Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 23:56:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717004.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_SRR9717004 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717004.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 23:56:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717004.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,947,380
Mapped reads	1,704,203 / 87.51%
Unmapped reads	243,177 / 12.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,129 / 0.31%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	45,179 / 2.32%
Duplication rate	1.86%
Clipped reads	1,706,705 / 87.64%

2.2. ACGT Content

Number/percentage of A's	23,719,582 / 24.66%
Number/percentage of C's	18,164,826 / 18.89%
Number/percentage of T's	30,769,790 / 31.99%
Number/percentage of G's	23,515,850 / 24.45%
Number/percentage of N's	680 / 0%
GC Percentage	43.34%

2.3. Coverage

Mean	0.0311

Standard Deviation	0.2566

2.4. Mapping Quality

Mean Mapping Quality	41.93

2.5. Mismatches and indels

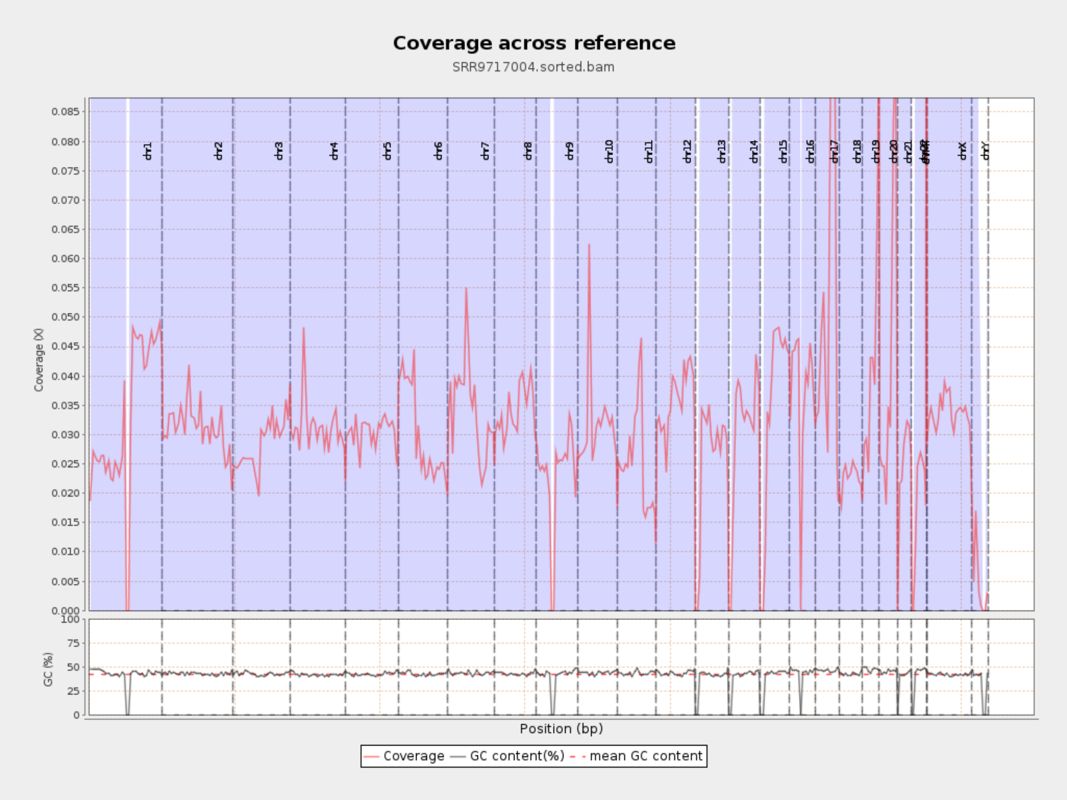
General error rate	0.55%
Mismatches	514,373
Insertions	6,993
Mapped reads with at least one insertion	0.41%
Deletions	18,012
Mapped reads with at least one deletion	1.05%
Homopolymer indels	40.38%

2.6. Chromosome stats

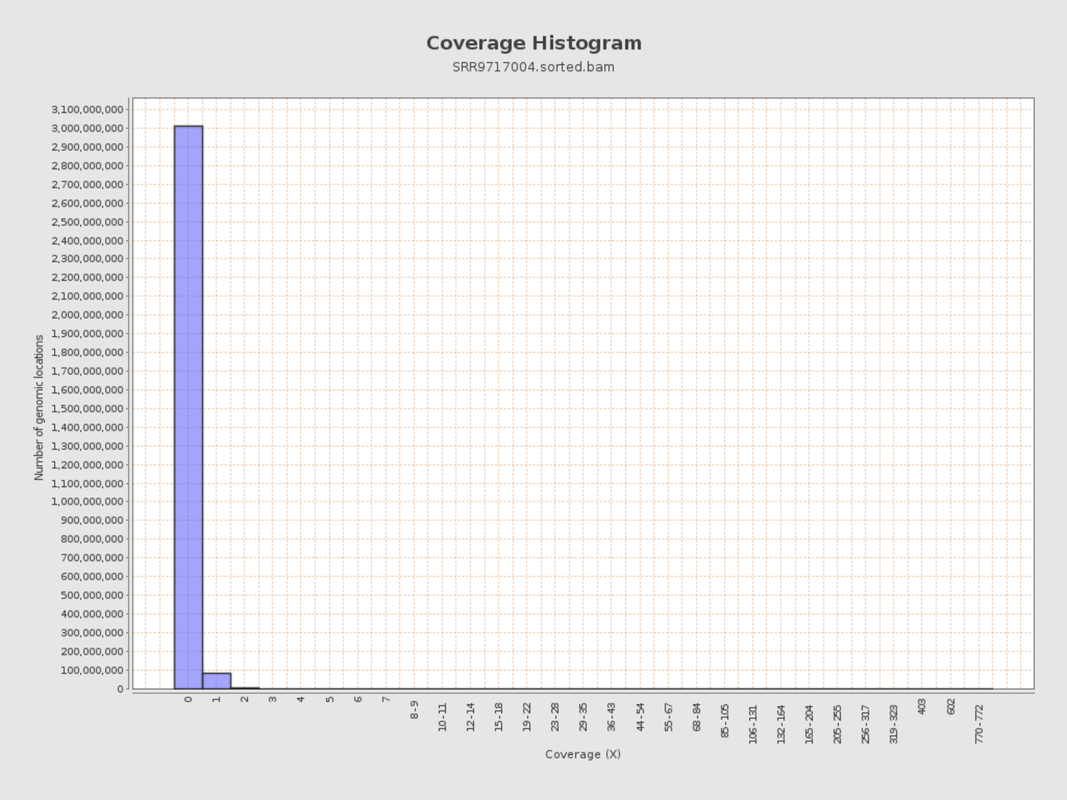
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8110835	0.0325	0.3176
chr2	243199373	7611909	0.0313	0.3699
chr3	198022430	5590675	0.0282	0.1865
chr4	191154276	5962840	0.0312	0.2123
chr5	180915260	5507697	0.0304	0.1892
chr6	171115067	5166240	0.0302	0.2245
chr7	159138663	5480301	0.0344	0.3781

chr8	146364022	5003214	0.0342	0.2491
chr9	141213431	3217560	0.0228	0.195
chr10	135534747	4303770	0.0318	0.3313
chr11	135006516	3438459	0.0255	0.2159
chr12	133851895	4808037	0.0359	0.2087
chr13	115169878	2947165	0.0256	0.1772
chr14	107349540	3210142	0.0299	0.1948
chr15	102531392	3533782	0.0345	0.2083
chr16	90354753	3360936	0.0372	0.225
chr17	81195210	4302172	0.053	0.2657
chr18	78077248	1784655	0.0229	0.2997
chr19	59128983	2469542	0.0418	0.3275
chr20	63025520	2769517	0.0439	0.24
chr21	48129895	1183898	0.0246	0.1837
chr22	51304566	893186	0.0174	0.1441
chrMT	16571	6833	0.4123	0.6884
chrX	155270560	5241638	0.0338	0.2149
chrY	59373566	294413	0.005	0.138

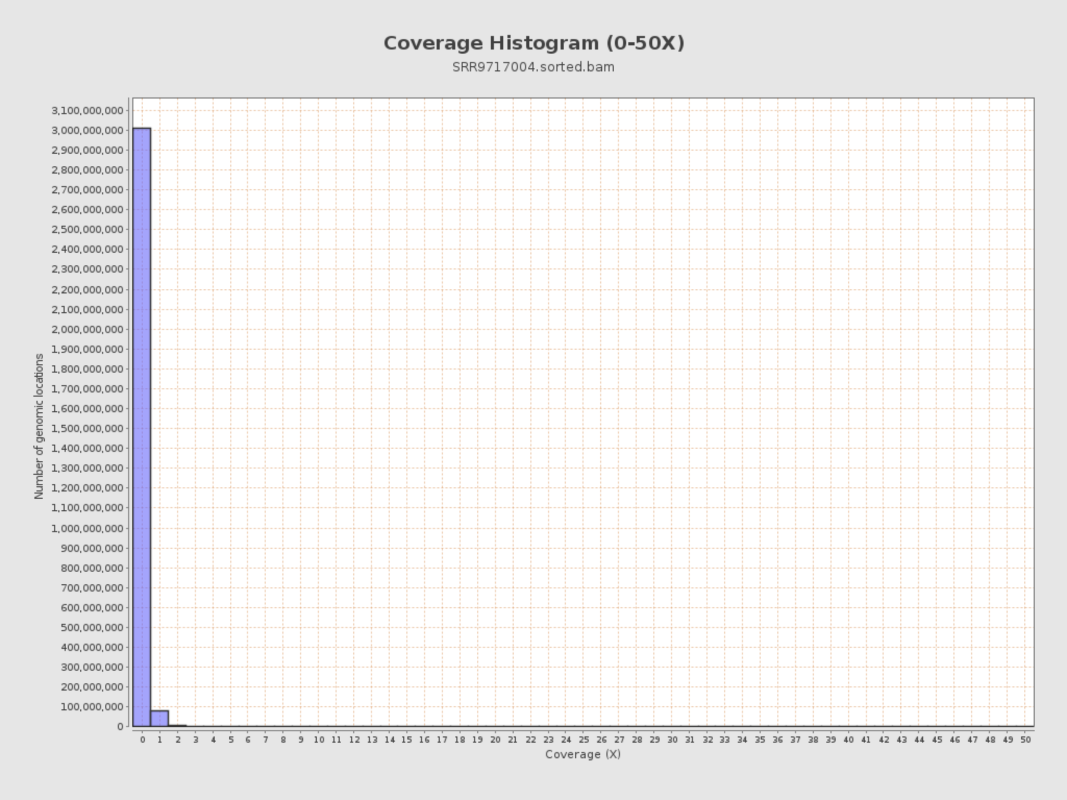
3. Results : Coverage across reference



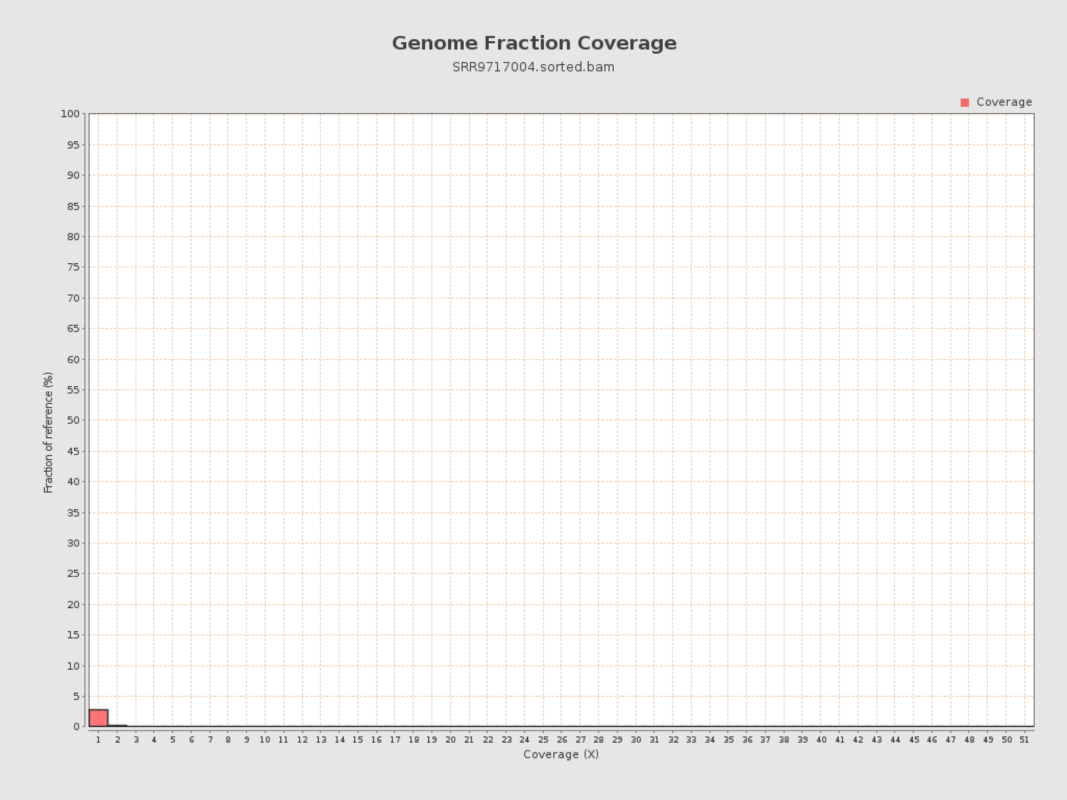
4. Results : Coverage Histogram



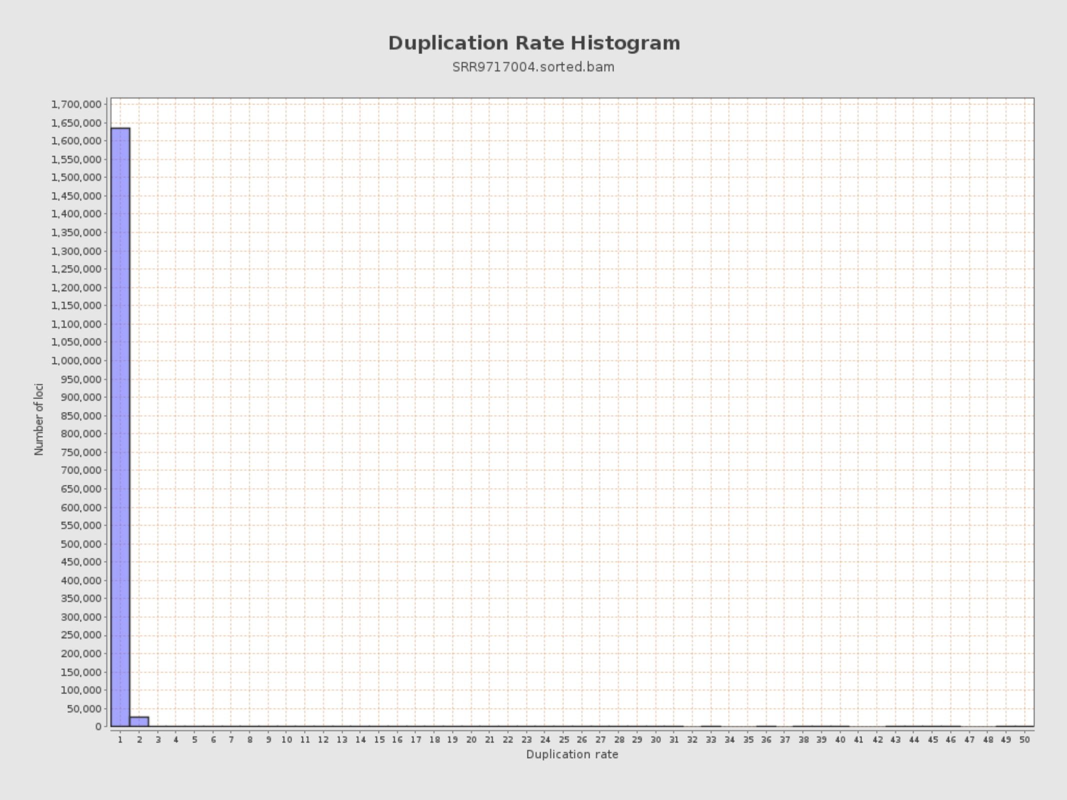
5. Results : Coverage Histogram (0-50X)



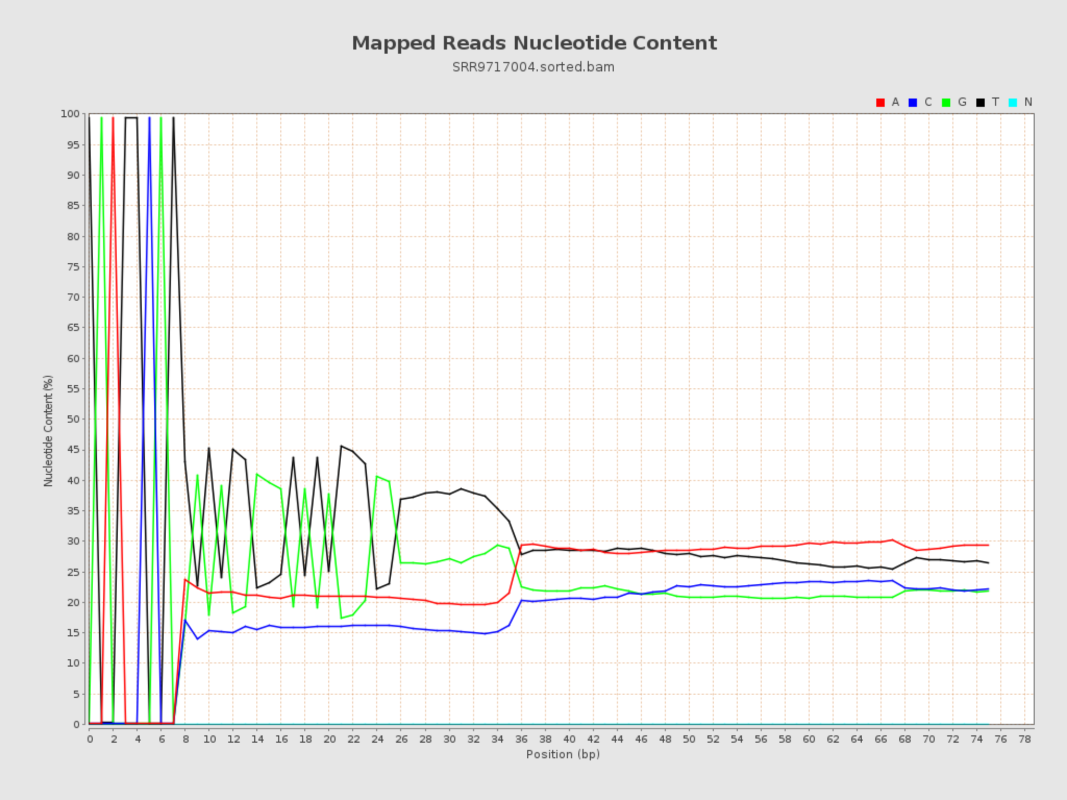
6. Results : Genome Fraction Coverage



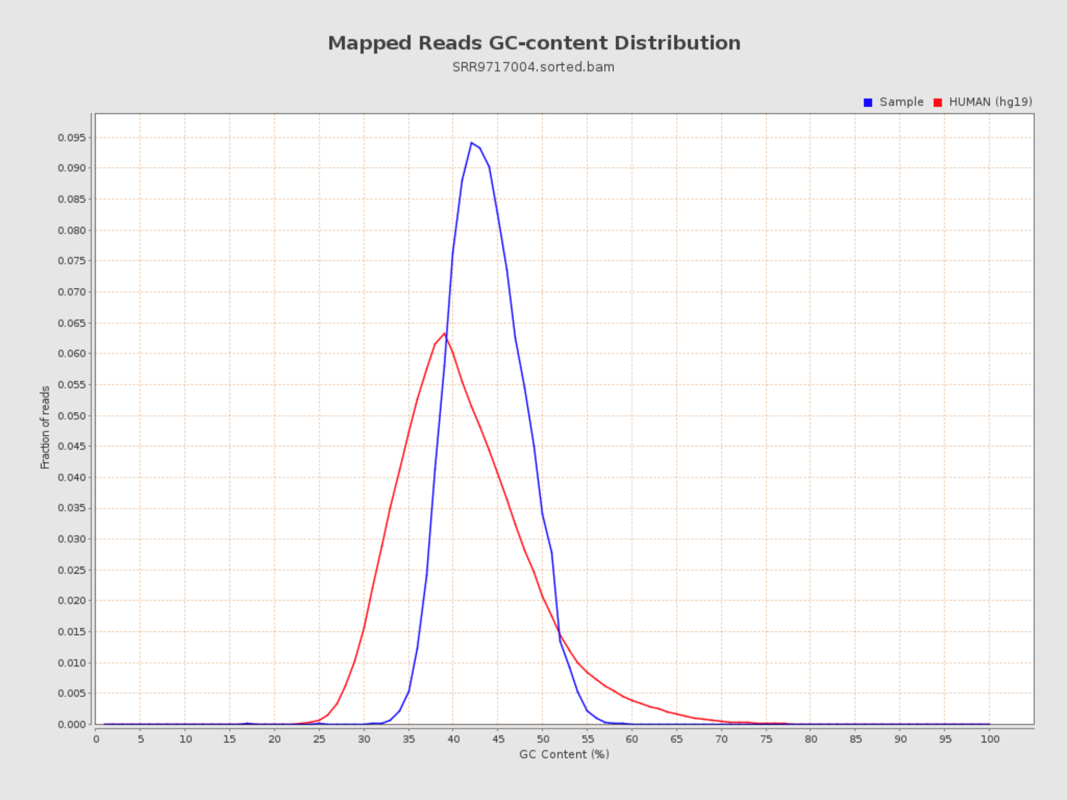
7. Results : Duplication Rate Histogram



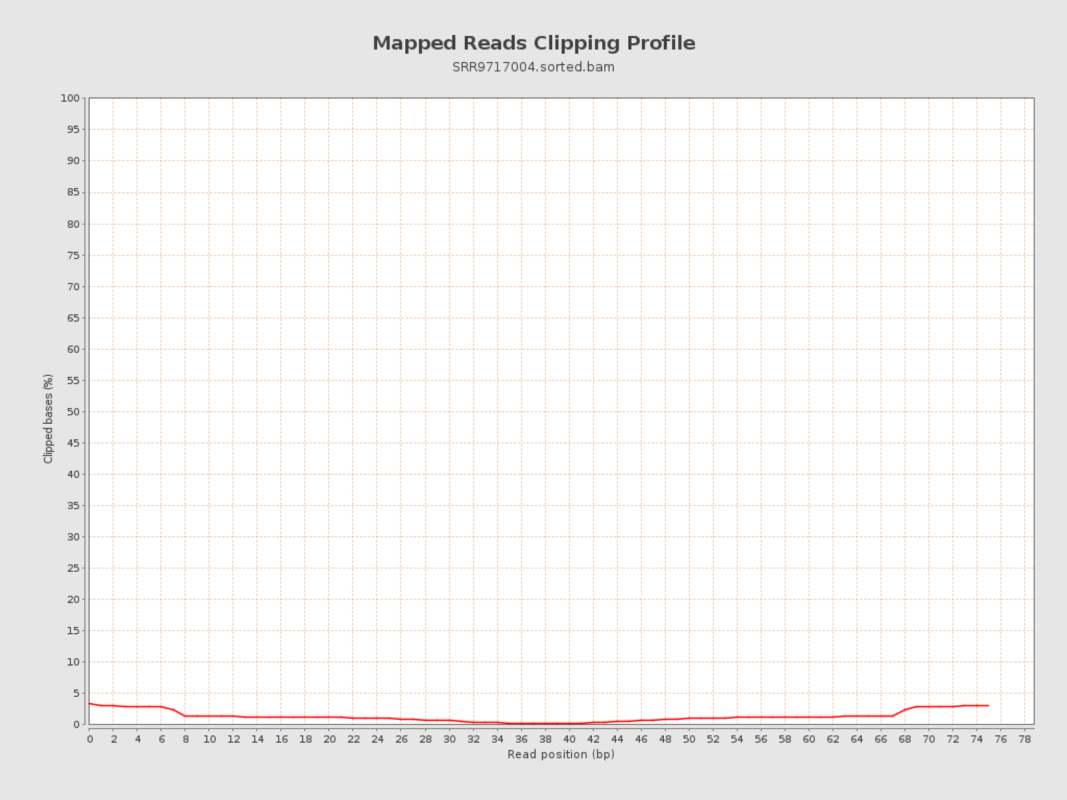
8. Results : Mapped Reads Nucleotide Content



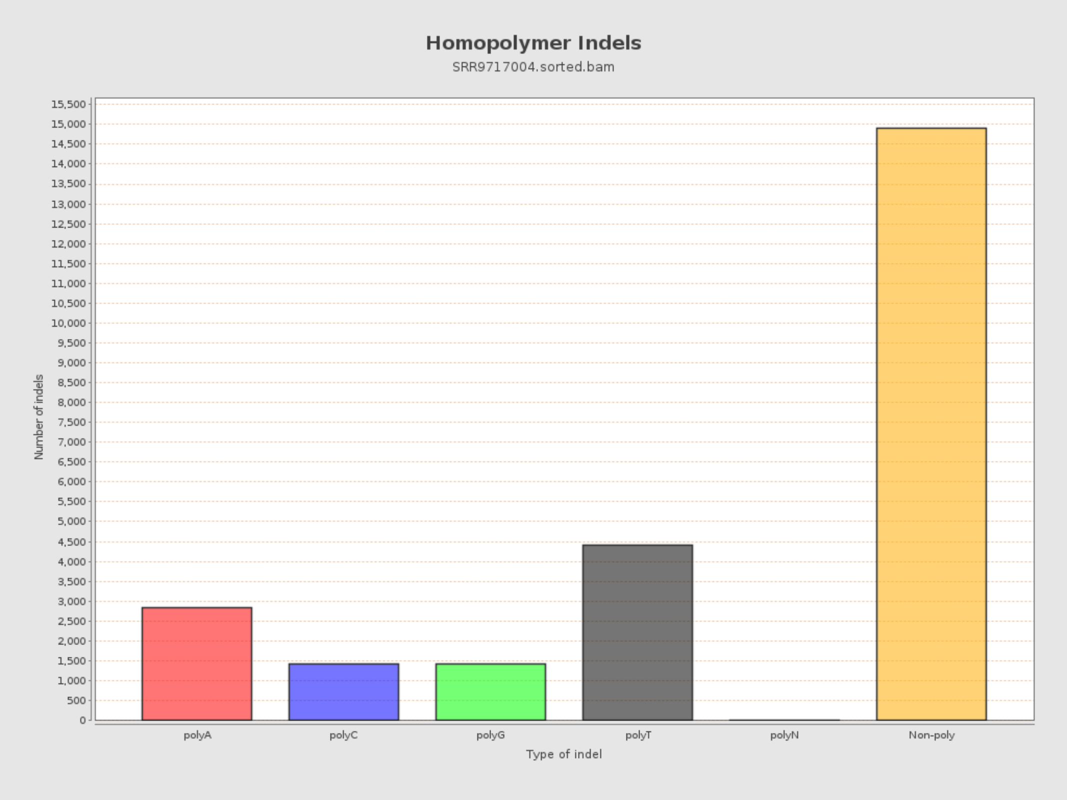
9. Results : Mapped Reads GC-content Distribution



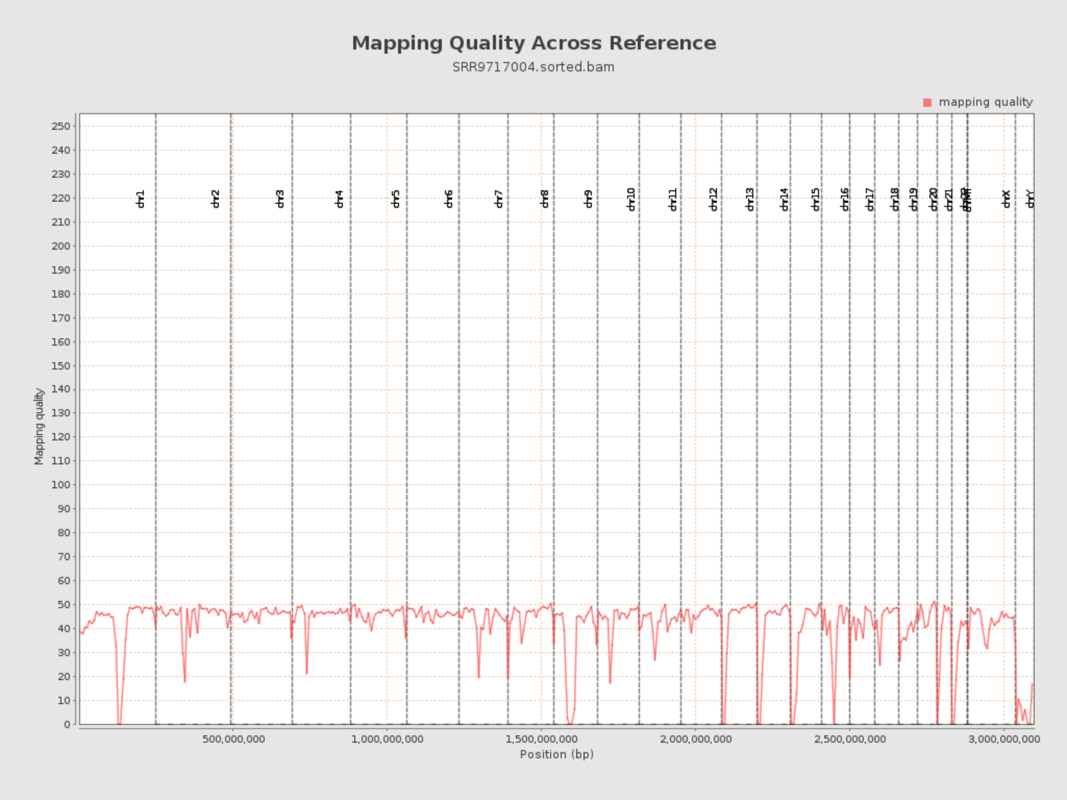
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram