

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 10:15:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524547.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_SRR10524547 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524547.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 10:15:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524547.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,083,117
Mapped reads	993,995 / 91.77%
Unmapped reads	89,122 / 8.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,936 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	28,353 / 2.62%
Duplication rate	2.14%
Clipped reads	996,693 / 92.02%

2.2. ACGT Content

Number/percentage of A's	13,764,509 / 23.79%
Number/percentage of C's	10,888,999 / 18.82%
Number/percentage of T's	18,540,884 / 32.05%
Number/percentage of G's	14,651,707 / 25.33%
Number/percentage of N's	782 / 0%
GC Percentage	44.15%

2.3. Coverage

Mean	0.0187

Standard Deviation	0.1879
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2.4. Mapping Quality

Mean Mapping Quality	44.86
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2.5. Mismatches and indels

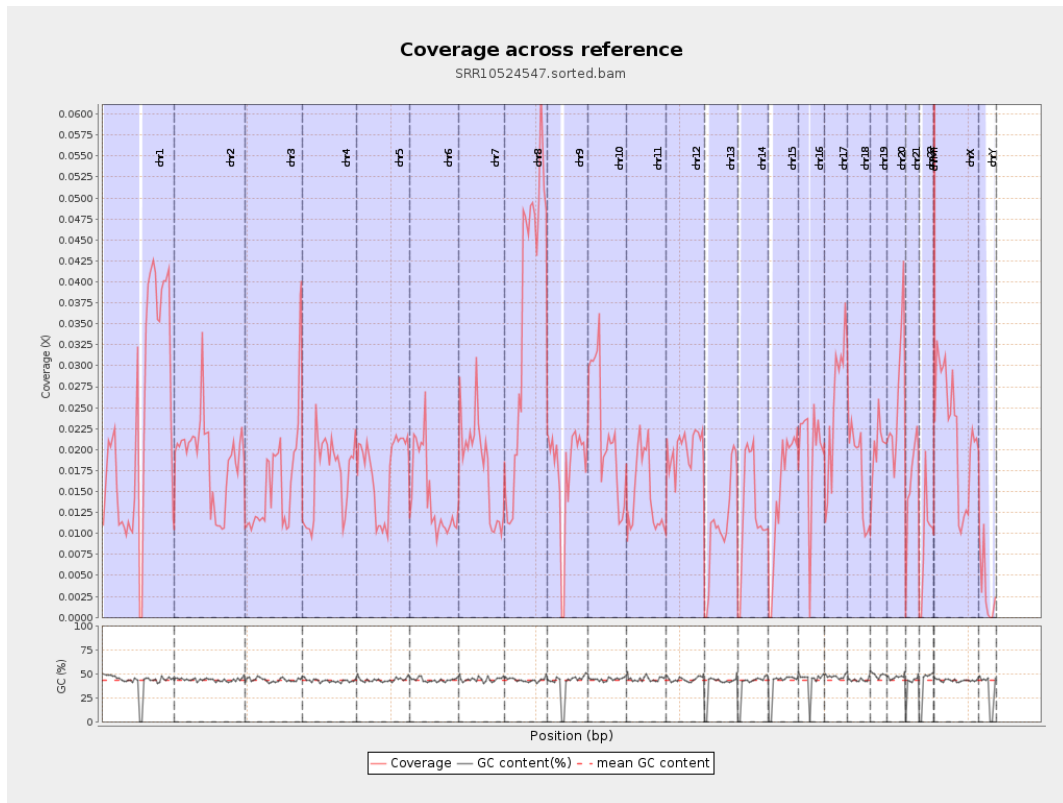
General error rate	0.52%
Mismatches	293,854
Insertions	3,157
Mapped reads with at least one insertion	0.32%
Deletions	10,823
Mapped reads with at least one deletion	1.08%
Homopolymer indels	43.81%

2.6. Chromosome stats

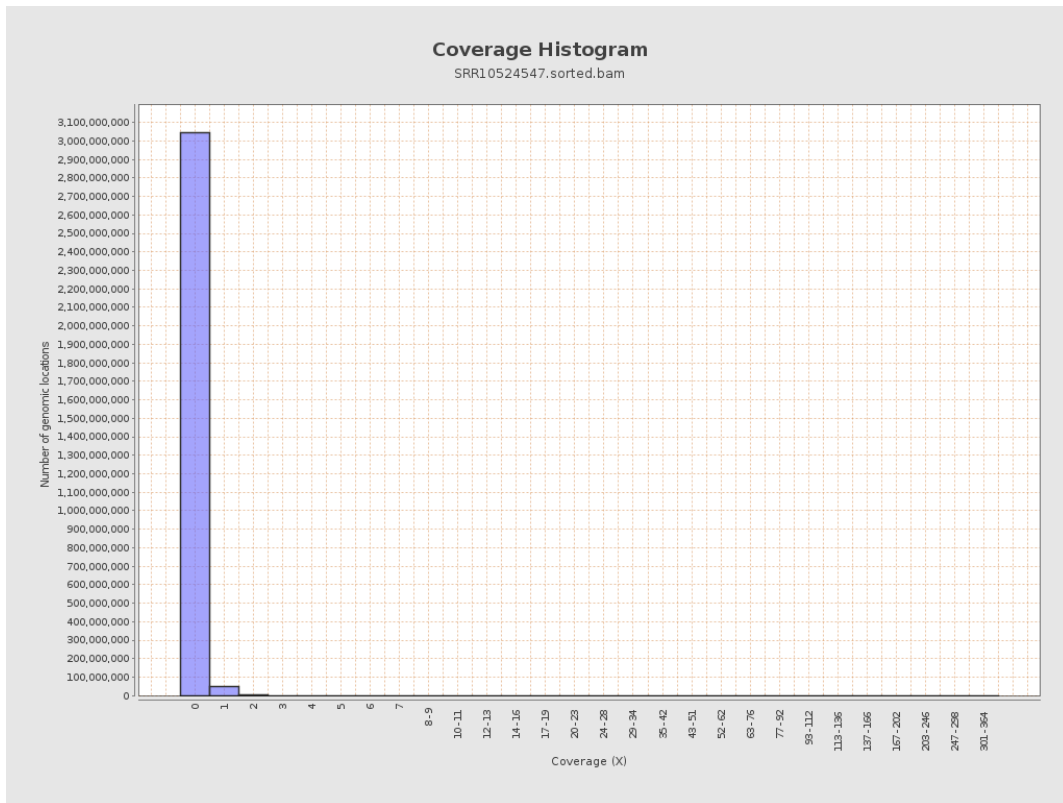
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5730648	0.023	0.3058
chr2	243199373	4588691	0.0189	0.2107
chr3	198022430	3154493	0.0159	0.1347
chr4	191154276	3243418	0.017	0.1495
chr5	180915260	3166107	0.0175	0.1407
chr6	171115067	2477493	0.0145	0.1513
chr7	159138663	2903397	0.0182	0.2306

chr8	146364022	5245629	0.0358	0.2251
chr9	141213431	2465830	0.0175	0.1703
chr10	135534747	3024159	0.0223	0.1978
chr11	135006516	2002149	0.0148	0.1701
chr12	133851895	2697644	0.0202	0.1505
chr13	115169878	1271348	0.011	0.1116
chr14	107349540	1359148	0.0127	0.1213
chr15	102531392	1534303	0.015	0.1321
chr16	90354753	1794333	0.0199	0.157
chr17	81195210	2045641	0.0252	0.1746
chr18	78077248	1369011	0.0175	0.275
chr19	59128983	1201669	0.0203	0.2429
chr20	63025520	1662066	0.0264	0.1746
chr21	48129895	793540	0.0165	0.1442
chr22	51304566	482513	0.0094	0.1025
chrMT	16571	4674	0.2821	0.5635
chrX	155270560	3454064	0.0222	0.1716
chrY	59373566	193080	0.0033	0.0983

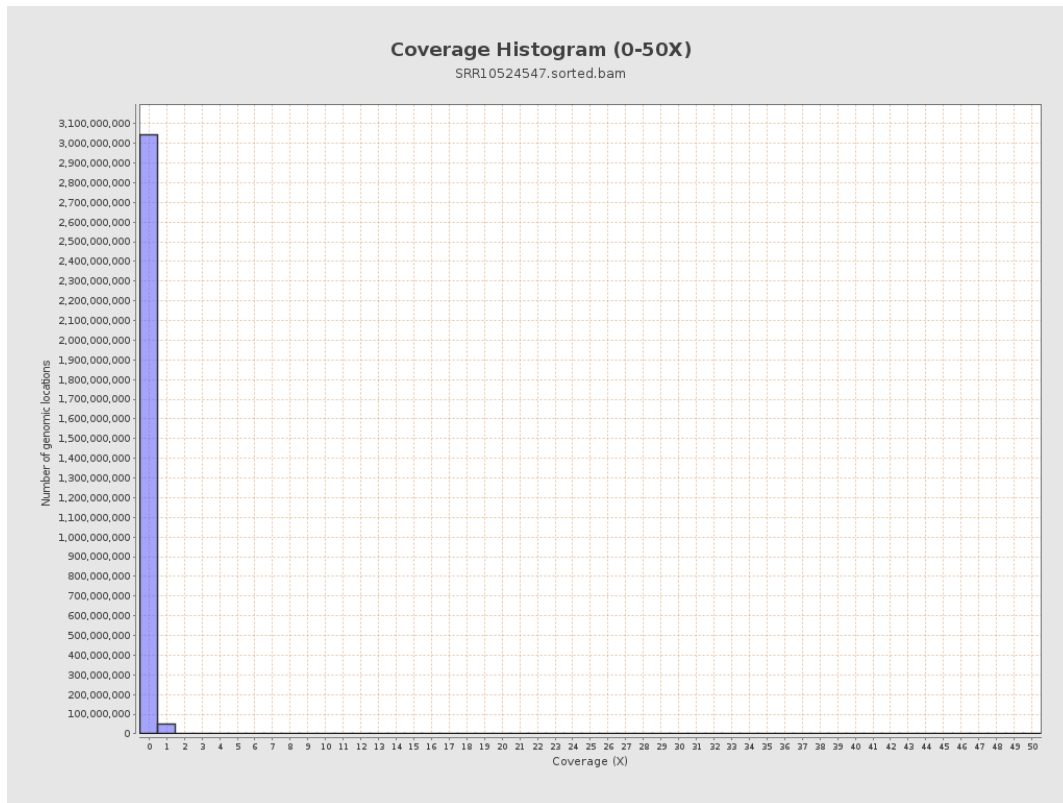
3. Results : Coverage across reference



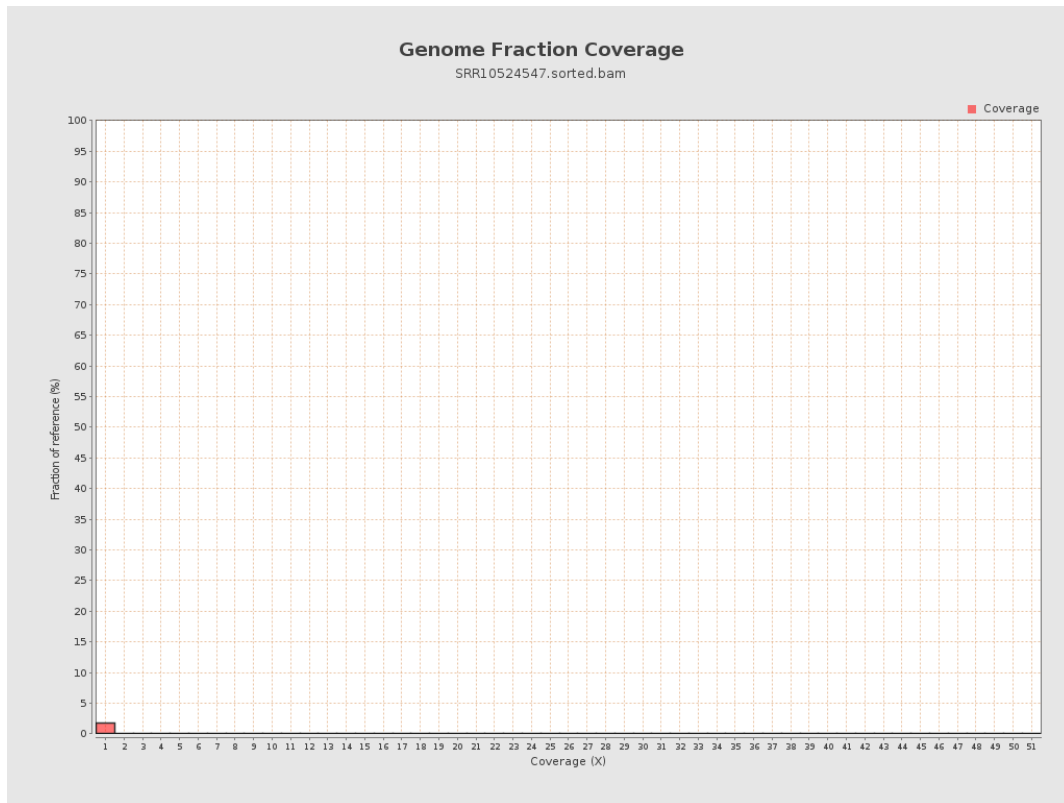
4. Results : Coverage Histogram



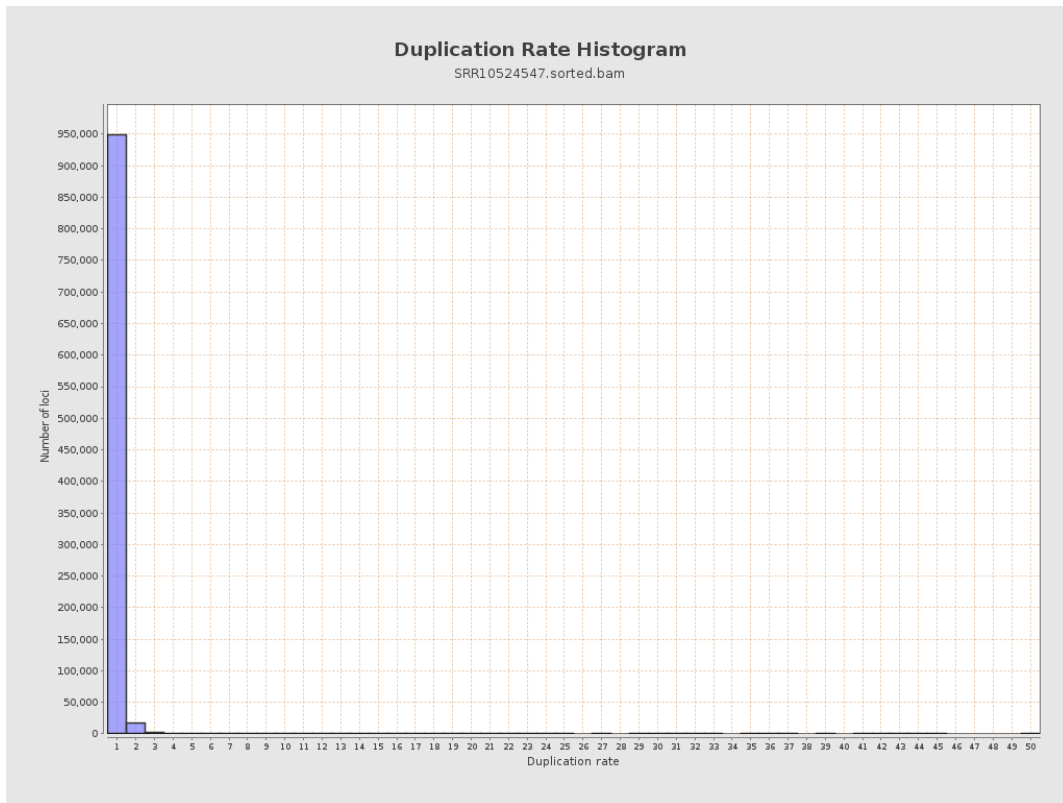
5. Results : Coverage Histogram (0-50X)



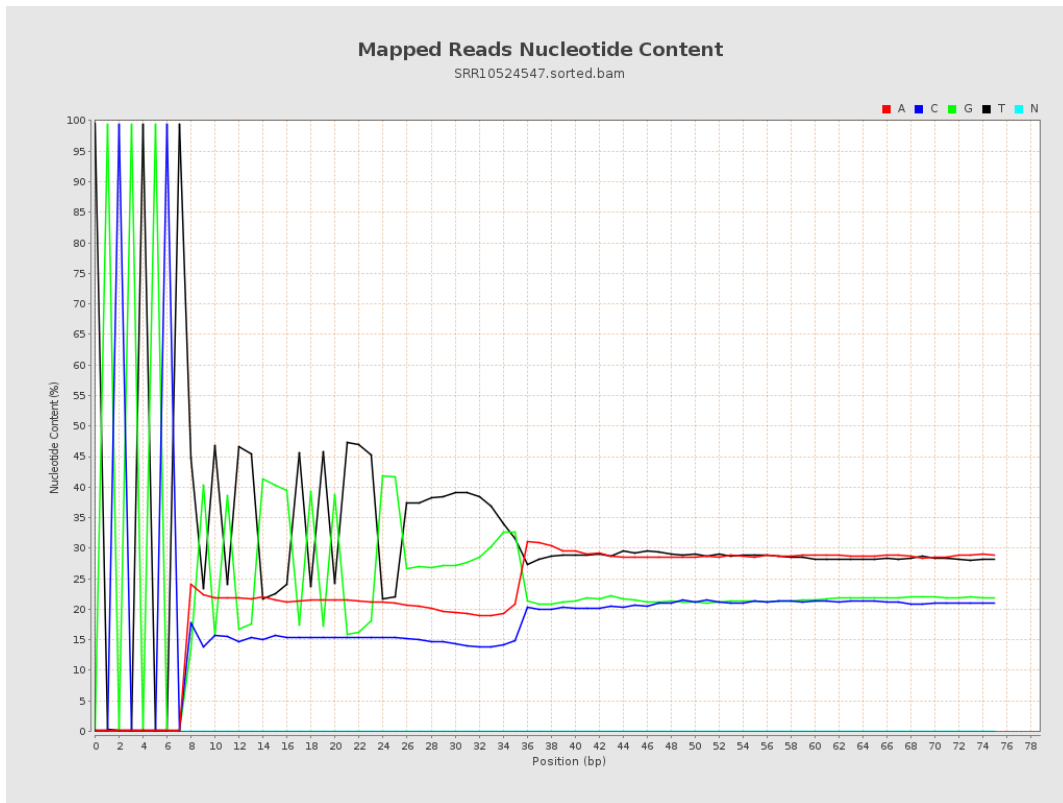
6. Results : Genome Fraction Coverage



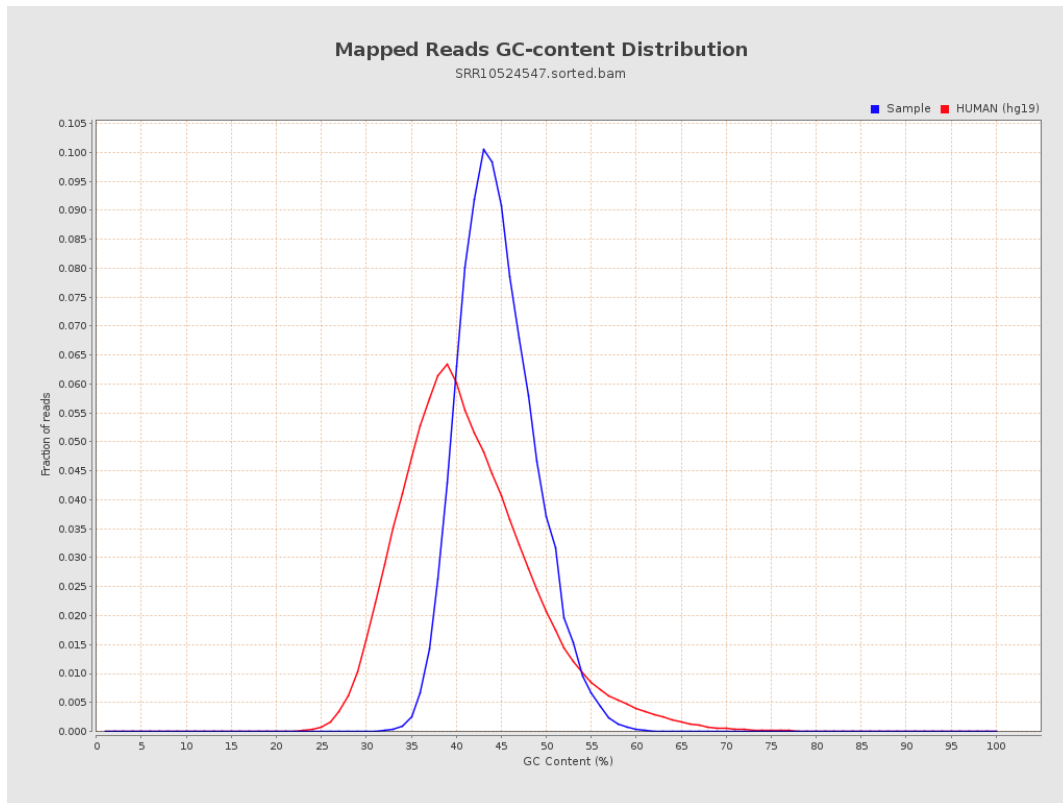
7. Results : Duplication Rate Histogram



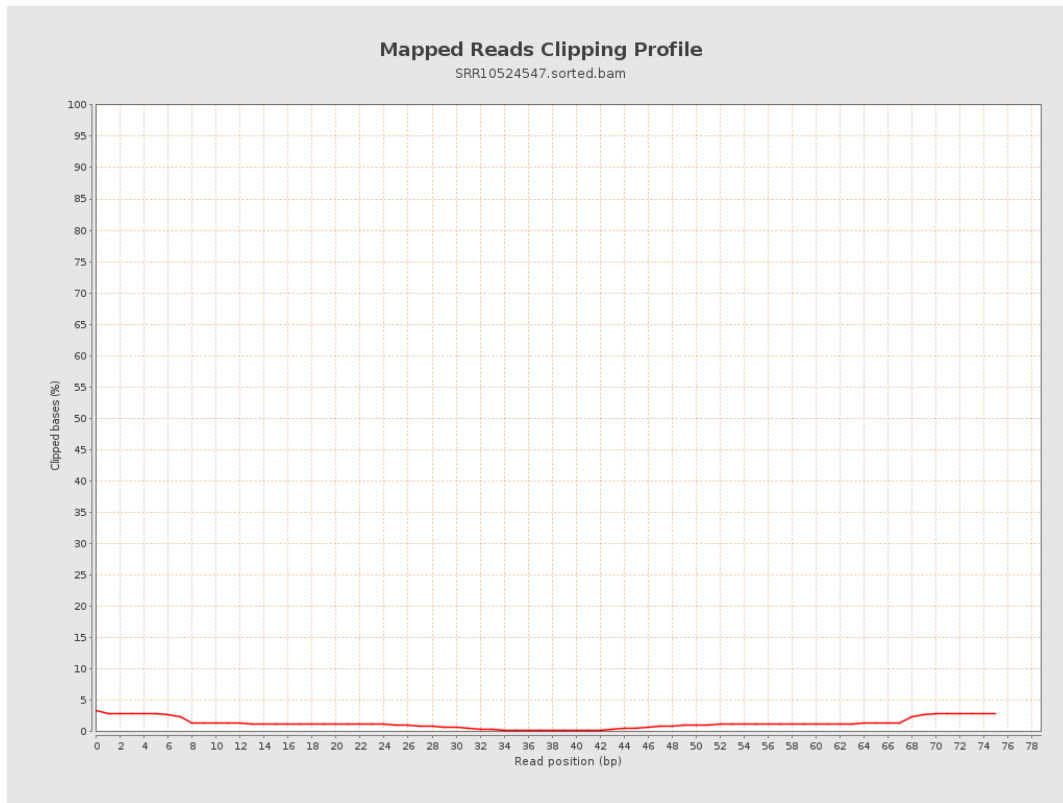
8. Results : Mapped Reads Nucleotide Content



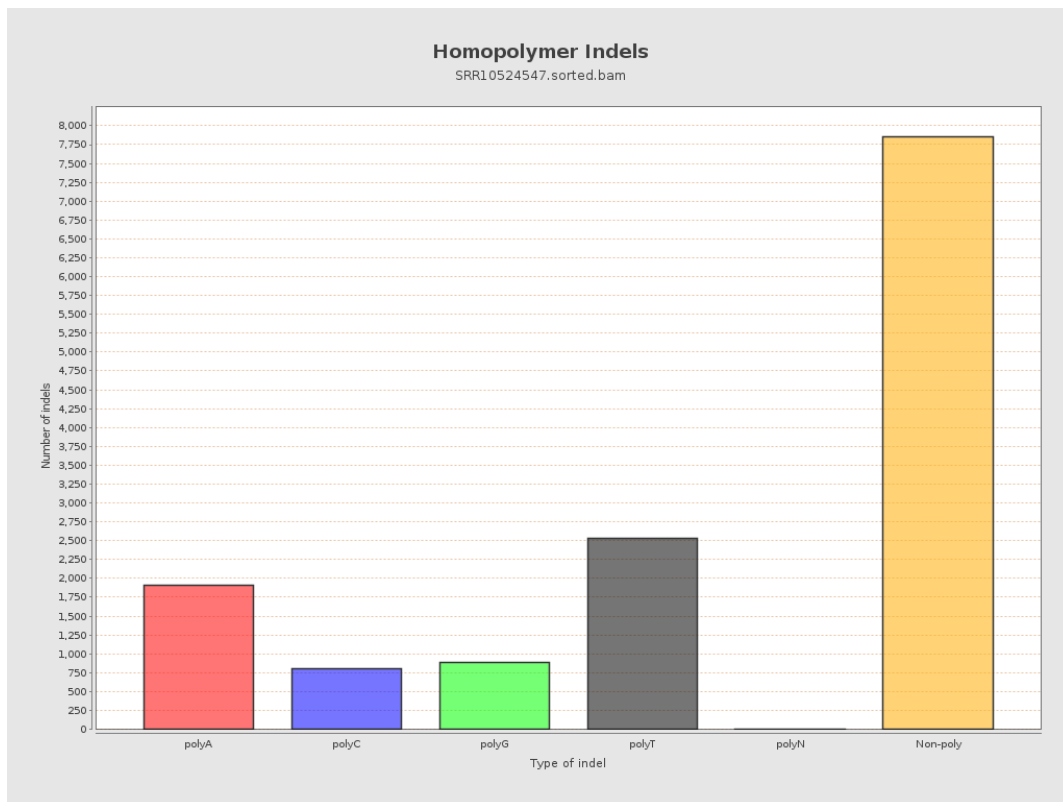
9. Results : Mapped Reads GC-content Distribution



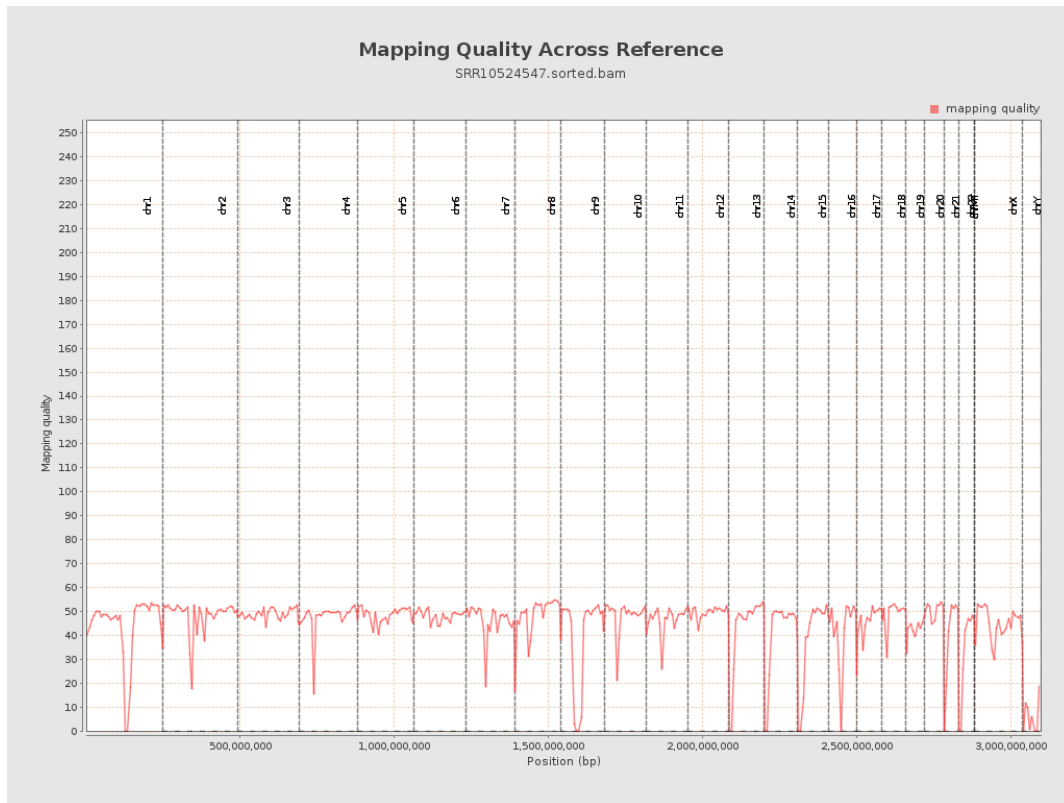
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

