Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 19:04:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716532.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_SRR9716532 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716532.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 19:04:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716532.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,688,861
Mapped reads	1,595,852 / 94.49%
Unmapped reads	93,009 / 5.51%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	33,403 / 1.98%
Read min/max/mean length	30 / 101 / 101.71
Duplicated reads (estimated)	59,272 / 3.51%
Duplication rate	2.62%
Clipped reads	1,628,558 / 96.43%

2.2. ACGT Content

Number/percentage of A's	31,808,541 / 25.71%
Number/percentage of C's	24,651,035 / 19.93%
Number/percentage of T's	37,514,809 / 30.32%
Number/percentage of G's	29,728,326 / 24.03%
Number/percentage of N's	8,200 / 0.01%
GC Percentage	43.96%

2.3. Coverage

Mean	0.04

Standard Deviation	0.3954

2.4. Mapping Quality

Mean Mapping Quality	46.98

2.5. Mismatches and indels

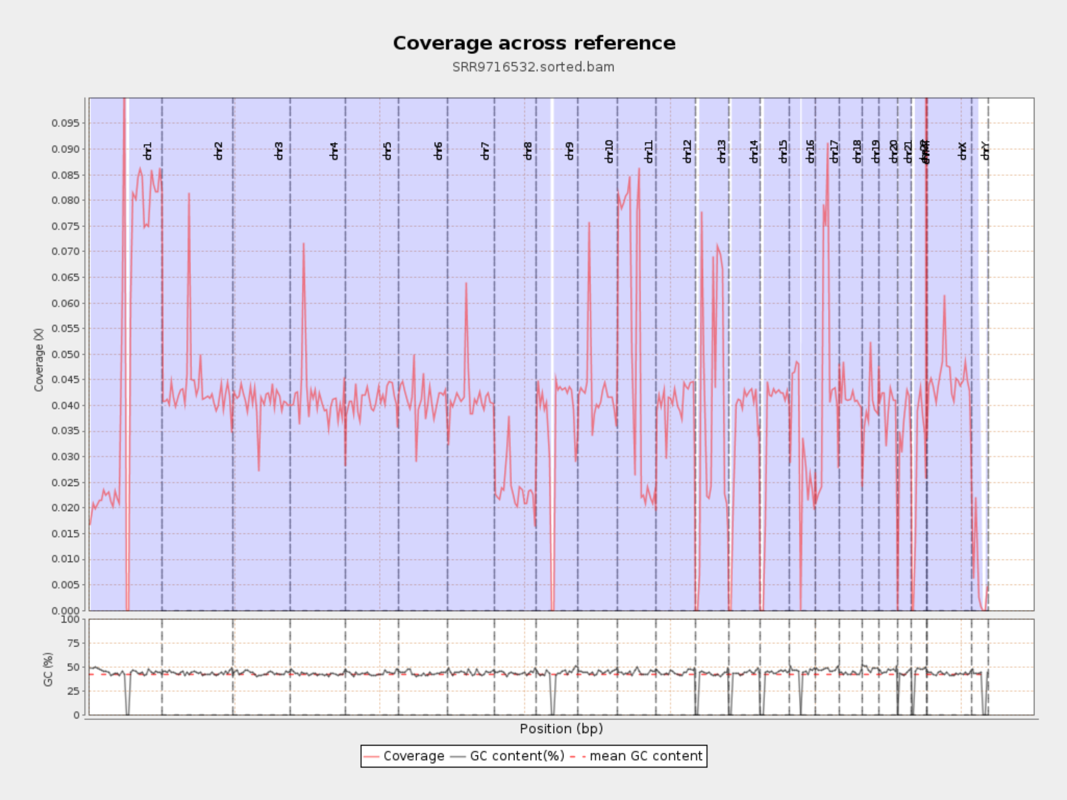
General error rate	0.63%
Mismatches	761,446
Insertions	8,823
Mapped reads with at least one insertion	0.55%
Deletions	28,148
Mapped reads with at least one deletion	1.74%
Homopolymer indels	43.29%

2.6. Chromosome stats

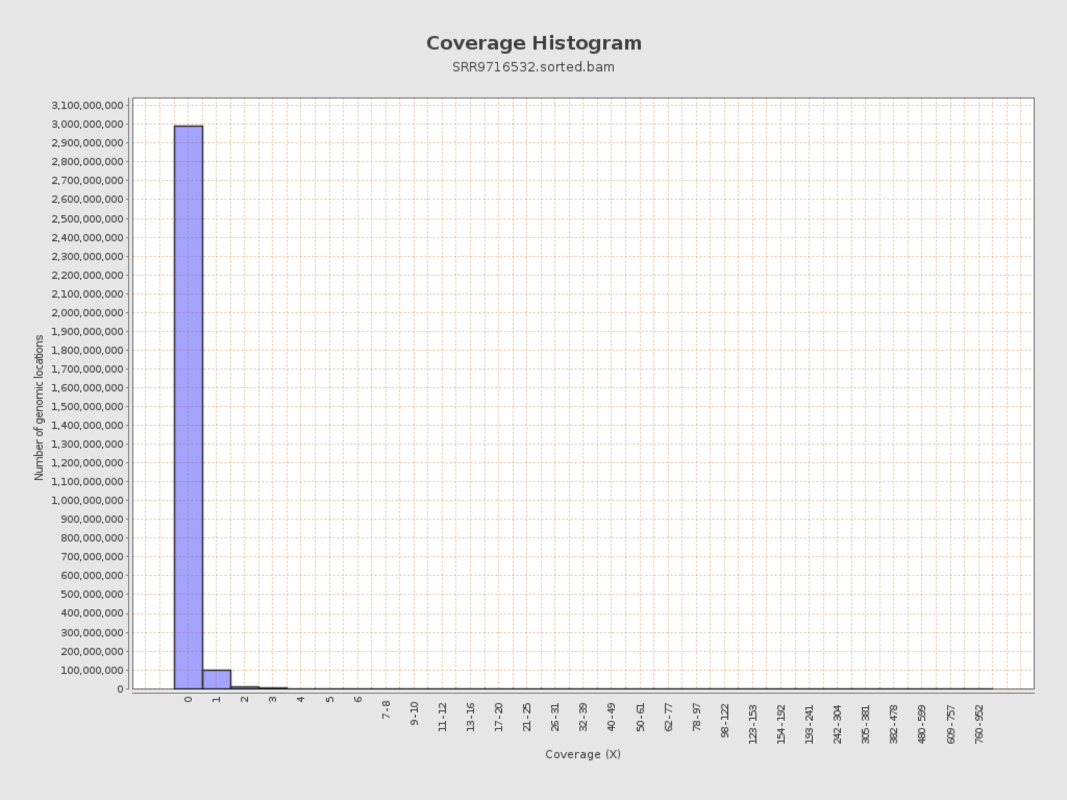
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12450413	0.05	0.8569
chr2	243199373	10547508	0.0434	0.4213
chr3	198022430	8089891	0.0409	0.2243
chr4	191154276	7996836	0.0418	0.2645
chr5	180915260	7429208	0.0411	0.2268
chr6	171115067	7056078	0.0412	0.2451
chr7	159138663	6677445	0.042	0.4639

chr8	146364022	3445810	0.0235	0.3993
chr9	141213431	5117165	0.0362	0.3096
chr10	135534747	5831457	0.043	0.3821
chr11	135006516	6971392	0.0516	0.4254
chr12	133851895	5456551	0.0408	0.2256
chr13	115169878	4406931	0.0383	0.2195
chr14	107349540	3672926	0.0342	0.2229
chr15	102531392	3537830	0.0345	0.2071
chr16	90354753	2800197	0.031	0.2138
chr17	81195210	3825244	0.0471	0.3103
chr18	78077248	3280594	0.042	0.5273
chr19	59128983	2356477	0.0399	0.6115
chr20	63025520	2488010	0.0395	0.2274
chr21	48129895	1607692	0.0334	0.2305
chr22	51304566	1354466	0.0264	0.1795
chrMT	16571	23859	1.4398	1.4114
chrX	155270560	6990969	0.045	0.2798
chrY	59373566	349302	0.0059	0.179

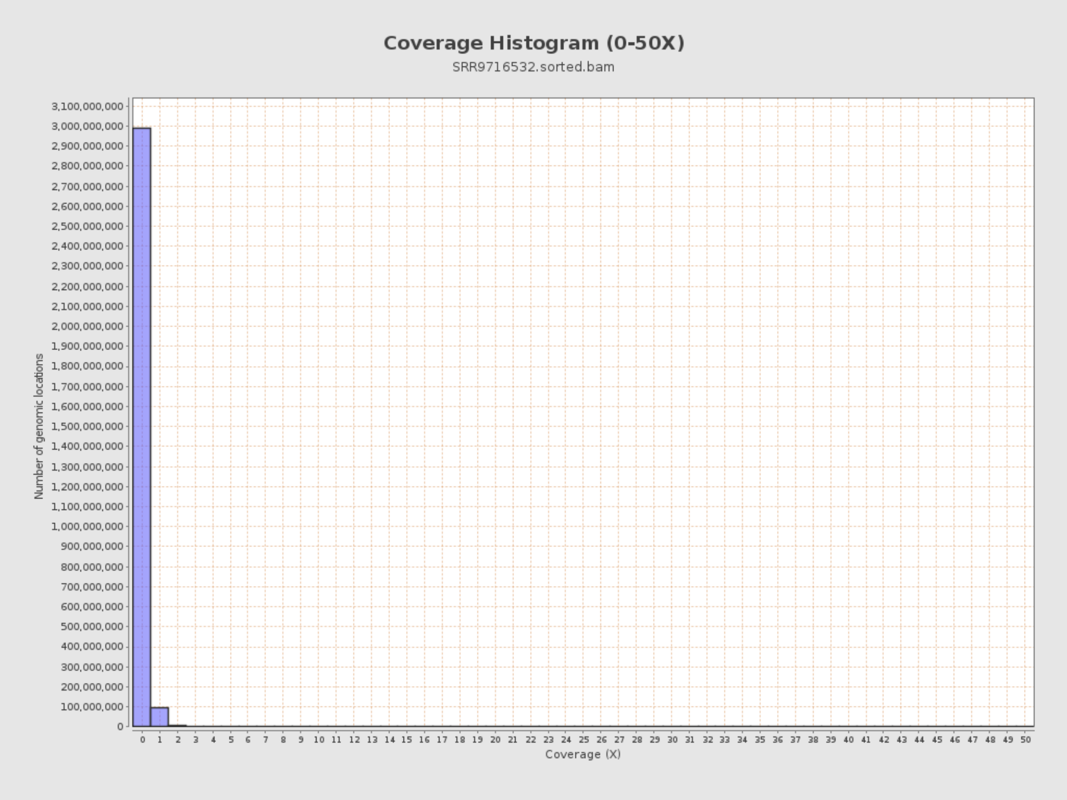
3. Results : Coverage across reference



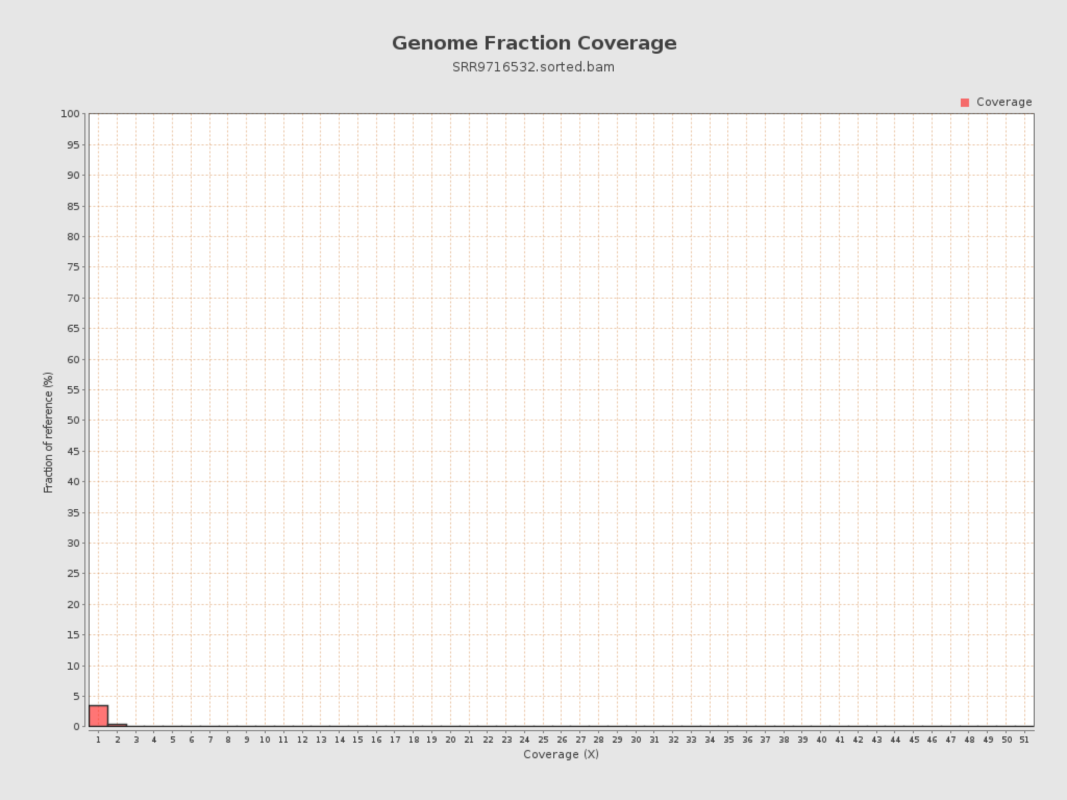
4. Results : Coverage Histogram



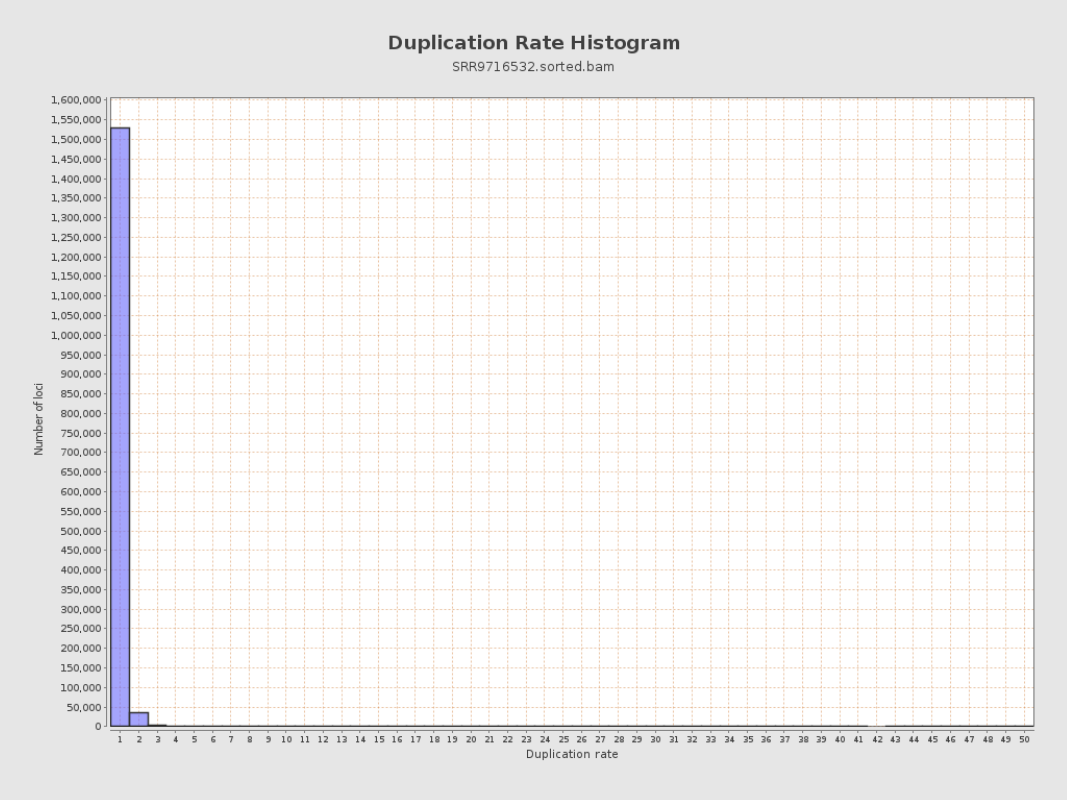
5. Results : Coverage Histogram (0-50X)



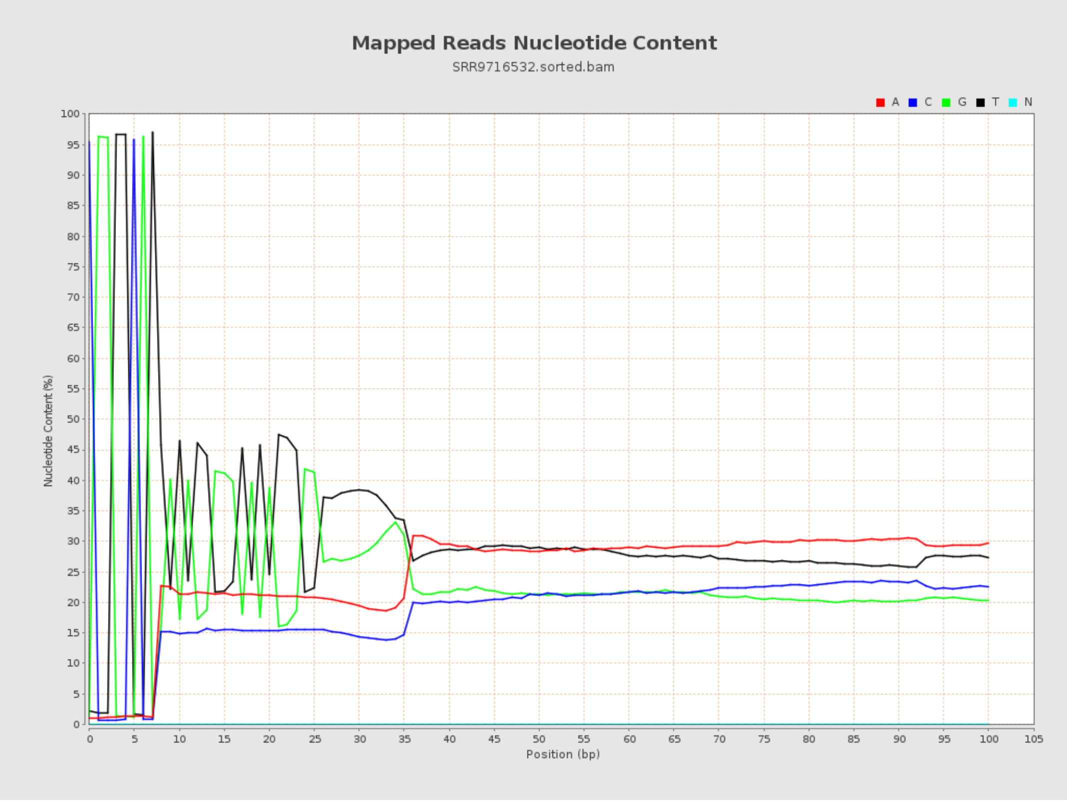
6. Results : Genome Fraction Coverage



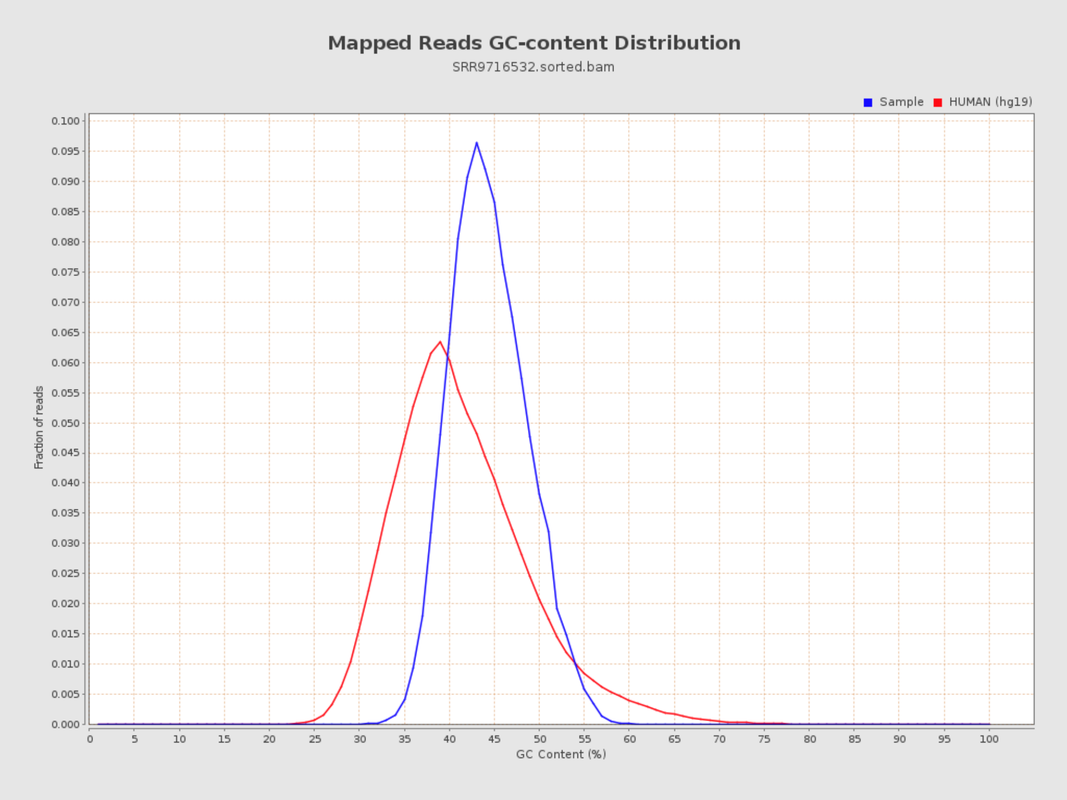
7. Results : Duplication Rate Histogram



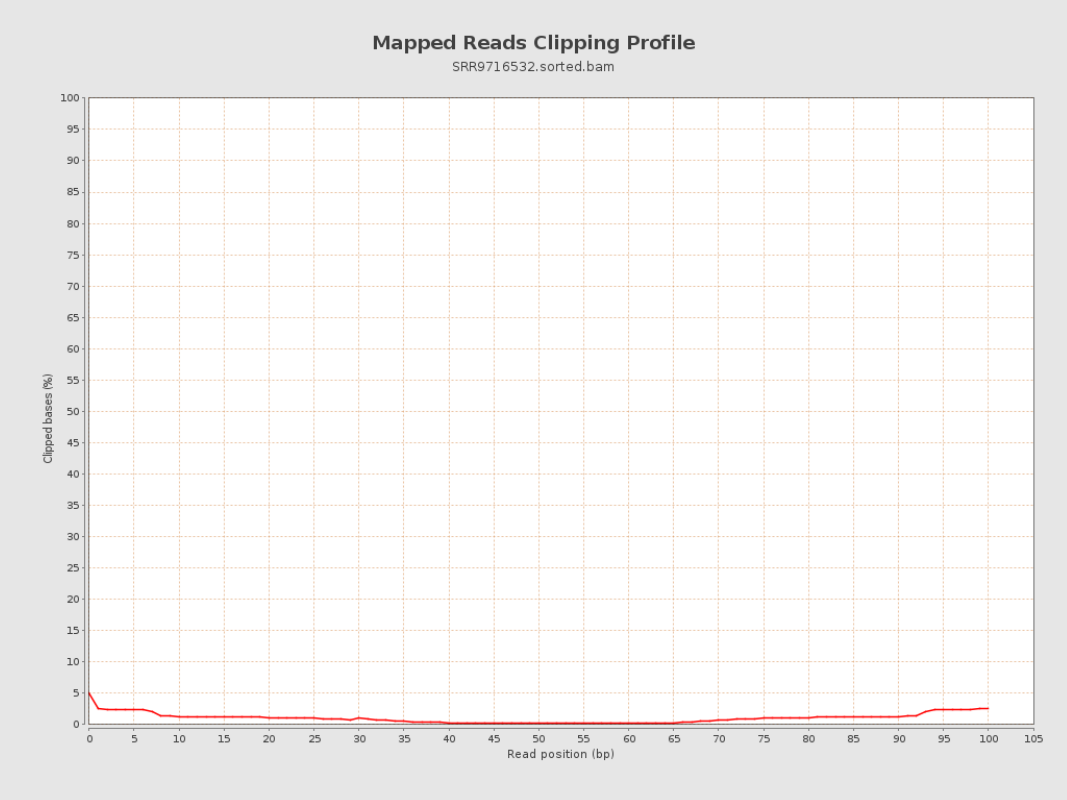
8. Results : Mapped Reads Nucleotide Content



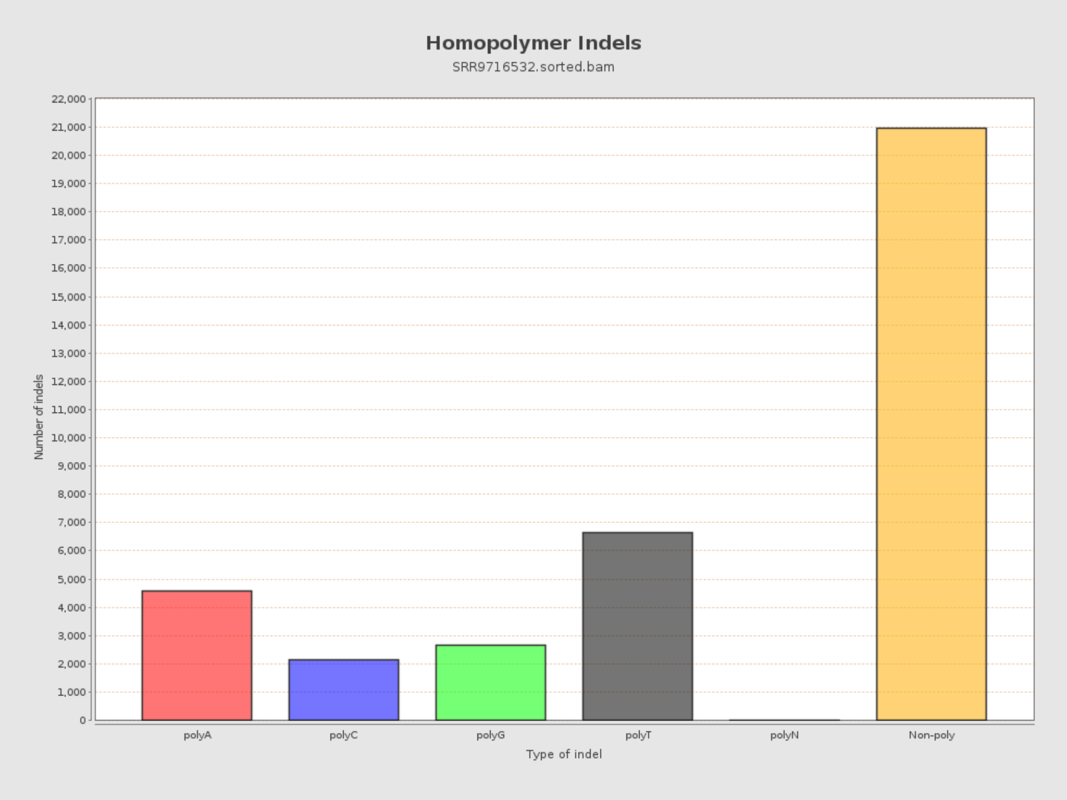
9. Results : Mapped Reads GC-content Distribution



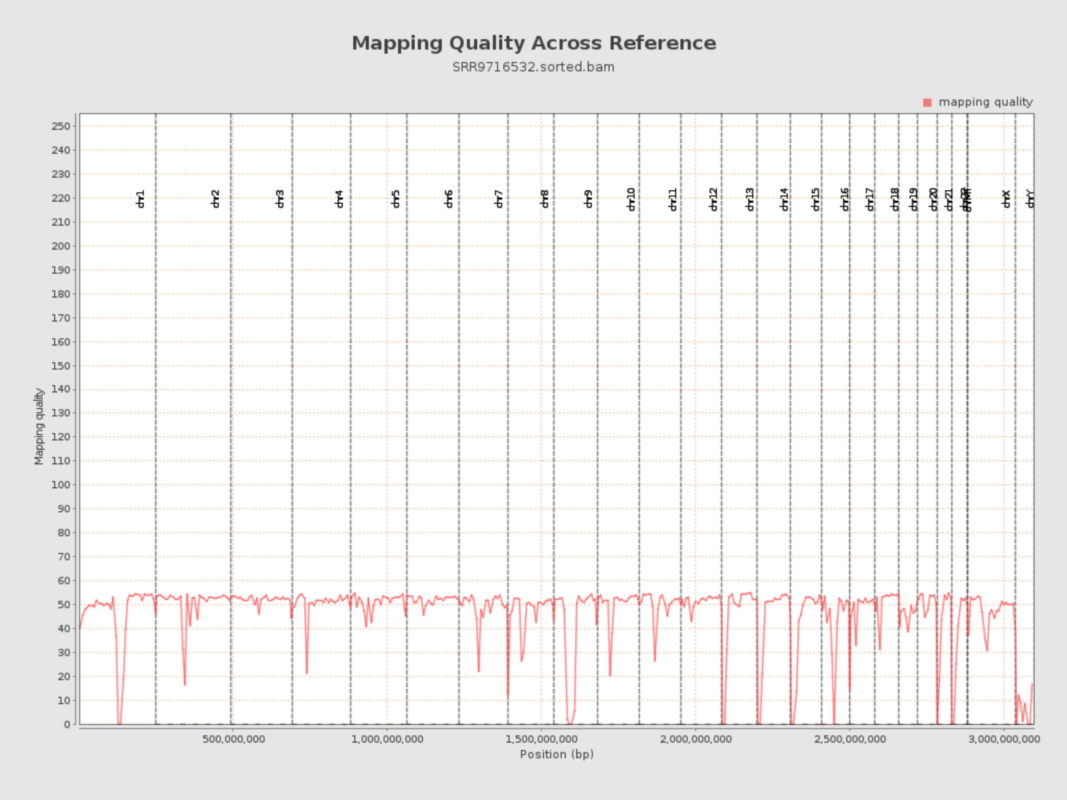
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram