

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 03:06:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006444.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_SRR1006444 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006444.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 03:06:22 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006444.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,379,277
Mapped reads	1,316,330 / 95.44%
Unmapped reads	62,947 / 4.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,361 / 0.32%
Read min/max/mean length	30 / 59 / 57.98
Duplicated reads (estimated)	25,267 / 1.83%
Duplication rate	1.41%
Clipped reads	156,268 / 11.33%

2.2. ACGT Content

Number/percentage of A's	21,475,115 / 28.82%
Number/percentage of C's	15,475,804 / 20.77%
Number/percentage of T's	21,389,107 / 28.71%
Number/percentage of G's	16,160,151 / 21.69%
Number/percentage of N's	2,165 / 0%
GC Percentage	42.46%

2.3. Coverage

Mean	0.0241

Standard Deviation	0.2192
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2.4. Mapping Quality

Mean Mapping Quality	46.22
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2.5. Mismatches and indels

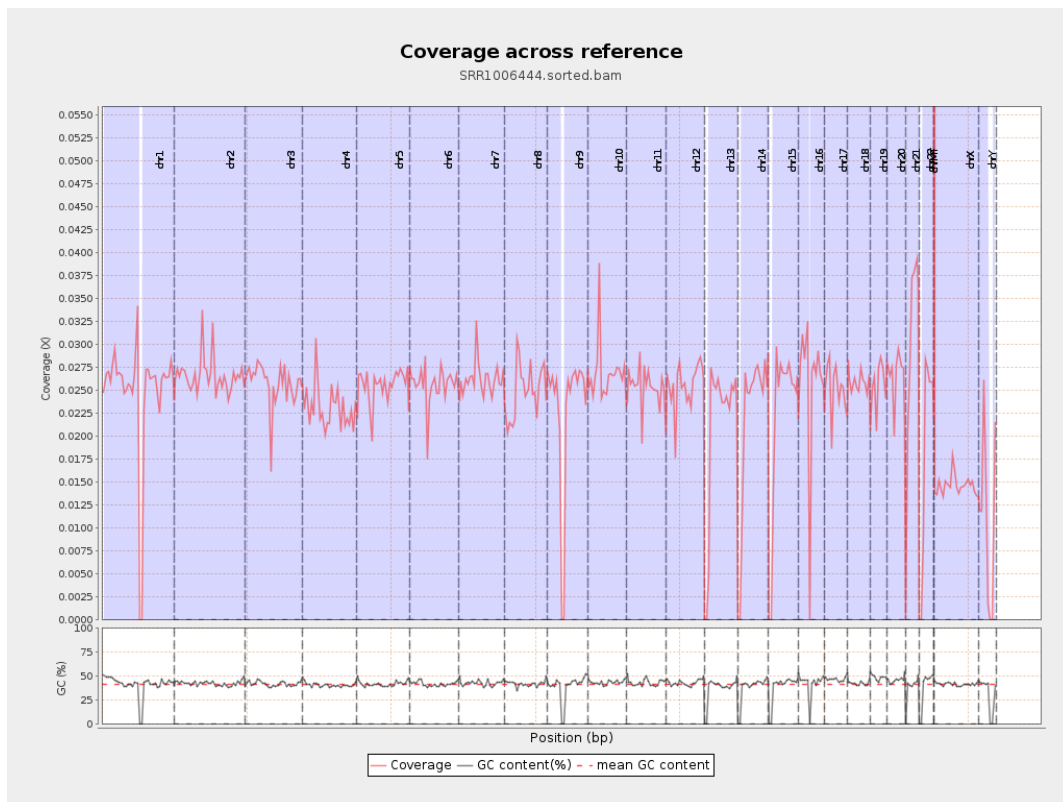
General error rate	0.45%
Mismatches	327,199
Insertions	4,612
Mapped reads with at least one insertion	0.35%
Deletions	15,277
Mapped reads with at least one deletion	1.16%
Homopolymer indels	45.28%

2.6. Chromosome stats

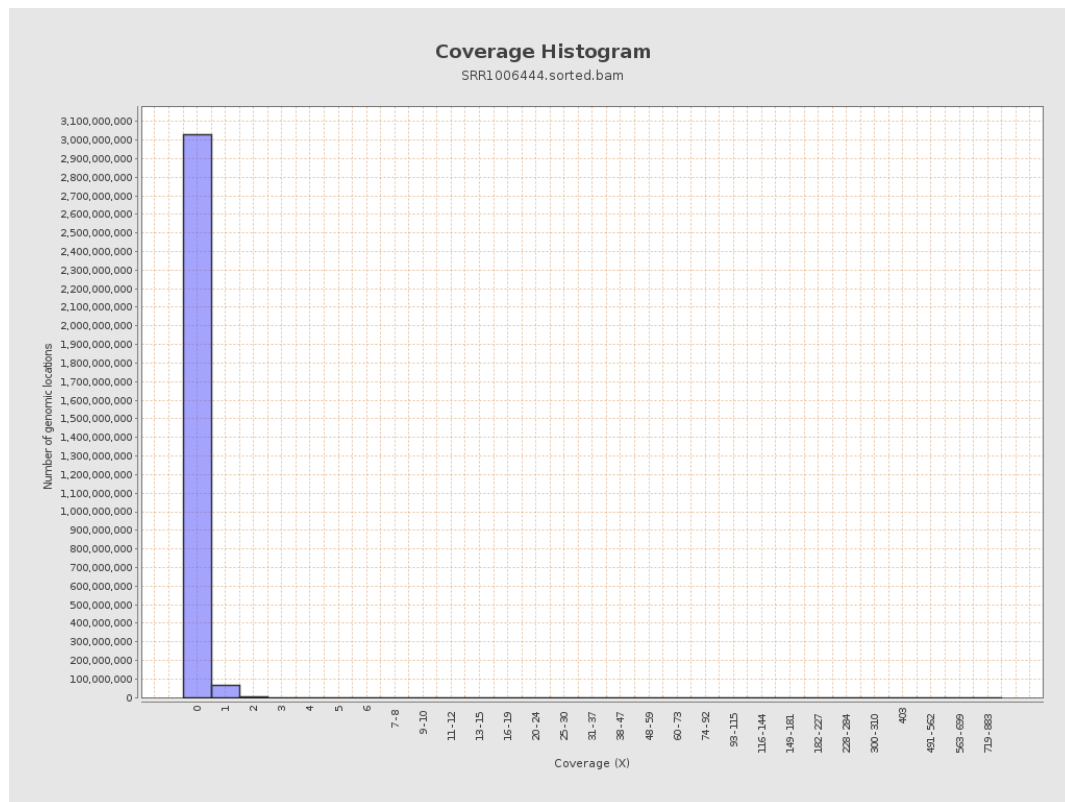
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6165078	0.0247	0.2823
chr2	243199373	6461429	0.0266	0.1973
chr3	198022430	5095500	0.0257	0.1681
chr4	191154276	4421168	0.0231	0.1651
chr5	180915260	4638837	0.0256	0.168
chr6	171115067	4380692	0.0256	0.1759
chr7	159138663	4166190	0.0262	0.2264

chr8	146364022	3643034	0.0249	0.5227
chr9	141213431	3205674	0.0227	0.179
chr10	135534747	3631052	0.0268	0.2141
chr11	135006516	3431401	0.0254	0.187
chr12	133851895	3415792	0.0255	0.1687
chr13	115169878	2404636	0.0209	0.1511
chr14	107349540	2332506	0.0217	0.1581
chr15	102531392	2252505	0.022	0.1556
chr16	90354753	2305250	0.0255	0.1841
chr17	81195210	2037816	0.0251	0.1783
chr18	78077248	2019541	0.0259	0.2526
chr19	59128983	1509499	0.0255	0.2299
chr20	63025520	1663794	0.0264	0.1728
chr21	48129895	1433201	0.0298	0.1924
chr22	51304566	945247	0.0184	0.1495
chrMT	16571	40650	2.4531	2.0815
chrX	155270560	2273789	0.0146	0.1322
chrY	59373566	653408	0.011	0.1602

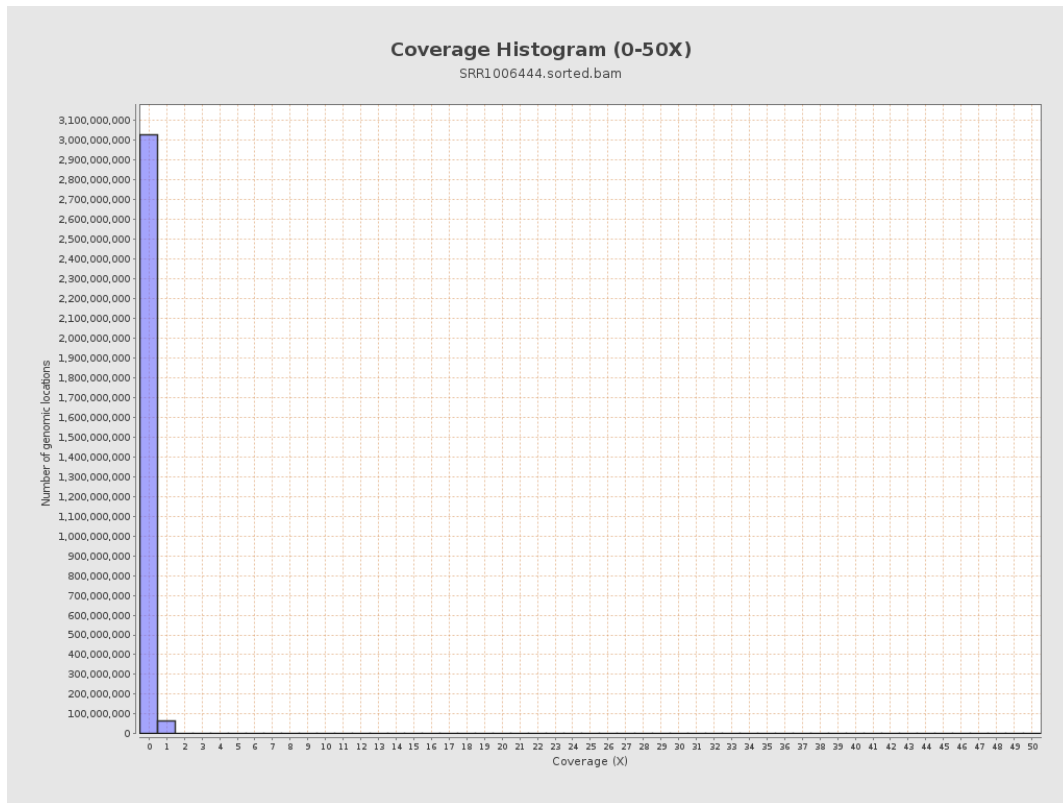
3. Results : Coverage across reference



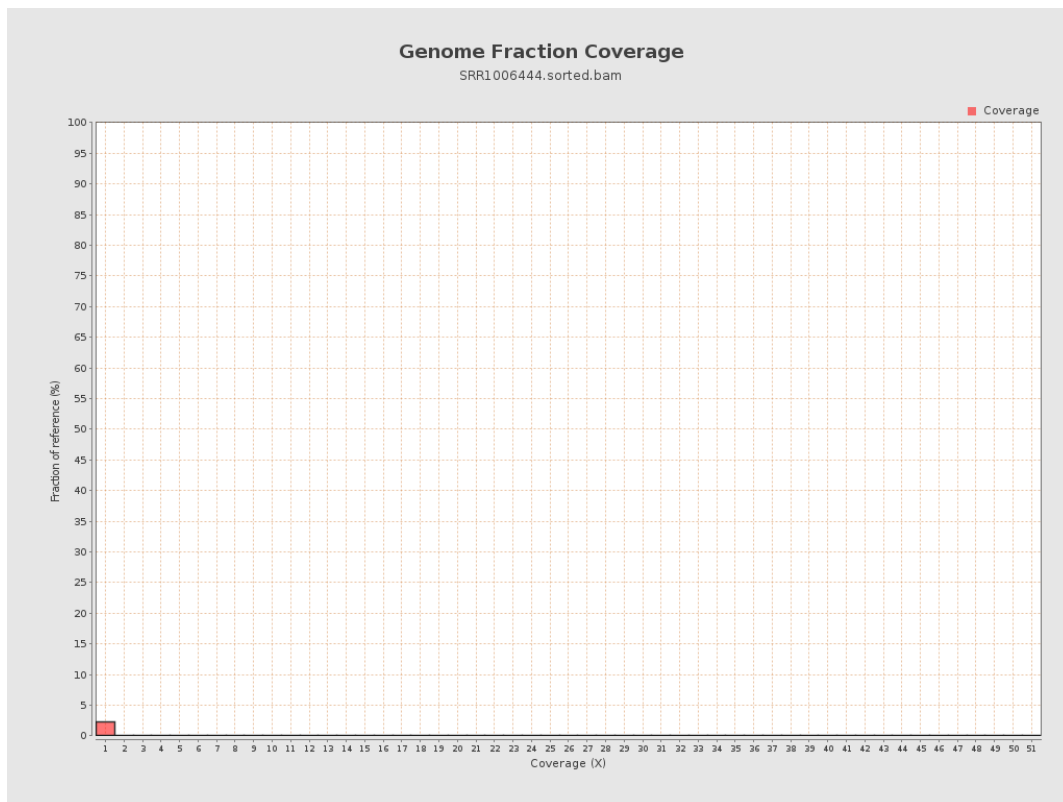
4. Results : Coverage Histogram



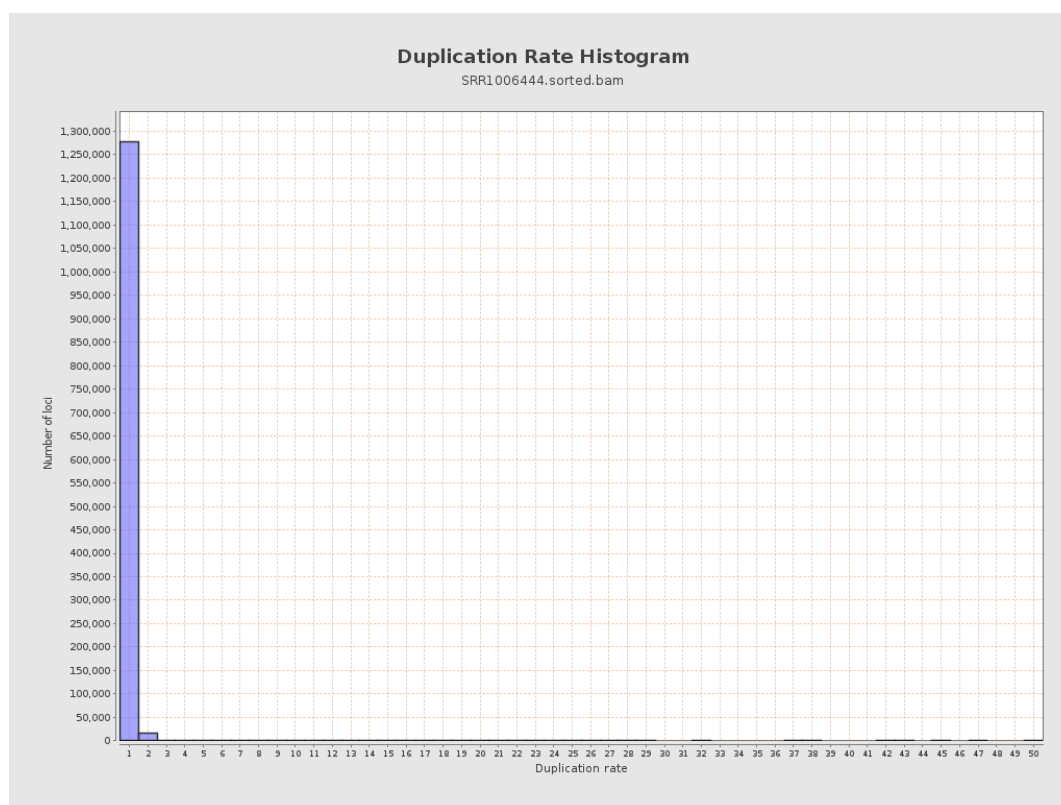
5. Results : Coverage Histogram (0-50X)



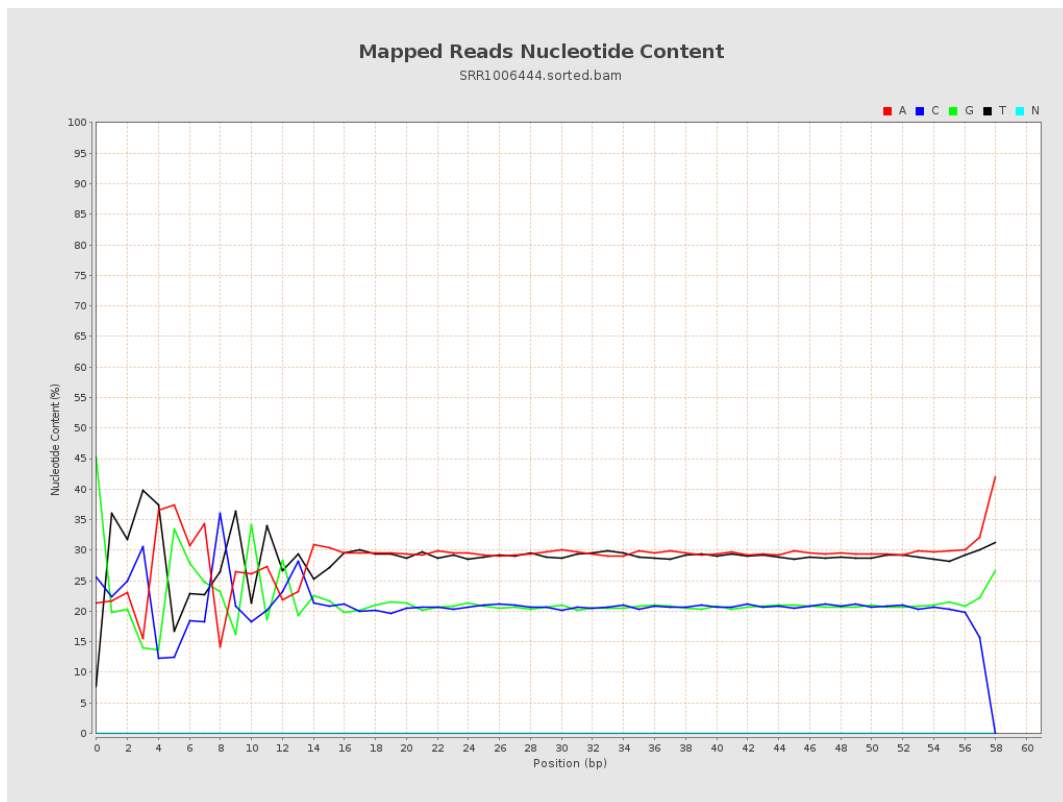
6. Results : Genome Fraction Coverage



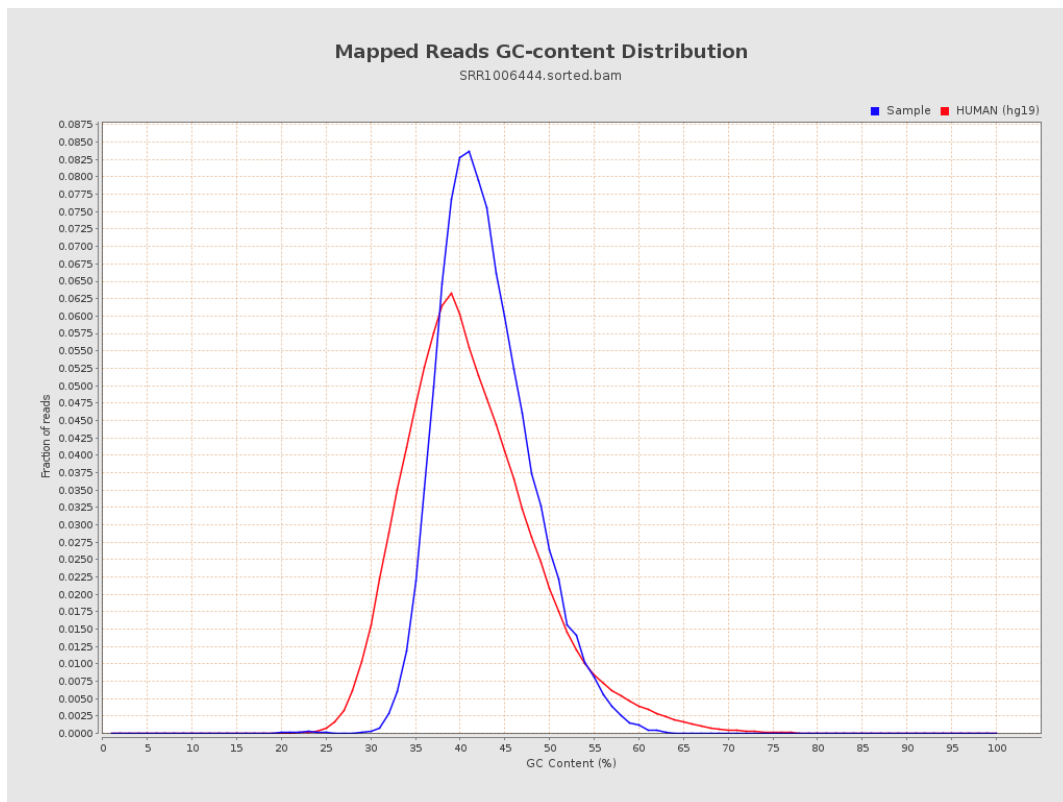
7. Results : Duplication Rate Histogram



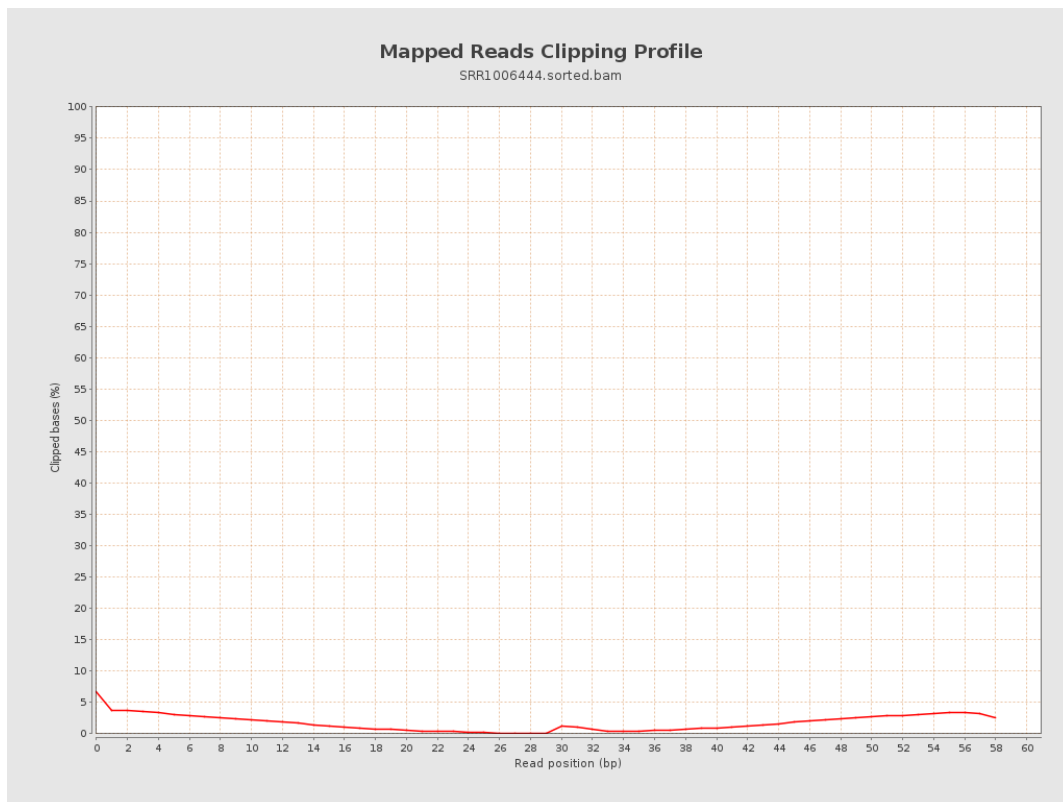
8. Results : Mapped Reads Nucleotide Content



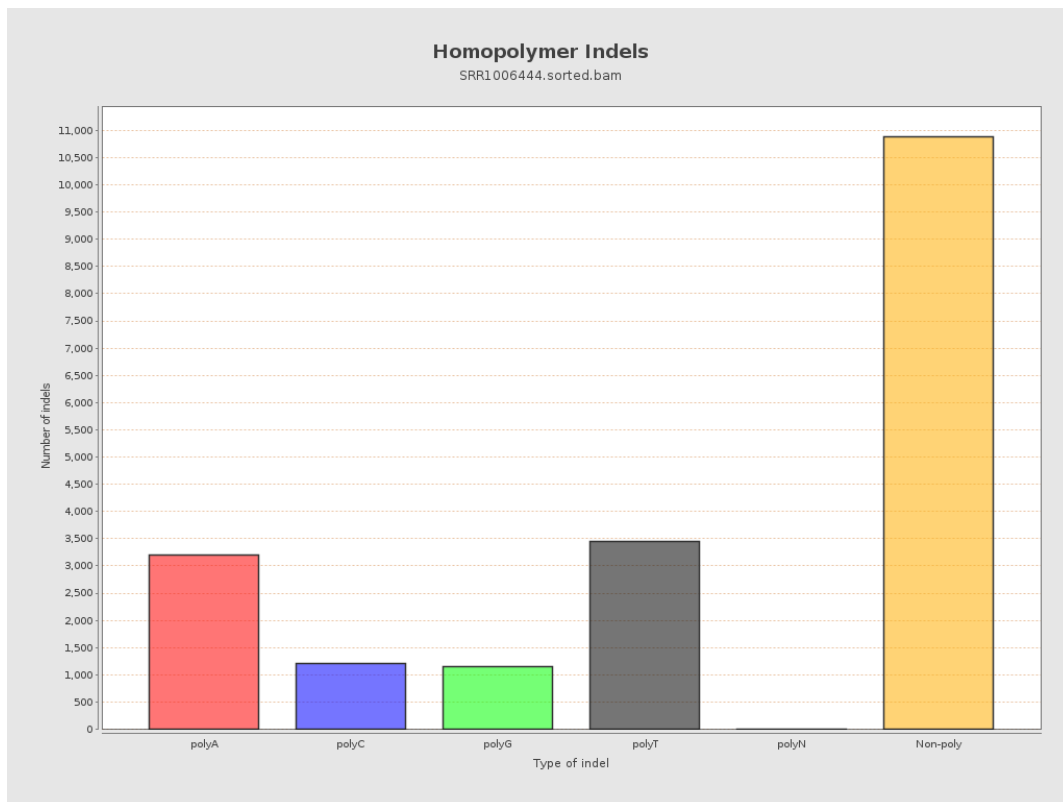
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

