Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 14:50:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716848.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_SRR9716848 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716848.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 14:50:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716848.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,333,856
Mapped reads	3,137,823 / 94.12%
Unmapped reads	196,033 / 5.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	54,504 / 1.63%
Read min/max/mean length	30 / 101 / 101.59
Duplicated reads (estimated)	196,118 / 5.88%
Duplication rate	4.62%
Clipped reads	3,185,307 / 95.54%

2.2. ACGT Content

Number/percentage of A's	62,584,751 / 25.11%
Number/percentage of C's	48,821,493 / 19.58%
Number/percentage of T's	76,432,579 / 30.66%
Number/percentage of G's	61,433,618 / 24.64%
Number/percentage of N's	18,217 / 0.01%
GC Percentage	44.23%

2.3. Coverage

Mean	0.0806

Standard Deviation	0.7034

2.4. Mapping Quality

Mean Mapping Quality	47.78

2.5. Mismatches and indels

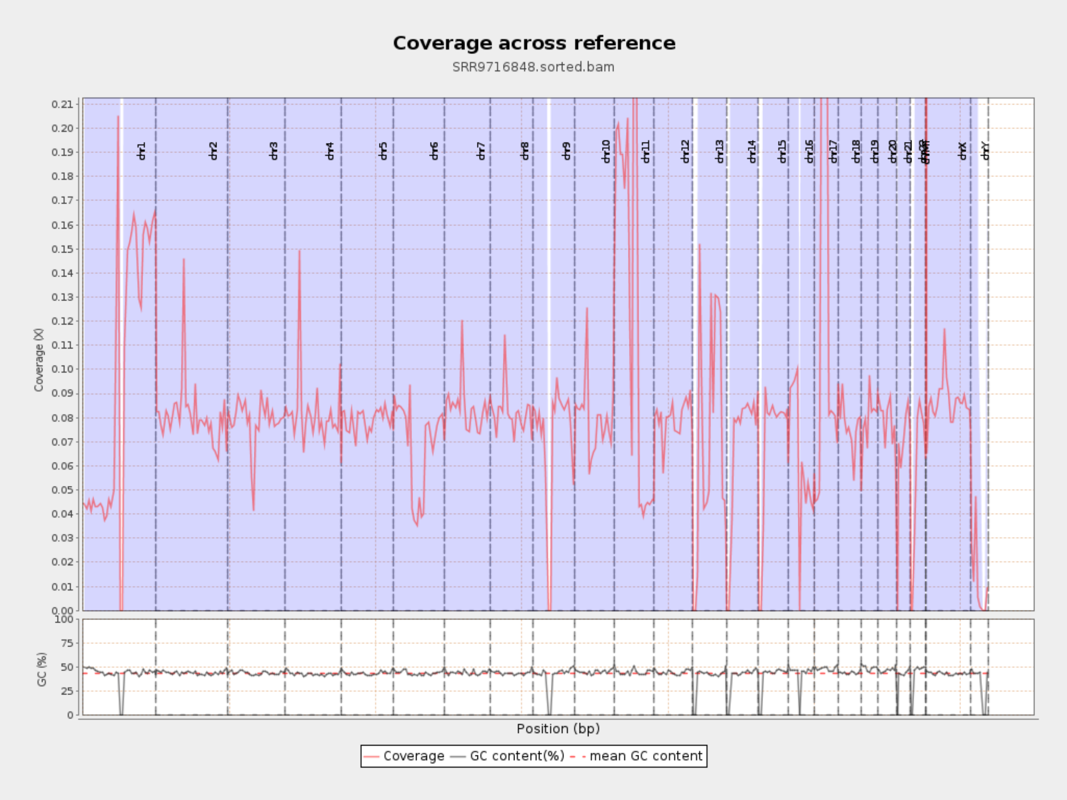
General error rate	0.66%
Mismatches	1,589,501
Insertions	19,997
Mapped reads with at least one insertion	0.63%
Deletions	57,932
Mapped reads with at least one deletion	1.82%
Homopolymer indels	42.75%

2.6. Chromosome stats

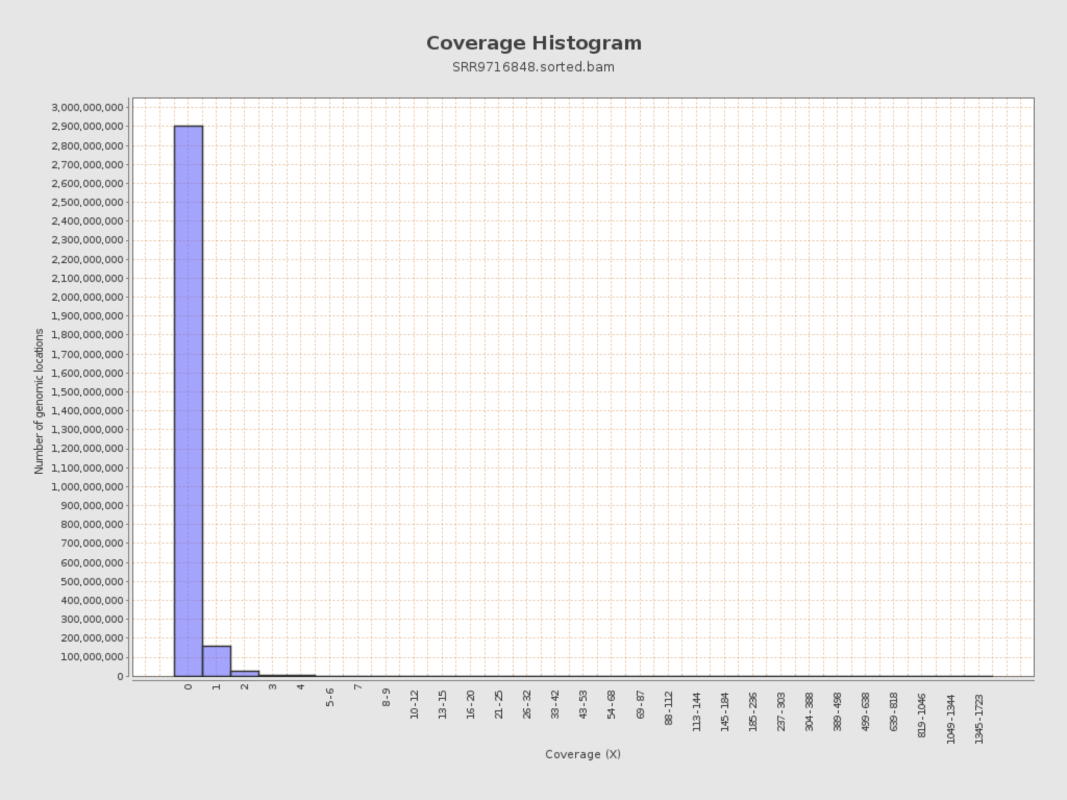
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23770274	0.0954	1.5166
chr2	243199373	19715909	0.0811	0.7211
chr3	198022430	15580518	0.0787	0.3381
chr4	191154276	15764143	0.0825	0.4694
chr5	180915260	14307934	0.0791	0.345
chr6	171115067	11736069	0.0686	0.3618
chr7	159138663	13390253	0.0841	0.86

chr8	146364022	11959954	0.0817	0.7755
chr9	141213431	10025014	0.071	0.5424
chr10	135534747	10660199	0.0787	0.6024
chr11	135006516	17331400	0.1284	0.9495
chr12	133851895	10717220	0.0801	0.3445
chr13	115169878	8474471	0.0736	0.3348
chr14	107349540	7324071	0.0682	0.3479
chr15	102531392	6921731	0.0675	0.3152
chr16	90354753	5599858	0.062	0.3483
chr17	81195210	9790252	0.1206	0.6584
chr18	78077248	5996553	0.0768	0.9408
chr19	59128983	4734157	0.0801	1.0605
chr20	63025520	4963379	0.0788	0.3674
chr21	48129895	3219228	0.0669	0.3861
chr22	51304566	2870022	0.0559	0.2903
chrMT	16571	328565	19.8277	11.9687
chrX	155270560	13492389	0.0869	0.4576
chrY	59373566	727537	0.0123	0.3866

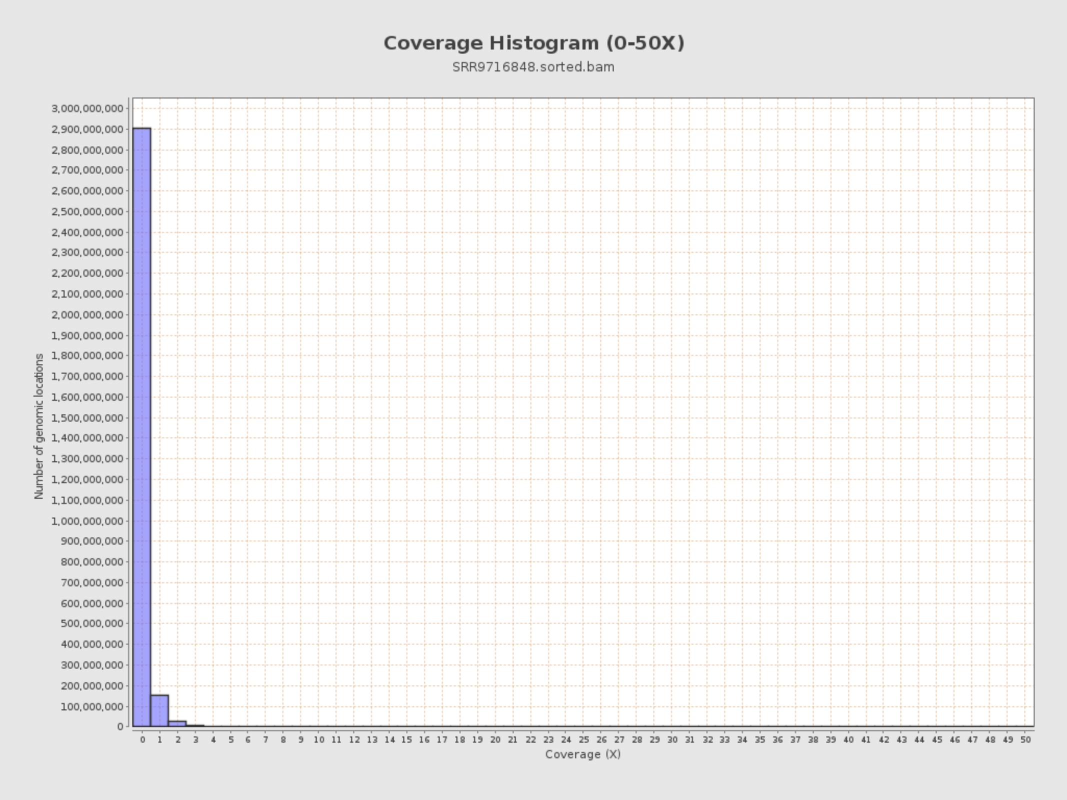
3. Results : Coverage across reference



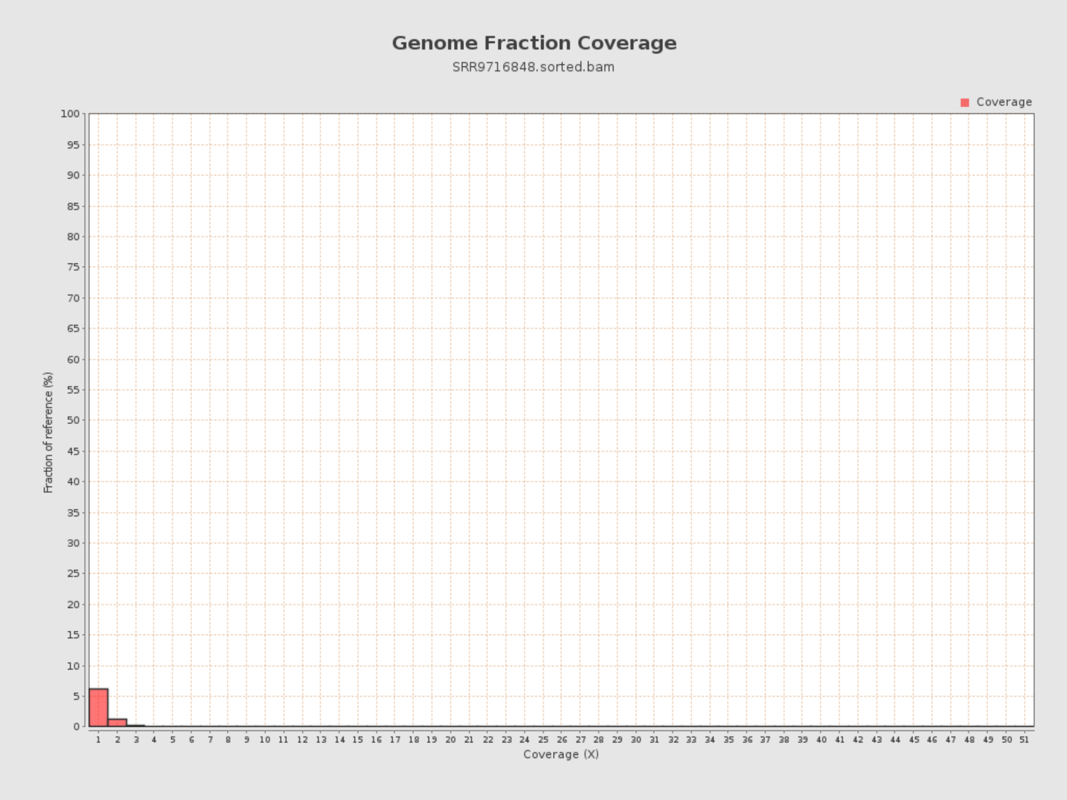
4. Results : Coverage Histogram



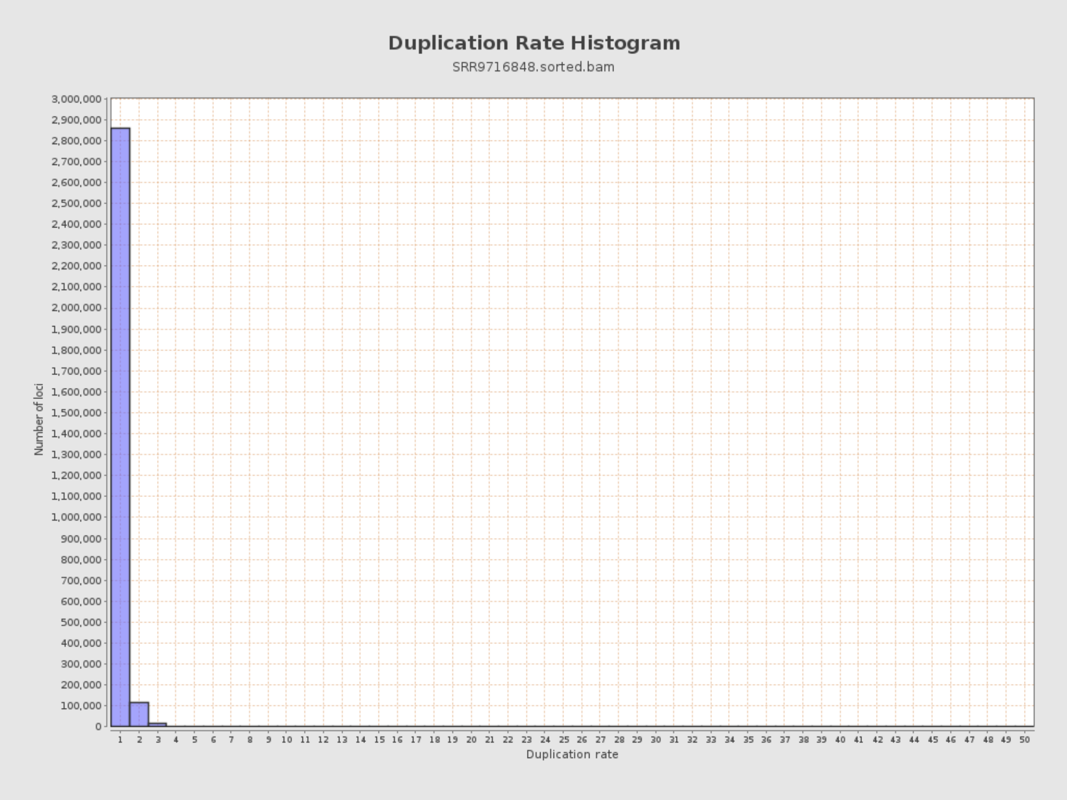
5. Results : Coverage Histogram (0-50X)



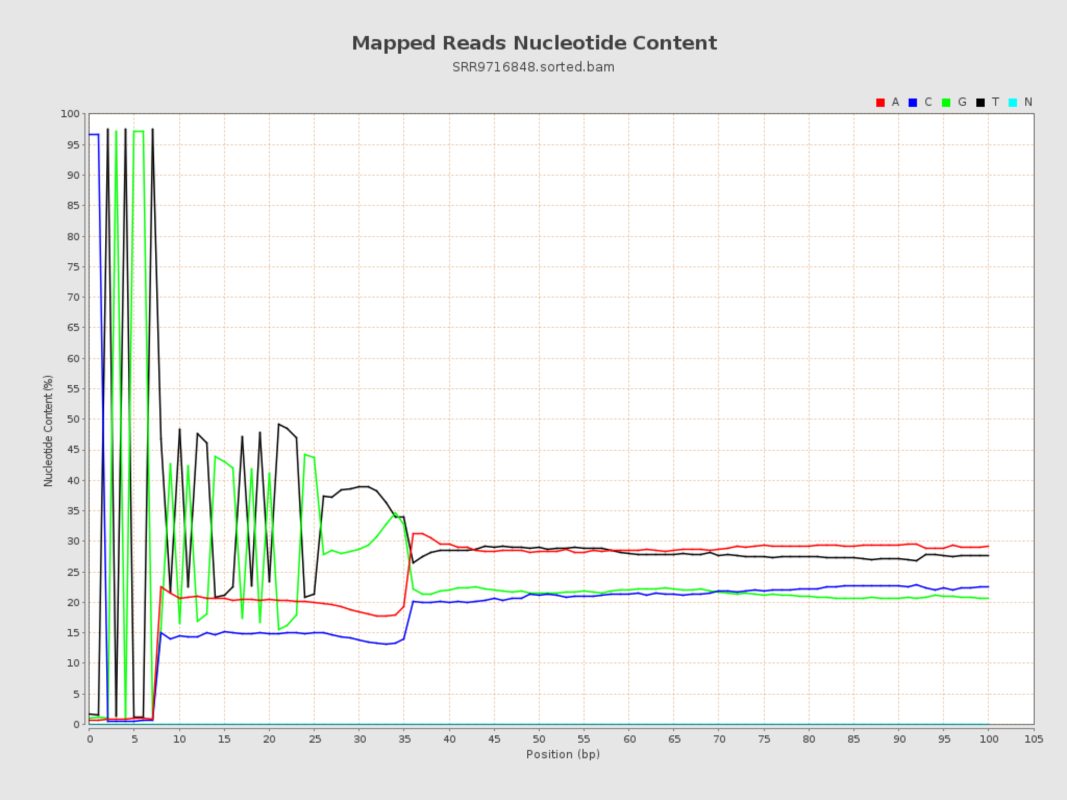
6. Results : Genome Fraction Coverage



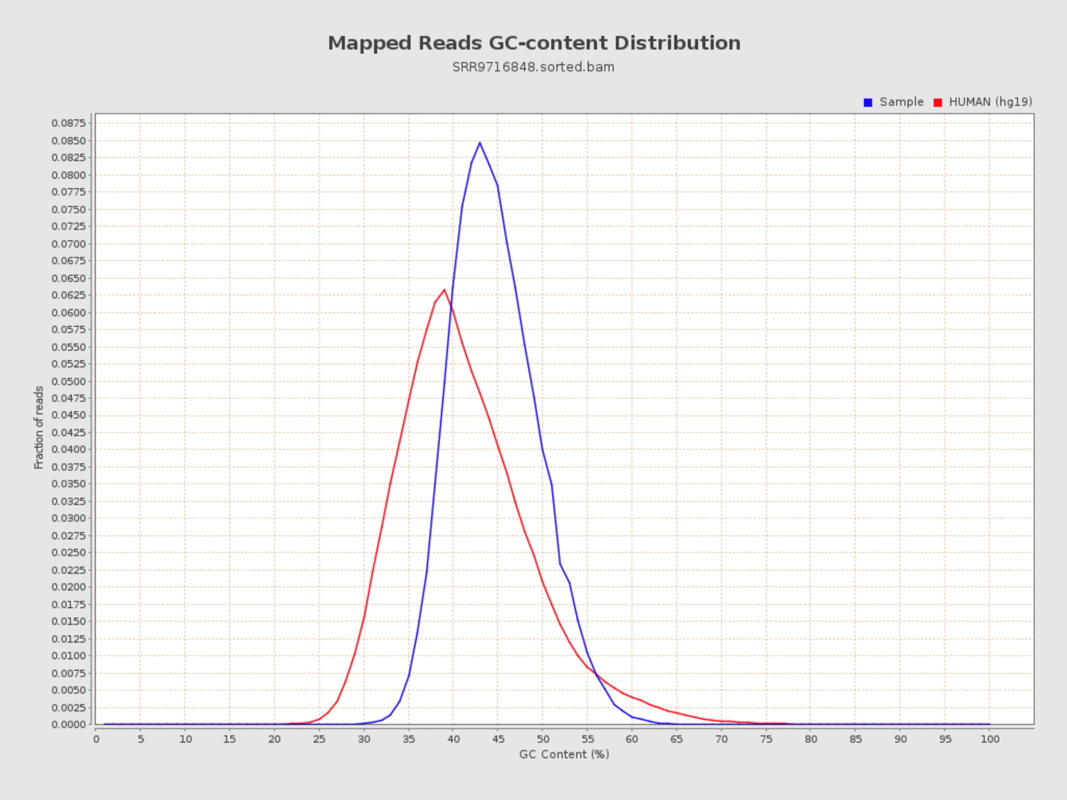
7. Results : Duplication Rate Histogram



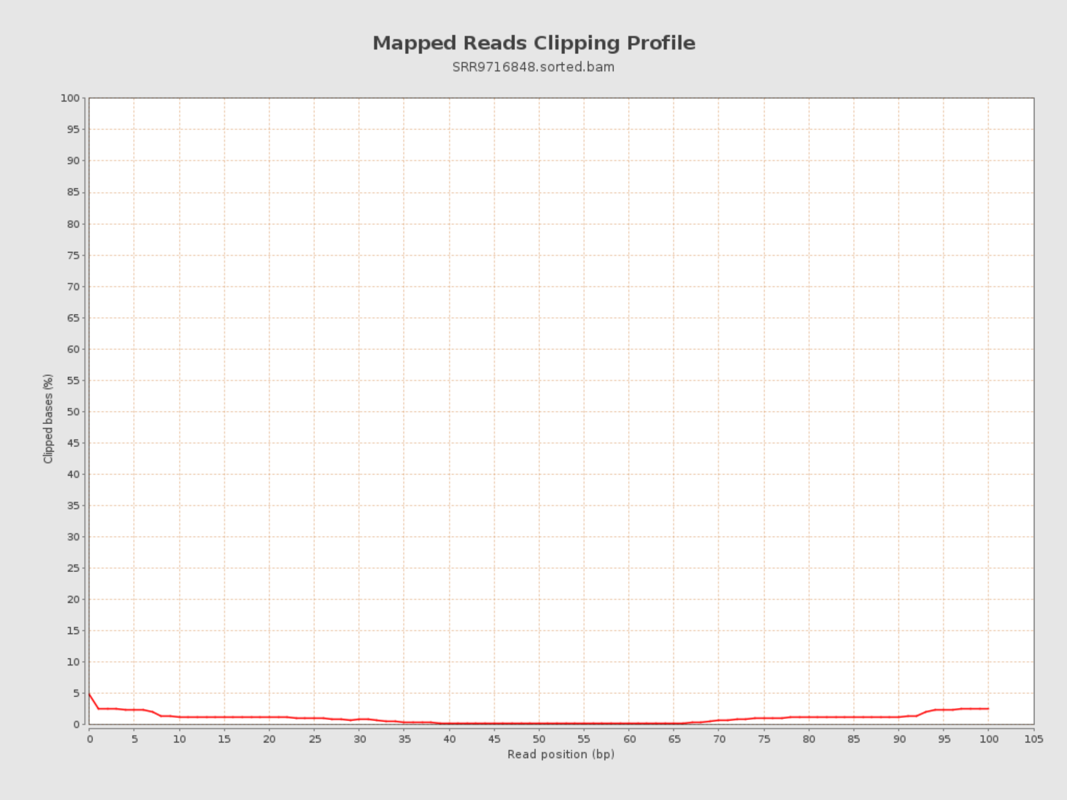
8. Results : Mapped Reads Nucleotide Content



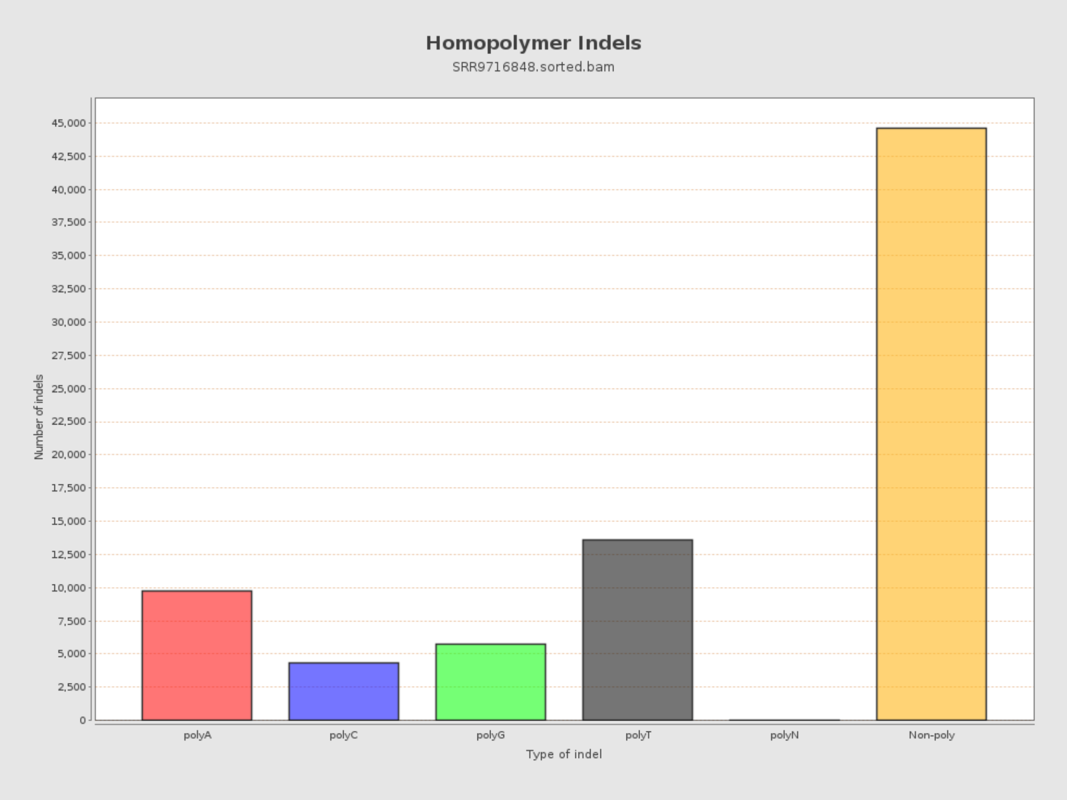
9. Results : Mapped Reads GC-content Distribution



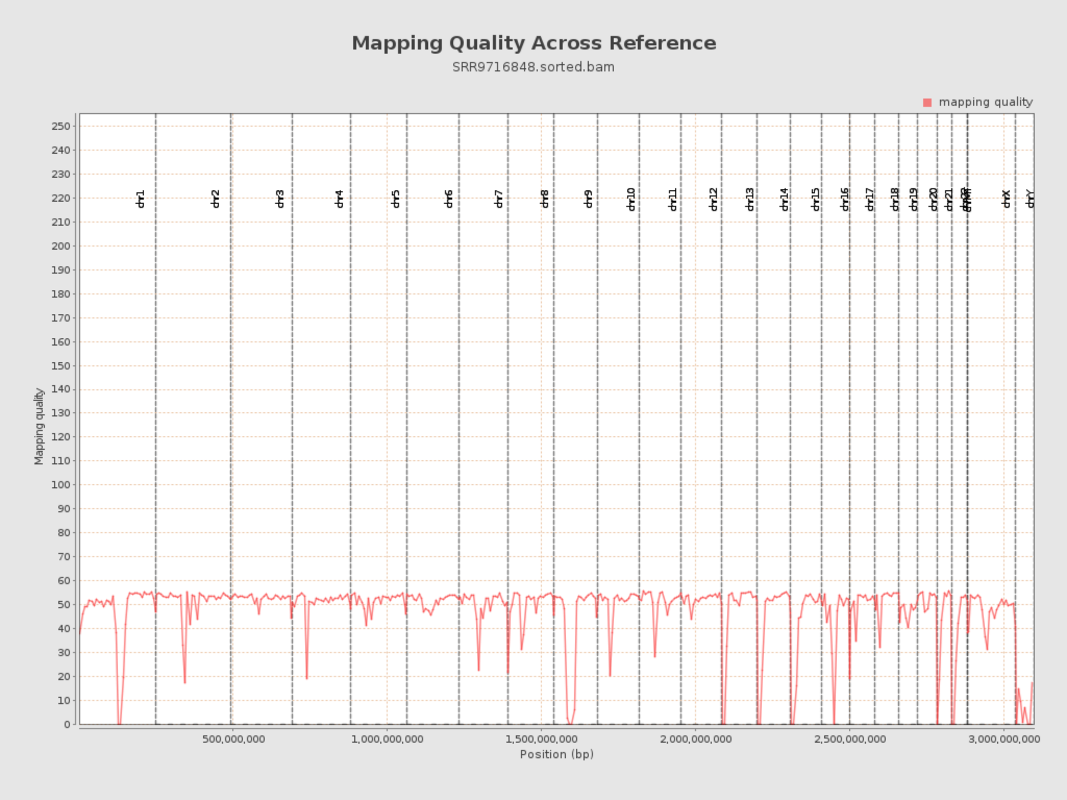
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram