Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 02:36:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716652.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_SRR9716652 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716652.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 02:36:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716652.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,093,831
Mapped reads	1,918,904 / 91.65%
Unmapped reads	174,927 / 8.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	45,820 / 2.19%
Read min/max/mean length	30 / 101 / 101.79
Duplicated reads (estimated)	59,954 / 2.86%
Duplication rate	2.17%
Clipped reads	1,963,635 / 93.78%

2.2. ACGT Content

Number/percentage of A's	36,254,323 / 26.14%
Number/percentage of C's	28,978,589 / 20.89%
Number/percentage of T's	40,629,134 / 29.29%
Number/percentage of G's	32,818,597 / 23.66%
Number/percentage of N's	15,328 / 0.01%
GC Percentage	44.56%

2.3. Coverage

Mean	0.0448

Standard Deviation	0.3637

2.4. Mapping Quality

Mean Mapping Quality	44.92

2.5. Mismatches and indels

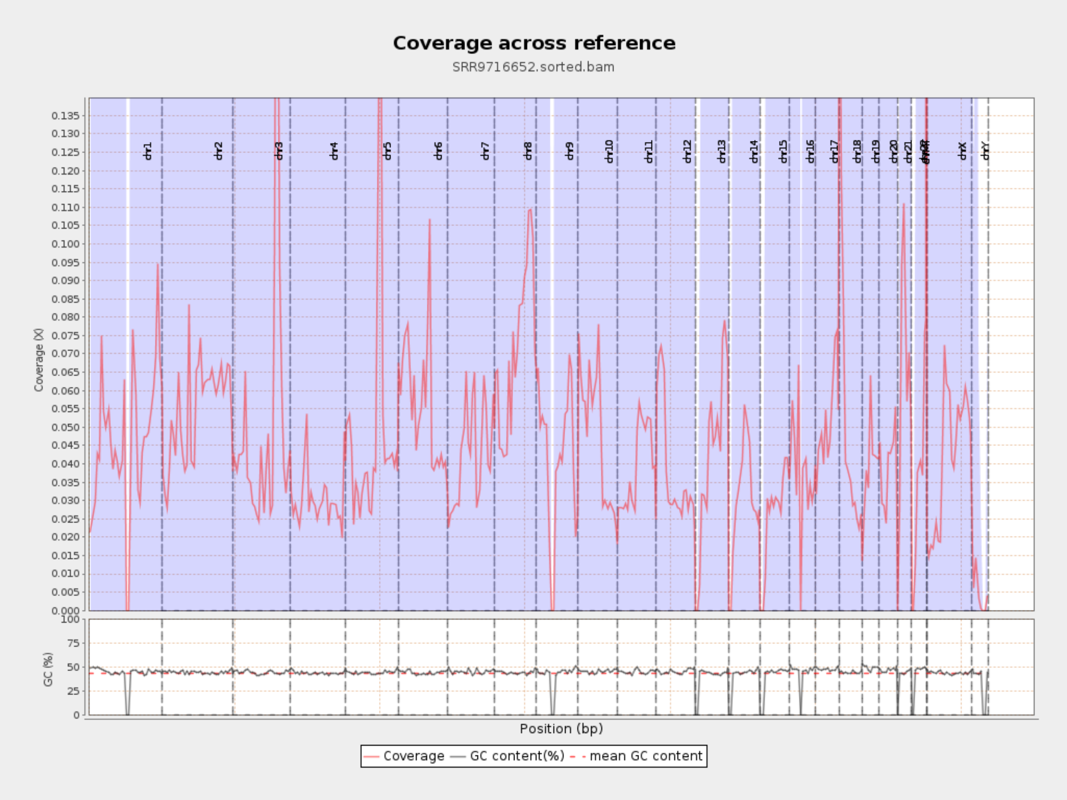
General error rate	0.74%
Mismatches	1,005,602
Insertions	9,939
Mapped reads with at least one insertion	0.51%
Deletions	26,759
Mapped reads with at least one deletion	1.38%
Homopolymer indels	39.49%

2.6. Chromosome stats

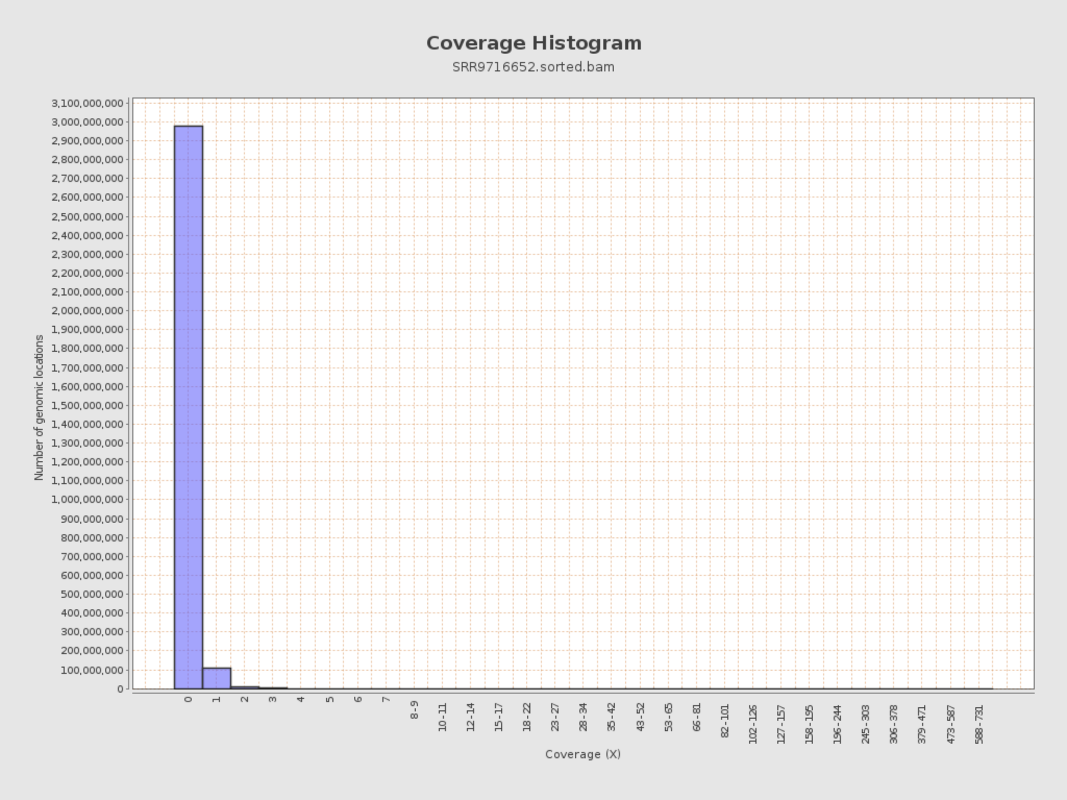
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11517419	0.0462	0.5177
chr2	243199373	13351300	0.0549	0.5495
chr3	198022430	10068063	0.0508	0.2604
chr4	191154276	5759447	0.0301	0.207
chr5	180915260	8803371	0.0487	0.2518
chr6	171115067	9761077	0.057	0.3038
chr7	159138663	6883800	0.0433	0.4888

chr8	146364022	10565189	0.0722	0.4765
chr9	141213431	5898317	0.0418	0.3224
chr10	135534747	6636862	0.049	0.337
chr11	135006516	5302908	0.0393	0.3041
chr12	133851895	5131541	0.0383	0.2204
chr13	115169878	4942857	0.0429	0.2327
chr14	107349540	3259302	0.0304	0.212
chr15	102531392	2673882	0.0261	0.1827
chr16	90354753	3376295	0.0374	0.24
chr17	81195210	4205491	0.0518	0.2845
chr18	78077248	4160209	0.0533	0.6863
chr19	59128983	2364678	0.04	0.4612
chr20	63025520	2454340	0.0389	0.2476
chr21	48129895	3048427	0.0633	0.2965
chr22	51304566	1737499	0.0339	0.2078
chrMT	16571	34393	2.0755	1.8752
chrX	155270560	6505635	0.0419	0.2831
chrY	59373566	299396	0.005	0.1322

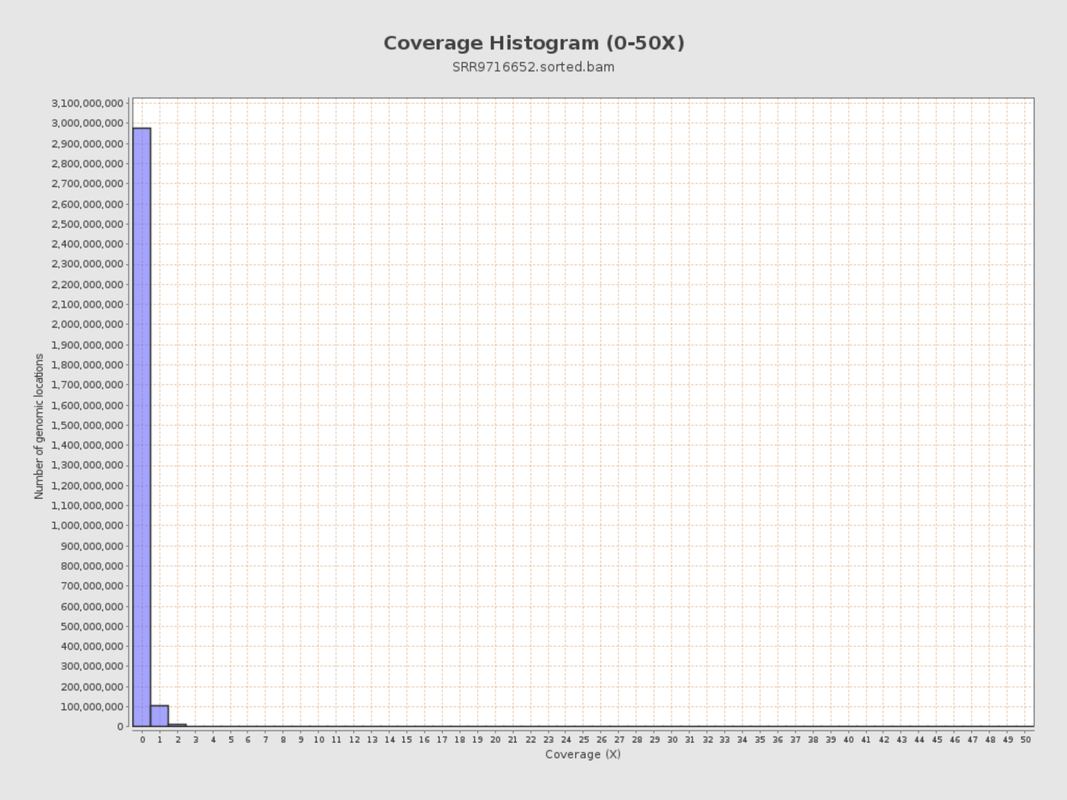
3. Results : Coverage across reference



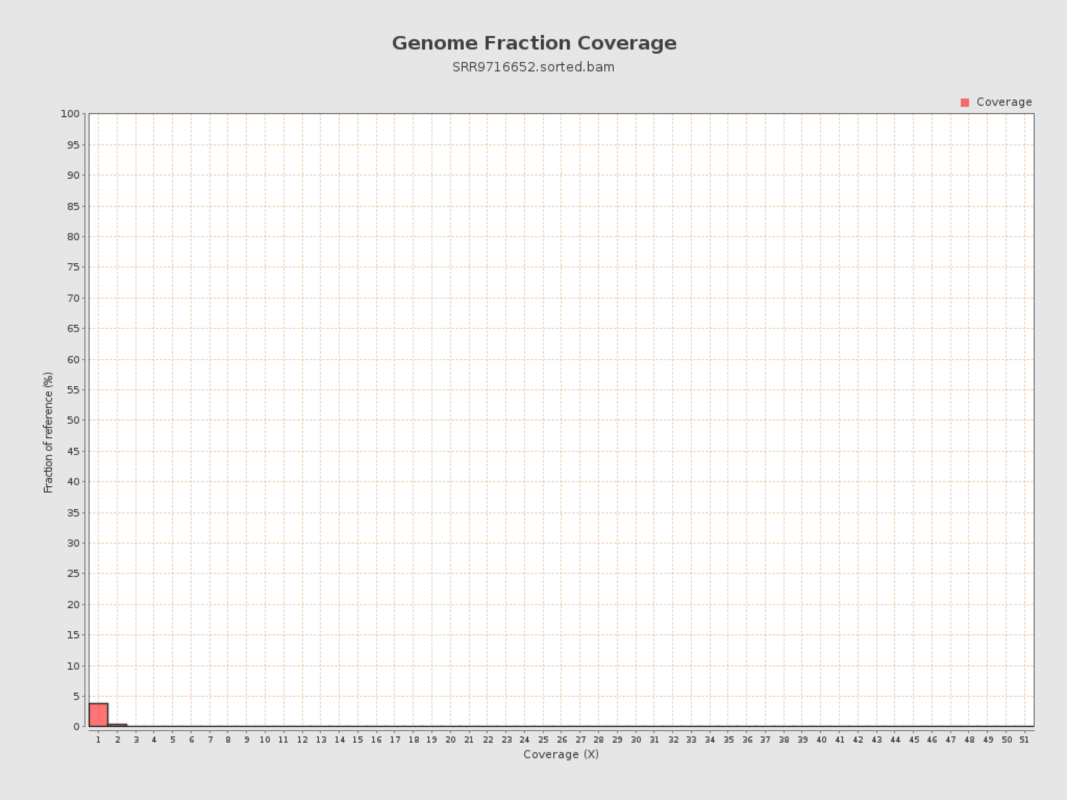
4. Results : Coverage Histogram



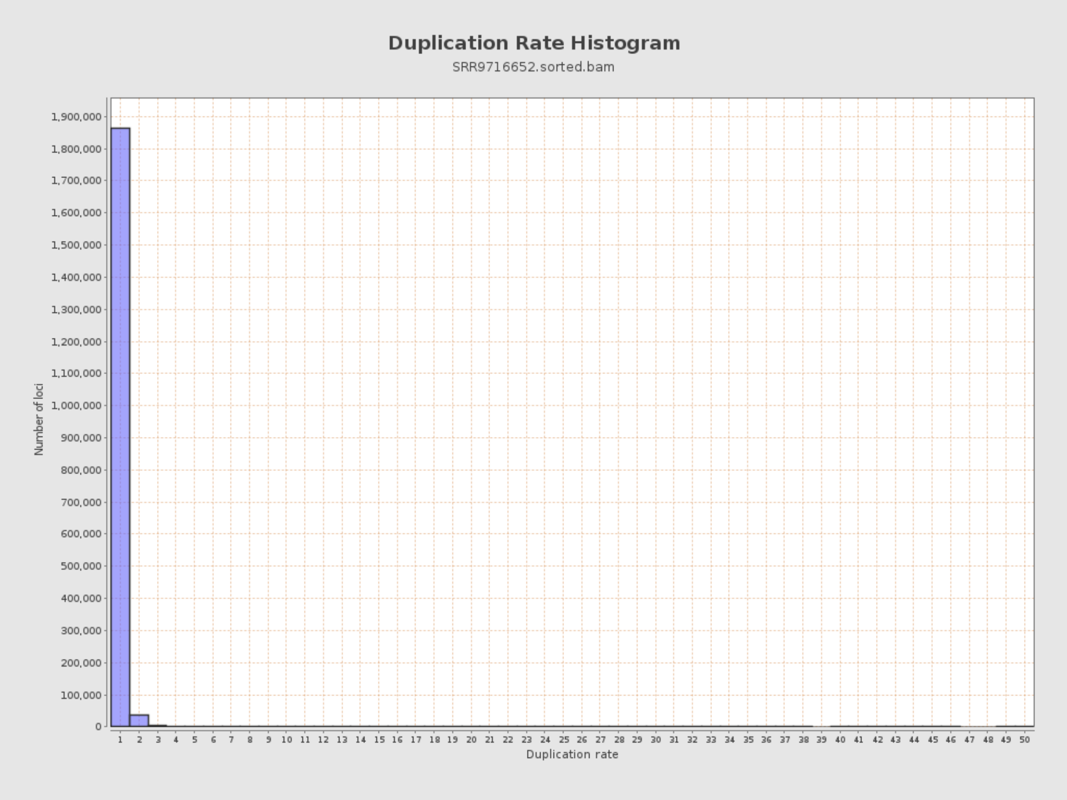
5. Results : Coverage Histogram (0-50X)



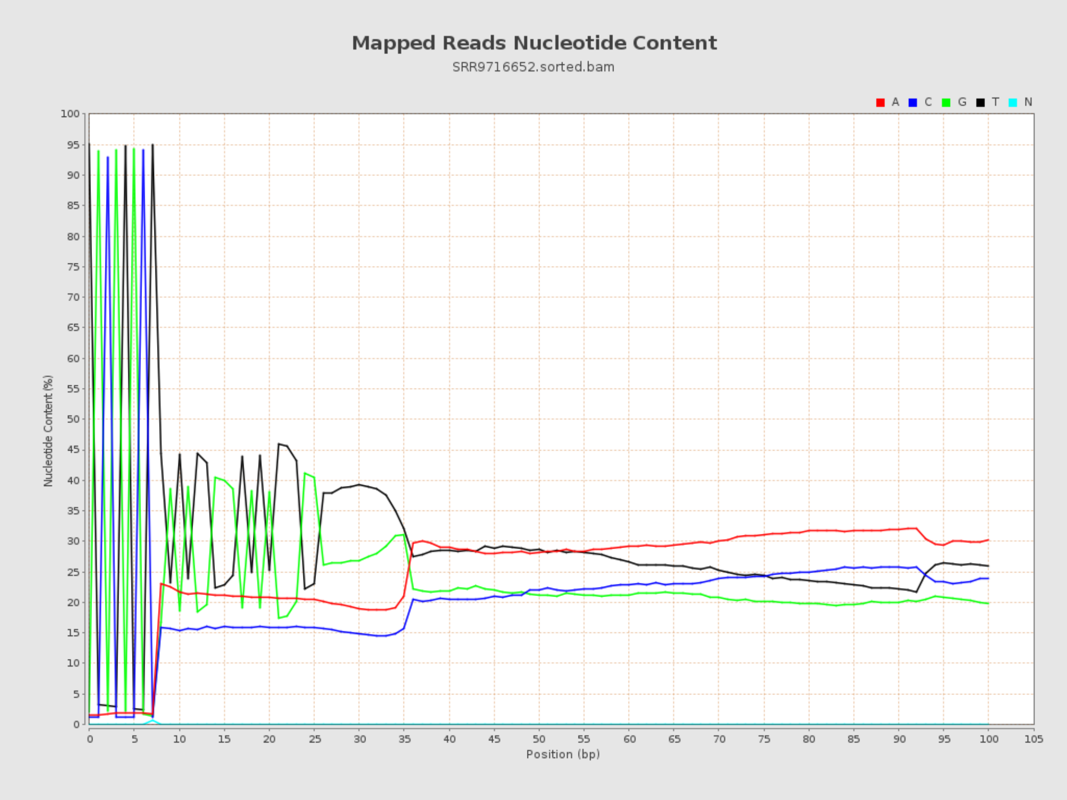
6. Results : Genome Fraction Coverage



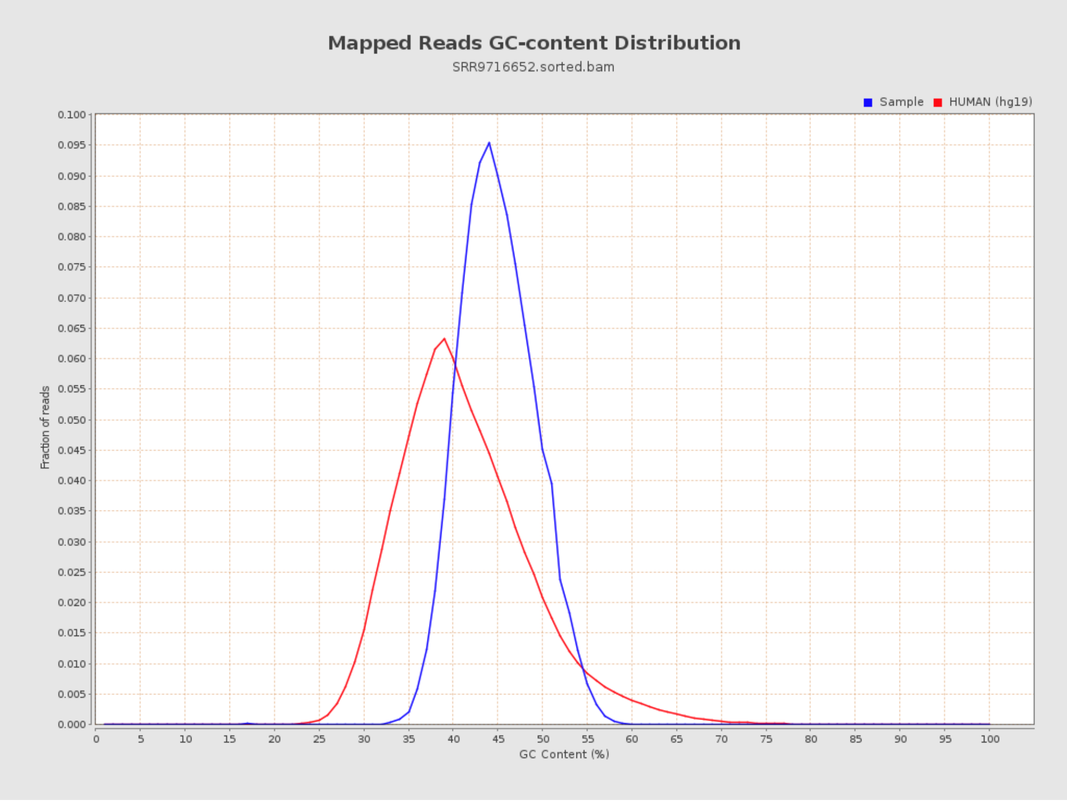
7. Results : Duplication Rate Histogram



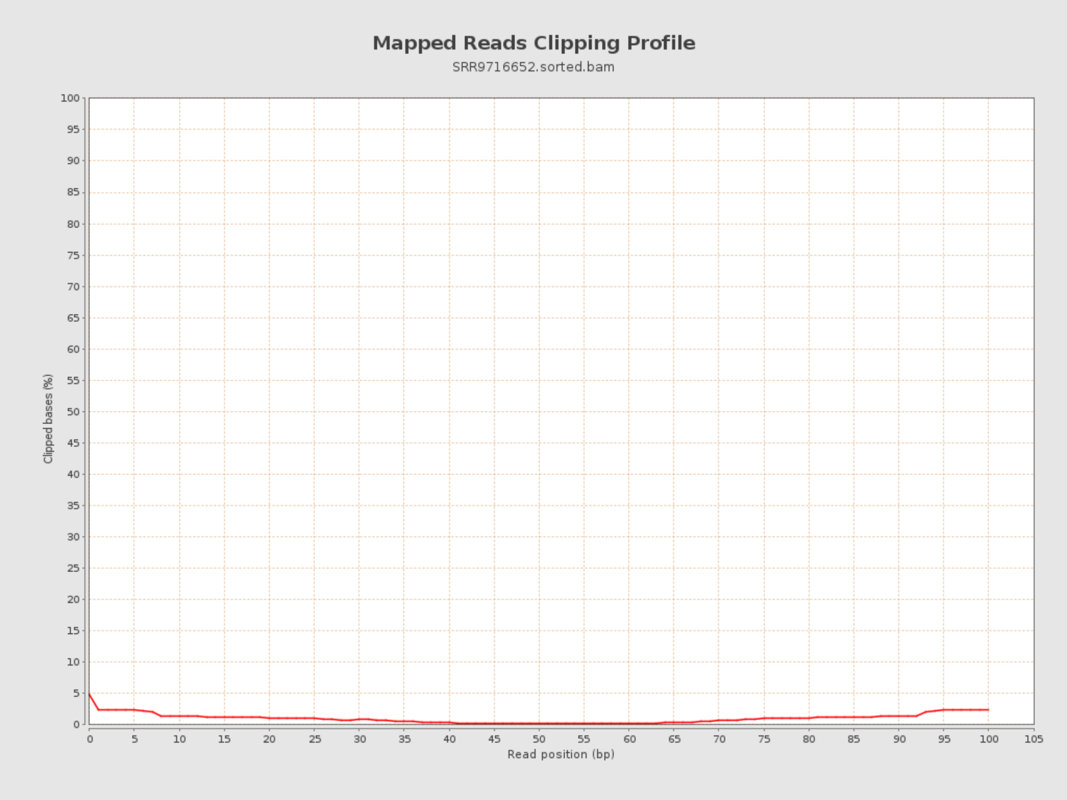
8. Results : Mapped Reads Nucleotide Content



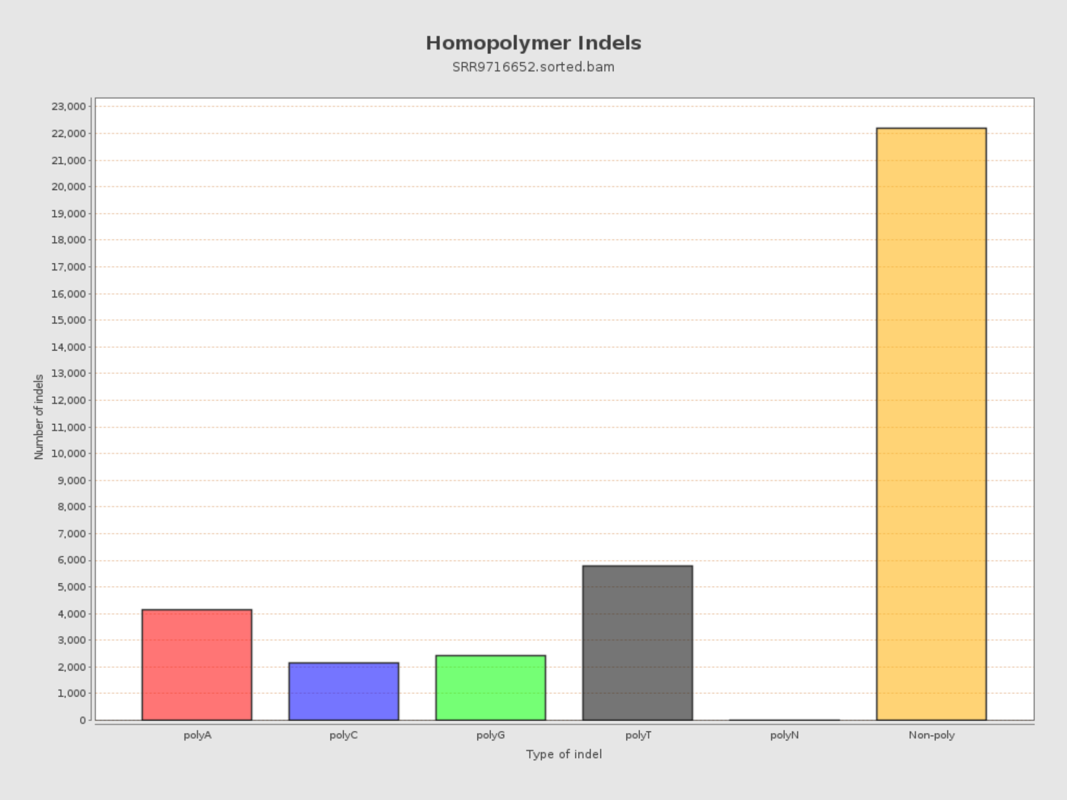
9. Results : Mapped Reads GC-content Distribution



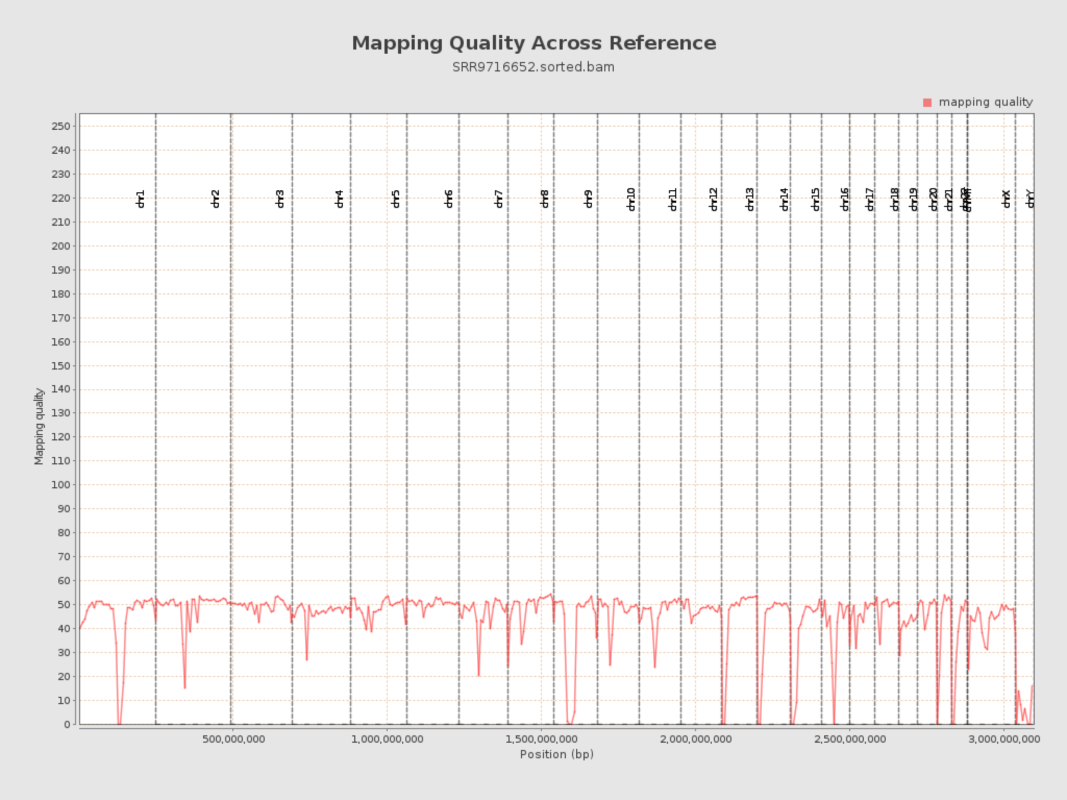
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram