Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 07:24:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716322.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_SRR9716322 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716322.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 07:24:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716322.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,668,425
Mapped reads	1,517,849 / 90.97%
Unmapped reads	150,576 / 9.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,146 / 0.43%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	54,342 / 3.26%
Duplication rate	2.68%
Clipped reads	1,520,903 / 91.16%

2.2. ACGT Content

Number/percentage of A's	22,742,067 / 25.74%
Number/percentage of C's	17,268,314 / 19.54%
Number/percentage of T's	27,637,478 / 31.28%
Number/percentage of G's	20,703,510 / 23.43%
Number/percentage of N's	2,541 / 0%
GC Percentage	42.98%

2.3. Coverage

Mean	0.0285

Standard Deviation	0.2727

2.4. Mapping Quality

Mean Mapping Quality	44.8

2.5. Mismatches and indels

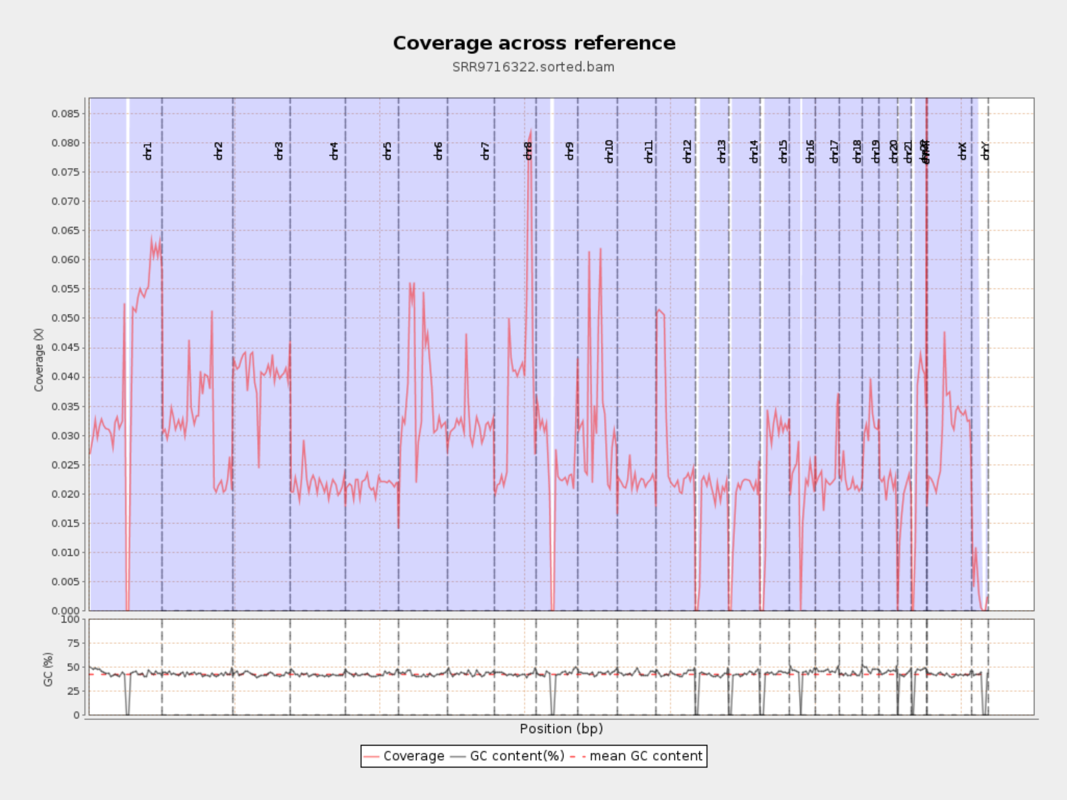
General error rate	0.5%
Mismatches	435,426
Insertions	5,632
Mapped reads with at least one insertion	0.37%
Deletions	16,357
Mapped reads with at least one deletion	1.07%
Homopolymer indels	43.63%

2.6. Chromosome stats

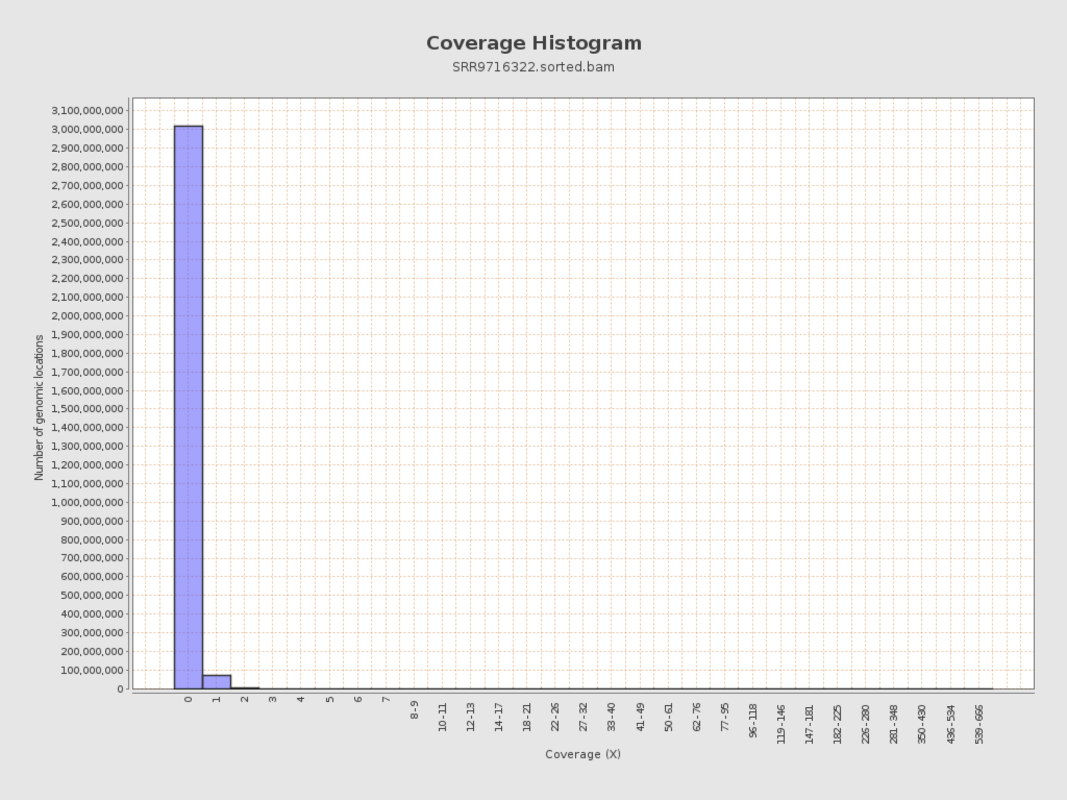
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10044006	0.0403	0.5213
chr2	243199373	7653110	0.0315	0.34
chr3	198022430	8035040	0.0406	0.2206
chr4	191154276	4127719	0.0216	0.1682
chr5	180915260	3895009	0.0215	0.162
chr6	171115067	6345220	0.0371	0.2876
chr7	159138663	5106706	0.0321	0.334

chr8	146364022	5837301	0.0399	0.2487
chr9	141213431	3321754	0.0235	0.2189
chr10	135534747	4544270	0.0335	0.2838
chr11	135006516	2988494	0.0221	0.2117
chr12	133851895	3916451	0.0293	0.1916
chr13	115169878	2029113	0.0176	0.1445
chr14	107349540	1930266	0.018	0.1594
chr15	102531392	2617635	0.0255	0.1761
chr16	90354753	1885459	0.0209	0.1752
chr17	81195210	1940601	0.0239	0.1747
chr18	78077248	1727499	0.0221	0.3874
chr19	59128983	1886988	0.0319	0.3522
chr20	63025520	1365131	0.0217	0.1625
chr21	48129895	825621	0.0172	0.1534
chr22	51304566	1428731	0.0278	0.1825
chrMT	16571	1730	0.1044	0.3484
chrX	155270560	4713391	0.0304	0.2146
chrY	59373566	212204	0.0036	0.0891

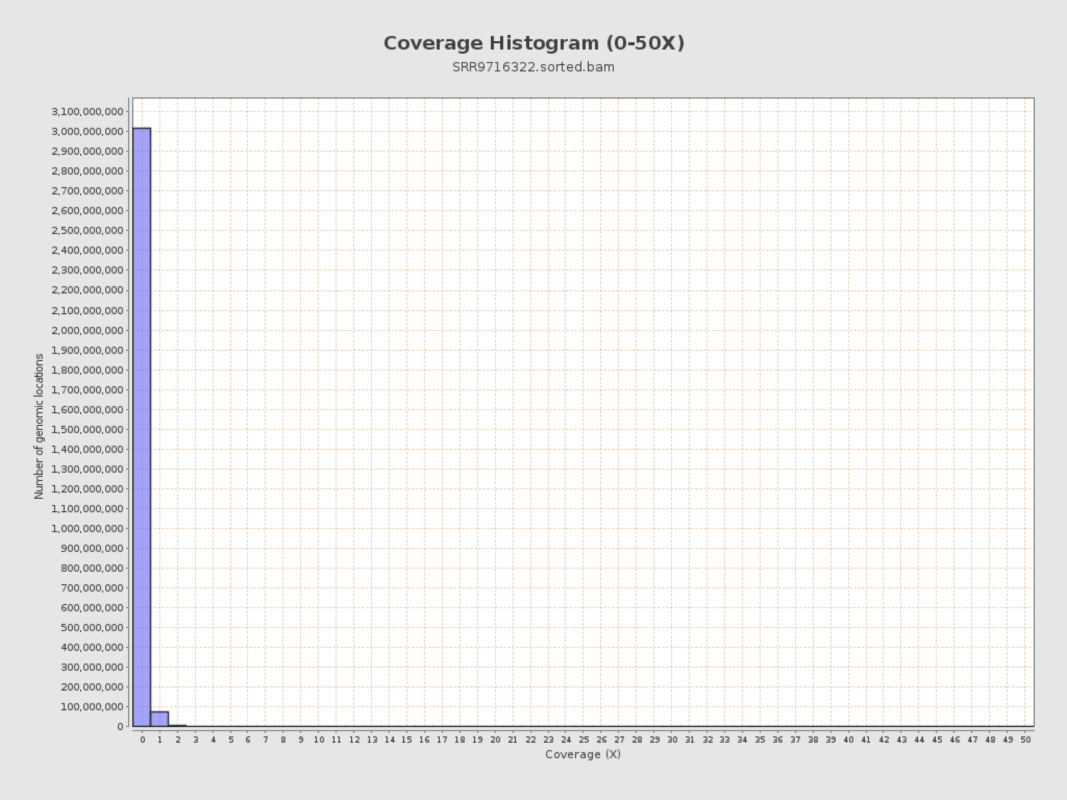
3. Results : Coverage across reference



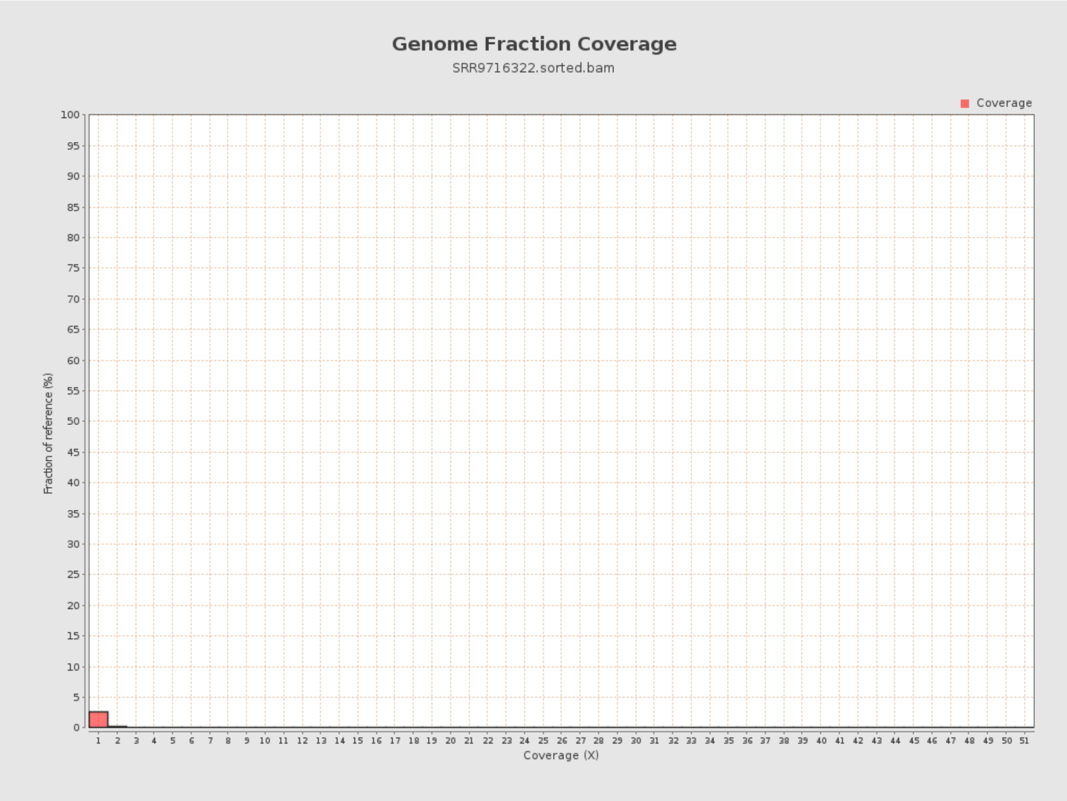
4. Results : Coverage Histogram



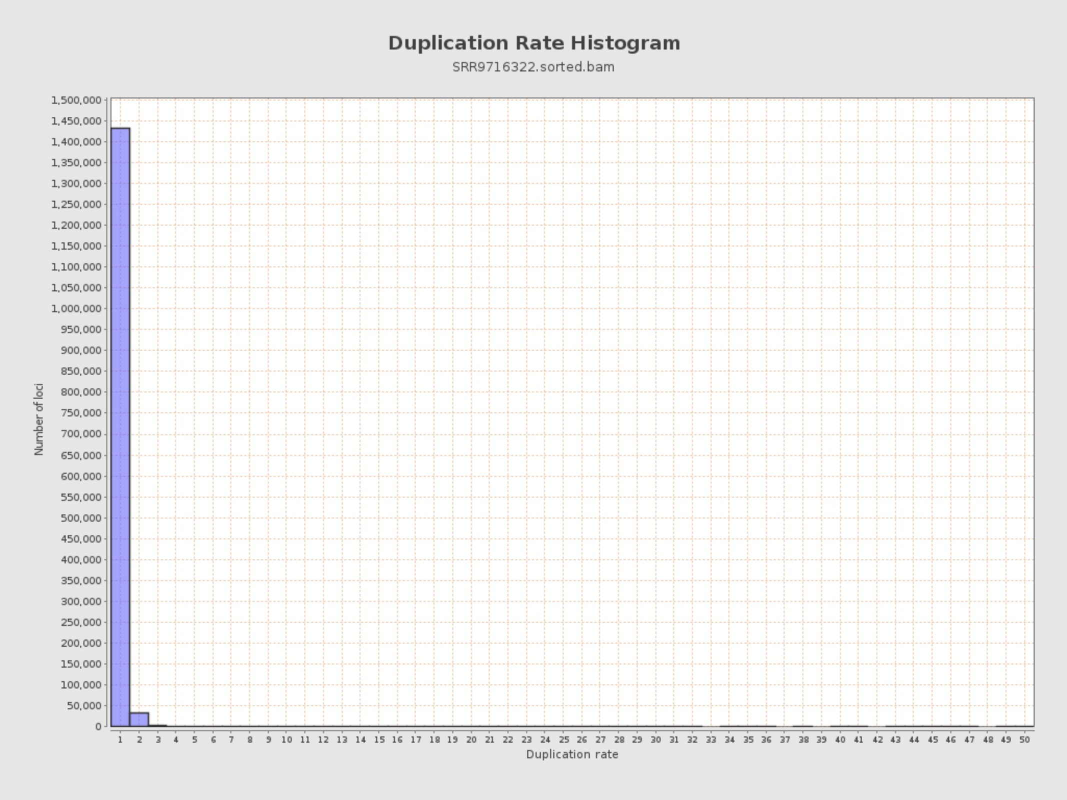
5. Results : Coverage Histogram (0-50X)



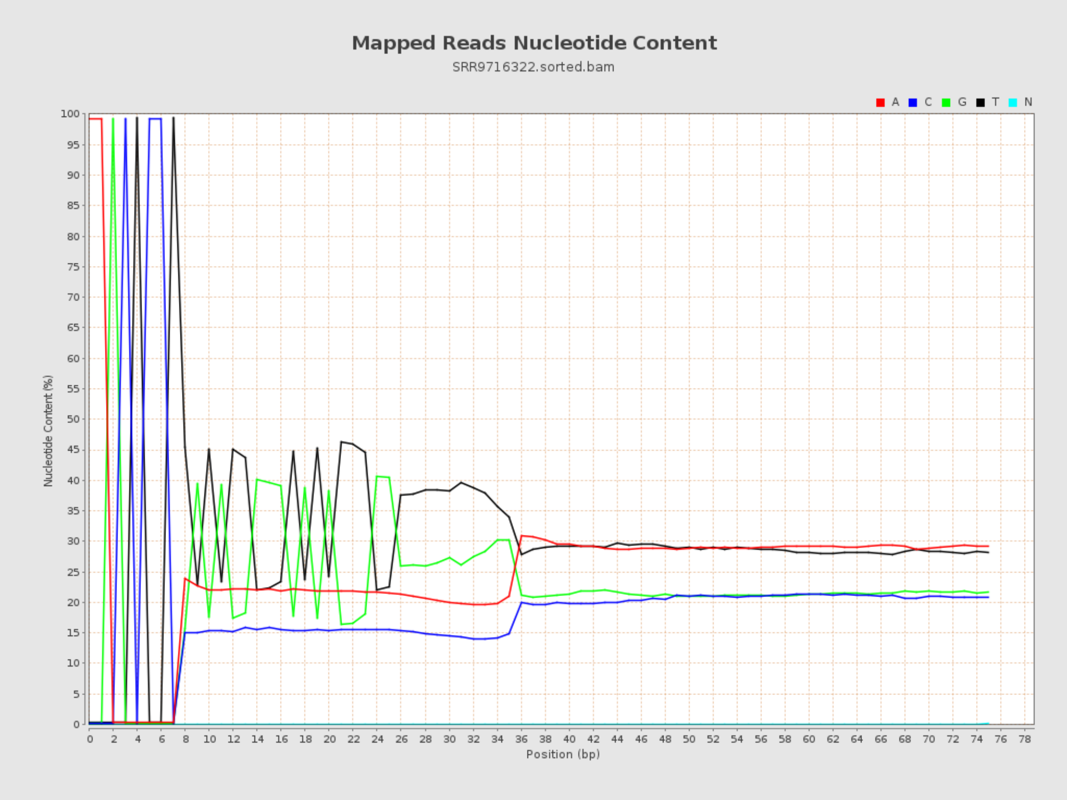
6. Results : Genome Fraction Coverage



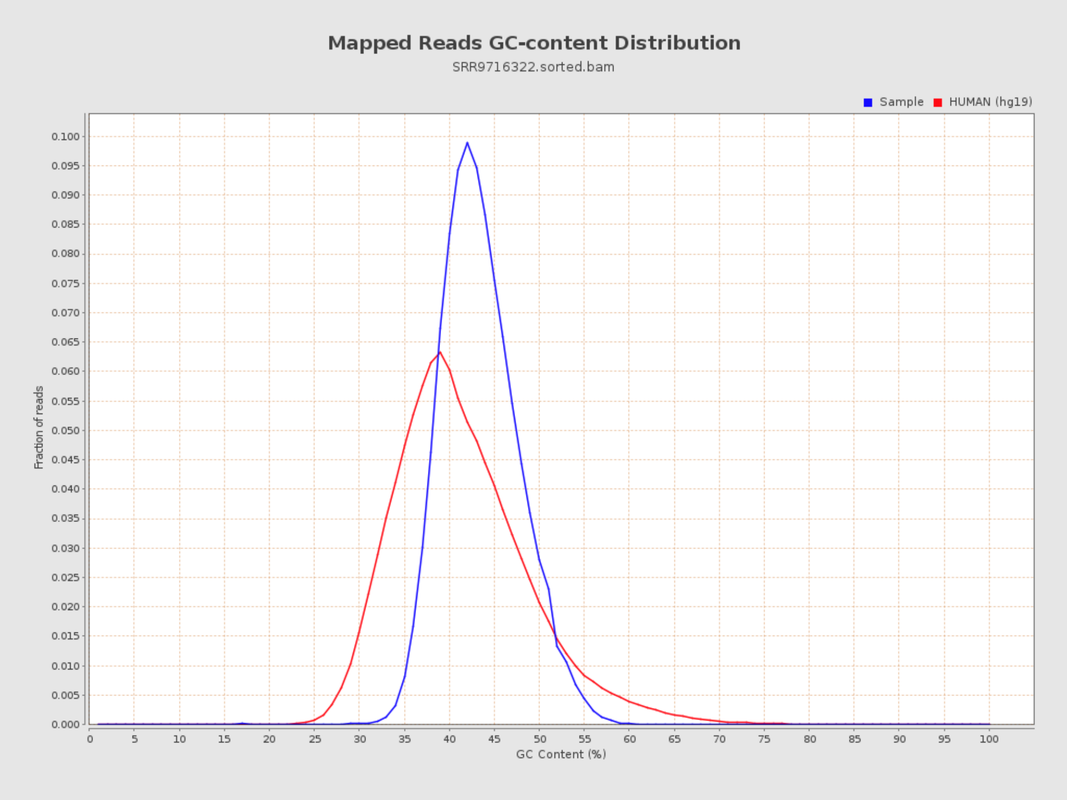
7. Results : Duplication Rate Histogram



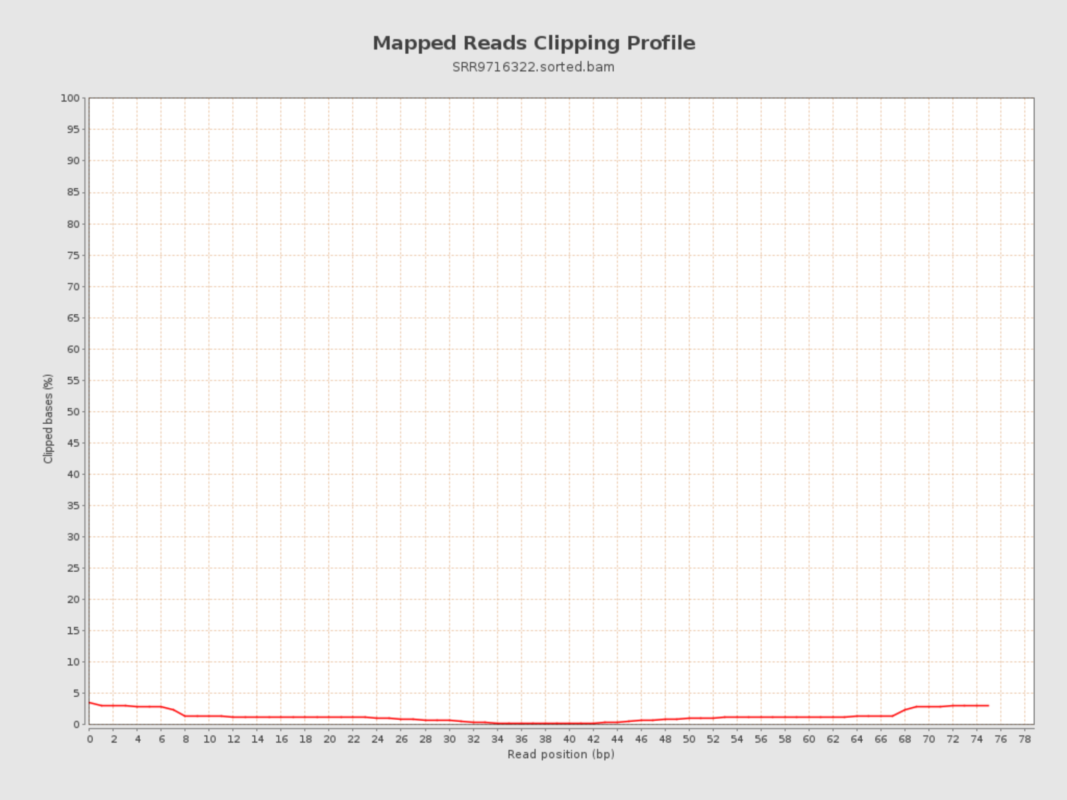
8. Results : Mapped Reads Nucleotide Content



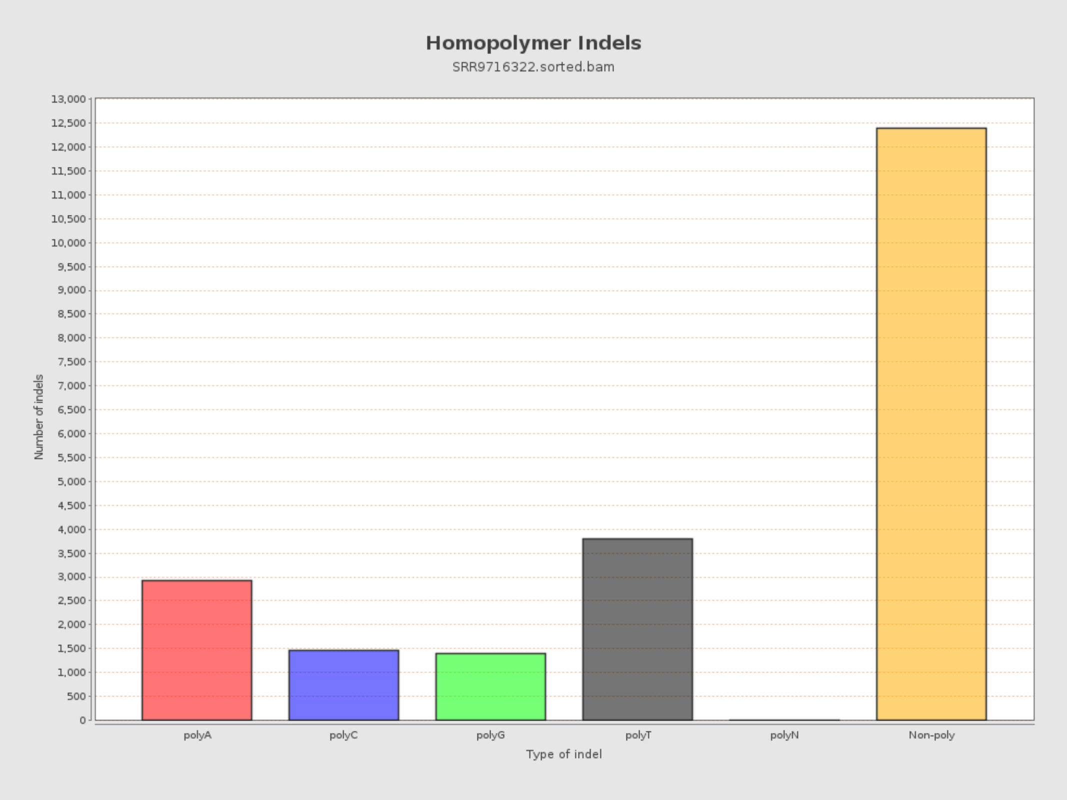
9. Results : Mapped Reads GC-content Distribution



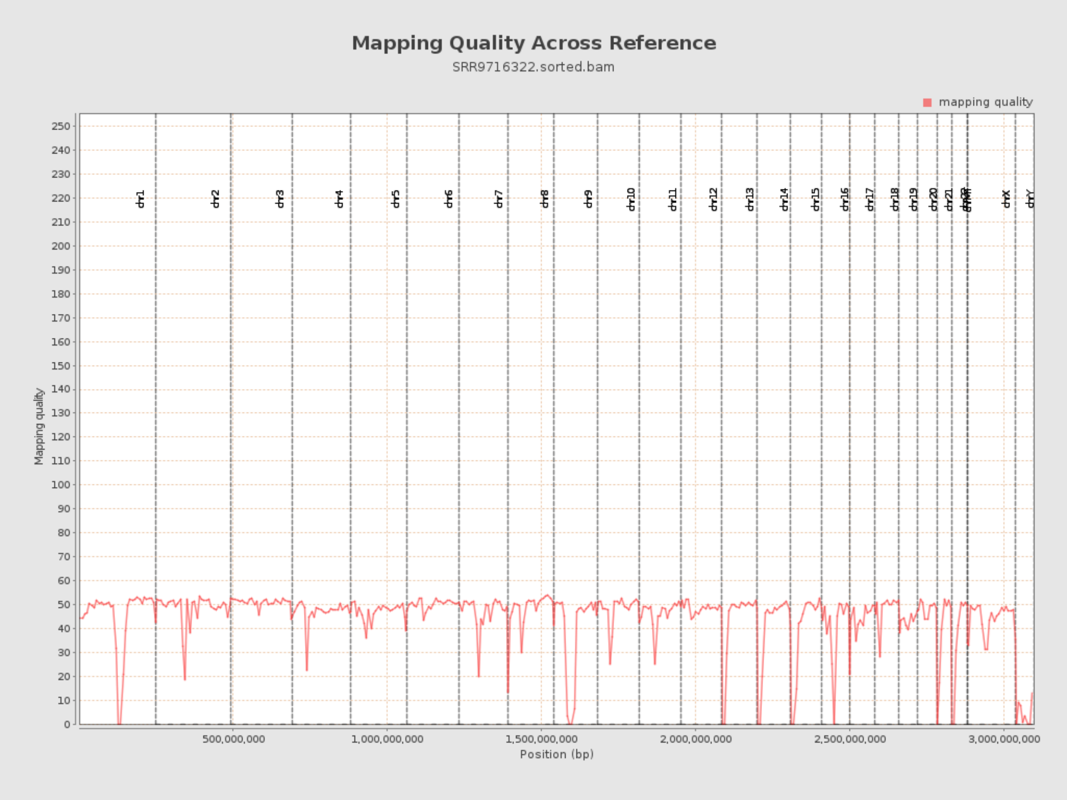
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram