Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 00:17:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717012.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_SRR9717012 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717012.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 00:17:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717012.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,246,144
Mapped reads	1,154,083 / 92.61%
Unmapped reads	92,061 / 7.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,226 / 1.54%
Read min/max/mean length	30 / 101 / 101.57
Duplicated reads (estimated)	41,371 / 3.32%
Duplication rate	2.02%
Clipped reads	1,170,627 / 93.94%

2.2. ACGT Content

Number/percentage of A's	23,211,908 / 25.37%
Number/percentage of C's	17,365,661 / 18.98%
Number/percentage of T's	27,806,653 / 30.39%
Number/percentage of G's	23,110,804 / 25.26%
Number/percentage of N's	5,744 / 0.01%
GC Percentage	44.24%

2.3. Coverage

Mean	0.0296

Standard Deviation	0.3904

2.4. Mapping Quality

Mean Mapping Quality	43.29

2.5. Mismatches and indels

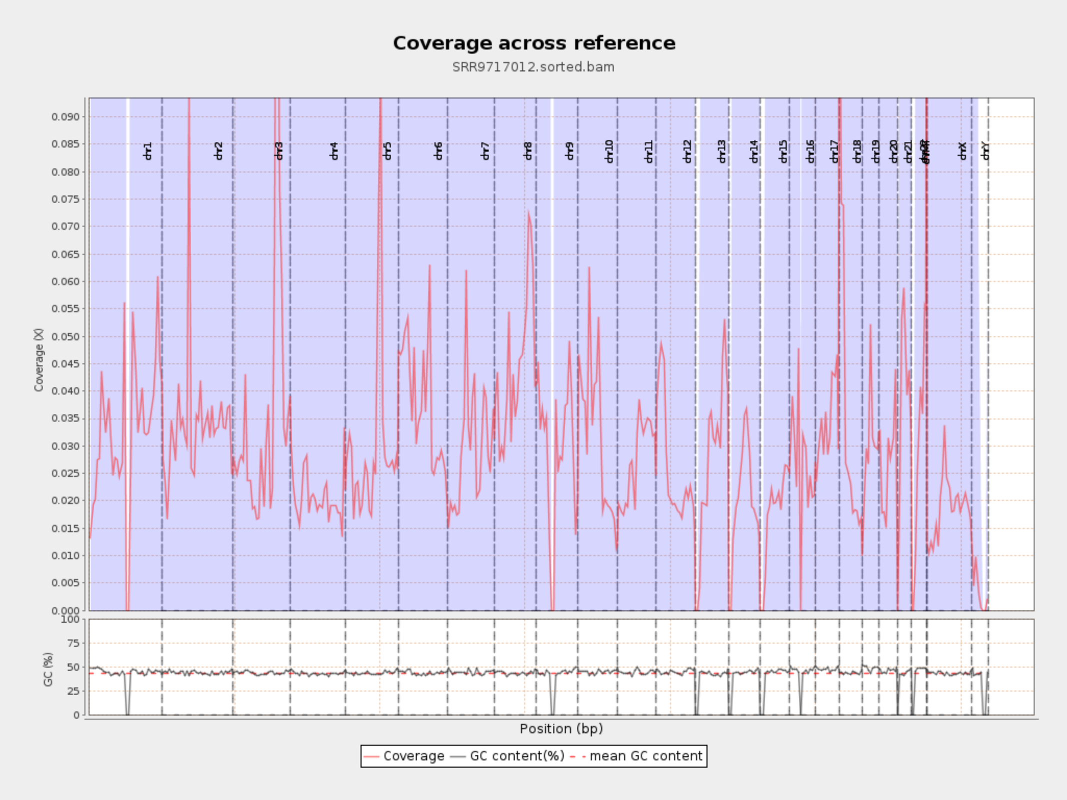
General error rate	0.83%
Mismatches	739,123
Insertions	9,268
Mapped reads with at least one insertion	0.79%
Deletions	22,144
Mapped reads with at least one deletion	1.89%
Homopolymer indels	41.58%

2.6. Chromosome stats

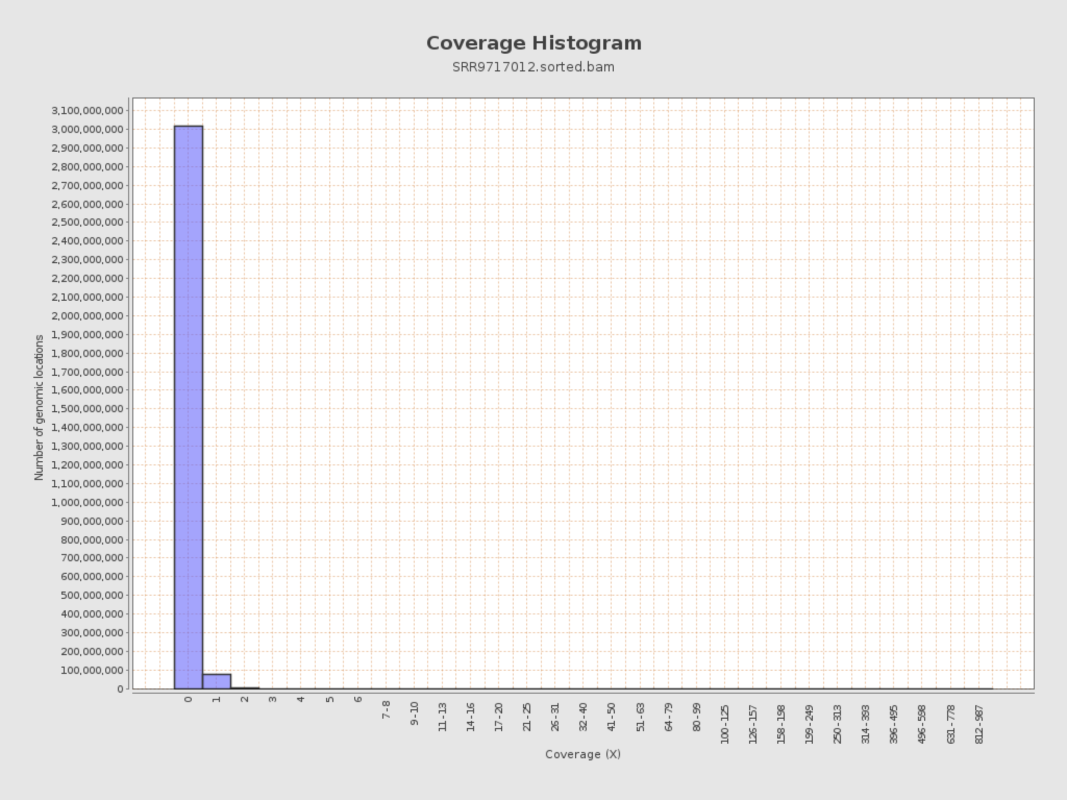
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8097996	0.0325	0.6201
chr2	243199373	8308739	0.0342	0.6981
chr3	198022430	7204284	0.0364	0.2139
chr4	191154276	3940144	0.0206	0.1636
chr5	180915260	5460508	0.0302	0.1936
chr6	171115067	6561323	0.0383	0.2551
chr7	159138663	4746852	0.0298	0.4912

chr8	146364022	6564756	0.0449	0.5299
chr9	141213431	4080678	0.0289	0.3927
chr10	135534747	4448280	0.0328	0.3454
chr11	135006516	3690739	0.0273	0.279
chr12	133851895	3455936	0.0258	0.1804
chr13	115169878	3190723	0.0277	0.1806
chr14	107349540	2163479	0.0202	0.1929
chr15	102531392	1773490	0.0173	0.1441
chr16	90354753	2380858	0.0264	0.218
chr17	81195210	2786684	0.0343	0.2433
chr18	78077248	2835850	0.0363	0.7524
chr19	59128983	1799843	0.0304	0.5108
chr20	63025520	1696433	0.0269	0.2159
chr21	48129895	1830232	0.038	0.2194
chr22	51304566	1405103	0.0274	0.1842
chrMT	16571	2784	0.168	0.4198
chrX	155270560	2910939	0.0187	0.2078
chrY	59373566	202830	0.0034	0.0917

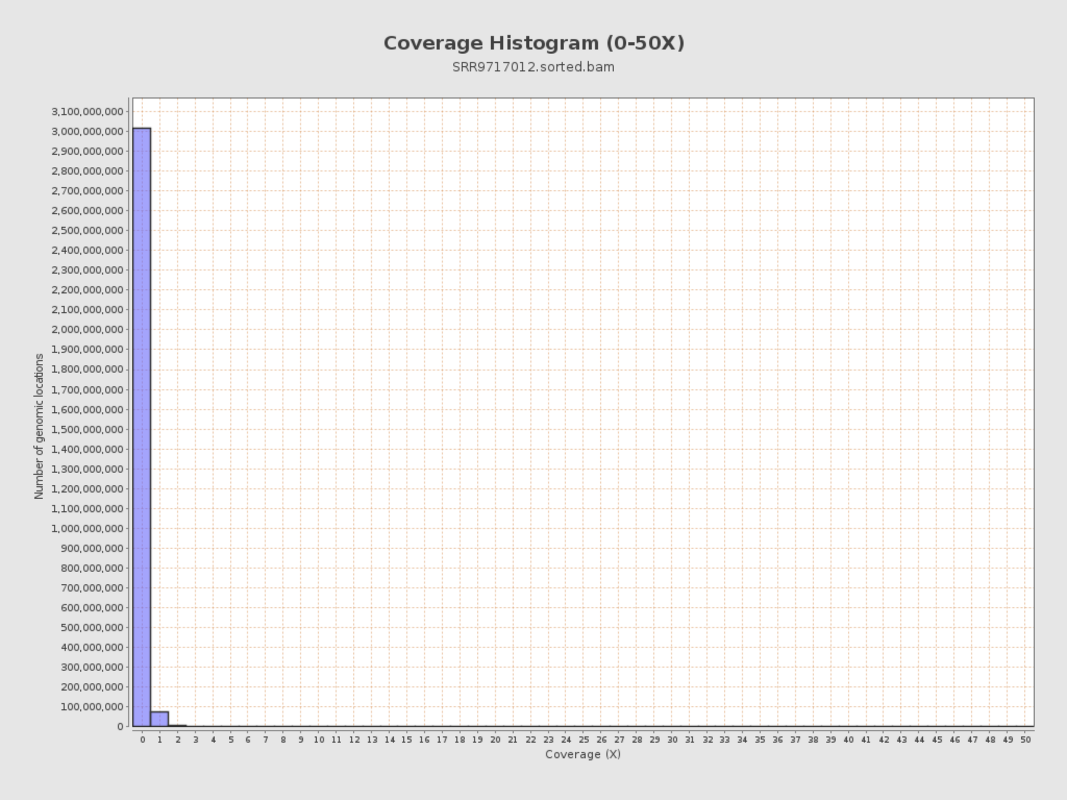
3. Results : Coverage across reference



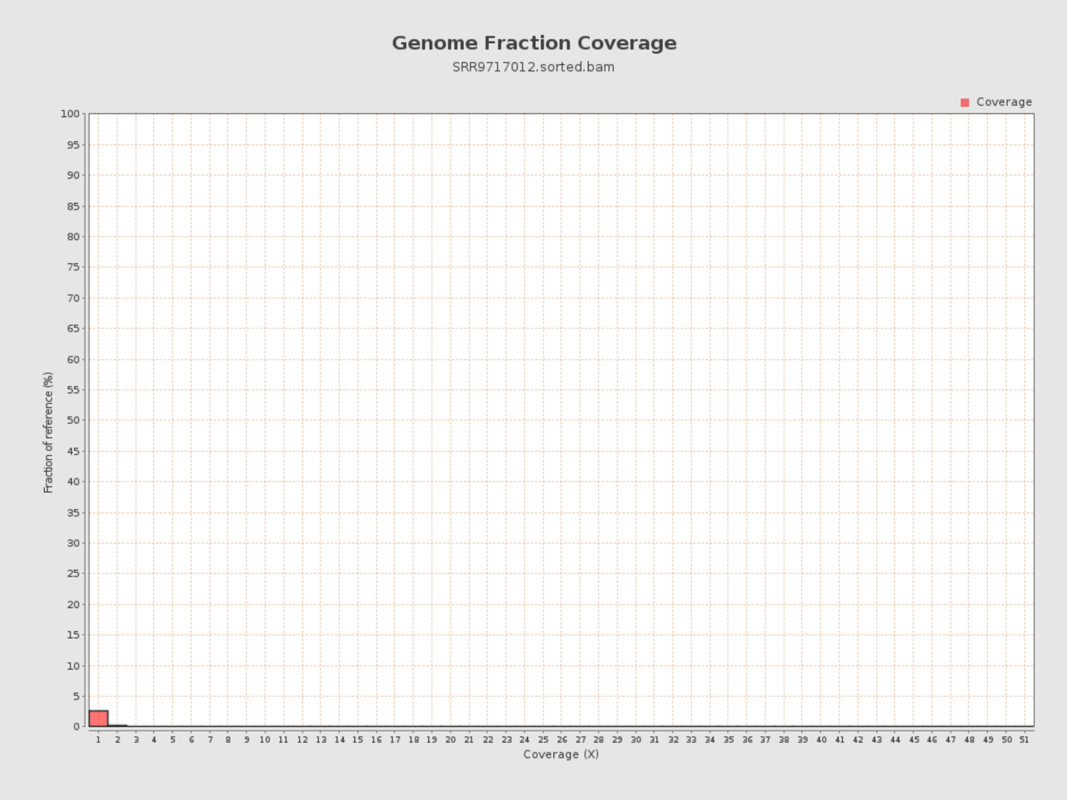
4. Results : Coverage Histogram



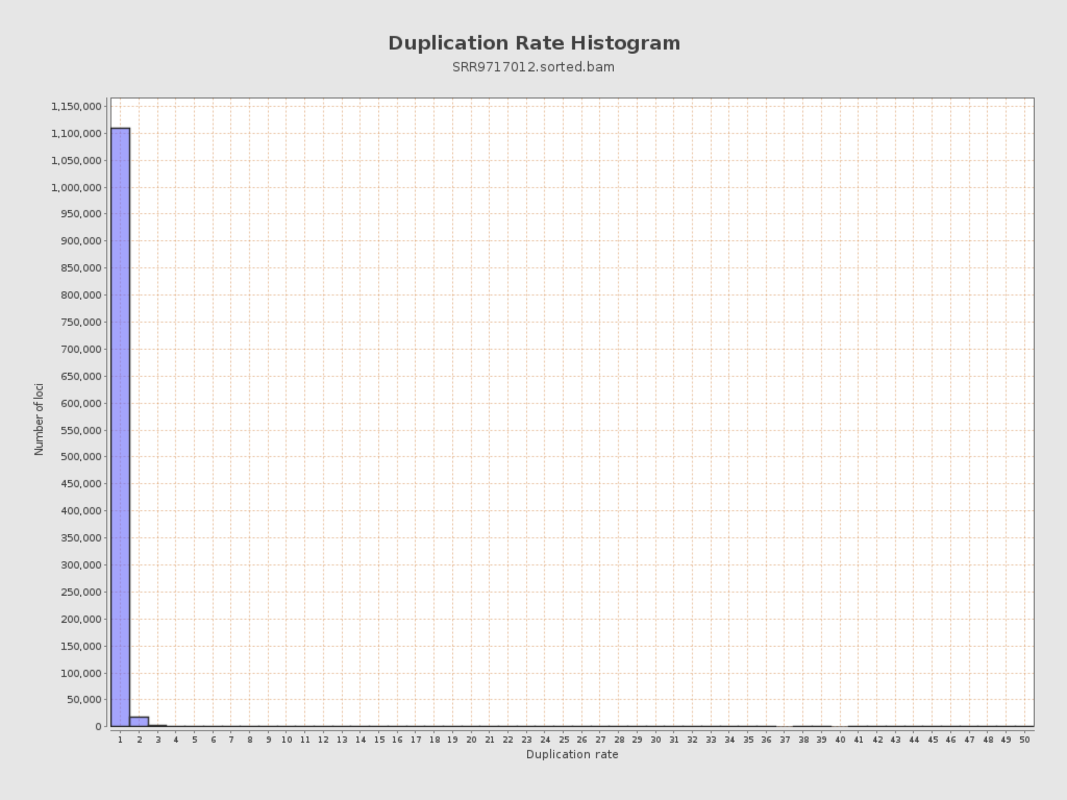
5. Results : Coverage Histogram (0-50X)



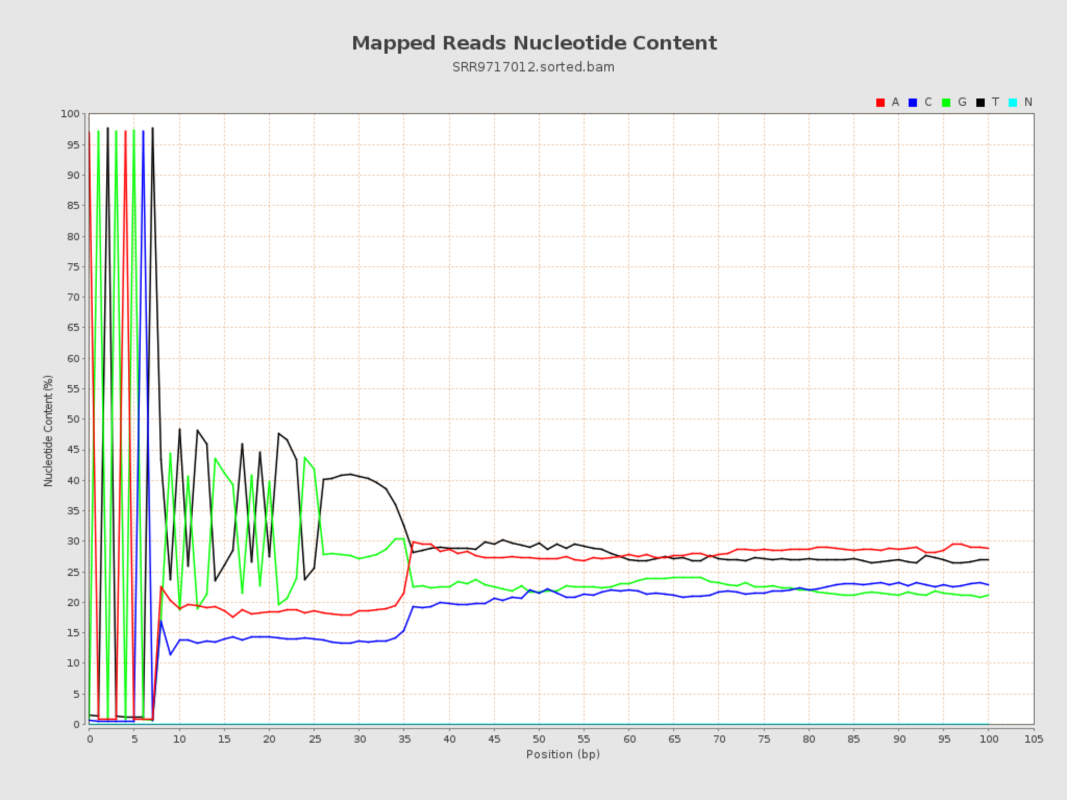
6. Results : Genome Fraction Coverage



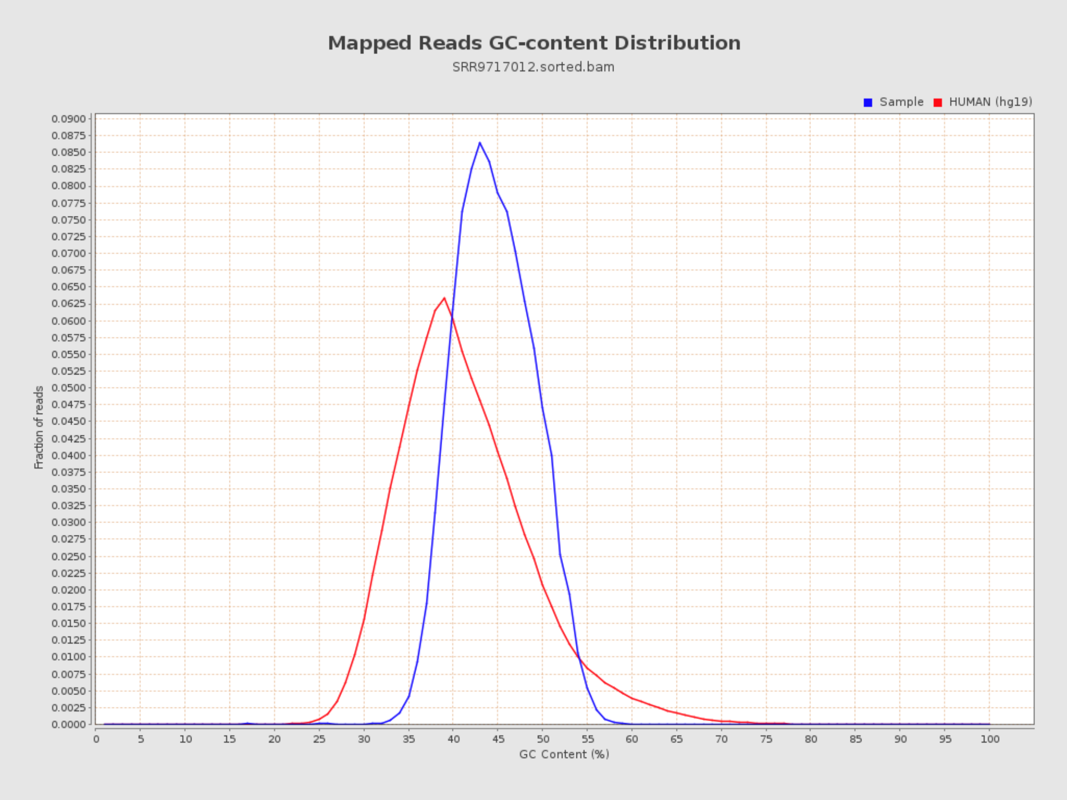
7. Results : Duplication Rate Histogram



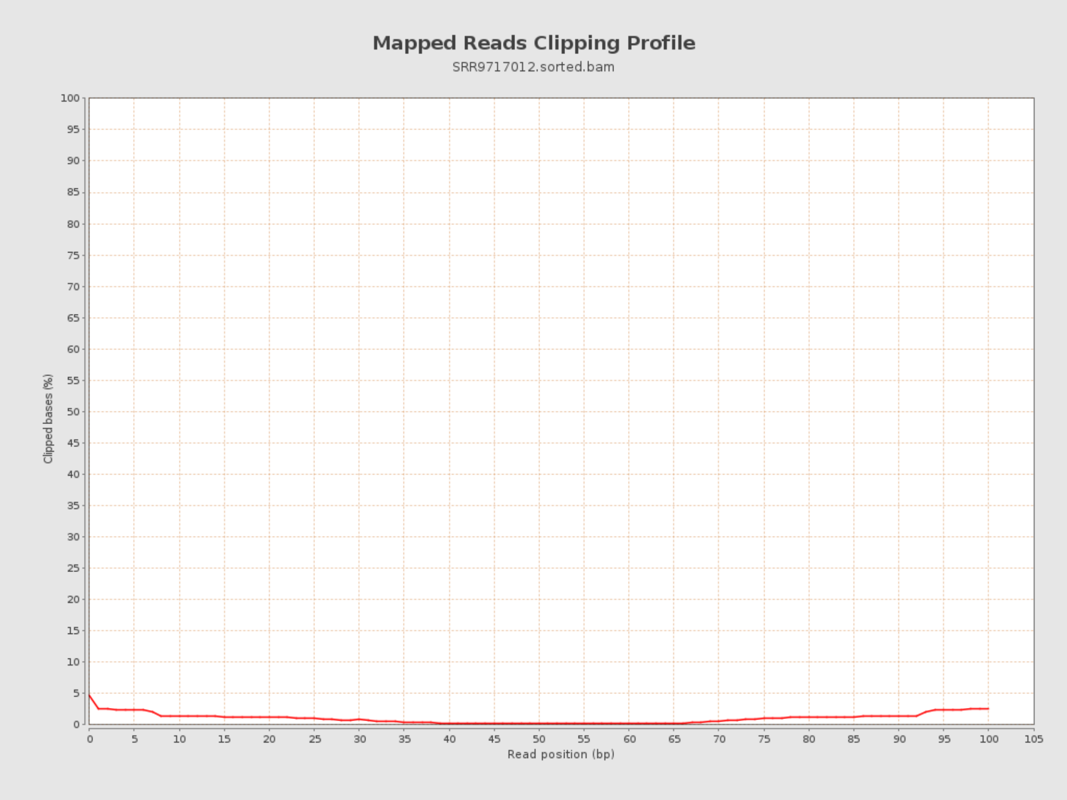
8. Results : Mapped Reads Nucleotide Content



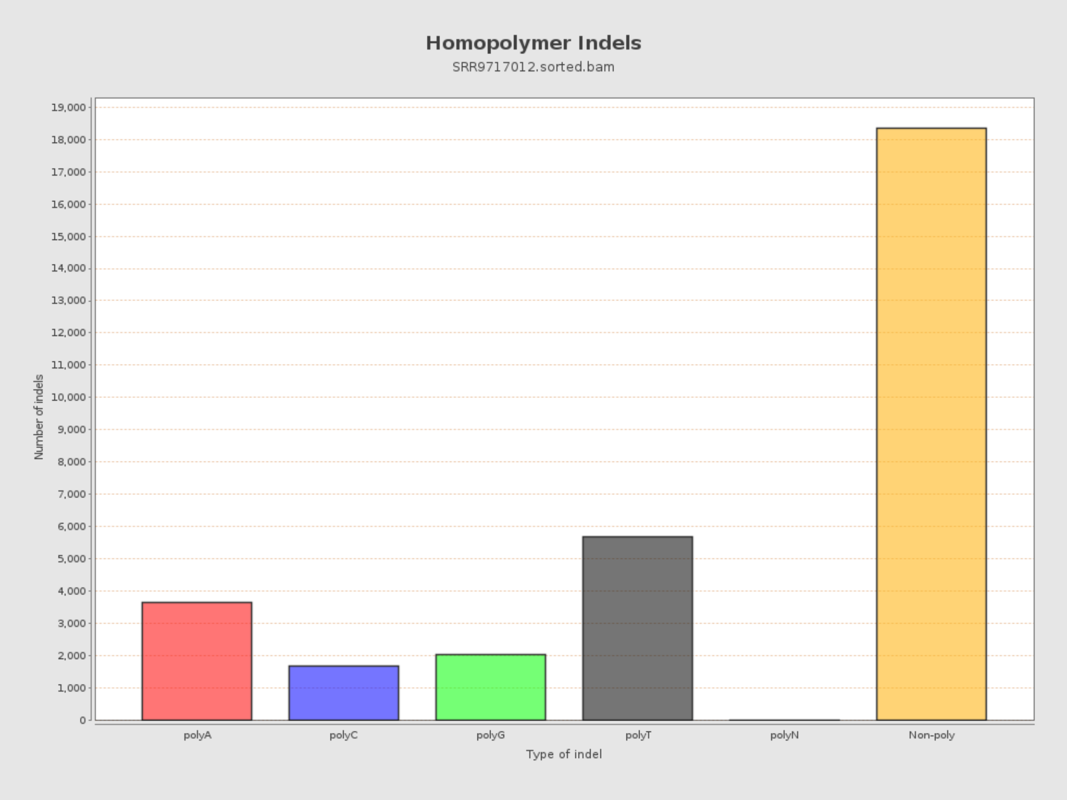
9. Results : Mapped Reads GC-content Distribution



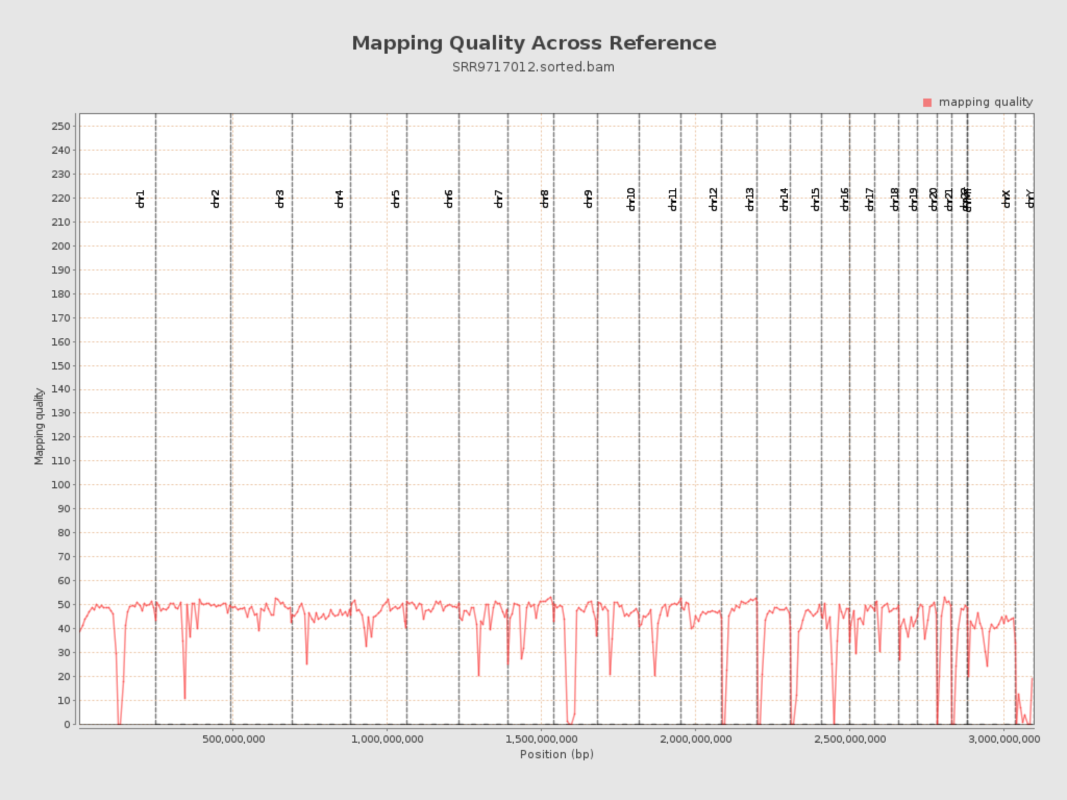
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram