Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 15:54:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716475.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_SRR9716475 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716475.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 15:54:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716475.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,889,908
Mapped reads	3,439,245 / 88.41%
Unmapped reads	450,663 / 11.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,549 / 0.55%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	254,341 / 6.54%
Duplication rate	5.59%
Clipped reads	3,454,294 / 88.8%

2.2. ACGT Content

Number/percentage of A's	51,431,294 / 25.96%
Number/percentage of C's	38,310,539 / 19.33%
Number/percentage of T's	62,124,796 / 31.35%
Number/percentage of G's	46,273,963 / 23.35%
Number/percentage of N's	1,348 / 0%
GC Percentage	42.69%

2.3. Coverage

Mean	0.064

Standard Deviation	0.6239

2.4. Mapping Quality

Mean Mapping Quality	44.34

2.5. Mismatches and indels

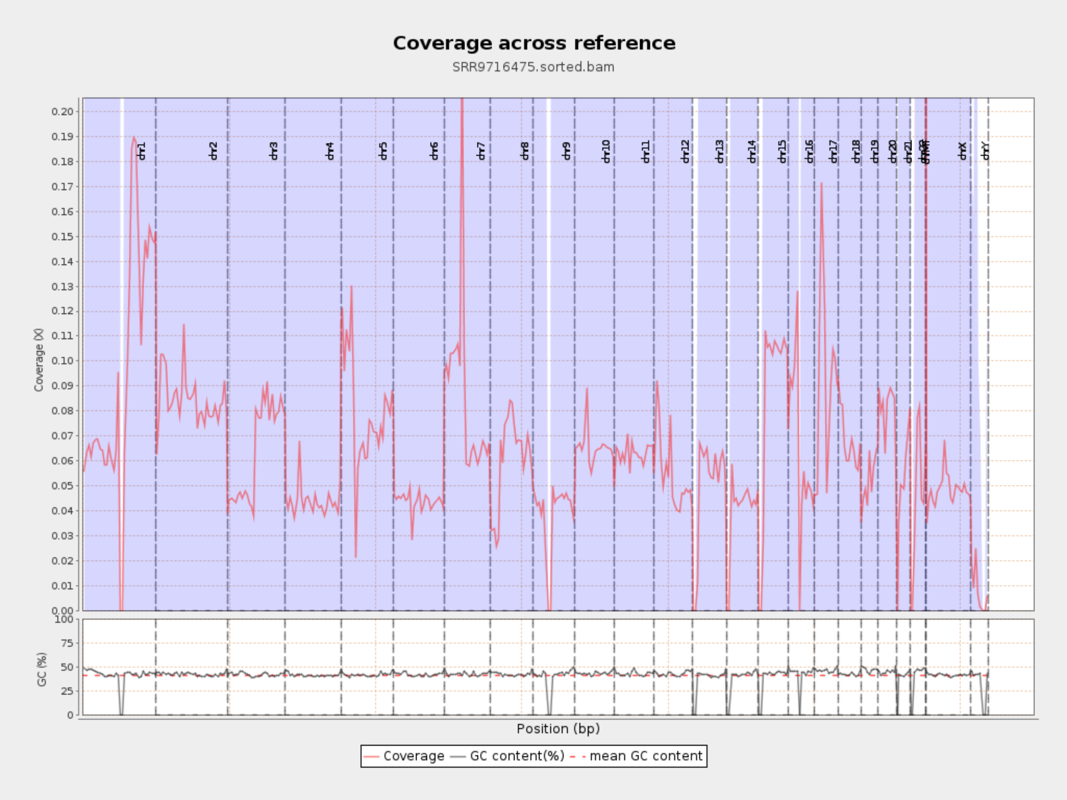
General error rate	0.52%
Mismatches	996,051
Insertions	14,172
Mapped reads with at least one insertion	0.41%
Deletions	35,432
Mapped reads with at least one deletion	1.02%
Homopolymer indels	40.31%

2.6. Chromosome stats

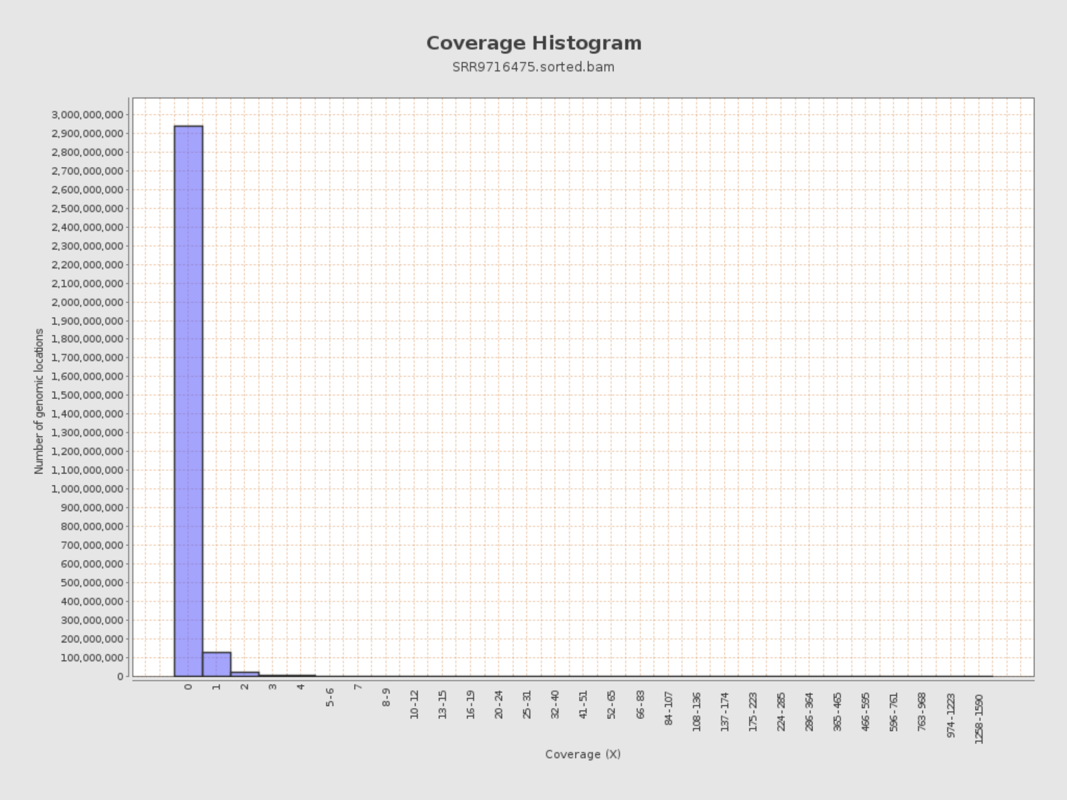
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23628022	0.0948	0.8135
chr2	243199373	20563835	0.0846	0.729
chr3	198022430	12586812	0.0636	0.309
chr4	191154276	8414865	0.044	0.313
chr5	180915260	14364024	0.0794	0.3497
chr6	171115067	7463179	0.0436	0.3007
chr7	159138663	13890040	0.0873	1.8641

chr8	146364022	8907226	0.0609	0.441
chr9	141213431	5417102	0.0384	0.364
chr10	135534747	8873205	0.0655	0.4202
chr11	135006516	8485155	0.0628	0.477
chr12	133851895	7387988	0.0552	0.2929
chr13	115169878	5725985	0.0497	0.2752
chr14	107349540	4273998	0.0398	0.2673
chr15	102531392	8751666	0.0854	0.3666
chr16	90354753	5738329	0.0635	0.337
chr17	81195210	7447547	0.0917	0.4245
chr18	78077248	5289562	0.0677	0.8354
chr19	59128983	3103060	0.0525	0.6398
chr20	63025520	5148478	0.0817	0.3606
chr21	48129895	2489920	0.0517	0.3016
chr22	51304566	2240603	0.0437	0.2552
chrMT	16571	5126	0.3093	0.5995
chrX	155270560	7534998	0.0485	0.3277
chrY	59373566	466880	0.0079	0.1753

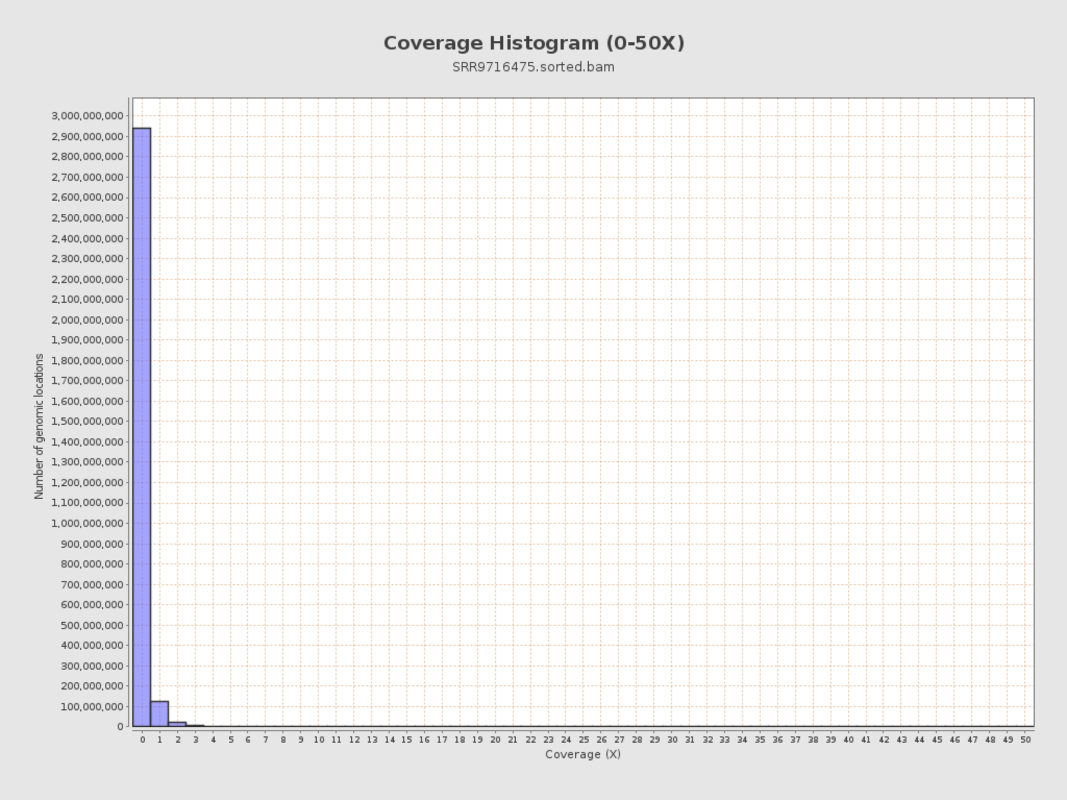
3. Results : Coverage across reference



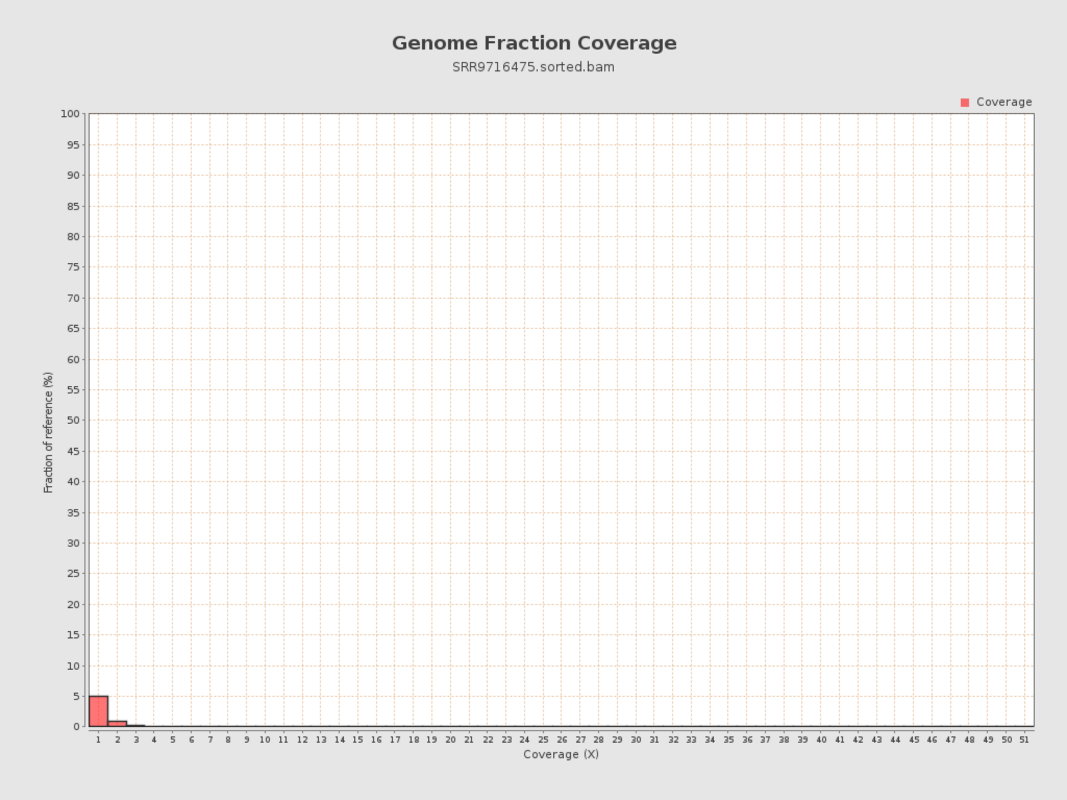
4. Results : Coverage Histogram



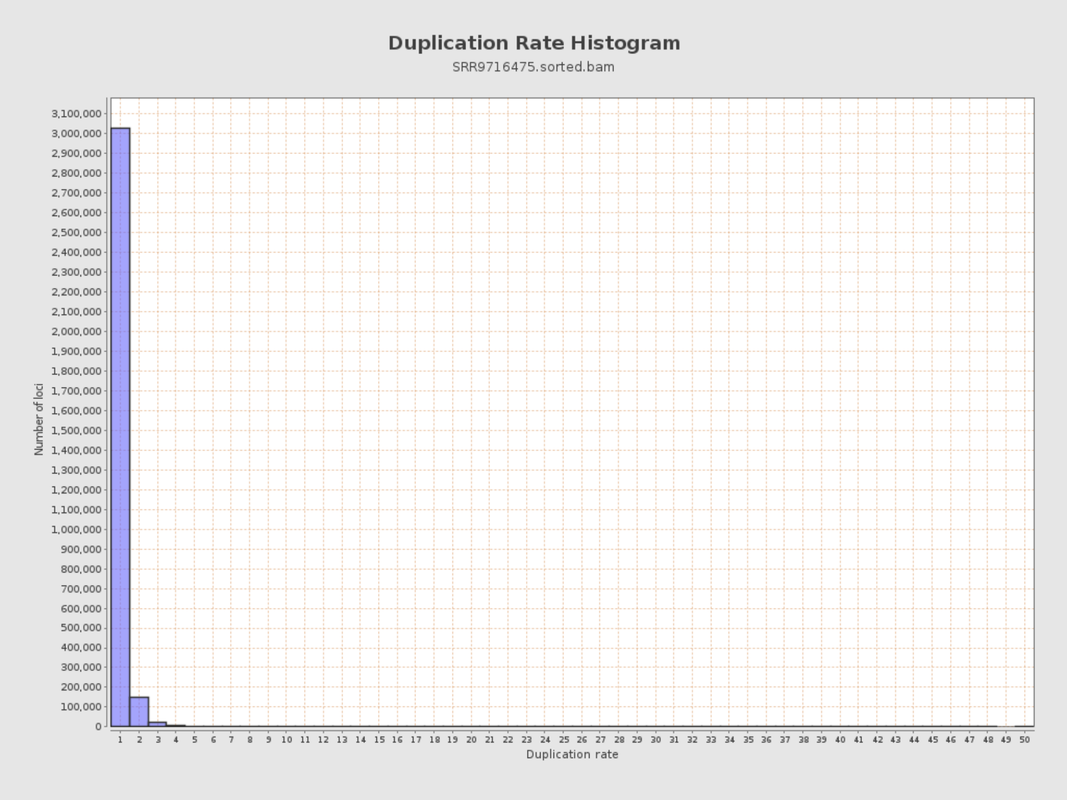
5. Results : Coverage Histogram (0-50X)



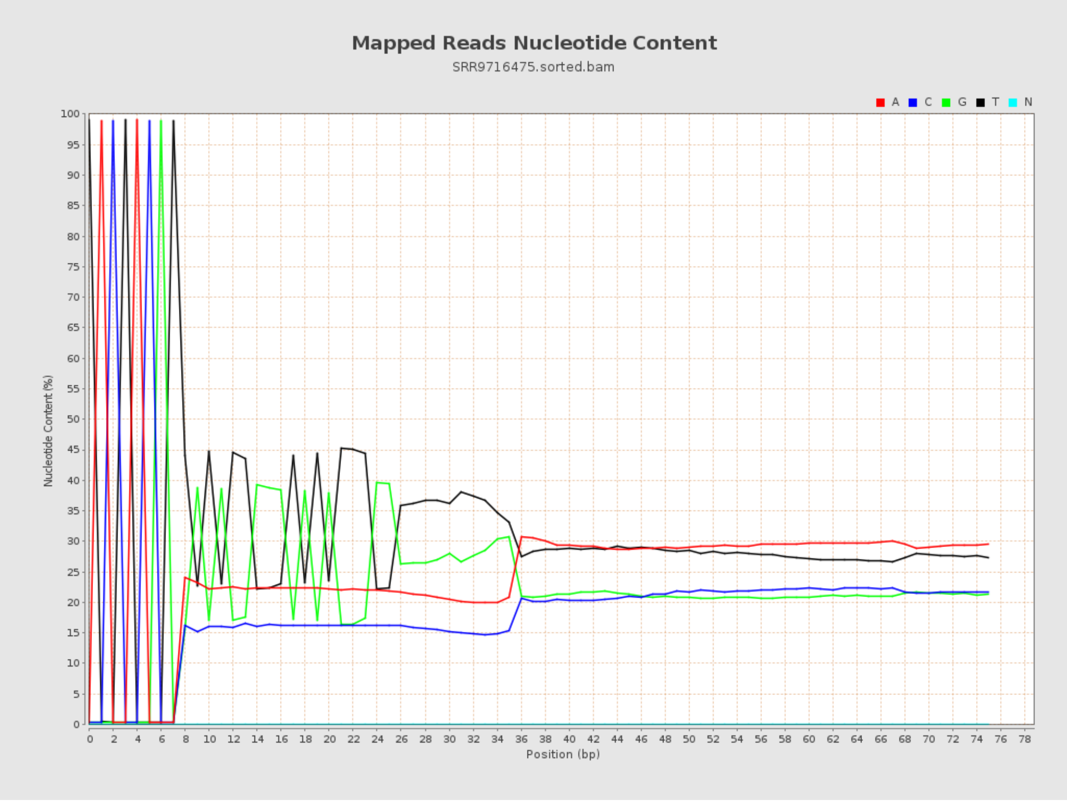
6. Results : Genome Fraction Coverage



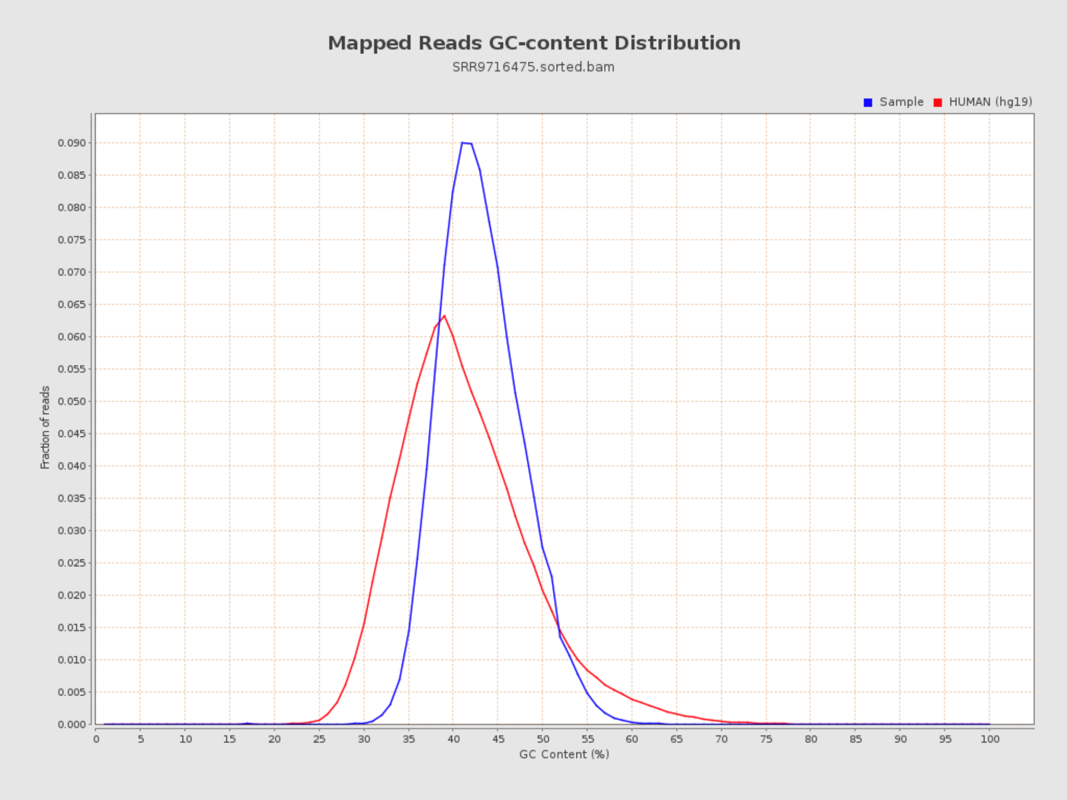
7. Results : Duplication Rate Histogram



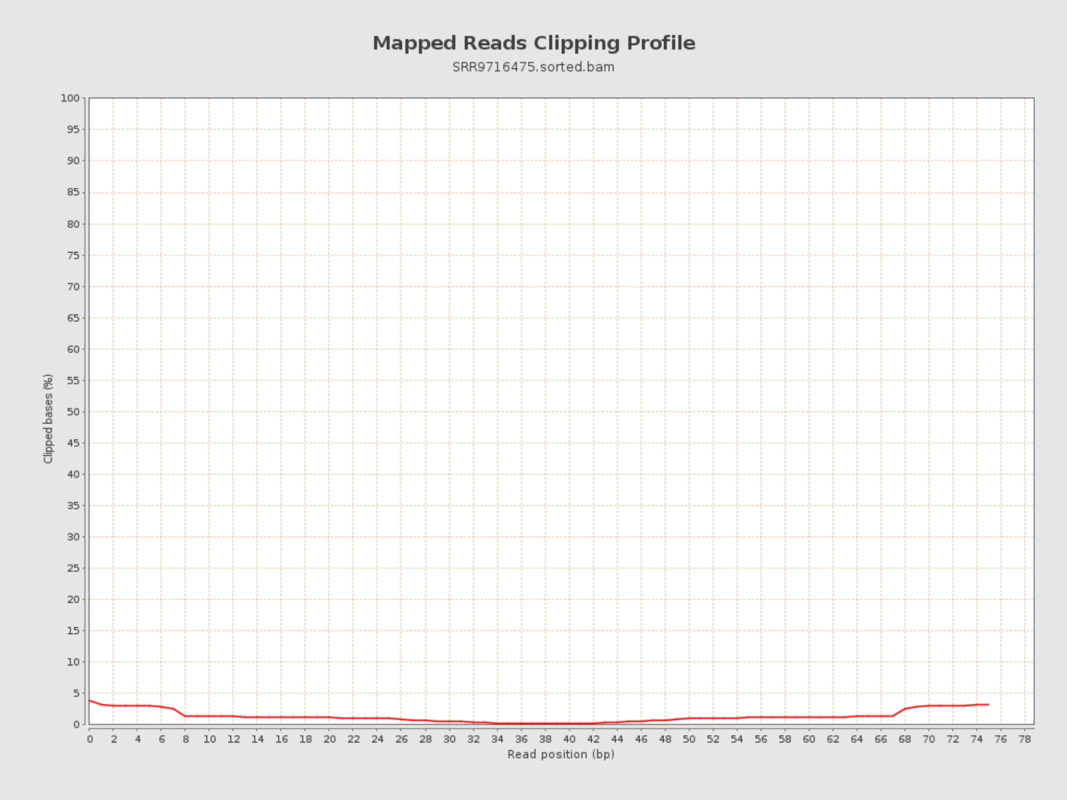
8. Results : Mapped Reads Nucleotide Content



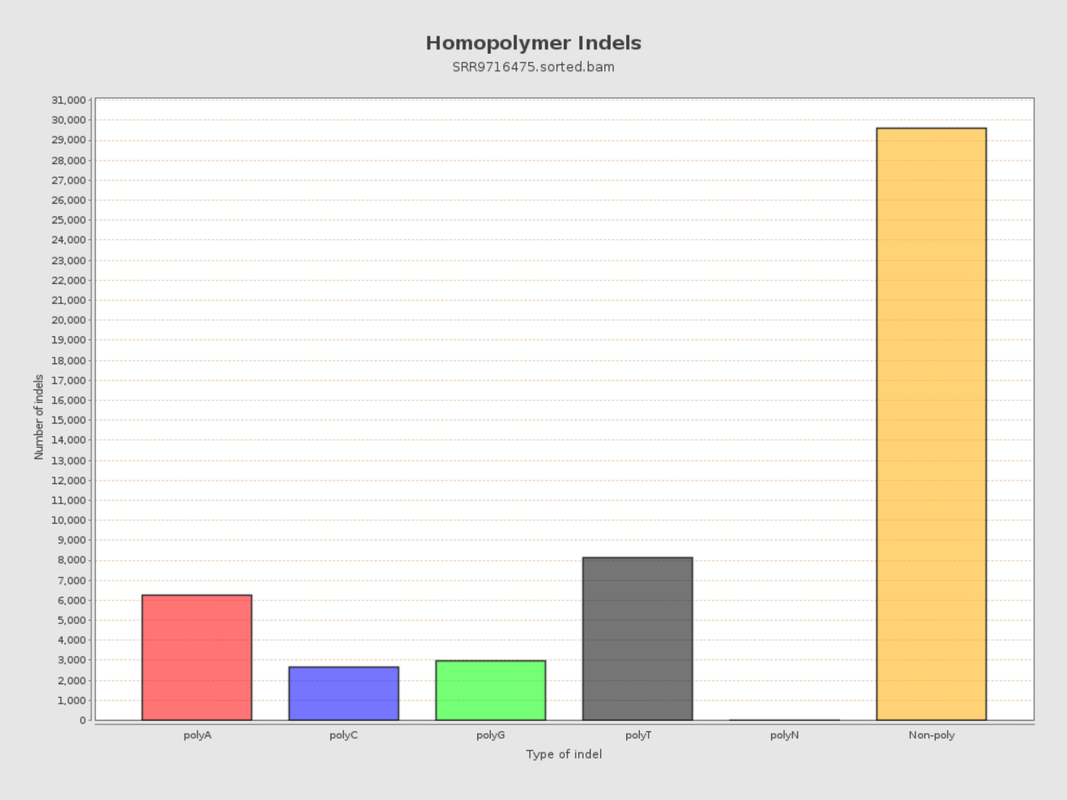
9. Results : Mapped Reads GC-content Distribution



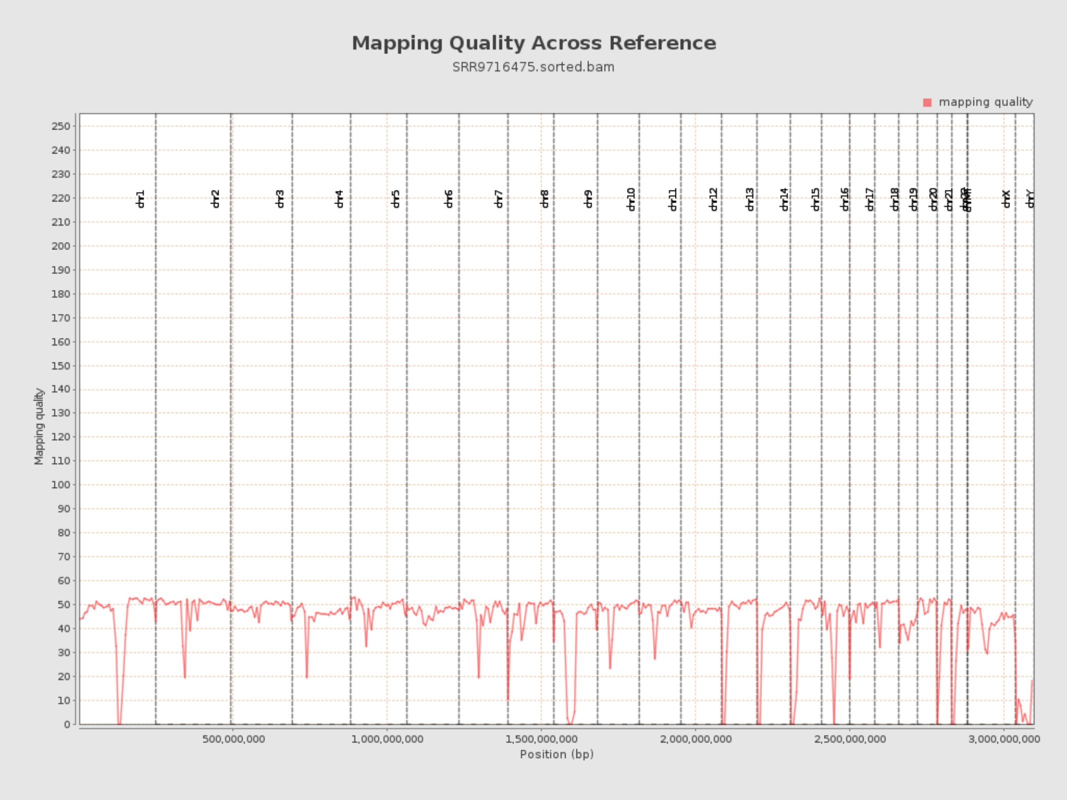
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram