Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 22:52:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716186.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_SRR9716186 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716186.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 22:52:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716186.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,683,682
Mapped reads	3,273,455 / 88.86%
Unmapped reads	410,227 / 11.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,162 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	122,617 / 3.33%
Duplication rate	2.65%
Clipped reads	3,283,881 / 89.15%

2.2. ACGT Content

Number/percentage of A's	46,102,511 / 24.67%
Number/percentage of C's	38,589,271 / 20.65%
Number/percentage of T's	56,494,553 / 30.23%
Number/percentage of G's	45,679,432 / 24.44%
Number/percentage of N's	1,344 / 0%
GC Percentage	45.1%

2.3. Coverage

Mean	0.0604

Standard Deviation	0.4249

2.4. Mapping Quality

Mean Mapping Quality	42.19

2.5. Mismatches and indels

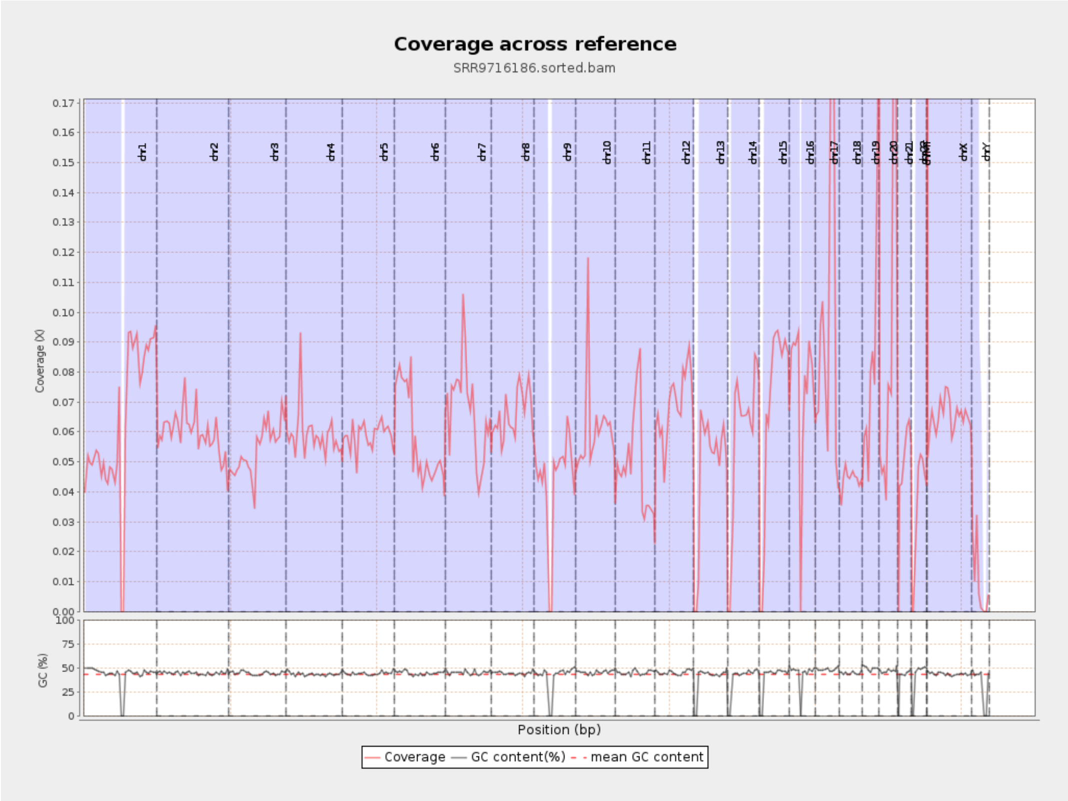
General error rate	0.53%
Mismatches	975,335
Insertions	10,810
Mapped reads with at least one insertion	0.33%
Deletions	33,347
Mapped reads with at least one deletion	1.01%
Homopolymer indels	41.09%

2.6. Chromosome stats

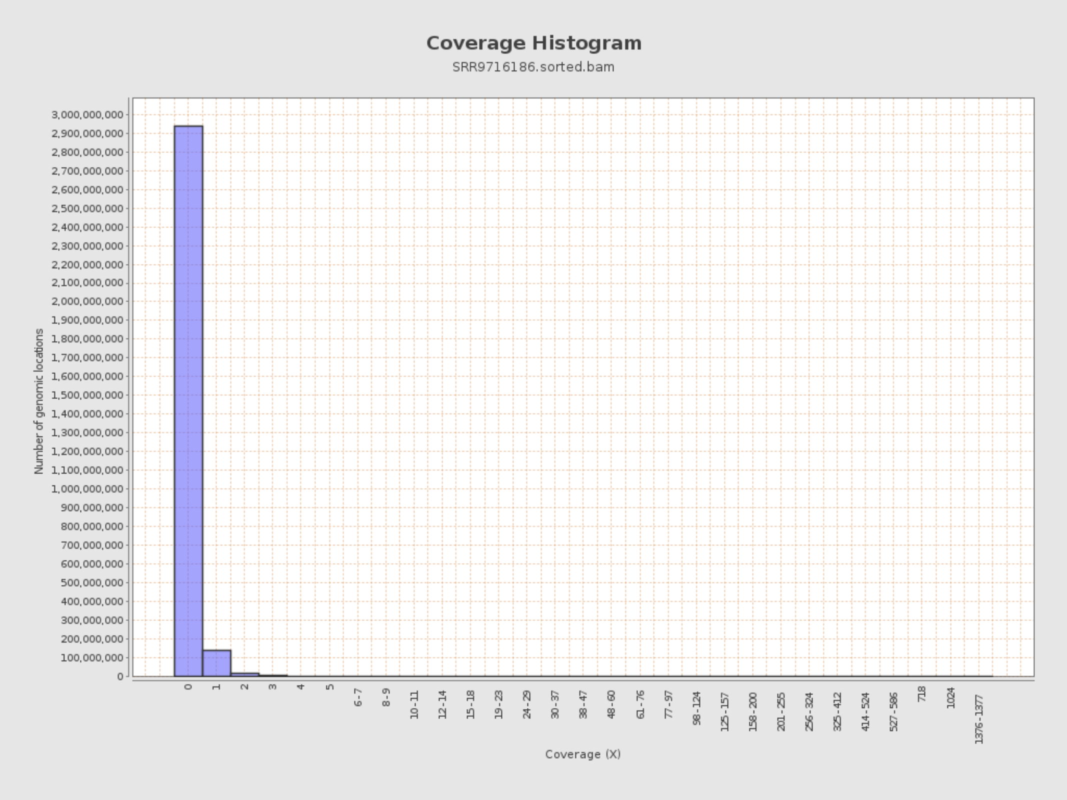
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15681983	0.0629	0.5457
chr2	243199373	14537870	0.0598	0.6453
chr3	198022430	10692559	0.054	0.275
chr4	191154276	11333354	0.0593	0.3272
chr5	180915260	10622644	0.0587	0.2795
chr6	171115067	9935910	0.0581	0.358
chr7	159138663	10725961	0.0674	0.6685

chr8	146364022	9663634	0.066	0.3912
chr9	141213431	6179901	0.0438	0.3096
chr10	135534747	8214649	0.0606	0.5713
chr11	135006516	6623419	0.0491	0.3533
chr12	133851895	9349024	0.0698	0.3116
chr13	115169878	5568734	0.0484	0.2548
chr14	107349540	6331589	0.059	0.3081
chr15	102531392	6860528	0.0669	0.3138
chr16	90354753	6622661	0.0733	0.3526
chr17	81195210	8451082	0.1041	0.4131
chr18	78077248	3436839	0.044	0.5238
chr19	59128983	5093610	0.0861	0.5402
chr20	63025520	6131085	0.0973	0.403
chr21	48129895	2332137	0.0485	0.2962
chr22	51304566	1770633	0.0345	0.2164
chrMT	16571	84841	5.1198	3.885
chrX	155270560	10111104	0.0651	0.3338
chrY	59373566	564722	0.0095	0.2523

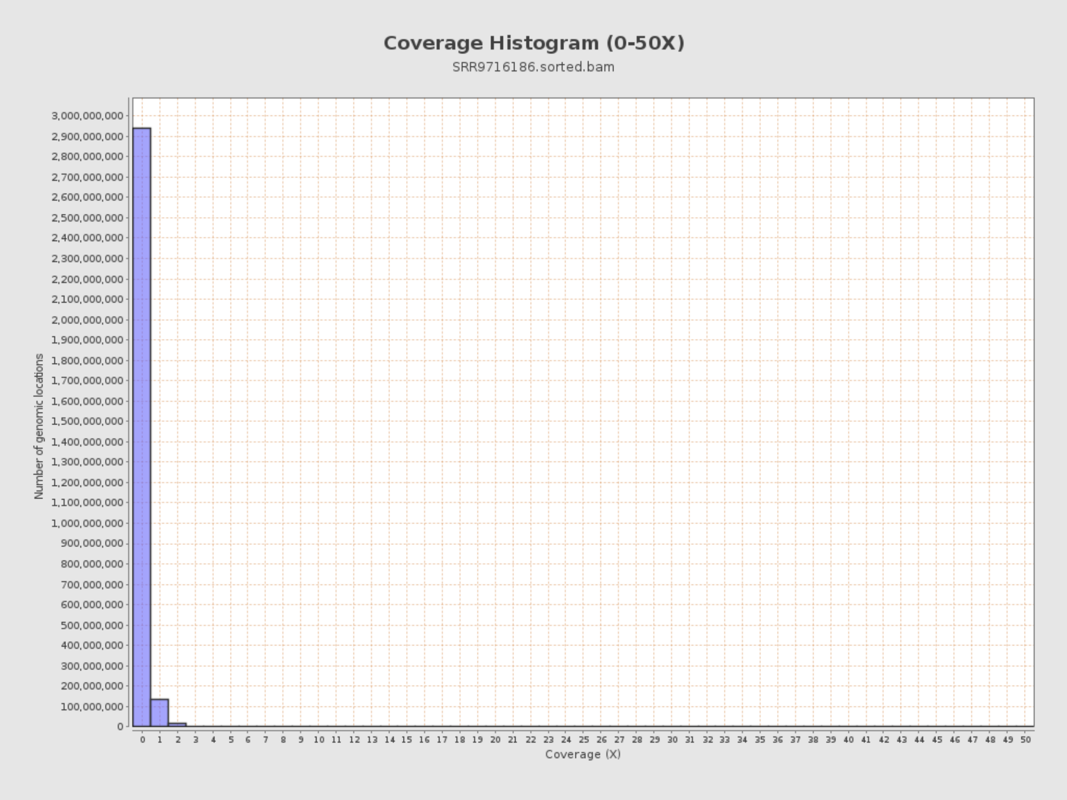
3. Results : Coverage across reference



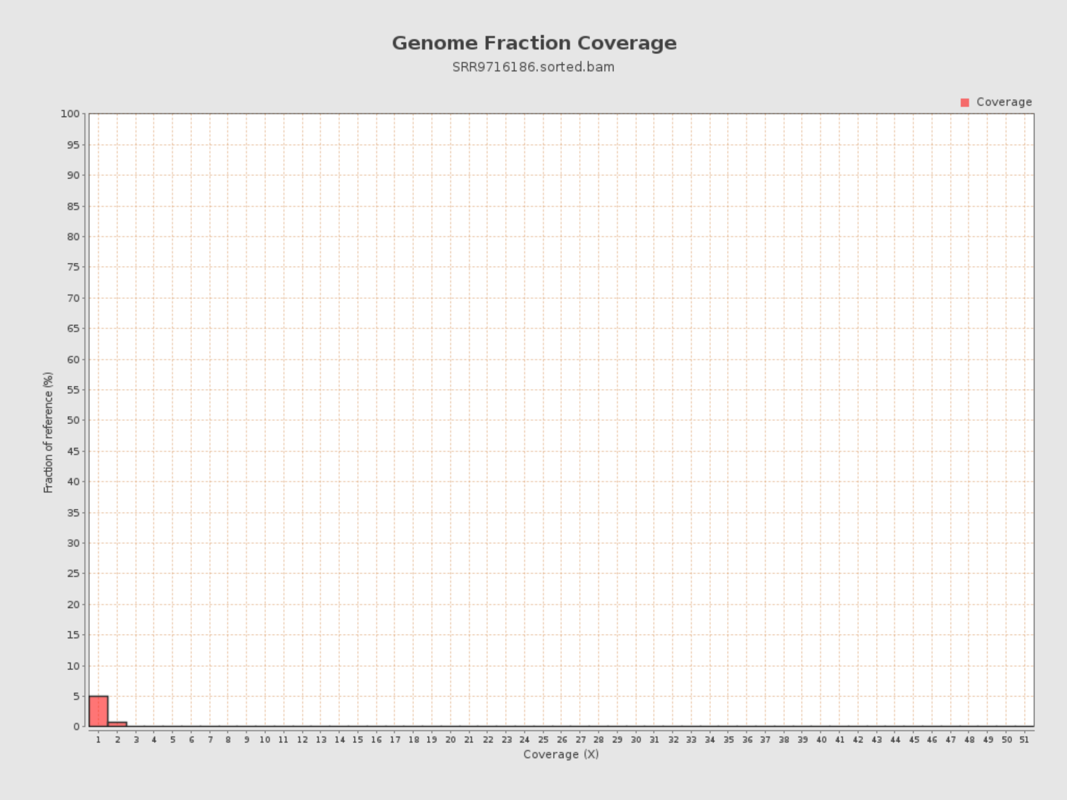
4. Results : Coverage Histogram



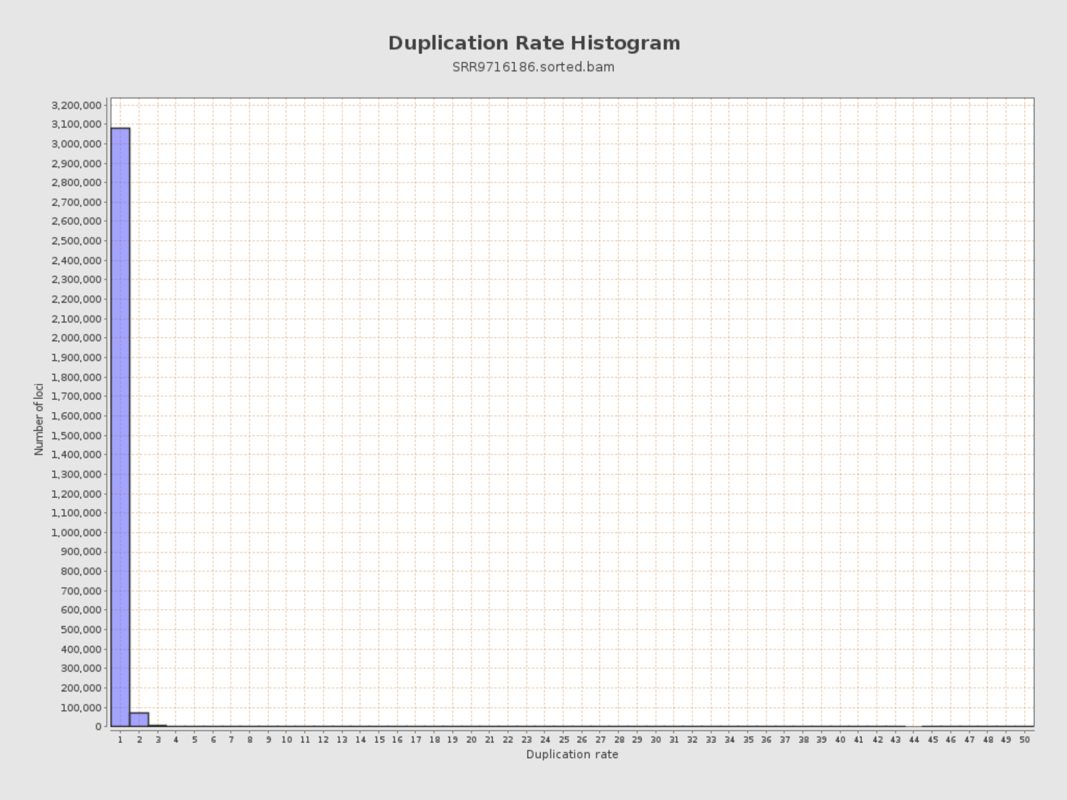
5. Results : Coverage Histogram (0-50X)



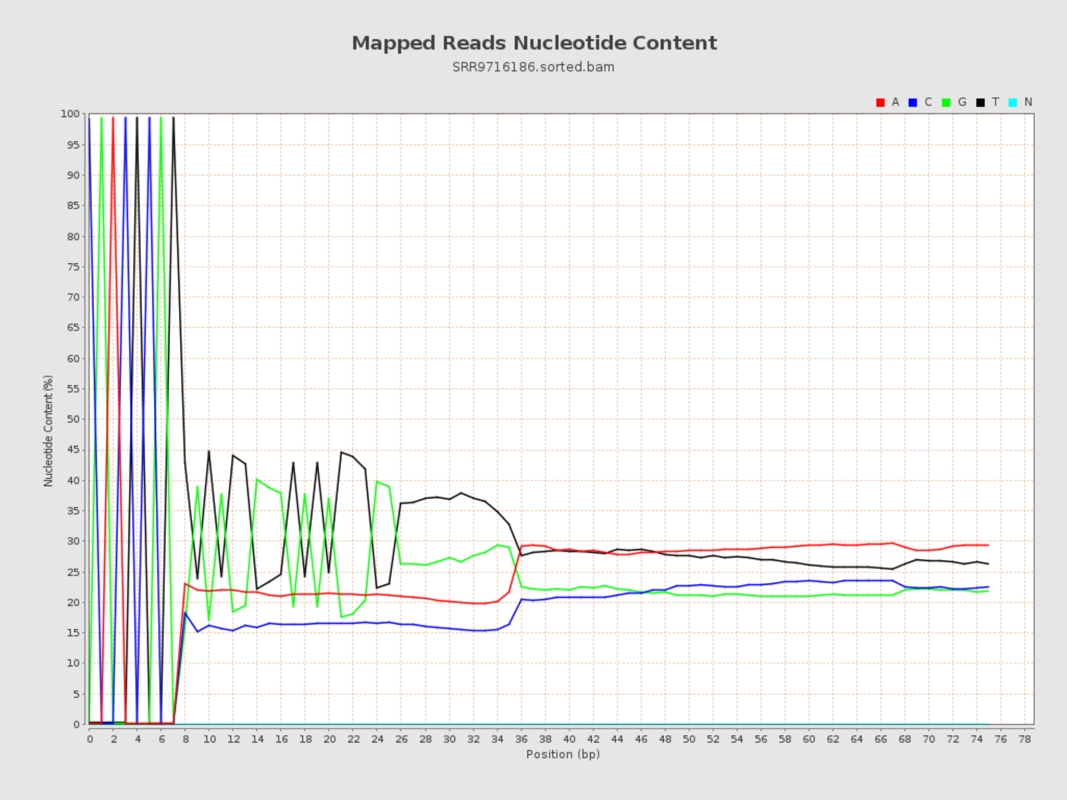
6. Results : Genome Fraction Coverage



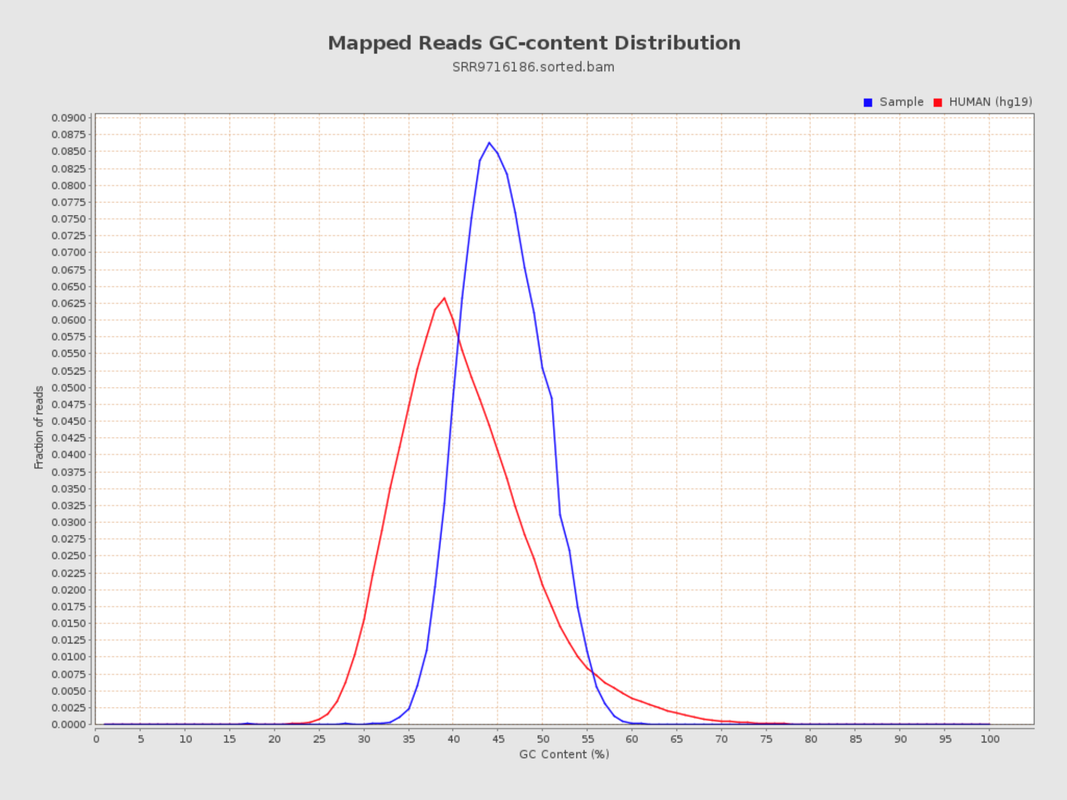
7. Results : Duplication Rate Histogram



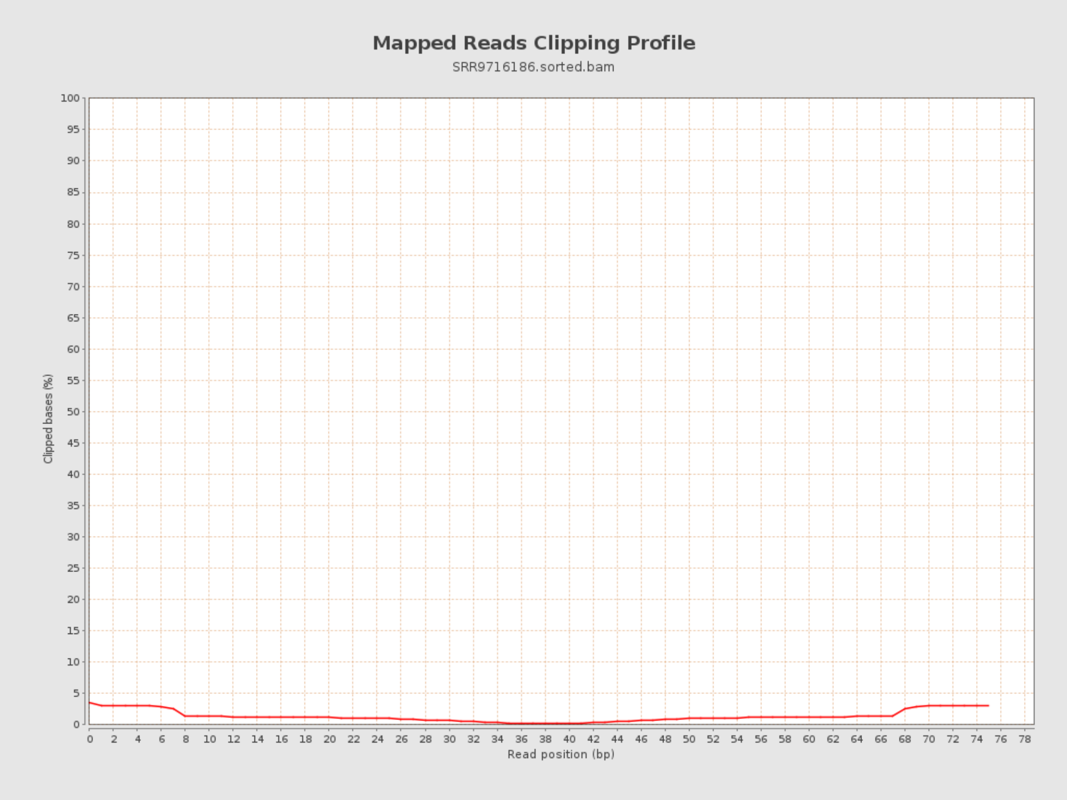
8. Results : Mapped Reads Nucleotide Content



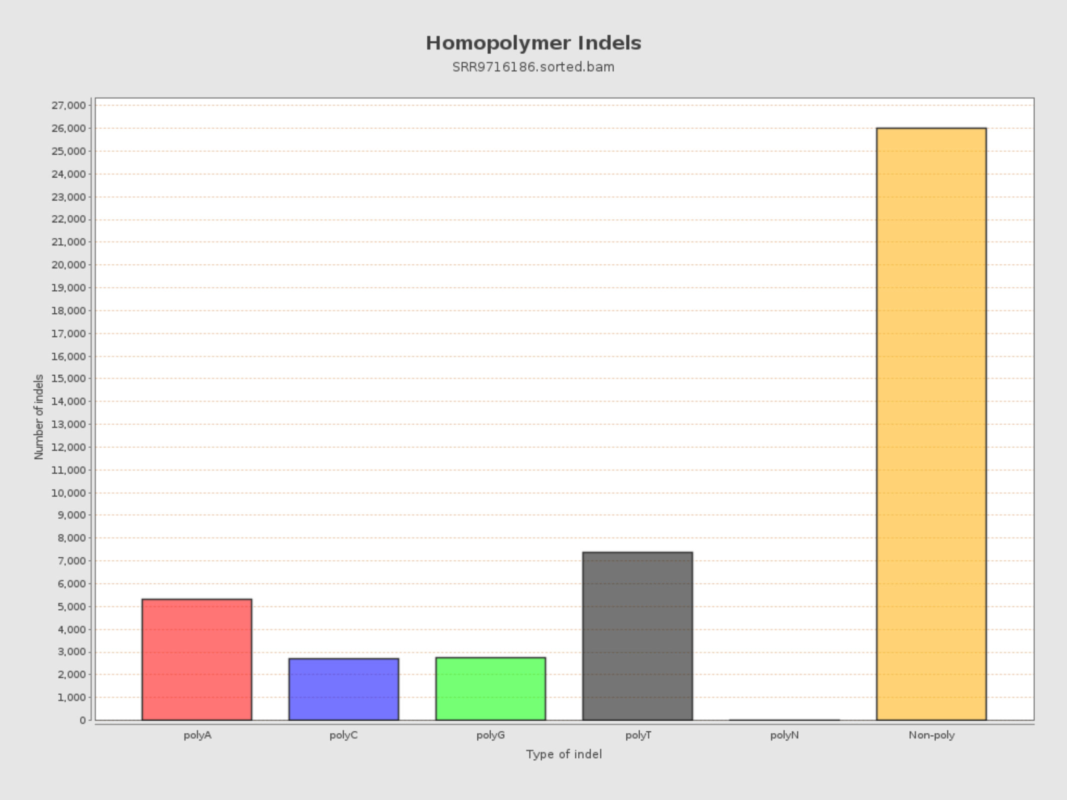
9. Results : Mapped Reads GC-content Distribution



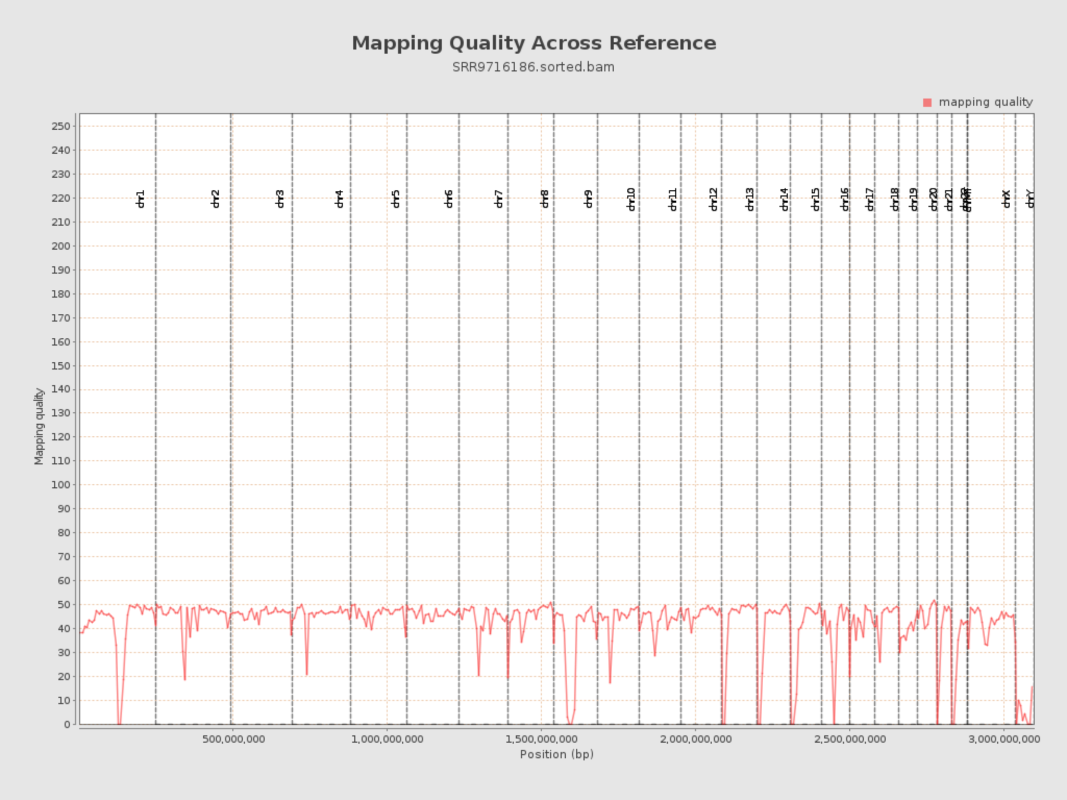
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram