Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 11:24:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716394.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_SRR9716394 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716394.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 11:24:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716394.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,479,784
Mapped reads	3,190,159 / 91.68%
Unmapped reads	289,625 / 8.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	52,758 / 1.52%
Read min/max/mean length	30 / 101 / 101.56
Duplicated reads (estimated)	205,546 / 5.91%
Duplication rate	4.11%
Clipped reads	3,235,399 / 92.98%

2.2. ACGT Content

Number/percentage of A's	62,358,376 / 24.82%
Number/percentage of C's	50,905,459 / 20.26%
Number/percentage of T's	79,042,168 / 31.46%
Number/percentage of G's	58,939,489 / 23.46%
Number/percentage of N's	15,204 / 0.01%
GC Percentage	43.72%

2.3. Coverage

Mean	0.0812

Standard Deviation	0.8998

2.4. Mapping Quality

Mean Mapping Quality	44.7

2.5. Mismatches and indels

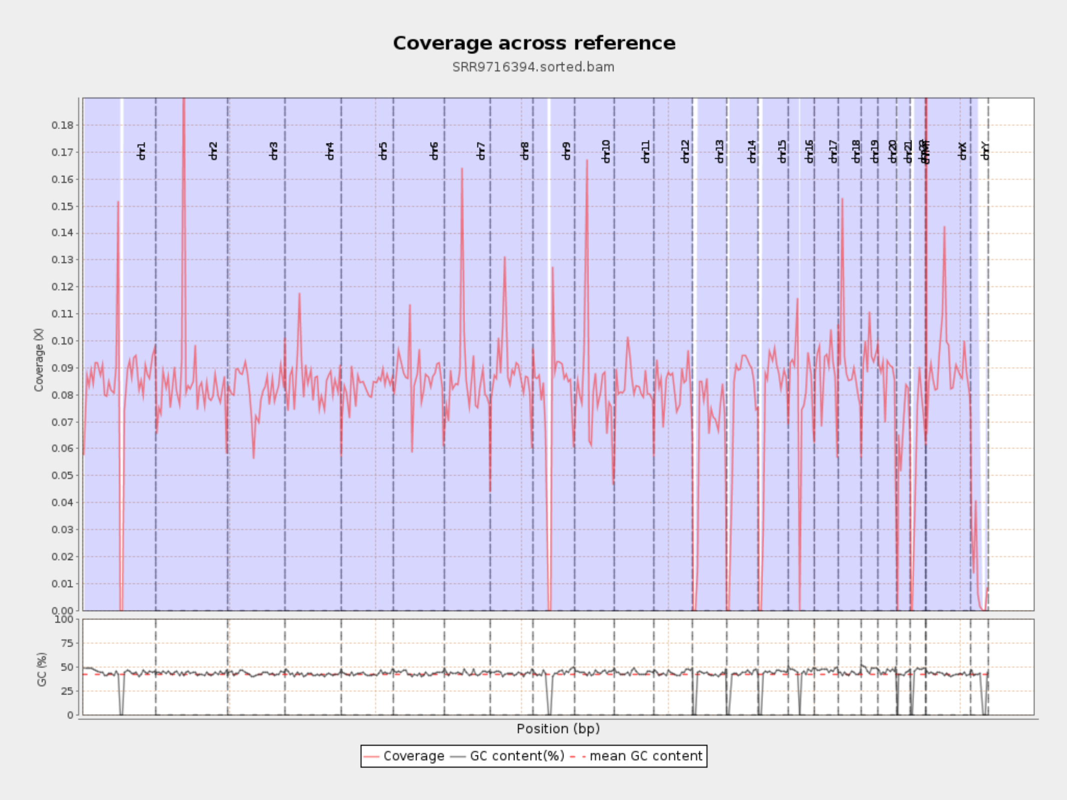
General error rate	0.85%
Mismatches	2,078,681
Insertions	24,904
Mapped reads with at least one insertion	0.77%
Deletions	62,996
Mapped reads with at least one deletion	1.94%
Homopolymer indels	44.02%

2.6. Chromosome stats

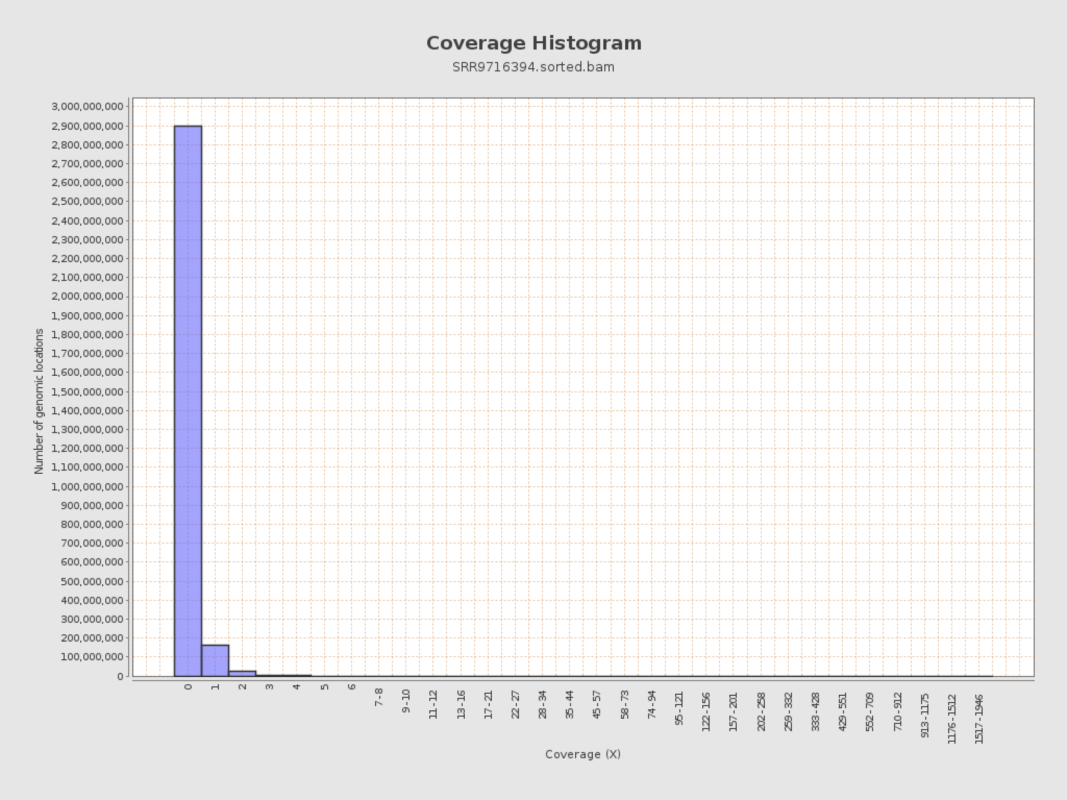
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20640578	0.0828	1.5106
chr2	243199373	20857494	0.0858	1.4112
chr3	198022430	16160863	0.0816	0.3629
chr4	191154276	16331354	0.0854	0.435
chr5	180915260	15008043	0.083	0.371
chr6	171115067	14823352	0.0866	0.5266
chr7	159138663	13776118	0.0866	1.1114

chr8	146364022	13016864	0.0889	1.2341
chr9	141213431	10876621	0.077	1.0121
chr10	135534747	11189137	0.0826	0.9144
chr11	135006516	11255920	0.0834	0.7641
chr12	133851895	11207669	0.0837	0.3778
chr13	115169878	7312953	0.0635	0.3067
chr14	107349540	7989436	0.0744	0.5682
chr15	102531392	7403079	0.0722	0.3427
chr16	90354753	7112288	0.0787	0.4723
chr17	81195210	7267295	0.0895	0.4387
chr18	78077248	7340647	0.094	1.9247
chr19	59128983	5585989	0.0945	1.1124
chr20	63025520	5387367	0.0855	0.4069
chr21	48129895	3061877	0.0636	0.3692
chr22	51304566	2818651	0.0549	0.2899
chrMT	16571	61681	3.7222	2.9464
chrX	155270560	14179920	0.0913	0.6125
chrY	59373566	705685	0.0119	0.3434

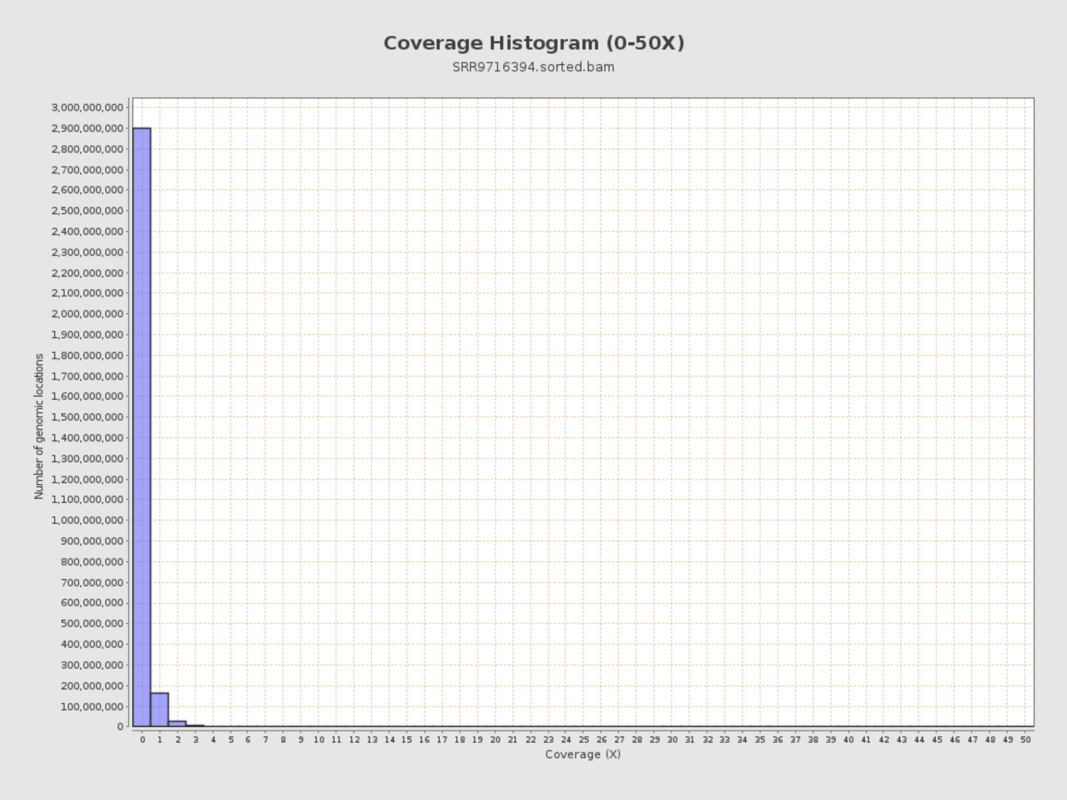
3. Results : Coverage across reference



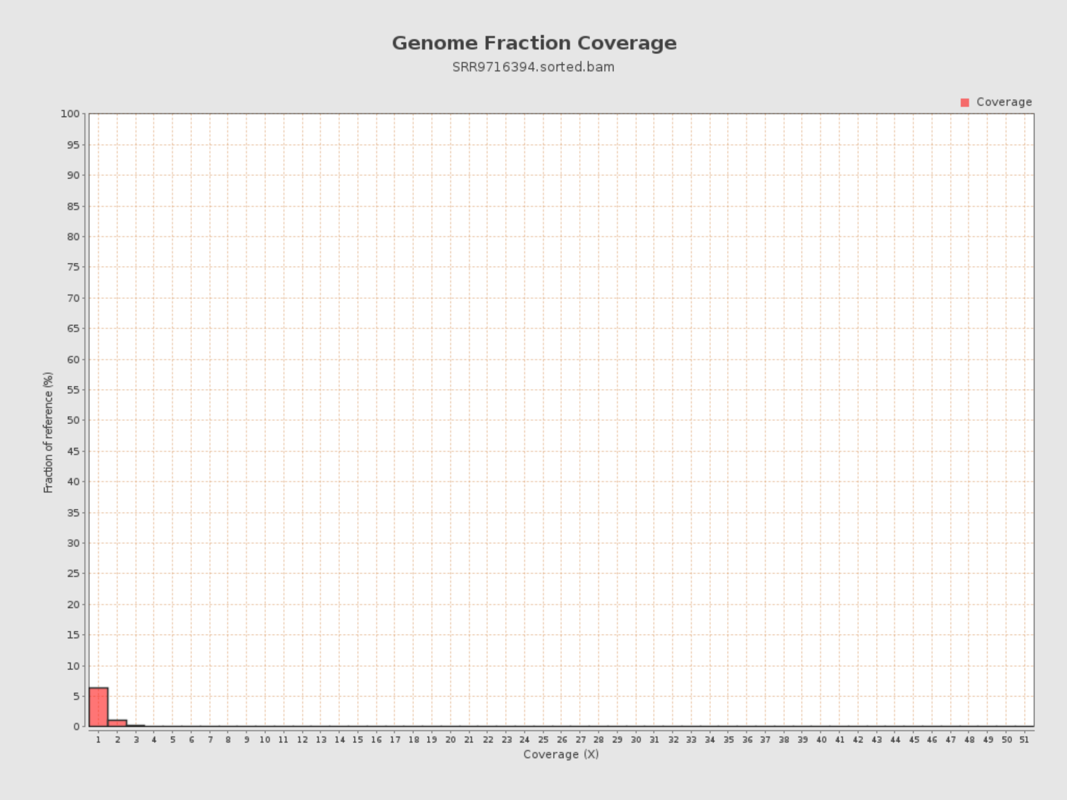
4. Results : Coverage Histogram



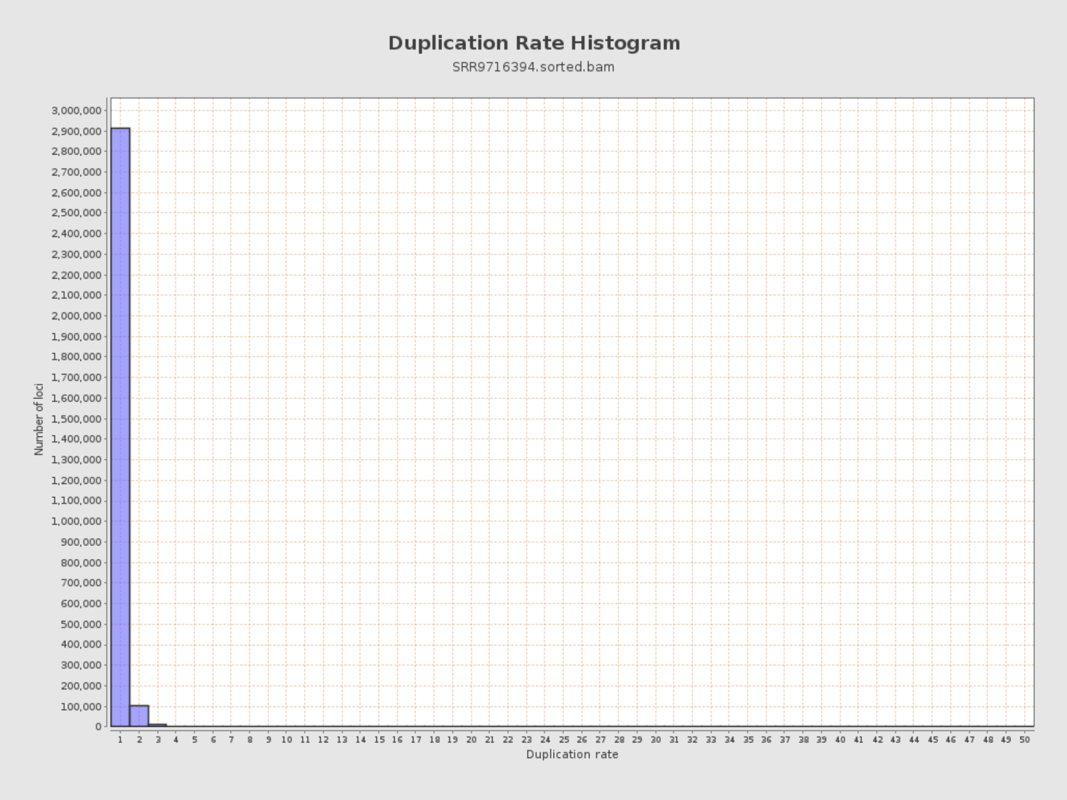
5. Results : Coverage Histogram (0-50X)



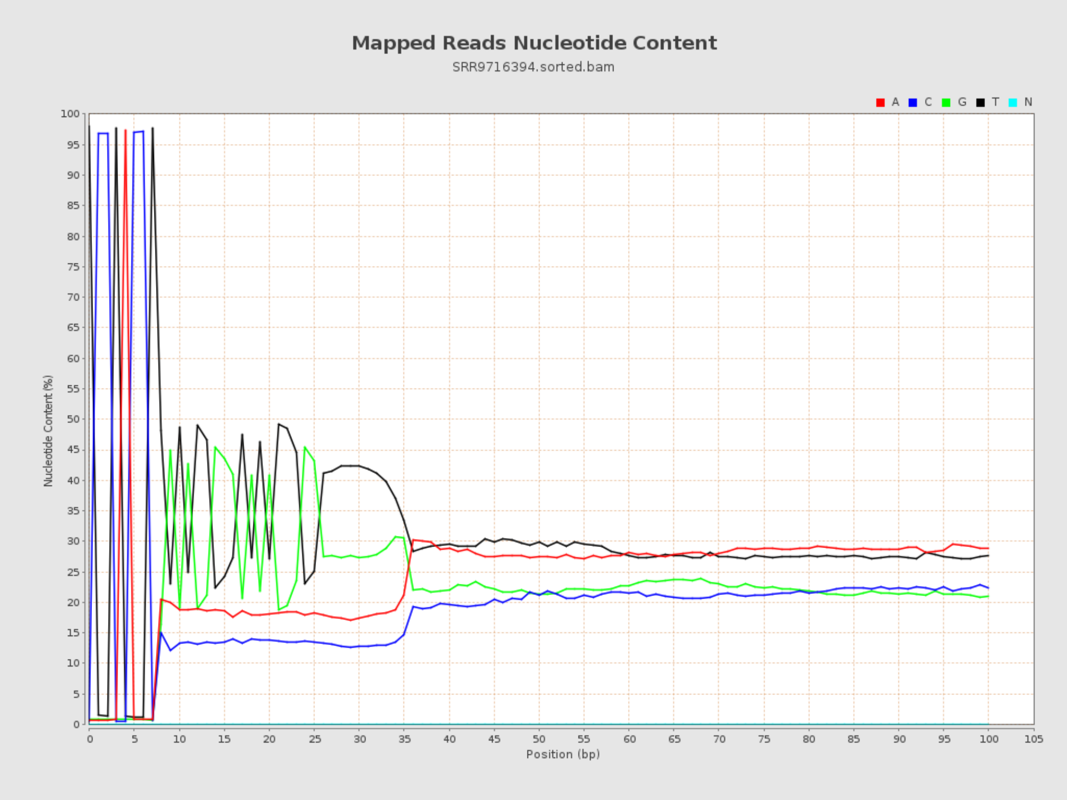
6. Results : Genome Fraction Coverage



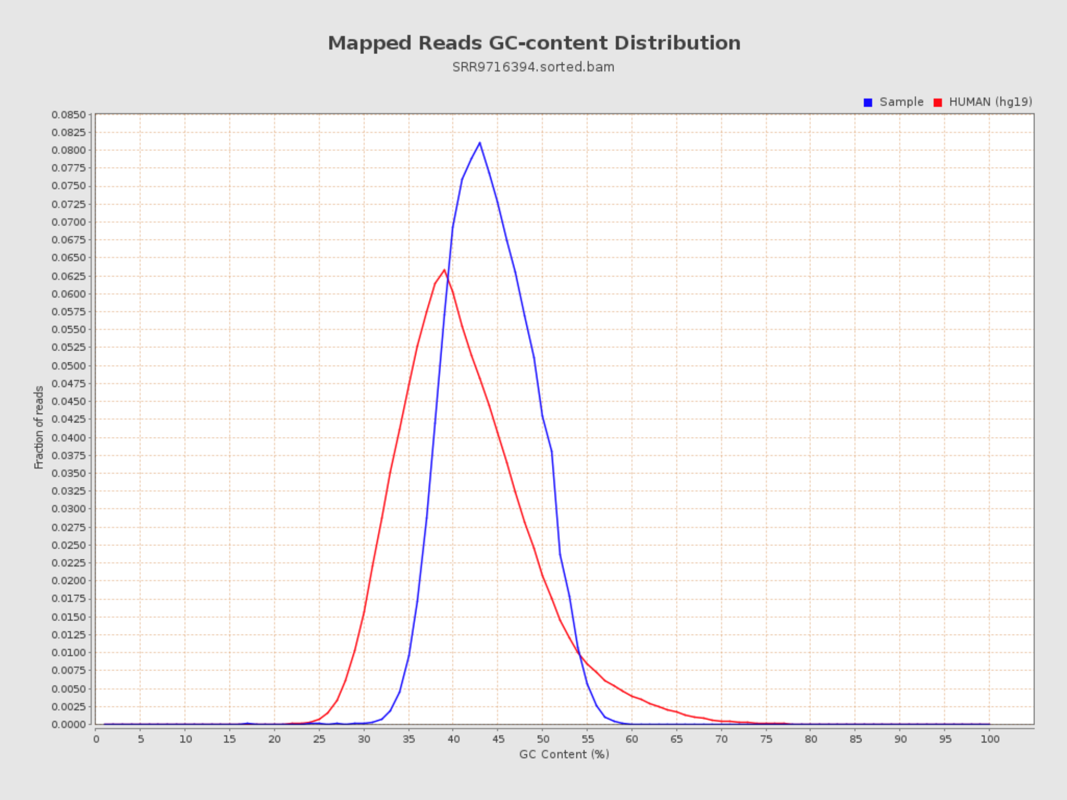
7. Results : Duplication Rate Histogram



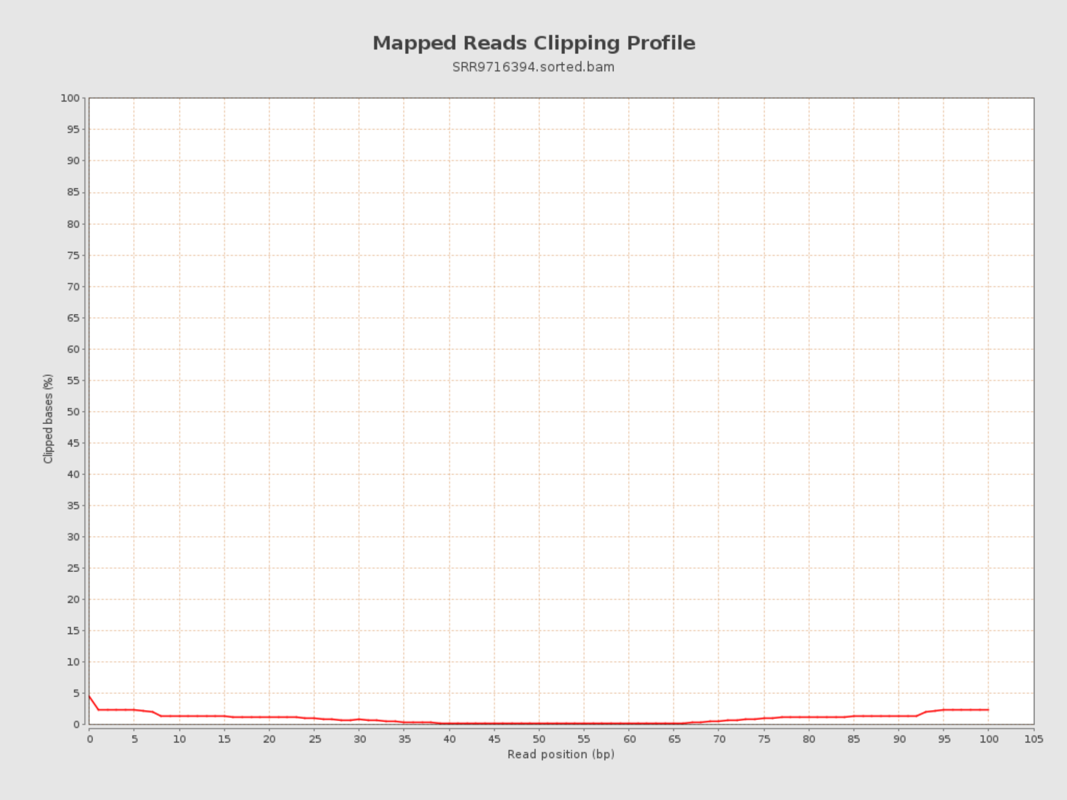
8. Results : Mapped Reads Nucleotide Content



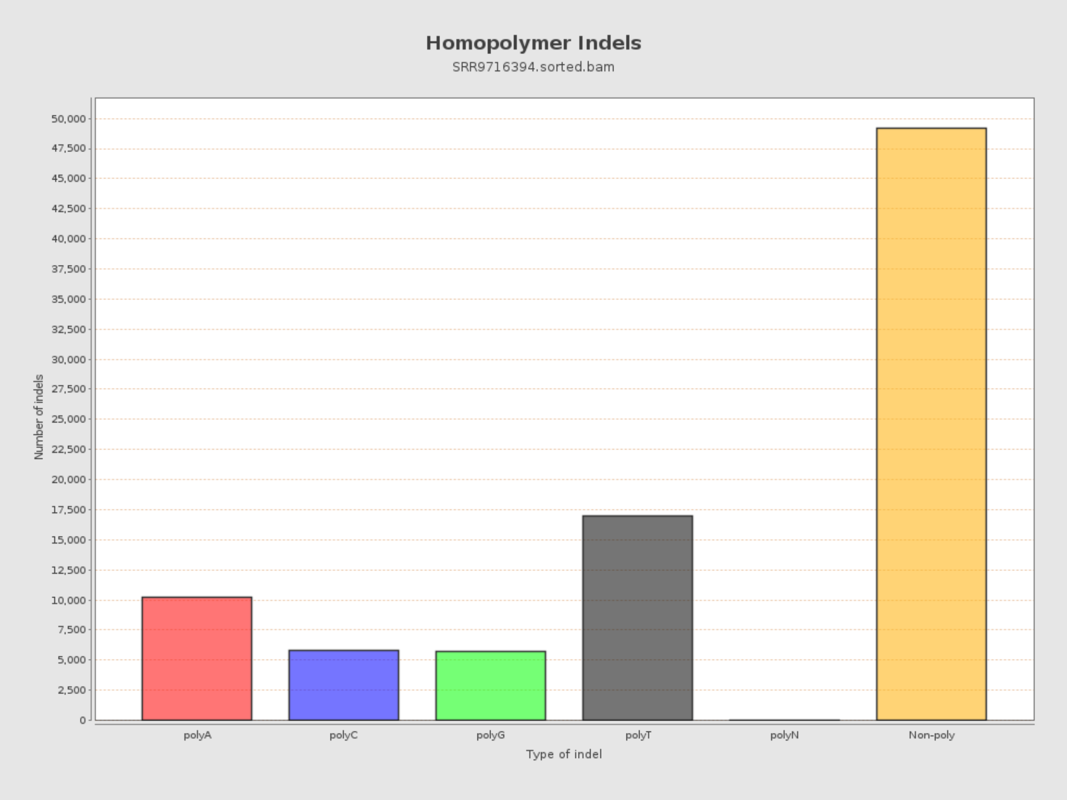
9. Results : Mapped Reads GC-content Distribution



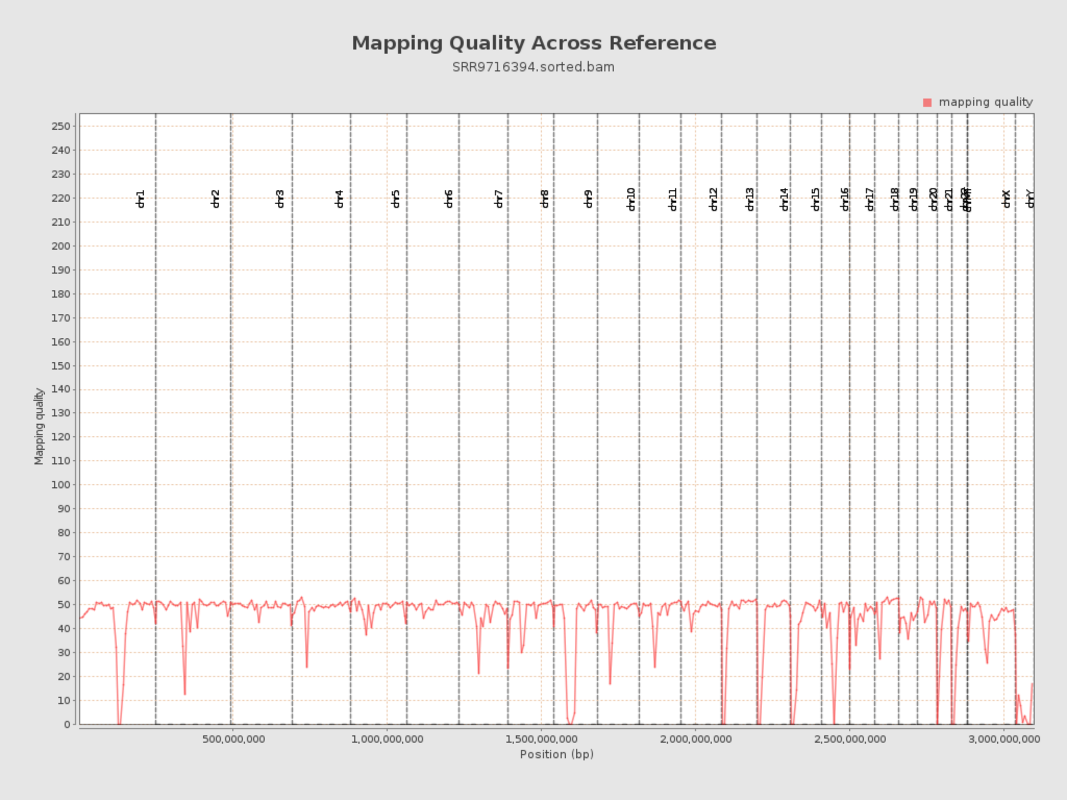
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram