Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 18:00:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081043.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_SRR3081043 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081043.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 18:00:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081043.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,544,416
Mapped reads	1,199,112 / 77.64%
Unmapped reads	345,304 / 22.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,521 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	23,407 / 1.52%
Duplication rate	1.52%
Clipped reads	484,380 / 31.36%

2.2. ACGT Content

Number/percentage of A's	24,230,877 / 30.03%
Number/percentage of C's	15,147,483 / 18.77%
Number/percentage of T's	23,818,491 / 29.51%
Number/percentage of G's	17,503,264 / 21.69%
Number/percentage of N's	1,035 / 0%
GC Percentage	40.46%

2.3. Coverage

Mean	0.0261

Standard Deviation	0.2222

2.4. Mapping Quality

Mean Mapping Quality	47.41

2.5. Mismatches and indels

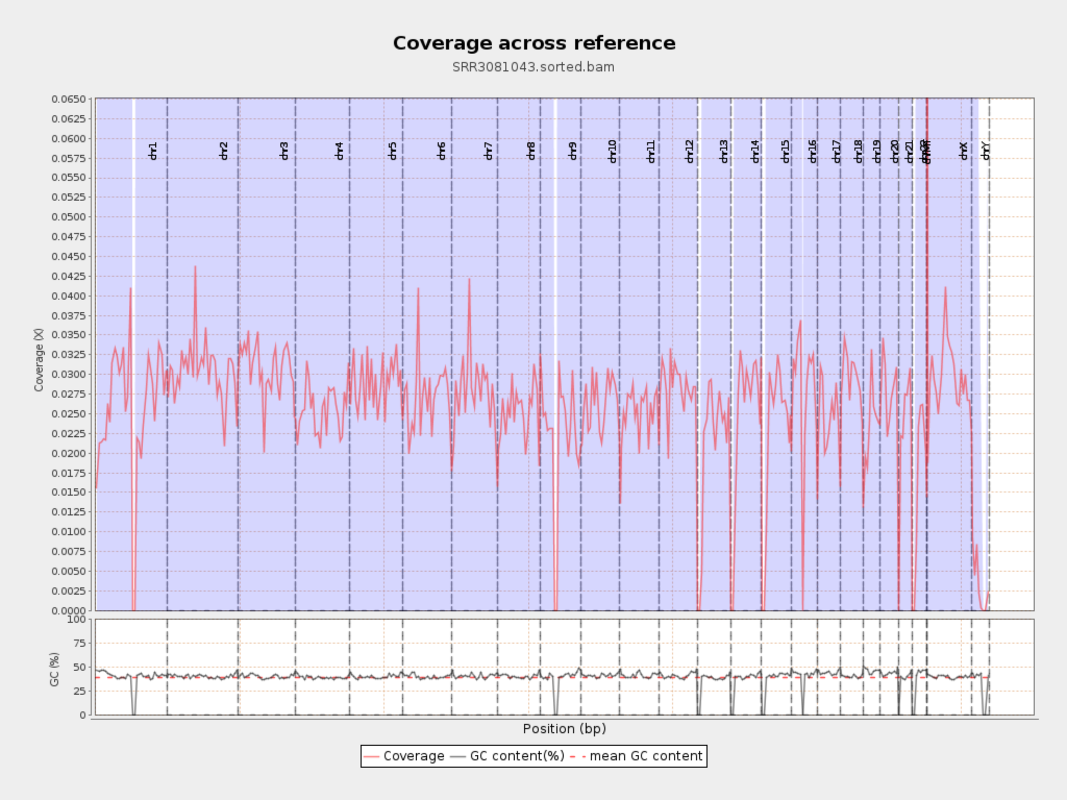
General error rate	0.83%
Mismatches	659,365
Insertions	5,279
Mapped reads with at least one insertion	0.44%
Deletions	17,167
Mapped reads with at least one deletion	1.42%
Homopolymer indels	48.13%

2.6. Chromosome stats

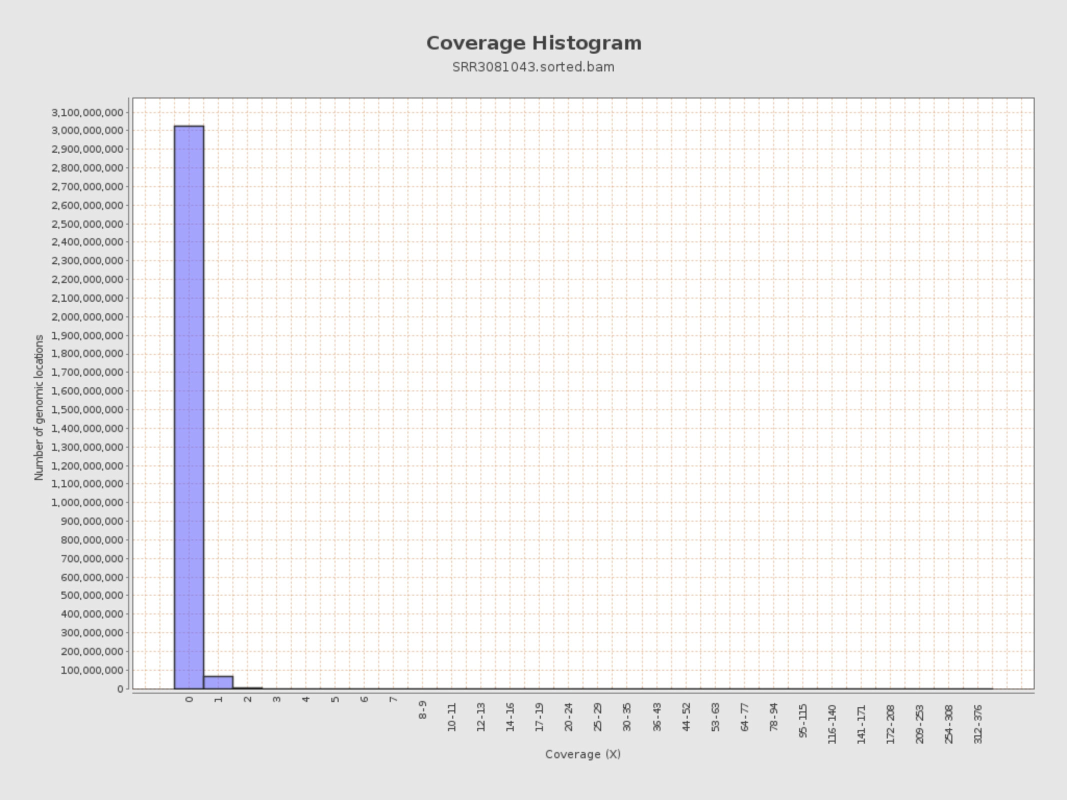
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6400378	0.0257	0.3367
chr2	243199373	7417210	0.0305	0.2402
chr3	198022430	6120001	0.0309	0.19
chr4	191154276	4894072	0.0256	0.1761
chr5	180915260	5264727	0.0291	0.1844
chr6	171115067	4655471	0.0272	0.2173
chr7	159138663	4447522	0.0279	0.3033

chr8	146364022	3670750	0.0251	0.2264
chr9	141213431	3126275	0.0221	0.2017
chr10	135534747	3557939	0.0263	0.2031
chr11	135006516	3395532	0.0252	0.2
chr12	133851895	3789634	0.0283	0.1831
chr13	115169878	2390420	0.0208	0.1549
chr14	107349540	2602383	0.0242	0.1741
chr15	102531392	2288239	0.0223	0.1648
chr16	90354753	2461444	0.0272	0.1902
chr17	81195210	1993674	0.0246	0.1805
chr18	78077248	2332281	0.0299	0.3689
chr19	59128983	1398188	0.0236	0.2464
chr20	63025520	1756808	0.0279	0.1829
chr21	48129895	1118052	0.0232	0.1718
chr22	51304566	836179	0.0163	0.1369
chrMT	16571	5595	0.3376	0.6441
chrX	155270560	4622854	0.0298	0.1986
chrY	59373566	185551	0.0031	0.0703

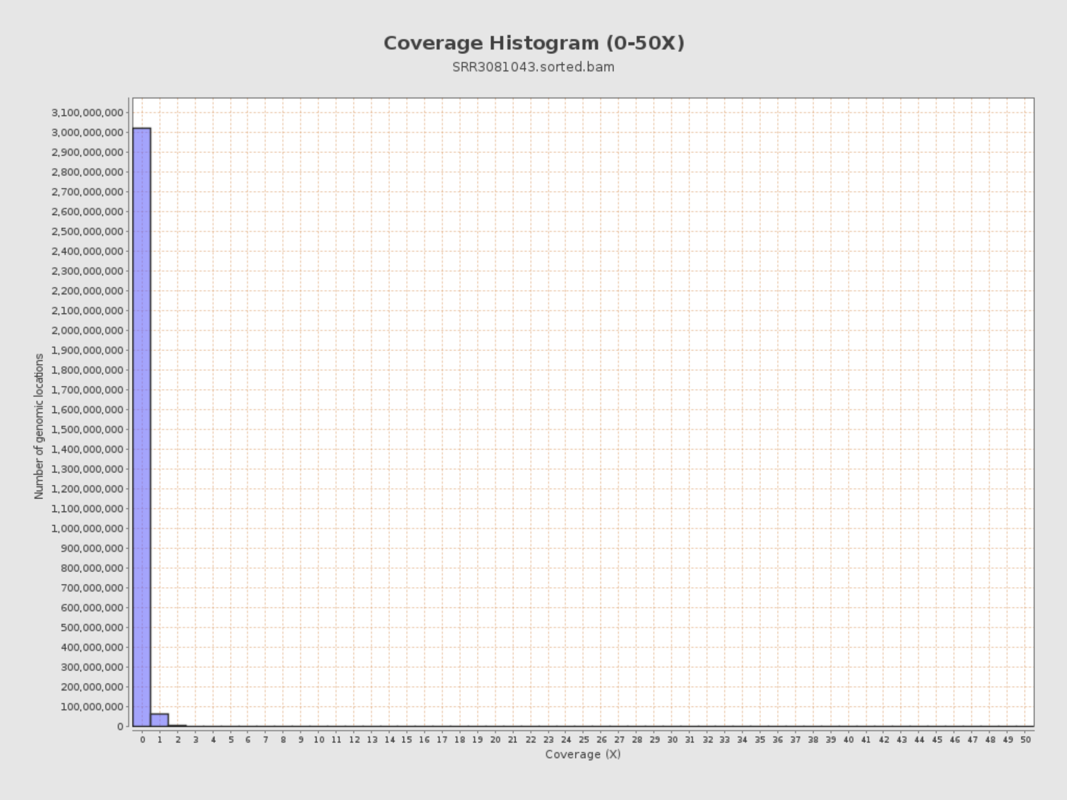
3. Results : Coverage across reference



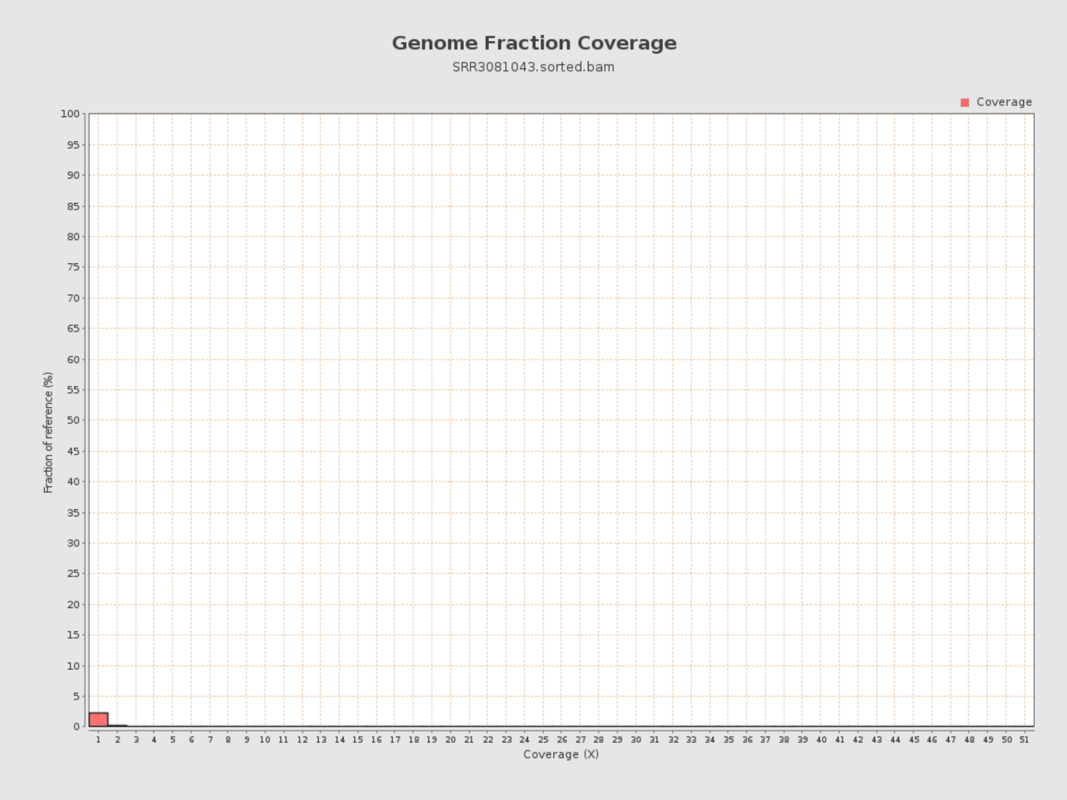
4. Results : Coverage Histogram



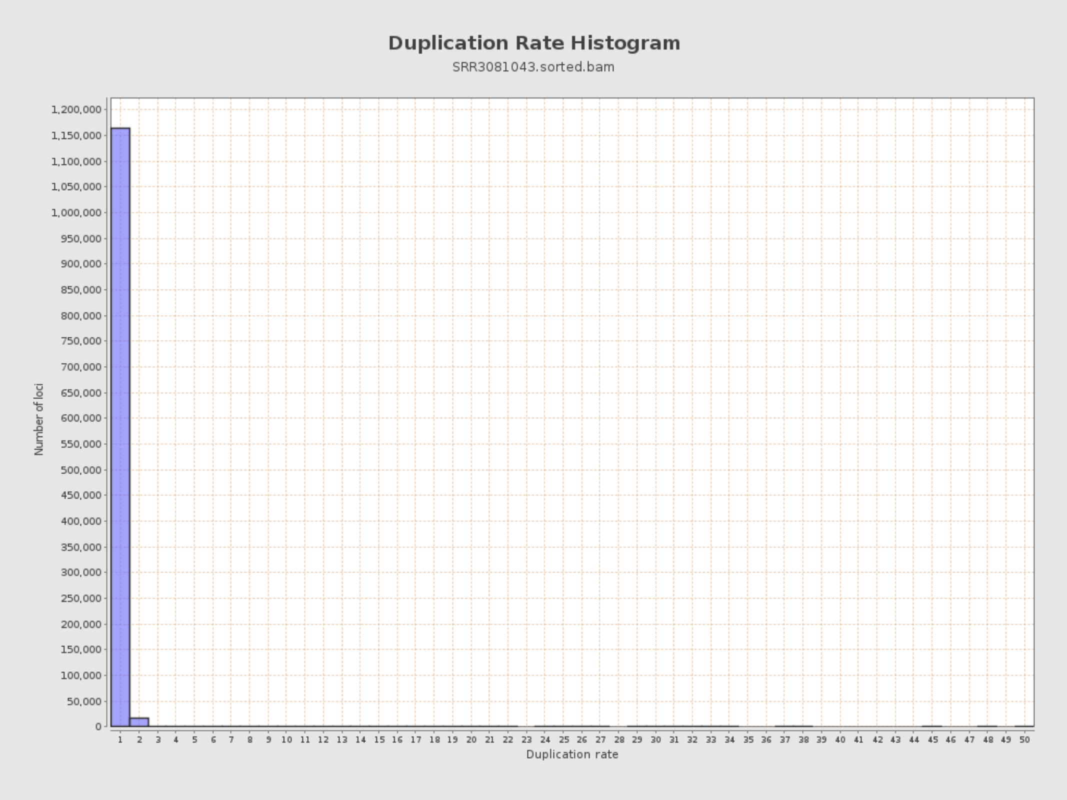
5. Results : Coverage Histogram (0-50X)



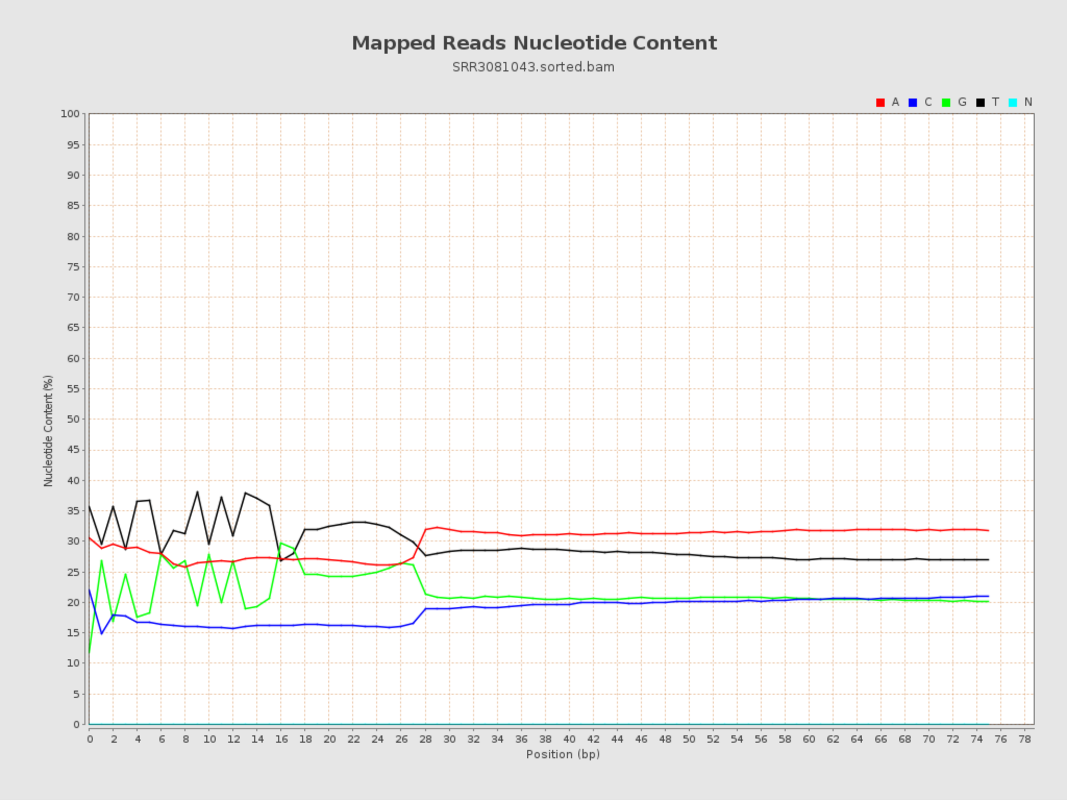
6. Results : Genome Fraction Coverage



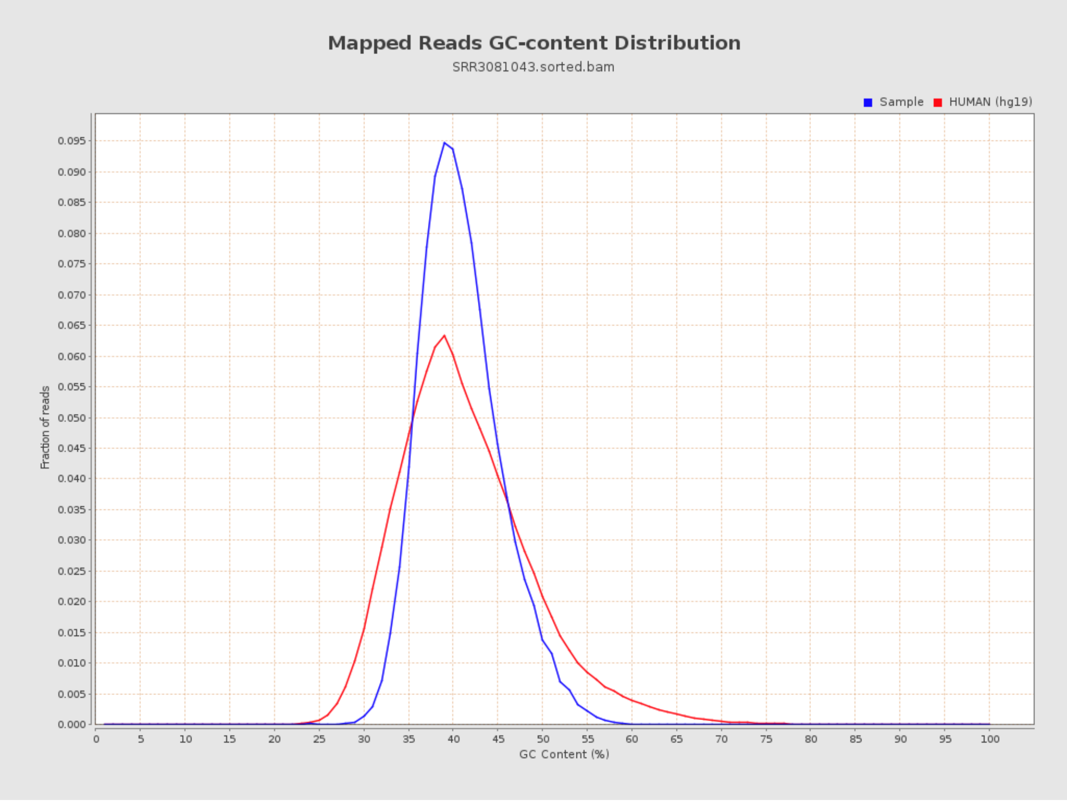
7. Results : Duplication Rate Histogram



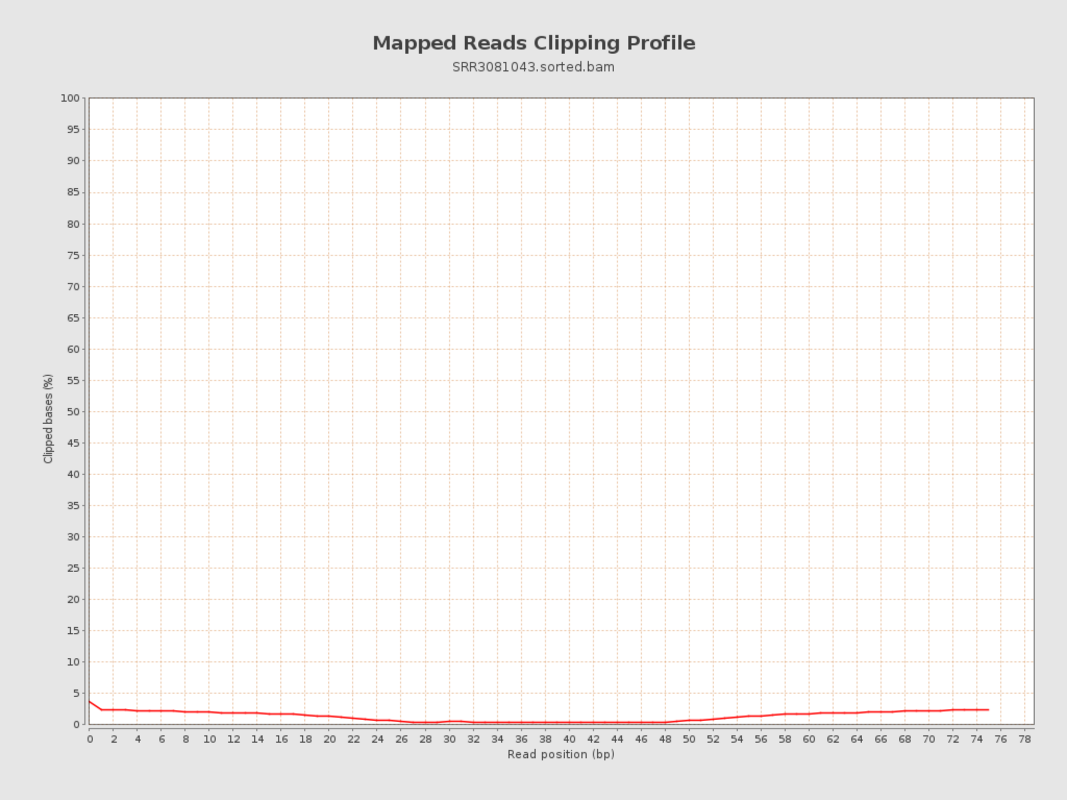
8. Results : Mapped Reads Nucleotide Content



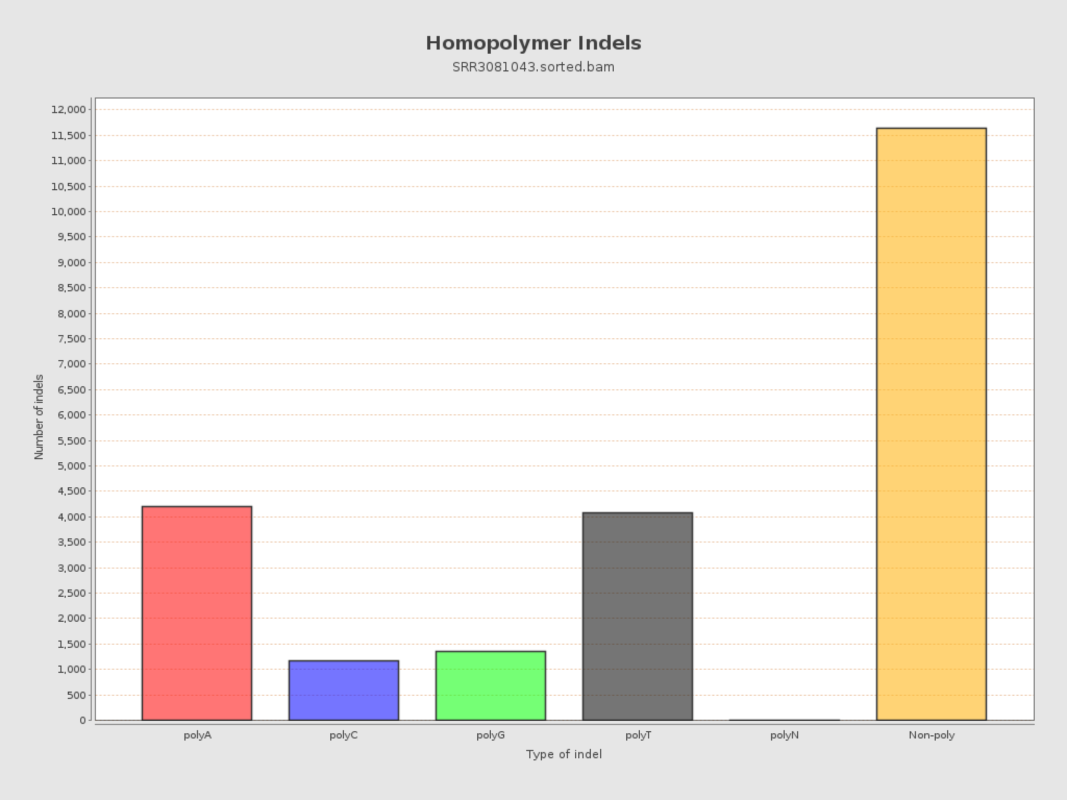
9. Results : Mapped Reads GC-content Distribution



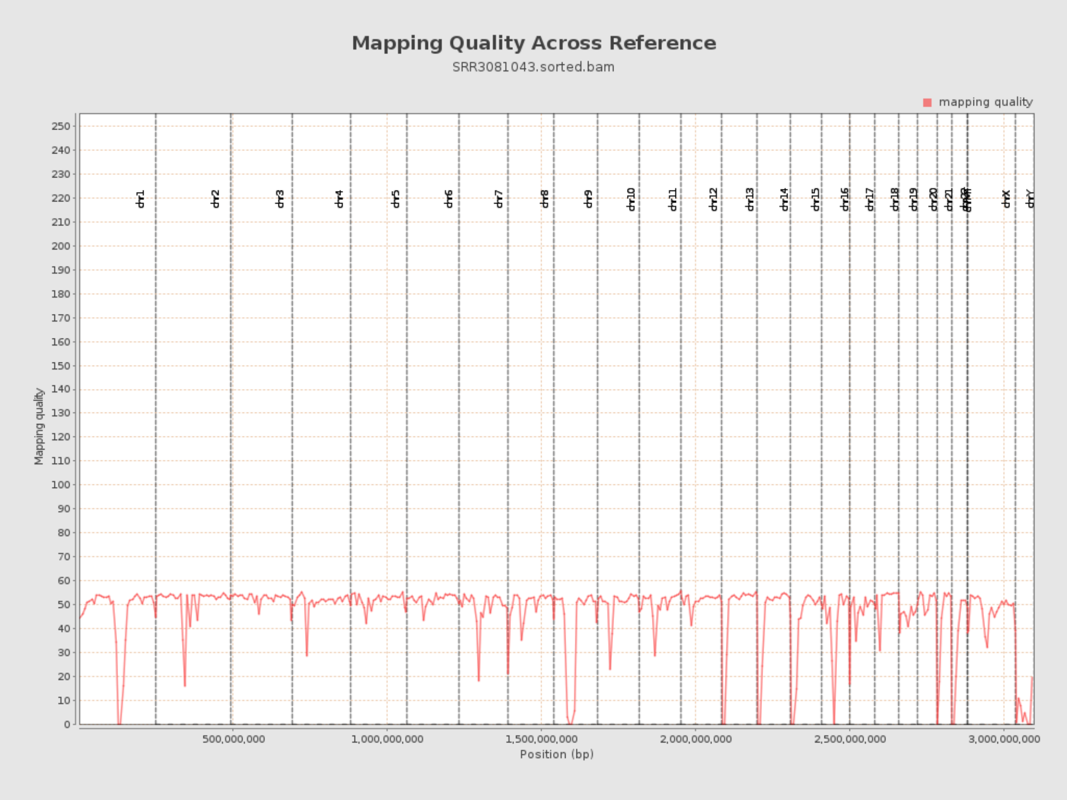
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram