Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 02:33:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083658.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_SRR3083658 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083658.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 02:33:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083658.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,231,378
Mapped reads	1,853,587 / 83.07%
Unmapped reads	377,791 / 16.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,916 / 0.62%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	57,653 / 2.58%
Duplication rate	2.4%
Clipped reads	1,245,150 / 55.8%

2.2. ACGT Content

Number/percentage of A's	33,232,253 / 29.45%
Number/percentage of C's	21,999,532 / 19.5%
Number/percentage of T's	33,241,868 / 29.46%
Number/percentage of G's	24,341,868 / 21.57%
Number/percentage of N's	15,930 / 0.01%
GC Percentage	41.07%

2.3. Coverage

Mean	0.0365

Standard Deviation	0.3866

2.4. Mapping Quality

Mean Mapping Quality	45.34

2.5. Mismatches and indels

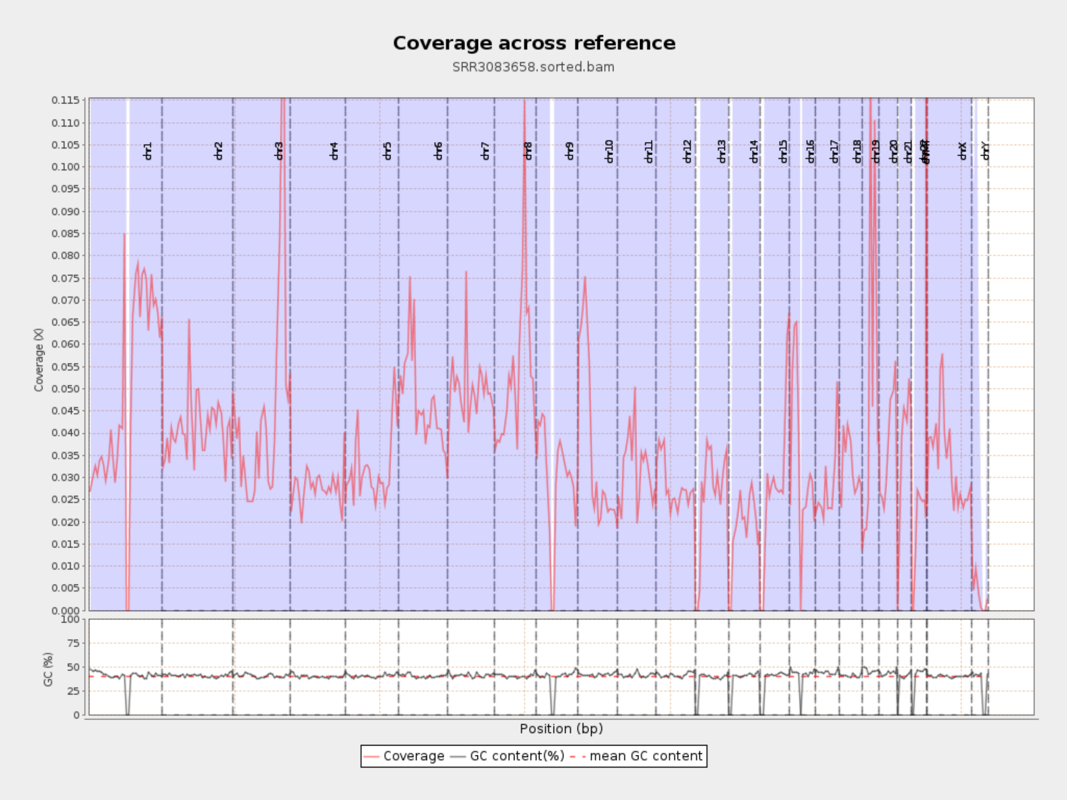
General error rate	0.83%
Mismatches	921,505
Insertions	8,046
Mapped reads with at least one insertion	0.43%
Deletions	23,223
Mapped reads with at least one deletion	1.24%
Homopolymer indels	45.56%

2.6. Chromosome stats

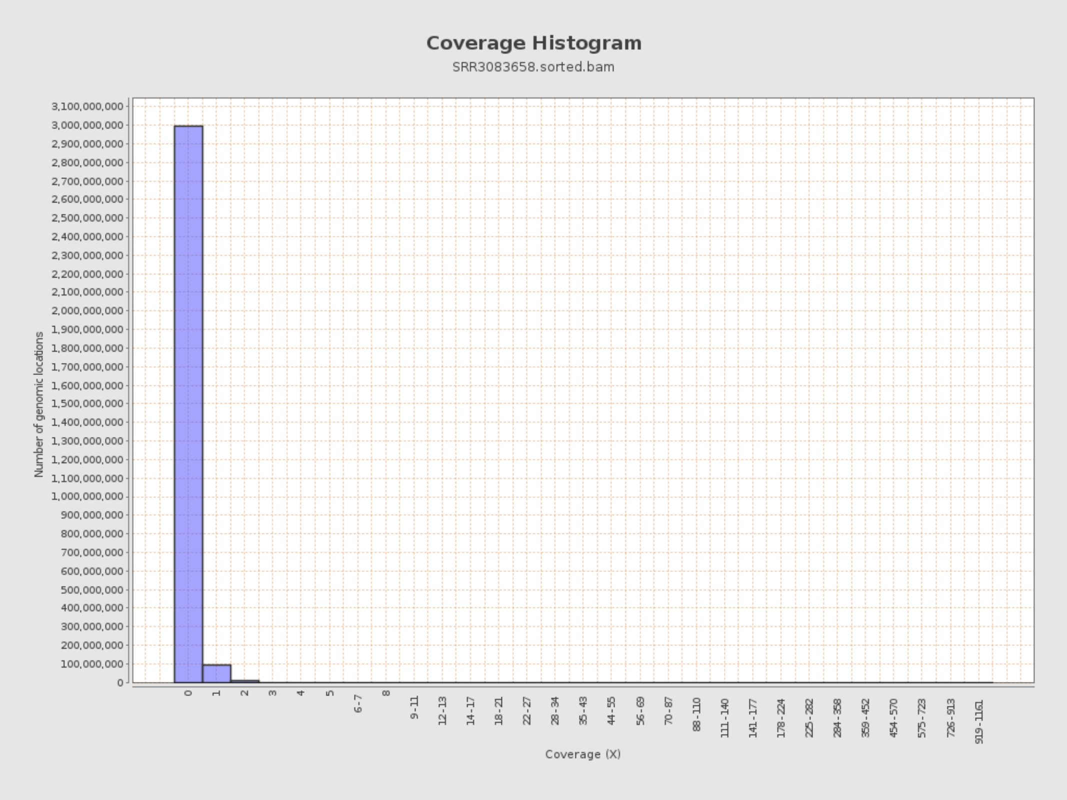
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12136061	0.0487	0.996
chr2	243199373	9996839	0.0411	0.2719
chr3	198022430	8982794	0.0454	0.2318
chr4	191154276	5298912	0.0277	0.1818
chr5	180915260	5864189	0.0324	0.1961
chr6	171115067	8111681	0.0474	0.2834
chr7	159138663	7990610	0.0502	0.5274

chr8	146364022	7843560	0.0536	0.4073
chr9	141213431	4191798	0.0297	0.2147
chr10	135534747	5098689	0.0376	0.2746
chr11	135006516	4301479	0.0319	0.2186
chr12	133851895	3752075	0.028	0.1824
chr13	115169878	2956923	0.0257	0.1719
chr14	107349540	2015786	0.0188	0.1503
chr15	102531392	2874550	0.028	0.1814
chr16	90354753	3047789	0.0337	0.2042
chr17	81195210	2340943	0.0288	0.19
chr18	78077248	2521117	0.0323	0.3491
chr19	59128983	3087739	0.0522	0.6484
chr20	63025520	2334265	0.037	0.2124
chr21	48129895	1766141	0.0367	0.2101
chr22	51304566	924948	0.018	0.1434
chrMT	16571	8250	0.4979	0.7086
chrX	155270560	5217338	0.0336	0.2079
chrY	59373566	203551	0.0034	0.0722

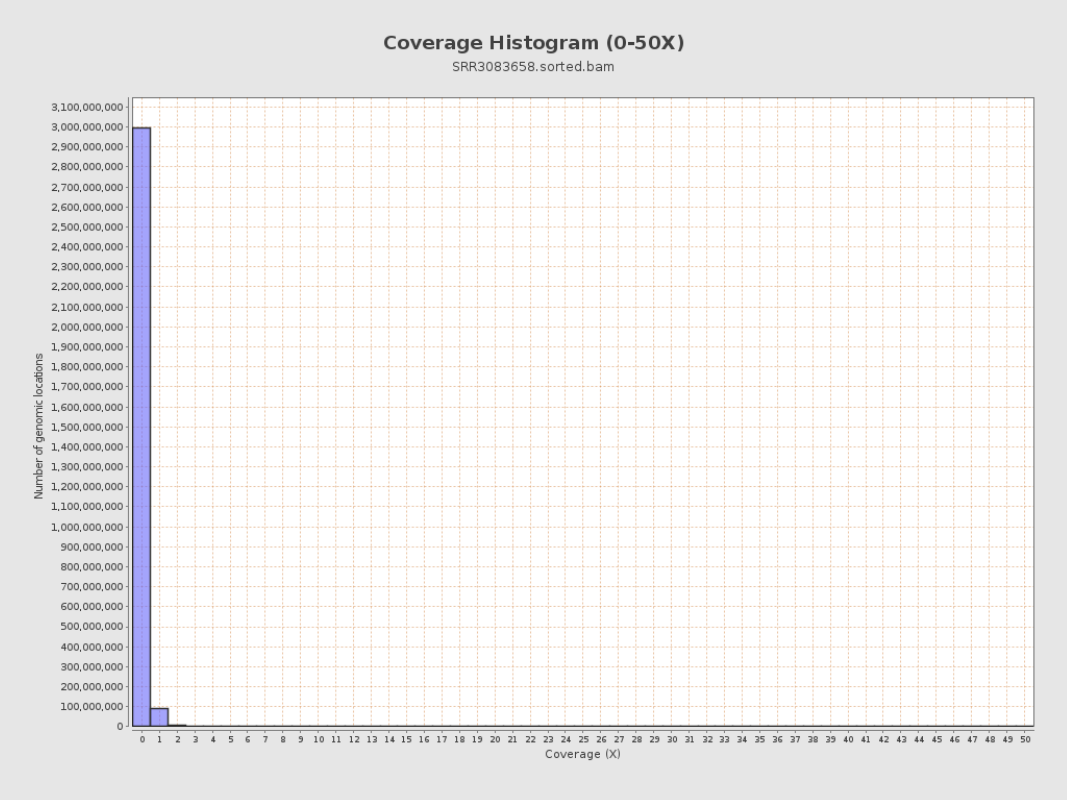
3. Results : Coverage across reference



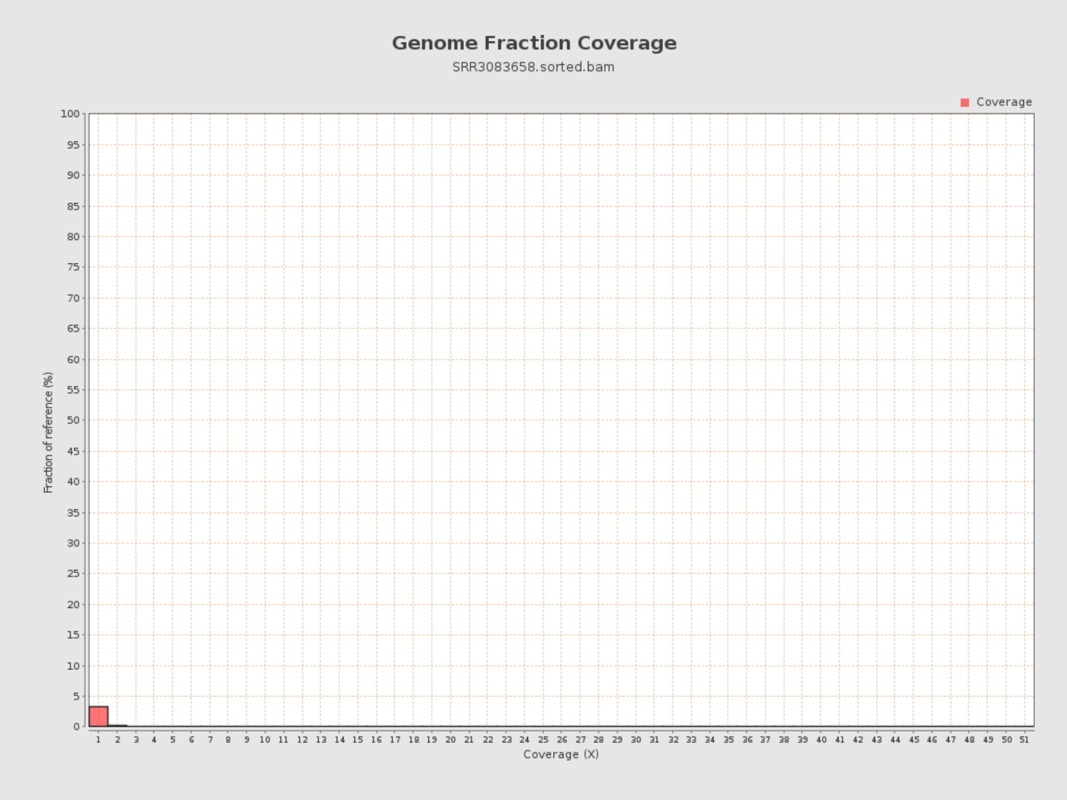
4. Results : Coverage Histogram



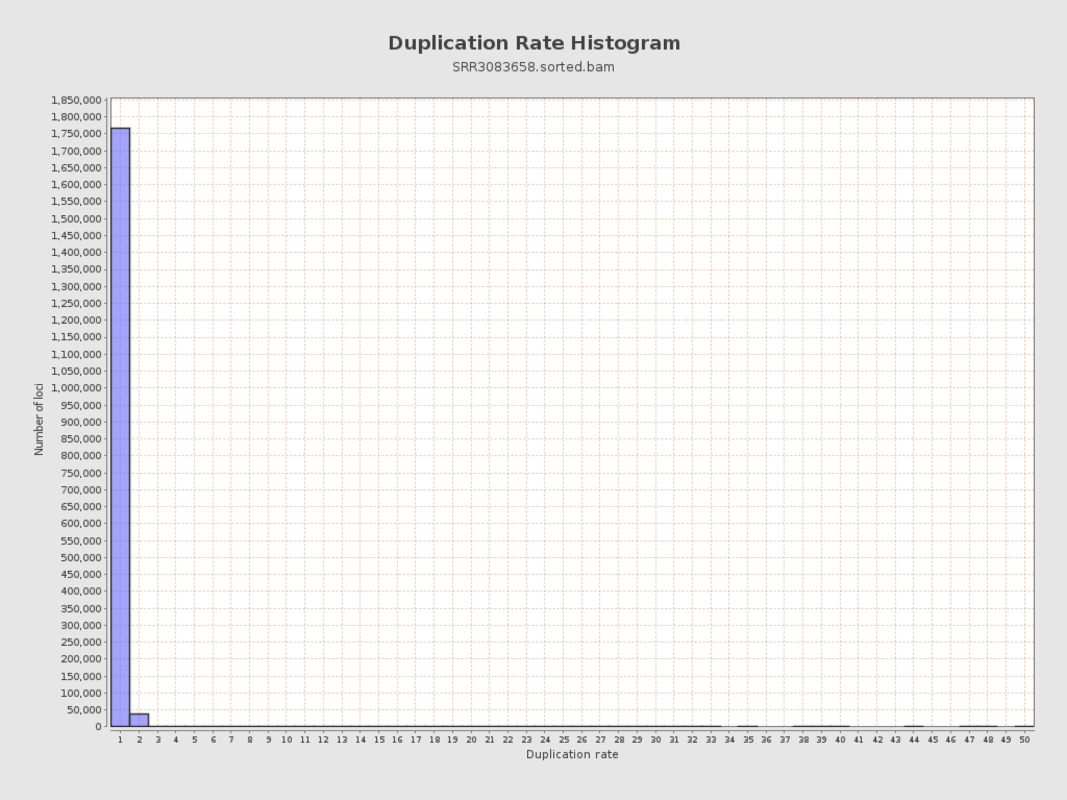
5. Results : Coverage Histogram (0-50X)



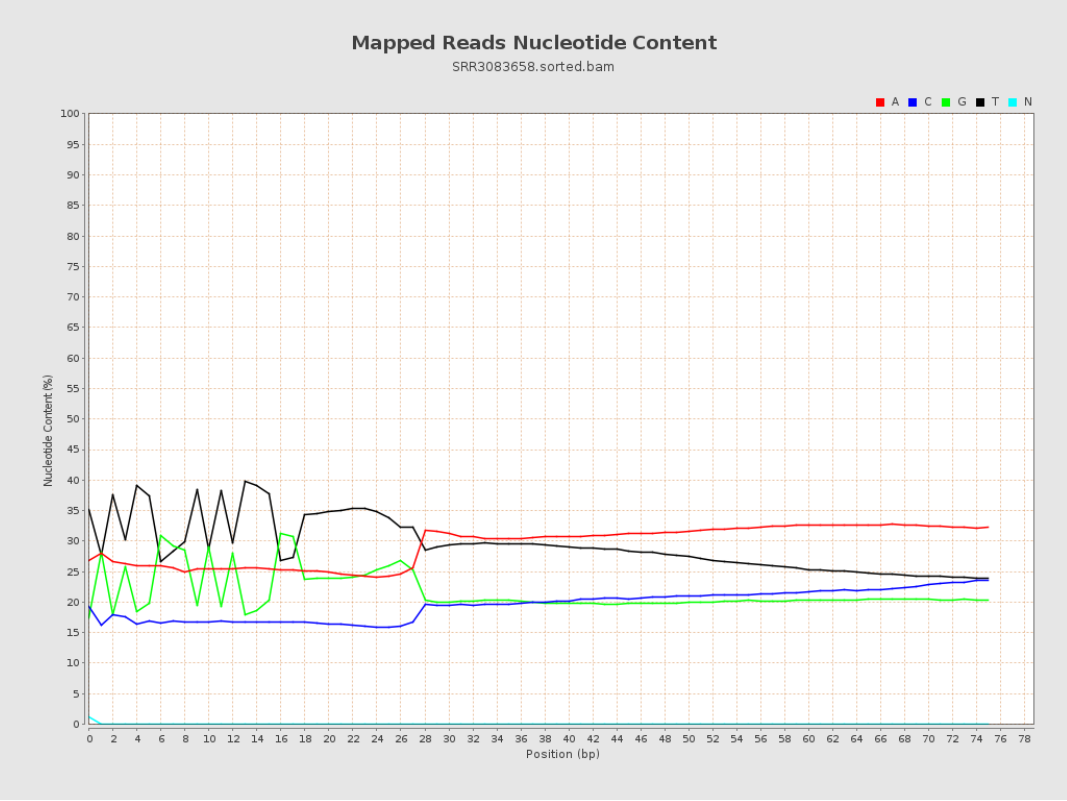
6. Results : Genome Fraction Coverage



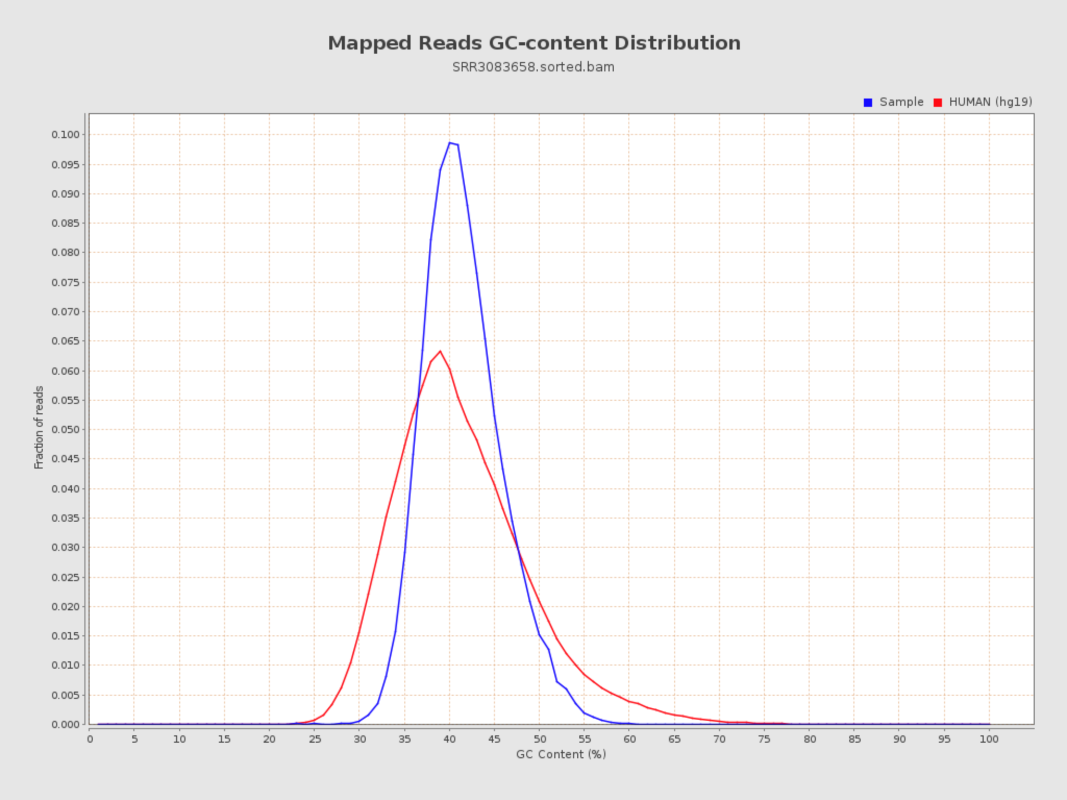
7. Results : Duplication Rate Histogram



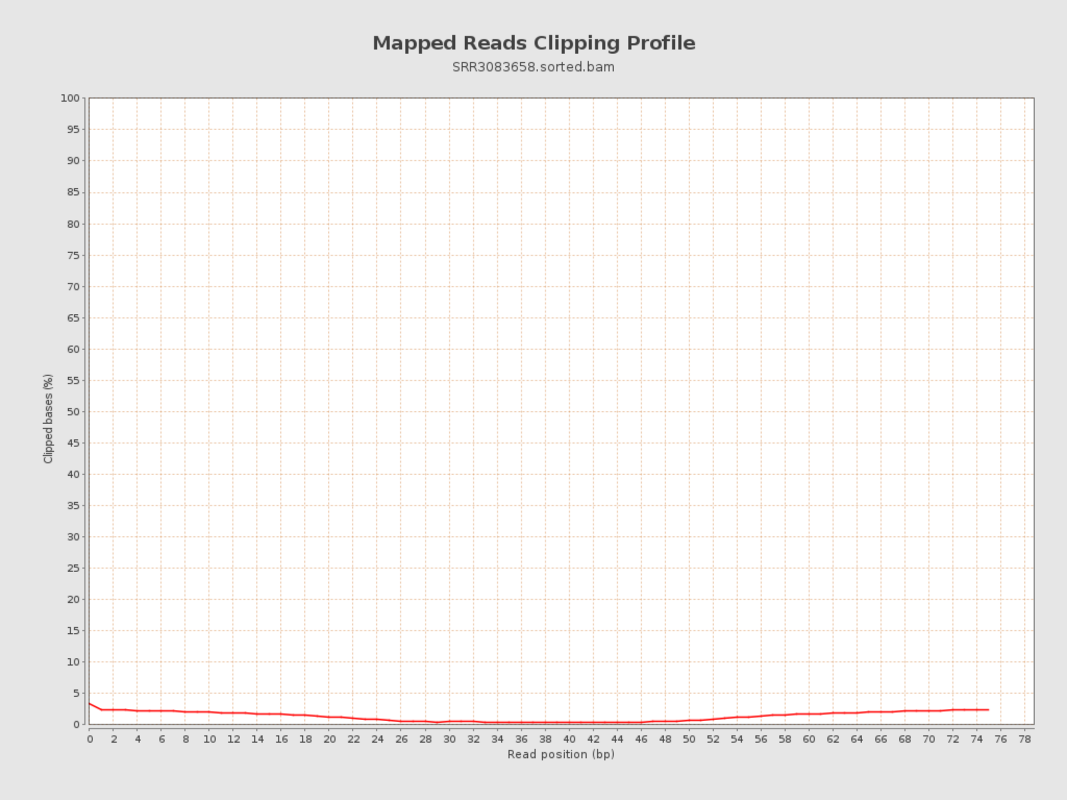
8. Results : Mapped Reads Nucleotide Content



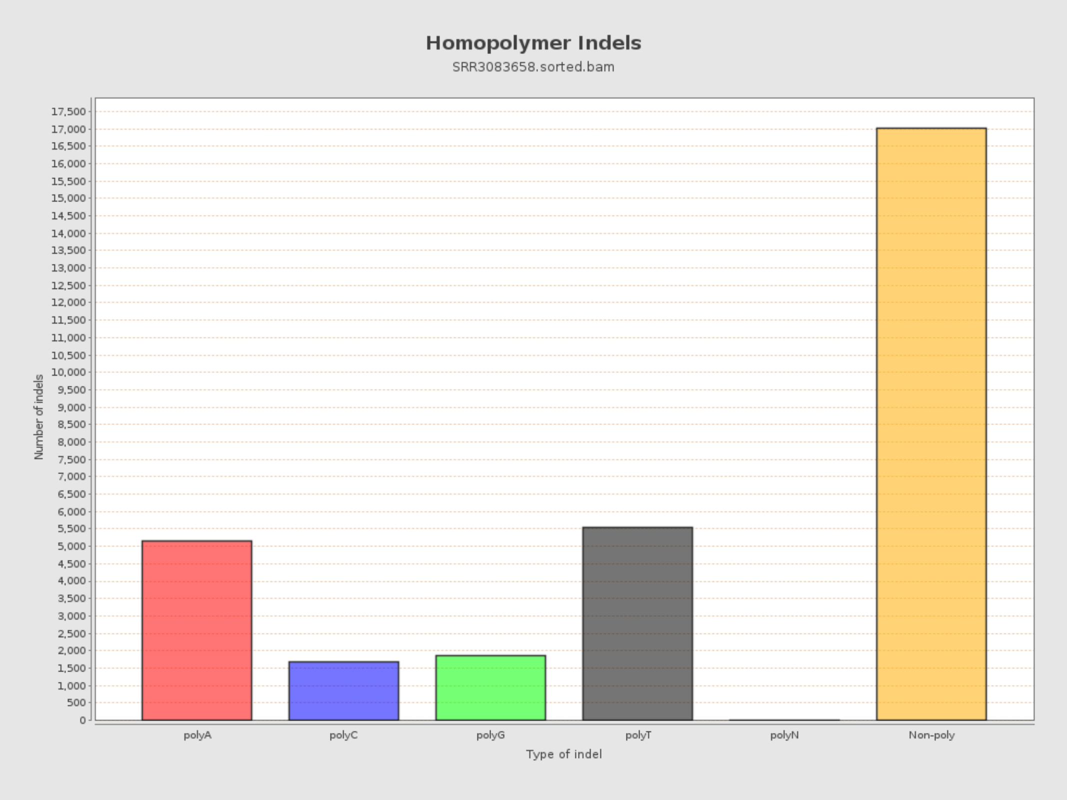
9. Results : Mapped Reads GC-content Distribution



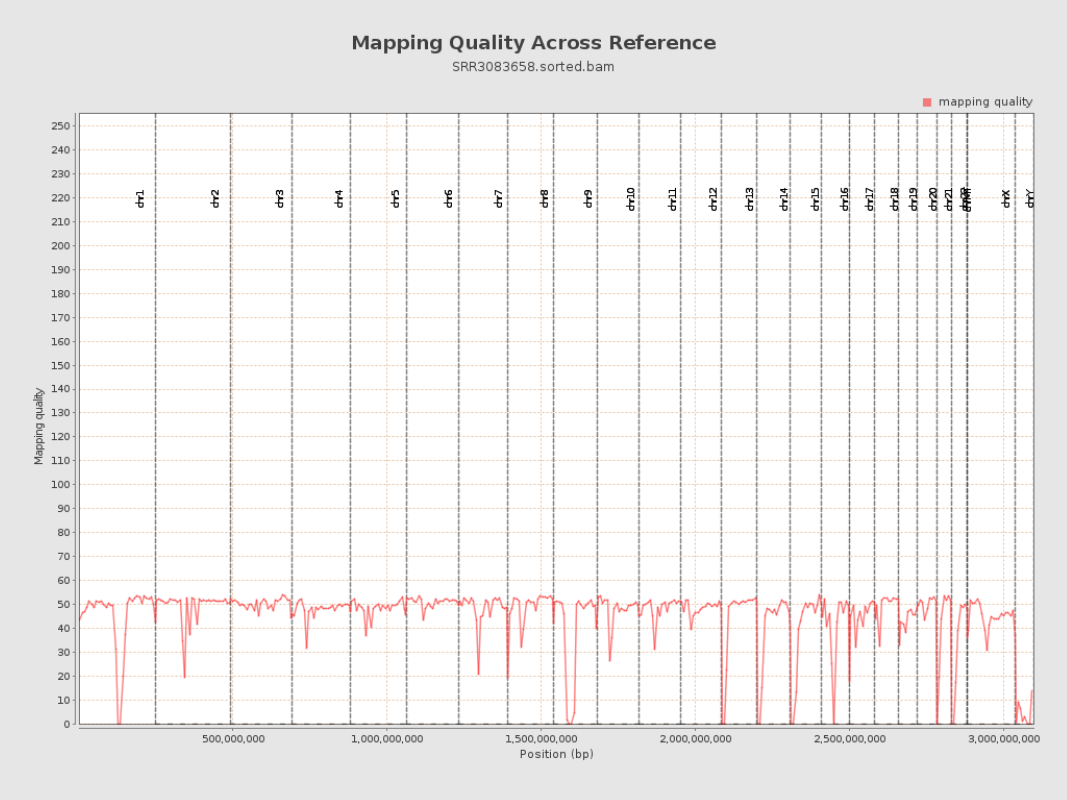
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram