

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 23:17:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524856.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_SRR10524856 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524856.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 23:17:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524856.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,609,346
Mapped reads	1,479,971 / 91.96%
Unmapped reads	129,375 / 8.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,306 / 0.45%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	44,359 / 2.76%
Duplication rate	2.04%
Clipped reads	1,483,848 / 92.2%

2.2. ACGT Content

Number/percentage of A's	22,024,264 / 25.51%
Number/percentage of C's	15,716,935 / 18.2%
Number/percentage of T's	28,060,772 / 32.5%
Number/percentage of G's	20,528,965 / 23.78%
Number/percentage of N's	11,003 / 0.01%
GC Percentage	41.98%

2.3. Coverage

Mean	0.0279

Standard Deviation	0.2792
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2.4. Mapping Quality

Mean Mapping Quality	45.16
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2.5. Mismatches and indels

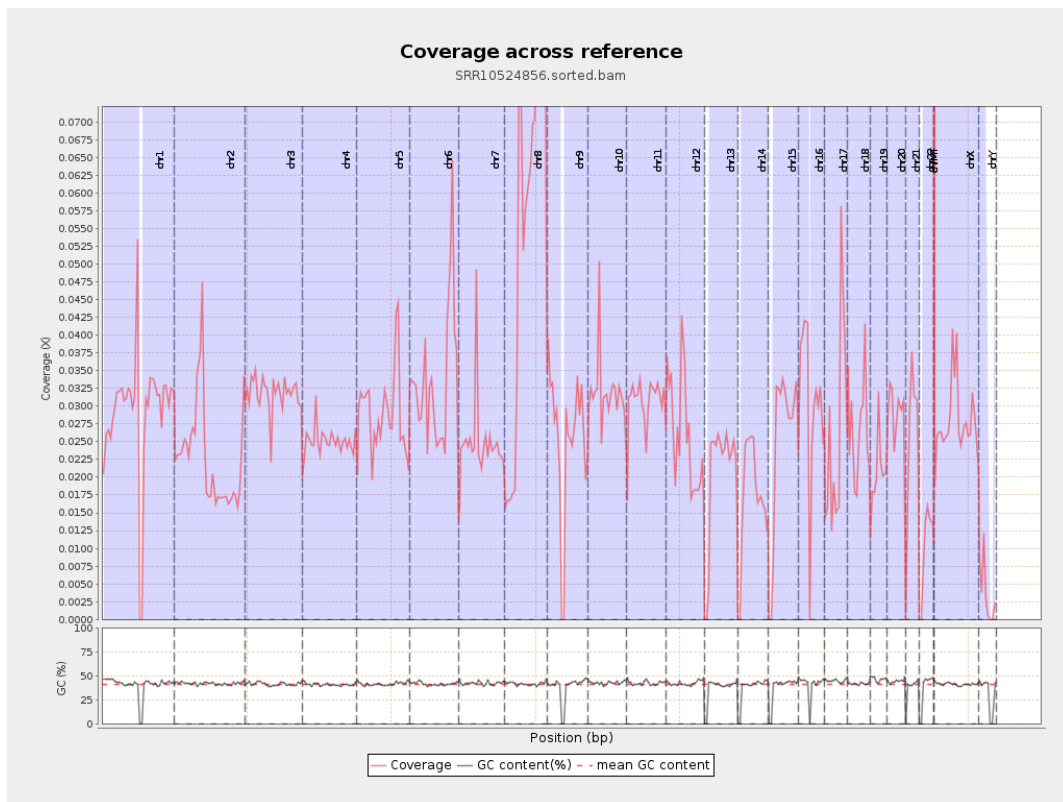
General error rate	0.5%
Mismatches	419,343
Insertions	5,835
Mapped reads with at least one insertion	0.39%
Deletions	16,032
Mapped reads with at least one deletion	1.08%
Homopolymer indels	43.87%

2.6. Chromosome stats

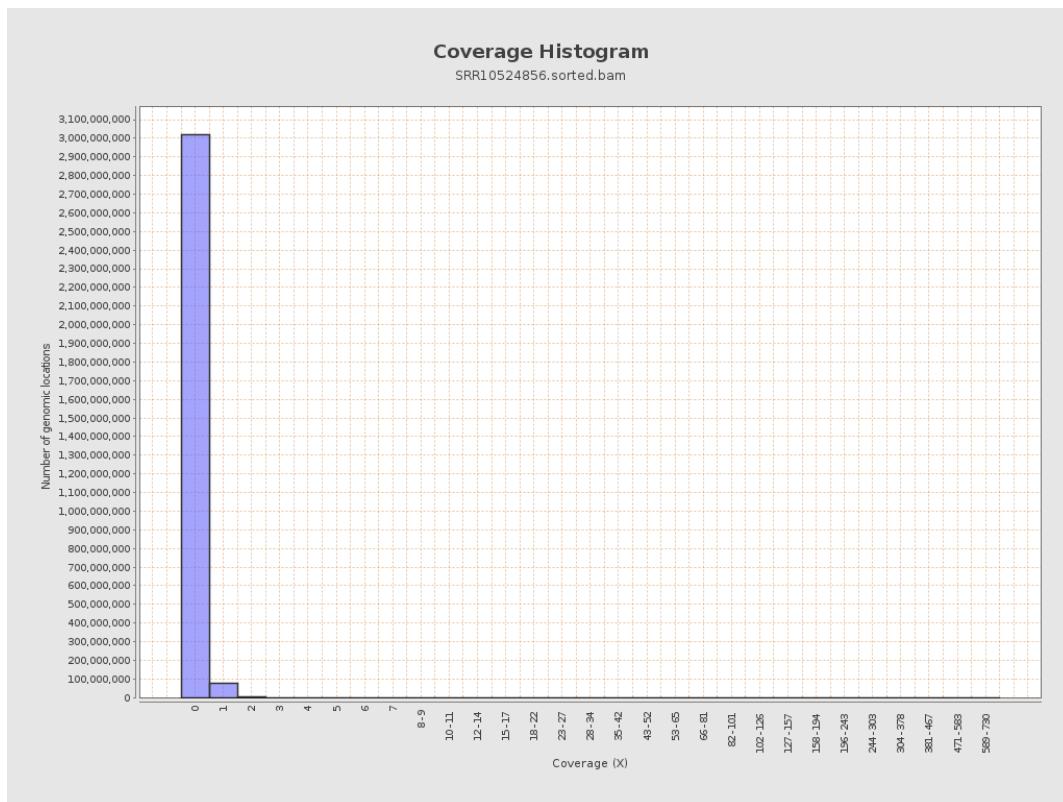
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7255068	0.0291	0.5485
chr2	243199373	5489941	0.0226	0.2649
chr3	198022430	6299588	0.0318	0.1901
chr4	191154276	4776501	0.025	0.1809
chr5	180915260	5293185	0.0293	0.1832
chr6	171115067	5681161	0.0332	0.2154
chr7	159138663	3975023	0.025	0.3793

chr8	146364022	8861785	0.0605	0.3795
chr9	141213431	3616893	0.0256	0.2332
chr10	135534747	4308679	0.0318	0.2593
chr11	135006516	4169367	0.0309	0.2531
chr12	133851895	3468572	0.0259	0.1766
chr13	115169878	2331744	0.0202	0.1518
chr14	107349540	1848857	0.0172	0.1518
chr15	102531392	2588189	0.0252	0.1699
chr16	90354753	2726065	0.0302	0.1996
chr17	81195210	2147878	0.0265	0.1967
chr18	78077248	2082241	0.0267	0.4248
chr19	59128983	1248294	0.0211	0.3588
chr20	63025520	1825330	0.029	0.1846
chr21	48129895	1247871	0.0259	0.1839
chr22	51304566	523310	0.0102	0.1072
chrMT	16571	25540	1.5412	1.5227
chrX	155270560	4365077	0.0281	0.2059
chrY	59373566	210814	0.0036	0.0948

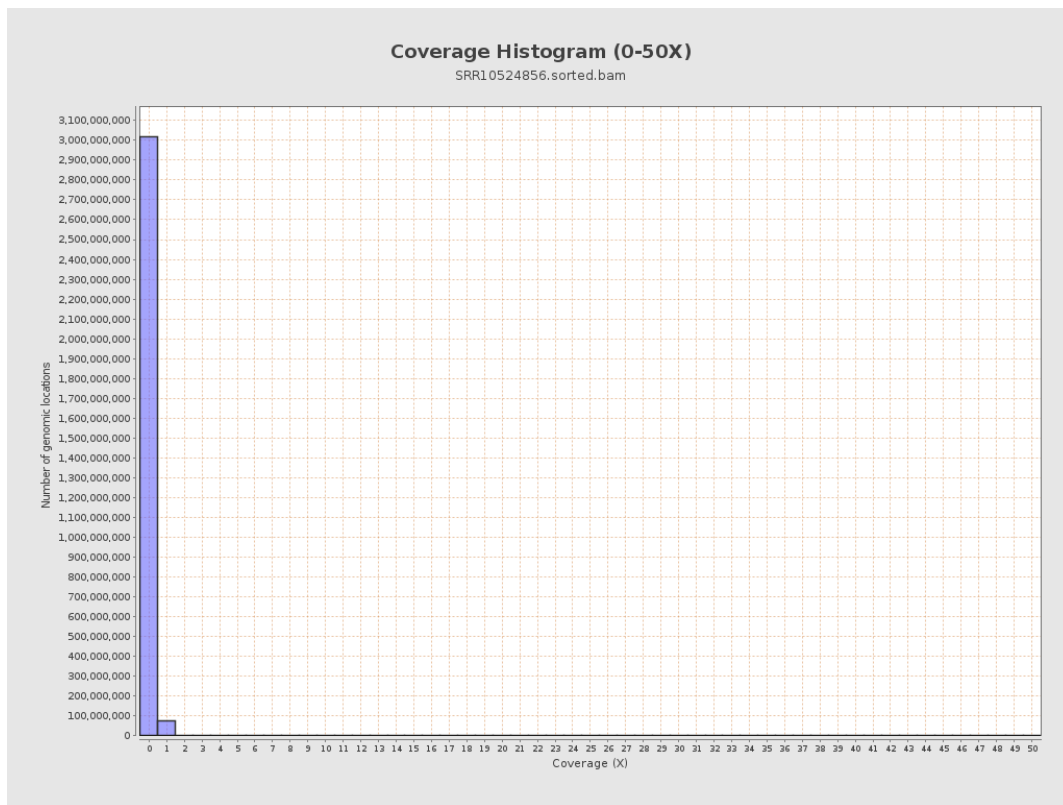
3. Results : Coverage across reference



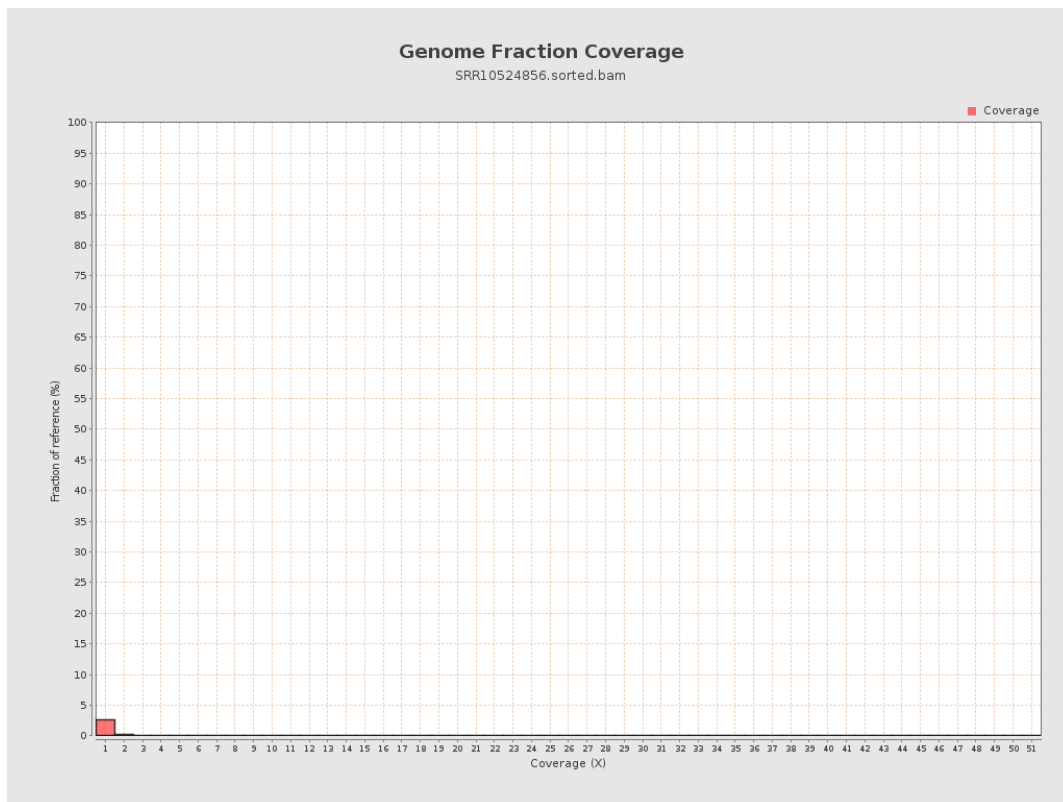
4. Results : Coverage Histogram



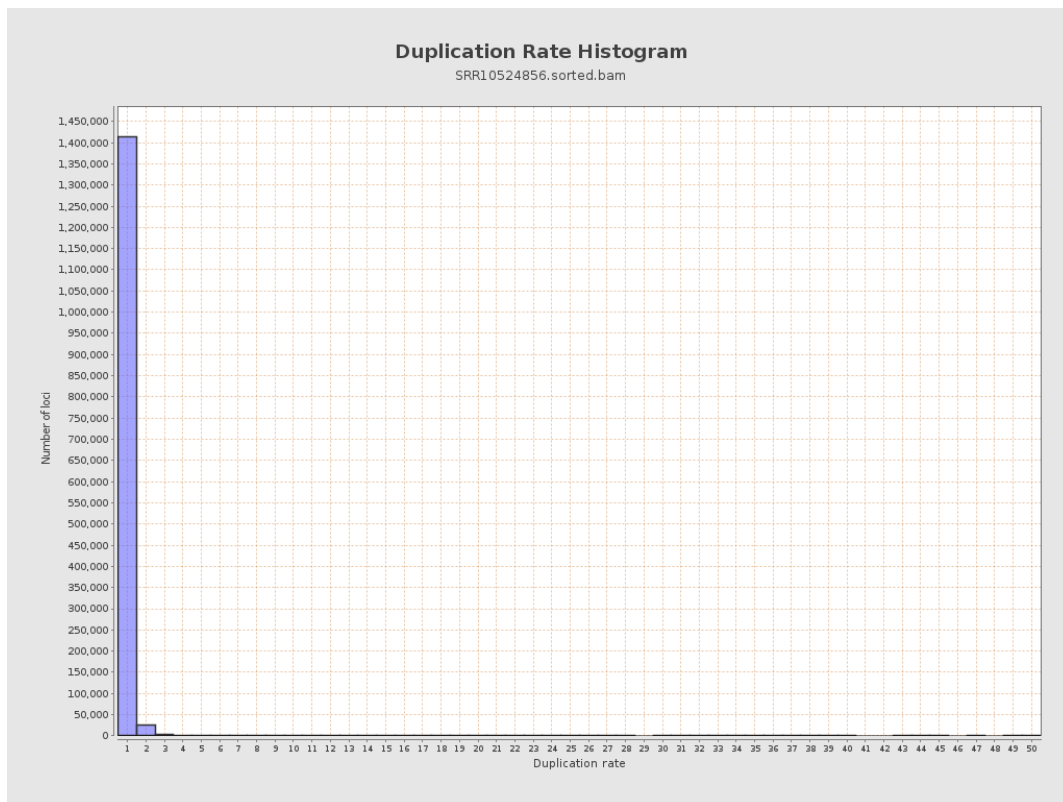
5. Results : Coverage Histogram (0-50X)



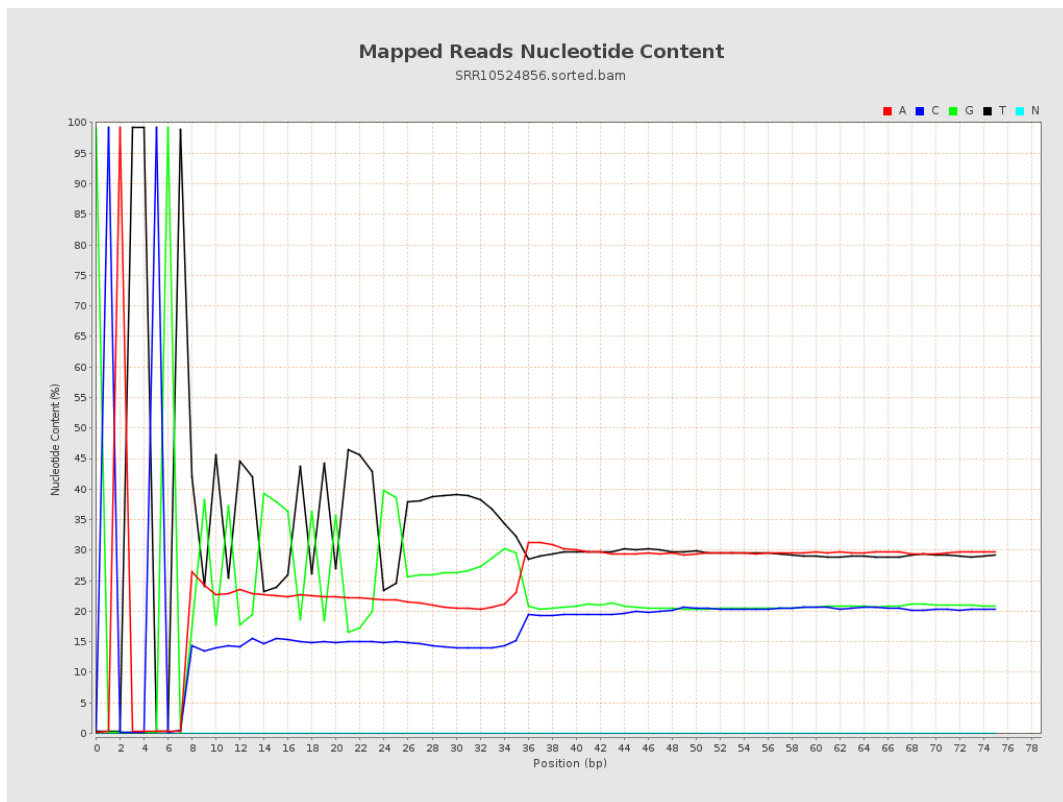
6. Results : Genome Fraction Coverage



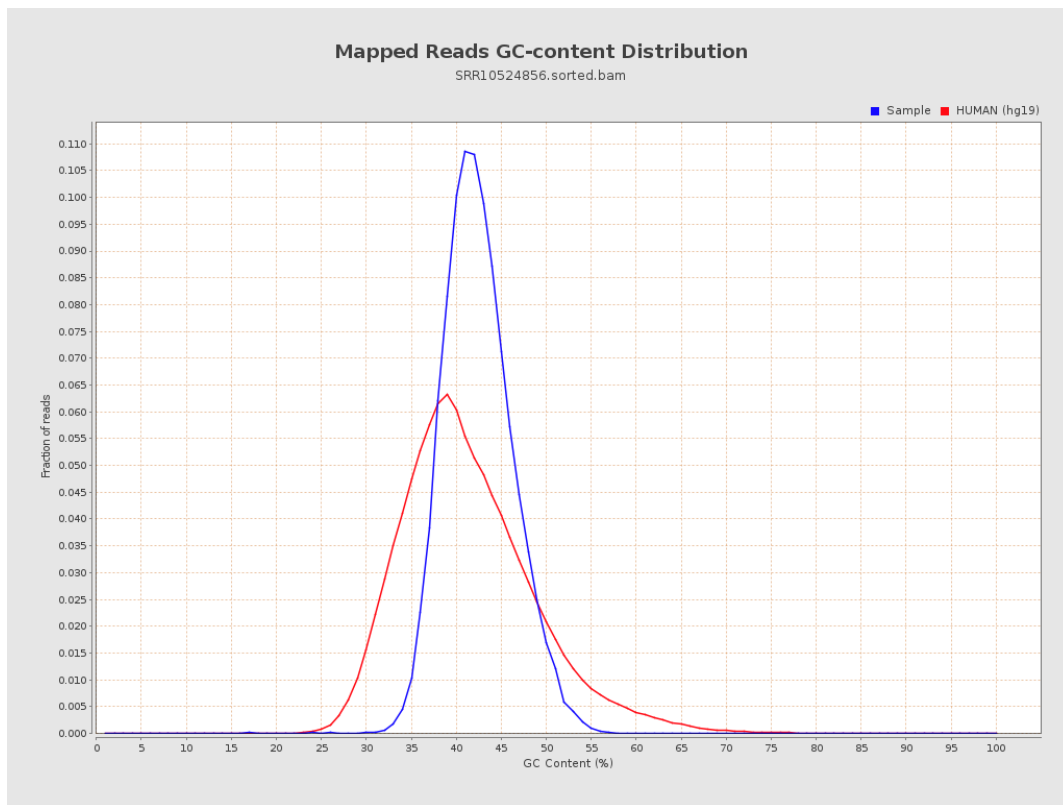
7. Results : Duplication Rate Histogram



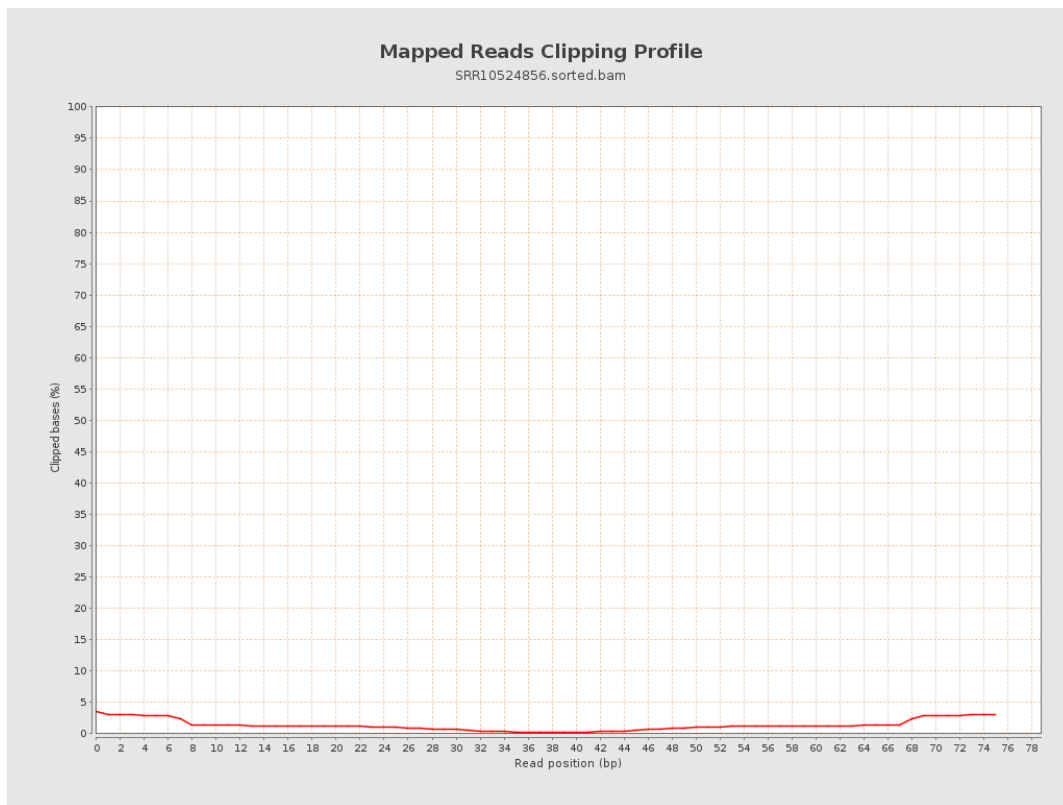
8. Results : Mapped Reads Nucleotide Content



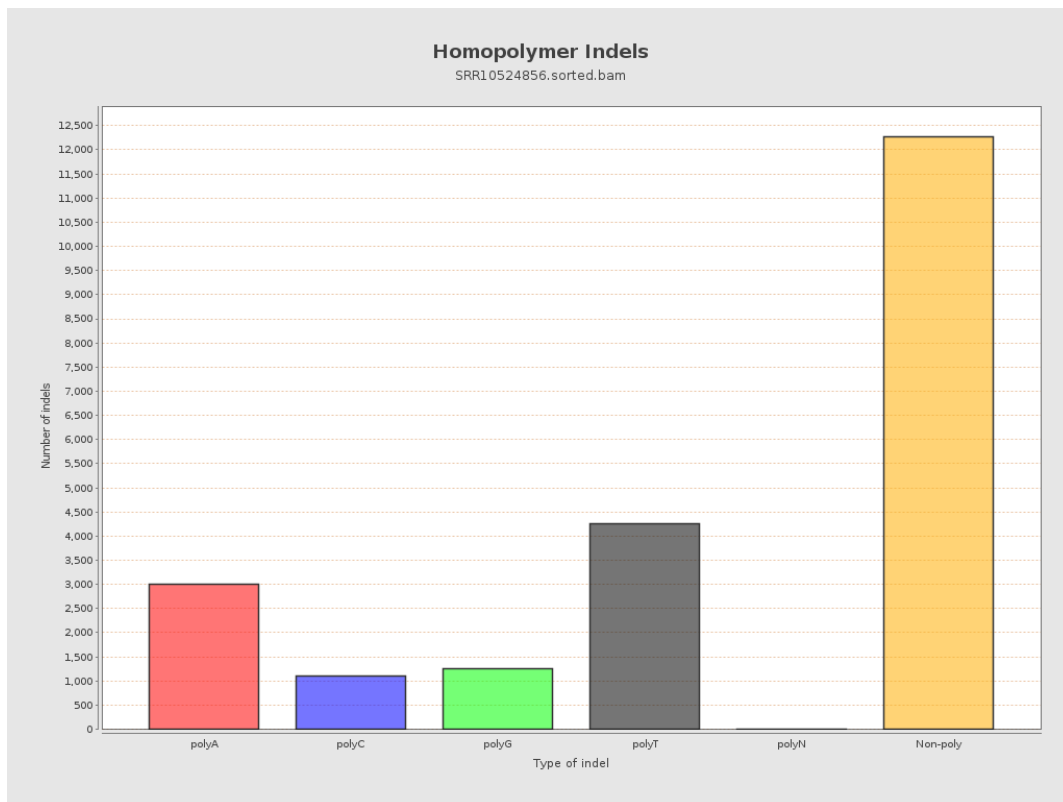
9. Results : Mapped Reads GC-content Distribution



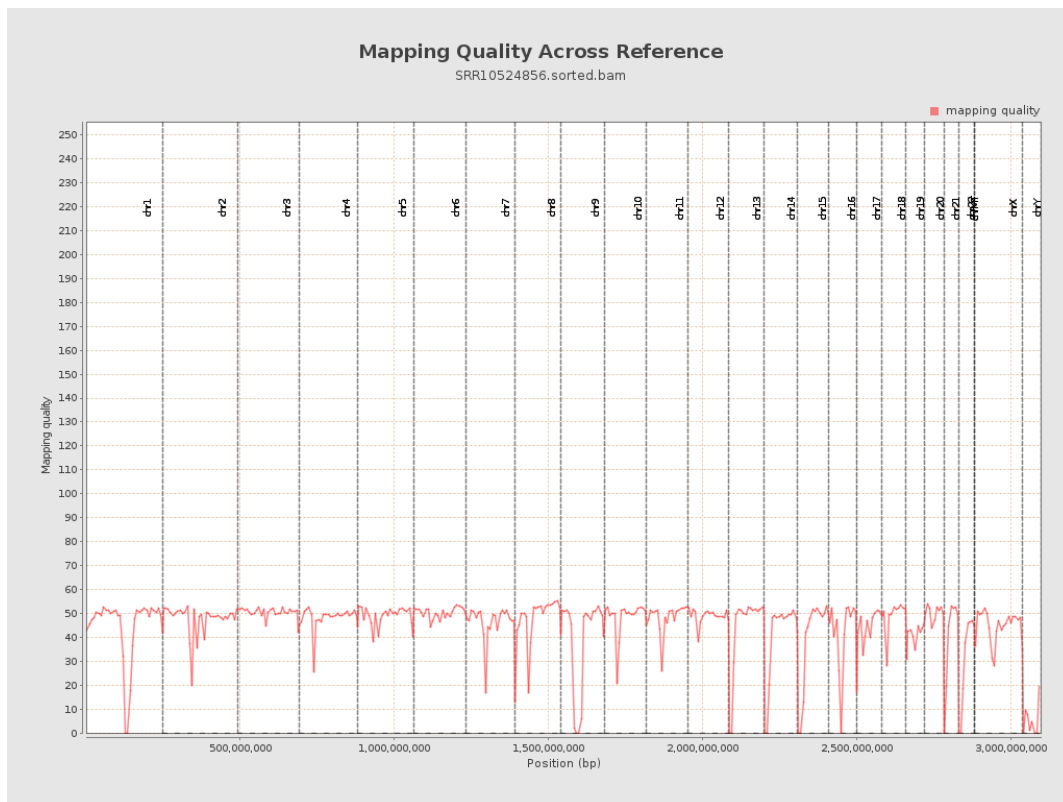
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

