Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 22:47:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716184.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_SRR9716184 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716184.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 22:47:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716184.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,621,360
Mapped reads	2,316,242 / 88.36%
Unmapped reads	305,118 / 11.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,443 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	74,077 / 2.83%
Duplication rate	2.23%
Clipped reads	2,318,262 / 88.44%

2.2. ACGT Content

Number/percentage of A's	33,134,835 / 25.23%
Number/percentage of C's	27,026,636 / 20.58%
Number/percentage of T's	39,795,173 / 30.3%
Number/percentage of G's	31,371,283 / 23.89%
Number/percentage of N's	1,007 / 0%
GC Percentage	44.47%

2.3. Coverage

Mean	0.0424

Standard Deviation	0.3313

2.4. Mapping Quality

Mean Mapping Quality	41.84

2.5. Mismatches and indels

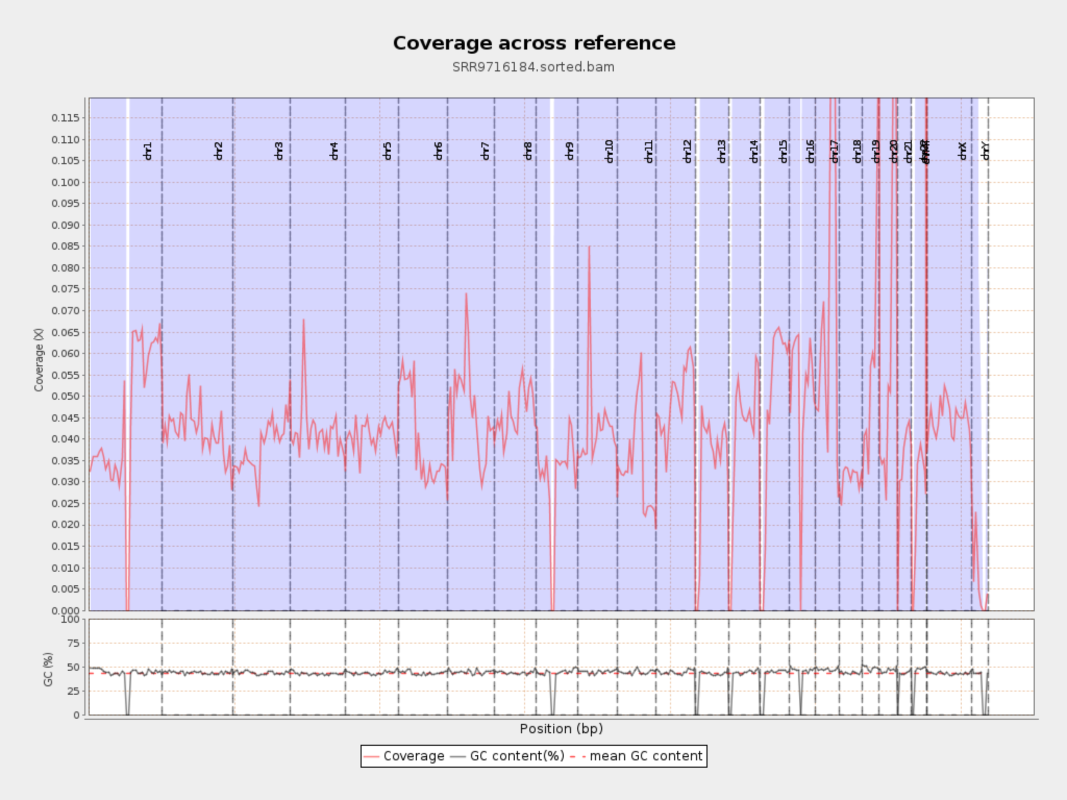
General error rate	0.54%
Mismatches	686,405
Insertions	10,908
Mapped reads with at least one insertion	0.47%
Deletions	24,346
Mapped reads with at least one deletion	1.04%
Homopolymer indels	39.2%

2.6. Chromosome stats

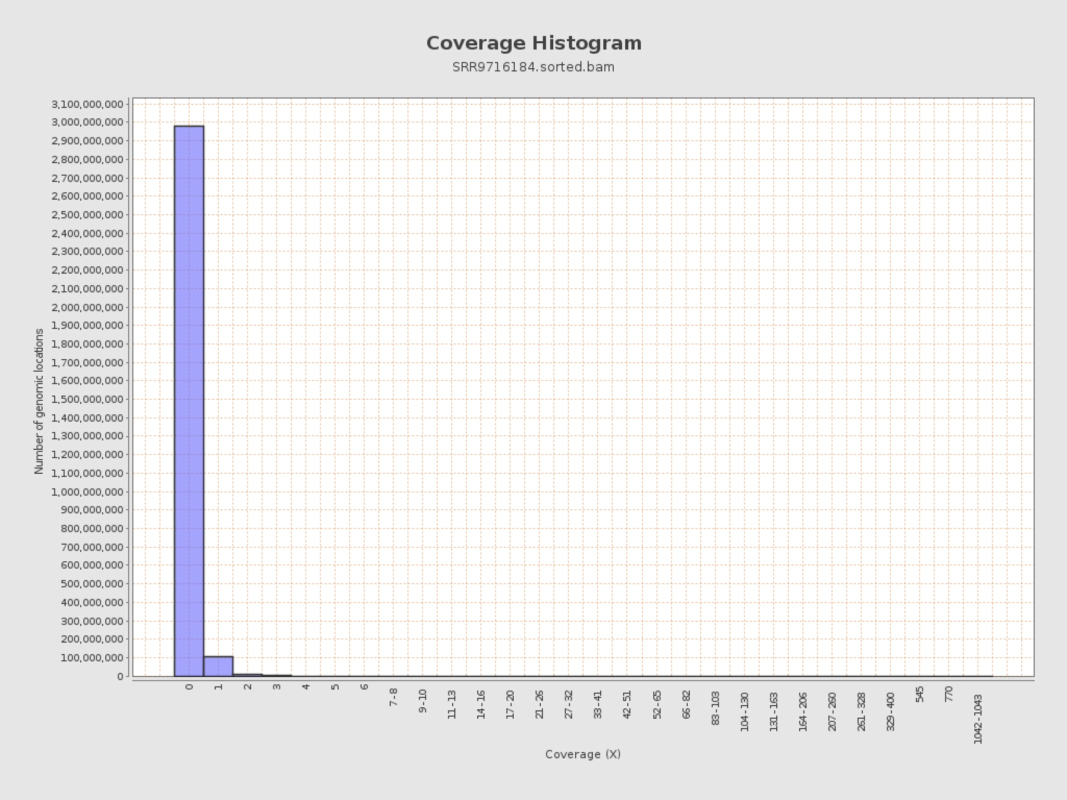
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11049328	0.0443	0.3988
chr2	243199373	10202552	0.042	0.4911
chr3	198022430	7519812	0.038	0.2229
chr4	191154276	7982495	0.0418	0.2625
chr5	180915260	7427746	0.0411	0.2261
chr6	171115067	6901951	0.0403	0.2717
chr7	159138663	7479343	0.047	0.4766

chr8	146364022	6794496	0.0464	0.3034
chr9	141213431	4348145	0.0308	0.2399
chr10	135534747	5788327	0.0427	0.4233
chr11	135006516	4613945	0.0342	0.2702
chr12	133851895	6592366	0.0493	0.2492
chr13	115169878	3881390	0.0337	0.2066
chr14	107349540	4373824	0.0407	0.2403
chr15	102531392	4848975	0.0473	0.2511
chr16	90354753	4662808	0.0516	0.2783
chr17	81195210	5881358	0.0724	0.3257
chr18	78077248	2419391	0.031	0.398
chr19	59128983	3607196	0.061	0.4054
chr20	63025520	4279750	0.0679	0.3117
chr21	48129895	1625777	0.0338	0.2316
chr22	51304566	1253855	0.0244	0.1759
chrMT	16571	451476	27.2449	18.337
chrX	155270560	6976156	0.0449	0.2598
chrY	59373566	405178	0.0068	0.1885

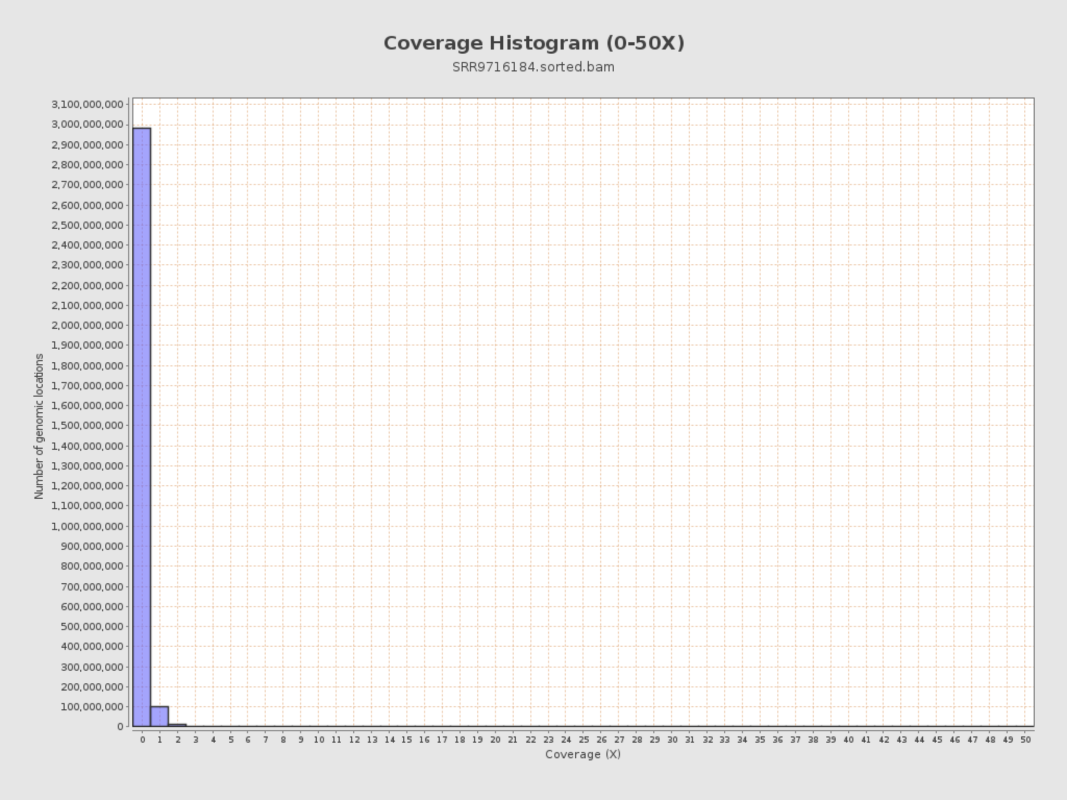
3. Results : Coverage across reference



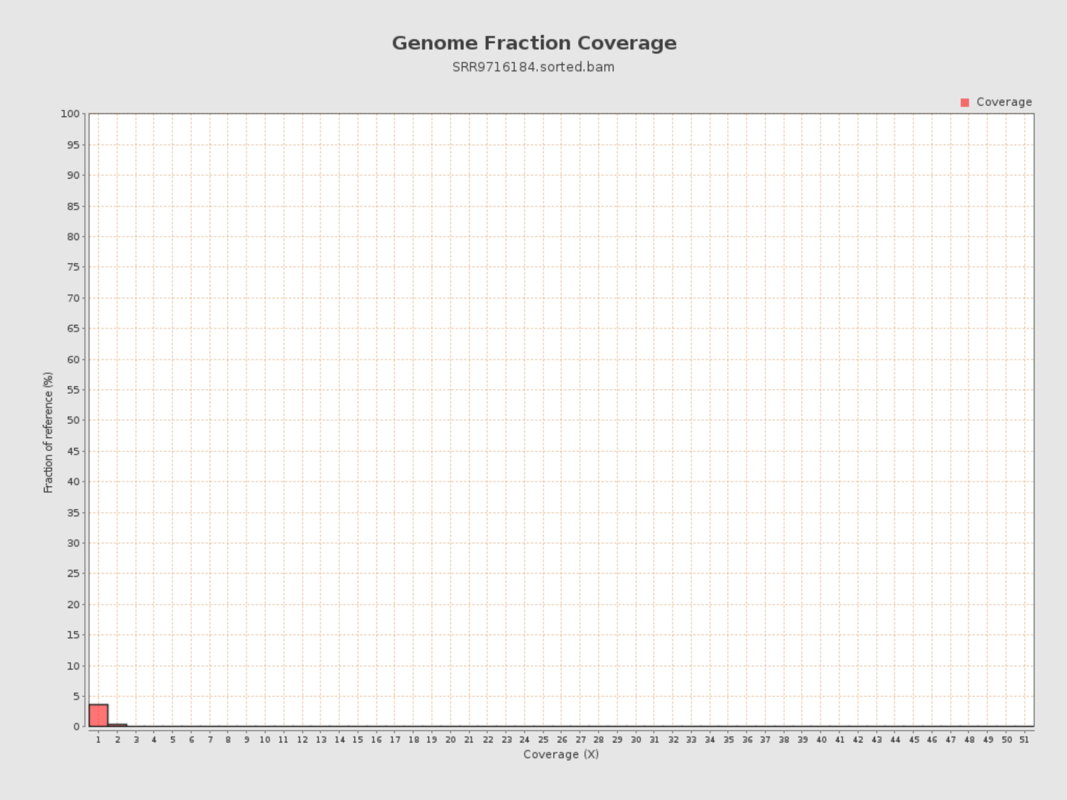
4. Results : Coverage Histogram



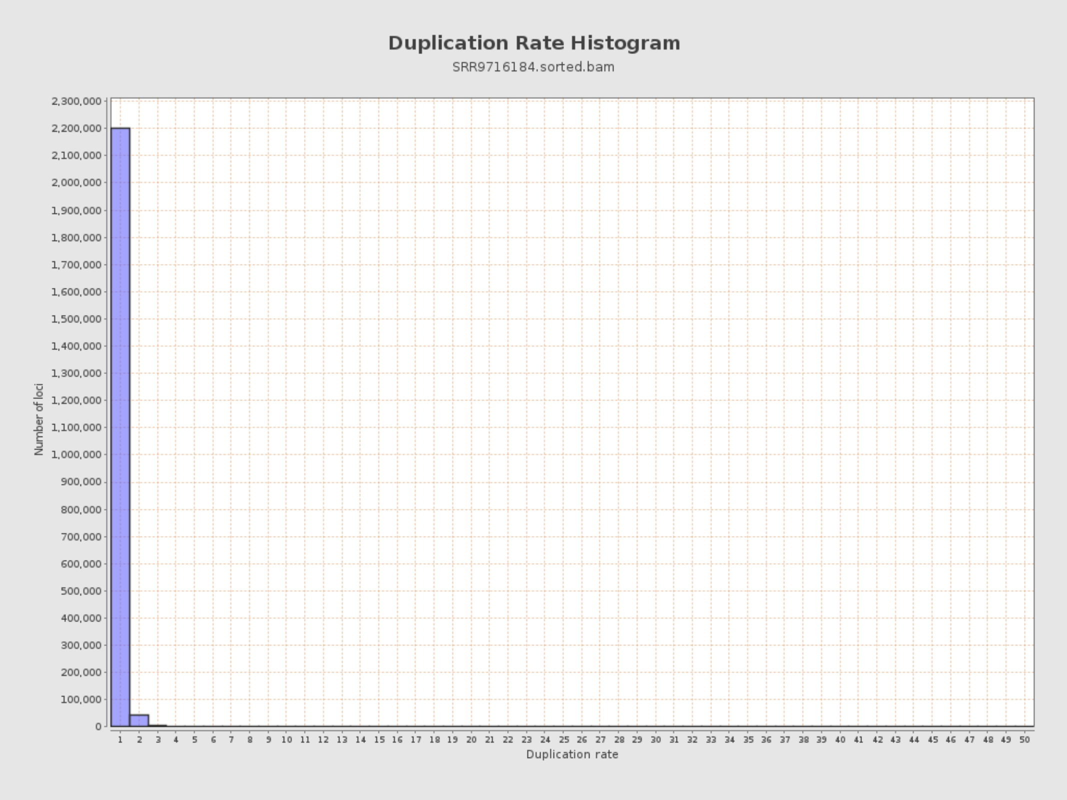
5. Results : Coverage Histogram (0-50X)



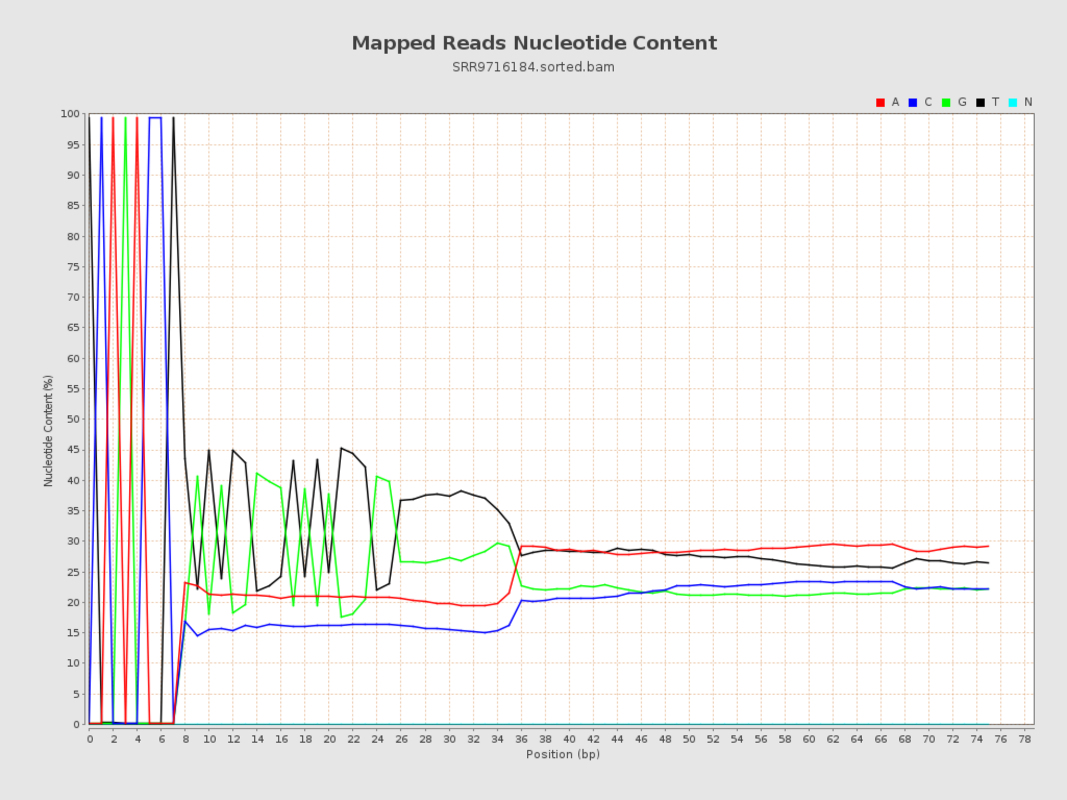
6. Results : Genome Fraction Coverage



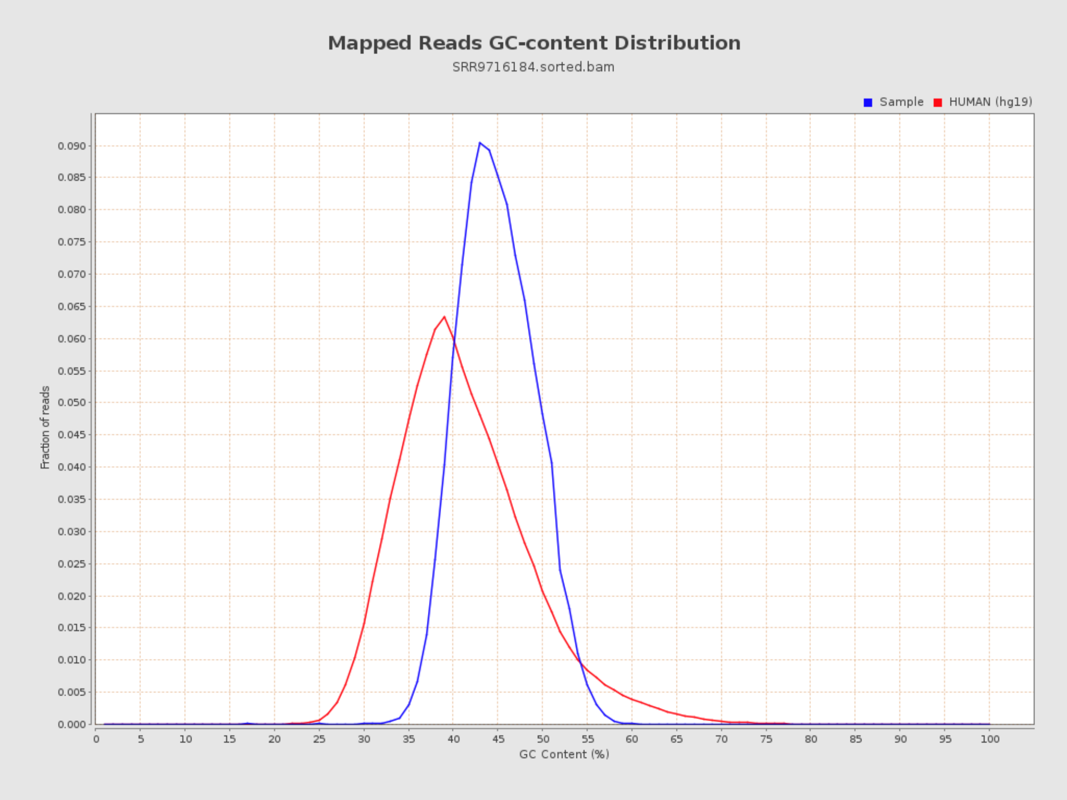
7. Results : Duplication Rate Histogram



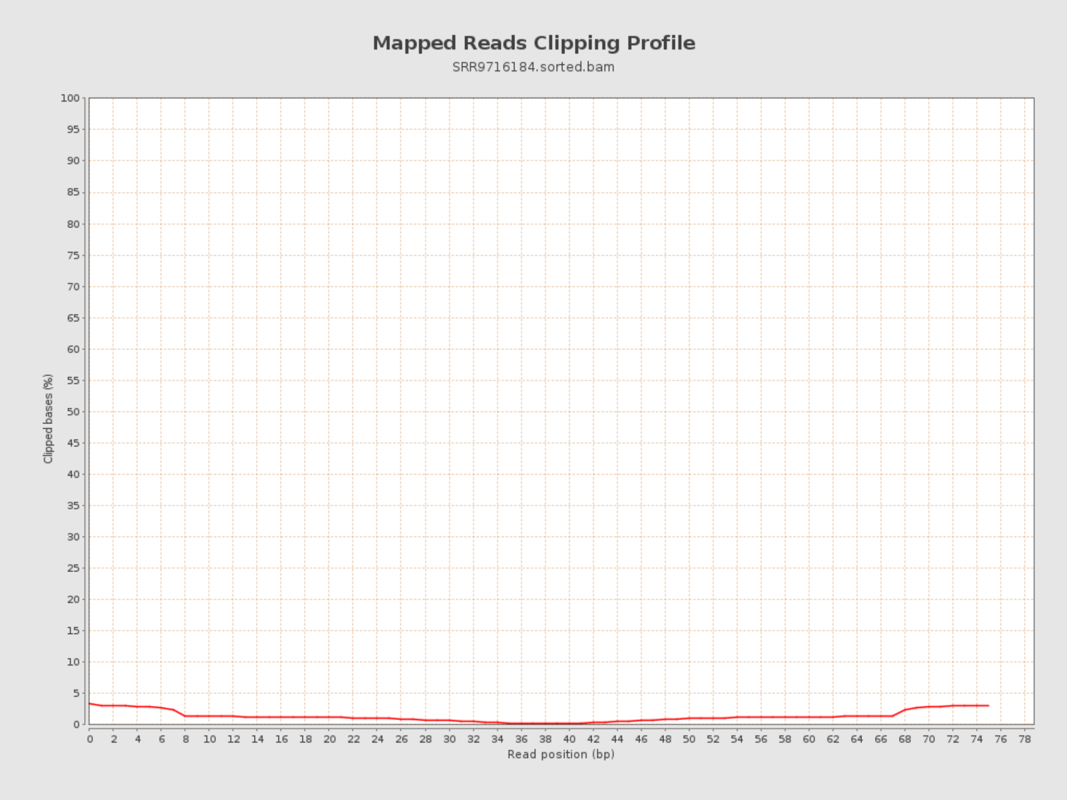
8. Results : Mapped Reads Nucleotide Content



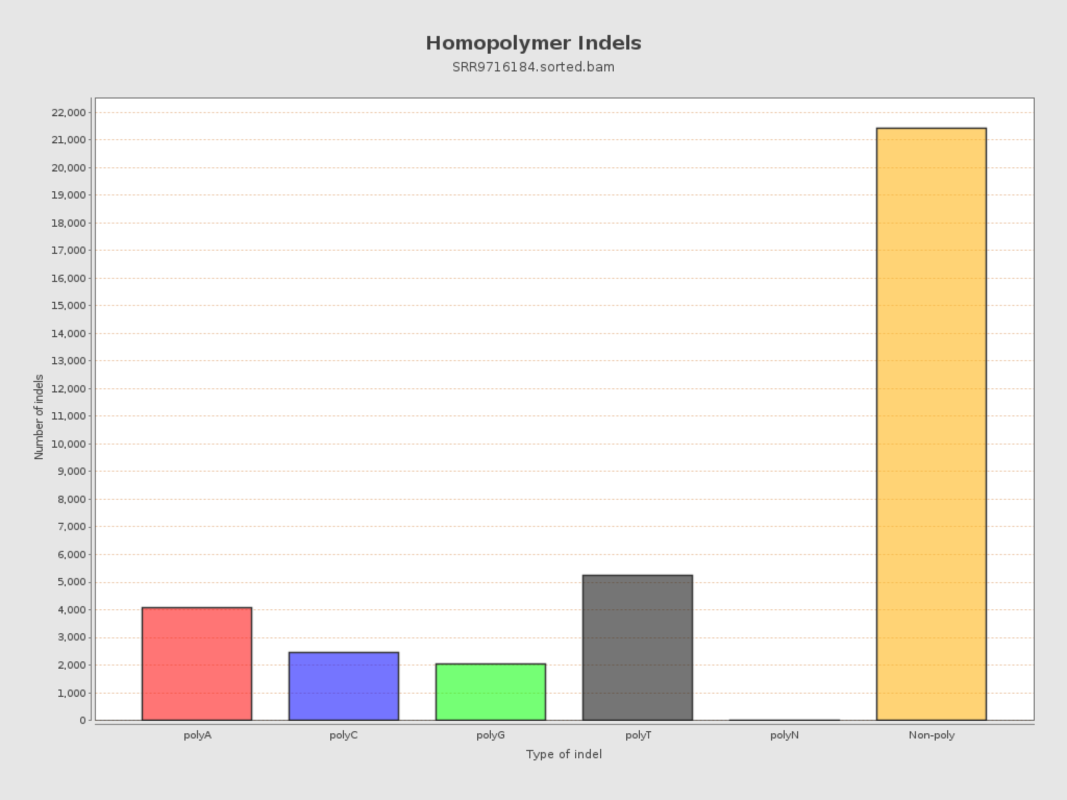
9. Results : Mapped Reads GC-content Distribution



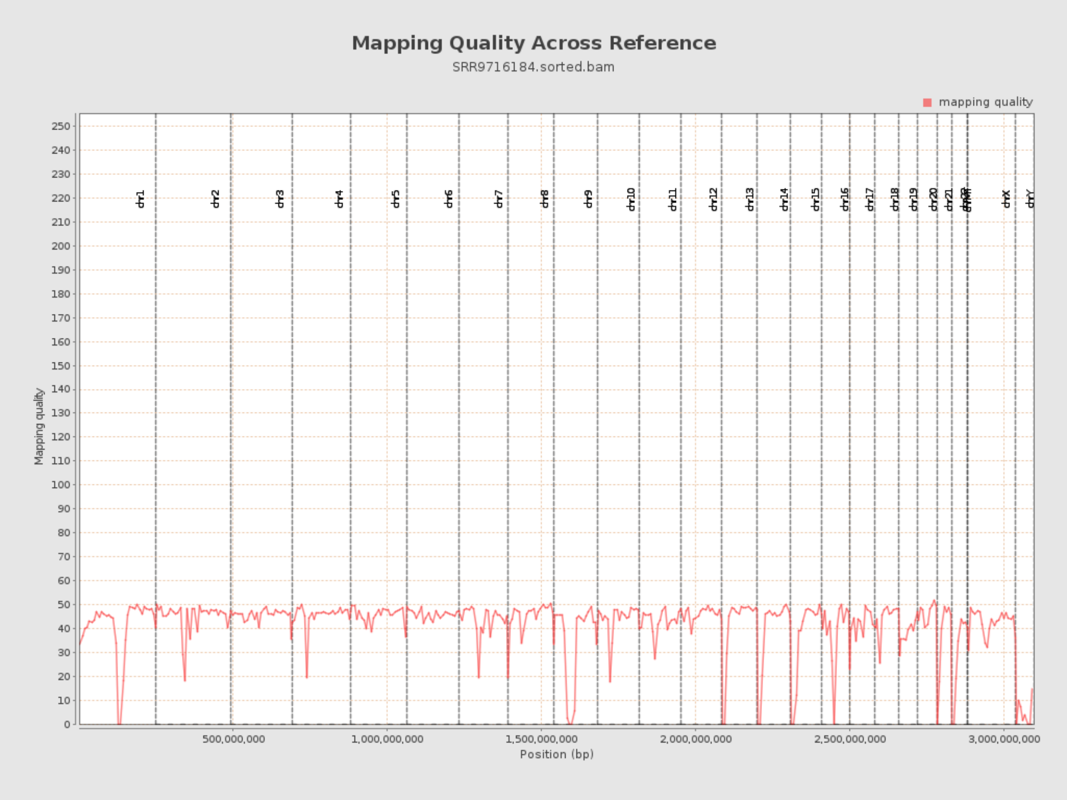
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram