Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 09:13:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716729.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_SRR9716729 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716729.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 09:13:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716729.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,995,783
Mapped reads	1,720,960 / 86.23%
Unmapped reads	274,823 / 13.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	47,605 / 2.39%
Read min/max/mean length	30 / 101 / 101.86
Duplicated reads (estimated)	49,036 / 2.46%
Duplication rate	1.86%
Clipped reads	1,767,848 / 88.58%

2.2. ACGT Content

Number/percentage of A's	34,054,604 / 25.96%
Number/percentage of C's	25,808,637 / 19.68%
Number/percentage of T's	39,413,203 / 30.05%
Number/percentage of G's	31,863,700 / 24.29%
Number/percentage of N's	16,143 / 0.01%
GC Percentage	43.97%

2.3. Coverage

Mean	0.0424

Standard Deviation	0.358

2.4. Mapping Quality

Mean Mapping Quality	45.52

2.5. Mismatches and indels

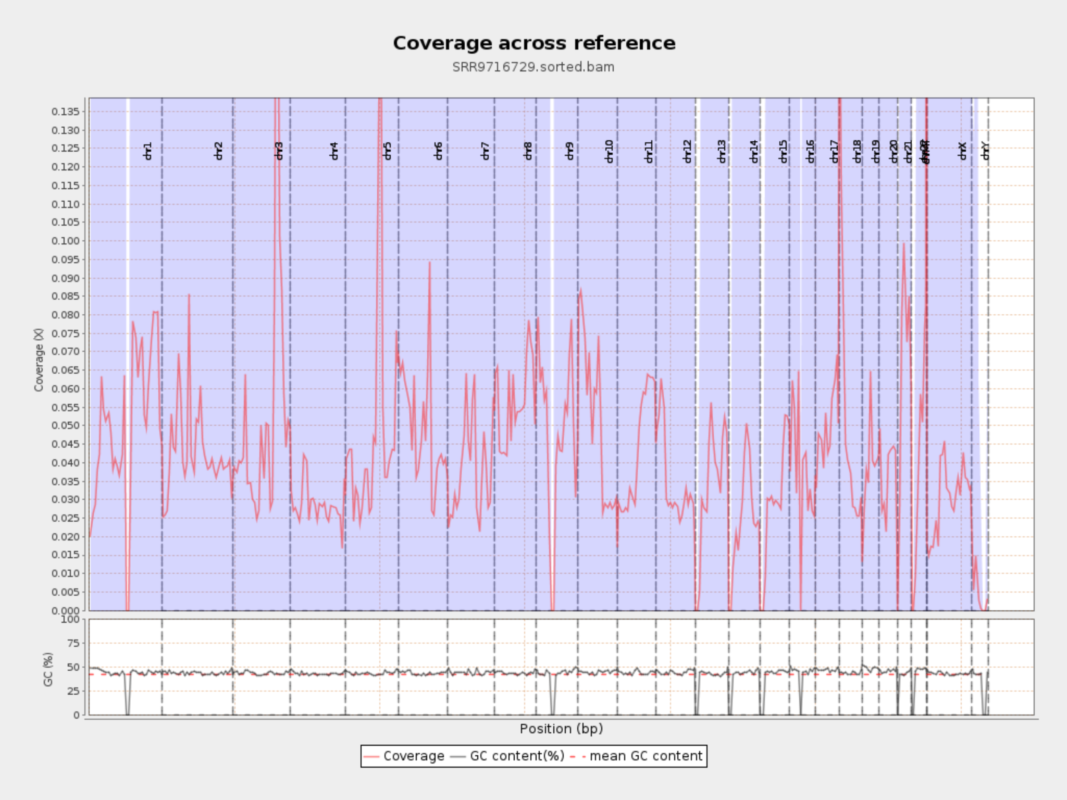
General error rate	0.73%
Mismatches	939,293
Insertions	9,950
Mapped reads with at least one insertion	0.57%
Deletions	27,830
Mapped reads with at least one deletion	1.59%
Homopolymer indels	42.09%

2.6. Chromosome stats

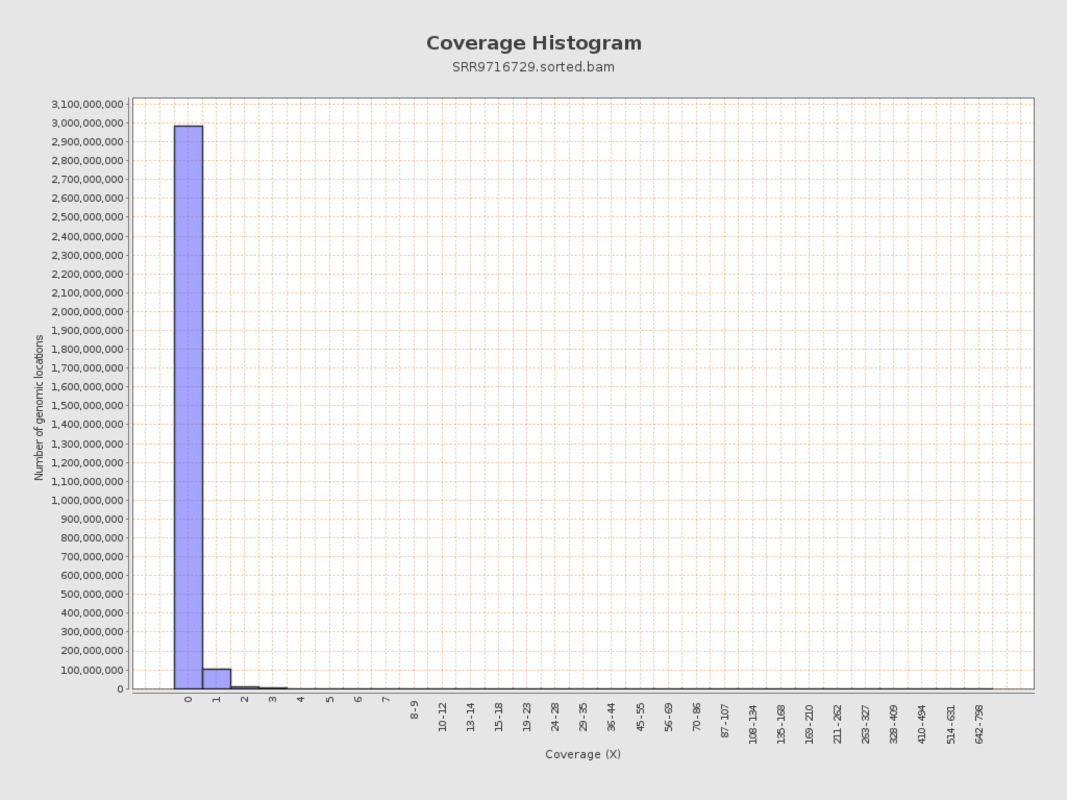
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12566836	0.0504	0.4849
chr2	243199373	10523873	0.0433	0.5841
chr3	198022430	10602508	0.0535	0.2664
chr4	191154276	5437669	0.0284	0.206
chr5	180915260	8906808	0.0492	0.2516
chr6	171115067	8616640	0.0504	0.2942
chr7	159138663	6168258	0.0388	0.4716

chr8	146364022	8369522	0.0572	0.4539
chr9	141213431	6730052	0.0477	0.3464
chr10	135534747	7139697	0.0527	0.37
chr11	135006516	5845599	0.0433	0.308
chr12	133851895	4625089	0.0346	0.2066
chr13	115169878	3913265	0.034	0.2035
chr14	107349540	2655042	0.0247	0.2059
chr15	102531392	2960632	0.0289	0.189
chr16	90354753	3367606	0.0373	0.2376
chr17	81195210	4033963	0.0497	0.2875
chr18	78077248	4071970	0.0522	0.6202
chr19	59128983	2340524	0.0396	0.4504
chr20	63025520	2296415	0.0364	0.2334
chr21	48129895	3125440	0.0649	0.2995
chr22	51304566	1895040	0.0369	0.2182
chrMT	16571	6618	0.3994	1.1988
chrX	155270560	4731317	0.0305	0.2355
chrY	59373566	274971	0.0046	0.14

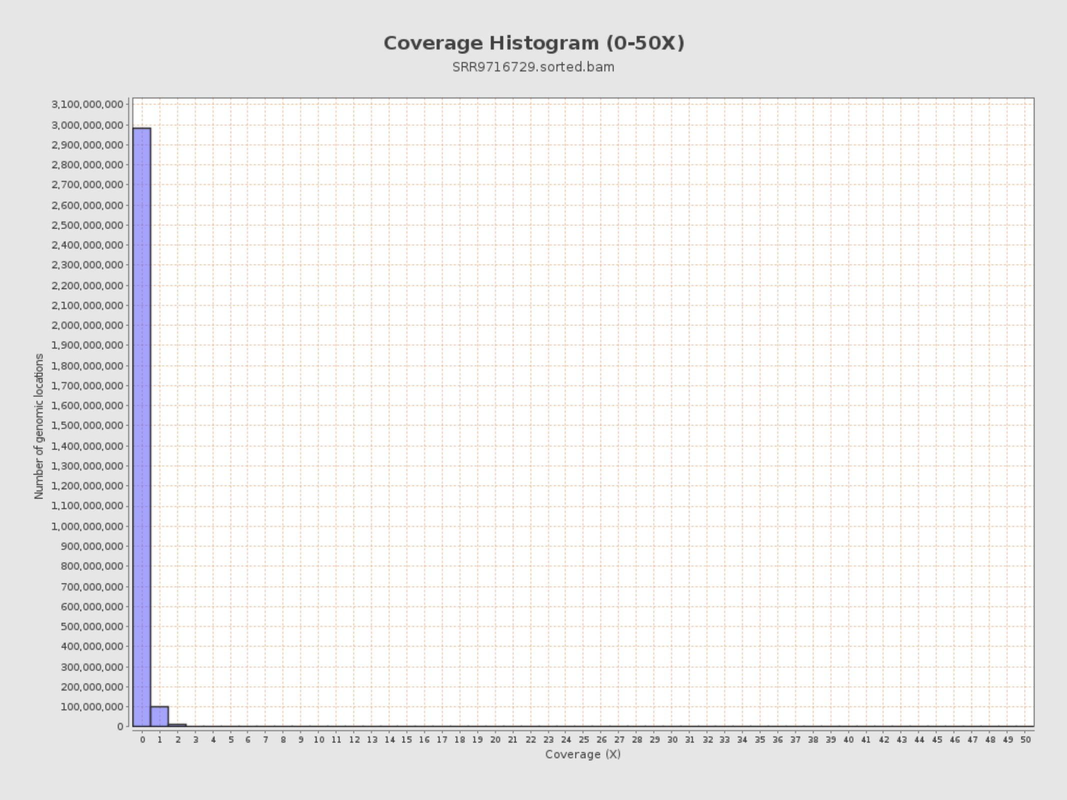
3. Results : Coverage across reference



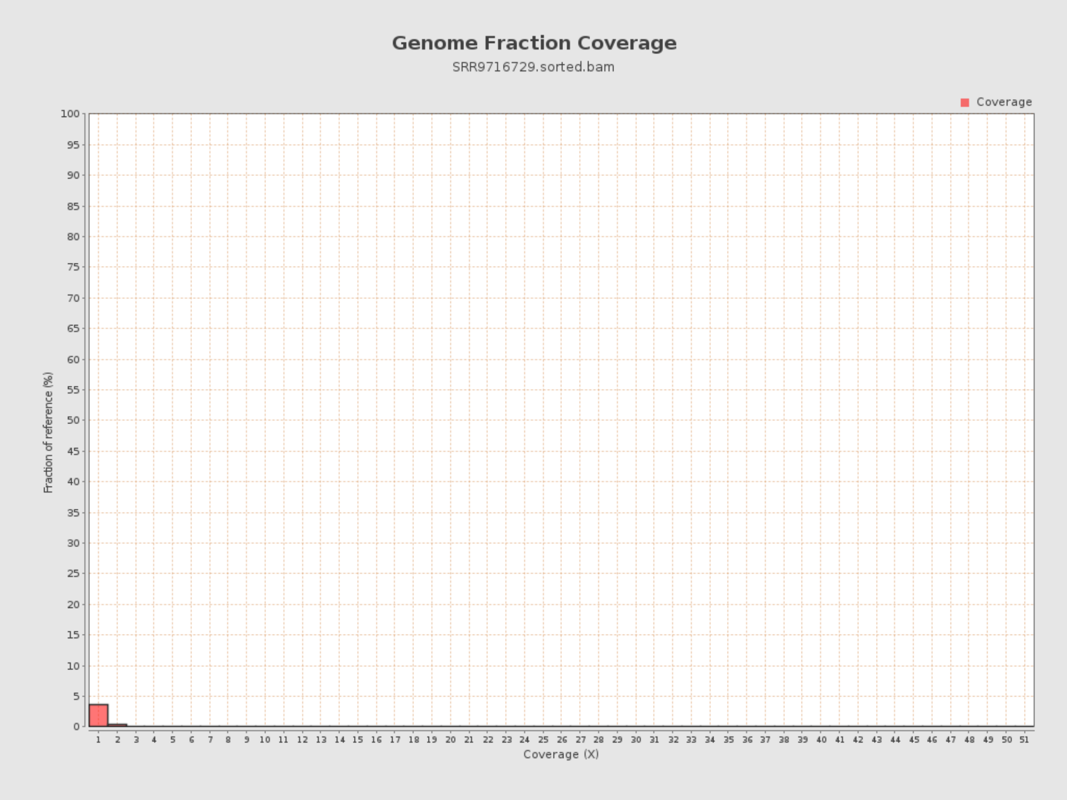
4. Results : Coverage Histogram



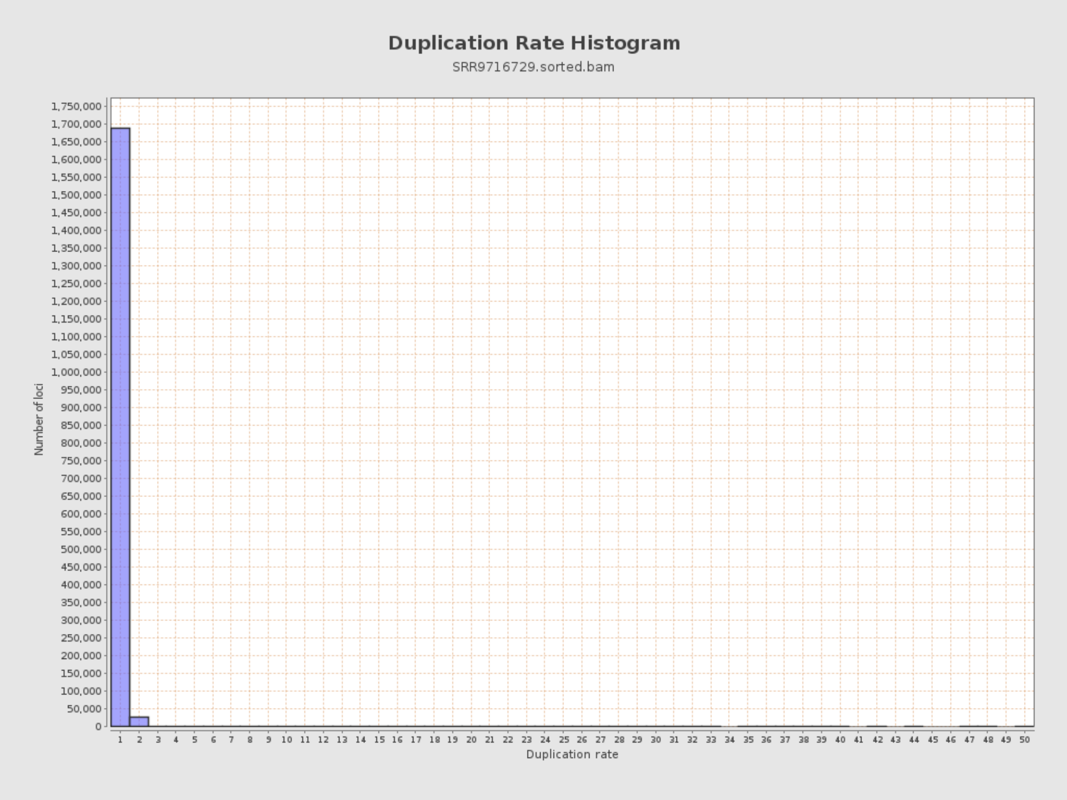
5. Results : Coverage Histogram (0-50X)



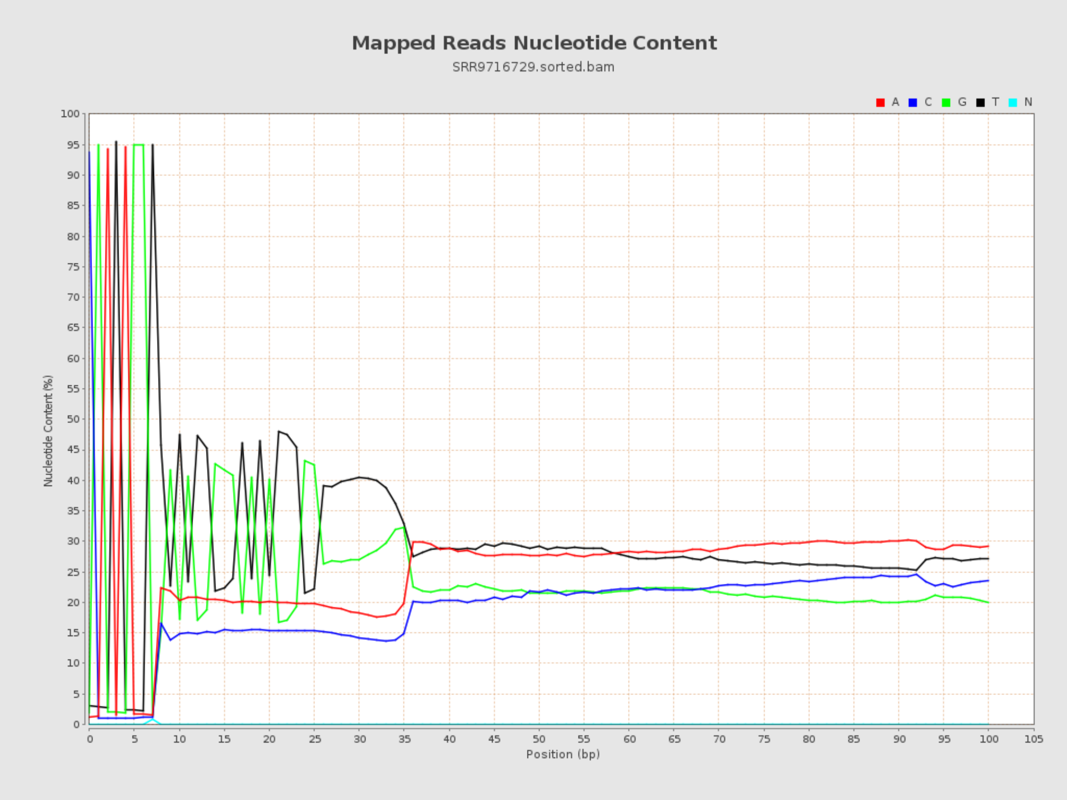
6. Results : Genome Fraction Coverage



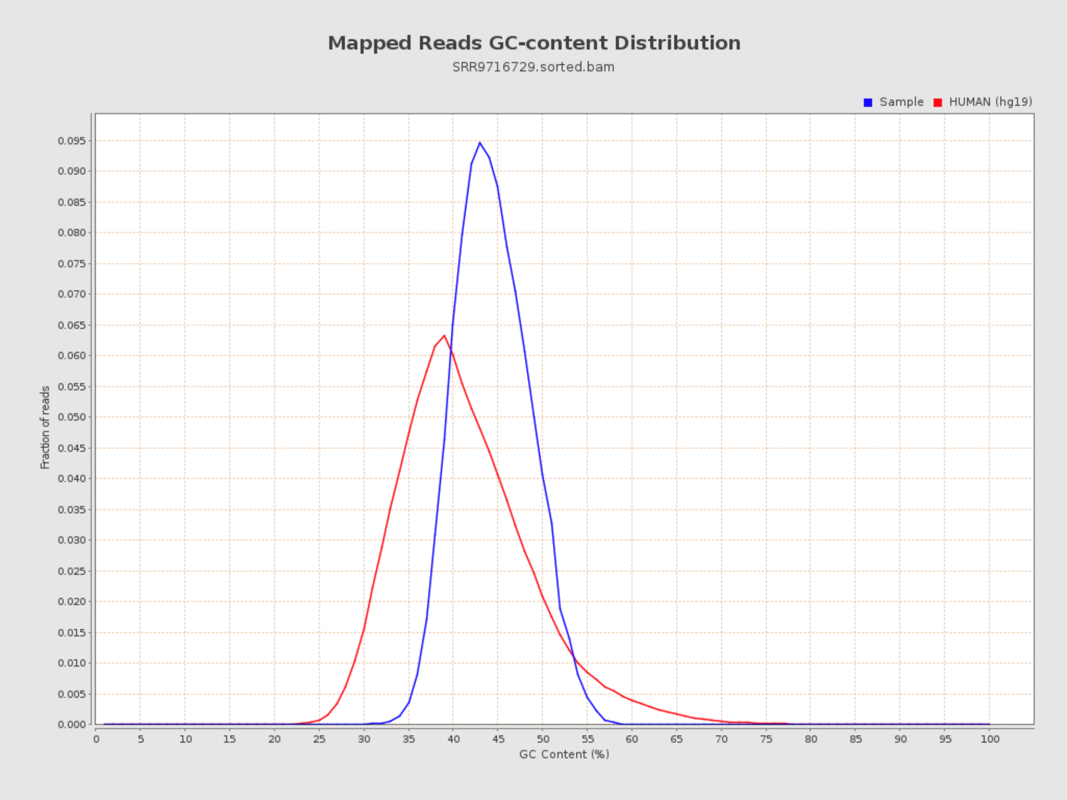
7. Results : Duplication Rate Histogram



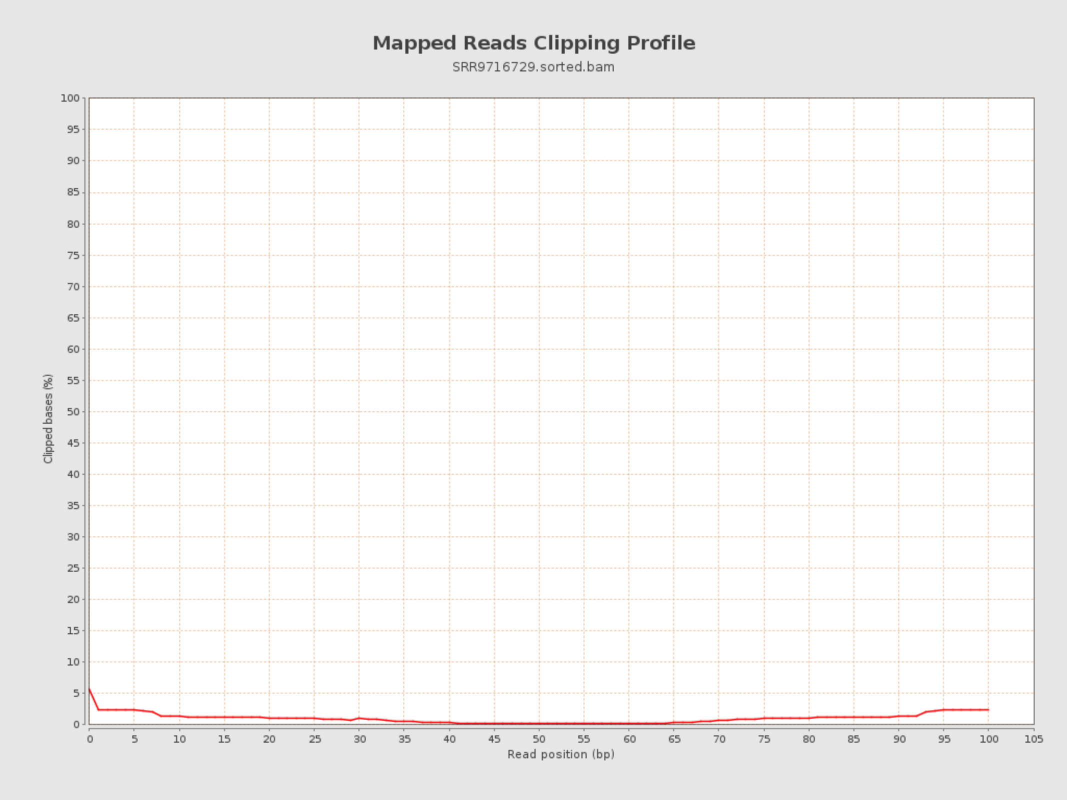
8. Results : Mapped Reads Nucleotide Content



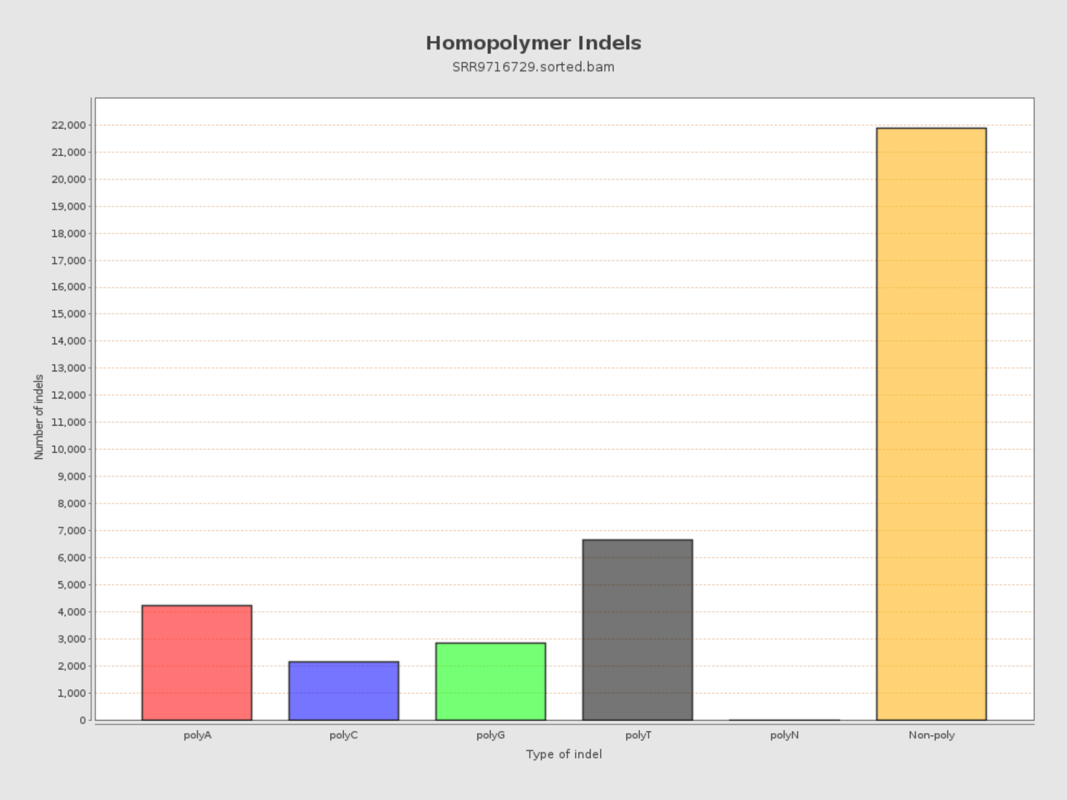
9. Results : Mapped Reads GC-content Distribution



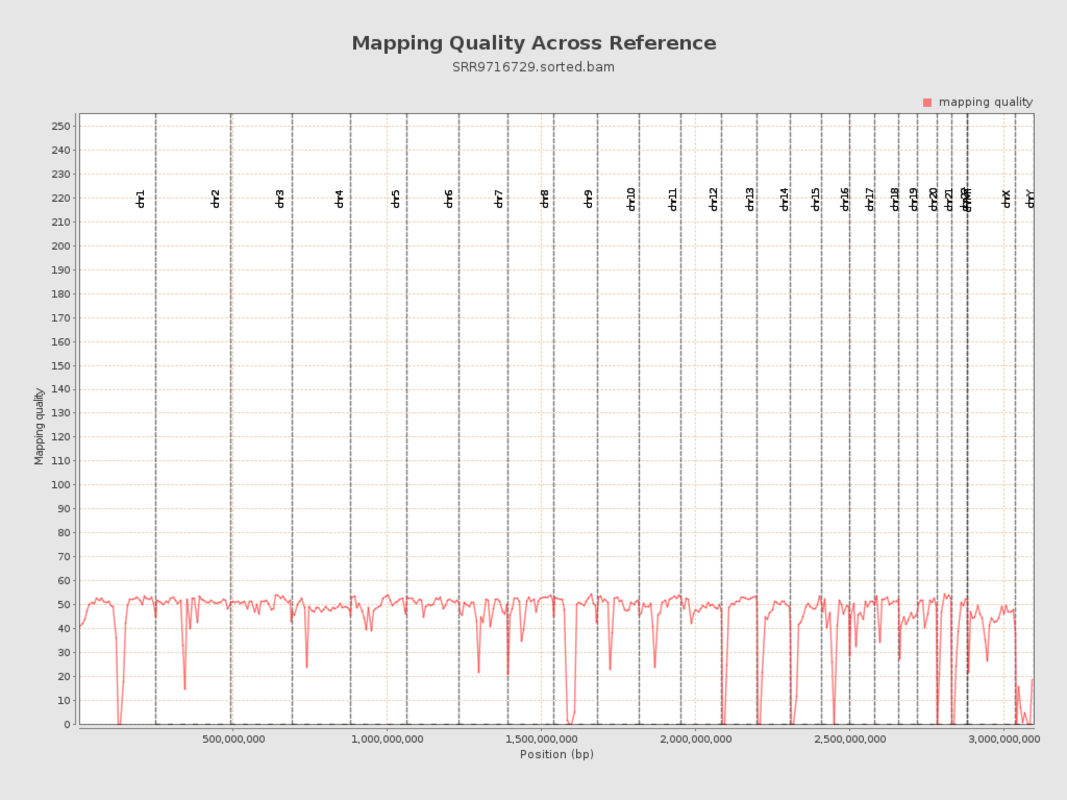
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram