Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 04:57:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081245.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_SRR3081245 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081245.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 04:57:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081245.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,508,097
Mapped reads	1,344,484 / 89.15%
Unmapped reads	163,613 / 10.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,575 / 0.77%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	37,748 / 2.5%
Duplication rate	2.14%
Clipped reads	715,225 / 47.43%

2.2. ACGT Content

Number/percentage of A's	25,756,125 / 29.31%
Number/percentage of C's	16,854,324 / 19.18%
Number/percentage of T's	26,656,140 / 30.33%
Number/percentage of G's	18,600,464 / 21.17%
Number/percentage of N's	10,770 / 0.01%
GC Percentage	40.35%

2.3. Coverage

Mean	0.0284

Standard Deviation	0.2731

2.4. Mapping Quality

Mean Mapping Quality	45.58

2.5. Mismatches and indels

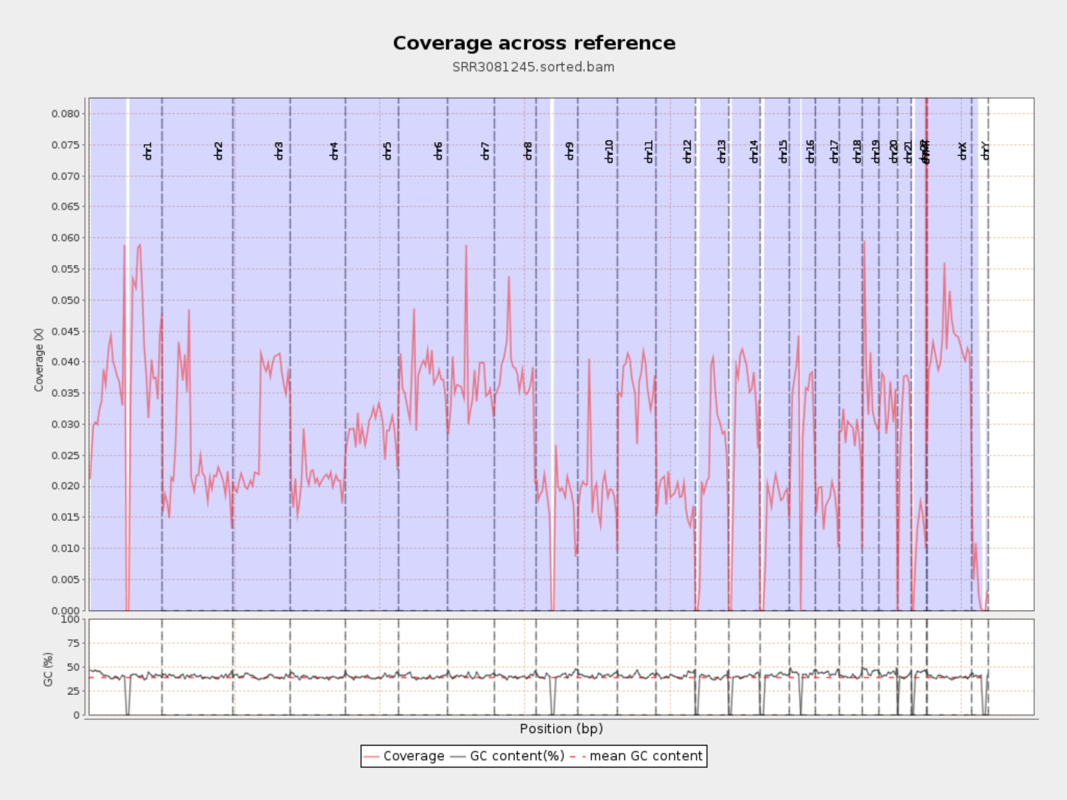
General error rate	0.95%
Mismatches	821,017
Insertions	6,651
Mapped reads with at least one insertion	0.49%
Deletions	21,544
Mapped reads with at least one deletion	1.59%
Homopolymer indels	47.4%

2.6. Chromosome stats

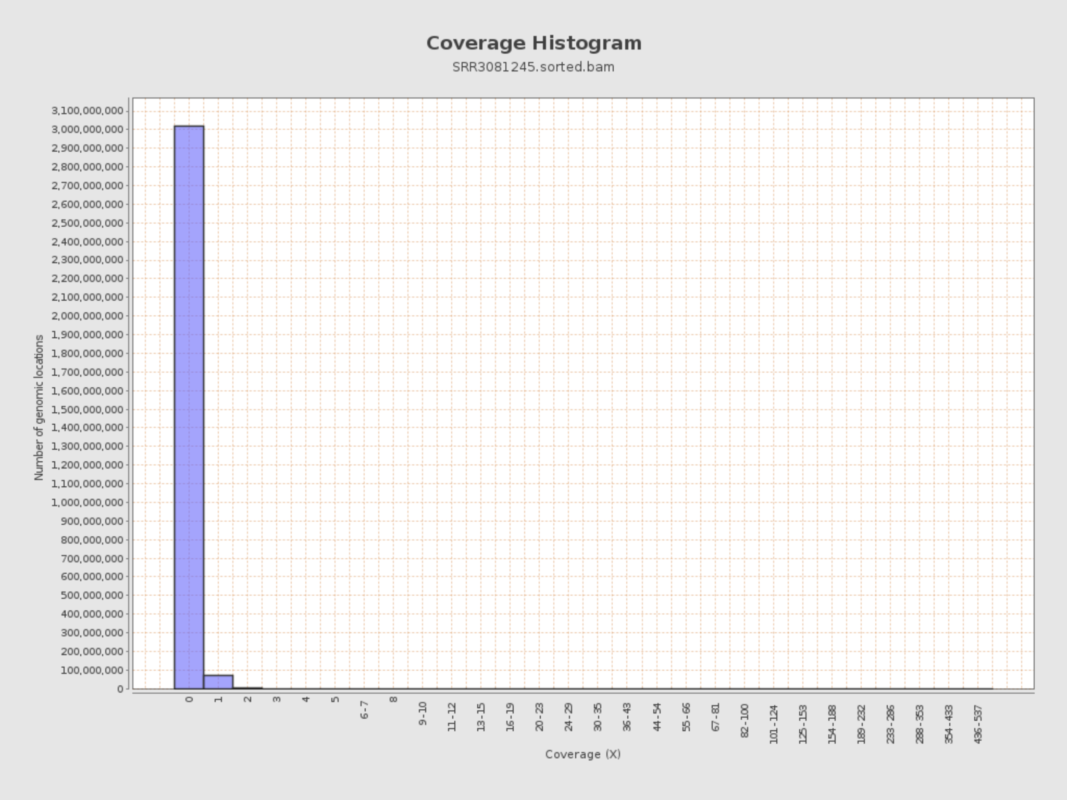
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9365921	0.0376	0.5015
chr2	243199373	5932850	0.0244	0.2687
chr3	198022430	5978596	0.0302	0.189
chr4	191154276	3980014	0.0208	0.1624
chr5	180915260	5276318	0.0292	0.1851
chr6	171115067	6414933	0.0375	0.2393
chr7	159138663	5811799	0.0365	0.3881

chr8	146364022	5535463	0.0378	0.3904
chr9	141213431	2375057	0.0168	0.1959
chr10	135534747	2708464	0.02	0.241
chr11	135006516	4903586	0.0363	0.3043
chr12	133851895	2437046	0.0182	0.1491
chr13	115169878	2707529	0.0235	0.1656
chr14	107349540	3320596	0.0309	0.1972
chr15	102531392	1578320	0.0154	0.1377
chr16	90354753	2903102	0.0321	0.2038
chr17	81195210	1395734	0.0172	0.1619
chr18	78077248	2257926	0.0289	0.3542
chr19	59128983	2124024	0.0359	0.3662
chr20	63025520	2090988	0.0332	0.199
chr21	48129895	1420747	0.0295	0.1935
chr22	51304566	533844	0.0104	0.109
chrMT	16571	18374	1.1088	1.237
chrX	155270560	6608193	0.0426	0.2406
chrY	59373566	233935	0.0039	0.0838

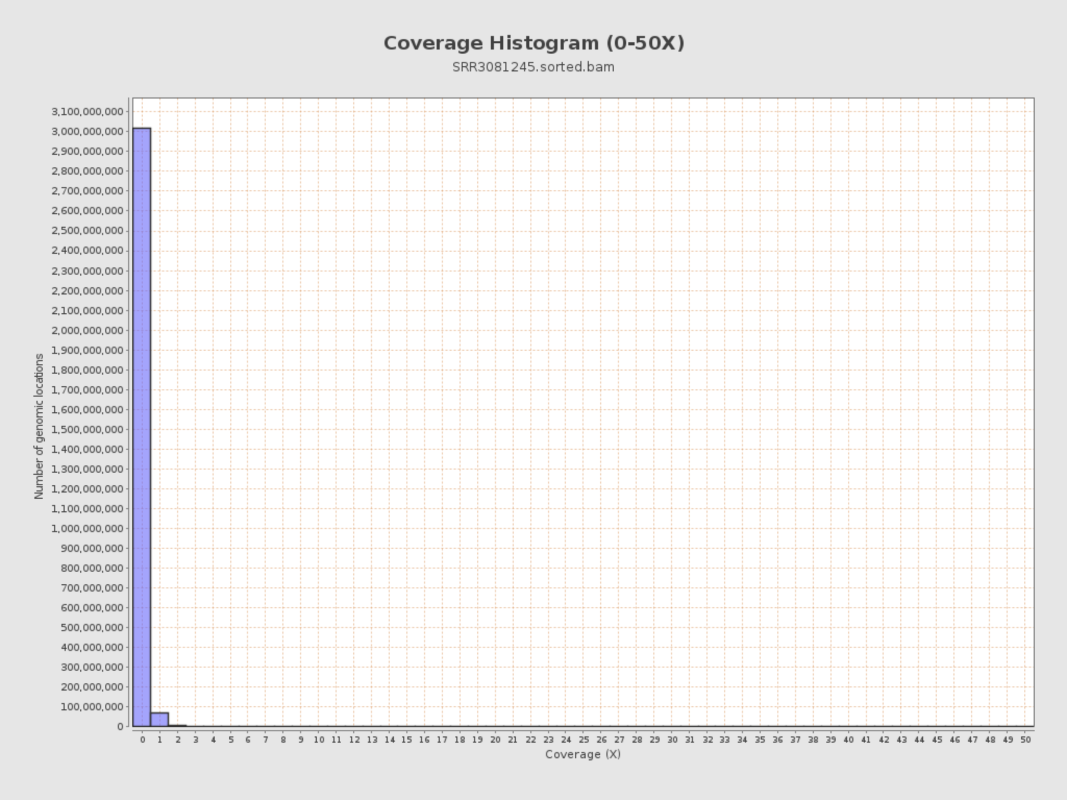
3. Results : Coverage across reference



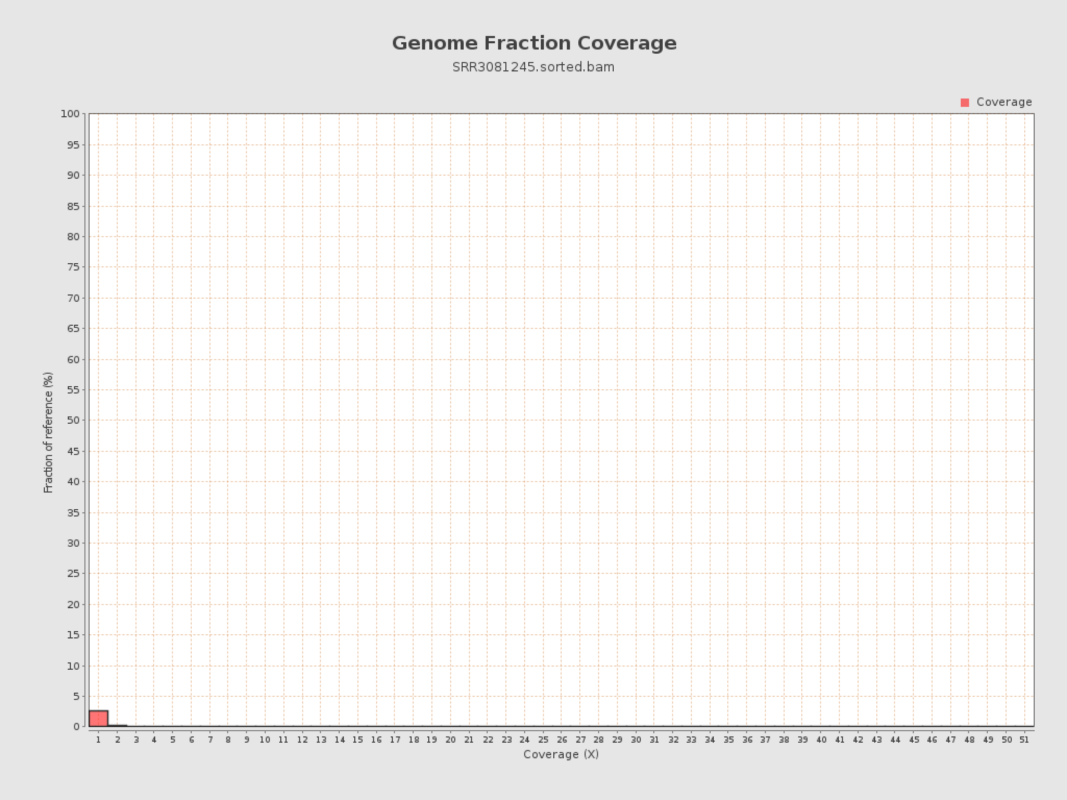
4. Results : Coverage Histogram



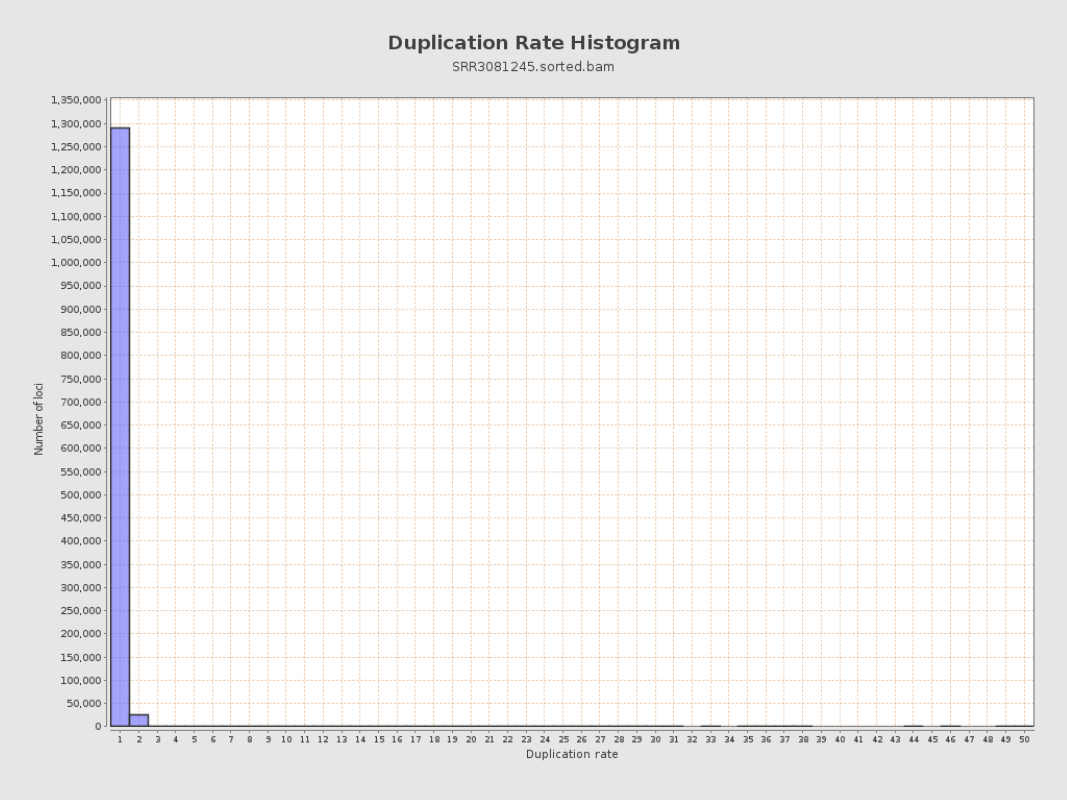
5. Results : Coverage Histogram (0-50X)



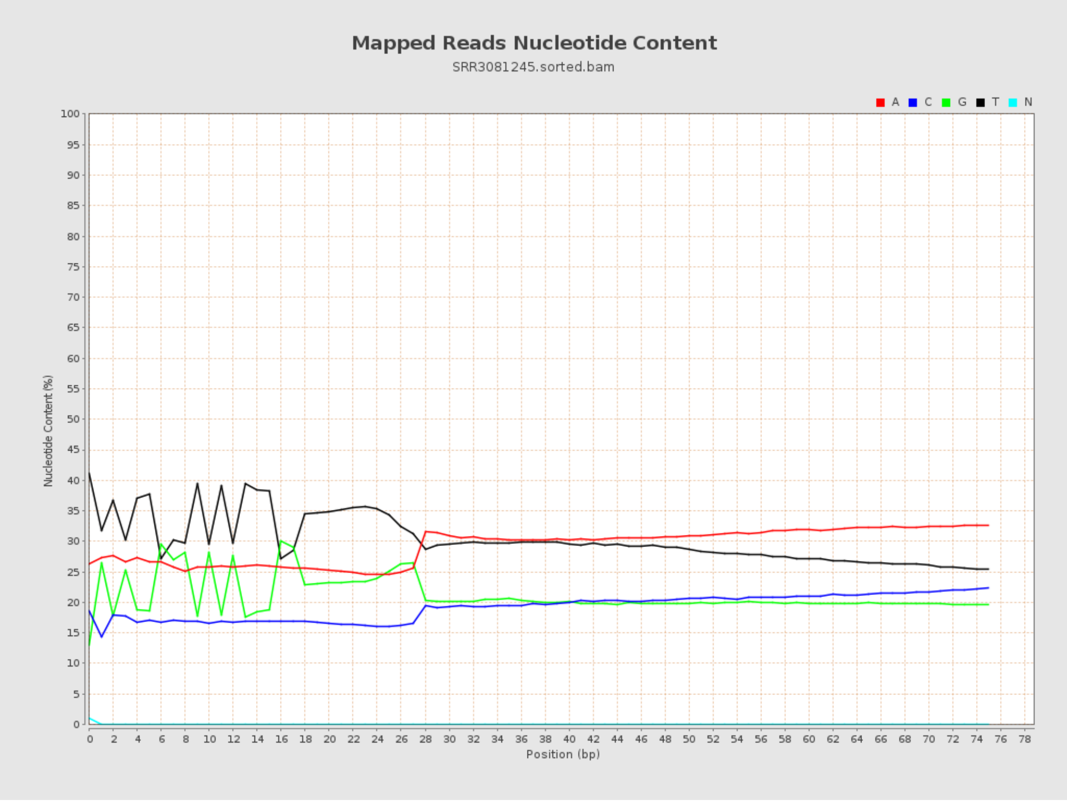
6. Results : Genome Fraction Coverage



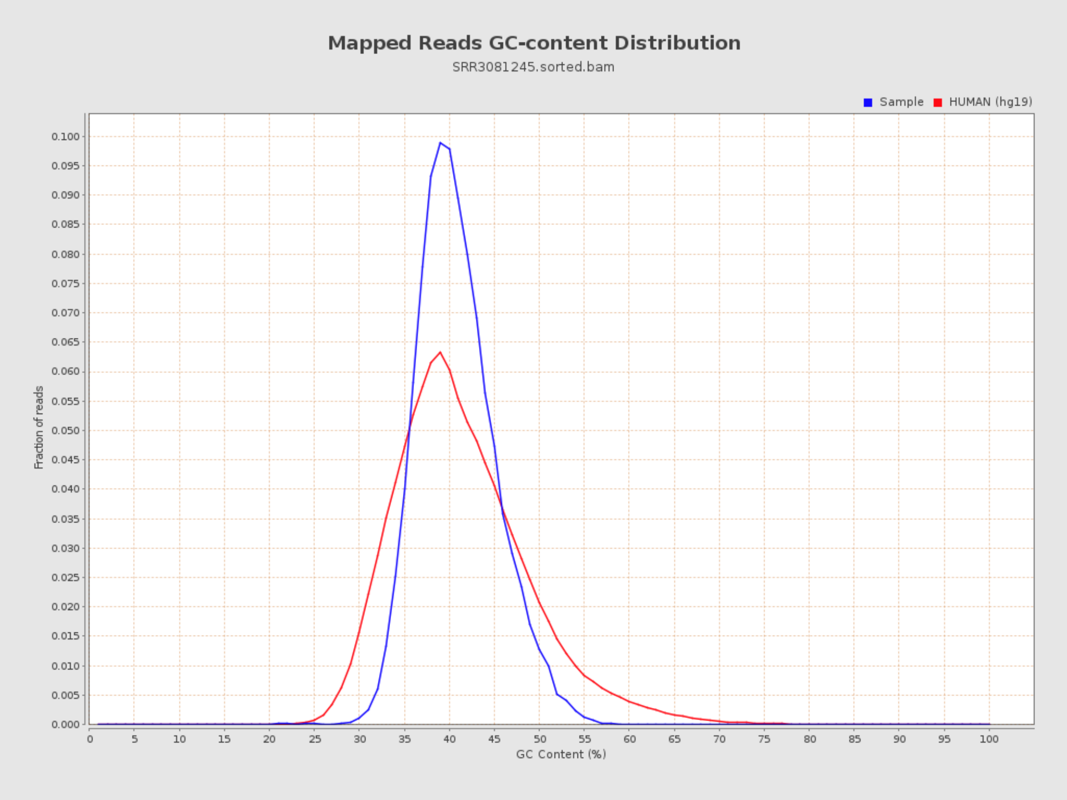
7. Results : Duplication Rate Histogram



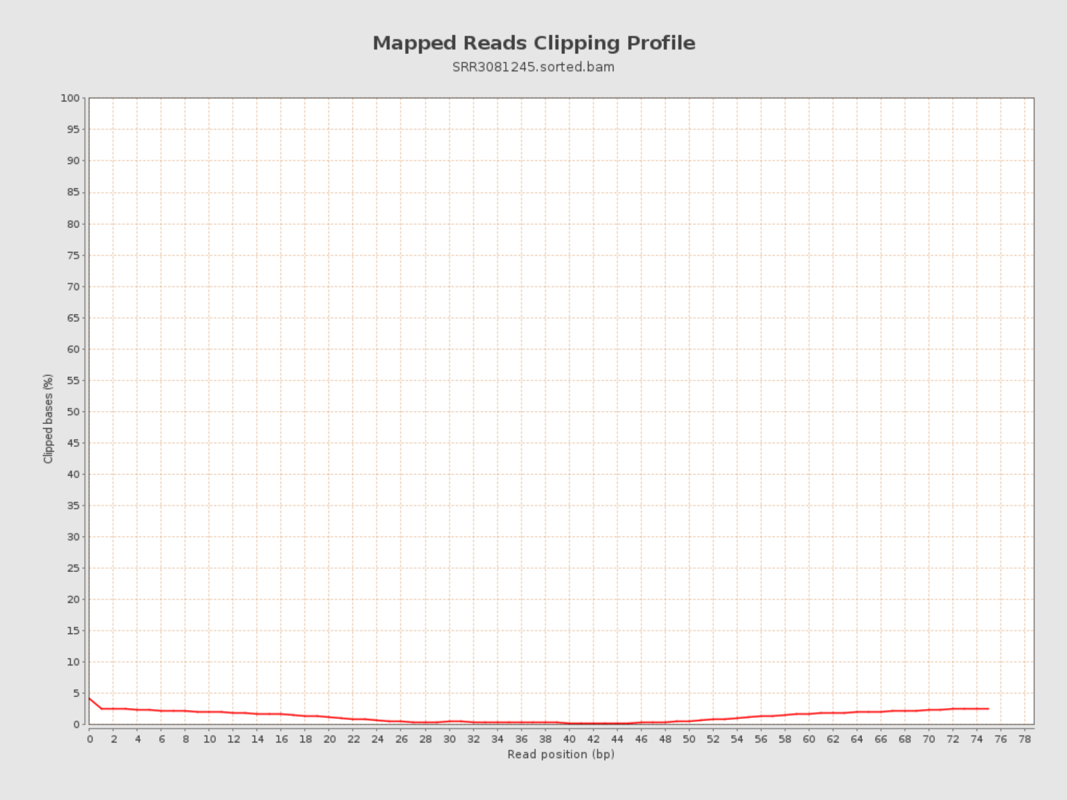
8. Results : Mapped Reads Nucleotide Content



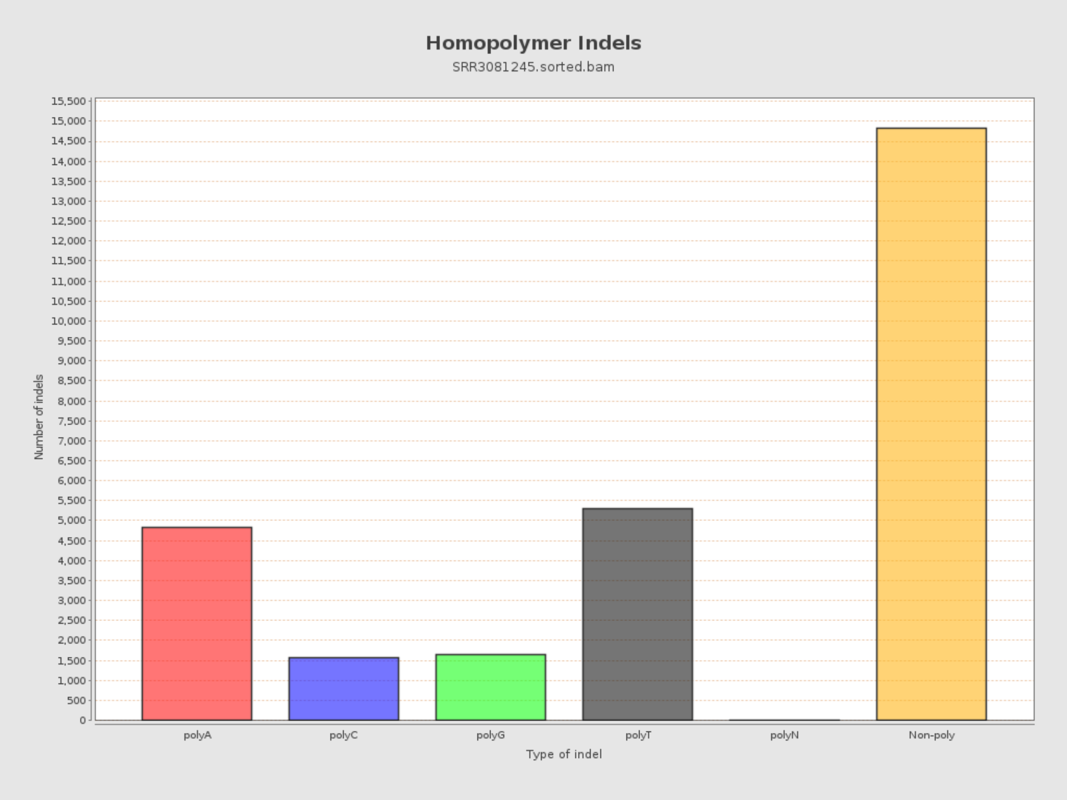
9. Results : Mapped Reads GC-content Distribution



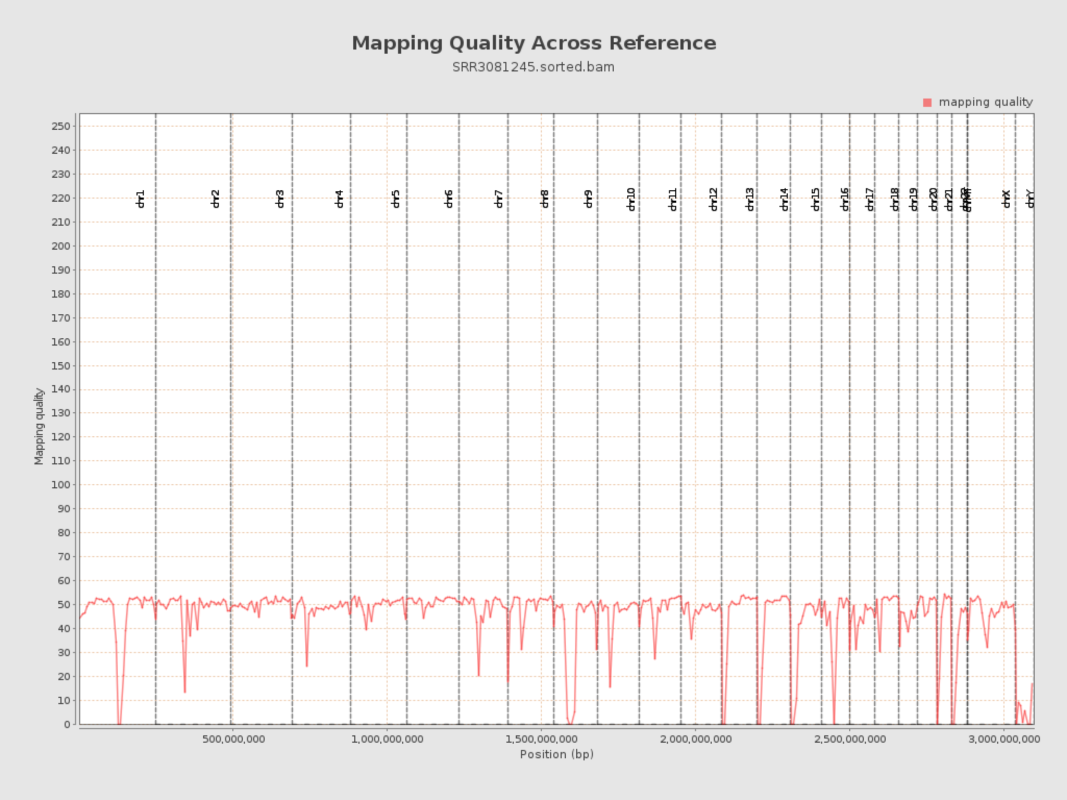
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram