Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 11:03:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716770.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_SRR9716770 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716770.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 11:03:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716770.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,322,120
Mapped reads	2,192,170 / 94.4%
Unmapped reads	129,950 / 5.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	45,392 / 1.95%
Read min/max/mean length	30 / 101 / 101.71
Duplicated reads (estimated)	135,285 / 5.83%
Duplication rate	4.78%
Clipped reads	2,234,298 / 96.22%

2.2. ACGT Content

Number/percentage of A's	41,203,848 / 24.16%
Number/percentage of C's	34,859,458 / 20.44%
Number/percentage of T's	51,188,520 / 30.01%
Number/percentage of G's	43,301,535 / 25.39%
Number/percentage of N's	6,677 / 0%
GC Percentage	45.83%

2.3. Coverage

Mean	0.0551

Standard Deviation	0.4425

2.4. Mapping Quality

Mean Mapping Quality	46.61

2.5. Mismatches and indels

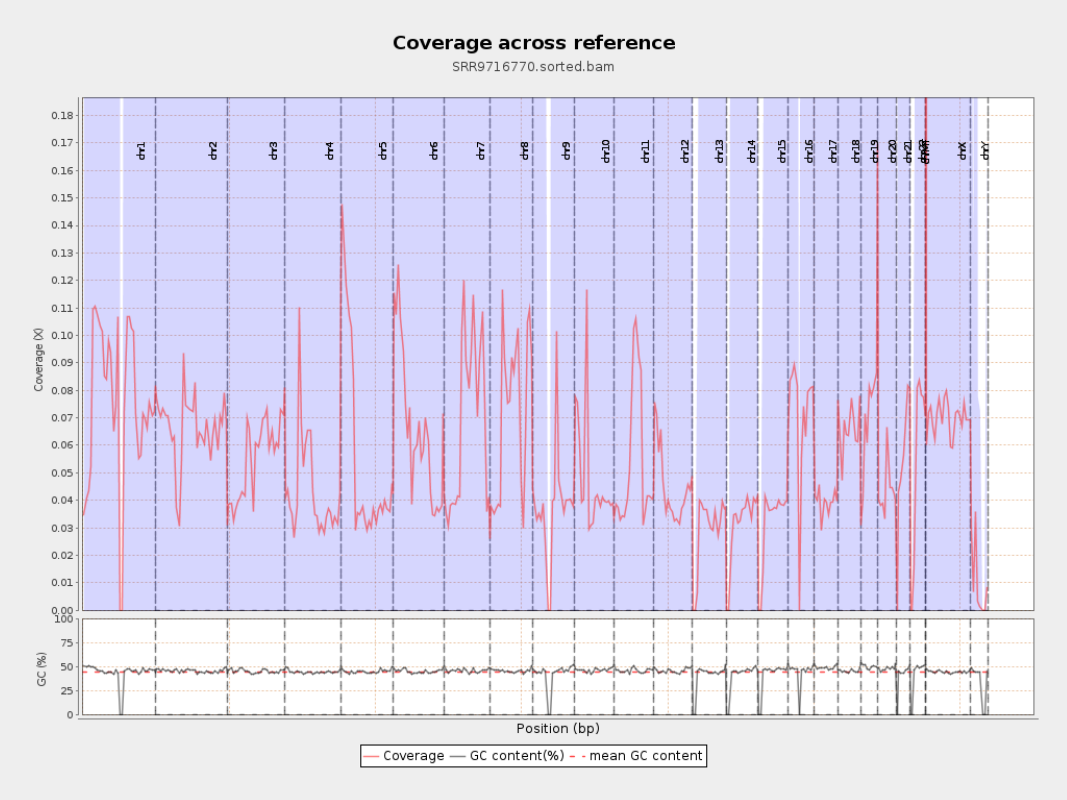
General error rate	0.66%
Mismatches	1,091,554
Insertions	14,011
Mapped reads with at least one insertion	0.63%
Deletions	31,126
Mapped reads with at least one deletion	1.4%
Homopolymer indels	39.87%

2.6. Chromosome stats

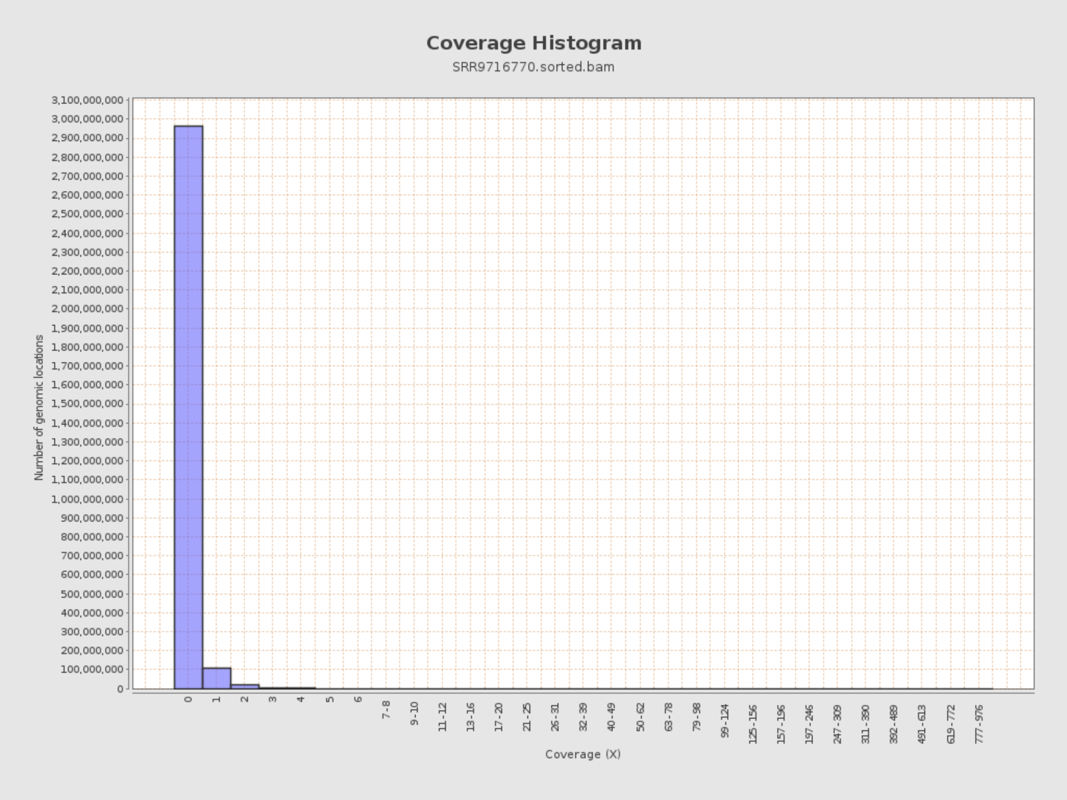
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18804991	0.0754	0.8846
chr2	243199373	16180558	0.0665	0.4585
chr3	198022430	10914238	0.0551	0.2912
chr4	191154276	8326689	0.0436	0.3786
chr5	180915260	10190367	0.0563	0.2972
chr6	171115067	11207330	0.0655	0.3357
chr7	159138663	10882132	0.0684	0.5754

chr8	146364022	10494160	0.0717	0.4639
chr9	141213431	5259940	0.0372	0.2997
chr10	135534747	6481354	0.0478	0.553
chr11	135006516	7281807	0.0539	0.362
chr12	133851895	6064573	0.0453	0.2609
chr13	115169878	3343698	0.029	0.2041
chr14	107349540	3337111	0.0311	0.2274
chr15	102531392	3196169	0.0312	0.2111
chr16	90354753	6336877	0.0701	0.3515
chr17	81195210	3203732	0.0395	0.2857
chr18	78077248	5116856	0.0655	0.4833
chr19	59128983	4312154	0.0729	0.6206
chr20	63025520	2742300	0.0435	0.2736
chr21	48129895	2693860	0.056	0.3617
chr22	51304566	2747649	0.0536	0.2962
chrMT	16571	48003	2.8968	2.5809
chrX	155270560	10876979	0.0701	0.3456
chrY	59373566	580972	0.0098	0.3326

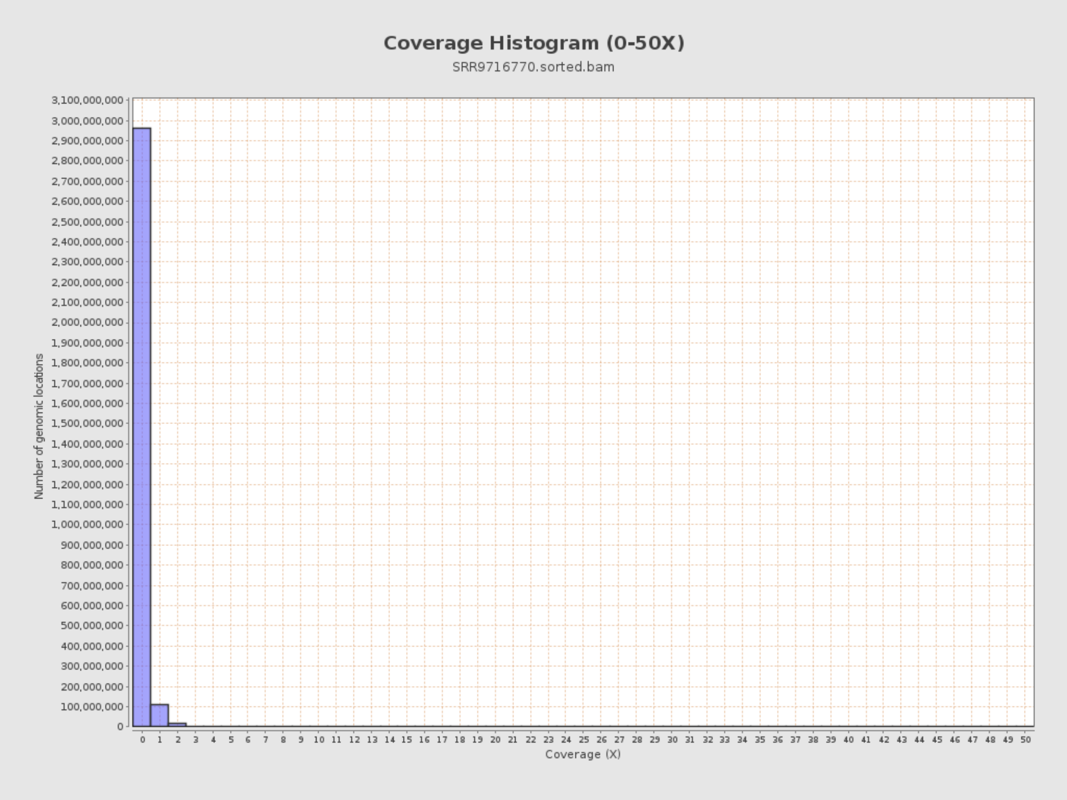
3. Results : Coverage across reference



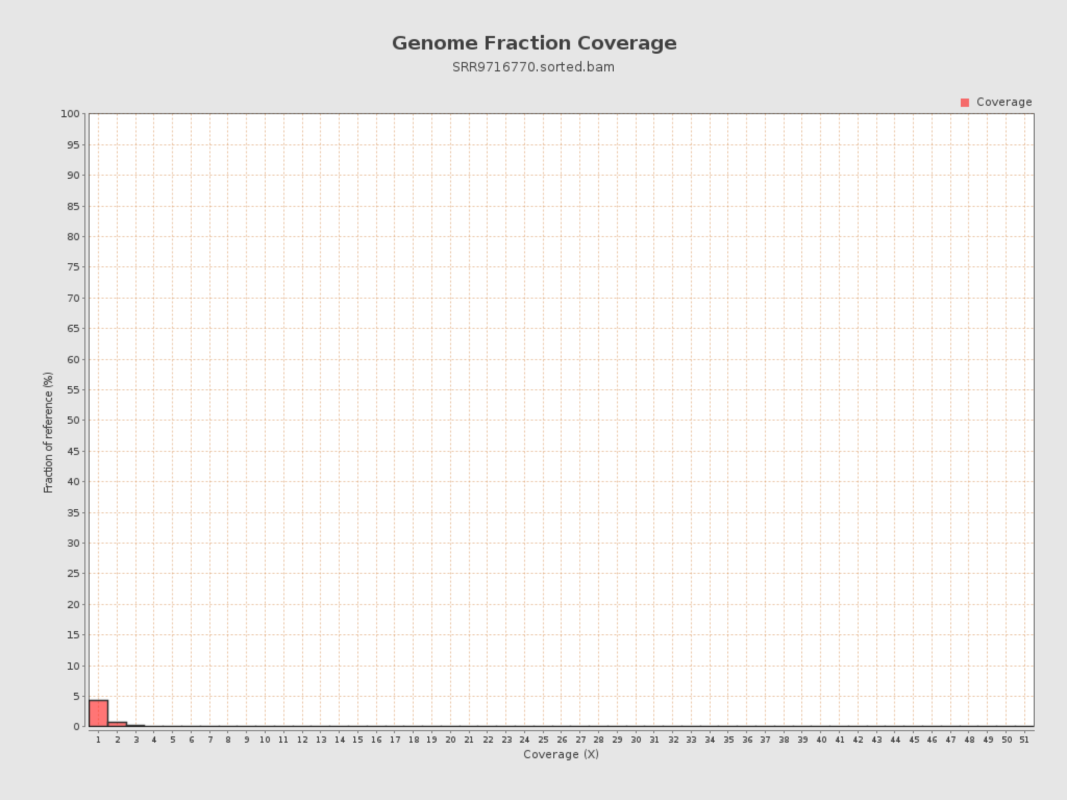
4. Results : Coverage Histogram



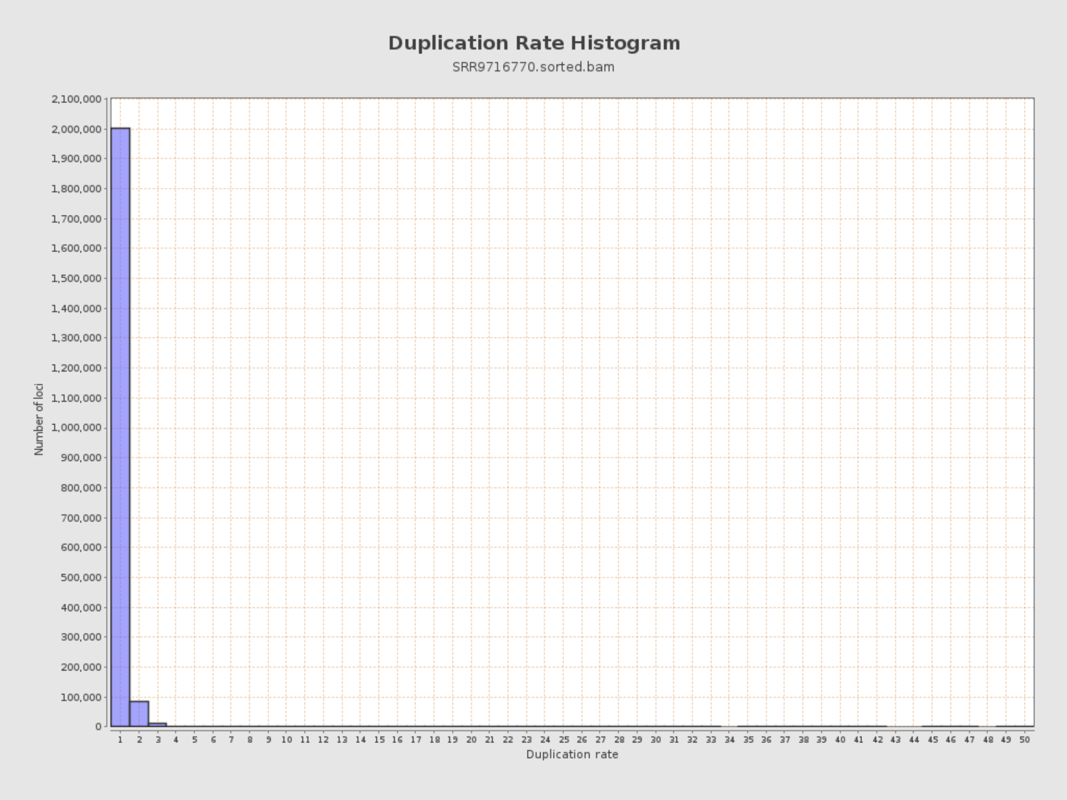
5. Results : Coverage Histogram (0-50X)



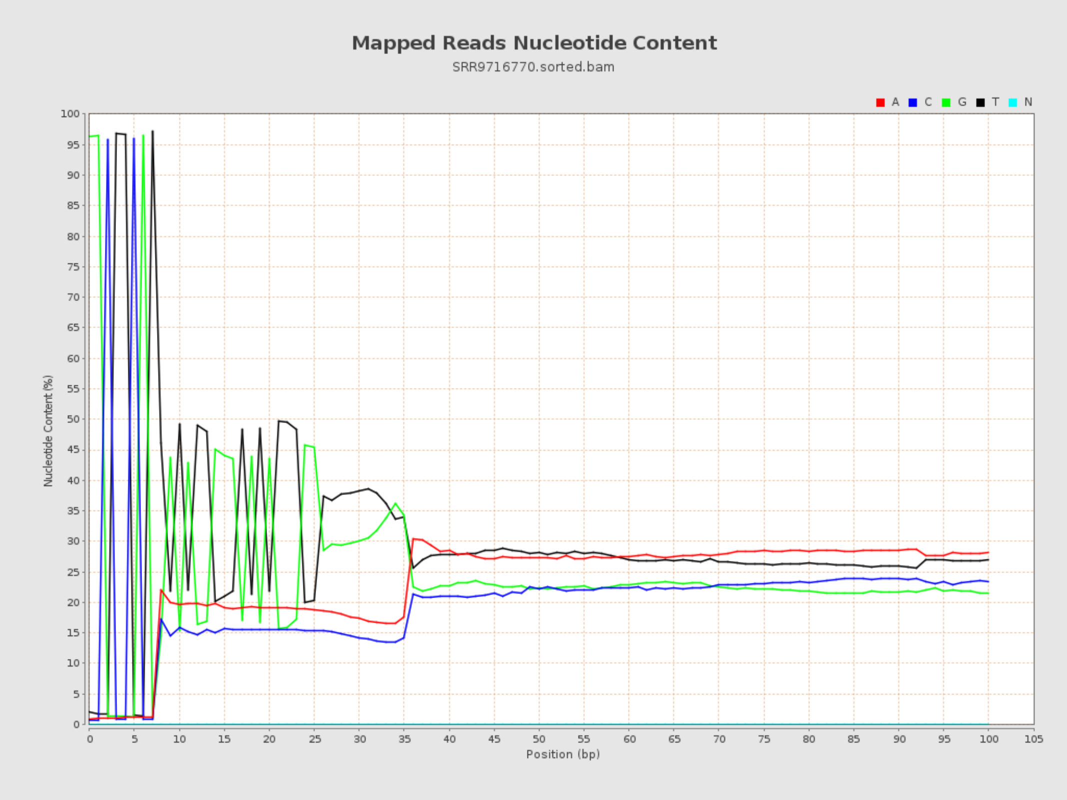
6. Results : Genome Fraction Coverage



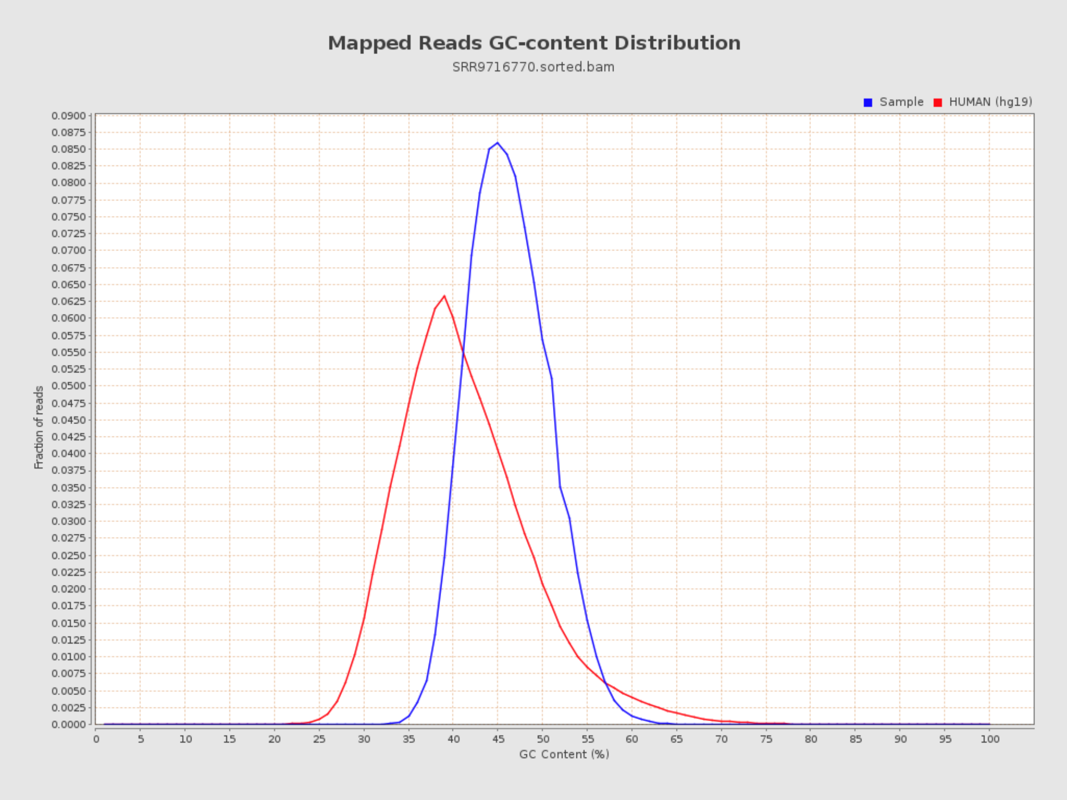
7. Results : Duplication Rate Histogram



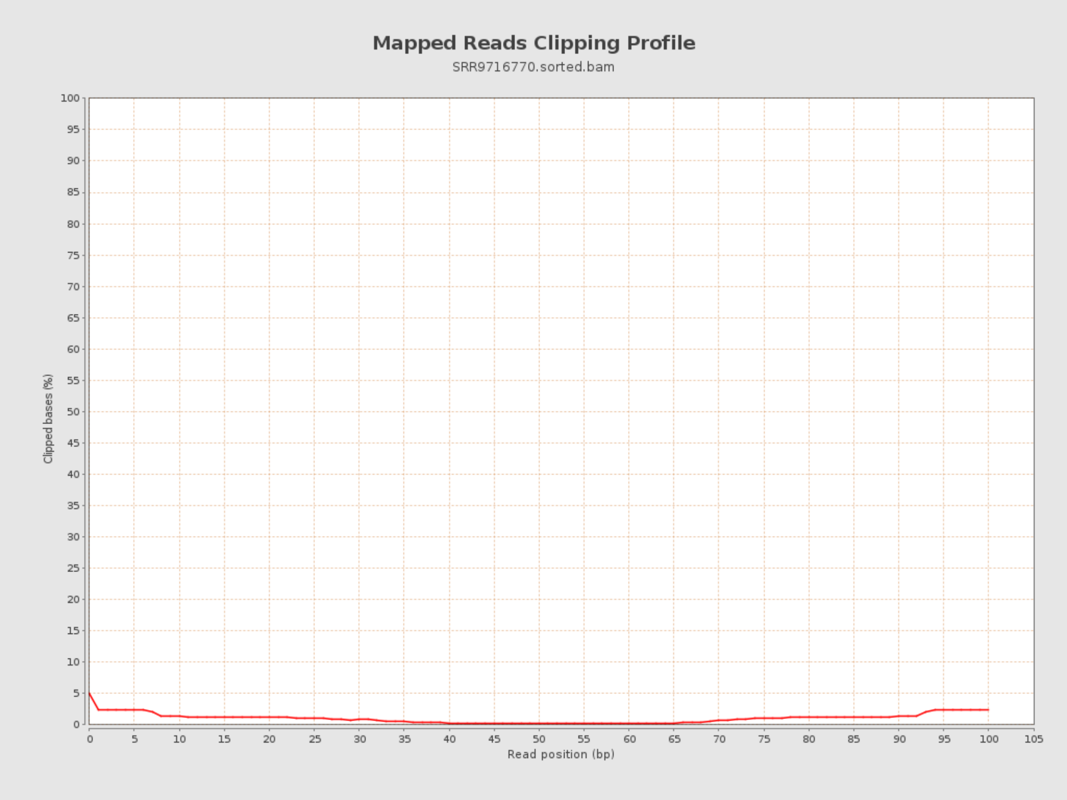
8. Results : Mapped Reads Nucleotide Content



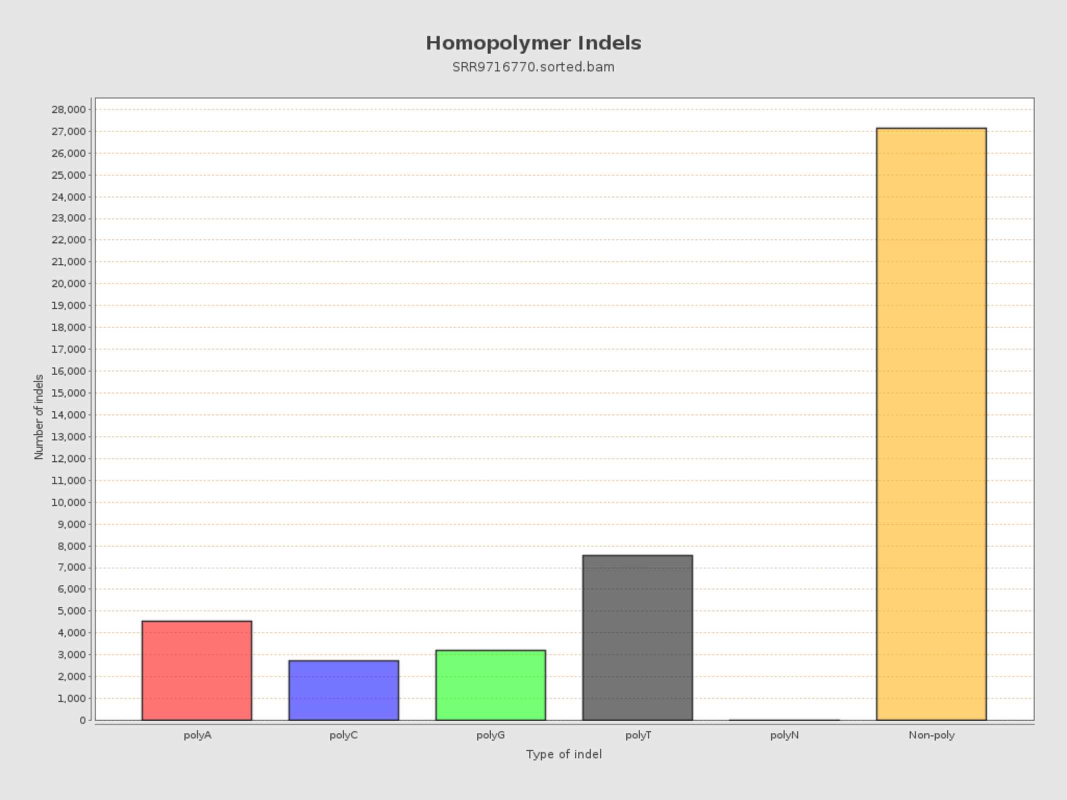
9. Results : Mapped Reads GC-content Distribution



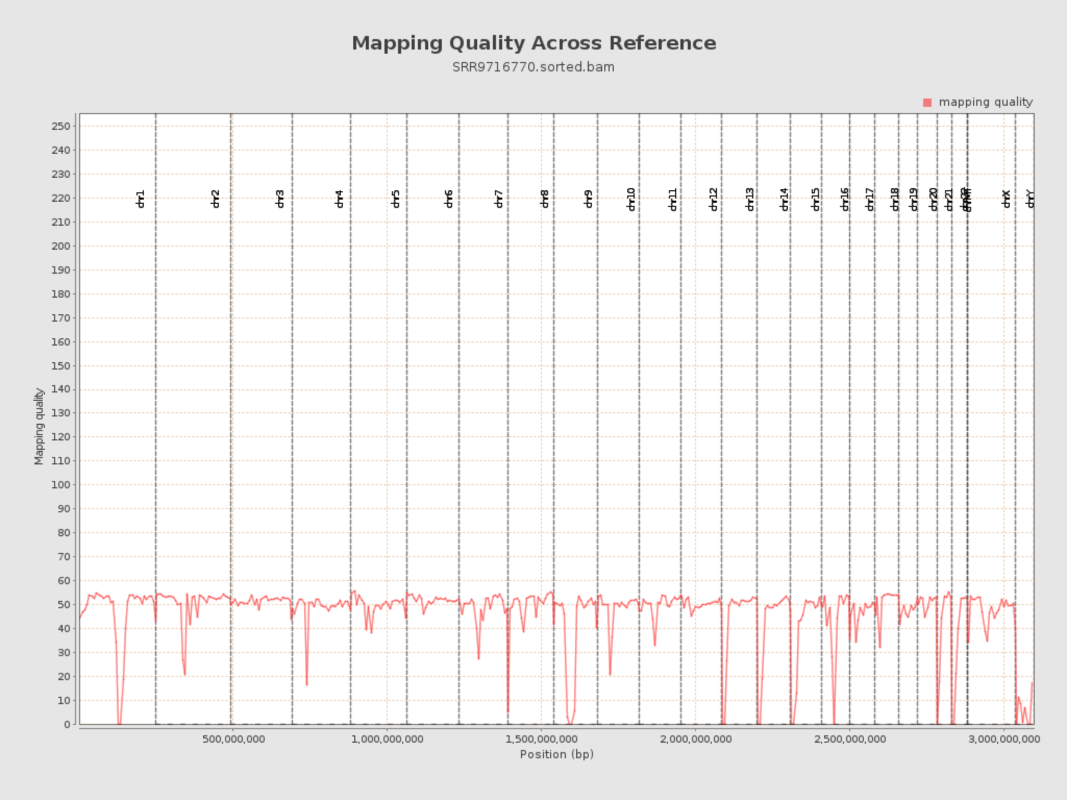
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram