Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 10:19:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716758.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_SRR9716758 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716758.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 10:19:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716758.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	405,669
Mapped reads	344,337 / 84.88%
Unmapped reads	61,332 / 15.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,496 / 0.37%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	5,021 / 1.24%
Duplication rate	1.15%
Clipped reads	344,818 / 85%

2.2. ACGT Content

Number/percentage of A's	5,328,936 / 26.27%
Number/percentage of C's	3,862,018 / 19.04%
Number/percentage of T's	6,122,085 / 30.18%
Number/percentage of G's	4,973,071 / 24.51%
Number/percentage of N's	543 / 0%
GC Percentage	43.55%

2.3. Coverage

Mean	0.0066

Standard Deviation	0.0937

2.4. Mapping Quality

Mean Mapping Quality	45.71

2.5. Mismatches and indels

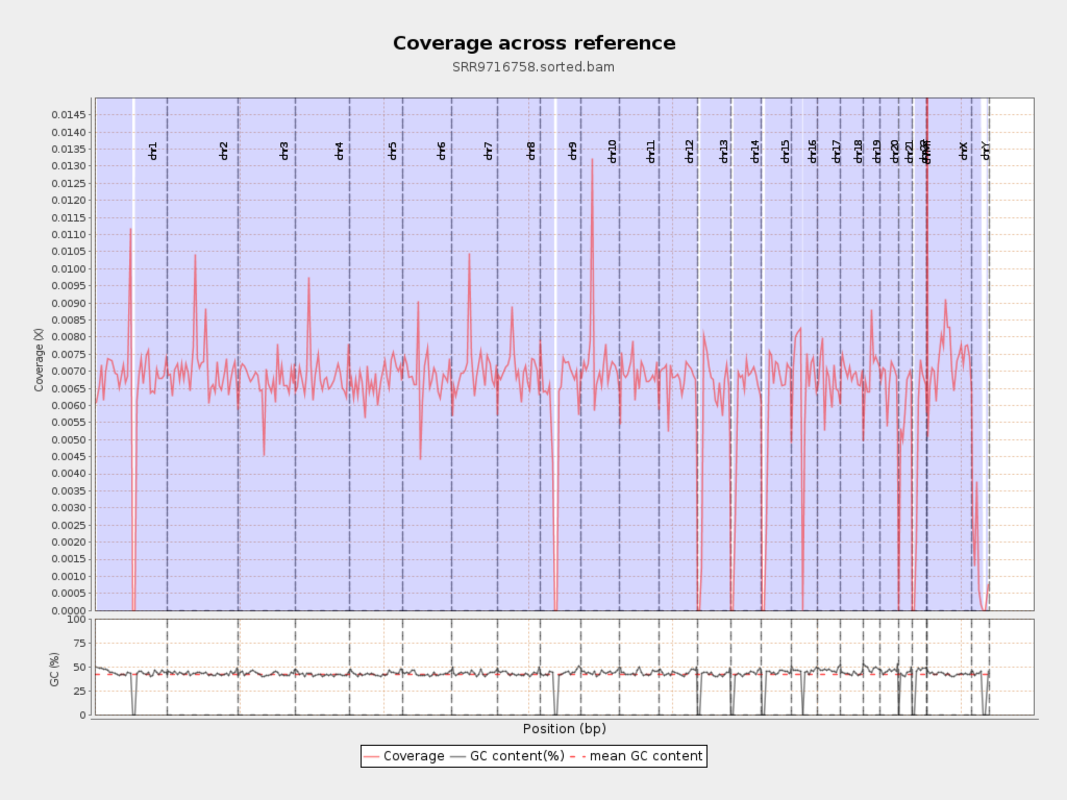
General error rate	0.52%
Mismatches	102,328
Insertions	1,589
Mapped reads with at least one insertion	0.46%
Deletions	3,985
Mapped reads with at least one deletion	1.15%
Homopolymer indels	43%

2.6. Chromosome stats

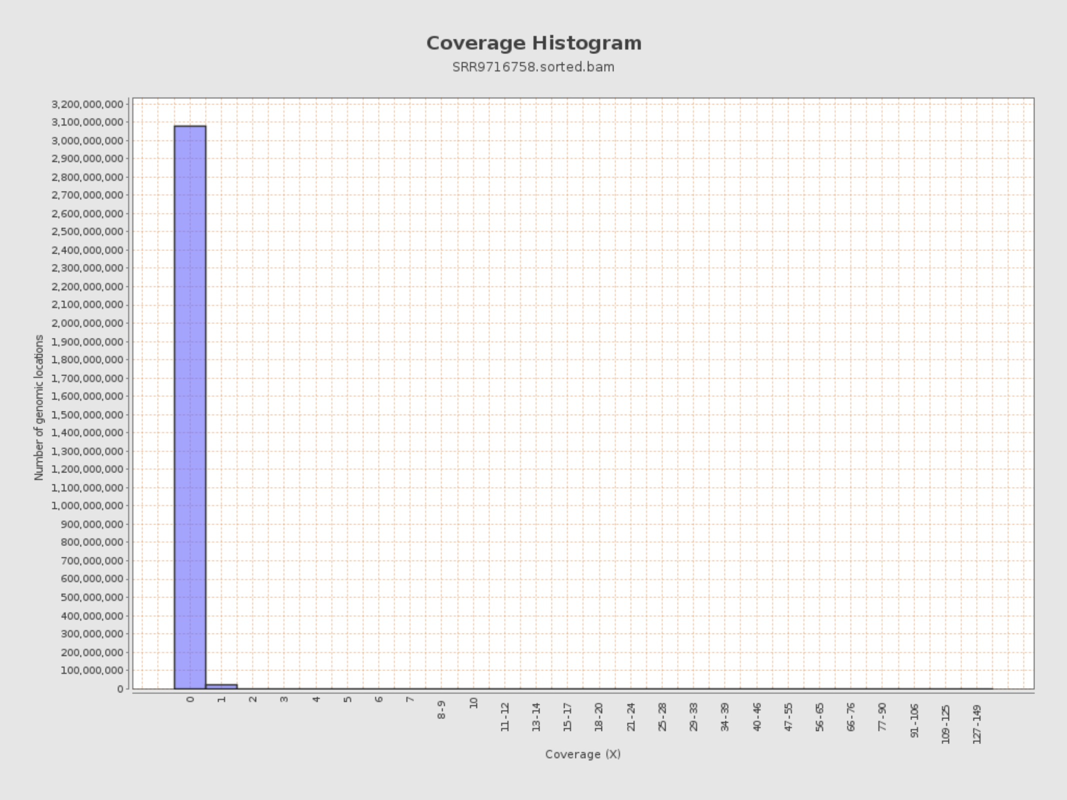
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1639839	0.0066	0.1345
chr2	243199373	1717616	0.0071	0.1025
chr3	198022430	1327559	0.0067	0.0839
chr4	191154276	1317174	0.0069	0.0867
chr5	180915260	1222419	0.0068	0.0842
chr6	171115067	1170451	0.0068	0.0891
chr7	159138663	1126332	0.0071	0.1028

chr8	146364022	1031982	0.0071	0.0969
chr9	141213431	833590	0.0059	0.0843
chr10	135534747	997277	0.0074	0.0999
chr11	135006516	936455	0.0069	0.0908
chr12	133851895	910104	0.0068	0.0848
chr13	115169878	650394	0.0056	0.0768
chr14	107349540	607164	0.0057	0.0779
chr15	102531392	585155	0.0057	0.0775
chr16	90354753	584648	0.0065	0.0844
chr17	81195210	543856	0.0067	0.0857
chr18	78077248	543014	0.007	0.1073
chr19	59128983	417963	0.0071	0.1094
chr20	63025520	420448	0.0067	0.0841
chr21	48129895	264293	0.0055	0.0776
chr22	51304566	237478	0.0046	0.0695
chrMT	16571	906	0.0547	0.2382
chrX	155270560	1141957	0.0074	0.09
chrY	59373566	64976	0.0011	0.0415

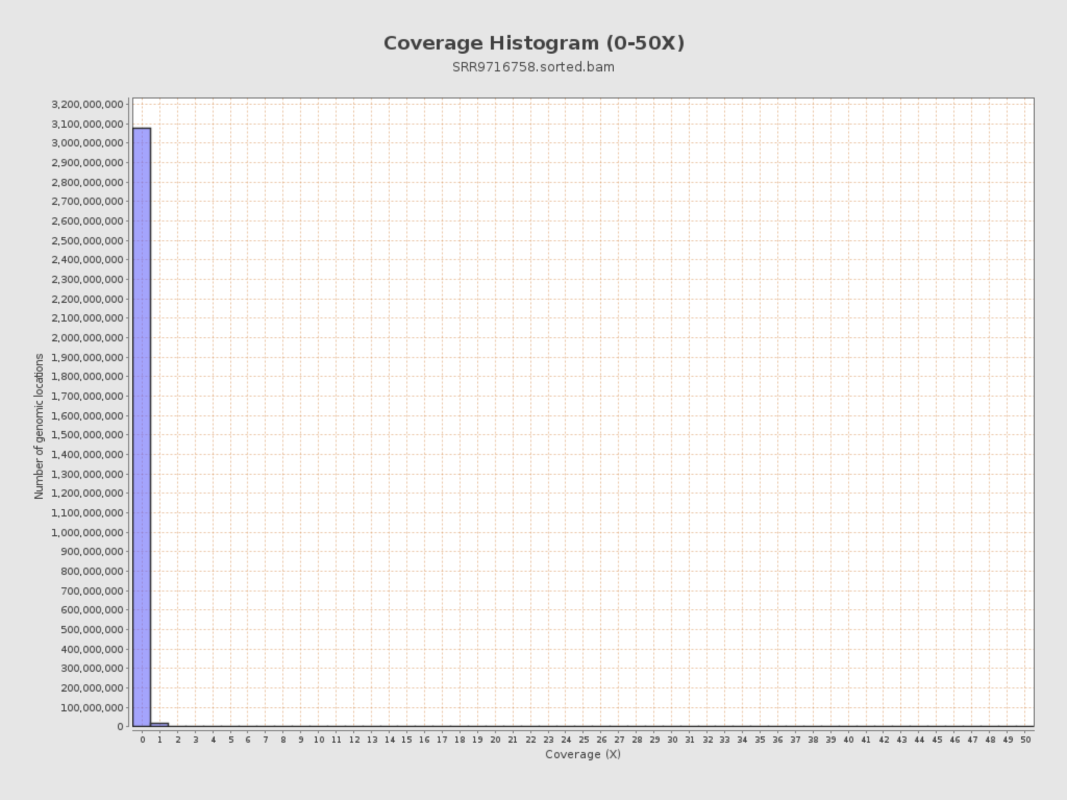
3. Results : Coverage across reference



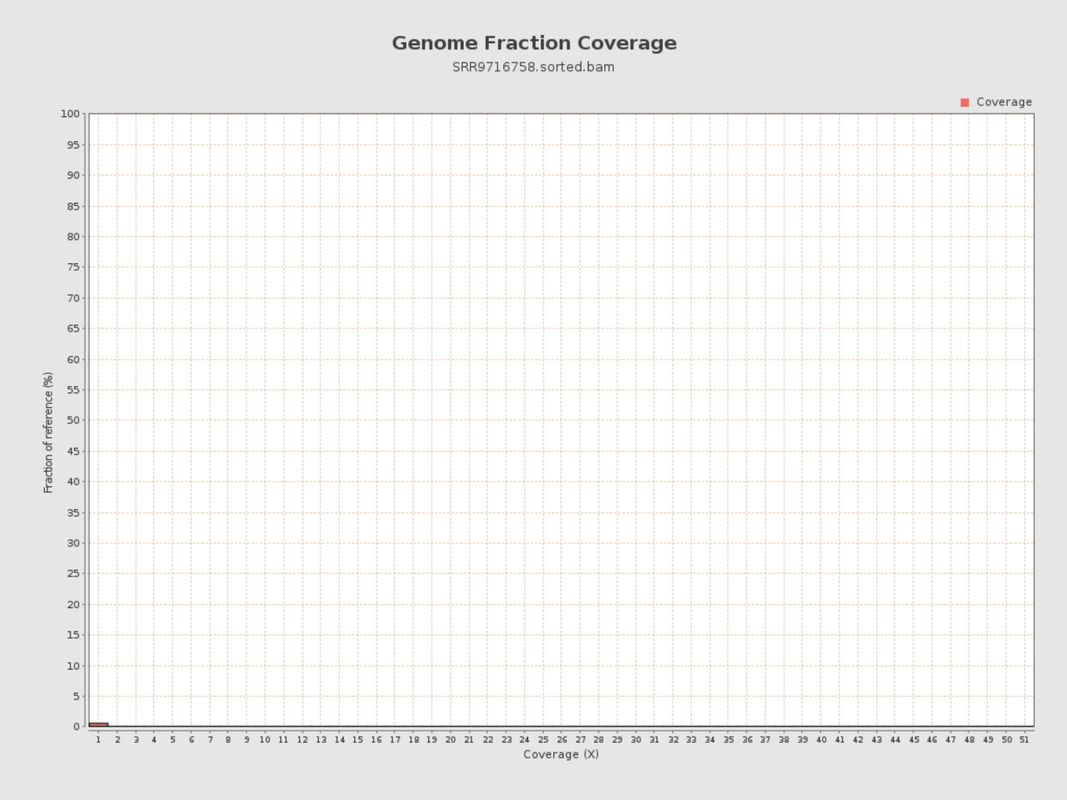
4. Results : Coverage Histogram



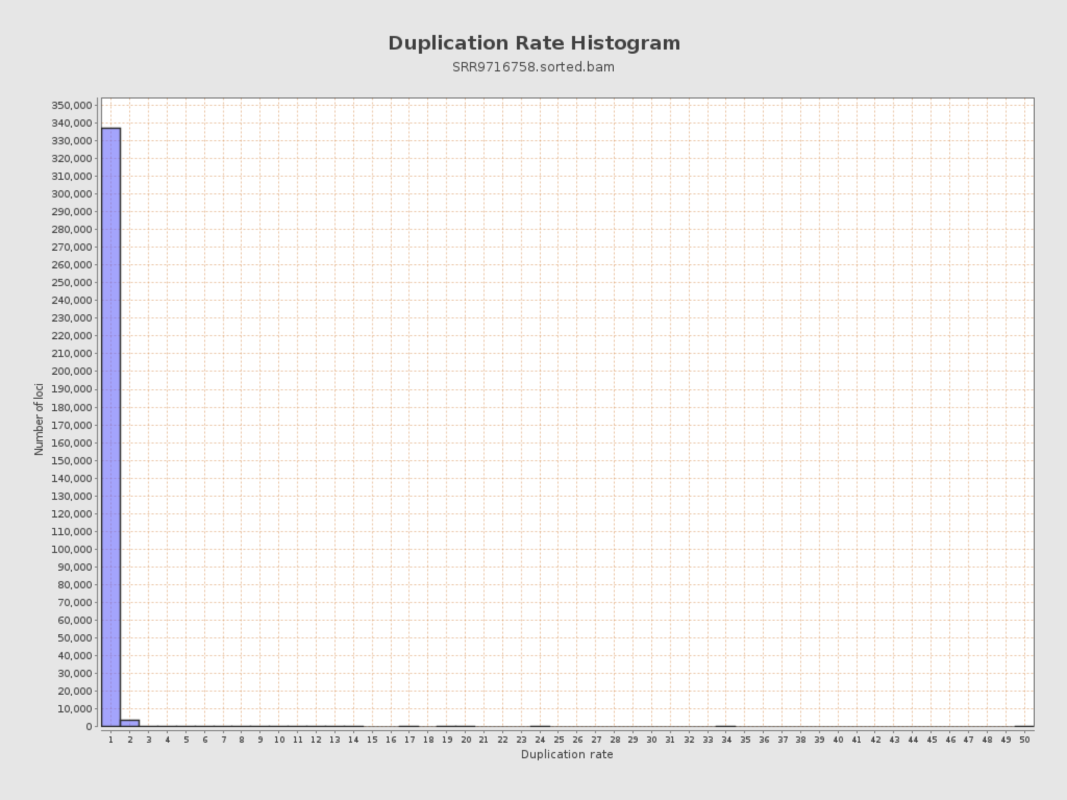
5. Results : Coverage Histogram (0-50X)



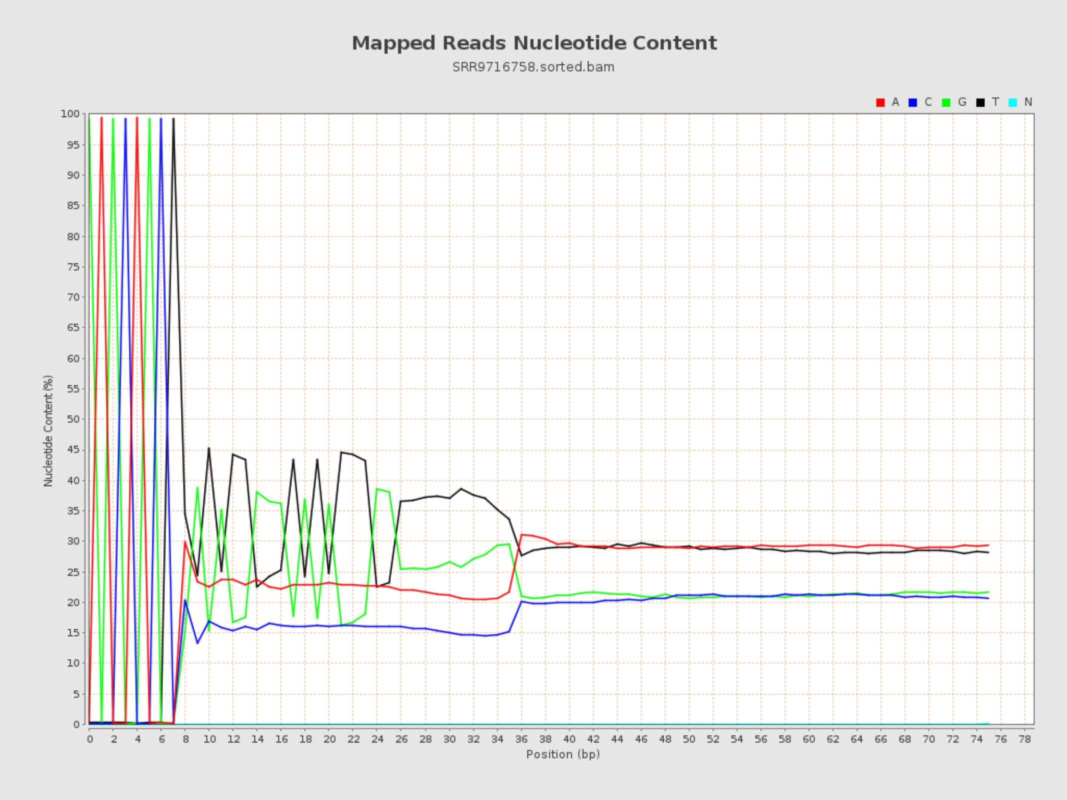
6. Results : Genome Fraction Coverage



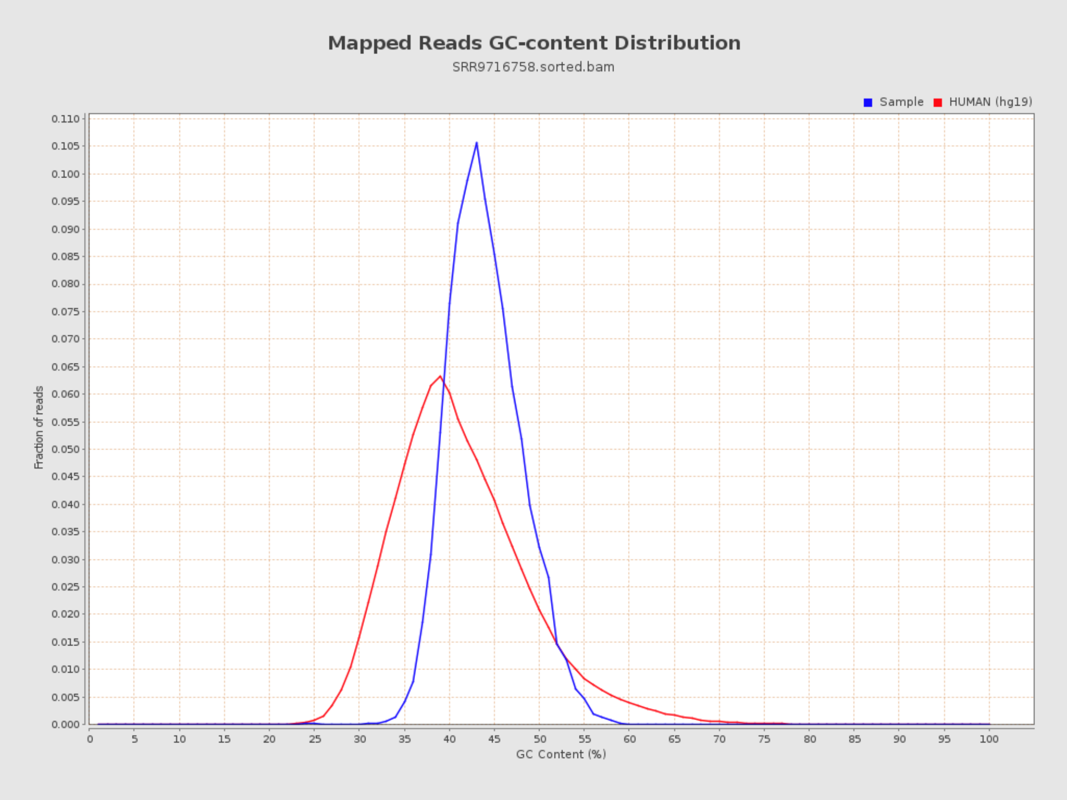
7. Results : Duplication Rate Histogram



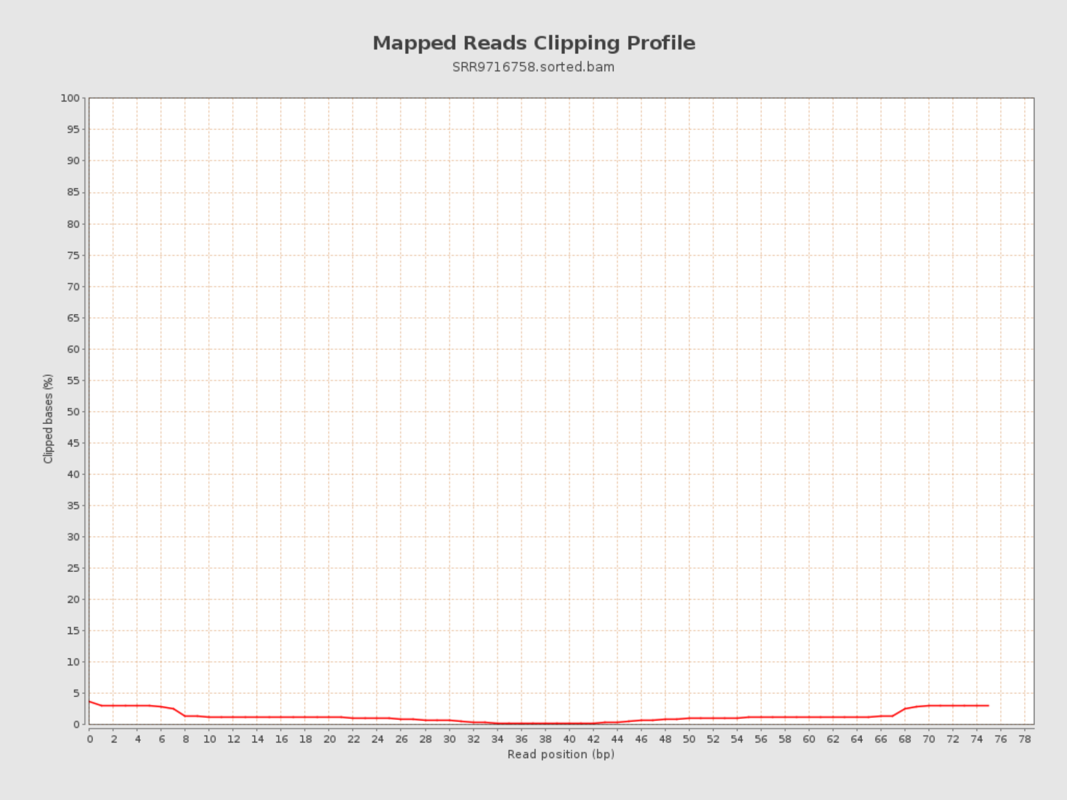
8. Results : Mapped Reads Nucleotide Content



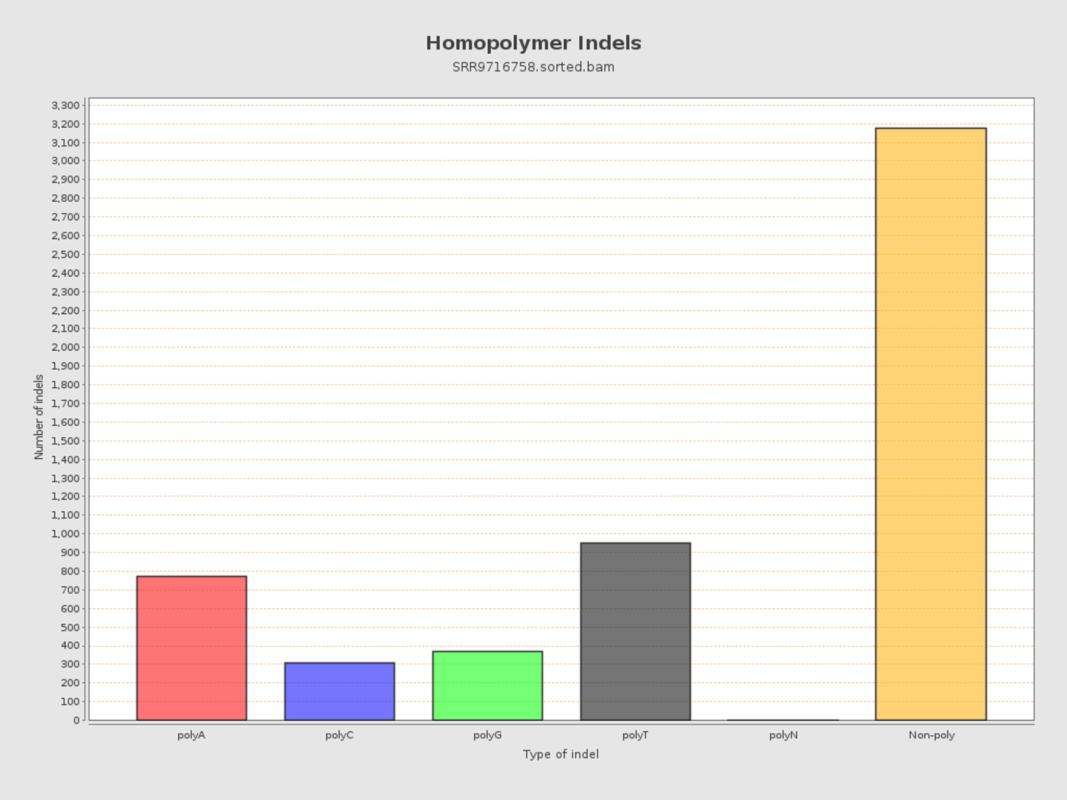
9. Results : Mapped Reads GC-content Distribution



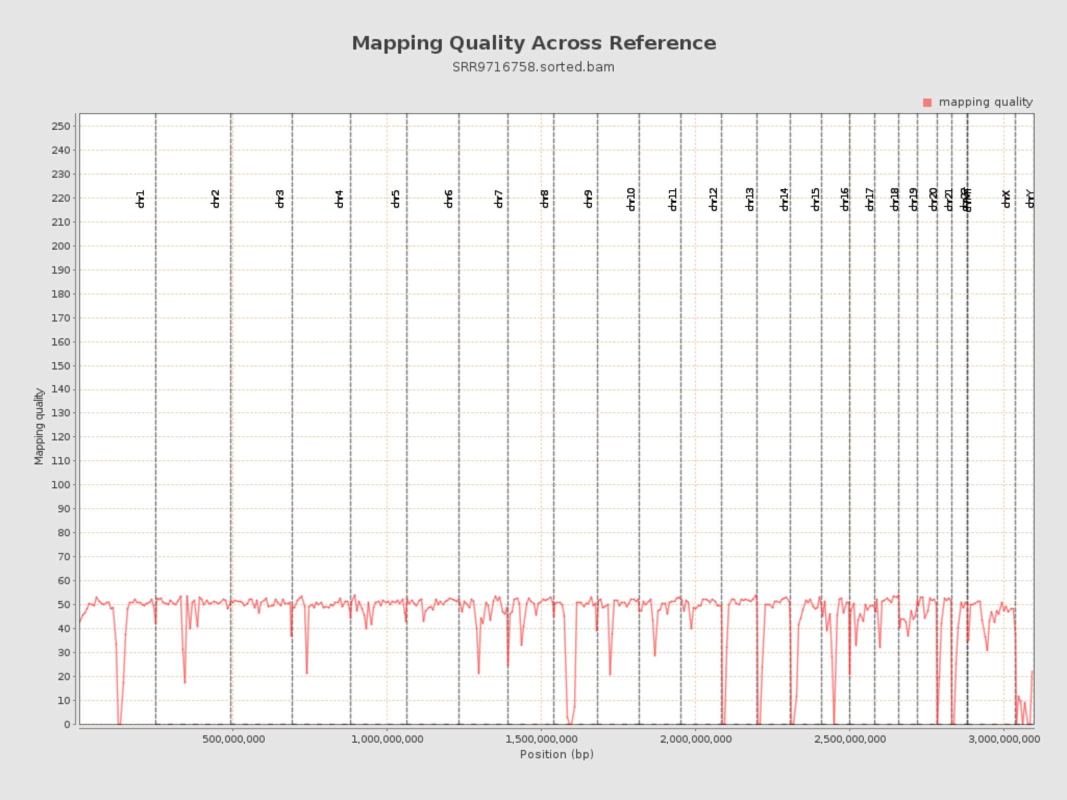
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram