Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 01:17:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716222.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_SRR9716222 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716222.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 01:17:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716222.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,530,630
Mapped reads	1,365,947 / 89.24%
Unmapped reads	164,683 / 10.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,861 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	42,135 / 2.75%
Duplication rate	2.3%
Clipped reads	1,368,206 / 89.39%

2.2. ACGT Content

Number/percentage of A's	19,395,881 / 24.59%
Number/percentage of C's	14,495,146 / 18.37%
Number/percentage of T's	24,445,150 / 30.99%
Number/percentage of G's	20,550,127 / 26.05%
Number/percentage of N's	686 / 0%
GC Percentage	44.42%

2.3. Coverage

Mean	0.0255

Standard Deviation	0.2246

2.4. Mapping Quality

Mean Mapping Quality	44.4

2.5. Mismatches and indels

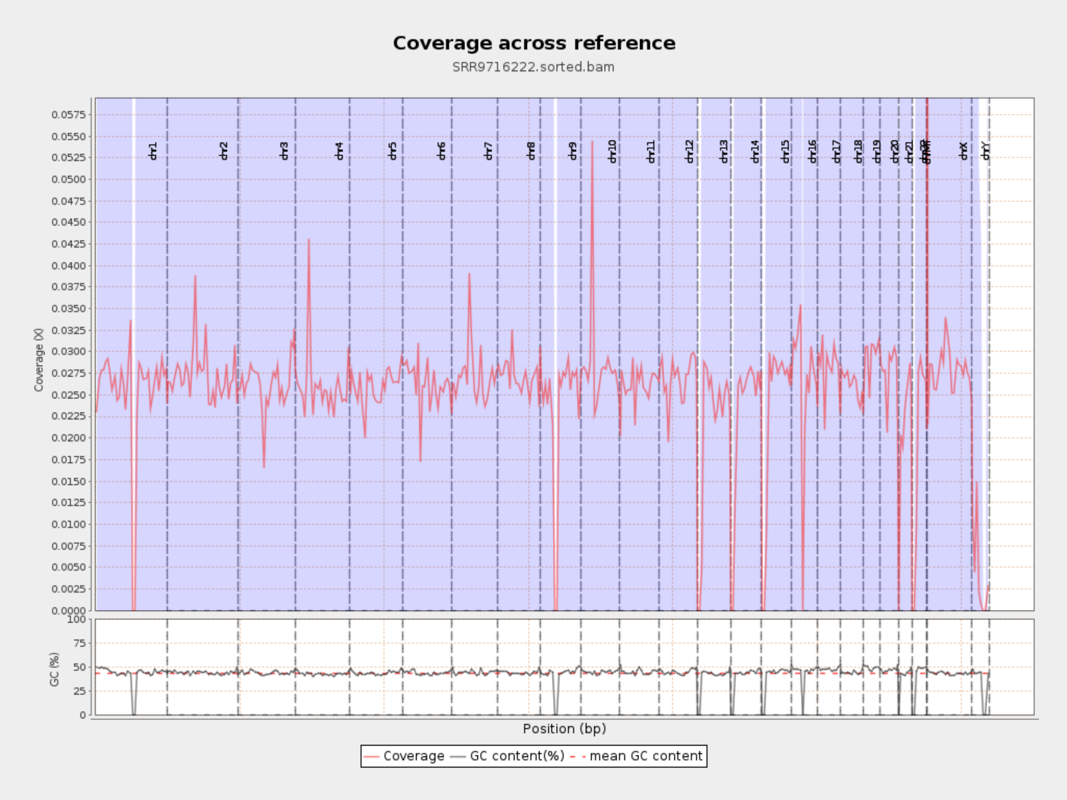
General error rate	0.53%
Mismatches	408,018
Insertions	5,117
Mapped reads with at least one insertion	0.37%
Deletions	14,791
Mapped reads with at least one deletion	1.07%
Homopolymer indels	42.23%

2.6. Chromosome stats

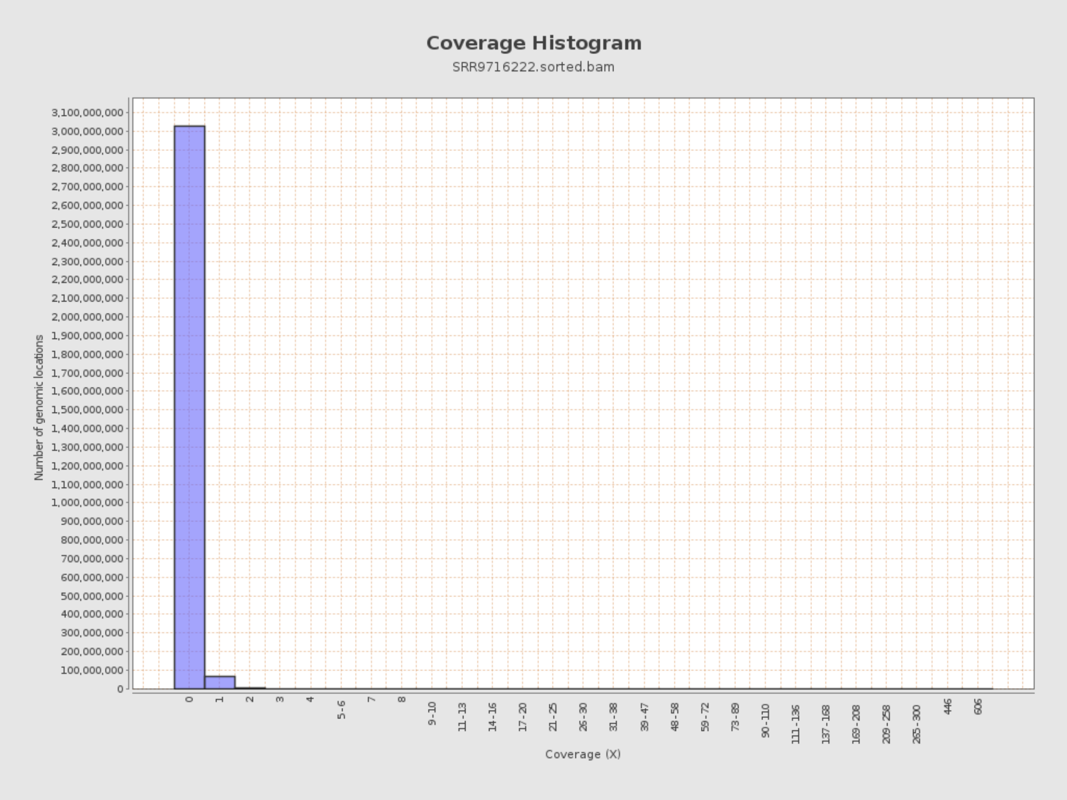
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6276757	0.0252	0.2874
chr2	243199373	6646023	0.0273	0.3259
chr3	198022430	5188567	0.0262	0.1781
chr4	191154276	5003286	0.0262	0.1932
chr5	180915260	4711753	0.026	0.175
chr6	171115067	4491208	0.0262	0.2
chr7	159138663	4349764	0.0273	0.2794

chr8	146364022	3972313	0.0271	0.2331
chr9	141213431	3286711	0.0233	0.1919
chr10	135534747	3886657	0.0287	0.2807
chr11	135006516	3546914	0.0263	0.207
chr12	133851895	3599912	0.0269	0.1809
chr13	115169878	2439875	0.0212	0.1584
chr14	107349540	2383356	0.0222	0.1666
chr15	102531392	2322577	0.0227	0.1658
chr16	90354753	2366118	0.0262	0.1923
chr17	81195210	2296906	0.0283	0.1895
chr18	78077248	2055280	0.0263	0.2947
chr19	59128983	1744182	0.0295	0.2586
chr20	63025520	1736045	0.0275	0.1845
chr21	48129895	1028705	0.0214	0.1784
chr22	51304566	974714	0.019	0.1512
chrMT	16571	5264	0.3177	0.6196
chrX	155270560	4346653	0.028	0.1942
chrY	59373566	251216	0.0042	0.135

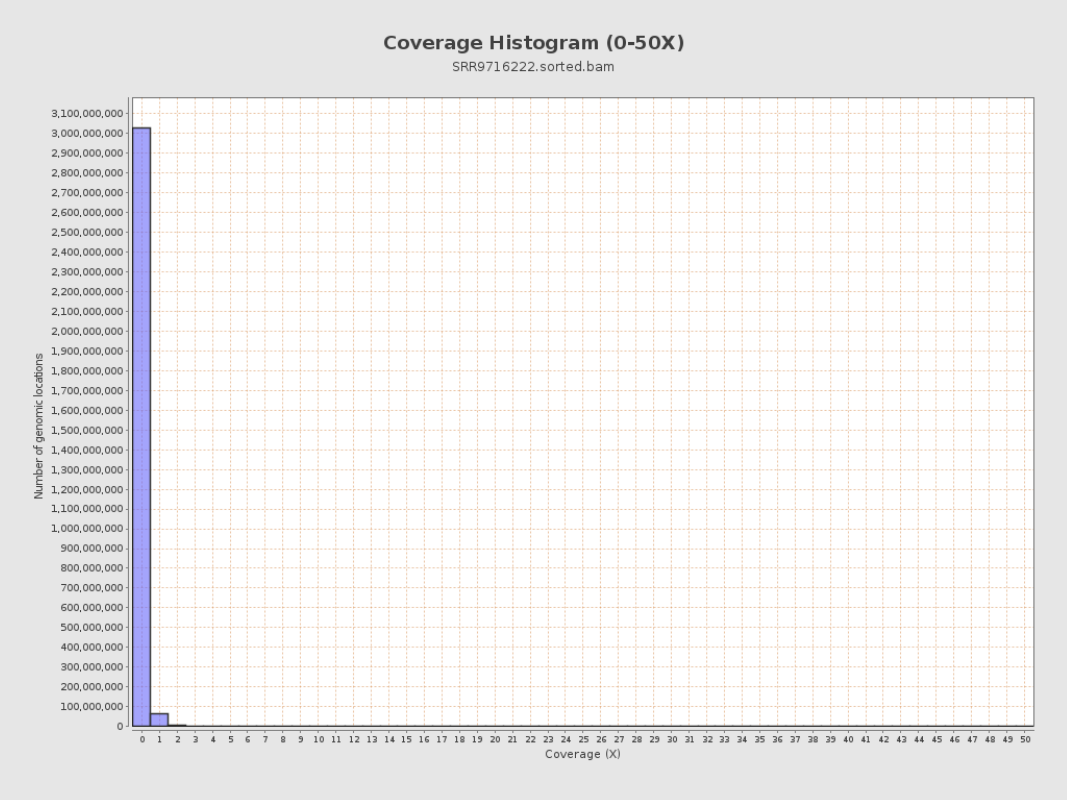
3. Results : Coverage across reference



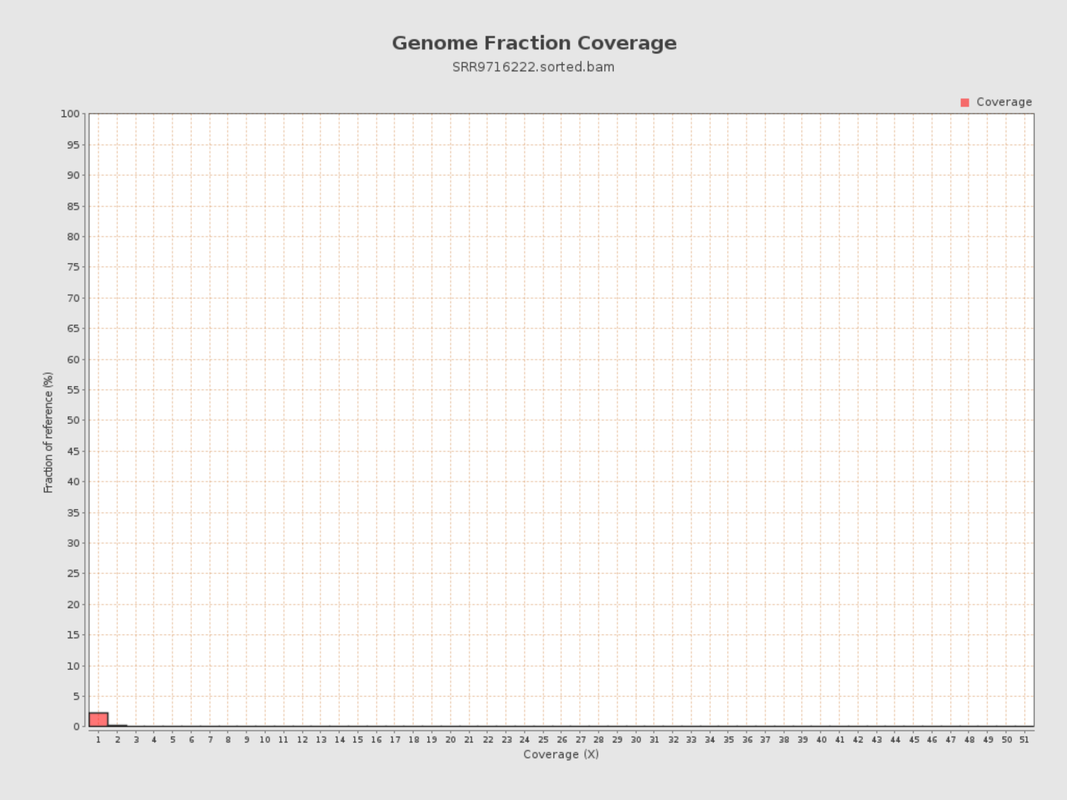
4. Results : Coverage Histogram



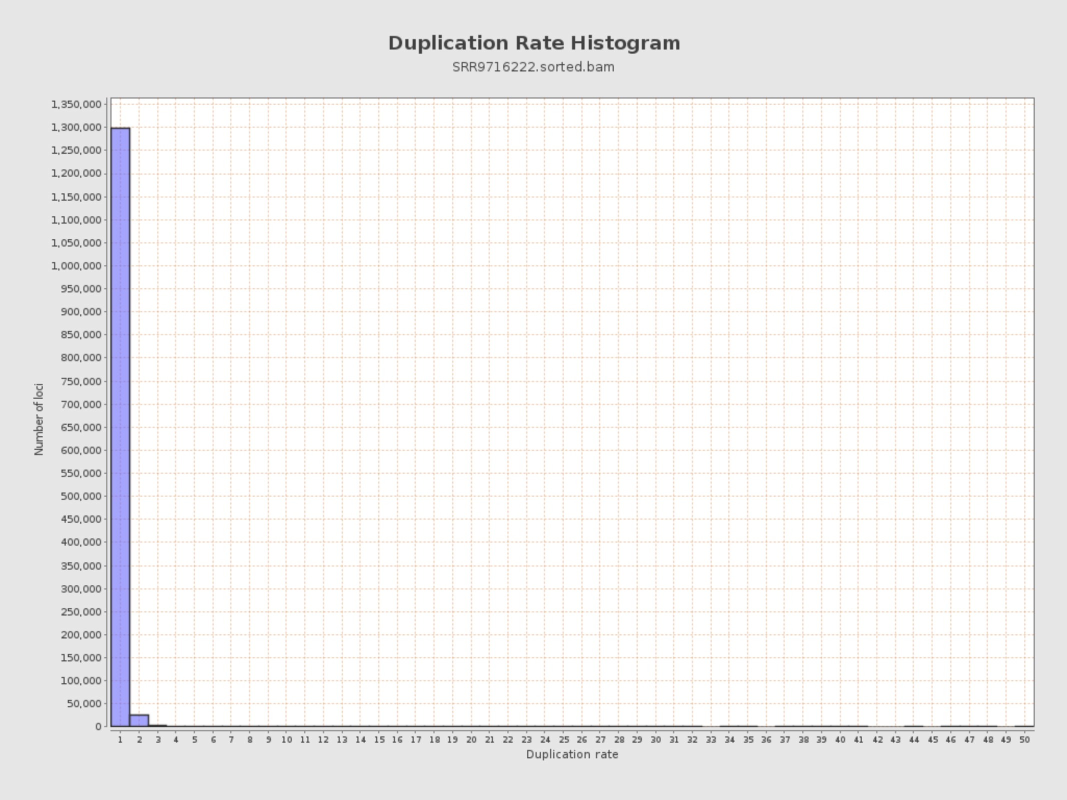
5. Results : Coverage Histogram (0-50X)



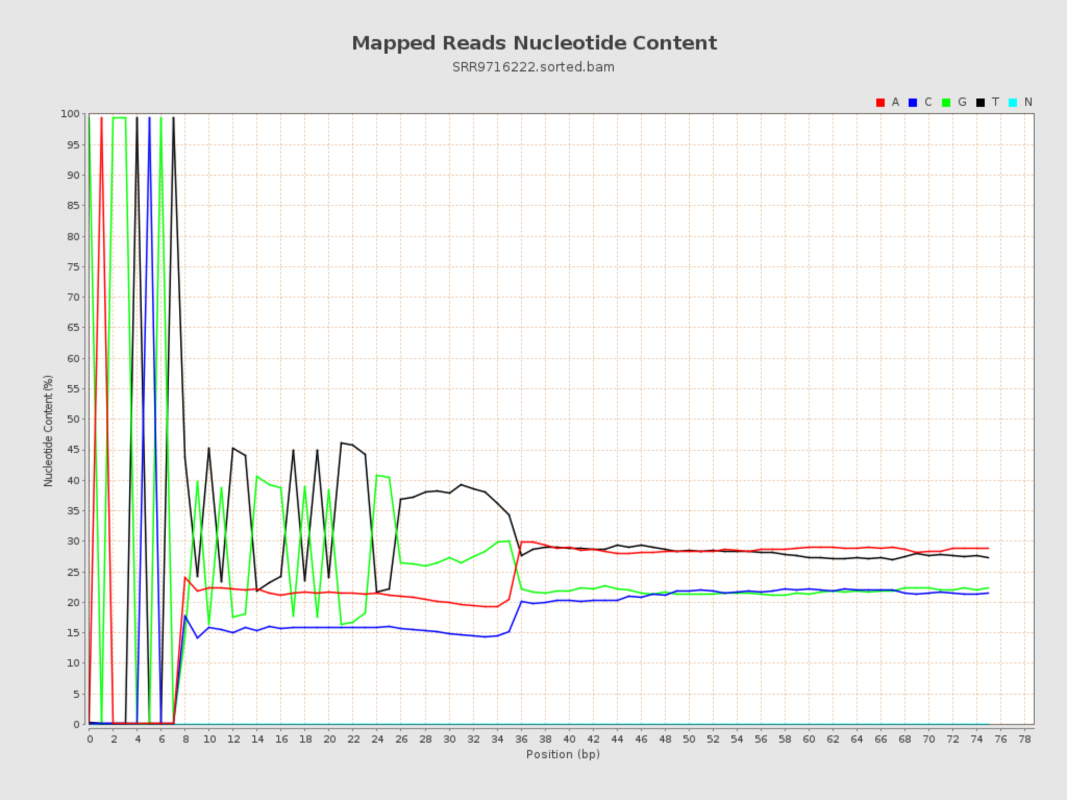
6. Results : Genome Fraction Coverage



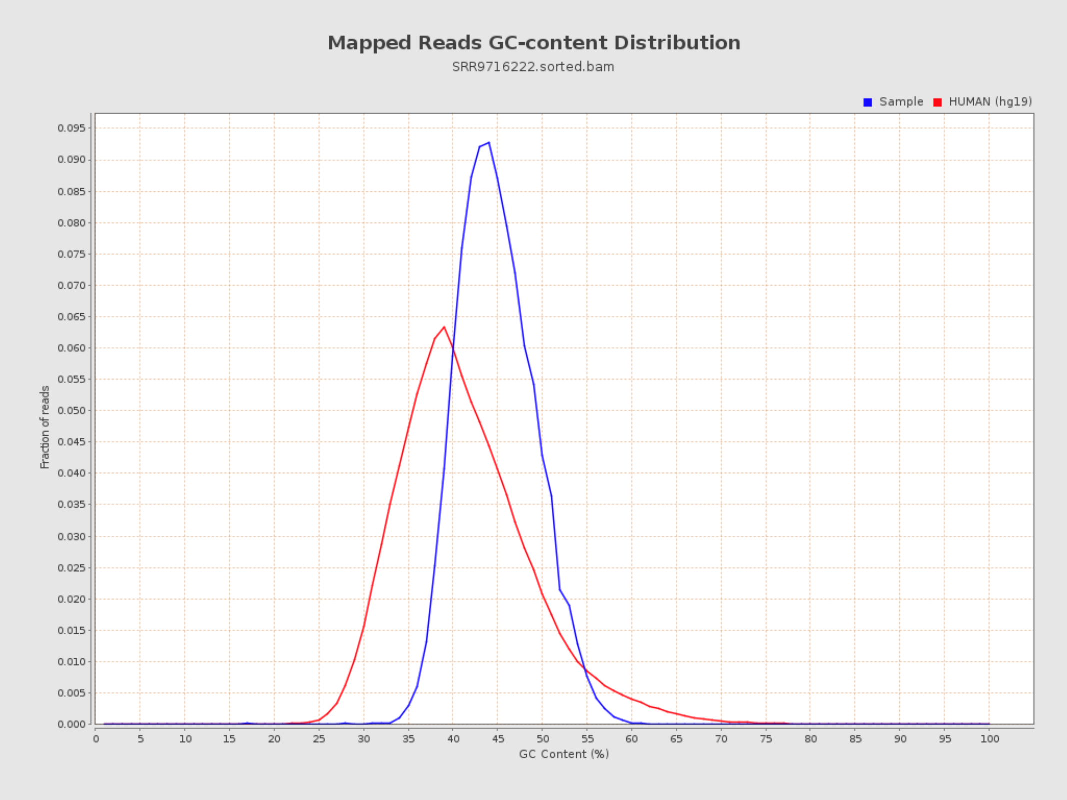
7. Results : Duplication Rate Histogram



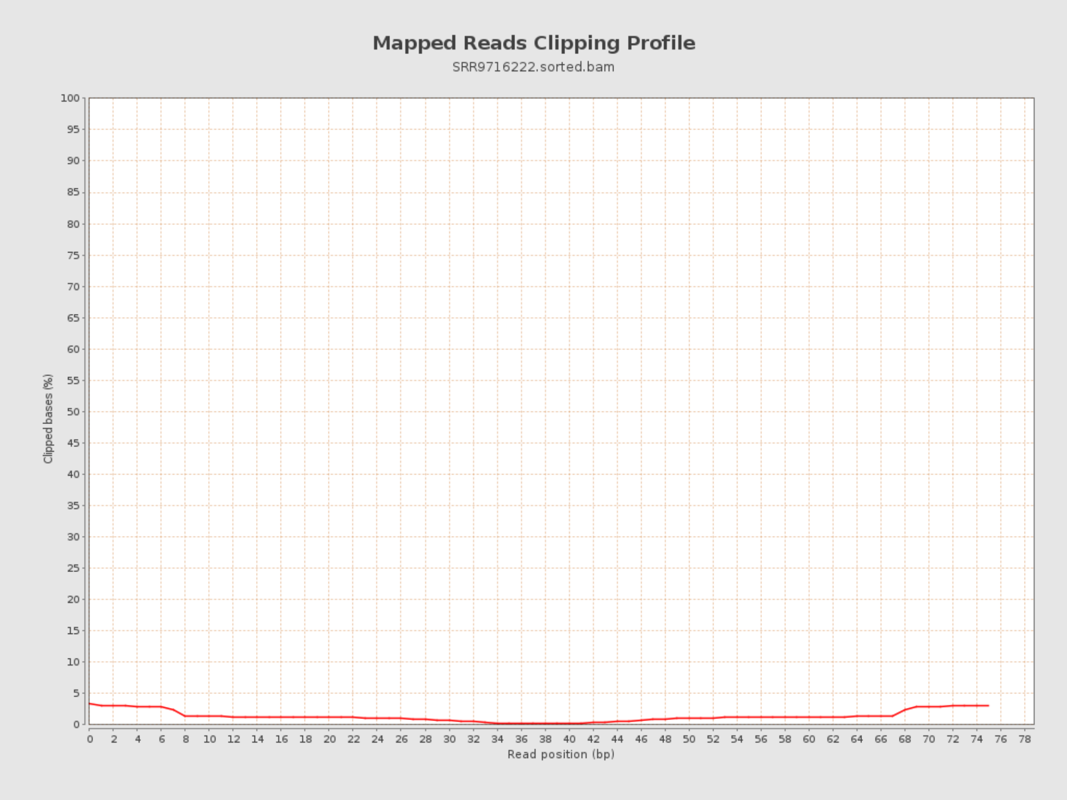
8. Results : Mapped Reads Nucleotide Content



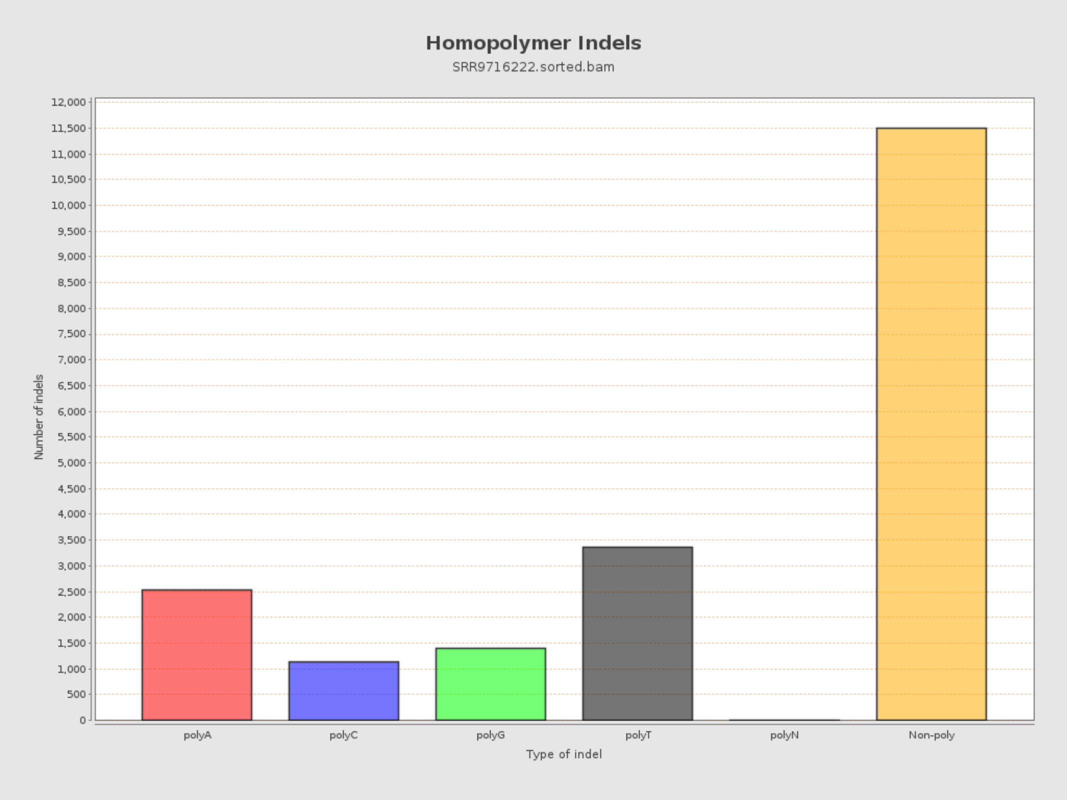
9. Results : Mapped Reads GC-content Distribution



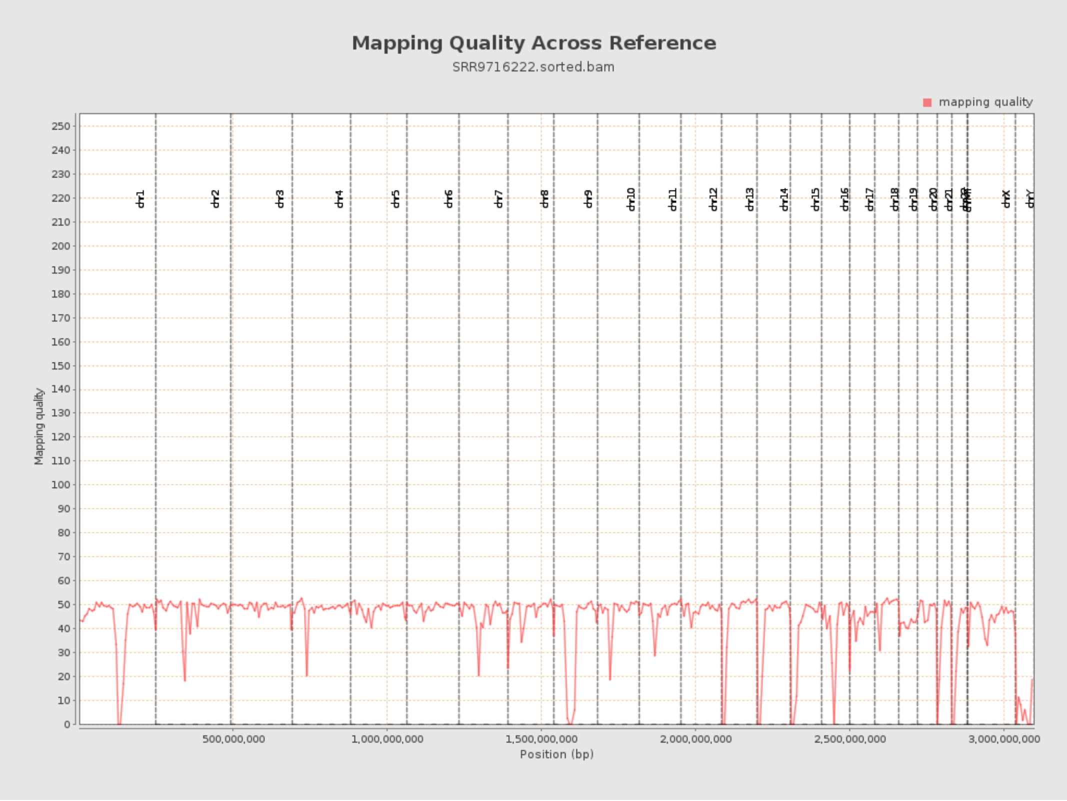
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram