Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 09:54:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716747.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_SRR9716747 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716747.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 09:54:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716747.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	413,424
Mapped reads	326,765 / 79.04%
Unmapped reads	86,659 / 20.96%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	342 / 0.08%
Read min/max/mean length	30 / 76 / 76.03
Duplicated reads (estimated)	14,358 / 3.47%
Duplication rate	3.97%
Clipped reads	326,457 / 78.96%

2.2. ACGT Content

Number/percentage of A's	3,680,884 / 21.45%
Number/percentage of C's	3,150,781 / 18.36%
Number/percentage of T's	5,584,466 / 32.55%
Number/percentage of G's	4,740,729 / 27.63%
Number/percentage of N's	330 / 0%
GC Percentage	46%

2.3. Coverage

Mean	0.0055

Standard Deviation	0.0835

2.4. Mapping Quality

Mean Mapping Quality	43.39

2.5. Mismatches and indels

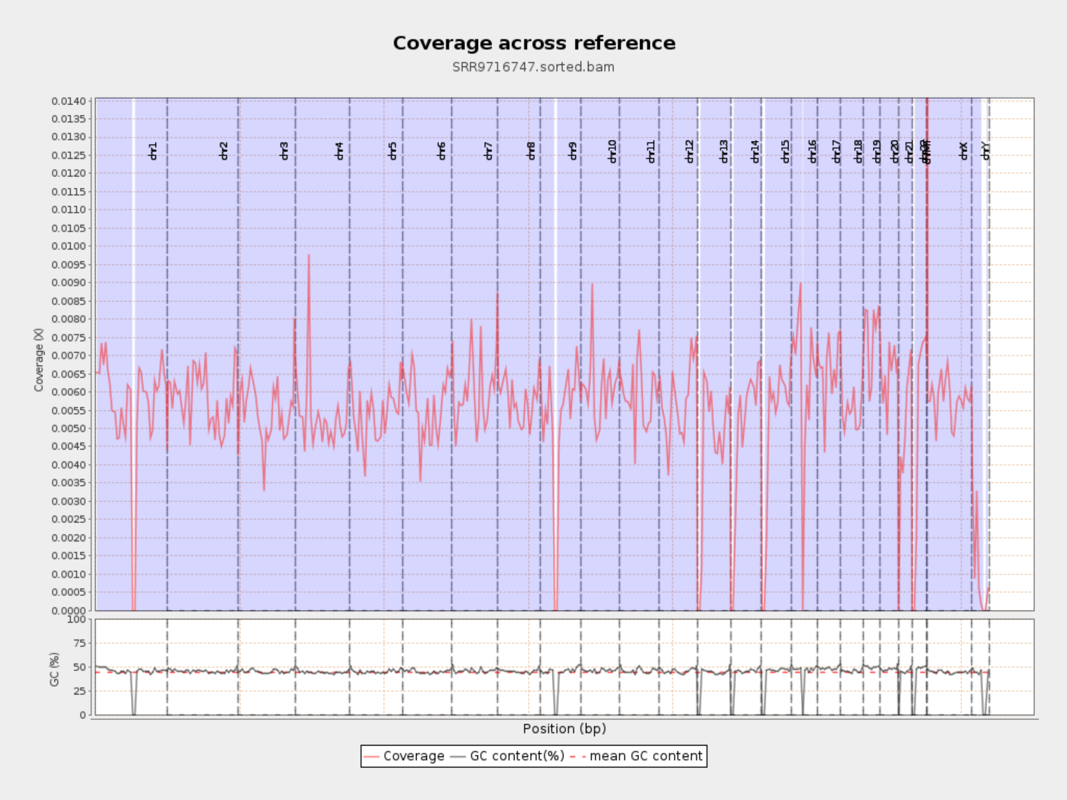
General error rate	0.65%
Mismatches	109,735
Insertions	1,110
Mapped reads with at least one insertion	0.34%
Deletions	2,592
Mapped reads with at least one deletion	0.79%
Homopolymer indels	39.36%

2.6. Chromosome stats

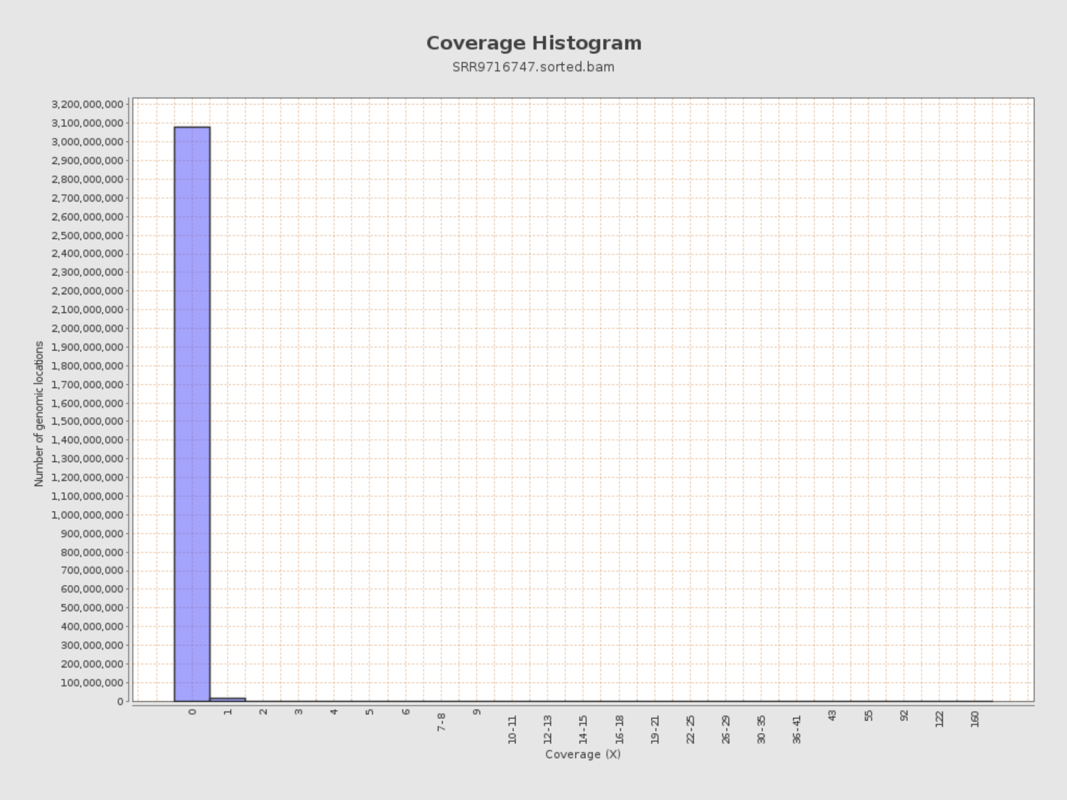
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1397410	0.0056	0.0838
chr2	243199373	1418554	0.0058	0.1041
chr3	198022430	1079266	0.0055	0.0785
chr4	191154276	1035357	0.0054	0.0802
chr5	180915260	978225	0.0054	0.0783
chr6	171115067	960490	0.0056	0.083
chr7	159138663	954218	0.006	0.088

chr8	146364022	844538	0.0058	0.0822
chr9	141213431	727890	0.0052	0.0787
chr10	135534747	835329	0.0062	0.089
chr11	135006516	799260	0.0059	0.085
chr12	133851895	765976	0.0057	0.081
chr13	115169878	511155	0.0044	0.0713
chr14	107349540	523718	0.0049	0.0752
chr15	102531392	496784	0.0048	0.0745
chr16	90354753	567304	0.0063	0.0874
chr17	81195210	535958	0.0066	0.0883
chr18	78077248	426071	0.0055	0.0847
chr19	59128983	444175	0.0075	0.1
chr20	63025520	406331	0.0064	0.0866
chr21	48129895	234792	0.0049	0.0767
chr22	51304566	251642	0.0049	0.0759
chrMT	16571	2554	0.1541	0.4381
chrX	155270560	903528	0.0058	0.0819
chrY	59373566	61018	0.001	0.039

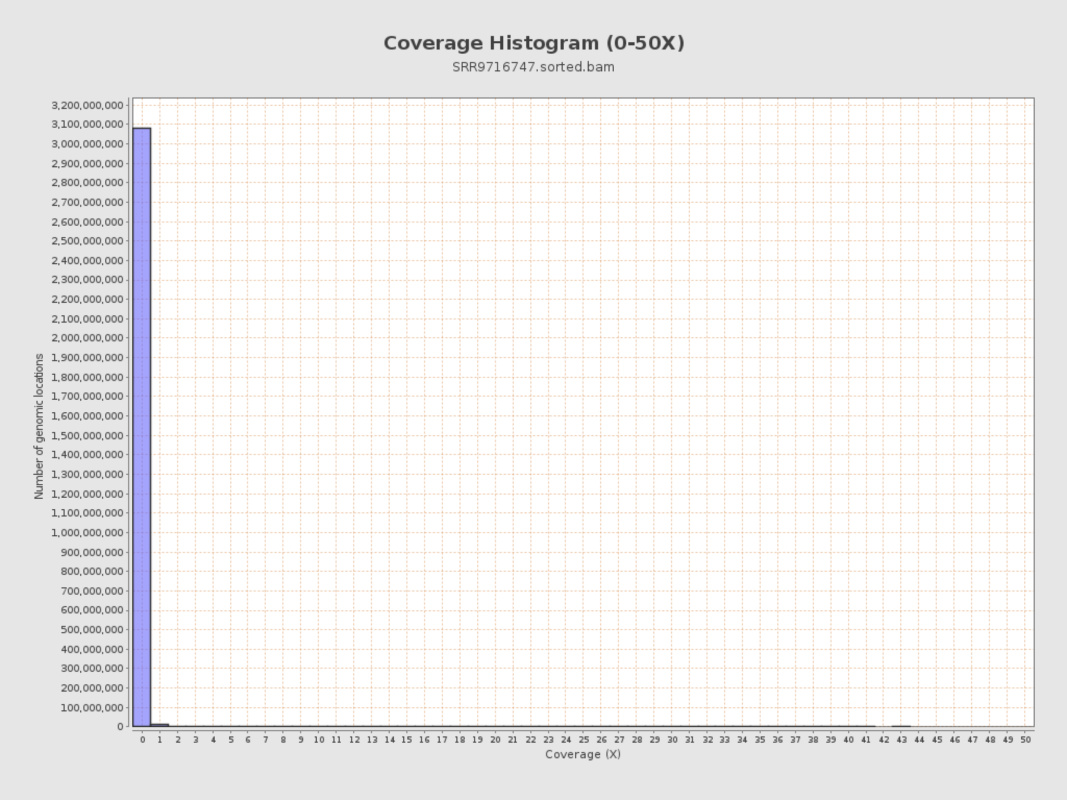
3. Results : Coverage across reference



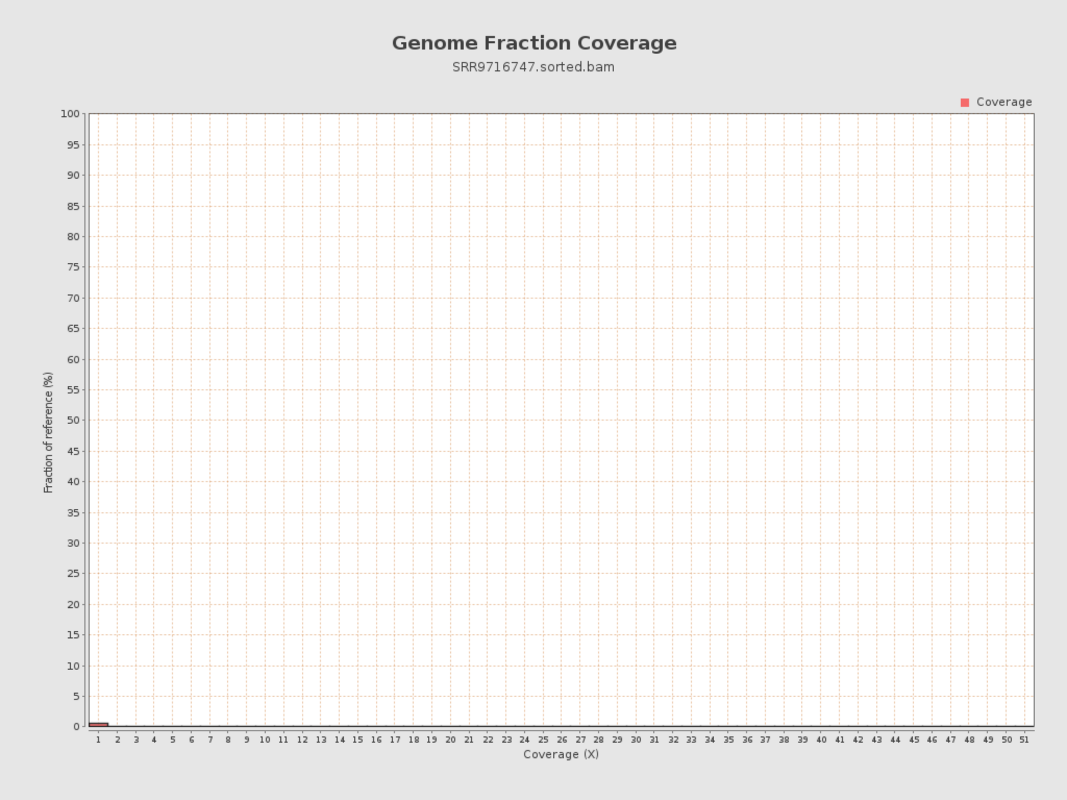
4. Results : Coverage Histogram



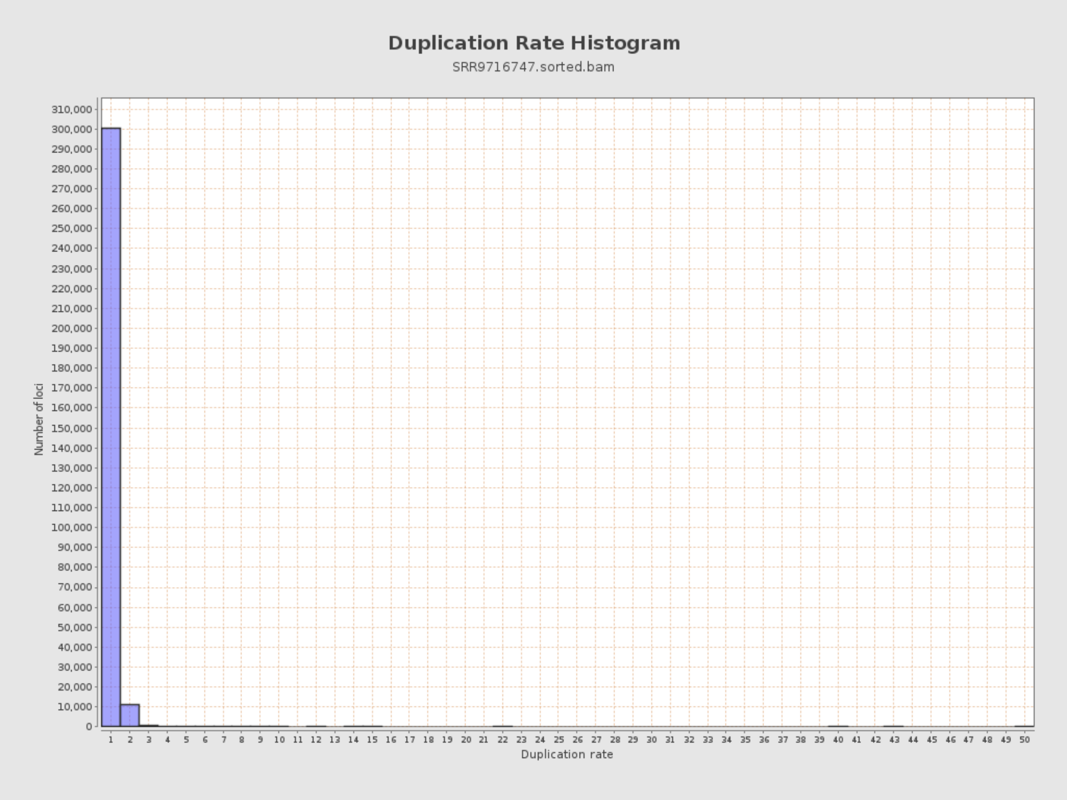
5. Results : Coverage Histogram (0-50X)



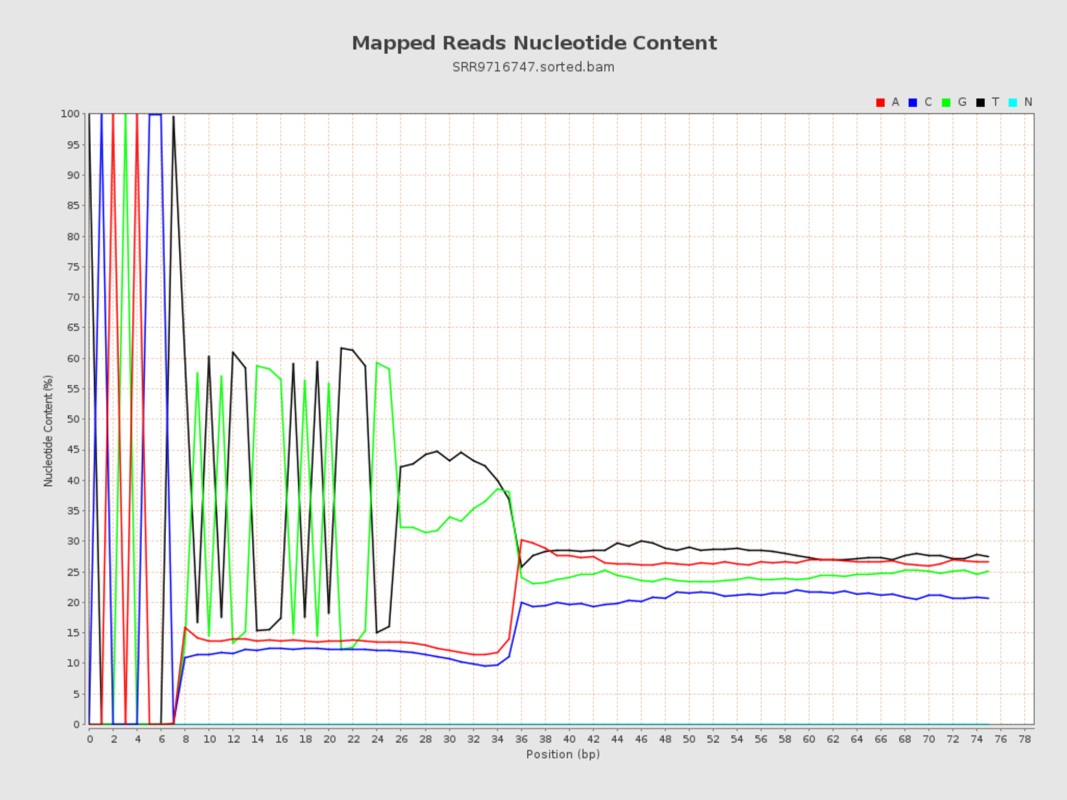
6. Results : Genome Fraction Coverage



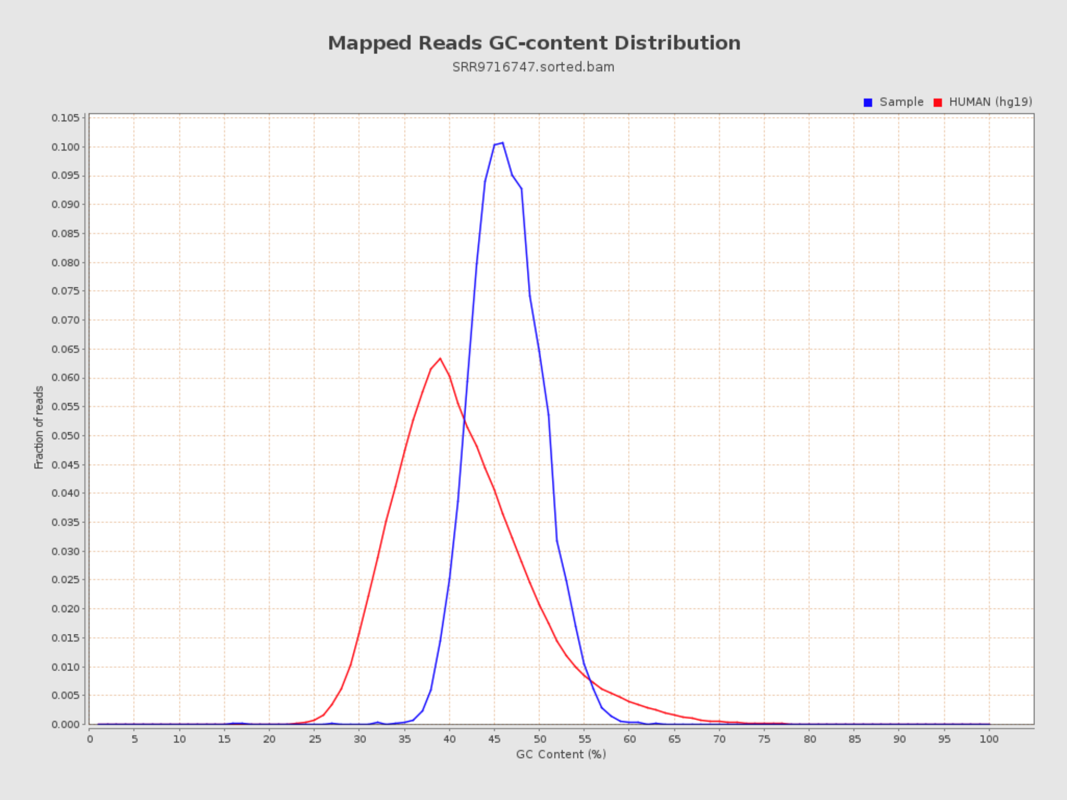
7. Results : Duplication Rate Histogram



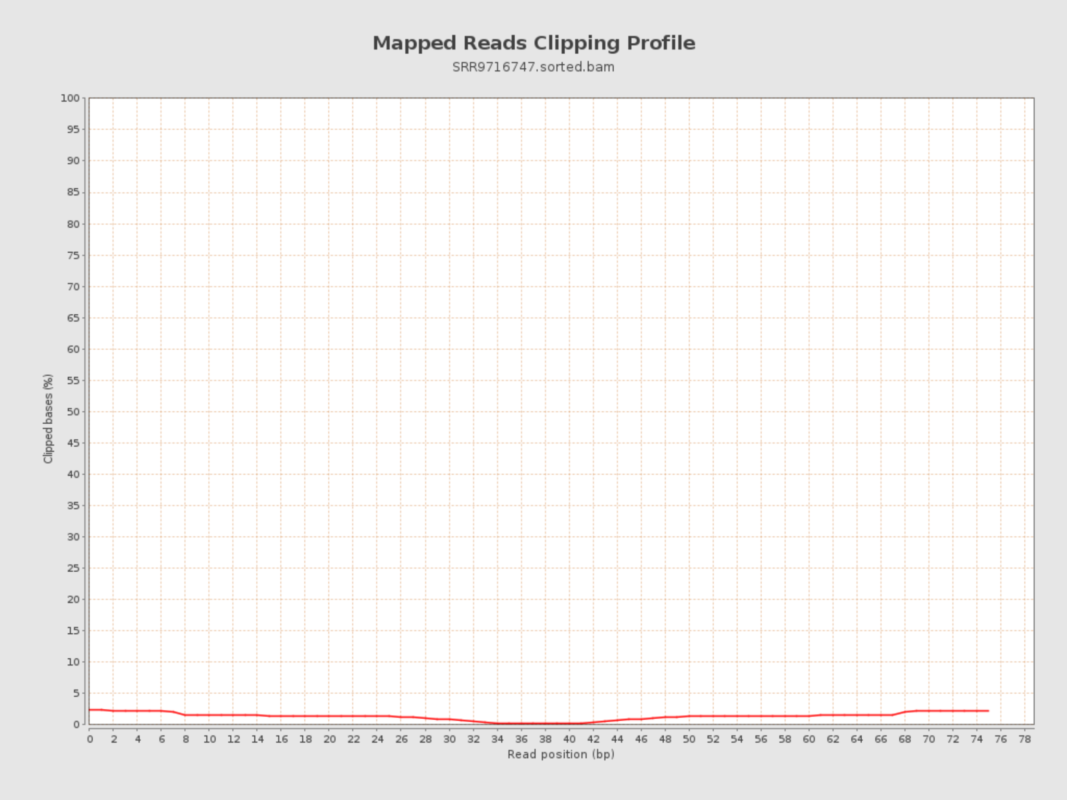
8. Results : Mapped Reads Nucleotide Content



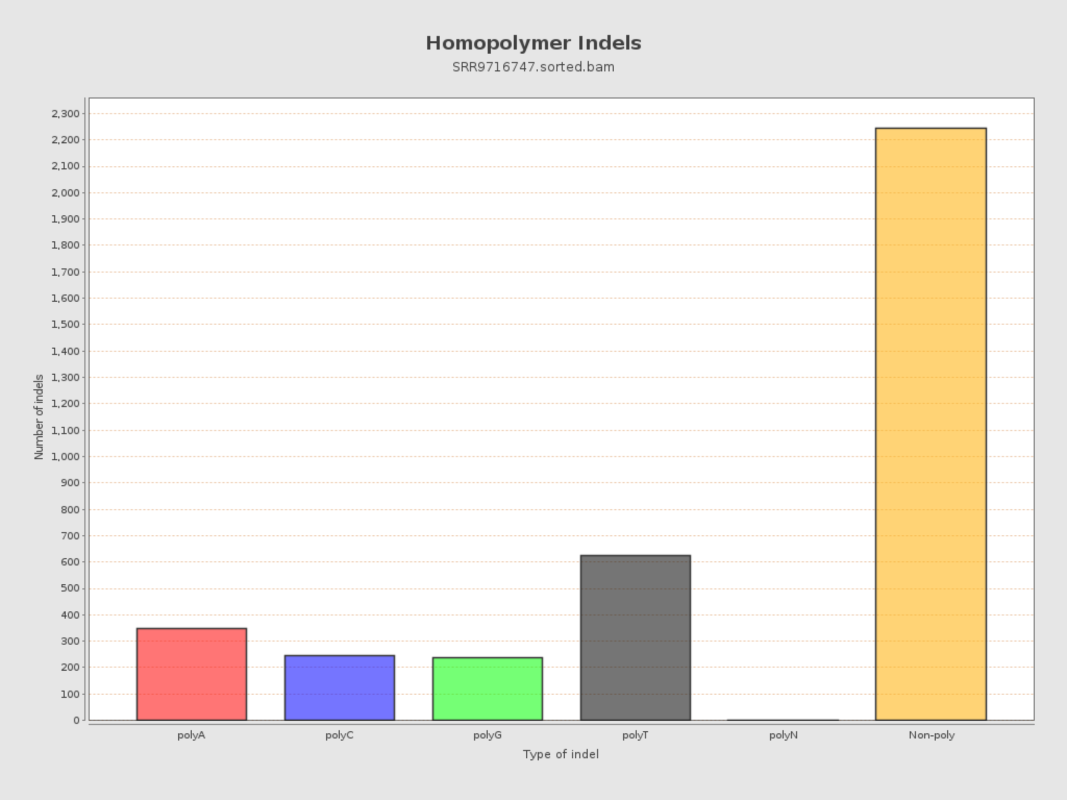
9. Results : Mapped Reads GC-content Distribution



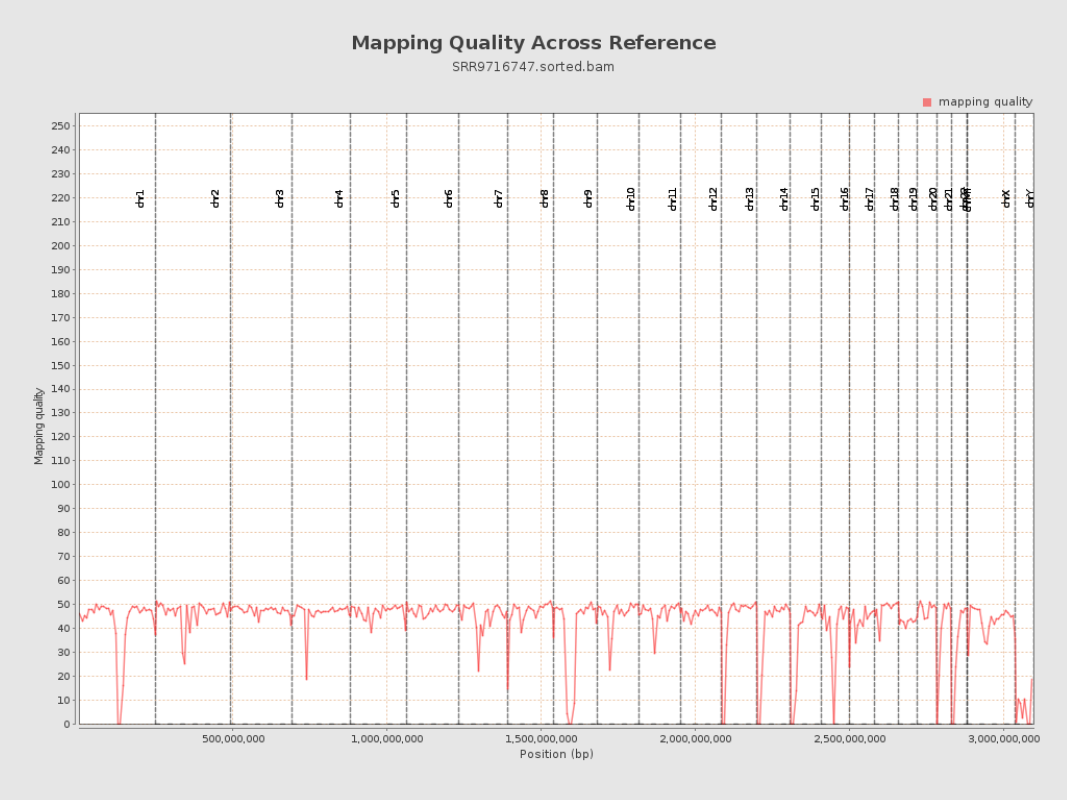
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram