Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 19:40:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716144.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_SRR9716144 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716144.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 19:40:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716144.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,006,666
Mapped reads	1,776,113 / 88.51%
Unmapped reads	230,553 / 11.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,394 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	55,964 / 2.79%
Duplication rate	2.26%
Clipped reads	1,775,983 / 88.5%

2.2. ACGT Content

Number/percentage of A's	25,363,970 / 25.07%
Number/percentage of C's	19,449,840 / 19.23%
Number/percentage of T's	32,134,840 / 31.77%
Number/percentage of G's	24,203,080 / 23.93%
Number/percentage of N's	881 / 0%
GC Percentage	43.16%

2.3. Coverage

Mean	0.0327

Standard Deviation	0.2694

2.4. Mapping Quality

Mean Mapping Quality	43.31

2.5. Mismatches and indels

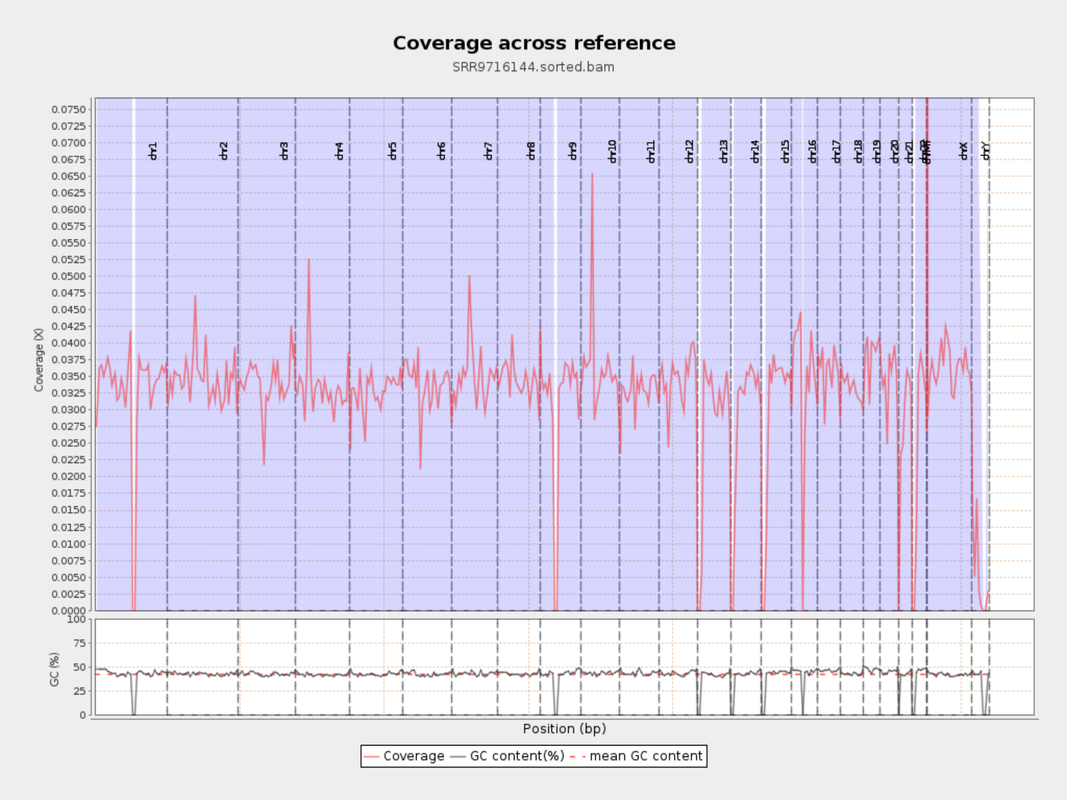
General error rate	0.54%
Mismatches	526,294
Insertions	8,421
Mapped reads with at least one insertion	0.47%
Deletions	18,440
Mapped reads with at least one deletion	1.03%
Homopolymer indels	40.83%

2.6. Chromosome stats

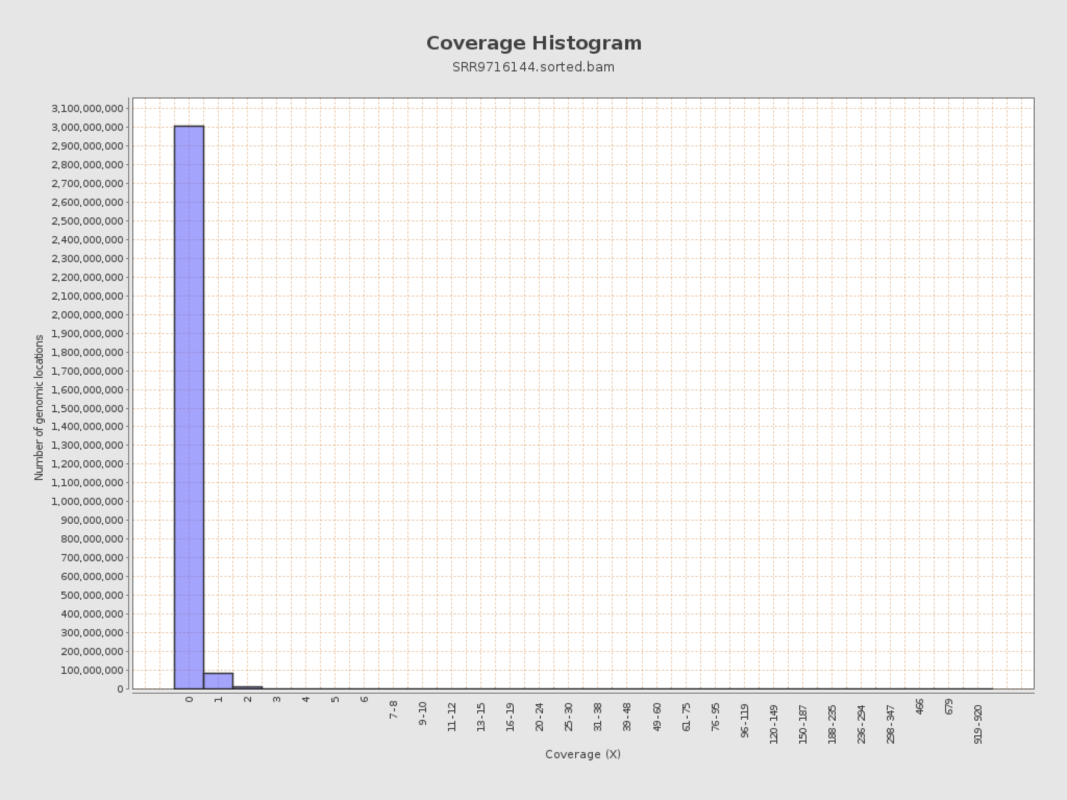
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8093794	0.0325	0.3333
chr2	243199373	8440811	0.0347	0.4329
chr3	198022430	6765927	0.0342	0.2082
chr4	191154276	6415160	0.0336	0.2249
chr5	180915260	5976242	0.033	0.2007
chr6	171115067	5779269	0.0338	0.2323
chr7	159138663	5609320	0.0352	0.3448

chr8	146364022	5036740	0.0344	0.2526
chr9	141213431	4283964	0.0303	0.2324
chr10	135534747	4945418	0.0365	0.3296
chr11	135006516	4469667	0.0331	0.2503
chr12	133851895	4640734	0.0347	0.2079
chr13	115169878	3144775	0.0273	0.1834
chr14	107349540	3058548	0.0285	0.1956
chr15	102531392	2957761	0.0288	0.1941
chr16	90354753	3063430	0.0339	0.2218
chr17	81195210	2908534	0.0358	0.2183
chr18	78077248	2613156	0.0335	0.3562
chr19	59128983	2261902	0.0383	0.3102
chr20	63025520	2173129	0.0345	0.2121
chr21	48129895	1314842	0.0273	0.2012
chr22	51304566	1248007	0.0243	0.1747
chrMT	16571	19735	1.1909	1.4268
chrX	155270560	5660613	0.0365	0.2328
chrY	59373566	300174	0.0051	0.1418

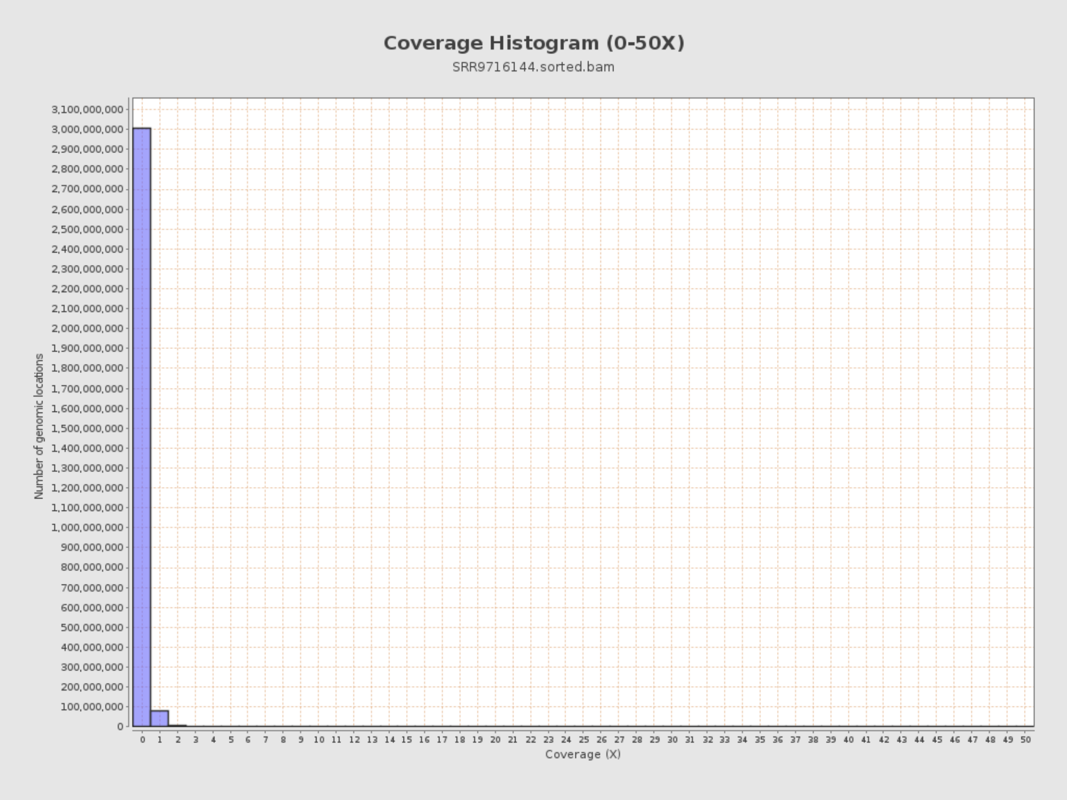
3. Results : Coverage across reference



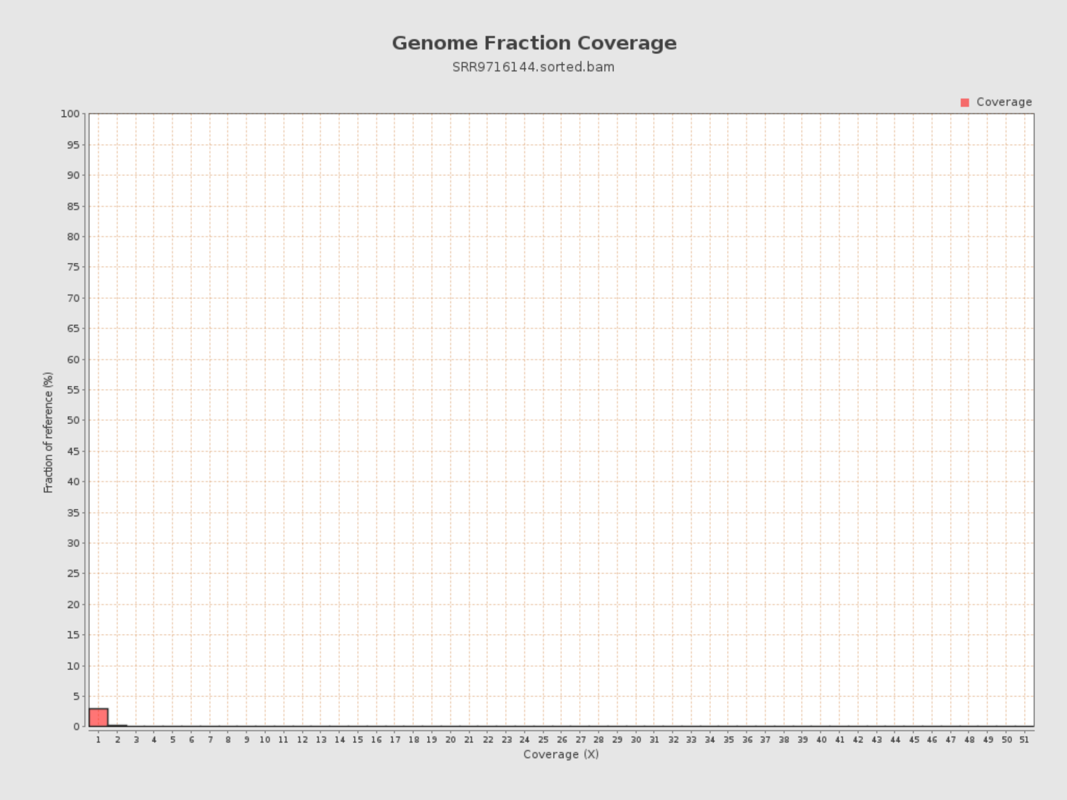
4. Results : Coverage Histogram



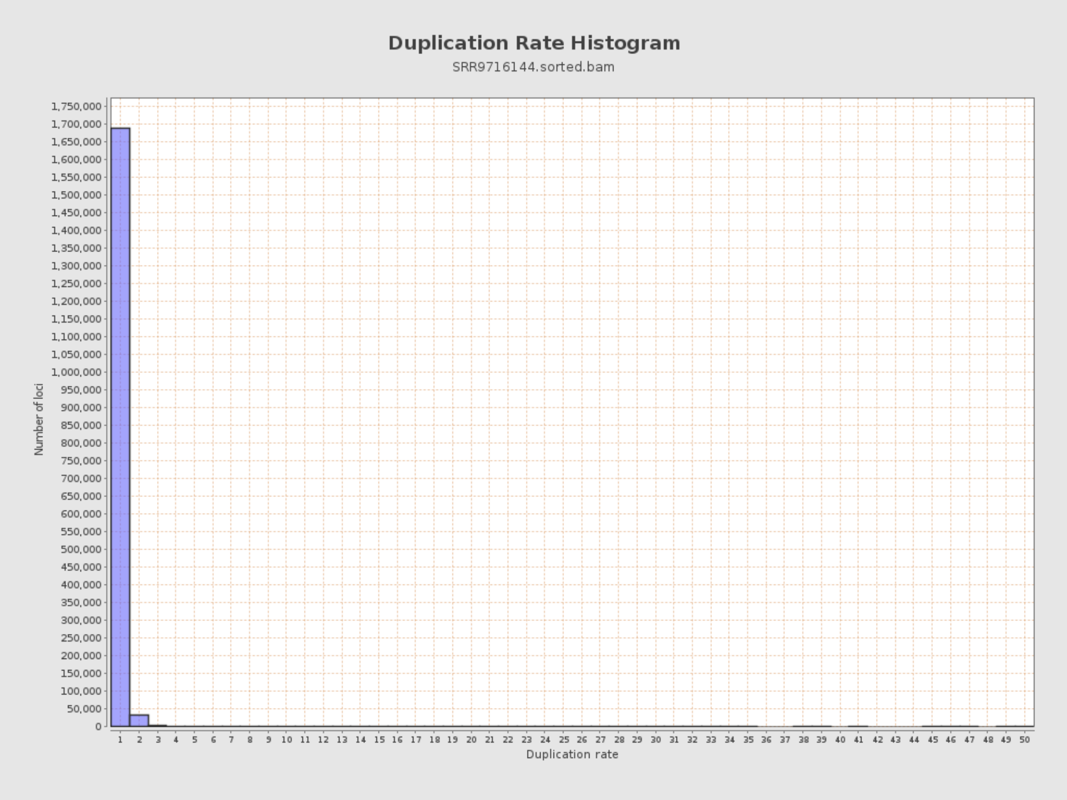
5. Results : Coverage Histogram (0-50X)



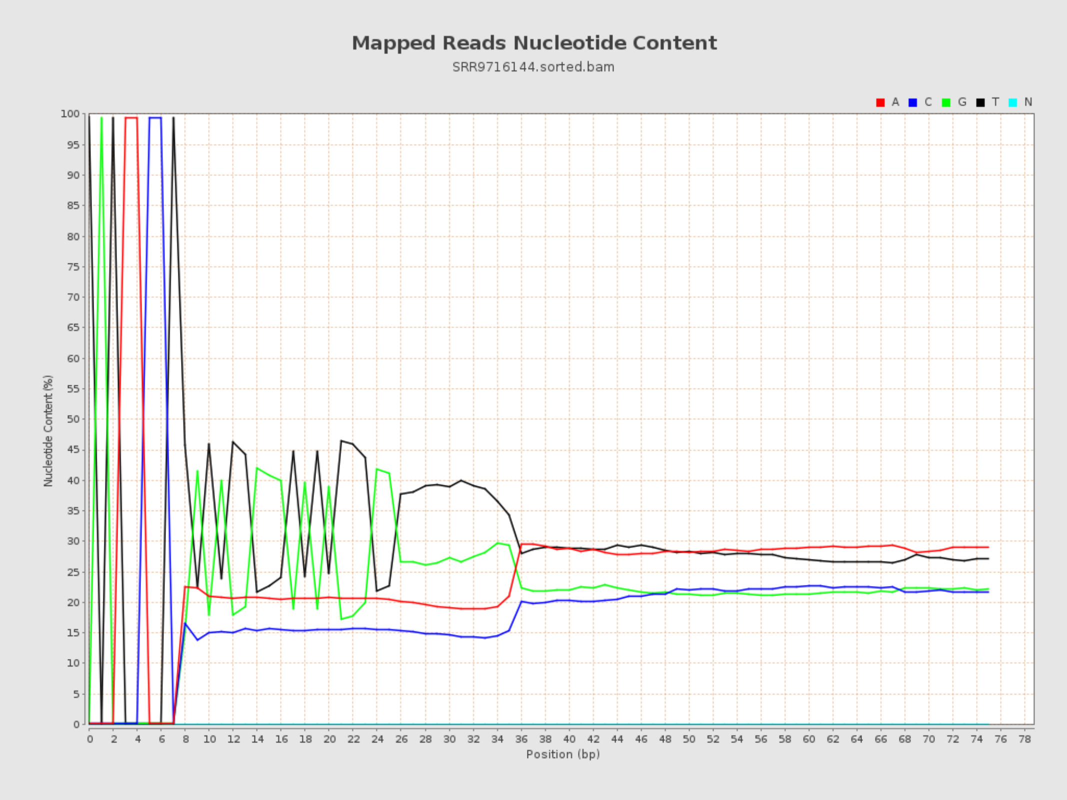
6. Results : Genome Fraction Coverage



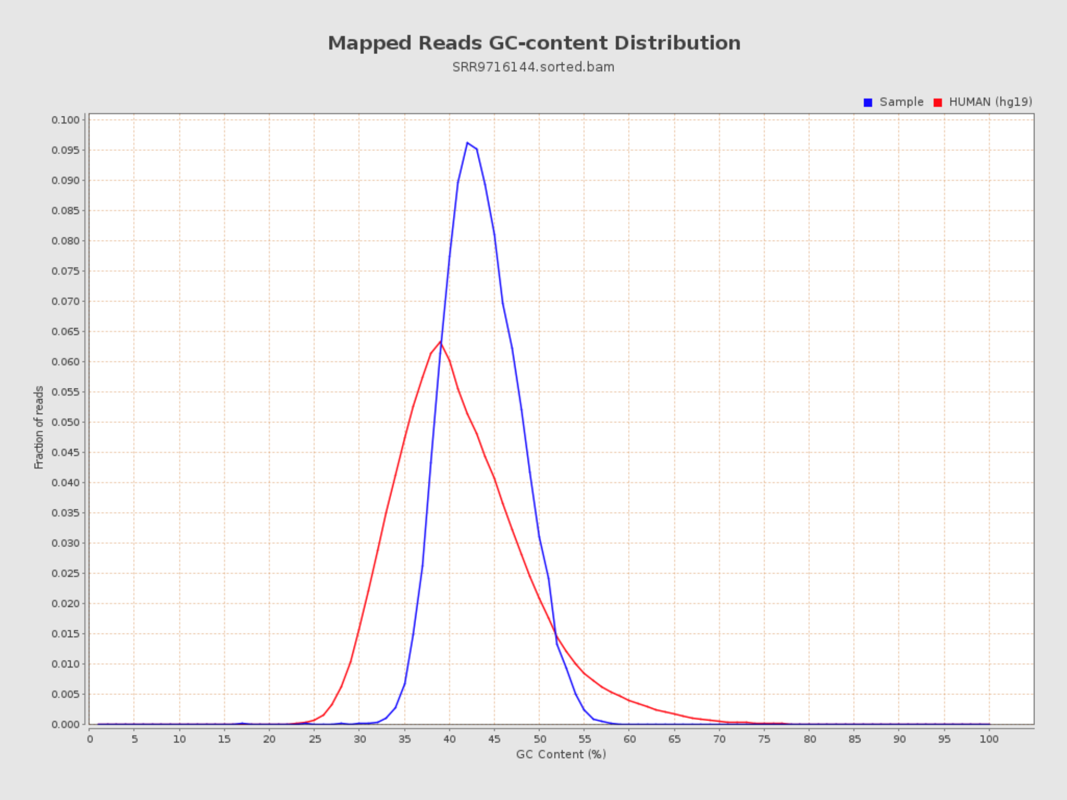
7. Results : Duplication Rate Histogram



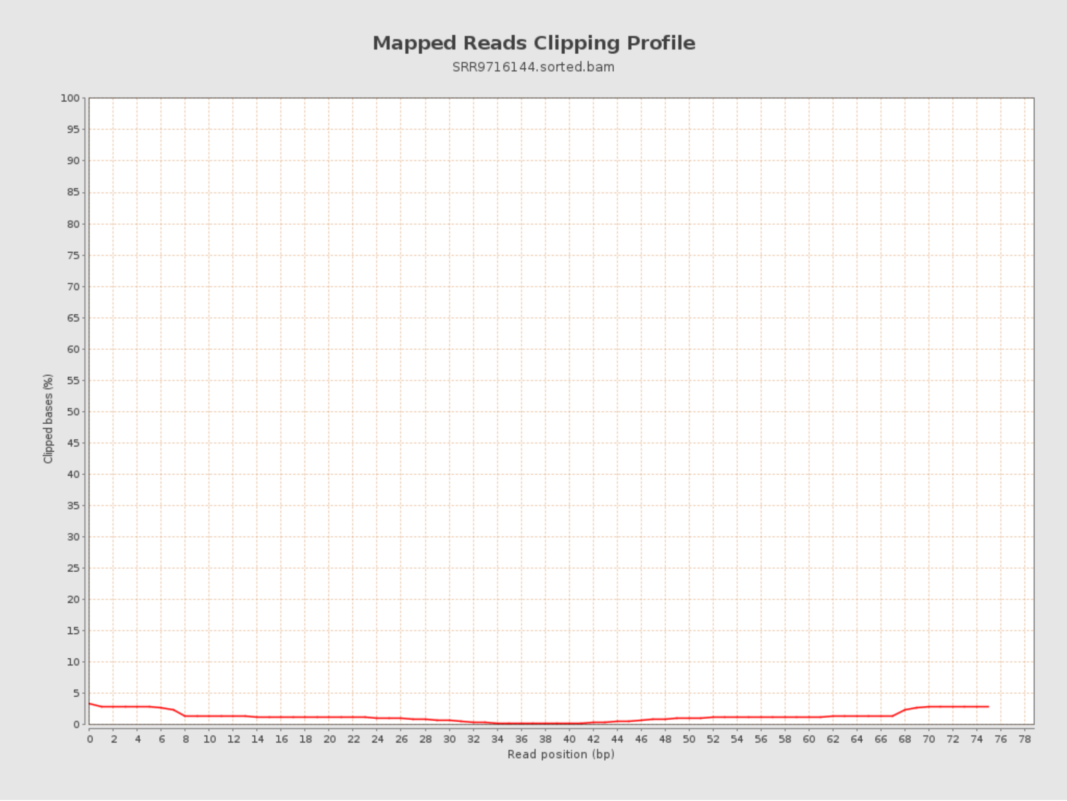
8. Results : Mapped Reads Nucleotide Content



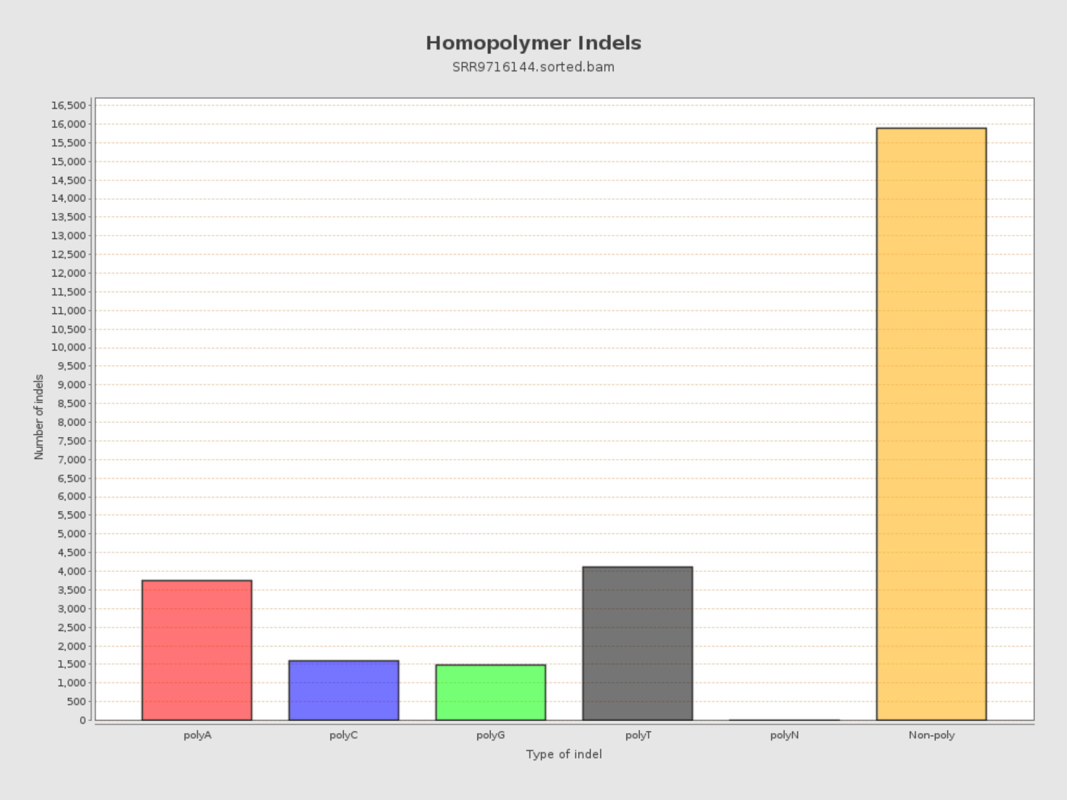
9. Results : Mapped Reads GC-content Distribution



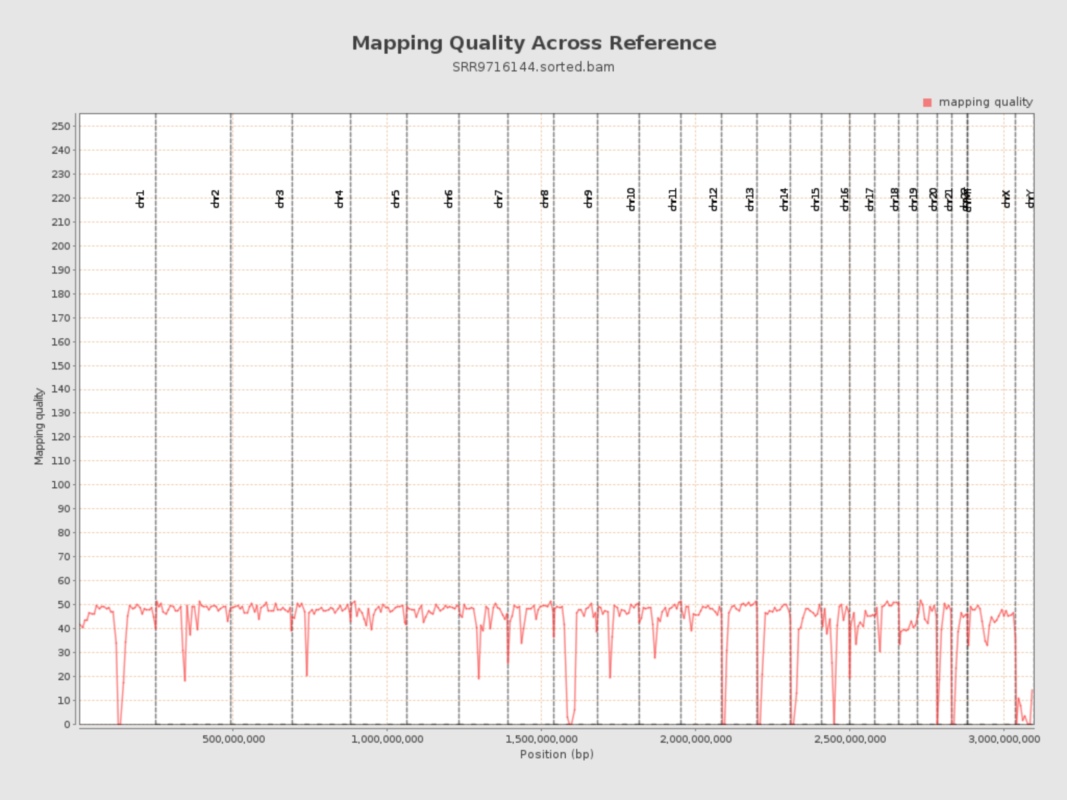
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram