Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 08:28:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231859.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_SRR6231859 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231859.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 08:28:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231859.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,158,795
Mapped reads	965,866 / 83.35%
Unmapped reads	192,929 / 16.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,286 / 0.54%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	32,028 / 2.76%
Duplication rate	2.79%
Clipped reads	425,725 / 36.74%

2.2. ACGT Content

Number/percentage of A's	18,094,605 / 28.19%
Number/percentage of C's	11,383,230 / 17.73%
Number/percentage of T's	20,953,965 / 32.64%
Number/percentage of G's	13,761,901 / 21.44%
Number/percentage of N's	3,009 / 0%
GC Percentage	39.17%

2.3. Coverage

Mean	0.0208

Standard Deviation	0.207

2.4. Mapping Quality

Mean Mapping Quality	46.31

2.5. Mismatches and indels

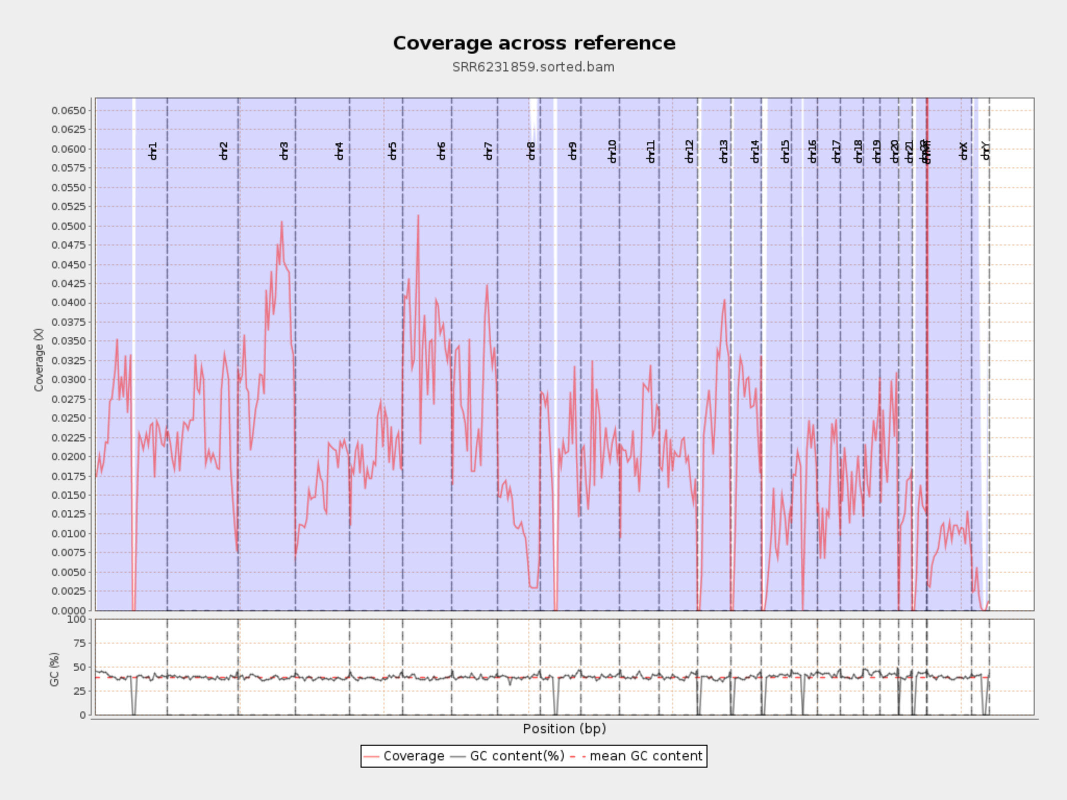
General error rate	0.77%
Mismatches	485,388
Insertions	4,713
Mapped reads with at least one insertion	0.48%
Deletions	22,776
Mapped reads with at least one deletion	2.33%
Homopolymer indels	45.3%

2.6. Chromosome stats

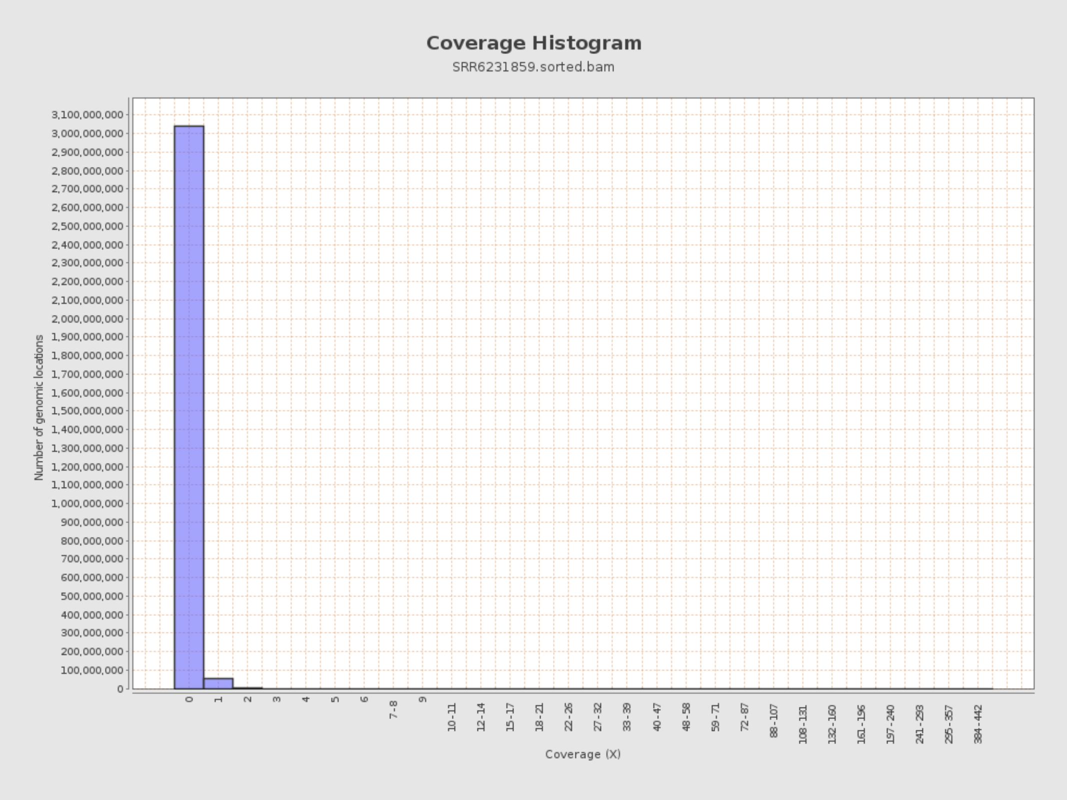
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5633858	0.0226	0.3239
chr2	243199373	5602592	0.023	0.2269
chr3	198022430	6996152	0.0353	0.2046
chr4	191154276	3142201	0.0164	0.1419
chr5	180915260	3728896	0.0206	0.1558
chr6	171115067	6111541	0.0357	0.2403
chr7	159138663	4477911	0.0281	0.2926

chr8	146364022	1523544	0.0104	0.2842
chr9	141213431	2877714	0.0204	0.1763
chr10	135534747	2869845	0.0212	0.2137
chr11	135006516	3070555	0.0227	0.1783
chr12	133851895	2575879	0.0192	0.1521
chr13	115169878	2880212	0.025	0.1732
chr14	107349540	2459809	0.0229	0.17
chr15	102531392	873735	0.0085	0.1001
chr16	90354753	1571044	0.0174	0.1489
chr17	81195210	1229215	0.0151	0.1354
chr18	78077248	1276048	0.0163	0.2445
chr19	59128983	1232173	0.0208	0.2223
chr20	63025520	1423025	0.0226	0.166
chr21	48129895	627377	0.013	0.1257
chr22	51304566	496520	0.0097	0.1051
chrMT	16571	42660	2.5744	2.5129
chrX	155270560	1410430	0.0091	0.1096
chrY	59373566	103187	0.0017	0.0519

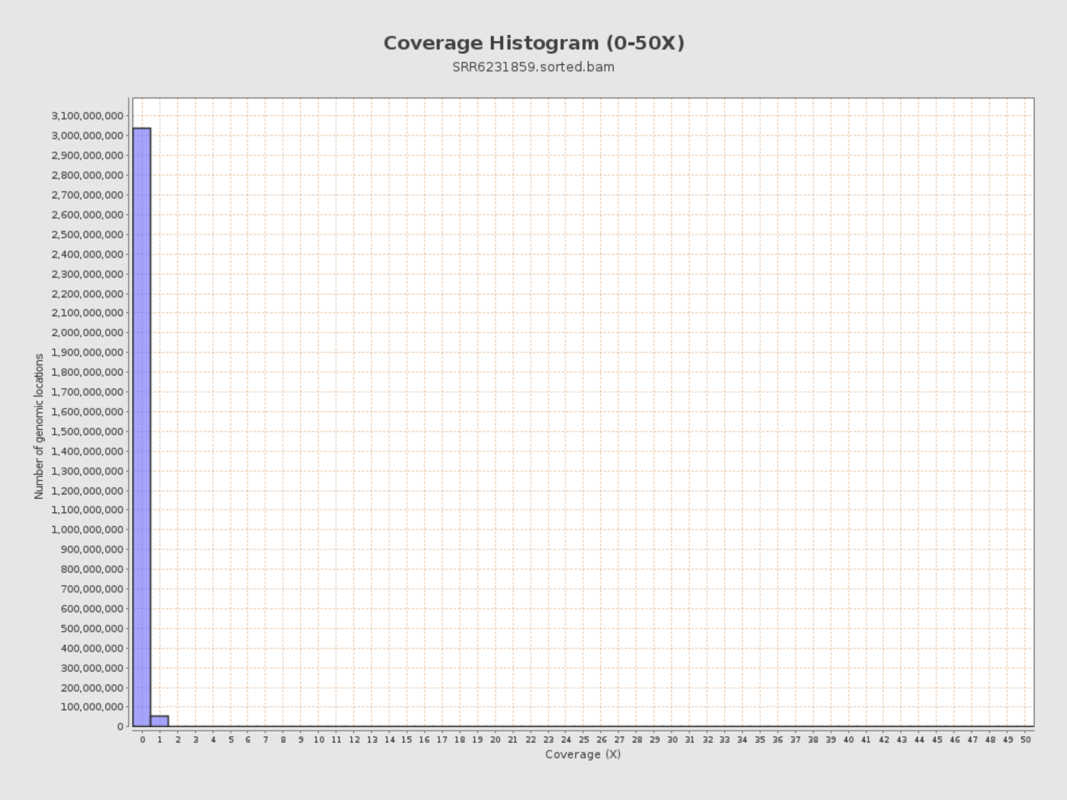
3. Results : Coverage across reference



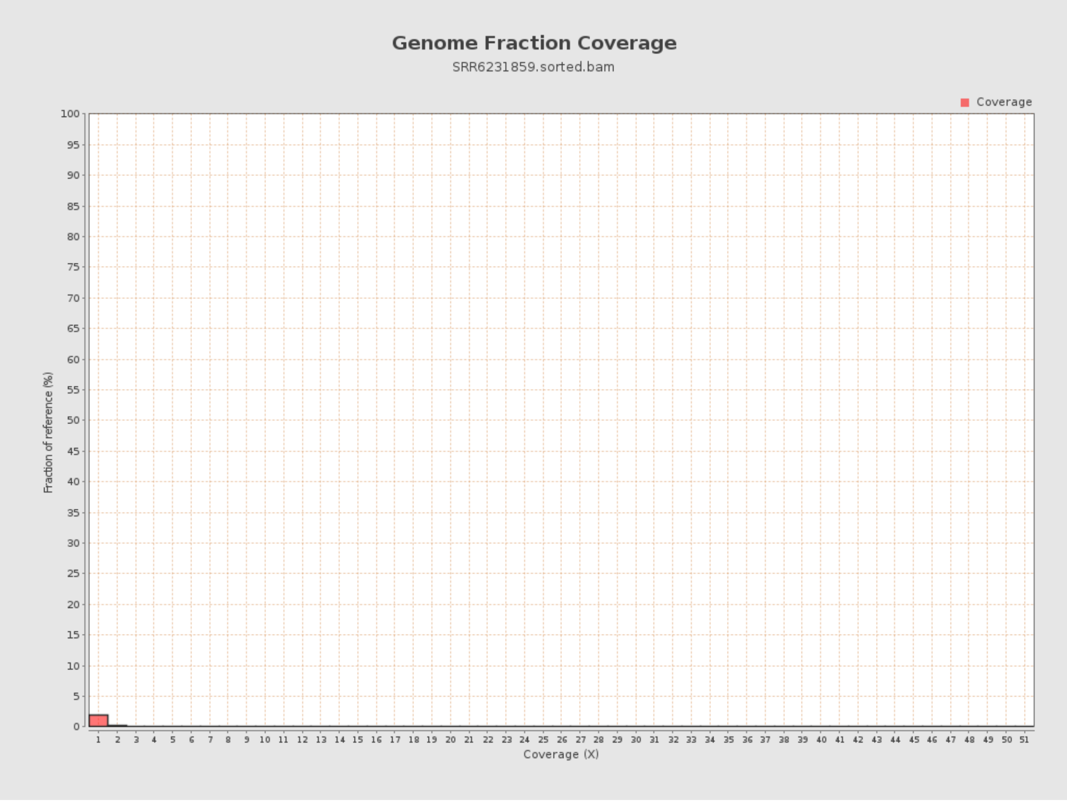
4. Results : Coverage Histogram



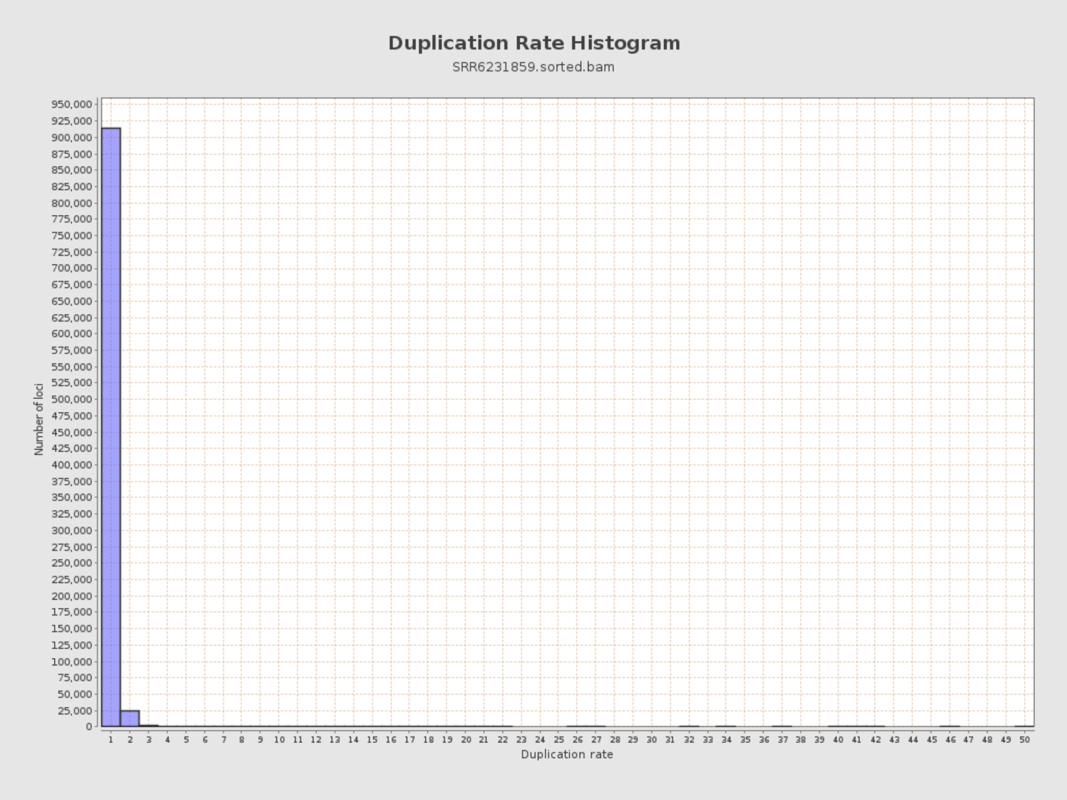
5. Results : Coverage Histogram (0-50X)



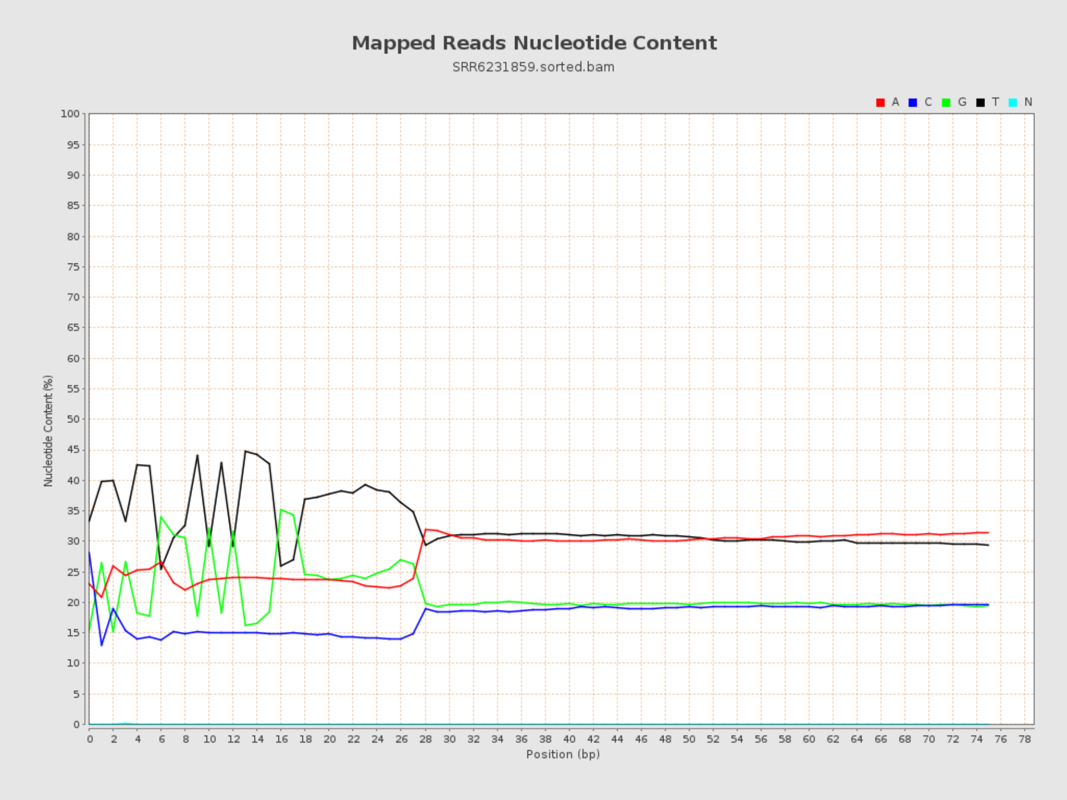
6. Results : Genome Fraction Coverage



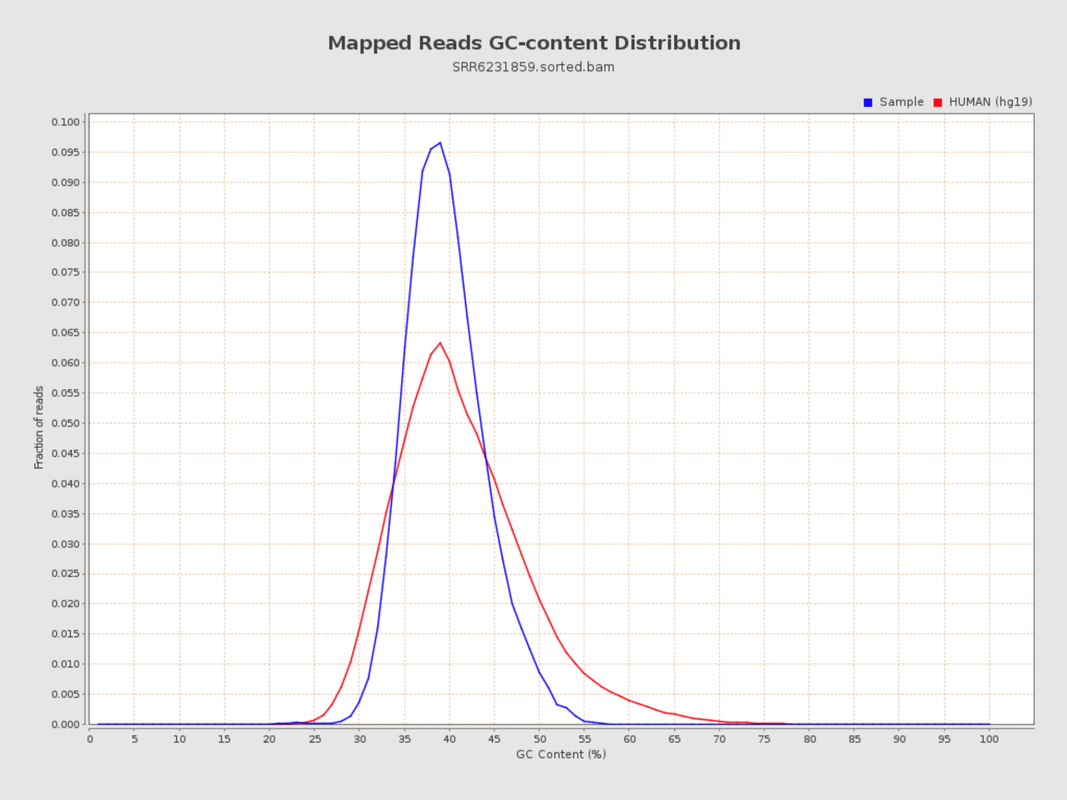
7. Results : Duplication Rate Histogram



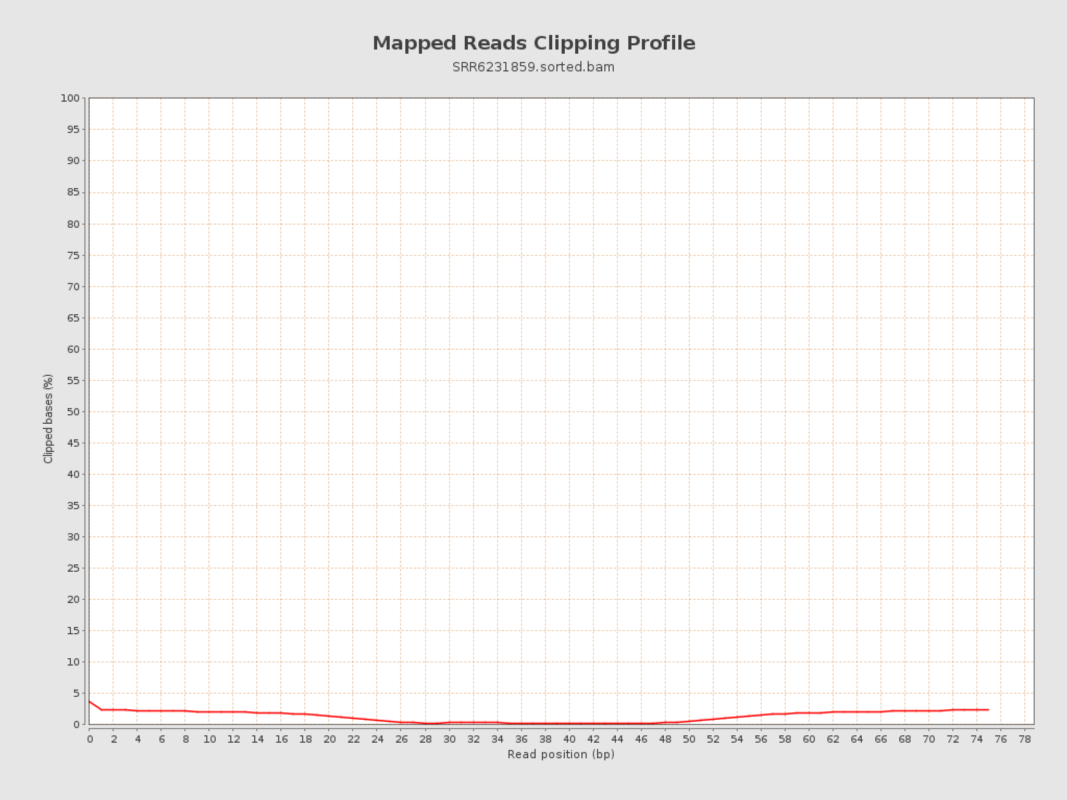
8. Results : Mapped Reads Nucleotide Content



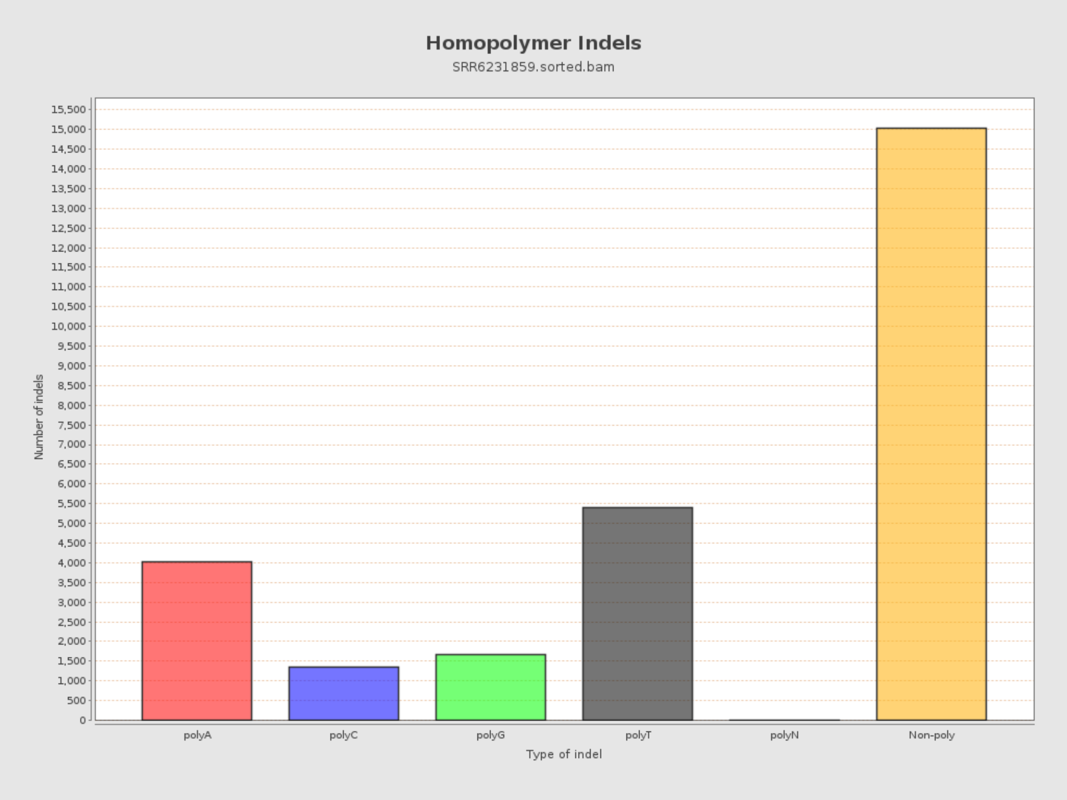
9. Results : Mapped Reads GC-content Distribution



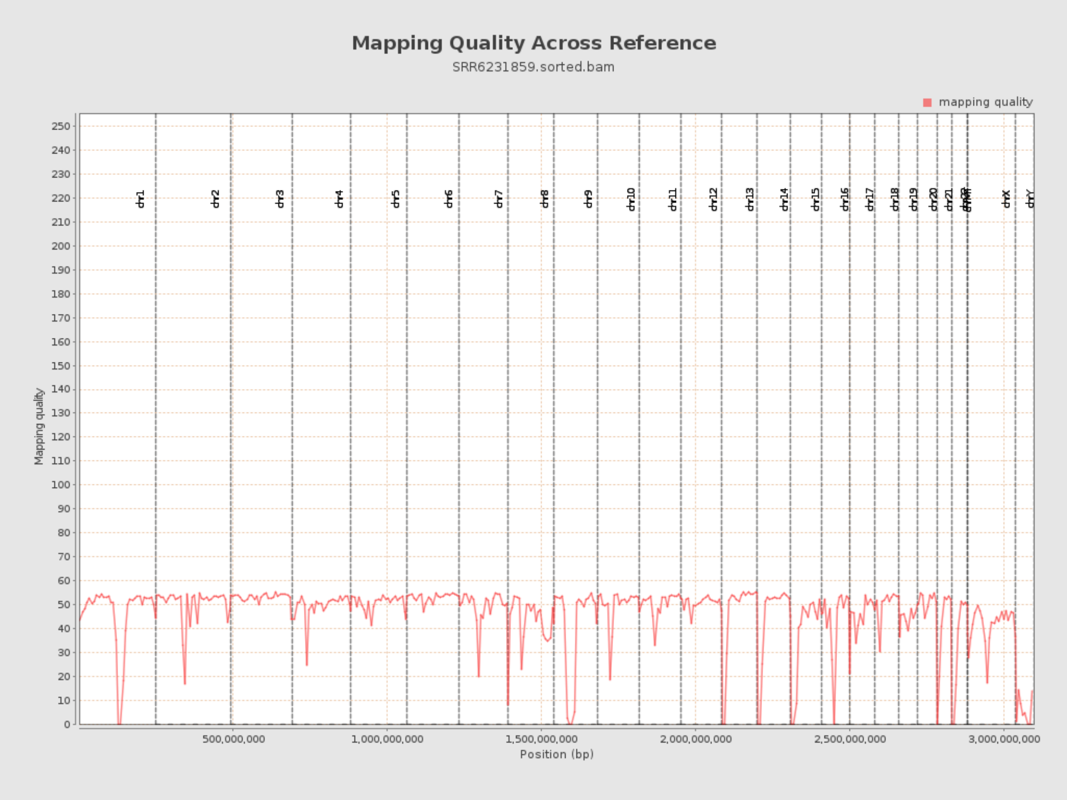
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram