Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 18:13:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716907.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_SRR9716907 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716907.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 18:13:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716907.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,157,911
Mapped reads	2,922,233 / 92.54%
Unmapped reads	235,678 / 7.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,678 / 0.62%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	187,145 / 5.93%
Duplication rate	4.97%
Clipped reads	2,938,039 / 93.04%

2.2. ACGT Content

Number/percentage of A's	42,432,625 / 24.91%
Number/percentage of C's	34,869,872 / 20.47%
Number/percentage of T's	51,535,443 / 30.25%
Number/percentage of G's	41,533,563 / 24.38%
Number/percentage of N's	2,218 / 0%
GC Percentage	44.84%

2.3. Coverage

Mean	0.0551

Standard Deviation	0.4151

2.4. Mapping Quality

Mean Mapping Quality	44.76

2.5. Mismatches and indels

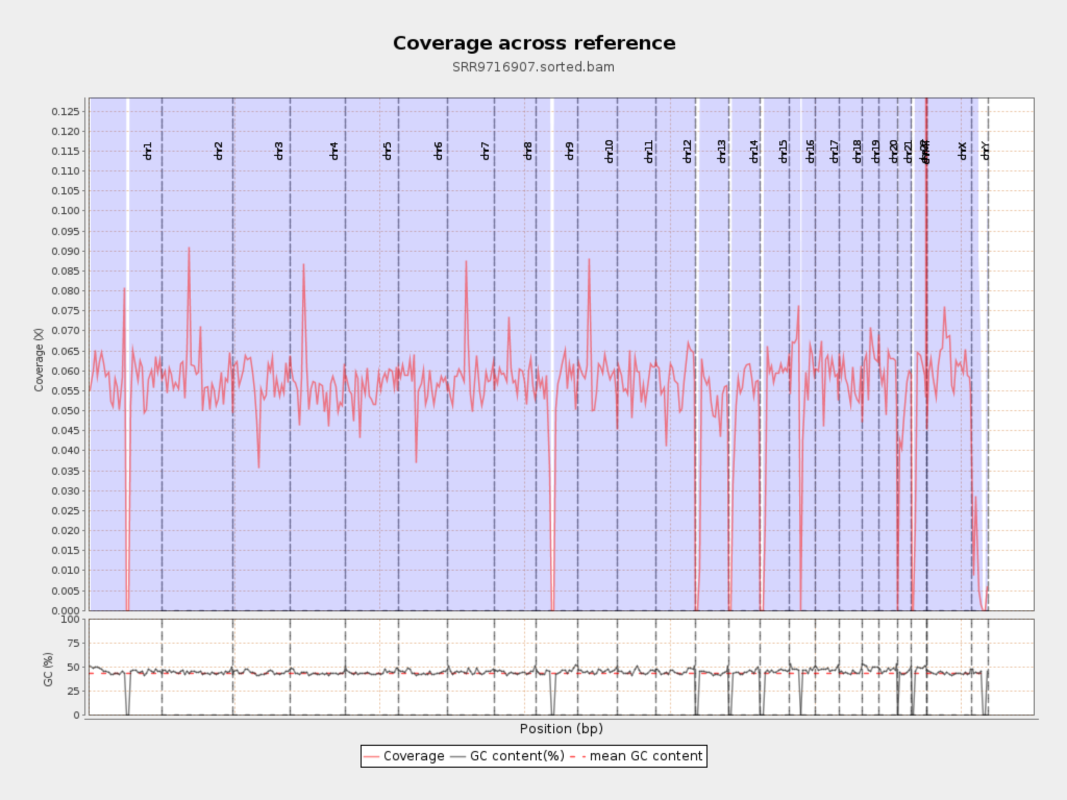
General error rate	0.51%
Mismatches	845,666
Insertions	10,189
Mapped reads with at least one insertion	0.35%
Deletions	30,434
Mapped reads with at least one deletion	1.03%
Homopolymer indels	41.75%

2.6. Chromosome stats

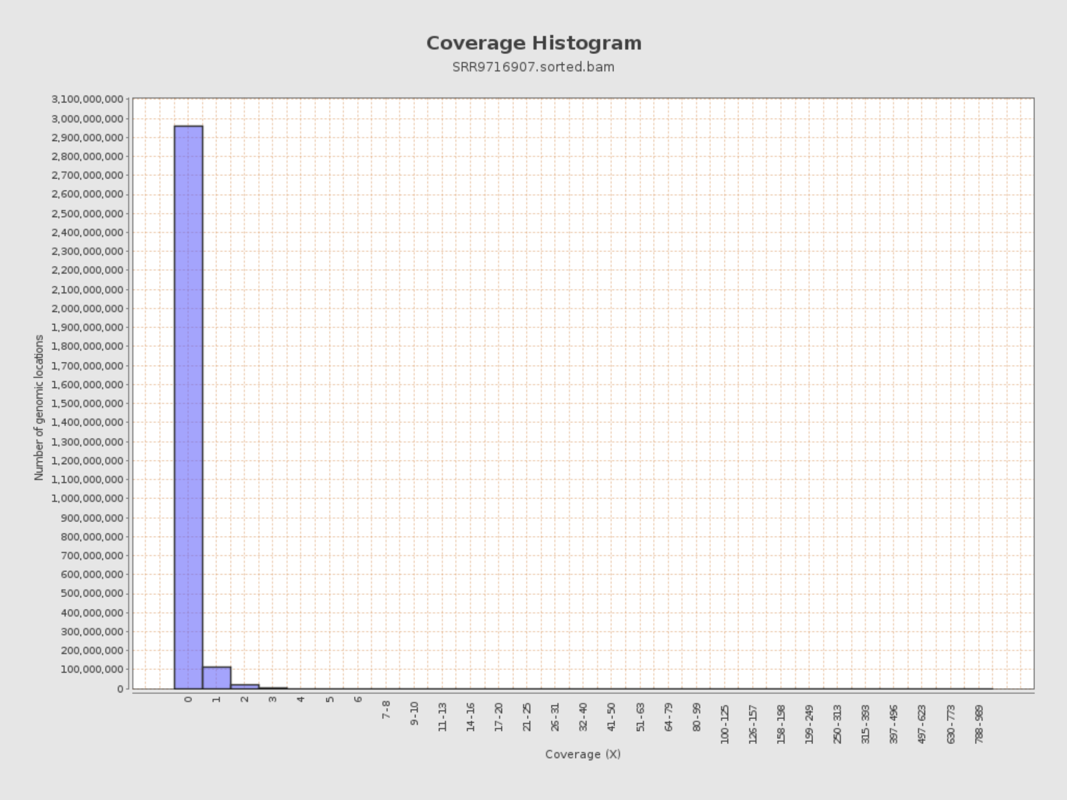
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13801776	0.0554	0.6777
chr2	243199373	14327132	0.0589	0.5551
chr3	198022430	11309102	0.0571	0.2855
chr4	191154276	10728557	0.0561	0.3324
chr5	180915260	10110641	0.0559	0.2826
chr6	171115067	9713464	0.0568	0.3227
chr7	159138663	9335585	0.0587	0.5583

chr8	146364022	8607246	0.0588	0.4385
chr9	141213431	7089225	0.0502	0.3393
chr10	135534747	8151970	0.0601	0.4339
chr11	135006516	7761288	0.0575	0.3887
chr12	133851895	7741075	0.0578	0.2942
chr13	115169878	5192600	0.0451	0.2549
chr14	107349540	5177819	0.0482	0.2783
chr15	102531392	5044825	0.0492	0.2736
chr16	90354753	5108791	0.0565	0.3119
chr17	81195210	4838494	0.0596	0.3306
chr18	78077248	4463290	0.0572	0.6339
chr19	59128983	3700061	0.0626	0.5282
chr20	63025520	3748680	0.0595	0.3041
chr21	48129895	2216562	0.0461	0.2961
chr22	51304566	2198982	0.0429	0.25
chrMT	16571	34078	2.0565	1.968
chrX	155270560	9514700	0.0613	0.3343
chrY	59373566	506291	0.0085	0.223

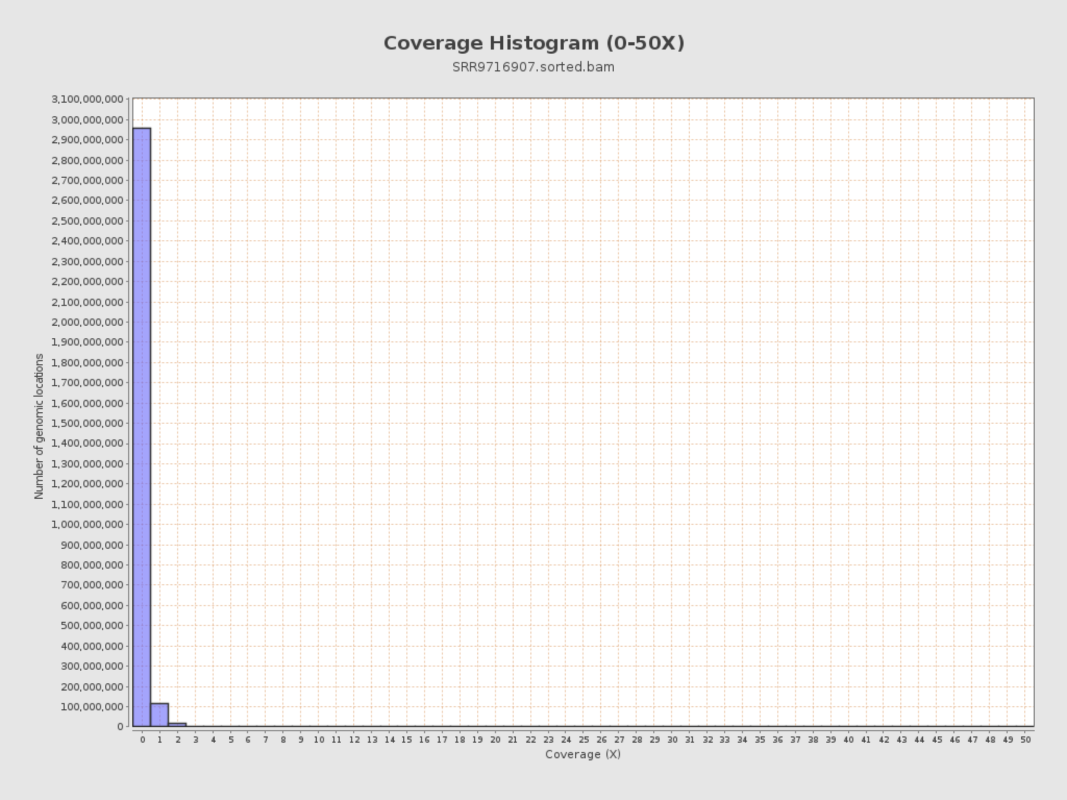
3. Results : Coverage across reference



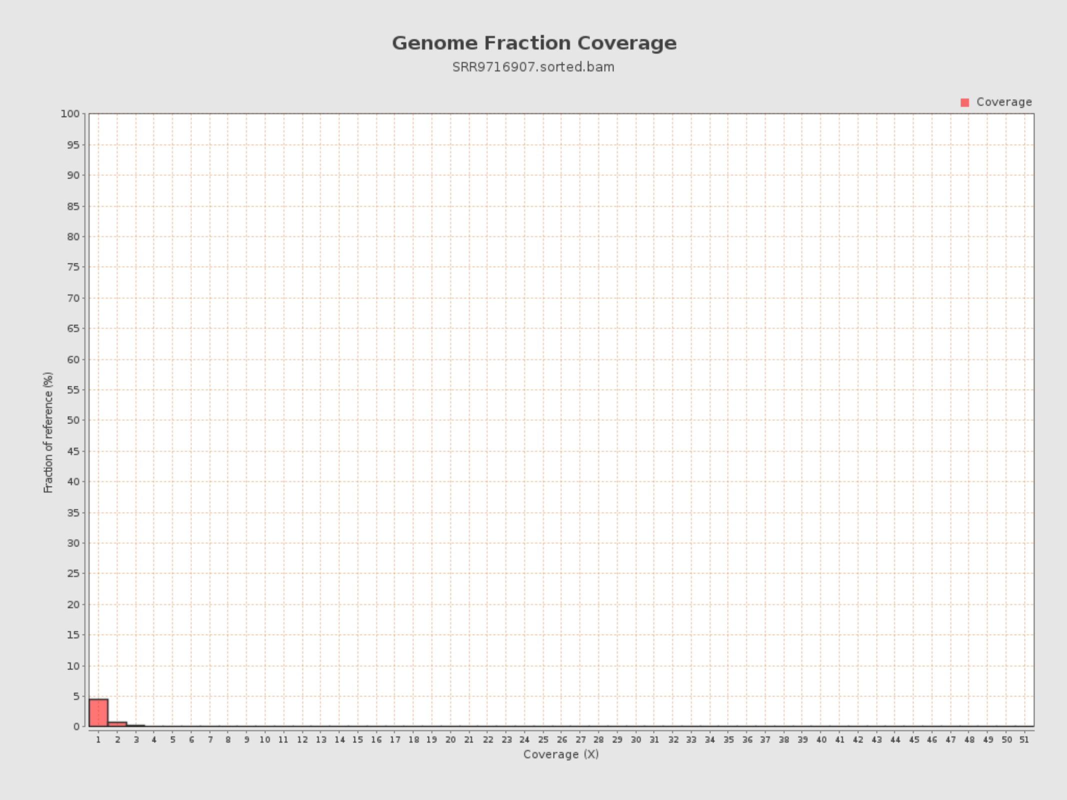
4. Results : Coverage Histogram



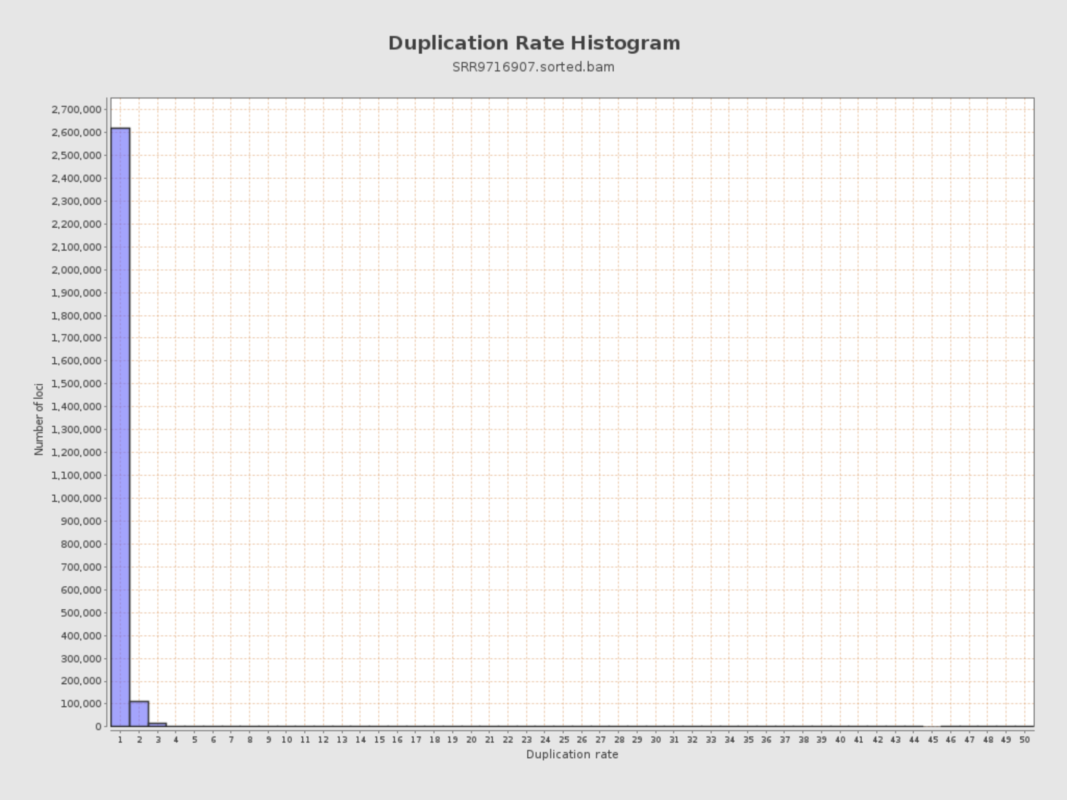
5. Results : Coverage Histogram (0-50X)



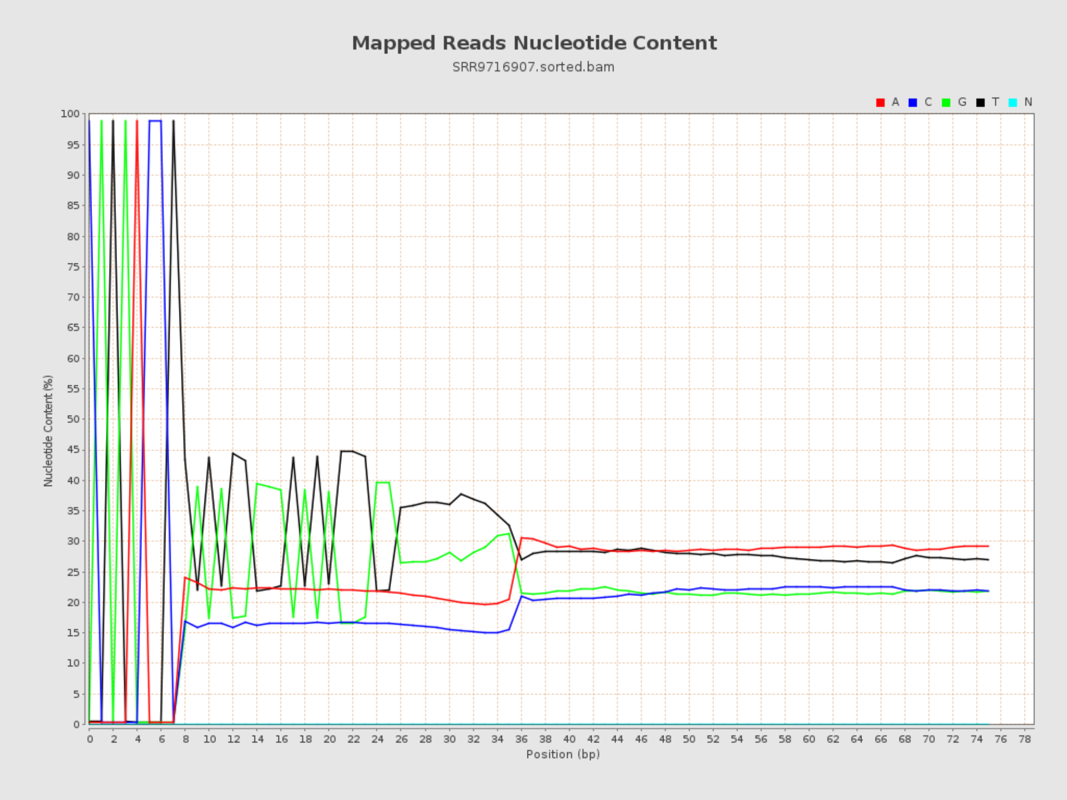
6. Results : Genome Fraction Coverage



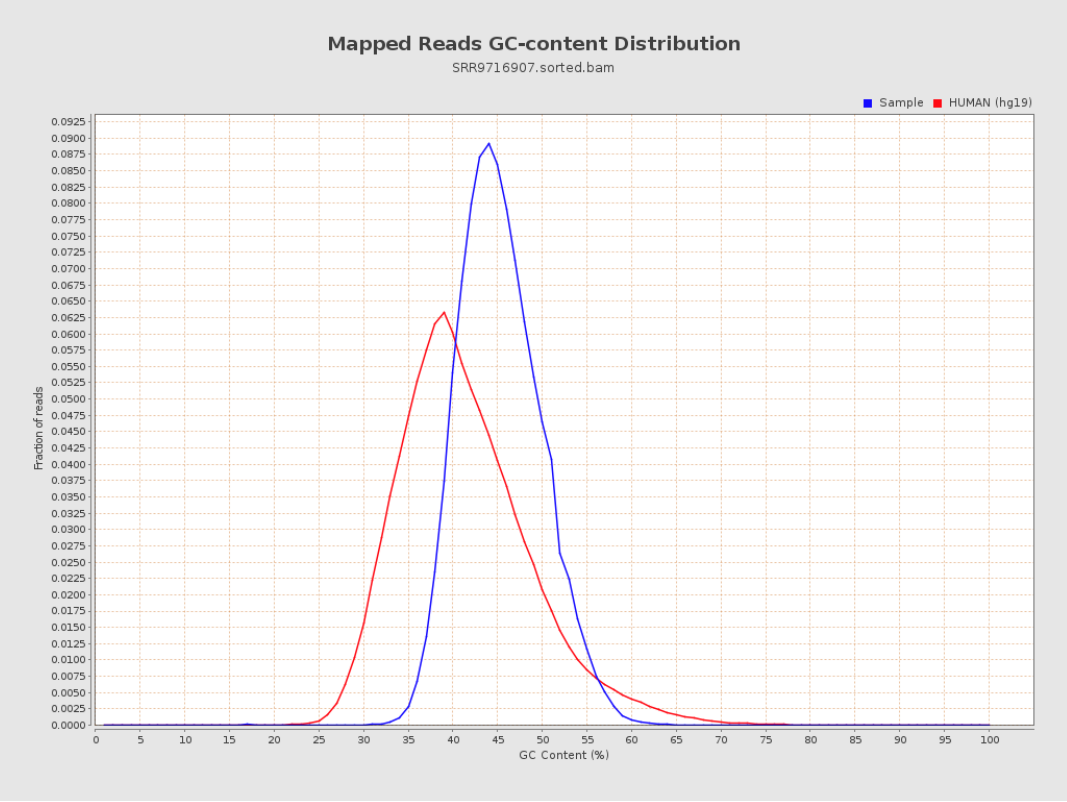
7. Results : Duplication Rate Histogram



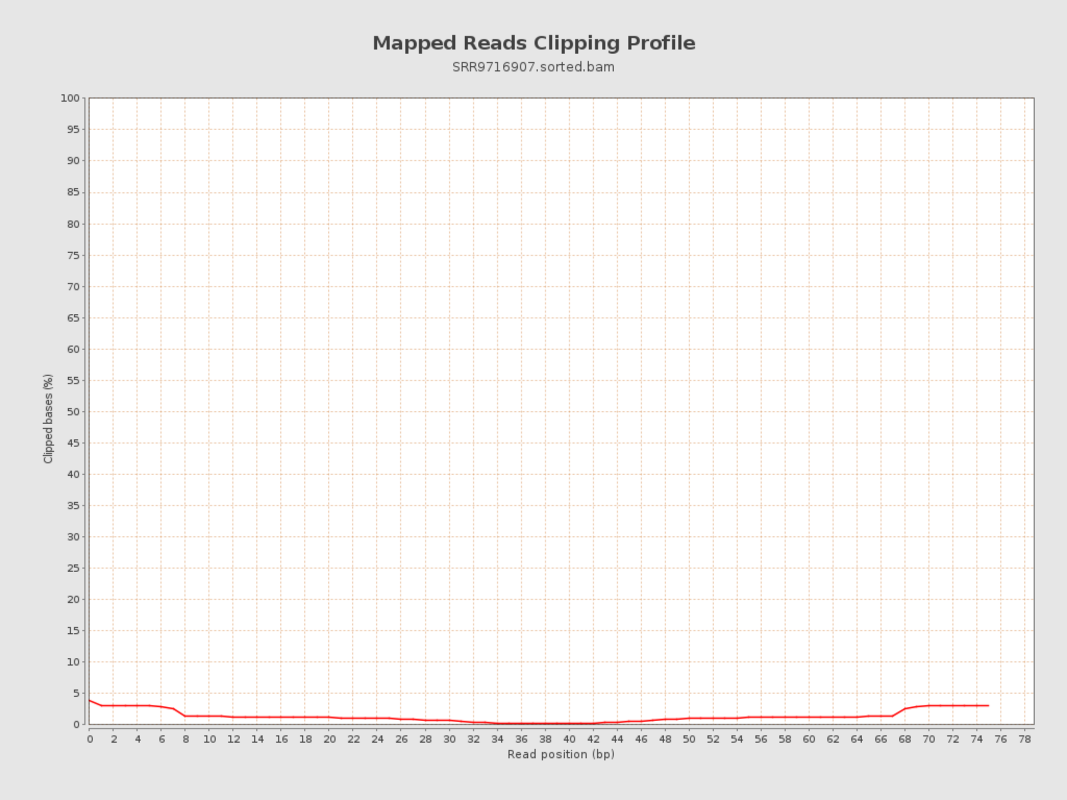
8. Results : Mapped Reads Nucleotide Content



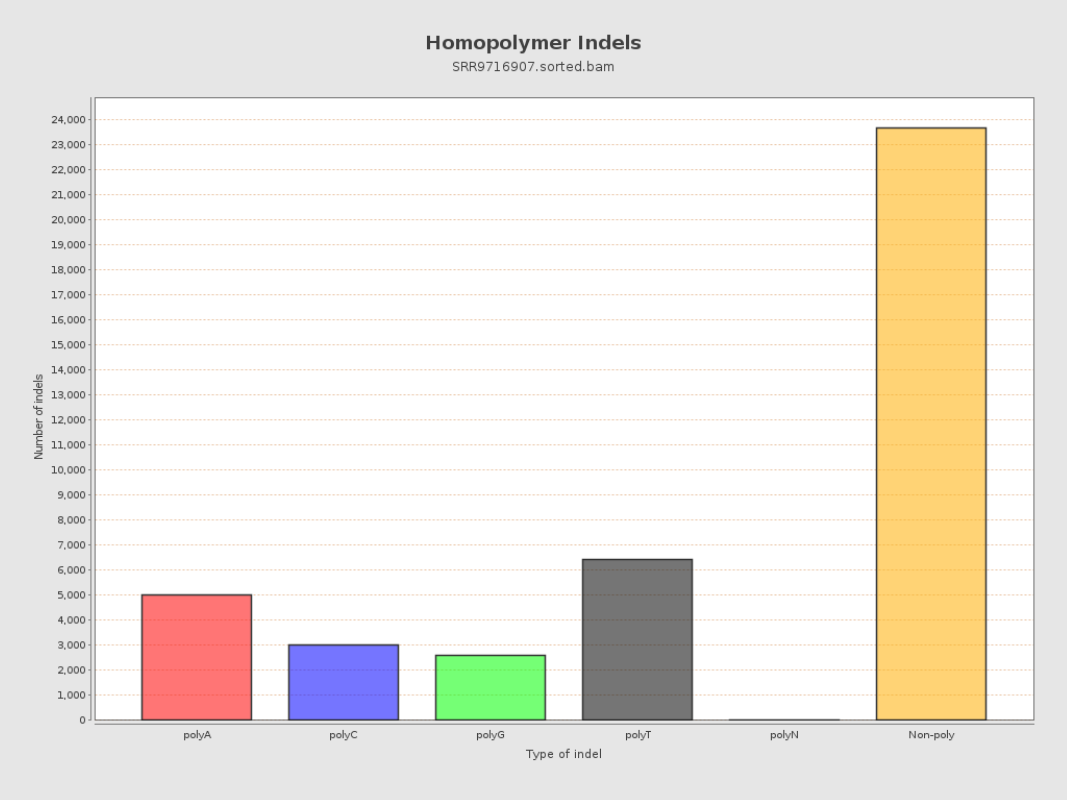
9. Results : Mapped Reads GC-content Distribution



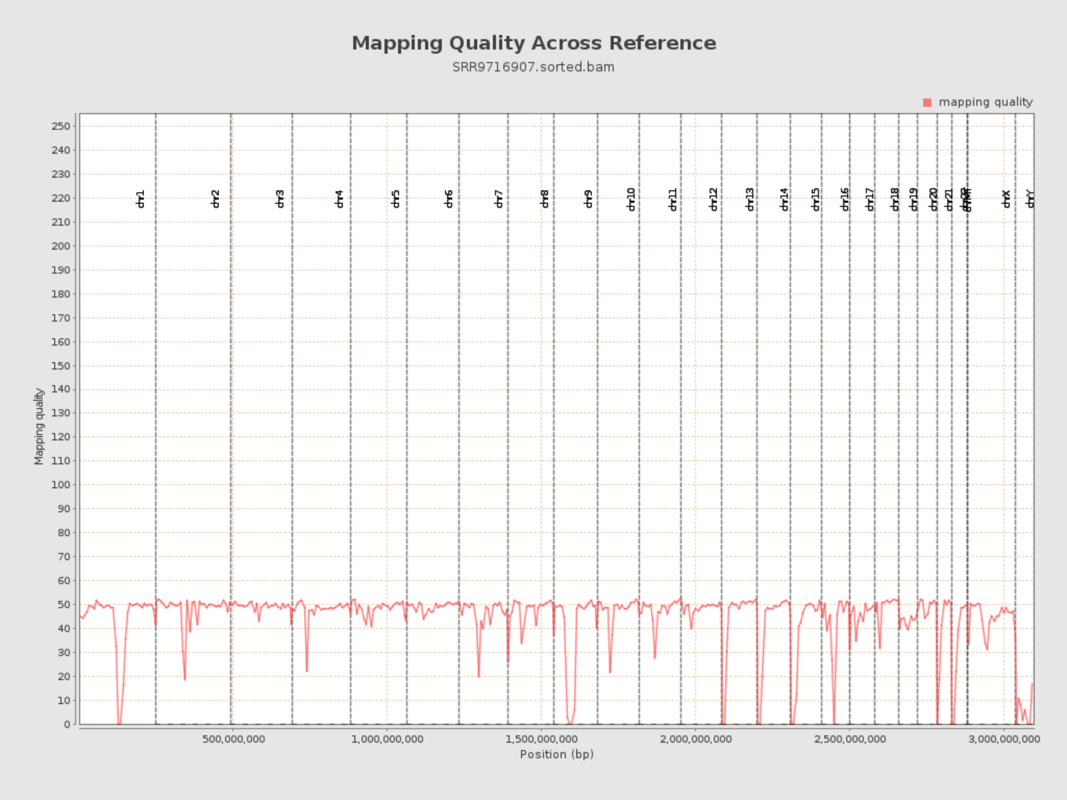
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram