Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 18:53:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818831.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_SRR1818831 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818831.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 18:53:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818831.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,472,351
Mapped reads	2,438,543 / 98.63%
Unmapped reads	33,808 / 1.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	35,916 / 1.45%
Read min/max/mean length	30 / 101 / 101.56
Duplicated reads (estimated)	644,306 / 26.06%
Duplication rate	22.68%
Clipped reads	2,457,133 / 99.38%

2.2. ACGT Content

Number/percentage of A's	65,281,674 / 28.9%
Number/percentage of C's	46,262,420 / 20.48%
Number/percentage of T's	63,902,917 / 28.29%
Number/percentage of G's	50,466,947 / 22.34%
Number/percentage of N's	3,583 / 0%
GC Percentage	42.82%

2.3. Coverage

Mean	0.073

Standard Deviation	0.8333

2.4. Mapping Quality

Mean Mapping Quality	49.34

2.5. Mismatches and indels

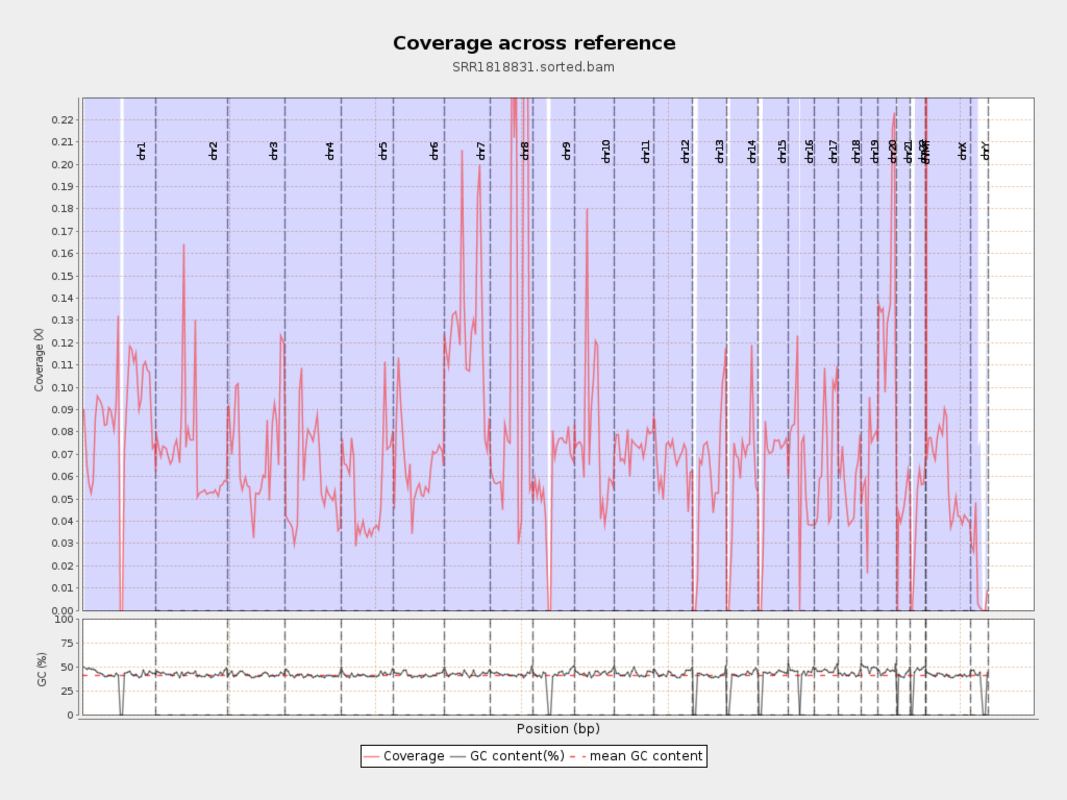
General error rate	0.62%
Mismatches	1,325,786
Insertions	30,547
Mapped reads with at least one insertion	1.21%
Deletions	70,940
Mapped reads with at least one deletion	2.84%
Homopolymer indels	40.18%

2.6. Chromosome stats

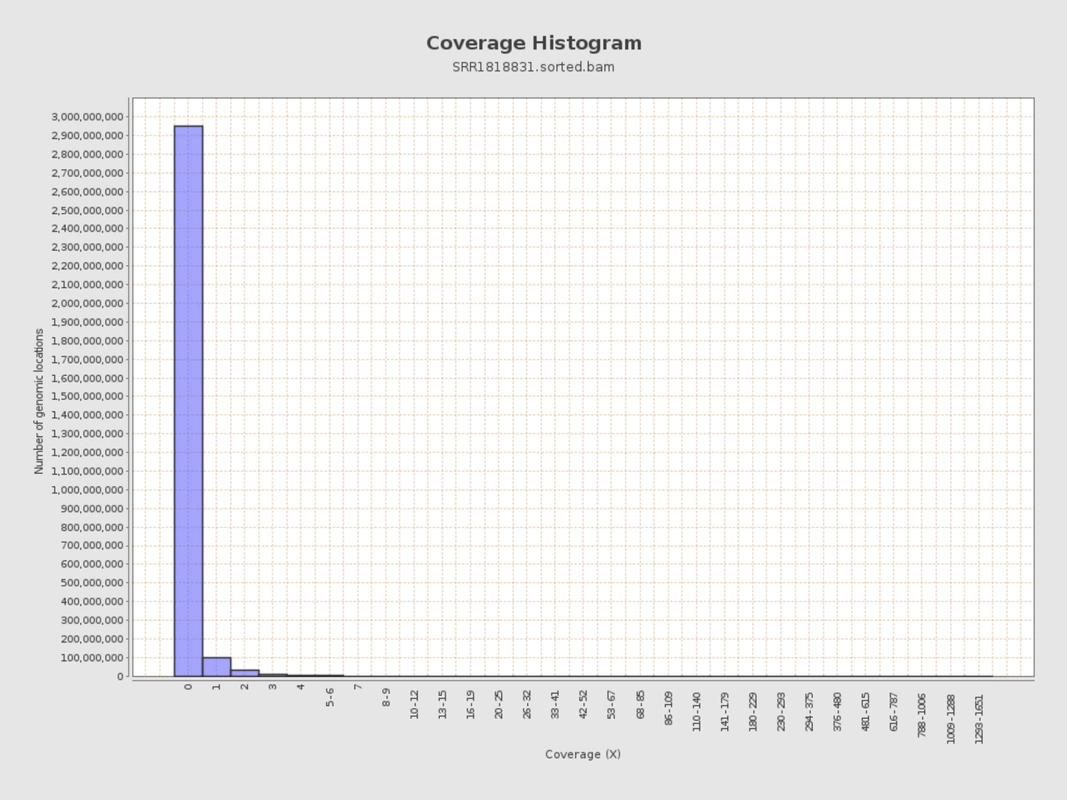
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21348489	0.0857	1.26
chr2	243199373	17001274	0.0699	1.1495
chr3	198022430	14275916	0.0721	0.3843
chr4	191154276	11334579	0.0593	0.4727
chr5	180915260	9961922	0.0551	0.3611
chr6	171115067	11128403	0.065	0.4112
chr7	159138663	20153295	0.1266	1.8422

chr8	146364022	19714937	0.1347	0.7255
chr9	141213431	8337085	0.059	0.7031
chr10	135534747	10489850	0.0774	1.1285
chr11	135006516	9978858	0.0739	0.4981
chr12	133851895	8975635	0.0671	0.3734
chr13	115169878	6979448	0.0606	0.3504
chr14	107349540	6631399	0.0618	0.4014
chr15	102531392	6259989	0.0611	0.3537
chr16	90354753	5643605	0.0625	0.8556
chr17	81195210	5666575	0.0698	0.5236
chr18	78077248	4392158	0.0563	0.8202
chr19	59128983	3861657	0.0653	1.1178
chr20	63025520	9426114	0.1496	0.6076
chr21	48129895	2164540	0.045	0.3862
chr22	51304566	2082176	0.0406	0.3266
chrMT	16571	135938	8.2034	5.7771
chrX	155270560	9280733	0.0598	0.429
chrY	59373566	831383	0.014	1.0799

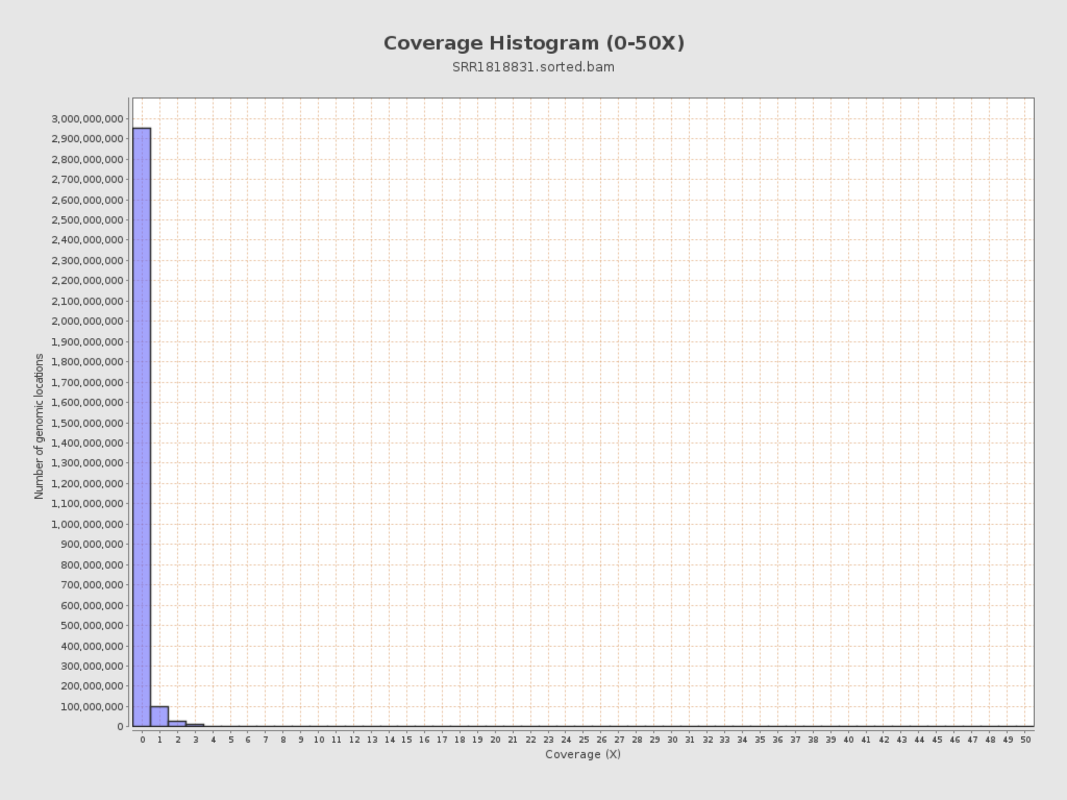
3. Results : Coverage across reference



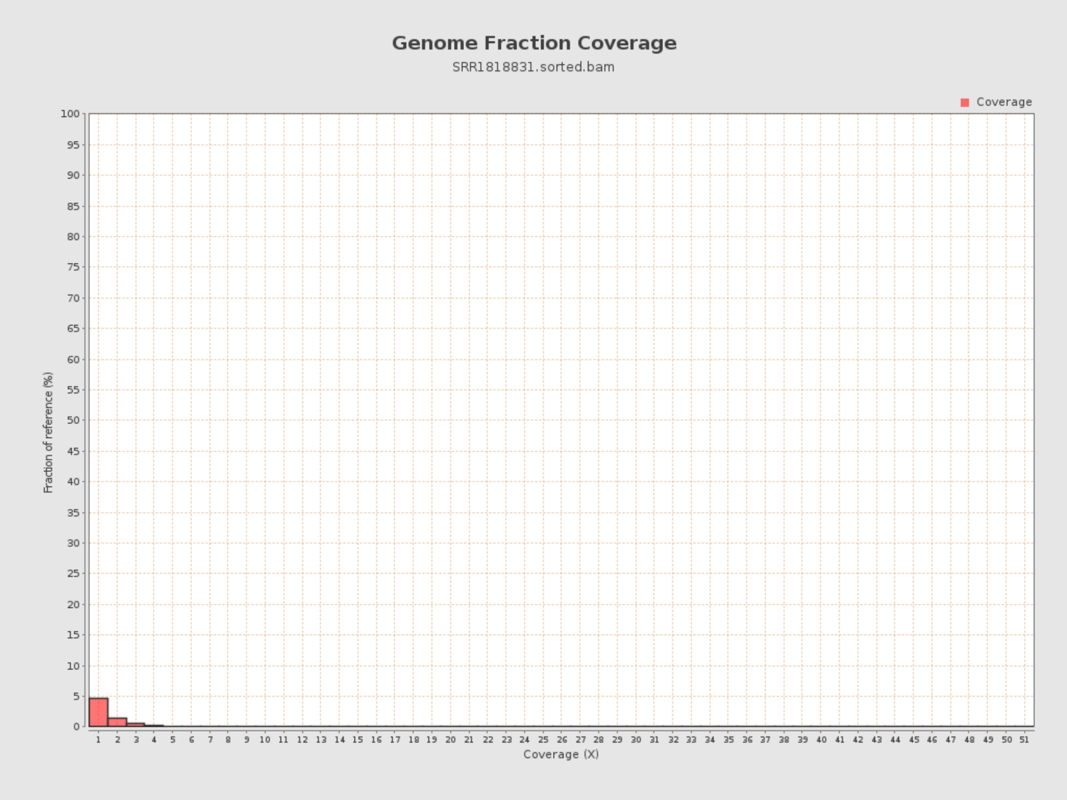
4. Results : Coverage Histogram



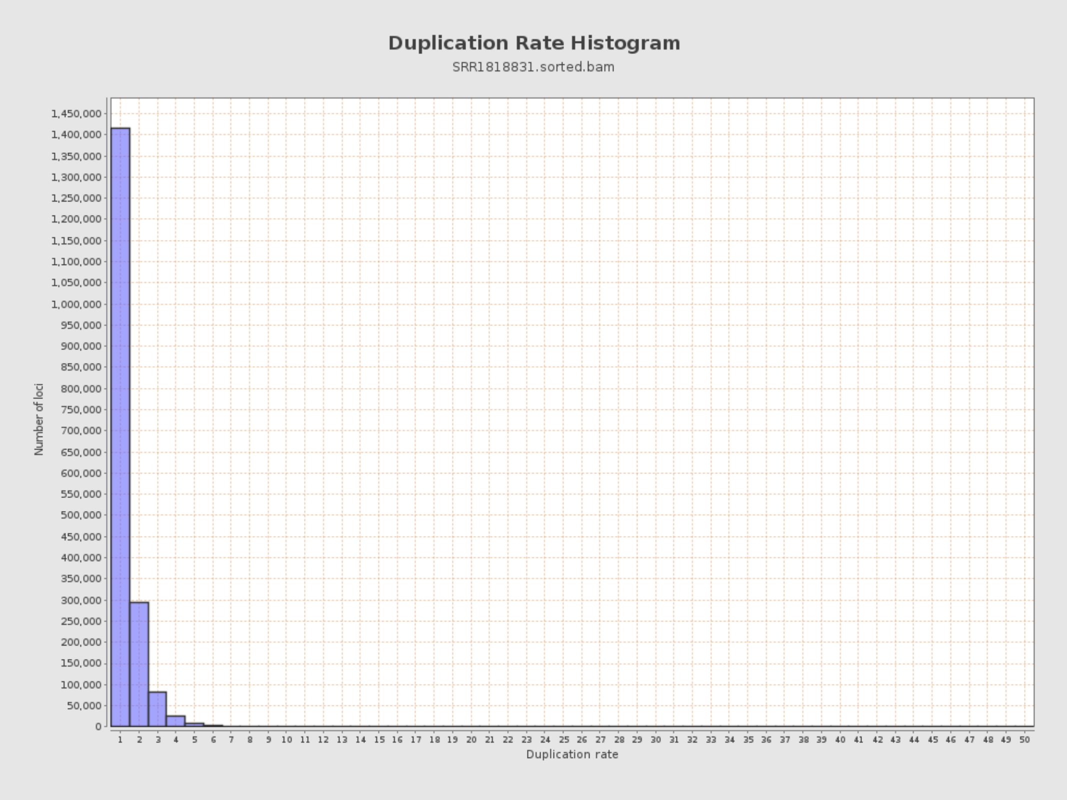
5. Results : Coverage Histogram (0-50X)



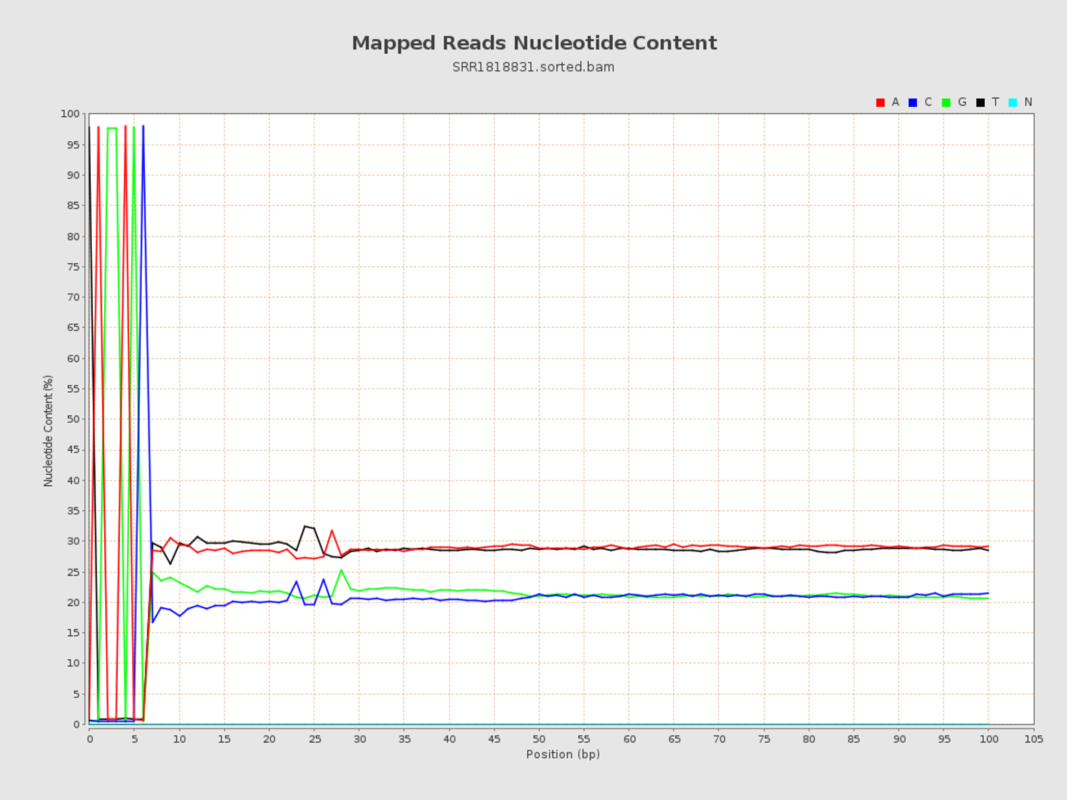
6. Results : Genome Fraction Coverage



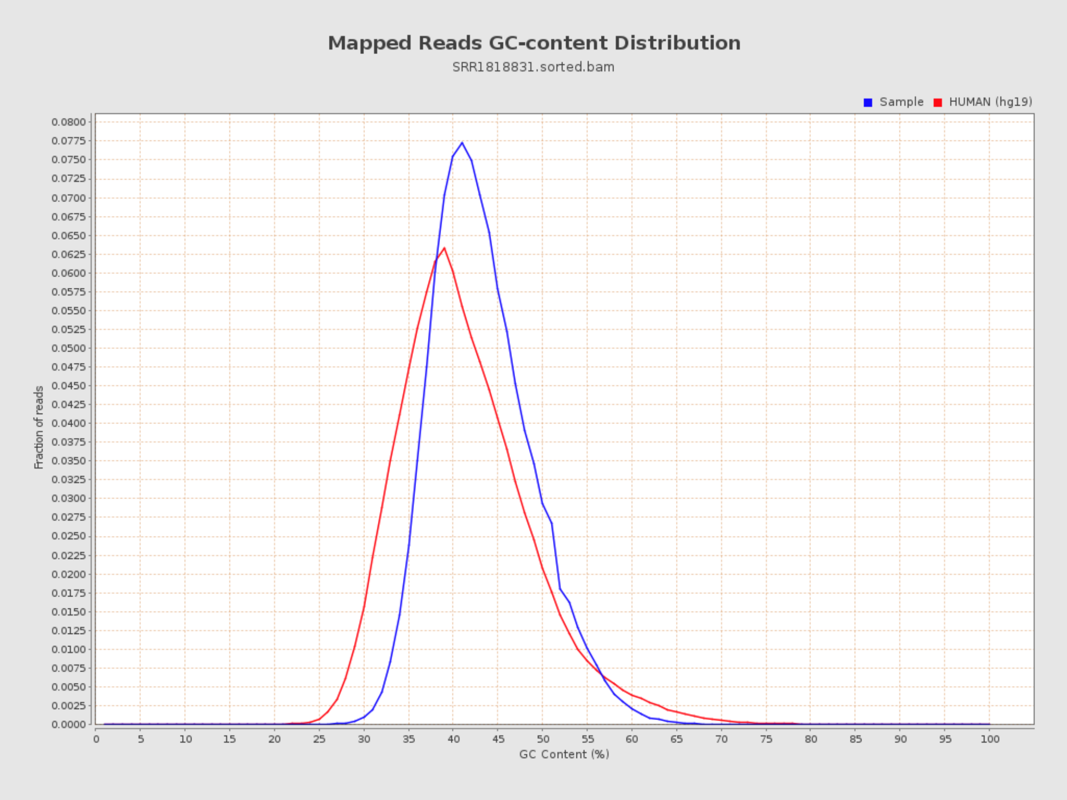
7. Results : Duplication Rate Histogram



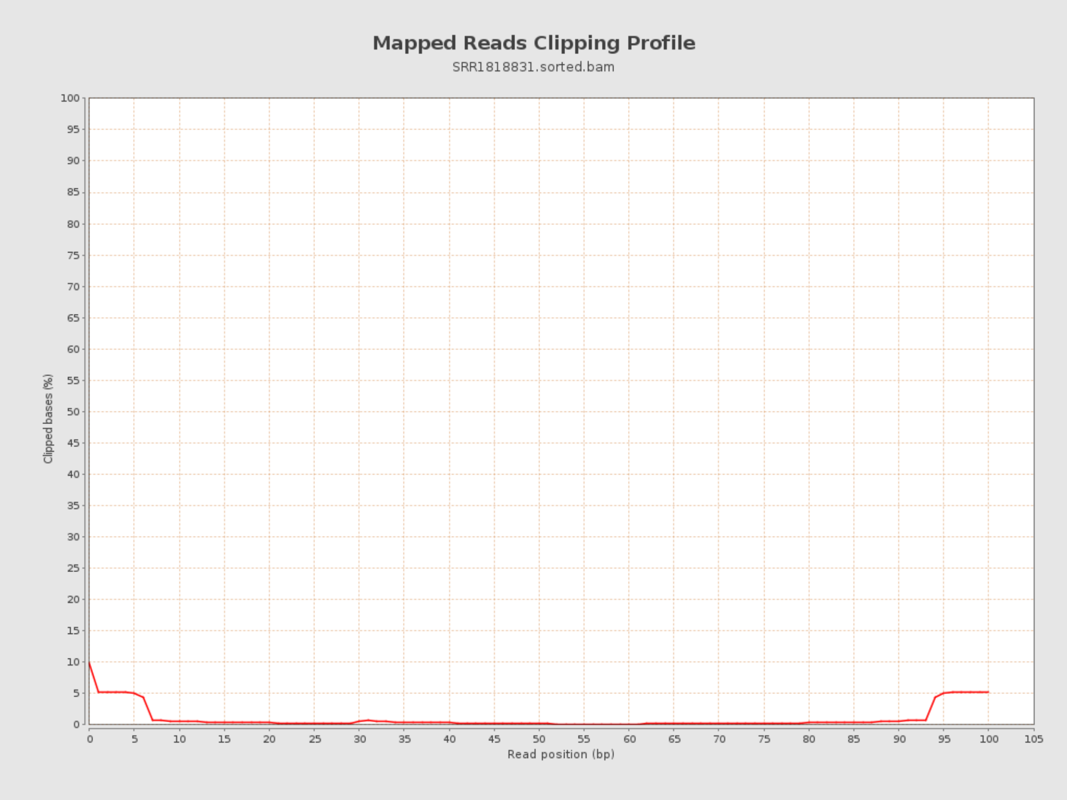
8. Results : Mapped Reads Nucleotide Content



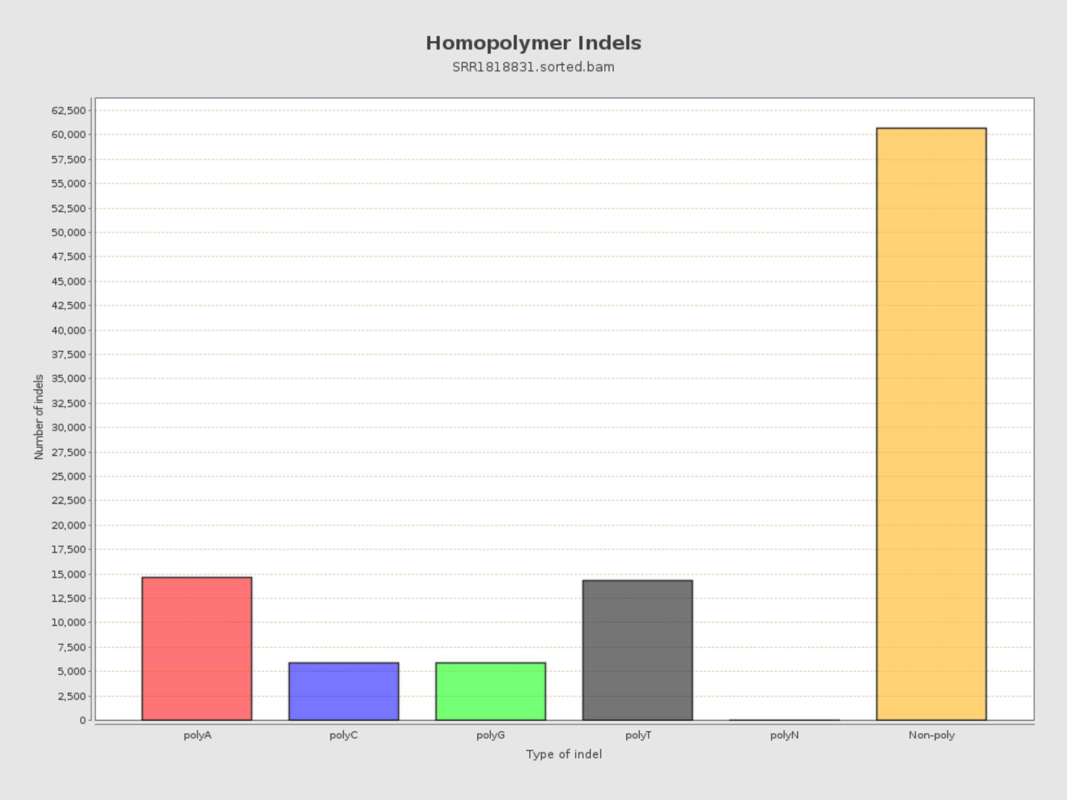
9. Results : Mapped Reads GC-content Distribution



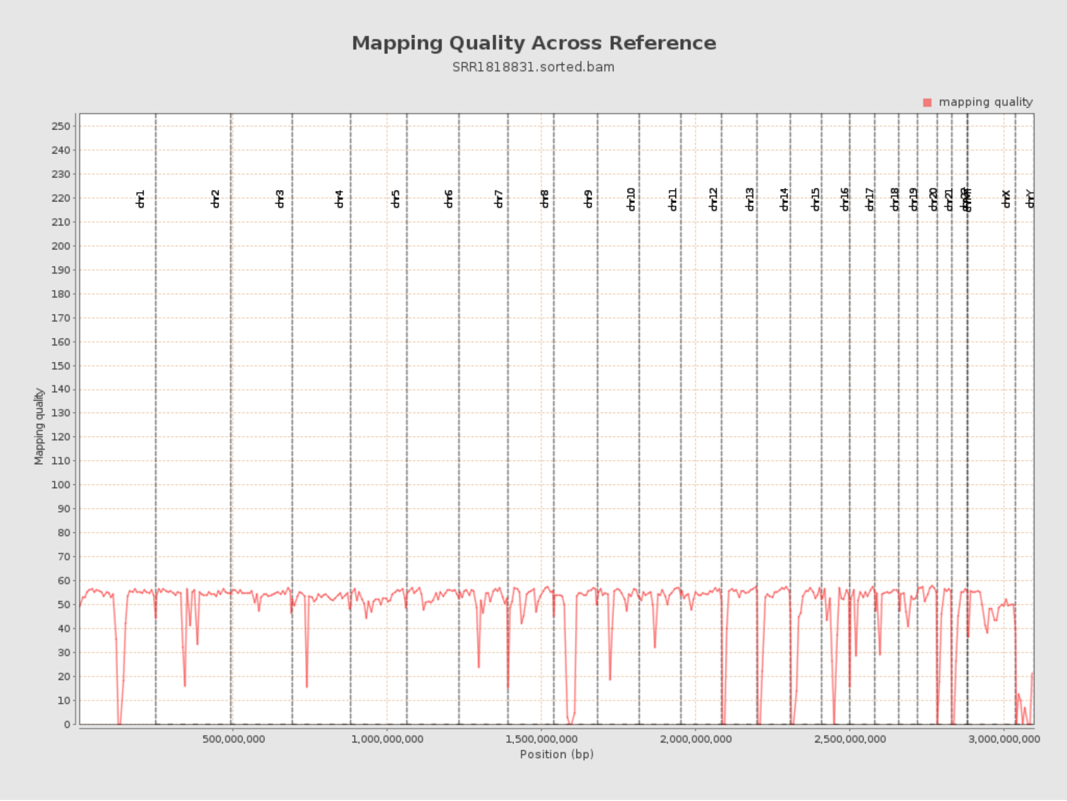
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram