Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 12:21:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716788.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_SRR9716788 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716788.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 12:21:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716788.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,453,074
Mapped reads	3,137,344 / 90.86%
Unmapped reads	315,730 / 9.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	67,871 / 1.97%
Read min/max/mean length	30 / 101 / 101.71
Duplicated reads (estimated)	159,536 / 4.62%
Duplication rate	3.7%
Clipped reads	3,200,956 / 92.7%

2.2. ACGT Content

Number/percentage of A's	61,560,405 / 26.42%
Number/percentage of C's	48,538,508 / 20.83%
Number/percentage of T's	69,037,373 / 29.63%
Number/percentage of G's	53,818,183 / 23.1%
Number/percentage of N's	26,898 / 0.01%
GC Percentage	43.93%

2.3. Coverage

Mean	0.0753

Standard Deviation	0.5449

2.4. Mapping Quality

Mean Mapping Quality	46.29

2.5. Mismatches and indels

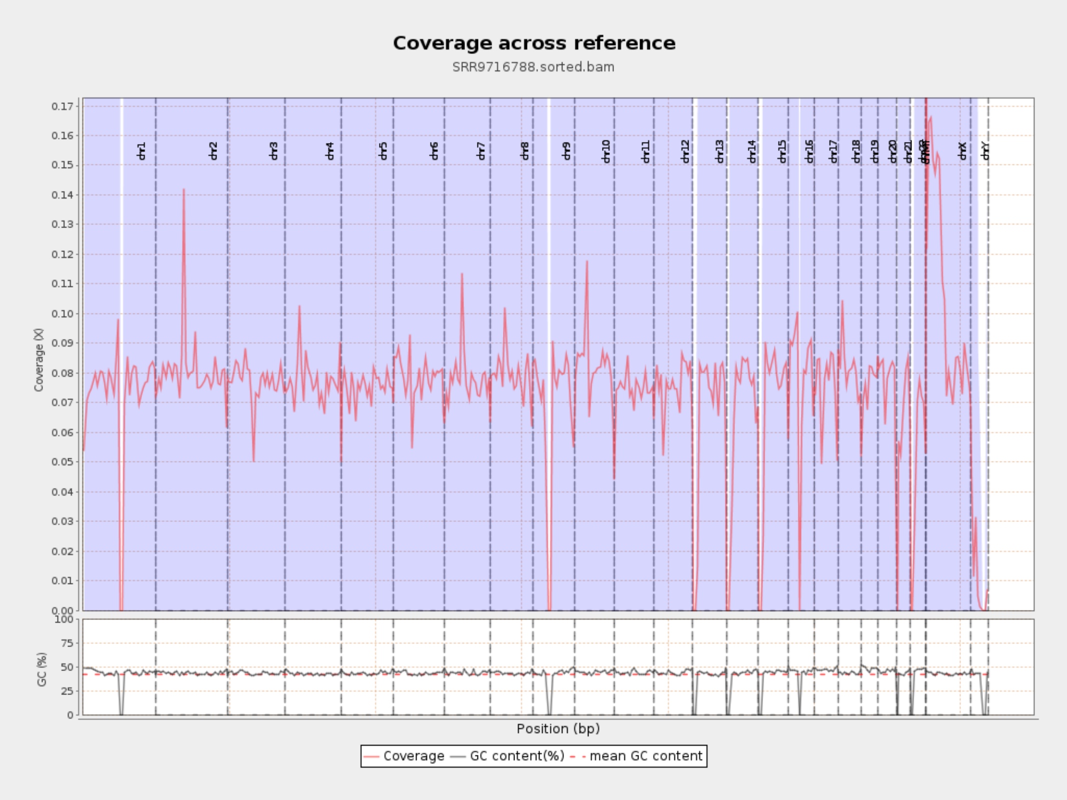
General error rate	0.77%
Mismatches	1,748,232
Insertions	20,008
Mapped reads with at least one insertion	0.63%
Deletions	46,756
Mapped reads with at least one deletion	1.47%
Homopolymer indels	39.53%

2.6. Chromosome stats

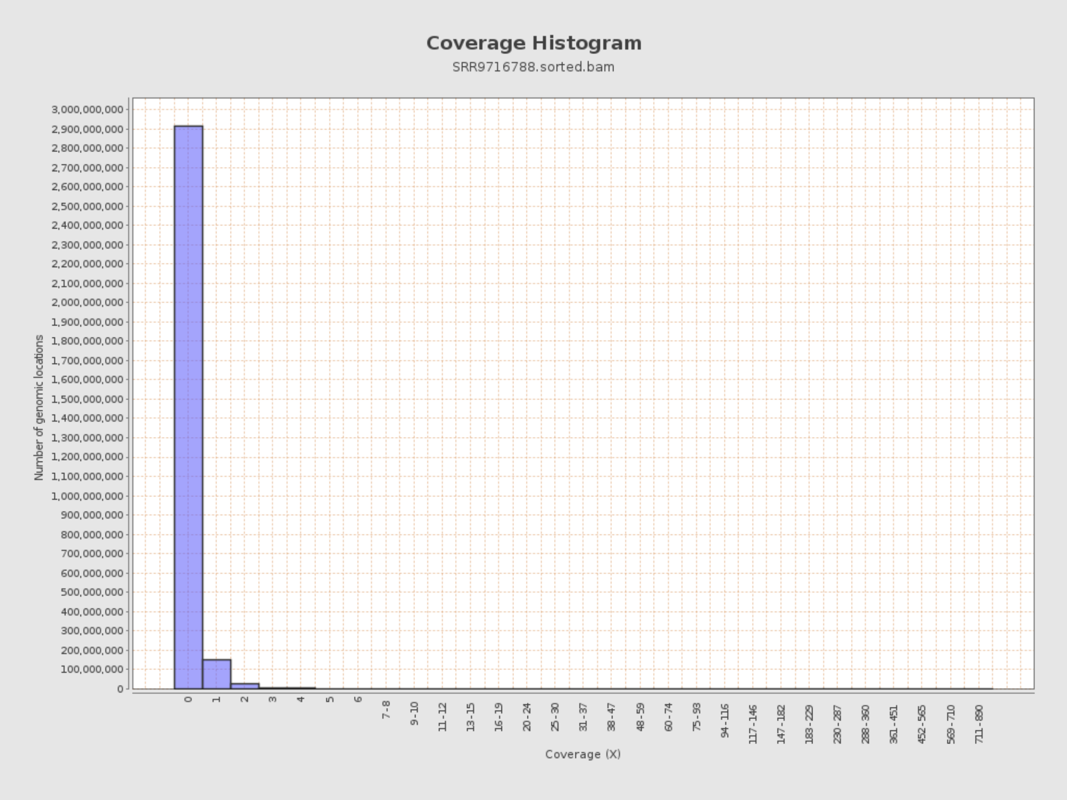
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18069192	0.0725	0.628
chr2	243199373	19734610	0.0811	0.7855
chr3	198022430	15256278	0.077	0.3385
chr4	191154276	14873090	0.0778	0.3835
chr5	180915260	13623420	0.0753	0.3431
chr6	171115067	13457316	0.0786	0.4016
chr7	159138663	12464217	0.0783	0.7304

chr8	146364022	11626624	0.0794	0.729
chr9	141213431	9592297	0.0679	0.5988
chr10	135534747	11274227	0.0832	0.5627
chr11	135006516	10055853	0.0745	0.5831
chr12	133851895	10213219	0.0763	0.351
chr13	115169878	7461835	0.0648	0.3098
chr14	107349540	6932449	0.0646	0.4005
chr15	102531392	6767769	0.066	0.3167
chr16	90354753	6833412	0.0756	0.3916
chr17	81195210	6198411	0.0763	0.3972
chr18	78077248	6428001	0.0823	1.1689
chr19	59128983	4493922	0.076	0.5374
chr20	63025520	4918250	0.078	0.3691
chr21	48129895	2991586	0.0622	0.3474
chr22	51304566	2554834	0.0498	0.2711
chrMT	16571	52077	3.1427	3.4659
chrX	155270560	16521562	0.1064	0.5095
chrY	59373566	666530	0.0112	0.2676

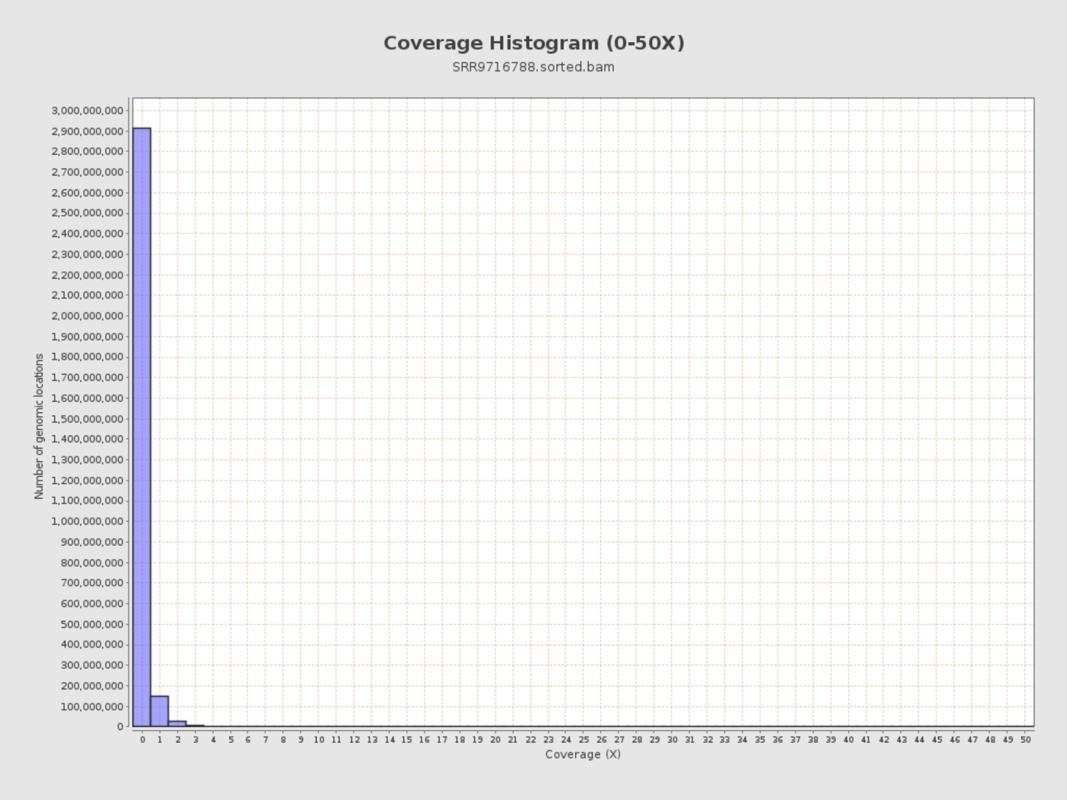
3. Results : Coverage across reference



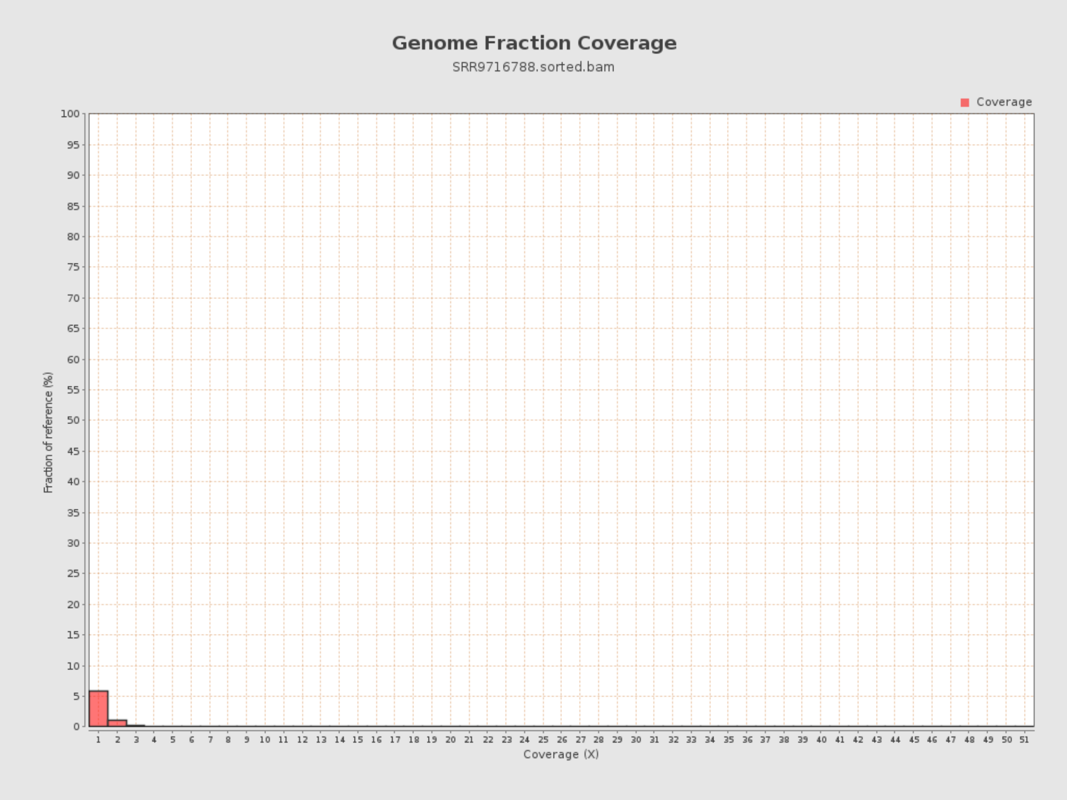
4. Results : Coverage Histogram



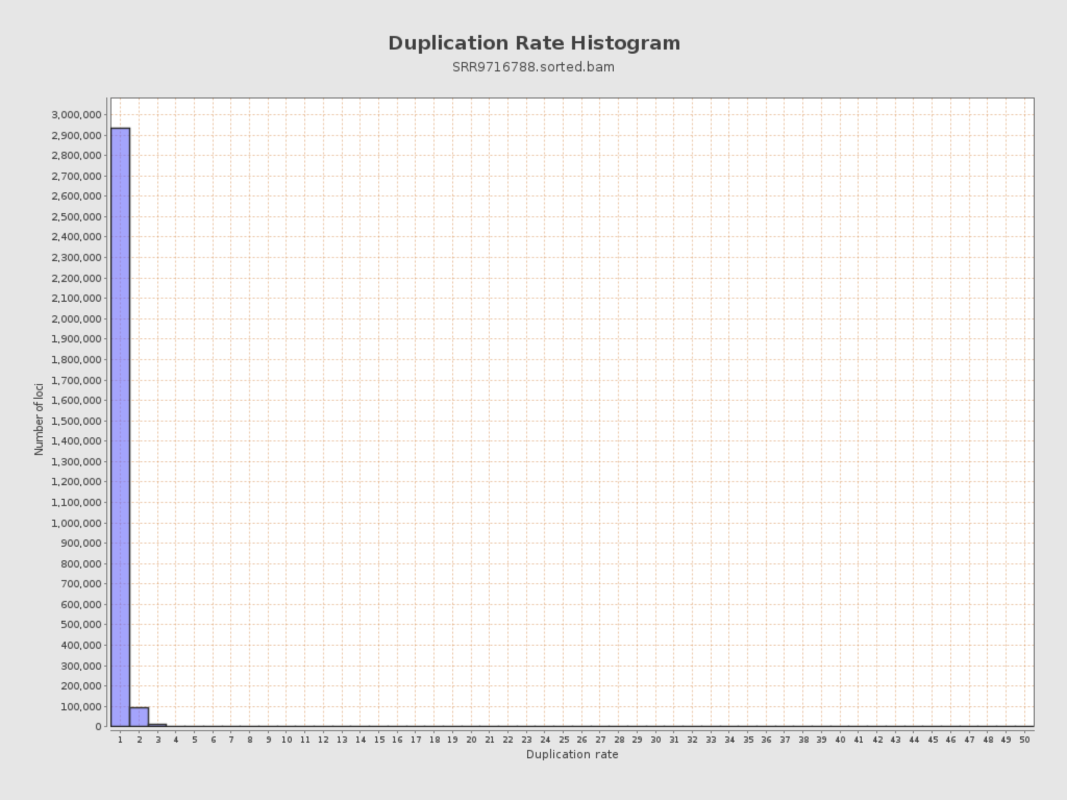
5. Results : Coverage Histogram (0-50X)



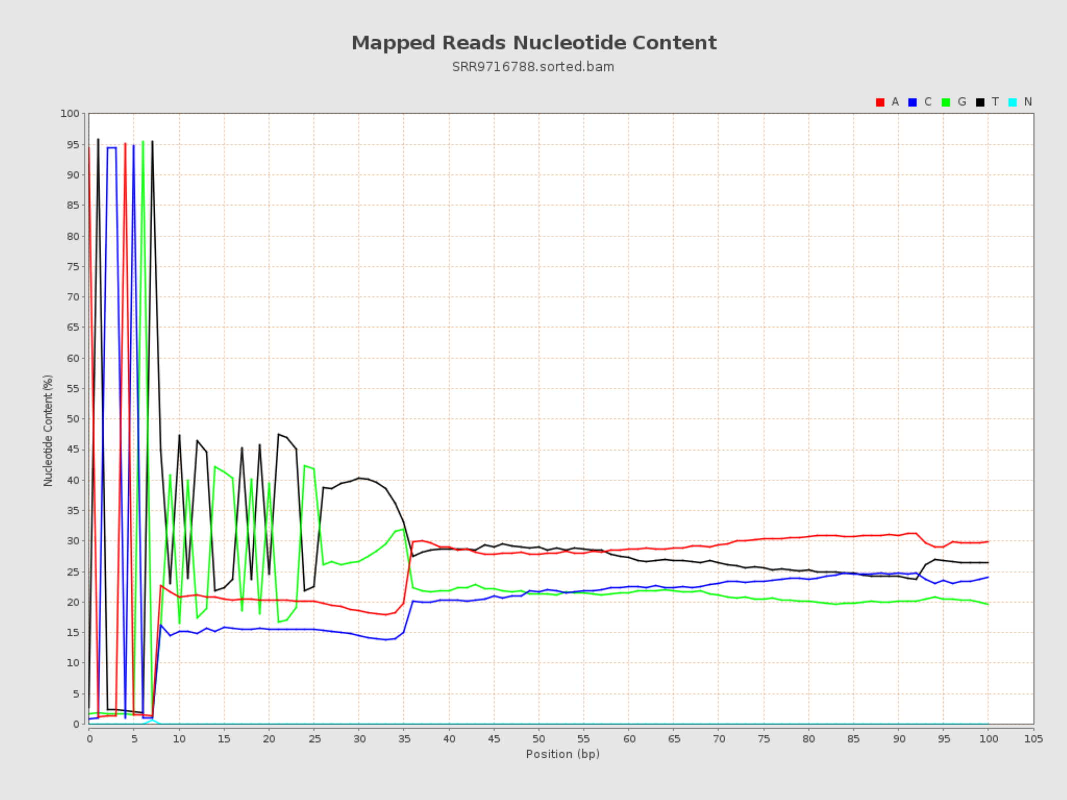
6. Results : Genome Fraction Coverage



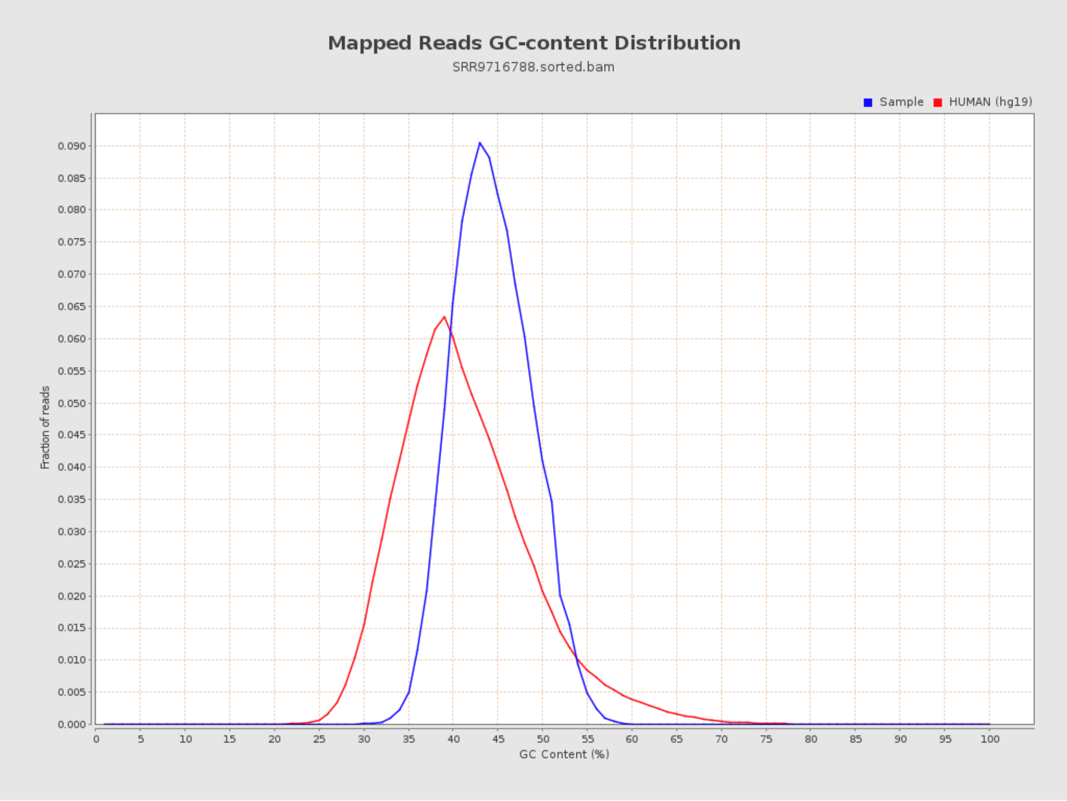
7. Results : Duplication Rate Histogram



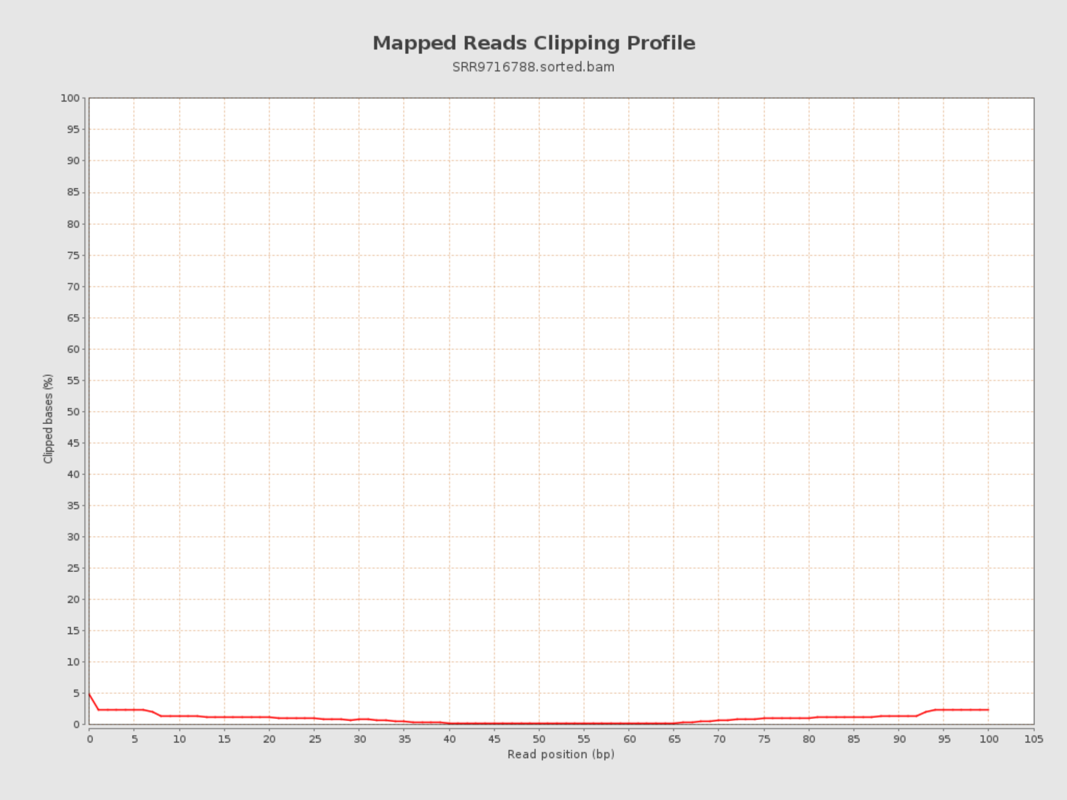
8. Results : Mapped Reads Nucleotide Content



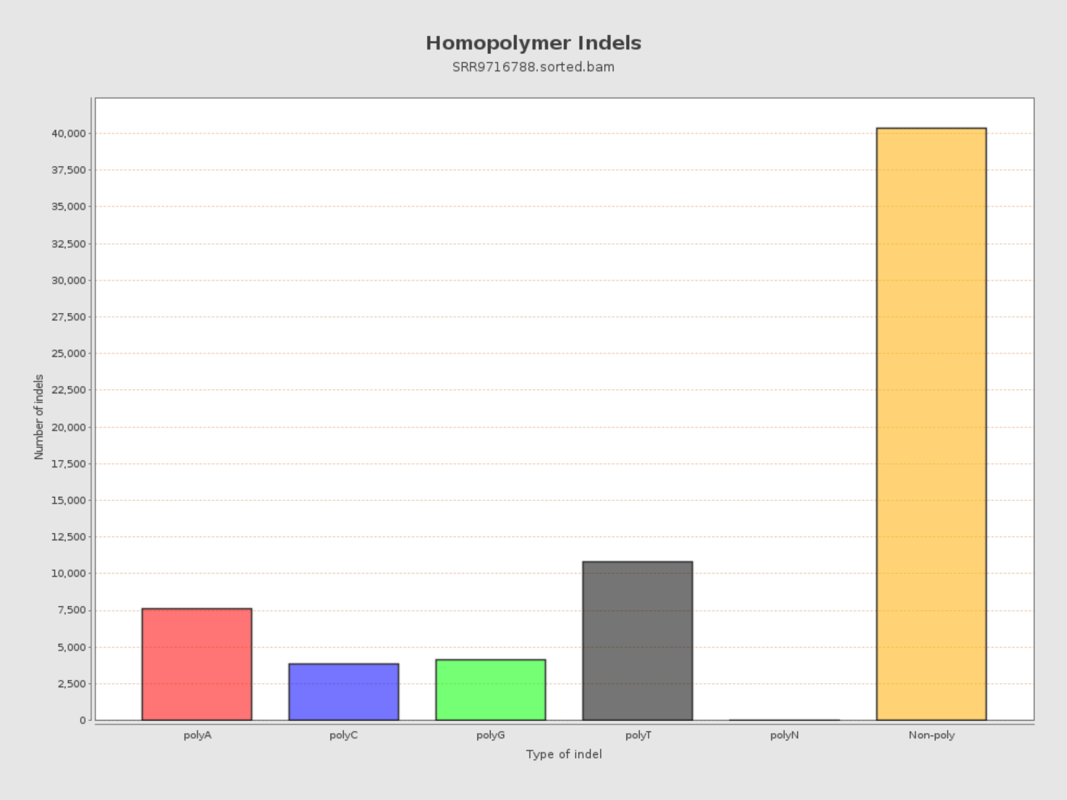
9. Results : Mapped Reads GC-content Distribution



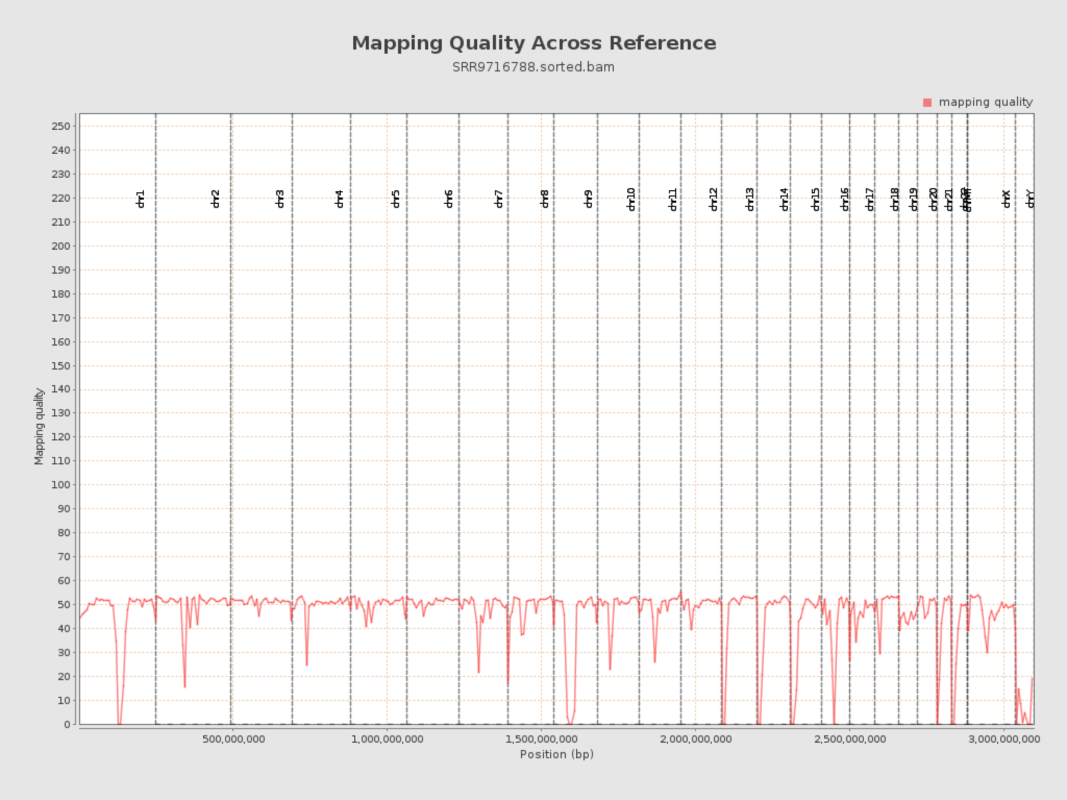
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram