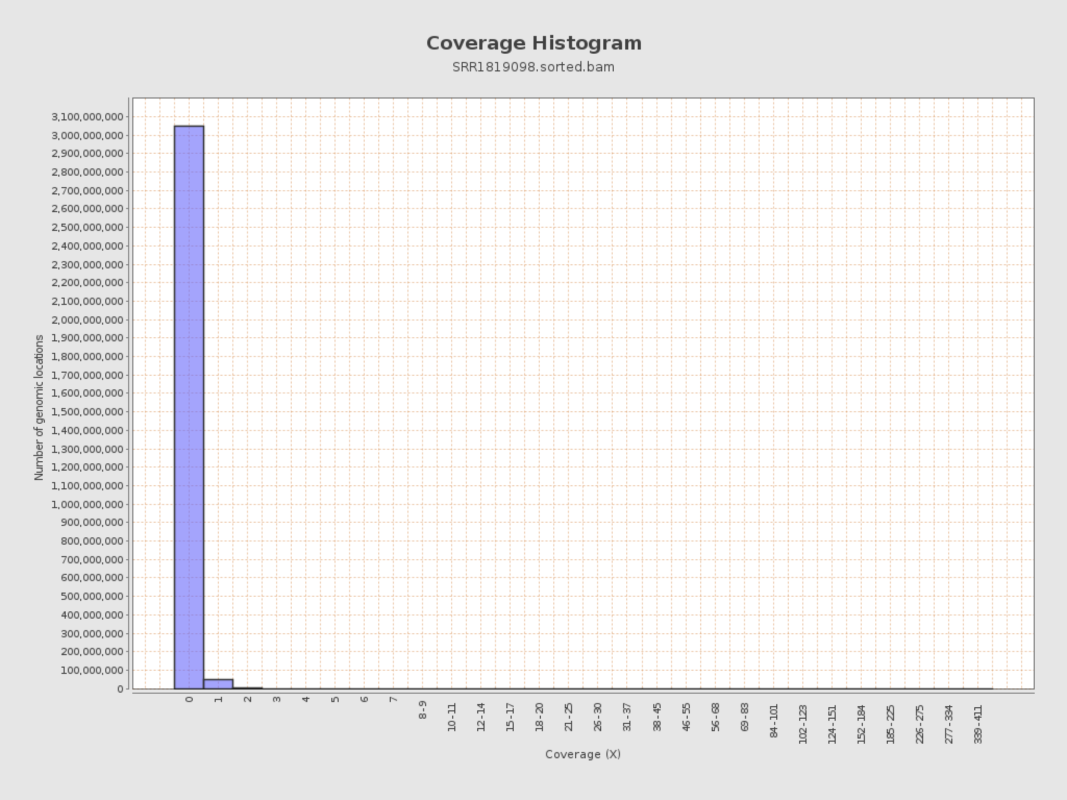
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5074012	0.0204	0.3212
chr2	243199373	4149673	0.0171	0.2102
chr3	198022430	2739524	0.0138	0.125
chr4	191154276	2811213	0.0147	0.1381
chr5	180915260	2968137	0.0164	0.1356
chr6	171115067	2262461	0.0132	0.1415
chr7	159138663	2578335	0.0162	0.2114

chr8	146364022	4661606	0.0318	0.208
chr9	141213431	2244968	0.0159	0.1631
chr10	135534747	2620108	0.0193	0.1841
chr11	135006516	1958925	0.0145	0.1698
chr12	133851895	2464927	0.0184	0.1434
chr13	115169878	1145099	0.0099	0.1049
chr14	107349540	1310122	0.0122	0.1179
chr15	102531392	1340688	0.0131	0.1228
chr16	90354753	1877394	0.0208	0.1581
chr17	81195210	1937925	0.0239	0.1713
chr18	78077248	1179317	0.0151	0.2521
chr19	59128983	1330168	0.0225	0.2447
chr20	63025520	1796254	0.0285	0.1793
chr21	48129895	886659	0.0184	0.1513
chr22	51304566	496347	0.0097	0.104
chrMT	16571	3194	0.1927	0.4637
chrX	155270560	3004771	0.0194	0.1565
chrY	59373566	166472	0.0028	0.0925

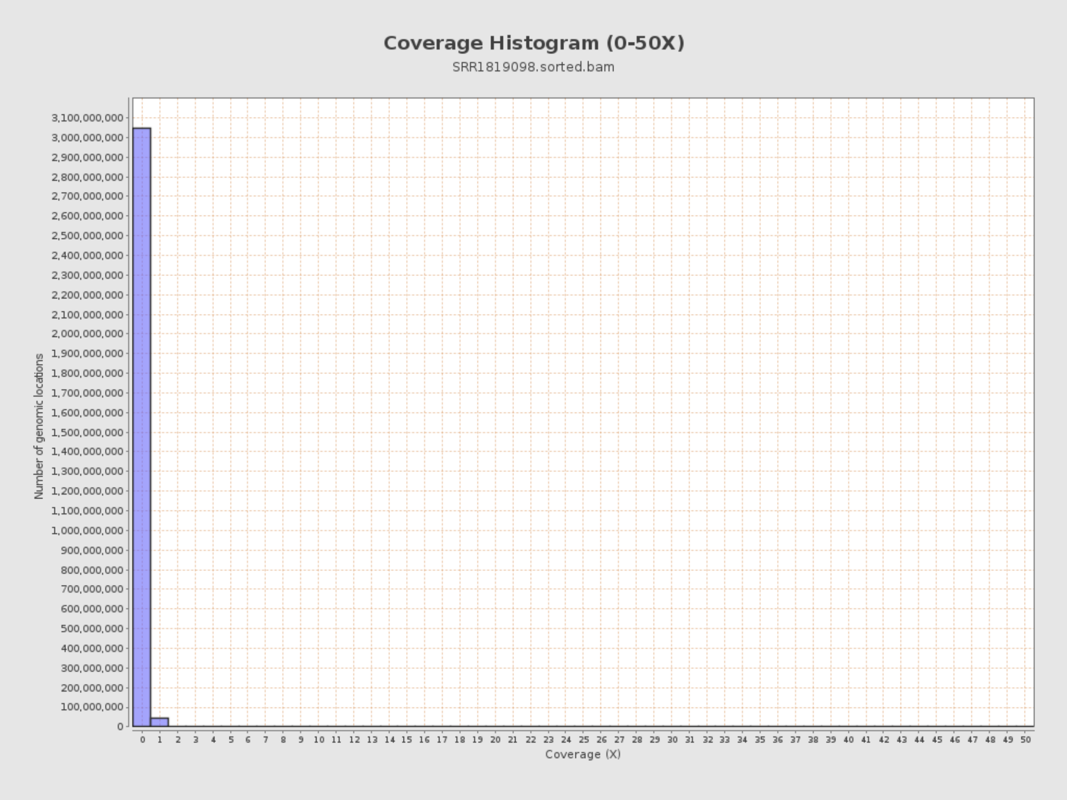
3. Results : Coverage across reference



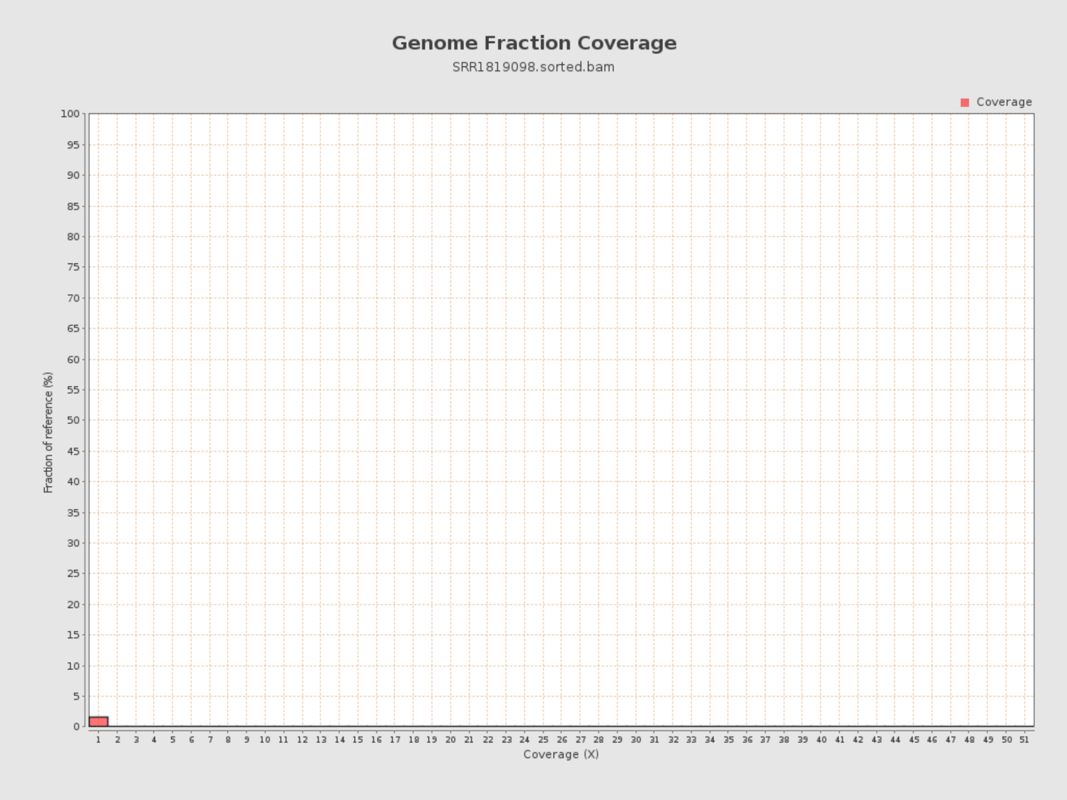
4. Results : Coverage Histogram



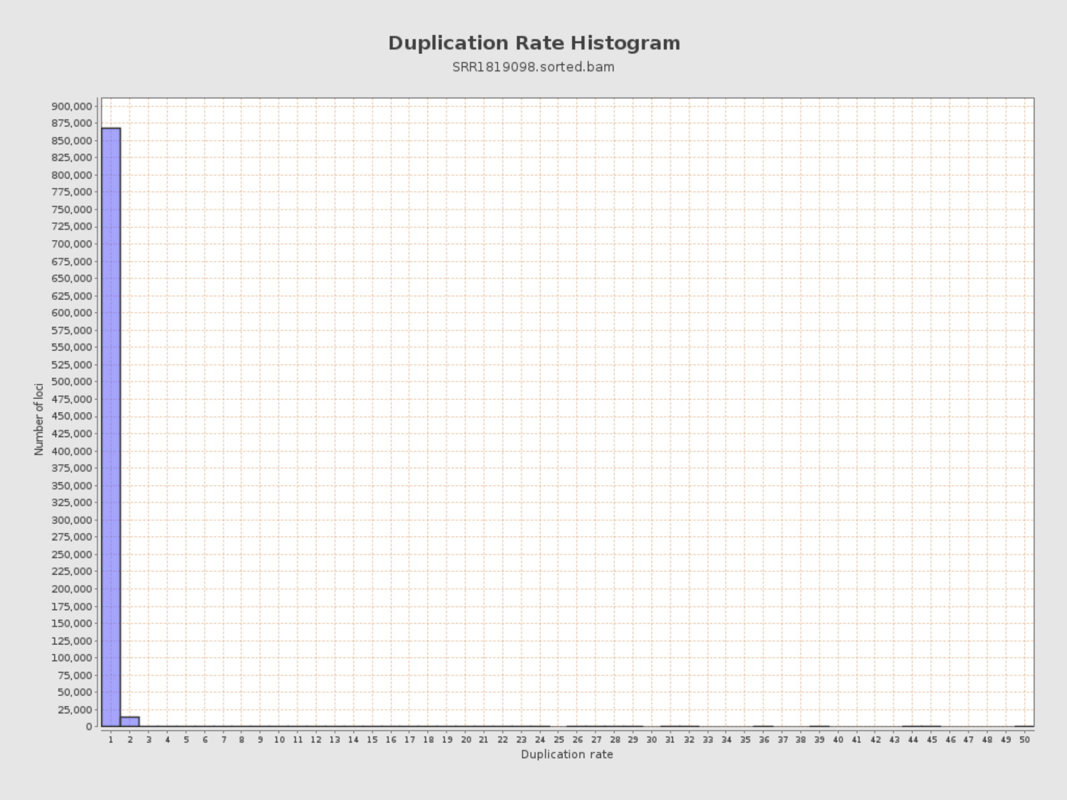
5. Results : Coverage Histogram (0-50X)



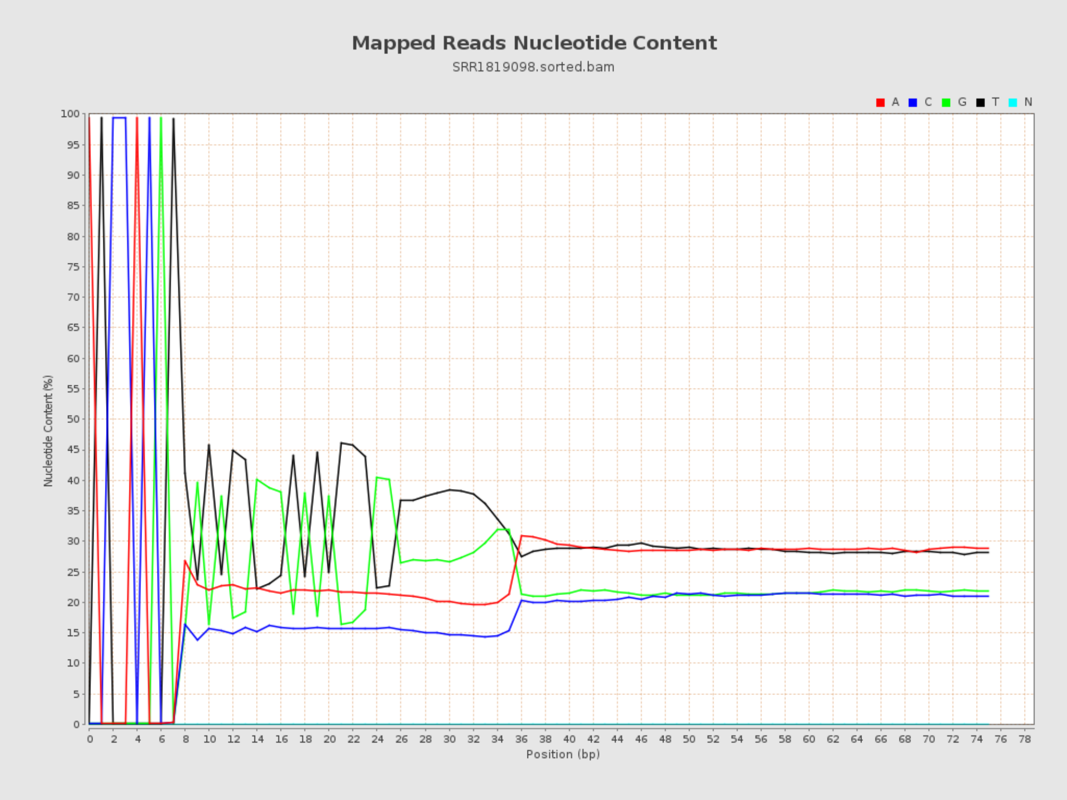
6. Results : Genome Fraction Coverage



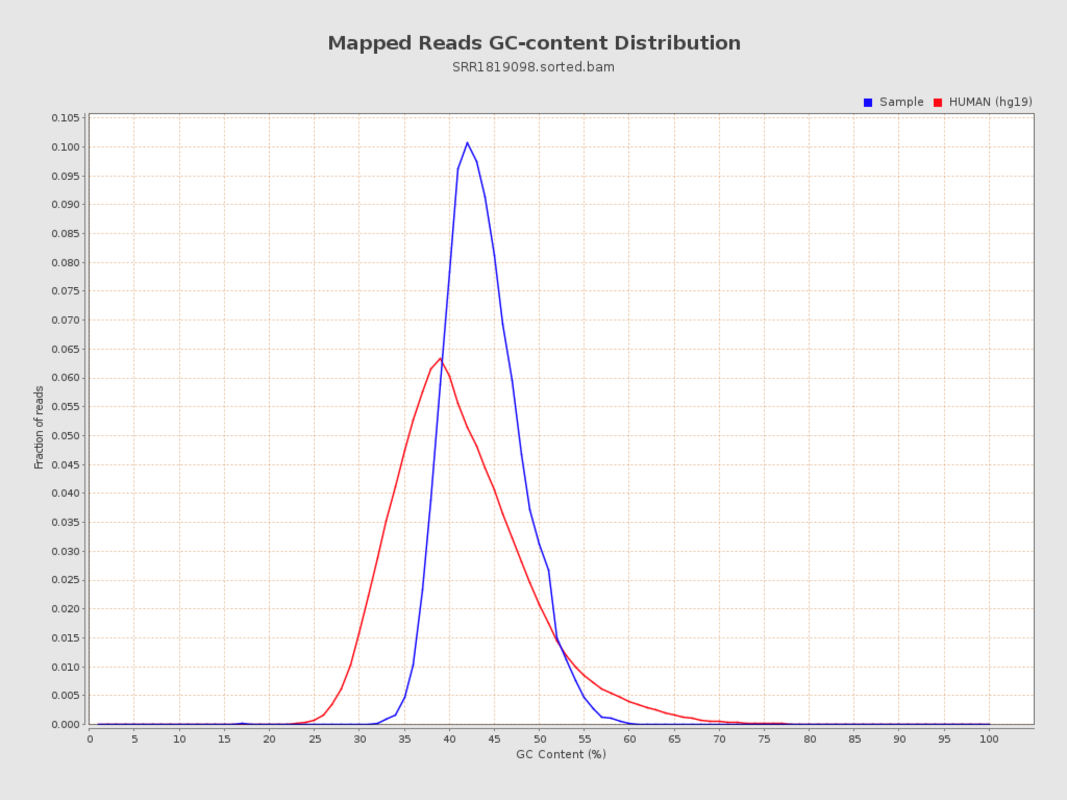
7. Results : Duplication Rate Histogram



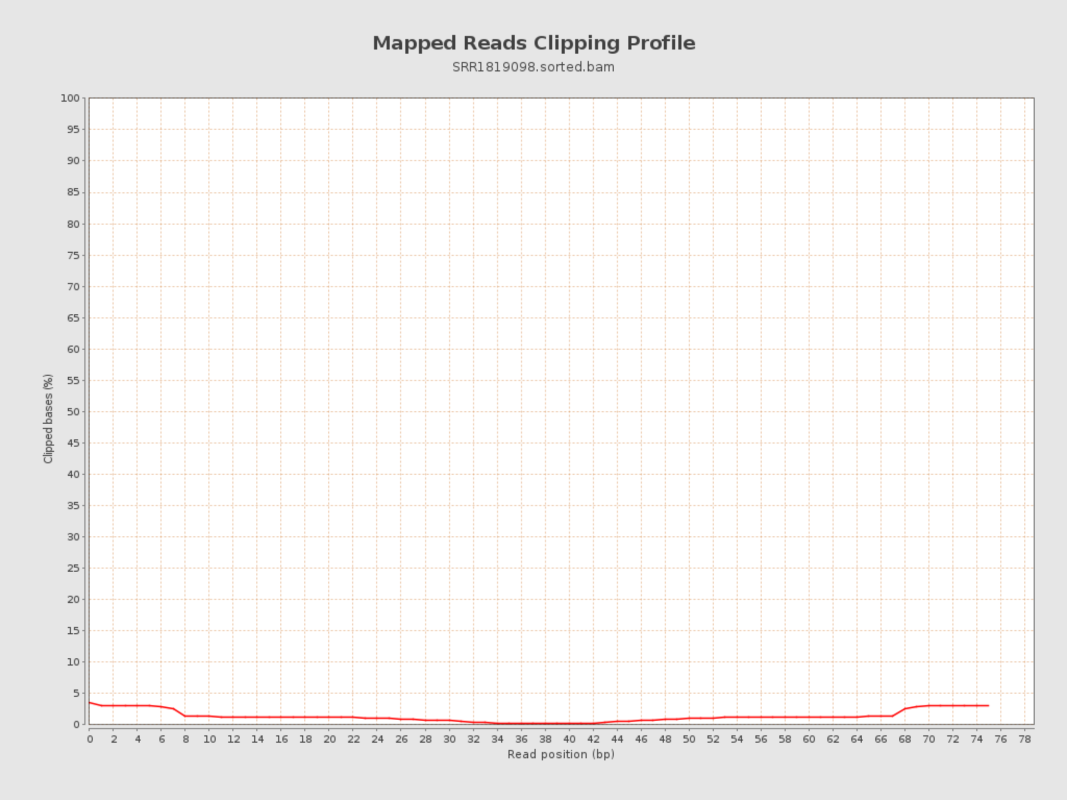
8. Results : Mapped Reads Nucleotide Content



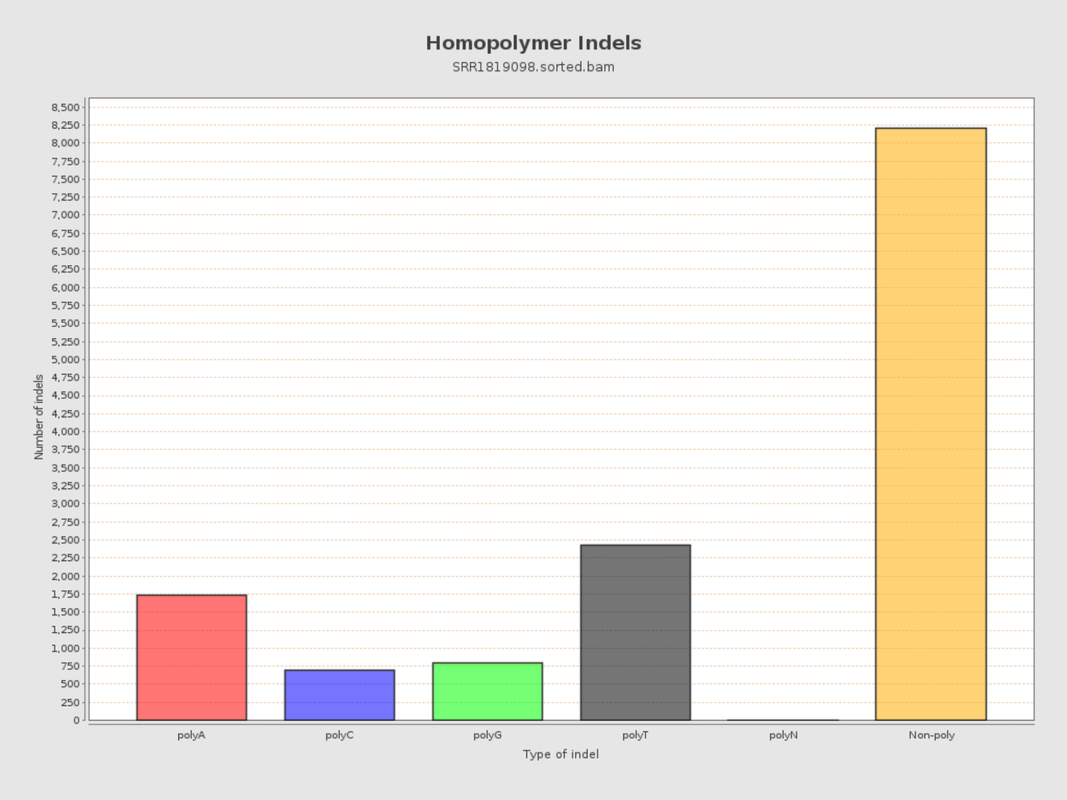
9. Results : Mapped Reads GC-content Distribution



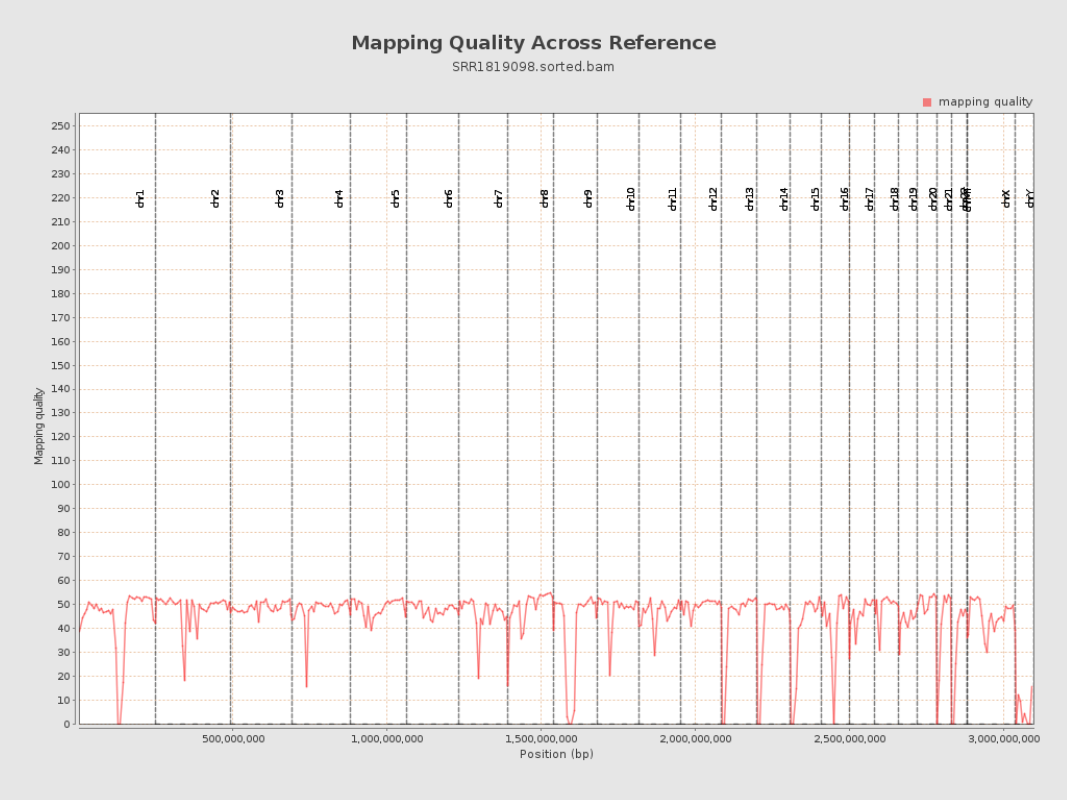
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram