Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 07:02:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716316.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_SRR9716316 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716316.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 07:02:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716316.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,775,047
Mapped reads	1,682,279 / 94.77%
Unmapped reads	92,768 / 5.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	35,101 / 1.98%
Read min/max/mean length	30 / 101 / 101.72
Duplicated reads (estimated)	63,724 / 3.59%
Duplication rate	2.81%
Clipped reads	1,716,008 / 96.67%

2.2. ACGT Content

Number/percentage of A's	35,430,870 / 26.33%
Number/percentage of C's	27,949,551 / 20.77%
Number/percentage of T's	39,750,571 / 29.54%
Number/percentage of G's	31,434,468 / 23.36%
Number/percentage of N's	9,553 / 0.01%
GC Percentage	44.13%

2.3. Coverage

Mean	0.0435

Standard Deviation	0.3614

2.4. Mapping Quality

Mean Mapping Quality	47.87

2.5. Mismatches and indels

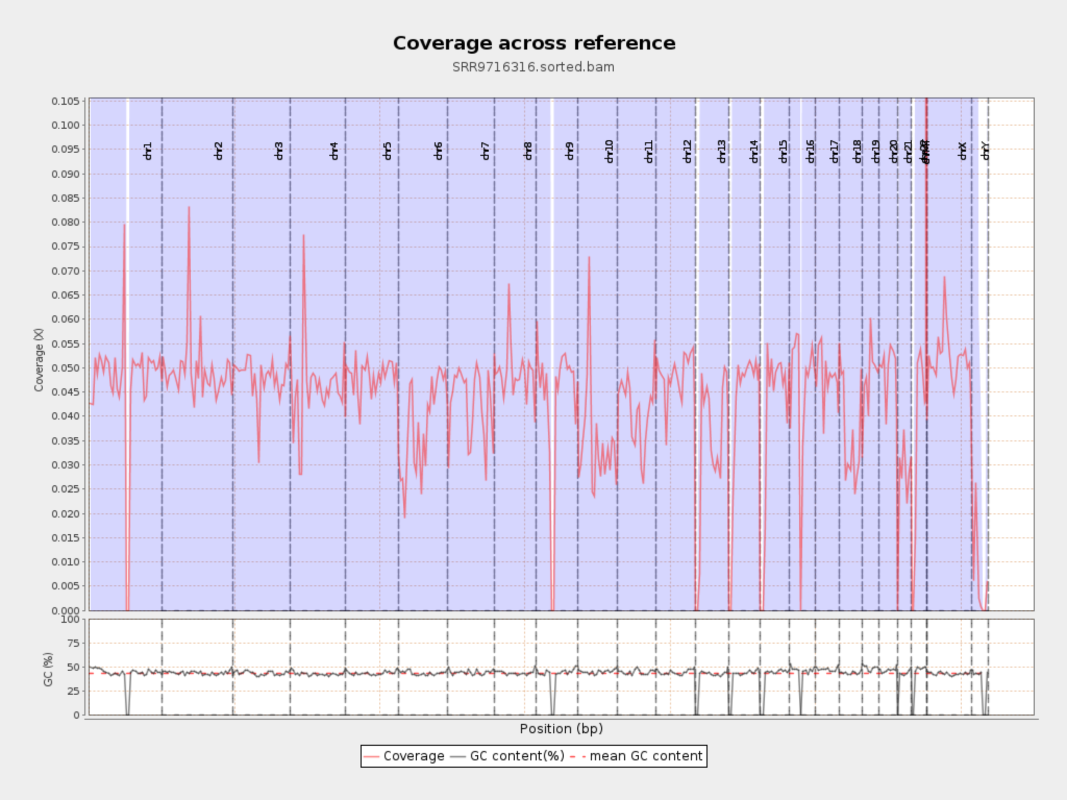
General error rate	0.61%
Mismatches	802,004
Insertions	10,522
Mapped reads with at least one insertion	0.62%
Deletions	29,808
Mapped reads with at least one deletion	1.74%
Homopolymer indels	44.26%

2.6. Chromosome stats

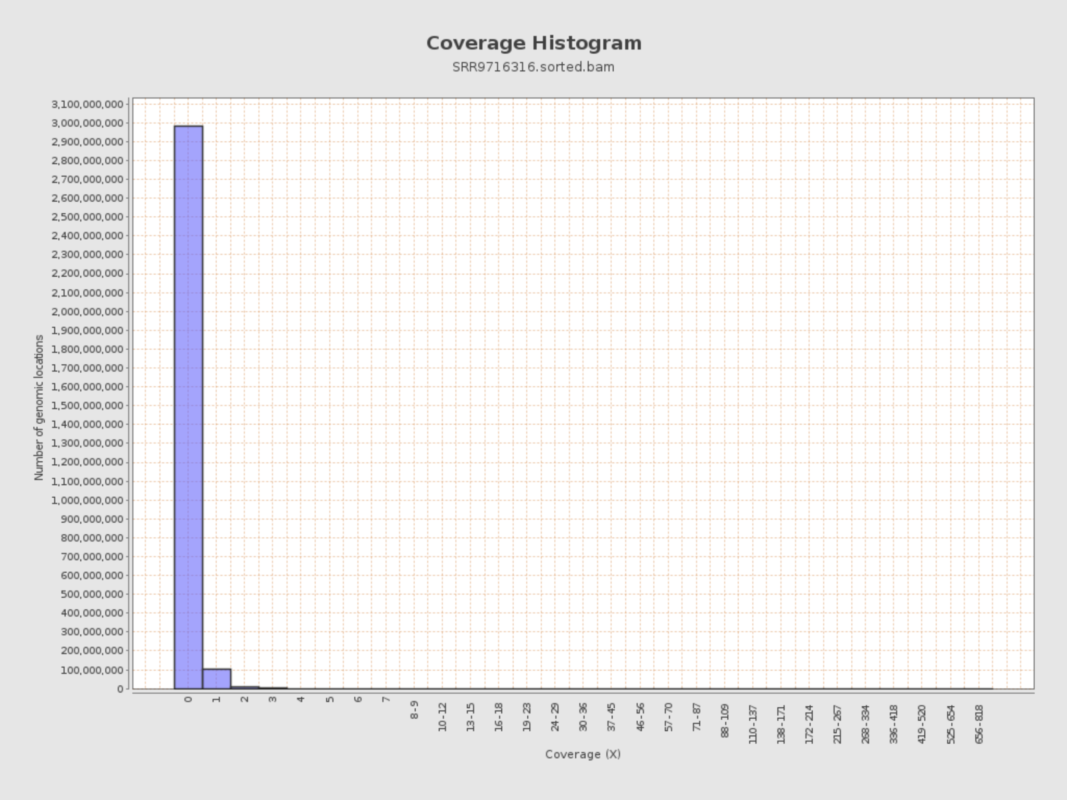
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11694090	0.0469	0.6971
chr2	243199373	12100950	0.0498	0.4273
chr3	198022430	9499754	0.048	0.2447
chr4	191154276	8735100	0.0457	0.3051
chr5	180915260	8735841	0.0483	0.2475
chr6	171115067	6573958	0.0384	0.2259
chr7	159138663	6772826	0.0426	0.3518

chr8	146364022	7187383	0.0491	0.4161
chr9	141213431	5978480	0.0423	0.3256
chr10	135534747	4703363	0.0347	0.3953
chr11	135006516	5560791	0.0412	0.3402
chr12	133851895	6485363	0.0485	0.2477
chr13	115169878	3831970	0.0333	0.2034
chr14	107349540	4391327	0.0409	0.2365
chr15	102531392	4026104	0.0393	0.2227
chr16	90354753	4142264	0.0458	0.2566
chr17	81195210	3897935	0.048	0.2786
chr18	78077248	2790426	0.0357	0.4769
chr19	59128983	2870360	0.0485	0.479
chr20	63025520	3135567	0.0498	0.2579
chr21	48129895	1287921	0.0268	0.224
chr22	51304566	1725295	0.0336	0.2114
chrMT	16571	21287	1.2846	1.477
chrX	155270560	8066012	0.0519	0.2876
chrY	59373566	418721	0.0071	0.2237

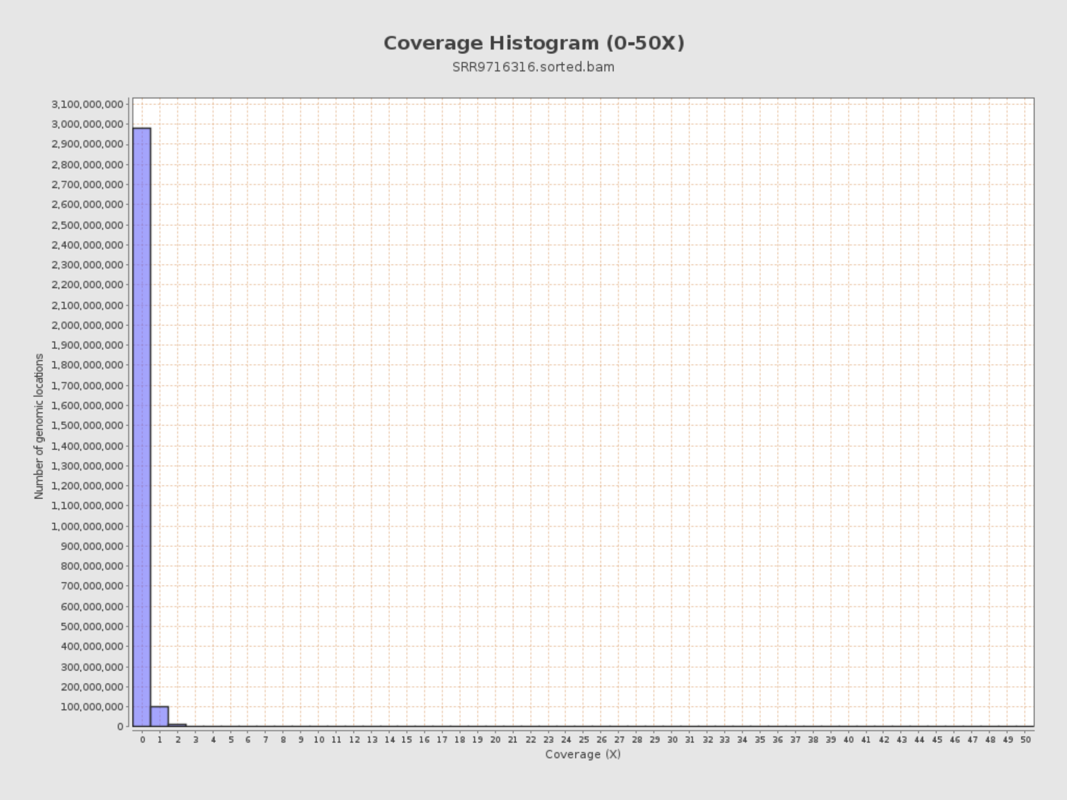
3. Results : Coverage across reference



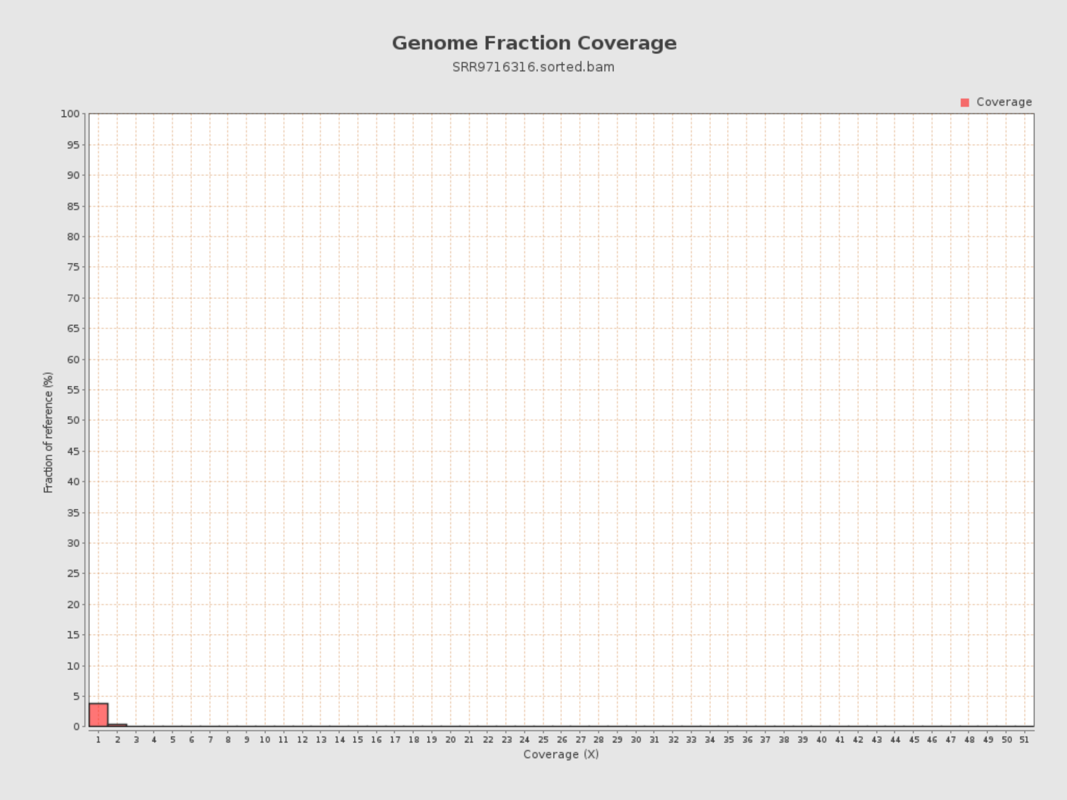
4. Results : Coverage Histogram



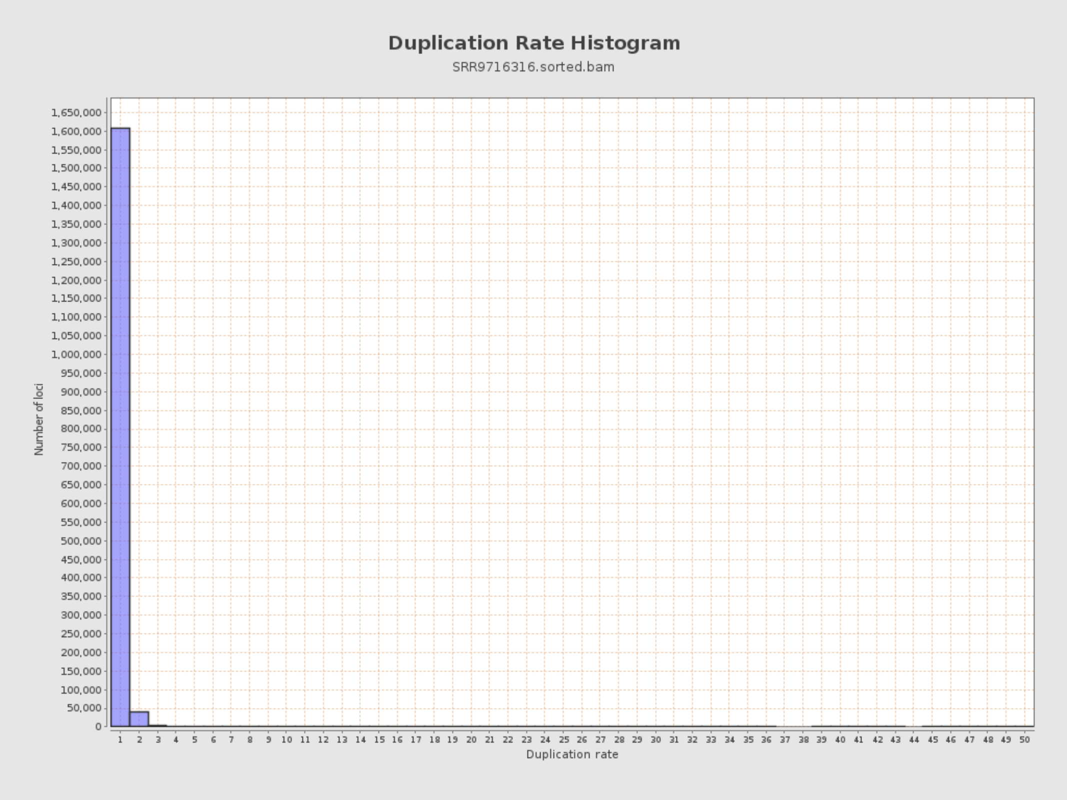
5. Results : Coverage Histogram (0-50X)



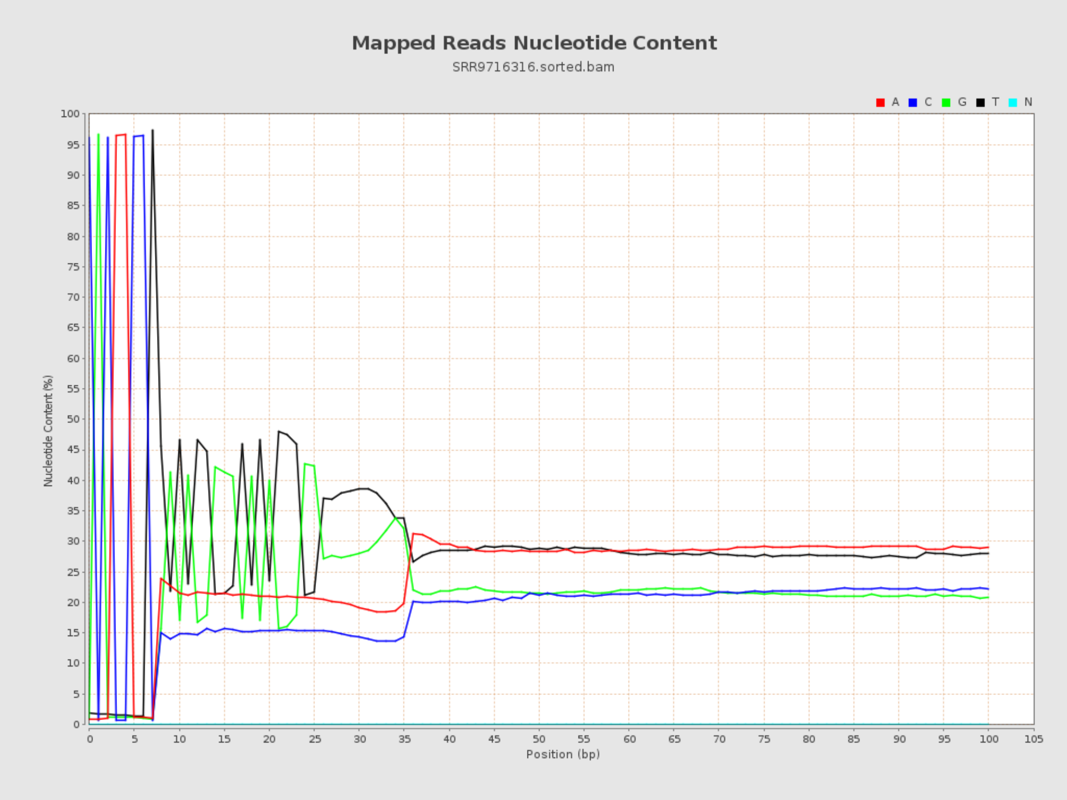
6. Results : Genome Fraction Coverage



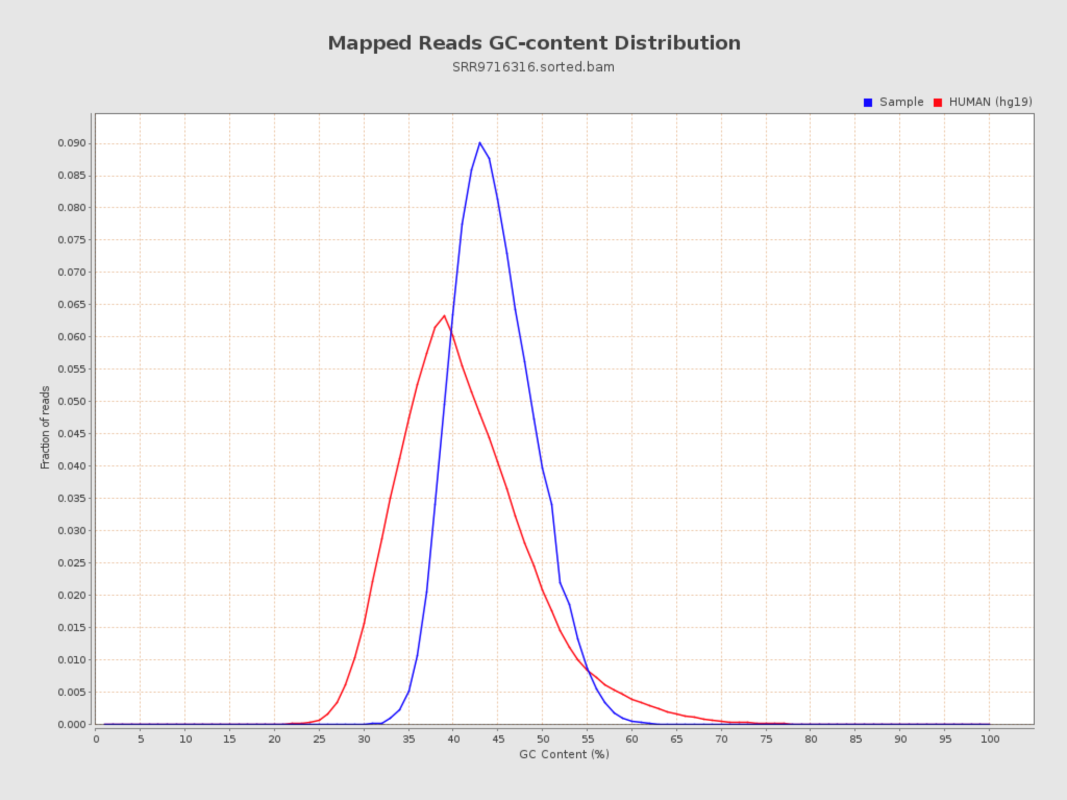
7. Results : Duplication Rate Histogram



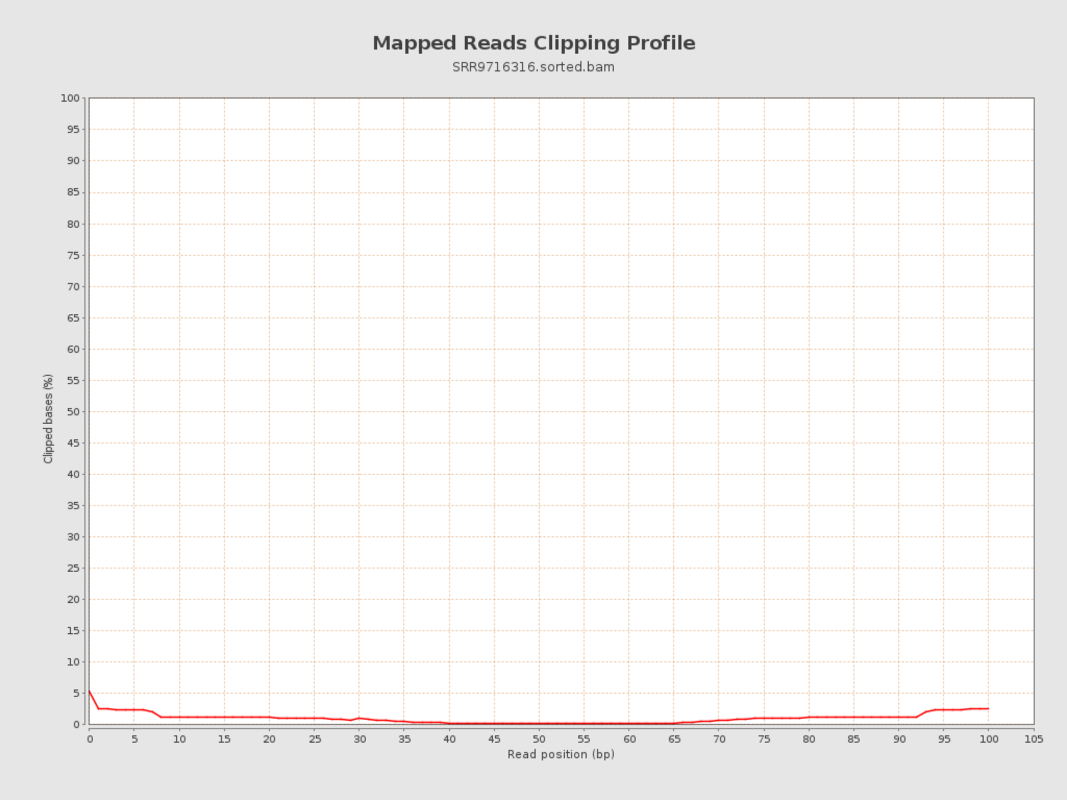
8. Results : Mapped Reads Nucleotide Content



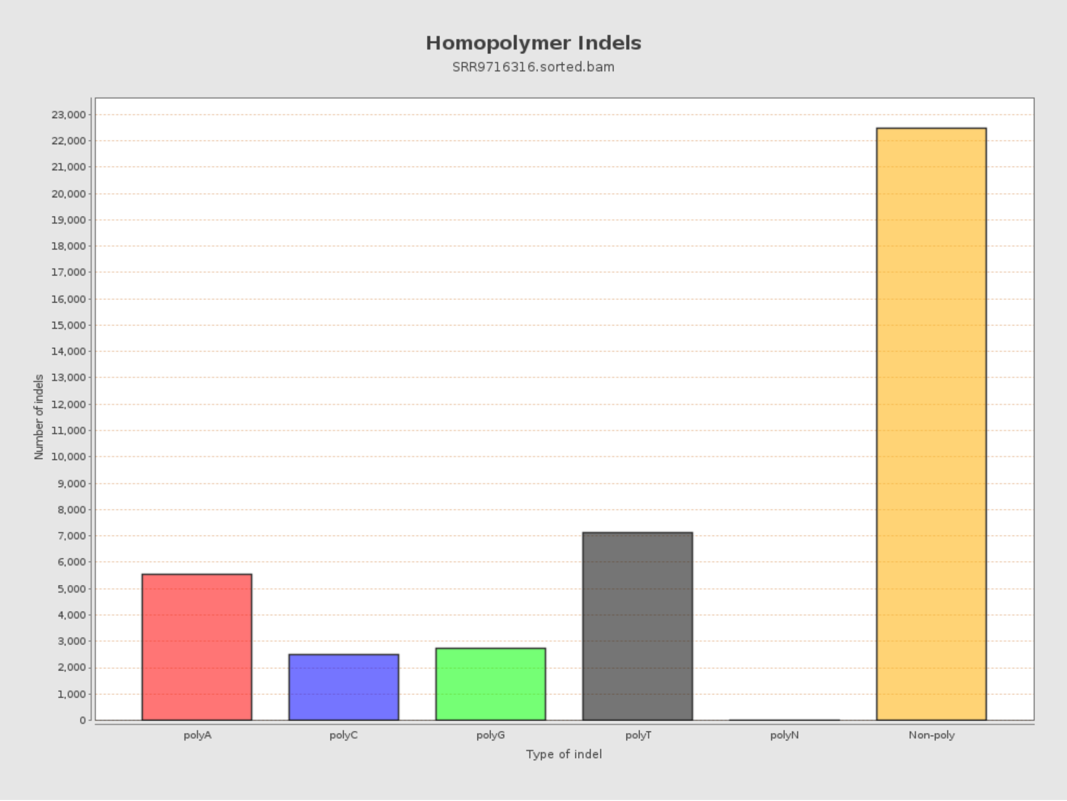
9. Results : Mapped Reads GC-content Distribution



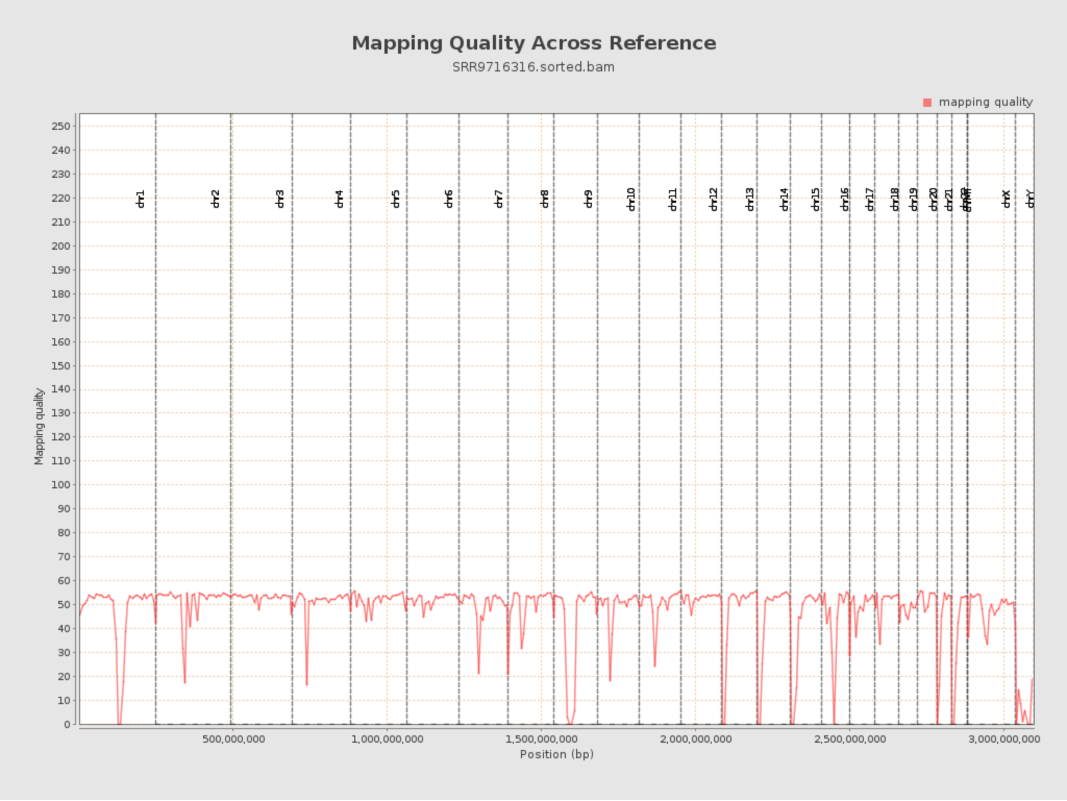
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram