Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 09:02:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818931.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_SRR1818931 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818931.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 09:02:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818931.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	696,651
Mapped reads	661,484 / 94.95%
Unmapped reads	35,167 / 5.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,063 / 1.3%
Read min/max/mean length	30 / 101 / 101.5
Duplicated reads (estimated)	166,444 / 23.89%
Duplication rate	22.07%
Clipped reads	668,077 / 95.9%

2.2. ACGT Content

Number/percentage of A's	17,867,244 / 29.17%
Number/percentage of C's	13,161,774 / 21.49%
Number/percentage of T's	17,744,813 / 28.97%
Number/percentage of G's	12,483,308 / 20.38%
Number/percentage of N's	2,821 / 0%
GC Percentage	41.86%

2.3. Coverage

Mean	0.0198

Standard Deviation	0.2611

2.4. Mapping Quality

Mean Mapping Quality	49.08

2.5. Mismatches and indels

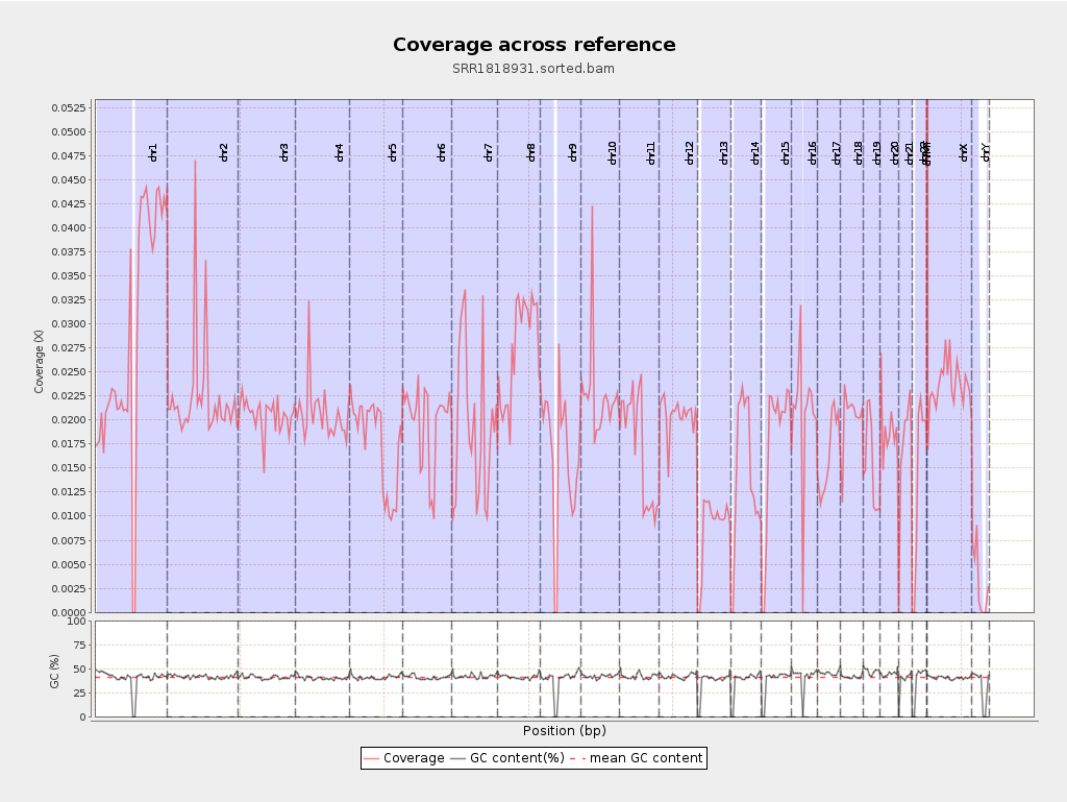
General error rate	0.66%
Mismatches	389,665
Insertions	7,831
Mapped reads with at least one insertion	1.15%
Deletions	18,129
Mapped reads with at least one deletion	2.68%
Homopolymer indels	42.62%

2.6. Chromosome stats

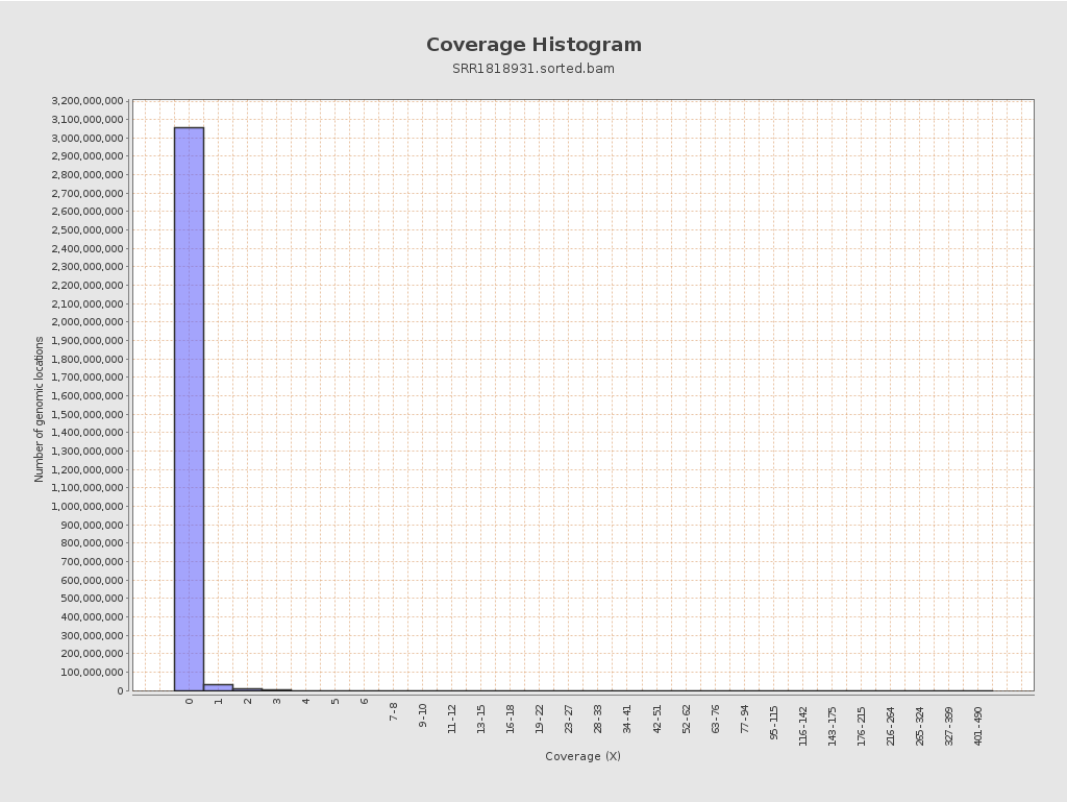
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7182513	0.0288	0.4404
chr2	243199373	5425950	0.0223	0.3532
chr3	198022430	4059651	0.0205	0.195
chr4	191154276	3945963	0.0206	0.2071
chr5	180915260	3166767	0.0175	0.1825
chr6	171115067	3364431	0.0197	0.2001
chr7	159138663	3102587	0.0195	0.2314

chr8	146364022	4018066	0.0275	0.2533
chr9	141213431	2277223	0.0161	0.2902
chr10	135534747	3064837	0.0226	0.3153
chr11	135006516	2316404	0.0172	0.1965
chr12	133851895	2747752	0.0205	0.198
chr13	115169878	1010603	0.0088	0.1255
chr14	107349540	1540383	0.0143	0.1742
chr15	102531392	1790120	0.0175	0.1789
chr16	90354753	1845844	0.0204	0.2686
chr17	81195210	1324375	0.0163	0.1874
chr18	78077248	1559441	0.02	0.3438
chr19	59128983	917950	0.0155	0.3456
chr20	63025520	1190207	0.0189	0.1959
chr21	48129895	832042	0.0173	0.1916
chr22	51304566	727690	0.0142	0.1687
chrMT	16571	23996	1.4481	1.8496
chrX	155270560	3676389	0.0237	0.2377
chrY	59373566	181880	0.0031	0.159

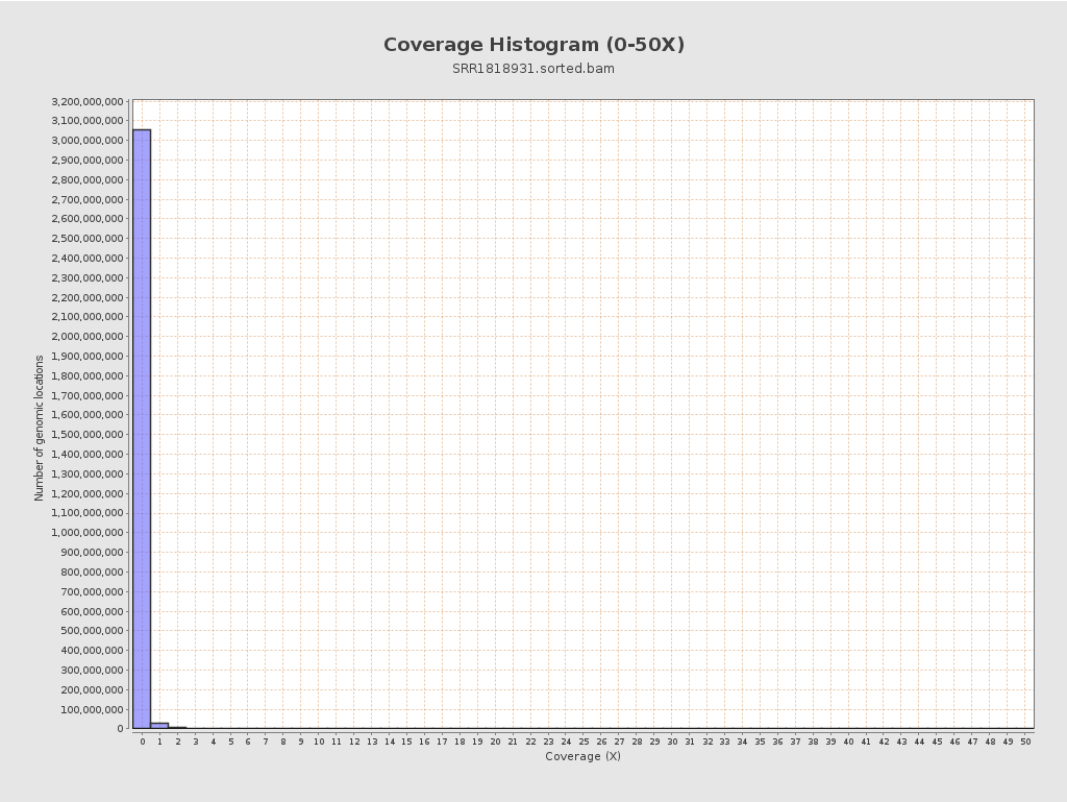
3. Results : Coverage across reference



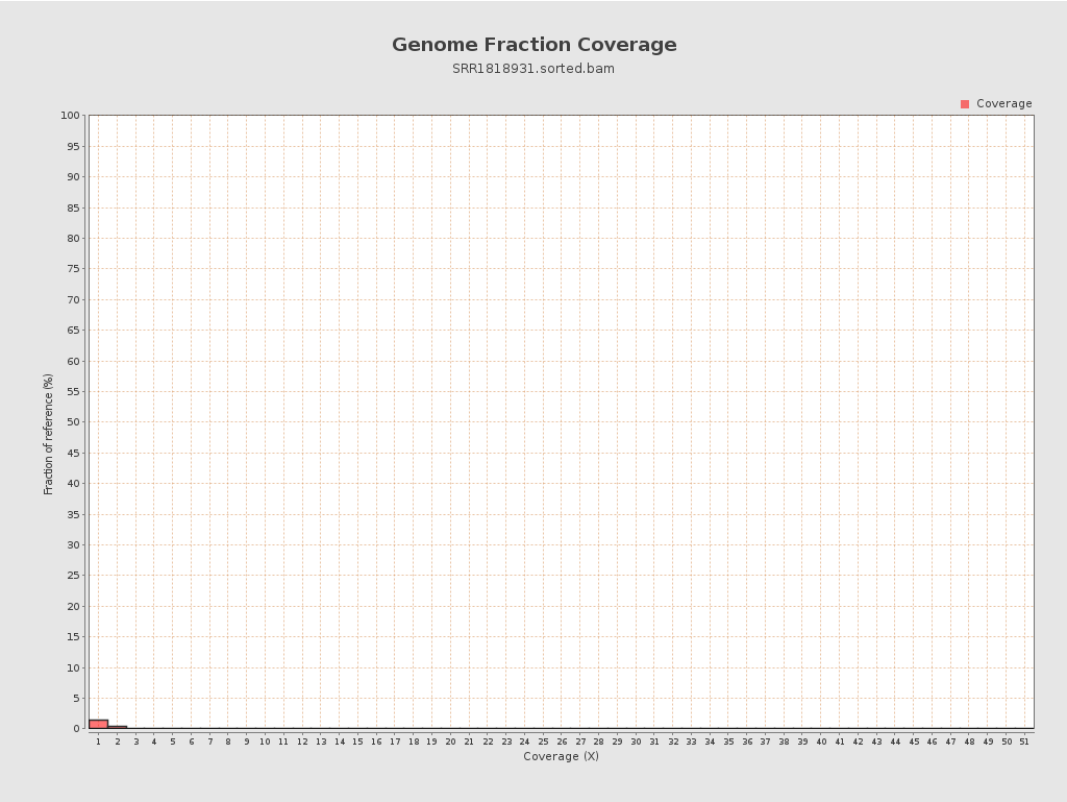
4. Results : Coverage Histogram



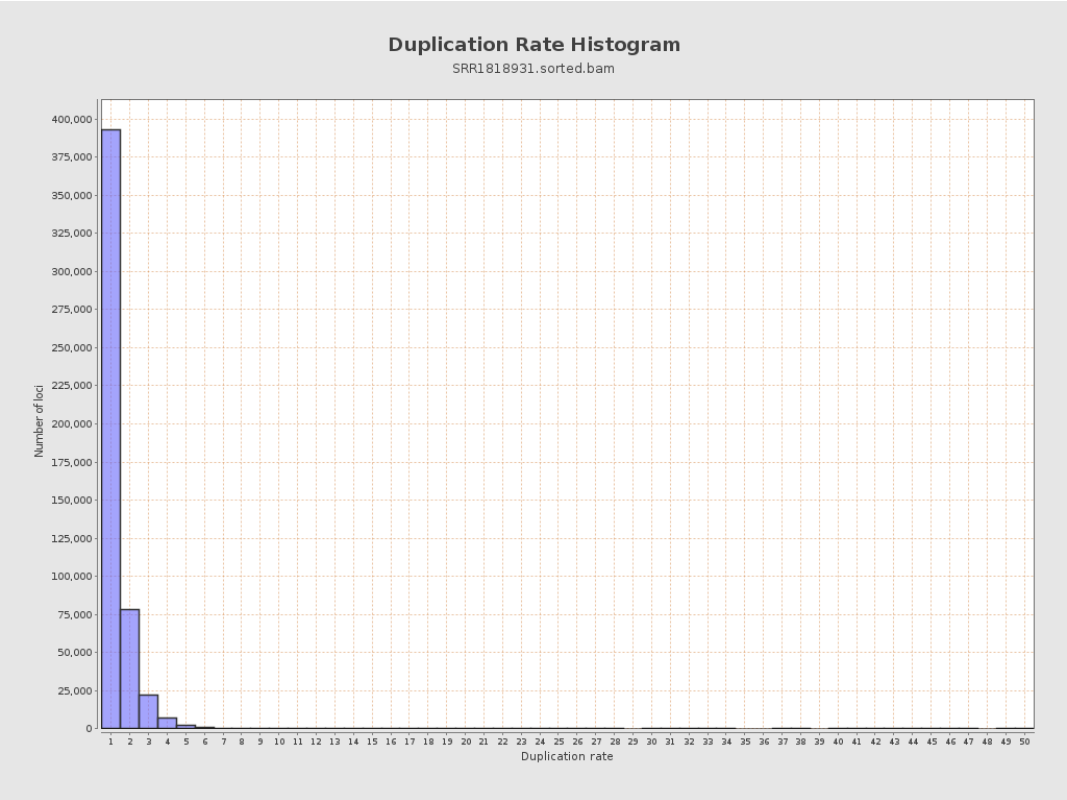
5. Results : Coverage Histogram (0-50X)



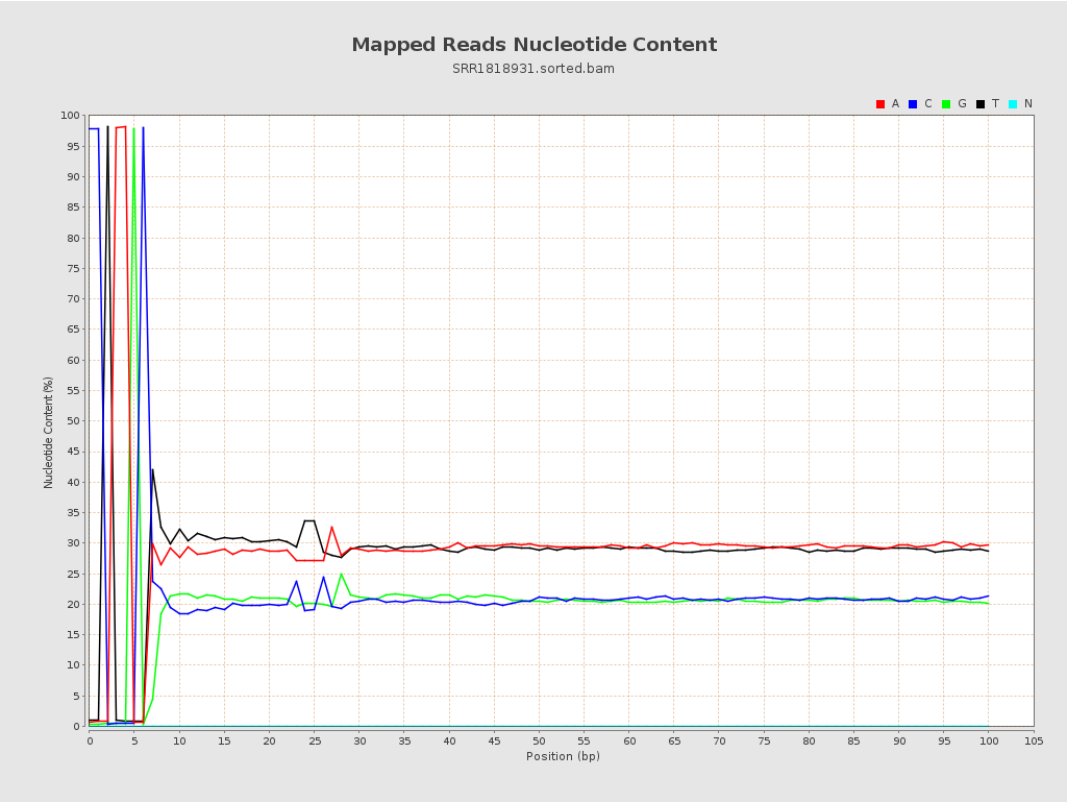
6. Results : Genome Fraction Coverage



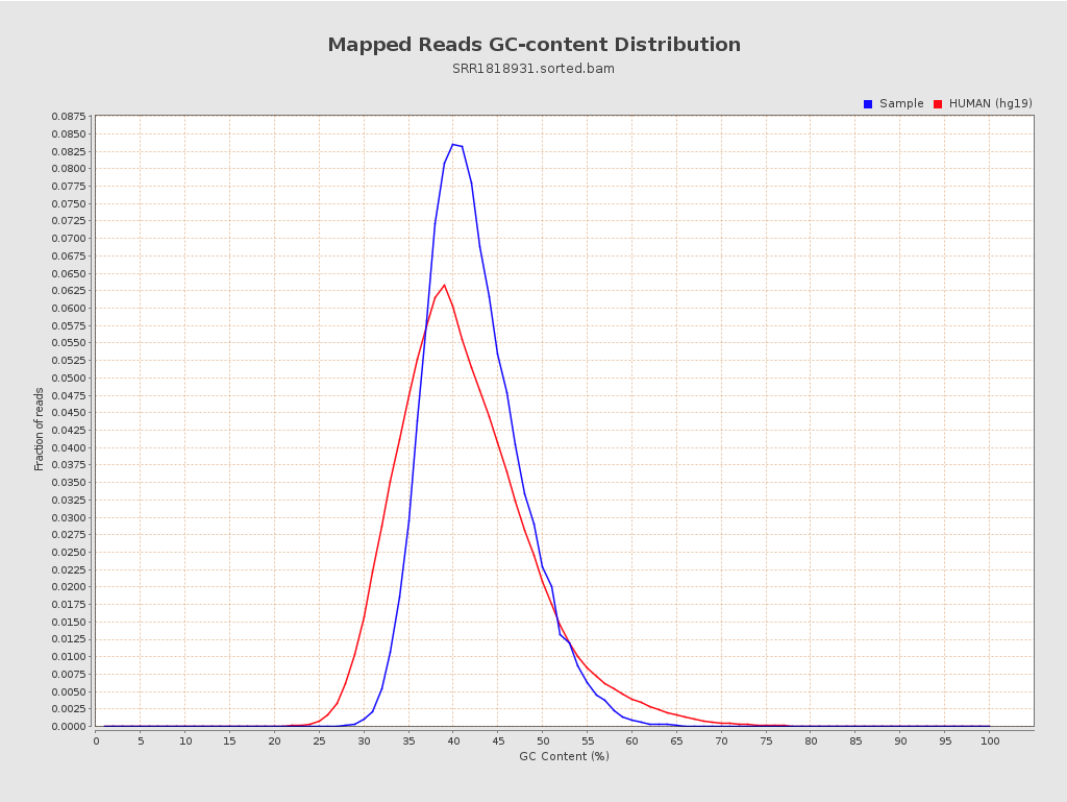
7. Results : Duplication Rate Histogram



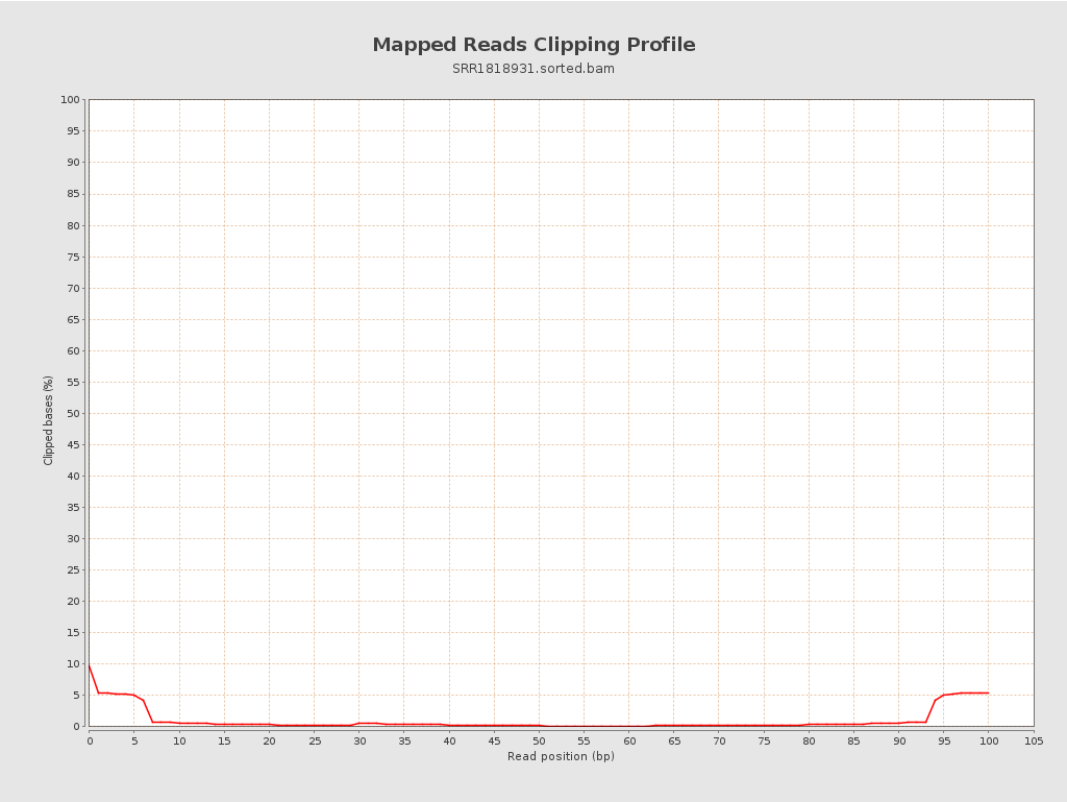
8. Results : Mapped Reads Nucleotide Content



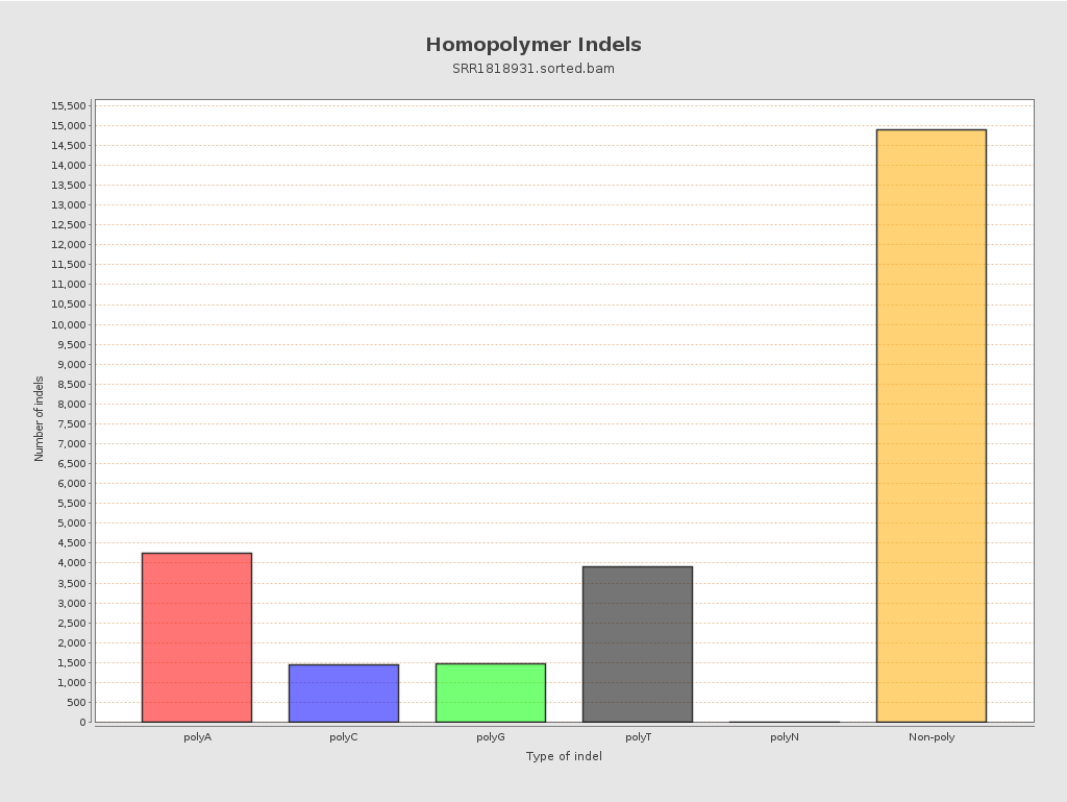
9. Results : Mapped Reads GC-content Distribution



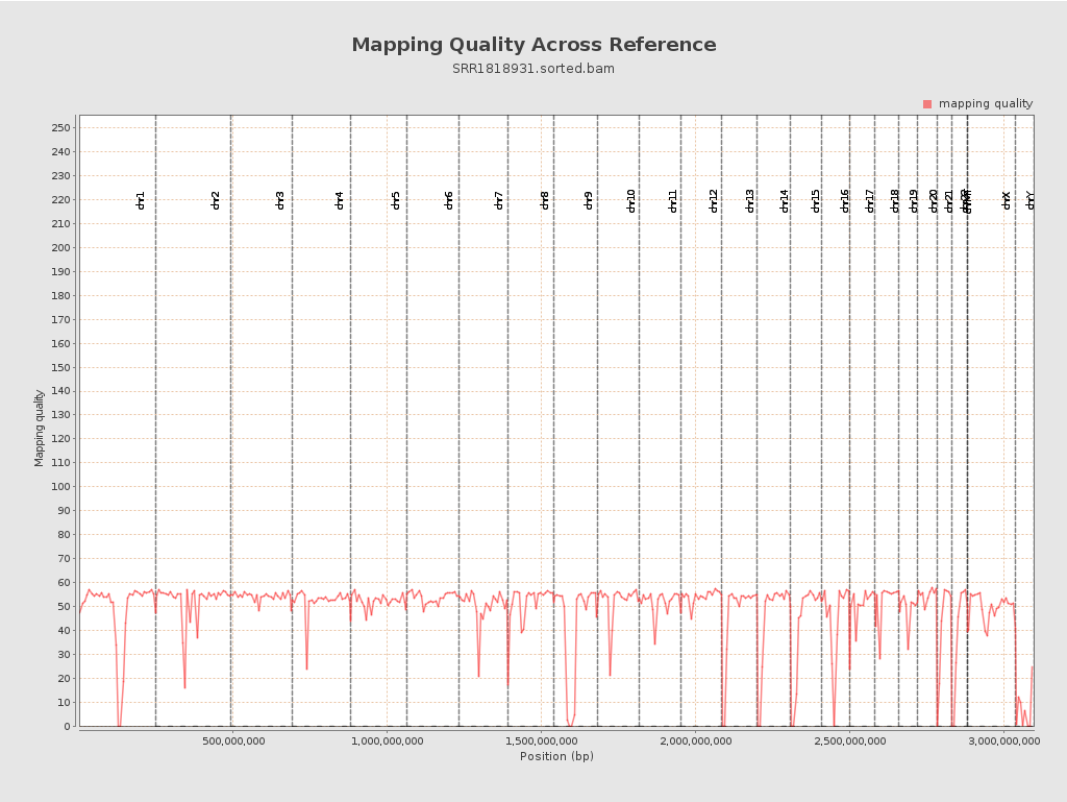
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram