Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 11:16:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716774.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_SRR9716774 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716774.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 11:16:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716774.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,294,848
Mapped reads	1,193,521 / 92.17%
Unmapped reads	101,327 / 7.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,914 / 2.23%
Read min/max/mean length	30 / 101 / 101.8
Duplicated reads (estimated)	43,622 / 3.37%
Duplication rate	2.84%
Clipped reads	1,220,294 / 94.24%

2.2. ACGT Content

Number/percentage of A's	23,284,491 / 25.8%
Number/percentage of C's	17,900,407 / 19.84%
Number/percentage of T's	26,649,783 / 29.53%
Number/percentage of G's	22,403,549 / 24.83%
Number/percentage of N's	2,992 / 0%
GC Percentage	44.66%

2.3. Coverage

Mean	0.0292

Standard Deviation	0.2605

2.4. Mapping Quality

Mean Mapping Quality	45.75

2.5. Mismatches and indels

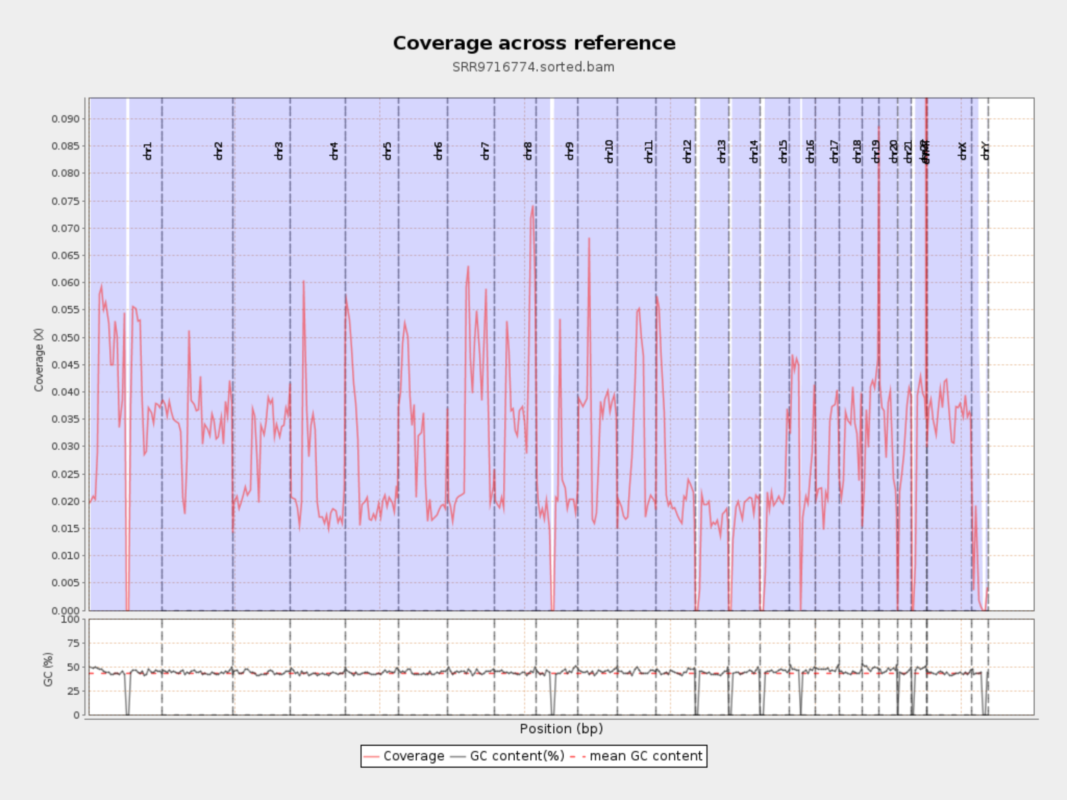
General error rate	0.7%
Mismatches	607,903
Insertions	8,121
Mapped reads with at least one insertion	0.67%
Deletions	17,778
Mapped reads with at least one deletion	1.46%
Homopolymer indels	39.25%

2.6. Chromosome stats

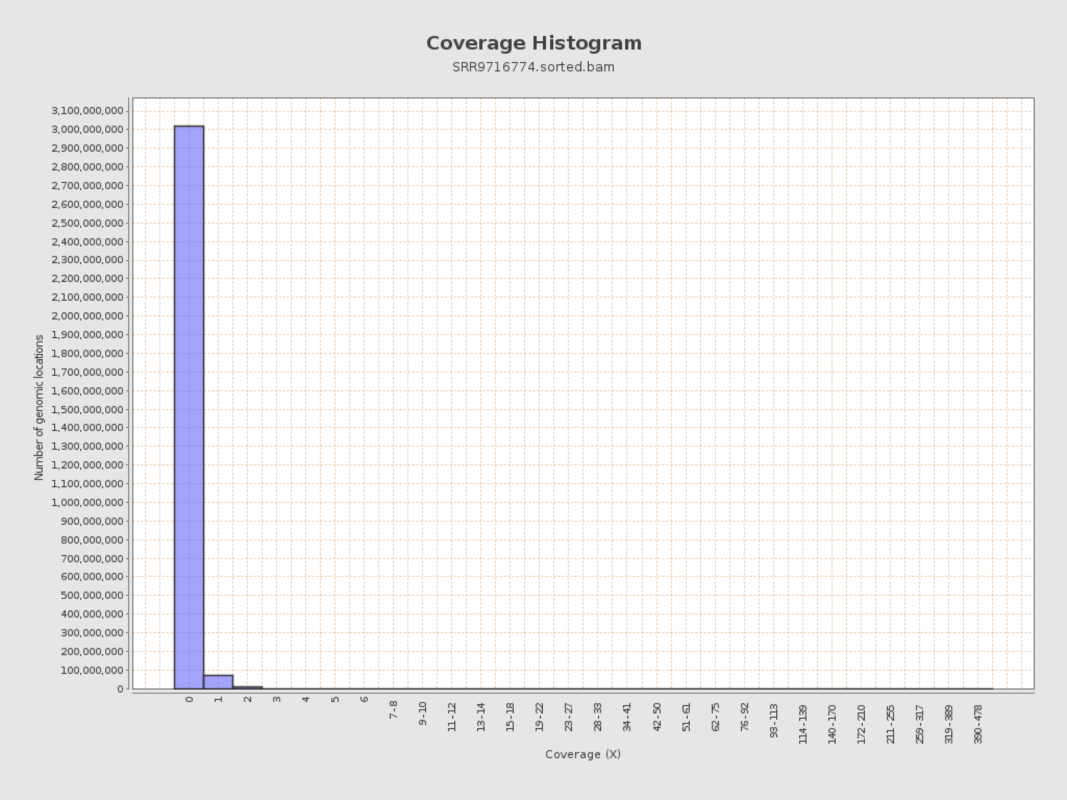
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9828211	0.0394	0.4638
chr2	243199373	8471058	0.0348	0.2792
chr3	198022430	5851517	0.0295	0.193
chr4	191154276	4382856	0.0229	0.2267
chr5	180915260	4651186	0.0257	0.1791
chr6	171115067	5047349	0.0295	0.2028
chr7	159138663	5700761	0.0358	0.3505

chr8	146364022	5583104	0.0381	0.2829
chr9	141213431	2720926	0.0193	0.1871
chr10	135534747	4808498	0.0355	0.349
chr11	135006516	3827622	0.0284	0.2326
chr12	133851895	3524188	0.0263	0.1809
chr13	115169878	1703481	0.0148	0.1333
chr14	107349540	1781216	0.0166	0.1511
chr15	102531392	1854411	0.0181	0.1487
chr16	90354753	2755394	0.0305	0.204
chr17	81195210	2248478	0.0277	0.1991
chr18	78077248	2455099	0.0314	0.2767
chr19	59128983	2230890	0.0377	0.3253
chr20	63025520	2039676	0.0324	0.2063
chr21	48129895	1383331	0.0287	0.2237
chr22	51304566	1382624	0.0269	0.1861
chrMT	16571	83704	5.0512	3.9988
chrX	155270560	5660293	0.0365	0.2204
chrY	59373566	301713	0.0051	0.1772

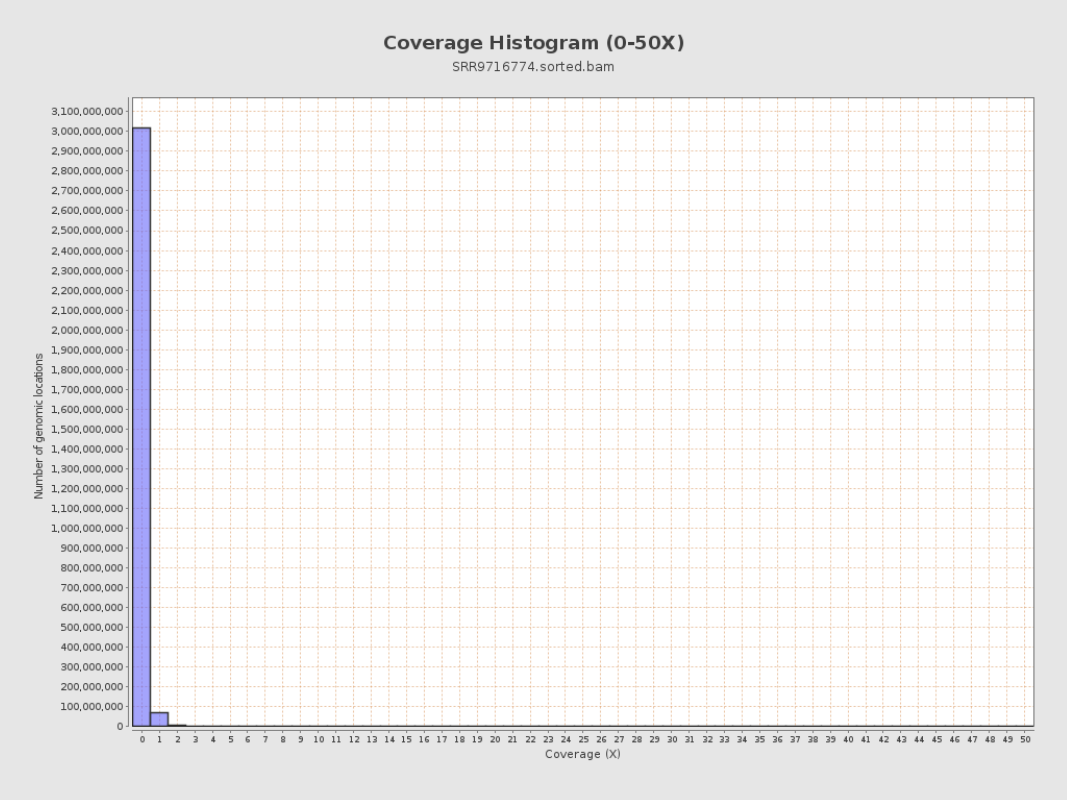
3. Results : Coverage across reference



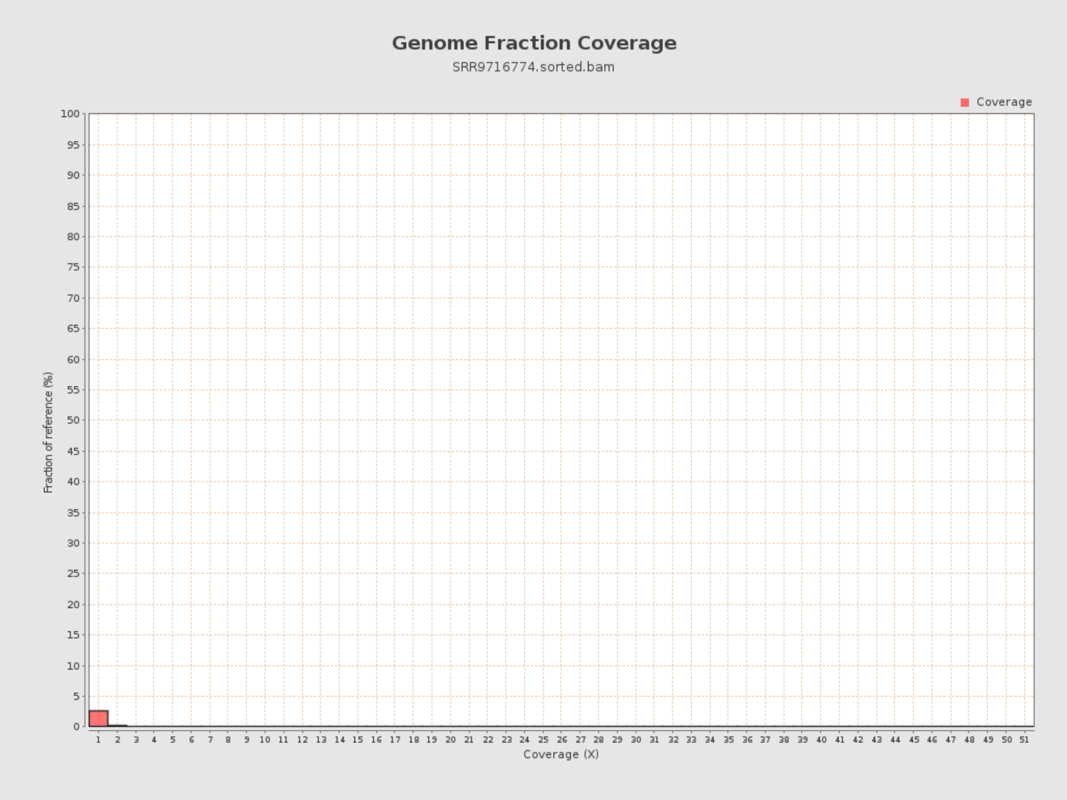
4. Results : Coverage Histogram



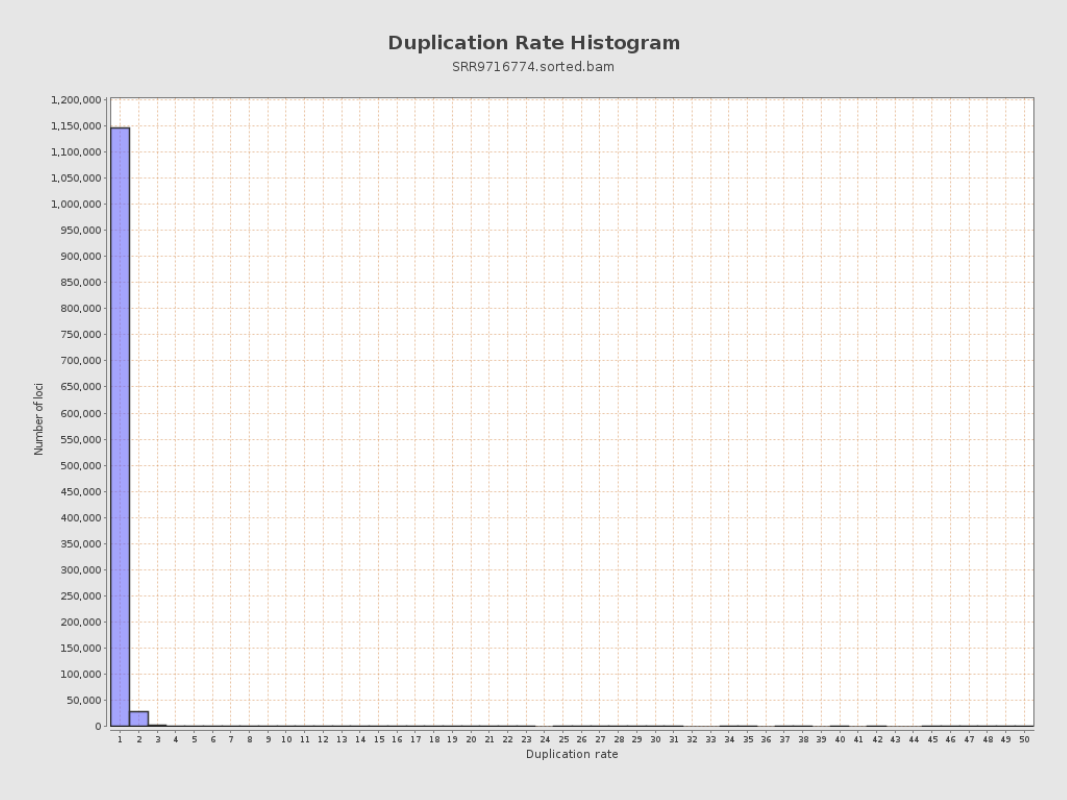
5. Results : Coverage Histogram (0-50X)



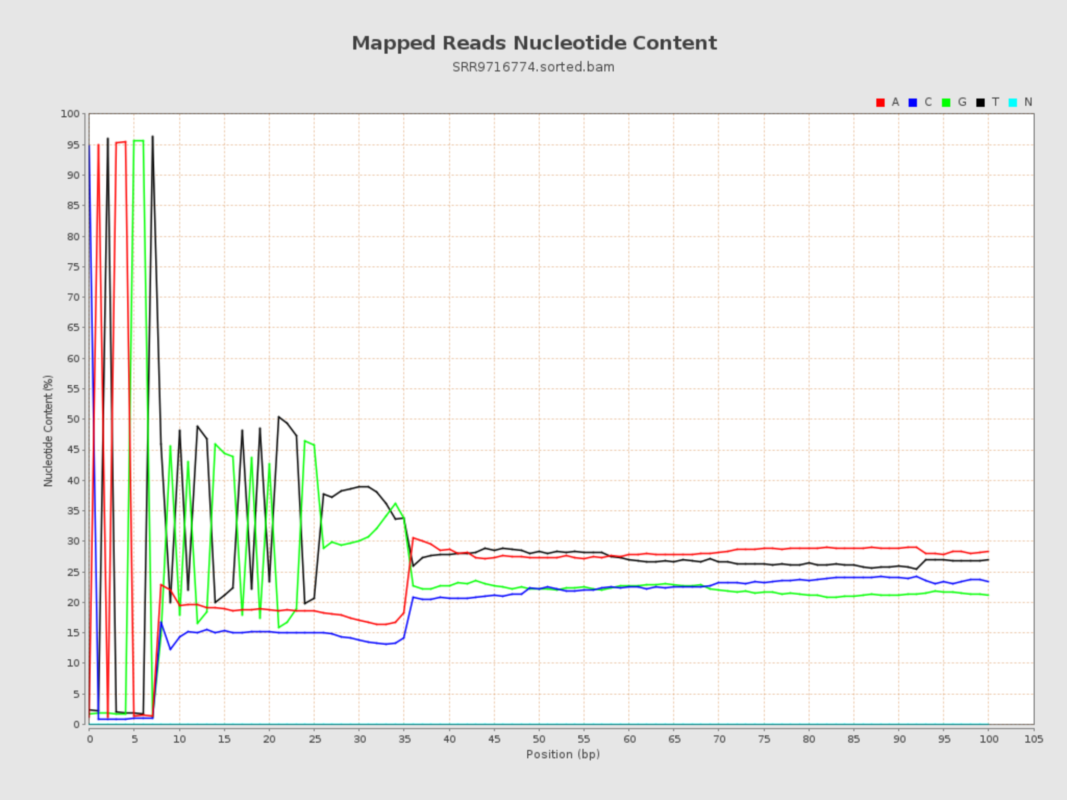
6. Results : Genome Fraction Coverage



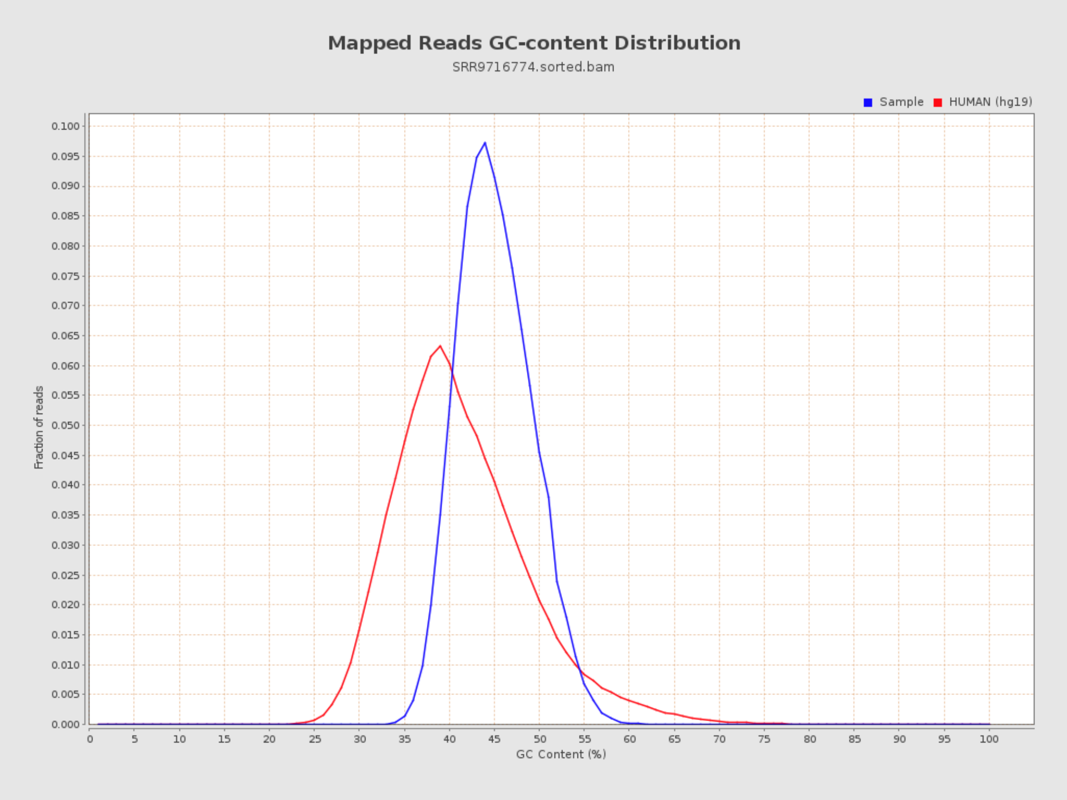
7. Results : Duplication Rate Histogram



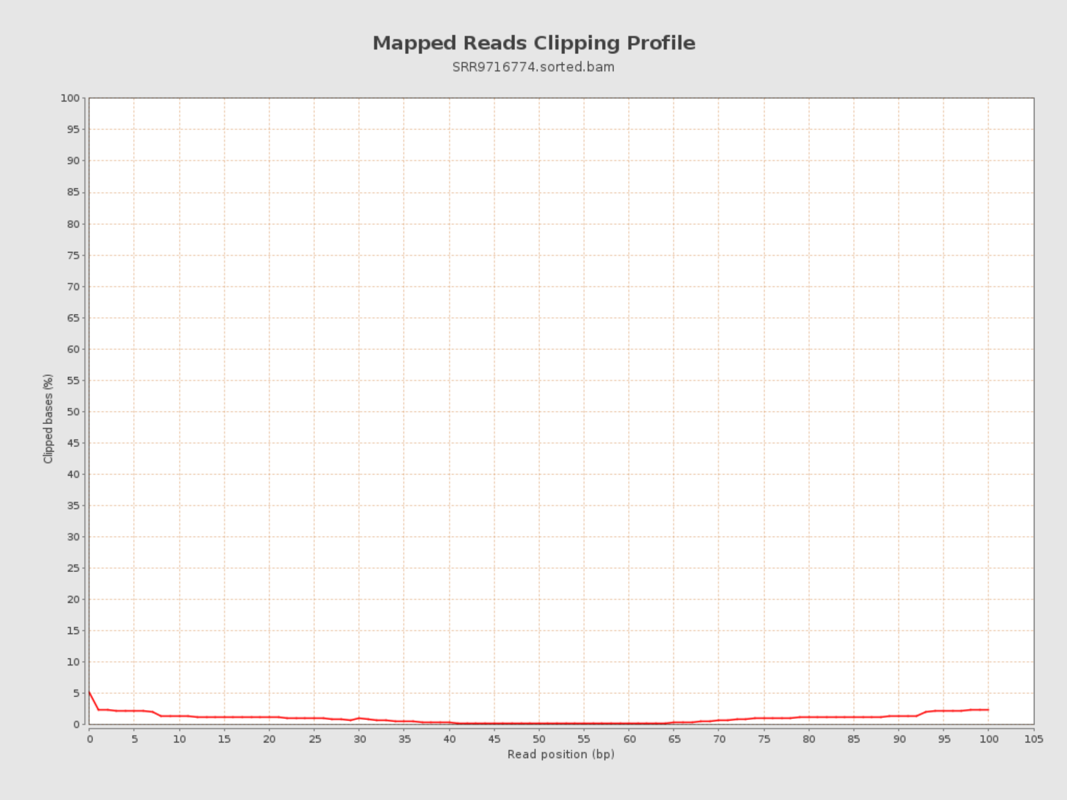
8. Results : Mapped Reads Nucleotide Content



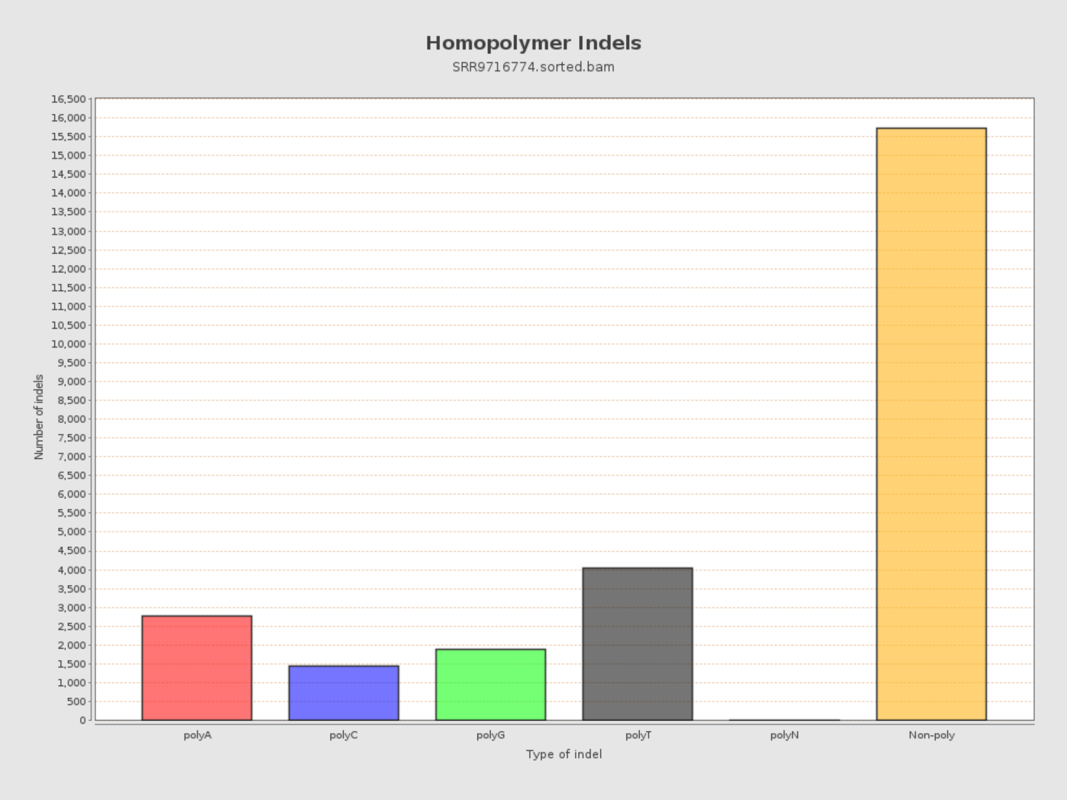
9. Results : Mapped Reads GC-content Distribution



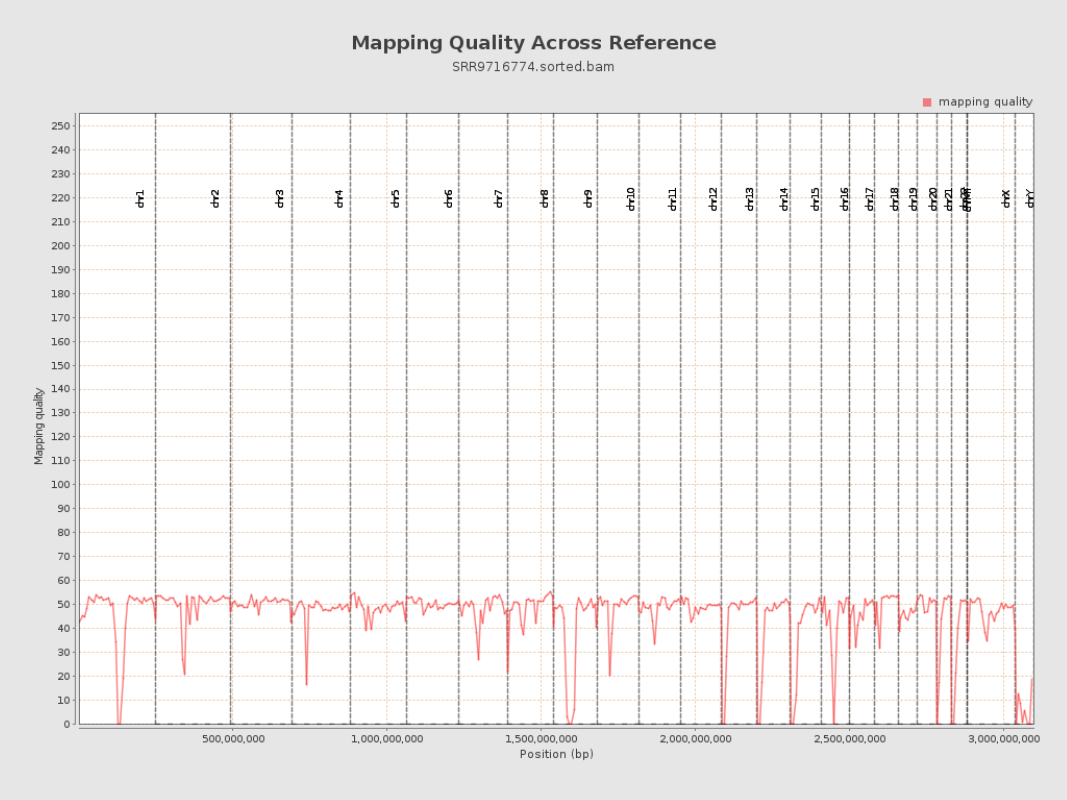
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram