

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 10:20:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818948.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_SRR1818948 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818948.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 10:20:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818948.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,252,339
Mapped reads	4,185,734 / 98.43%
Unmapped reads	66,605 / 1.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	51,884 / 1.22%
Read min/max/mean length	30 / 101 / 101.47
Duplicated reads (estimated)	2,359,831 / 55.49%
Duplication rate	45.46%
Clipped reads	4,191,290 / 98.56%

2.2. ACGT Content

Number/percentage of A's	108,762,574 / 28.02%
Number/percentage of C's	81,647,817 / 21.04%
Number/percentage of T's	111,215,192 / 28.65%
Number/percentage of G's	86,494,857 / 22.28%
Number/percentage of N's	15,975 / 0%
GC Percentage	43.32%

2.3. Coverage

Mean	0.1254

Standard Deviation	1.3408
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2.4. Mapping Quality

Mean Mapping Quality	49.26
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2.5. Mismatches and indels

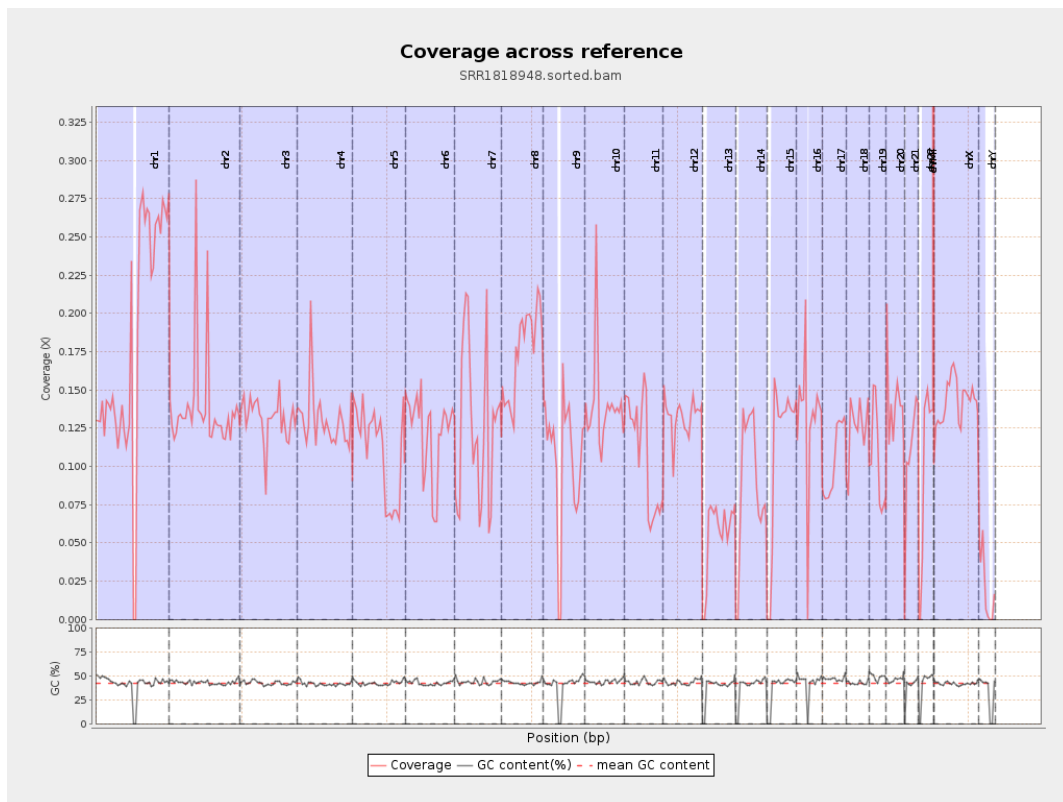
General error rate	0.65%
Mismatches	2,406,785
Insertions	51,189
Mapped reads with at least one insertion	1.19%
Deletions	118,673
Mapped reads with at least one deletion	2.78%
Homopolymer indels	42.07%

2.6. Chromosome stats

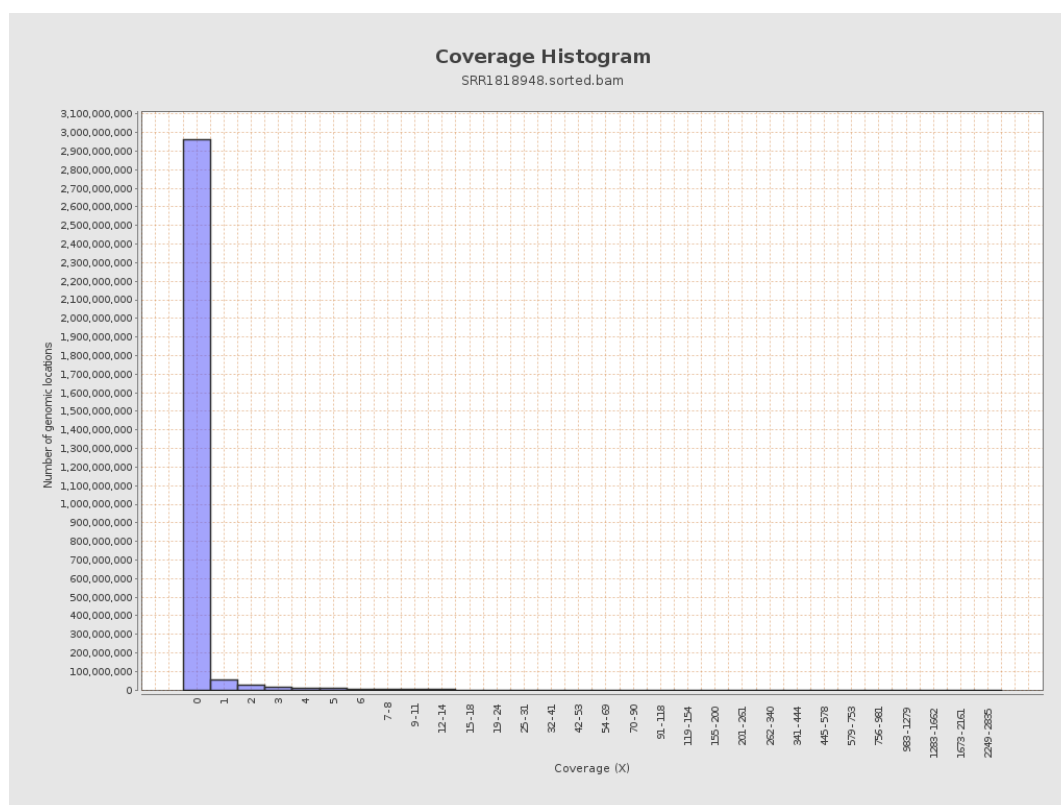
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	44986467	0.1805	2.4284
chr2	243199373	33673517	0.1385	1.9205
chr3	198022430	25969792	0.1311	0.8259
chr4	191154276	24838582	0.1299	0.9451
chr5	180915260	19902726	0.11	0.7846
chr6	171115067	20822739	0.1217	0.8965
chr7	159138663	19903095	0.1251	1.041

chr8	146364022	25691345	0.1755	1.1411
chr9	141213431	14566658	0.1032	1.5297
chr10	135534747	18838066	0.139	1.6673
chr11	135006516	14694404	0.1088	0.9145
chr12	133851895	17715742	0.1324	0.8507
chr13	115169878	6336833	0.055	0.5223
chr14	107349540	9488017	0.0884	0.7946
chr15	102531392	11564619	0.1128	0.7869
chr16	90354753	11912414	0.1318	1.419
chr17	81195210	8510864	0.1048	0.8631
chr18	78077248	9769912	0.1251	1.8511
chr19	59128983	6268091	0.106	2.2003
chr20	63025520	8866226	0.1407	0.9404
chr21	48129895	5279562	0.1097	0.866
chr22	51304566	4926055	0.096	0.8033
chrMT	16571	587136	35.4315	22.9767
chrX	155270560	22061780	0.1421	1.0276
chrY	59373566	1178642	0.0199	1.1875

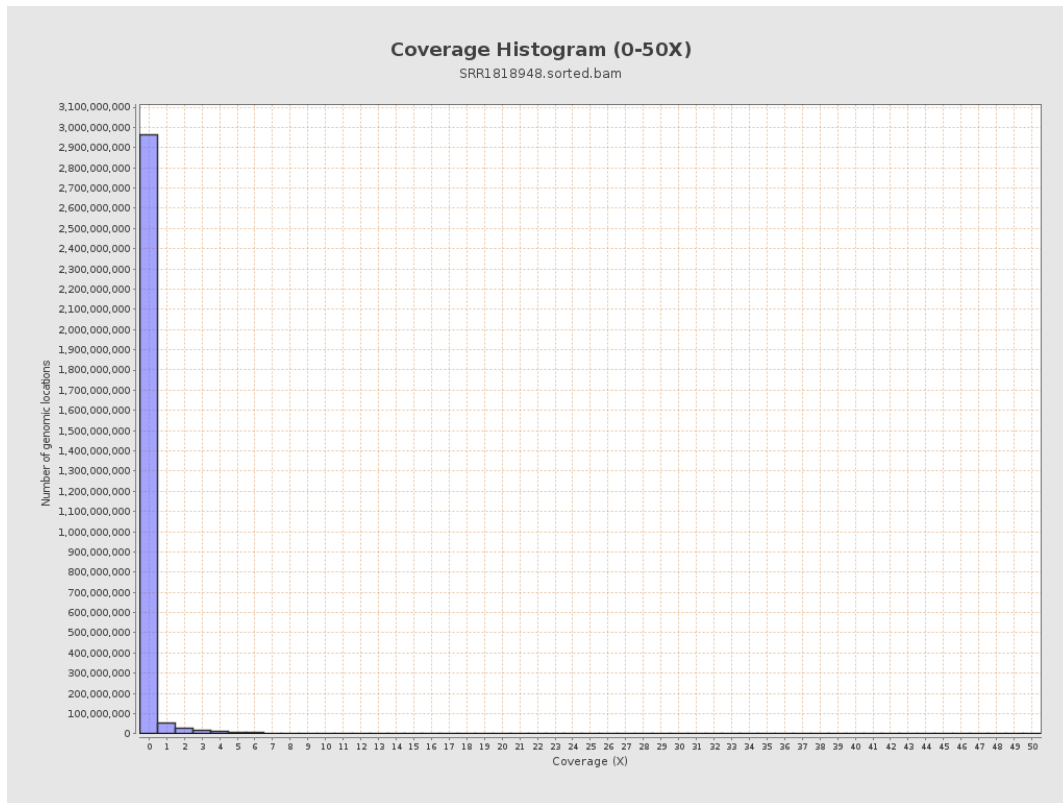
3. Results : Coverage across reference



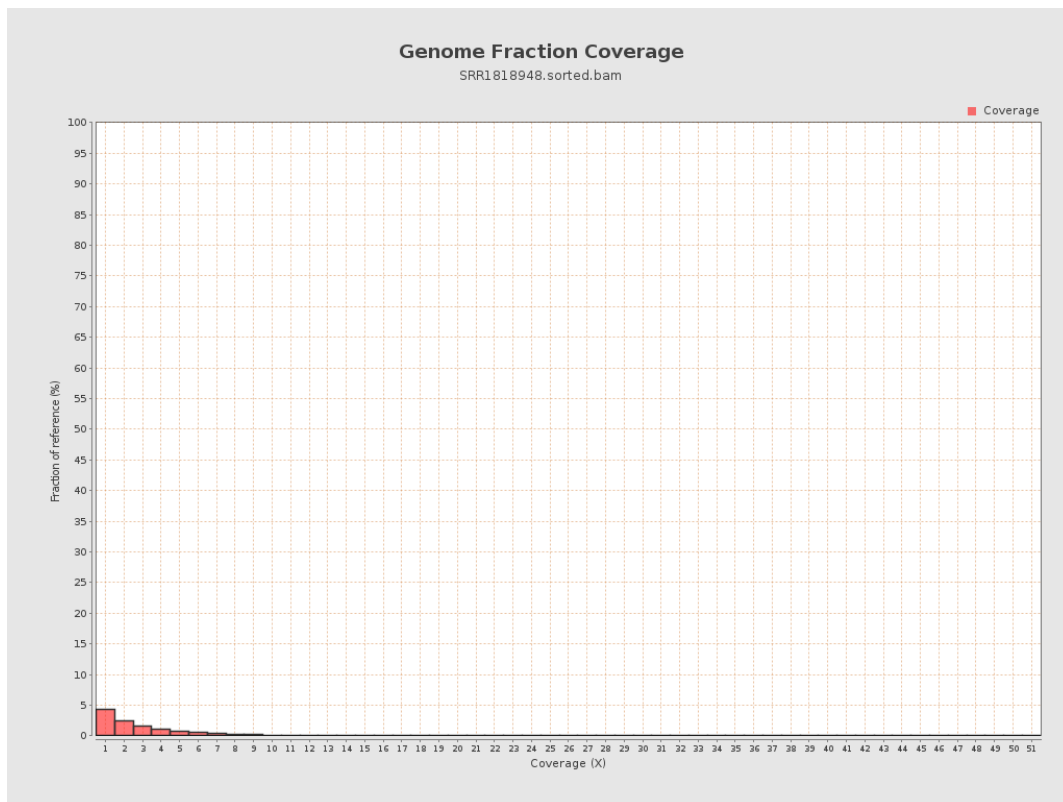
4. Results : Coverage Histogram



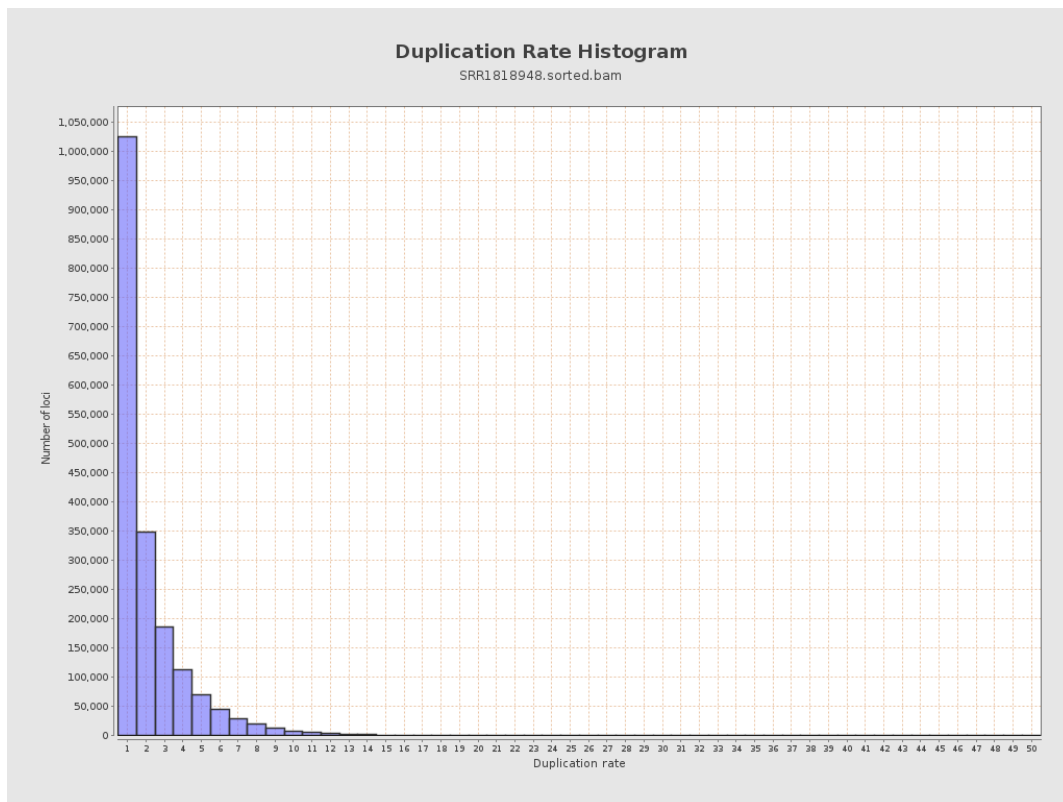
5. Results : Coverage Histogram (0-50X)



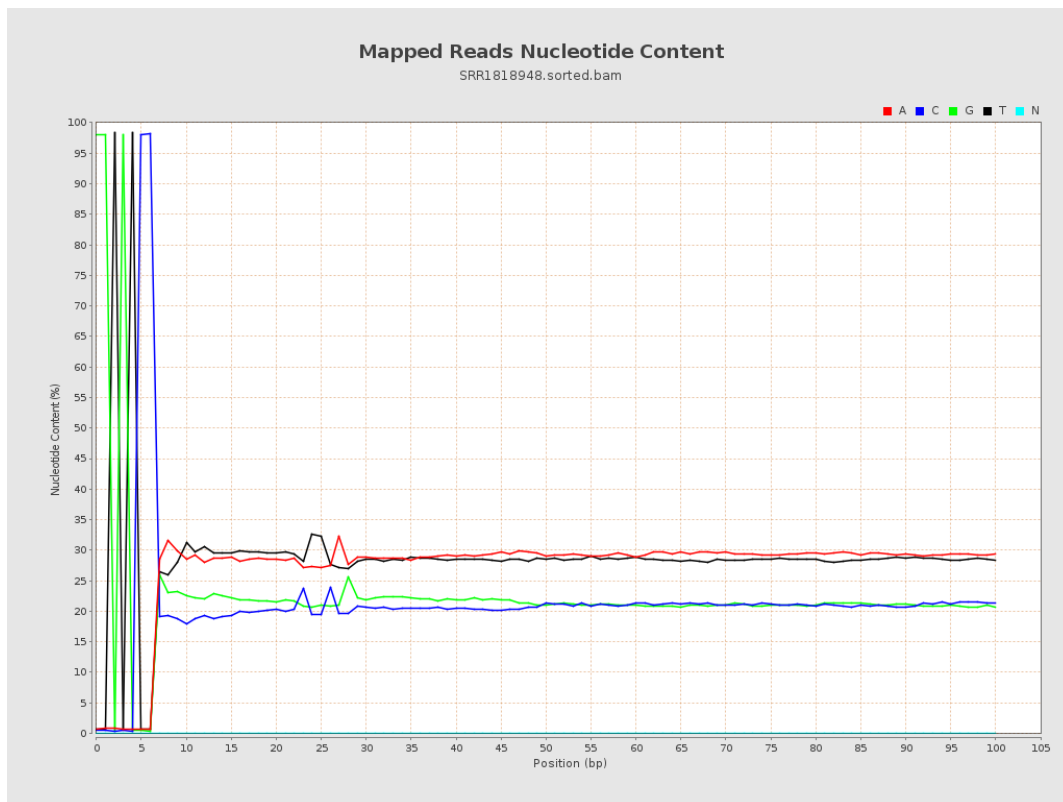
6. Results : Genome Fraction Coverage



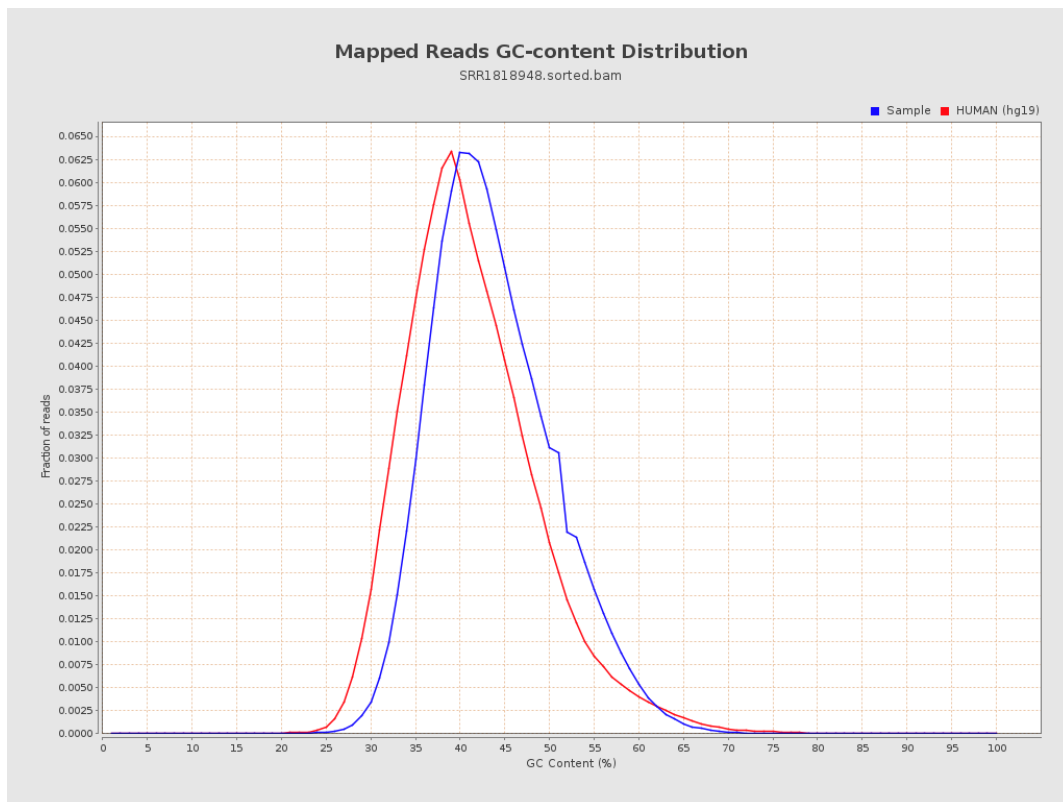
7. Results : Duplication Rate Histogram



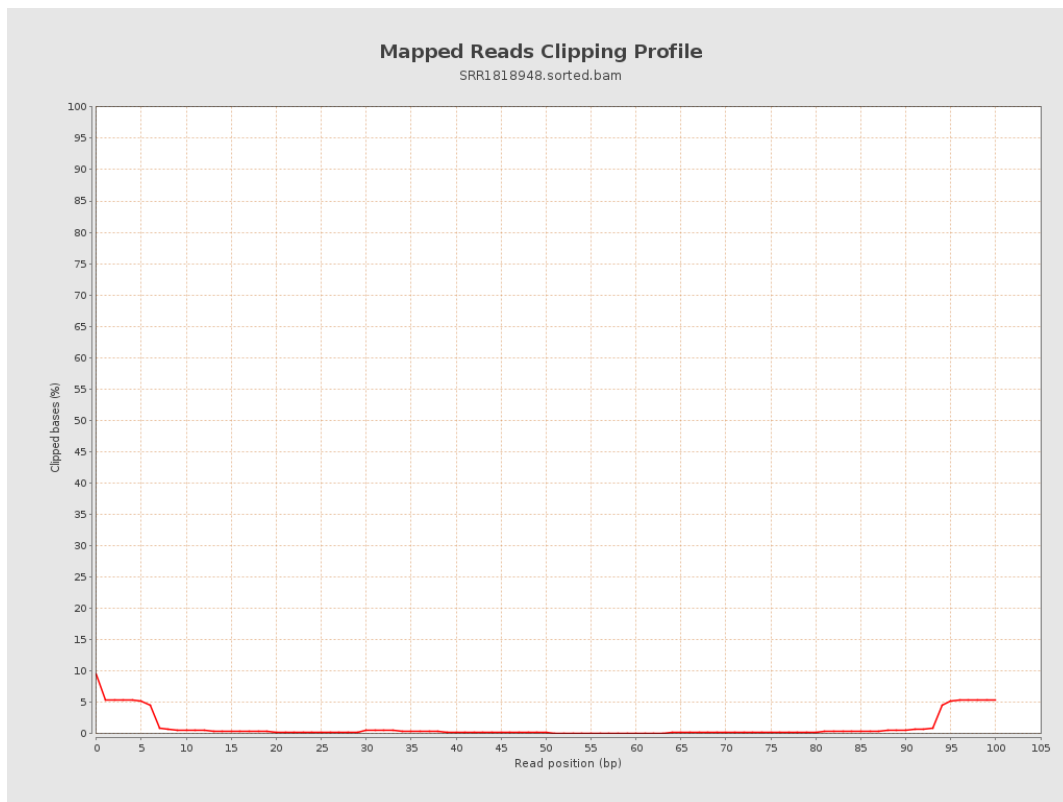
8. Results : Mapped Reads Nucleotide Content



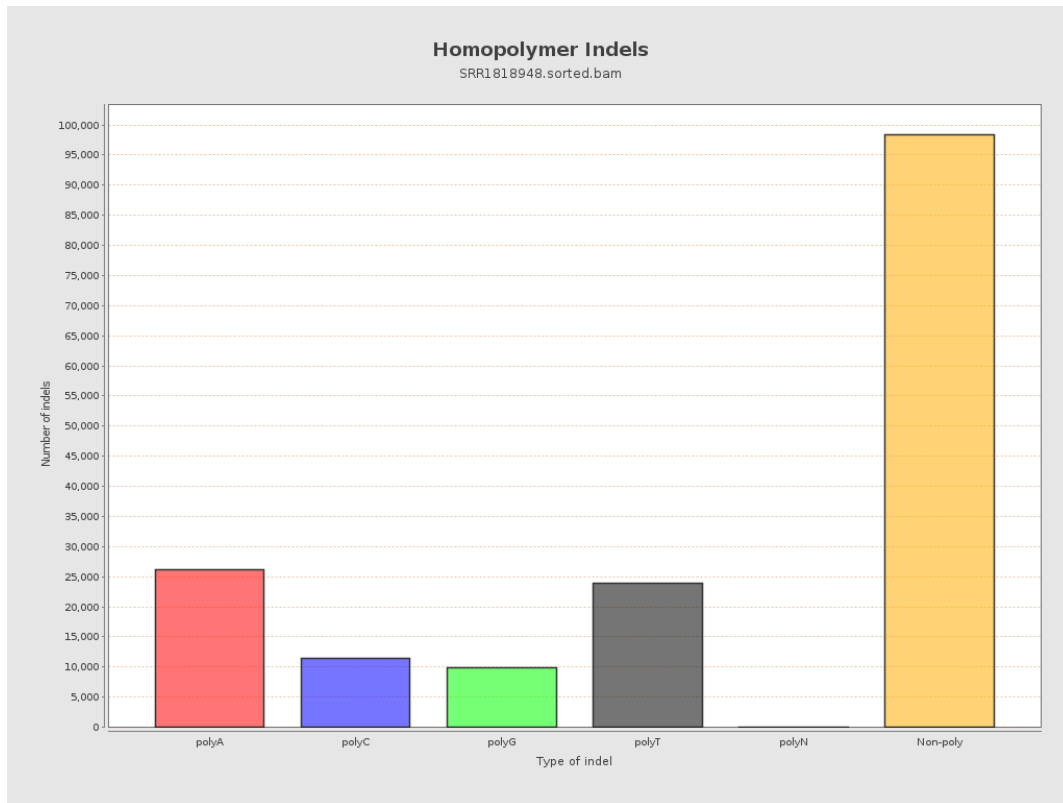
9. Results : Mapped Reads GC-content Distribution



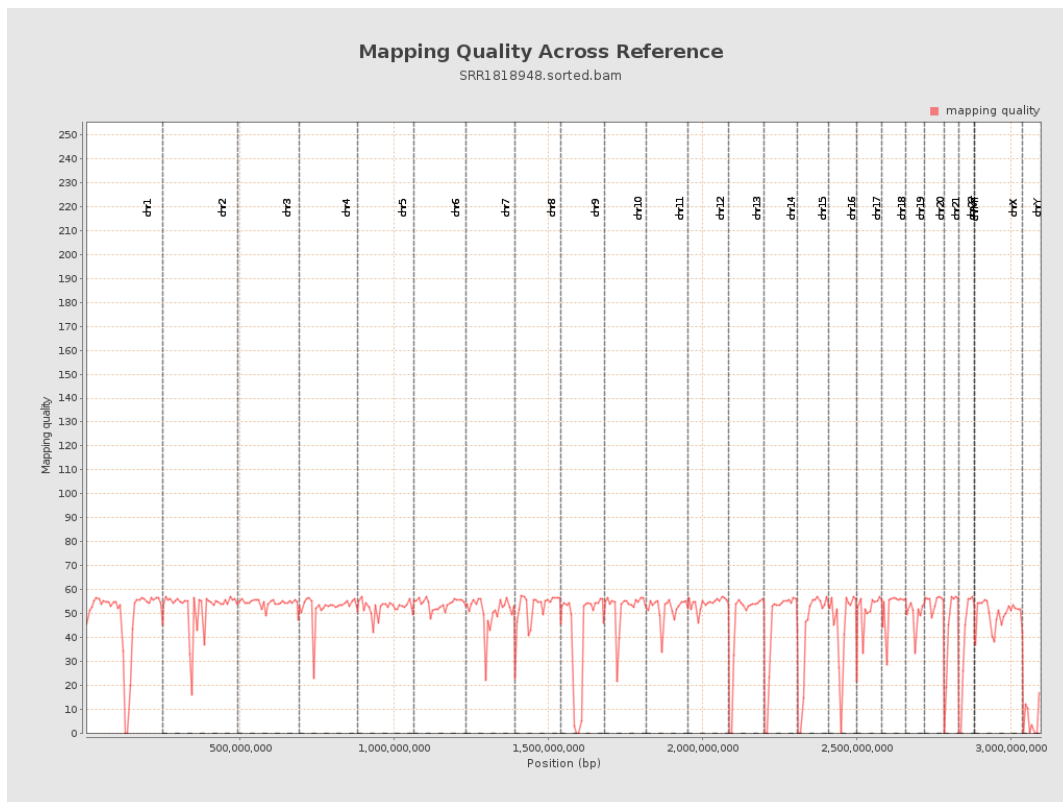
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

