Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 23:53:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717003.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_SRR9717003 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717003.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 23:53:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717003.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,088,062
Mapped reads	1,884,421 / 90.25%
Unmapped reads	203,641 / 9.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,650 / 0.46%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	74,073 / 3.55%
Duplication rate	2.82%
Clipped reads	1,889,517 / 90.49%

2.2. ACGT Content

Number/percentage of A's	28,070,371 / 25.94%
Number/percentage of C's	20,862,210 / 19.28%
Number/percentage of T's	33,925,281 / 31.35%
Number/percentage of G's	25,358,825 / 23.43%
Number/percentage of N's	1,772 / 0%
GC Percentage	42.71%

2.3. Coverage

Mean	0.035

Standard Deviation	0.3294

2.4. Mapping Quality

Mean Mapping Quality	44.46

2.5. Mismatches and indels

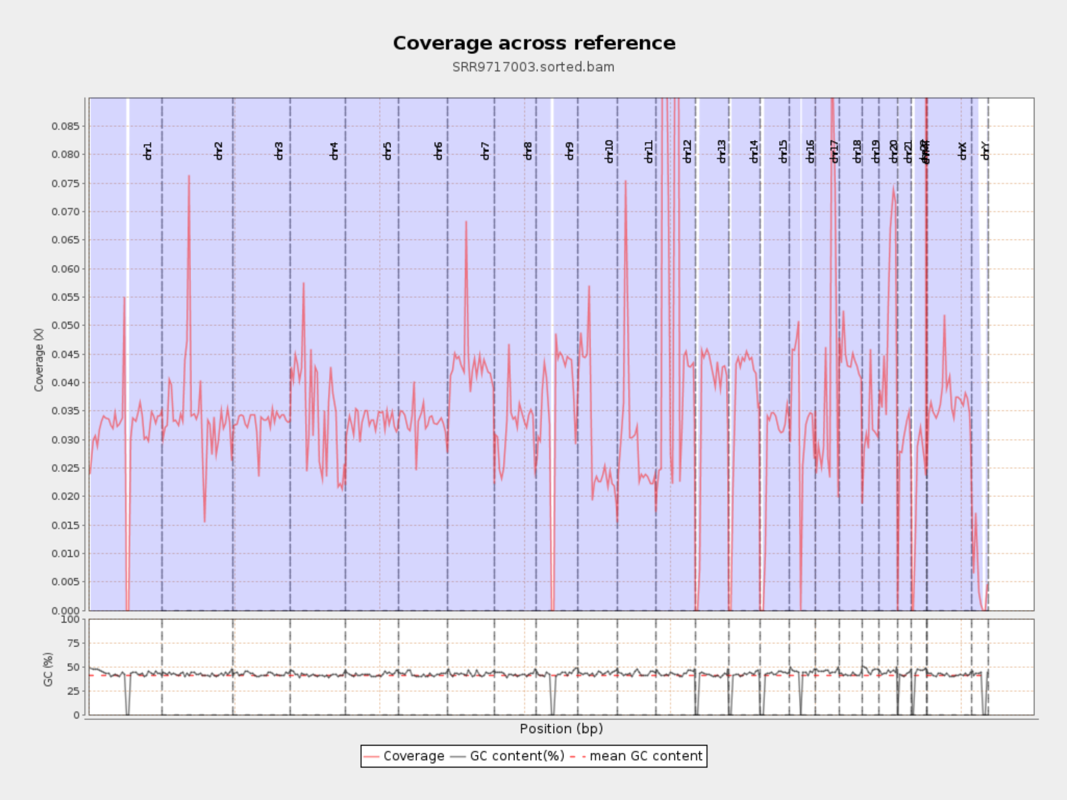
General error rate	0.55%
Mismatches	583,553
Insertions	6,531
Mapped reads with at least one insertion	0.34%
Deletions	18,641
Mapped reads with at least one deletion	0.98%
Homopolymer indels	43.41%

2.6. Chromosome stats

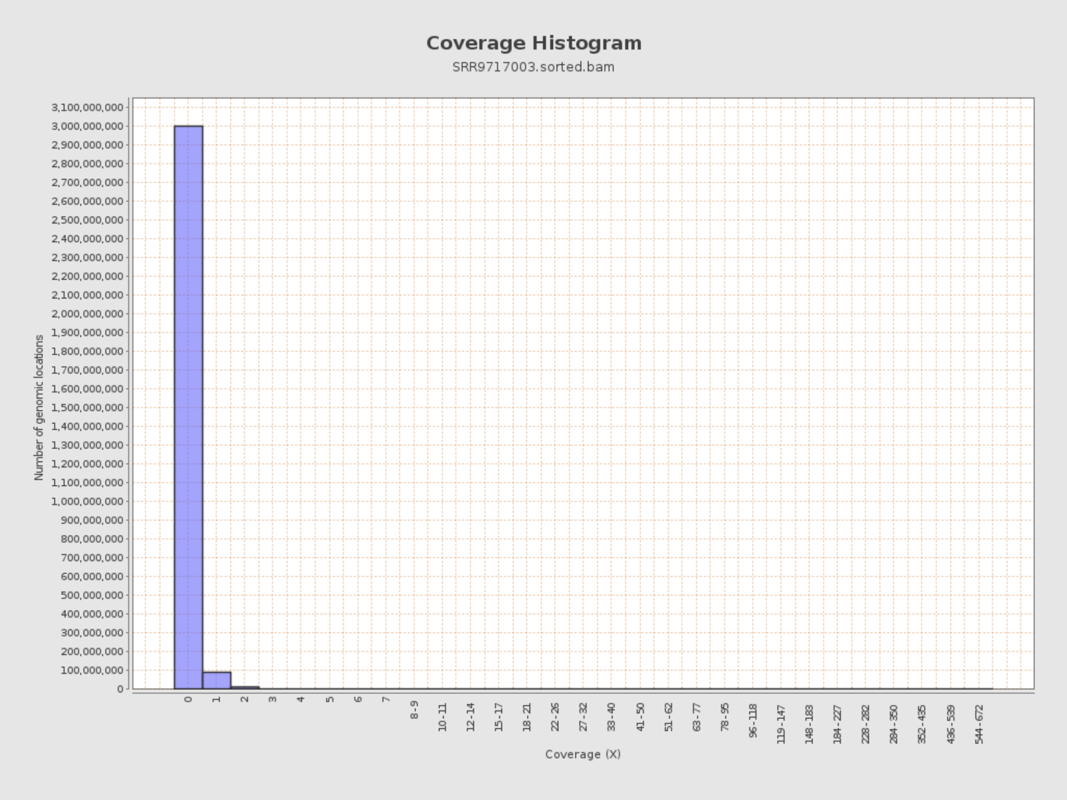
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7768750	0.0312	0.5755
chr2	243199373	8455533	0.0348	0.3654
chr3	198022430	6563798	0.0331	0.198
chr4	191154276	6717356	0.0351	0.2273
chr5	180915260	6008033	0.0332	0.2034
chr6	171115067	5687818	0.0332	0.2281
chr7	159138663	6927406	0.0435	0.4495

chr8	146364022	4722084	0.0323	0.3196
chr9	141213431	5028295	0.0356	0.3573
chr10	135534747	4170176	0.0308	0.3121
chr11	135006516	4149955	0.0307	0.2786
chr12	133851895	7930199	0.0592	0.3024
chr13	115169878	4094765	0.0356	0.2042
chr14	107349540	3855617	0.0359	0.2369
chr15	102531392	2762929	0.0269	0.1803
chr16	90354753	3080468	0.0341	0.2221
chr17	81195210	3256542	0.0401	0.2277
chr18	78077248	3463673	0.0444	0.6435
chr19	59128983	1886771	0.0319	0.4383
chr20	63025520	3304257	0.0524	0.258
chr21	48129895	1323183	0.0275	0.2101
chr22	51304566	1042234	0.0203	0.1538
chrMT	16571	35270	2.1284	1.8012
chrX	155270560	5700577	0.0367	0.2598
chrY	59373566	313967	0.0053	0.1244

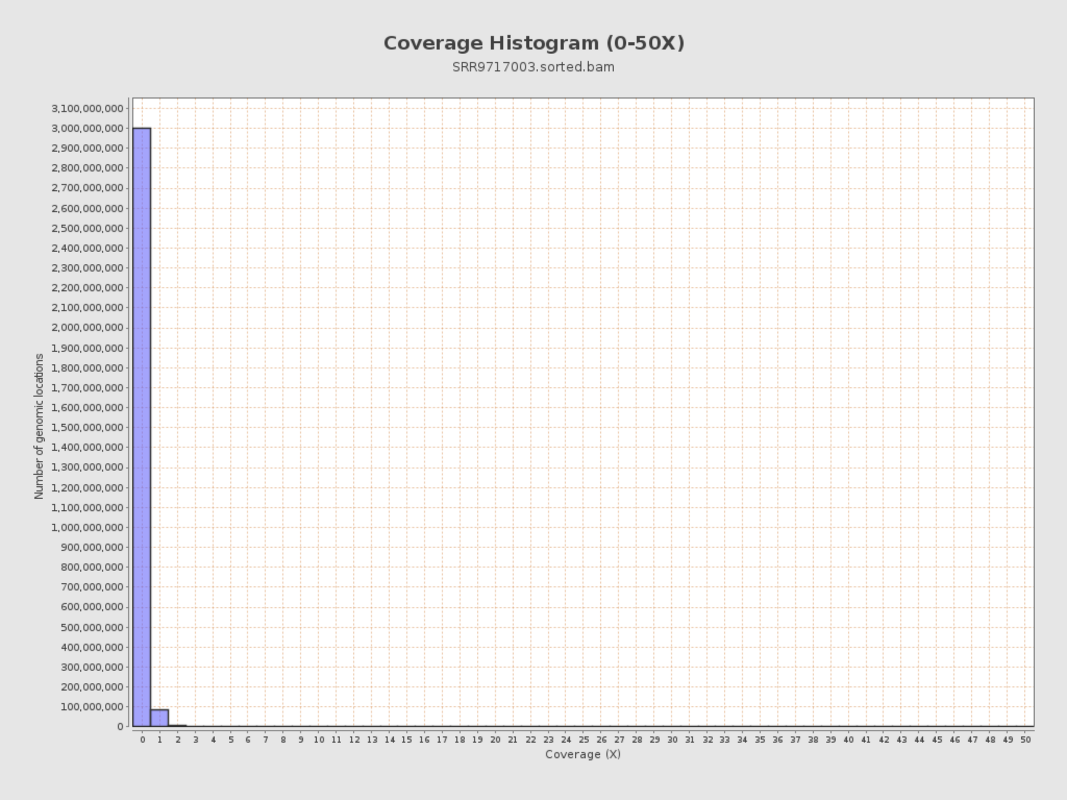
3. Results : Coverage across reference



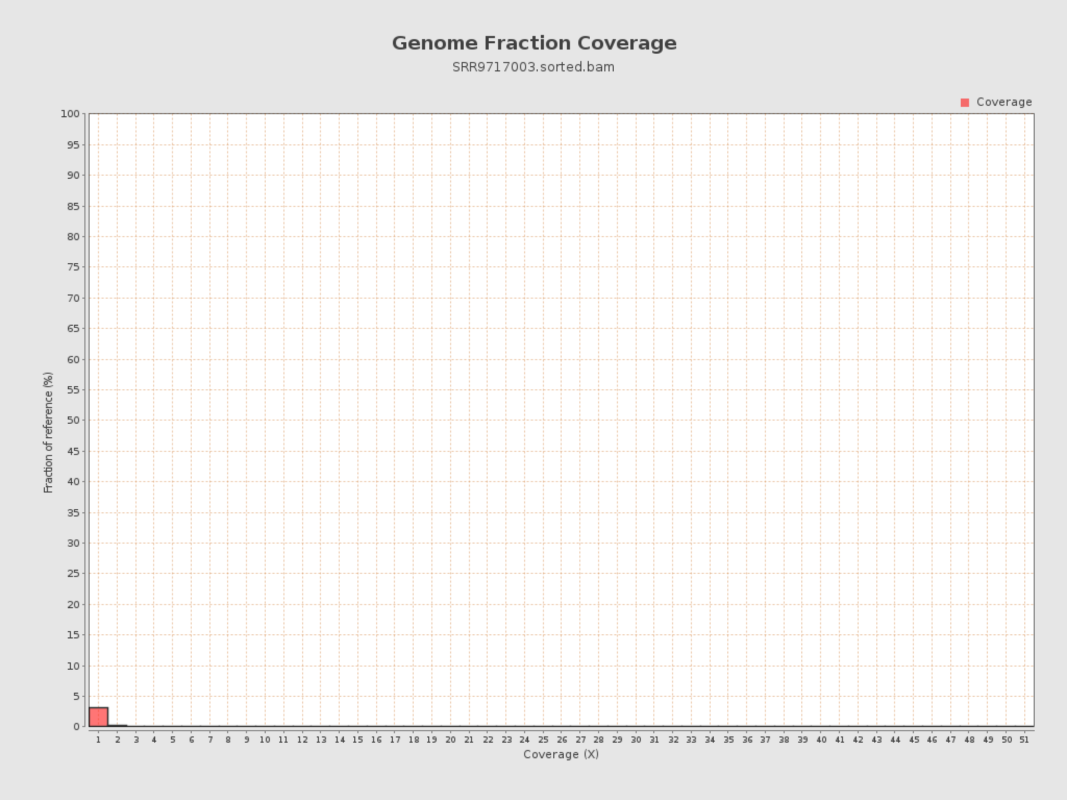
4. Results : Coverage Histogram



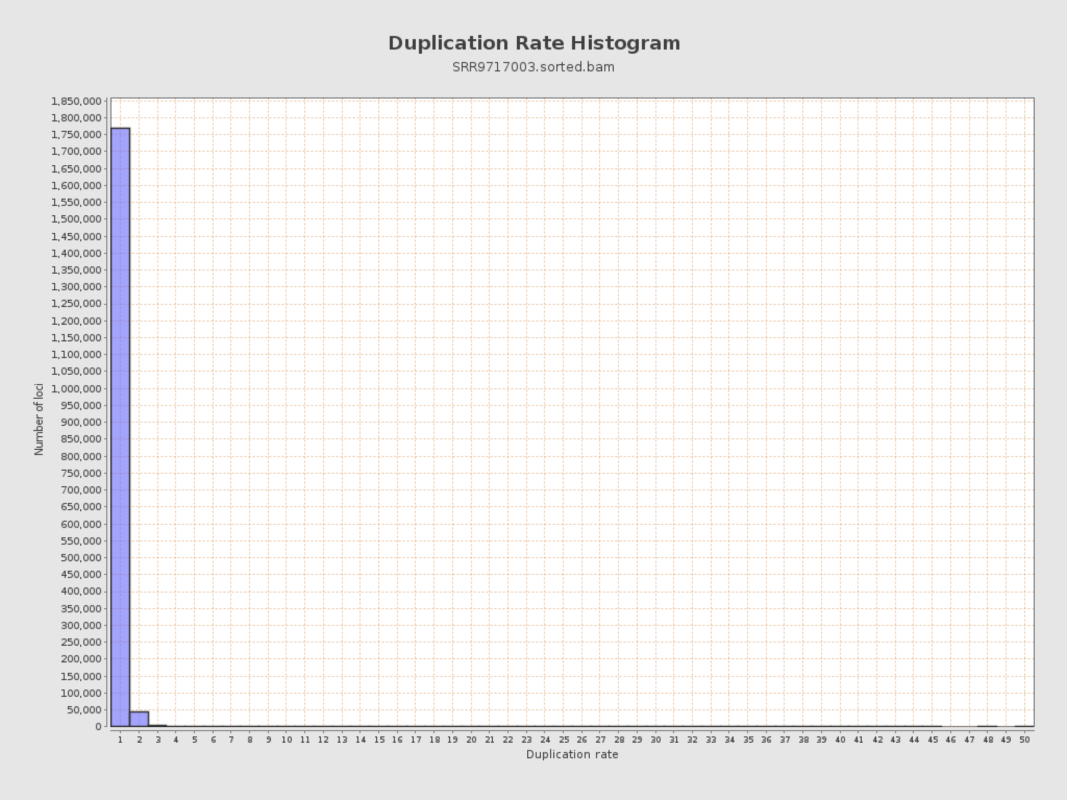
5. Results : Coverage Histogram (0-50X)



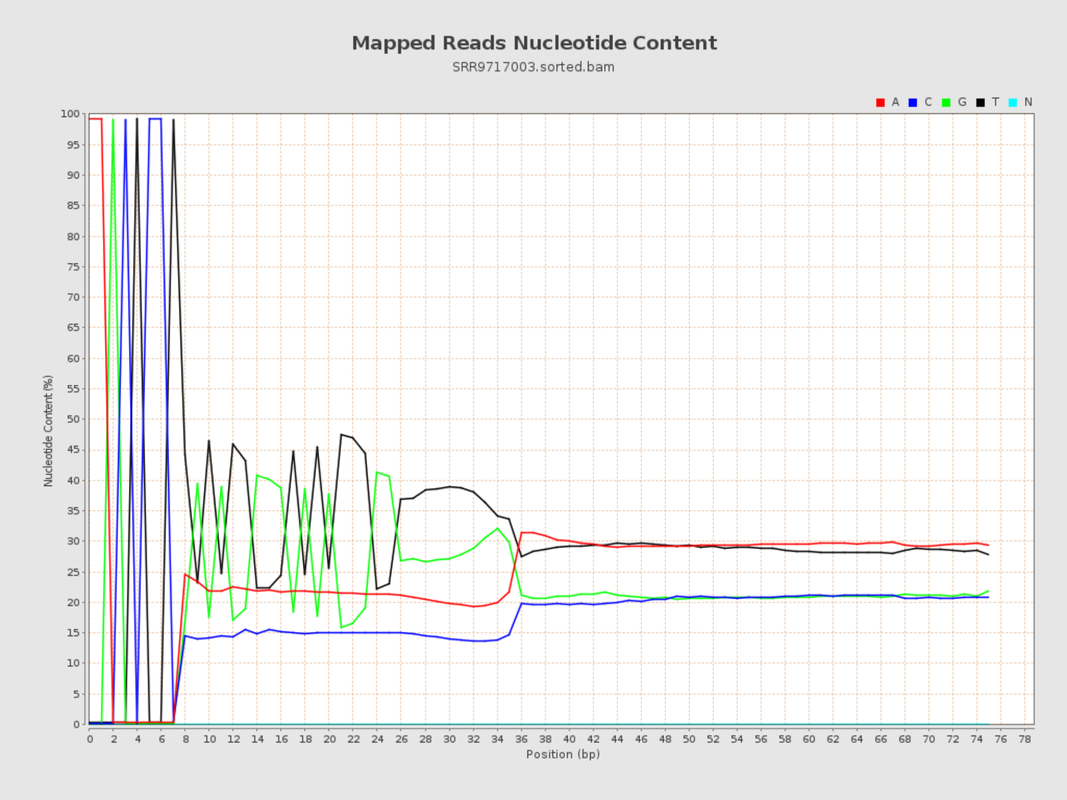
6. Results : Genome Fraction Coverage



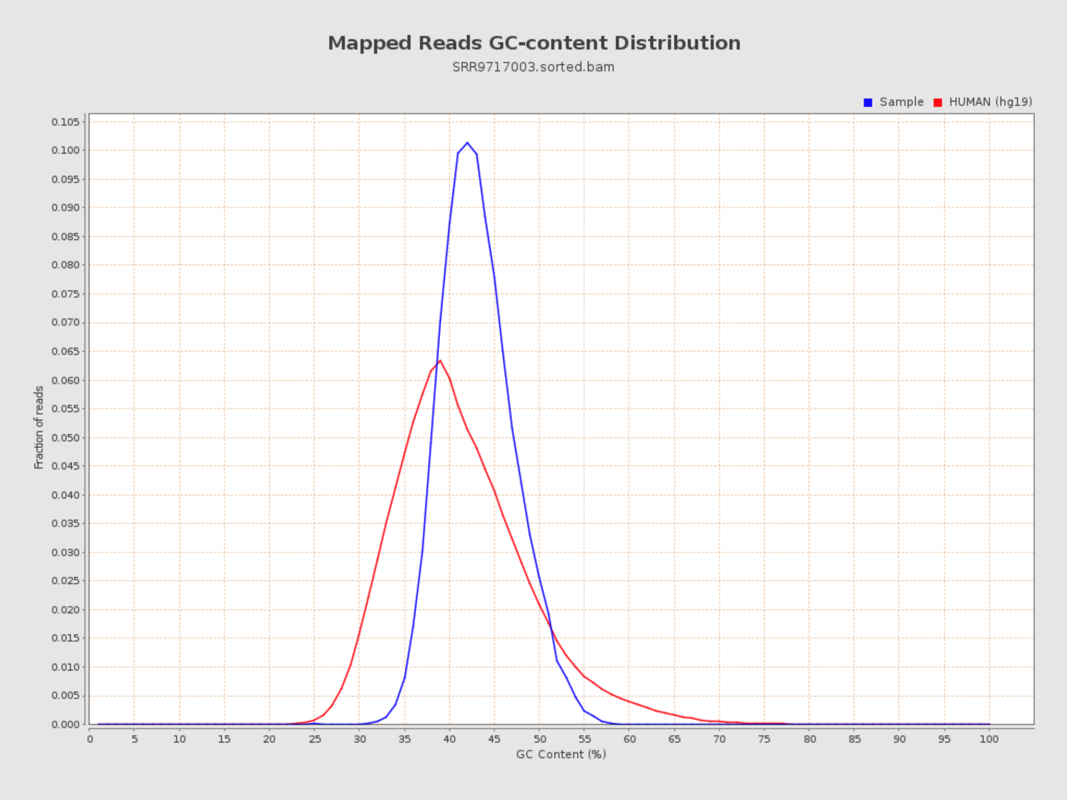
7. Results : Duplication Rate Histogram



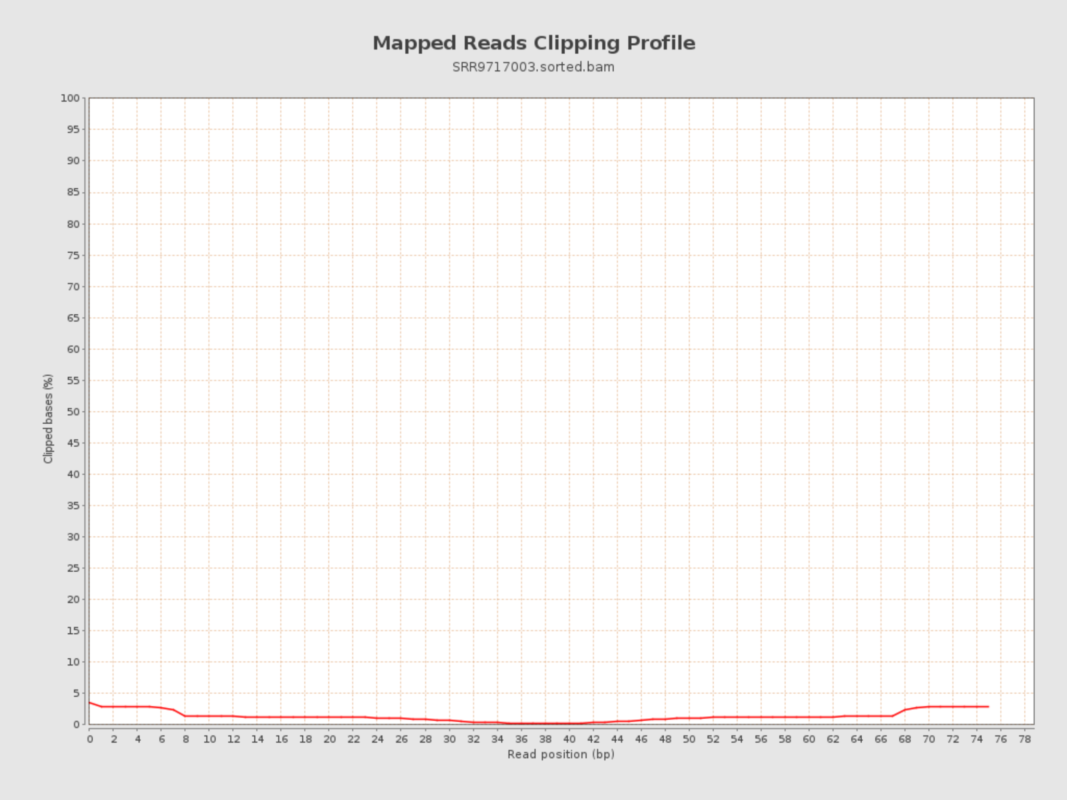
8. Results : Mapped Reads Nucleotide Content



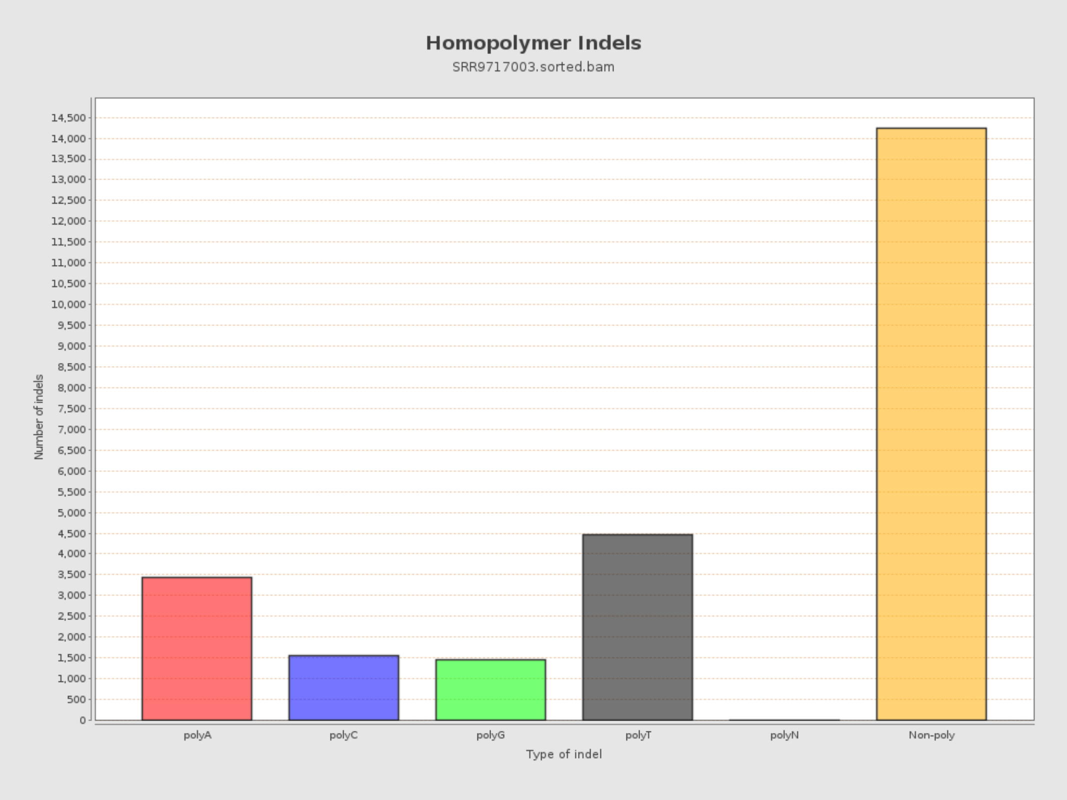
9. Results : Mapped Reads GC-content Distribution



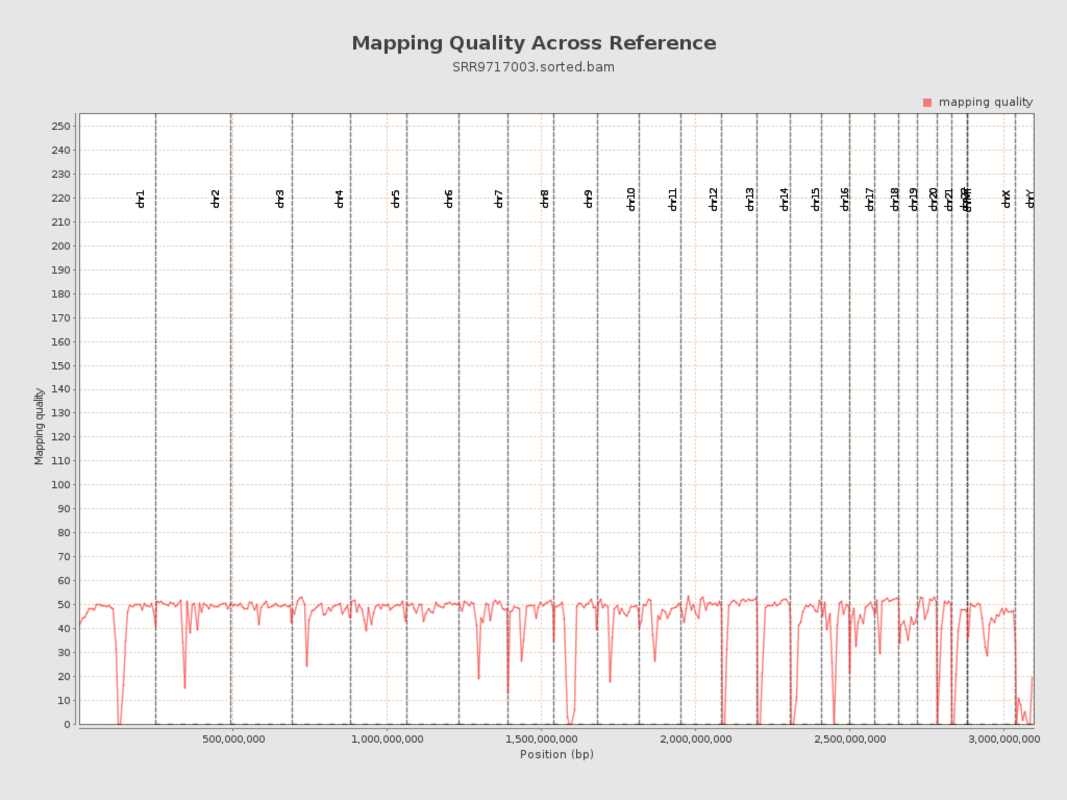
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram