Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 06:48:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716697.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_SRR9716697 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716697.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 06:48:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716697.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,146,548
Mapped reads	1,062,971 / 92.71%
Unmapped reads	83,577 / 7.29%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,491 / 1.53%
Read min/max/mean length	30 / 101 / 101.56
Duplicated reads (estimated)	35,024 / 3.05%
Duplication rate	1.89%
Clipped reads	1,078,636 / 94.08%

2.2. ACGT Content

Number/percentage of A's	20,441,957 / 24.25%
Number/percentage of C's	17,493,932 / 20.75%
Number/percentage of T's	25,108,798 / 29.79%
Number/percentage of G's	21,244,366 / 25.2%
Number/percentage of N's	4,685 / 0.01%
GC Percentage	45.96%

2.3. Coverage

Mean	0.0272

Standard Deviation	0.3419

2.4. Mapping Quality

Mean Mapping Quality	42.86

2.5. Mismatches and indels

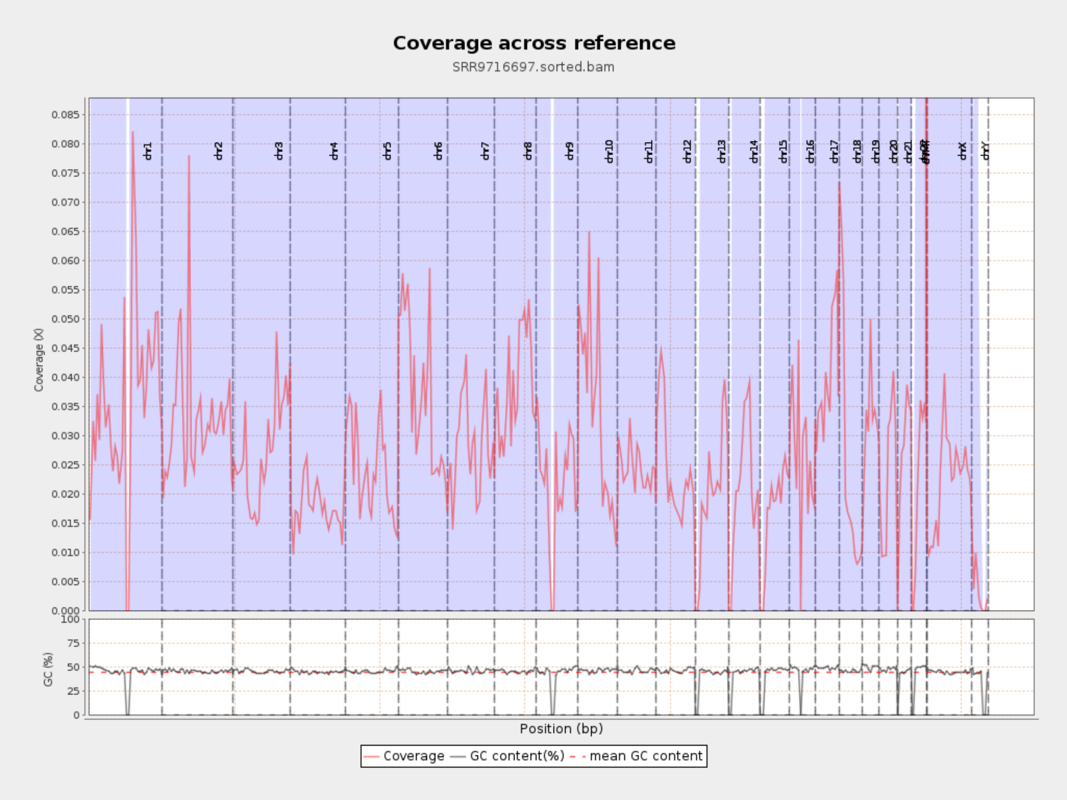
General error rate	0.86%
Mismatches	705,010
Insertions	7,937
Mapped reads with at least one insertion	0.74%
Deletions	21,004
Mapped reads with at least one deletion	1.95%
Homopolymer indels	44.44%

2.6. Chromosome stats

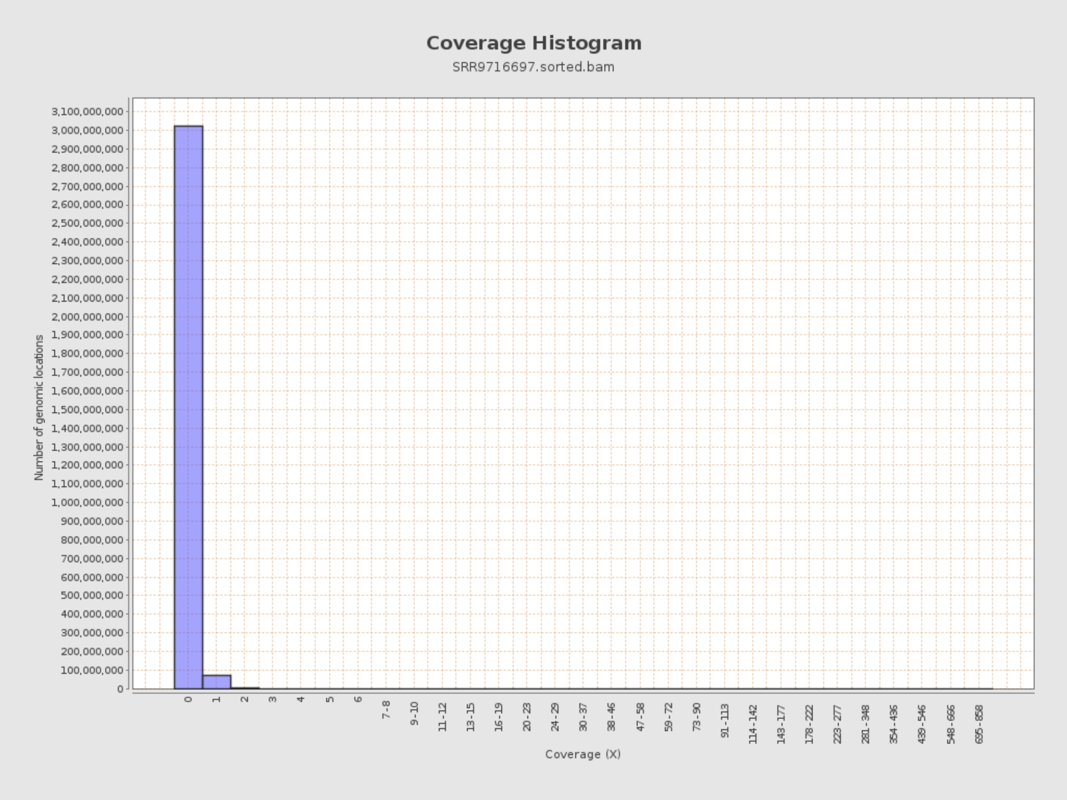
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8941809	0.0359	0.5643
chr2	243199373	8039504	0.0331	0.6161
chr3	198022430	5354511	0.027	0.1835
chr4	191154276	3350640	0.0175	0.15
chr5	180915260	4401368	0.0243	0.1713
chr6	171115067	6344720	0.0371	0.2549
chr7	159138663	4543903	0.0286	0.337

chr8	146364022	5689842	0.0389	0.4564
chr9	141213431	3020134	0.0214	0.3206
chr10	135534747	4684722	0.0346	0.3837
chr11	135006516	3305098	0.0245	0.2669
chr12	133851895	3249481	0.0243	0.172
chr13	115169878	2349714	0.0204	0.1547
chr14	107349540	2239420	0.0209	0.1819
chr15	102531392	1735007	0.0169	0.1419
chr16	90354753	2359314	0.0261	0.1985
chr17	81195210	3264573	0.0402	0.2464
chr18	78077248	1964197	0.0252	0.5687
chr19	59128983	1930092	0.0326	0.4461
chr20	63025520	1438350	0.0228	0.1826
chr21	48129895	1312420	0.0273	0.1846
chr22	51304566	1083786	0.0211	0.1625
chrMT	16571	38441	2.3198	2.0207
chrX	155270560	3495485	0.0225	0.2034
chrY	59373566	193932	0.0033	0.0952

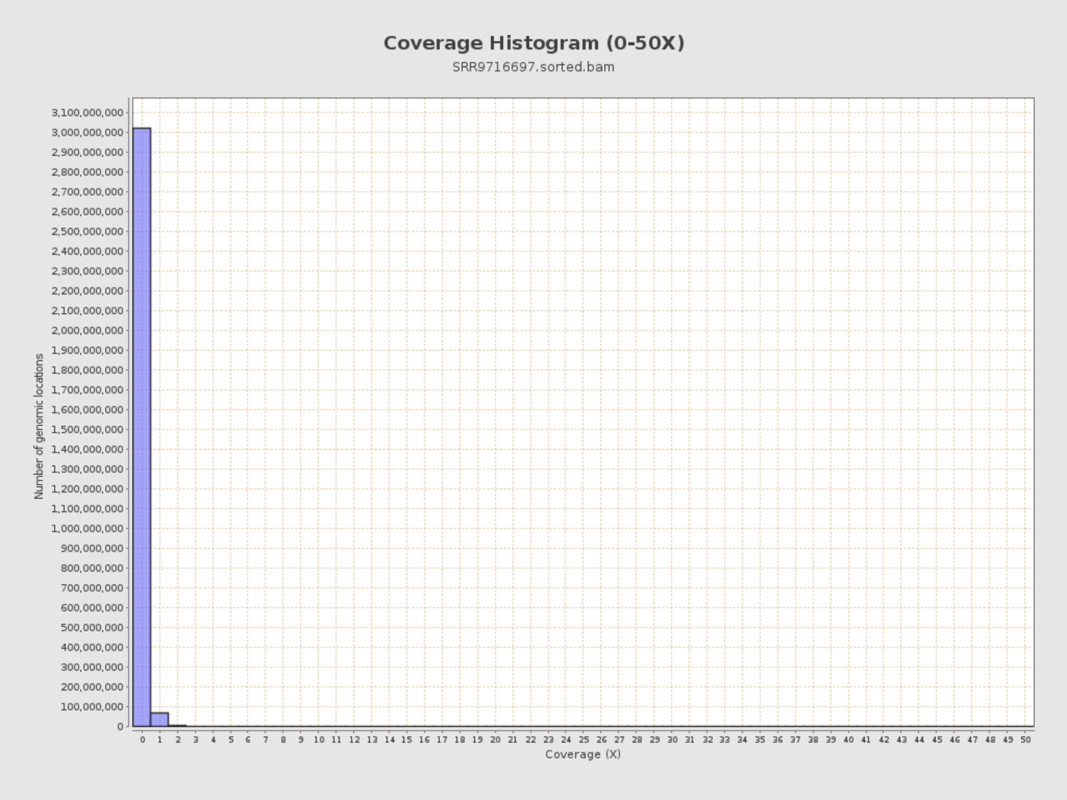
3. Results : Coverage across reference



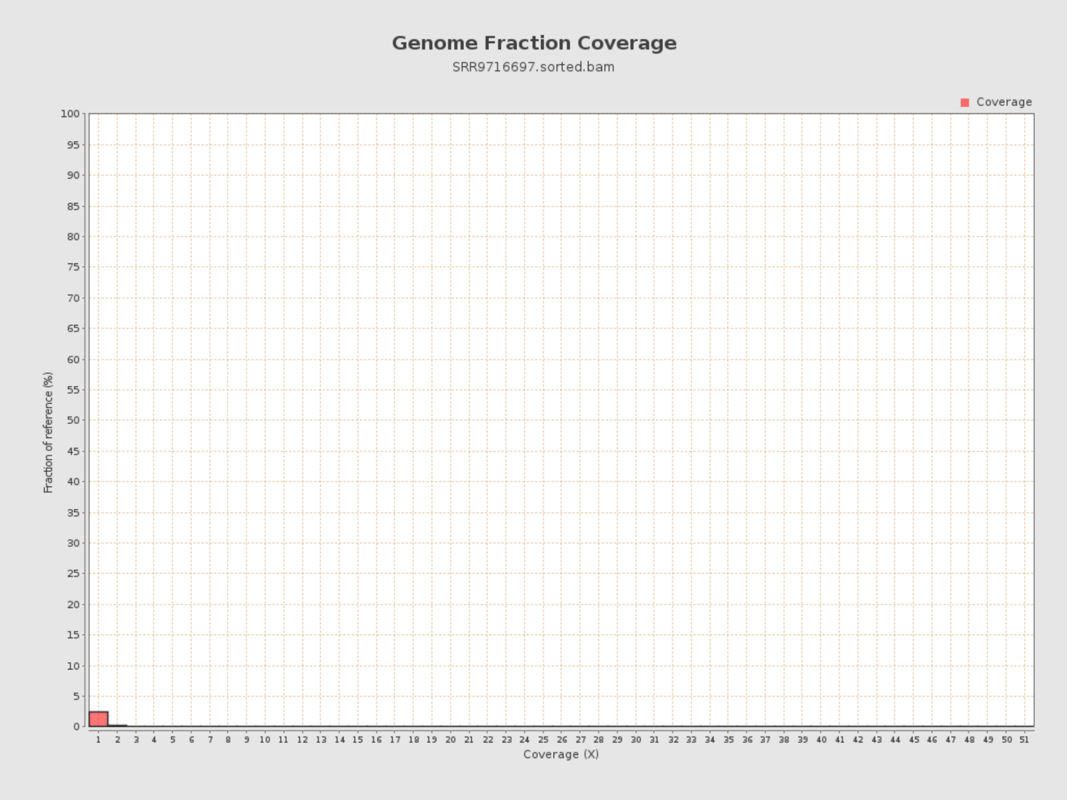
4. Results : Coverage Histogram



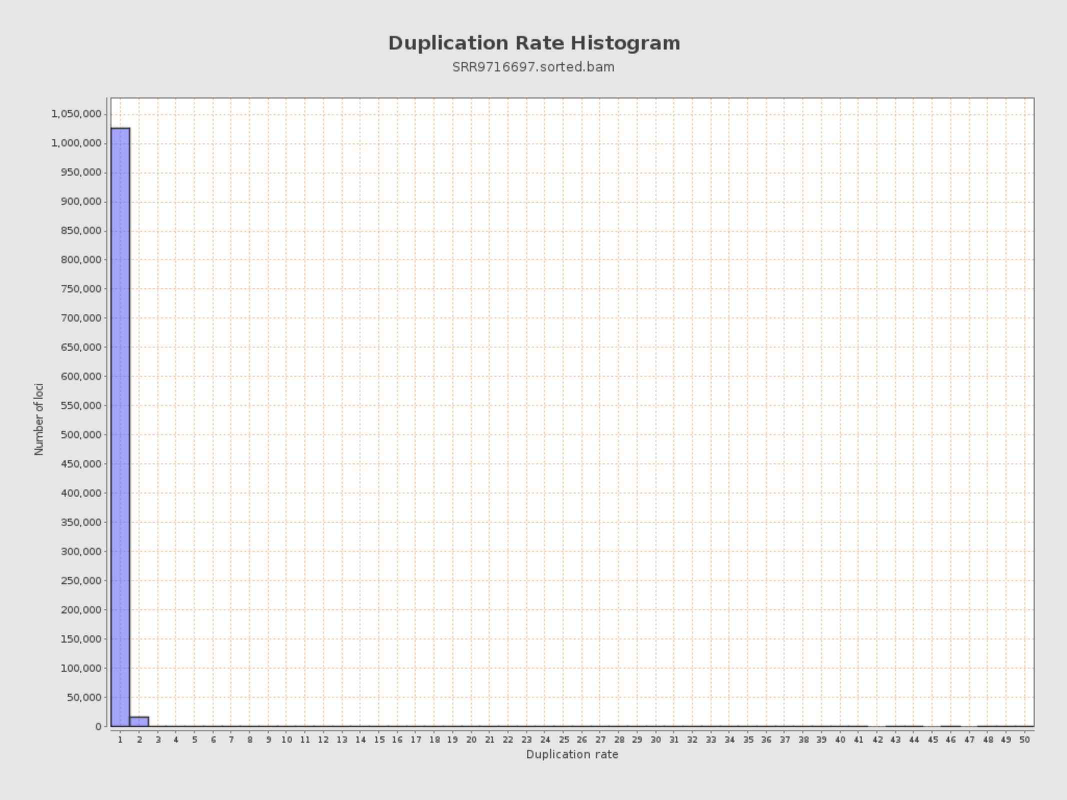
5. Results : Coverage Histogram (0-50X)



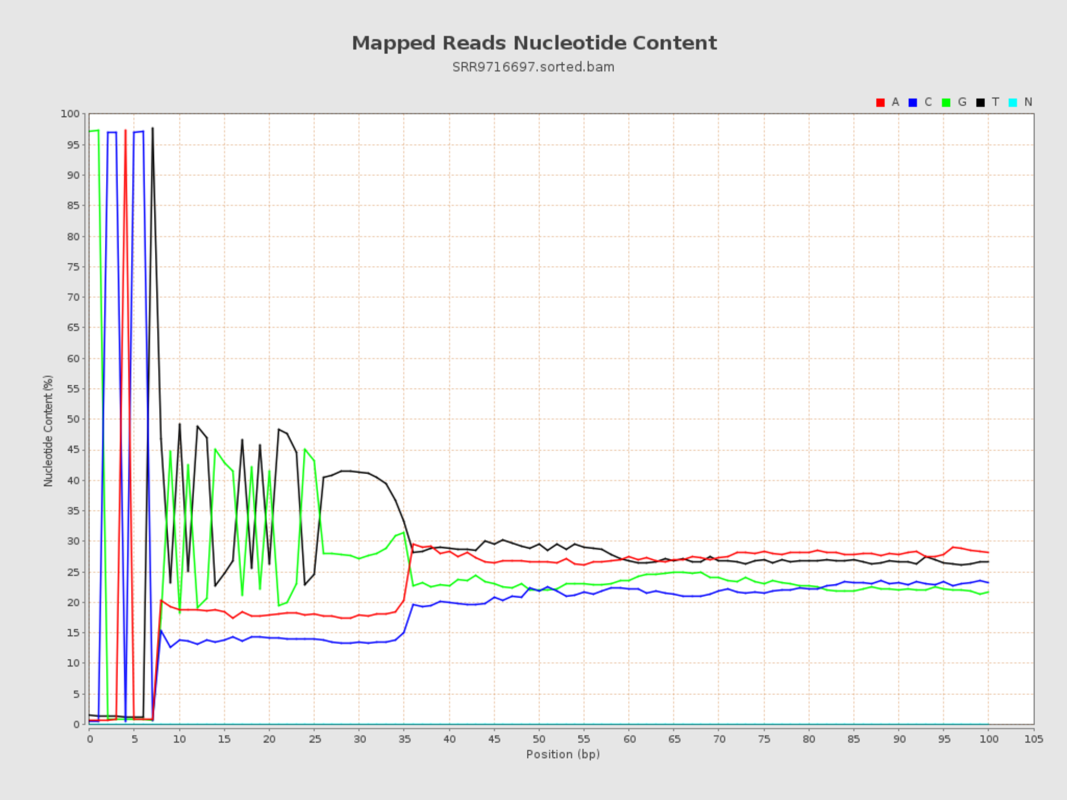
6. Results : Genome Fraction Coverage



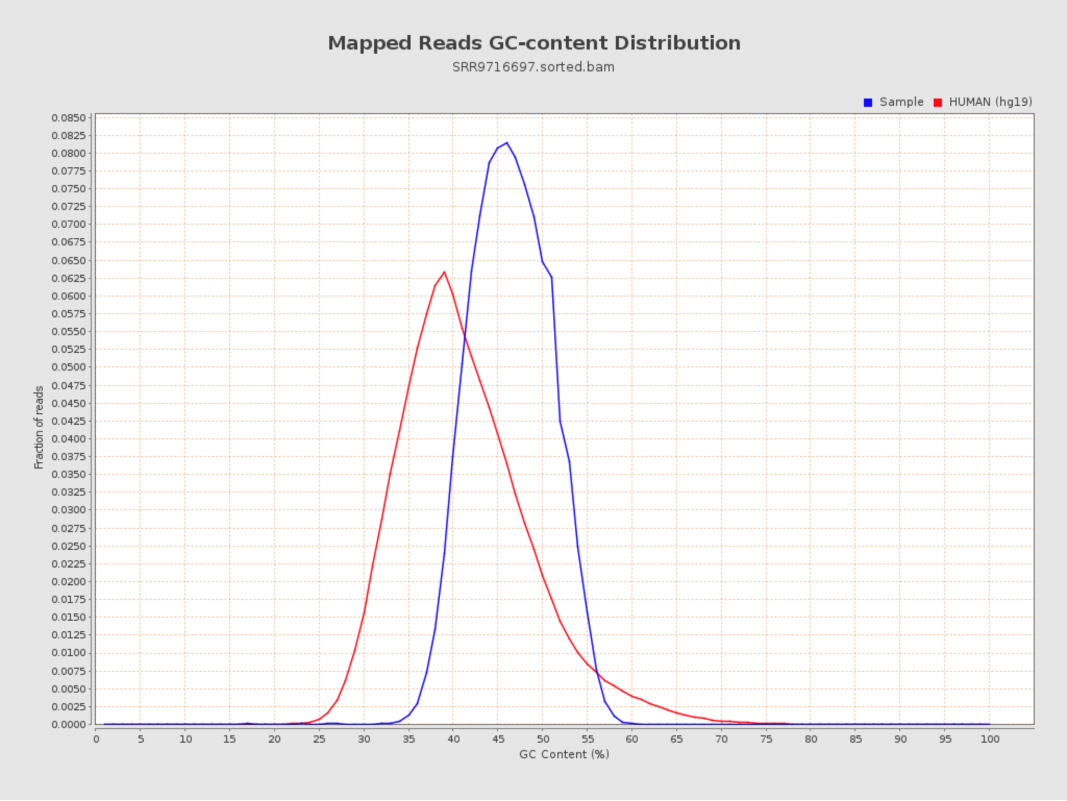
7. Results : Duplication Rate Histogram



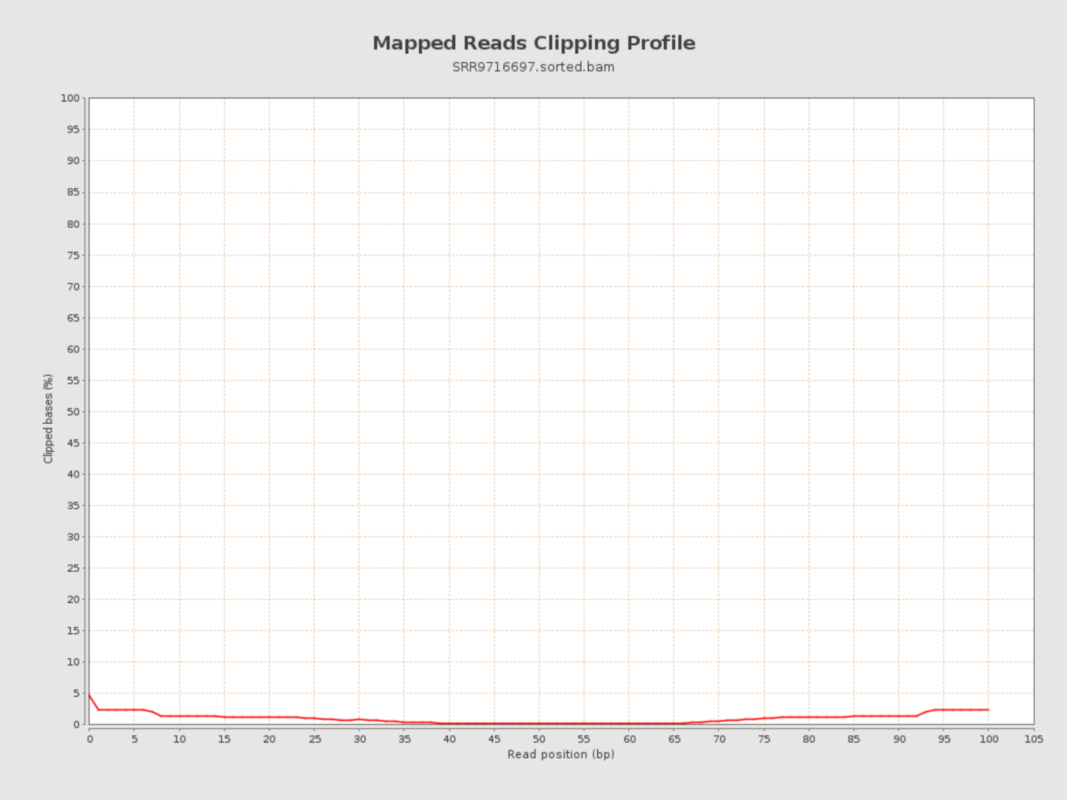
8. Results : Mapped Reads Nucleotide Content



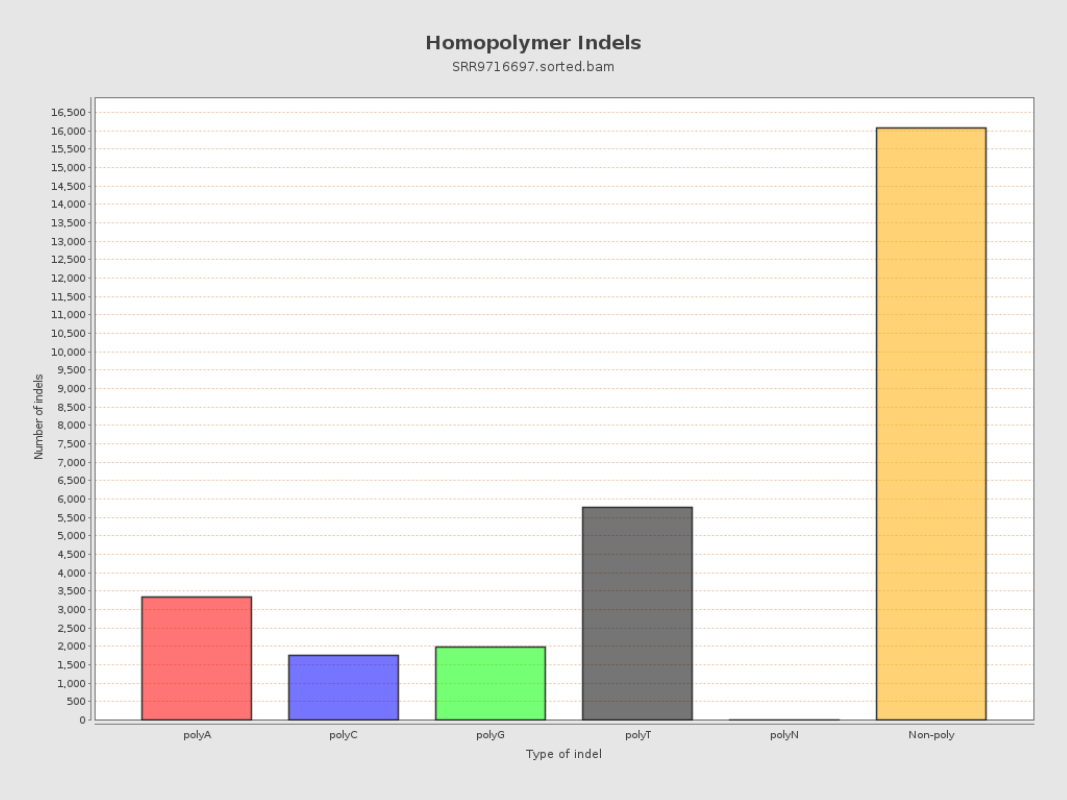
9. Results : Mapped Reads GC-content Distribution



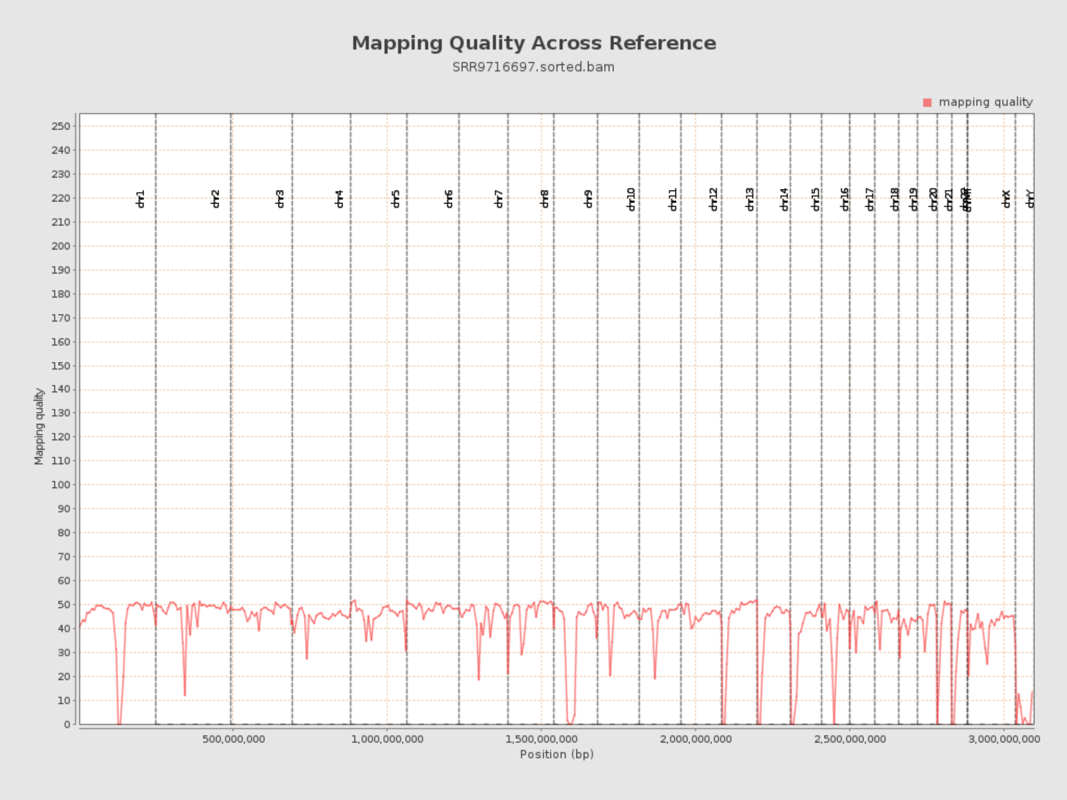
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram