Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 17:57:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716900.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_SRR9716900 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716900.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 17:57:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716900.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,215,443
Mapped reads	1,017,549 / 83.72%
Unmapped reads	197,894 / 16.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,487 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	21,936 / 1.8%
Duplication rate	1.55%
Clipped reads	1,018,470 / 83.79%

2.2. ACGT Content

Number/percentage of A's	12,472,529 / 21.96%
Number/percentage of C's	12,257,294 / 21.58%
Number/percentage of T's	17,481,857 / 30.78%
Number/percentage of G's	14,588,623 / 25.68%
Number/percentage of N's	1,690 / 0%
GC Percentage	47.26%

2.3. Coverage

Mean	0.0184

Standard Deviation	0.1665

2.4. Mapping Quality

Mean Mapping Quality	39.34

2.5. Mismatches and indels

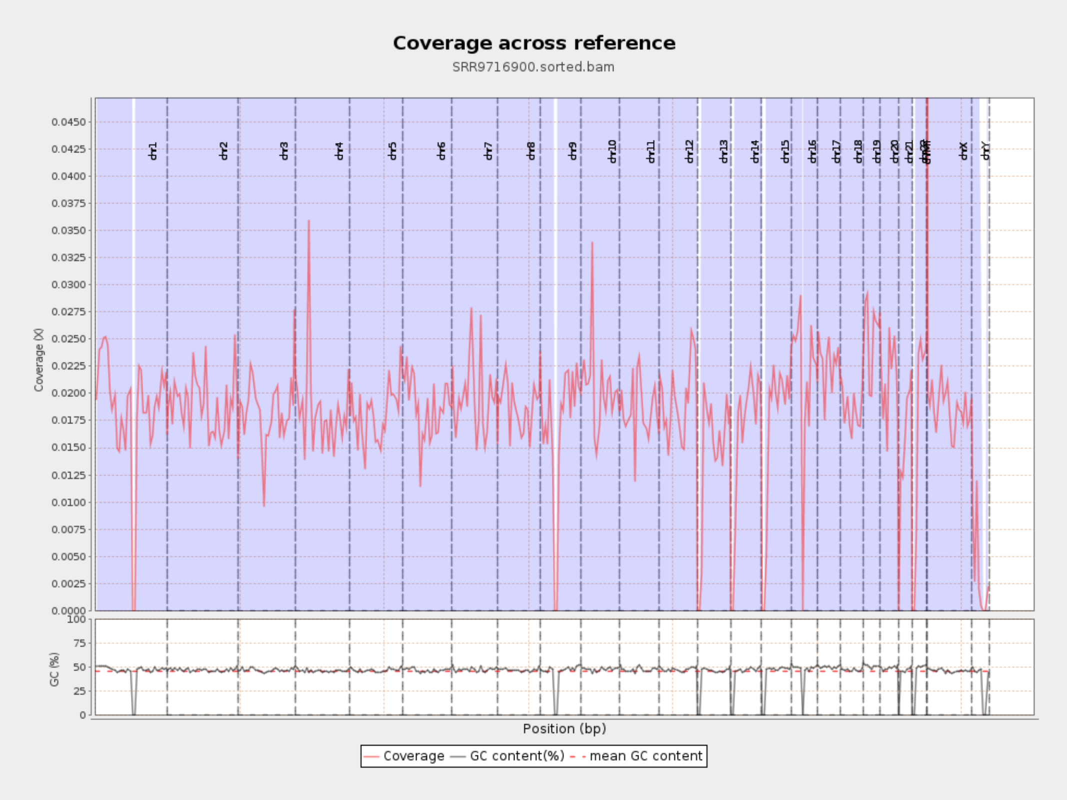
General error rate	0.54%
Mismatches	297,636
Insertions	4,295
Mapped reads with at least one insertion	0.42%
Deletions	9,662
Mapped reads with at least one deletion	0.94%
Homopolymer indels	36.81%

2.6. Chromosome stats

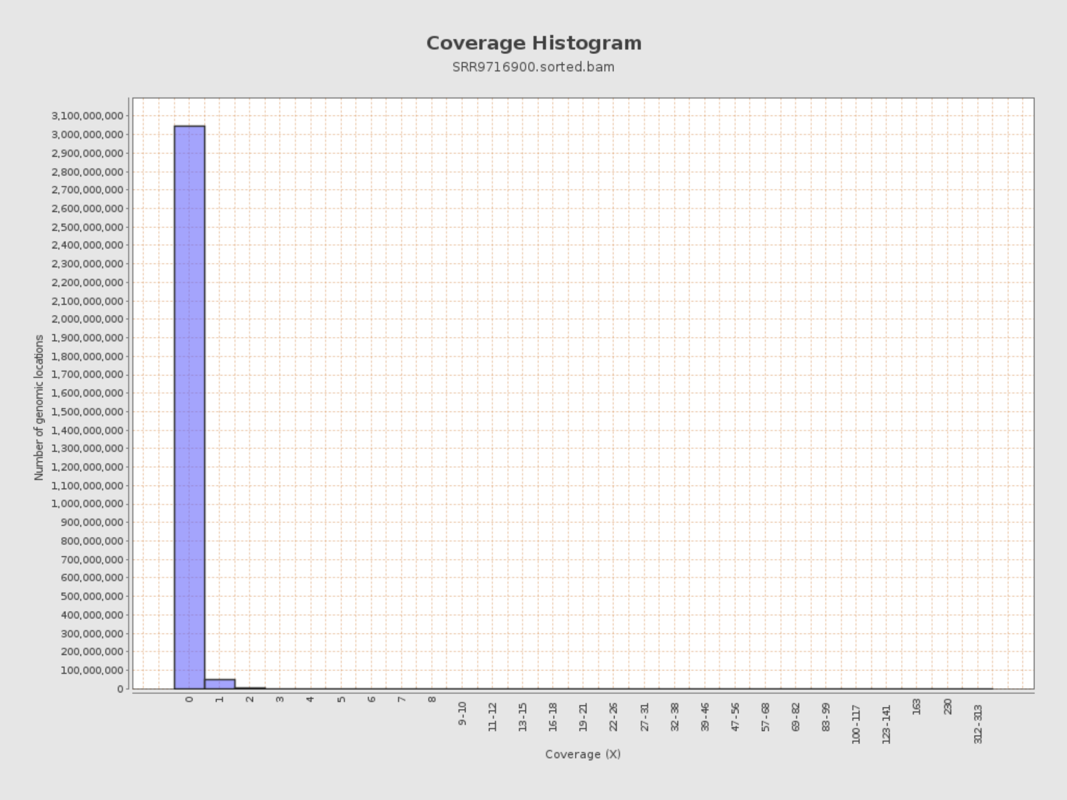
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4611731	0.0185	0.1745
chr2	243199373	4614835	0.019	0.2128
chr3	198022430	3602438	0.0182	0.1523
chr4	191154276	3538797	0.0185	0.1684
chr5	180915260	3305299	0.0183	0.1481
chr6	171115067	3205359	0.0187	0.1523
chr7	159138663	3142761	0.0197	0.1845

chr8	146364022	2749046	0.0188	0.1549
chr9	141213431	2370608	0.0168	0.1488
chr10	135534747	2792285	0.0206	0.2048
chr11	135006516	2513239	0.0186	0.1705
chr12	133851895	2591565	0.0194	0.1529
chr13	115169878	1635667	0.0142	0.1303
chr14	107349540	1720033	0.016	0.1413
chr15	102531392	1687596	0.0165	0.1417
chr16	90354753	1927331	0.0213	0.1692
chr17	81195210	1853211	0.0228	0.1696
chr18	78077248	1437826	0.0184	0.1851
chr19	59128983	1499365	0.0254	0.1969
chr20	63025520	1337474	0.0212	0.165
chr21	48129895	733109	0.0152	0.1518
chr22	51304566	847758	0.0165	0.1463
chrMT	16571	4769	0.2878	0.6099
chrX	155270560	2895662	0.0186	0.1566
chrY	59373566	200404	0.0034	0.1062

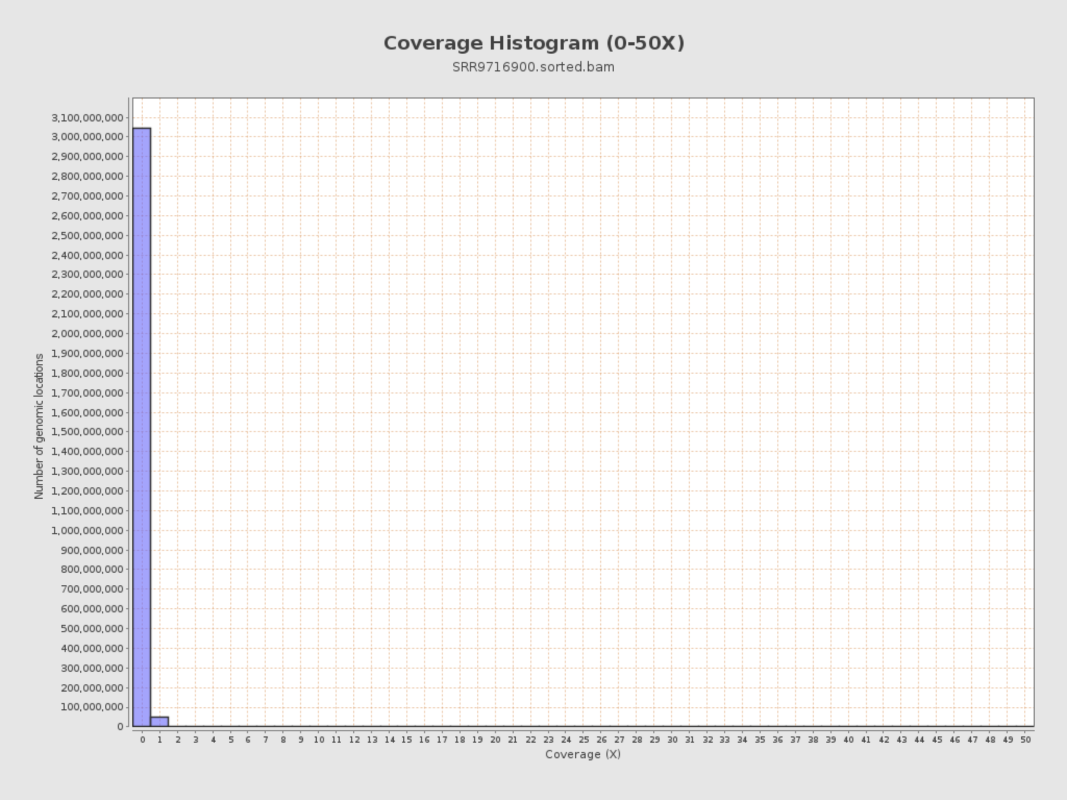
3. Results : Coverage across reference



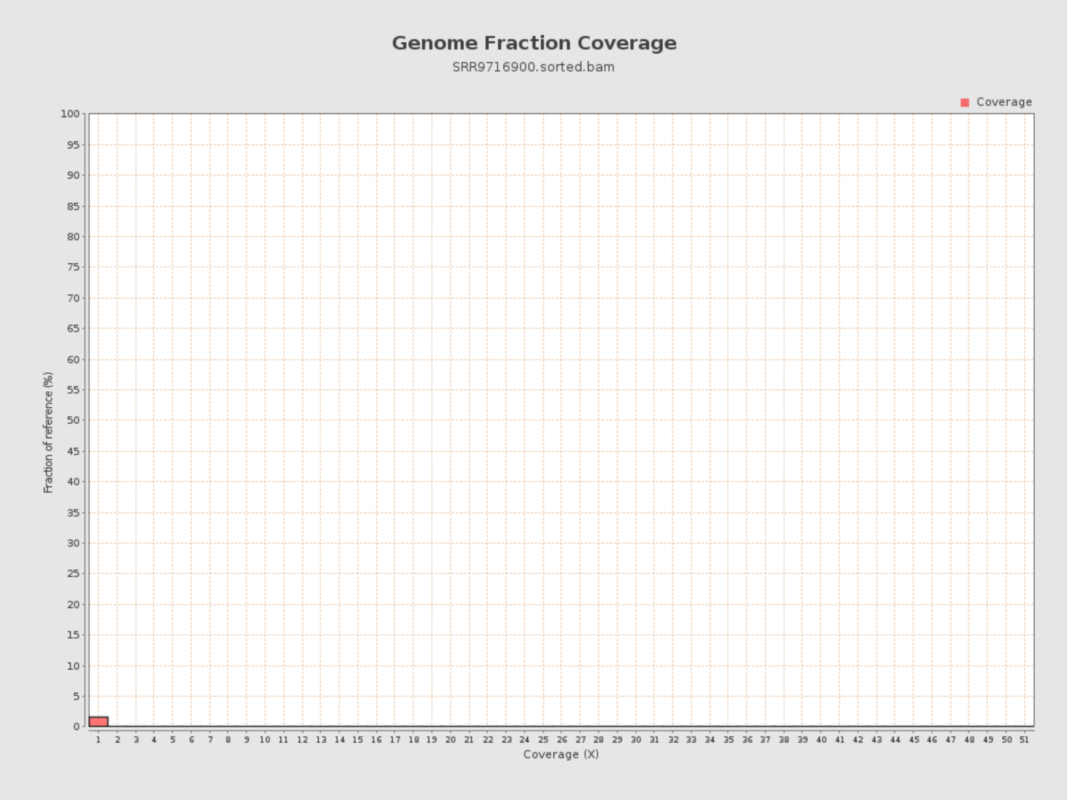
4. Results : Coverage Histogram



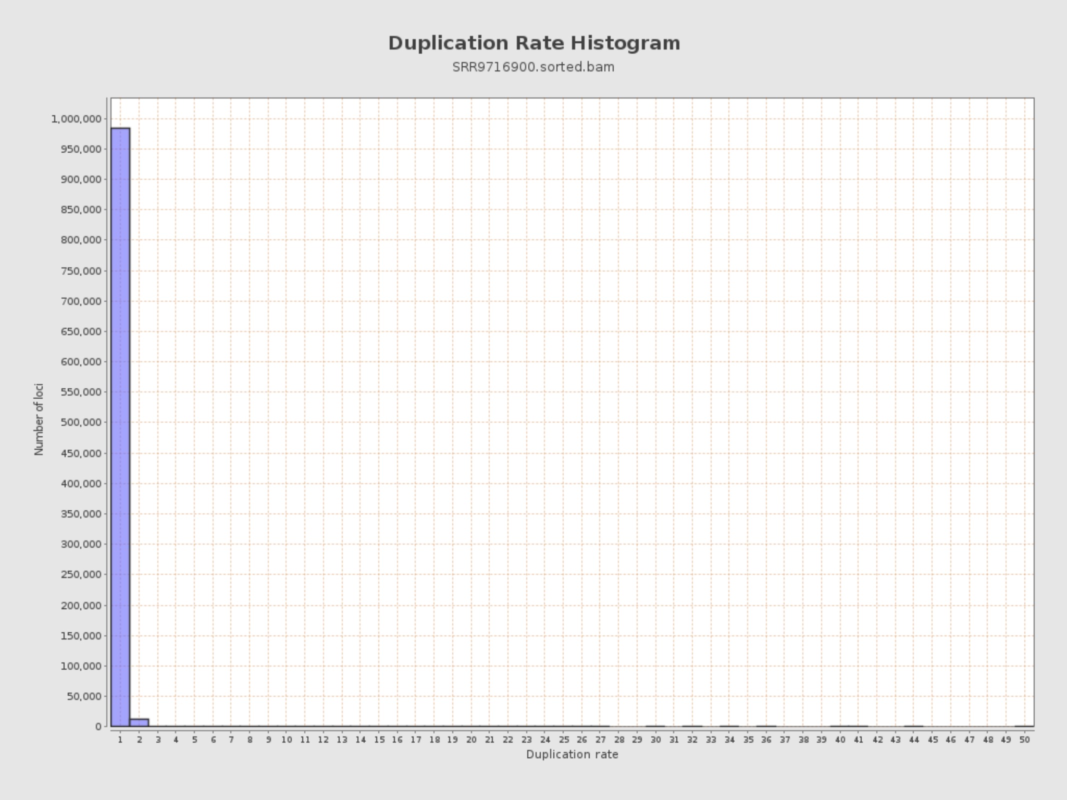
5. Results : Coverage Histogram (0-50X)



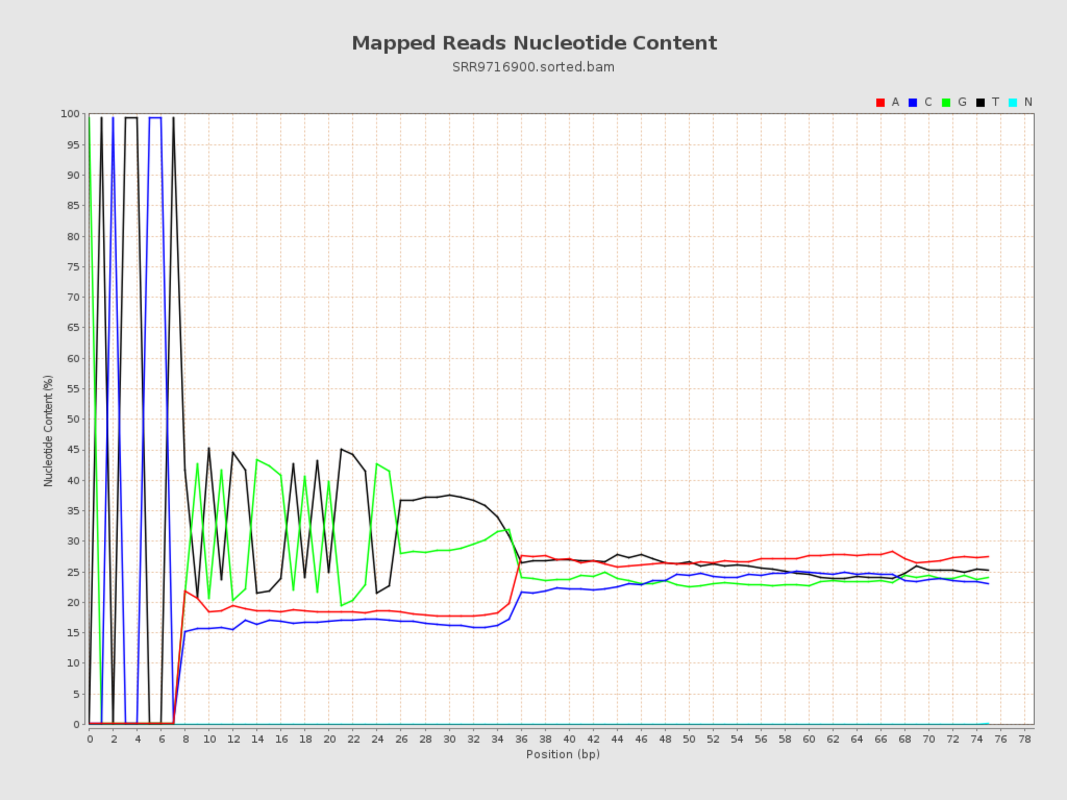
6. Results : Genome Fraction Coverage



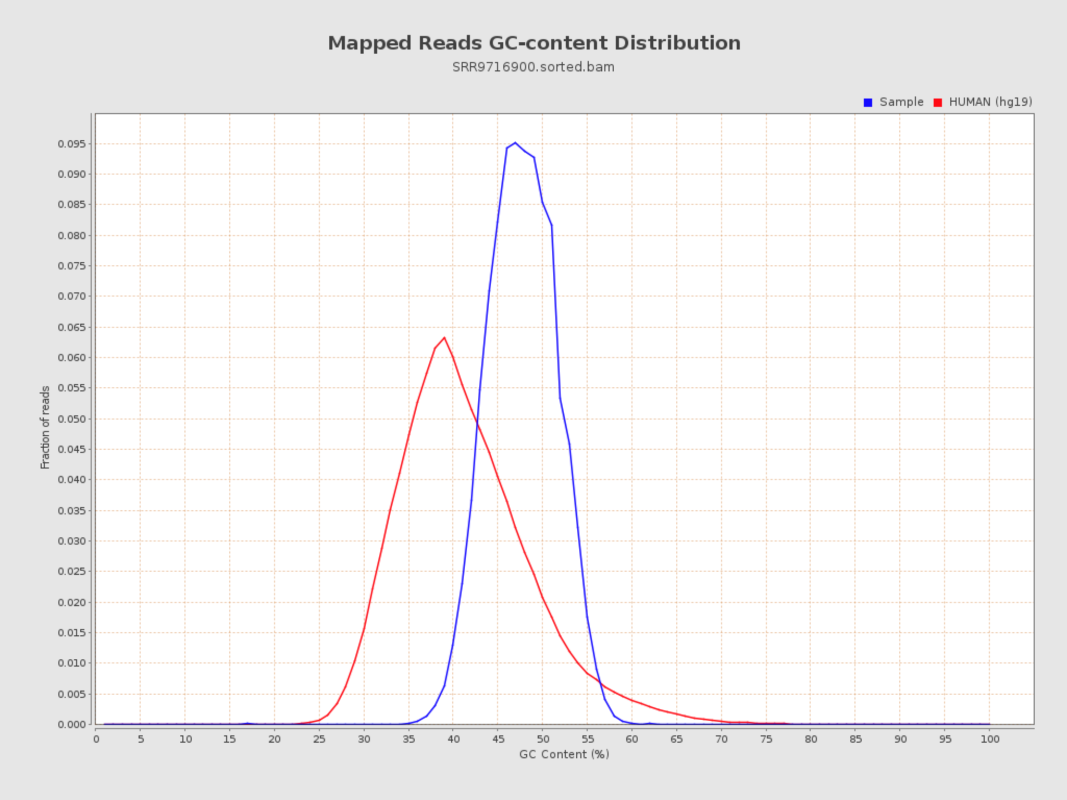
7. Results : Duplication Rate Histogram



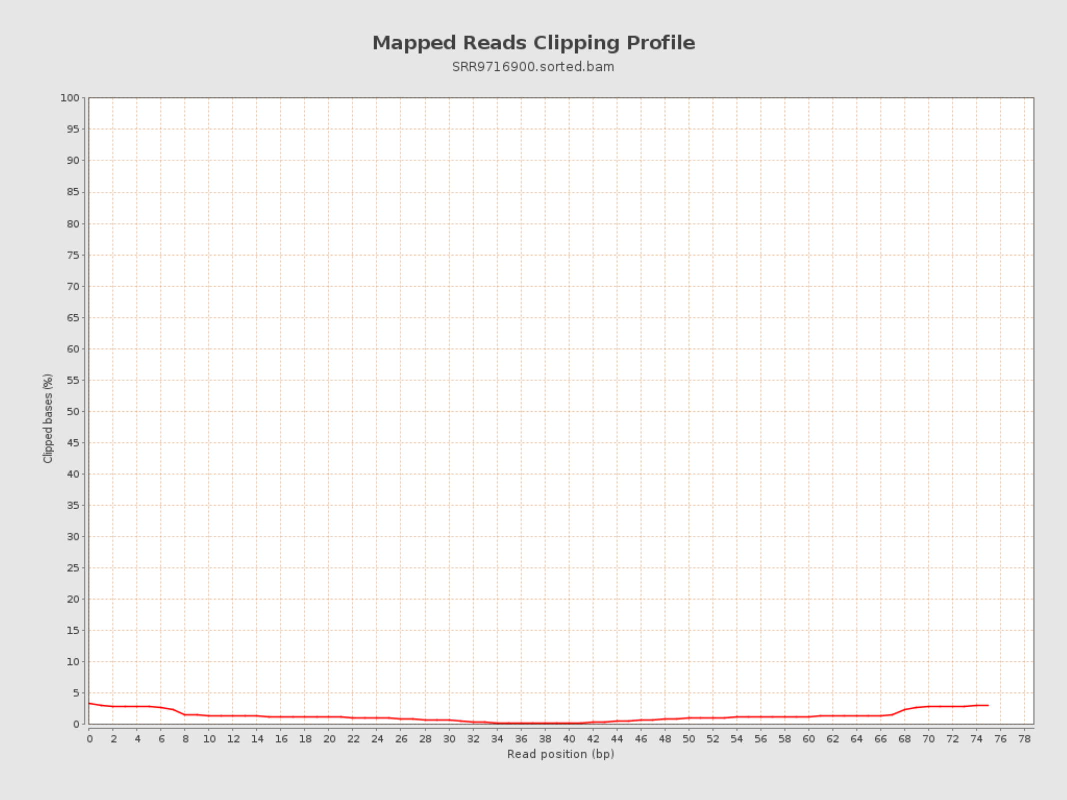
8. Results : Mapped Reads Nucleotide Content



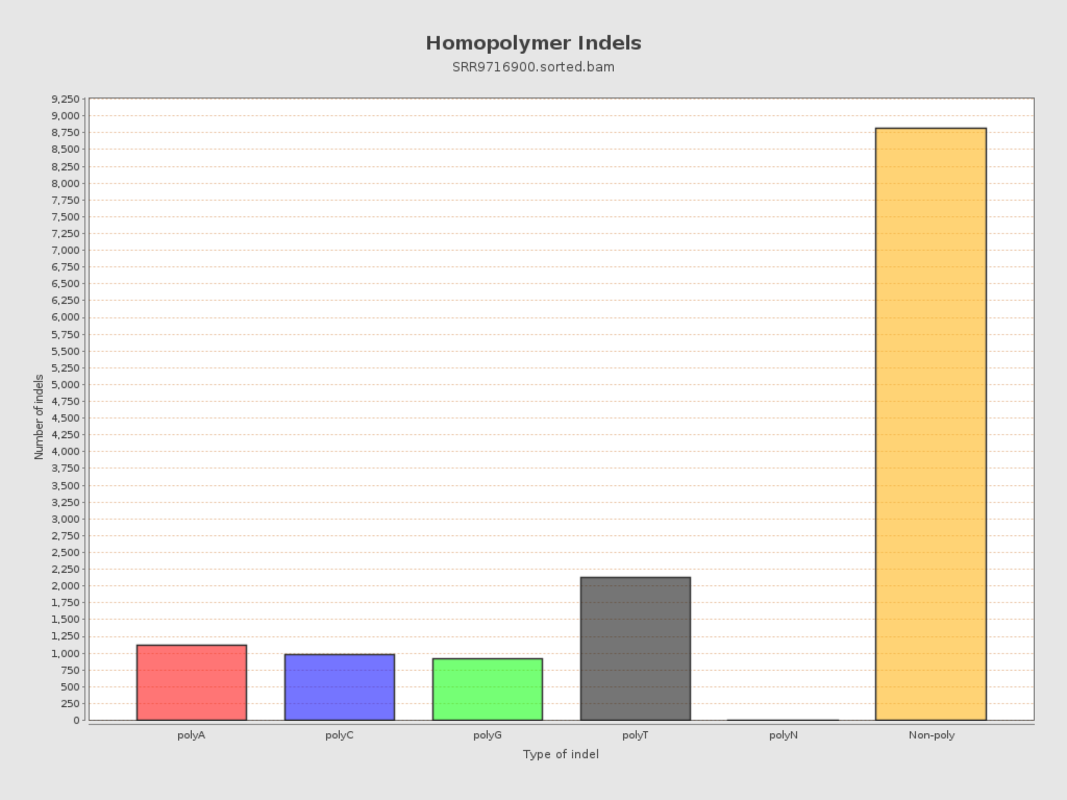
9. Results : Mapped Reads GC-content Distribution



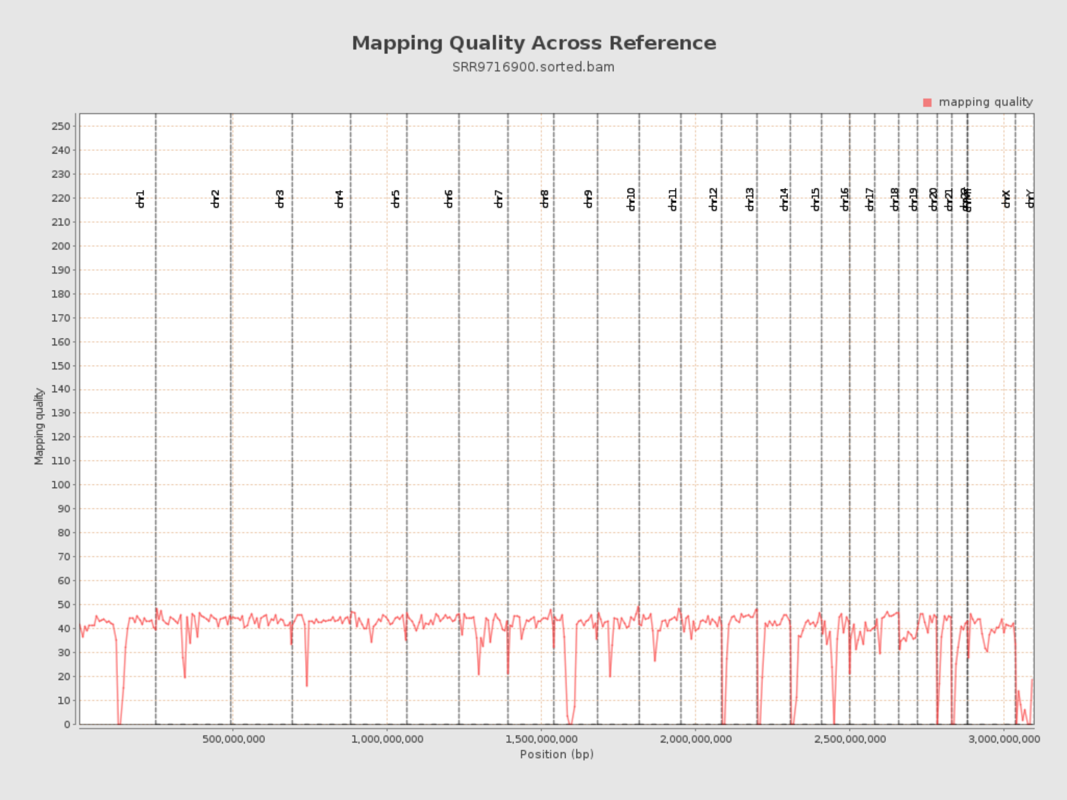
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram