Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 19:01:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716126.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_SRR9716126 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716126.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 19:01:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716126.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	800,732
Mapped reads	712,269 / 88.95%
Unmapped reads	88,463 / 11.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,276 / 1.78%
Read min/max/mean length	30 / 101 / 101.64
Duplicated reads (estimated)	17,090 / 2.13%
Duplication rate	1.68%
Clipped reads	725,069 / 90.55%

2.2. ACGT Content

Number/percentage of A's	14,620,024 / 26.28%
Number/percentage of C's	10,793,130 / 19.4%
Number/percentage of T's	17,171,367 / 30.87%
Number/percentage of G's	13,039,056 / 23.44%
Number/percentage of N's	3,926 / 0.01%
GC Percentage	42.84%

2.3. Coverage

Mean	0.018

Standard Deviation	0.2004

2.4. Mapping Quality

Mean Mapping Quality	46.9

2.5. Mismatches and indels

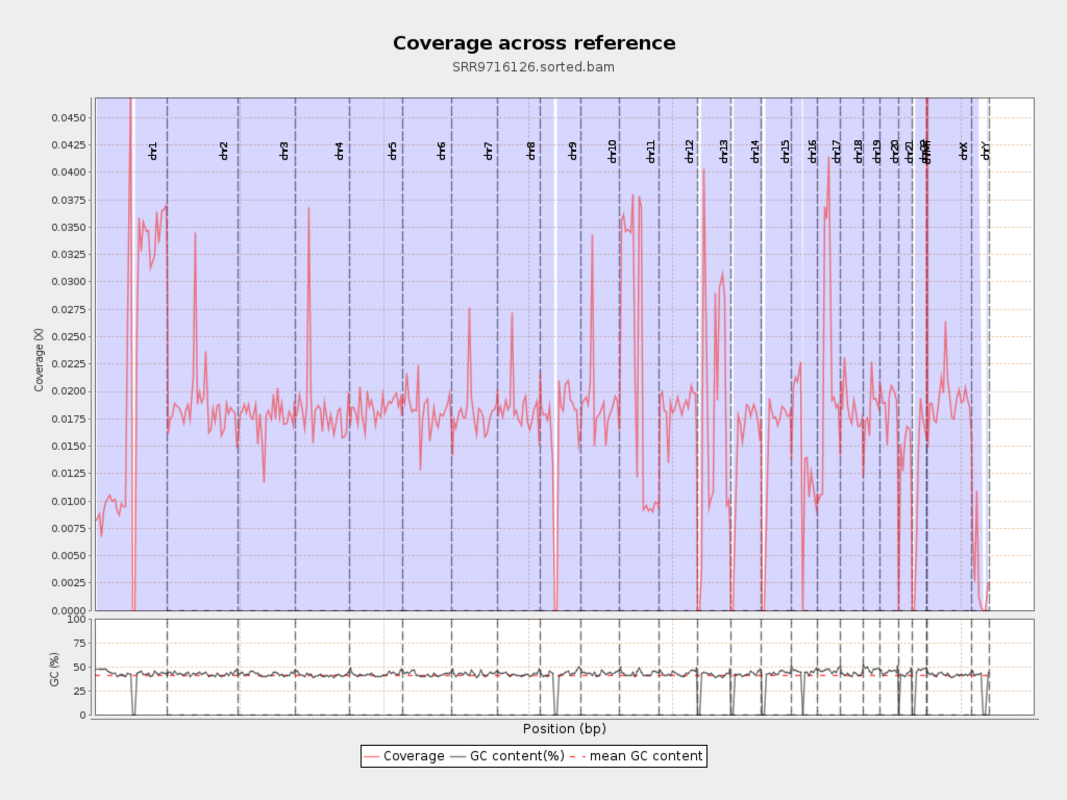
General error rate	0.72%
Mismatches	386,574
Insertions	5,036
Mapped reads with at least one insertion	0.7%
Deletions	13,487
Mapped reads with at least one deletion	1.86%
Homopolymer indels	42.89%

2.6. Chromosome stats

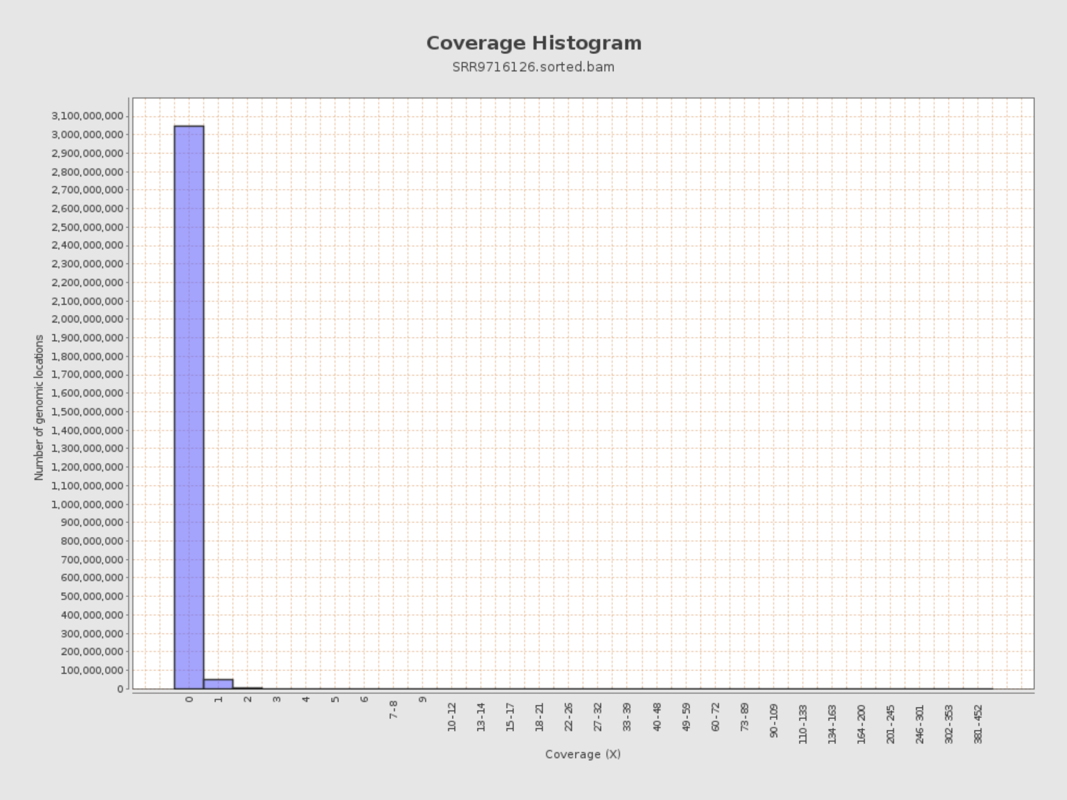
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5307121	0.0213	0.3912
chr2	243199373	4564897	0.0188	0.2069
chr3	198022430	3486115	0.0176	0.1393
chr4	191154276	3527887	0.0185	0.1633
chr5	180915260	3356406	0.0186	0.1436
chr6	171115067	3119837	0.0182	0.1497
chr7	159138663	2880661	0.0181	0.2196

chr8	146364022	2702670	0.0185	0.2053
chr9	141213431	2308180	0.0163	0.1738
chr10	135534747	2592171	0.0191	0.1971
chr11	135006516	3076027	0.0228	0.2123
chr12	133851895	2489977	0.0186	0.1434
chr13	115169878	1975148	0.0171	0.138
chr14	107349540	1563219	0.0146	0.1318
chr15	102531392	1504070	0.0147	0.1271
chr16	90354753	1283074	0.0142	0.1318
chr17	81195210	1768171	0.0218	0.169
chr18	78077248	1442489	0.0185	0.2706
chr19	59128983	1089687	0.0184	0.27
chr20	63025520	1187247	0.0188	0.1488
chr21	48129895	653645	0.0136	0.1325
chr22	51304566	599418	0.0117	0.1138
chrMT	16571	10194	0.6152	0.9131
chrX	155270560	2992580	0.0193	0.1588
chrY	59373566	172429	0.0029	0.1011

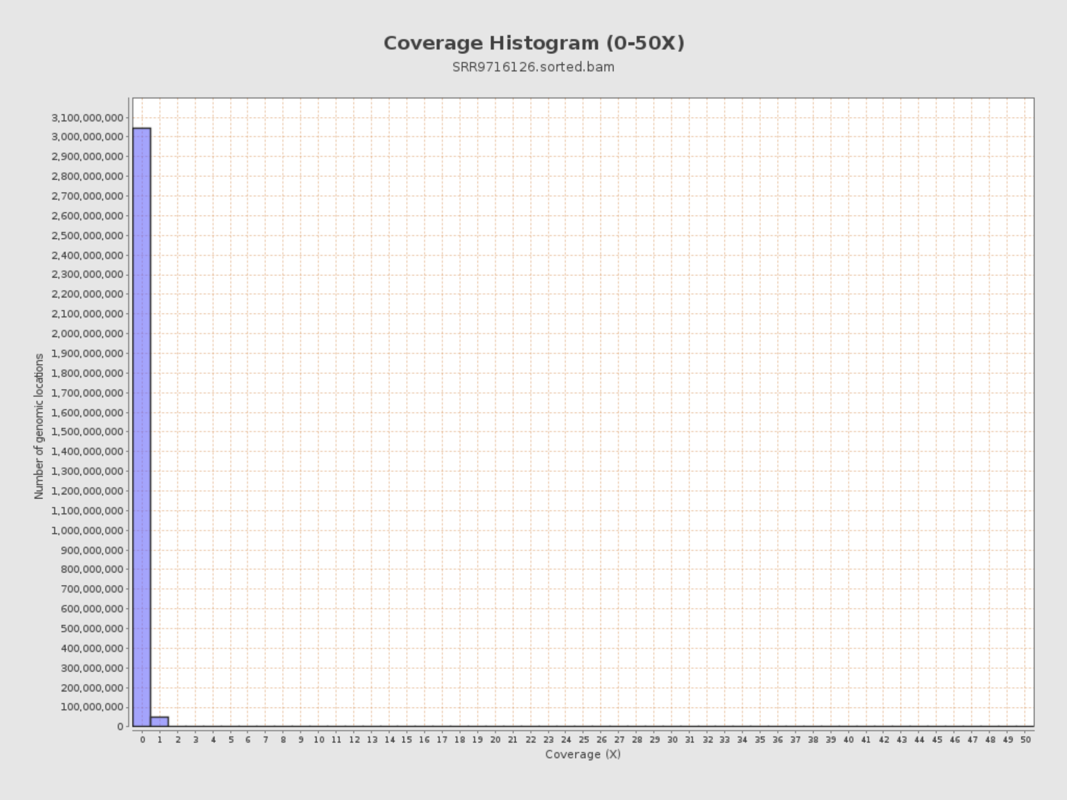
3. Results : Coverage across reference



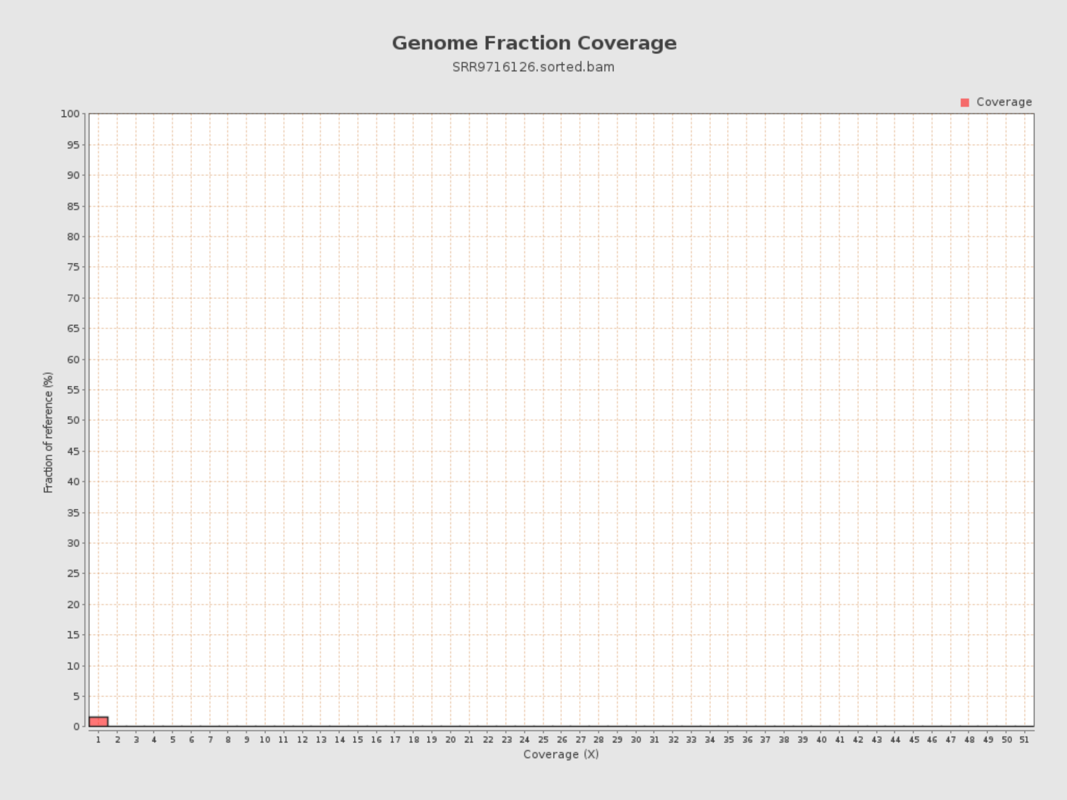
4. Results : Coverage Histogram



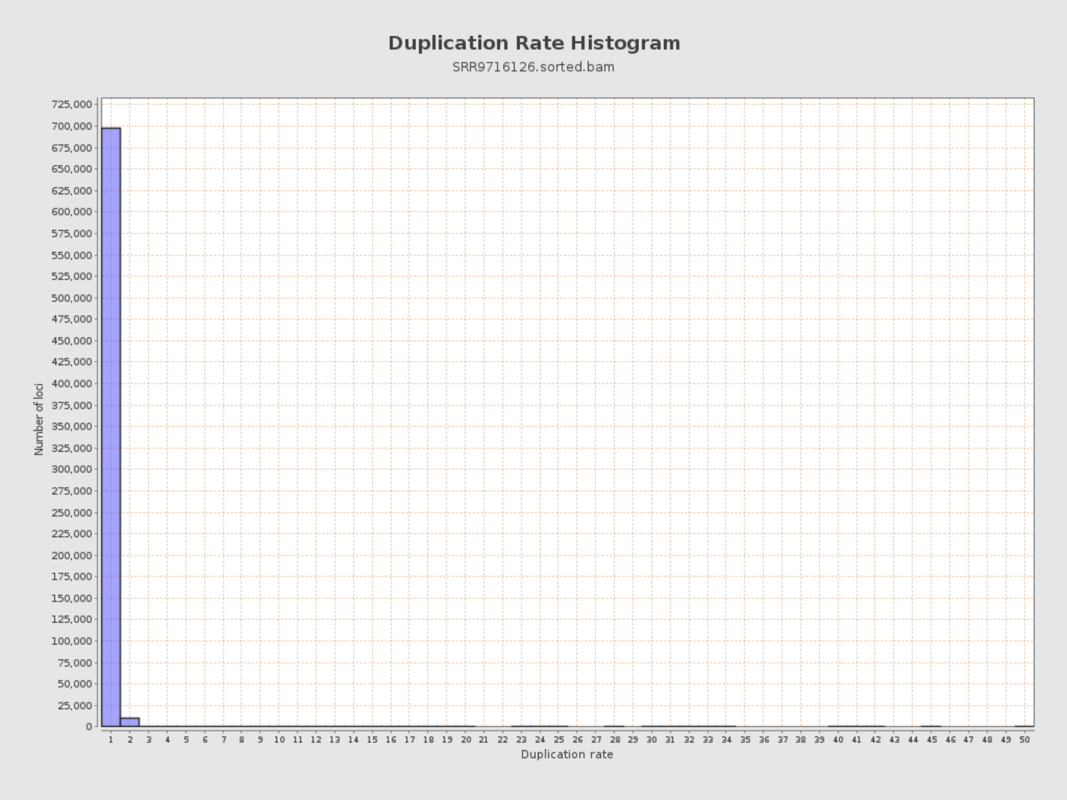
5. Results : Coverage Histogram (0-50X)



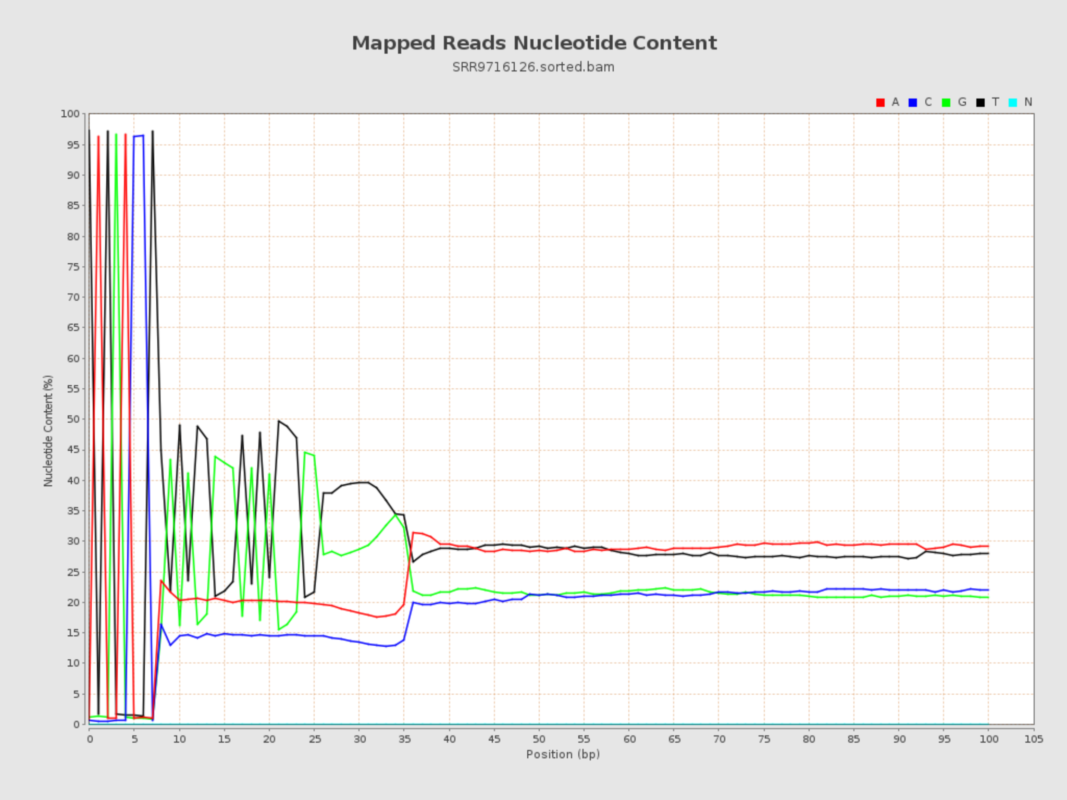
6. Results : Genome Fraction Coverage



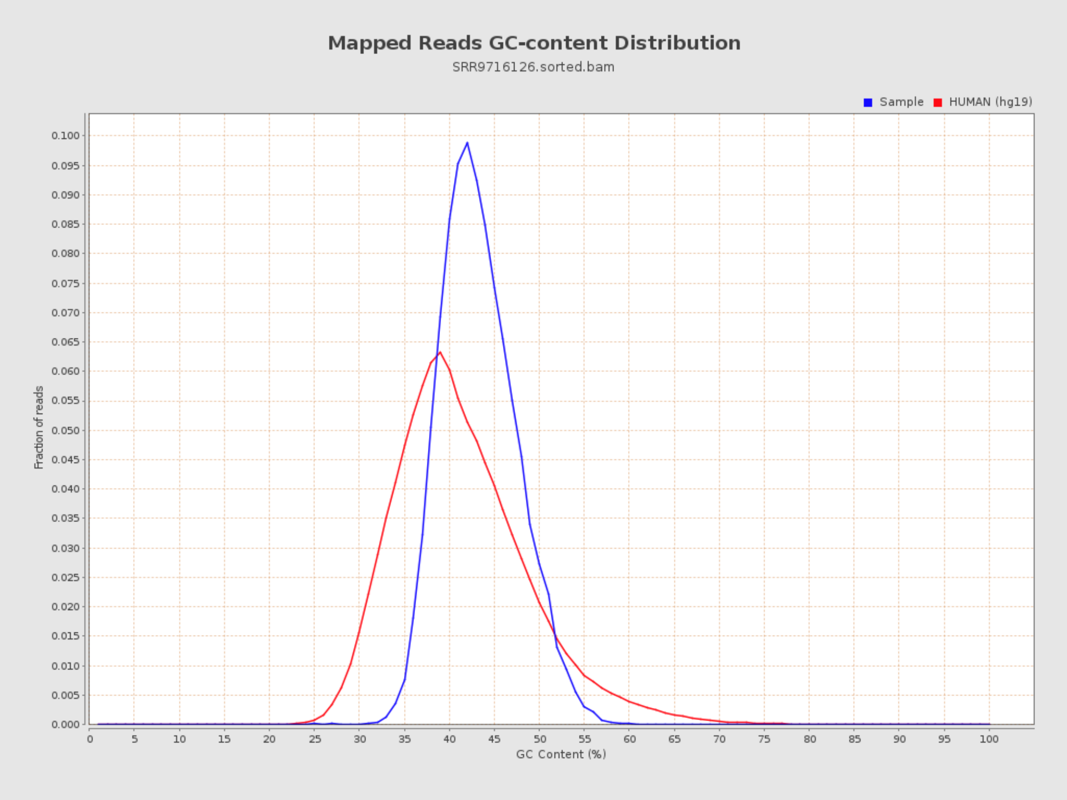
7. Results : Duplication Rate Histogram



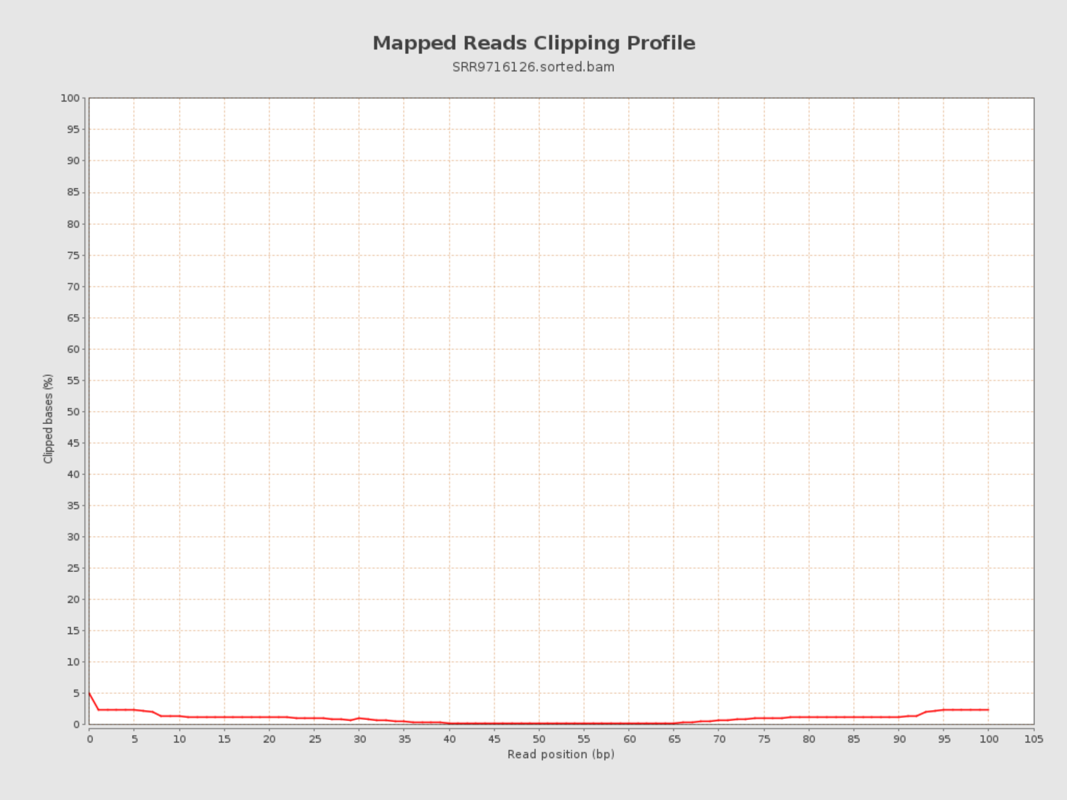
8. Results : Mapped Reads Nucleotide Content



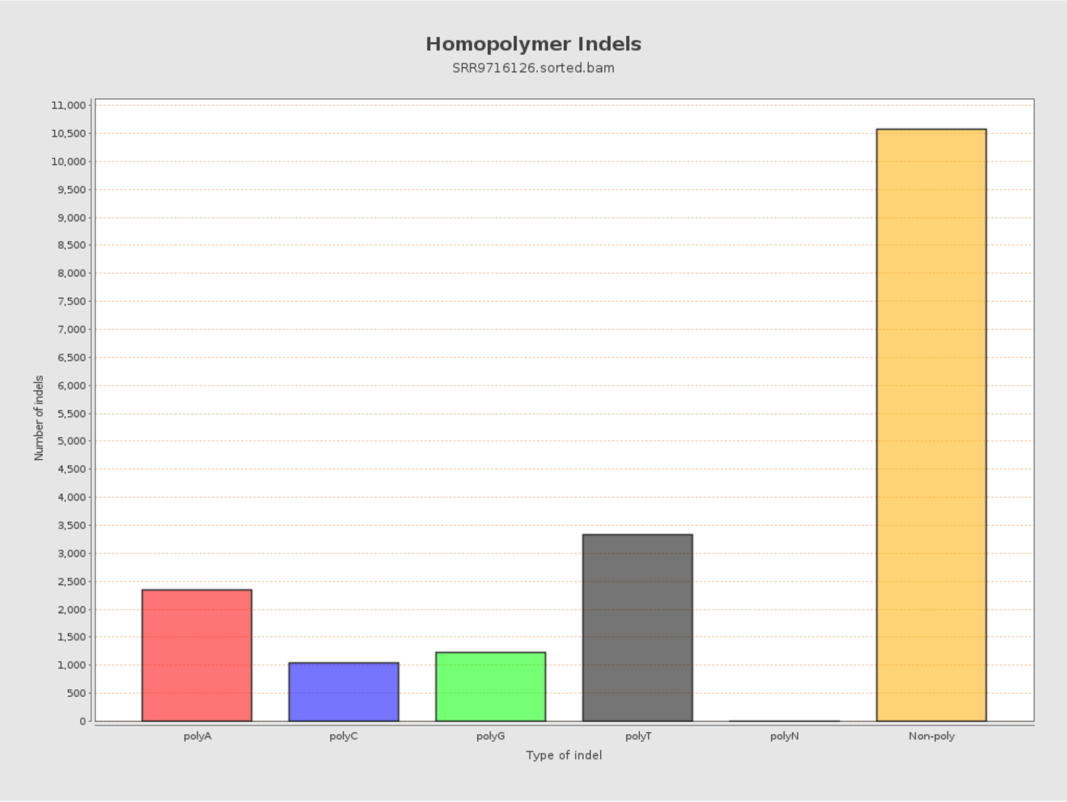
9. Results : Mapped Reads GC-content Distribution



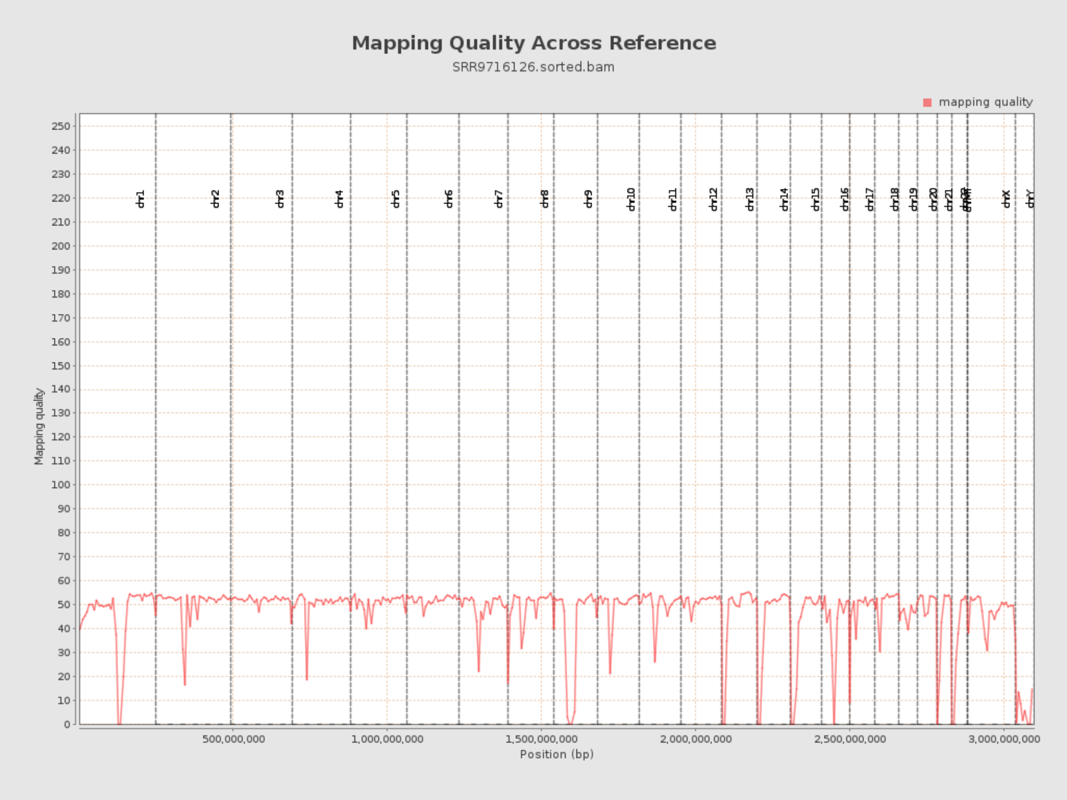
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram