Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 19:14:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716534.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_SRR9716534 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716534.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 19:14:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716534.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,789,513
Mapped reads	1,658,614 / 92.69%
Unmapped reads	130,899 / 7.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	34,031 / 1.9%
Read min/max/mean length	30 / 101 / 101.69
Duplicated reads (estimated)	62,754 / 3.51%
Duplication rate	2.65%
Clipped reads	1,689,416 / 94.41%

2.2. ACGT Content

Number/percentage of A's	34,238,941 / 26.27%
Number/percentage of C's	26,194,430 / 20.09%
Number/percentage of T's	39,449,302 / 30.26%
Number/percentage of G's	30,462,935 / 23.37%
Number/percentage of N's	9,429 / 0.01%
GC Percentage	43.46%

2.3. Coverage

Mean	0.0421

Standard Deviation	0.4091

2.4. Mapping Quality

Mean Mapping Quality	47.19

2.5. Mismatches and indels

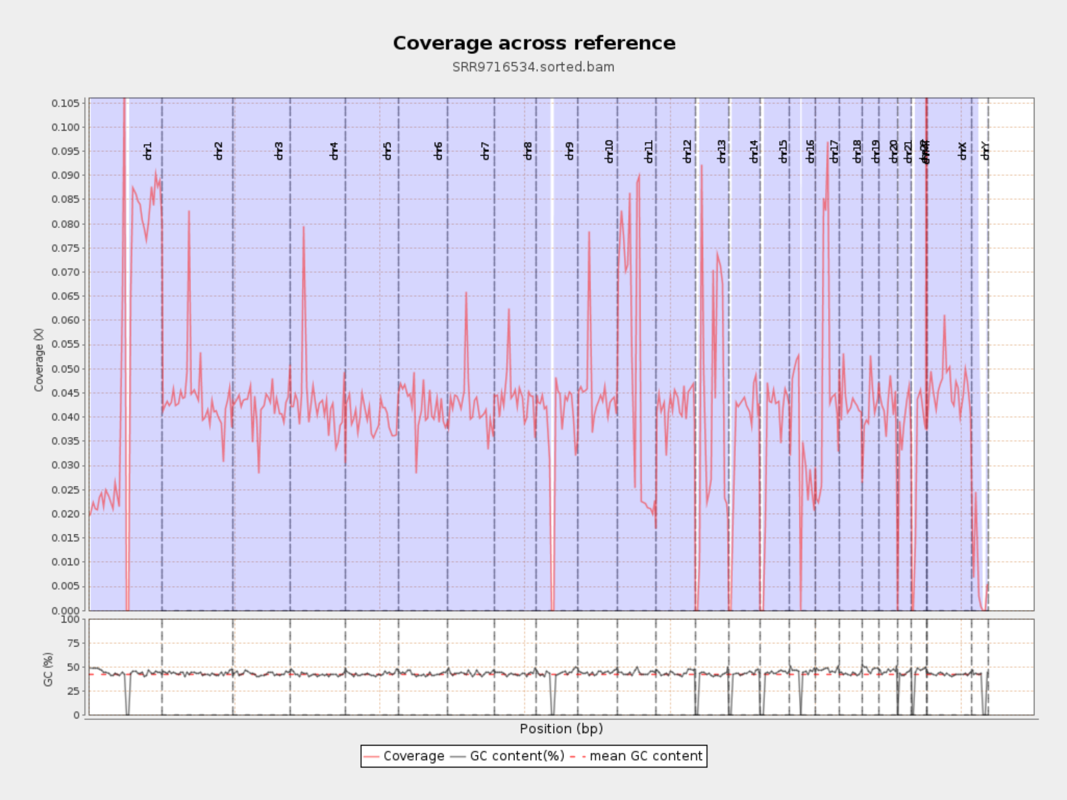
General error rate	0.69%
Mismatches	873,260
Insertions	10,453
Mapped reads with at least one insertion	0.62%
Deletions	31,447
Mapped reads with at least one deletion	1.86%
Homopolymer indels	42.53%

2.6. Chromosome stats

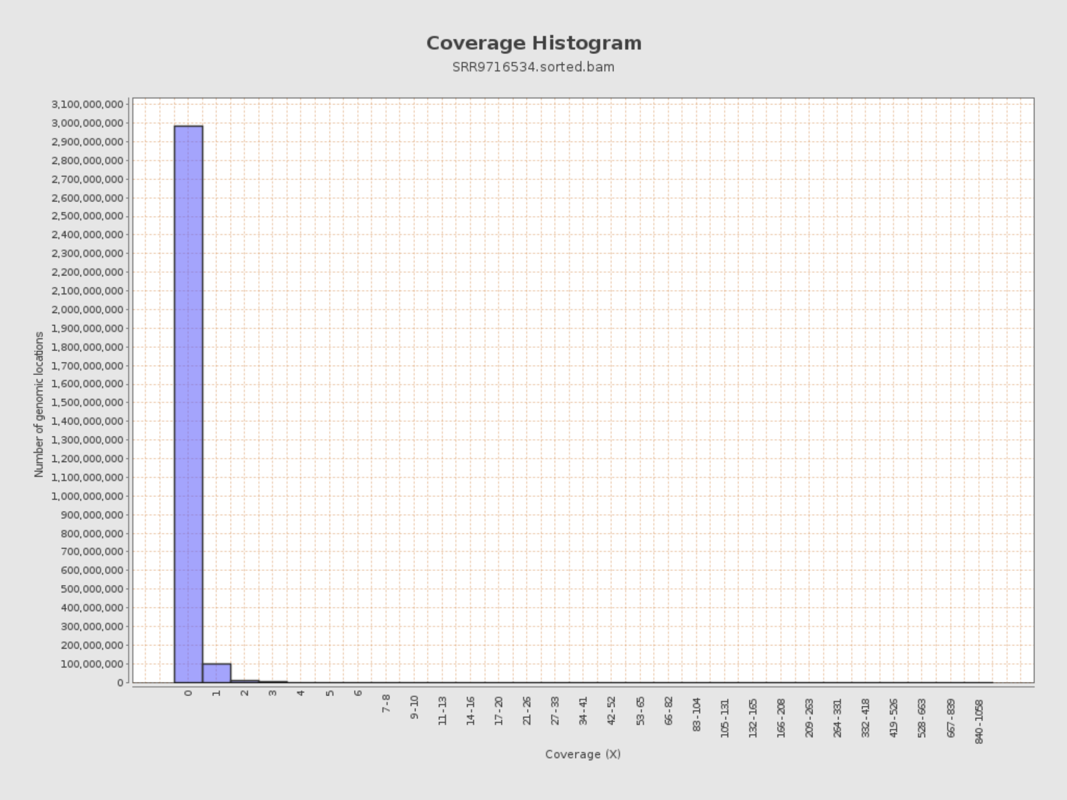
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12942890	0.0519	0.8816
chr2	243199373	10697409	0.044	0.4256
chr3	198022430	8360447	0.0422	0.2304
chr4	191154276	8248833	0.0432	0.2799
chr5	180915260	7190267	0.0397	0.2238
chr6	171115067	7211287	0.0421	0.2541
chr7	159138663	6798042	0.0427	0.4839

chr8	146364022	6501766	0.0444	0.4426
chr9	141213431	5269000	0.0373	0.3276
chr10	135534747	6147872	0.0454	0.4007
chr11	135006516	6862058	0.0508	0.444
chr12	133851895	5688094	0.0425	0.2304
chr13	115169878	4660817	0.0405	0.225
chr14	107349540	3852934	0.0359	0.2313
chr15	102531392	3603503	0.0351	0.2079
chr16	90354753	2985248	0.033	0.2214
chr17	81195210	4067498	0.0501	0.3002
chr18	78077248	3398159	0.0435	0.5671
chr19	59128983	2495469	0.0422	0.607
chr20	63025520	2646085	0.042	0.24
chr21	48129895	1730031	0.0359	0.2453
chr22	51304566	1497735	0.0292	0.1906
chrMT	16571	5963	0.3598	0.6806
chrX	155270560	7168396	0.0462	0.2844
chrY	59373566	385105	0.0065	0.2043

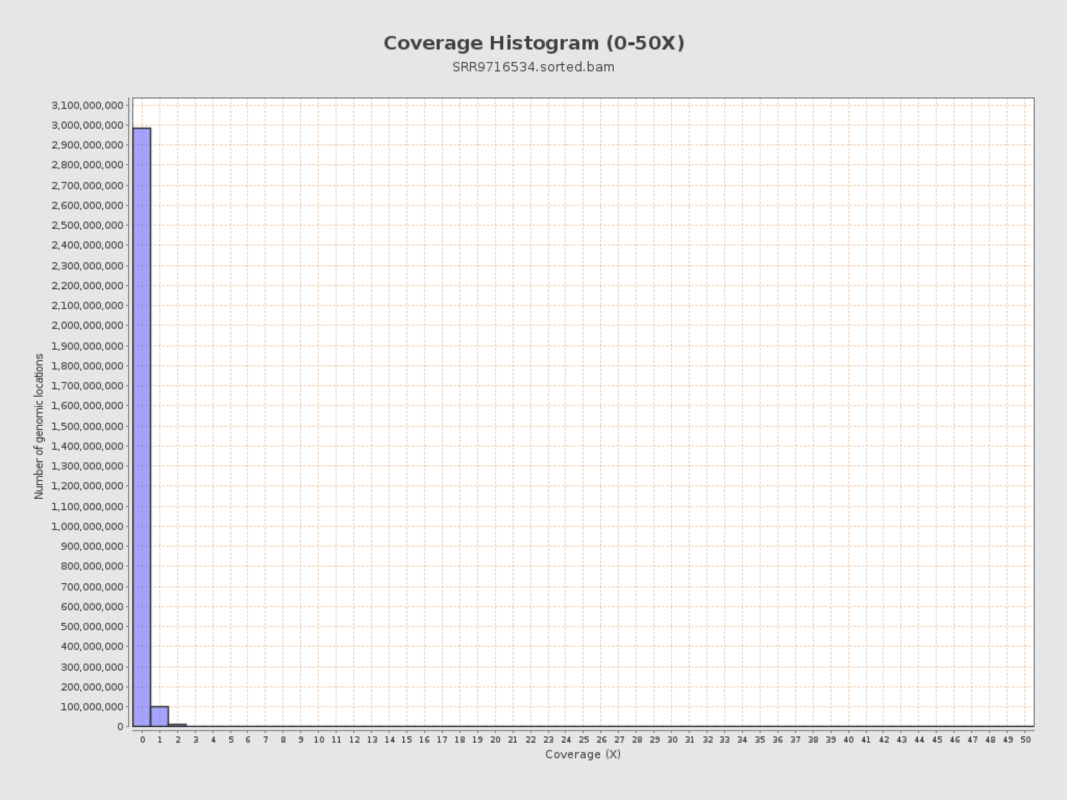
3. Results : Coverage across reference



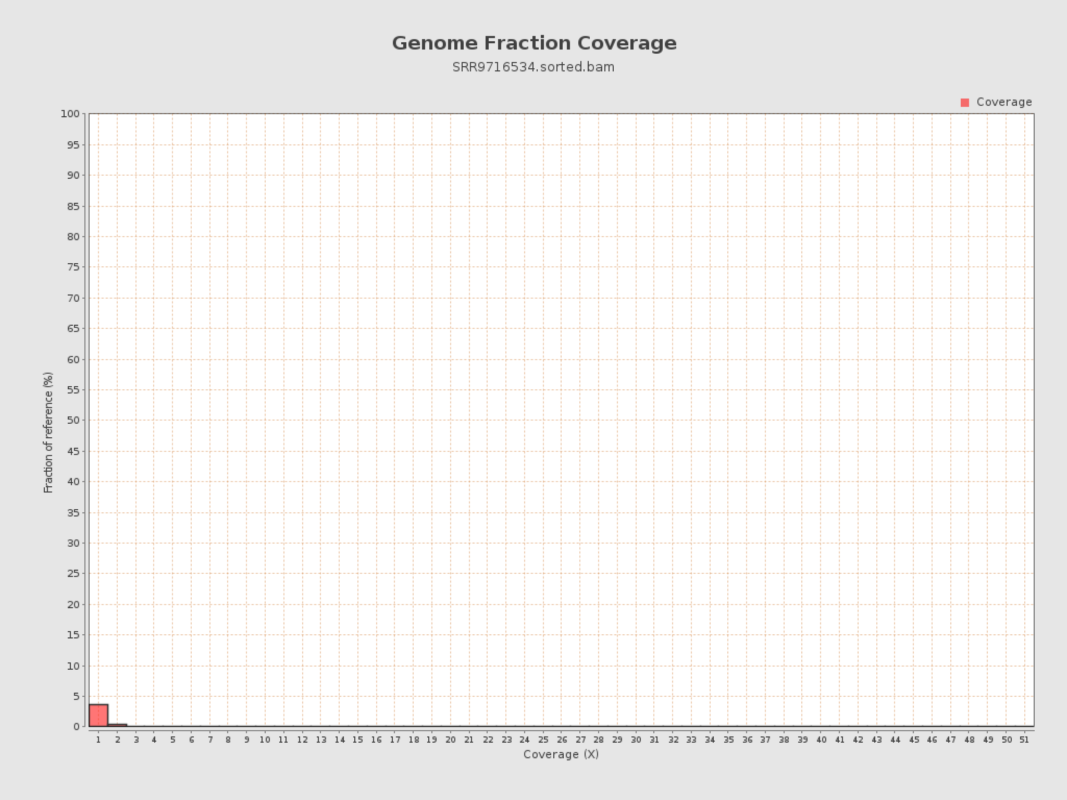
4. Results : Coverage Histogram



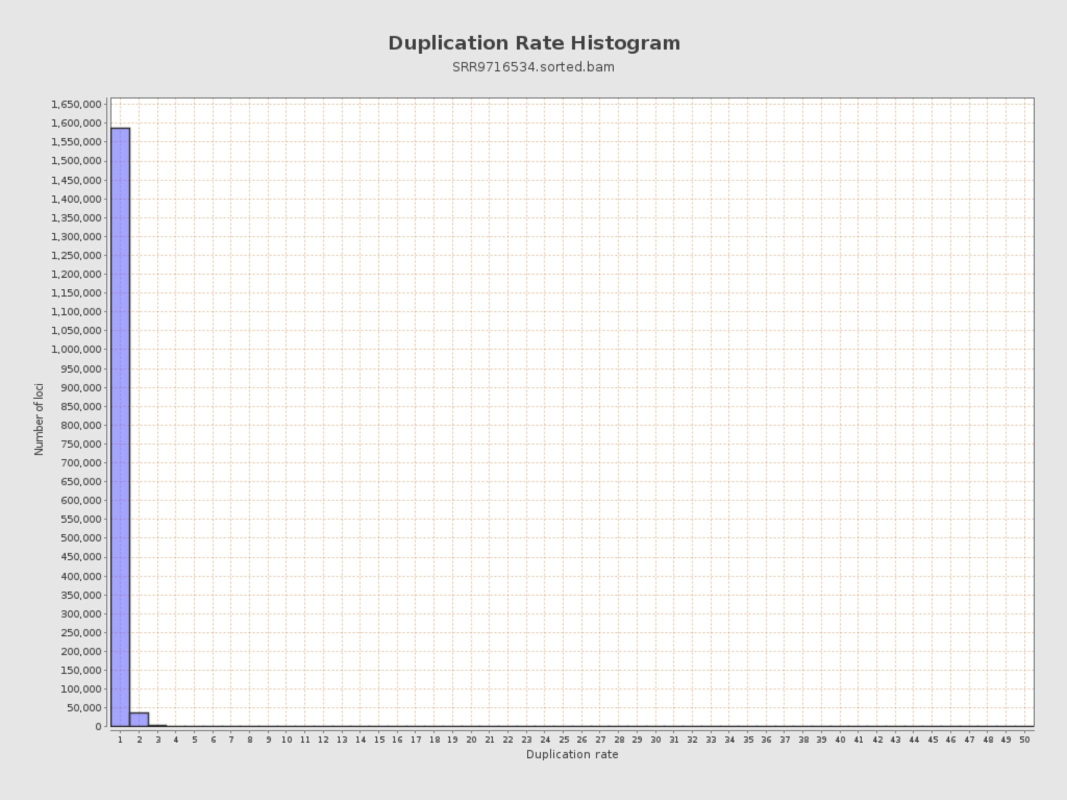
5. Results : Coverage Histogram (0-50X)



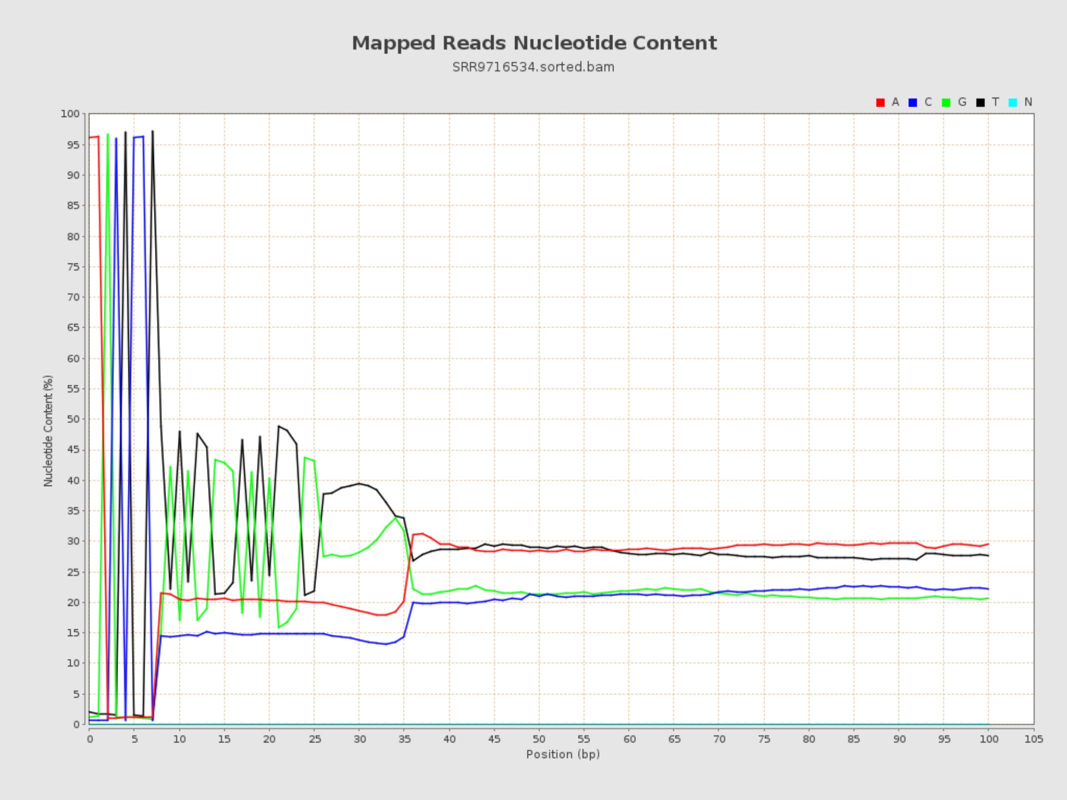
6. Results : Genome Fraction Coverage



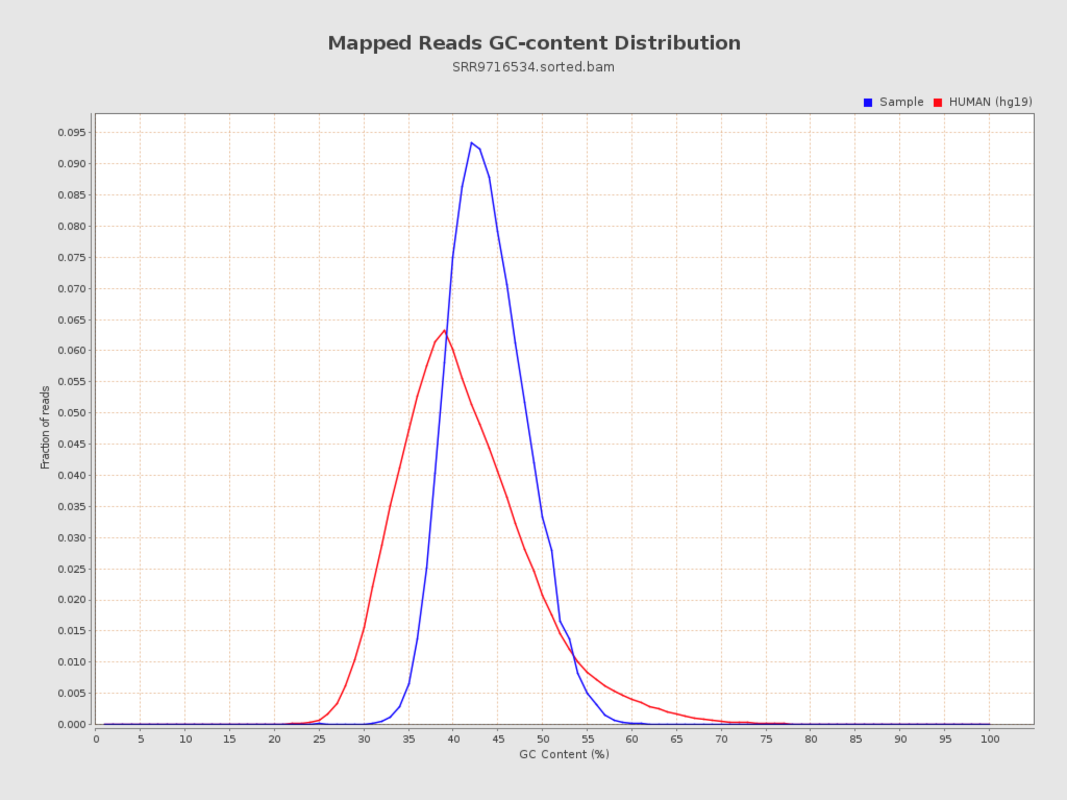
7. Results : Duplication Rate Histogram



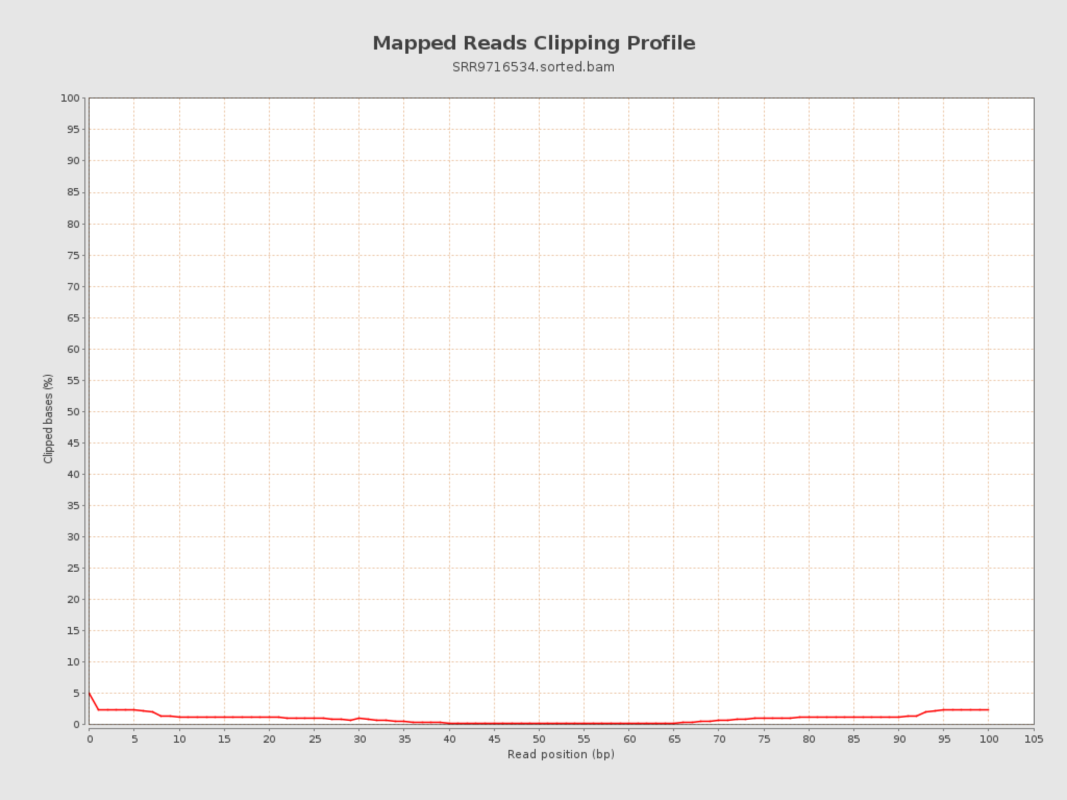
8. Results : Mapped Reads Nucleotide Content



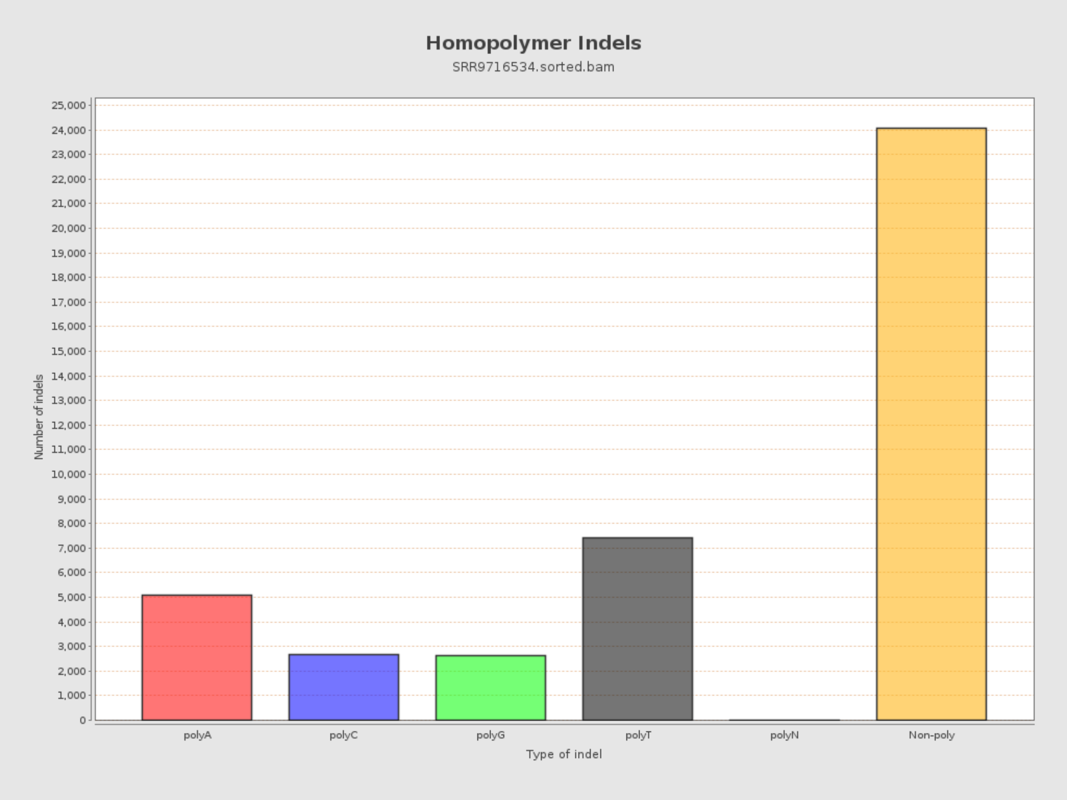
9. Results : Mapped Reads GC-content Distribution



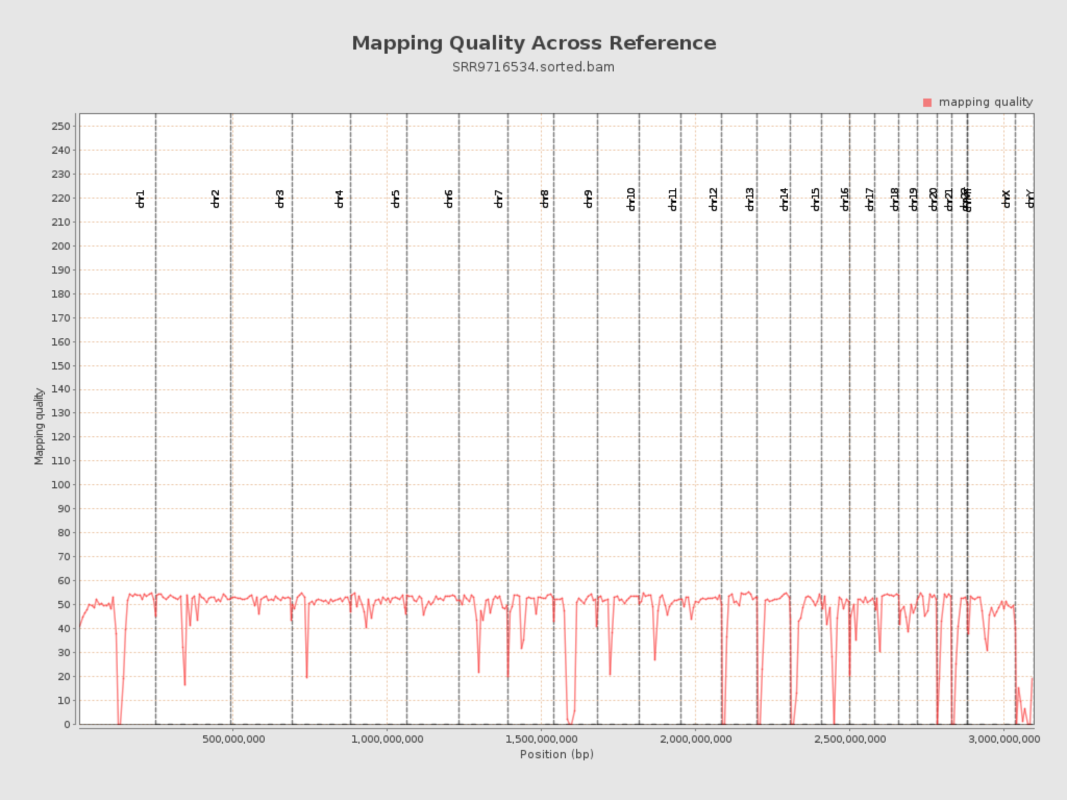
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram