Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 18:44:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716922.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_SRR9716922 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716922.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 18:44:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716922.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,183,129
Mapped reads	1,062,437 / 89.8%
Unmapped reads	120,692 / 10.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,543 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	25,723 / 2.17%
Duplication rate	1.85%
Clipped reads	1,064,740 / 89.99%

2.2. ACGT Content

Number/percentage of A's	15,305,867 / 25.41%
Number/percentage of C's	12,100,537 / 20.09%
Number/percentage of T's	18,451,121 / 30.63%
Number/percentage of G's	14,374,873 / 23.87%
Number/percentage of N's	1,247 / 0%
GC Percentage	43.95%

2.3. Coverage

Mean	0.0195

Standard Deviation	0.1816

2.4. Mapping Quality

Mean Mapping Quality	44.58

2.5. Mismatches and indels

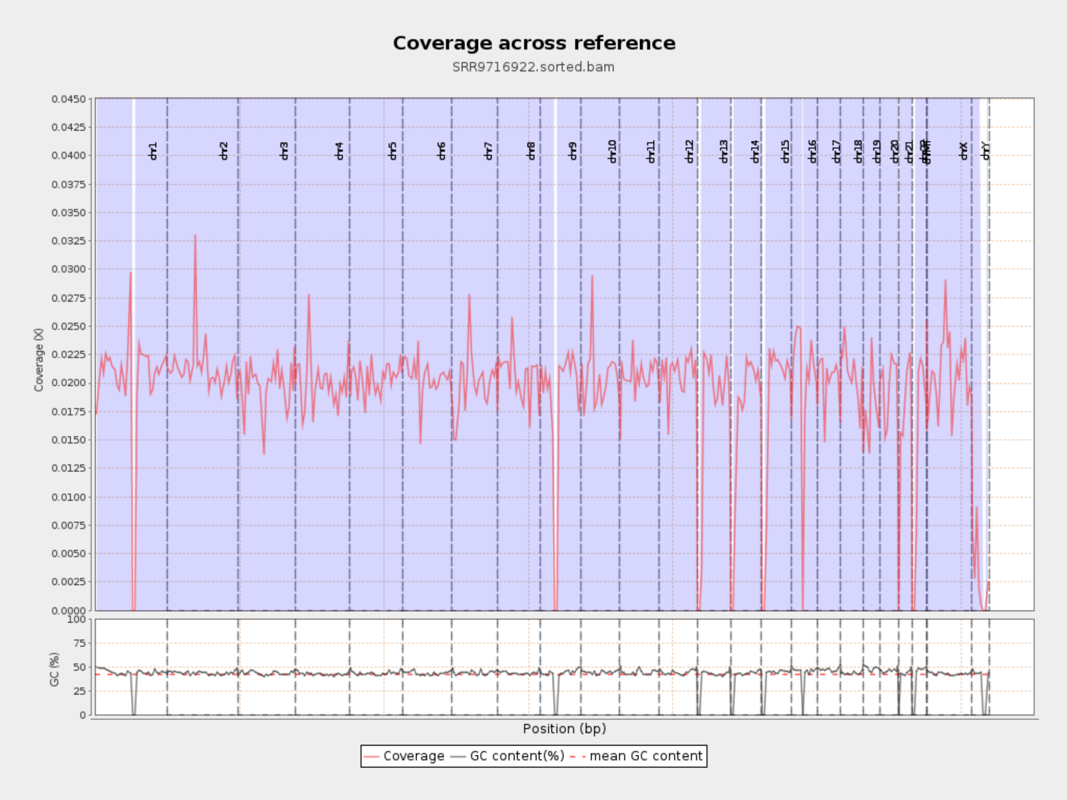
General error rate	0.51%
Mismatches	298,946
Insertions	3,803
Mapped reads with at least one insertion	0.36%
Deletions	9,422
Mapped reads with at least one deletion	0.88%
Homopolymer indels	41.57%

2.6. Chromosome stats

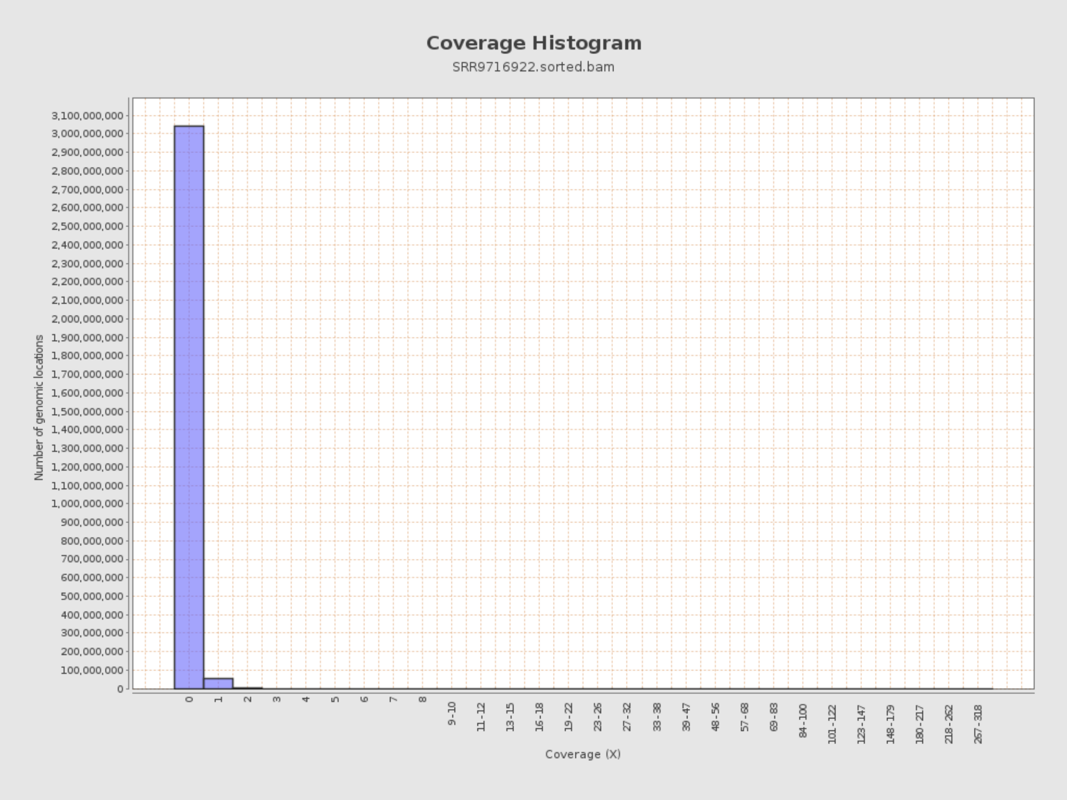
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4999223	0.0201	0.2743
chr2	243199373	5216613	0.0214	0.2032
chr3	198022430	3901830	0.0197	0.149
chr4	191154276	3834271	0.0201	0.1578
chr5	180915260	3708015	0.0205	0.1525
chr6	171115067	3509359	0.0205	0.1599
chr7	159138663	3188286	0.02	0.1965

chr8	146364022	3031900	0.0207	0.1713
chr9	141213431	2586936	0.0183	0.1818
chr10	135534747	2792655	0.0206	0.1772
chr11	135006516	2800946	0.0207	0.1828
chr12	133851895	2778770	0.0208	0.1537
chr13	115169878	1966093	0.0171	0.1378
chr14	107349540	1794129	0.0167	0.1434
chr15	102531392	1800460	0.0176	0.1412
chr16	90354753	1800200	0.0199	0.1584
chr17	81195210	1655855	0.0204	0.1587
chr18	78077248	1624866	0.0208	0.3011
chr19	59128983	1054090	0.0178	0.21
chr20	63025520	1235562	0.0196	0.1515
chr21	48129895	813901	0.0169	0.147
chr22	51304566	729527	0.0142	0.1257
chrMT	16571	424	0.0256	0.1718
chrX	155270560	3259069	0.021	0.1697
chrY	59373566	166537	0.0028	0.074

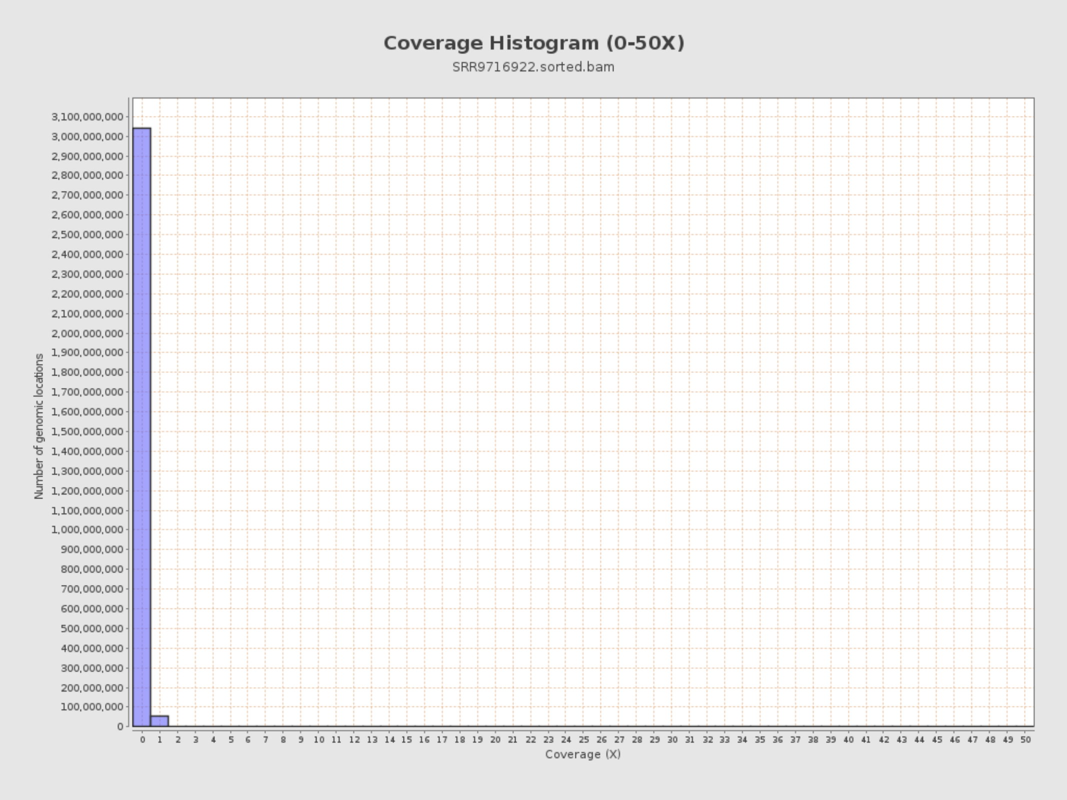
3. Results : Coverage across reference



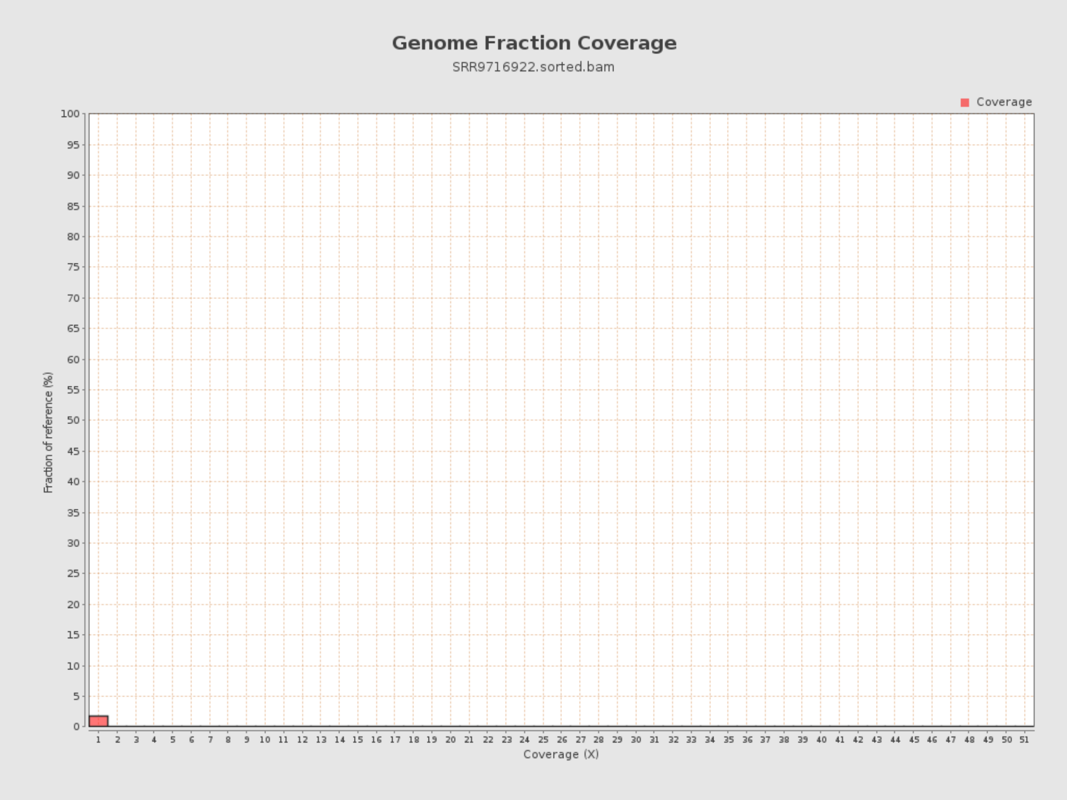
4. Results : Coverage Histogram



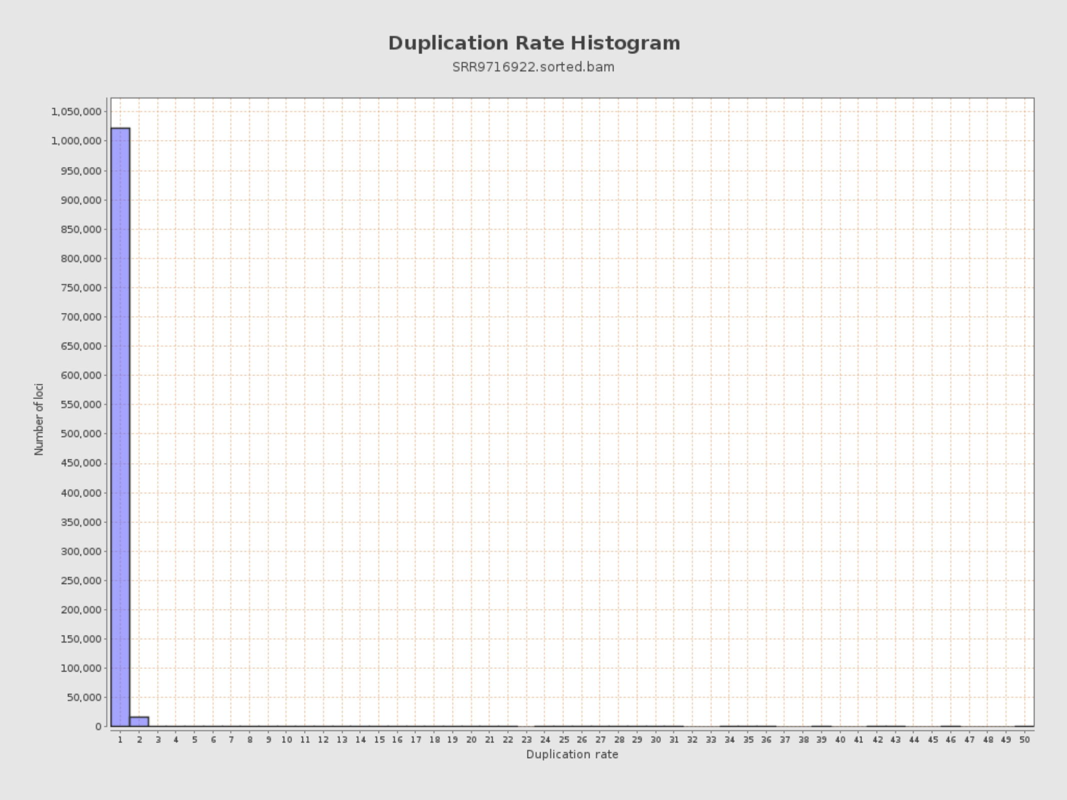
5. Results : Coverage Histogram (0-50X)



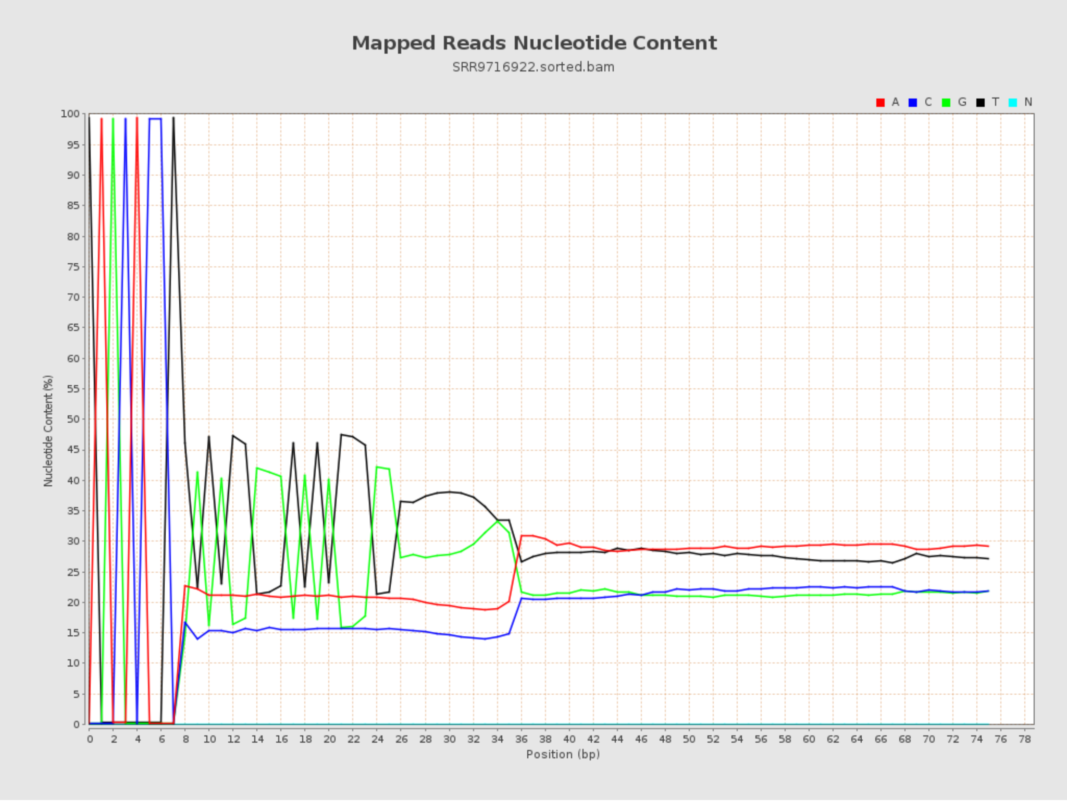
6. Results : Genome Fraction Coverage



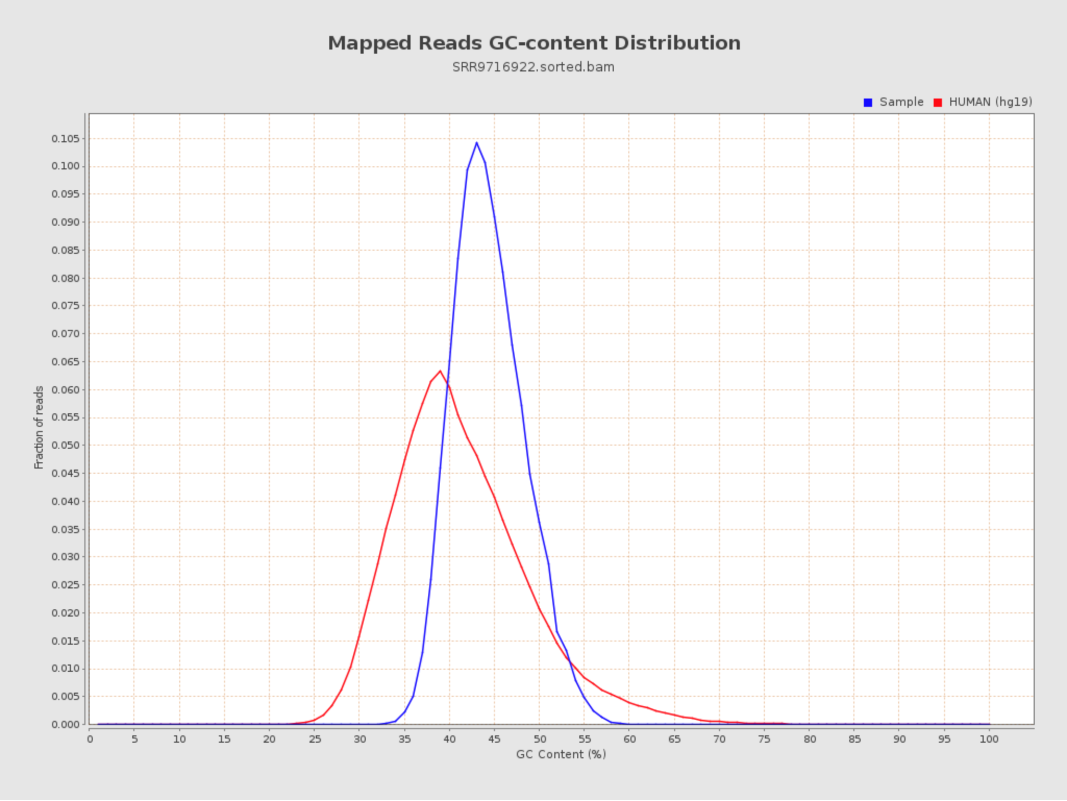
7. Results : Duplication Rate Histogram



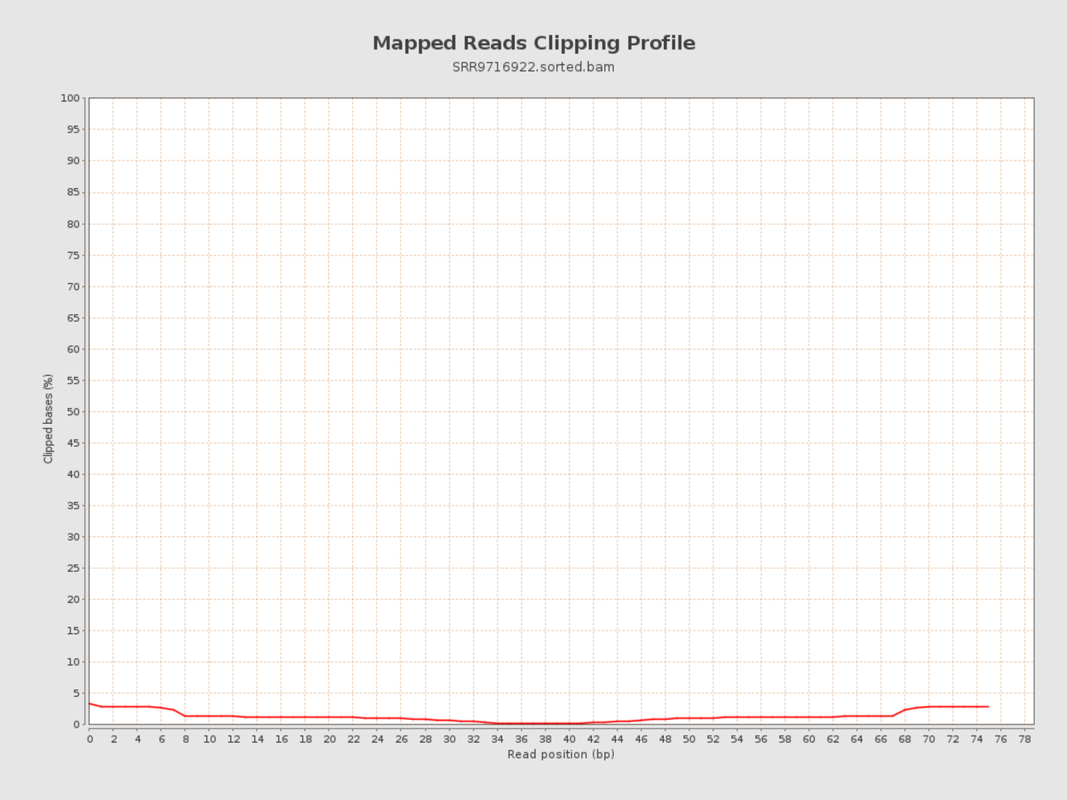
8. Results : Mapped Reads Nucleotide Content



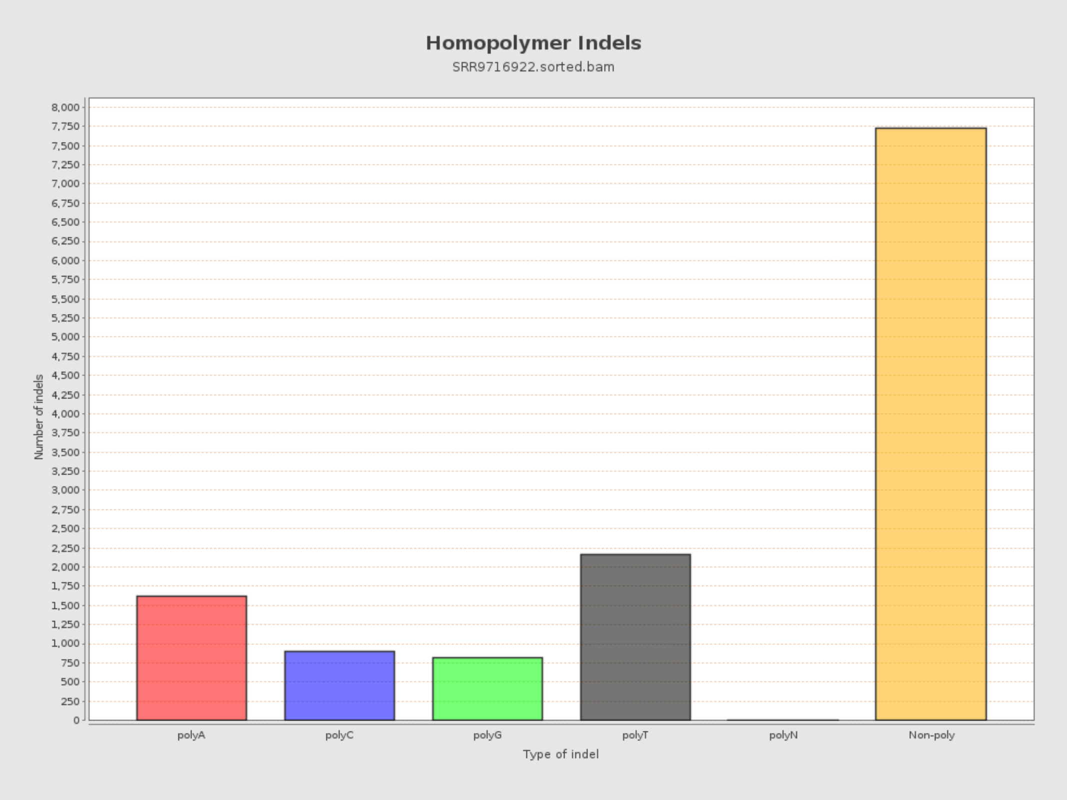
9. Results : Mapped Reads GC-content Distribution



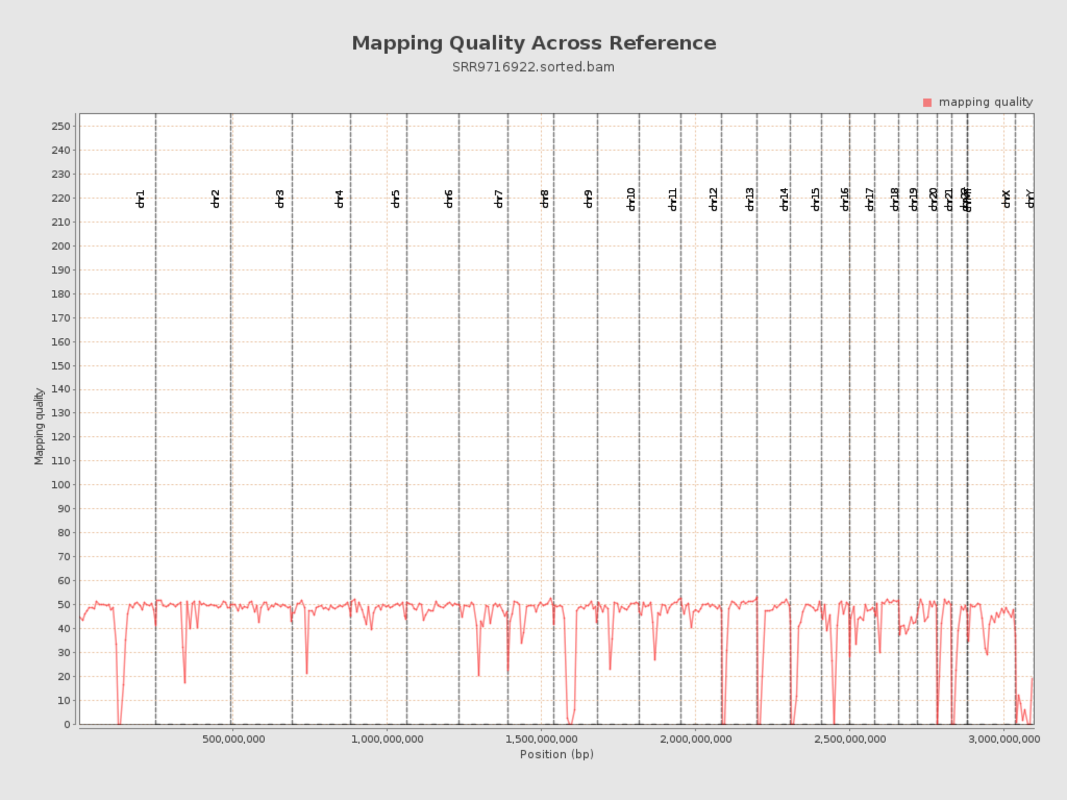
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram