Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 19:13:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2971315.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_SRR2971315 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2971315.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 19:13:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2971315.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,913,884
Mapped reads	11,653,009 / 90.24%
Unmapped reads	1,260,875 / 9.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,616 / 0.01%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	1,262,480 / 9.78%
Duplication rate	9.27%
Clipped reads	2,377,022 / 18.41%

2.2. ACGT Content

Number/percentage of A's	158,948,914 / 28.44%
Number/percentage of C's	116,591,041 / 20.86%
Number/percentage of T's	162,967,146 / 29.16%
Number/percentage of G's	120,376,064 / 21.54%
Number/percentage of N's	29,951 / 0.01%
GC Percentage	42.4%

2.3. Coverage

Mean	0.1806

Standard Deviation	1.4119

2.4. Mapping Quality

Mean Mapping Quality	39.26

2.5. Mismatches and indels

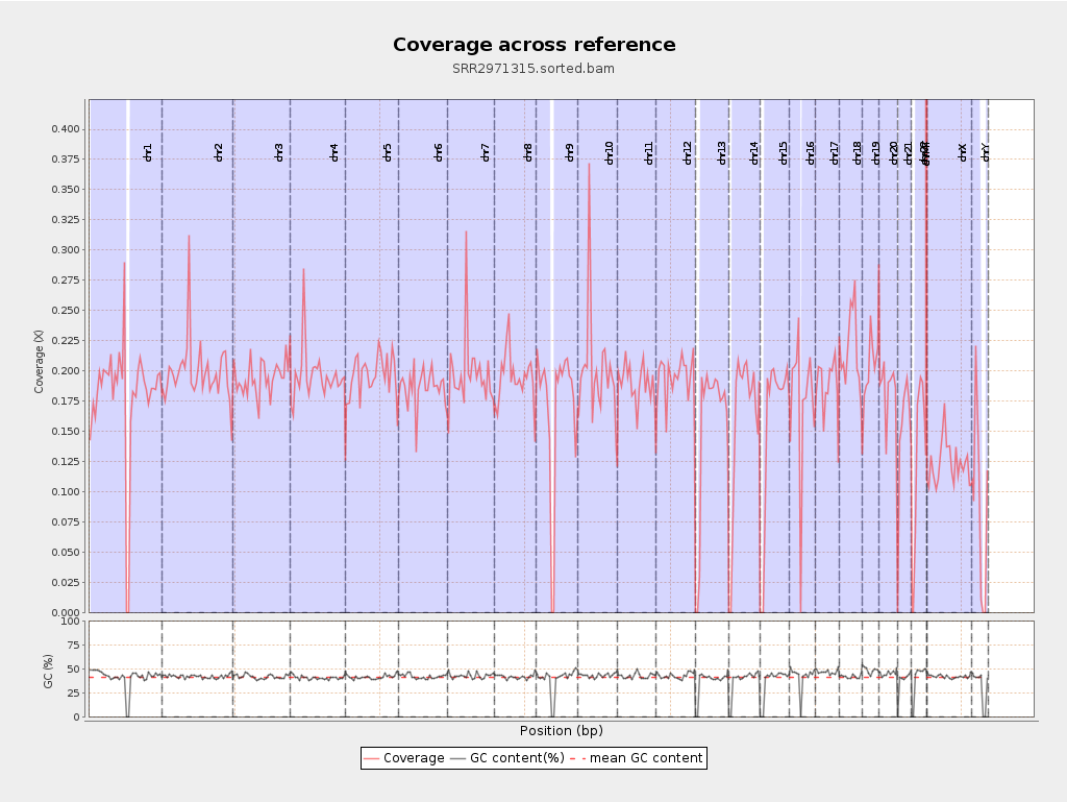
General error rate	0.47%
Mismatches	2,568,675
Insertions	34,673
Mapped reads with at least one insertion	0.3%
Deletions	83,213
Mapped reads with at least one deletion	0.71%
Homopolymer indels	41.76%

2.6. Chromosome stats

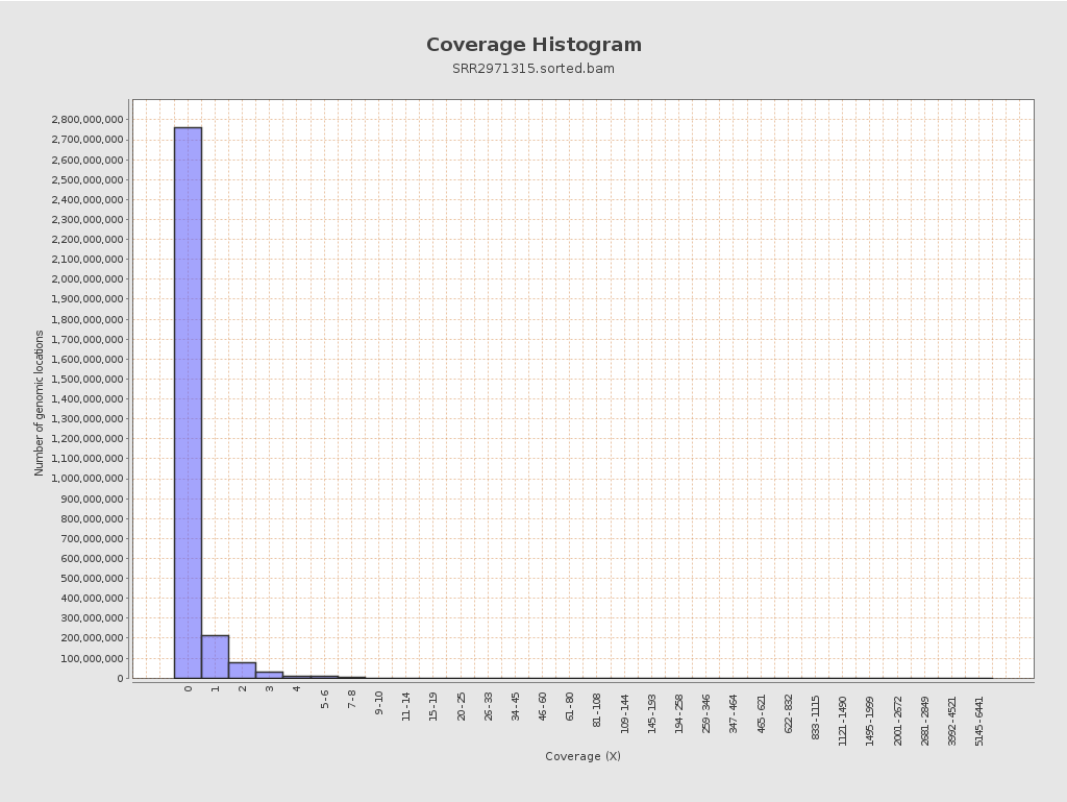
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	44820965	0.1798	2.3924
chr2	243199373	48463754	0.1993	1.2595
chr3	198022430	38349471	0.1937	0.6818
chr4	191154276	37351870	0.1954	0.8933
chr5	180915260	35572437	0.1966	0.6892
chr6	171115067	31901121	0.1864	0.7357
chr7	159138663	31541667	0.1982	1.748

chr8	146364022	28415378	0.1941	3.3332
chr9	141213431	23791494	0.1685	1.1346
chr10	135534747	27139893	0.2002	1.5957
chr11	135006516	25500479	0.1889	1.0382
chr12	133851895	26046502	0.1946	0.6988
chr13	115169878	17645411	0.1532	0.5901
chr14	107349540	16875597	0.1572	0.7543
chr15	102531392	16077667	0.1568	0.6013
chr16	90354753	15858857	0.1755	0.8158
chr17	81195210	15158820	0.1867	0.7731
chr18	78077248	17086091	0.2188	2.2012
chr19	59128983	12150926	0.2055	2.0604
chr20	63025520	11477310	0.1821	0.6975
chr21	48129895	7197121	0.1495	0.8714
chr22	51304566	6306807	0.1229	0.6506
chrMT	16571	188507	11.3757	8.2239
chrX	155270560	19182874	0.1235	0.6856
chrY	59373566	4933780	0.0831	0.8385

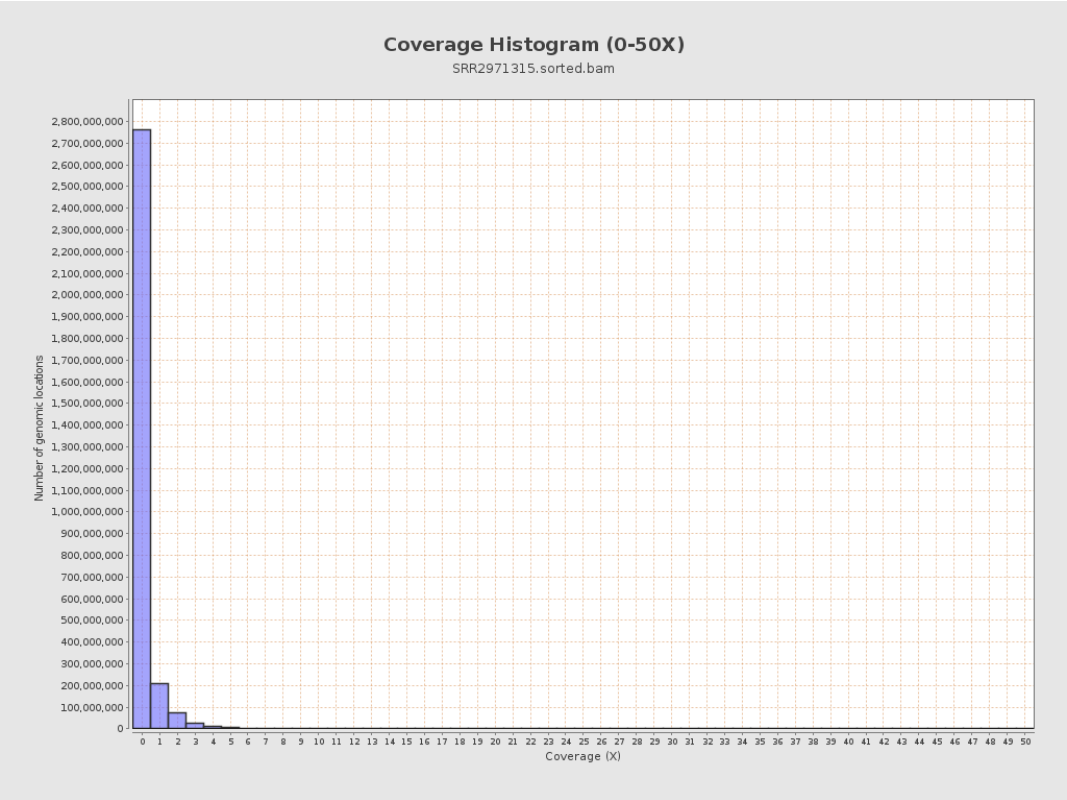
3. Results : Coverage across reference



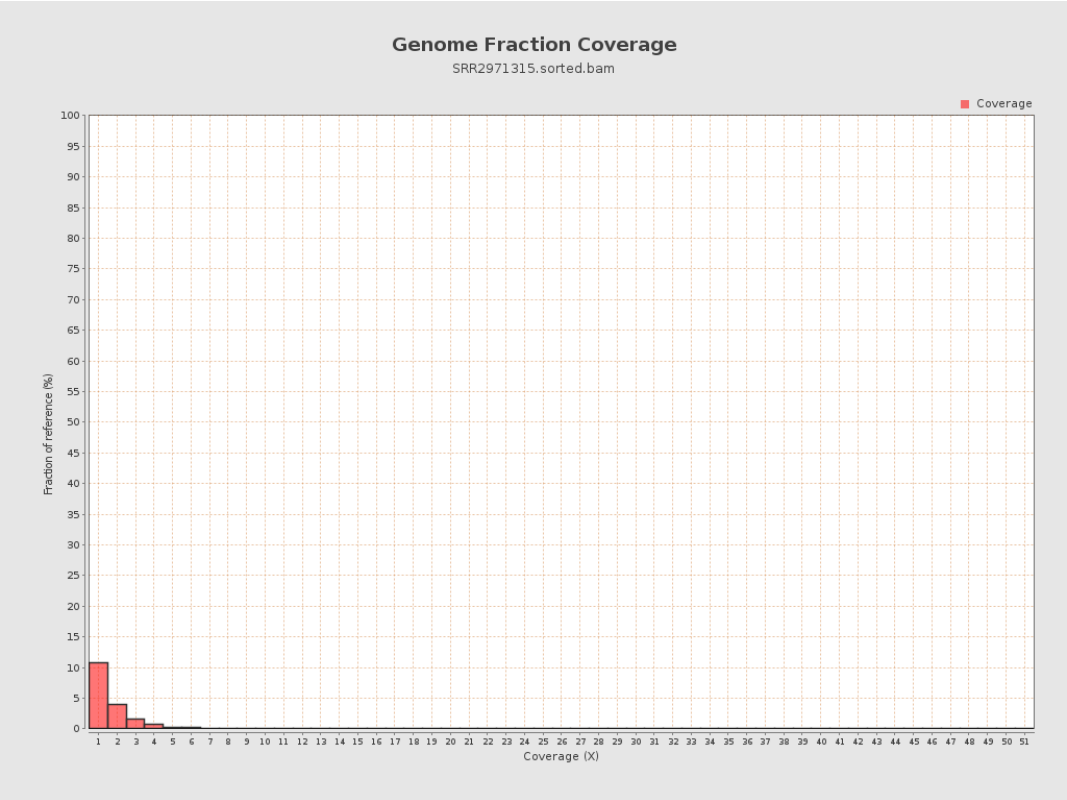
4. Results : Coverage Histogram



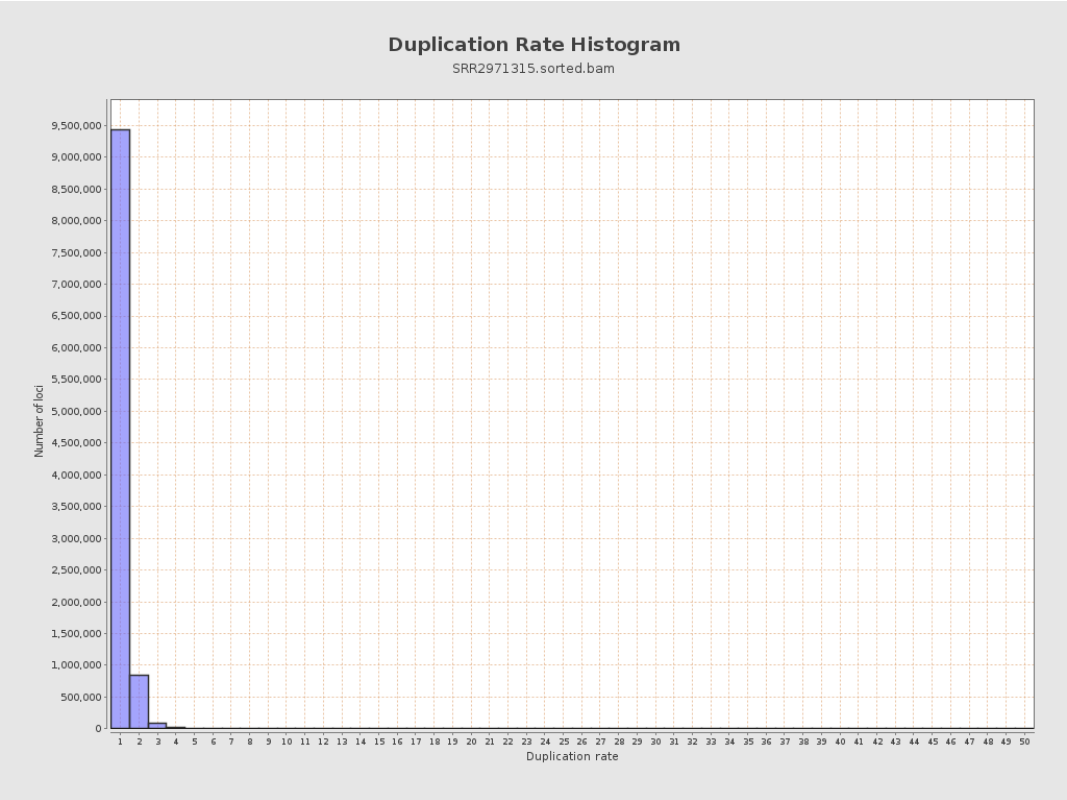
5. Results : Coverage Histogram (0-50X)



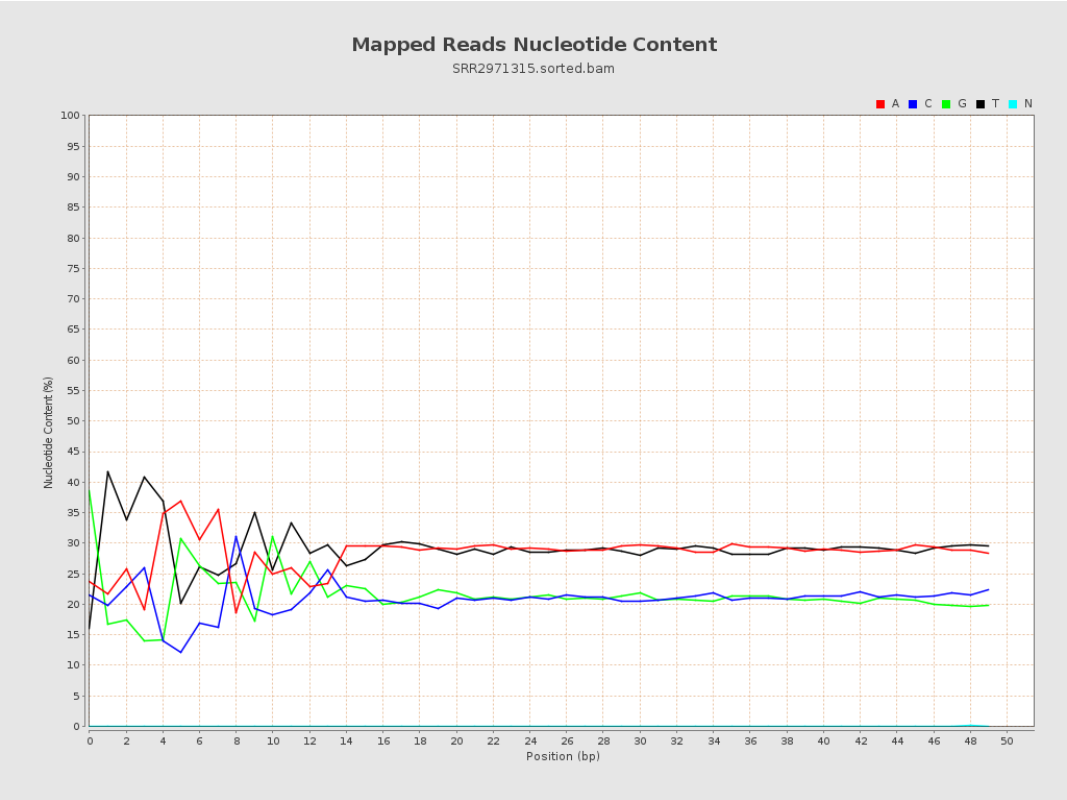
6. Results : Genome Fraction Coverage



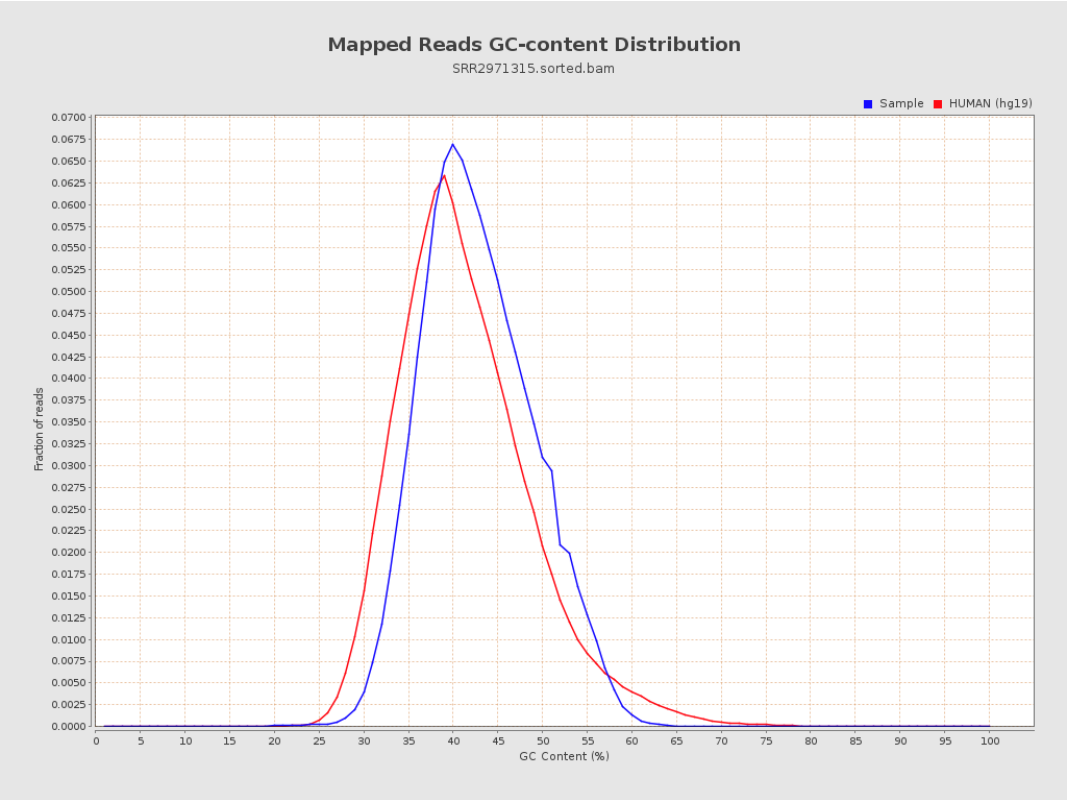
7. Results : Duplication Rate Histogram



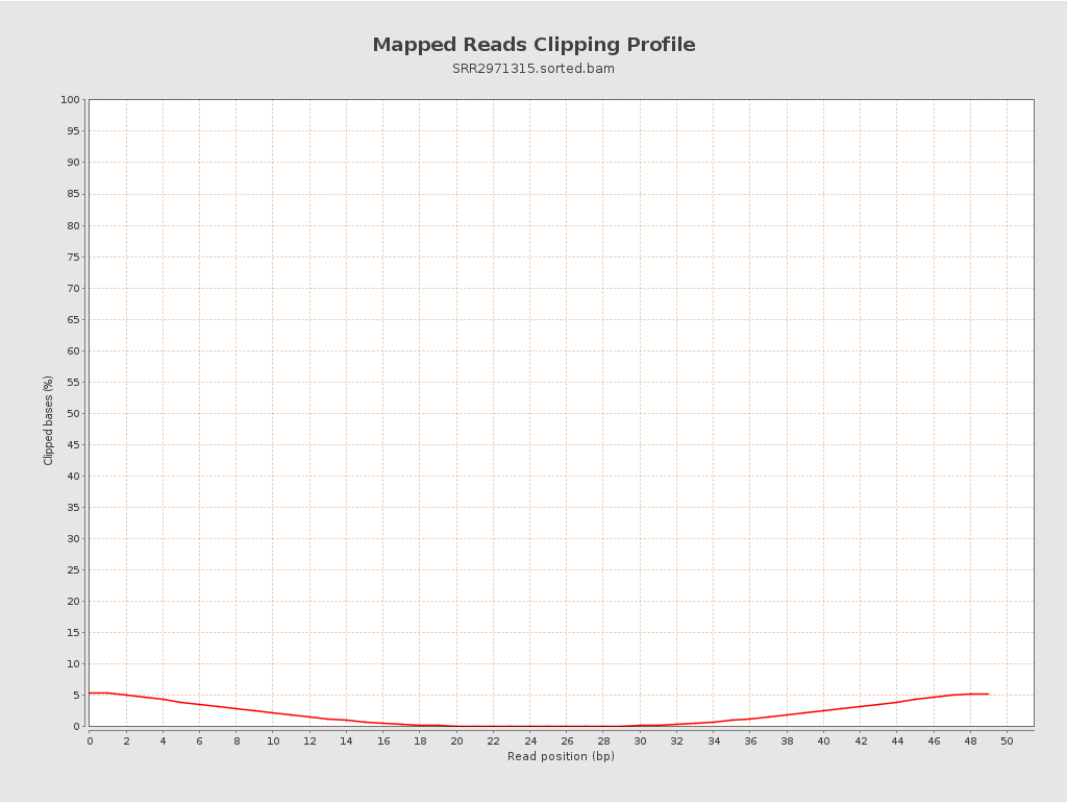
8. Results : Mapped Reads Nucleotide Content



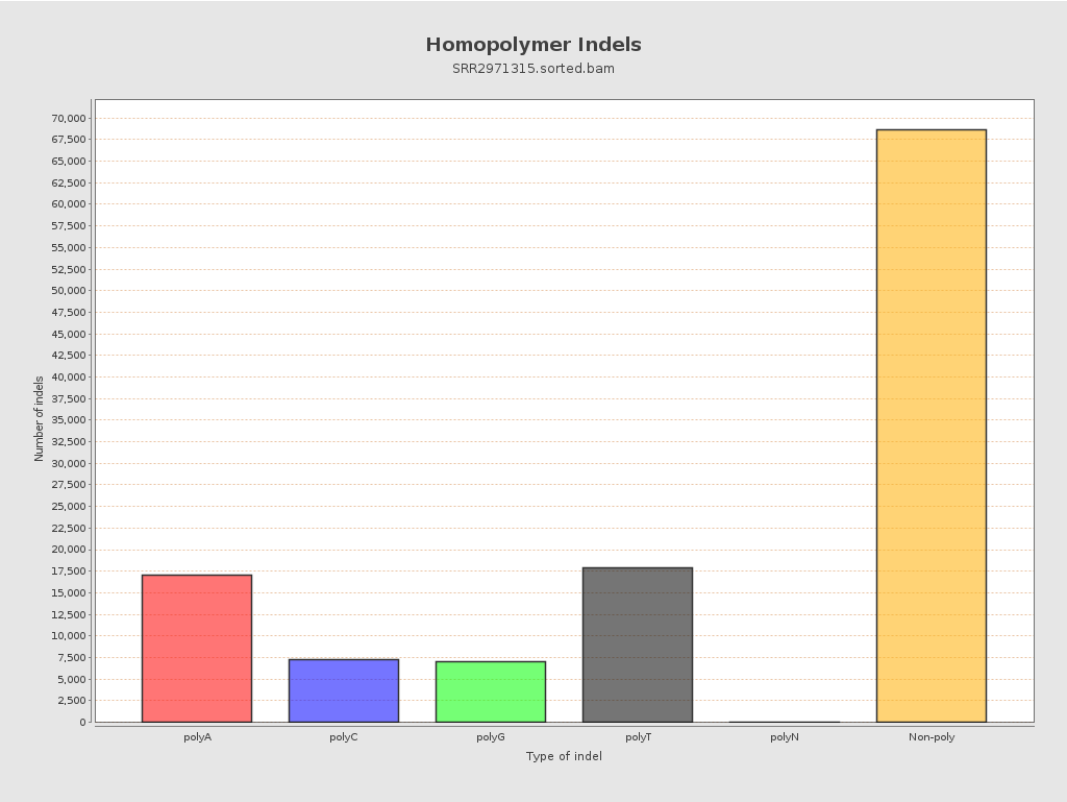
9. Results : Mapped Reads GC-content Distribution



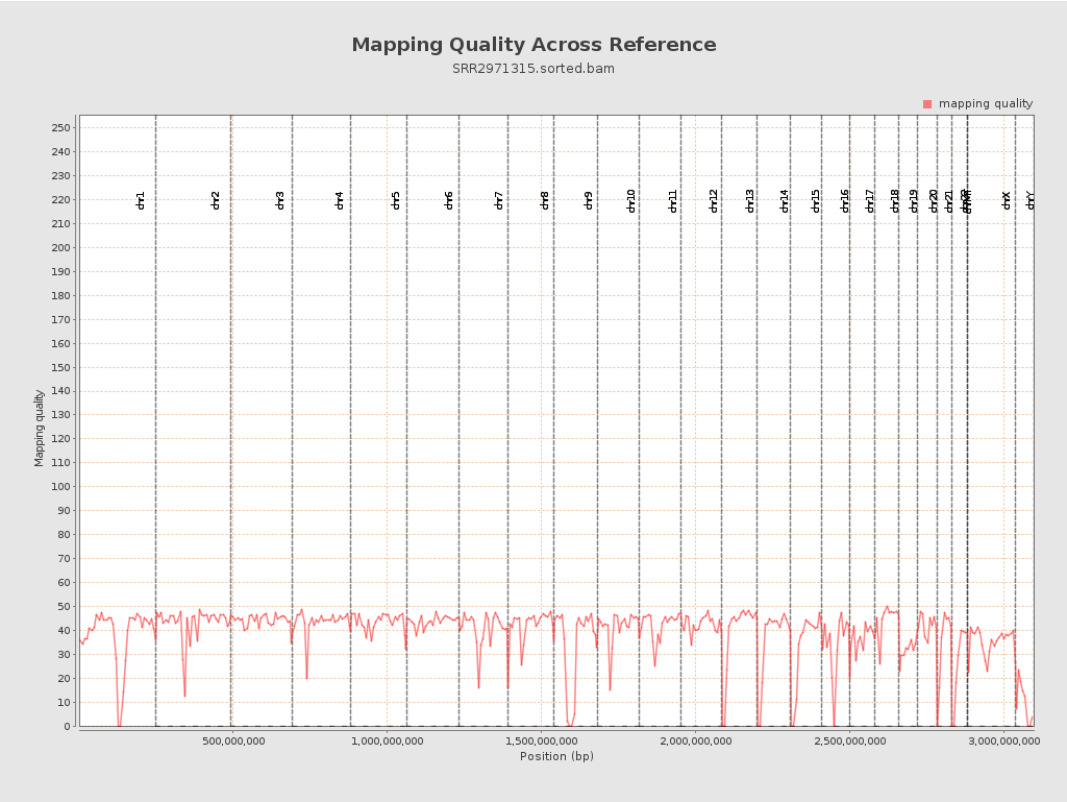
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram