Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 03:14:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081219.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_SRR3081219 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081219.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 03:14:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081219.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,552,641
Mapped reads	2,254,417 / 88.32%
Unmapped reads	298,224 / 11.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,404 / 1.07%
Read min/max/mean length	30 / 76 / 76.37
Duplicated reads (estimated)	108,256 / 4.24%
Duplication rate	4.03%
Clipped reads	1,201,441 / 47.07%

2.2. ACGT Content

Number/percentage of A's	41,898,440 / 28.54%
Number/percentage of C's	28,492,939 / 19.41%
Number/percentage of T's	44,852,660 / 30.55%
Number/percentage of G's	31,530,189 / 21.48%
Number/percentage of N's	19,272 / 0.01%
GC Percentage	40.89%

2.3. Coverage

Mean	0.0474

Standard Deviation	0.3388

2.4. Mapping Quality

Mean Mapping Quality	45.33

2.5. Mismatches and indels

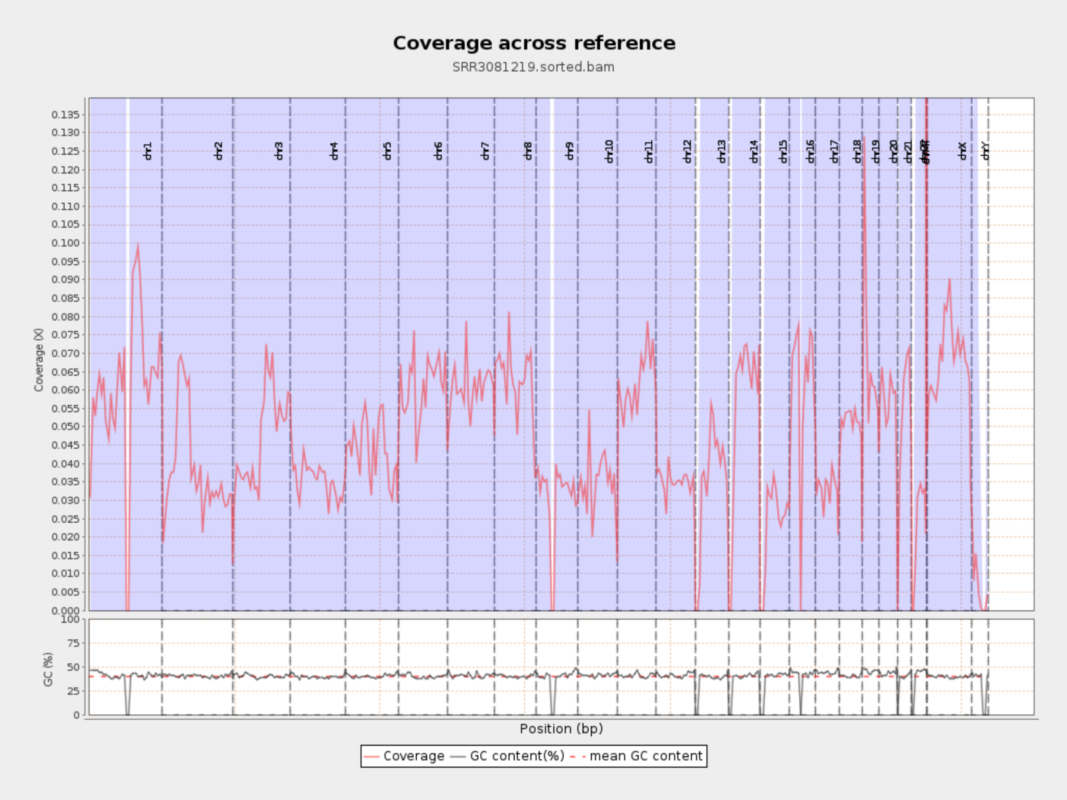
General error rate	0.91%
Mismatches	1,313,956
Insertions	10,947
Mapped reads with at least one insertion	0.48%
Deletions	33,471
Mapped reads with at least one deletion	1.47%
Homopolymer indels	47.86%

2.6. Chromosome stats

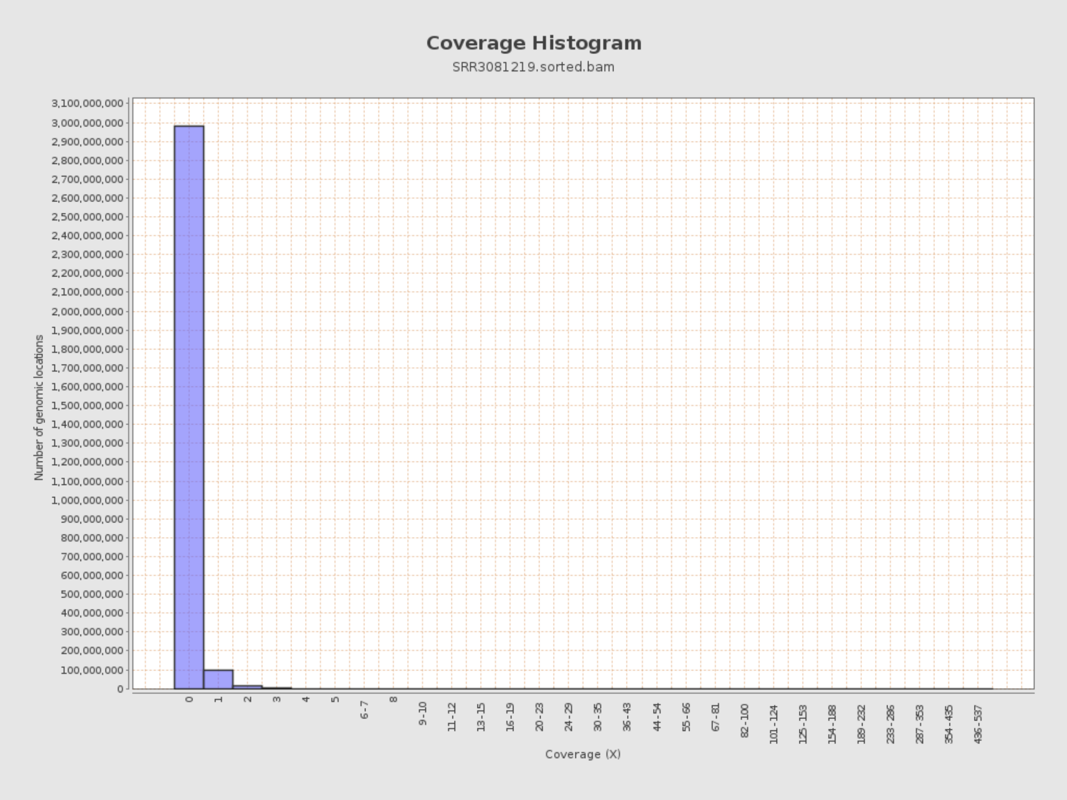
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15137617	0.0607	0.5335
chr2	243199373	9390958	0.0386	0.3597
chr3	198022430	9276665	0.0468	0.2637
chr4	191154276	6794264	0.0355	0.2321
chr5	180915260	7938017	0.0439	0.2533
chr6	171115067	10436641	0.061	0.3261
chr7	159138663	9708094	0.061	0.4613

chr8	146364022	9224807	0.063	0.4154
chr9	141213431	4308592	0.0305	0.2647
chr10	135534747	4759077	0.0351	0.3132
chr11	135006516	8282121	0.0613	0.397
chr12	133851895	4700823	0.0351	0.2275
chr13	115169878	4035944	0.035	0.2277
chr14	107349540	5915235	0.0551	0.2951
chr15	102531392	2436964	0.0238	0.1888
chr16	90354753	5530436	0.0612	0.3073
chr17	81195210	2644048	0.0326	0.2332
chr18	78077248	4019514	0.0515	0.4274
chr19	59128983	4040266	0.0683	0.4643
chr20	63025520	3623820	0.0575	0.2959
chr21	48129895	2491530	0.0518	0.2835
chr22	51304566	1147996	0.0224	0.1793
chrMT	16571	38002	2.2933	2.2574
chrX	155270560	10604399	0.0683	0.3316
chrY	59373566	362886	0.0061	0.1096

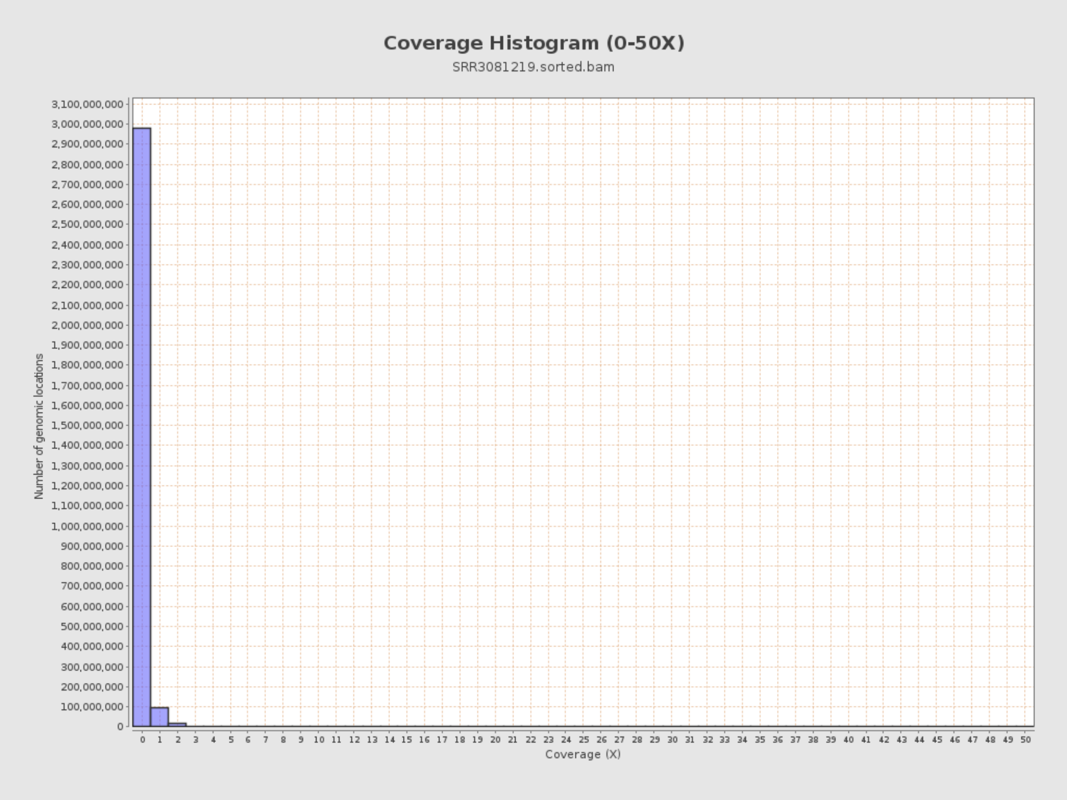
3. Results : Coverage across reference



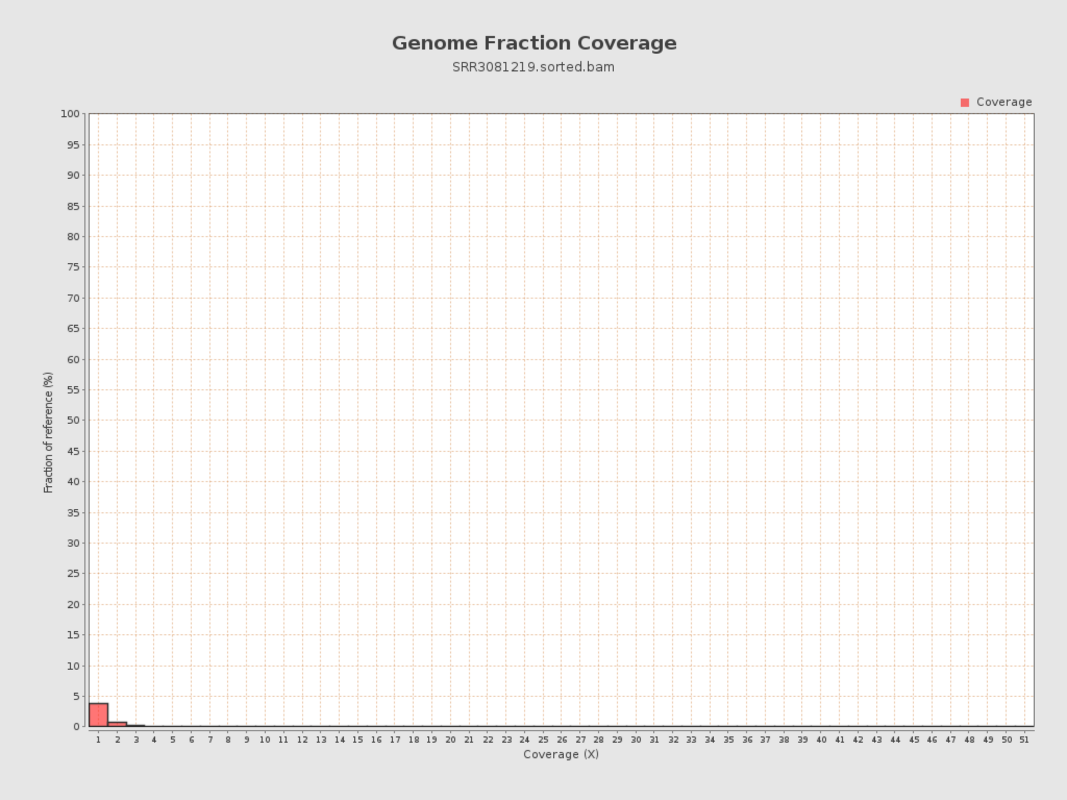
4. Results : Coverage Histogram



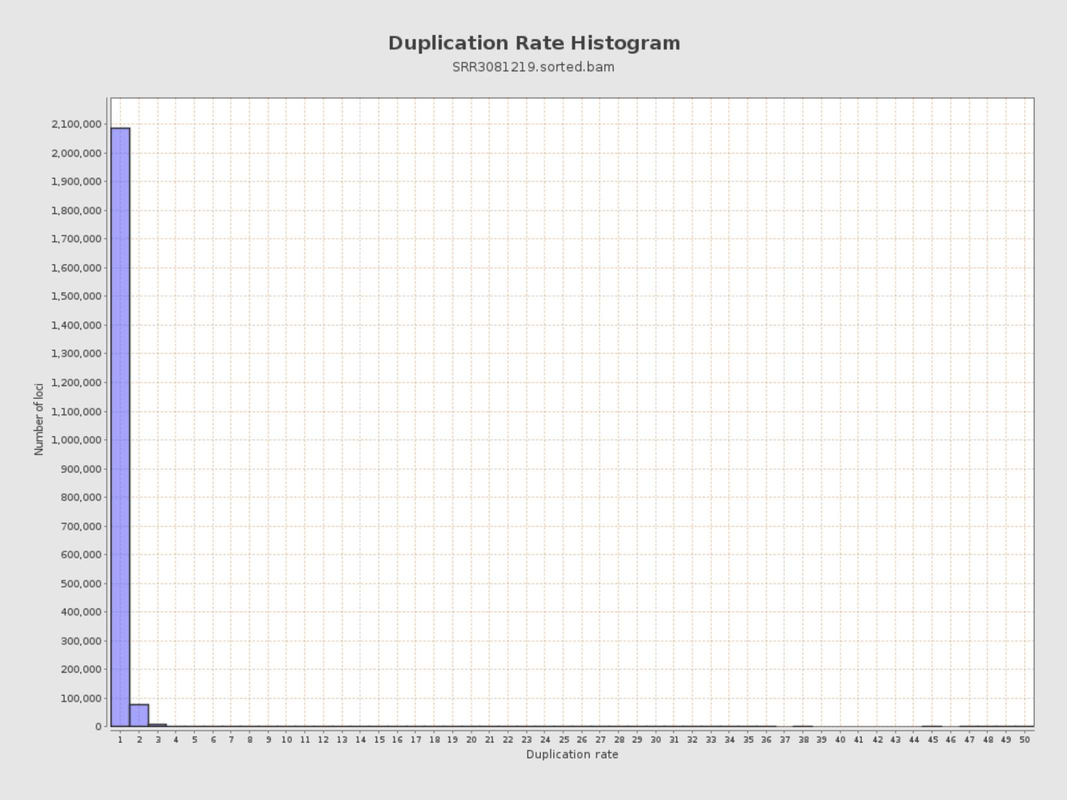
5. Results : Coverage Histogram (0-50X)



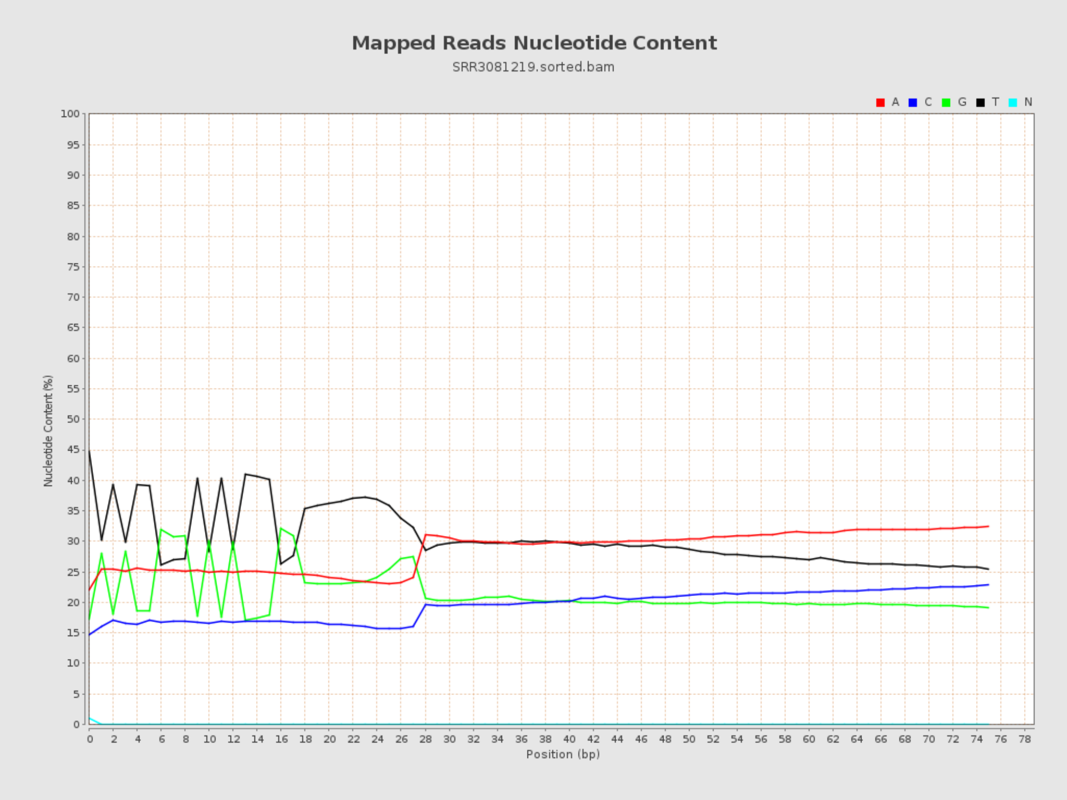
6. Results : Genome Fraction Coverage



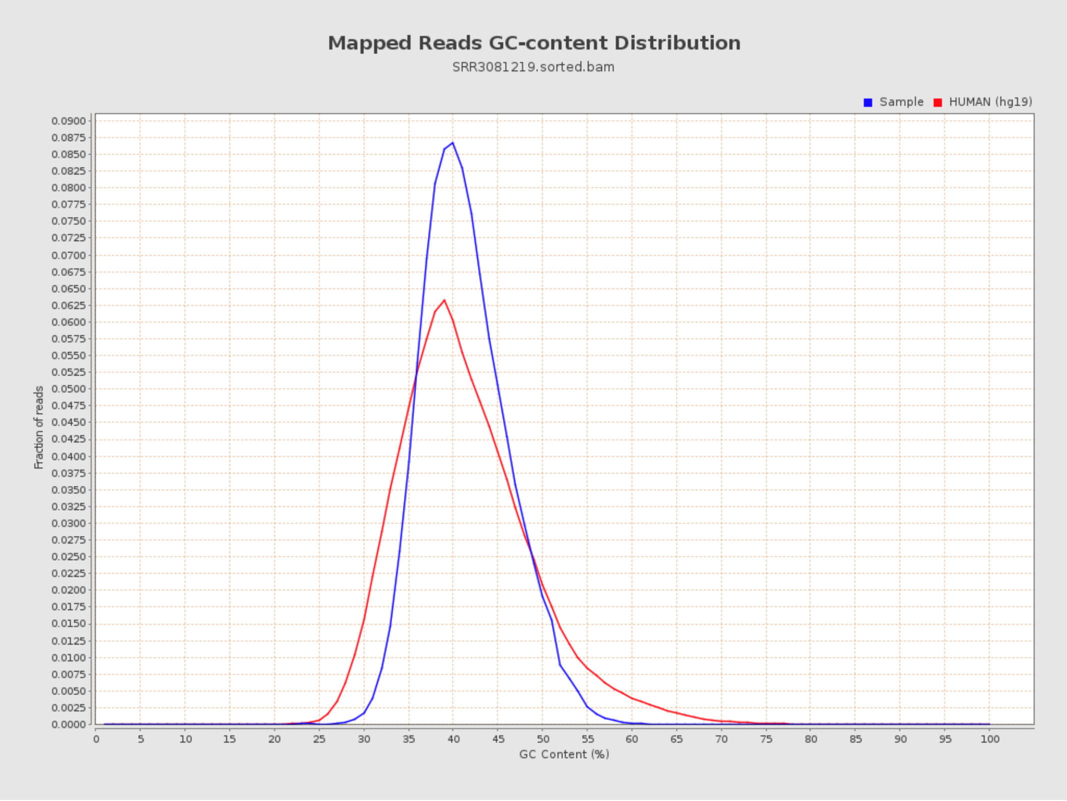
7. Results : Duplication Rate Histogram



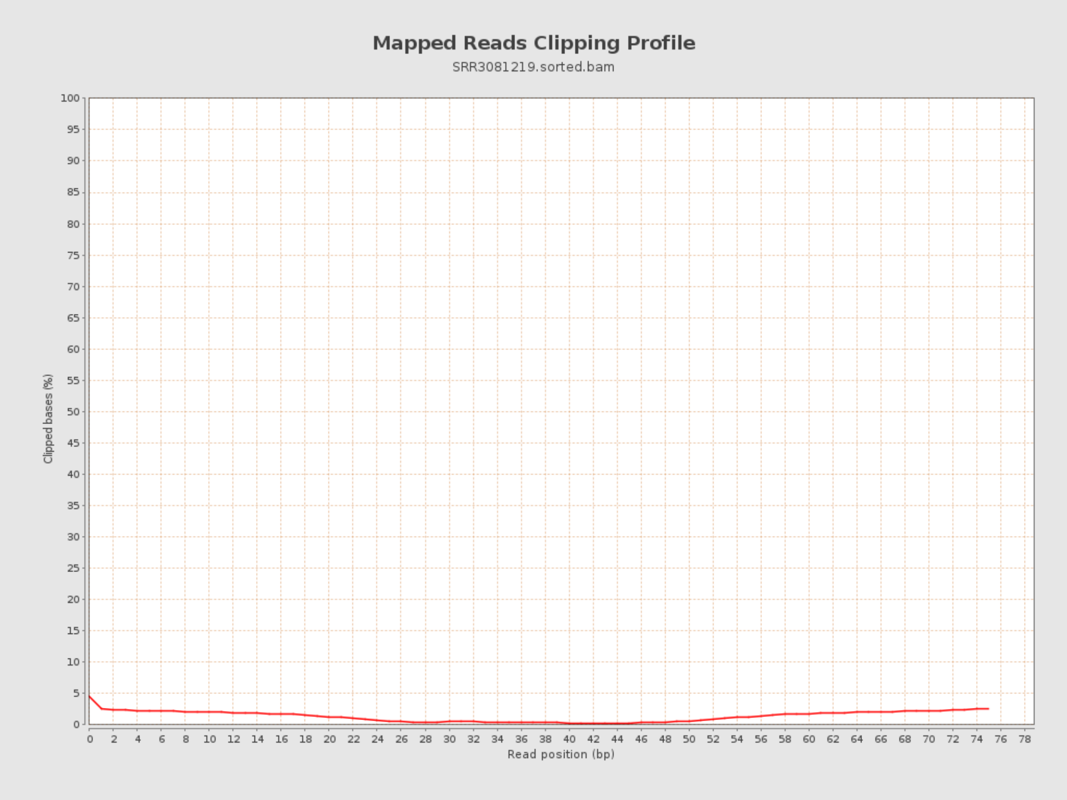
8. Results : Mapped Reads Nucleotide Content



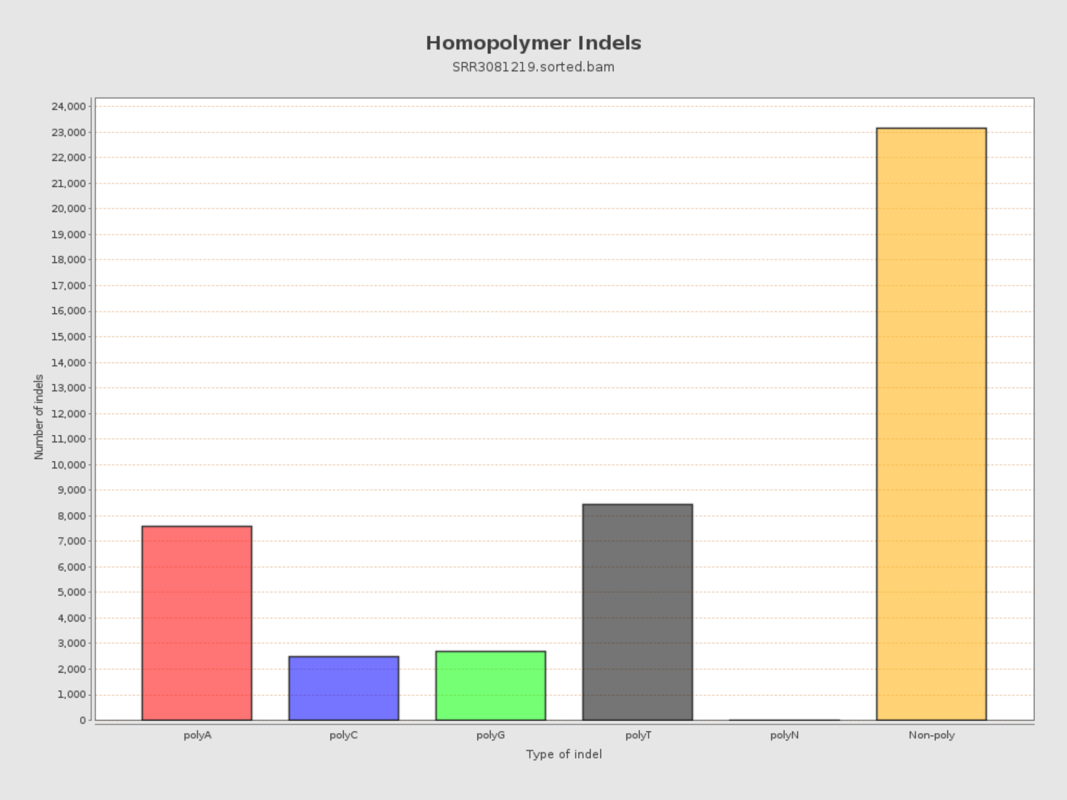
9. Results : Mapped Reads GC-content Distribution



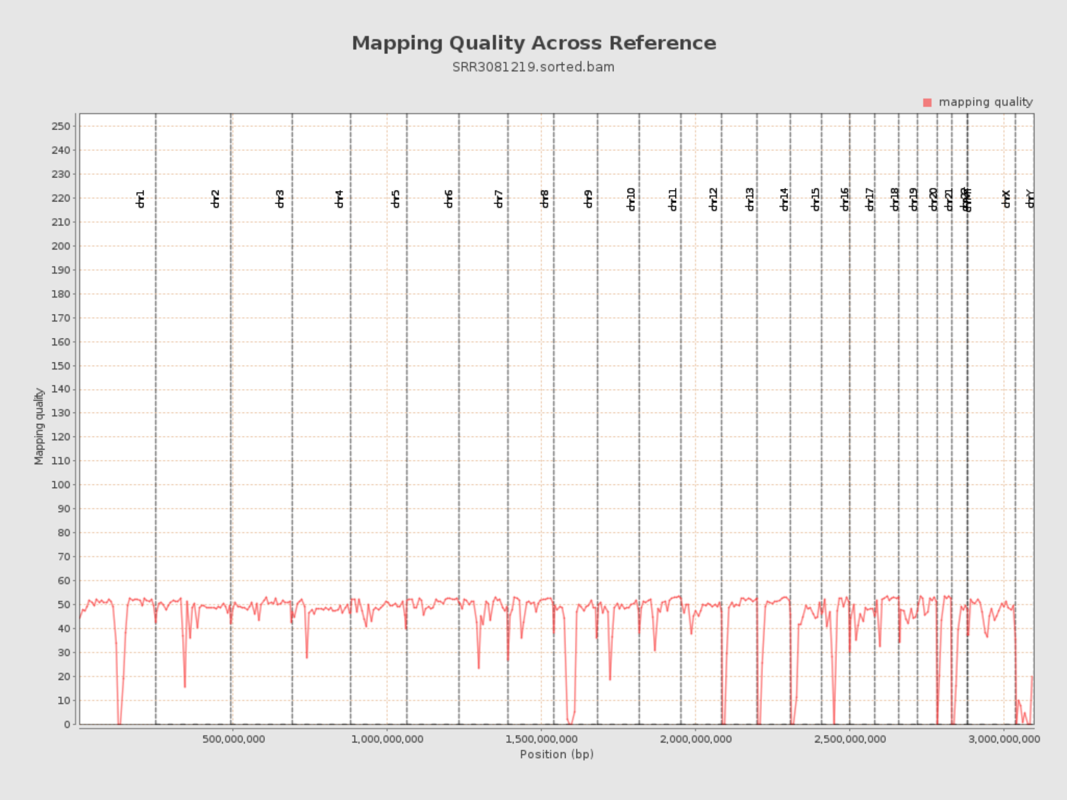
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram