

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 05:25:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818892.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_SRR1818892 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818892.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 05:25:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818892.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,408,266
Mapped reads	1,385,999 / 98.42%
Unmapped reads	22,267 / 1.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,557 / 1.39%
Read min/max/mean length	30 / 101 / 101.53
Duplicated reads (estimated)	237,557 / 16.87%
Duplication rate	14.02%
Clipped reads	1,400,450 / 99.44%

2.2. ACGT Content

Number/percentage of A's	37,746,527 / 29.43%
Number/percentage of C's	28,362,980 / 22.12%
Number/percentage of T's	35,578,655 / 27.74%
Number/percentage of G's	26,552,669 / 20.7%
Number/percentage of N's	1,992 / 0%
GC Percentage	42.82%

2.3. Coverage

Mean	0.0415

Standard Deviation	0.5571
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2.4. Mapping Quality

Mean Mapping Quality	49.17
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2.5. Mismatches and indels

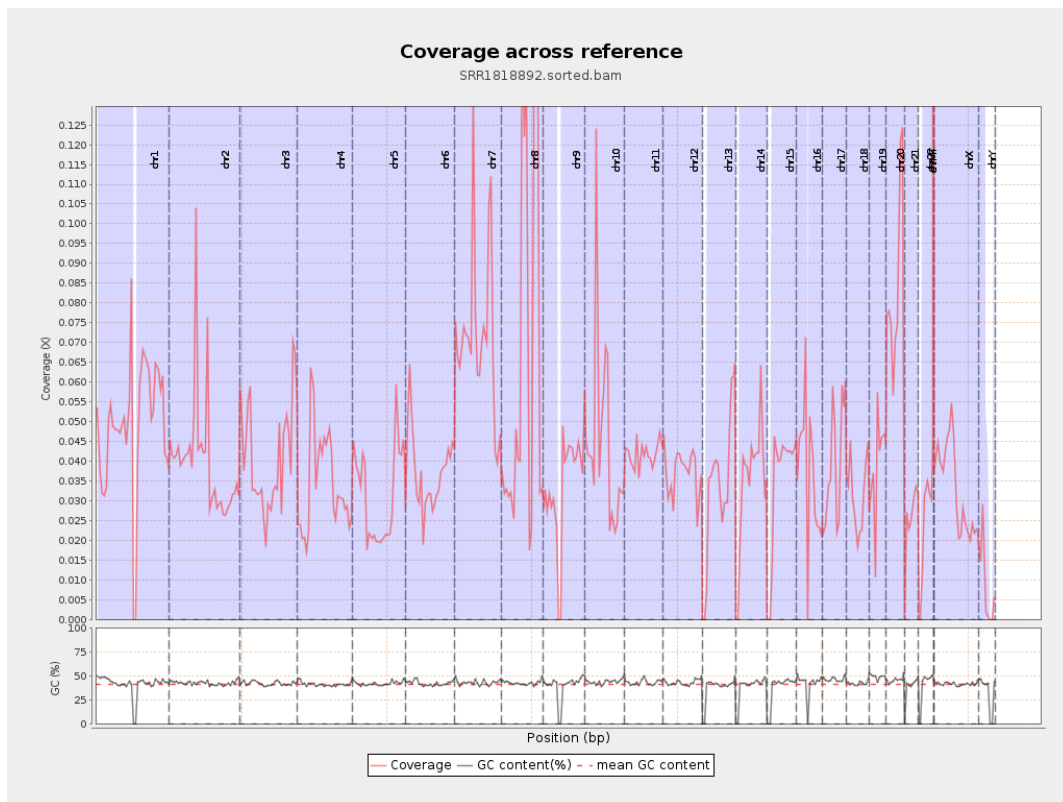
General error rate	0.65%
Mismatches	787,052
Insertions	17,494
Mapped reads with at least one insertion	1.22%
Deletions	40,967
Mapped reads with at least one deletion	2.89%
Homopolymer indels	40.82%

2.6. Chromosome stats

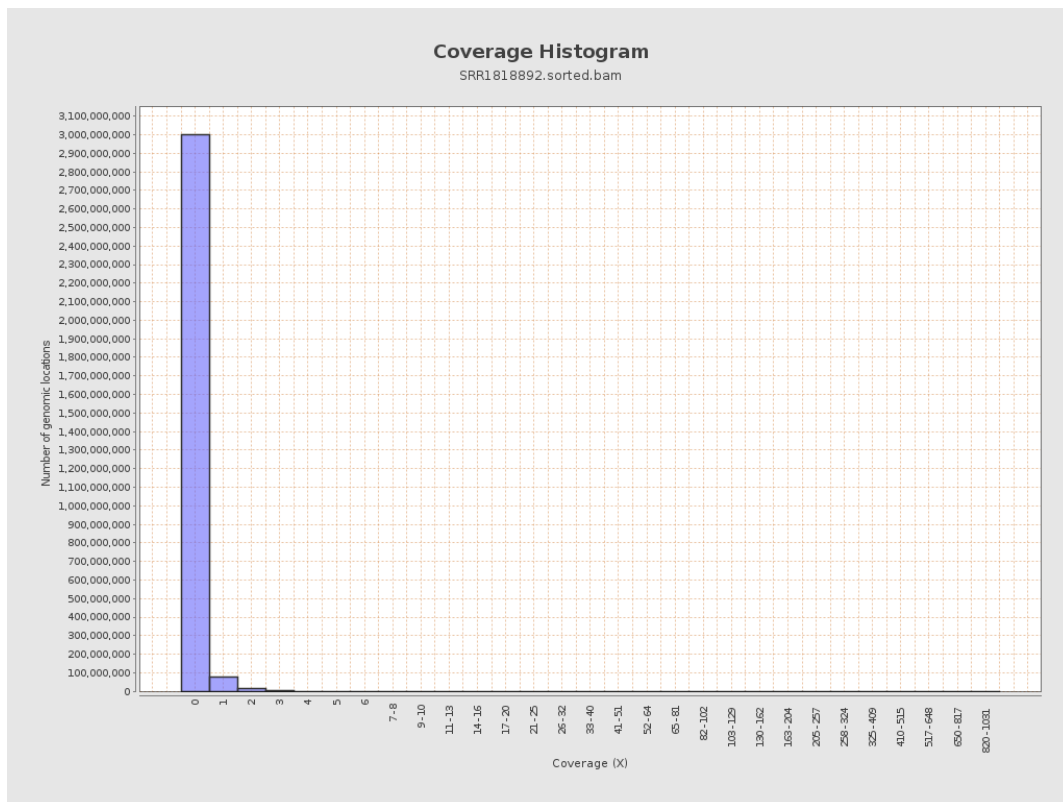
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	12181184	0.0489	0.825
chr2	243199373	9741071	0.0401	0.7637
chr3	198022430	8088137	0.0408	0.2526
chr4	191154276	6463489	0.0338	0.3151
chr5	180915260	5660065	0.0313	0.2342
chr6	171115067	6319021	0.0369	0.2683
chr7	159138663	11503601	0.0723	1.2766

chr8	146364022	11110814	0.0759	0.4561
chr9	141213431	4698546	0.0333	0.4652
chr10	135534747	6041371	0.0446	0.8349
chr11	135006516	5626140	0.0417	0.3255
chr12	133851895	5005919	0.0374	0.2438
chr13	115169878	3866103	0.0336	0.2259
chr14	107349540	3738032	0.0348	0.2582
chr15	102531392	3541345	0.0345	0.2314
chr16	90354753	3273174	0.0362	0.5455
chr17	81195210	3207463	0.0395	0.3587
chr18	78077248	2468898	0.0316	0.5274
chr19	59128983	2286729	0.0387	0.7115
chr20	63025520	5271410	0.0836	0.3919
chr21	48129895	1236854	0.0257	0.2712
chr22	51304566	1172836	0.0229	0.2099
chrMT	16571	151941	9.1691	6.3187
chrX	155270560	5182892	0.0334	0.2864
chrY	59373566	486485	0.0082	0.5787

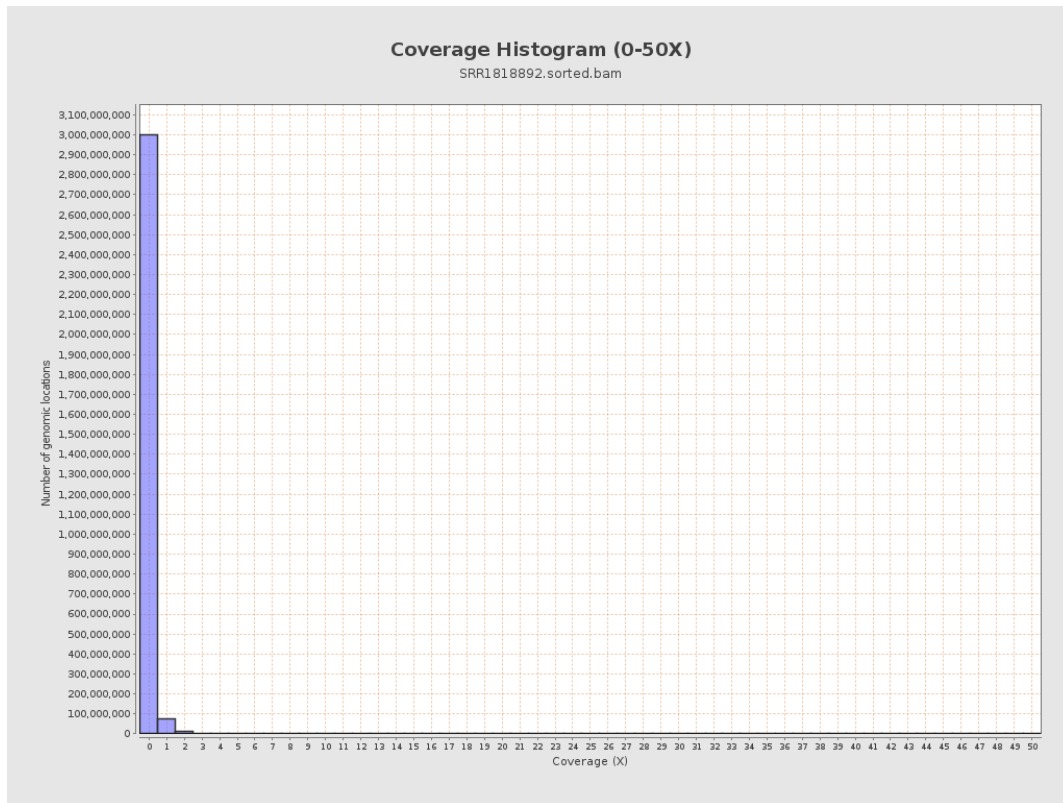
3. Results : Coverage across reference



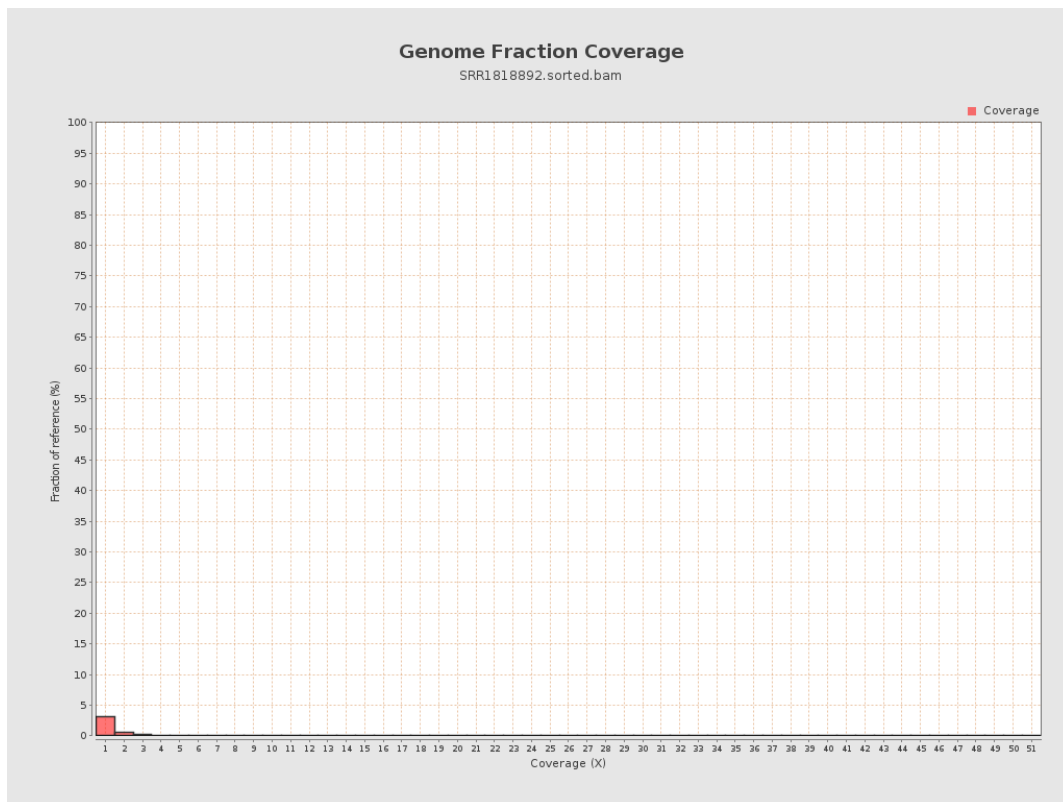
4. Results : Coverage Histogram



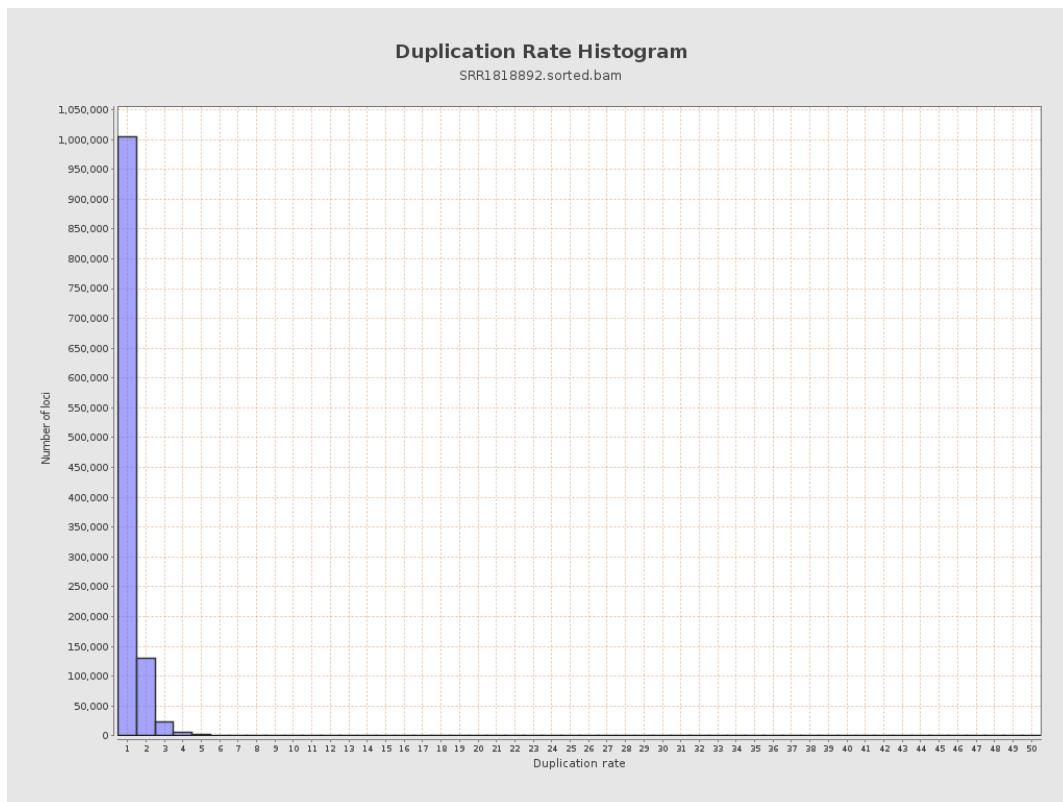
5. Results : Coverage Histogram (0-50X)



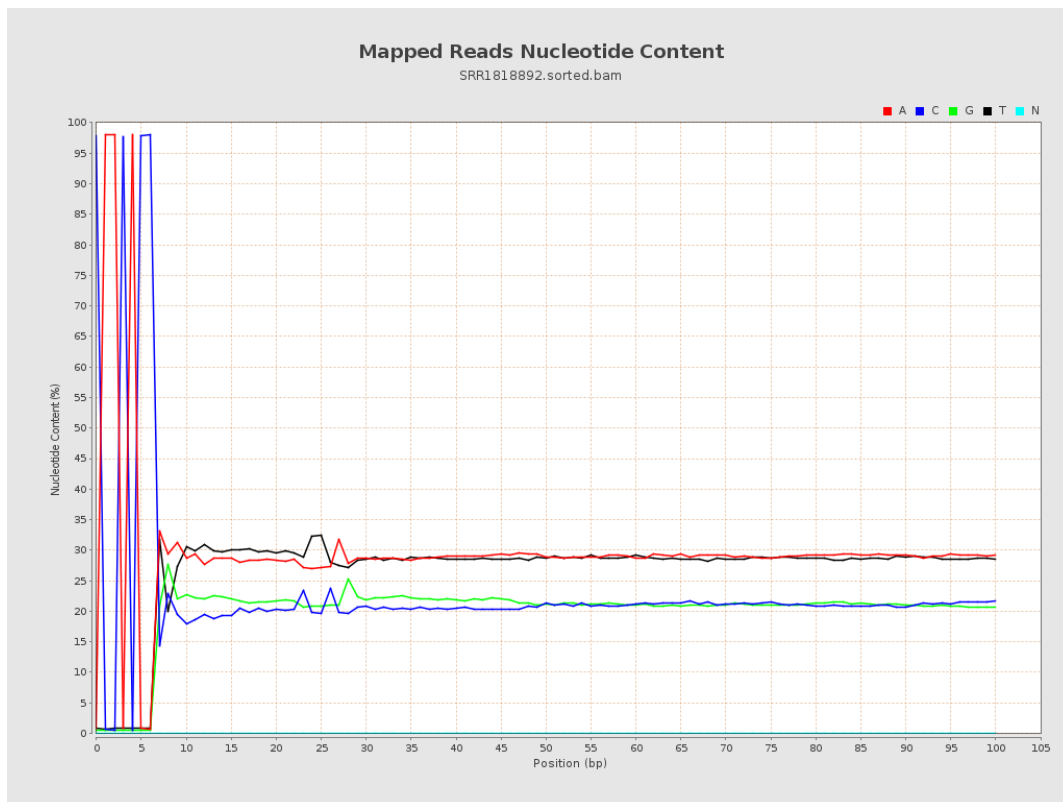
6. Results : Genome Fraction Coverage



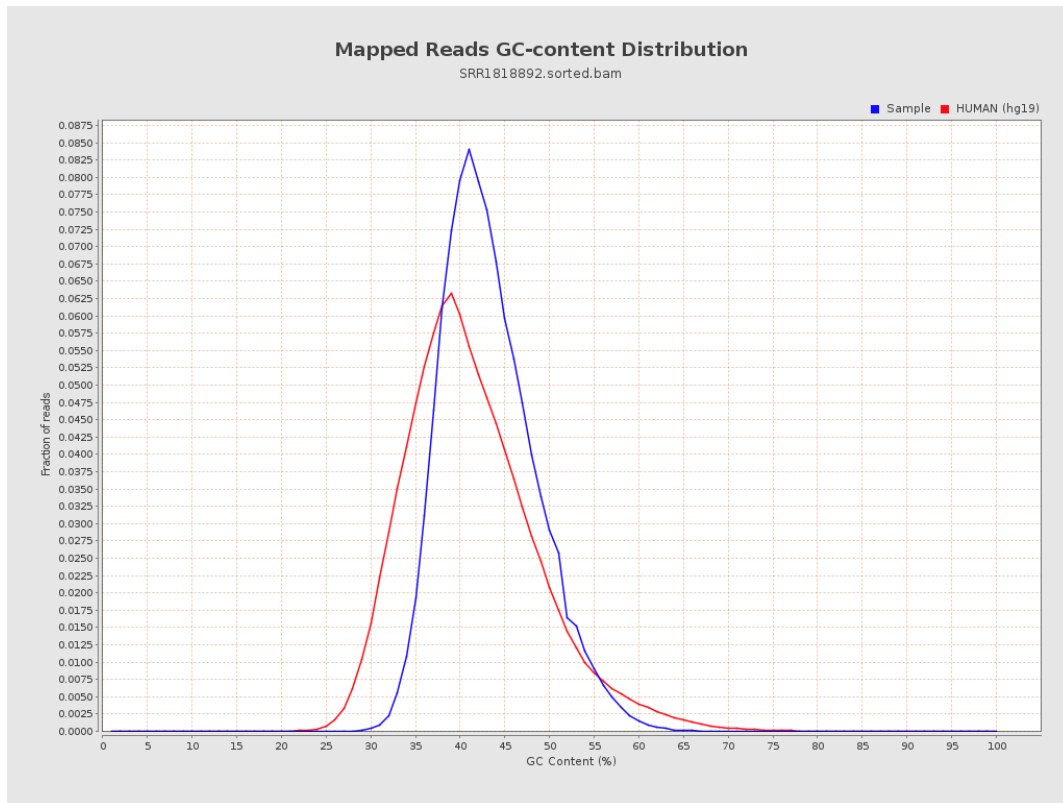
7. Results : Duplication Rate Histogram



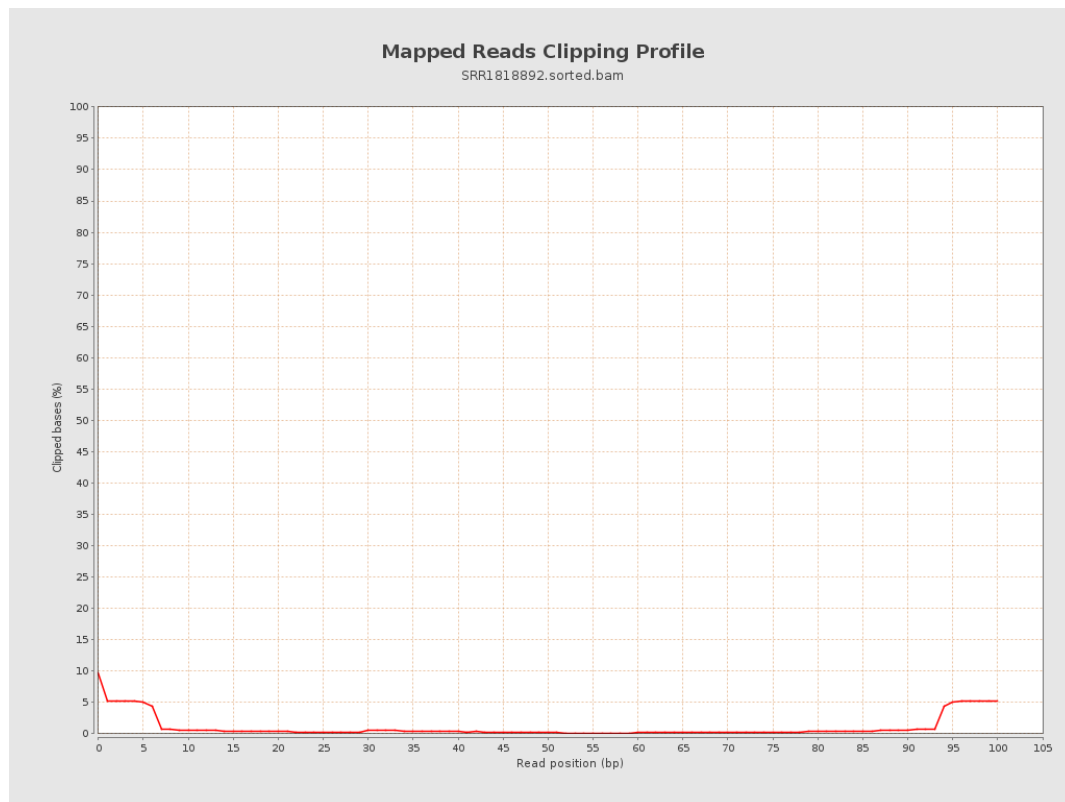
8. Results : Mapped Reads Nucleotide Content



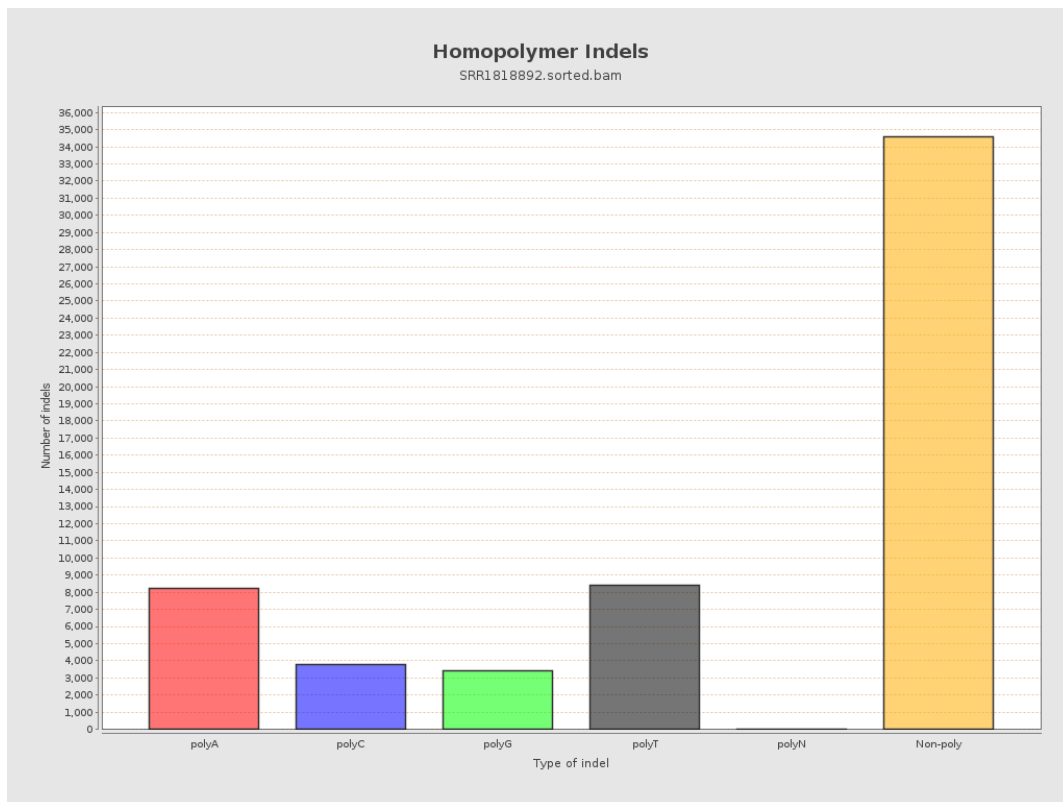
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

