

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 06:56:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818906.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_SRR1818906 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818906.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 06:56:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818906.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,978,575
Mapped reads	1,944,496 / 98.28%
Unmapped reads	34,079 / 1.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,216 / 1.43%
Read min/max/mean length	30 / 101 / 101.55
Duplicated reads (estimated)	385,591 / 19.49%
Duplication rate	16.71%
Clipped reads	1,944,012 / 98.25%

2.2. ACGT Content

Number/percentage of A's	49,809,907 / 27.65%
Number/percentage of C's	38,092,153 / 21.14%
Number/percentage of T's	51,614,255 / 28.65%
Number/percentage of G's	40,636,557 / 22.56%
Number/percentage of N's	2,679 / 0%
GC Percentage	43.7%

2.3. Coverage

Mean	0.0582

Standard Deviation	0.6459
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2.4. Mapping Quality

Mean Mapping Quality	49.38
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2.5. Mismatches and indels

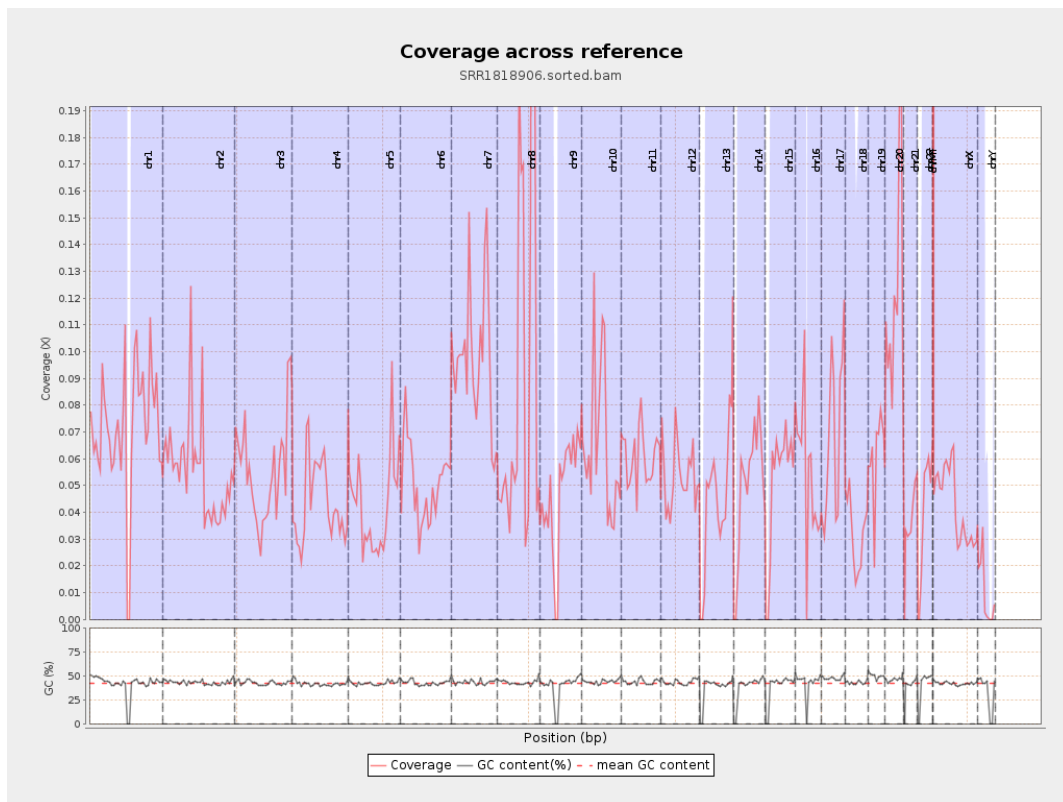
General error rate	0.64%
Mismatches	1,080,145
Insertions	27,317
Mapped reads with at least one insertion	1.36%
Deletions	58,764
Mapped reads with at least one deletion	2.96%
Homopolymer indels	40.6%

2.6. Chromosome stats

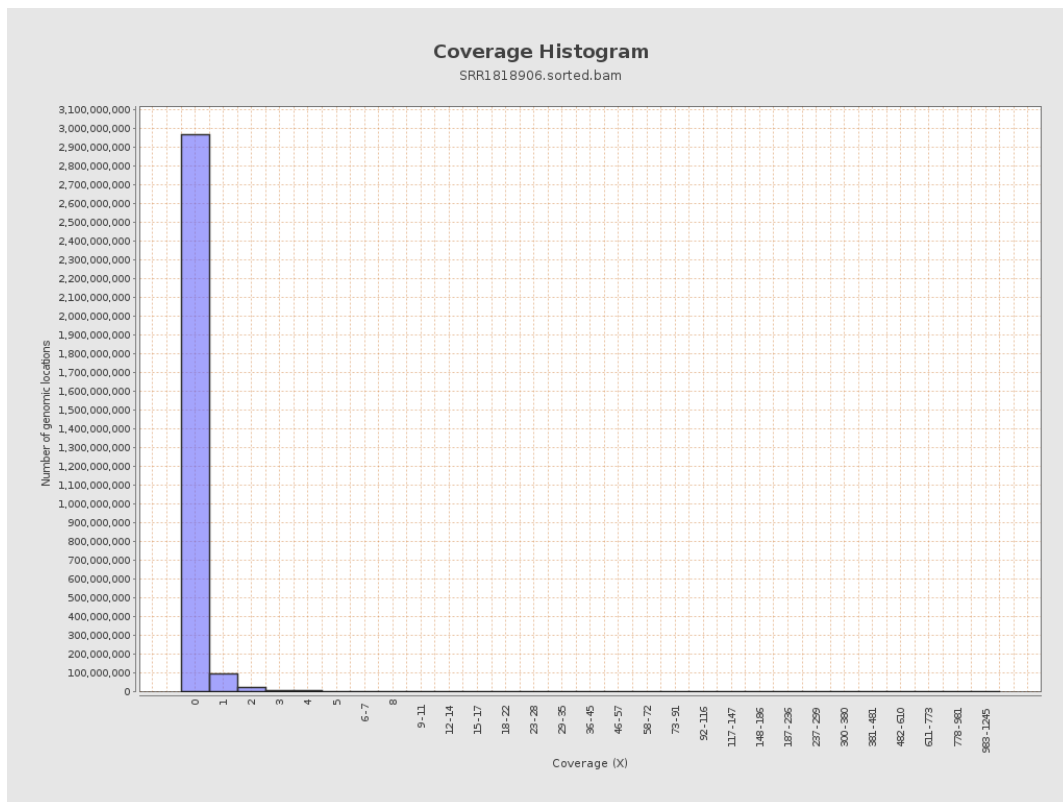
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	17841601	0.0716	0.9404
chr2	243199373	13518359	0.0556	0.959
chr3	198022430	10938191	0.0552	0.3115
chr4	191154276	8391522	0.0439	0.3789
chr5	180915260	7802153	0.0431	0.2943
chr6	171115067	8693780	0.0508	0.33
chr7	159138663	15527954	0.0976	1.3449

chr8	146364022	15077564	0.103	0.552
chr9	141213431	6679643	0.0473	0.5442
chr10	135534747	8709912	0.0643	0.832
chr11	135006516	8173869	0.0605	0.392
chr12	133851895	7261723	0.0543	0.3135
chr13	115169878	5174128	0.0449	0.2771
chr14	107349540	5524828	0.0515	0.3351
chr15	102531392	5205703	0.0508	0.3014
chr16	90354753	4876580	0.054	0.7147
chr17	81195210	5390271	0.0664	0.4249
chr18	78077248	2524625	0.0323	0.5902
chr19	59128983	3595633	0.0608	0.8668
chr20	63025520	7936339	0.1259	0.5153
chr21	48129895	1754335	0.0365	0.2933
chr22	51304566	1993031	0.0388	0.2894
chrMT	16571	457173	27.5887	16.5939
chrX	155270560	6621862	0.0426	0.343
chrY	59373566	599326	0.0101	0.8197

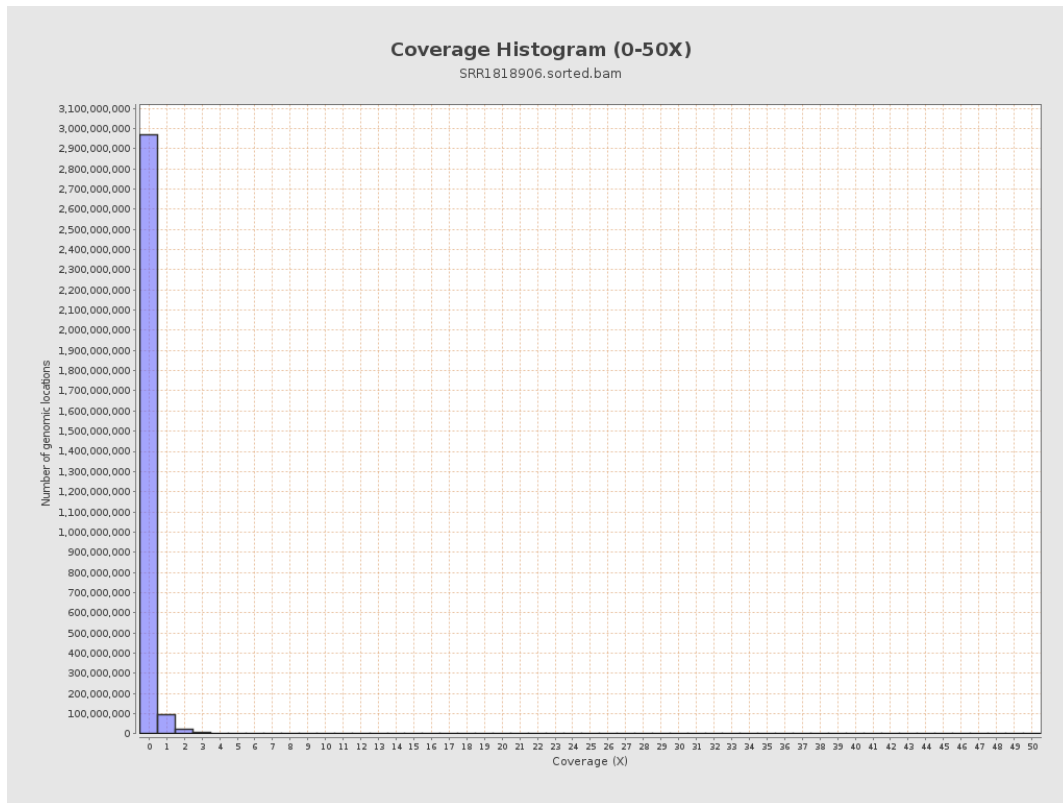
3. Results : Coverage across reference



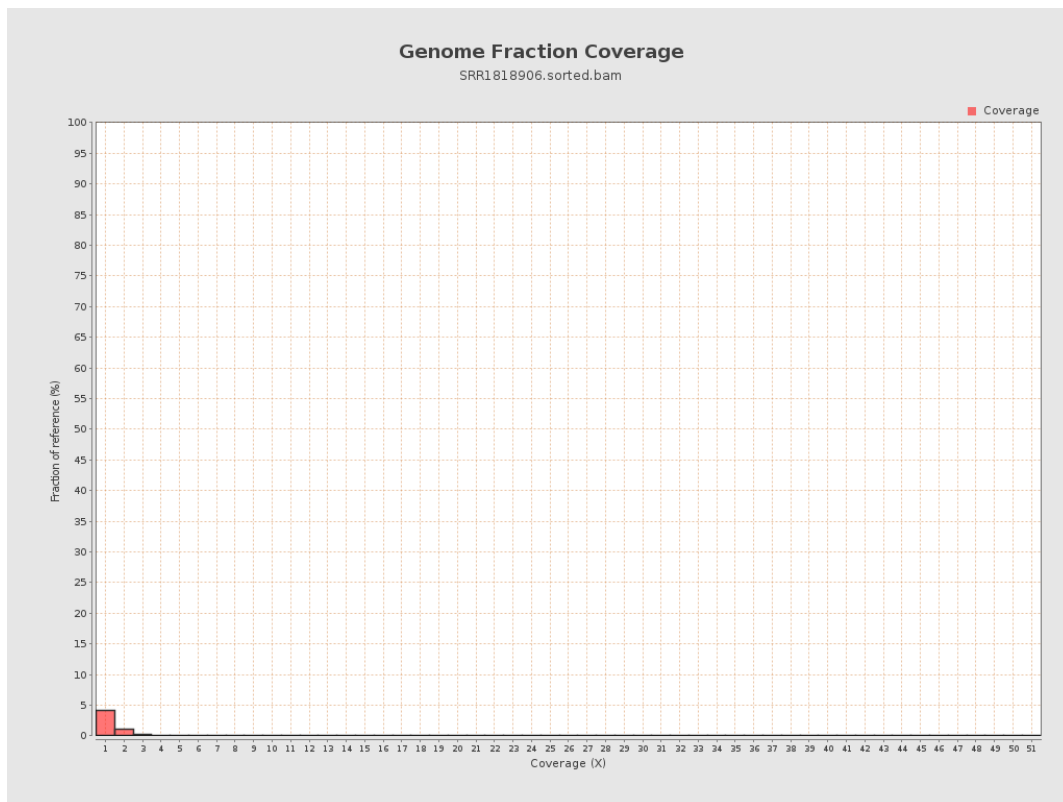
4. Results : Coverage Histogram



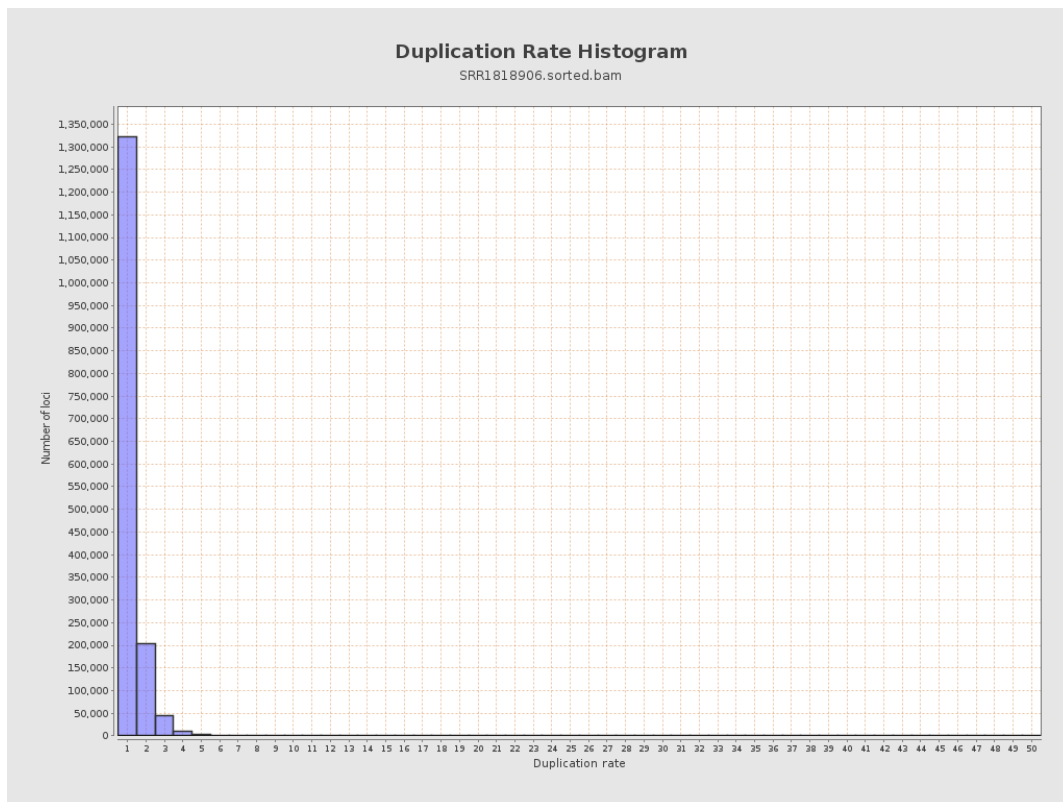
5. Results : Coverage Histogram (0-50X)



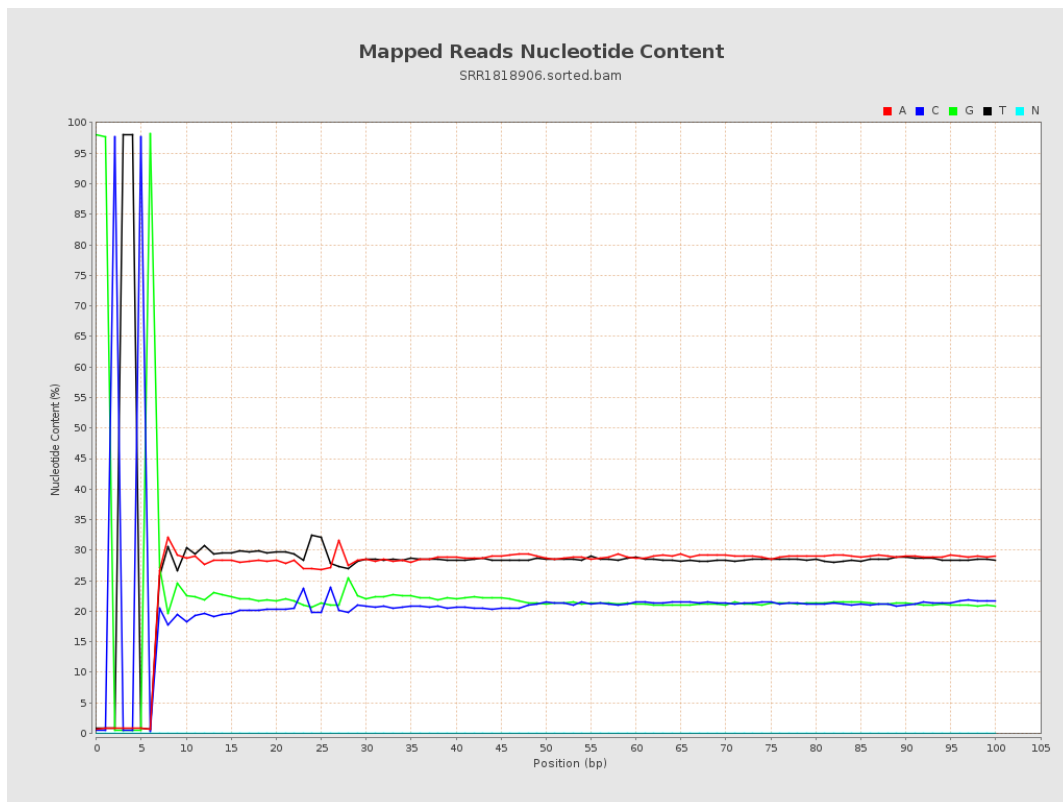
6. Results : Genome Fraction Coverage



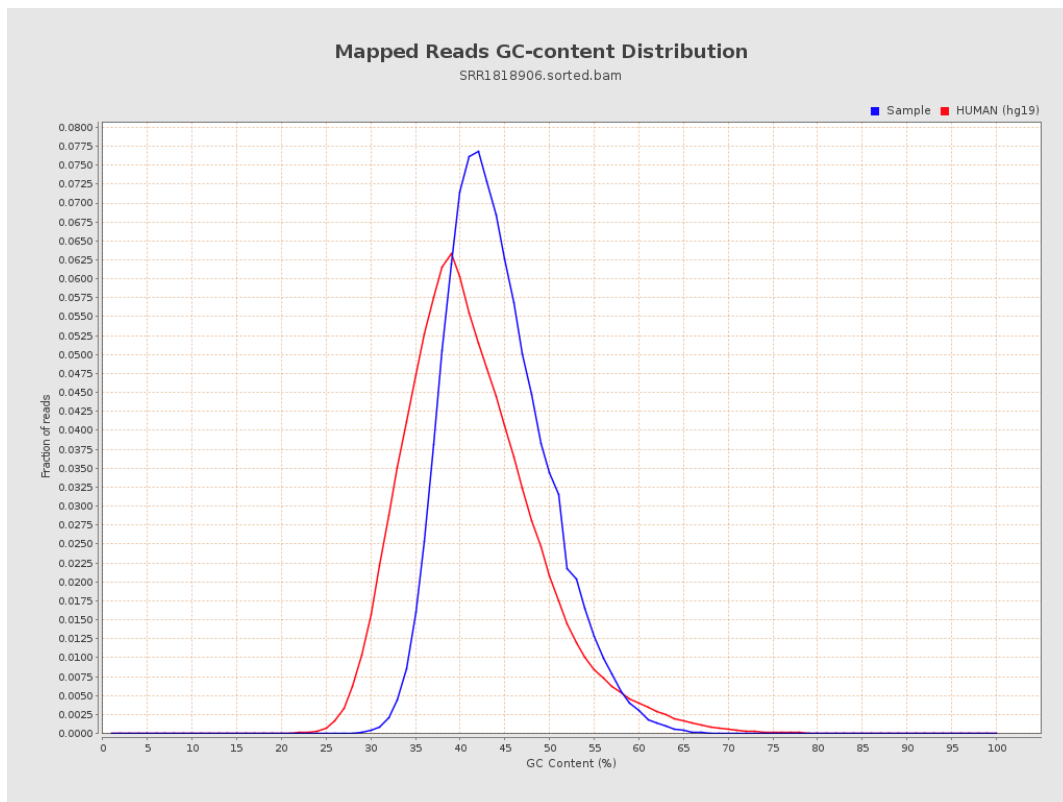
7. Results : Duplication Rate Histogram



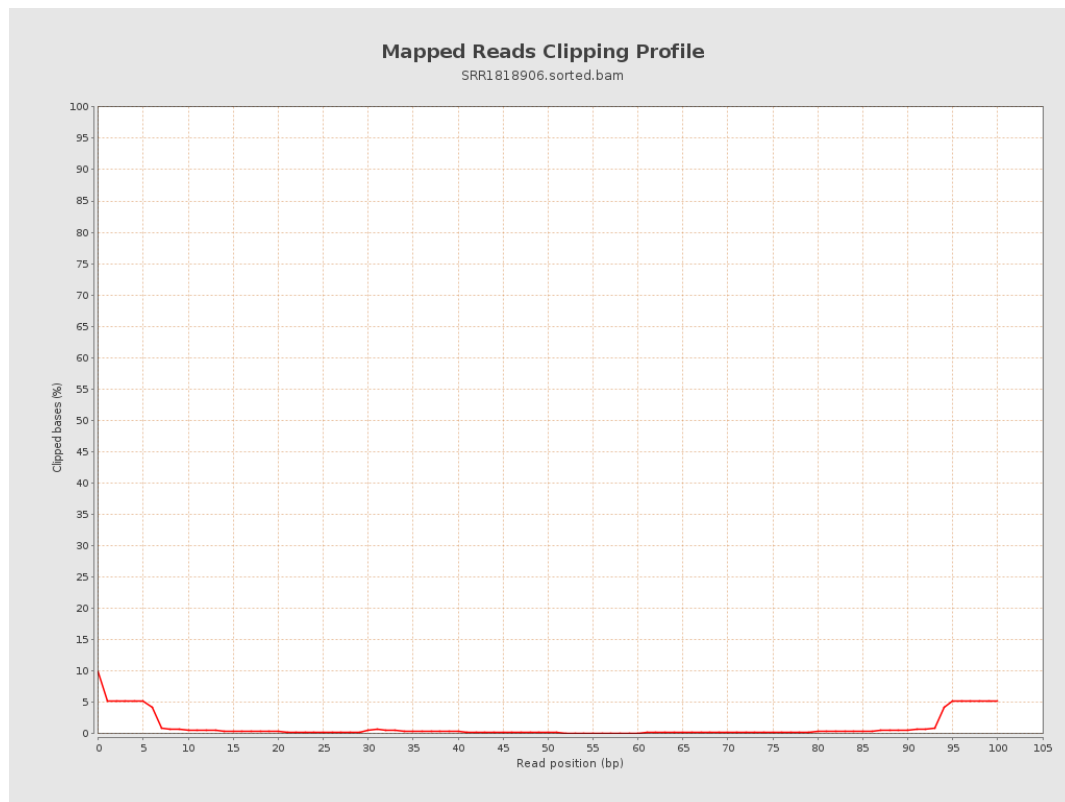
8. Results : Mapped Reads Nucleotide Content



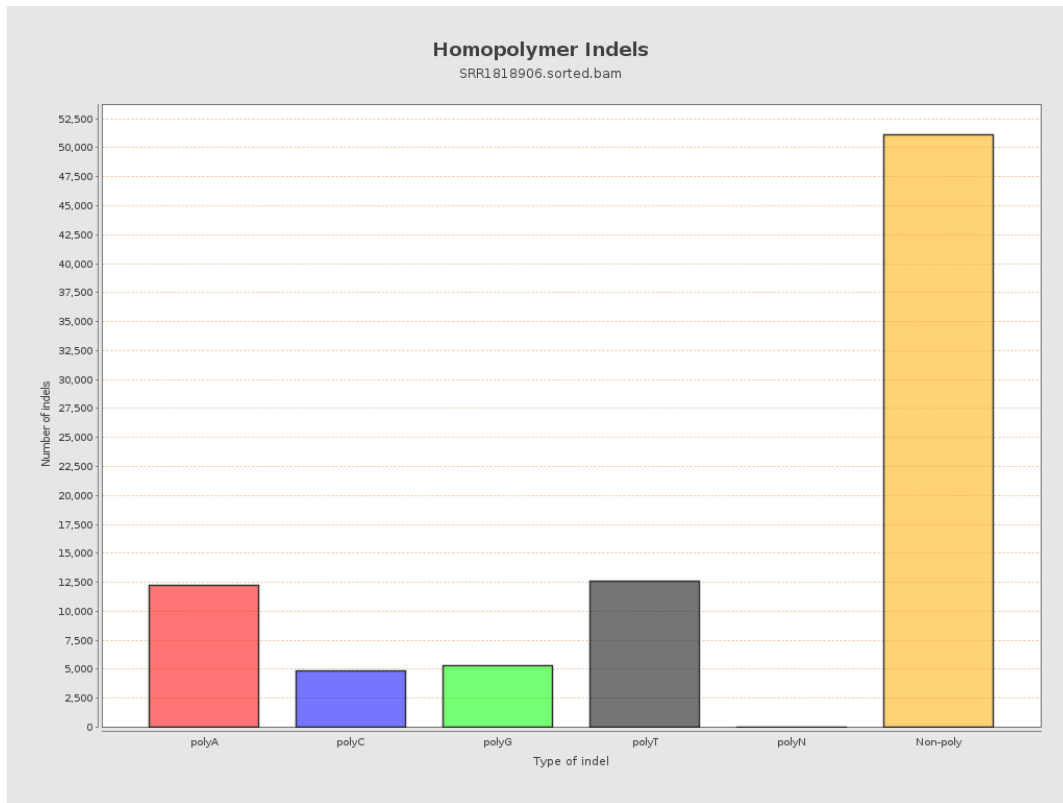
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

