Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 02:52:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717050.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_SRR9717050 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717050.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 02:52:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717050.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	990,841
Mapped reads	803,346 / 81.08%
Unmapped reads	187,495 / 18.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,772 / 0.28%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	14,804 / 1.49%
Duplication rate	1.3%
Clipped reads	804,292 / 81.17%

2.2. ACGT Content

Number/percentage of A's	10,999,564 / 24.43%
Number/percentage of C's	8,646,527 / 19.2%
Number/percentage of T's	13,493,305 / 29.96%
Number/percentage of G's	11,891,452 / 26.41%
Number/percentage of N's	1,237 / 0%
GC Percentage	45.61%

2.3. Coverage

Mean	0.0146

Standard Deviation	0.1491

2.4. Mapping Quality

Mean Mapping Quality	40.32

2.5. Mismatches and indels

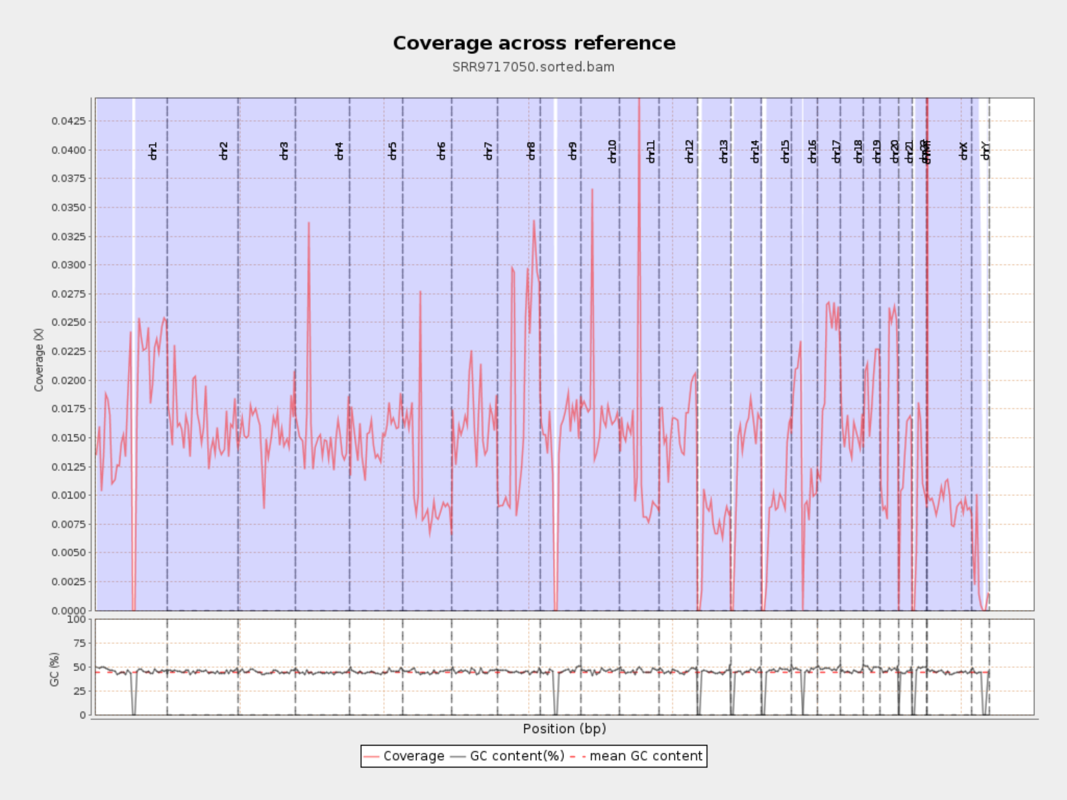
General error rate	0.54%
Mismatches	235,824
Insertions	3,546
Mapped reads with at least one insertion	0.44%
Deletions	7,713
Mapped reads with at least one deletion	0.95%
Homopolymer indels	34.73%

2.6. Chromosome stats

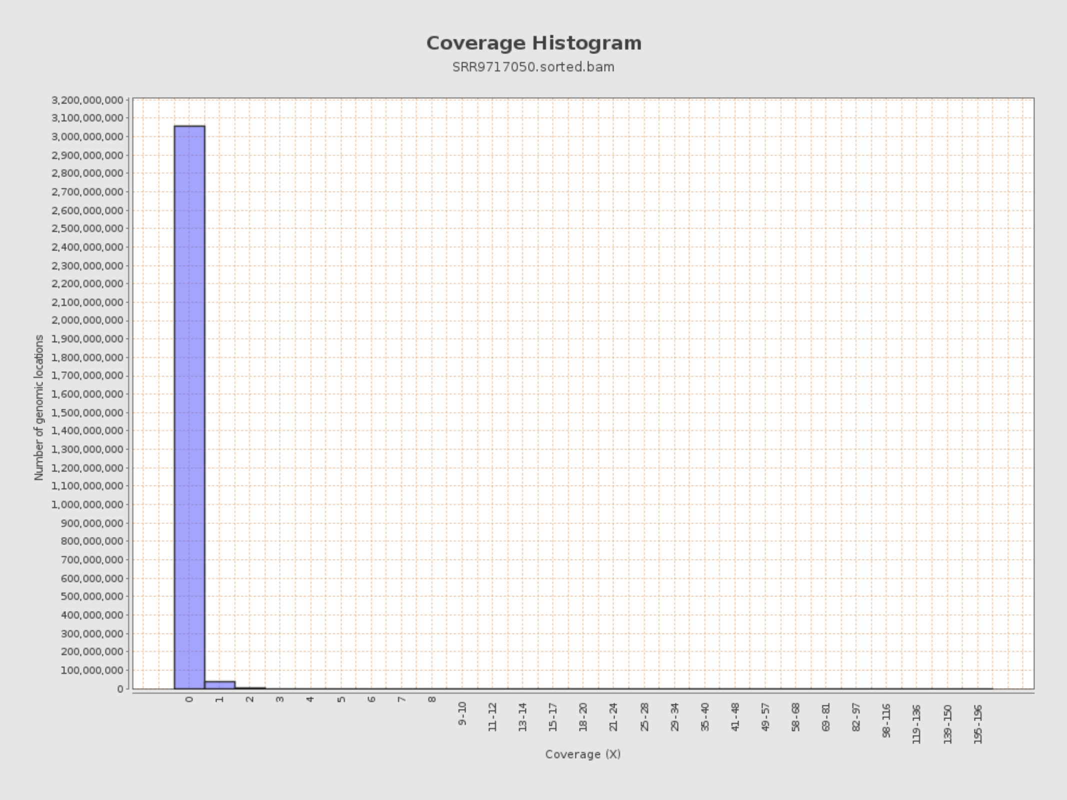
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4357693	0.0175	0.1841
chr2	243199373	3892409	0.016	0.1791
chr3	198022430	3064083	0.0155	0.1352
chr4	191154276	2961059	0.0155	0.1515
chr5	180915260	2769968	0.0153	0.1324
chr6	171115067	1916960	0.0112	0.1143
chr7	159138663	2629171	0.0165	0.1684

chr8	146364022	2754633	0.0188	0.1518
chr9	141213431	2012193	0.0142	0.1379
chr10	135534747	2394678	0.0177	0.2205
chr11	135006516	1853214	0.0137	0.1456
chr12	133851895	2184516	0.0163	0.1373
chr13	115169878	790431	0.0069	0.0905
chr14	107349540	1425612	0.0133	0.1258
chr15	102531392	881387	0.0086	0.1004
chr16	90354753	1188662	0.0132	0.1308
chr17	81195210	1742306	0.0215	0.162
chr18	78077248	1195961	0.0153	0.1628
chr19	59128983	1172393	0.0198	0.1736
chr20	63025520	1127439	0.0179	0.1493
chr21	48129895	607629	0.0126	0.1325
chr22	51304566	485214	0.0095	0.1062
chrMT	16571	35459	2.1398	2.1244
chrX	155270560	1451397	0.0093	0.1094
chrY	59373566	150864	0.0025	0.091

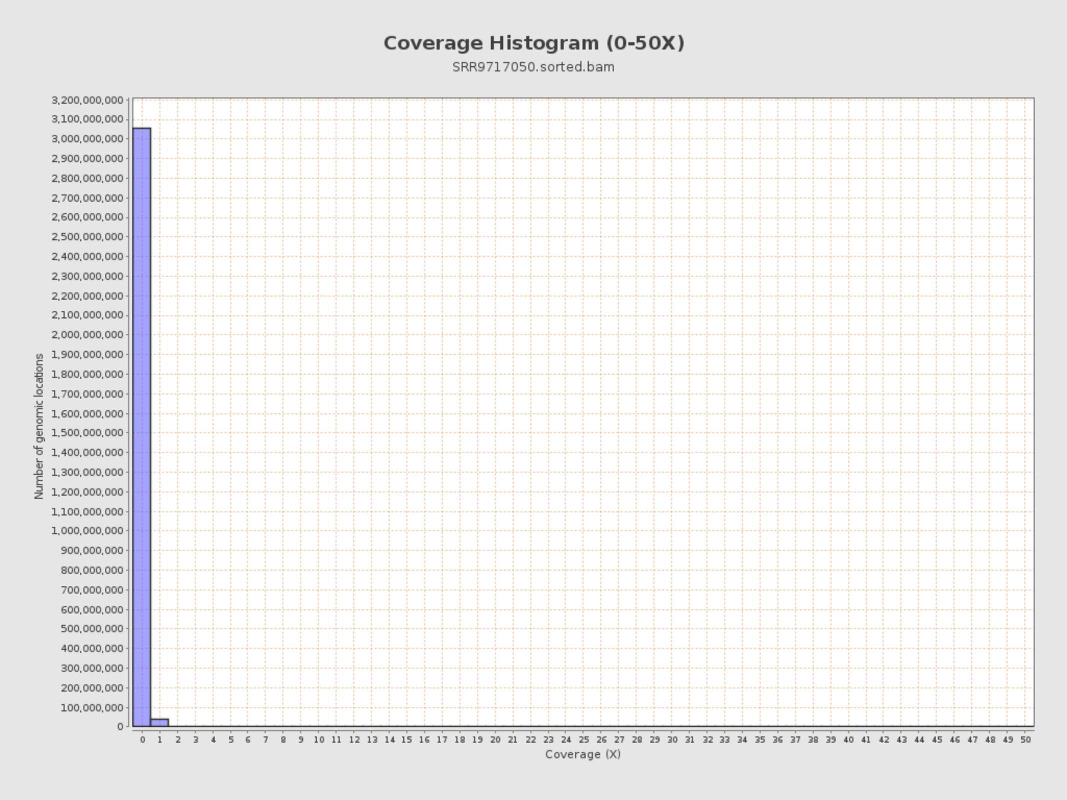
3. Results : Coverage across reference



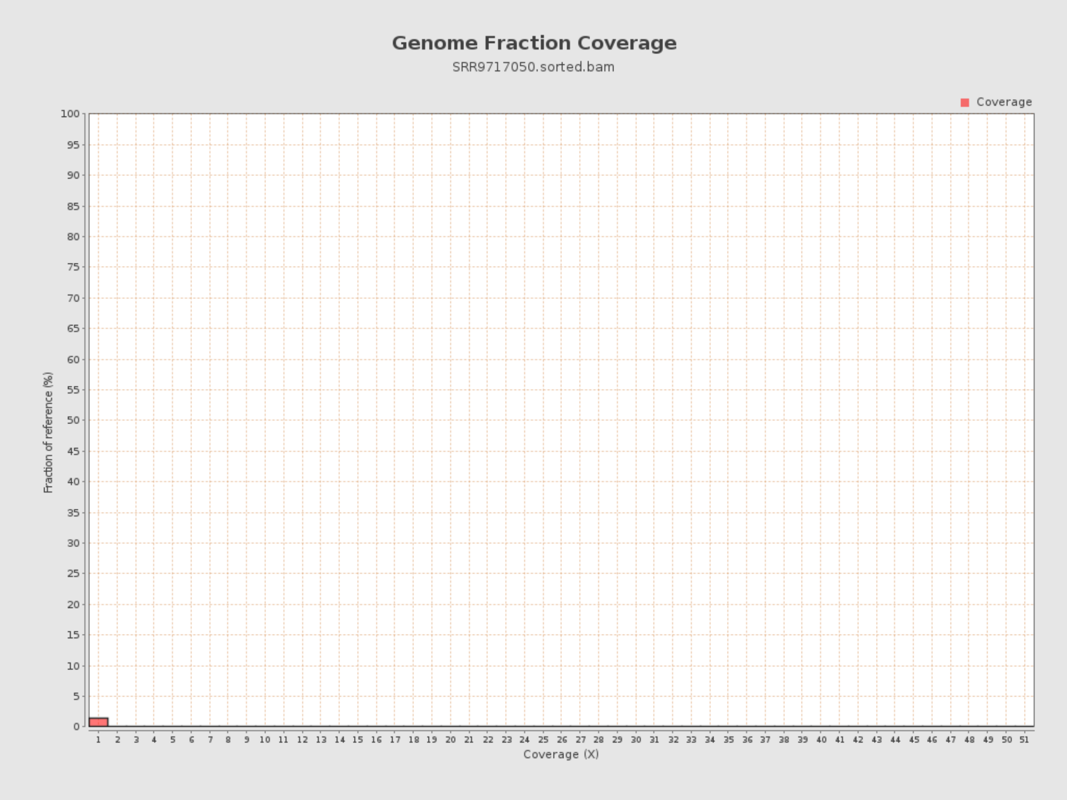
4. Results : Coverage Histogram



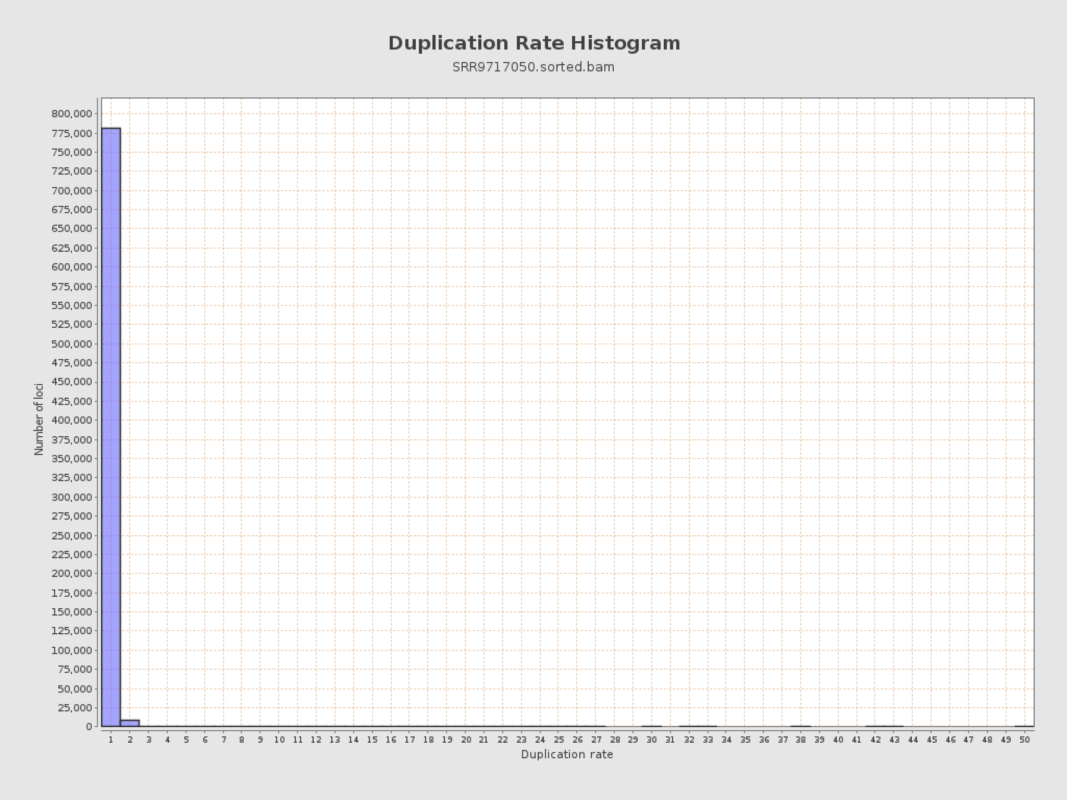
5. Results : Coverage Histogram (0-50X)



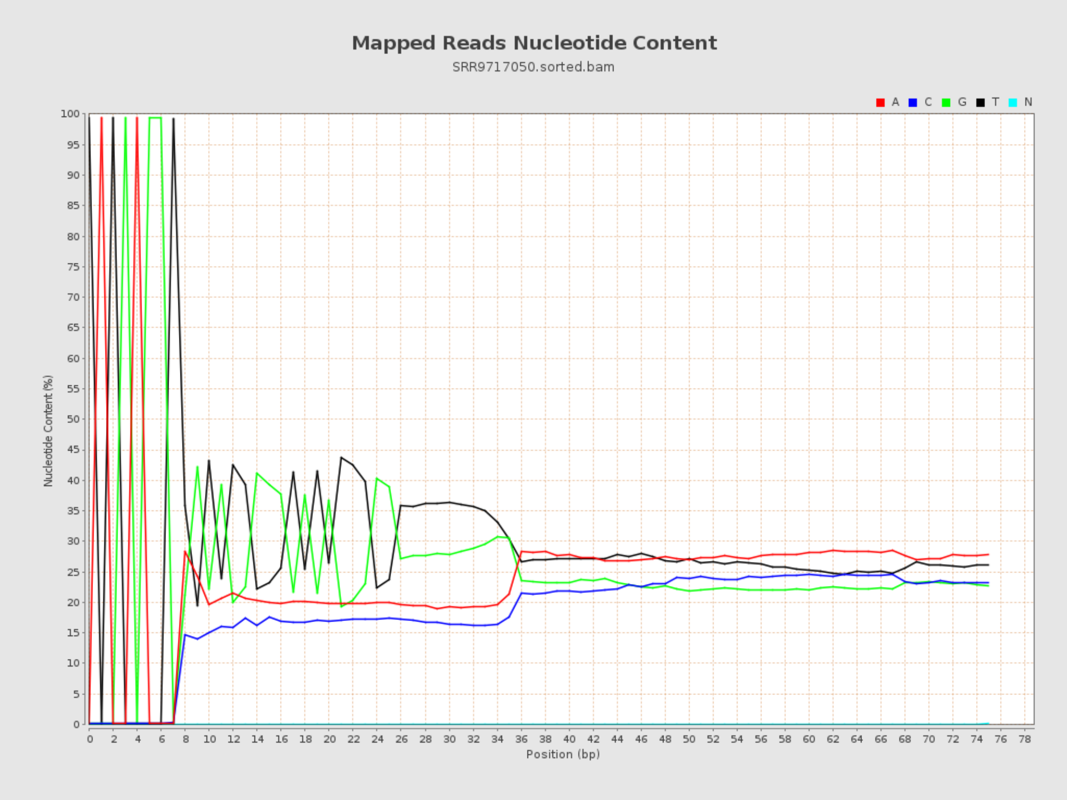
6. Results : Genome Fraction Coverage



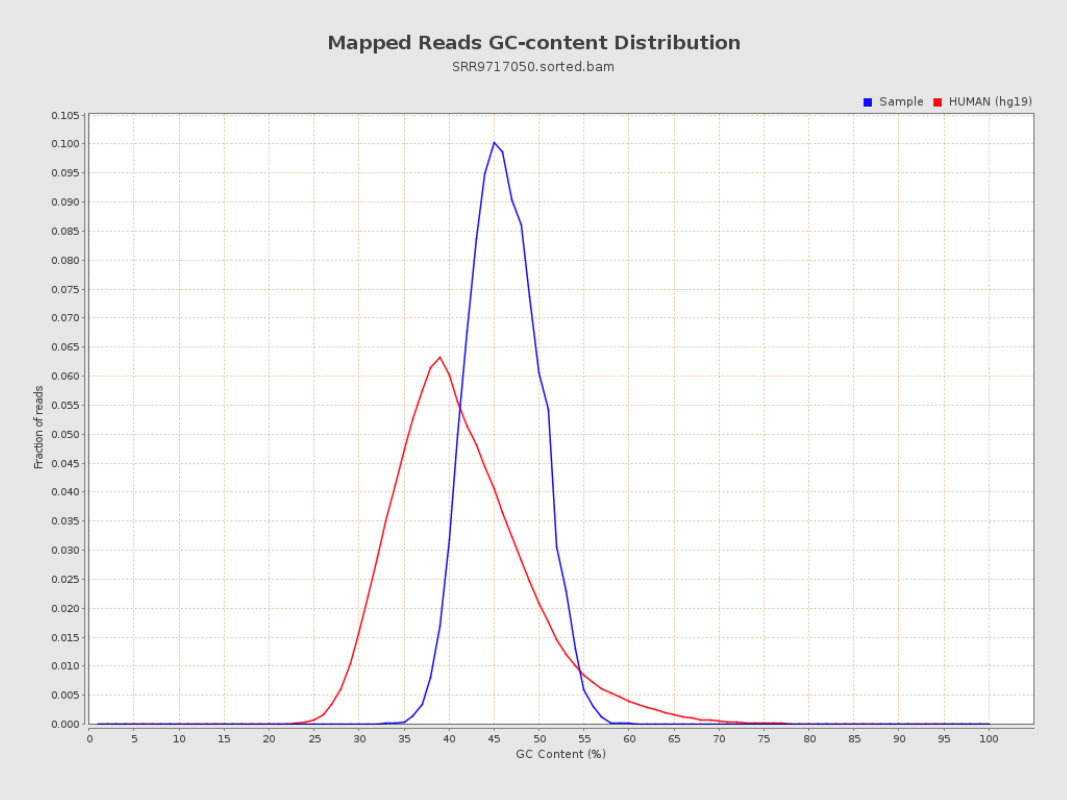
7. Results : Duplication Rate Histogram



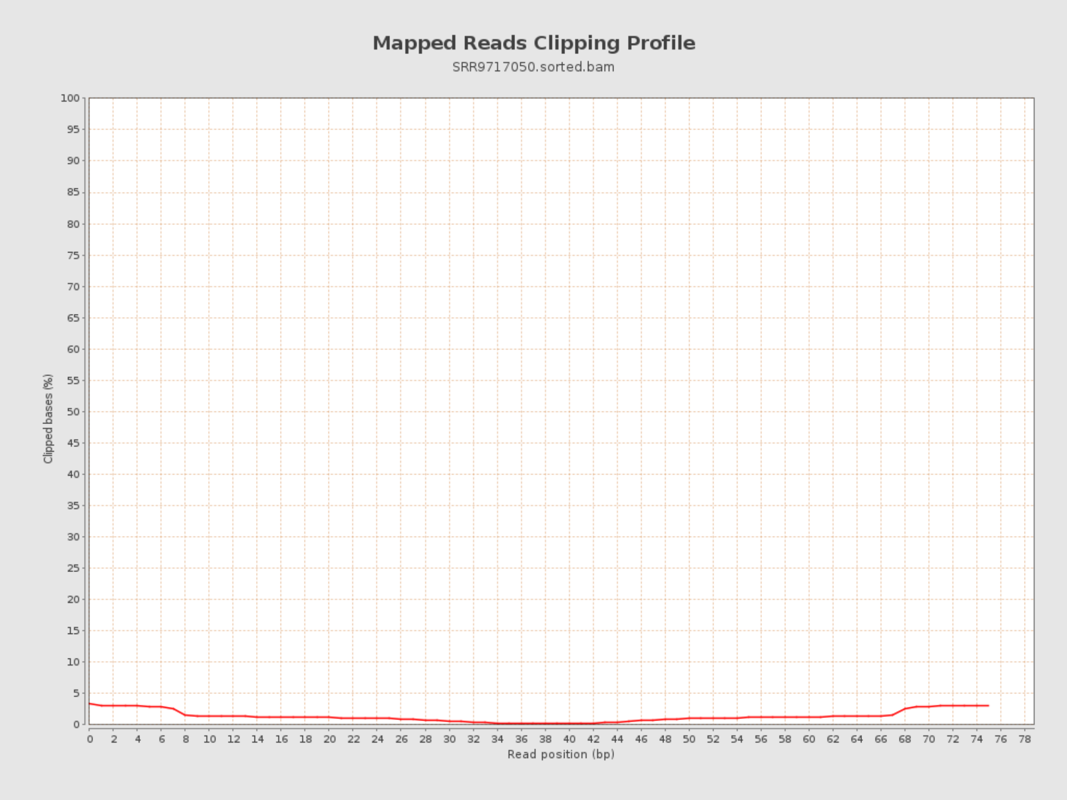
8. Results : Mapped Reads Nucleotide Content



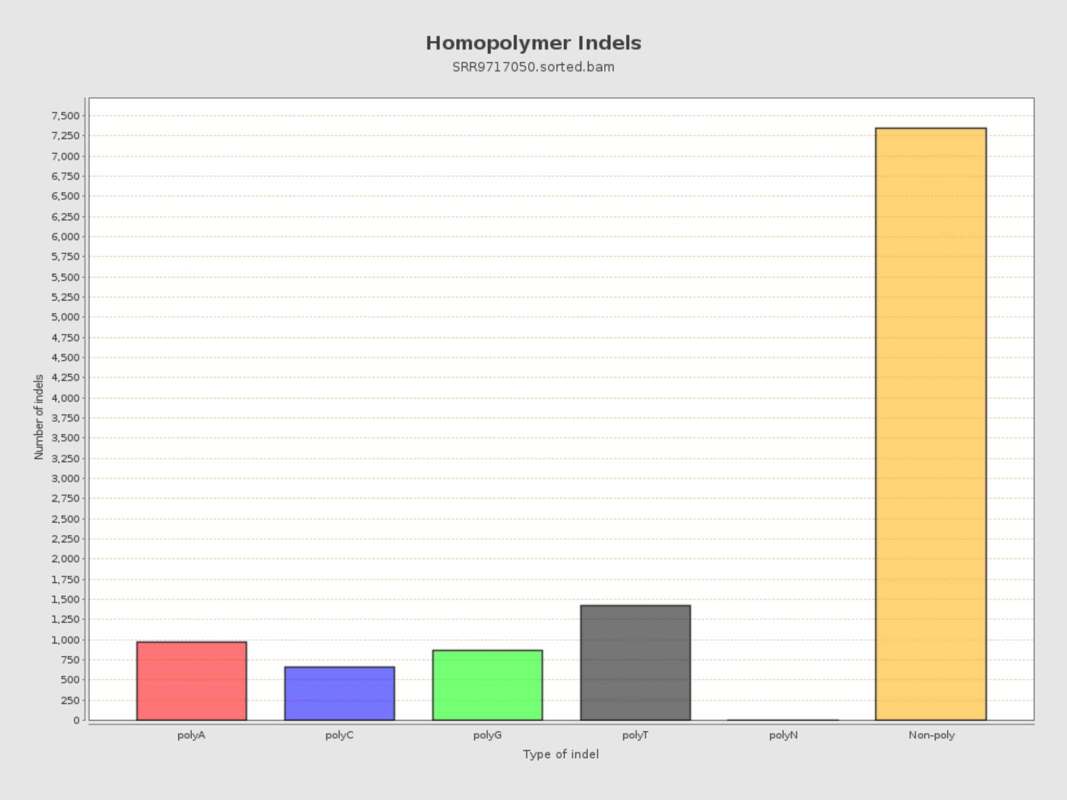
9. Results : Mapped Reads GC-content Distribution



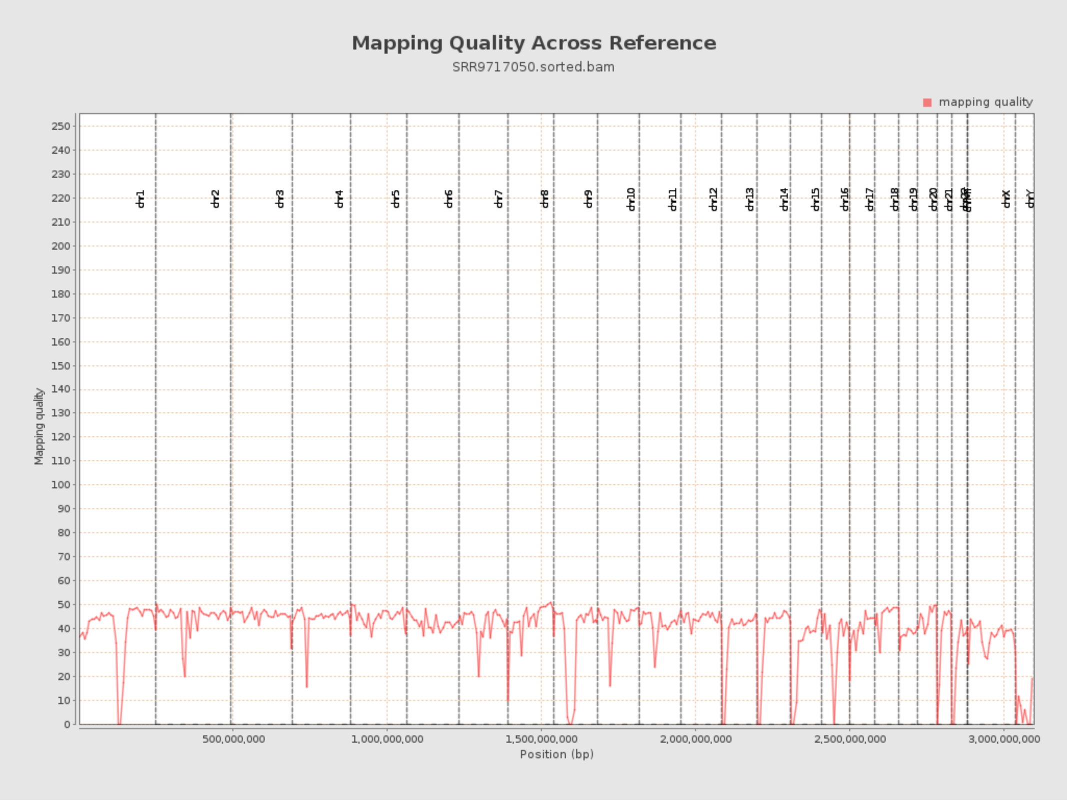
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram