Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 20:34:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716557.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_SRR9716557 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716557.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 20:34:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716557.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,419,281
Mapped reads	16,012,643 / 97.52%
Unmapped reads	406,638 / 2.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,654 / 0.05%
Read min/max/mean length	30 / 76 / 76.02
Duplicated reads (estimated)	779,336 / 4.75%
Duplication rate	1.61%
Clipped reads	15,920,100 / 96.96%

2.2. ACGT Content

Number/percentage of A's	306,247,107 / 28.09%
Number/percentage of C's	236,497,832 / 21.7%
Number/percentage of T's	323,246,440 / 29.65%
Number/percentage of G's	224,003,559 / 20.55%
Number/percentage of N's	54,556 / 0.01%
GC Percentage	42.25%

2.3. Coverage

Mean	0.3522

Standard Deviation	3.575

2.4. Mapping Quality

Mean Mapping Quality	48.96

2.5. Mismatches and indels

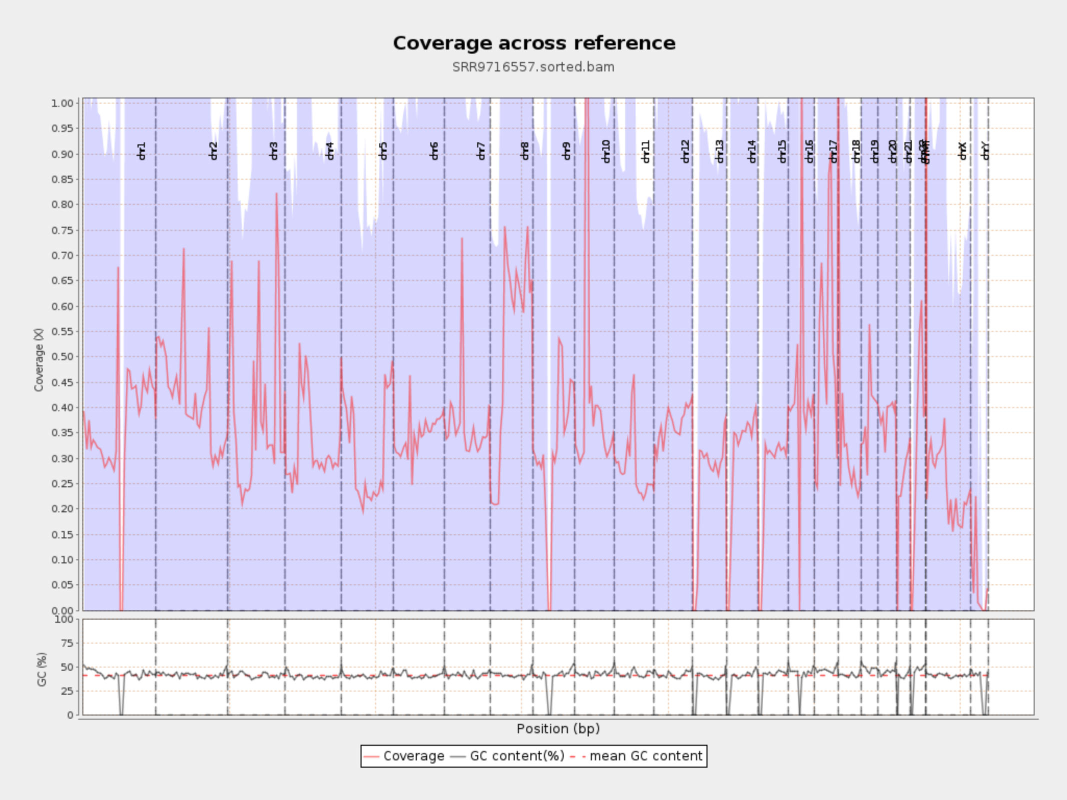
General error rate	0.32%
Mismatches	3,257,860
Insertions	87,662
Mapped reads with at least one insertion	0.54%
Deletions	90,476
Mapped reads with at least one deletion	0.56%
Homopolymer indels	37.41%

2.6. Chromosome stats

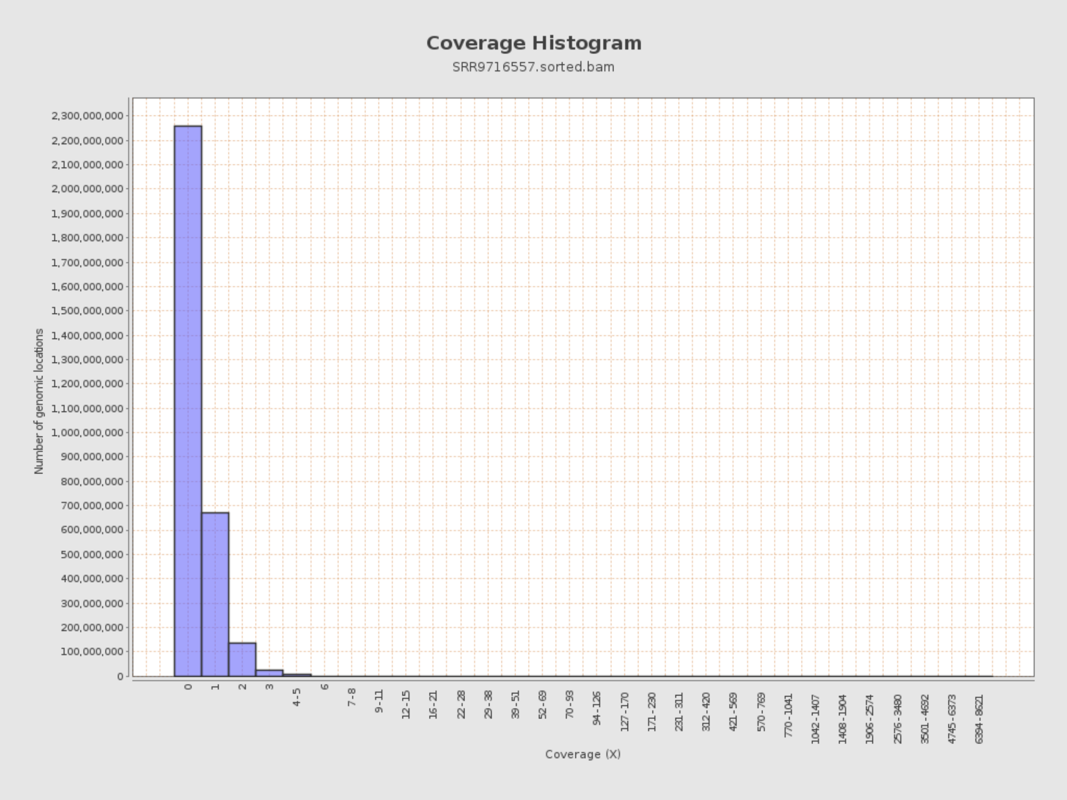
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	89545658	0.3593	7.4551
chr2	243199373	102625798	0.422	2.4237
chr3	198022430	75873117	0.3832	1.3658
chr4	191154276	62301399	0.3259	1.7342
chr5	180915260	57387328	0.3172	0.6871
chr6	171115067	59137026	0.3456	1.3306
chr7	159138663	58666670	0.3687	5.1567

chr8	146364022	77974142	0.5327	2.0962
chr9	141213431	44588071	0.3157	1.4621
chr10	135534747	57647346	0.4253	8.8183
chr11	135006516	38464774	0.2849	1.3002
chr12	133851895	49118653	0.367	1.3397
chr13	115169878	29052258	0.2523	0.5395
chr14	107349540	32266584	0.3006	0.7626
chr15	102531392	26419442	0.2577	0.548
chr16	90354753	39043345	0.4321	4.3206
chr17	81195210	42754789	0.5266	1.2076
chr18	78077248	25397869	0.3253	2.9889
chr19	59128983	23280341	0.3937	6.2467
chr20	63025520	24282898	0.3853	1.2544
chr21	48129895	11983313	0.249	1.6626
chr22	51304566	16945684	0.3303	0.7233
chrMT	16571	4137195	249.6648	66.5967
chrX	155270560	38257707	0.2464	1.083
chrY	59373566	3074945	0.0518	2.1048

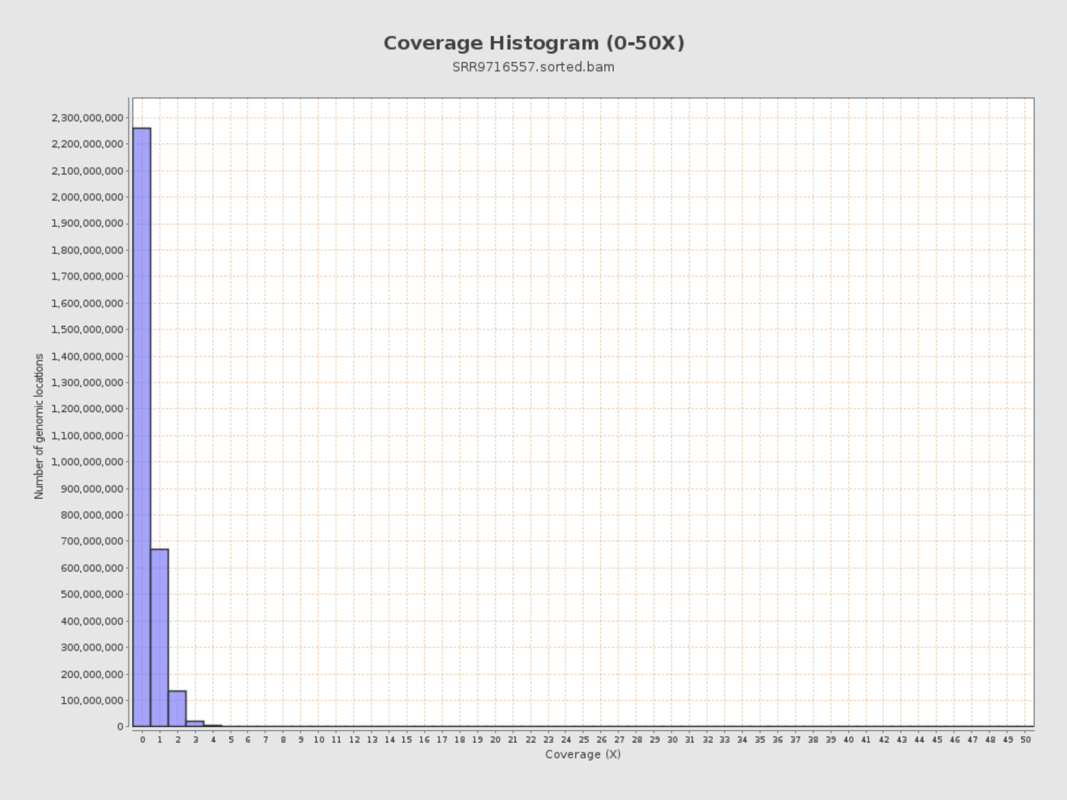
3. Results : Coverage across reference



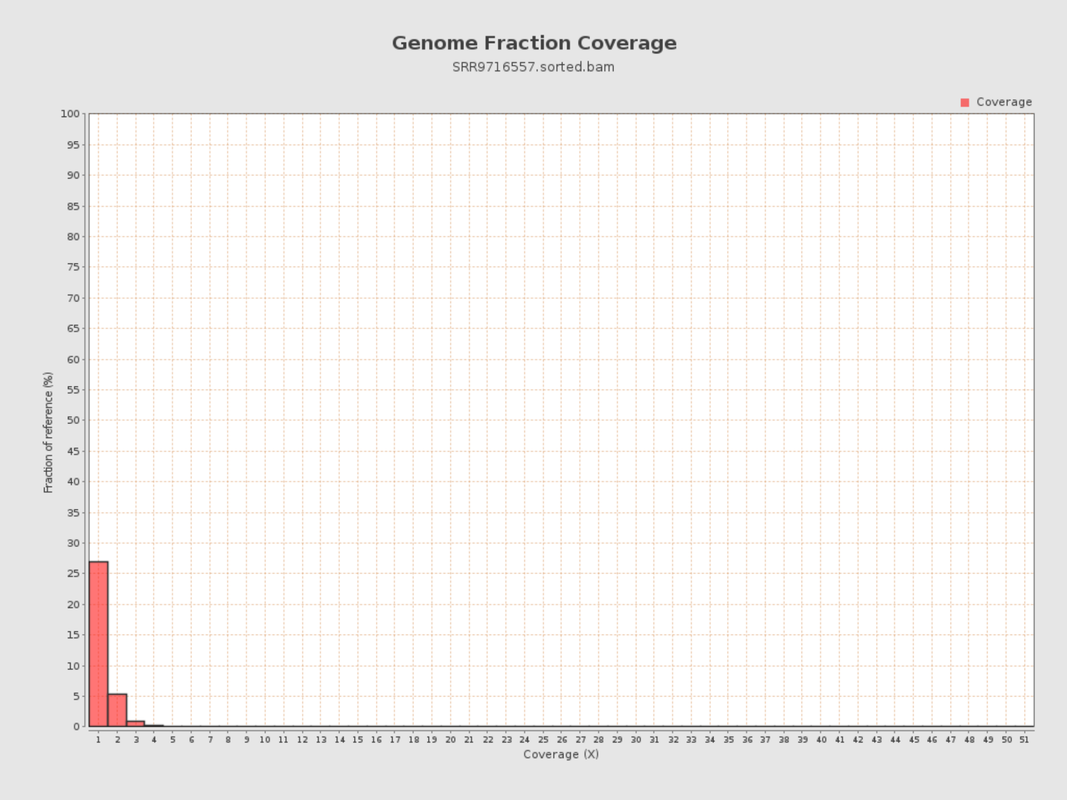
4. Results : Coverage Histogram



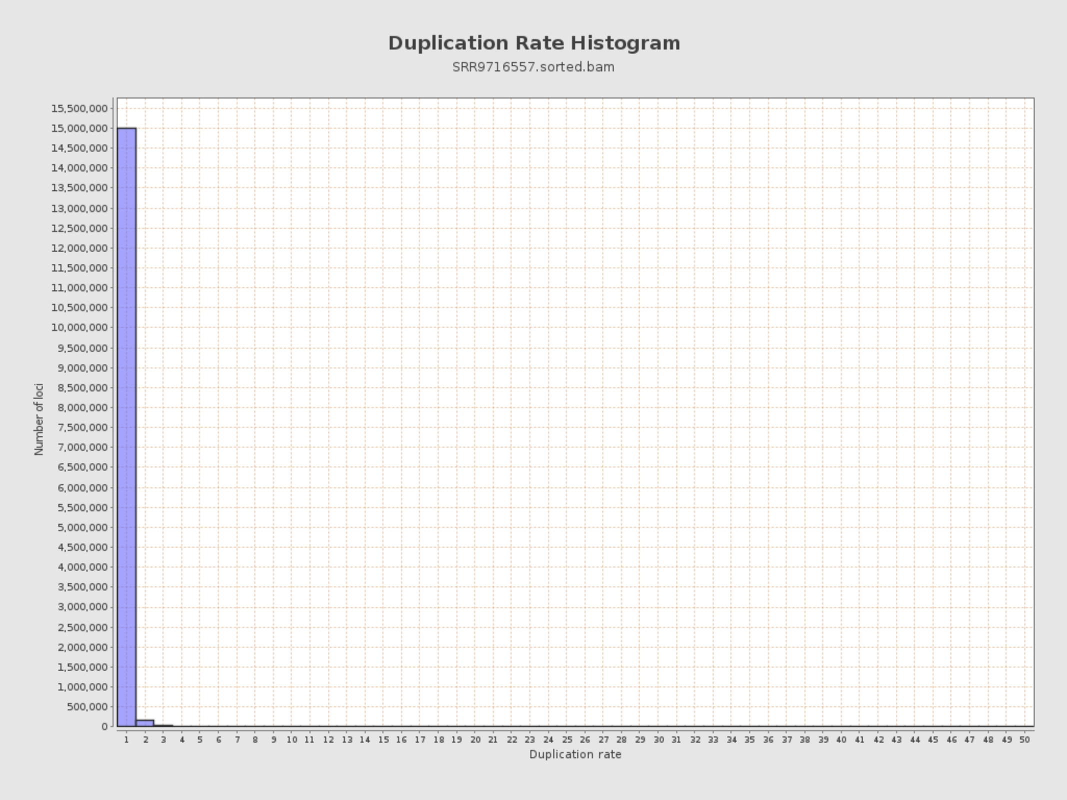
5. Results : Coverage Histogram (0-50X)



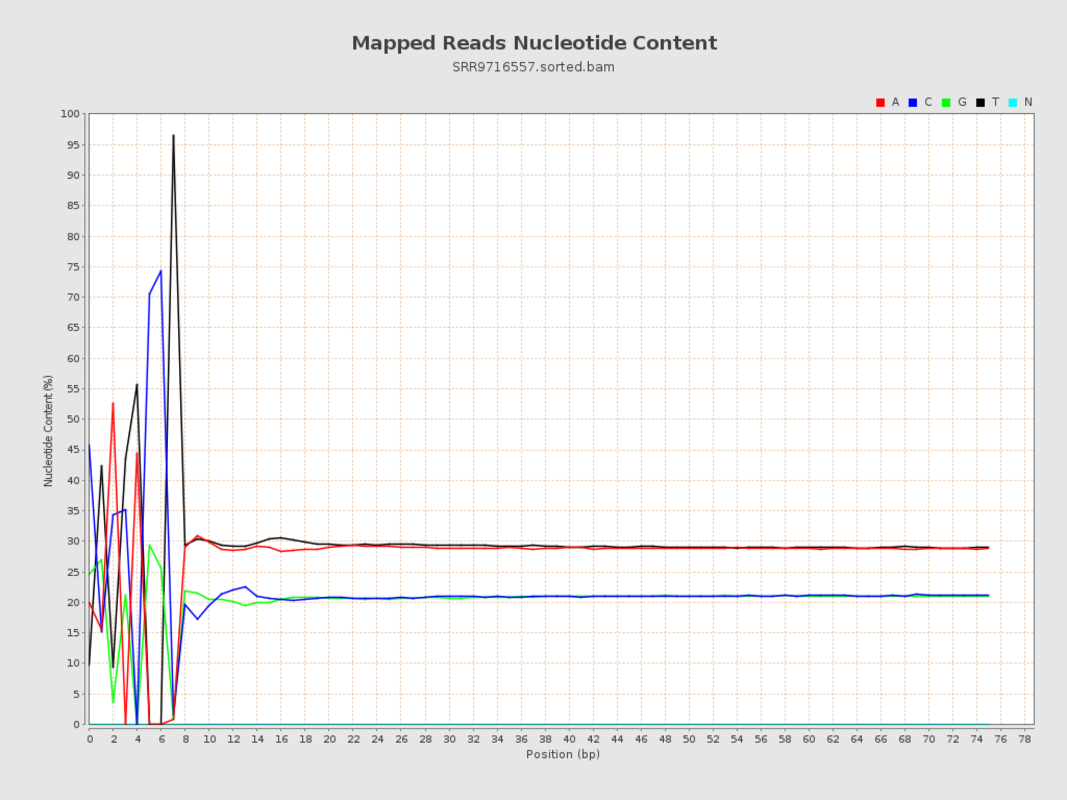
6. Results : Genome Fraction Coverage



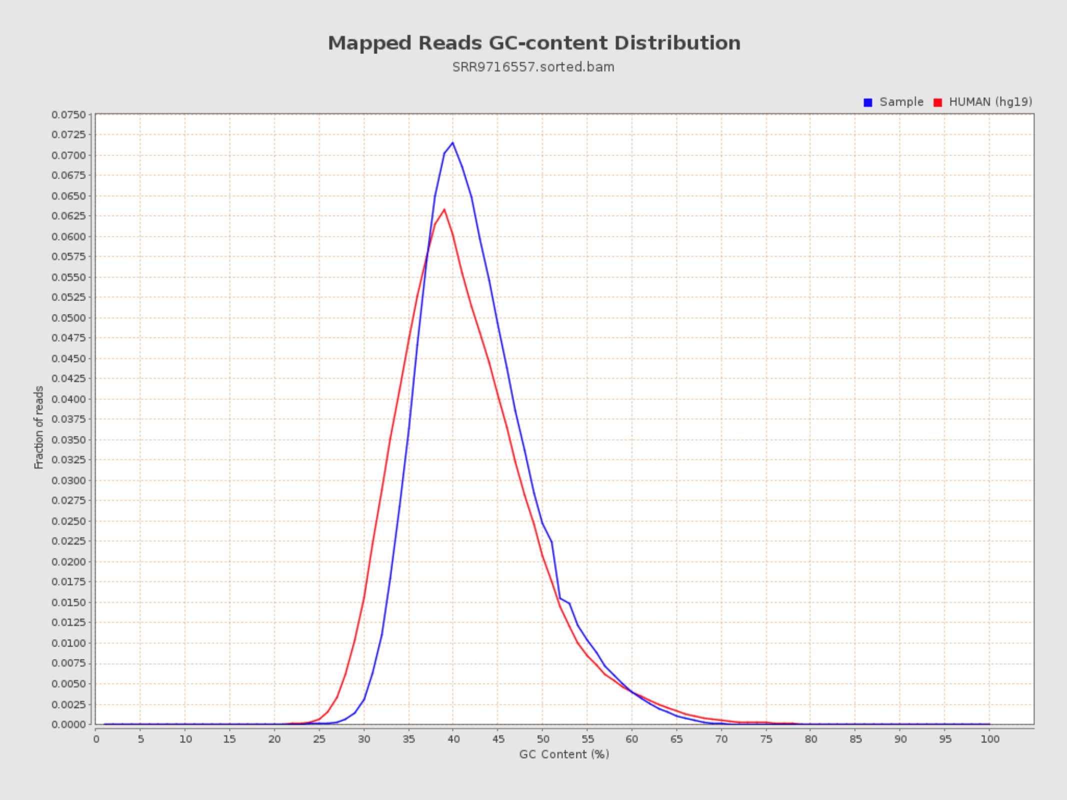
7. Results : Duplication Rate Histogram



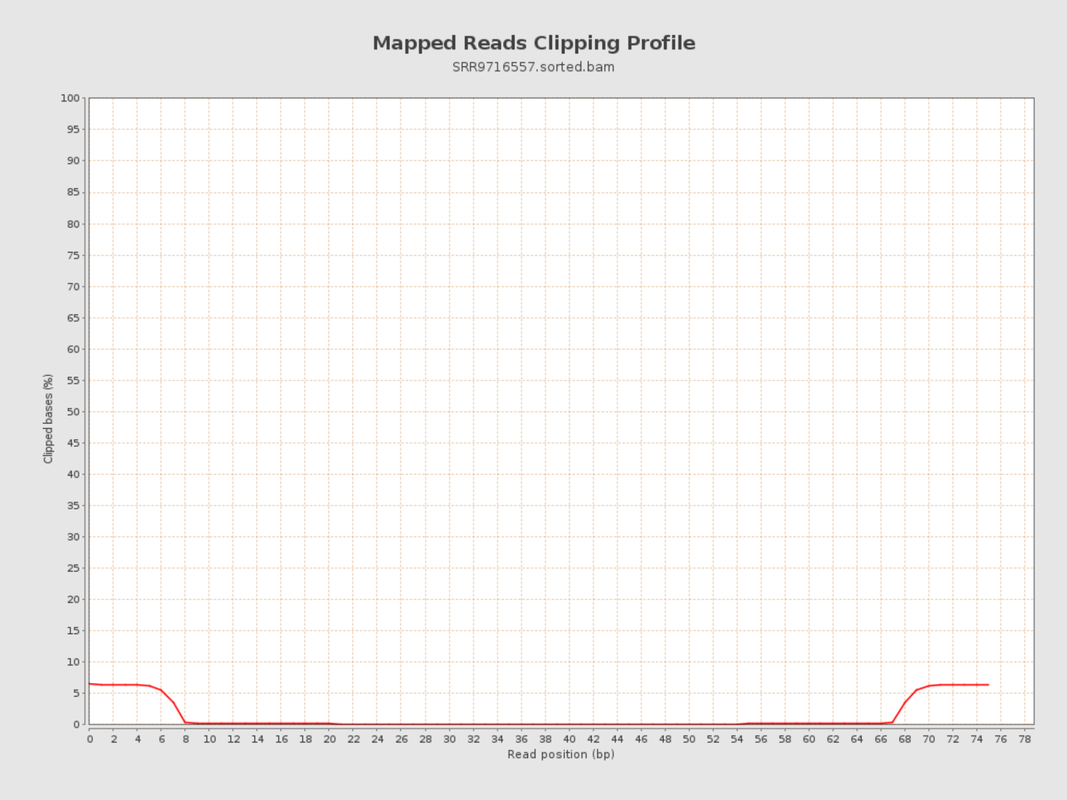
8. Results : Mapped Reads Nucleotide Content



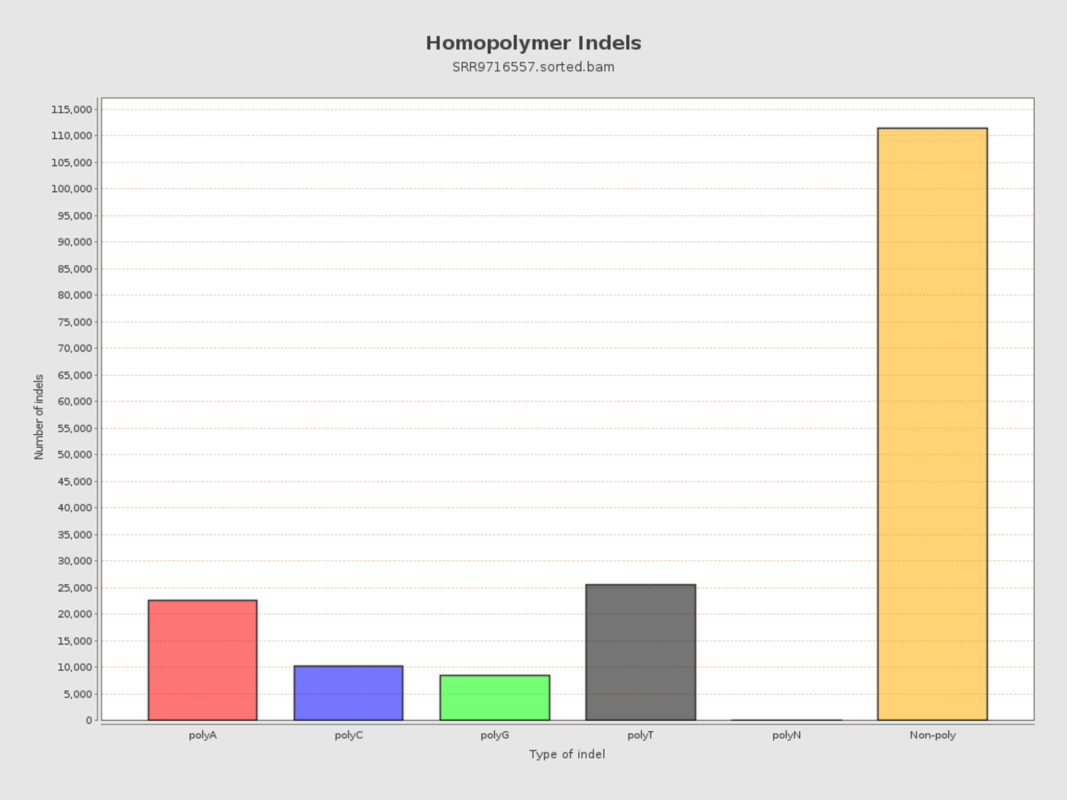
9. Results : Mapped Reads GC-content Distribution



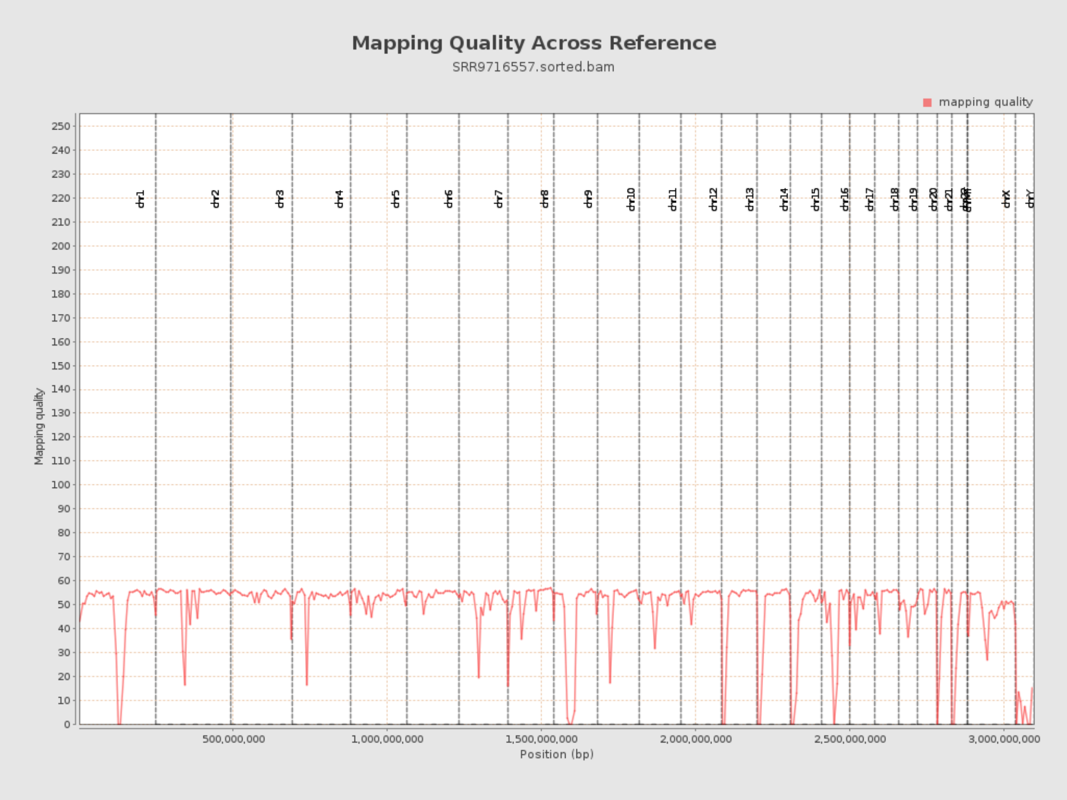
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram