Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 14:15:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716838.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_SRR9716838 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716838.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 14:15:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716838.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,816,323
Mapped reads	3,199,435 / 83.84%
Unmapped reads	616,888 / 16.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,304 / 0.53%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	246,631 / 6.46%
Duplication rate	5.99%
Clipped reads	3,213,192 / 84.2%

2.2. ACGT Content

Number/percentage of A's	47,694,947 / 25.73%
Number/percentage of C's	35,694,586 / 19.26%
Number/percentage of T's	58,388,172 / 31.5%
Number/percentage of G's	43,589,521 / 23.52%
Number/percentage of N's	1,332 / 0%
GC Percentage	42.77%

2.3. Coverage

Mean	0.0599

Standard Deviation	0.4803

2.4. Mapping Quality

Mean Mapping Quality	44.16

2.5. Mismatches and indels

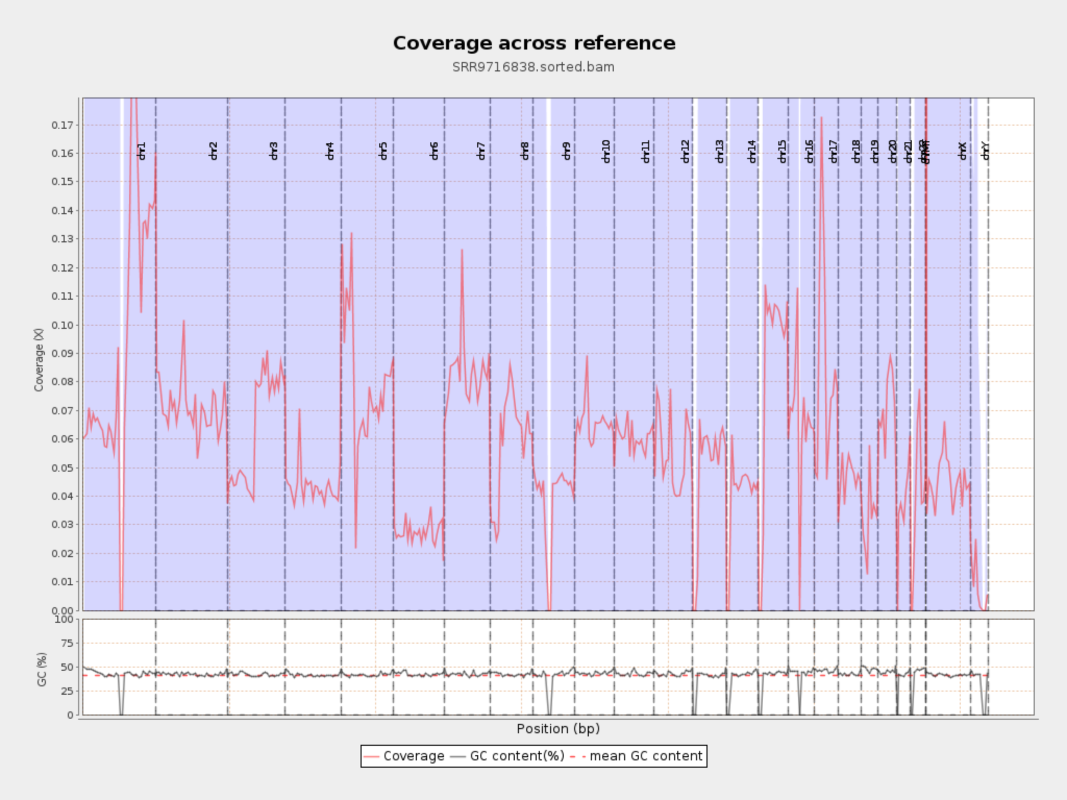
General error rate	0.51%
Mismatches	915,969
Insertions	11,871
Mapped reads with at least one insertion	0.37%
Deletions	32,016
Mapped reads with at least one deletion	0.99%
Homopolymer indels	42.15%

2.6. Chromosome stats

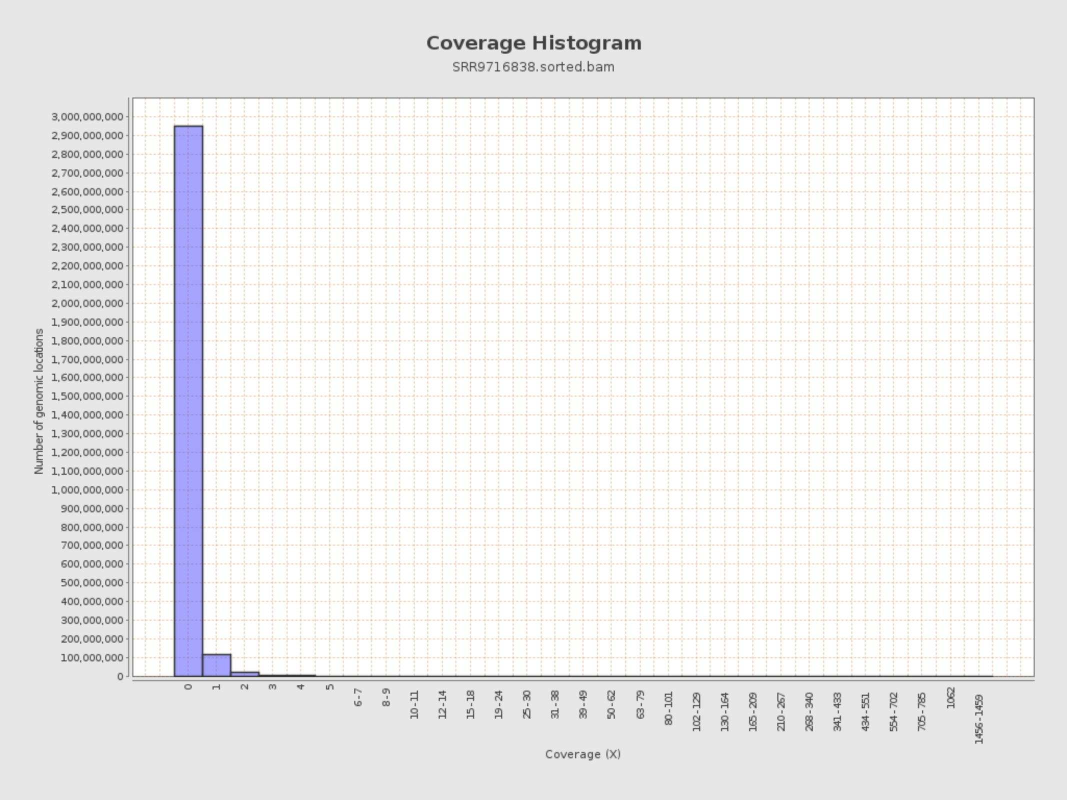
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23294291	0.0935	0.7432
chr2	243199373	17350383	0.0713	0.6963
chr3	198022430	12562540	0.0634	0.3104
chr4	191154276	8318148	0.0435	0.3151
chr5	180915260	14420591	0.0797	0.3527
chr6	171115067	4710584	0.0275	0.2415
chr7	159138663	13327644	0.0837	0.8658

chr8	146364022	8749326	0.0598	0.4332
chr9	141213431	5463958	0.0387	0.3508
chr10	135534747	8906532	0.0657	0.4242
chr11	135006516	8181765	0.0606	0.4722
chr12	133851895	7412754	0.0554	0.2944
chr13	115169878	5643363	0.049	0.275
chr14	107349540	4304595	0.0401	0.2717
chr15	102531392	8574573	0.0836	0.3647
chr16	90354753	5868120	0.0649	0.3421
chr17	81195210	6820577	0.084	0.4173
chr18	78077248	3647110	0.0467	0.8051
chr19	59128983	1922466	0.0325	0.5405
chr20	63025520	4551766	0.0722	0.3418
chr21	48129895	1798053	0.0374	0.2701
chr22	51304566	1966866	0.0383	0.2422
chrMT	16571	169320	10.2179	6.7881
chrX	155270560	7008963	0.0451	0.3136
chrY	59373566	444764	0.0075	0.1838

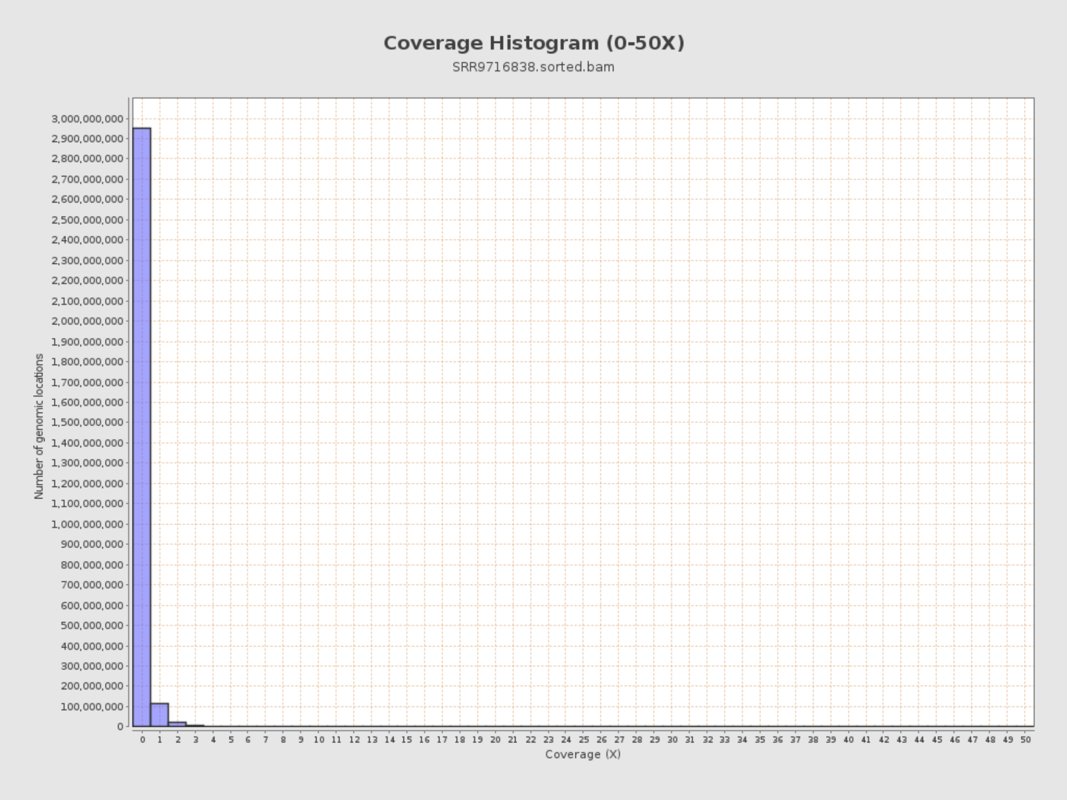
3. Results : Coverage across reference



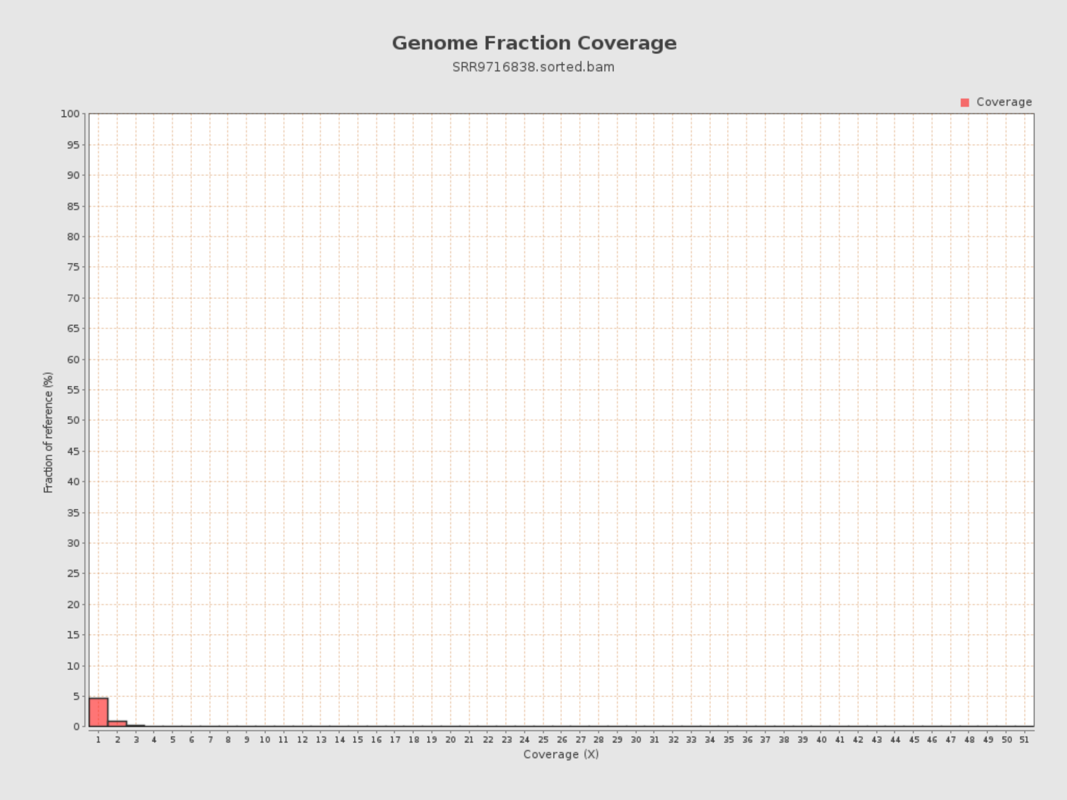
4. Results : Coverage Histogram



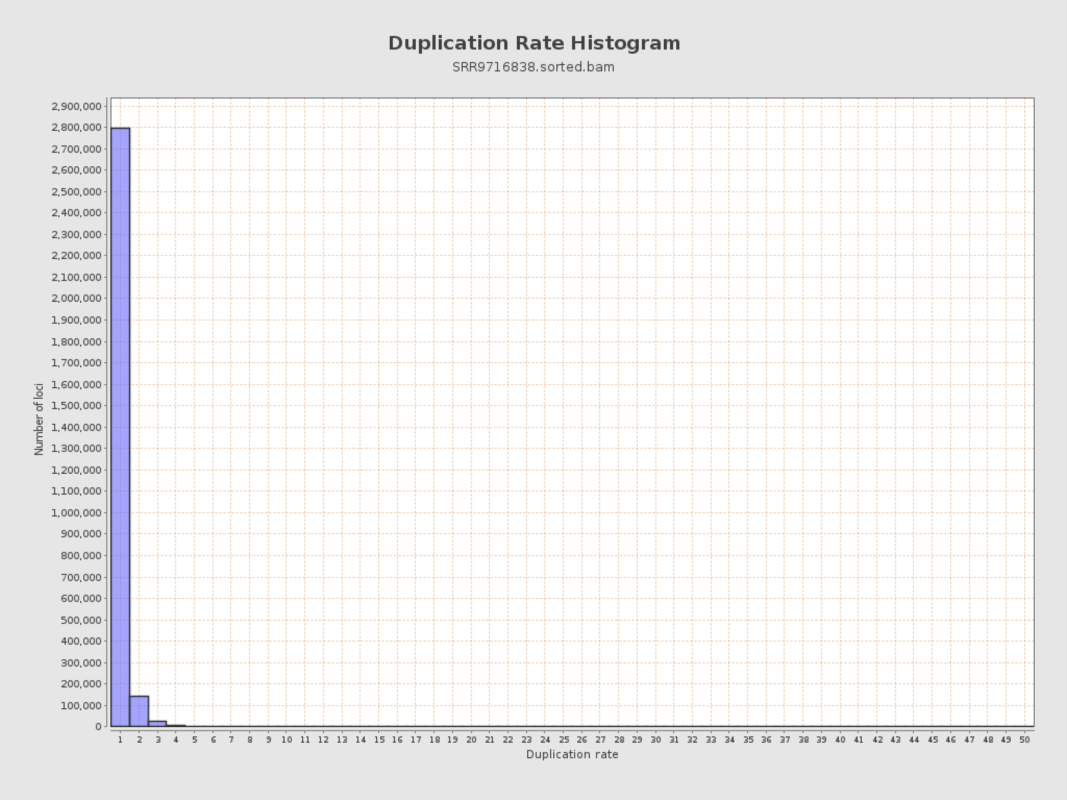
5. Results : Coverage Histogram (0-50X)



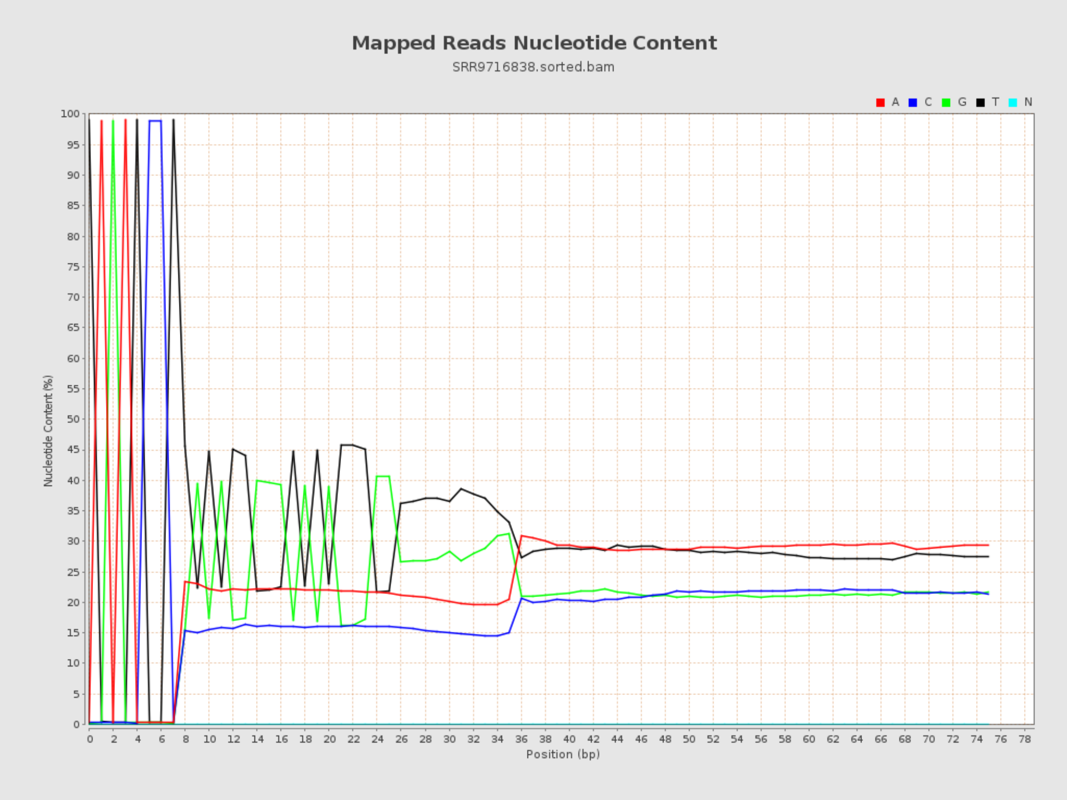
6. Results : Genome Fraction Coverage



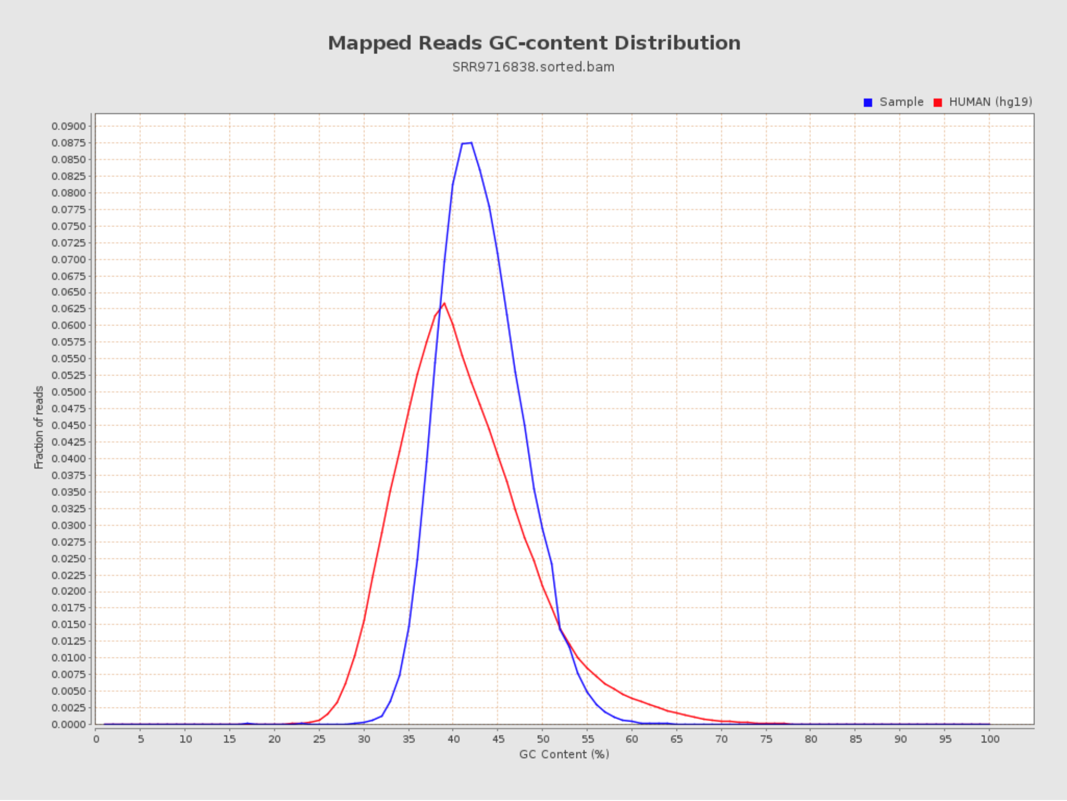
7. Results : Duplication Rate Histogram



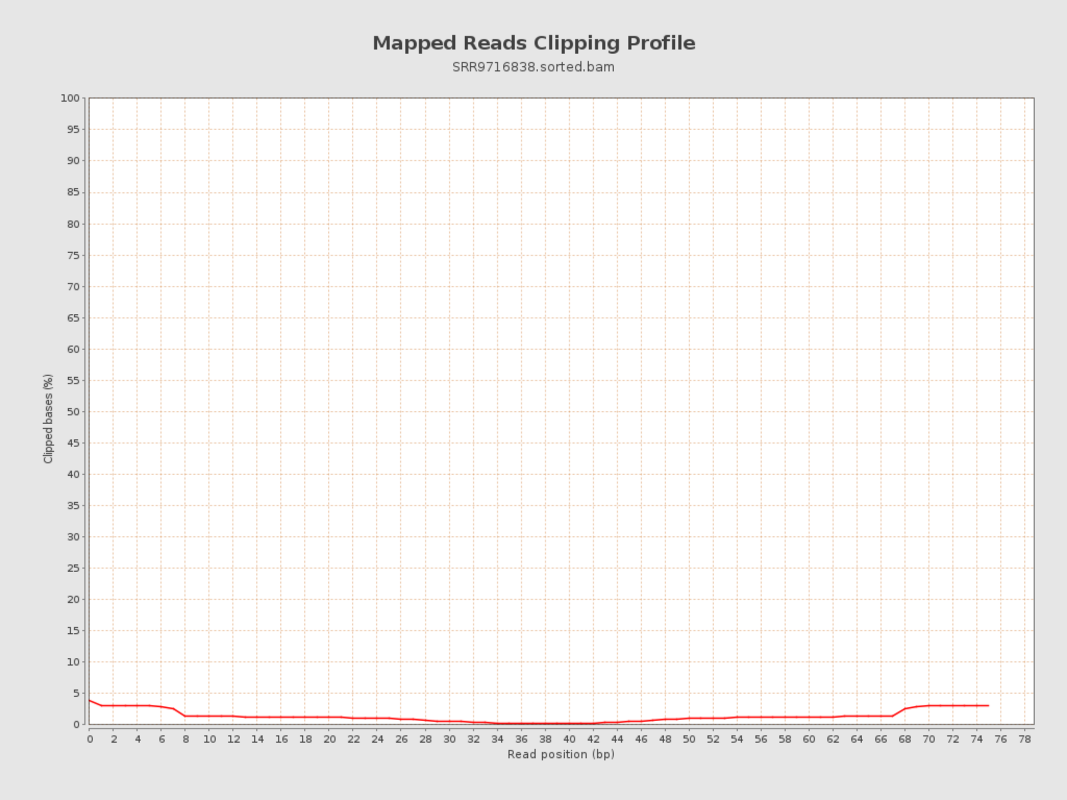
8. Results : Mapped Reads Nucleotide Content



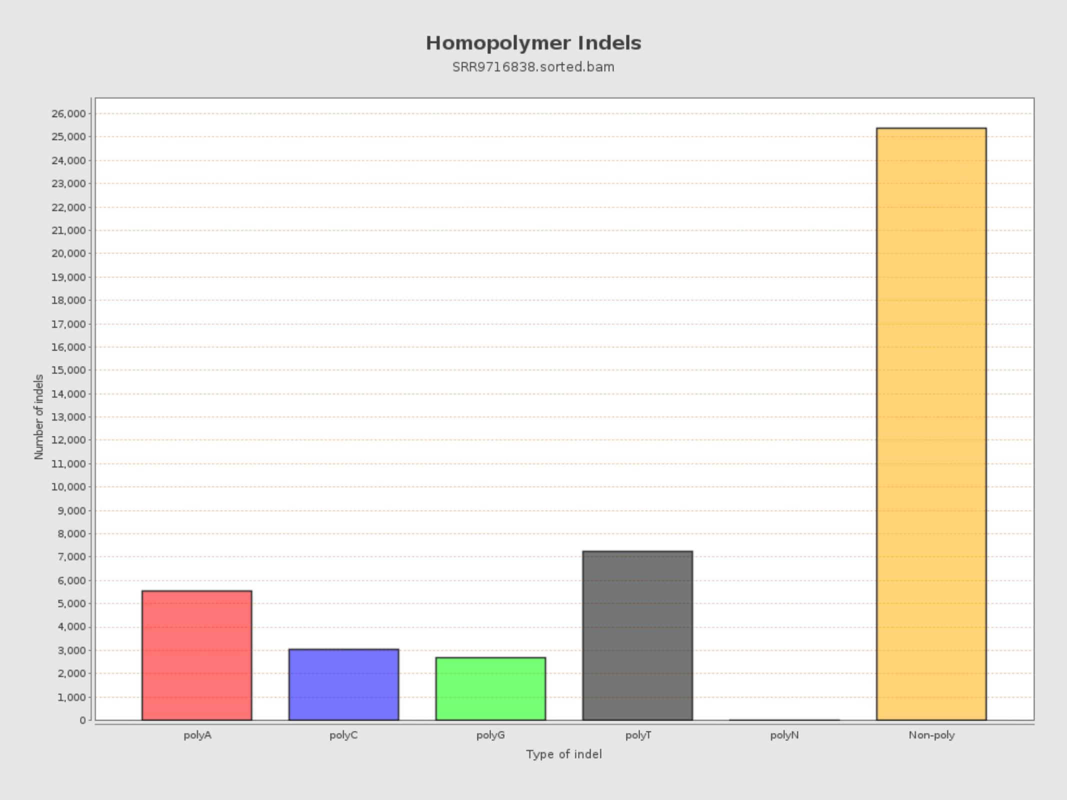
9. Results : Mapped Reads GC-content Distribution



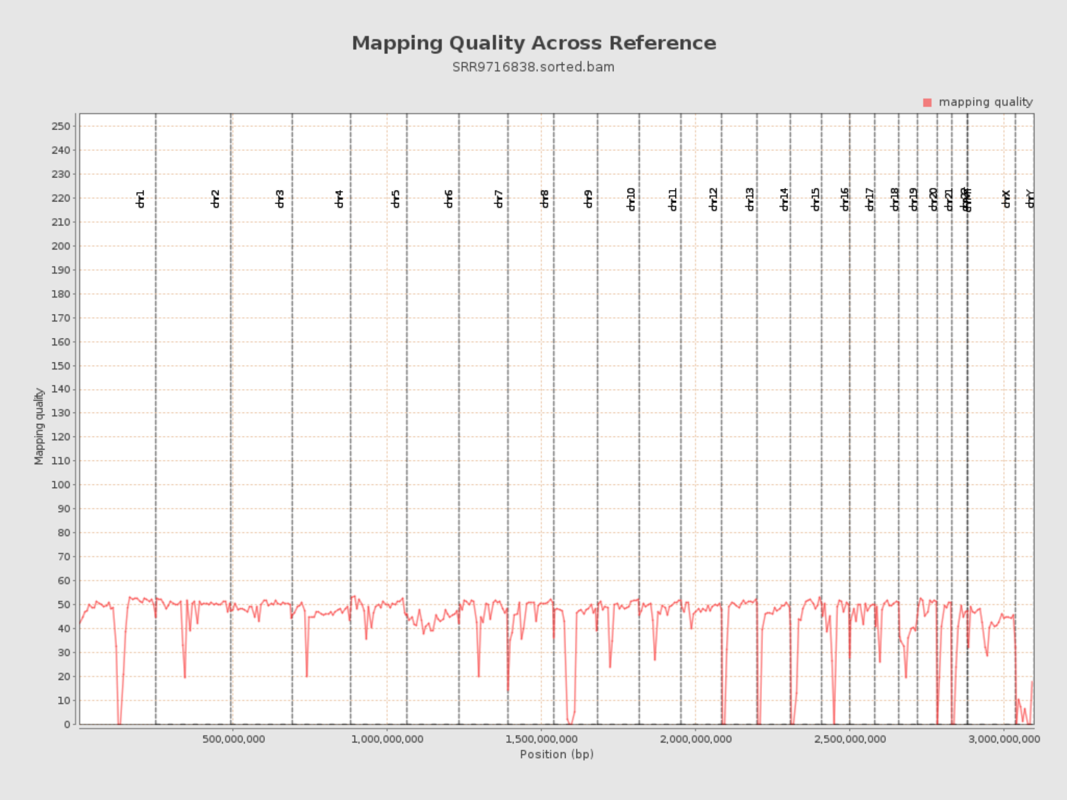
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram