Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 13:20:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716813.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_SRR9716813 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716813.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 13:20:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716813.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	766,158
Mapped reads	693,669 / 90.54%
Unmapped reads	72,489 / 9.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,012 / 0.52%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	17,274 / 2.25%
Duplication rate	1.96%
Clipped reads	695,890 / 90.83%

2.2. ACGT Content

Number/percentage of A's	10,371,964 / 25.89%
Number/percentage of C's	8,059,192 / 20.12%
Number/percentage of T's	12,268,713 / 30.63%
Number/percentage of G's	9,354,151 / 23.35%
Number/percentage of N's	249 / 0%
GC Percentage	43.47%

2.3. Coverage

Mean	0.0129

Standard Deviation	0.1438

2.4. Mapping Quality

Mean Mapping Quality	44.75

2.5. Mismatches and indels

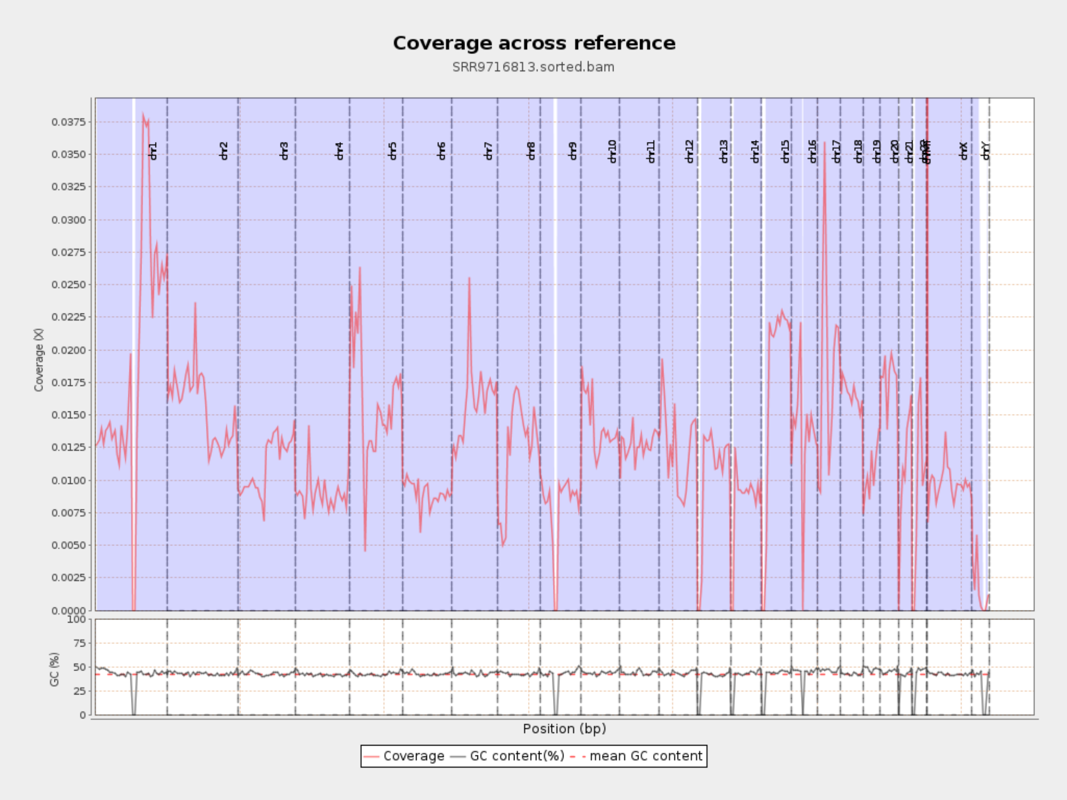
General error rate	0.5%
Mismatches	196,539
Insertions	2,833
Mapped reads with at least one insertion	0.41%
Deletions	6,859
Mapped reads with at least one deletion	0.98%
Homopolymer indels	42.52%

2.6. Chromosome stats

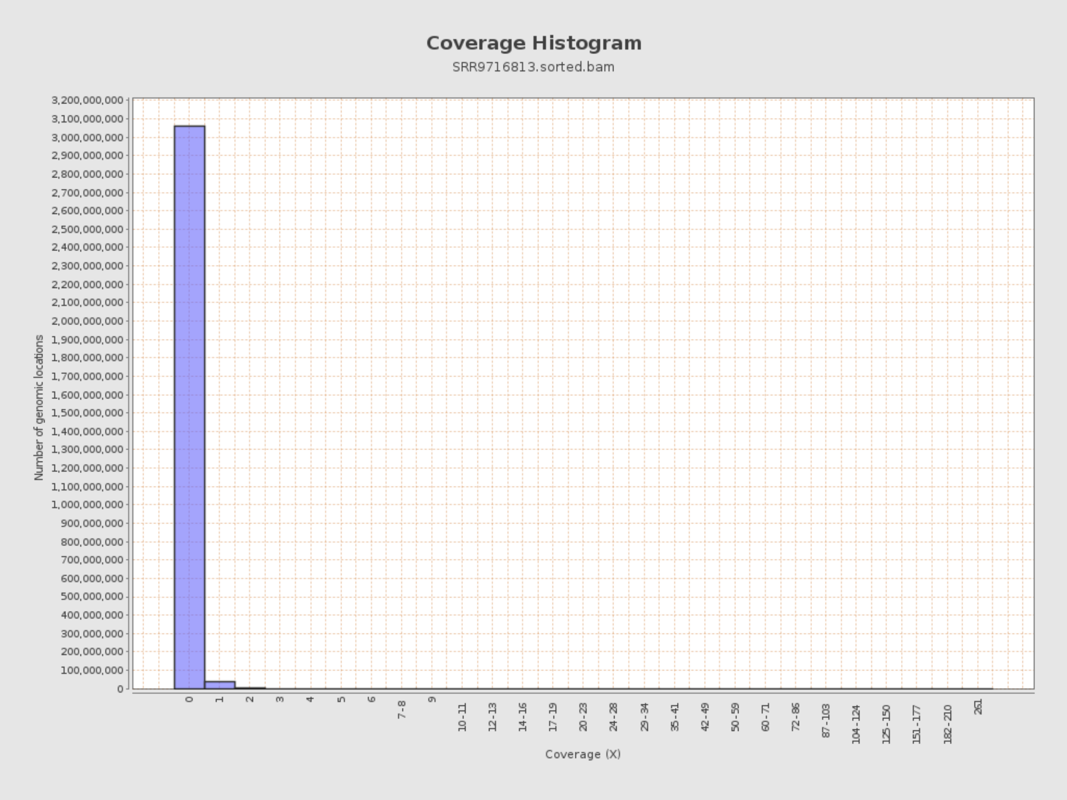
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4684862	0.0188	0.2095
chr2	243199373	3790948	0.0156	0.1803
chr3	198022430	2205536	0.0111	0.1111
chr4	191154276	1719789	0.009	0.1059
chr5	180915260	2931453	0.0162	0.134
chr6	171115067	1535333	0.009	0.1044
chr7	159138663	2559205	0.0161	0.2025

chr8	146364022	1834903	0.0125	0.1362
chr9	141213431	1113899	0.0079	0.1124
chr10	135534747	1938071	0.0143	0.1377
chr11	135006516	1722277	0.0128	0.1388
chr12	133851895	1664491	0.0124	0.1178
chr13	115169878	1185154	0.0103	0.1067
chr14	107349540	880145	0.0082	0.098
chr15	102531392	1801096	0.0176	0.1398
chr16	90354753	1210723	0.0134	0.1247
chr17	81195210	1557233	0.0192	0.151
chr18	78077248	1298375	0.0166	0.2173
chr19	59128983	633987	0.0107	0.1559
chr20	63025520	1122124	0.0178	0.1419
chr21	48129895	530041	0.011	0.1121
chr22	51304566	489663	0.0095	0.1023
chrMT	16571	36774	2.2192	2.0125
chrX	155270560	1522151	0.0098	0.1106
chrY	59373566	97143	0.0016	0.0543

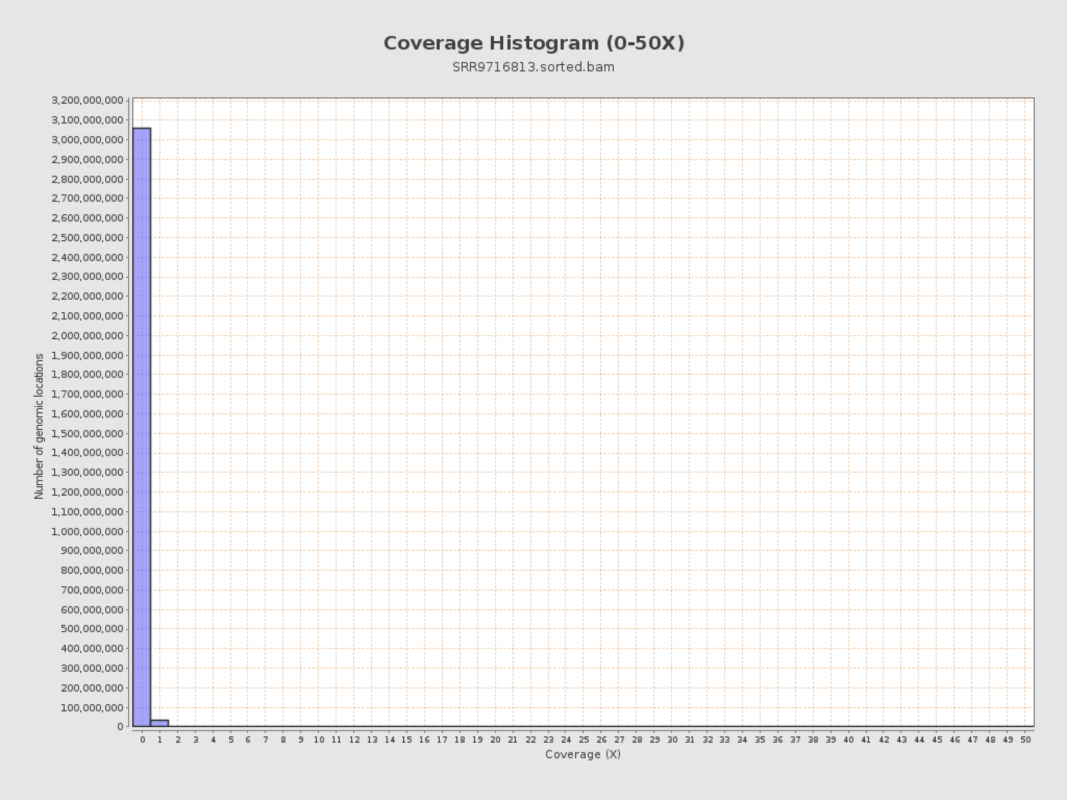
3. Results : Coverage across reference



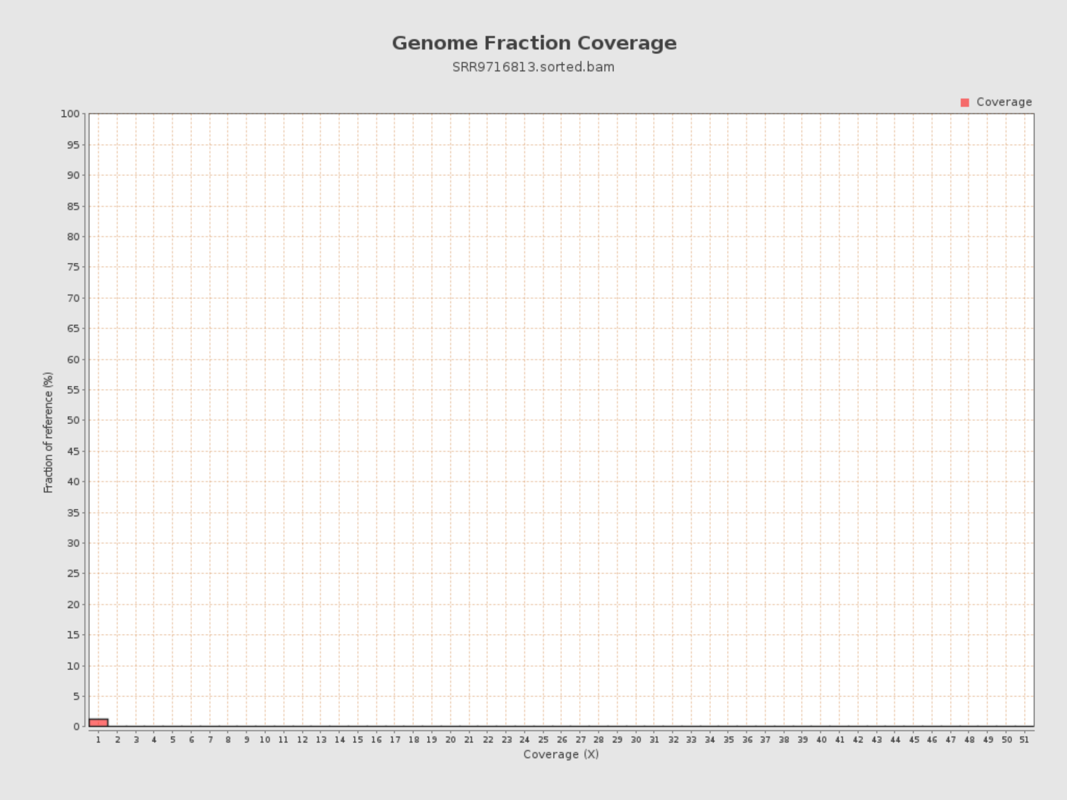
4. Results : Coverage Histogram



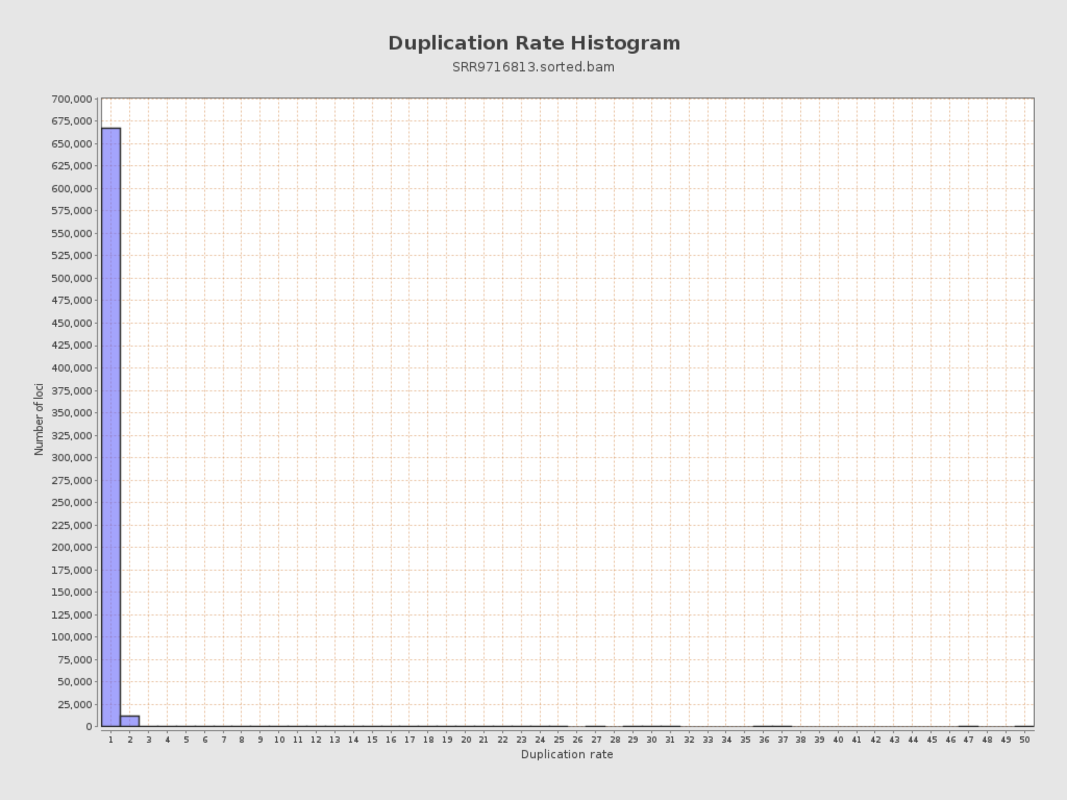
5. Results : Coverage Histogram (0-50X)



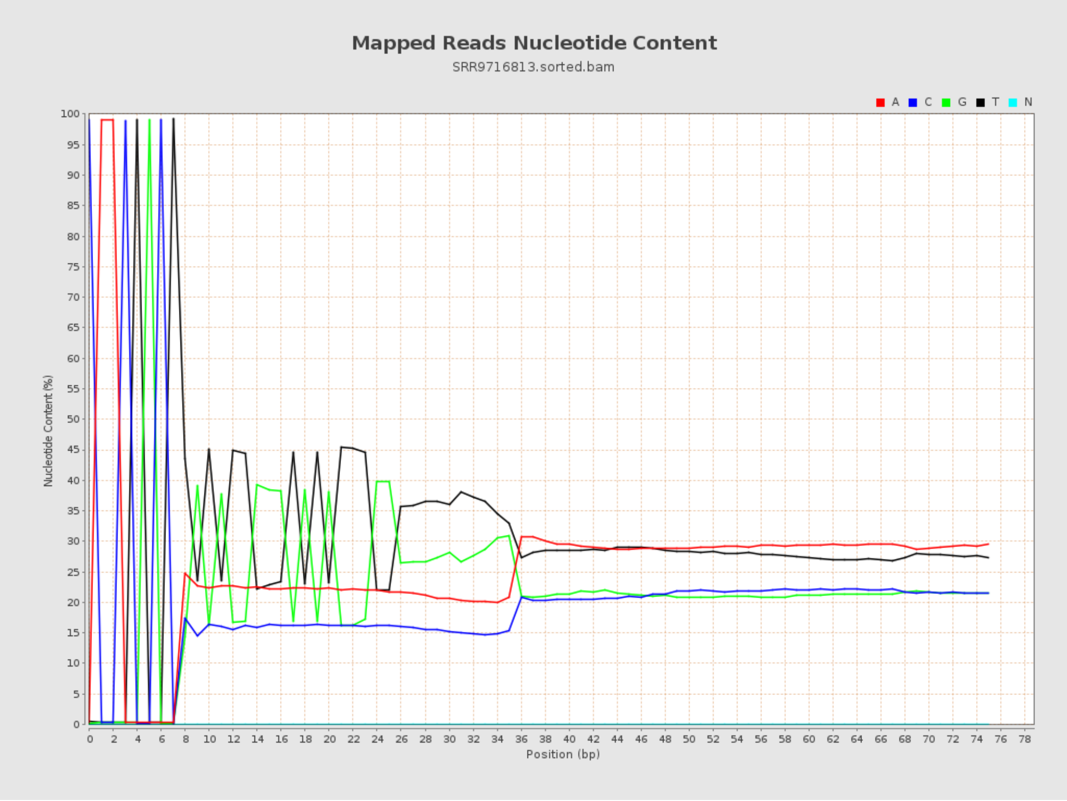
6. Results : Genome Fraction Coverage



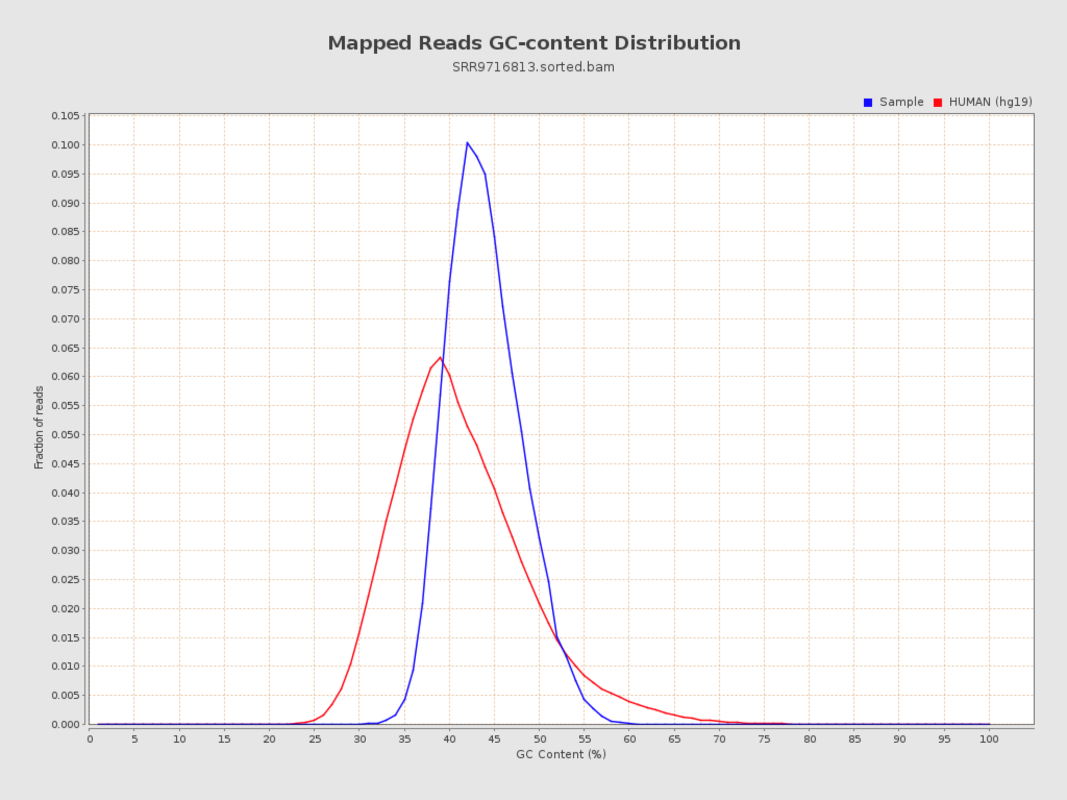
7. Results : Duplication Rate Histogram



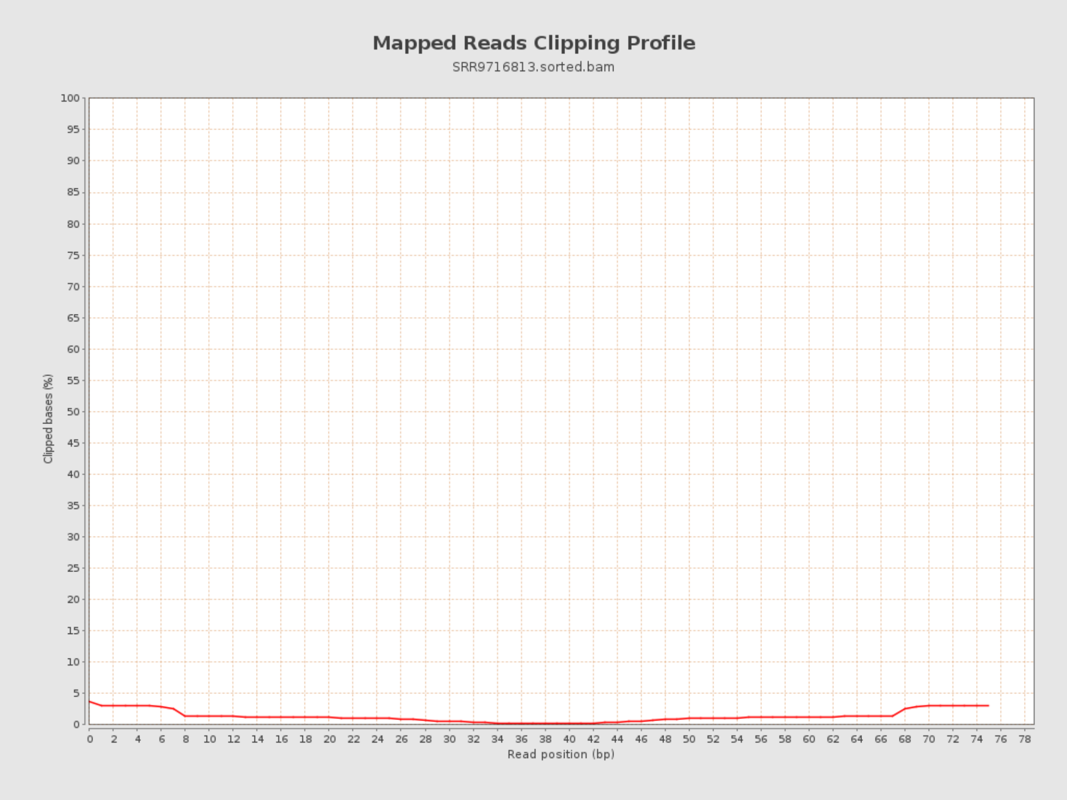
8. Results : Mapped Reads Nucleotide Content



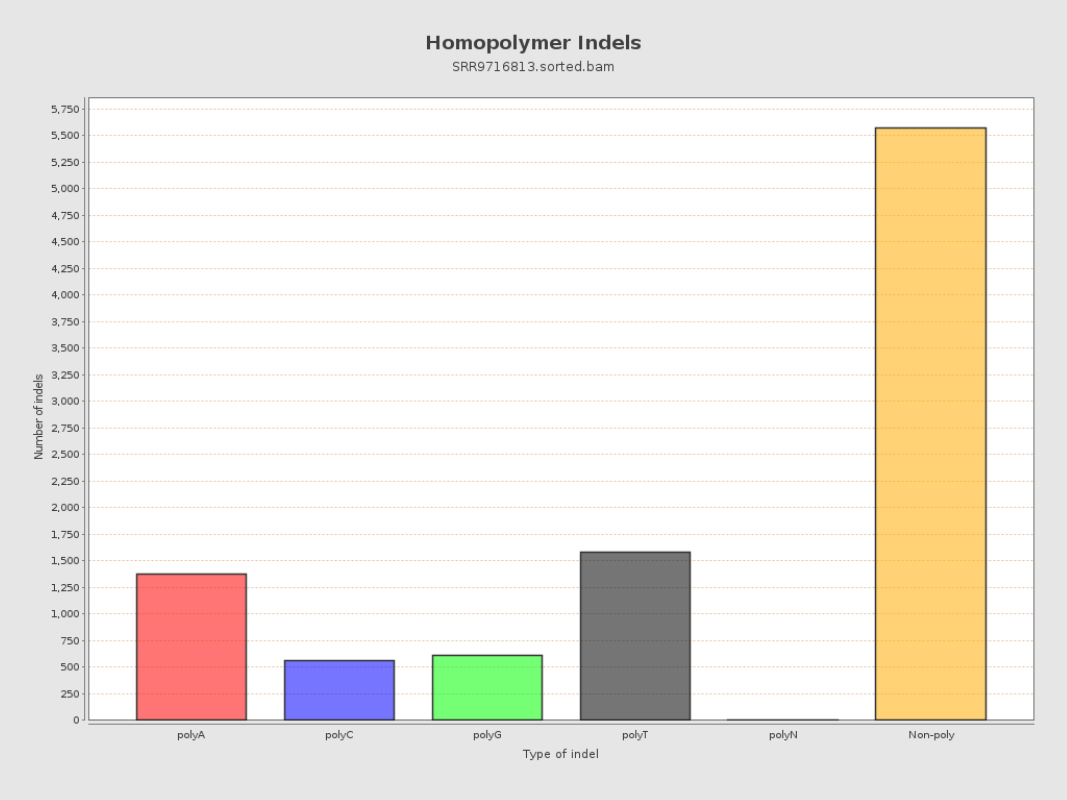
9. Results : Mapped Reads GC-content Distribution



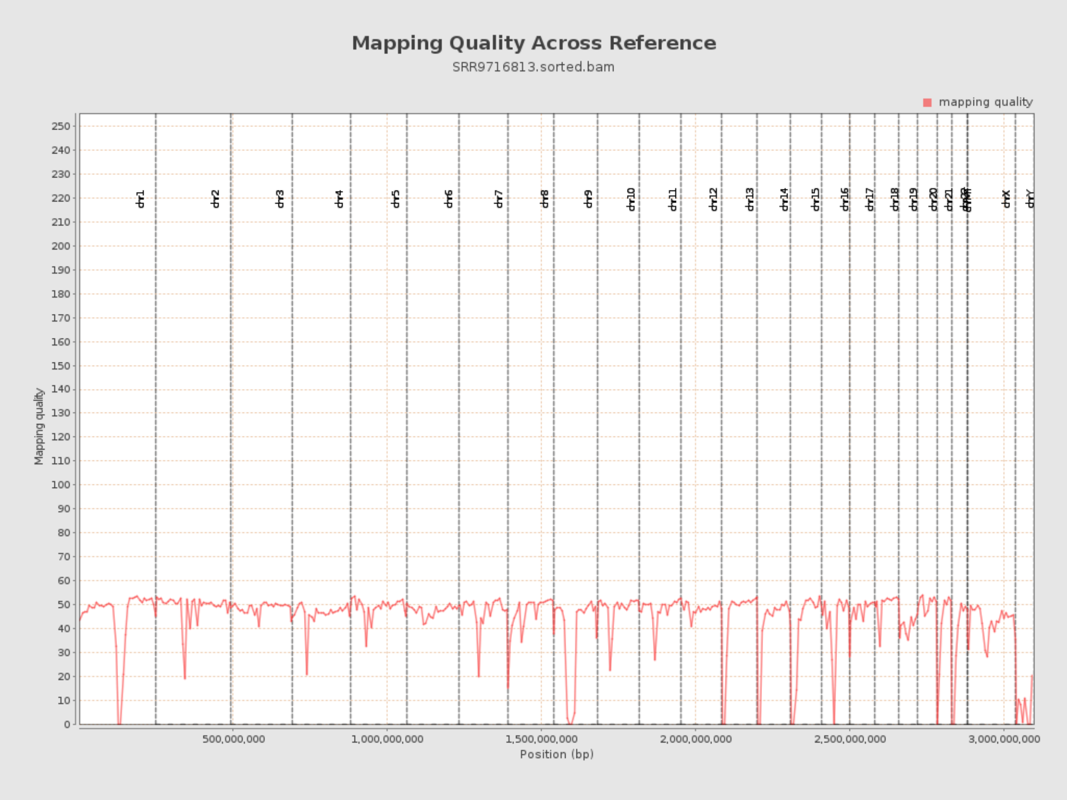
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram