Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 17:03:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716890.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_SRR9716890 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716890.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 17:03:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716890.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,806,500
Mapped reads	9,497,571 / 87.89%
Unmapped reads	1,308,929 / 12.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	54,741 / 0.51%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	729,100 / 6.75%
Duplication rate	5.41%
Clipped reads	9,547,395 / 88.35%

2.2. ACGT Content

Number/percentage of A's	137,921,187 / 25.35%
Number/percentage of C's	108,760,674 / 19.99%
Number/percentage of T's	167,351,651 / 30.76%
Number/percentage of G's	129,934,309 / 23.89%
Number/percentage of N's	7,993 / 0%
GC Percentage	43.88%

2.3. Coverage

Mean	0.1758

Standard Deviation	1.2716

2.4. Mapping Quality

Mean Mapping Quality	43.25

2.5. Mismatches and indels

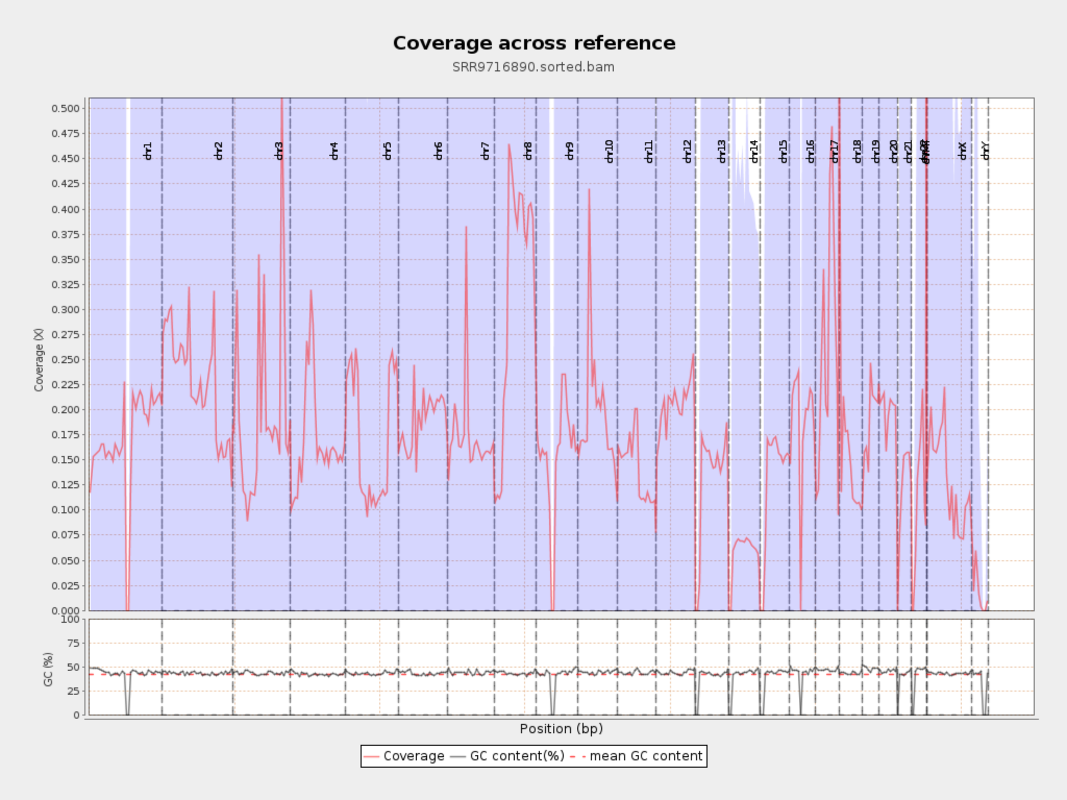
General error rate	0.52%
Mismatches	2,758,275
Insertions	31,187
Mapped reads with at least one insertion	0.33%
Deletions	102,737
Mapped reads with at least one deletion	1.07%
Homopolymer indels	41.64%

2.6. Chromosome stats

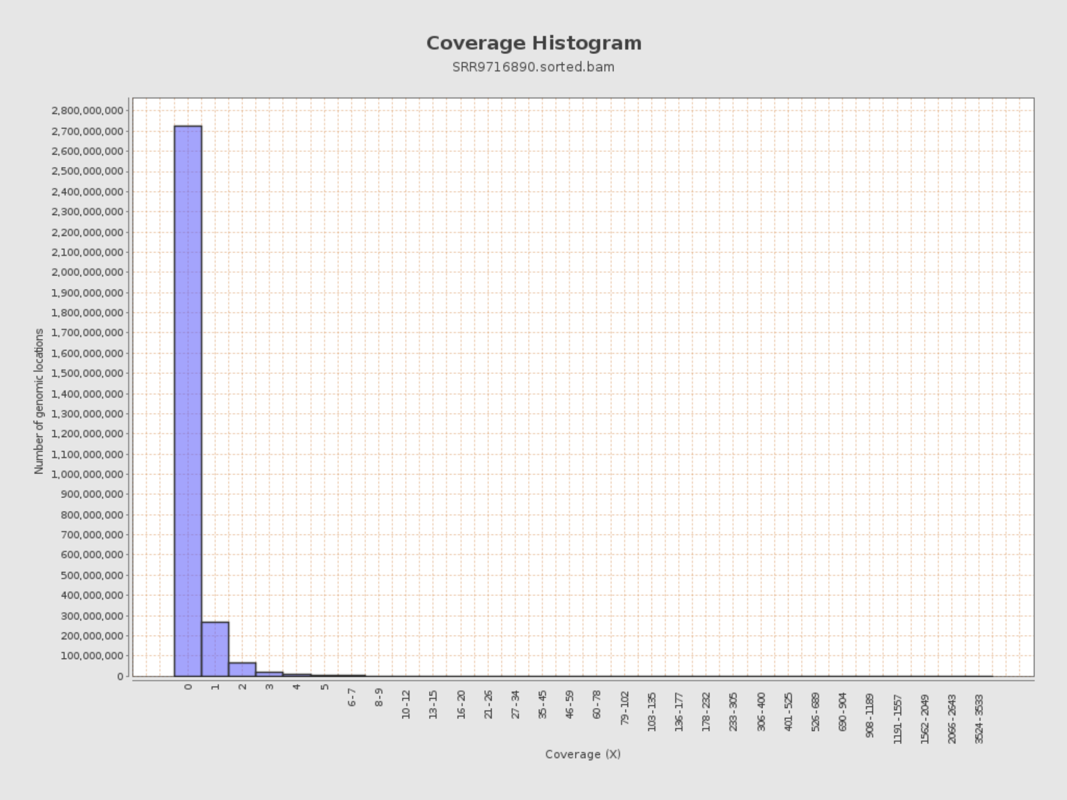
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	42089008	0.1689	1.8215
chr2	243199373	55994488	0.2302	1.7533
chr3	198022430	39355200	0.1987	0.7454
chr4	191154276	32426283	0.1696	0.6585
chr5	180915260	30940105	0.171	0.5842
chr6	171115067	32450735	0.1896	0.8247
chr7	159138663	27904171	0.1753	2.9398

chr8	146364022	46883310	0.3203	1.2772
chr9	141213431	21462086	0.152	0.8376
chr10	135534747	26762353	0.1975	1.8713
chr11	135006516	18979999	0.1406	0.8106
chr12	133851895	27418645	0.2048	0.767
chr13	115169878	15059279	0.1308	0.5022
chr14	107349540	6197690	0.0577	0.4575
chr15	102531392	13420496	0.1309	0.5344
chr16	90354753	16960316	0.1877	0.7307
chr17	81195210	21023207	0.2589	0.811
chr18	78077248	12371185	0.1584	1.477
chr19	59128983	11136795	0.1883	1.7593
chr20	63025520	12406809	0.1969	0.6991
chr21	48129895	5800213	0.1205	0.5511
chr22	51304566	5380473	0.1049	0.4517
chrMT	16571	33835	2.0418	2.5421
chrX	155270560	20520894	0.1322	0.7822
chrY	59373566	1160880	0.0196	0.3856

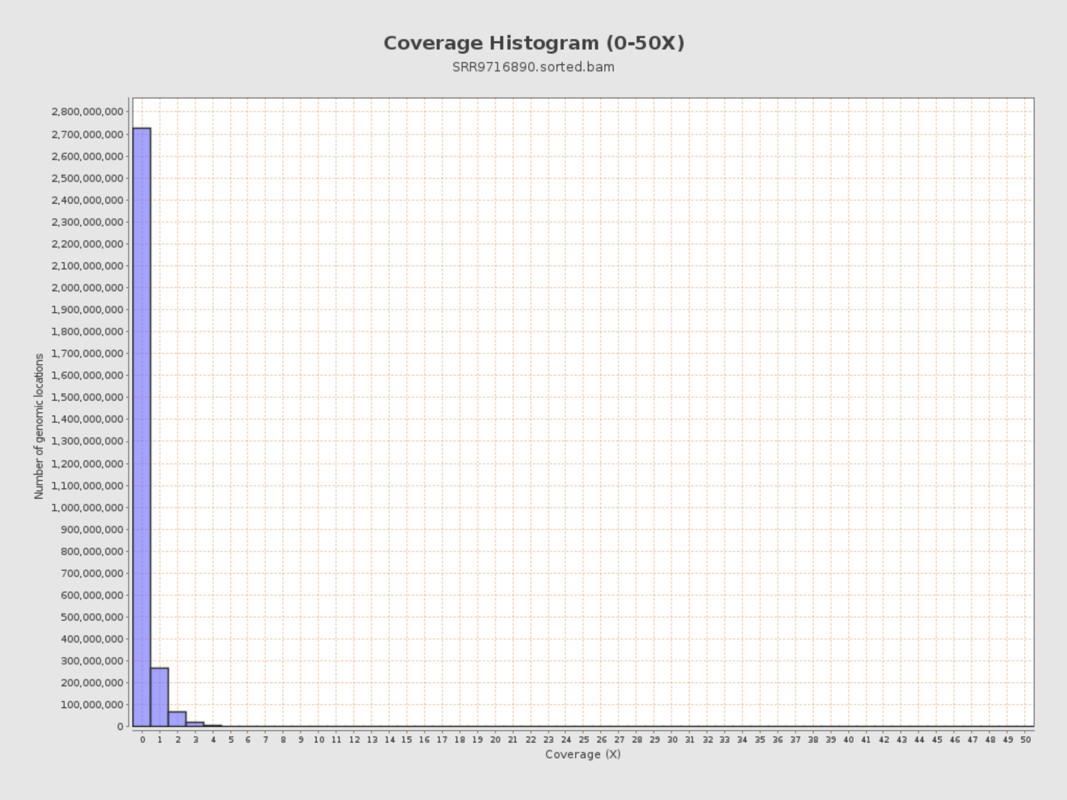
3. Results : Coverage across reference



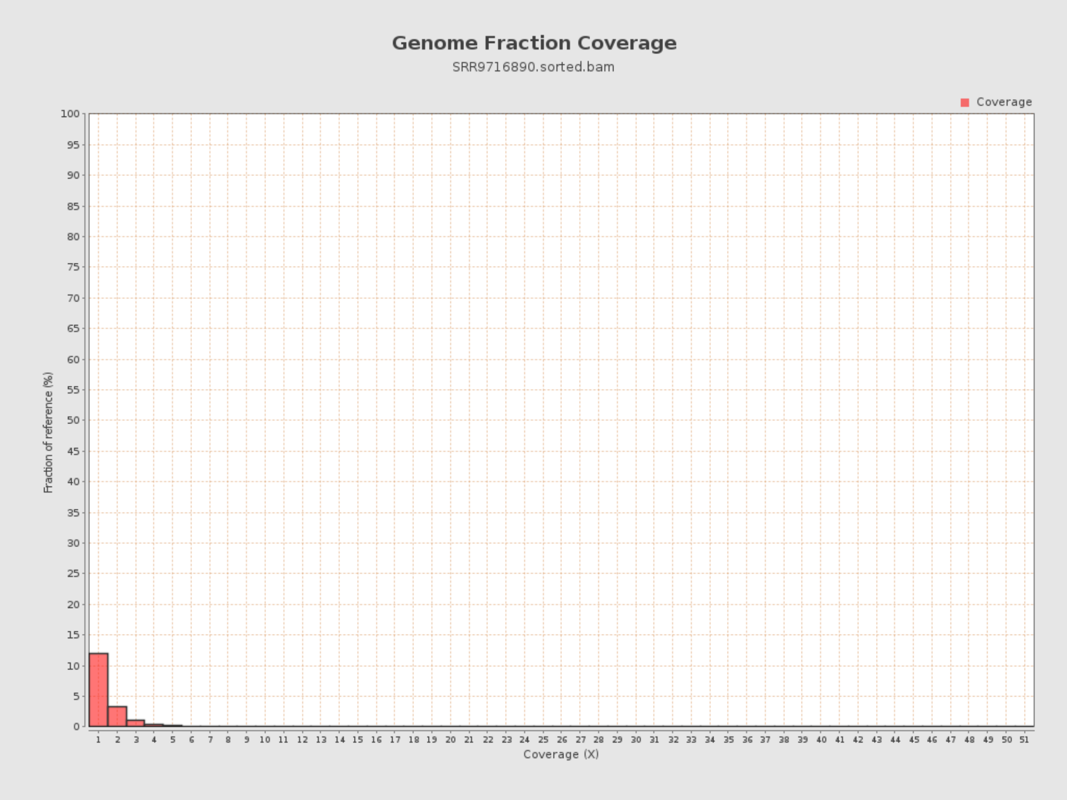
4. Results : Coverage Histogram



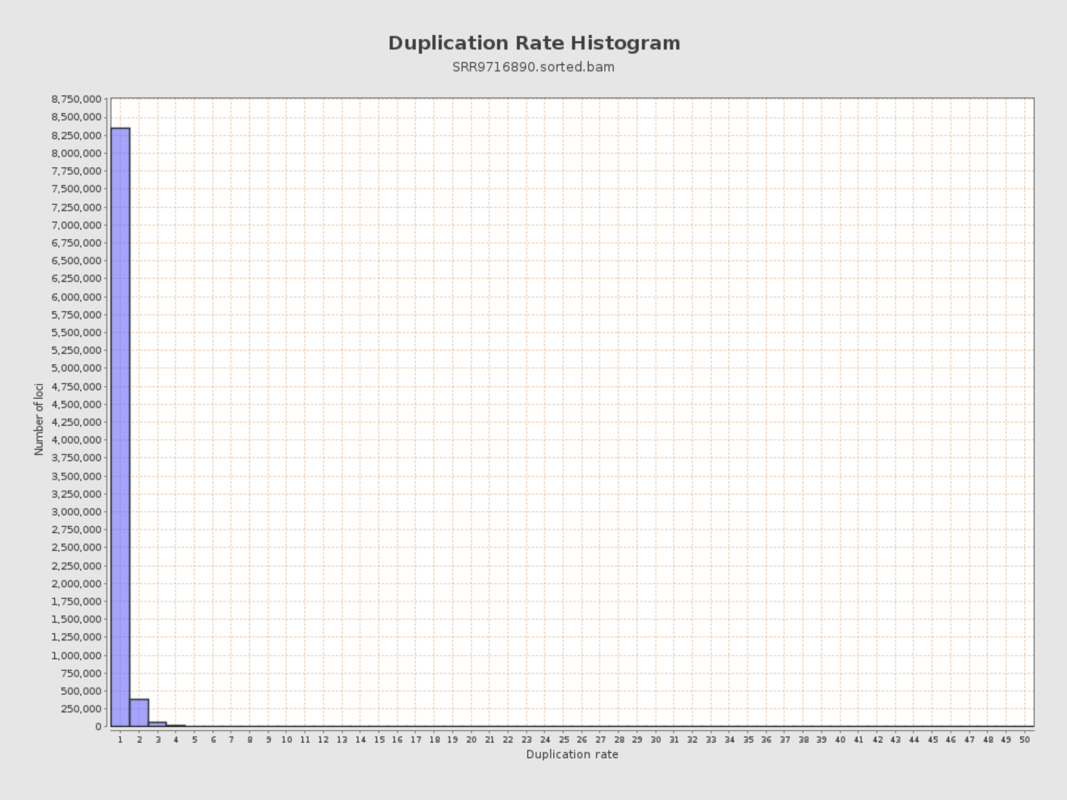
5. Results : Coverage Histogram (0-50X)



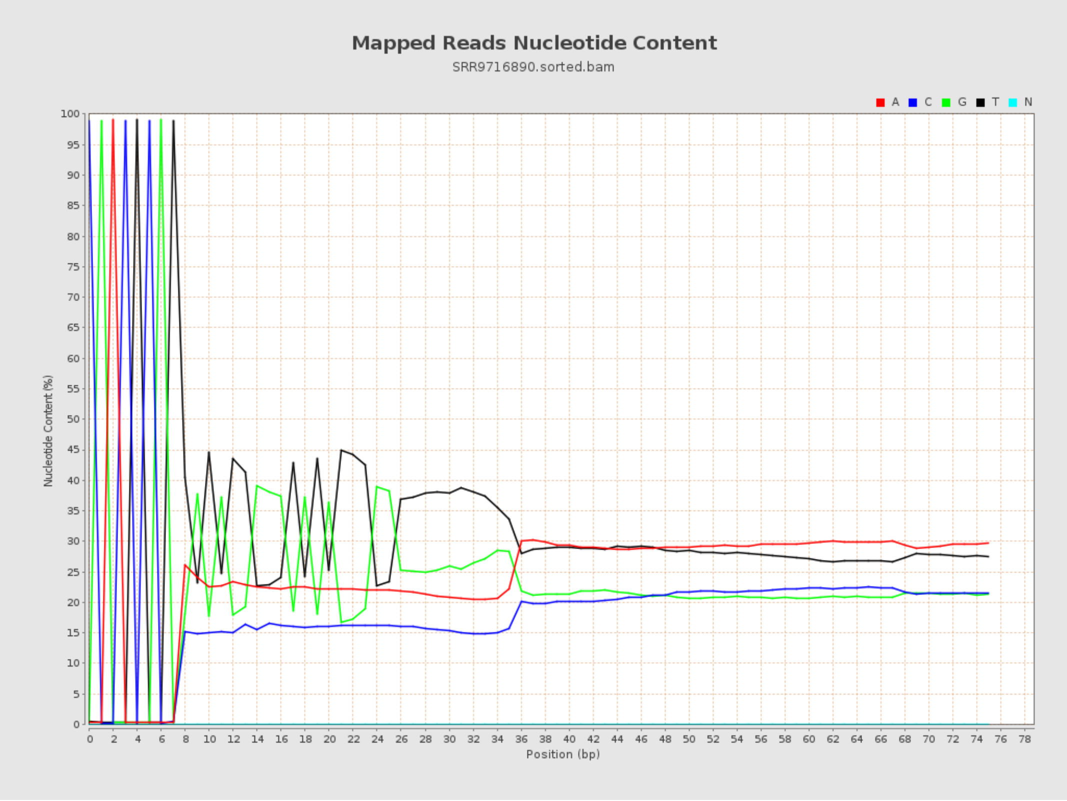
6. Results : Genome Fraction Coverage



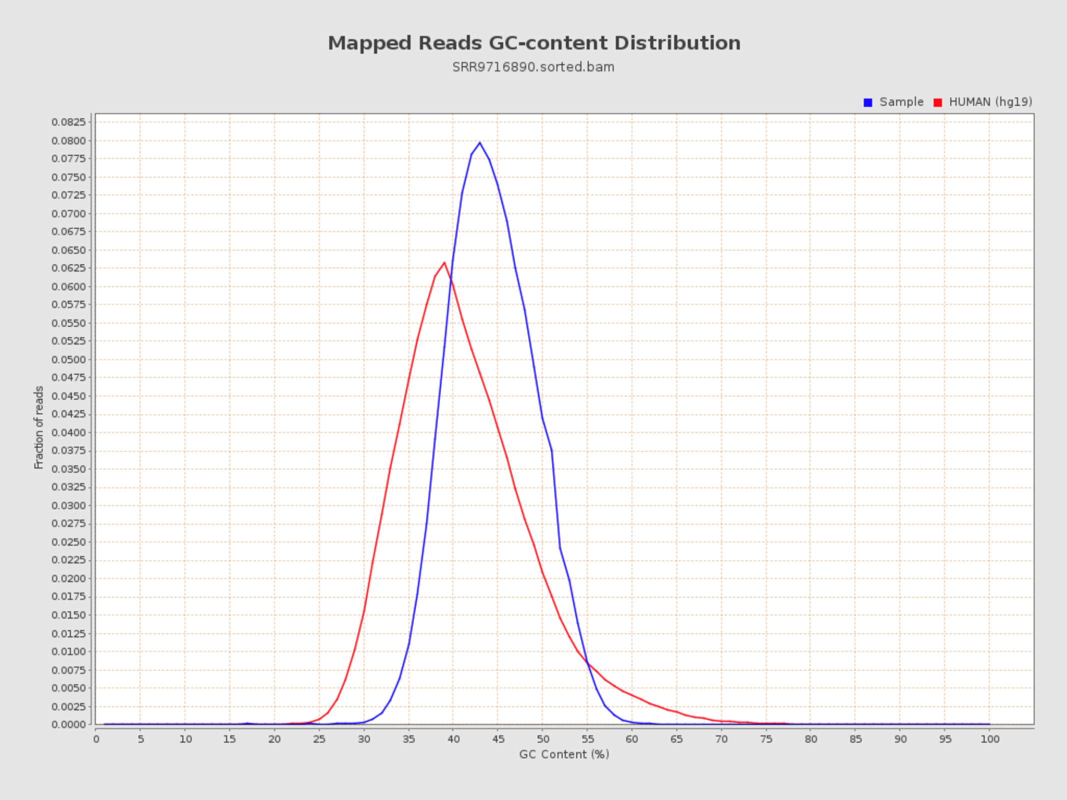
7. Results : Duplication Rate Histogram



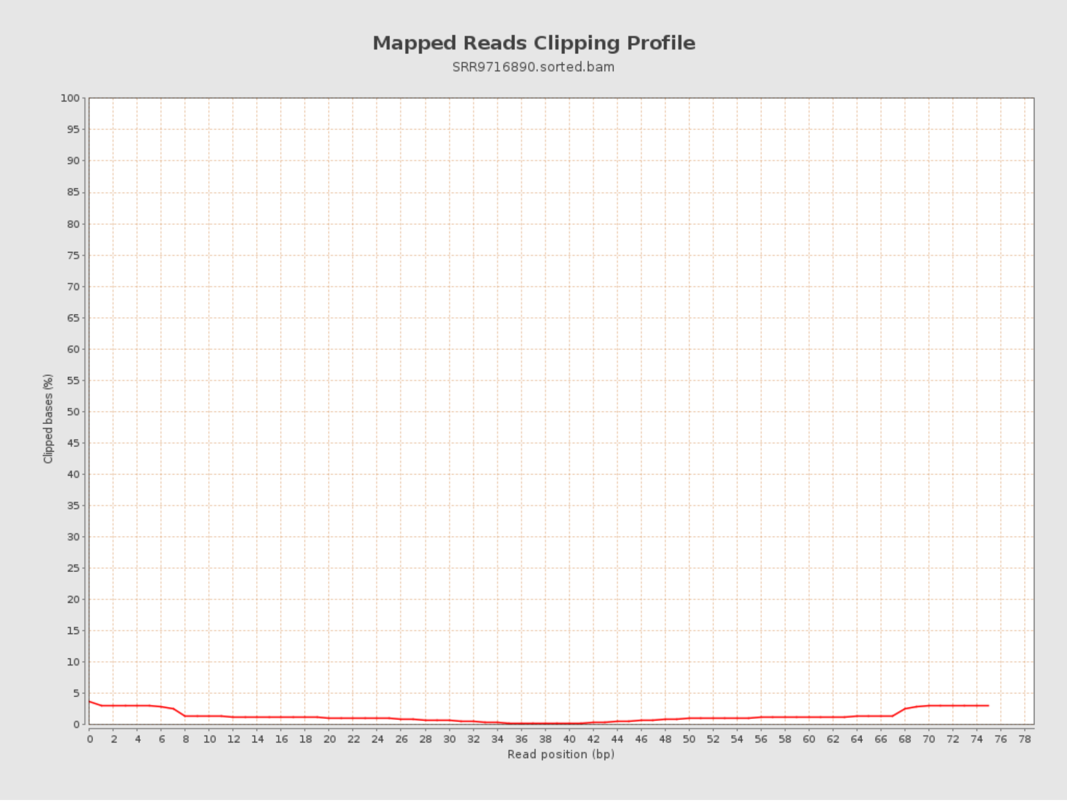
8. Results : Mapped Reads Nucleotide Content



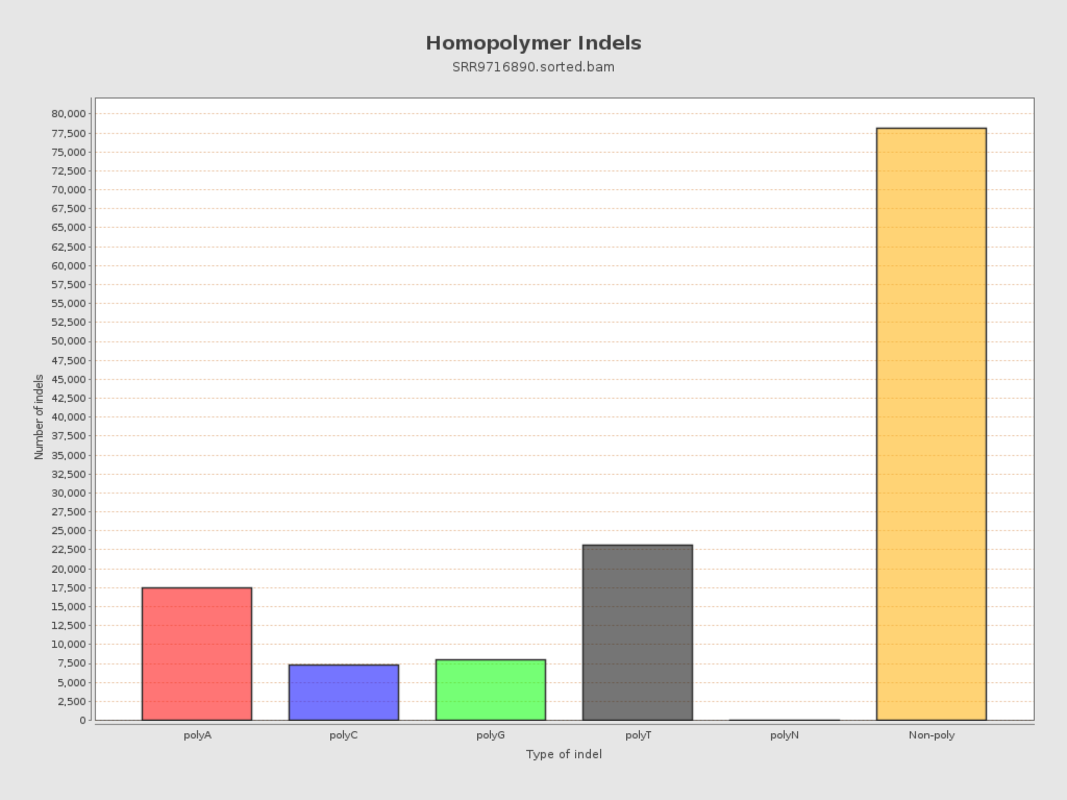
9. Results : Mapped Reads GC-content Distribution



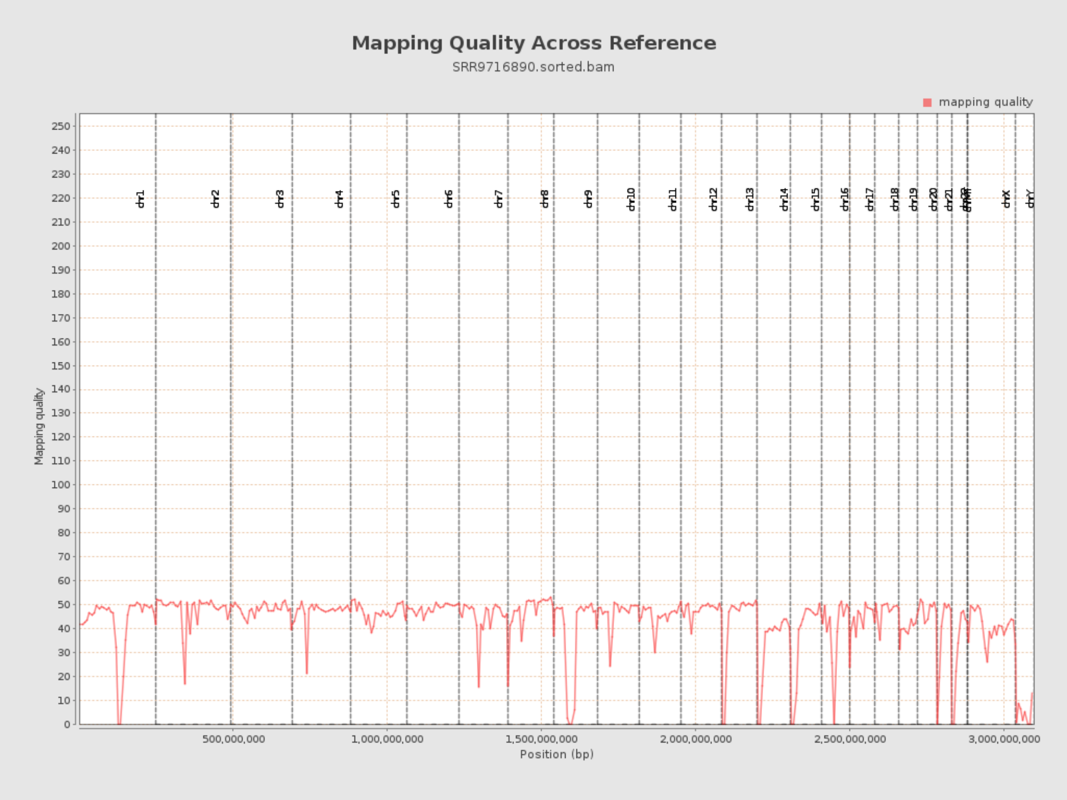
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram