Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 21:55:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716165.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_SRR9716165 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716165.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 21:55:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716165.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,227,310
Mapped reads	2,022,464 / 90.8%
Unmapped reads	204,846 / 9.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,874 / 0.44%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	80,961 / 3.63%
Duplication rate	2.84%
Clipped reads	2,025,134 / 90.92%

2.2. ACGT Content

Number/percentage of A's	30,431,574 / 26.14%
Number/percentage of C's	22,536,321 / 19.35%
Number/percentage of T's	36,334,155 / 31.21%
Number/percentage of G's	27,132,842 / 23.3%
Number/percentage of N's	1,878 / 0%
GC Percentage	42.66%

2.3. Coverage

Mean	0.0376

Standard Deviation	0.3602

2.4. Mapping Quality

Mean Mapping Quality	44.33

2.5. Mismatches and indels

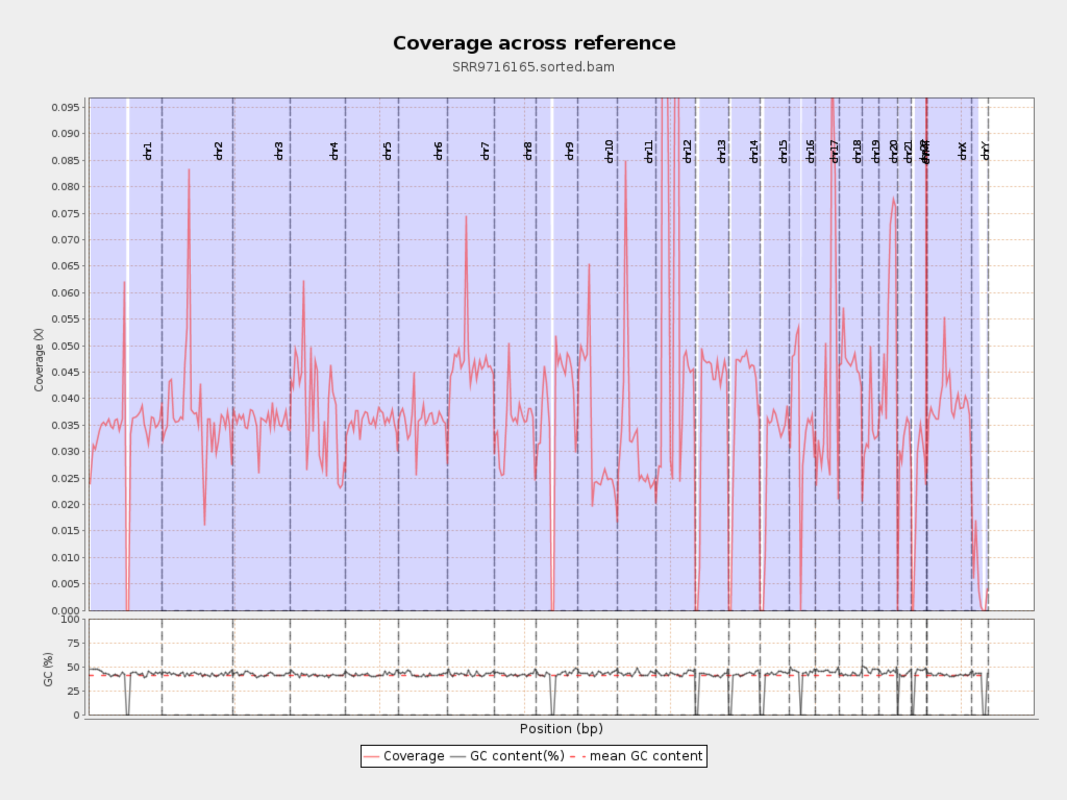
General error rate	0.55%
Mismatches	622,181
Insertions	8,934
Mapped reads with at least one insertion	0.44%
Deletions	19,769
Mapped reads with at least one deletion	0.97%
Homopolymer indels	41.84%

2.6. Chromosome stats

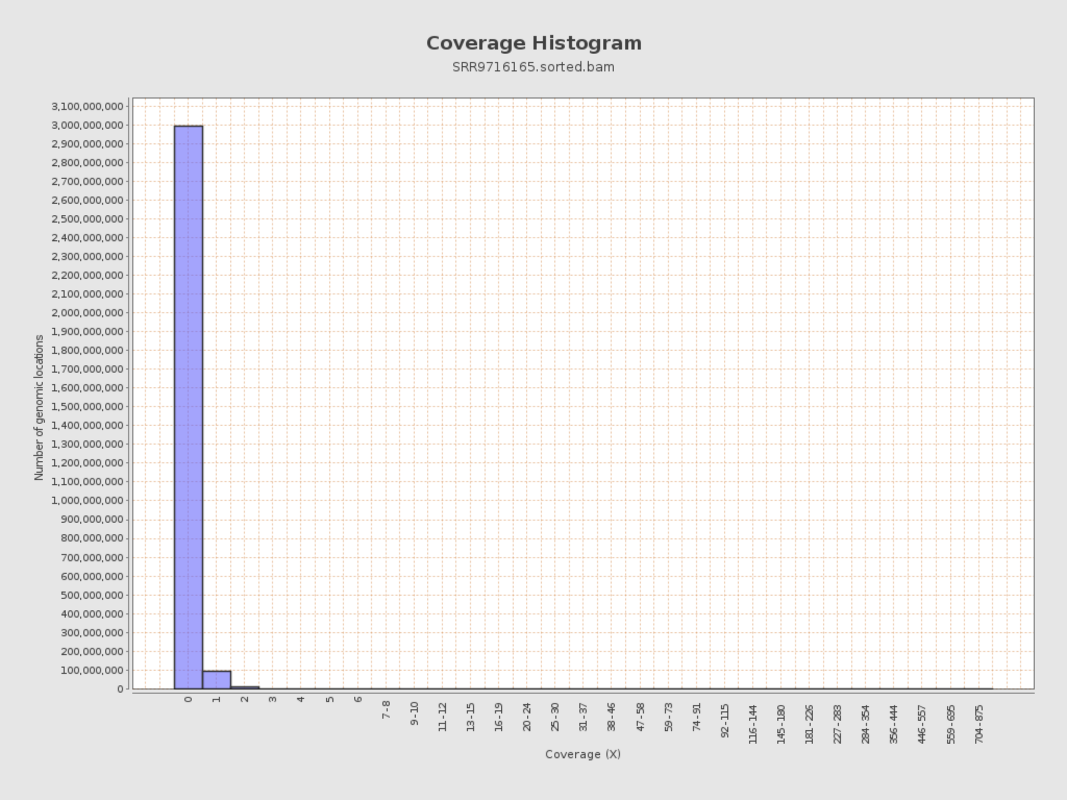
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8308272	0.0333	0.6625
chr2	243199373	9107612	0.0374	0.3983
chr3	198022430	7080816	0.0358	0.2057
chr4	191154276	7273155	0.038	0.2405
chr5	180915260	6478423	0.0358	0.2119
chr6	171115067	6146045	0.0359	0.2397
chr7	159138663	7540144	0.0474	0.4886

chr8	146364022	5109124	0.0349	0.3329
chr9	141213431	5313359	0.0376	0.3792
chr10	135534747	4461515	0.0329	0.3588
chr11	135006516	4489519	0.0333	0.2866
chr12	133851895	8769588	0.0655	0.3195
chr13	115169878	4383585	0.0381	0.2125
chr14	107349540	4135146	0.0385	0.2481
chr15	102531392	2949025	0.0288	0.1863
chr16	90354753	3261597	0.0361	0.2379
chr17	81195210	3514353	0.0433	0.238
chr18	78077248	3705617	0.0475	0.7059
chr19	59128983	1998600	0.0338	0.4993
chr20	63025520	3516755	0.0558	0.2687
chr21	48129895	1391666	0.0289	0.222
chr22	51304566	1124490	0.0219	0.1596
chrMT	16571	4941	0.2982	0.5917
chrX	155270560	6091865	0.0392	0.2709
chrY	59373566	314205	0.0053	0.1236

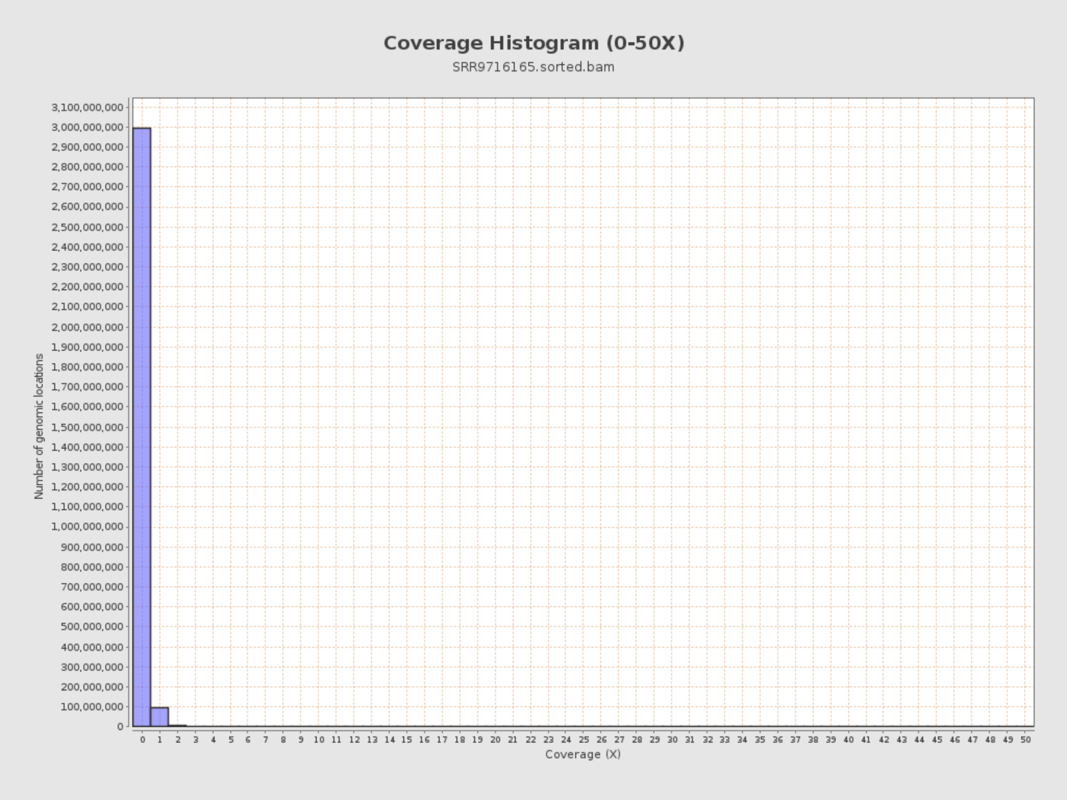
3. Results : Coverage across reference



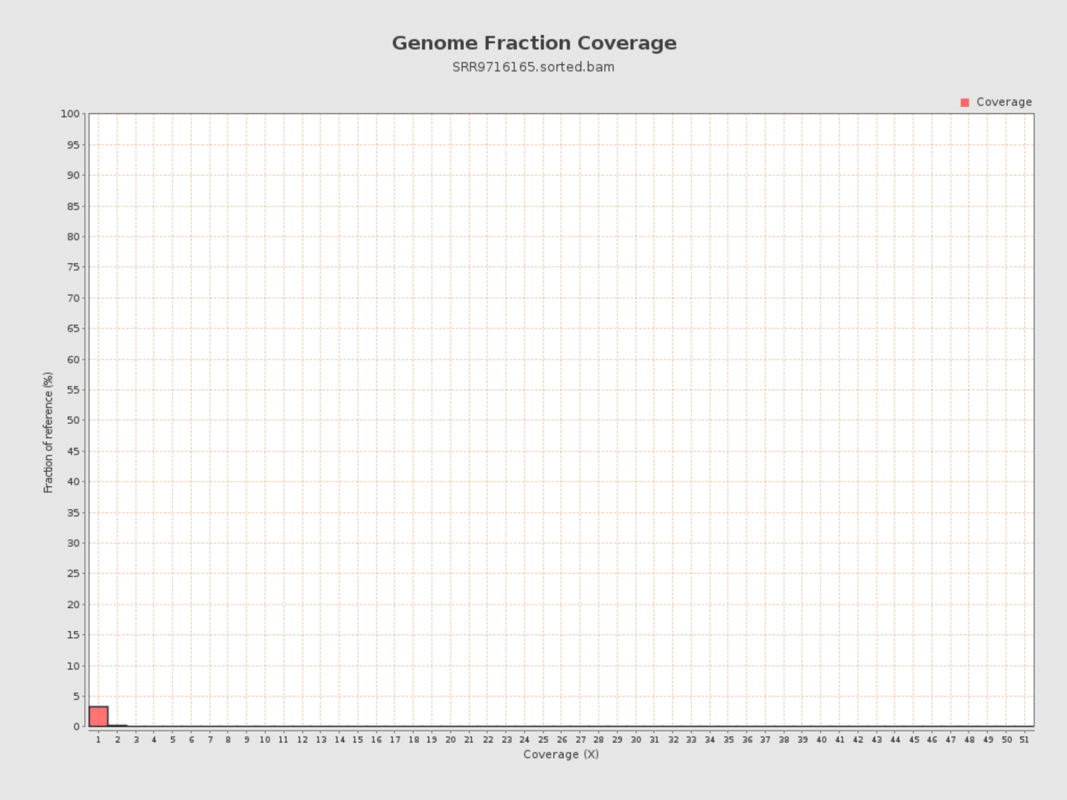
4. Results : Coverage Histogram



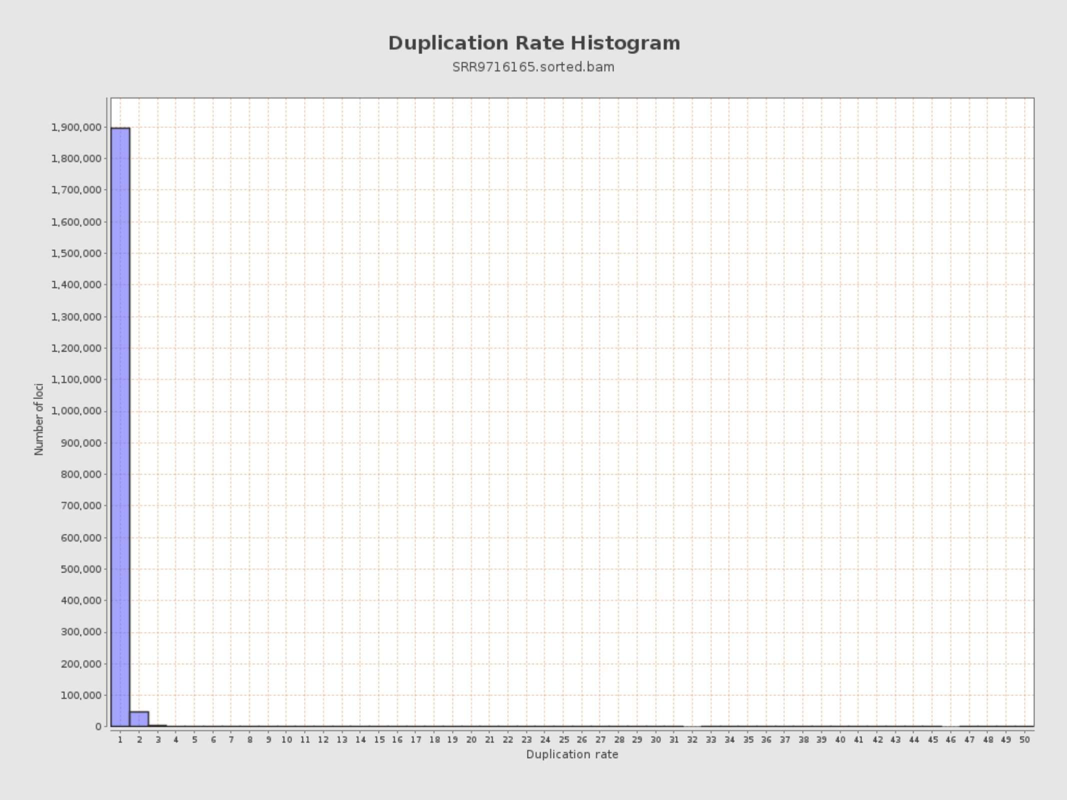
5. Results : Coverage Histogram (0-50X)



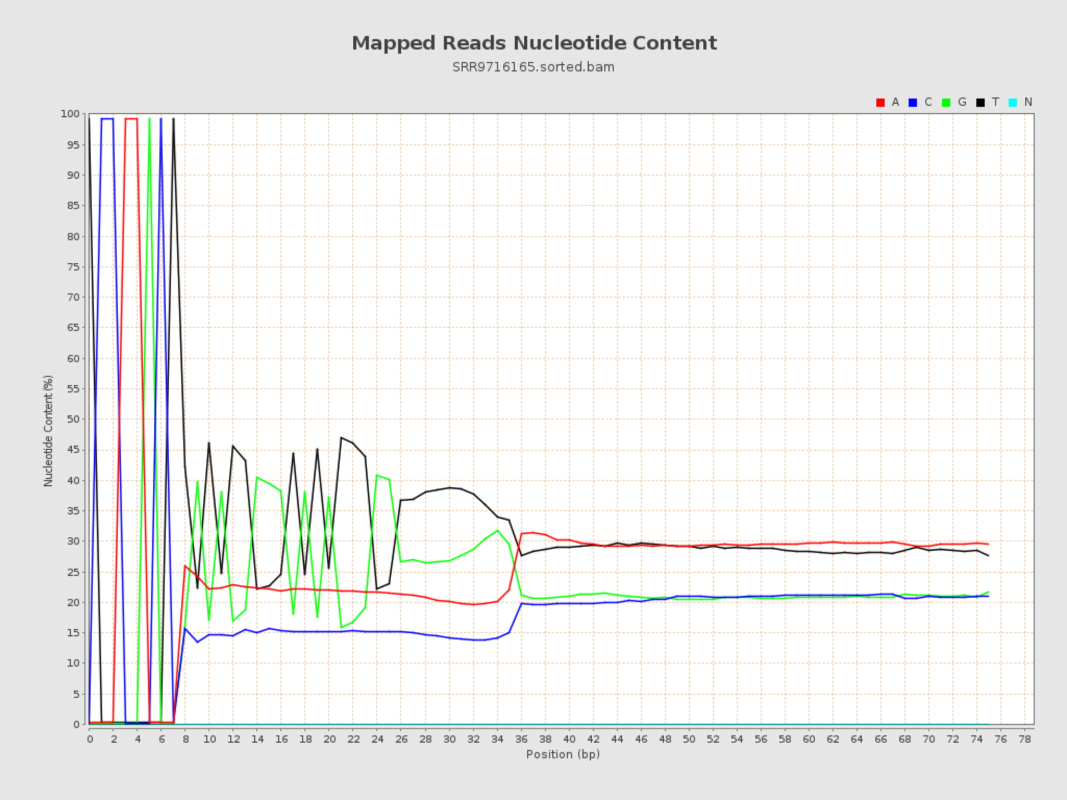
6. Results : Genome Fraction Coverage



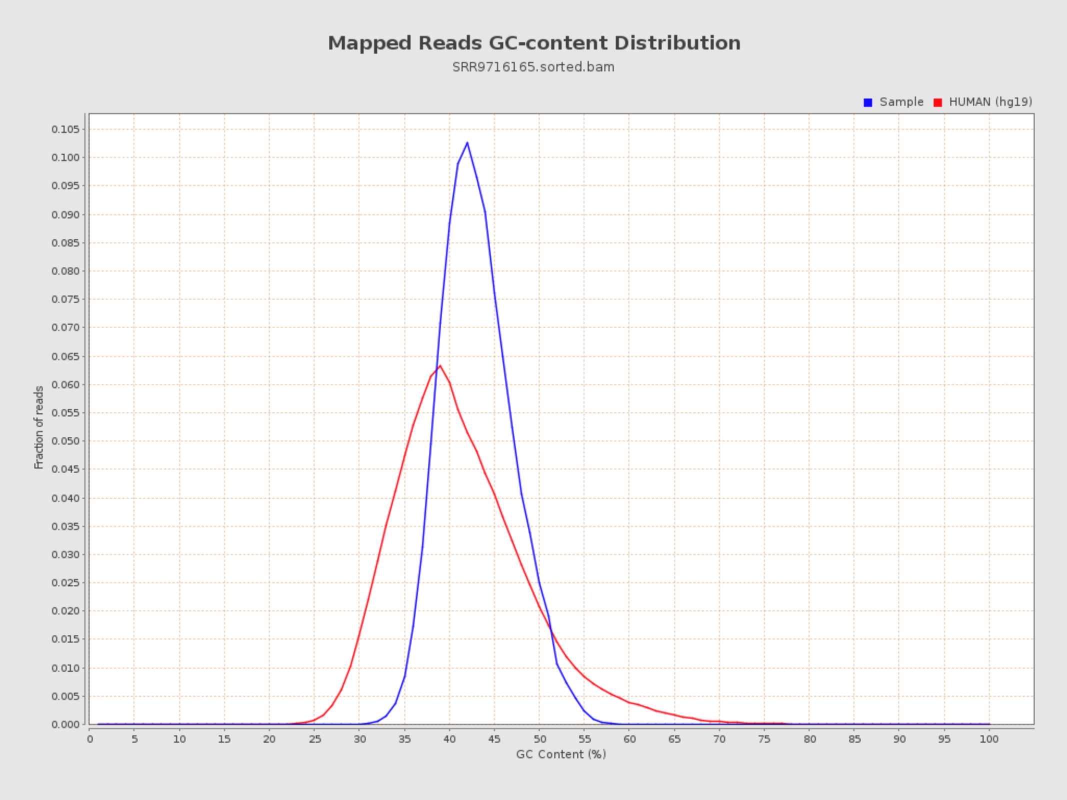
7. Results : Duplication Rate Histogram



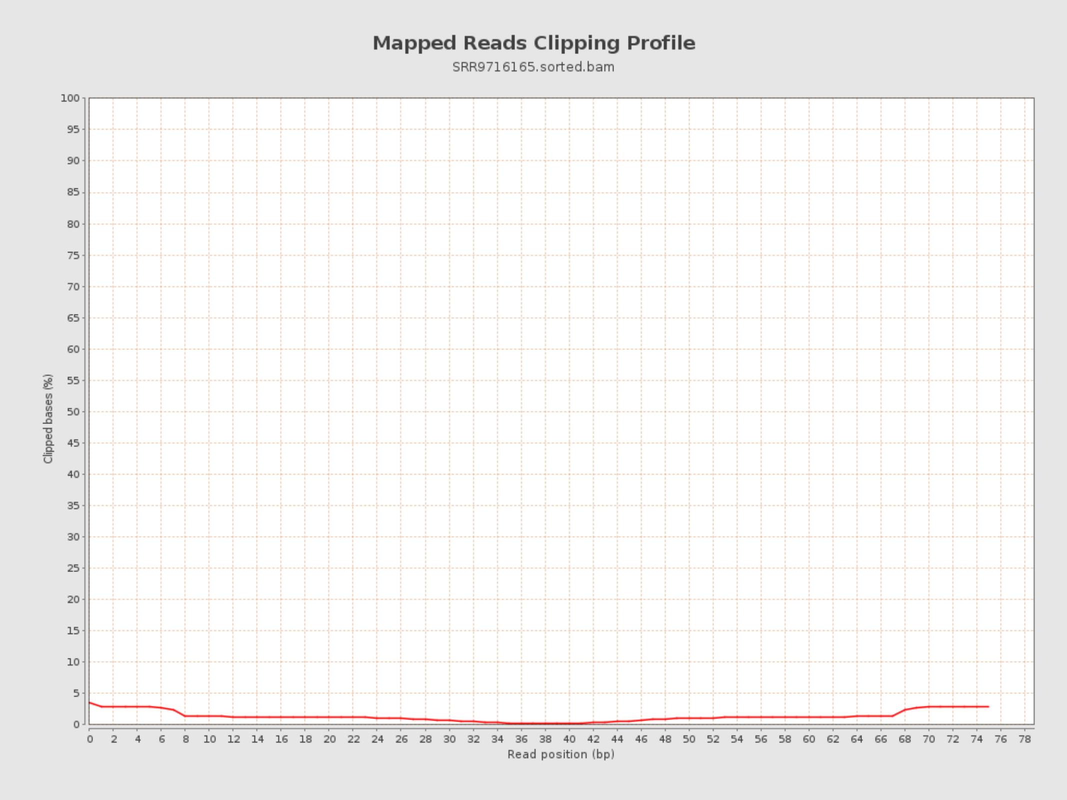
8. Results : Mapped Reads Nucleotide Content



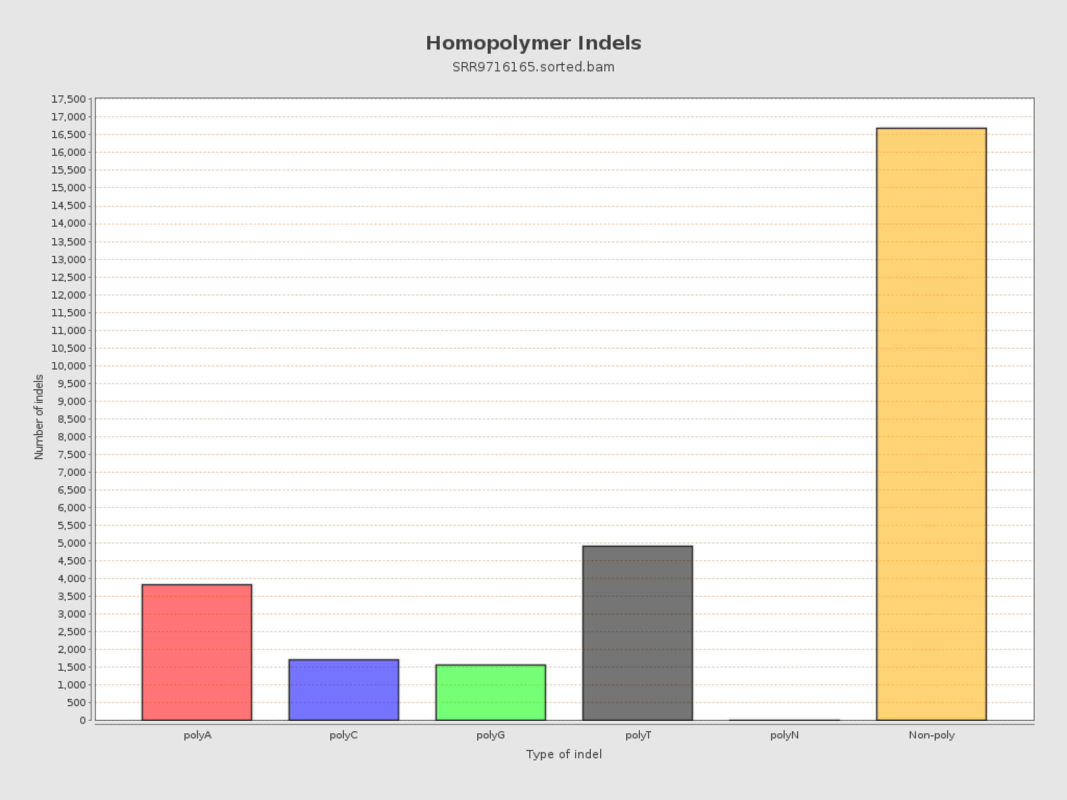
9. Results : Mapped Reads GC-content Distribution



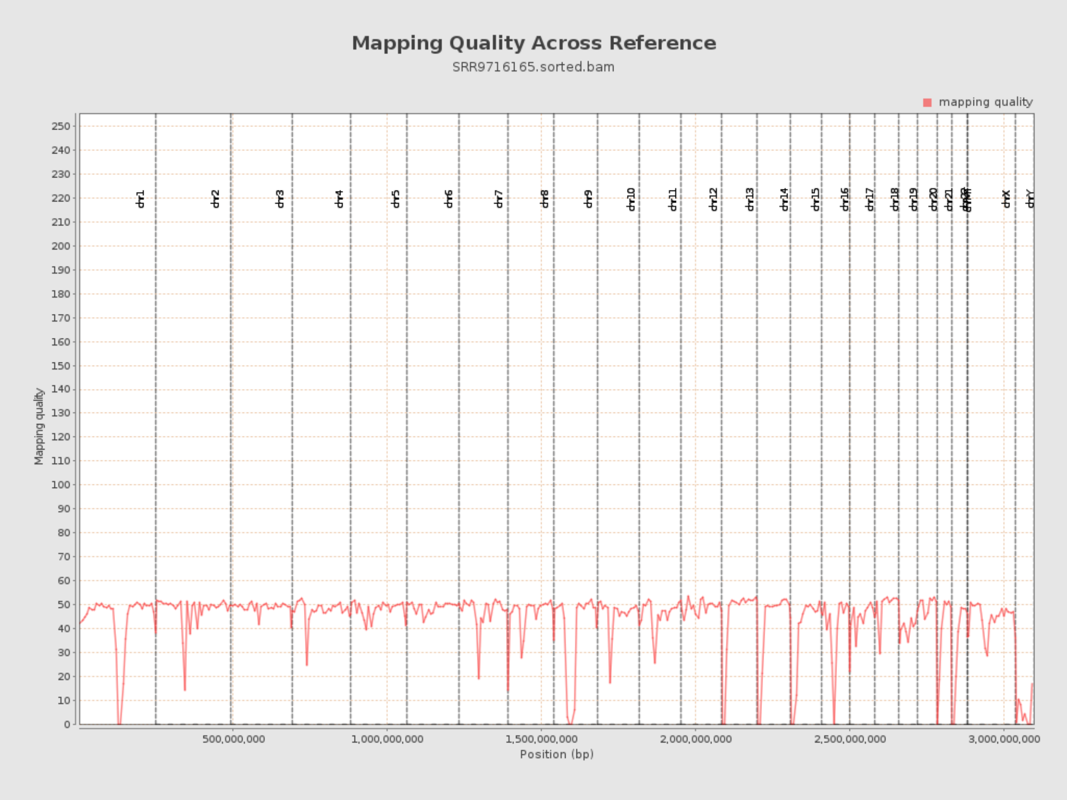
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram