

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 16:10:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2971299.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_SRR2971299 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2971299.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 16:10:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2971299.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,241,900
Mapped reads	8,659,048 / 84.55%
Unmapped reads	1,582,852 / 15.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	1,450,953 / 14.17%
Duplication rate	15.28%
Clipped reads	1,008,381 / 9.85%

2.2. ACGT Content

Number/percentage of A's	96,250,295 / 28.28%
Number/percentage of C's	71,227,500 / 20.93%
Number/percentage of T's	99,521,418 / 29.24%
Number/percentage of G's	73,373,068 / 21.56%
Number/percentage of N's	2,616 / 0%
GC Percentage	42.48%

2.3. Coverage

Mean	0.11
Standard Deviation	1.0481

2.4. Mapping Quality

Mean Mapping Quality	35.71
----------------------	-------

2.5. Mismatches and indels

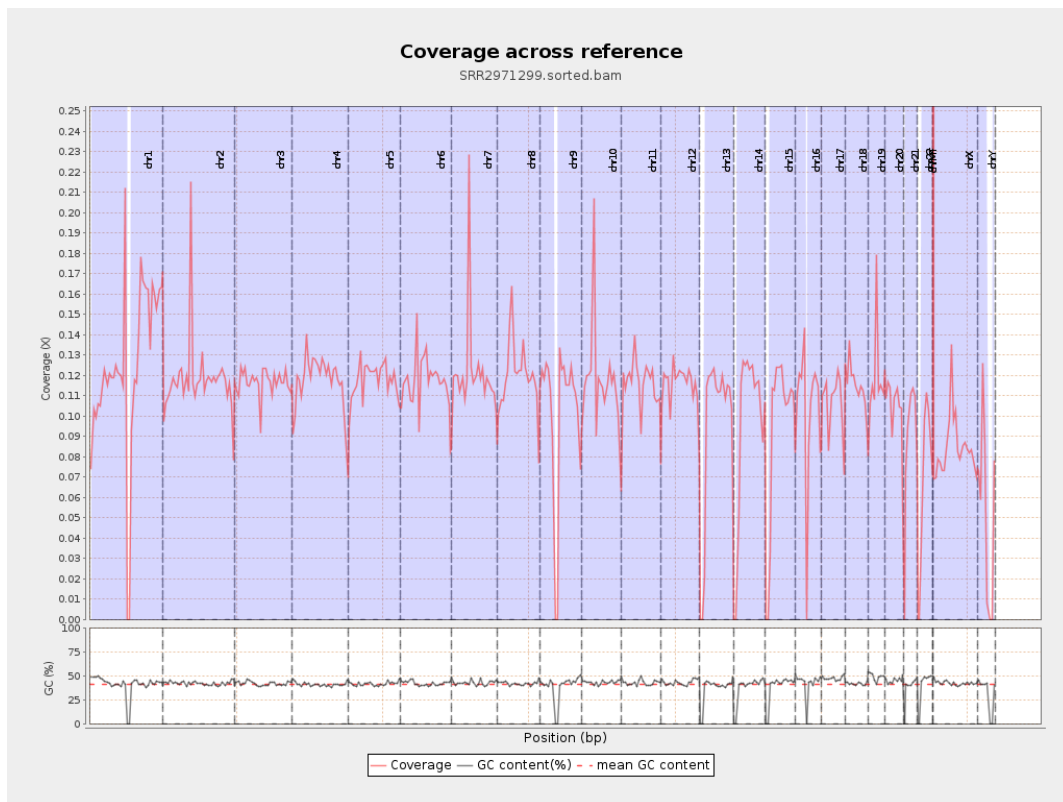
General error rate	0.34%
Mismatches	1,148,009
Insertions	13,888
Mapped reads with at least one insertion	0.16%
Deletions	28,116
Mapped reads with at least one deletion	0.32%
Homopolymer indels	37.53%

2.6. Chromosome stats

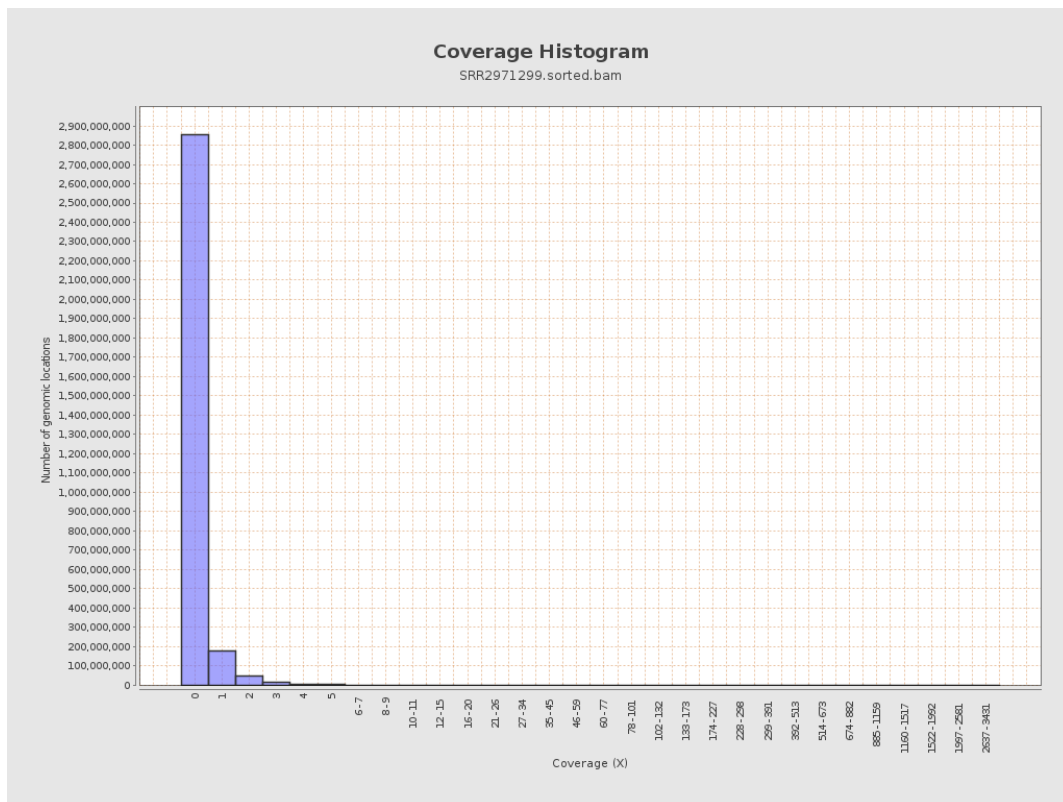
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	30974225	0.1243	2.2873
chr2	243199373	28732565	0.1181	0.8908
chr3	198022430	23108148	0.1167	0.4614
chr4	191154276	22455716	0.1175	0.4962
chr5	180915260	21215969	0.1173	0.4903
chr6	171115067	20130388	0.1176	0.5902
chr7	159138663	19263092	0.121	1.258
chr8	146364022	17569536	0.12	1.7316

chr9	141213431	14386238	0.1019	0.8807
chr10	135534747	15939786	0.1176	0.919
chr11	135006516	15644215	0.1159	0.7527
chr12	133851895	15535943	0.1161	0.4941
chr13	115169878	10939291	0.095	0.4039
chr14	107349540	10398173	0.0969	0.5267
chr15	102531392	9437322	0.092	0.4014
chr16	90354753	9121385	0.101	0.5031
chr17	81195210	8755096	0.1078	0.4789
chr18	78077248	9028945	0.1156	1.7245
chr19	59128983	7039675	0.1191	2.0539
chr20	63025520	6614187	0.1049	0.4922
chr21	48129895	4260431	0.0885	0.5036
chr22	51304566	3530220	0.0688	0.4065
chrMT	16571	49732	3.0011	3.2365
chrX	155270560	13133301	0.0846	0.5652
chrY	59373566	3145896	0.053	0.459

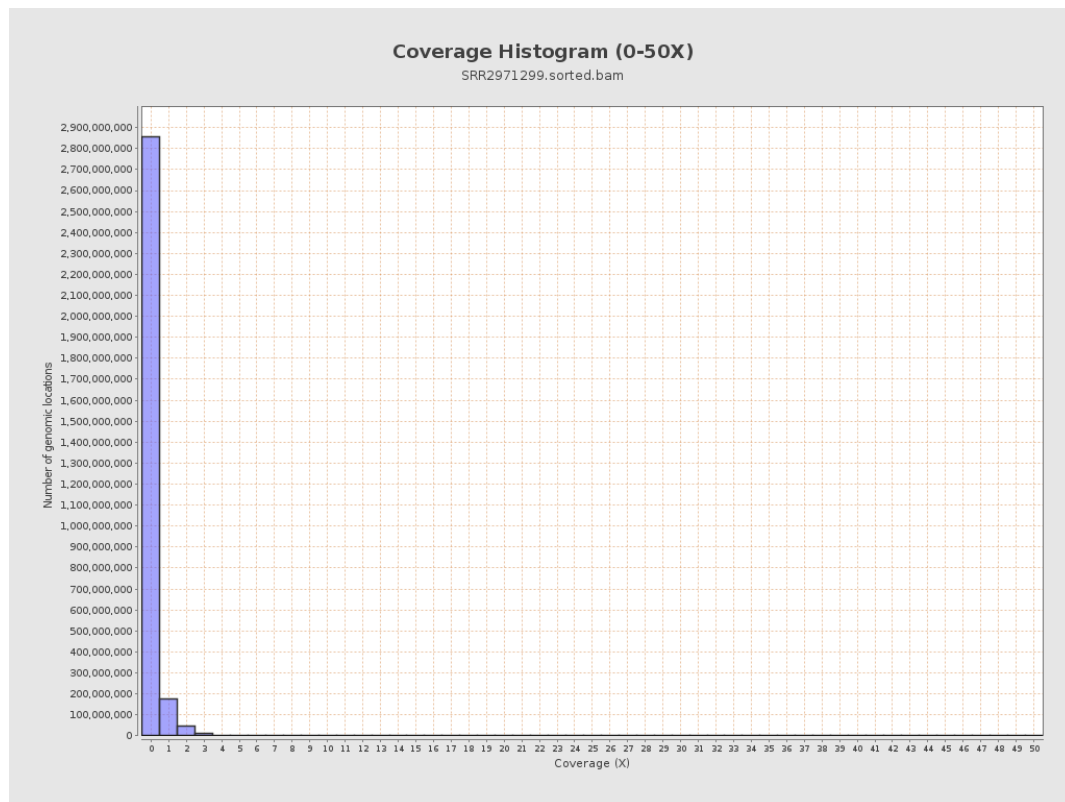
3. Results : Coverage across reference



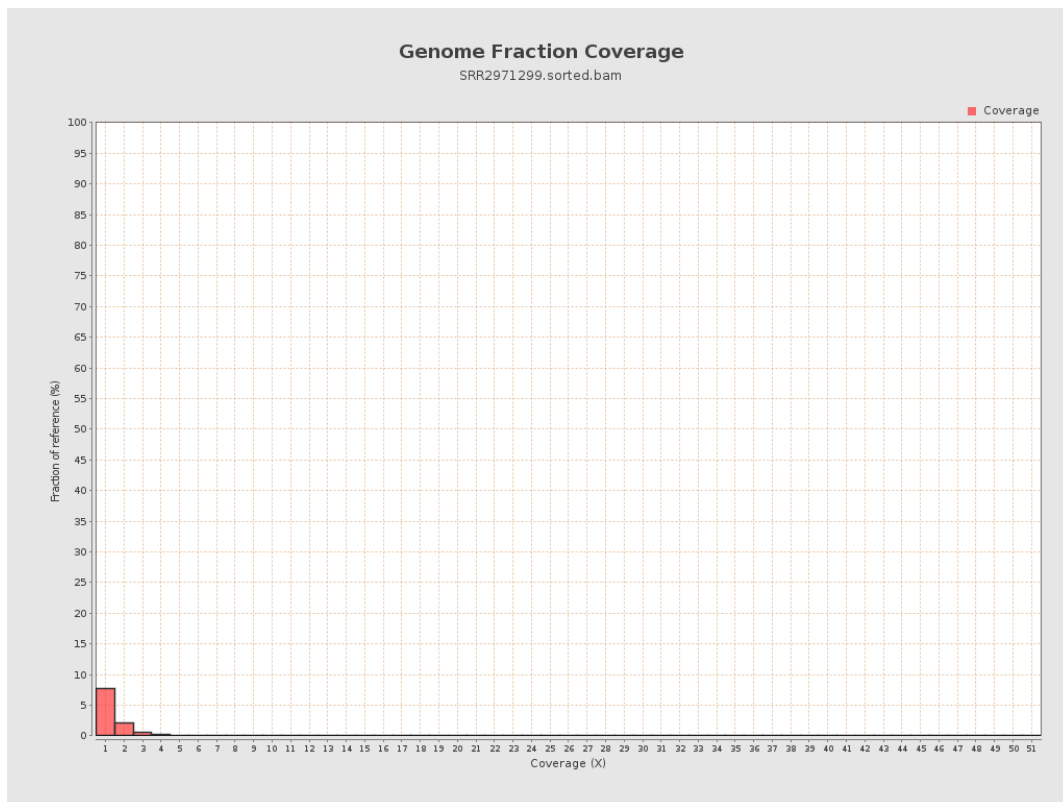
4. Results : Coverage Histogram



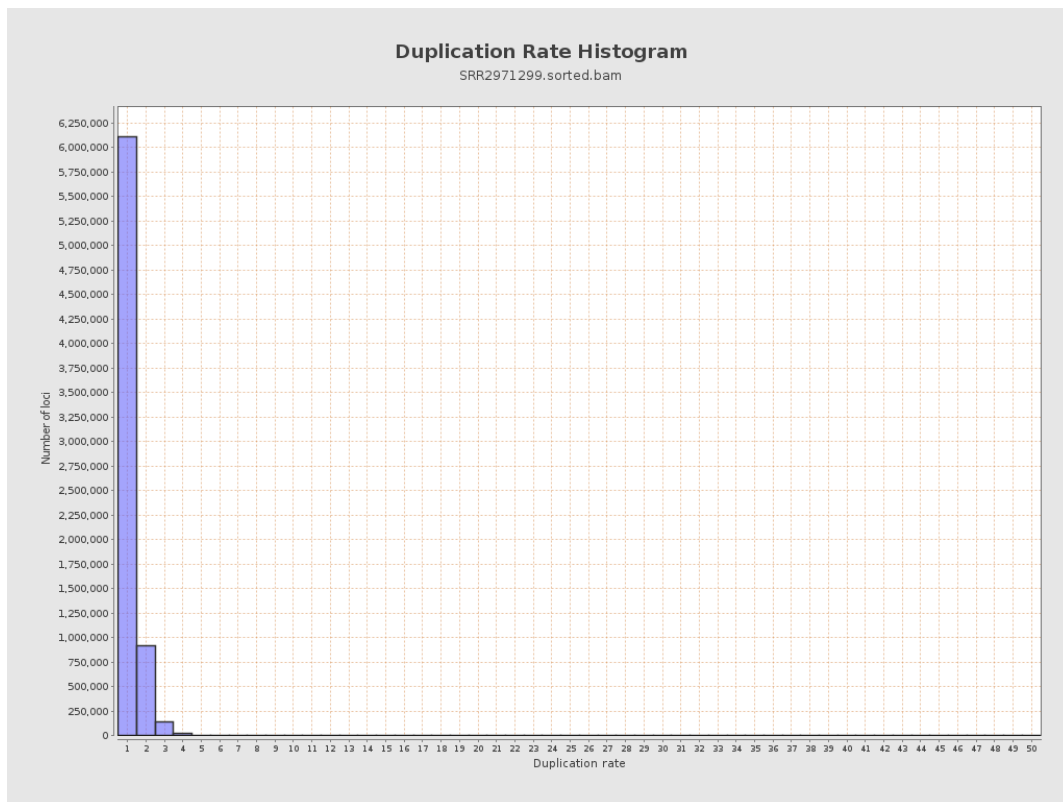
5. Results : Coverage Histogram (0-50X)



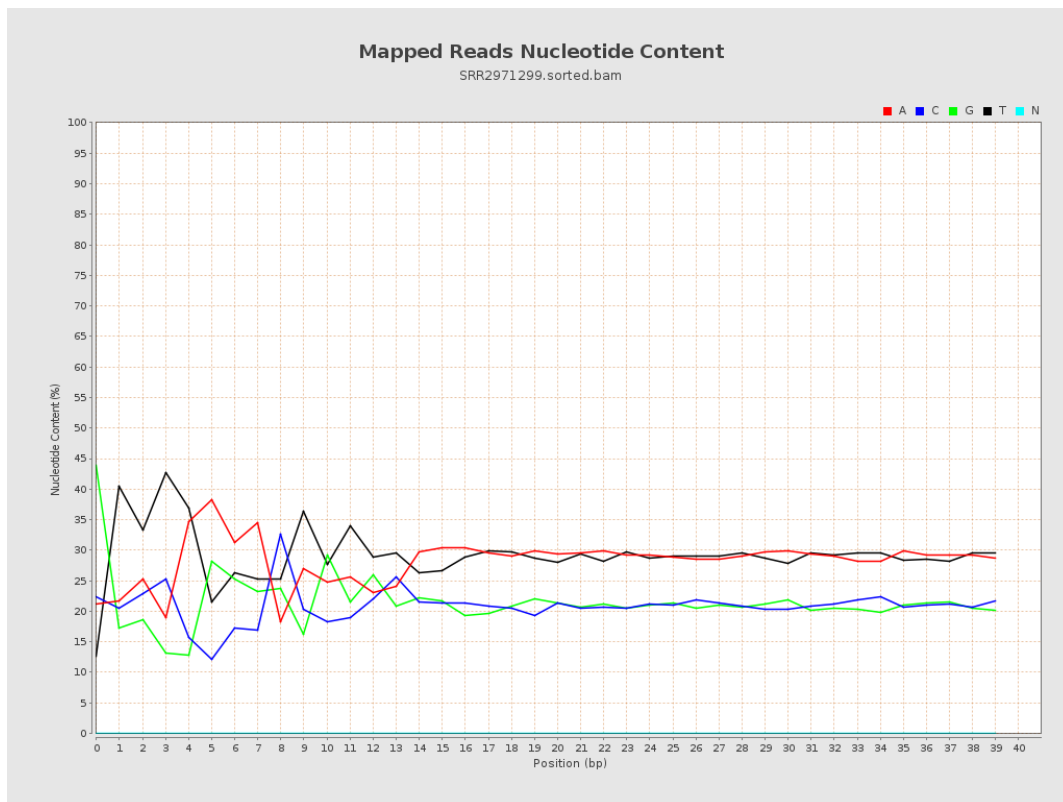
6. Results : Genome Fraction Coverage



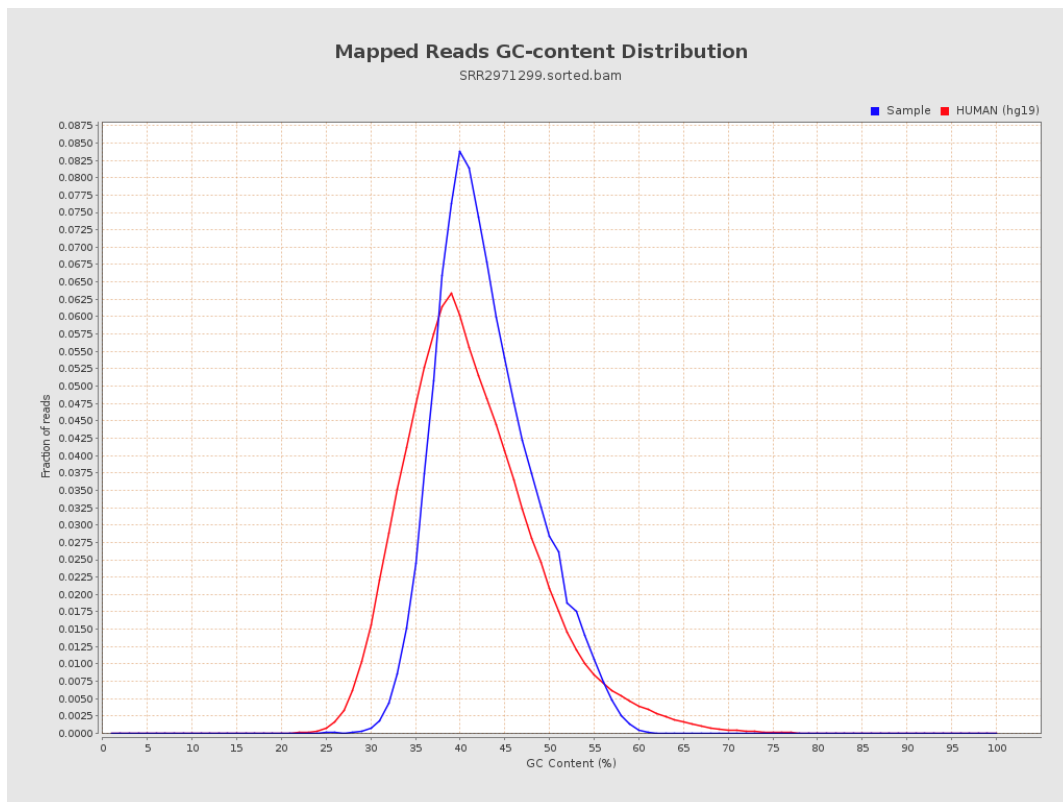
7. Results : Duplication Rate Histogram



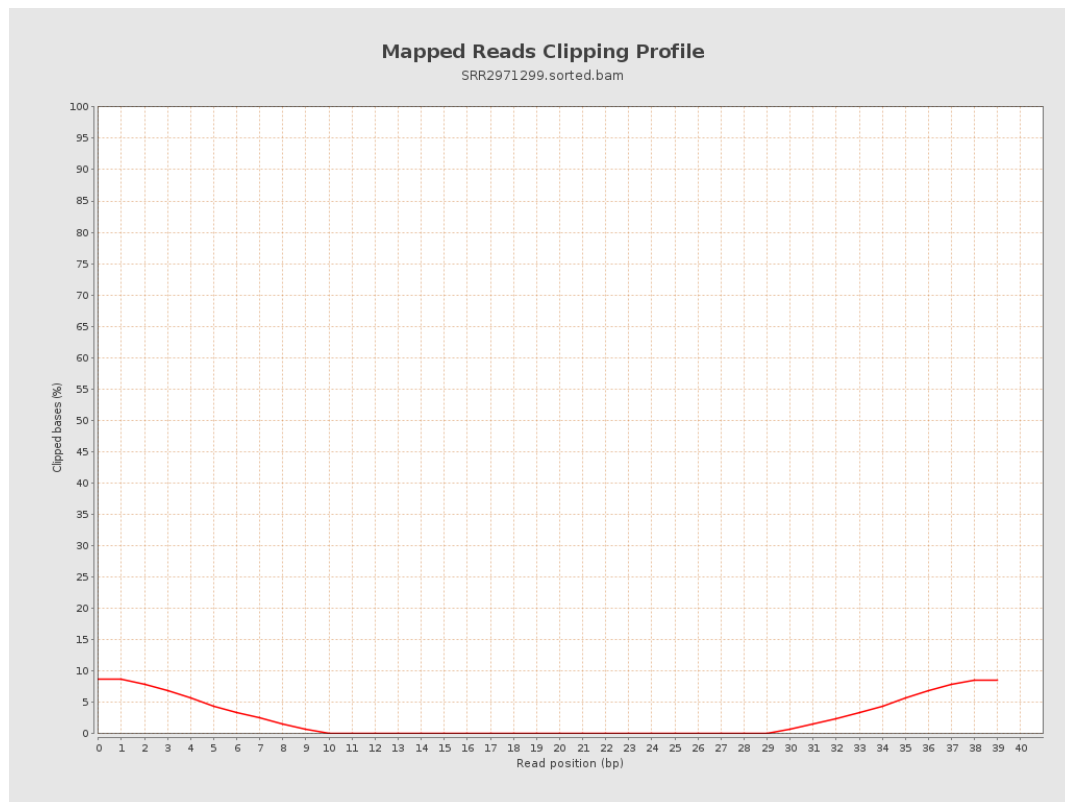
8. Results : Mapped Reads Nucleotide Content



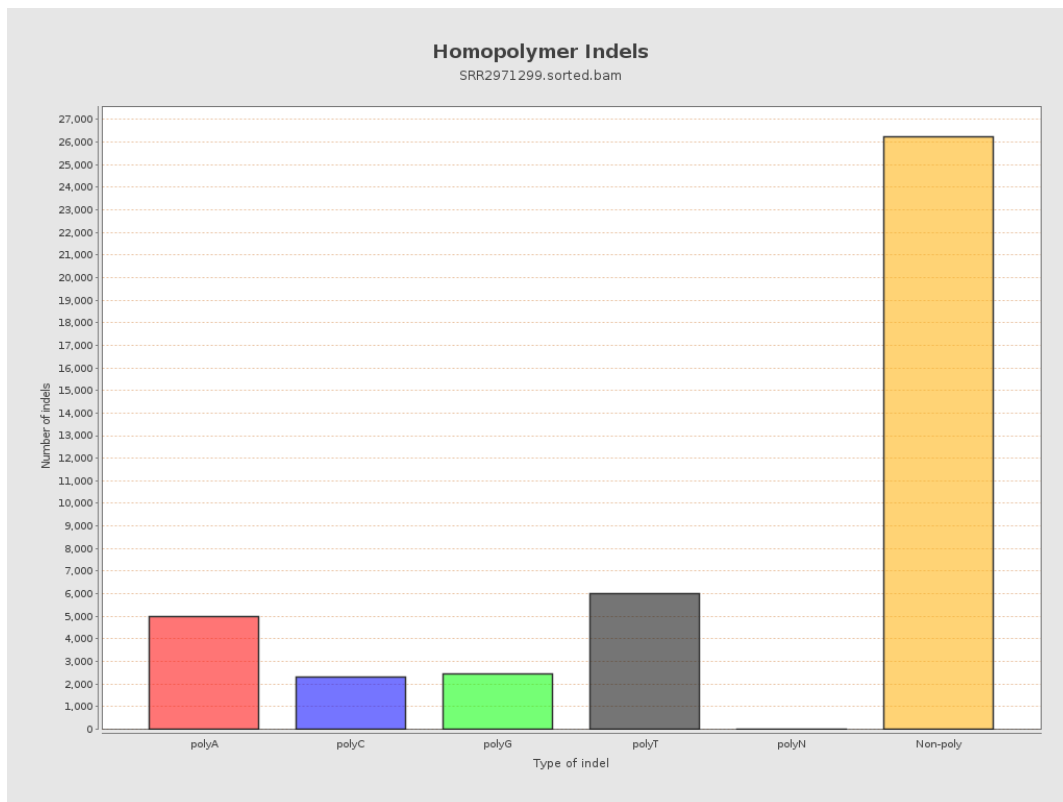
9. Results : Mapped Reads GC-content Distribution



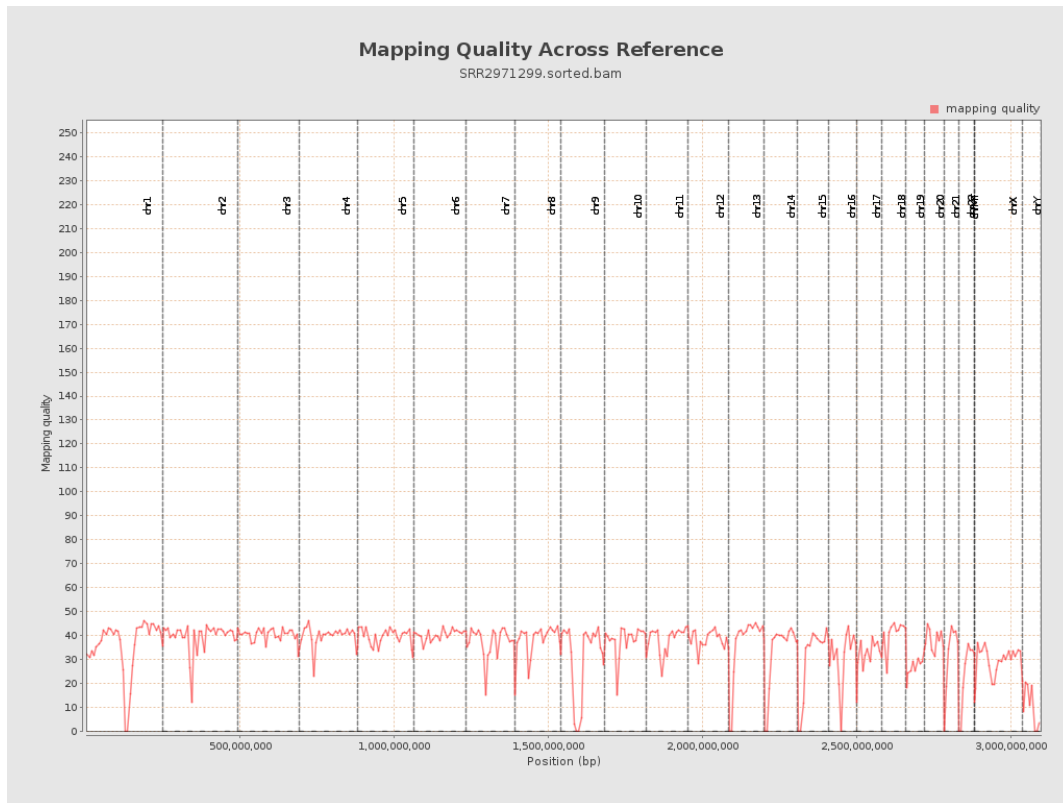
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

