Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 20:15:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716955.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_SRR9716955 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716955.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 20:15:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716955.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,216,833
Mapped reads	1,975,827 / 89.13%
Unmapped reads	241,006 / 10.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,599 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	56,966 / 2.57%
Duplication rate	2.03%
Clipped reads	1,977,580 / 89.21%

2.2. ACGT Content

Number/percentage of A's	28,728,661 / 25.35%
Number/percentage of C's	23,701,759 / 20.92%
Number/percentage of T's	34,026,628 / 30.03%
Number/percentage of G's	26,853,403 / 23.7%
Number/percentage of N's	979 / 0%
GC Percentage	44.62%

2.3. Coverage

Mean	0.0366

Standard Deviation	0.2907

2.4. Mapping Quality

Mean Mapping Quality	42.83

2.5. Mismatches and indels

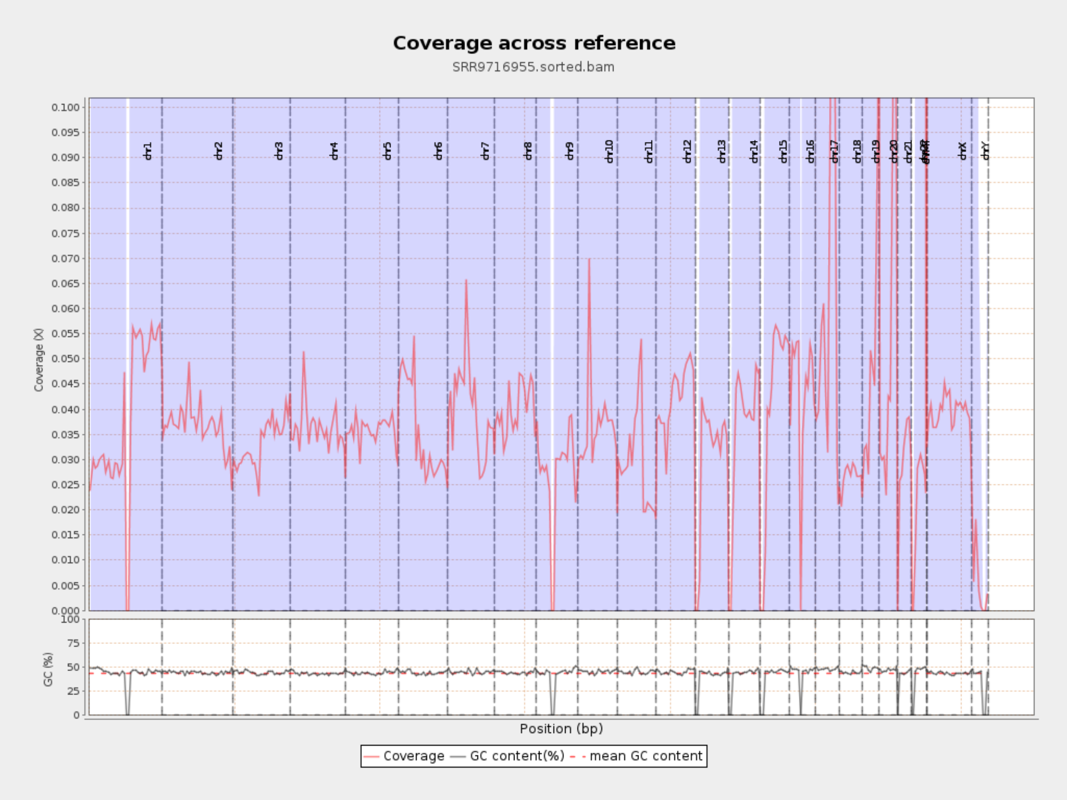
General error rate	0.52%
Mismatches	577,604
Insertions	8,615
Mapped reads with at least one insertion	0.43%
Deletions	21,271
Mapped reads with at least one deletion	1.07%
Homopolymer indels	40.13%

2.6. Chromosome stats

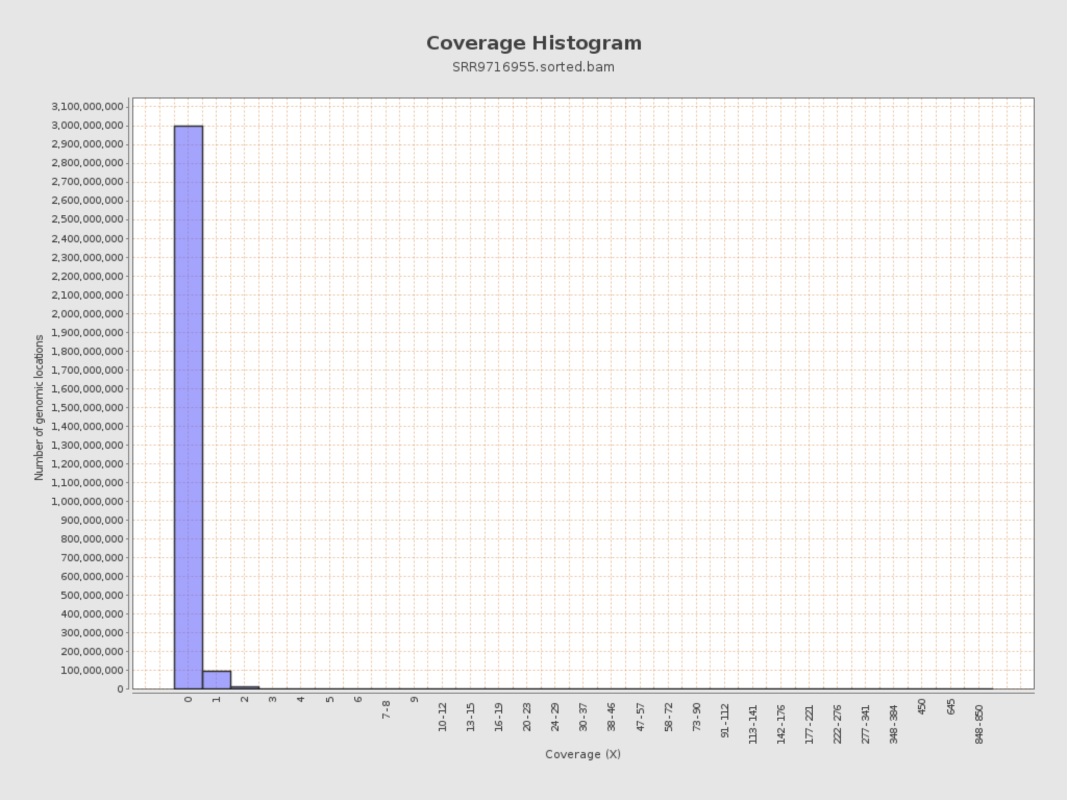
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9483723	0.038	0.3822
chr2	243199373	8956919	0.0368	0.4076
chr3	198022430	6573874	0.0332	0.2045
chr4	191154276	6920495	0.0362	0.225
chr5	180915260	6485404	0.0358	0.2082
chr6	171115067	6103260	0.0357	0.2549
chr7	159138663	6465670	0.0406	0.4303

chr8	146364022	5861336	0.04	0.2831
chr9	141213431	3772540	0.0267	0.2189
chr10	135534747	4993955	0.0368	0.3728
chr11	135006516	3993188	0.0296	0.2438
chr12	133851895	5679318	0.0424	0.2292
chr13	115169878	3459806	0.03	0.1928
chr14	107349540	3820691	0.0356	0.2141
chr15	102531392	4134700	0.0403	0.2313
chr16	90354753	3917958	0.0434	0.2454
chr17	81195210	4995184	0.0615	0.289
chr18	78077248	2089664	0.0268	0.3634
chr19	59128983	2964072	0.0501	0.3828
chr20	63025520	3633845	0.0577	0.2807
chr21	48129895	1398903	0.0291	0.2035
chr22	51304566	1033489	0.0201	0.156
chrMT	16571	134988	8.146	6.0711
chrX	155270560	6141485	0.0396	0.2361
chrY	59373566	330476	0.0056	0.1496

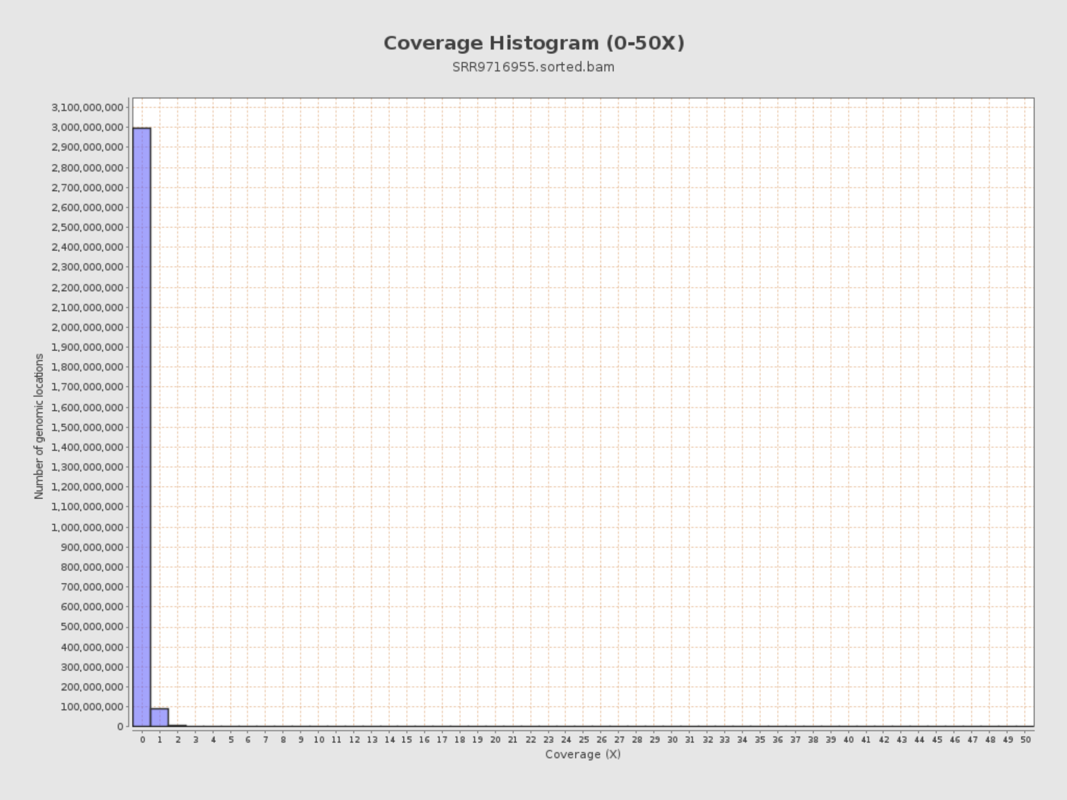
3. Results : Coverage across reference



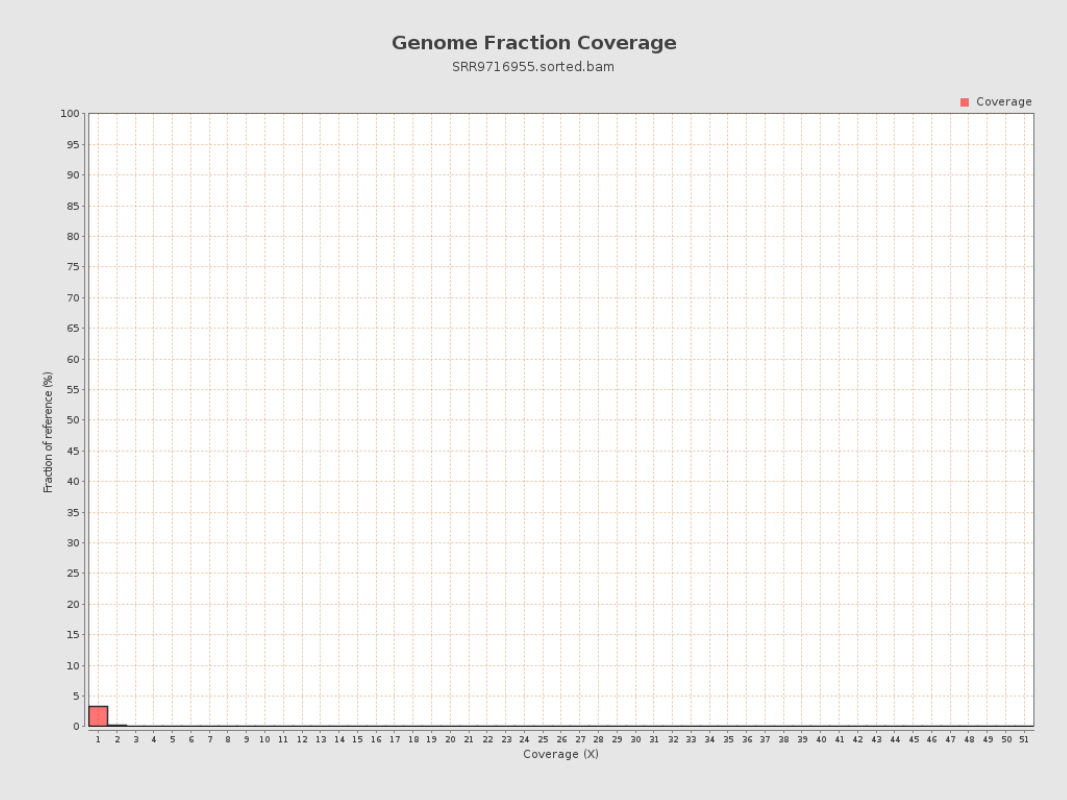
4. Results : Coverage Histogram



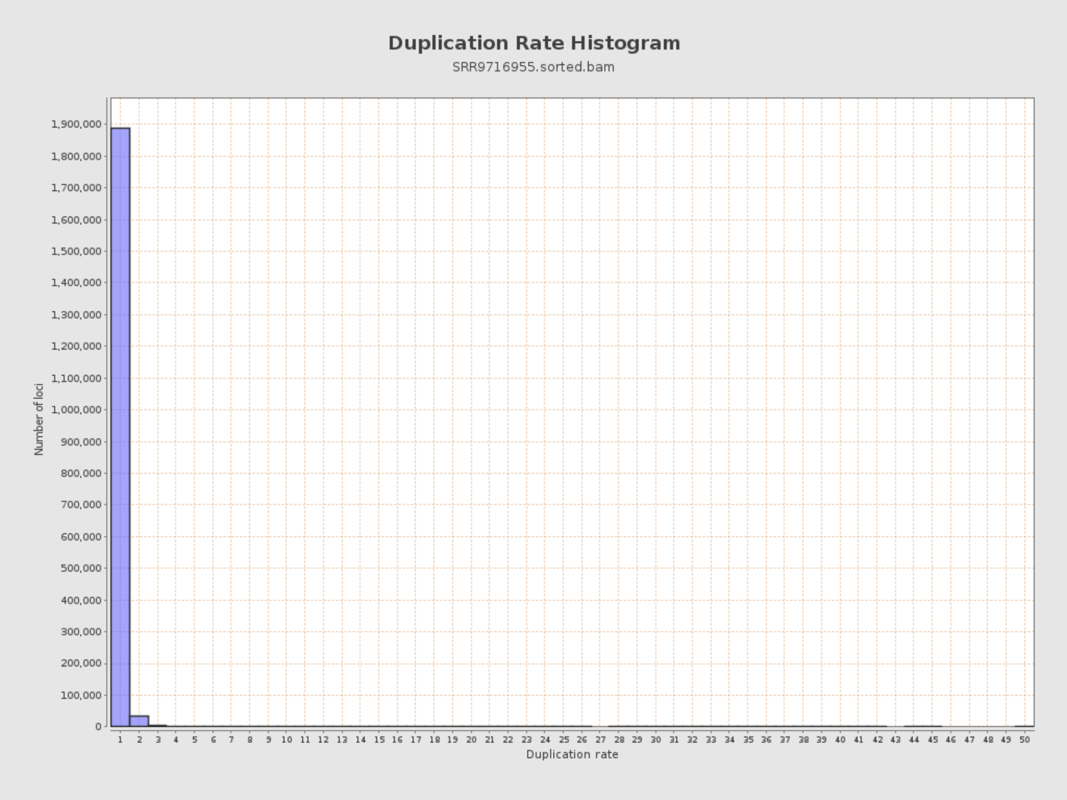
5. Results : Coverage Histogram (0-50X)



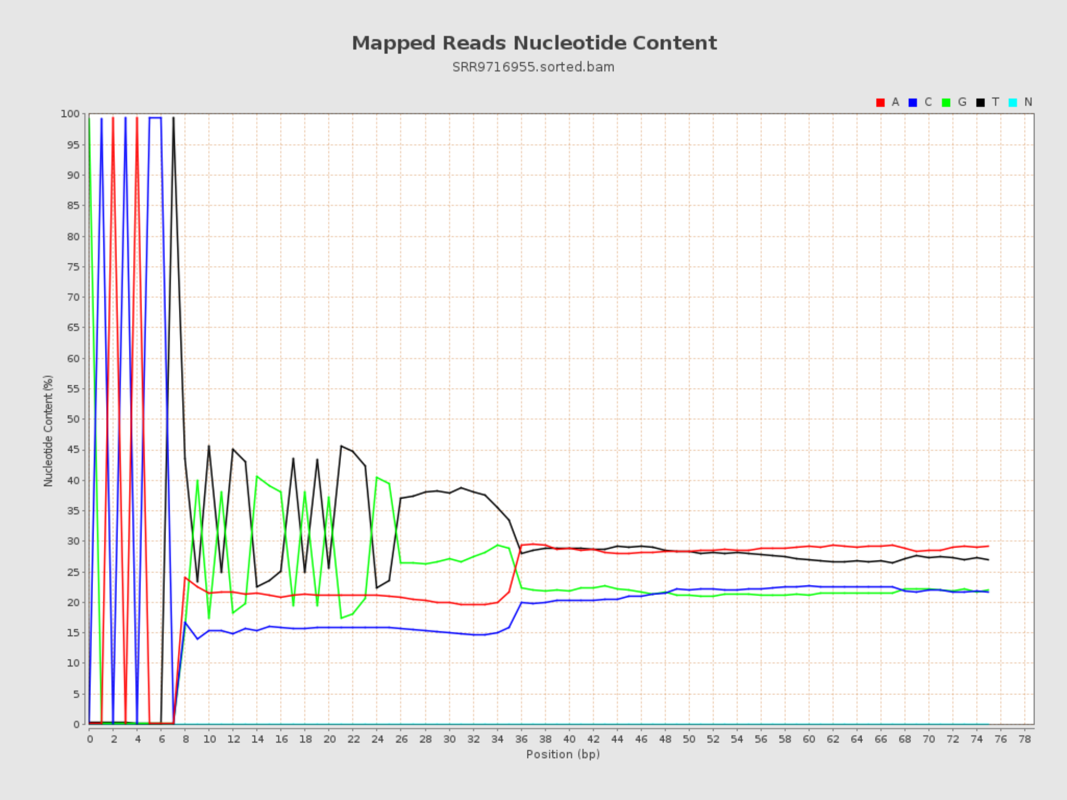
6. Results : Genome Fraction Coverage



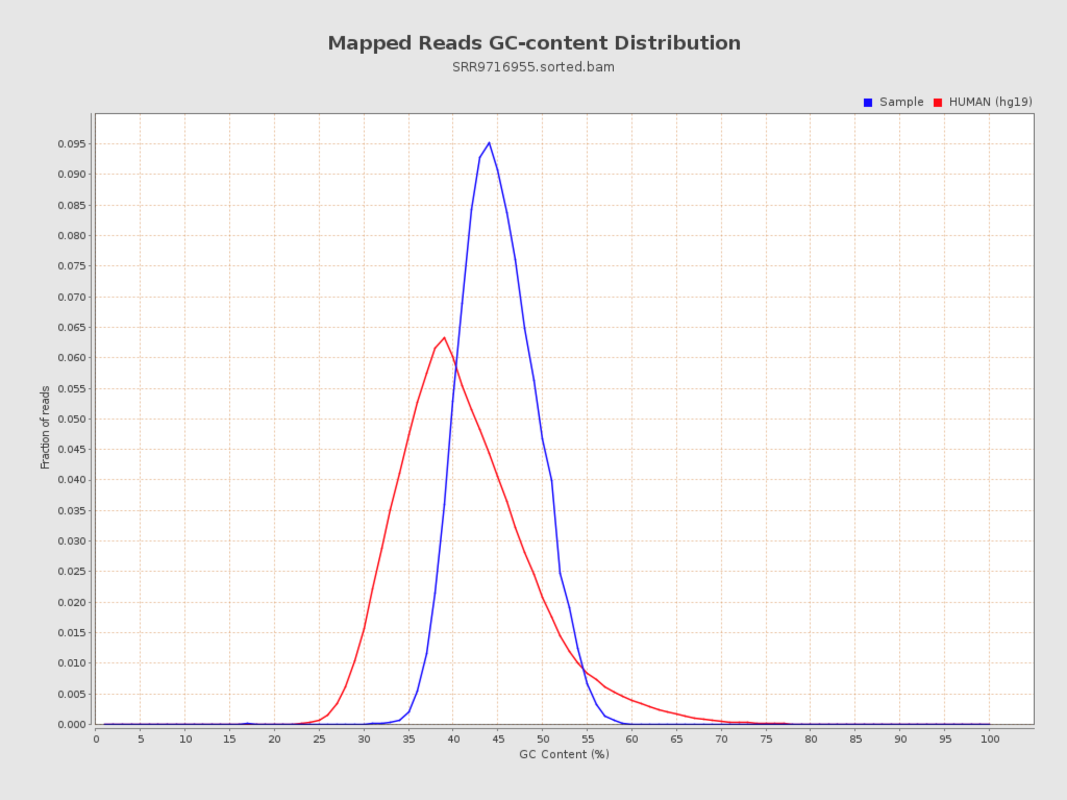
7. Results : Duplication Rate Histogram



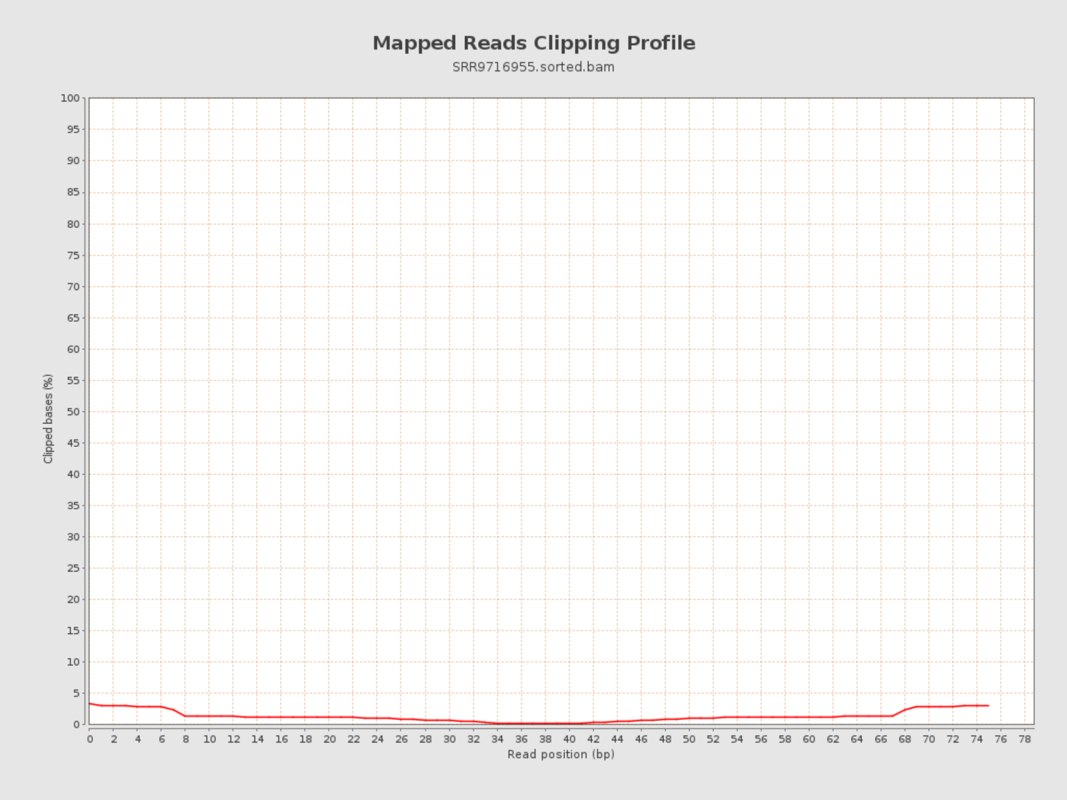
8. Results : Mapped Reads Nucleotide Content



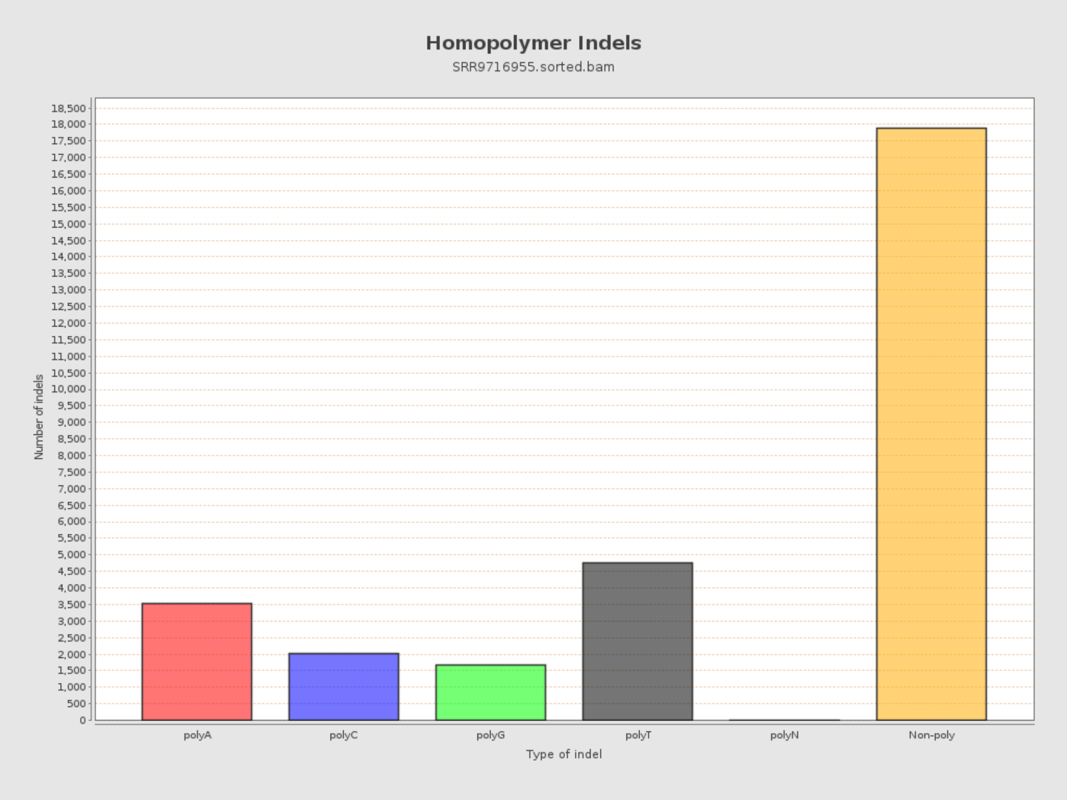
9. Results : Mapped Reads GC-content Distribution



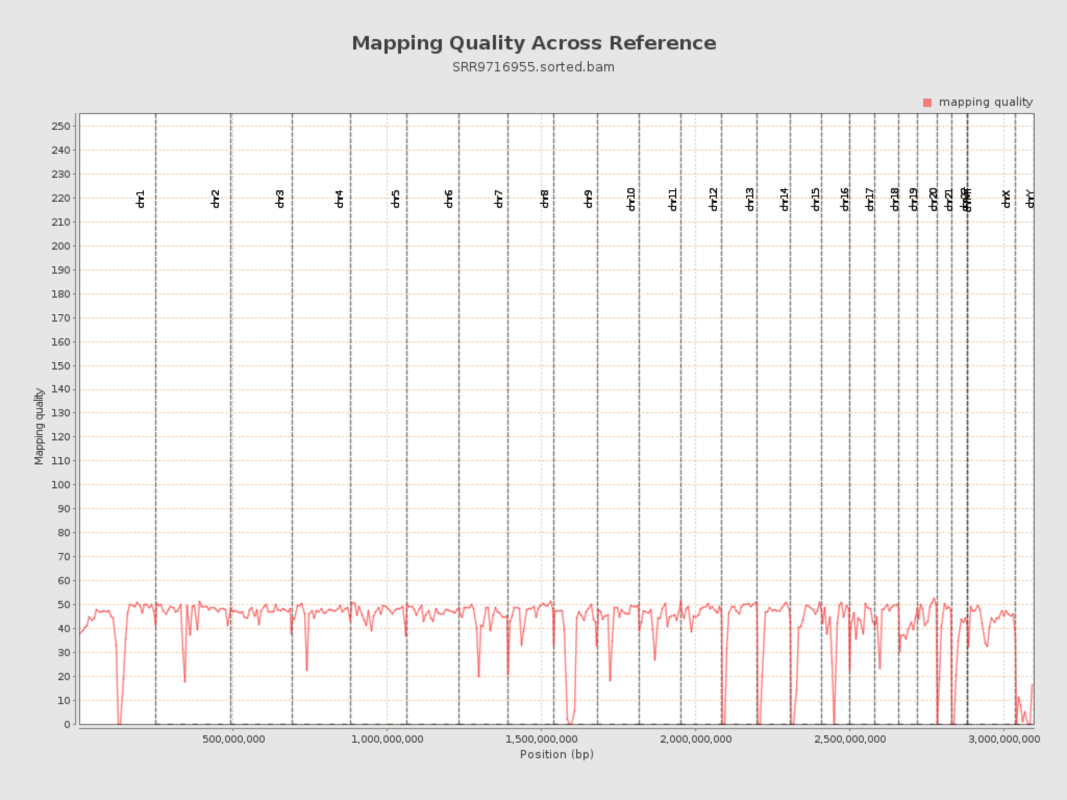
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram