Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 12:24:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716416.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_SRR9716416 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716416.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 12:24:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716416.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,019,488
Mapped reads	922,847 / 90.52%
Unmapped reads	96,641 / 9.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,225 / 0.51%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	24,580 / 2.41%
Duplication rate	2.01%
Clipped reads	926,141 / 90.84%

2.2. ACGT Content

Number/percentage of A's	13,230,110 / 24.69%
Number/percentage of C's	10,715,769 / 20%
Number/percentage of T's	16,534,480 / 30.86%
Number/percentage of G's	13,100,763 / 24.45%
Number/percentage of N's	729 / 0%
GC Percentage	44.45%

2.3. Coverage

Mean	0.0173

Standard Deviation	0.1796

2.4. Mapping Quality

Mean Mapping Quality	44.29

2.5. Mismatches and indels

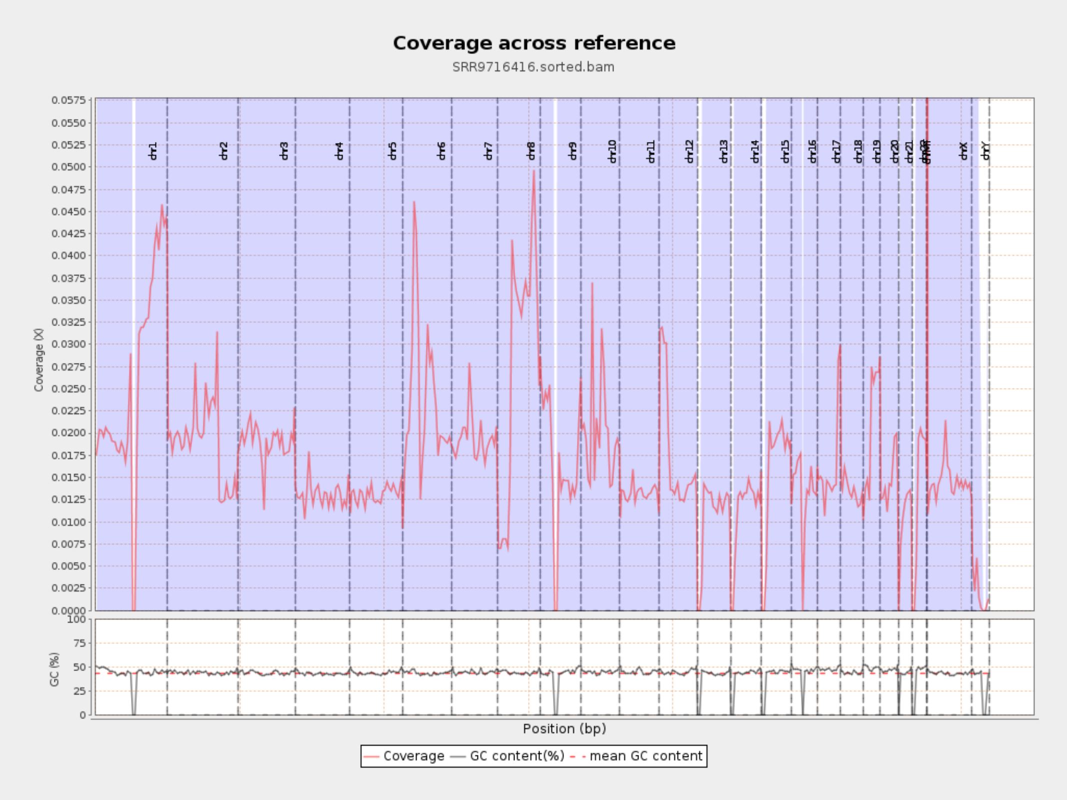
General error rate	0.5%
Mismatches	262,350
Insertions	3,346
Mapped reads with at least one insertion	0.36%
Deletions	9,519
Mapped reads with at least one deletion	1.02%
Homopolymer indels	42.81%

2.6. Chromosome stats

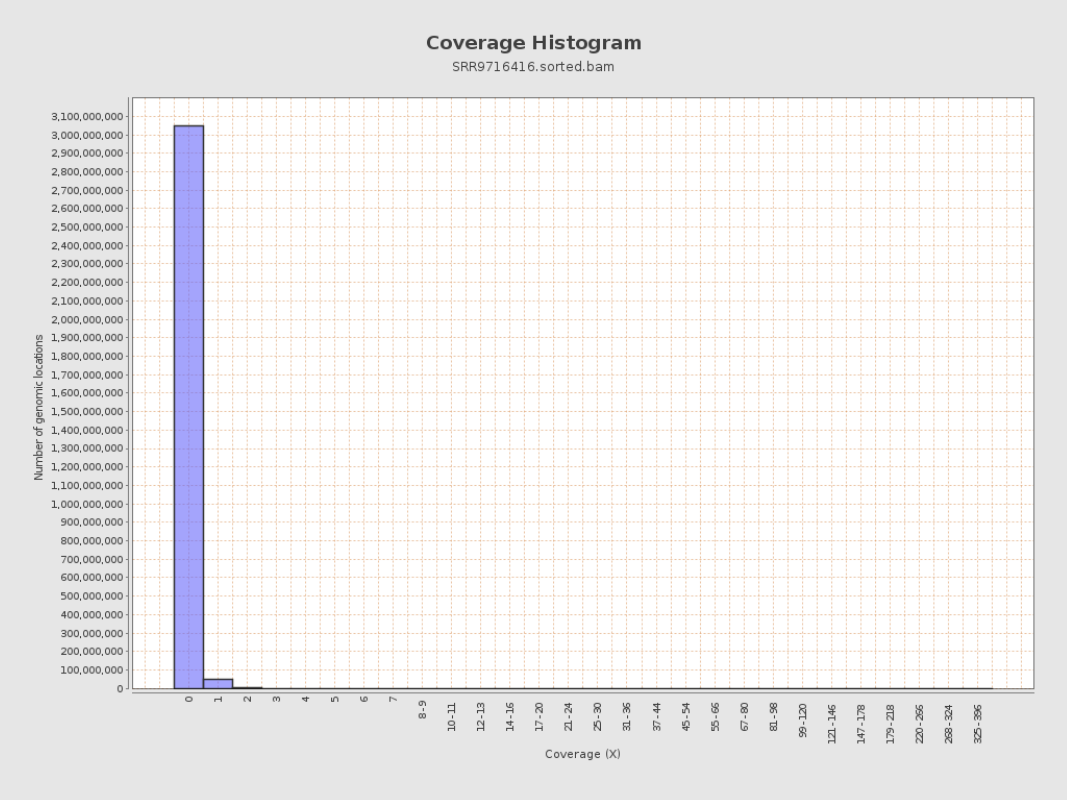
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6467484	0.0259	0.305
chr2	243199373	4637216	0.0191	0.2221
chr3	198022430	3766150	0.019	0.1477
chr4	191154276	2496573	0.0131	0.1251
chr5	180915260	2386088	0.0132	0.1221
chr6	171115067	4058156	0.0237	0.1895
chr7	159138663	3110550	0.0195	0.2184

chr8	146364022	4123927	0.0282	0.1906
chr9	141213431	2275170	0.0161	0.1687
chr10	135534747	2768364	0.0204	0.1935
chr11	135006516	1797768	0.0133	0.1436
chr12	133851895	2401206	0.0179	0.1443
chr13	115169878	1211677	0.0105	0.109
chr14	107349540	1184017	0.011	0.1213
chr15	102531392	1606697	0.0157	0.135
chr16	90354753	1187001	0.0131	0.1312
chr17	81195210	1312628	0.0162	0.1366
chr18	78077248	1048211	0.0134	0.2432
chr19	59128983	1233799	0.0209	0.2118
chr20	63025520	936533	0.0149	0.1297
chr21	48129895	501411	0.0104	0.1157
chr22	51304566	684743	0.0133	0.1226
chrMT	16571	18091	1.0917	1.2871
chrX	155270560	2267227	0.0146	0.1395
chrY	59373566	116059	0.002	0.0563

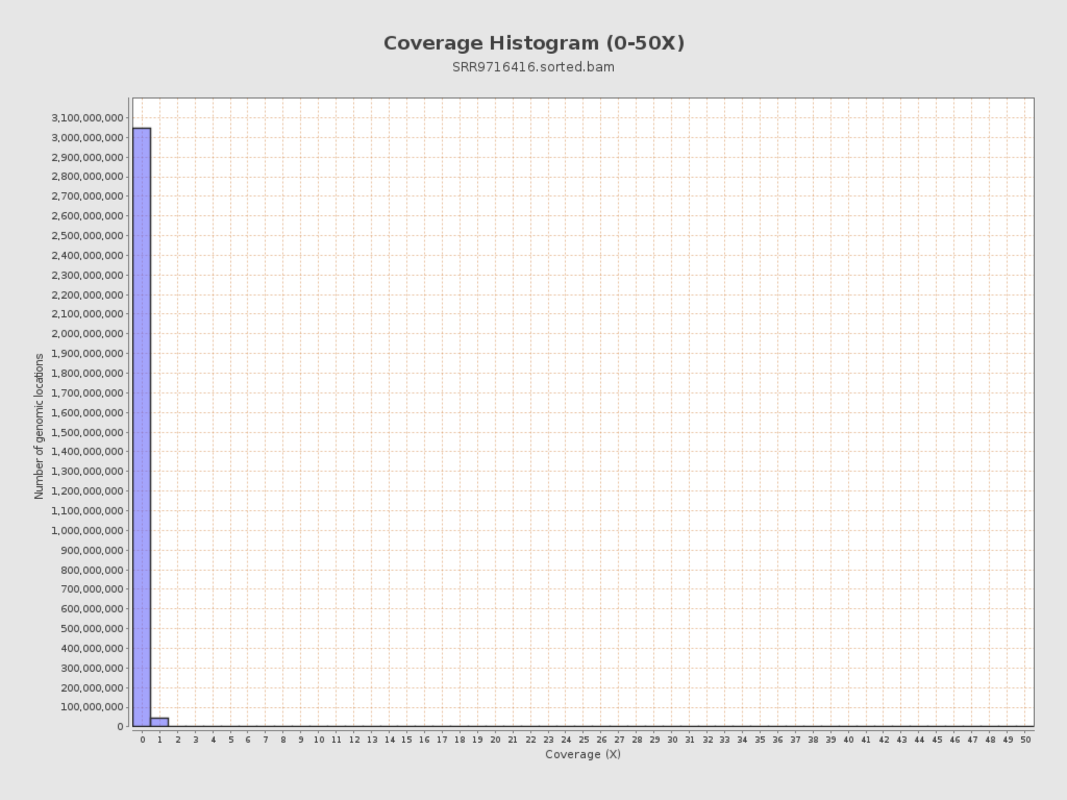
3. Results : Coverage across reference



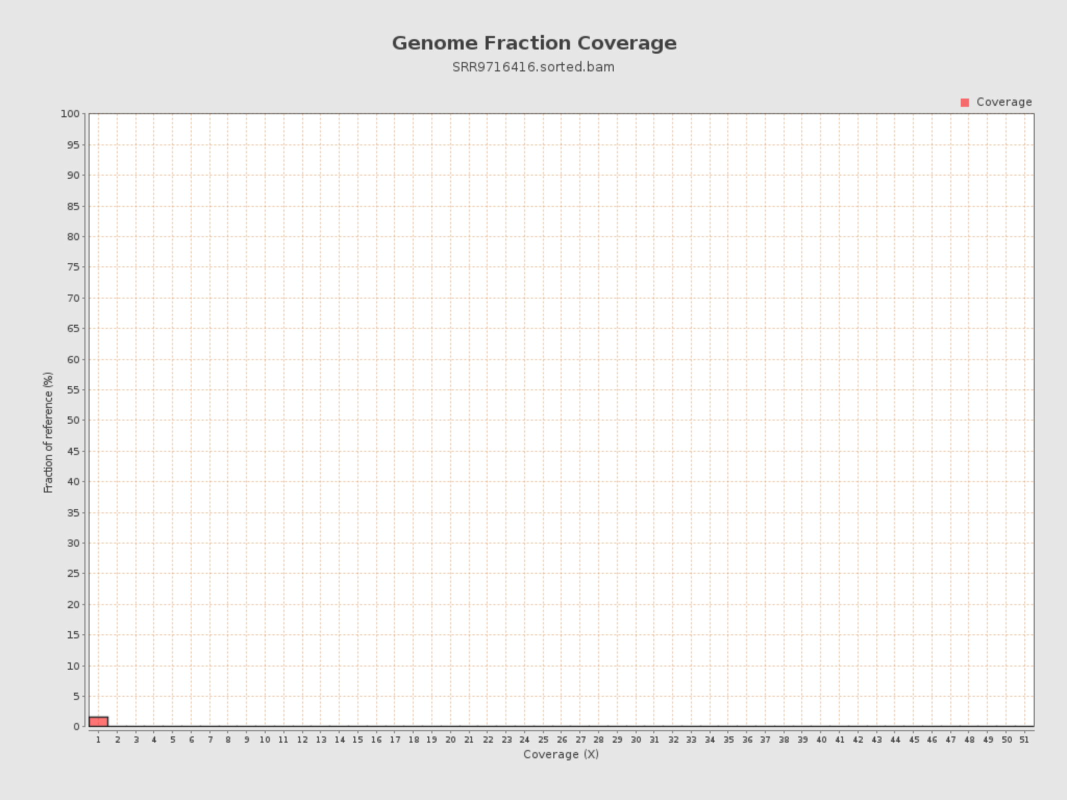
4. Results : Coverage Histogram



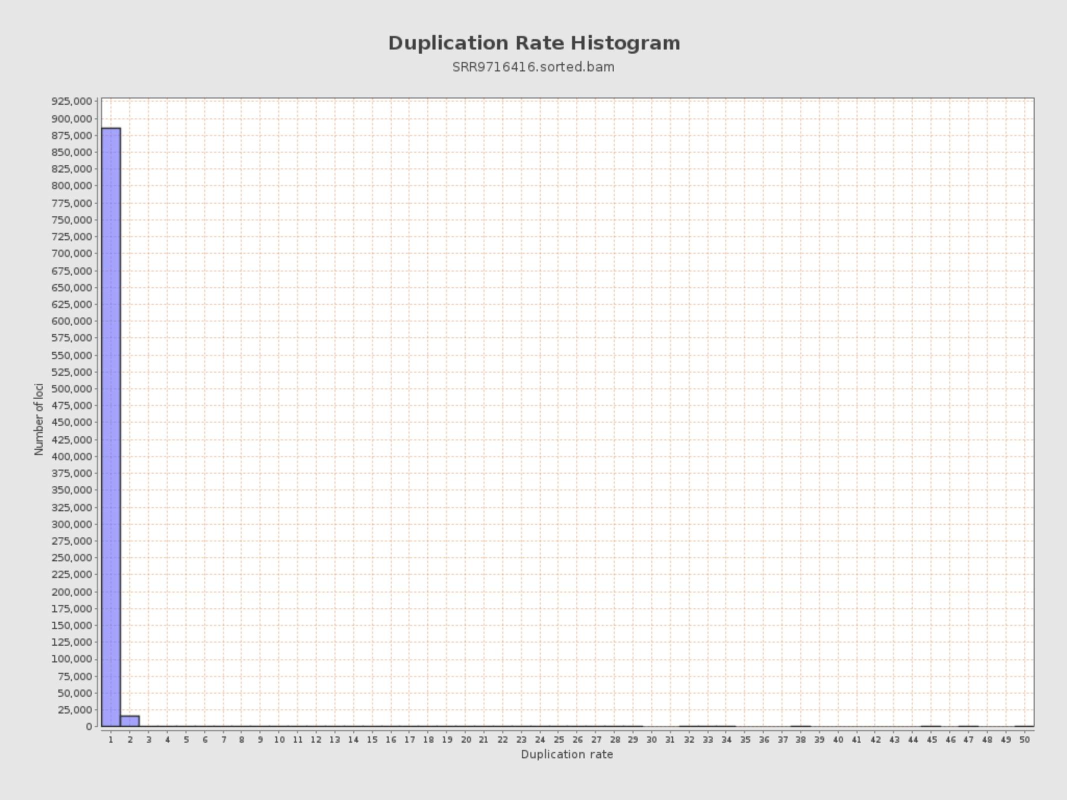
5. Results : Coverage Histogram (0-50X)



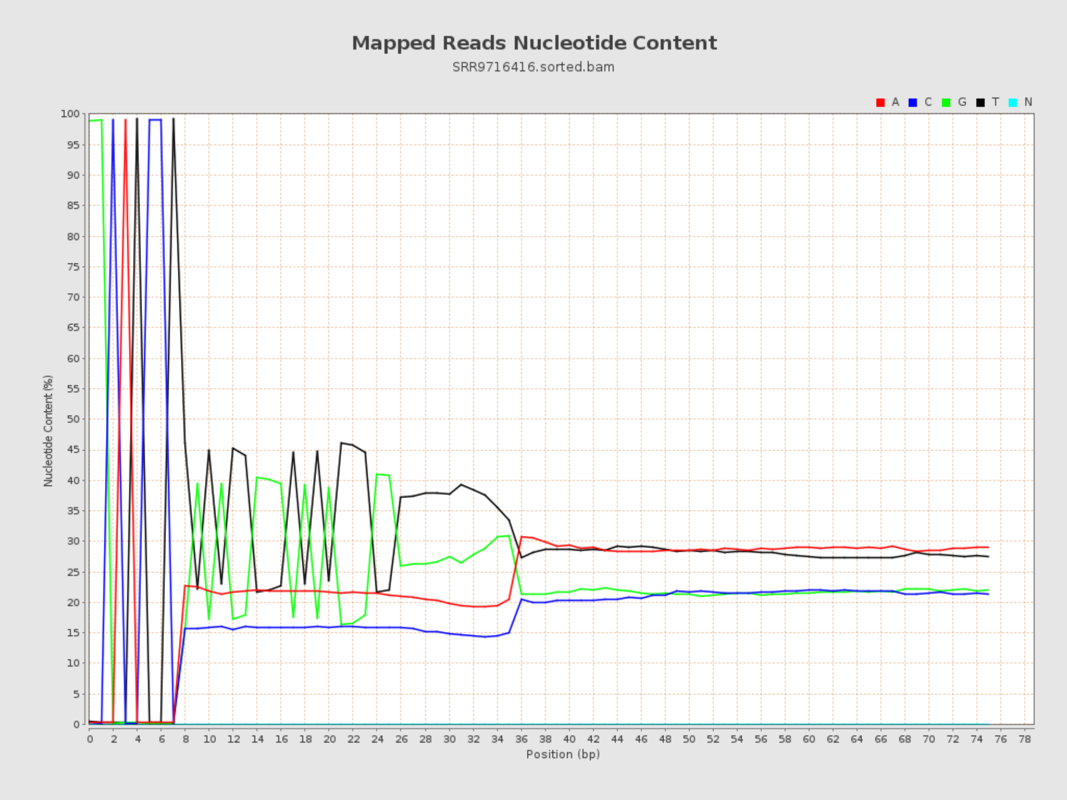
6. Results : Genome Fraction Coverage



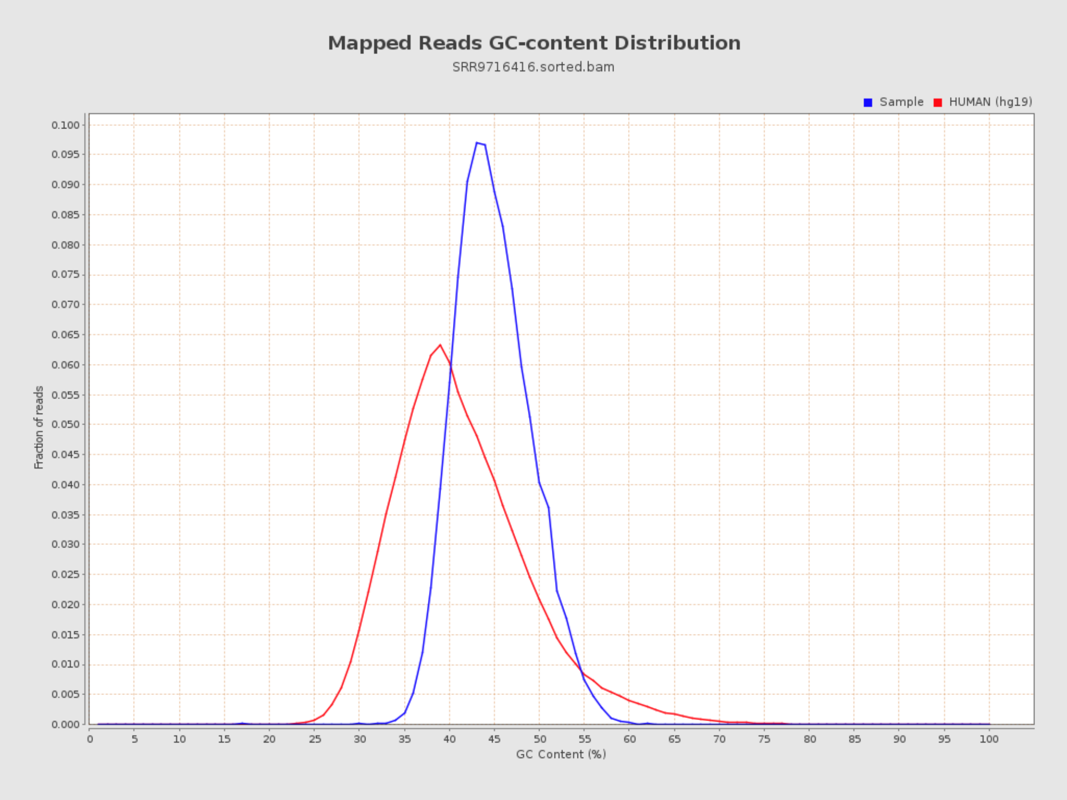
7. Results : Duplication Rate Histogram



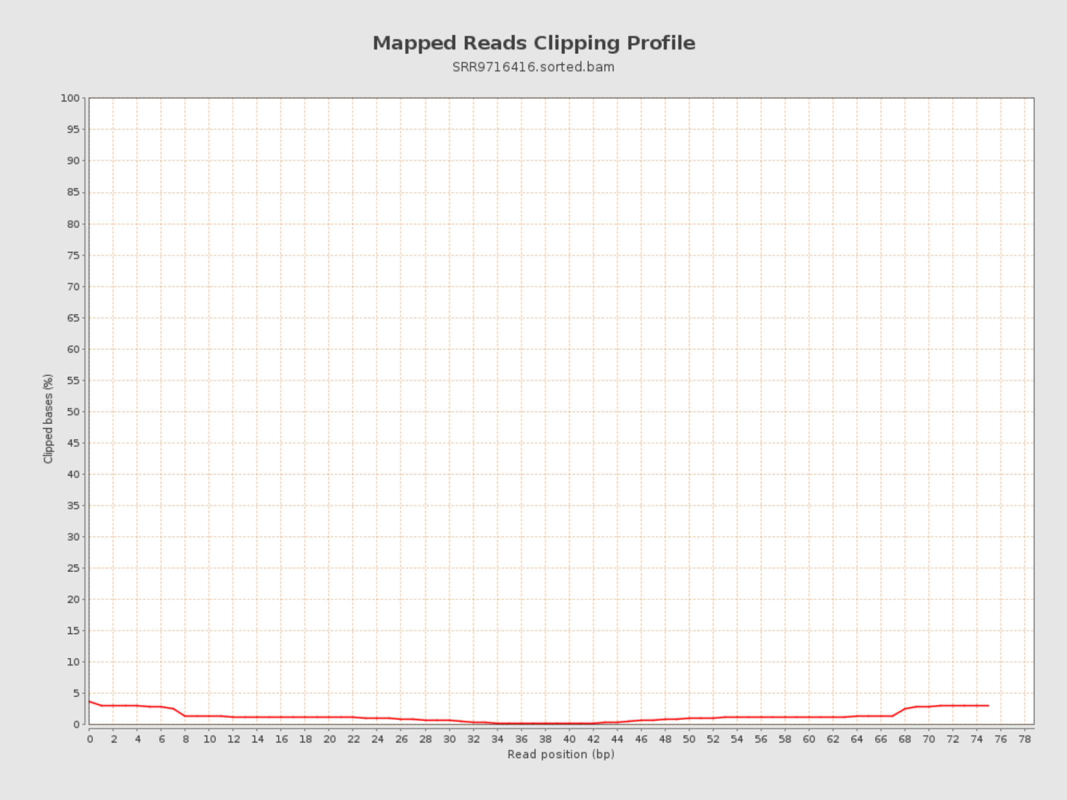
8. Results : Mapped Reads Nucleotide Content



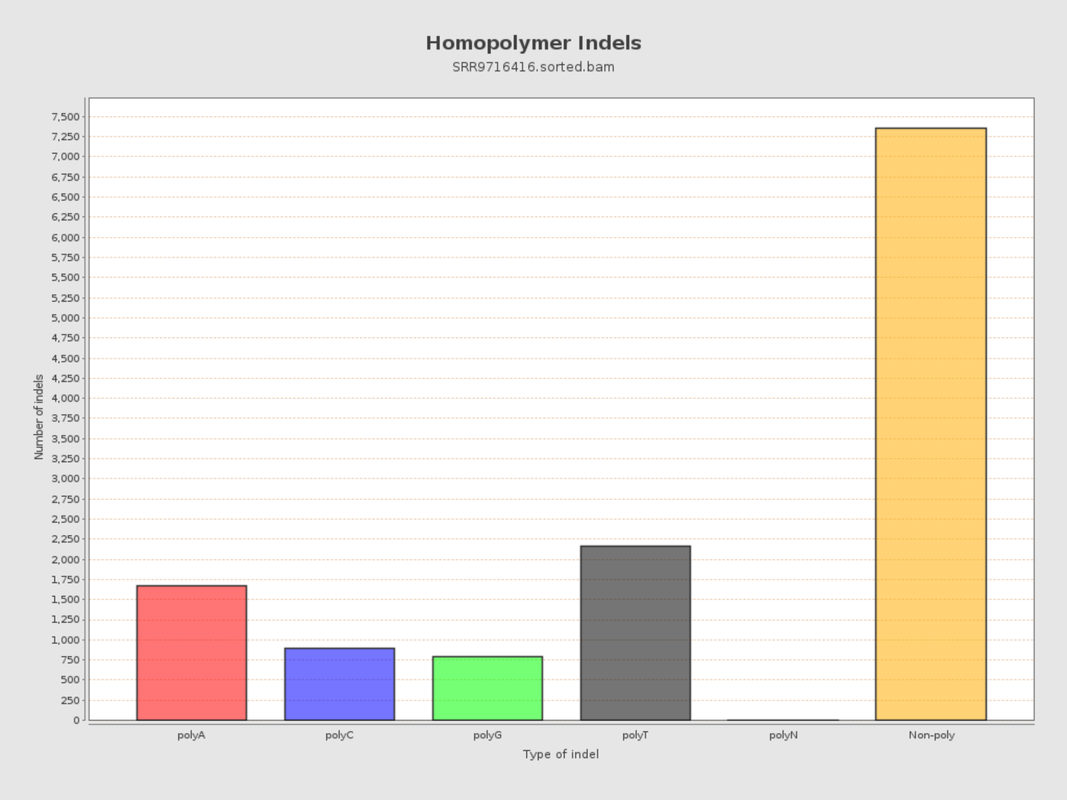
9. Results : Mapped Reads GC-content Distribution



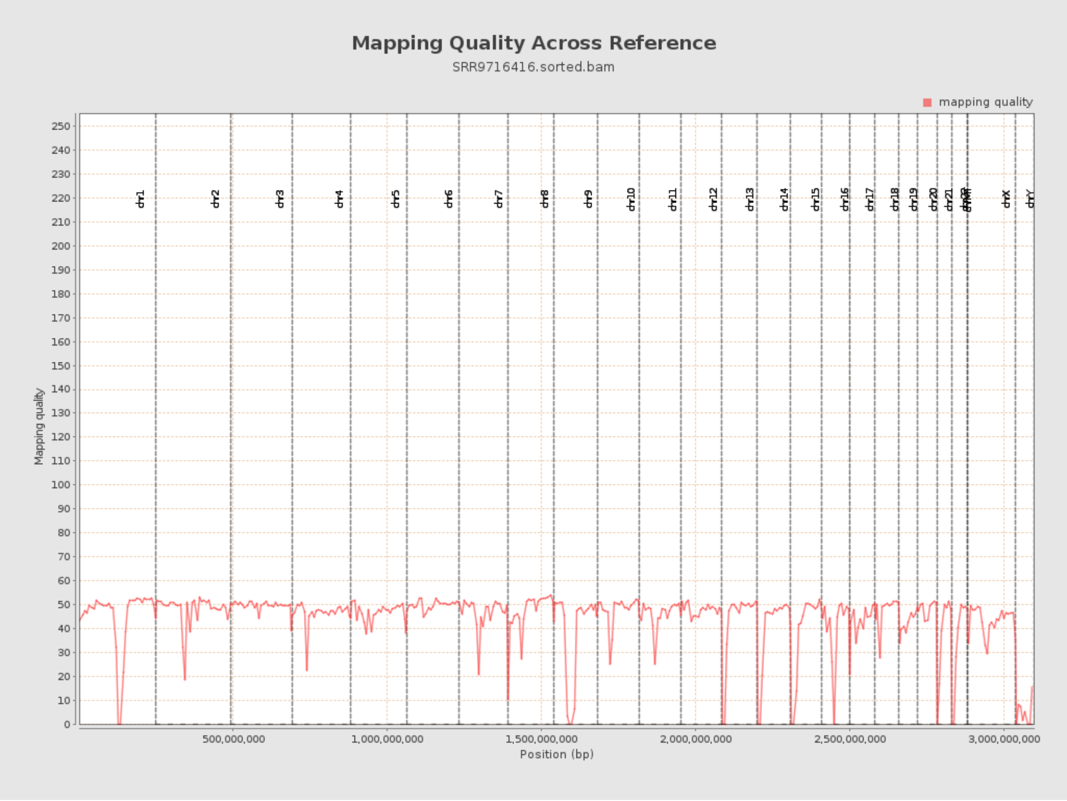
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram