Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 01:40:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717031.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_SRR9717031 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717031.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 01:40:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717031.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	807,385
Mapped reads	738,063 / 91.41%
Unmapped reads	69,322 / 8.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,657 / 0.45%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	14,530 / 1.8%
Duplication rate	1.35%
Clipped reads	739,540 / 91.6%

2.2. ACGT Content

Number/percentage of A's	10,426,205 / 24.25%
Number/percentage of C's	8,255,480 / 19.2%
Number/percentage of T's	13,582,201 / 31.58%
Number/percentage of G's	10,738,792 / 24.97%
Number/percentage of N's	496 / 0%
GC Percentage	44.17%

2.3. Coverage

Mean	0.0139

Standard Deviation	0.1605

2.4. Mapping Quality

Mean Mapping Quality	44.36

2.5. Mismatches and indels

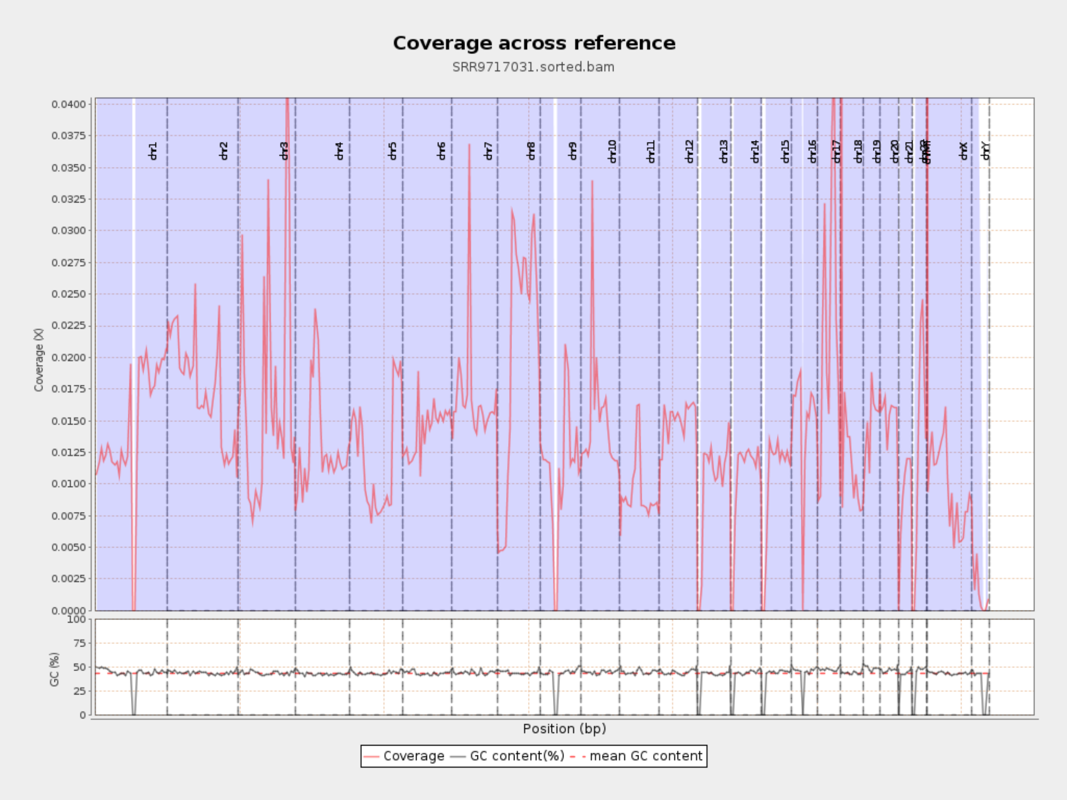
General error rate	0.52%
Mismatches	219,709
Insertions	2,854
Mapped reads with at least one insertion	0.38%
Deletions	8,330
Mapped reads with at least one deletion	1.12%
Homopolymer indels	42.69%

2.6. Chromosome stats

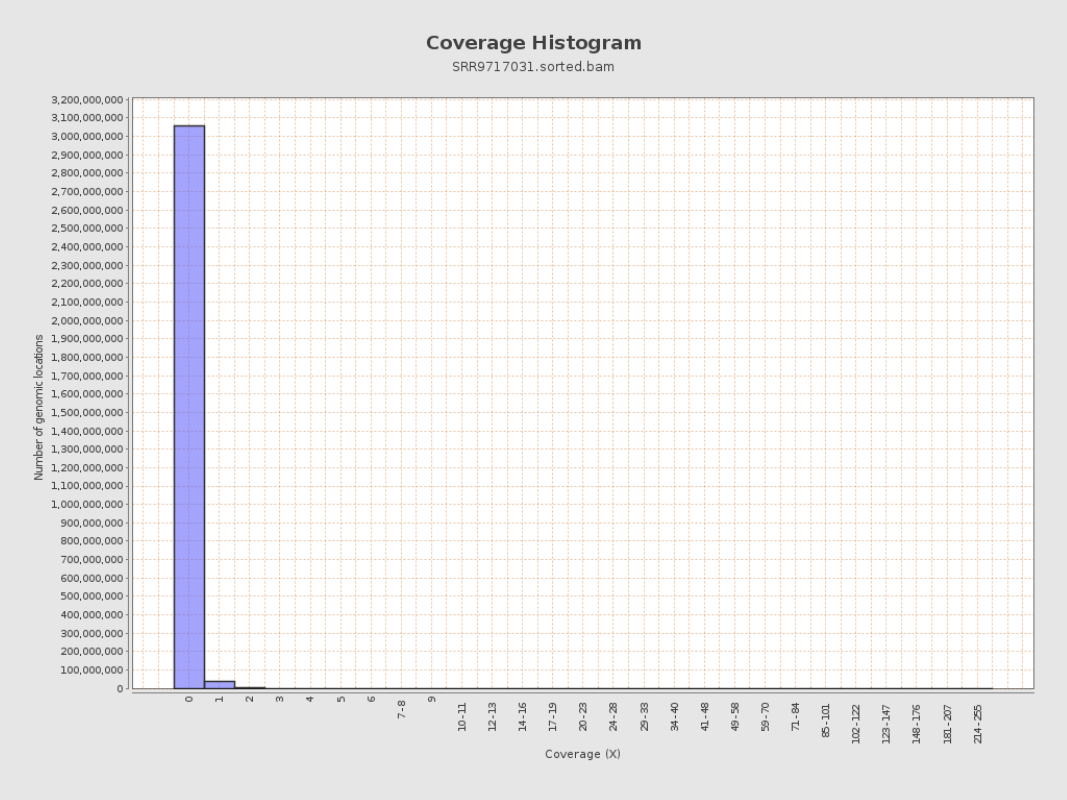
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3594337	0.0144	0.2084
chr2	243199373	4287788	0.0176	0.1796
chr3	198022430	3342384	0.0169	0.1397
chr4	191154276	2462720	0.0129	0.12
chr5	180915260	2177548	0.012	0.114
chr6	171115067	2443579	0.0143	0.1298
chr7	159138663	2709052	0.017	0.3199

chr8	146364022	3059236	0.0209	0.1745
chr9	141213431	1544923	0.0109	0.1212
chr10	135534747	2048442	0.0151	0.2047
chr11	135006516	1284917	0.0095	0.1165
chr12	133851895	2005105	0.015	0.1349
chr13	115169878	1145863	0.0099	0.1036
chr14	107349540	1098502	0.0102	0.1073
chr15	102531392	1036206	0.0101	0.1058
chr16	90354753	1330775	0.0147	0.1296
chr17	81195210	1814847	0.0224	0.1587
chr18	78077248	1032945	0.0132	0.1809
chr19	59128983	873716	0.0148	0.1892
chr20	63025520	972459	0.0154	0.1328
chr21	48129895	441318	0.0092	0.1004
chr22	51304566	653404	0.0127	0.1174
chrMT	16571	44863	2.7073	2.1238
chrX	155270560	1520157	0.0098	0.1119
chrY	59373566	91378	0.0015	0.0464

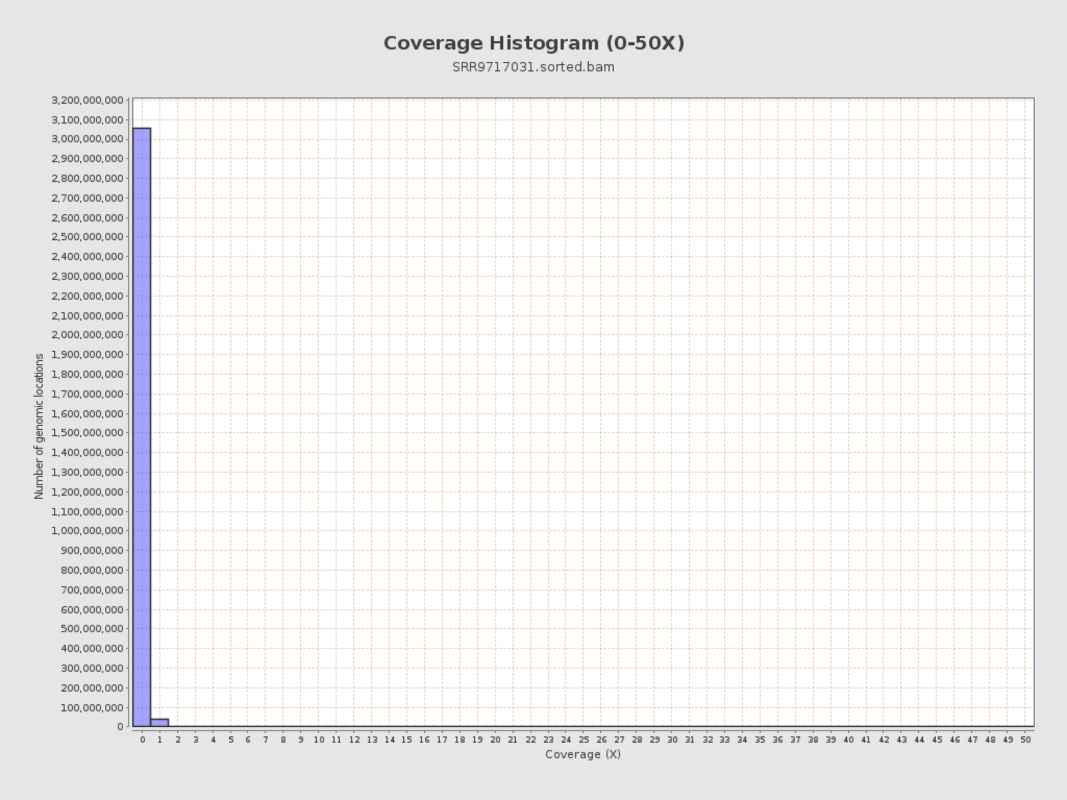
3. Results : Coverage across reference



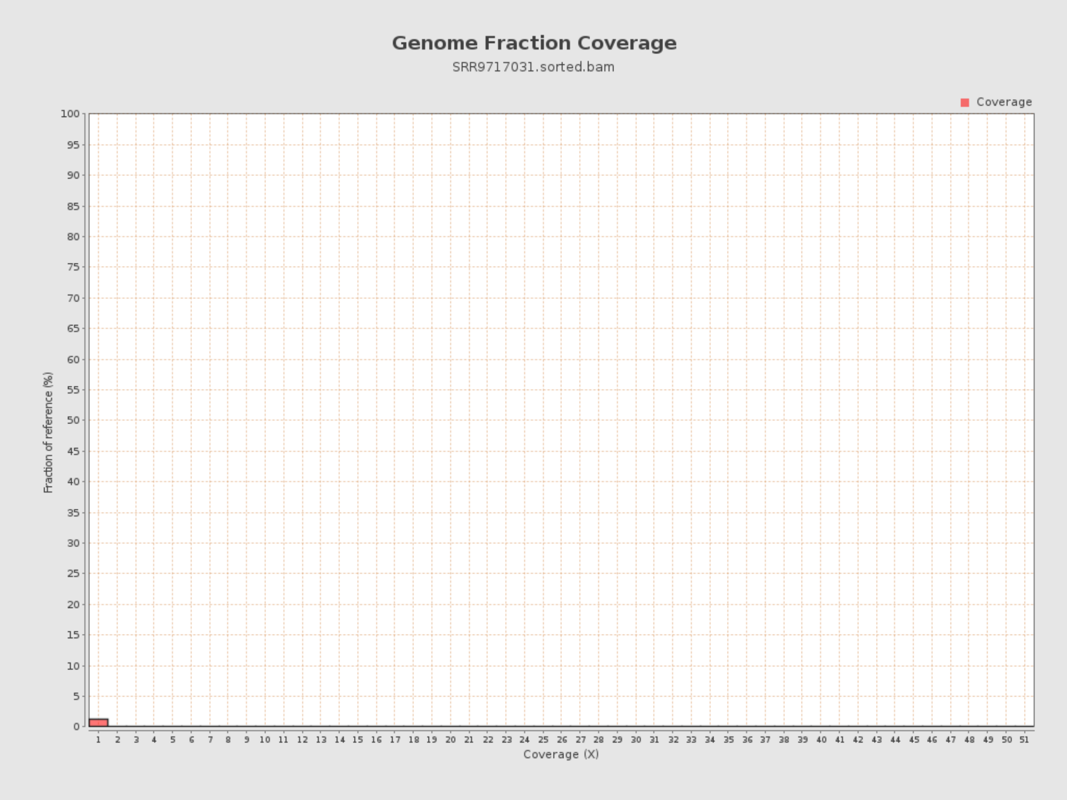
4. Results : Coverage Histogram



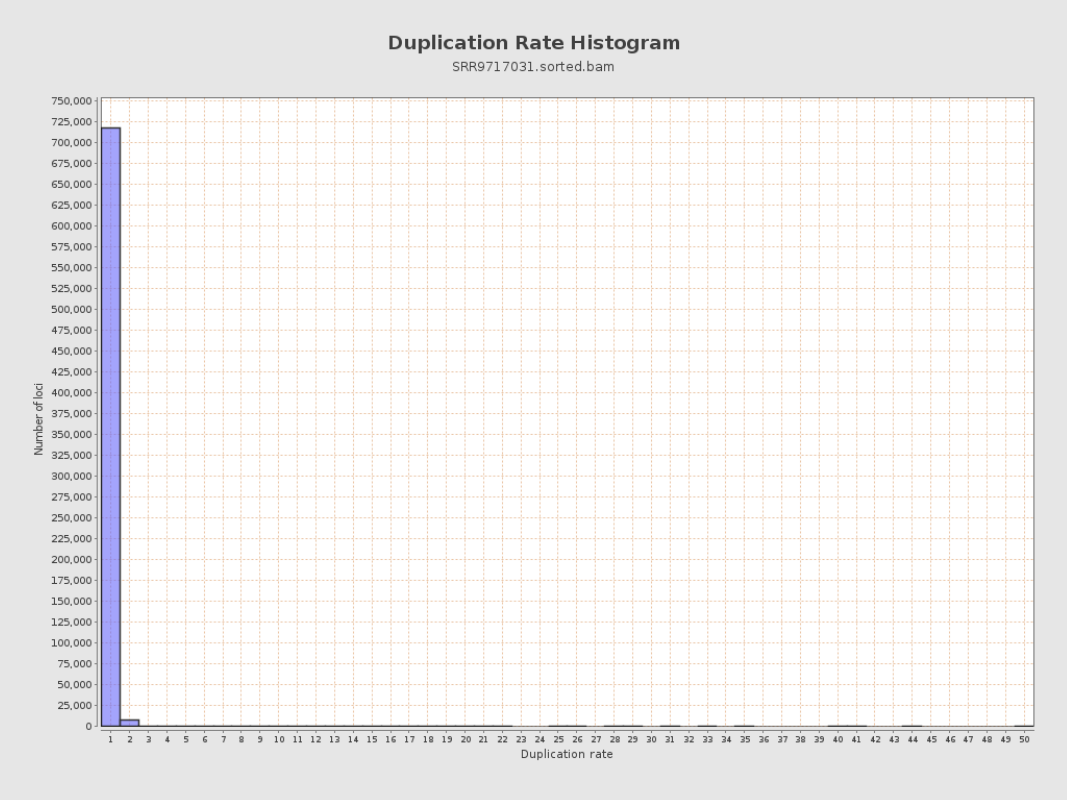
5. Results : Coverage Histogram (0-50X)



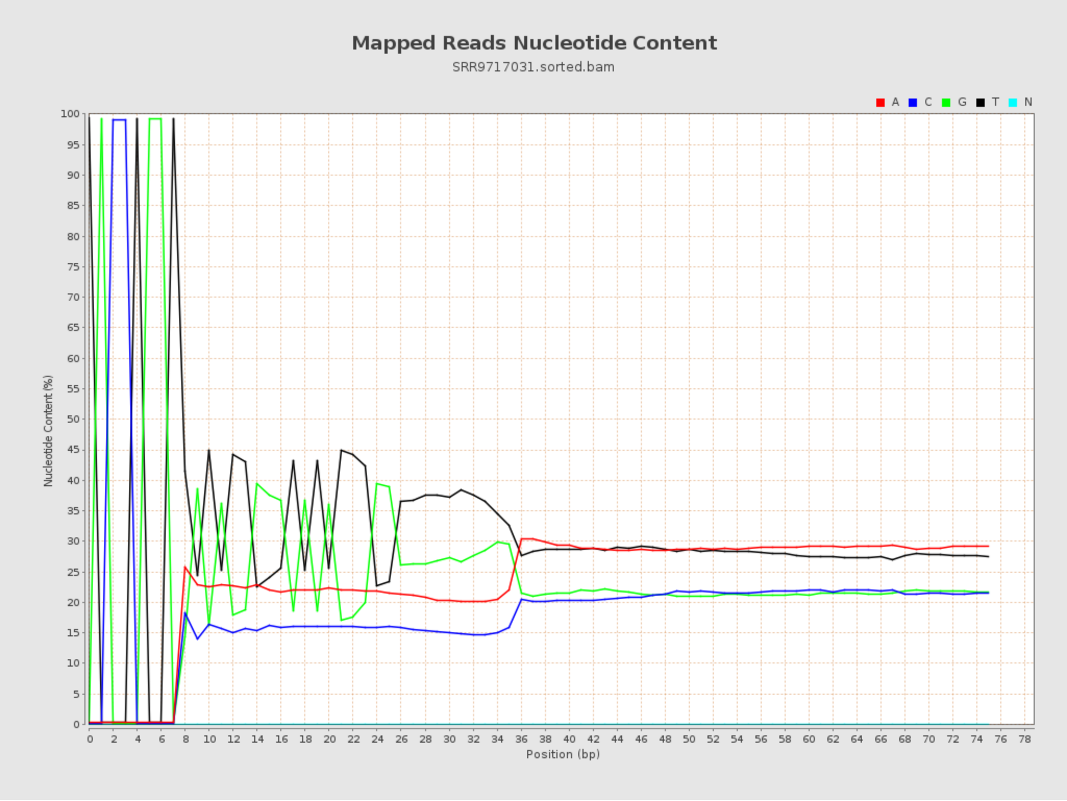
6. Results : Genome Fraction Coverage



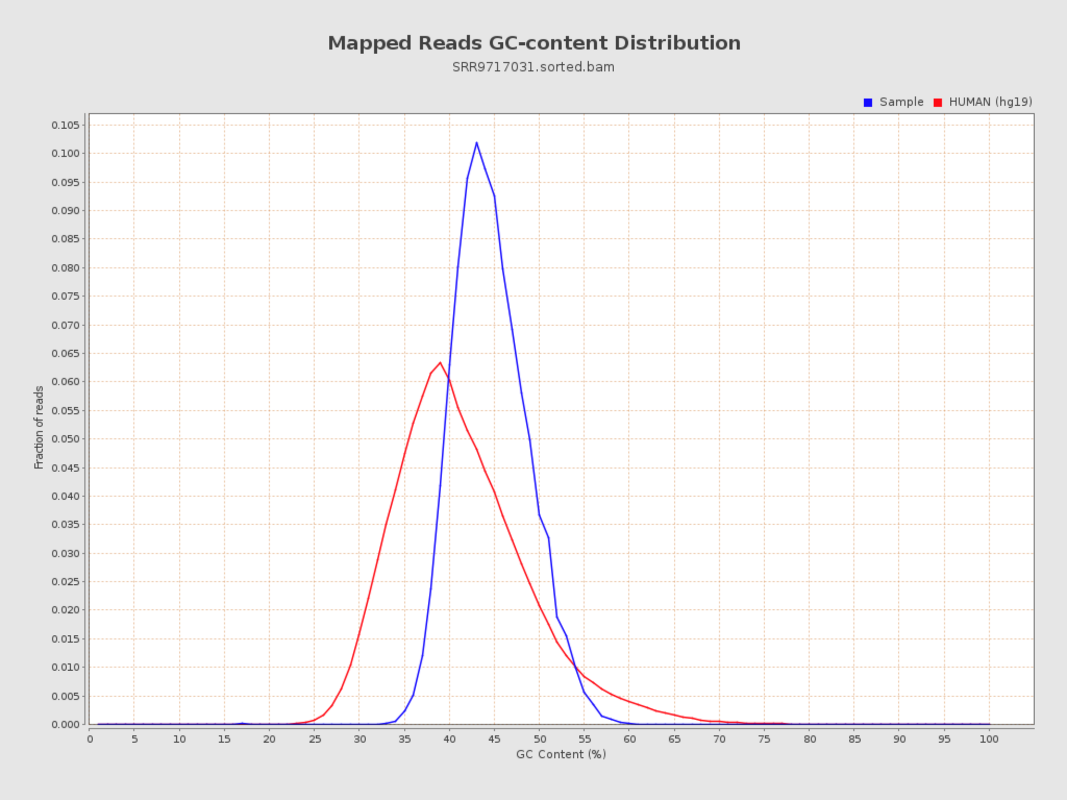
7. Results : Duplication Rate Histogram



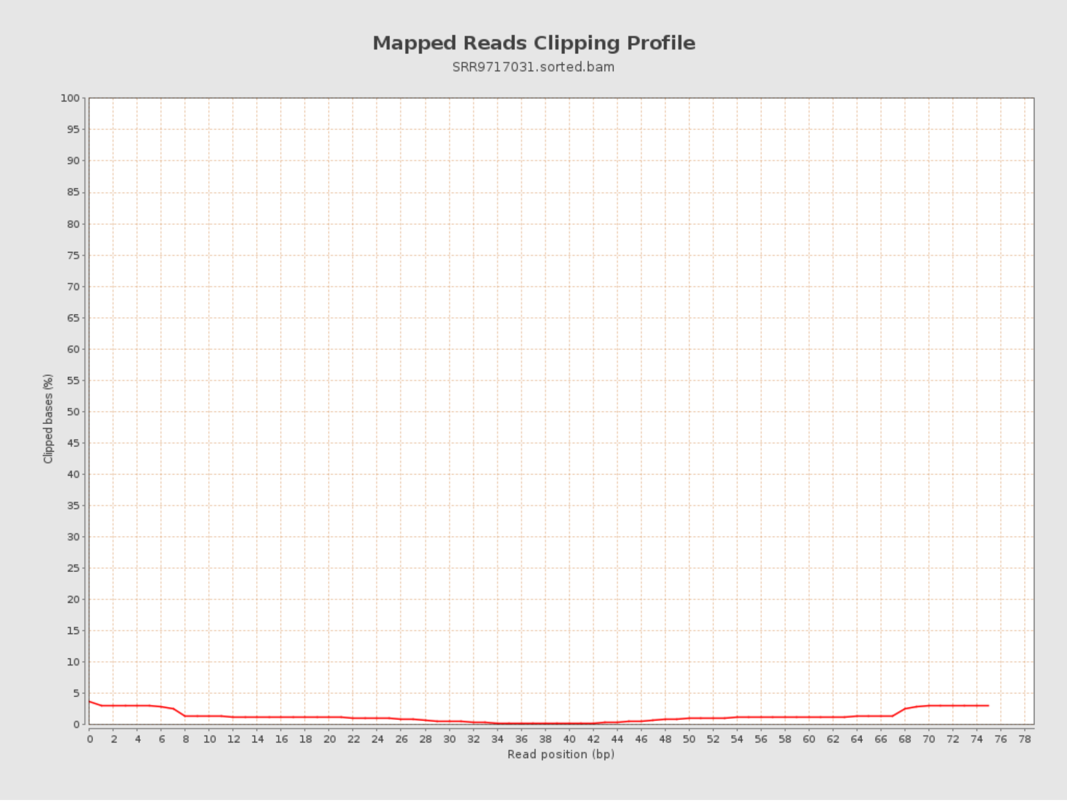
8. Results : Mapped Reads Nucleotide Content



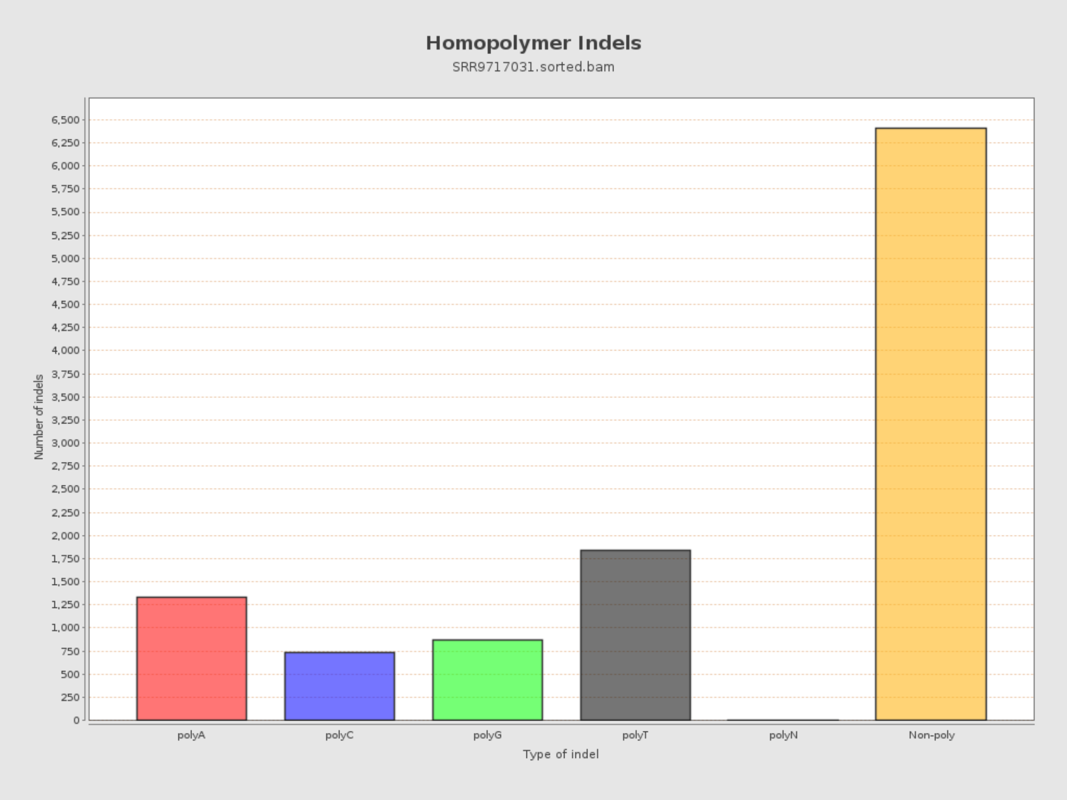
9. Results : Mapped Reads GC-content Distribution



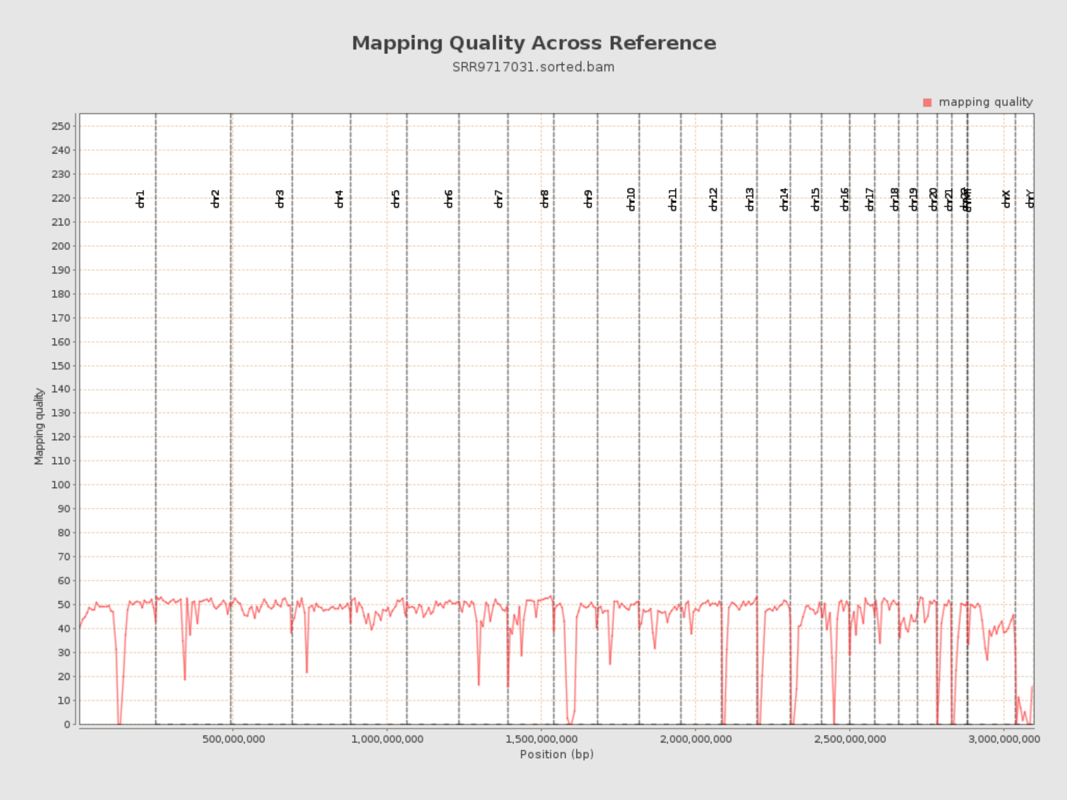
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram