Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 23:12:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716586.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_SRR9716586 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716586.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 23:12:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716586.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,027,790
Mapped reads	4,399,473 / 87.5%
Unmapped reads	628,317 / 12.5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,164 / 0.46%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	288,579 / 5.74%
Duplication rate	4.91%
Clipped reads	4,408,935 / 87.69%

2.2. ACGT Content

Number/percentage of A's	65,126,378 / 25.59%
Number/percentage of C's	50,748,796 / 19.94%
Number/percentage of T's	78,755,219 / 30.94%
Number/percentage of G's	59,881,739 / 23.53%
Number/percentage of N's	3,584 / 0%
GC Percentage	43.47%

2.3. Coverage

Mean	0.0822

Standard Deviation	0.6261

2.4. Mapping Quality

Mean Mapping Quality	44.22

2.5. Mismatches and indels

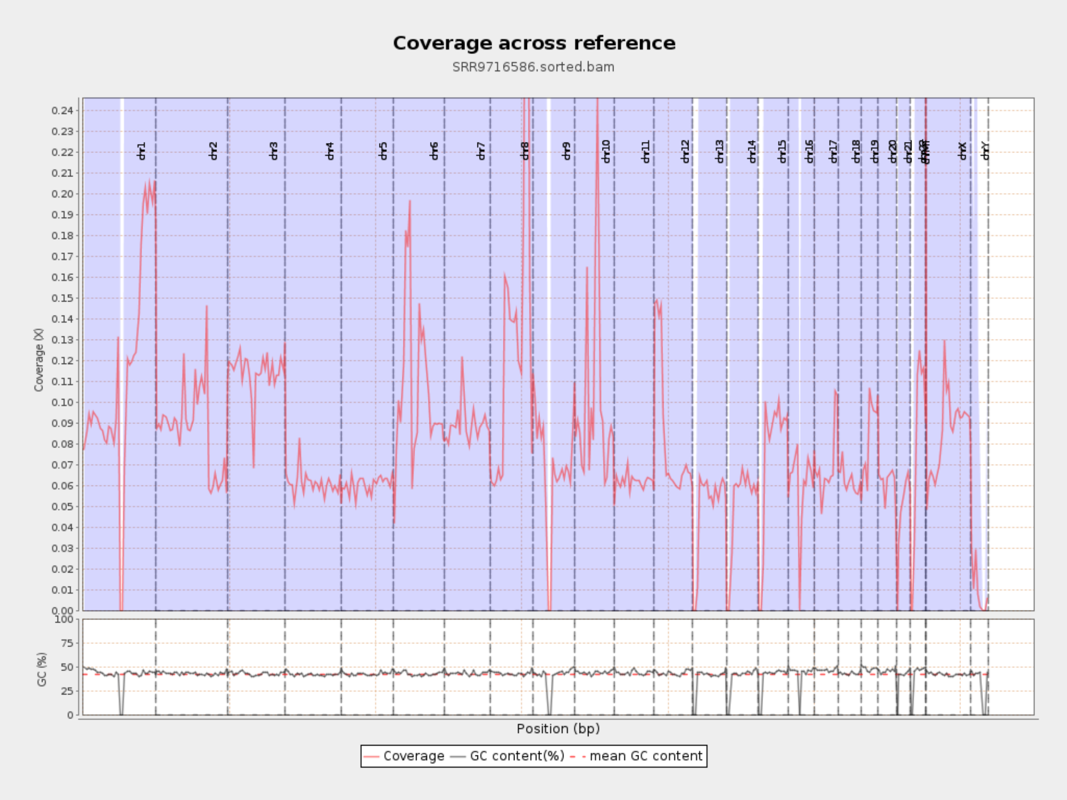
General error rate	0.5%
Mismatches	1,238,078
Insertions	20,056
Mapped reads with at least one insertion	0.45%
Deletions	43,794
Mapped reads with at least one deletion	0.99%
Homopolymer indels	39.86%

2.6. Chromosome stats

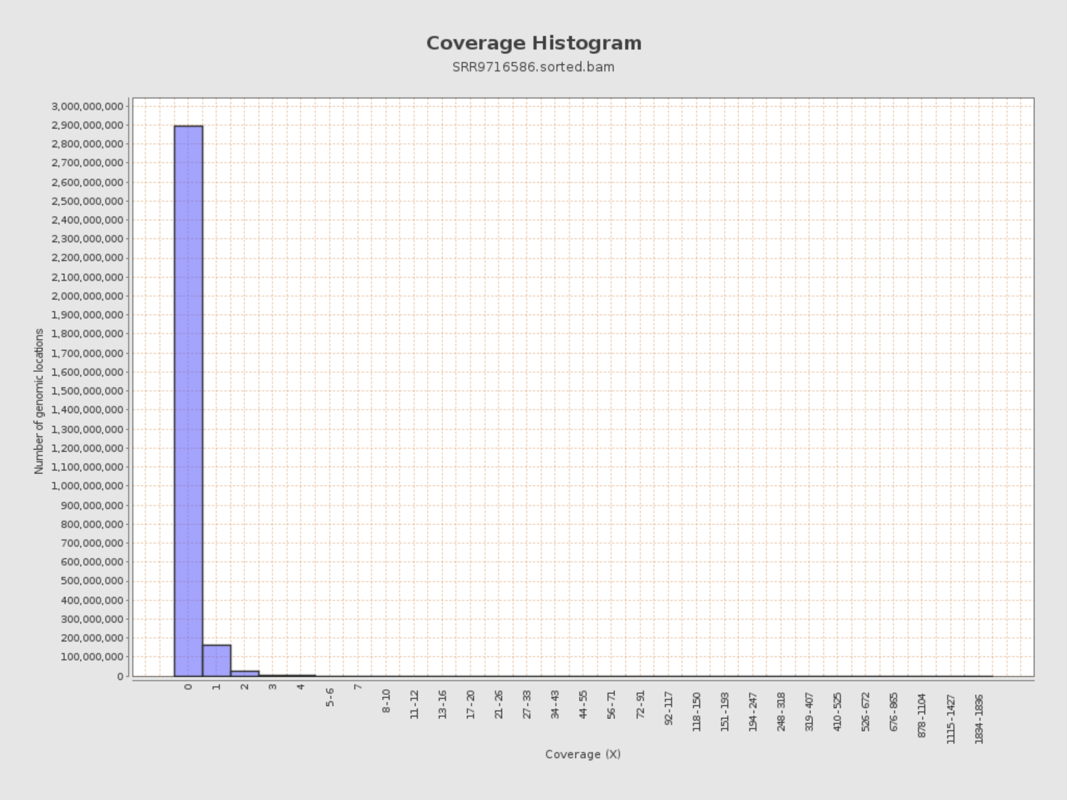
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	28421285	0.114	1.1569
chr2	243199373	21240730	0.0873	0.8388
chr3	198022430	22620403	0.1142	0.4215
chr4	191154276	11724330	0.0613	0.3358
chr5	180915260	10960913	0.0606	0.3091
chr6	171115067	18532378	0.1083	0.9183
chr7	159138663	14324619	0.09	0.7164

chr8	146364022	20494910	0.14	0.5533
chr9	141213431	9450943	0.0669	0.5056
chr10	135534747	13600410	0.1003	0.6463
chr11	135006516	8384945	0.0621	0.4945
chr12	133851895	11269161	0.0842	0.3701
chr13	115169878	5638602	0.049	0.2722
chr14	107349540	5459767	0.0509	0.3413
chr15	102531392	7580158	0.0739	0.3428
chr16	90354753	5332731	0.059	0.3598
chr17	81195210	5576372	0.0687	0.3528
chr18	78077248	4858284	0.0622	0.9833
chr19	59128983	4951849	0.0837	0.7872
chr20	63025520	3906074	0.062	0.3127
chr21	48129895	2327827	0.0484	0.313
chr22	51304566	4050961	0.079	0.347
chrMT	16571	4288	0.2588	0.5545
chrX	155270560	13290016	0.0856	0.453
chrY	59373566	581493	0.0098	0.1867

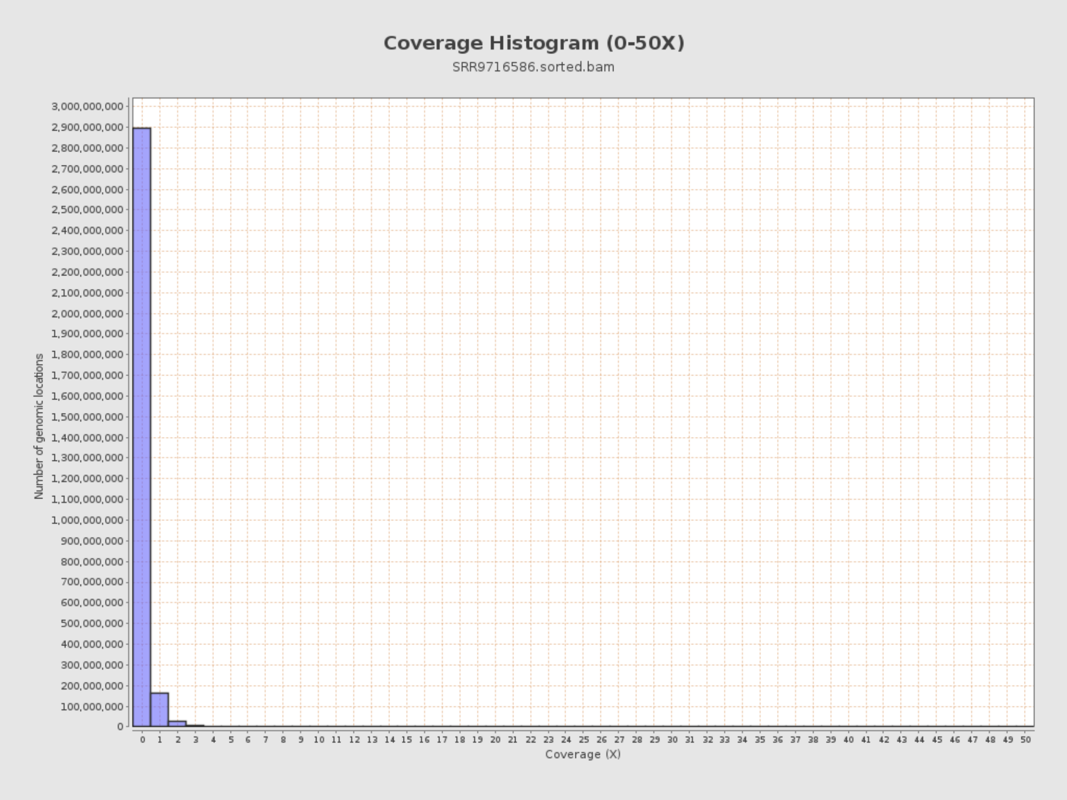
3. Results : Coverage across reference



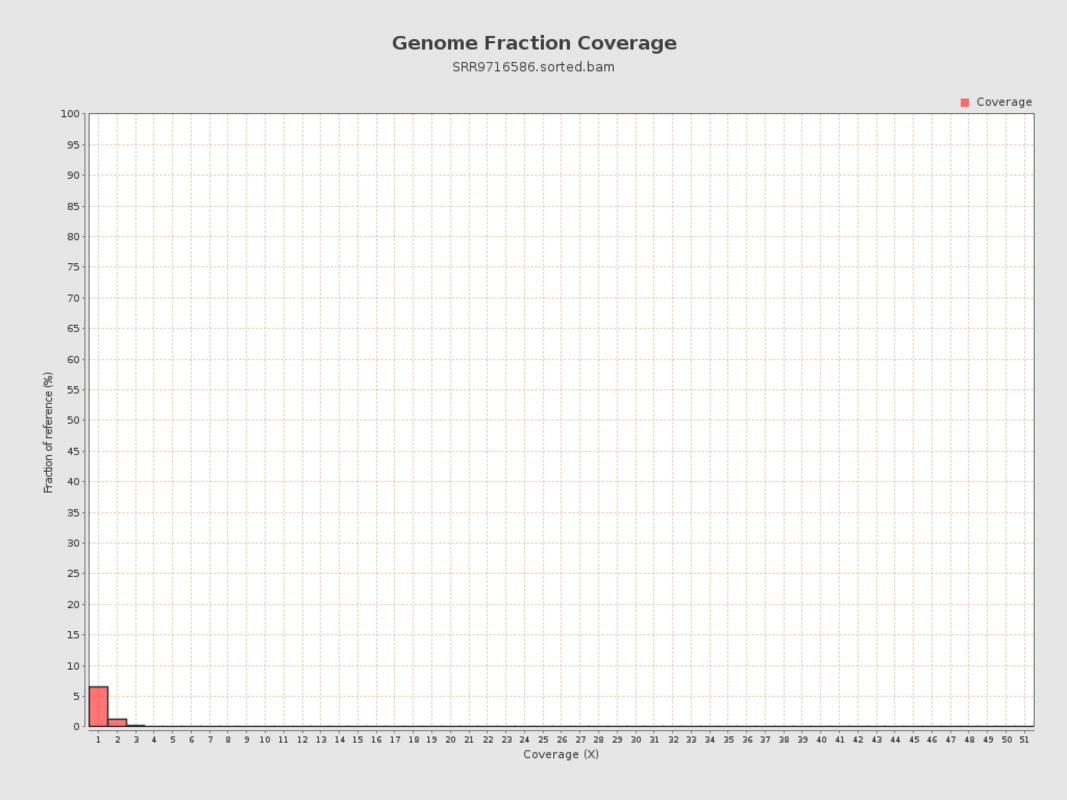
4. Results : Coverage Histogram



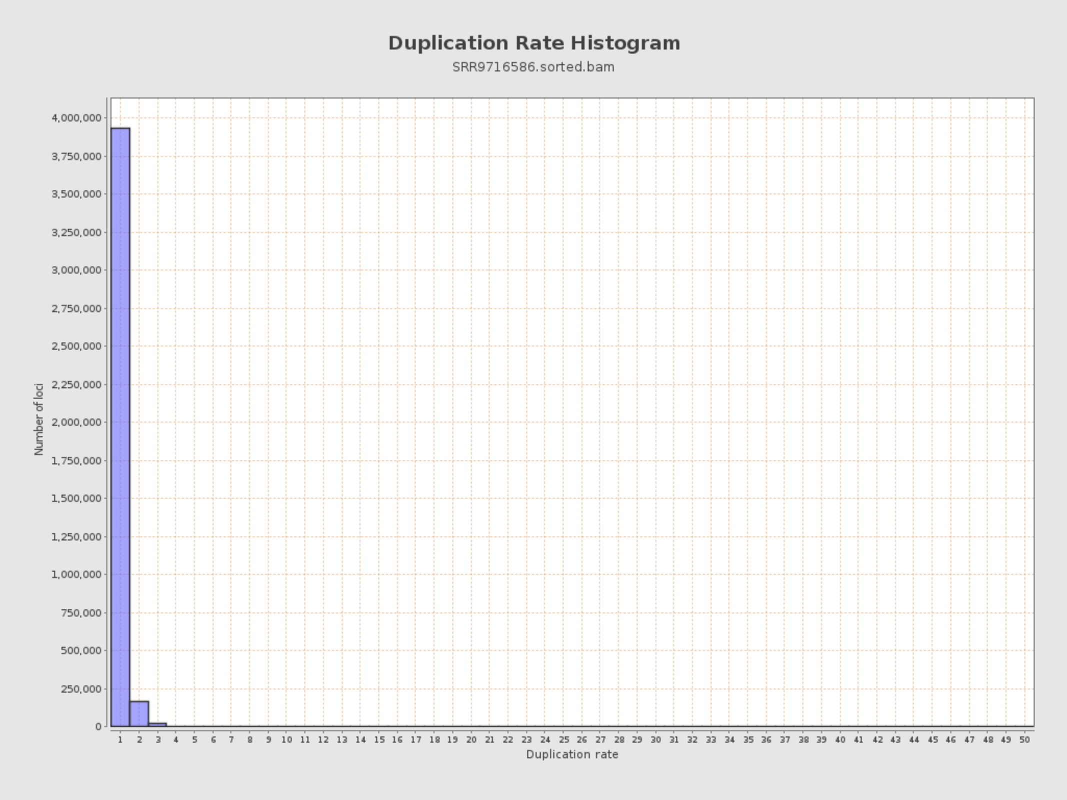
5. Results : Coverage Histogram (0-50X)



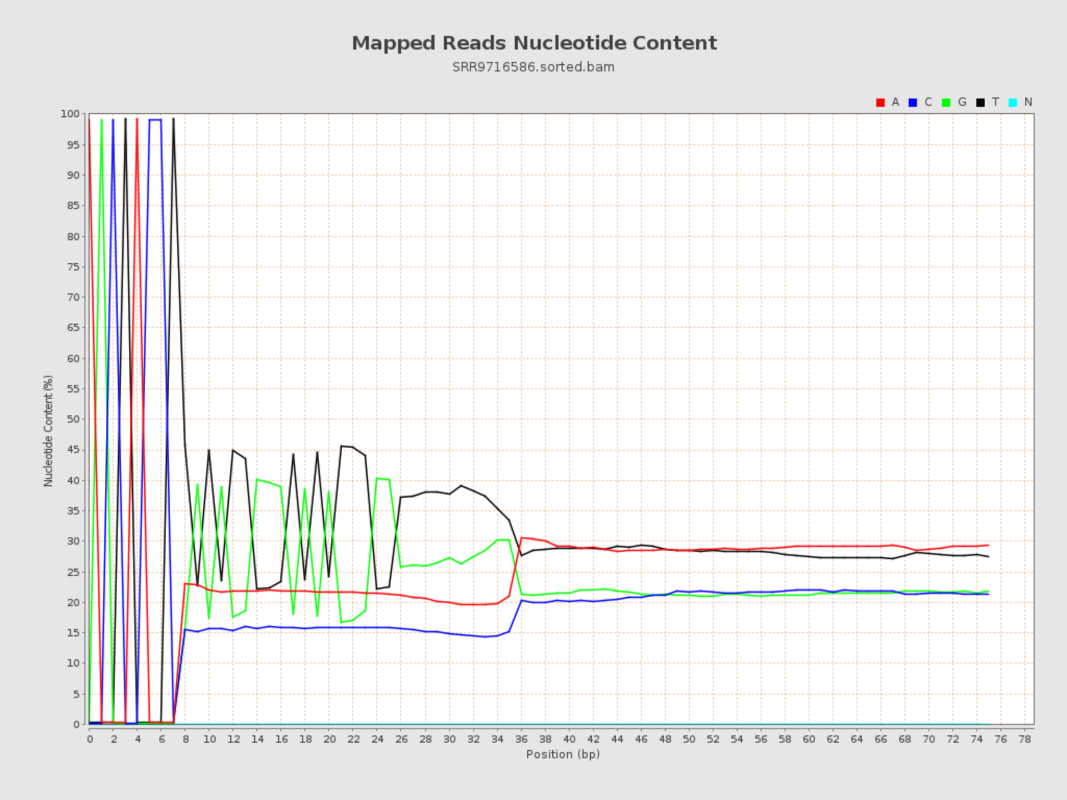
6. Results : Genome Fraction Coverage



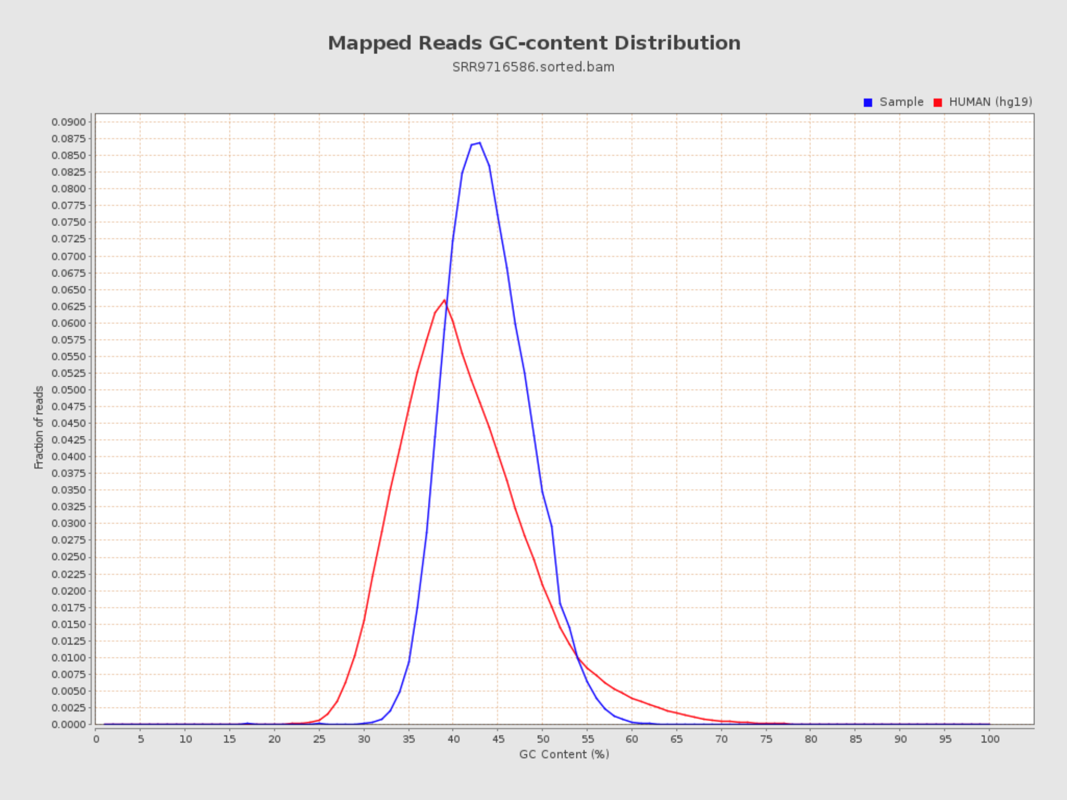
7. Results : Duplication Rate Histogram



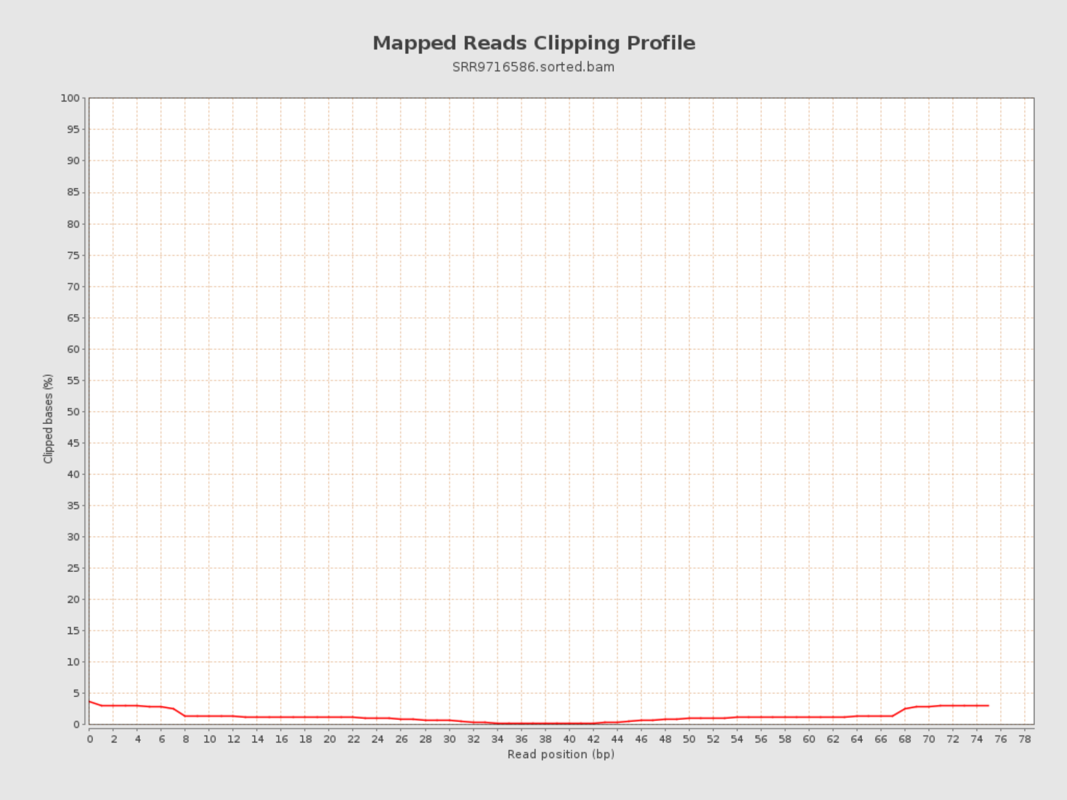
8. Results : Mapped Reads Nucleotide Content



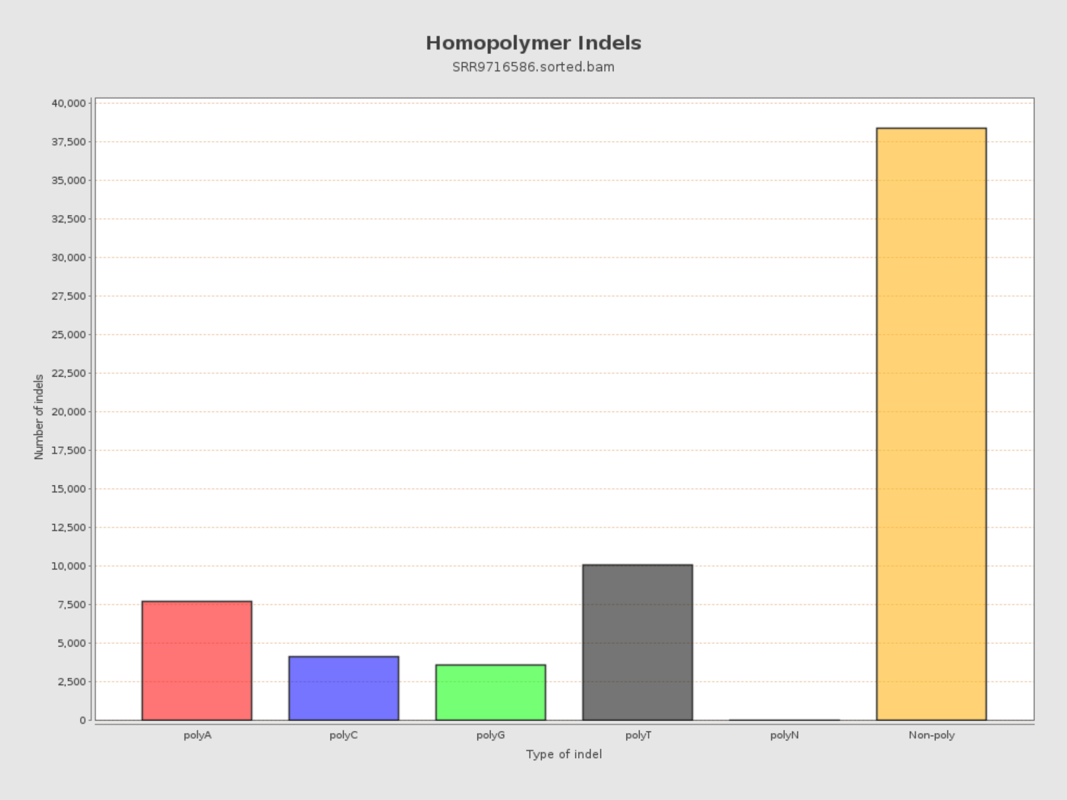
9. Results : Mapped Reads GC-content Distribution



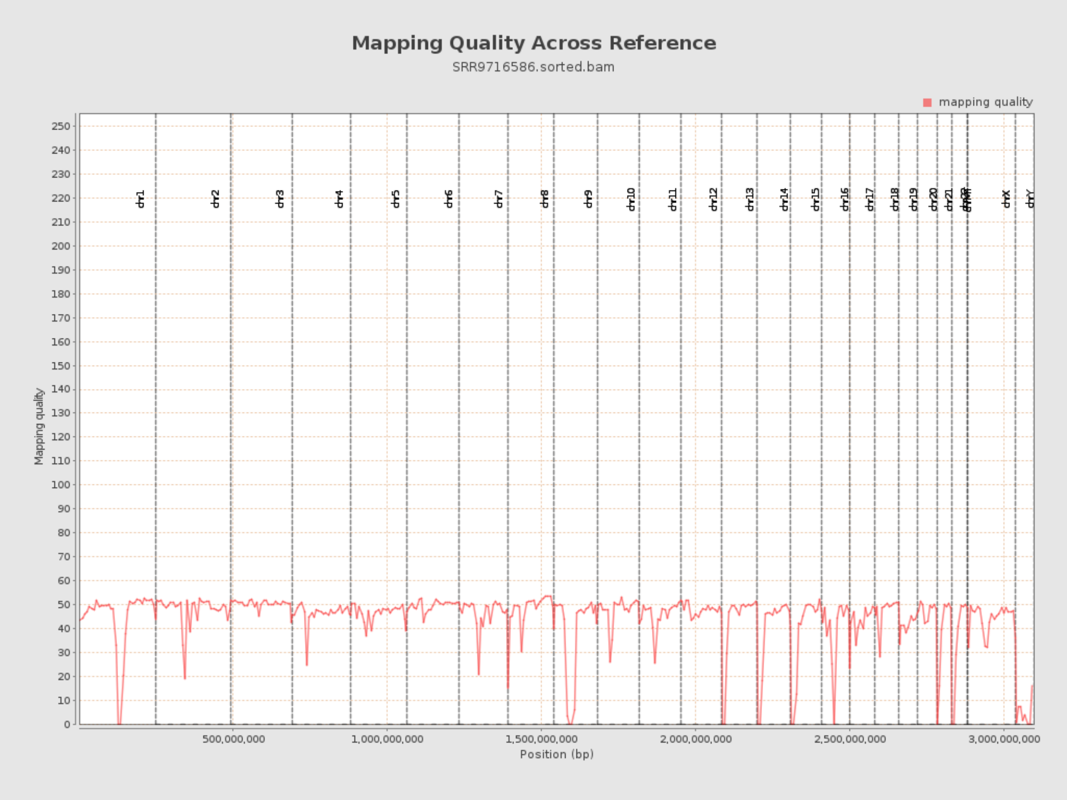
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram