Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 17:26:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819039.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_SRR1819039 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819039.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 17:26:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819039.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	827,813
Mapped reads	713,012 / 86.13%
Unmapped reads	114,801 / 13.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,941 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	13,021 / 1.57%
Duplication rate	1.41%
Clipped reads	713,667 / 86.21%

2.2. ACGT Content

Number/percentage of A's	9,810,416 / 24.28%
Number/percentage of C's	8,377,883 / 20.73%
Number/percentage of T's	12,745,008 / 31.54%
Number/percentage of G's	9,471,412 / 23.44%
Number/percentage of N's	809 / 0%
GC Percentage	44.18%

2.3. Coverage

Mean	0.0131

Standard Deviation	0.1351

2.4. Mapping Quality

Mean Mapping Quality	43.64

2.5. Mismatches and indels

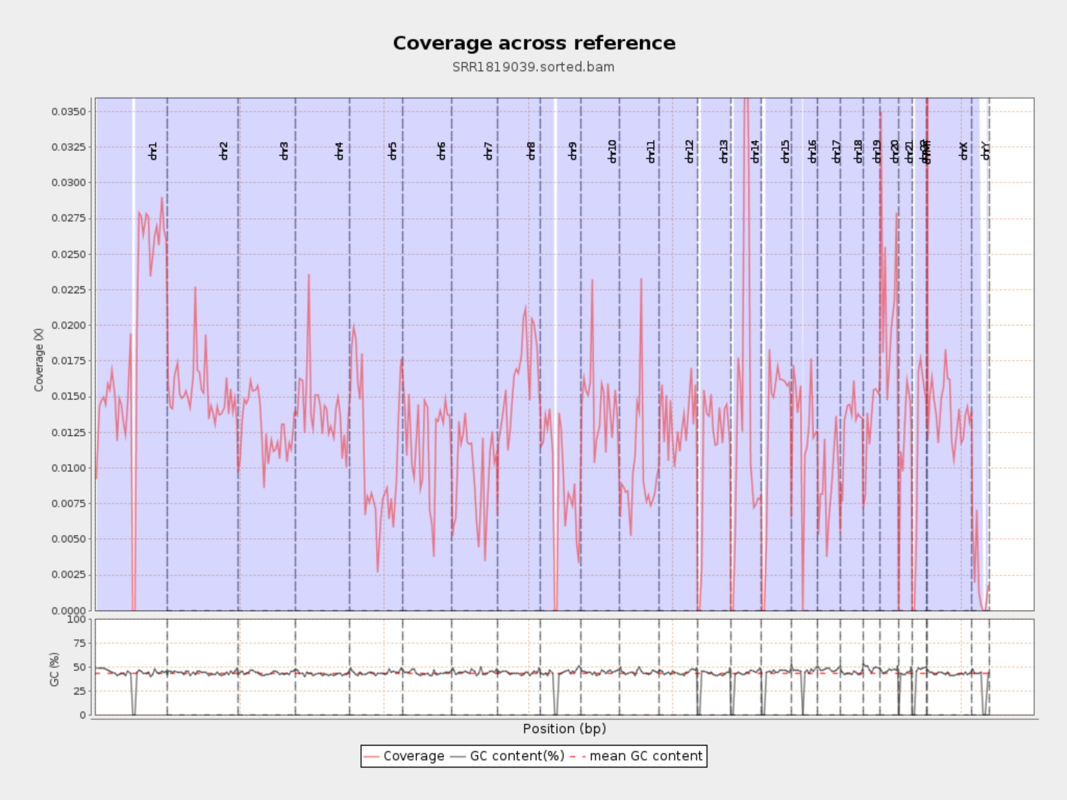
General error rate	0.5%
Mismatches	196,493
Insertions	3,180
Mapped reads with at least one insertion	0.44%
Deletions	6,177
Mapped reads with at least one deletion	0.86%
Homopolymer indels	38.79%

2.6. Chromosome stats

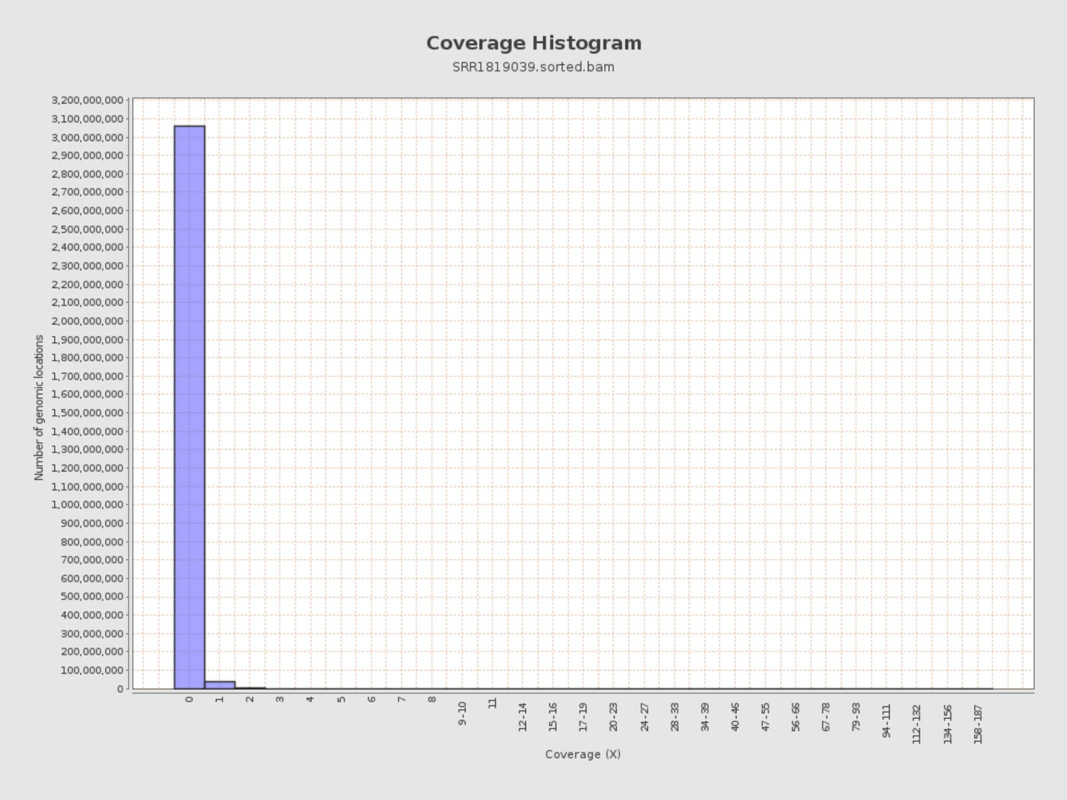
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4657877	0.0187	0.1898
chr2	243199373	3721004	0.0153	0.1542
chr3	198022430	2514151	0.0127	0.1181
chr4	191154276	2692409	0.0141	0.1303
chr5	180915260	1947545	0.0108	0.11
chr6	171115067	2024575	0.0118	0.1179
chr7	159138663	1520192	0.0096	0.1134

chr8	146364022	2374306	0.0162	0.1422
chr9	141213431	1247313	0.0088	0.1202
chr10	135534747	1958554	0.0145	0.1501
chr11	135006516	1335723	0.0099	0.1188
chr12	133851895	1778131	0.0133	0.1213
chr13	115169878	1295038	0.0112	0.1102
chr14	107349540	1568018	0.0146	0.1293
chr15	102531392	1331723	0.013	0.1192
chr16	90354753	1123982	0.0124	0.1228
chr17	81195210	702988	0.0087	0.0993
chr18	78077248	1029239	0.0132	0.2027
chr19	59128983	777484	0.0131	0.15
chr20	63025520	1370899	0.0218	0.1572
chr21	48129895	566388	0.0118	0.1198
chr22	51304566	574161	0.0112	0.1115
chrMT	16571	3858	0.2328	0.5175
chrX	155270560	2173583	0.014	0.1307
chrY	59373566	126815	0.0021	0.0617

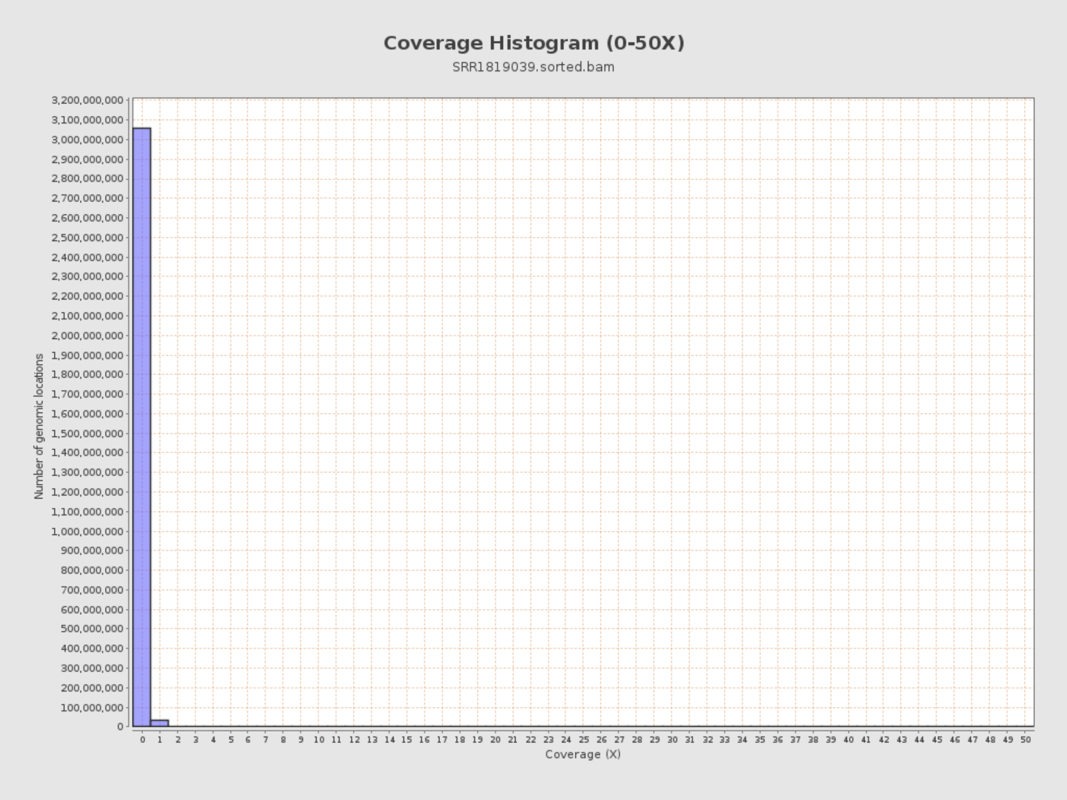
3. Results : Coverage across reference



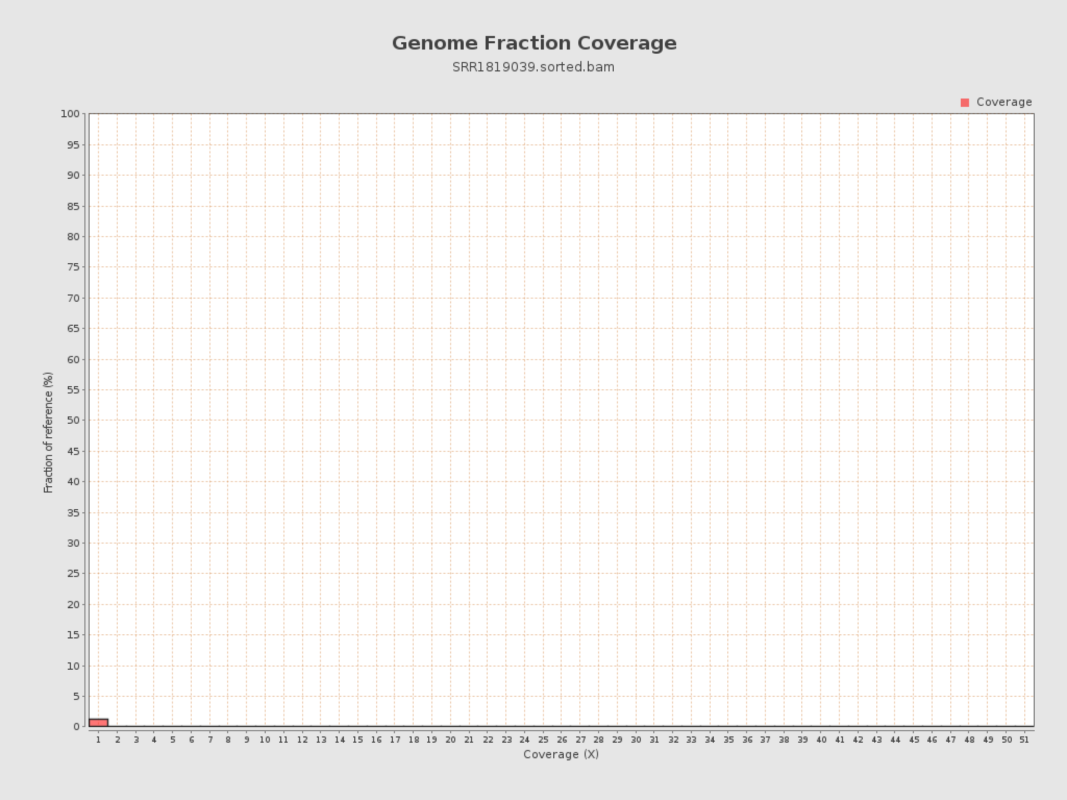
4. Results : Coverage Histogram



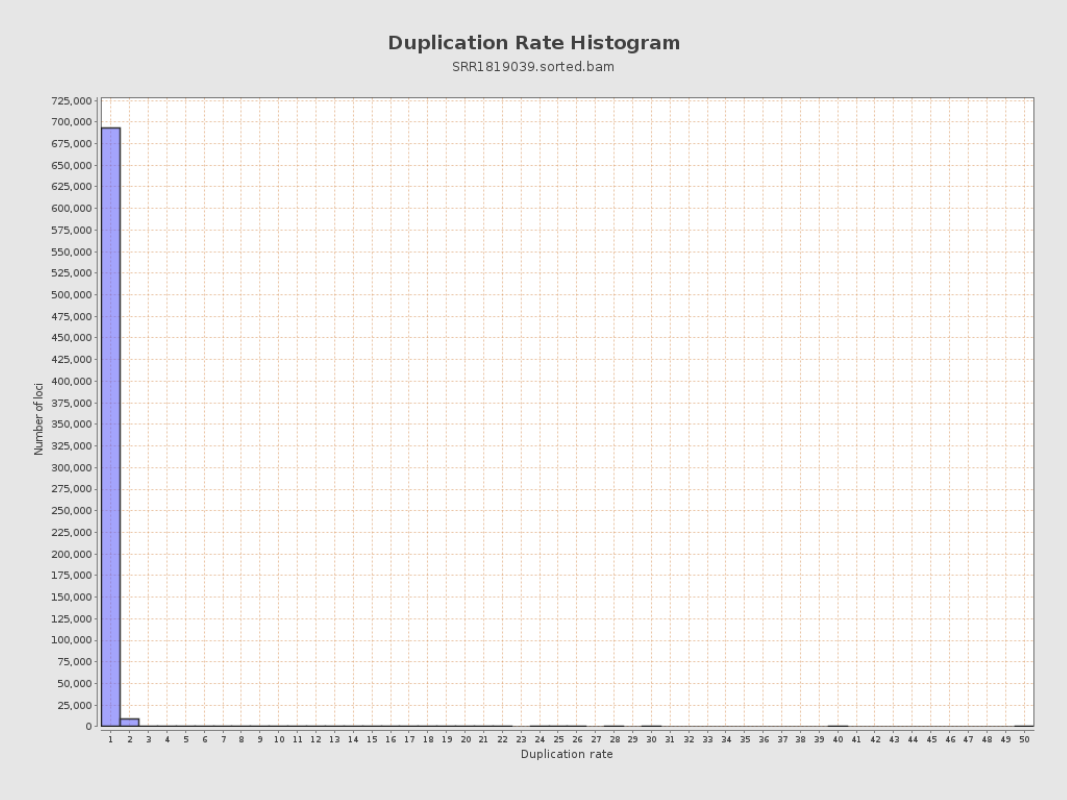
5. Results : Coverage Histogram (0-50X)



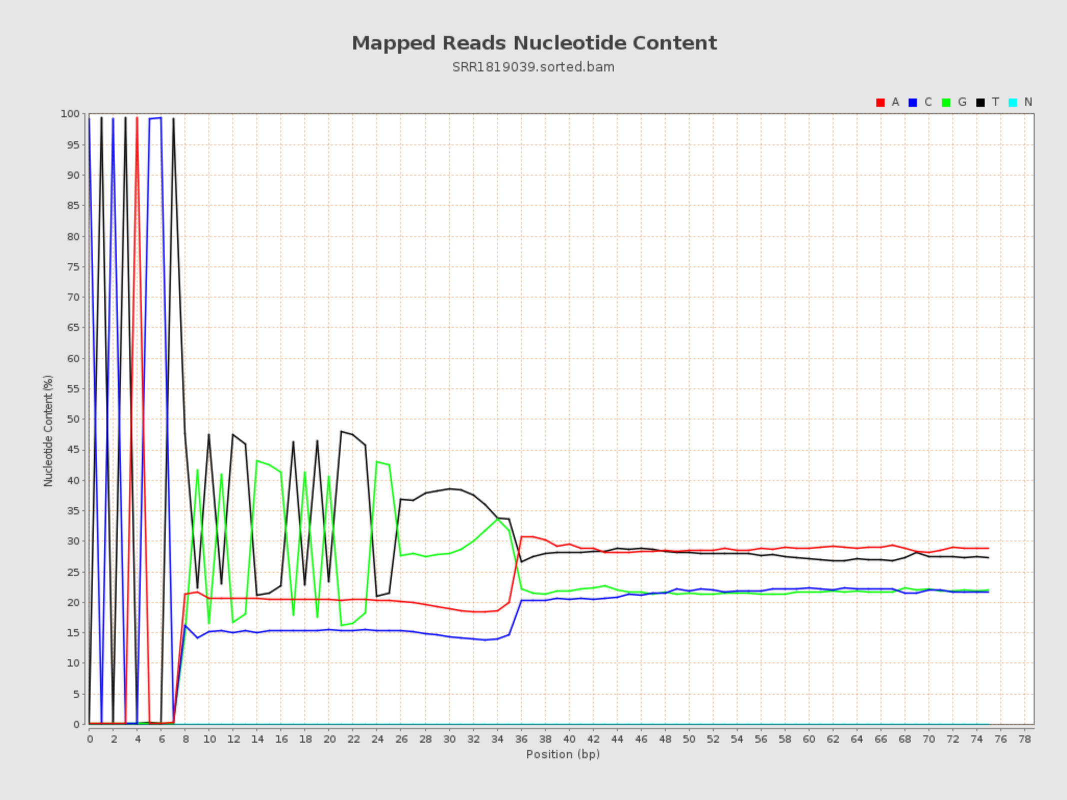
6. Results : Genome Fraction Coverage



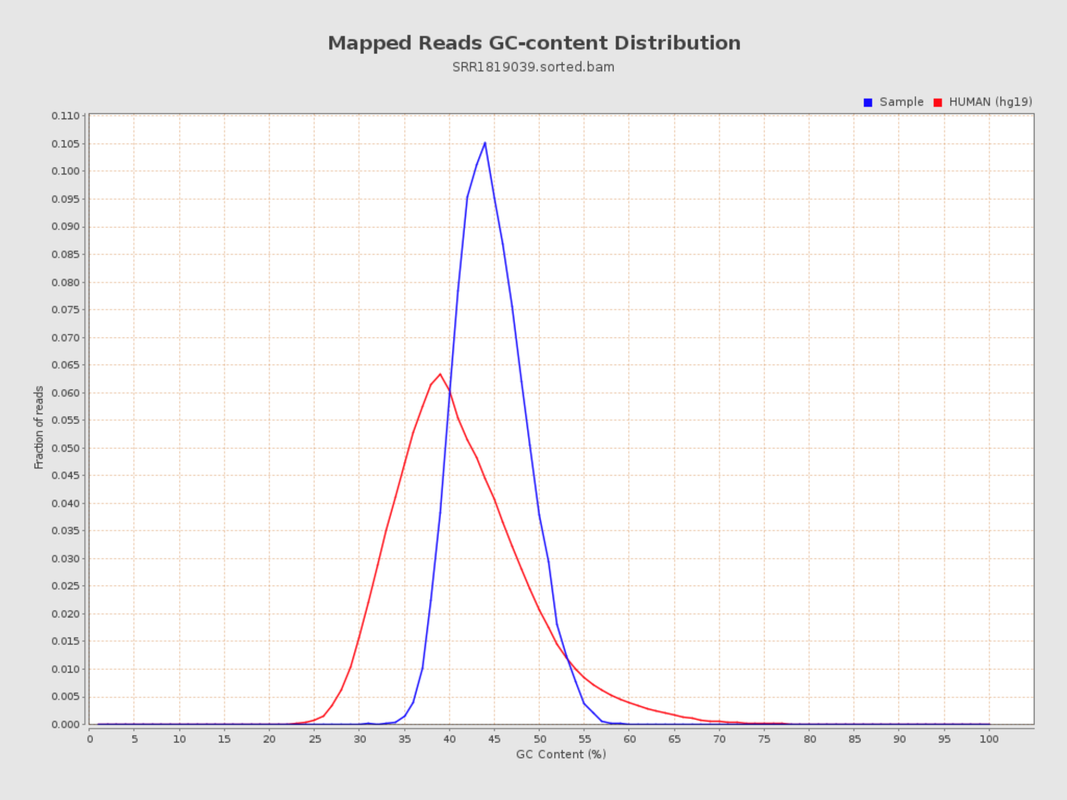
7. Results : Duplication Rate Histogram



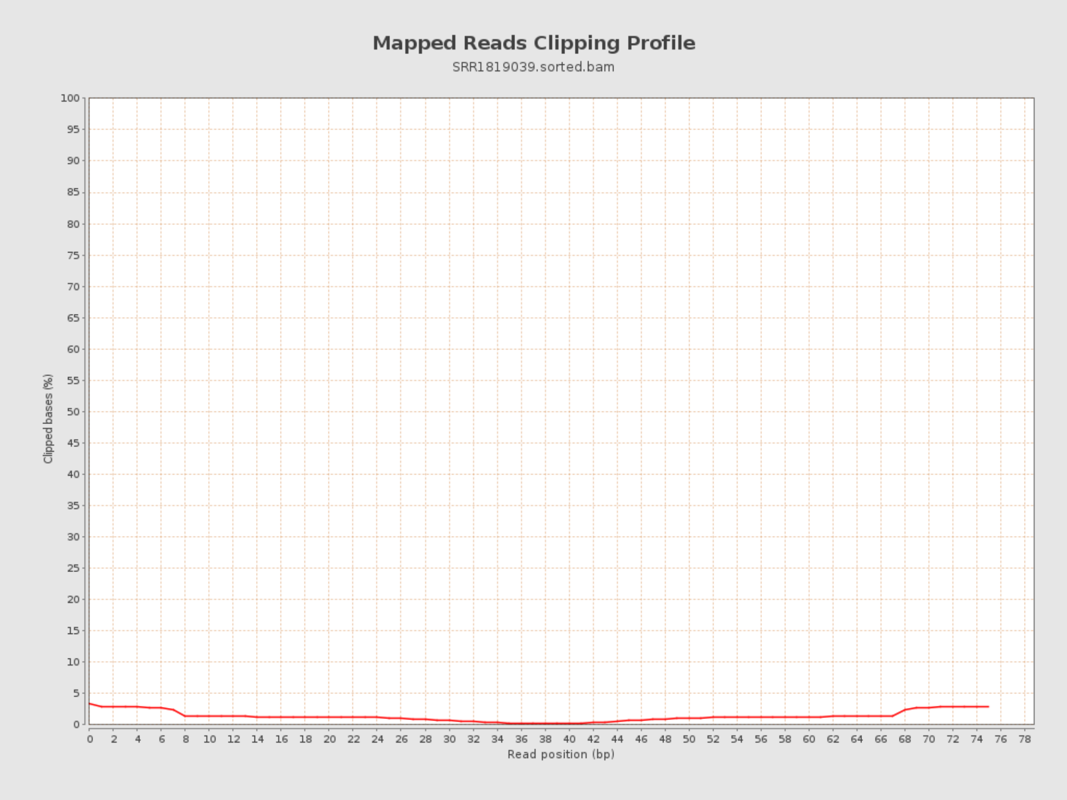
8. Results : Mapped Reads Nucleotide Content



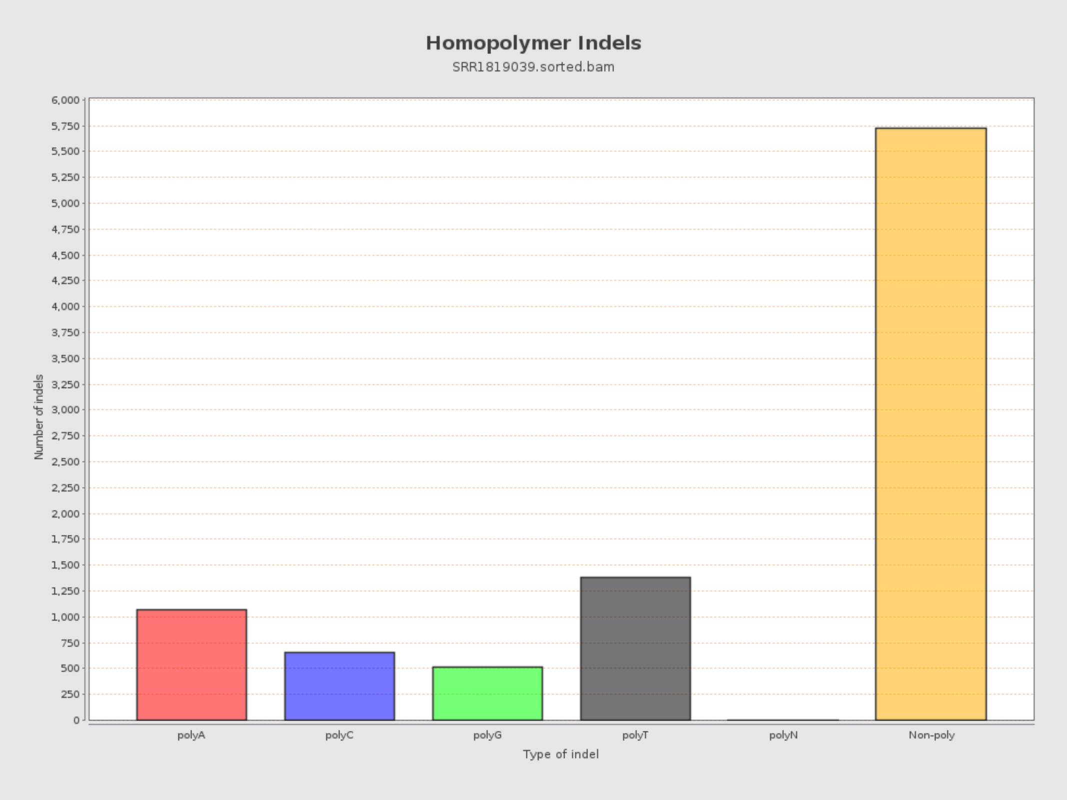
9. Results : Mapped Reads GC-content Distribution



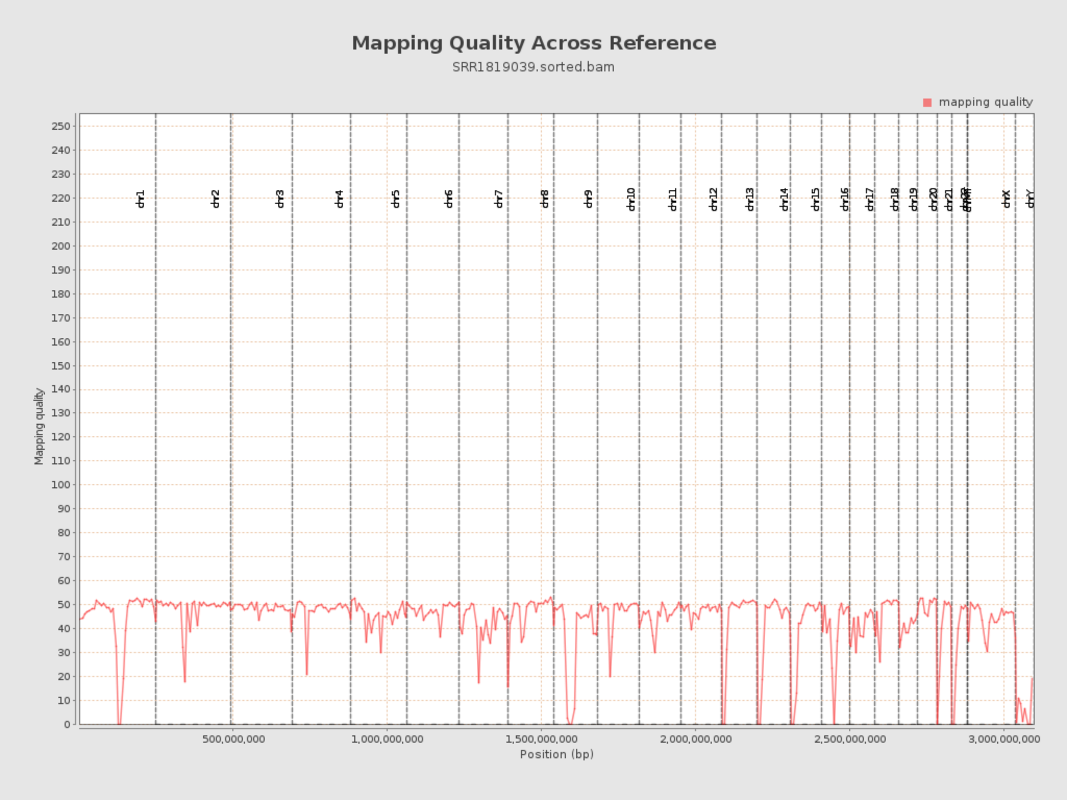
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram