Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 05:57:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716292.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_SRR9716292 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716292.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 05:57:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716292.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,336,570
Mapped reads	1,095,990 / 82%
Unmapped reads	240,580 / 18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,091 / 0.23%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	25,646 / 1.92%
Duplication rate	1.71%
Clipped reads	1,097,356 / 82.1%

2.2. ACGT Content

Number/percentage of A's	13,883,494 / 22.83%
Number/percentage of C's	12,461,984 / 20.49%
Number/percentage of T's	18,531,535 / 30.47%
Number/percentage of G's	15,937,252 / 26.21%
Number/percentage of N's	1,451 / 0%
GC Percentage	46.7%

2.3. Coverage

Mean	0.0197

Standard Deviation	0.1767

2.4. Mapping Quality

Mean Mapping Quality	39.25

2.5. Mismatches and indels

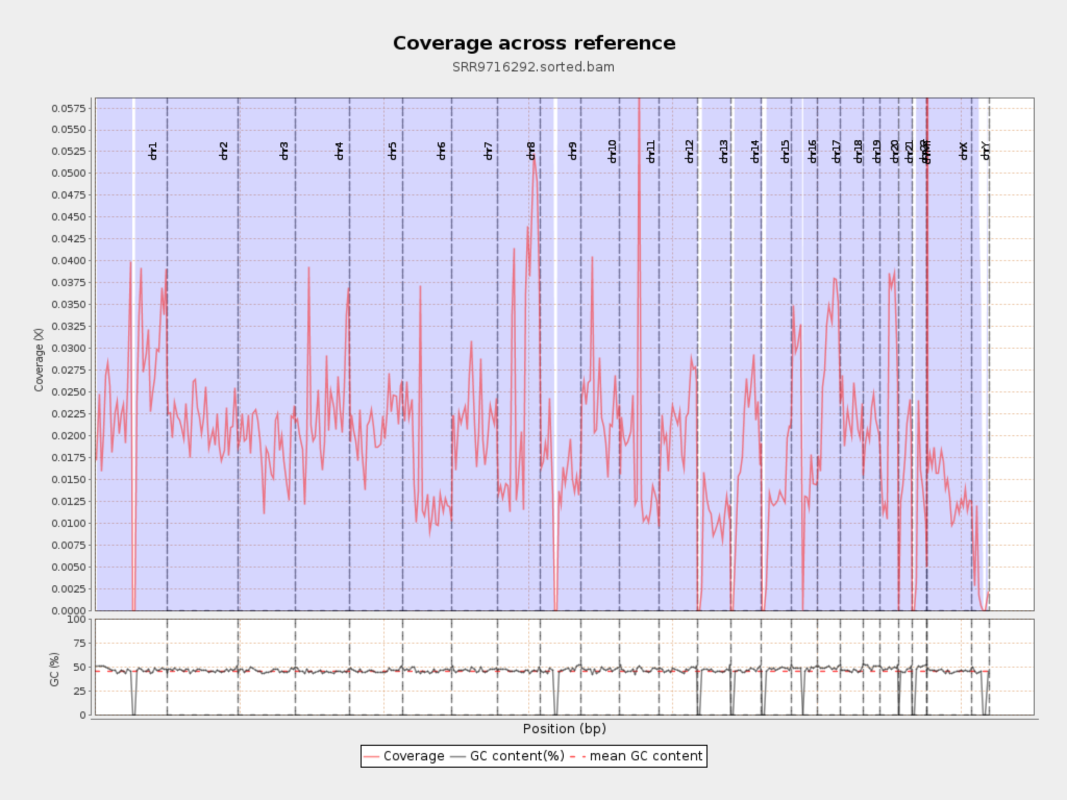
General error rate	0.53%
Mismatches	314,127
Insertions	4,273
Mapped reads with at least one insertion	0.39%
Deletions	9,596
Mapped reads with at least one deletion	0.87%
Homopolymer indels	36.92%

2.6. Chromosome stats

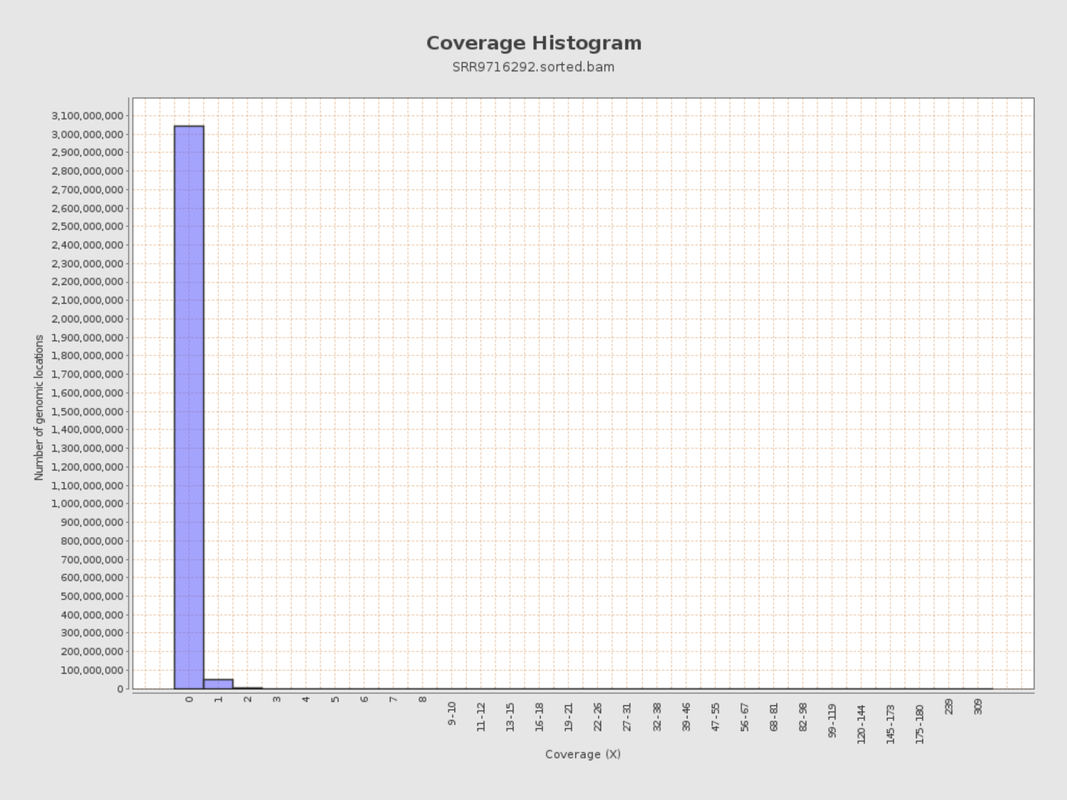
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6265437	0.0251	0.2249
chr2	243199373	5203013	0.0214	0.2203
chr3	198022430	3762317	0.019	0.1573
chr4	191154276	4409766	0.0231	0.1853
chr5	180915260	3852348	0.0213	0.1603
chr6	171115067	2628315	0.0154	0.1395
chr7	159138663	3502393	0.022	0.199

chr8	146364022	3989317	0.0273	0.1937
chr9	141213431	2038269	0.0144	0.1413
chr10	135534747	3232292	0.0238	0.2259
chr11	135006516	2445124	0.0181	0.177
chr12	133851895	2912621	0.0218	0.1629
chr13	115169878	1069587	0.0093	0.1057
chr14	107349540	1911840	0.0178	0.1496
chr15	102531392	1185512	0.0116	0.1206
chr16	90354753	1750866	0.0194	0.1622
chr17	81195210	2404411	0.0296	0.1982
chr18	78077248	1747985	0.0224	0.1878
chr19	59128983	1239056	0.021	0.1965
chr20	63025520	1561092	0.0248	0.1823
chr21	48129895	791875	0.0165	0.156
chr22	51304566	533498	0.0104	0.1145
chrMT	16571	9796	0.5912	0.8886
chrX	155270560	2191140	0.0141	0.1403
chrY	59373566	194099	0.0033	0.1014

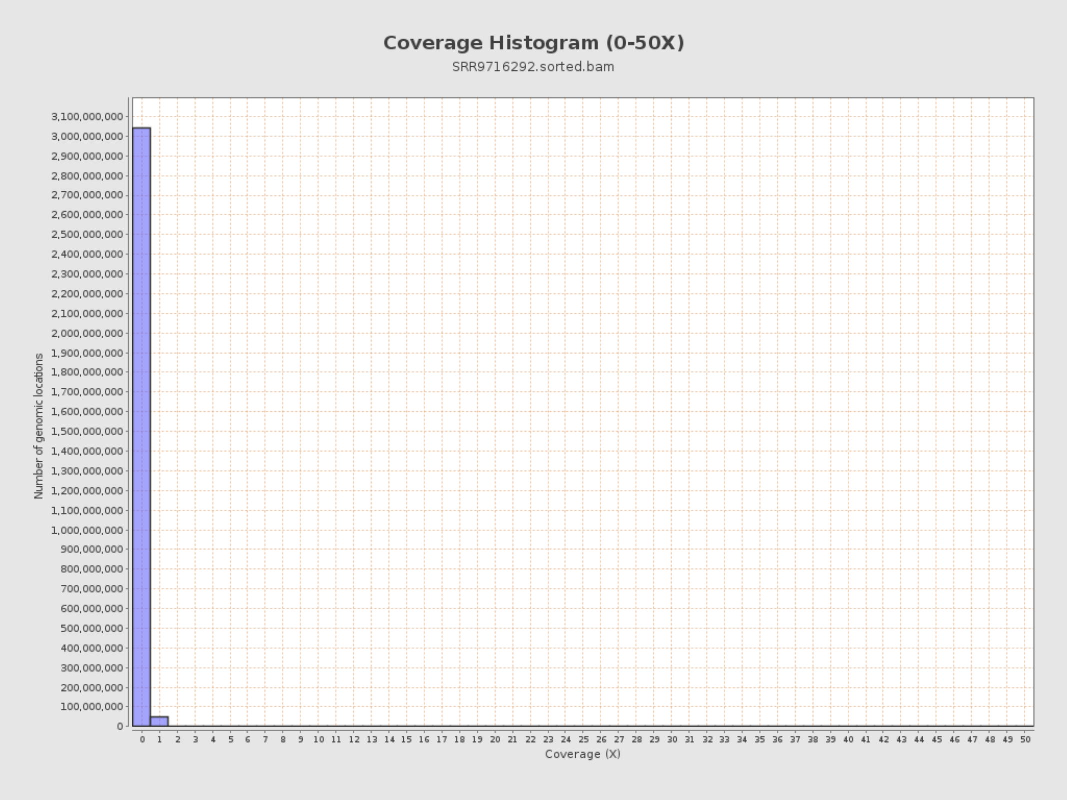
3. Results : Coverage across reference



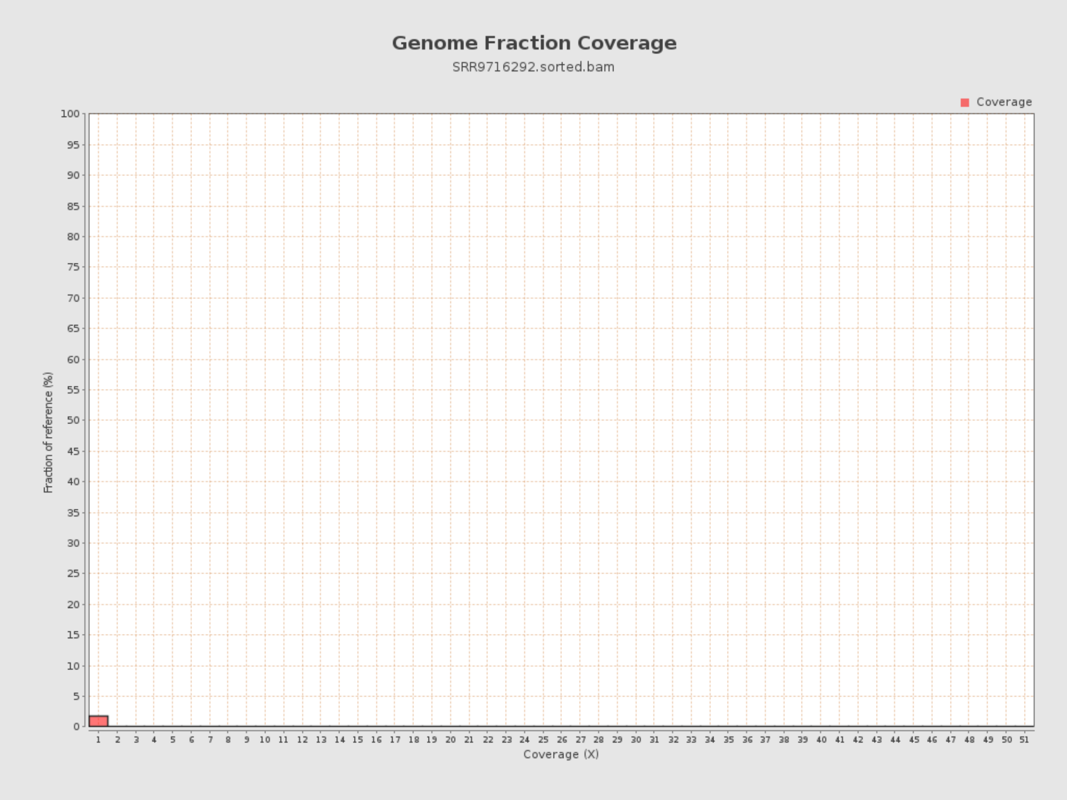
4. Results : Coverage Histogram



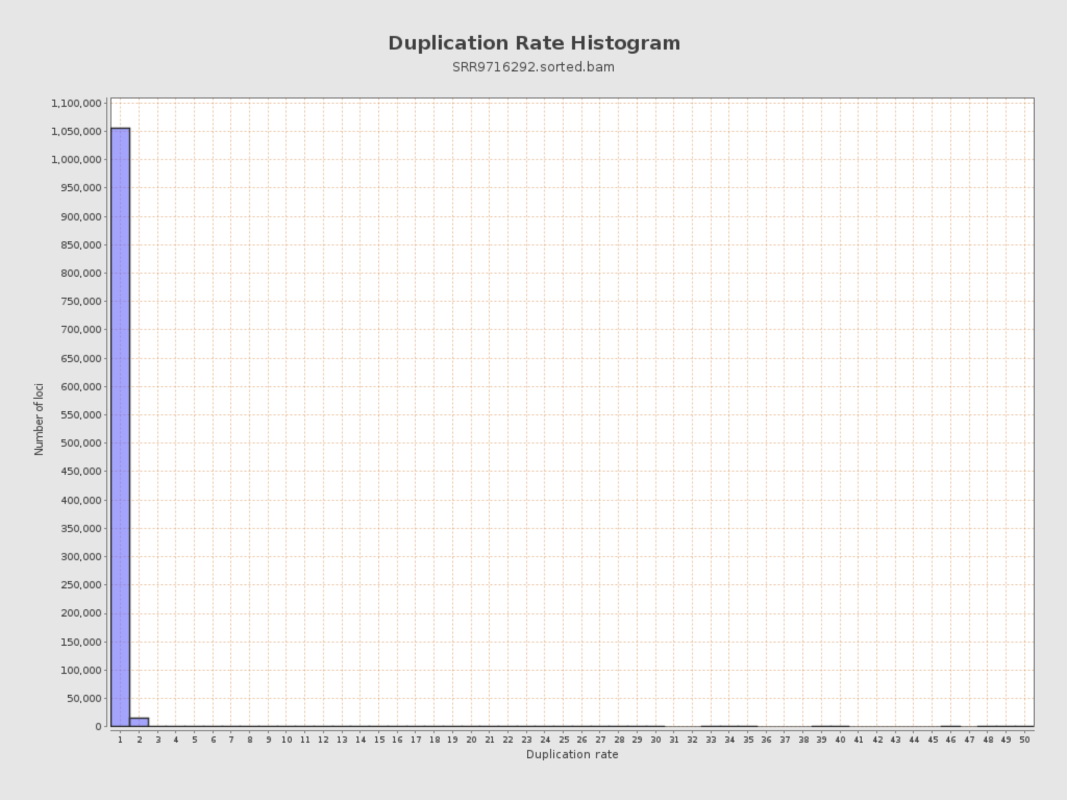
5. Results : Coverage Histogram (0-50X)



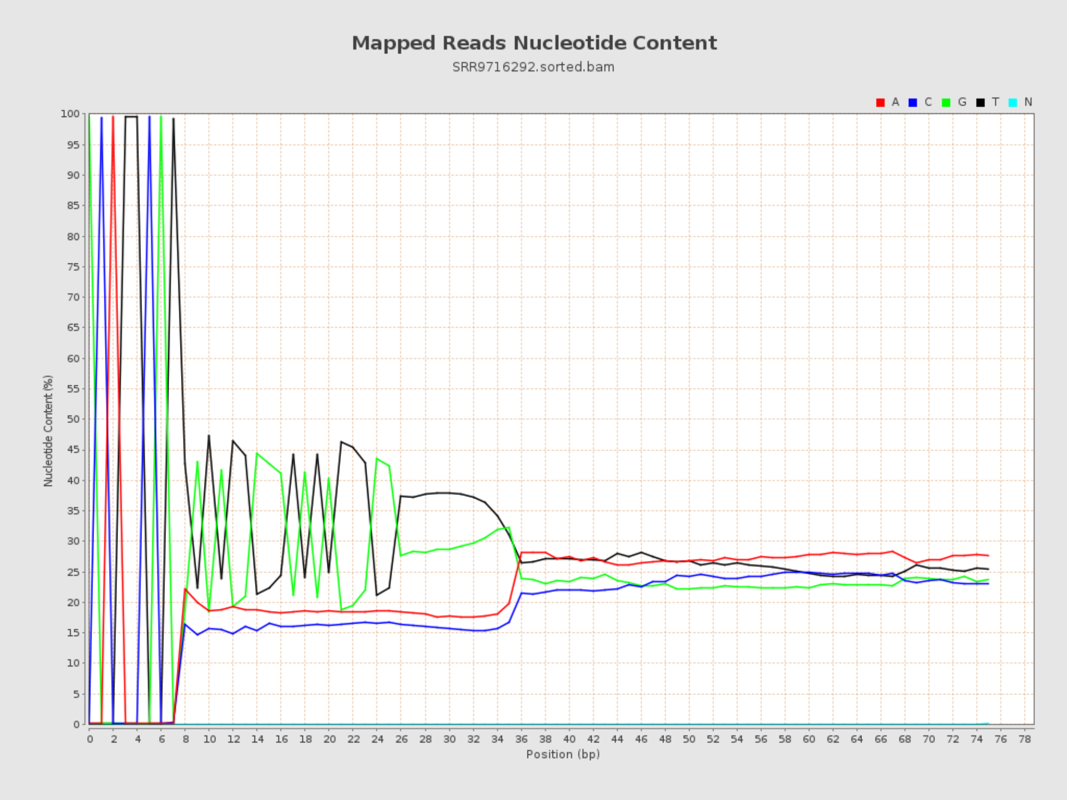
6. Results : Genome Fraction Coverage



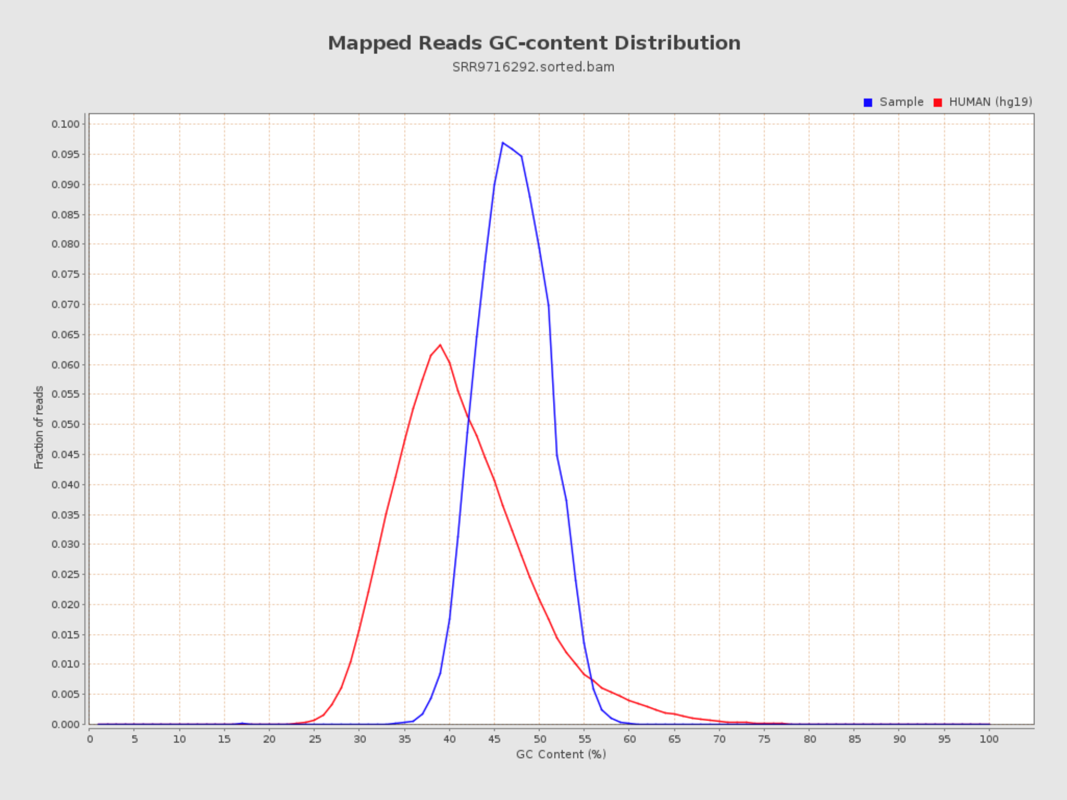
7. Results : Duplication Rate Histogram



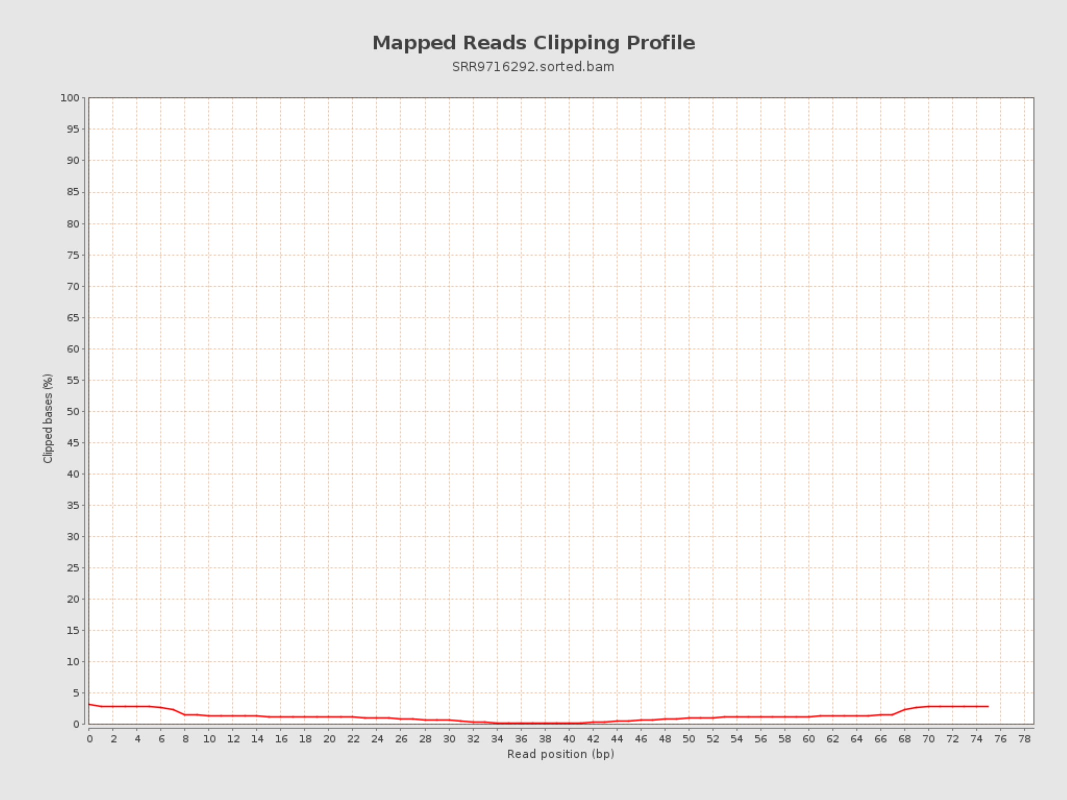
8. Results : Mapped Reads Nucleotide Content



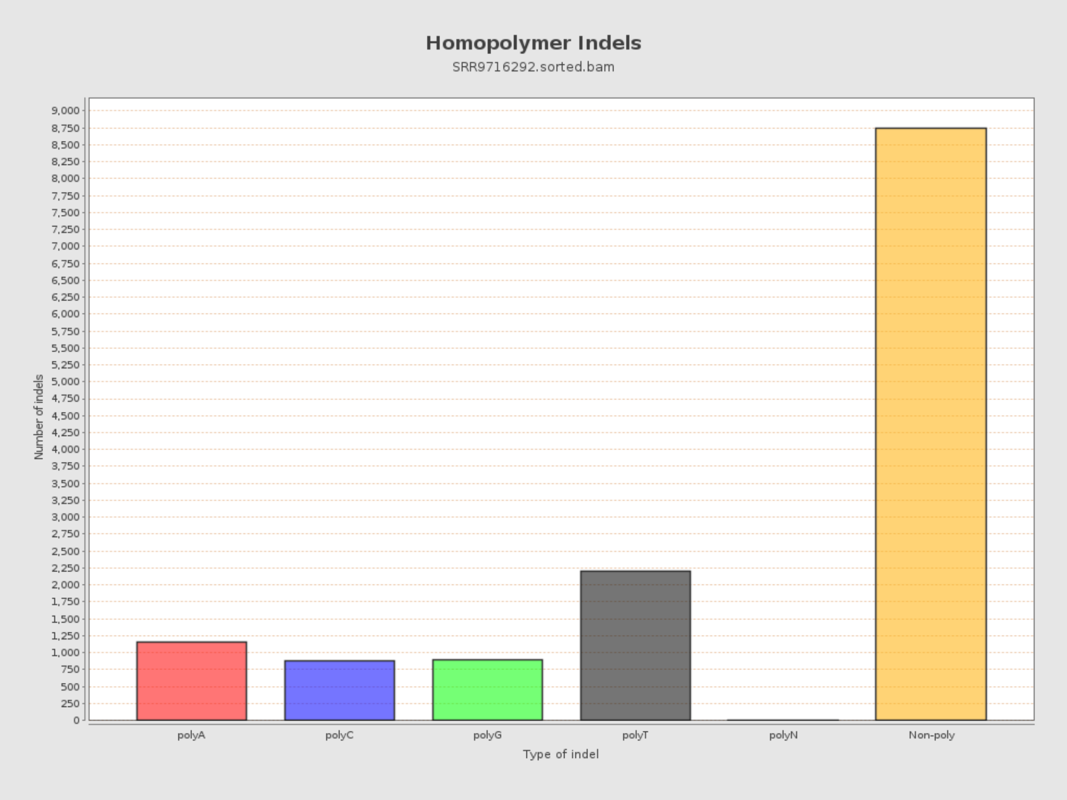
9. Results : Mapped Reads GC-content Distribution



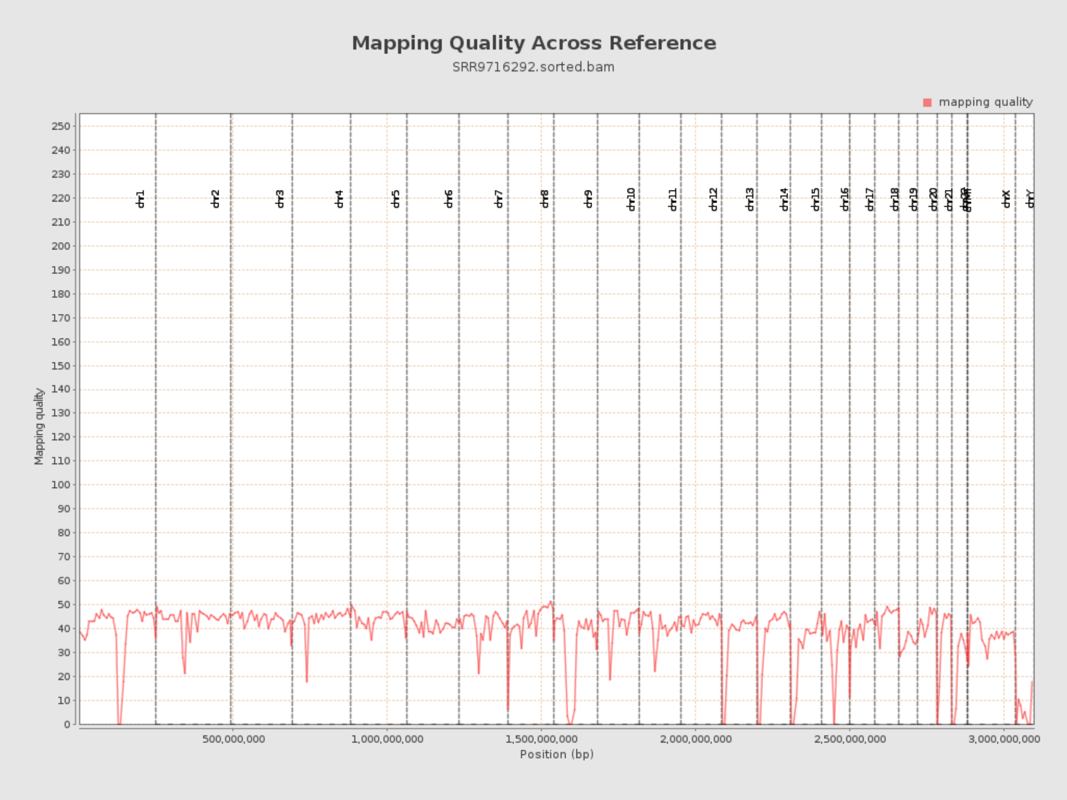
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram