Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 14:45:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716847.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_SRR9716847 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716847.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 14:45:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716847.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,639,970
Mapped reads	1,525,906 / 93.04%
Unmapped reads	114,064 / 6.96%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,175 / 1.78%
Read min/max/mean length	30 / 101 / 101.64
Duplicated reads (estimated)	57,081 / 3.48%
Duplication rate	2.68%
Clipped reads	1,553,544 / 94.73%

2.2. ACGT Content

Number/percentage of A's	30,563,690 / 25.15%
Number/percentage of C's	25,033,015 / 20.6%
Number/percentage of T's	37,524,403 / 30.88%
Number/percentage of G's	28,399,483 / 23.37%
Number/percentage of N's	8,928 / 0.01%
GC Percentage	43.97%

2.3. Coverage

Mean	0.0393

Standard Deviation	0.3532

2.4. Mapping Quality

Mean Mapping Quality	47.88

2.5. Mismatches and indels

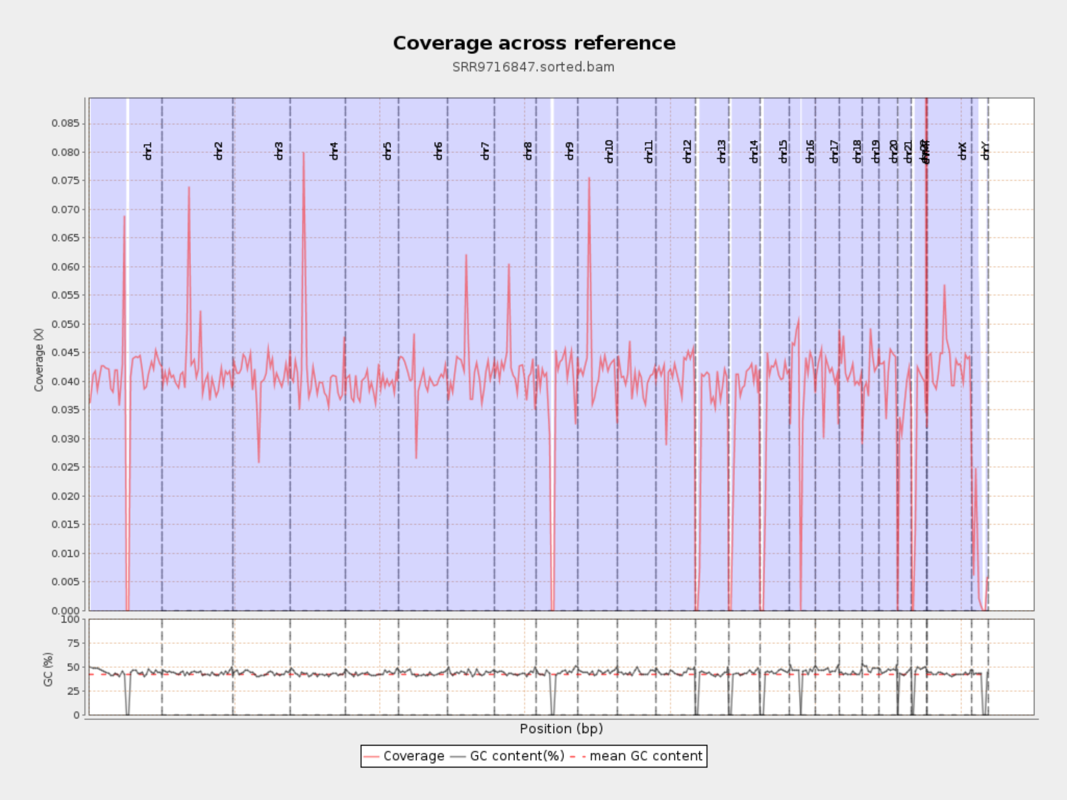
General error rate	0.66%
Mismatches	778,131
Insertions	9,552
Mapped reads with at least one insertion	0.62%
Deletions	28,589
Mapped reads with at least one deletion	1.84%
Homopolymer indels	43.92%

2.6. Chromosome stats

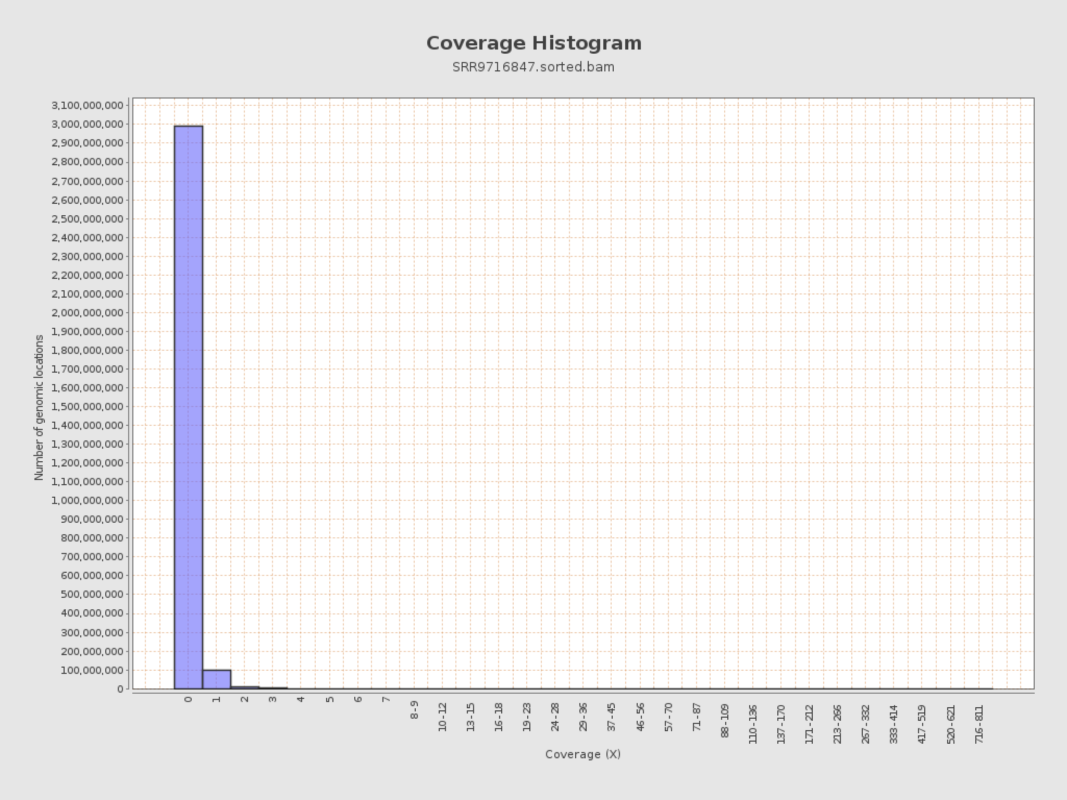
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9927577	0.0398	0.676
chr2	243199373	10246065	0.0421	0.3938
chr3	198022430	8114392	0.041	0.2226
chr4	191154276	7910173	0.0414	0.2819
chr5	180915260	7130519	0.0394	0.2213
chr6	171115067	6954450	0.0406	0.245
chr7	159138663	6694294	0.0421	0.4386

chr8	146364022	6188000	0.0423	0.427
chr9	141213431	5182856	0.0367	0.3134
chr10	135534747	5880419	0.0434	0.3773
chr11	135006516	5459633	0.0404	0.3148
chr12	133851895	5539574	0.0414	0.2263
chr13	115169878	3792670	0.0329	0.1994
chr14	107349540	3632276	0.0338	0.2209
chr15	102531392	3521297	0.0343	0.2043
chr16	90354753	3591606	0.0398	0.2419
chr17	81195210	3311809	0.0408	0.2549
chr18	78077248	3285178	0.0421	0.5163
chr19	59128983	2457638	0.0416	0.4532
chr20	63025520	2643359	0.0419	0.2366
chr21	48129895	1584009	0.0329	0.2335
chr22	51304566	1450122	0.0283	0.1864
chrMT	16571	9059	0.5467	0.7932
chrX	155270560	6697130	0.0431	0.2644
chrY	59373566	380711	0.0064	0.2334

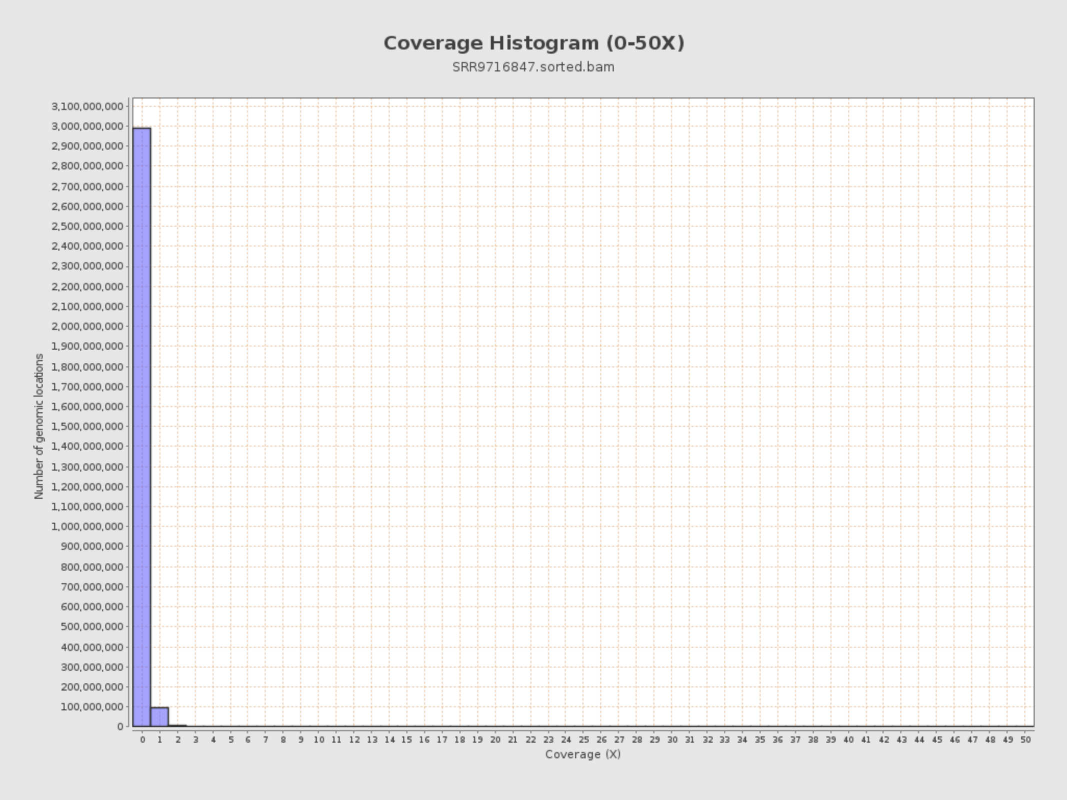
3. Results : Coverage across reference



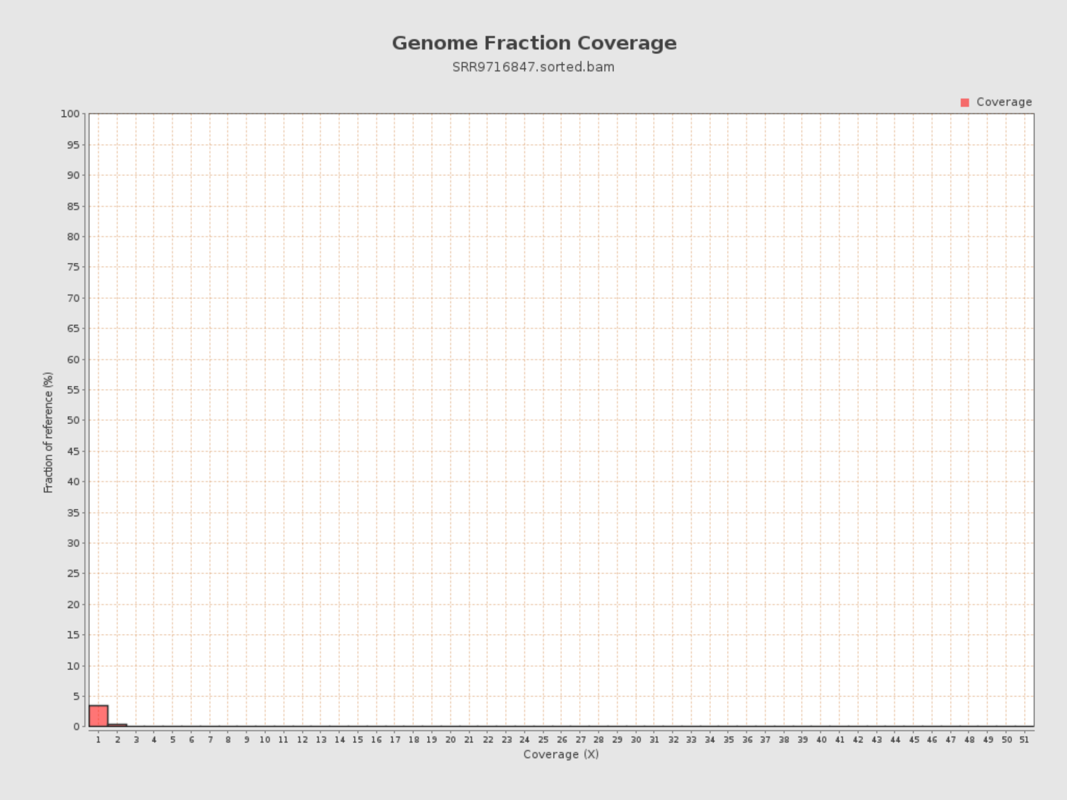
4. Results : Coverage Histogram



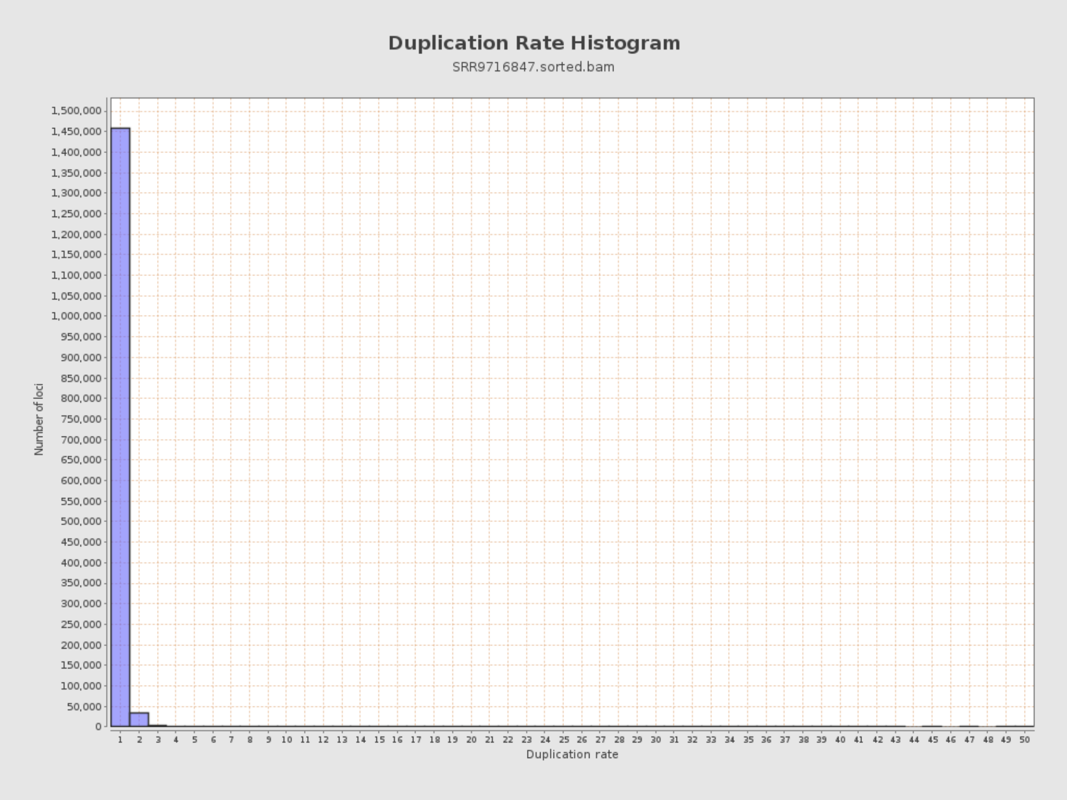
5. Results : Coverage Histogram (0-50X)



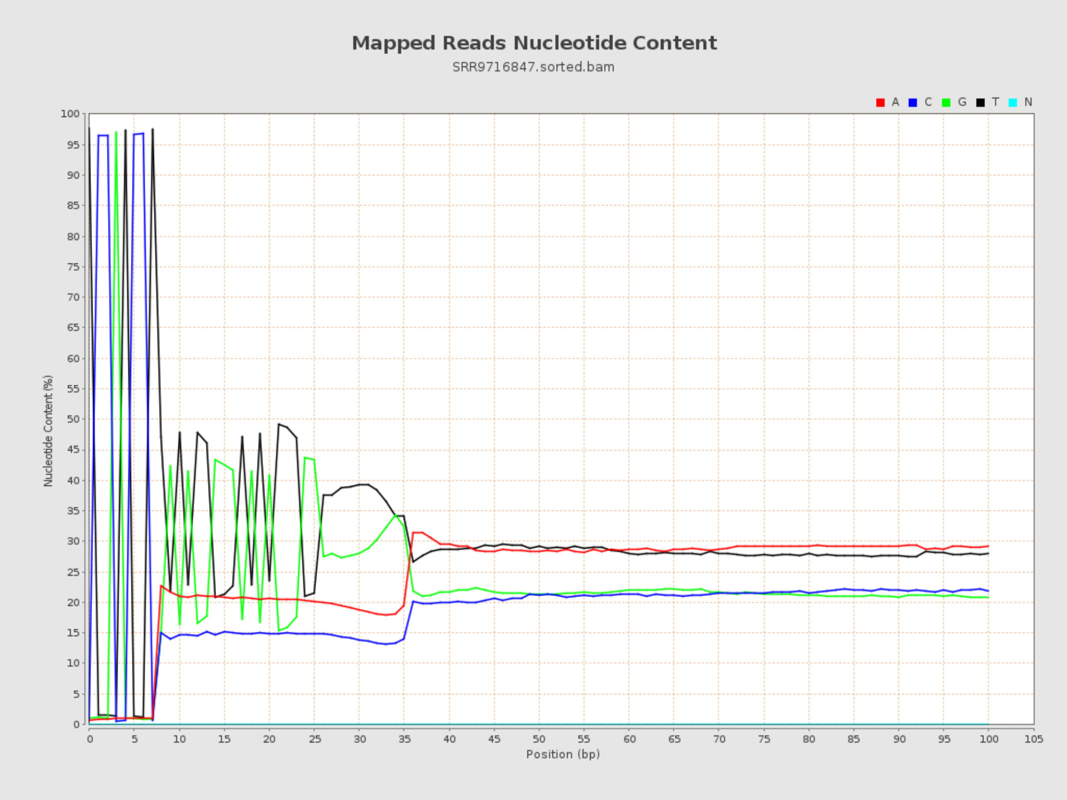
6. Results : Genome Fraction Coverage



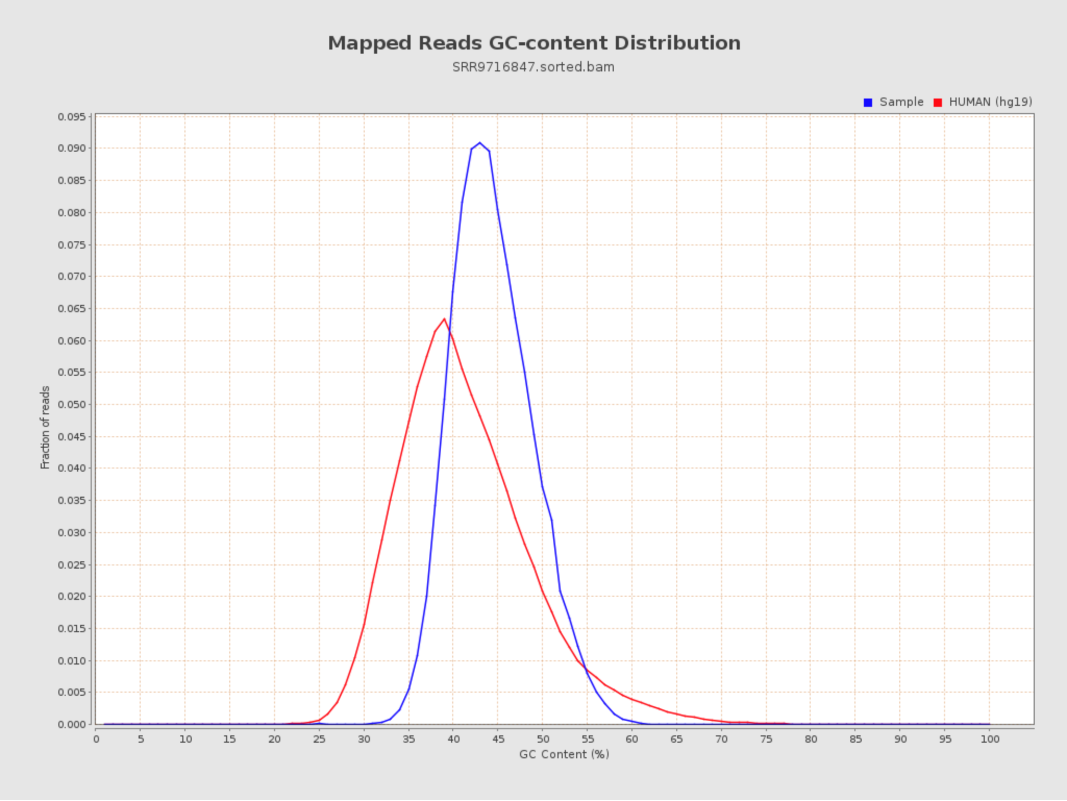
7. Results : Duplication Rate Histogram



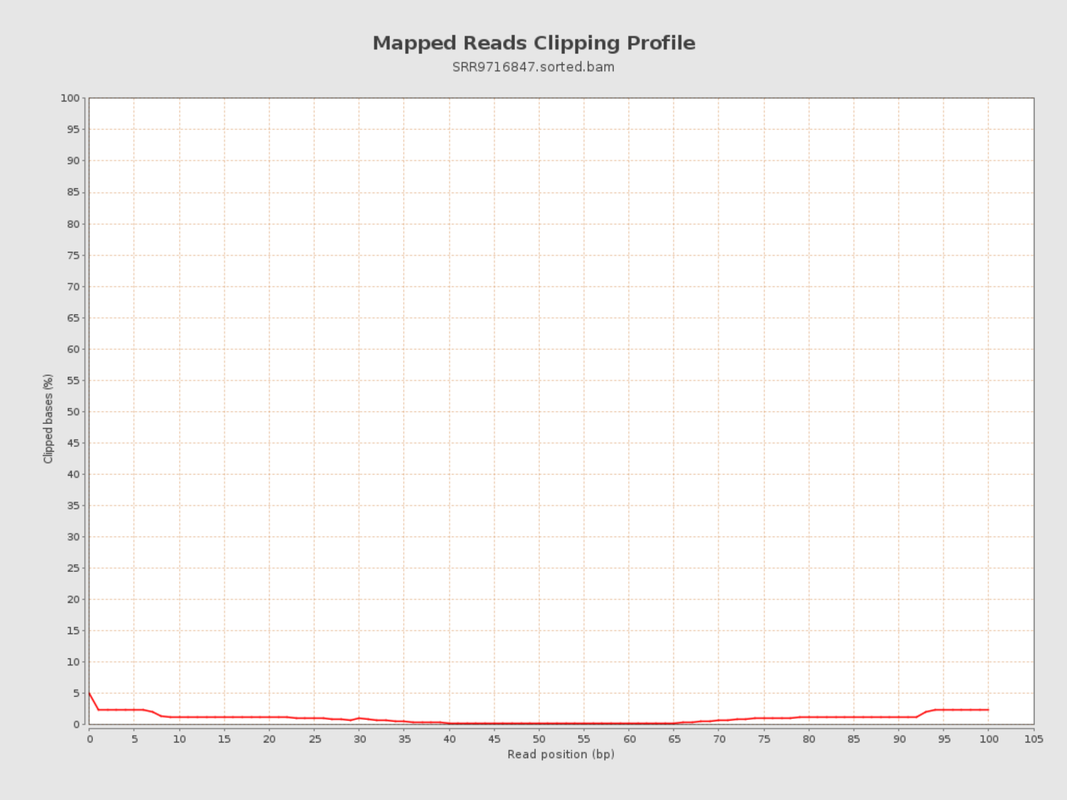
8. Results : Mapped Reads Nucleotide Content



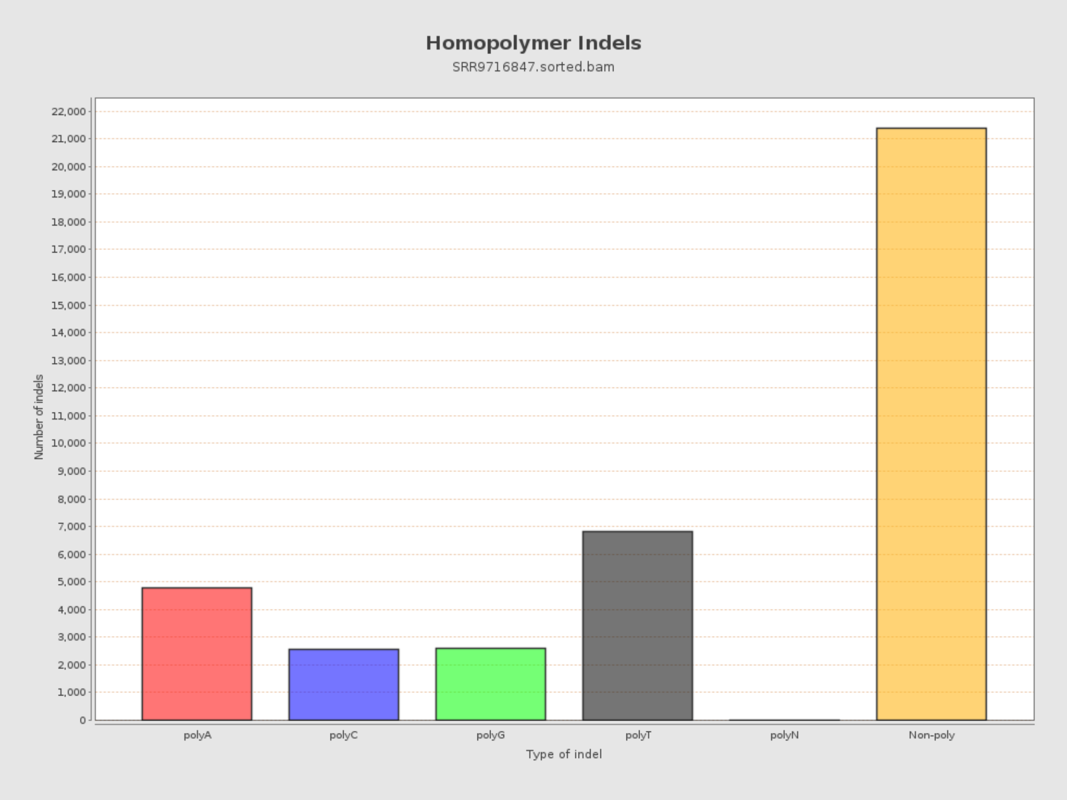
9. Results : Mapped Reads GC-content Distribution



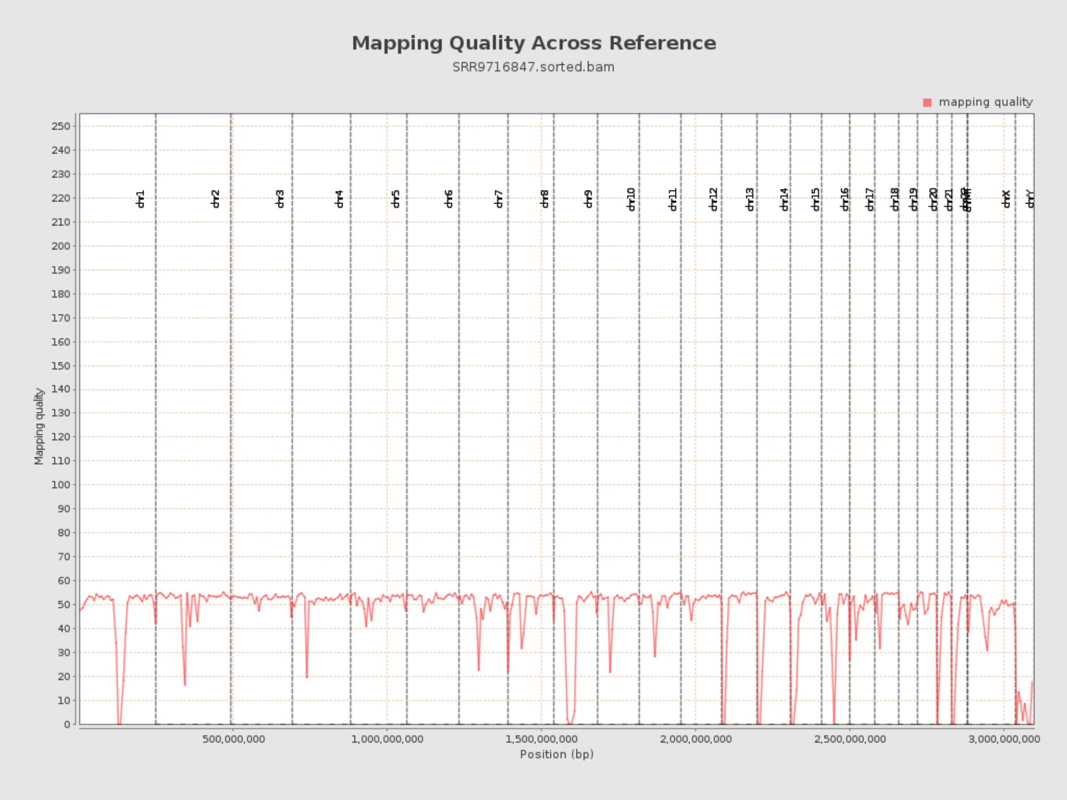
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram