Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 18:42:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716118.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_SRR9716118 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716118.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 18:42:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716118.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,250,895
Mapped reads	1,142,477 / 91.33%
Unmapped reads	108,418 / 8.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,043 / 1.92%
Read min/max/mean length	30 / 101 / 101.69
Duplicated reads (estimated)	35,050 / 2.8%
Duplication rate	2.08%
Clipped reads	1,164,021 / 93.06%

2.2. ACGT Content

Number/percentage of A's	23,642,368 / 26.37%
Number/percentage of C's	16,826,414 / 18.77%
Number/percentage of T's	27,284,249 / 30.44%
Number/percentage of G's	21,887,876 / 24.42%
Number/percentage of N's	6,092 / 0.01%
GC Percentage	43.19%

2.3. Coverage

Mean	0.029

Standard Deviation	0.2993

2.4. Mapping Quality

Mean Mapping Quality	47.08

2.5. Mismatches and indels

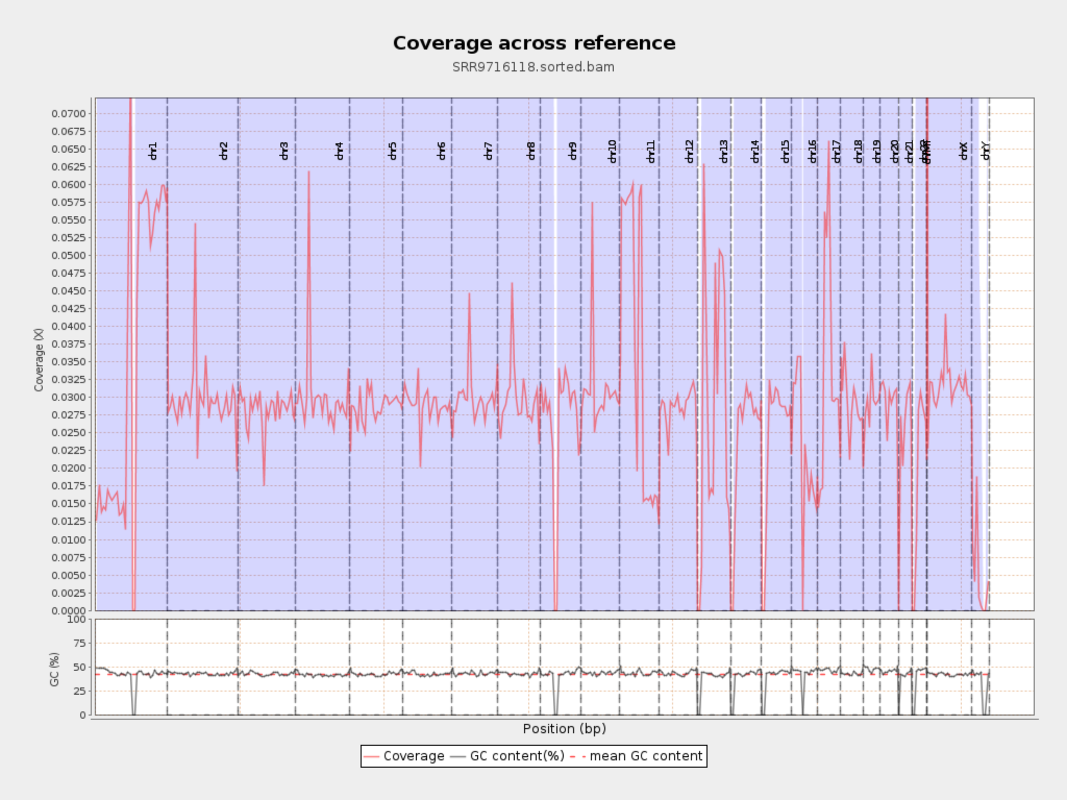
General error rate	0.7%
Mismatches	613,169
Insertions	7,768
Mapped reads with at least one insertion	0.67%
Deletions	21,993
Mapped reads with at least one deletion	1.89%
Homopolymer indels	43.53%

2.6. Chromosome stats

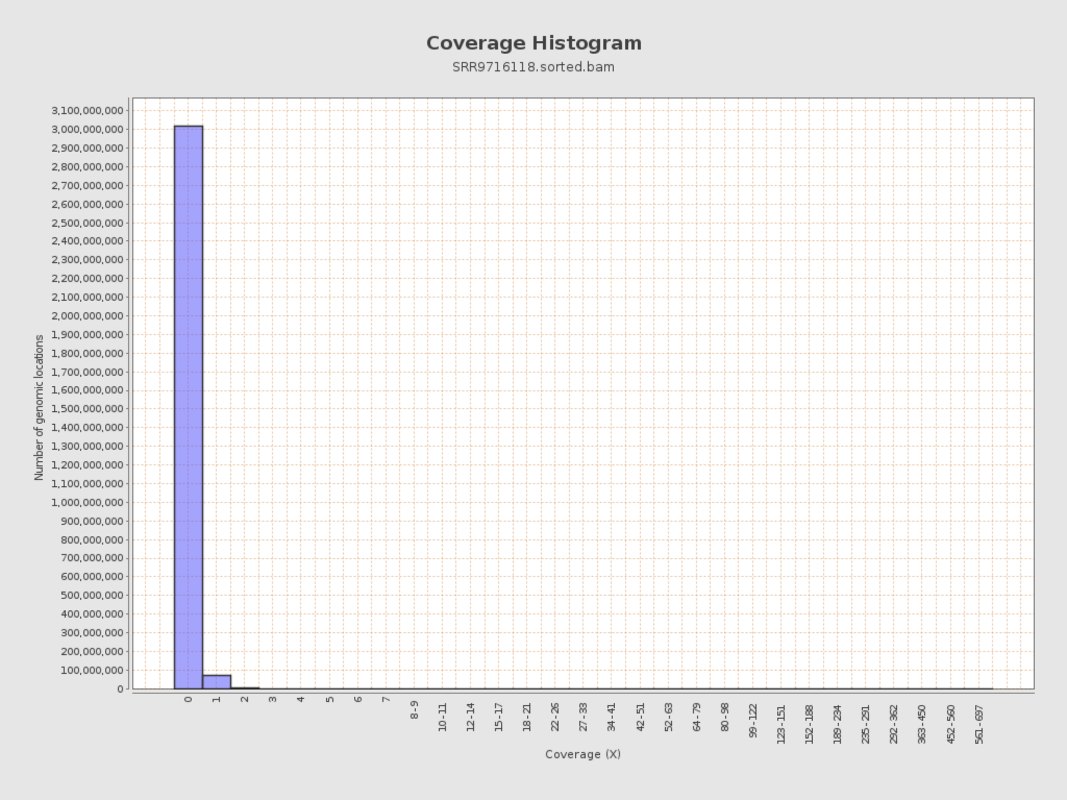
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8701350	0.0349	0.6224
chr2	243199373	7245845	0.0298	0.3118
chr3	198022430	5592877	0.0282	0.1805
chr4	191154276	5804606	0.0304	0.2322
chr5	180915260	5232009	0.0289	0.1836
chr6	171115067	4944843	0.0289	0.195
chr7	159138663	4770168	0.03	0.3476

chr8	146364022	4356612	0.0298	0.323
chr9	141213431	3709957	0.0263	0.2455
chr10	135534747	4225183	0.0312	0.2964
chr11	135006516	4999276	0.037	0.3114
chr12	133851895	3841487	0.0287	0.184
chr13	115169878	3178323	0.0276	0.1804
chr14	107349540	2576200	0.024	0.1779
chr15	102531392	2459308	0.024	0.1666
chr16	90354753	2005673	0.0222	0.1724
chr17	81195210	2732199	0.0336	0.2246
chr18	78077248	2286426	0.0293	0.4179
chr19	59128983	1730753	0.0293	0.4181
chr20	63025520	1862079	0.0295	0.1932
chr21	48129895	1187034	0.0247	0.1891
chr22	51304566	1004433	0.0196	0.1503
chrMT	16571	50212	3.0301	2.5404
chrX	155270560	4914156	0.0316	0.2167
chrY	59373566	278082	0.0047	0.1691

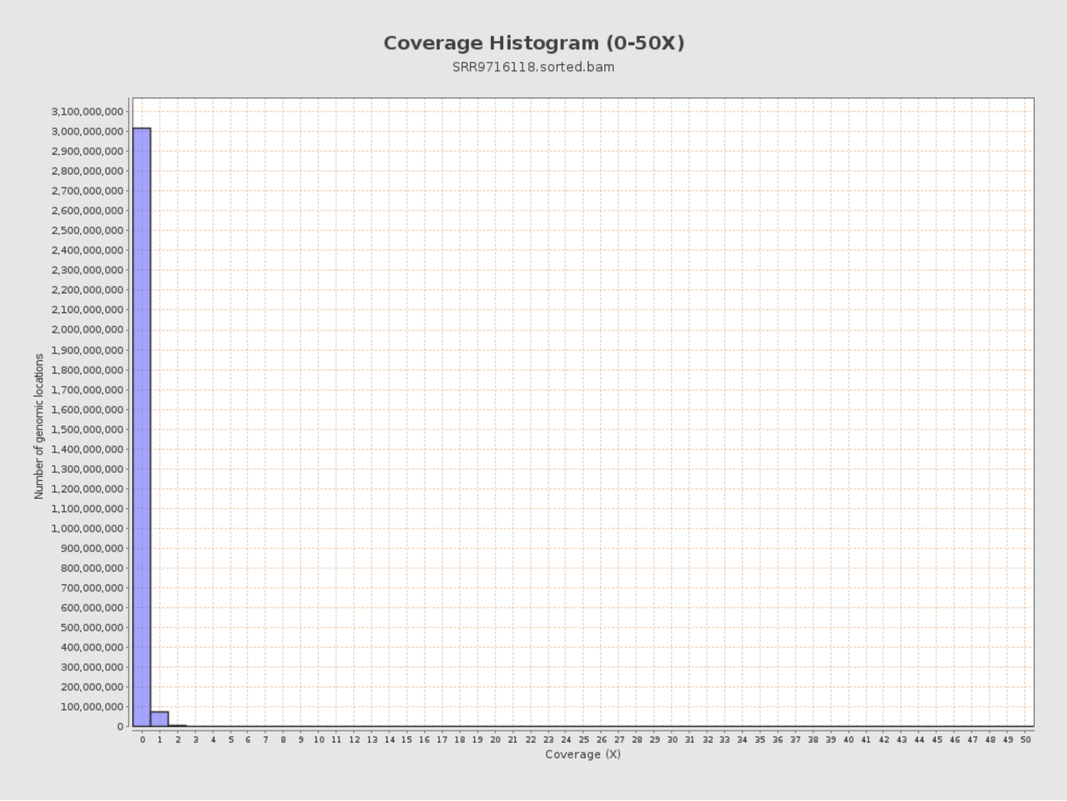
3. Results : Coverage across reference



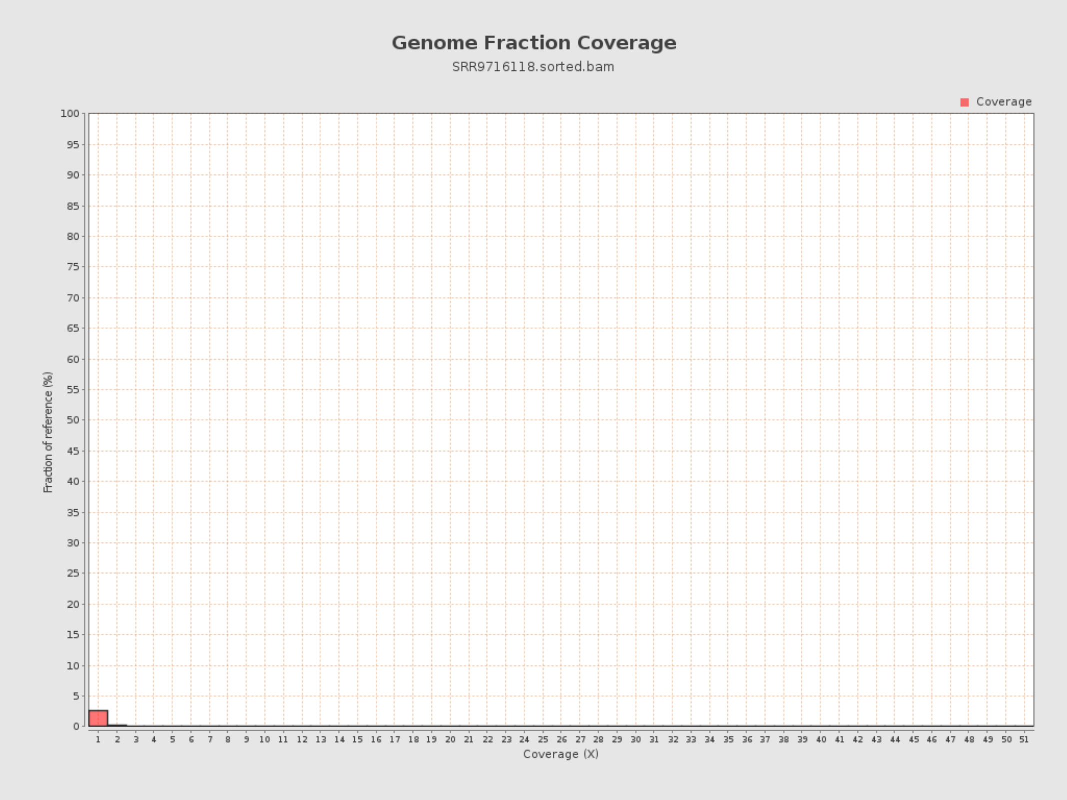
4. Results : Coverage Histogram



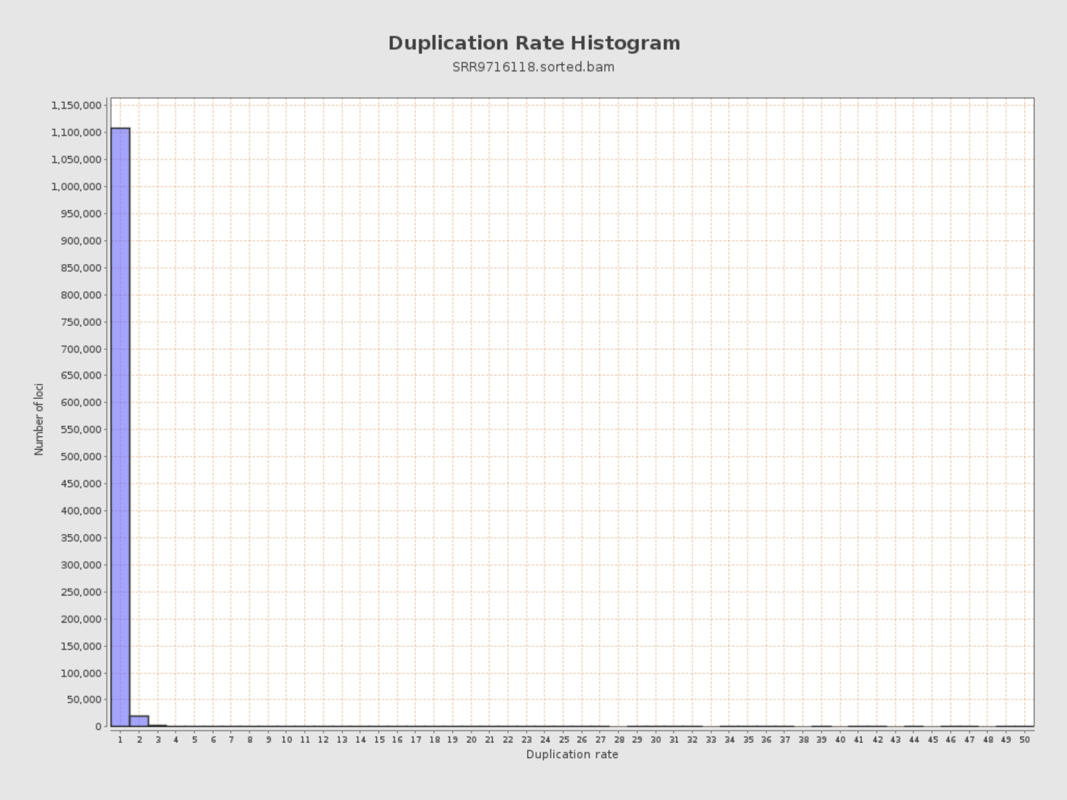
5. Results : Coverage Histogram (0-50X)



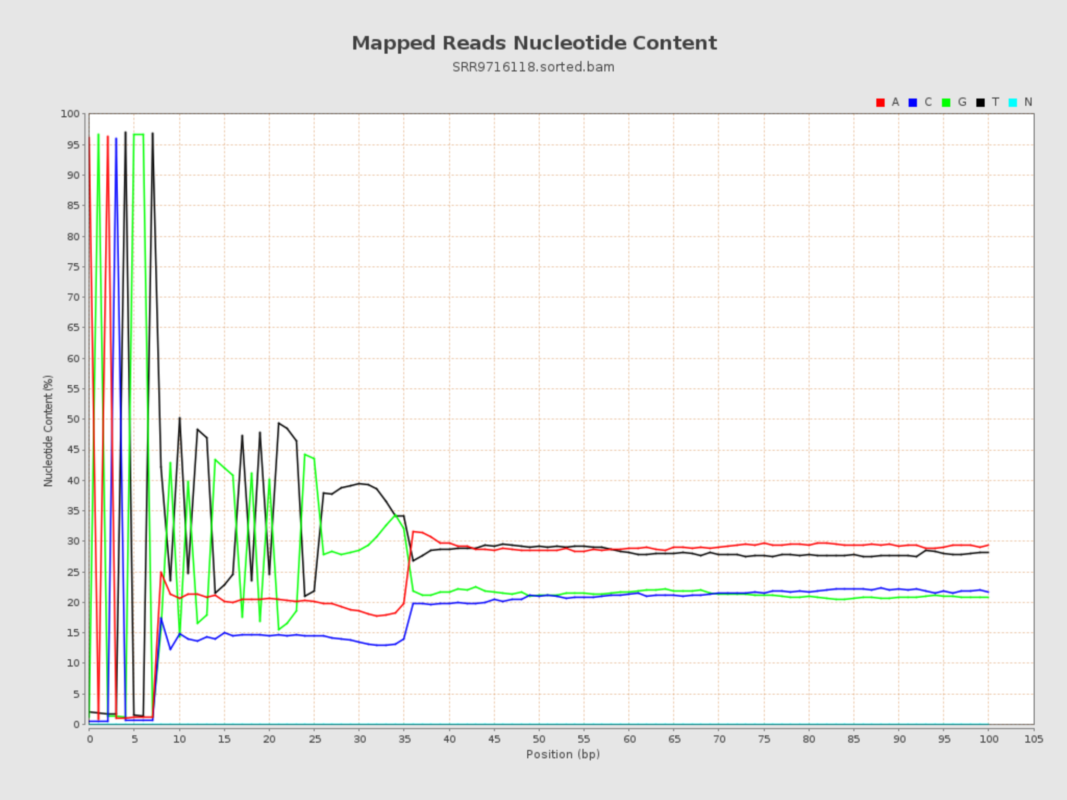
6. Results : Genome Fraction Coverage



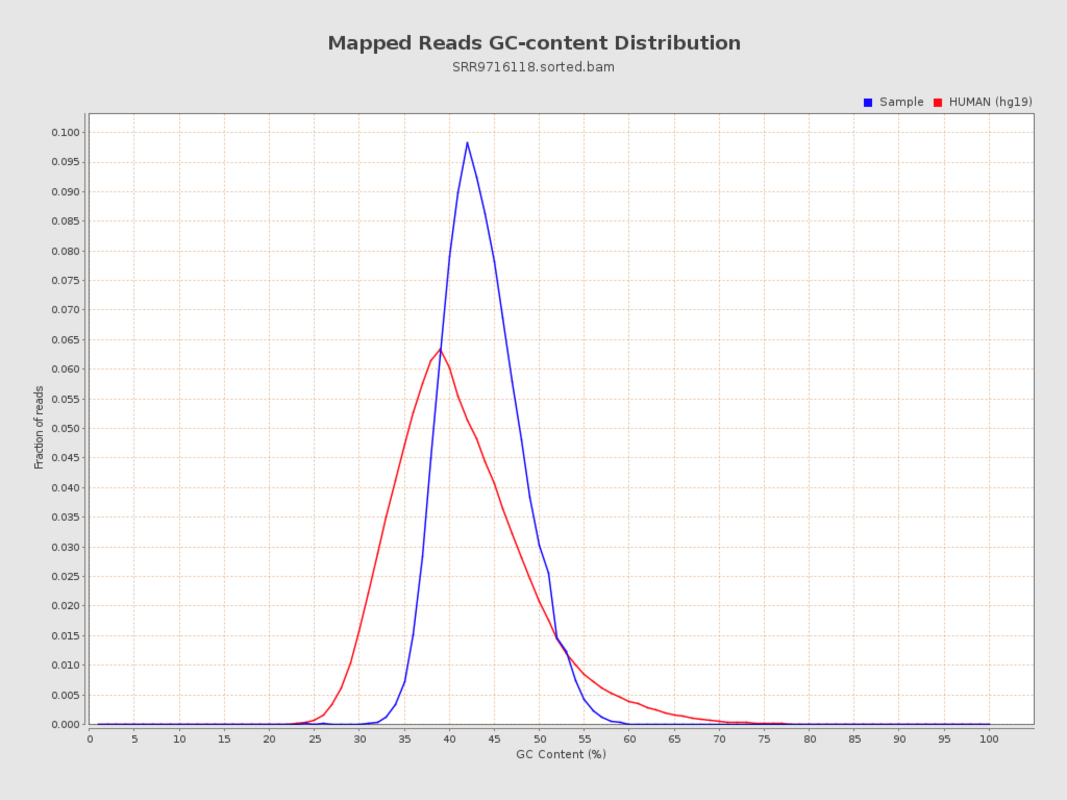
7. Results : Duplication Rate Histogram



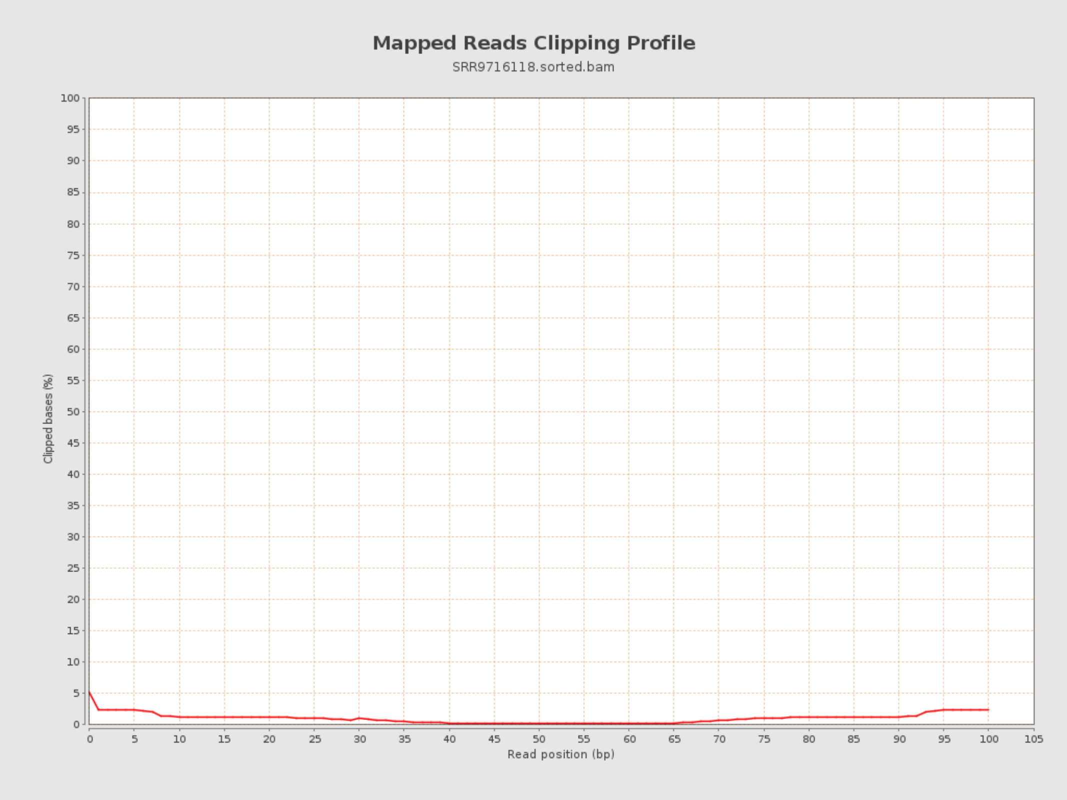
8. Results : Mapped Reads Nucleotide Content



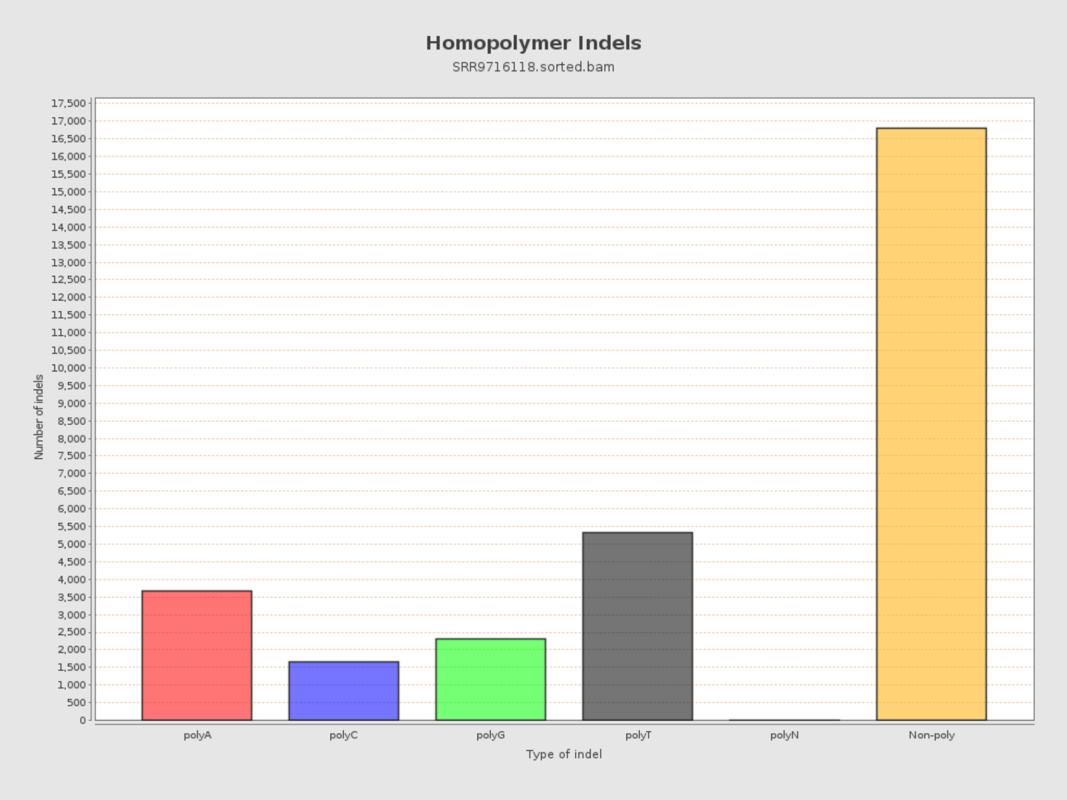
9. Results : Mapped Reads GC-content Distribution



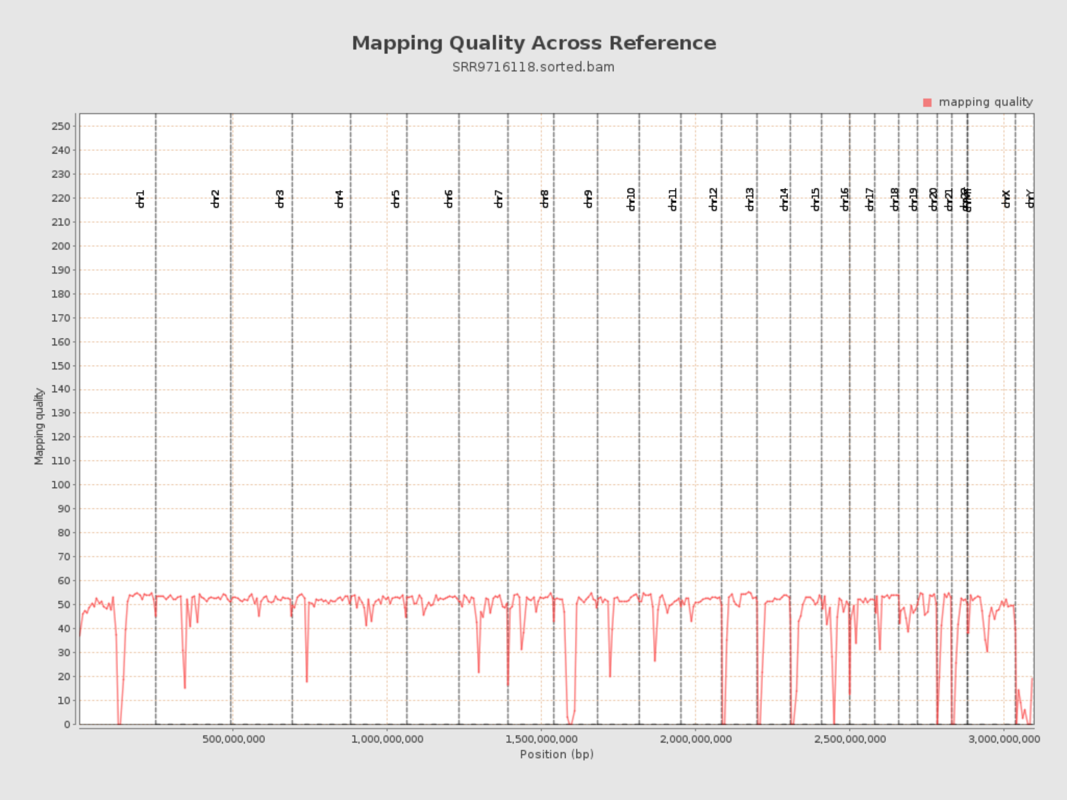
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram