Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 04:39:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716268.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_SRR9716268 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716268.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 04:39:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716268.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,902,212
Mapped reads	1,292,437 / 67.94%
Unmapped reads	609,775 / 32.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,510 / 0.08%
Read min/max/mean length	30 / 76 / 76.03
Duplicated reads (estimated)	107,773 / 5.67%
Duplication rate	7.13%
Clipped reads	1,292,318 / 67.94%

2.2. ACGT Content

Number/percentage of A's	14,305,297 / 21.73%
Number/percentage of C's	10,370,914 / 15.75%
Number/percentage of T's	22,065,676 / 33.52%
Number/percentage of G's	19,088,437 / 29%
Number/percentage of N's	1,053 / 0%
GC Percentage	44.75%

2.3. Coverage

Mean	0.0213

Standard Deviation	0.2142

2.4. Mapping Quality

Mean Mapping Quality	41.35

2.5. Mismatches and indels

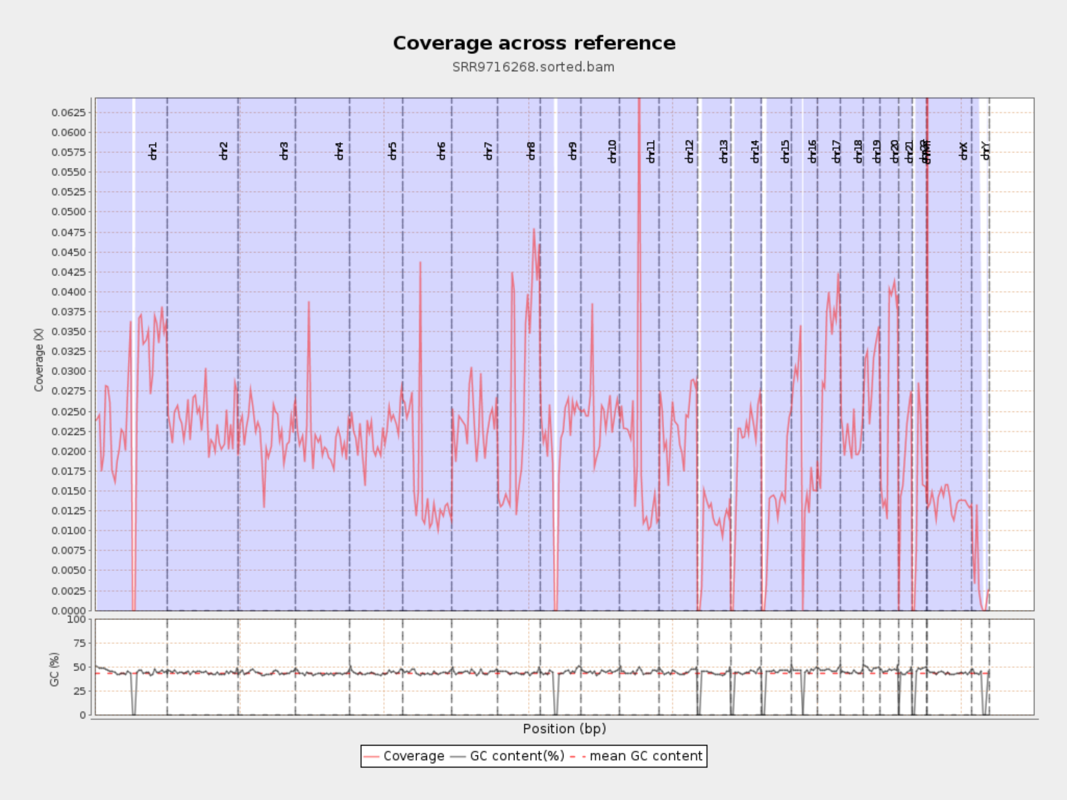
General error rate	0.8%
Mismatches	519,651
Insertions	4,045
Mapped reads with at least one insertion	0.31%
Deletions	10,454
Mapped reads with at least one deletion	0.8%
Homopolymer indels	41.38%

2.6. Chromosome stats

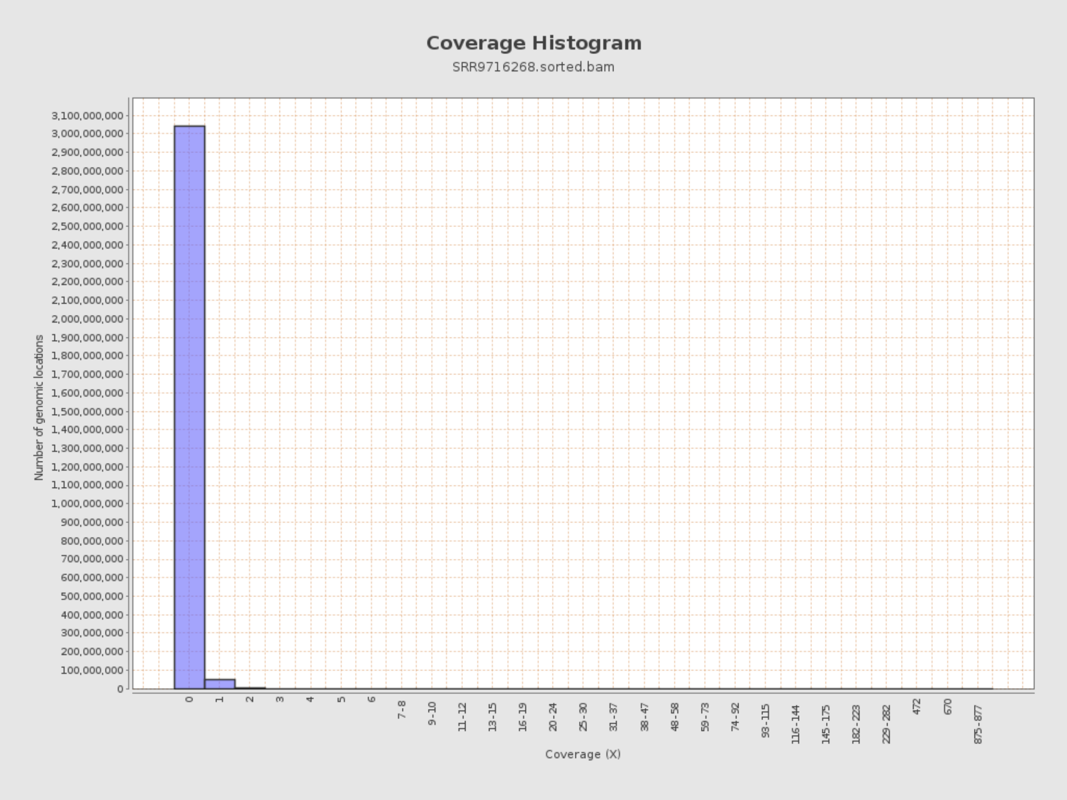
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6576093	0.0264	0.2637
chr2	243199373	5720710	0.0235	0.3889
chr3	198022430	4409962	0.0223	0.1754
chr4	191154276	4150447	0.0217	0.184
chr5	180915260	4026188	0.0223	0.1728
chr6	171115067	2849223	0.0167	0.1973
chr7	159138663	3770746	0.0237	0.2106

chr8	146364022	3974443	0.0272	0.2011
chr9	141213431	2908714	0.0206	0.183
chr10	135534747	3363549	0.0248	0.2293
chr11	135006516	2764096	0.0205	0.1876
chr12	133851895	3141017	0.0235	0.1792
chr13	115169878	1172730	0.0102	0.1231
chr14	107349540	2089300	0.0195	0.1648
chr15	102531392	1313994	0.0128	0.1335
chr16	90354753	1765217	0.0195	0.1773
chr17	81195210	2604970	0.0321	0.2163
chr18	78077248	1674011	0.0214	0.2004
chr19	59128983	1797509	0.0304	0.2596
chr20	63025520	1748691	0.0277	0.2084
chr21	48129895	906507	0.0188	0.168
chr22	51304566	741332	0.0144	0.1417
chrMT	16571	34046	2.0546	2.1886
chrX	155270560	2130801	0.0137	0.144
chrY	59373566	214538	0.0036	0.1018

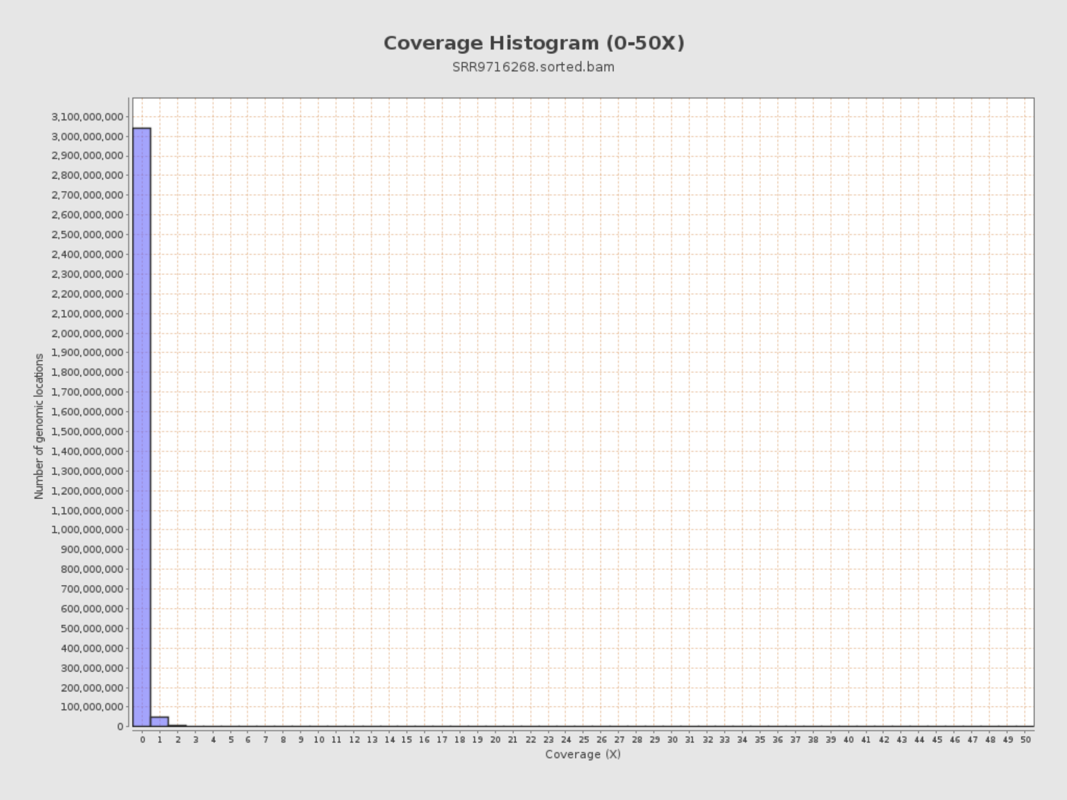
3. Results : Coverage across reference



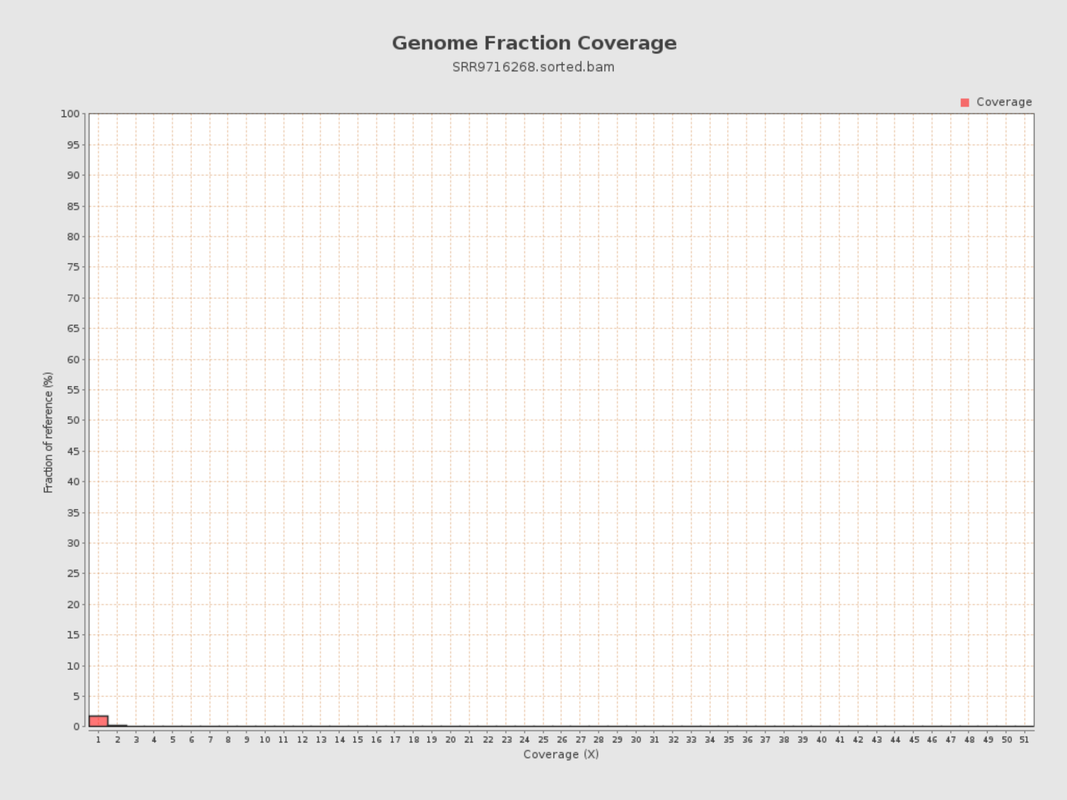
4. Results : Coverage Histogram



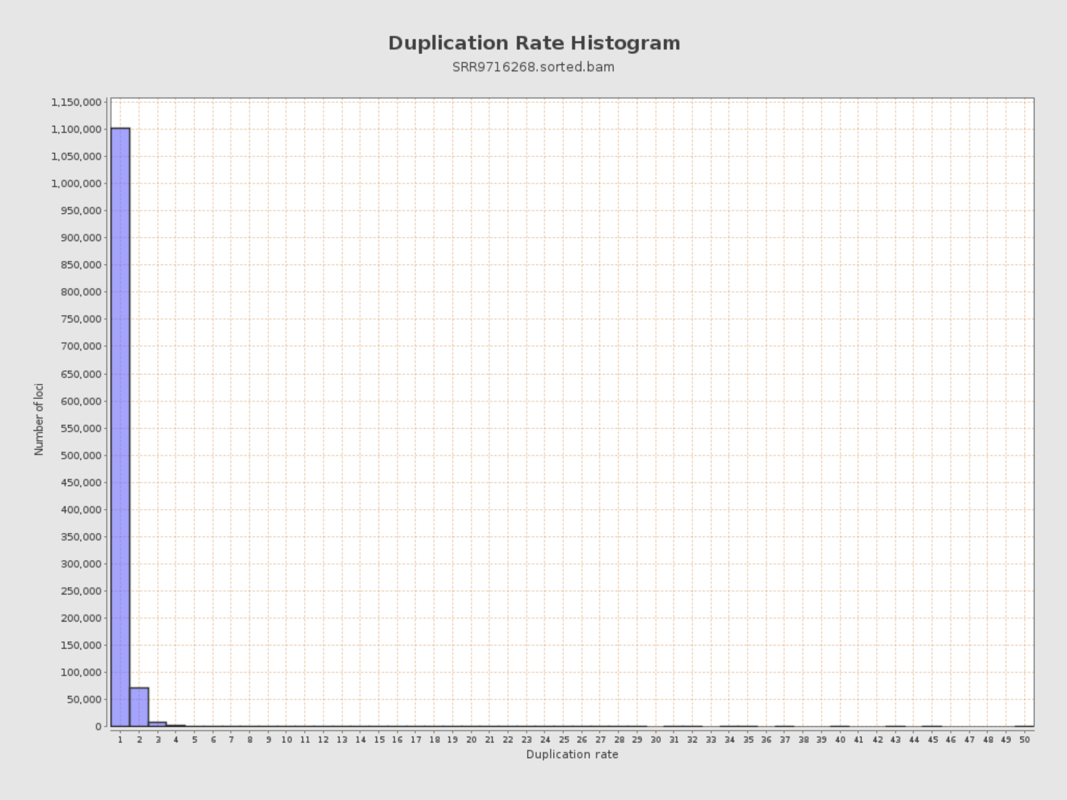
5. Results : Coverage Histogram (0-50X)



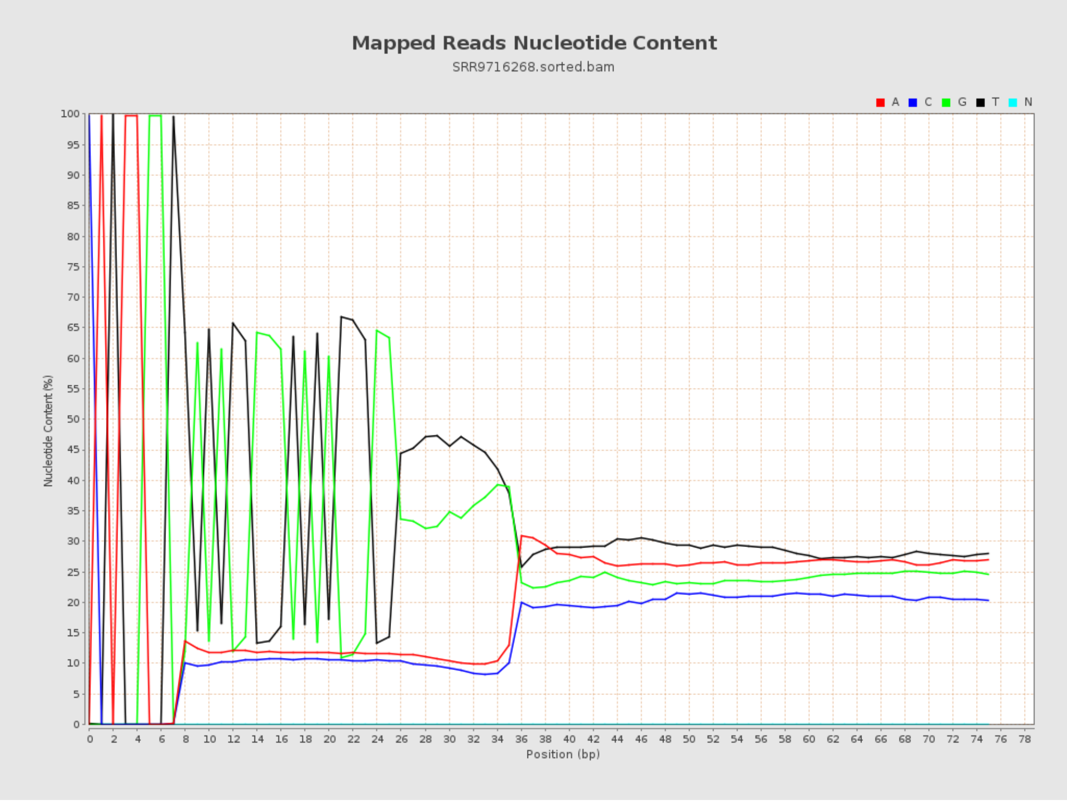
6. Results : Genome Fraction Coverage



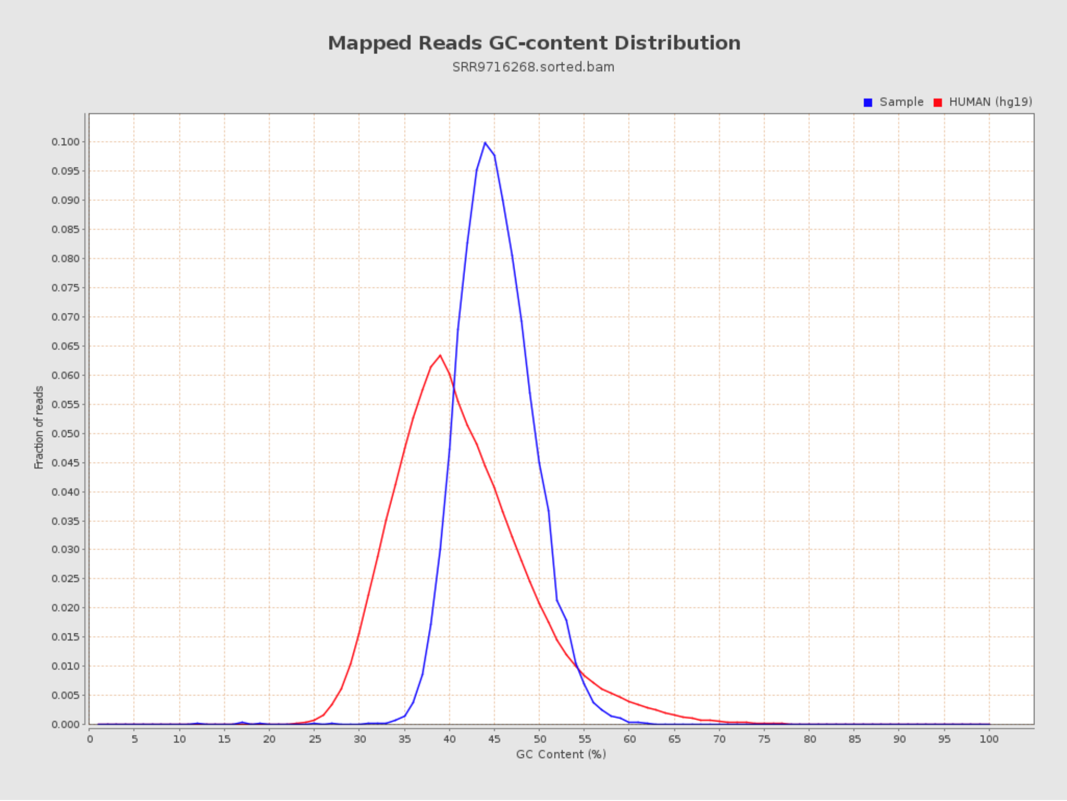
7. Results : Duplication Rate Histogram



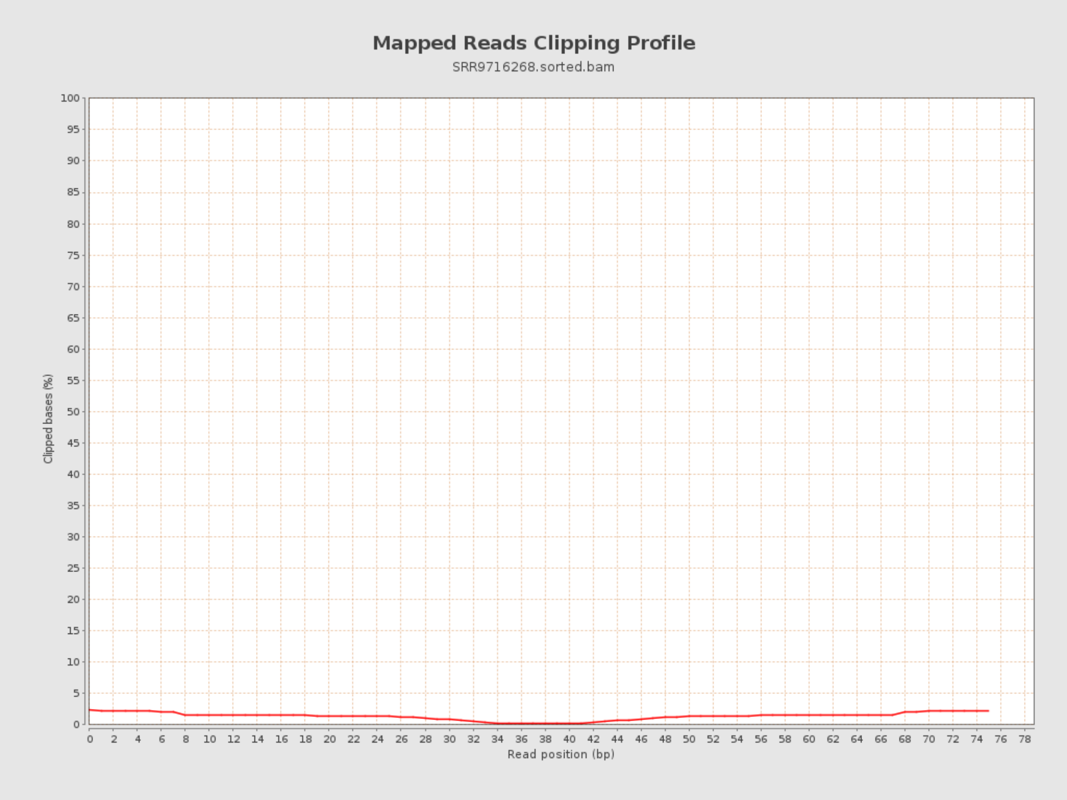
8. Results : Mapped Reads Nucleotide Content



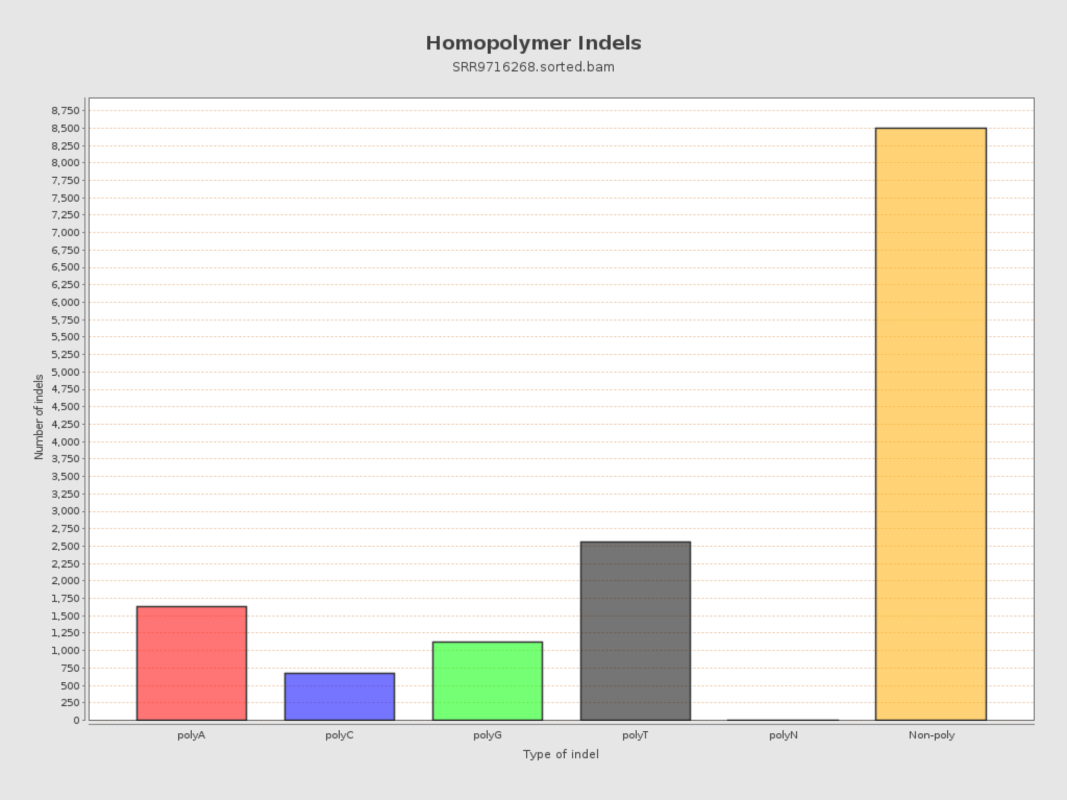
9. Results : Mapped Reads GC-content Distribution



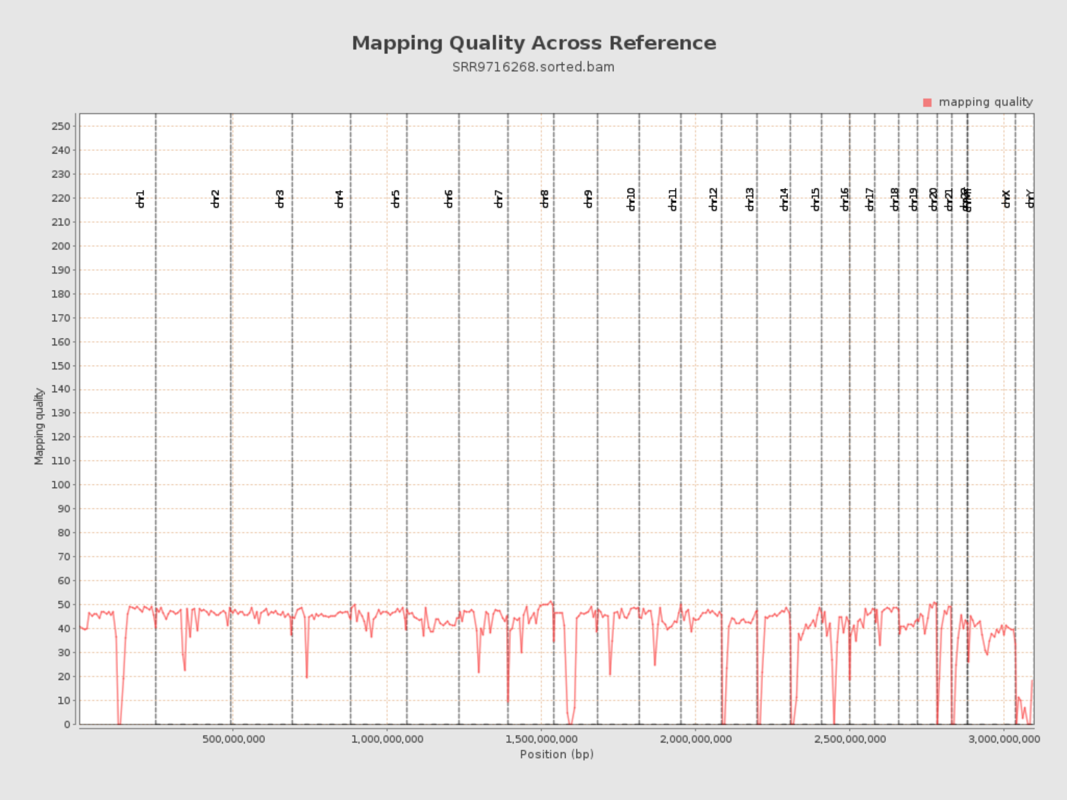
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram