Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 15:23:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716464.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_SRR9716464 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716464.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 15:23:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716464.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,284,823
Mapped reads	1,134,411 / 88.29%
Unmapped reads	150,412 / 11.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,942 / 0.31%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	25,575 / 1.99%
Duplication rate	1.6%
Clipped reads	1,137,176 / 88.51%

2.2. ACGT Content

Number/percentage of A's	15,566,531 / 24.05%
Number/percentage of C's	13,283,721 / 20.52%
Number/percentage of T's	20,674,133 / 31.94%
Number/percentage of G's	15,211,133 / 23.5%
Number/percentage of N's	962 / 0%
GC Percentage	44.02%

2.3. Coverage

Mean	0.0209

Standard Deviation	0.2006

2.4. Mapping Quality

Mean Mapping Quality	43.21

2.5. Mismatches and indels

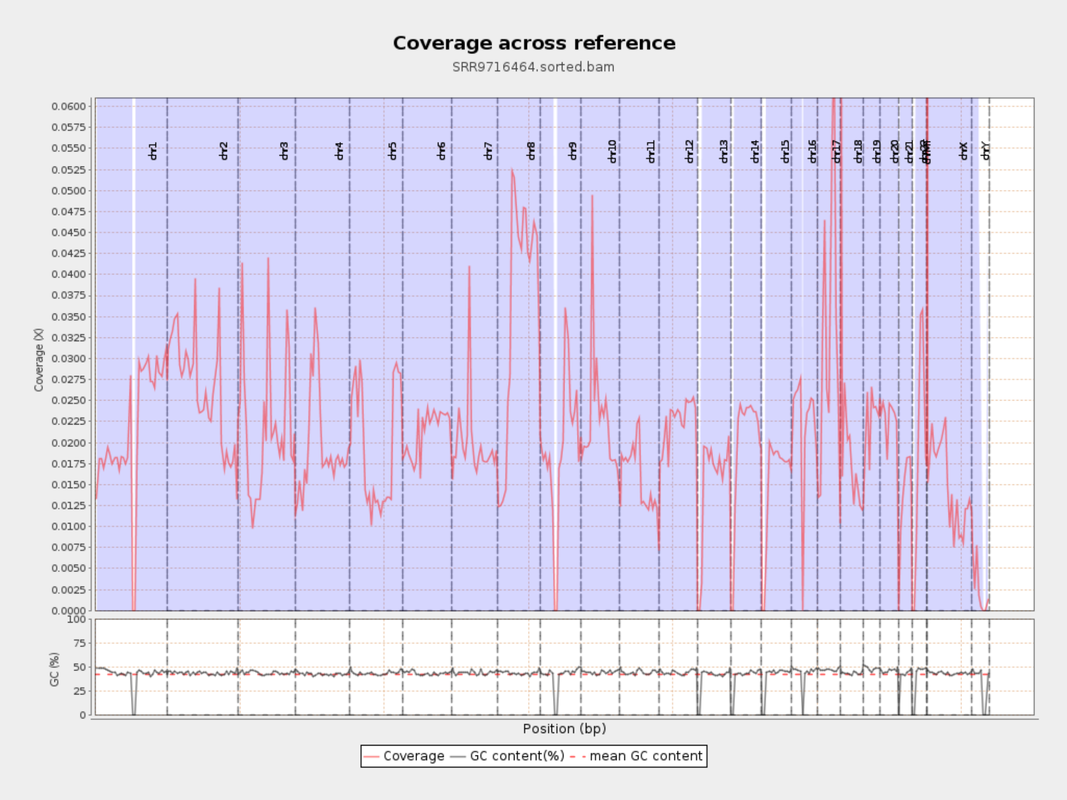
General error rate	0.52%
Mismatches	327,844
Insertions	3,913
Mapped reads with at least one insertion	0.34%
Deletions	12,476
Mapped reads with at least one deletion	1.09%
Homopolymer indels	44.49%

2.6. Chromosome stats

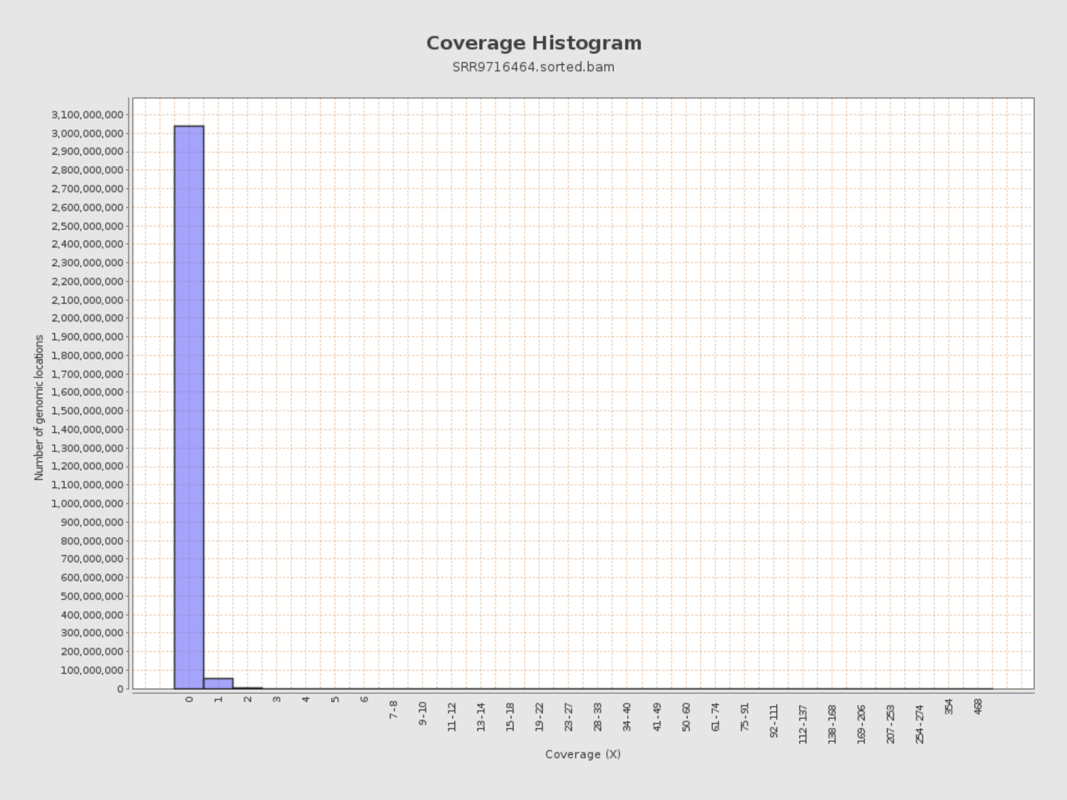
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5354400	0.0215	0.2699
chr2	243199373	6417448	0.0264	0.2751
chr3	198022430	4283067	0.0216	0.1569
chr4	191154276	3717799	0.0194	0.1527
chr5	180915260	3519677	0.0195	0.1478
chr6	171115067	3624654	0.0212	0.1675
chr7	159138663	3179041	0.02	0.3203

chr8	146364022	5329906	0.0364	0.2384
chr9	141213431	2674550	0.0189	0.166
chr10	135534747	3072408	0.0227	0.2257
chr11	135006516	2171973	0.0161	0.154
chr12	133851895	3003539	0.0224	0.1601
chr13	115169878	1736198	0.0151	0.1297
chr14	107349540	2100837	0.0196	0.1508
chr15	102531392	1541283	0.015	0.1317
chr16	90354753	1965117	0.0217	0.1651
chr17	81195210	2665965	0.0328	0.2001
chr18	78077248	1510166	0.0193	0.2506
chr19	59128983	1328523	0.0225	0.2467
chr20	63025520	1424898	0.0226	0.1608
chr21	48129895	660918	0.0137	0.1262
chr22	51304566	954862	0.0186	0.1455
chrMT	16571	54666	3.2989	2.6858
chrX	155270560	2318008	0.0149	0.145
chrY	59373566	146474	0.0025	0.0704

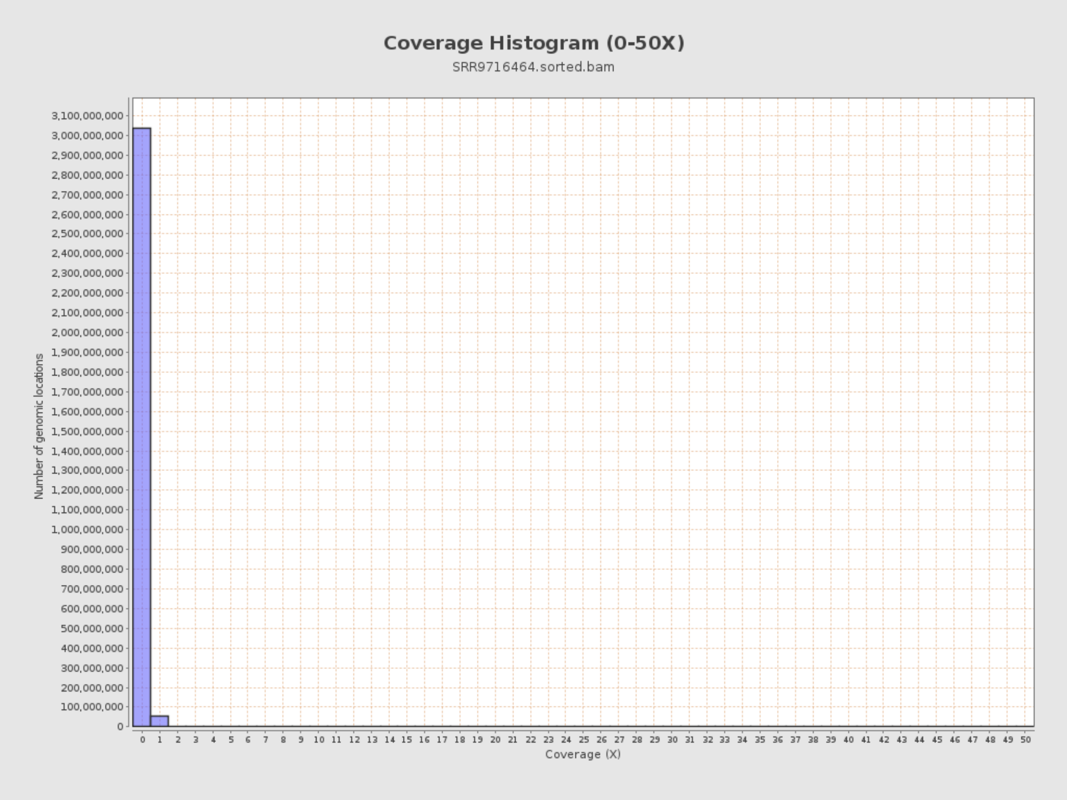
3. Results : Coverage across reference



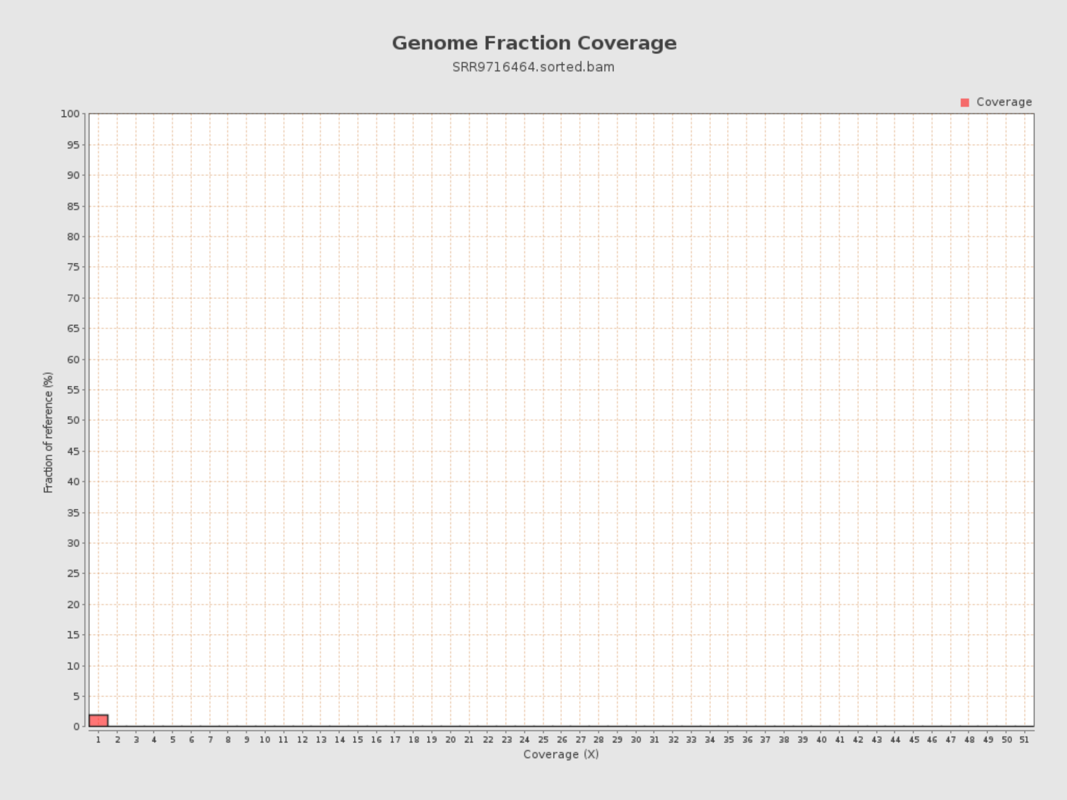
4. Results : Coverage Histogram



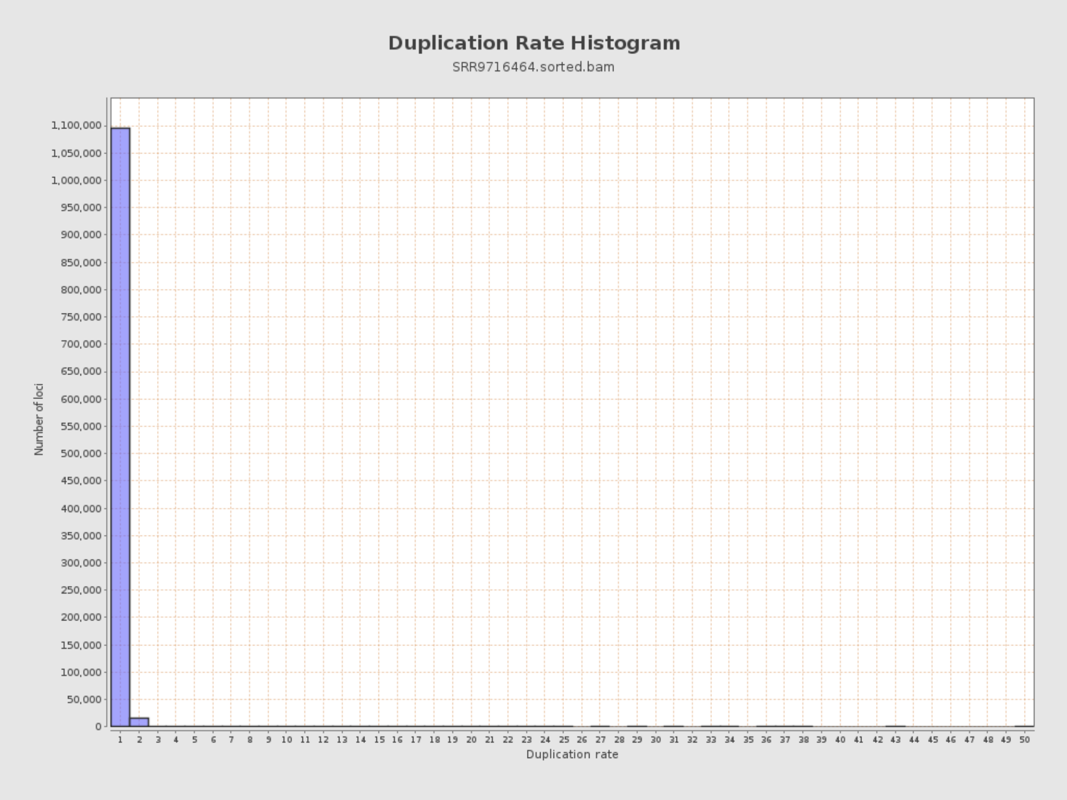
5. Results : Coverage Histogram (0-50X)



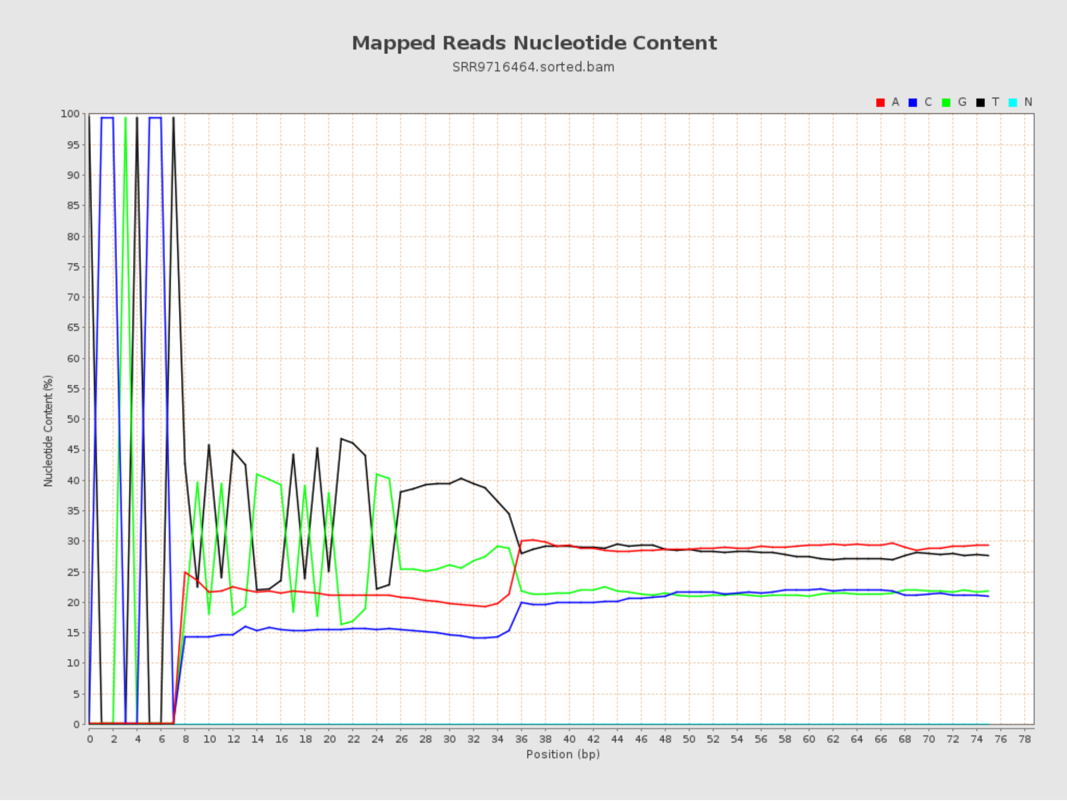
6. Results : Genome Fraction Coverage



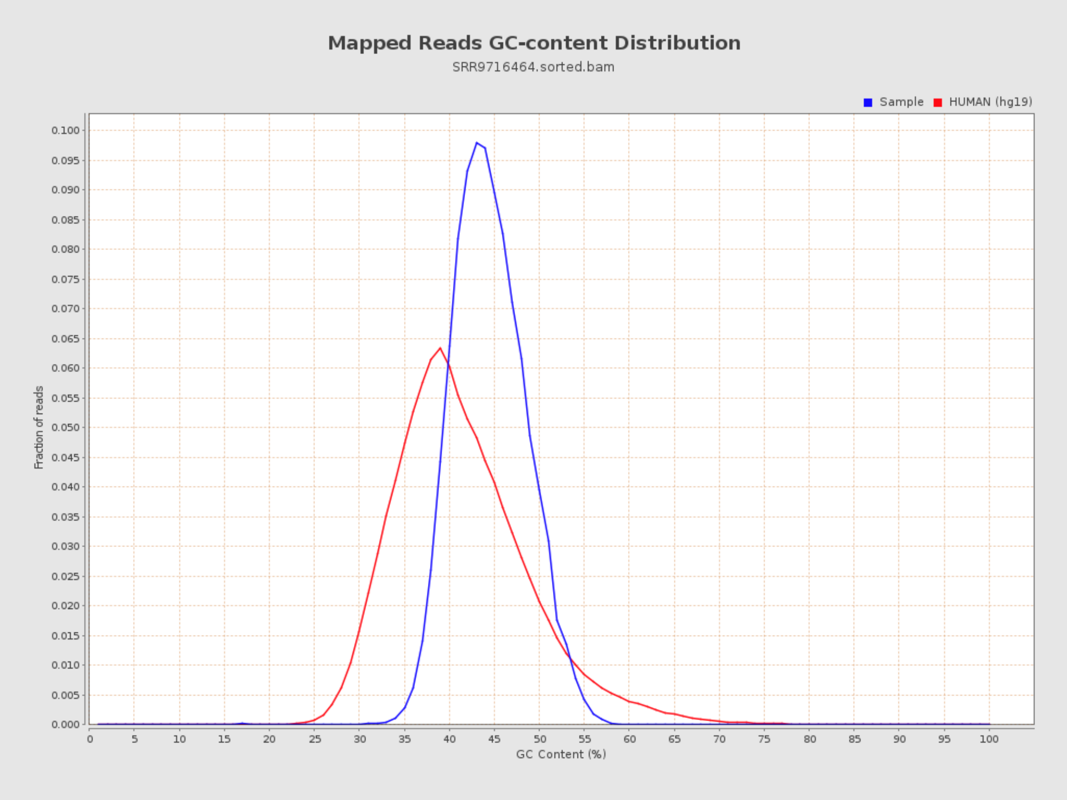
7. Results : Duplication Rate Histogram



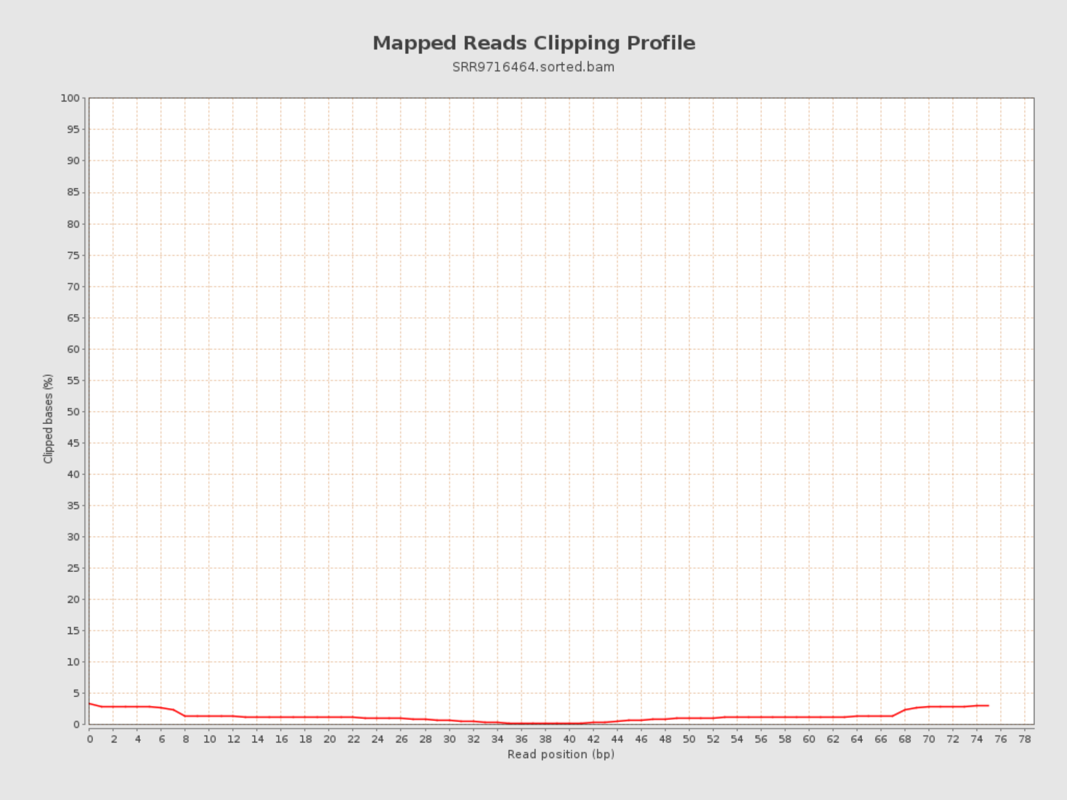
8. Results : Mapped Reads Nucleotide Content



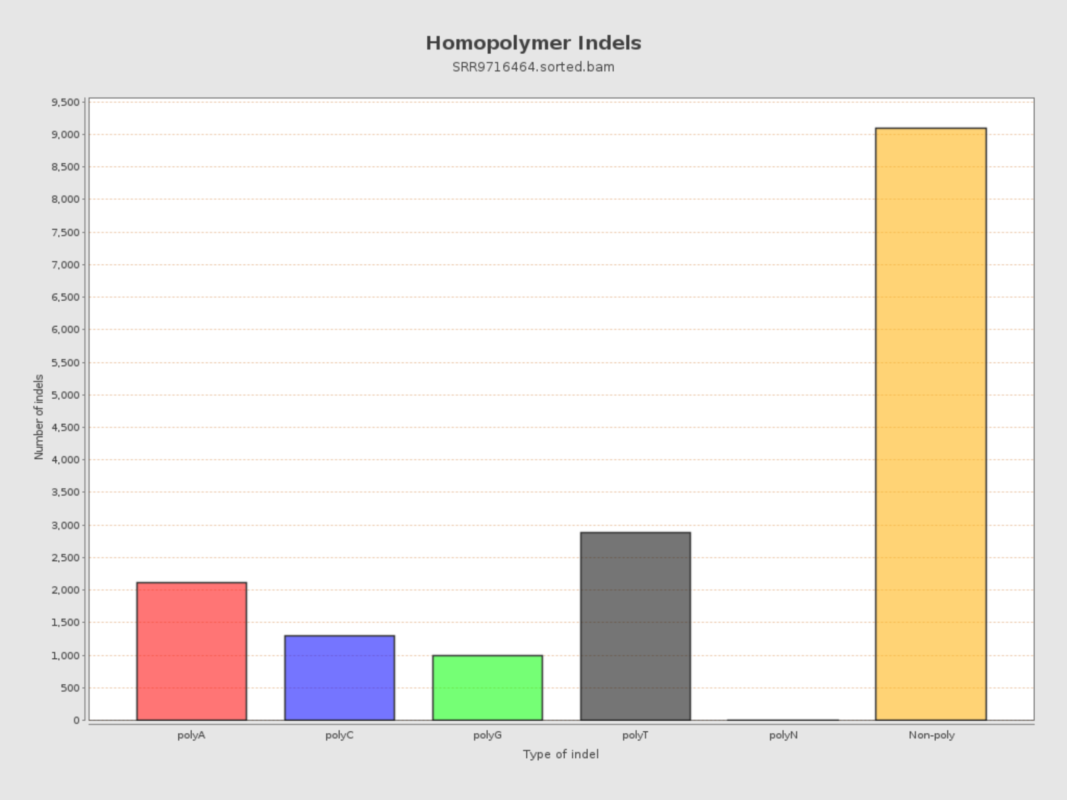
9. Results : Mapped Reads GC-content Distribution



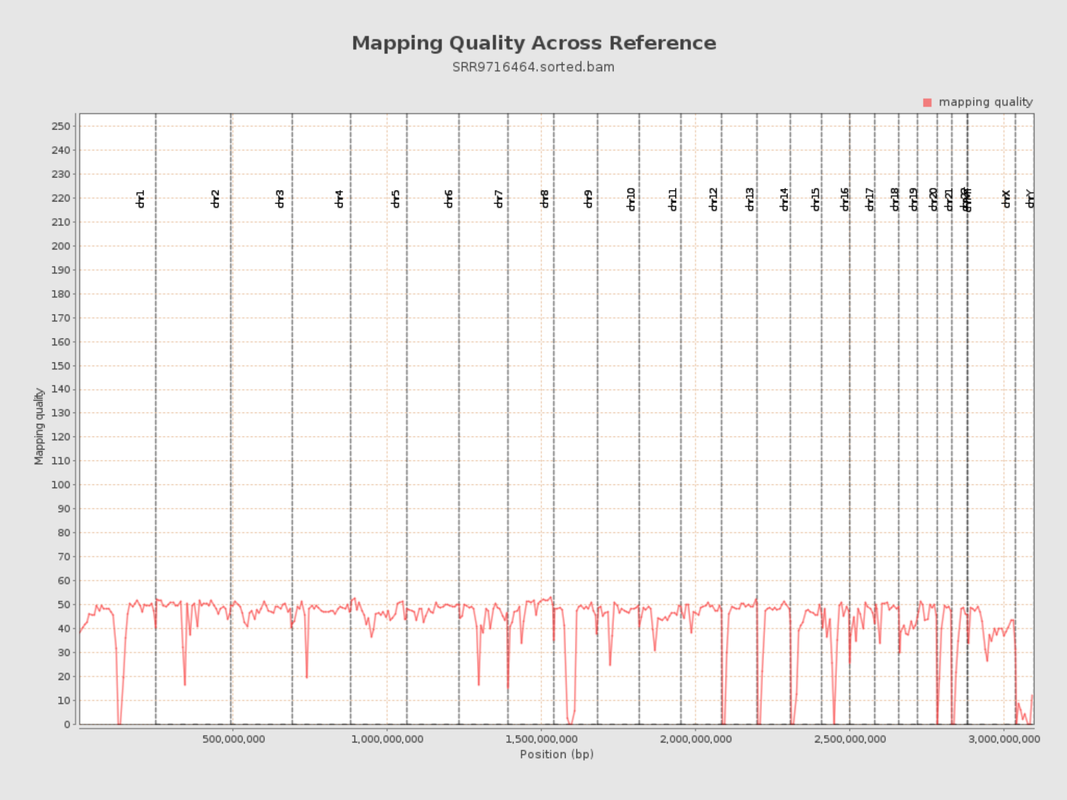
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram