Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 12:12:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716786.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_SRR9716786 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716786.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 12:12:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716786.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,668,797
Mapped reads	2,217,434 / 83.09%
Unmapped reads	451,363 / 16.91%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	46,908 / 1.76%
Read min/max/mean length	30 / 101 / 101.63
Duplicated reads (estimated)	82,994 / 3.11%
Duplication rate	2.64%
Clipped reads	2,261,092 / 84.72%

2.2. ACGT Content

Number/percentage of A's	43,429,540 / 26.46%
Number/percentage of C's	32,260,712 / 19.66%
Number/percentage of T's	49,242,360 / 30%
Number/percentage of G's	39,164,368 / 23.86%
Number/percentage of N's	20,005 / 0.01%
GC Percentage	43.52%

2.3. Coverage

Mean	0.053

Standard Deviation	0.4078

2.4. Mapping Quality

Mean Mapping Quality	46.18

2.5. Mismatches and indels

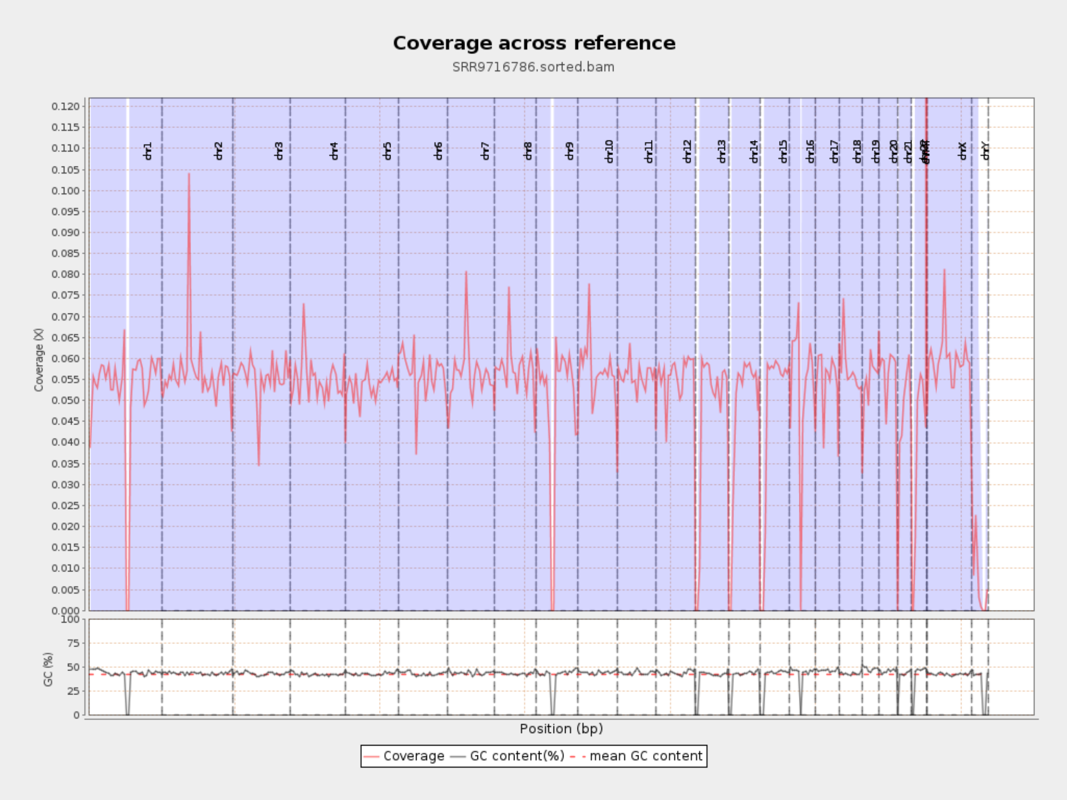
General error rate	0.76%
Mismatches	1,214,650
Insertions	13,827
Mapped reads with at least one insertion	0.62%
Deletions	33,957
Mapped reads with at least one deletion	1.51%
Homopolymer indels	40.49%

2.6. Chromosome stats

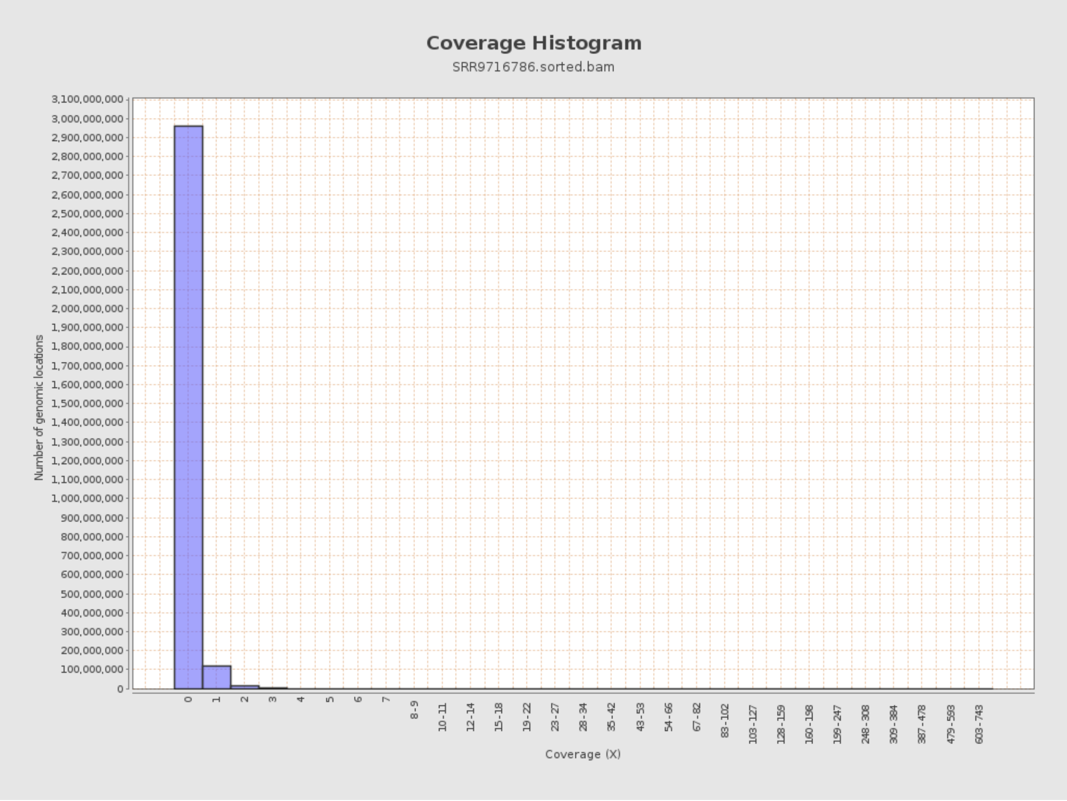
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12972607	0.052	0.4555
chr2	243199373	13864215	0.057	0.6027
chr3	198022430	10982312	0.0555	0.2713
chr4	191154276	10510685	0.055	0.2991
chr5	180915260	9735126	0.0538	0.2709
chr6	171115067	9658614	0.0564	0.3209
chr7	159138663	9041093	0.0568	0.5331

chr8	146364022	8416007	0.0575	0.5297
chr9	141213431	6976465	0.0494	0.4461
chr10	135534747	7791650	0.0575	0.3851
chr11	135006516	7485668	0.0554	0.4551
chr12	133851895	7440376	0.0556	0.2772
chr13	115169878	5299150	0.046	0.2466
chr14	107349540	4974185	0.0463	0.303
chr15	102531392	4772531	0.0465	0.2518
chr16	90354753	4849265	0.0537	0.2974
chr17	81195210	4413989	0.0544	0.2992
chr18	78077248	4514322	0.0578	0.8325
chr19	59128983	3261429	0.0552	0.4447
chr20	63025520	3532667	0.0561	0.2907
chr21	48129895	2151334	0.0447	0.2721
chr22	51304566	1836210	0.0358	0.2191
chrMT	16571	19220	1.1599	1.4291
chrX	155270560	9263542	0.0597	0.3657
chrY	59373566	411786	0.0069	0.2053

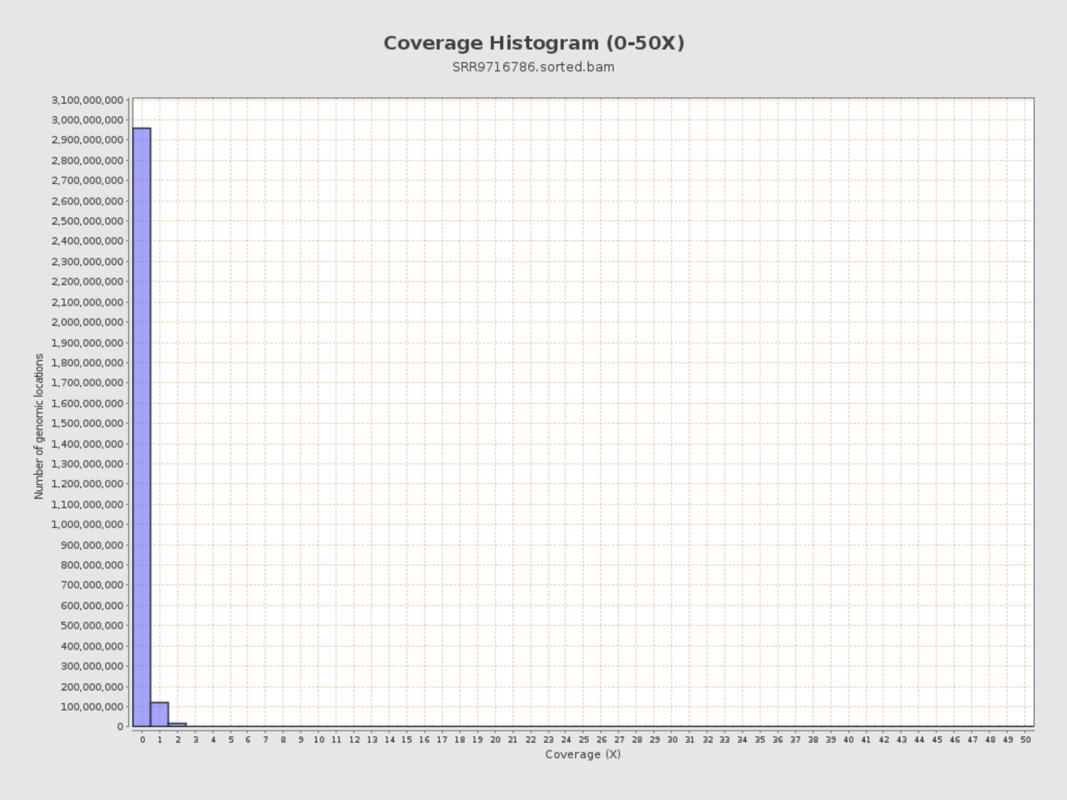
3. Results : Coverage across reference



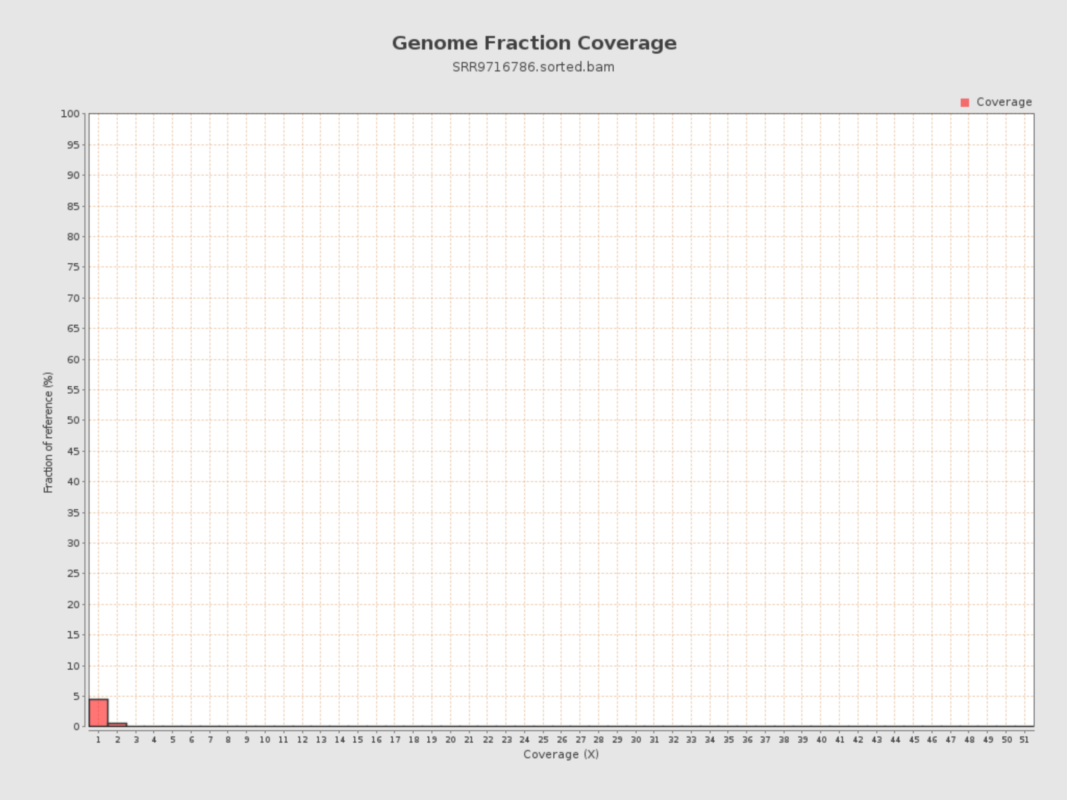
4. Results : Coverage Histogram



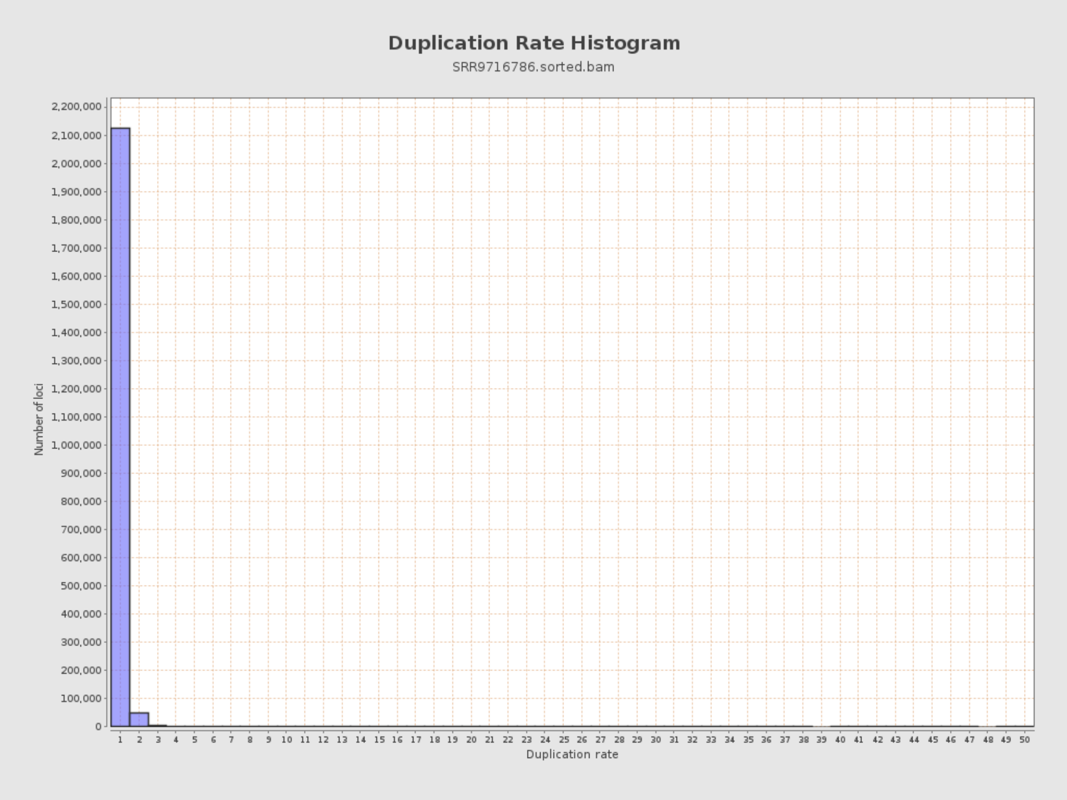
5. Results : Coverage Histogram (0-50X)



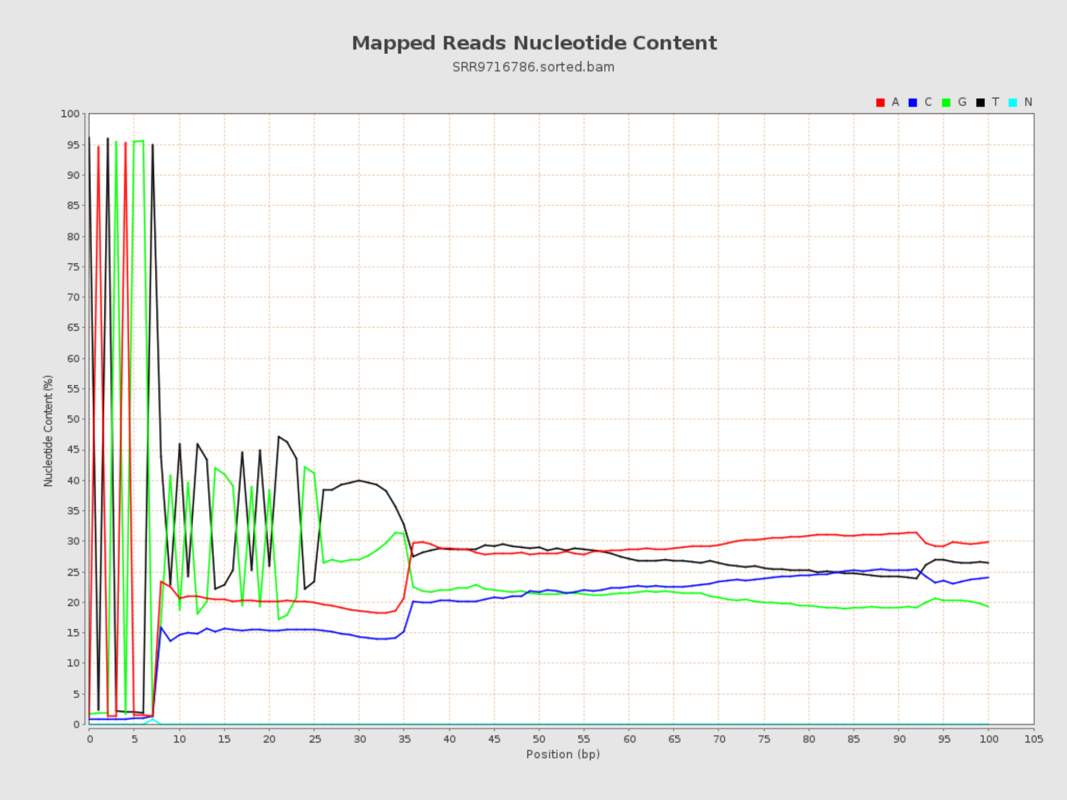
6. Results : Genome Fraction Coverage



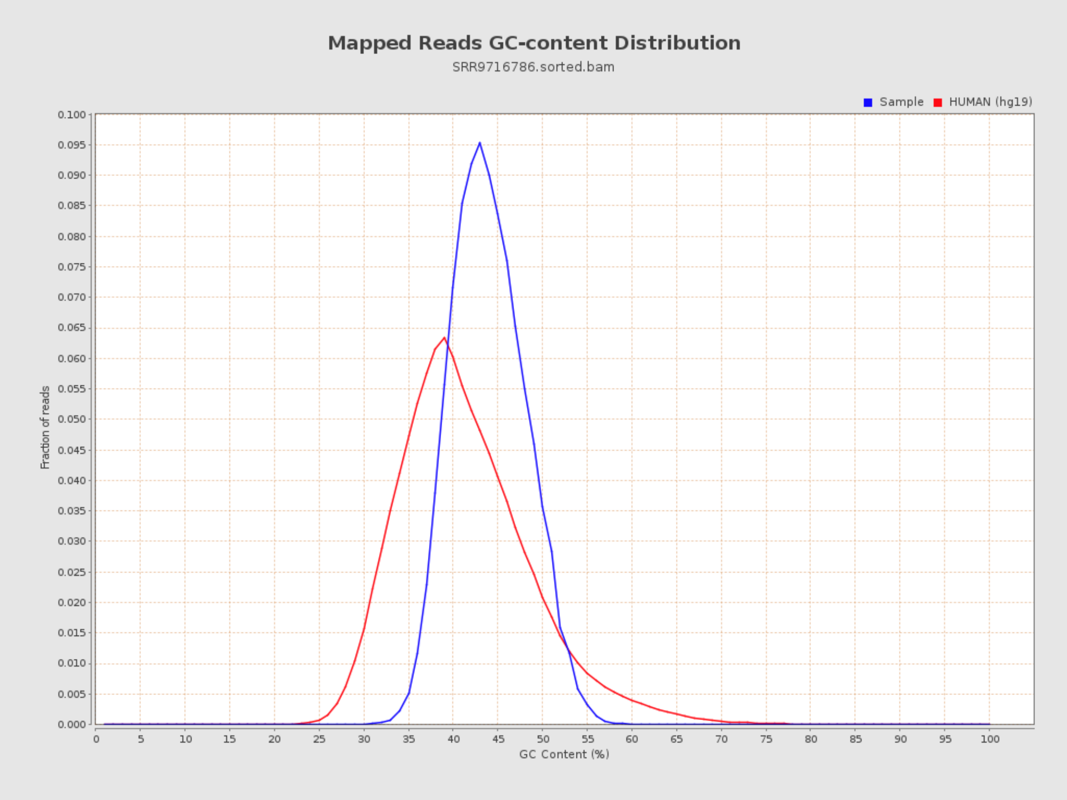
7. Results : Duplication Rate Histogram



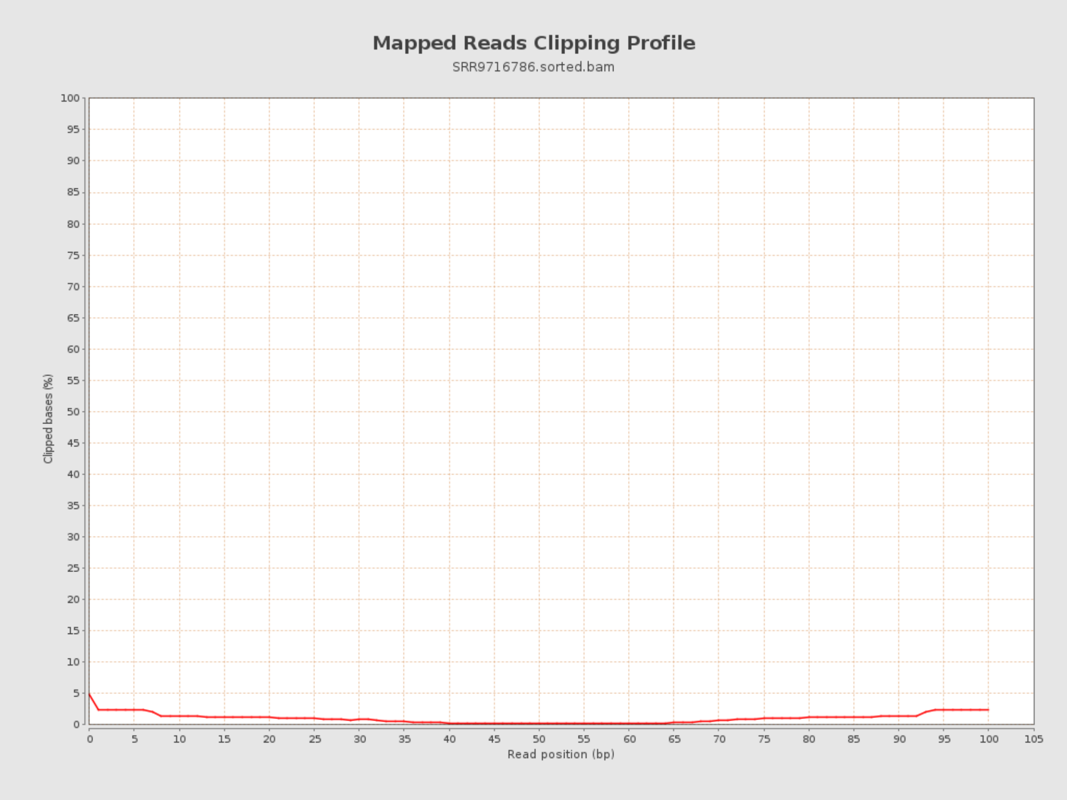
8. Results : Mapped Reads Nucleotide Content



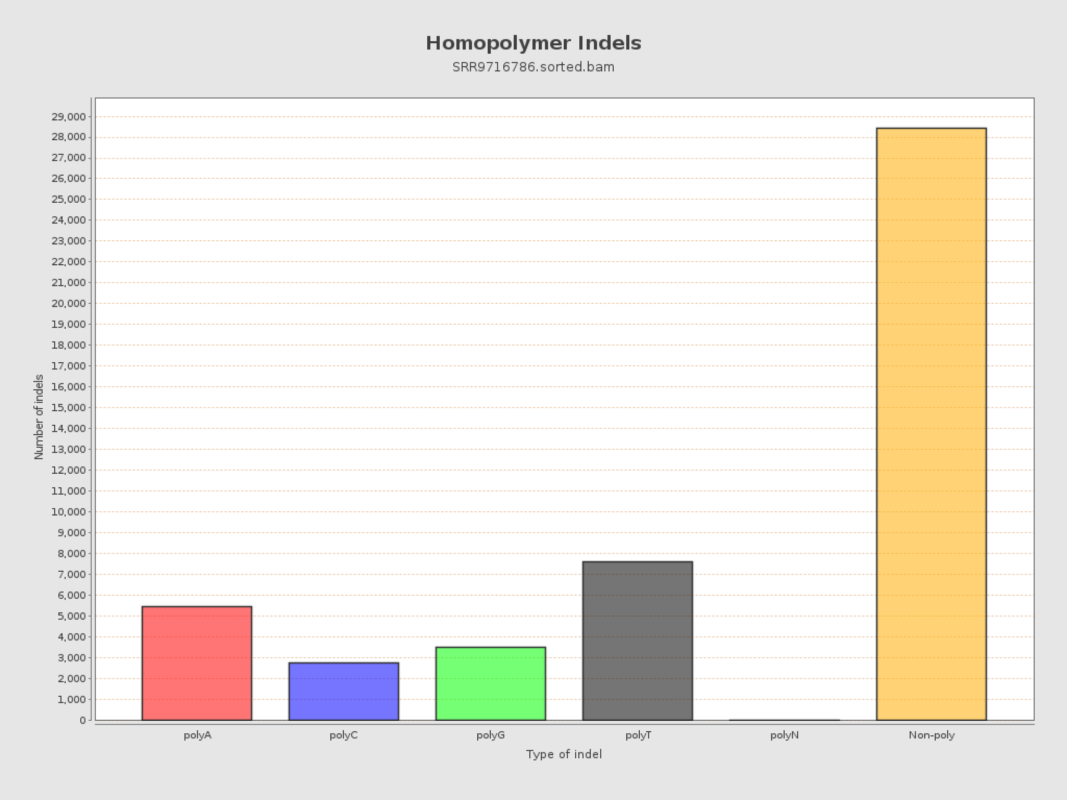
9. Results : Mapped Reads GC-content Distribution



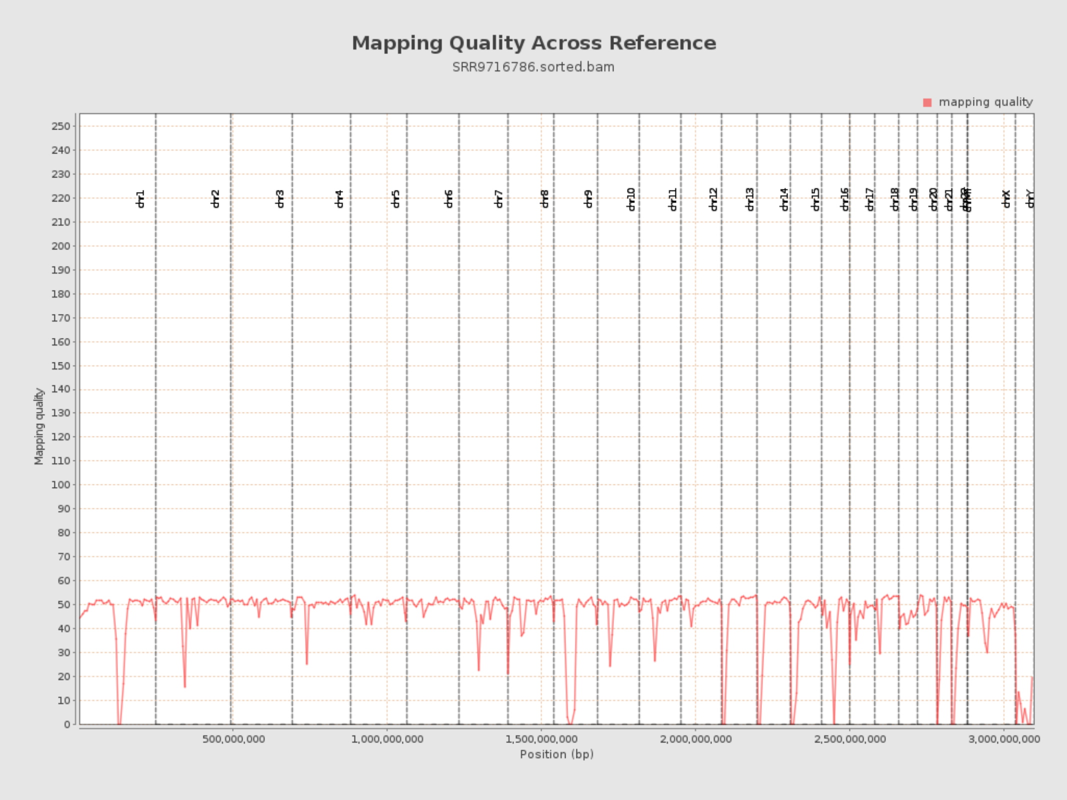
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram