Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 05:56:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716683.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_SRR9716683 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716683.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 05:56:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716683.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,561,473
Mapped reads	1,385,578 / 88.74%
Unmapped reads	175,895 / 11.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,949 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	32,771 / 2.1%
Duplication rate	1.6%
Clipped reads	1,389,103 / 88.96%

2.2. ACGT Content

Number/percentage of A's	18,458,708 / 23.38%
Number/percentage of C's	16,540,729 / 20.95%
Number/percentage of T's	24,967,305 / 31.62%
Number/percentage of G's	18,981,645 / 24.04%
Number/percentage of N's	582 / 0%
GC Percentage	44.99%

2.3. Coverage

Mean	0.0255

Standard Deviation	0.2264

2.4. Mapping Quality

Mean Mapping Quality	42.17

2.5. Mismatches and indels

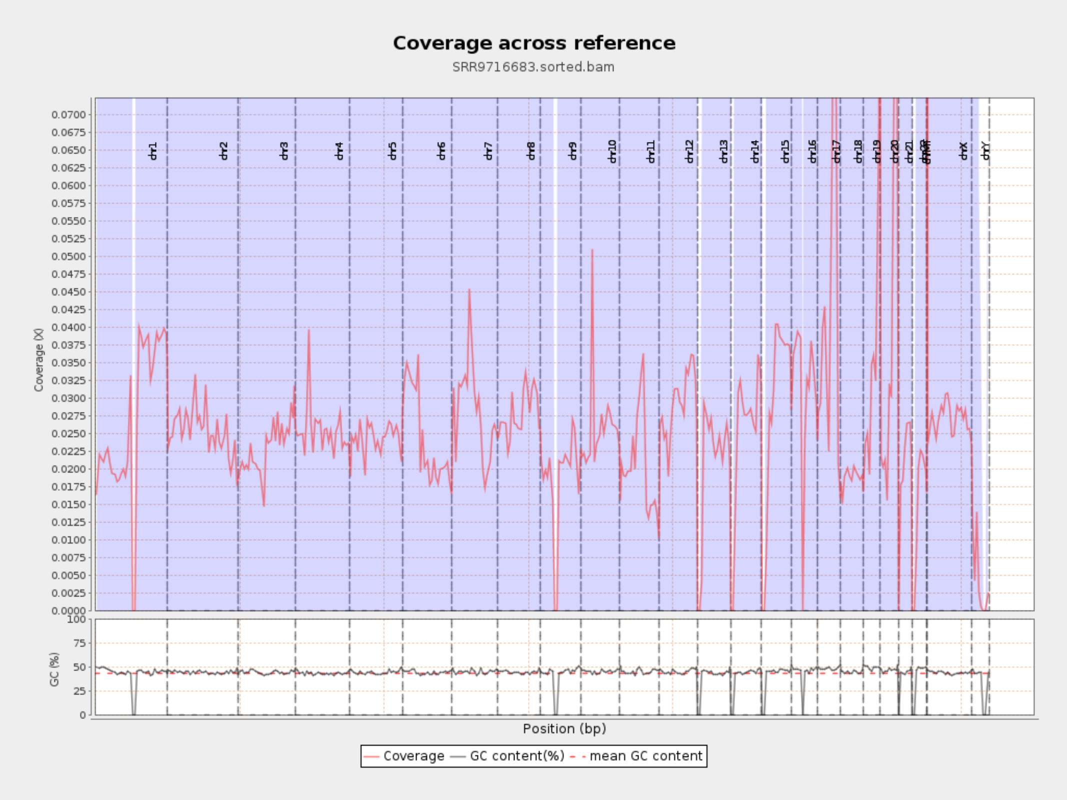
General error rate	0.54%
Mismatches	415,125
Insertions	4,932
Mapped reads with at least one insertion	0.35%
Deletions	15,165
Mapped reads with at least one deletion	1.09%
Homopolymer indels	42.88%

2.6. Chromosome stats

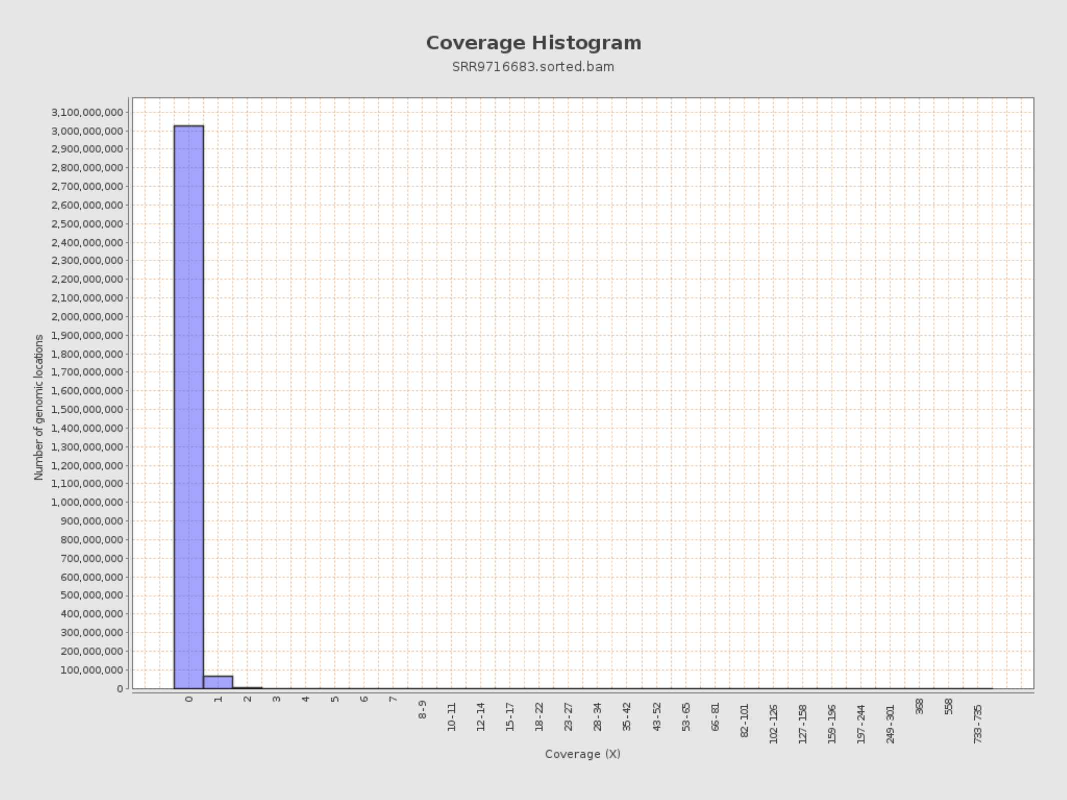
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6651664	0.0267	0.28
chr2	243199373	6174373	0.0254	0.3428
chr3	198022430	4522680	0.0228	0.1676
chr4	191154276	4865297	0.0255	0.1847
chr5	180915260	4426564	0.0245	0.1678
chr6	171115067	4180961	0.0244	0.1955
chr7	159138663	4505766	0.0283	0.3239

chr8	146364022	4078288	0.0279	0.2117
chr9	141213431	2615110	0.0185	0.1686
chr10	135534747	3519746	0.026	0.2835
chr11	135006516	2809464	0.0208	0.1883
chr12	133851895	3902755	0.0292	0.1847
chr13	115169878	2376215	0.0206	0.1555
chr14	107349540	2653721	0.0247	0.1766
chr15	102531392	2918298	0.0285	0.1854
chr16	90354753	2796156	0.0309	0.204
chr17	81195210	3562565	0.0439	0.2349
chr18	78077248	1461860	0.0187	0.2488
chr19	59128983	2127832	0.036	0.2708
chr20	63025520	2574291	0.0408	0.2277
chr21	48129895	979902	0.0204	0.1642
chr22	51304566	751752	0.0147	0.1325
chrMT	16571	55770	3.3655	2.8317
chrX	155270560	4211134	0.0271	0.1886
chrY	59373566	251476	0.0042	0.1222

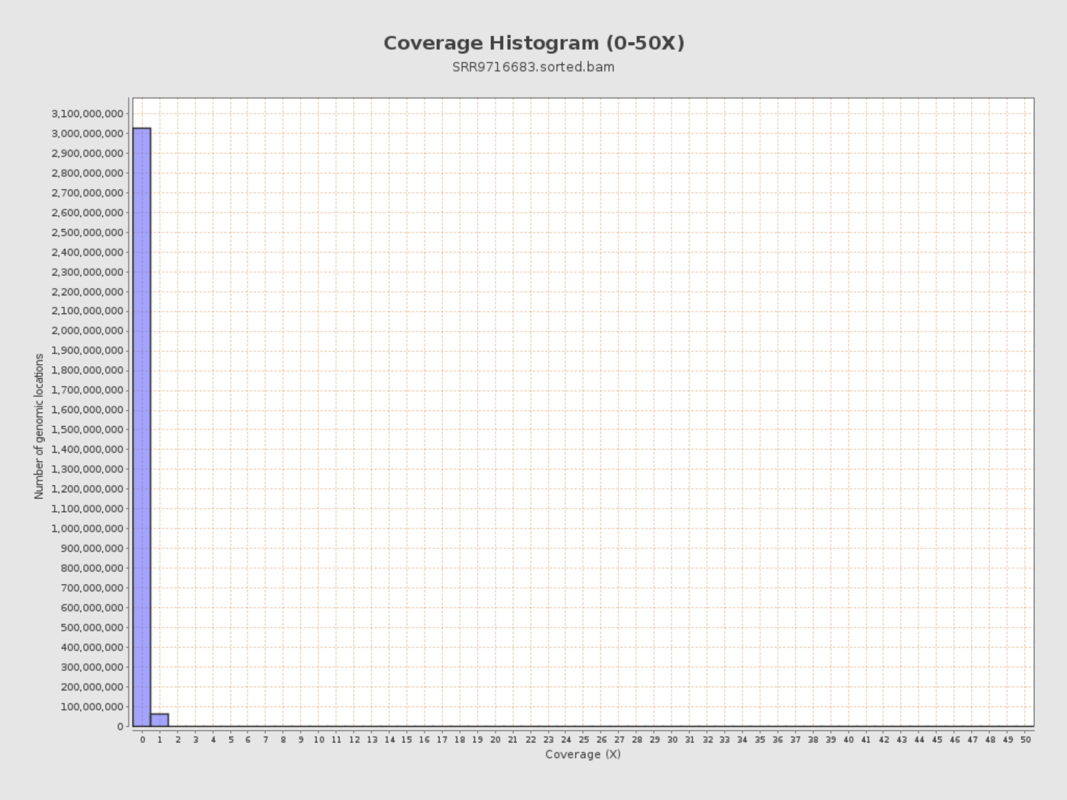
3. Results : Coverage across reference



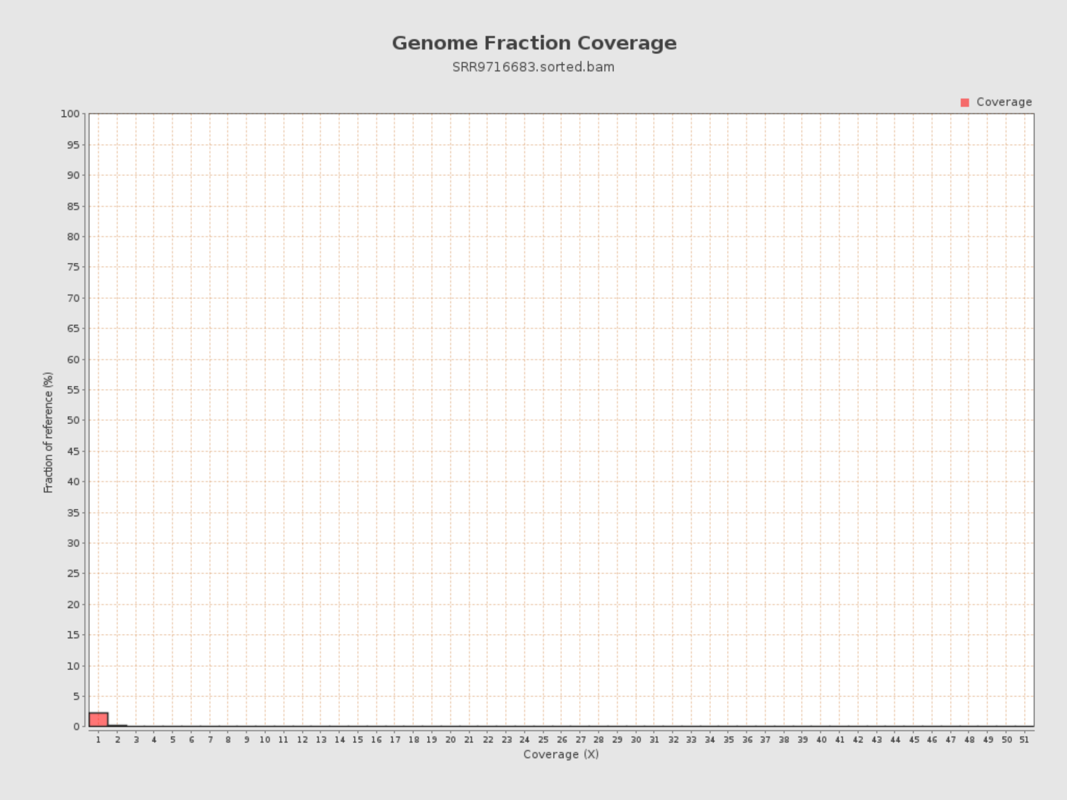
4. Results : Coverage Histogram



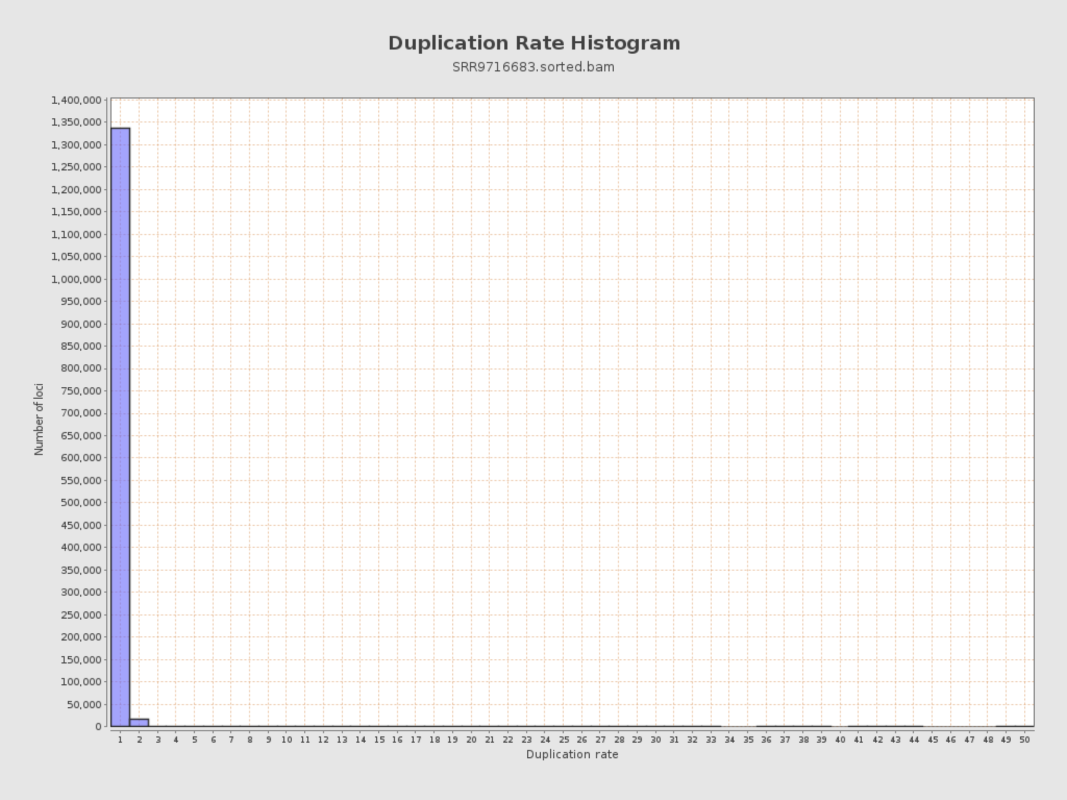
5. Results : Coverage Histogram (0-50X)



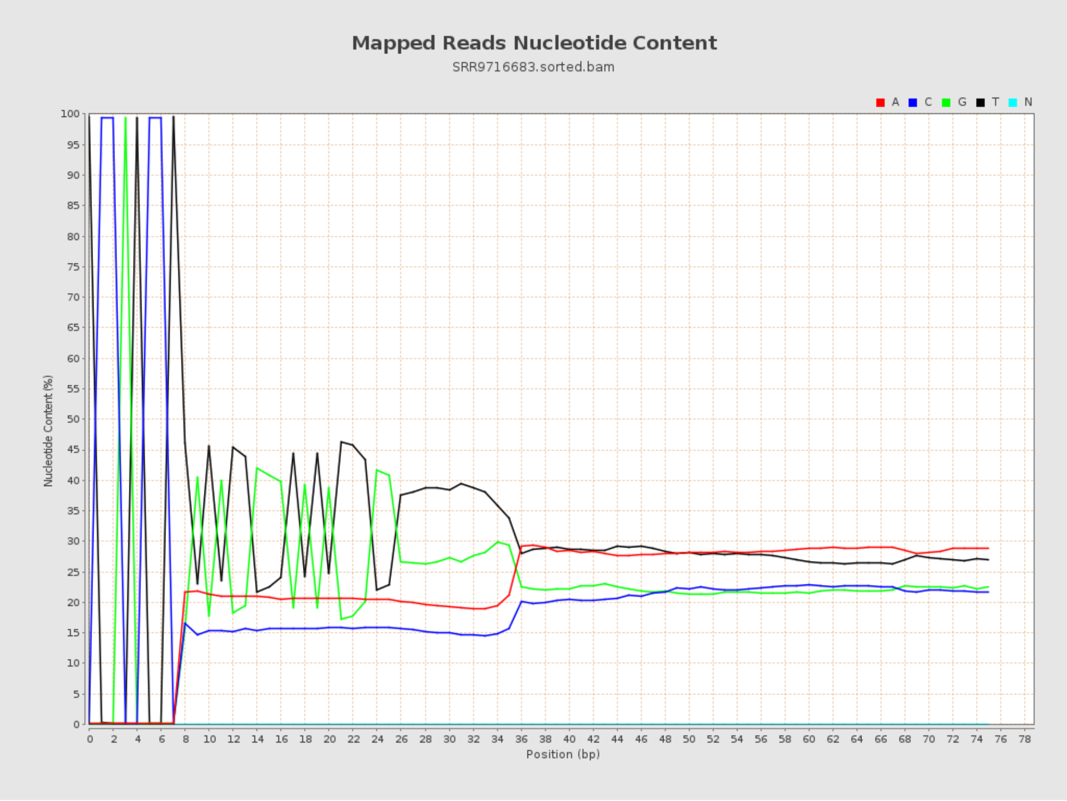
6. Results : Genome Fraction Coverage



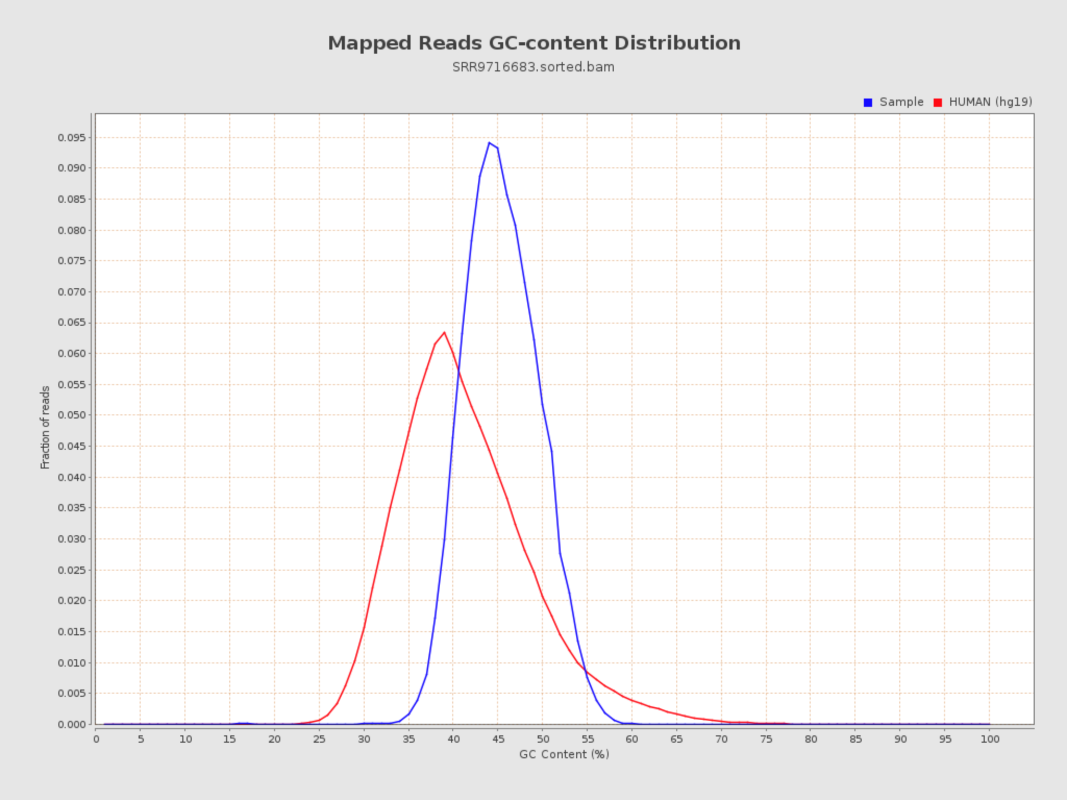
7. Results : Duplication Rate Histogram



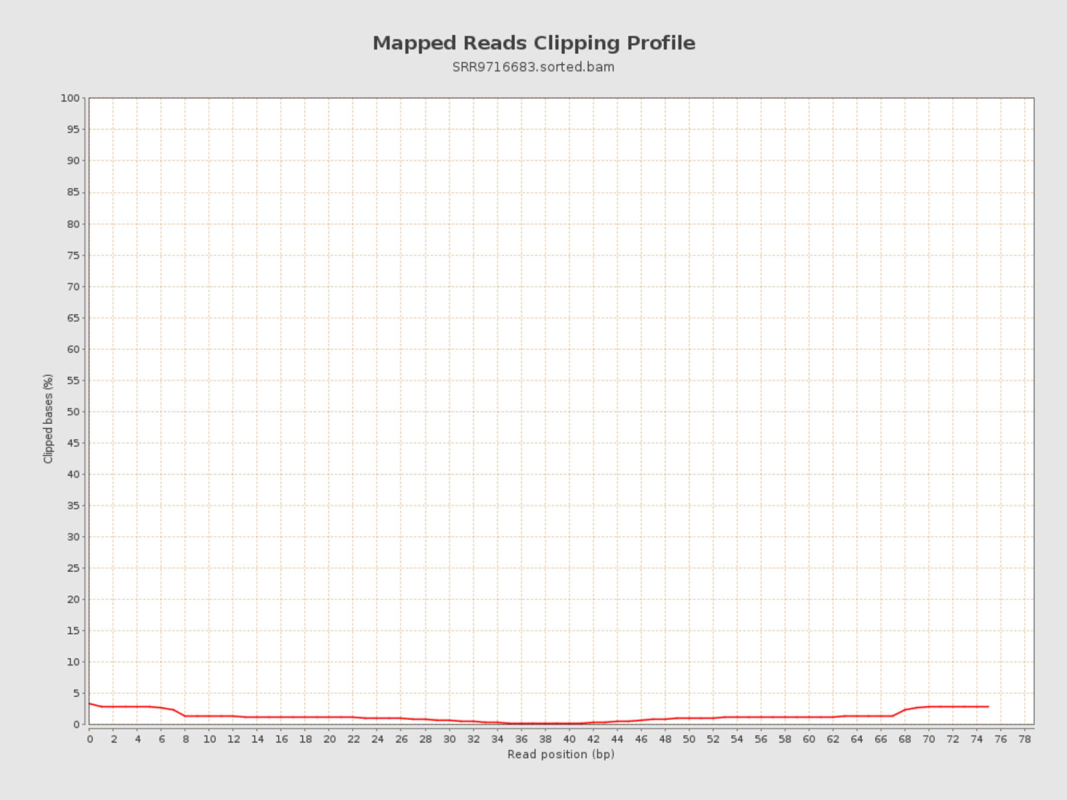
8. Results : Mapped Reads Nucleotide Content



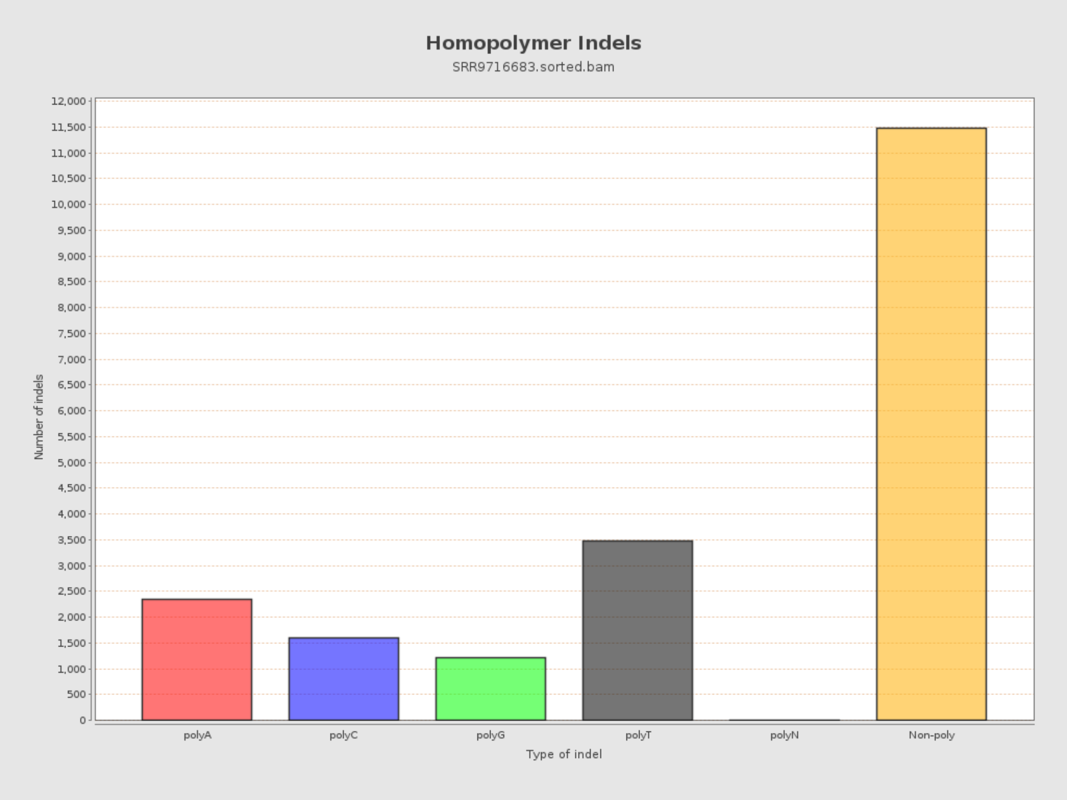
9. Results : Mapped Reads GC-content Distribution



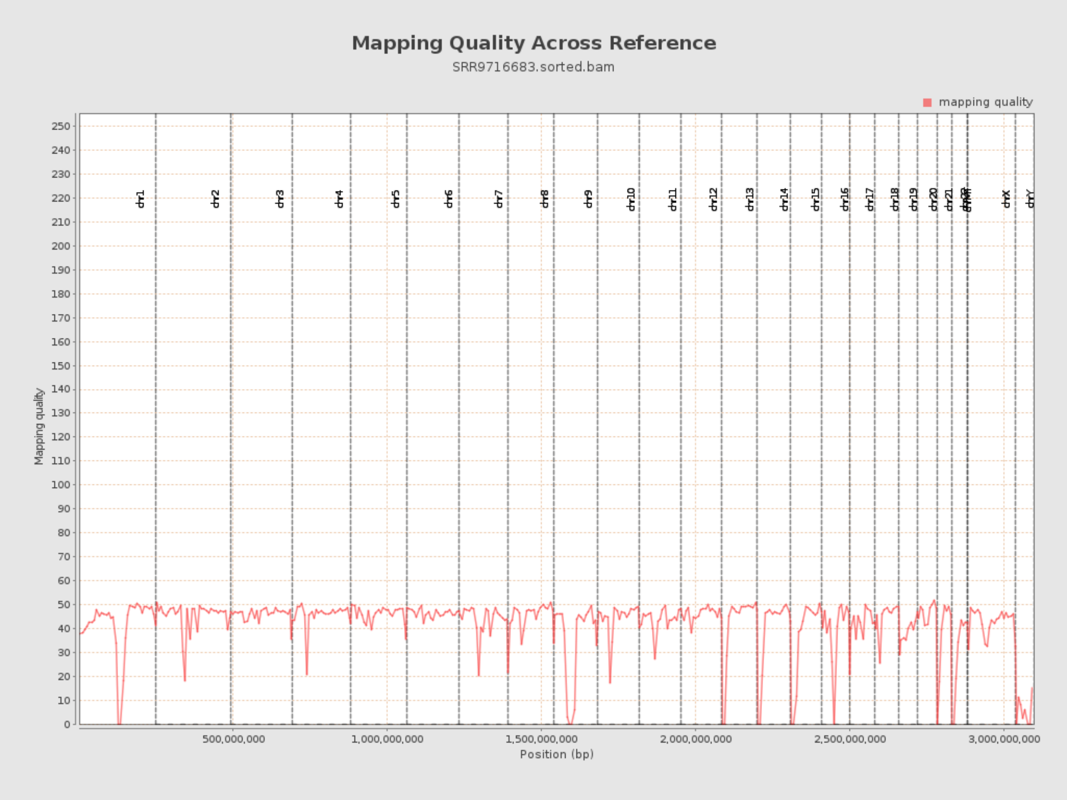
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram