

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 23:59:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081163.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_SRR3081163 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081163.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 23:59:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081163.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,537,739
Mapped reads	2,287,388 / 90.13%
Unmapped reads	250,351 / 9.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,418 / 0.8%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	93,577 / 3.69%
Duplication rate	3.25%
Clipped reads	973,947 / 38.38%

2.2. ACGT Content

Number/percentage of A's	44,214,228 / 28.65%
Number/percentage of C's	28,343,378 / 18.37%
Number/percentage of T's	48,690,398 / 31.55%
Number/percentage of G's	33,011,759 / 21.39%
Number/percentage of N's	46,561 / 0.03%
GC Percentage	39.76%

2.3. Coverage

Mean	0.0499

Standard Deviation	0.3886
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2.4. Mapping Quality

Mean Mapping Quality	47.02
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2.5. Mismatches and indels

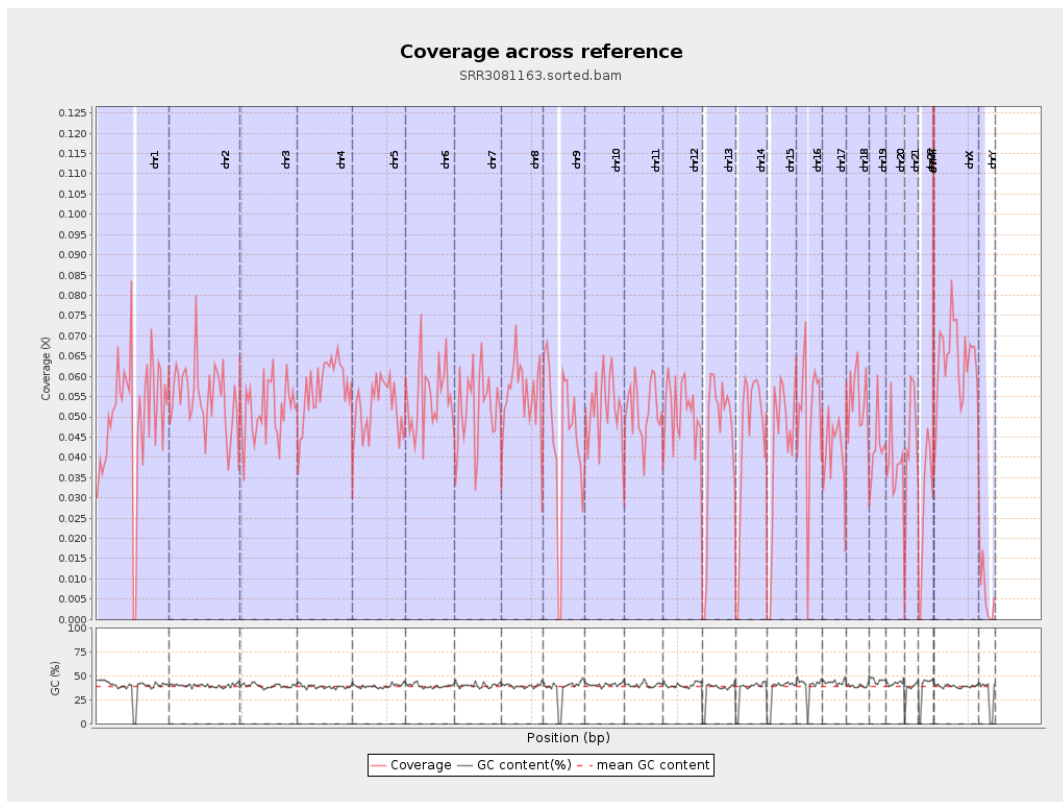
General error rate	0.84%
Mismatches	1,268,498
Insertions	12,137
Mapped reads with at least one insertion	0.53%
Deletions	35,113
Mapped reads with at least one deletion	1.52%
Homopolymer indels	47.67%

2.6. Chromosome stats

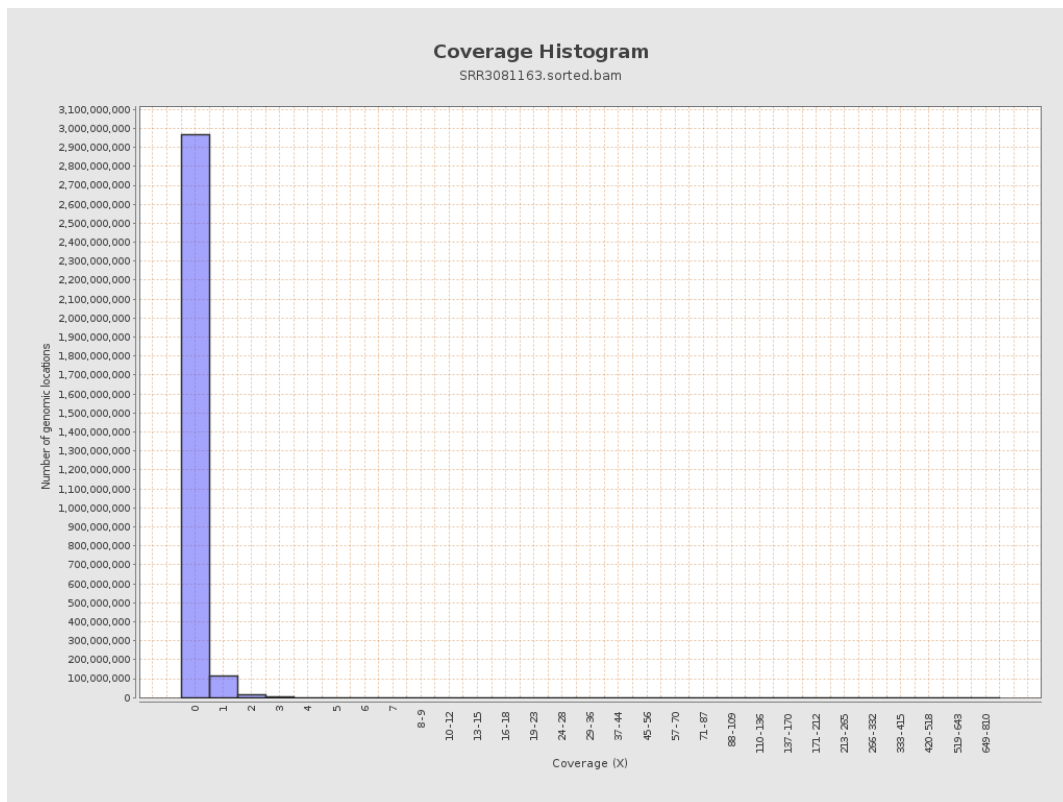
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	12350734	0.0496	0.6357
chr2	243199373	13332685	0.0548	0.4508
chr3	198022430	10288845	0.052	0.2582
chr4	191154276	10942760	0.0572	0.2831
chr5	180915260	9483875	0.0524	0.2614
chr6	171115067	9399531	0.0549	0.3494
chr7	159138663	8283662	0.0521	0.4909

chr8	146364022	8129210	0.0555	0.564
chr9	141213431	6384956	0.0452	0.3732
chr10	135534747	7107163	0.0524	0.3378
chr11	135006516	6948806	0.0515	0.3364
chr12	133851895	6814114	0.0509	0.2618
chr13	115169878	5029908	0.0437	0.2367
chr14	107349540	4789847	0.0446	0.2668
chr15	102531392	4271915	0.0417	0.2379
chr16	90354753	4565199	0.0505	0.2861
chr17	81195210	3333158	0.0411	0.2714
chr18	78077248	4230671	0.0542	0.6949
chr19	59128983	2528476	0.0428	0.4974
chr20	63025520	2420560	0.0384	0.2326
chr21	48129895	2073990	0.0431	0.2527
chr22	51304566	1432256	0.0279	0.1881
chrMT	16571	8930	0.5389	0.8664
chrX	155270560	9838137	0.0634	0.3193
chrY	59373566	373966	0.0063	0.1307

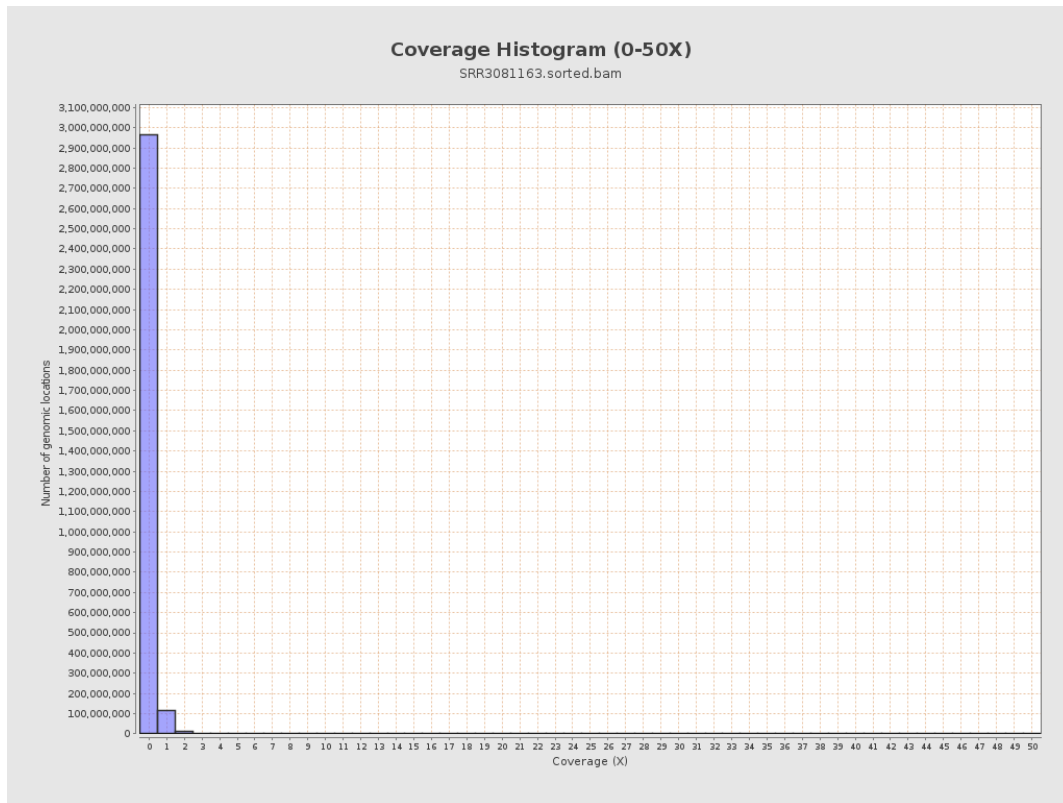
3. Results : Coverage across reference



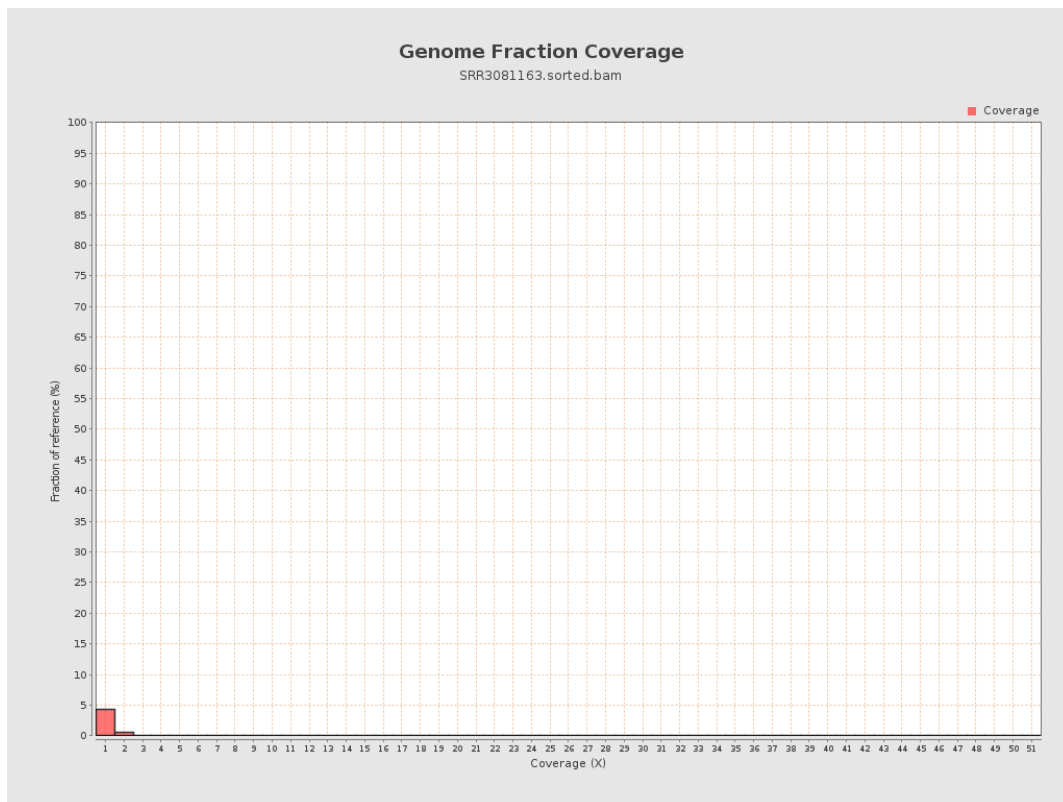
4. Results : Coverage Histogram



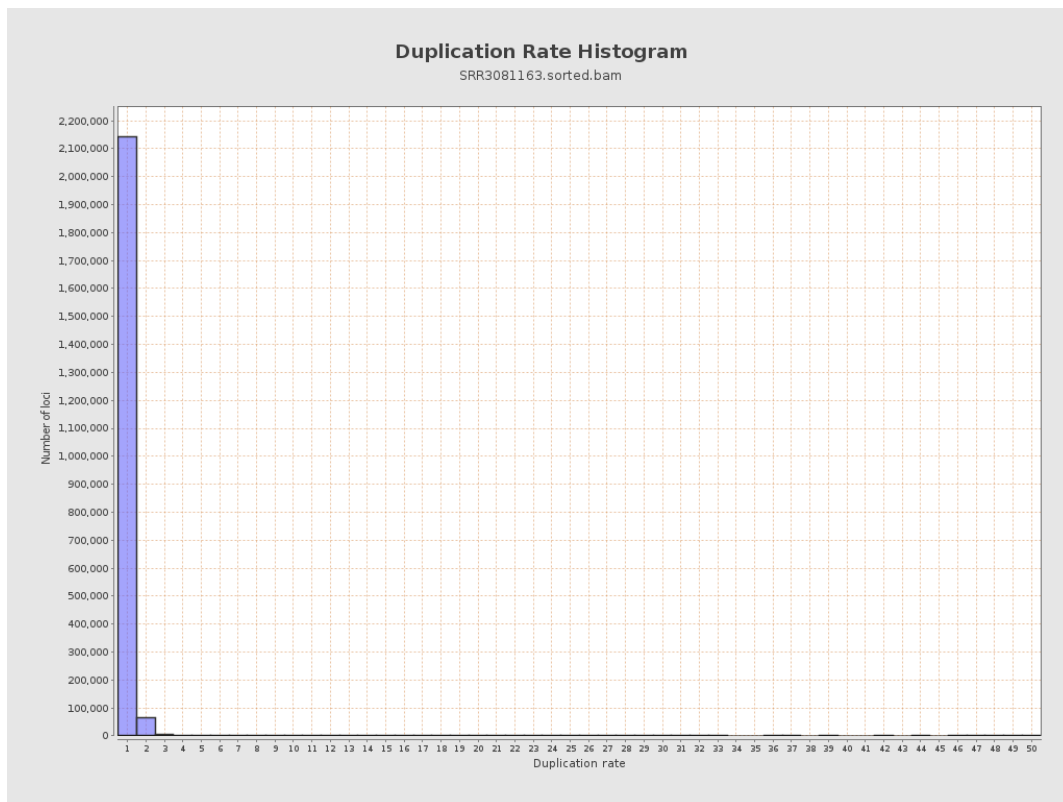
5. Results : Coverage Histogram (0-50X)



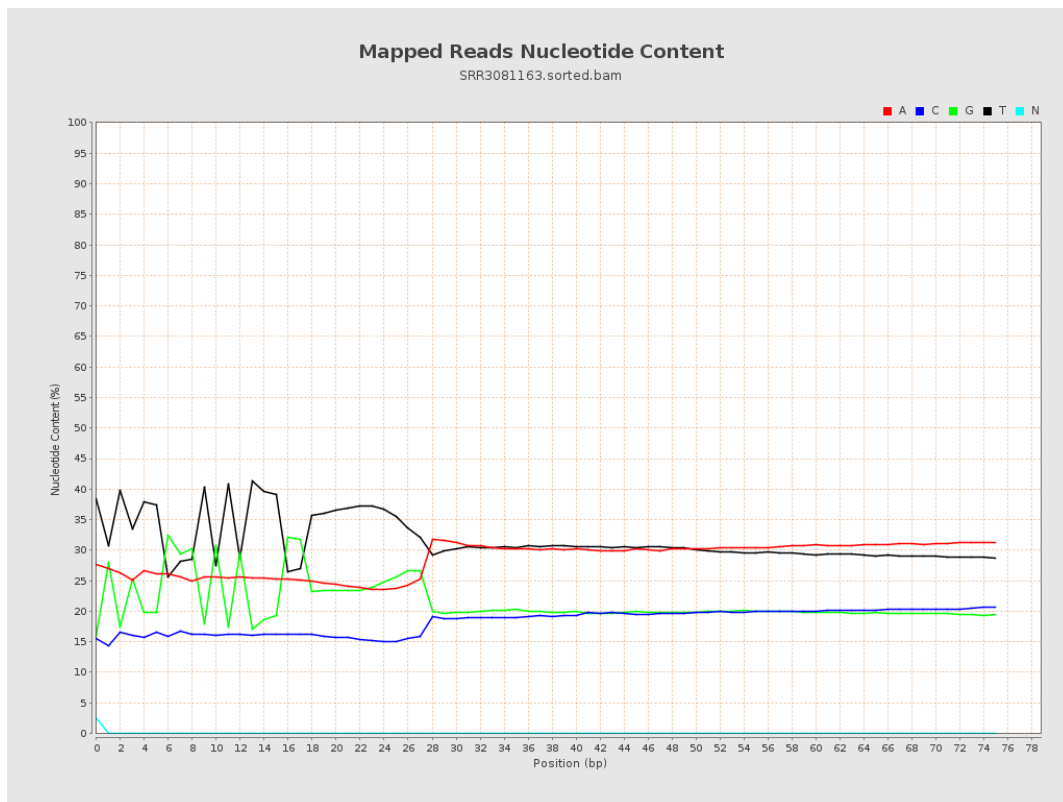
6. Results : Genome Fraction Coverage



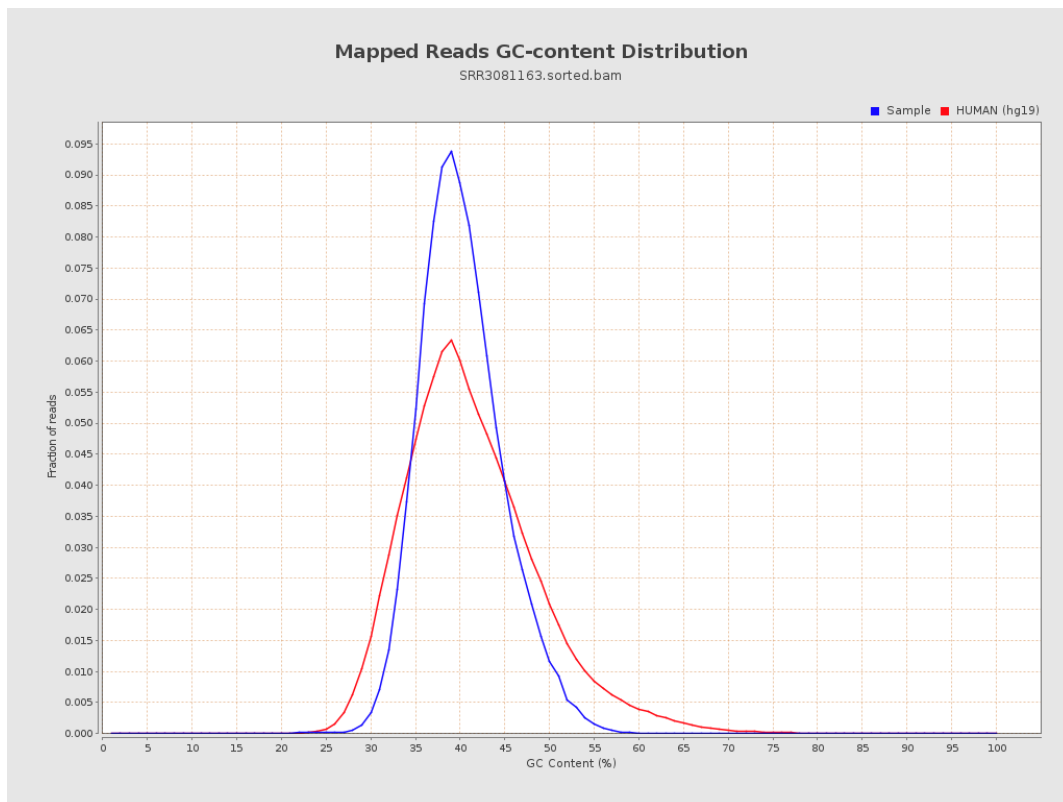
7. Results : Duplication Rate Histogram



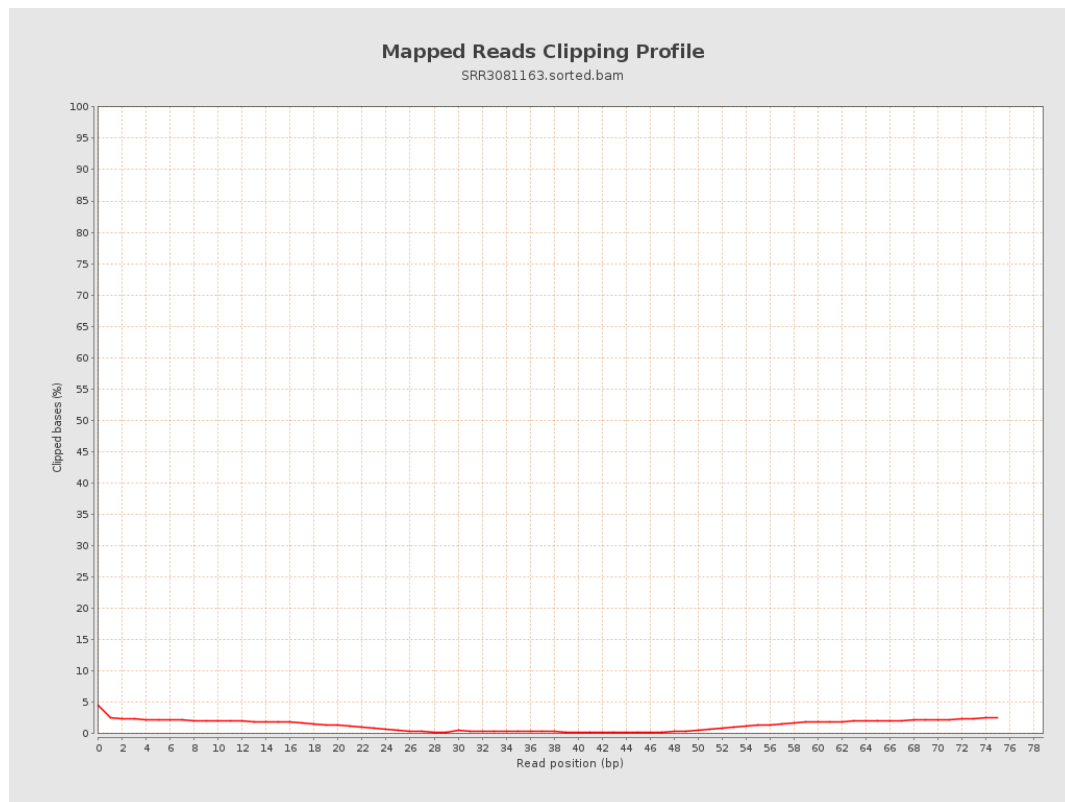
8. Results : Mapped Reads Nucleotide Content



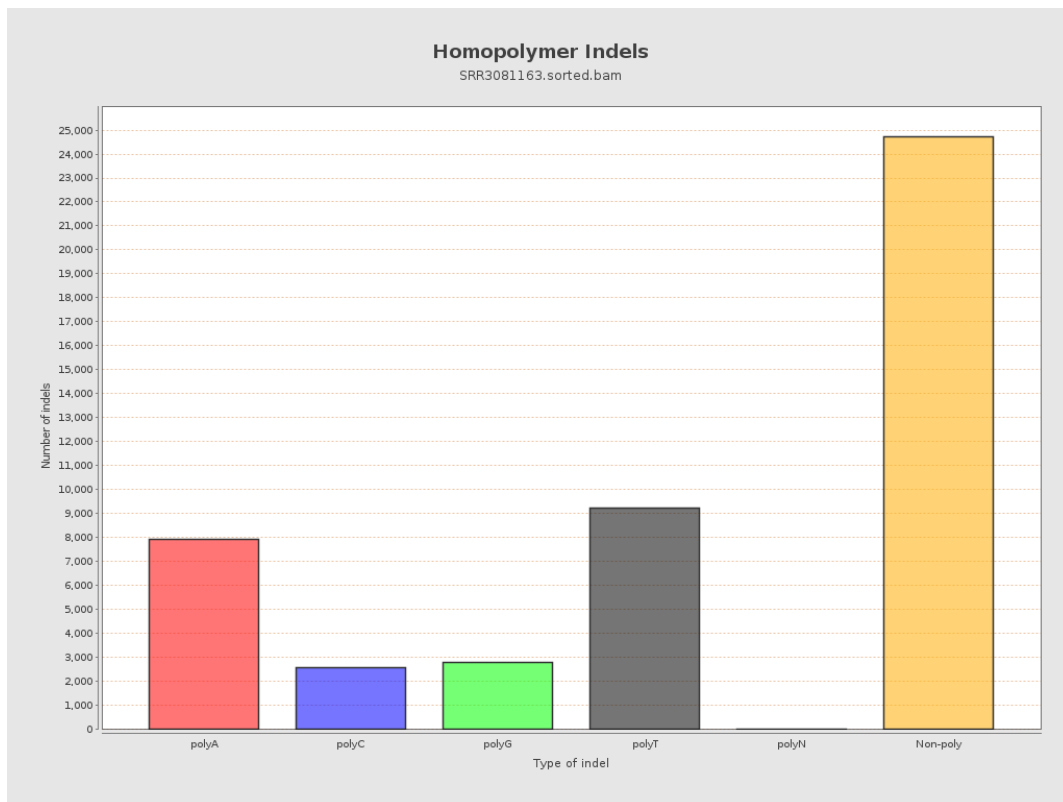
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

