Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 11:53:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716403.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_SRR9716403 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716403.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 11:53:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716403.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,340,402
Mapped reads	1,216,735 / 90.77%
Unmapped reads	123,667 / 9.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,850 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	29,863 / 2.23%
Duplication rate	1.85%
Clipped reads	1,219,113 / 90.95%

2.2. ACGT Content

Number/percentage of A's	17,083,856 / 24.46%
Number/percentage of C's	13,512,914 / 19.34%
Number/percentage of T's	21,885,206 / 31.33%
Number/percentage of G's	17,373,605 / 24.87%
Number/percentage of N's	1,523 / 0%
GC Percentage	44.21%

2.3. Coverage

Mean	0.0226

Standard Deviation	0.1982

2.4. Mapping Quality

Mean Mapping Quality	44.71

2.5. Mismatches and indels

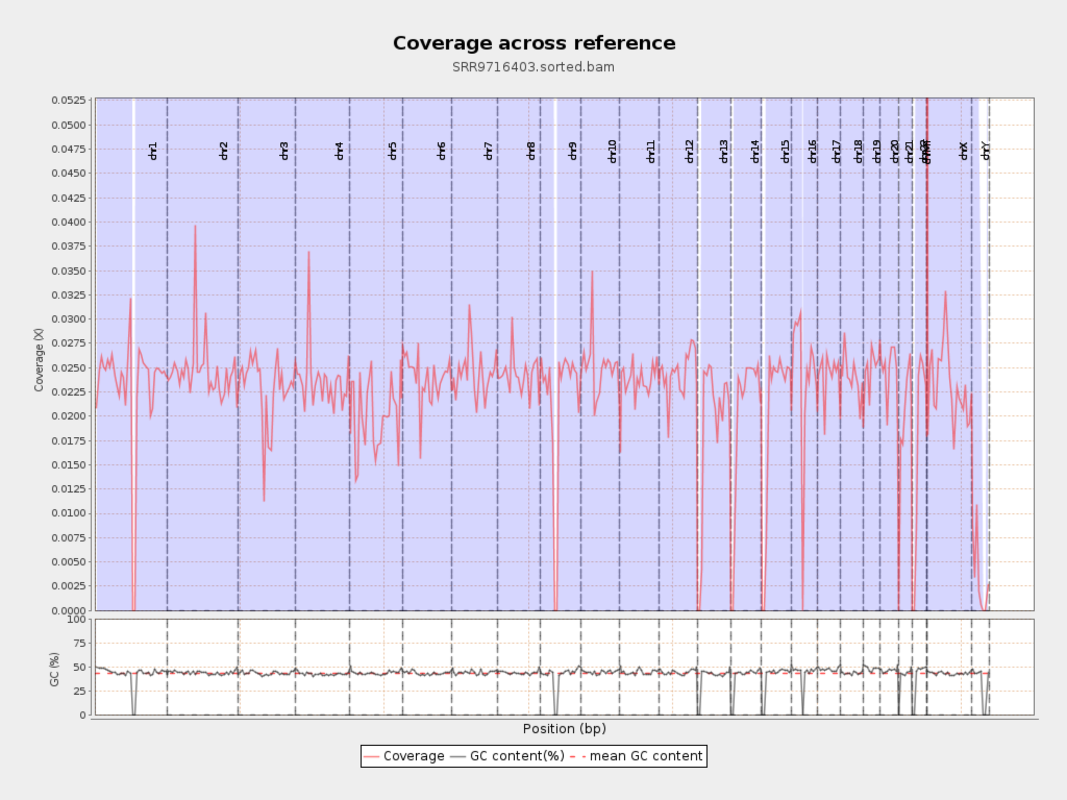
General error rate	0.5%
Mismatches	340,747
Insertions	4,137
Mapped reads with at least one insertion	0.34%
Deletions	10,593
Mapped reads with at least one deletion	0.86%
Homopolymer indels	42.04%

2.6. Chromosome stats

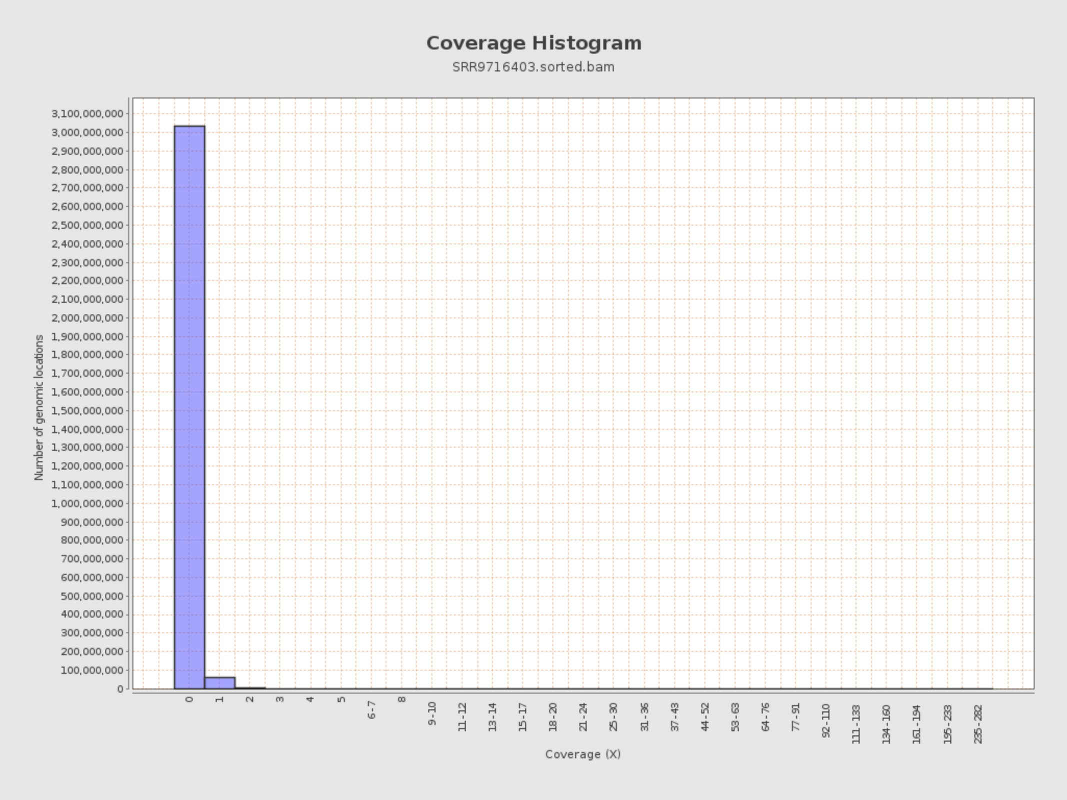
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5723419	0.023	0.2737
chr2	243199373	6012954	0.0247	0.2293
chr3	198022430	4543391	0.0229	0.162
chr4	191154276	4539153	0.0237	0.1755
chr5	180915260	3646878	0.0202	0.1535
chr6	171115067	4095476	0.0239	0.174
chr7	159138663	3898233	0.0245	0.2228

chr8	146364022	3544500	0.0242	0.1875
chr9	141213431	3014654	0.0213	0.2024
chr10	135534747	3404271	0.0251	0.2
chr11	135006516	3205330	0.0237	0.2148
chr12	133851895	3271335	0.0244	0.1688
chr13	115169878	2153647	0.0187	0.1456
chr14	107349540	2136990	0.0199	0.1579
chr15	102531392	2055253	0.02	0.152
chr16	90354753	2146631	0.0238	0.1735
chr17	81195210	1967267	0.0242	0.1745
chr18	78077248	1877725	0.024	0.3571
chr19	59128983	1474125	0.0249	0.2231
chr20	63025520	1551198	0.0246	0.1715
chr21	48129895	929183	0.0193	0.1596
chr22	51304566	867559	0.0169	0.139
chrMT	16571	5316	0.3208	0.612
chrX	155270560	3614111	0.0233	0.1828
chrY	59373566	196922	0.0033	0.0843

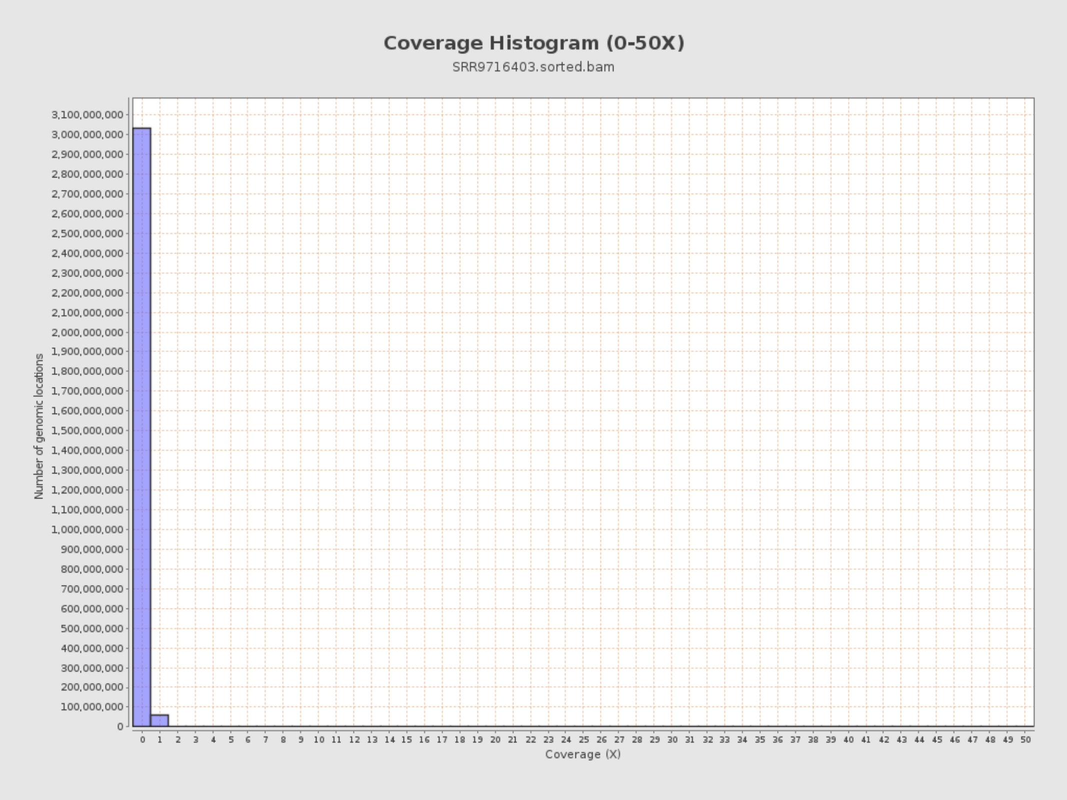
3. Results : Coverage across reference



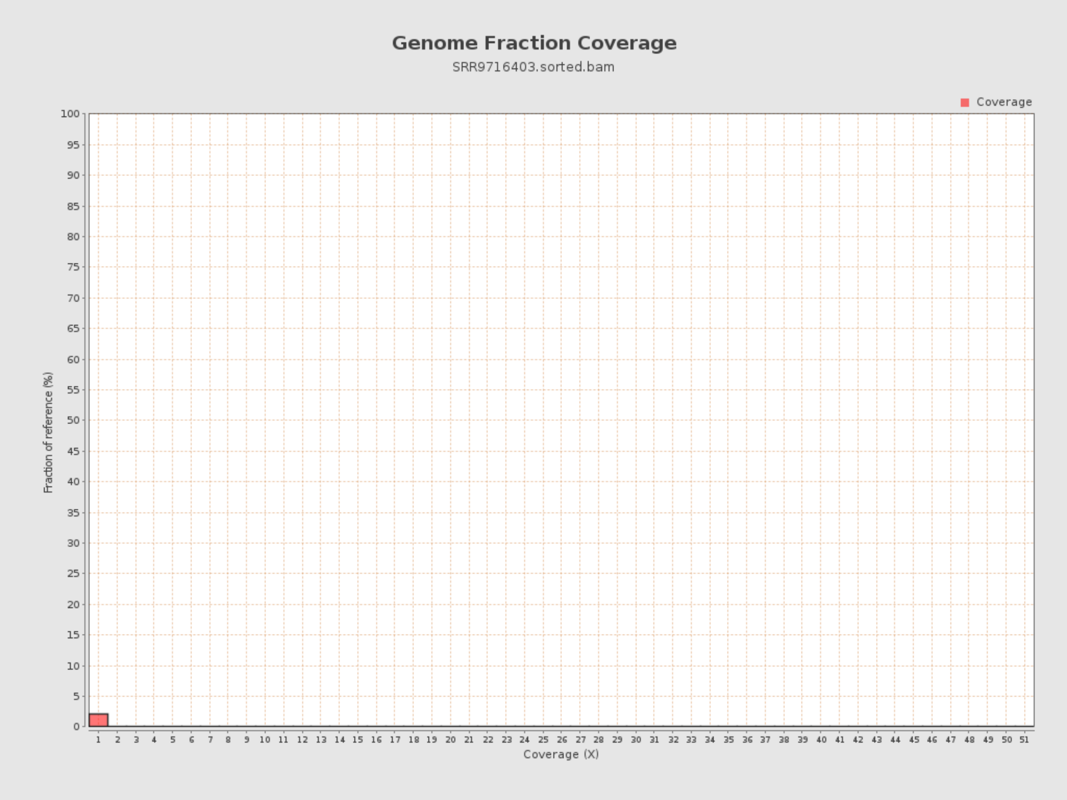
4. Results : Coverage Histogram



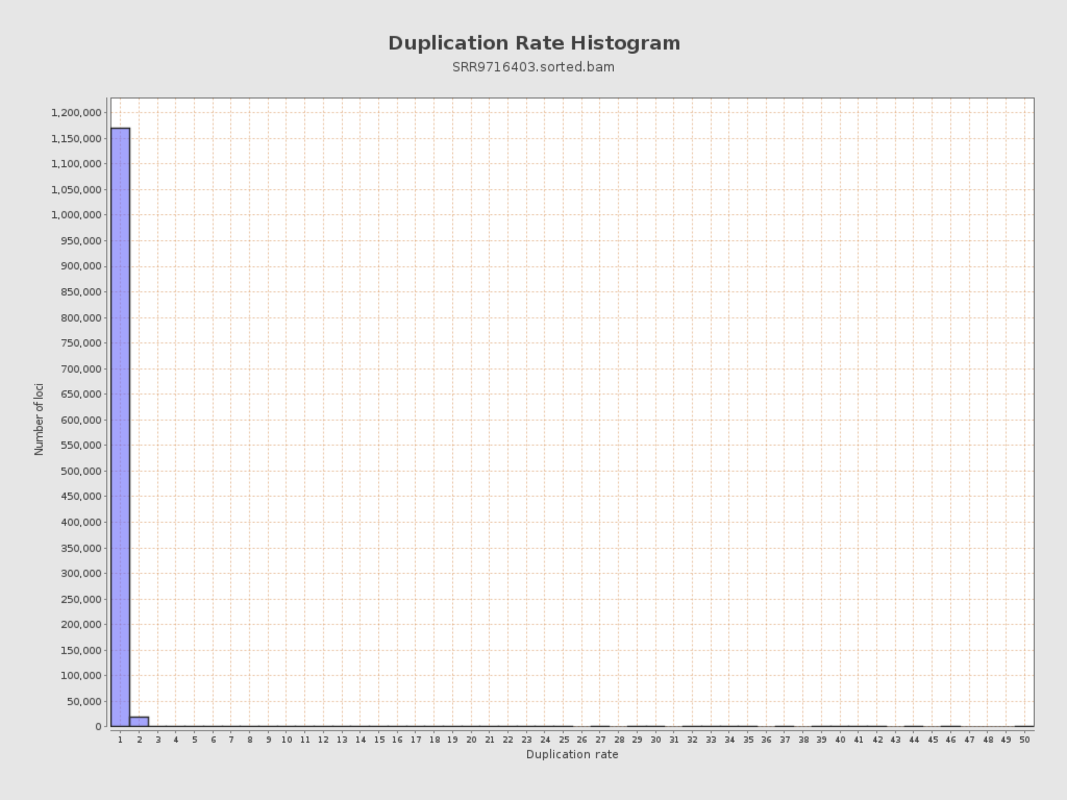
5. Results : Coverage Histogram (0-50X)



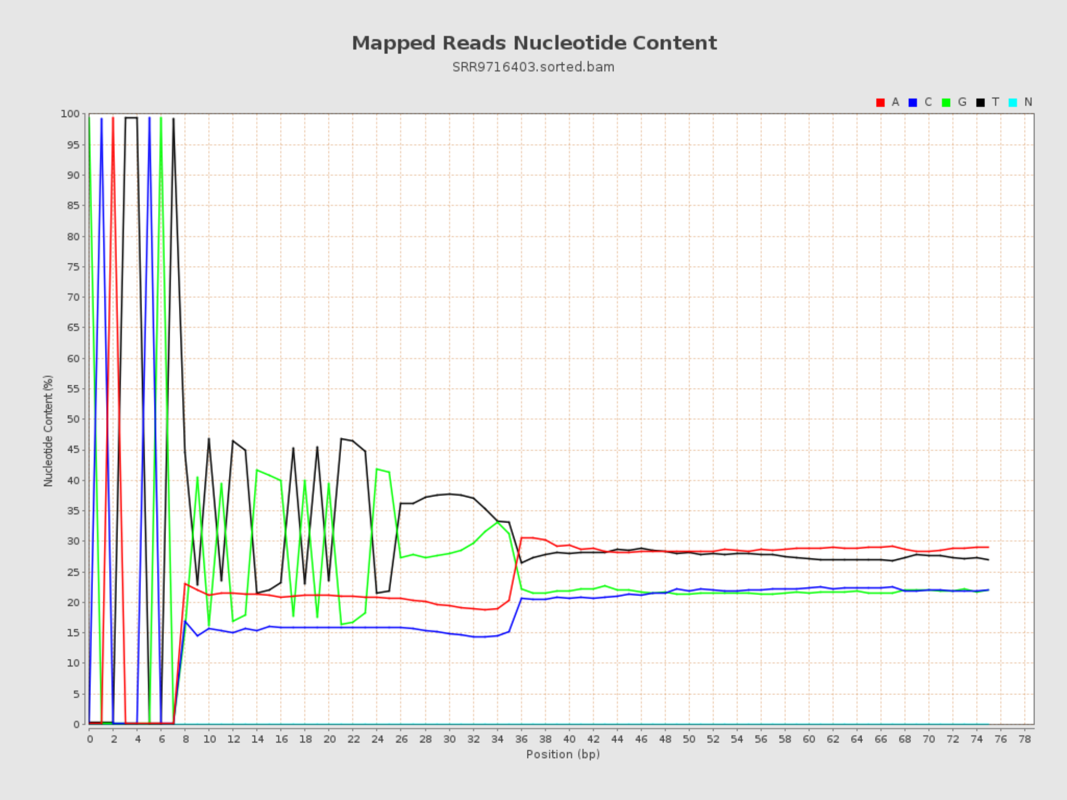
6. Results : Genome Fraction Coverage



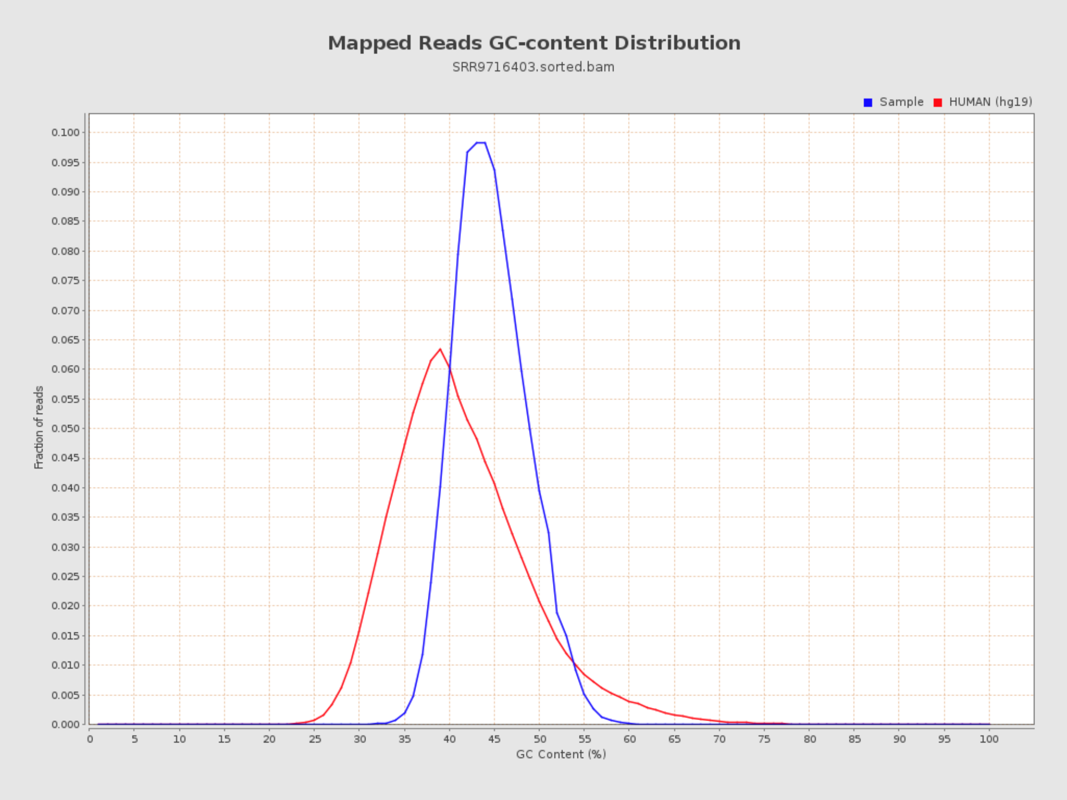
7. Results : Duplication Rate Histogram



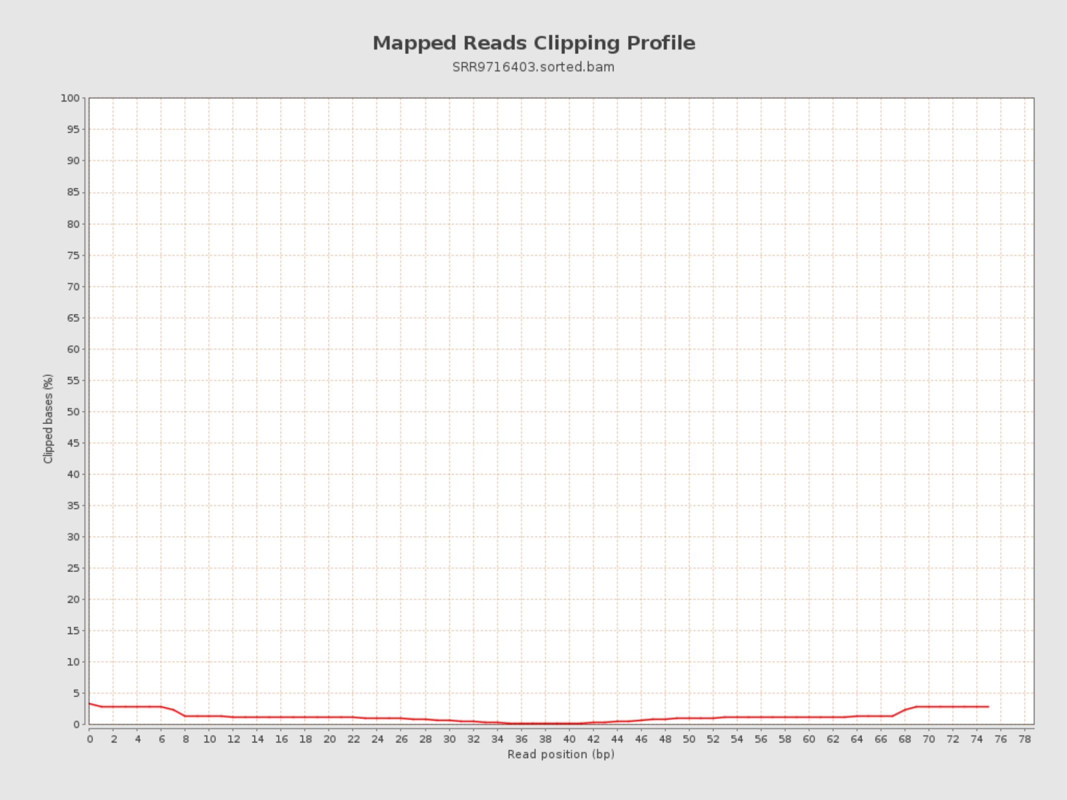
8. Results : Mapped Reads Nucleotide Content



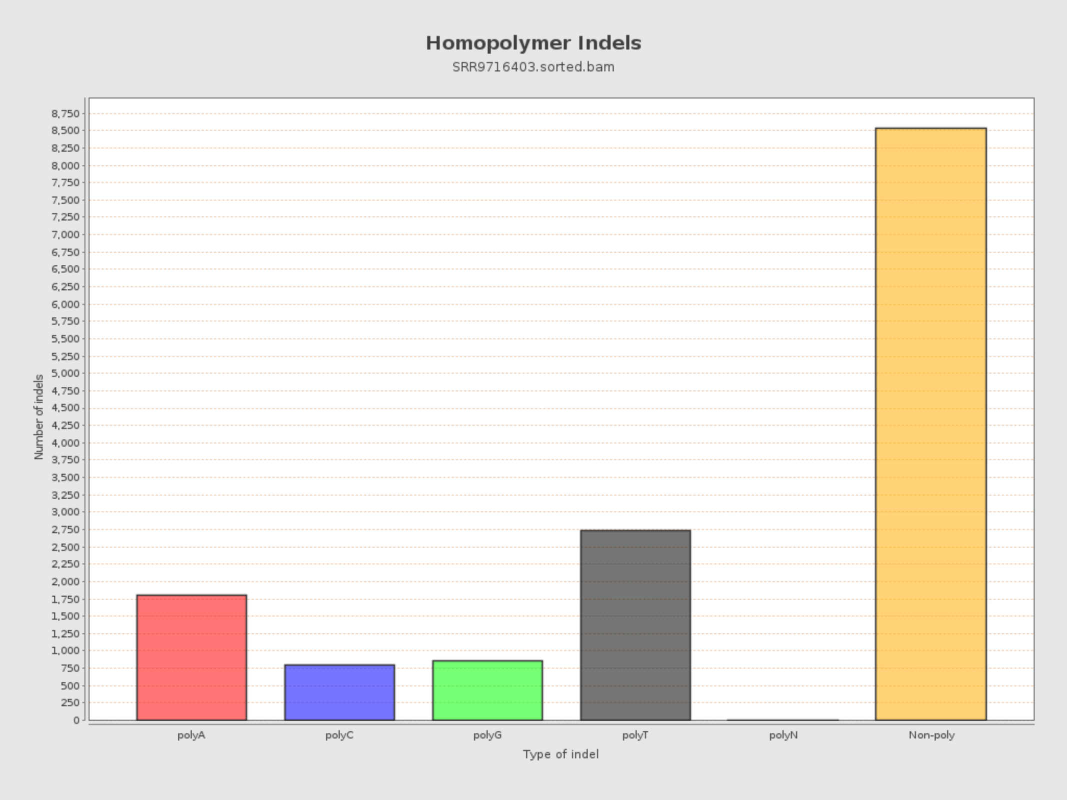
9. Results : Mapped Reads GC-content Distribution



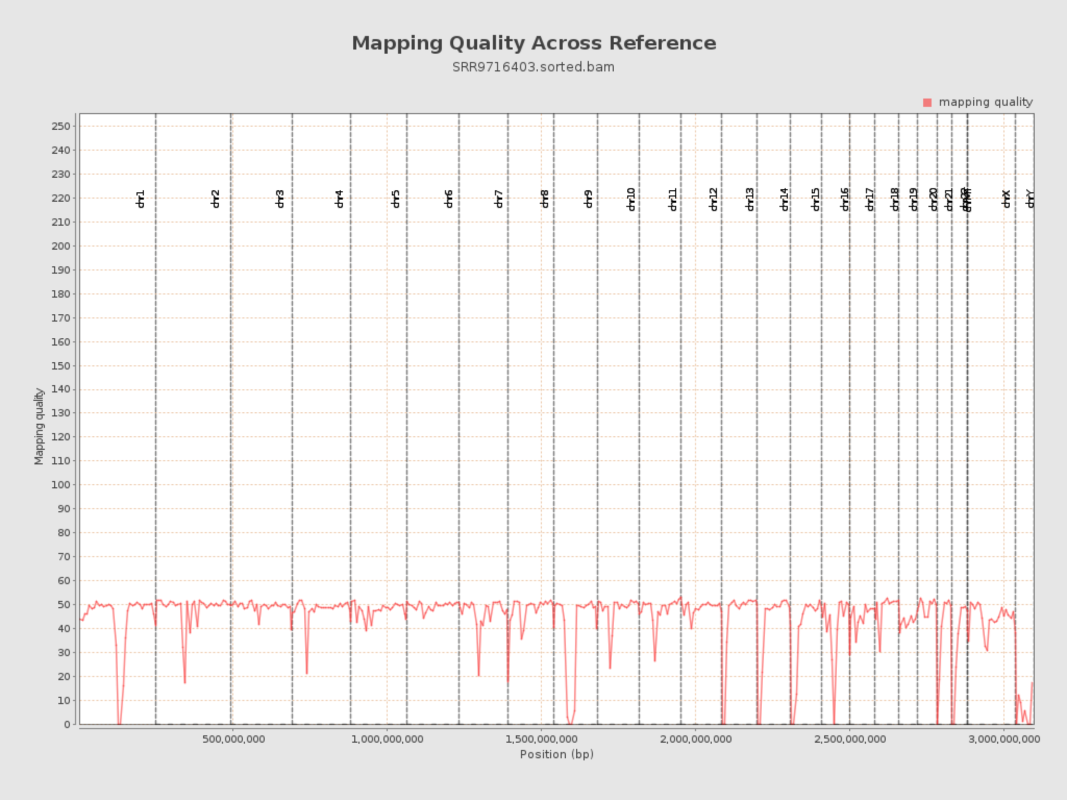
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram