

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 14:38:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819008.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_SRR1819008 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819008.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 14:38:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819008.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	891,485
Mapped reads	874,853 / 98.13%
Unmapped reads	16,632 / 1.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,849 / 1.55%
Read min/max/mean length	30 / 101 / 101.6
Duplicated reads (estimated)	309,233 / 34.69%
Duplication rate	30.55%
Clipped reads	882,011 / 98.94%

2.2. ACGT Content

Number/percentage of A's	23,656,367 / 29.31%
Number/percentage of C's	17,451,140 / 21.63%
Number/percentage of T's	22,839,744 / 28.3%
Number/percentage of G's	16,746,846 / 20.75%
Number/percentage of N's	4,252 / 0.01%
GC Percentage	42.38%

2.3. Coverage

Mean	0.0261

Standard Deviation	0.3923
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2.4. Mapping Quality

Mean Mapping Quality	49.05
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2.5. Mismatches and indels

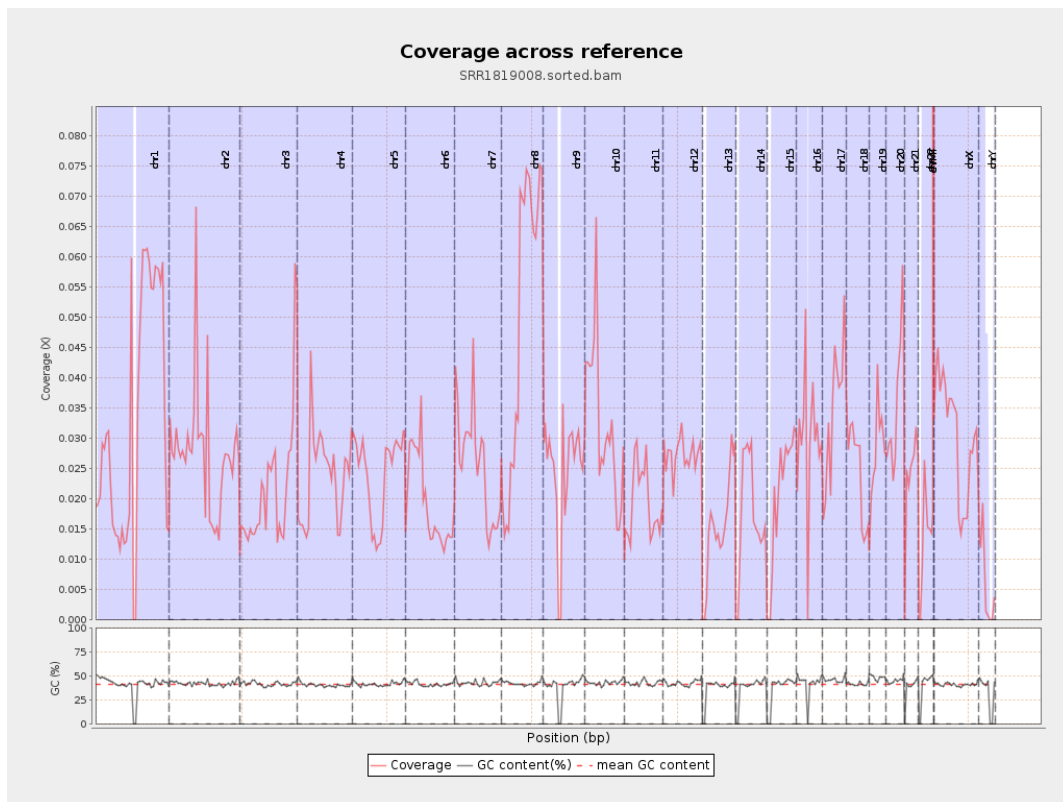
General error rate	0.73%
Mismatches	553,307
Insertions	14,375
Mapped reads with at least one insertion	1.59%
Deletions	26,992
Mapped reads with at least one deletion	3.02%
Homopolymer indels	40.83%

2.6. Chromosome stats

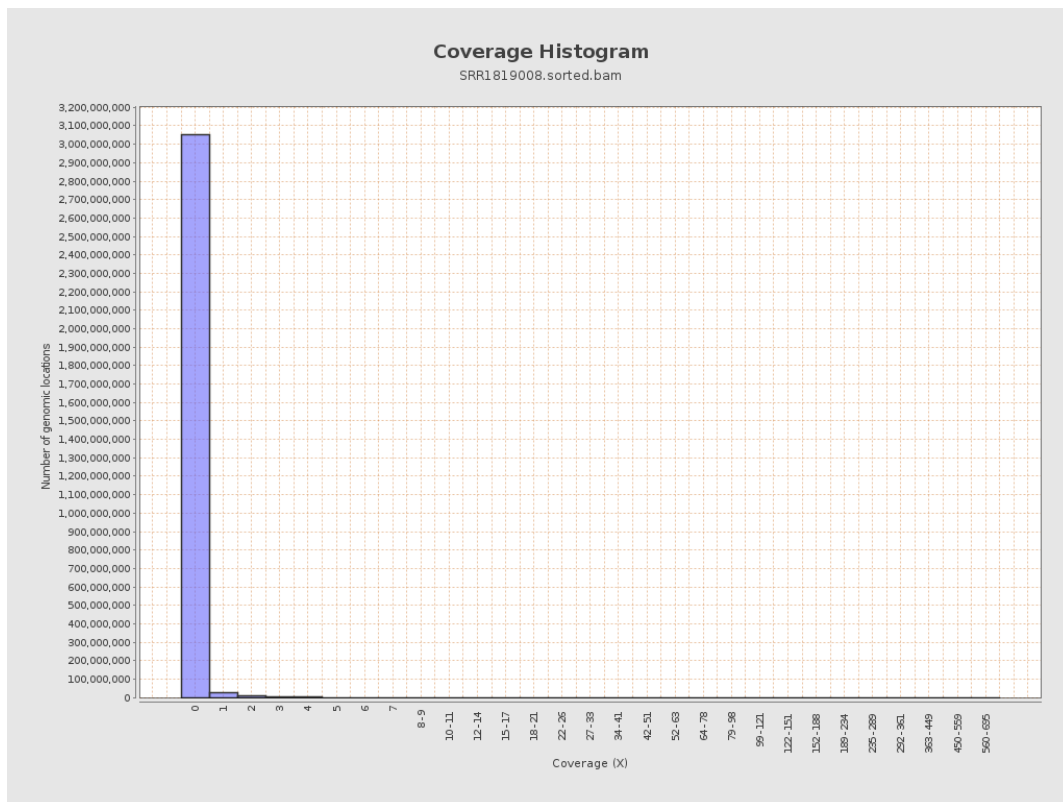
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8276989	0.0332	0.6962
chr2	243199373	6720602	0.0276	0.5851
chr3	198022430	4166715	0.021	0.2266
chr4	191154276	4517970	0.0236	0.2802
chr5	180915260	4331373	0.0239	0.2513
chr6	171115067	3295890	0.0193	0.2508
chr7	159138663	4053062	0.0255	0.3912

chr8	146364022	7293123	0.0498	0.376
chr9	141213431	3436030	0.0243	0.3355
chr10	135534747	4363019	0.0322	0.4955
chr11	135006516	2605886	0.0193	0.2495
chr12	133851895	3647091	0.0272	0.264
chr13	115169878	1748713	0.0152	0.1911
chr14	107349540	1865735	0.0174	0.2185
chr15	102531392	2110832	0.0206	0.2243
chr16	90354753	2684476	0.0297	0.4665
chr17	81195210	2854274	0.0352	0.3199
chr18	78077248	1912637	0.0245	0.3964
chr19	59128983	1671436	0.0283	0.5524
chr20	63025520	2262742	0.0359	0.3169
chr21	48129895	1148693	0.0239	0.2729
chr22	51304566	652577	0.0127	0.1906
chrMT	16571	47185	2.8474	3.2739
chrX	155270560	4730349	0.0305	0.3284
chrY	59373566	351859	0.0059	0.4337

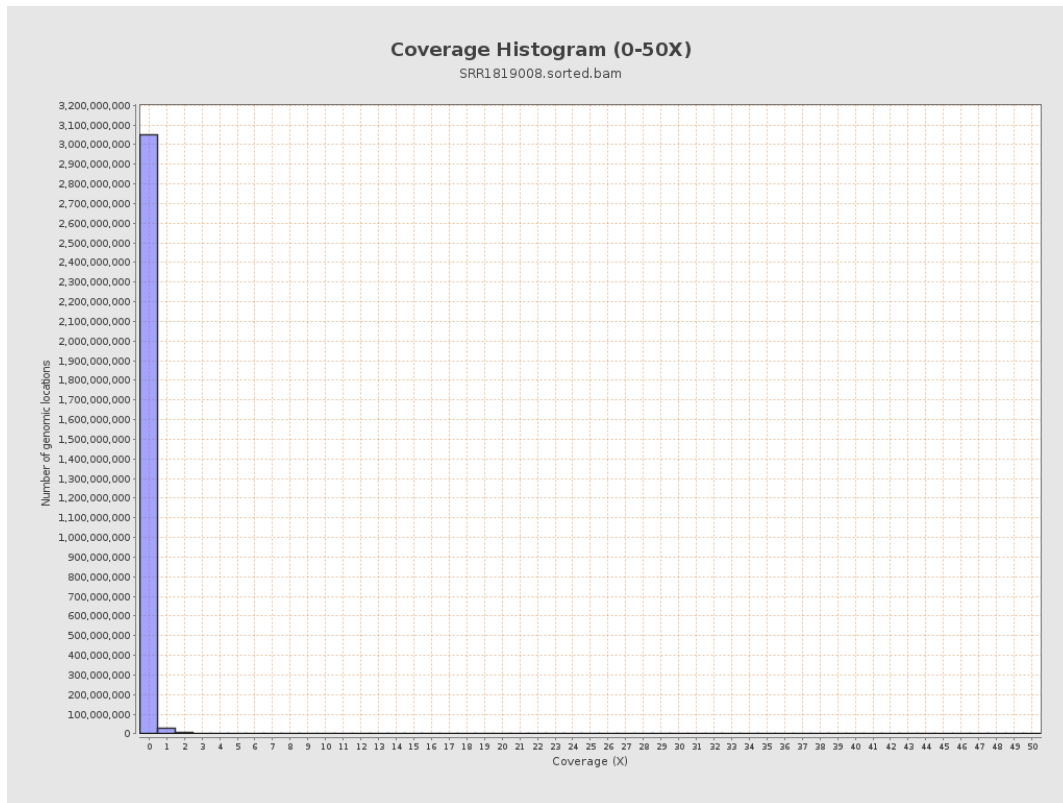
3. Results : Coverage across reference



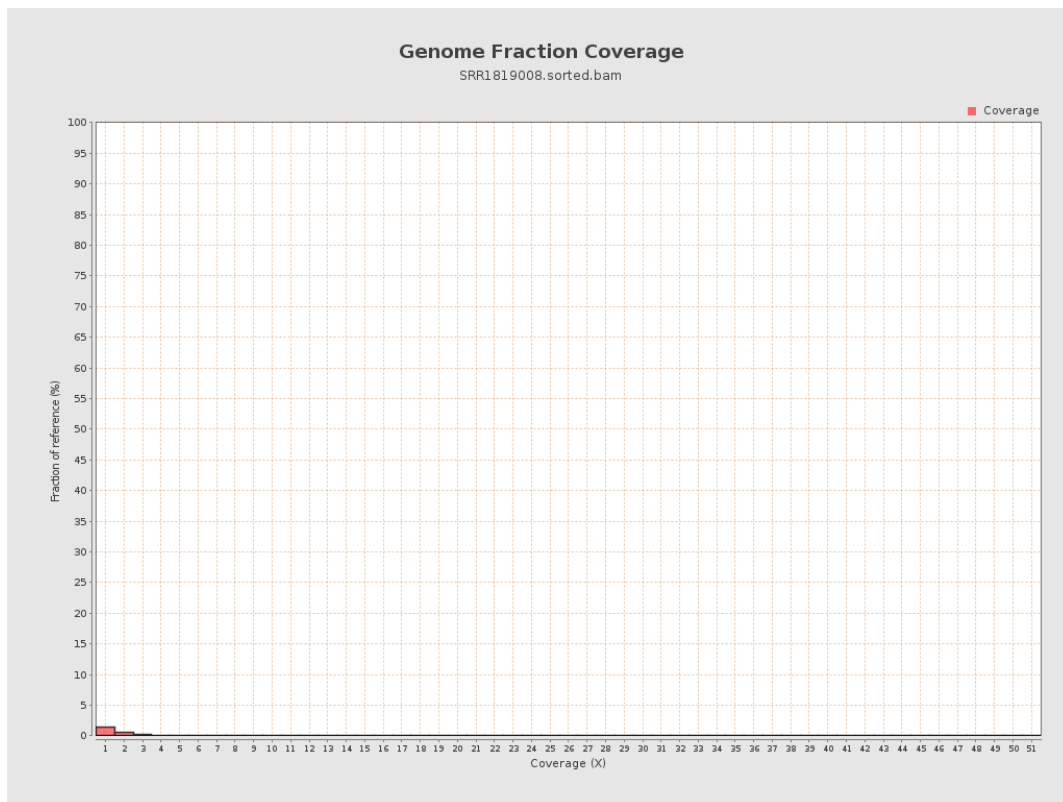
4. Results : Coverage Histogram



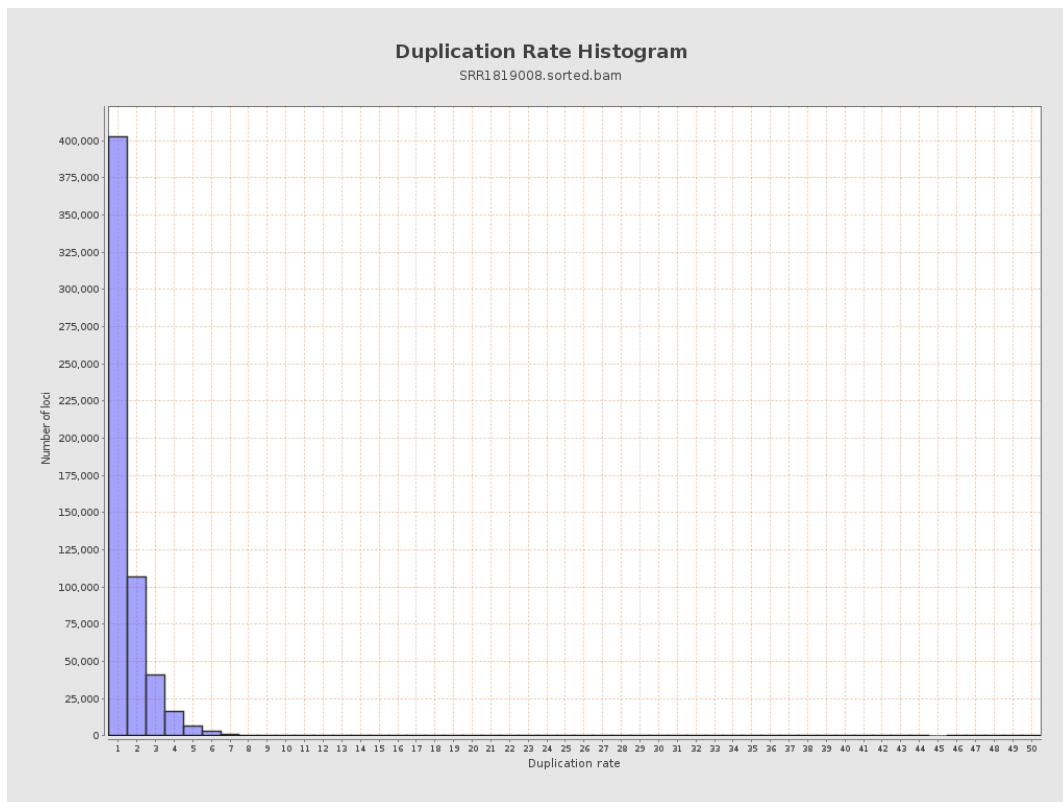
5. Results : Coverage Histogram (0-50X)



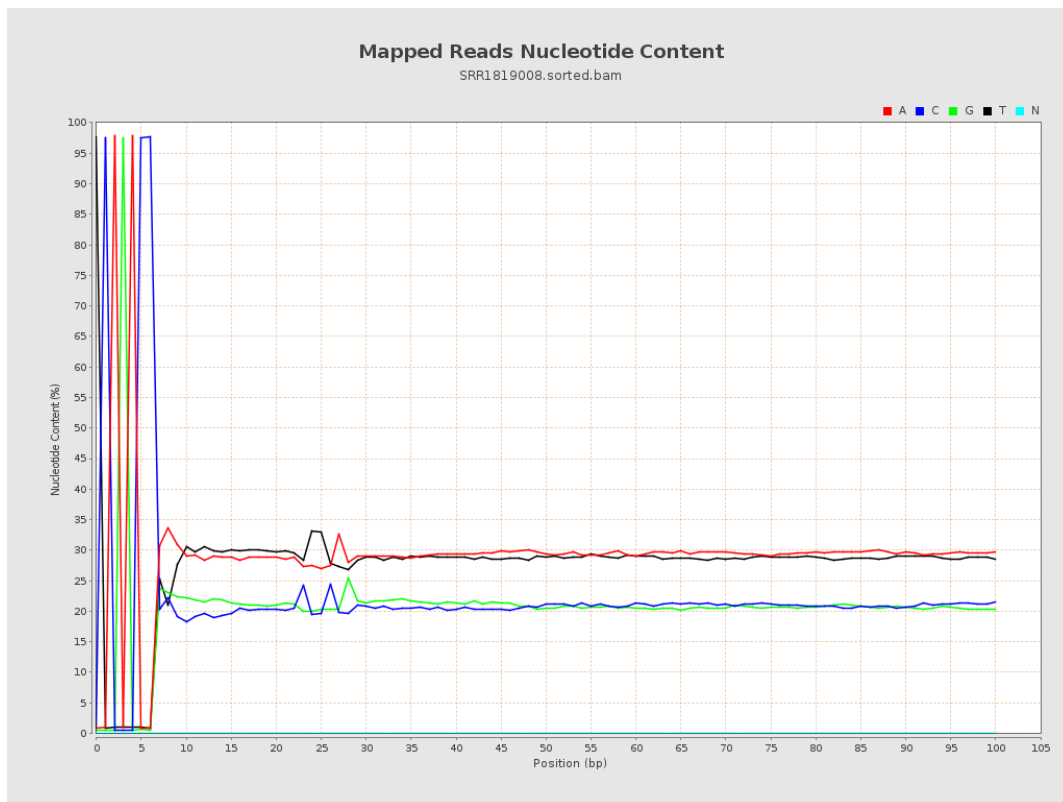
6. Results : Genome Fraction Coverage



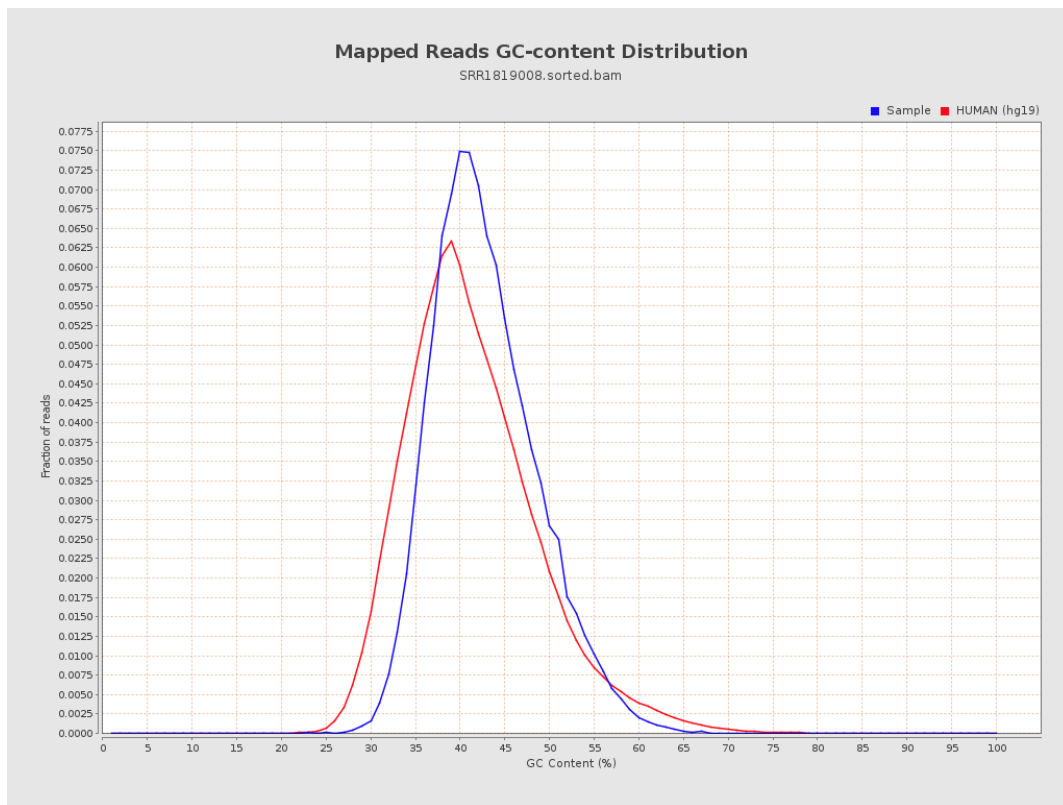
7. Results : Duplication Rate Histogram



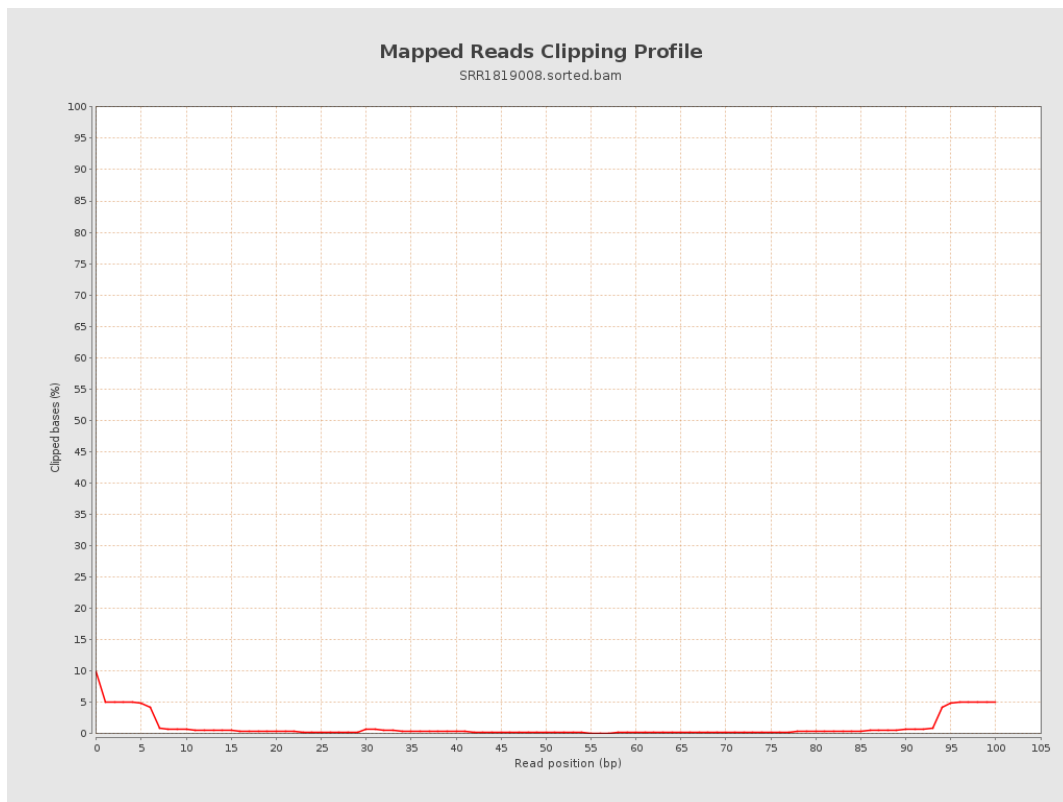
8. Results : Mapped Reads Nucleotide Content



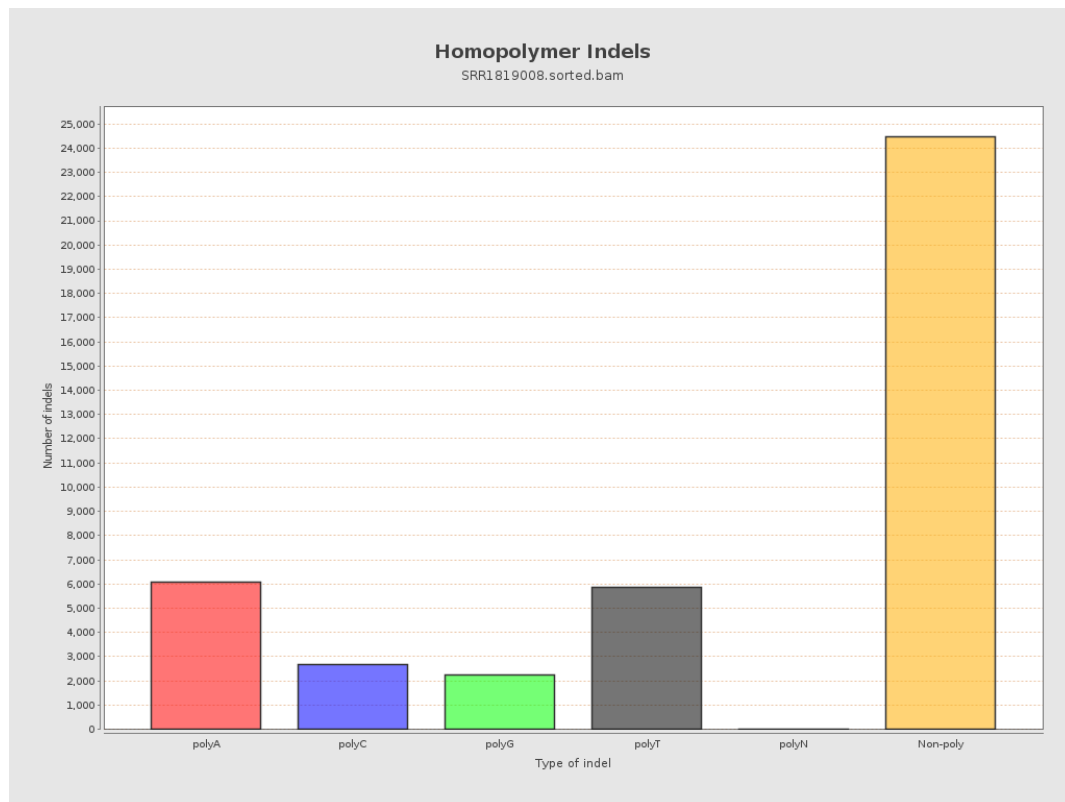
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

