Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 17:47:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716096.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_SRR9716096 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716096.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 17:47:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716096.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,193,226
Mapped reads	1,072,843 / 89.91%
Unmapped reads	120,383 / 10.09%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,451 / 1.55%
Read min/max/mean length	30 / 101 / 101.57
Duplicated reads (estimated)	39,974 / 3.35%
Duplication rate	2.19%
Clipped reads	1,089,174 / 91.28%

2.2. ACGT Content

Number/percentage of A's	21,066,404 / 25.08%
Number/percentage of C's	15,938,066 / 18.98%
Number/percentage of T's	26,423,312 / 31.46%
Number/percentage of G's	20,547,633 / 24.47%
Number/percentage of N's	5,099 / 0.01%
GC Percentage	43.45%

2.3. Coverage

Mean	0.0271

Standard Deviation	0.343

2.4. Mapping Quality

Mean Mapping Quality	44.41

2.5. Mismatches and indels

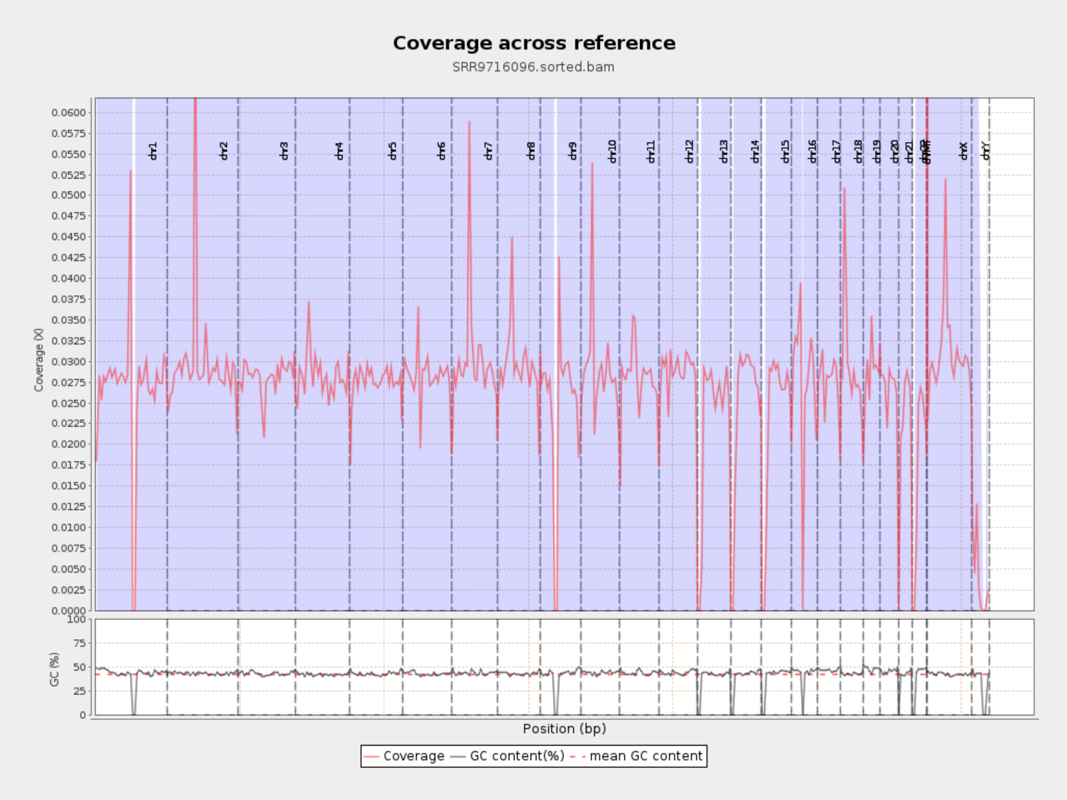
General error rate	0.87%
Mismatches	714,058
Insertions	7,727
Mapped reads with at least one insertion	0.71%
Deletions	20,956
Mapped reads with at least one deletion	1.92%
Homopolymer indels	43.98%

2.6. Chromosome stats

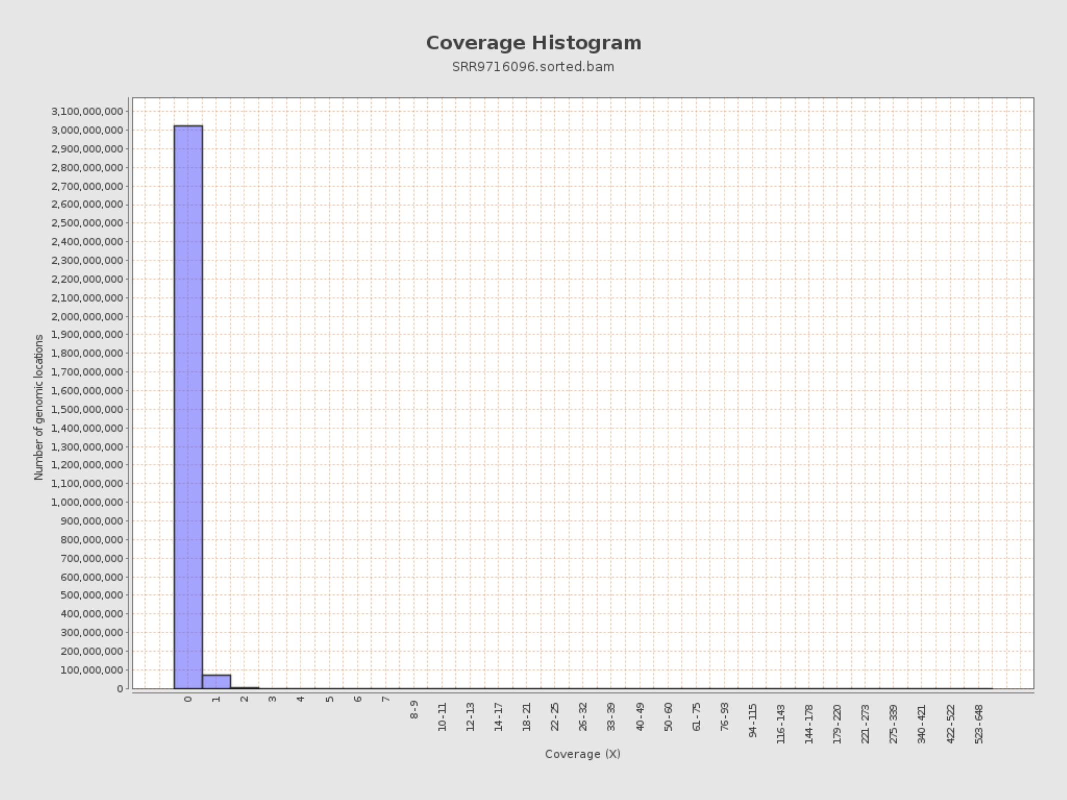
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6629218	0.0266	0.5514
chr2	243199373	7310970	0.0301	0.5094
chr3	198022430	5567916	0.0281	0.1826
chr4	191154276	5412915	0.0283	0.1946
chr5	180915260	5030683	0.0278	0.1852
chr6	171115067	4825533	0.0282	0.2233
chr7	159138663	4834841	0.0304	0.4766

chr8	146364022	4337964	0.0296	0.4507
chr9	141213431	3492178	0.0247	0.3614
chr10	135534747	3952984	0.0292	0.3062
chr11	135006516	3827903	0.0284	0.3359
chr12	133851895	3855903	0.0288	0.1884
chr13	115169878	2586850	0.0225	0.1613
chr14	107349540	2592984	0.0242	0.2247
chr15	102531392	2340349	0.0228	0.1676
chr16	90354753	2436966	0.027	0.2061
chr17	81195210	2239116	0.0276	0.1989
chr18	78077248	2322783	0.0297	0.6792
chr19	59128983	1705367	0.0288	0.388
chr20	63025520	1675017	0.0266	0.1883
chr21	48129895	1076786	0.0224	0.1733
chr22	51304566	869777	0.017	0.1406
chrMT	16571	8906	0.5374	0.8953
chrX	155270560	4851996	0.0312	0.2649
chrY	59373566	230927	0.0039	0.1188

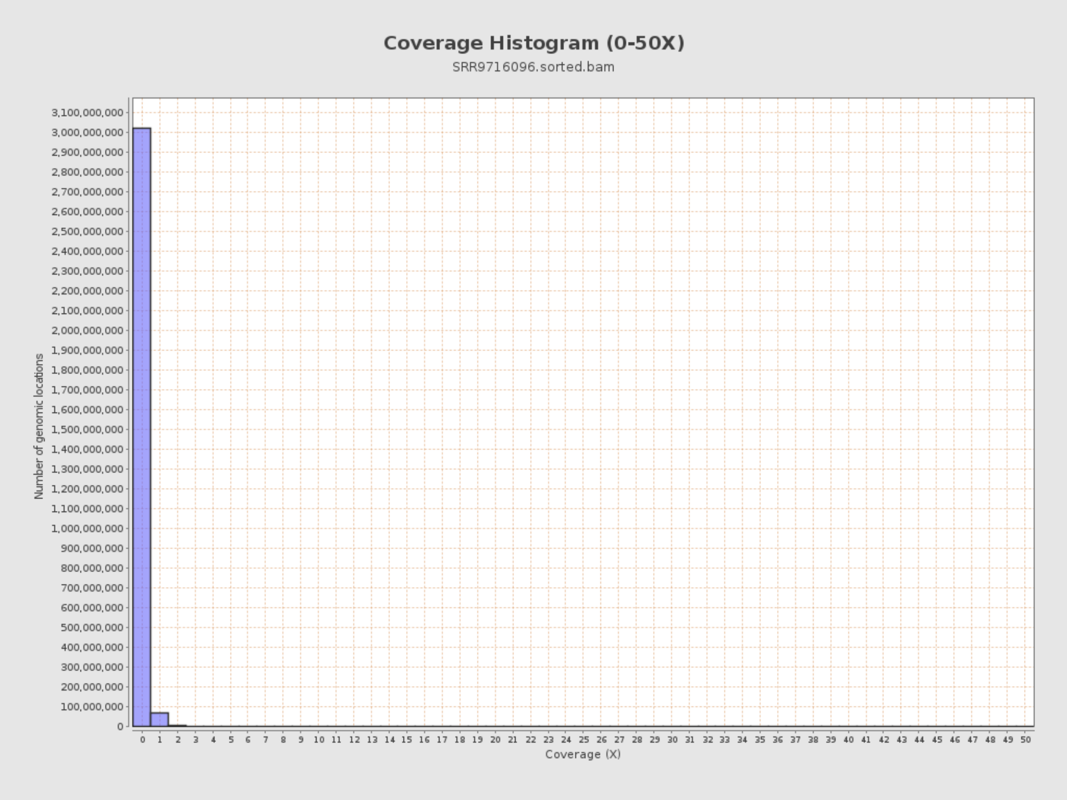
3. Results : Coverage across reference



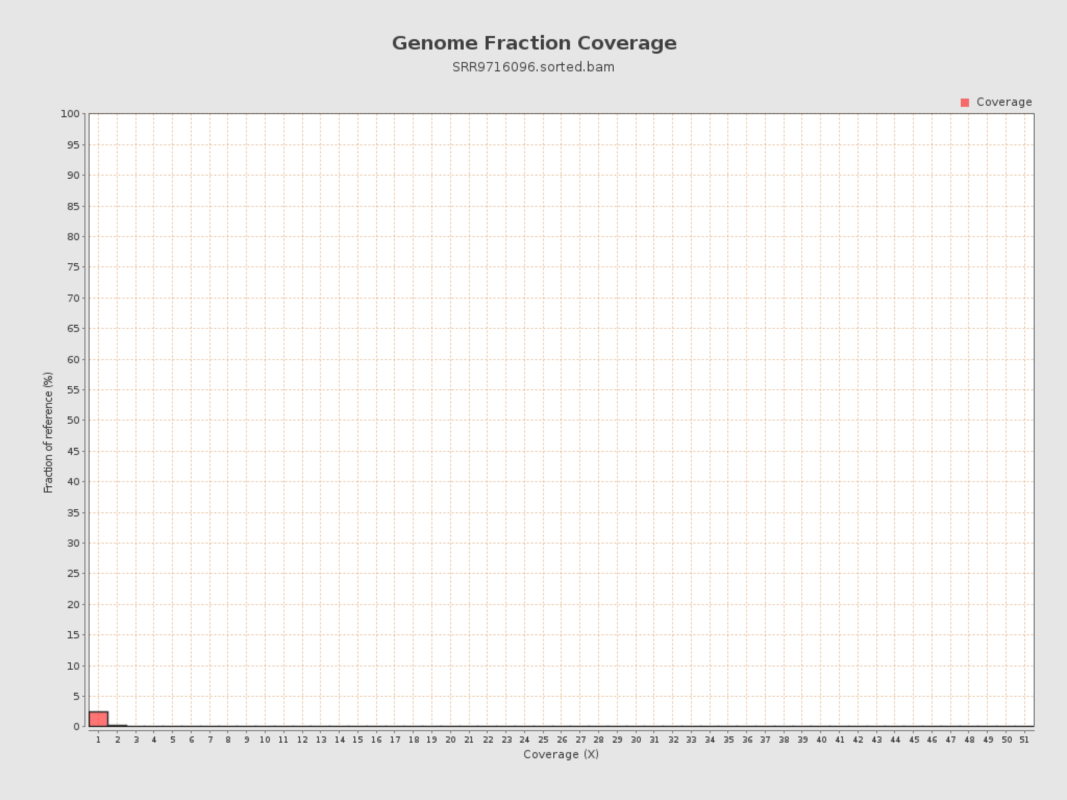
4. Results : Coverage Histogram



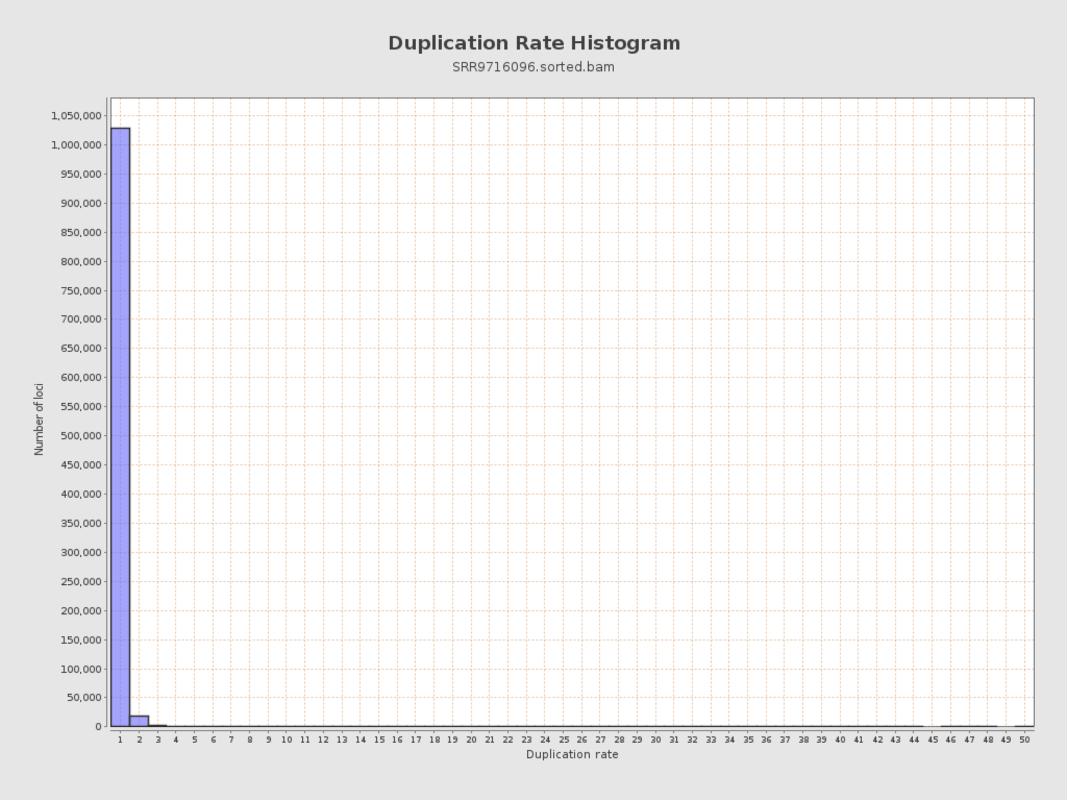
5. Results : Coverage Histogram (0-50X)



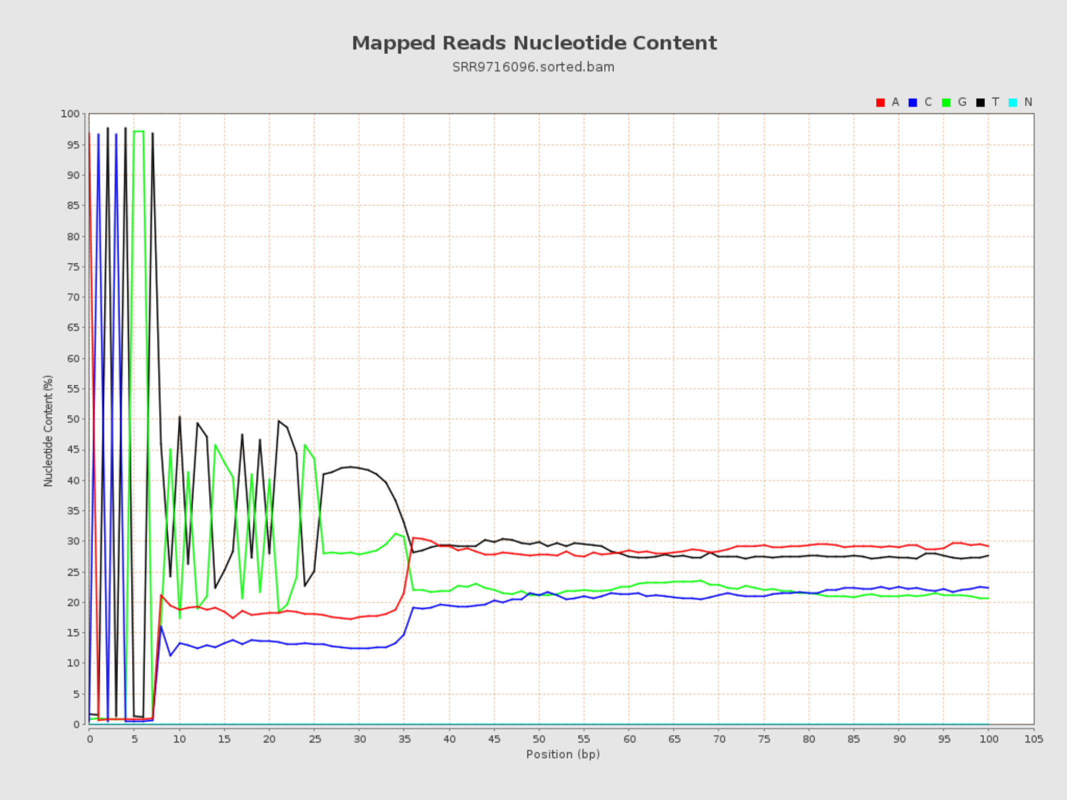
6. Results : Genome Fraction Coverage



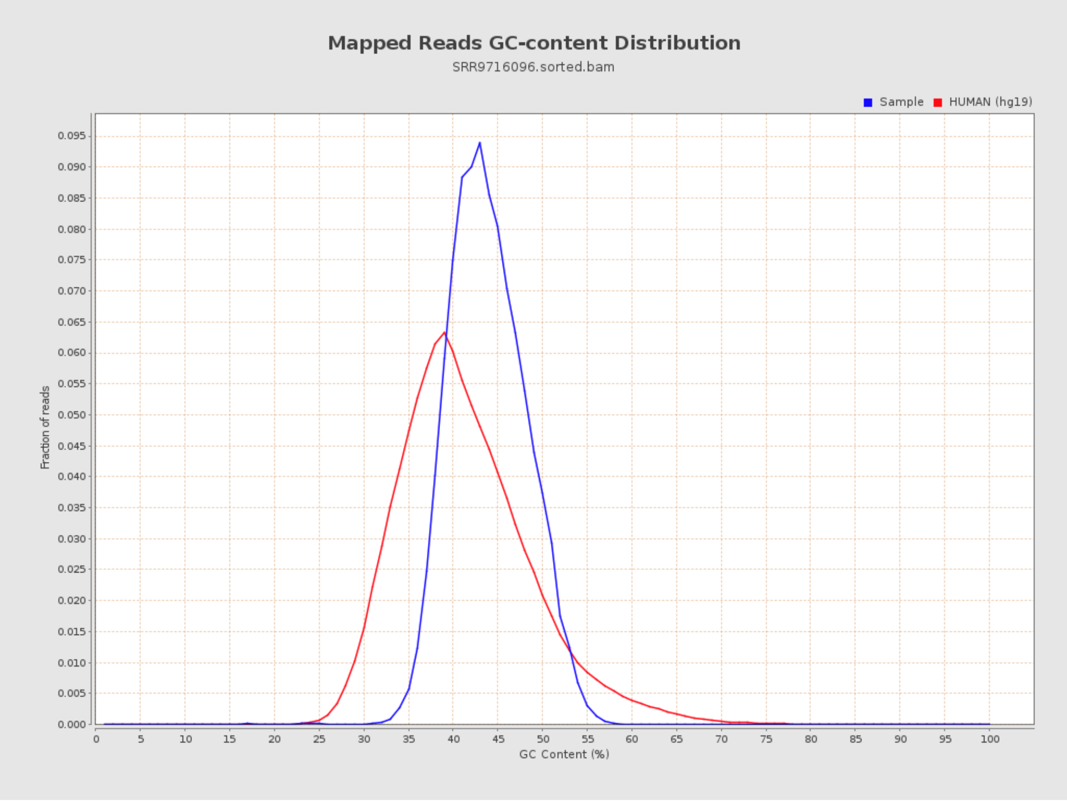
7. Results : Duplication Rate Histogram



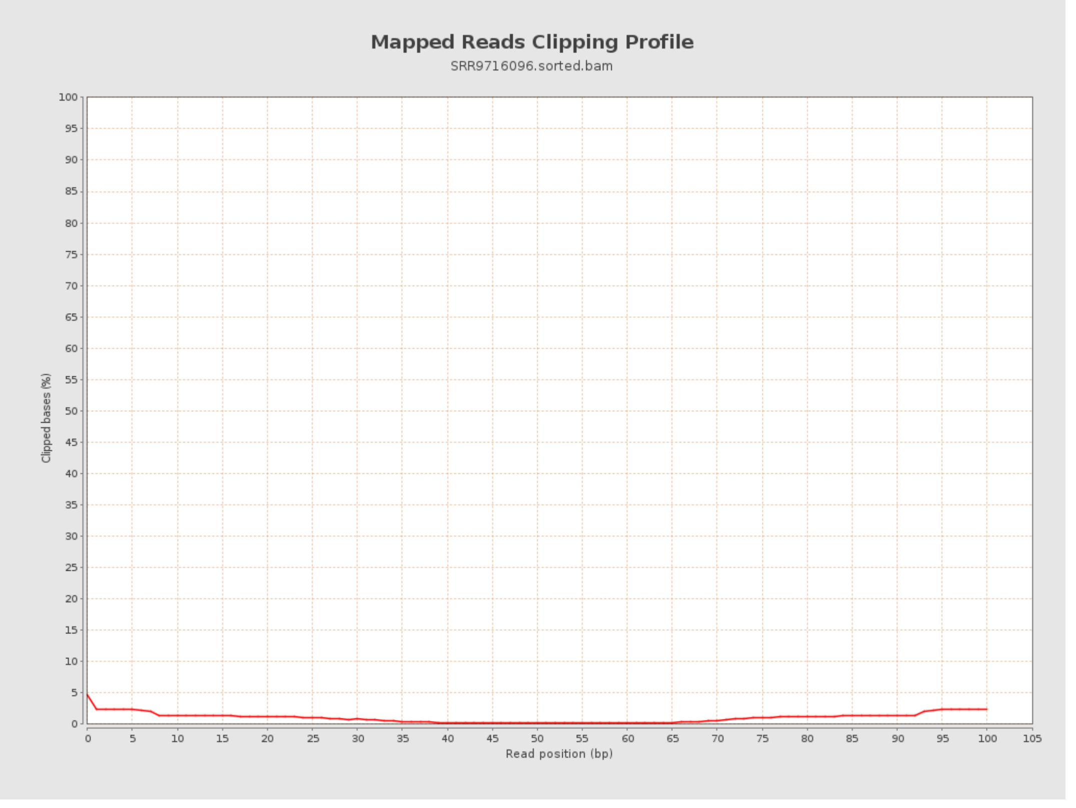
8. Results : Mapped Reads Nucleotide Content



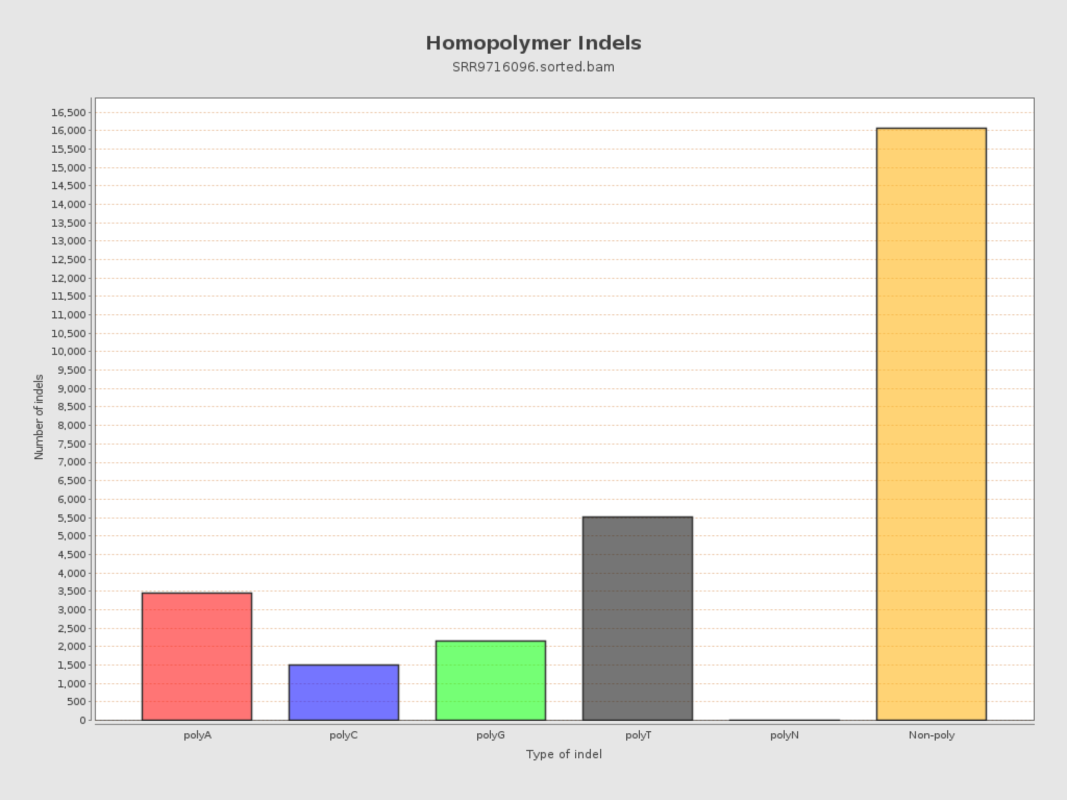
9. Results : Mapped Reads GC-content Distribution



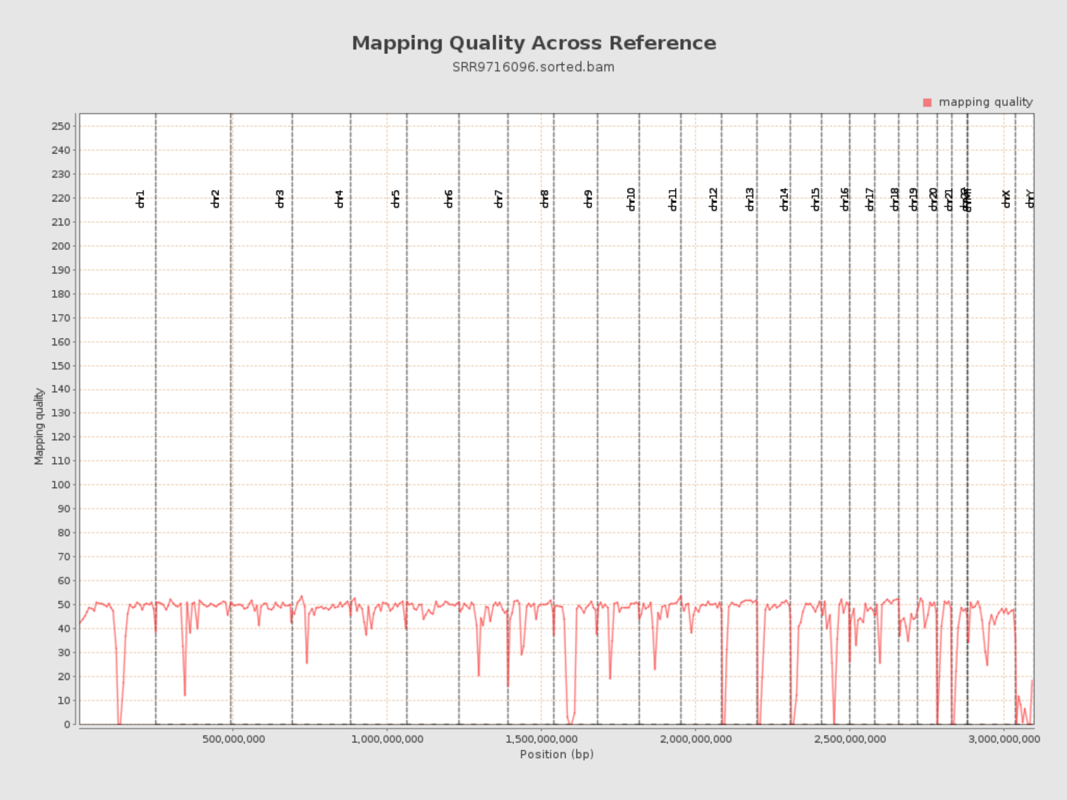
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram