Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 04:06:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717064.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_SRR9717064 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717064.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 04:06:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717064.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,008,745
Mapped reads	823,789 / 81.66%
Unmapped reads	184,956 / 18.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,974 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	15,741 / 1.56%
Duplication rate	1.35%
Clipped reads	824,665 / 81.75%

2.2. ACGT Content

Number/percentage of A's	10,011,507 / 22.25%
Number/percentage of C's	9,376,993 / 20.84%
Number/percentage of T's	14,111,570 / 31.36%
Number/percentage of G's	11,498,729 / 25.55%
Number/percentage of N's	1,336 / 0%
GC Percentage	46.39%

2.3. Coverage

Mean	0.0145

Standard Deviation	0.143

2.4. Mapping Quality

Mean Mapping Quality	39.5

2.5. Mismatches and indels

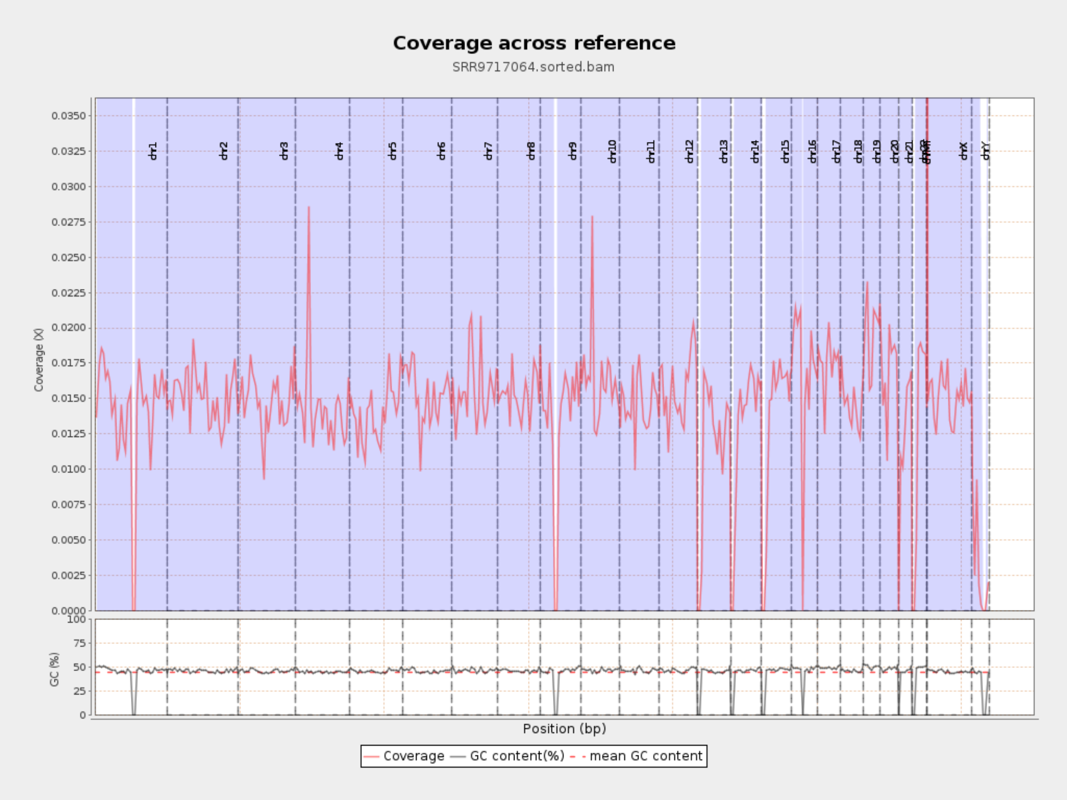
General error rate	0.54%
Mismatches	238,272
Insertions	3,704
Mapped reads with at least one insertion	0.45%
Deletions	7,502
Mapped reads with at least one deletion	0.9%
Homopolymer indels	33.43%

2.6. Chromosome stats

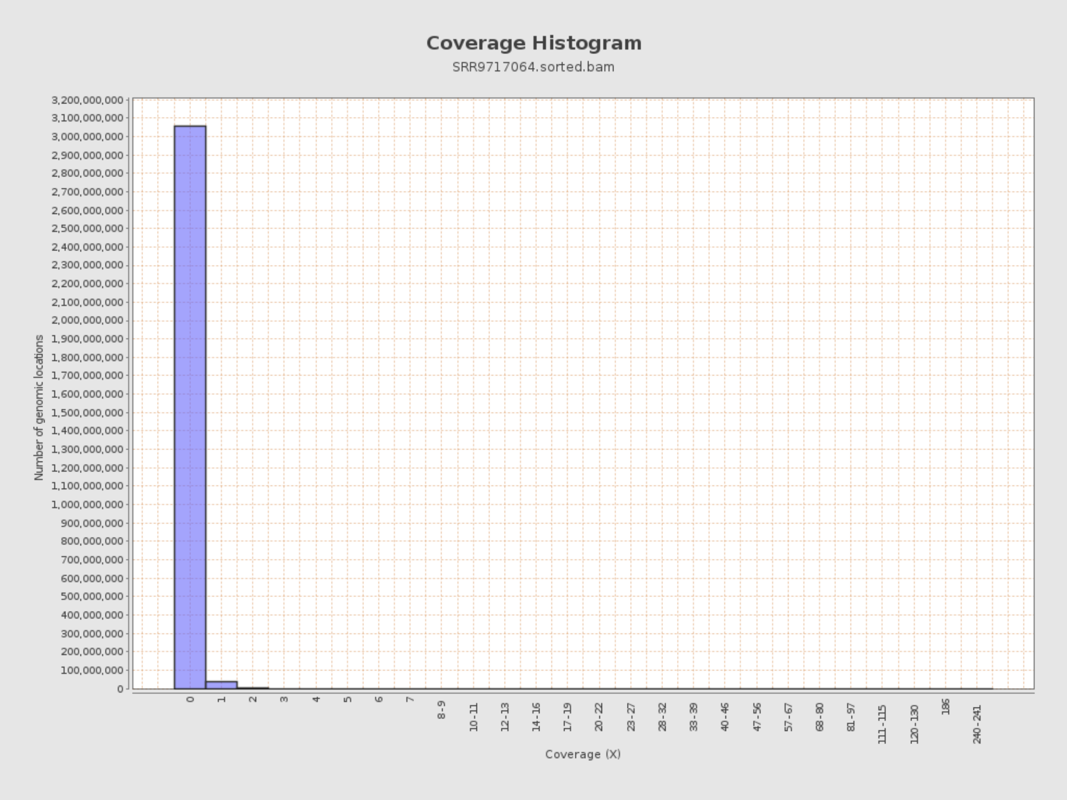
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3489214	0.014	0.1477
chr2	243199373	3698087	0.0152	0.1774
chr3	198022430	2920070	0.0147	0.1325
chr4	191154276	2776185	0.0145	0.1418
chr5	180915260	2541340	0.014	0.1263
chr6	171115067	2608520	0.0152	0.1336
chr7	159138663	2485146	0.0156	0.157

chr8	146364022	2225174	0.0152	0.1378
chr9	141213431	1882963	0.0133	0.1316
chr10	135534747	2222581	0.0164	0.1727
chr11	135006516	1992753	0.0148	0.1478
chr12	133851895	2114755	0.0158	0.1341
chr13	115169878	1322750	0.0115	0.1152
chr14	107349540	1366921	0.0127	0.1244
chr15	102531392	1332723	0.013	0.1229
chr16	90354753	1505233	0.0167	0.1462
chr17	81195210	1414202	0.0174	0.1442
chr18	78077248	1132073	0.0145	0.16
chr19	59128983	1162162	0.0197	0.1732
chr20	63025520	1056217	0.0168	0.1418
chr21	48129895	594281	0.0123	0.1312
chr22	51304566	639925	0.0125	0.1227
chrMT	16571	12951	0.7815	1.1165
chrX	155270560	2347107	0.0151	0.1376
chrY	59373566	169207	0.0028	0.0874

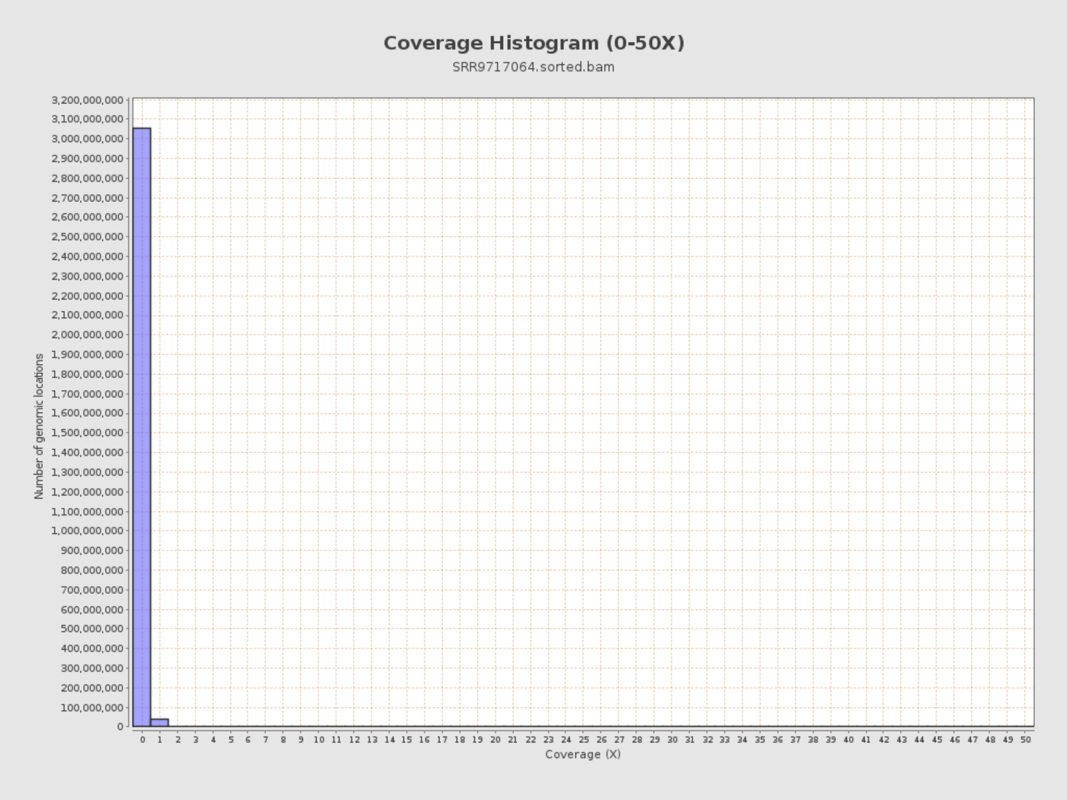
3. Results : Coverage across reference



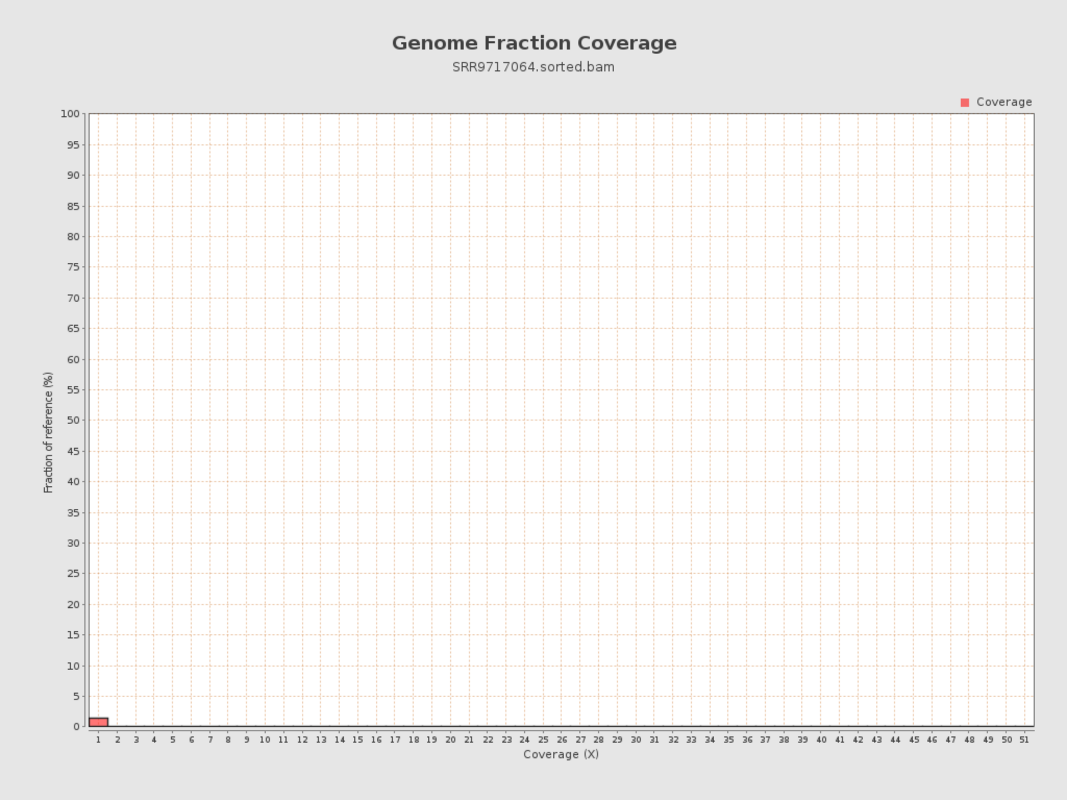
4. Results : Coverage Histogram



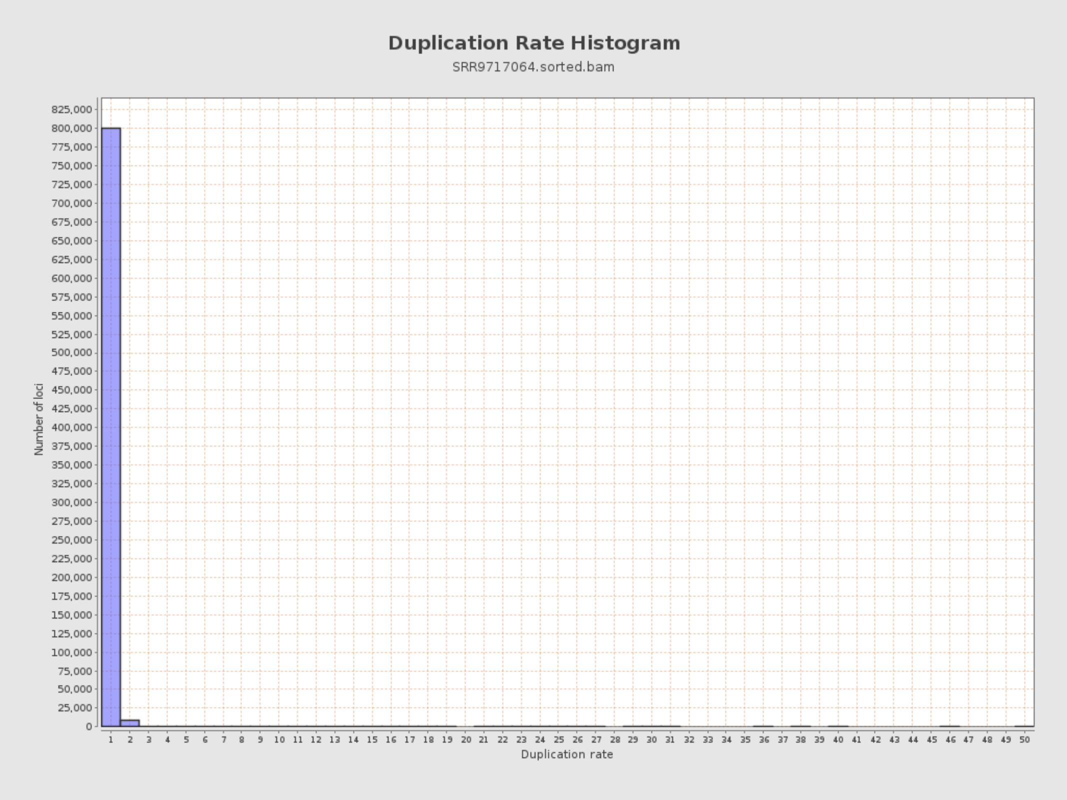
5. Results : Coverage Histogram (0-50X)



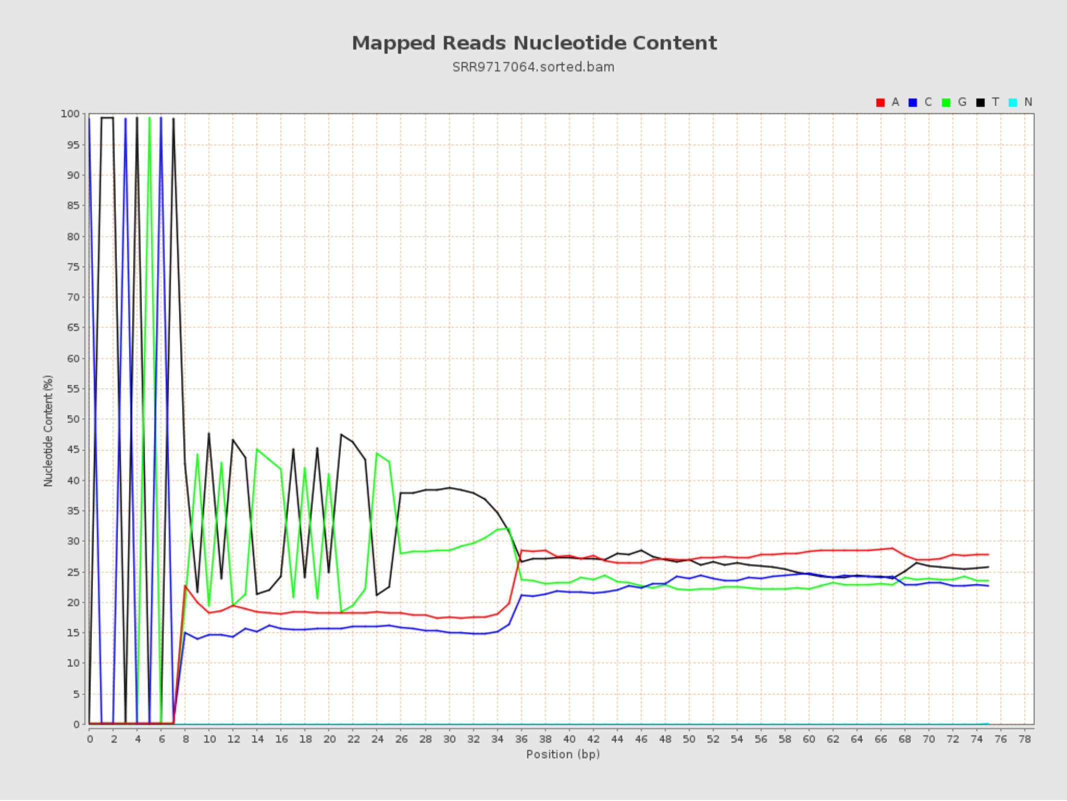
6. Results : Genome Fraction Coverage



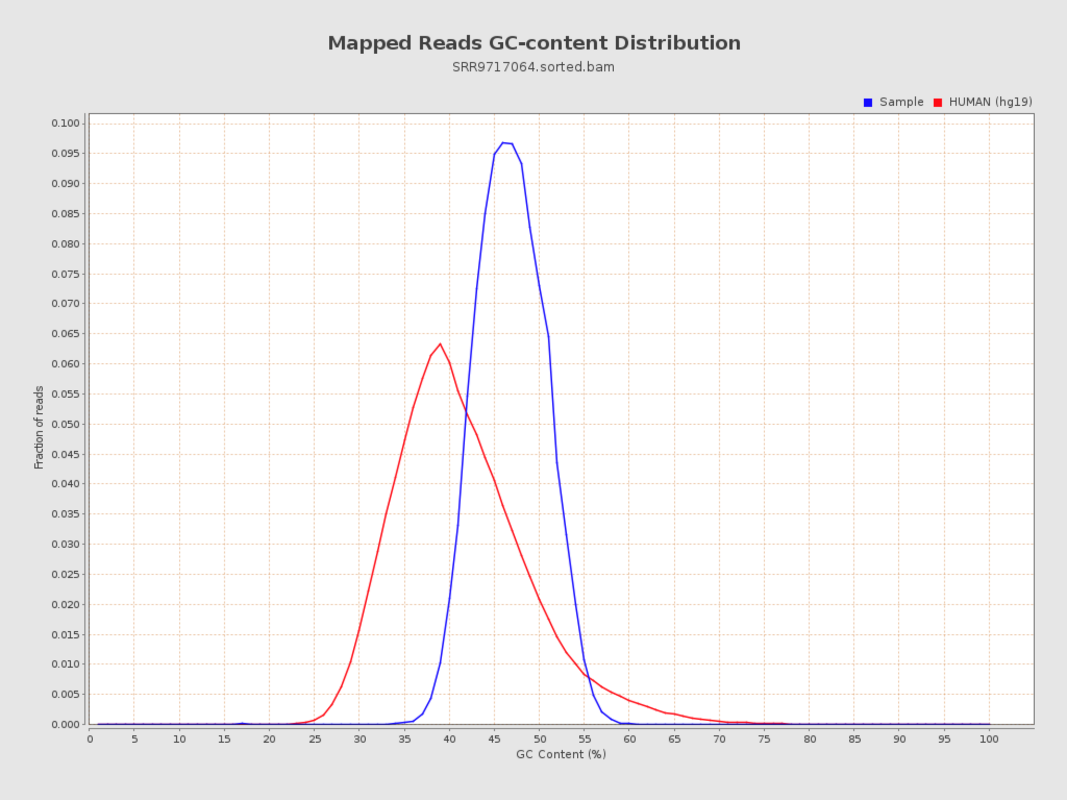
7. Results : Duplication Rate Histogram



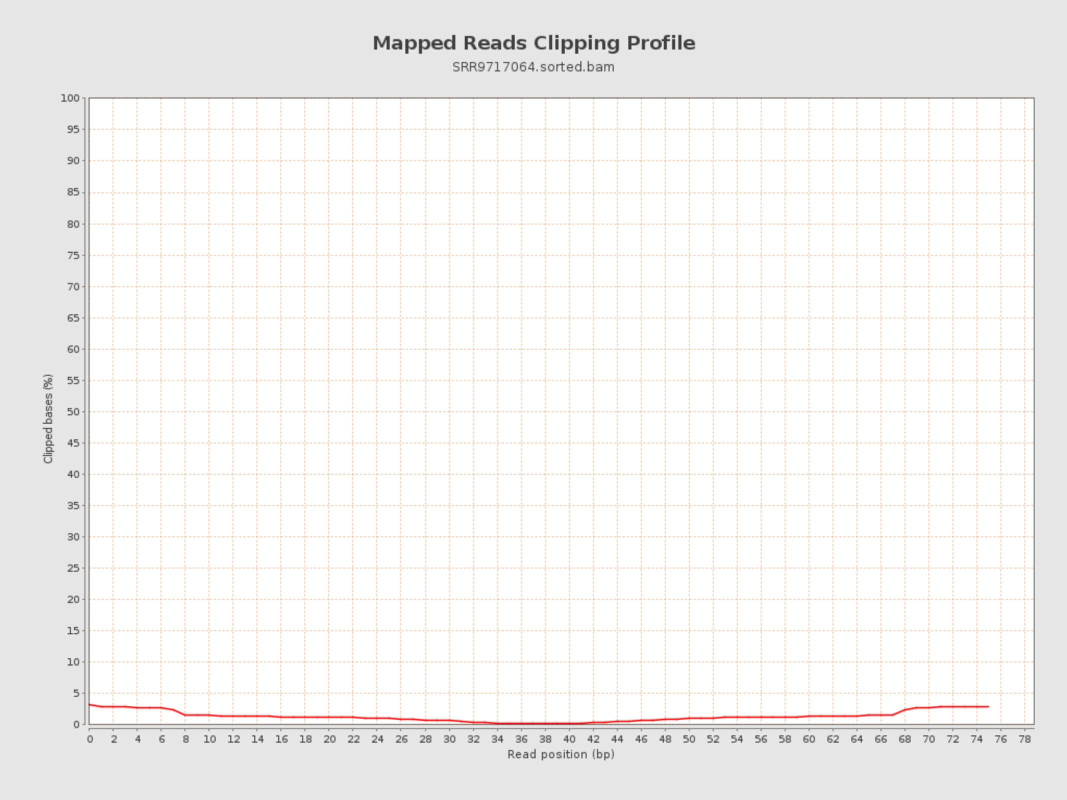
8. Results : Mapped Reads Nucleotide Content



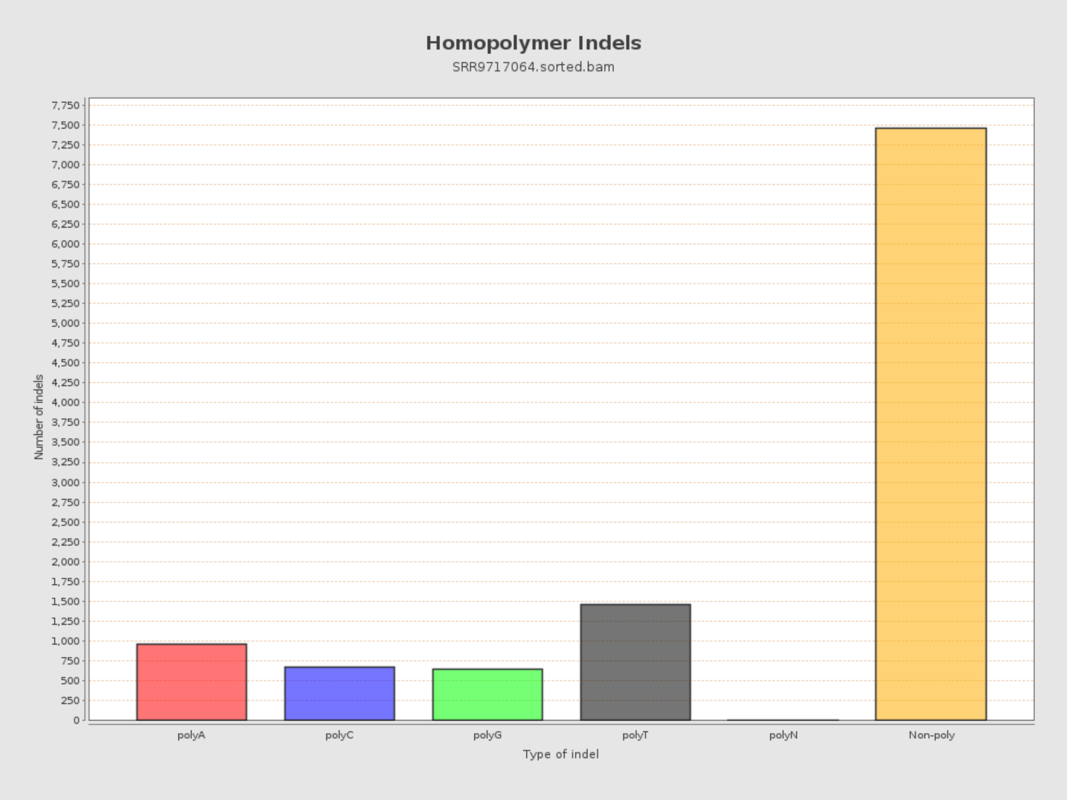
9. Results : Mapped Reads GC-content Distribution



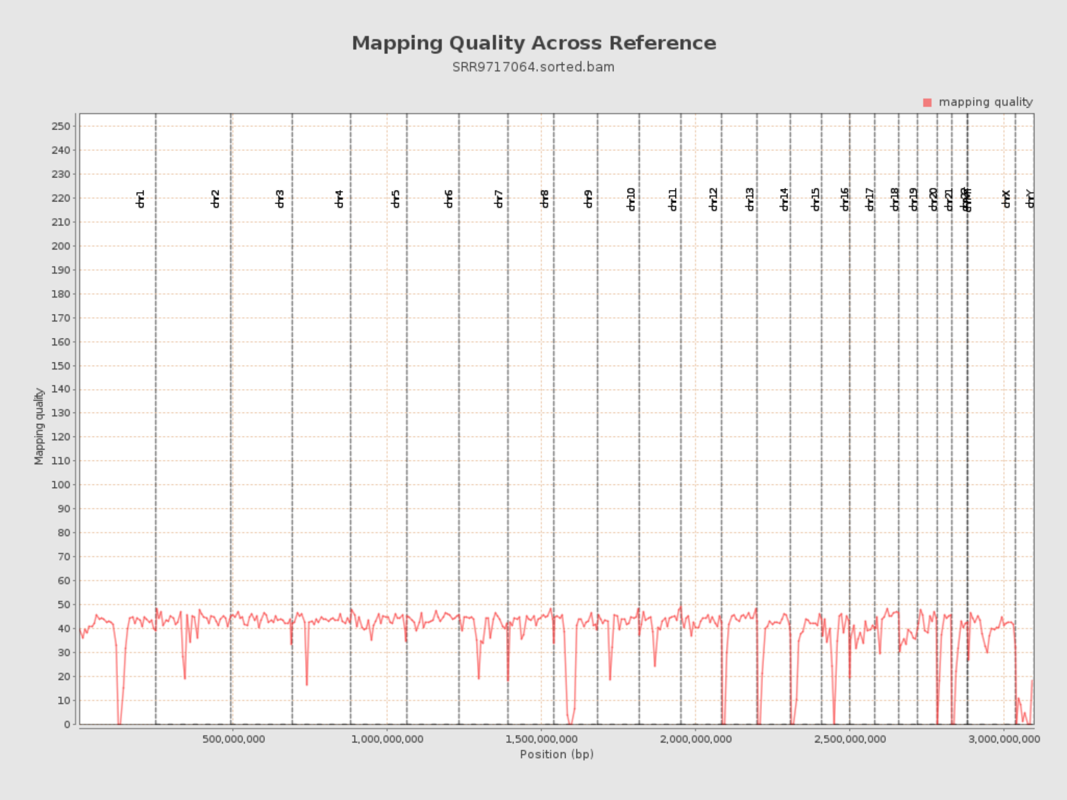
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram