Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 15:32:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716861.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_SRR9716861 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716861.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 15:32:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716861.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,994,854
Mapped reads	3,733,118 / 93.45%
Unmapped reads	261,736 / 6.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	79,620 / 1.99%
Read min/max/mean length	30 / 101 / 101.71
Duplicated reads (estimated)	295,813 / 7.4%
Duplication rate	6.01%
Clipped reads	3,807,423 / 95.31%

2.2. ACGT Content

Number/percentage of A's	70,862,431 / 24.75%
Number/percentage of C's	58,856,388 / 20.56%
Number/percentage of T's	85,441,986 / 29.84%
Number/percentage of G's	71,131,137 / 24.84%
Number/percentage of N's	10,768 / 0%
GC Percentage	45.4%

2.3. Coverage

Mean	0.0925

Standard Deviation	0.7046

2.4. Mapping Quality

Mean Mapping Quality	46.02

2.5. Mismatches and indels

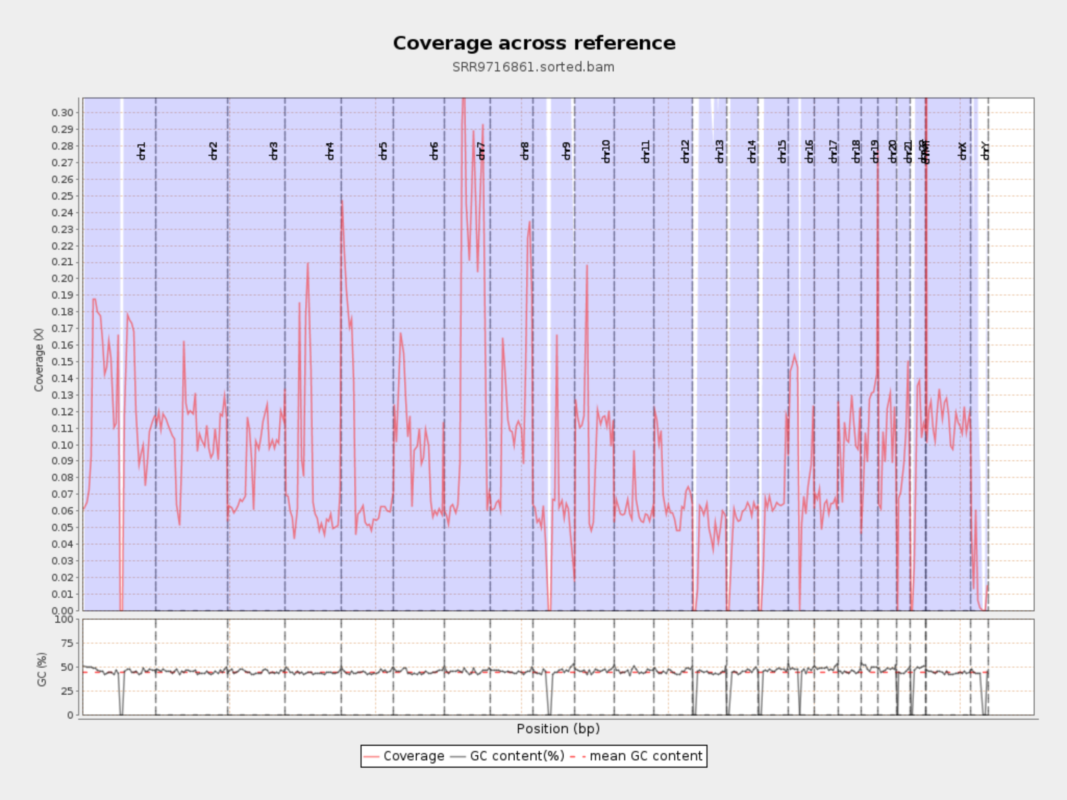
General error rate	0.67%
Mismatches	1,851,555
Insertions	23,451
Mapped reads with at least one insertion	0.62%
Deletions	51,086
Mapped reads with at least one deletion	1.35%
Homopolymer indels	39.3%

2.6. Chromosome stats

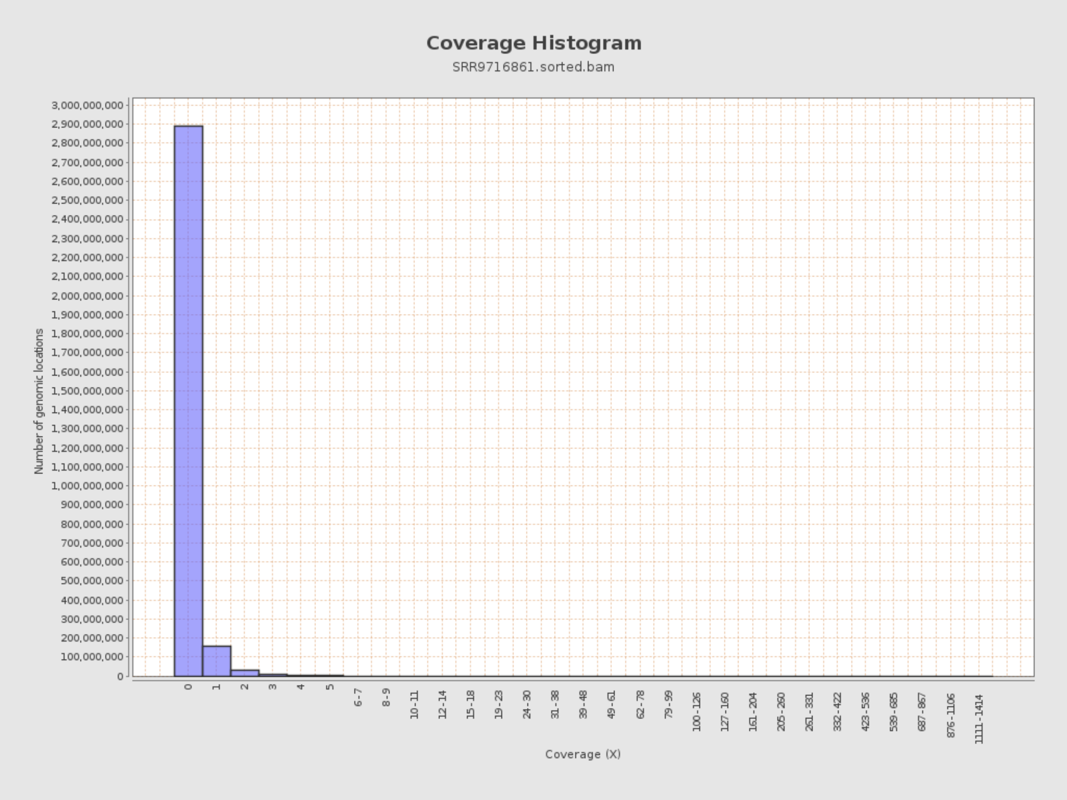
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	30377028	0.1219	1.2749
chr2	243199373	26351204	0.1084	0.7183
chr3	198022430	18071792	0.0913	0.4079
chr4	191154276	15074443	0.0789	0.6148
chr5	180915260	16662769	0.0921	0.4221
chr6	171115067	16685198	0.0975	0.4571
chr7	159138663	26273839	0.1651	1.3839

chr8	146364022	17438683	0.1191	0.6973
chr9	141213431	7886664	0.0558	0.4466
chr10	135534747	14616310	0.1078	0.9743
chr11	135006516	8260461	0.0612	0.5288
chr12	133851895	9767938	0.073	0.3596
chr13	115169878	5156284	0.0448	0.2744
chr14	107349540	5461361	0.0509	0.3298
chr15	102531392	5909064	0.0576	0.3174
chr16	90354753	8669486	0.0959	0.4591
chr17	81195210	5218031	0.0643	0.4014
chr18	78077248	8151449	0.1044	0.6977
chr19	59128983	6929193	0.1172	0.9209
chr20	63025520	6304355	0.1	0.4649
chr21	48129895	4045070	0.084	0.5044
chr22	51304566	4227530	0.0824	0.4087
chrMT	16571	41608	2.5109	2.5082
chrX	155270560	17850217	0.115	0.4938
chrY	59373566	979062	0.0165	0.5671

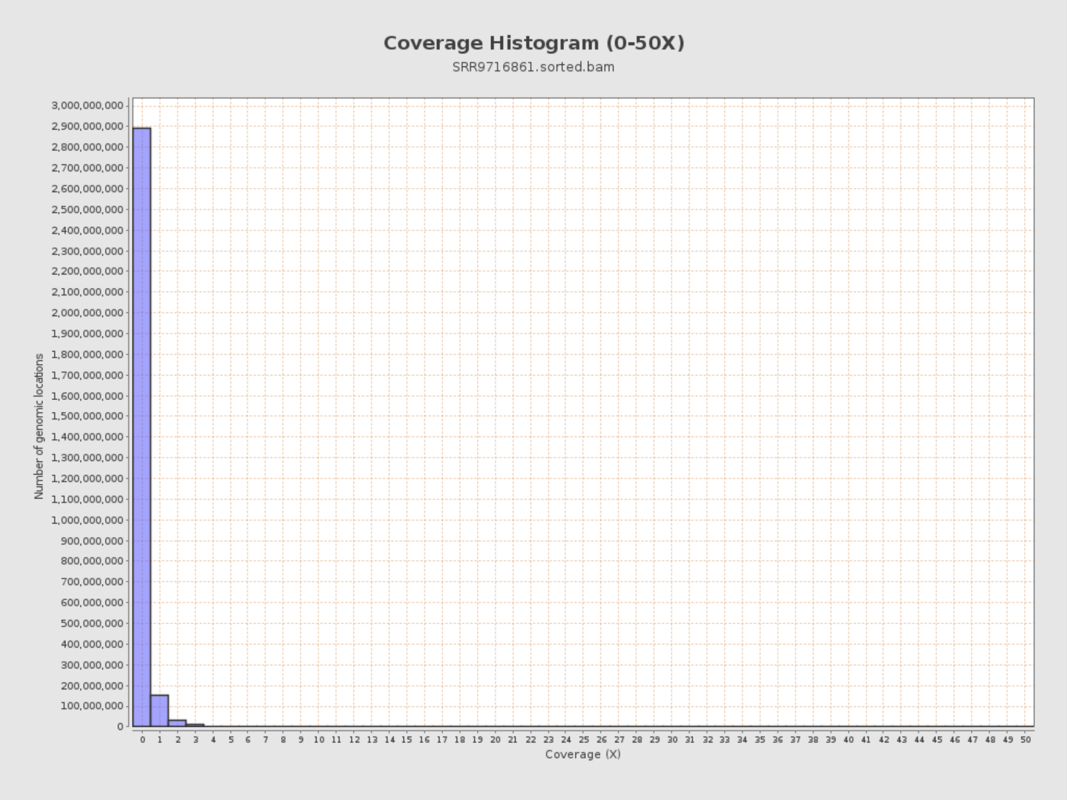
3. Results : Coverage across reference



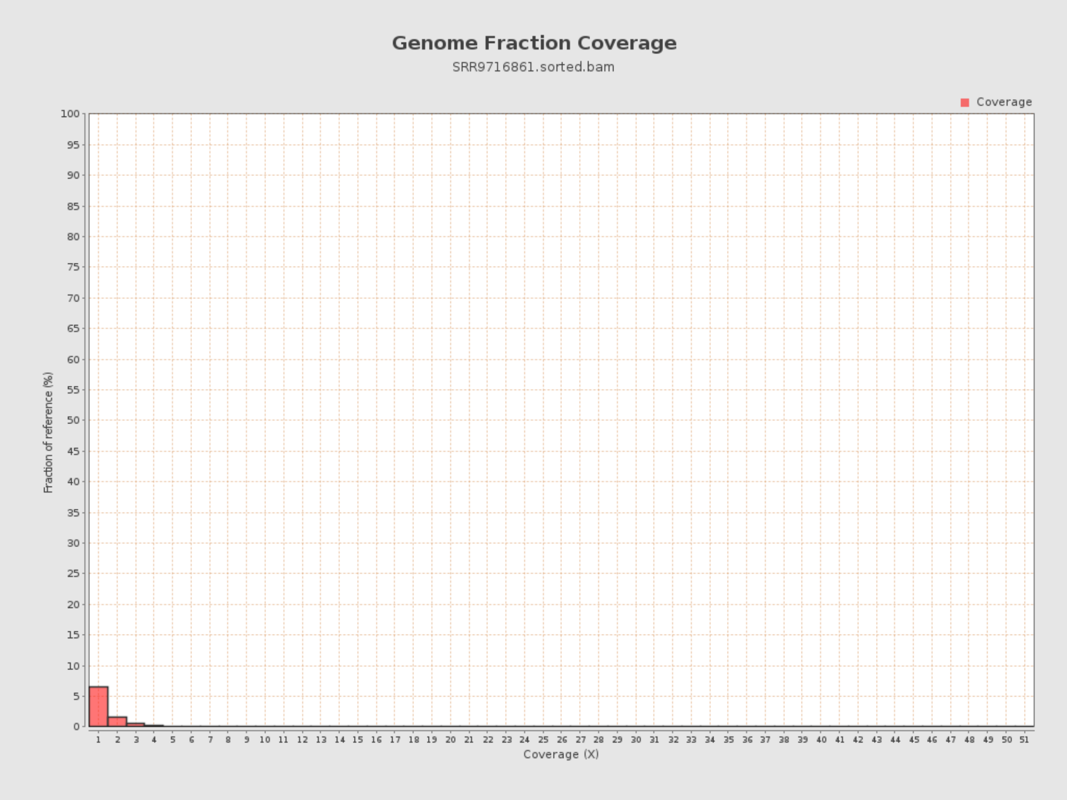
4. Results : Coverage Histogram



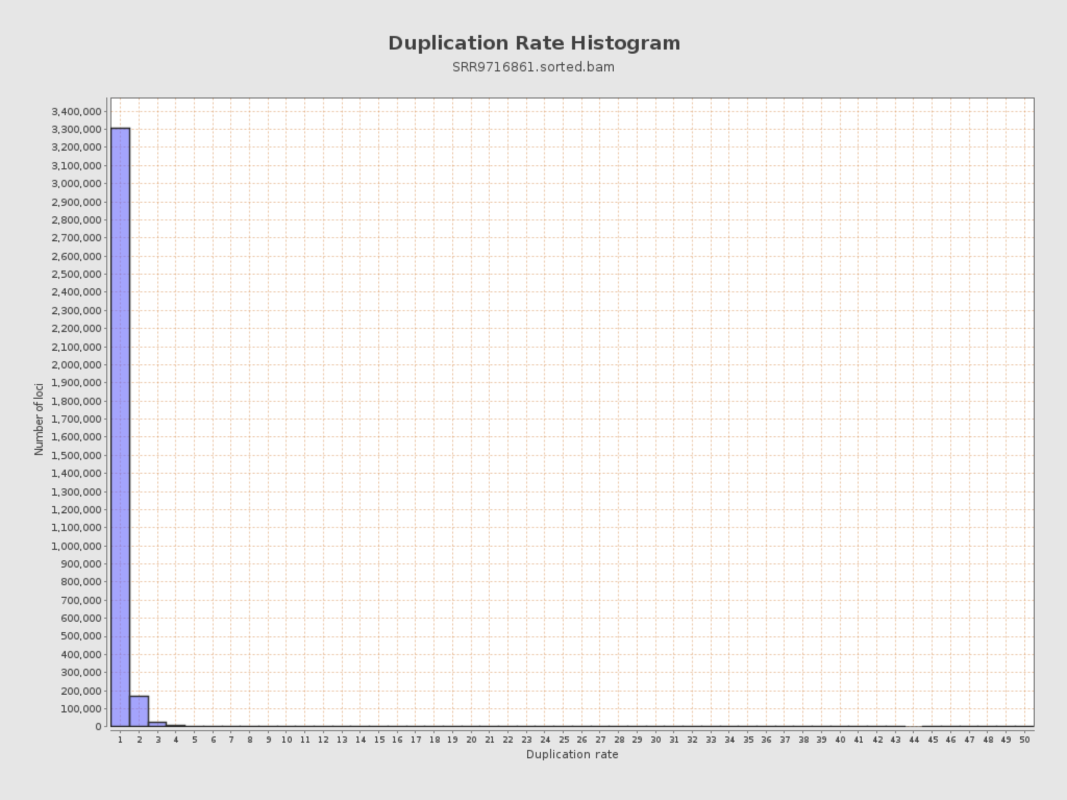
5. Results : Coverage Histogram (0-50X)



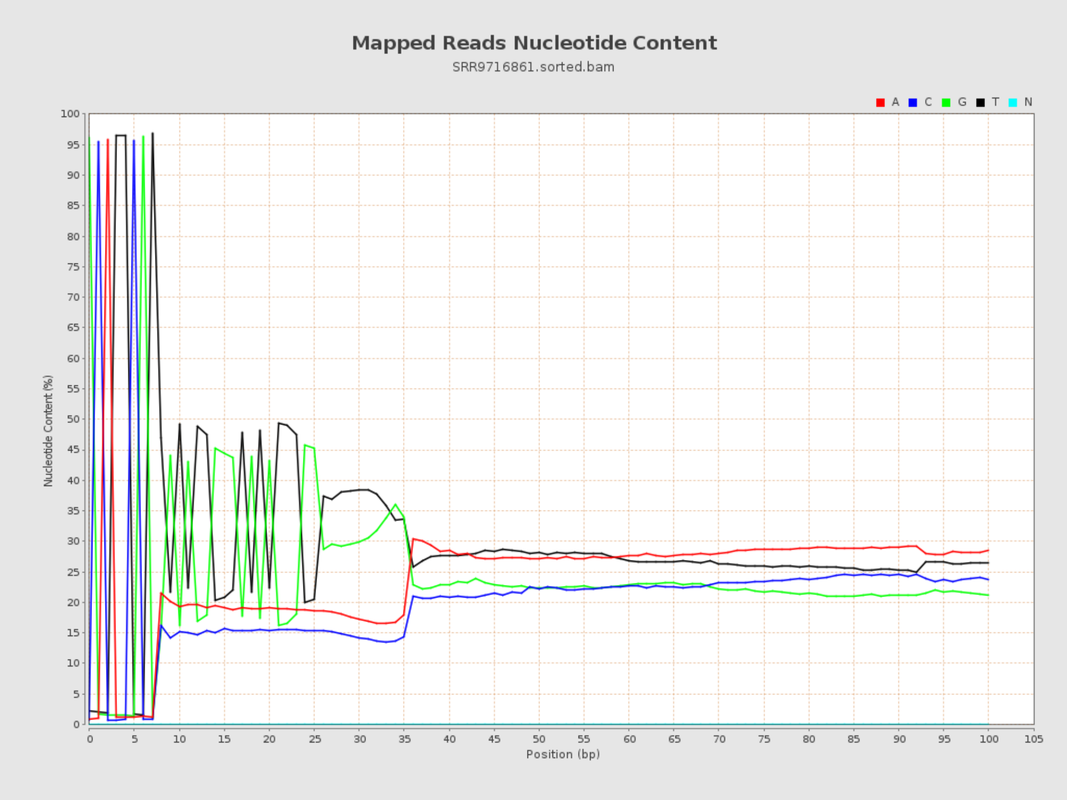
6. Results : Genome Fraction Coverage



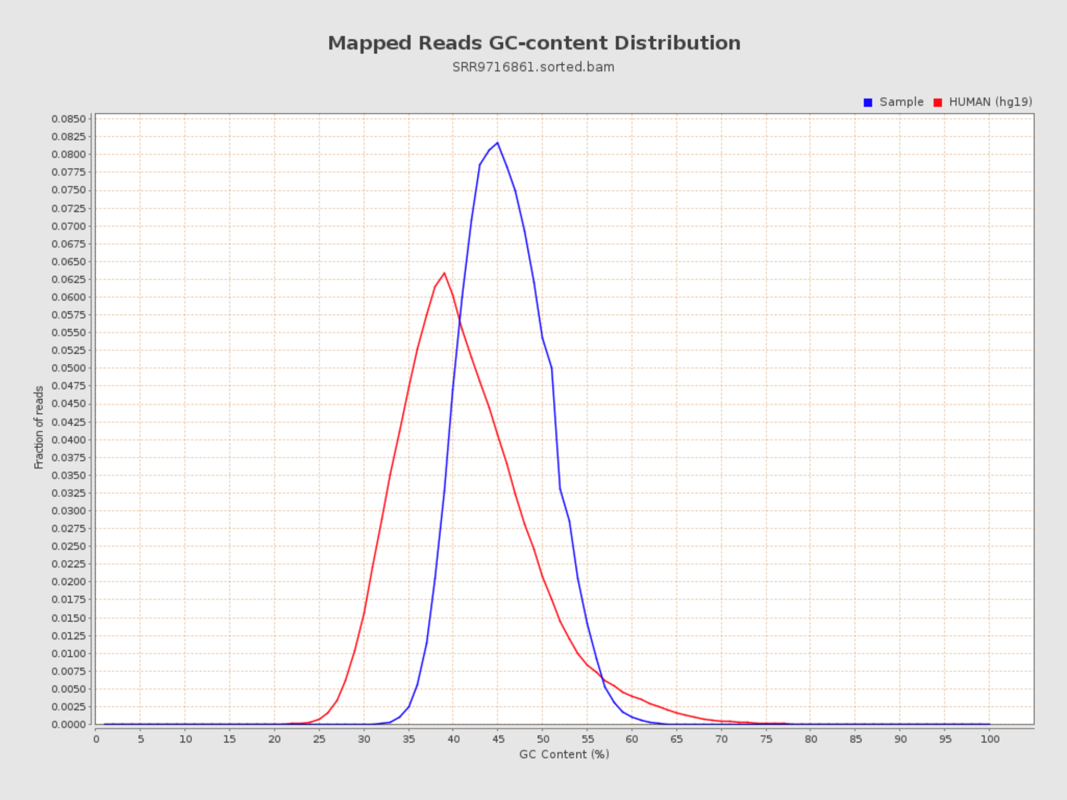
7. Results : Duplication Rate Histogram



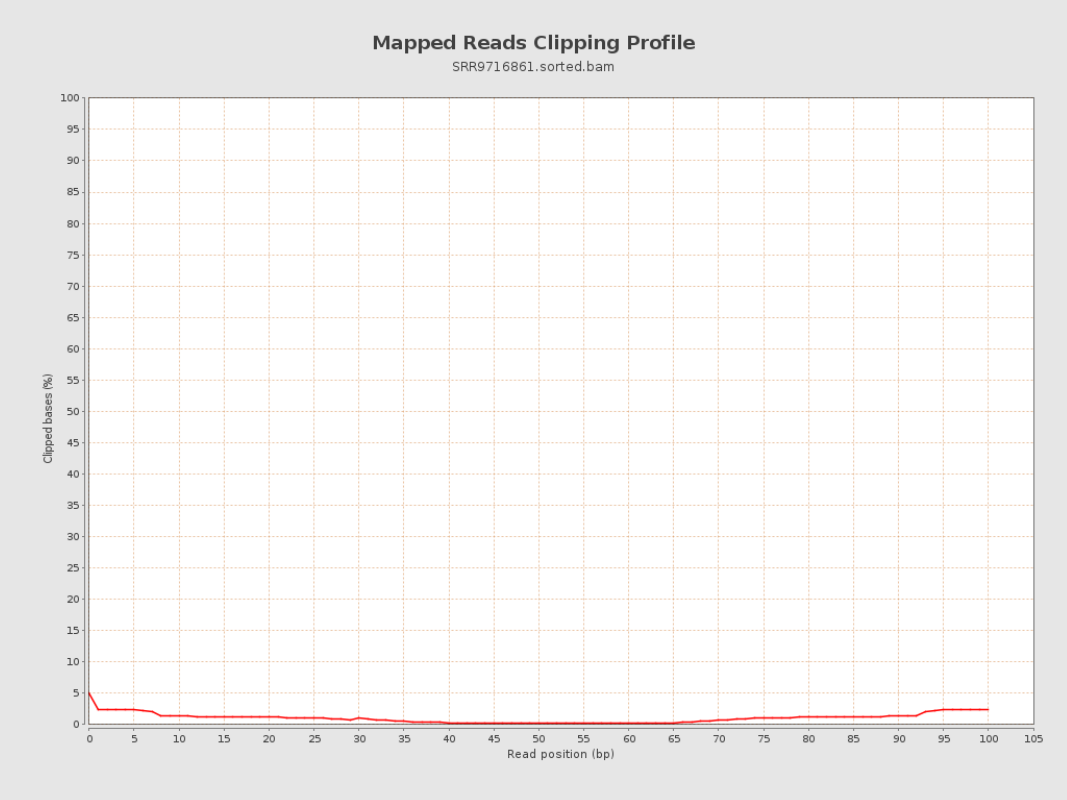
8. Results : Mapped Reads Nucleotide Content



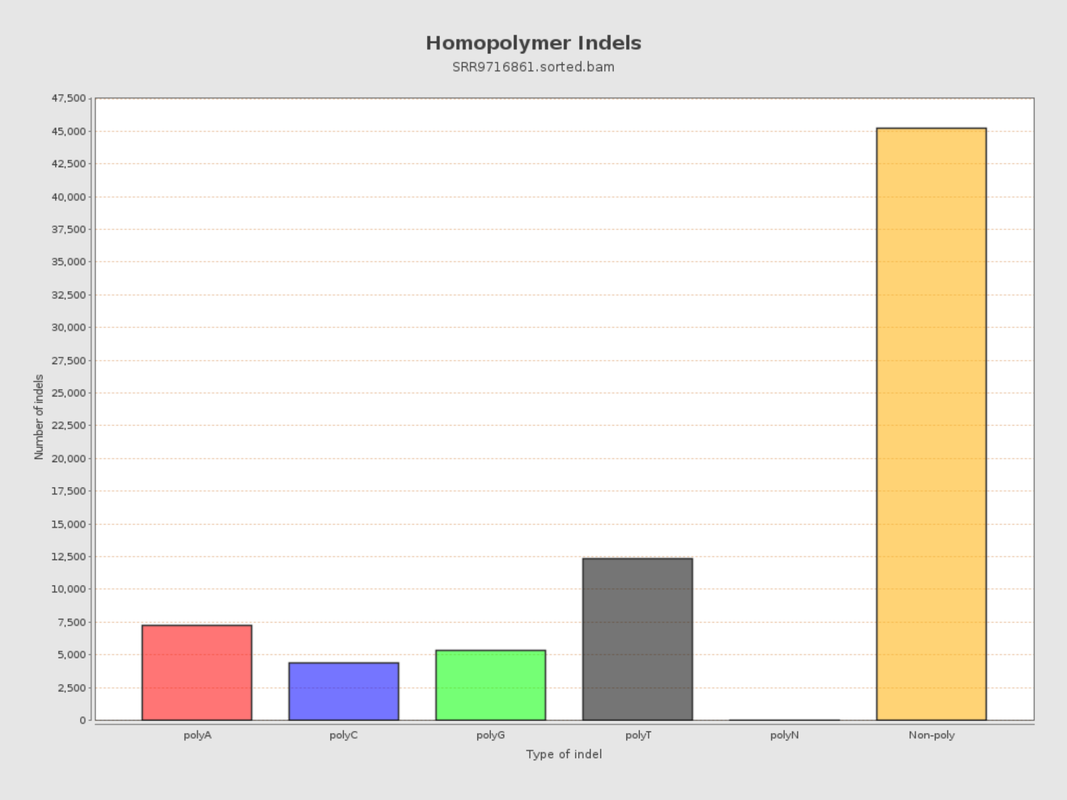
9. Results : Mapped Reads GC-content Distribution



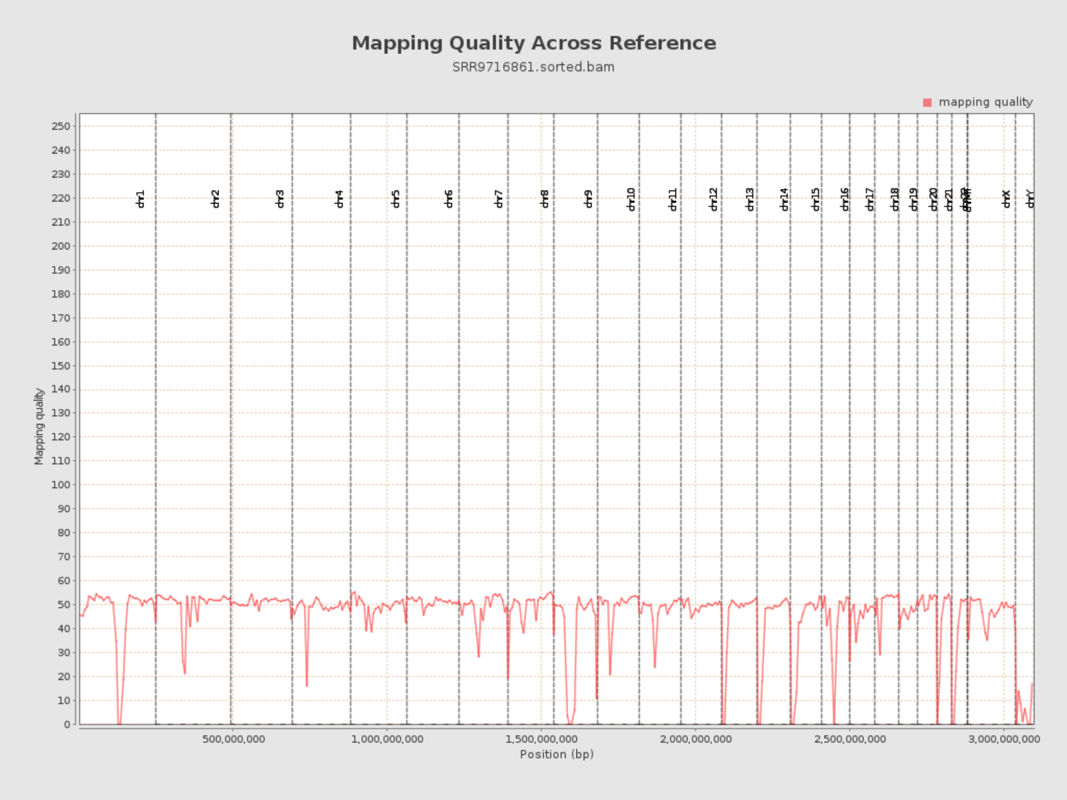
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram