Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 02:29:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716651.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_SRR9716651 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716651.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 02:29:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716651.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,645,800
Mapped reads	2,434,437 / 92.01%
Unmapped reads	211,363 / 7.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	72,192 / 2.73%
Read min/max/mean length	30 / 101 / 101.98
Duplicated reads (estimated)	77,070 / 2.91%
Duplication rate	2.16%
Clipped reads	2,503,243 / 94.61%

2.2. ACGT Content

Number/percentage of A's	46,446,570 / 25.57%
Number/percentage of C's	37,843,712 / 20.84%
Number/percentage of T's	53,835,987 / 29.64%
Number/percentage of G's	43,466,002 / 23.93%
Number/percentage of N's	21,668 / 0.01%
GC Percentage	44.77%

2.3. Coverage

Mean	0.0587

Standard Deviation	0.4462

2.4. Mapping Quality

Mean Mapping Quality	44.84

2.5. Mismatches and indels

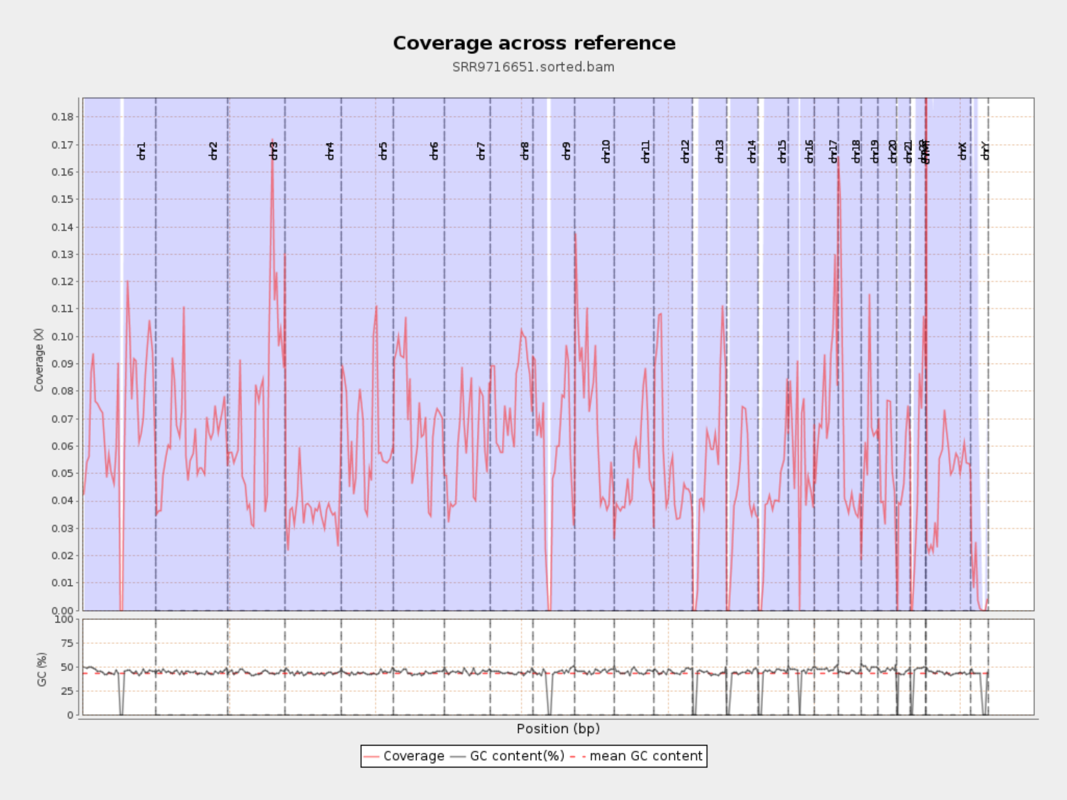
General error rate	0.77%
Mismatches	1,363,596
Insertions	15,433
Mapped reads with at least one insertion	0.62%
Deletions	37,561
Mapped reads with at least one deletion	1.52%
Homopolymer indels	38.87%

2.6. Chromosome stats

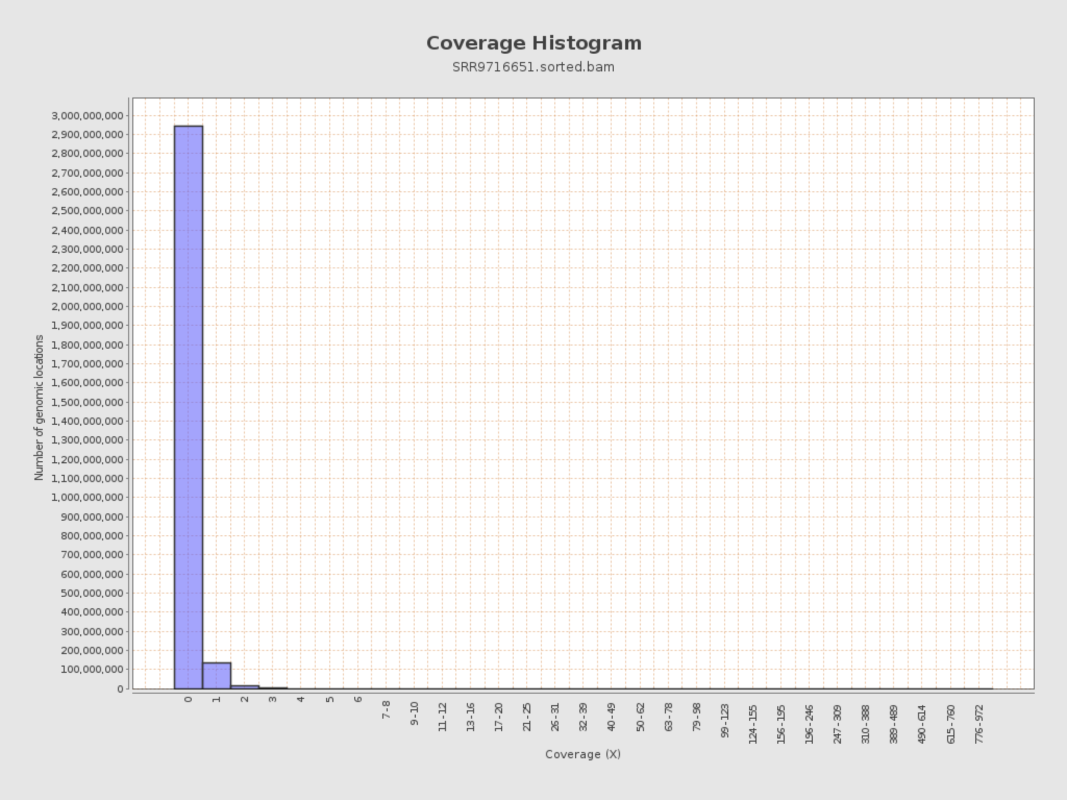
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17351066	0.0696	0.7102
chr2	243199373	15213294	0.0626	0.7081
chr3	198022430	14394567	0.0727	0.3148
chr4	191154276	7030253	0.0368	0.2448
chr5	180915260	11393181	0.063	0.2859
chr6	171115067	12233243	0.0715	0.3537
chr7	159138663	9448287	0.0594	0.5919

chr8	146364022	11409995	0.078	0.5758
chr9	141213431	8157370	0.0578	0.3964
chr10	135534747	9896390	0.073	0.5059
chr11	135006516	7005789	0.0519	0.3689
chr12	133851895	7565001	0.0565	0.2745
chr13	115169878	6273618	0.0545	0.2684
chr14	107349540	4366454	0.0407	0.2496
chr15	102531392	3846578	0.0375	0.2227
chr16	90354753	4998951	0.0553	0.299
chr17	81195210	6445174	0.0794	0.3709
chr18	78077248	4733891	0.0606	0.5128
chr19	59128983	3794728	0.0642	0.6238
chr20	63025520	3252679	0.0516	0.266
chr21	48129895	2352329	0.0489	0.2718
chr22	51304566	2660783	0.0519	0.2677
chrMT	16571	18411	1.111	1.8635
chrX	155270560	7400098	0.0477	0.2902
chrY	59373566	437626	0.0074	0.2439

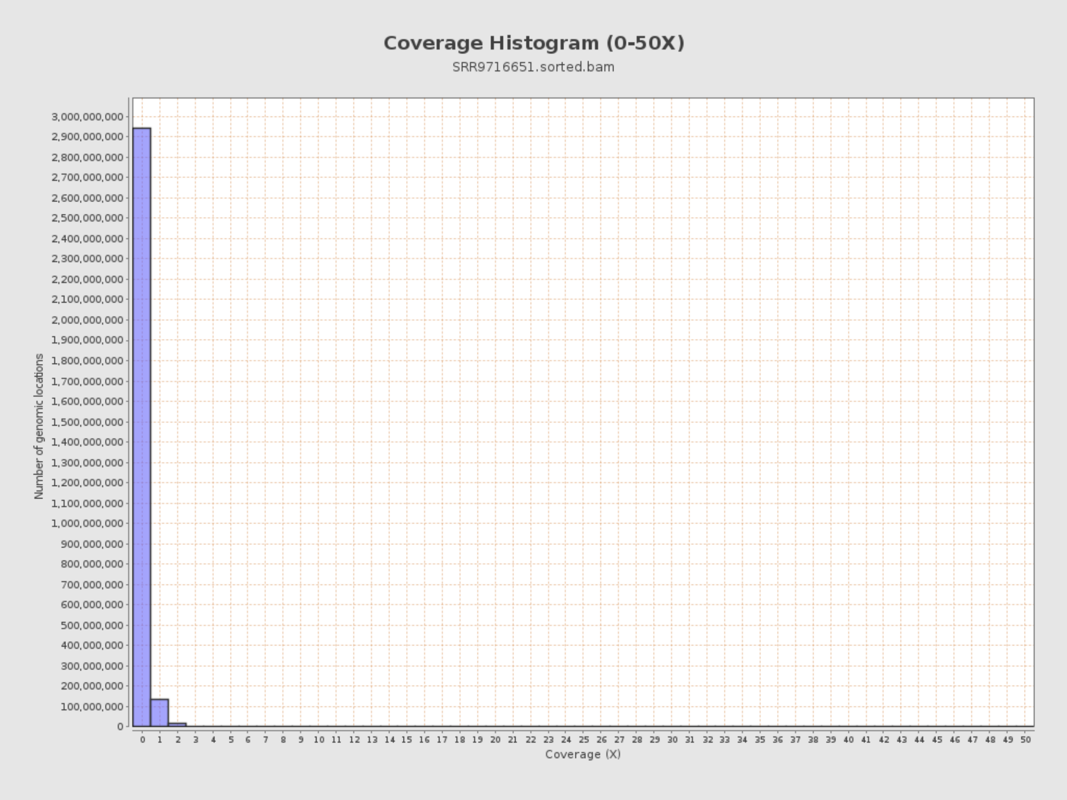
3. Results : Coverage across reference



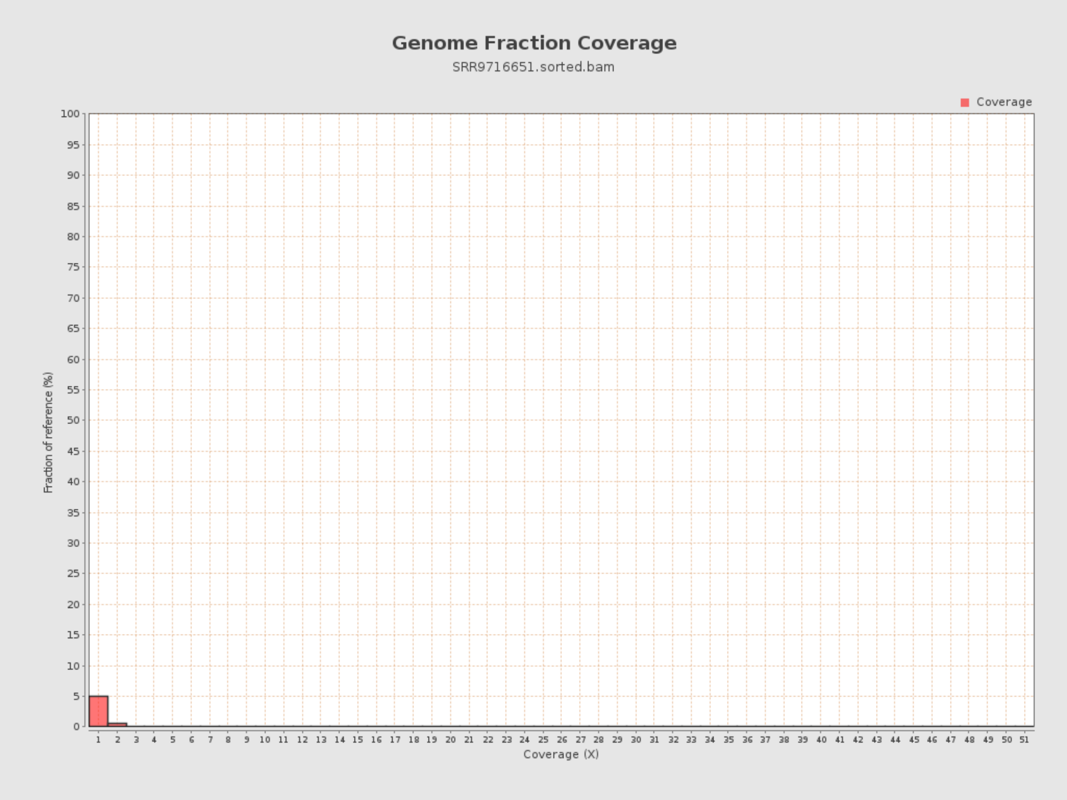
4. Results : Coverage Histogram



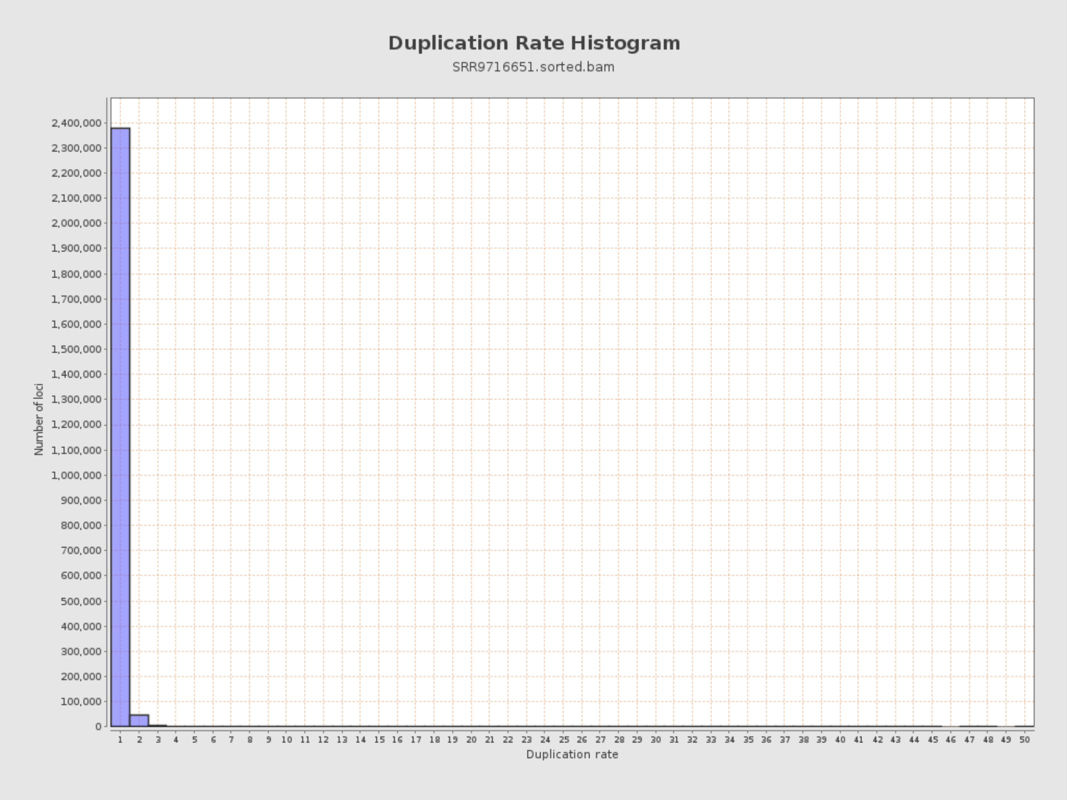
5. Results : Coverage Histogram (0-50X)



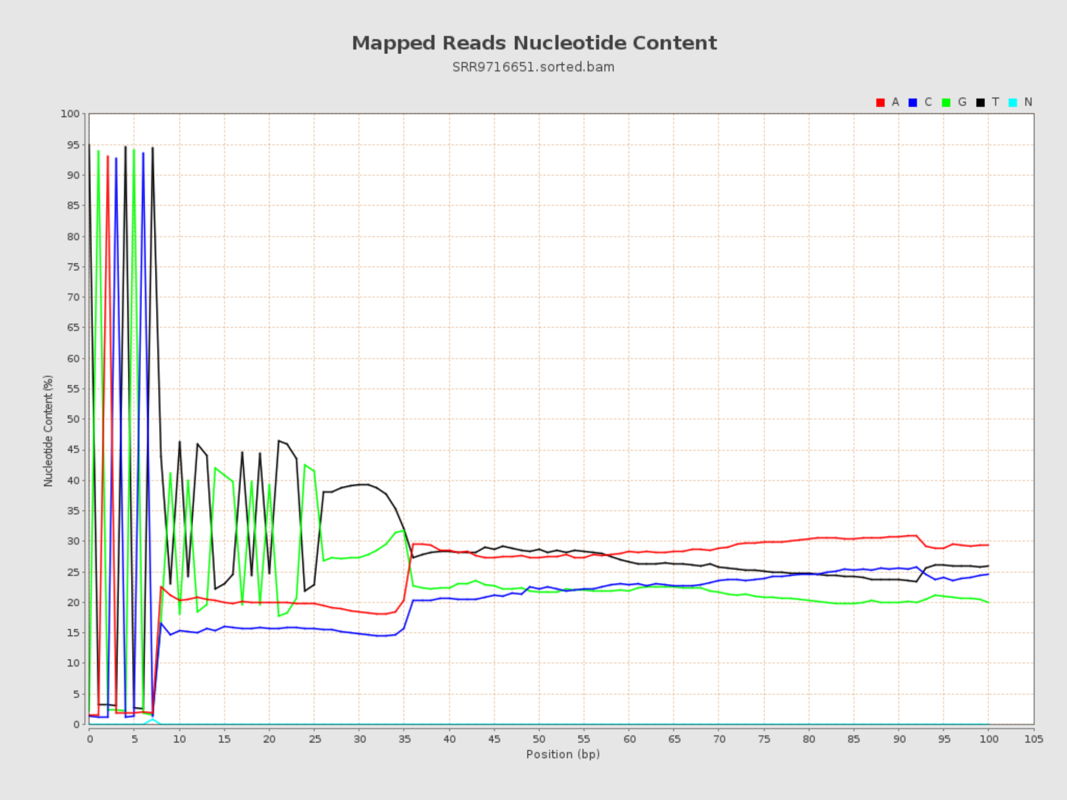
6. Results : Genome Fraction Coverage



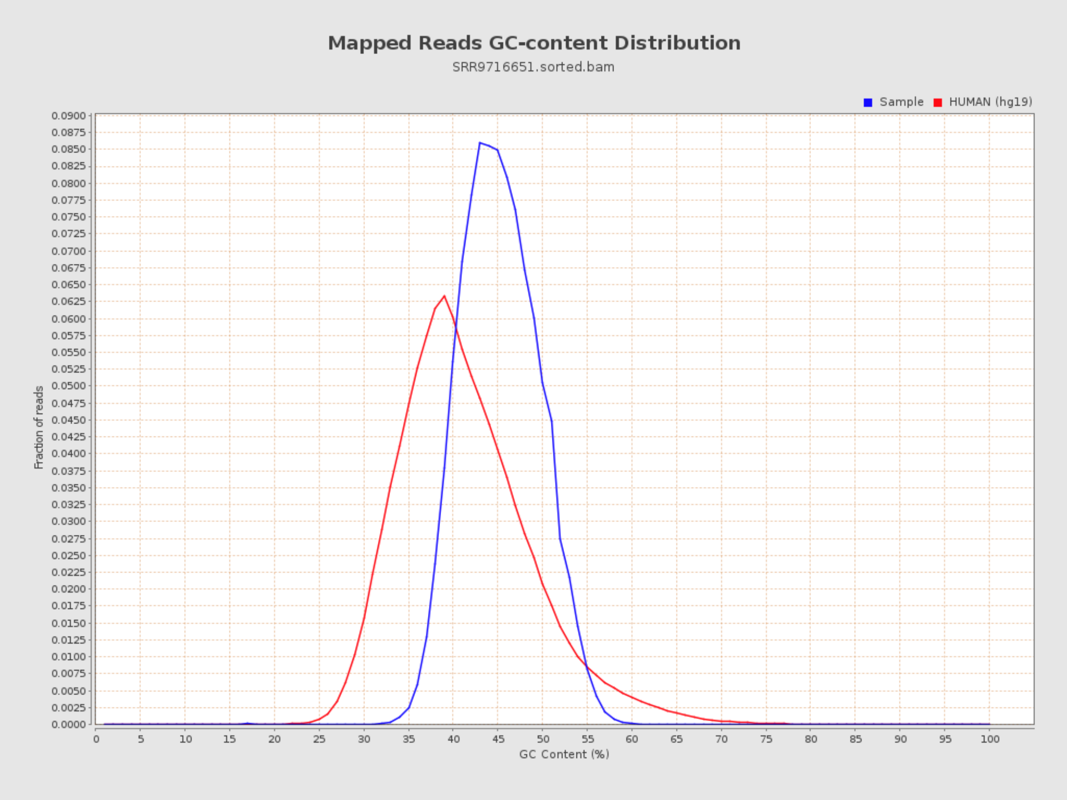
7. Results : Duplication Rate Histogram



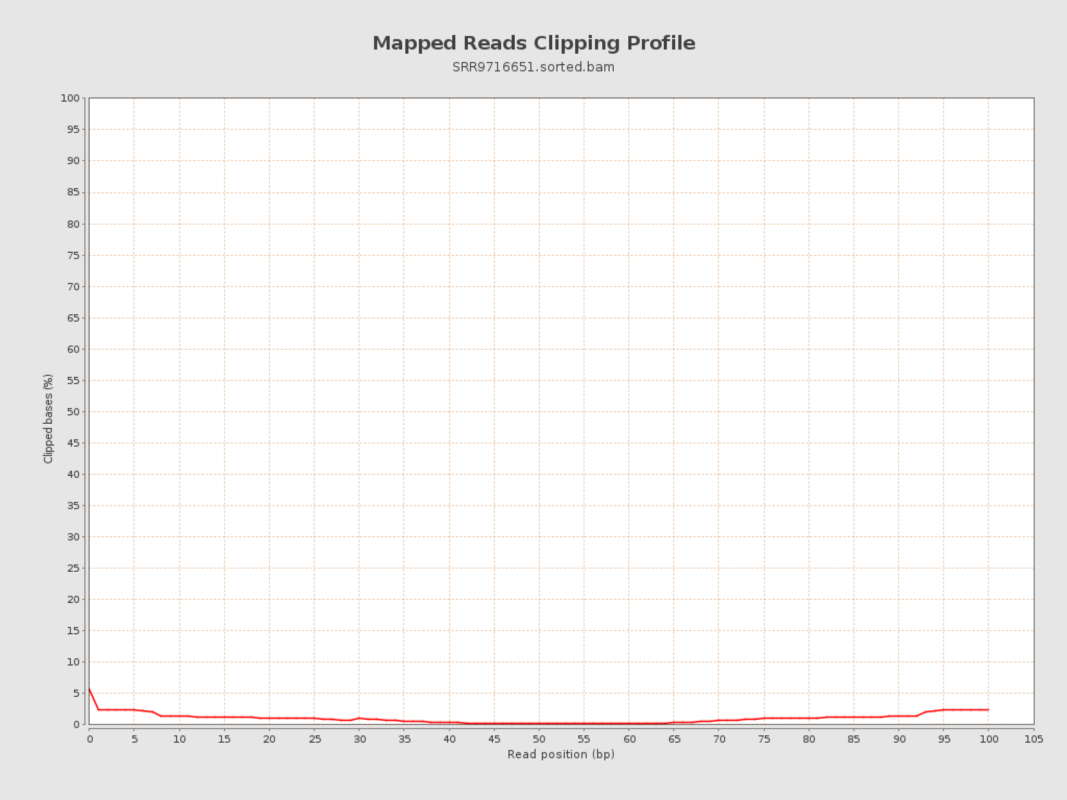
8. Results : Mapped Reads Nucleotide Content



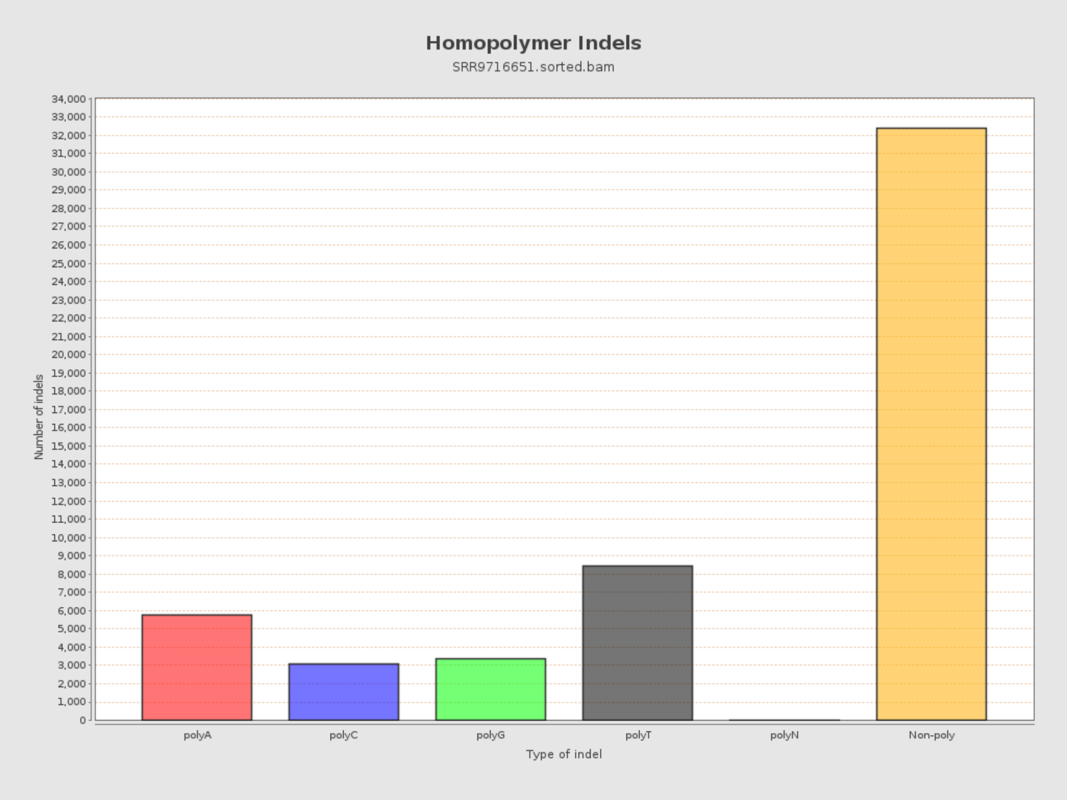
9. Results : Mapped Reads GC-content Distribution



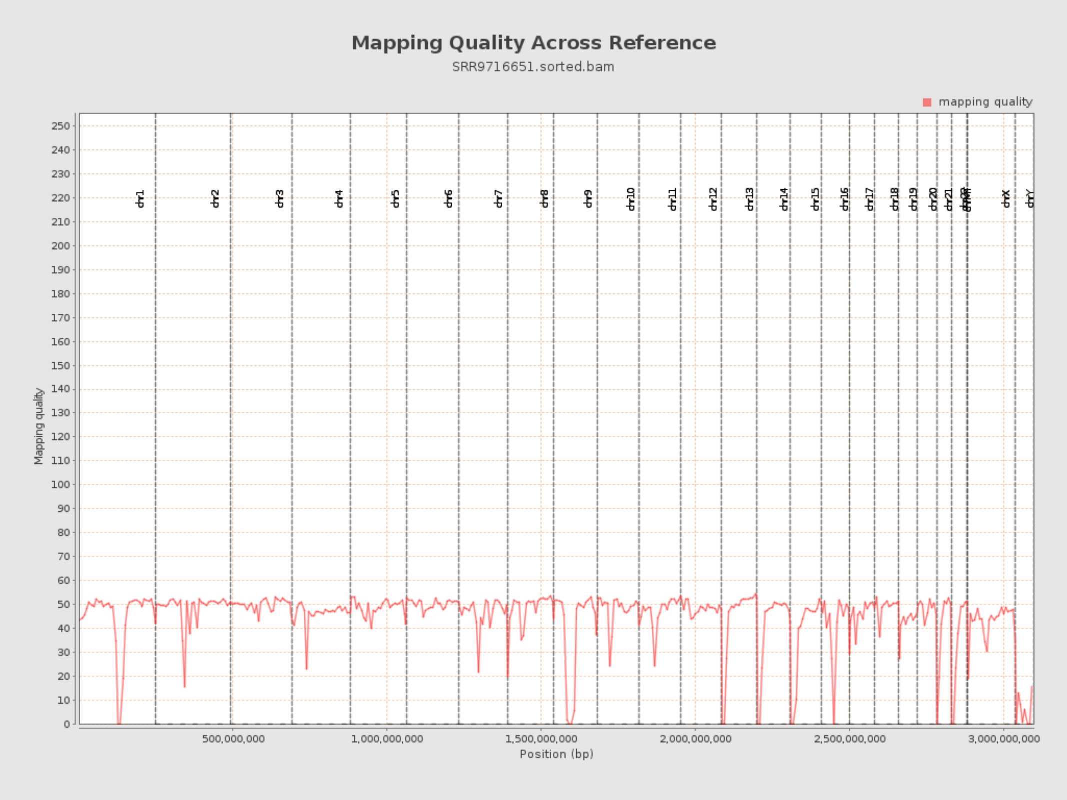
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram