Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 12:16:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716787.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_SRR9716787 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716787.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 12:16:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716787.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,735,429
Mapped reads	1,480,475 / 85.31%
Unmapped reads	254,954 / 14.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	32,109 / 1.85%
Read min/max/mean length	30 / 101 / 101.67
Duplicated reads (estimated)	41,770 / 2.41%
Duplication rate	1.94%
Clipped reads	1,510,680 / 87.05%

2.2. ACGT Content

Number/percentage of A's	29,017,589 / 26.55%
Number/percentage of C's	22,970,915 / 21.02%
Number/percentage of T's	32,065,905 / 29.34%
Number/percentage of G's	25,207,600 / 23.07%
Number/percentage of N's	13,170 / 0.01%
GC Percentage	44.09%

2.3. Coverage

Mean	0.0353

Standard Deviation	0.2908

2.4. Mapping Quality

Mean Mapping Quality	46.06

2.5. Mismatches and indels

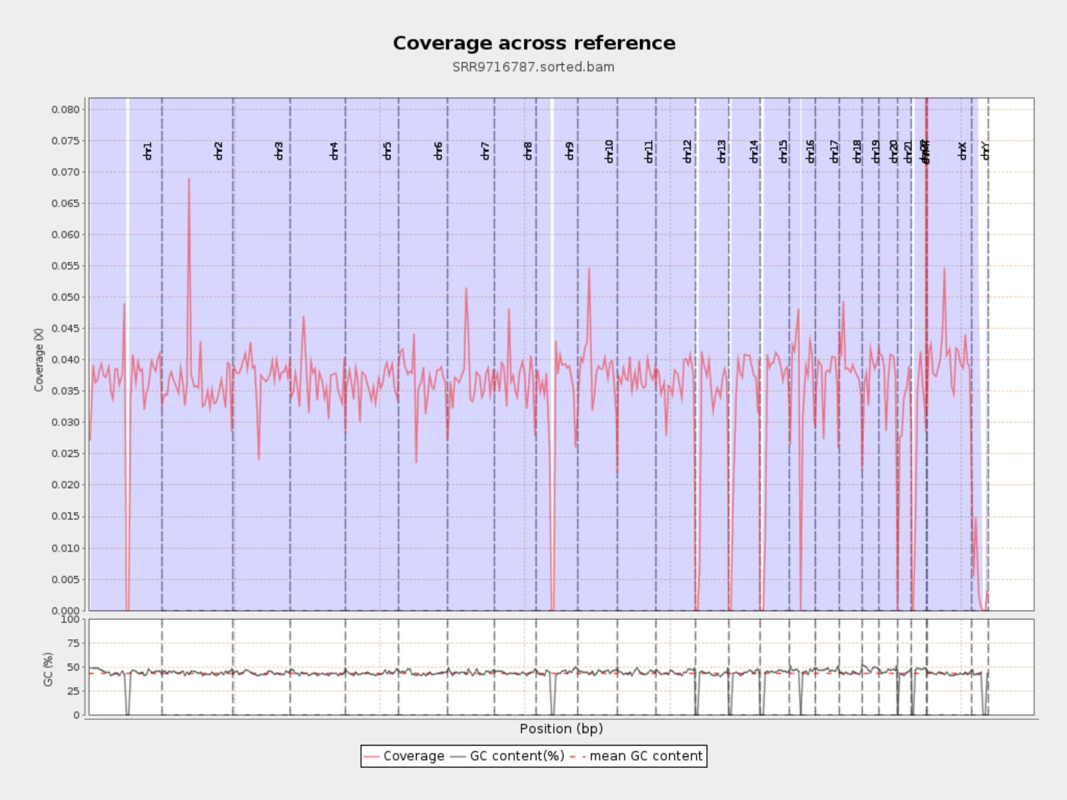
General error rate	0.74%
Mismatches	784,291
Insertions	9,552
Mapped reads with at least one insertion	0.64%
Deletions	22,212
Mapped reads with at least one deletion	1.48%
Homopolymer indels	38.52%

2.6. Chromosome stats

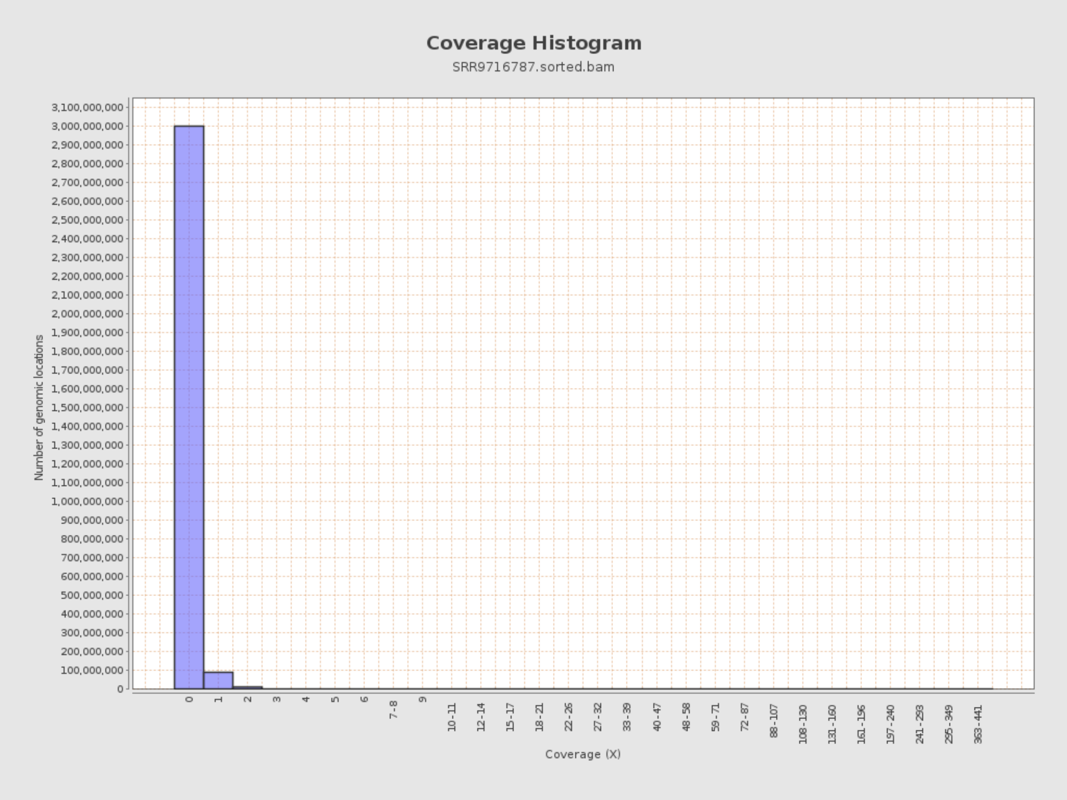
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8779725	0.0352	0.3593
chr2	243199373	8888929	0.0365	0.3976
chr3	198022430	7468894	0.0377	0.214
chr4	191154276	6977064	0.0365	0.2245
chr5	180915260	6539718	0.0361	0.2114
chr6	171115067	6318793	0.0369	0.2357
chr7	159138663	5907510	0.0371	0.3448

chr8	146364022	5409848	0.037	0.3497
chr9	141213431	4586721	0.0325	0.3075
chr10	135534747	5292561	0.039	0.2983
chr11	135006516	5004454	0.0371	0.32
chr12	133851895	4891402	0.0365	0.2138
chr13	115169878	3521286	0.0306	0.1924
chr14	107349540	3399638	0.0317	0.2271
chr15	102531392	3226833	0.0315	0.1968
chr16	90354753	3226530	0.0357	0.2329
chr17	81195210	2983125	0.0367	0.2309
chr18	78077248	3088896	0.0396	0.5578
chr19	59128983	2220145	0.0375	0.3205
chr20	63025520	2344585	0.0372	0.219
chr21	48129895	1419207	0.0295	0.2036
chr22	51304566	1282046	0.025	0.1749
chrMT	16571	14390	0.8684	1.2138
chrX	155270560	6247563	0.0402	0.2735
chrY	59373566	273065	0.0046	0.1257

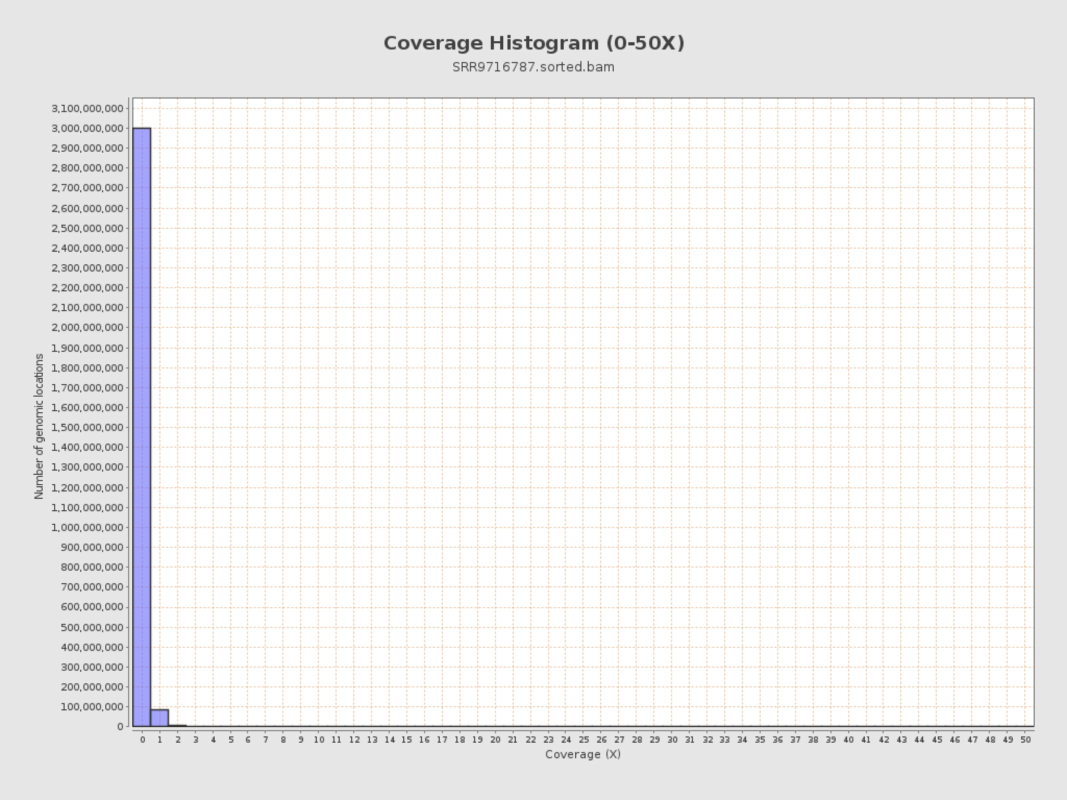
3. Results : Coverage across reference



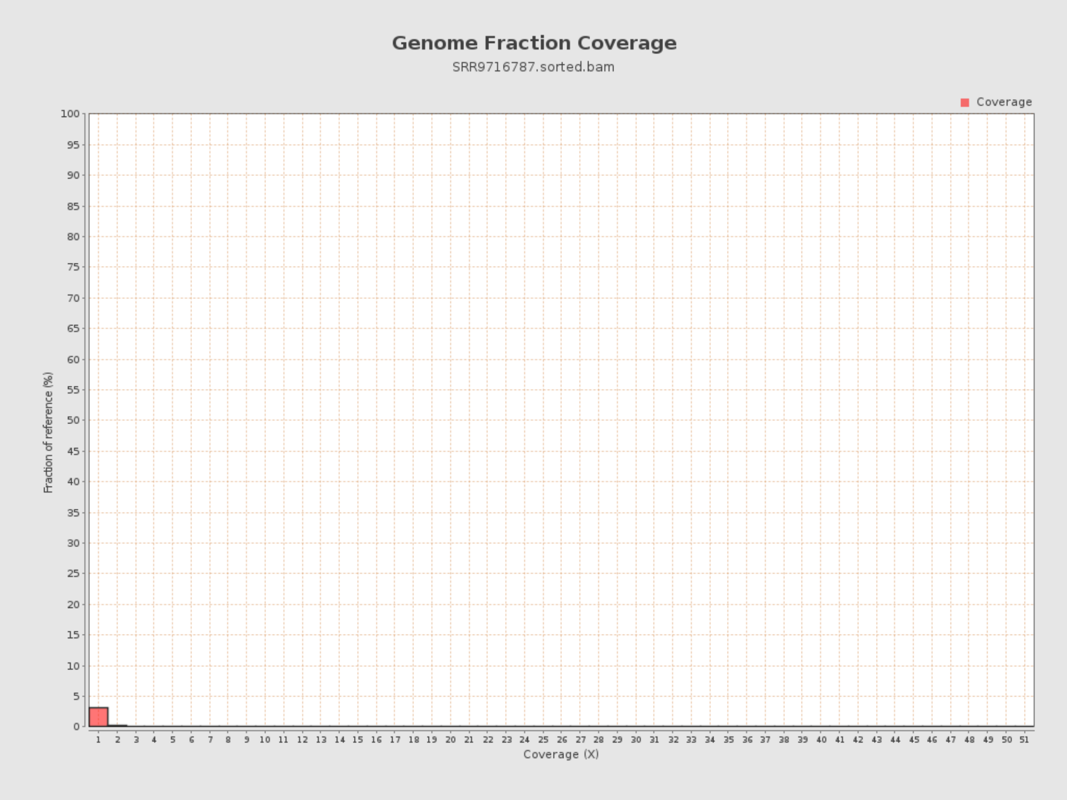
4. Results : Coverage Histogram



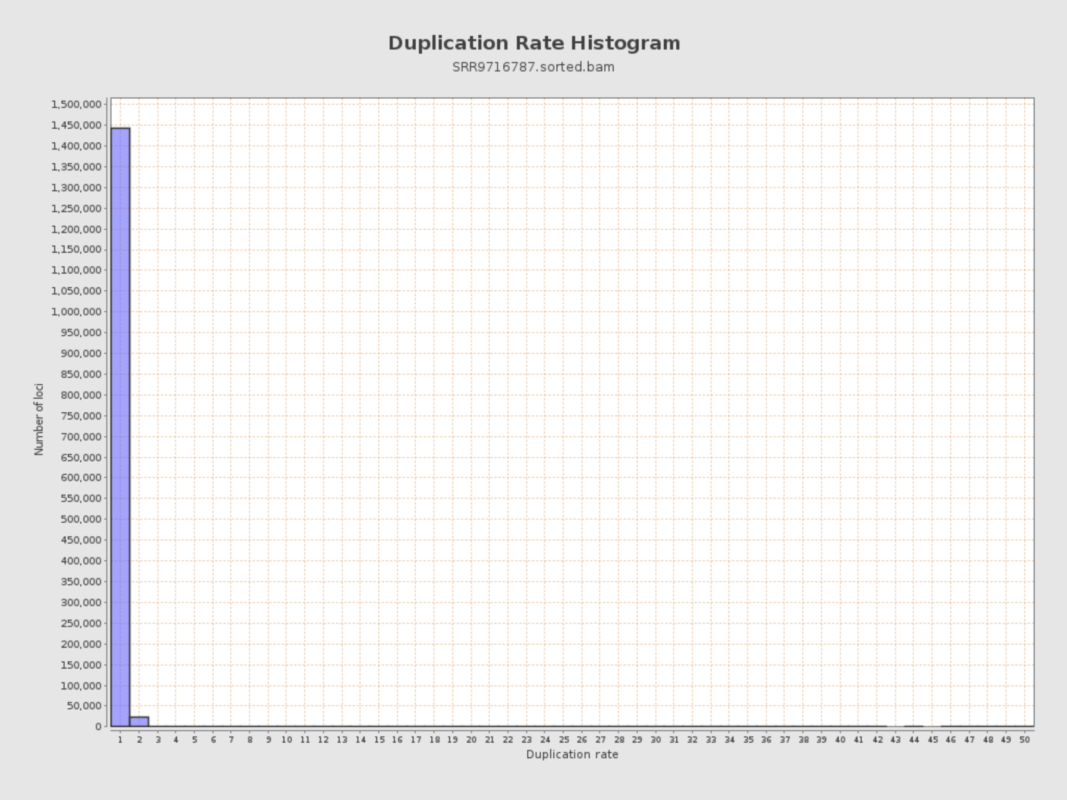
5. Results : Coverage Histogram (0-50X)



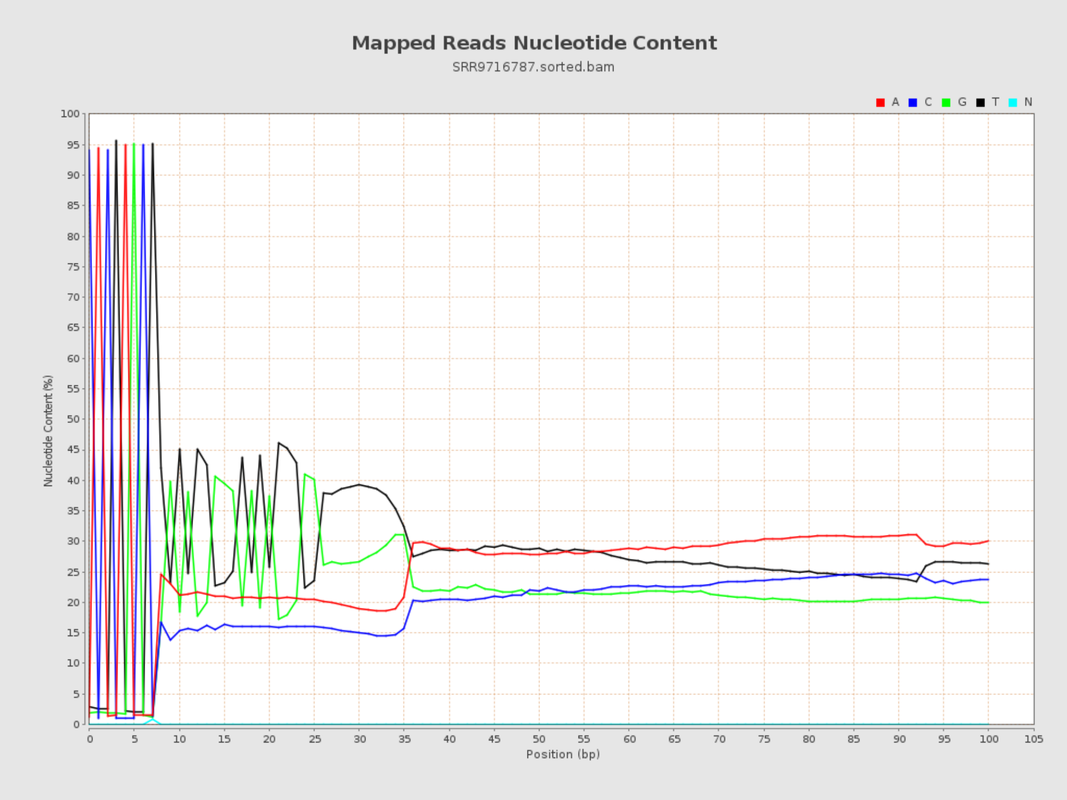
6. Results : Genome Fraction Coverage



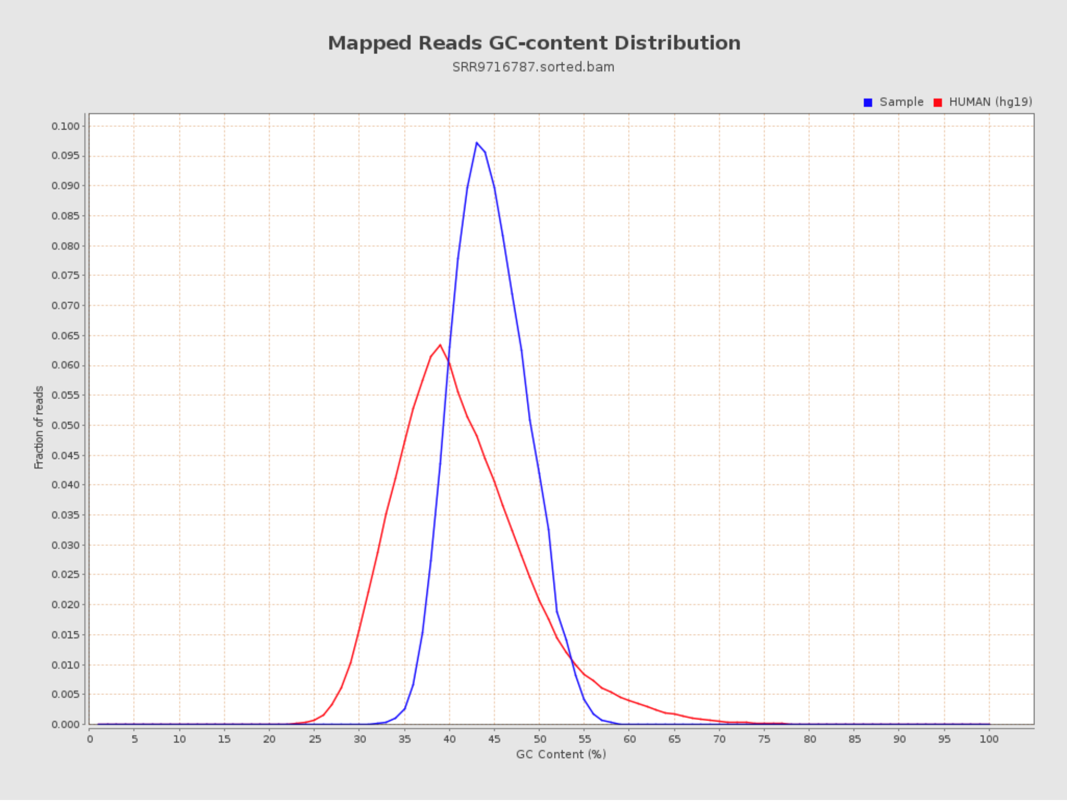
7. Results : Duplication Rate Histogram



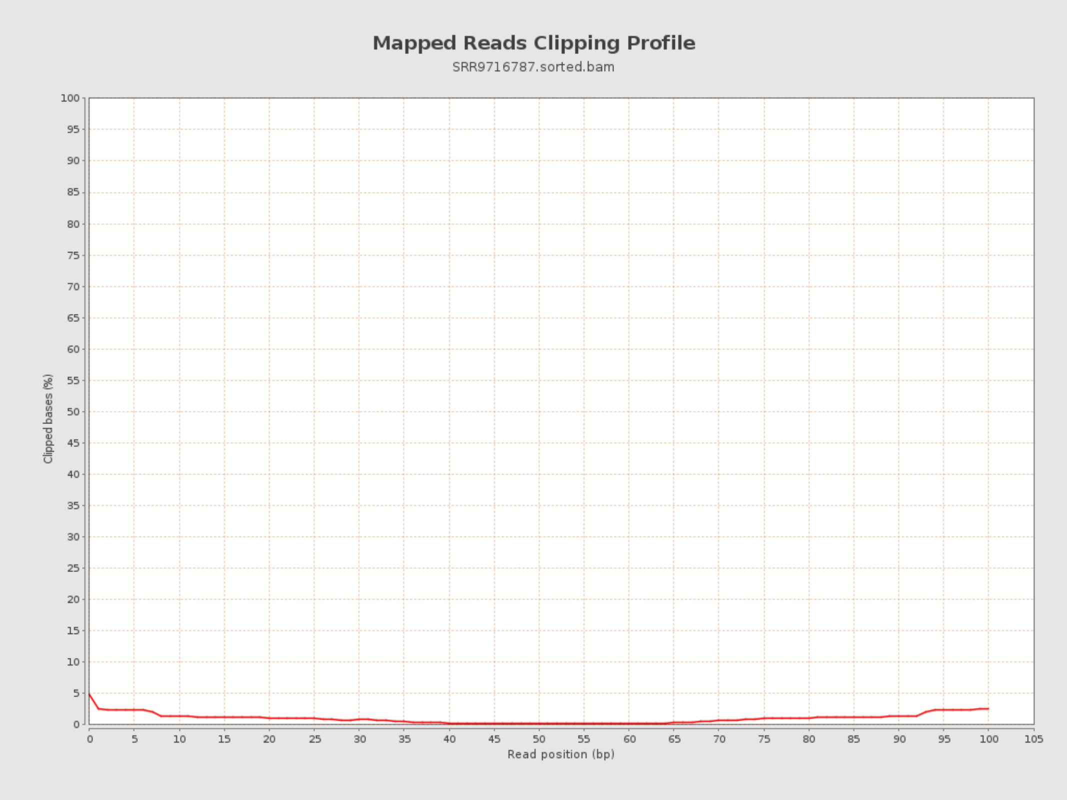
8. Results : Mapped Reads Nucleotide Content



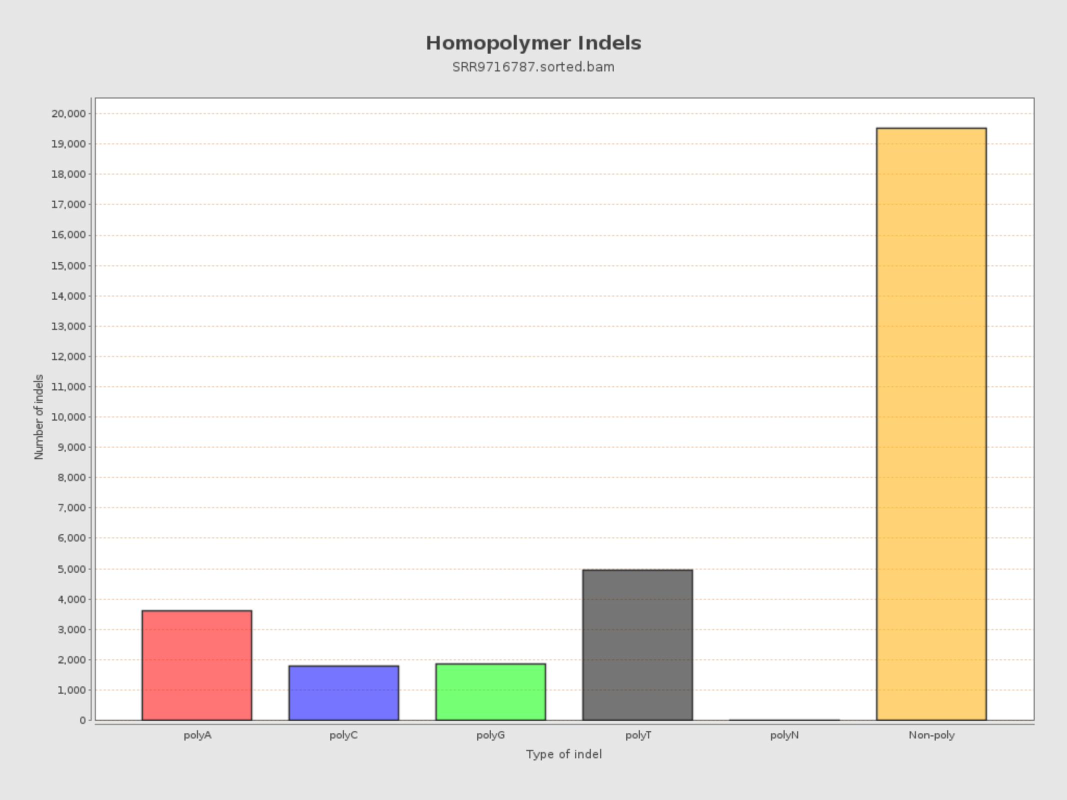
9. Results : Mapped Reads GC-content Distribution



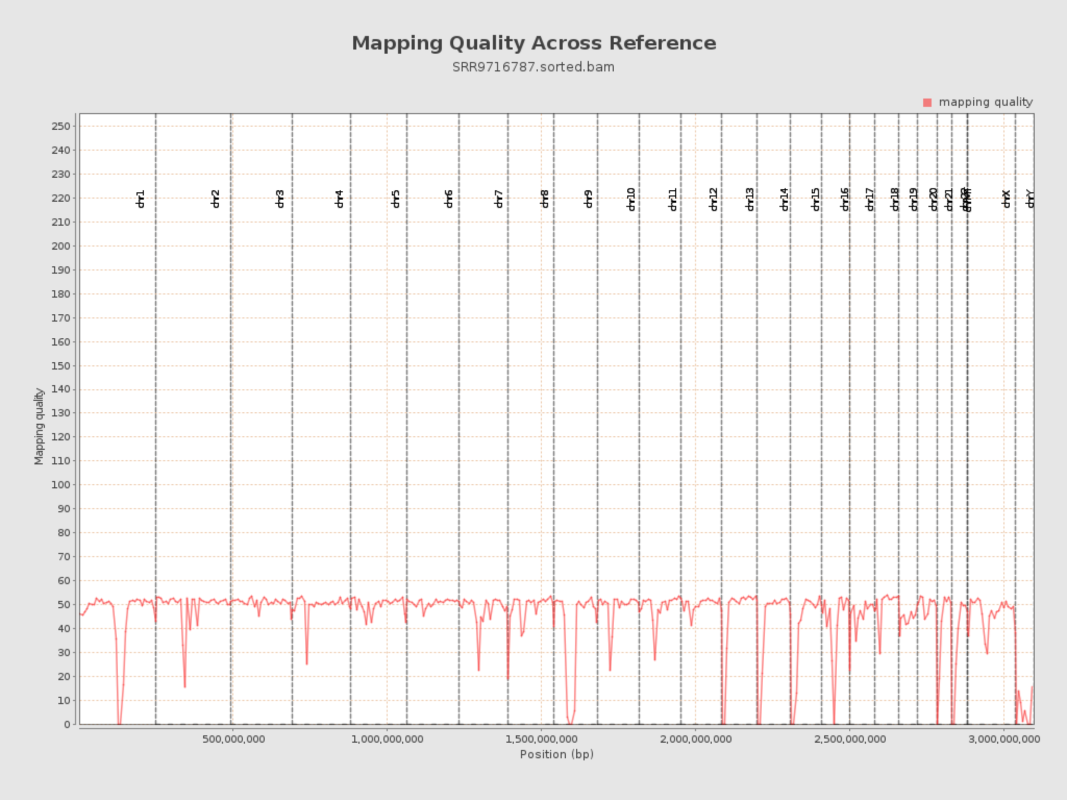
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram