Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 02:39:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717045.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_SRR9717045 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717045.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 02:39:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717045.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,593,344
Mapped reads	2,395,678 / 92.38%
Unmapped reads	197,666 / 7.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	67,904 / 2.62%
Read min/max/mean length	30 / 101 / 101.94
Duplicated reads (estimated)	82,596 / 3.18%
Duplication rate	2.28%
Clipped reads	2,460,048 / 94.86%

2.2. ACGT Content

Number/percentage of A's	45,337,298 / 25.61%
Number/percentage of C's	36,036,147 / 20.36%
Number/percentage of T's	53,017,736 / 29.95%
Number/percentage of G's	42,624,450 / 24.08%
Number/percentage of N's	20,534 / 0.01%
GC Percentage	44.43%

2.3. Coverage

Mean	0.0572

Standard Deviation	0.4606

2.4. Mapping Quality

Mean Mapping Quality	44.76

2.5. Mismatches and indels

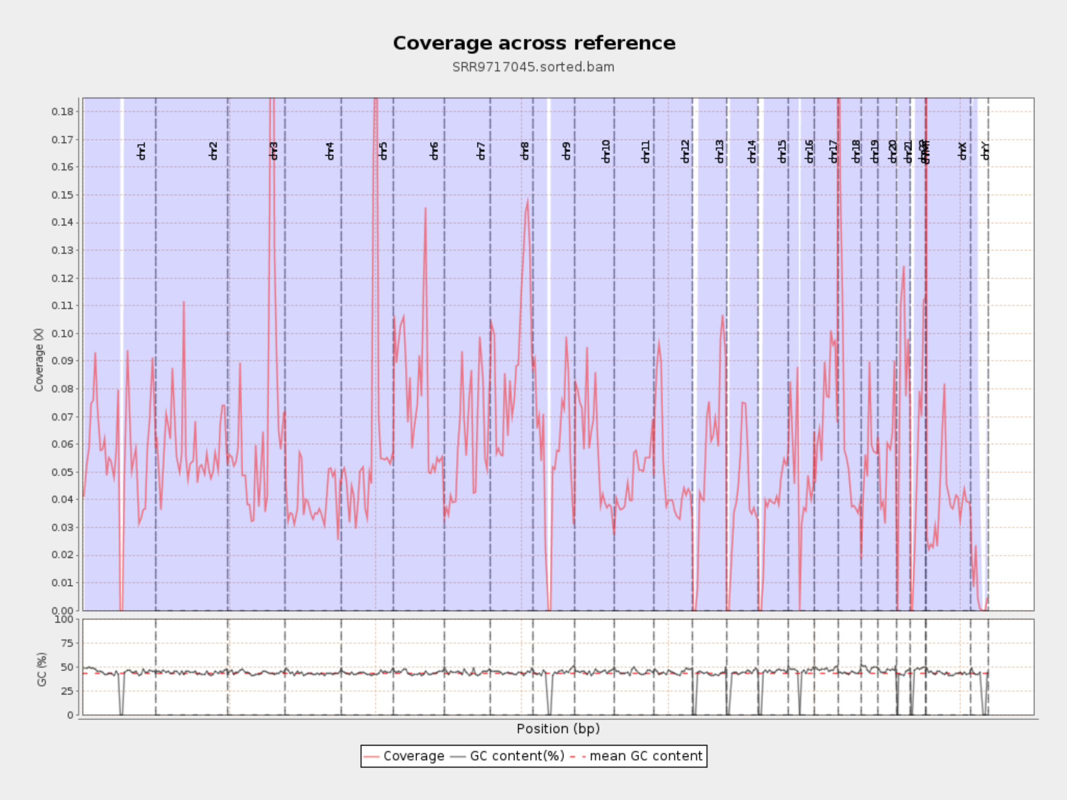
General error rate	0.76%
Mismatches	1,319,998
Insertions	15,101
Mapped reads with at least one insertion	0.62%
Deletions	36,116
Mapped reads with at least one deletion	1.49%
Homopolymer indels	39.42%

2.6. Chromosome stats

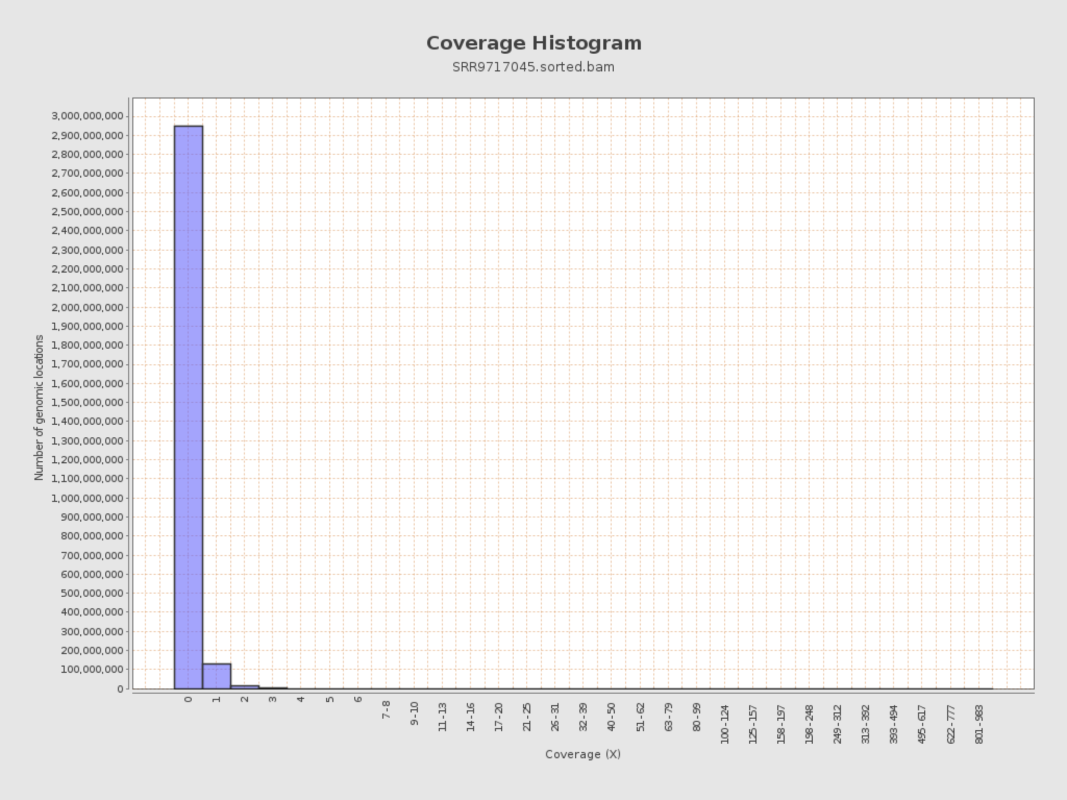
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14009146	0.0562	0.6298
chr2	243199373	14409933	0.0593	0.7331
chr3	198022430	13905344	0.0702	0.3167
chr4	191154276	7605042	0.0398	0.2507
chr5	180915260	10911210	0.0603	0.2863
chr6	171115067	13355907	0.0781	0.3828
chr7	159138663	9626177	0.0605	0.6522

chr8	146364022	13446714	0.0919	0.5983
chr9	141213431	7948735	0.0563	0.4285
chr10	135534747	8097547	0.0597	0.451
chr11	135006516	6420905	0.0476	0.3655
chr12	133851895	6806848	0.0509	0.2602
chr13	115169878	6618824	0.0575	0.2737
chr14	107349540	4279904	0.0399	0.2675
chr15	102531392	3566802	0.0348	0.2136
chr16	90354753	4312895	0.0477	0.2927
chr17	81195210	6185102	0.0762	0.3583
chr18	78077248	5629466	0.0721	0.8792
chr19	59128983	3358796	0.0568	0.5846
chr20	63025520	3472531	0.0551	0.3101
chr21	48129895	3854258	0.0801	0.3447
chr22	51304566	2807796	0.0547	0.2729
chrMT	16571	18488	1.1157	1.4549
chrX	155270560	6024220	0.0388	0.3201
chrY	59373566	426488	0.0072	0.2165

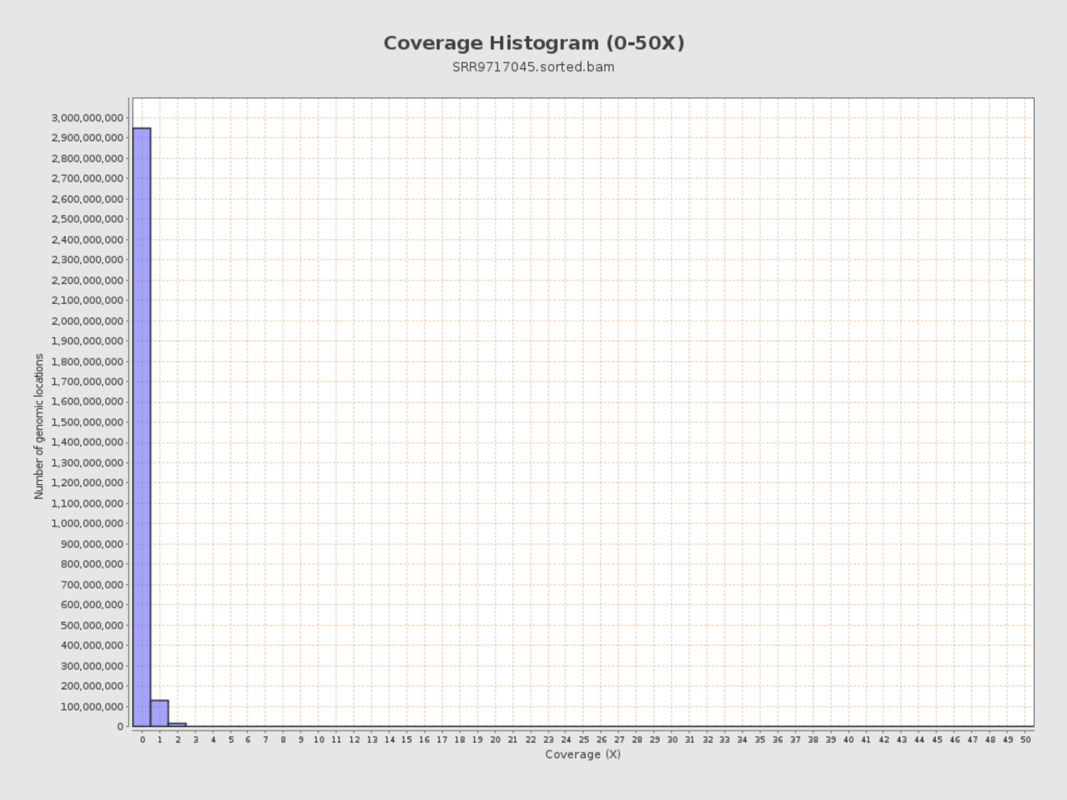
3. Results : Coverage across reference



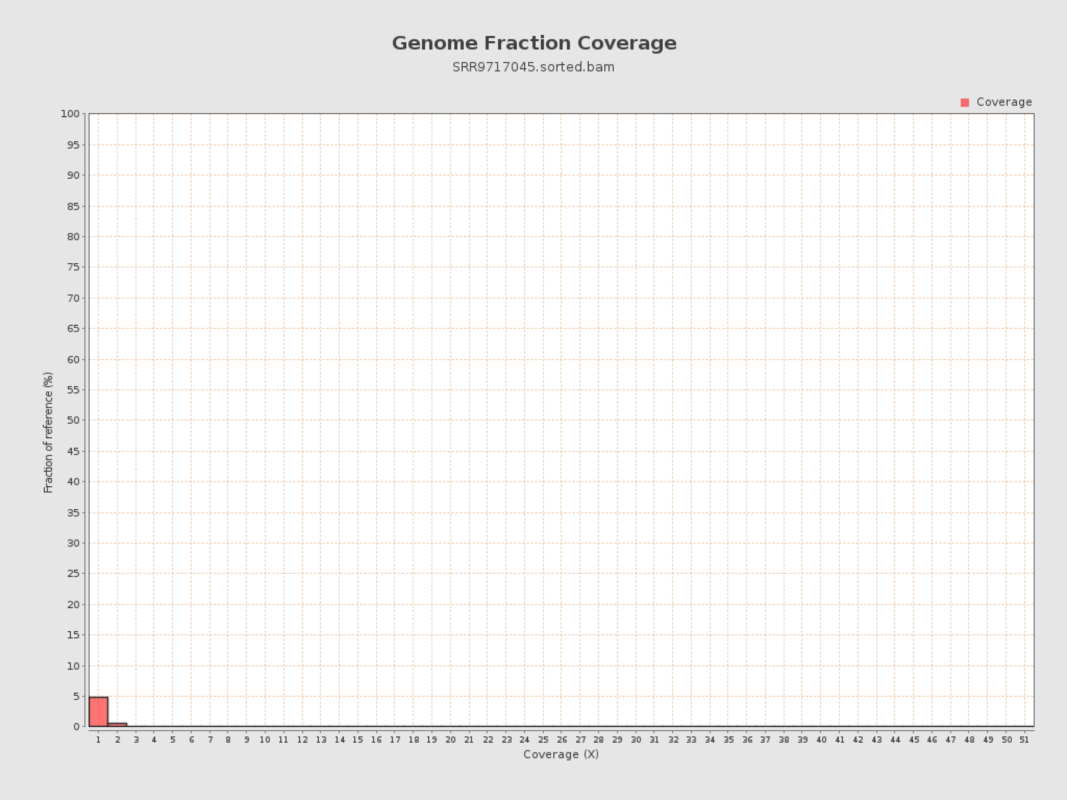
4. Results : Coverage Histogram



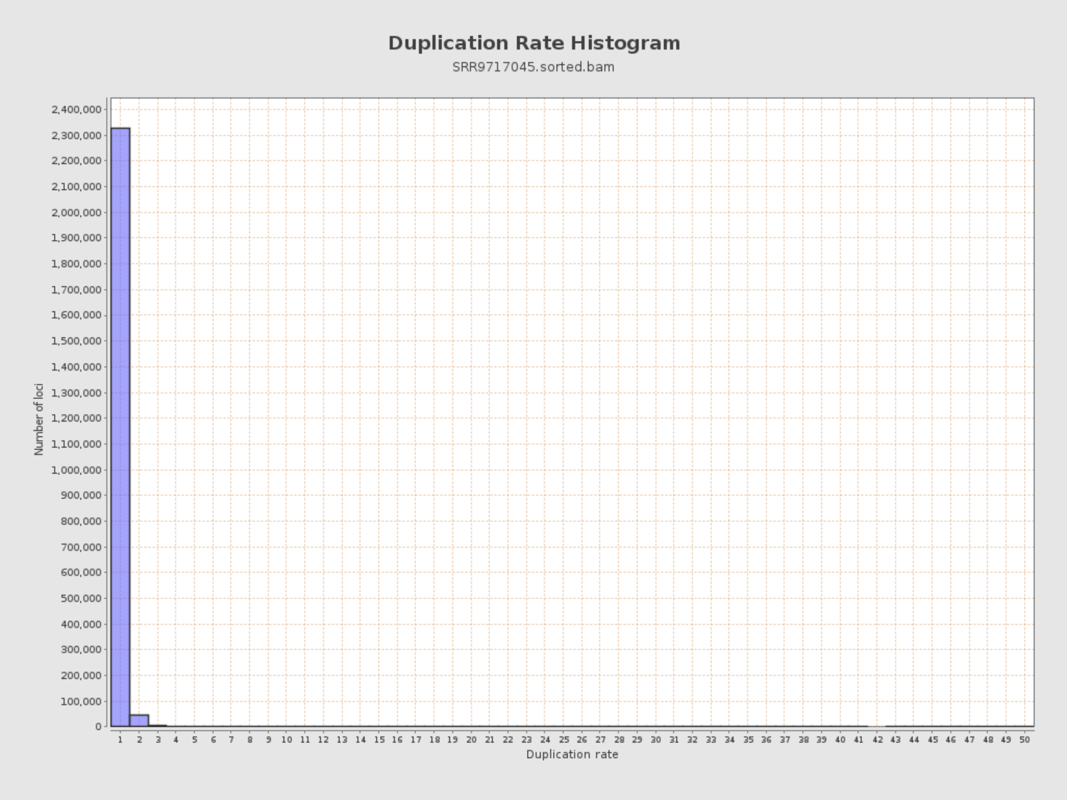
5. Results : Coverage Histogram (0-50X)



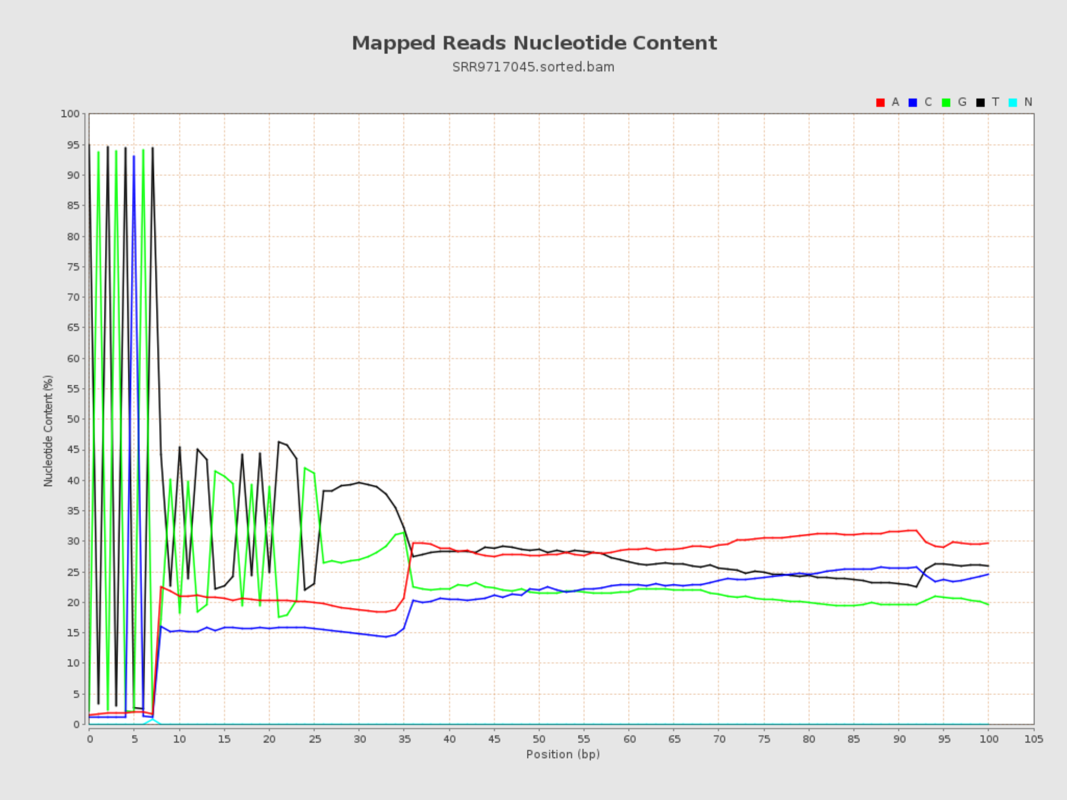
6. Results : Genome Fraction Coverage



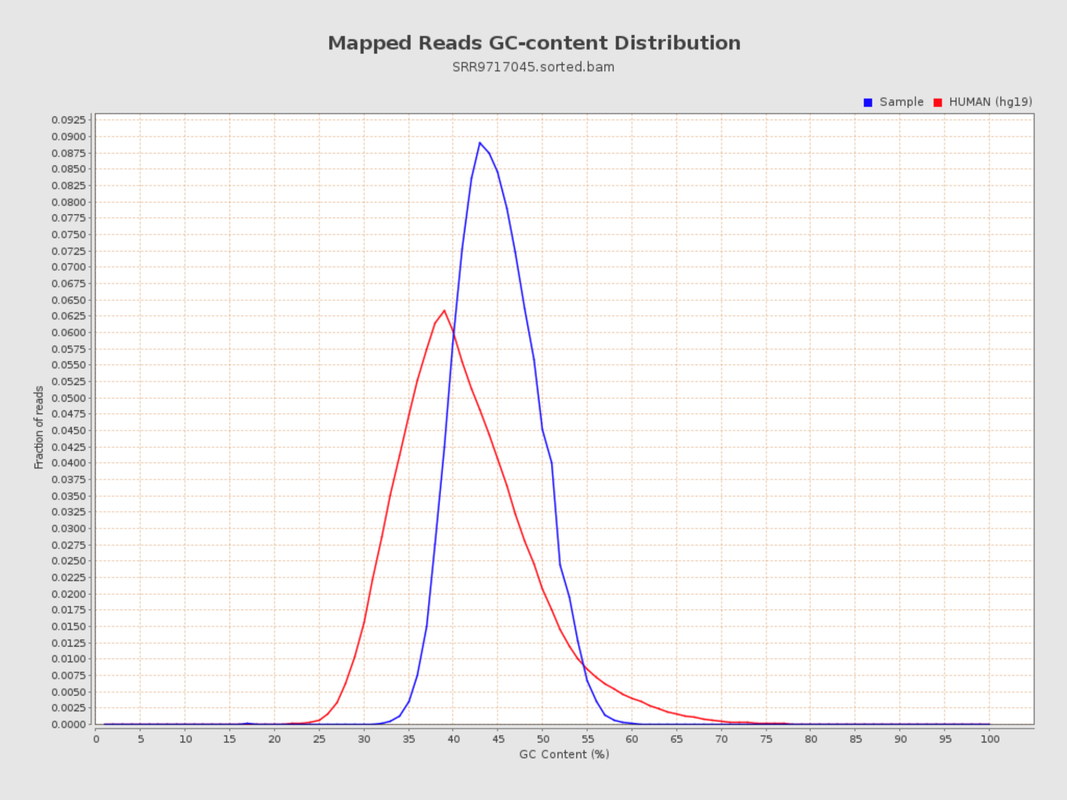
7. Results : Duplication Rate Histogram



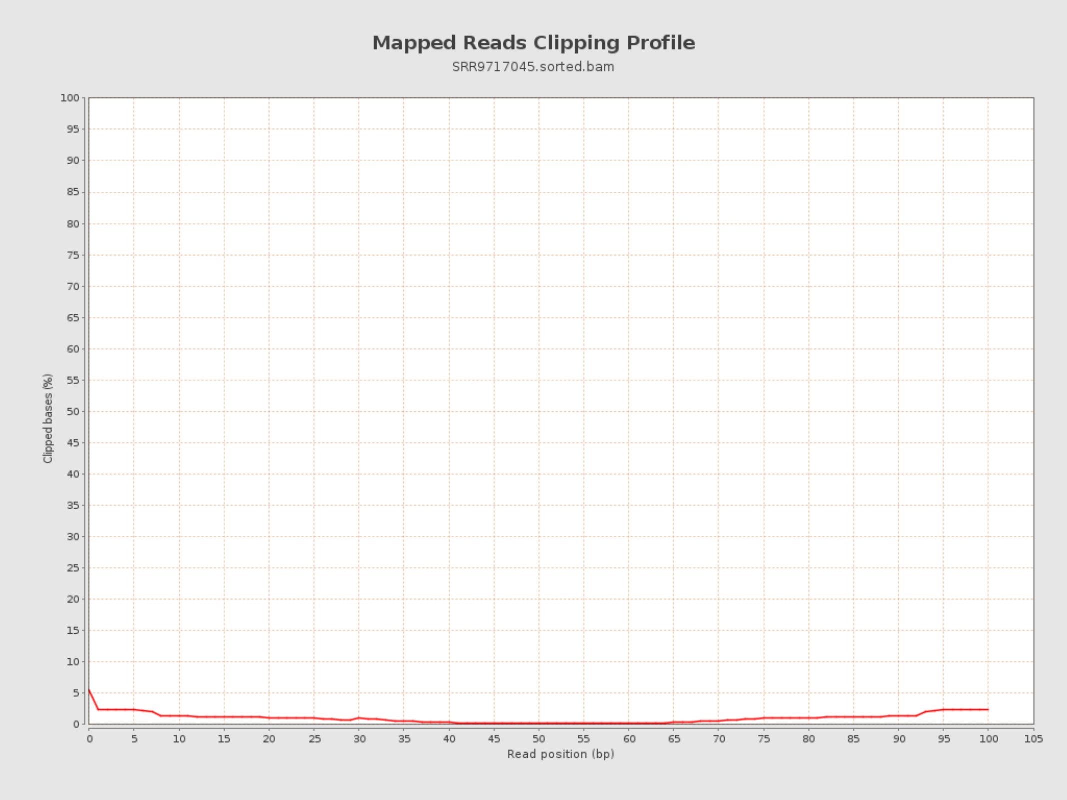
8. Results : Mapped Reads Nucleotide Content



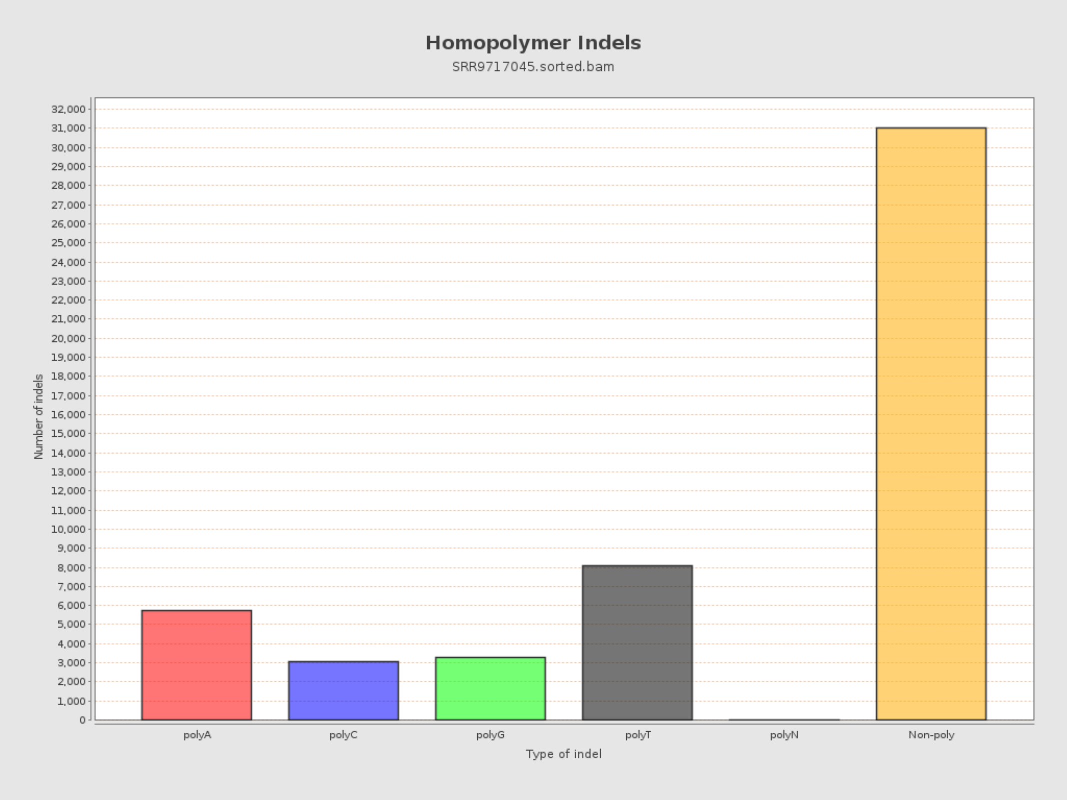
9. Results : Mapped Reads GC-content Distribution



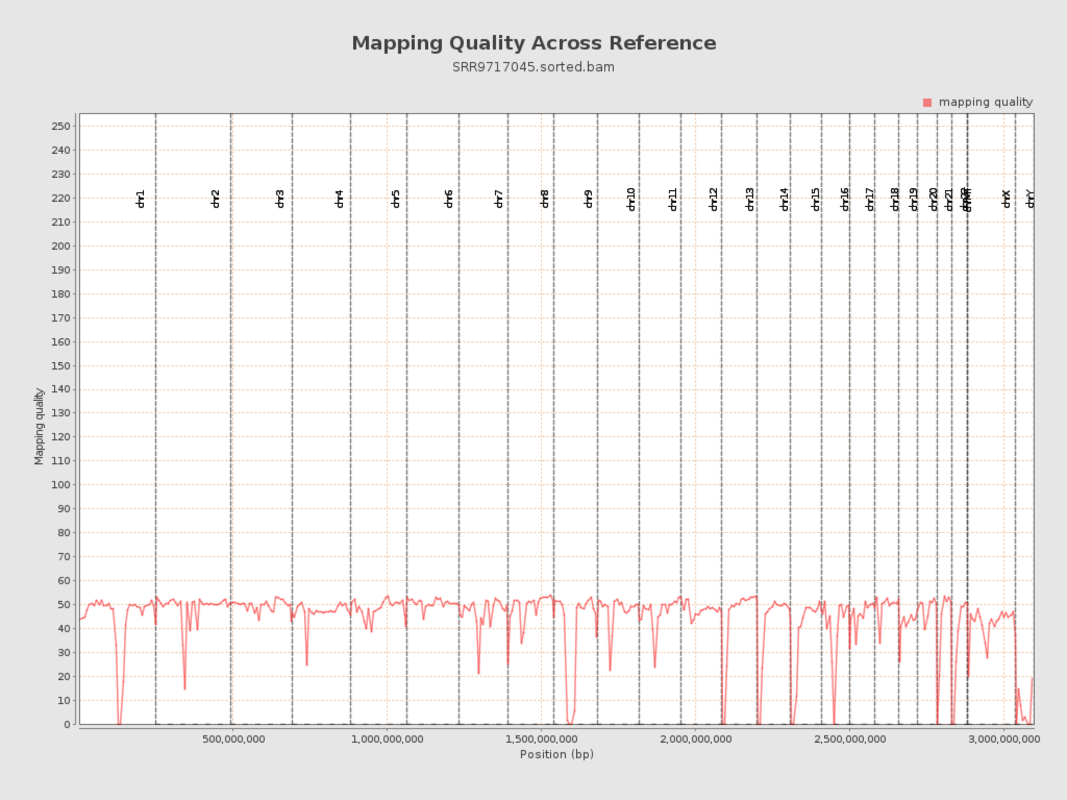
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram