Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 08:29:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716715.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_SRR9716715 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716715.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 08:29:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716715.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	473,819
Mapped reads	429,422 / 90.63%
Unmapped reads	44,397 / 9.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,823 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	5,727 / 1.21%
Duplication rate	1.05%
Clipped reads	430,817 / 90.92%

2.2. ACGT Content

Number/percentage of A's	5,765,643 / 23.59%
Number/percentage of C's	4,470,144 / 18.29%
Number/percentage of T's	7,907,752 / 32.36%
Number/percentage of G's	6,292,173 / 25.75%
Number/percentage of N's	528 / 0%
GC Percentage	44.04%

2.3. Coverage

Mean	0.0079

Standard Deviation	0.0999

2.4. Mapping Quality

Mean Mapping Quality	44.47

2.5. Mismatches and indels

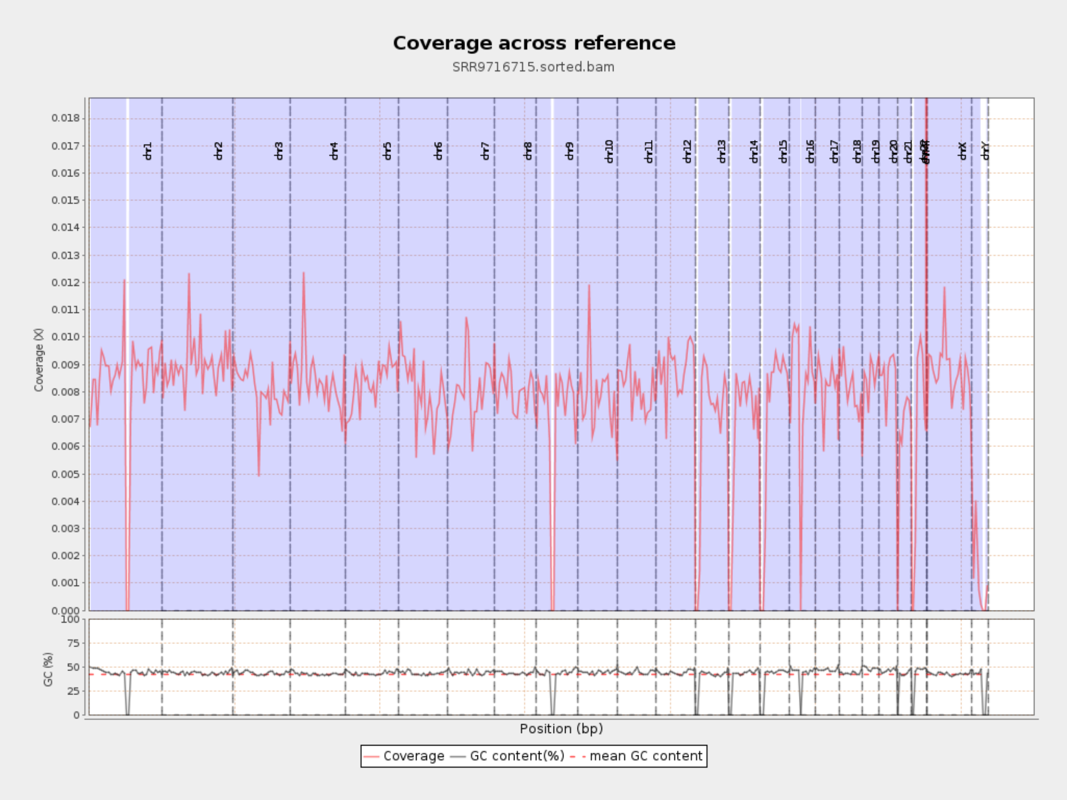
General error rate	0.49%
Mismatches	117,997
Insertions	1,280
Mapped reads with at least one insertion	0.3%
Deletions	3,662
Mapped reads with at least one deletion	0.85%
Homopolymer indels	44.37%

2.6. Chromosome stats

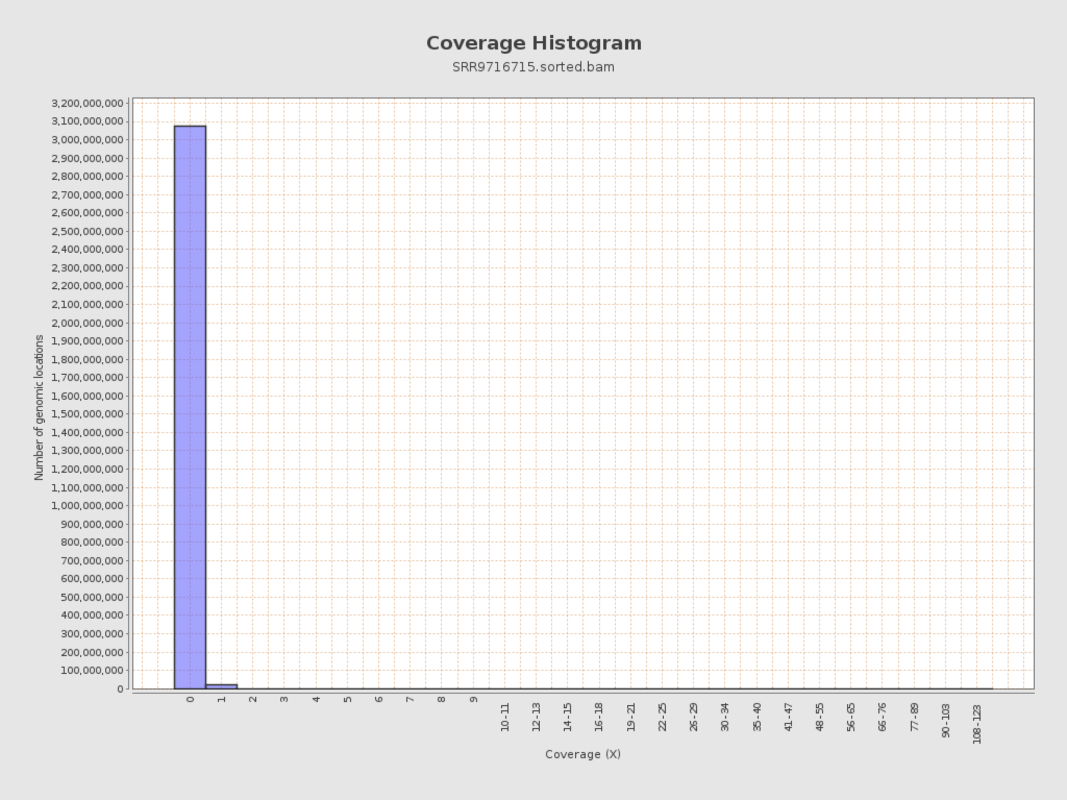
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2047287	0.0082	0.1298
chr2	243199373	2185395	0.009	0.1077
chr3	198022430	1596973	0.0081	0.0924
chr4	191154276	1614336	0.0084	0.0967
chr5	180915260	1505362	0.0083	0.0939
chr6	171115067	1378553	0.0081	0.0938
chr7	159138663	1273285	0.008	0.1038

chr8	146364022	1174613	0.008	0.0974
chr9	141213431	990075	0.007	0.0951
chr10	135534747	1063424	0.0078	0.0991
chr11	135006516	1092466	0.0081	0.1005
chr12	133851895	1188276	0.0089	0.0971
chr13	115169878	762388	0.0066	0.0832
chr14	107349540	699630	0.0065	0.0843
chr15	102531392	722989	0.0071	0.0863
chr16	90354753	751588	0.0083	0.0959
chr17	81195210	663707	0.0082	0.0943
chr18	78077248	640169	0.0082	0.1392
chr19	59128983	500721	0.0085	0.1046
chr20	63025520	536748	0.0085	0.0955
chr21	48129895	307613	0.0064	0.0848
chr22	51304566	308699	0.006	0.0801
chrMT	16571	4271	0.2577	0.5043
chrX	155270560	1360961	0.0088	0.0995
chrY	59373566	72961	0.0012	0.0423

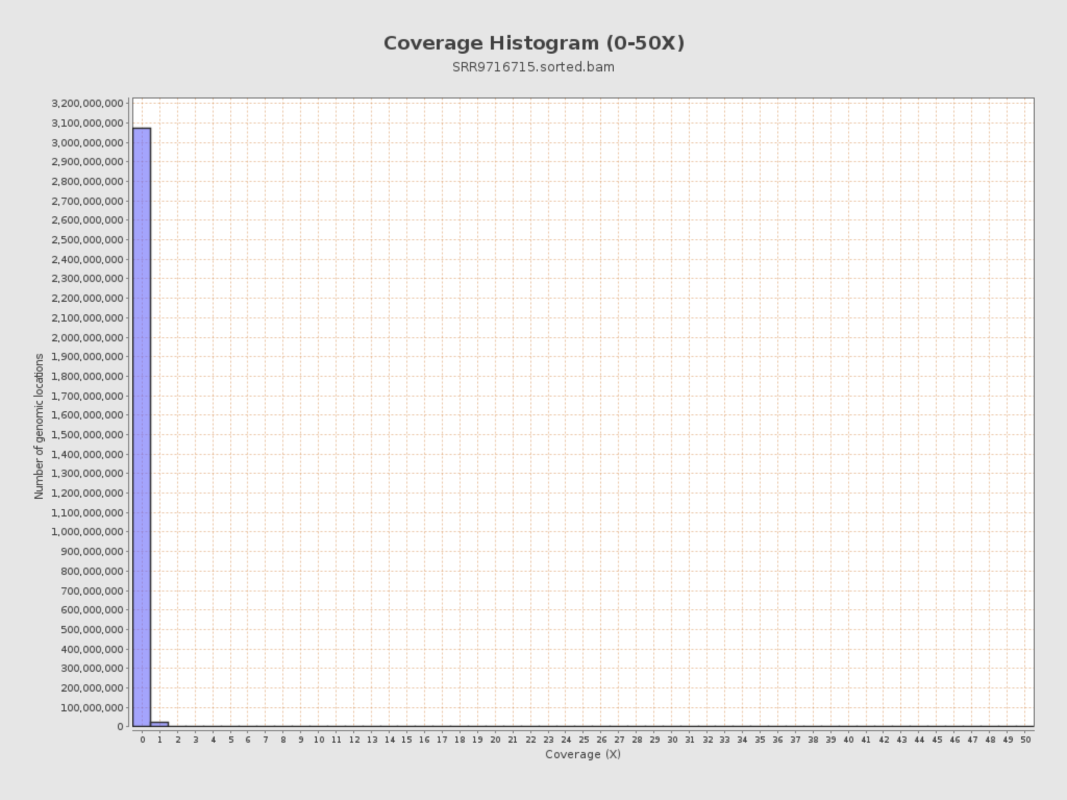
3. Results : Coverage across reference



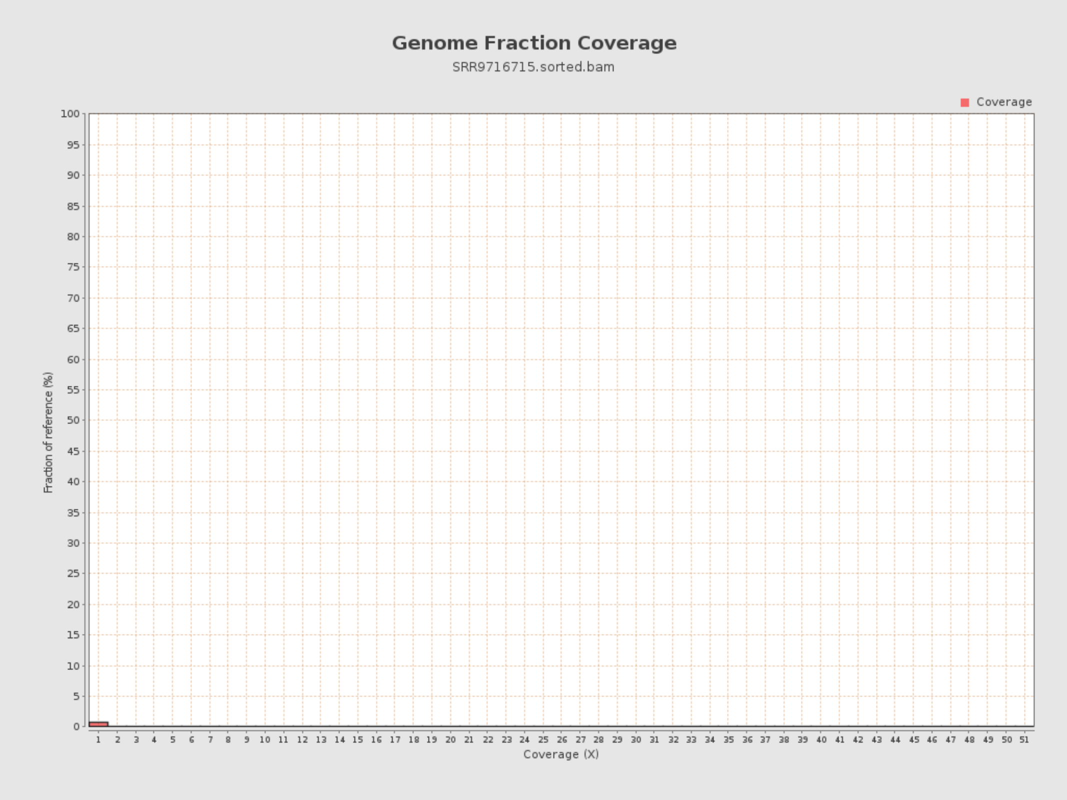
4. Results : Coverage Histogram



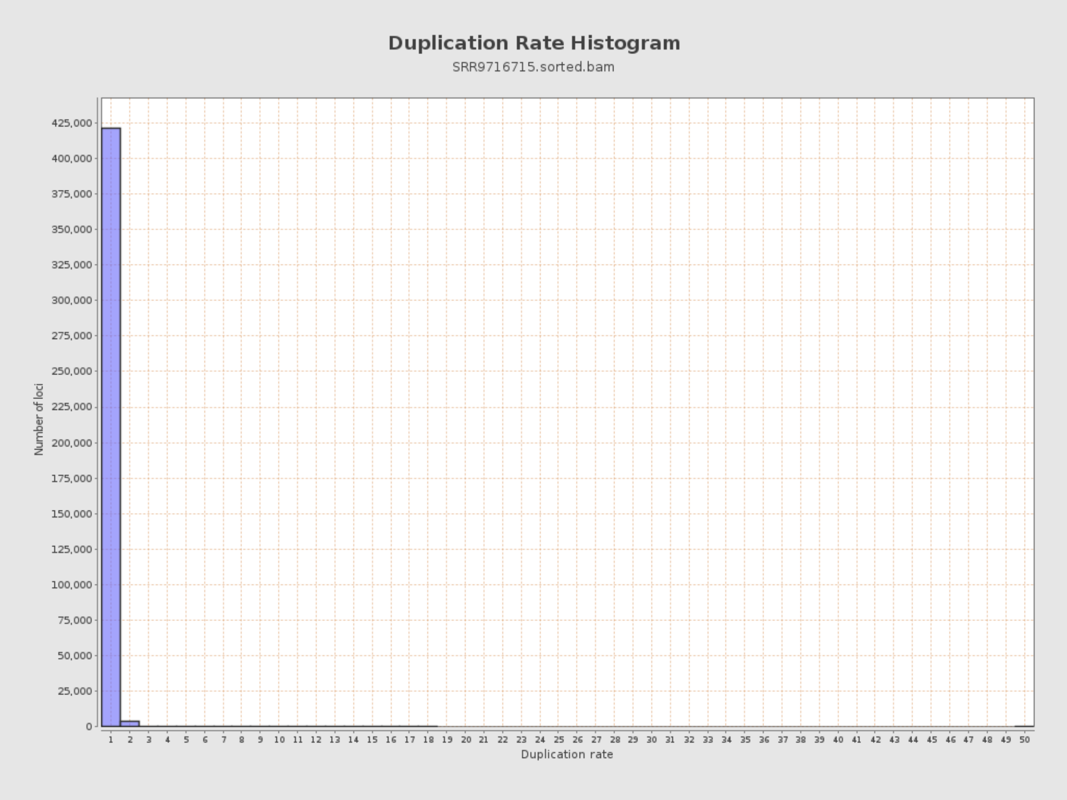
5. Results : Coverage Histogram (0-50X)



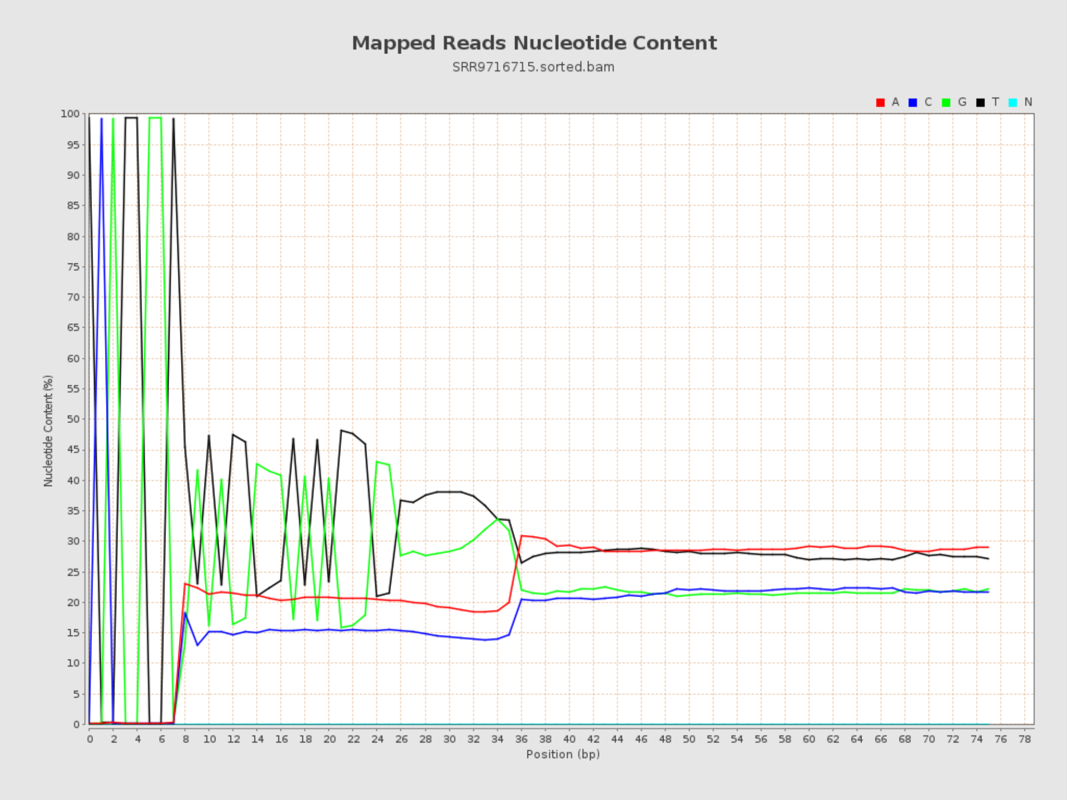
6. Results : Genome Fraction Coverage



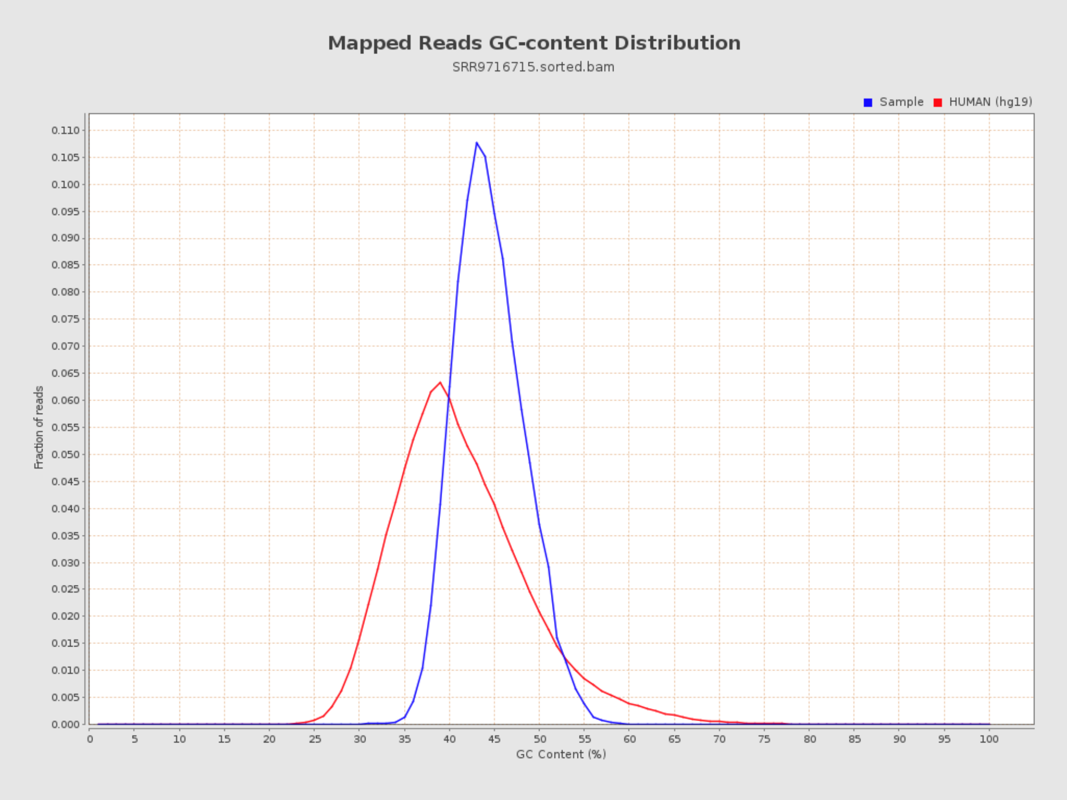
7. Results : Duplication Rate Histogram



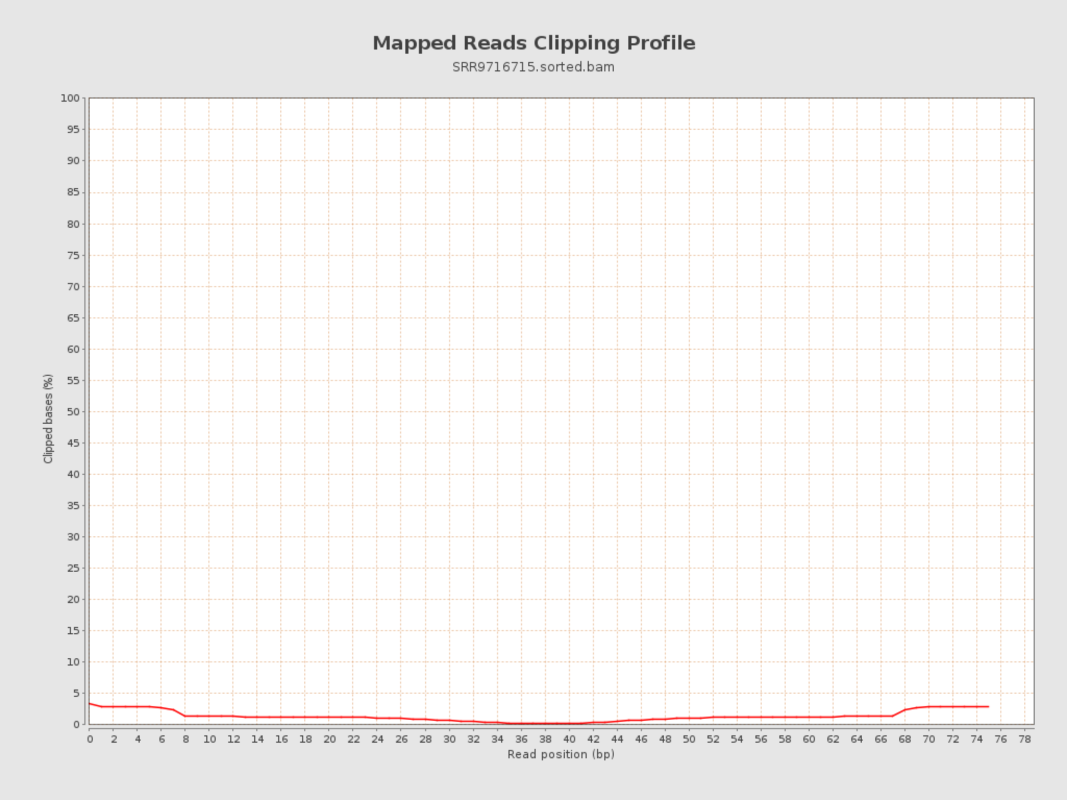
8. Results : Mapped Reads Nucleotide Content



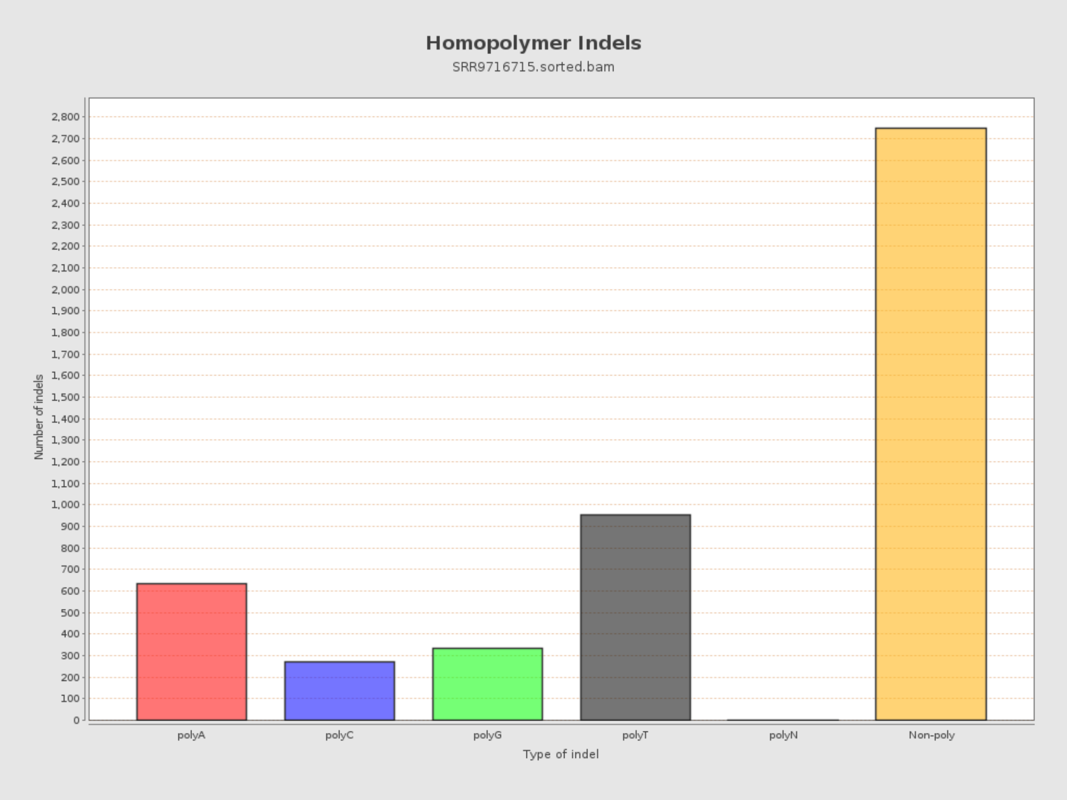
9. Results : Mapped Reads GC-content Distribution



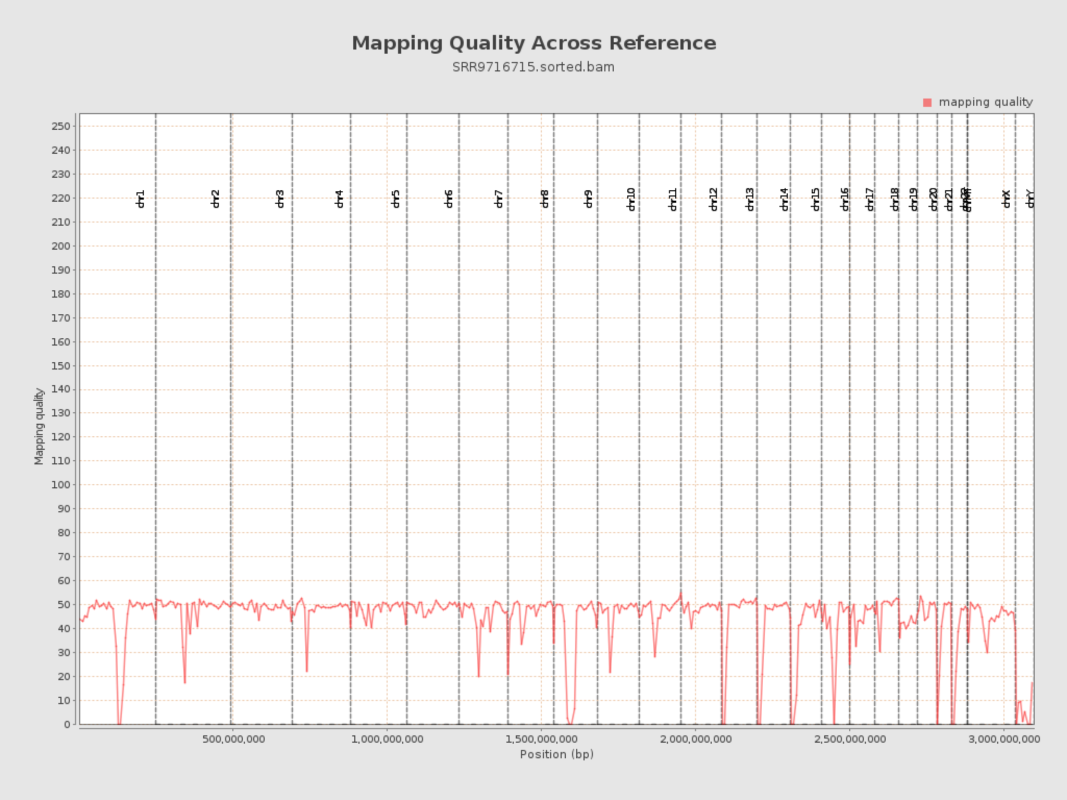
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram