Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 14:53:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716849.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_SRR9716849 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716849.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 14:53:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716849.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	738,545
Mapped reads	626,396 / 84.81%
Unmapped reads	112,149 / 15.19%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,405 / 0.46%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	14,839 / 2.01%
Duplication rate	1.88%
Clipped reads	628,487 / 85.1%

2.2. ACGT Content

Number/percentage of A's	9,311,924 / 25.91%
Number/percentage of C's	6,935,670 / 19.29%
Number/percentage of T's	11,288,649 / 31.4%
Number/percentage of G's	8,409,754 / 23.4%
Number/percentage of N's	257 / 0%
GC Percentage	42.69%

2.3. Coverage

Mean	0.0116

Standard Deviation	0.1342

2.4. Mapping Quality

Mean Mapping Quality	44.51

2.5. Mismatches and indels

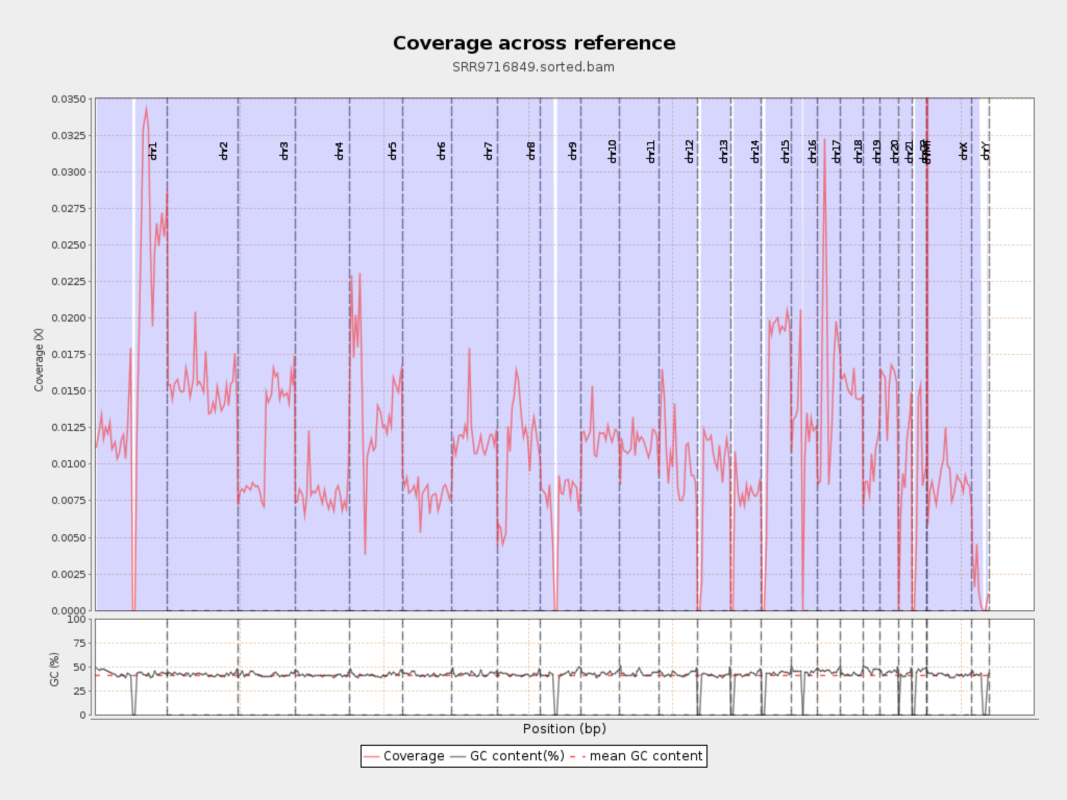
General error rate	0.5%
Mismatches	174,739
Insertions	2,566
Mapped reads with at least one insertion	0.41%
Deletions	6,190
Mapped reads with at least one deletion	0.98%
Homopolymer indels	42.01%

2.6. Chromosome stats

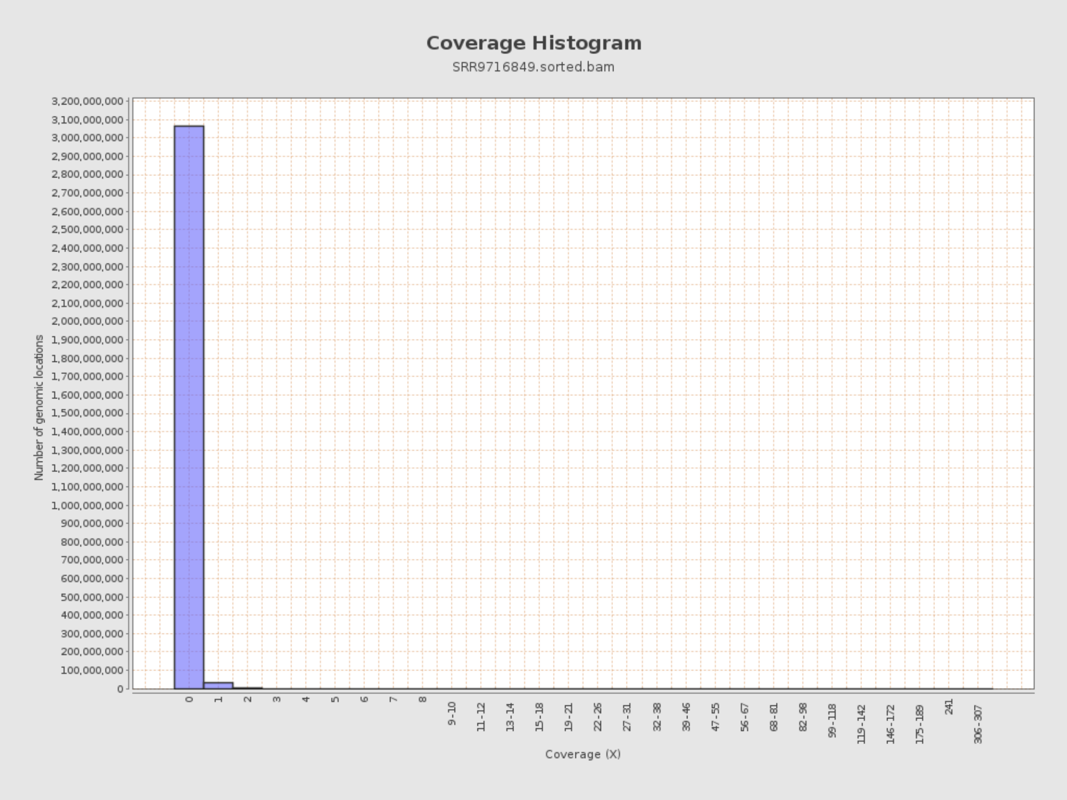
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4310751	0.0173	0.1991
chr2	243199373	3719337	0.0153	0.1834
chr3	198022430	2337653	0.0118	0.114
chr4	191154276	1516648	0.0079	0.1009
chr5	180915260	2598794	0.0144	0.1262
chr6	171115067	1367950	0.008	0.0981
chr7	159138663	1889469	0.0119	0.156

chr8	146364022	1636561	0.0112	0.1303
chr9	141213431	1011910	0.0072	0.103
chr10	135534747	1635272	0.0121	0.1236
chr11	135006516	1543058	0.0114	0.1312
chr12	133851895	1403069	0.0105	0.108
chr13	115169878	1050439	0.0091	0.0999
chr14	107349540	772502	0.0072	0.0904
chr15	102531392	1605584	0.0157	0.1322
chr16	90354753	1094348	0.0121	0.1177
chr17	81195210	1384472	0.0171	0.1419
chr18	78077248	1186182	0.0152	0.1973
chr19	59128983	578178	0.0098	0.1387
chr20	63025520	968740	0.0154	0.1306
chr21	48129895	458126	0.0095	0.1036
chr22	51304566	429746	0.0084	0.0966
chrMT	16571	5055	0.3051	0.6083
chrX	155270560	1364256	0.0088	0.1043
chrY	59373566	87692	0.0015	0.0463

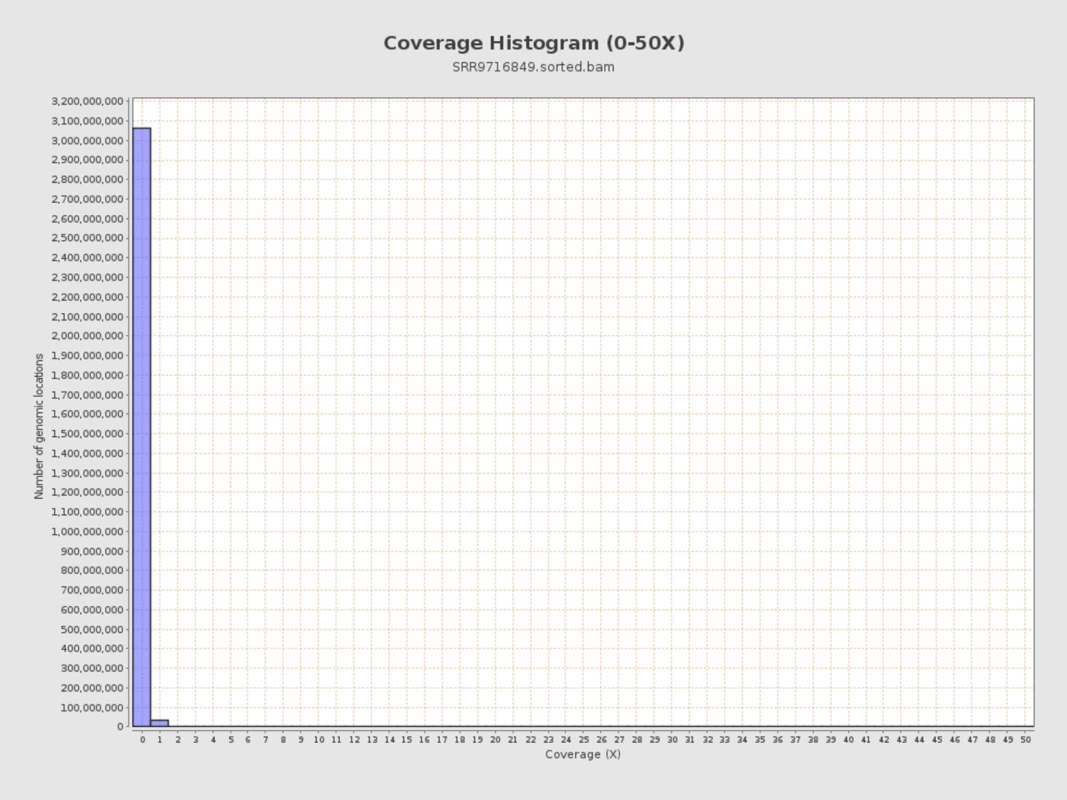
3. Results : Coverage across reference



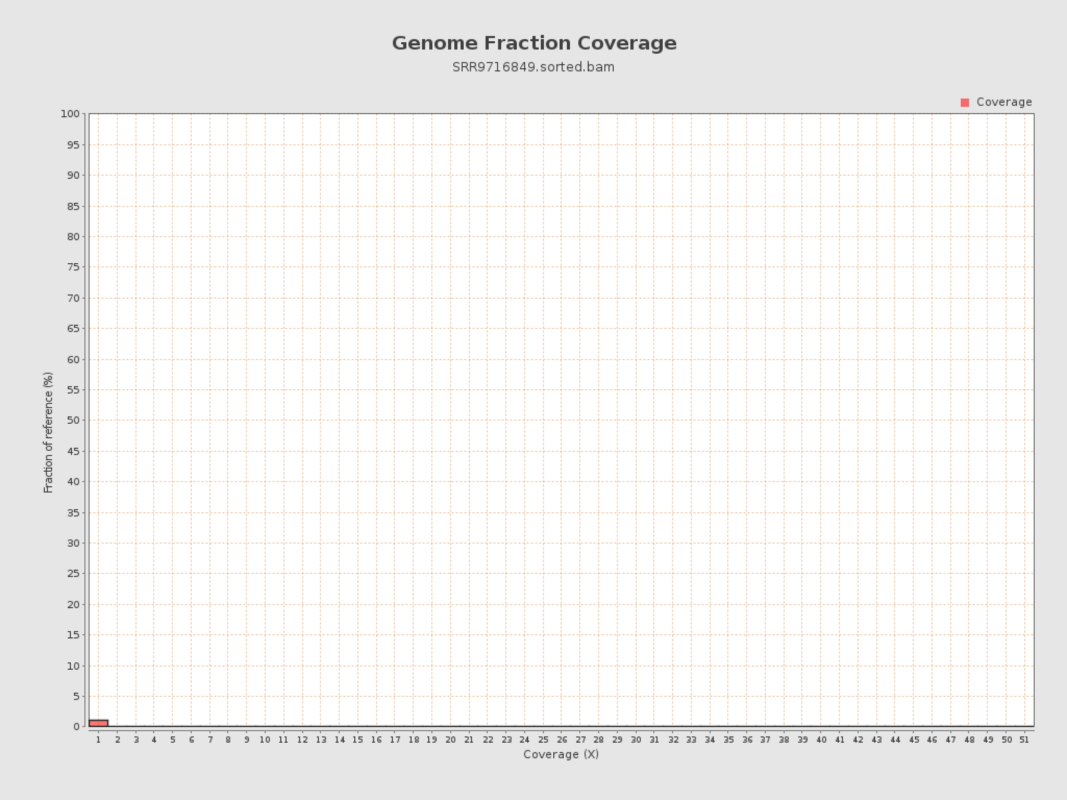
4. Results : Coverage Histogram



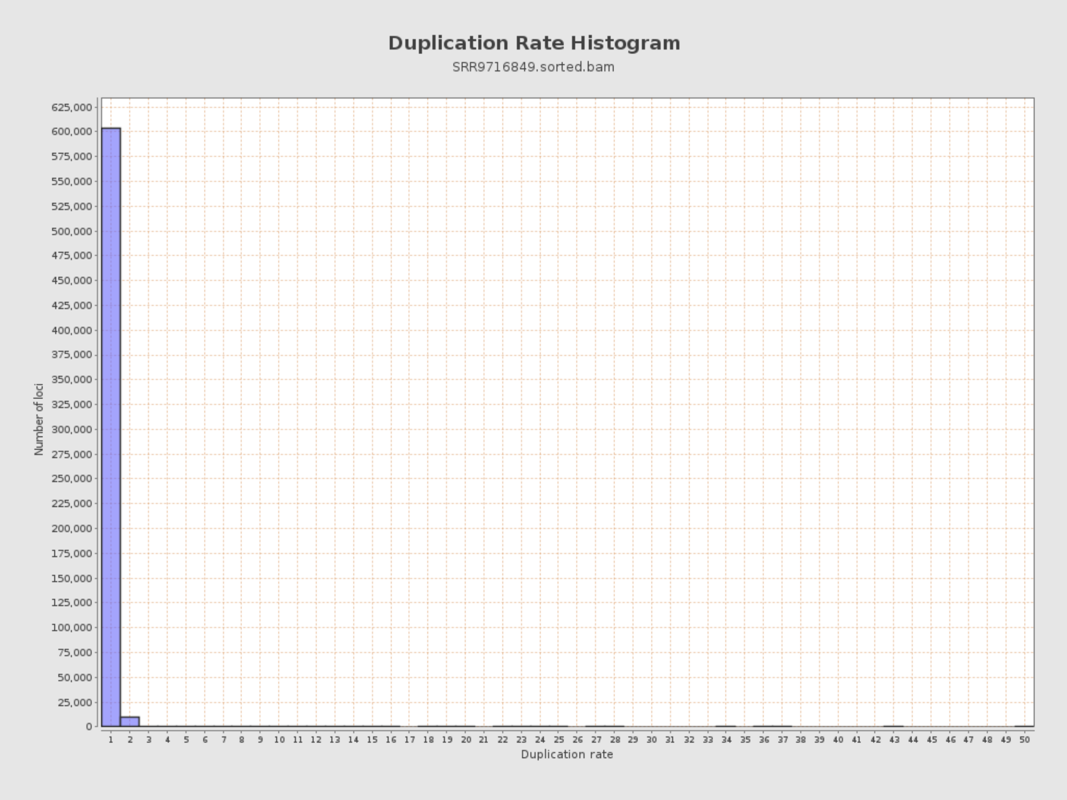
5. Results : Coverage Histogram (0-50X)



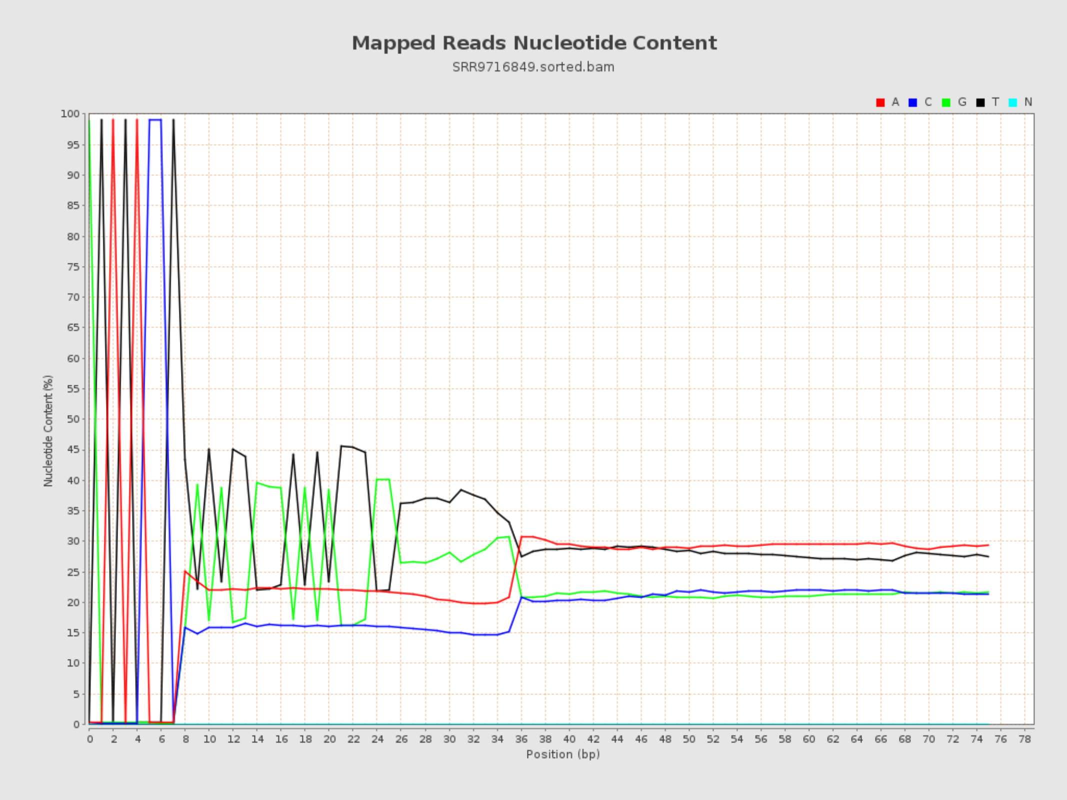
6. Results : Genome Fraction Coverage



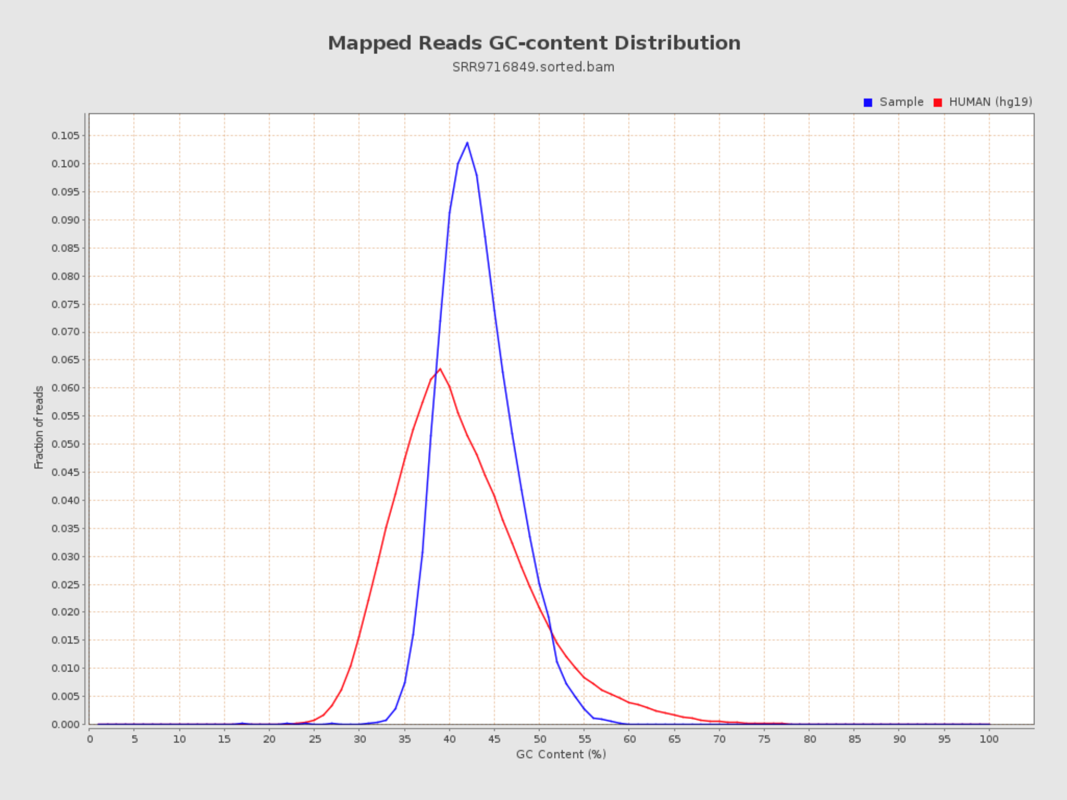
7. Results : Duplication Rate Histogram



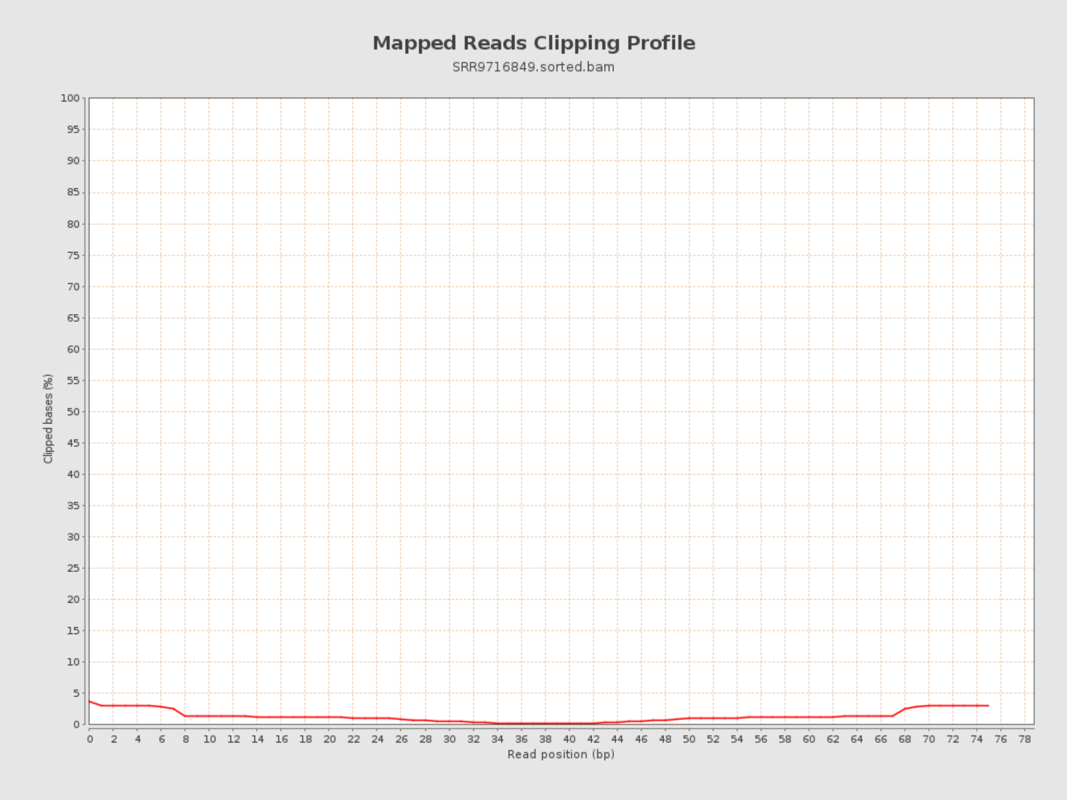
8. Results : Mapped Reads Nucleotide Content



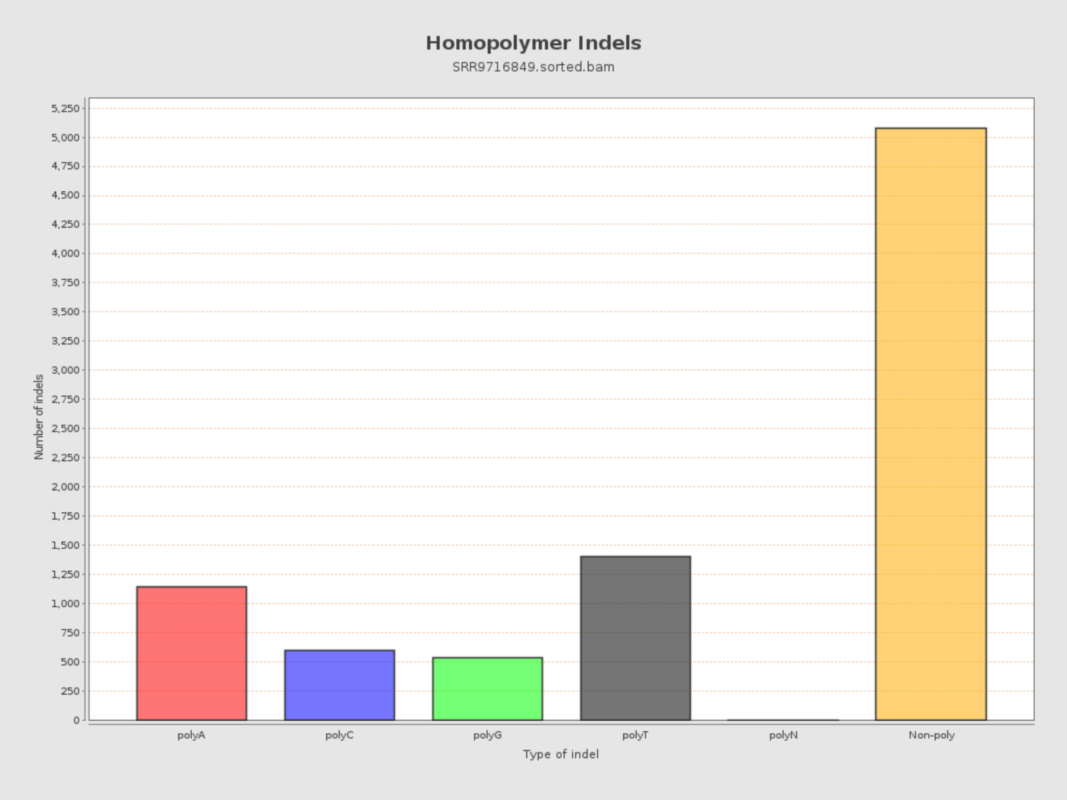
9. Results : Mapped Reads GC-content Distribution



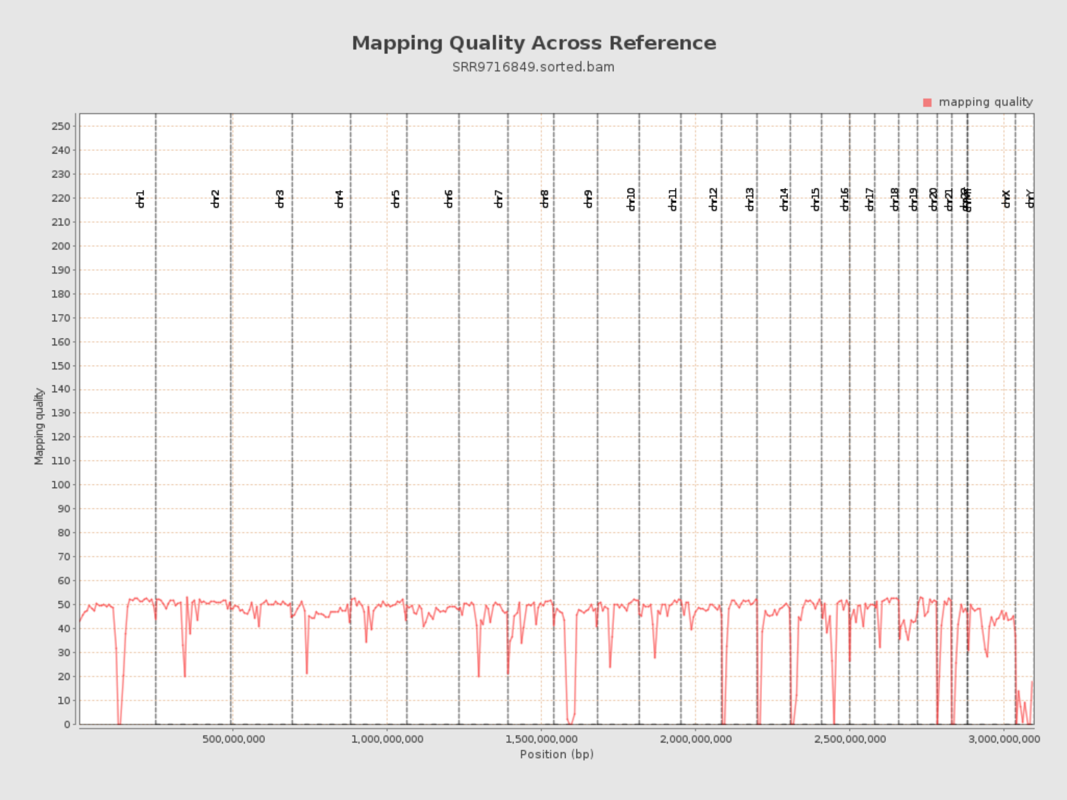
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram