Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 11:10:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716392.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_SRR9716392 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716392.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 11:10:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716392.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,578,242
Mapped reads	1,456,625 / 92.29%
Unmapped reads	121,617 / 7.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,659 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	52,751 / 3.34%
Duplication rate	2.61%
Clipped reads	1,457,748 / 92.37%

2.2. ACGT Content

Number/percentage of A's	20,328,954 / 23.81%
Number/percentage of C's	16,051,750 / 18.8%
Number/percentage of T's	27,370,691 / 32.06%
Number/percentage of G's	21,614,630 / 25.32%
Number/percentage of N's	1,819 / 0%
GC Percentage	44.12%

2.3. Coverage

Mean	0.0276

Standard Deviation	0.26

2.4. Mapping Quality

Mean Mapping Quality	44.85

2.5. Mismatches and indels

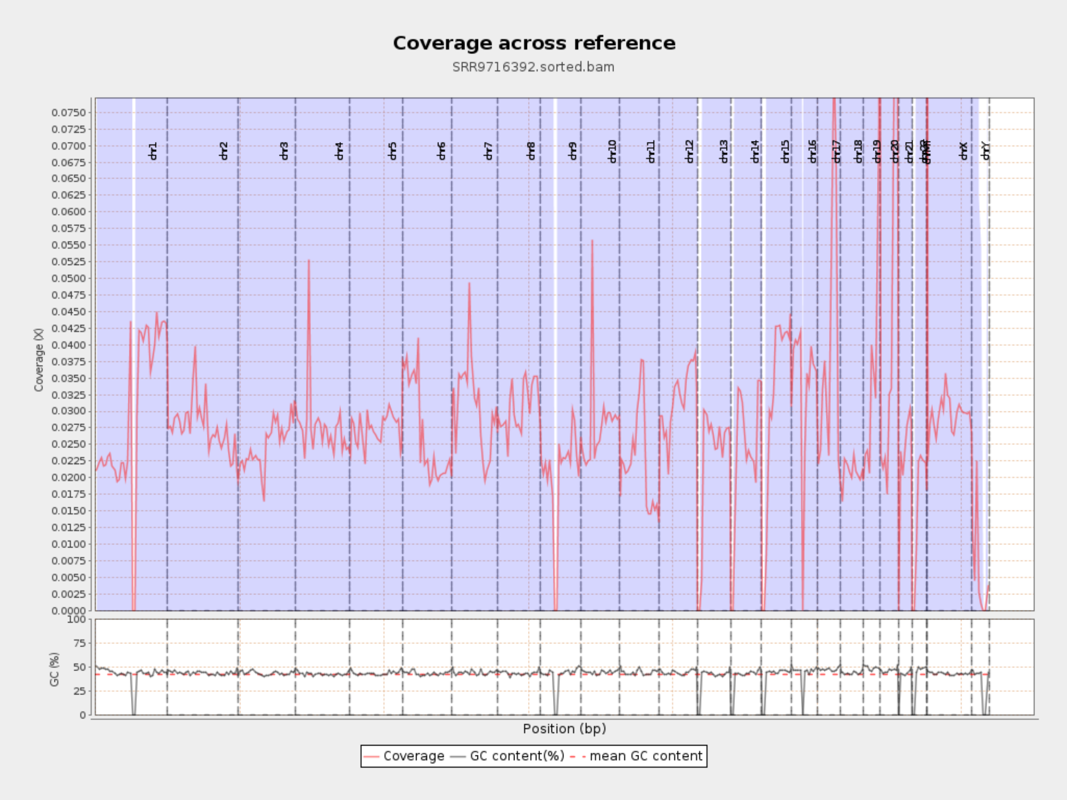
General error rate	0.52%
Mismatches	433,027
Insertions	6,197
Mapped reads with at least one insertion	0.42%
Deletions	17,558
Mapped reads with at least one deletion	1.2%
Homopolymer indels	42.99%

2.6. Chromosome stats

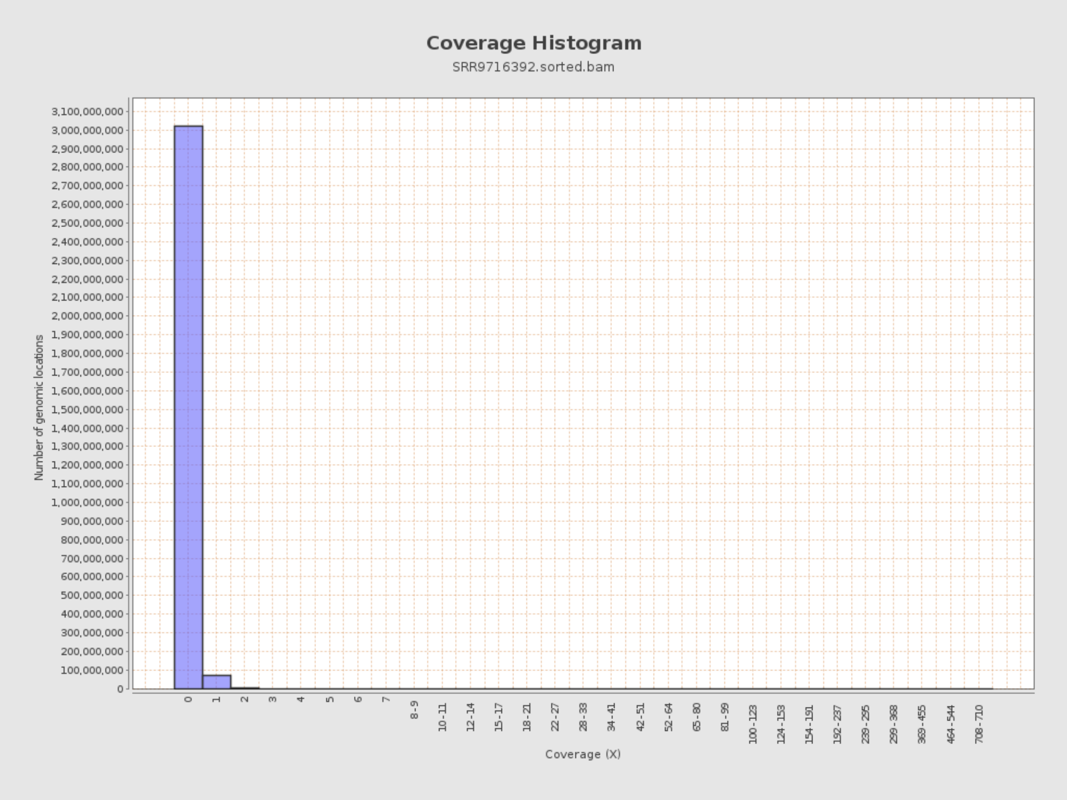
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7333526	0.0294	0.4132
chr2	243199373	6740106	0.0277	0.3505
chr3	198022430	4916376	0.0248	0.1717
chr4	191154276	5326081	0.0279	0.2192
chr5	180915260	4979345	0.0275	0.1791
chr6	171115067	4597001	0.0269	0.2003
chr7	159138663	4923230	0.0309	0.335

chr8	146364022	4495927	0.0307	0.3434
chr9	141213431	2885791	0.0204	0.1883
chr10	135534747	3811603	0.0281	0.2793
chr11	135006516	3059812	0.0227	0.1971
chr12	133851895	4253256	0.0318	0.1942
chr13	115169878	2581103	0.0224	0.162
chr14	107349540	2512173	0.0234	0.1687
chr15	102531392	3180439	0.031	0.1913
chr16	90354753	3011679	0.0333	0.2102
chr17	81195210	3205706	0.0395	0.2249
chr18	78077248	1610966	0.0206	0.3121
chr19	59128983	2236412	0.0378	0.3276
chr20	63025520	2891287	0.0459	0.2429
chr21	48129895	1120313	0.0233	0.2093
chr22	51304566	808210	0.0158	0.1363
chrMT	16571	7557	0.456	0.7187
chrX	155270560	4579140	0.0295	0.1978
chrY	59373566	329122	0.0055	0.2359

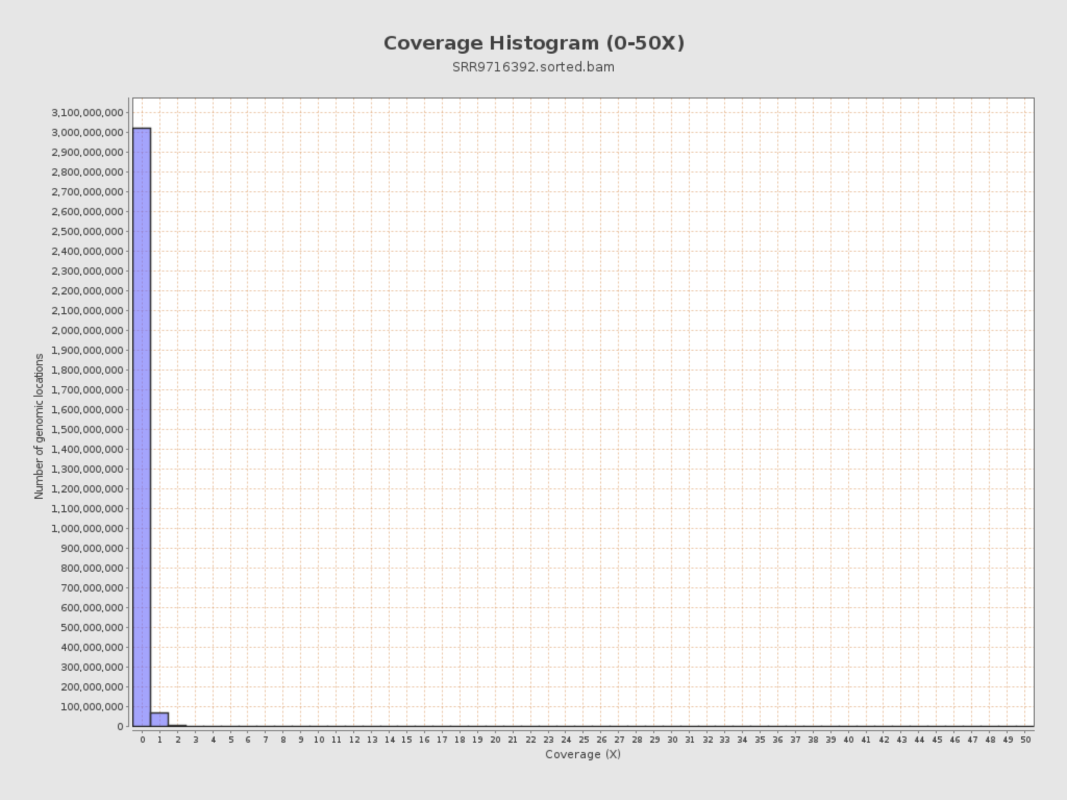
3. Results : Coverage across reference



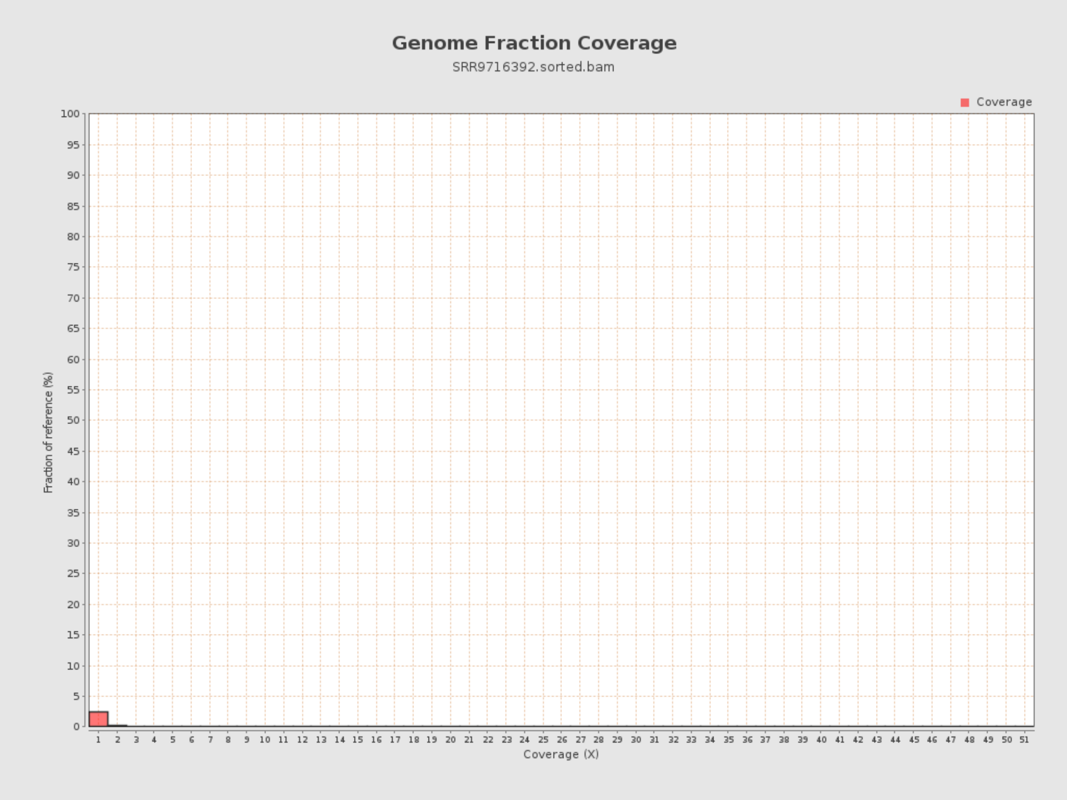
4. Results : Coverage Histogram



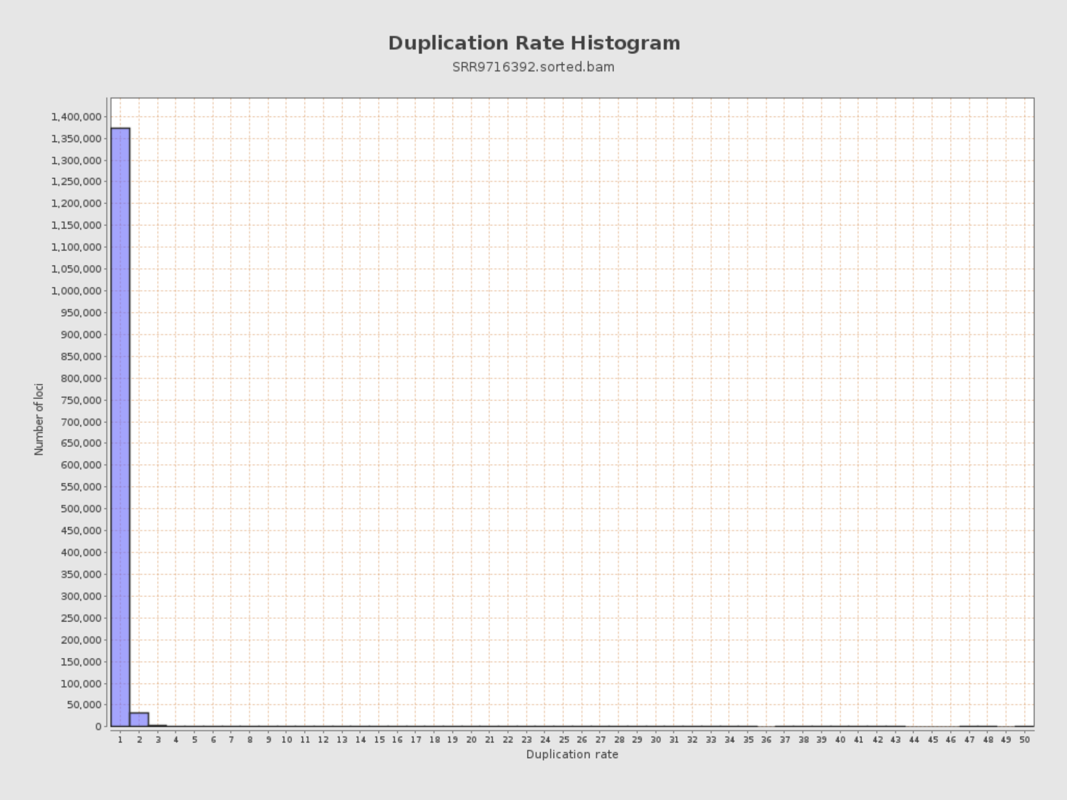
5. Results : Coverage Histogram (0-50X)



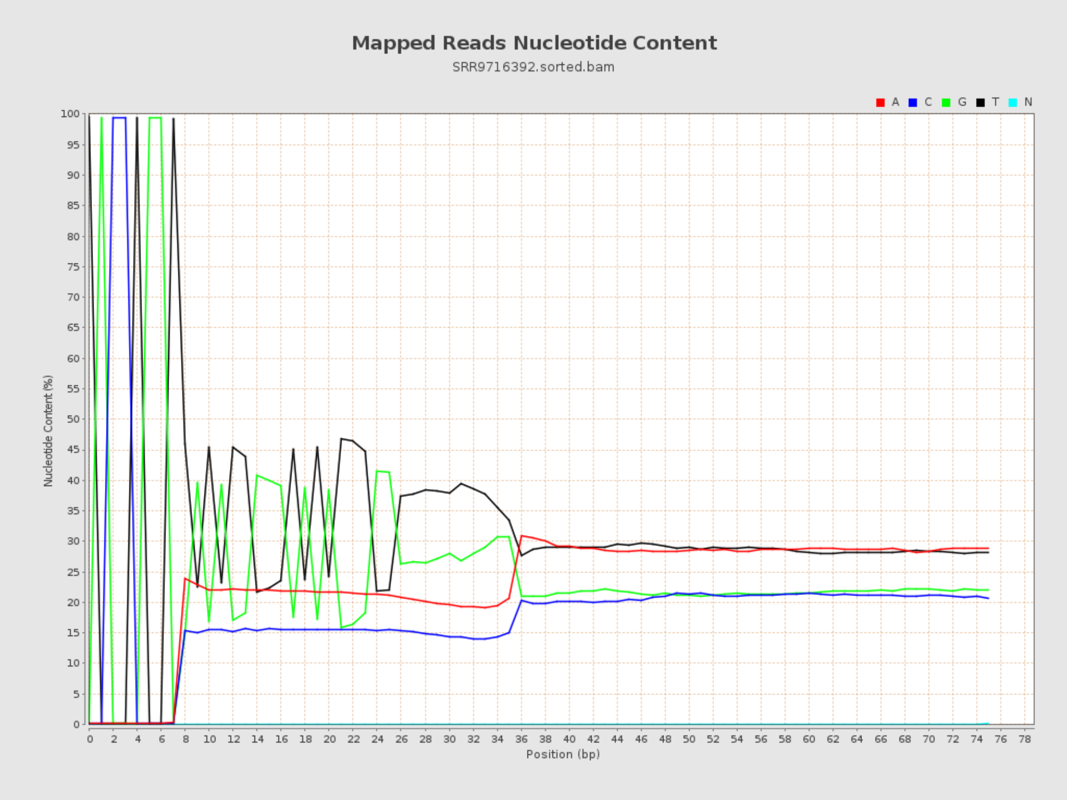
6. Results : Genome Fraction Coverage



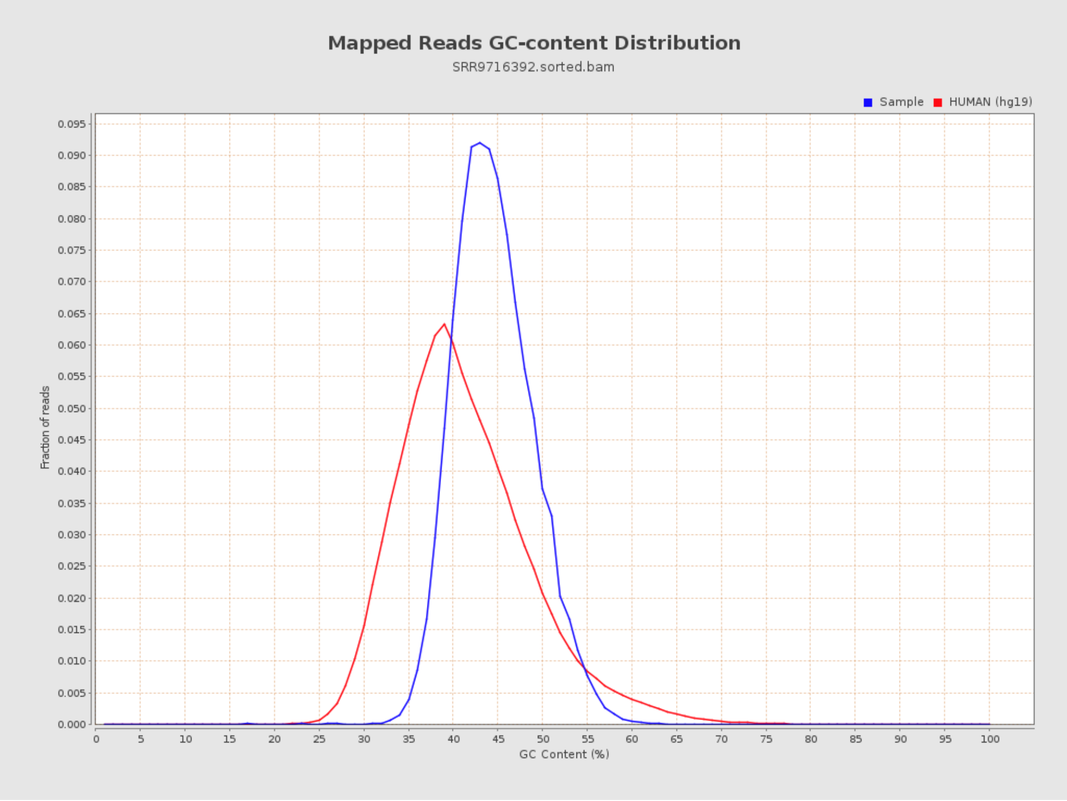
7. Results : Duplication Rate Histogram



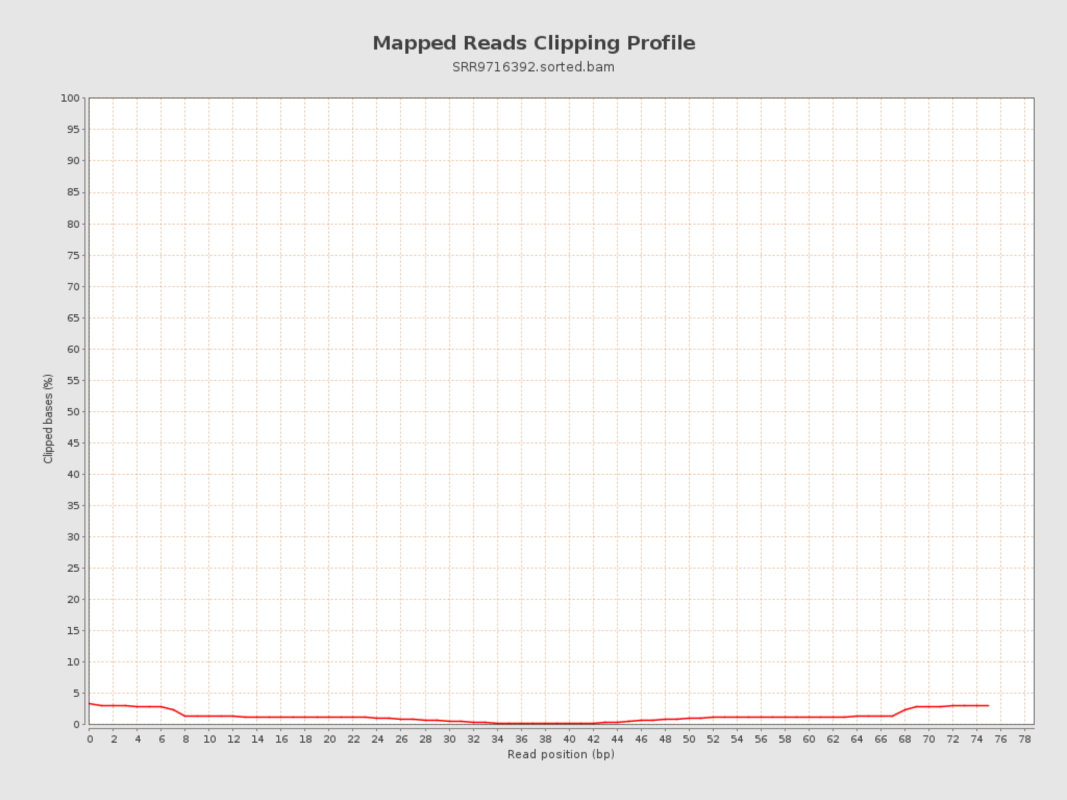
8. Results : Mapped Reads Nucleotide Content



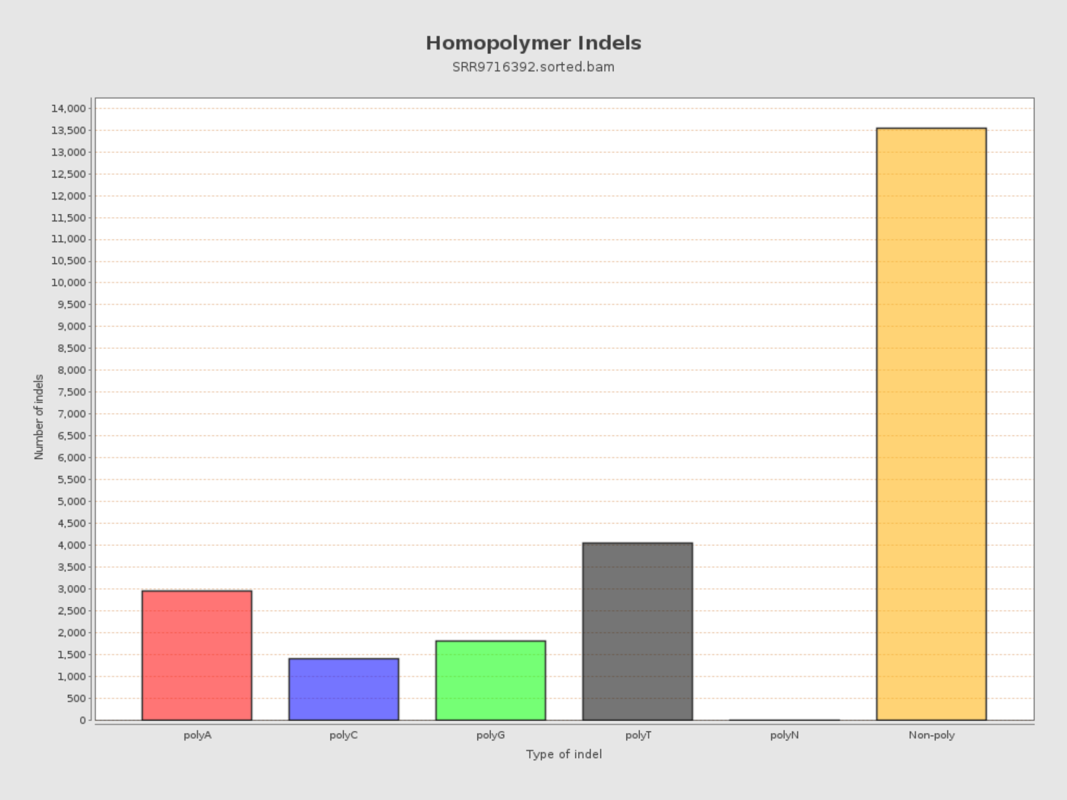
9. Results : Mapped Reads GC-content Distribution



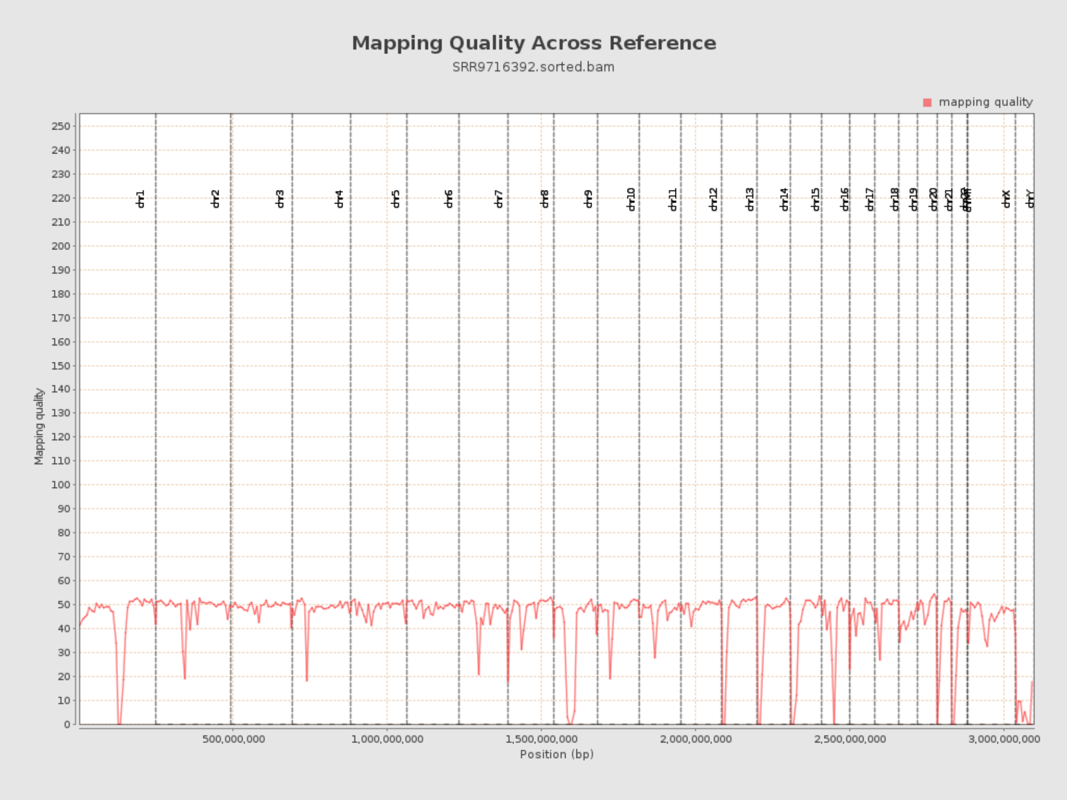
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram