

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 16:52:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084842.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_SRR3084842 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084842.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 16:52:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084842.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,564,133
Mapped reads	2,330,795 / 90.9%
Unmapped reads	233,338 / 9.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,709 / 0.85%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	119,899 / 4.68%
Duplication rate	4.28%
Clipped reads	755,790 / 29.48%

2.2. ACGT Content

Number/percentage of A's	47,634,941 / 29.3%
Number/percentage of C's	29,877,947 / 18.38%
Number/percentage of T's	52,231,932 / 32.12%
Number/percentage of G's	32,826,302 / 20.19%
Number/percentage of N's	25,945 / 0.02%
GC Percentage	38.56%

2.3. Coverage

Mean	0.0525

Standard Deviation	0.4637
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2.4. Mapping Quality

Mean Mapping Quality	48.42
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2.5. Mismatches and indels

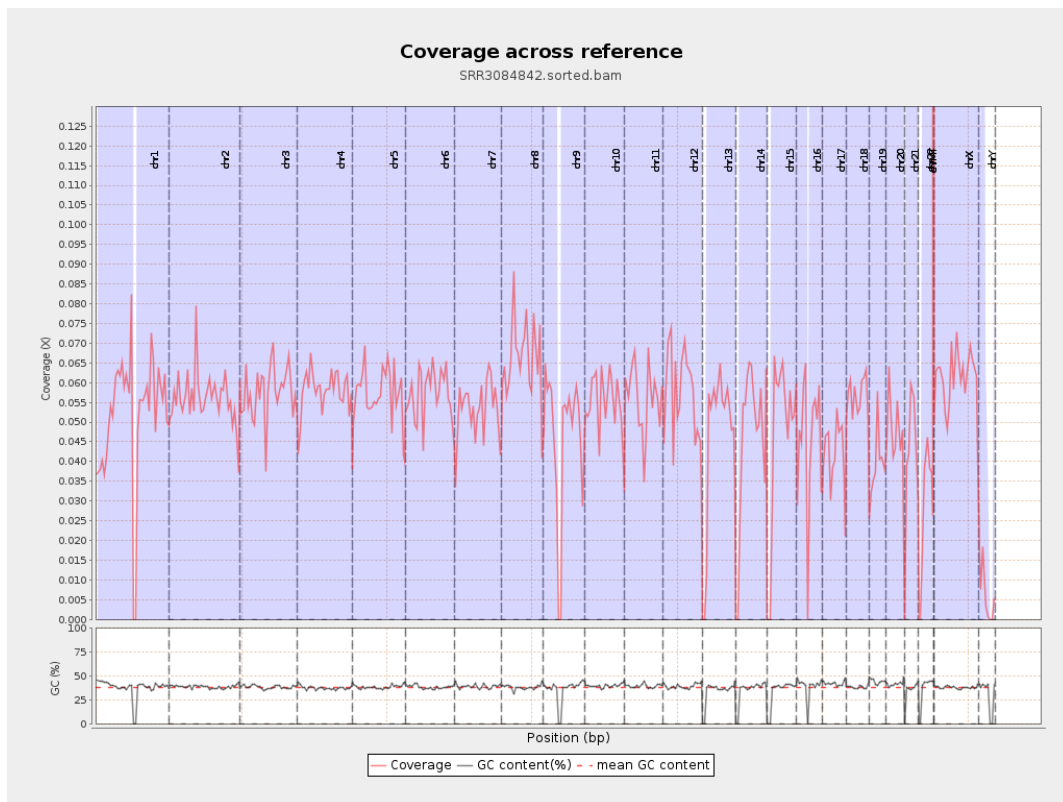
General error rate	0.84%
Mismatches	1,338,433
Insertions	13,052
Mapped reads with at least one insertion	0.55%
Deletions	35,629
Mapped reads with at least one deletion	1.51%
Homopolymer indels	48.29%

2.6. Chromosome stats

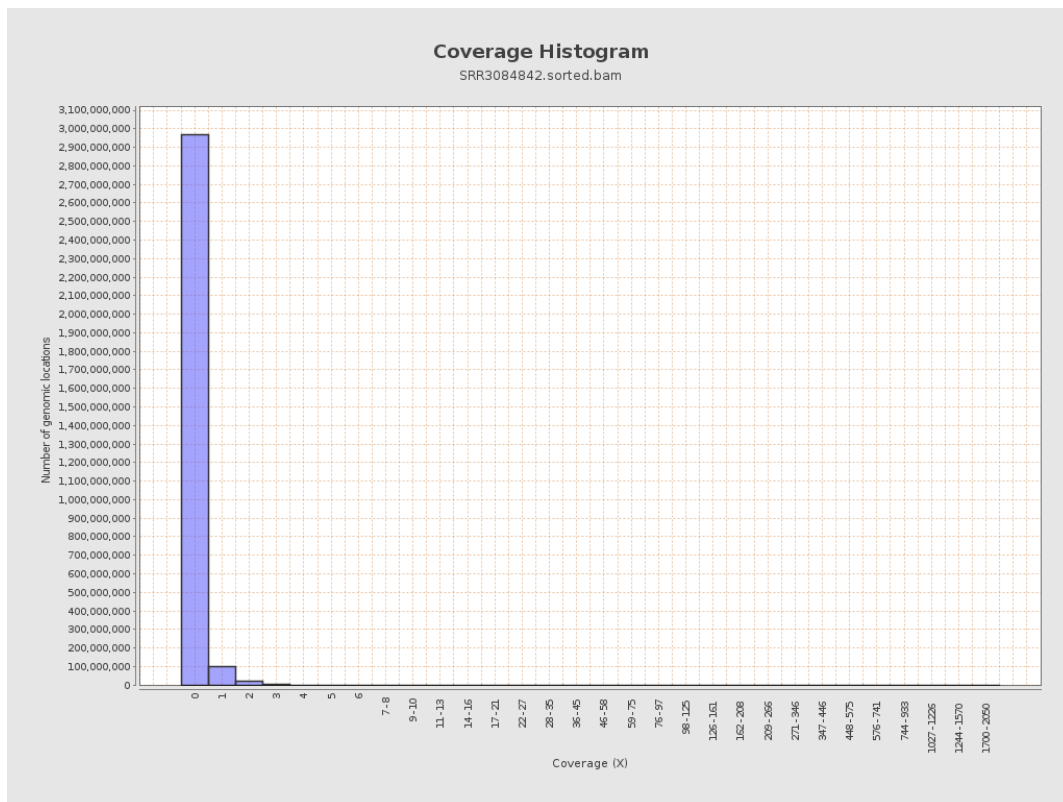
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	12961997	0.052	0.682
chr2	243199373	13651561	0.0561	0.3753
chr3	198022430	11423317	0.0577	0.2935
chr4	191154276	11089582	0.058	0.3044
chr5	180915260	10379586	0.0574	0.2941
chr6	171115067	9781249	0.0572	0.298
chr7	159138663	8528994	0.0536	0.3223

chr8	146364022	9673962	0.0661	1.3023
chr9	141213431	6520193	0.0462	0.3697
chr10	135534747	7564716	0.0558	0.3417
chr11	135006516	7554995	0.056	0.335
chr12	133851895	7640274	0.0571	0.2946
chr13	115169878	5306392	0.0461	0.263
chr14	107349540	4842443	0.0451	0.2726
chr15	102531392	4829209	0.0471	0.2644
chr16	90354753	4072936	0.0451	0.2765
chr17	81195210	3383147	0.0417	0.308
chr18	78077248	4444945	0.0569	0.6765
chr19	59128983	2347689	0.0397	0.4734
chr20	63025520	3008546	0.0477	0.274
chr21	48129895	2006778	0.0417	0.26
chr22	51304566	1422694	0.0277	0.1988
chrMT	16571	354345	21.3834	11.0605
chrX	155270560	9513509	0.0613	0.3179
chrY	59373566	356980	0.006	0.1316

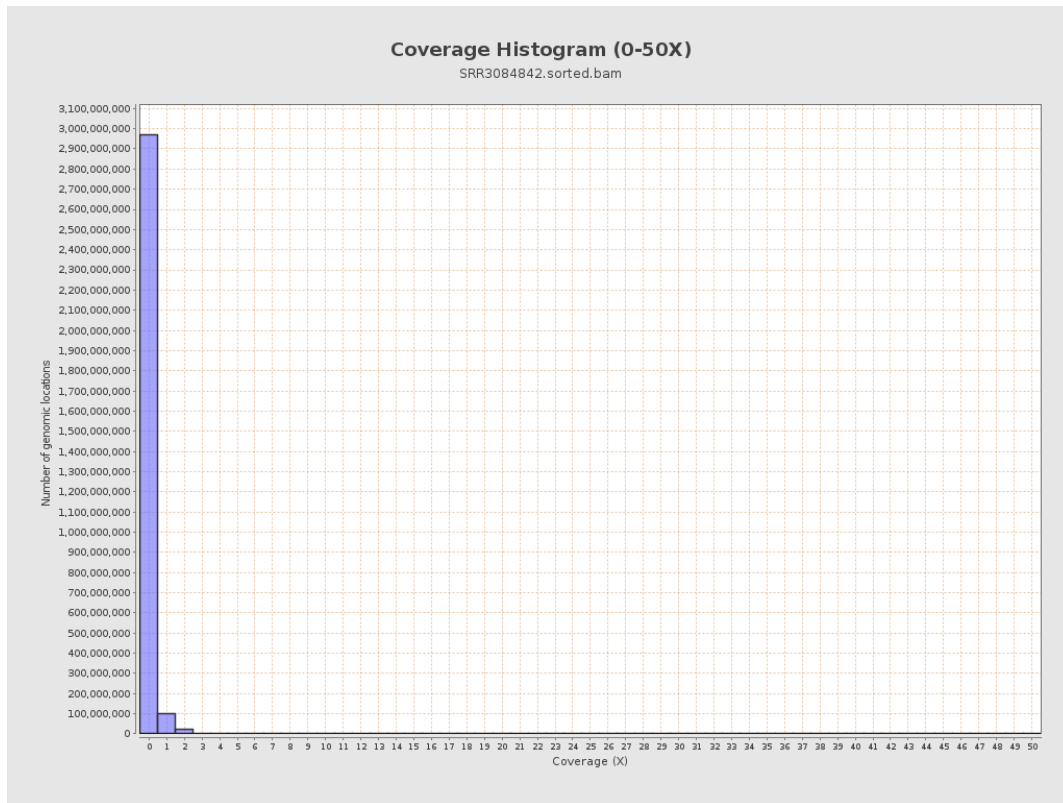
3. Results : Coverage across reference



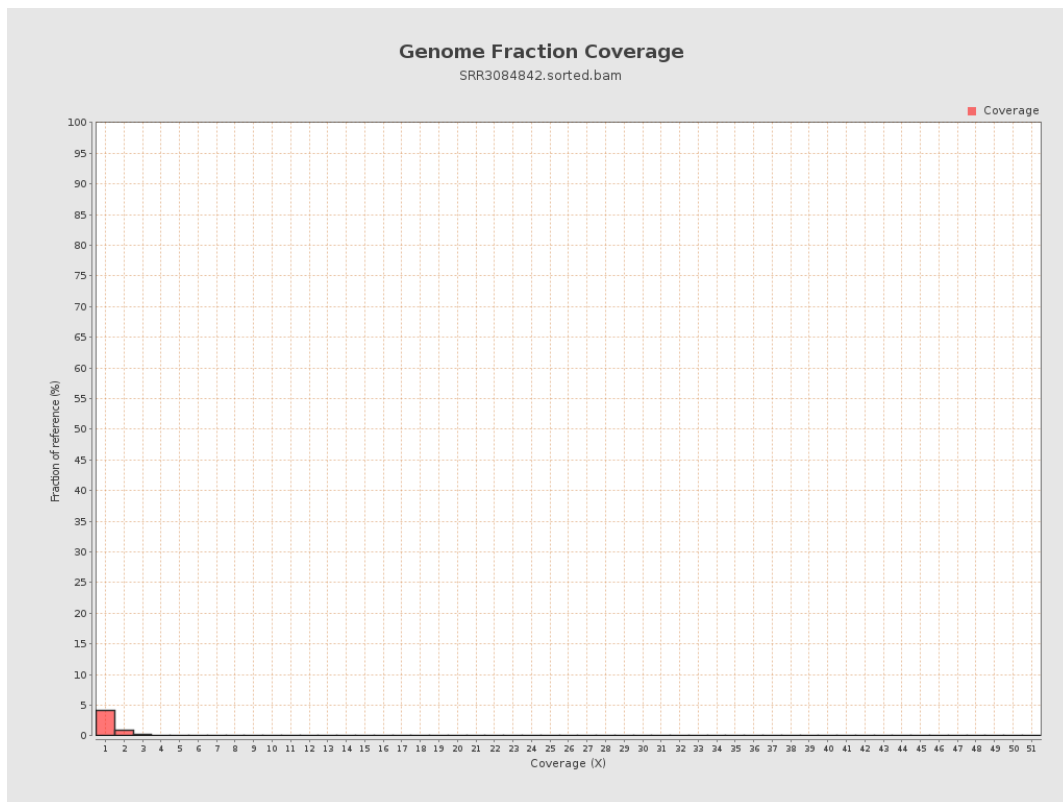
4. Results : Coverage Histogram



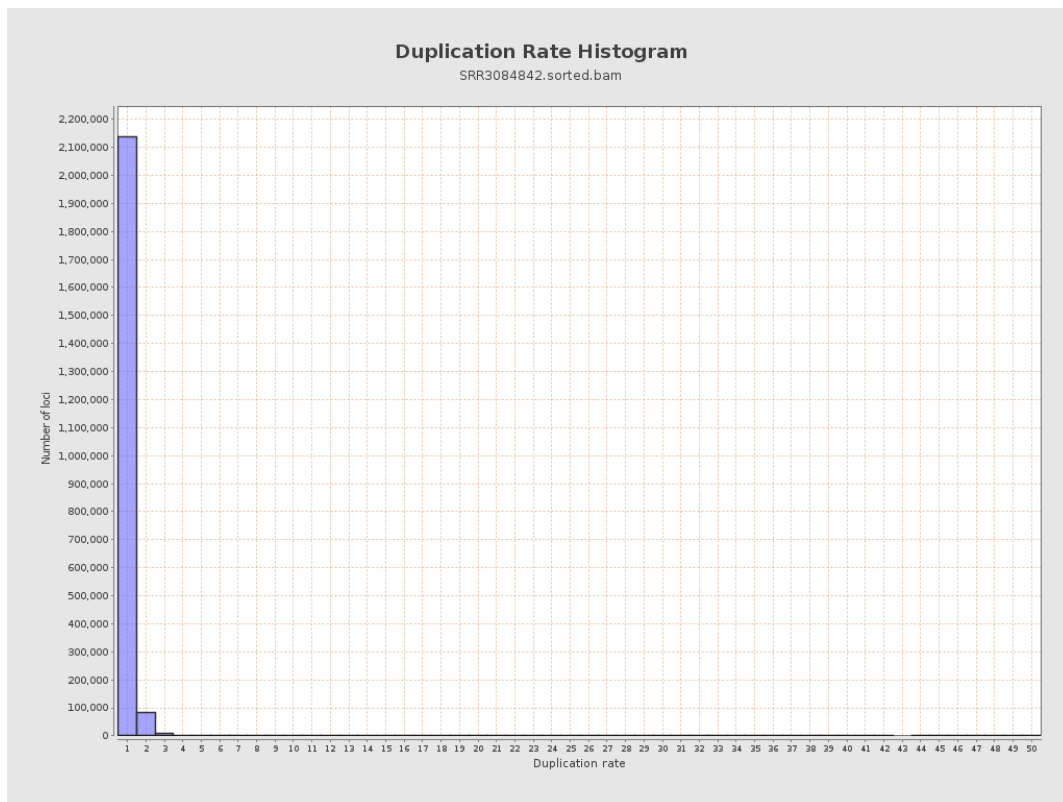
5. Results : Coverage Histogram (0-50X)



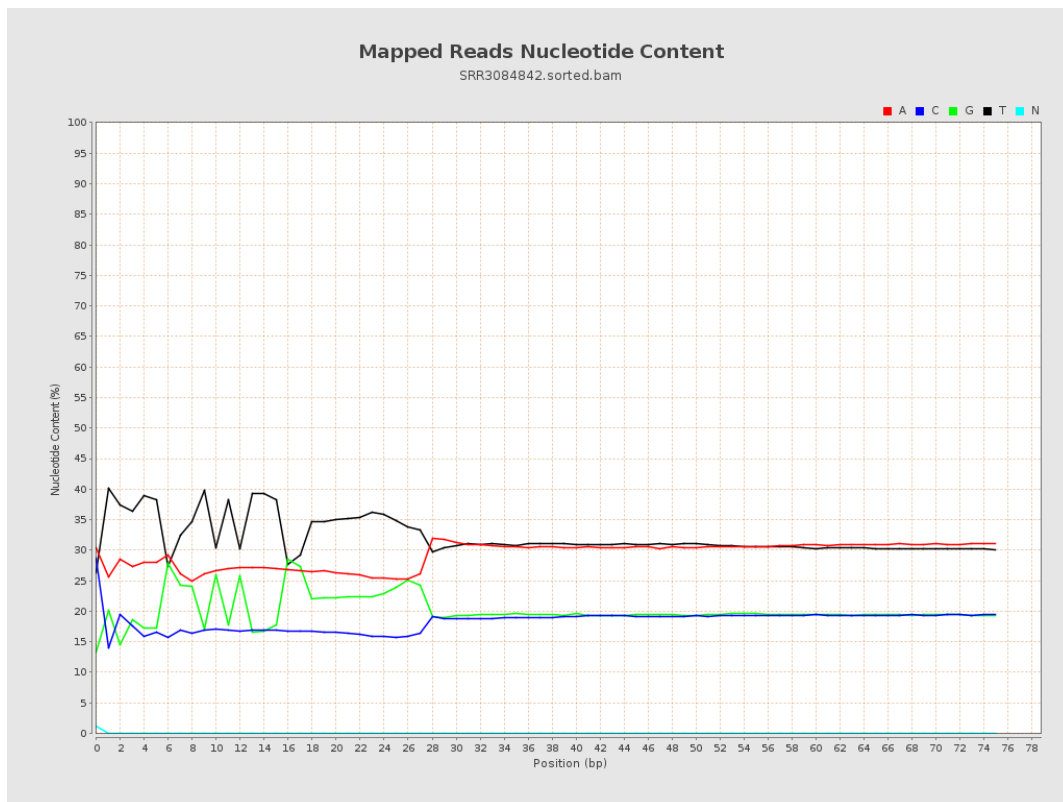
6. Results : Genome Fraction Coverage



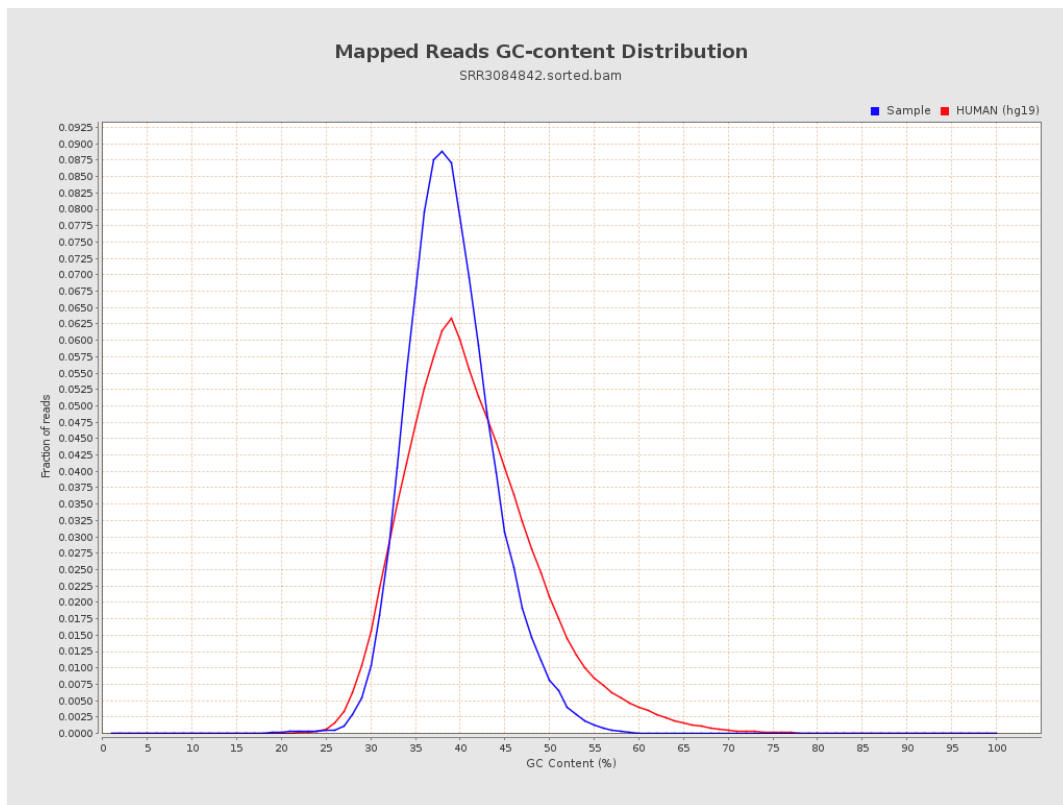
7. Results : Duplication Rate Histogram



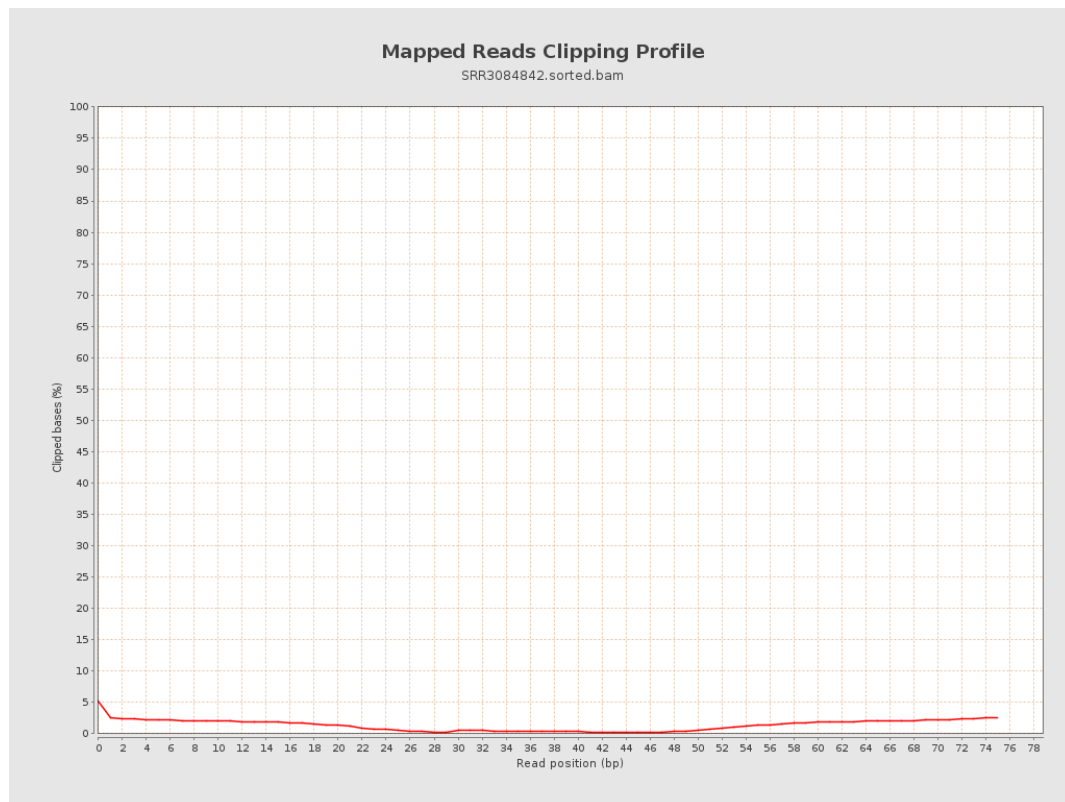
8. Results : Mapped Reads Nucleotide Content



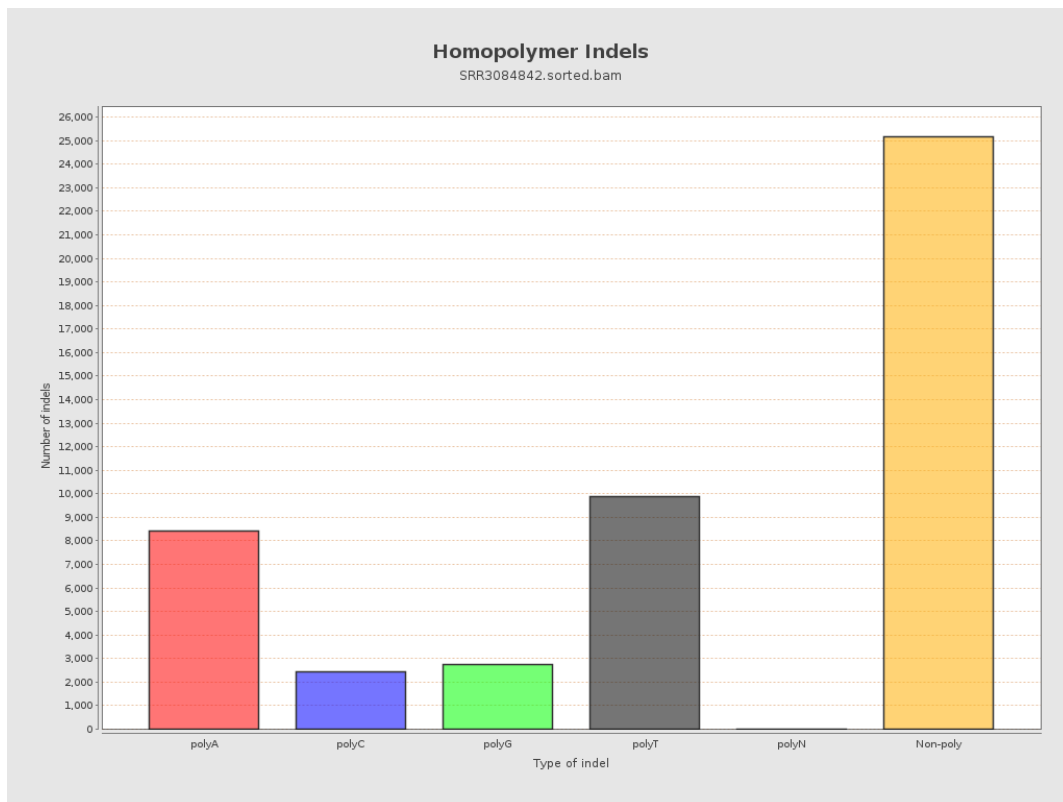
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

