

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 02:19:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549106.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_SRR1549106 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549106.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 02:19:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549106.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,601,805
Mapped reads	9,139,052 / 86.2%
Unmapped reads	1,462,753 / 13.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	393,158 / 3.71%
Duplication rate	3.22%
Clipped reads	413,185 / 3.9%

2.2. ACGT Content

Number/percentage of A's	107,859,046 / 29.71%
Number/percentage of C's	73,887,179 / 20.35%
Number/percentage of T's	107,919,978 / 29.73%
Number/percentage of G's	73,346,921 / 20.2%
Number/percentage of N's	1,394 / 0%
GC Percentage	40.56%

2.3. Coverage

Mean	0.1173
Standard Deviation	0.7596

2.4. Mapping Quality

Mean Mapping Quality	44.31
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2.5. Mismatches and indels

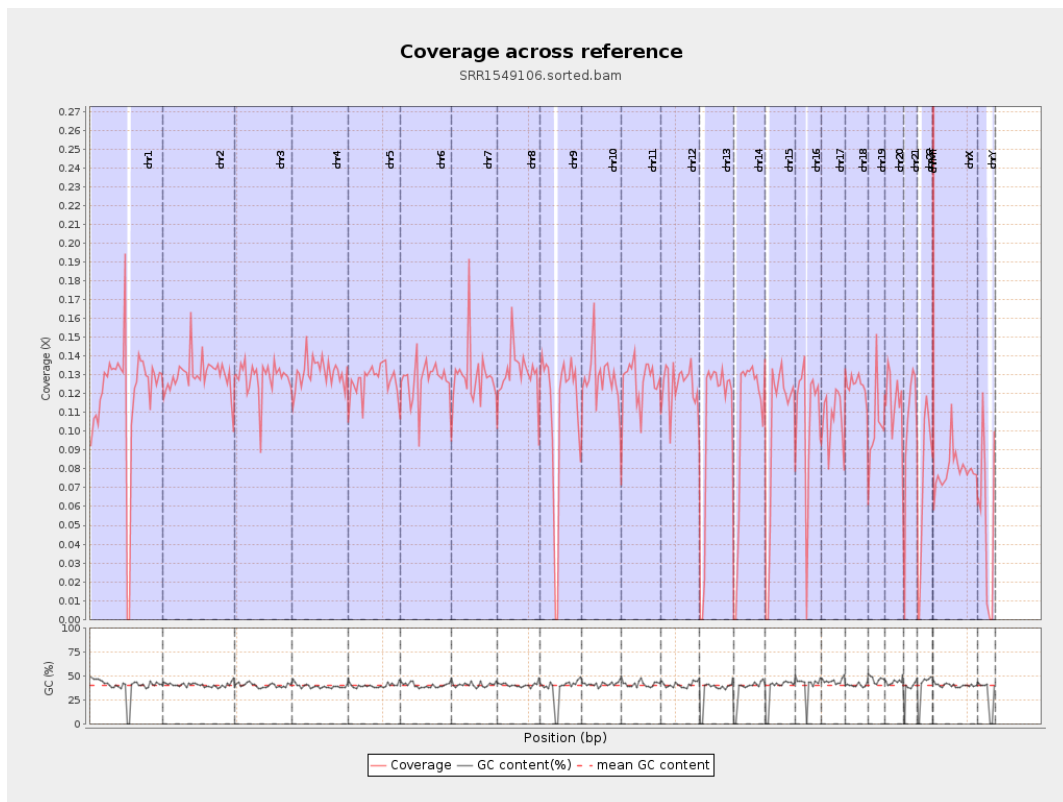
General error rate	0.3%
Mismatches	1,077,193
Insertions	8,820
Mapped reads with at least one insertion	0.1%
Deletions	26,611
Mapped reads with at least one deletion	0.29%
Homopolymer indels	46.1%

2.6. Chromosome stats

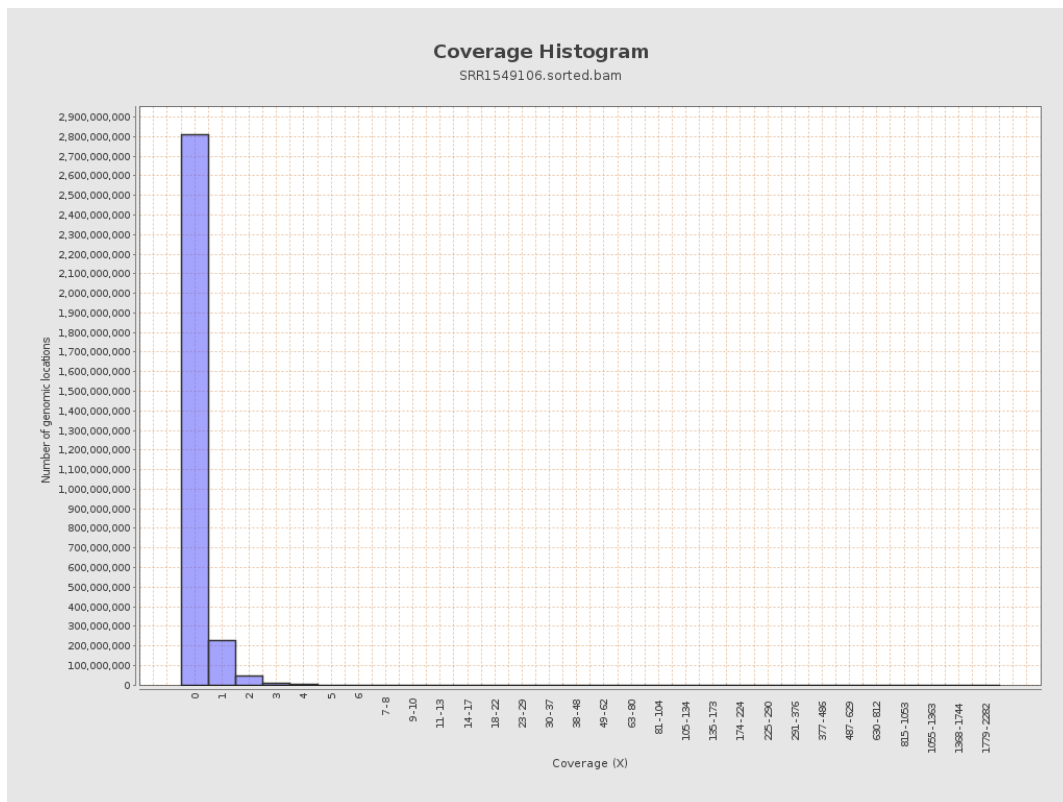
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	29832470	0.1197	1.6257
chr2	243199373	31584593	0.1299	0.6411
chr3	198022430	25436894	0.1285	0.4348
chr4	191154276	25121908	0.1314	0.4794
chr5	180915260	22893417	0.1265	0.445
chr6	171115067	21814603	0.1275	0.4879
chr7	159138663	20553147	0.1292	1.0395
chr8	146364022	19201705	0.1312	0.89

chr9	141213431	15677348	0.111	0.5921
chr10	135534747	17399466	0.1284	0.6777
chr11	135006516	17074687	0.1265	0.6189
chr12	133851895	16648823	0.1244	0.4536
chr13	115169878	12148886	0.1055	0.3898
chr14	107349540	11304733	0.1053	0.5083
chr15	102531392	10380978	0.1012	0.3806
chr16	90354753	9628688	0.1066	0.4492
chr17	81195210	8743050	0.1077	0.4441
chr18	78077248	9742969	0.1248	1.2763
chr19	59128983	6153726	0.1041	1.2278
chr20	63025520	7354185	0.1167	0.4504
chr21	48129895	4953371	0.1029	0.4752
chr22	51304566	3795746	0.074	0.3475
chrMT	16571	101532	6.1271	8.0058
chrX	155270560	12304509	0.0792	0.4502
chrY	59373566	3196587	0.0538	0.5174

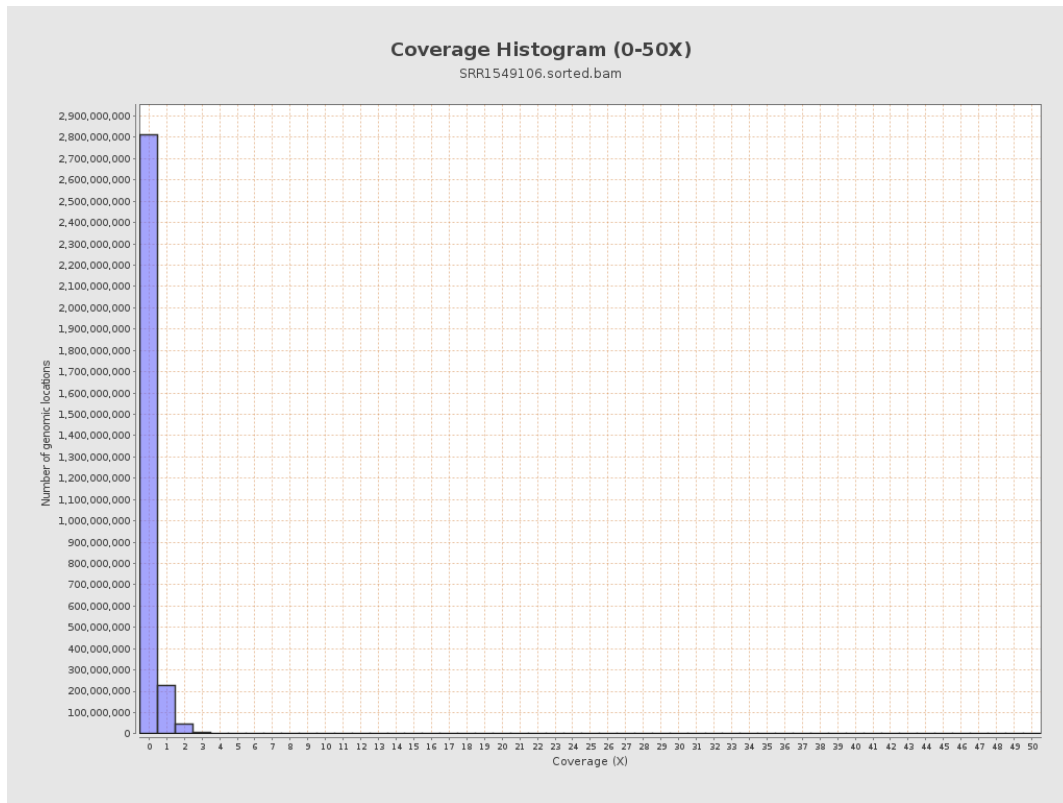
3. Results : Coverage across reference



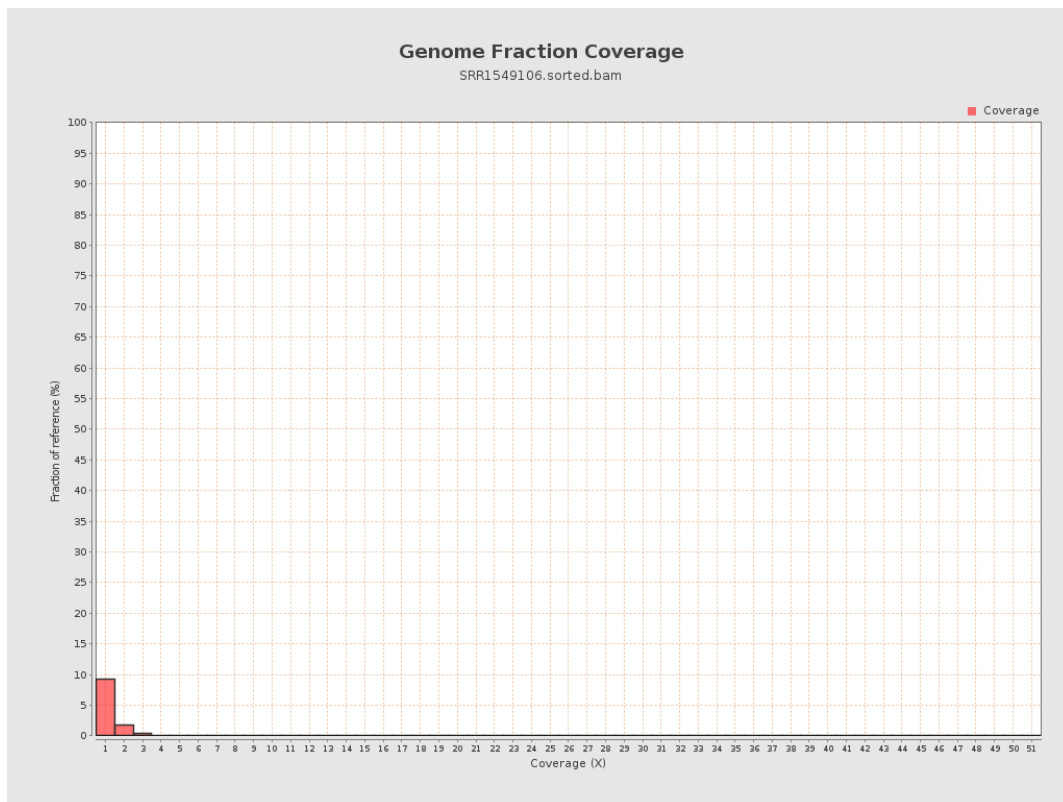
4. Results : Coverage Histogram



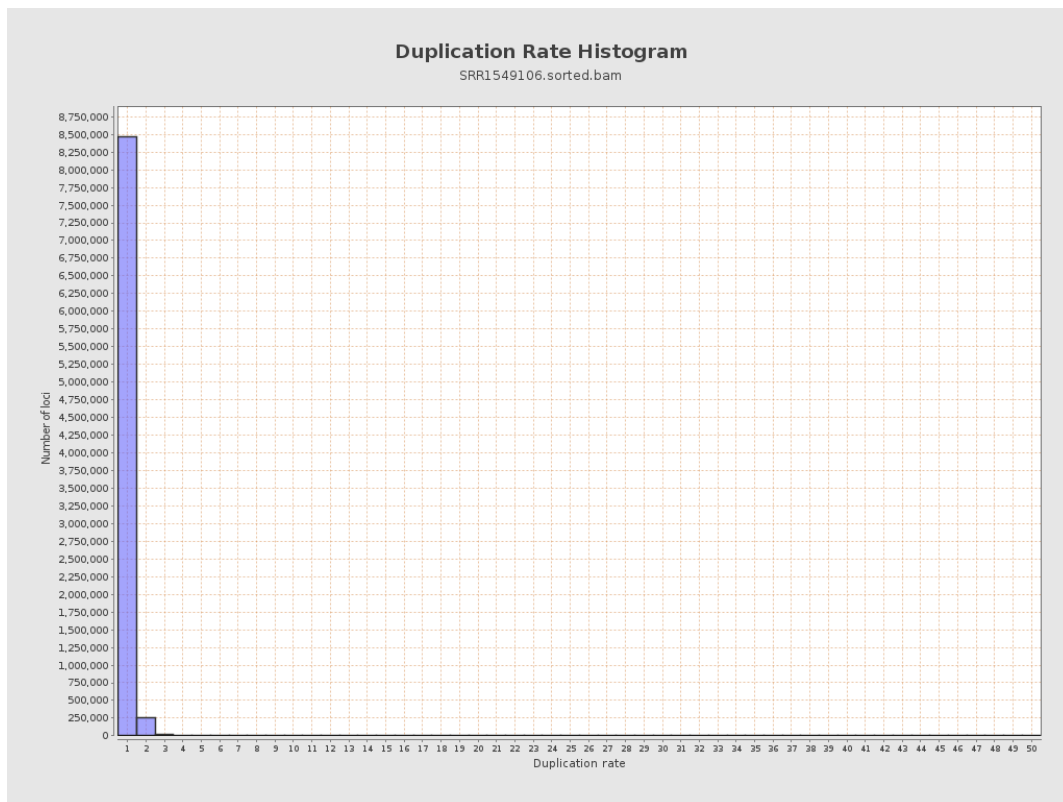
5. Results : Coverage Histogram (0-50X)



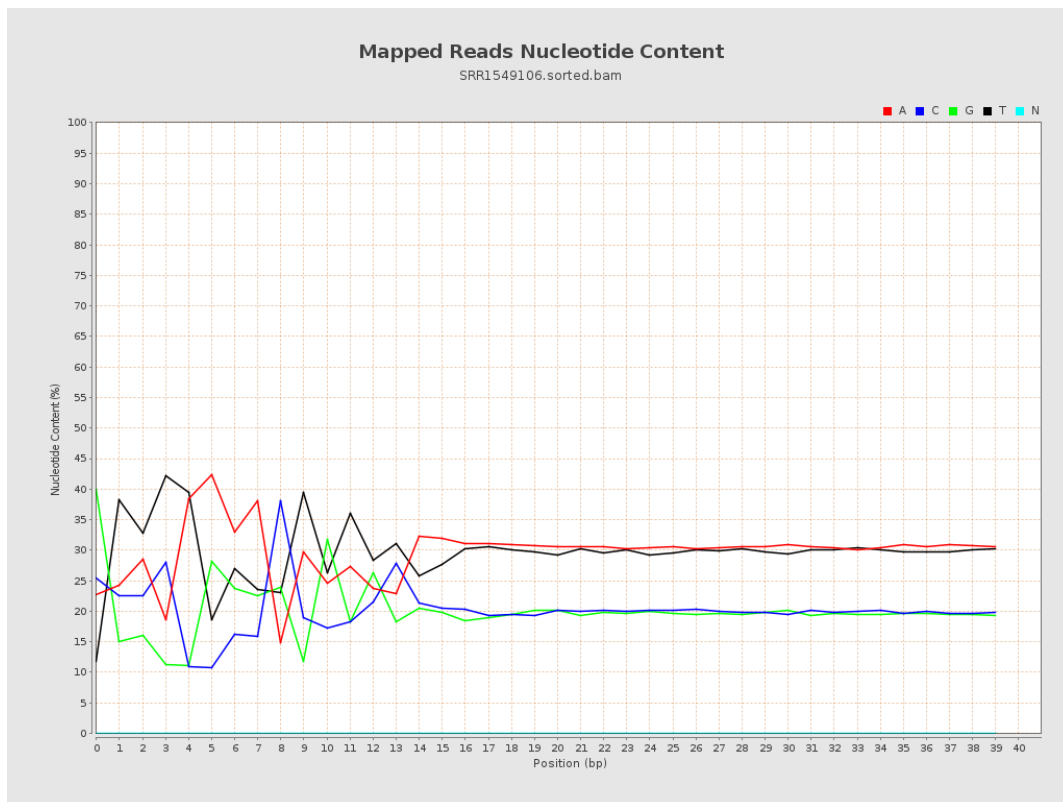
6. Results : Genome Fraction Coverage



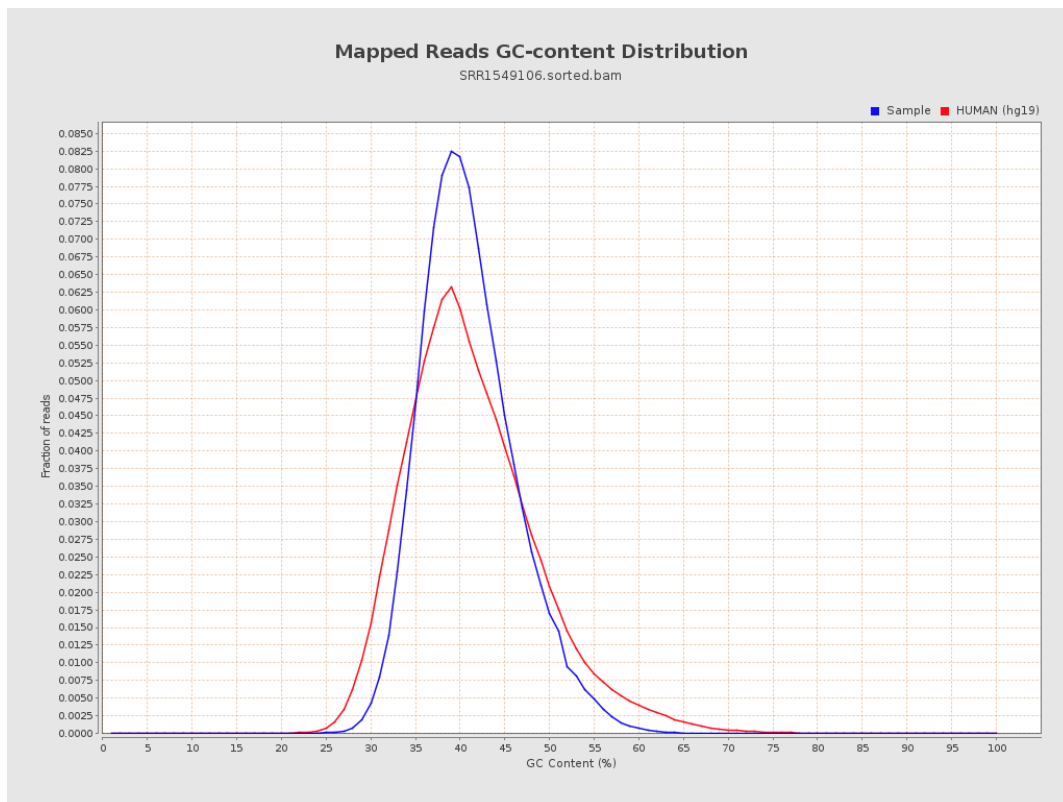
7. Results : Duplication Rate Histogram



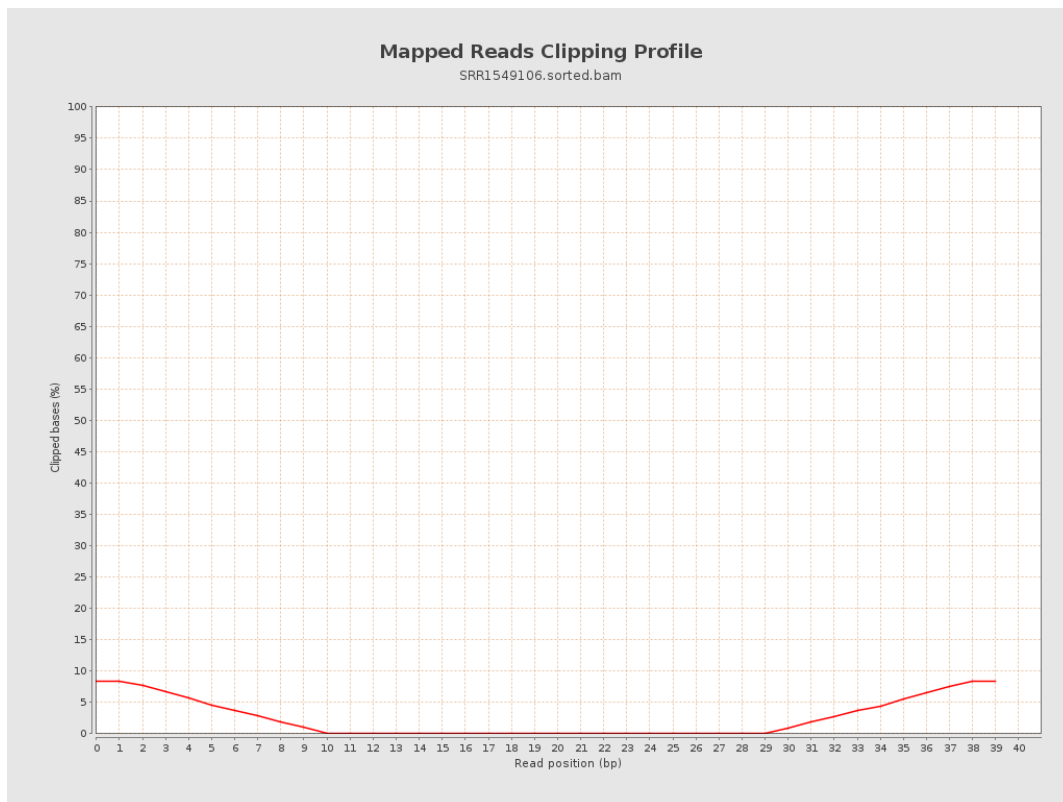
8. Results : Mapped Reads Nucleotide Content



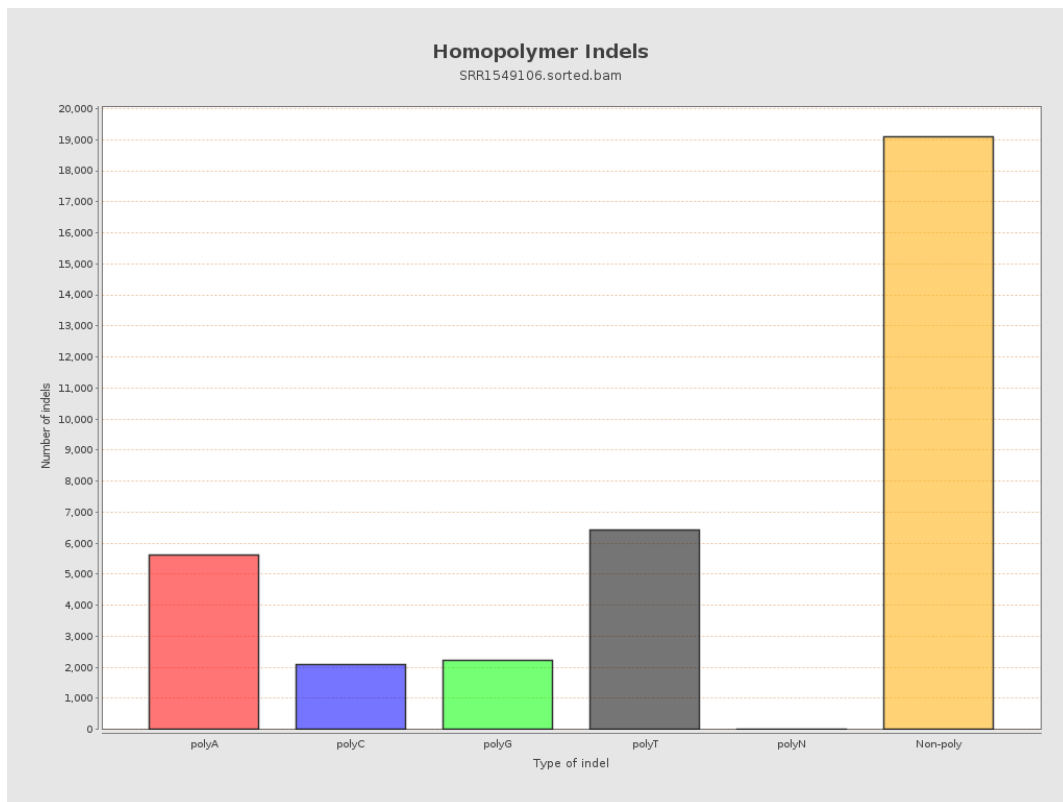
9. Results : Mapped Reads GC-content Distribution



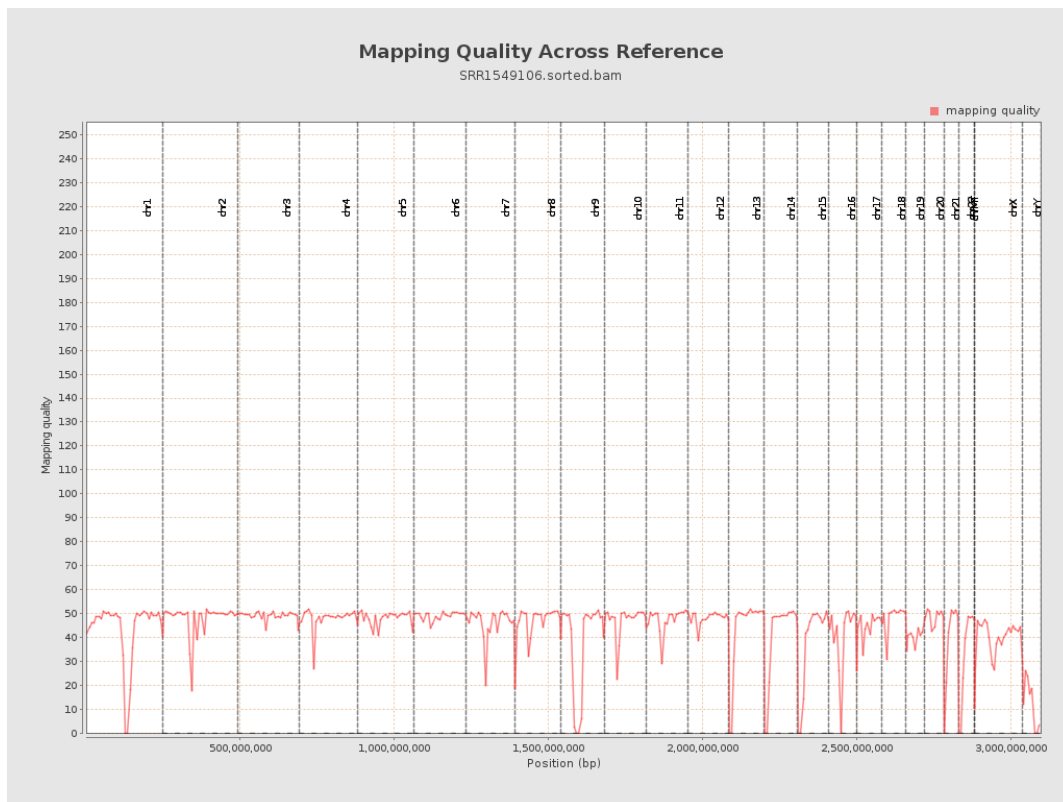
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

