Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 17:54:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716099.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_SRR9716099 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716099.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 17:54:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716099.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,753,324
Mapped reads	1,607,861 / 91.7%
Unmapped reads	145,463 / 8.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,980 / 0.51%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	56,640 / 3.23%
Duplication rate	2.47%
Clipped reads	1,615,968 / 92.17%

2.2. ACGT Content

Number/percentage of A's	23,369,764 / 24.82%
Number/percentage of C's	18,949,610 / 20.13%
Number/percentage of T's	28,838,681 / 30.63%
Number/percentage of G's	22,993,080 / 24.42%
Number/percentage of N's	1,136 / 0%
GC Percentage	44.55%

2.3. Coverage

Mean	0.0304

Standard Deviation	0.2967

2.4. Mapping Quality

Mean Mapping Quality	44.54

2.5. Mismatches and indels

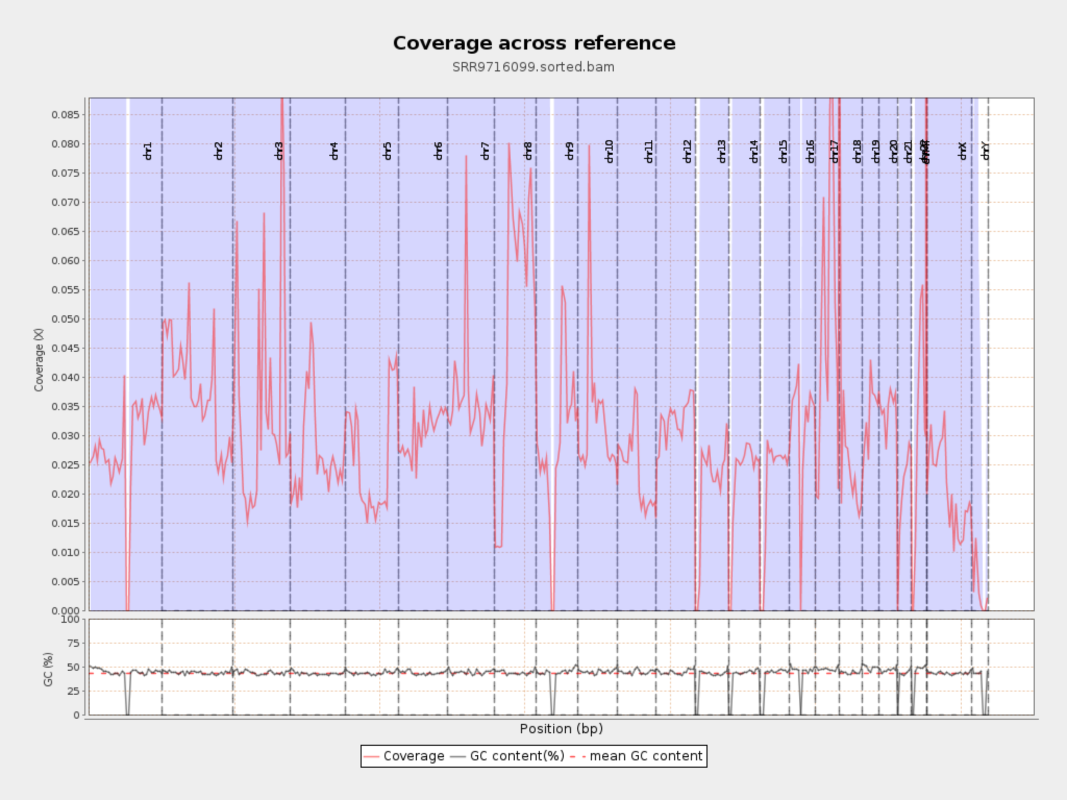
General error rate	0.5%
Mismatches	464,106
Insertions	5,275
Mapped reads with at least one insertion	0.33%
Deletions	17,042
Mapped reads with at least one deletion	1.05%
Homopolymer indels	41.95%

2.6. Chromosome stats

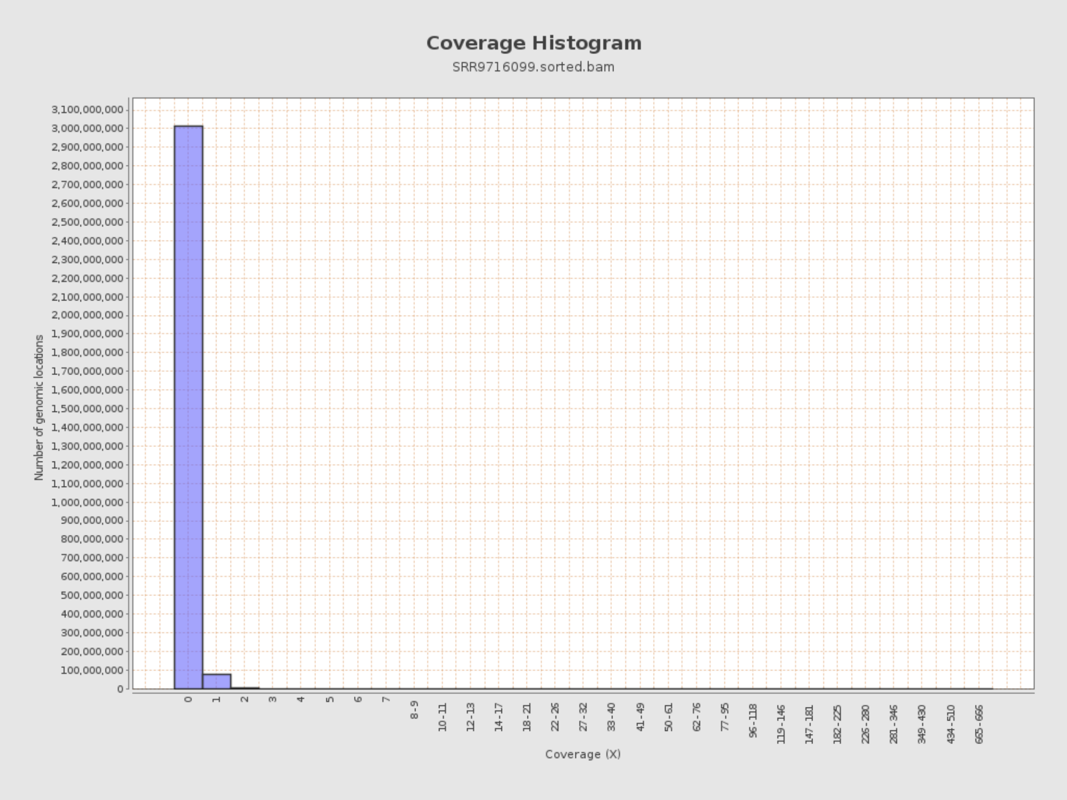
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6981379	0.028	0.4032
chr2	243199373	9234726	0.038	0.3598
chr3	198022430	7078803	0.0357	0.2178
chr4	191154276	5172344	0.0271	0.2004
chr5	180915260	4718448	0.0261	0.1768
chr6	171115067	5244374	0.0306	0.2056
chr7	159138663	5864597	0.0369	0.6476

chr8	146364022	7454453	0.0509	0.3234
chr9	141213431	3972185	0.0281	0.2157
chr10	135534747	4449544	0.0328	0.4141
chr11	135006516	3252725	0.0241	0.2085
chr12	133851895	4367819	0.0326	0.2174
chr13	115169878	2433760	0.0211	0.1569
chr14	107349540	2390545	0.0223	0.1667
chr15	102531392	2225745	0.0217	0.1627
chr16	90354753	2900137	0.0321	0.2058
chr17	81195210	4094515	0.0504	0.255
chr18	78077248	2174633	0.0279	0.3257
chr19	59128983	1987819	0.0336	0.3687
chr20	63025520	2172970	0.0345	0.2151
chr21	48129895	985049	0.0205	0.1713
chr22	51304566	1476193	0.0288	0.1848
chrMT	16571	59196	3.5723	2.8928
chrX	155270560	3269318	0.0211	0.1836
chrY	59373566	218281	0.0037	0.1081

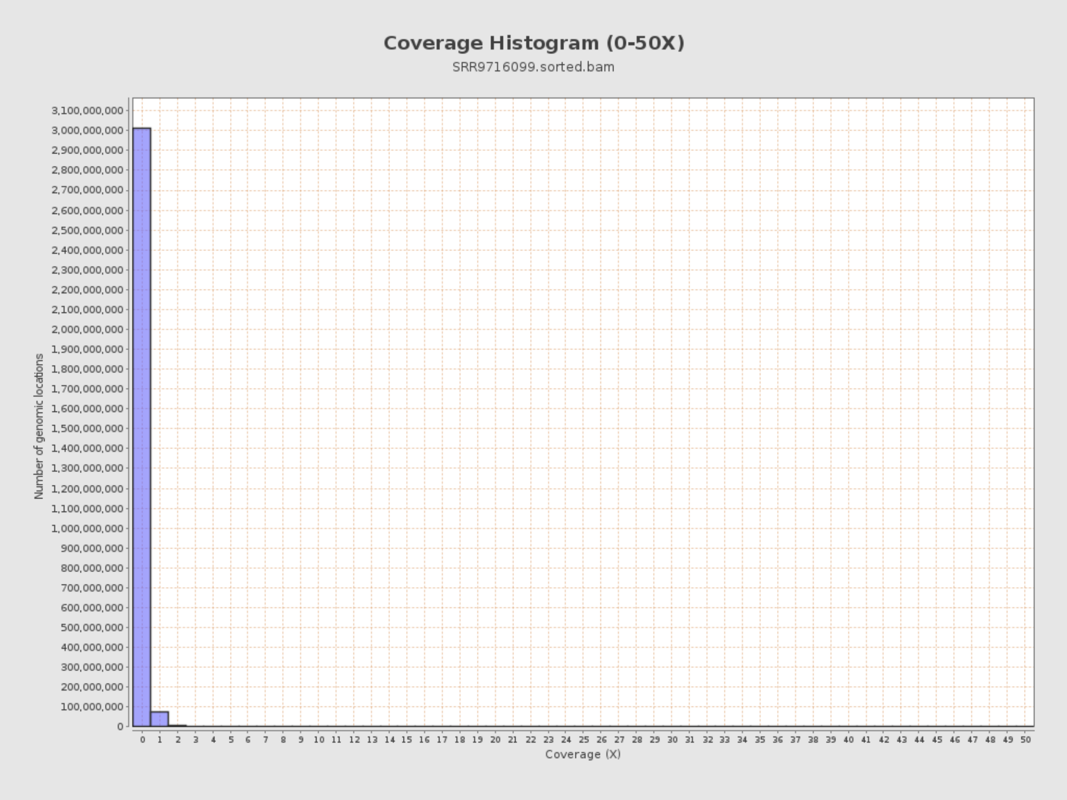
3. Results : Coverage across reference



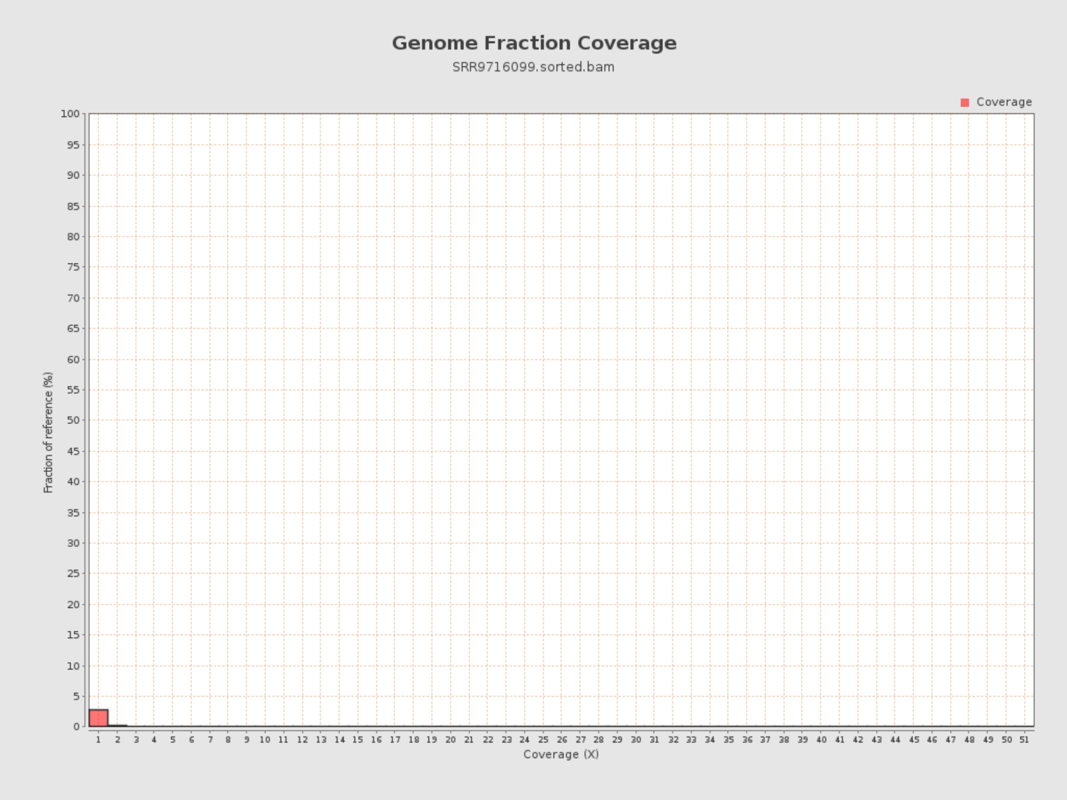
4. Results : Coverage Histogram



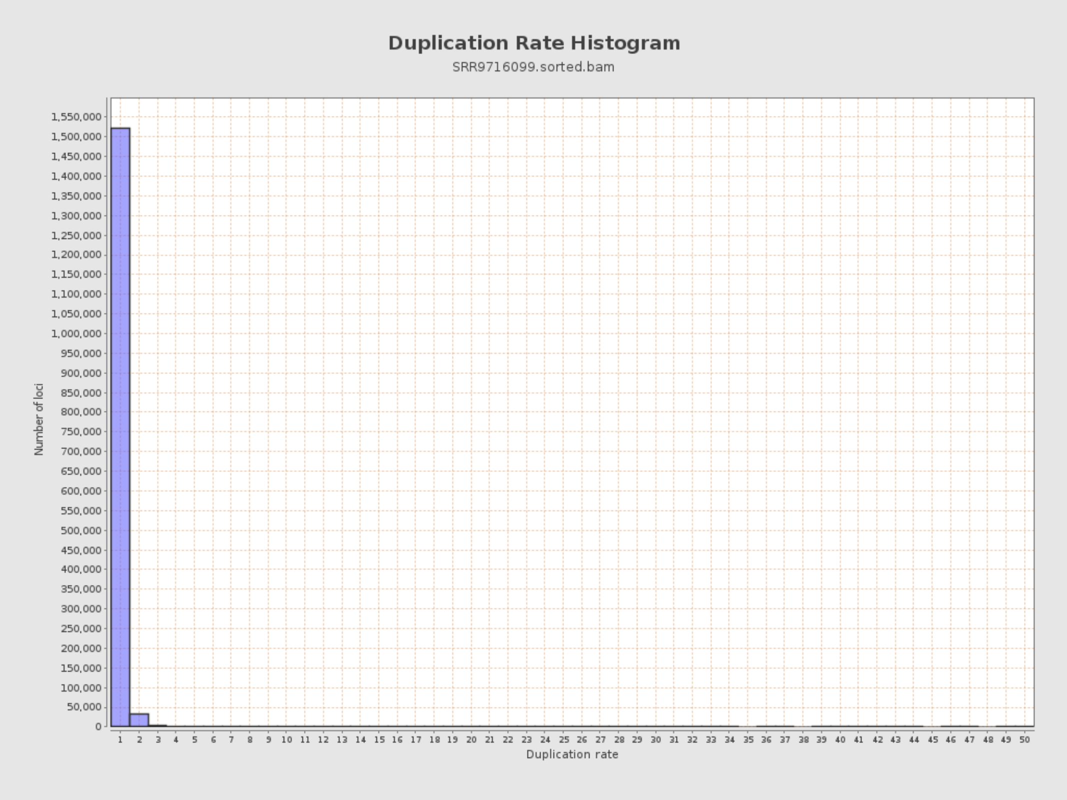
5. Results : Coverage Histogram (0-50X)



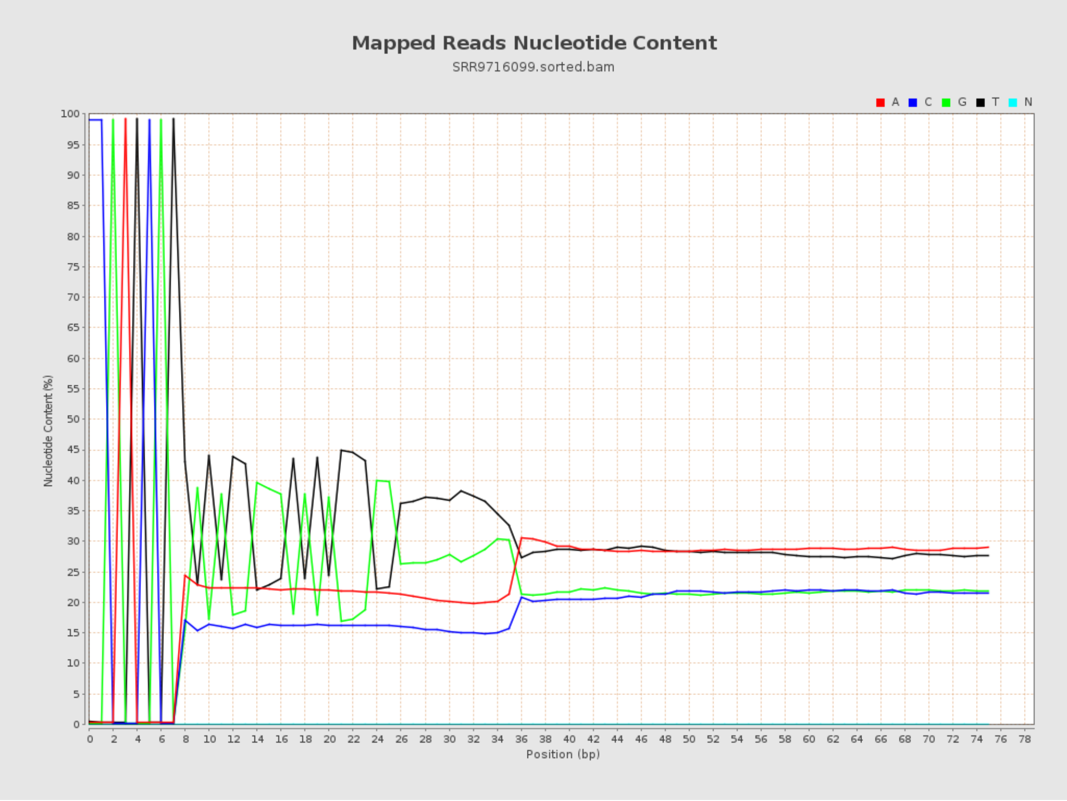
6. Results : Genome Fraction Coverage



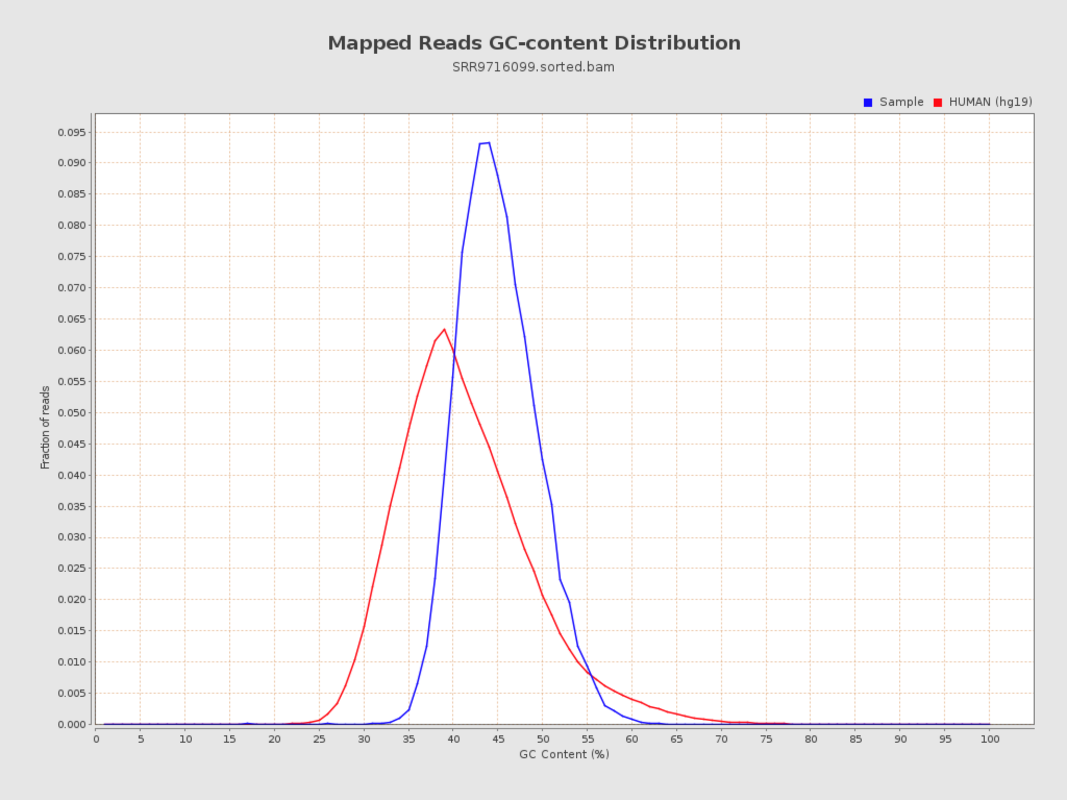
7. Results : Duplication Rate Histogram



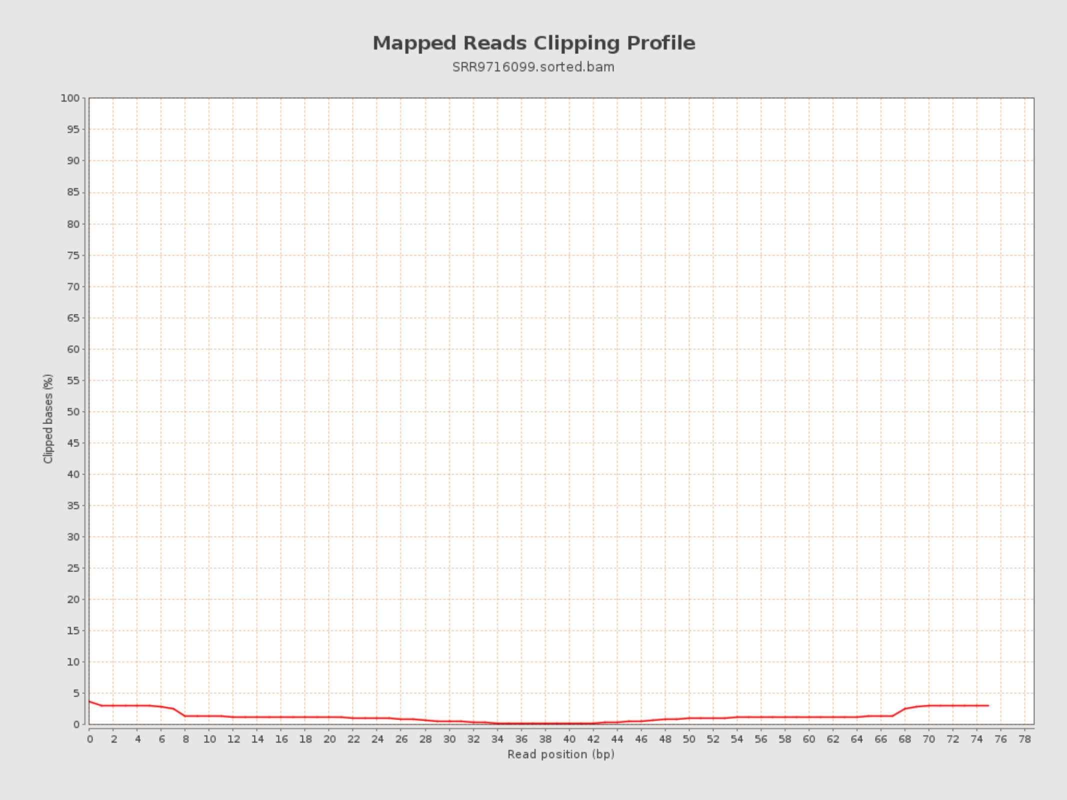
8. Results : Mapped Reads Nucleotide Content



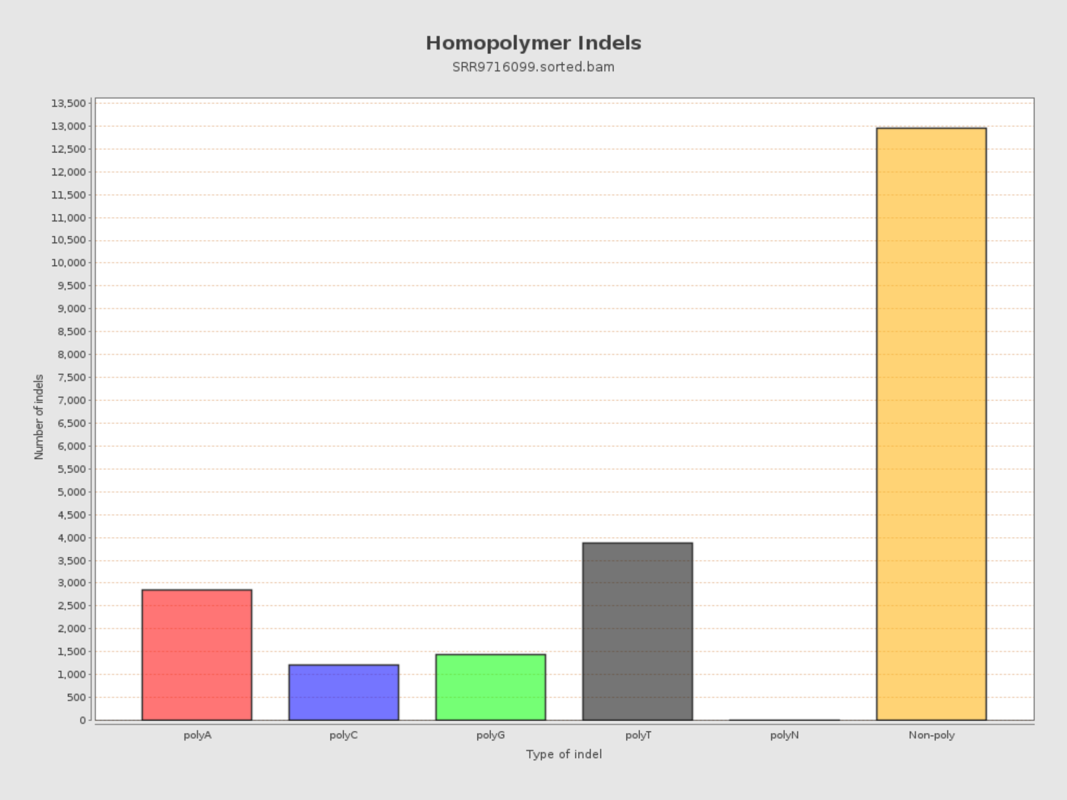
9. Results : Mapped Reads GC-content Distribution



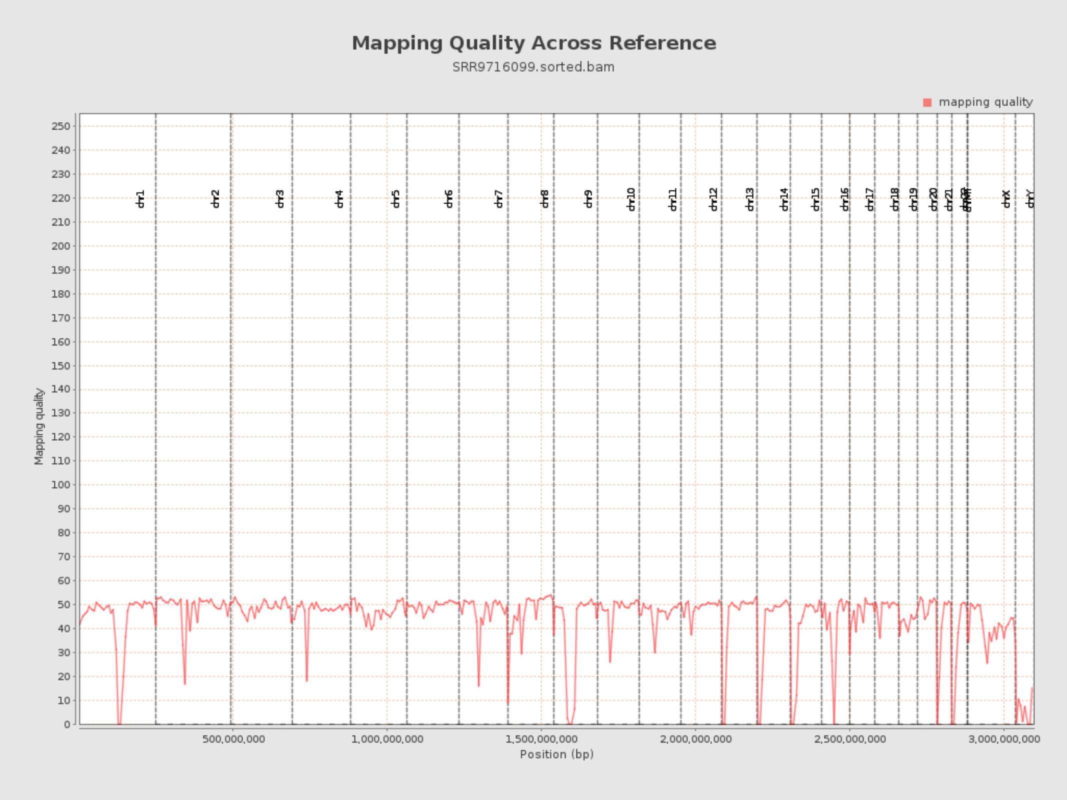
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram