

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 14:30:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819005.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_SRR1819005 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819005.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 14:30:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819005.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	955,569
Mapped reads	898,825 / 94.06%
Unmapped reads	56,744 / 5.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,136 / 1.58%
Read min/max/mean length	30 / 101 / 101.61
Duplicated reads (estimated)	279,838 / 29.28%
Duplication rate	26.61%
Clipped reads	909,255 / 95.15%

2.2. ACGT Content

Number/percentage of A's	24,395,185 / 29.45%
Number/percentage of C's	17,382,252 / 20.98%
Number/percentage of T's	23,959,662 / 28.92%
Number/percentage of G's	17,099,220 / 20.64%
Number/percentage of N's	4,038 / 0%
GC Percentage	41.62%

2.3. Coverage

Mean	0.0268

Standard Deviation	0.391
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2.4. Mapping Quality

Mean Mapping Quality	49.04
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2.5. Mismatches and indels

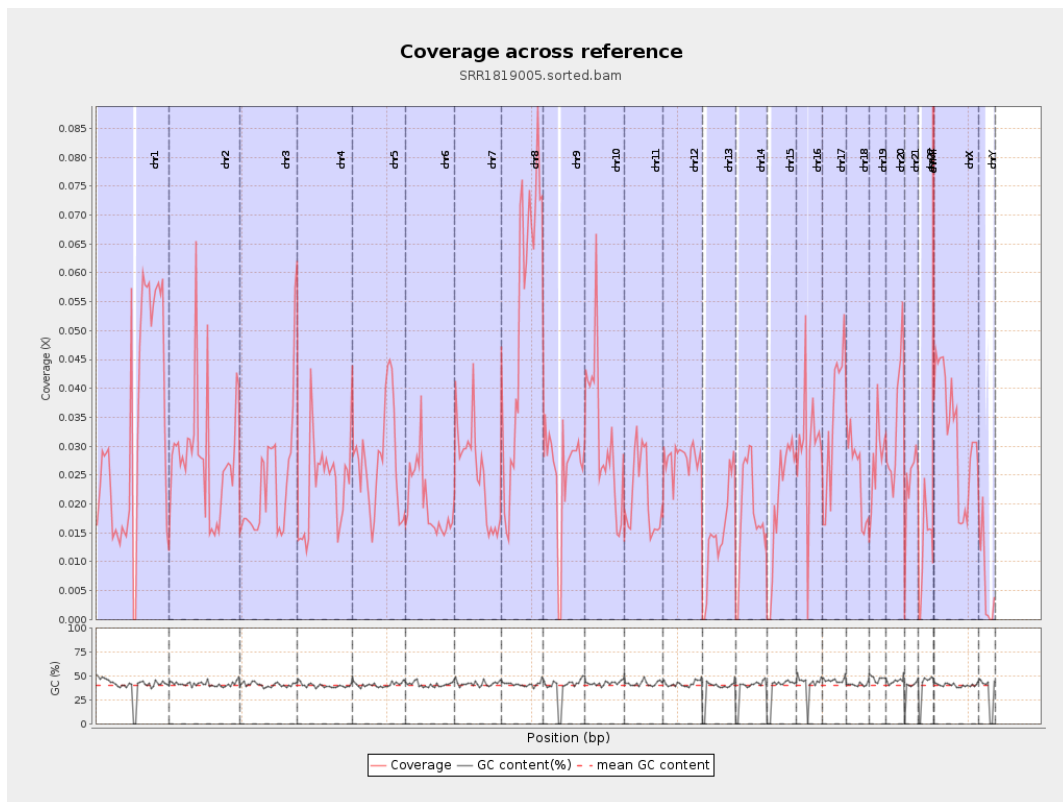
General error rate	0.7%
Mismatches	549,764
Insertions	14,229
Mapped reads with at least one insertion	1.53%
Deletions	26,786
Mapped reads with at least one deletion	2.91%
Homopolymer indels	40.09%

2.6. Chromosome stats

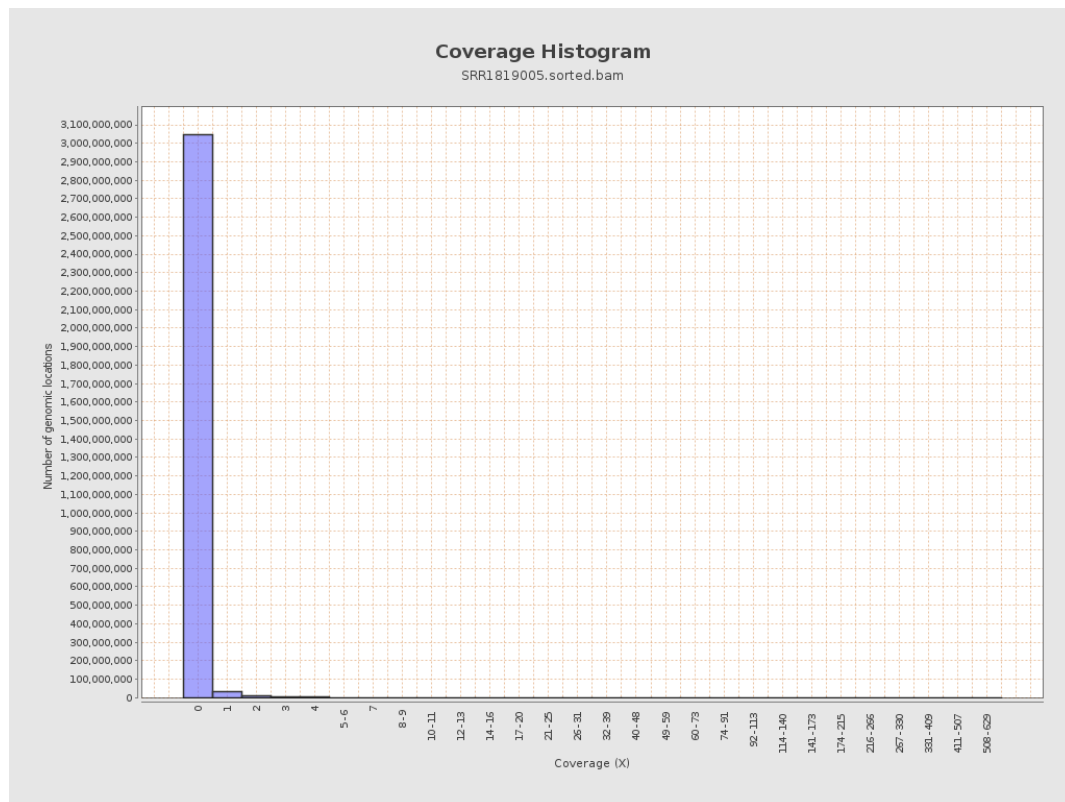
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8171017	0.0328	0.6445
chr2	243199373	6819170	0.028	0.6378
chr3	198022430	4611723	0.0233	0.2249
chr4	191154276	4440804	0.0232	0.2768
chr5	180915260	4994181	0.0276	0.2599
chr6	171115067	3451706	0.0202	0.2459
chr7	159138663	4008279	0.0252	0.4019

chr8	146364022	7635347	0.0522	0.3706
chr9	141213431	3619624	0.0256	0.338
chr10	135534747	4229364	0.0312	0.5054
chr11	135006516	2880655	0.0213	0.2513
chr12	133851895	3747278	0.028	0.2516
chr13	115169878	1708500	0.0148	0.179
chr14	107349540	1956017	0.0182	0.2102
chr15	102531392	2122845	0.0207	0.2162
chr16	90354753	2735029	0.0303	0.5133
chr17	81195210	2848185	0.0351	0.3002
chr18	78077248	1955045	0.025	0.3812
chr19	59128983	1658689	0.0281	0.5474
chr20	63025520	2154672	0.0342	0.2991
chr21	48129895	1130237	0.0235	0.2548
chr22	51304566	634903	0.0124	0.1867
chrMT	16571	12373	0.7467	1.2438
chrX	155270560	4995911	0.0322	0.305
chrY	59373566	370739	0.0062	0.4362

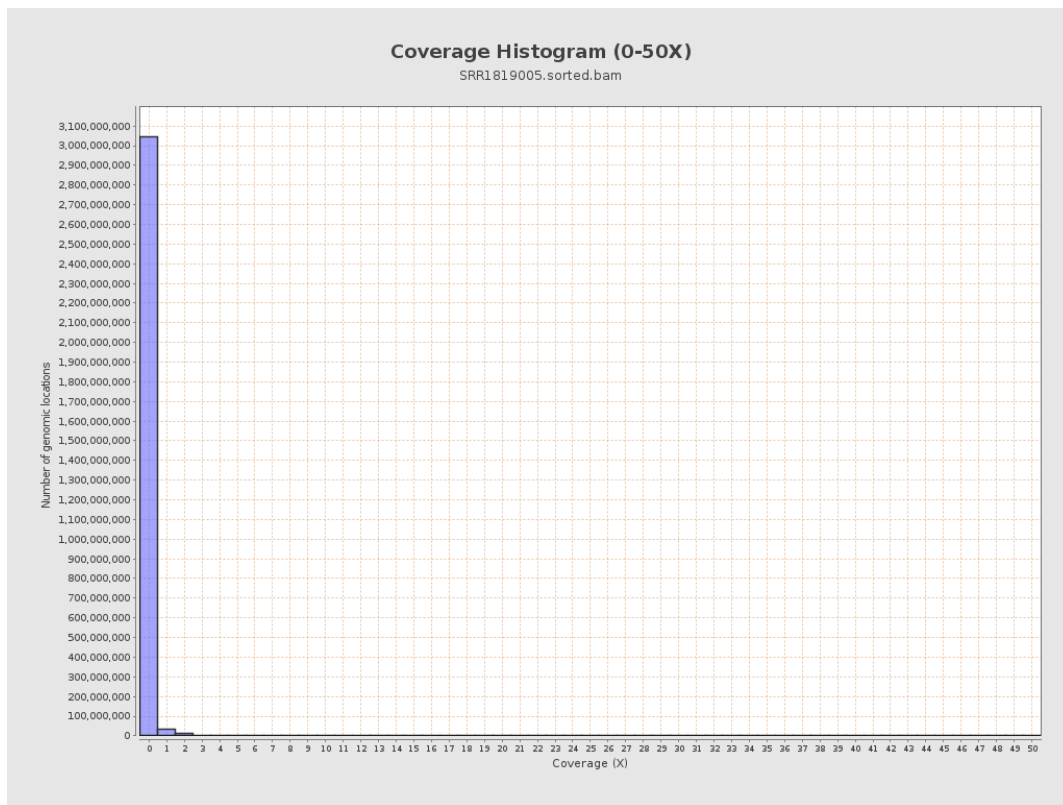
3. Results : Coverage across reference



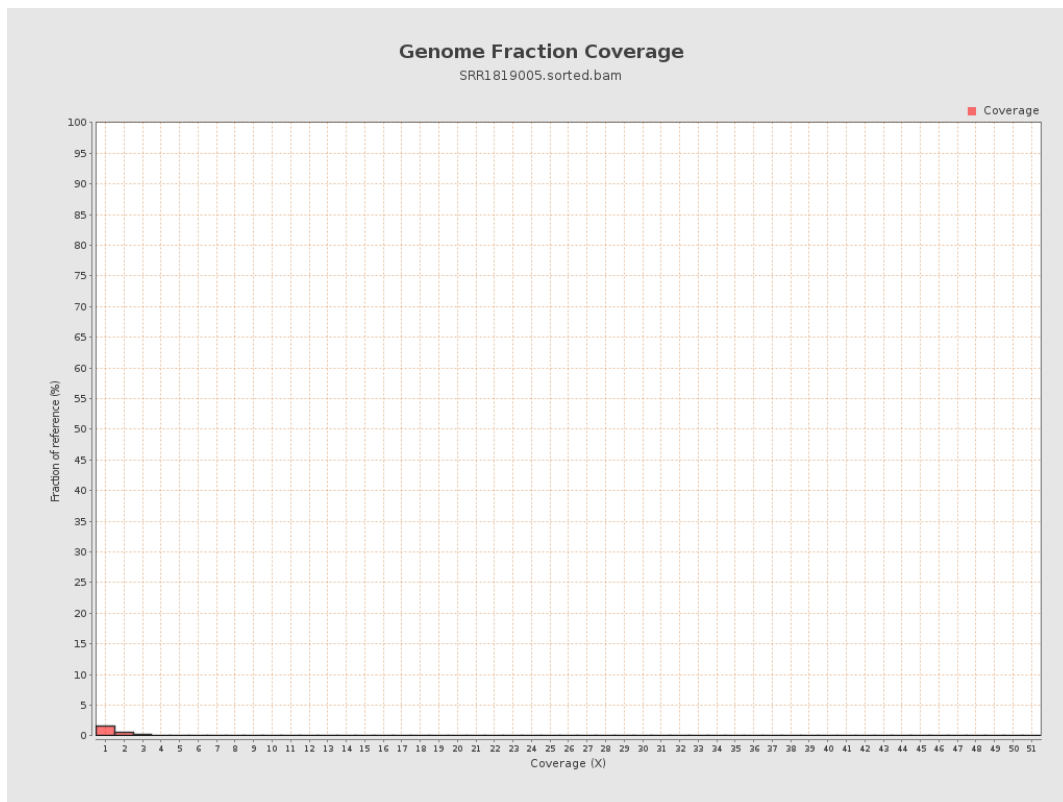
4. Results : Coverage Histogram



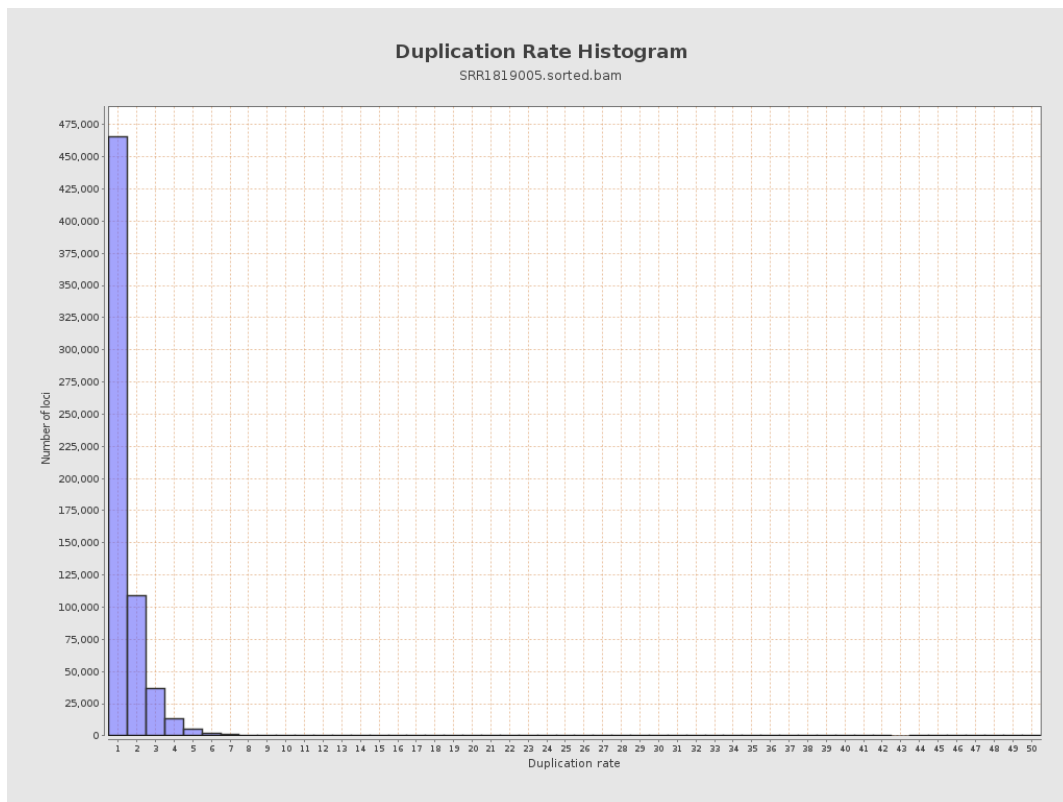
5. Results : Coverage Histogram (0-50X)



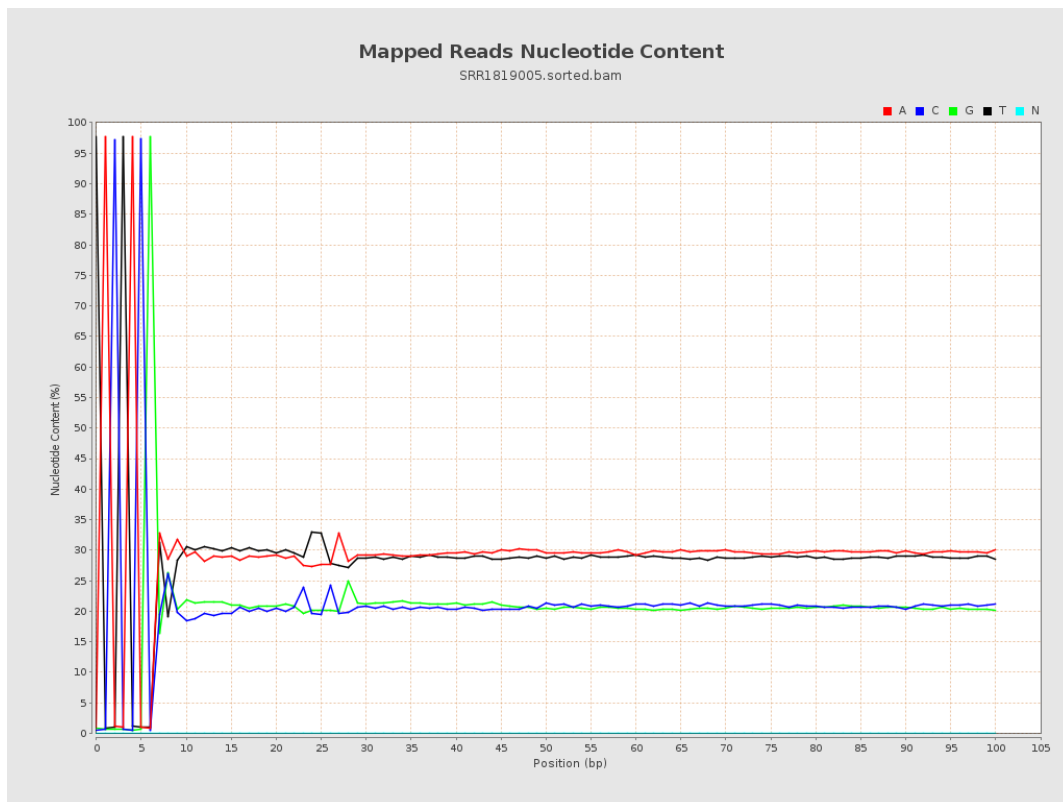
6. Results : Genome Fraction Coverage



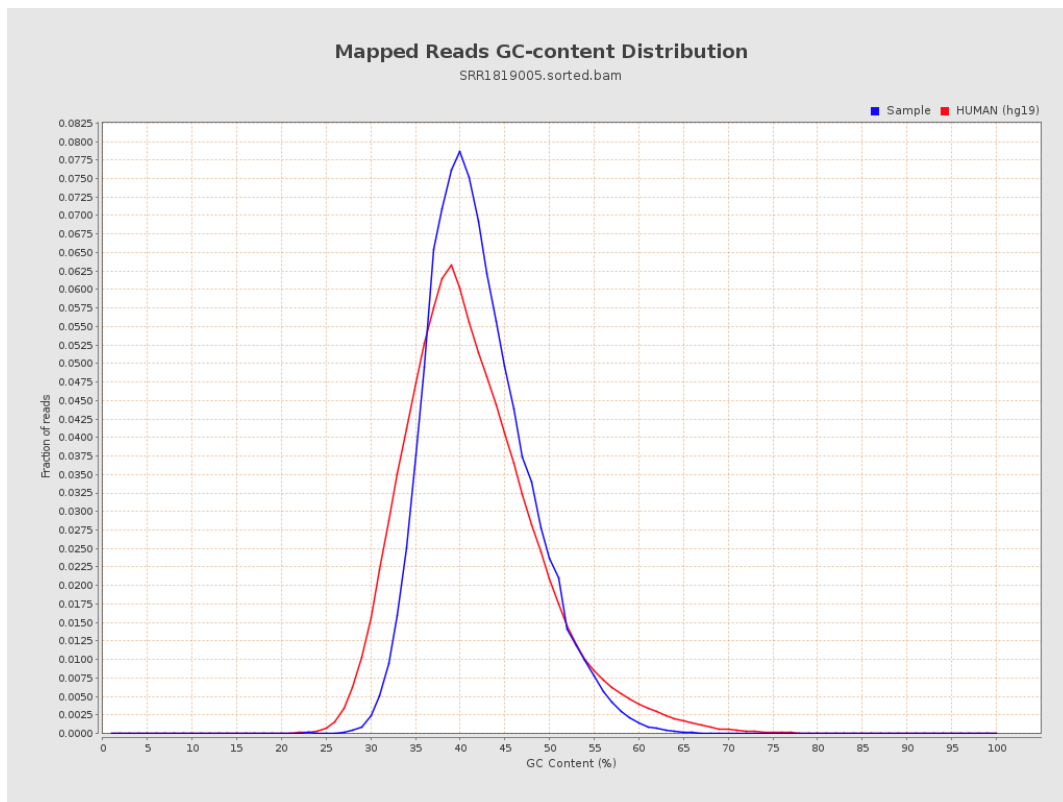
7. Results : Duplication Rate Histogram



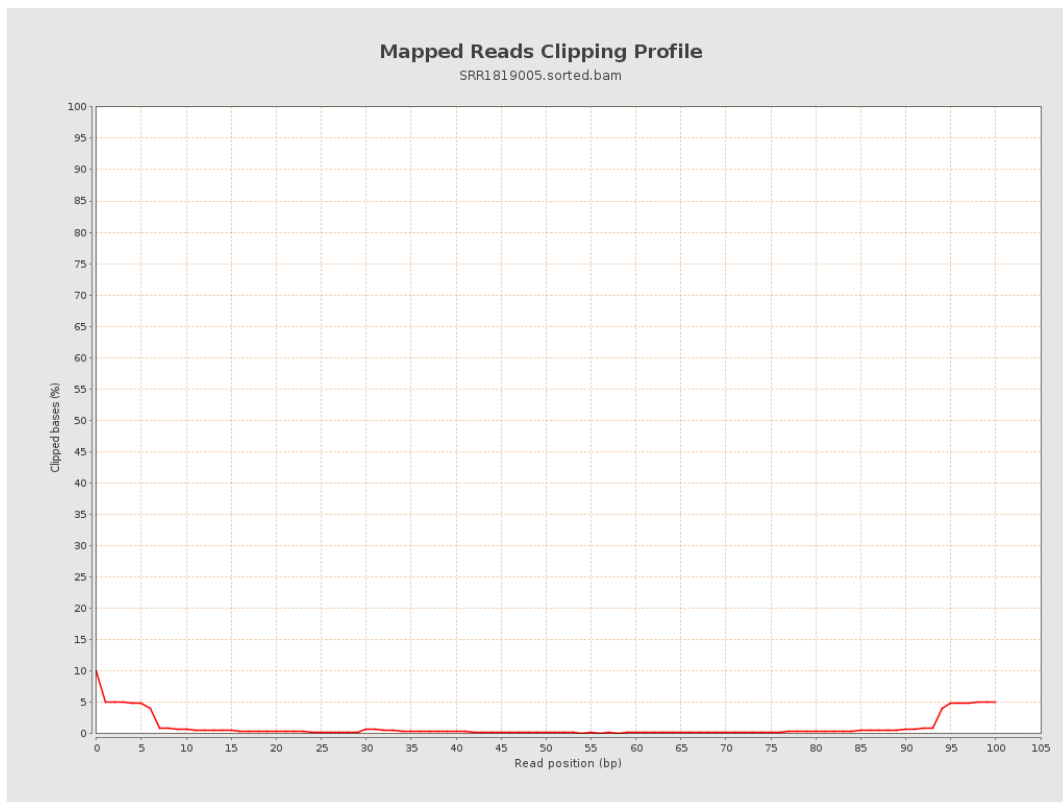
8. Results : Mapped Reads Nucleotide Content



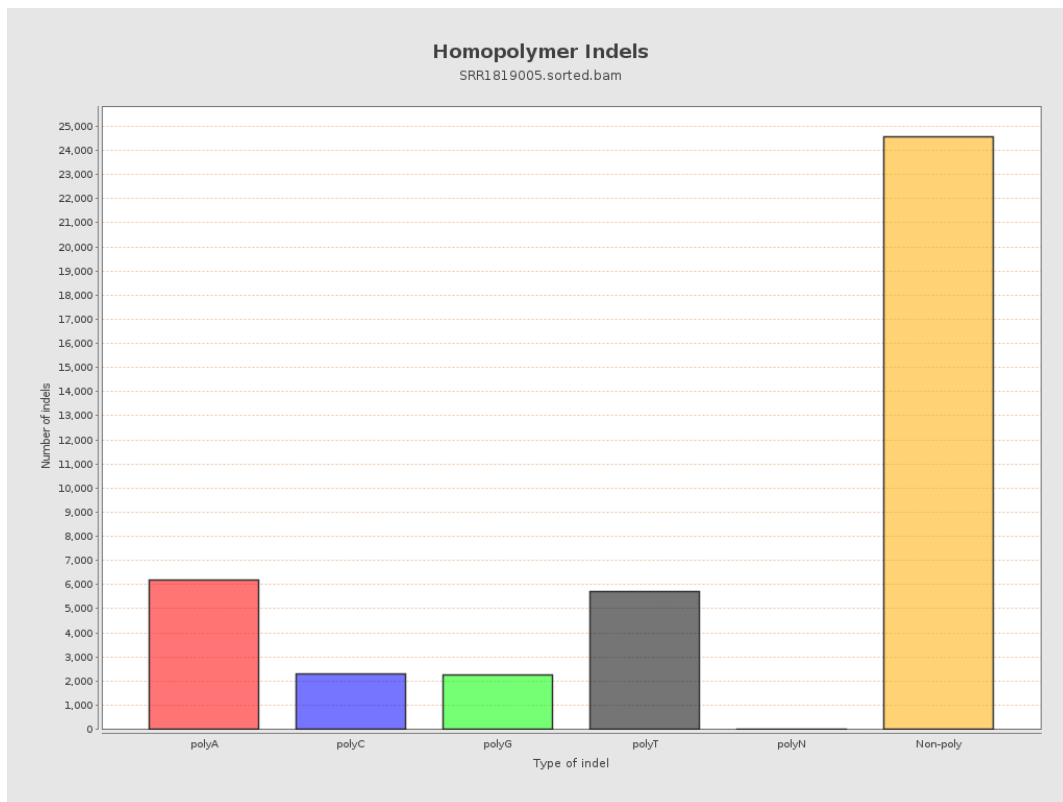
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

