

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 01:23:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080549.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_SRR3080549 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080549.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 01:23:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080549.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,041,220
Mapped reads	2,502,643 / 82.29%
Unmapped reads	538,577 / 17.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,367 / 0.77%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	139,000 / 4.57%
Duplication rate	4.86%
Clipped reads	1,167,892 / 38.4%

2.2. ACGT Content

Number/percentage of A's	45,580,635 / 27.41%
Number/percentage of C's	29,851,424 / 17.95%
Number/percentage of T's	53,955,414 / 32.44%
Number/percentage of G's	36,780,399 / 22.12%
Number/percentage of N's	138,334 / 0.08%
GC Percentage	40.07%

2.3. Coverage

Mean	0.0537

Standard Deviation	0.3372
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2.4. Mapping Quality

Mean Mapping Quality	47.49
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2.5. Mismatches and indels

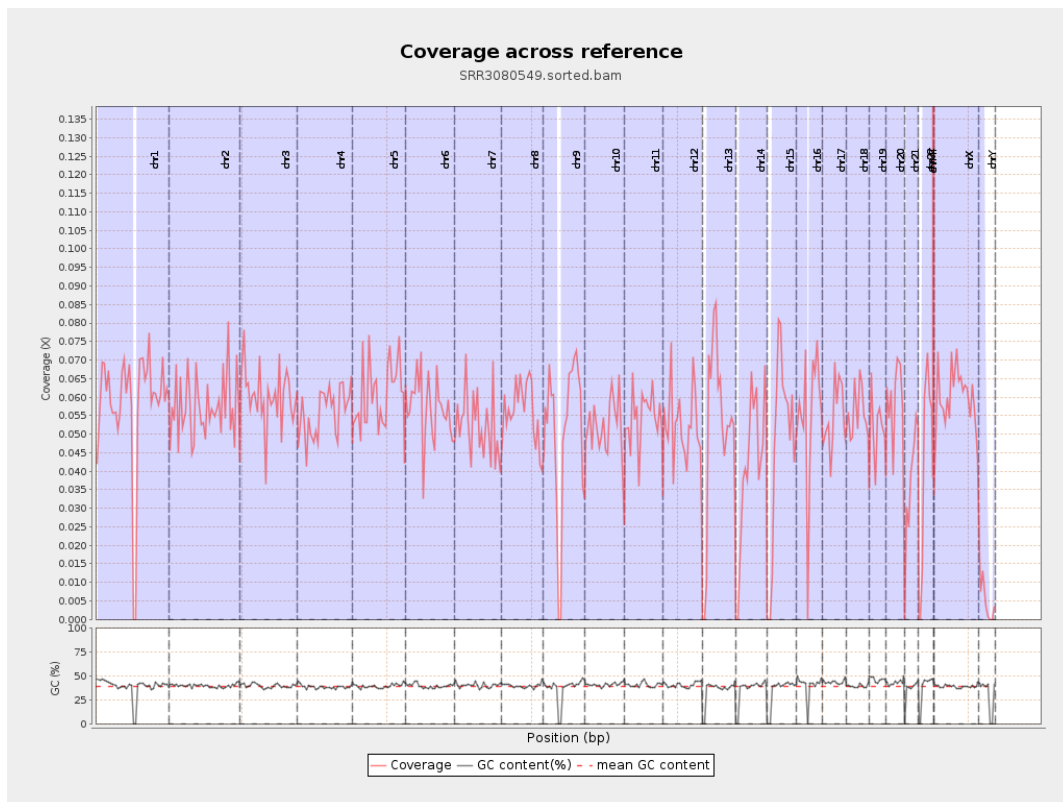
General error rate	0.9%
Mismatches	1,473,619
Insertions	13,603
Mapped reads with at least one insertion	0.54%
Deletions	39,703
Mapped reads with at least one deletion	1.57%
Homopolymer indels	48.97%

2.6. Chromosome stats

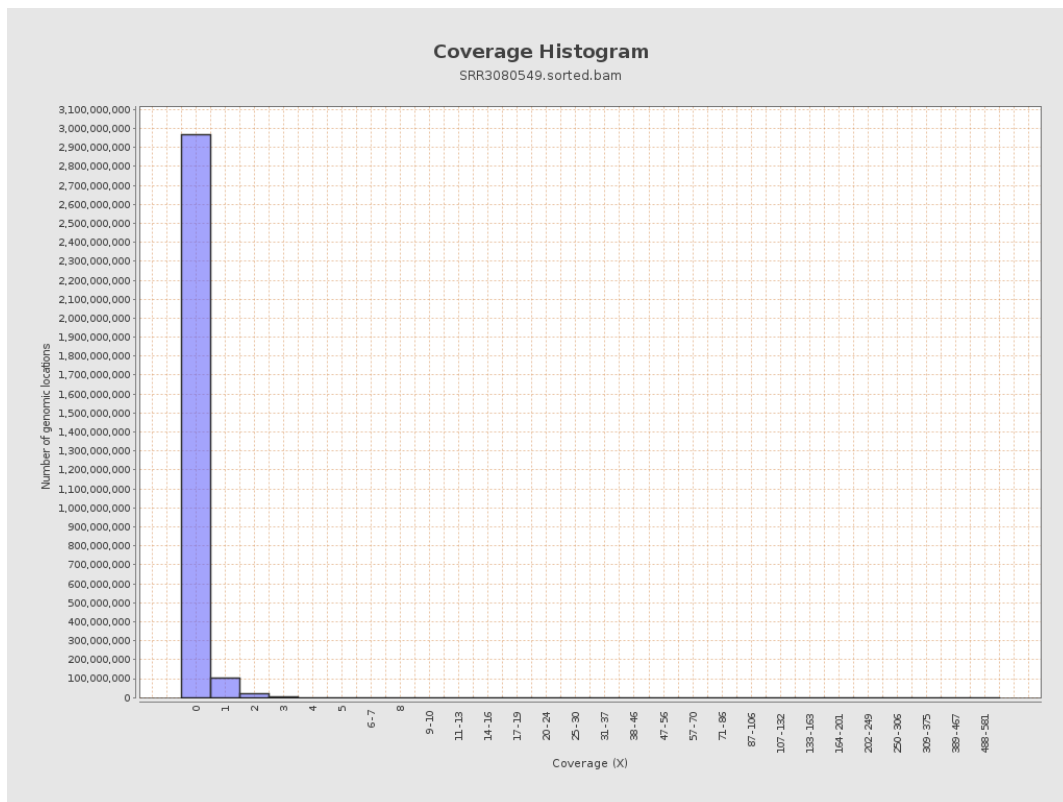
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	14530121	0.0583	0.3729
chr2	243199373	13947163	0.0573	0.3522
chr3	198022430	11844744	0.0598	0.3004
chr4	191154276	10655248	0.0557	0.2974
chr5	180915260	10991234	0.0608	0.3014
chr6	171115067	9739124	0.0569	0.3291
chr7	159138663	8341698	0.0524	0.3562

chr8	146364022	8207569	0.0561	0.4508
chr9	141213431	7258245	0.0514	0.3401
chr10	135534747	7093013	0.0523	0.3288
chr11	135006516	7325355	0.0543	0.3128
chr12	133851895	7033703	0.0525	0.2838
chr13	115169878	5875060	0.051	0.2828
chr14	107349540	4430227	0.0413	0.2623
chr15	102531392	4874176	0.0475	0.2715
chr16	90354753	4996948	0.0553	0.3024
chr17	81195210	4421751	0.0545	0.2907
chr18	78077248	4365855	0.0559	0.5325
chr19	59128983	3023112	0.0511	0.3515
chr20	63025520	3670276	0.0582	0.2987
chr21	48129895	1780539	0.037	0.24
chr22	51304566	2108099	0.0411	0.2499
chrMT	16571	335734	20.2603	23.7823
chrX	155270560	9219827	0.0594	0.3121
chrY	59373566	302763	0.0051	0.1044

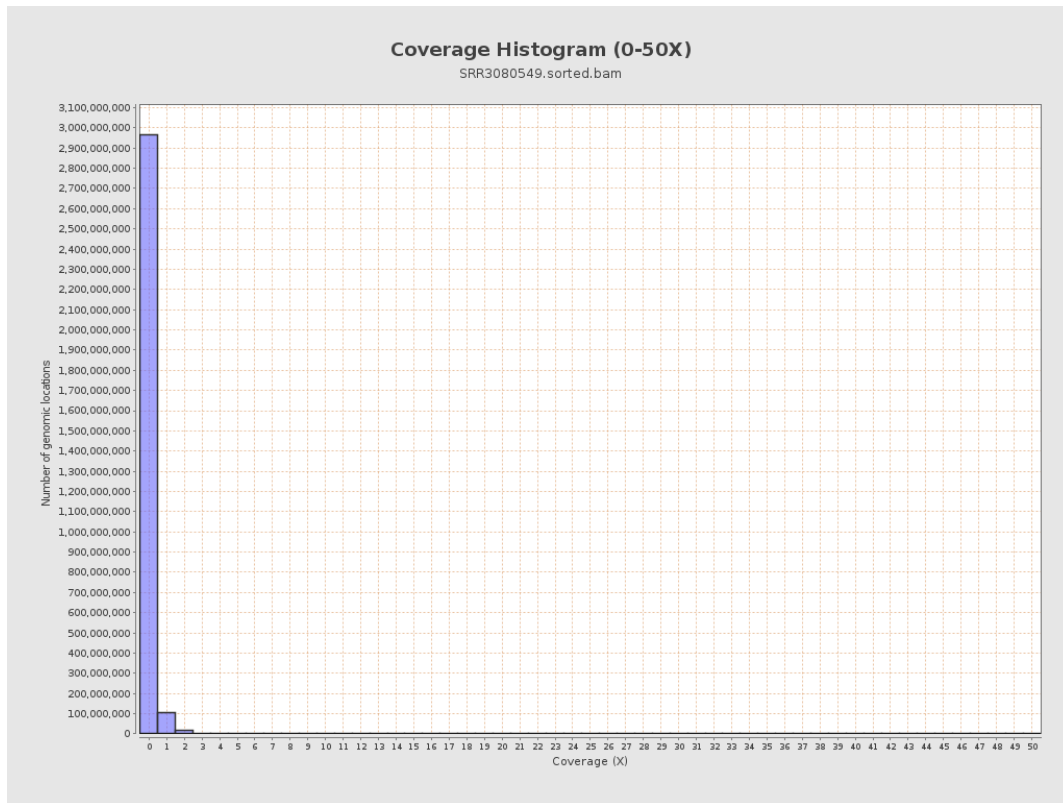
3. Results : Coverage across reference



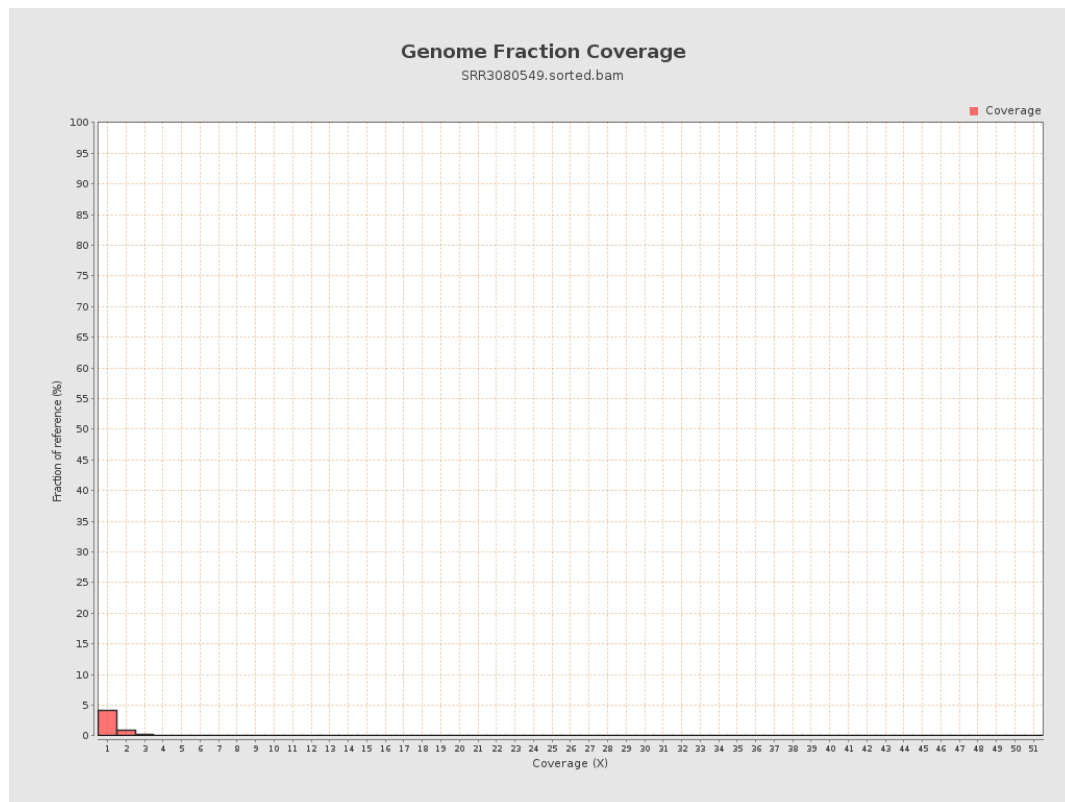
4. Results : Coverage Histogram



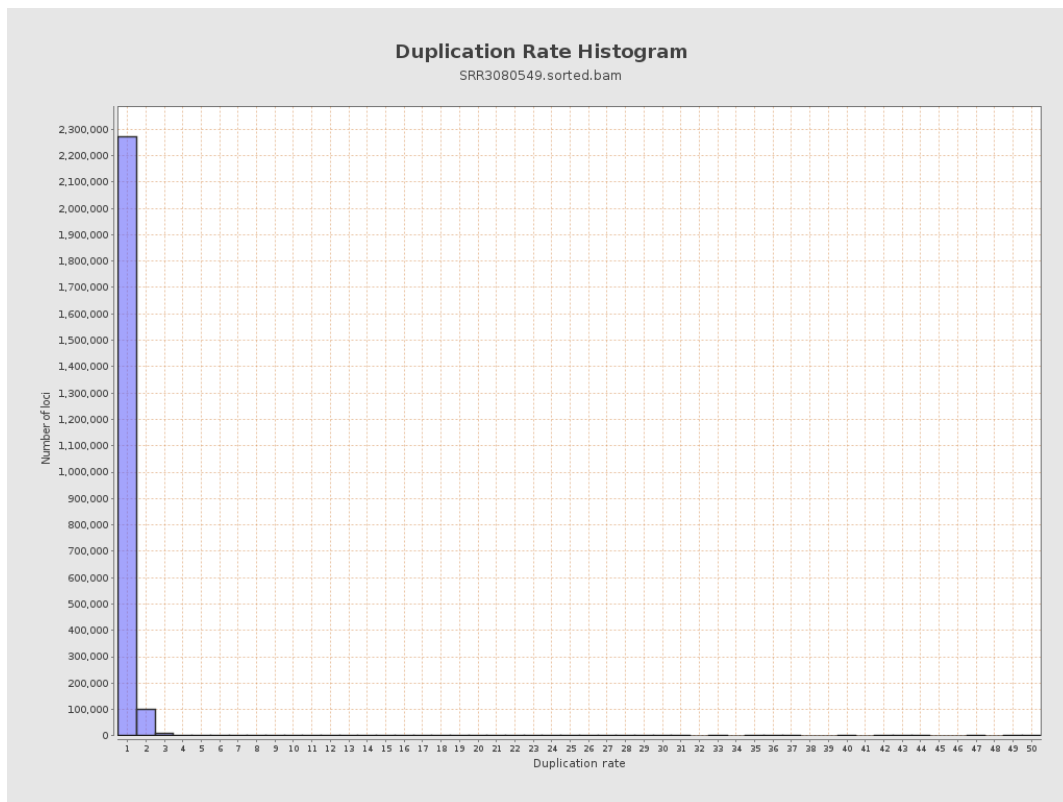
5. Results : Coverage Histogram (0-50X)



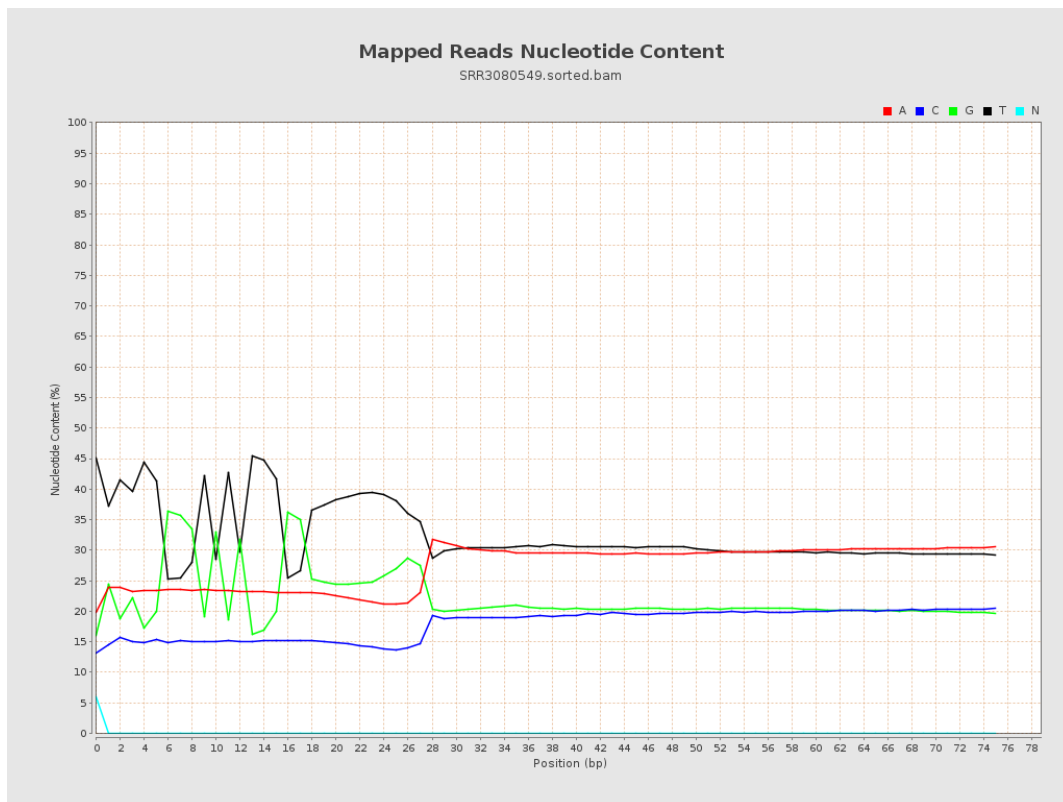
6. Results : Genome Fraction Coverage



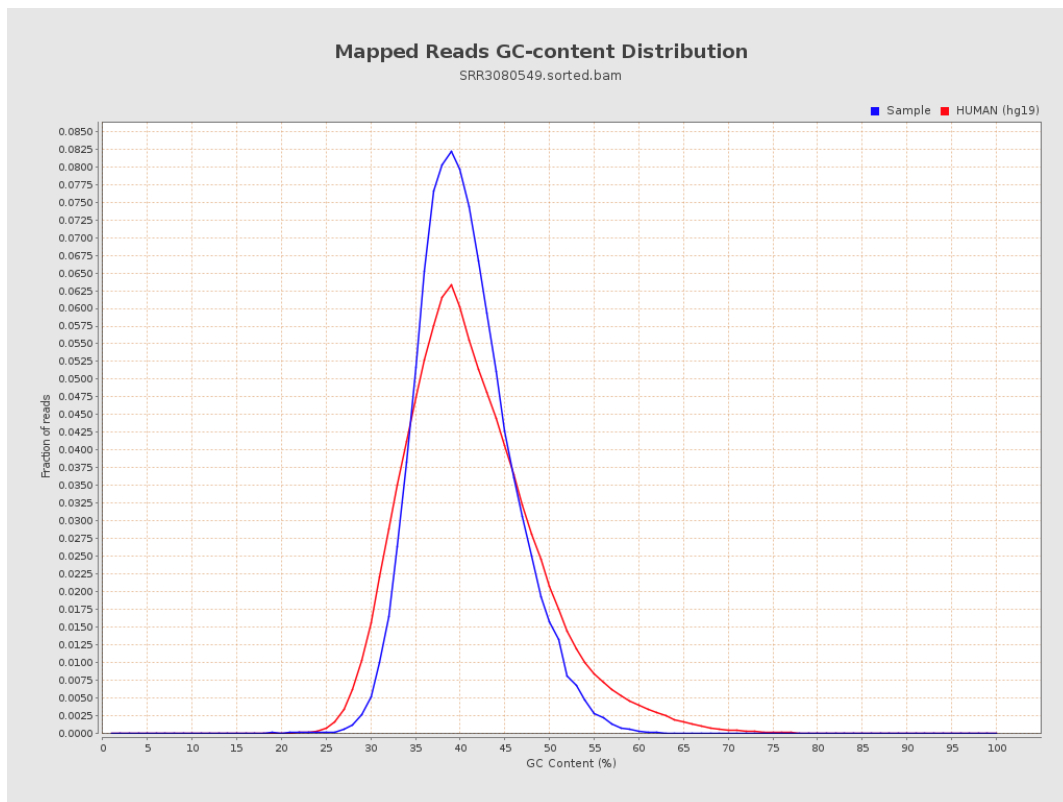
7. Results : Duplication Rate Histogram



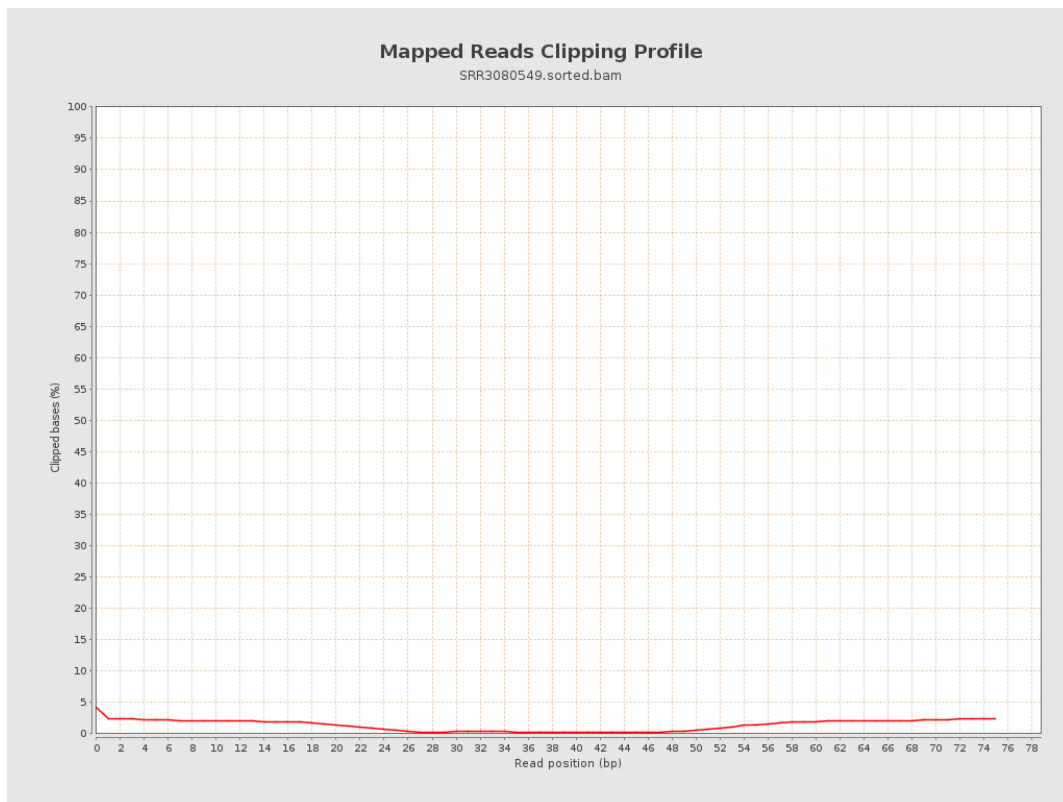
8. Results : Mapped Reads Nucleotide Content



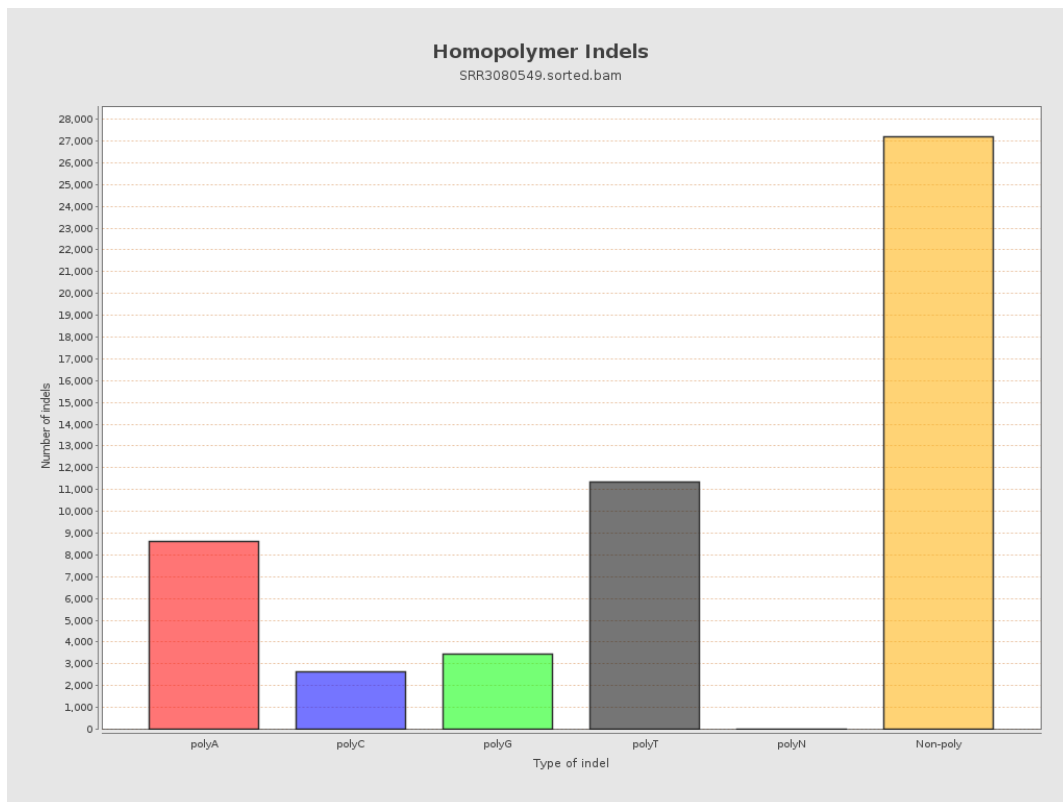
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

