

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 10:44:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR23117304.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_SRR23117304 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR23117304.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 10:44:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR23117304.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	902,652
Mapped reads	869,026 / 96.27%
Unmapped reads	33,626 / 3.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,984 / 0.55%
Read min/max/mean length	25 / 593 / 263.4
Duplicated reads (estimated)	294,502 / 32.63%
Duplication rate	27.13%
Clipped reads	874,006 / 96.83%

2.2. ACGT Content

Number/percentage of A's	59,496,704 / 29.44%
Number/percentage of C's	41,798,834 / 20.69%
Number/percentage of T's	58,853,967 / 29.13%
Number/percentage of G's	41,922,183 / 20.75%
Number/percentage of N's	0 / 0%
GC Percentage	41.43%

2.3. Coverage

Mean	0.0654

Standard Deviation	1.1437
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	53.77
----------------------	-------

2.5. Mismatches and indels

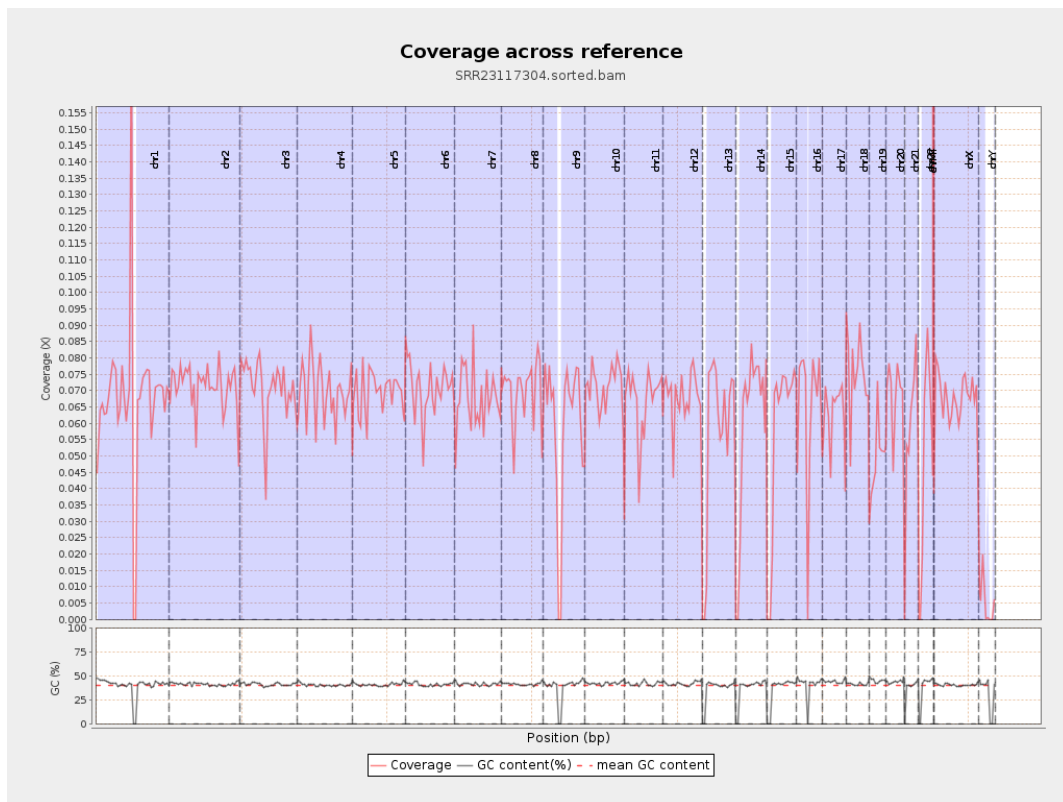
General error rate	0.88%
Mismatches	1,051,886
Insertions	629,918
Mapped reads with at least one insertion	33.47%
Deletions	275,001
Mapped reads with at least one deletion	22.46%
Homopolymer indels	32.88%

2.6. Chromosome stats

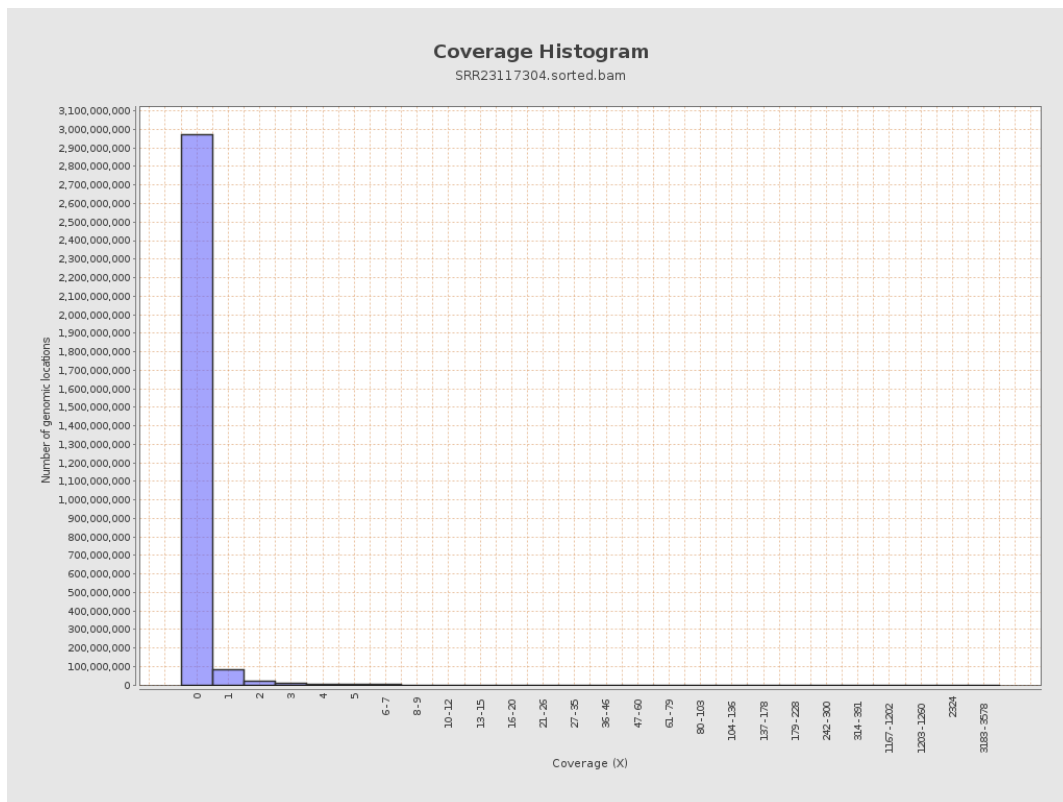
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	16845866	0.0676	3.5407
chr2	243199373	17351397	0.0713	0.4286
chr3	198022430	14032302	0.0709	0.4077
chr4	191154276	13317597	0.0697	0.4959
chr5	180915260	12559484	0.0694	0.4045
chr6	171115067	12126798	0.0709	0.4107
chr7	159138663	10822442	0.068	1.562

chr8	146364022	10237188	0.0699	0.4097
chr9	141213431	8414258	0.0596	0.393
chr10	135534747	9720787	0.0717	0.5711
chr11	135006516	9032977	0.0669	0.4002
chr12	133851895	9090911	0.0679	0.4069
chr13	115169878	6505584	0.0565	0.3592
chr14	107349540	6367886	0.0593	0.3844
chr15	102531392	5876430	0.0573	0.3727
chr16	90354753	5860151	0.0649	0.5386
chr17	81195210	5044292	0.0621	0.5057
chr18	78077248	5886037	0.0754	0.5177
chr19	59128983	2930544	0.0496	0.7624
chr20	63025520	4261951	0.0676	0.4662
chr21	48129895	2801460	0.0582	0.492
chr22	51304566	2484780	0.0484	0.3866
chrMT	16571	76724	4.63	12.7047
chrX	155270560	10478853	0.0675	0.4057
chrY	59373566	293084	0.0049	0.4006

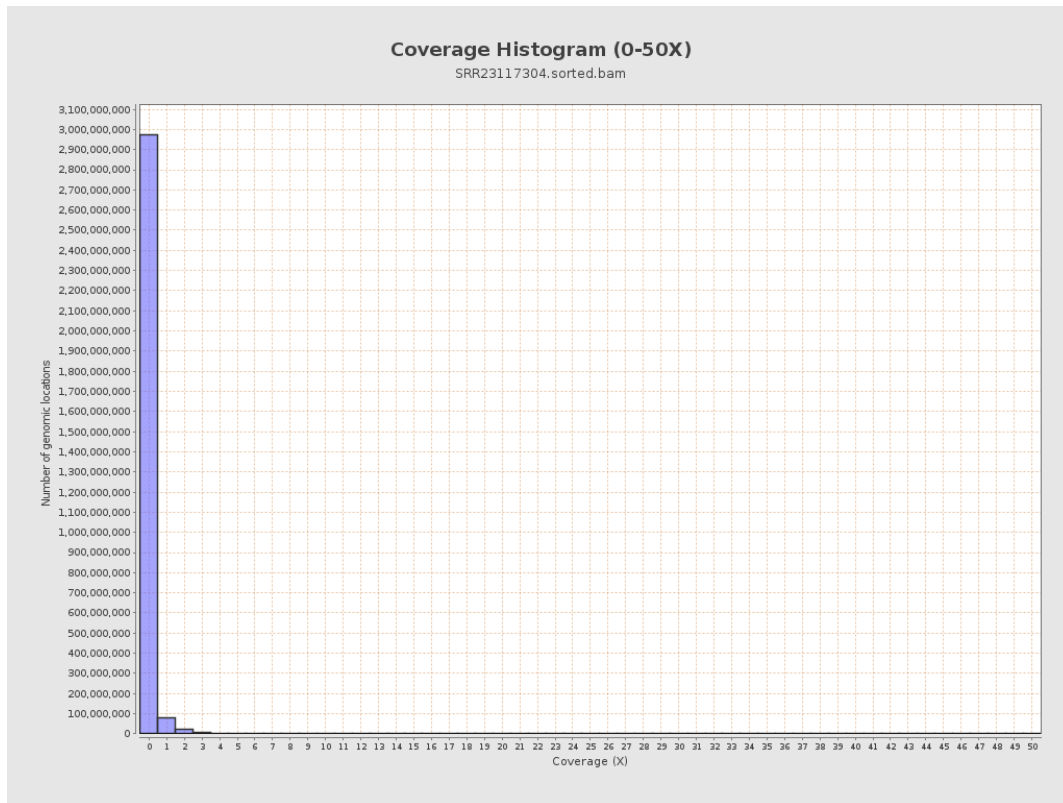
3. Results : Coverage across reference



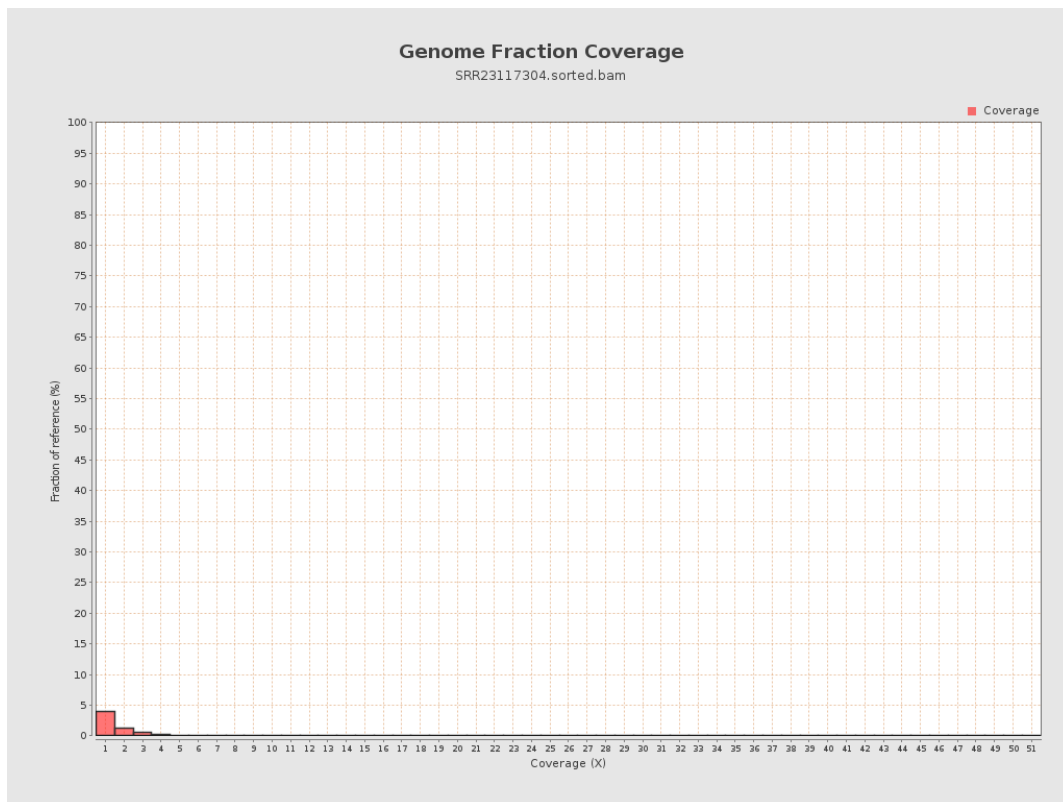
4. Results : Coverage Histogram



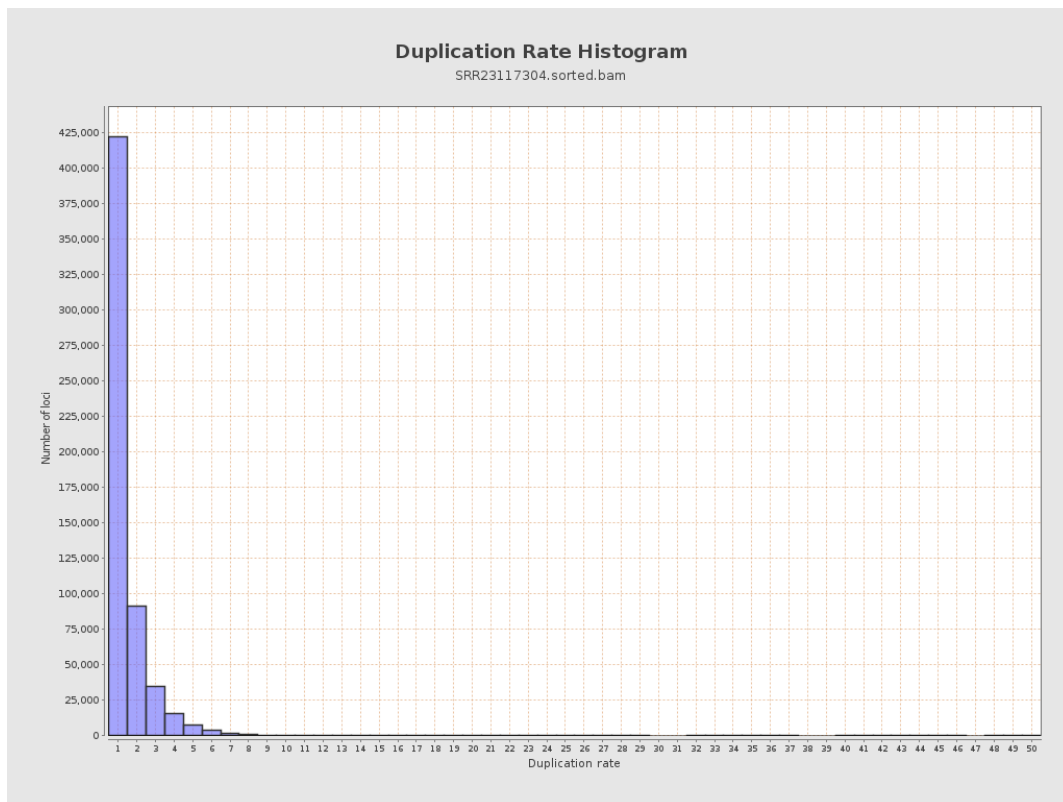
5. Results : Coverage Histogram (0-50X)



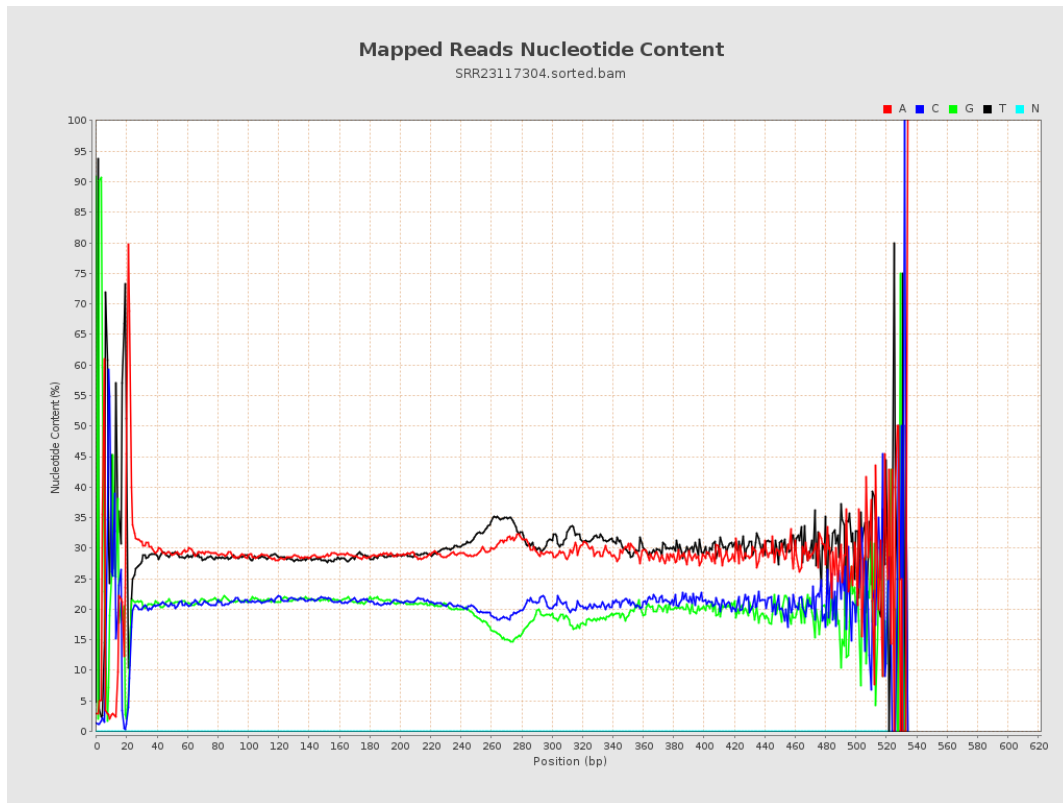
6. Results : Genome Fraction Coverage



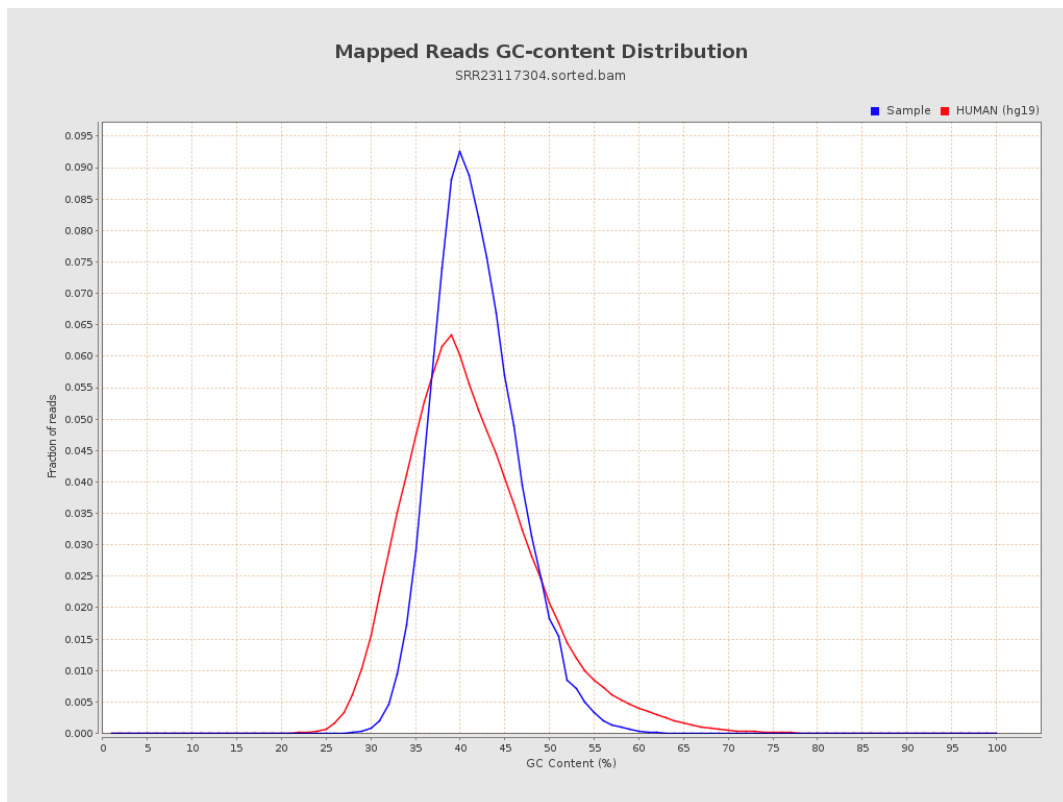
7. Results : Duplication Rate Histogram



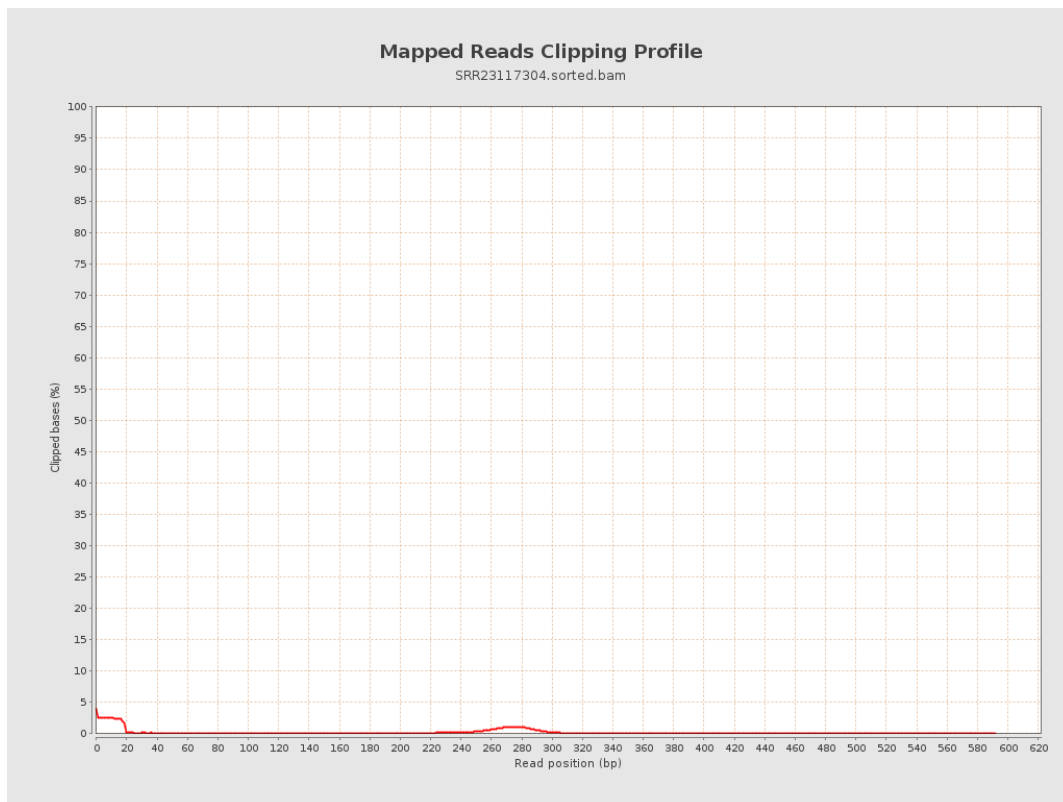
8. Results : Mapped Reads Nucleotide Content



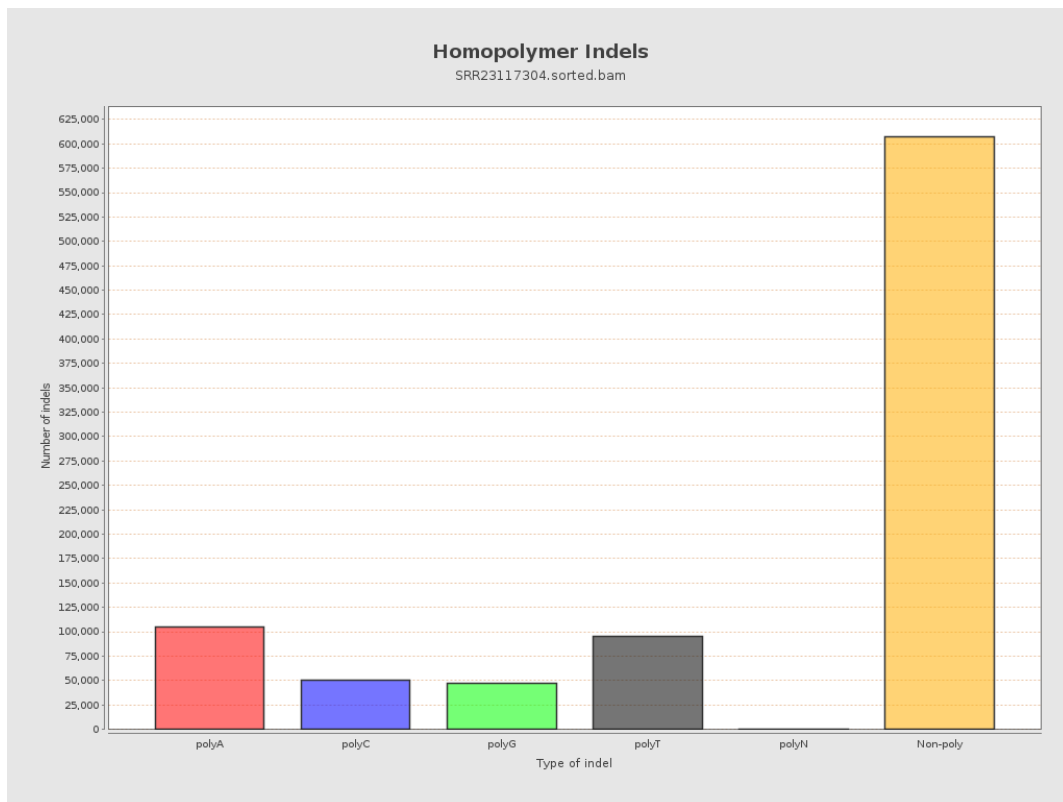
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

