

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 13:00:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818983.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_SRR1818983 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818983.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 13:00:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818983.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,209,869
Mapped reads	2,141,994 / 96.93%
Unmapped reads	67,875 / 3.07%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	32,187 / 1.46%
Read min/max/mean length	30 / 101 / 101.56
Duplicated reads (estimated)	944,398 / 42.74%
Duplication rate	37.27%
Clipped reads	2,147,984 / 97.2%

2.2. ACGT Content

Number/percentage of A's	55,424,122 / 27.97%
Number/percentage of C's	43,071,138 / 21.73%
Number/percentage of T's	57,769,474 / 29.15%
Number/percentage of G's	41,895,572 / 21.14%
Number/percentage of N's	9,224 / 0%
GC Percentage	42.88%

2.3. Coverage

Mean	0.0641

Standard Deviation	0.7852
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2.4. Mapping Quality

Mean Mapping Quality	49.05
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2.5. Mismatches and indels

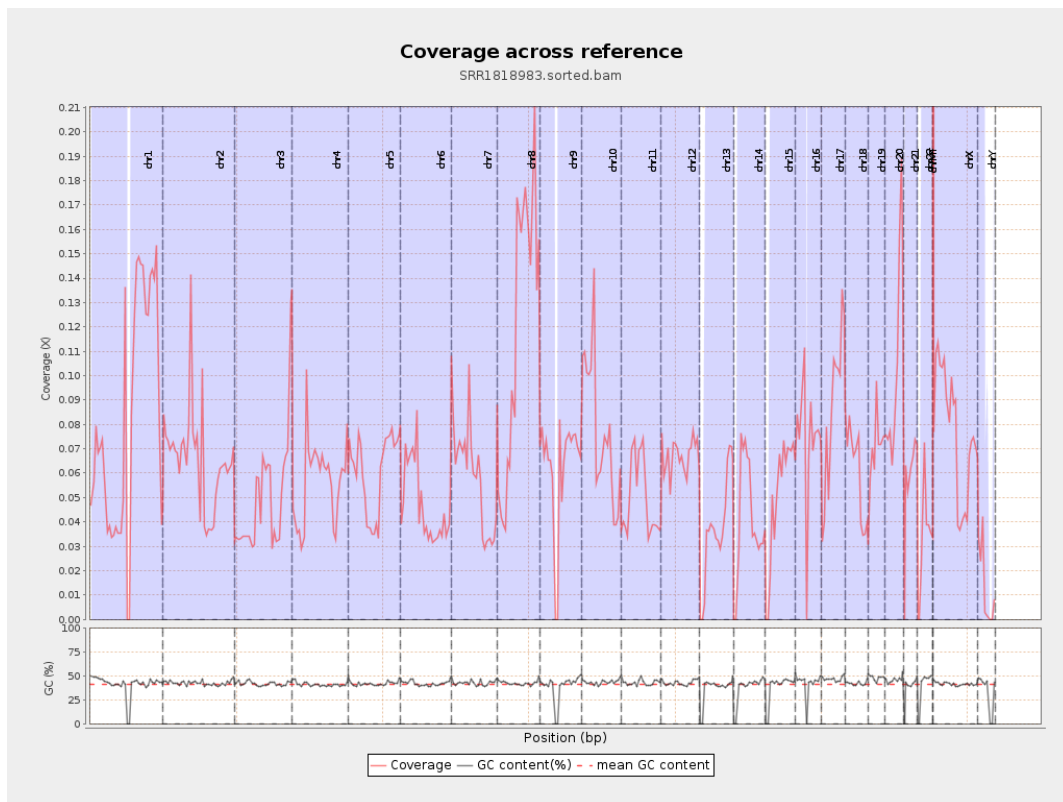
General error rate	0.68%
Mismatches	1,270,413
Insertions	32,084
Mapped reads with at least one insertion	1.45%
Deletions	63,307
Mapped reads with at least one deletion	2.89%
Homopolymer indels	41%

2.6. Chromosome stats

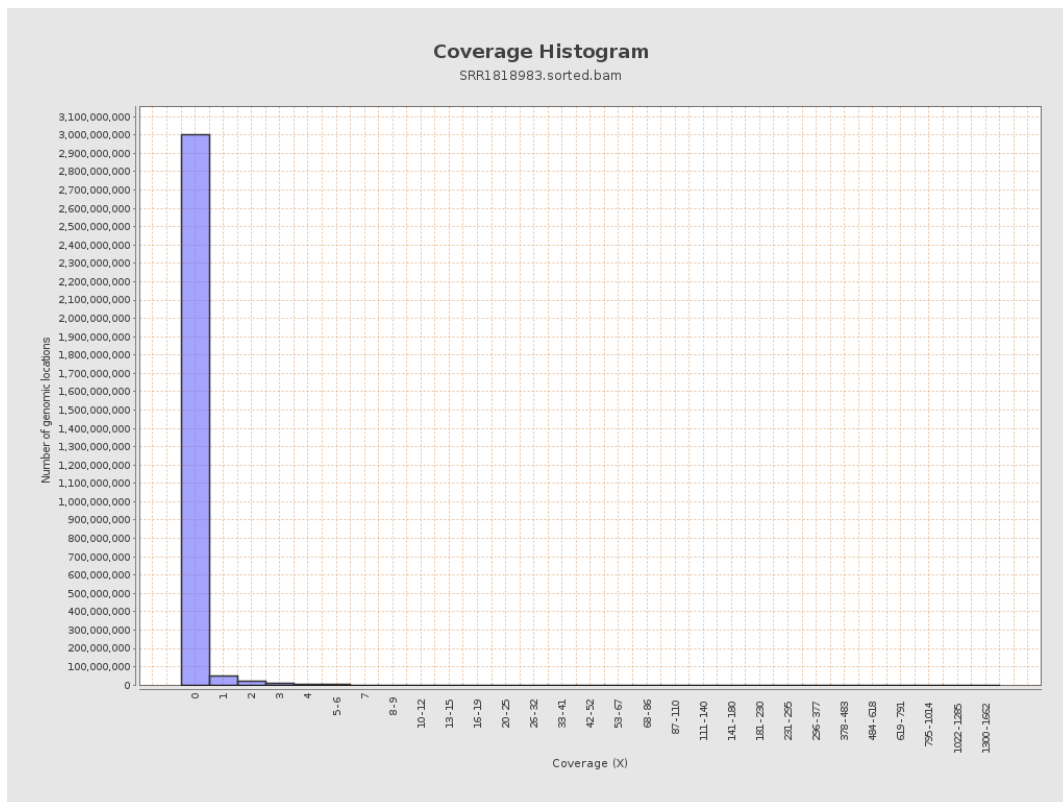
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	20406767	0.0819	1.4813
chr2	243199373	15962331	0.0656	1.0791
chr3	198022430	9758361	0.0493	0.4004
chr4	191154276	10747105	0.0562	0.5219
chr5	180915260	11015950	0.0609	0.4609
chr6	171115067	8058283	0.0471	0.4762
chr7	159138663	9324495	0.0586	0.8867

chr8	146364022	17699894	0.1209	0.7162
chr9	141213431	8785484	0.0622	0.7761
chr10	135534747	10360158	0.0764	0.9337
chr11	135006516	6678224	0.0495	0.5049
chr12	133851895	9022908	0.0674	0.4813
chr13	115169878	4295735	0.0373	0.3434
chr14	107349540	4491480	0.0418	0.4024
chr15	102531392	5053114	0.0493	0.4075
chr16	90354753	6634939	0.0734	0.8815
chr17	81195210	6984240	0.086	0.6172
chr18	78077248	4743278	0.0608	0.8143
chr19	59128983	4170709	0.0705	1.3391
chr20	63025520	6671649	0.1059	0.6452
chr21	48129895	2817857	0.0585	0.4945
chr22	51304566	1681260	0.0328	0.3705
chrMT	16571	139340	8.4087	7.5195
chrX	155270560	12000463	0.0773	0.5776
chrY	59373566	785989	0.0132	0.8352

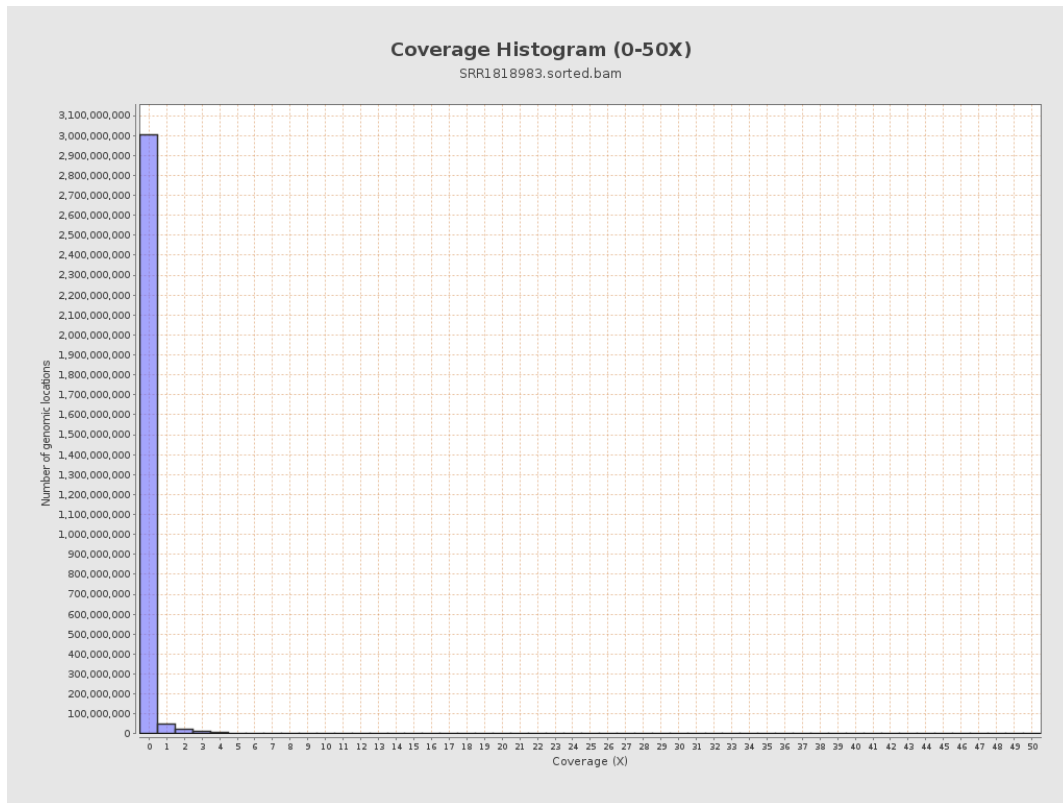
3. Results : Coverage across reference



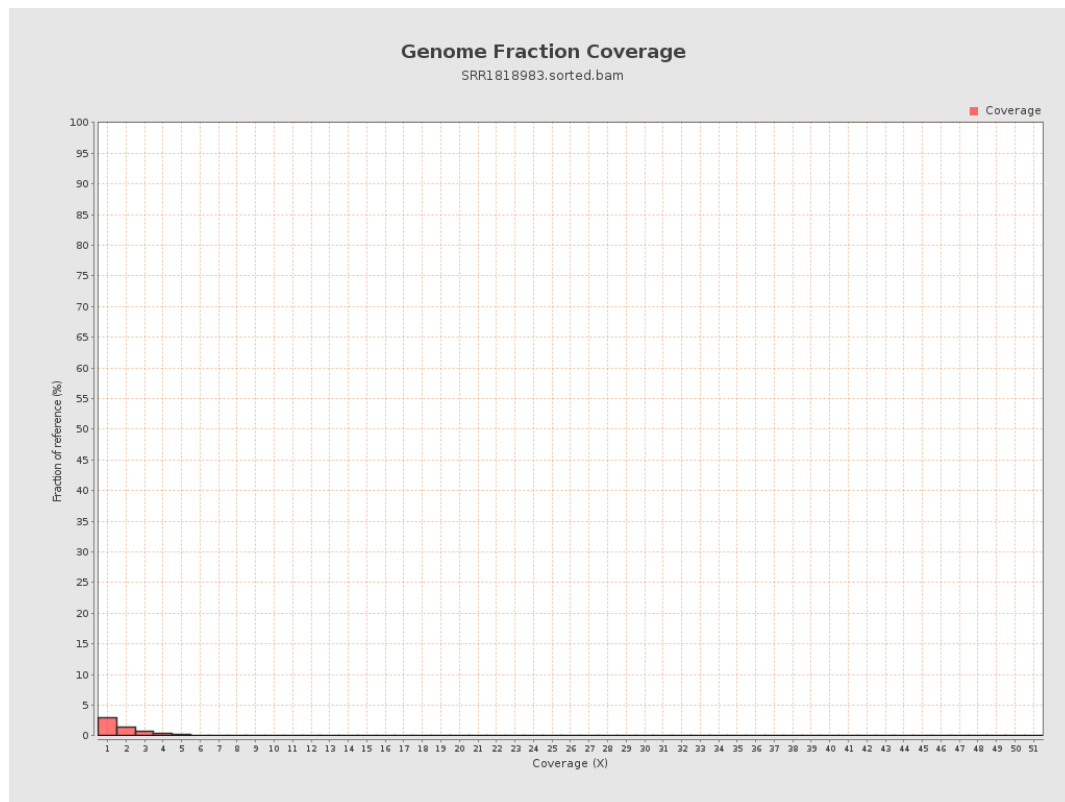
4. Results : Coverage Histogram



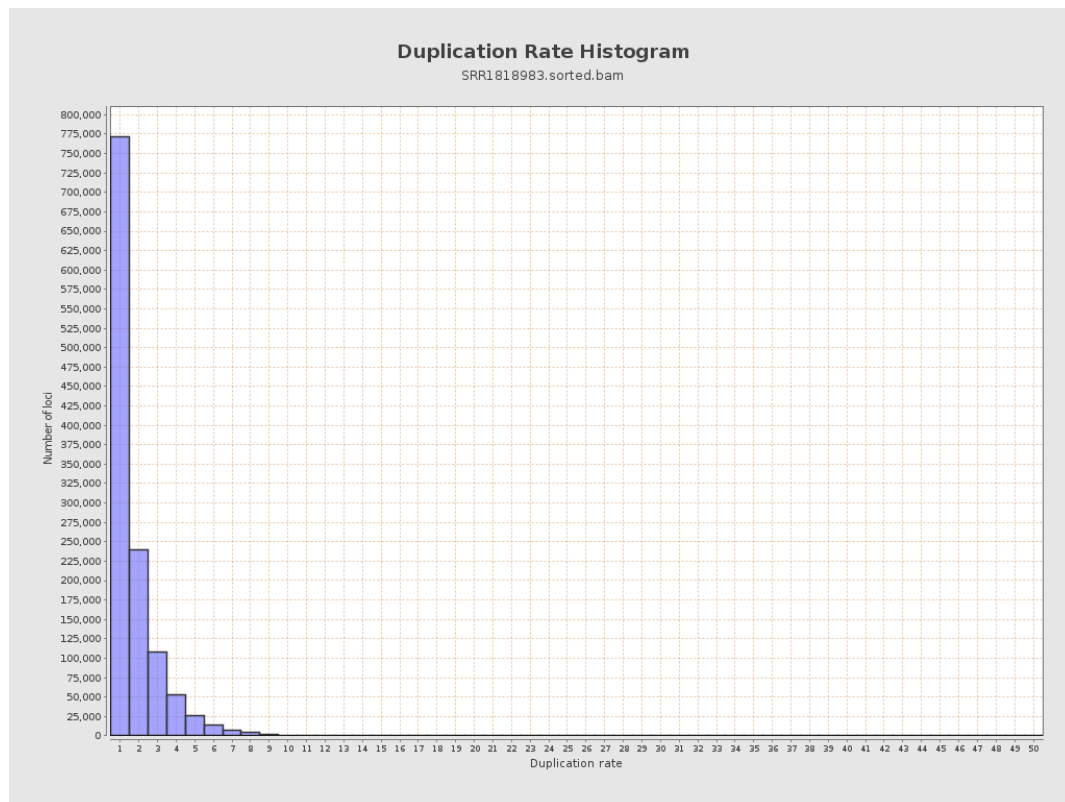
5. Results : Coverage Histogram (0-50X)



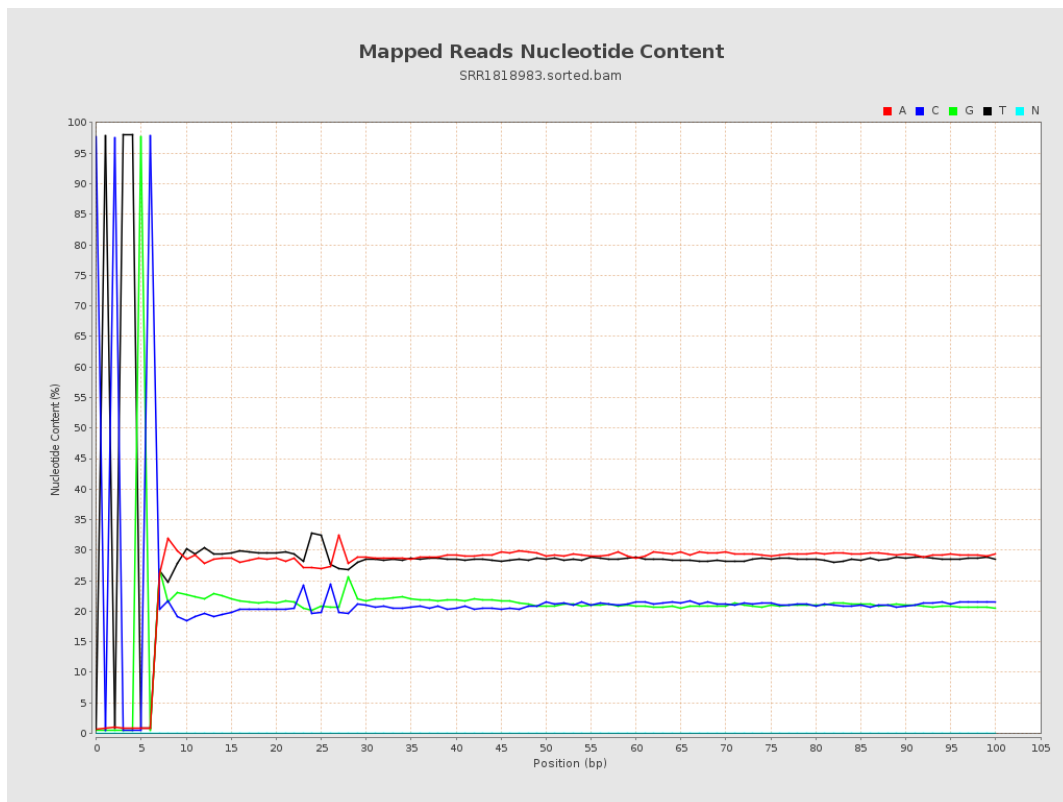
6. Results : Genome Fraction Coverage



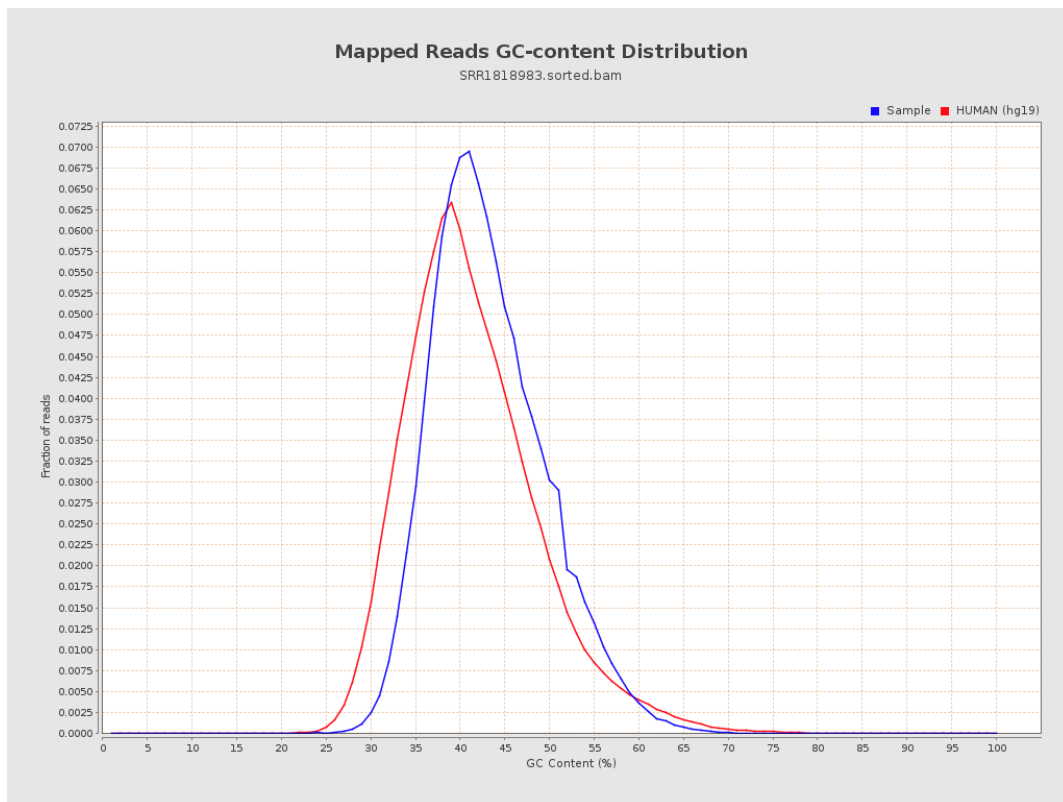
7. Results : Duplication Rate Histogram



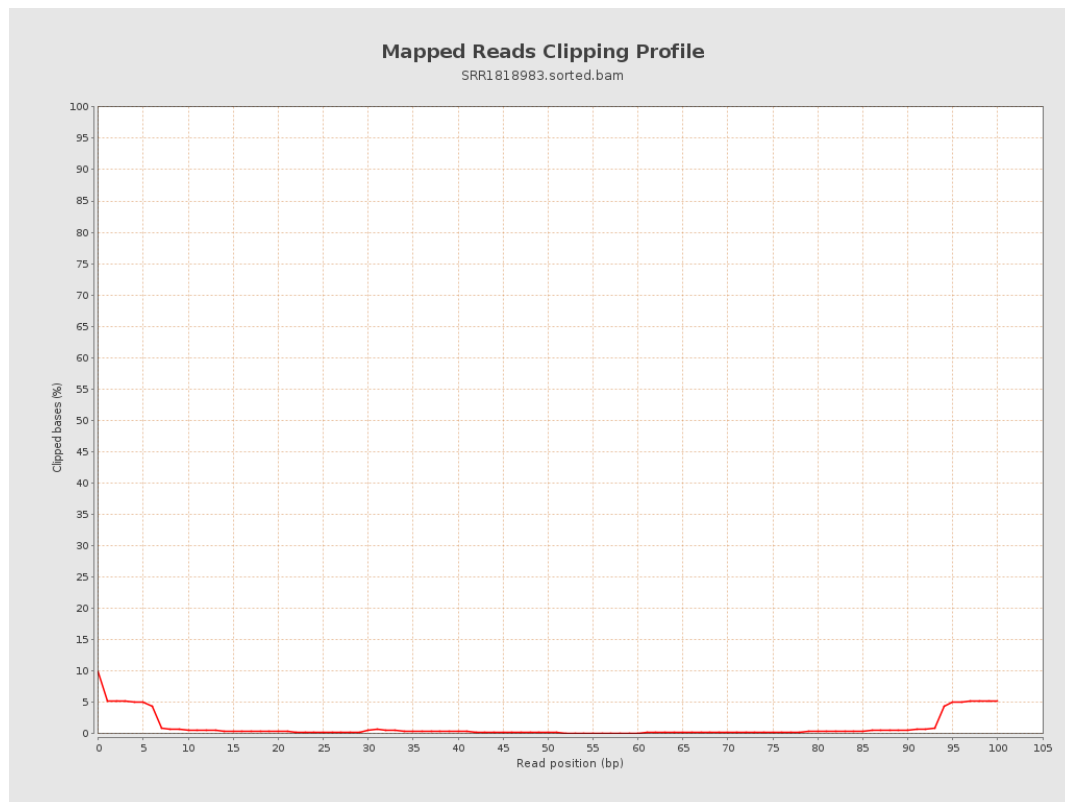
8. Results : Mapped Reads Nucleotide Content



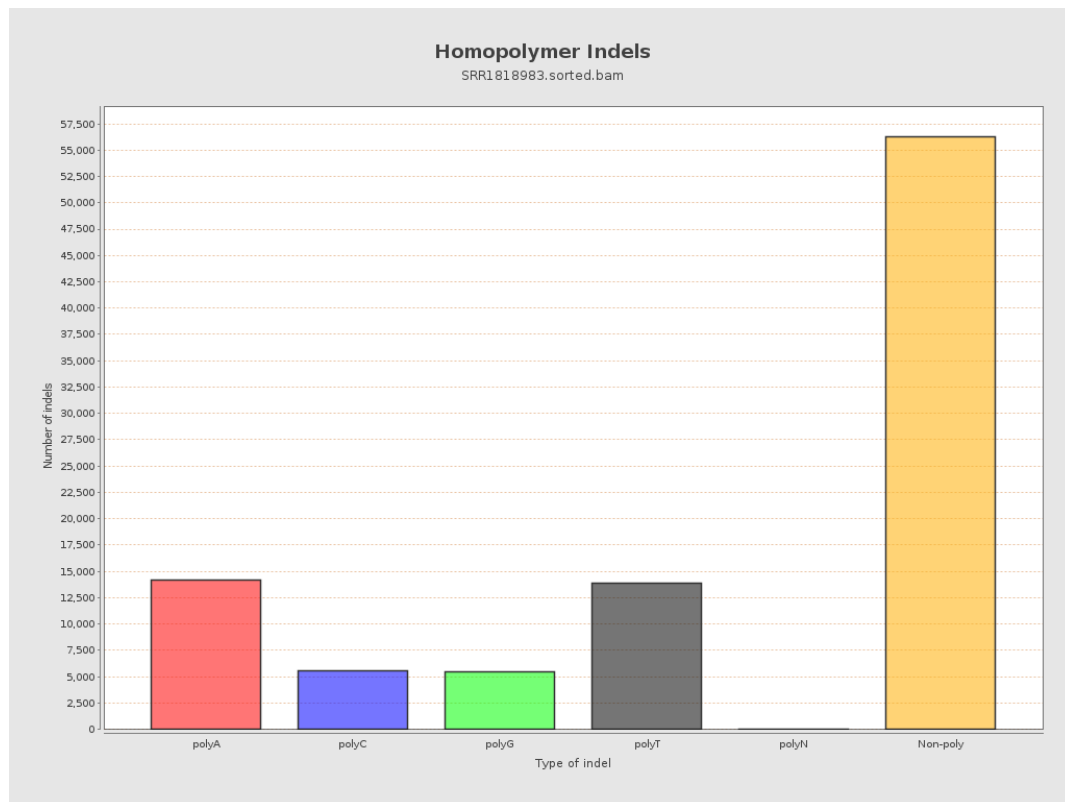
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

