Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 00:54:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717014.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_SRR9717014 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717014.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 00:54:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717014.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	937,693
Mapped reads	855,340 / 91.22%
Unmapped reads	82,353 / 8.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,578 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	16,923 / 1.8%
Duplication rate	1.51%
Clipped reads	858,013 / 91.5%

2.2. ACGT Content

Number/percentage of A's	11,985,654 / 24.45%
Number/percentage of C's	9,080,416 / 18.52%
Number/percentage of T's	14,990,566 / 30.58%
Number/percentage of G's	12,967,830 / 26.45%
Number/percentage of N's	1,040 / 0%
GC Percentage	44.97%

2.3. Coverage

Mean	0.0158

Standard Deviation	0.1559

2.4. Mapping Quality

Mean Mapping Quality	44.6

2.5. Mismatches and indels

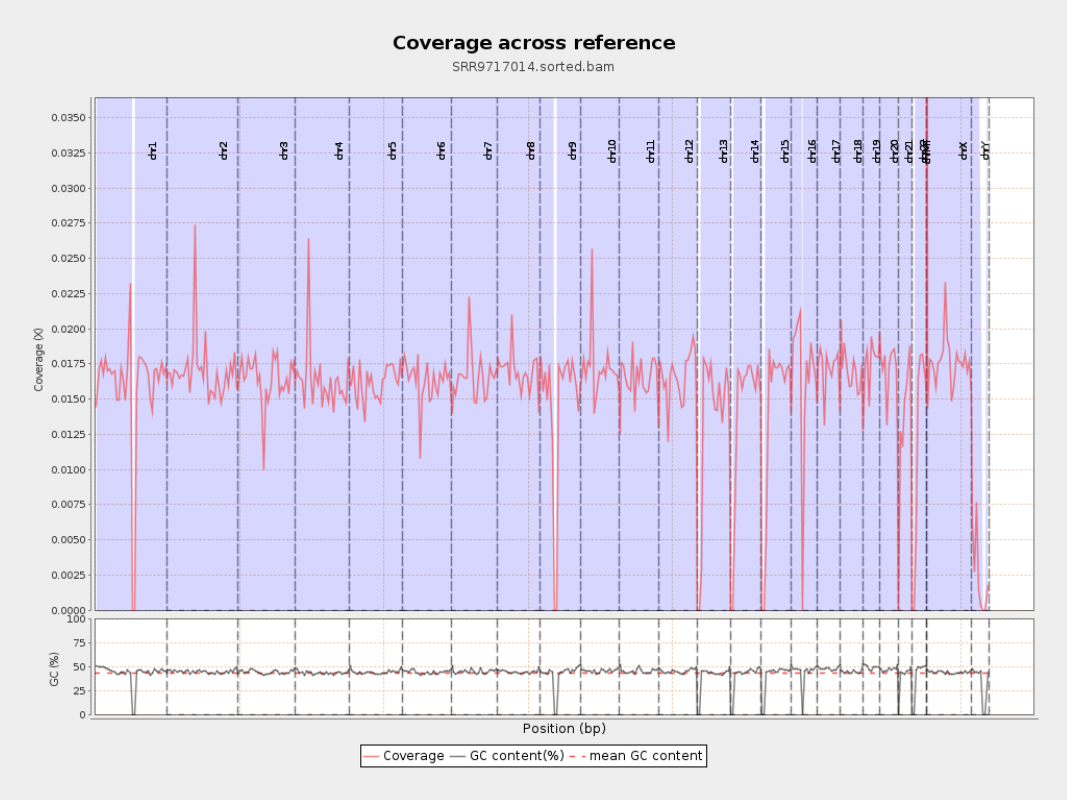
General error rate	0.51%
Mismatches	243,869
Insertions	2,481
Mapped reads with at least one insertion	0.29%
Deletions	7,593
Mapped reads with at least one deletion	0.88%
Homopolymer indels	43.08%

2.6. Chromosome stats

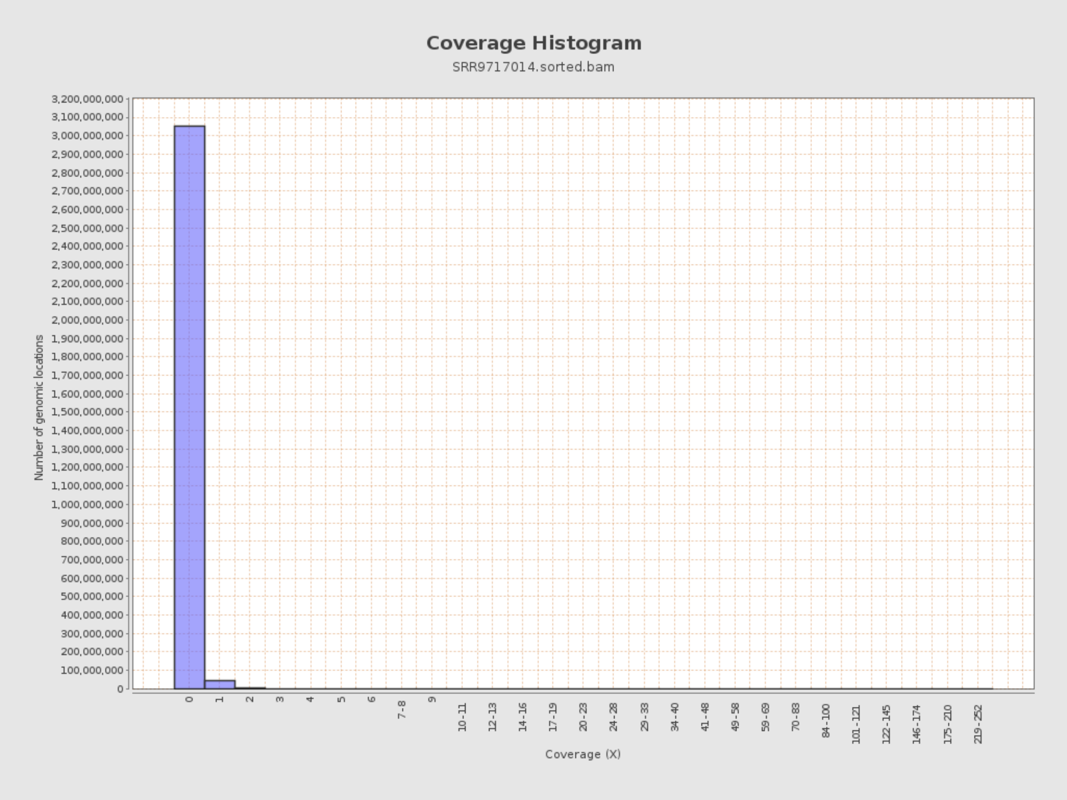
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3941597	0.0158	0.223
chr2	243199373	4134476	0.017	0.1686
chr3	198022430	3249632	0.0164	0.1343
chr4	191154276	3129727	0.0164	0.1412
chr5	180915260	2937117	0.0162	0.1346
chr6	171115067	2787899	0.0163	0.1392
chr7	159138663	2648899	0.0166	0.1666

chr8	146364022	2483339	0.017	0.149
chr9	141213431	2054673	0.0146	0.1535
chr10	135534747	2340284	0.0173	0.1608
chr11	135006516	2247330	0.0166	0.155
chr12	133851895	2220818	0.0166	0.1366
chr13	115169878	1526946	0.0133	0.1201
chr14	107349540	1482153	0.0138	0.129
chr15	102531392	1422466	0.0139	0.1235
chr16	90354753	1475662	0.0163	0.1406
chr17	81195210	1392921	0.0172	0.1422
chr18	78077248	1324228	0.017	0.249
chr19	59128983	1041196	0.0176	0.179
chr20	63025520	1069486	0.017	0.1392
chr21	48129895	643623	0.0134	0.1301
chr22	51304566	606458	0.0118	0.1141
chrMT	16571	2169	0.1309	0.3676
chrX	155270560	2734980	0.0176	0.151
chrY	59373566	140318	0.0024	0.0647

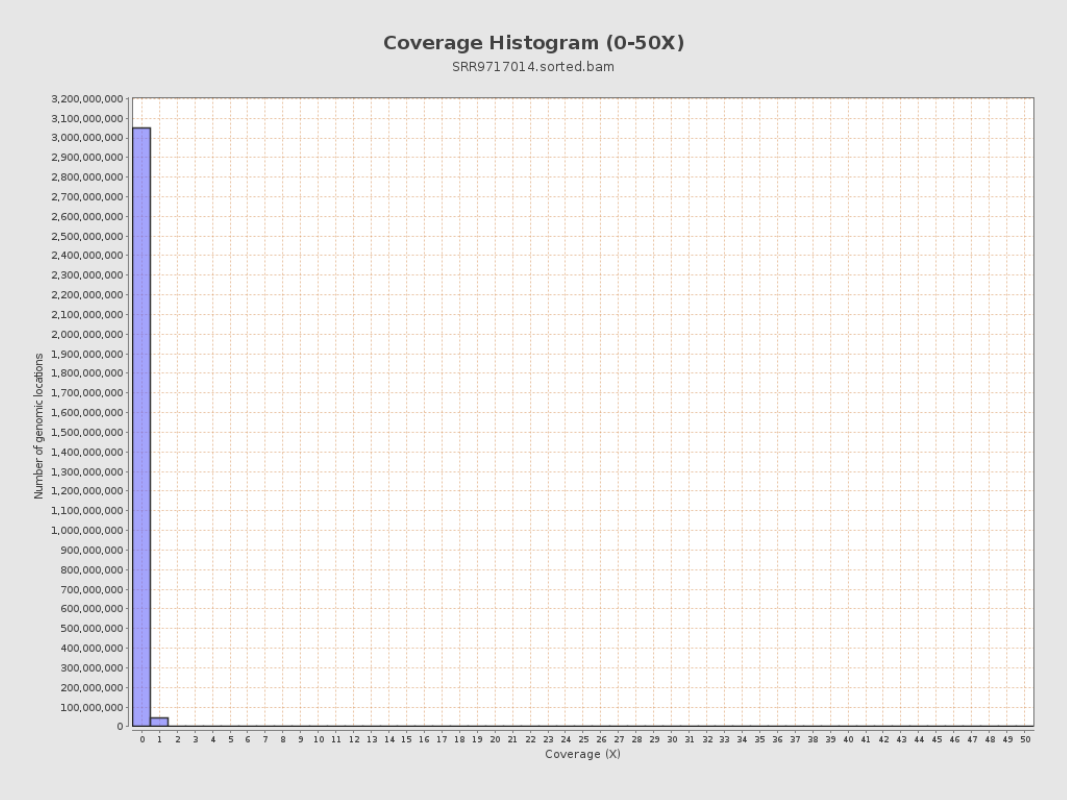
3. Results : Coverage across reference



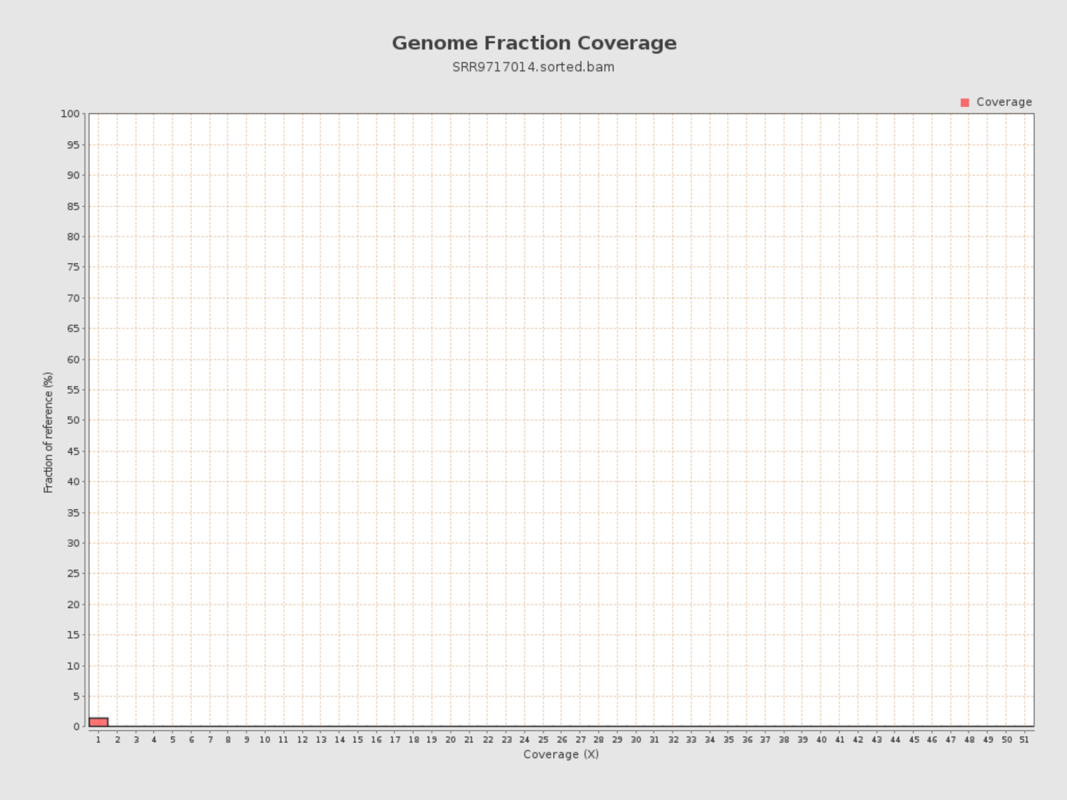
4. Results : Coverage Histogram



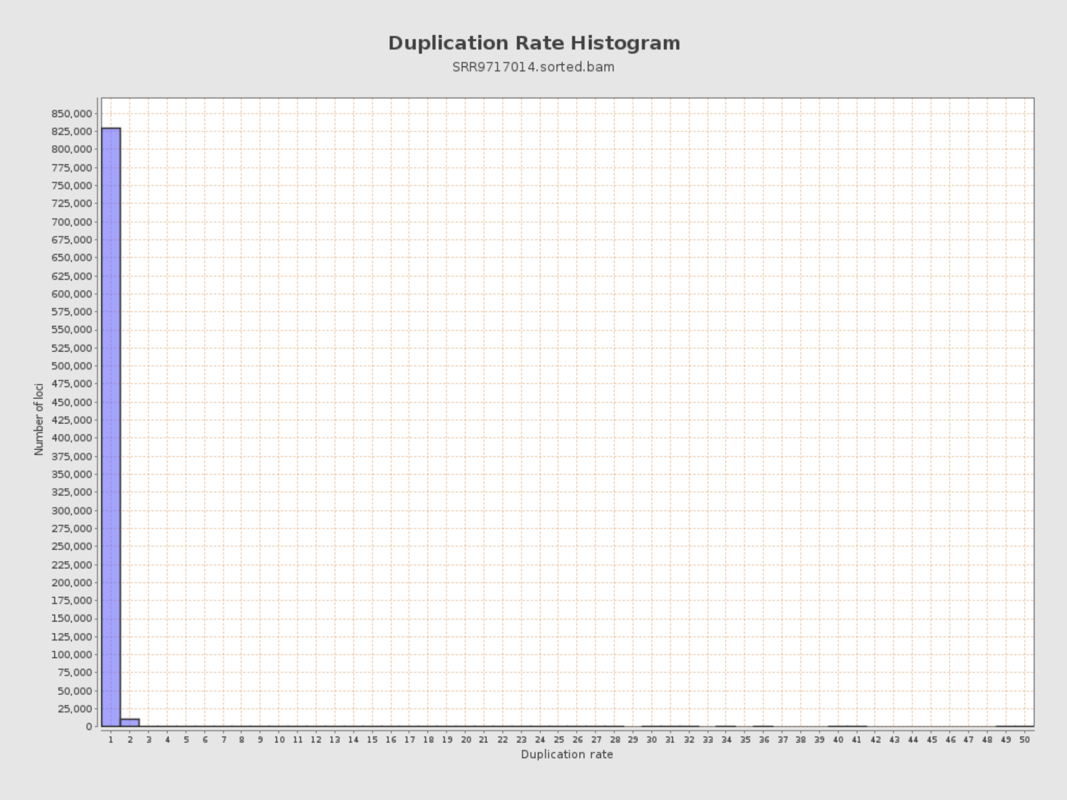
5. Results : Coverage Histogram (0-50X)



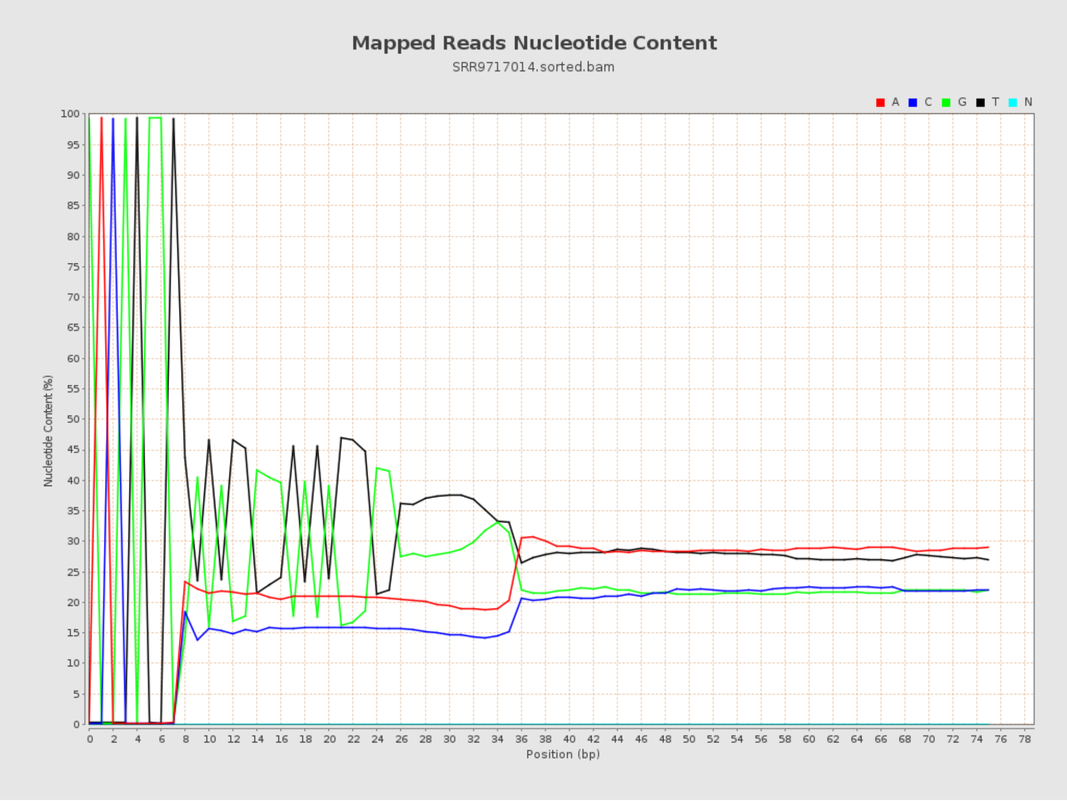
6. Results : Genome Fraction Coverage



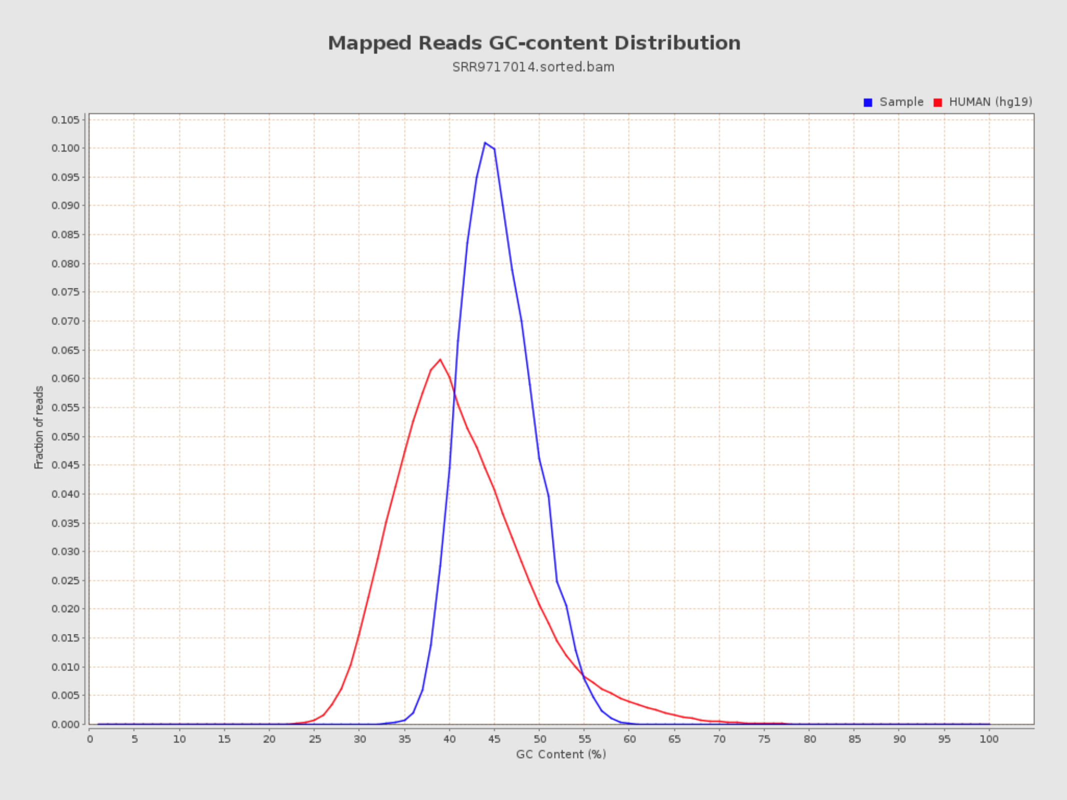
7. Results : Duplication Rate Histogram



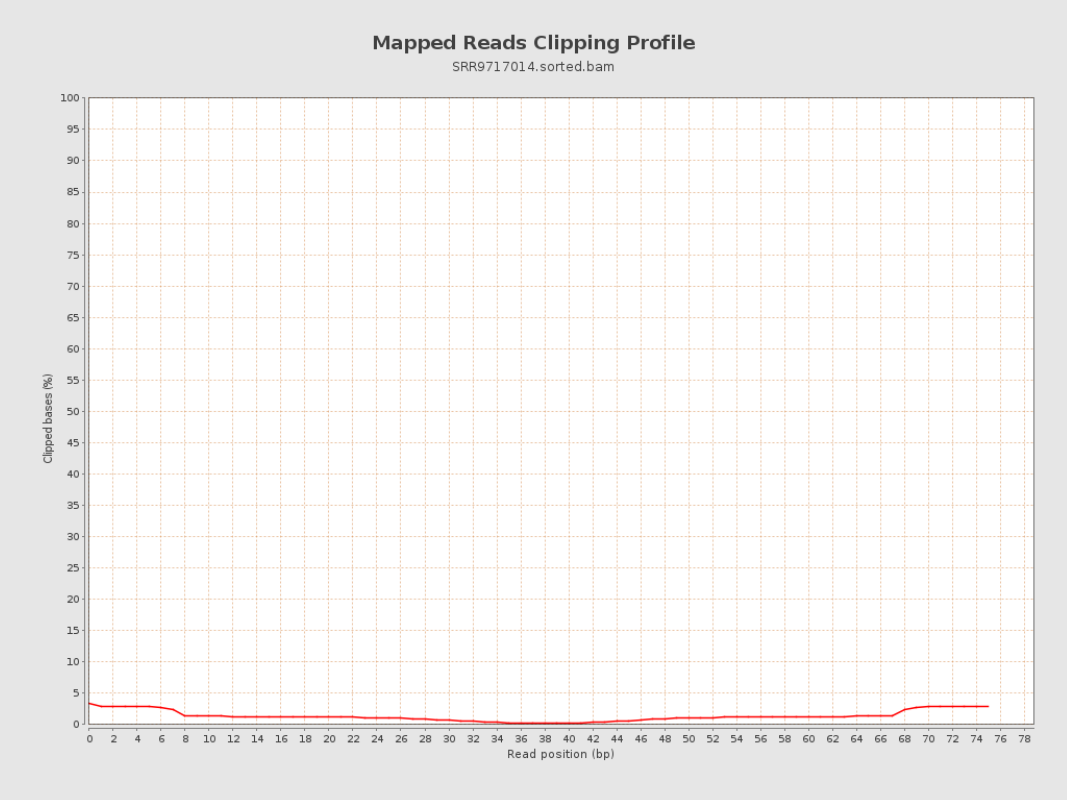
8. Results : Mapped Reads Nucleotide Content



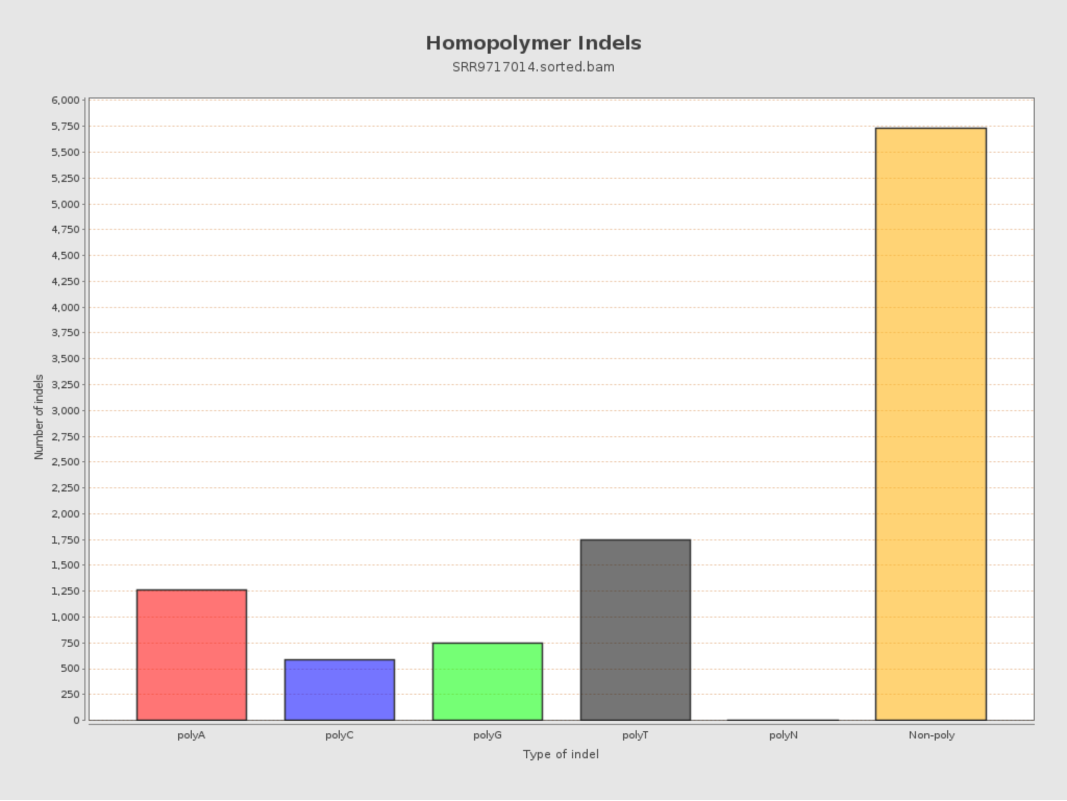
9. Results : Mapped Reads GC-content Distribution



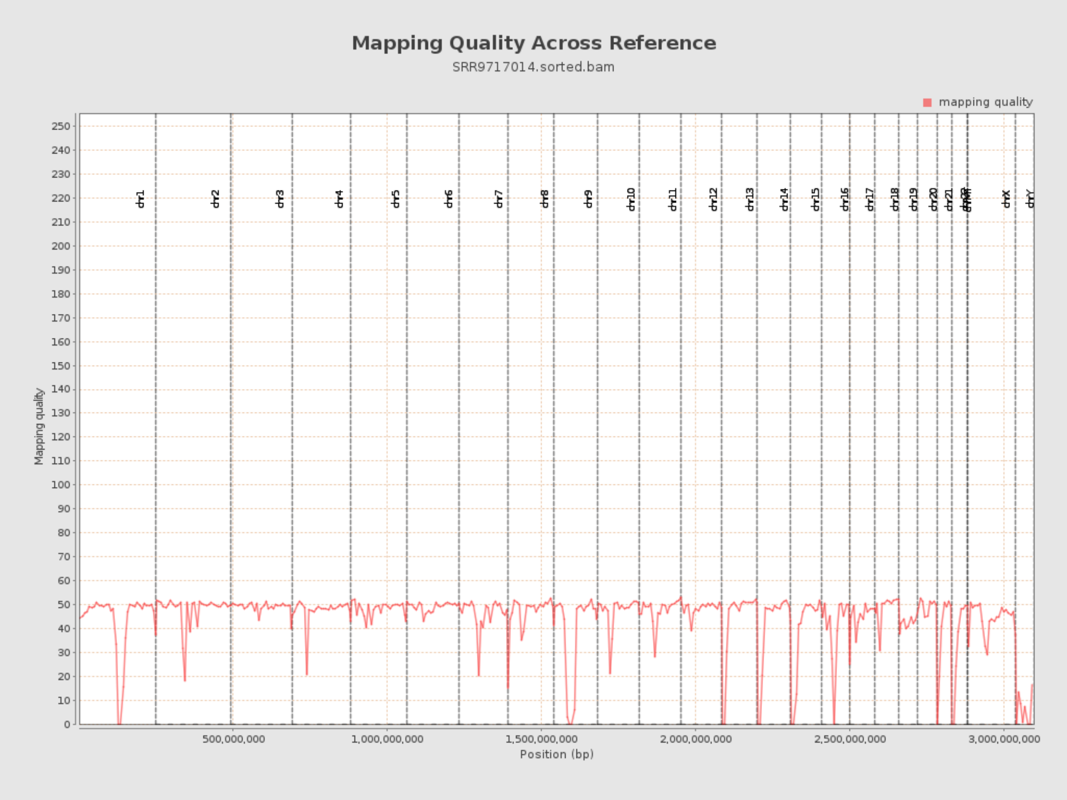
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram