Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 18:47:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716923.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_SRR9716923 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716923.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 18:47:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716923.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,192,900
Mapped reads	1,093,655 / 91.68%
Unmapped reads	99,245 / 8.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,626 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	27,784 / 2.33%
Duplication rate	1.95%
Clipped reads	1,095,489 / 91.83%

2.2. ACGT Content

Number/percentage of A's	15,640,846 / 24.75%
Number/percentage of C's	11,604,624 / 18.37%
Number/percentage of T's	20,436,599 / 32.35%
Number/percentage of G's	15,499,265 / 24.53%
Number/percentage of N's	1,385 / 0%
GC Percentage	42.9%

2.3. Coverage

Mean	0.0204

Standard Deviation	0.1929

2.4. Mapping Quality

Mean Mapping Quality	45.49

2.5. Mismatches and indels

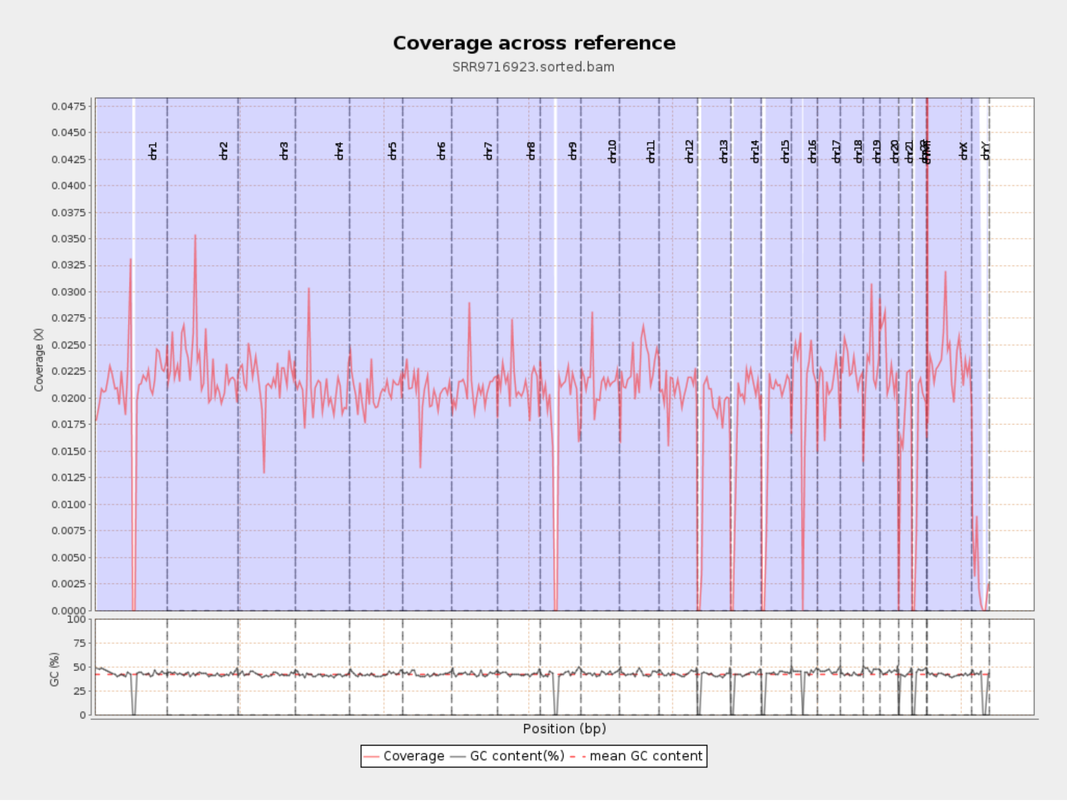
General error rate	0.49%
Mismatches	303,450
Insertions	4,075
Mapped reads with at least one insertion	0.37%
Deletions	9,543
Mapped reads with at least one deletion	0.87%
Homopolymer indels	42.3%

2.6. Chromosome stats

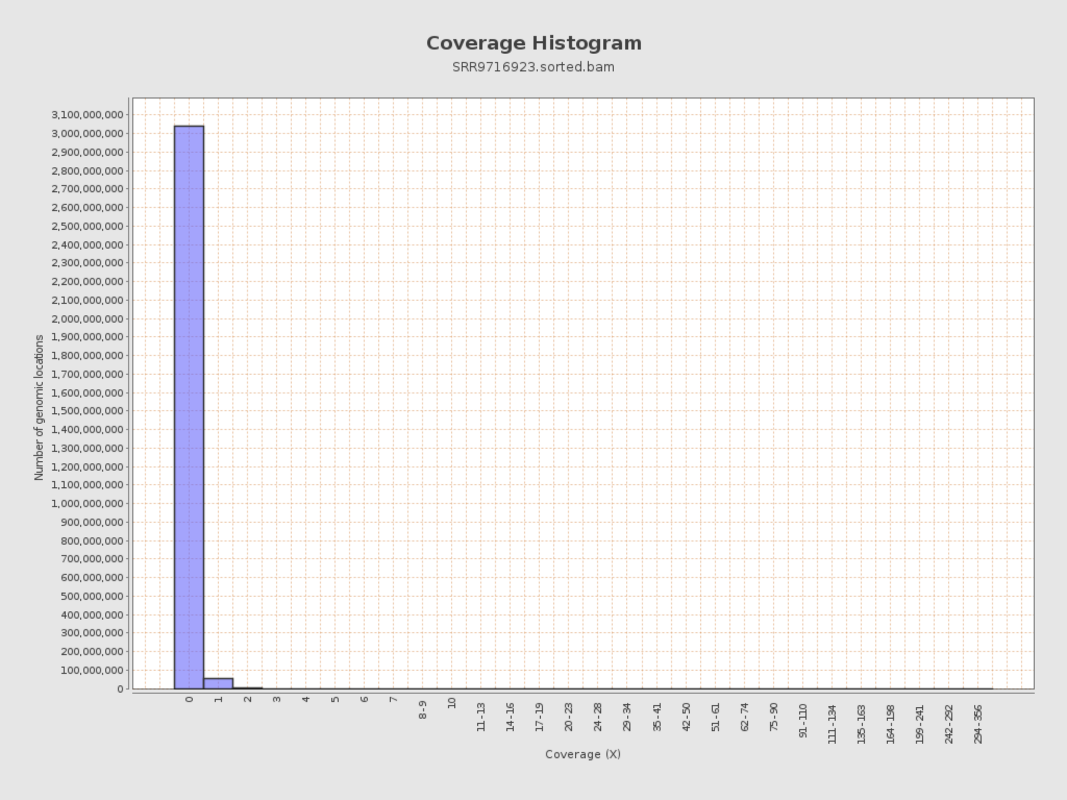
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5103100	0.0205	0.3314
chr2	243199373	5580951	0.0229	0.2068
chr3	198022430	4311247	0.0218	0.1565
chr4	191154276	3958942	0.0207	0.1603
chr5	180915260	3732823	0.0206	0.1545
chr6	171115067	3521828	0.0206	0.1599
chr7	159138663	3360859	0.0211	0.2038

chr8	146364022	3130839	0.0214	0.1763
chr9	141213431	2577321	0.0183	0.1852
chr10	135534747	2925485	0.0216	0.1748
chr11	135006516	3072768	0.0228	0.1954
chr12	133851895	2784316	0.0208	0.1545
chr13	115169878	1904583	0.0165	0.1364
chr14	107349540	1877065	0.0175	0.1452
chr15	102531392	1767165	0.0172	0.1401
chr16	90354753	1862435	0.0206	0.1601
chr17	81195210	1711429	0.0211	0.1603
chr18	78077248	1787850	0.0229	0.3119
chr19	59128983	1379808	0.0233	0.228
chr20	63025520	1462294	0.0232	0.1658
chr21	48129895	833065	0.0173	0.1507
chr22	51304566	733157	0.0143	0.1266
chrMT	16571	4291	0.2589	0.5242
chrX	155270560	3642295	0.0235	0.1803
chrY	59373566	172725	0.0029	0.0708

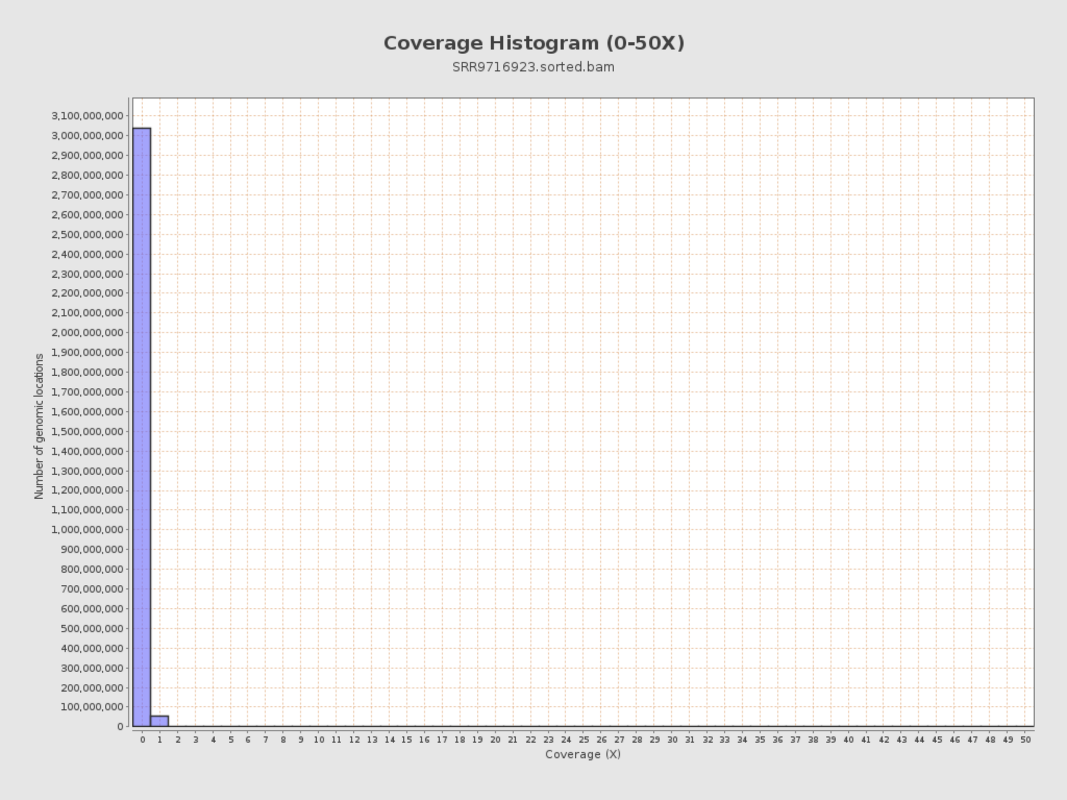
3. Results : Coverage across reference



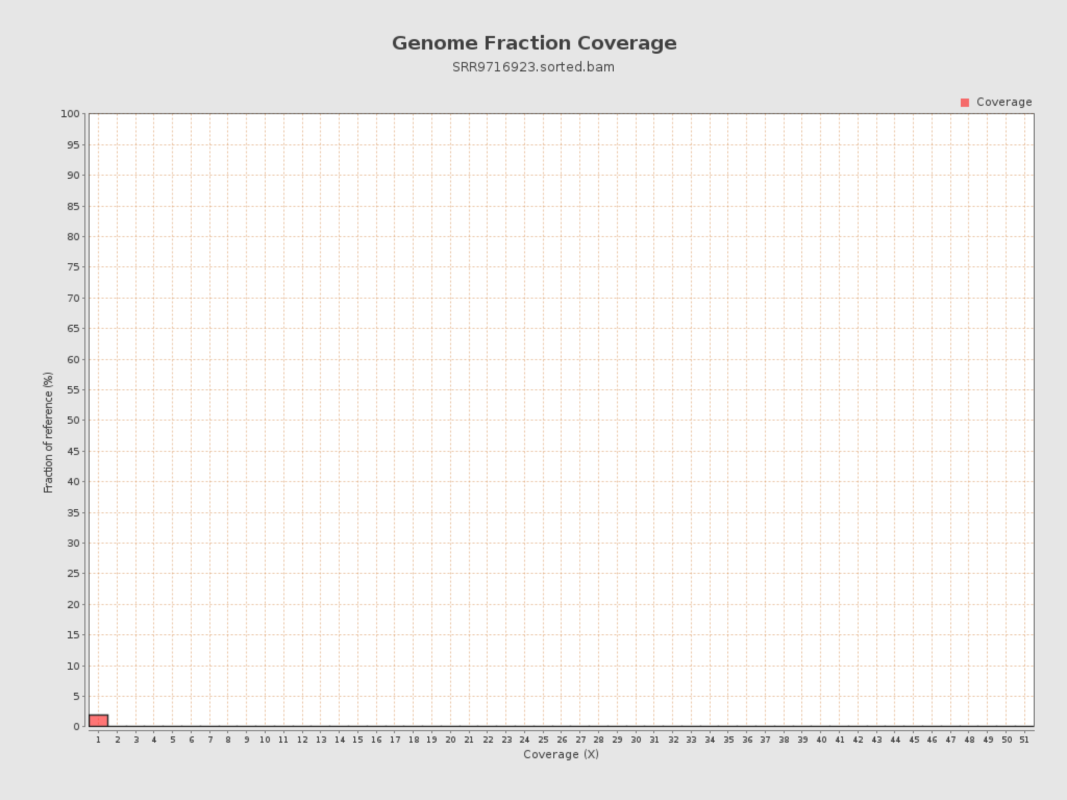
4. Results : Coverage Histogram



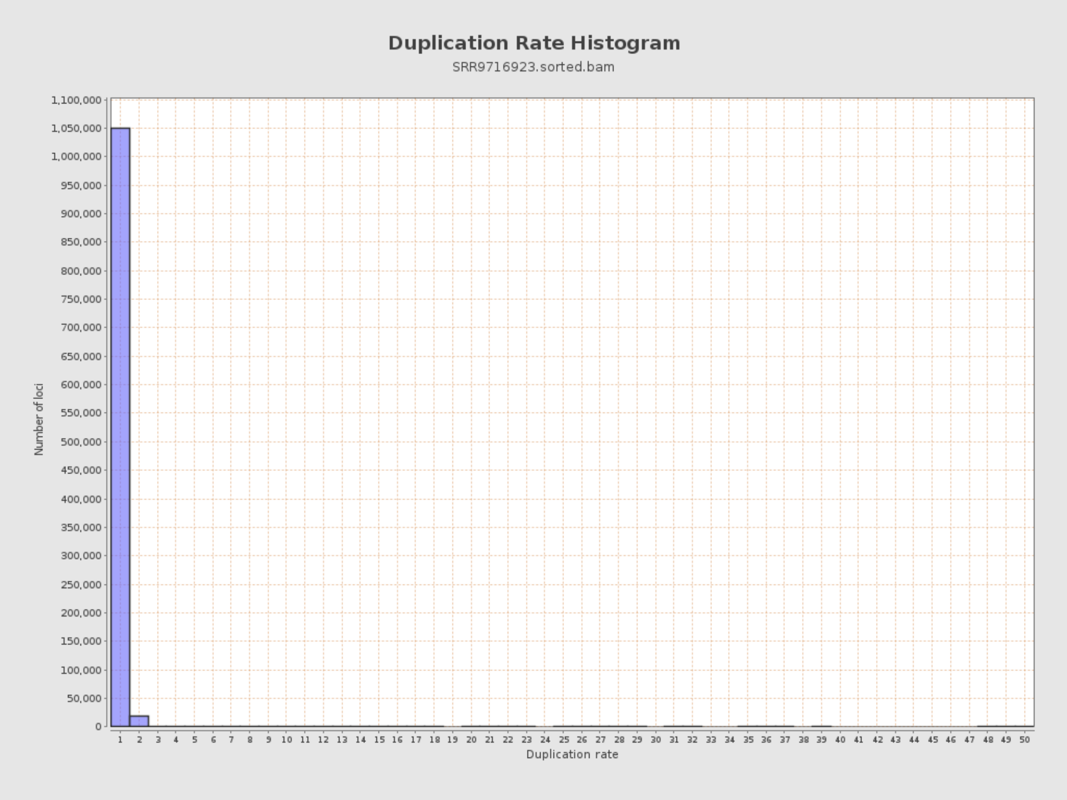
5. Results : Coverage Histogram (0-50X)



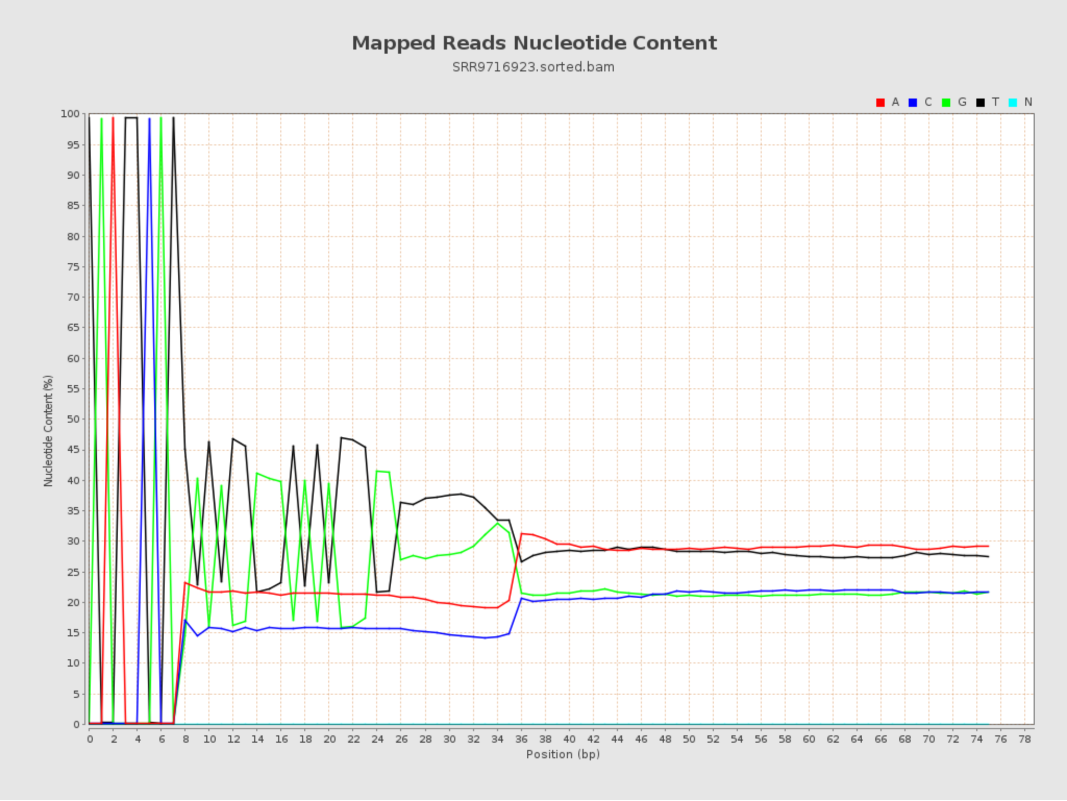
6. Results : Genome Fraction Coverage



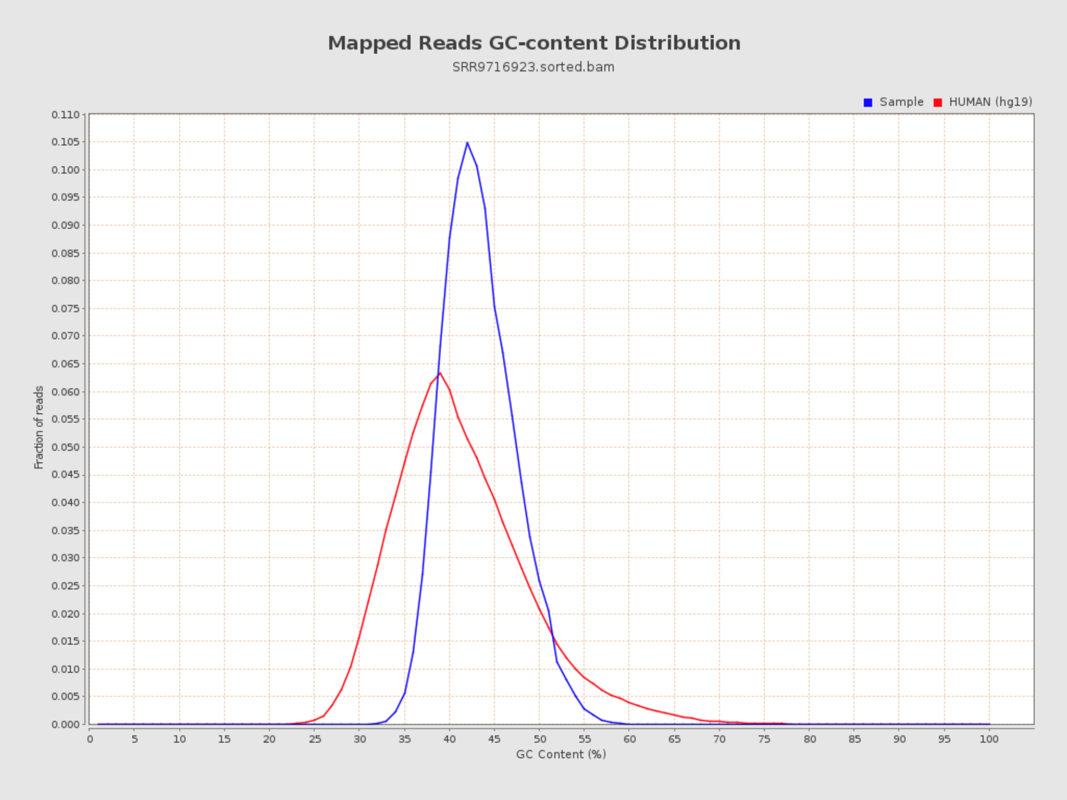
7. Results : Duplication Rate Histogram



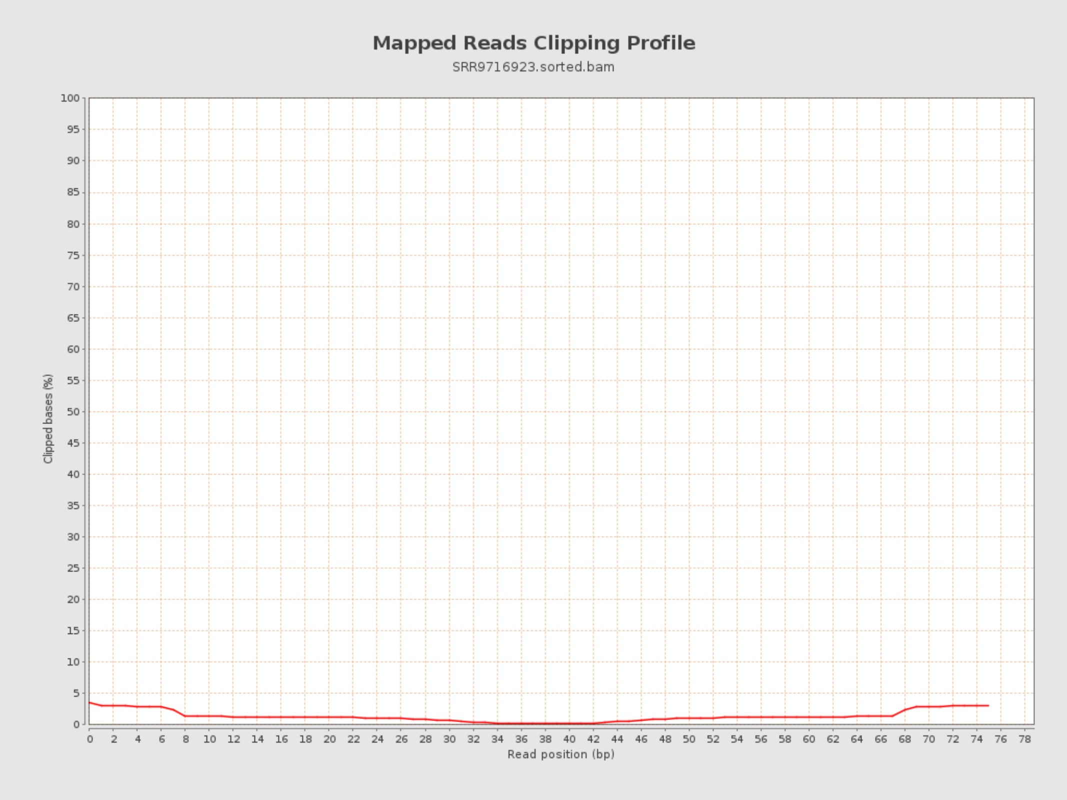
8. Results : Mapped Reads Nucleotide Content



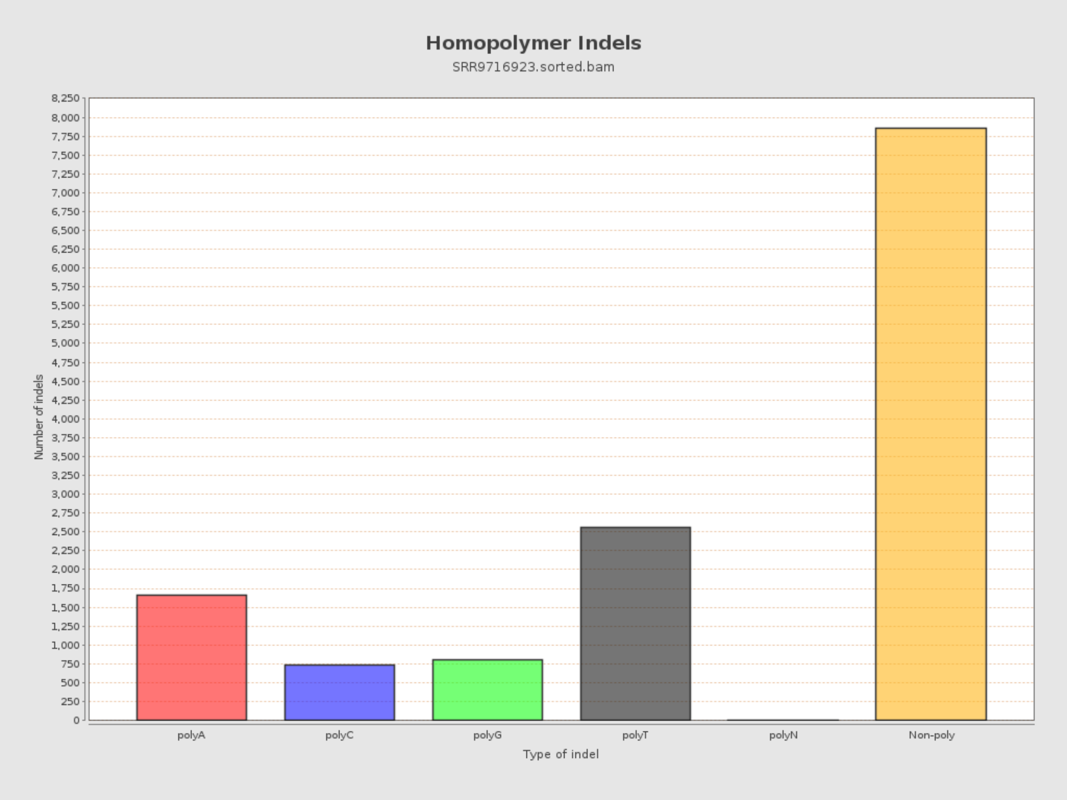
9. Results : Mapped Reads GC-content Distribution



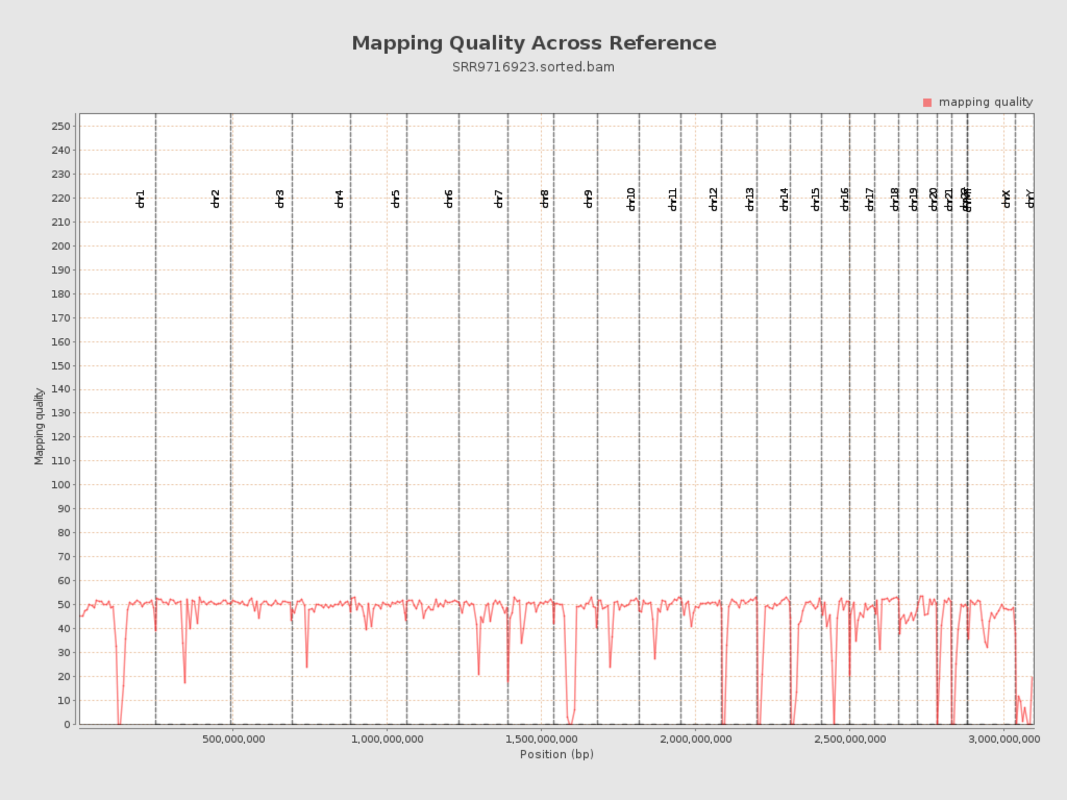
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram