Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 10:54:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716387.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_SRR9716387 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716387.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 10:54:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716387.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,205,927
Mapped reads	1,070,802 / 88.79%
Unmapped reads	135,125 / 11.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,638 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	22,193 / 1.84%
Duplication rate	1.41%
Clipped reads	1,072,926 / 88.97%

2.2. ACGT Content

Number/percentage of A's	14,945,255 / 24.49%
Number/percentage of C's	12,399,412 / 20.31%
Number/percentage of T's	18,684,734 / 30.61%
Number/percentage of G's	15,005,952 / 24.59%
Number/percentage of N's	518 / 0%
GC Percentage	44.9%

2.3. Coverage

Mean	0.0197

Standard Deviation	0.187

2.4. Mapping Quality

Mean Mapping Quality	42.21

2.5. Mismatches and indels

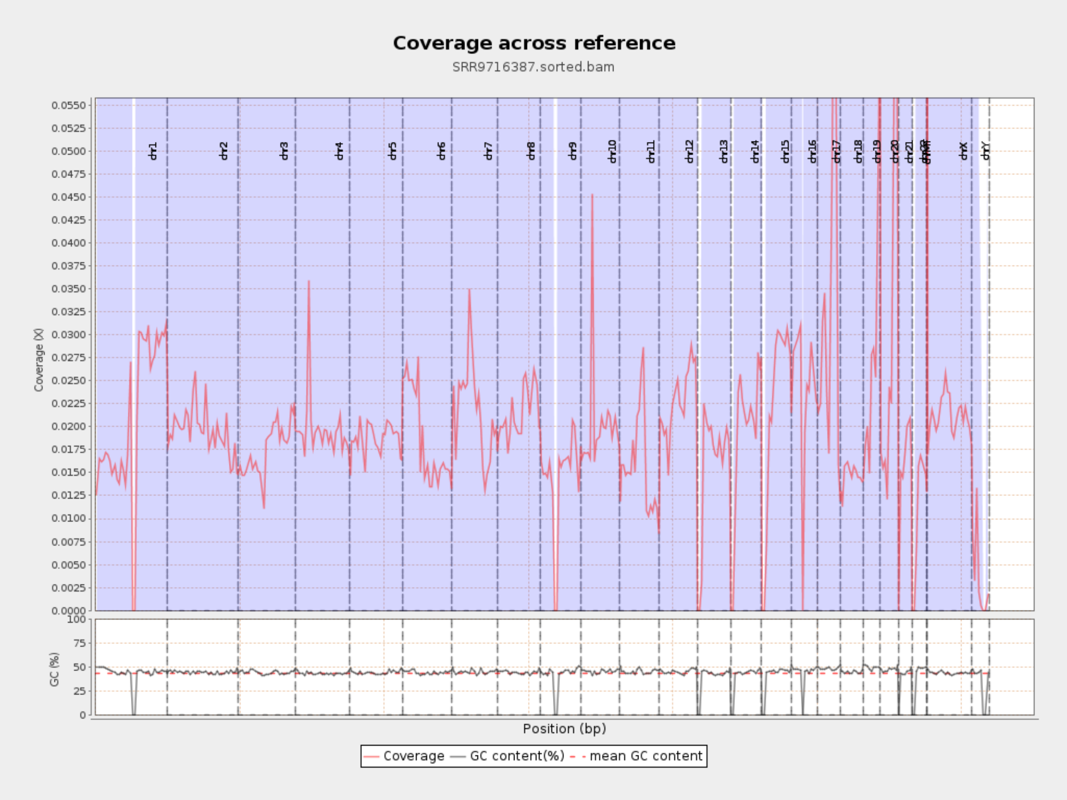
General error rate	0.55%
Mismatches	325,471
Insertions	4,415
Mapped reads with at least one insertion	0.41%
Deletions	11,847
Mapped reads with at least one deletion	1.1%
Homopolymer indels	38.83%

2.6. Chromosome stats

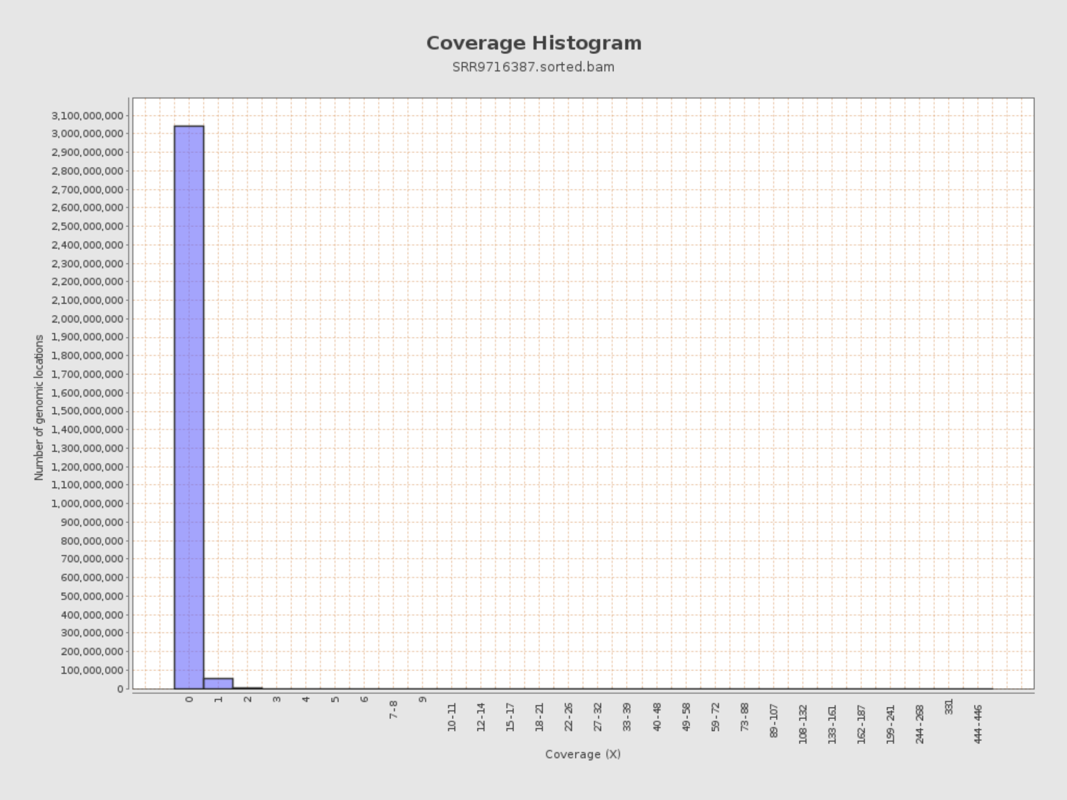
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5169568	0.0207	0.2474
chr2	243199373	4760779	0.0196	0.2444
chr3	198022430	3458470	0.0175	0.1423
chr4	191154276	3777547	0.0198	0.1638
chr5	180915260	3419605	0.0189	0.1442
chr6	171115067	3212572	0.0188	0.1622
chr7	159138663	3488637	0.0219	0.2445

chr8	146364022	3150262	0.0215	0.1846
chr9	141213431	2027009	0.0144	0.1407
chr10	135534747	2752300	0.0203	0.2474
chr11	135006516	2160751	0.016	0.1548
chr12	133851895	3039270	0.0227	0.1601
chr13	115169878	1800900	0.0156	0.1315
chr14	107349540	2041377	0.019	0.1502
chr15	102531392	2250231	0.0219	0.1581
chr16	90354753	2156488	0.0239	0.1766
chr17	81195210	2718909	0.0335	0.2018
chr18	78077248	1141890	0.0146	0.2094
chr19	59128983	1681576	0.0284	0.2361
chr20	63025520	1994782	0.0317	0.1958
chr21	48129895	760838	0.0158	0.1415
chr22	51304566	566778	0.011	0.111
chrMT	16571	4479	0.2703	0.5742
chrX	155270560	3313792	0.0213	0.1622
chrY	59373566	206111	0.0035	0.1165

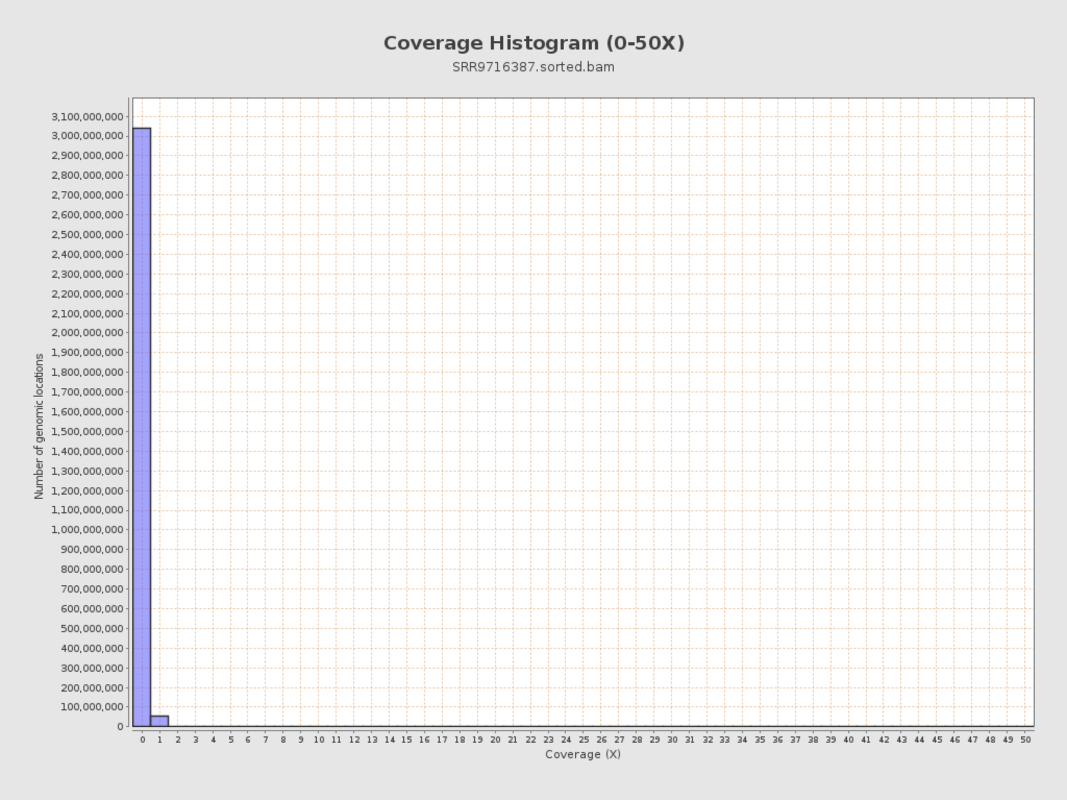
3. Results : Coverage across reference



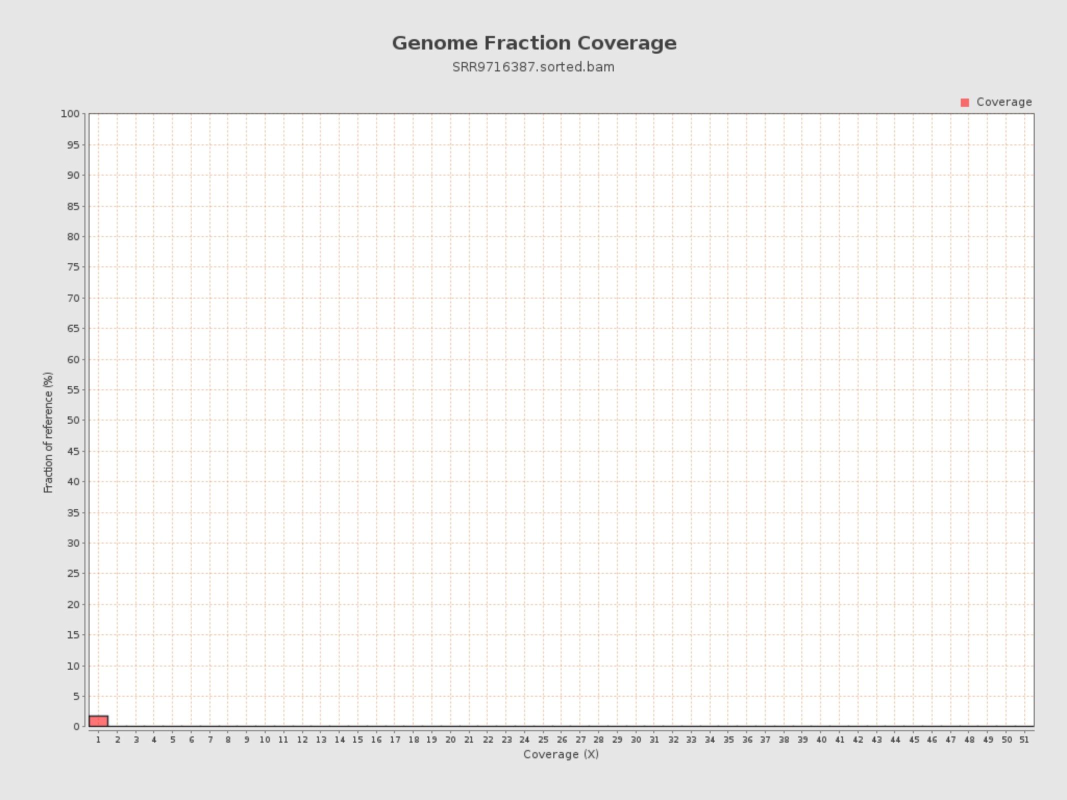
4. Results : Coverage Histogram



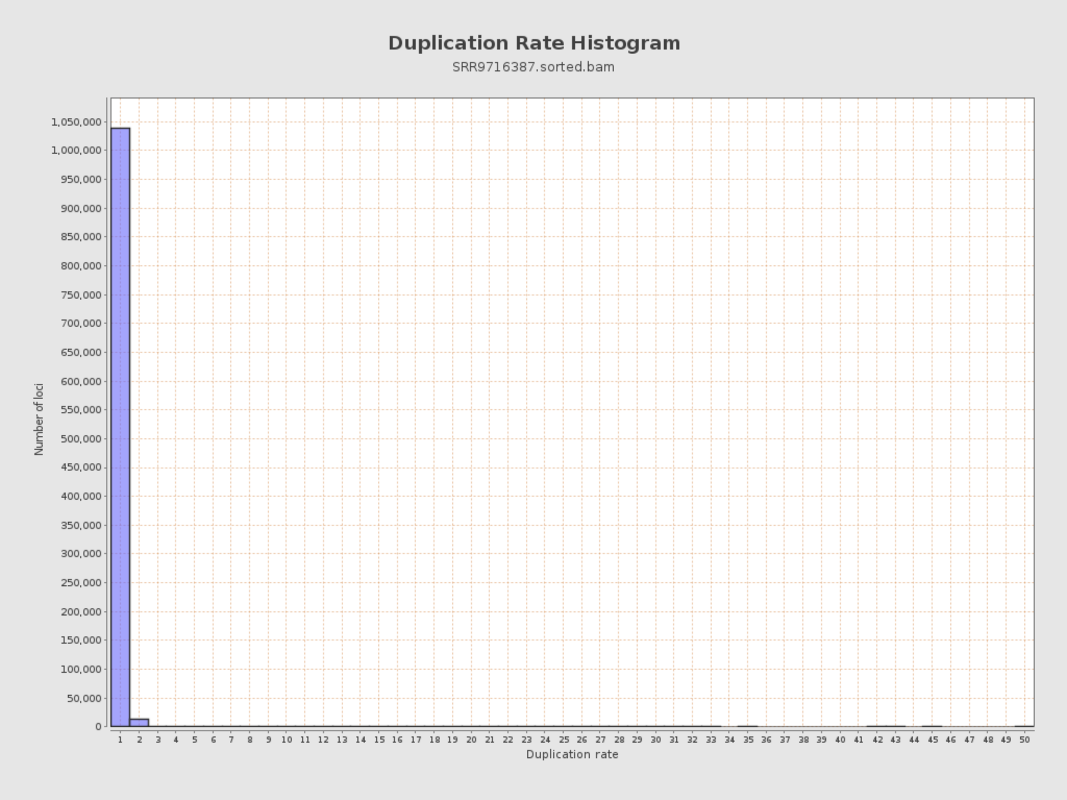
5. Results : Coverage Histogram (0-50X)



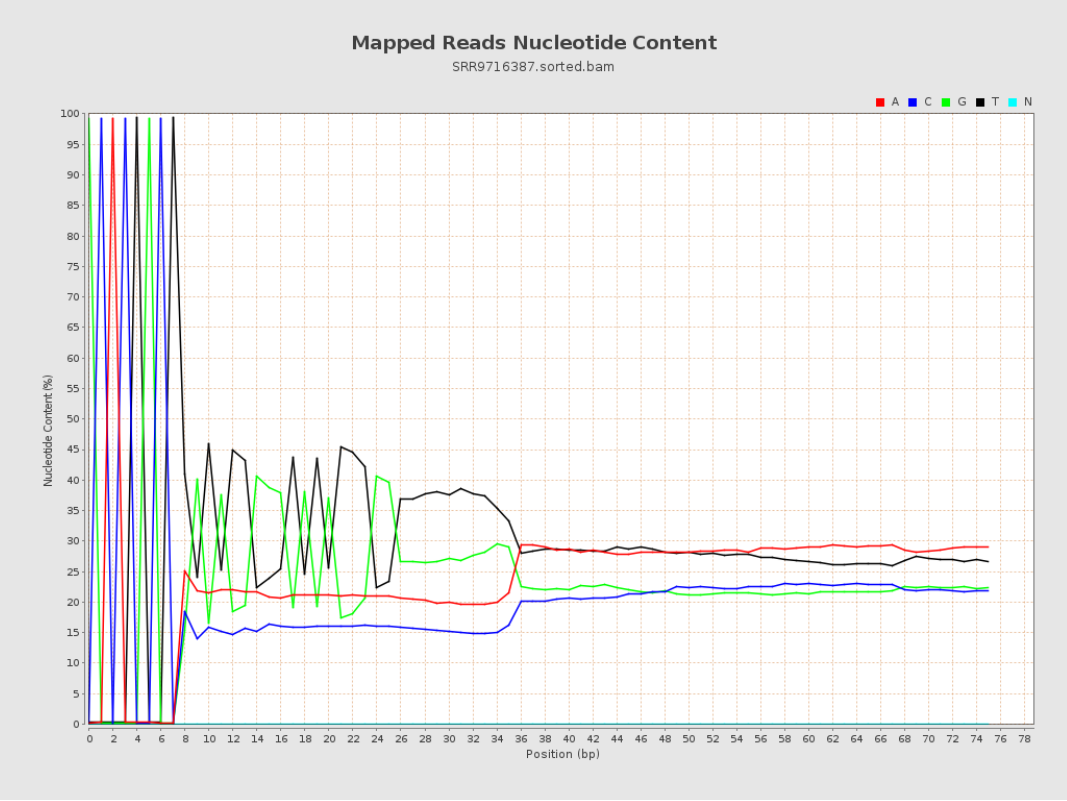
6. Results : Genome Fraction Coverage



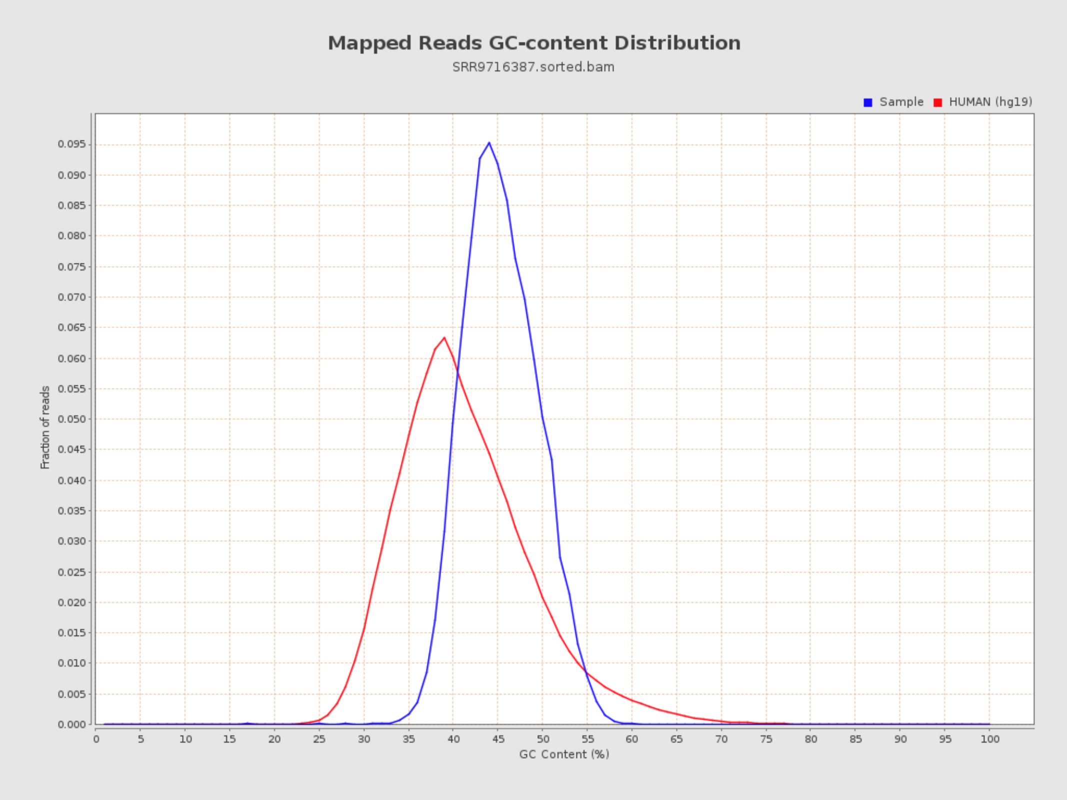
7. Results : Duplication Rate Histogram



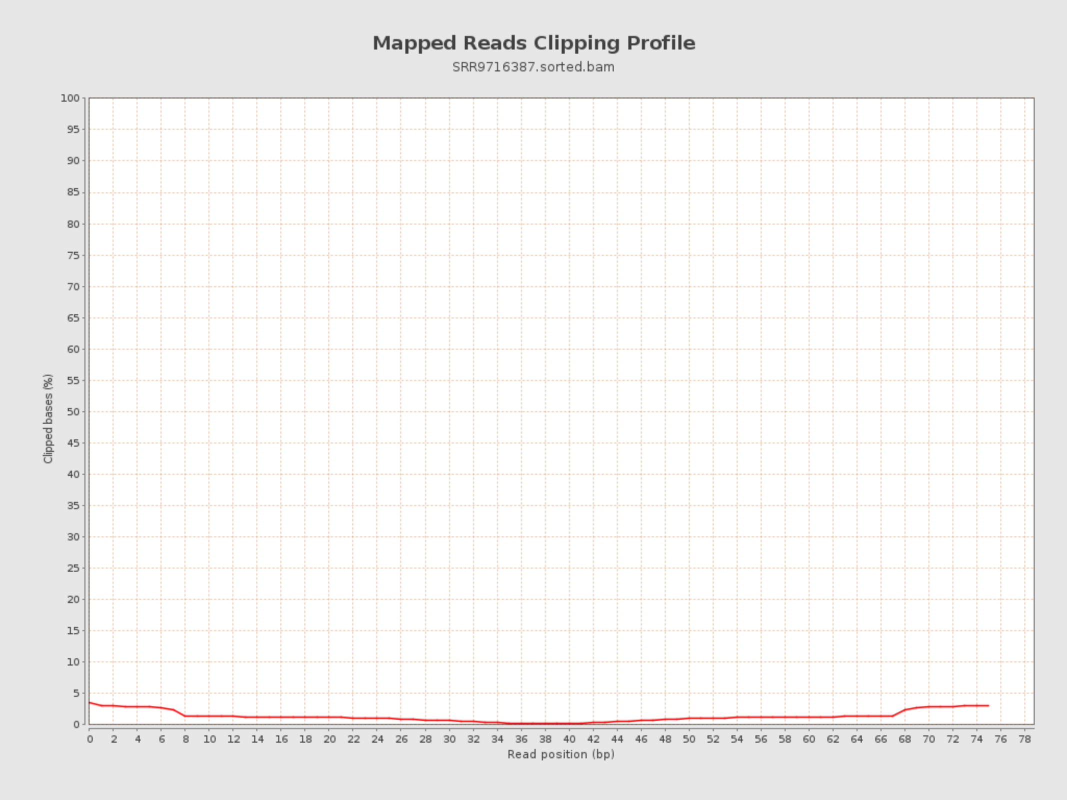
8. Results : Mapped Reads Nucleotide Content



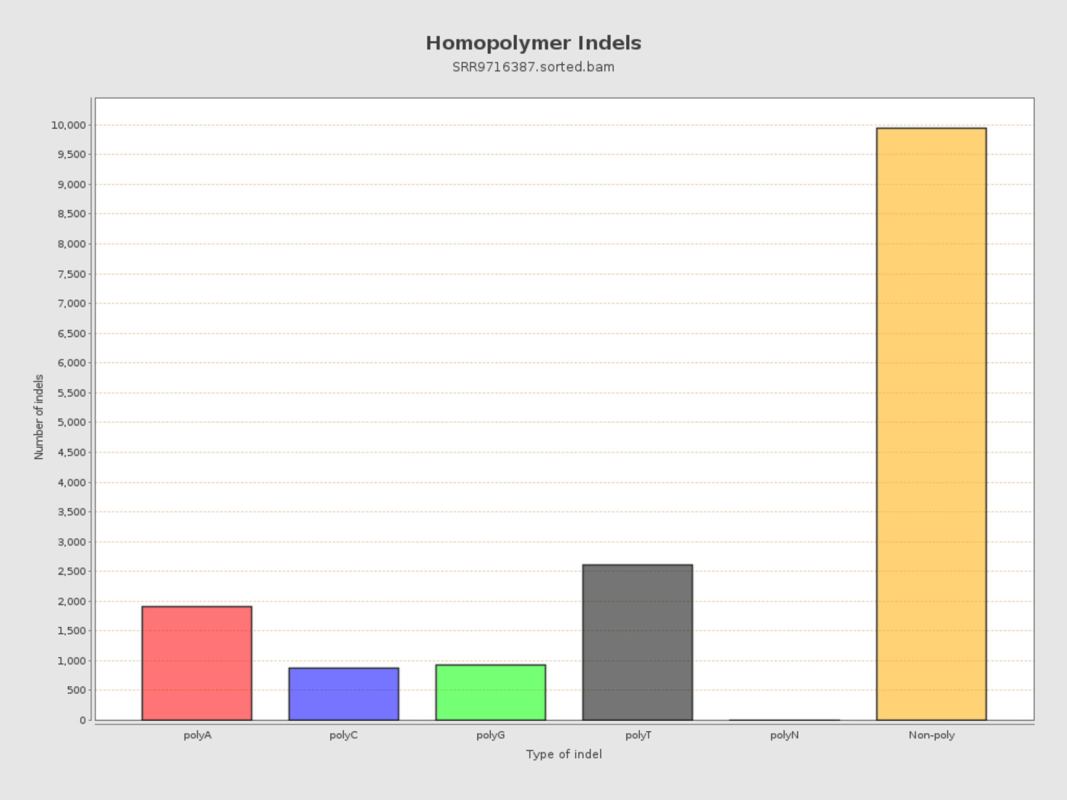
9. Results : Mapped Reads GC-content Distribution



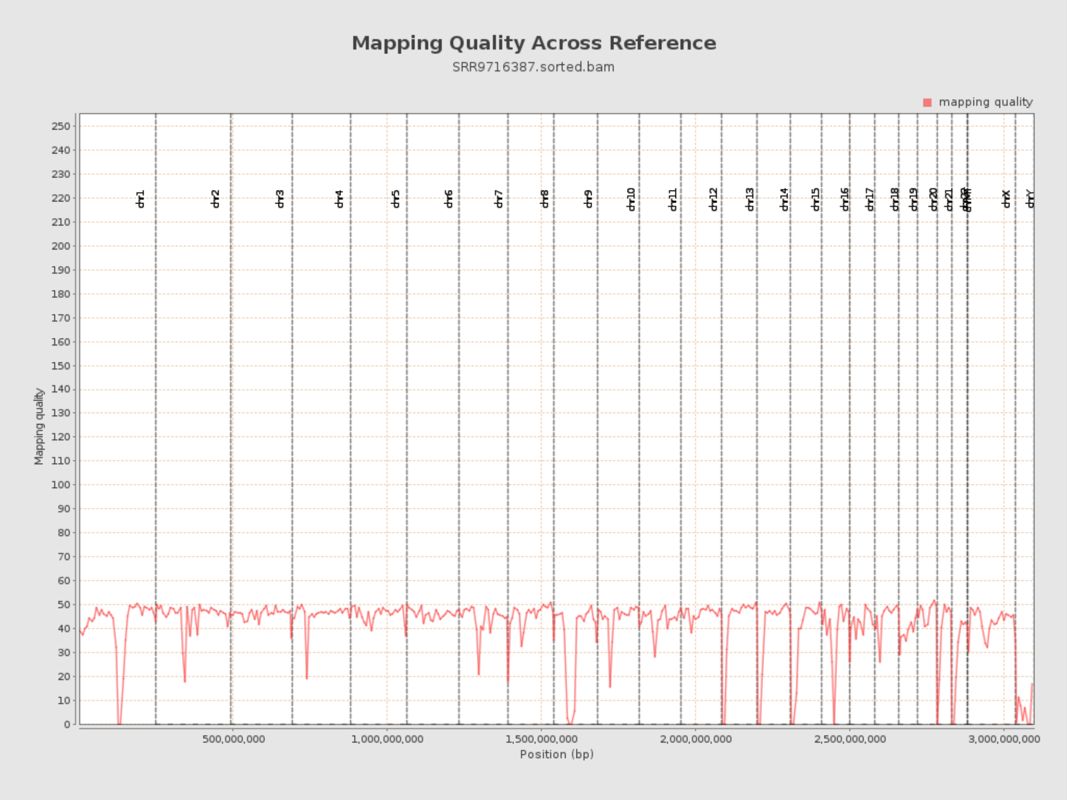
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram