Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 01:27:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717026.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_SRR9717026 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717026.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 01:27:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717026.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,173,383
Mapped reads	2,035,811 / 93.67%
Unmapped reads	137,572 / 6.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	44,394 / 2.04%
Read min/max/mean length	30 / 101 / 101.74
Duplicated reads (estimated)	105,099 / 4.84%
Duplication rate	4.01%
Clipped reads	2,075,476 / 95.5%

2.2. ACGT Content

Number/percentage of A's	39,912,435 / 25.28%
Number/percentage of C's	33,239,223 / 21.06%
Number/percentage of T's	46,250,261 / 29.3%
Number/percentage of G's	38,443,408 / 24.35%
Number/percentage of N's	6,163 / 0%
GC Percentage	45.41%

2.3. Coverage

Mean	0.051

Standard Deviation	0.411

2.4. Mapping Quality

Mean Mapping Quality	46.22

2.5. Mismatches and indels

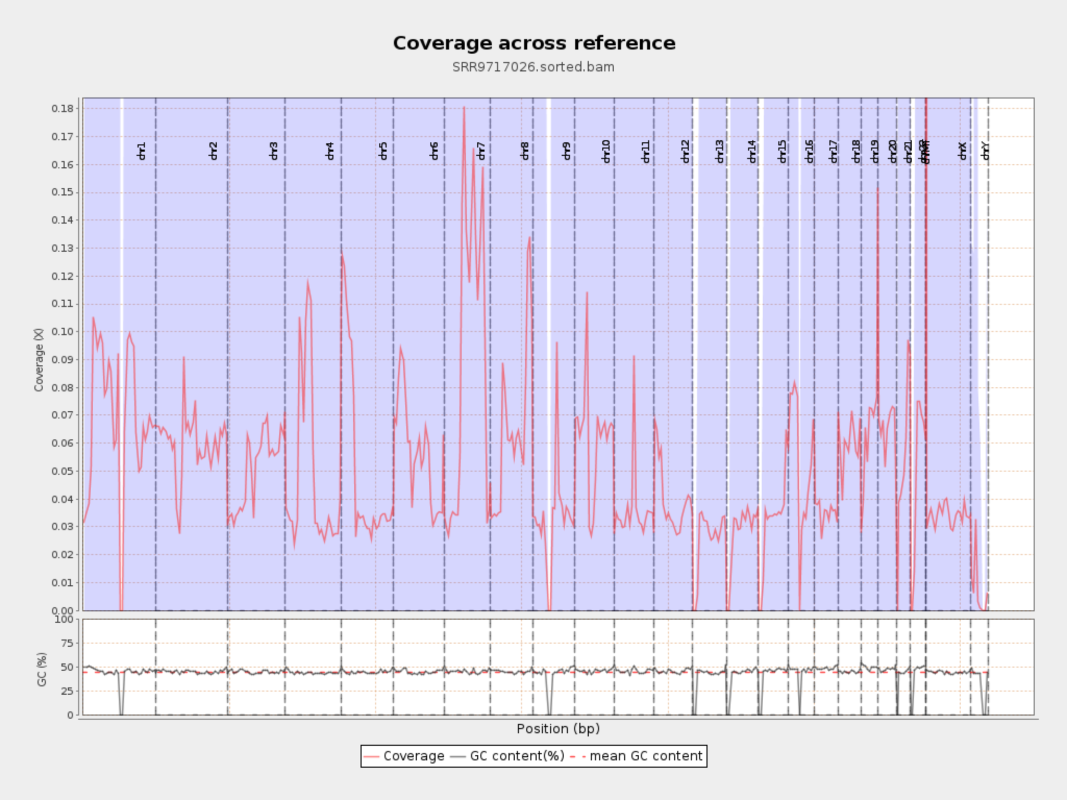
General error rate	0.67%
Mismatches	1,024,703
Insertions	14,285
Mapped reads with at least one insertion	0.69%
Deletions	28,512
Mapped reads with at least one deletion	1.38%
Homopolymer indels	38.7%

2.6. Chromosome stats

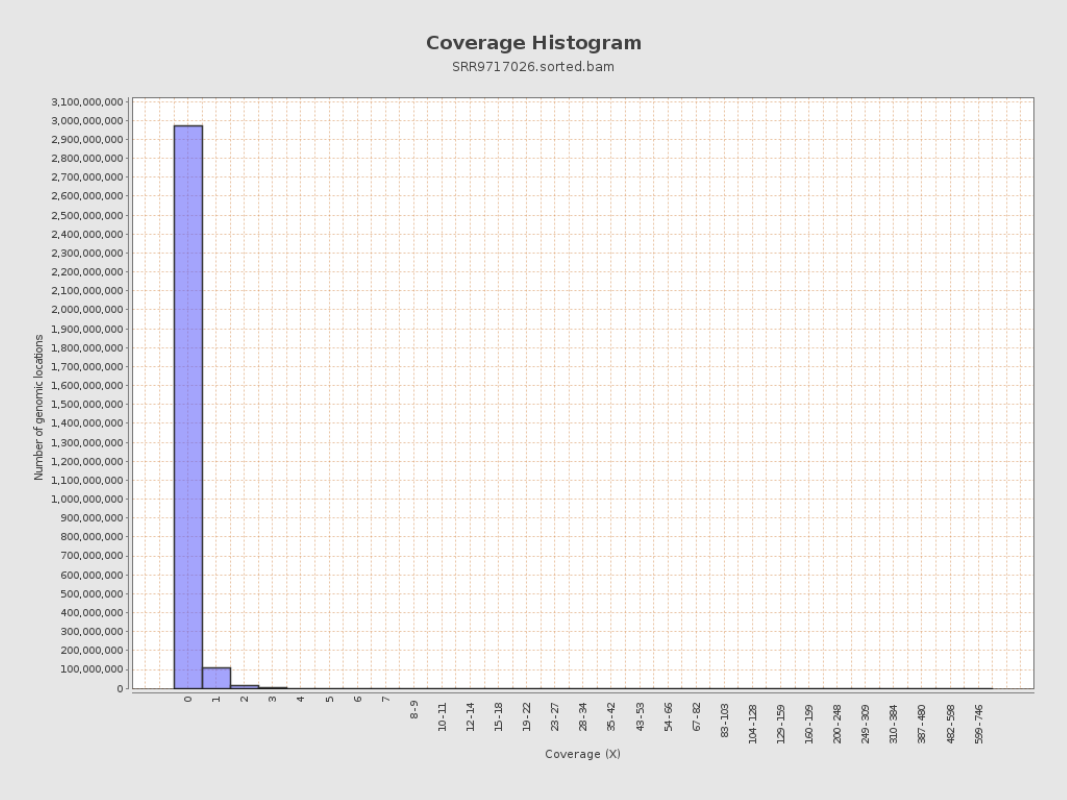
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17200692	0.069	0.7274
chr2	243199373	14659010	0.0603	0.431
chr3	198022430	10053176	0.0508	0.2721
chr4	191154276	9249722	0.0484	0.3813
chr5	180915260	9253506	0.0511	0.2761
chr6	171115067	9698097	0.0567	0.2987
chr7	159138663	14360940	0.0902	0.7407

chr8	146364022	9719575	0.0664	0.4214
chr9	141213431	4707964	0.0333	0.2818
chr10	135534747	8333205	0.0615	0.5473
chr11	135006516	4920199	0.0364	0.3137
chr12	133851895	5412837	0.0404	0.2413
chr13	115169878	2914611	0.0253	0.1859
chr14	107349540	2982530	0.0278	0.2081
chr15	102531392	3190845	0.0311	0.2108
chr16	90354753	4753916	0.0526	0.296
chr17	81195210	2871628	0.0354	0.2465
chr18	78077248	4639188	0.0594	0.4258
chr19	59128983	3877410	0.0656	0.526
chr20	63025520	4161484	0.066	0.3223
chr21	48129895	2676497	0.0556	0.3695
chr22	51304566	2457778	0.0479	0.2682
chrMT	16571	30614	1.8474	1.859
chrX	155270560	5337656	0.0344	0.2357
chrY	59373566	447017	0.0075	0.2923

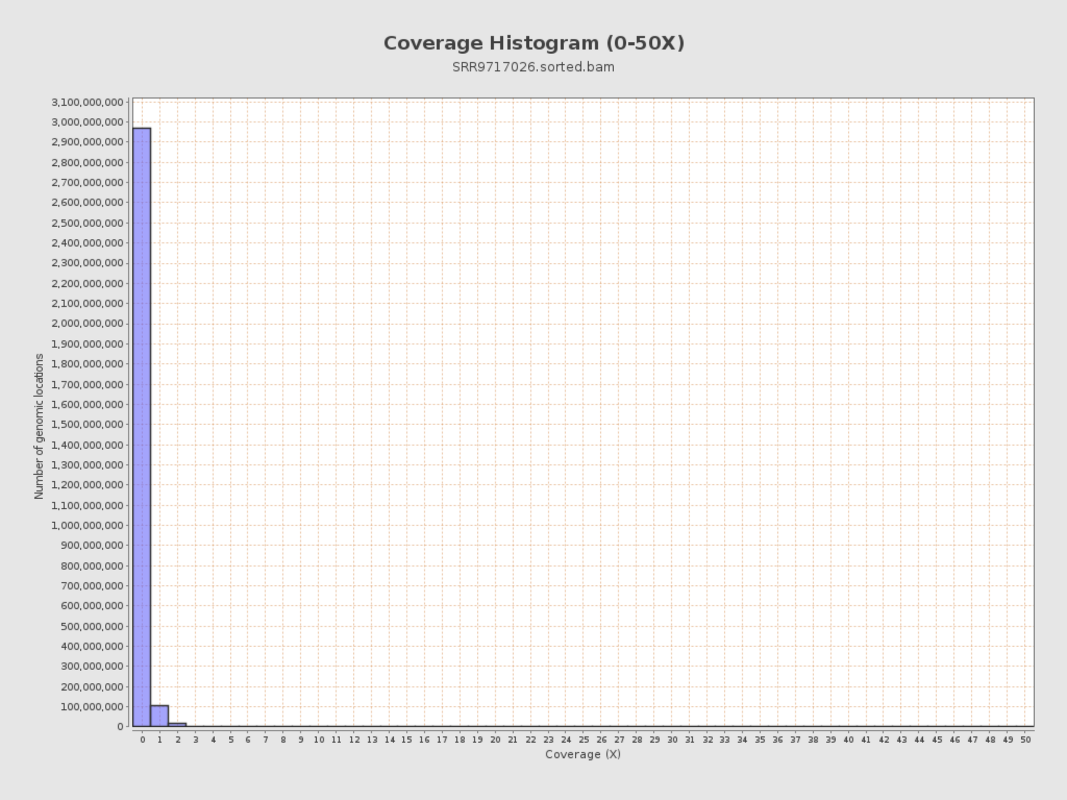
3. Results : Coverage across reference



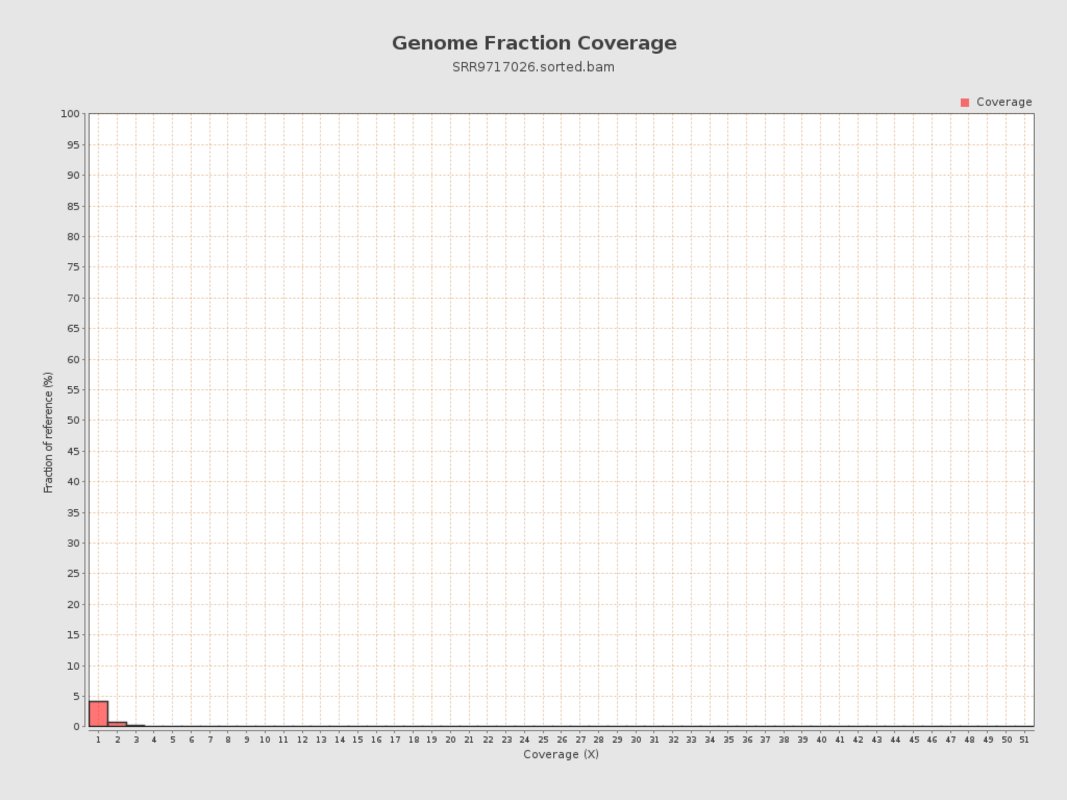
4. Results : Coverage Histogram



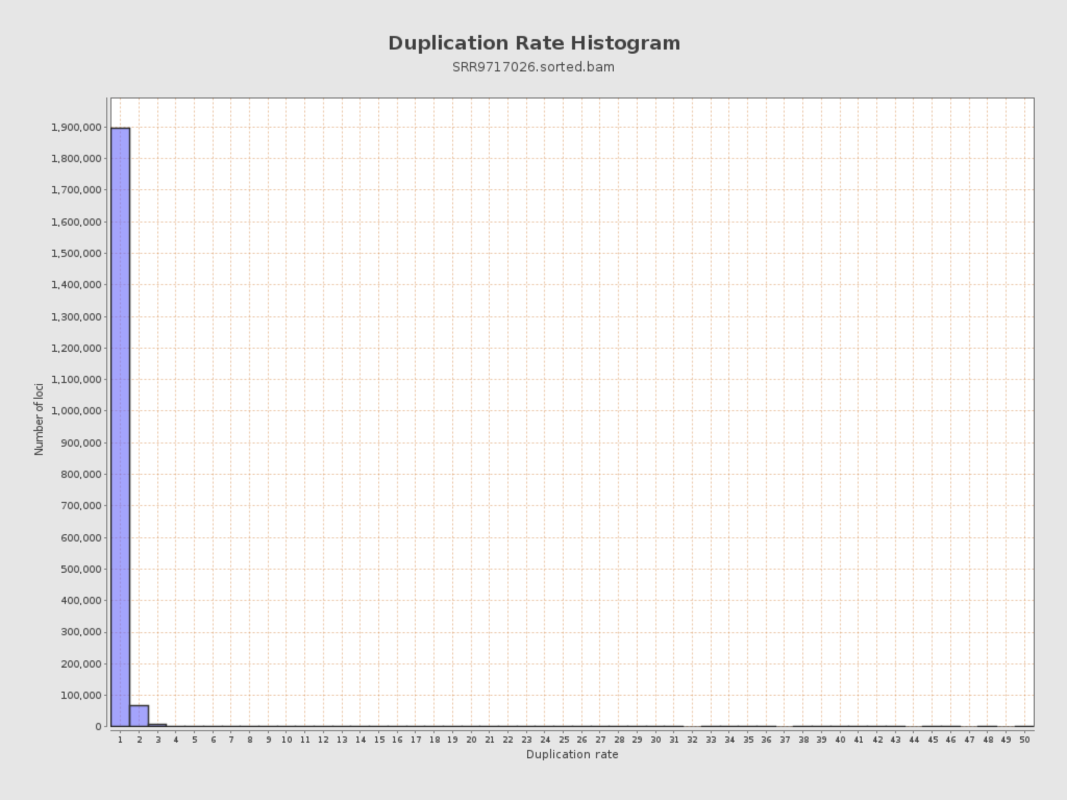
5. Results : Coverage Histogram (0-50X)



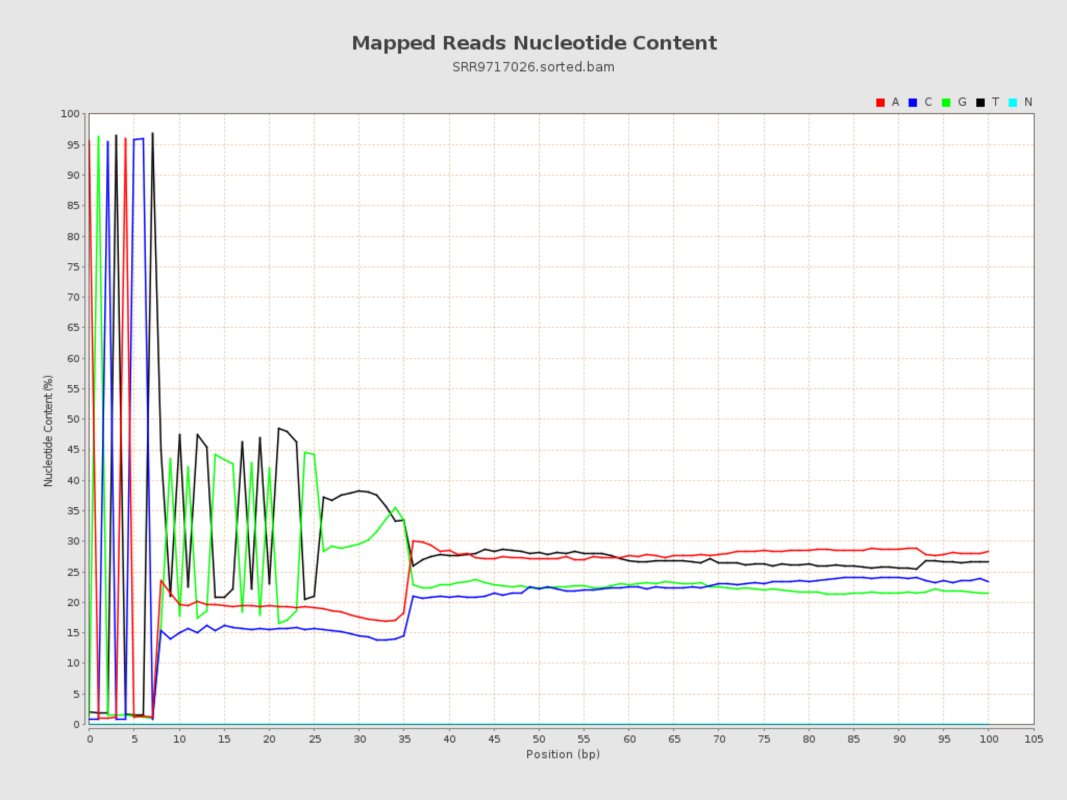
6. Results : Genome Fraction Coverage



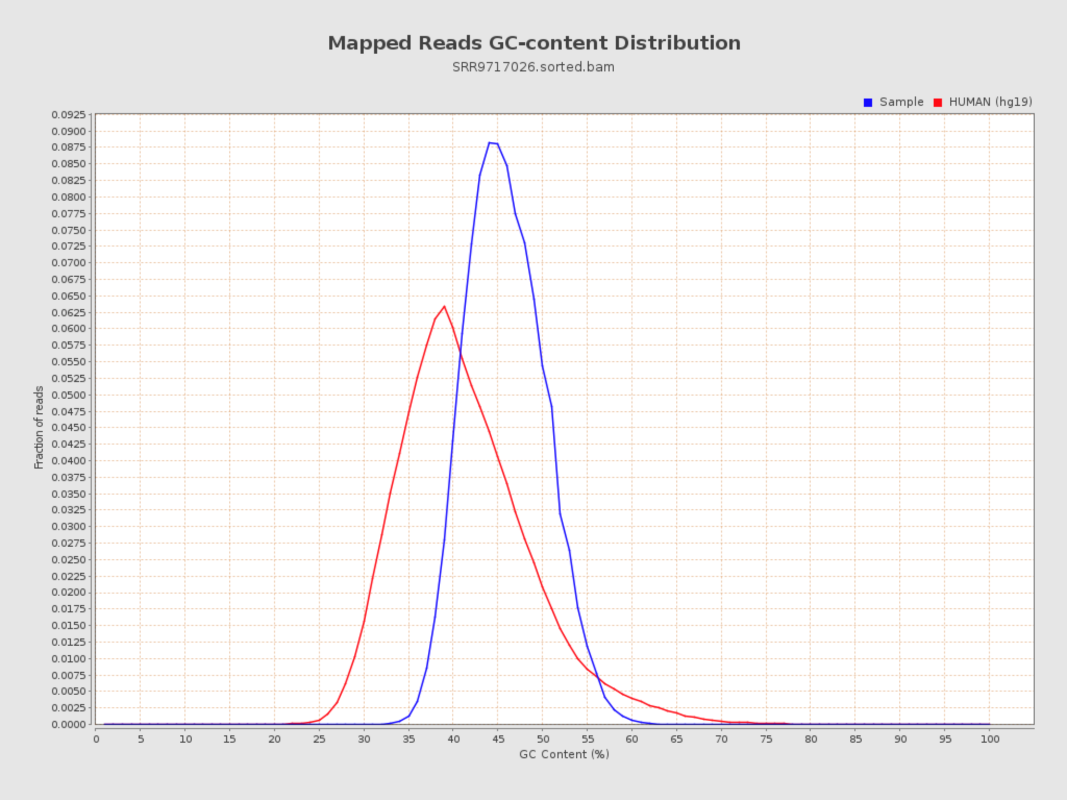
7. Results : Duplication Rate Histogram



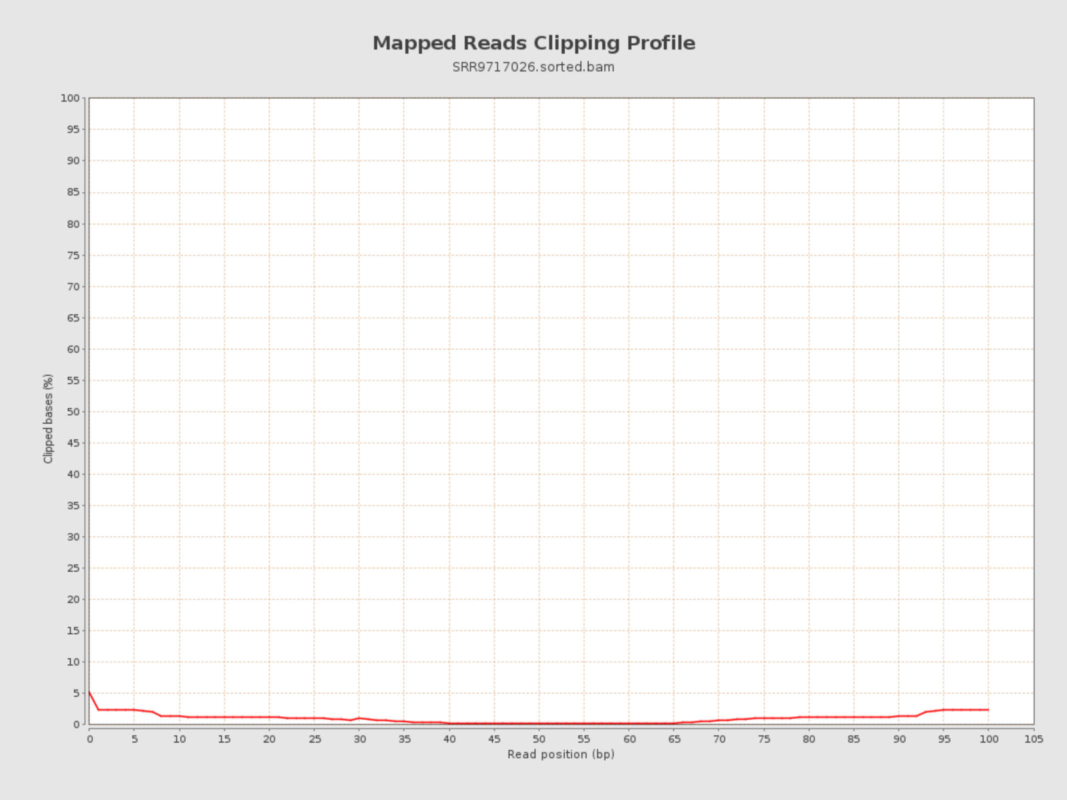
8. Results : Mapped Reads Nucleotide Content



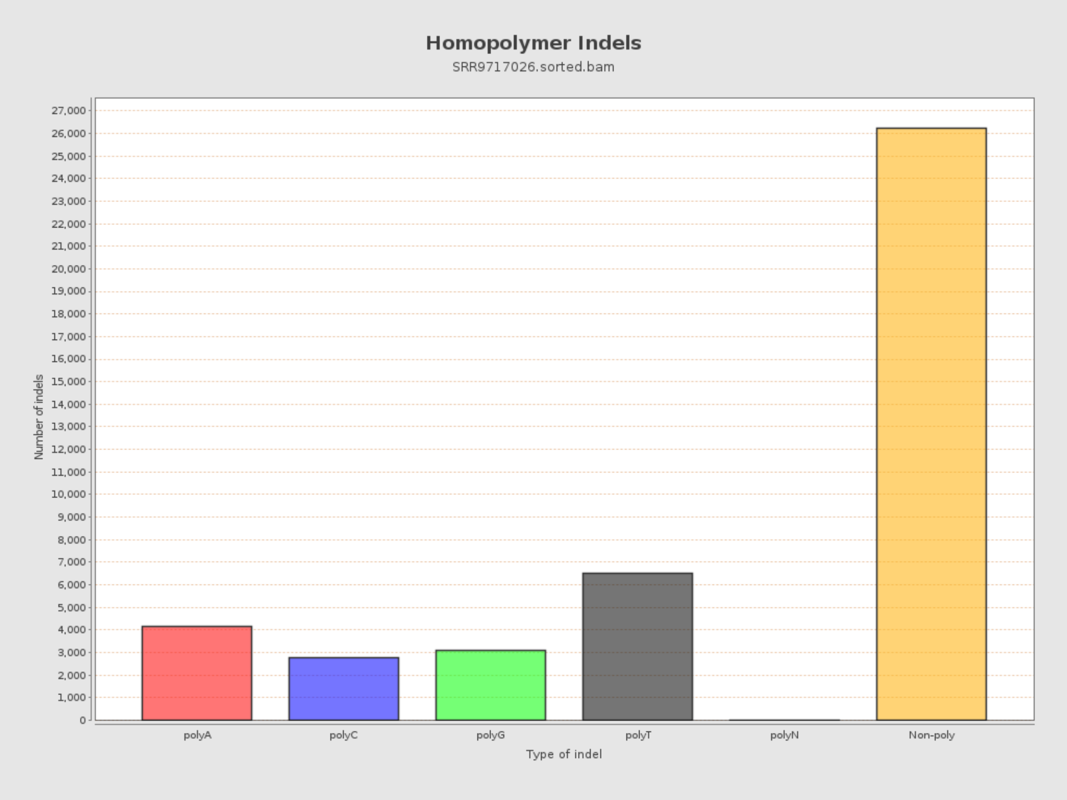
9. Results : Mapped Reads GC-content Distribution



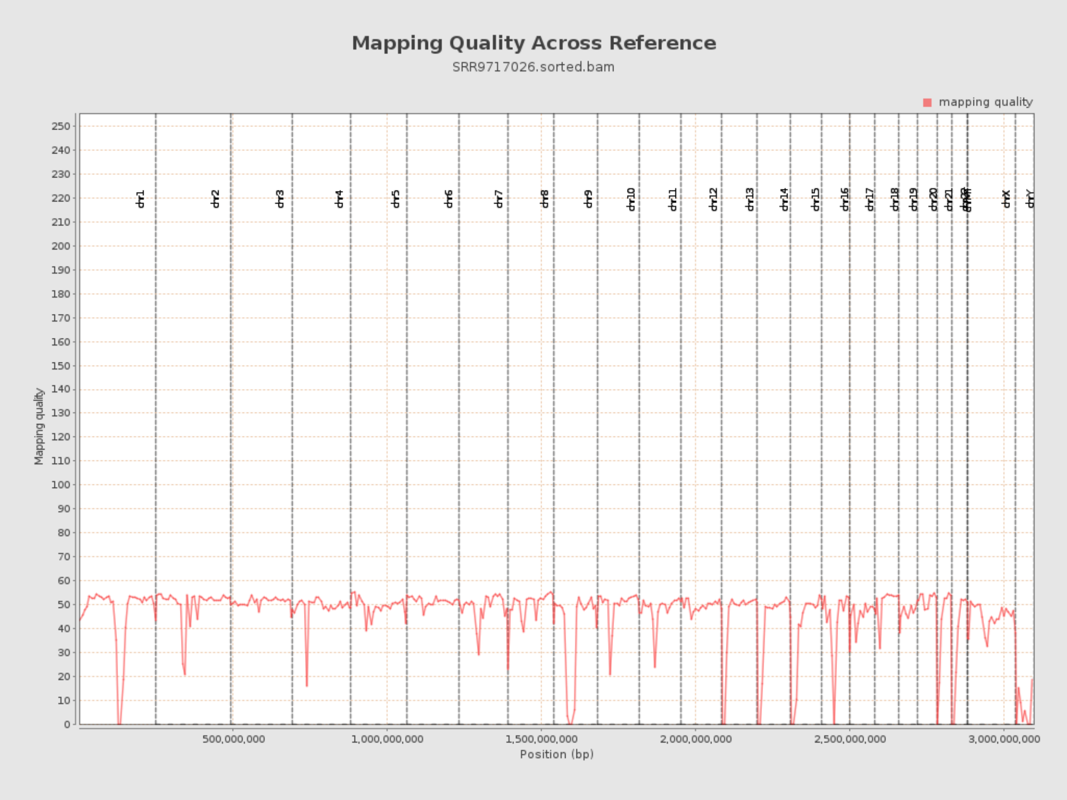
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram