Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 12:05:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716408.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_SRR9716408 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716408.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 12:05:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716408.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,114,125
Mapped reads	1,021,024 / 91.64%
Unmapped reads	93,101 / 8.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,385 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	29,897 / 2.68%
Duplication rate	2.04%
Clipped reads	1,021,620 / 91.7%

2.2. ACGT Content

Number/percentage of A's	14,859,606 / 25.19%
Number/percentage of C's	11,919,076 / 20.21%
Number/percentage of T's	18,164,235 / 30.8%
Number/percentage of G's	14,040,260 / 23.8%
Number/percentage of N's	1,082 / 0%
GC Percentage	44.01%

2.3. Coverage

Mean	0.0191

Standard Deviation	0.2015

2.4. Mapping Quality

Mean Mapping Quality	44.16

2.5. Mismatches and indels

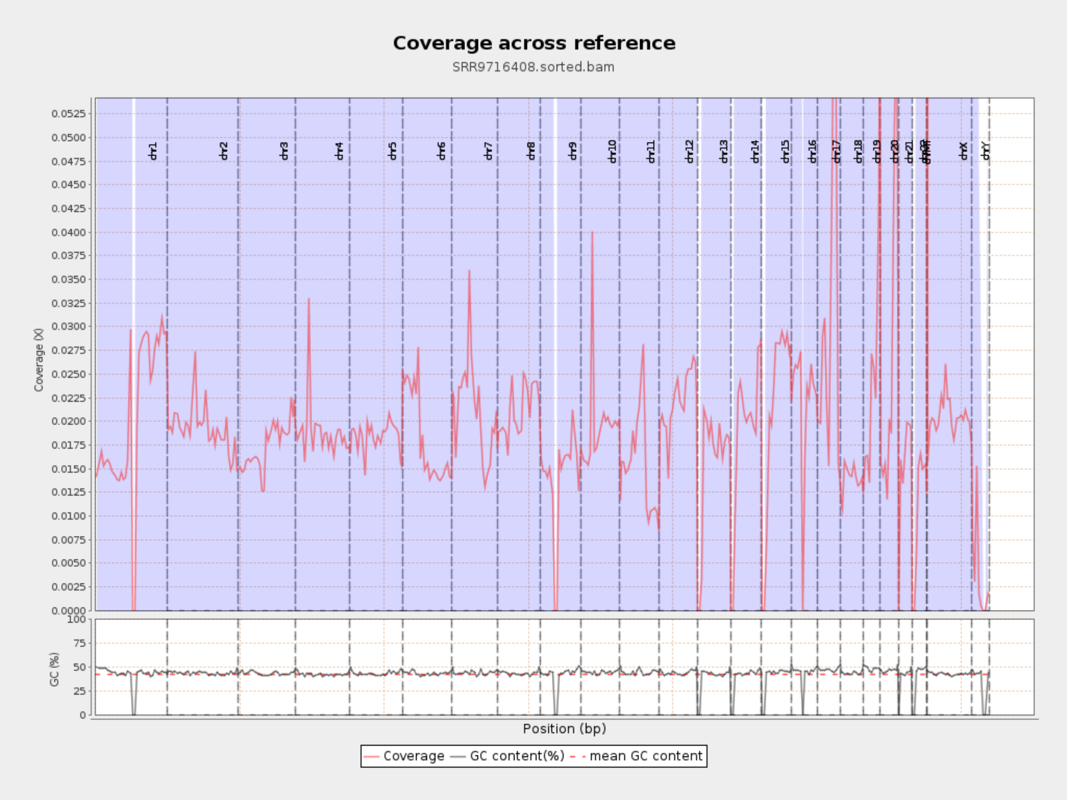
General error rate	0.52%
Mismatches	299,178
Insertions	4,523
Mapped reads with at least one insertion	0.44%
Deletions	11,712
Mapped reads with at least one deletion	1.14%
Homopolymer indels	42.11%

2.6. Chromosome stats

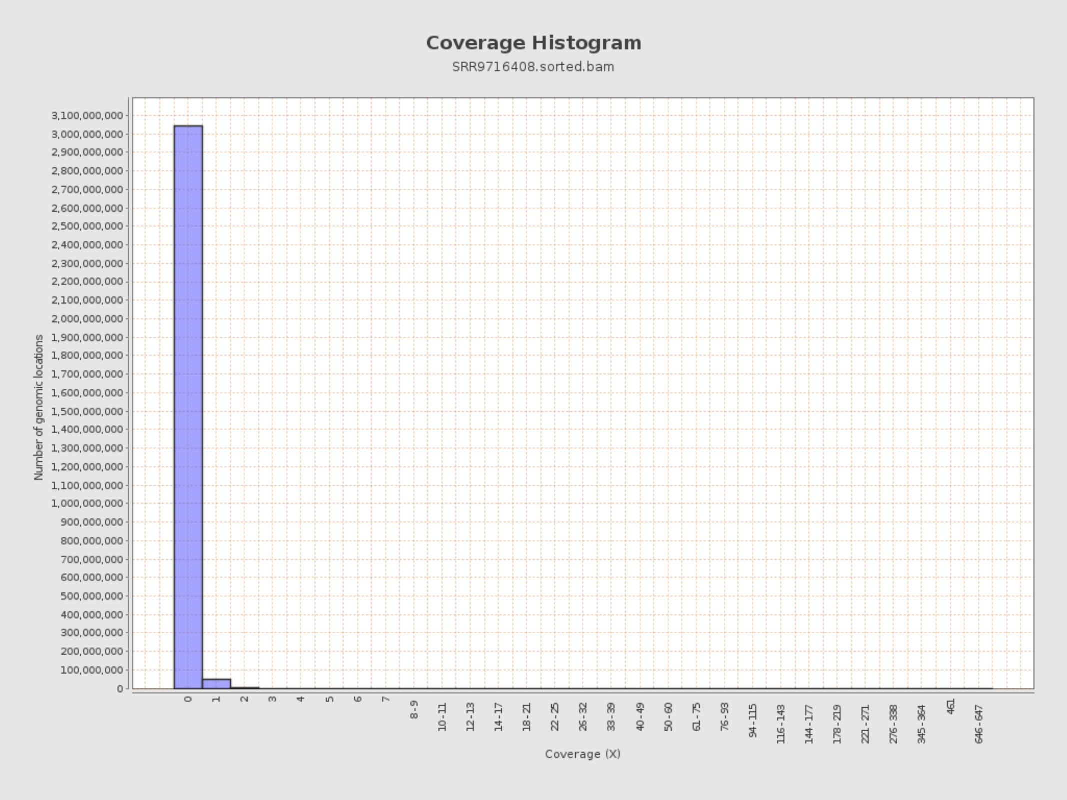
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5001525	0.0201	0.294
chr2	243199373	4684805	0.0193	0.2971
chr3	198022430	3432065	0.0173	0.1405
chr4	191154276	3618366	0.0189	0.1648
chr5	180915260	3354347	0.0185	0.1437
chr6	171115067	3132644	0.0183	0.162
chr7	159138663	3387896	0.0213	0.2566

chr8	146364022	3113756	0.0213	0.2469
chr9	141213431	1994426	0.0141	0.1509
chr10	135534747	2657864	0.0196	0.2152
chr11	135006516	2126721	0.0158	0.1585
chr12	133851895	2967697	0.0222	0.1581
chr13	115169878	1768417	0.0154	0.1318
chr14	107349540	2007822	0.0187	0.147
chr15	102531392	2160396	0.0211	0.1557
chr16	90354753	1966709	0.0218	0.1635
chr17	81195210	2552400	0.0314	0.1919
chr18	78077248	1086264	0.0139	0.2259
chr19	59128983	1468175	0.0248	0.2467
chr20	63025520	1745751	0.0277	0.1807
chr21	48129895	754385	0.0157	0.1531
chr22	51304566	551050	0.0107	0.1103
chrMT	16571	71897	4.3387	3.2481
chrX	155270560	3182976	0.0205	0.1612
chrY	59373566	214824	0.0036	0.1598

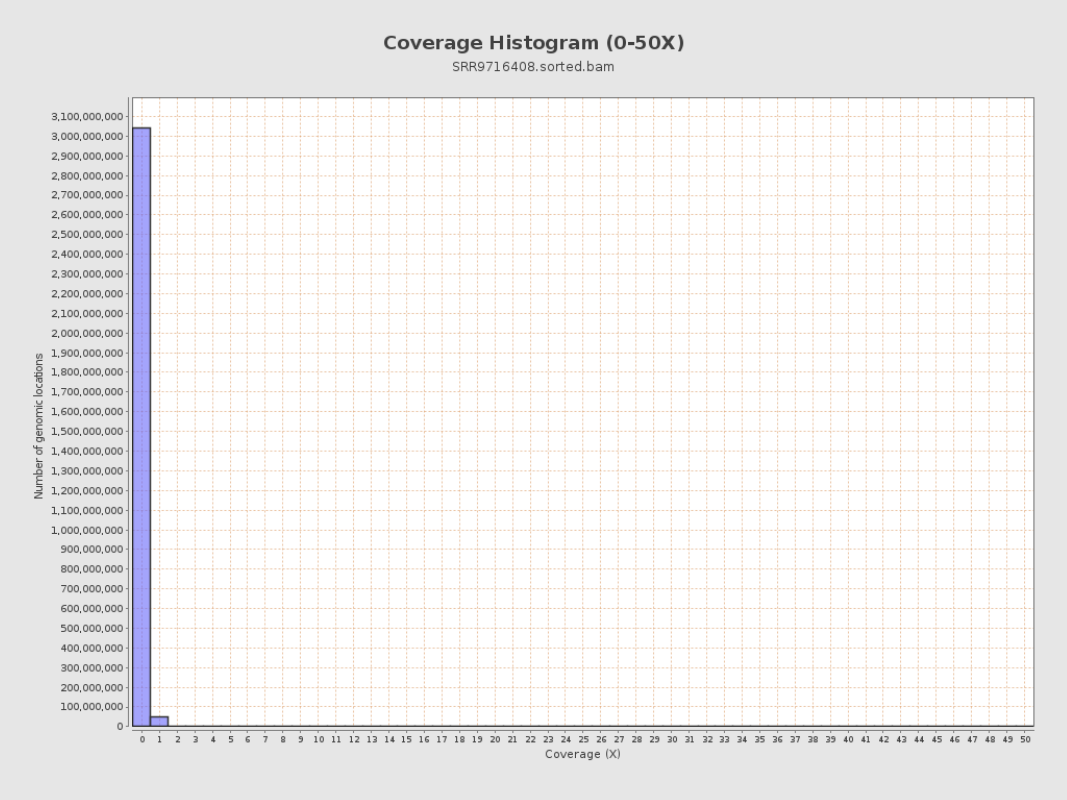
3. Results : Coverage across reference



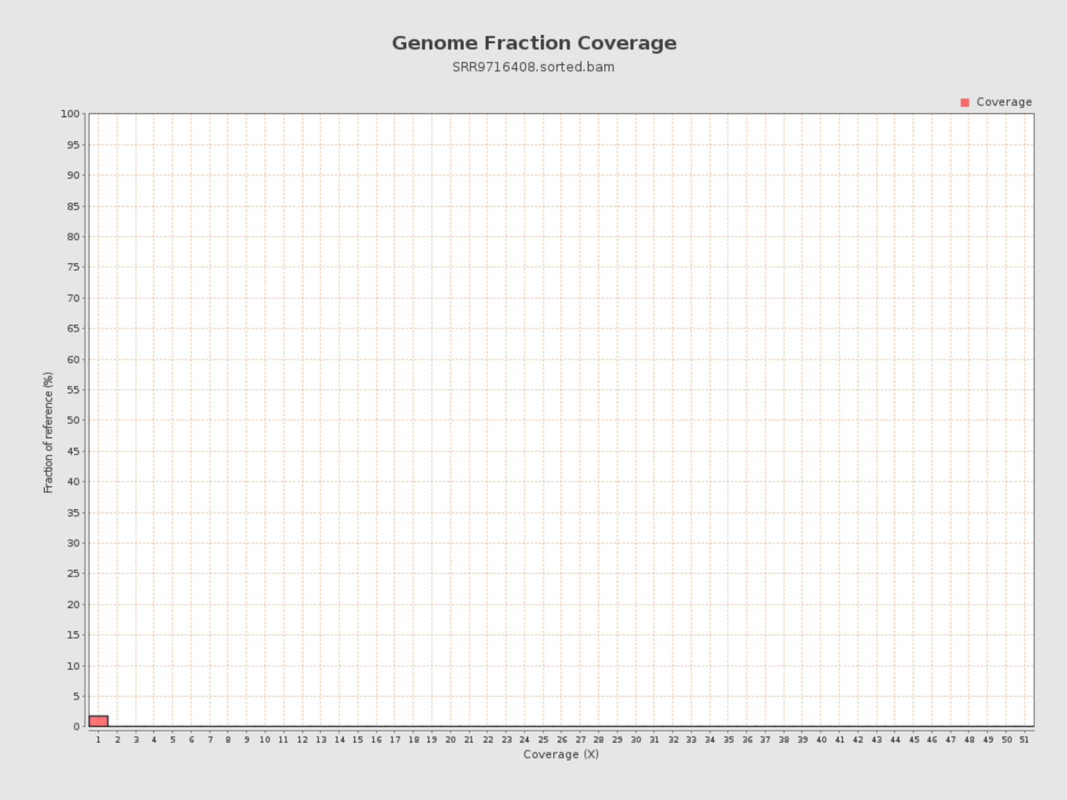
4. Results : Coverage Histogram



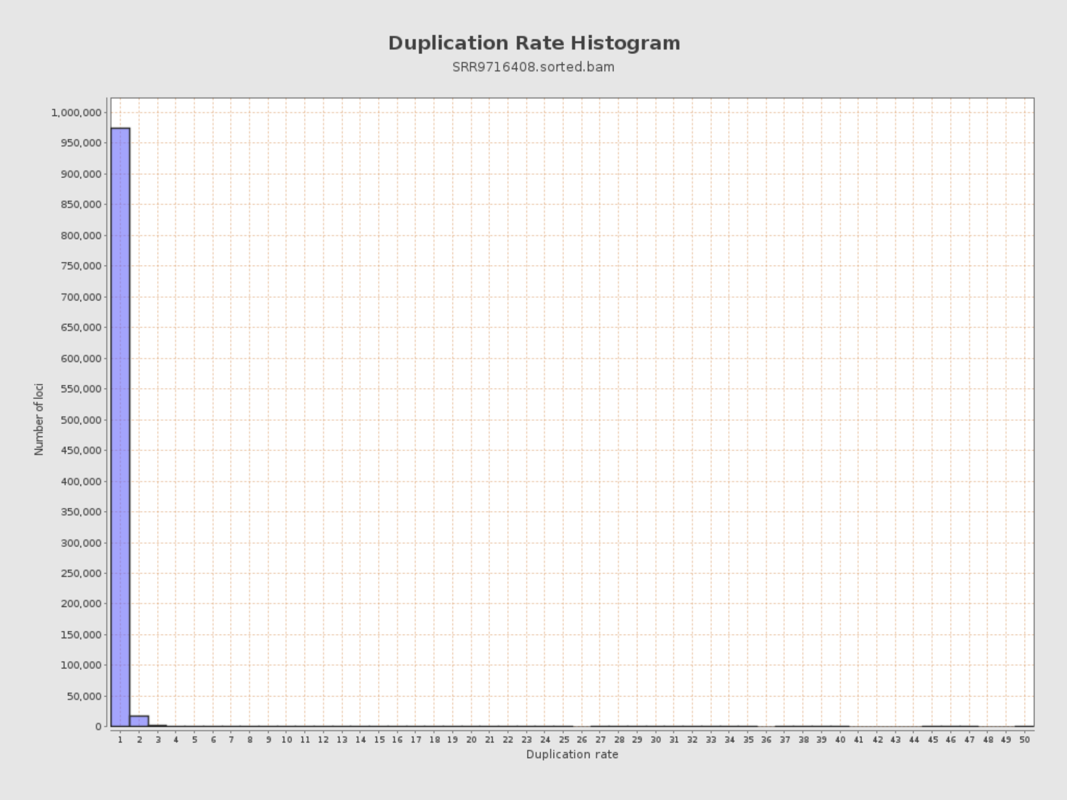
5. Results : Coverage Histogram (0-50X)



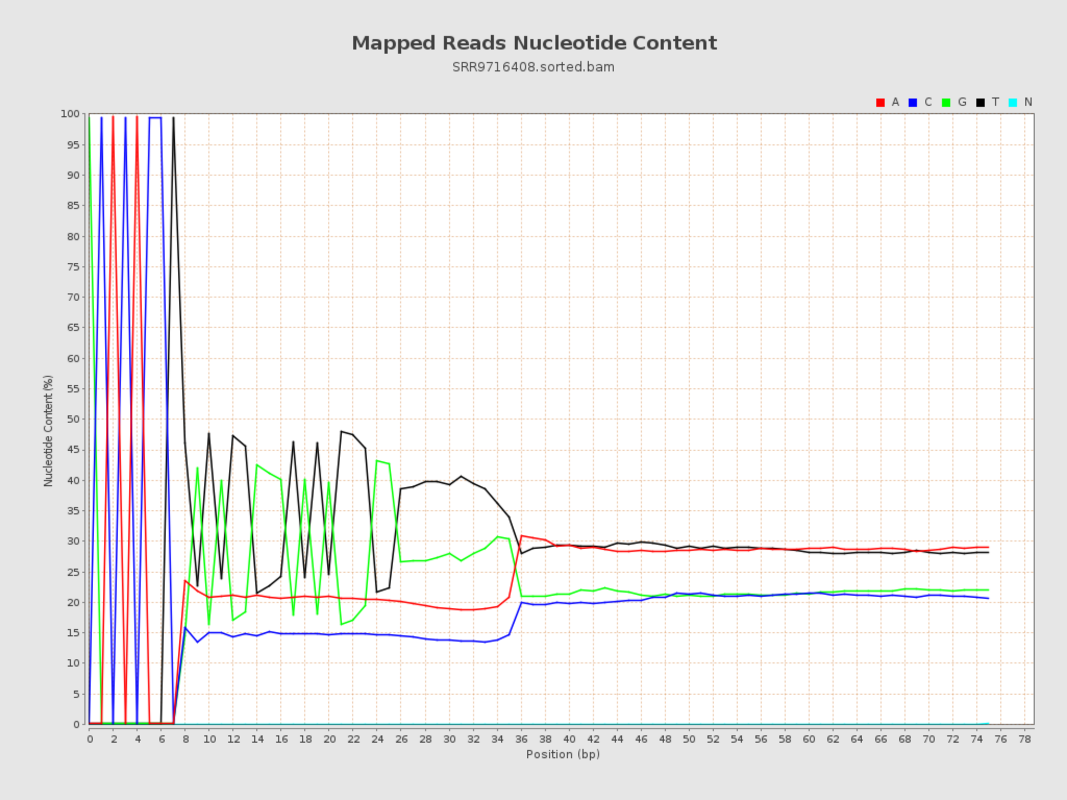
6. Results : Genome Fraction Coverage



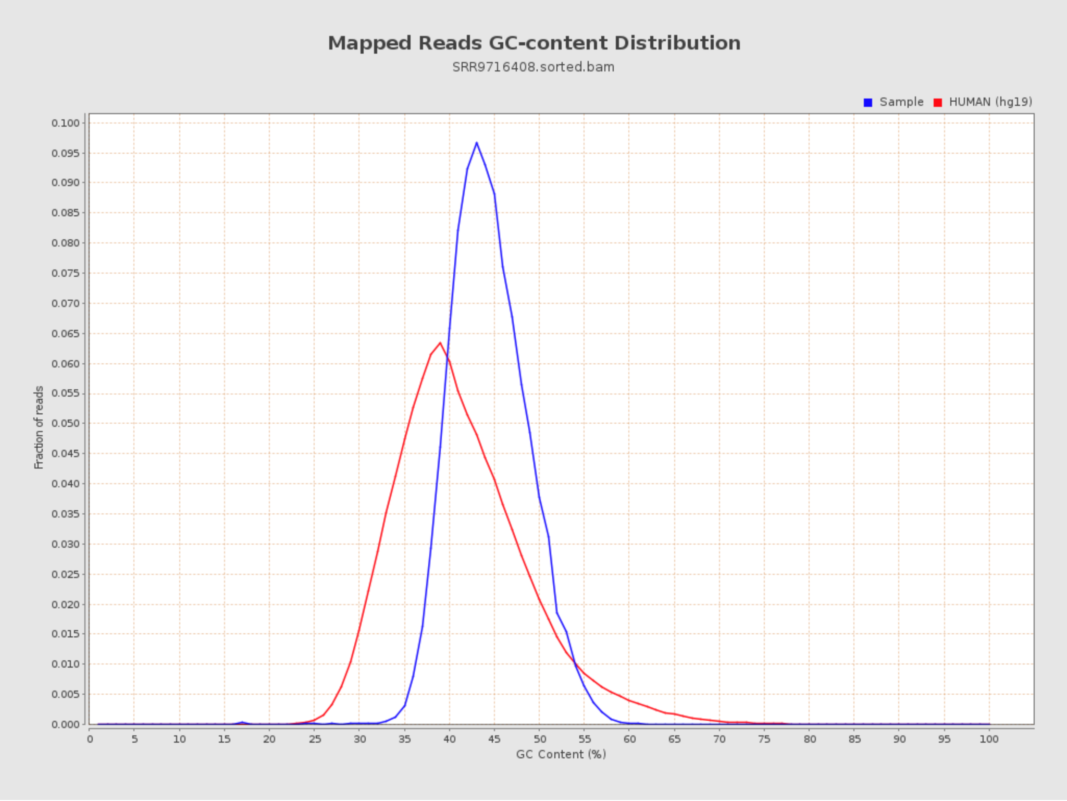
7. Results : Duplication Rate Histogram



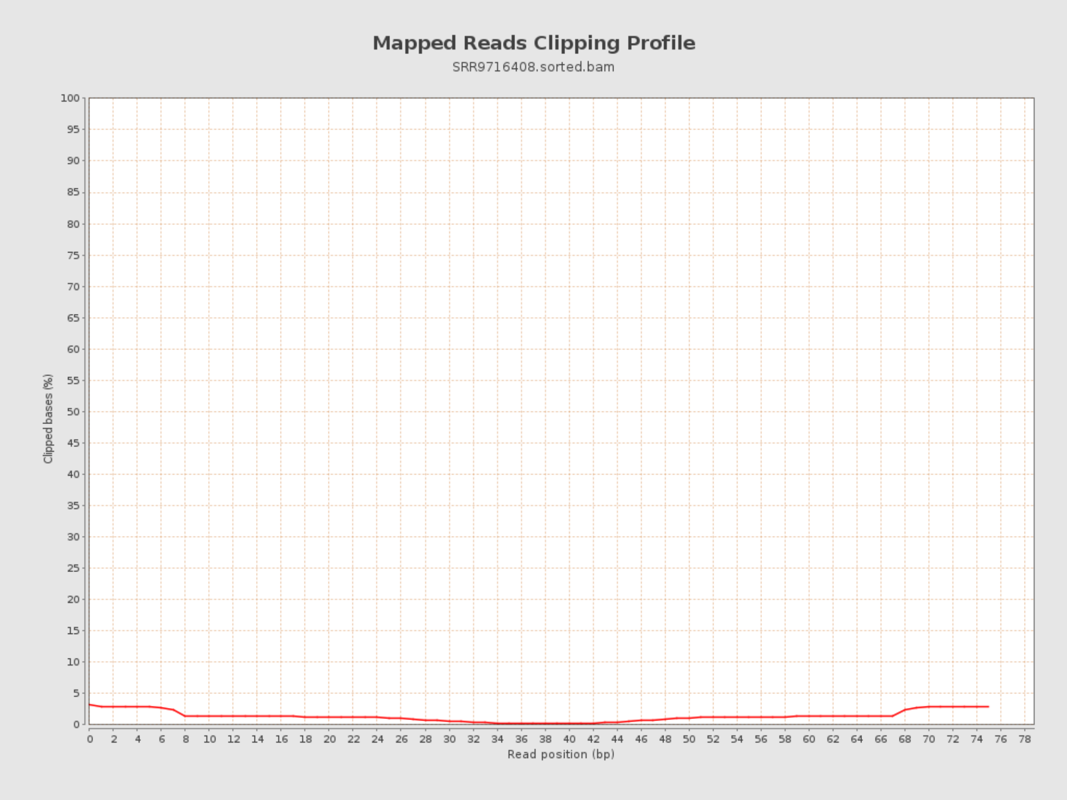
8. Results : Mapped Reads Nucleotide Content



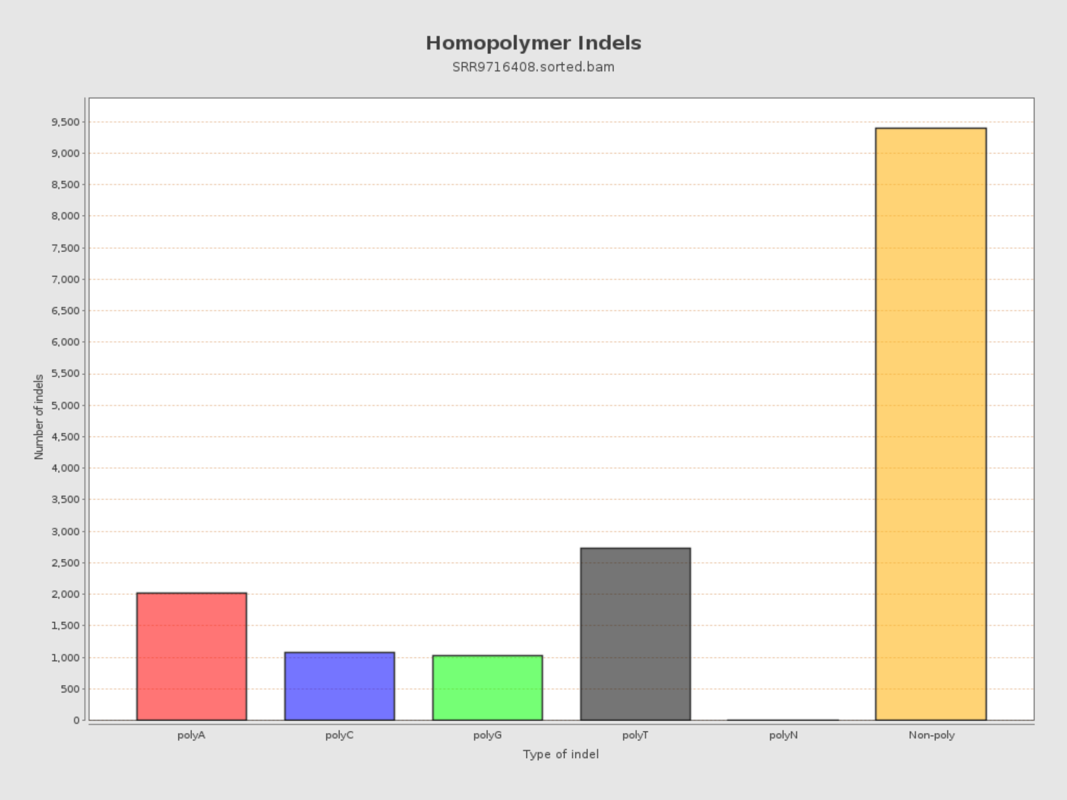
9. Results : Mapped Reads GC-content Distribution



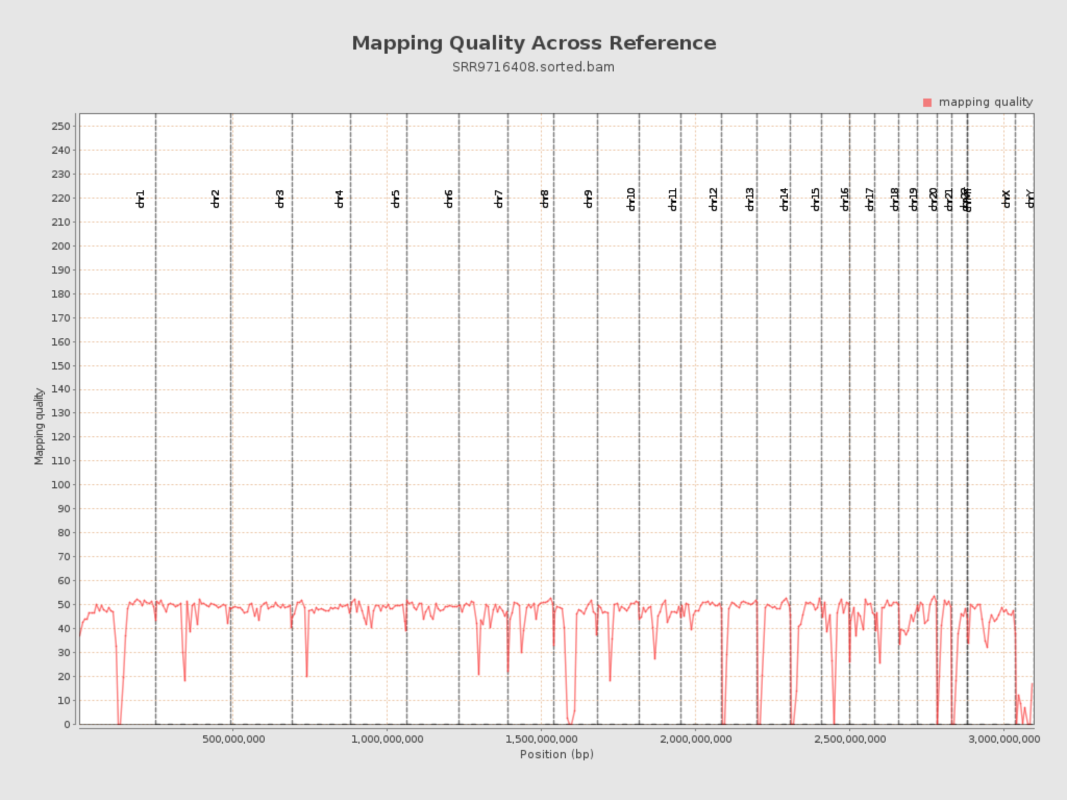
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram