

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 10:31:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR23117300.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_SRR23117300 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR23117300.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 10:31:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR23117300.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	465,924
Mapped reads	439,591 / 94.35%
Unmapped reads	26,333 / 5.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,915 / 0.63%
Read min/max/mean length	25 / 551 / 252.4
Duplicated reads (estimated)	98,245 / 21.09%
Duplication rate	18.28%
Clipped reads	442,505 / 94.97%

2.2. ACGT Content

Number/percentage of A's	28,391,556 / 28.57%
Number/percentage of C's	21,021,020 / 21.16%
Number/percentage of T's	29,439,913 / 29.63%
Number/percentage of G's	20,514,019 / 20.64%
Number/percentage of N's	0 / 0%
GC Percentage	41.8%

2.3. Coverage

Mean	0.0322

Standard Deviation	0.5895
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2.4. Mapping Quality

Mean Mapping Quality	53.56
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2.5. Mismatches and indels

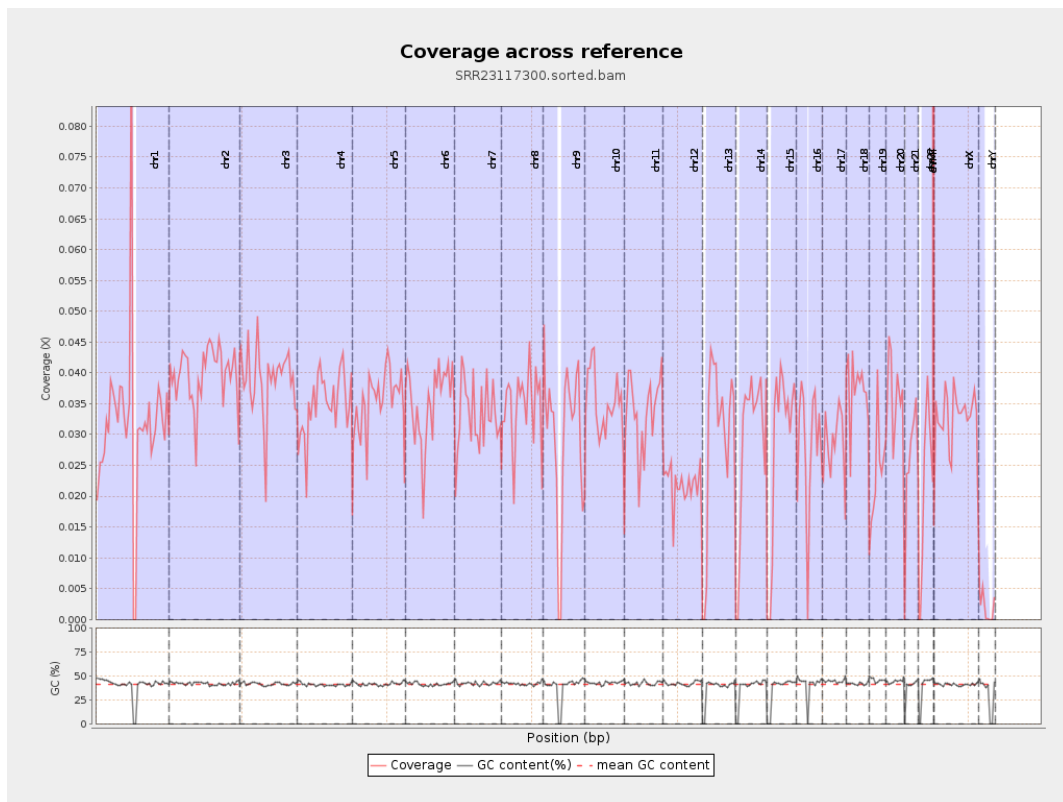
General error rate	1.42%
Mismatches	549,363
Insertions	782,517
Mapped reads with at least one insertion	65.02%
Deletions	181,172
Mapped reads with at least one deletion	28.08%
Homopolymer indels	26.42%

2.6. Chromosome stats

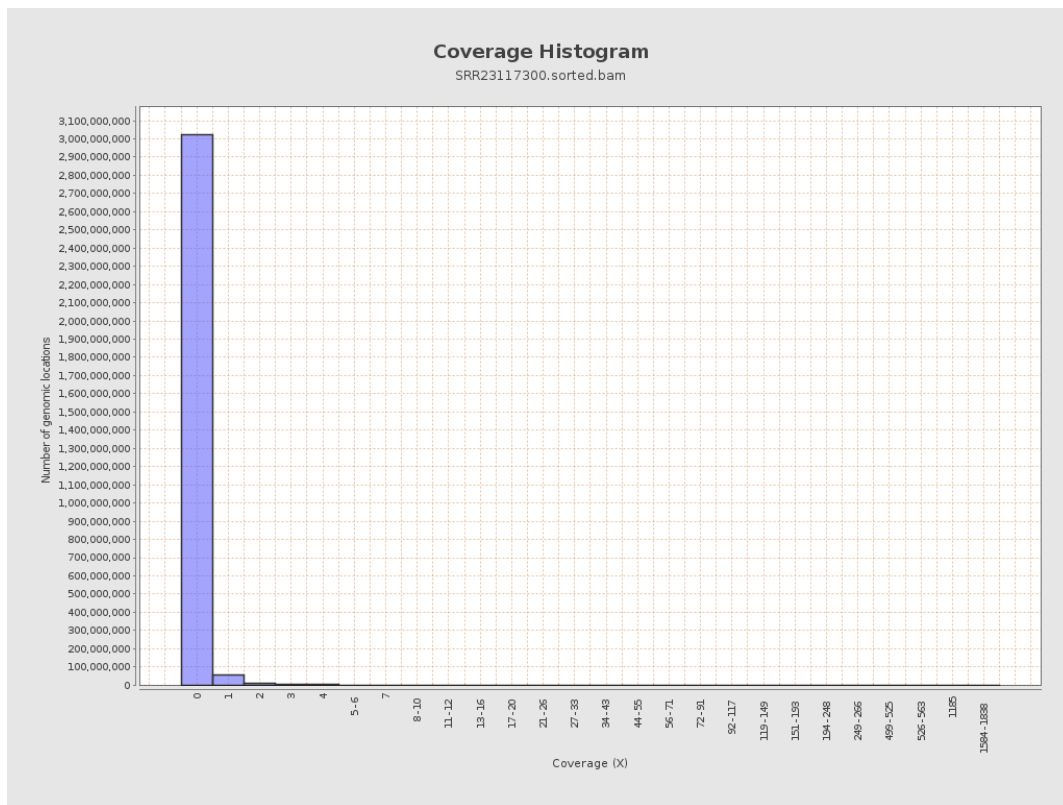
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7959251	0.0319	1.8103
chr2	243199373	9675274	0.0398	0.2744
chr3	198022430	7708465	0.0389	0.27
chr4	191154276	6681335	0.035	0.2569
chr5	180915260	6425175	0.0355	0.2523
chr6	171115067	6031705	0.0352	0.2531
chr7	159138663	5305510	0.0333	0.7256

chr8	146364022	5076131	0.0347	0.2539
chr9	141213431	4139170	0.0293	0.2331
chr10	135534747	4787722	0.0353	0.2916
chr11	135006516	4519616	0.0335	0.2477
chr12	133851895	2906394	0.0217	0.1906
chr13	115169878	3393008	0.0295	0.231
chr14	107349540	3076731	0.0287	0.2282
chr15	102531392	2956835	0.0288	0.2275
chr16	90354753	2534683	0.0281	0.2542
chr17	81195210	2287835	0.0282	0.236
chr18	78077248	2919704	0.0374	0.2856
chr19	59128983	1421836	0.024	0.4559
chr20	63025520	2259902	0.0359	0.2664
chr21	48129895	1233849	0.0256	0.2399
chr22	51304566	1089206	0.0212	0.2074
chrMT	16571	22694	1.3695	2.8142
chrX	155270560	5061304	0.0326	0.2423
chrY	59373566	111478	0.0019	0.0906

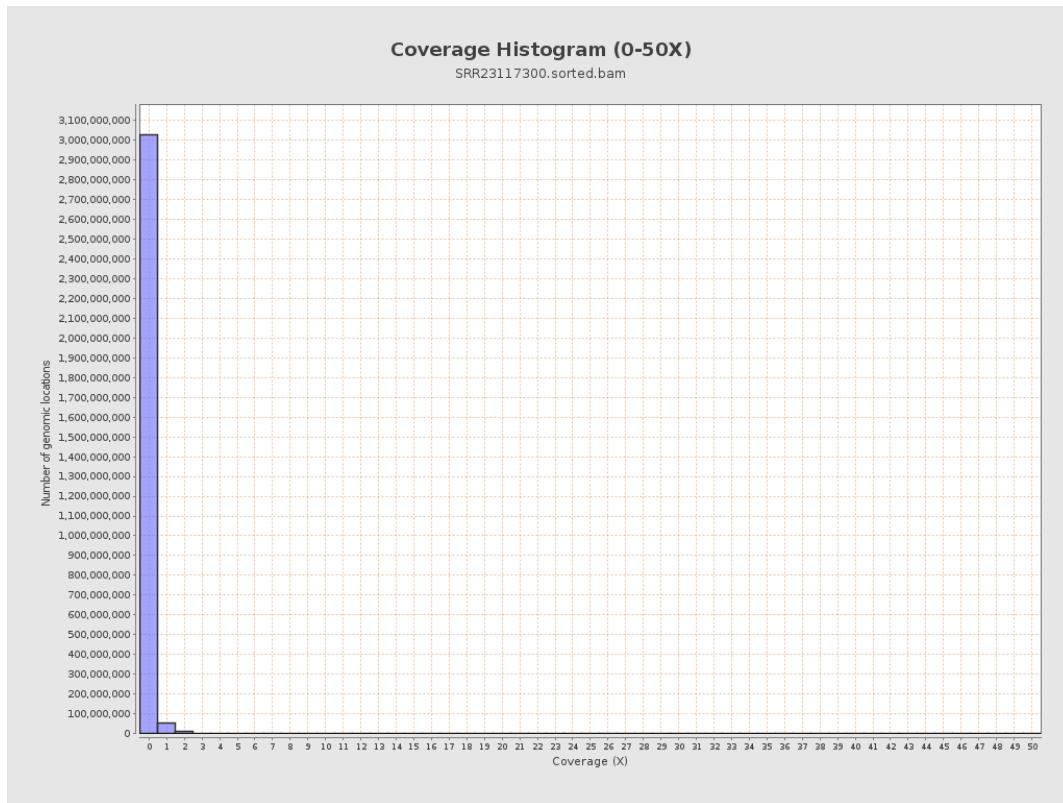
3. Results : Coverage across reference



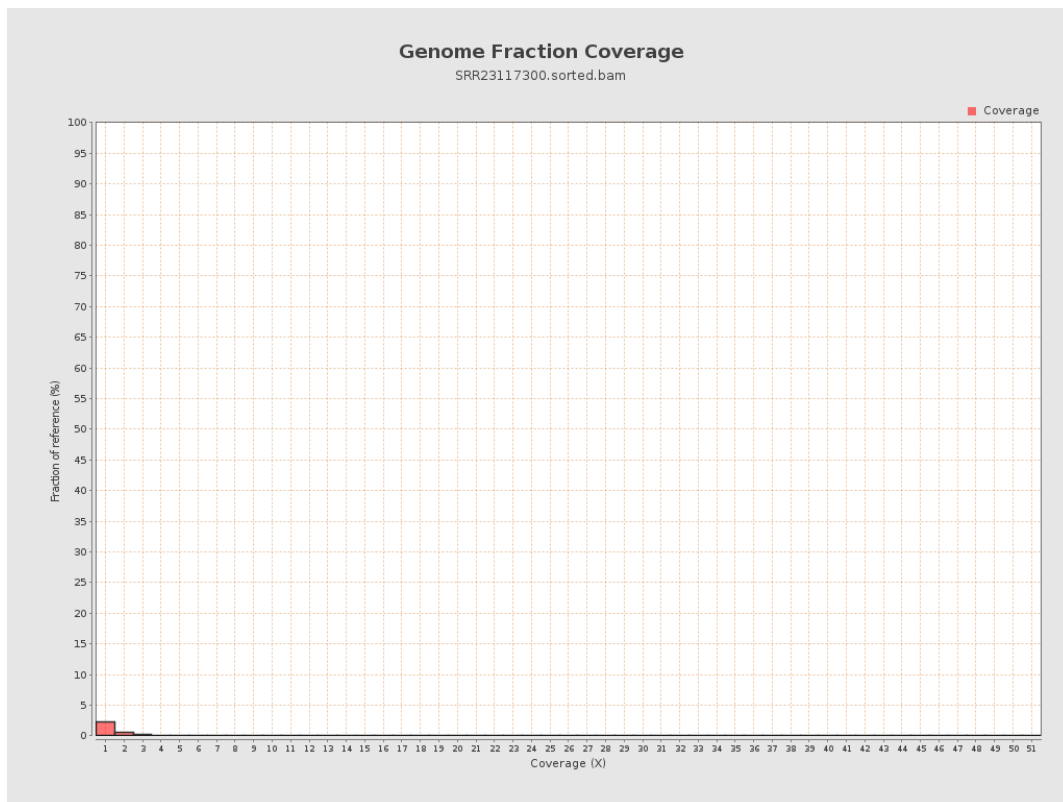
4. Results : Coverage Histogram



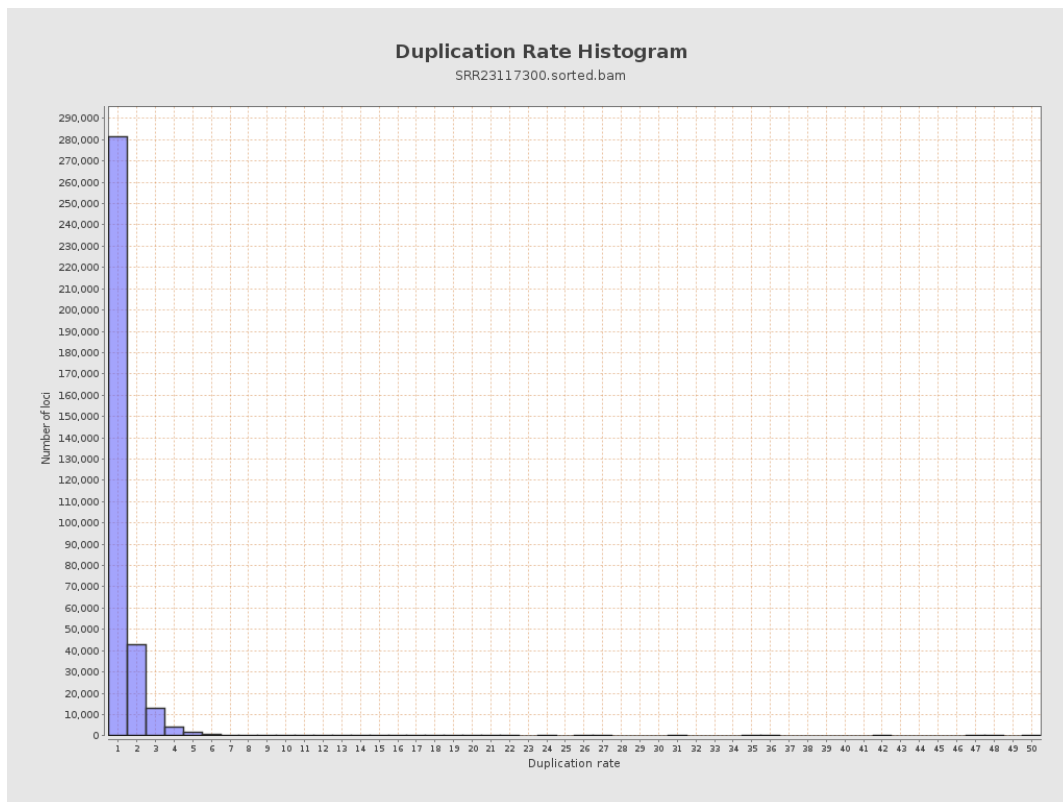
5. Results : Coverage Histogram (0-50X)



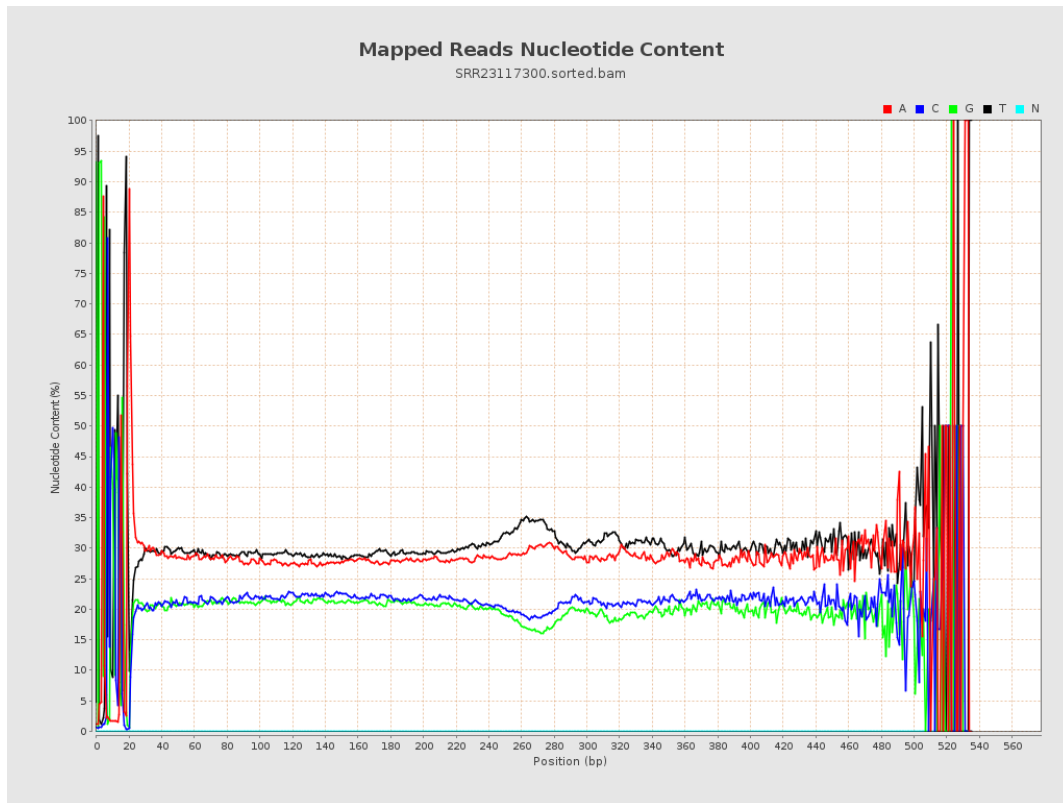
6. Results : Genome Fraction Coverage



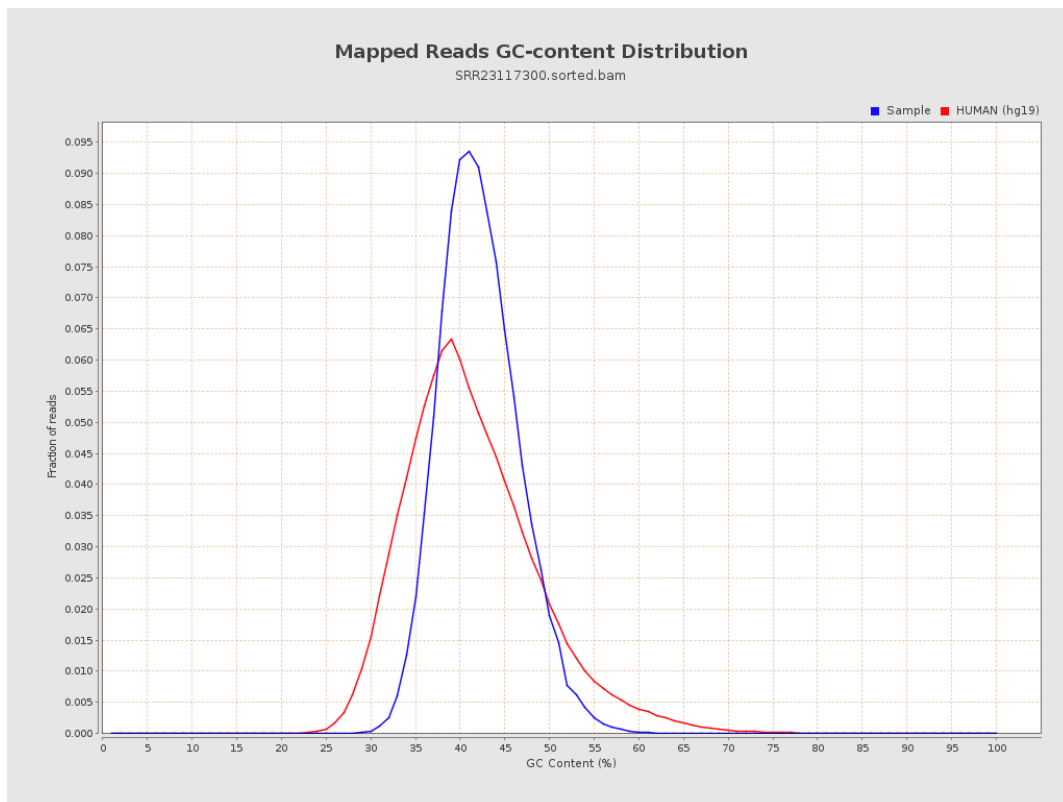
7. Results : Duplication Rate Histogram



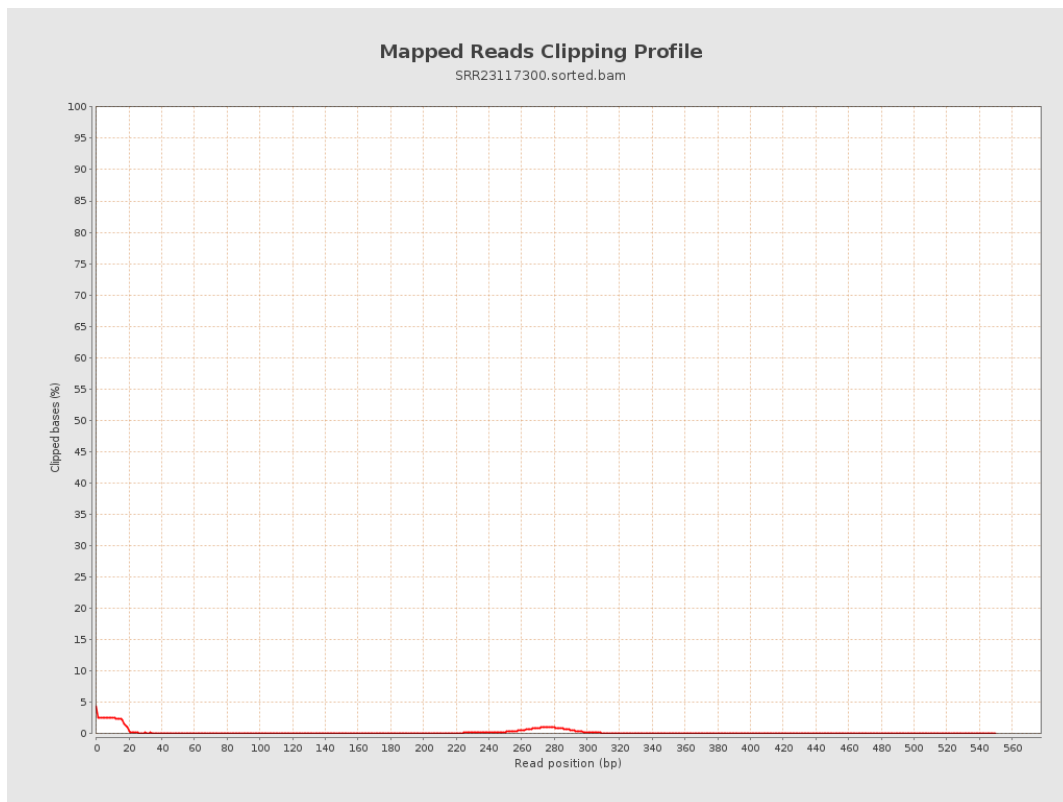
8. Results : Mapped Reads Nucleotide Content



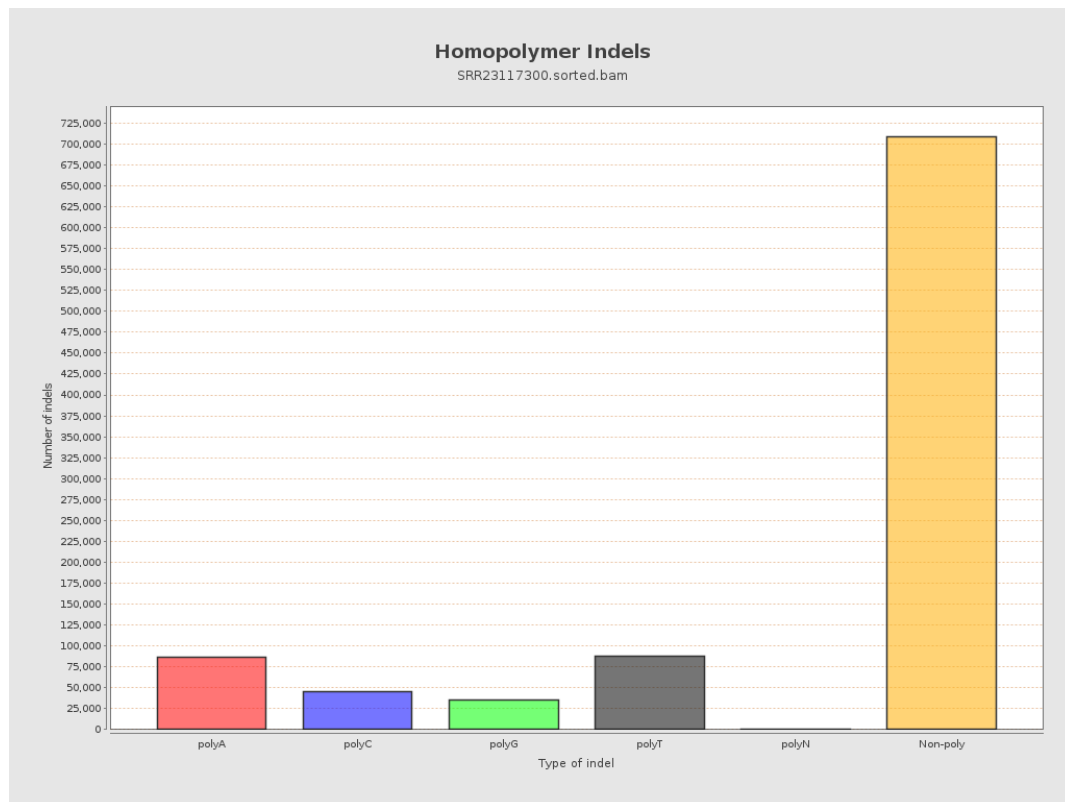
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

