Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 04:47:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717074.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_SRR9717074 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717074.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 04:47:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717074.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,161,005
Mapped reads	972,108 / 83.73%
Unmapped reads	188,897 / 16.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,234 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	21,085 / 1.82%
Duplication rate	1.53%
Clipped reads	973,693 / 83.87%

2.2. ACGT Content

Number/percentage of A's	13,636,198 / 25.05%
Number/percentage of C's	10,372,208 / 19.06%
Number/percentage of T's	17,250,953 / 31.69%
Number/percentage of G's	13,169,322 / 24.2%
Number/percentage of N's	924 / 0%
GC Percentage	43.25%

2.3. Coverage

Mean	0.0176

Standard Deviation	0.1824

2.4. Mapping Quality

Mean Mapping Quality	41.64

2.5. Mismatches and indels

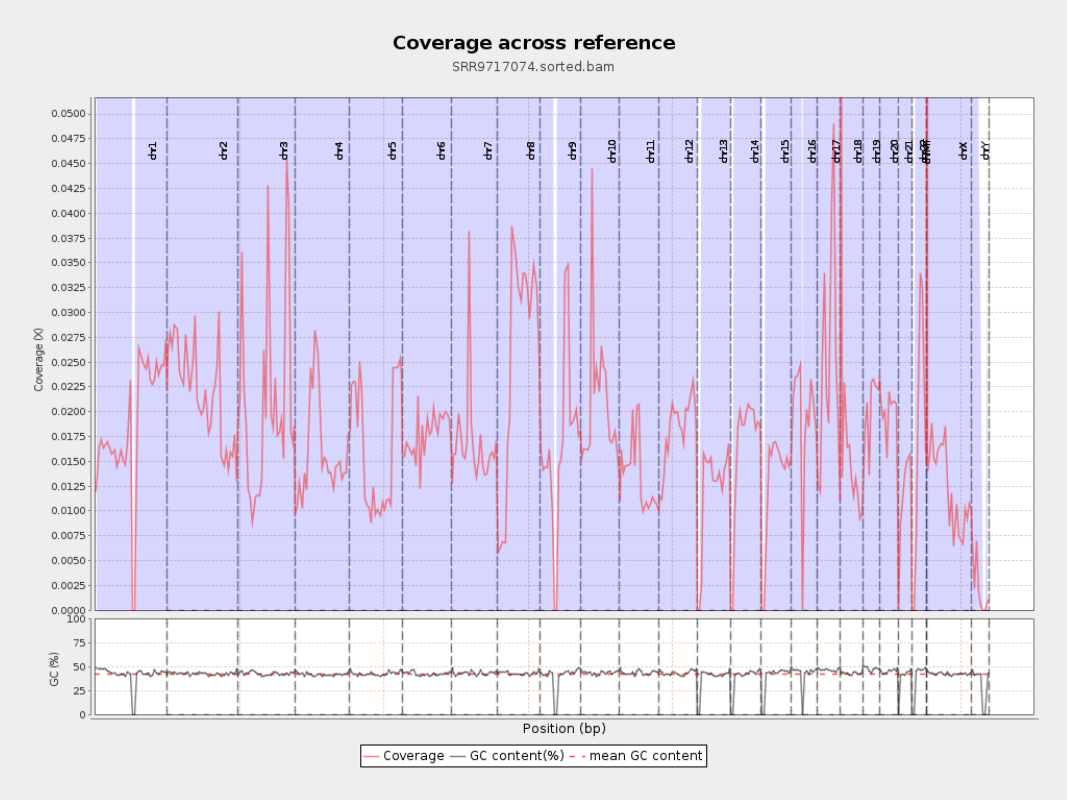
General error rate	0.54%
Mismatches	285,854
Insertions	3,994
Mapped reads with at least one insertion	0.41%
Deletions	10,022
Mapped reads with at least one deletion	1.02%
Homopolymer indels	40.72%

2.6. Chromosome stats

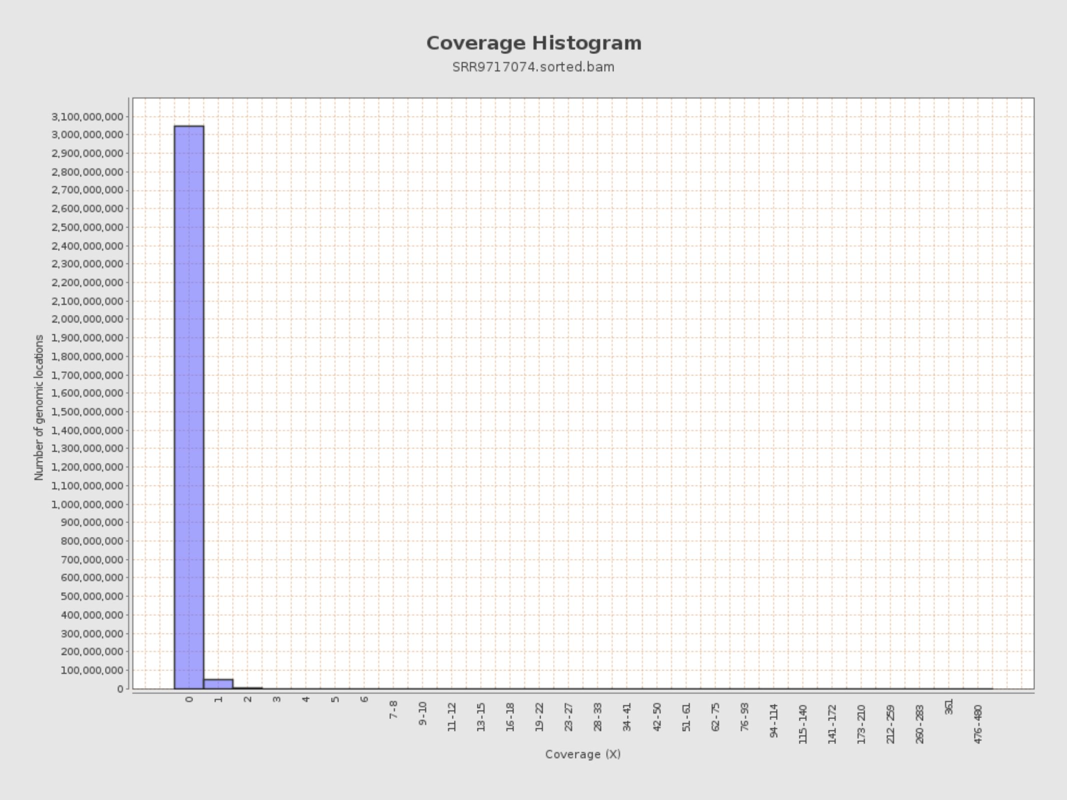
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4644261	0.0186	0.2207
chr2	243199373	5325426	0.0219	0.251
chr3	198022430	4102674	0.0207	0.1564
chr4	191154276	3036339	0.0159	0.1372
chr5	180915260	2928006	0.0162	0.1344
chr6	171115067	3029969	0.0177	0.1499
chr7	159138663	2692148	0.0169	0.3358

chr8	146364022	3790421	0.0259	0.1879
chr9	141213431	2323728	0.0165	0.1491
chr10	135534747	2812089	0.0207	0.2193
chr11	135006516	1864331	0.0138	0.1431
chr12	133851895	2433300	0.0182	0.1459
chr13	115169878	1378675	0.012	0.1144
chr14	107349540	1742076	0.0162	0.1369
chr15	102531392	1305488	0.0127	0.1231
chr16	90354753	1714741	0.019	0.152
chr17	81195210	2051744	0.0253	0.1732
chr18	78077248	1301326	0.0167	0.2037
chr19	59128983	1198953	0.0203	0.2143
chr20	63025520	1239541	0.0197	0.1498
chr21	48129895	564196	0.0117	0.1158
chr22	51304566	889291	0.0173	0.1406
chrMT	16571	19426	1.1723	1.3936
chrX	155270560	1924571	0.0124	0.1286
chrY	59373566	132816	0.0022	0.0642

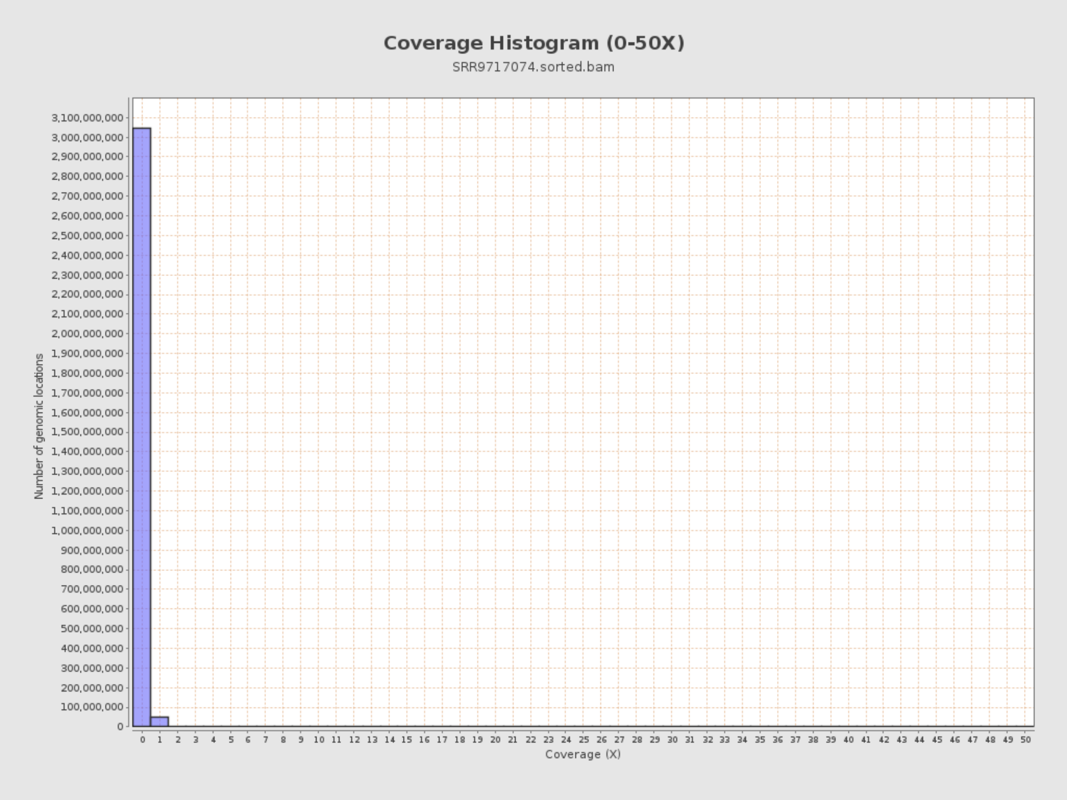
3. Results : Coverage across reference



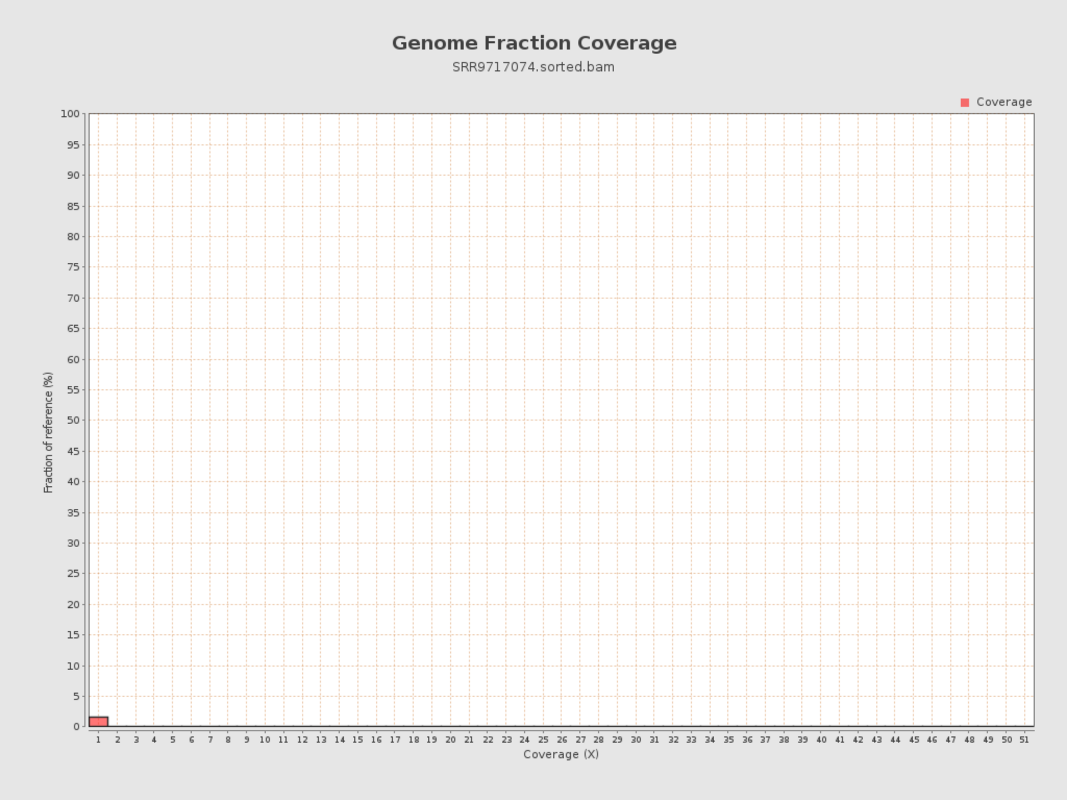
4. Results : Coverage Histogram



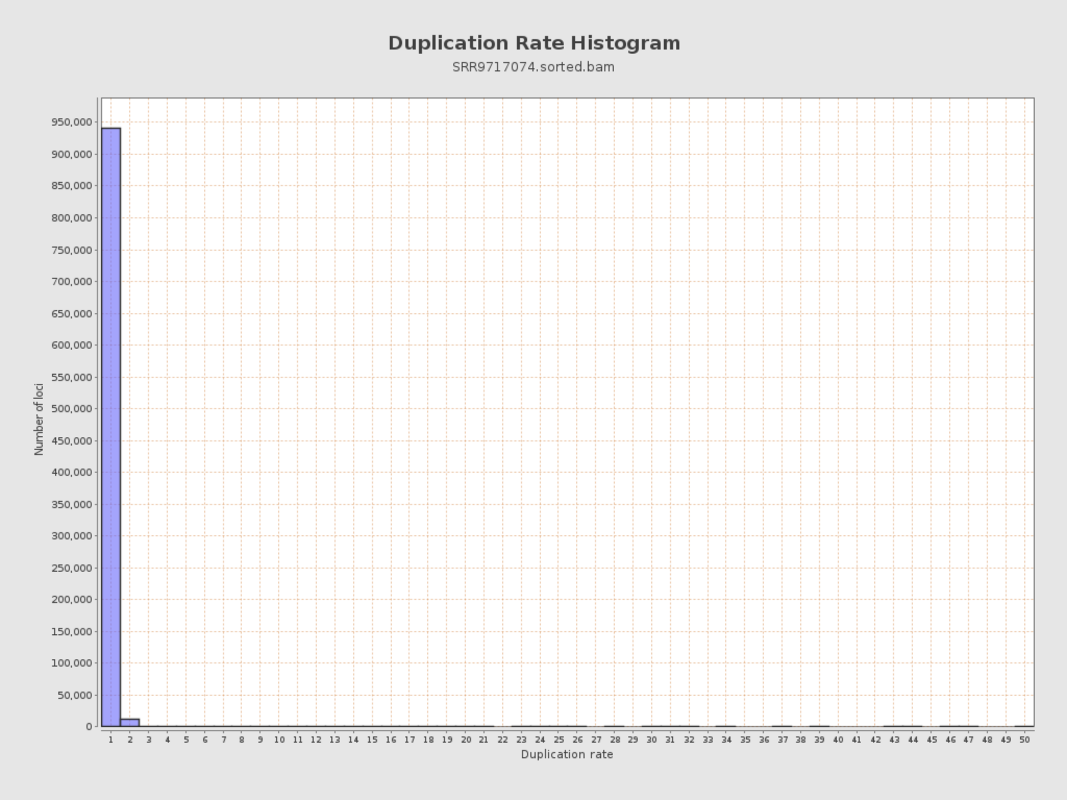
5. Results : Coverage Histogram (0-50X)



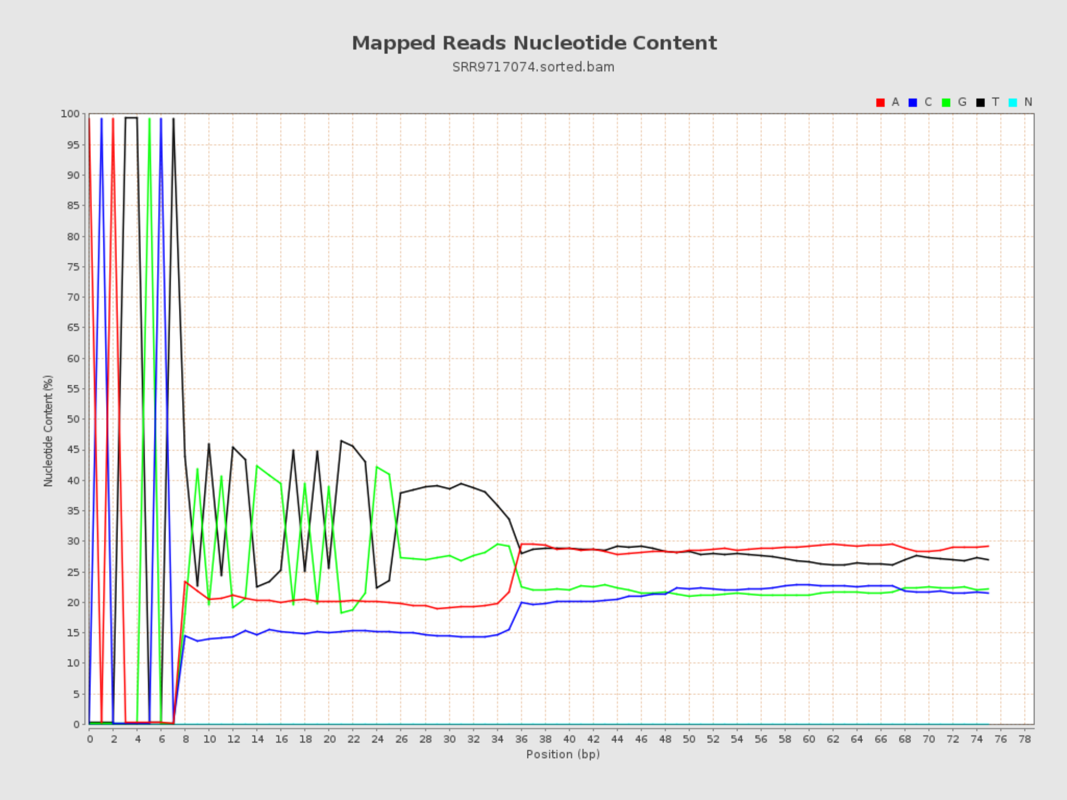
6. Results : Genome Fraction Coverage



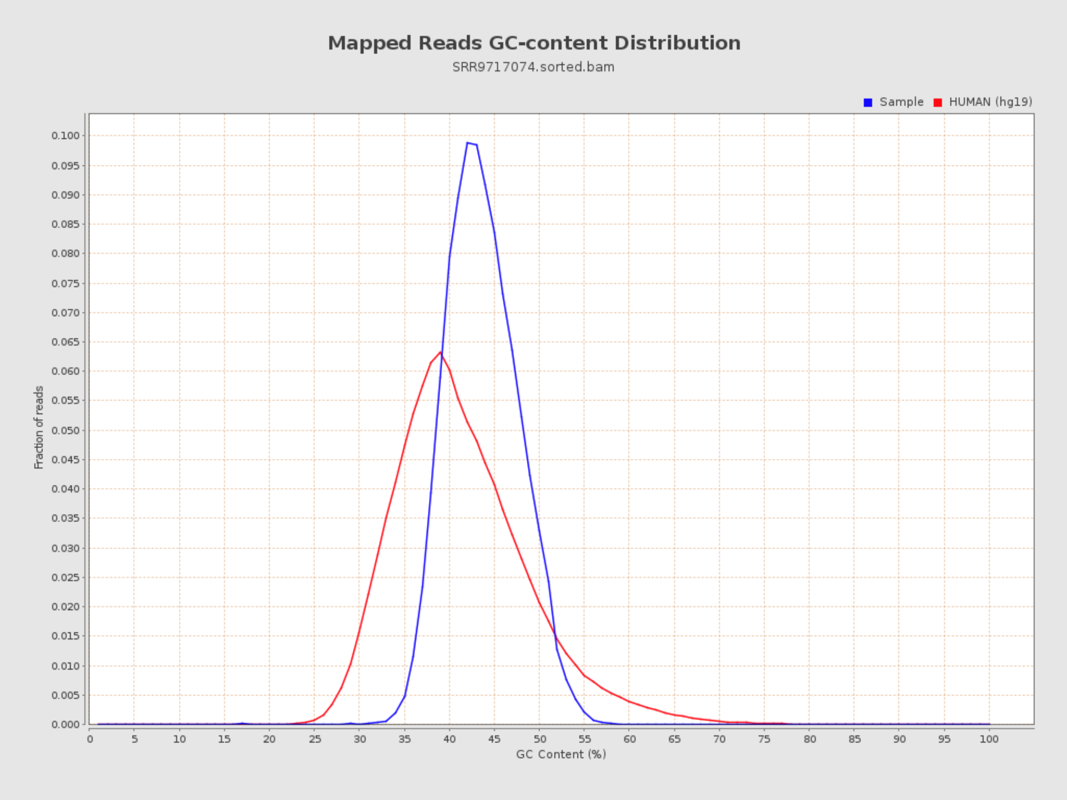
7. Results : Duplication Rate Histogram



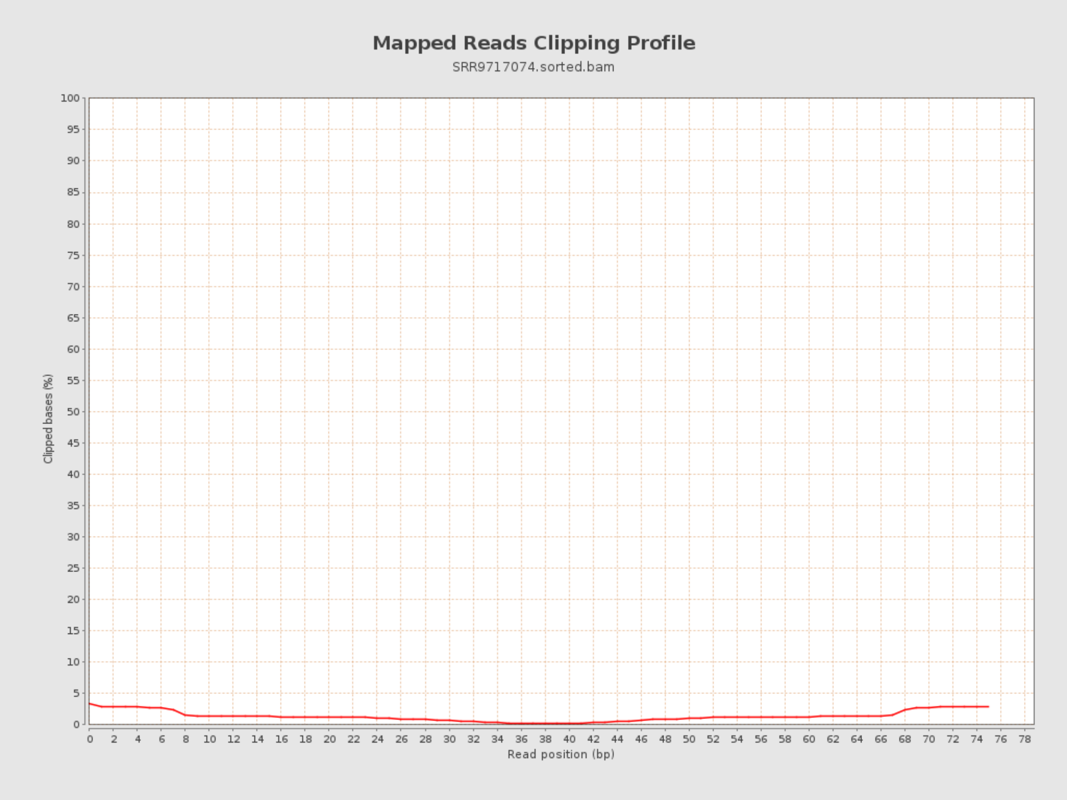
8. Results : Mapped Reads Nucleotide Content



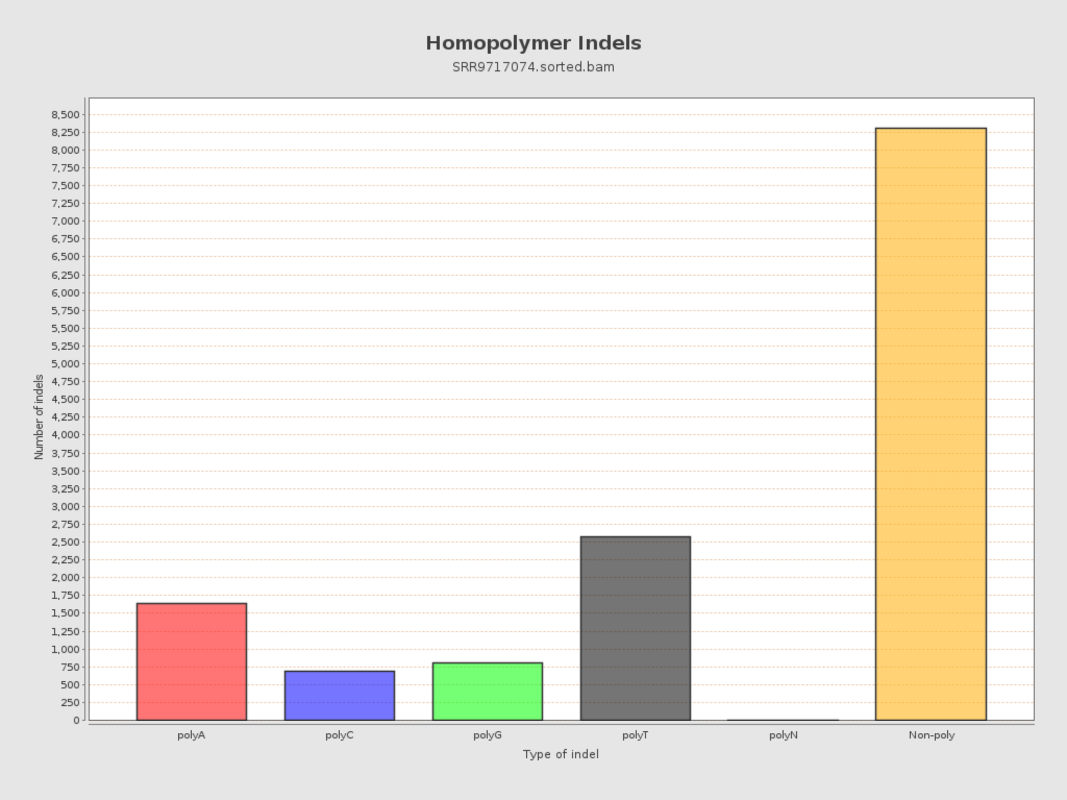
9. Results : Mapped Reads GC-content Distribution



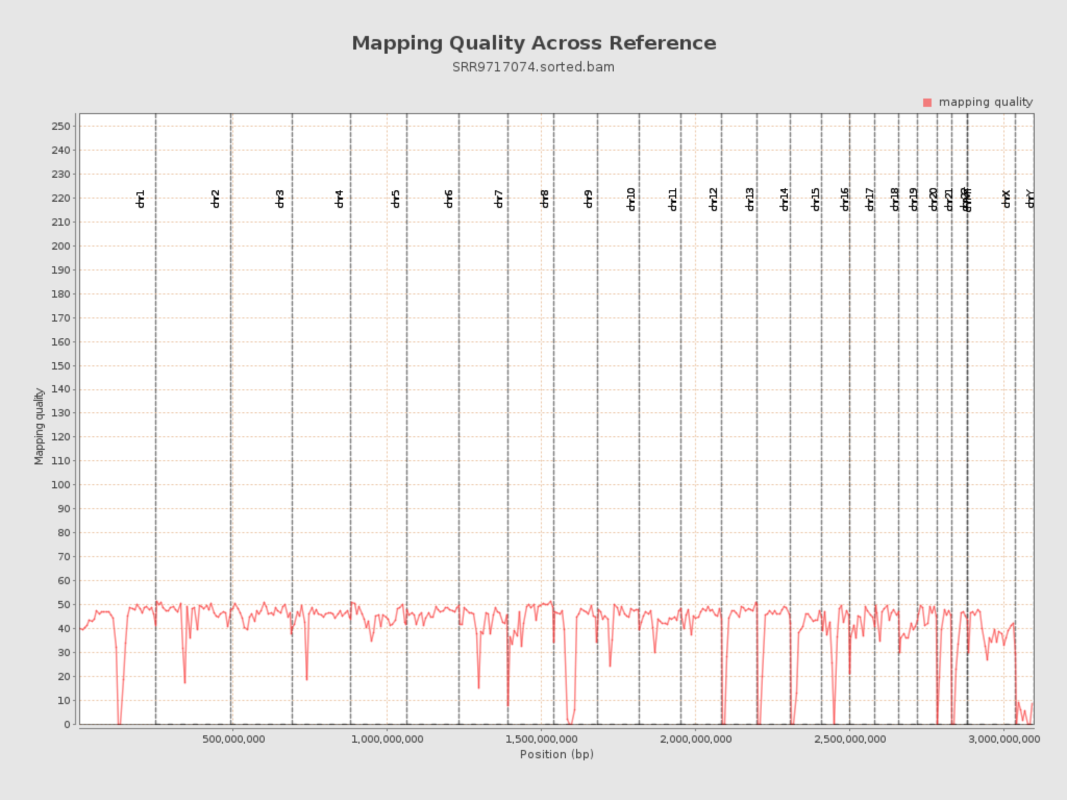
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram