

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 18:19:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081055.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_SRR3081055 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081055.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 18:19:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081055.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,001,546
Mapped reads	2,740,104 / 91.29%
Unmapped reads	261,442 / 8.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,484 / 0.95%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	137,735 / 4.59%
Duplication rate	3.5%
Clipped reads	1,344,427 / 44.79%

2.2. ACGT Content

Number/percentage of A's	49,212,915 / 27.11%
Number/percentage of C's	34,510,316 / 19.01%
Number/percentage of T's	55,401,114 / 30.52%
Number/percentage of G's	42,376,897 / 23.35%
Number/percentage of N's	1,928 / 0%
GC Percentage	42.36%

2.3. Coverage

Mean	0.0587

Standard Deviation	0.6042
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2.4. Mapping Quality

Mean Mapping Quality	43.58
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2.5. Mismatches and indels

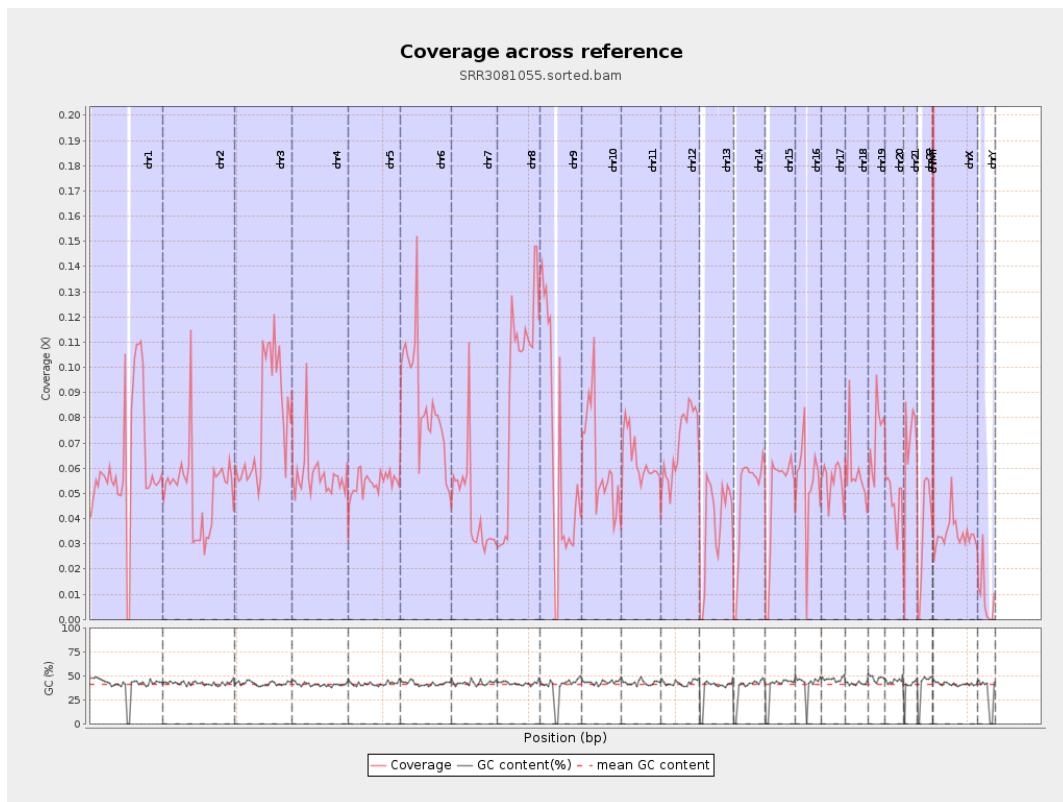
General error rate	0.91%
Mismatches	1,627,250
Insertions	15,198
Mapped reads with at least one insertion	0.55%
Deletions	40,447
Mapped reads with at least one deletion	1.46%
Homopolymer indels	45.98%

2.6. Chromosome stats

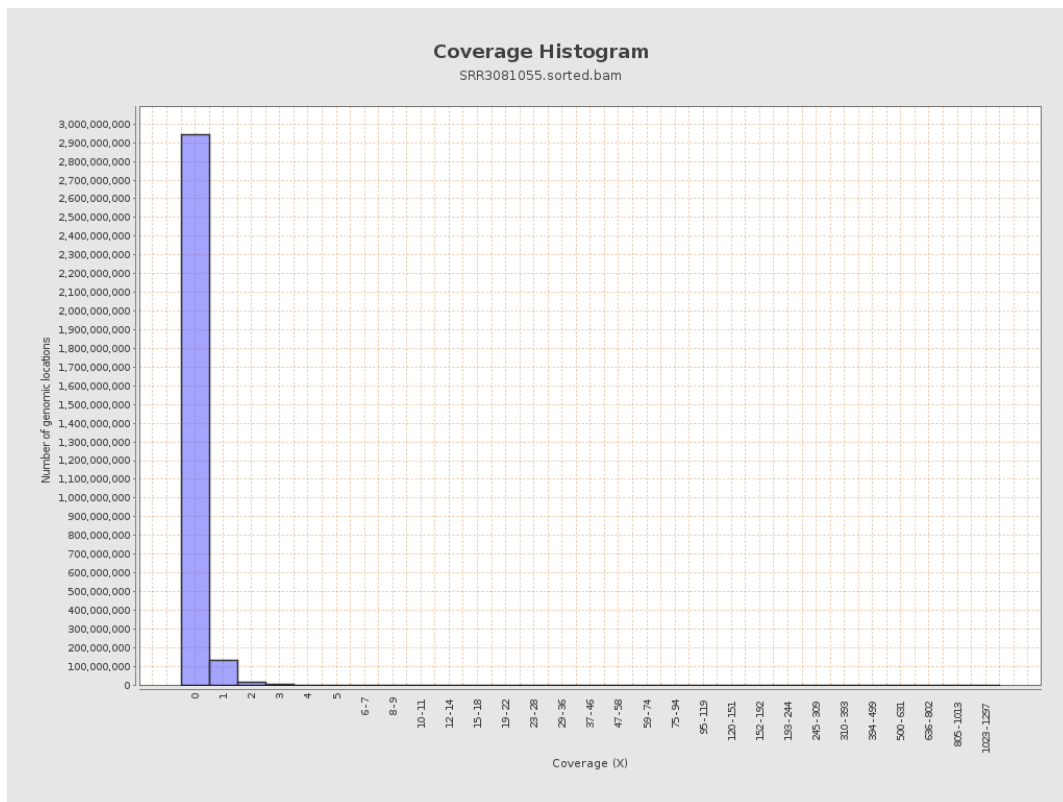
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	15265808	0.0612	1.0782
chr2	243199373	12507859	0.0514	0.6588
chr3	198022430	15284026	0.0772	0.3244
chr4	191154276	10964437	0.0574	0.3321
chr5	180915260	9817316	0.0543	0.2777
chr6	171115067	14731762	0.0861	0.5914
chr7	159138663	7004955	0.044	0.8541

chr8	146364022	13658007	0.0933	0.5662
chr9	141213431	8989214	0.0637	0.7593
chr10	135534747	8399305	0.062	0.5415
chr11	135006516	8544478	0.0633	0.4502
chr12	133851895	9357633	0.0699	0.336
chr13	115169878	4404858	0.0382	0.2238
chr14	107349540	5253661	0.0489	0.4111
chr15	102531392	4972948	0.0485	0.2684
chr16	90354753	4818845	0.0533	0.4434
chr17	81195210	4511376	0.0556	0.2892
chr18	78077248	4556415	0.0584	1.4253
chr19	59128983	4271086	0.0722	0.7937
chr20	63025520	3002796	0.0476	0.284
chr21	48129895	3313454	0.0688	0.4137
chr22	51304566	1839942	0.0359	0.214
chrMT	16571	311052	18.7709	9.7786
chrX	155270560	5259232	0.0339	0.2931
chrY	59373566	531522	0.009	0.2412

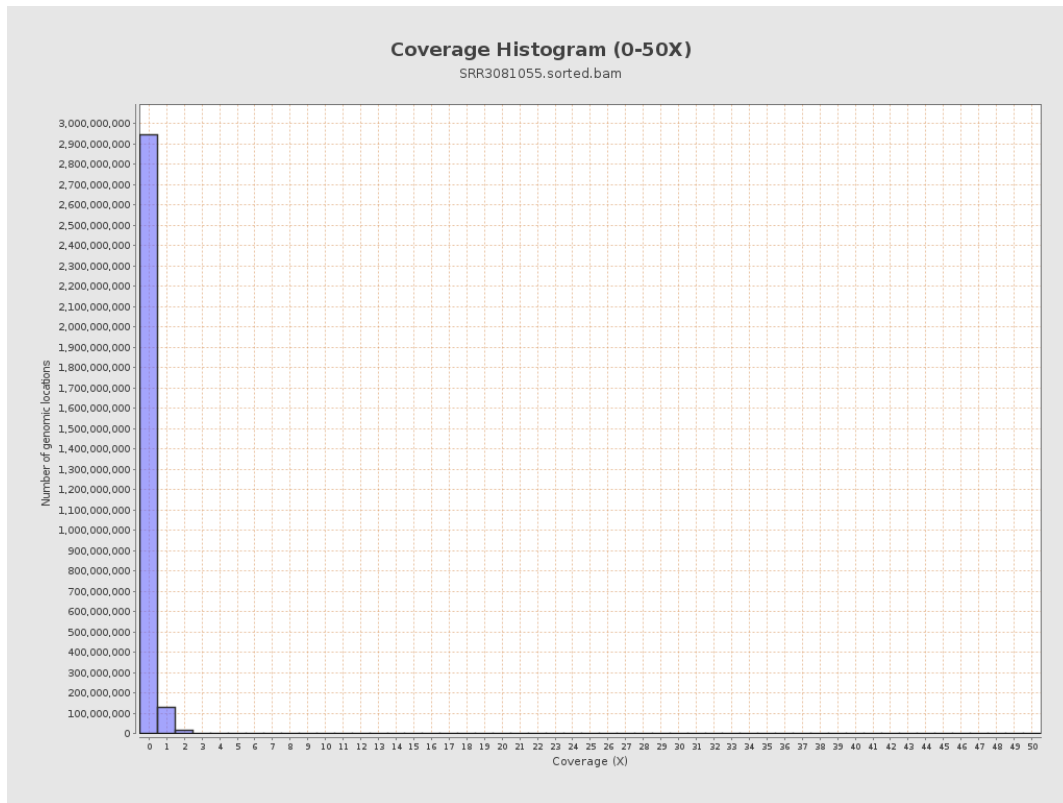
3. Results : Coverage across reference



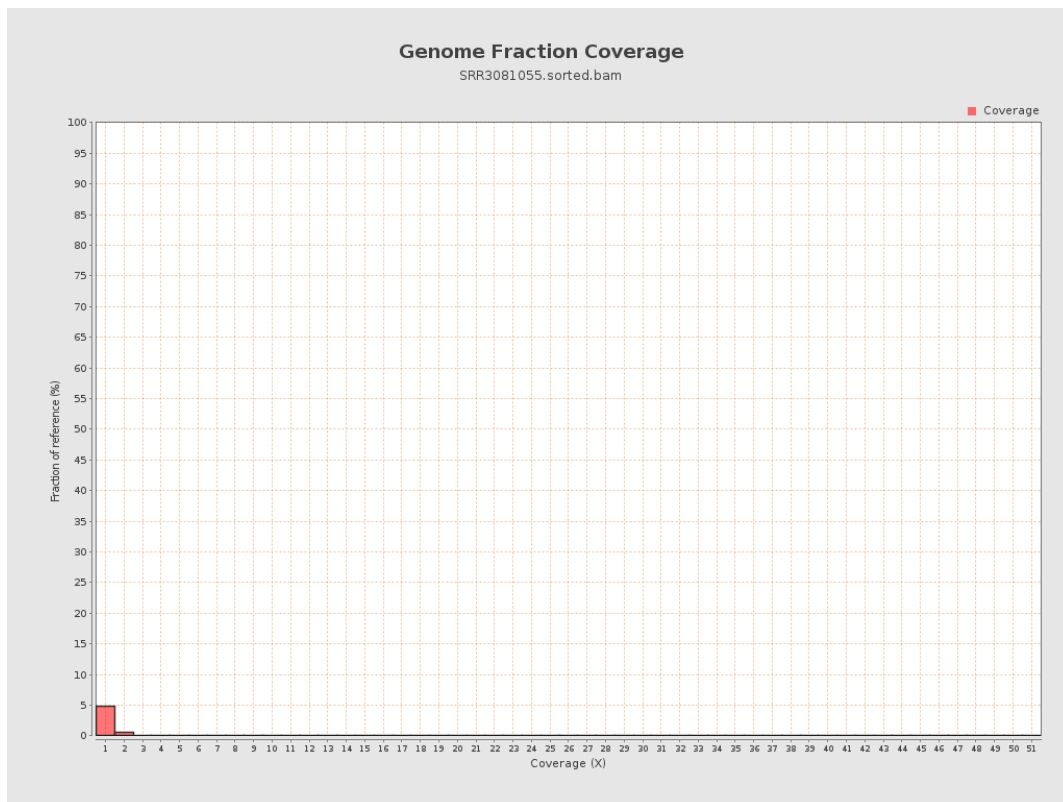
4. Results : Coverage Histogram



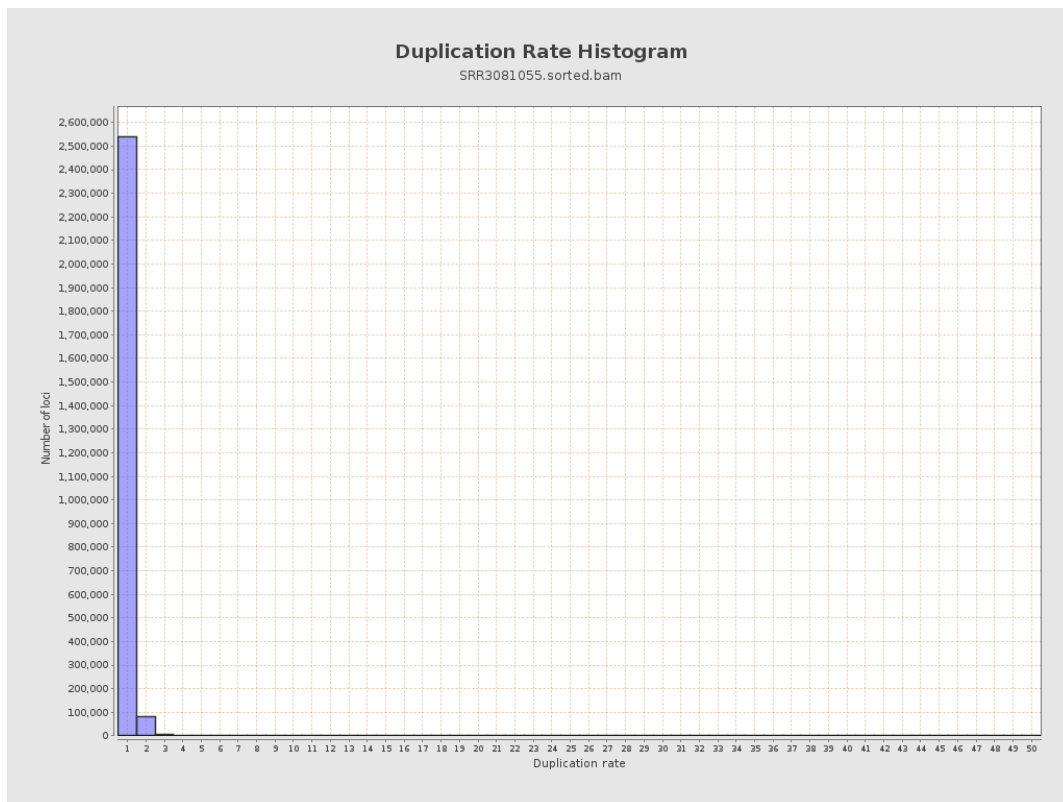
5. Results : Coverage Histogram (0-50X)



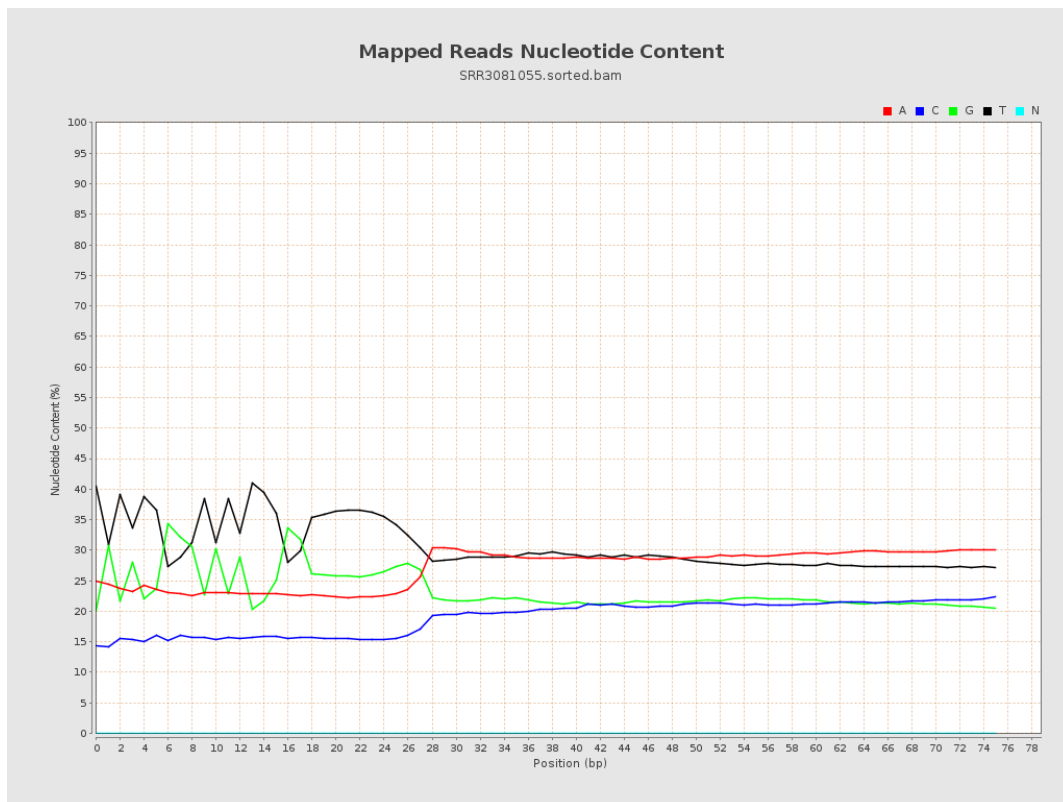
6. Results : Genome Fraction Coverage



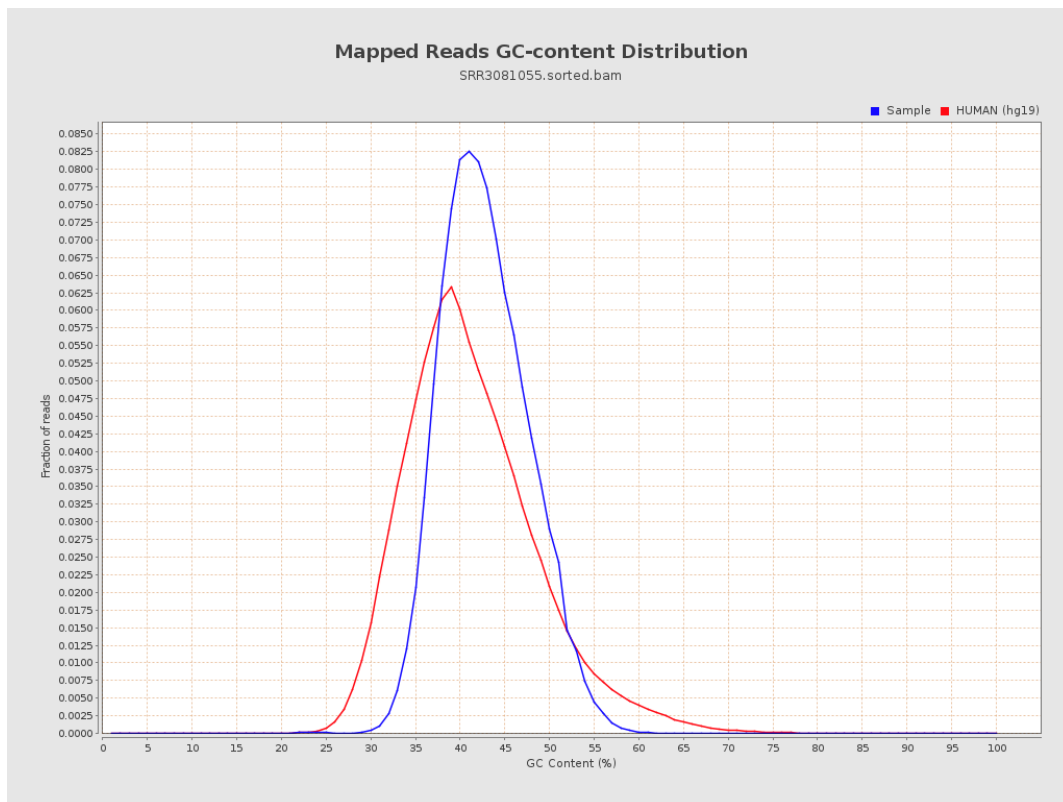
7. Results : Duplication Rate Histogram



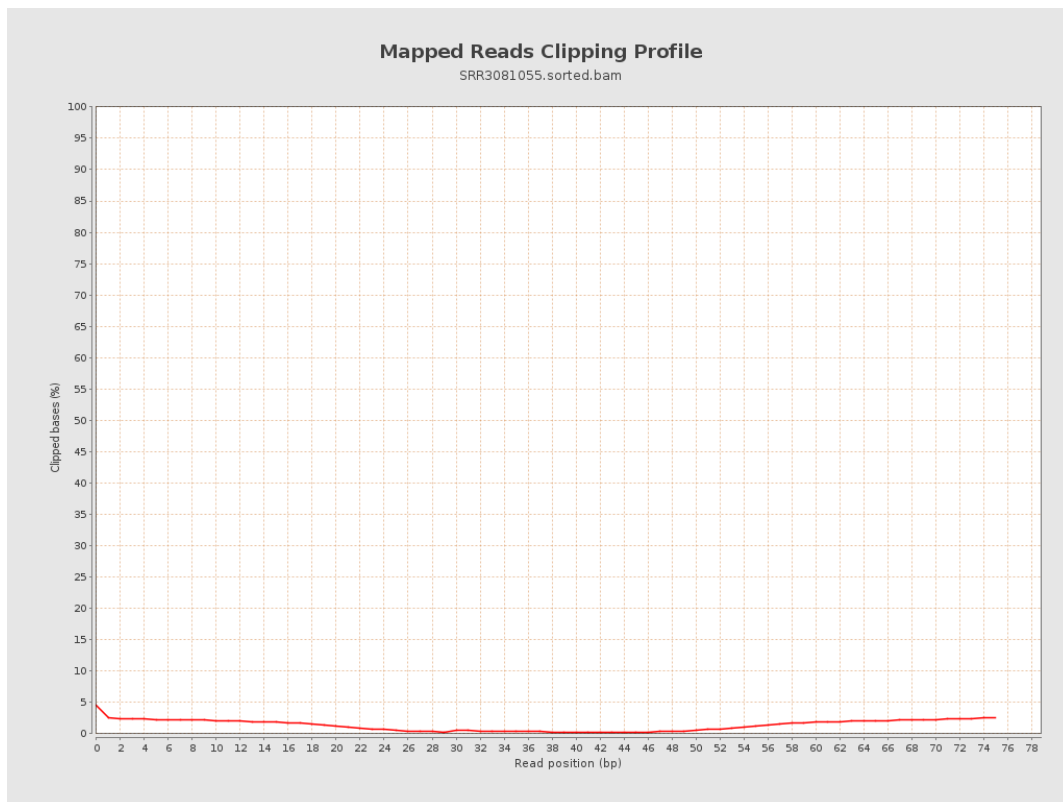
8. Results : Mapped Reads Nucleotide Content



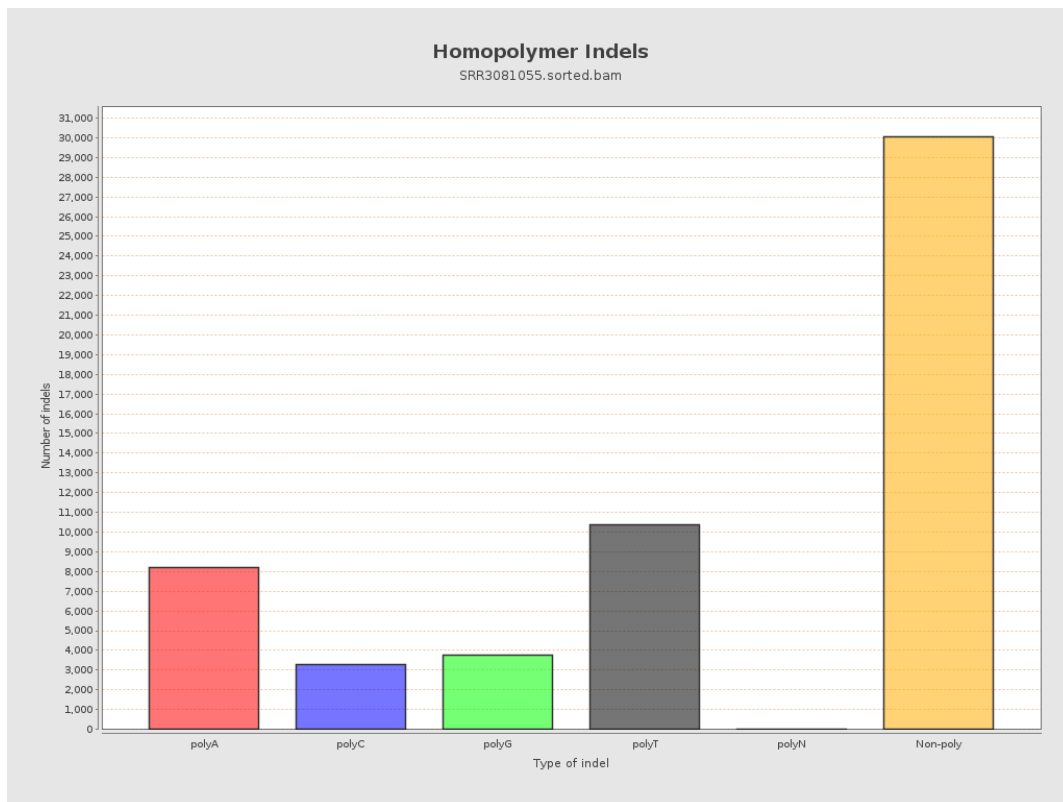
9. Results : Mapped Reads GC-content Distribution



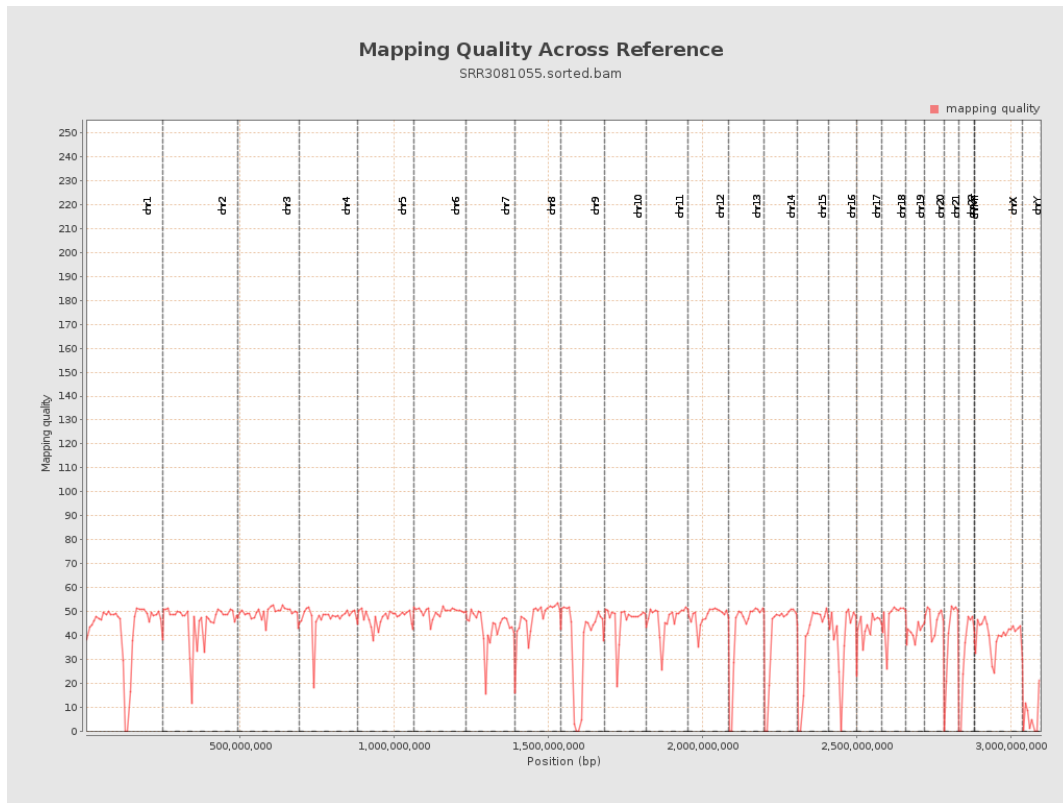
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

