

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 15:37:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084814.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_SRR3084814 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084814.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 15:37:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084814.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	984,354
Mapped reads	906,819 / 92.12%
Unmapped reads	77,535 / 7.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,805 / 0.89%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	25,206 / 2.56%
Duplication rate	2.51%
Clipped reads	308,313 / 31.32%

2.2. ACGT Content

Number/percentage of A's	17,976,300 / 28.7%
Number/percentage of C's	11,387,624 / 18.18%
Number/percentage of T's	20,232,856 / 32.3%
Number/percentage of G's	13,038,819 / 20.81%
Number/percentage of N's	8,966 / 0.01%
GC Percentage	38.99%

2.3. Coverage

Mean	0.0202

Standard Deviation	0.1715
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2.4. Mapping Quality

Mean Mapping Quality	47.25
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2.5. Mismatches and indels

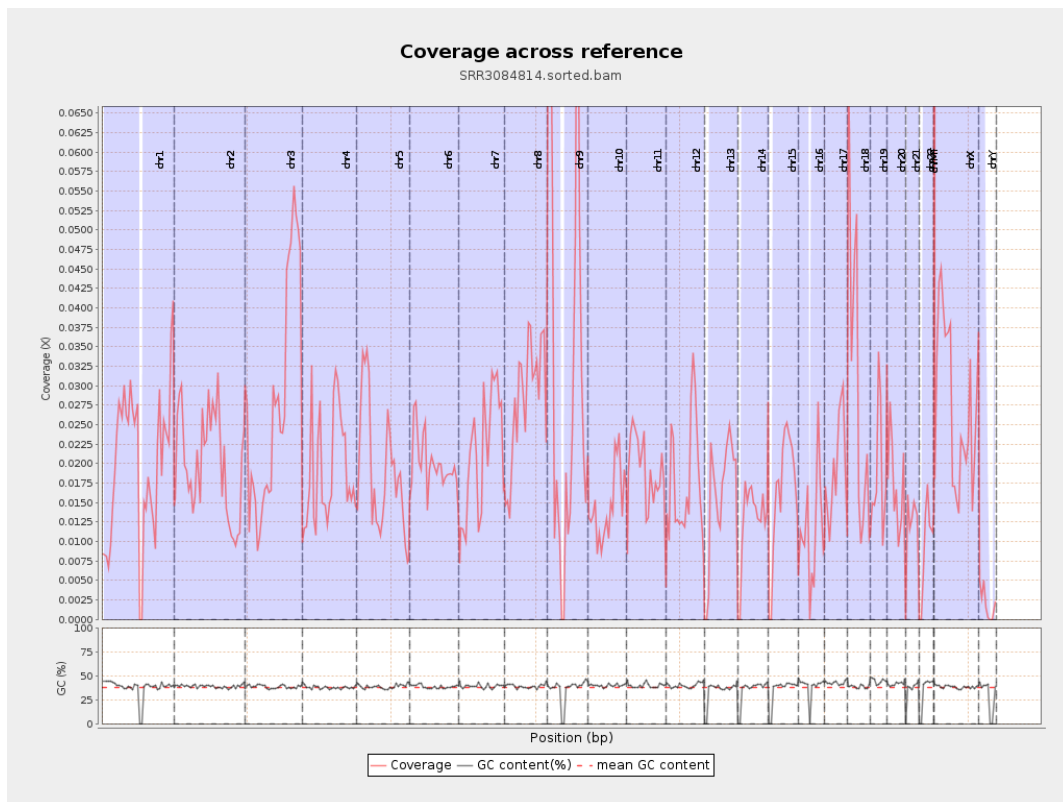
General error rate	0.8%
Mismatches	493,133
Insertions	5,175
Mapped reads with at least one insertion	0.57%
Deletions	14,673
Mapped reads with at least one deletion	1.6%
Homopolymer indels	48.46%

2.6. Chromosome stats

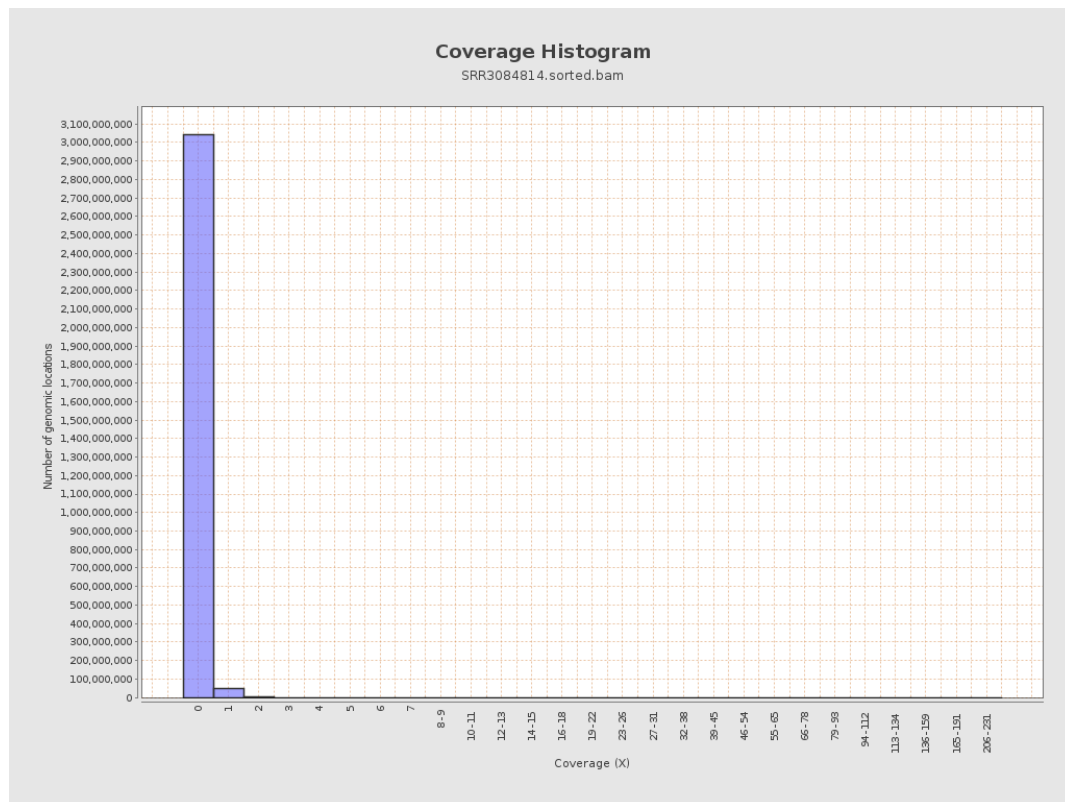
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4993362	0.02	0.2013
chr2	243199373	4849038	0.0199	0.1995
chr3	198022430	5528147	0.0279	0.1832
chr4	191154276	3652511	0.0191	0.1516
chr5	180915260	3481556	0.0192	0.1521
chr6	171115067	3400722	0.0199	0.1566
chr7	159138663	3401195	0.0214	0.1725

chr8	146364022	4103244	0.028	0.236
chr9	141213431	4770034	0.0338	0.2185
chr10	135534747	1974811	0.0146	0.137
chr11	135006516	2595561	0.0192	0.1631
chr12	133851895	2359808	0.0176	0.1449
chr13	115169878	1814013	0.0158	0.1369
chr14	107349540	1369340	0.0128	0.1239
chr15	102531392	1677152	0.0164	0.1409
chr16	90354753	1012942	0.0112	0.1173
chr17	81195210	1566468	0.0193	0.1532
chr18	78077248	2398713	0.0307	0.2308
chr19	59128983	1146732	0.0194	0.168
chr20	63025520	1099181	0.0174	0.145
chr21	48129895	573554	0.0119	0.1218
chr22	51304566	493948	0.0096	0.1065
chrMT	16571	61575	3.7158	2.7715
chrX	155270560	4226011	0.0272	0.1837
chrY	59373566	119136	0.002	0.0534

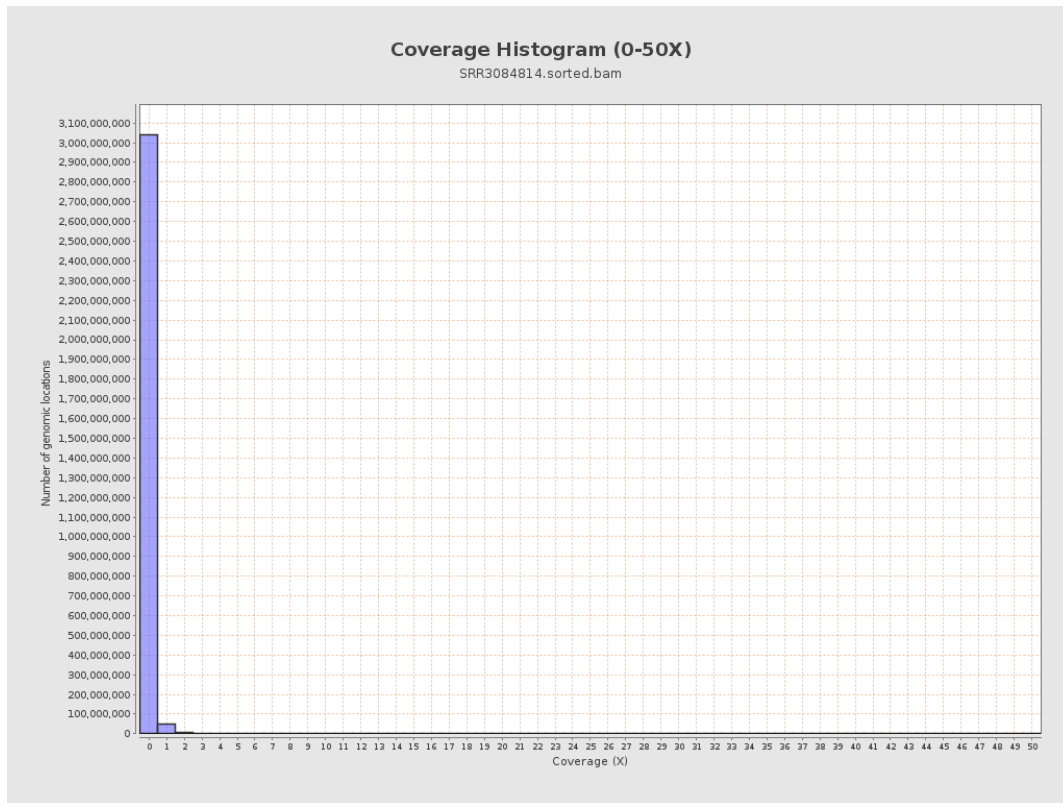
3. Results : Coverage across reference



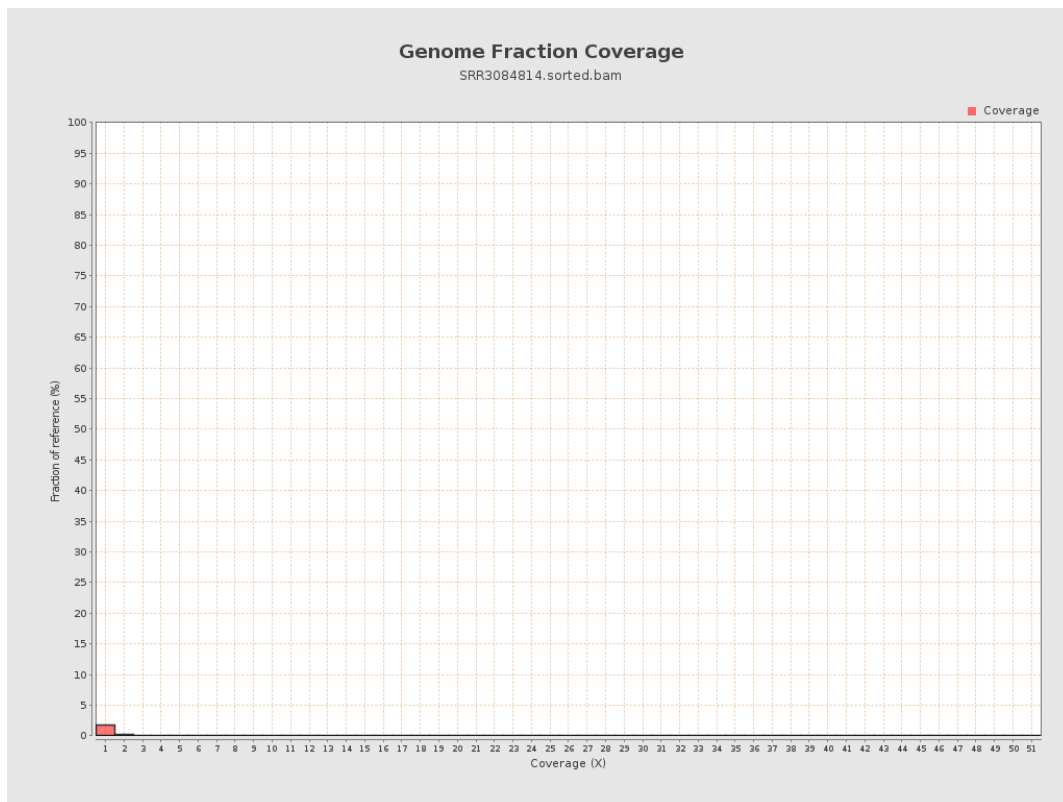
4. Results : Coverage Histogram



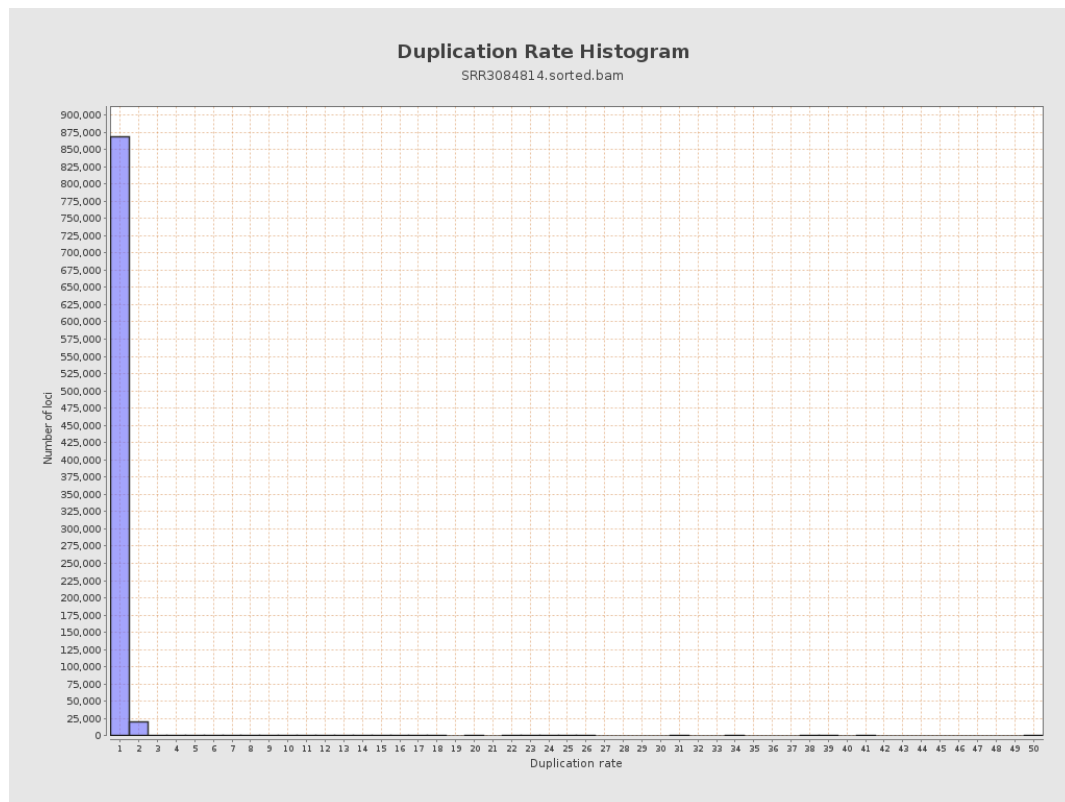
5. Results : Coverage Histogram (0-50X)



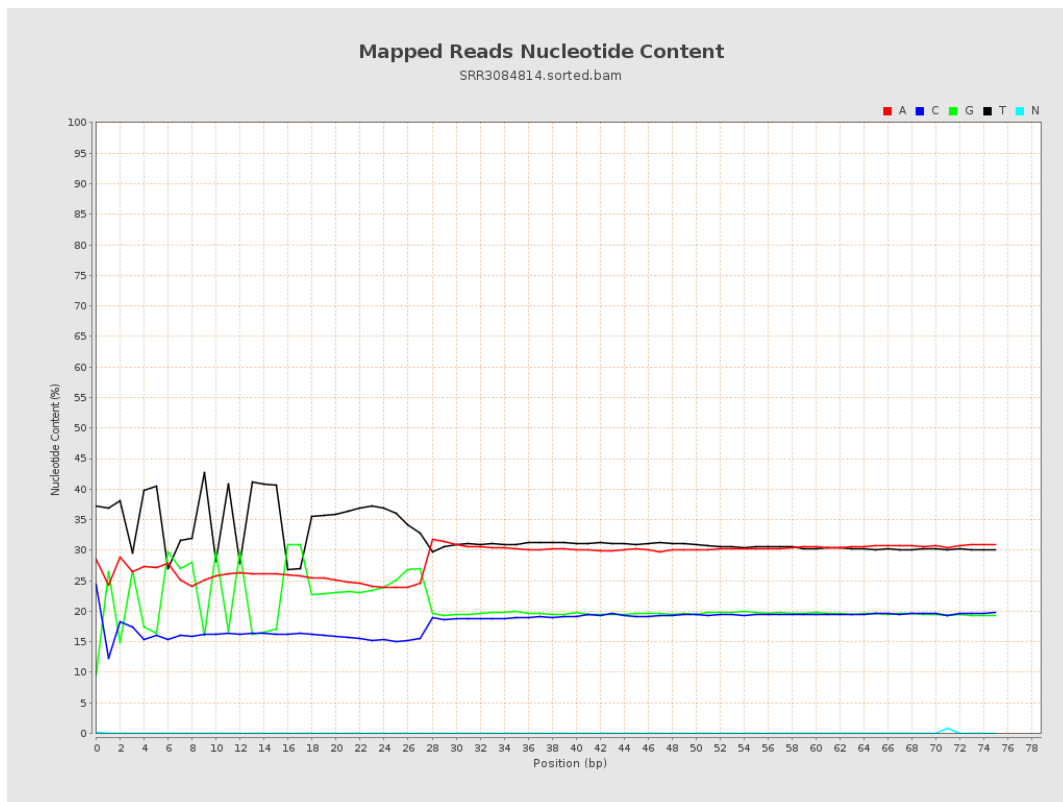
6. Results : Genome Fraction Coverage



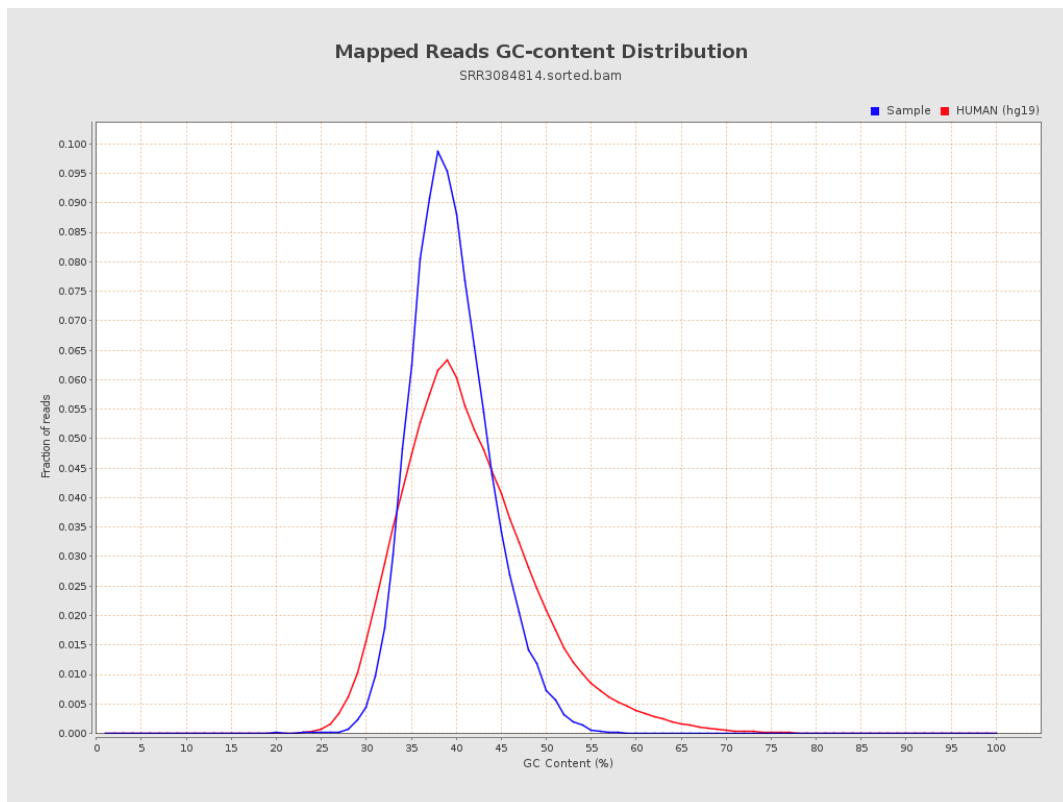
7. Results : Duplication Rate Histogram



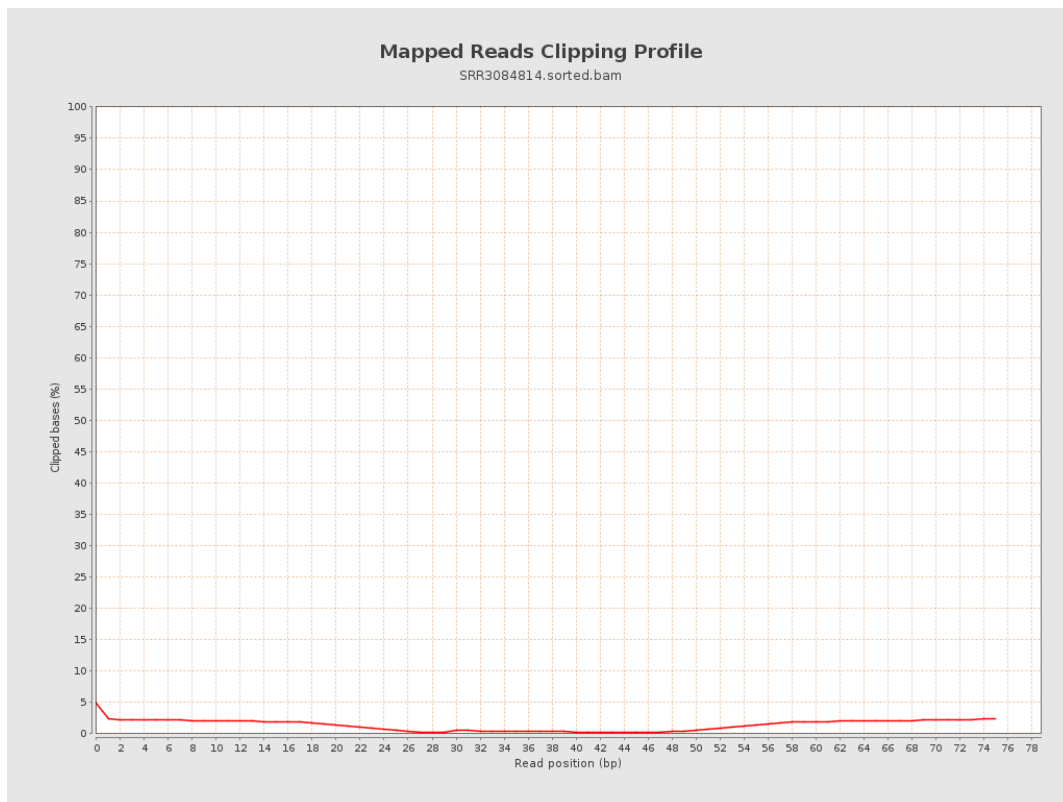
8. Results : Mapped Reads Nucleotide Content



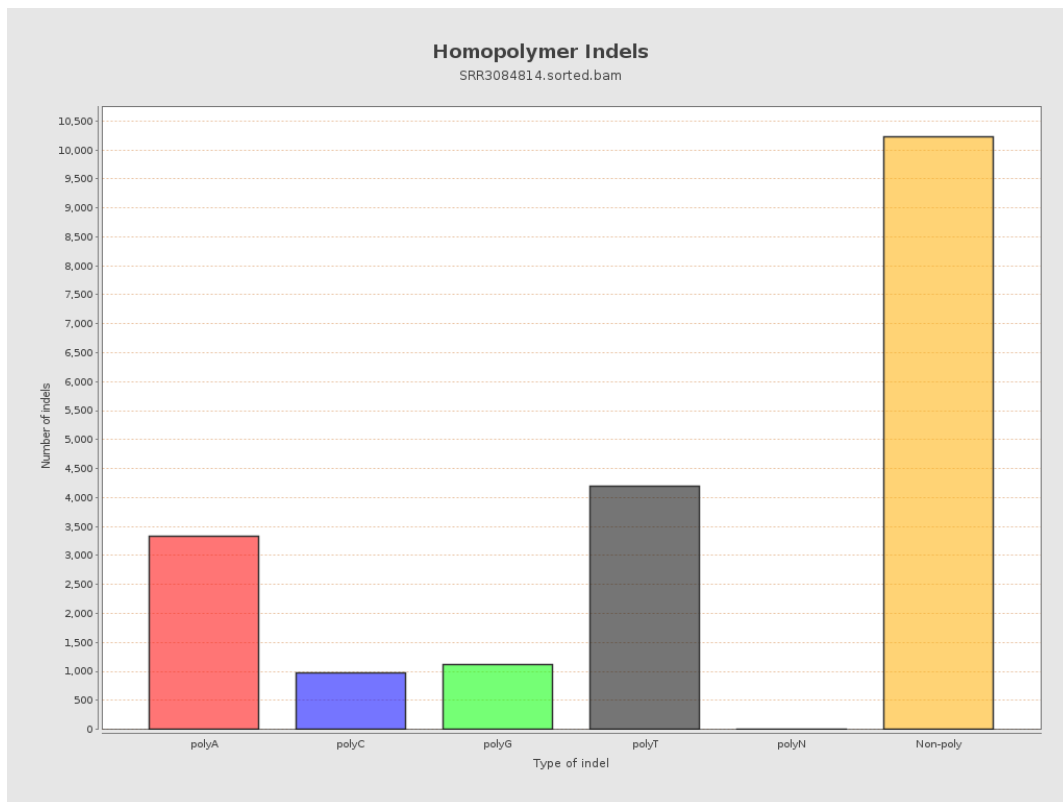
9. Results : Mapped Reads GC-content Distribution



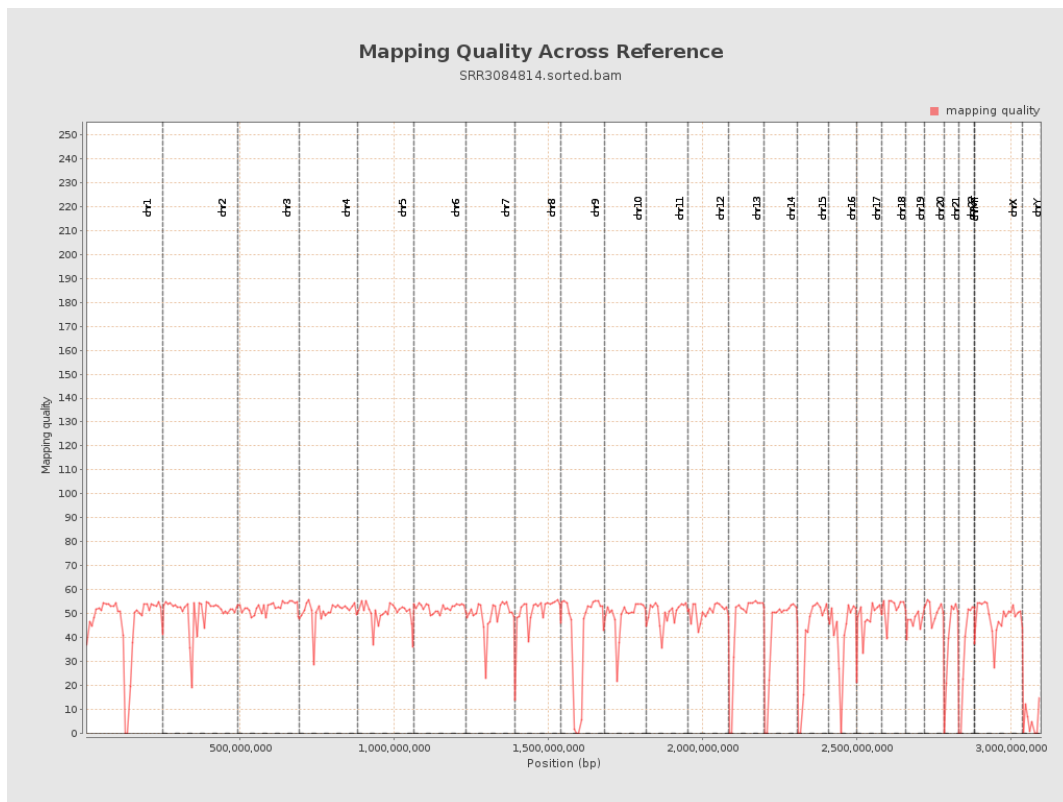
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

