Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 07:17:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716321.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_SRR9716321 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716321.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 07:17:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716321.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,732,331
Mapped reads	1,597,615 / 92.22%
Unmapped reads	134,716 / 7.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,565 / 0.49%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	53,951 / 3.11%
Duplication rate	2.48%
Clipped reads	1,605,200 / 92.66%

2.2. ACGT Content

Number/percentage of A's	22,698,346 / 24.35%
Number/percentage of C's	17,520,420 / 18.8%
Number/percentage of T's	29,813,441 / 31.98%
Number/percentage of G's	23,182,583 / 24.87%
Number/percentage of N's	2,781 / 0%
GC Percentage	43.66%

2.3. Coverage

Mean	0.0301

Standard Deviation	0.2726

2.4. Mapping Quality

Mean Mapping Quality	44.72

2.5. Mismatches and indels

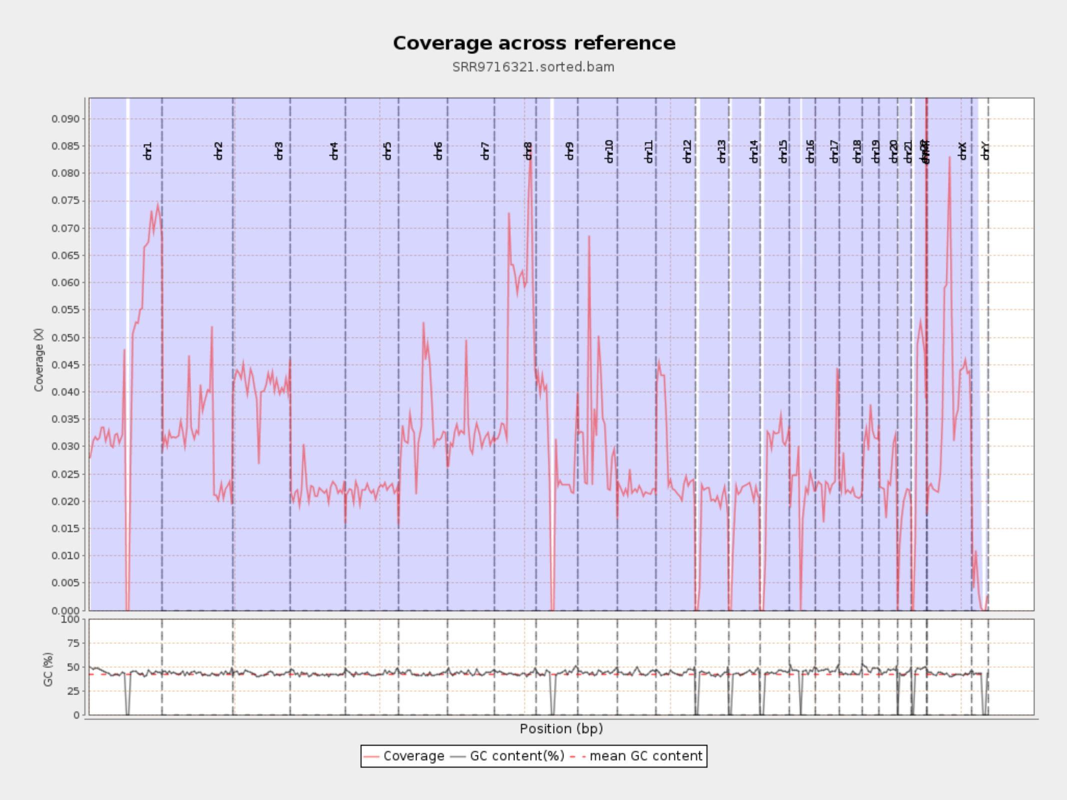
General error rate	0.49%
Mismatches	450,776
Insertions	5,129
Mapped reads with at least one insertion	0.32%
Deletions	16,148
Mapped reads with at least one deletion	1%
Homopolymer indels	45.31%

2.6. Chromosome stats

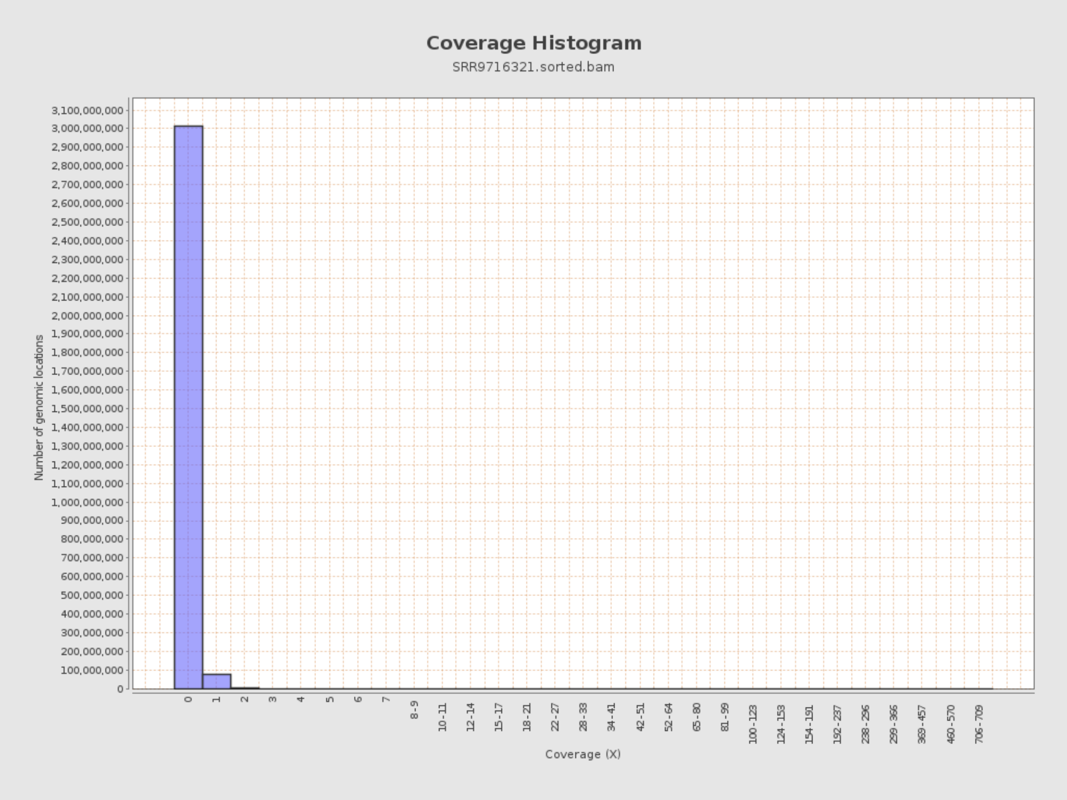
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10764318	0.0432	0.4596
chr2	243199373	7652755	0.0315	0.3545
chr3	198022430	8141717	0.0411	0.2241
chr4	191154276	4223439	0.0221	0.1718
chr5	180915260	3988286	0.022	0.1629
chr6	171115067	5835098	0.0341	0.2294
chr7	159138663	5168606	0.0325	0.3482

chr8	146364022	7877825	0.0538	0.2822
chr9	141213431	3767853	0.0267	0.2505
chr10	135534747	4511860	0.0333	0.3274
chr11	135006516	2969987	0.022	0.223
chr12	133851895	3746400	0.028	0.1867
chr13	115169878	2031805	0.0176	0.146
chr14	107349540	1990283	0.0185	0.1664
chr15	102531392	2651723	0.0259	0.177
chr16	90354753	1925750	0.0213	0.1896
chr17	81195210	2061711	0.0254	0.1795
chr18	78077248	1740369	0.0223	0.437
chr19	59128983	1892073	0.032	0.3415
chr20	63025520	1524794	0.0242	0.1706
chr21	48129895	823575	0.0171	0.1633
chr22	51304566	1716264	0.0335	0.2003
chrMT	16571	4002	0.2415	0.4915
chrX	155270560	6016882	0.0388	0.2469
chrY	59373566	215960	0.0036	0.092

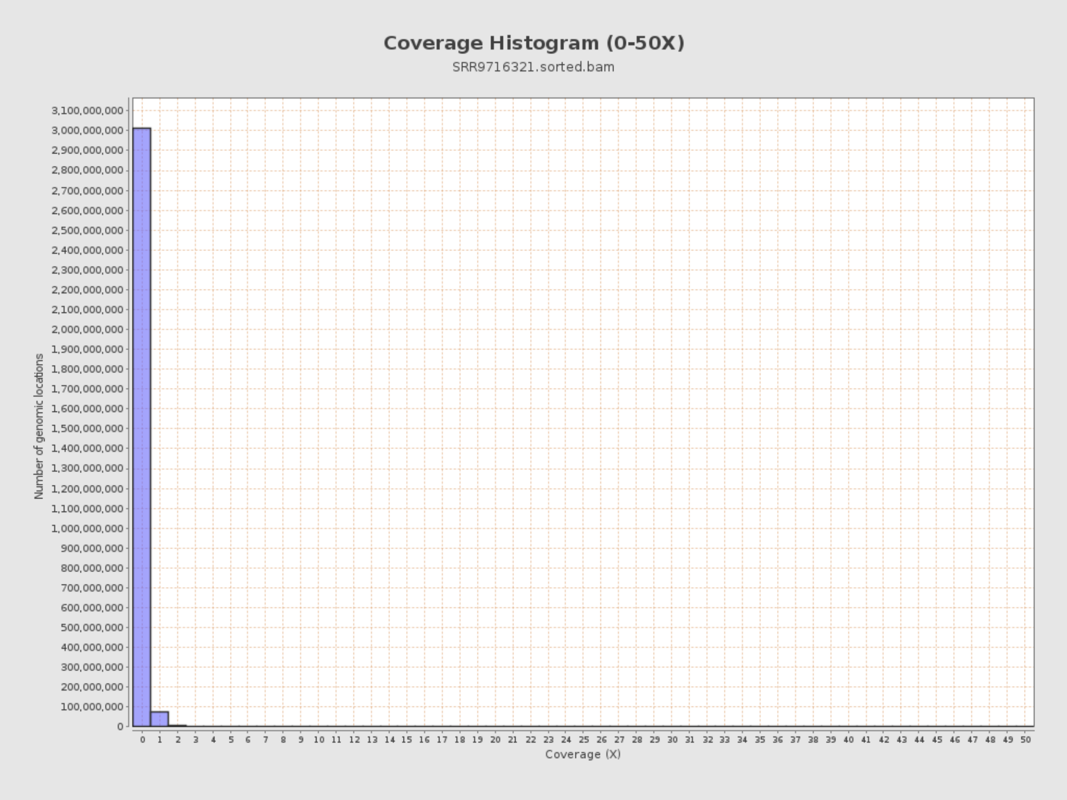
3. Results : Coverage across reference



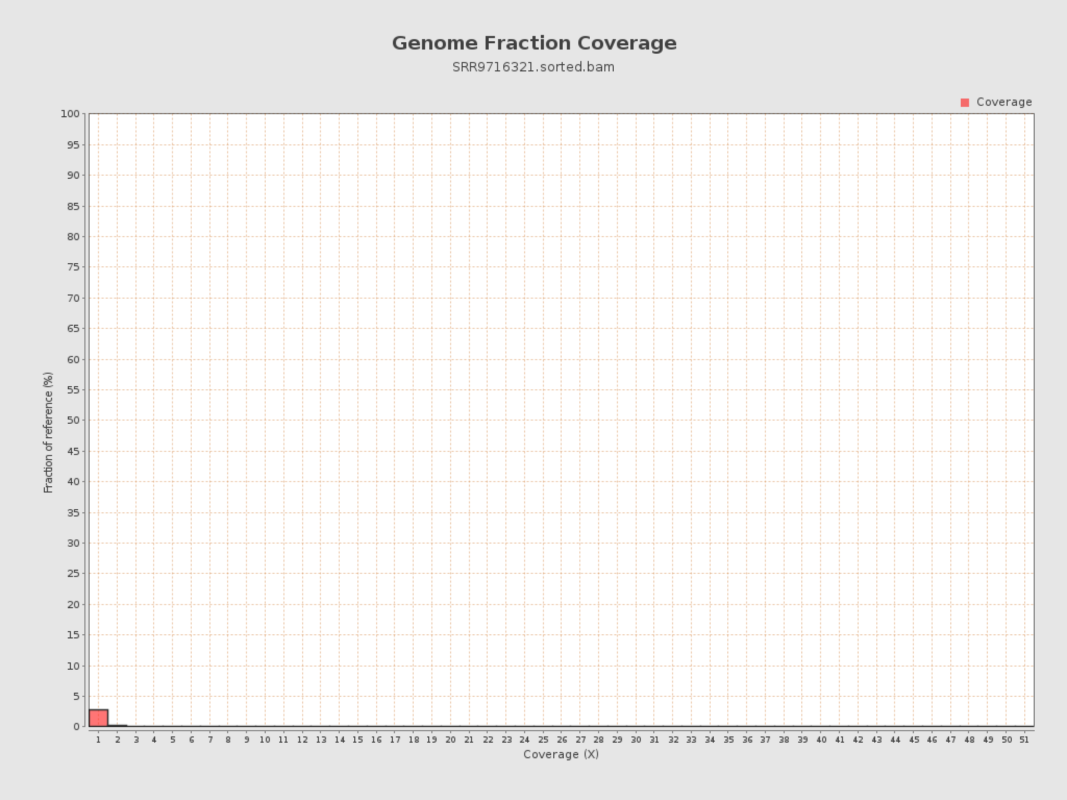
4. Results : Coverage Histogram



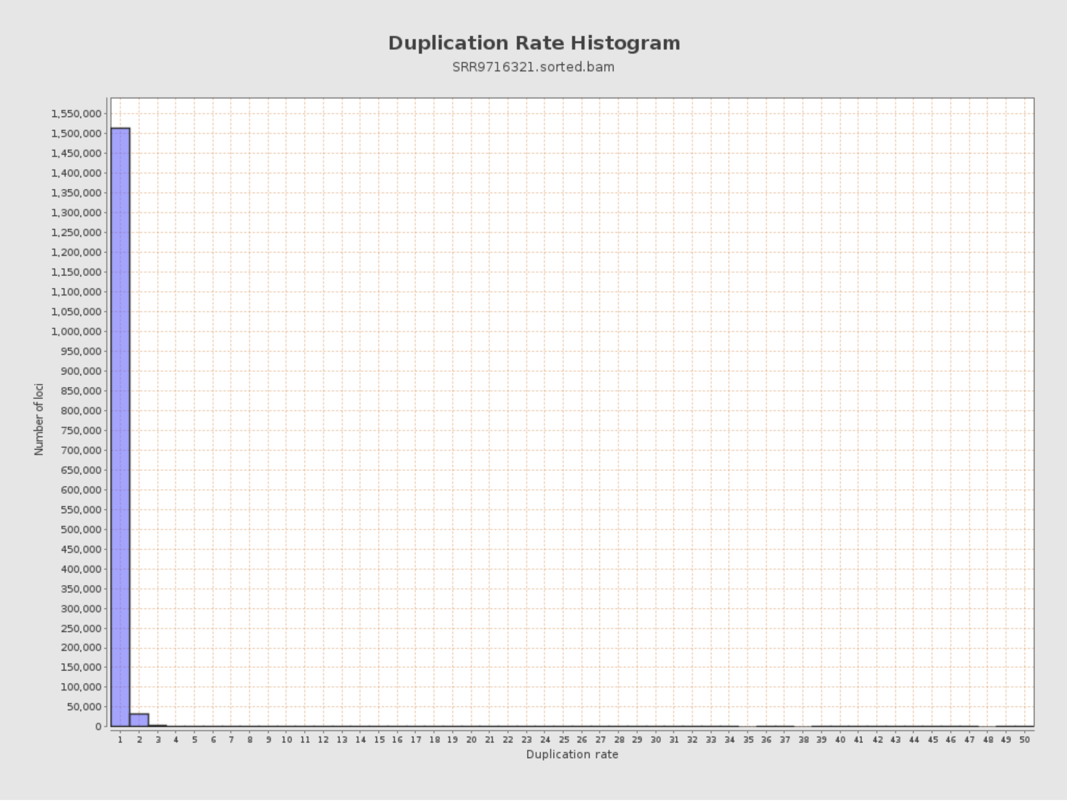
5. Results : Coverage Histogram (0-50X)



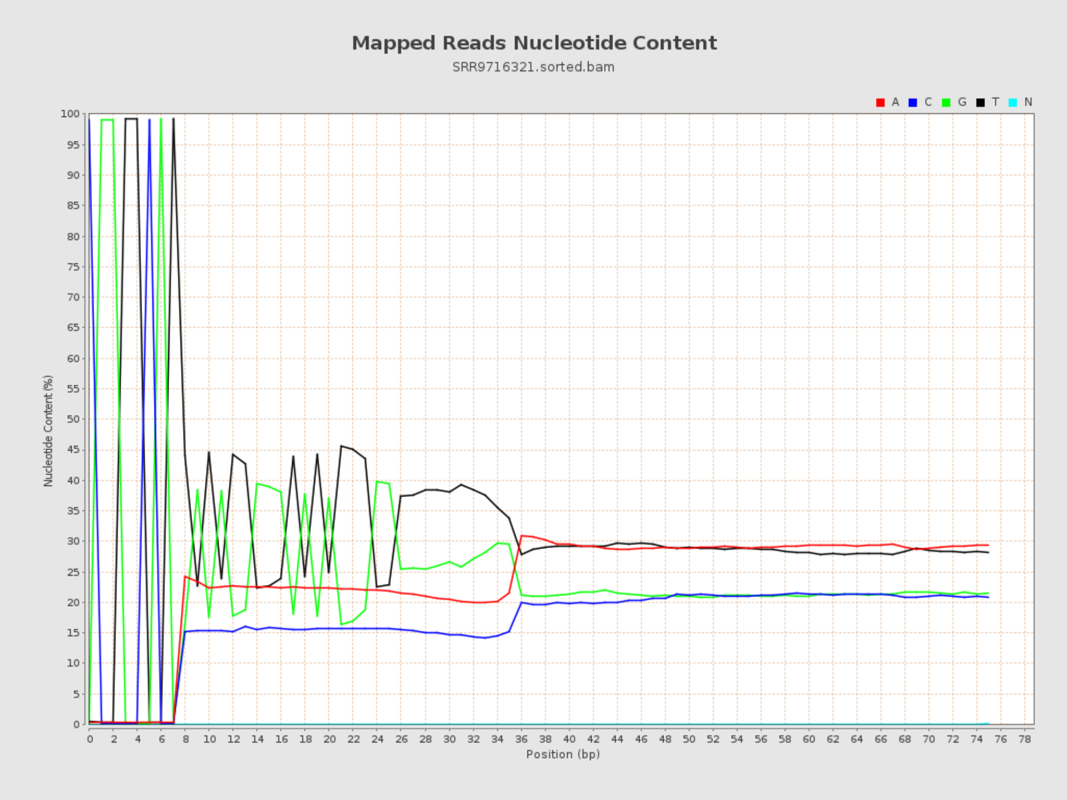
6. Results : Genome Fraction Coverage



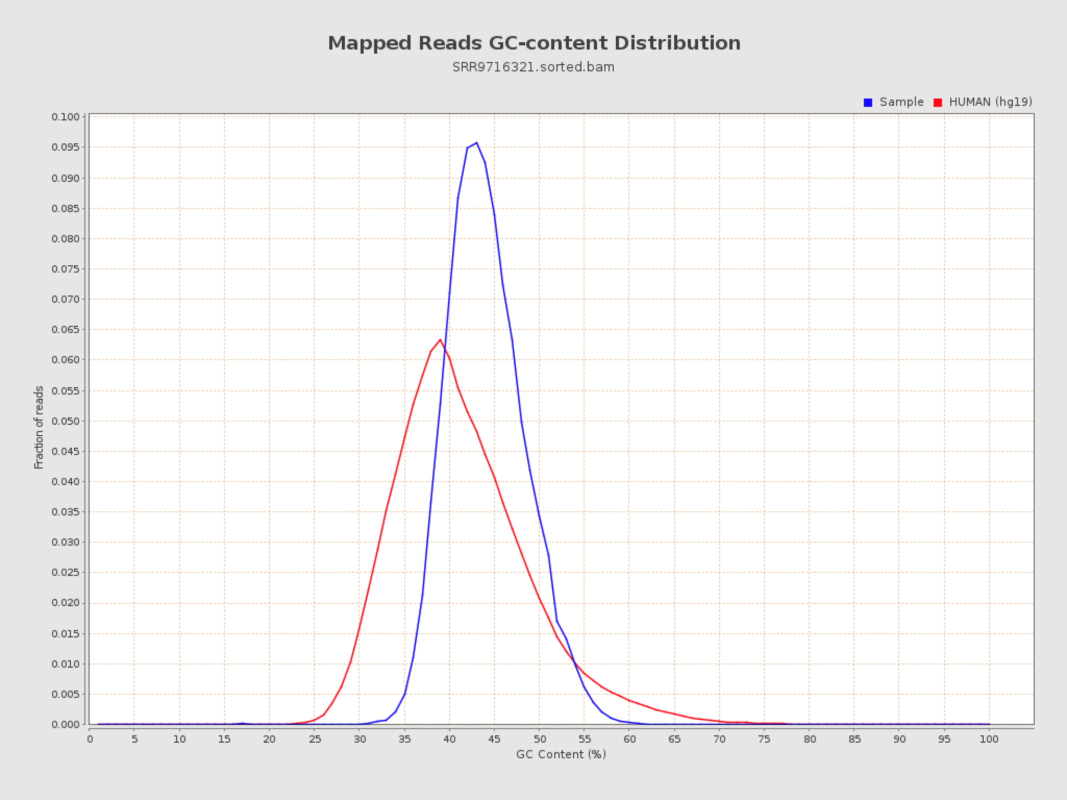
7. Results : Duplication Rate Histogram



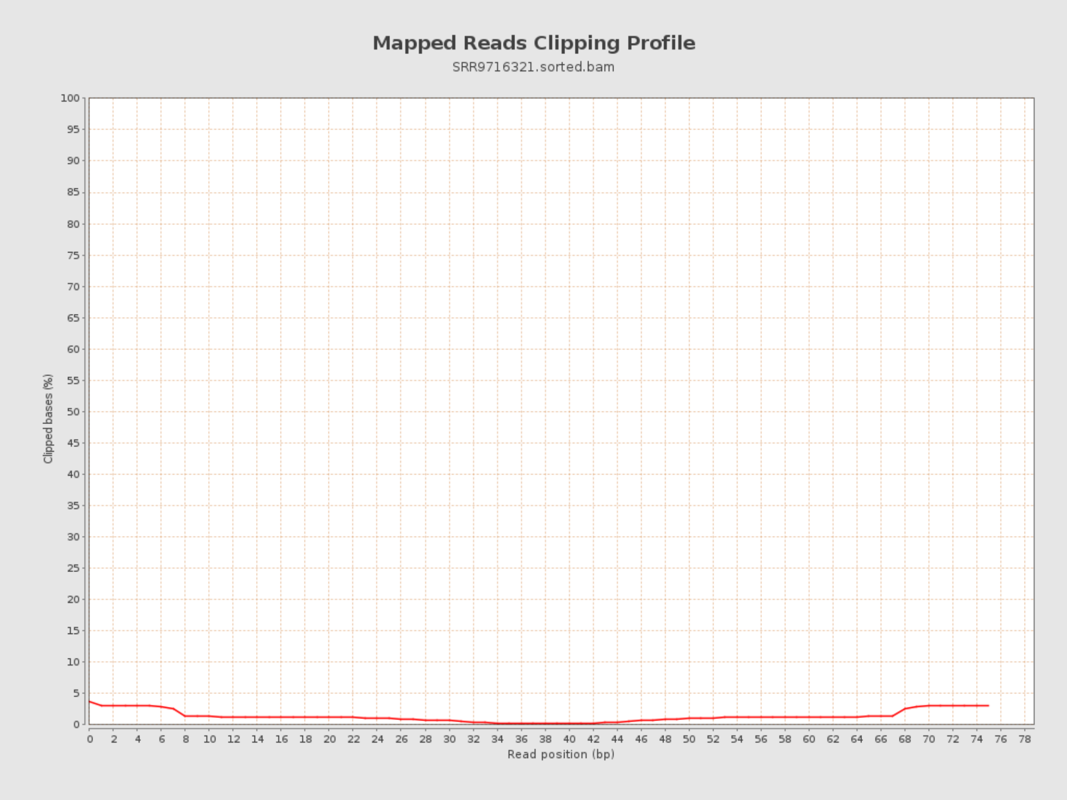
8. Results : Mapped Reads Nucleotide Content



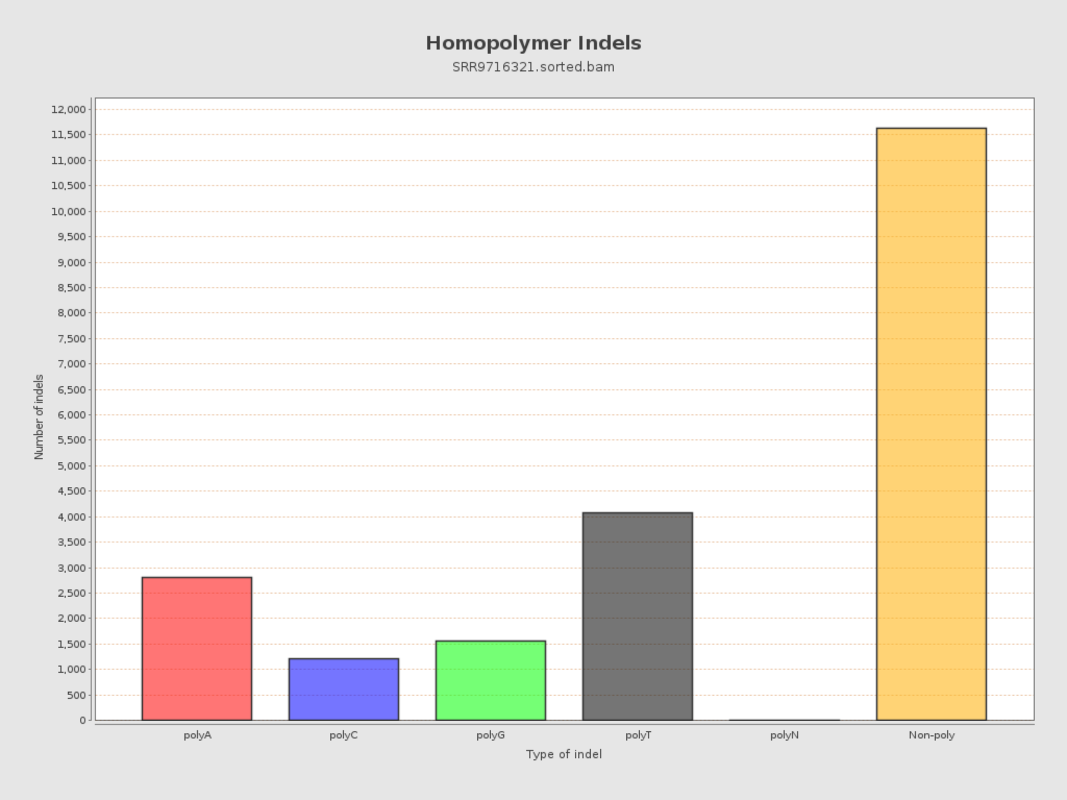
9. Results : Mapped Reads GC-content Distribution



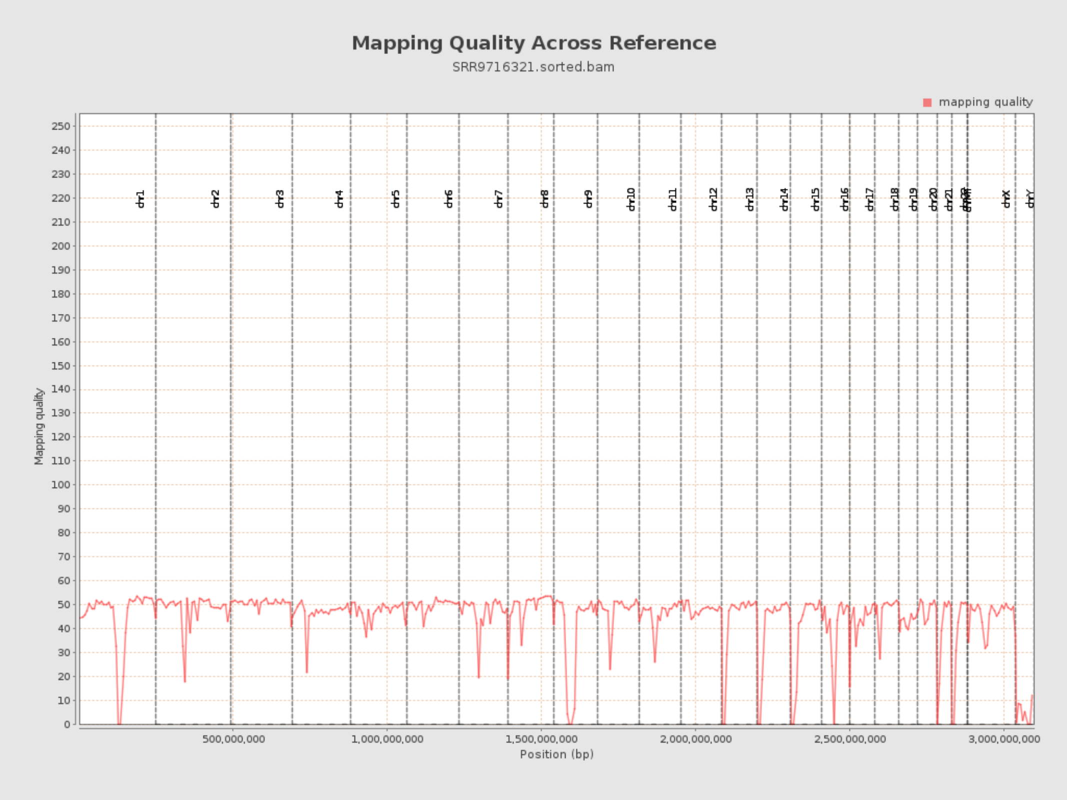
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram