Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 15:12:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716855.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_SRR9716855 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716855.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 15:12:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716855.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,574,701
Mapped reads	2,400,724 / 93.24%
Unmapped reads	173,977 / 6.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	50,826 / 1.97%
Read min/max/mean length	30 / 101 / 101.71
Duplicated reads (estimated)	150,331 / 5.84%
Duplication rate	4.78%
Clipped reads	2,447,039 / 95.04%

2.2. ACGT Content

Number/percentage of A's	45,998,911 / 24.86%
Number/percentage of C's	36,527,032 / 19.74%
Number/percentage of T's	54,961,905 / 29.71%
Number/percentage of G's	47,516,575 / 25.68%
Number/percentage of N's	6,865 / 0%
GC Percentage	45.43%

2.3. Coverage

Mean	0.0598

Standard Deviation	0.4739

2.4. Mapping Quality

Mean Mapping Quality	46.13

2.5. Mismatches and indels

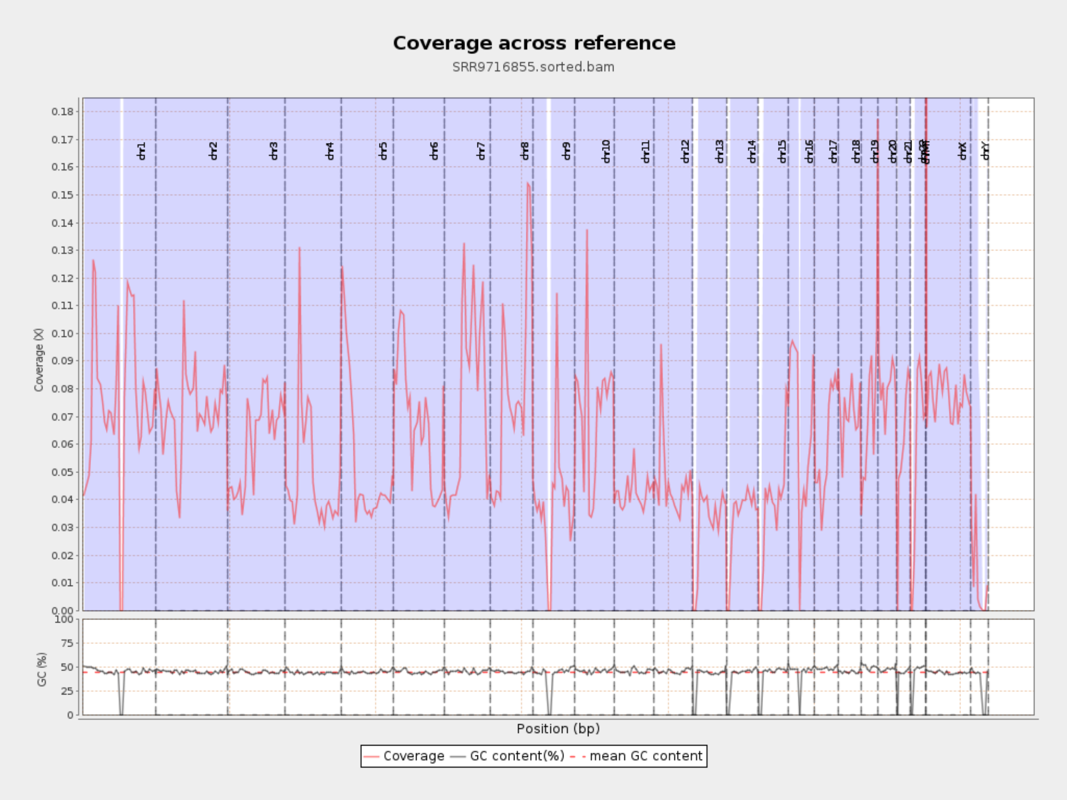
General error rate	0.68%
Mismatches	1,214,246
Insertions	15,839
Mapped reads with at least one insertion	0.65%
Deletions	34,546
Mapped reads with at least one deletion	1.41%
Homopolymer indels	38.44%

2.6. Chromosome stats

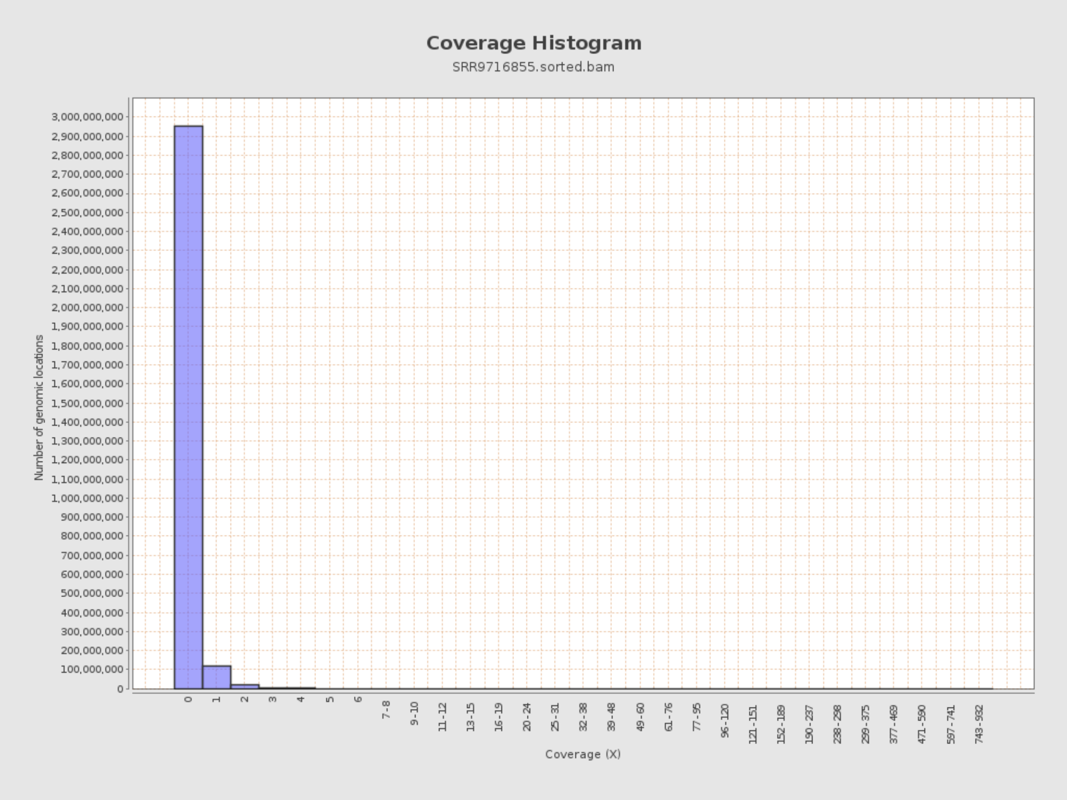
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18708664	0.0751	0.8632
chr2	243199373	17730988	0.0729	0.5422
chr3	198022430	12073737	0.061	0.3093
chr4	191154276	9292144	0.0486	0.4336
chr5	180915260	9711004	0.0537	0.2902
chr6	171115067	11513331	0.0673	0.3459
chr7	159138663	11938872	0.075	0.643

chr8	146364022	11690719	0.0799	0.5026
chr9	141213431	5537430	0.0392	0.3226
chr10	135534747	9745032	0.0719	0.6949
chr11	135006516	5736817	0.0425	0.3702
chr12	133851895	6260206	0.0468	0.268
chr13	115169878	3597239	0.0312	0.214
chr14	107349540	3596475	0.0335	0.2474
chr15	102531392	3776786	0.0368	0.234
chr16	90354753	5842003	0.0647	0.3467
chr17	81195210	4866939	0.0599	0.3492
chr18	78077248	5537901	0.0709	0.5322
chr19	59128983	4289204	0.0725	0.6462
chr20	63025520	5121472	0.0813	0.3803
chr21	48129895	2910133	0.0605	0.3899
chr22	51304566	2848084	0.0555	0.2982
chrMT	16571	44616	2.6924	2.719
chrX	155270560	12055590	0.0776	0.3655
chrY	59373566	657982	0.0111	0.3798

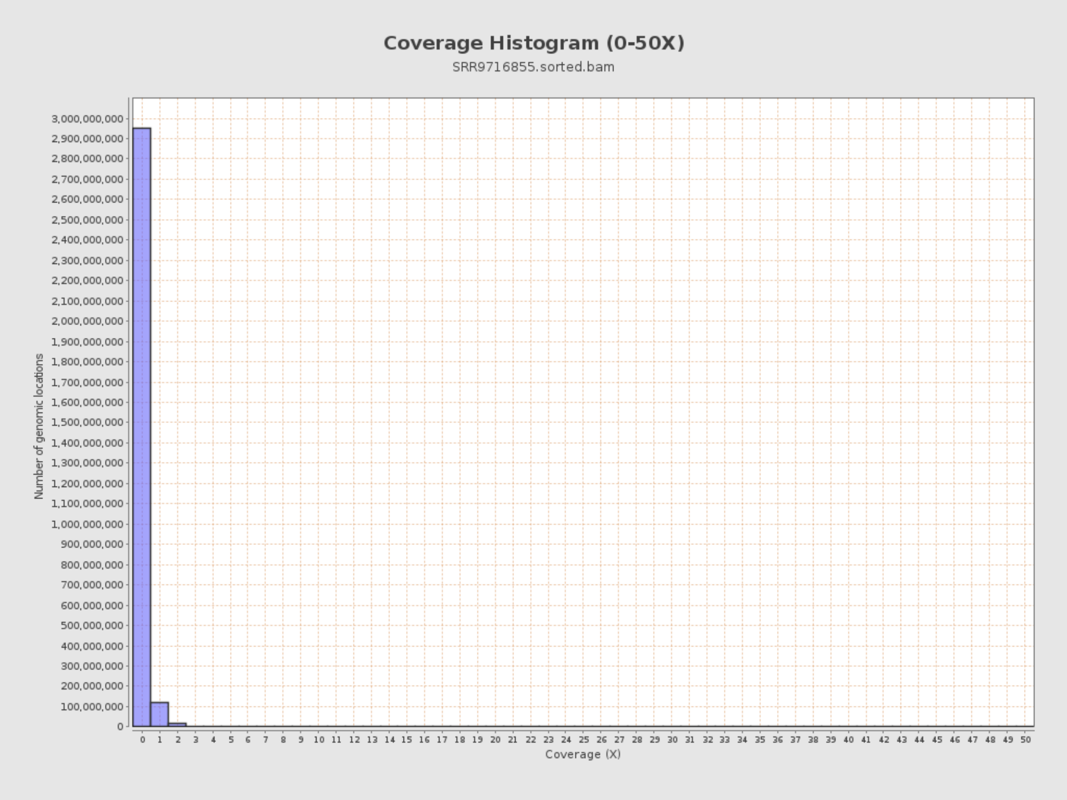
3. Results : Coverage across reference



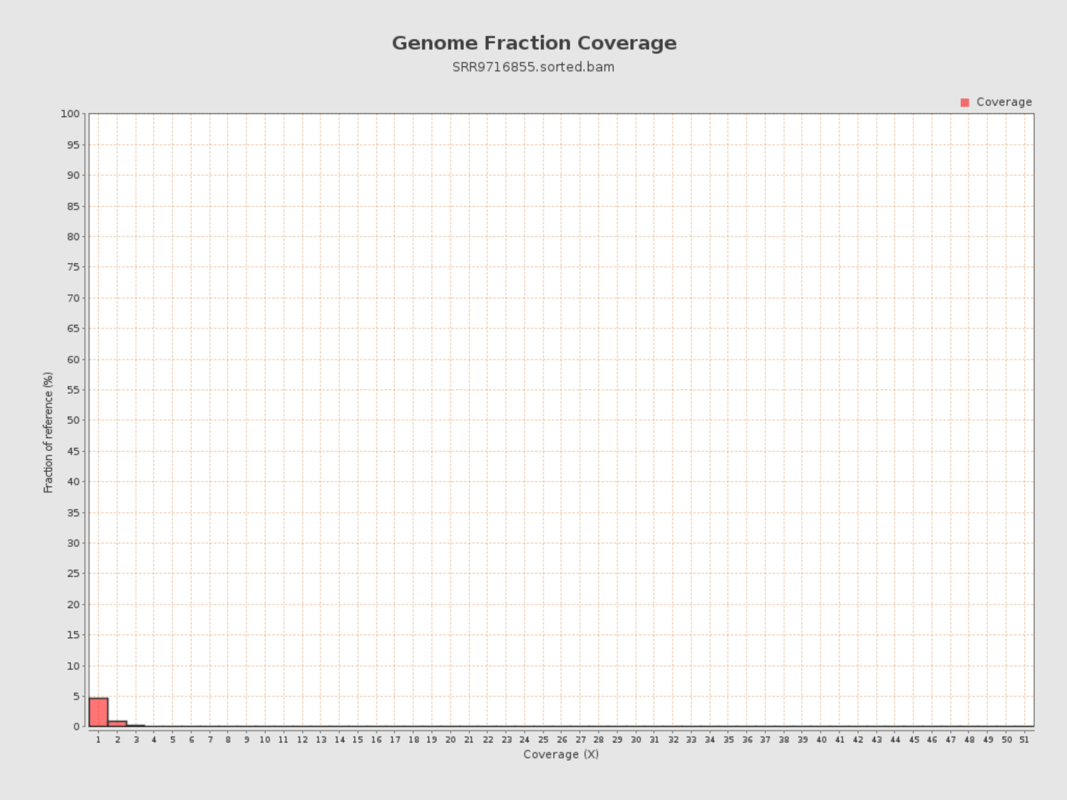
4. Results : Coverage Histogram



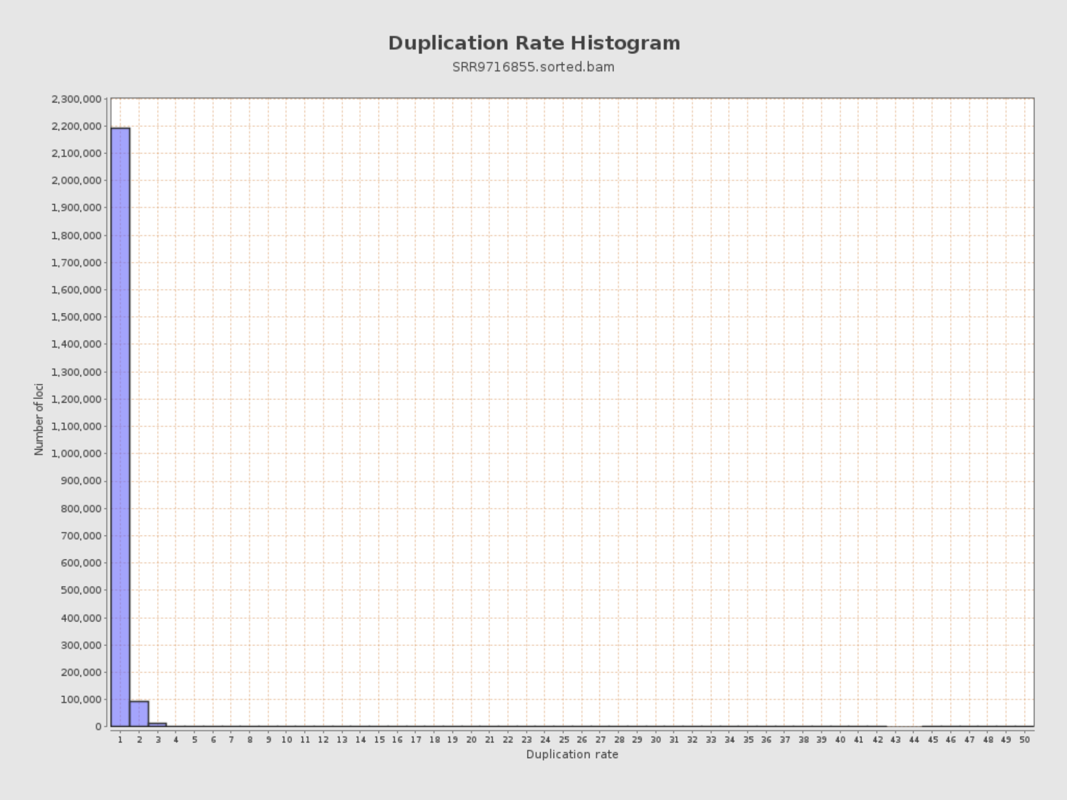
5. Results : Coverage Histogram (0-50X)



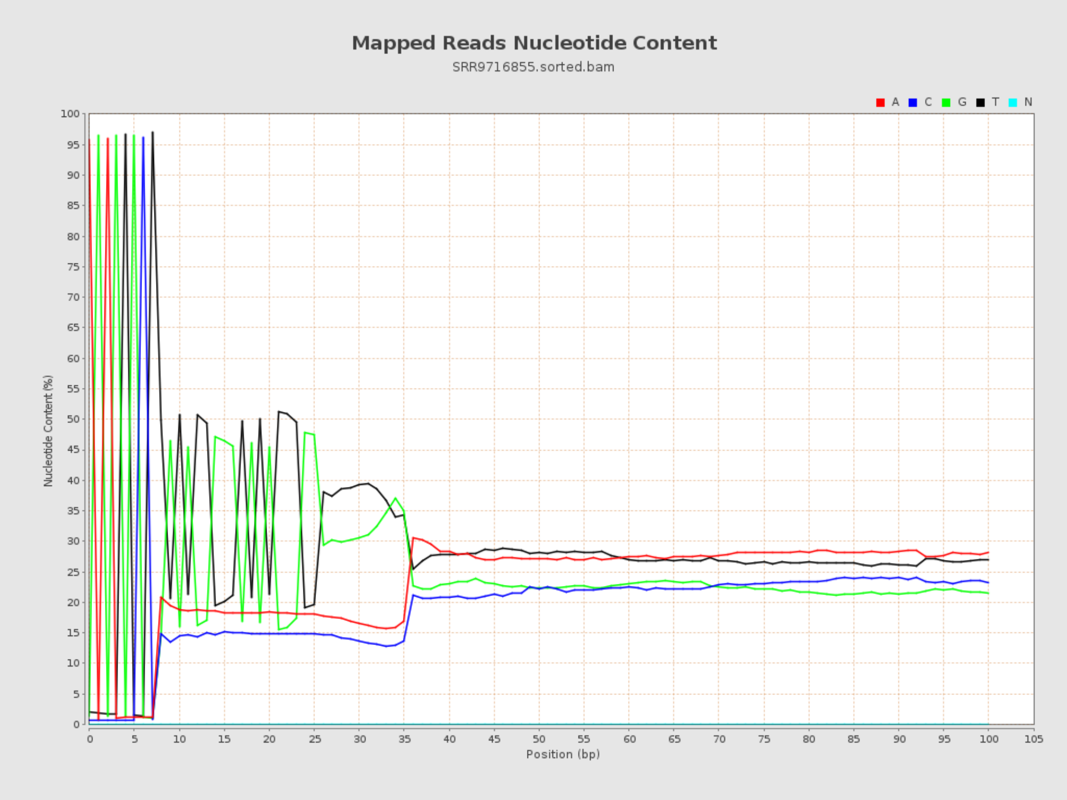
6. Results : Genome Fraction Coverage



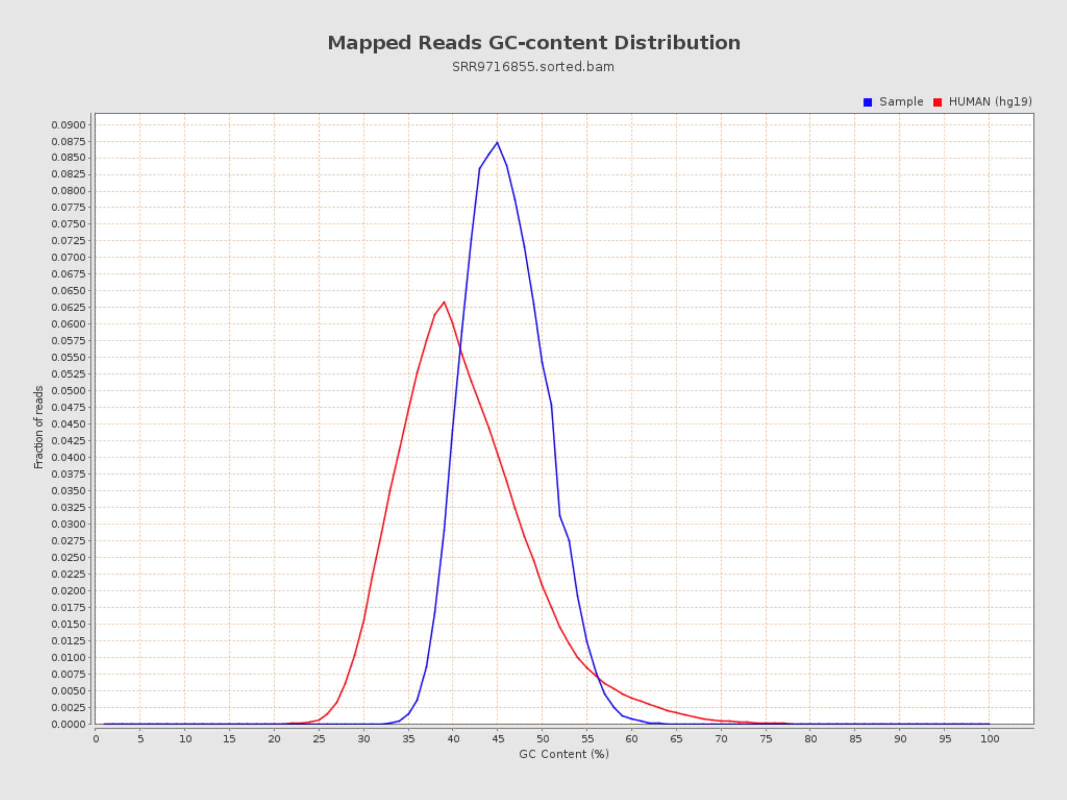
7. Results : Duplication Rate Histogram



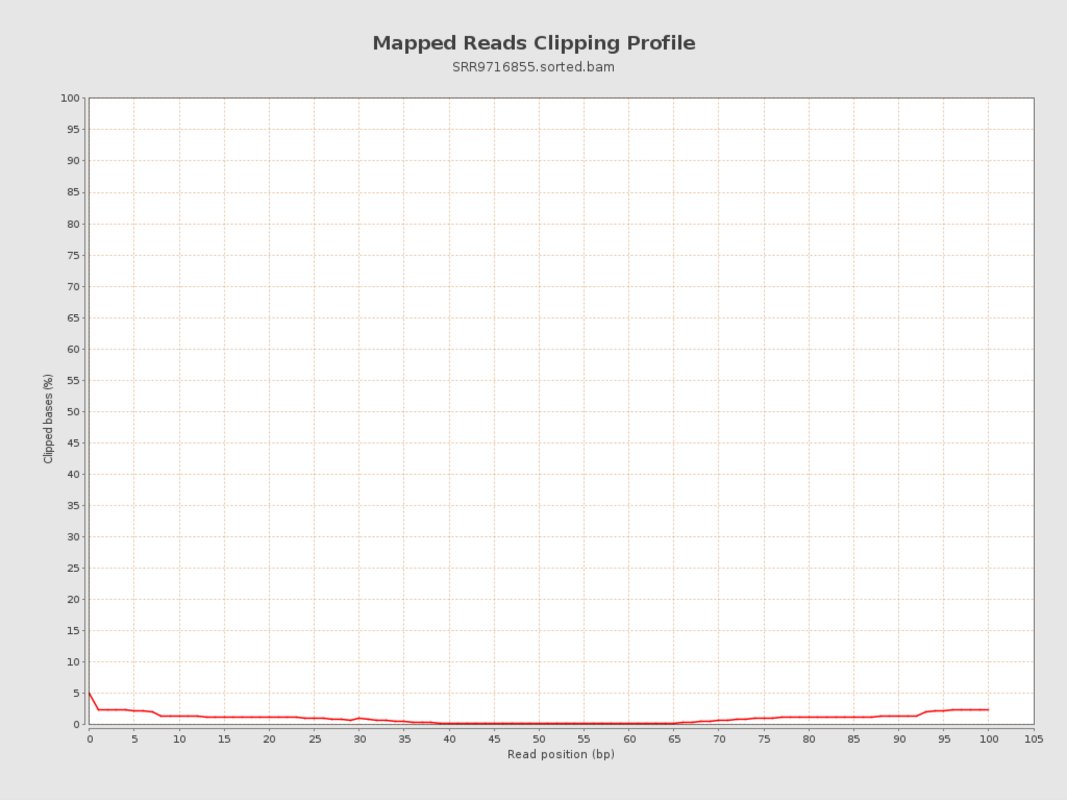
8. Results : Mapped Reads Nucleotide Content



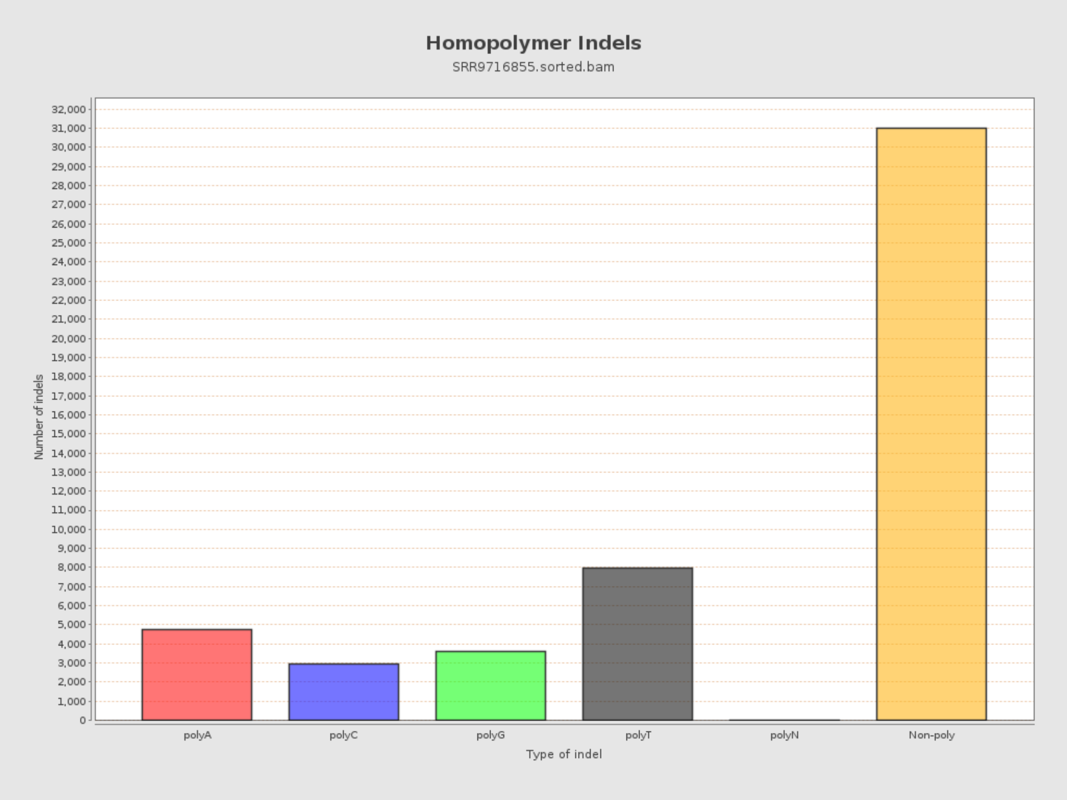
9. Results : Mapped Reads GC-content Distribution



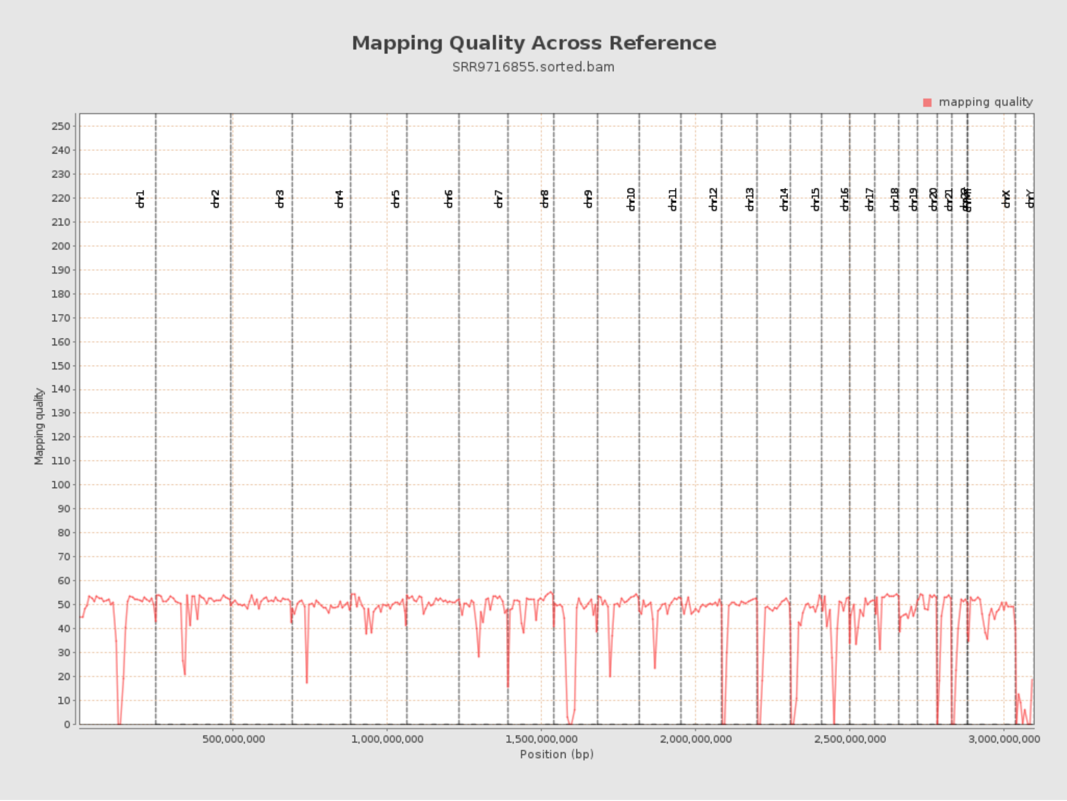
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram