Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 06:04:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716294.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_SRR9716294 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716294.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 06:04:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716294.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,380,266
Mapped reads	1,292,229 / 93.62%
Unmapped reads	88,037 / 6.38%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,327 / 1.91%
Read min/max/mean length	30 / 101 / 101.69
Duplicated reads (estimated)	52,822 / 3.83%
Duplication rate	3.24%
Clipped reads	1,316,498 / 95.38%

2.2. ACGT Content

Number/percentage of A's	25,167,181 / 25.19%
Number/percentage of C's	20,900,704 / 20.92%
Number/percentage of T's	29,504,445 / 29.53%
Number/percentage of G's	24,351,834 / 24.37%
Number/percentage of N's	4,069 / 0%
GC Percentage	45.29%

2.3. Coverage

Mean	0.0323

Standard Deviation	0.2572

2.4. Mapping Quality

Mean Mapping Quality	46.88

2.5. Mismatches and indels

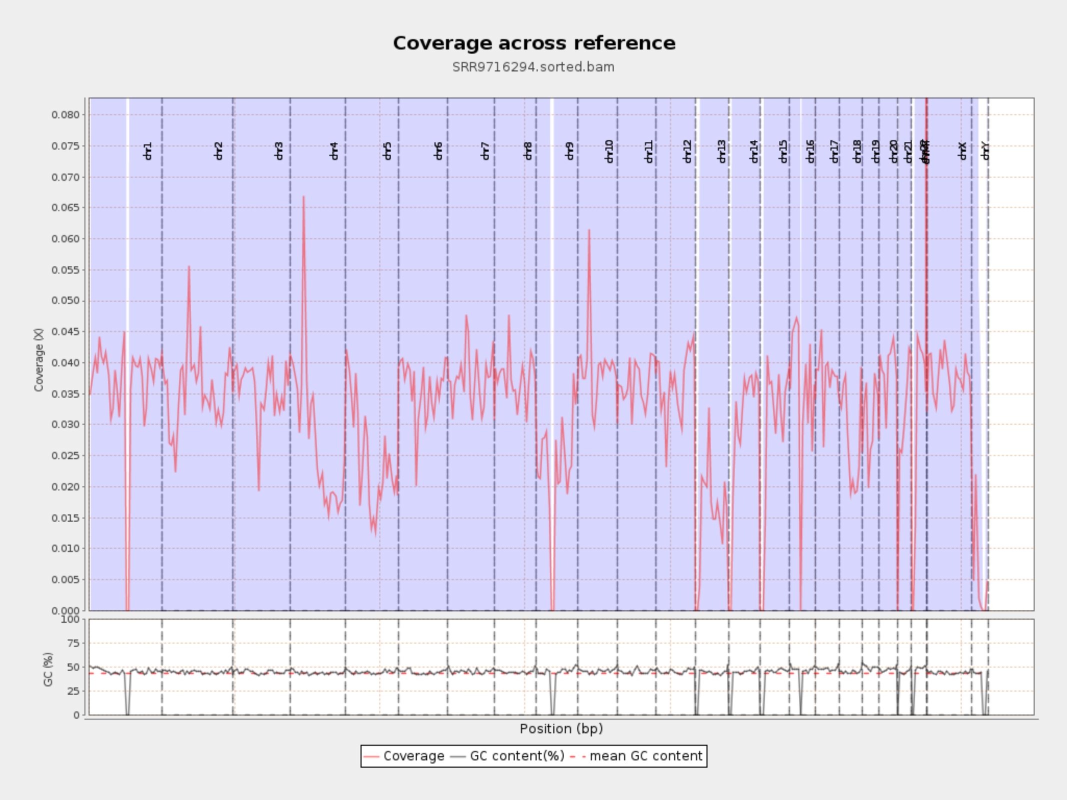
General error rate	0.68%
Mismatches	657,995
Insertions	8,513
Mapped reads with at least one insertion	0.65%
Deletions	18,678
Mapped reads with at least one deletion	1.42%
Homopolymer indels	38.64%

2.6. Chromosome stats

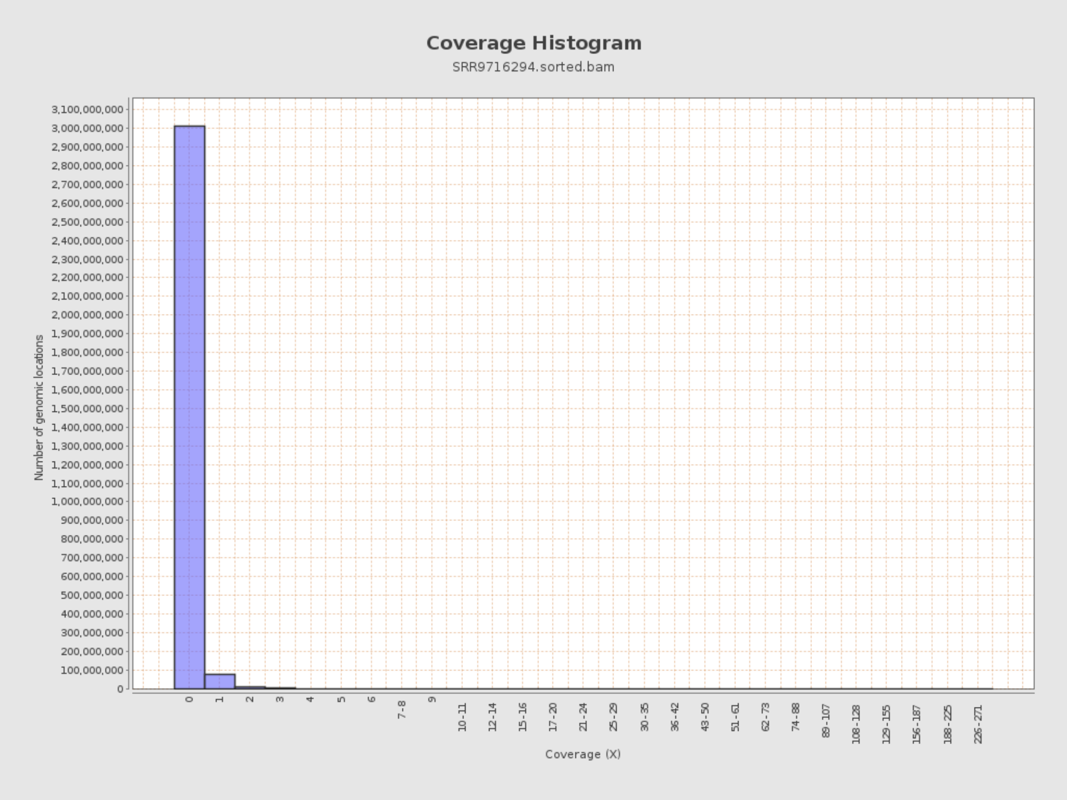
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8932285	0.0358	0.3194
chr2	243199373	8695752	0.0358	0.3022
chr3	198022430	7071261	0.0357	0.2136
chr4	191154276	5299216	0.0277	0.2416
chr5	180915260	4452575	0.0246	0.1763
chr6	171115067	6109000	0.0357	0.2213
chr7	159138663	5951801	0.0374	0.3407

chr8	146364022	5493269	0.0375	0.2915
chr9	141213431	3189314	0.0226	0.2273
chr10	135534747	5331549	0.0393	0.3253
chr11	135006516	4946868	0.0366	0.2869
chr12	133851895	4895109	0.0366	0.2179
chr13	115169878	1760129	0.0153	0.1392
chr14	107349540	3113909	0.029	0.2086
chr15	102531392	2903346	0.0283	0.1902
chr16	90354753	3201379	0.0354	0.2269
chr17	81195210	3069750	0.0378	0.2435
chr18	78077248	2150588	0.0275	0.3488
chr19	59128983	1806617	0.0306	0.2698
chr20	63025520	2470353	0.0392	0.2344
chr21	48129895	1435231	0.0298	0.2269
chr22	51304566	1473863	0.0287	0.201
chrMT	16571	6245	0.3769	0.6394
chrX	155270560	5870691	0.0378	0.2329
chrY	59373566	336918	0.0057	0.2026

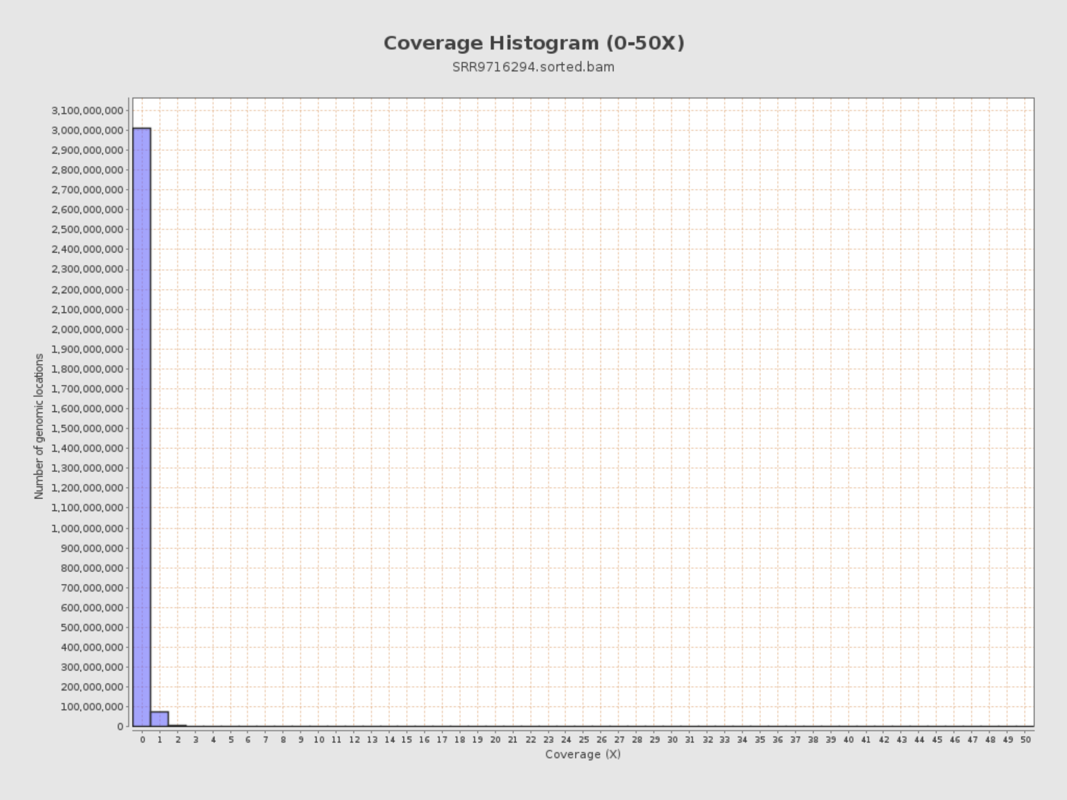
3. Results : Coverage across reference



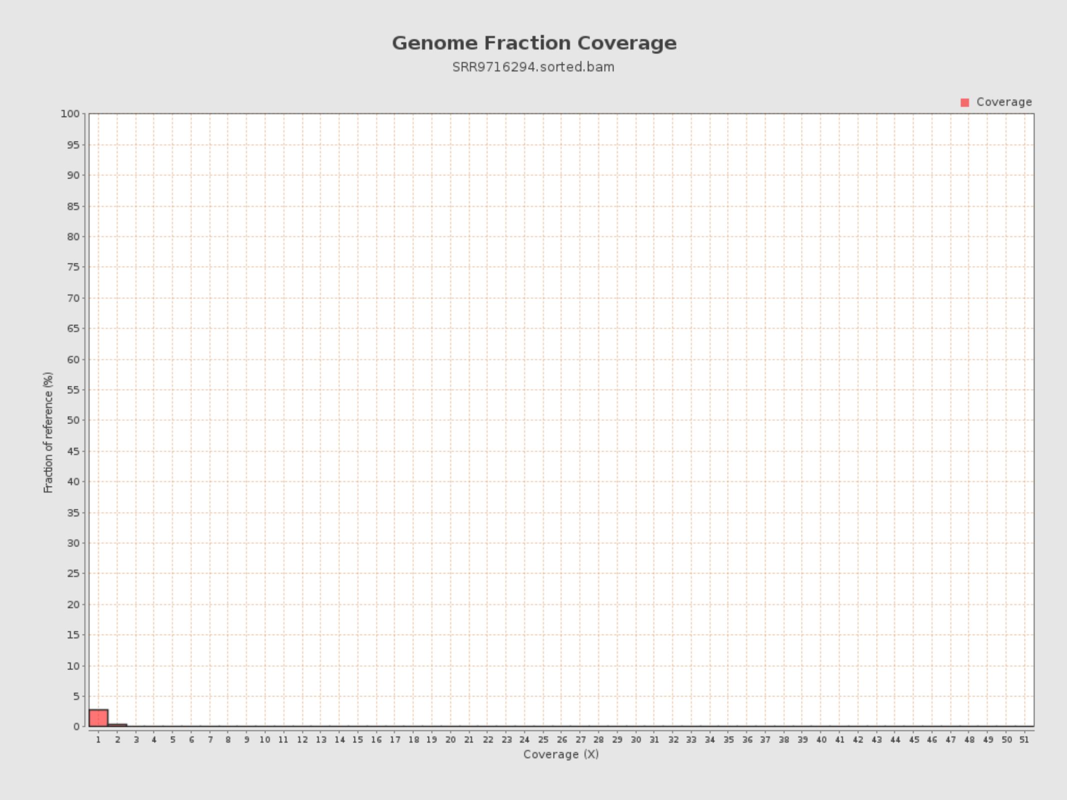
4. Results : Coverage Histogram



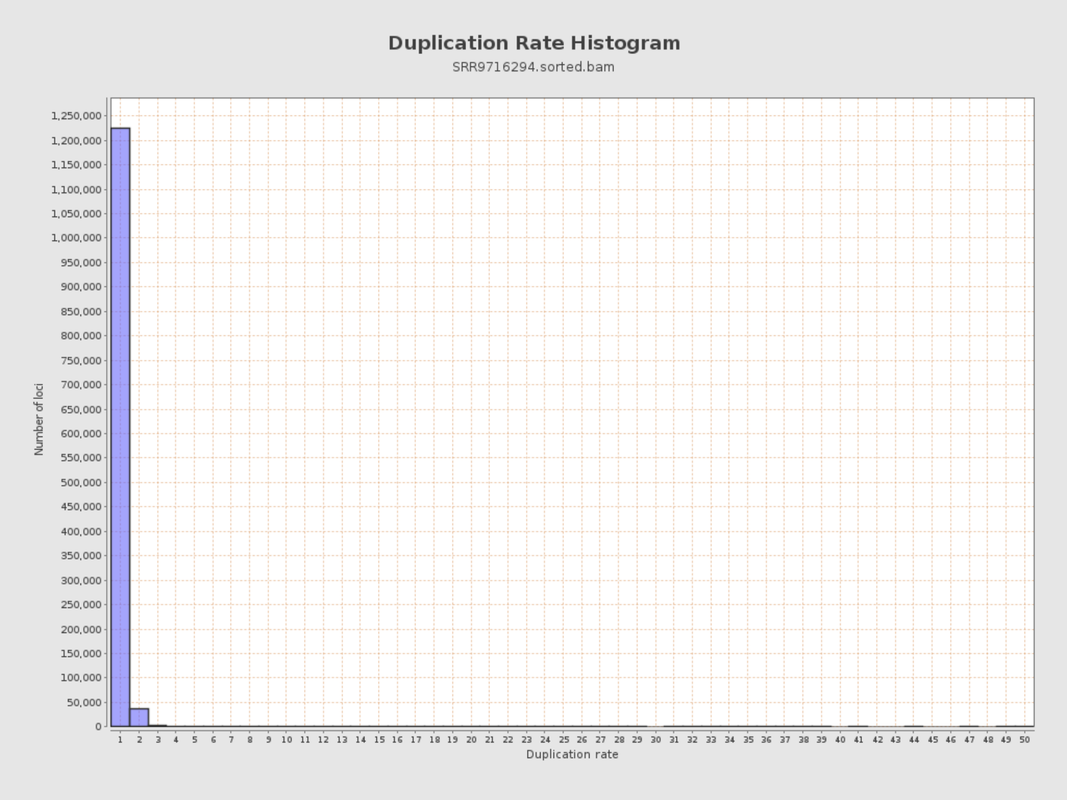
5. Results : Coverage Histogram (0-50X)



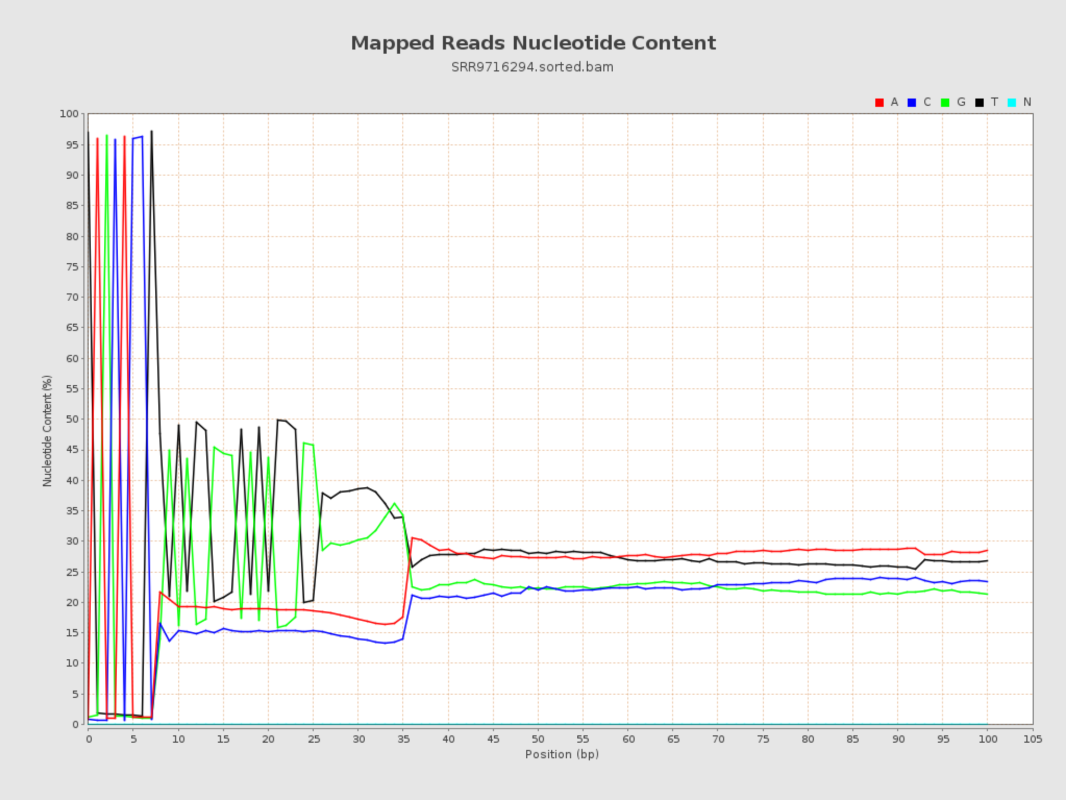
6. Results : Genome Fraction Coverage



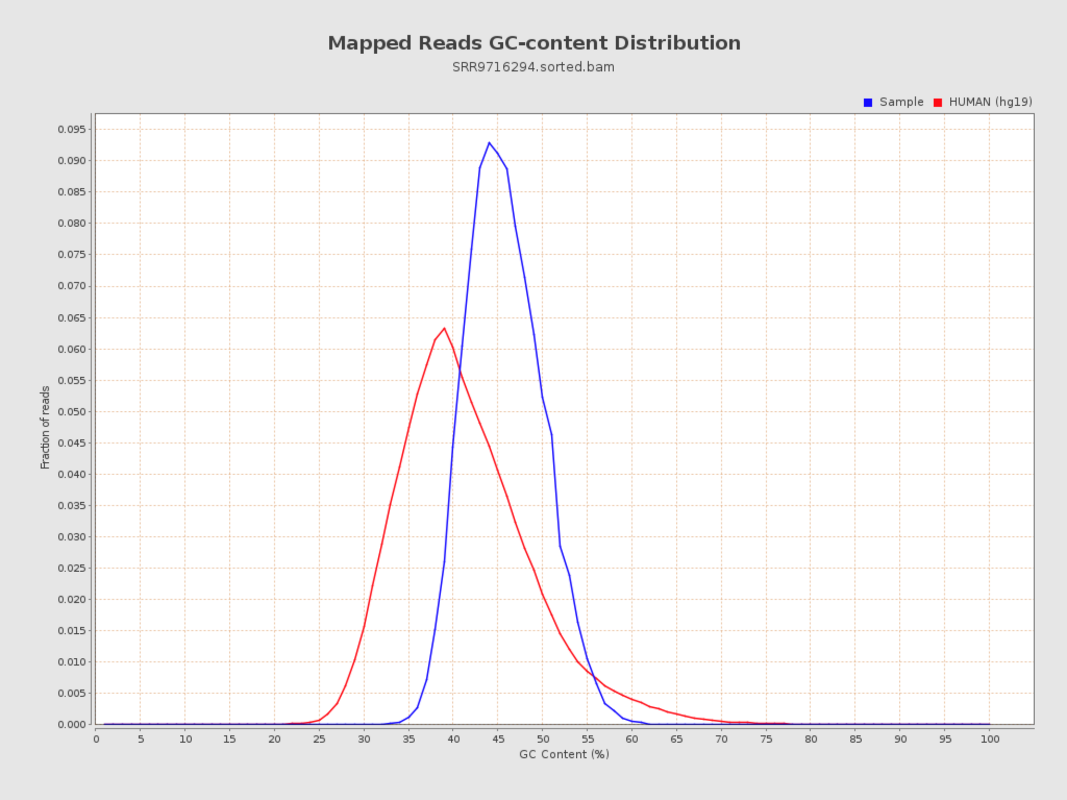
7. Results : Duplication Rate Histogram



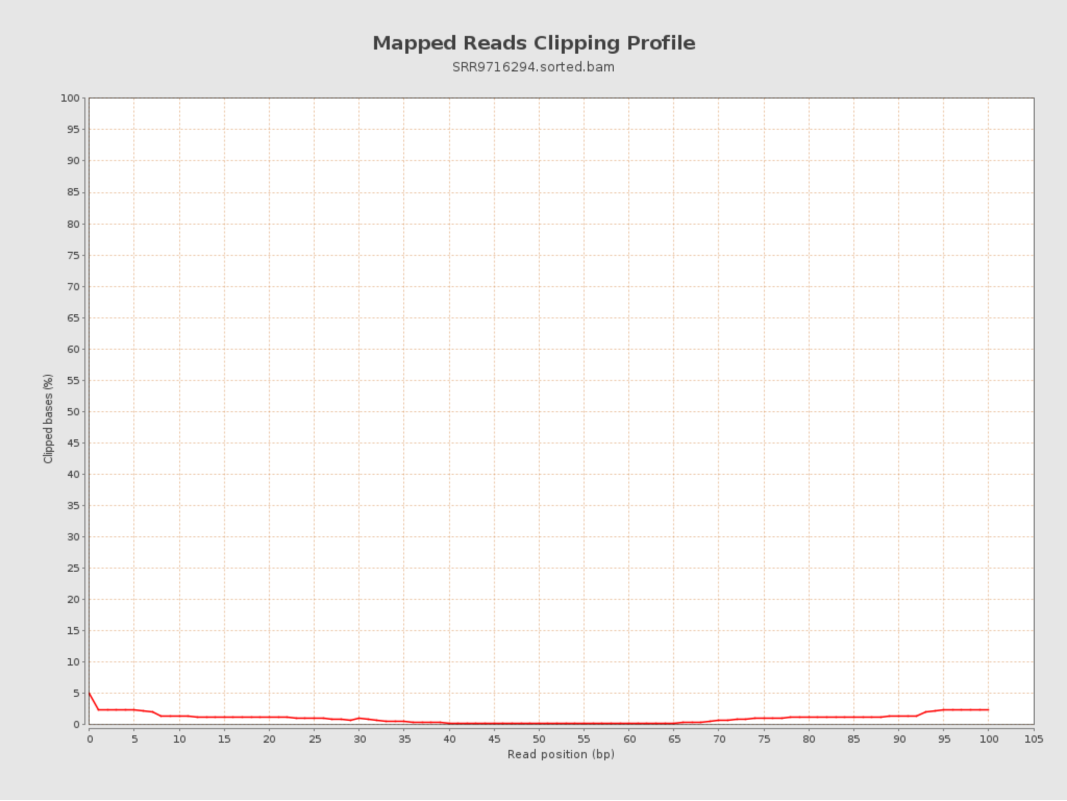
8. Results : Mapped Reads Nucleotide Content



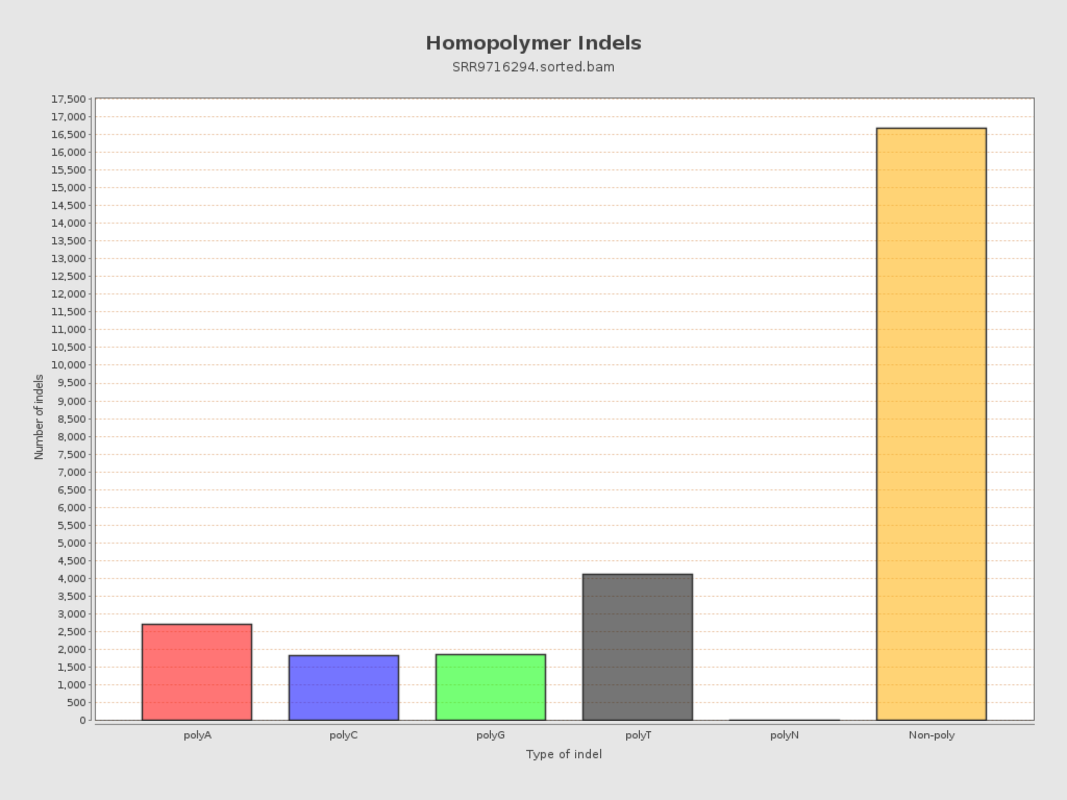
9. Results : Mapped Reads GC-content Distribution



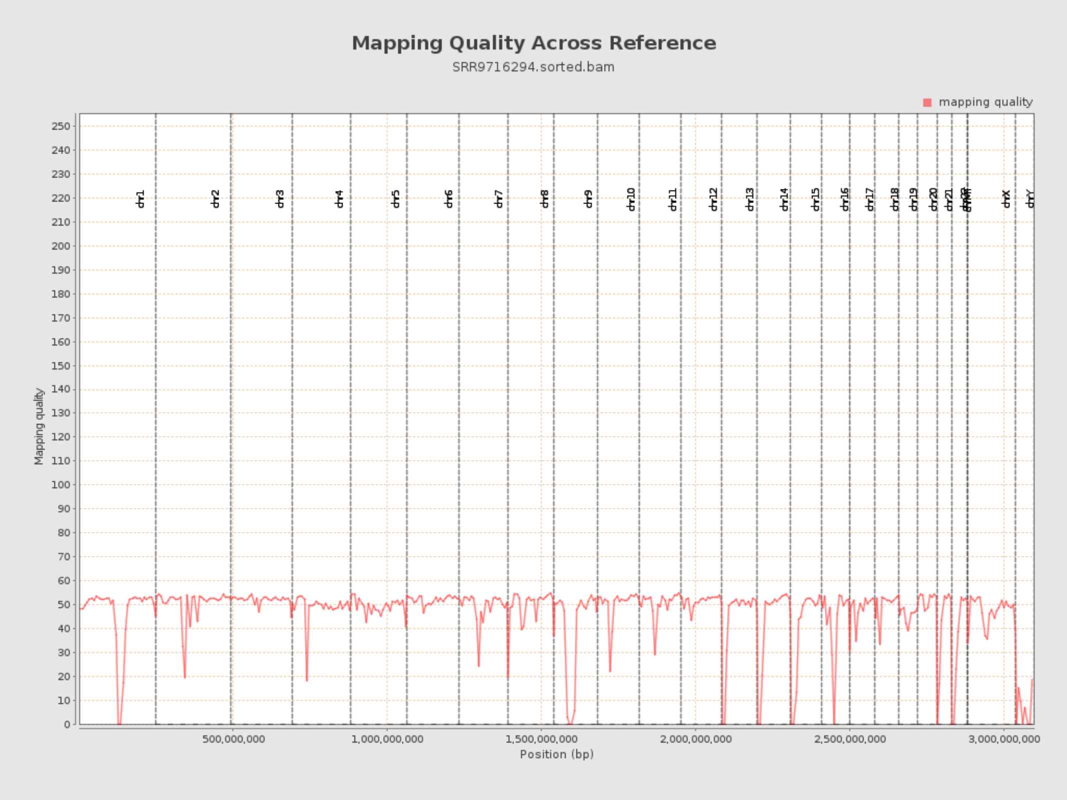
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram