

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 22:09:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081140.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_SRR3081140 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081140.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 22:09:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081140.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,462,865
Mapped reads	2,144,708 / 87.08%
Unmapped reads	318,157 / 12.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,735 / 0.76%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	80,631 / 3.27%
Duplication rate	2.98%
Clipped reads	970,812 / 39.42%

2.2. ACGT Content

Number/percentage of A's	41,041,879 / 28.62%
Number/percentage of C's	26,436,524 / 18.43%
Number/percentage of T's	45,029,381 / 31.4%
Number/percentage of G's	30,876,892 / 21.53%
Number/percentage of N's	42,336 / 0.03%
GC Percentage	39.96%

2.3. Coverage

Mean	0.0463

Standard Deviation	0.3724
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2.4. Mapping Quality

Mean Mapping Quality	46.68
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2.5. Mismatches and indels

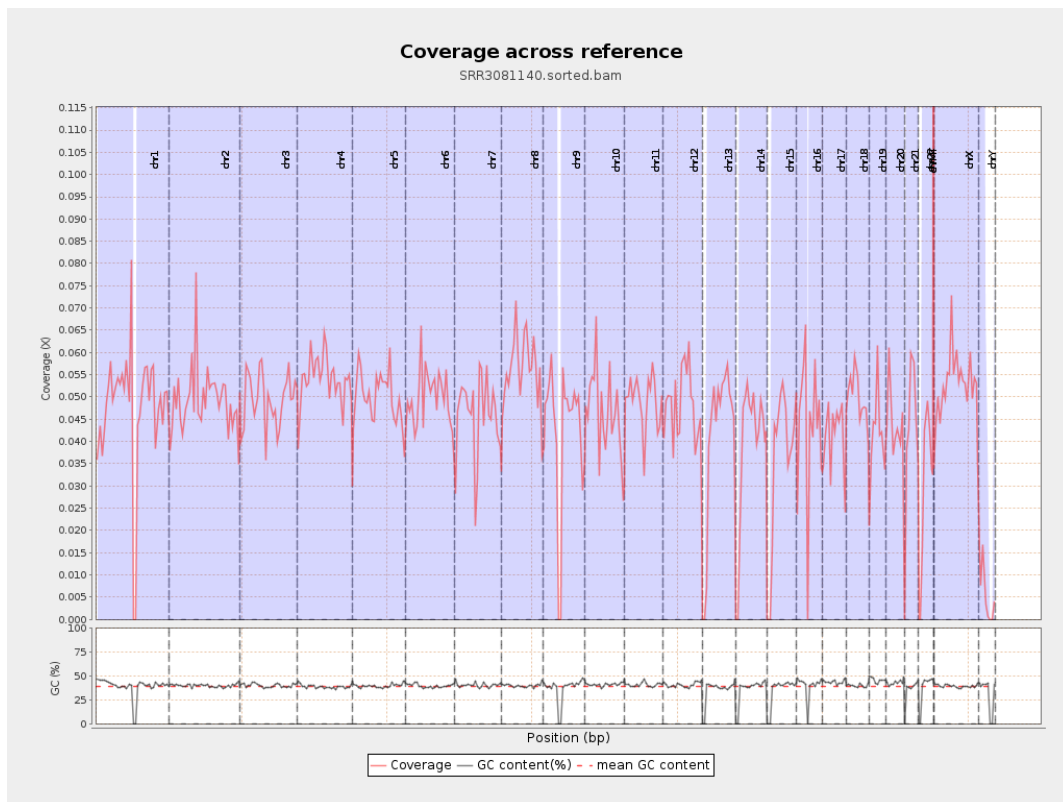
General error rate	0.84%
Mismatches	1,190,859
Insertions	11,383
Mapped reads with at least one insertion	0.53%
Deletions	30,751
Mapped reads with at least one deletion	1.42%
Homopolymer indels	46.93%

2.6. Chromosome stats

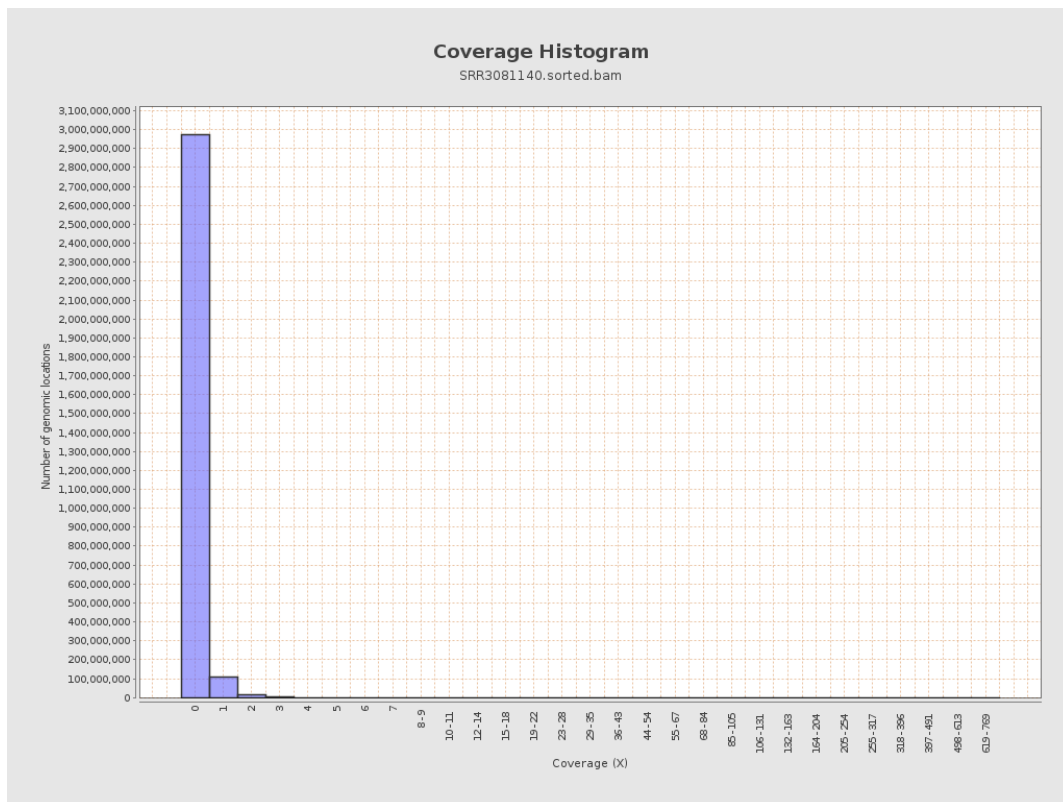
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	11845201	0.0475	0.7073
chr2	243199373	12015414	0.0494	0.4255
chr3	198022430	9797303	0.0495	0.248
chr4	191154276	10329599	0.054	0.2709
chr5	180915260	9062848	0.0501	0.2516
chr6	171115067	8501945	0.0497	0.3192
chr7	159138663	7351448	0.0462	0.3605

chr8	146364022	8228622	0.0562	0.4921
chr9	141213431	6017636	0.0426	0.3387
chr10	135534747	6336156	0.0467	0.3337
chr11	135006516	6589595	0.0488	0.3436
chr12	133851895	6405035	0.0479	0.2473
chr13	115169878	4673413	0.0406	0.2242
chr14	107349540	4175798	0.0389	0.2358
chr15	102531392	3654551	0.0356	0.2131
chr16	90354753	3957456	0.0438	0.268
chr17	81195210	3289544	0.0405	0.2598
chr18	78077248	3904960	0.05	0.5991
chr19	59128983	2497272	0.0422	0.5146
chr20	63025520	2766454	0.0439	0.2403
chr21	48129895	2057799	0.0428	0.2438
chr22	51304566	1494653	0.0291	0.1883
chrMT	16571	4988	0.301	0.5979
chrX	155270560	8187642	0.0527	0.283
chrY	59373566	332384	0.0056	0.121

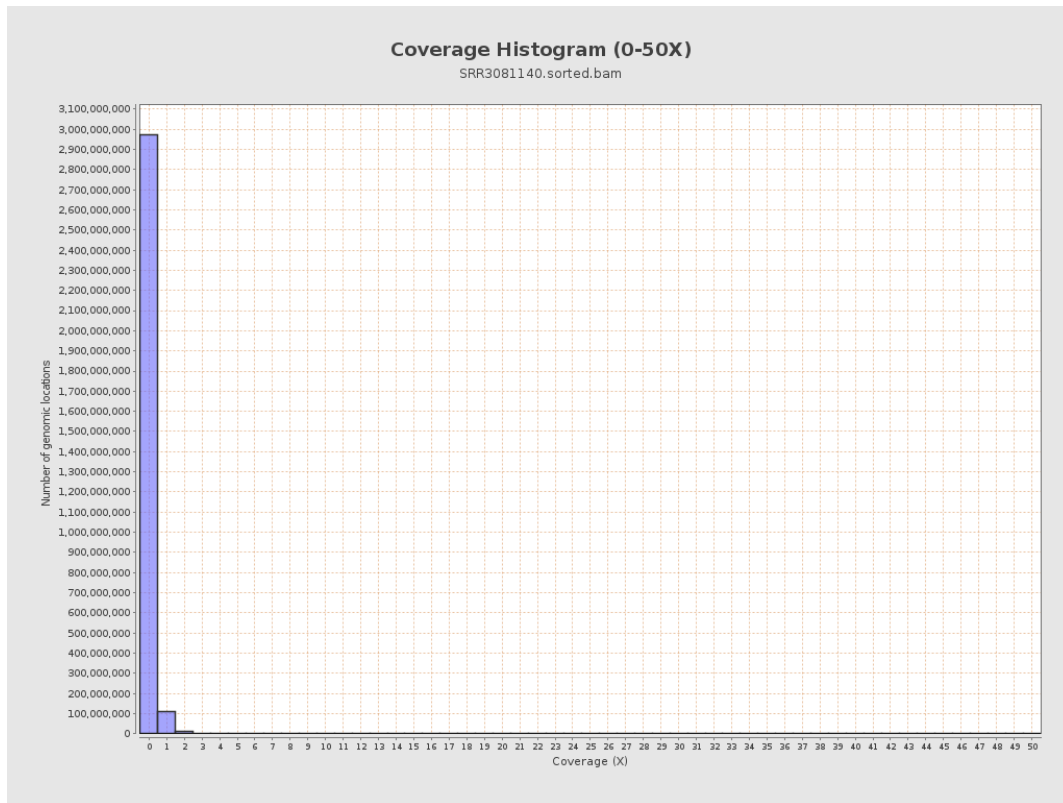
3. Results : Coverage across reference



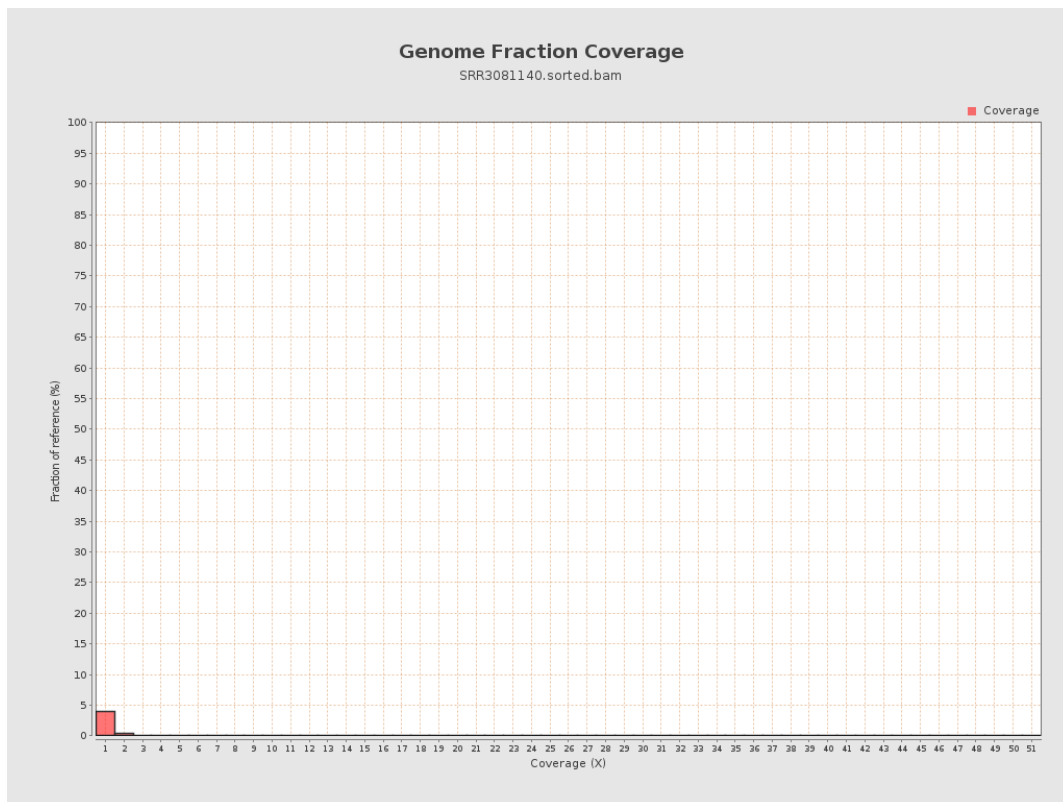
4. Results : Coverage Histogram



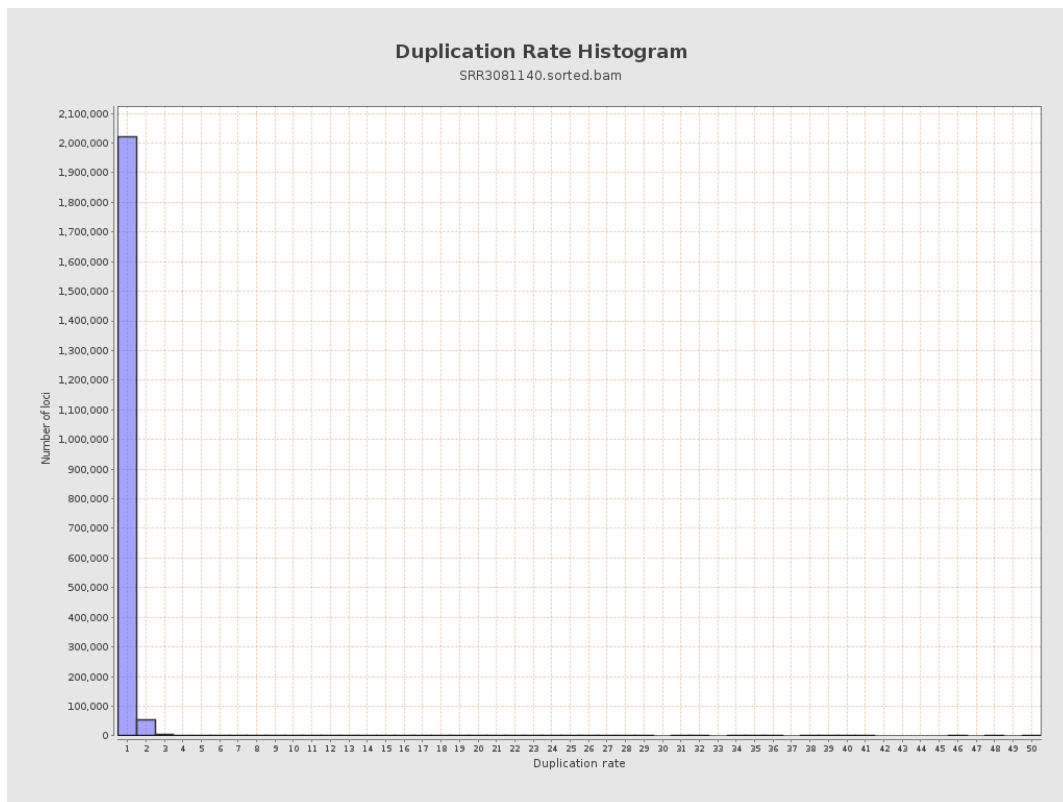
5. Results : Coverage Histogram (0-50X)



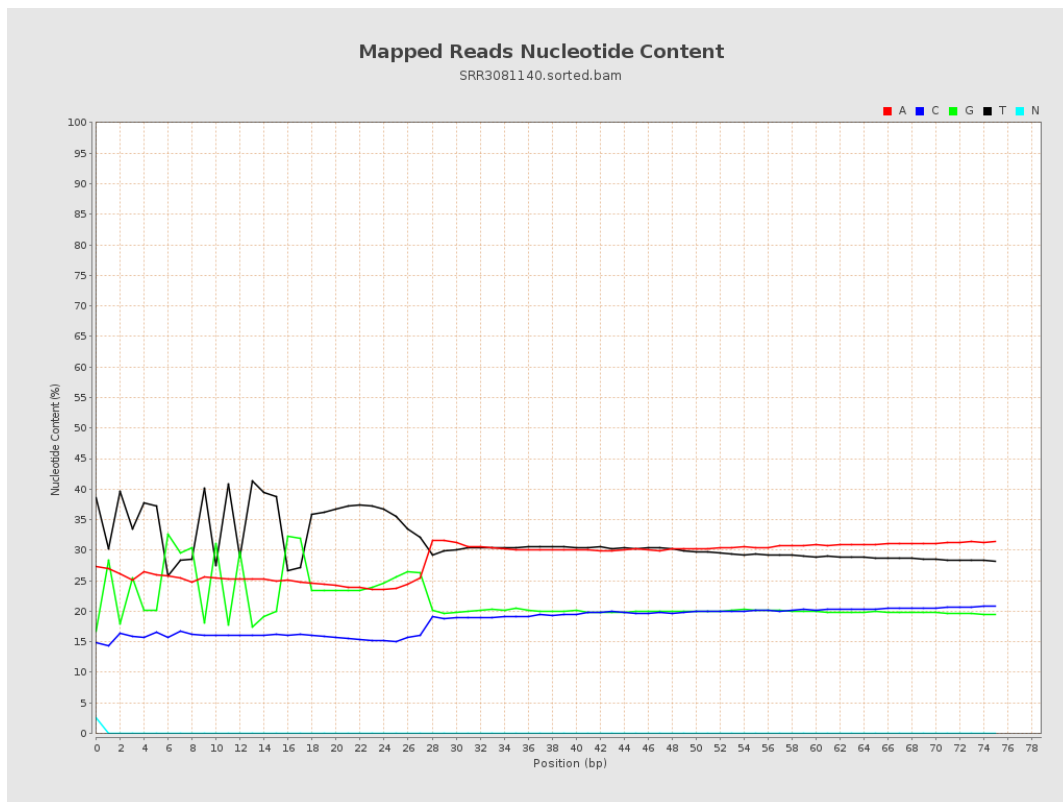
6. Results : Genome Fraction Coverage



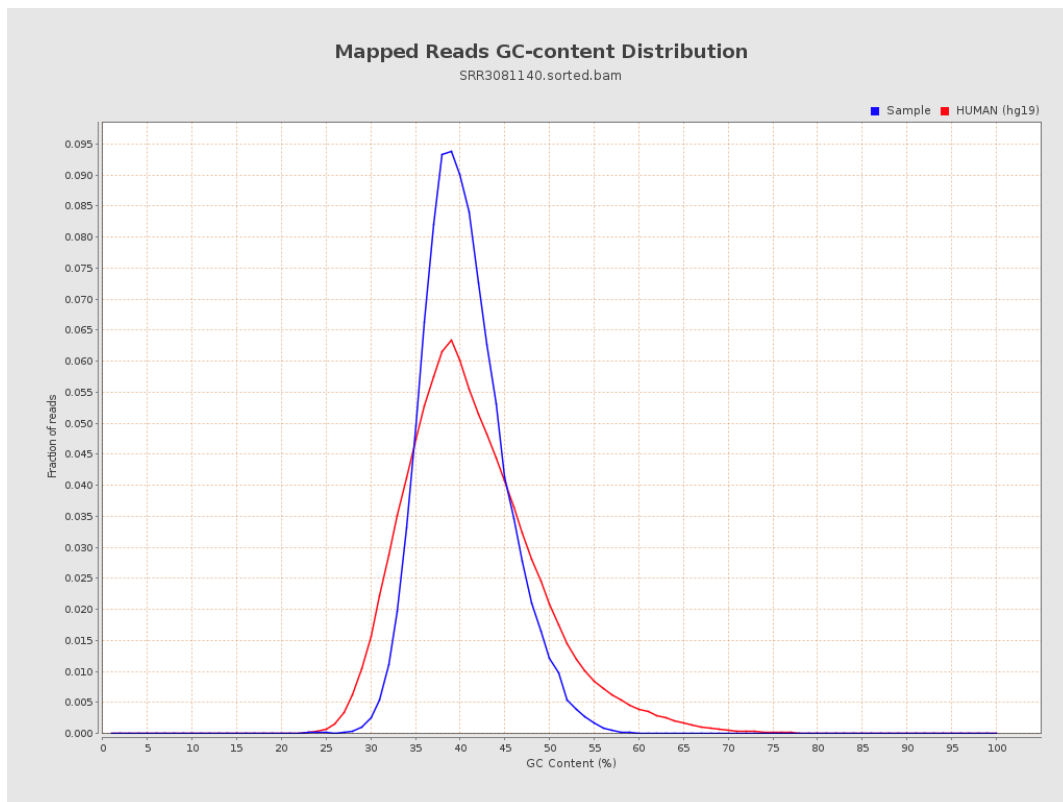
7. Results : Duplication Rate Histogram



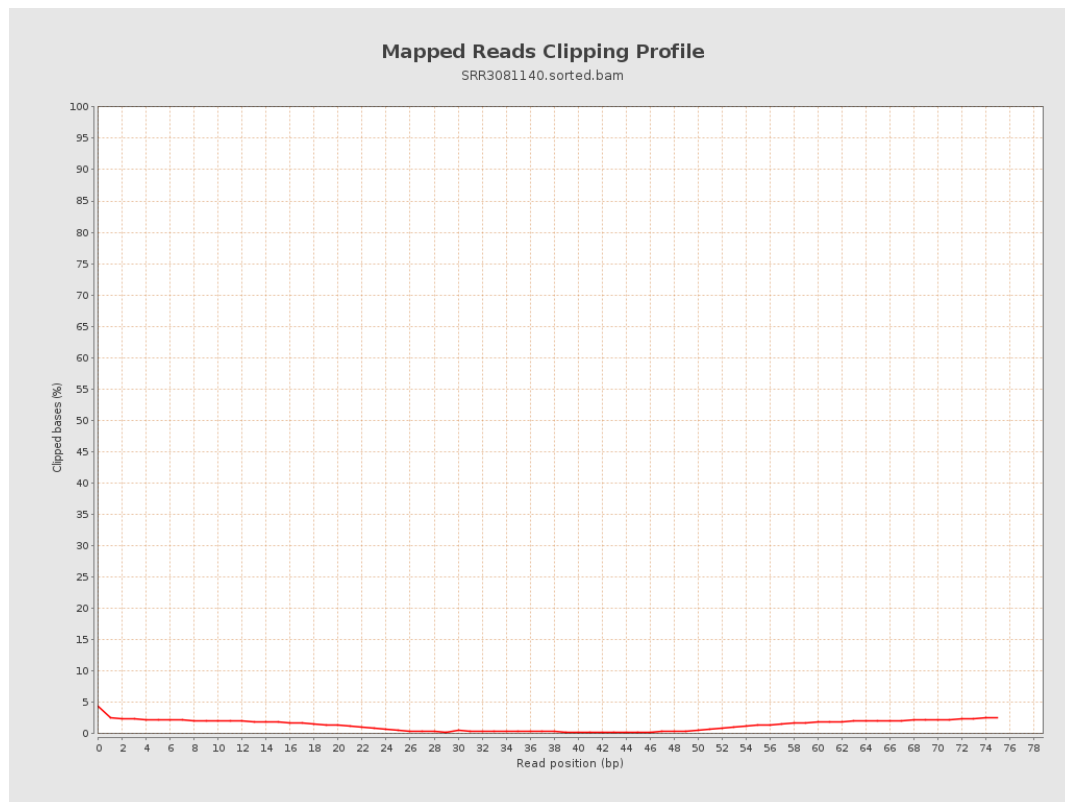
8. Results : Mapped Reads Nucleotide Content



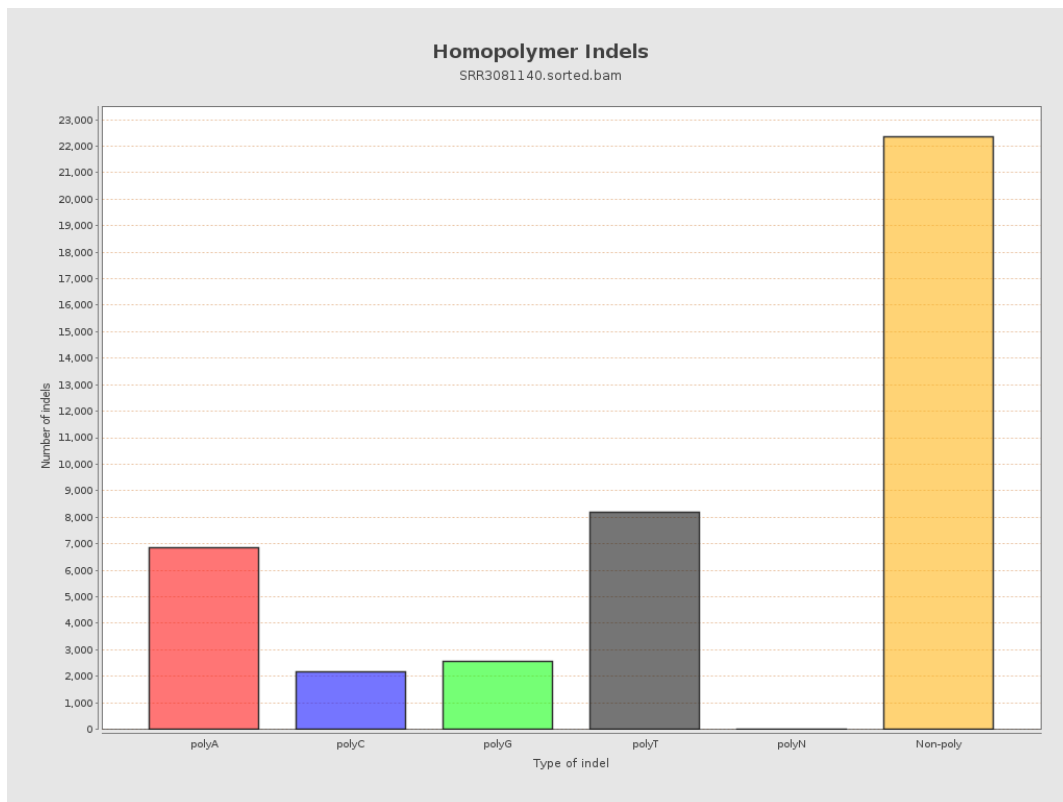
9. Results : Mapped Reads GC-content Distribution



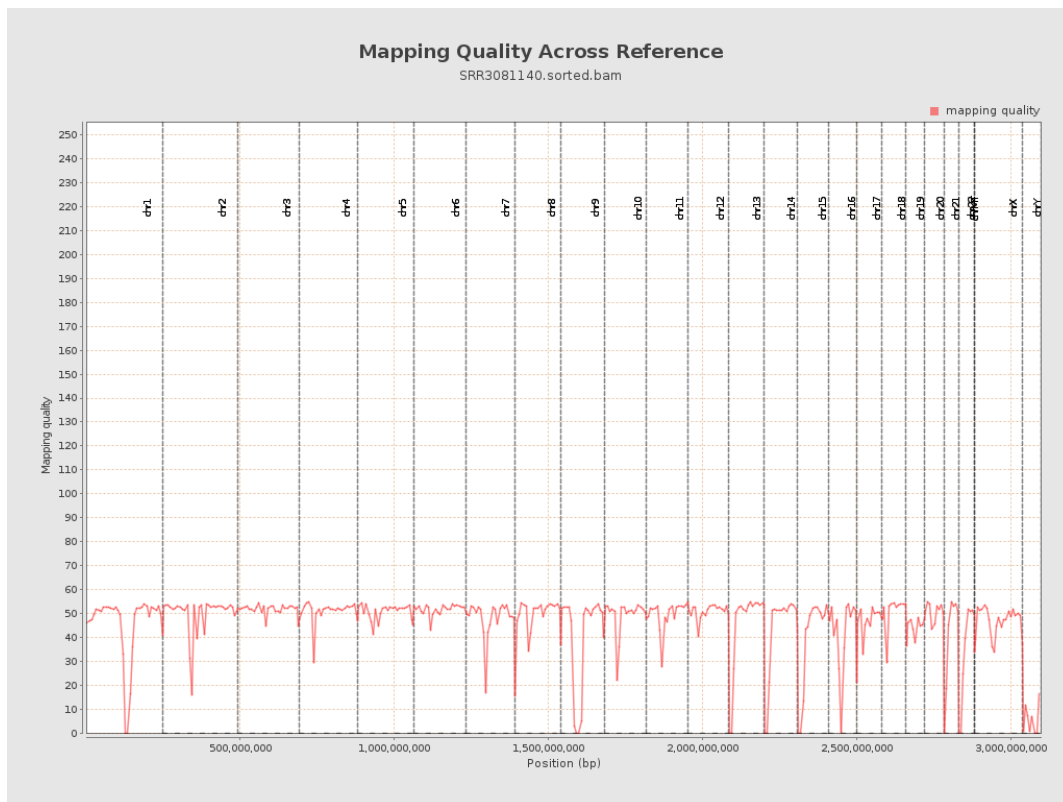
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

