

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 10:30:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708640.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_SRR1708640 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708640.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 10:30:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708640.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,398,614
Mapped reads	2,313,984 / 96.47%
Unmapped reads	84,630 / 3.53%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	56 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	9,951 / 0.41%
Duplication rate	0.43%
Clipped reads	31,474 / 1.31%

2.2. ACGT Content

Number/percentage of A's	35,665,543 / 30.91%
Number/percentage of C's	21,946,686 / 19.02%
Number/percentage of T's	35,592,890 / 30.84%
Number/percentage of G's	22,186,092 / 19.23%
Number/percentage of N's	4,113 / 0%
GC Percentage	38.24%

2.3. Coverage

Mean	0.0373

Standard Deviation	0.2001
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2.4. Mapping Quality

Mean Mapping Quality	46.14
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2.5. Mismatches and indels

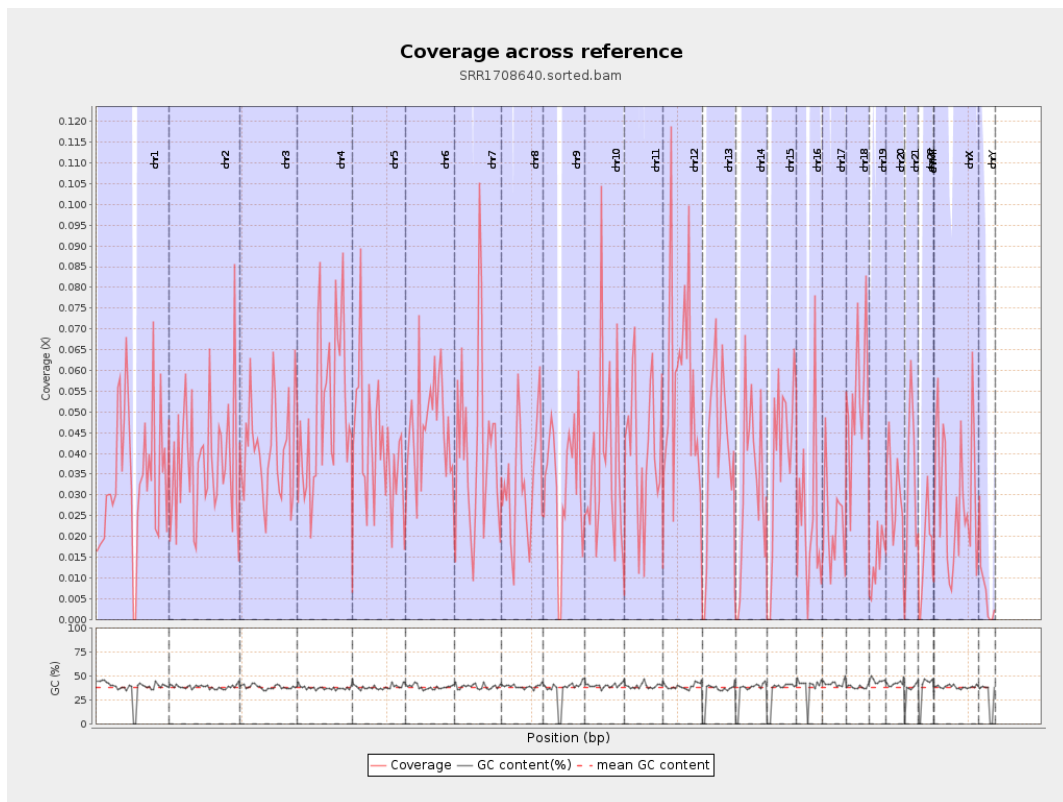
General error rate	0.17%
Mismatches	190,340
Insertions	7,949
Mapped reads with at least one insertion	0.34%
Deletions	6,776
Mapped reads with at least one deletion	0.29%
Homopolymer indels	48.56%

2.6. Chromosome stats

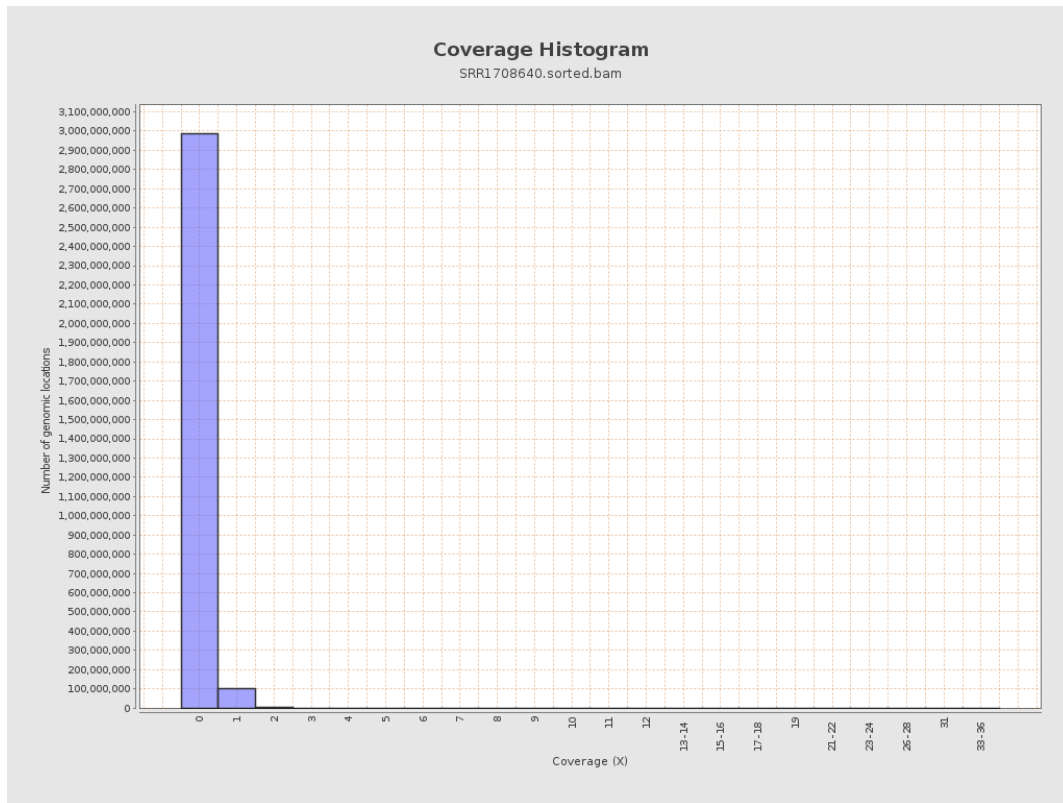
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8424716	0.0338	0.1908
chr2	243199373	9132739	0.0376	0.2004
chr3	198022430	8102299	0.0409	0.2087
chr4	191154276	9580297	0.0501	0.2315
chr5	180915260	7462710	0.0412	0.2094
chr6	171115067	7828139	0.0457	0.2211
chr7	159138663	6700739	0.0421	0.2128

chr8	146364022	4967073	0.0339	0.1895
chr9	141213431	4711852	0.0334	0.1889
chr10	135534747	5204466	0.0384	0.203
chr11	135006516	5602790	0.0415	0.2122
chr12	133851895	7501606	0.056	0.2462
chr13	115169878	4651087	0.0404	0.208
chr14	107349540	3448248	0.0321	0.1865
chr15	102531392	4010773	0.0391	0.2051
chr16	90354753	2149594	0.0238	0.1597
chr17	81195210	1801859	0.0222	0.1531
chr18	78077248	4164965	0.0533	0.2397
chr19	59128983	837623	0.0142	0.1221
chr20	63025520	1908945	0.0303	0.1789
chr21	48129895	1520457	0.0316	0.1844
chr22	51304566	813851	0.0159	0.1292
chrMT	16571	150	0.0091	0.0947
chrX	155270560	4469503	0.0288	0.1756
chrY	59373566	410249	0.0069	0.0857

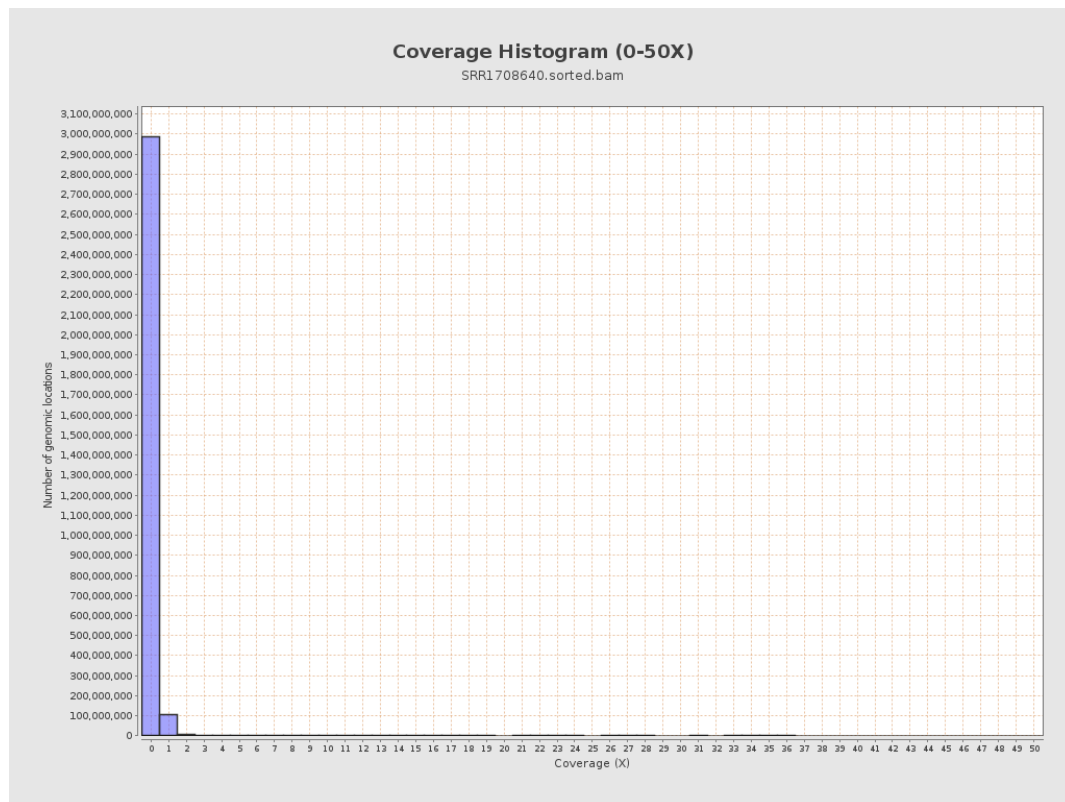
3. Results : Coverage across reference



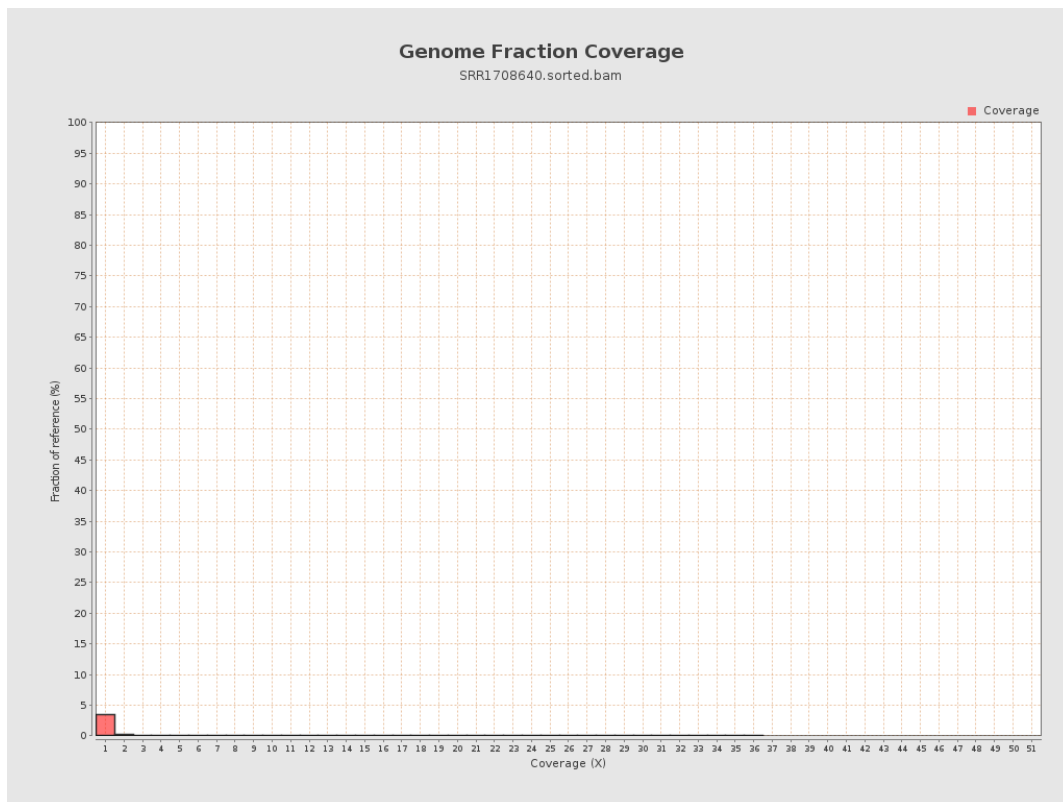
4. Results : Coverage Histogram



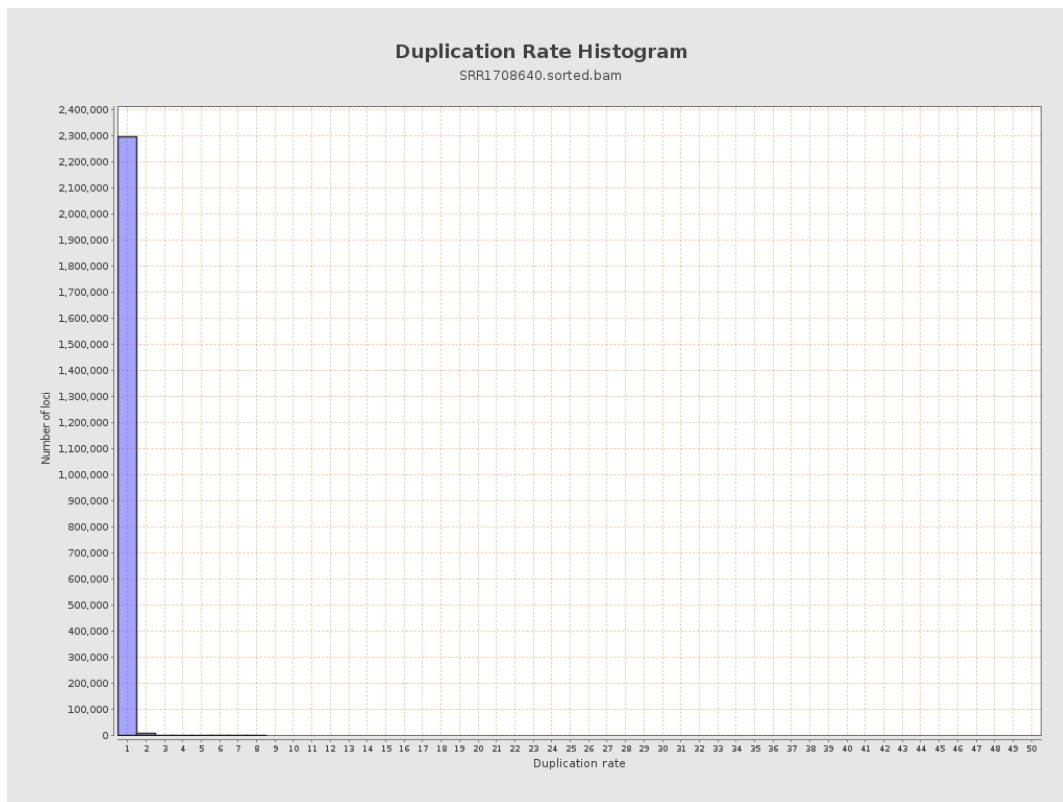
5. Results : Coverage Histogram (0-50X)



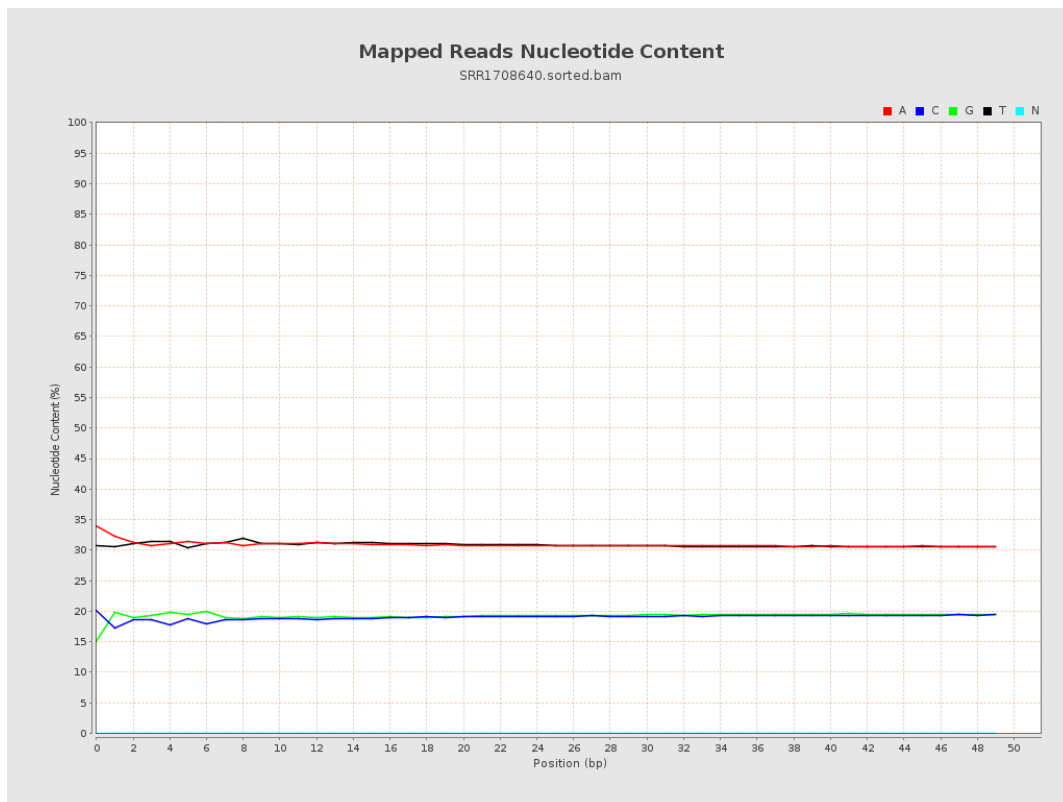
6. Results : Genome Fraction Coverage



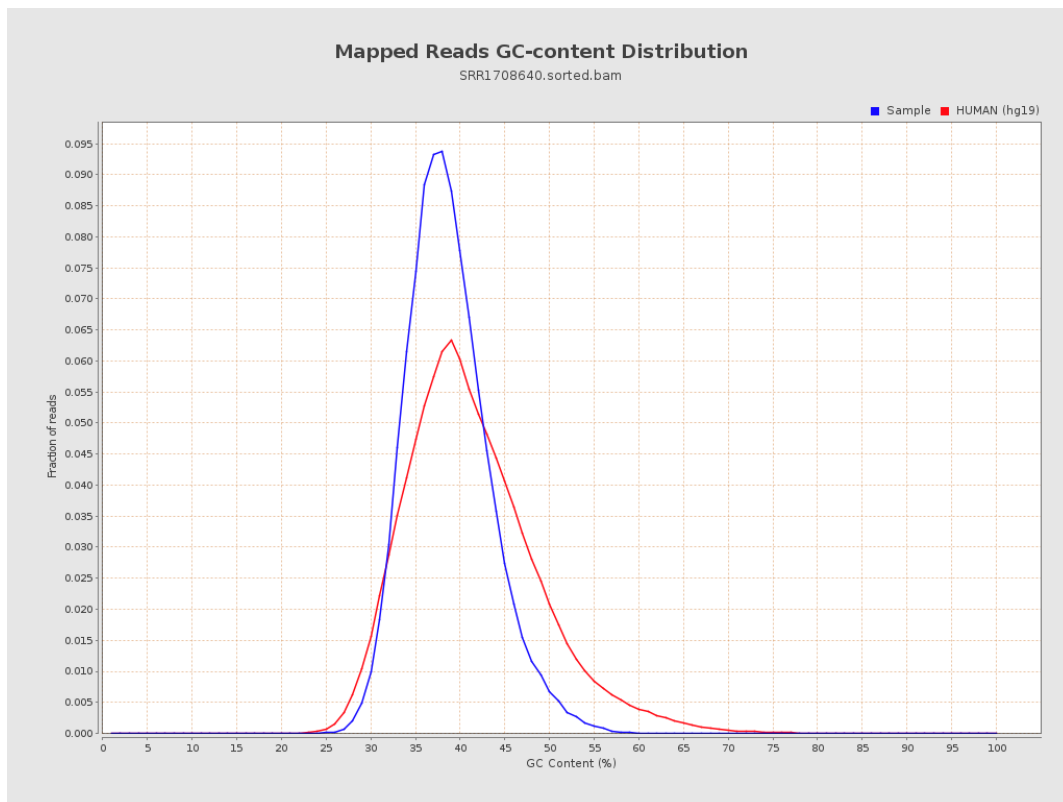
7. Results : Duplication Rate Histogram



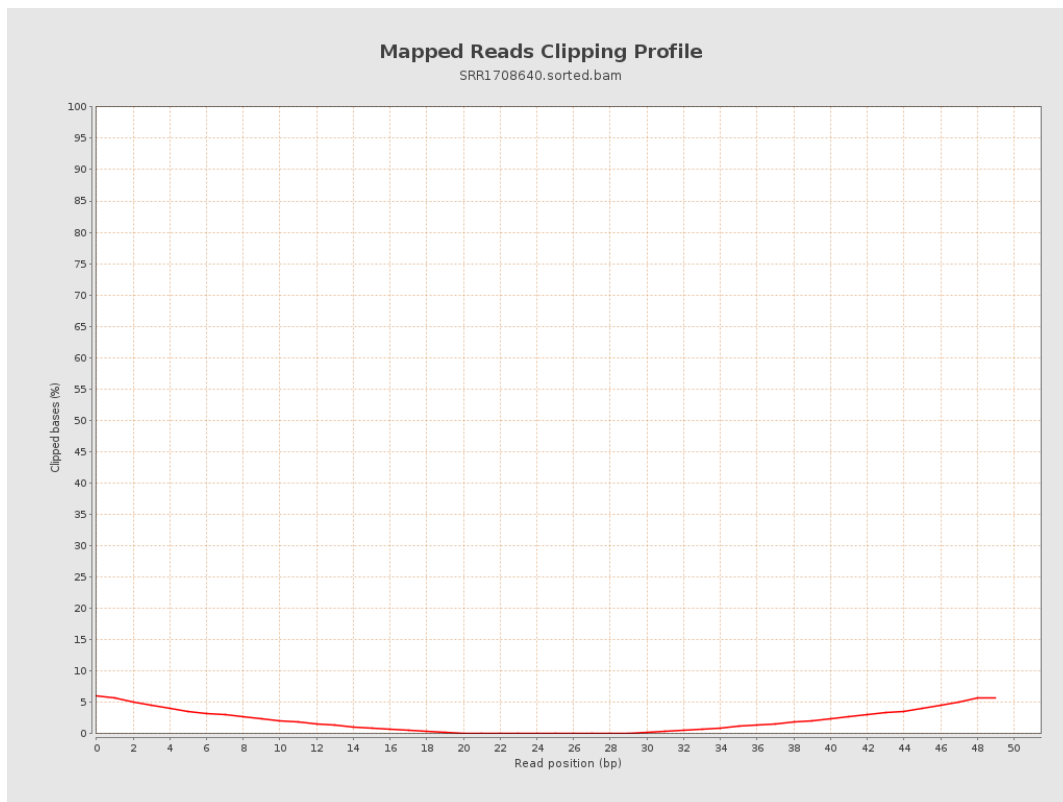
8. Results : Mapped Reads Nucleotide Content



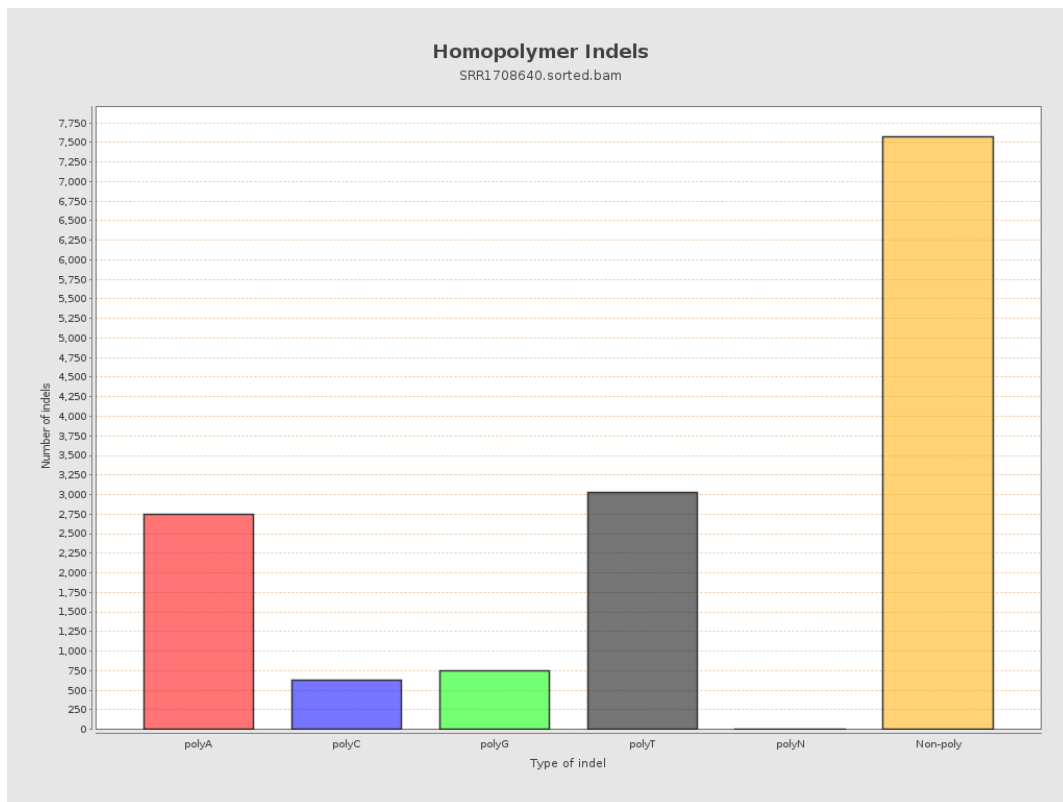
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

