

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 14:33:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819006.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_SRR1819006 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819006.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 14:33:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819006.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,287,925
Mapped reads	1,205,555 / 93.6%
Unmapped reads	82,370 / 6.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,427 / 1.51%
Read min/max/mean length	30 / 101 / 101.58
Duplicated reads (estimated)	393,655 / 30.57%
Duplication rate	27.08%
Clipped reads	1,216,468 / 94.45%

2.2. ACGT Content

Number/percentage of A's	32,691,559 / 29.39%
Number/percentage of C's	23,435,696 / 21.07%
Number/percentage of T's	32,102,551 / 28.86%
Number/percentage of G's	23,007,710 / 20.68%
Number/percentage of N's	5,606 / 0.01%
GC Percentage	41.75%

2.3. Coverage

Mean	0.036

Standard Deviation	0.4978
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2.4. Mapping Quality

Mean Mapping Quality	49.08
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2.5. Mismatches and indels

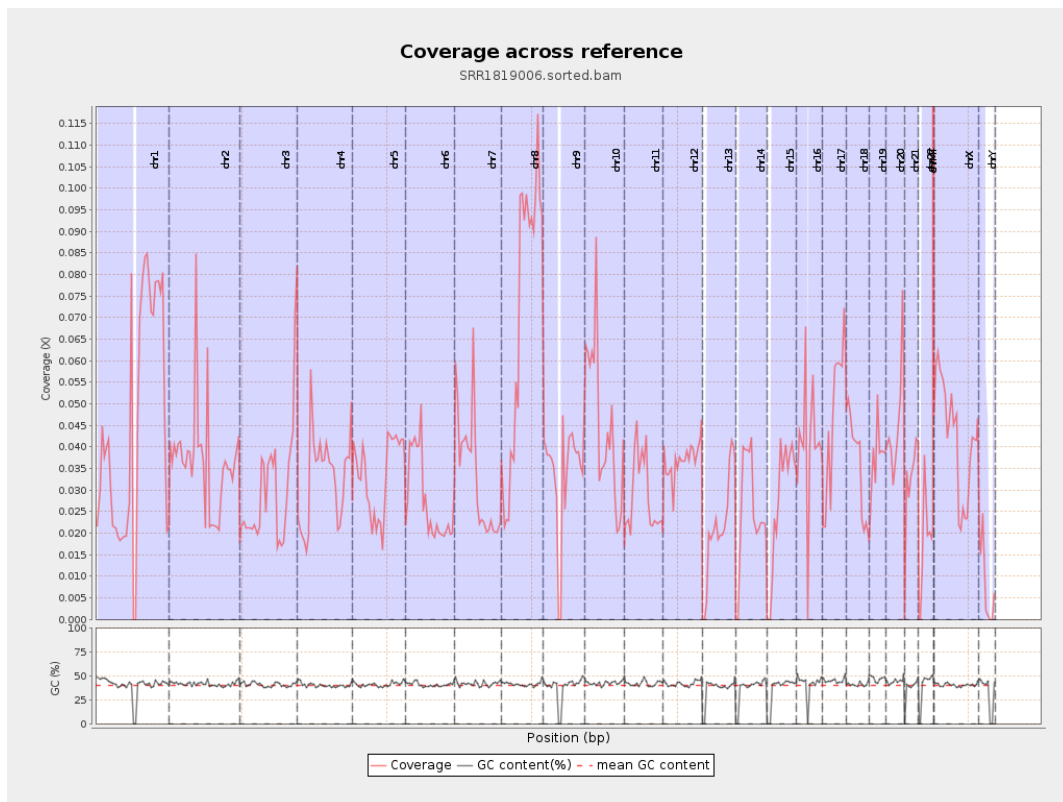
General error rate	0.71%
Mismatches	745,969
Insertions	19,596
Mapped reads with at least one insertion	1.58%
Deletions	36,812
Mapped reads with at least one deletion	2.99%
Homopolymer indels	41.11%

2.6. Chromosome stats

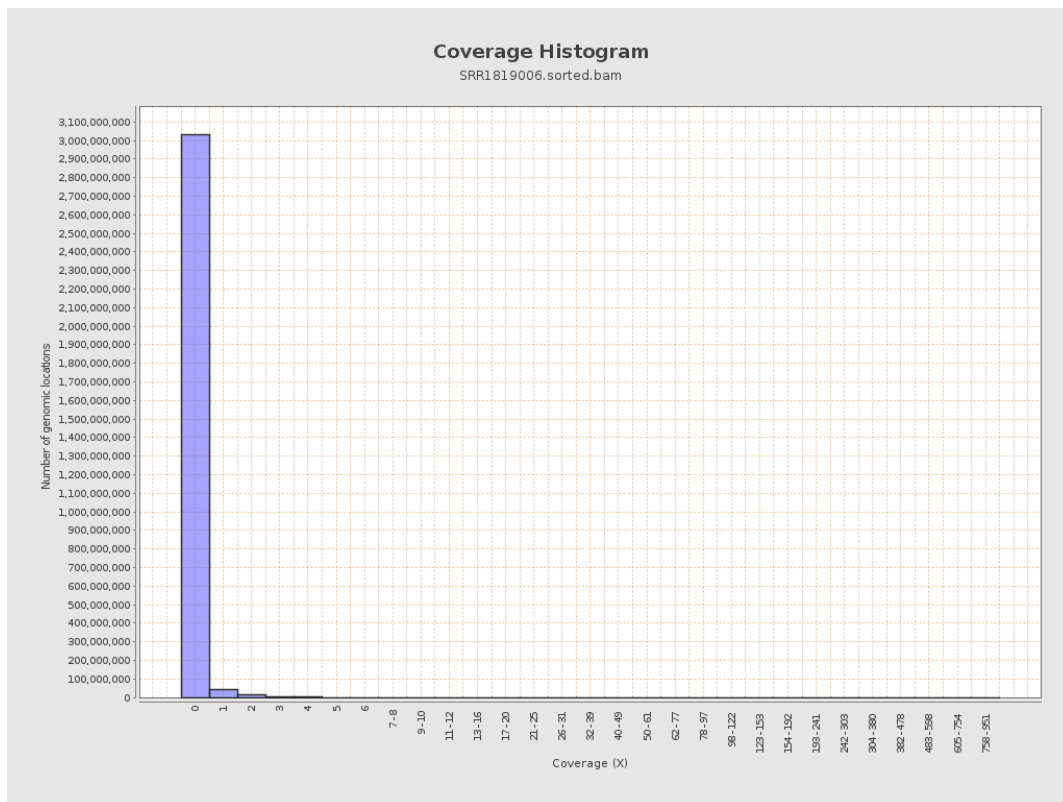
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	11304268	0.0454	0.9088
chr2	243199373	8906848	0.0366	0.7524
chr3	198022430	5821356	0.0294	0.2612
chr4	191154276	6240296	0.0326	0.3422
chr5	180915260	6078091	0.0336	0.2974
chr6	171115067	4708063	0.0275	0.3025
chr7	159138663	5240142	0.0329	0.5789

chr8	146364022	10374367	0.0709	0.4538
chr9	141213431	4721055	0.0334	0.427
chr10	135534747	6033441	0.0445	0.6313
chr11	135006516	3894503	0.0288	0.3198
chr12	133851895	4947149	0.037	0.2989
chr13	115169878	2479933	0.0215	0.2217
chr14	107349540	2705250	0.0252	0.2625
chr15	102531392	2794639	0.0273	0.2519
chr16	90354753	3648262	0.0404	0.5761
chr17	81195210	3875938	0.0477	0.3678
chr18	78077248	2829447	0.0362	0.5271
chr19	59128983	2218948	0.0375	0.7183
chr20	63025520	2888706	0.0458	0.3484
chr21	48129895	1551543	0.0322	0.2983
chr22	51304566	889838	0.0173	0.2186
chrMT	16571	124580	7.518	5.8341
chrX	155270560	6567363	0.0423	0.3761
chrY	59373566	468866	0.0079	0.5211

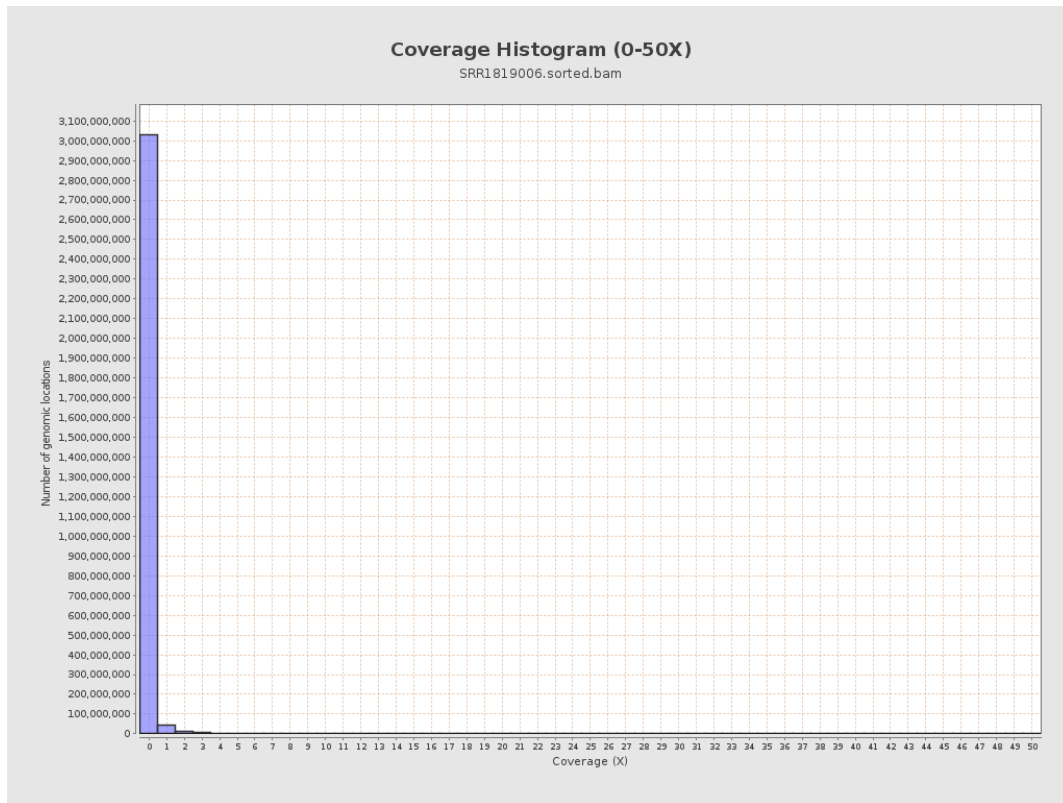
3. Results : Coverage across reference



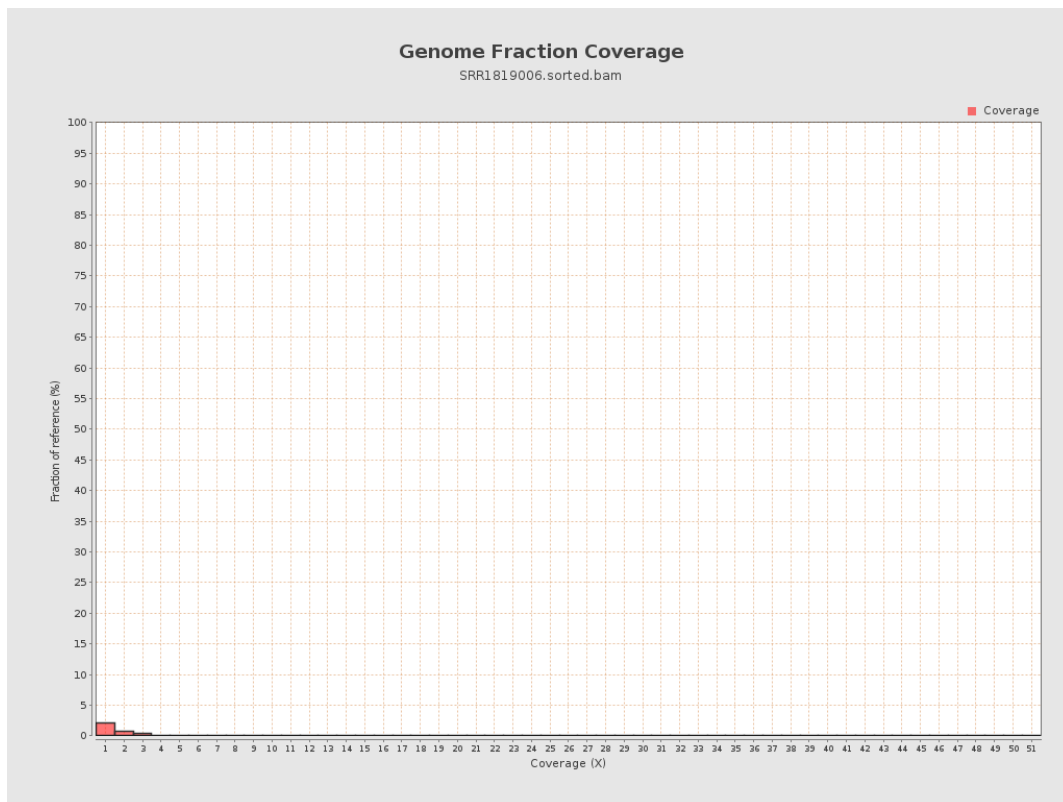
4. Results : Coverage Histogram



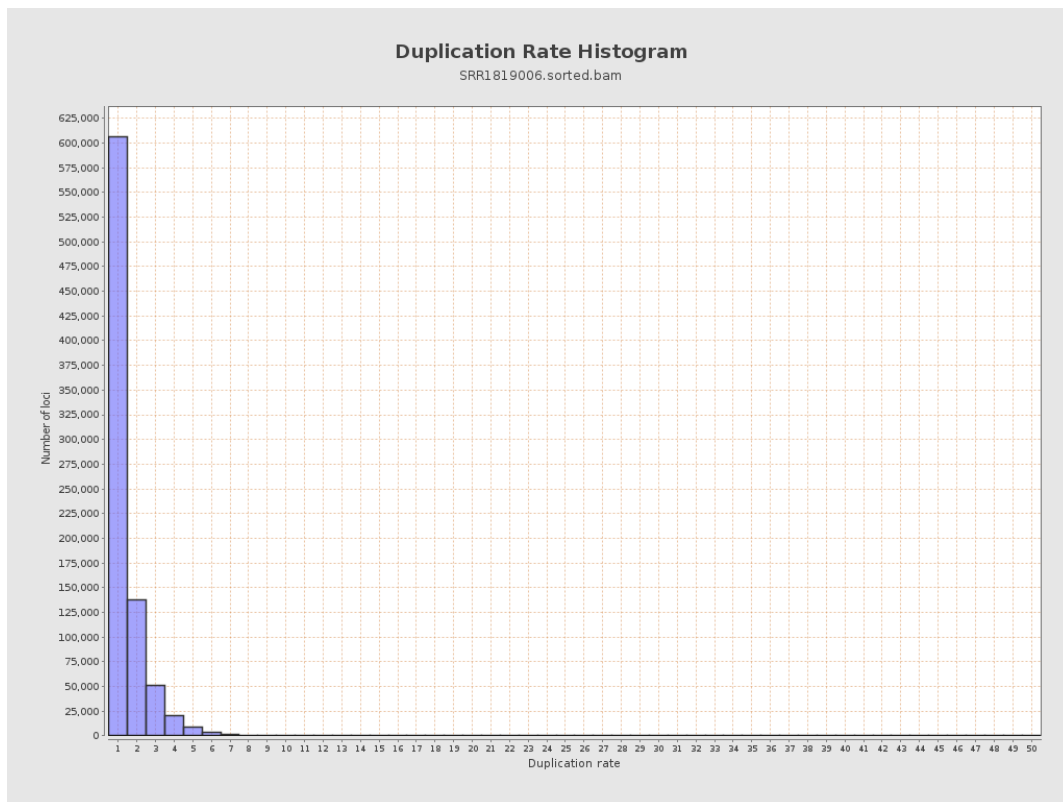
5. Results : Coverage Histogram (0-50X)



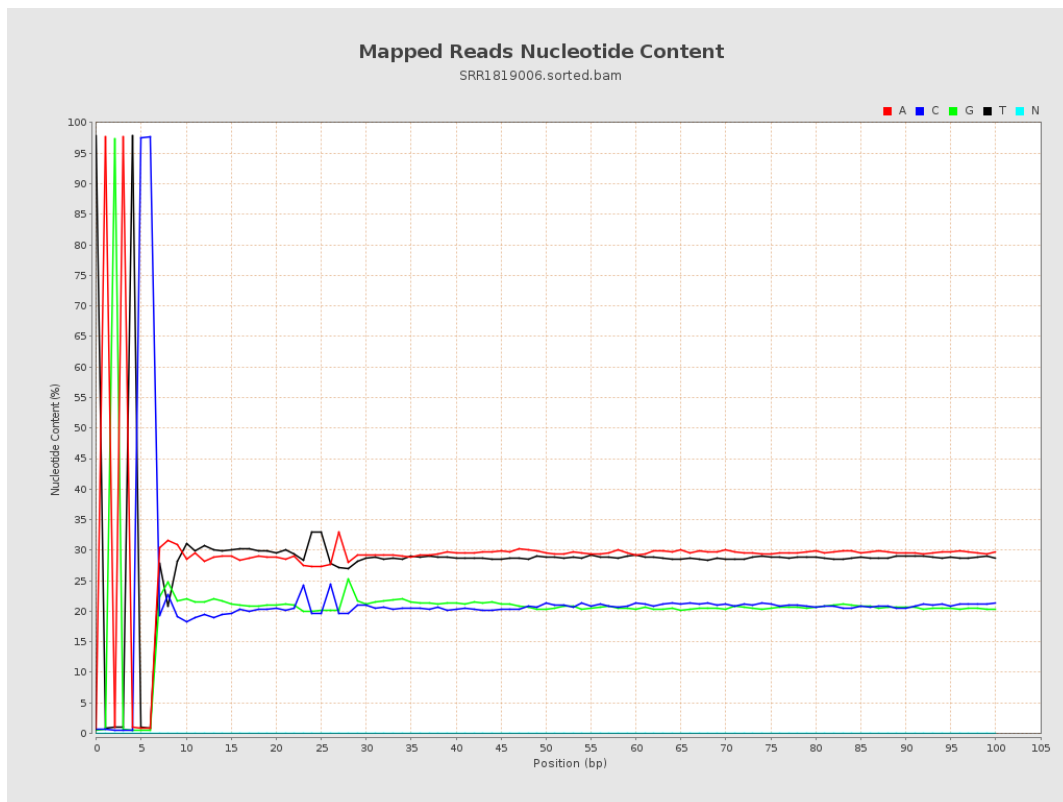
6. Results : Genome Fraction Coverage



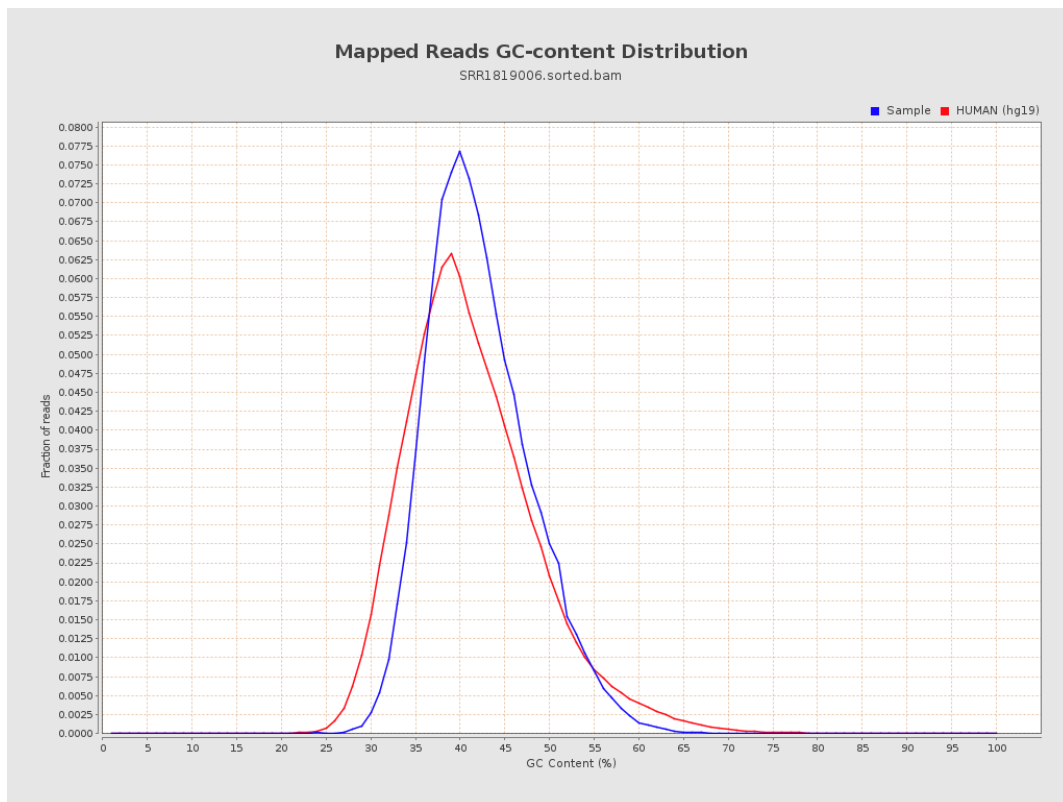
7. Results : Duplication Rate Histogram



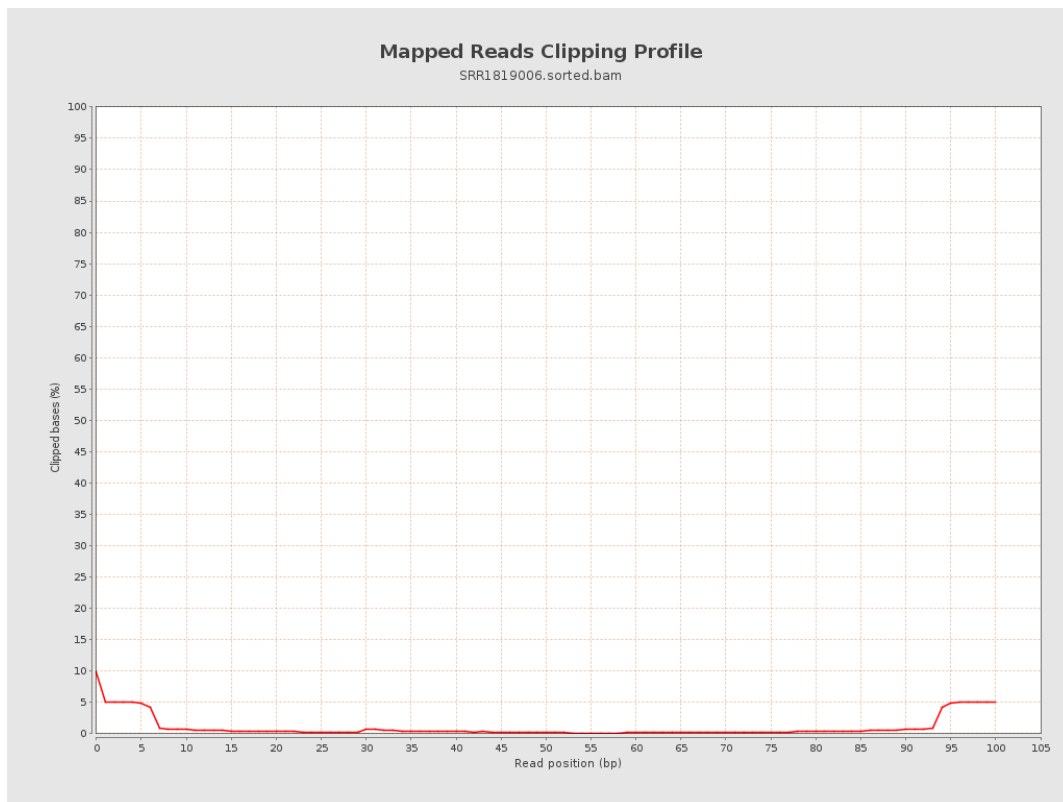
8. Results : Mapped Reads Nucleotide Content



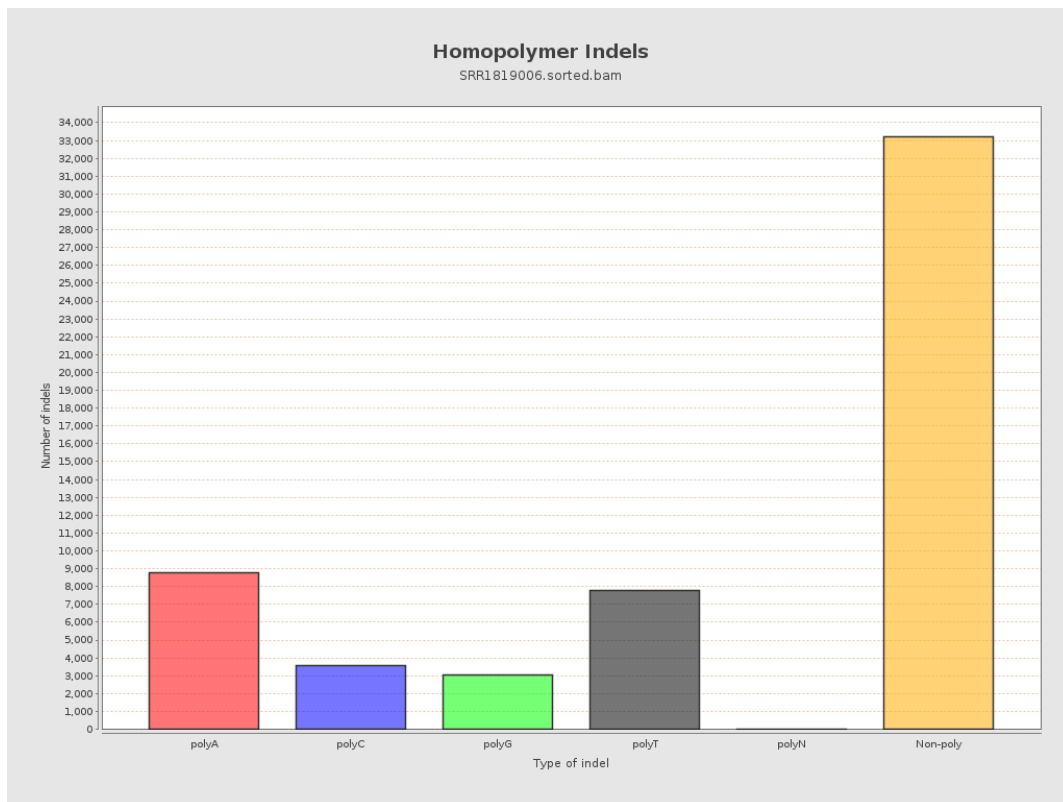
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

