Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 01:49:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717035.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_SRR9717035 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717035.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 01:49:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717035.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,328,487
Mapped reads	1,958,268 / 84.1%
Unmapped reads	370,219 / 15.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	44,474 / 1.91%
Read min/max/mean length	30 / 101 / 101.7
Duplicated reads (estimated)	66,948 / 2.88%
Duplication rate	2.22%
Clipped reads	1,999,178 / 85.86%

2.2. ACGT Content

Number/percentage of A's	38,625,471 / 26.06%
Number/percentage of C's	28,575,556 / 19.28%
Number/percentage of T's	44,997,516 / 30.36%
Number/percentage of G's	36,016,587 / 24.3%
Number/percentage of N's	18,853 / 0.01%
GC Percentage	43.57%

2.3. Coverage

Mean	0.0479

Standard Deviation	0.4275

2.4. Mapping Quality

Mean Mapping Quality	45.44

2.5. Mismatches and indels

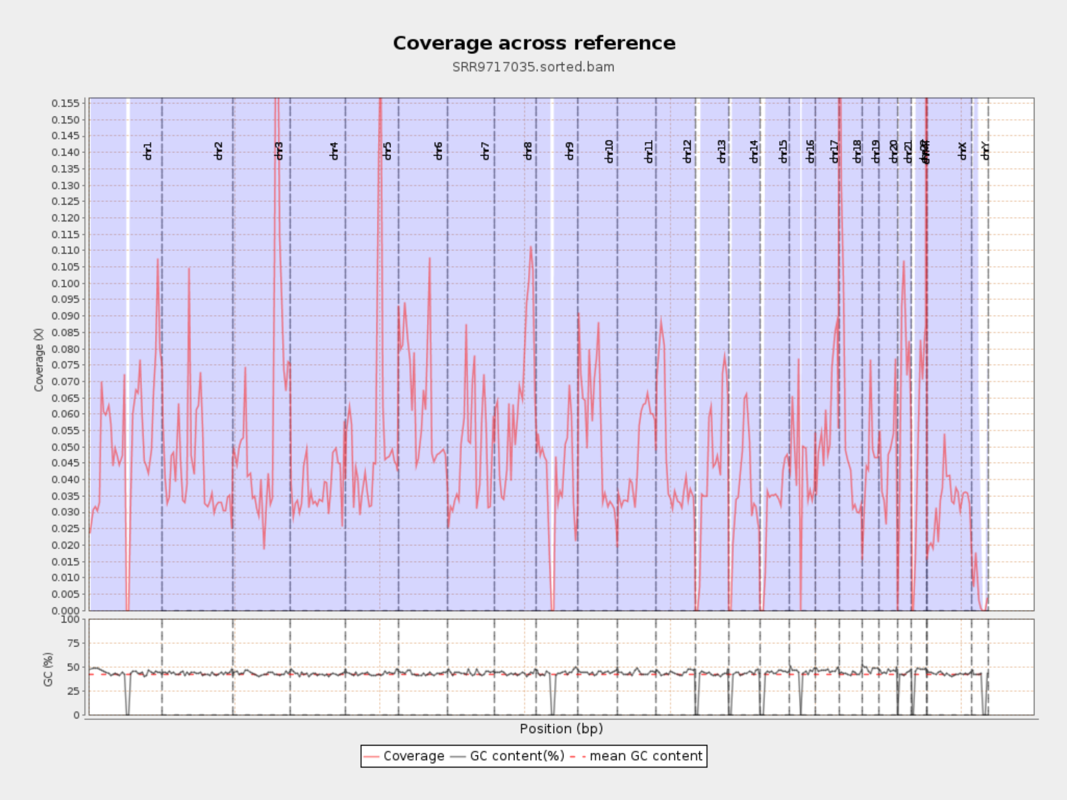
General error rate	0.76%
Mismatches	1,107,750
Insertions	12,513
Mapped reads with at least one insertion	0.63%
Deletions	32,230
Mapped reads with at least one deletion	1.62%
Homopolymer indels	41.13%

2.6. Chromosome stats

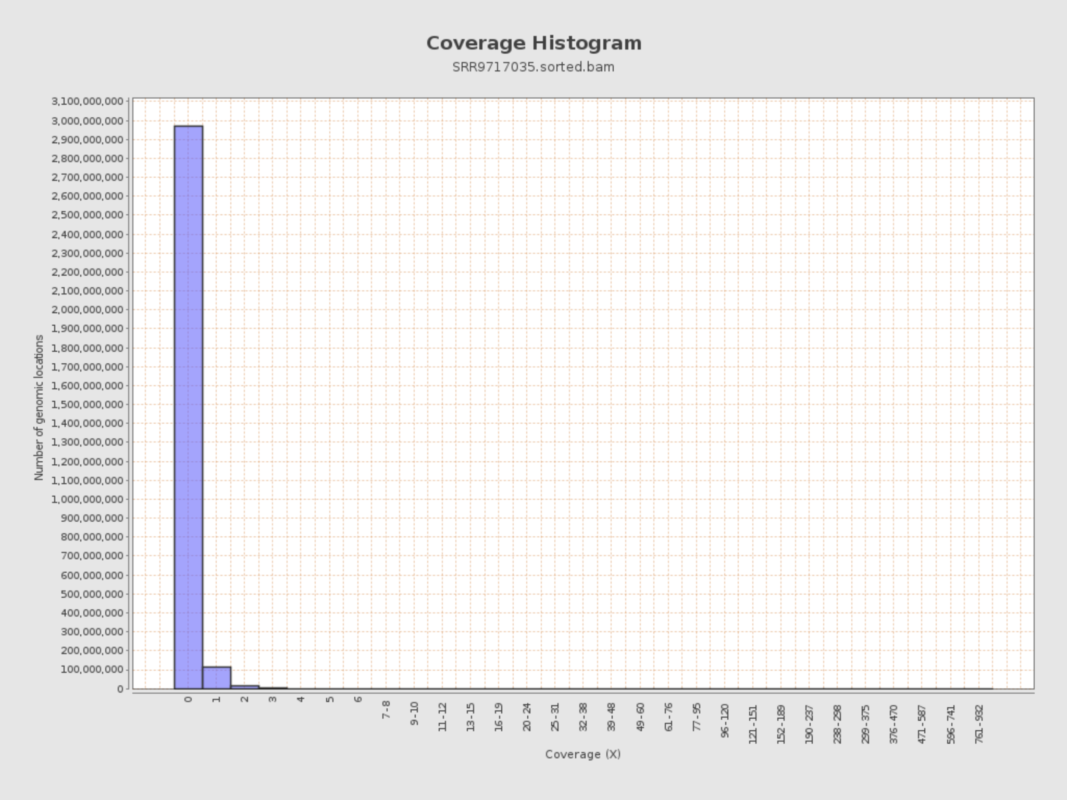
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12840490	0.0515	0.62
chr2	243199373	10496452	0.0432	0.6745
chr3	198022430	11829876	0.0597	0.2786
chr4	191154276	7167207	0.0375	0.2272
chr5	180915260	9721769	0.0537	0.2647
chr6	171115067	11115938	0.065	0.3331
chr7	159138663	7795523	0.049	0.6528

chr8	146364022	9556067	0.0653	0.556
chr9	141213431	5478607	0.0388	0.3978
chr10	135534747	7572027	0.0559	0.3778
chr11	135006516	6348893	0.047	0.3506
chr12	133851895	6114421	0.0457	0.2436
chr13	115169878	5036962	0.0437	0.2329
chr14	107349540	3760857	0.035	0.2411
chr15	102531392	3165218	0.0309	0.1964
chr16	90354753	3882396	0.043	0.2685
chr17	81195210	4784707	0.0589	0.3125
chr18	78077248	4791395	0.0614	0.791
chr19	59128983	2763002	0.0467	0.5417
chr20	63025520	2953520	0.0469	0.2829
chr21	48129895	3296319	0.0685	0.309
chr22	51304566	2463463	0.048	0.2524
chrMT	16571	21784	1.3146	1.6311
chrX	155270560	5032053	0.0324	0.2666
chrY	59373566	300564	0.0051	0.159

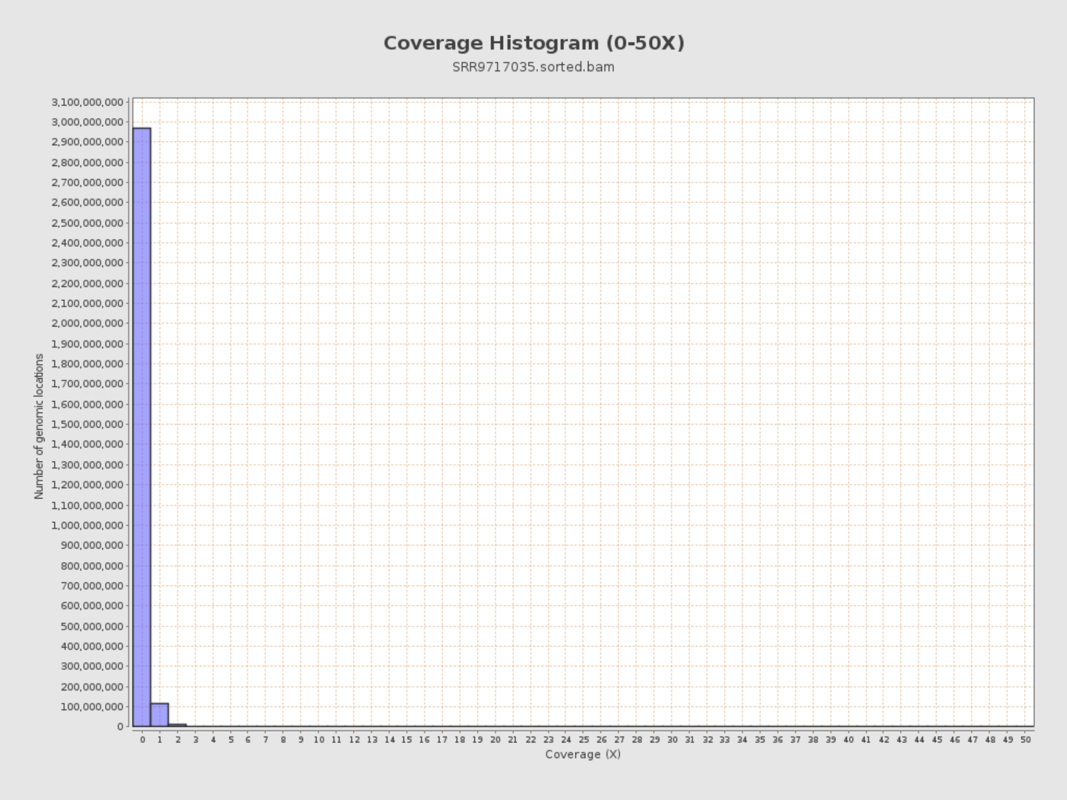
3. Results : Coverage across reference



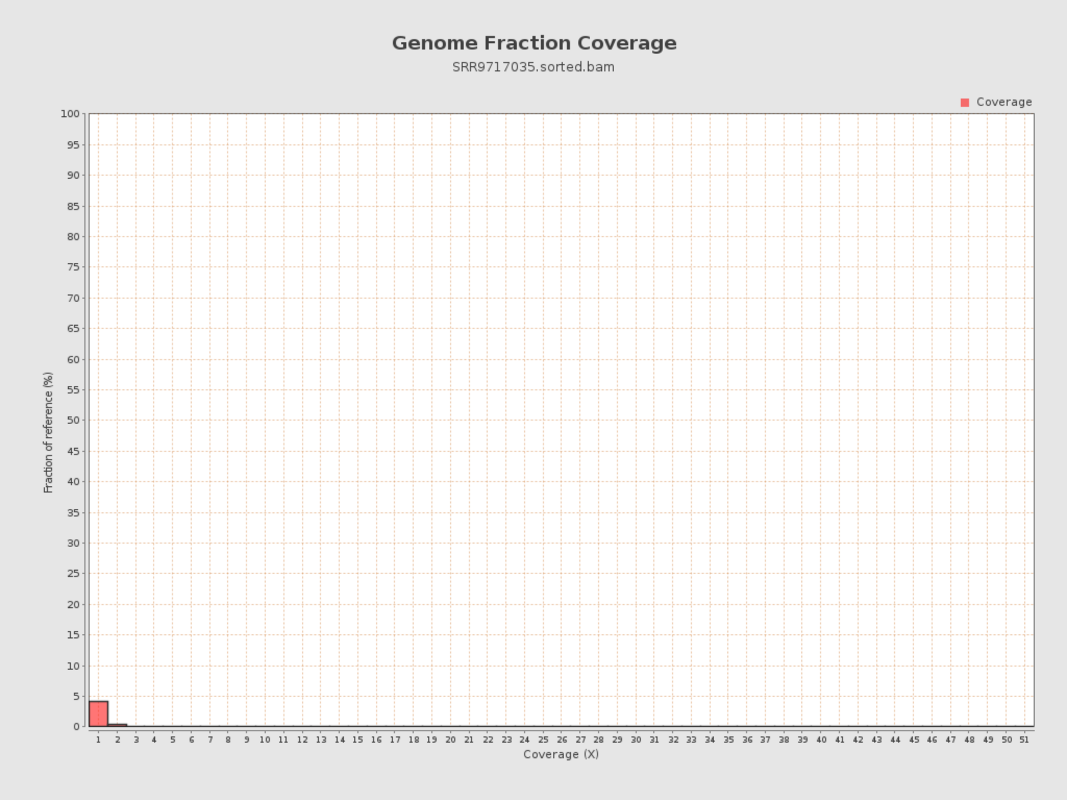
4. Results : Coverage Histogram



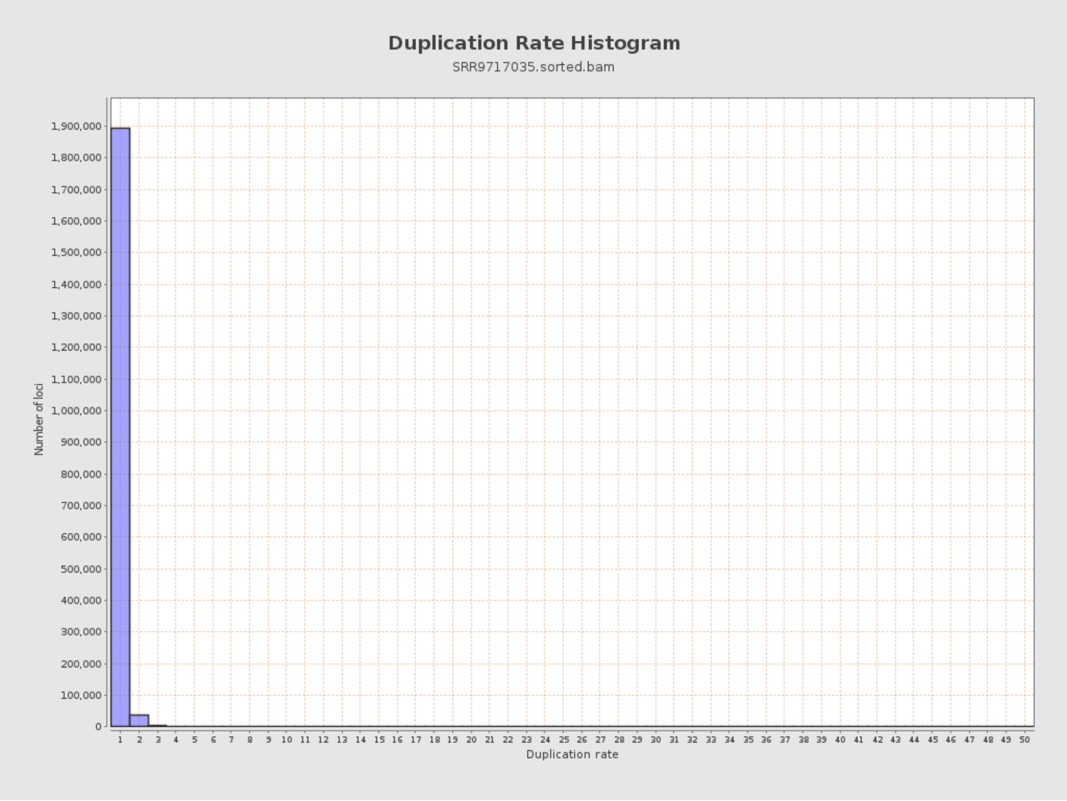
5. Results : Coverage Histogram (0-50X)



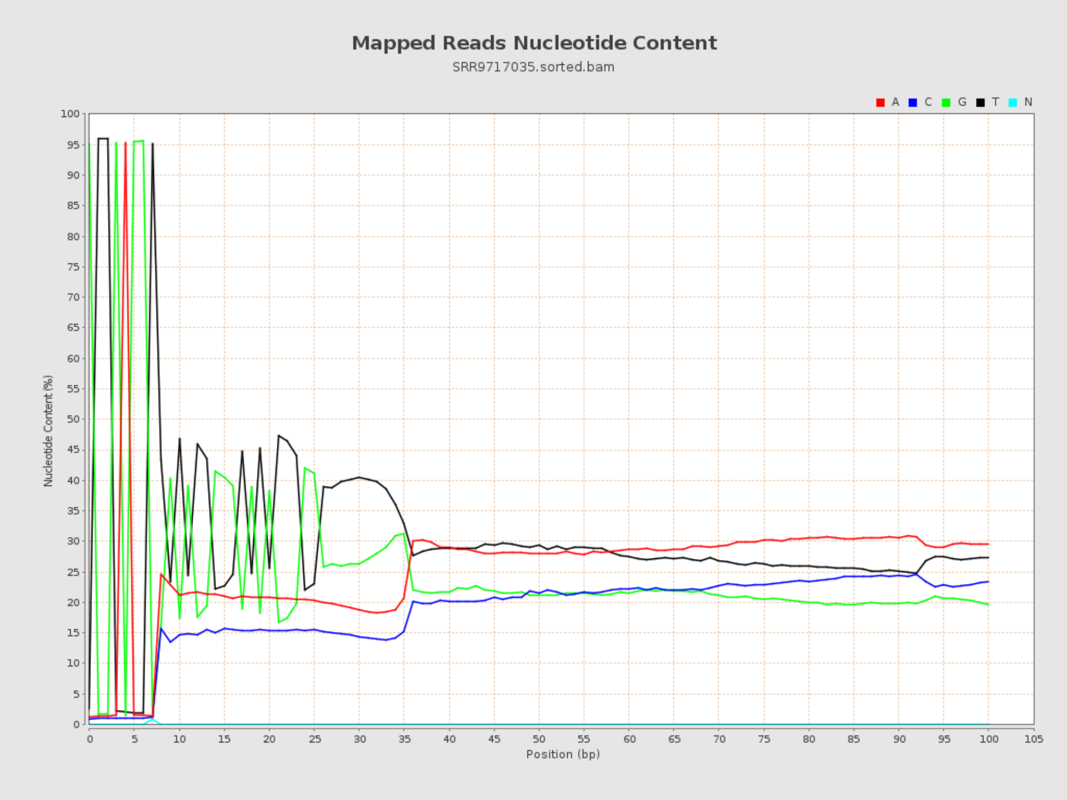
6. Results : Genome Fraction Coverage



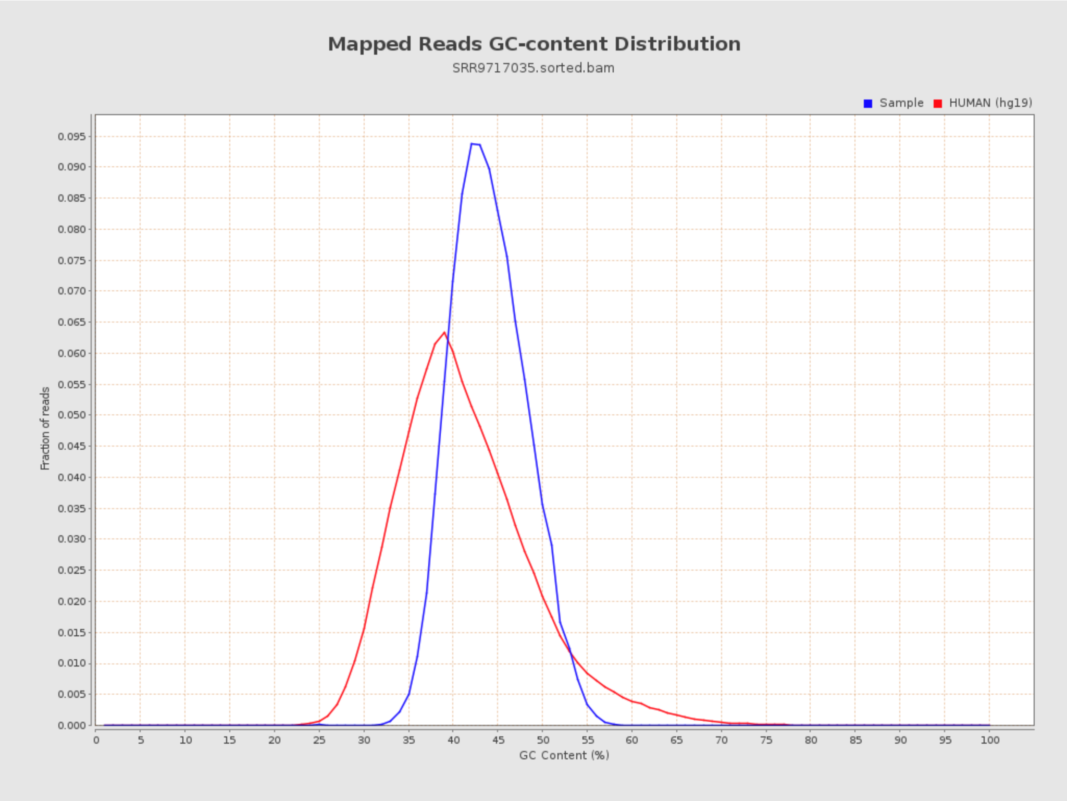
7. Results : Duplication Rate Histogram



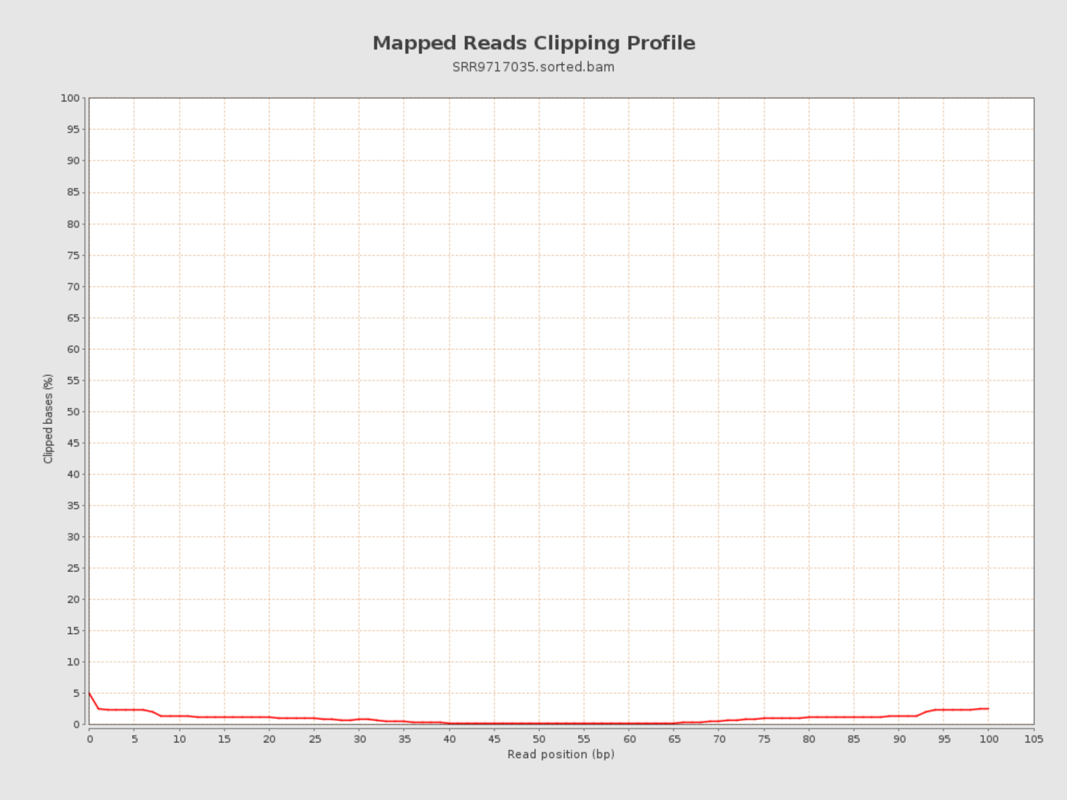
8. Results : Mapped Reads Nucleotide Content



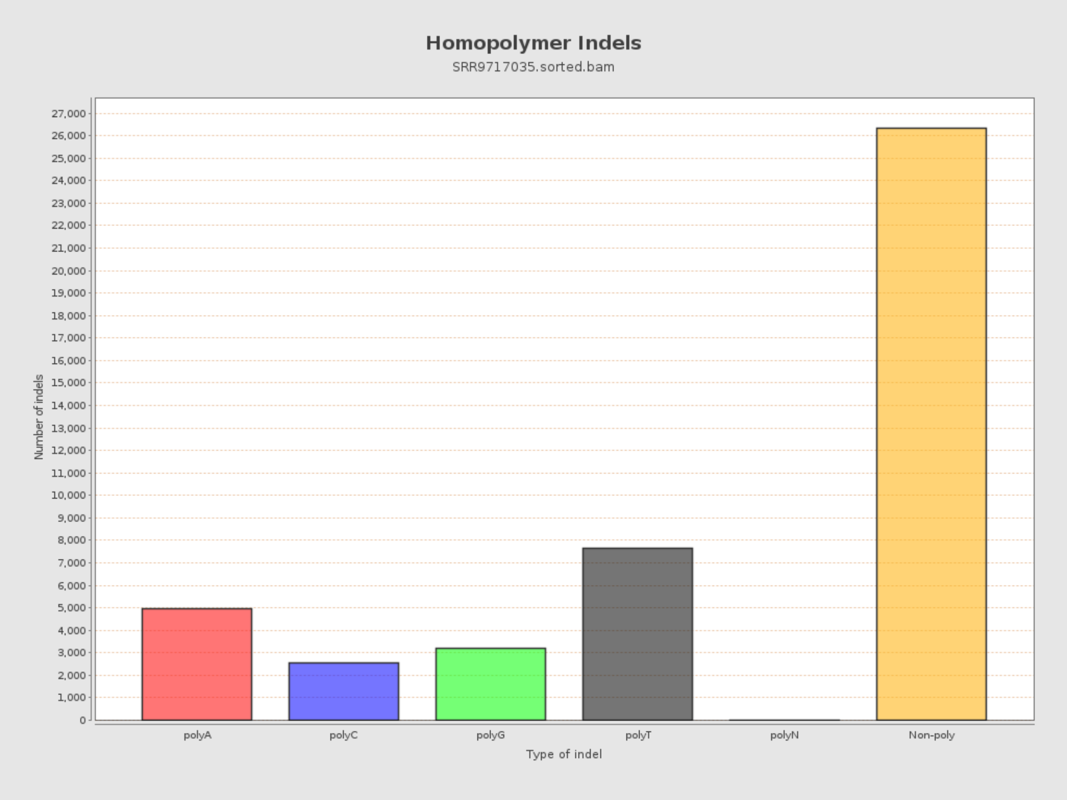
9. Results : Mapped Reads GC-content Distribution



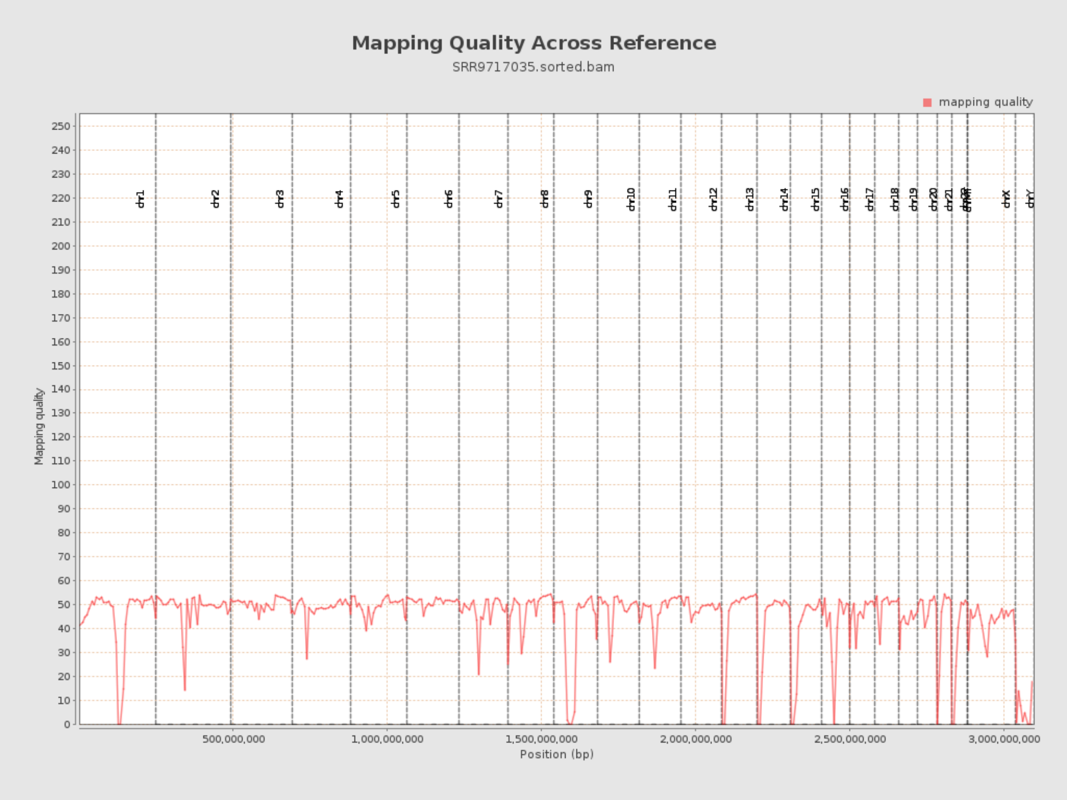
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram