

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 12:48:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818980.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_SRR1818980 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818980.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 12:48:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818980.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	689,213
Mapped reads	678,387 / 98.43%
Unmapped reads	10,826 / 1.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,707 / 1.41%
Read min/max/mean length	30 / 101 / 101.54
Duplicated reads (estimated)	202,074 / 29.32%
Duplication rate	24.83%
Clipped reads	683,826 / 99.22%

2.2. ACGT Content

Number/percentage of A's	18,335,878 / 29.19%
Number/percentage of C's	13,774,648 / 21.93%
Number/percentage of T's	17,720,682 / 28.22%
Number/percentage of G's	12,970,343 / 20.65%
Number/percentage of N's	3,336 / 0.01%
GC Percentage	42.58%

2.3. Coverage

Mean	0.0203

Standard Deviation	0.282
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2.4. Mapping Quality

Mean Mapping Quality	49.3
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2.5. Mismatches and indels

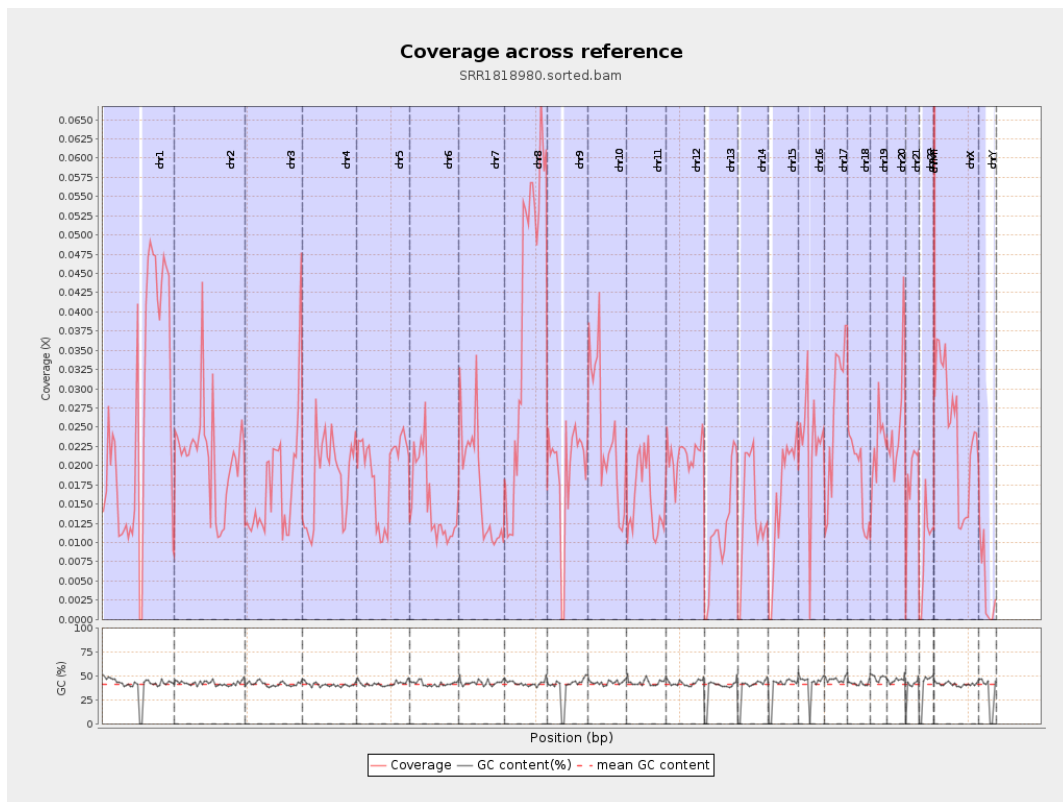
General error rate	0.66%
Mismatches	397,008
Insertions	8,878
Mapped reads with at least one insertion	1.27%
Deletions	19,971
Mapped reads with at least one deletion	2.88%
Homopolymer indels	41.67%

2.6. Chromosome stats

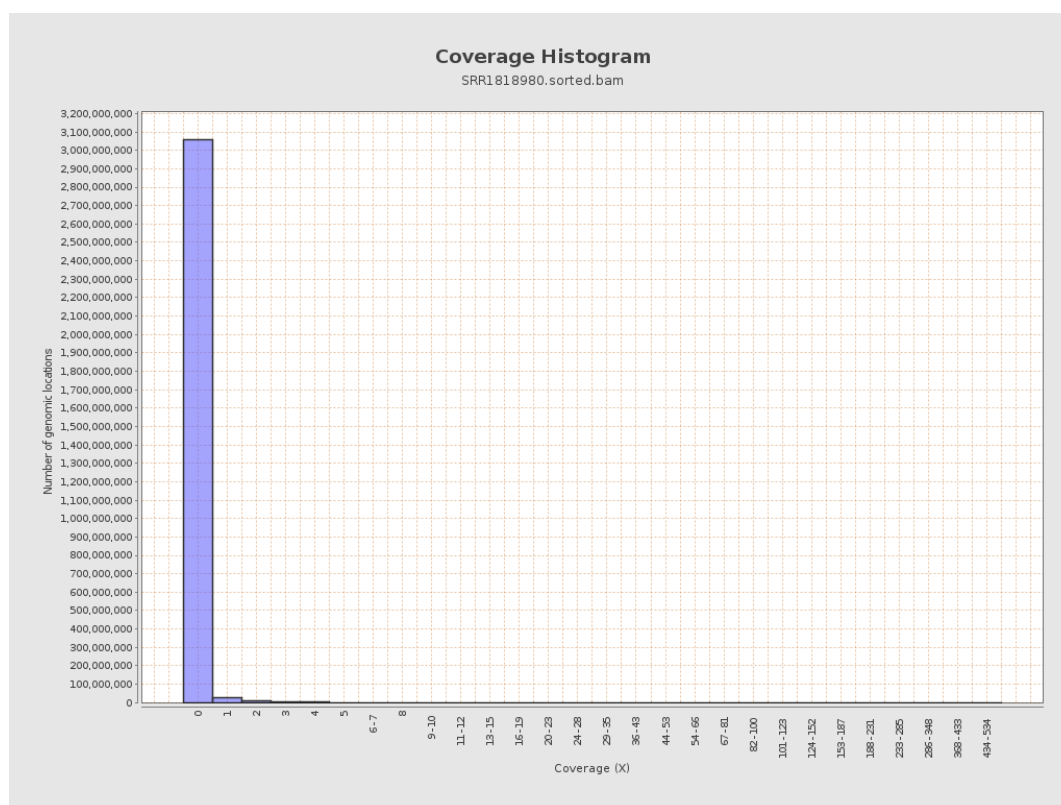
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6438518	0.0258	0.4754
chr2	243199373	5122656	0.0211	0.3654
chr3	198022430	3439204	0.0174	0.1936
chr4	191154276	3549942	0.0186	0.2172
chr5	180915260	3482952	0.0193	0.2084
chr6	171115067	2609940	0.0153	0.1986
chr7	159138663	2785373	0.0175	0.2988

chr8	146364022	5865116	0.0401	0.3119
chr9	141213431	2737569	0.0194	0.2607
chr10	135534747	3317941	0.0245	0.3245
chr11	135006516	2106583	0.0156	0.2017
chr12	133851895	2863409	0.0214	0.2188
chr13	115169878	1332350	0.0116	0.1588
chr14	107349540	1472748	0.0137	0.1781
chr15	102531392	1638761	0.016	0.194
chr16	90354753	2040483	0.0226	0.3192
chr17	81195210	2177542	0.0268	0.2602
chr18	78077248	1441951	0.0185	0.2719
chr19	59128983	1332341	0.0225	0.413
chr20	63025520	1651631	0.0262	0.2548
chr21	48129895	872675	0.0181	0.2125
chr22	51304566	483307	0.0094	0.153
chrMT	16571	7360	0.4441	1.218
chrX	155270560	3830352	0.0247	0.246
chrY	59373566	240547	0.0041	0.2734

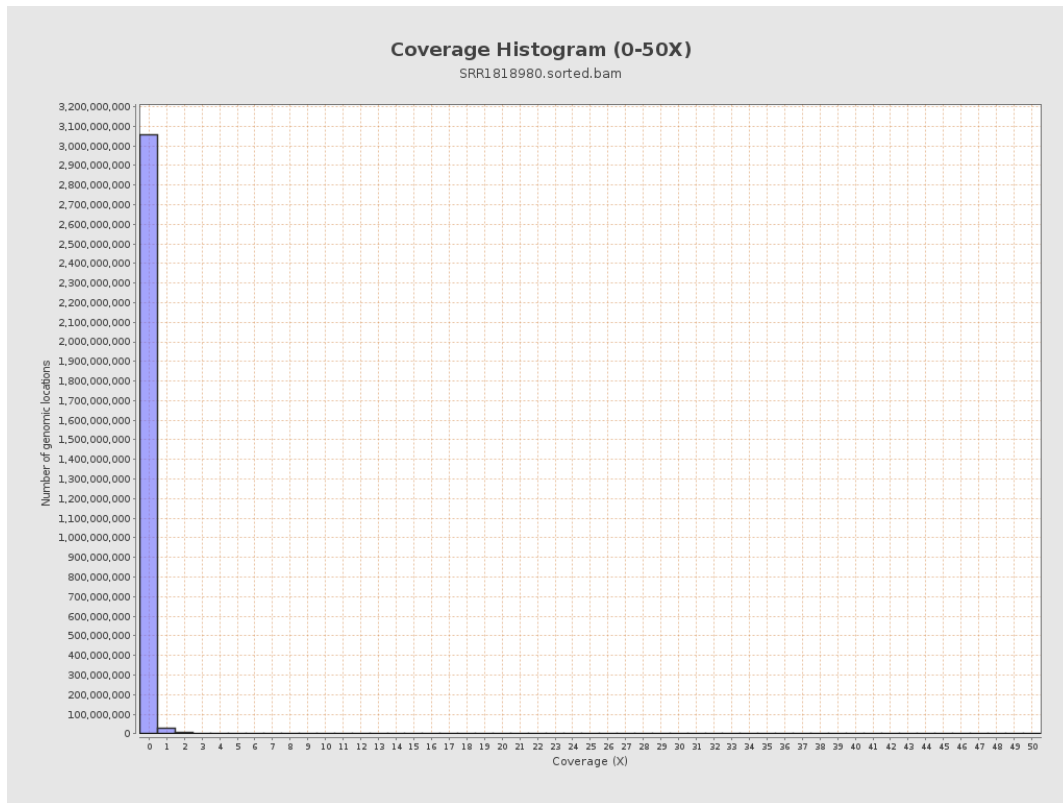
3. Results : Coverage across reference



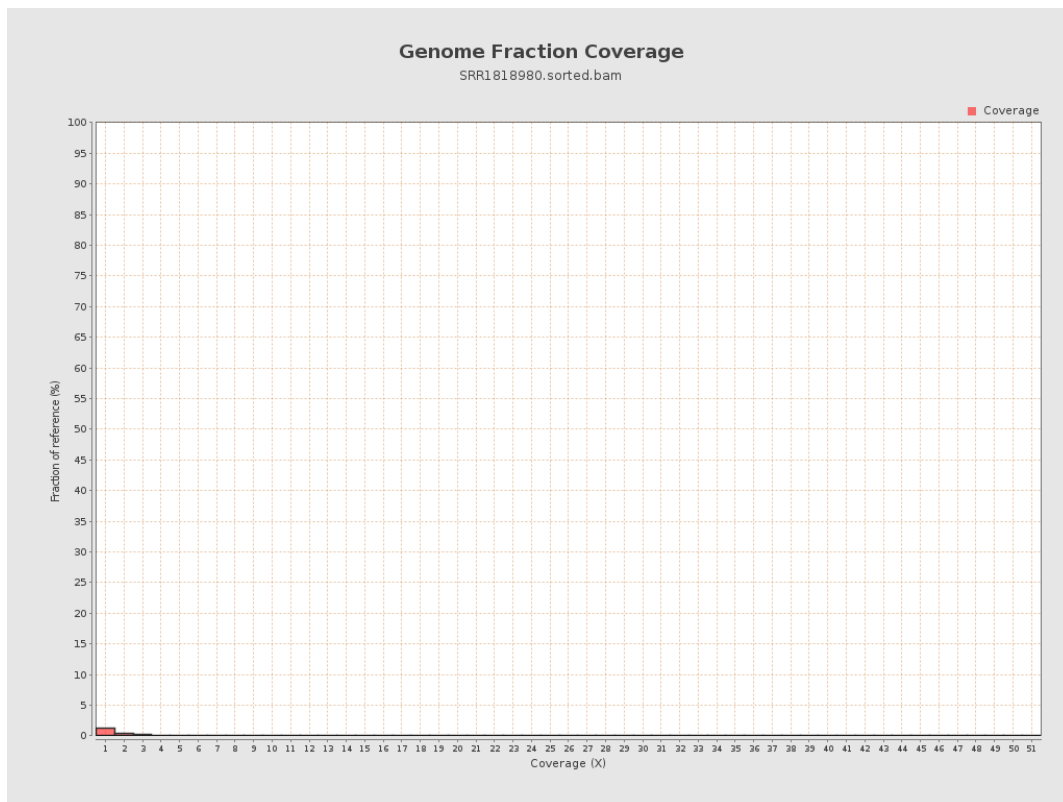
4. Results : Coverage Histogram



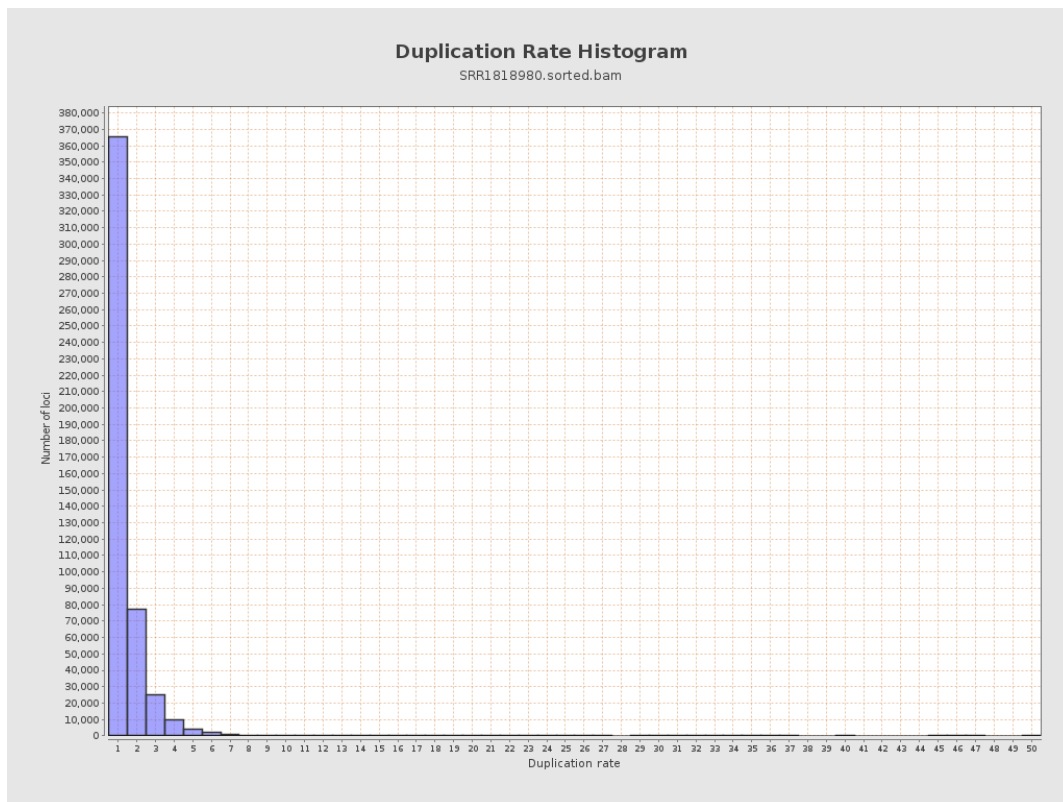
5. Results : Coverage Histogram (0-50X)



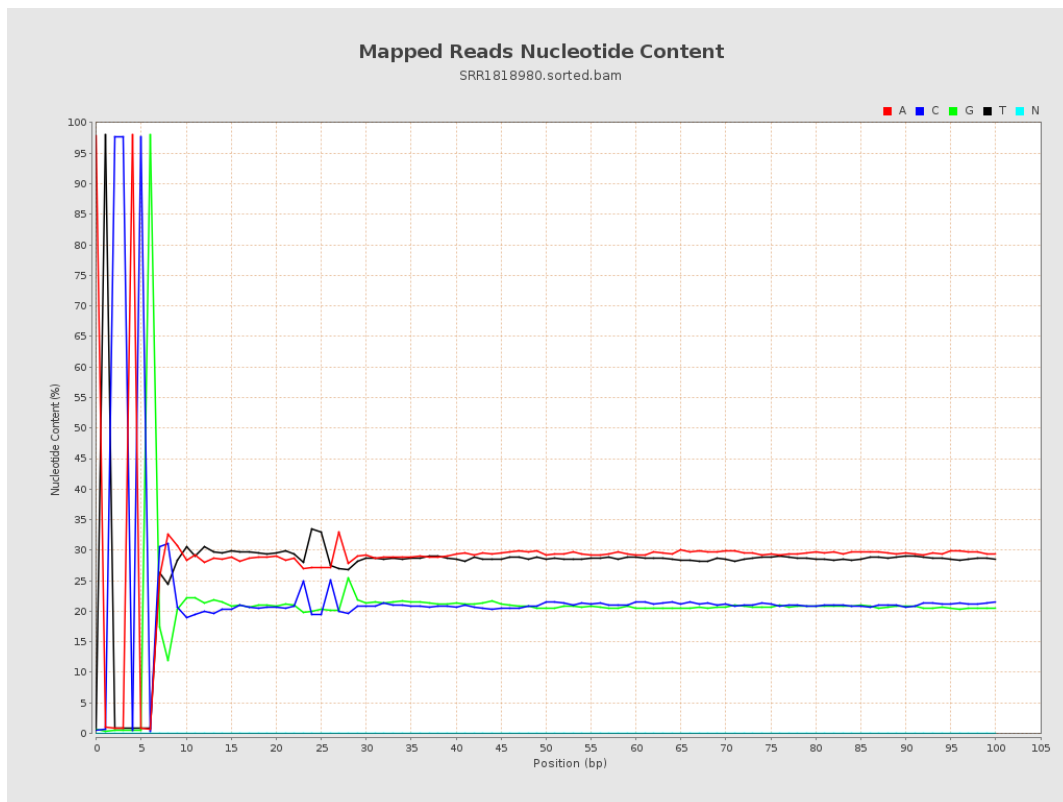
6. Results : Genome Fraction Coverage



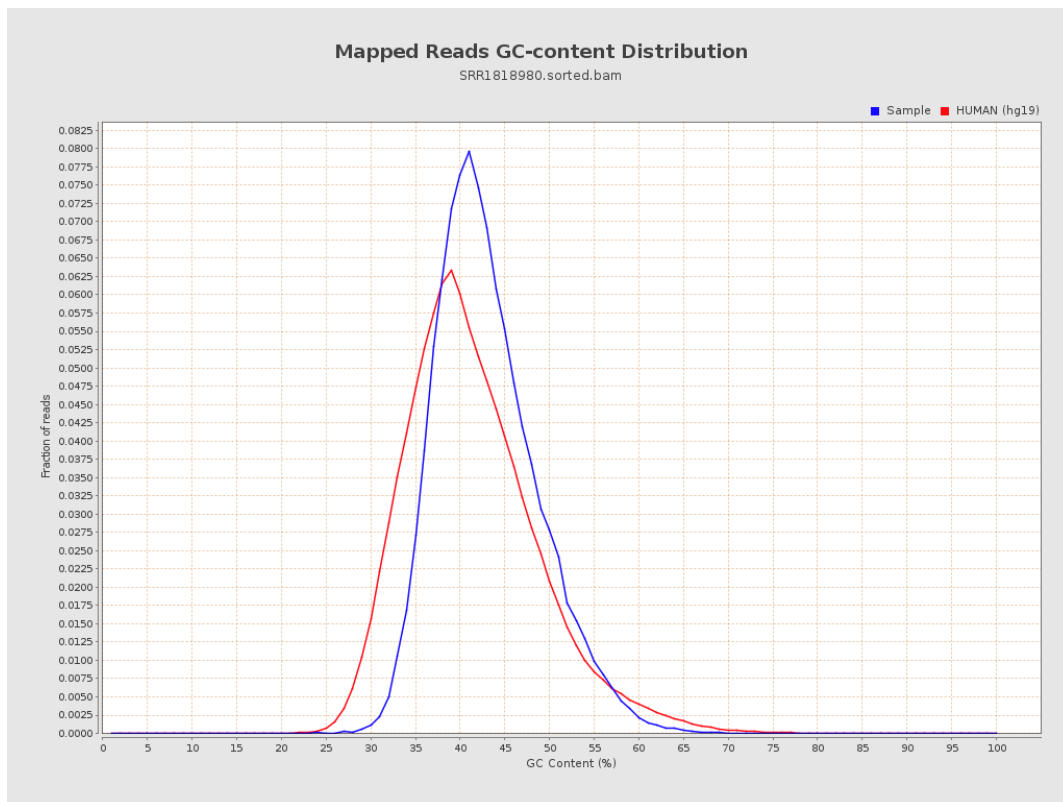
7. Results : Duplication Rate Histogram



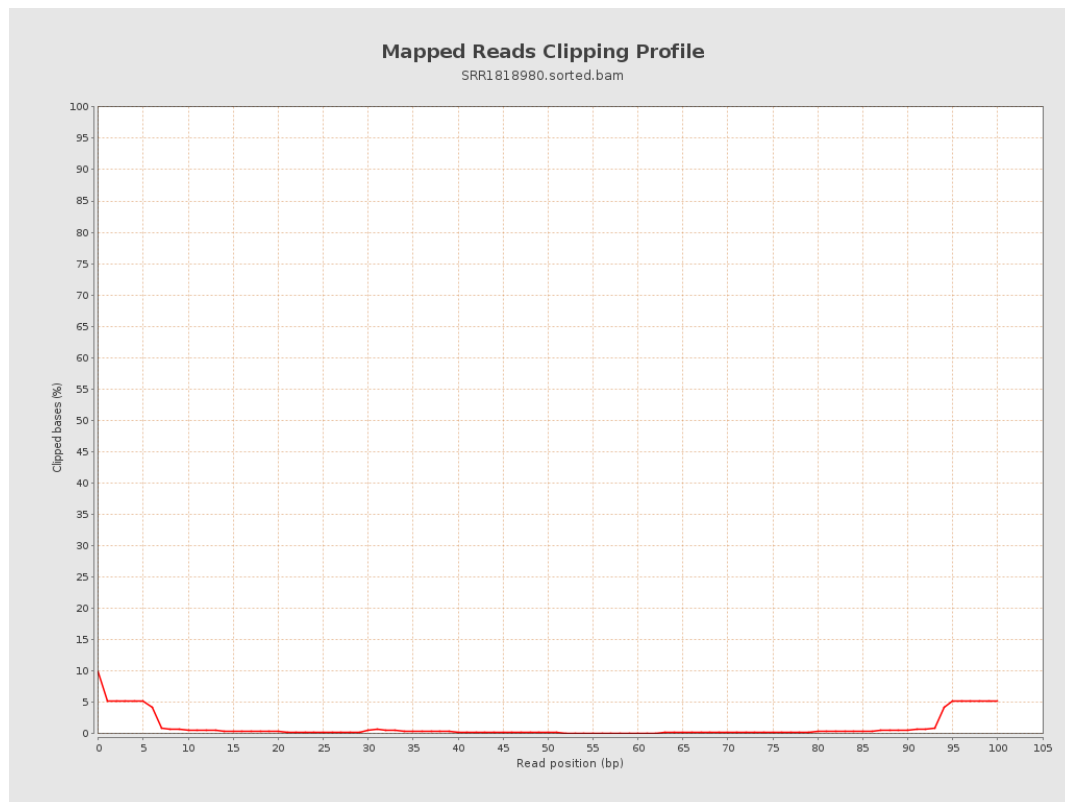
8. Results : Mapped Reads Nucleotide Content



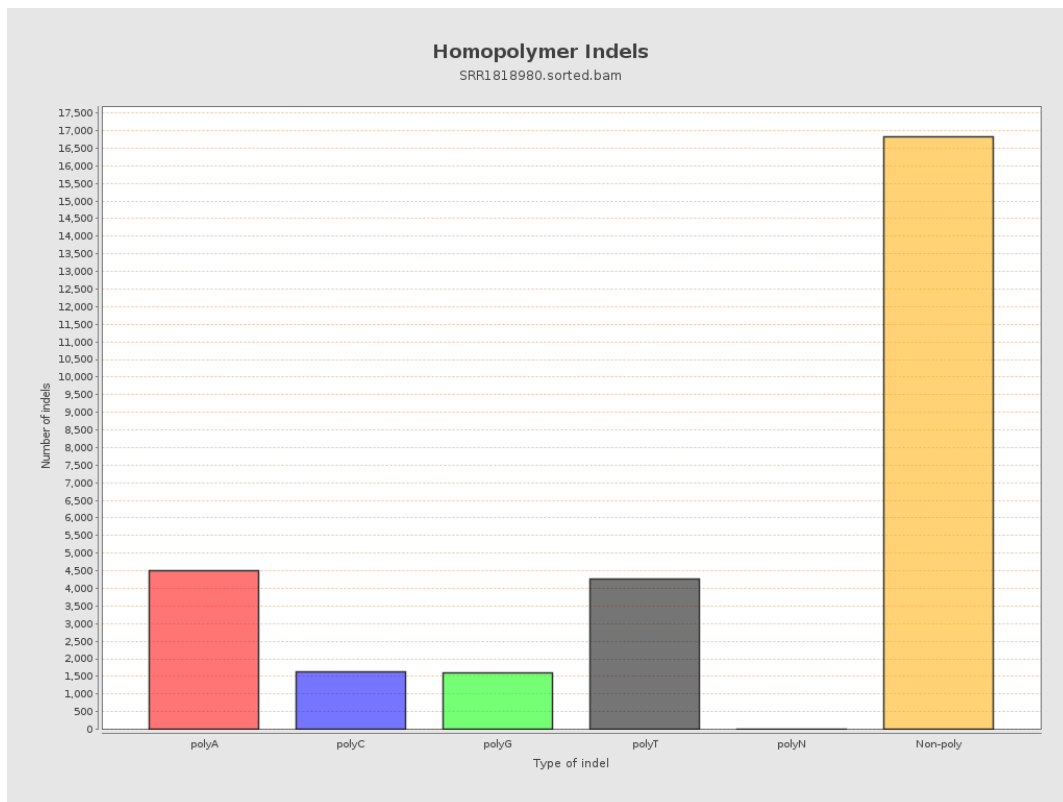
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

