Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 15:54:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716869.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_SRR9716869 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716869.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 15:54:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716869.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,528,941
Mapped reads	2,328,130 / 92.06%
Unmapped reads	200,811 / 7.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,528 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	82,727 / 3.27%
Duplication rate	2.77%
Clipped reads	2,333,300 / 92.26%

2.2. ACGT Content

Number/percentage of A's	32,442,821 / 24.09%
Number/percentage of C's	26,072,142 / 19.36%
Number/percentage of T's	41,984,871 / 31.17%
Number/percentage of G's	34,176,669 / 25.38%
Number/percentage of N's	2,925 / 0%
GC Percentage	44.73%

2.3. Coverage

Mean	0.0435

Standard Deviation	0.3049

2.4. Mapping Quality

Mean Mapping Quality	45

2.5. Mismatches and indels

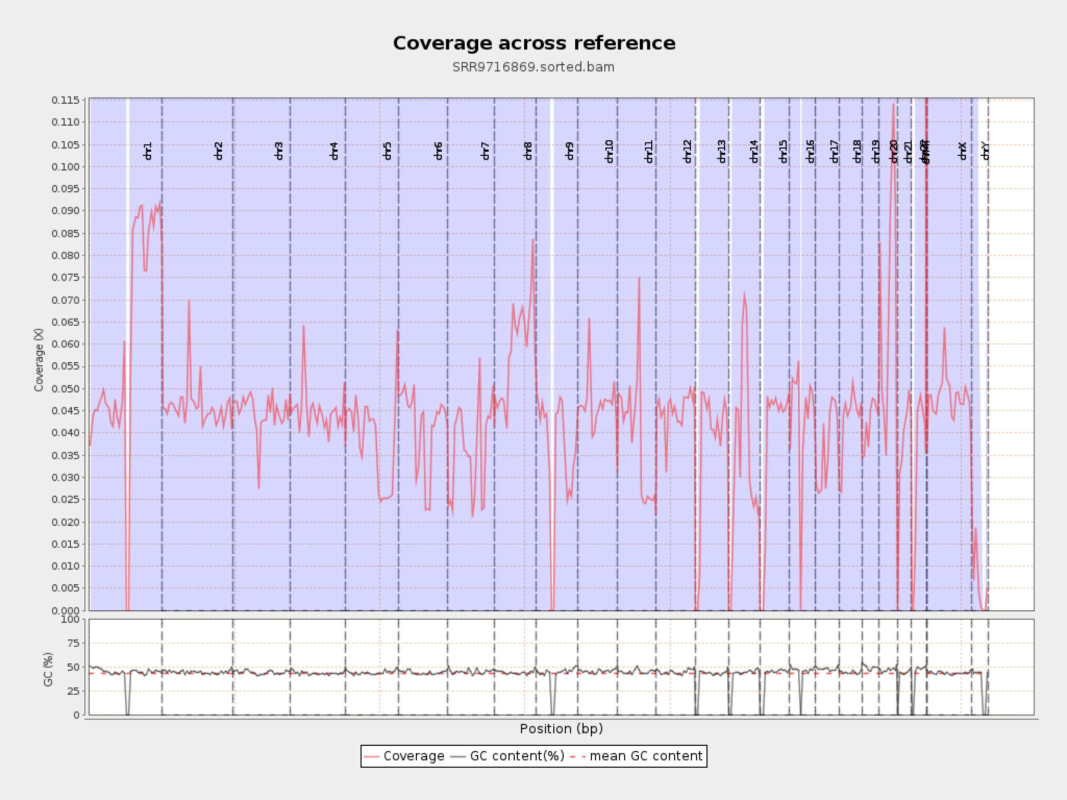
General error rate	0.5%
Mismatches	653,217
Insertions	7,927
Mapped reads with at least one insertion	0.34%
Deletions	20,387
Mapped reads with at least one deletion	0.87%
Homopolymer indels	42.2%

2.6. Chromosome stats

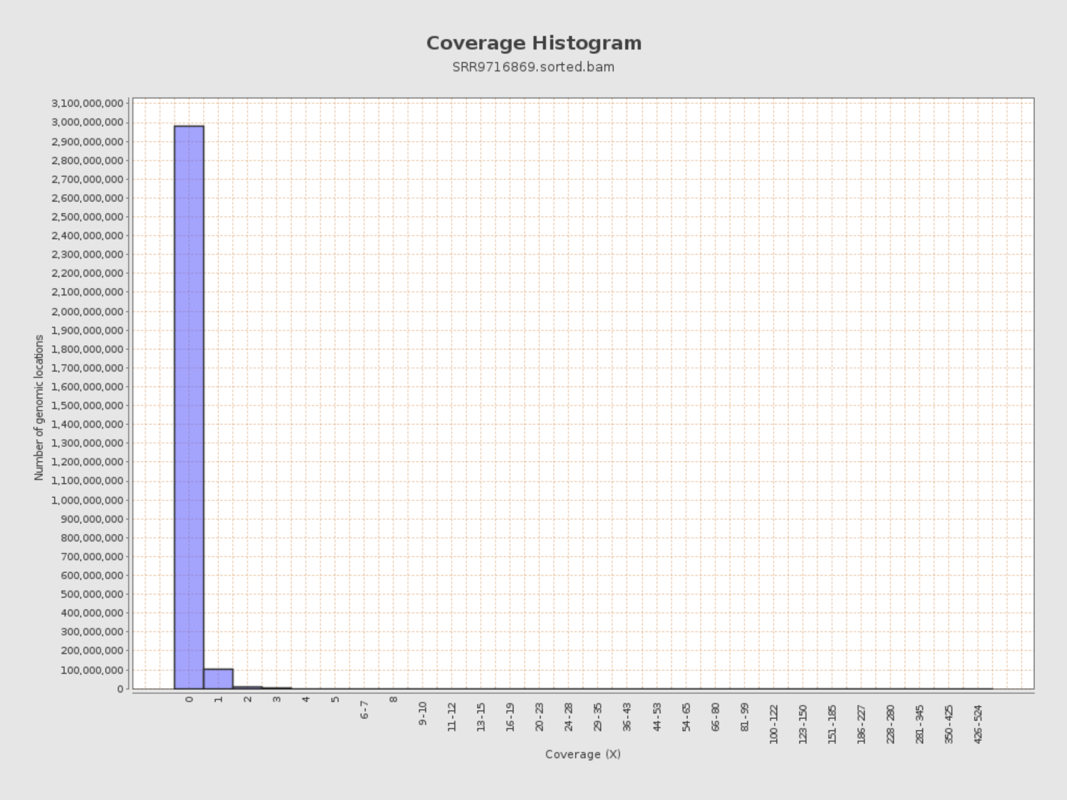
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15011092	0.0602	0.4727
chr2	243199373	11225074	0.0462	0.3458
chr3	198022430	8837448	0.0446	0.2377
chr4	191154276	8572039	0.0448	0.2578
chr5	180915260	6934285	0.0383	0.2228
chr6	171115067	7098580	0.0415	0.2501
chr7	159138663	5752991	0.0362	0.2657

chr8	146364022	8664726	0.0592	0.3297
chr9	141213431	4888672	0.0346	0.3054
chr10	135534747	6344367	0.0468	0.3176
chr11	135006516	5254467	0.0389	0.3175
chr12	133851895	6047760	0.0452	0.2439
chr13	115169878	4217762	0.0366	0.2128
chr14	107349540	3646394	0.034	0.2272
chr15	102531392	3840968	0.0375	0.2187
chr16	90354753	3930913	0.0435	0.2596
chr17	81195210	2995237	0.0369	0.2305
chr18	78077248	3387980	0.0434	0.5763
chr19	59128983	2518995	0.0426	0.3584
chr20	63025520	4336521	0.0688	0.3062
chr21	48129895	1766597	0.0367	0.2387
chr22	51304566	1583834	0.0309	0.1974
chrMT	16571	13122	0.7919	1.0084
chrX	155270560	7485919	0.0482	0.2826
chrY	59373566	358447	0.006	0.1313

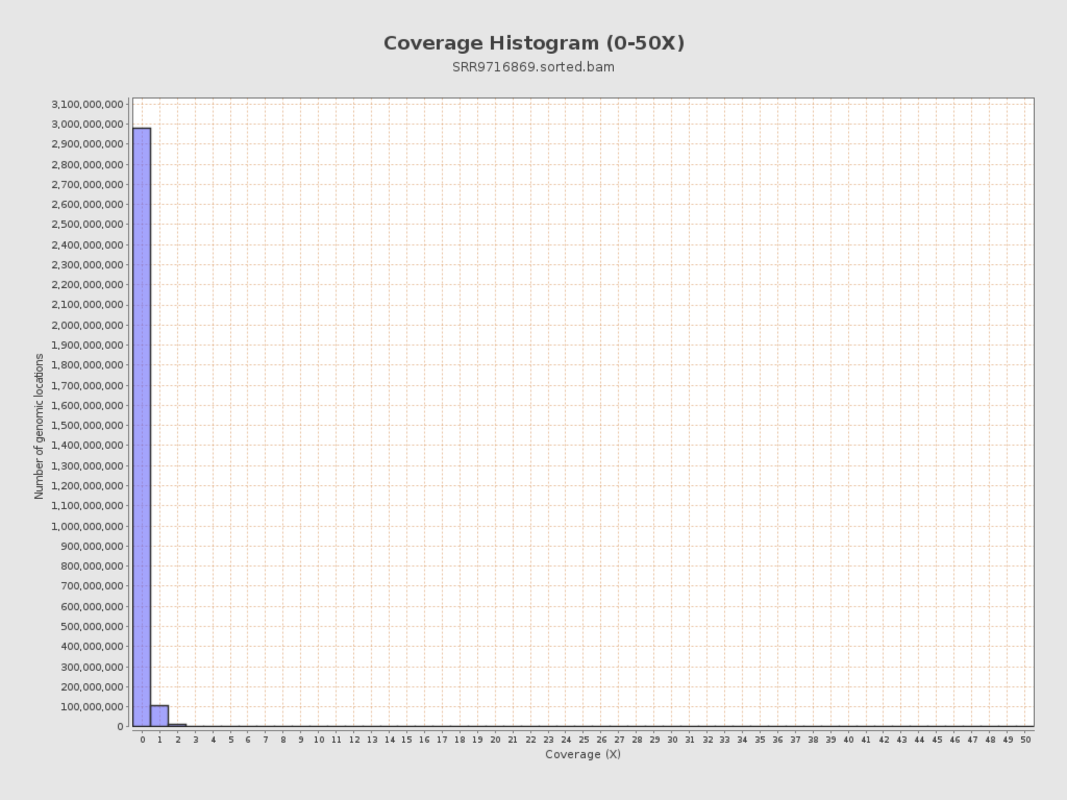
3. Results : Coverage across reference



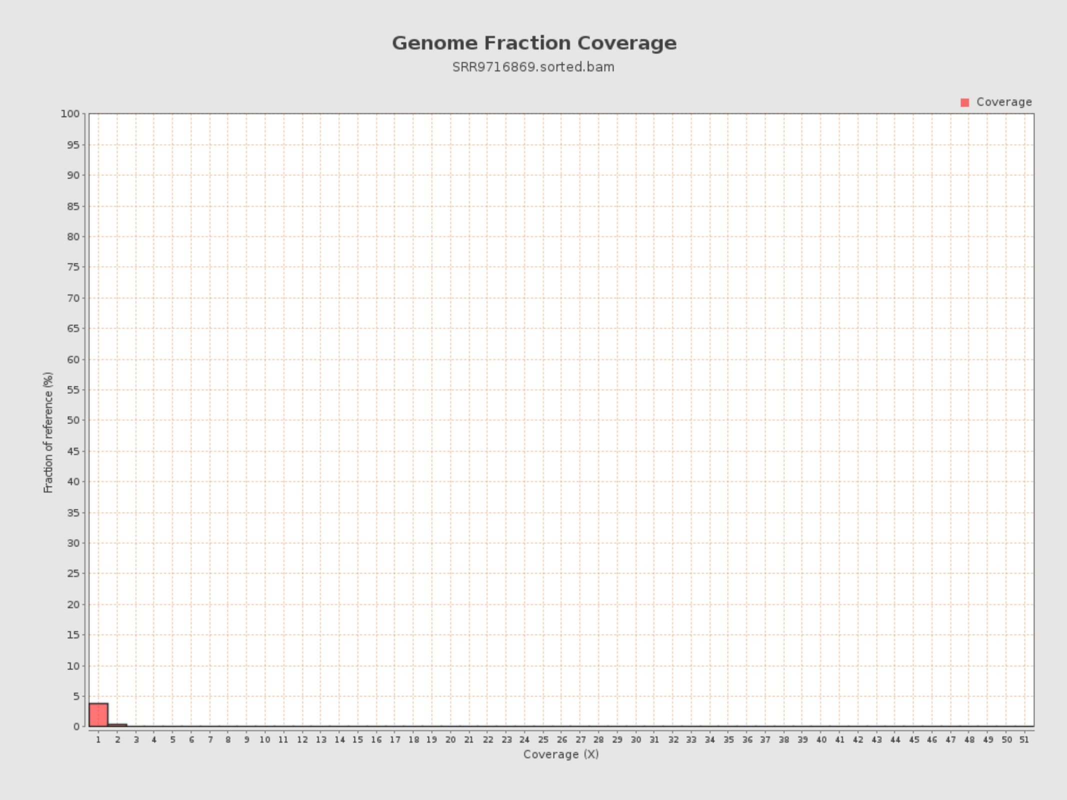
4. Results : Coverage Histogram



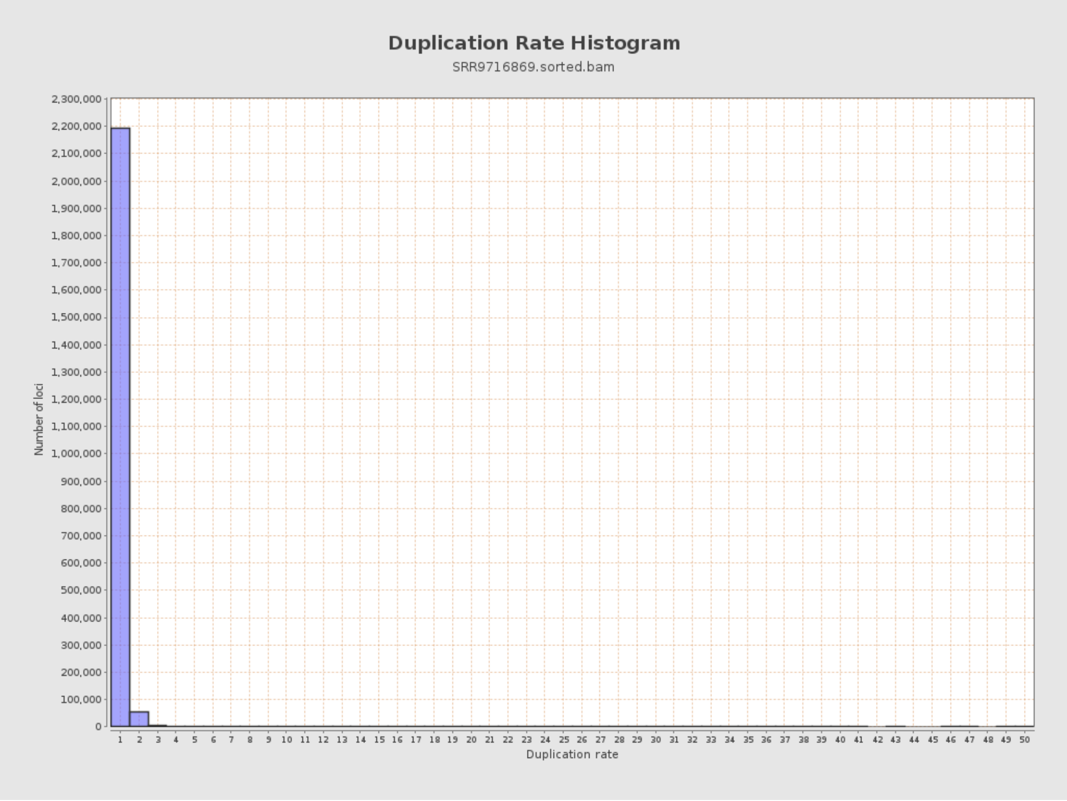
5. Results : Coverage Histogram (0-50X)



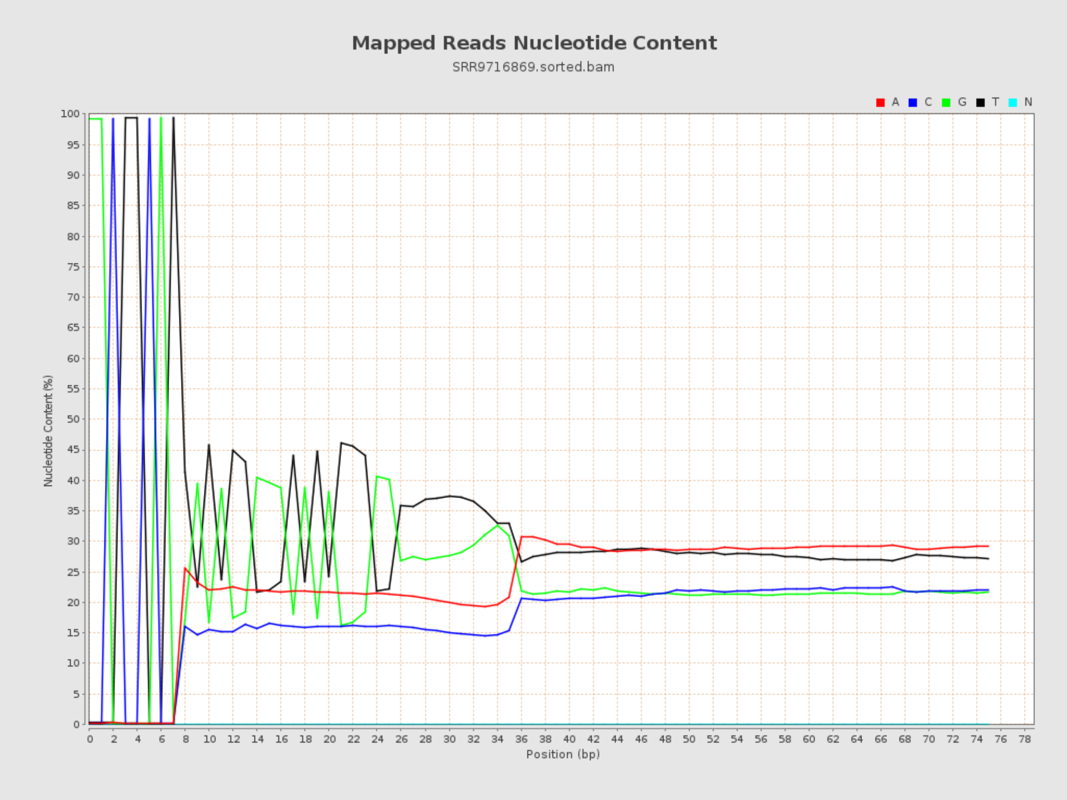
6. Results : Genome Fraction Coverage



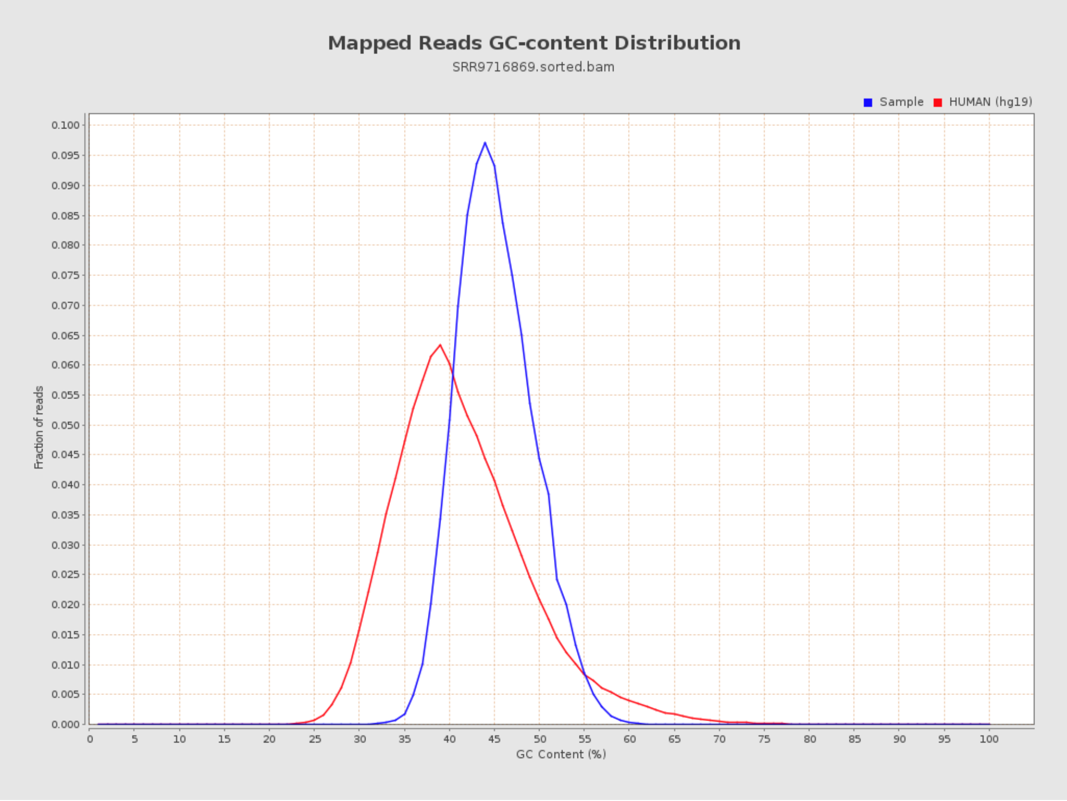
7. Results : Duplication Rate Histogram



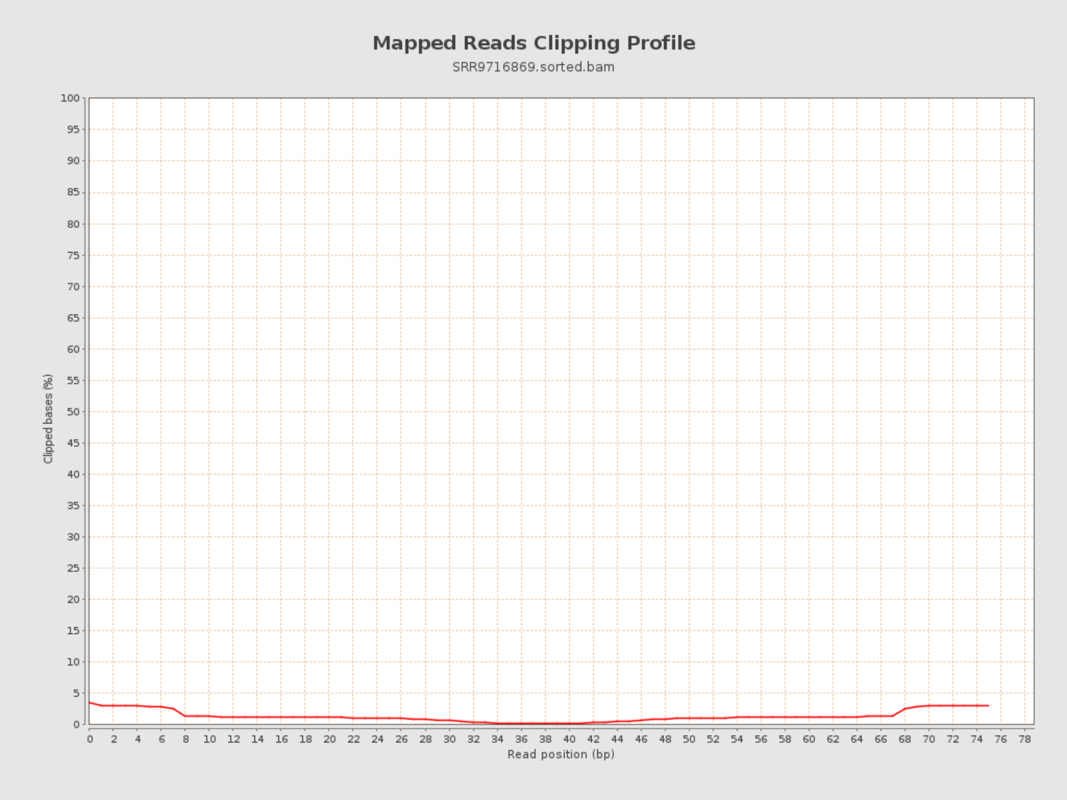
8. Results : Mapped Reads Nucleotide Content



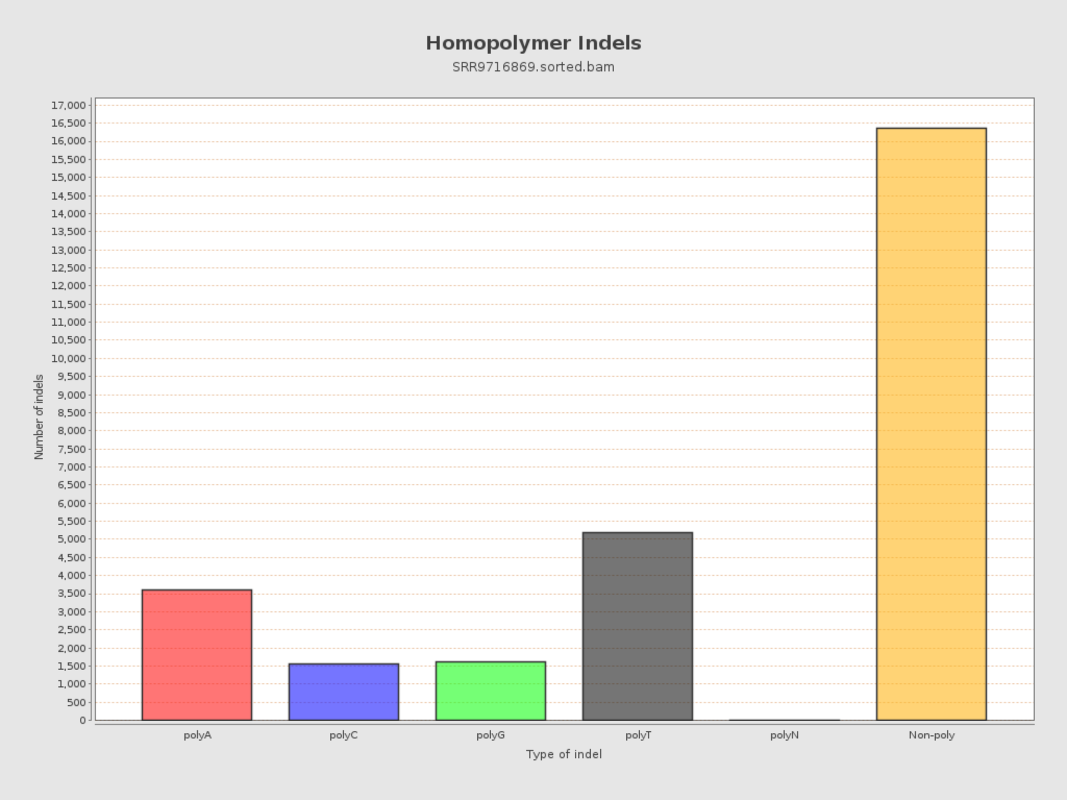
9. Results : Mapped Reads GC-content Distribution



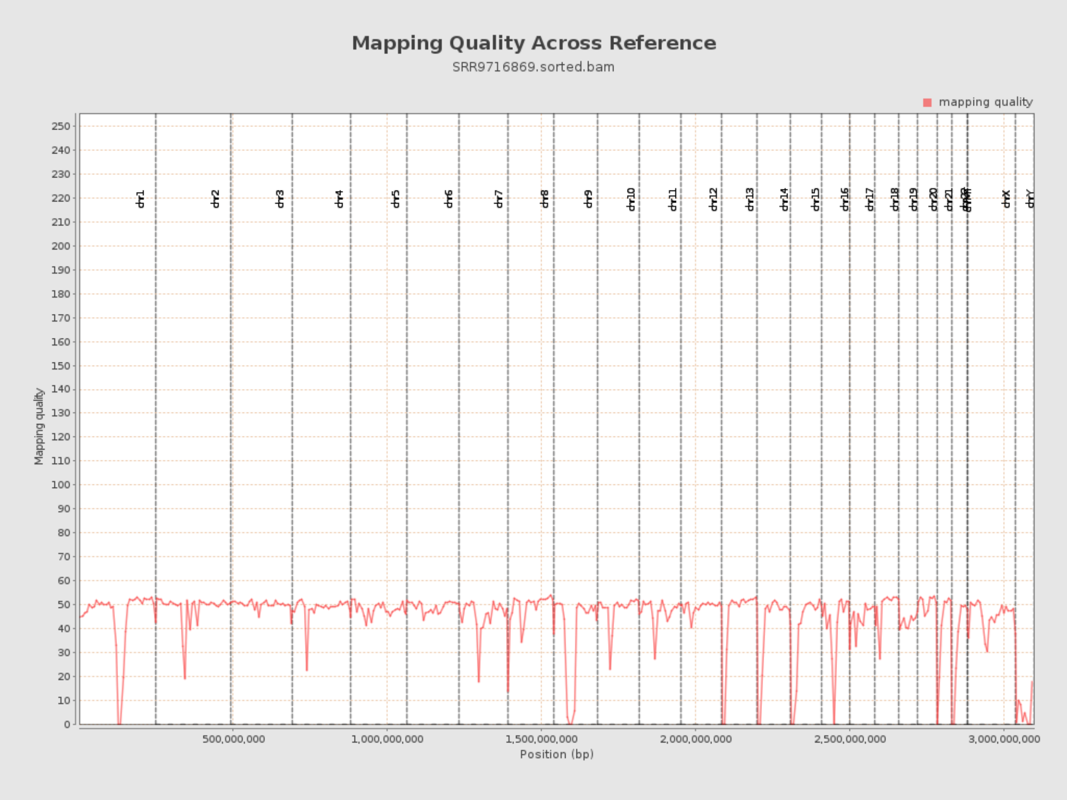
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram