Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 12:07:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081958.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_SRR3081958 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081958.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 12:07:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081958.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,086,366
Mapped reads	2,874,016 / 93.12%
Unmapped reads	212,350 / 6.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,106 / 0.46%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	128,451 / 4.16%
Duplication rate	3.63%
Clipped reads	890,162 / 28.84%

2.2. ACGT Content

Number/percentage of A's	58,031,930 / 29.04%
Number/percentage of C's	37,055,434 / 18.54%
Number/percentage of T's	63,469,322 / 31.76%
Number/percentage of G's	41,271,856 / 20.65%
Number/percentage of N's	26,455 / 0.01%
GC Percentage	39.19%

2.3. Coverage

Mean	0.0646

Standard Deviation	0.4796

2.4. Mapping Quality

Mean Mapping Quality	47.47

2.5. Mismatches and indels

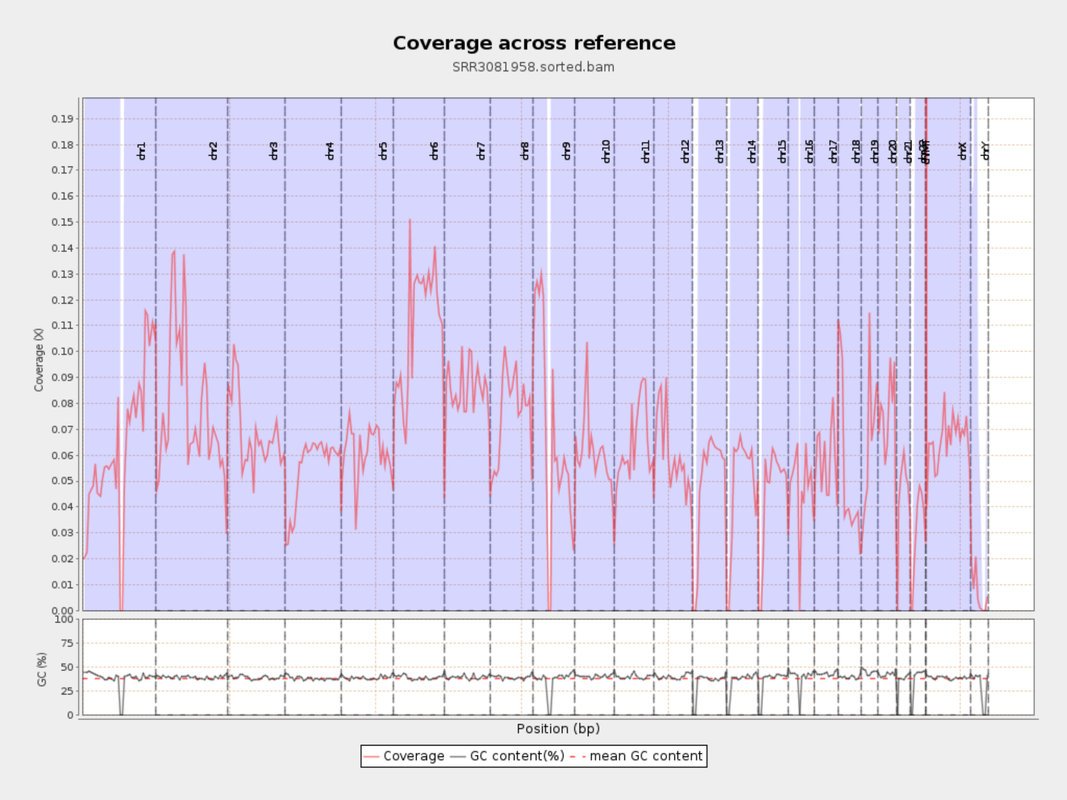
General error rate	0.75%
Mismatches	1,476,862
Insertions	14,443
Mapped reads with at least one insertion	0.5%
Deletions	44,662
Mapped reads with at least one deletion	1.54%
Homopolymer indels	48.64%

2.6. Chromosome stats

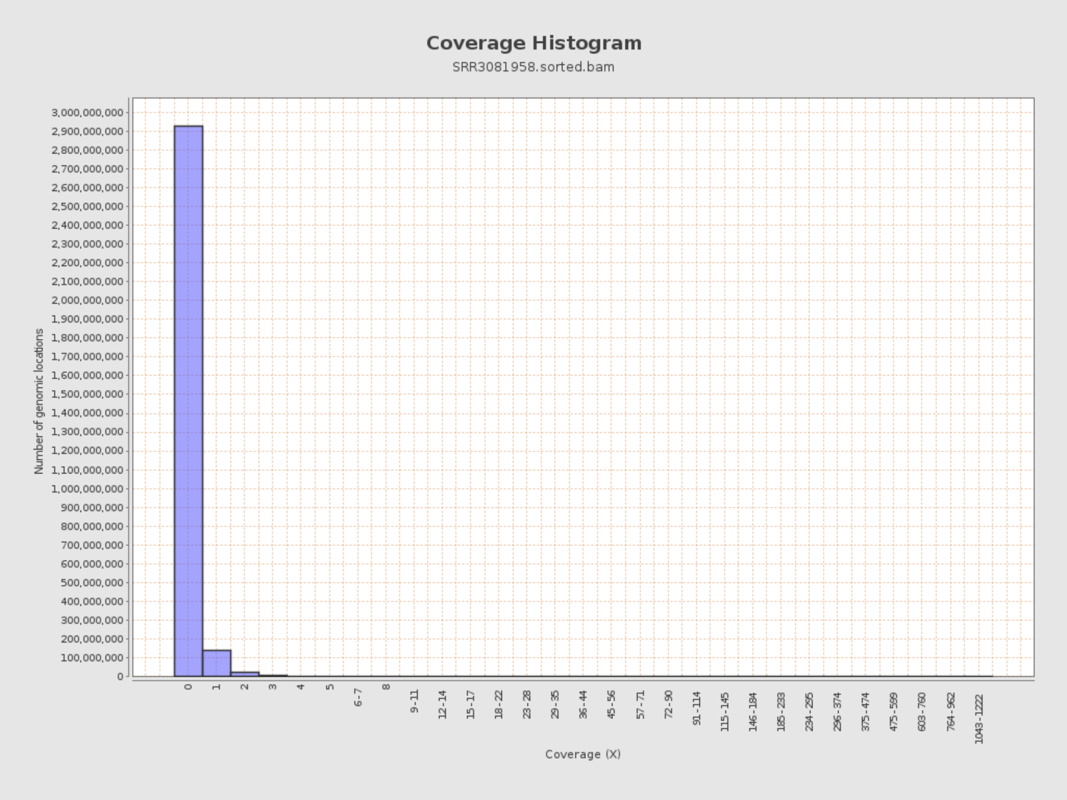
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15797116	0.0634	0.8122
chr2	243199373	18971801	0.078	0.566
chr3	198022430	13596613	0.0687	0.301
chr4	191154276	10519619	0.055	0.2892
chr5	180915260	11000957	0.0608	0.2872
chr6	171115067	18959913	0.1108	0.5159
chr7	159138663	13509107	0.0849	0.5531

chr8	146364022	11199821	0.0765	0.8299
chr9	141213431	9712754	0.0688	0.4663
chr10	135534747	8302541	0.0613	0.4399
chr11	135006516	8689763	0.0644	0.3671
chr12	133851895	8035041	0.06	0.2892
chr13	115169878	5696138	0.0495	0.2565
chr14	107349540	5249078	0.0489	0.2744
chr15	102531392	4590290	0.0448	0.2434
chr16	90354753	4133633	0.0457	0.2874
chr17	81195210	4785165	0.0589	0.3104
chr18	78077248	4069441	0.0521	0.745
chr19	59128983	3819505	0.0646	0.5849
chr20	63025520	4779465	0.0758	0.3223
chr21	48129895	2151796	0.0447	0.2673
chr22	51304566	1548069	0.0302	0.1973
chrMT	16571	318953	19.2477	11.4533
chrX	155270560	10102117	0.0651	0.3253
chrY	59373566	395670	0.0067	0.1524

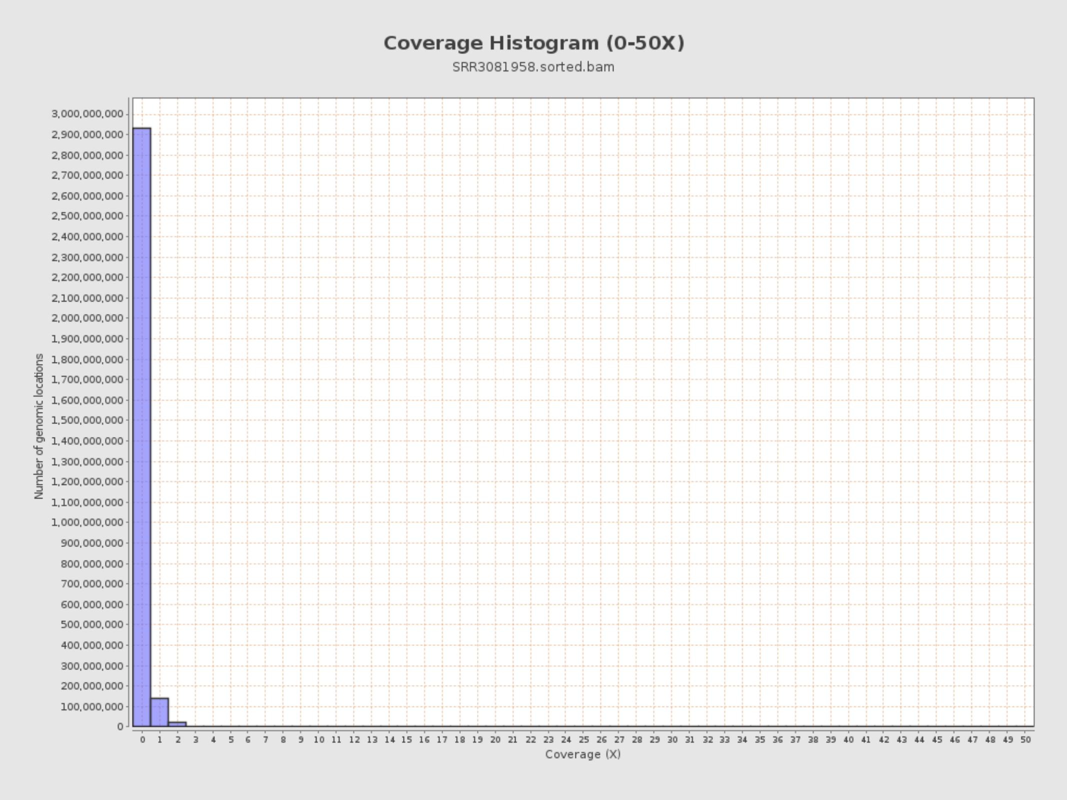
3. Results : Coverage across reference



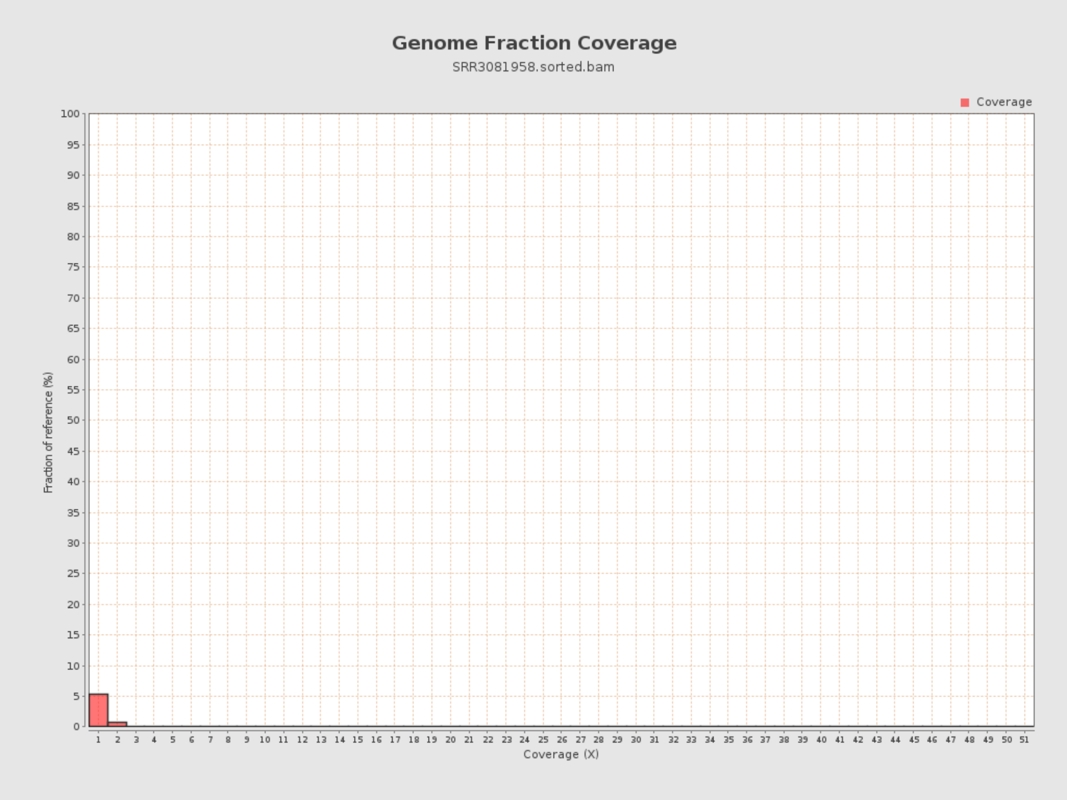
4. Results : Coverage Histogram



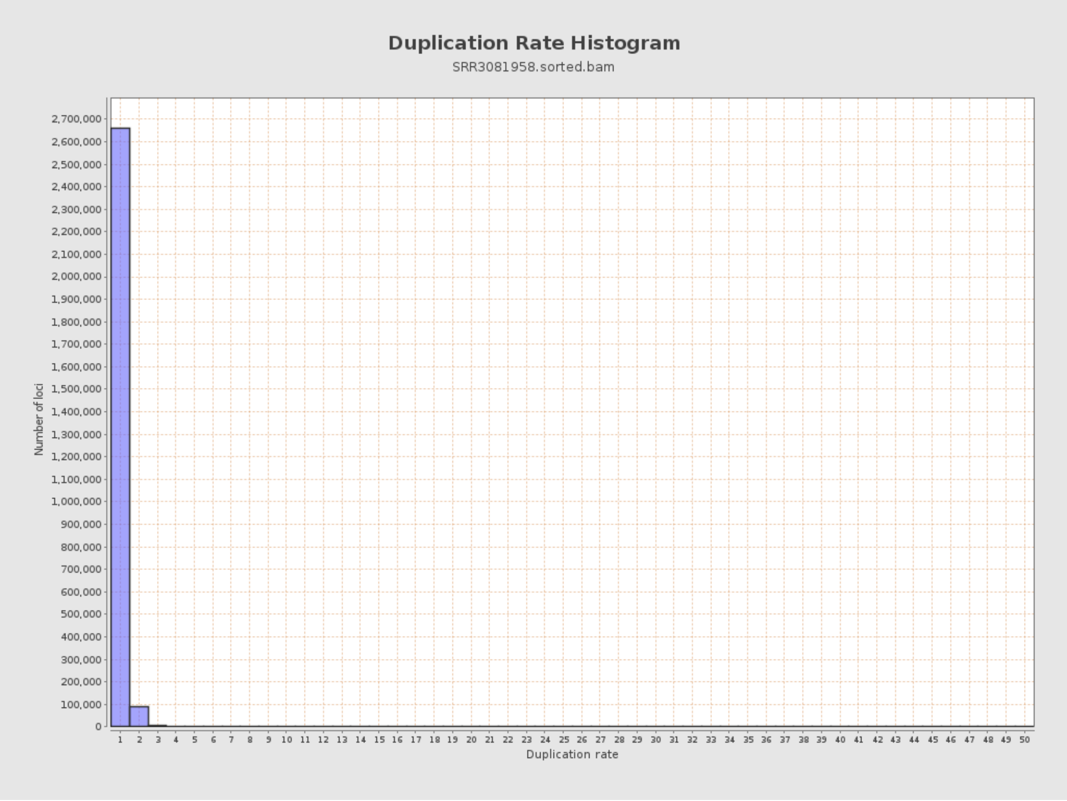
5. Results : Coverage Histogram (0-50X)



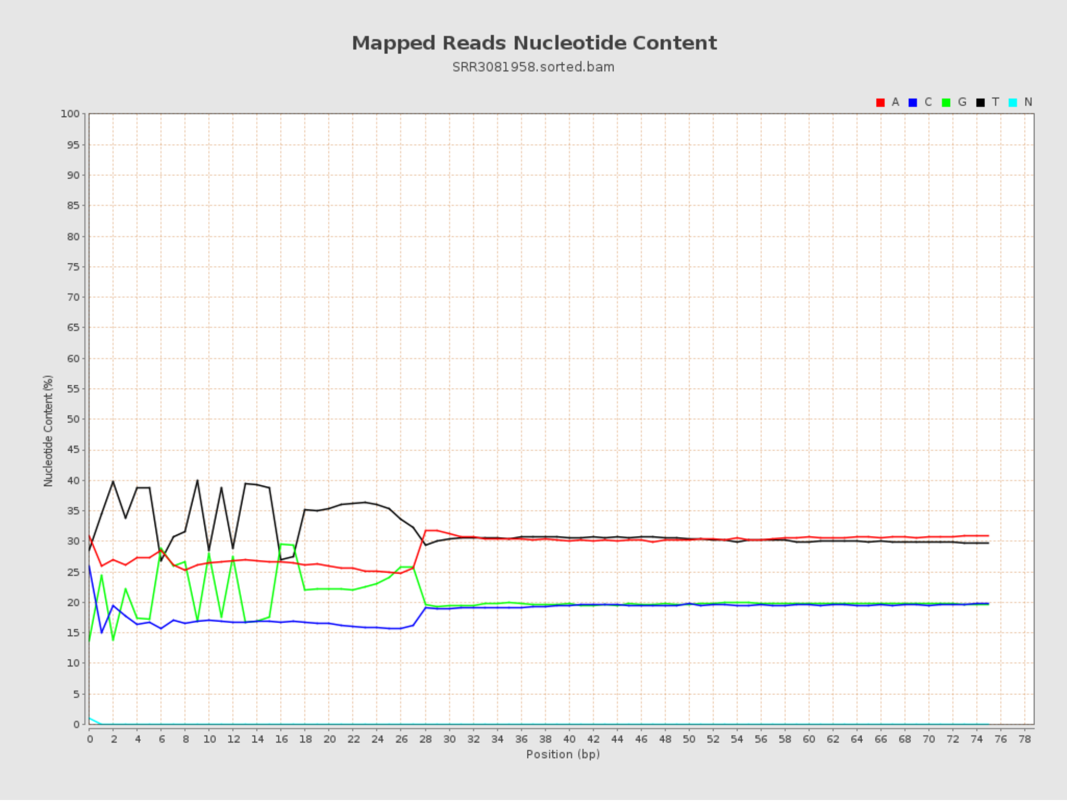
6. Results : Genome Fraction Coverage



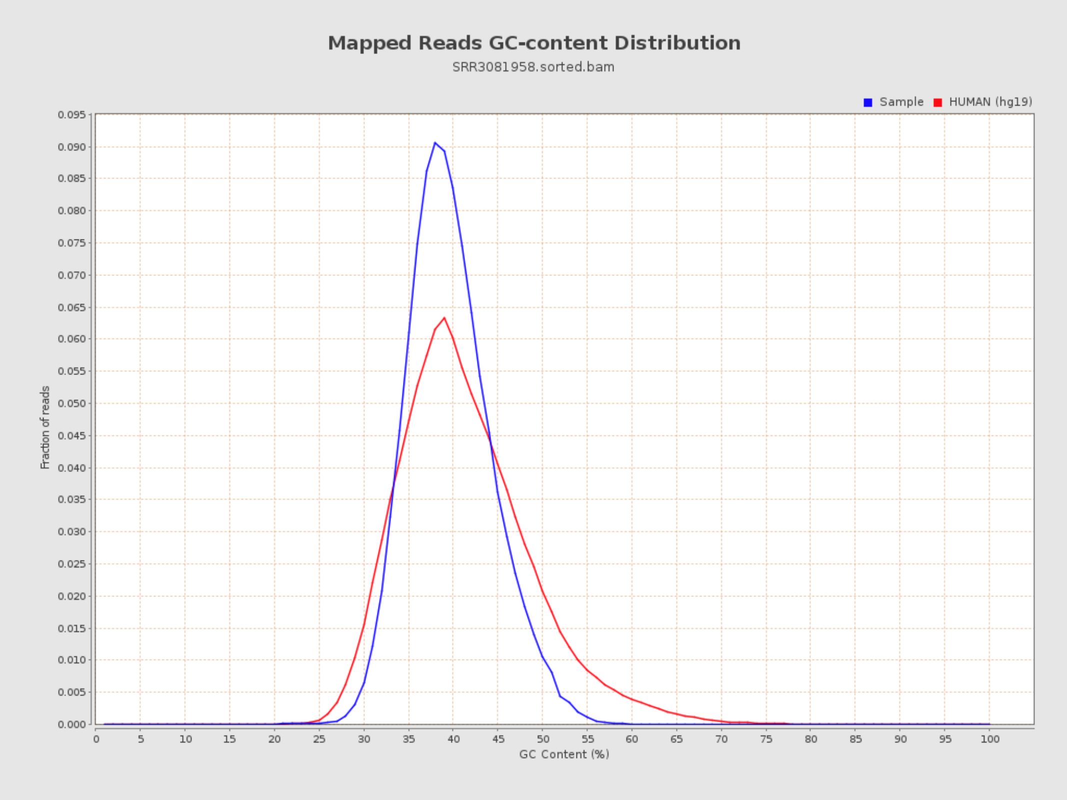
7. Results : Duplication Rate Histogram



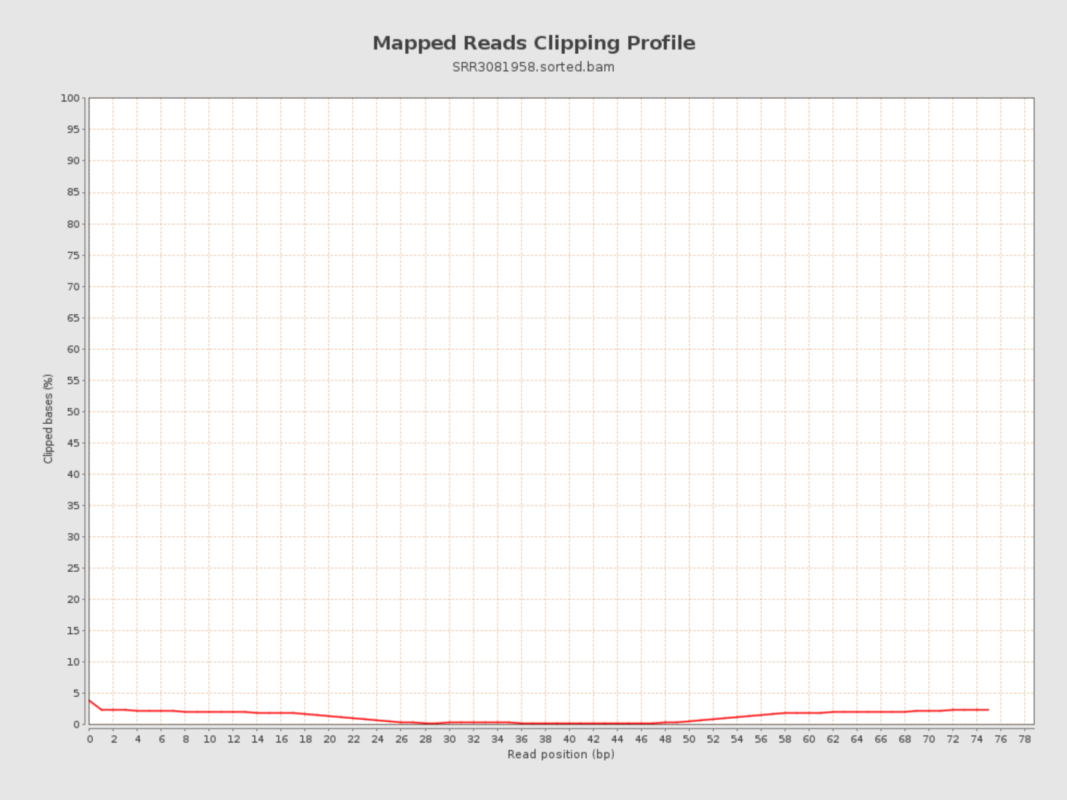
8. Results : Mapped Reads Nucleotide Content



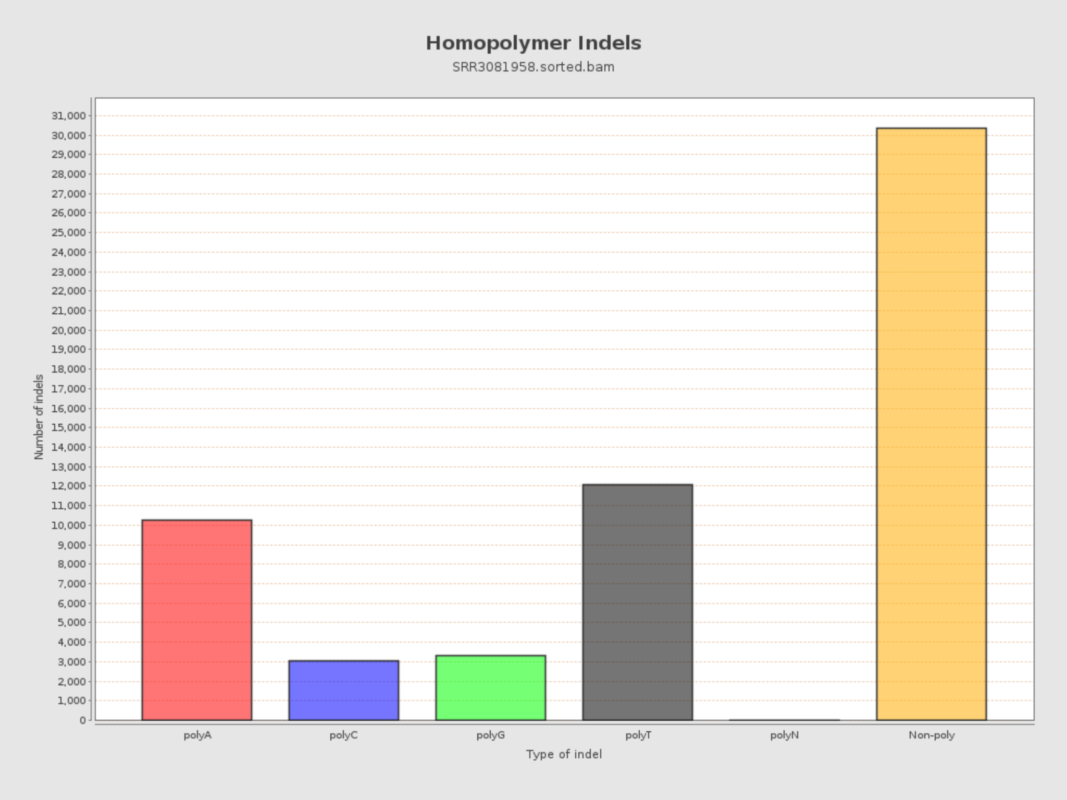
9. Results : Mapped Reads GC-content Distribution



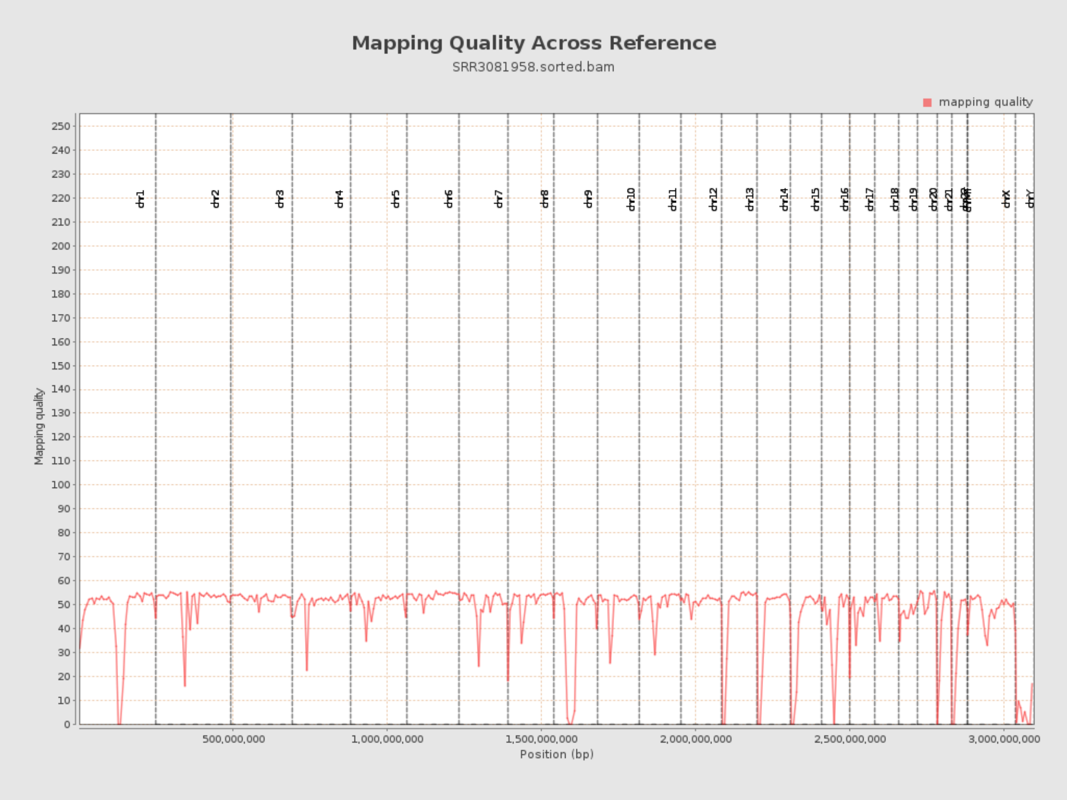
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram