

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 10:37:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR23117302.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_SRR23117302 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR23117302.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 10:37:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR23117302.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,144,147
Mapped reads	1,105,281 / 96.6%
Unmapped reads	38,866 / 3.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,157 / 0.71%
Read min/max/mean length	25 / 548 / 262.04
Duplicated reads (estimated)	347,296 / 30.35%
Duplication rate	24.79%
Clipped reads	1,113,435 / 97.32%

2.2. ACGT Content

Number/percentage of A's	72,033,366 / 28.23%
Number/percentage of C's	55,170,106 / 21.62%
Number/percentage of T's	73,953,349 / 28.98%
Number/percentage of G's	54,022,264 / 21.17%
Number/percentage of N's	0 / 0%
GC Percentage	42.79%

2.3. Coverage

Mean	0.0826

Standard Deviation	1.1745
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2.4. Mapping Quality

Mean Mapping Quality	53.57
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2.5. Mismatches and indels

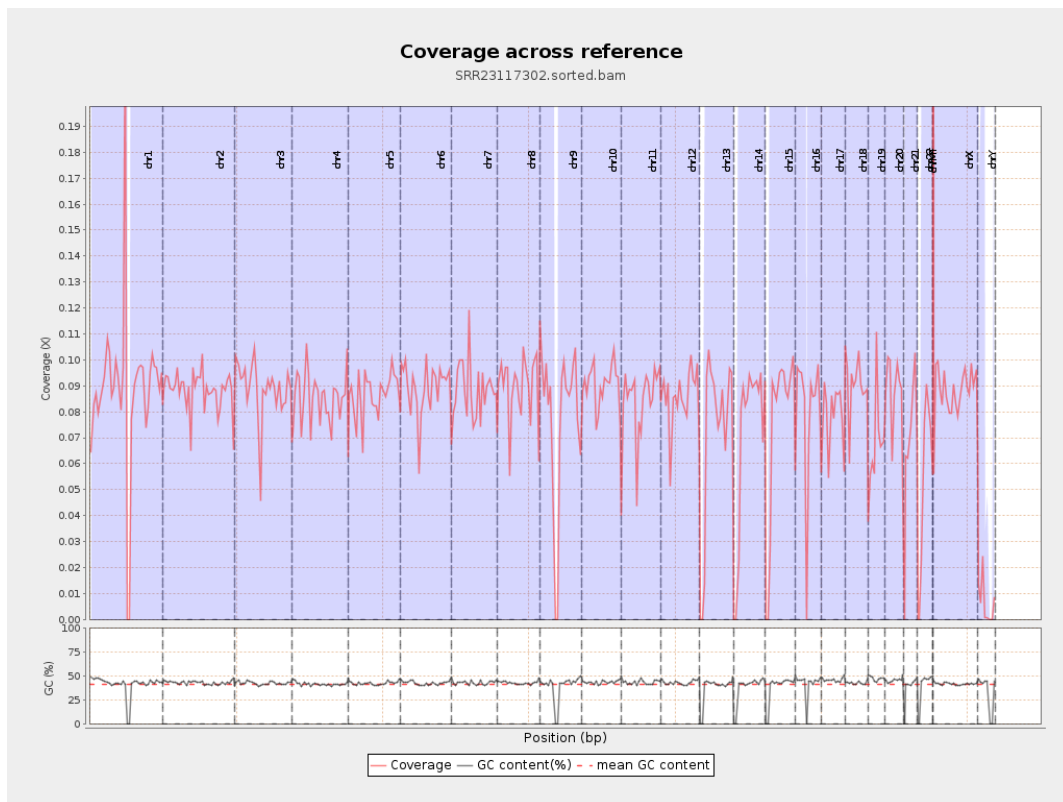
General error rate	1.08%
Mismatches	1,371,615
Insertions	1,237,972
Mapped reads with at least one insertion	49.26%
Deletions	397,100
Mapped reads with at least one deletion	25.31%
Homopolymer indels	29.97%

2.6. Chromosome stats

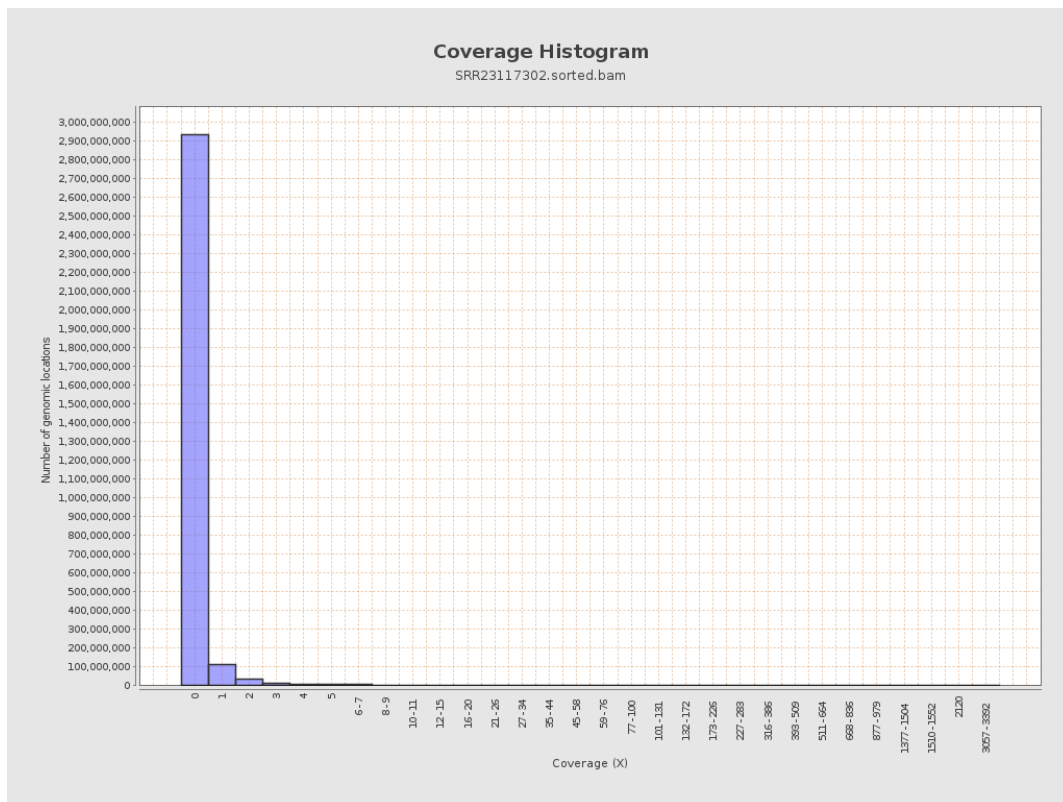
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	22189132	0.089	3.4679
chr2	243199373	21501631	0.0884	0.4708
chr3	198022430	17505602	0.0884	0.4481
chr4	191154276	16389338	0.0857	0.5272
chr5	180915260	15662469	0.0866	0.4436
chr6	171115067	15293399	0.0894	0.455
chr7	159138663	14024518	0.0881	1.9046

chr8	146364022	13073711	0.0893	0.4784
chr9	141213431	10897186	0.0772	0.4492
chr10	135534747	12280073	0.0906	0.6563
chr11	135006516	11386053	0.0843	0.4374
chr12	133851895	11541857	0.0862	0.4454
chr13	115169878	8312885	0.0722	0.4059
chr14	107349540	7663556	0.0714	0.4047
chr15	102531392	7614639	0.0743	0.4177
chr16	90354753	7092602	0.0785	0.5941
chr17	81195210	6416723	0.079	0.5386
chr18	78077248	7015530	0.0899	0.5264
chr19	59128983	4072200	0.0689	1.2494
chr20	63025520	5538480	0.0879	0.5326
chr21	48129895	3367735	0.07	0.5314
chr22	51304566	2790348	0.0544	0.3679
chrMT	16571	17924	1.0816	3.7651
chrX	155270560	13644249	0.0879	0.459
chrY	59373566	381363	0.0064	0.4018

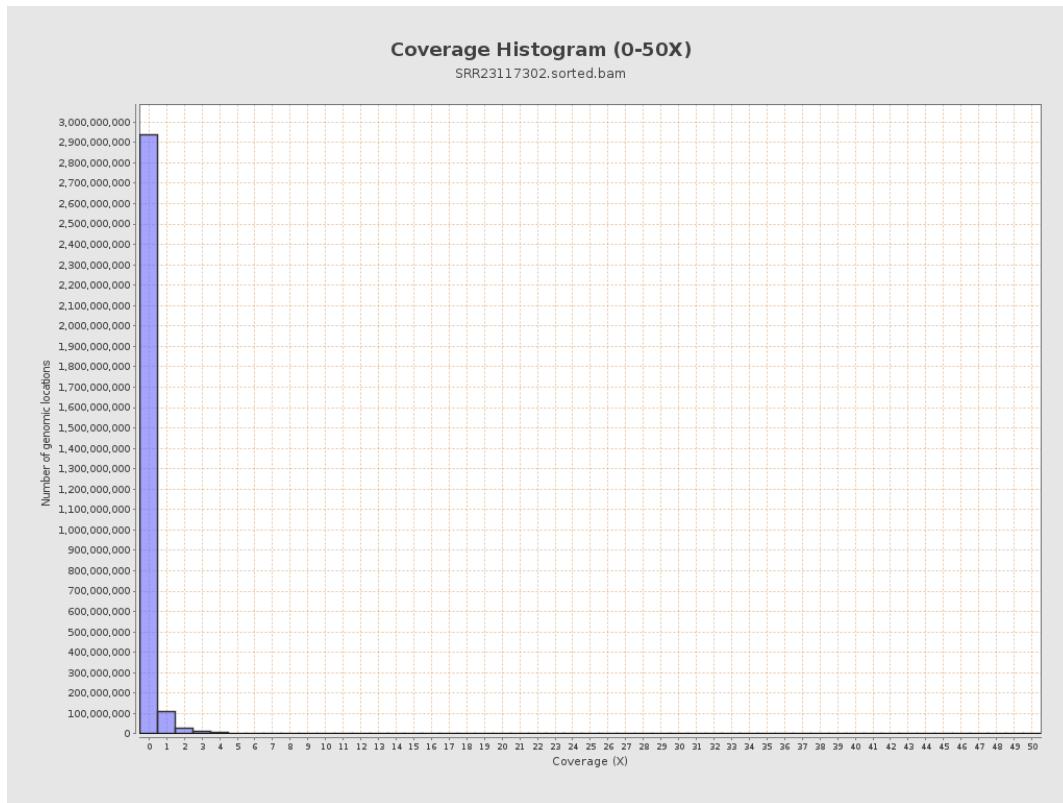
3. Results : Coverage across reference



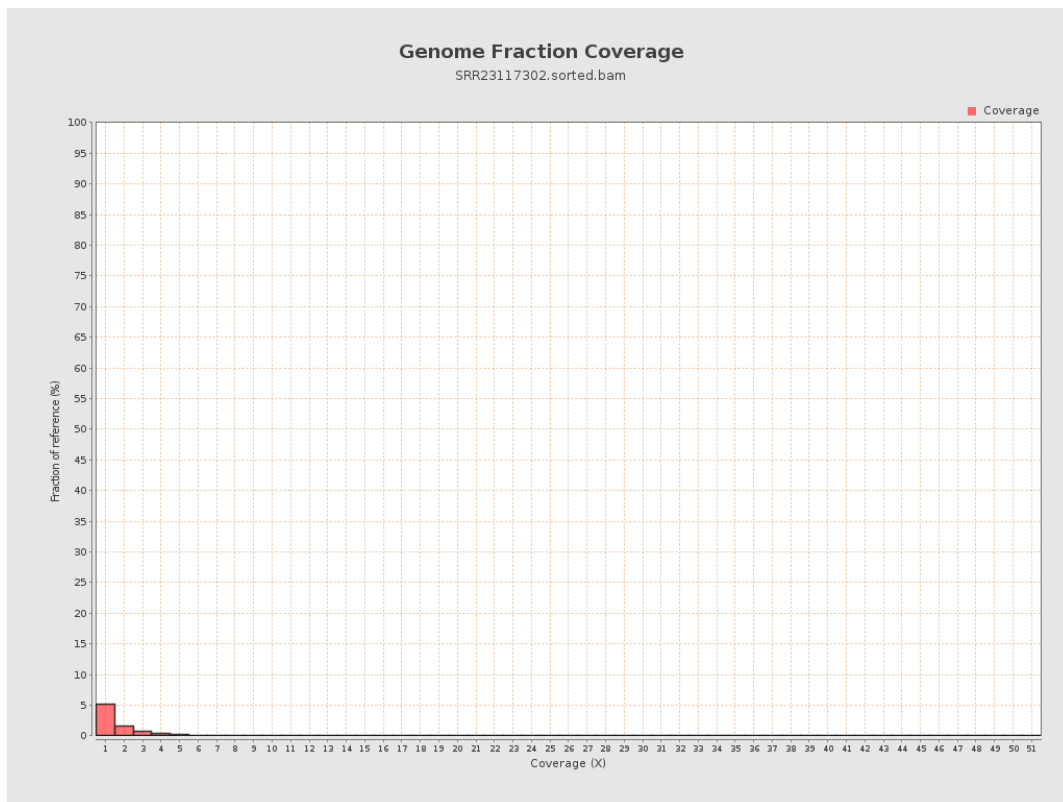
4. Results : Coverage Histogram



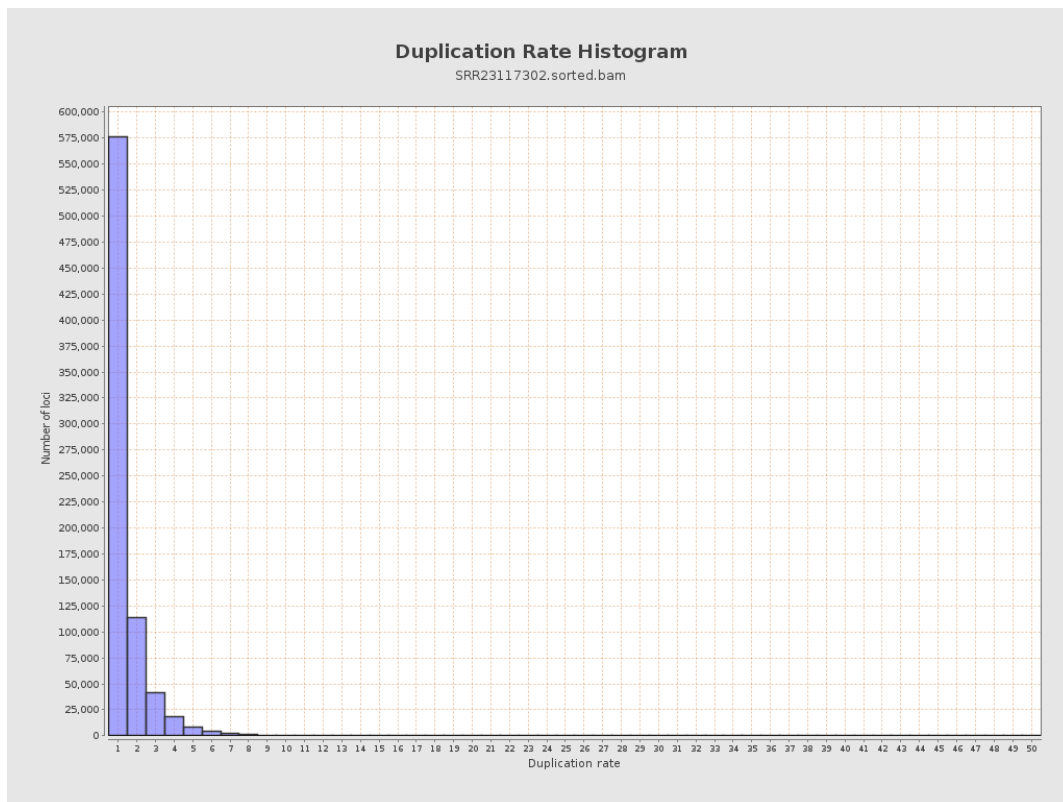
5. Results : Coverage Histogram (0-50X)



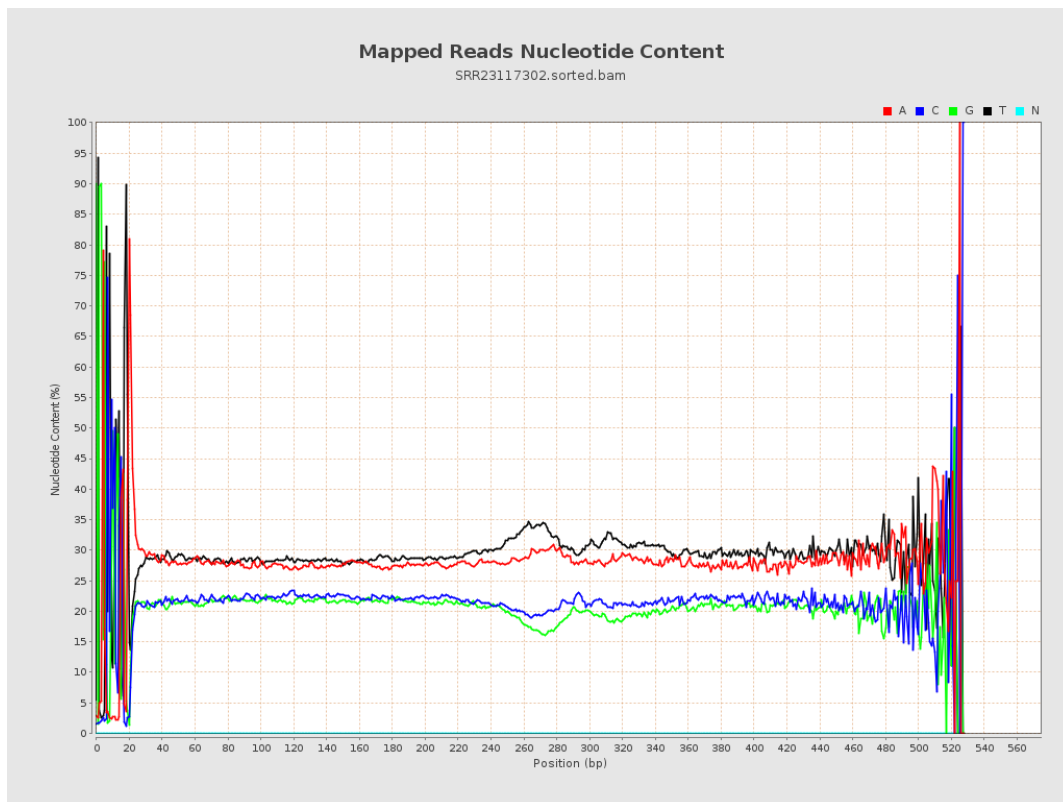
6. Results : Genome Fraction Coverage



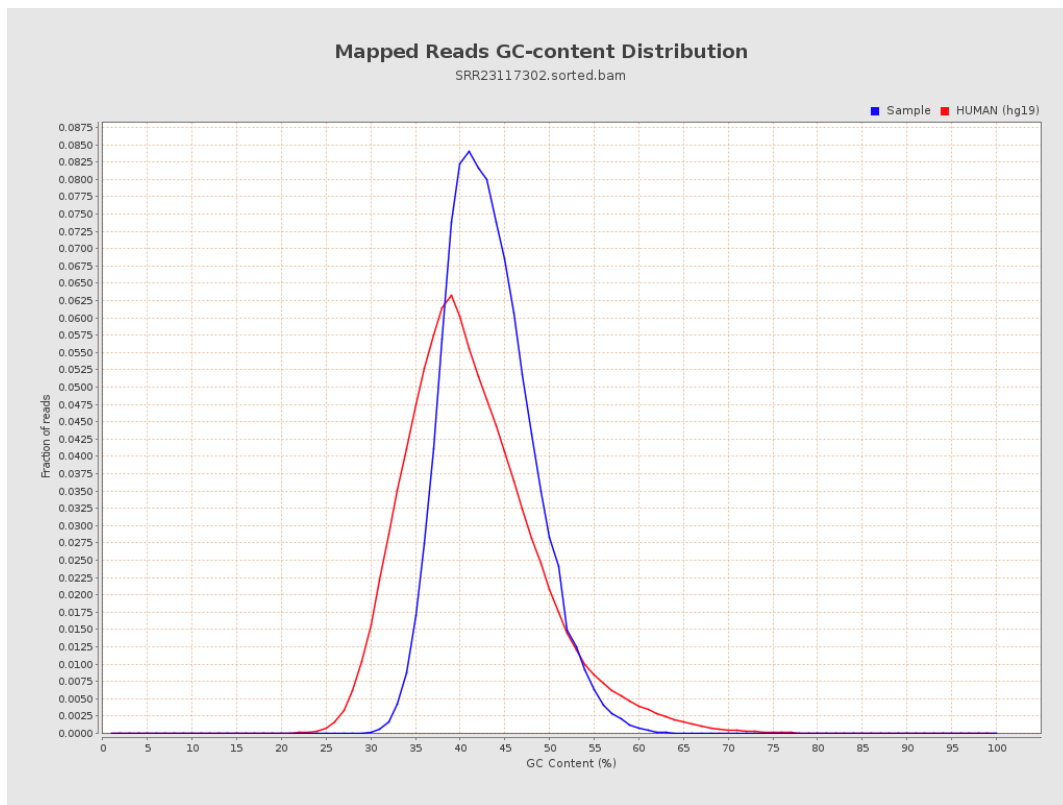
7. Results : Duplication Rate Histogram



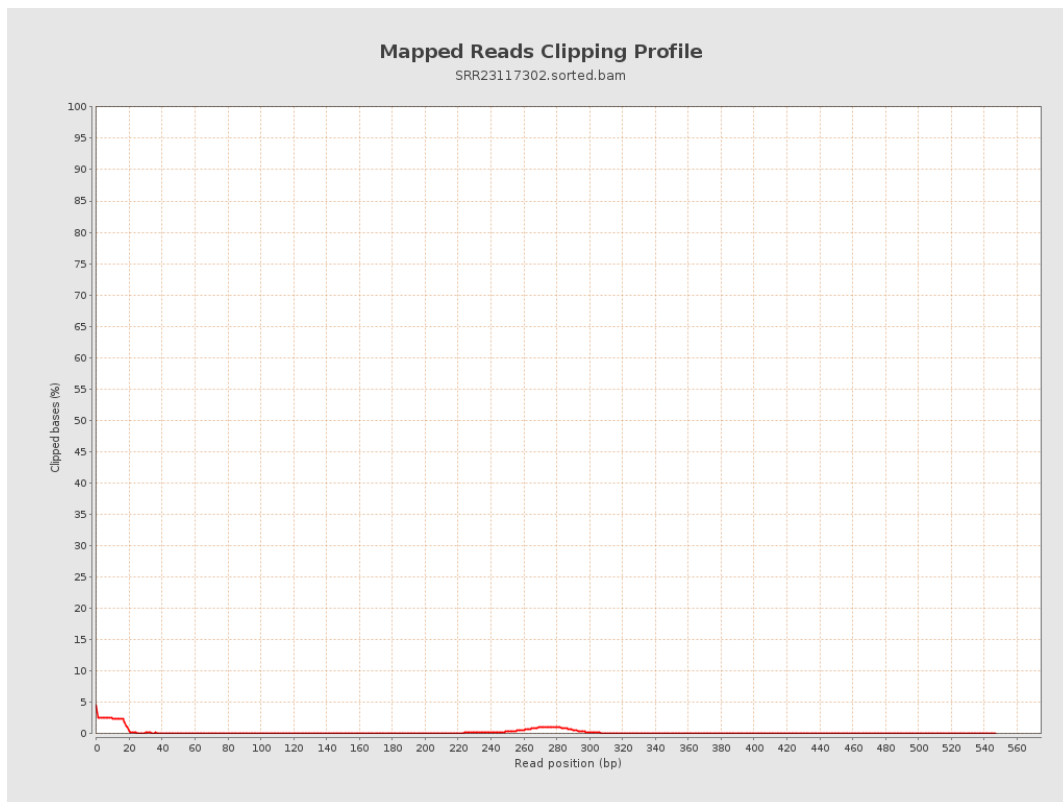
8. Results : Mapped Reads Nucleotide Content



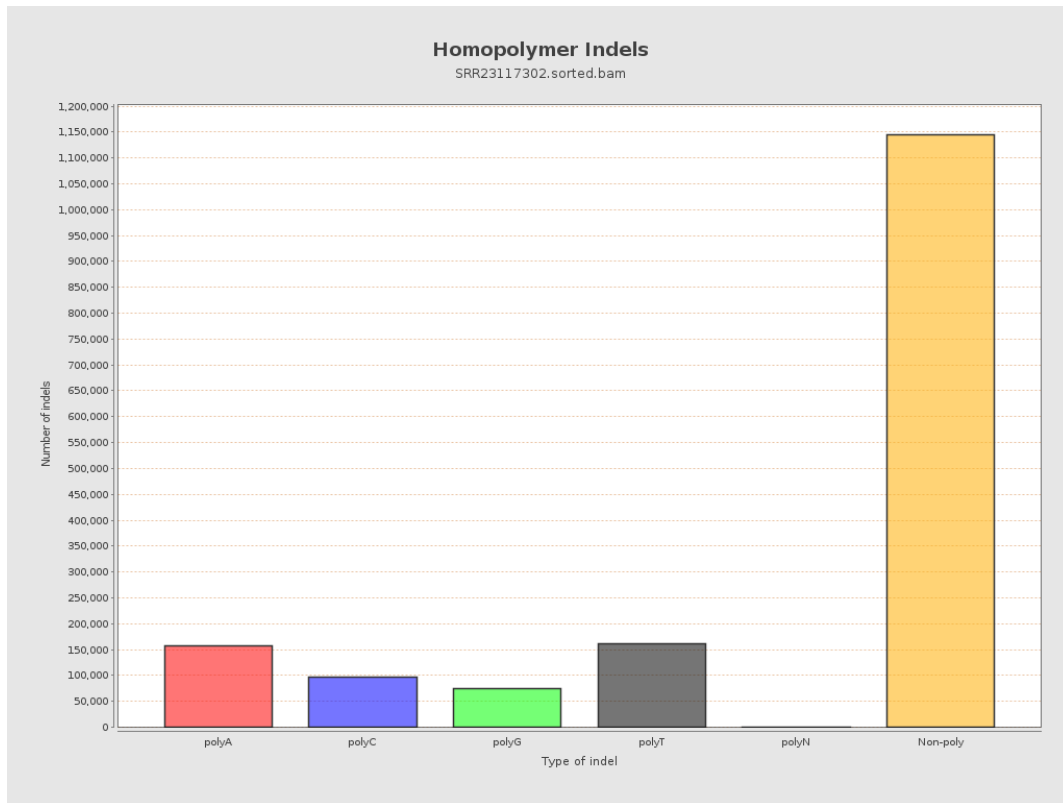
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

