

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 04:01:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818881.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_SRR1818881 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818881.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 04:01:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818881.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,614,322
Mapped reads	1,575,344 / 97.59%
Unmapped reads	38,978 / 2.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,321 / 1.44%
Read min/max/mean length	30 / 101 / 101.56
Duplicated reads (estimated)	258,778 / 16.03%
Duplication rate	13.39%
Clipped reads	1,586,531 / 98.28%

2.2. ACGT Content

Number/percentage of A's	42,918,688 / 29.45%
Number/percentage of C's	30,790,974 / 21.13%
Number/percentage of T's	40,376,762 / 27.71%
Number/percentage of G's	31,630,981 / 21.71%
Number/percentage of N's	2,129 / 0%
GC Percentage	42.84%

2.3. Coverage

Mean	0.0471

Standard Deviation	0.6163
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2.4. Mapping Quality

Mean Mapping Quality	49.2
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2.5. Mismatches and indels

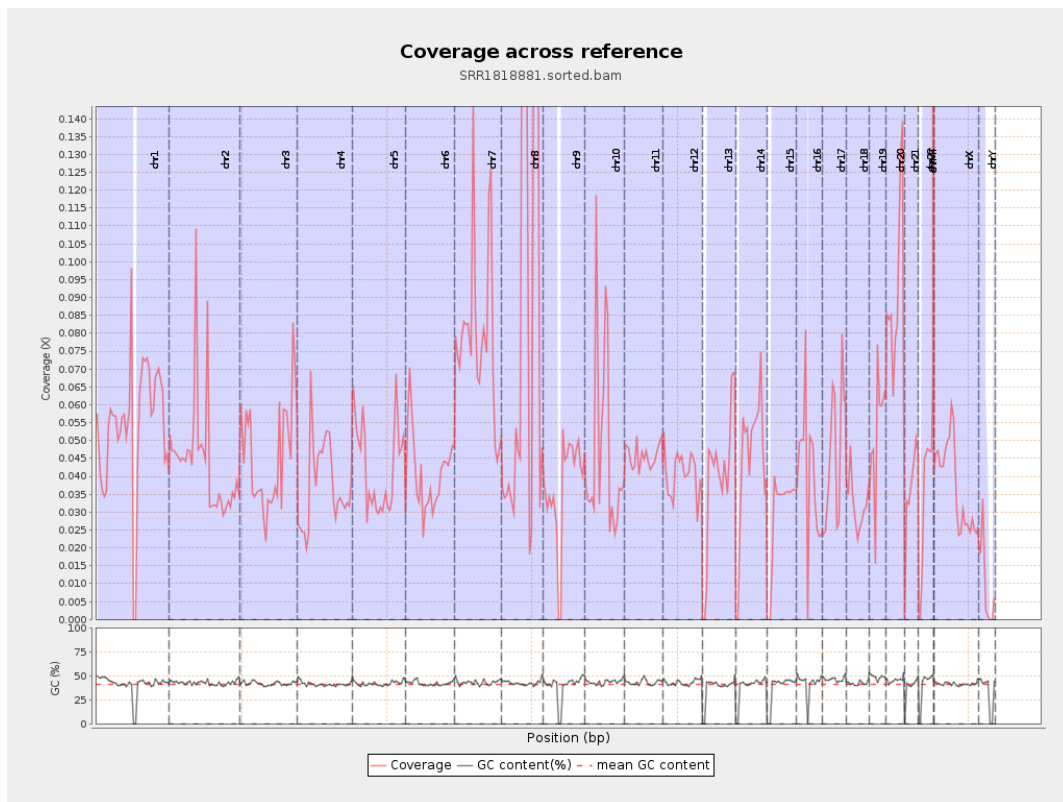
General error rate	0.65%
Mismatches	882,292
Insertions	24,773
Mapped reads with at least one insertion	1.52%
Deletions	47,791
Mapped reads with at least one deletion	2.96%
Homopolymer indels	40.02%

2.6. Chromosome stats

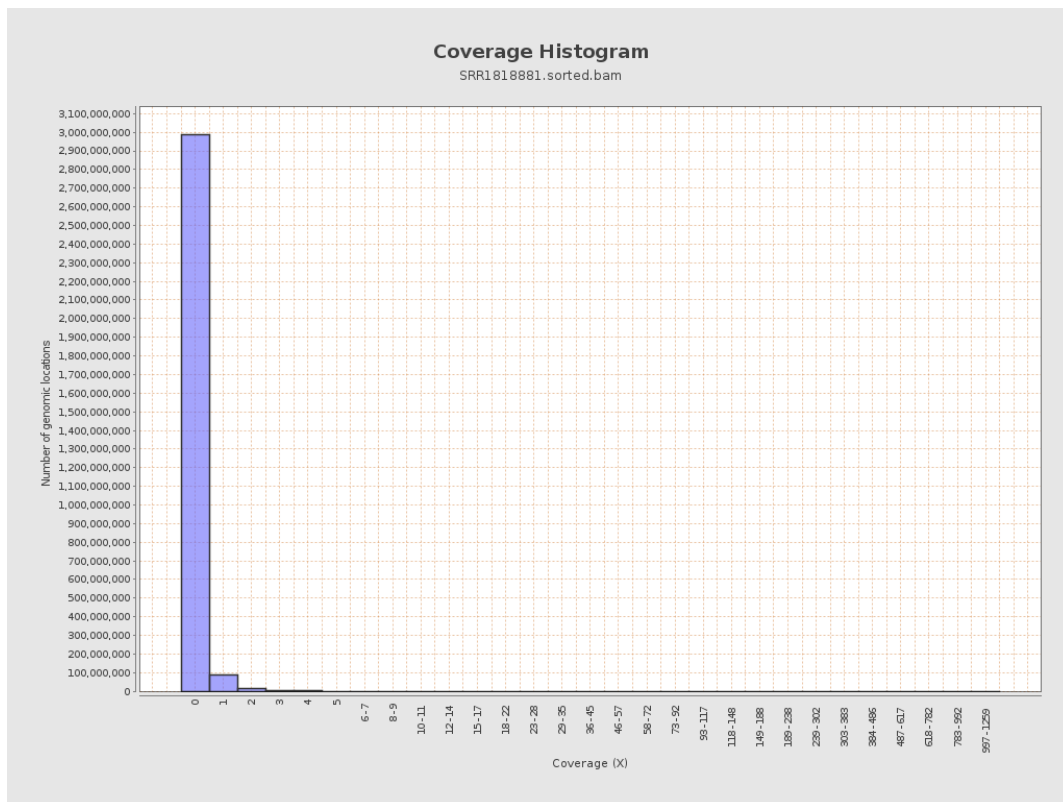
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	13433559	0.0539	0.9712
chr2	243199373	10779390	0.0443	0.8613
chr3	198022430	9013058	0.0455	0.2685
chr4	191154276	7119933	0.0372	0.3405
chr5	180915260	7694314	0.0425	0.2727
chr6	171115067	6971638	0.0407	0.2879
chr7	159138663	12734266	0.08	1.3692

chr8	146364022	13787561	0.0942	0.5181
chr9	141213431	5182868	0.0367	0.4892
chr10	135534747	6292797	0.0464	0.8123
chr11	135006516	6157475	0.0456	0.3444
chr12	133851895	5484924	0.041	0.2551
chr13	115169878	4573478	0.0397	0.2478
chr14	107349540	4747476	0.0442	0.2927
chr15	102531392	3017209	0.0294	0.2114
chr16	90354753	3568476	0.0395	0.6386
chr17	81195210	3798805	0.0468	0.3751
chr18	78077248	2526390	0.0324	0.5684
chr19	59128983	3086180	0.0522	0.8897
chr20	63025520	5809305	0.0922	0.411
chr21	48129895	1755256	0.0365	0.2963
chr22	51304566	1704508	0.0332	0.2563
chrMT	16571	227344	13.7194	9.2494
chrX	155270560	5776624	0.0372	0.3108
chrY	59373566	571239	0.0096	0.7235

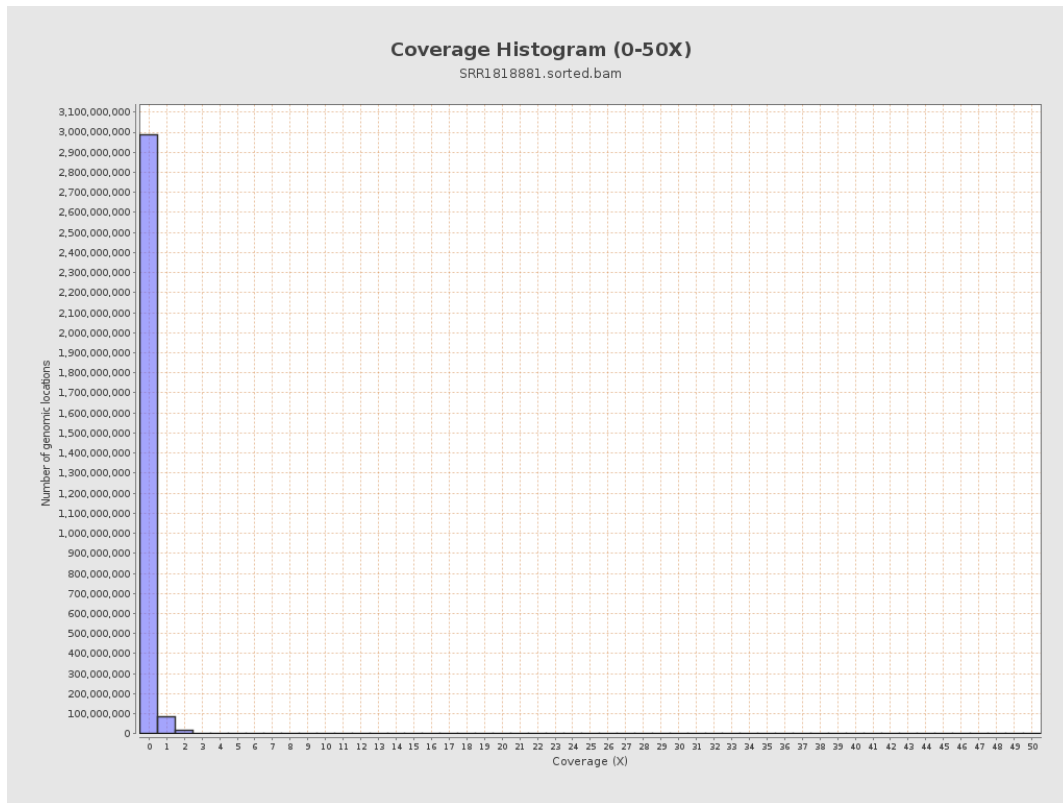
3. Results : Coverage across reference



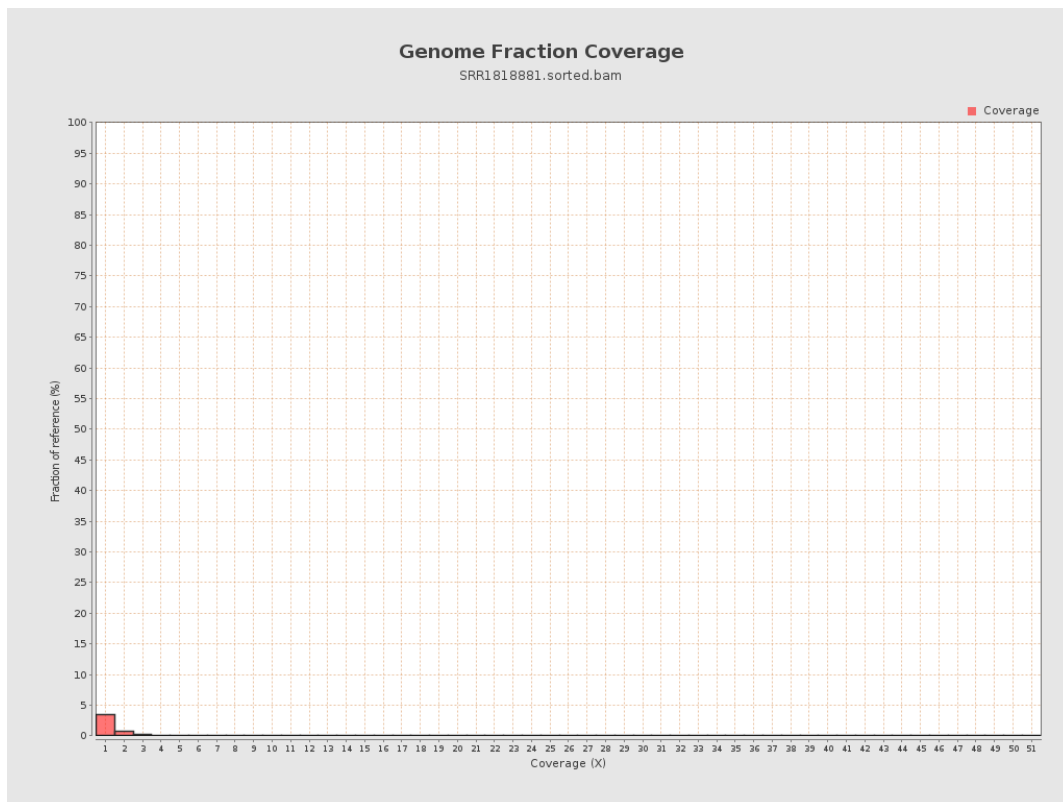
4. Results : Coverage Histogram



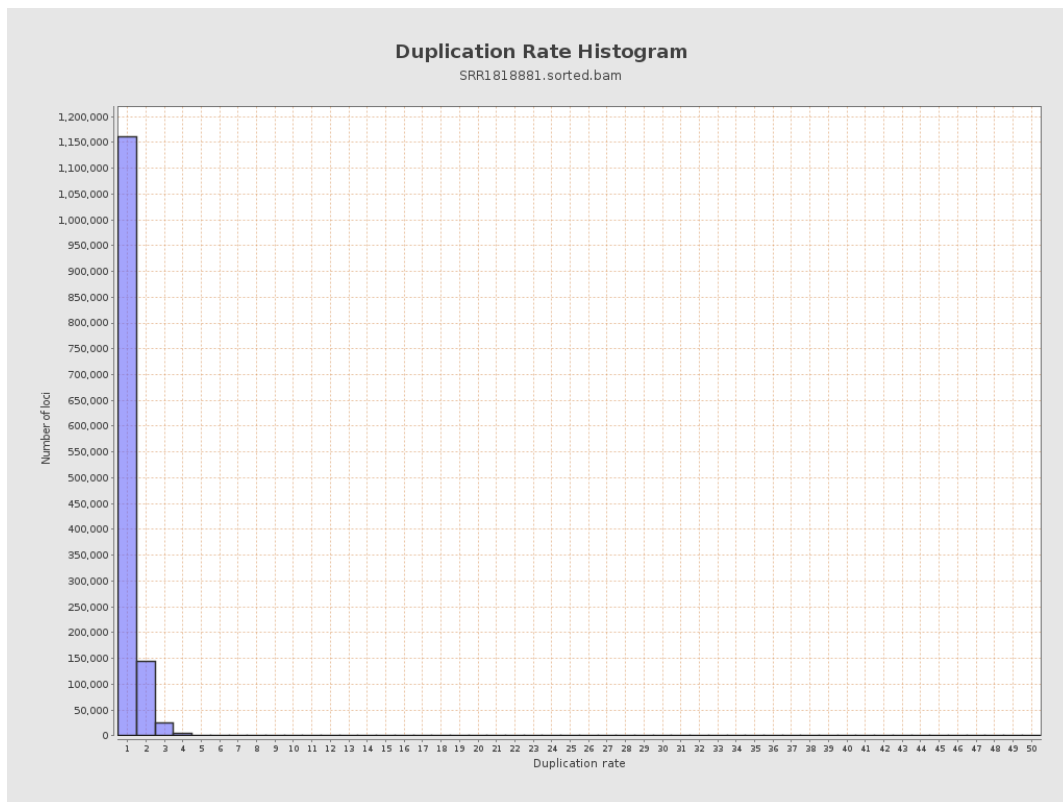
5. Results : Coverage Histogram (0-50X)



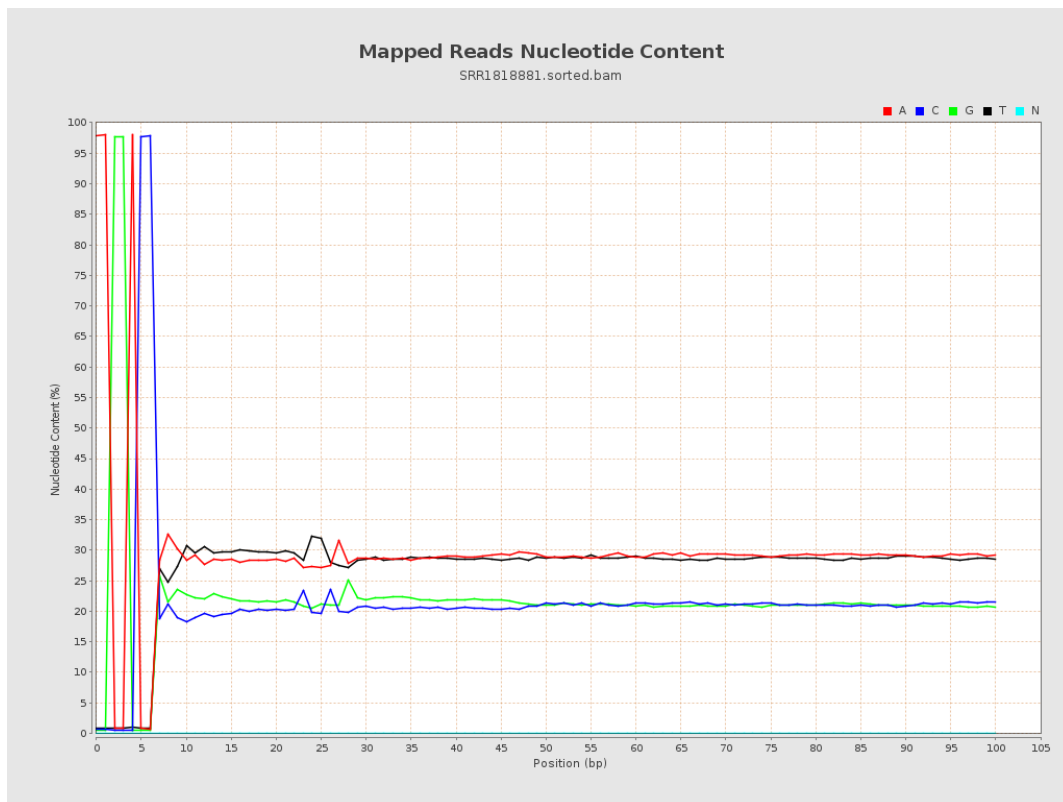
6. Results : Genome Fraction Coverage



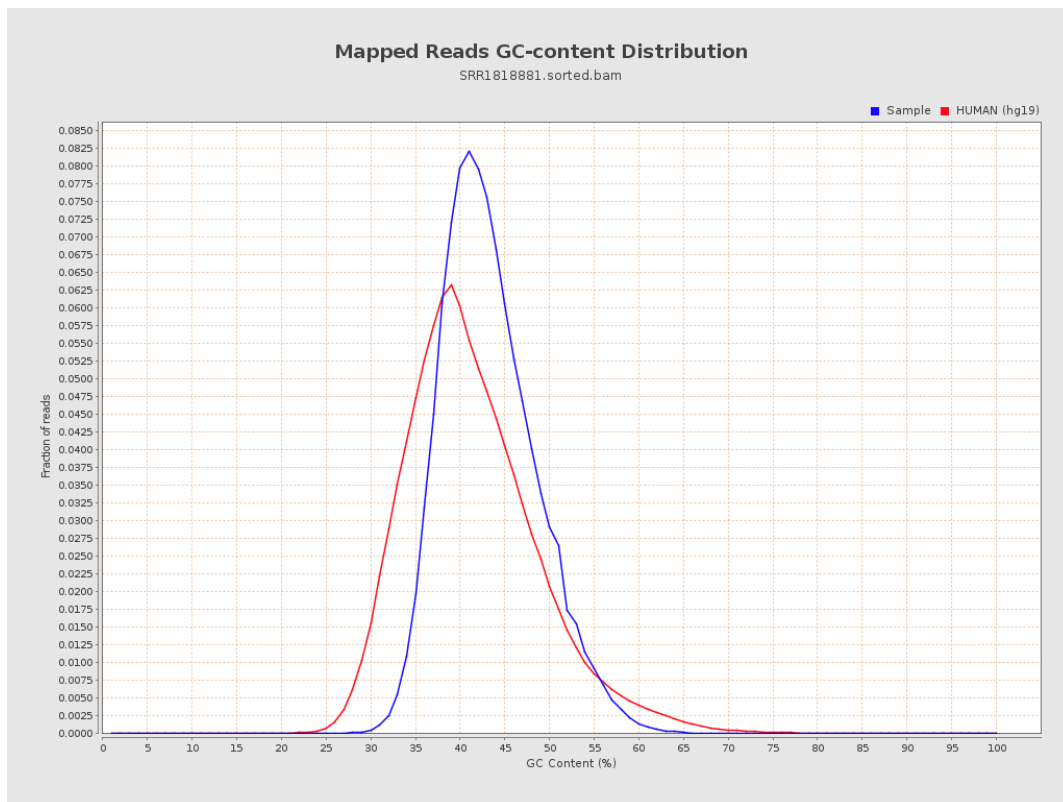
7. Results : Duplication Rate Histogram



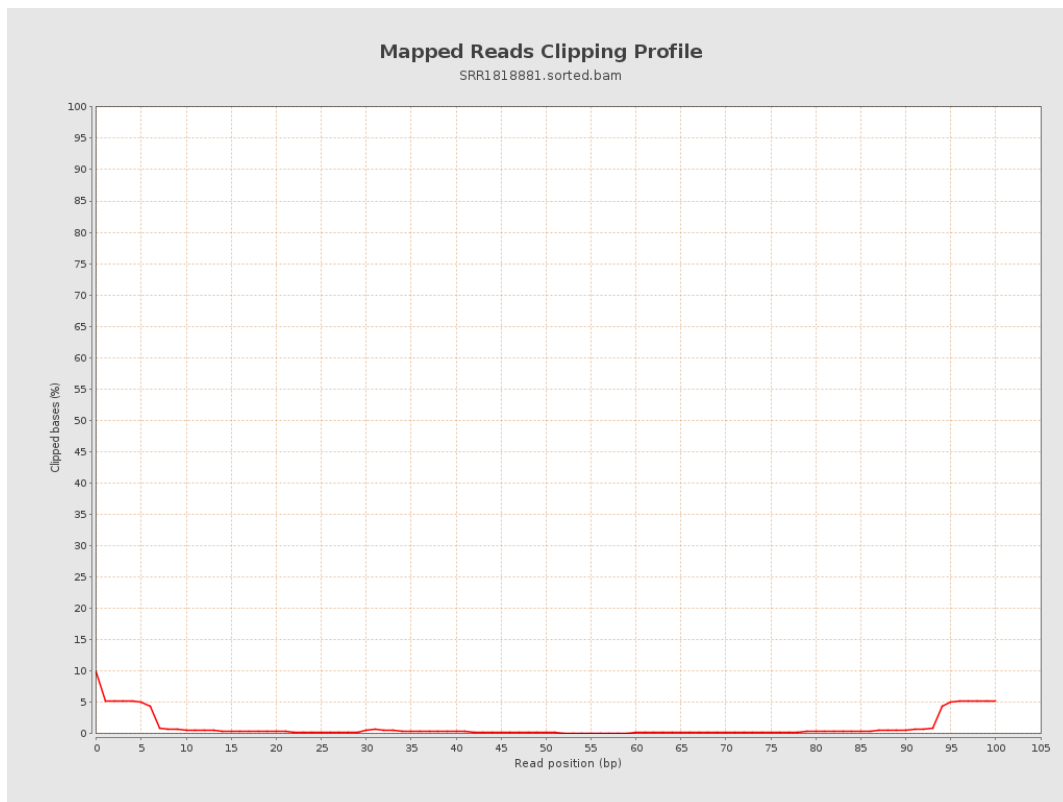
8. Results : Mapped Reads Nucleotide Content



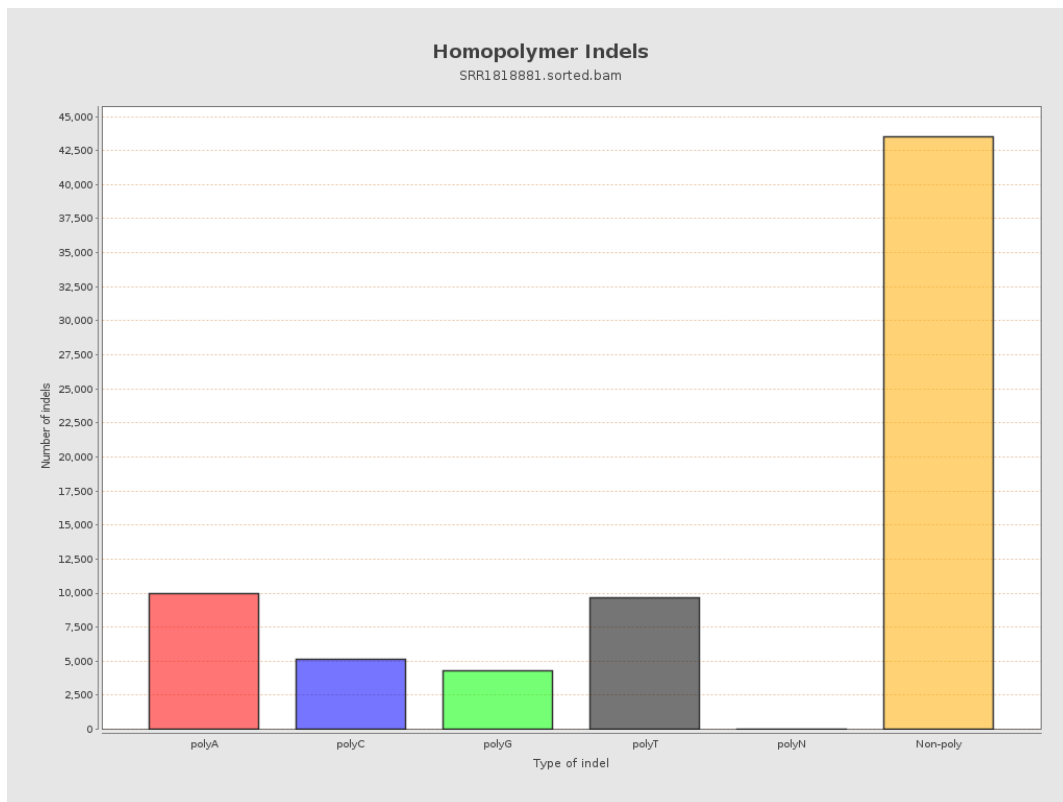
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

