

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 11:03:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549021.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_SRR1549021 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549021.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 11:03:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549021.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,289,136
Mapped reads	7,301,168 / 88.08%
Unmapped reads	987,968 / 11.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	270,187 / 3.26%
Duplication rate	2.68%
Clipped reads	534,563 / 6.45%

2.2. ACGT Content

Number/percentage of A's	83,322,003 / 28.83%
Number/percentage of C's	60,854,652 / 21.06%
Number/percentage of T's	83,851,744 / 29.01%
Number/percentage of G's	60,981,641 / 21.1%
Number/percentage of N's	2,850 / 0%
GC Percentage	42.16%

2.3. Coverage

Mean	0.0934
Standard Deviation	0.8477

2.4. Mapping Quality

Mean Mapping Quality	39.96
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2.5. Mismatches and indels

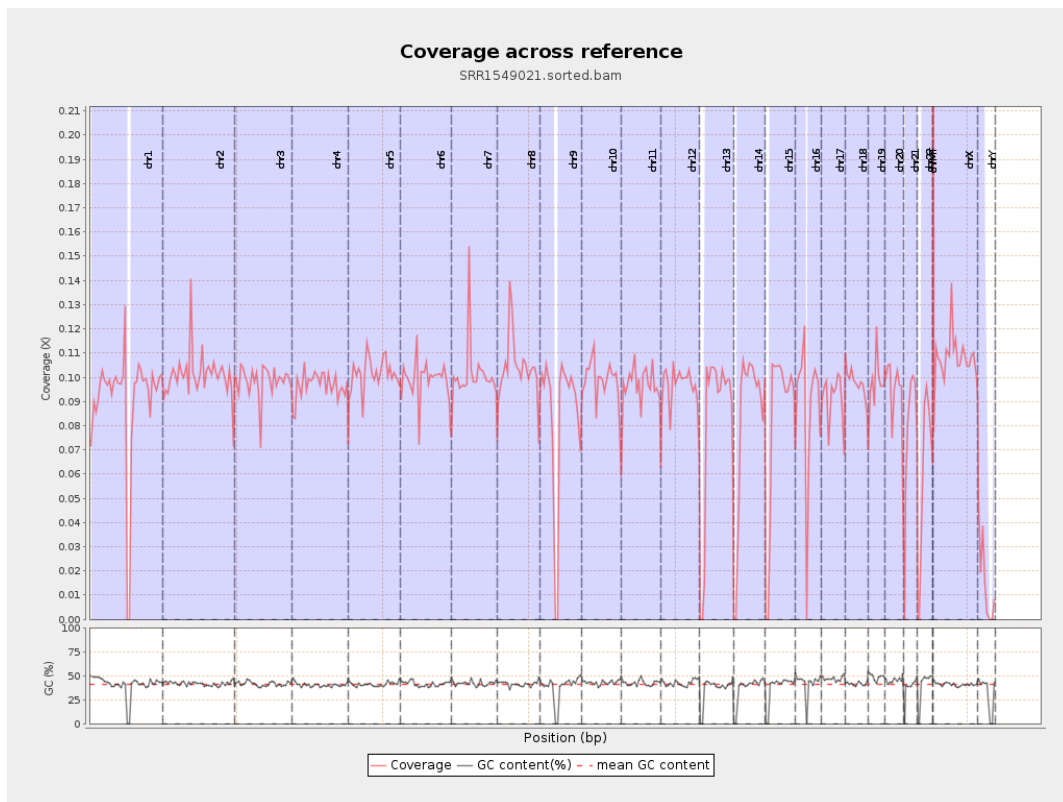
General error rate	0.29%
Mismatches	836,962
Insertions	9,114
Mapped reads with at least one insertion	0.12%
Deletions	23,611
Mapped reads with at least one deletion	0.32%
Homopolymer indels	40.58%

2.6. Chromosome stats

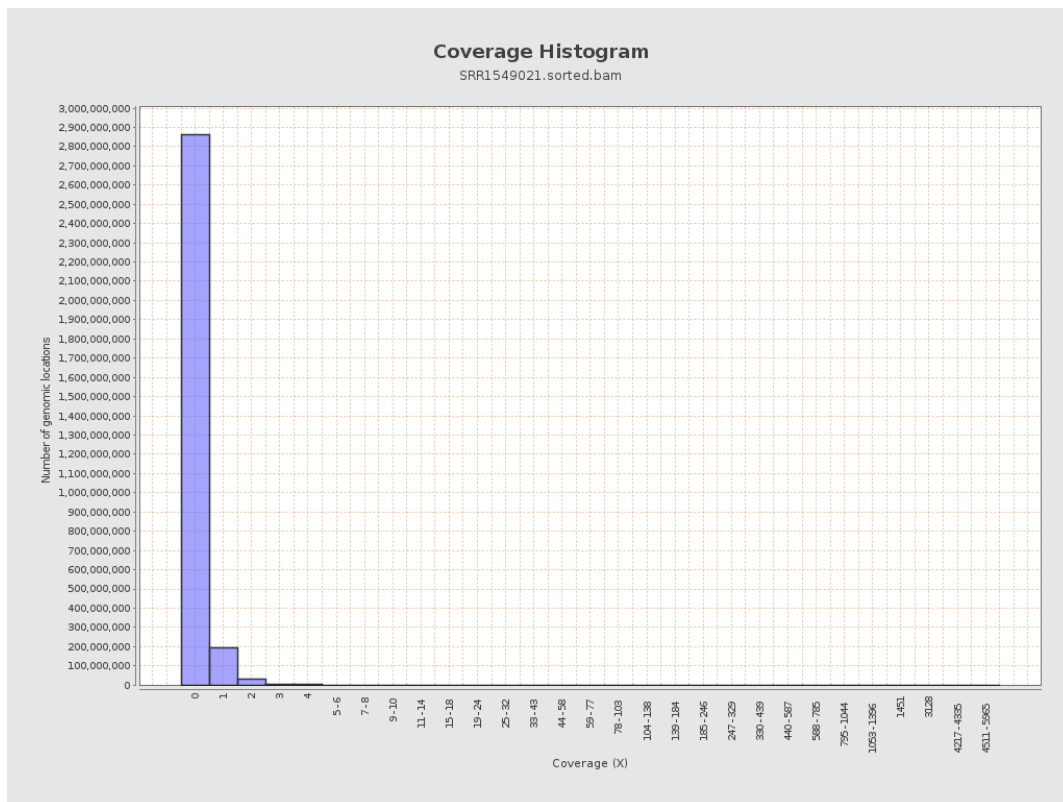
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	22601045	0.0907	1.0142
chr2	243199373	24571387	0.101	0.5744
chr3	198022430	19506099	0.0985	0.3732
chr4	191154276	18470015	0.0966	0.381
chr5	180915260	18304914	0.1012	0.3867
chr6	171115067	16963449	0.0991	0.4289
chr7	159138663	16092345	0.1011	0.8366
chr8	146364022	15261182	0.1043	2.9191

chr9	141213431	11947456	0.0846	0.5457
chr10	135534747	13428211	0.0991	0.4968
chr11	135006516	13059996	0.0967	0.6018
chr12	133851895	12965420	0.0969	0.3871
chr13	115169878	9457012	0.0821	0.337
chr14	107349540	8869103	0.0826	0.413
chr15	102531392	8353051	0.0815	0.3396
chr16	90354753	7802106	0.0863	0.3903
chr17	81195210	7471433	0.092	0.3941
chr18	78077248	7643666	0.0979	1.0504
chr19	59128983	5808291	0.0982	0.9714
chr20	63025520	5985659	0.095	0.3849
chr21	48129895	3725289	0.0774	0.3728
chr22	51304566	3114169	0.0607	0.3277
chrMT	16571	10671	0.644	1.0669
chrX	155270560	16728216	0.1077	0.4793
chrY	59373566	903463	0.0152	0.1764

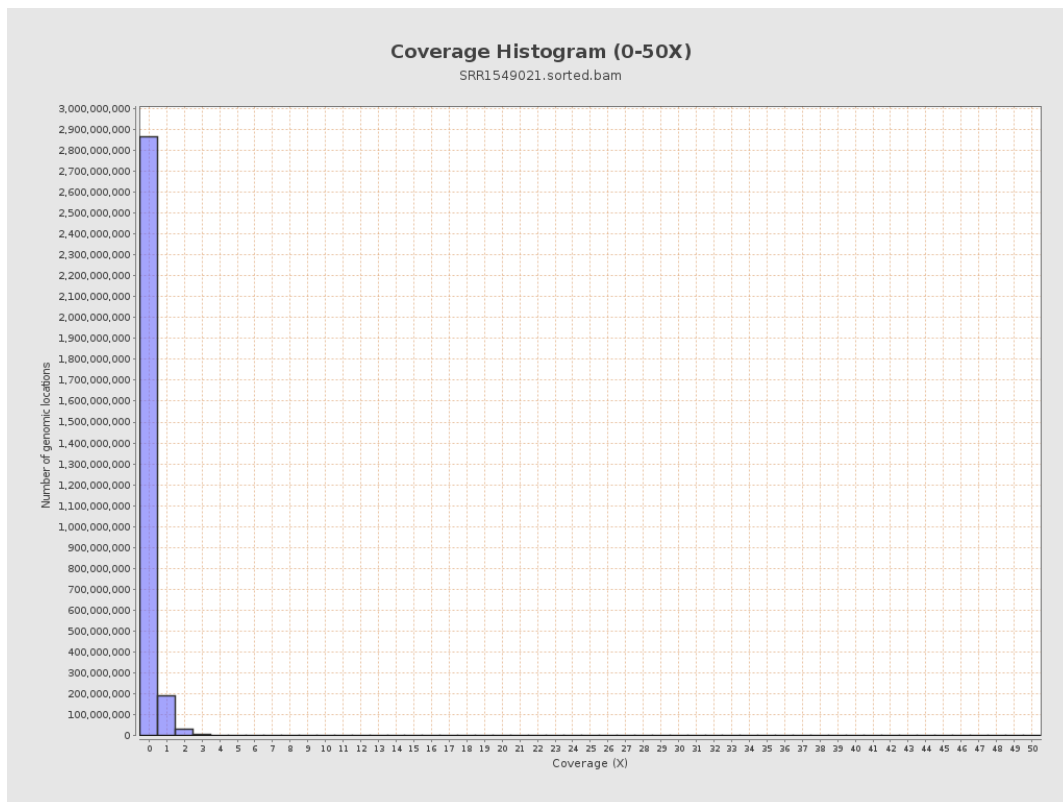
3. Results : Coverage across reference



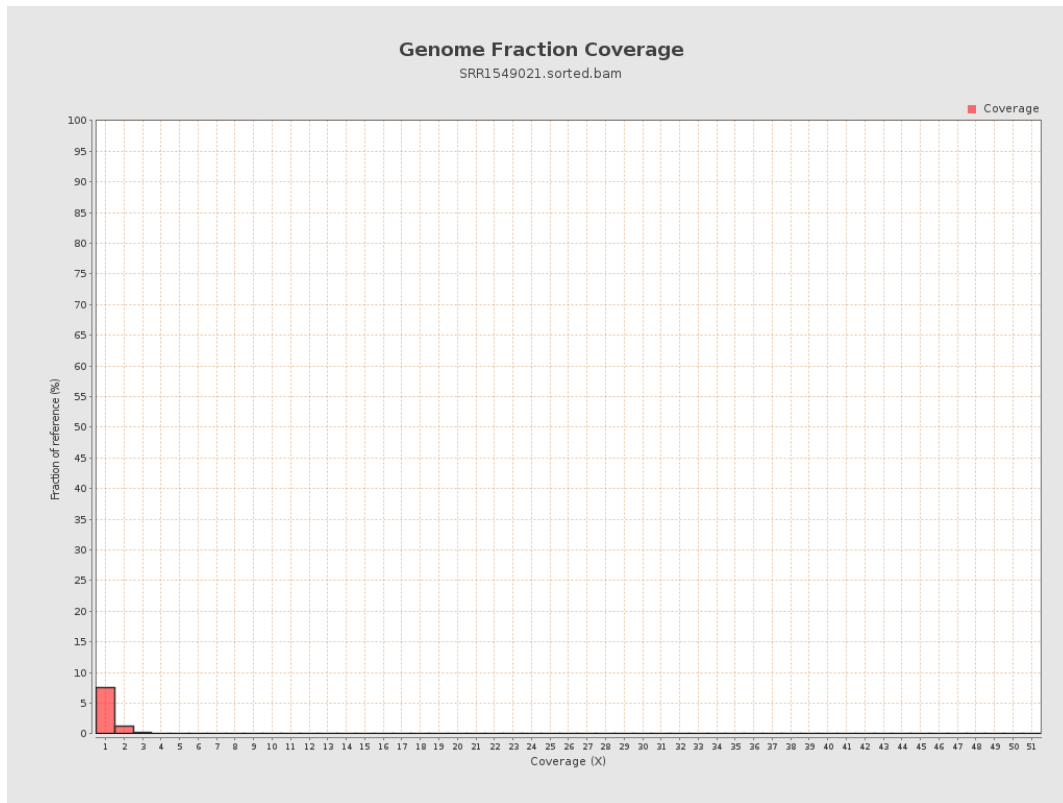
4. Results : Coverage Histogram



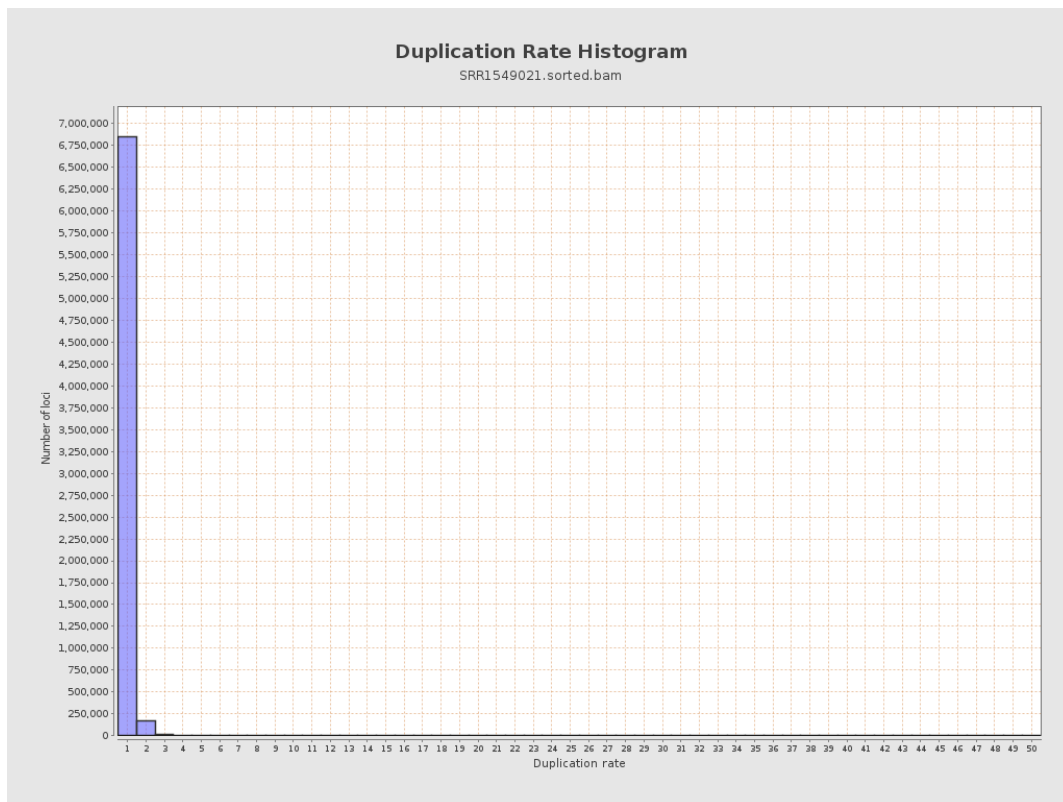
5. Results : Coverage Histogram (0-50X)



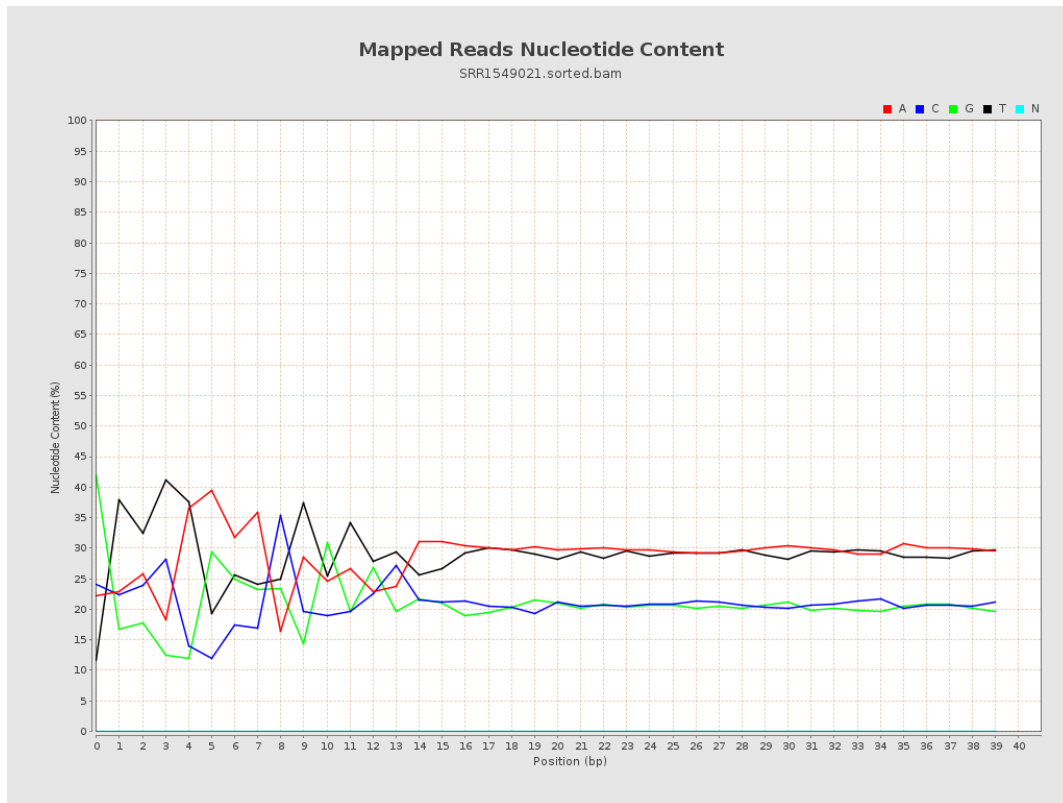
6. Results : Genome Fraction Coverage



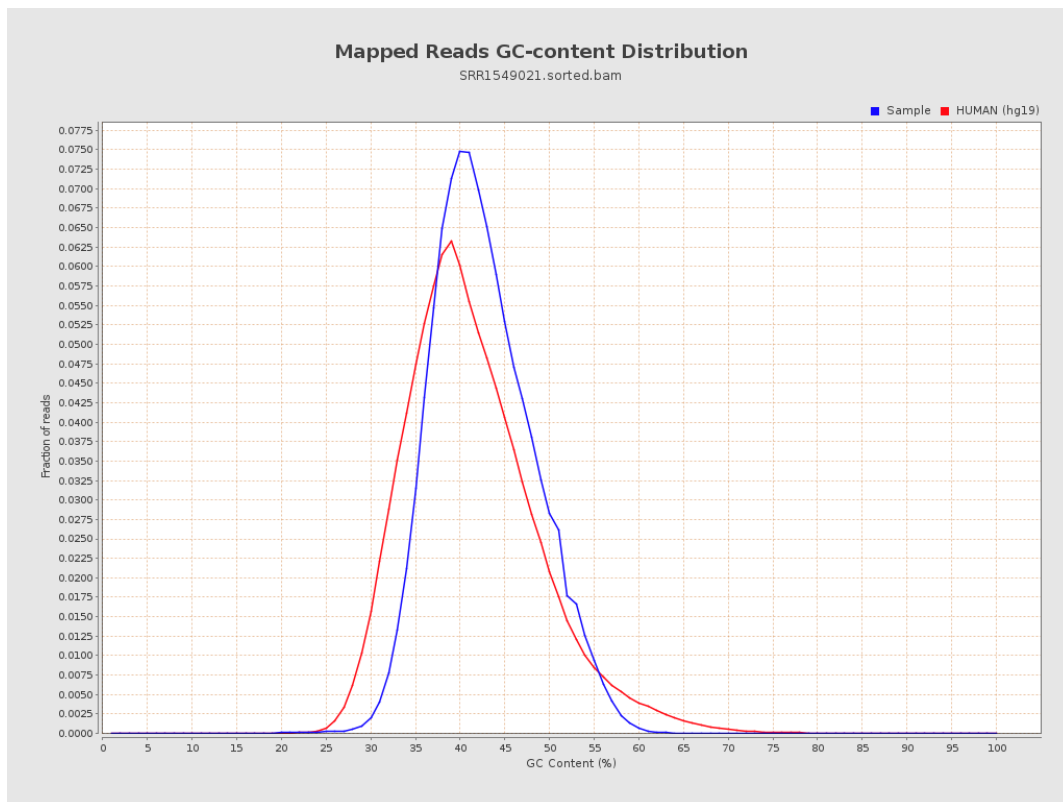
7. Results : Duplication Rate Histogram



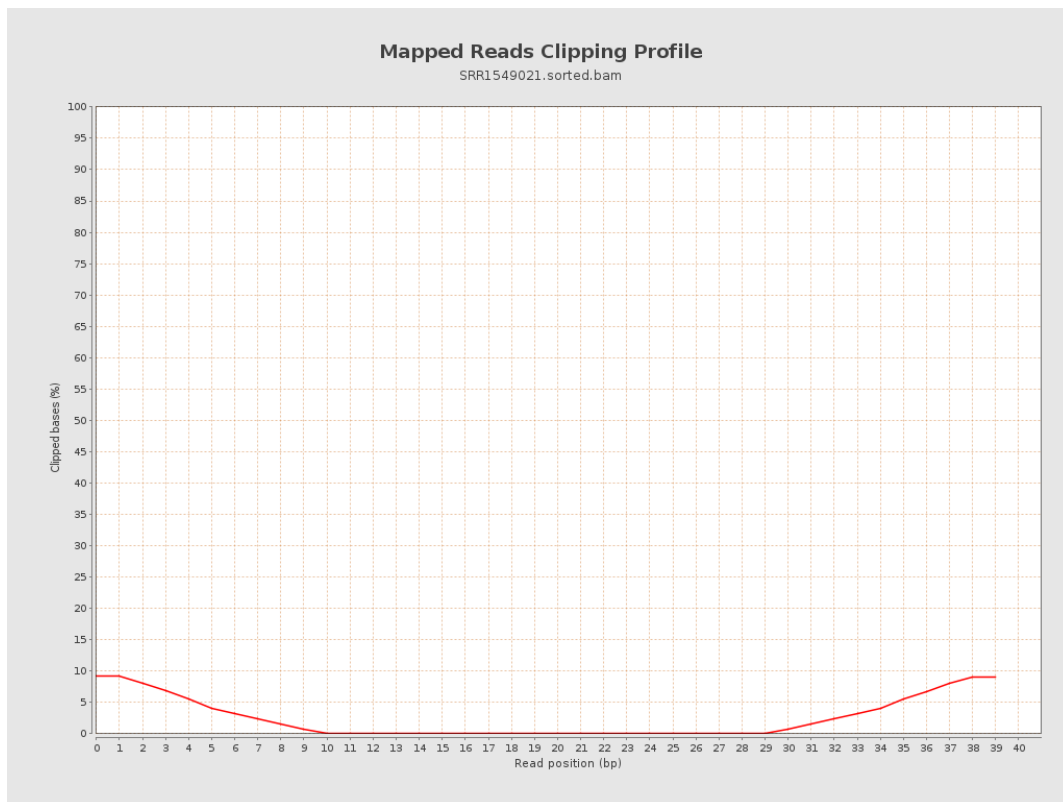
8. Results : Mapped Reads Nucleotide Content



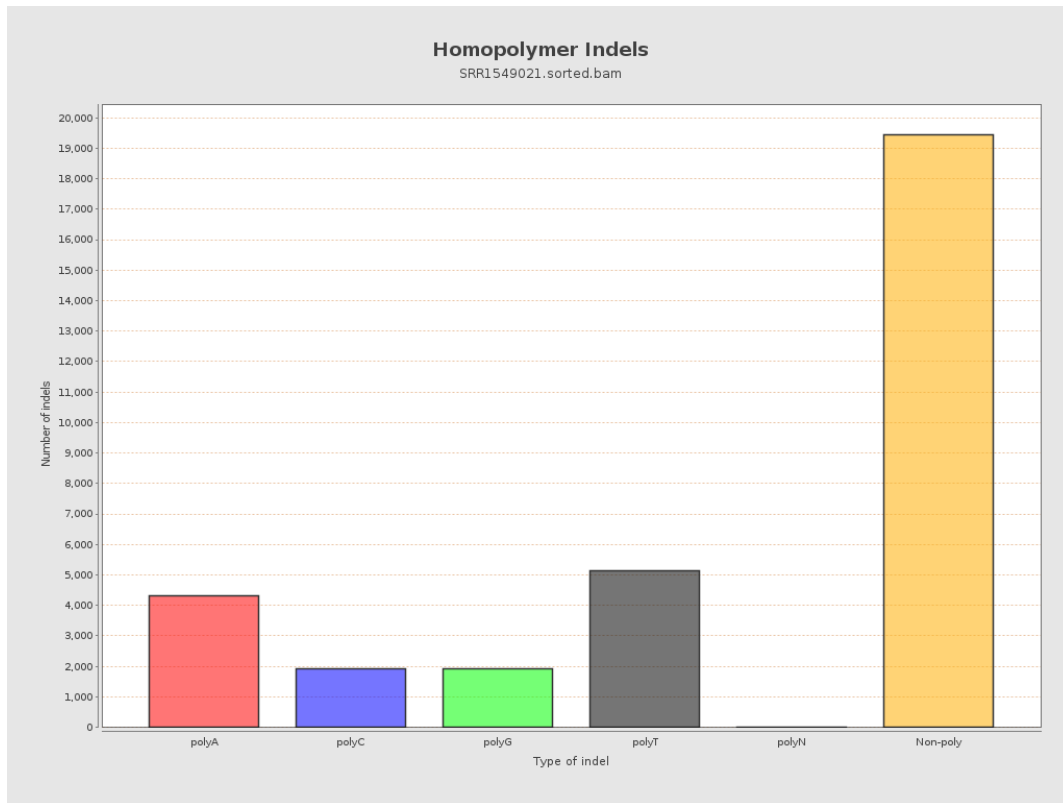
9. Results : Mapped Reads GC-content Distribution



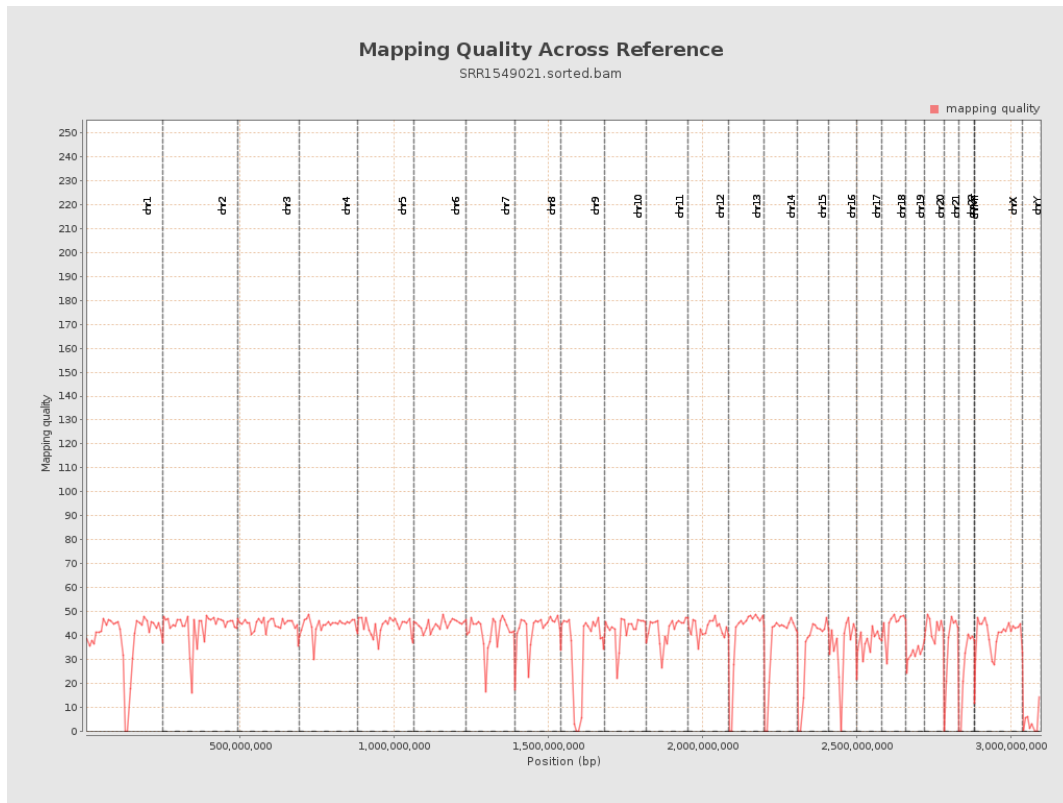
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

