Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 03:14:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717057.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_SRR9717057 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717057.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 03:14:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717057.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,267,504
Mapped reads	2,928,885 / 89.64%
Unmapped reads	338,619 / 10.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,580 / 0.51%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	167,617 / 5.13%
Duplication rate	4.31%
Clipped reads	2,936,194 / 89.86%

2.2. ACGT Content

Number/percentage of A's	43,478,779 / 25.67%
Number/percentage of C's	33,745,011 / 19.92%
Number/percentage of T's	52,316,780 / 30.89%
Number/percentage of G's	39,825,577 / 23.51%
Number/percentage of N's	4,605 / 0%
GC Percentage	43.44%

2.3. Coverage

Mean	0.0547

Standard Deviation	0.4707

2.4. Mapping Quality

Mean Mapping Quality	43.78

2.5. Mismatches and indels

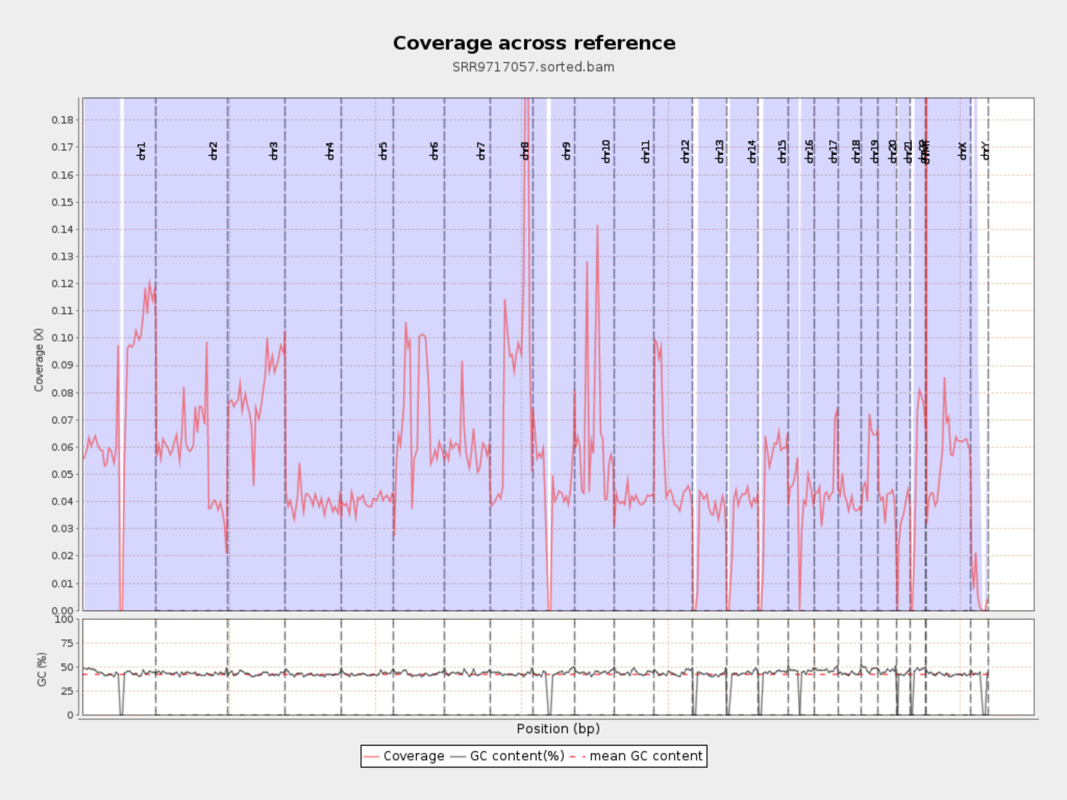
General error rate	0.51%
Mismatches	837,257
Insertions	13,486
Mapped reads with at least one insertion	0.46%
Deletions	28,071
Mapped reads with at least one deletion	0.95%
Homopolymer indels	40.11%

2.6. Chromosome stats

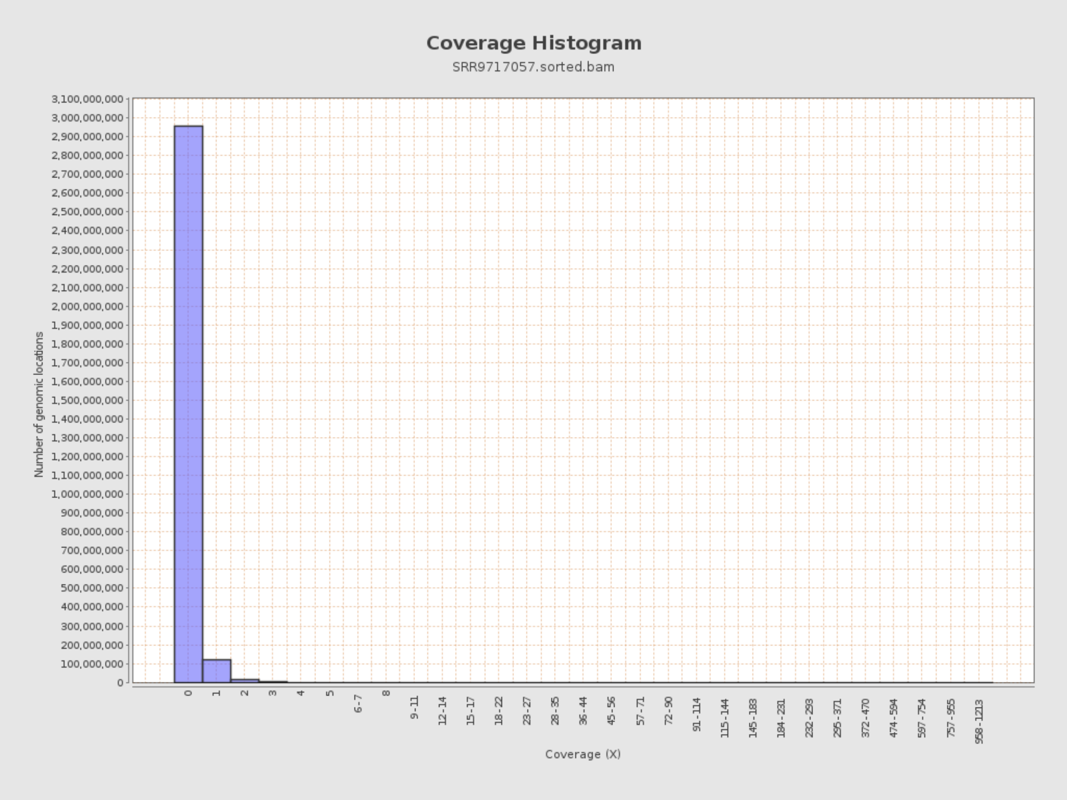
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18865340	0.0757	0.9113
chr2	243199373	13925142	0.0573	0.5671
chr3	198022430	15899180	0.0803	0.3427
chr4	191154276	7673494	0.0401	0.2606
chr5	180915260	7281212	0.0402	0.2421
chr6	171115067	12234614	0.0715	0.4644
chr7	159138663	9597479	0.0603	0.6211

chr8	146364022	13283244	0.0908	0.4243
chr9	141213431	6152705	0.0436	0.3706
chr10	135534747	8902981	0.0657	0.5342
chr11	135006516	5511334	0.0408	0.3712
chr12	133851895	7432642	0.0555	0.2906
chr13	115169878	3758524	0.0326	0.2145
chr14	107349540	3717301	0.0346	0.2712
chr15	102531392	4958787	0.0484	0.2699
chr16	90354753	3596524	0.0398	0.2837
chr17	81195210	3751769	0.0462	0.2719
chr18	78077248	3173852	0.0407	0.7024
chr19	59128983	3335458	0.0564	0.6409
chr20	63025520	2554333	0.0405	0.2418
chr21	48129895	1549024	0.0322	0.2384
chr22	51304566	2687747	0.0524	0.2718
chrMT	16571	424931	25.6431	14.4072
chrX	155270560	8739024	0.0563	0.3393
chrY	59373566	407381	0.0069	0.1418

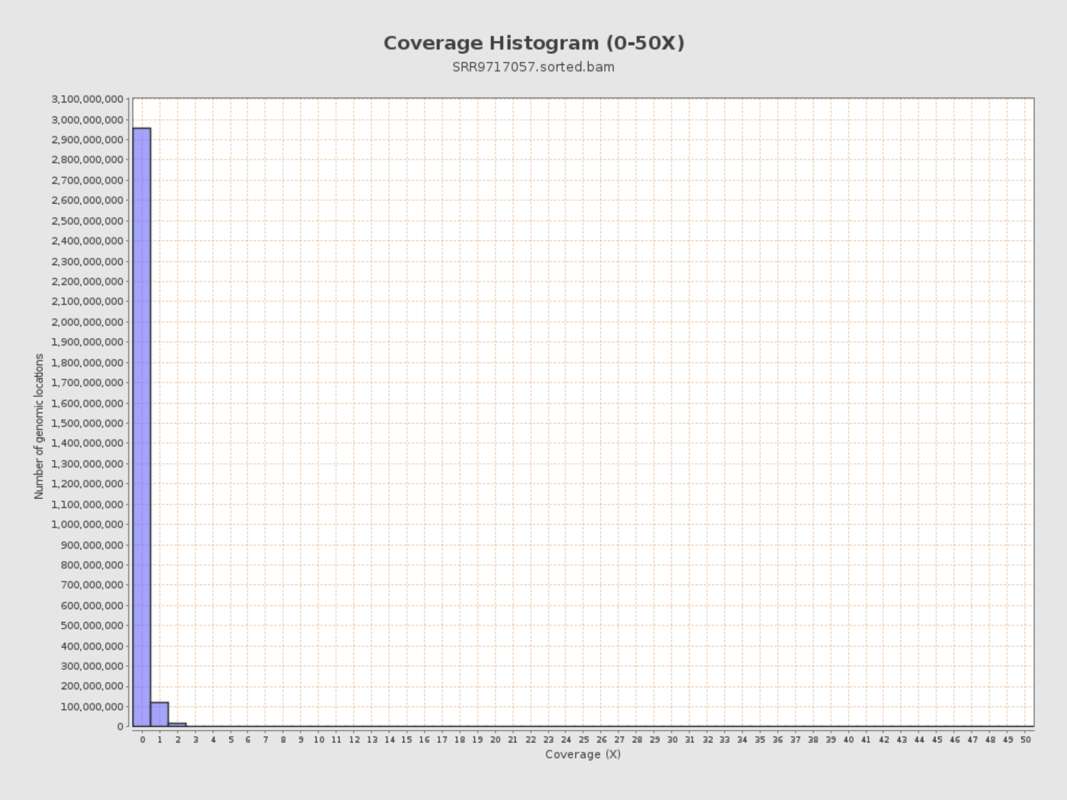
3. Results : Coverage across reference



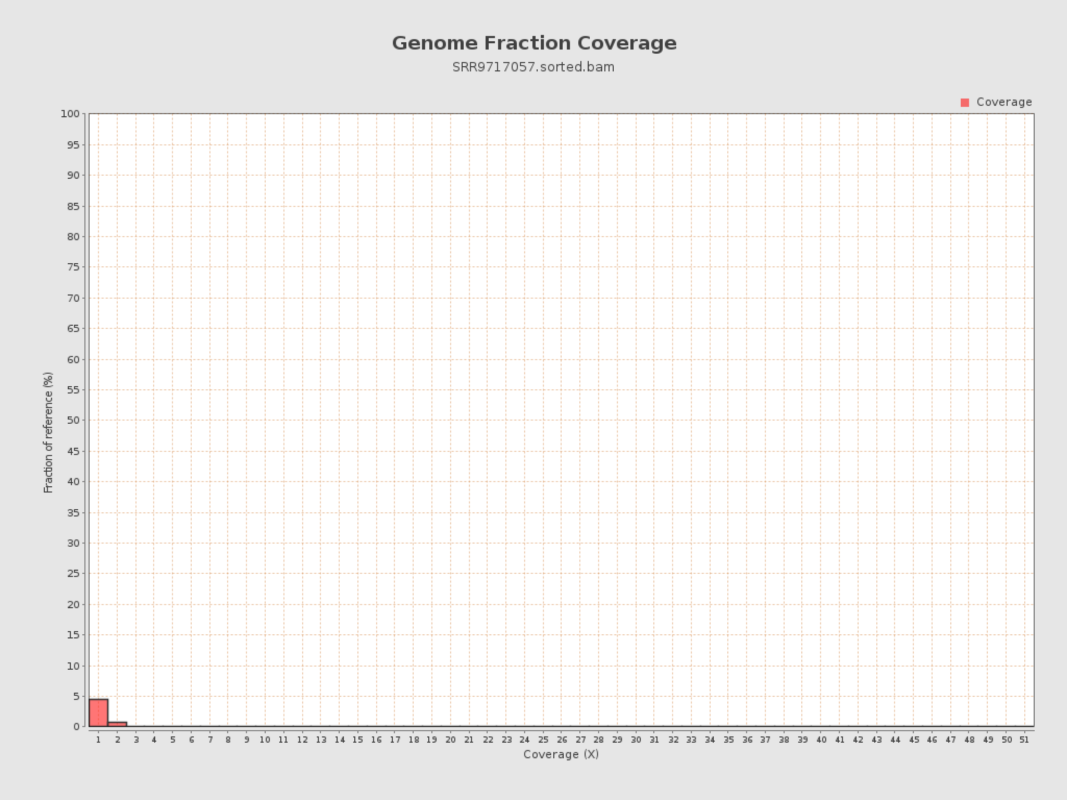
4. Results : Coverage Histogram



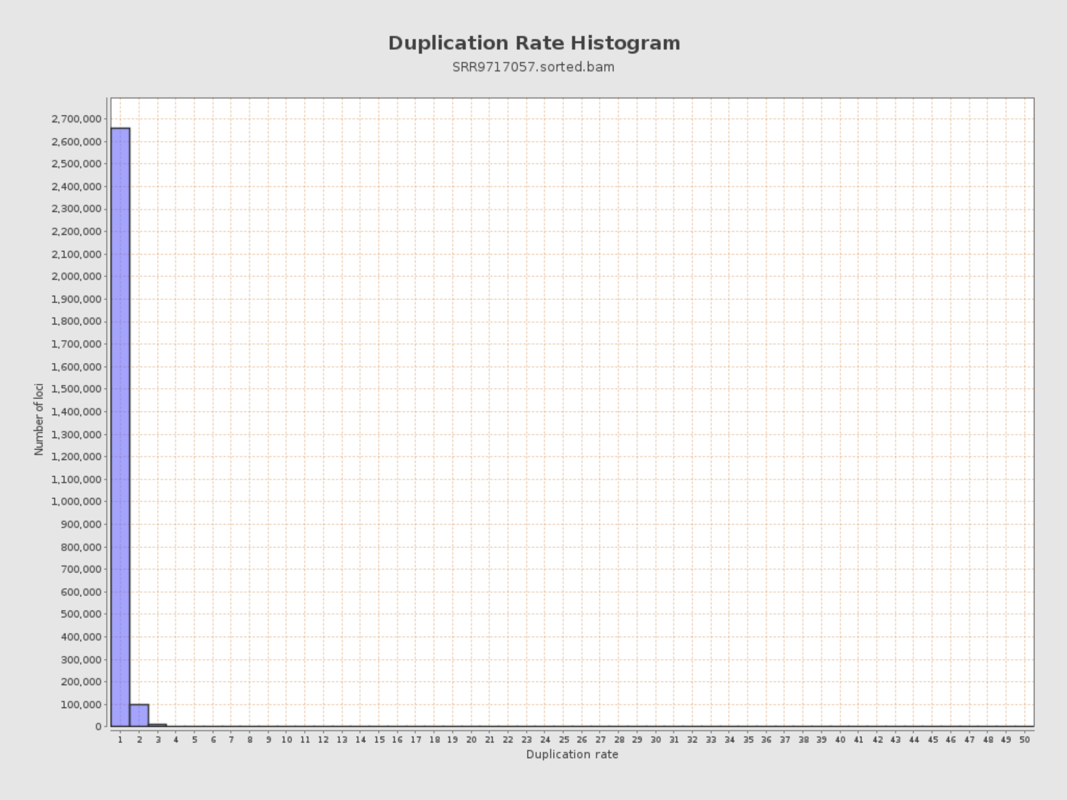
5. Results : Coverage Histogram (0-50X)



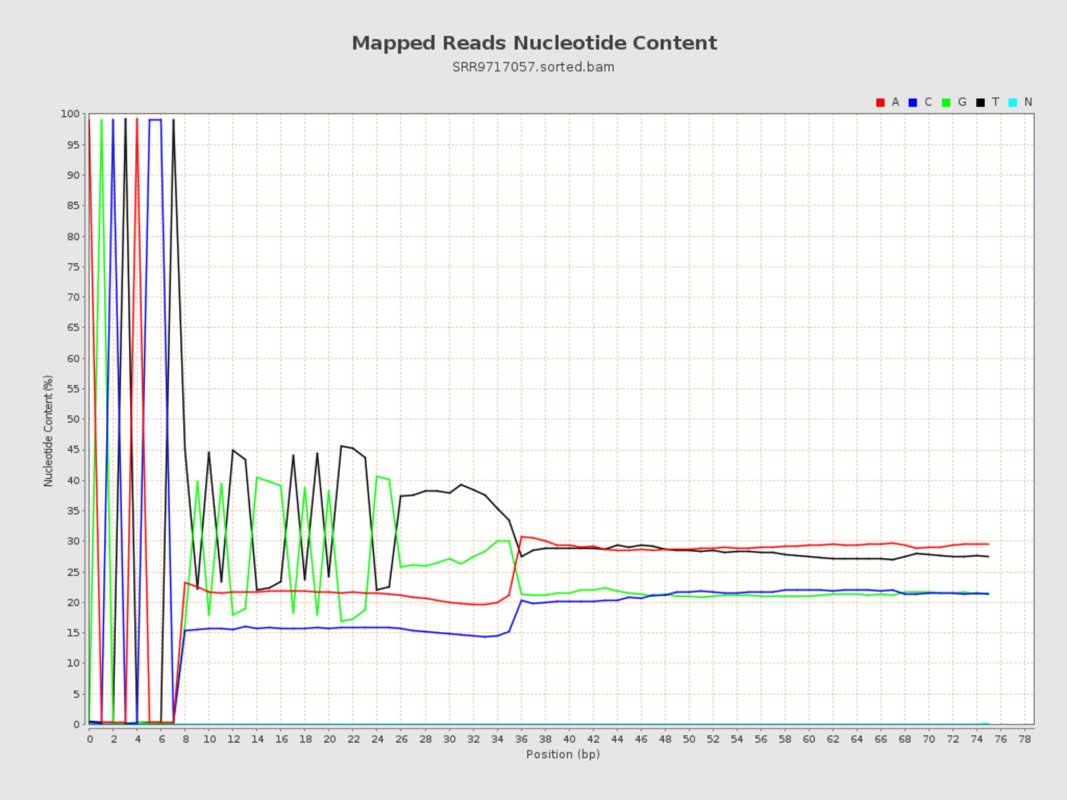
6. Results : Genome Fraction Coverage



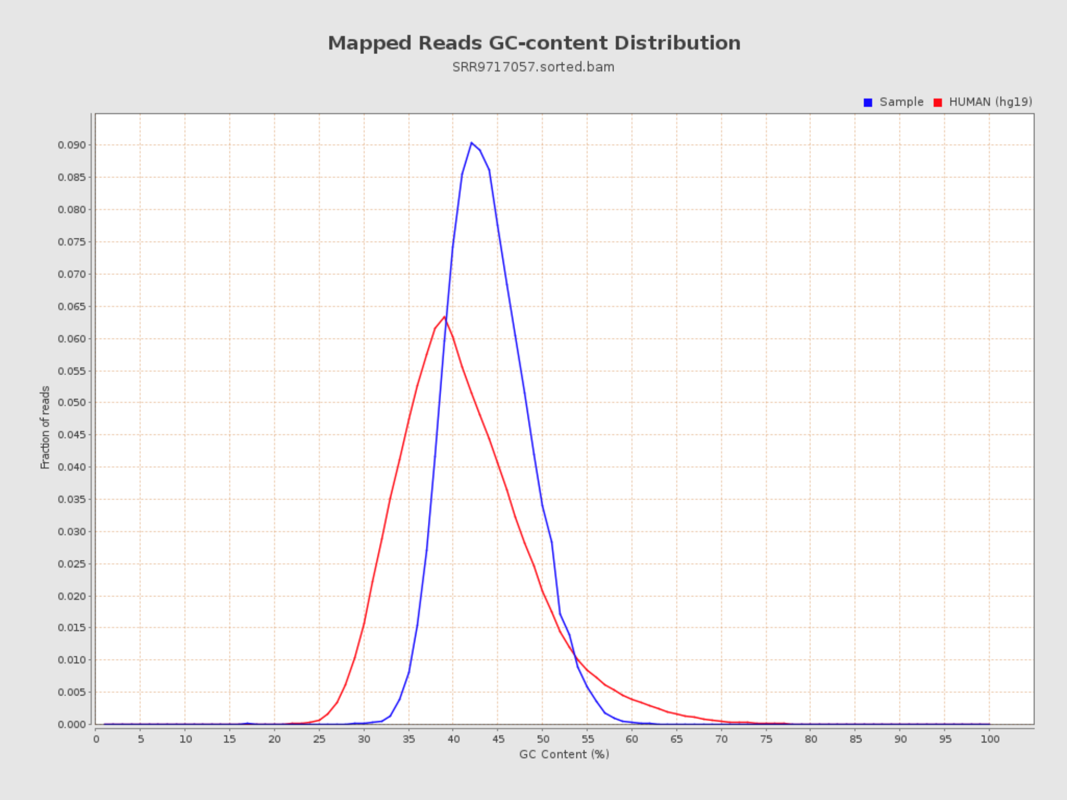
7. Results : Duplication Rate Histogram



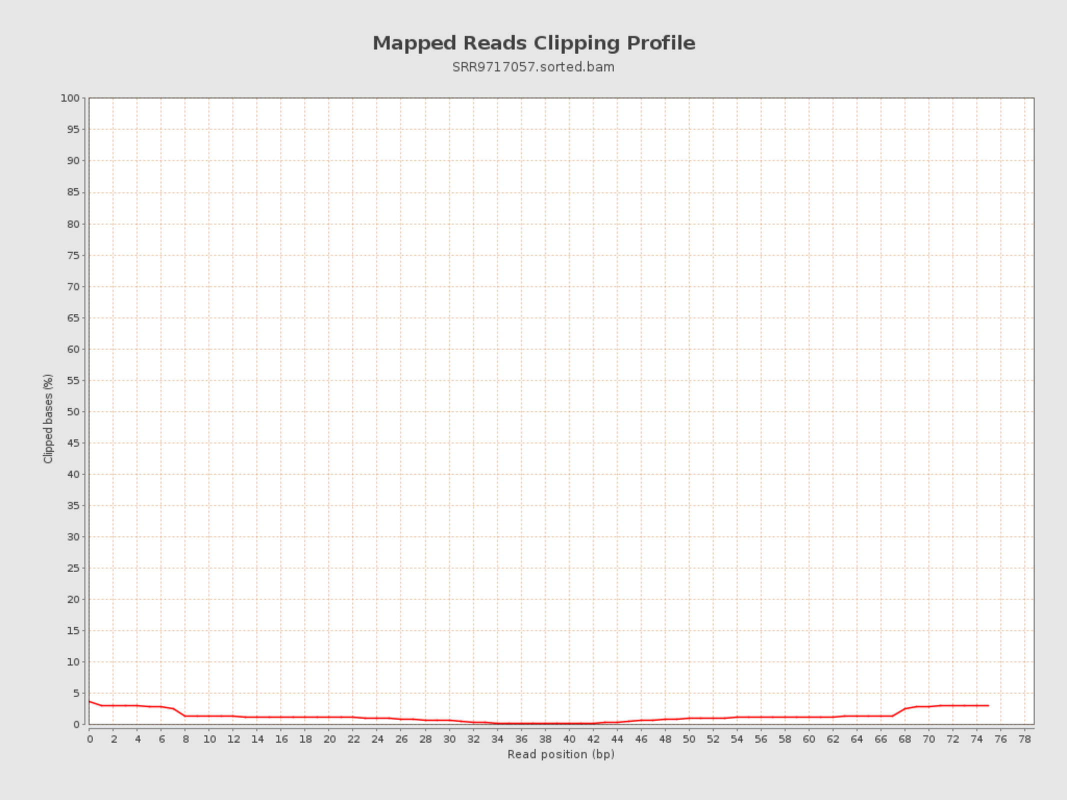
8. Results : Mapped Reads Nucleotide Content



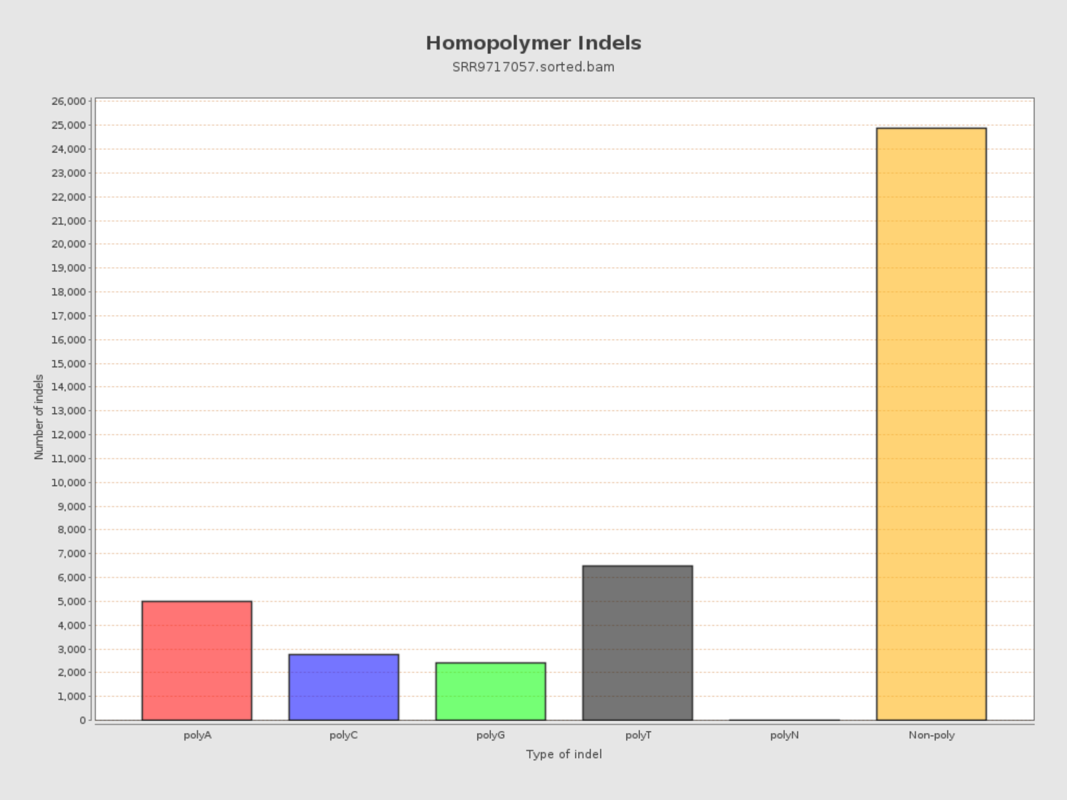
9. Results : Mapped Reads GC-content Distribution



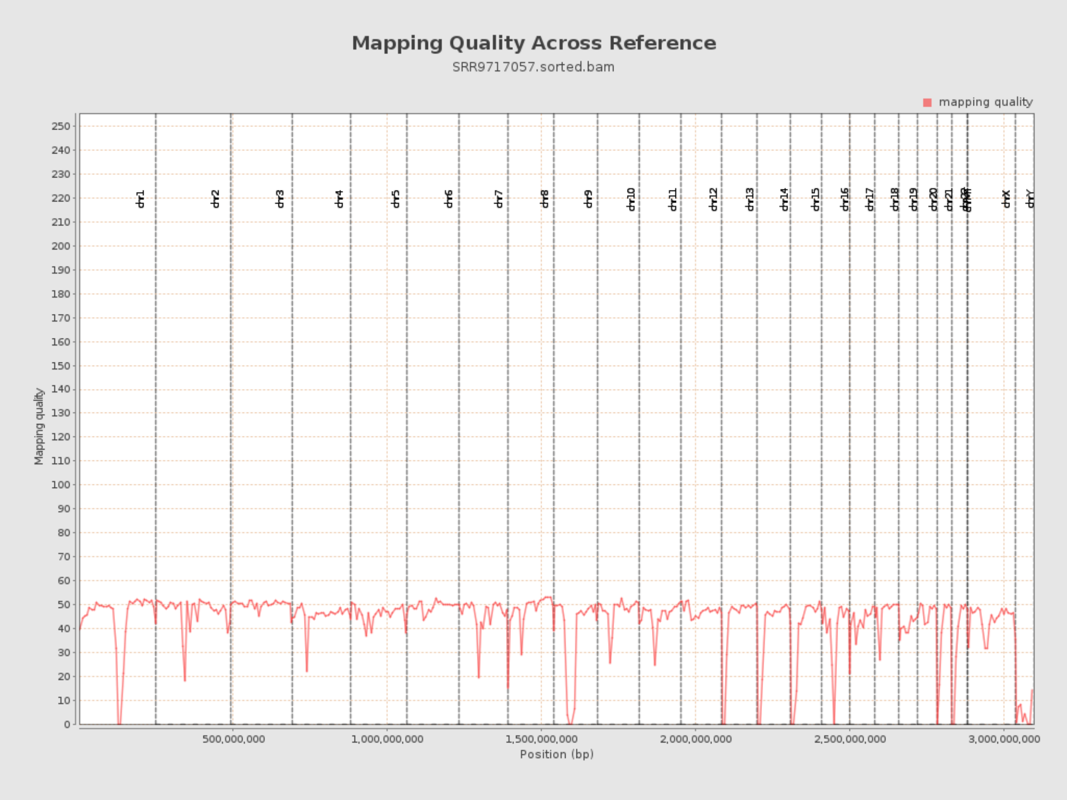
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram