

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 11:57:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234044.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_SRR6234044 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234044.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 11:57:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234044.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,836,118
Mapped reads	276,277 / 15.05%
Unmapped reads	1,559,841 / 84.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,717 / 0.09%
Read min/max/mean length	30 / 76 / 76.03
Duplicated reads (estimated)	29,938 / 1.63%
Duplication rate	5.13%
Clipped reads	130,031 / 7.08%

2.2. ACGT Content

Number/percentage of A's	4,725,962 / 25.91%
Number/percentage of C's	3,403,746 / 18.66%
Number/percentage of T's	6,059,492 / 33.22%
Number/percentage of G's	4,049,477 / 22.2%
Number/percentage of N's	1,167 / 0.01%
GC Percentage	40.86%

2.3. Coverage

Mean	0.0059

Standard Deviation	0.4124
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	42.45
----------------------	-------

2.5. Mismatches and indels

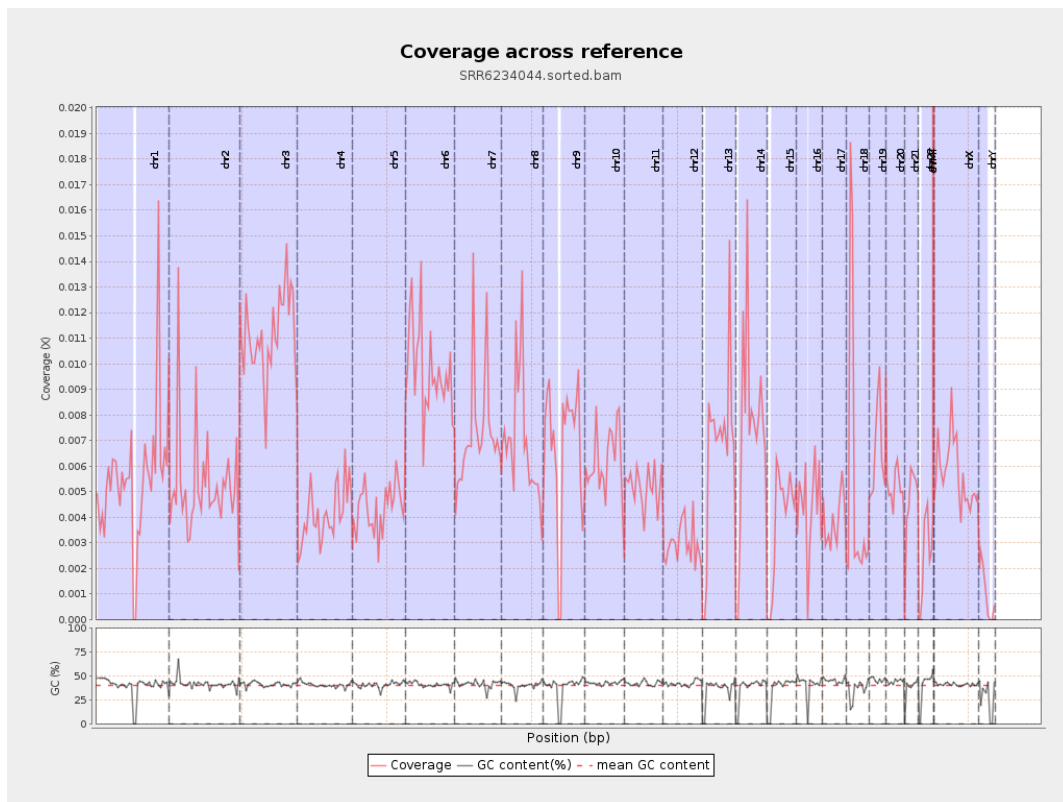
General error rate	1.08%
Mismatches	194,301
Insertions	1,479
Mapped reads with at least one insertion	0.53%
Deletions	4,530
Mapped reads with at least one deletion	1.62%
Homopolymer indels	42.85%

2.6. Chromosome stats

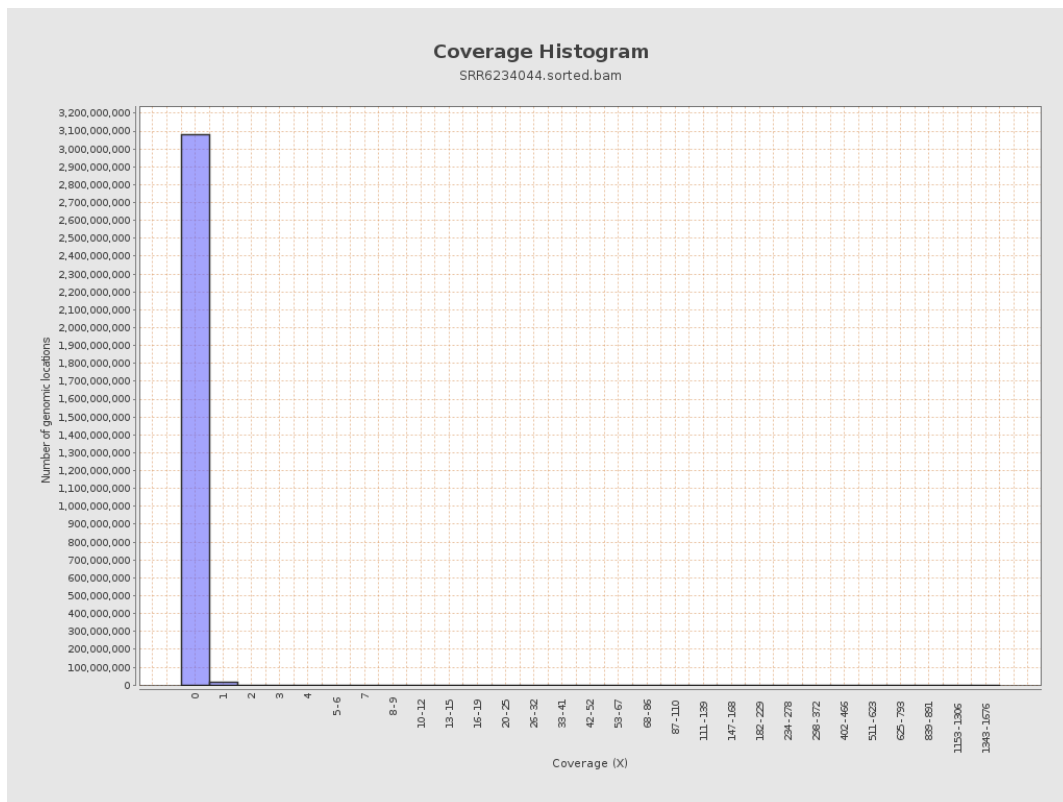
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	1351090	0.0054	0.1472
chr2	243199373	1276034	0.0052	0.4261
chr3	198022430	2212166	0.0112	0.205
chr4	191154276	784755	0.0041	0.1134
chr5	180915260	790874	0.0044	0.1273
chr6	171115067	1661800	0.0097	0.2694
chr7	159138663	1164627	0.0073	0.448

chr8	146364022	1023400	0.007	0.4587
chr9	141213431	950982	0.0067	0.1236
chr10	135534747	841642	0.0062	0.1147
chr11	135006516	694661	0.0051	0.097
chr12	133851895	394119	0.0029	0.114
chr13	115169878	763960	0.0066	0.6119
chr14	107349540	792517	0.0074	0.135
chr15	102531392	396540	0.0039	0.0941
chr16	90354753	395254	0.0044	0.1364
chr17	81195210	316732	0.0039	0.0822
chr18	78077248	419508	0.0054	2.038
chr19	59128983	399097	0.0067	0.1856
chr20	63025520	324153	0.0051	0.098
chr21	48129895	219442	0.0046	0.0922
chr22	51304566	120455	0.0023	0.0799
chrMT	16571	10364	0.6254	1.9259
chrX	155270560	881822	0.0057	0.1001
chrY	59373566	61398	0.001	0.2438

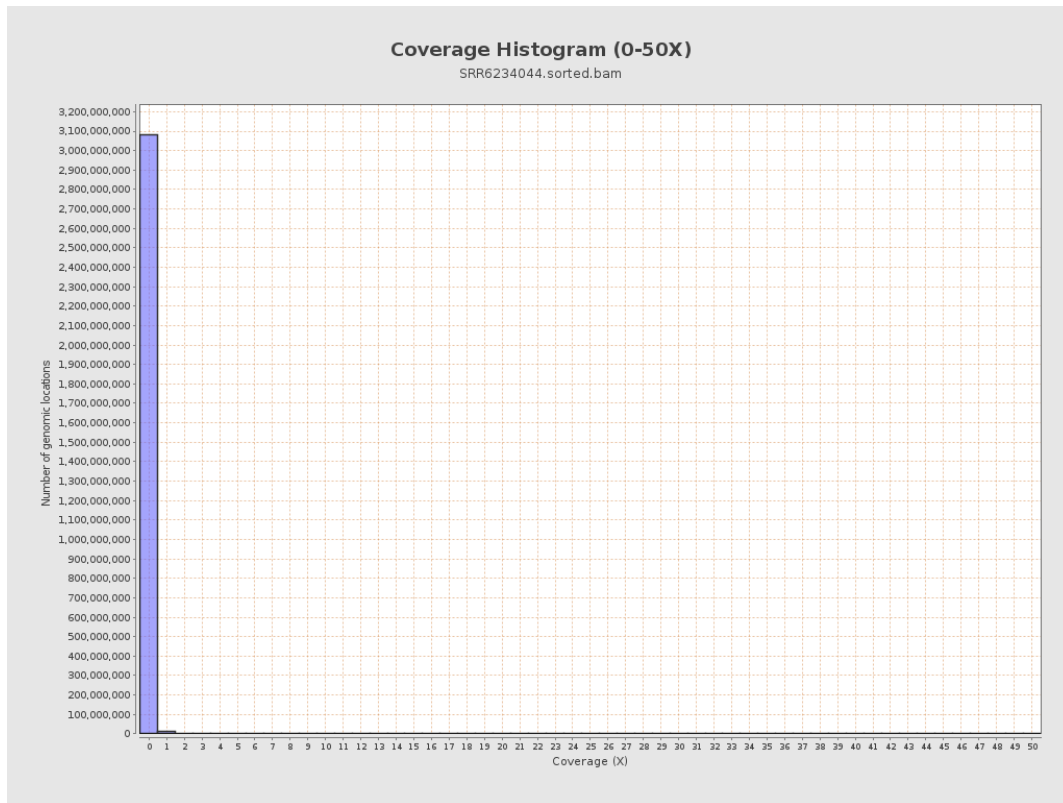
3. Results : Coverage across reference



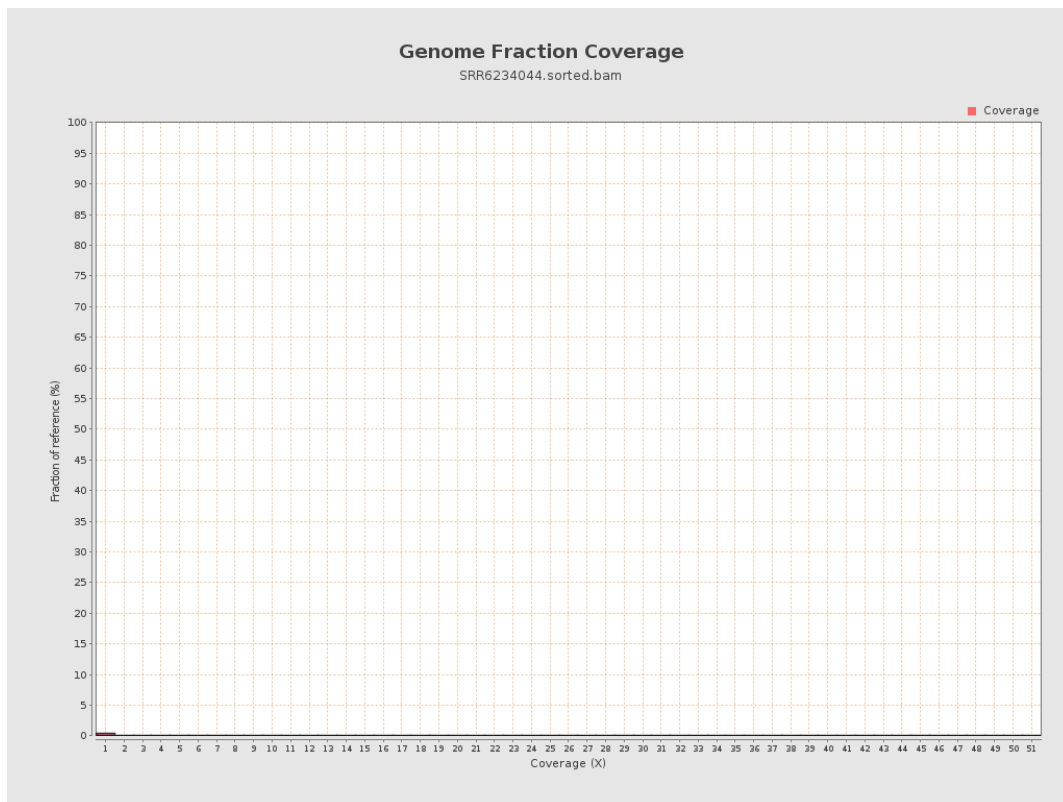
4. Results : Coverage Histogram



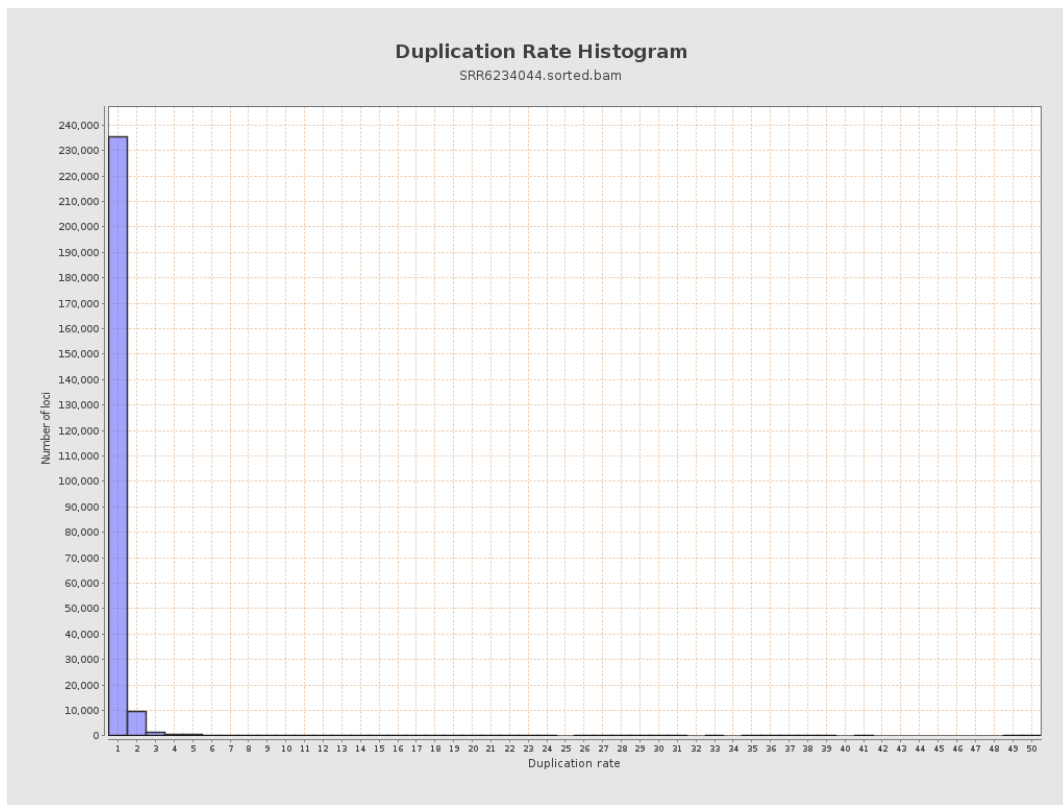
5. Results : Coverage Histogram (0-50X)



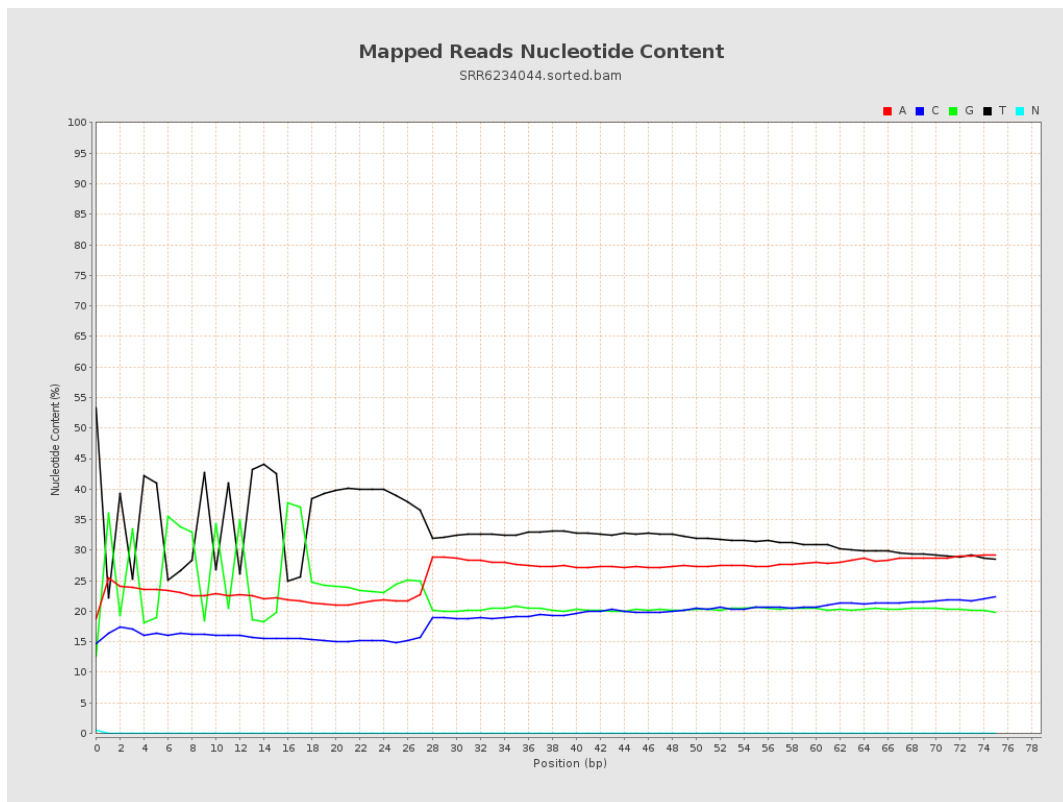
6. Results : Genome Fraction Coverage



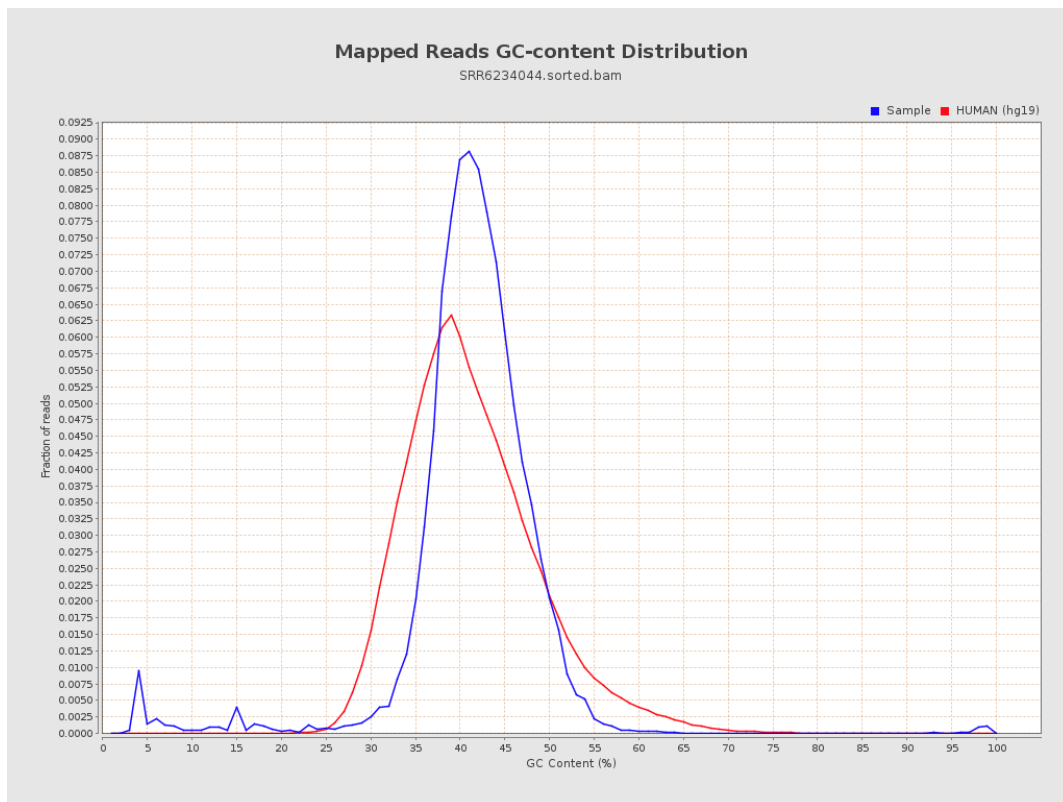
7. Results : Duplication Rate Histogram



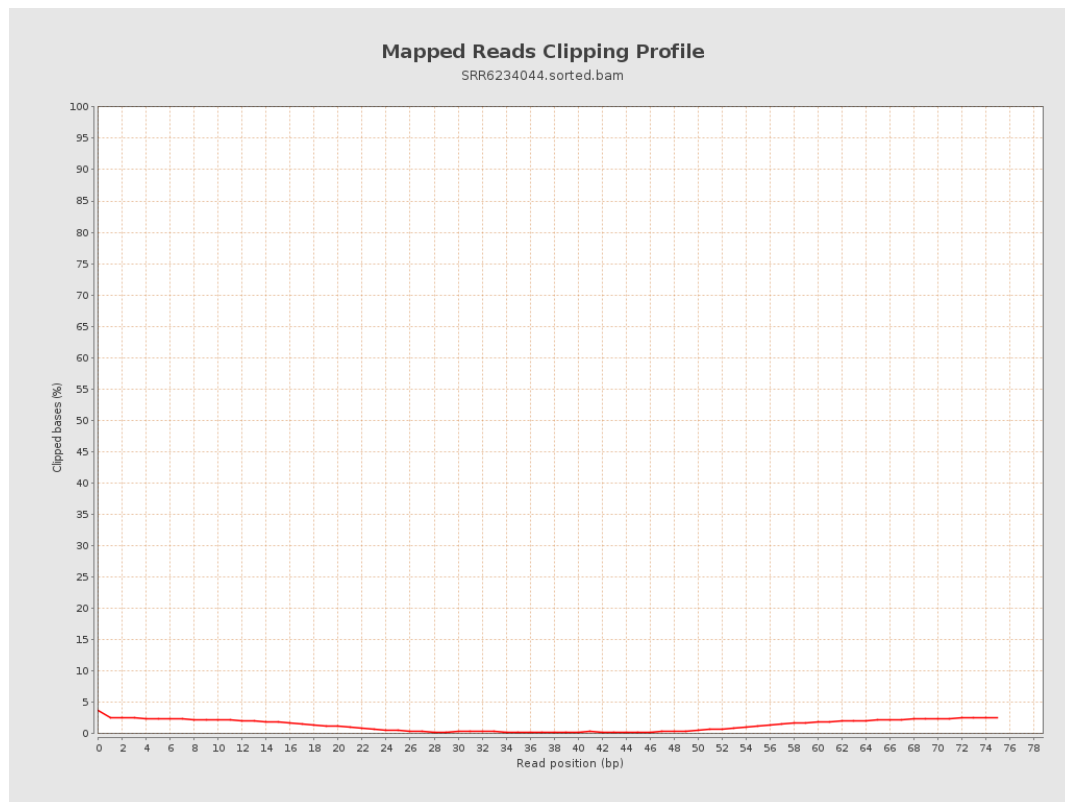
8. Results : Mapped Reads Nucleotide Content



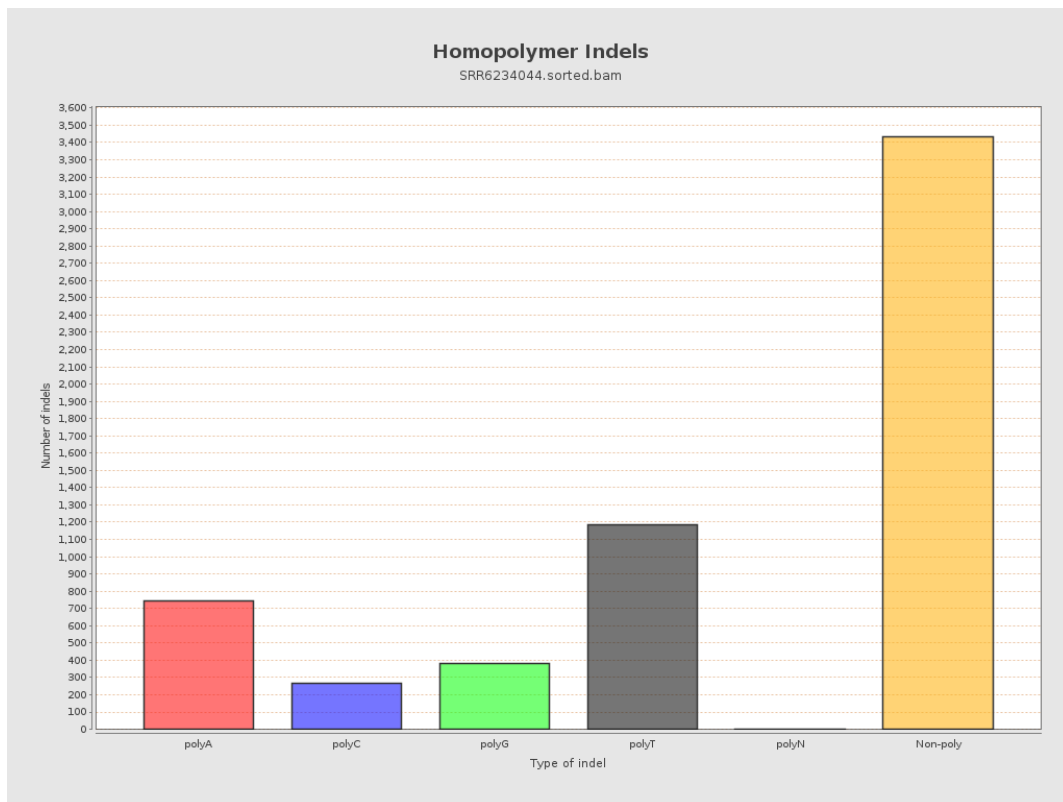
9. Results : Mapped Reads GC-content Distribution



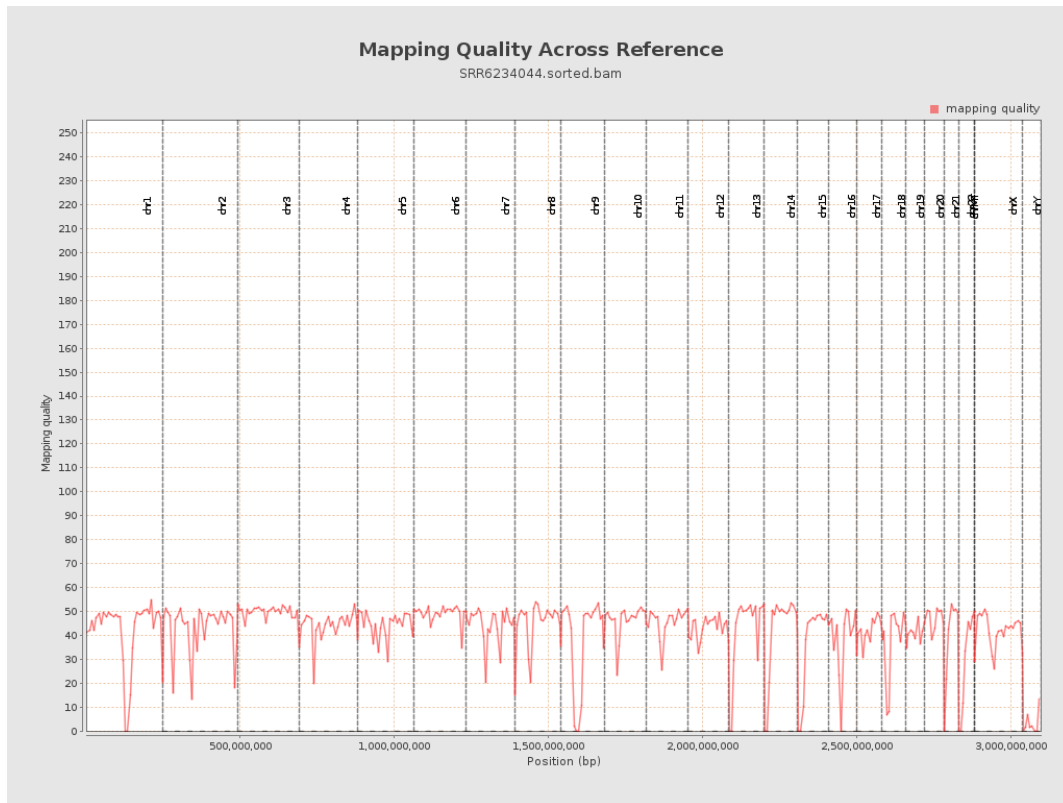
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

