Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 21:59:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081134.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_SRR3081134 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081134.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 21:59:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081134.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,941,346
Mapped reads	1,718,740 / 88.53%
Unmapped reads	222,606 / 11.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,945 / 0.72%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	62,374 / 3.21%
Duplication rate	2.87%
Clipped reads	811,033 / 41.78%

2.2. ACGT Content

Number/percentage of A's	31,891,047 / 27.97%
Number/percentage of C's	21,135,893 / 18.54%
Number/percentage of T's	35,677,555 / 31.29%
Number/percentage of G's	25,286,910 / 22.18%
Number/percentage of N's	33,698 / 0.03%
GC Percentage	40.71%

2.3. Coverage

Mean	0.0368

Standard Deviation	0.3117

2.4. Mapping Quality

Mean Mapping Quality	46.07

2.5. Mismatches and indels

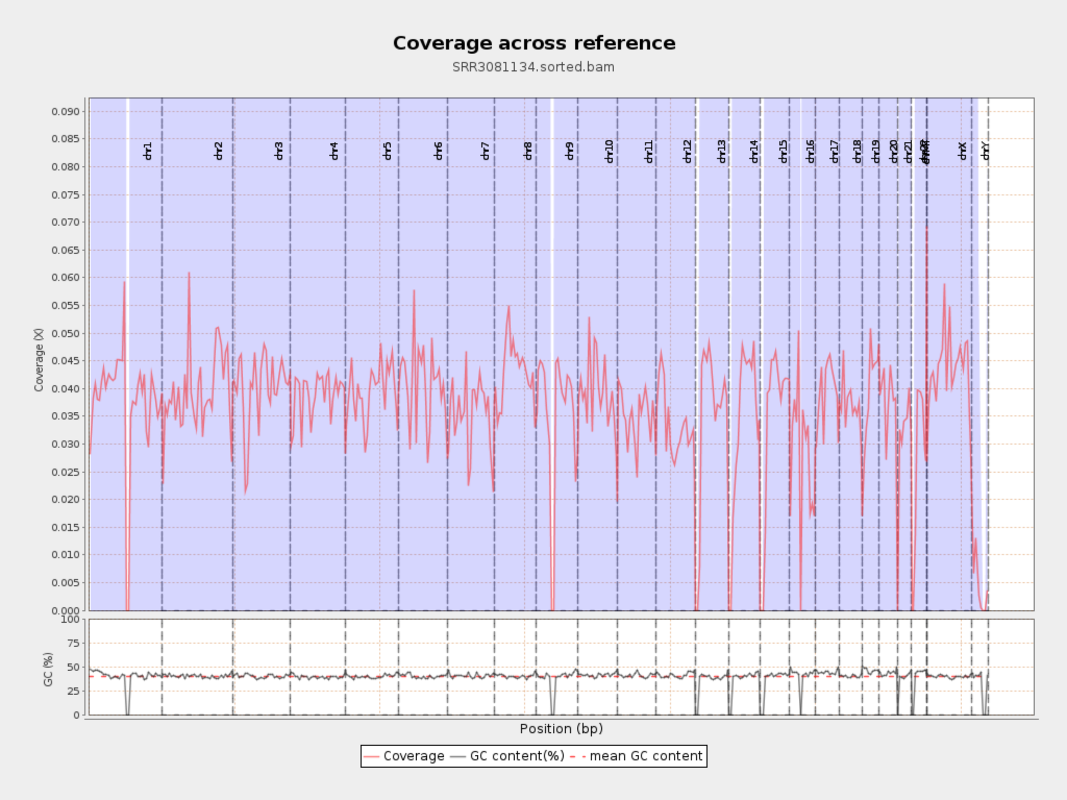
General error rate	0.85%
Mismatches	953,602
Insertions	8,948
Mapped reads with at least one insertion	0.52%
Deletions	25,986
Mapped reads with at least one deletion	1.5%
Homopolymer indels	46.85%

2.6. Chromosome stats

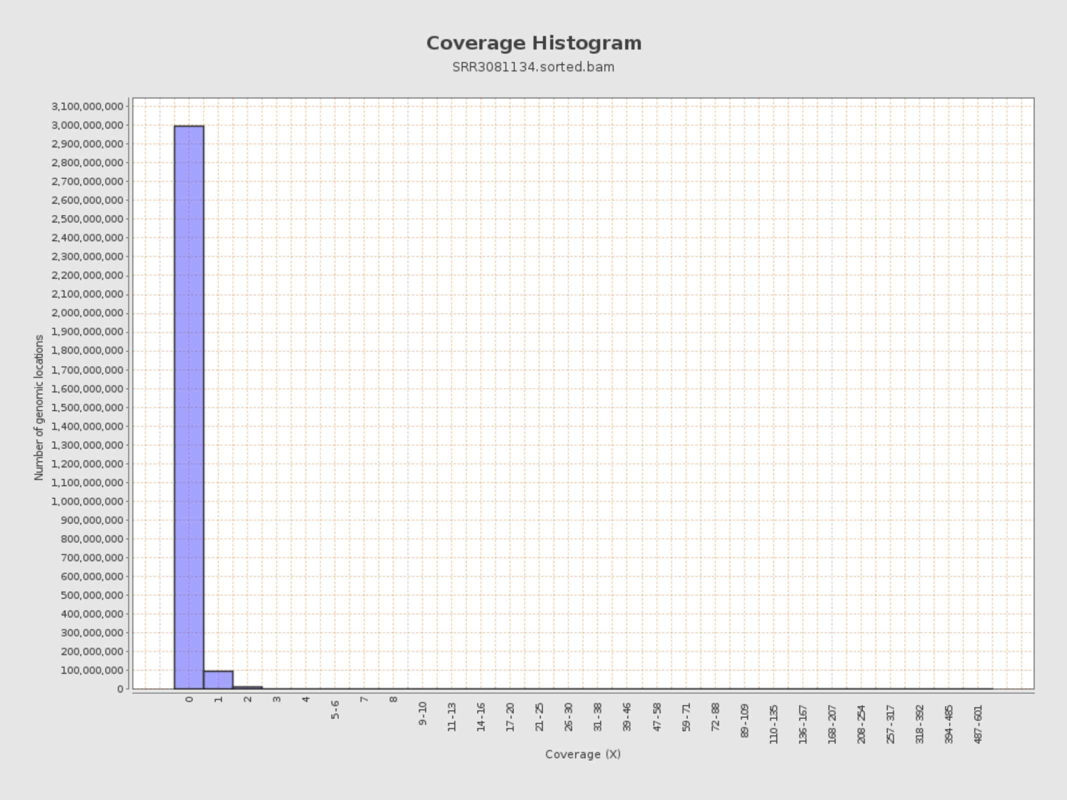
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9354428	0.0375	0.5269
chr2	243199373	9623315	0.0396	0.391
chr3	198022430	7968936	0.0402	0.2198
chr4	191154276	7419552	0.0388	0.2248
chr5	180915260	7172140	0.0396	0.2197
chr6	171115067	6968058	0.0407	0.2915
chr7	159138663	5644227	0.0355	0.3516

chr8	146364022	6289944	0.043	0.3847
chr9	141213431	4975724	0.0352	0.2876
chr10	135534747	5365174	0.0396	0.2805
chr11	135006516	4691535	0.0348	0.2756
chr12	133851895	4469613	0.0334	0.2033
chr13	115169878	3945167	0.0343	0.2021
chr14	107349540	3588476	0.0334	0.2129
chr15	102531392	3483866	0.034	0.2065
chr16	90354753	2497126	0.0276	0.209
chr17	81195210	3189760	0.0393	0.2469
chr18	78077248	2901847	0.0372	0.5496
chr19	59128983	2324256	0.0393	0.3828
chr20	63025520	2366502	0.0375	0.2182
chr21	48129895	1484639	0.0308	0.2063
chr22	51304566	1291795	0.0252	0.1727
chrMT	16571	1147	0.0692	0.3371
chrX	155270560	6769900	0.0436	0.2559
chrY	59373566	279608	0.0047	0.0994

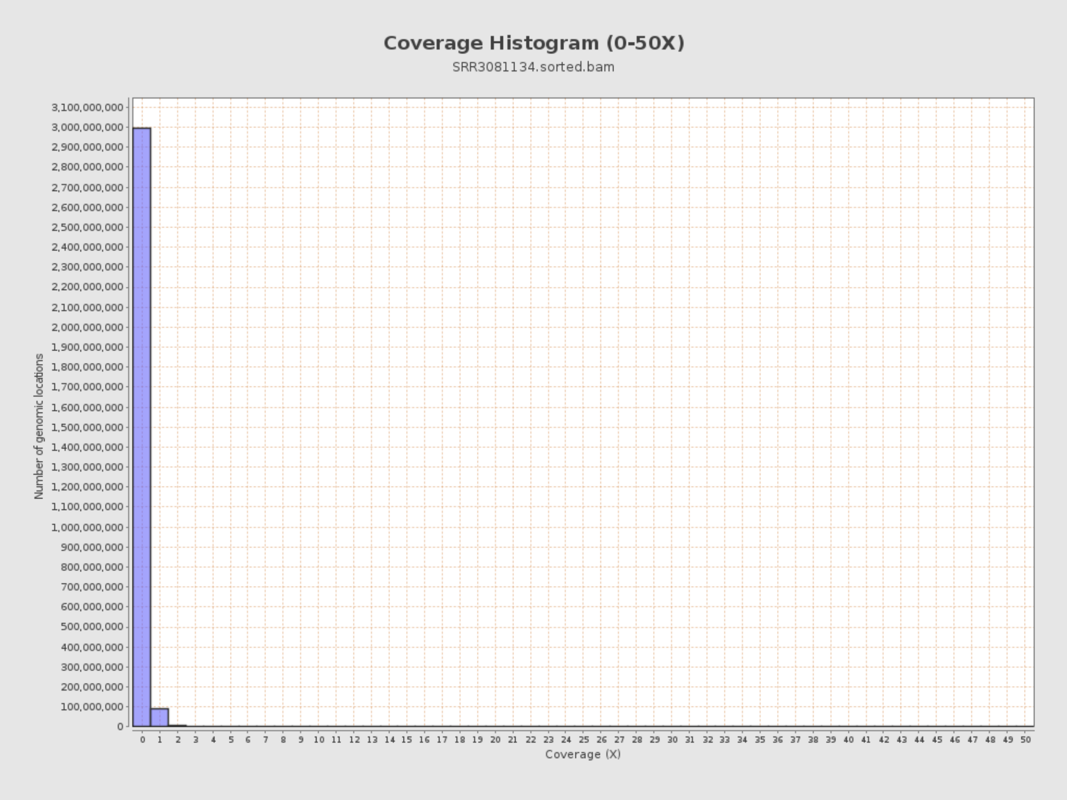
3. Results : Coverage across reference



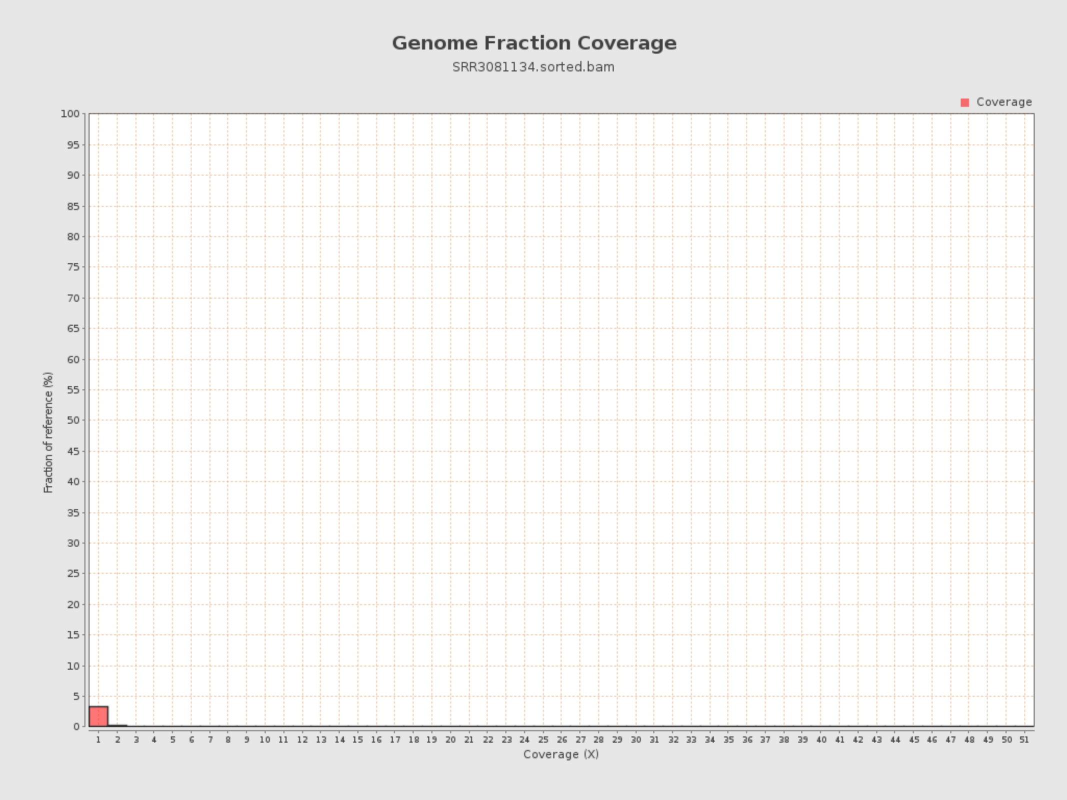
4. Results : Coverage Histogram



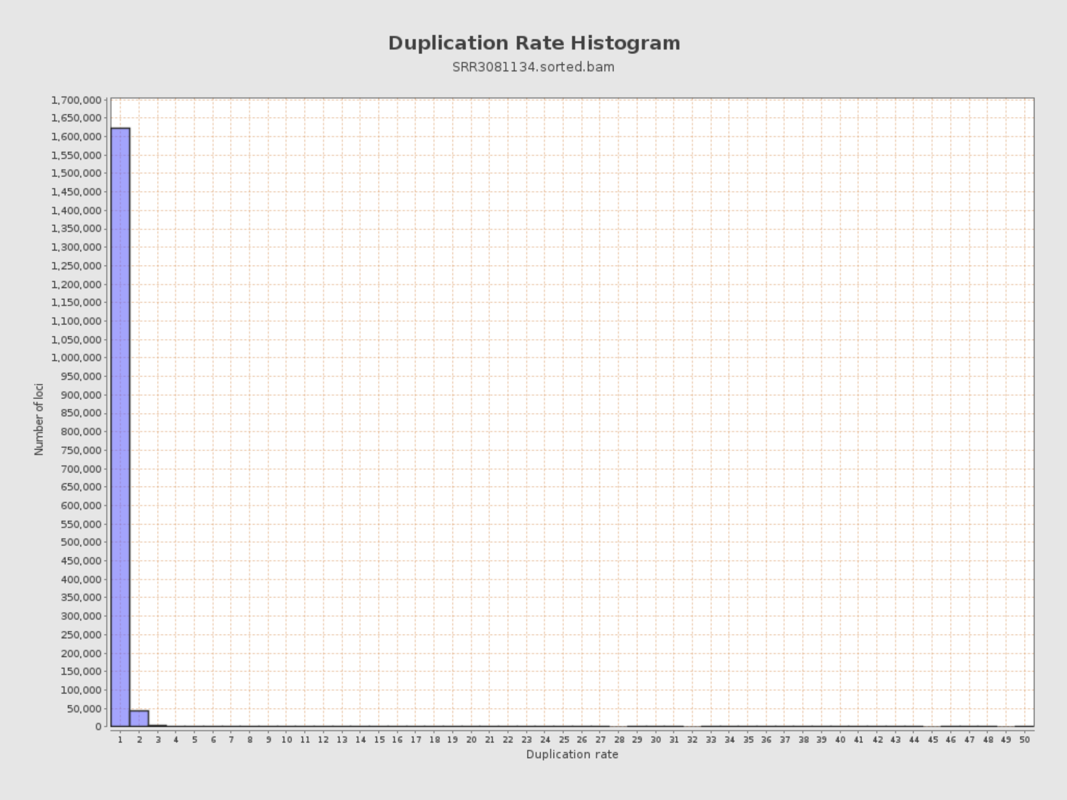
5. Results : Coverage Histogram (0-50X)



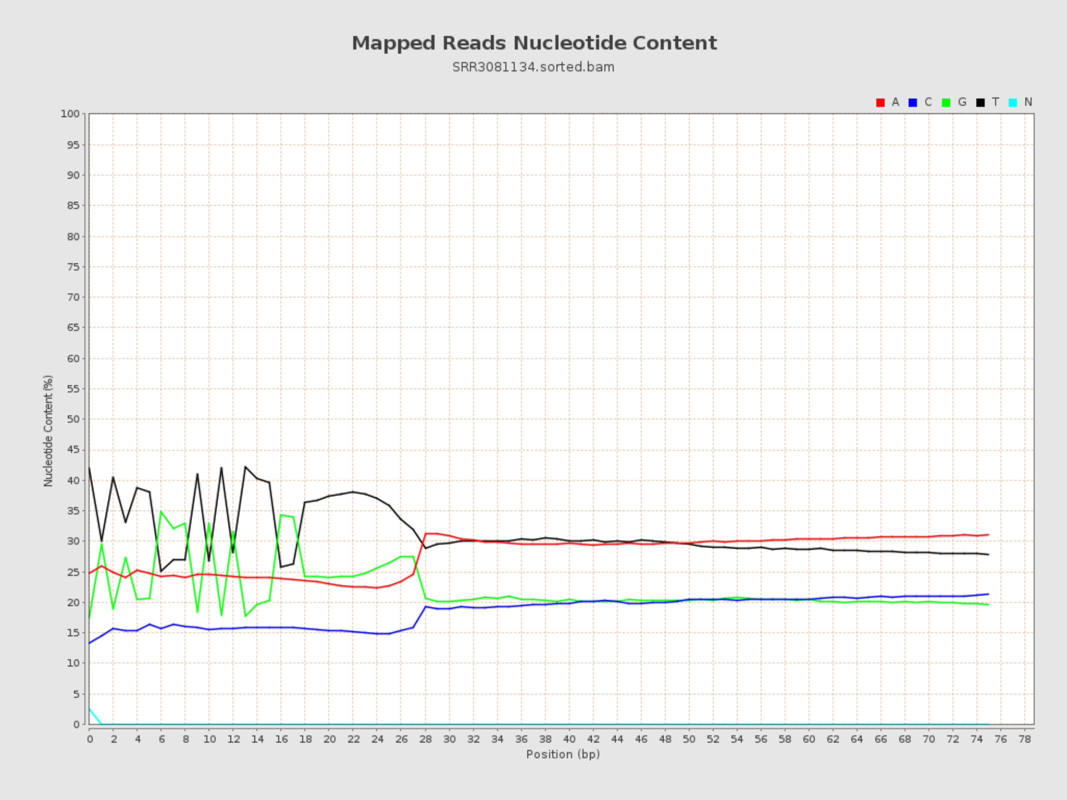
6. Results : Genome Fraction Coverage



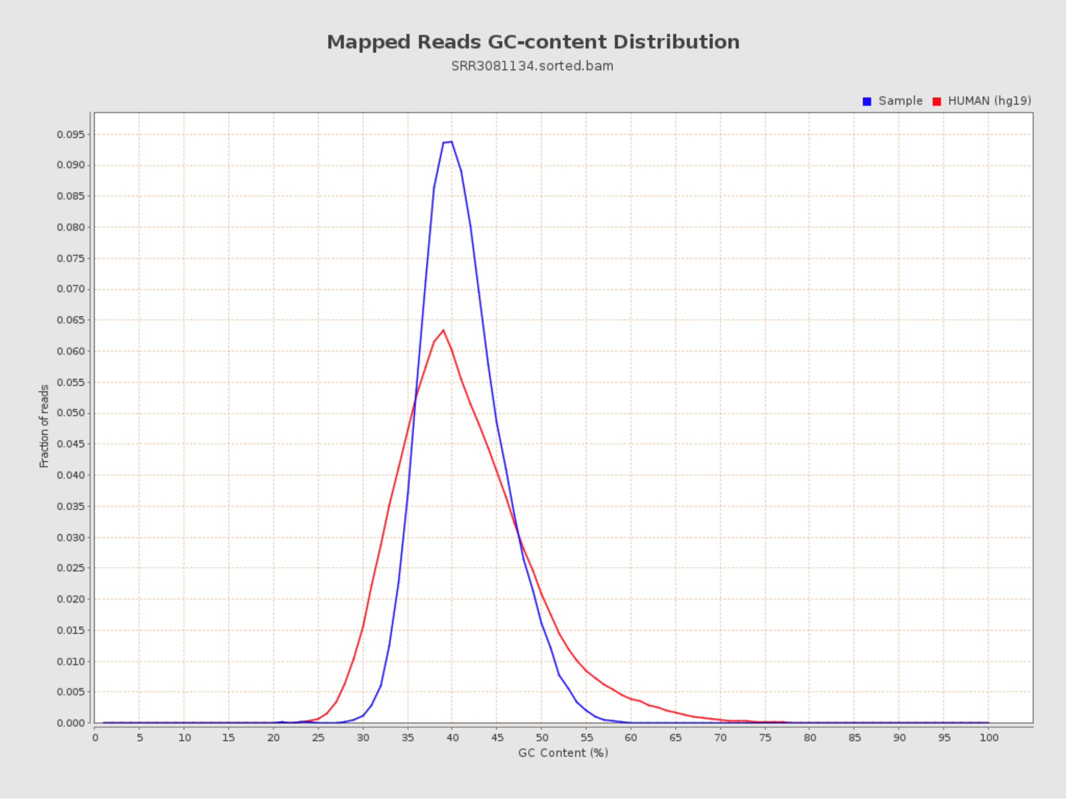
7. Results : Duplication Rate Histogram



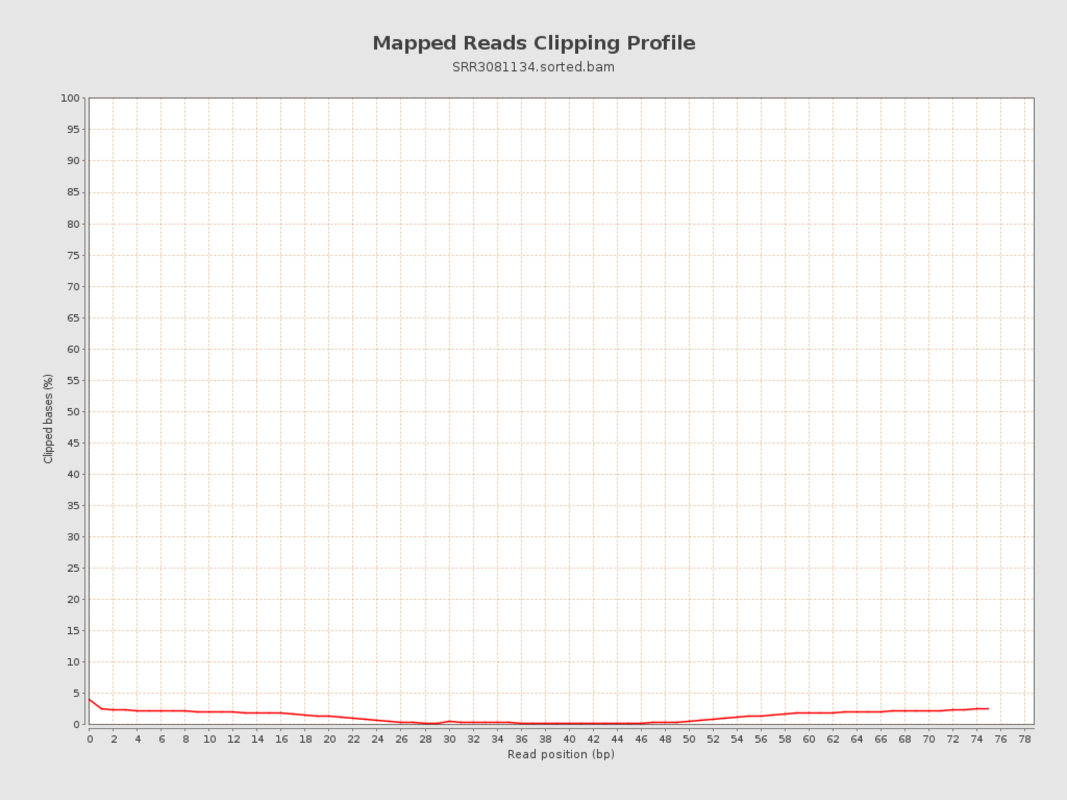
8. Results : Mapped Reads Nucleotide Content



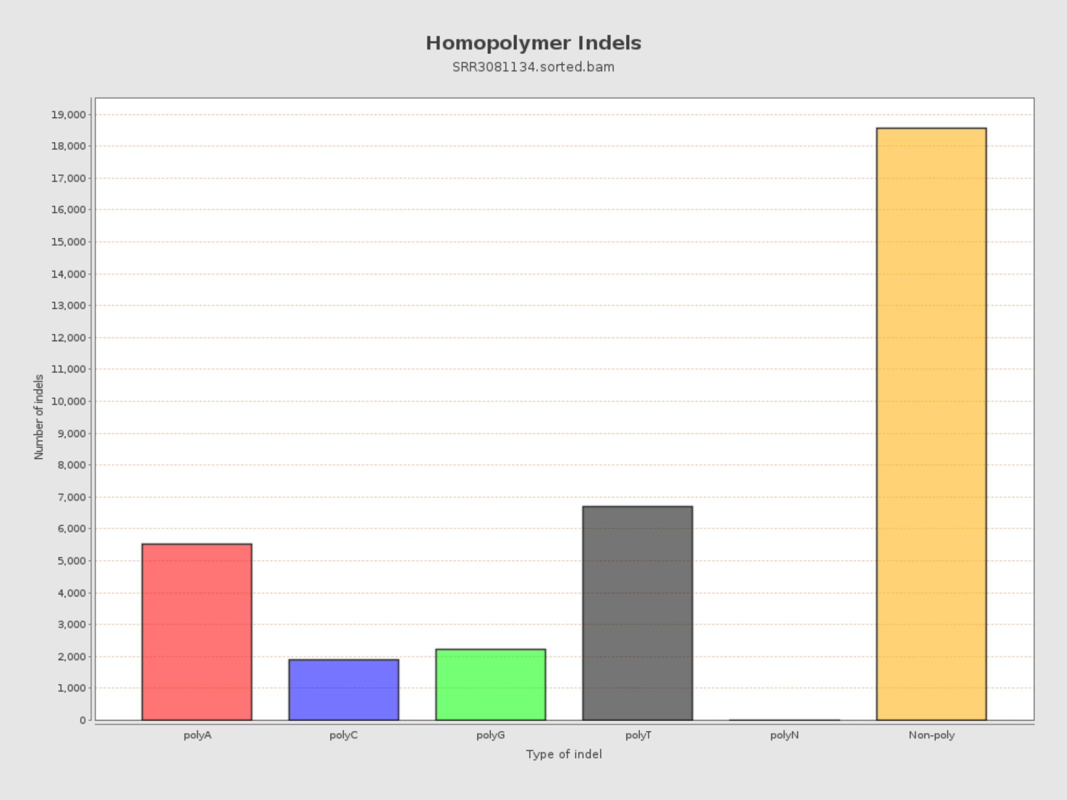
9. Results : Mapped Reads GC-content Distribution



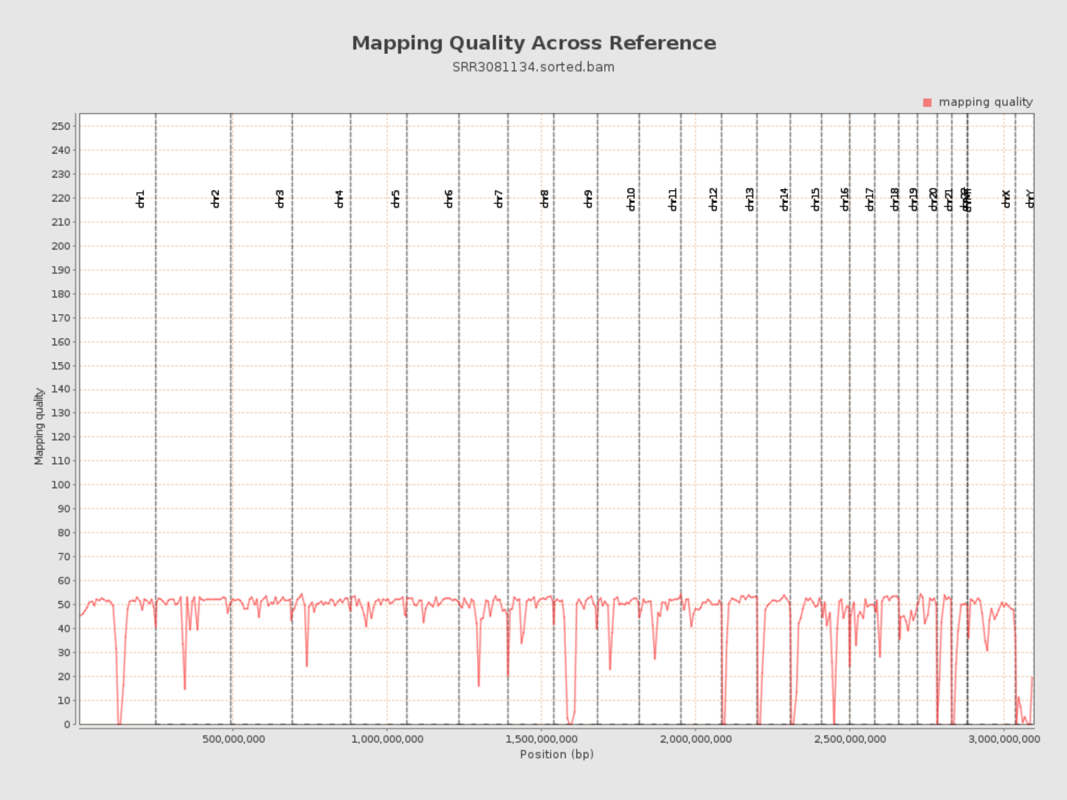
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram