Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 11:10:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10251062.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_SRR10251062 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10251062.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 11:10:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10251062.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,472,814
Mapped reads	3,370,898 / 97.07%
Unmapped reads	101,916 / 2.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	31,291 / 0.9%
Read min/max/mean length	30 / 80 / 80.32
Duplicated reads (estimated)	727,578 / 20.95%
Duplication rate	19.37%
Clipped reads	457,979 / 13.19%

2.2. ACGT Content

Number/percentage of A's	76,725,057 / 29.27%
Number/percentage of C's	52,500,380 / 20.03%
Number/percentage of T's	77,495,117 / 29.56%
Number/percentage of G's	55,406,250 / 21.14%
Number/percentage of N's	21,360 / 0.01%
GC Percentage	41.16%

2.3. Coverage

Mean	0.0847

Standard Deviation	0.7787

2.4. Mapping Quality

Mean Mapping Quality	48.29

2.5. Mismatches and indels

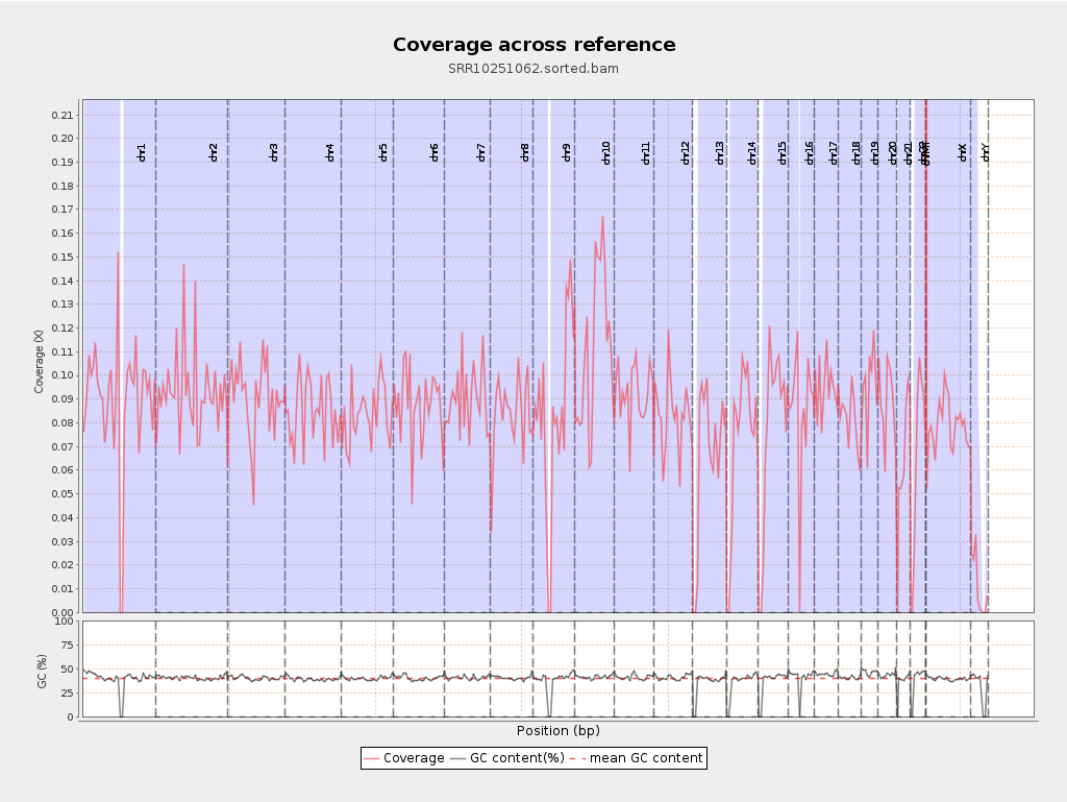
General error rate	0.58%
Mismatches	1,464,717
Insertions	32,679
Mapped reads with at least one insertion	0.95%
Deletions	88,472
Mapped reads with at least one deletion	2.58%
Homopolymer indels	46.34%

2.6. Chromosome stats

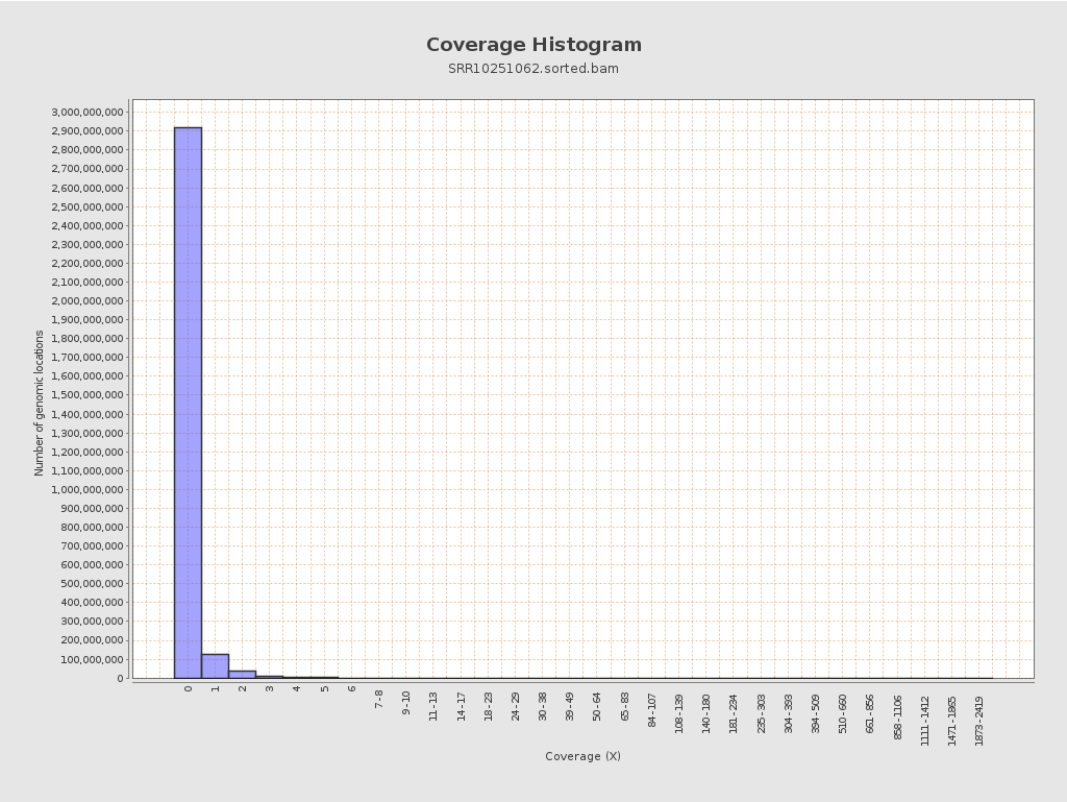
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	22272725	0.0894	1.6502
chr2	243199373	22741281	0.0935	0.9687
chr3	198022430	17909899	0.0904	0.4171
chr4	191154276	16268740	0.0851	0.4585
chr5	180915260	15208610	0.0841	0.4117
chr6	171115067	14995643	0.0876	0.4692
chr7	159138663	14284691	0.0898	0.9449

chr8	146364022	12236517	0.0836	0.56
chr9	141213431	11859072	0.084	0.7982
chr10	135534747	15070706	0.1112	0.8183
chr11	135006516	12463966	0.0923	0.512
chr12	133851895	11284229	0.0843	0.4111
chr13	115169878	7618002	0.0661	0.3529
chr14	107349540	7887768	0.0735	0.5247
chr15	102531392	7699524	0.0751	0.3783
chr16	90354753	7590319	0.084	0.6294
chr17	81195210	7756286	0.0955	0.4886
chr18	78077248	6370021	0.0816	0.8901
chr19	59128983	5614316	0.095	1.5044
chr20	63025520	5554830	0.0881	0.4398
chr21	48129895	3142905	0.0653	0.3835
chr22	51304566	3335769	0.065	0.3704
chrMT	16571	258272	15.5858	9.3844
chrX	155270560	12221534	0.0787	0.4296
chrY	59373566	658684	0.0111	0.712

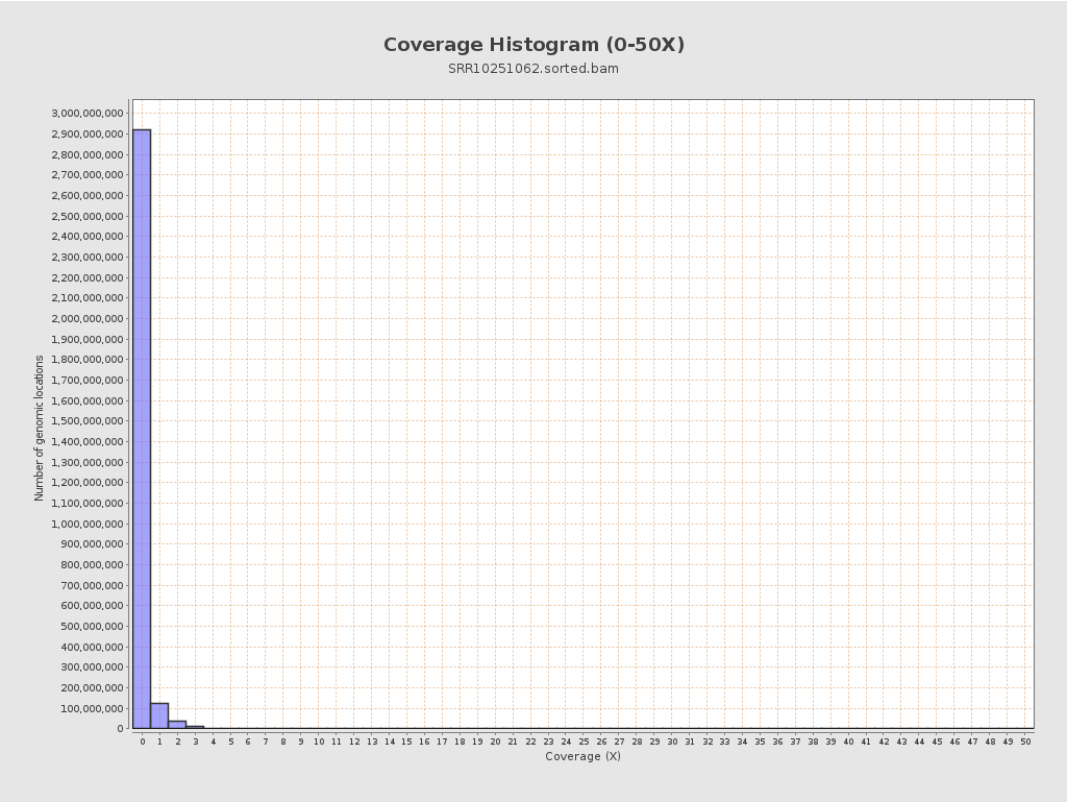
3. Results : Coverage across reference



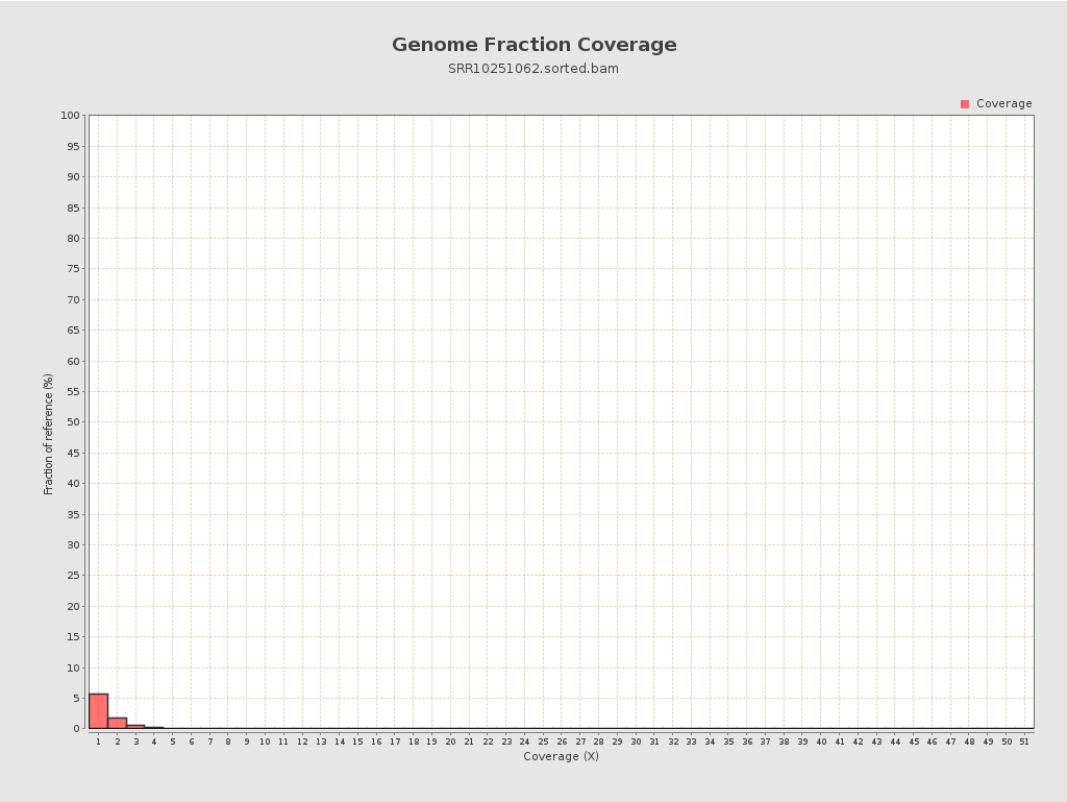
4. Results : Coverage Histogram



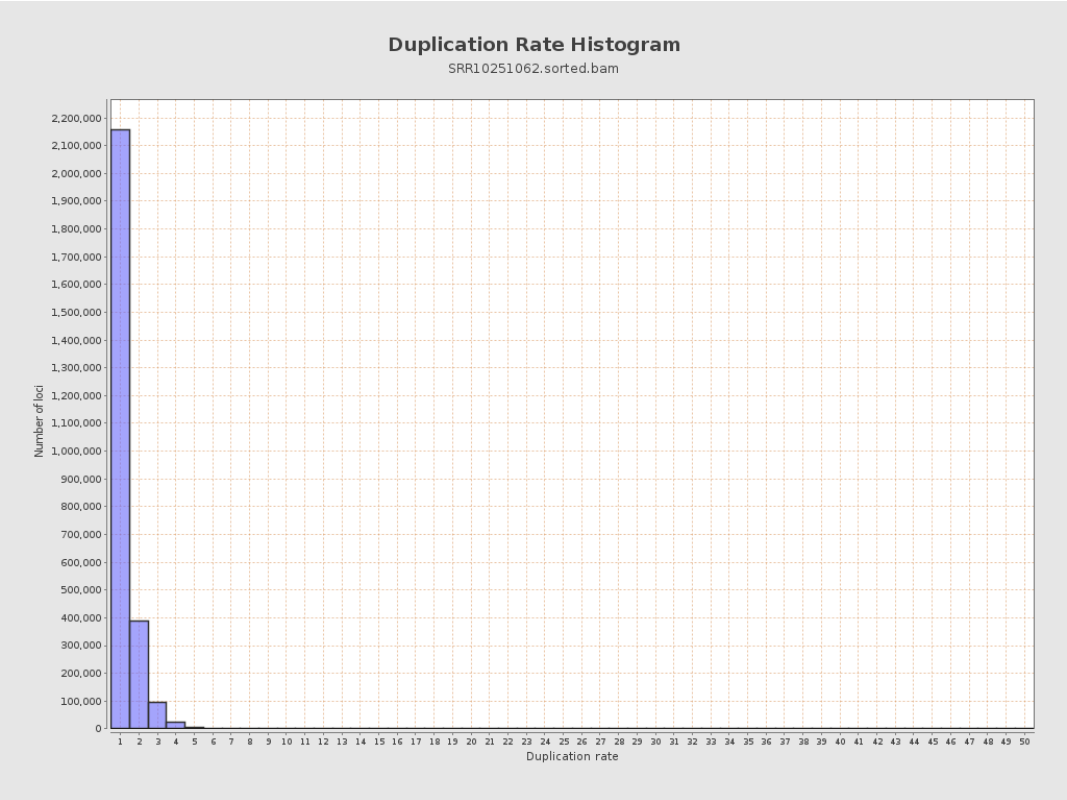
5. Results : Coverage Histogram (0-50X)



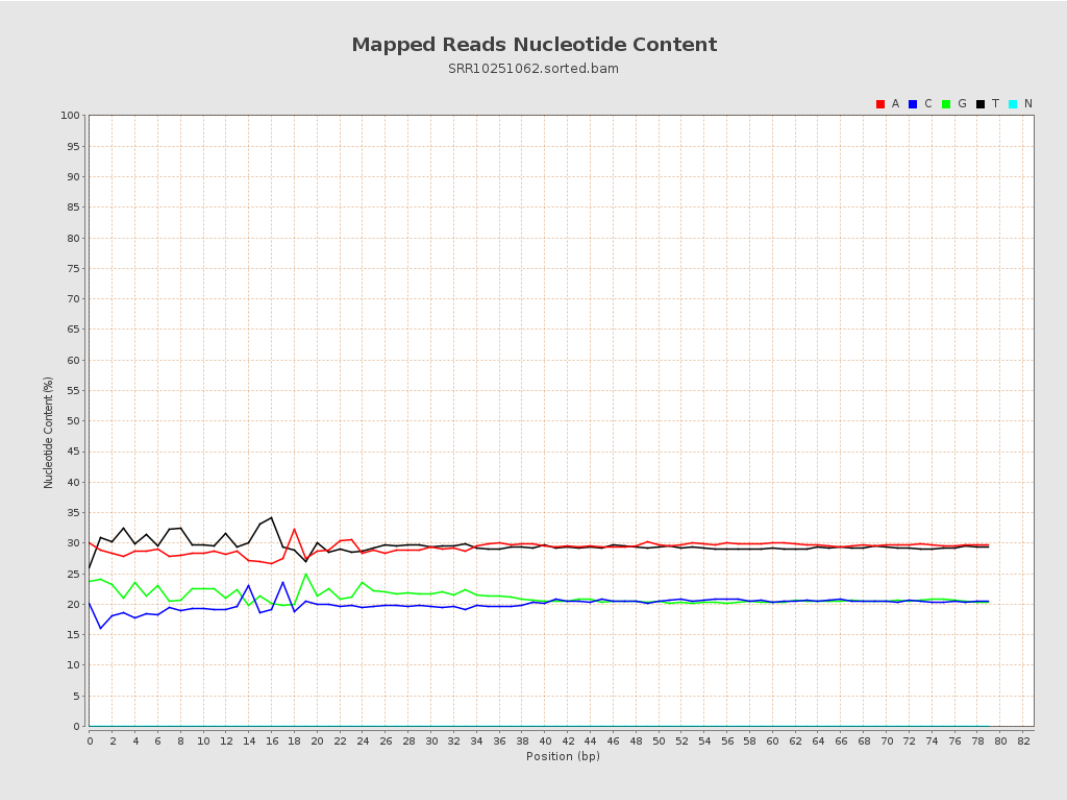
6. Results : Genome Fraction Coverage



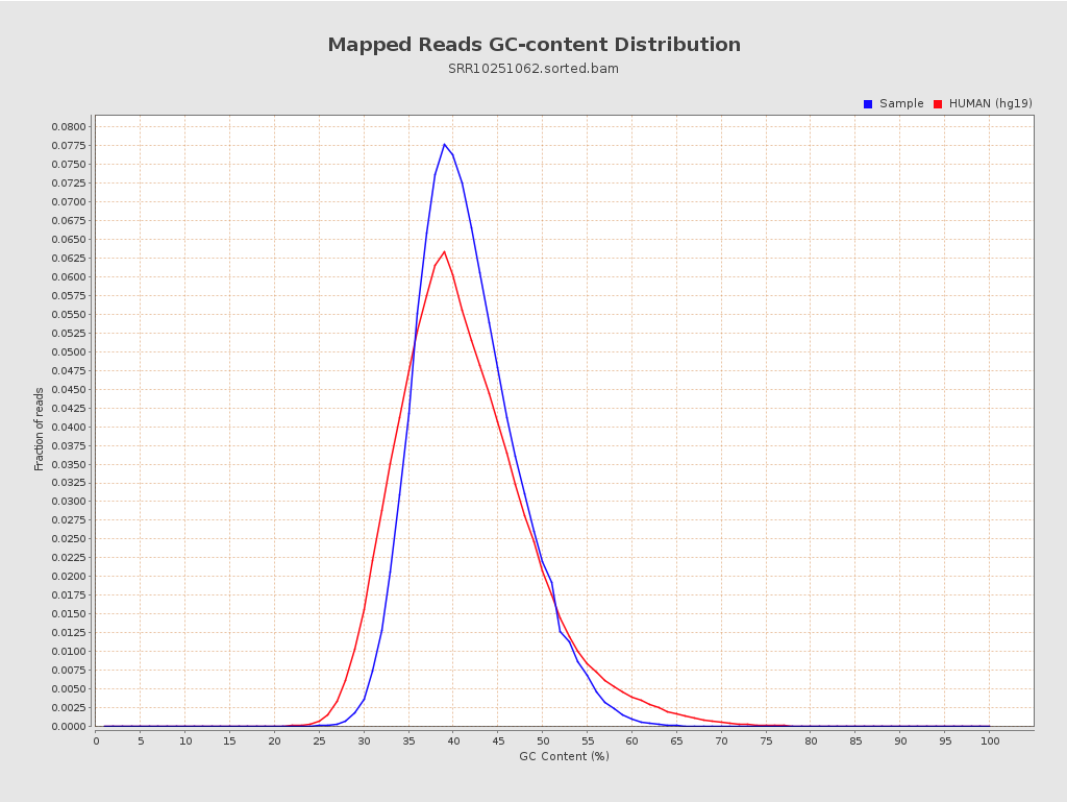
7. Results : Duplication Rate Histogram



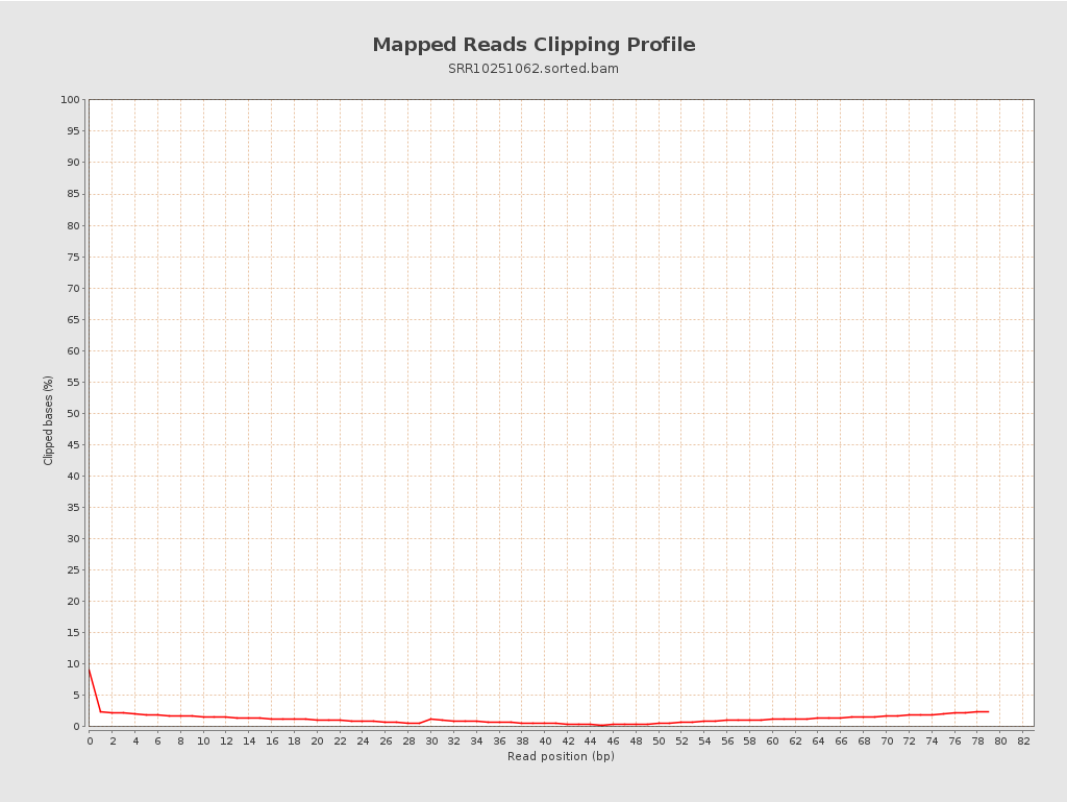
8. Results : Mapped Reads Nucleotide Content



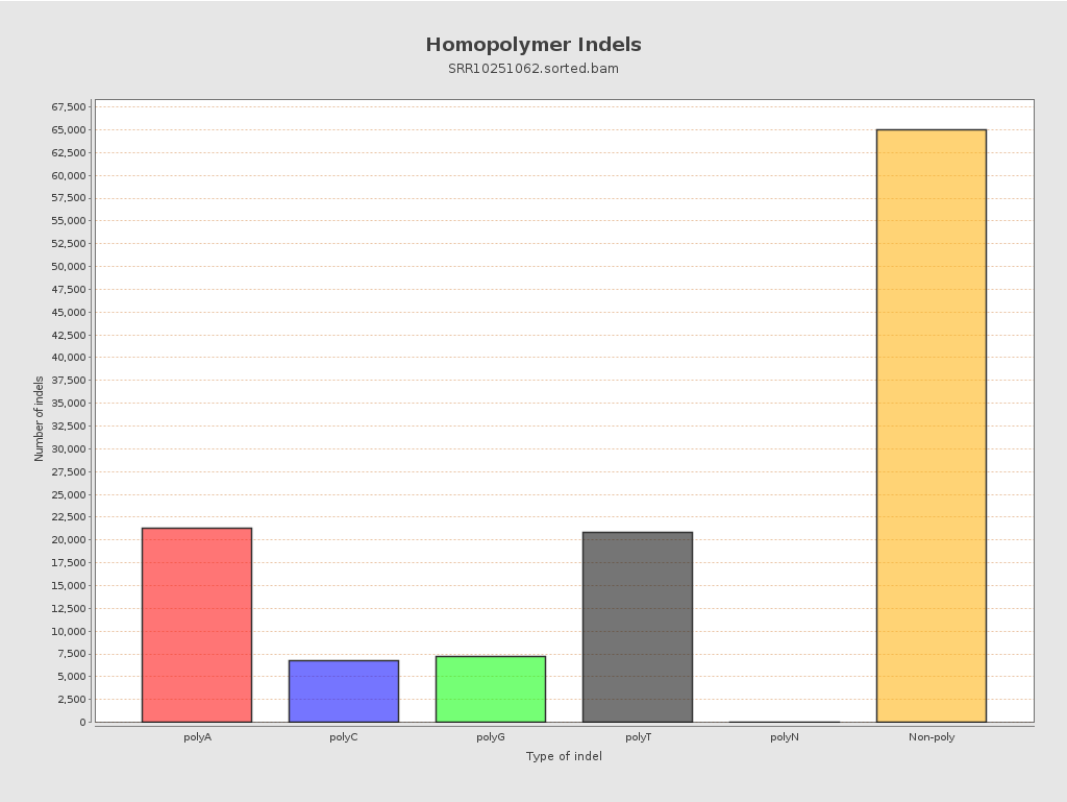
9. Results : Mapped Reads GC-content Distribution



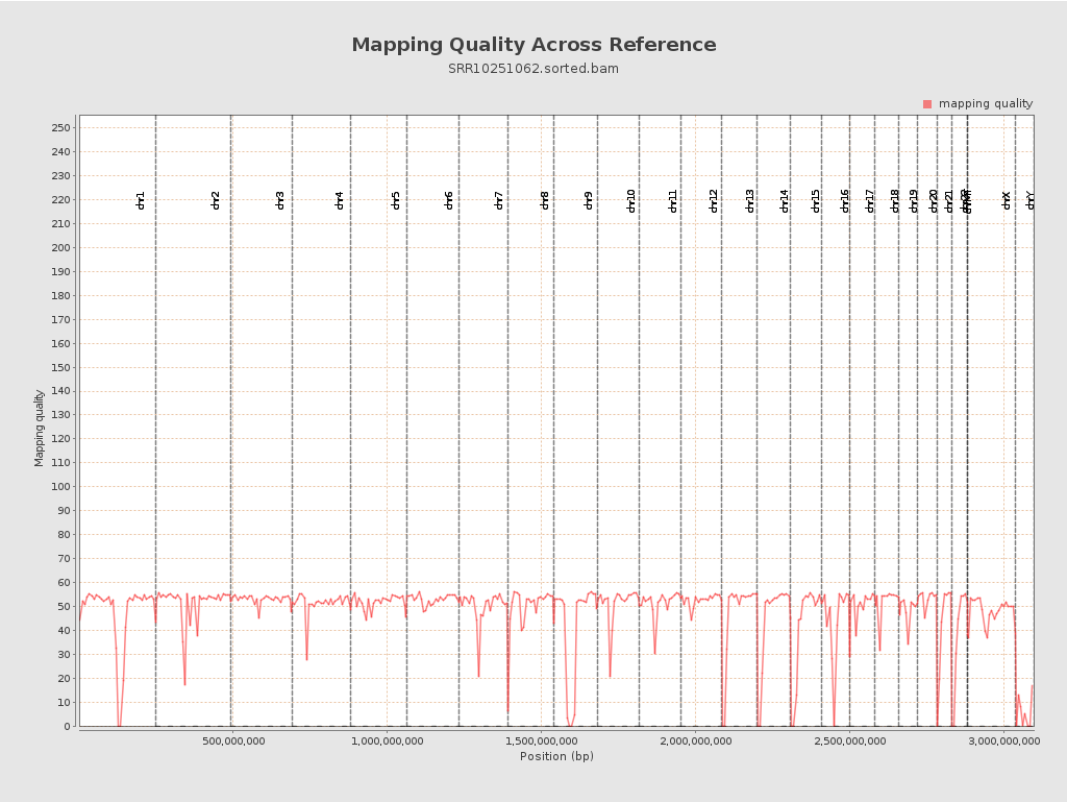
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram