Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 05:13:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717086.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_SRR9717086 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717086.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 05:13:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717086.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,261,097
Mapped reads	1,141,327 / 90.5%
Unmapped reads	119,770 / 9.5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,367 / 1.46%
Read min/max/mean length	30 / 101 / 101.53
Duplicated reads (estimated)	42,456 / 3.37%
Duplication rate	2.34%
Clipped reads	1,158,966 / 91.9%

2.2. ACGT Content

Number/percentage of A's	22,858,950 / 25.36%
Number/percentage of C's	17,753,006 / 19.69%
Number/percentage of T's	27,825,212 / 30.86%
Number/percentage of G's	21,710,126 / 24.08%
Number/percentage of N's	5,632 / 0.01%
GC Percentage	43.77%

2.3. Coverage

Mean	0.0291

Standard Deviation	0.3309

2.4. Mapping Quality

Mean Mapping Quality	44.92

2.5. Mismatches and indels

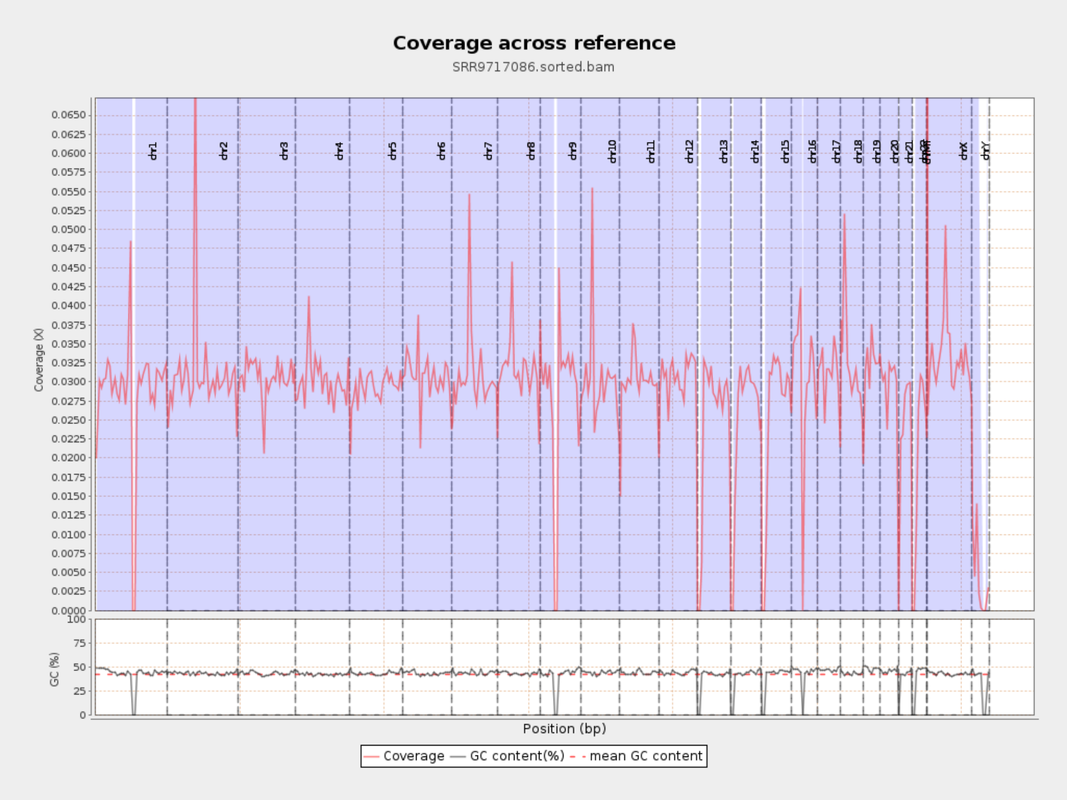
General error rate	0.86%
Mismatches	756,668
Insertions	7,974
Mapped reads with at least one insertion	0.69%
Deletions	22,719
Mapped reads with at least one deletion	1.97%
Homopolymer indels	44.76%

2.6. Chromosome stats

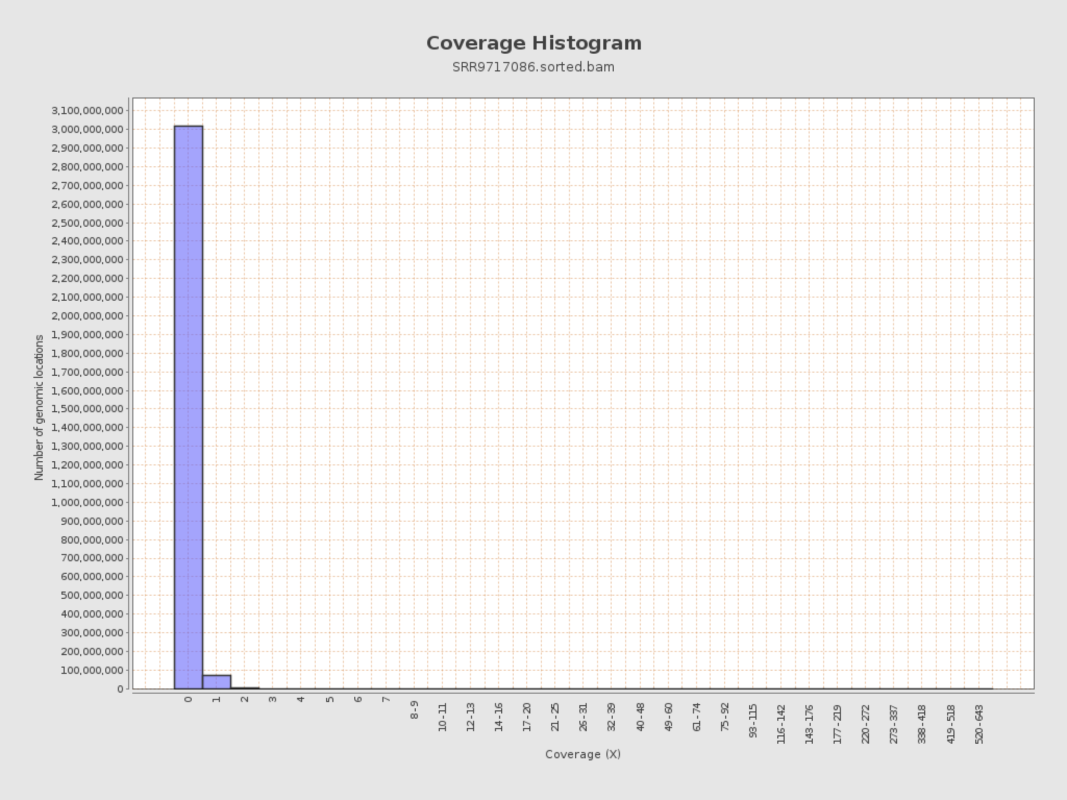
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7097997	0.0285	0.4941
chr2	243199373	7609848	0.0313	0.4905
chr3	198022430	6050250	0.0306	0.192
chr4	191154276	5785460	0.0303	0.2057
chr5	180915260	5339381	0.0295	0.1902
chr6	171115067	5253753	0.0307	0.2285
chr7	159138663	4953465	0.0311	0.4159

chr8	146364022	4637780	0.0317	0.4312
chr9	141213431	3945886	0.0279	0.3724
chr10	135534747	4111871	0.0303	0.3135
chr11	135006516	4110596	0.0304	0.3248
chr12	133851895	4121747	0.0308	0.1979
chr13	115169878	2813694	0.0244	0.17
chr14	107349540	2644437	0.0246	0.2173
chr15	102531392	2567592	0.025	0.1745
chr16	90354753	2683596	0.0297	0.2104
chr17	81195210	2529237	0.0312	0.2089
chr18	78077248	2553568	0.0327	0.6834
chr19	59128983	1914563	0.0324	0.3894
chr20	63025520	1865435	0.0296	0.2018
chr21	48129895	1149634	0.0239	0.1815
chr22	51304566	1008951	0.0197	0.1529
chrMT	16571	6548	0.3951	0.6923
chrX	155270560	5191097	0.0334	0.262
chrY	59373566	245595	0.0041	0.1295

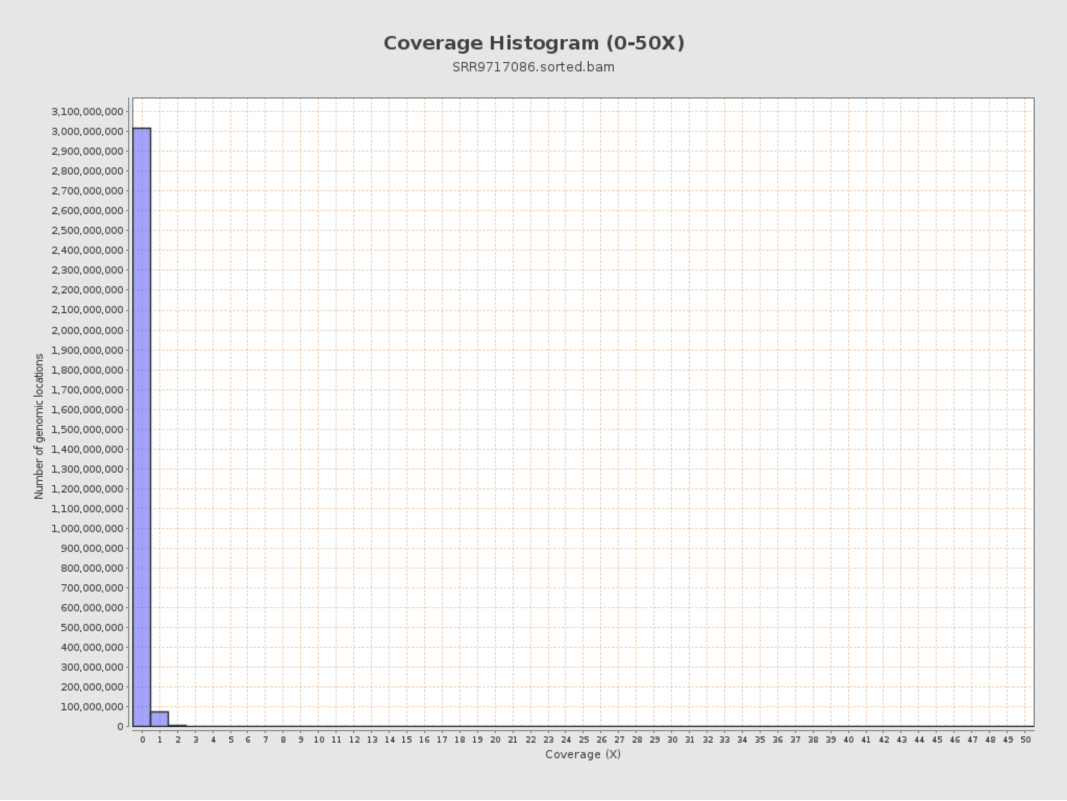
3. Results : Coverage across reference



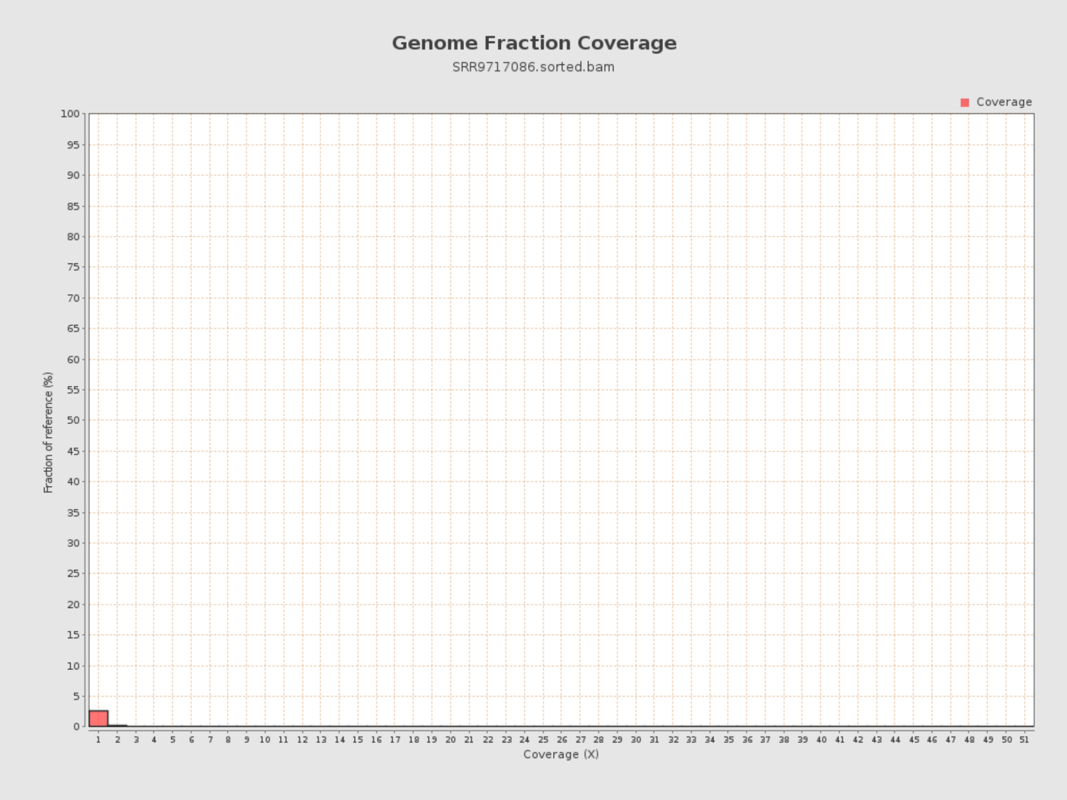
4. Results : Coverage Histogram



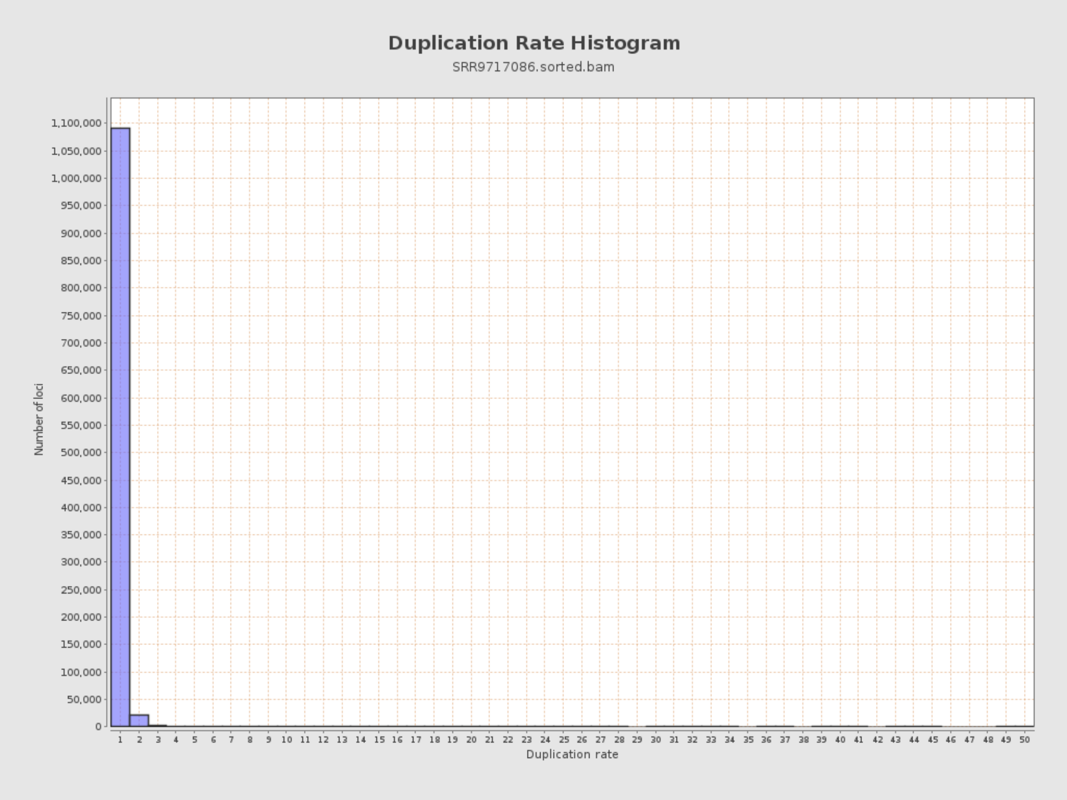
5. Results : Coverage Histogram (0-50X)



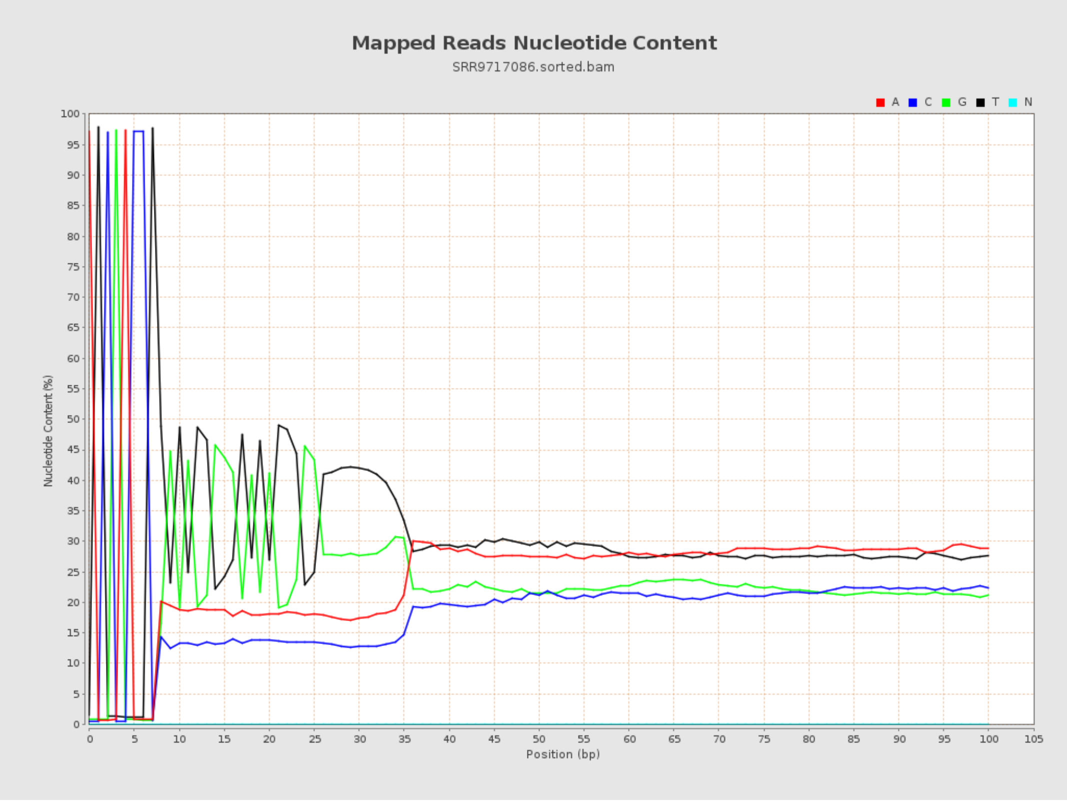
6. Results : Genome Fraction Coverage



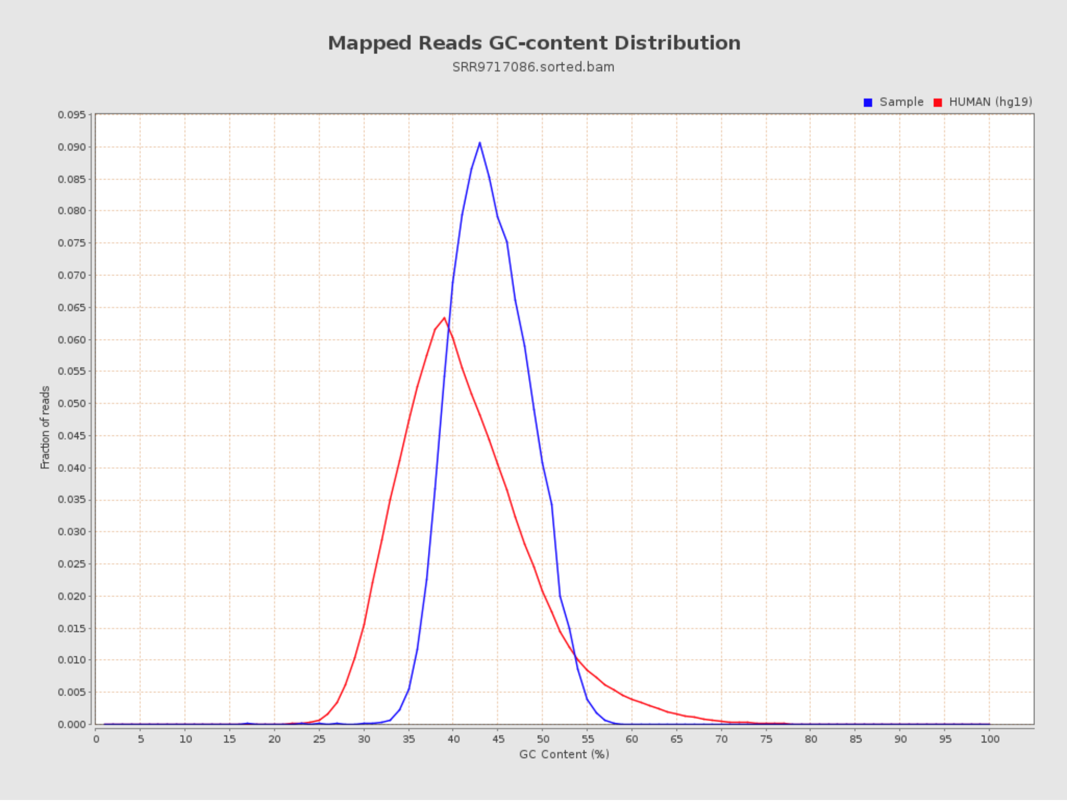
7. Results : Duplication Rate Histogram



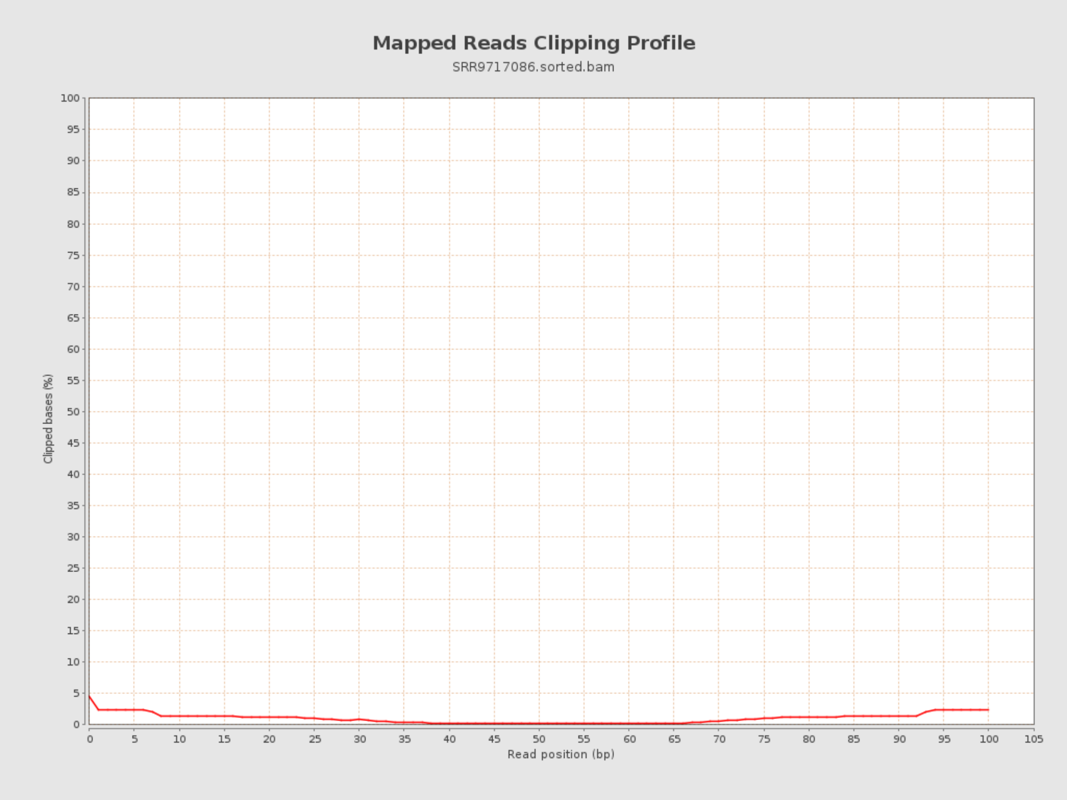
8. Results : Mapped Reads Nucleotide Content



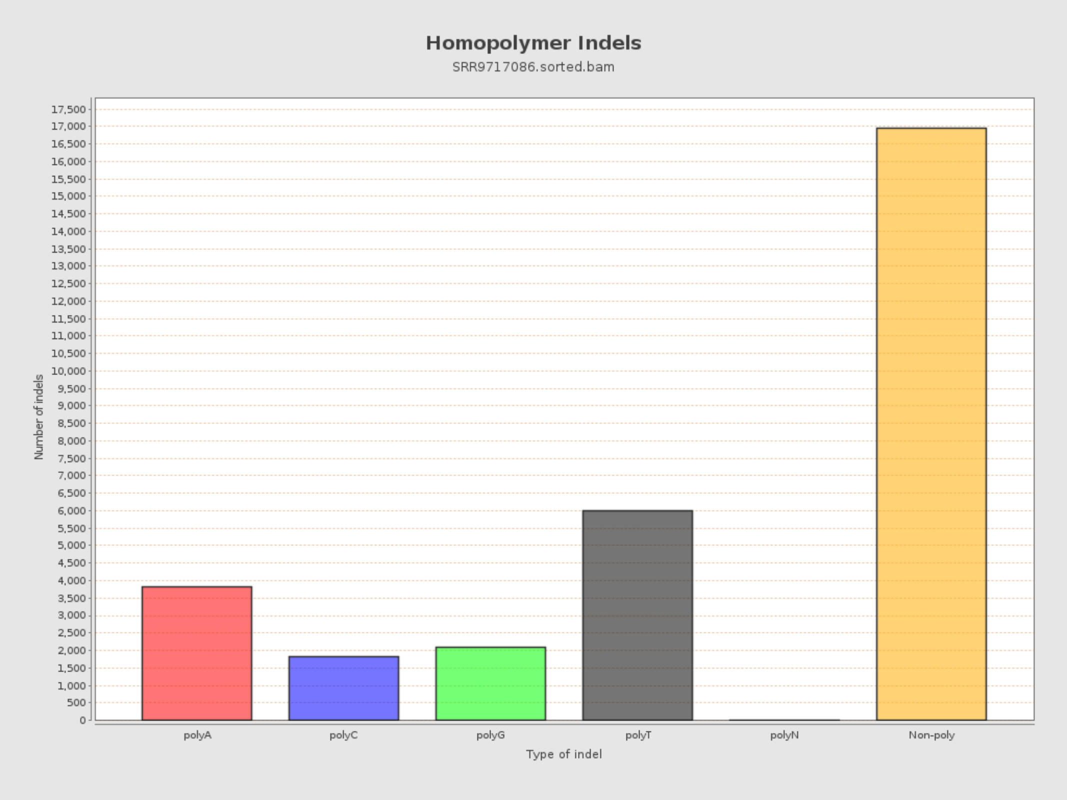
9. Results : Mapped Reads GC-content Distribution



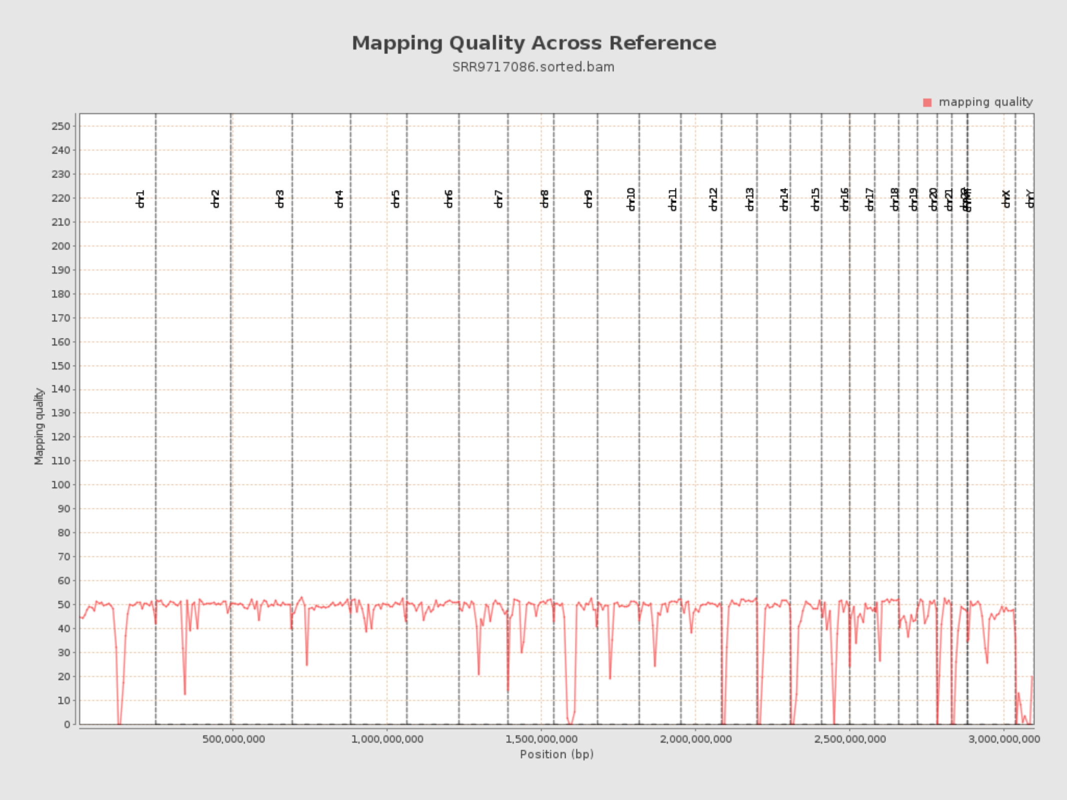
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram