Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 13:04:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081980.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_SRR3081980 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081980.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 13:04:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081980.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,222,562
Mapped reads	2,063,076 / 92.82%
Unmapped reads	159,486 / 7.18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,386 / 0.56%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	99,228 / 4.46%
Duplication rate	3.93%
Clipped reads	792,358 / 35.65%

2.2. ACGT Content

Number/percentage of A's	39,462,395 / 28.2%
Number/percentage of C's	25,557,420 / 18.27%
Number/percentage of T's	44,753,354 / 31.98%
Number/percentage of G's	30,129,294 / 21.53%
Number/percentage of N's	18,129 / 0.01%
GC Percentage	39.8%

2.3. Coverage

Mean	0.0452

Standard Deviation	0.3853

2.4. Mapping Quality

Mean Mapping Quality	46.87

2.5. Mismatches and indels

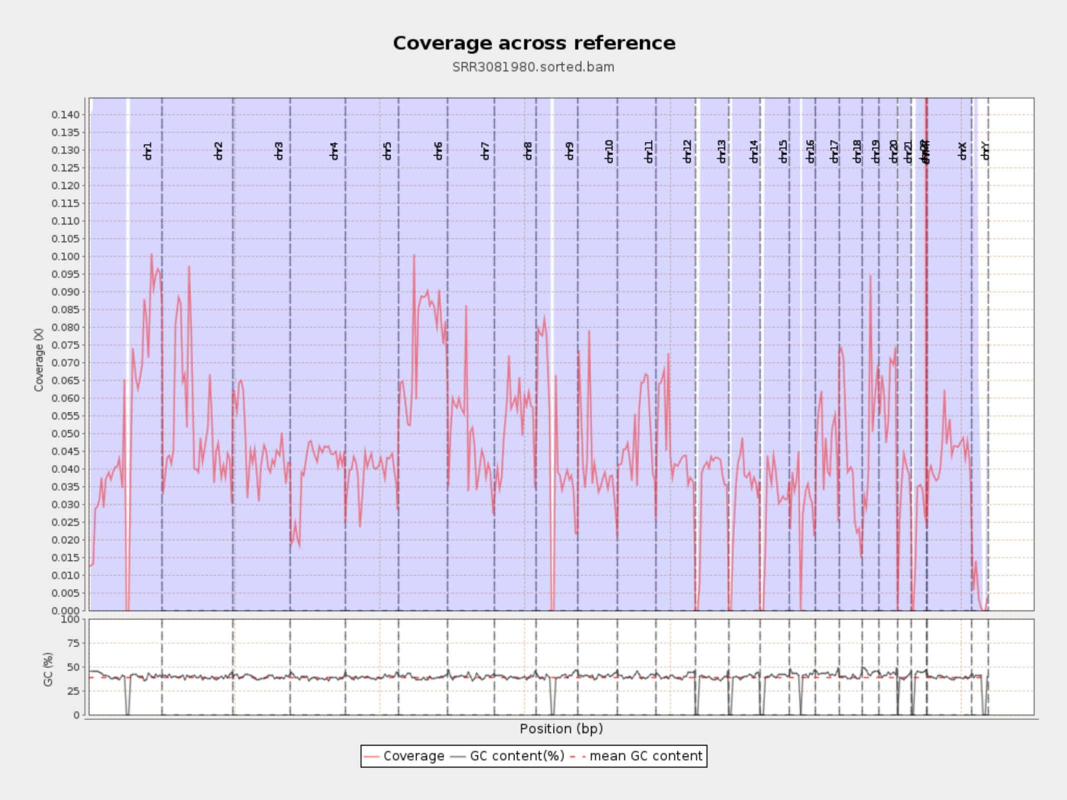
General error rate	0.74%
Mismatches	1,021,417
Insertions	9,689
Mapped reads with at least one insertion	0.47%
Deletions	29,285
Mapped reads with at least one deletion	1.4%
Homopolymer indels	48.23%

2.6. Chromosome stats

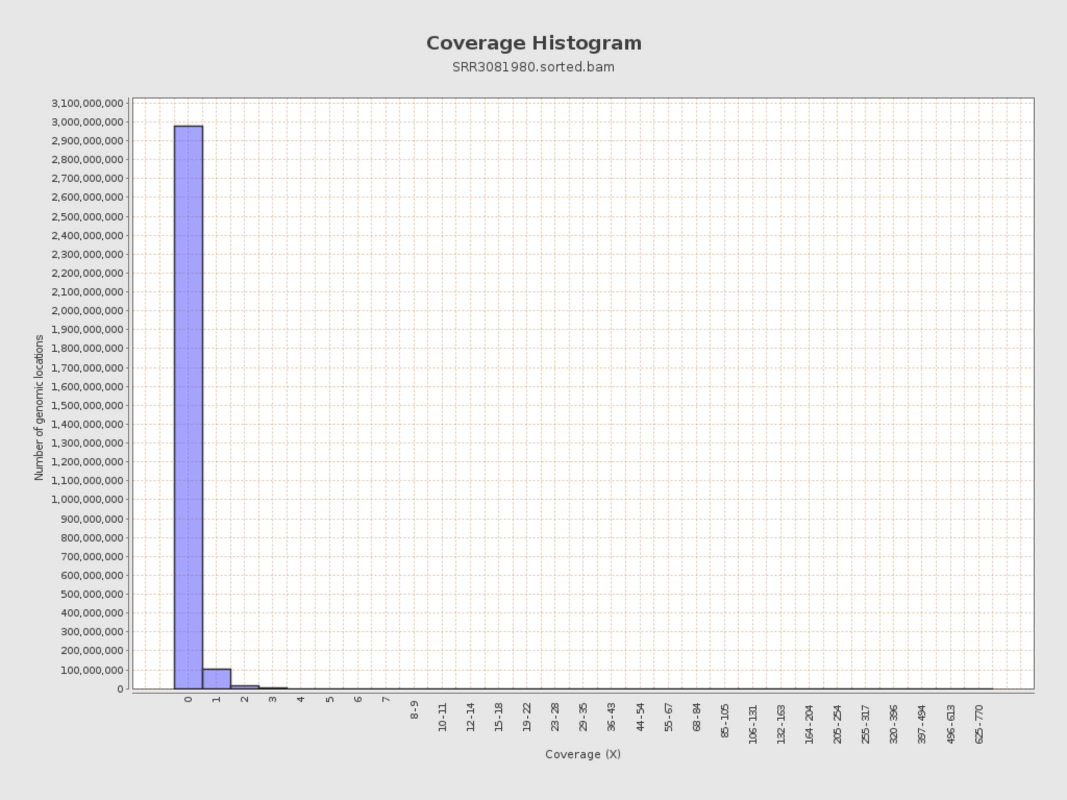
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12963704	0.052	0.6818
chr2	243199373	12632848	0.0519	0.4843
chr3	198022430	9130604	0.0461	0.2413
chr4	191154276	7545226	0.0395	0.234
chr5	180915260	7115786	0.0393	0.2246
chr6	171115067	13081126	0.0764	0.3946
chr7	159138663	7705217	0.0484	0.5382

chr8	146364022	7744258	0.0529	0.5158
chr9	141213431	6560360	0.0465	0.3734
chr10	135534747	5716247	0.0422	0.3785
chr11	135006516	6535762	0.0484	0.2874
chr12	133851895	6257118	0.0467	0.2505
chr13	115169878	3862627	0.0335	0.204
chr14	107349540	3478593	0.0324	0.2151
chr15	102531392	3005627	0.0293	0.1935
chr16	90354753	2711202	0.03	0.2113
chr17	81195210	3752539	0.0462	0.2723
chr18	78077248	3341045	0.0428	0.5557
chr19	59128983	3078009	0.0521	0.5218
chr20	63025520	3857321	0.0612	0.286
chr21	48129895	1572636	0.0327	0.2176
chr22	51304566	1164979	0.0227	0.1671
chrMT	16571	47779	2.8833	2.2773
chrX	155270560	6839955	0.0441	0.2666
chrY	59373566	271833	0.0046	0.1093

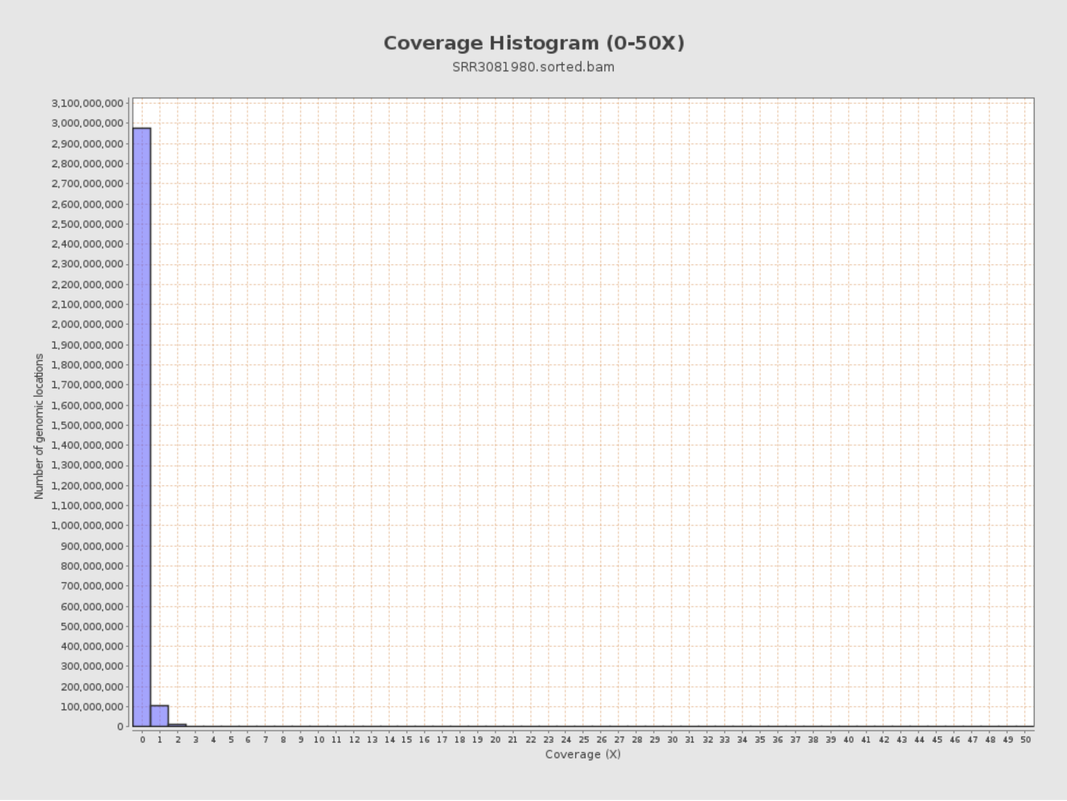
3. Results : Coverage across reference



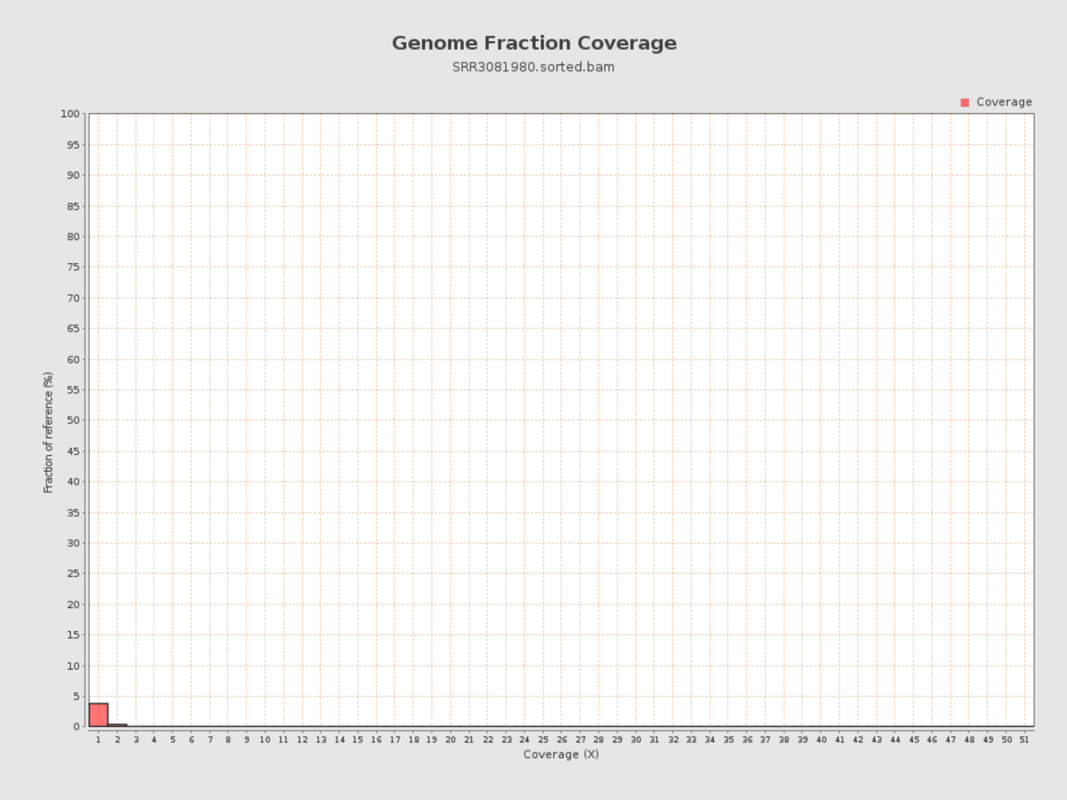
4. Results : Coverage Histogram



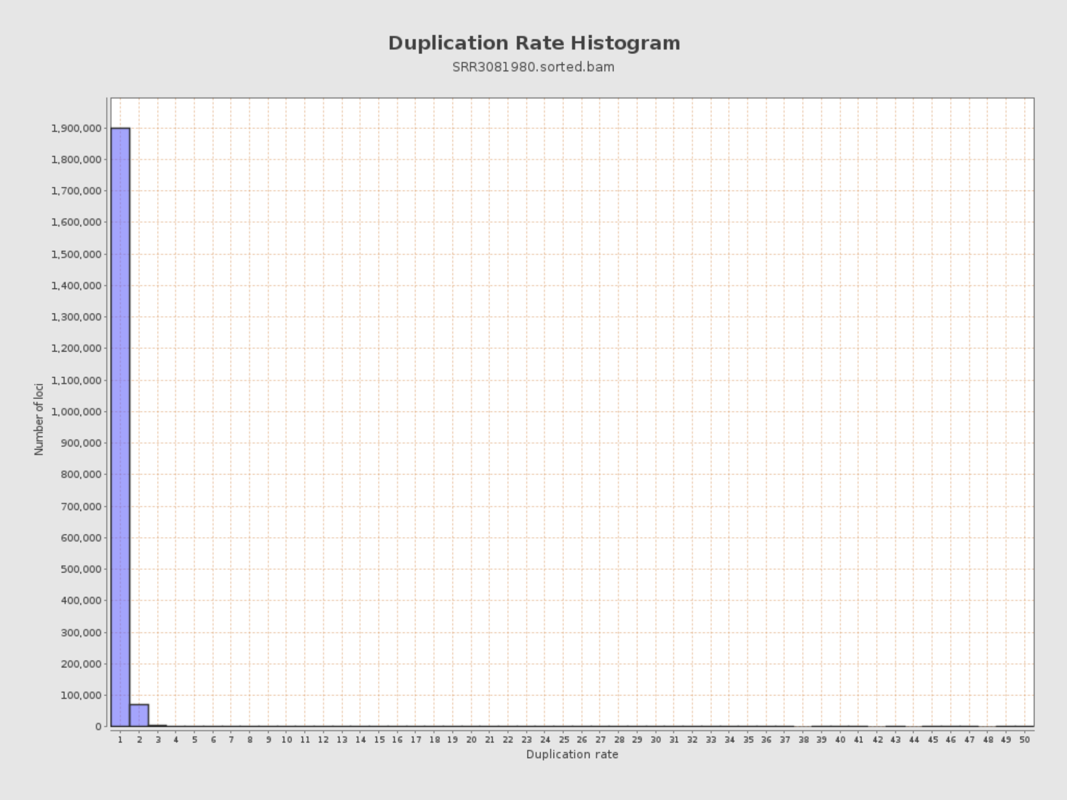
5. Results : Coverage Histogram (0-50X)



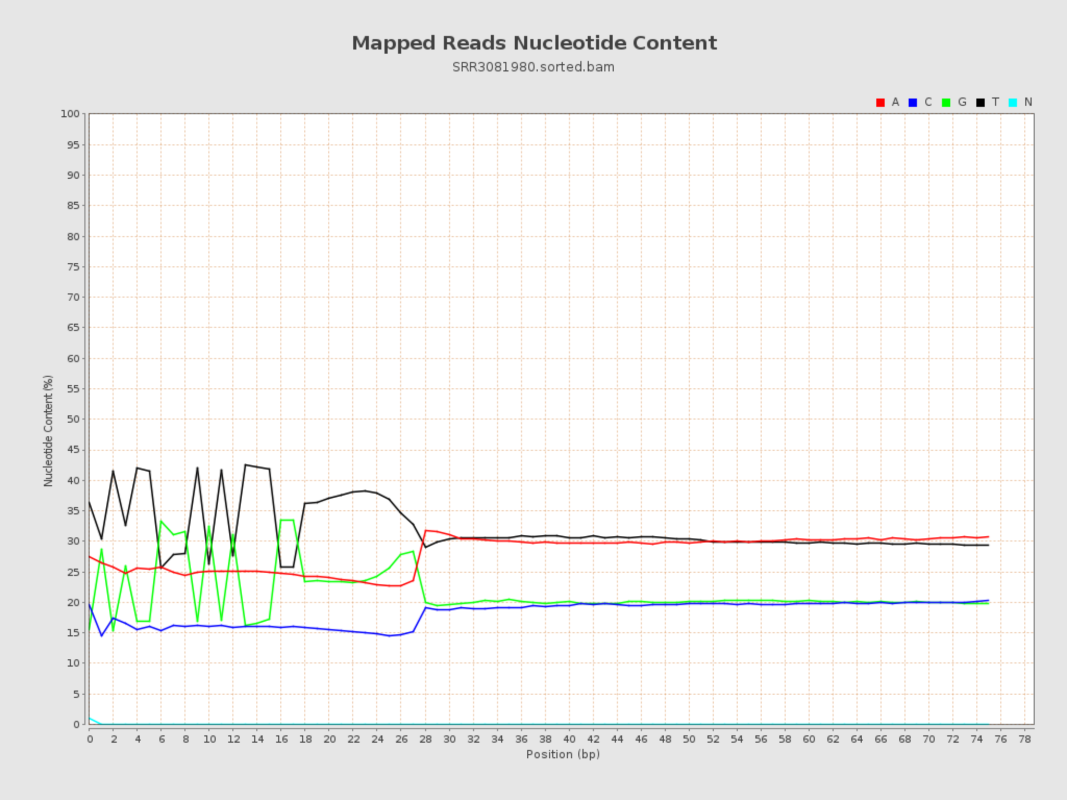
6. Results : Genome Fraction Coverage



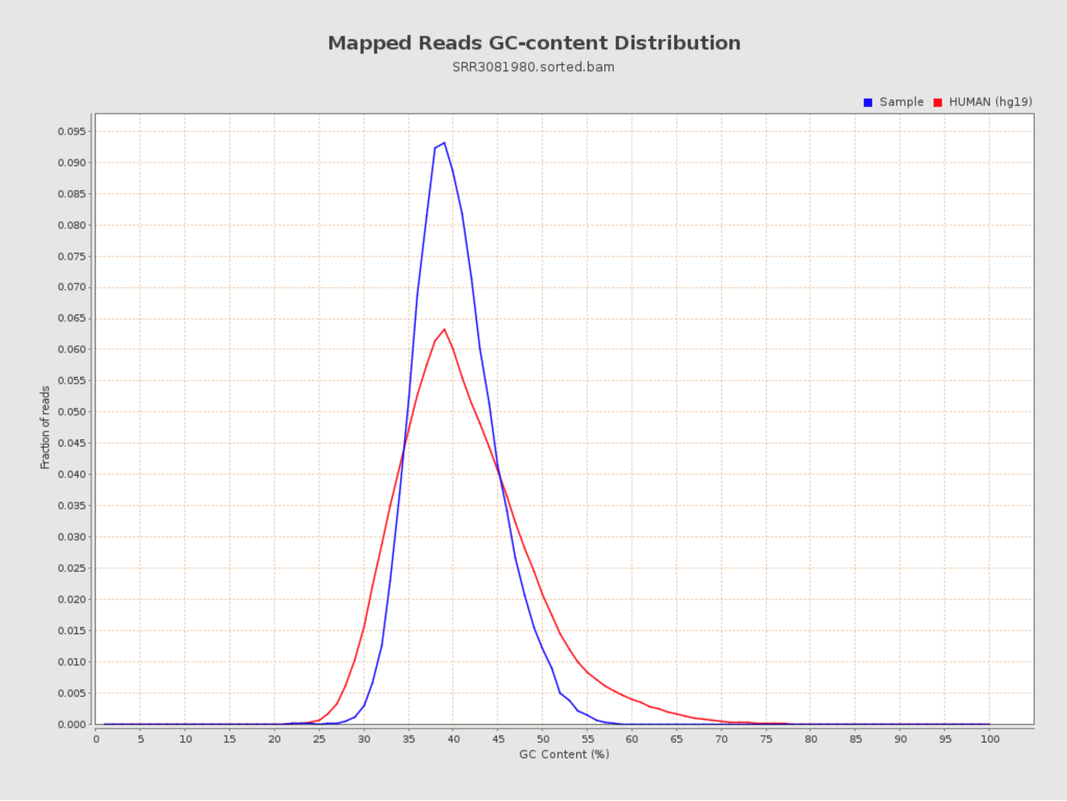
7. Results : Duplication Rate Histogram



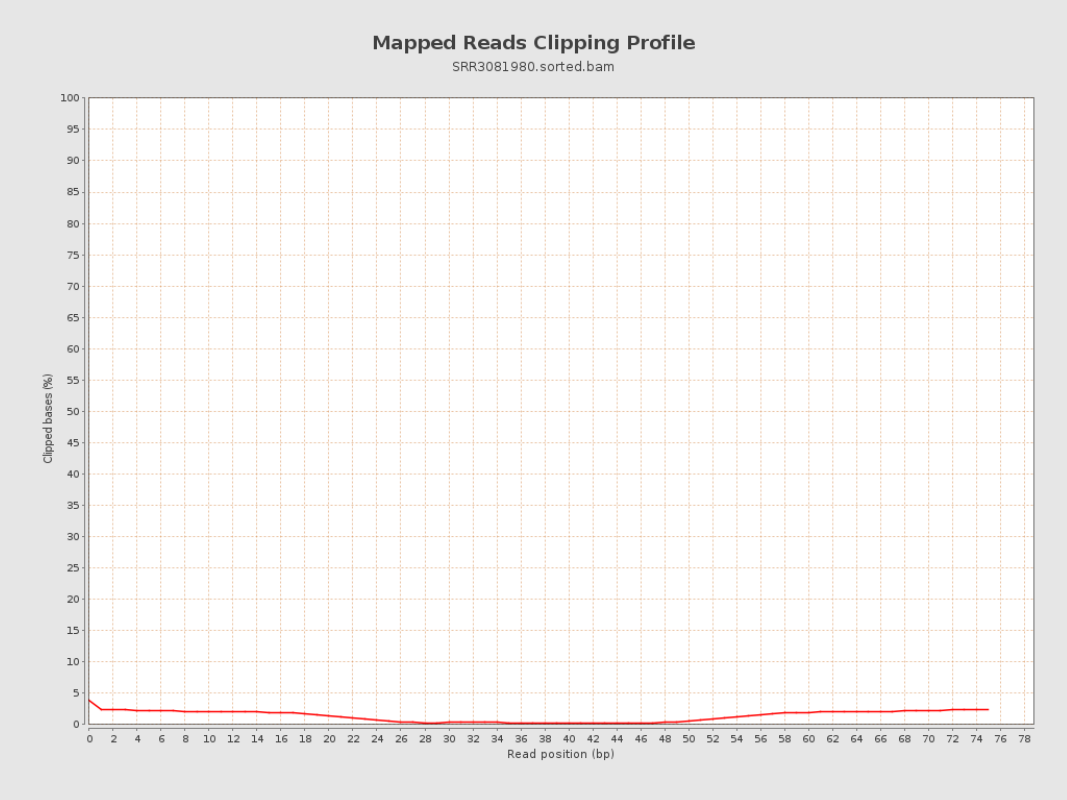
8. Results : Mapped Reads Nucleotide Content



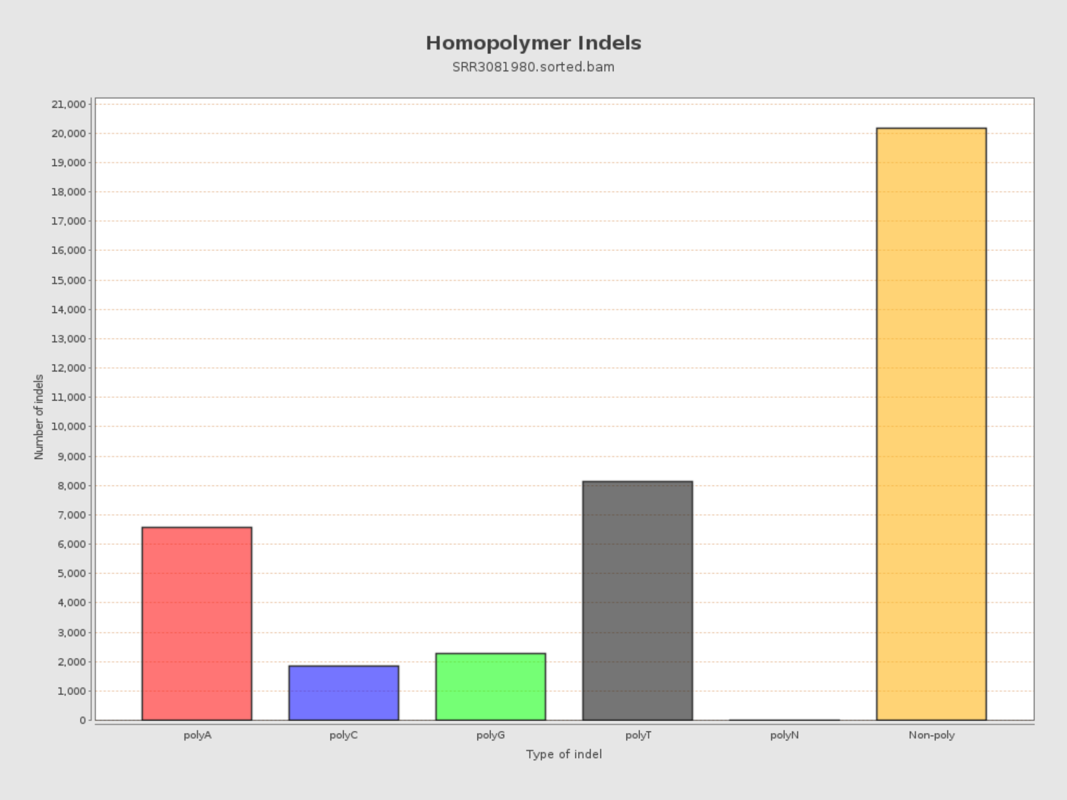
9. Results : Mapped Reads GC-content Distribution



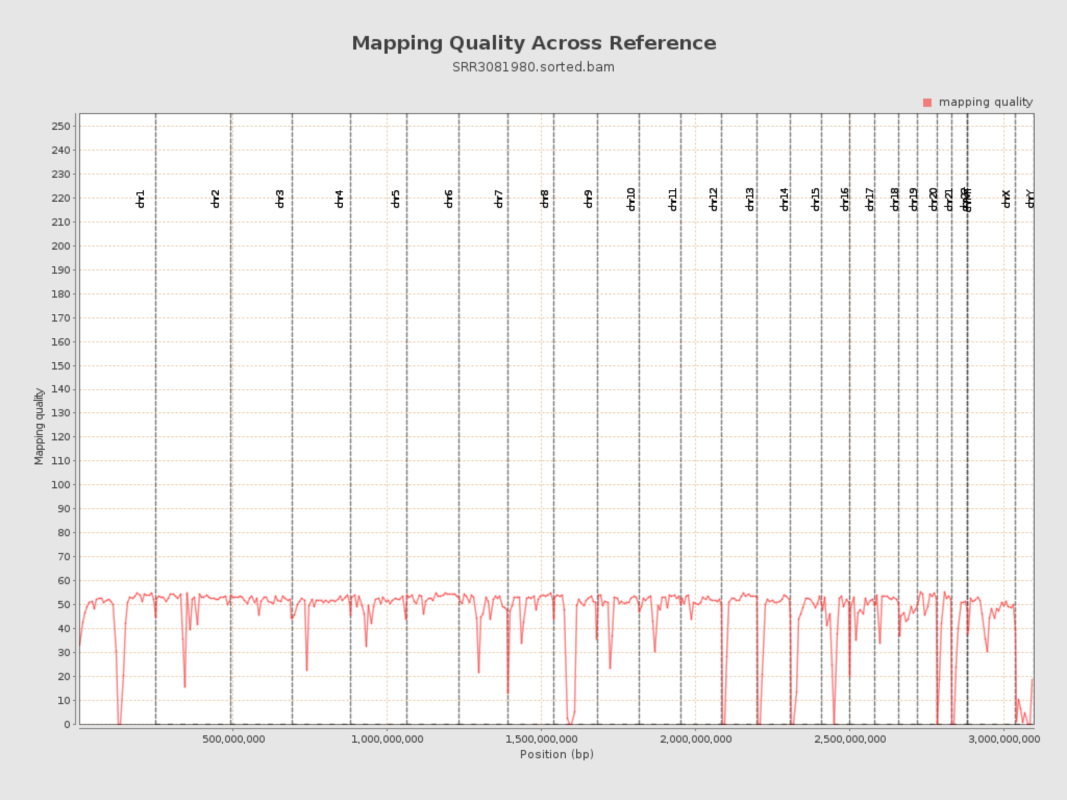
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram