Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 23:50:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717002.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_SRR9717002 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717002.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 23:50:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717002.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,928,443
Mapped reads	1,762,445 / 91.39%
Unmapped reads	165,998 / 8.61%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,606 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	71,708 / 3.72%
Duplication rate	3.07%
Clipped reads	1,768,893 / 91.73%

2.2. ACGT Content

Number/percentage of A's	26,383,470 / 25.93%
Number/percentage of C's	17,991,173 / 17.68%
Number/percentage of T's	31,826,056 / 31.28%
Number/percentage of G's	25,553,176 / 25.11%
Number/percentage of N's	1,711 / 0%
GC Percentage	42.79%

2.3. Coverage

Mean	0.0329

Standard Deviation	0.2993

2.4. Mapping Quality

Mean Mapping Quality	45.02

2.5. Mismatches and indels

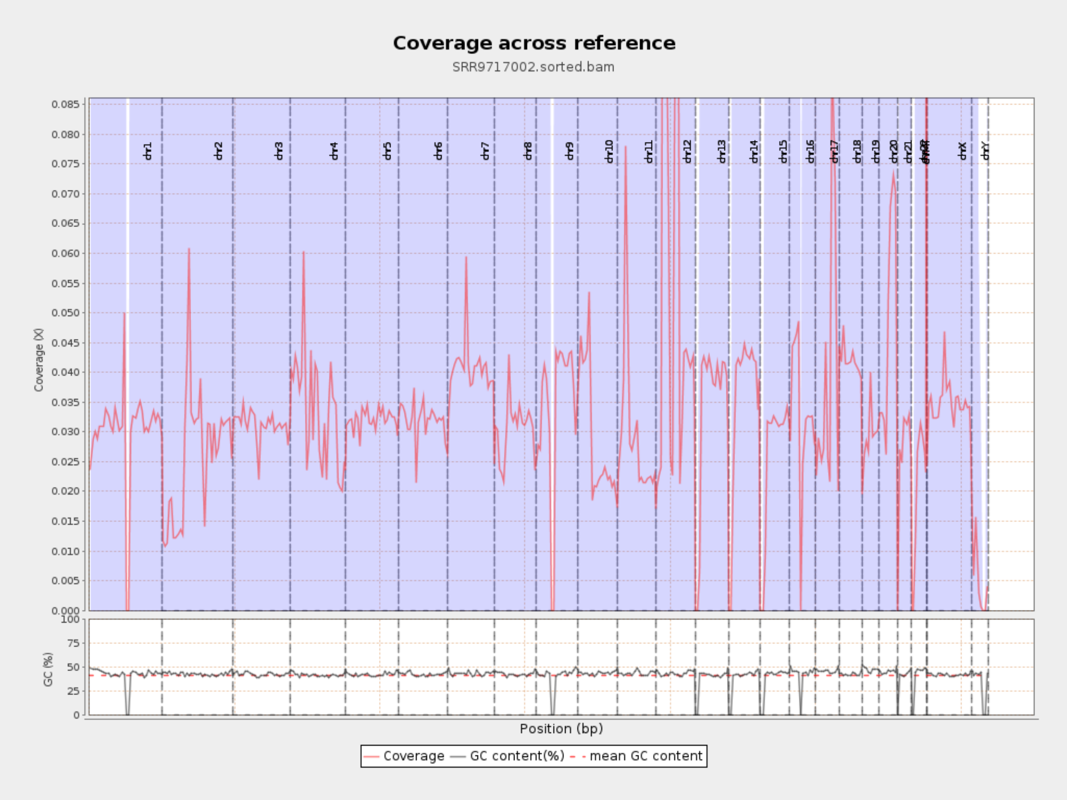
General error rate	0.53%
Mismatches	530,300
Insertions	5,634
Mapped reads with at least one insertion	0.32%
Deletions	17,032
Mapped reads with at least one deletion	0.96%
Homopolymer indels	44.87%

2.6. Chromosome stats

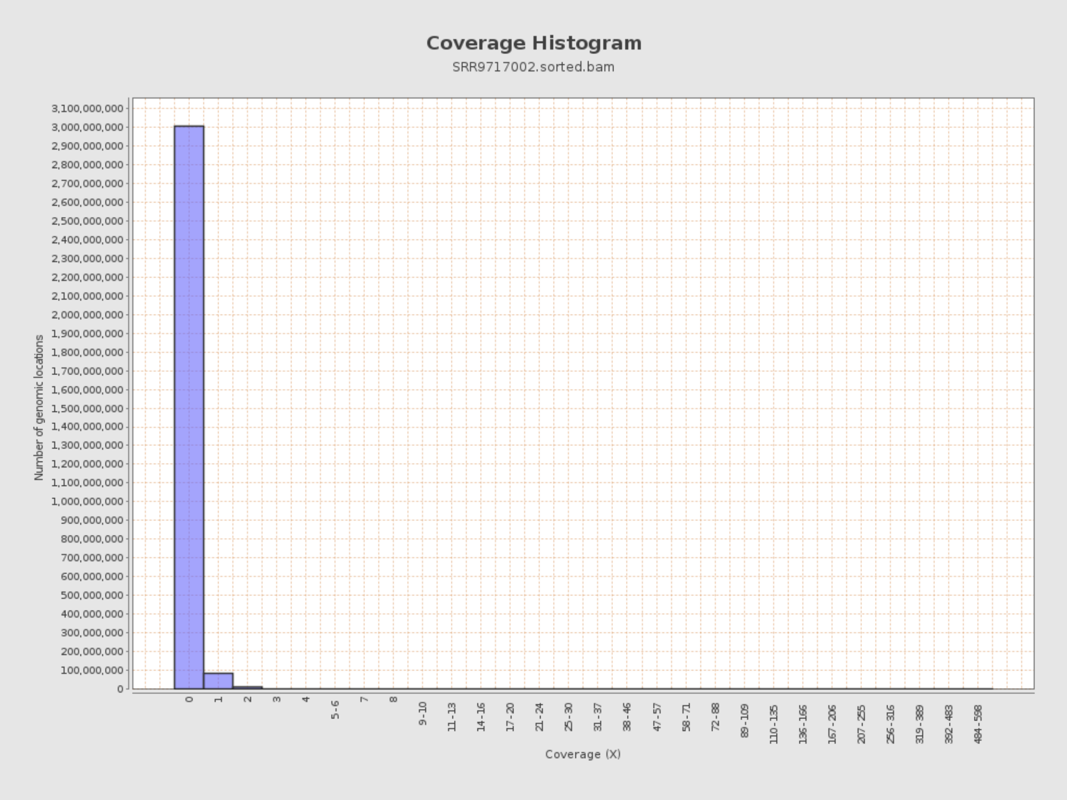
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7480835	0.03	0.5001
chr2	243199373	6355908	0.0261	0.3156
chr3	198022430	6174954	0.0312	0.1933
chr4	191154276	6425300	0.0336	0.23
chr5	180915260	5803874	0.0321	0.1995
chr6	171115067	5470894	0.032	0.2196
chr7	159138663	6529551	0.041	0.4064

chr8	146364022	4495569	0.0307	0.2777
chr9	141213431	4799548	0.034	0.327
chr10	135534747	3966950	0.0293	0.2883
chr11	135006516	4037653	0.0299	0.2598
chr12	133851895	7758019	0.058	0.2973
chr13	115169878	3866920	0.0336	0.2009
chr14	107349540	3747403	0.0349	0.228
chr15	102531392	2636635	0.0257	0.1749
chr16	90354753	2999381	0.0332	0.2141
chr17	81195210	3126853	0.0385	0.2267
chr18	78077248	3295045	0.0422	0.5724
chr19	59128983	1753825	0.0297	0.3788
chr20	63025520	3074556	0.0488	0.2503
chr21	48129895	1275516	0.0265	0.2053
chr22	51304566	1017469	0.0198	0.1538
chrMT	16571	4545	0.2743	0.5682
chrX	155270560	5397923	0.0348	0.2393
chrY	59373566	289002	0.0049	0.1209

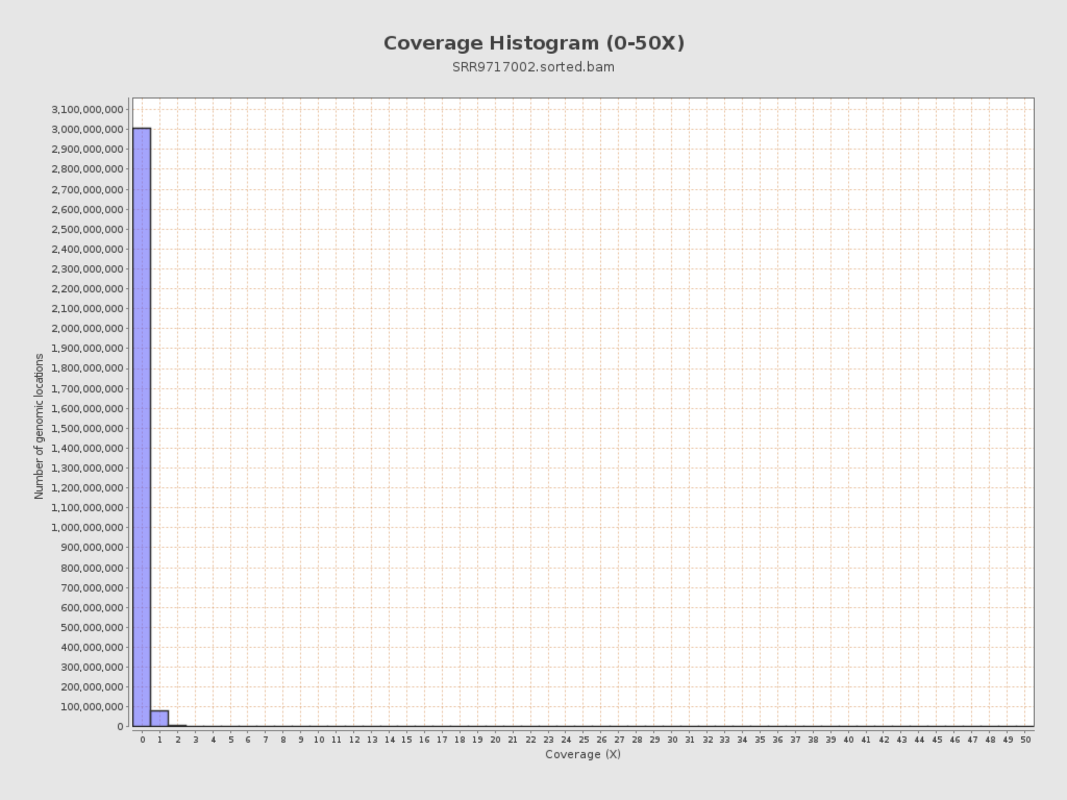
3. Results : Coverage across reference



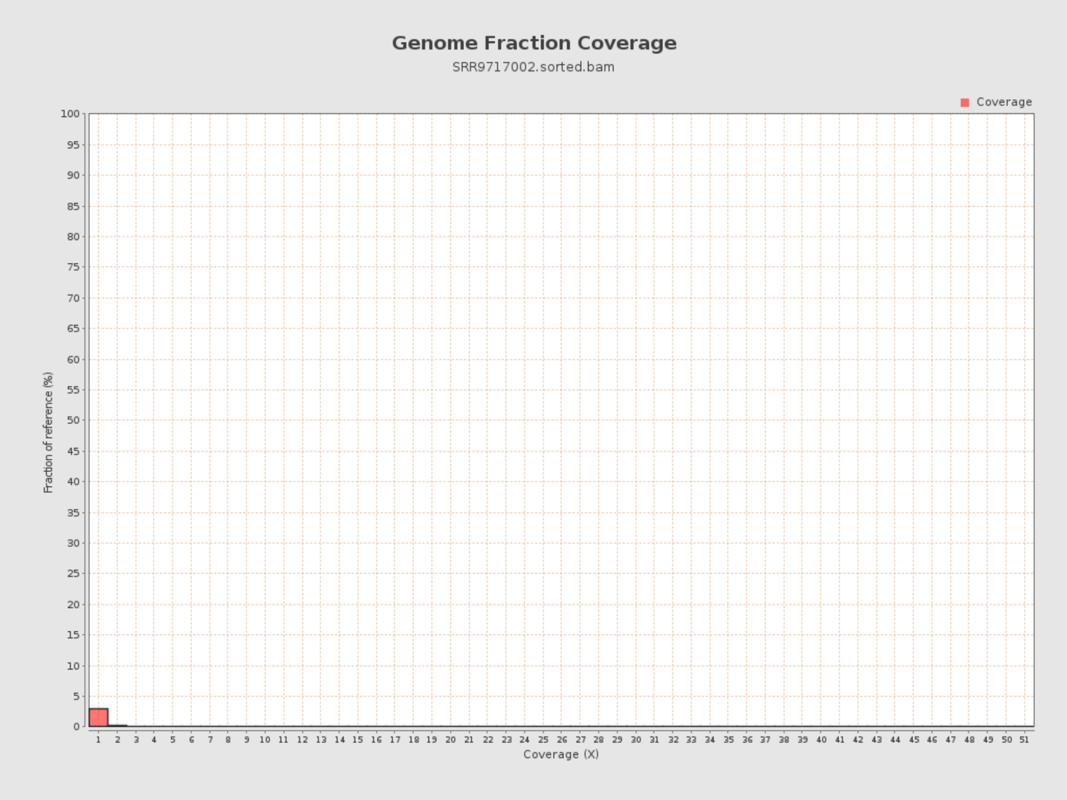
4. Results : Coverage Histogram



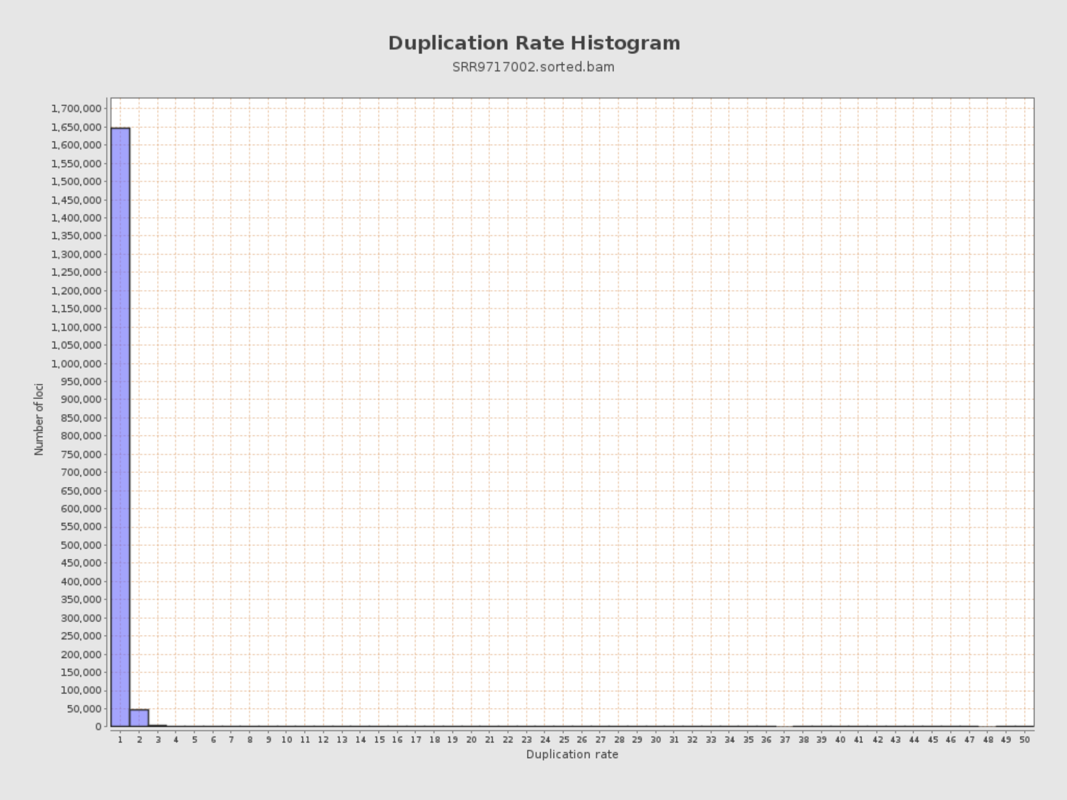
5. Results : Coverage Histogram (0-50X)



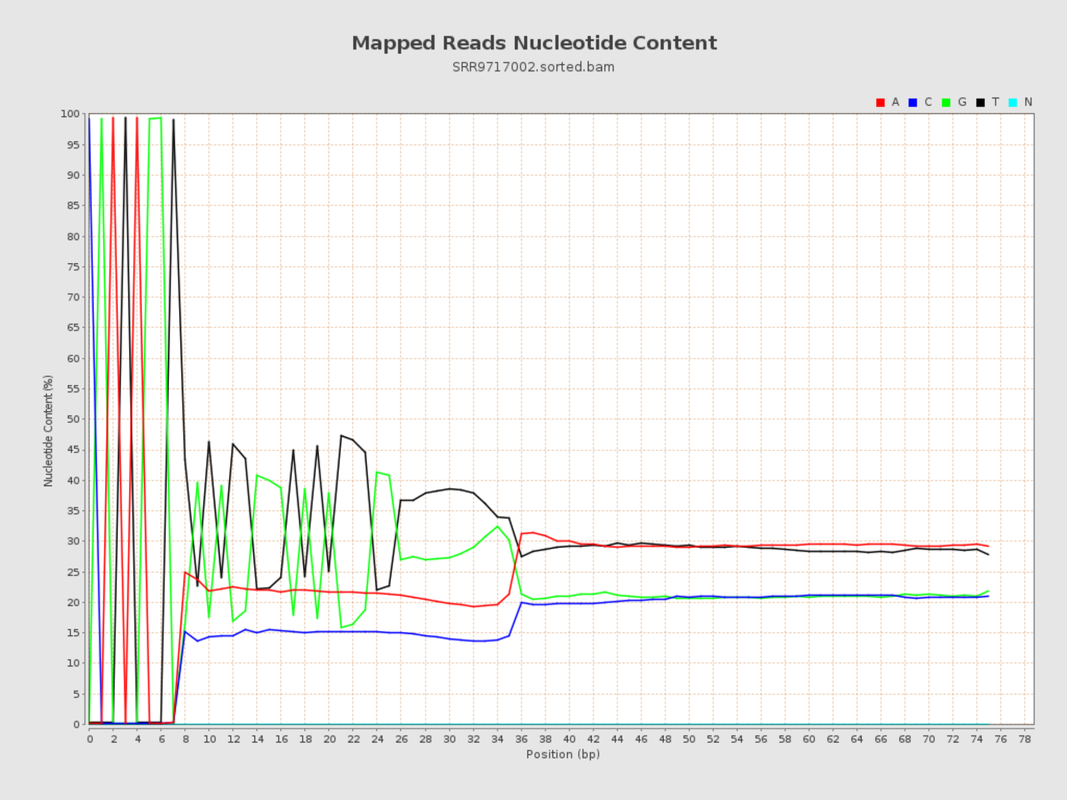
6. Results : Genome Fraction Coverage



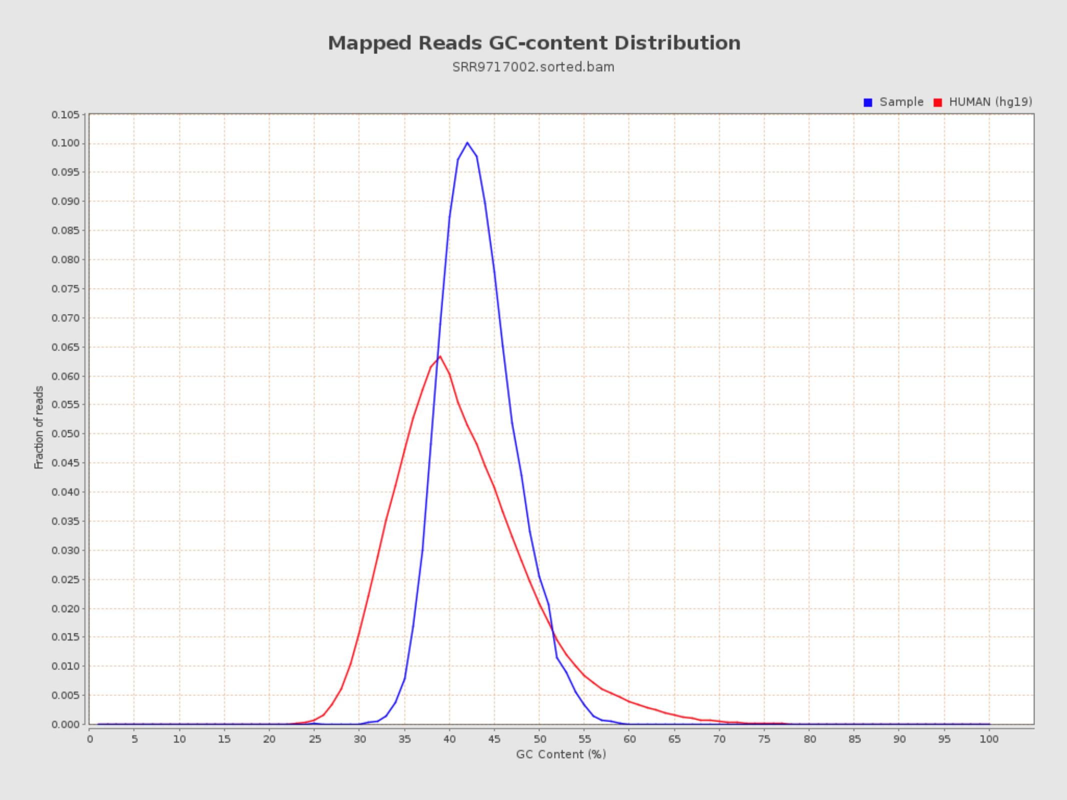
7. Results : Duplication Rate Histogram



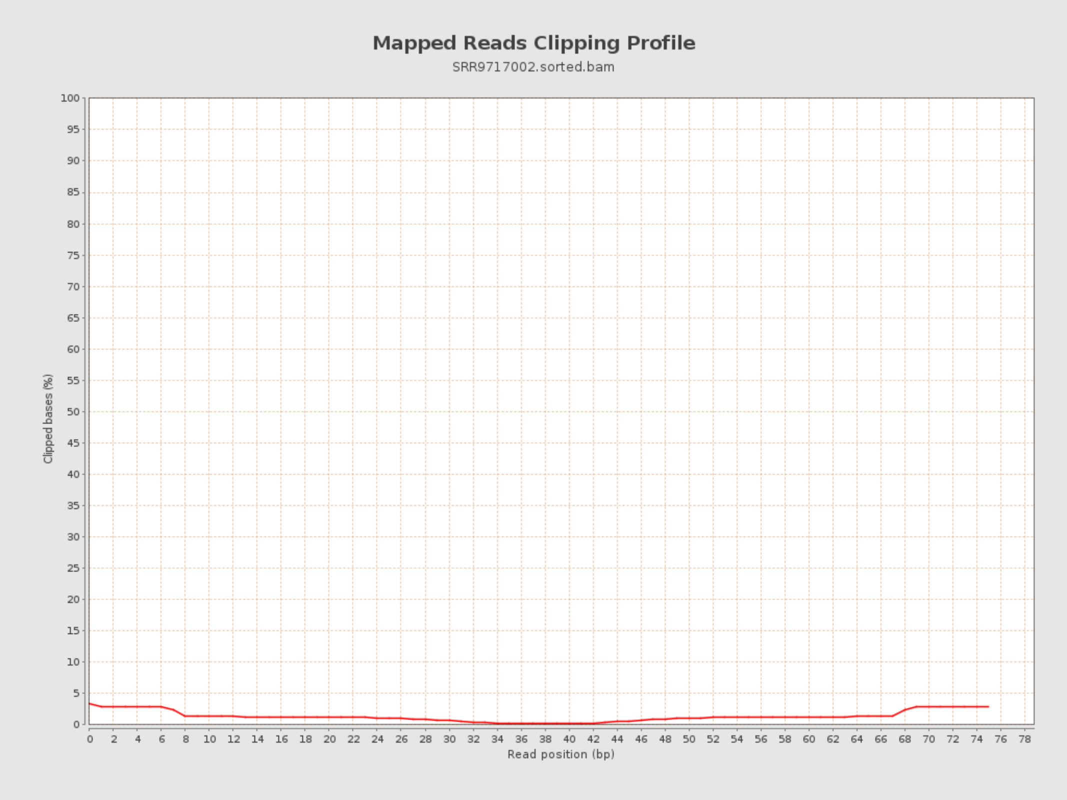
8. Results : Mapped Reads Nucleotide Content



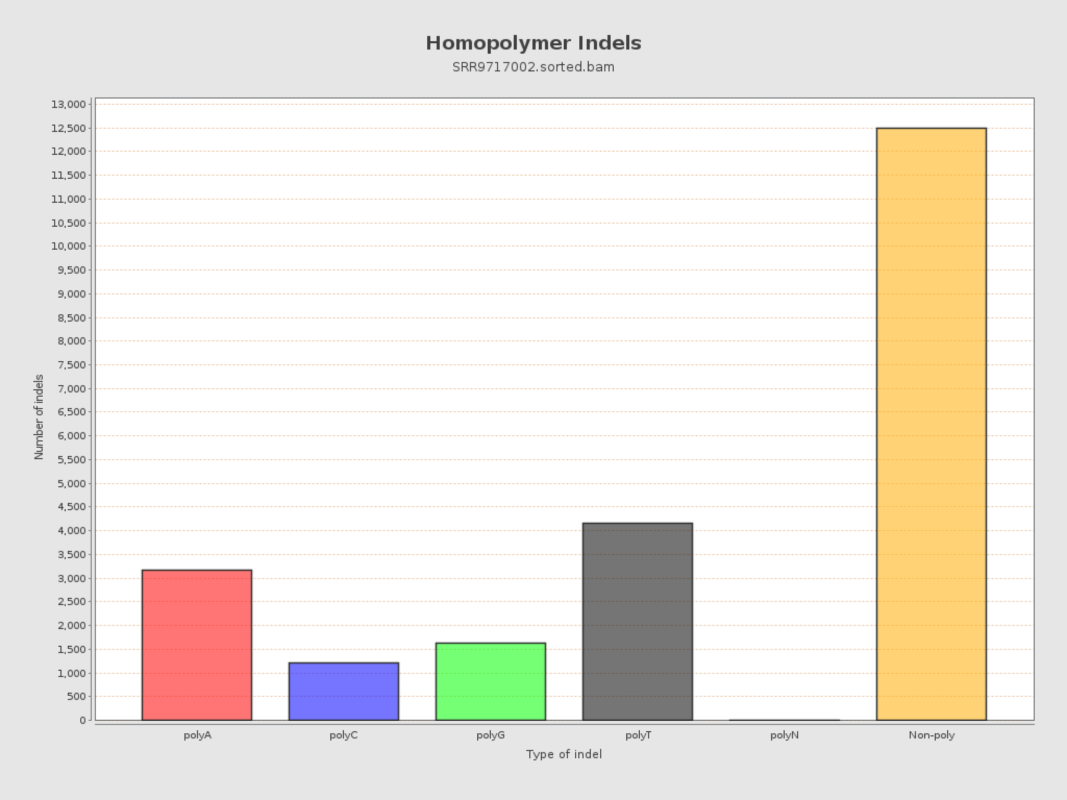
9. Results : Mapped Reads GC-content Distribution



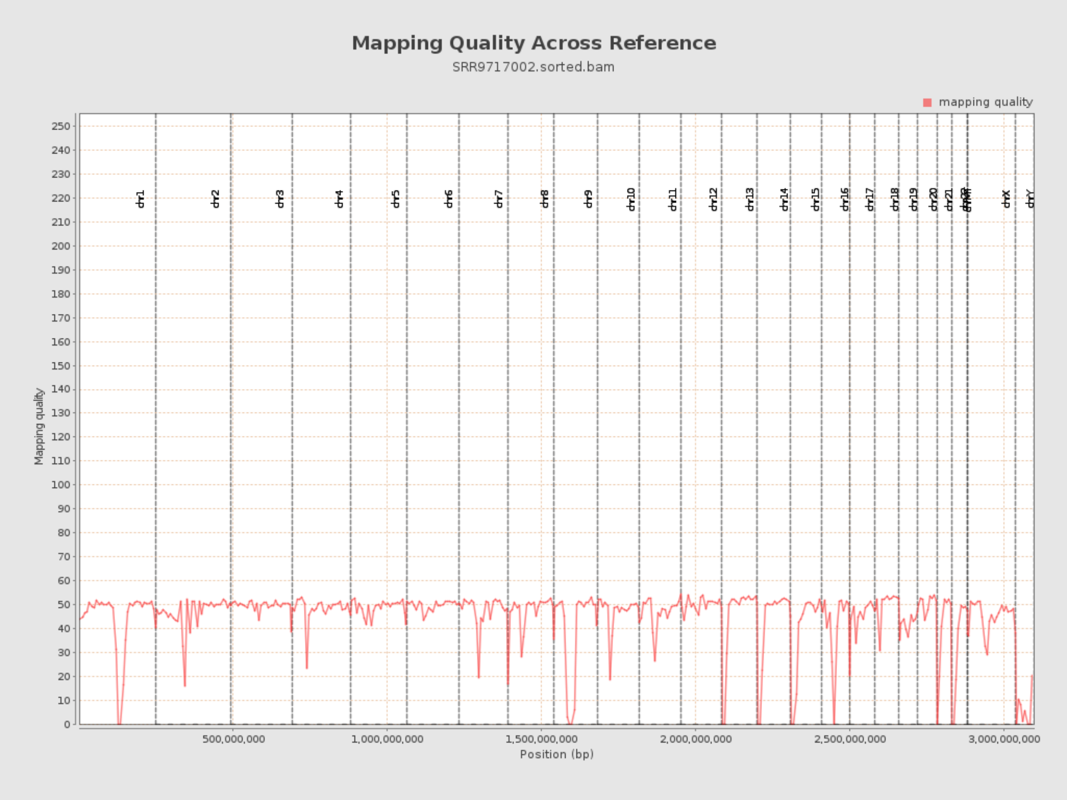
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram