Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 21:04:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525019.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_SRR10525019 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525019.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 21:04:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525019.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,772,200
Mapped reads	1,592,371 / 89.85%
Unmapped reads	179,829 / 10.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,143 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	46,848 / 2.64%
Duplication rate	2%
Clipped reads	1,594,273 / 89.96%

2.2. ACGT Content

Number/percentage of A's	21,615,831 / 23.88%
Number/percentage of C's	18,397,848 / 20.33%
Number/percentage of T's	28,934,525 / 31.97%
Number/percentage of G's	21,566,072 / 23.83%
Number/percentage of N's	846 / 0%
GC Percentage	44.15%

2.3. Coverage

Mean	0.0292

Standard Deviation	0.2597

2.4. Mapping Quality

Mean Mapping Quality	42.55

2.5. Mismatches and indels

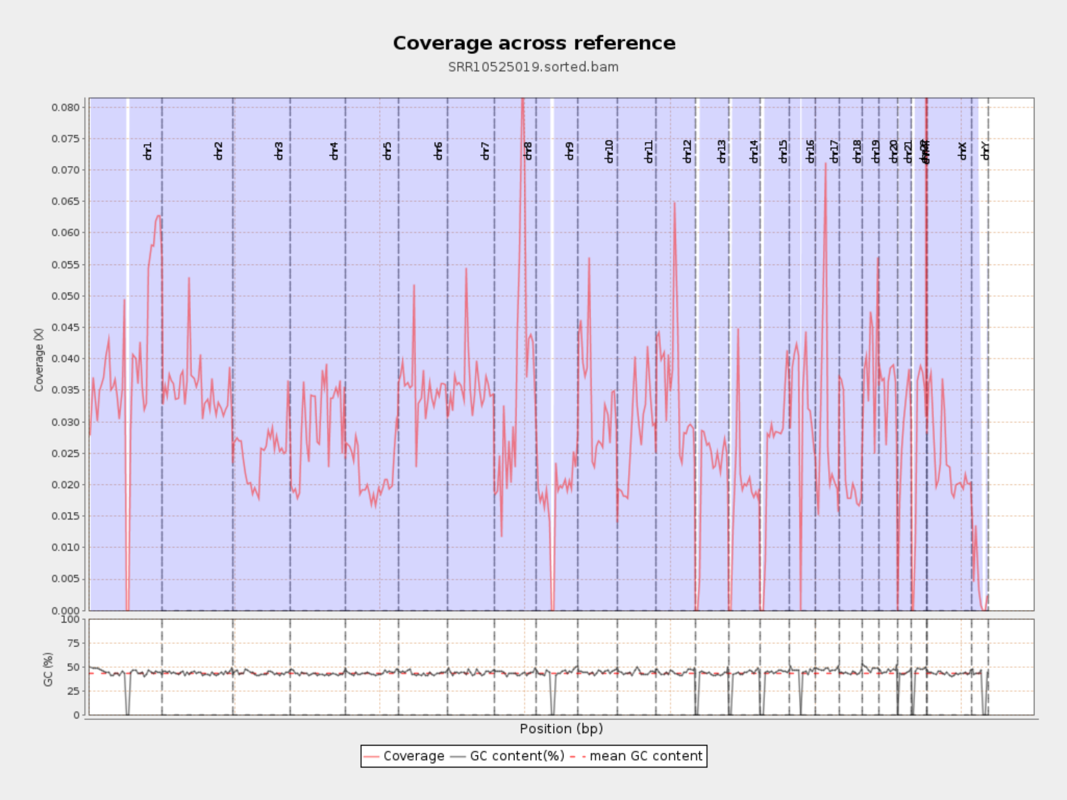
General error rate	0.52%
Mismatches	463,954
Insertions	5,646
Mapped reads with at least one insertion	0.35%
Deletions	17,433
Mapped reads with at least one deletion	1.09%
Homopolymer indels	43.32%

2.6. Chromosome stats

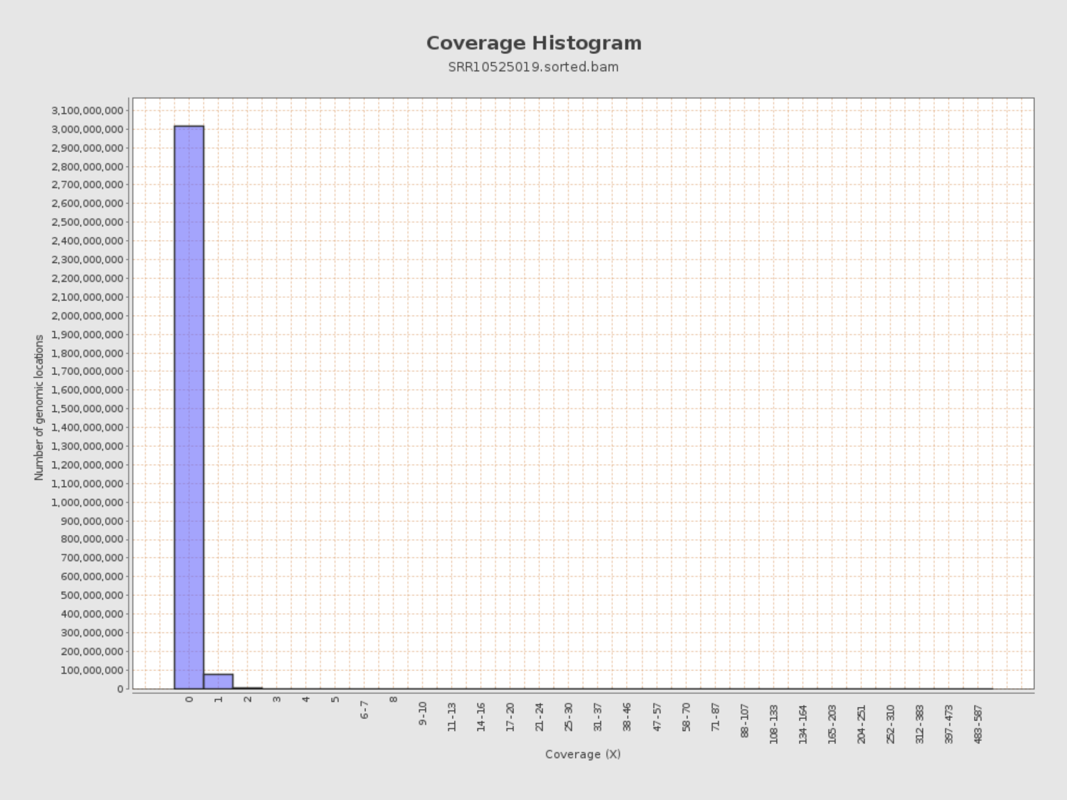
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9551699	0.0383	0.4391
chr2	243199373	8568030	0.0352	0.3222
chr3	198022430	4932058	0.0249	0.1722
chr4	191154276	5636657	0.0295	0.1997
chr5	180915260	3931861	0.0217	0.1628
chr6	171115067	6039509	0.0353	0.2795
chr7	159138663	5730262	0.036	0.3732

chr8	146364022	5265571	0.036	0.2483
chr9	141213431	2489311	0.0176	0.1994
chr10	135534747	4538976	0.0335	0.2669
chr11	135006516	3720014	0.0276	0.2339
chr12	133851895	4799861	0.0359	0.2068
chr13	115169878	2439767	0.0212	0.1581
chr14	107349540	2024256	0.0189	0.1554
chr15	102531392	2517368	0.0246	0.1805
chr16	90354753	2929901	0.0324	0.207
chr17	81195210	2427785	0.0299	0.2537
chr18	78077248	1775093	0.0227	0.3083
chr19	59128983	2359174	0.0399	0.3043
chr20	63025520	2237114	0.0355	0.2081
chr21	48129895	1286977	0.0267	0.1833
chr22	51304566	1293975	0.0252	0.1711
chrMT	16571	13961	0.8425	1.0613
chrX	155270560	3776698	0.0243	0.2099
chrY	59373566	257889	0.0043	0.0985

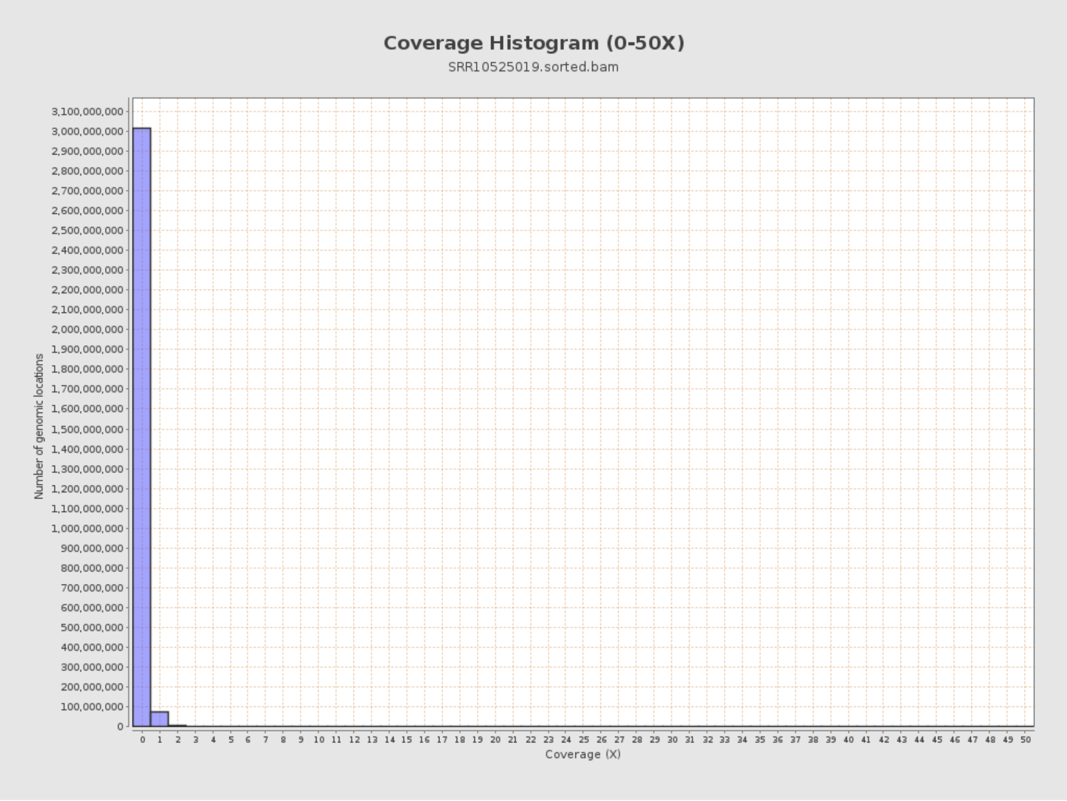
3. Results : Coverage across reference



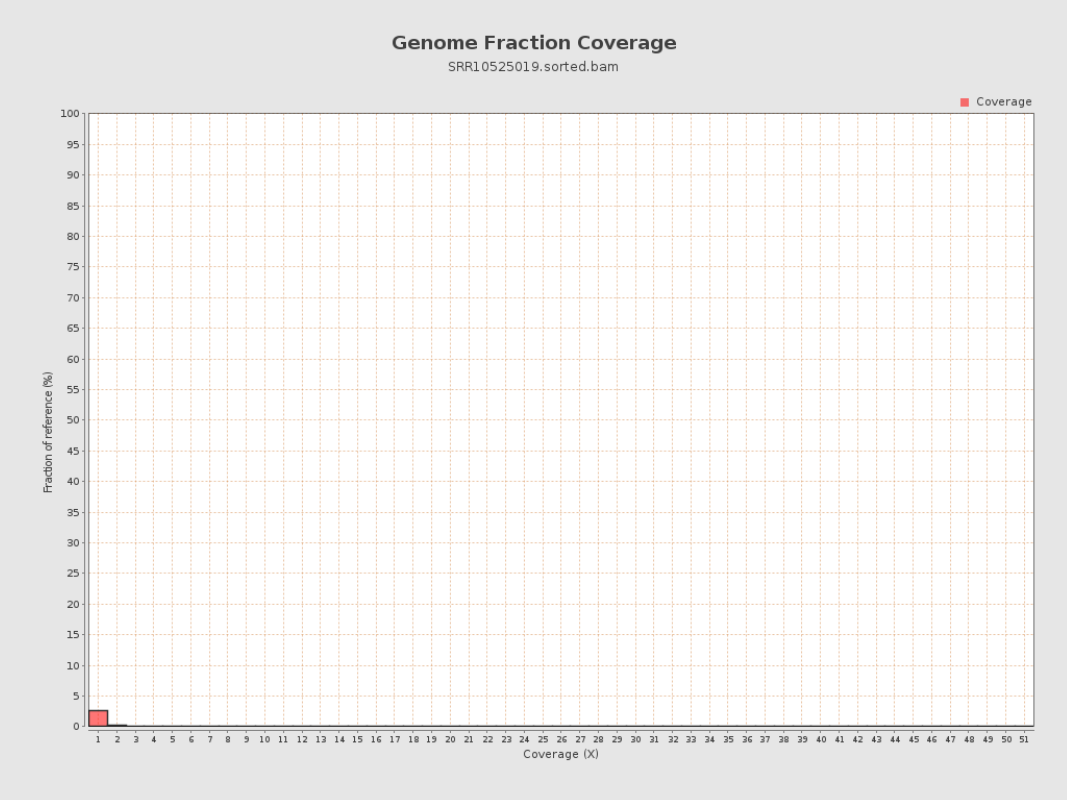
4. Results : Coverage Histogram



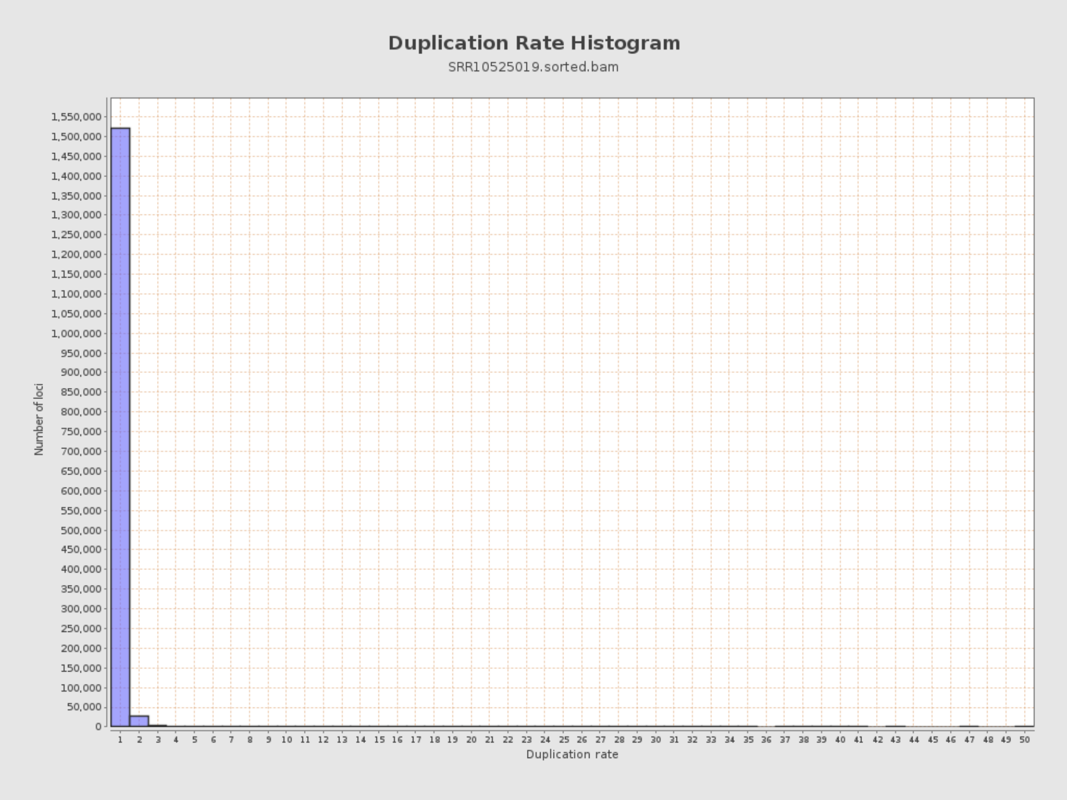
5. Results : Coverage Histogram (0-50X)



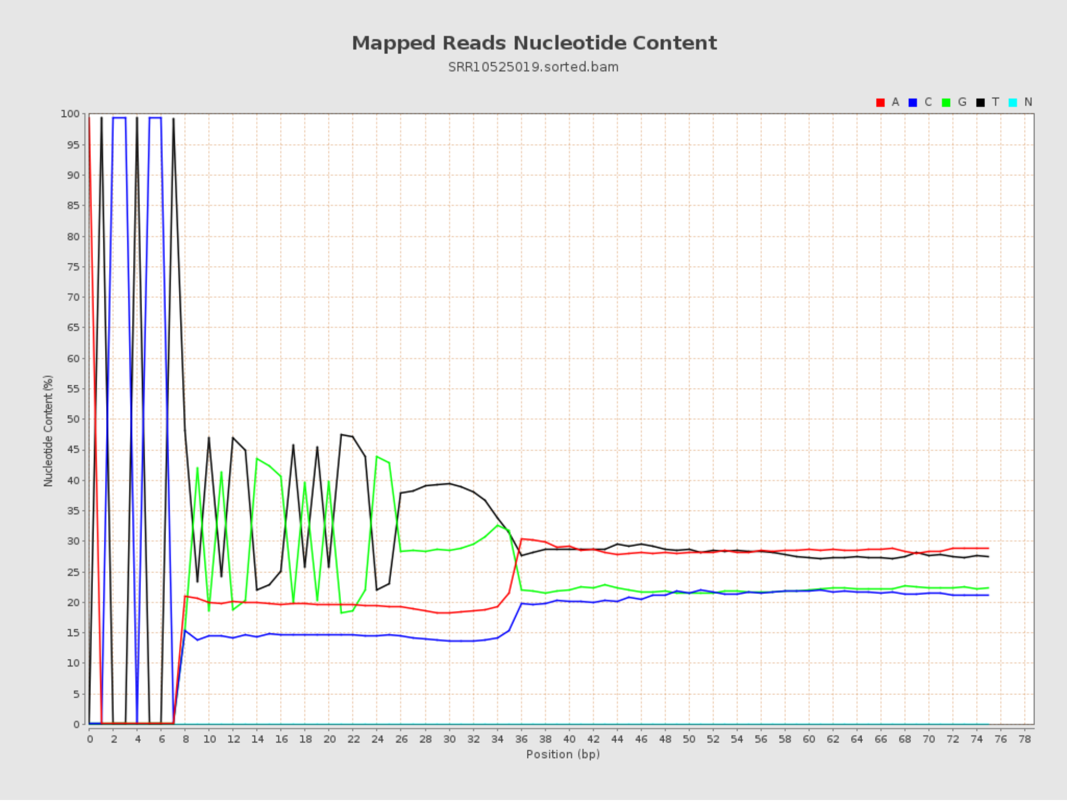
6. Results : Genome Fraction Coverage



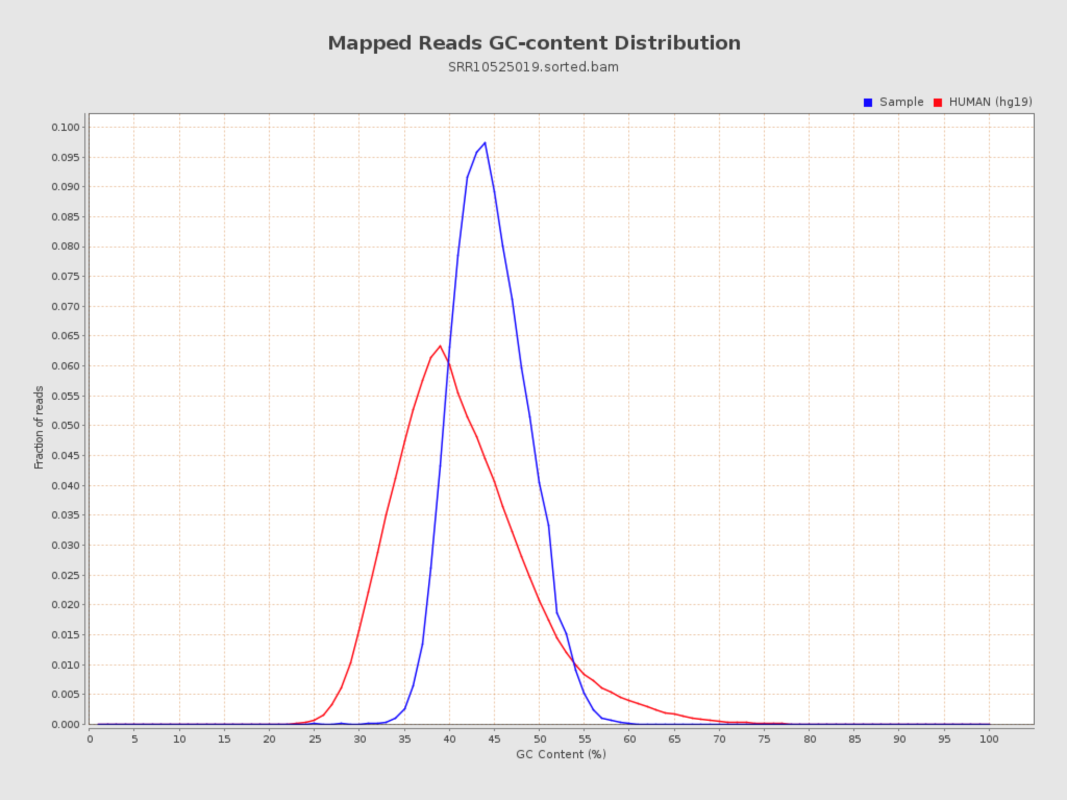
7. Results : Duplication Rate Histogram



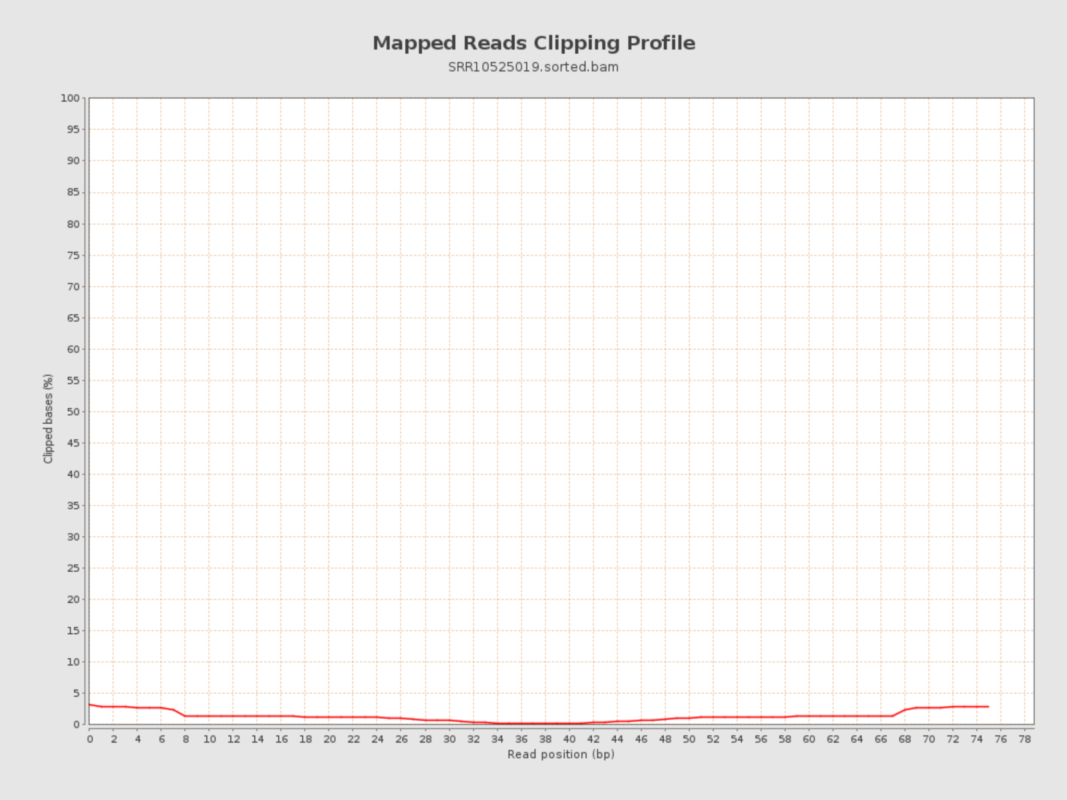
8. Results : Mapped Reads Nucleotide Content



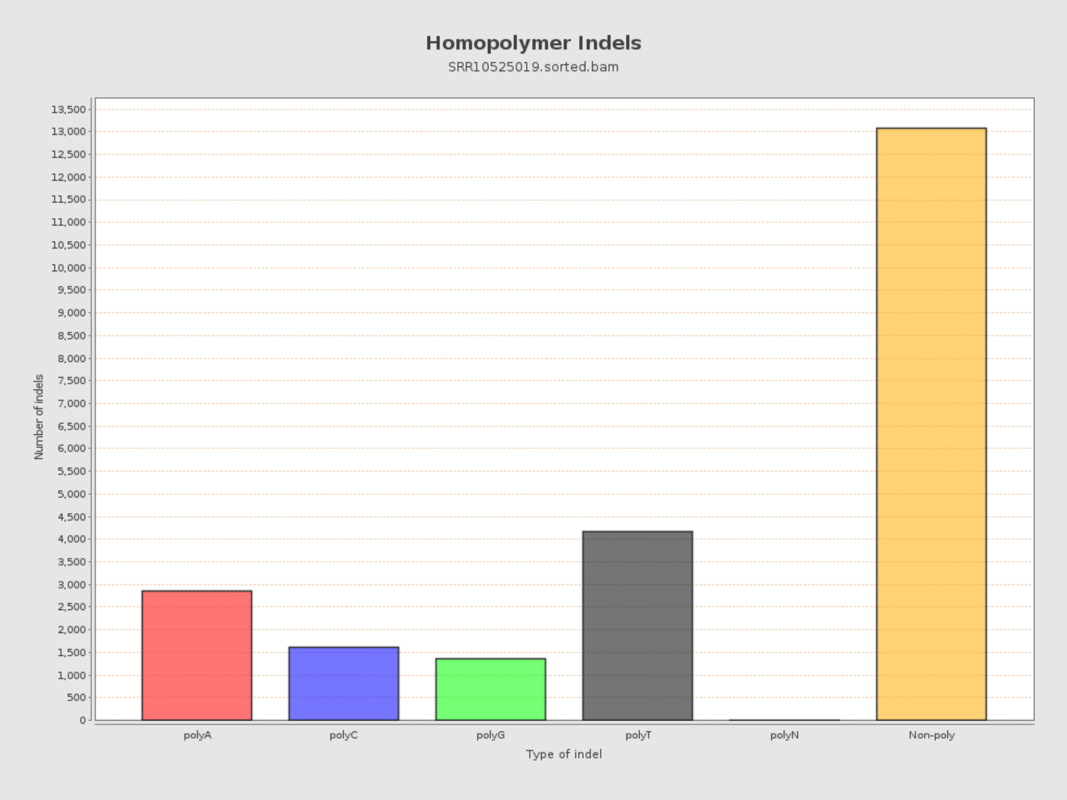
9. Results : Mapped Reads GC-content Distribution



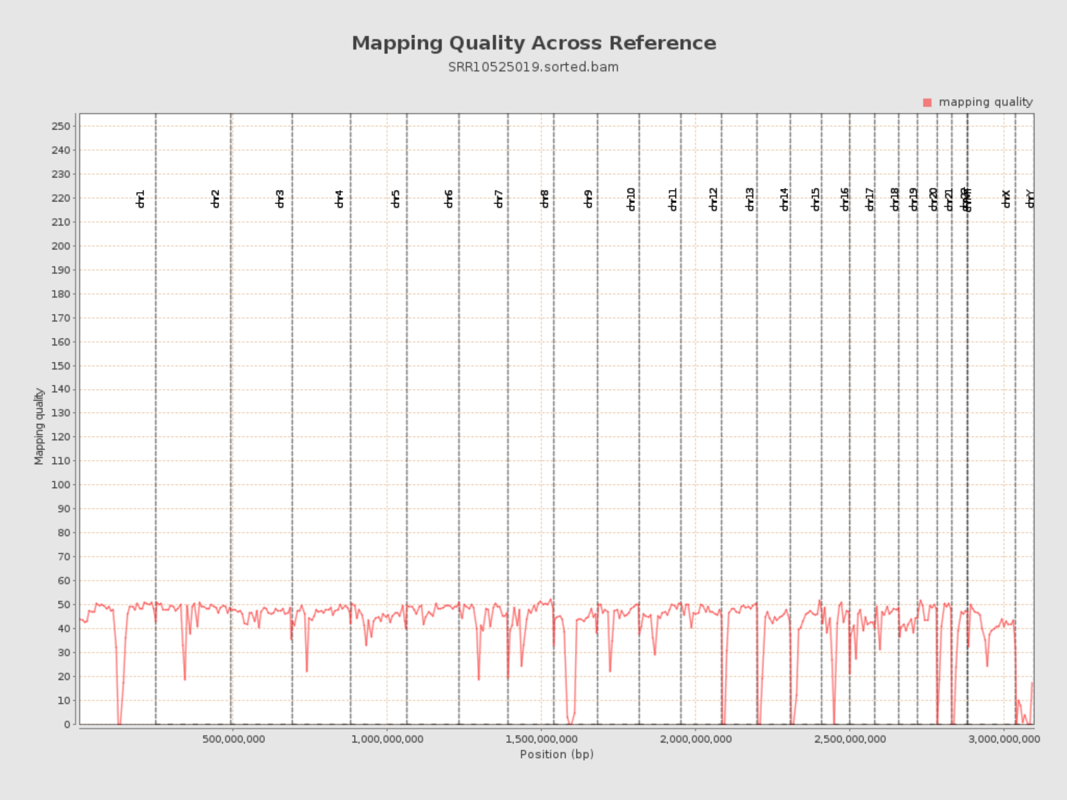
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram