Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 08:06:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716334.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_SRR9716334 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716334.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 08:06:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716334.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	435,247
Mapped reads	390,829 / 89.79%
Unmapped reads	44,418 / 10.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,750 / 0.4%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	7,813 / 1.8%
Duplication rate	1.62%
Clipped reads	391,877 / 90.04%

2.2. ACGT Content

Number/percentage of A's	5,706,098 / 25.37%
Number/percentage of C's	4,181,879 / 18.59%
Number/percentage of T's	7,187,954 / 31.96%
Number/percentage of G's	5,413,260 / 24.07%
Number/percentage of N's	399 / 0%
GC Percentage	42.66%

2.3. Coverage

Mean	0.0073

Standard Deviation	0.0998

2.4. Mapping Quality

Mean Mapping Quality	45.24

2.5. Mismatches and indels

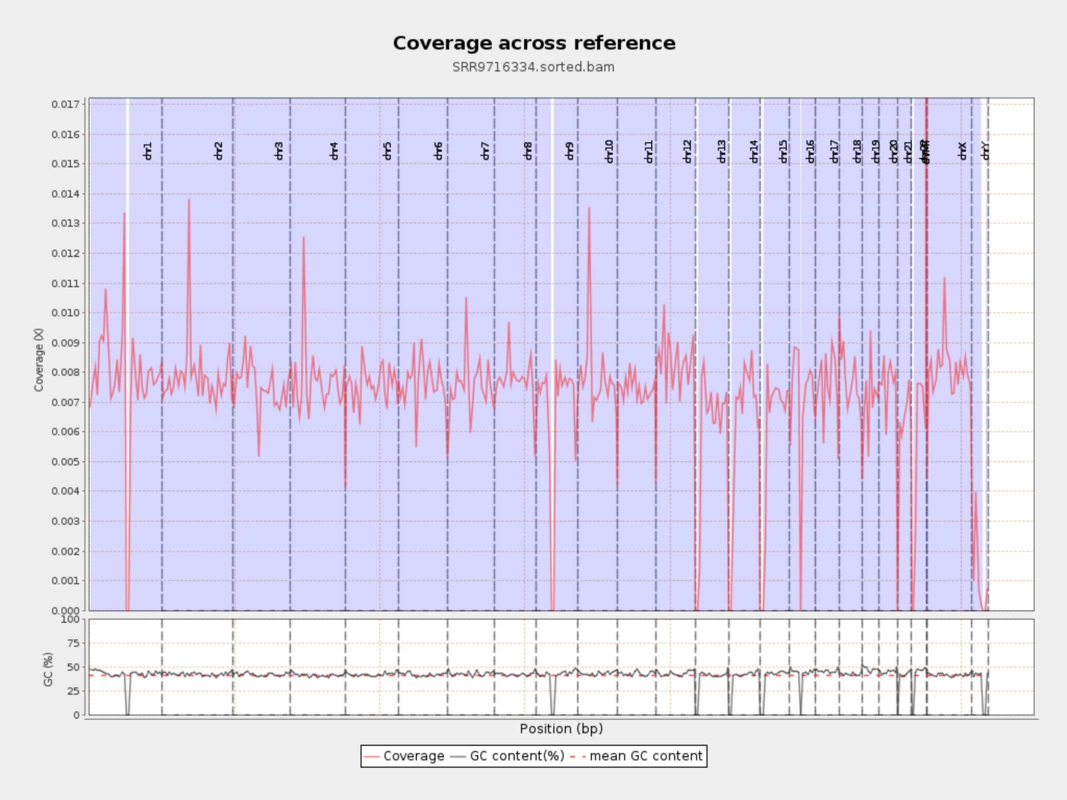
General error rate	0.55%
Mismatches	121,649
Insertions	1,464
Mapped reads with at least one insertion	0.37%
Deletions	3,830
Mapped reads with at least one deletion	0.97%
Homopolymer indels	41.97%

2.6. Chromosome stats

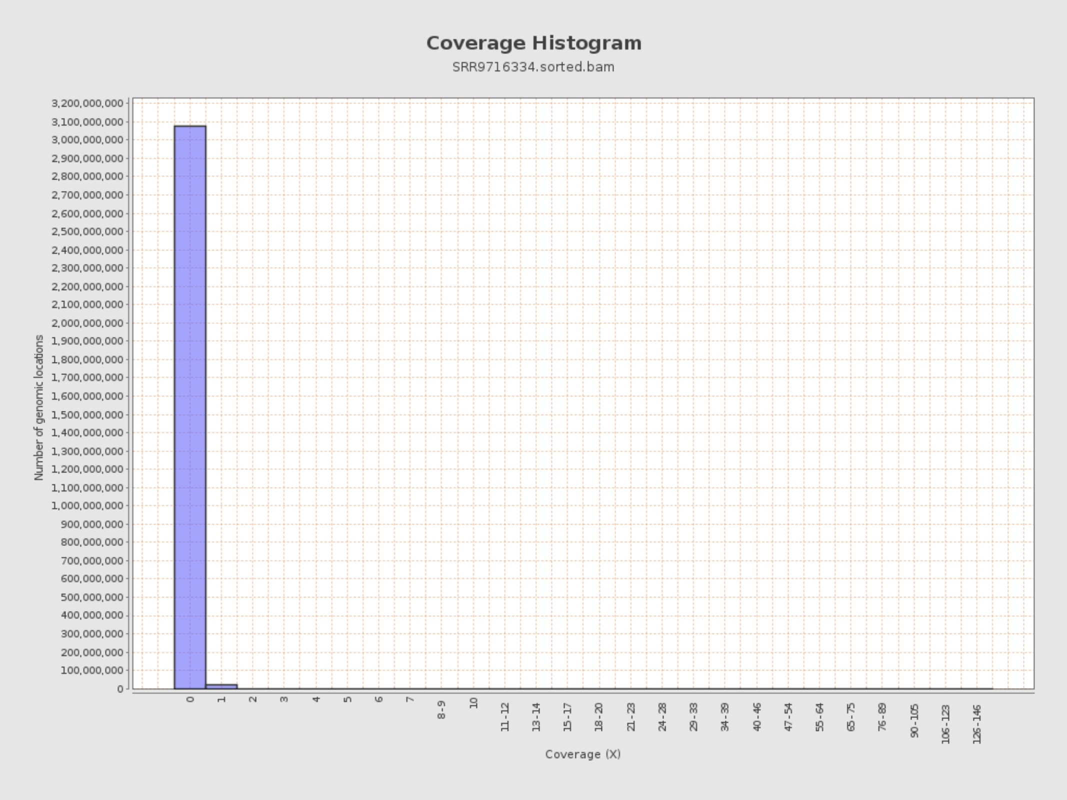
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1919520	0.0077	0.1381
chr2	243199373	1921984	0.0079	0.1079
chr3	198022430	1491710	0.0075	0.0892
chr4	191154276	1472931	0.0077	0.0928
chr5	180915260	1372959	0.0076	0.0896
chr6	171115067	1308572	0.0076	0.0926
chr7	159138663	1207454	0.0076	0.1036

chr8	146364022	1134980	0.0078	0.1011
chr9	141213431	929271	0.0066	0.0985
chr10	135534747	1071645	0.0079	0.1046
chr11	135006516	997691	0.0074	0.0977
chr12	133851895	1111607	0.0083	0.0945
chr13	115169878	670231	0.0058	0.0785
chr14	107349540	660470	0.0062	0.0836
chr15	102531392	598720	0.0058	0.0783
chr16	90354753	640055	0.0071	0.0891
chr17	81195210	609134	0.0075	0.0904
chr18	78077248	608639	0.0078	0.1441
chr19	59128983	420366	0.0071	0.1159
chr20	63025520	479389	0.0076	0.0904
chr21	48129895	288331	0.006	0.0828
chr22	51304566	257219	0.005	0.0729
chrMT	16571	8126	0.4904	0.7279
chrX	155270560	1251464	0.0081	0.0967
chrY	59373566	63510	0.0011	0.0398

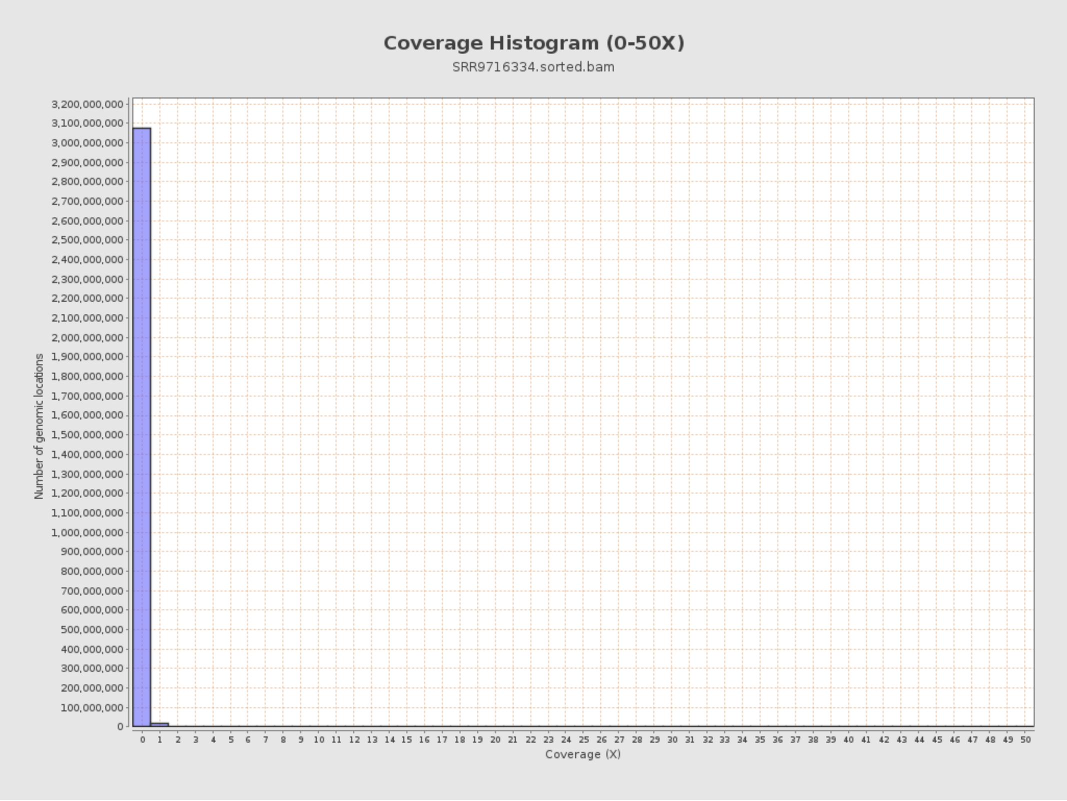
3. Results : Coverage across reference



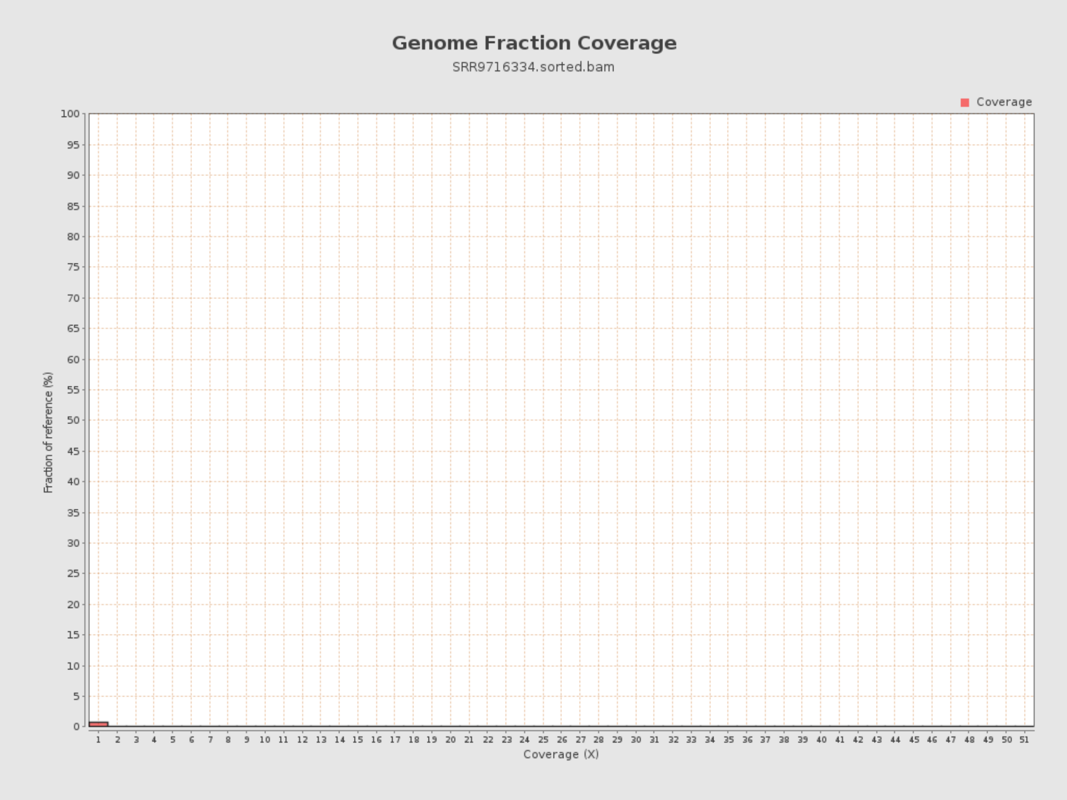
4. Results : Coverage Histogram



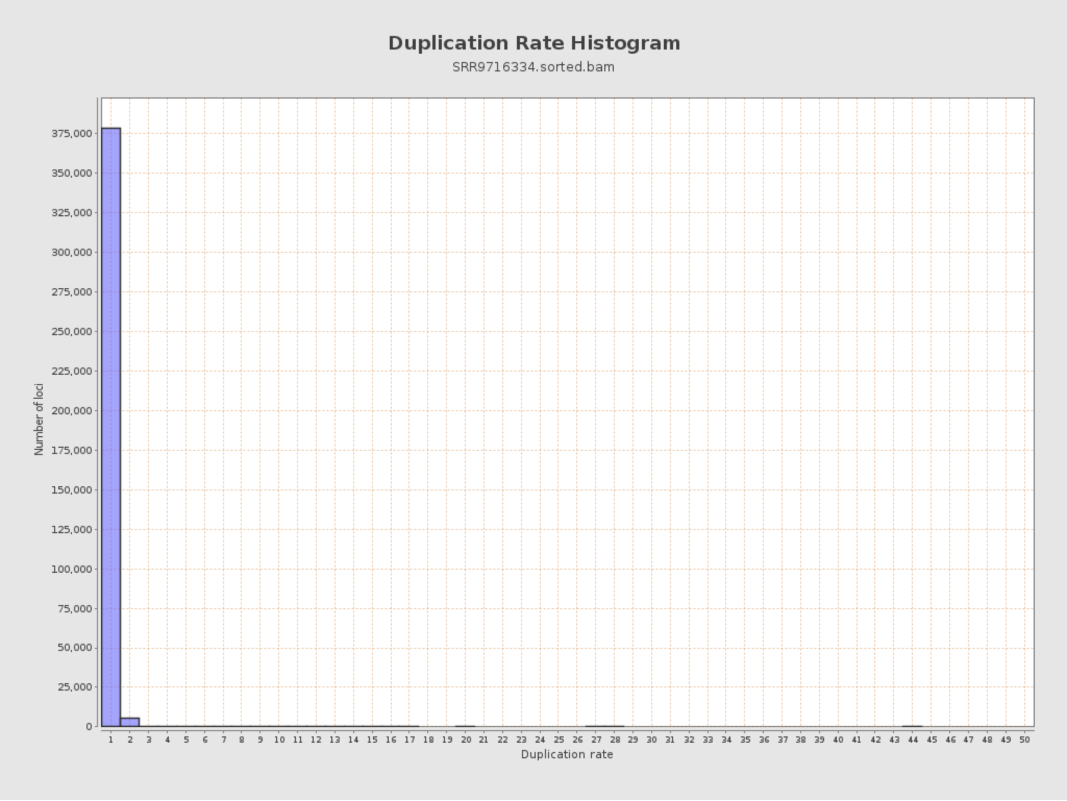
5. Results : Coverage Histogram (0-50X)



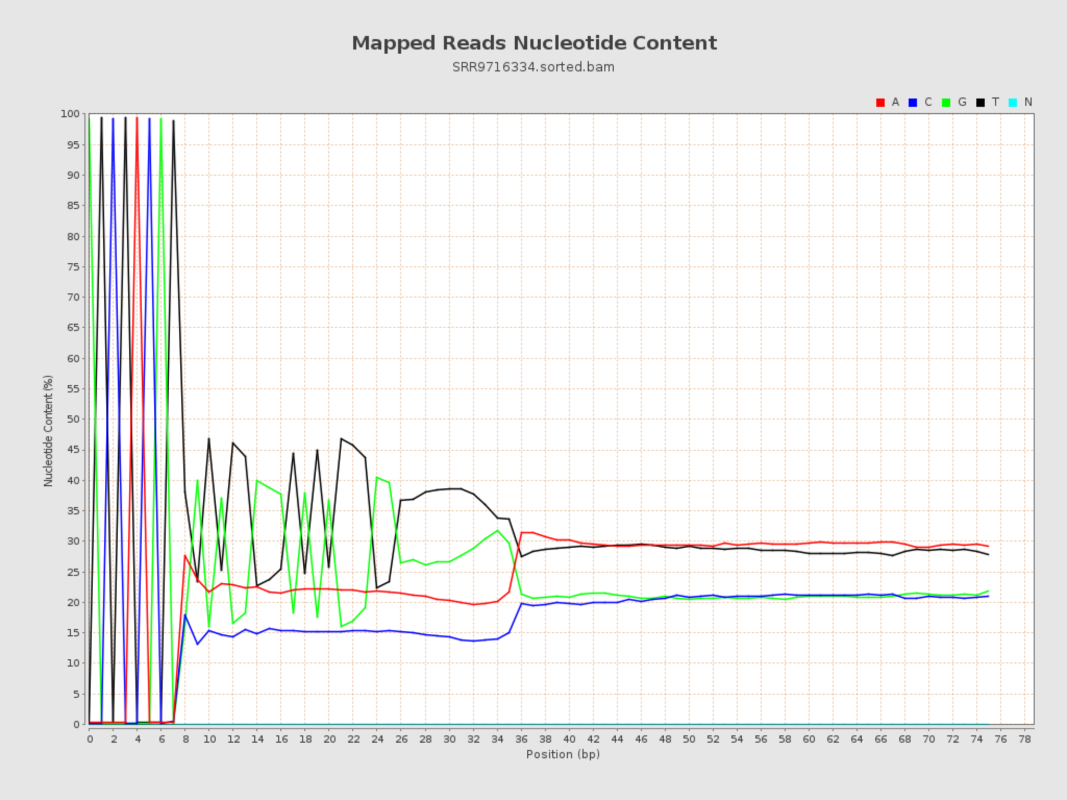
6. Results : Genome Fraction Coverage



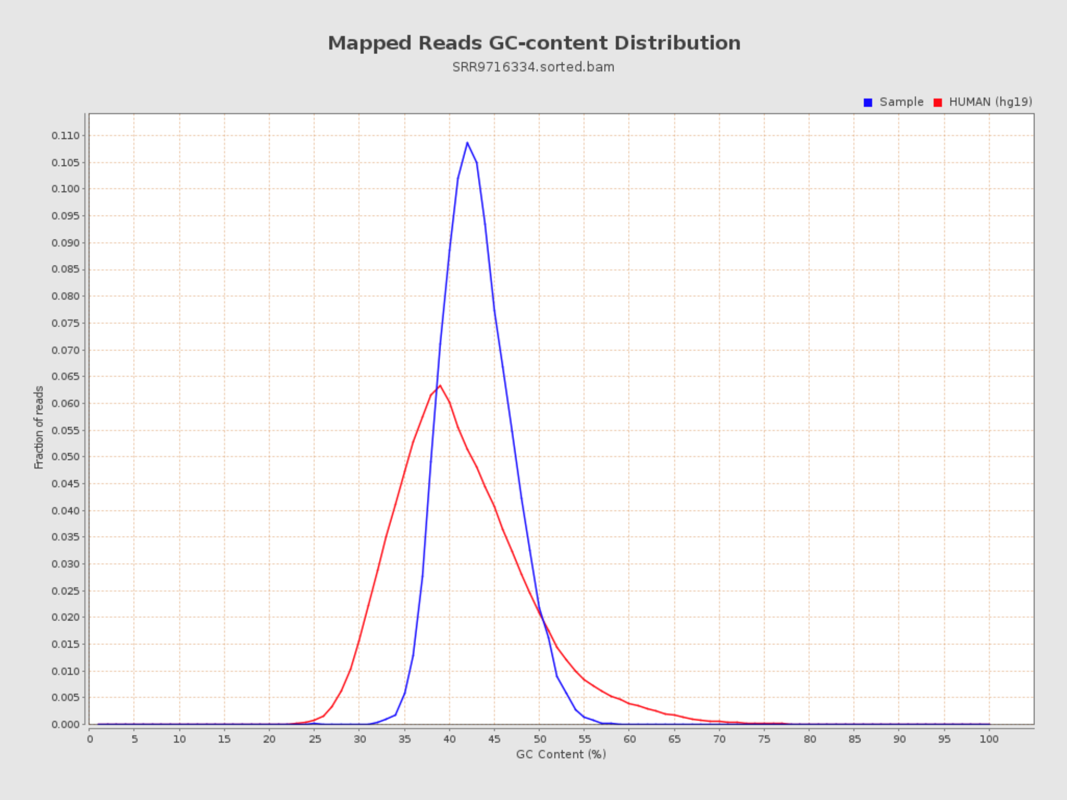
7. Results : Duplication Rate Histogram



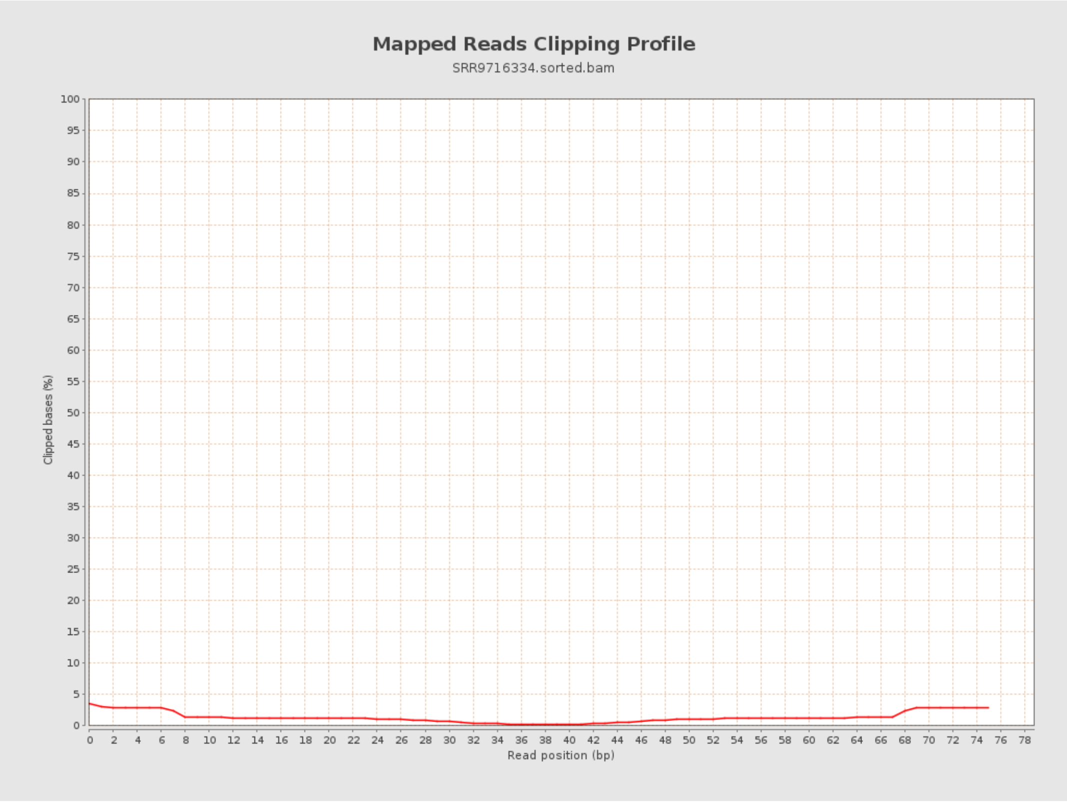
8. Results : Mapped Reads Nucleotide Content



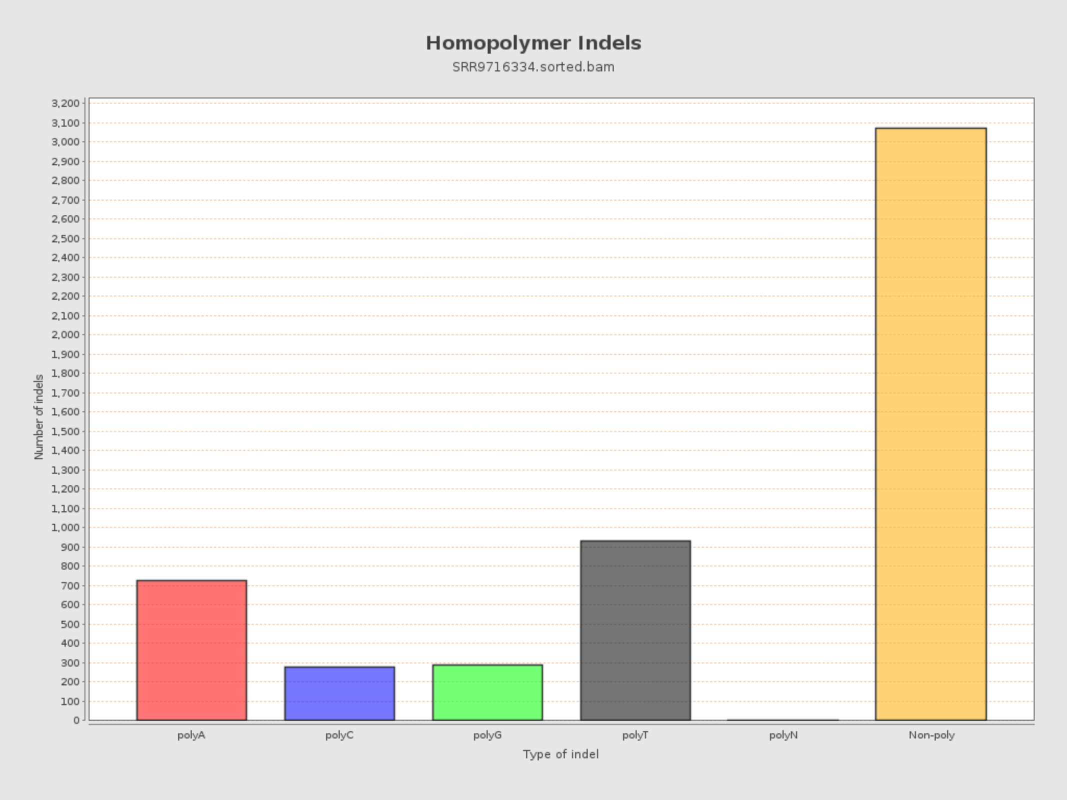
9. Results : Mapped Reads GC-content Distribution



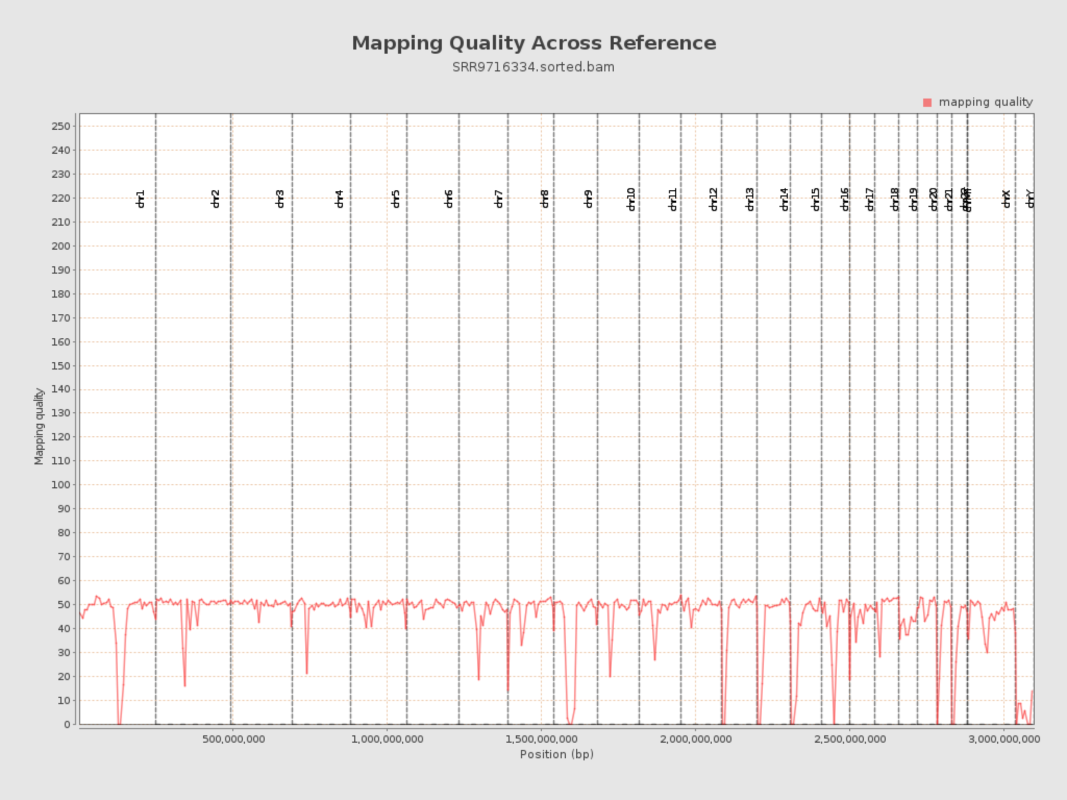
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram