Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 01:19:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716629.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_SRR9716629 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716629.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 01:19:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716629.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	896,909
Mapped reads	807,905 / 90.08%
Unmapped reads	89,004 / 9.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,212 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	23,494 / 2.62%
Duplication rate	2.24%
Clipped reads	807,923 / 90.08%

2.2. ACGT Content

Number/percentage of A's	11,145,289 / 23.95%
Number/percentage of C's	9,066,879 / 19.48%
Number/percentage of T's	15,355,878 / 32.99%
Number/percentage of G's	10,975,237 / 23.58%
Number/percentage of N's	1,225 / 0%
GC Percentage	43.06%

2.3. Coverage

Mean	0.015

Standard Deviation	0.1672

2.4. Mapping Quality

Mean Mapping Quality	45.16

2.5. Mismatches and indels

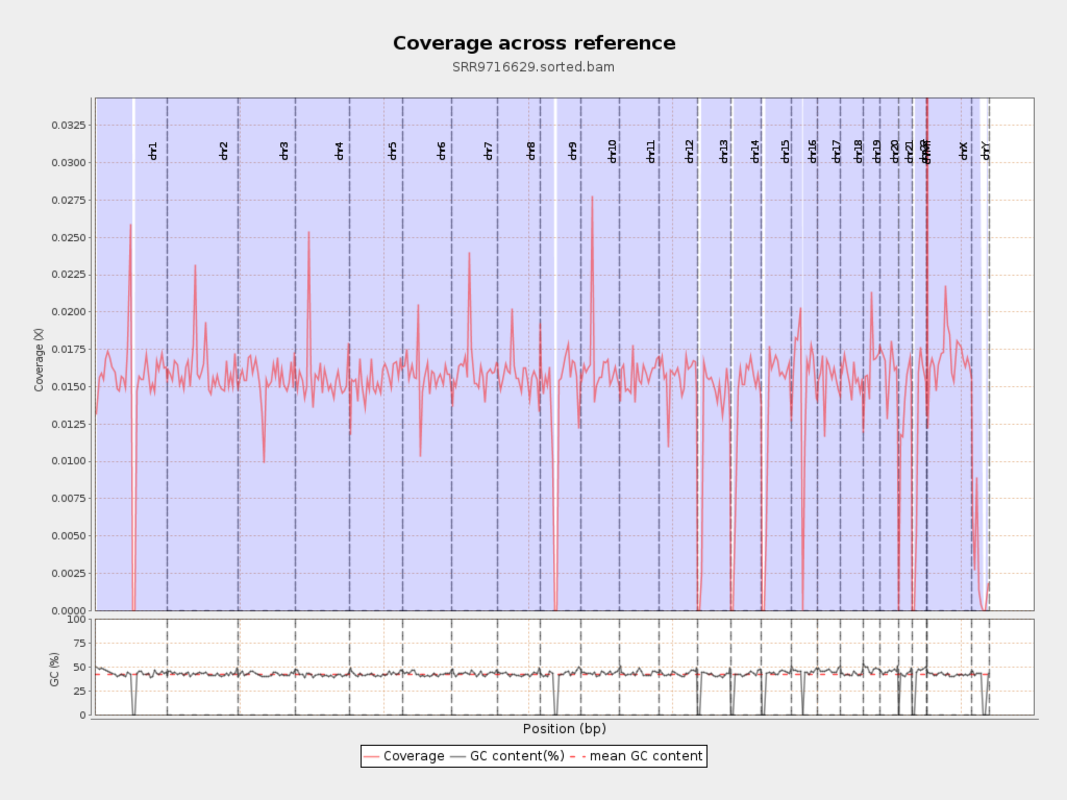
General error rate	0.53%
Mismatches	239,736
Insertions	3,755
Mapped reads with at least one insertion	0.46%
Deletions	9,007
Mapped reads with at least one deletion	1.1%
Homopolymer indels	40.31%

2.6. Chromosome stats

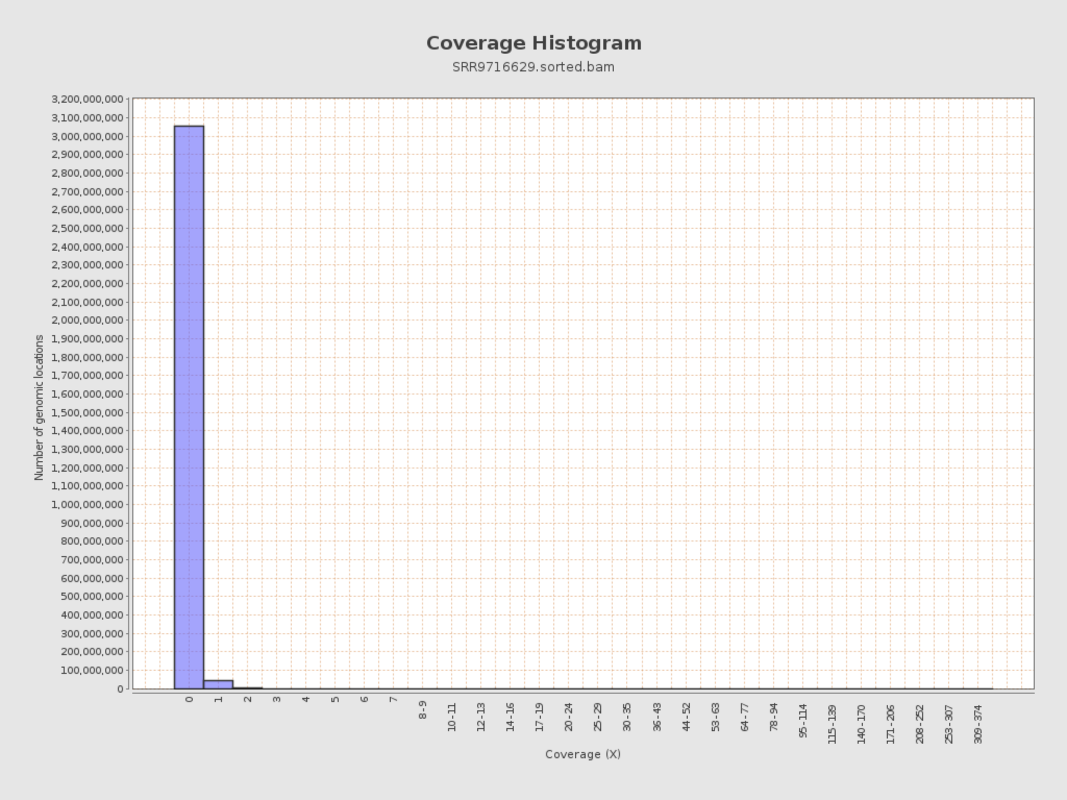
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3773211	0.0151	0.2797
chr2	243199373	3908618	0.0161	0.208
chr3	198022430	3062111	0.0155	0.1316
chr4	191154276	3005572	0.0157	0.1397
chr5	180915260	2810060	0.0155	0.1319
chr6	171115067	2696378	0.0158	0.147
chr7	159138663	2580529	0.0162	0.1917

chr8	146364022	2307766	0.0158	0.1632
chr9	141213431	1943420	0.0138	0.1458
chr10	135534747	2234624	0.0165	0.1671
chr11	135006516	2128802	0.0158	0.1505
chr12	133851895	2104423	0.0157	0.1334
chr13	115169878	1443840	0.0125	0.1192
chr14	107349540	1390593	0.013	0.122
chr15	102531392	1355099	0.0132	0.1223
chr16	90354753	1347484	0.0149	0.1336
chr17	81195210	1257401	0.0155	0.1357
chr18	78077248	1222096	0.0157	0.2176
chr19	59128983	984059	0.0166	0.2117
chr20	63025520	1012734	0.0161	0.1362
chr21	48129895	620800	0.0129	0.1266
chr22	51304566	571961	0.0111	0.1118
chrMT	16571	17187	1.0372	1.2172
chrX	155270560	2629954	0.0169	0.1454
chrY	59373566	150119	0.0025	0.0794

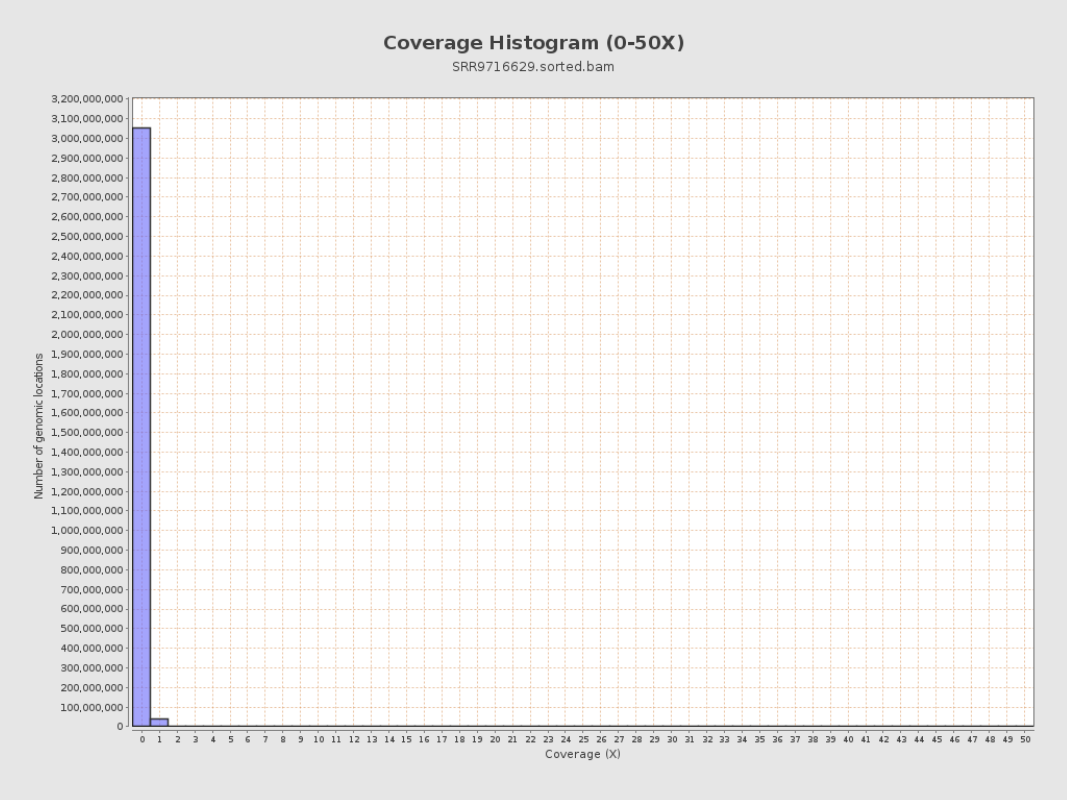
3. Results : Coverage across reference



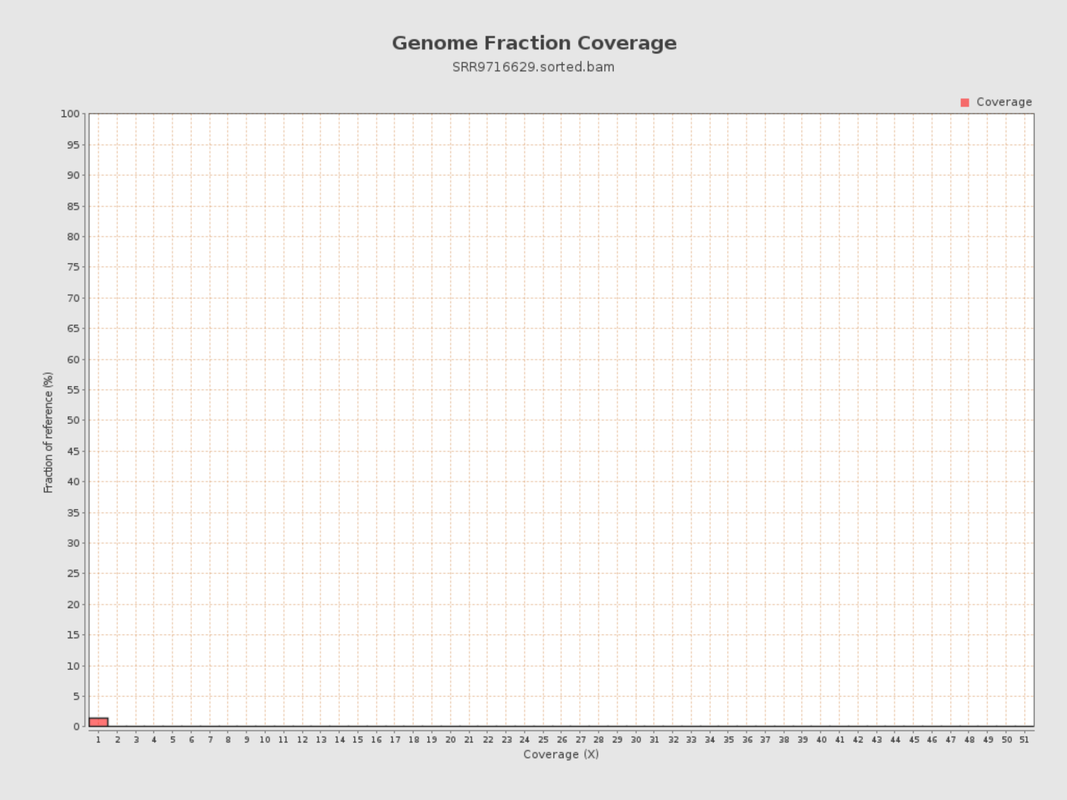
4. Results : Coverage Histogram



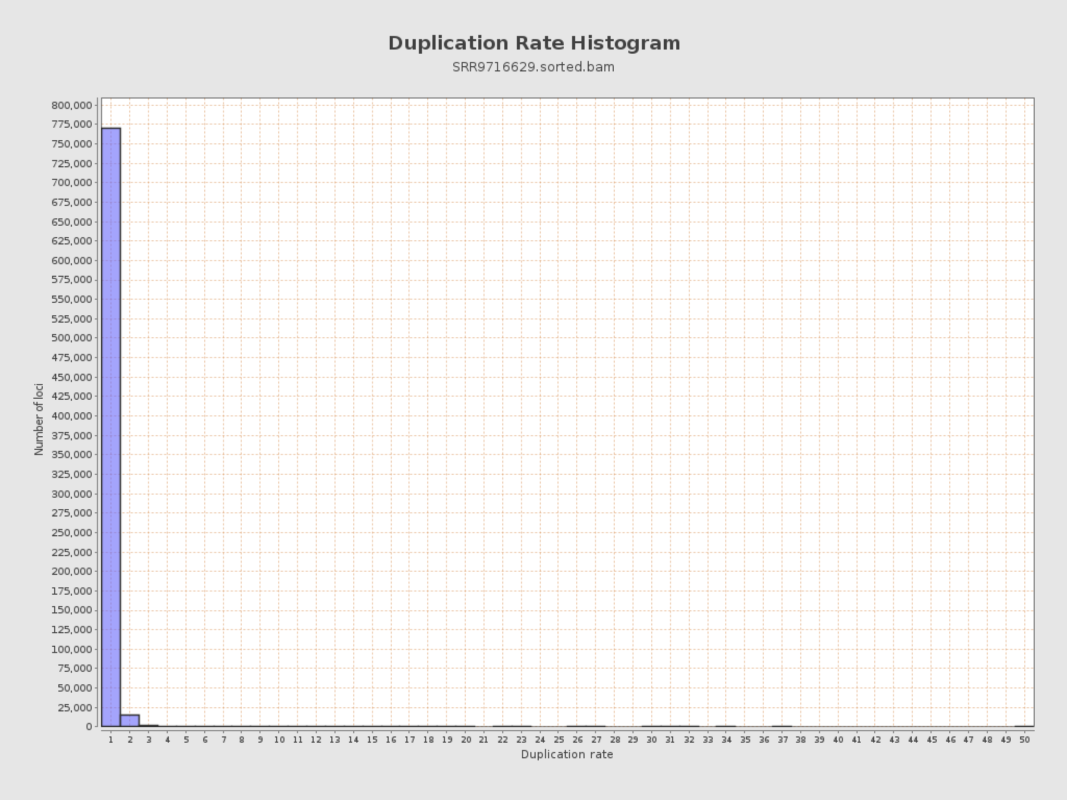
5. Results : Coverage Histogram (0-50X)



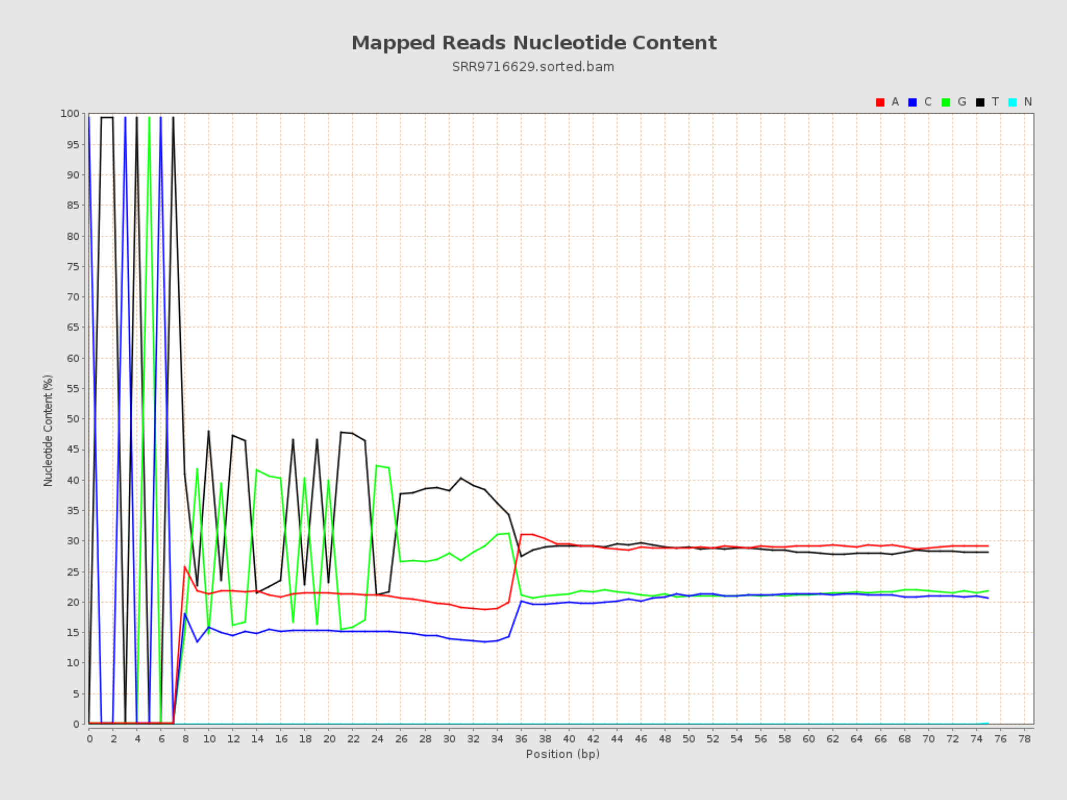
6. Results : Genome Fraction Coverage



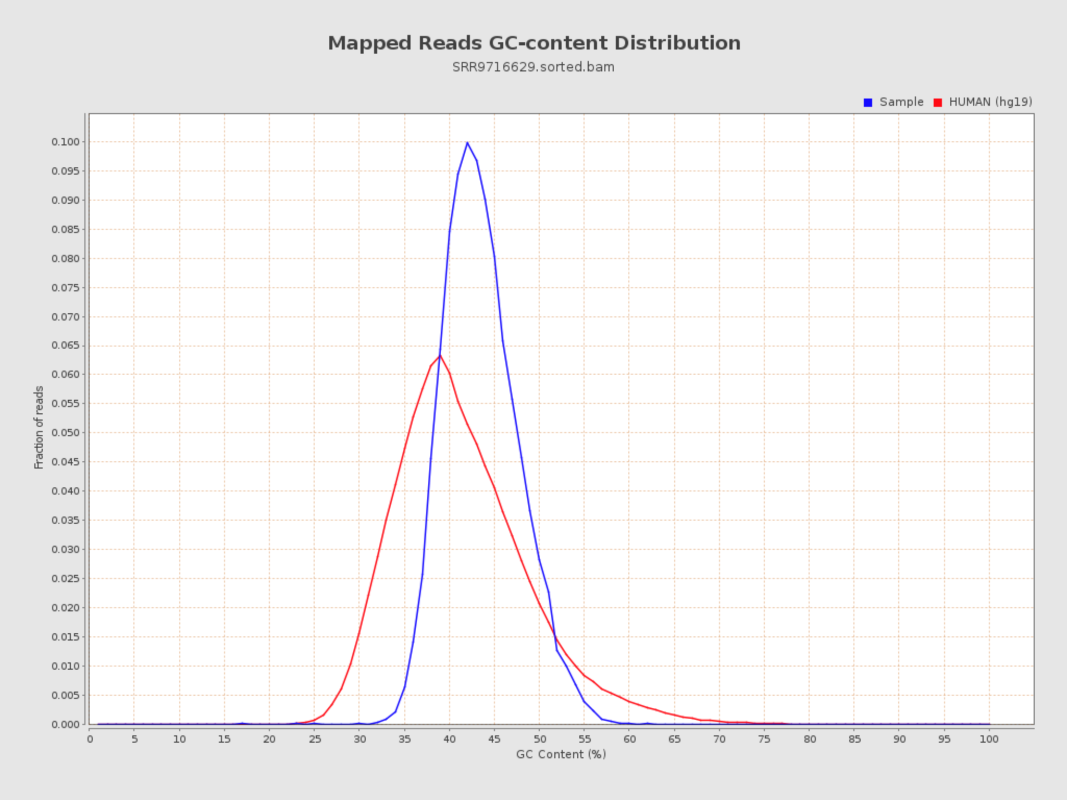
7. Results : Duplication Rate Histogram



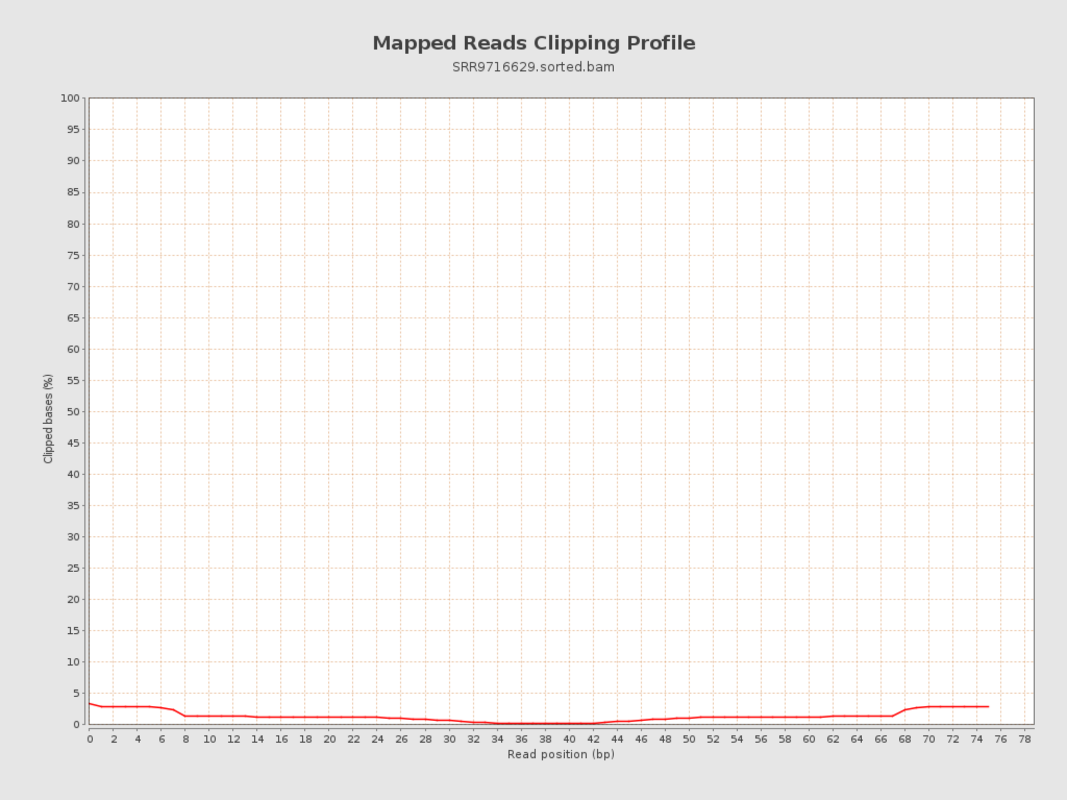
8. Results : Mapped Reads Nucleotide Content



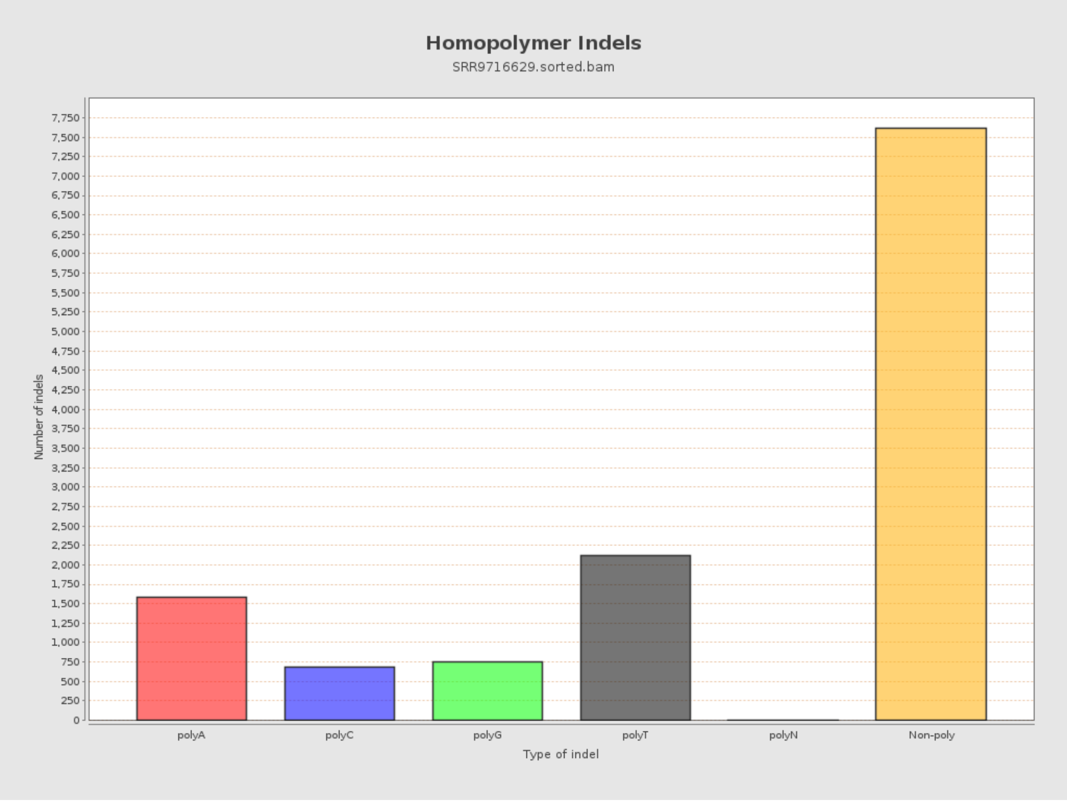
9. Results : Mapped Reads GC-content Distribution



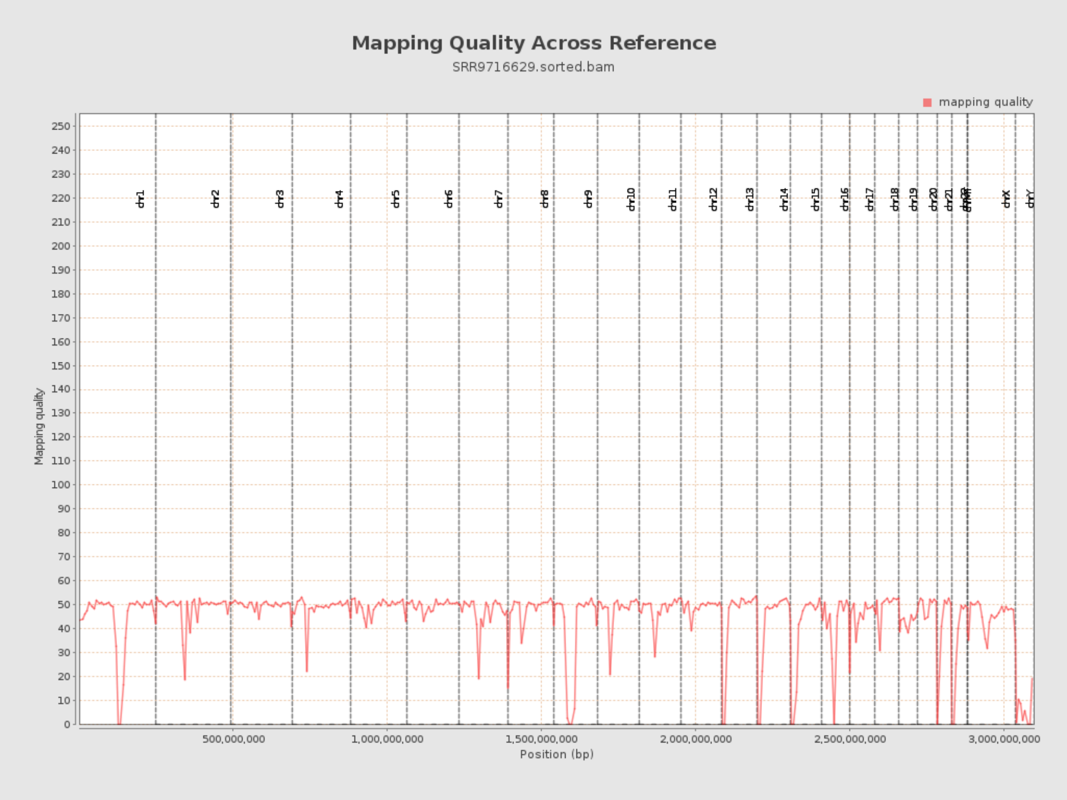
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram