

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 10:40:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR23117303.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_SRR23117303 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR23117303.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 10:40:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR23117303.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	635,255
Mapped reads	609,331 / 95.92%
Unmapped reads	25,924 / 4.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,736 / 0.75%
Read min/max/mean length	25 / 615 / 266.43
Duplicated reads (estimated)	158,984 / 25.03%
Duplication rate	22.09%
Clipped reads	614,066 / 96.66%

2.2. ACGT Content

Number/percentage of A's	42,659,973 / 29.64%
Number/percentage of C's	29,490,843 / 20.49%
Number/percentage of T's	42,146,245 / 29.28%
Number/percentage of G's	29,626,326 / 20.58%
Number/percentage of N's	0 / 0%
GC Percentage	41.08%

2.3. Coverage

Mean	0.0466

Standard Deviation	0.8672
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2.4. Mapping Quality

Mean Mapping Quality	53.5
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2.5. Mismatches and indels

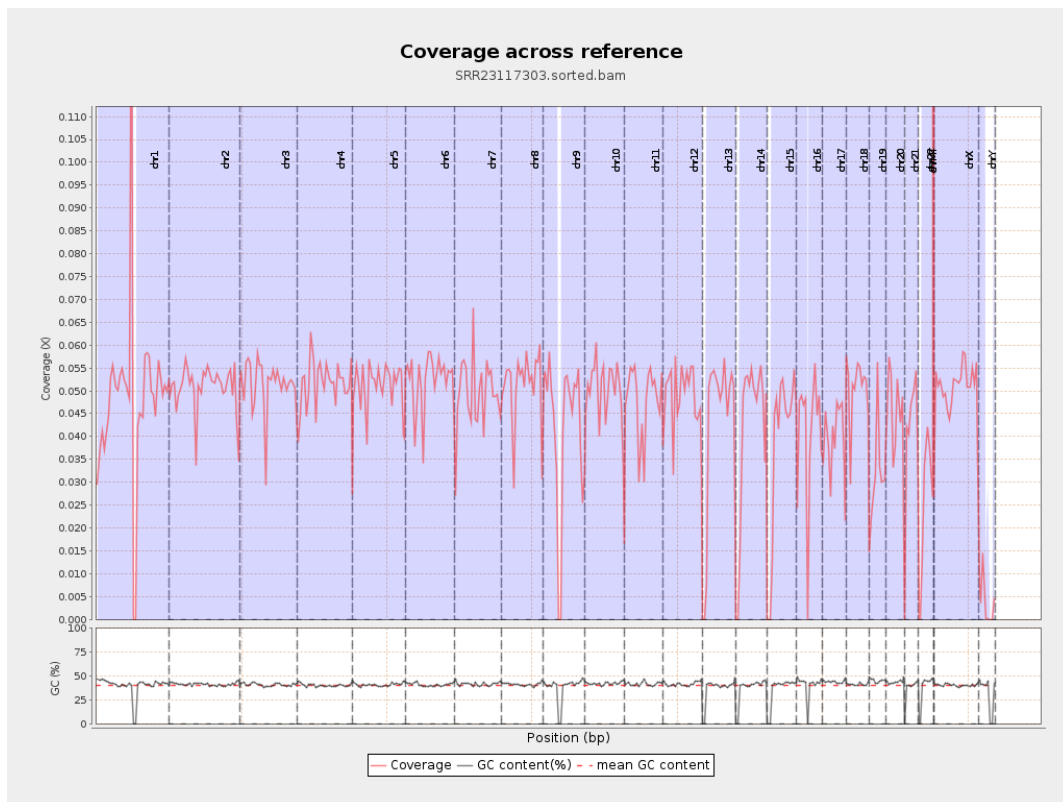
General error rate	0.87%
Mismatches	732,473
Insertions	449,952
Mapped reads with at least one insertion	33.41%
Deletions	208,189
Mapped reads with at least one deletion	23.77%
Homopolymer indels	33.45%

2.6. Chromosome stats

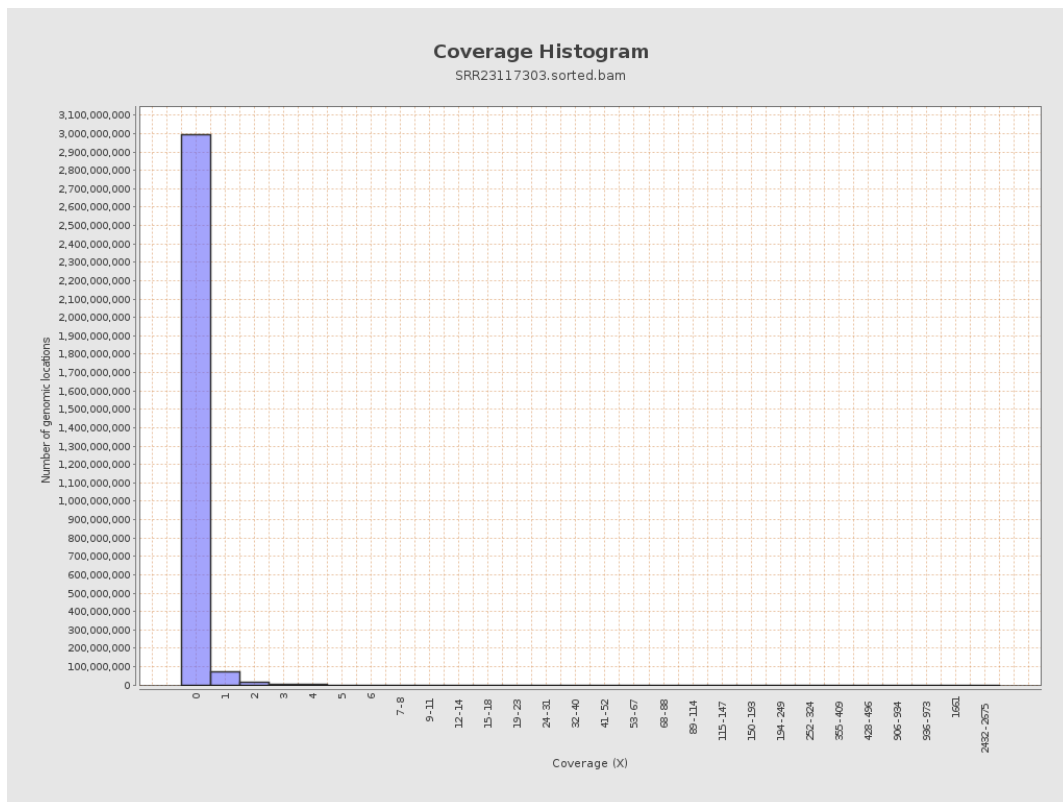
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	12152702	0.0488	2.6792
chr2	243199373	12357227	0.0508	0.3183
chr3	198022430	10195062	0.0515	0.3069
chr4	191154276	9864202	0.0516	0.3571
chr5	180915260	9231955	0.051	0.3054
chr6	171115067	8952960	0.0523	0.3105
chr7	159138663	7934288	0.0499	1.2154

chr8	146364022	7524745	0.0514	0.3135
chr9	141213431	5908811	0.0418	0.2901
chr10	135534747	6853884	0.0506	0.5115
chr11	135006516	6438641	0.0477	0.2962
chr12	133851895	6551738	0.0489	0.3002
chr13	115169878	4907491	0.0426	0.2767
chr14	107349540	4436837	0.0413	0.2769
chr15	102531392	3923428	0.0383	0.2627
chr16	90354753	3716092	0.0411	0.3536
chr17	81195210	3170753	0.0391	0.3329
chr18	78077248	3934604	0.0504	0.3449
chr19	59128983	1915877	0.0324	0.6798
chr20	63025520	2846850	0.0452	0.3301
chr21	48129895	1960416	0.0407	0.3652
chr22	51304566	1274340	0.0248	0.2211
chrMT	16571	60706	3.6634	6.9843
chrX	155270560	7853093	0.0506	0.308
chrY	59373566	218950	0.0037	0.27

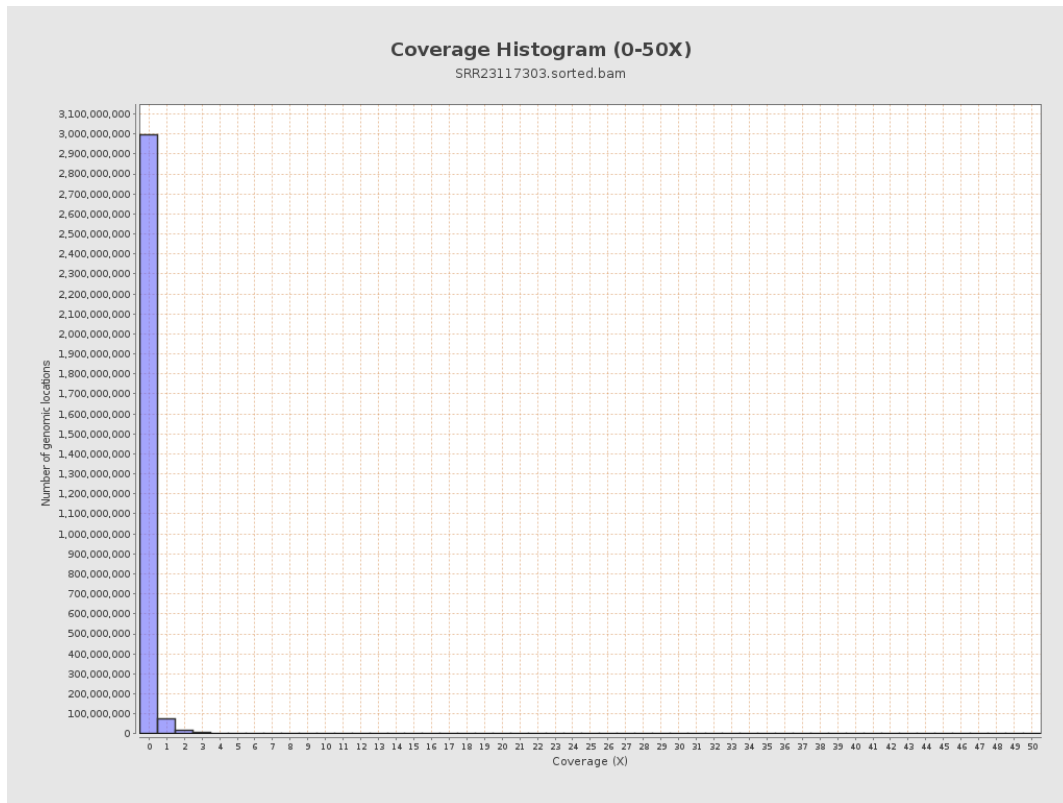
3. Results : Coverage across reference



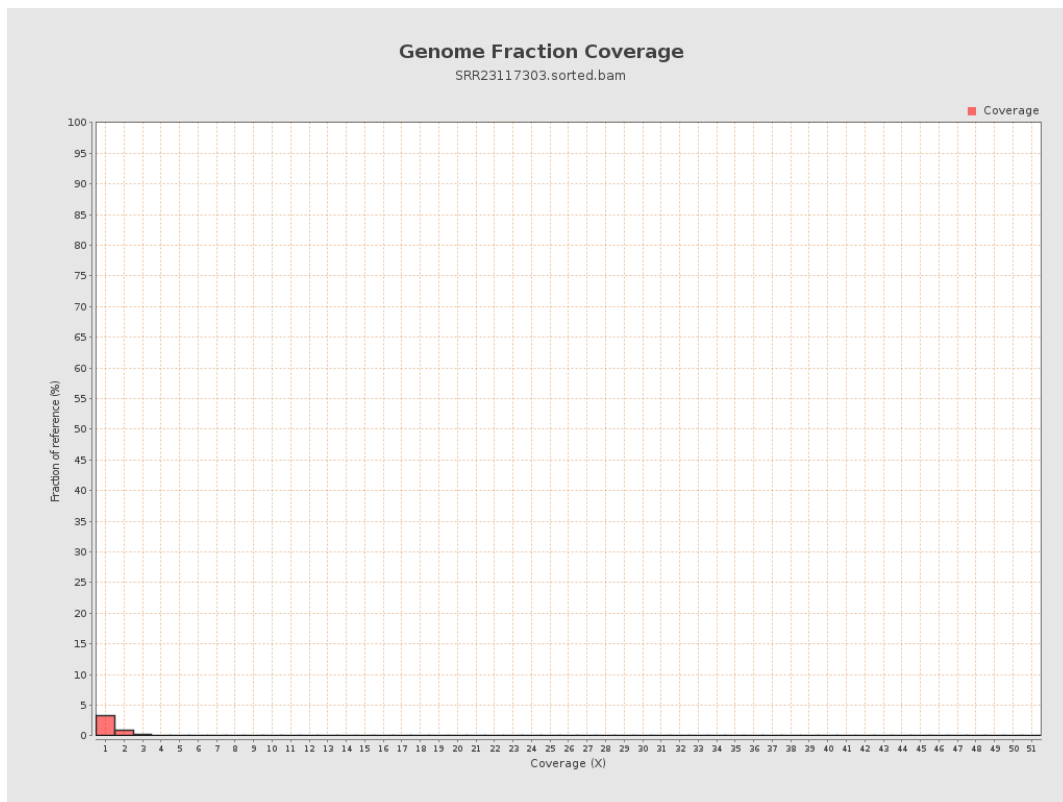
4. Results : Coverage Histogram



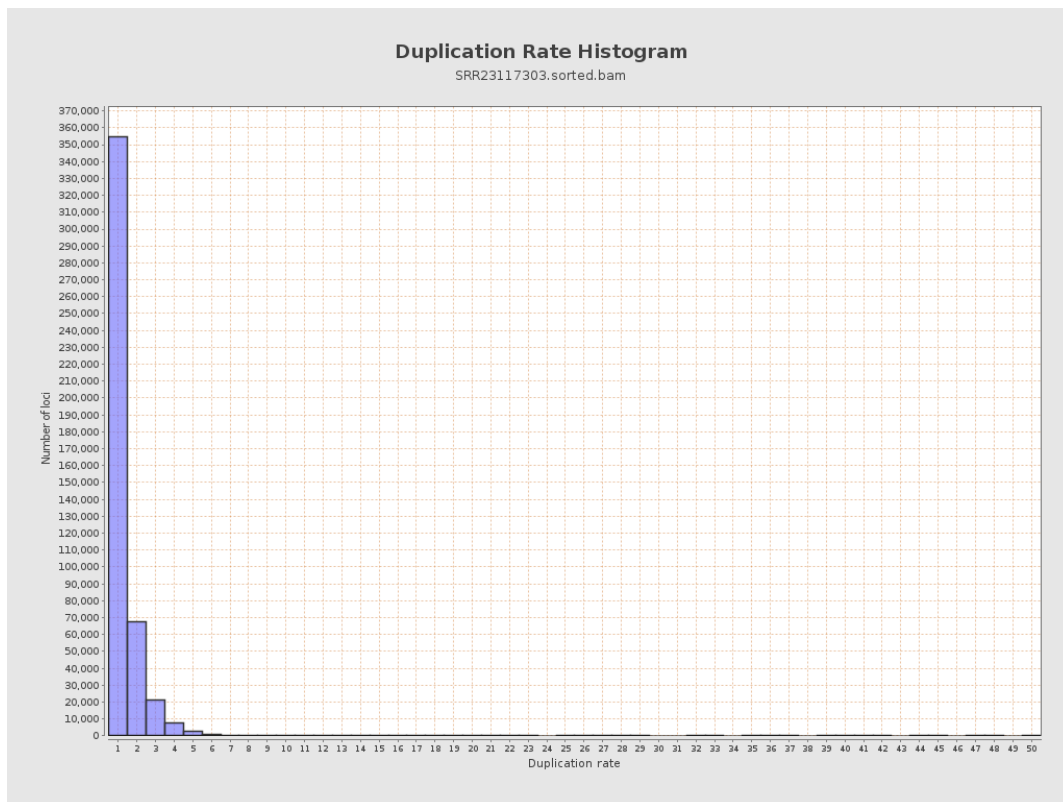
5. Results : Coverage Histogram (0-50X)



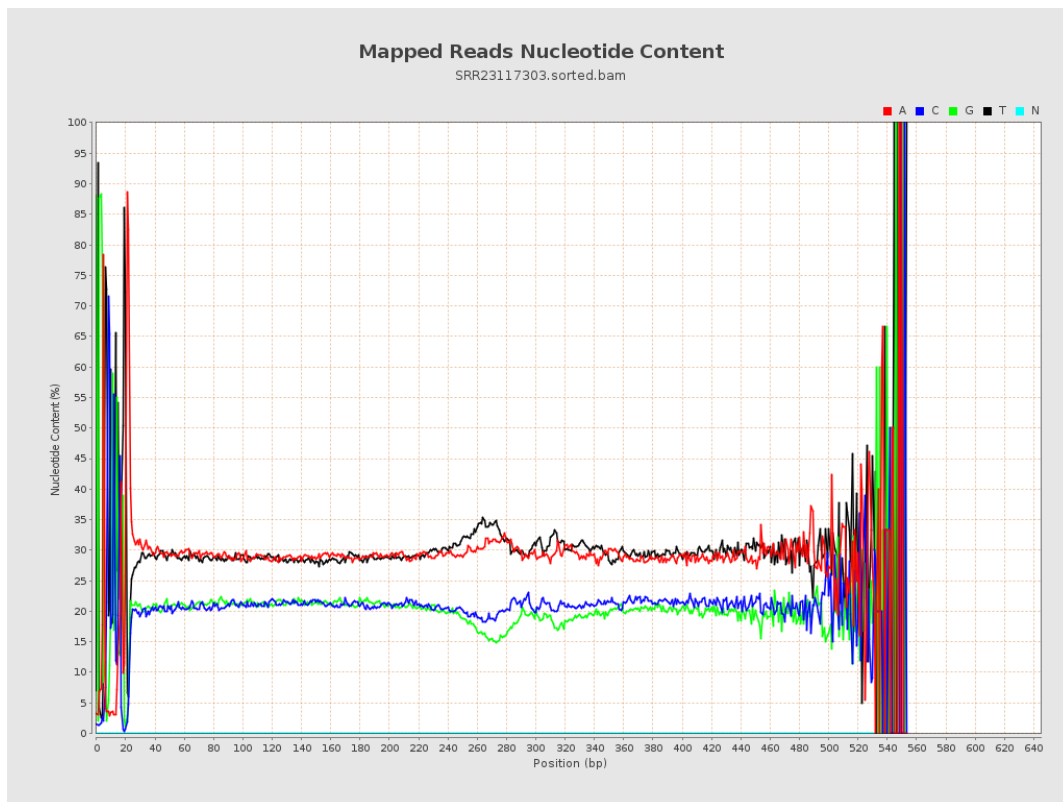
6. Results : Genome Fraction Coverage



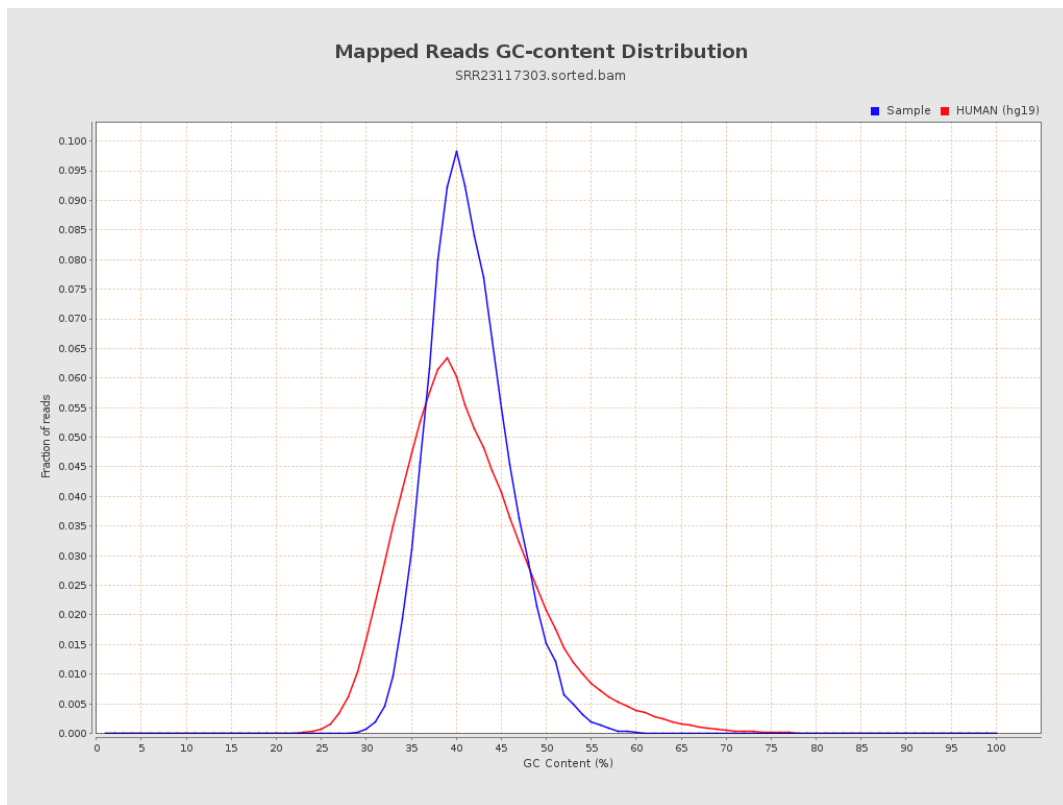
7. Results : Duplication Rate Histogram



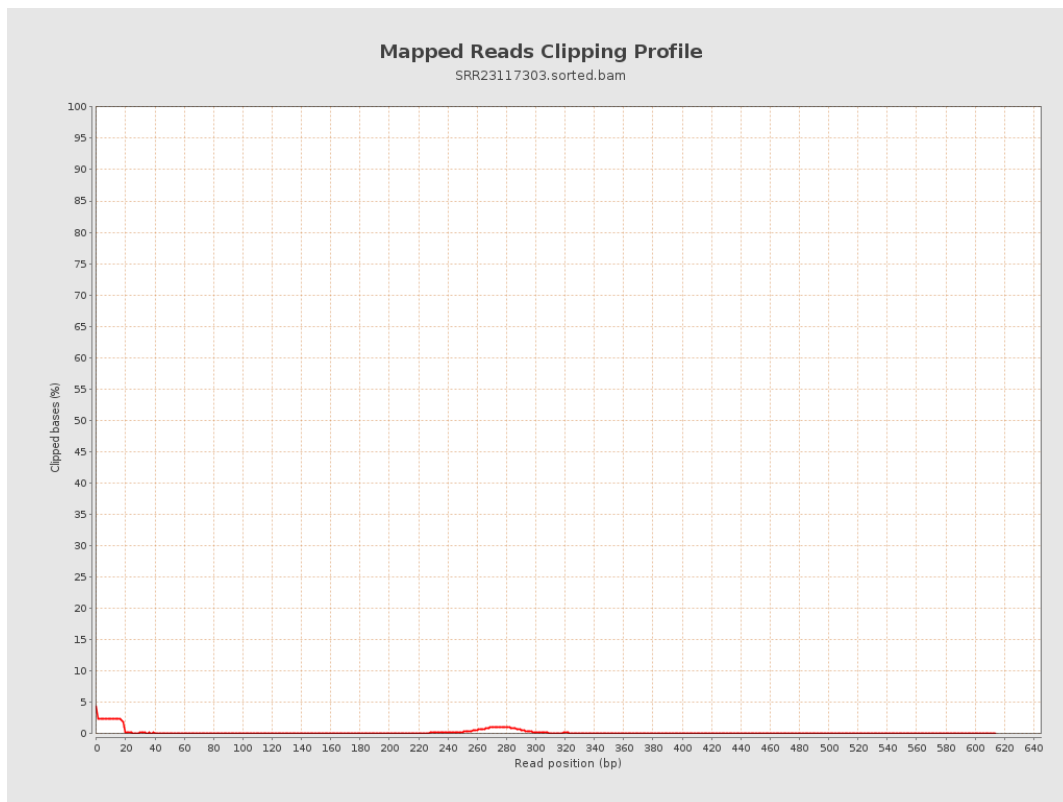
8. Results : Mapped Reads Nucleotide Content



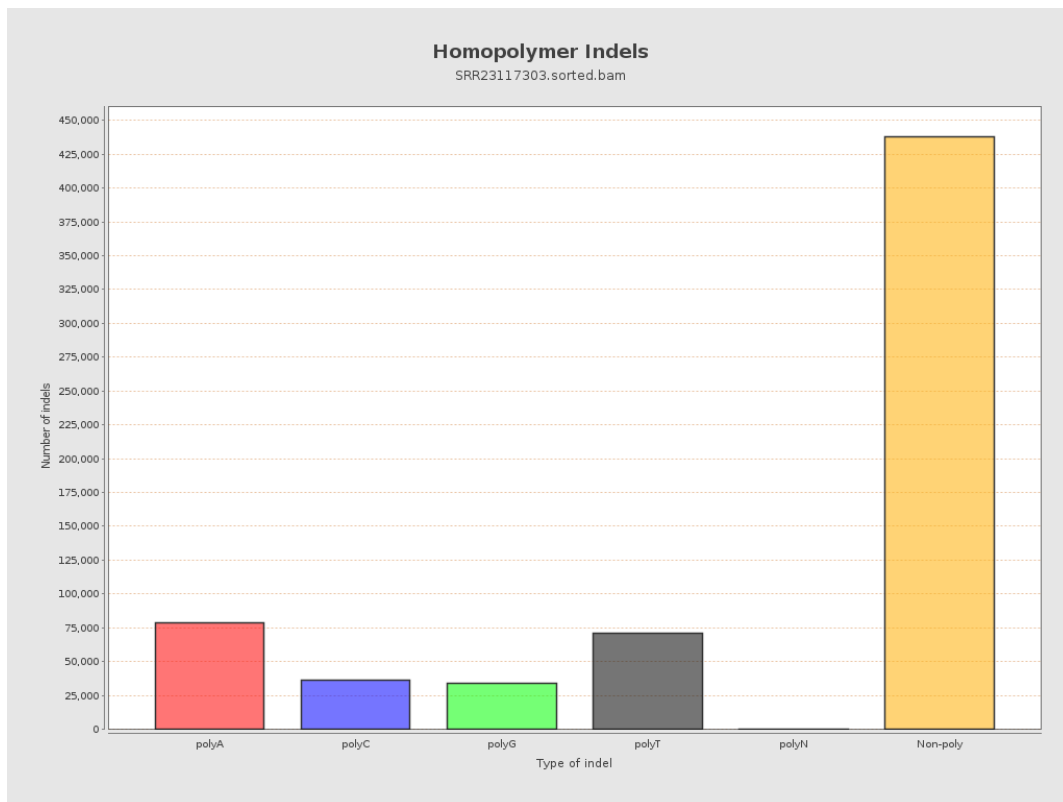
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

