Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 19:03:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716127.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_SRR9716127 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716127.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 19:03:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716127.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,229,128
Mapped reads	1,124,263 / 91.47%
Unmapped reads	104,865 / 8.53%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,902 / 1.86%
Read min/max/mean length	30 / 101 / 101.67
Duplicated reads (estimated)	34,354 / 2.79%
Duplication rate	2.1%
Clipped reads	1,144,728 / 93.13%

2.2. ACGT Content

Number/percentage of A's	22,139,827 / 25.17%
Number/percentage of C's	16,525,406 / 18.78%
Number/percentage of T's	27,638,264 / 31.42%
Number/percentage of G's	21,664,030 / 24.63%
Number/percentage of N's	5,139 / 0.01%
GC Percentage	43.41%

2.3. Coverage

Mean	0.0284

Standard Deviation	0.2876

2.4. Mapping Quality

Mean Mapping Quality	47.07

2.5. Mismatches and indels

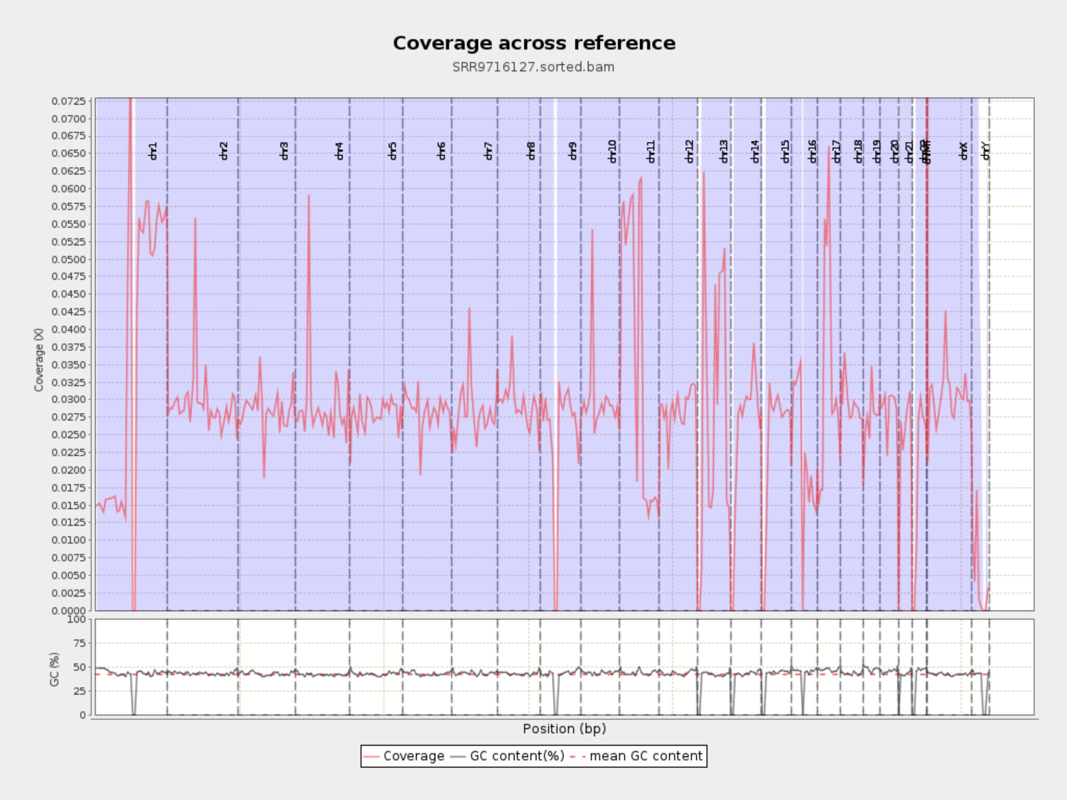
General error rate	0.68%
Mismatches	584,408
Insertions	7,493
Mapped reads with at least one insertion	0.66%
Deletions	20,684
Mapped reads with at least one deletion	1.81%
Homopolymer indels	43.07%

2.6. Chromosome stats

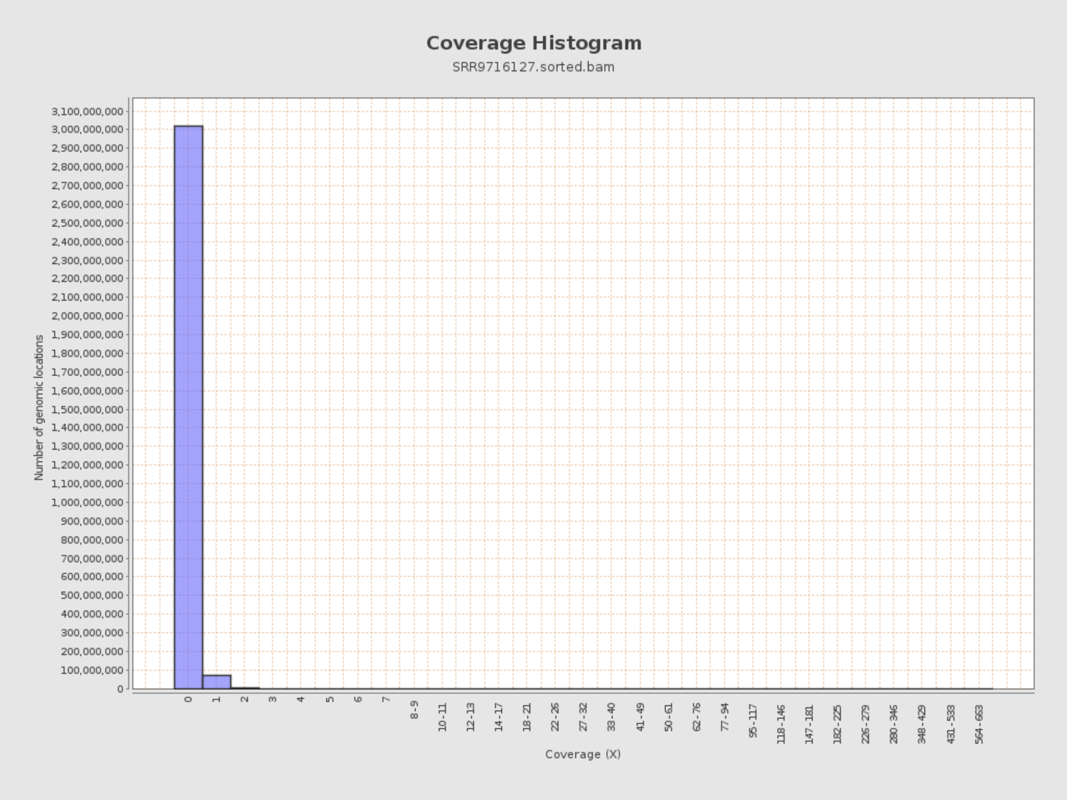
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8567564	0.0344	0.568
chr2	243199373	7219059	0.0297	0.308
chr3	198022430	5664108	0.0286	0.182
chr4	191154276	5594696	0.0293	0.2272
chr5	180915260	5097663	0.0282	0.1818
chr6	171115067	4851113	0.0284	0.1935
chr7	159138663	4518462	0.0284	0.3363

chr8	146364022	4308217	0.0294	0.3178
chr9	141213431	3526043	0.025	0.2414
chr10	135534747	4075333	0.0301	0.2909
chr11	135006516	4924729	0.0365	0.311
chr12	133851895	3829075	0.0286	0.1831
chr13	115169878	3131935	0.0272	0.1792
chr14	107349540	2699549	0.0251	0.1836
chr15	102531392	2426703	0.0237	0.1664
chr16	90354753	1965155	0.0217	0.1701
chr17	81195210	2690396	0.0331	0.2272
chr18	78077248	2316262	0.0297	0.4072
chr19	59128983	1635841	0.0277	0.4066
chr20	63025520	1794714	0.0285	0.1924
chr21	48129895	1163452	0.0242	0.1939
chr22	51304566	969975	0.0189	0.1493
chrMT	16571	27965	1.6876	1.5578
chrX	155270560	4752124	0.0306	0.2148
chrY	59373566	262212	0.0044	0.1553

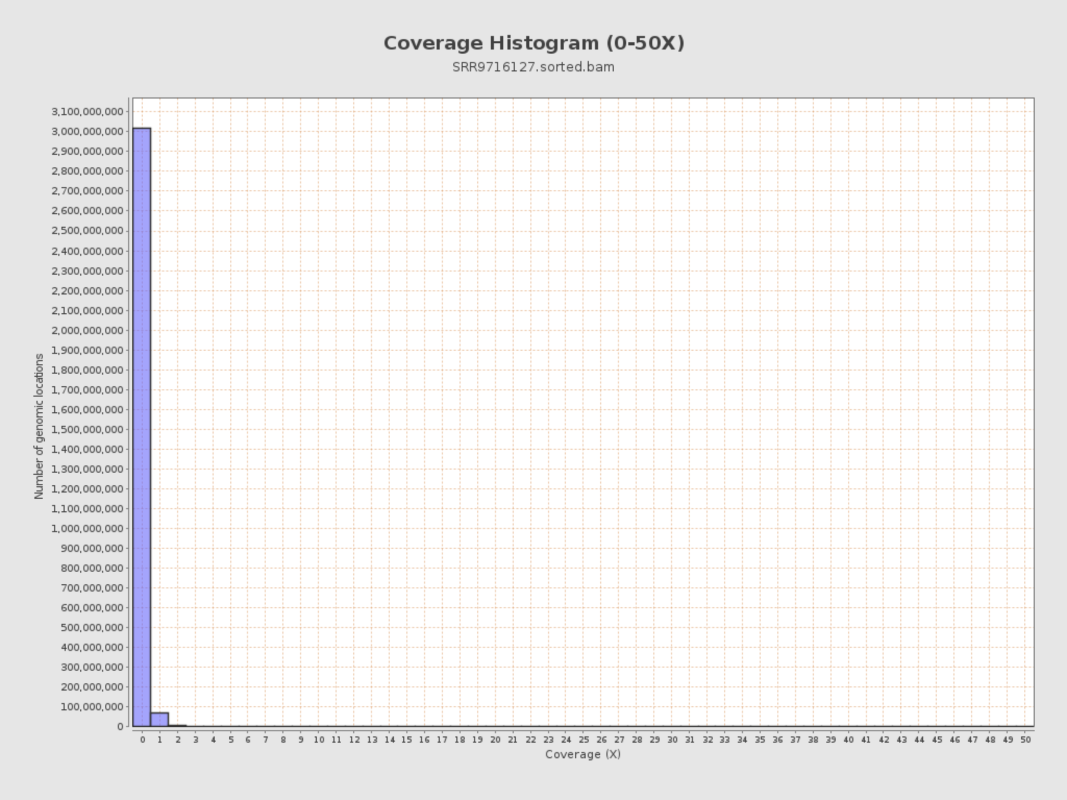
3. Results : Coverage across reference



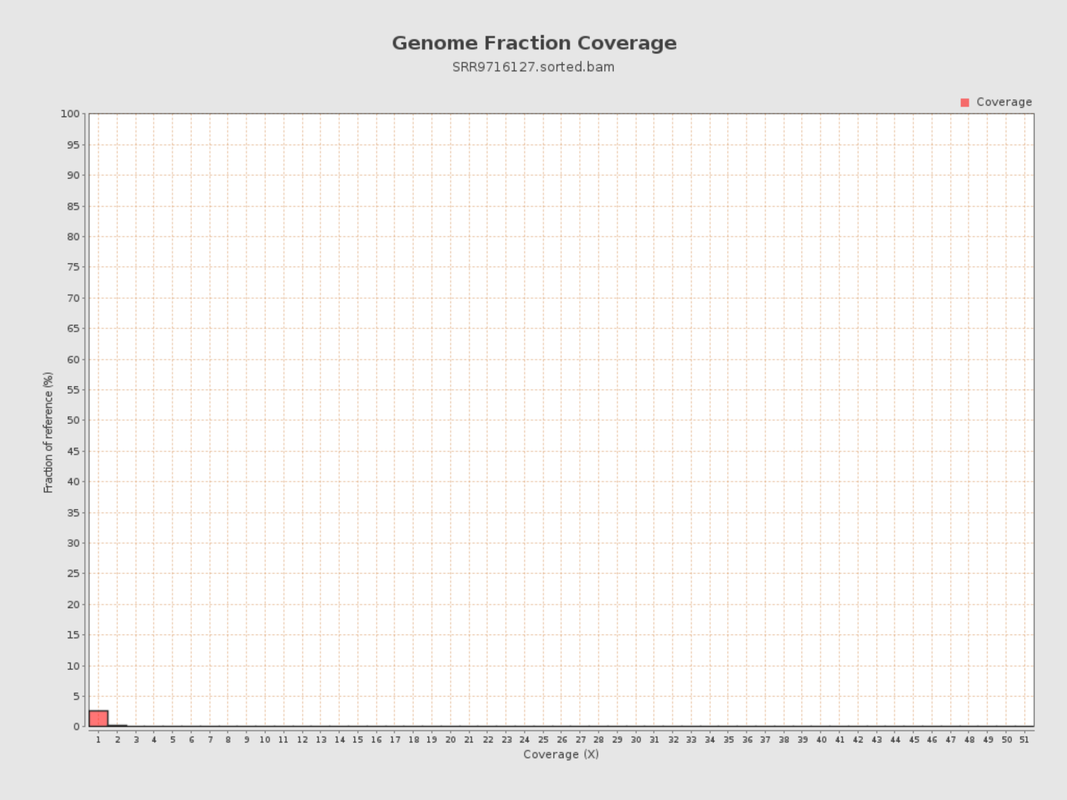
4. Results : Coverage Histogram



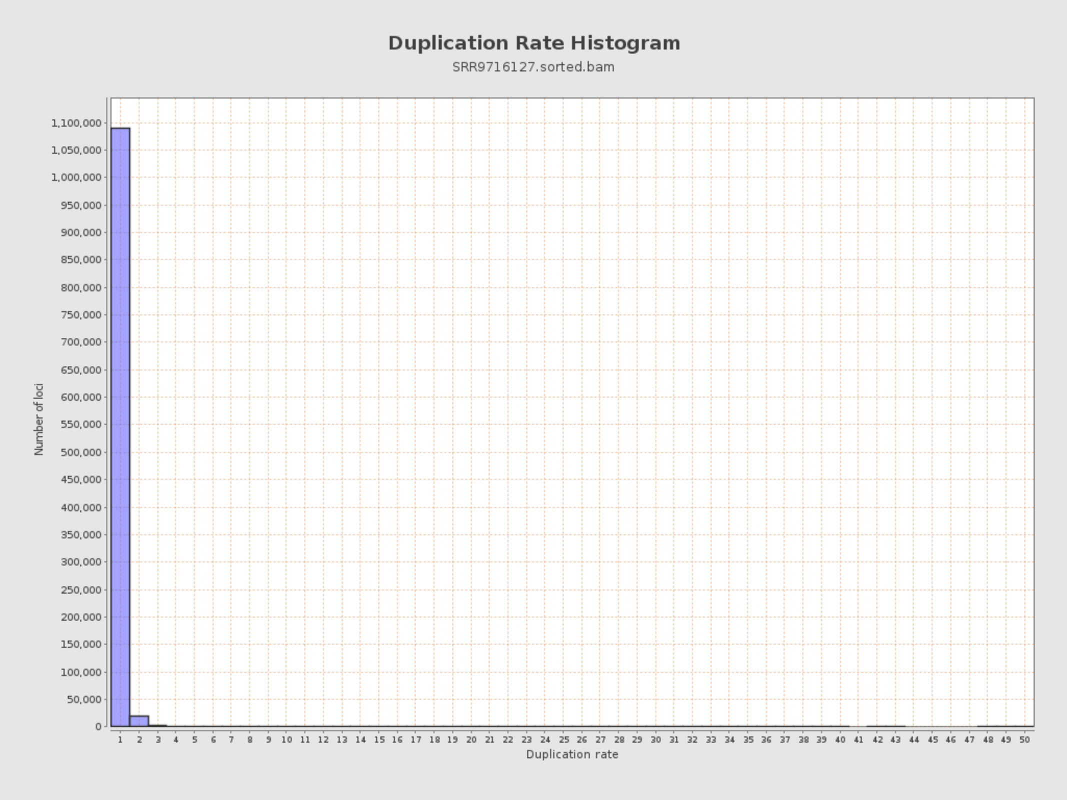
5. Results : Coverage Histogram (0-50X)



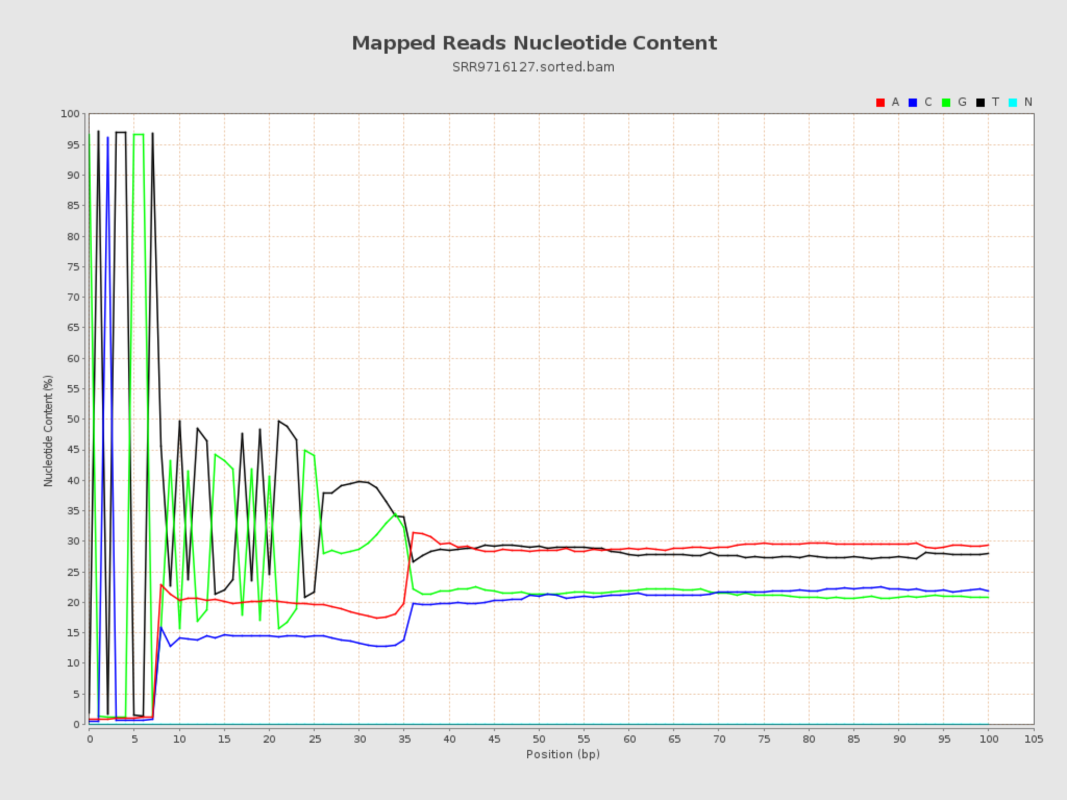
6. Results : Genome Fraction Coverage



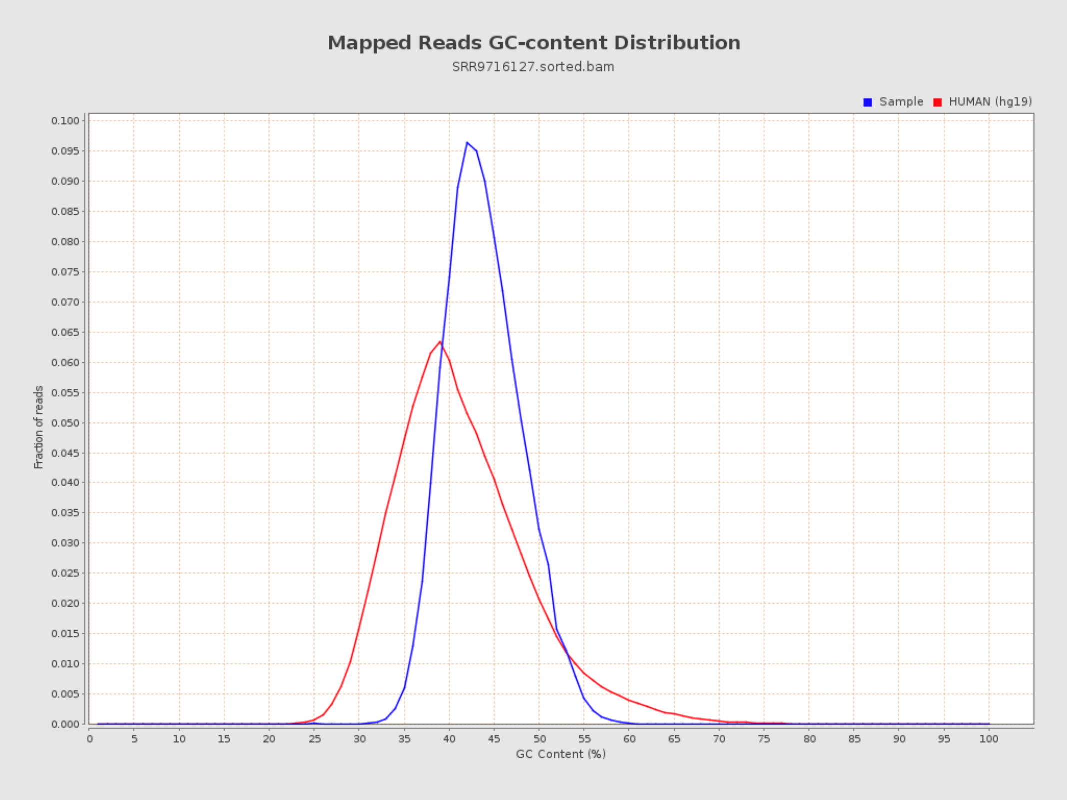
7. Results : Duplication Rate Histogram



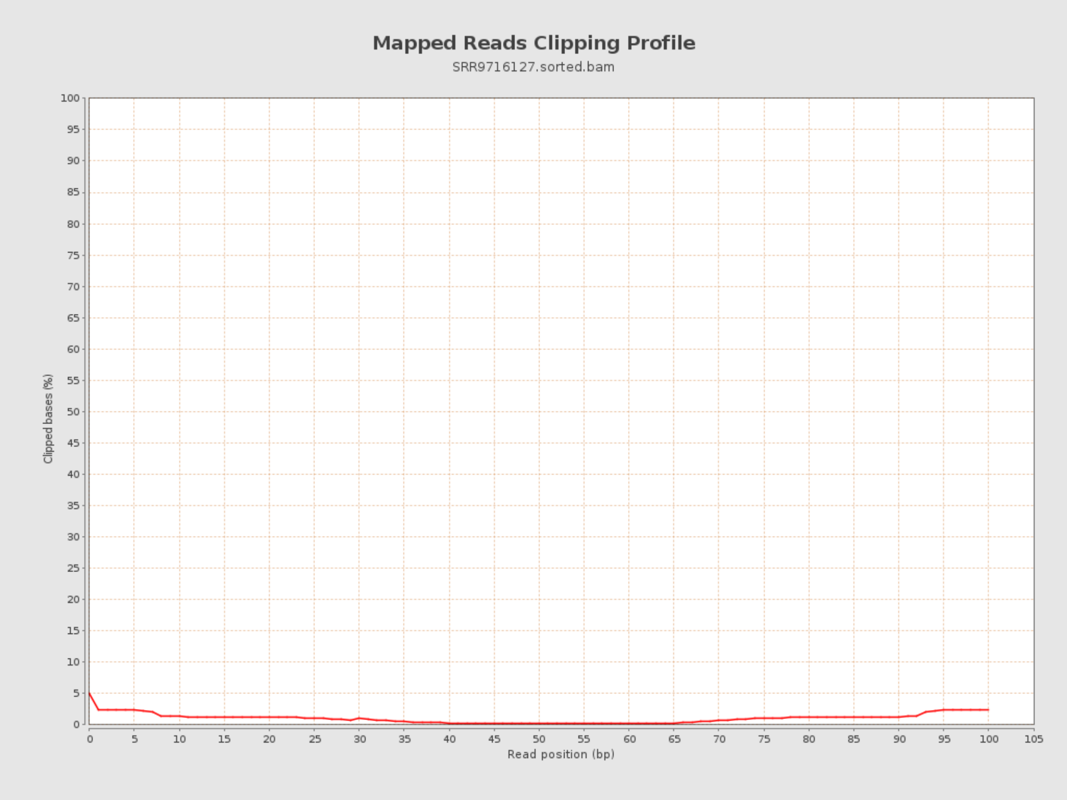
8. Results : Mapped Reads Nucleotide Content



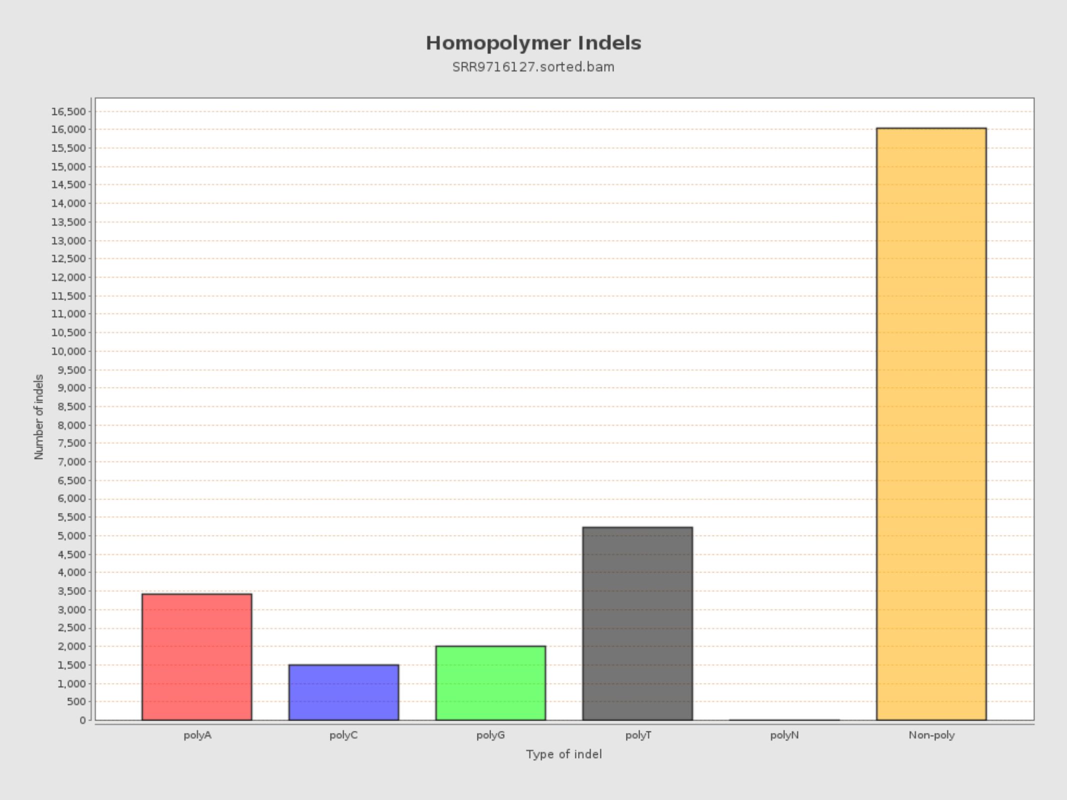
9. Results : Mapped Reads GC-content Distribution



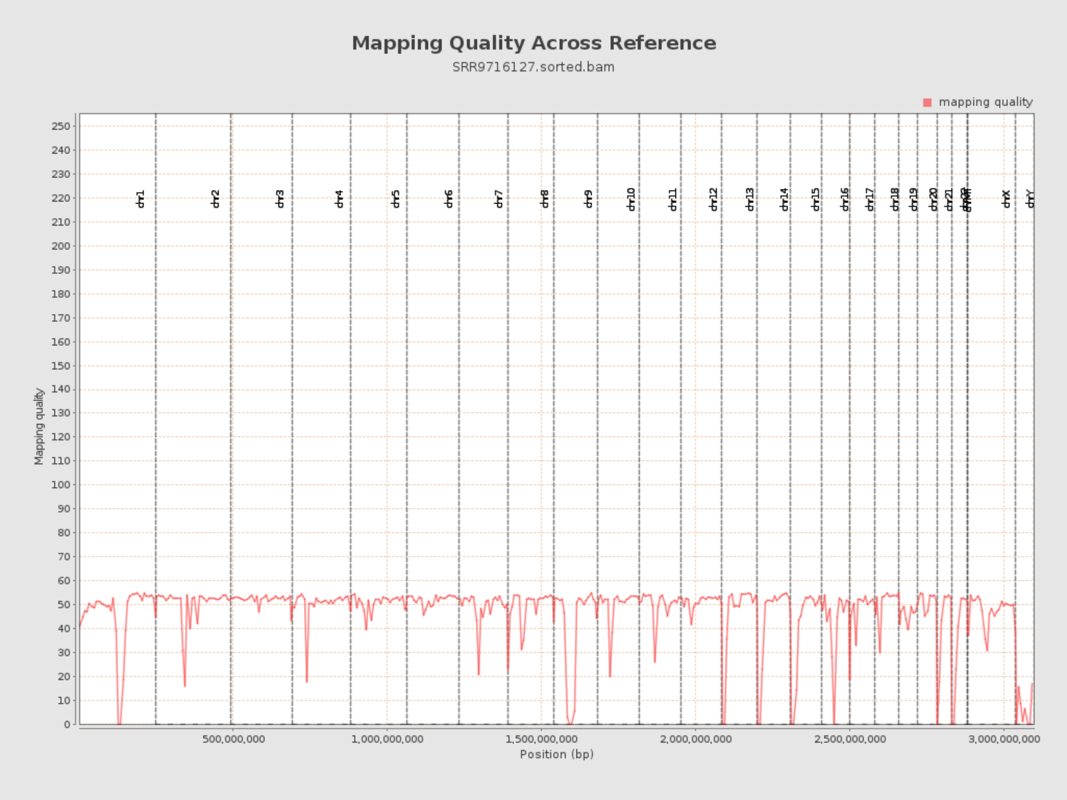
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram