Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 13:56:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716830.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_SRR9716830 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716830.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 13:56:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716830.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,475,134
Mapped reads	1,094,126 / 74.17%
Unmapped reads	381,008 / 25.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,203 / 0.08%
Read min/max/mean length	30 / 76 / 76.03
Duplicated reads (estimated)	89,798 / 6.09%
Duplication rate	6.79%
Clipped reads	1,093,356 / 74.12%

2.2. ACGT Content

Number/percentage of A's	10,970,161 / 19.29%
Number/percentage of C's	10,335,014 / 18.17%
Number/percentage of T's	19,664,305 / 34.58%
Number/percentage of G's	15,899,981 / 27.96%
Number/percentage of N's	943 / 0%
GC Percentage	46.13%

2.3. Coverage

Mean	0.0184

Standard Deviation	0.1866

2.4. Mapping Quality

Mean Mapping Quality	42.62

2.5. Mismatches and indels

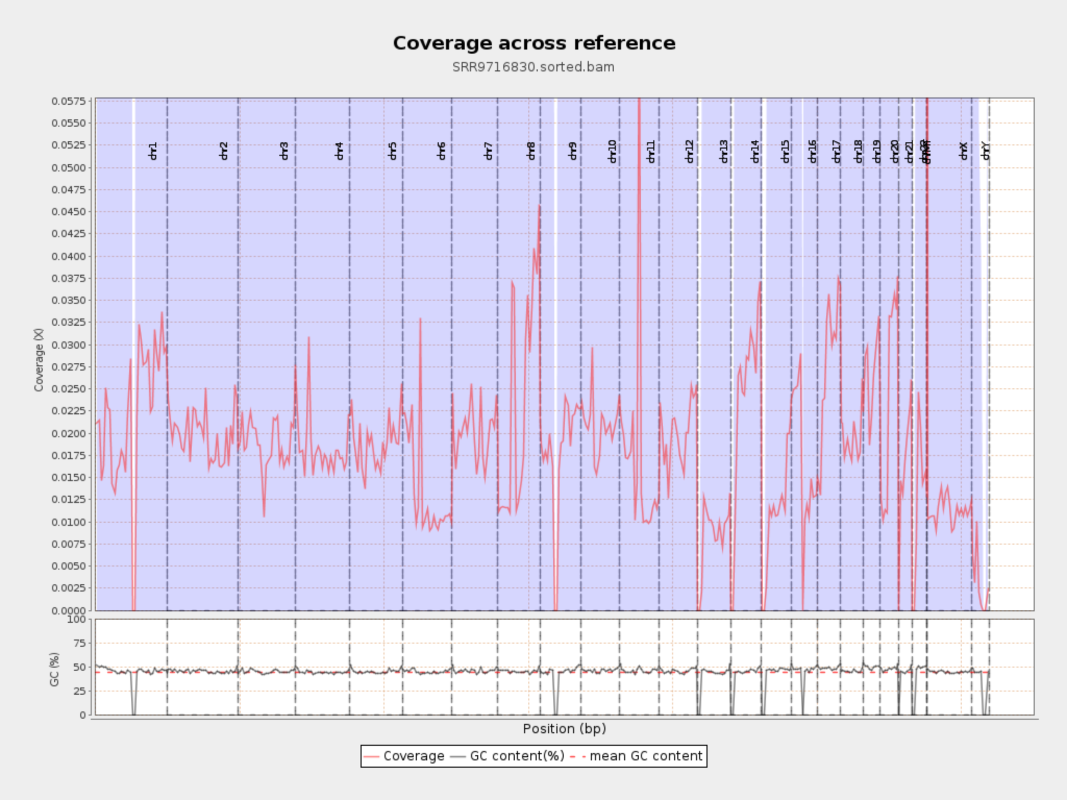
General error rate	0.69%
Mismatches	387,982
Insertions	3,521
Mapped reads with at least one insertion	0.32%
Deletions	9,078
Mapped reads with at least one deletion	0.82%
Homopolymer indels	40.23%

2.6. Chromosome stats

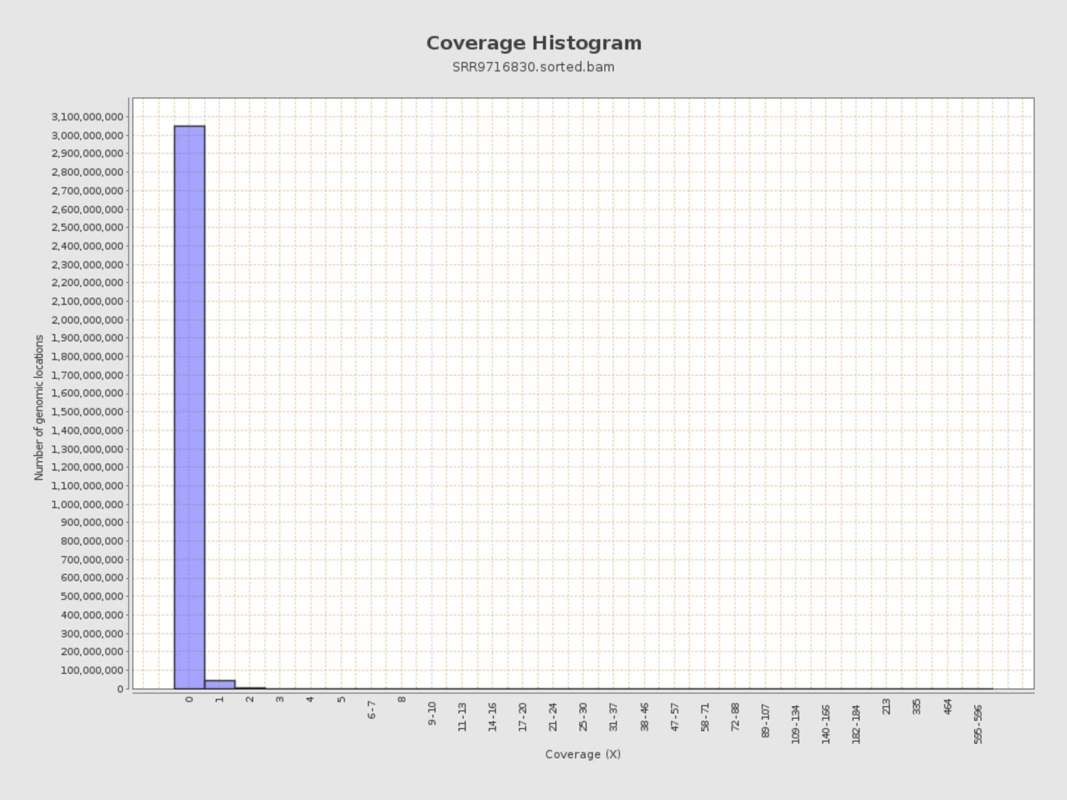
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5477481	0.022	0.2073
chr2	243199373	4828580	0.0199	0.2882
chr3	198022430	3717802	0.0188	0.159
chr4	191154276	3543225	0.0185	0.1763
chr5	180915260	3410316	0.0189	0.16
chr6	171115067	2353185	0.0138	0.1692
chr7	159138663	3206738	0.0202	0.1936

chr8	146364022	3461030	0.0236	0.1903
chr9	141213431	2494805	0.0177	0.1769
chr10	135534747	2848695	0.021	0.1962
chr11	135006516	2399074	0.0178	0.1744
chr12	133851895	2666987	0.0199	0.1694
chr13	115169878	952900	0.0083	0.1081
chr14	107349540	2581752	0.024	0.1851
chr15	102531392	1104259	0.0108	0.1212
chr16	90354753	1498825	0.0166	0.163
chr17	81195210	2263416	0.0279	0.2053
chr18	78077248	1504889	0.0193	0.1961
chr19	59128983	1575230	0.0266	0.245
chr20	63025520	1498636	0.0238	0.1925
chr21	48129895	805885	0.0167	0.1634
chr22	51304566	671417	0.0131	0.1432
chrMT	16571	98882	5.9672	4.8845
chrX	155270560	1746627	0.0112	0.1272
chrY	59373566	175075	0.0029	0.0873

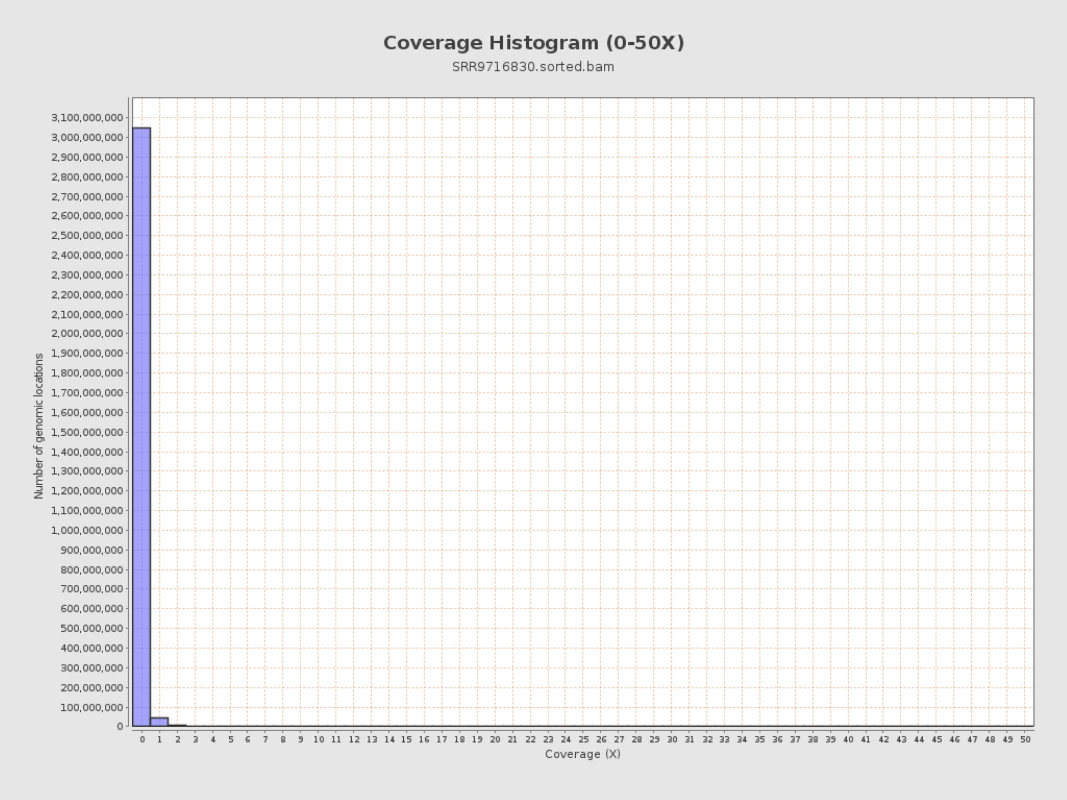
3. Results : Coverage across reference



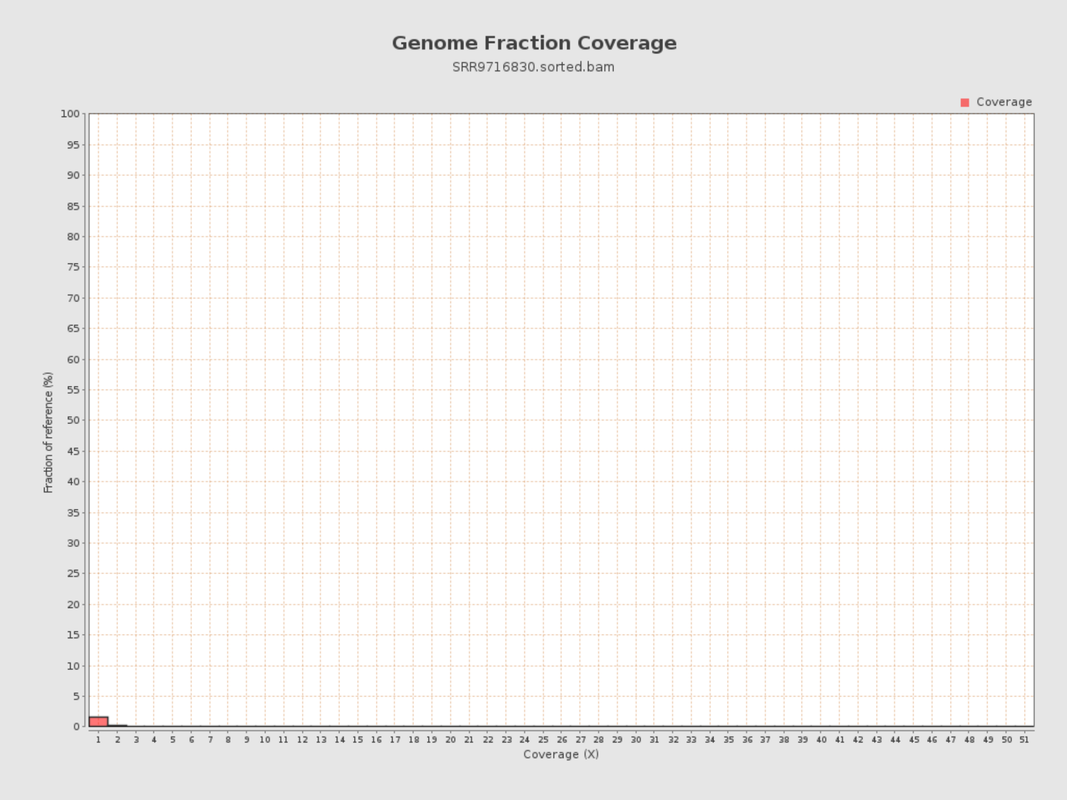
4. Results : Coverage Histogram



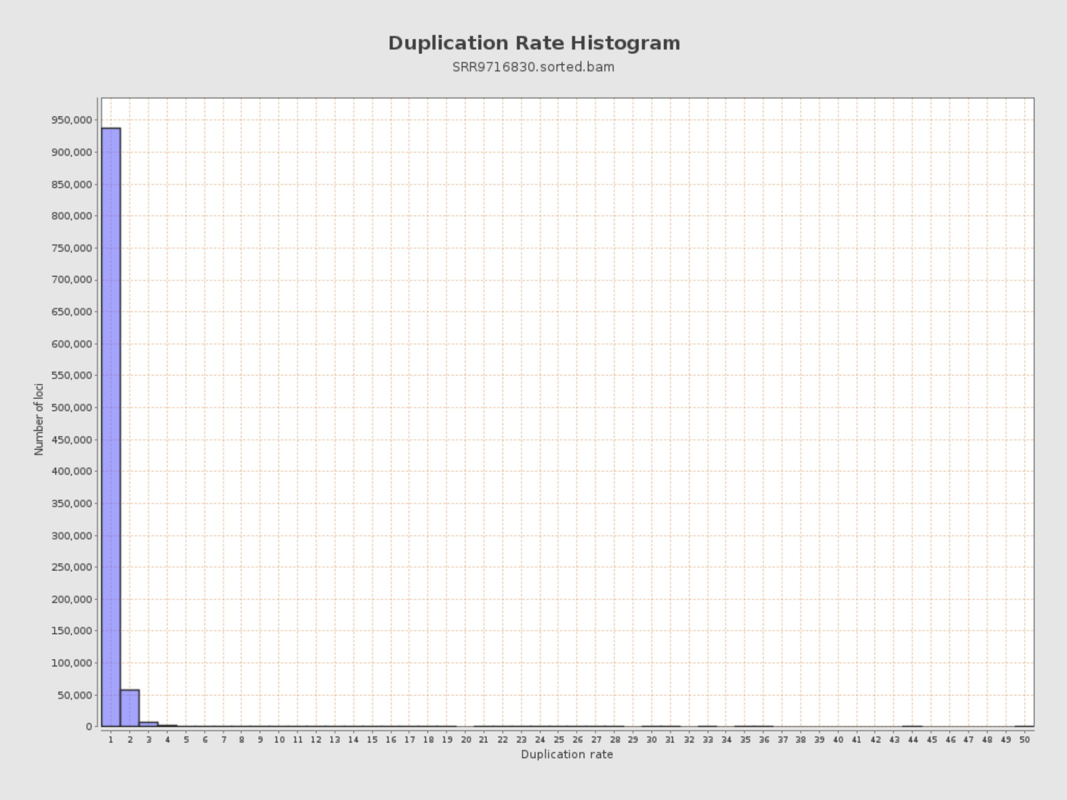
5. Results : Coverage Histogram (0-50X)



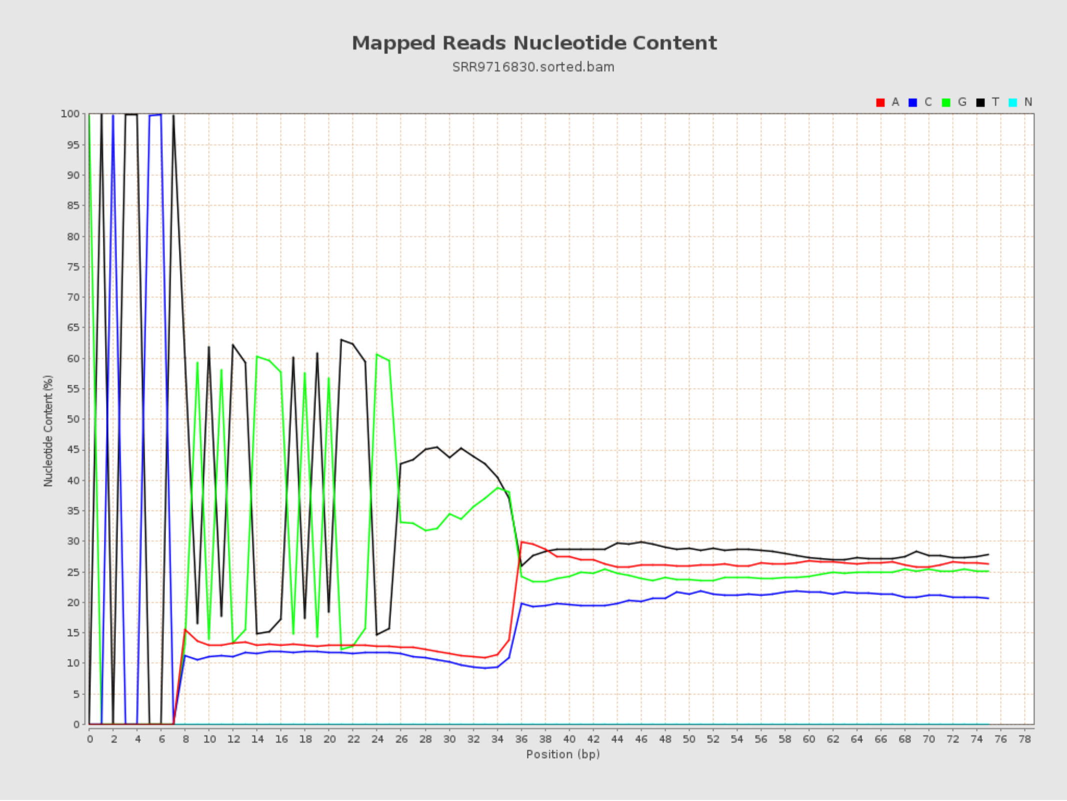
6. Results : Genome Fraction Coverage



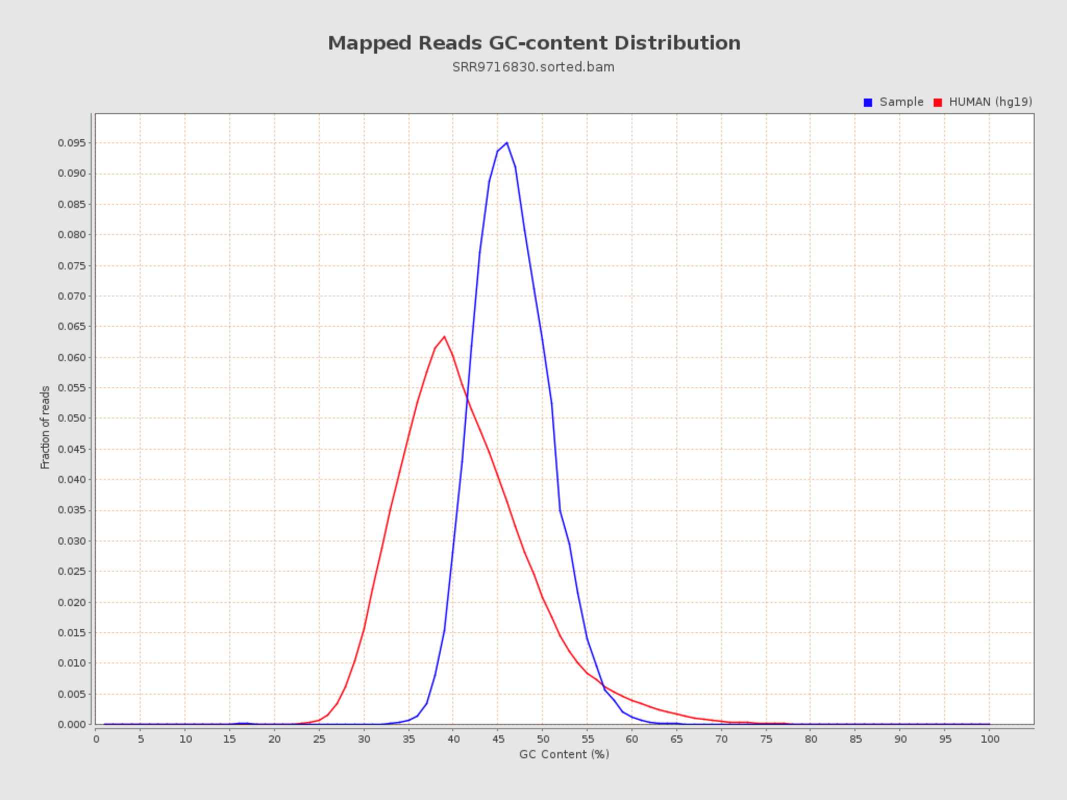
7. Results : Duplication Rate Histogram



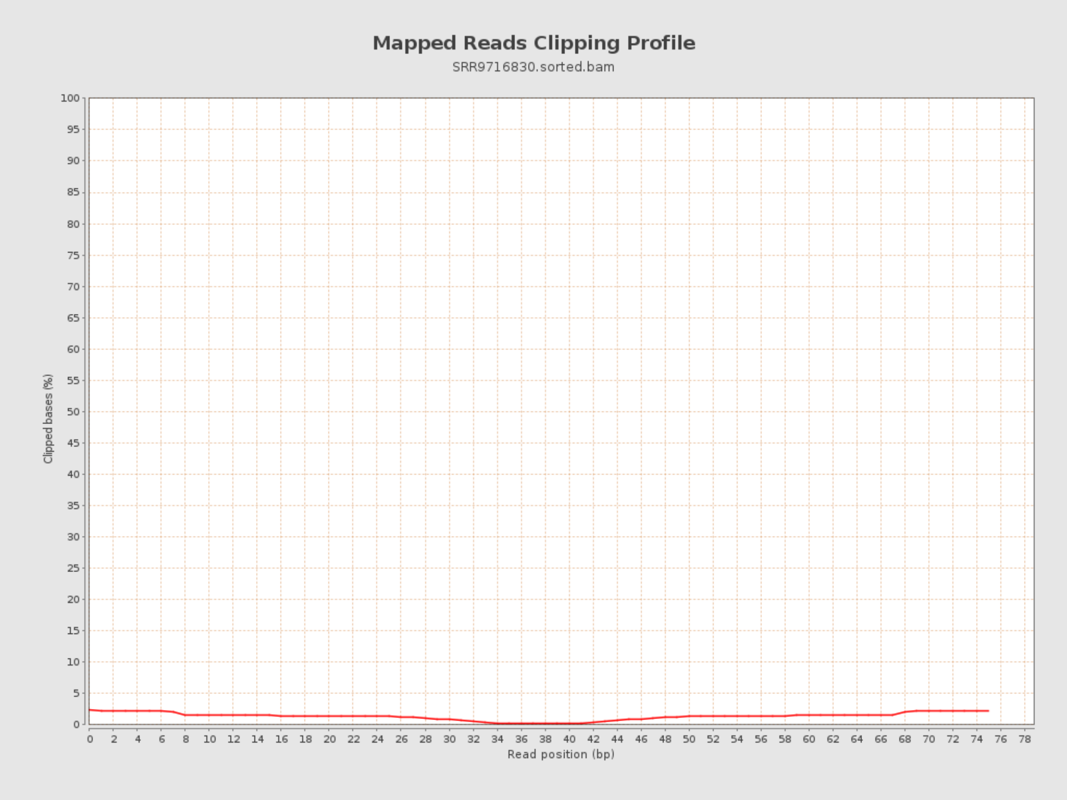
8. Results : Mapped Reads Nucleotide Content



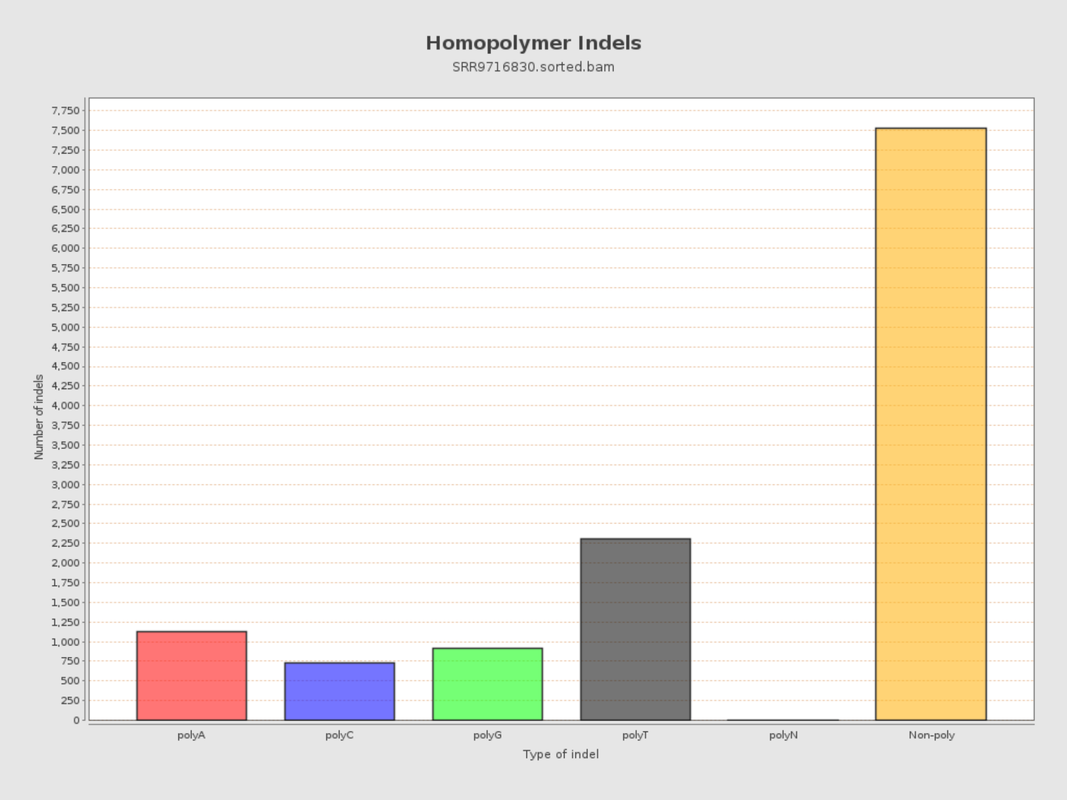
9. Results : Mapped Reads GC-content Distribution



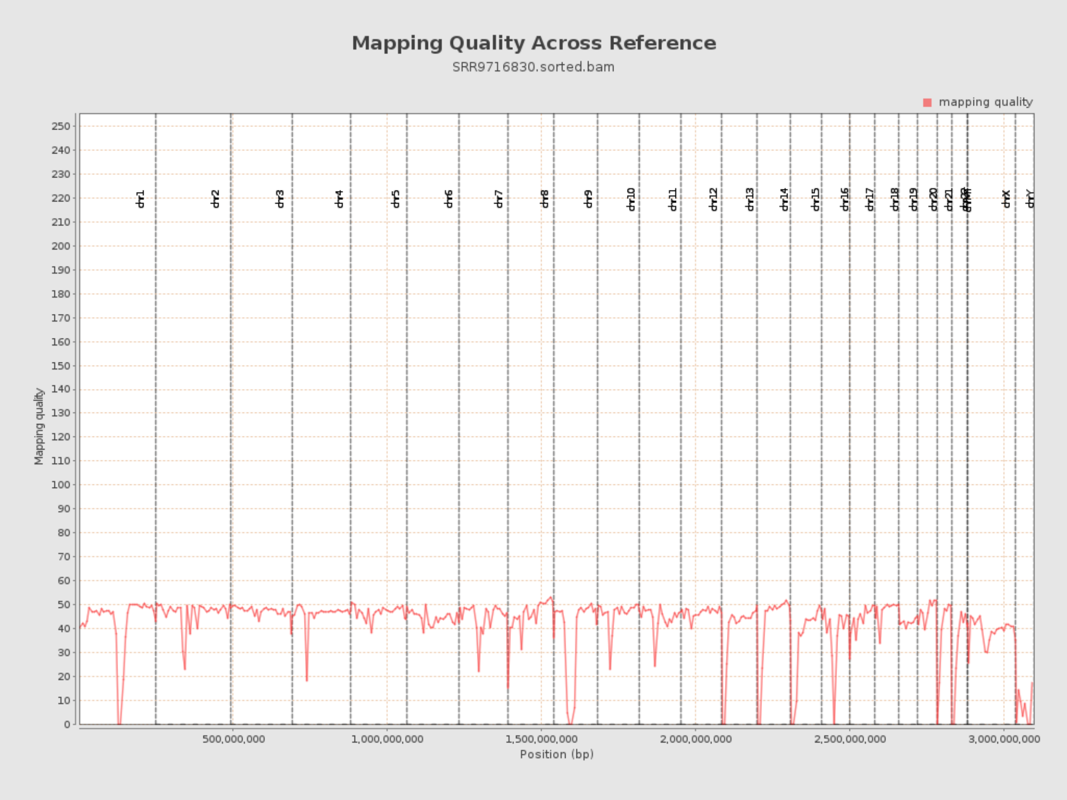
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram