Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 09:59:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716749.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_SRR9716749 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716749.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 09:59:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716749.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	619,390
Mapped reads	456,039 / 73.63%
Unmapped reads	163,351 / 26.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	399 / 0.06%
Read min/max/mean length	30 / 76 / 76.02
Duplicated reads (estimated)	20,846 / 3.37%
Duplication rate	4.13%
Clipped reads	455,675 / 73.57%

2.2. ACGT Content

Number/percentage of A's	5,091,047 / 21.41%
Number/percentage of C's	4,111,379 / 17.29%
Number/percentage of T's	8,010,178 / 33.69%
Number/percentage of G's	6,564,124 / 27.61%
Number/percentage of N's	453 / 0%
GC Percentage	44.9%

2.3. Coverage

Mean	0.0077

Standard Deviation	0.101

2.4. Mapping Quality

Mean Mapping Quality	43.19

2.5. Mismatches and indels

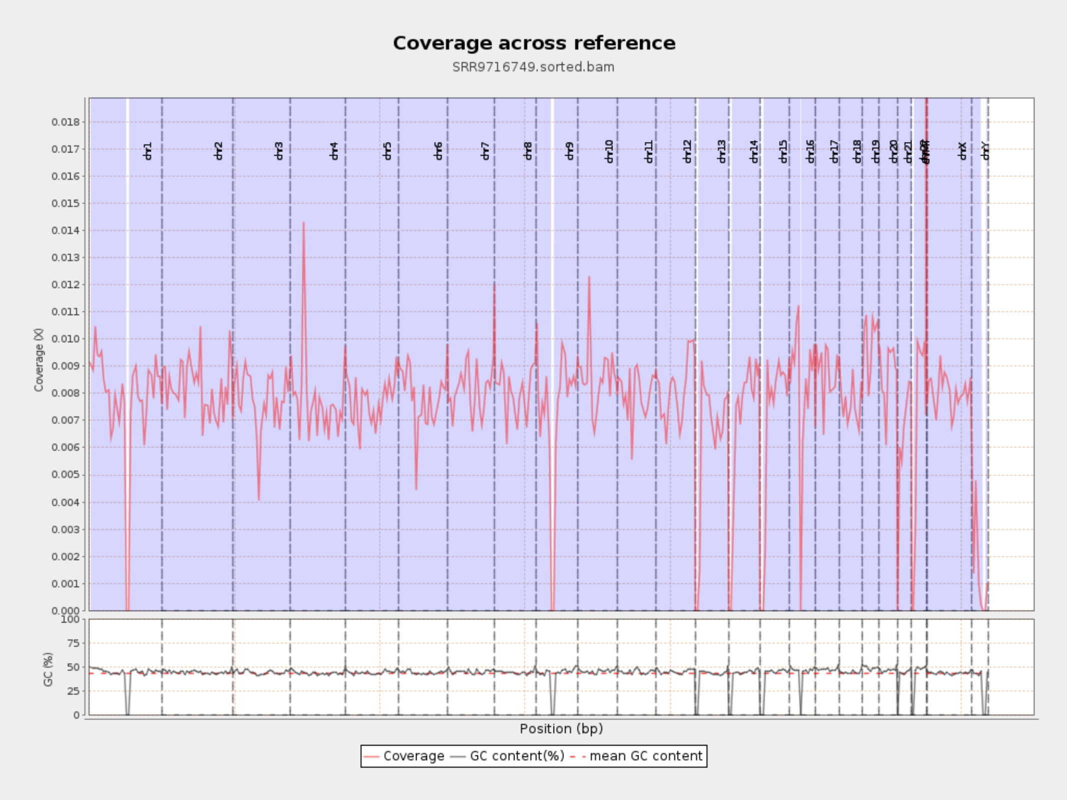
General error rate	0.69%
Mismatches	162,059
Insertions	1,513
Mapped reads with at least one insertion	0.33%
Deletions	3,704
Mapped reads with at least one deletion	0.81%
Homopolymer indels	39.2%

2.6. Chromosome stats

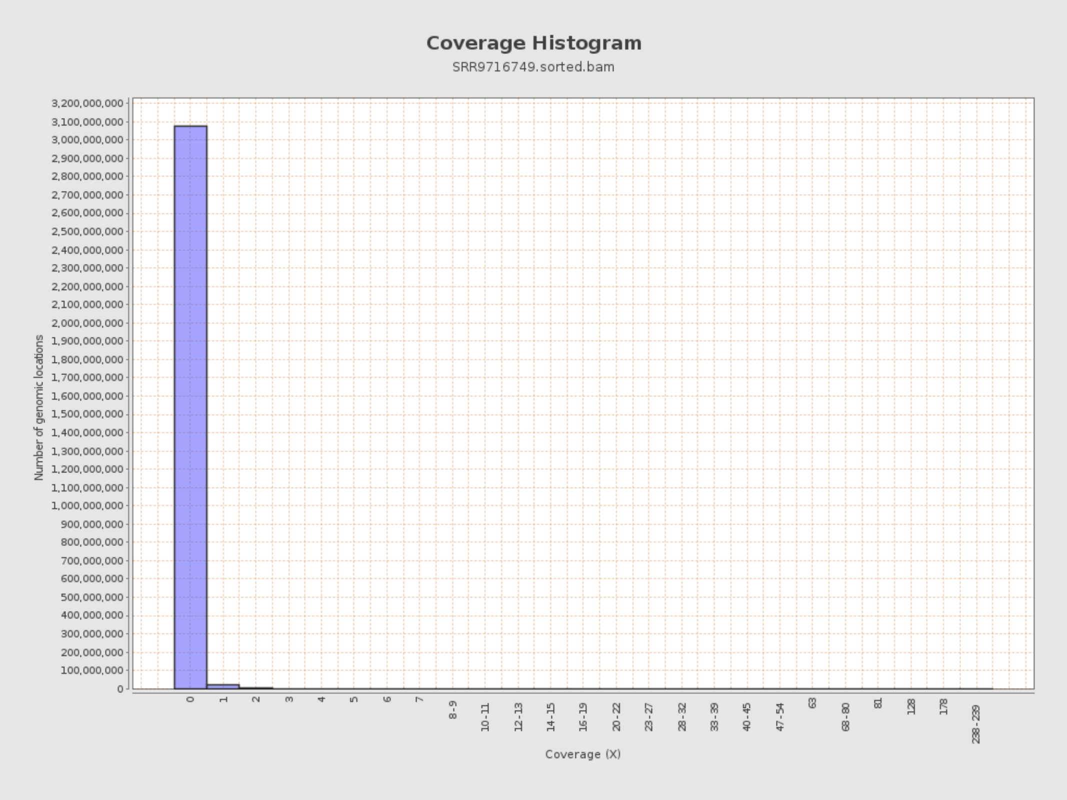
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1921095	0.0077	0.1008
chr2	243199373	1999512	0.0082	0.1375
chr3	198022430	1536695	0.0078	0.0947
chr4	191154276	1479345	0.0077	0.0975
chr5	180915260	1396694	0.0077	0.0943
chr6	171115067	1346609	0.0079	0.103
chr7	159138663	1286189	0.0081	0.1029

chr8	146364022	1179747	0.0081	0.0981
chr9	141213431	1003328	0.0071	0.0943
chr10	135534747	1161519	0.0086	0.1078
chr11	135006516	1078584	0.008	0.0993
chr12	133851895	1085615	0.0081	0.0969
chr13	115169878	713554	0.0062	0.0847
chr14	107349540	729519	0.0068	0.0892
chr15	102531392	697330	0.0068	0.0892
chr16	90354753	747769	0.0083	0.1009
chr17	81195210	714635	0.0088	0.1024
chr18	78077248	594164	0.0076	0.1023
chr19	59128983	581588	0.0098	0.1145
chr20	63025520	547232	0.0087	0.1018
chr21	48129895	307964	0.0064	0.0885
chr22	51304566	336800	0.0066	0.0885
chrMT	16571	3246	0.1959	0.4637
chrX	155270560	1250086	0.0081	0.0973
chrY	59373566	84521	0.0014	0.0482

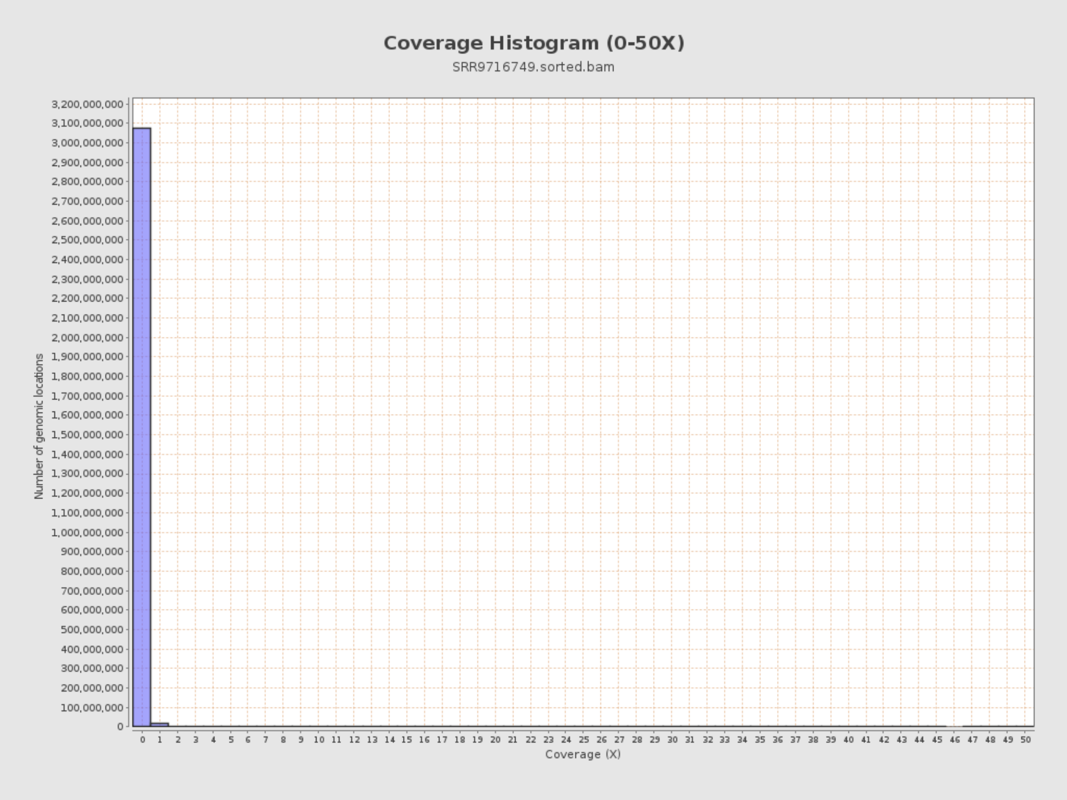
3. Results : Coverage across reference



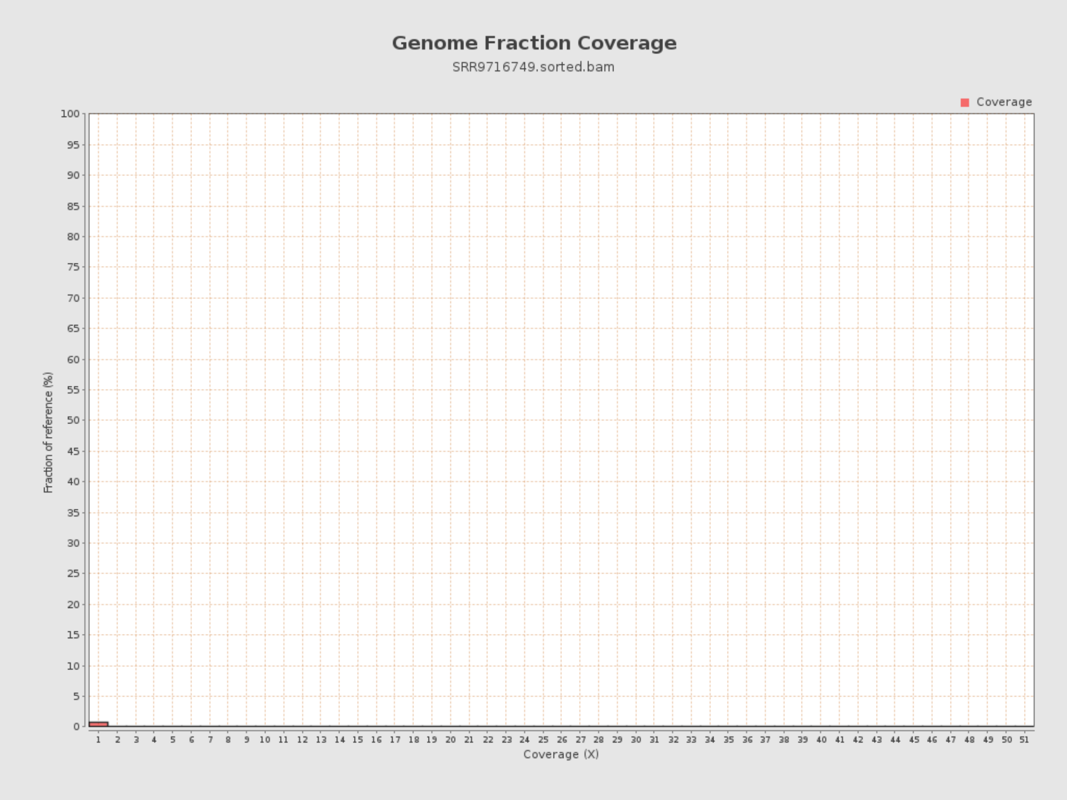
4. Results : Coverage Histogram



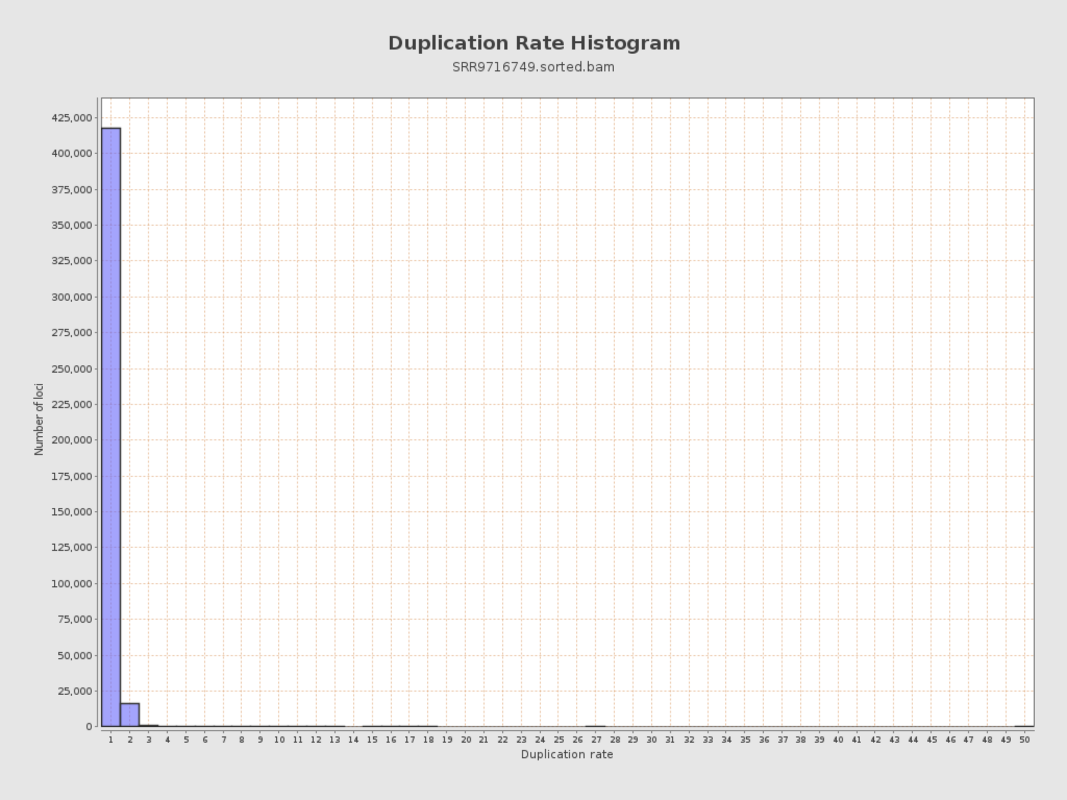
5. Results : Coverage Histogram (0-50X)



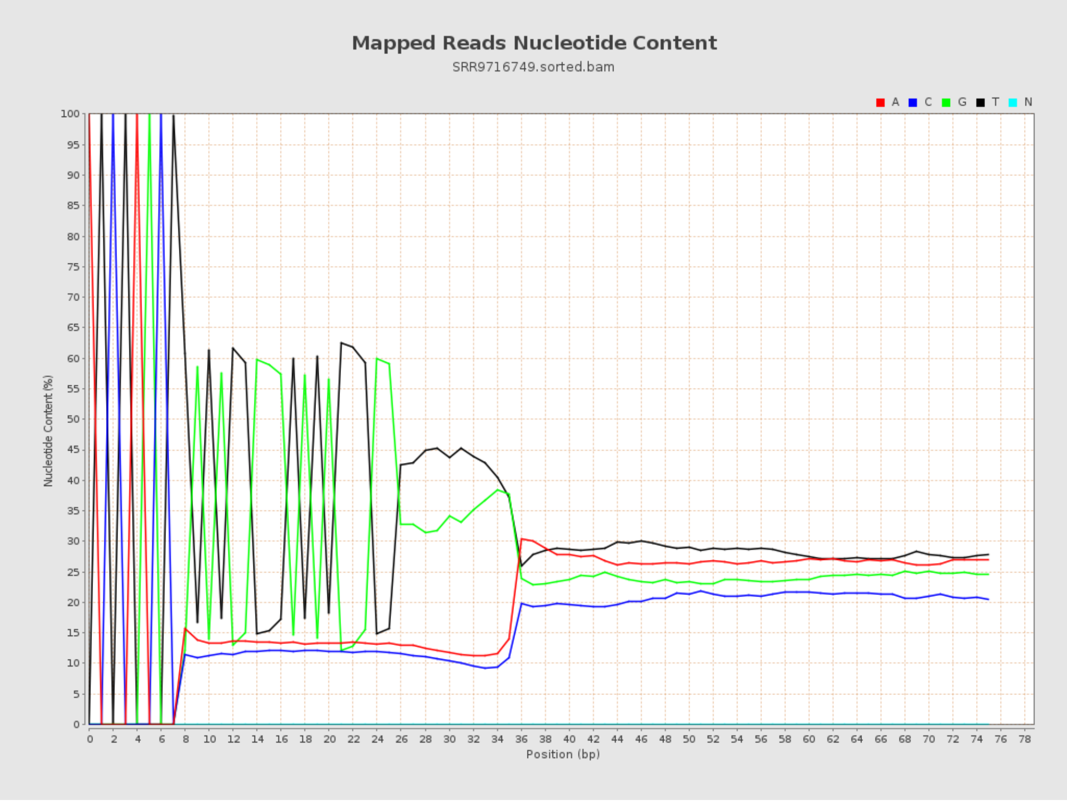
6. Results : Genome Fraction Coverage



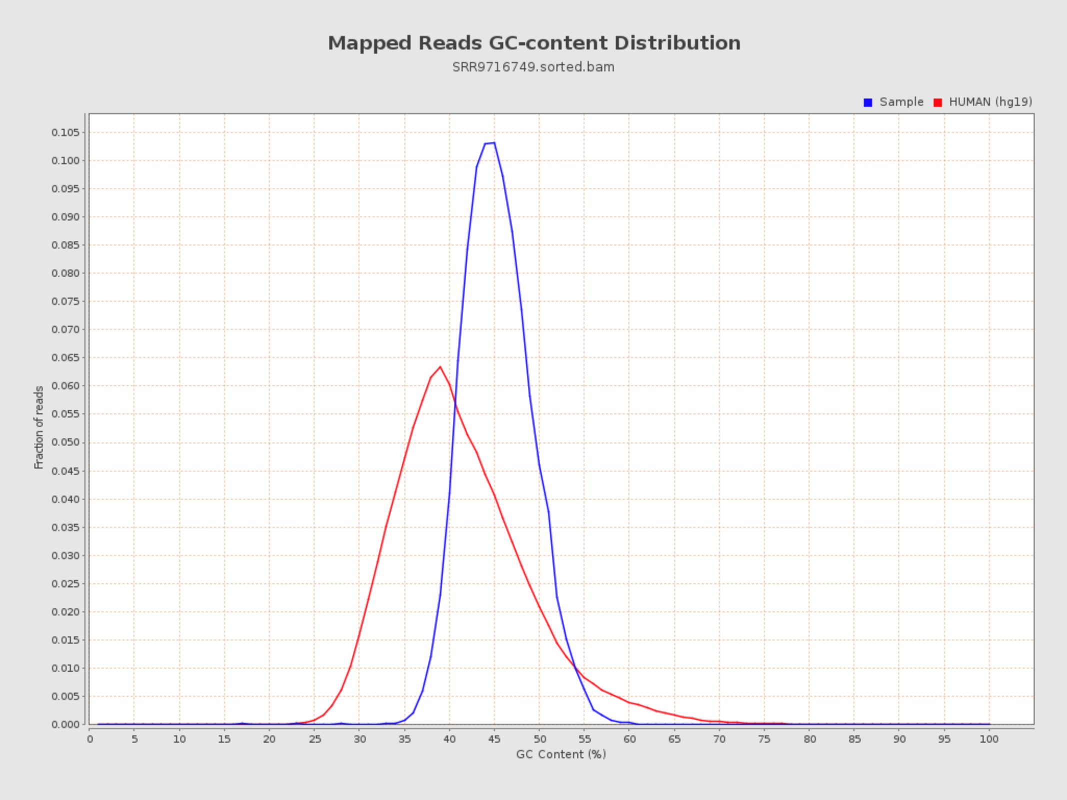
7. Results : Duplication Rate Histogram



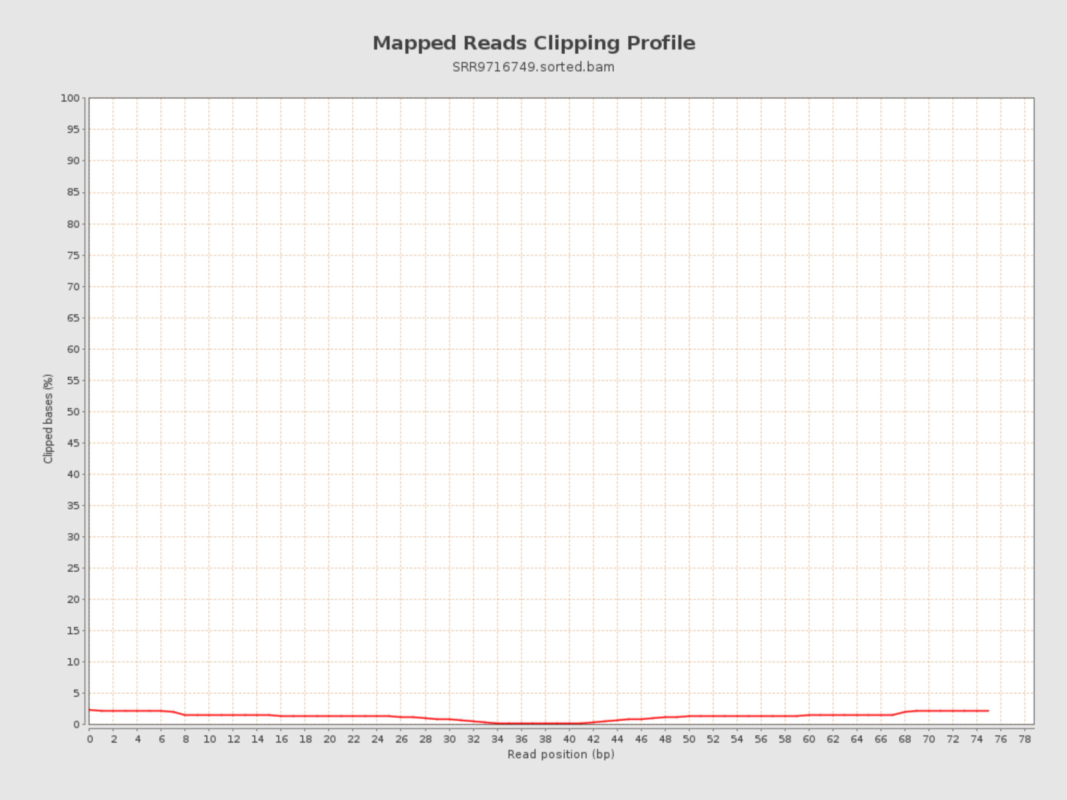
8. Results : Mapped Reads Nucleotide Content



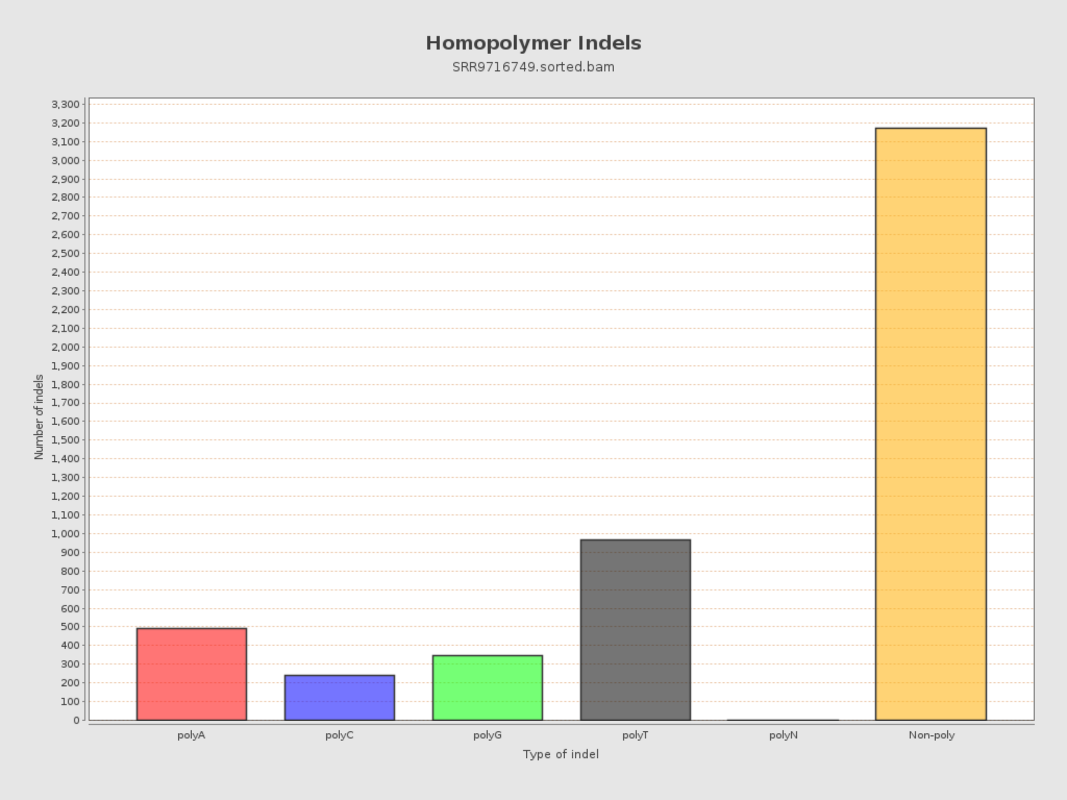
9. Results : Mapped Reads GC-content Distribution



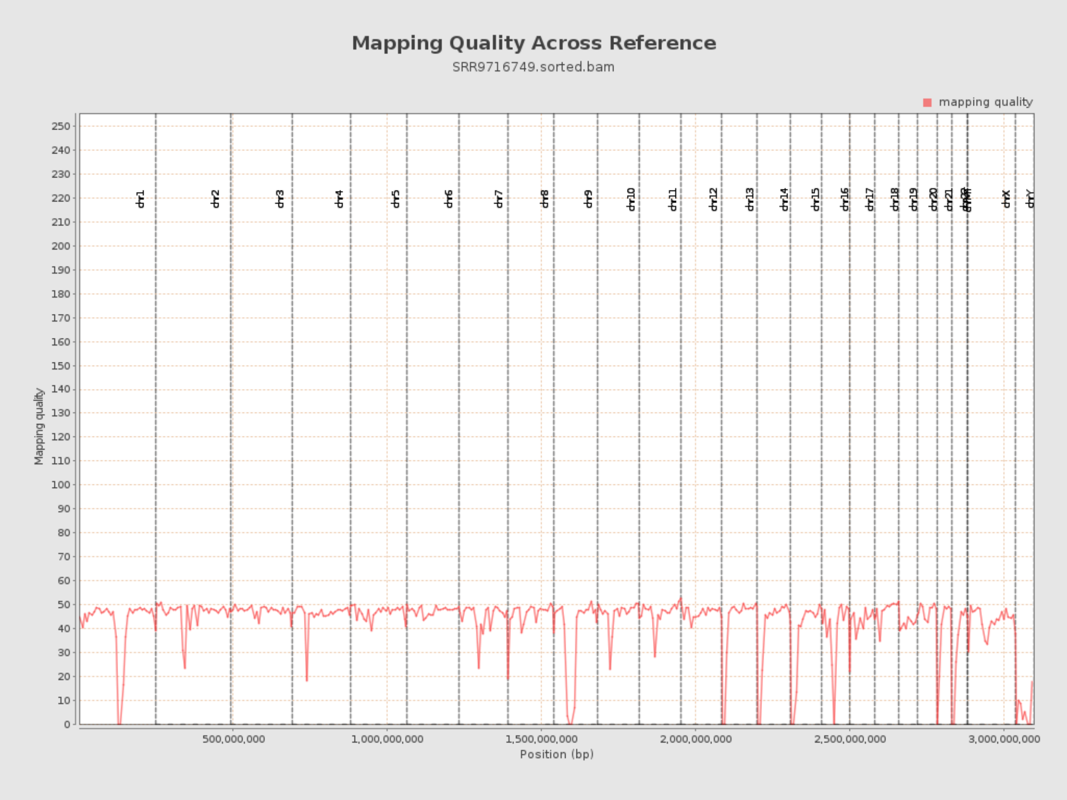
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram