Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 20:10:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716552.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_SRR9716552 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716552.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 20:10:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716552.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,998,558
Mapped reads	1,785,718 / 89.35%
Unmapped reads	212,840 / 10.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,732 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	46,666 / 2.33%
Duplication rate	1.85%
Clipped reads	1,791,417 / 89.64%

2.2. ACGT Content

Number/percentage of A's	24,246,712 / 23.71%
Number/percentage of C's	19,978,975 / 19.54%
Number/percentage of T's	31,996,749 / 31.29%
Number/percentage of G's	26,042,603 / 25.47%
Number/percentage of N's	799 / 0%
GC Percentage	45%

2.3. Coverage

Mean	0.033

Standard Deviation	0.2641

2.4. Mapping Quality

Mean Mapping Quality	42.32

2.5. Mismatches and indels

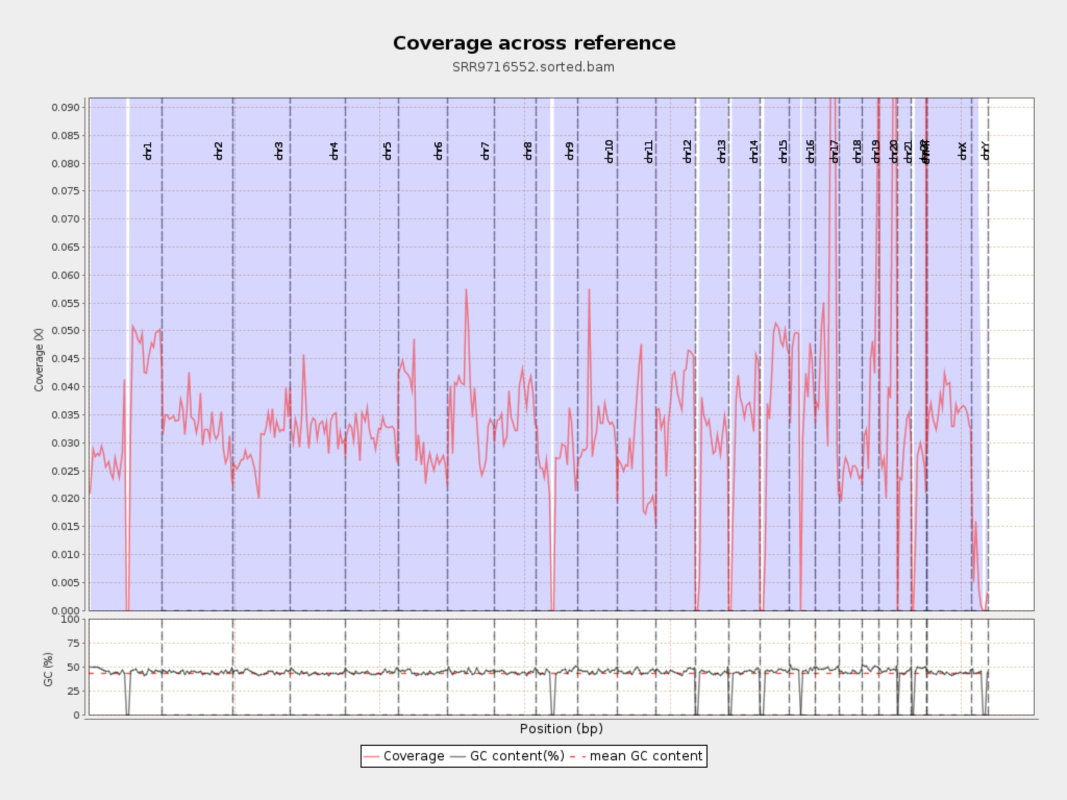
General error rate	0.53%
Mismatches	527,831
Insertions	5,893
Mapped reads with at least one insertion	0.33%
Deletions	18,779
Mapped reads with at least one deletion	1.04%
Homopolymer indels	42.89%

2.6. Chromosome stats

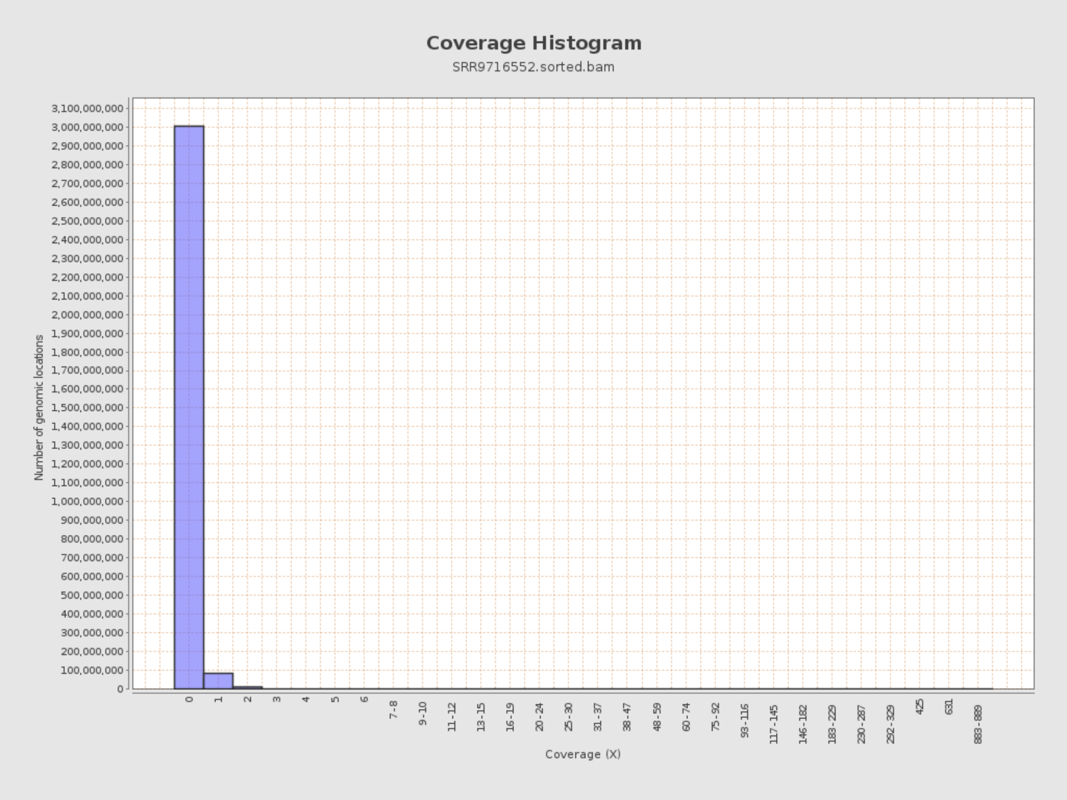
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8520447	0.0342	0.3225
chr2	243199373	8064959	0.0332	0.4044
chr3	198022430	5897617	0.0298	0.1915
chr4	191154276	6274459	0.0328	0.2098
chr5	180915260	5809913	0.0321	0.1953
chr6	171115067	5567513	0.0325	0.2379
chr7	159138663	5816441	0.0365	0.3774

chr8	146364022	5255355	0.0359	0.2611
chr9	141213431	3437801	0.0243	0.1986
chr10	135534747	4470863	0.033	0.2964
chr11	135006516	3642894	0.027	0.2254
chr12	133851895	5137479	0.0384	0.2161
chr13	115169878	3081525	0.0268	0.1789
chr14	107349540	3426554	0.0319	0.2047
chr15	102531392	3747026	0.0365	0.2151
chr16	90354753	3557472	0.0394	0.2332
chr17	81195210	4546685	0.056	0.2758
chr18	78077248	1922836	0.0246	0.3195
chr19	59128983	2744572	0.0464	0.3334
chr20	63025520	3239312	0.0514	0.2615
chr21	48129895	1277096	0.0265	0.1911
chr22	51304566	989757	0.0193	0.1535
chrMT	16571	5713	0.3448	0.7338
chrX	155270560	5564534	0.0358	0.2219
chrY	59373566	297068	0.005	0.1323

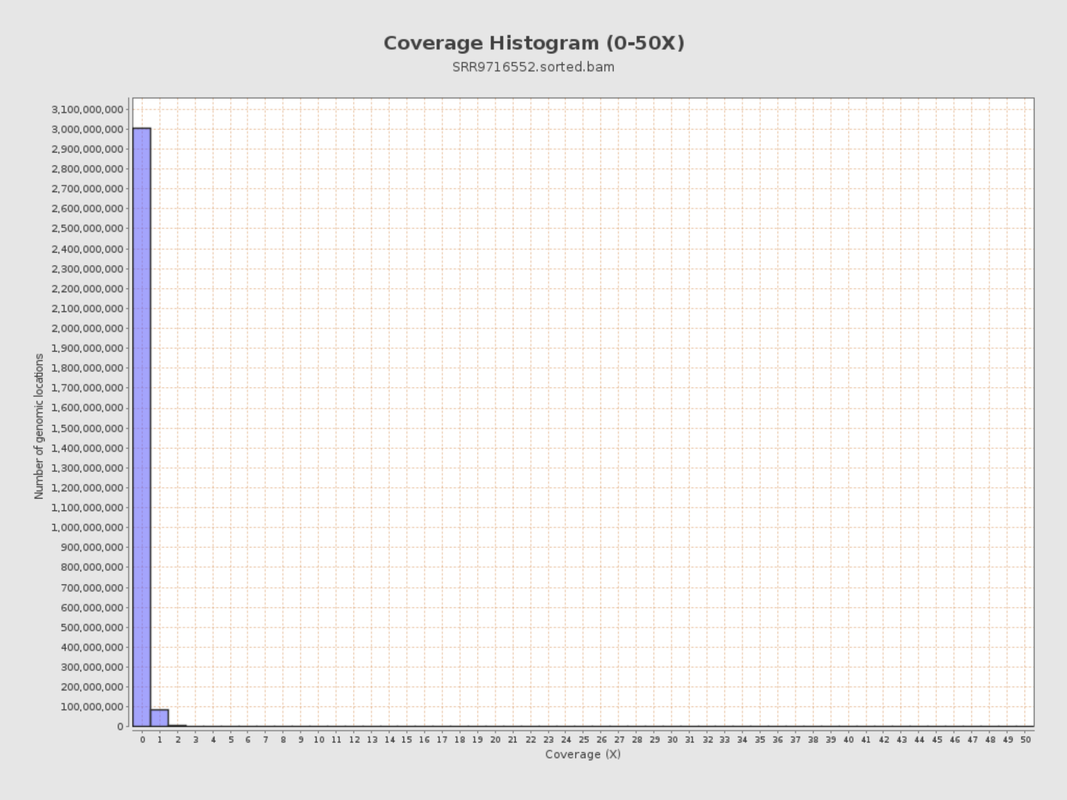
3. Results : Coverage across reference



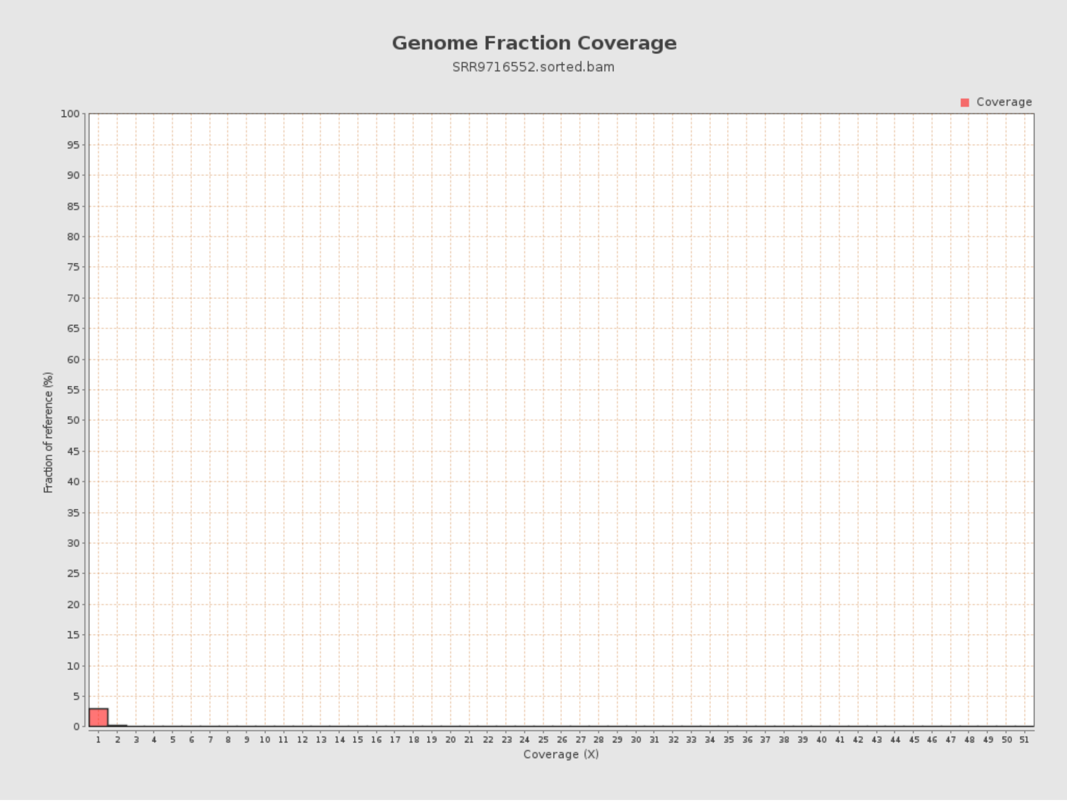
4. Results : Coverage Histogram



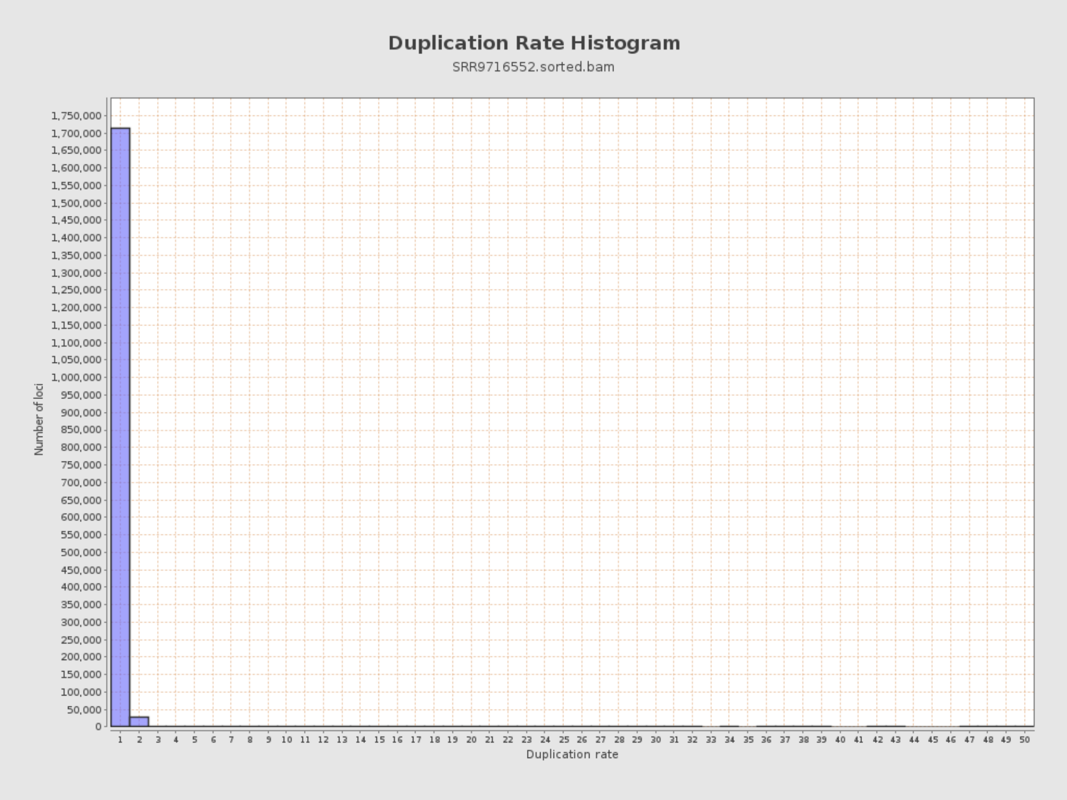
5. Results : Coverage Histogram (0-50X)



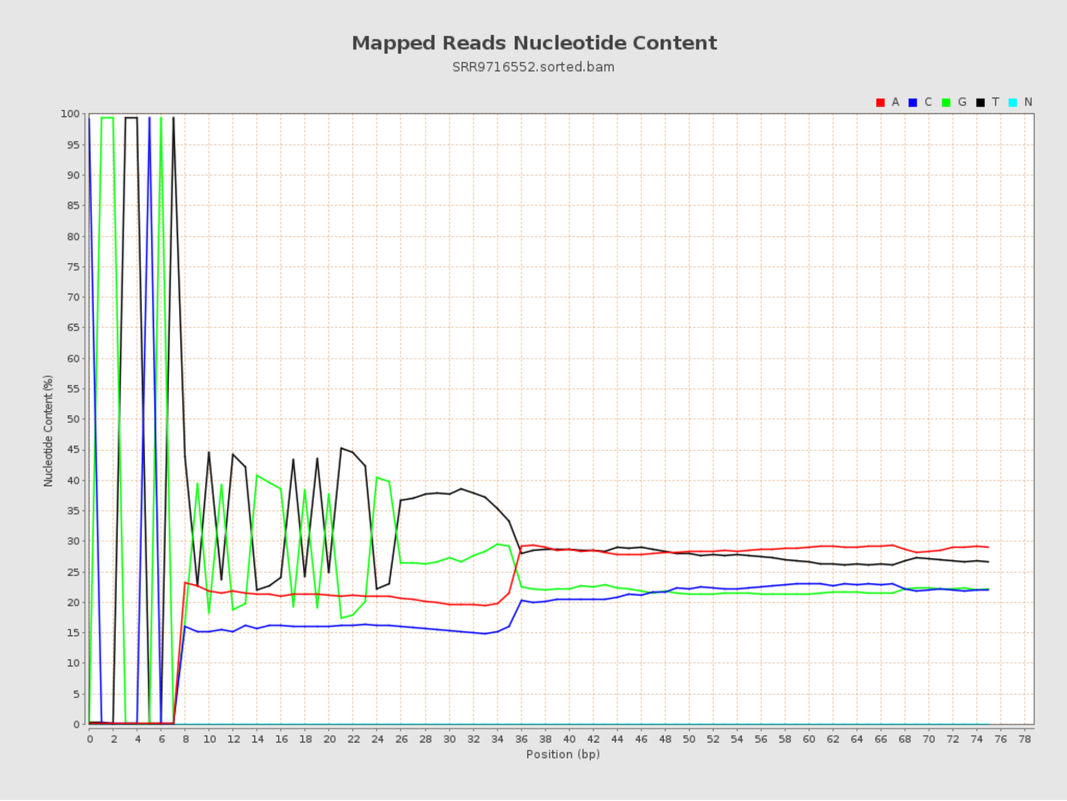
6. Results : Genome Fraction Coverage



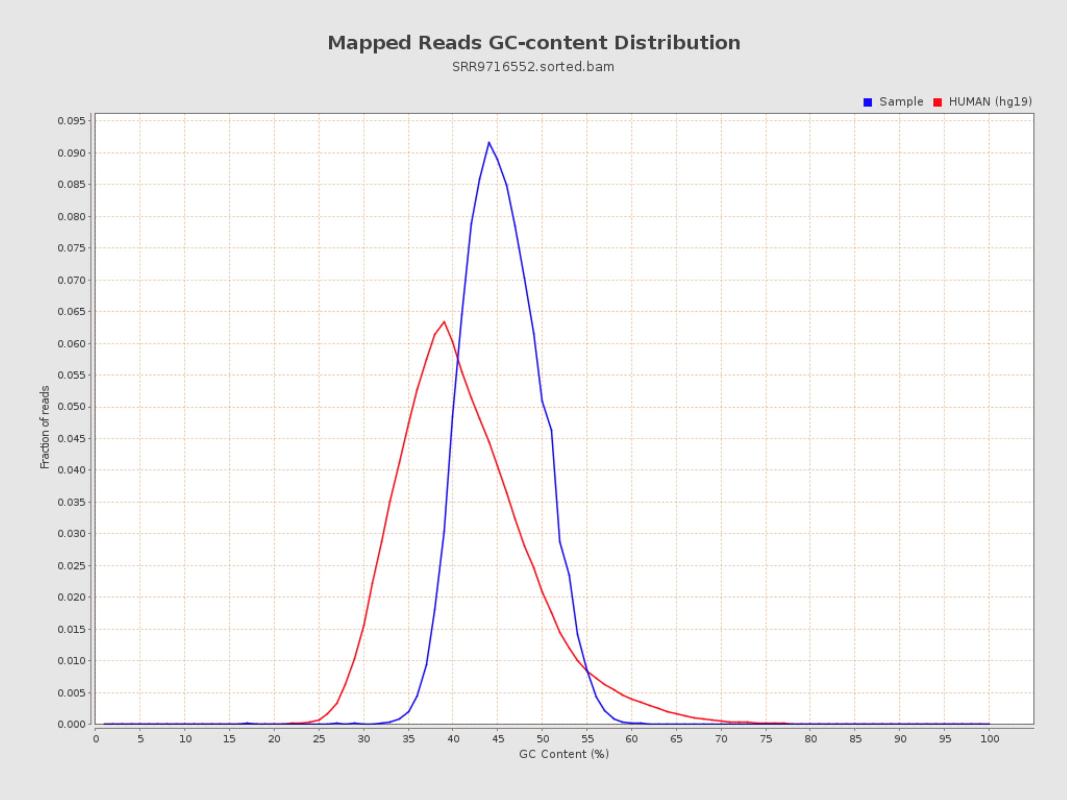
7. Results : Duplication Rate Histogram



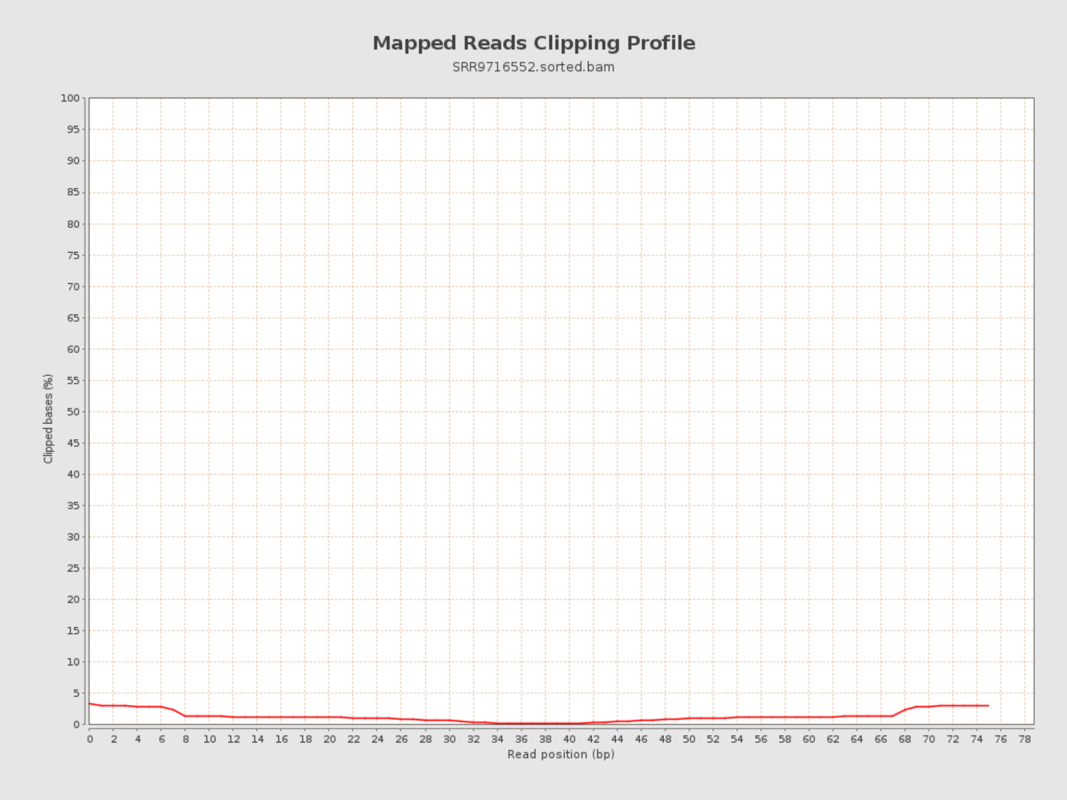
8. Results : Mapped Reads Nucleotide Content



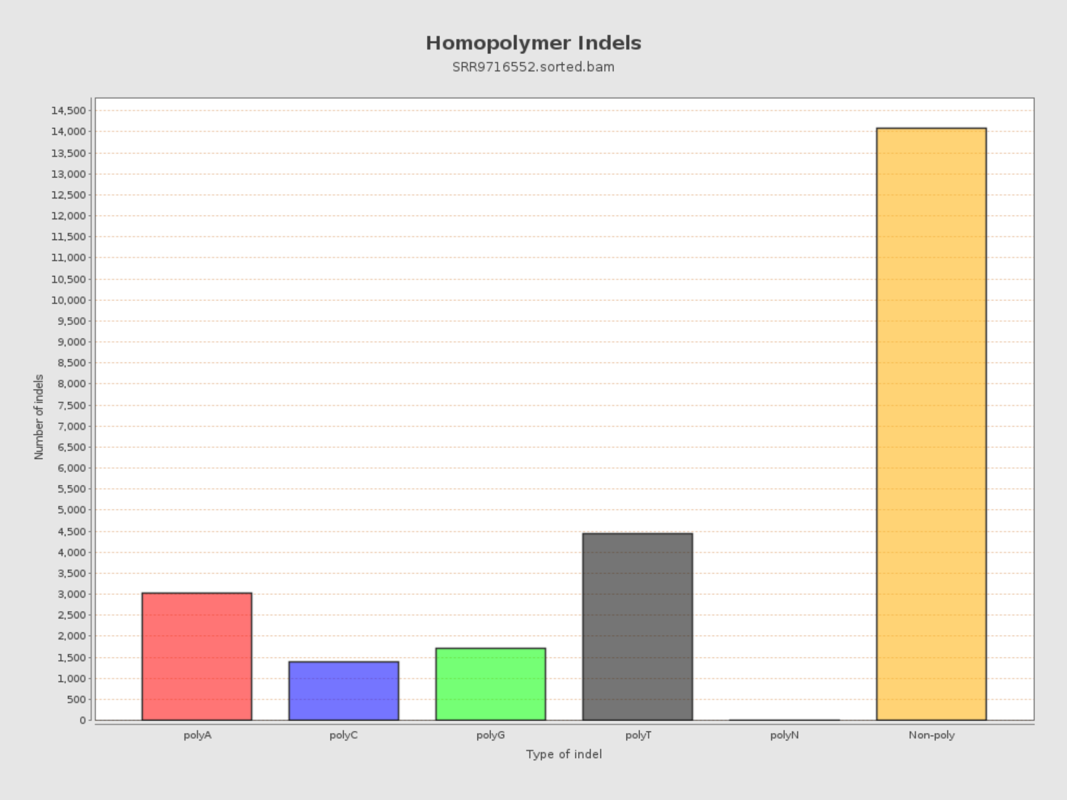
9. Results : Mapped Reads GC-content Distribution



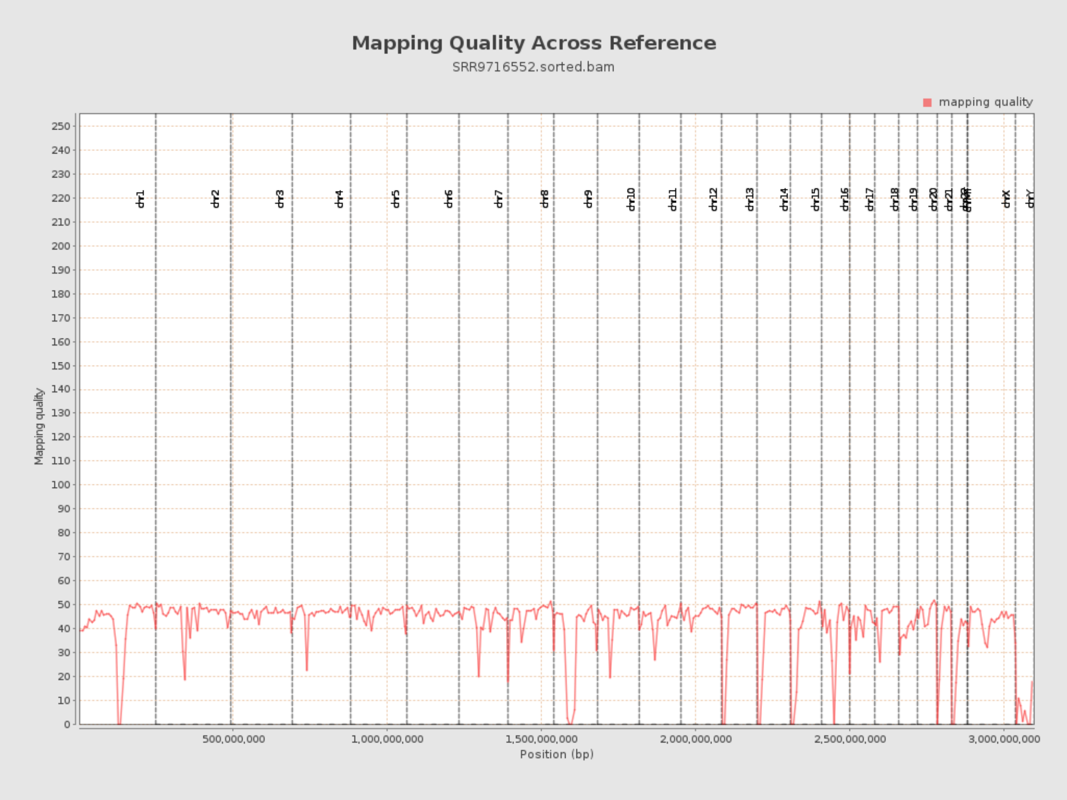
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram