Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 11:50:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716402.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_SRR9716402 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716402.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 11:50:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716402.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,695,394
Mapped reads	1,551,216 / 91.5%
Unmapped reads	144,178 / 8.5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,822 / 0.4%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	46,484 / 2.74%
Duplication rate	2.34%
Clipped reads	1,553,256 / 91.62%

2.2. ACGT Content

Number/percentage of A's	23,296,014 / 26.18%
Number/percentage of C's	18,658,710 / 20.97%
Number/percentage of T's	26,523,124 / 29.81%
Number/percentage of G's	20,509,018 / 23.05%
Number/percentage of N's	1,898 / 0%
GC Percentage	44.01%

2.3. Coverage

Mean	0.0288

Standard Deviation	0.2358

2.4. Mapping Quality

Mean Mapping Quality	44.97

2.5. Mismatches and indels

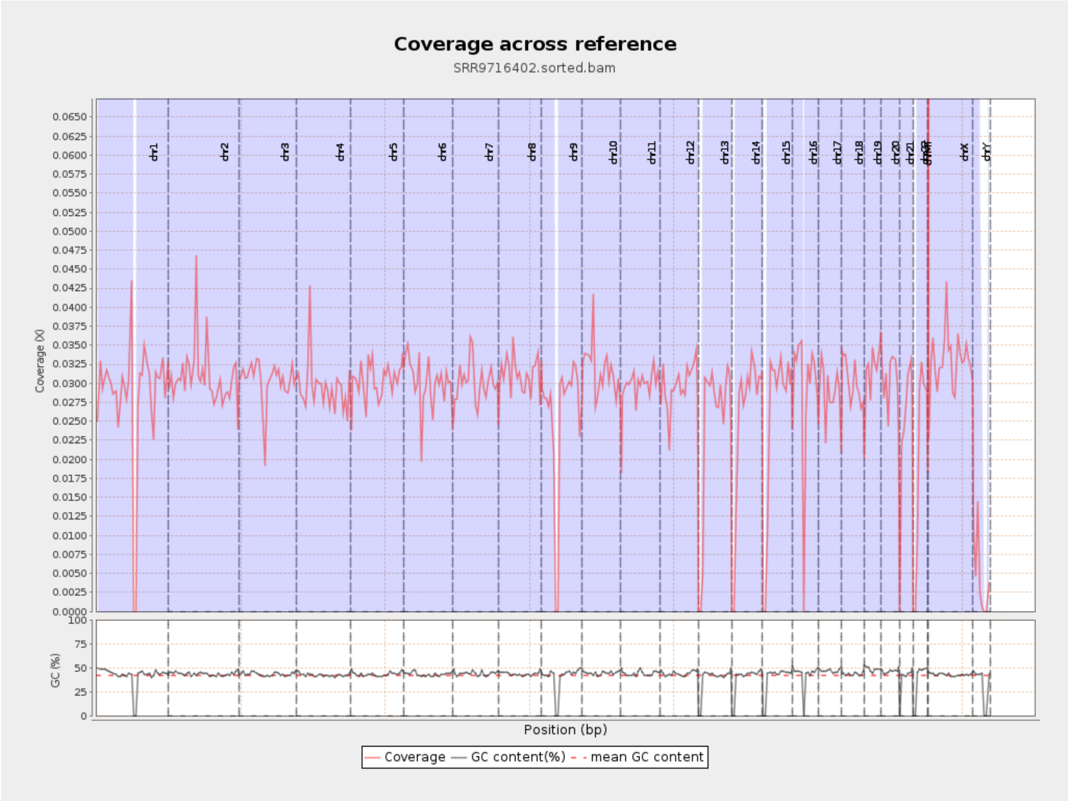
General error rate	0.5%
Mismatches	428,757
Insertions	6,176
Mapped reads with at least one insertion	0.4%
Deletions	13,247
Mapped reads with at least one deletion	0.85%
Homopolymer indels	40.19%

2.6. Chromosome stats

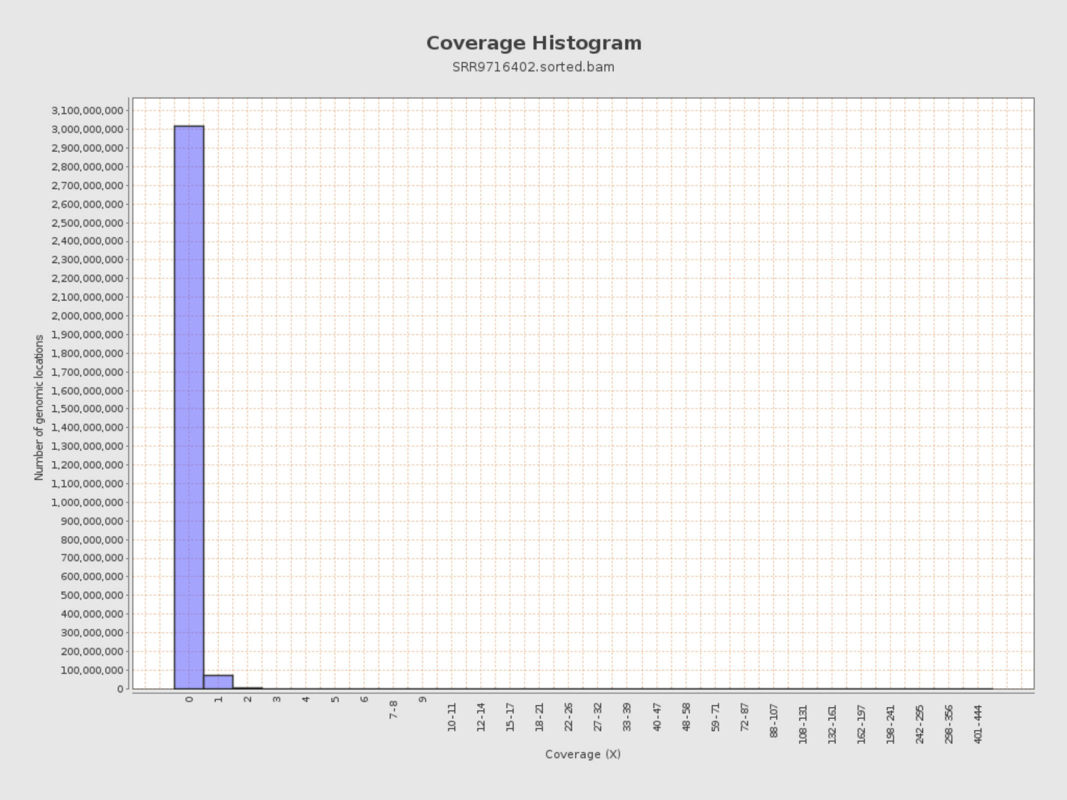
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7056619	0.0283	0.3861
chr2	243199373	7497402	0.0308	0.2544
chr3	198022430	6006331	0.0303	0.1897
chr4	191154276	5644241	0.0295	0.1999
chr5	180915260	5537681	0.0306	0.1921
chr6	171115067	5144941	0.0301	0.2014
chr7	159138663	4787466	0.0301	0.2397

chr8	146364022	4554267	0.0311	0.2159
chr9	141213431	3608802	0.0256	0.23
chr10	135534747	4309375	0.0318	0.2281
chr11	135006516	4032935	0.0299	0.2388
chr12	133851895	3970737	0.0297	0.1895
chr13	115169878	2809806	0.0244	0.1695
chr14	107349540	2698480	0.0251	0.1797
chr15	102531392	2587398	0.0252	0.1746
chr16	90354753	2608151	0.0289	0.1971
chr17	81195210	2342092	0.0288	0.1927
chr18	78077248	2354479	0.0302	0.4036
chr19	59128983	1888206	0.0319	0.2823
chr20	63025520	1904633	0.0302	0.1974
chr21	48129895	1195210	0.0248	0.1876
chr22	51304566	1044839	0.0204	0.1559
chrMT	16571	47353	2.8576	2.197
chrX	155270560	5124714	0.033	0.2222
chrY	59373566	255198	0.0043	0.1058

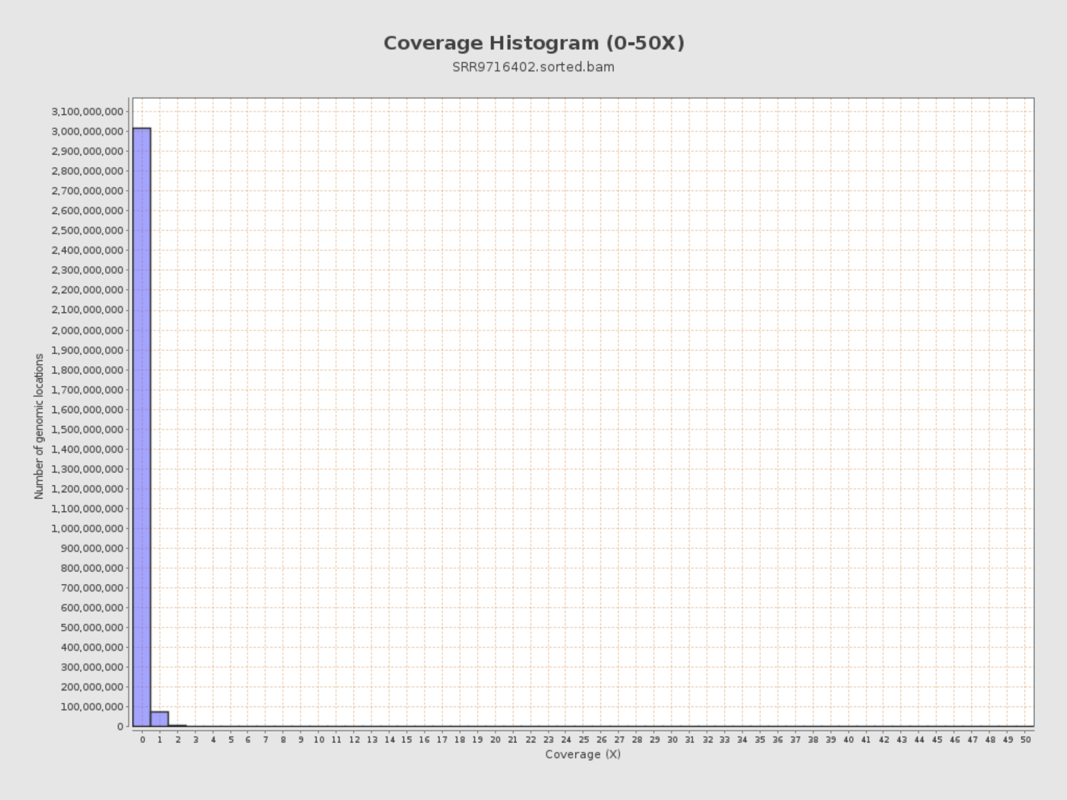
3. Results : Coverage across reference



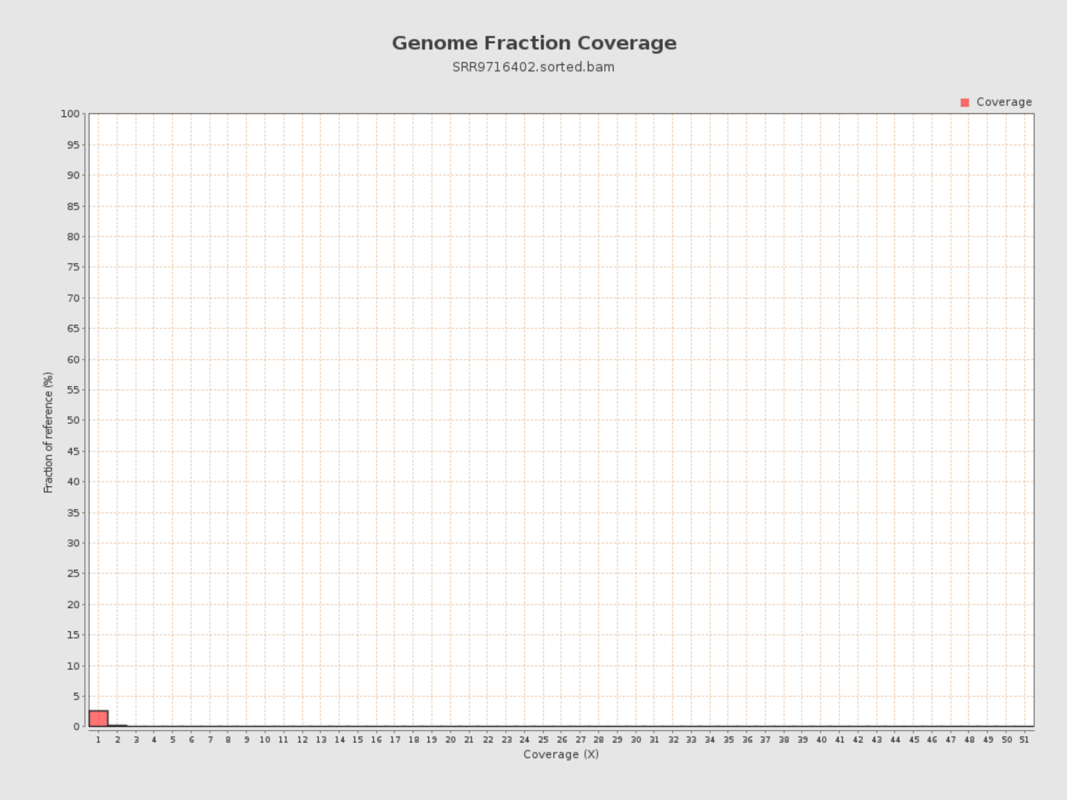
4. Results : Coverage Histogram



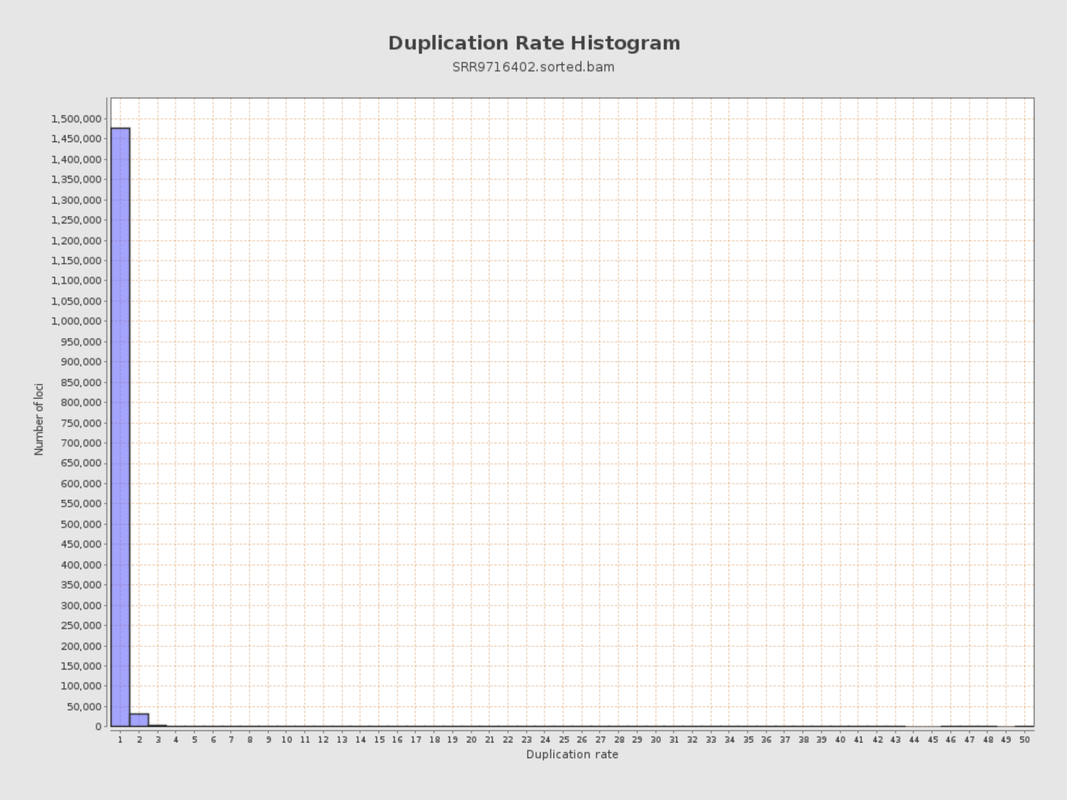
5. Results : Coverage Histogram (0-50X)



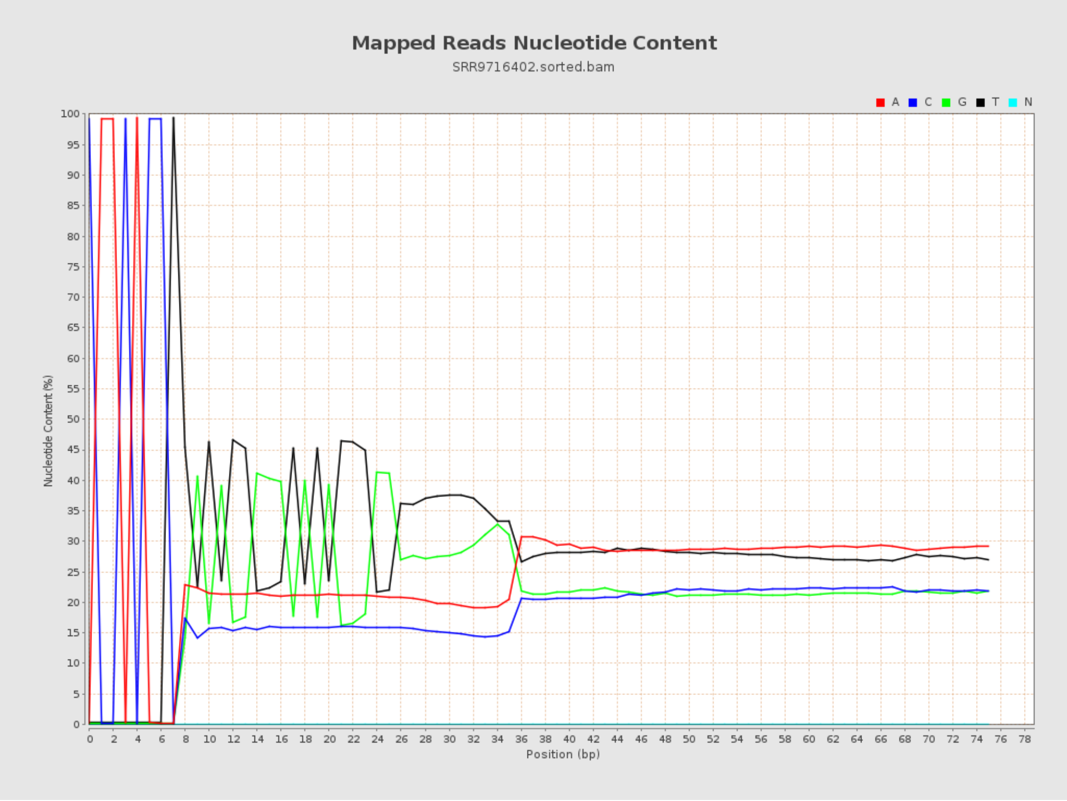
6. Results : Genome Fraction Coverage



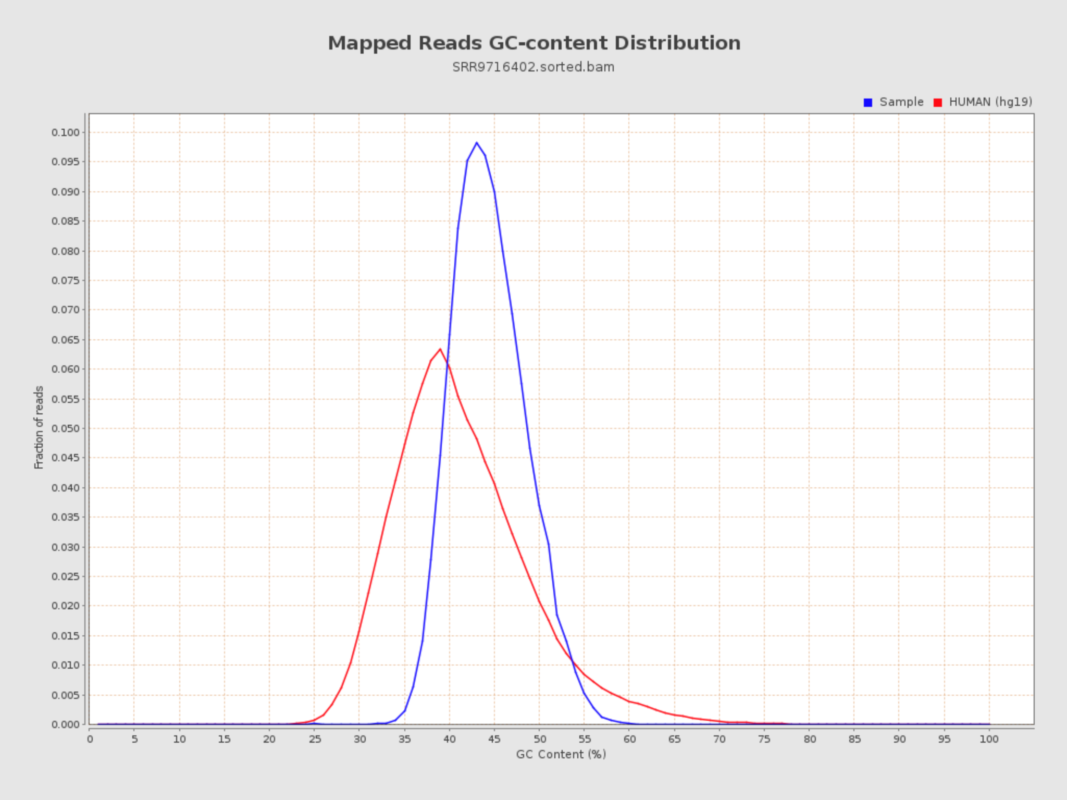
7. Results : Duplication Rate Histogram



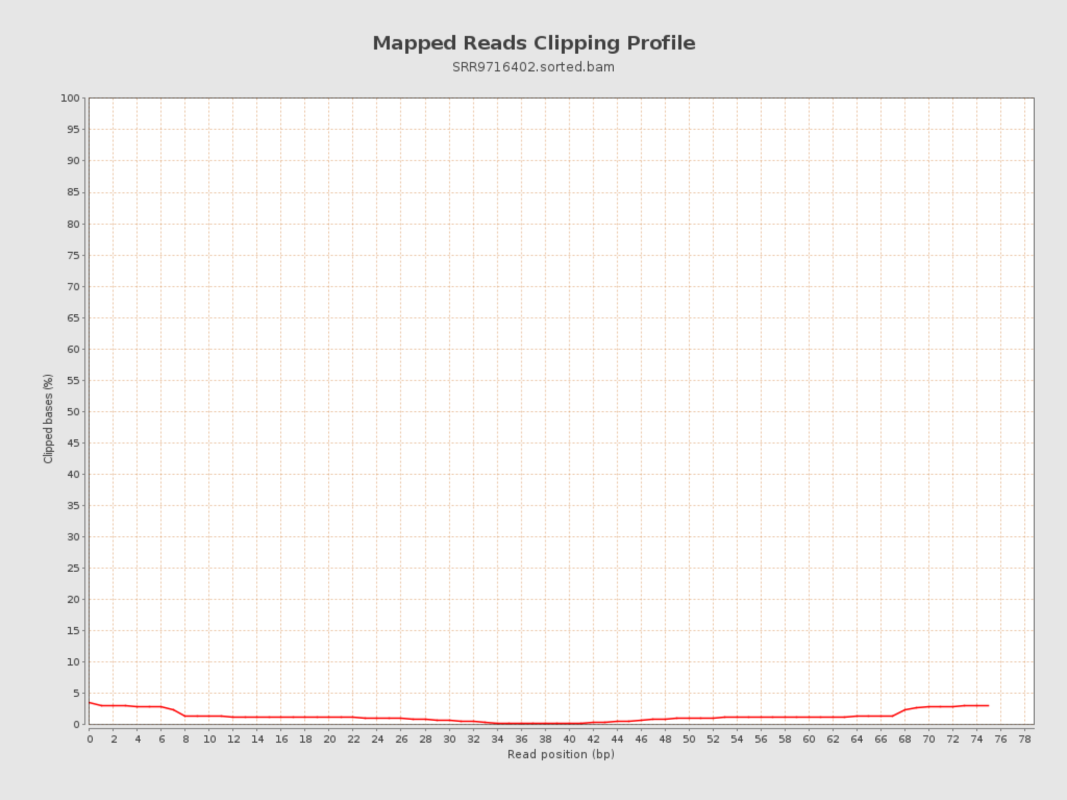
8. Results : Mapped Reads Nucleotide Content



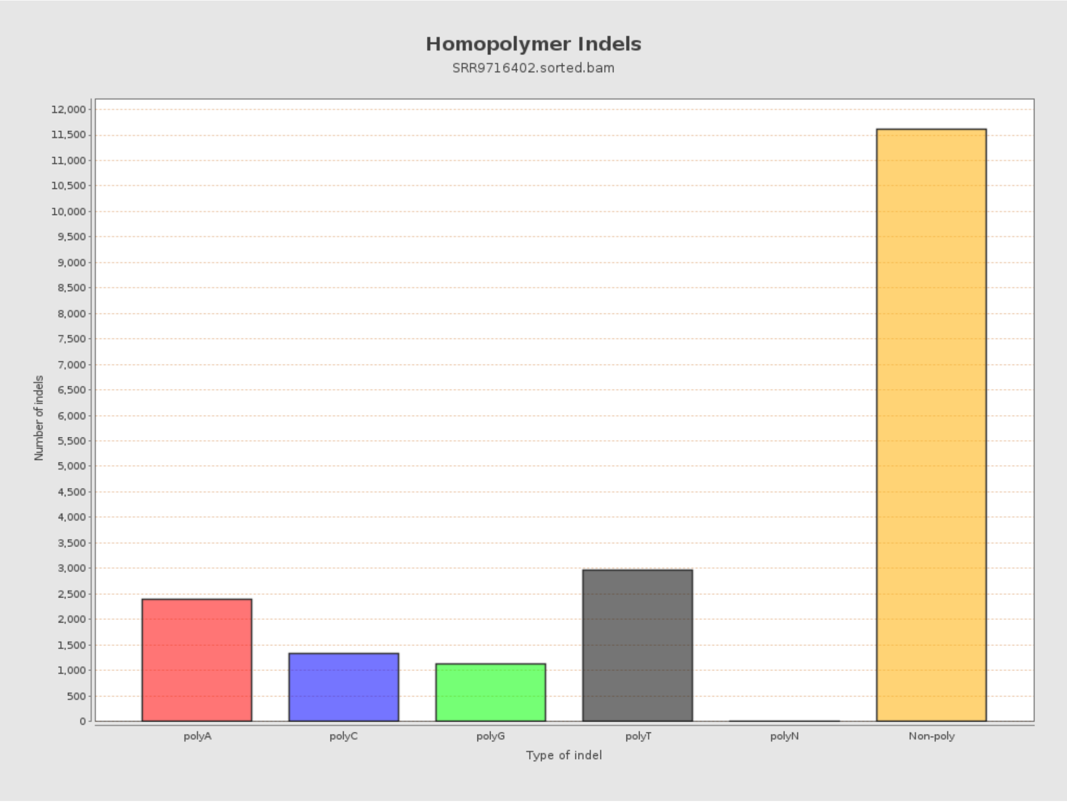
9. Results : Mapped Reads GC-content Distribution



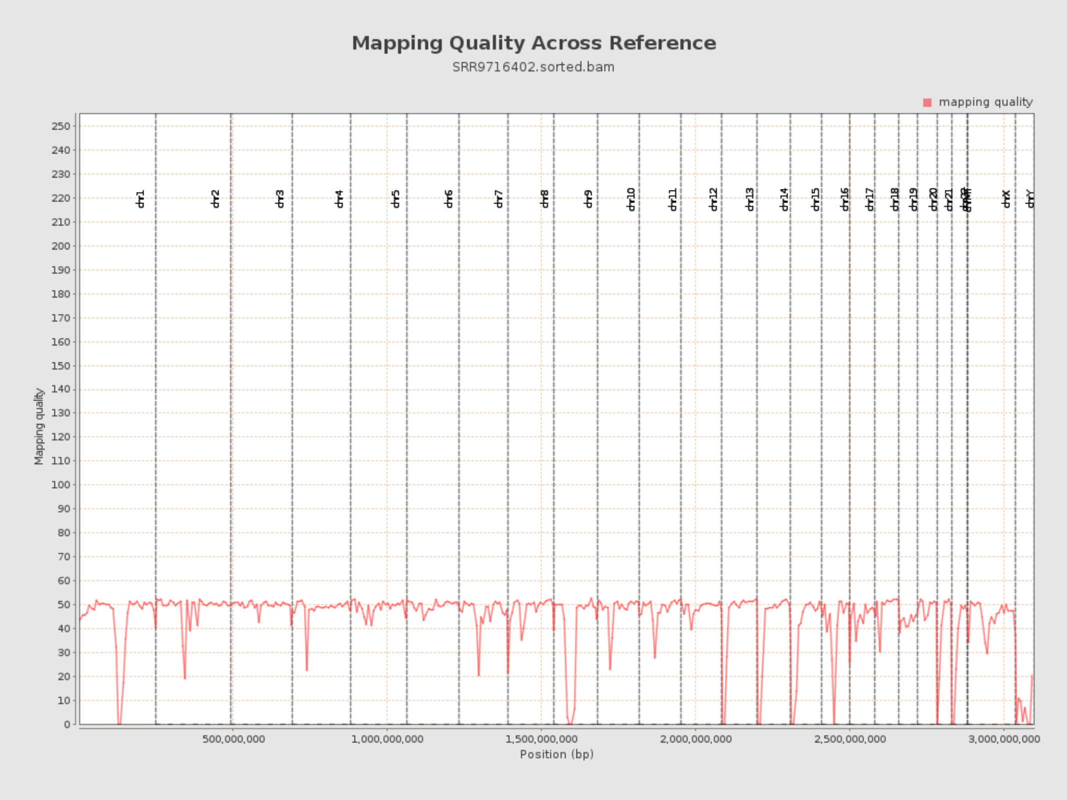
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram