

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 01:48:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549103.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_SRR1549103 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549103.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 01:48:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549103.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,402,388
Mapped reads	8,897,730 / 85.54%
Unmapped reads	1,504,658 / 14.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	386,354 / 3.71%
Duplication rate	3.19%
Clipped reads	445,133 / 4.28%

2.2. ACGT Content

Number/percentage of A's	106,363,510 / 30.12%
Number/percentage of C's	69,734,619 / 19.75%
Number/percentage of T's	107,286,562 / 30.38%
Number/percentage of G's	69,744,110 / 19.75%
Number/percentage of N's	1,465 / 0%
GC Percentage	39.5%

2.3. Coverage

Mean	0.1141
Standard Deviation	0.831

2.4. Mapping Quality

Mean Mapping Quality	44.32
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2.5. Mismatches and indels

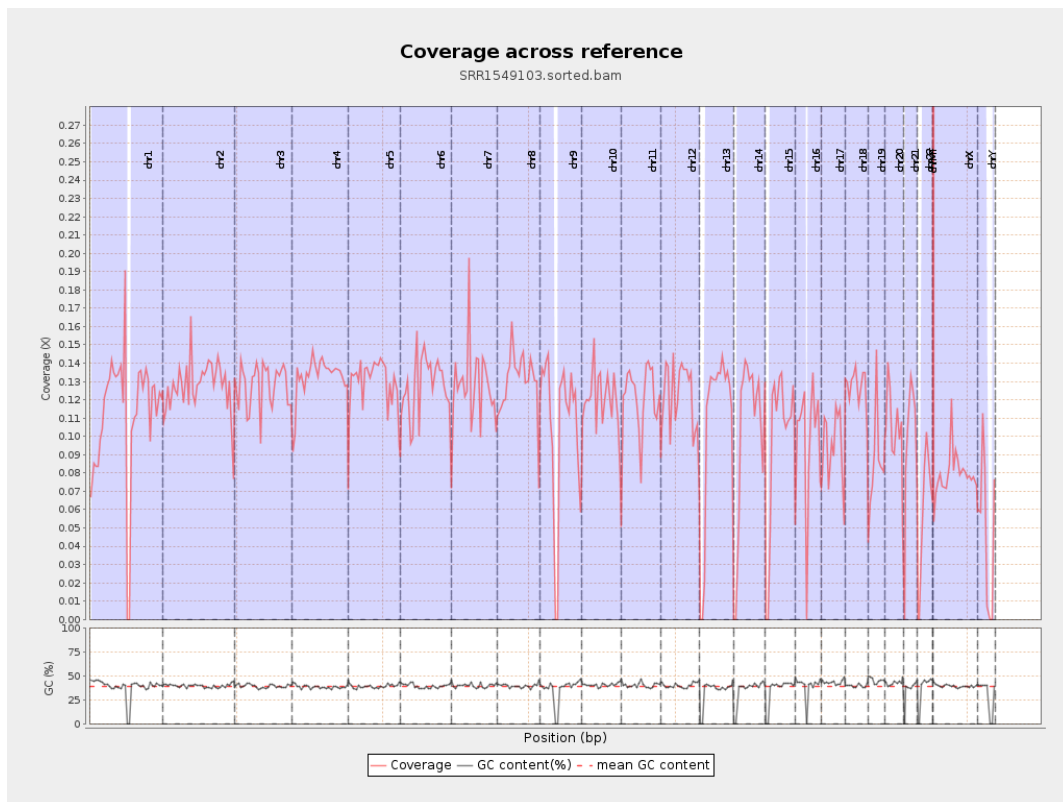
General error rate	0.3%
Mismatches	1,044,839
Insertions	8,681
Mapped reads with at least one insertion	0.1%
Deletions	26,120
Mapped reads with at least one deletion	0.29%
Homopolymer indels	45.52%

2.6. Chromosome stats

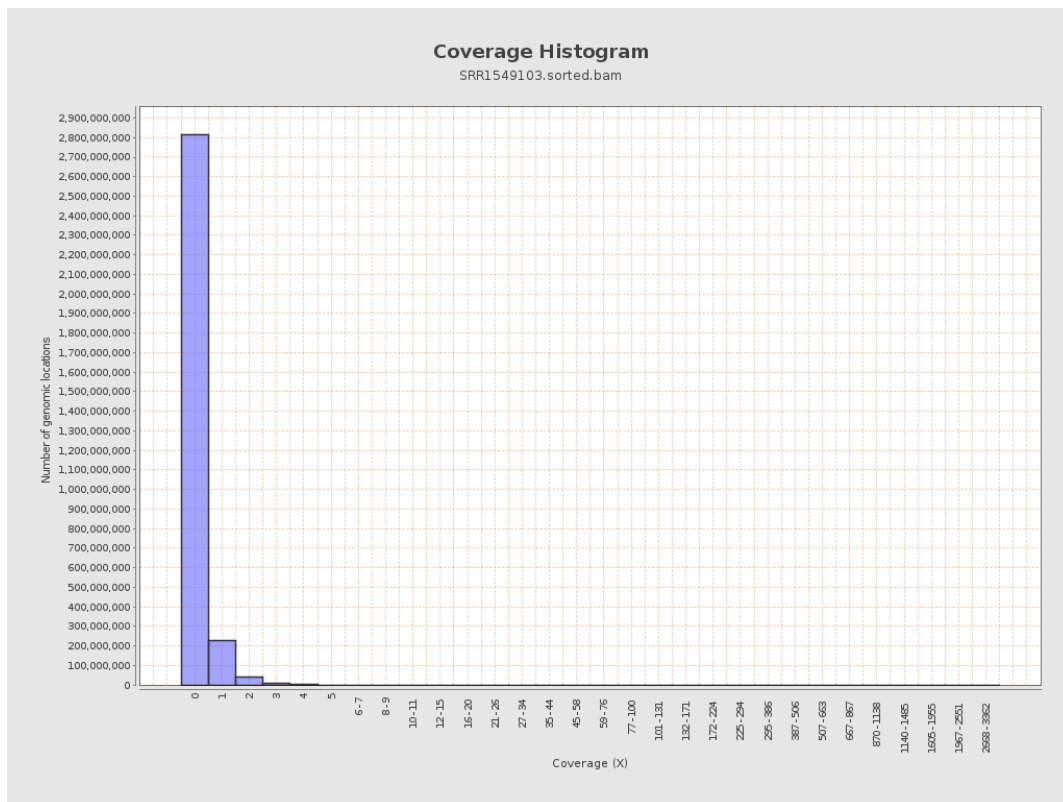
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	28009251	0.1124	1.6201
chr2	243199373	31087609	0.1278	0.6541
chr3	198022430	25314183	0.1278	0.4332
chr4	191154276	25402925	0.1329	0.4542
chr5	180915260	23377407	0.1292	0.4411
chr6	171115067	21941491	0.1282	0.5049
chr7	159138663	20196585	0.1269	1.1169
chr8	146364022	19079233	0.1304	1.7212

chr9	141213431	15028873	0.1064	0.616
chr10	135534747	16295341	0.1202	0.6331
chr11	135006516	16340541	0.121	0.6434
chr12	133851895	16316532	0.1219	0.4499
chr13	115169878	12355470	0.1073	0.3879
chr14	107349540	11017382	0.1026	0.52
chr15	102531392	9954572	0.0971	0.37
chr16	90354753	8676676	0.096	0.4412
chr17	81195210	7765120	0.0956	0.4188
chr18	78077248	9982965	0.1279	1.3591
chr19	59128983	5184963	0.0877	1.2438
chr20	63025520	6725439	0.1067	0.4395
chr21	48129895	4691775	0.0975	0.4631
chr22	51304566	3098939	0.0604	0.3152
chrMT	16571	76744	4.6312	5.5921
chrX	155270560	12317359	0.0793	0.4612
chrY	59373566	2925416	0.0493	0.4204

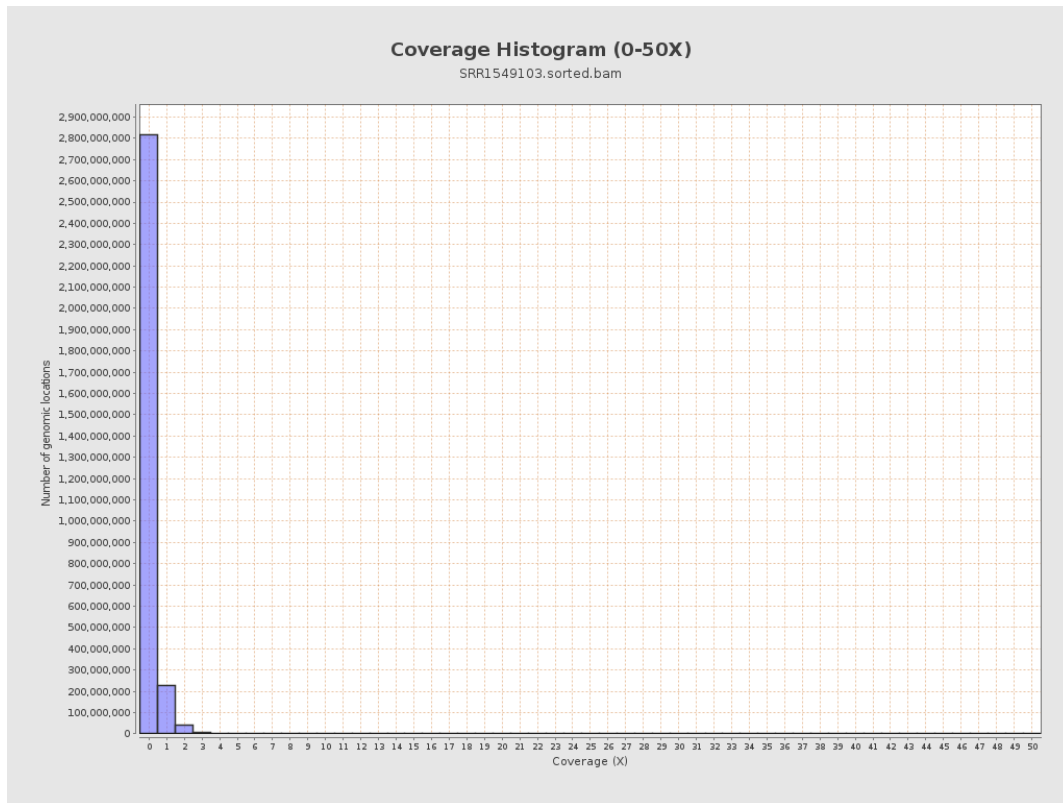
3. Results : Coverage across reference



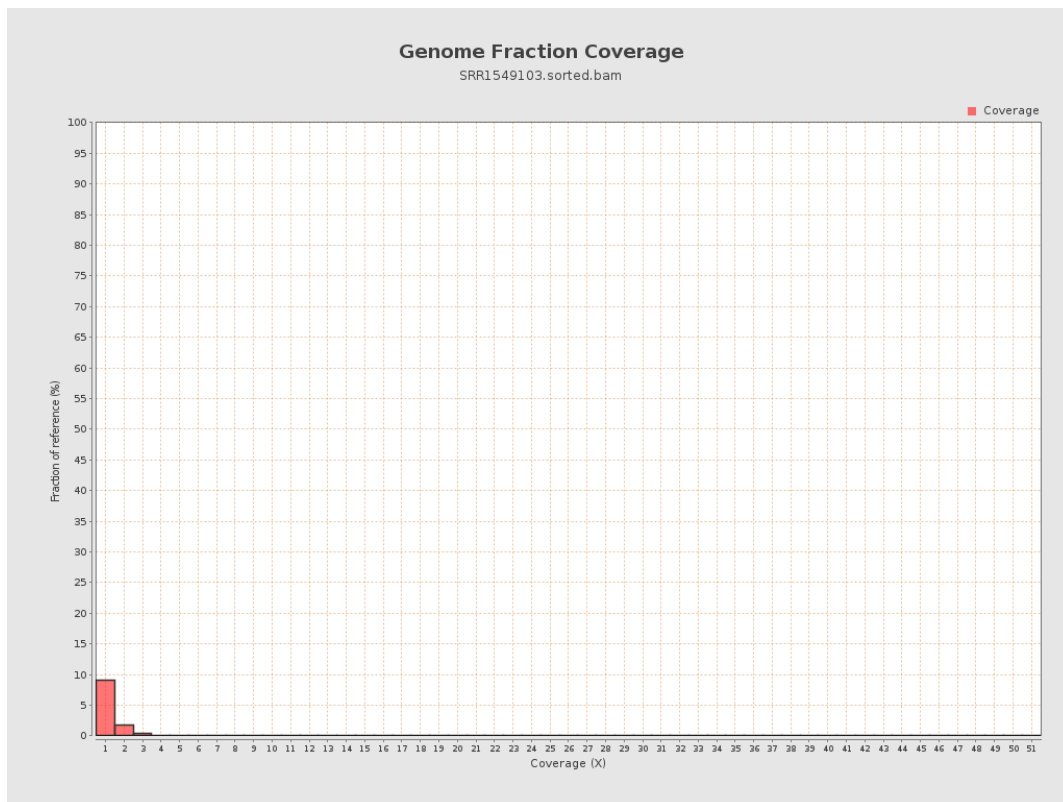
4. Results : Coverage Histogram



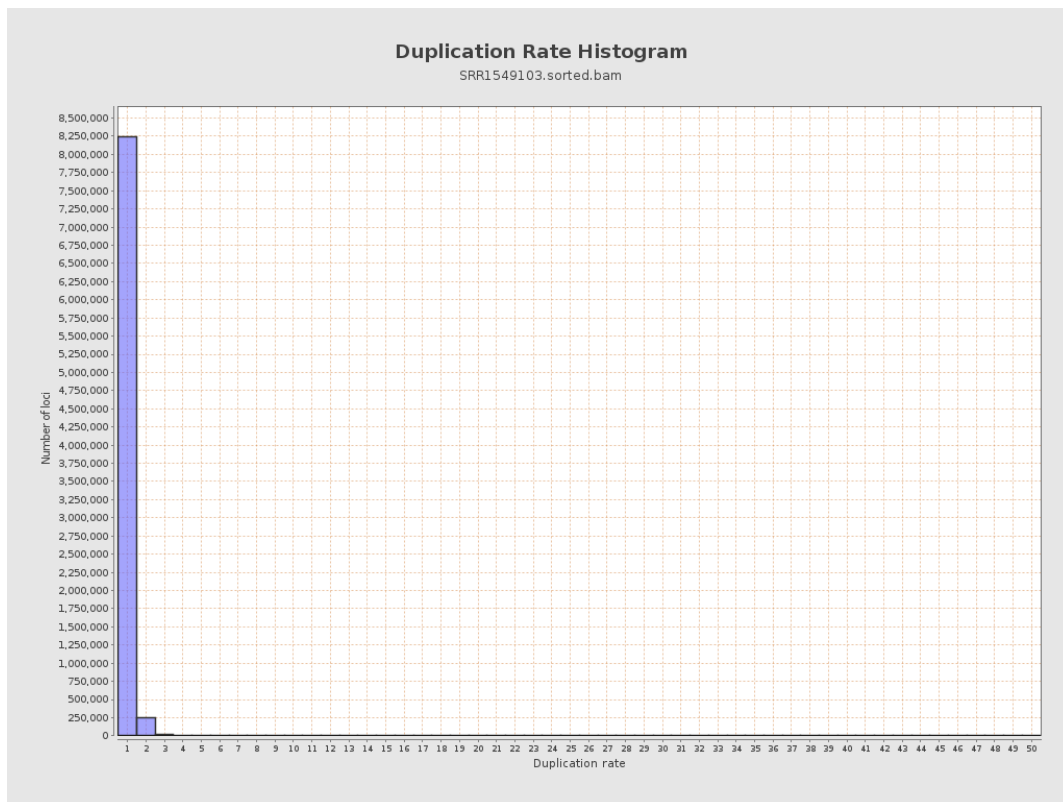
5. Results : Coverage Histogram (0-50X)



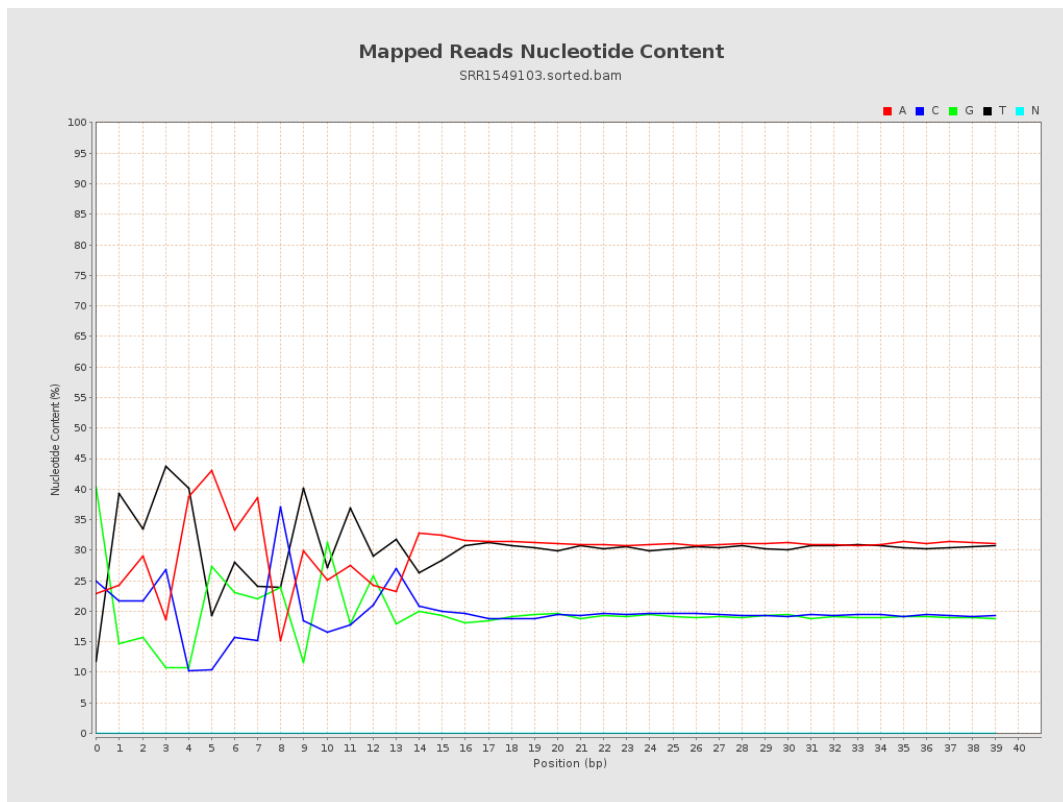
6. Results : Genome Fraction Coverage



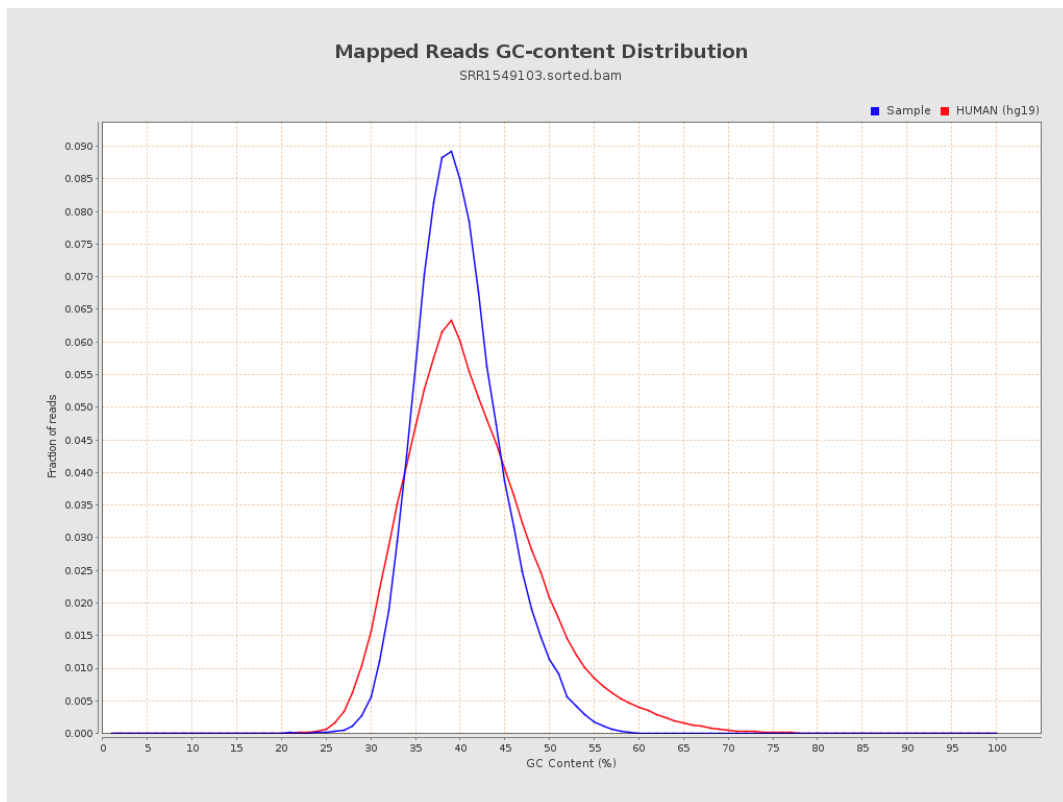
7. Results : Duplication Rate Histogram



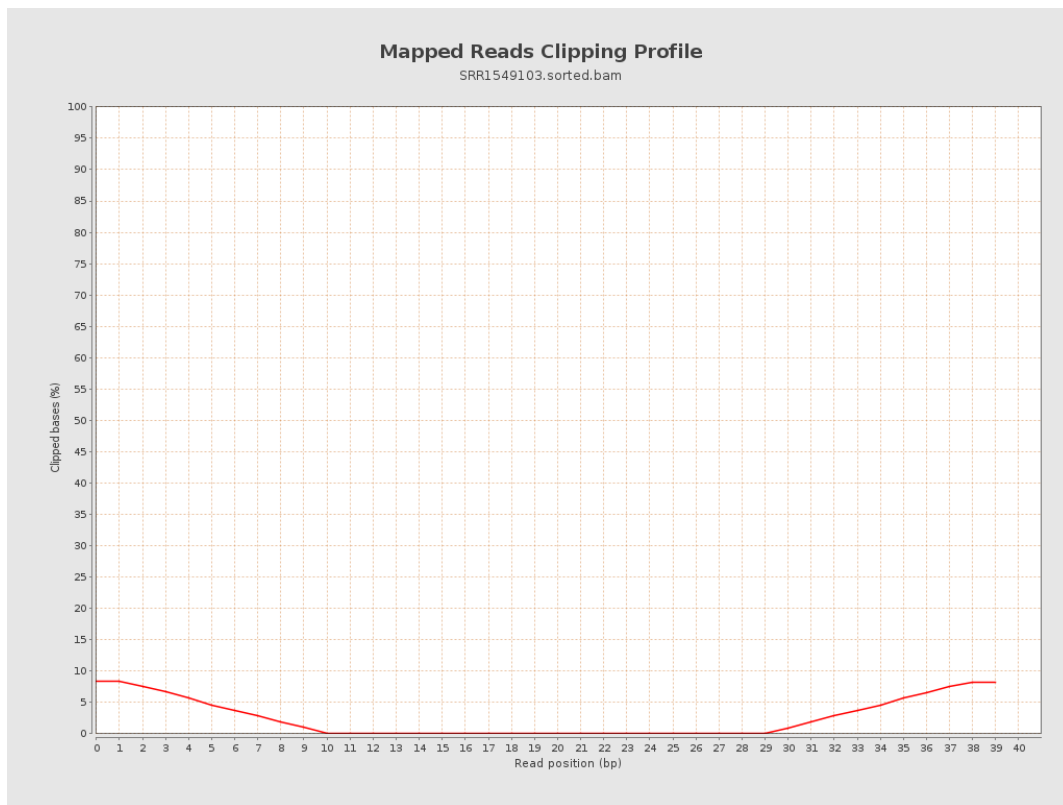
8. Results : Mapped Reads Nucleotide Content



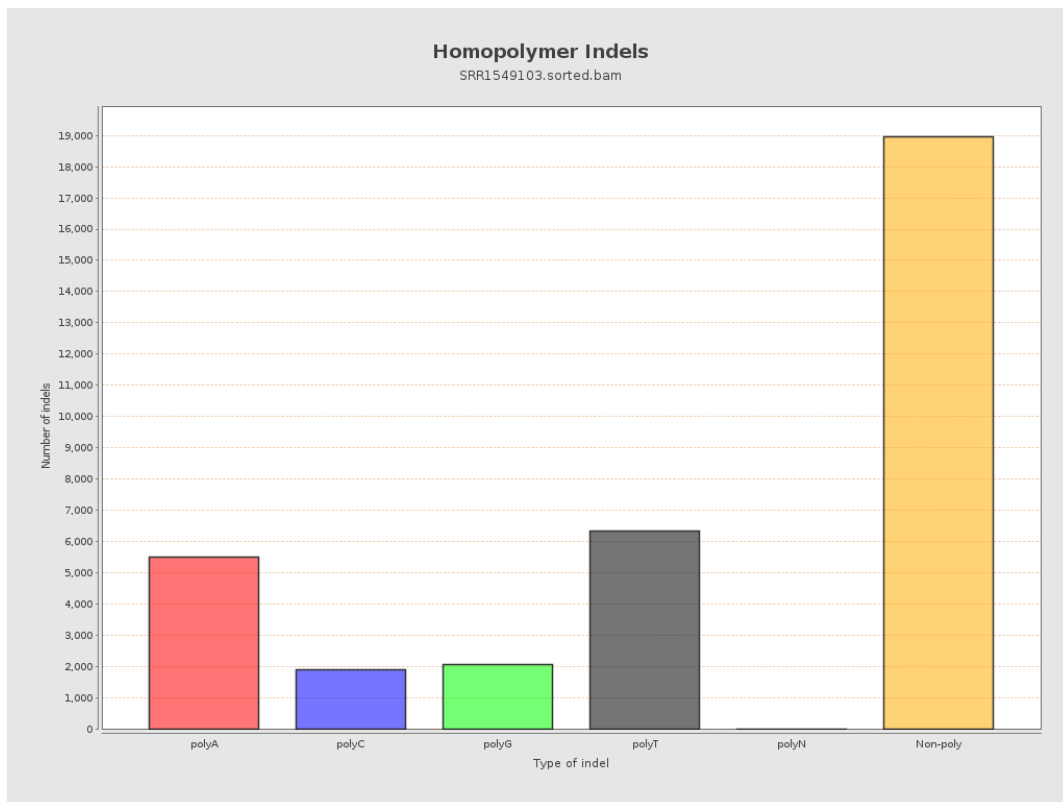
9. Results : Mapped Reads GC-content Distribution



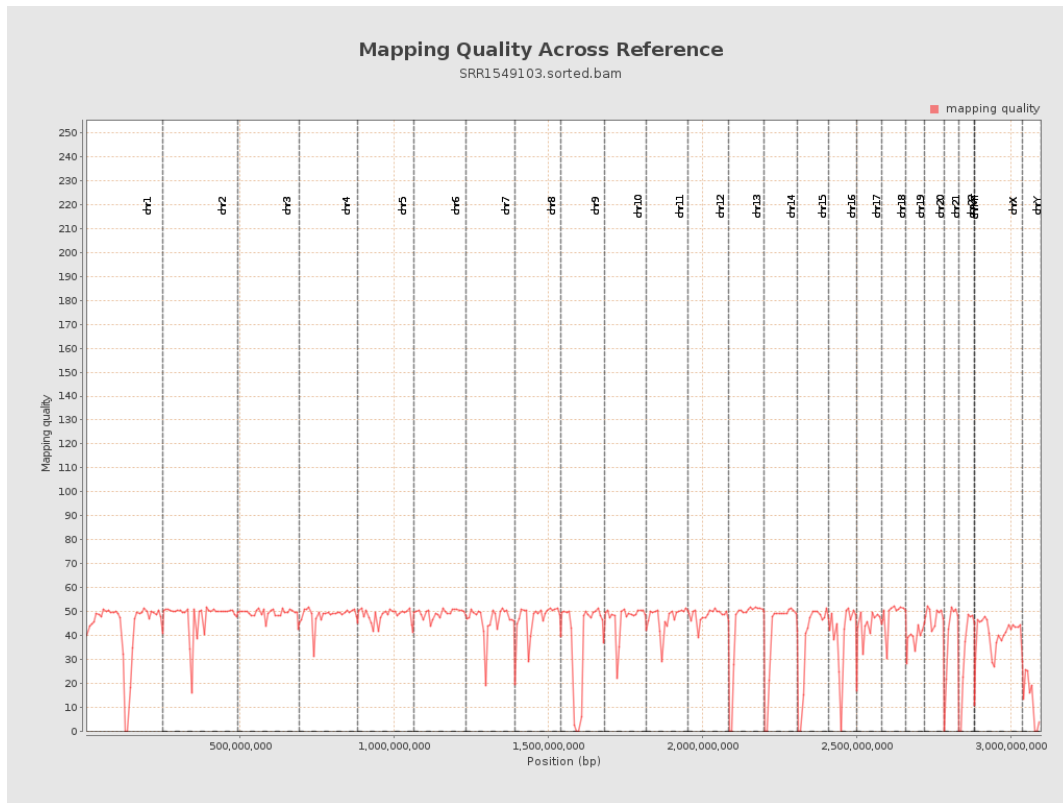
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

