

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 03:17:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006449.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_SRR1006449 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006449.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 03:17:58 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006449.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,222,940
Mapped reads	1,139,826 / 93.2%
Unmapped reads	83,114 / 6.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,431 / 0.28%
Read min/max/mean length	30 / 59 / 56.17
Duplicated reads (estimated)	14,204 / 1.16%
Duplication rate	0.81%
Clipped reads	148,313 / 12.13%

2.2. ACGT Content

Number/percentage of A's	17,941,103 / 28.62%
Number/percentage of C's	13,137,454 / 20.96%
Number/percentage of T's	17,954,870 / 28.65%
Number/percentage of G's	13,643,264 / 21.77%
Number/percentage of N's	1,178 / 0%
GC Percentage	42.73%

2.3. Coverage

Mean	0.0203

Standard Deviation	0.1901
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2.4. Mapping Quality

Mean Mapping Quality	45.31
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2.5. Mismatches and indels

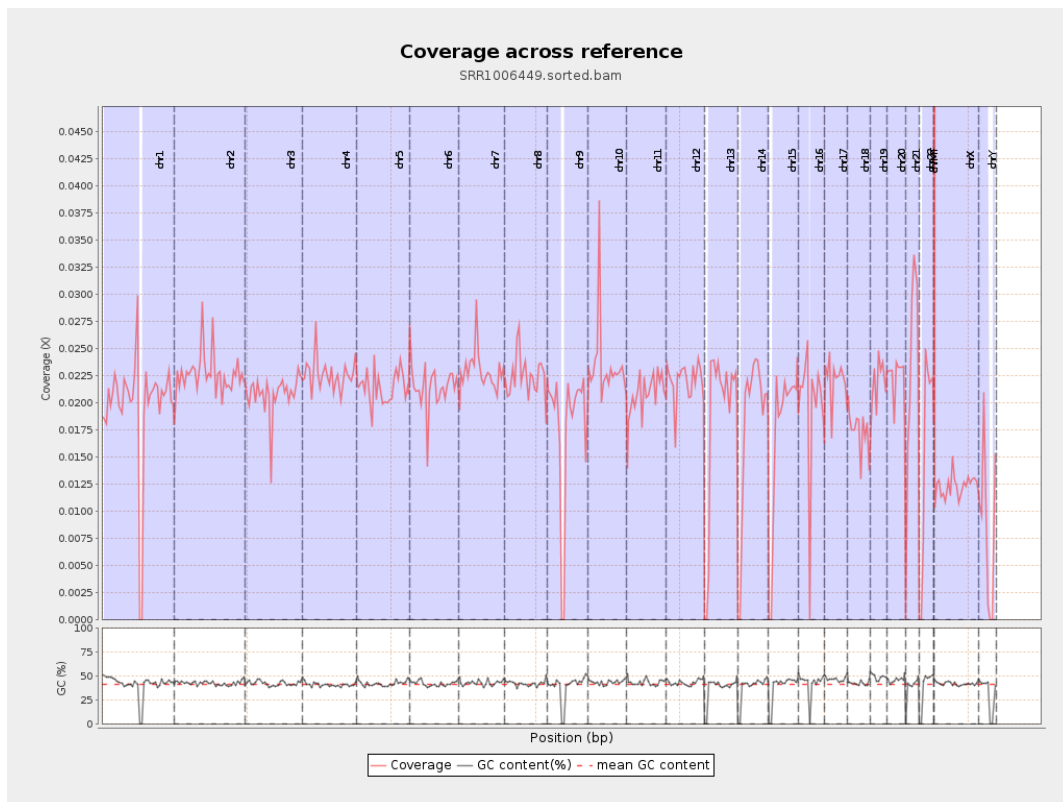
General error rate	0.42%
Mismatches	255,739
Insertions	3,887
Mapped reads with at least one insertion	0.34%
Deletions	11,299
Mapped reads with at least one deletion	0.99%
Homopolymer indels	45.32%

2.6. Chromosome stats

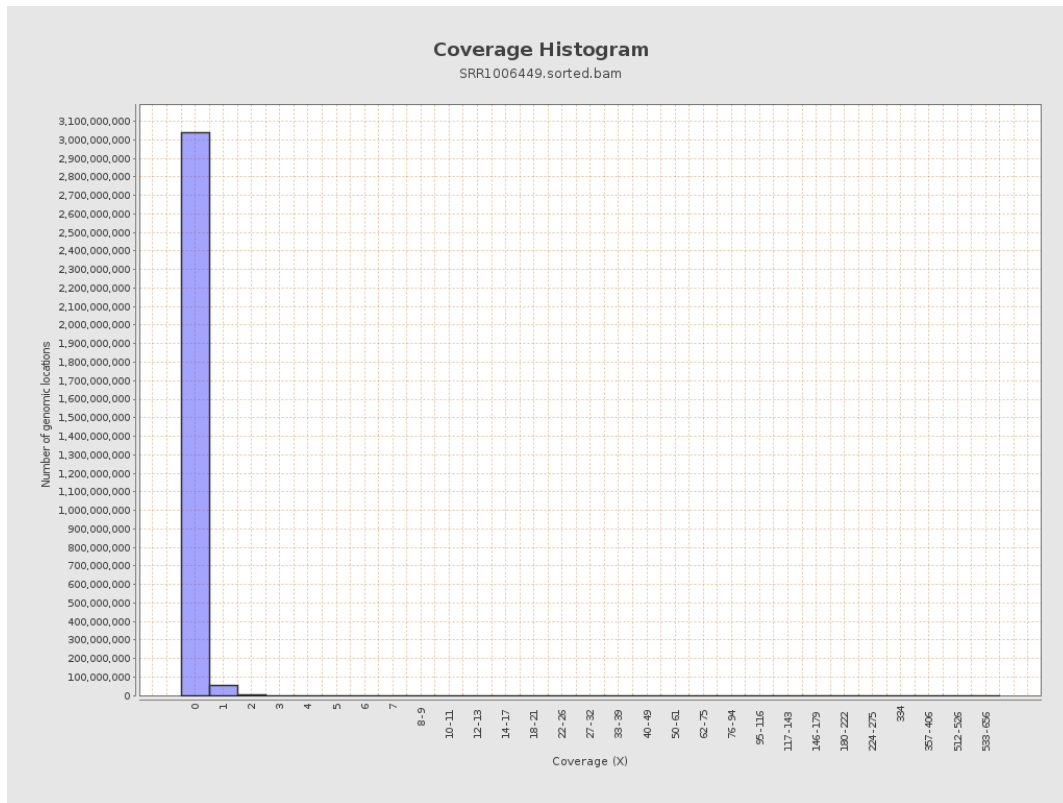
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4919249	0.0197	0.2607
chr2	243199373	5521017	0.0227	0.1775
chr3	198022430	4124843	0.0208	0.1494
chr4	191154276	4321396	0.0226	0.1598
chr5	180915260	3880136	0.0214	0.1521
chr6	171115067	3672517	0.0215	0.1585
chr7	159138663	3652319	0.023	0.2057

chr8	146364022	3283128	0.0224	0.3921
chr9	141213431	2512196	0.0178	0.1525
chr10	135534747	3179253	0.0235	0.2075
chr11	135006516	2813116	0.0208	0.1636
chr12	133851895	2940410	0.022	0.154
chr13	115169878	2139422	0.0186	0.1408
chr14	107349540	1943255	0.0181	0.1422
chr15	102531392	1753457	0.0171	0.1356
chr16	90354753	1776423	0.0197	0.1593
chr17	81195210	1797146	0.0221	0.1638
chr18	78077248	1359416	0.0174	0.2018
chr19	59128983	1294975	0.0219	0.2252
chr20	63025520	1407236	0.0223	0.1564
chr21	48129895	1118237	0.0232	0.1637
chr22	51304566	807931	0.0157	0.1368
chrMT	16571	64635	3.9005	2.4466
chrX	155270560	1912159	0.0123	0.119
chrY	59373566	502429	0.0085	0.1285

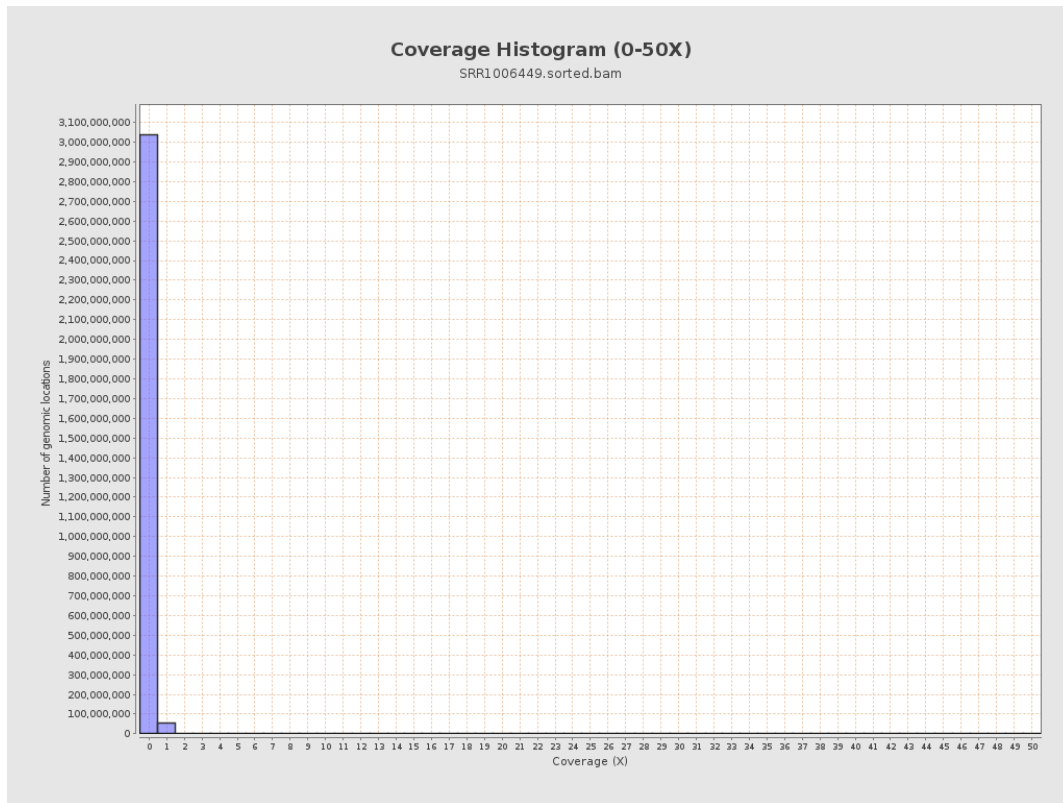
3. Results : Coverage across reference



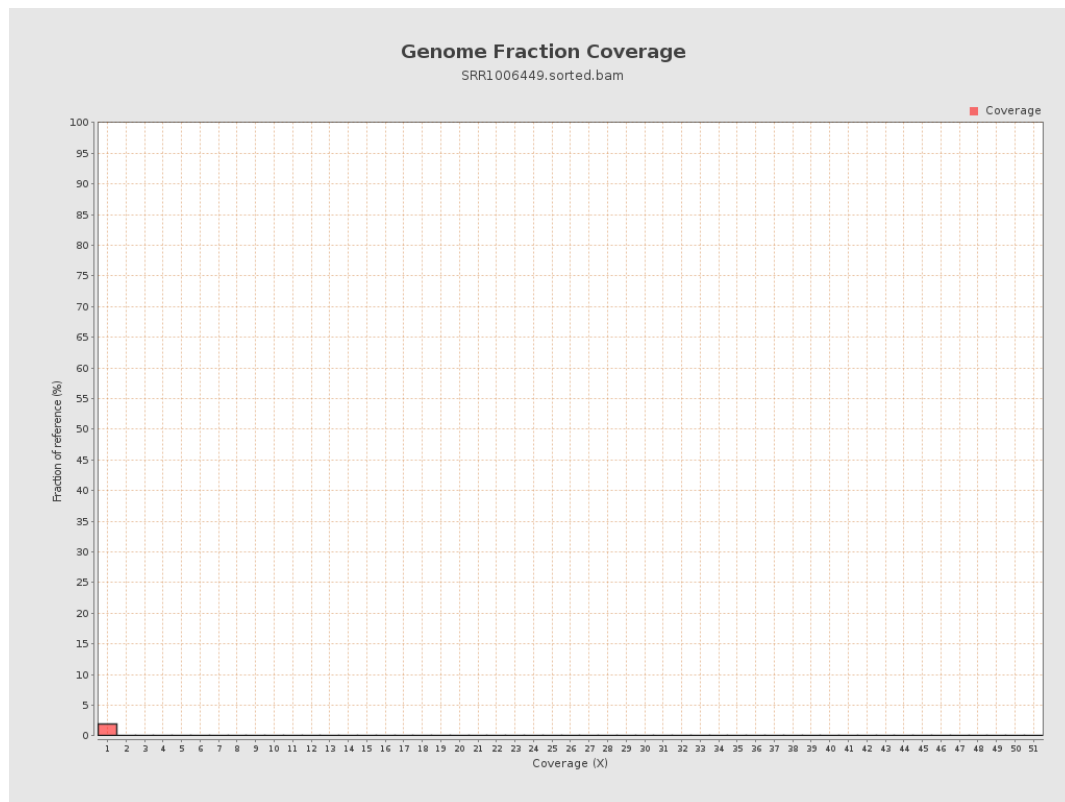
4. Results : Coverage Histogram



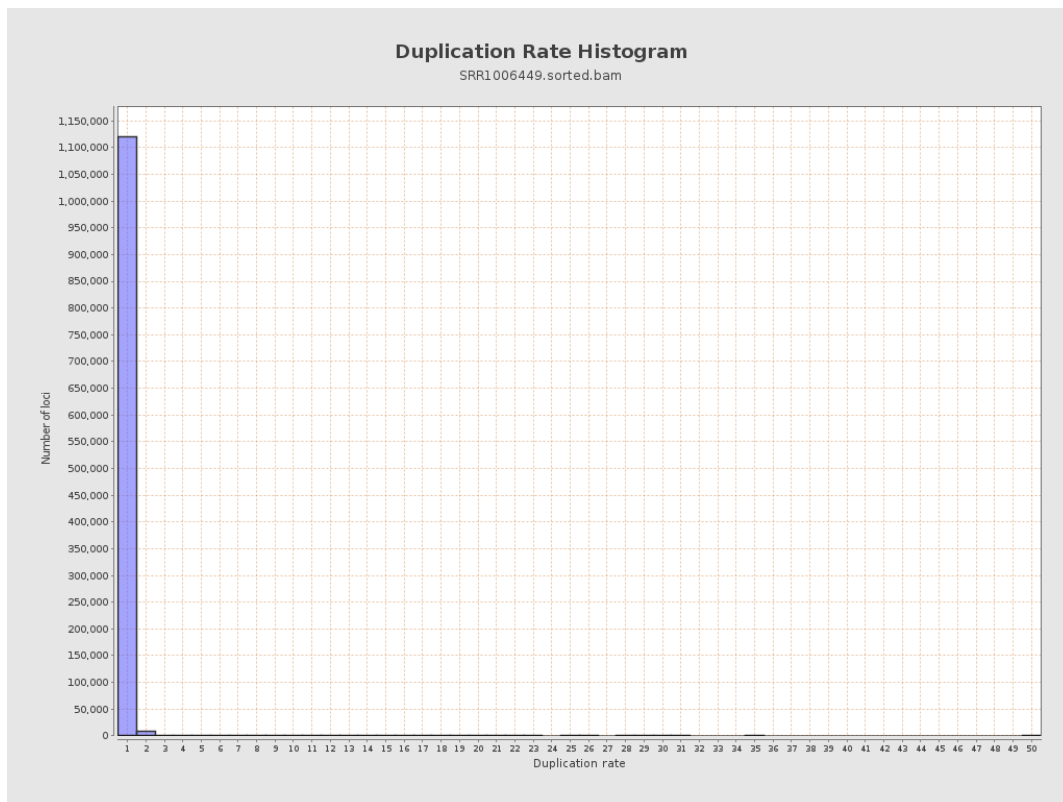
5. Results : Coverage Histogram (0-50X)



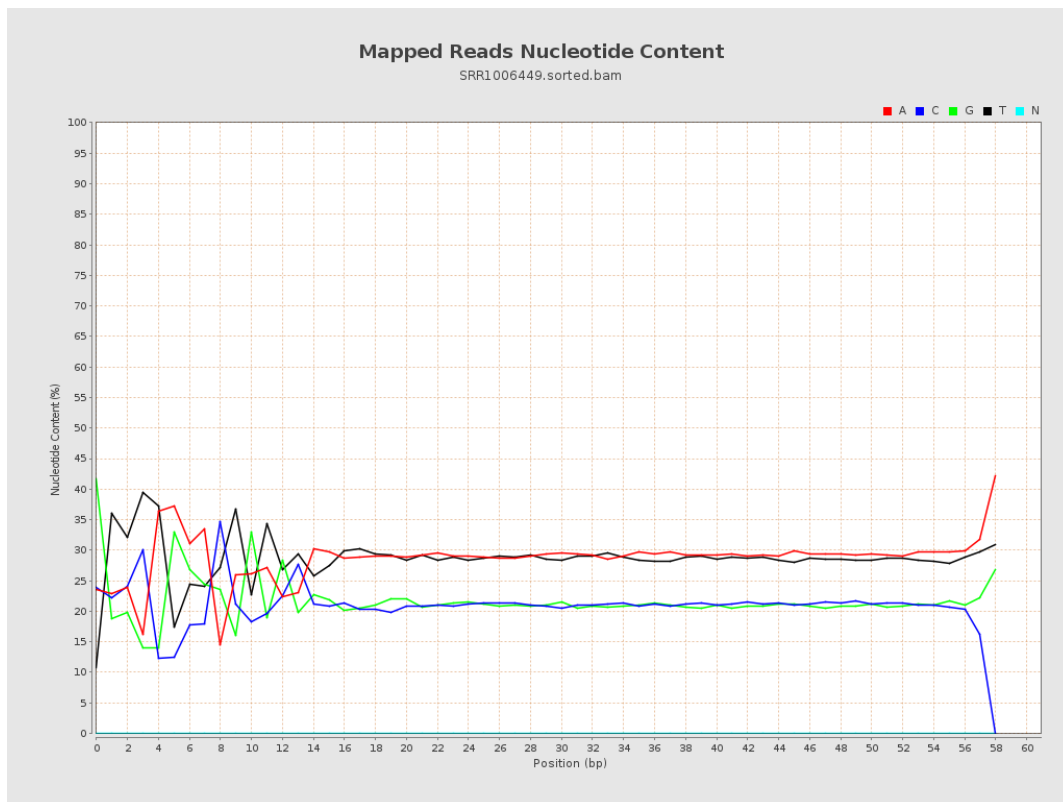
6. Results : Genome Fraction Coverage



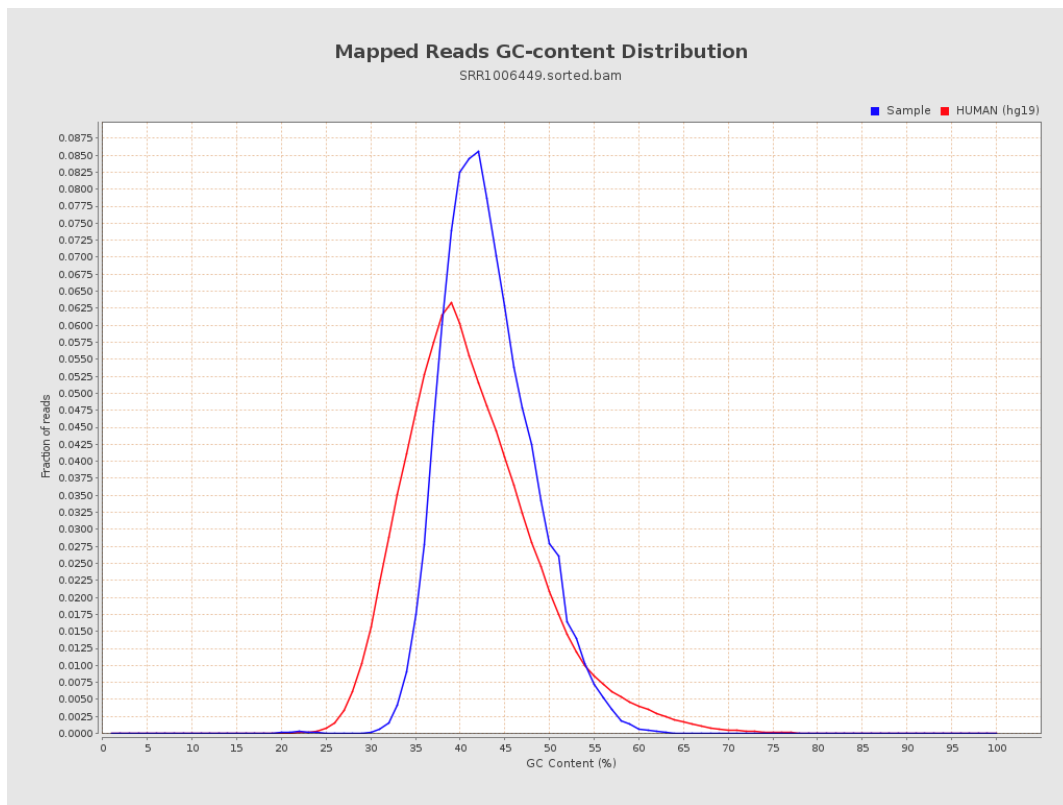
7. Results : Duplication Rate Histogram



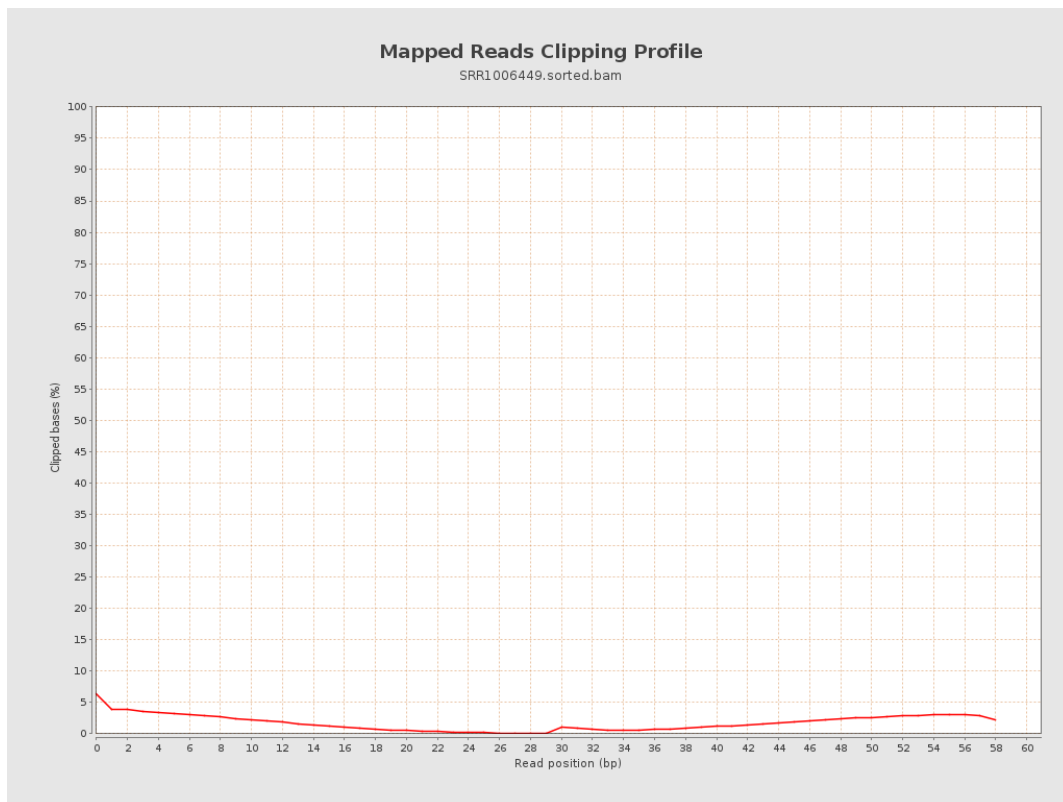
8. Results : Mapped Reads Nucleotide Content



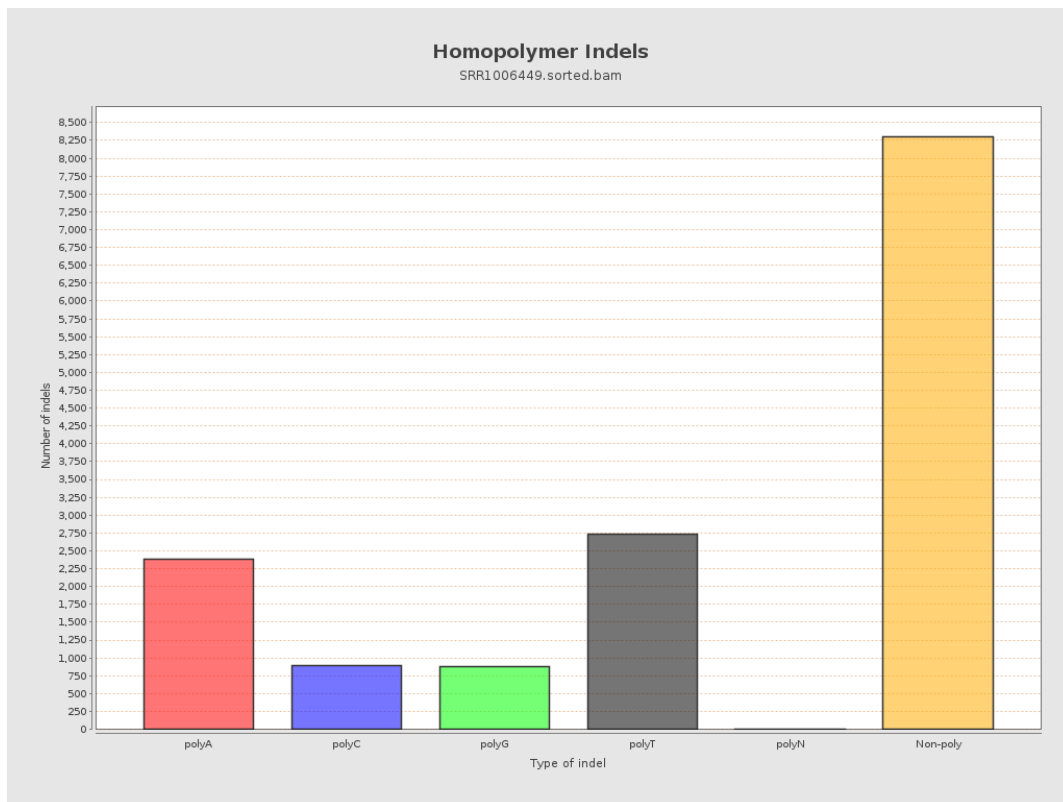
9. Results : Mapped Reads GC-content Distribution



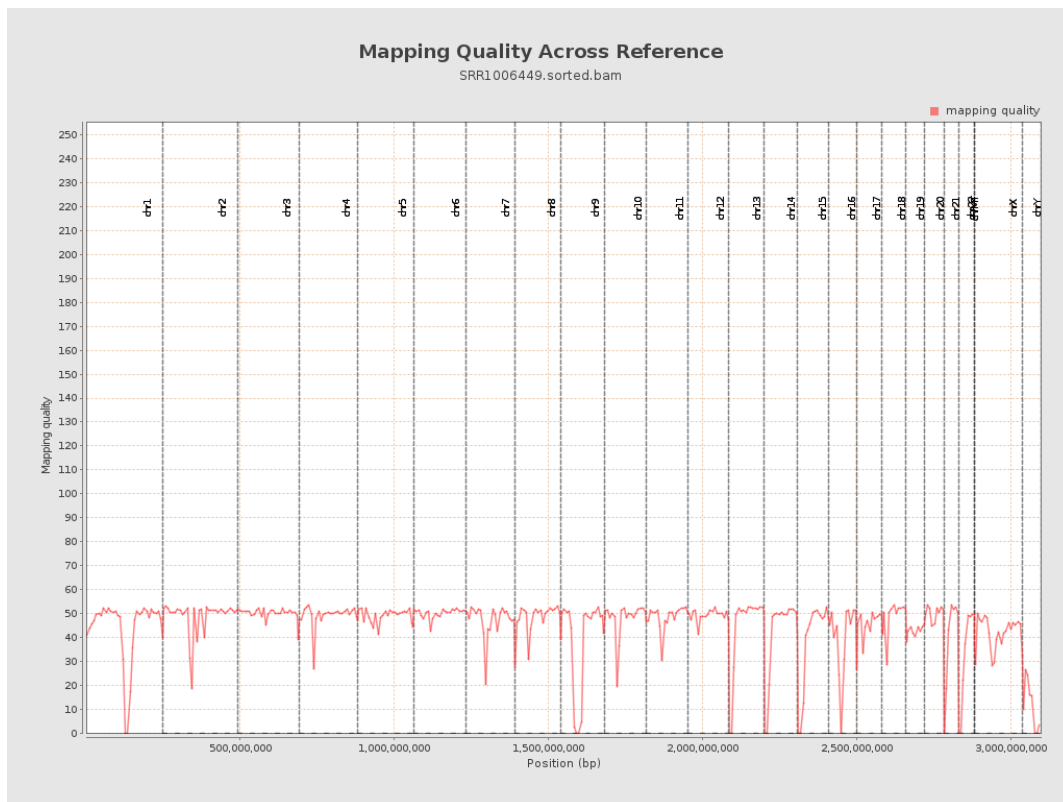
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

