Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 18:50:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716924.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_SRR9716924 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716924.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 18:50:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716924.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,811,748
Mapped reads	2,577,607 / 91.67%
Unmapped reads	234,141 / 8.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,769 / 0.49%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	122,254 / 4.35%
Duplication rate	3.54%
Clipped reads	2,589,039 / 92.08%

2.2. ACGT Content

Number/percentage of A's	38,404,212 / 25.64%
Number/percentage of C's	29,542,781 / 19.72%
Number/percentage of T's	46,593,492 / 31.11%
Number/percentage of G's	35,237,650 / 23.53%
Number/percentage of N's	4,182 / 0%
GC Percentage	43.25%

2.3. Coverage

Mean	0.0484

Standard Deviation	0.4195

2.4. Mapping Quality

Mean Mapping Quality	44.62

2.5. Mismatches and indels

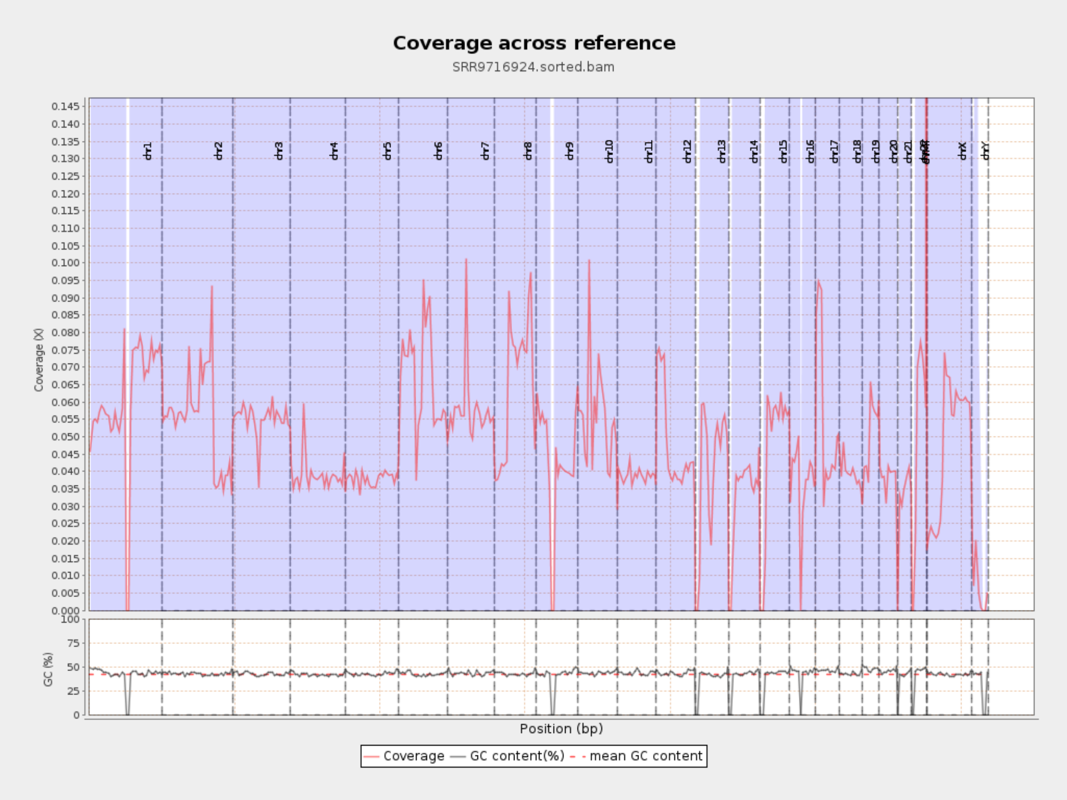
General error rate	0.51%
Mismatches	745,329
Insertions	8,332
Mapped reads with at least one insertion	0.32%
Deletions	26,224
Mapped reads with at least one deletion	1.01%
Homopolymer indels	43.92%

2.6. Chromosome stats

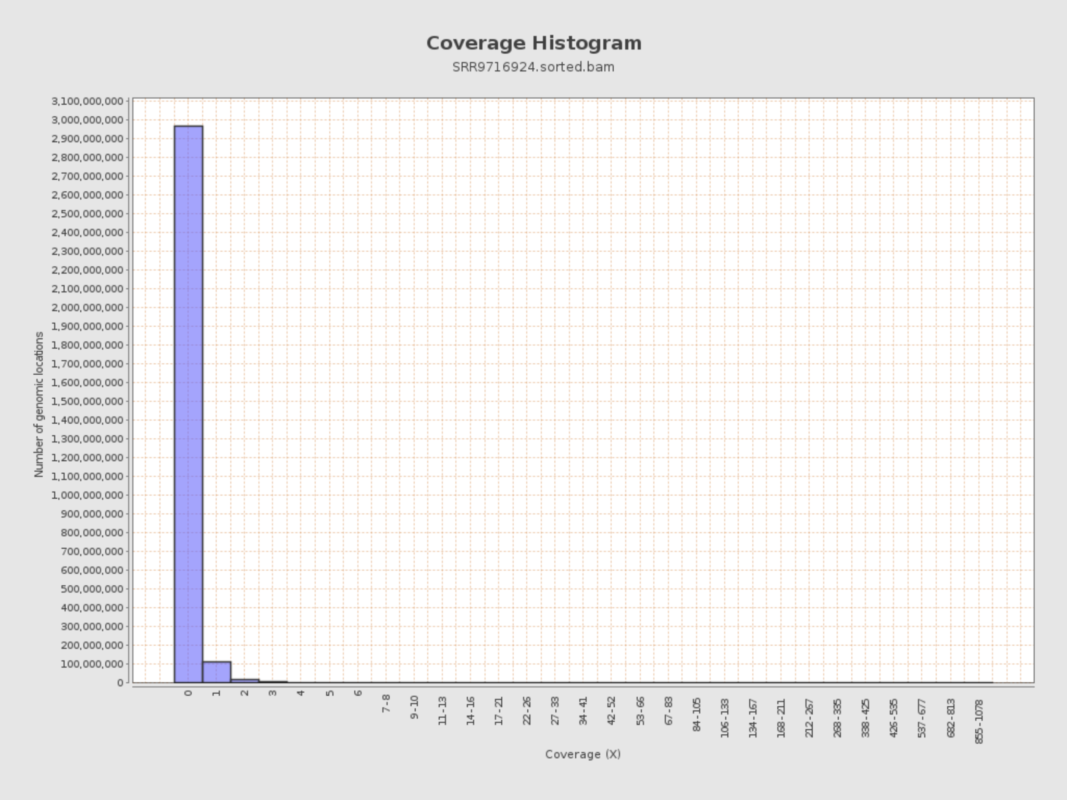
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14978998	0.0601	0.7429
chr2	243199373	13490148	0.0555	0.5236
chr3	198022430	10920841	0.0551	0.2711
chr4	191154276	7451557	0.039	0.2446
chr5	180915260	6853055	0.0379	0.2263
chr6	171115067	11457812	0.067	0.3844
chr7	159138663	9249946	0.0581	0.7912

chr8	146364022	9536755	0.0652	0.3806
chr9	141213431	5821520	0.0412	0.3174
chr10	135534747	7635849	0.0563	0.3859
chr11	135006516	5226594	0.0387	0.3463
chr12	133851895	6404388	0.0478	0.2563
chr13	115169878	4537295	0.0394	0.2299
chr14	107349540	3428556	0.0319	0.2331
chr15	102531392	4750415	0.0463	0.2552
chr16	90354753	3309151	0.0366	0.2476
chr17	81195210	4442349	0.0547	0.2841
chr18	78077248	3118303	0.0399	0.6258
chr19	59128983	2980001	0.0504	0.4887
chr20	63025520	2399032	0.0381	0.2281
chr21	48129895	1550278	0.0322	0.2326
chr22	51304566	2489677	0.0485	0.2525
chrMT	16571	42097	2.5404	2.245
chrX	155270560	7378682	0.0475	0.2958
chrY	59373566	370095	0.0062	0.1337

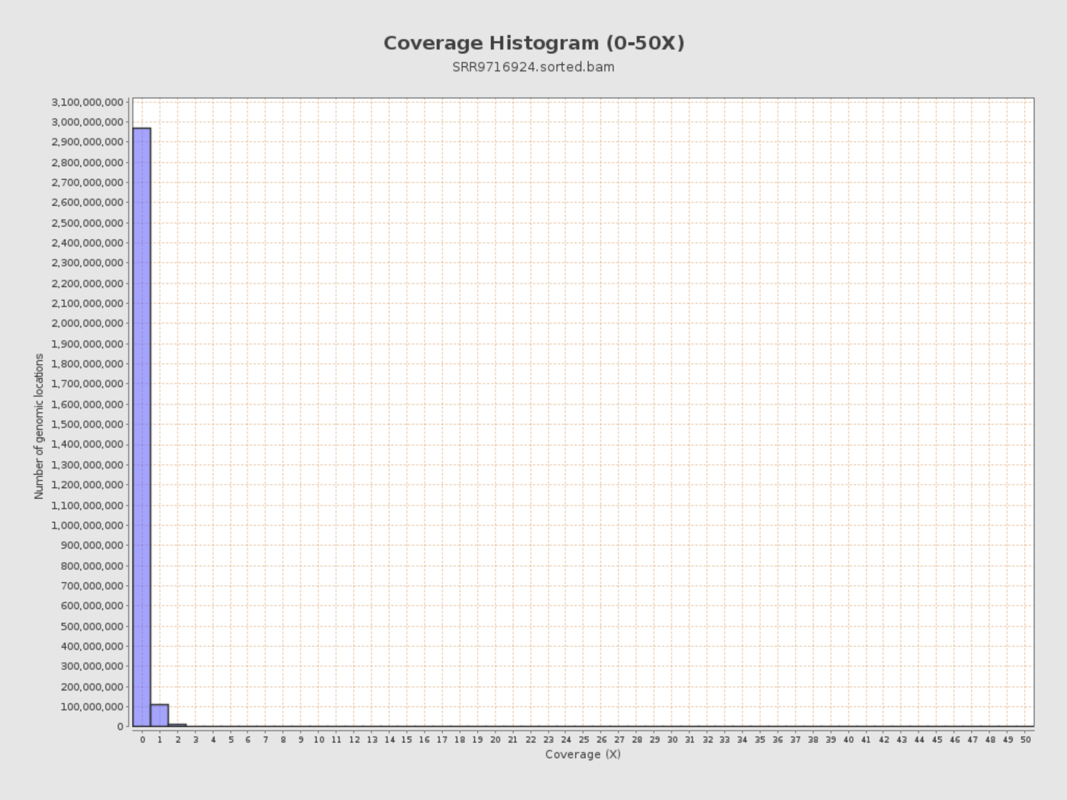
3. Results : Coverage across reference



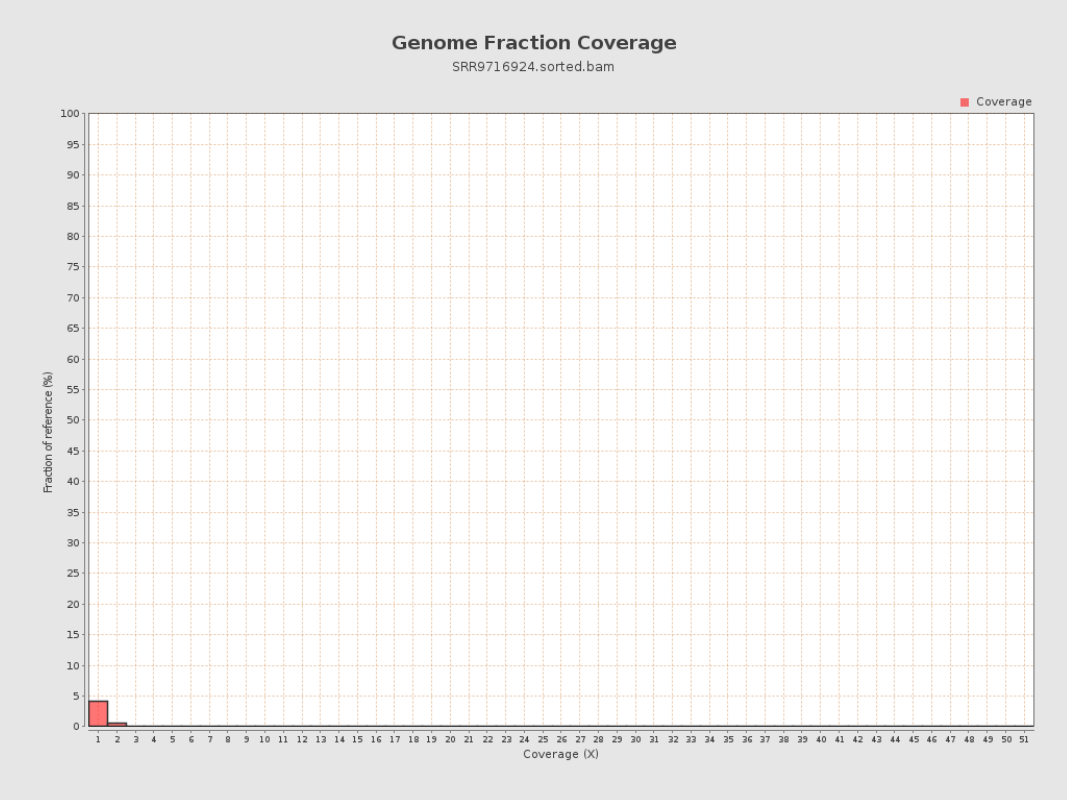
4. Results : Coverage Histogram



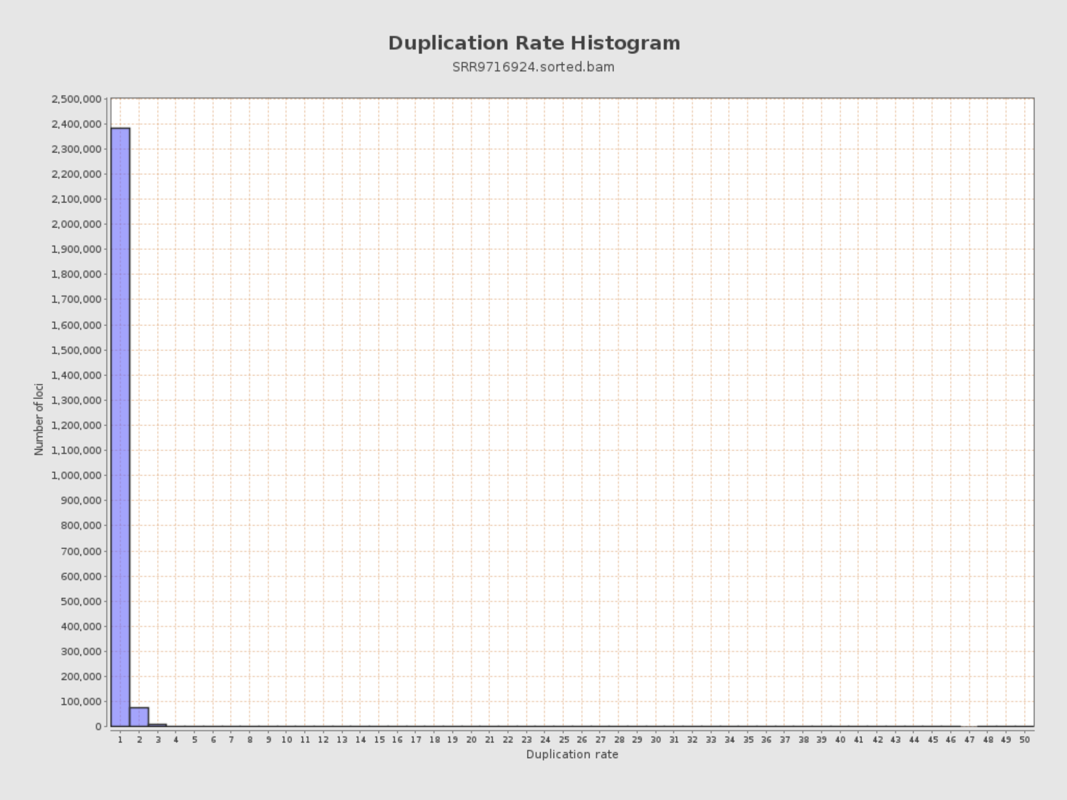
5. Results : Coverage Histogram (0-50X)



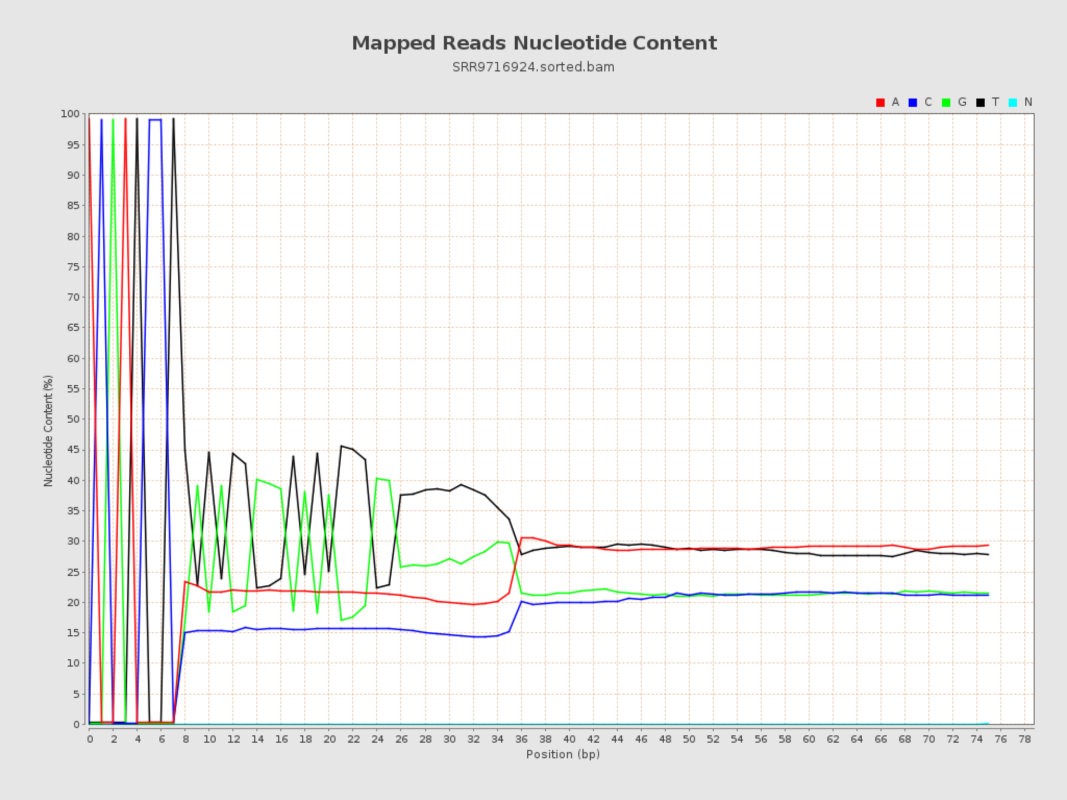
6. Results : Genome Fraction Coverage



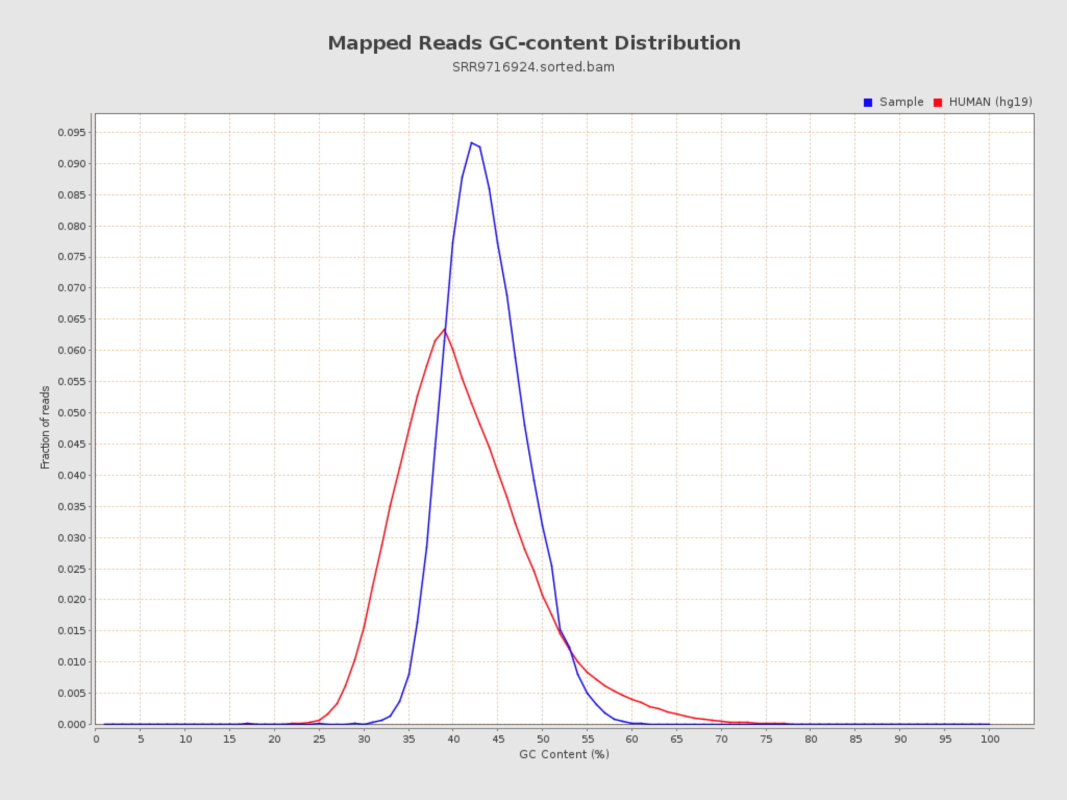
7. Results : Duplication Rate Histogram



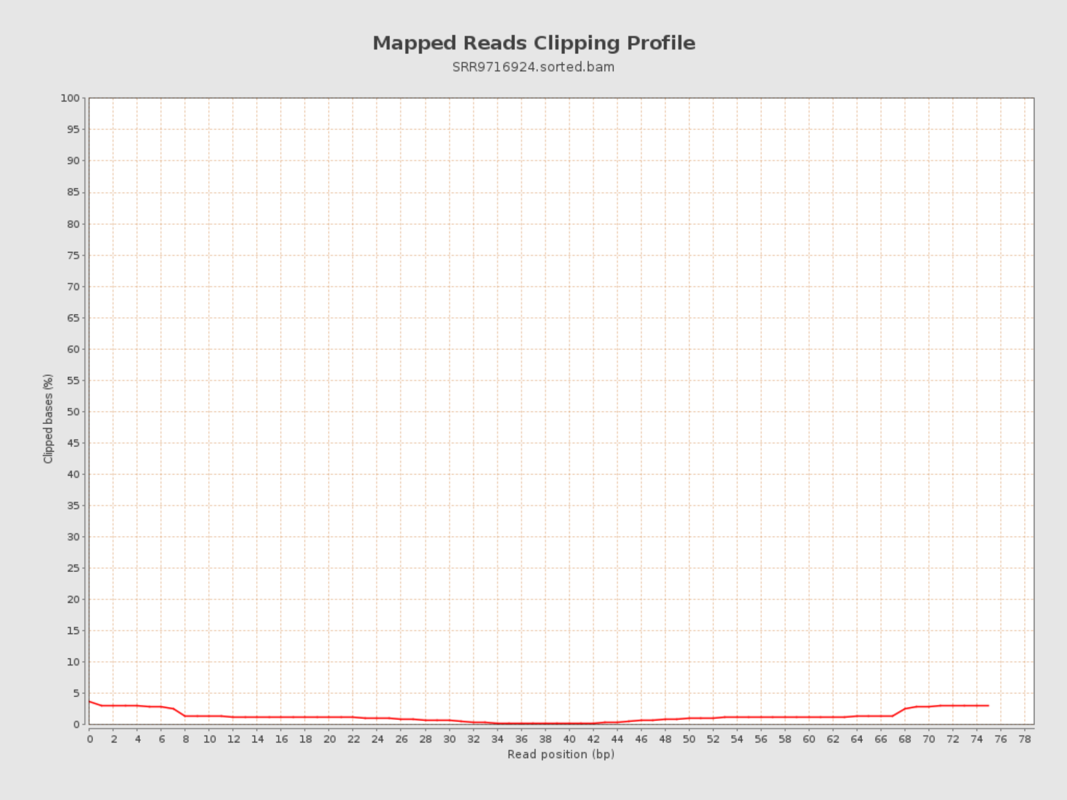
8. Results : Mapped Reads Nucleotide Content



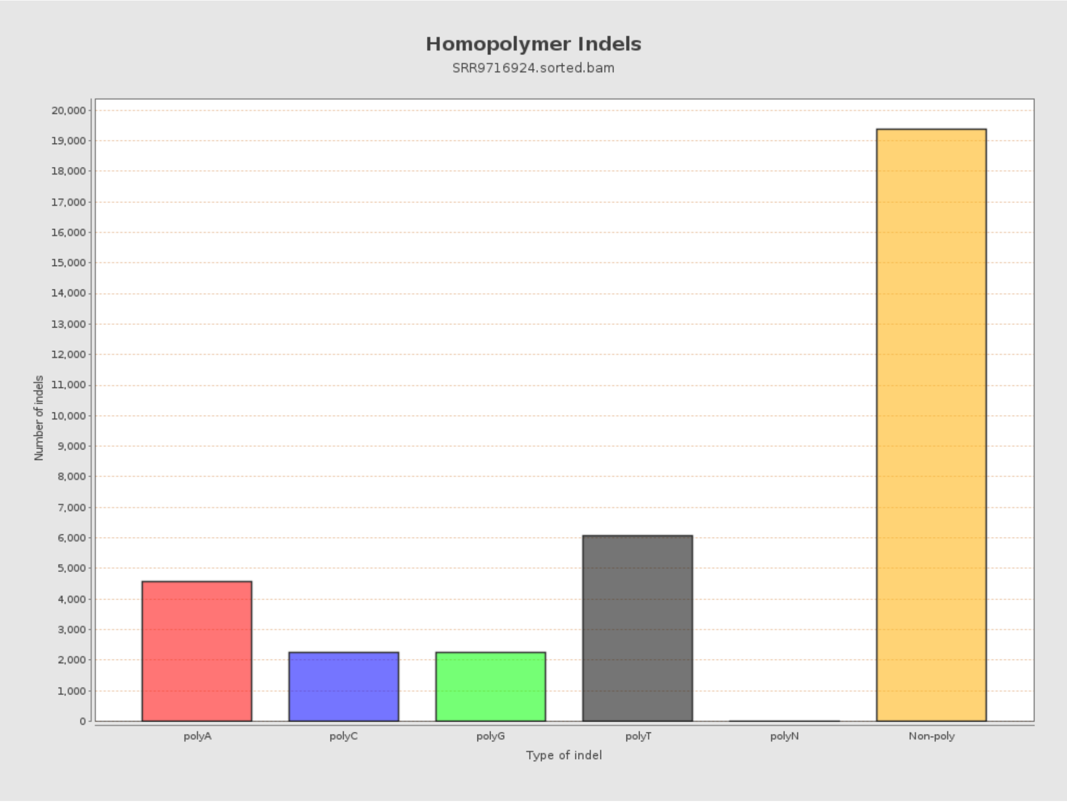
9. Results : Mapped Reads GC-content Distribution



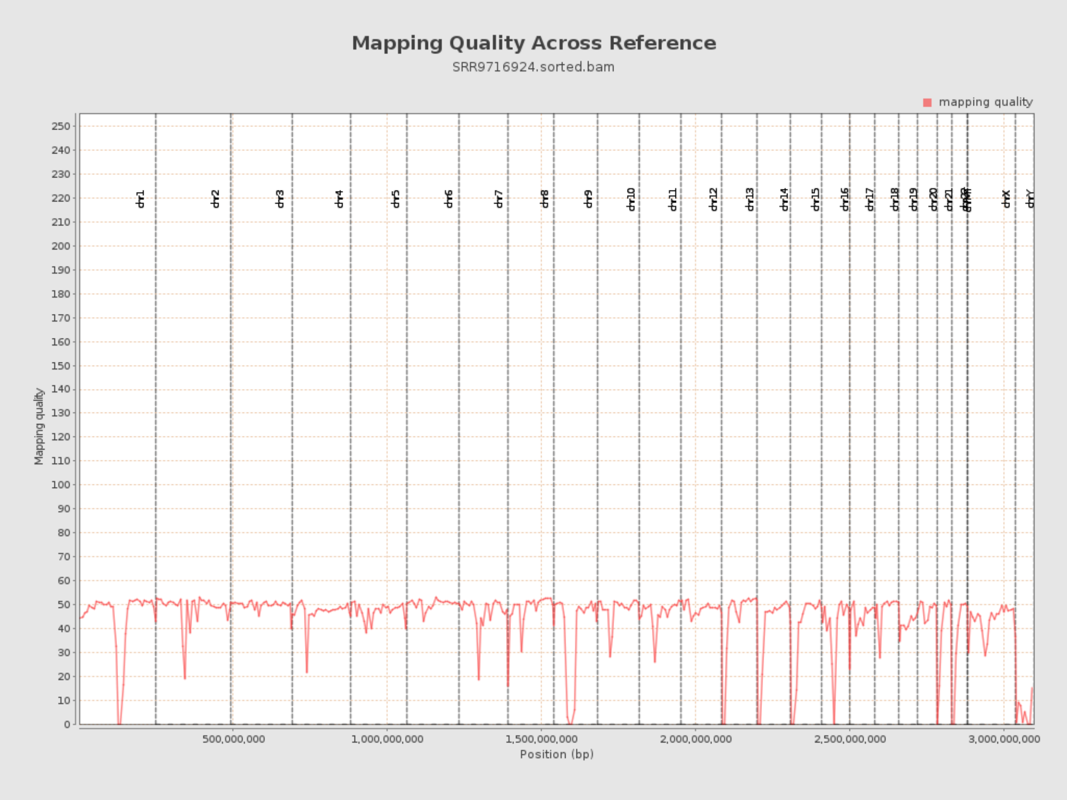
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram