Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 09:02:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716359.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_SRR9716359 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716359.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 09:02:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716359.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,332,532
Mapped reads	5,826,937 / 92.02%
Unmapped reads	505,595 / 7.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	32,327 / 0.51%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	483,348 / 7.63%
Duplication rate	6.26%
Clipped reads	5,840,941 / 92.24%

2.2. ACGT Content

Number/percentage of A's	90,610,282 / 26.73%
Number/percentage of C's	68,552,870 / 20.23%
Number/percentage of T's	103,162,722 / 30.44%
Number/percentage of G's	76,605,970 / 22.6%
Number/percentage of N's	5,269 / 0%
GC Percentage	42.83%

2.3. Coverage

Mean	0.1095

Standard Deviation	0.8535

2.4. Mapping Quality

Mean Mapping Quality	45.7

2.5. Mismatches and indels

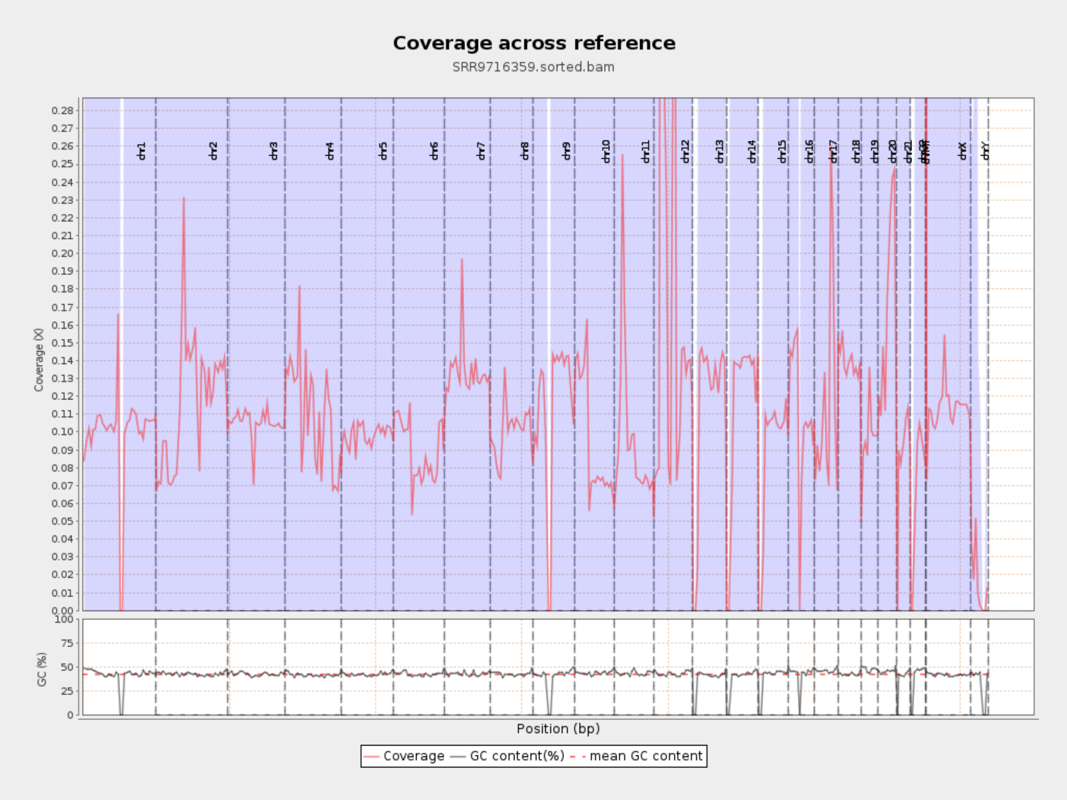
General error rate	0.53%
Mismatches	1,745,371
Insertions	24,634
Mapped reads with at least one insertion	0.42%
Deletions	56,059
Mapped reads with at least one deletion	0.96%
Homopolymer indels	42.07%

2.6. Chromosome stats

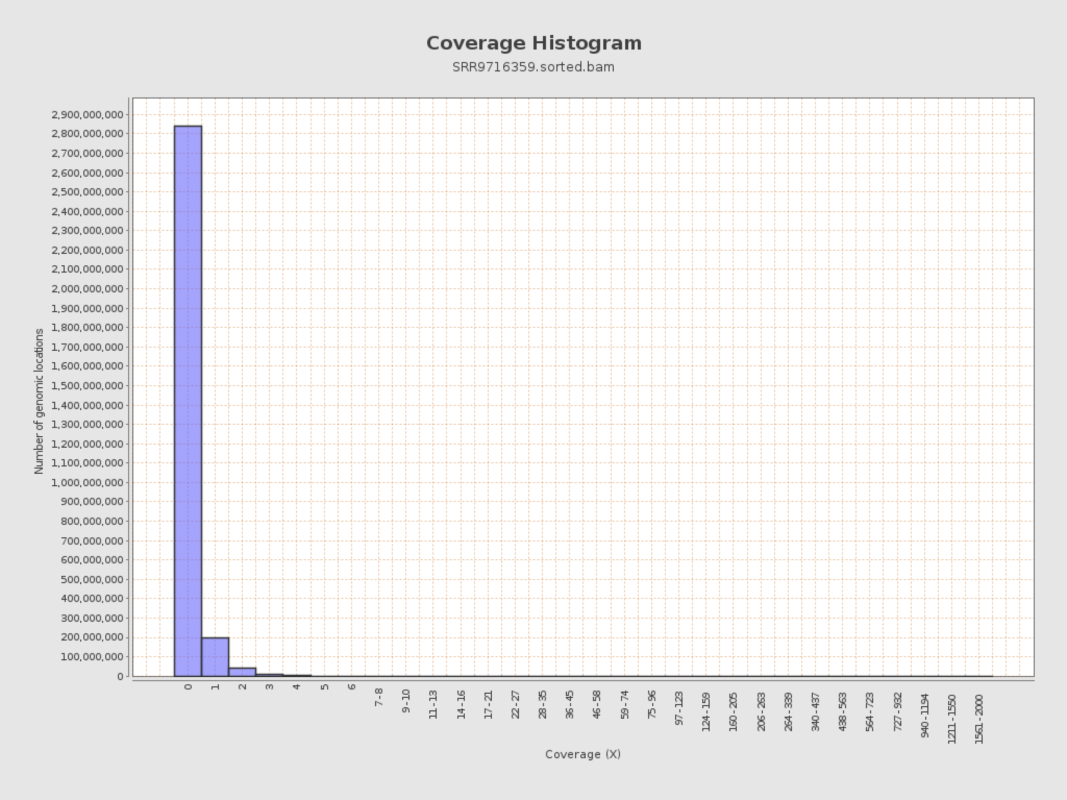
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	24631241	0.0988	1.627
chr2	243199373	28721434	0.1181	0.9864
chr3	198022430	20802377	0.1051	0.4049
chr4	191154276	21266616	0.1113	0.5432
chr5	180915260	17800027	0.0984	0.41
chr6	171115067	15270002	0.0892	0.4835
chr7	159138663	21331155	0.134	1.1745

chr8	146364022	14734593	0.1007	0.842
chr9	141213431	16056606	0.1137	0.9208
chr10	135534747	12737026	0.094	0.8029
chr11	135006516	13089198	0.097	0.7105
chr12	133851895	25258070	0.1887	0.7134
chr13	115169878	13034183	0.1132	0.4225
chr14	107349540	12378813	0.1153	0.5138
chr15	102531392	8852393	0.0863	0.3694
chr16	90354753	9671839	0.107	0.4951
chr17	81195210	9533195	0.1174	0.4741
chr18	78077248	10897437	0.1396	1.7547
chr19	59128983	5783766	0.0978	1.1989
chr20	63025520	10927569	0.1734	0.5675
chr21	48129895	4232918	0.0879	0.4862
chr22	51304566	3450441	0.0673	0.3186
chrMT	16571	83300	5.0269	3.9134
chrX	155270560	17567734	0.1131	0.6127
chrY	59373566	918823	0.0155	0.3231

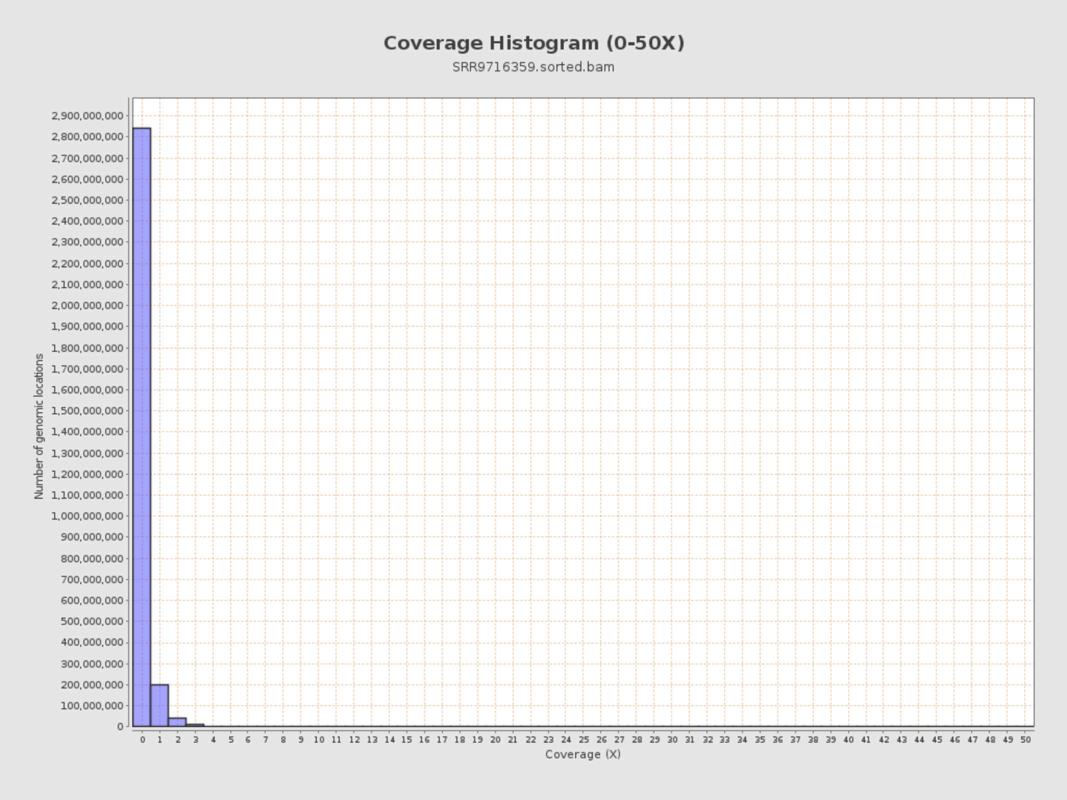
3. Results : Coverage across reference



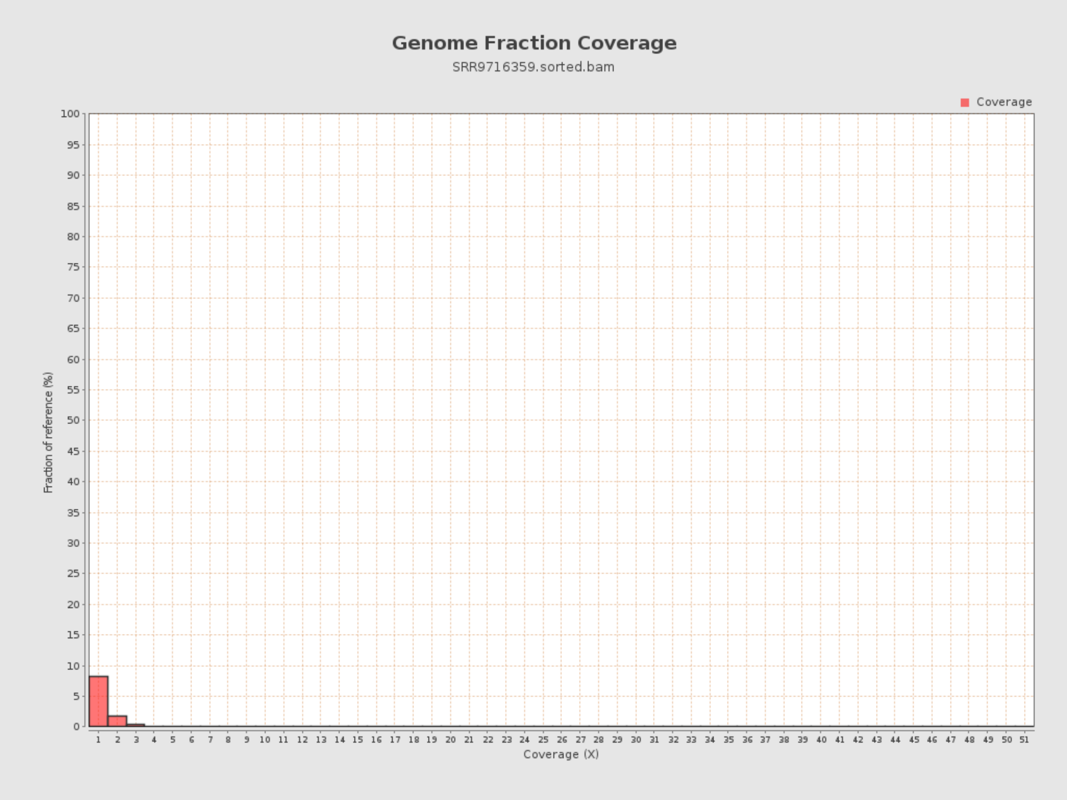
4. Results : Coverage Histogram



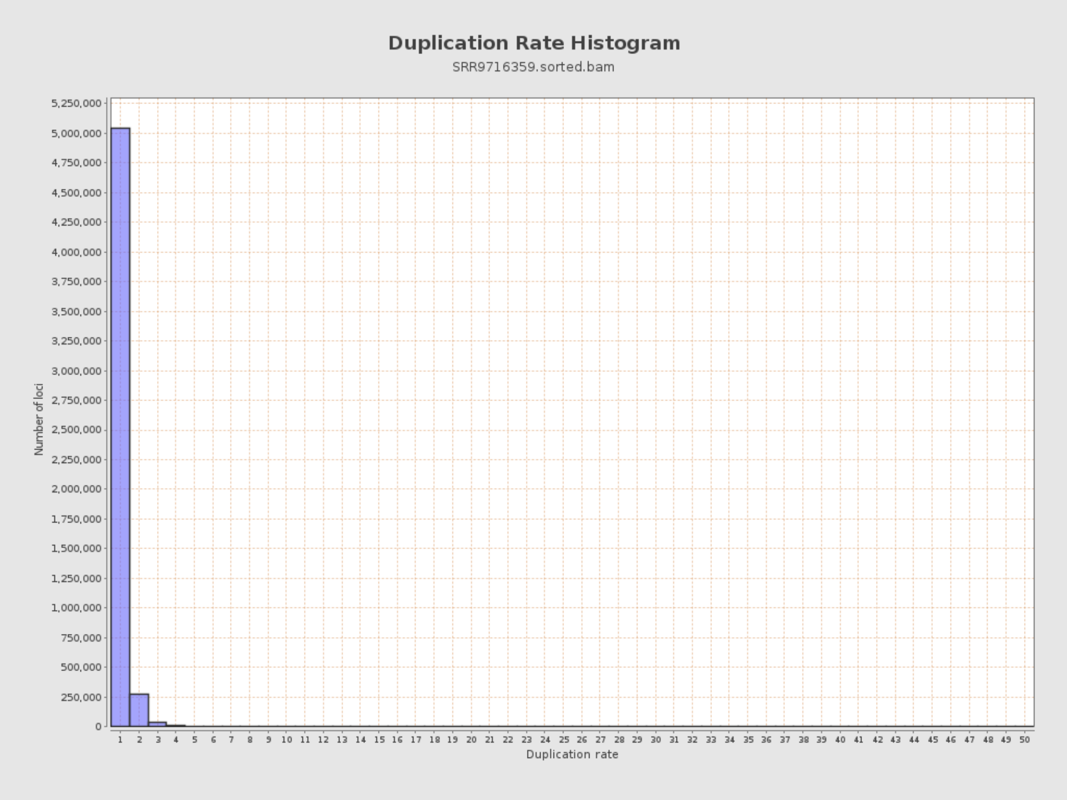
5. Results : Coverage Histogram (0-50X)



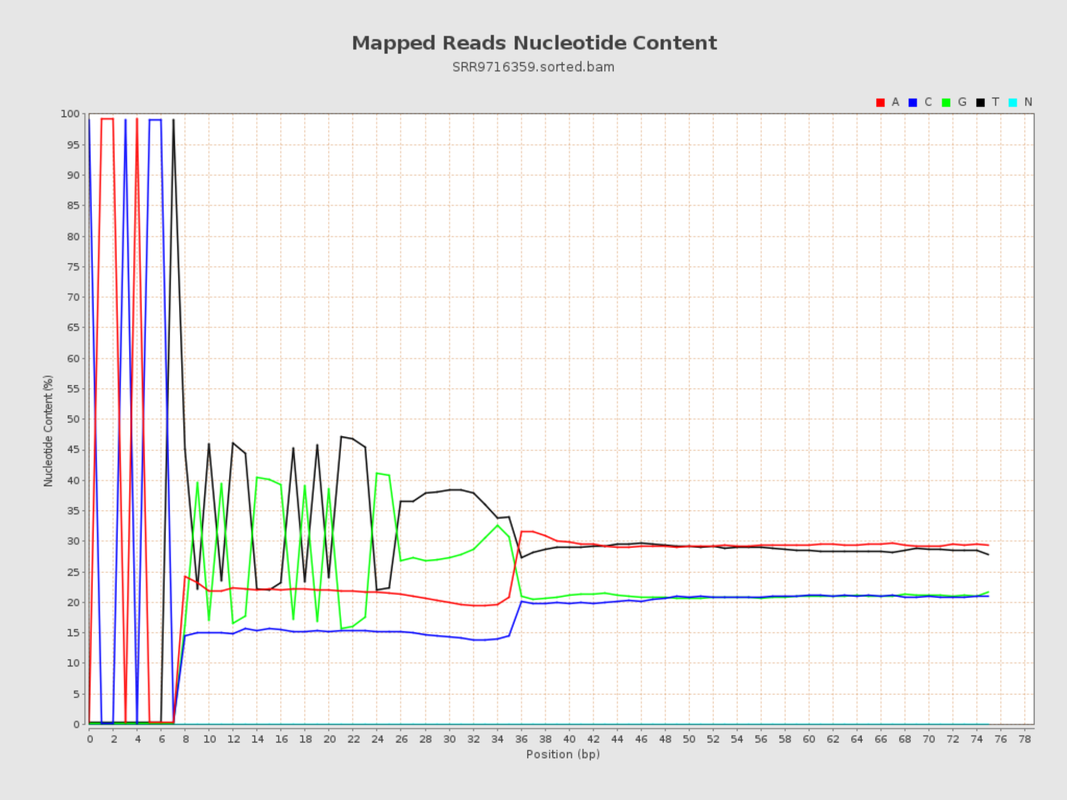
6. Results : Genome Fraction Coverage



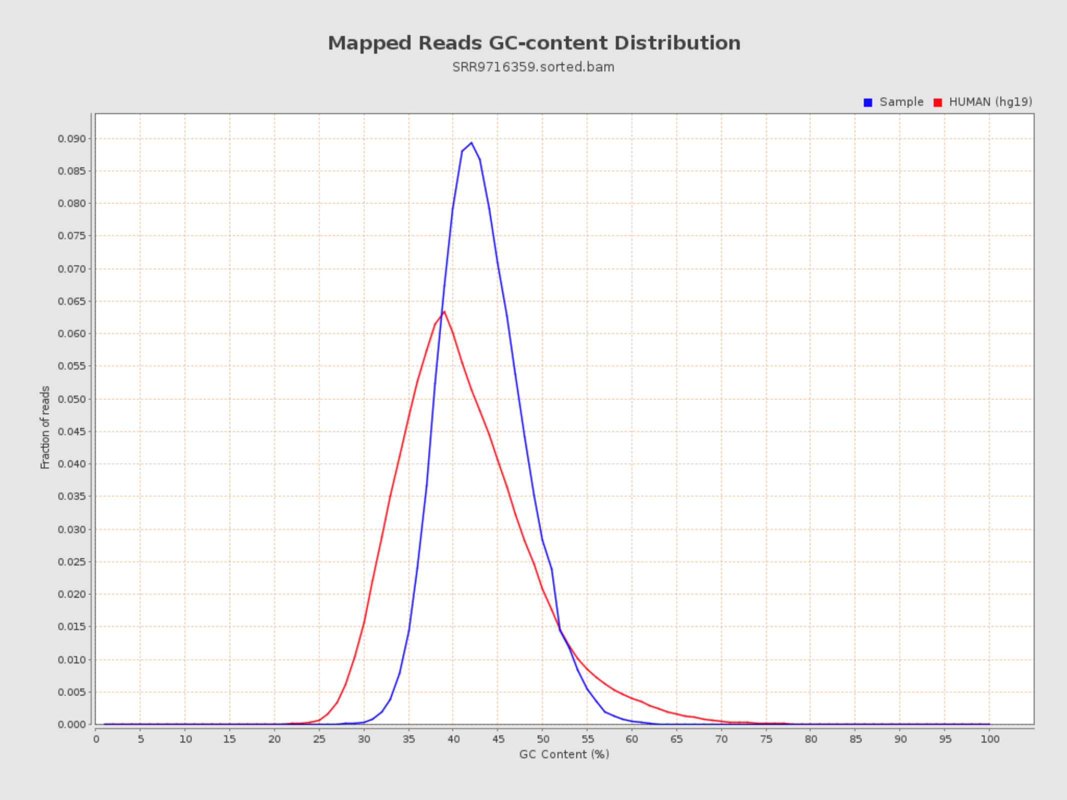
7. Results : Duplication Rate Histogram



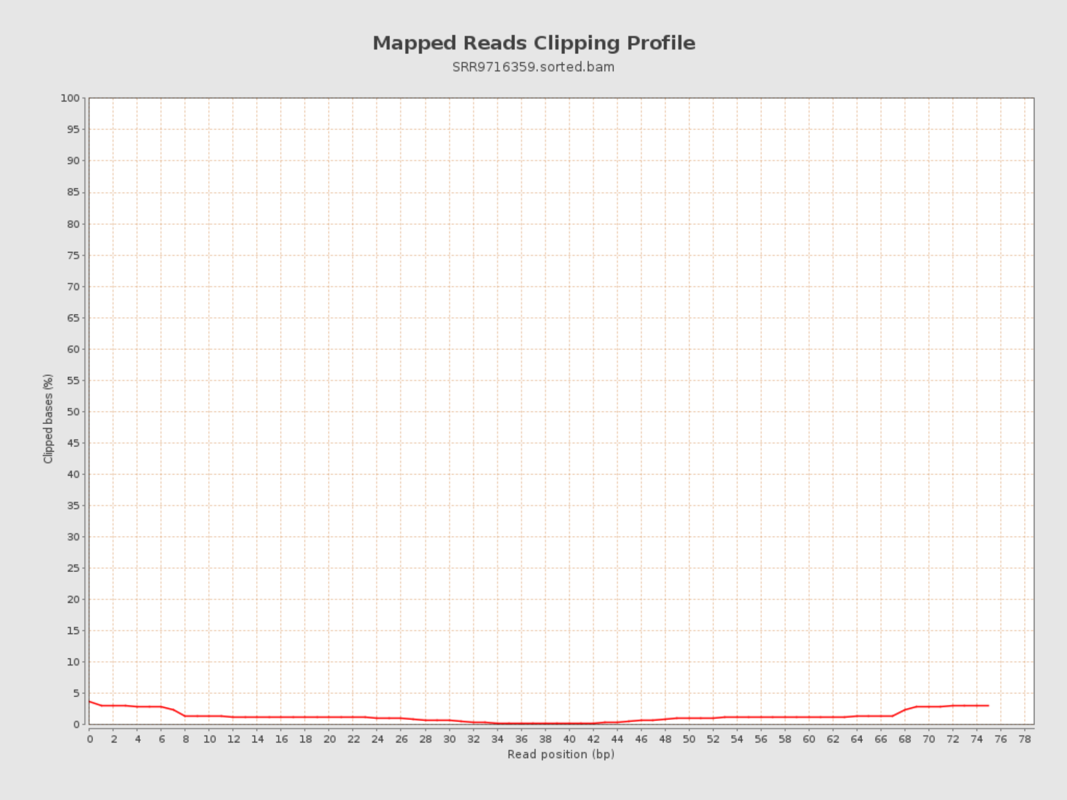
8. Results : Mapped Reads Nucleotide Content



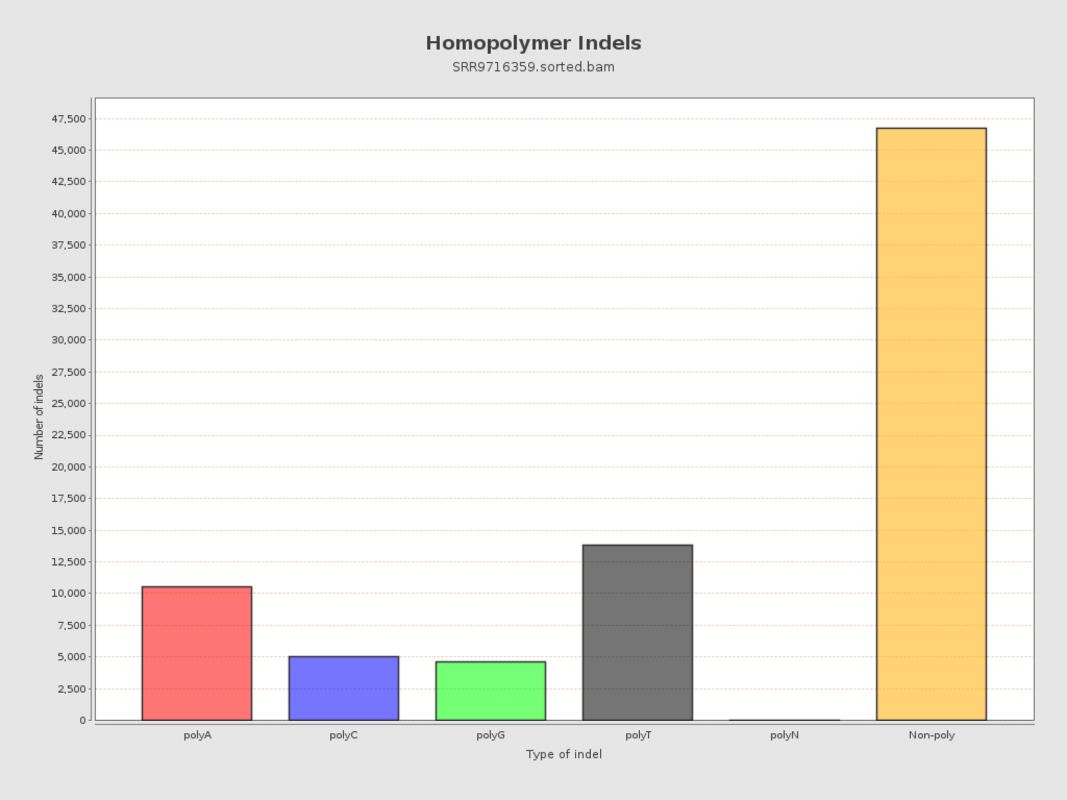
9. Results : Mapped Reads GC-content Distribution



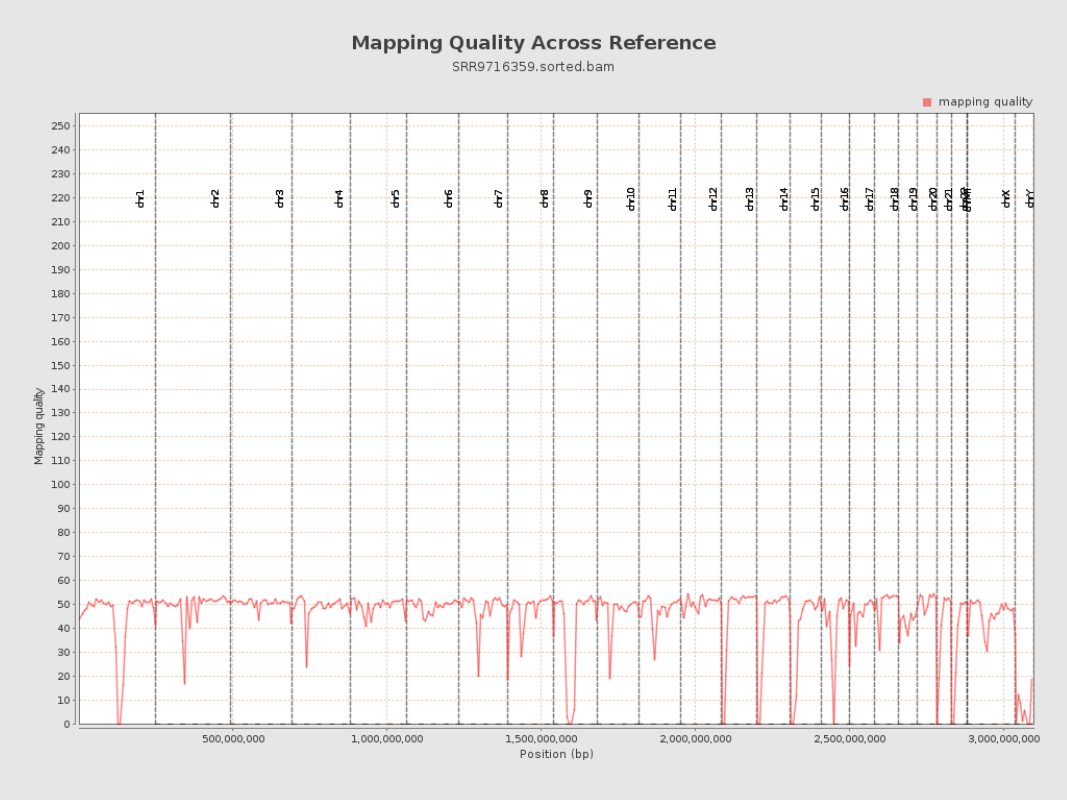
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram