

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 08:13:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237836.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_SRR6237836 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237836.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 08:13:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237836.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,523,187
Mapped reads	1,084,197 / 71.18%
Unmapped reads	438,990 / 28.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,348 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	36,687 / 2.41%
Duplication rate	2.52%
Clipped reads	599,358 / 39.35%

2.2. ACGT Content

Number/percentage of A's	20,353,644 / 29.29%
Number/percentage of C's	11,751,013 / 16.91%
Number/percentage of T's	21,462,970 / 30.89%
Number/percentage of G's	15,864,998 / 22.83%
Number/percentage of N's	59,768 / 0.09%
GC Percentage	39.74%

2.3. Coverage

Mean	0.0225

Standard Deviation	0.2058
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2.4. Mapping Quality

Mean Mapping Quality	46.62
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2.5. Mismatches and indels

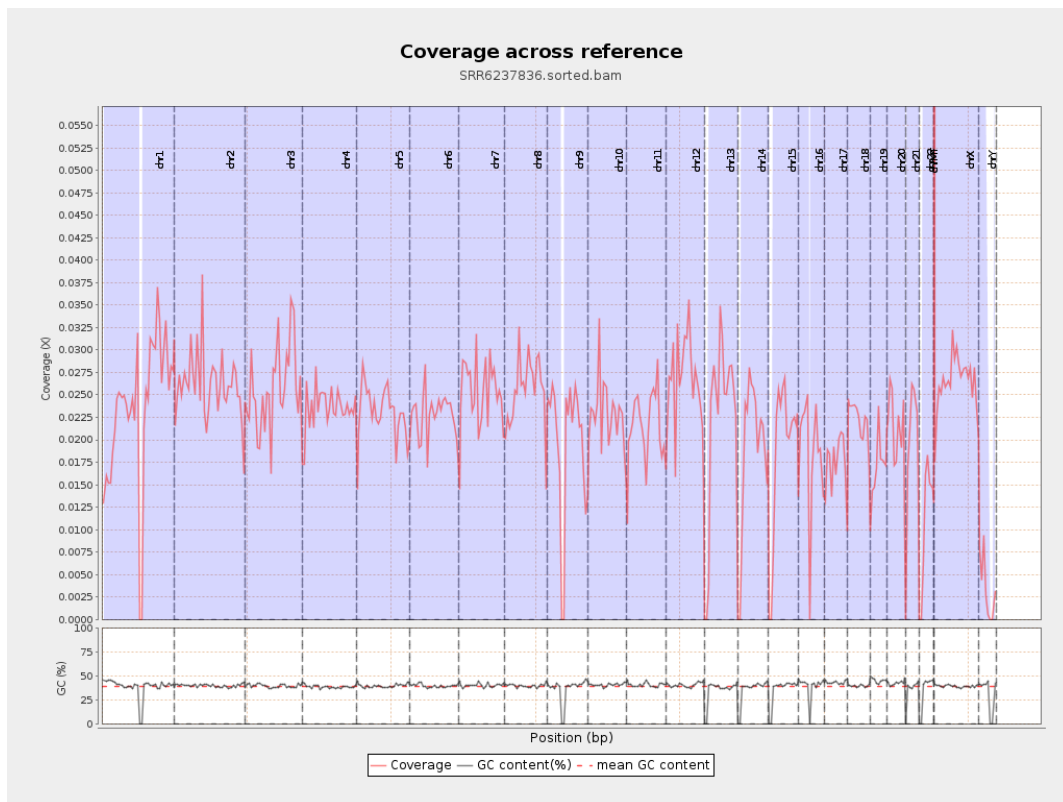
General error rate	1.1%
Mismatches	750,736
Insertions	6,287
Mapped reads with at least one insertion	0.57%
Deletions	27,365
Mapped reads with at least one deletion	2.48%
Homopolymer indels	48.74%

2.6. Chromosome stats

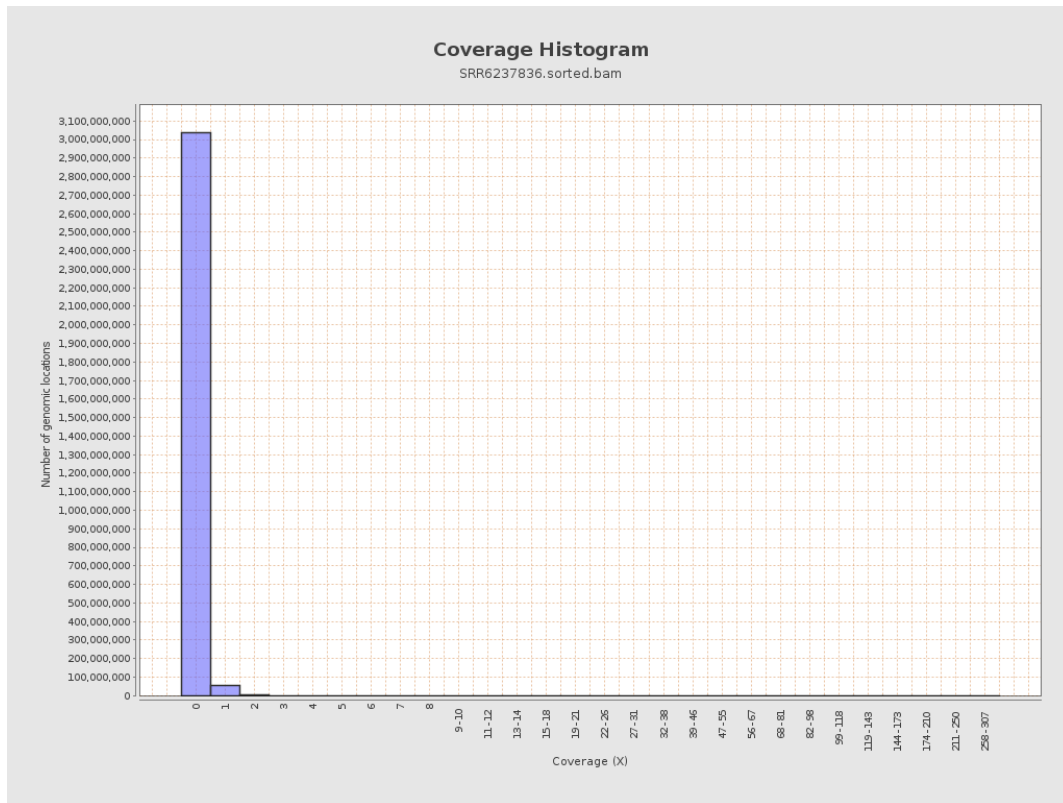
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5866809	0.0235	0.2697
chr2	243199373	6345679	0.0261	0.2323
chr3	198022430	5069437	0.0256	0.188
chr4	191154276	4486399	0.0235	0.1781
chr5	180915260	4207026	0.0233	0.1736
chr6	171115067	3889549	0.0227	0.1834
chr7	159138663	4041343	0.0254	0.2557

chr8	146364022	3737956	0.0255	0.2655
chr9	141213431	2772549	0.0196	0.1933
chr10	135534747	3080225	0.0227	0.2056
chr11	135006516	2924506	0.0217	0.2068
chr12	133851895	3581756	0.0268	0.1946
chr13	115169878	2553898	0.0222	0.1737
chr14	107349540	2011188	0.0187	0.1618
chr15	102531392	1919071	0.0187	0.1592
chr16	90354753	1648040	0.0182	0.1666
chr17	81195210	1412746	0.0174	0.157
chr18	78077248	1737850	0.0223	0.3019
chr19	59128983	1019369	0.0172	0.1913
chr20	63025520	1345939	0.0214	0.1693
chr21	48129895	952674	0.0198	0.1683
chr22	51304566	572727	0.0112	0.1213
chrMT	16571	36527	2.2043	2.2506
chrX	155270560	4126680	0.0266	0.1929
chrY	59373566	195836	0.0033	0.0786

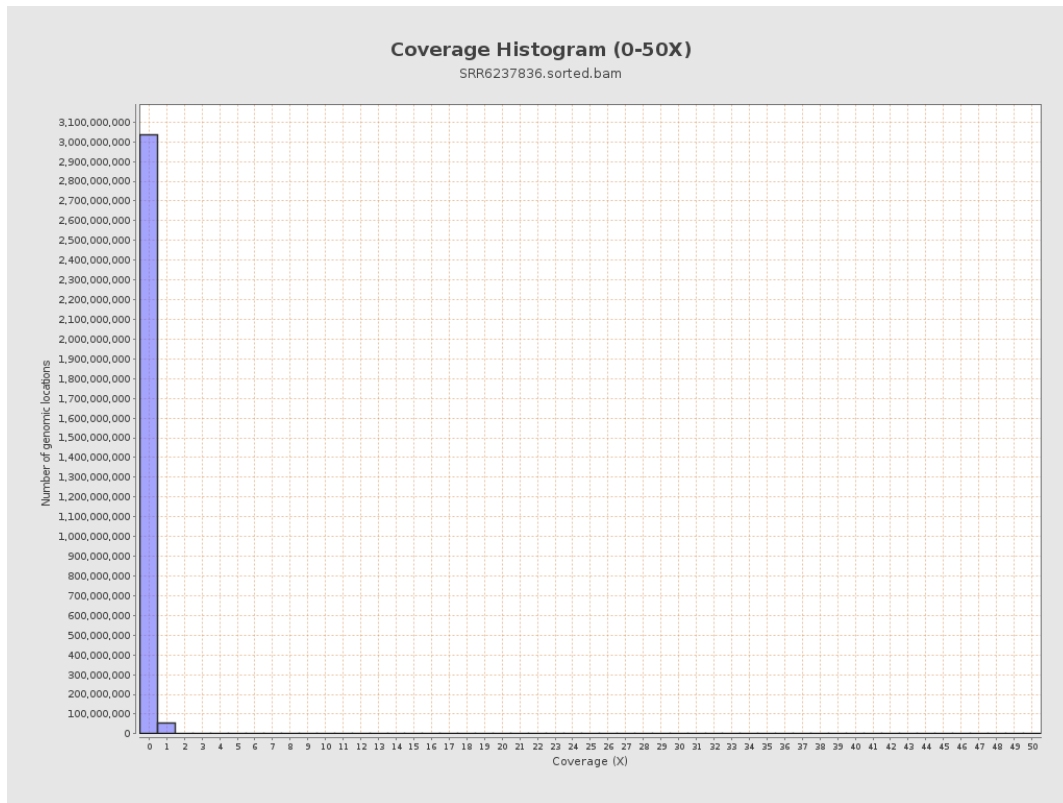
3. Results : Coverage across reference



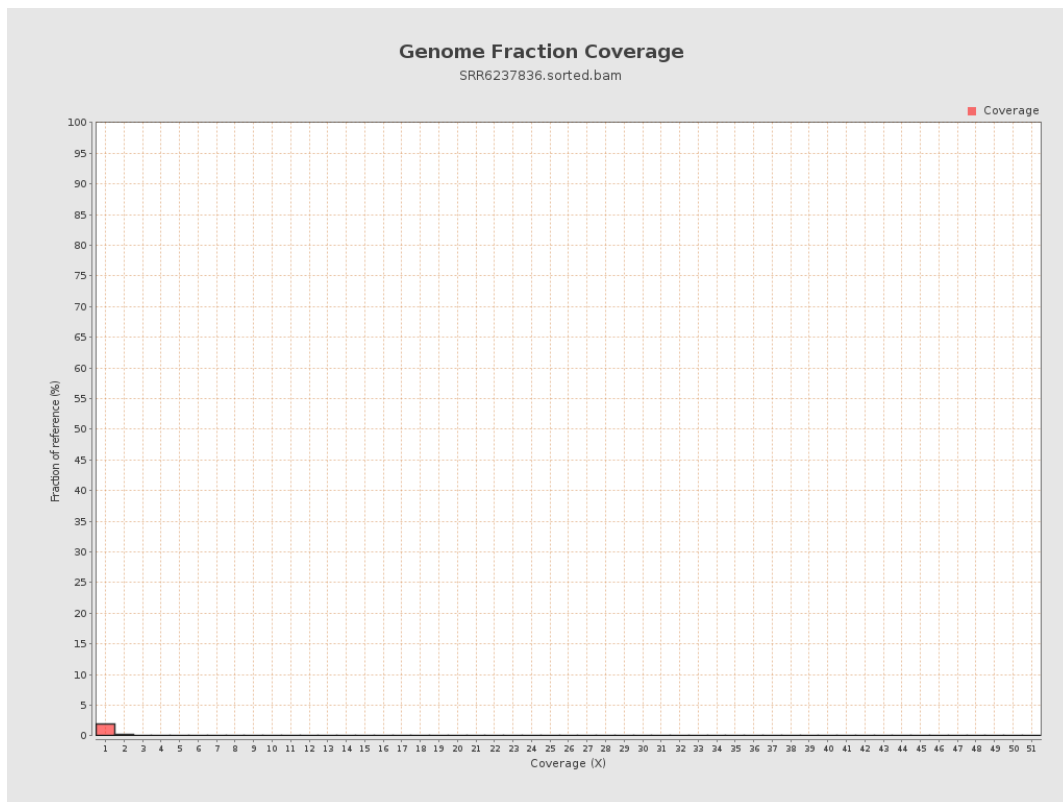
4. Results : Coverage Histogram



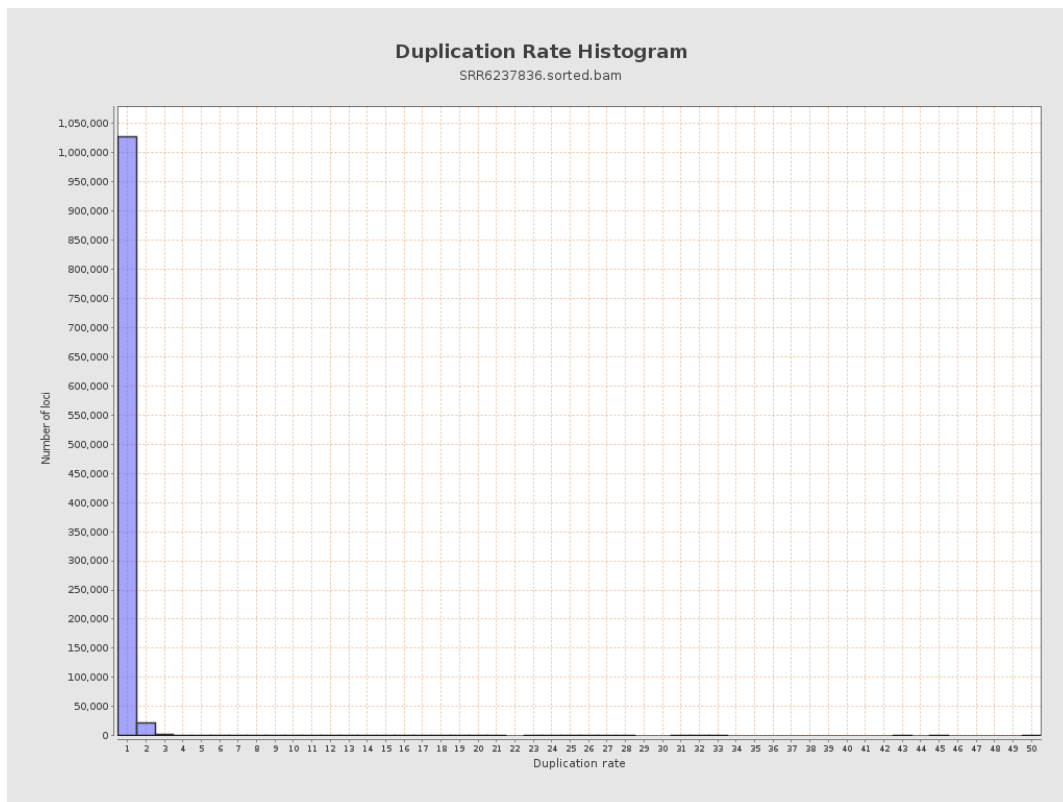
5. Results : Coverage Histogram (0-50X)



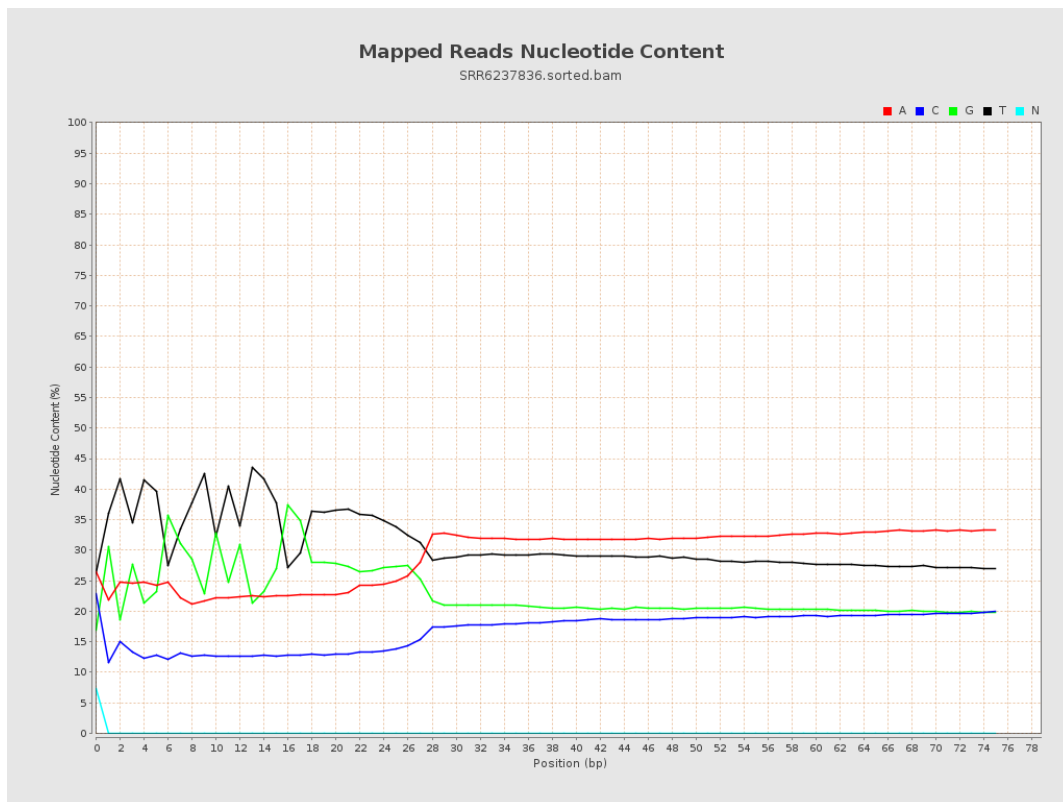
6. Results : Genome Fraction Coverage



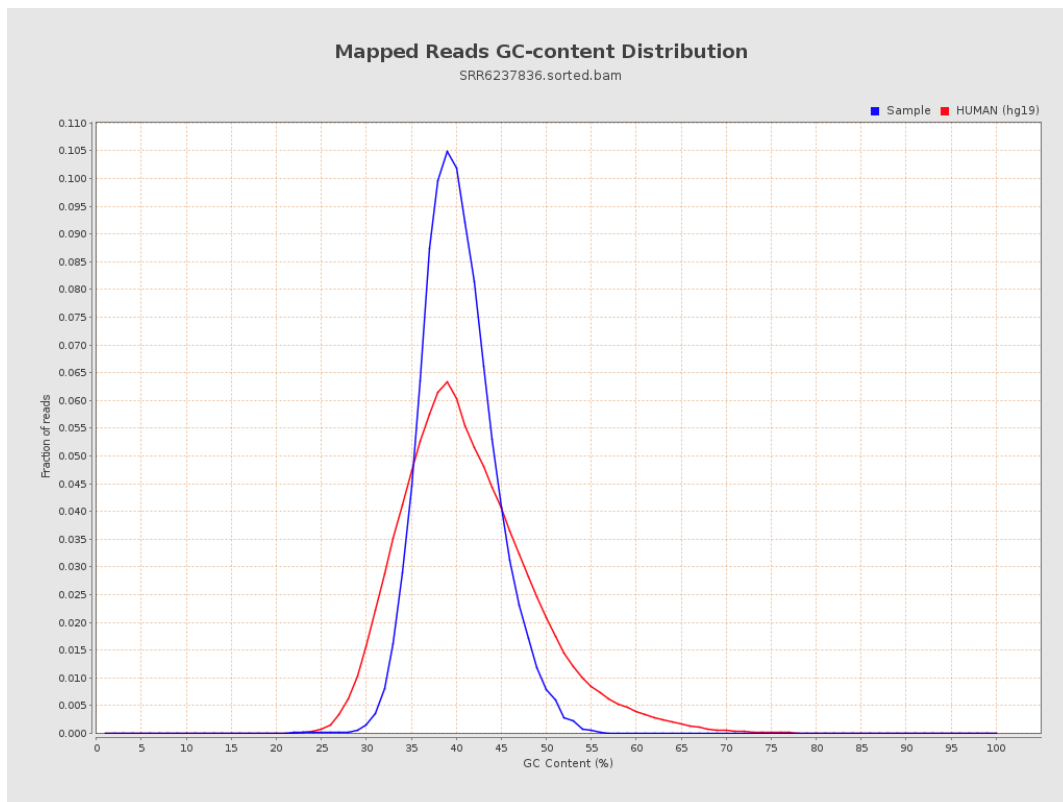
7. Results : Duplication Rate Histogram



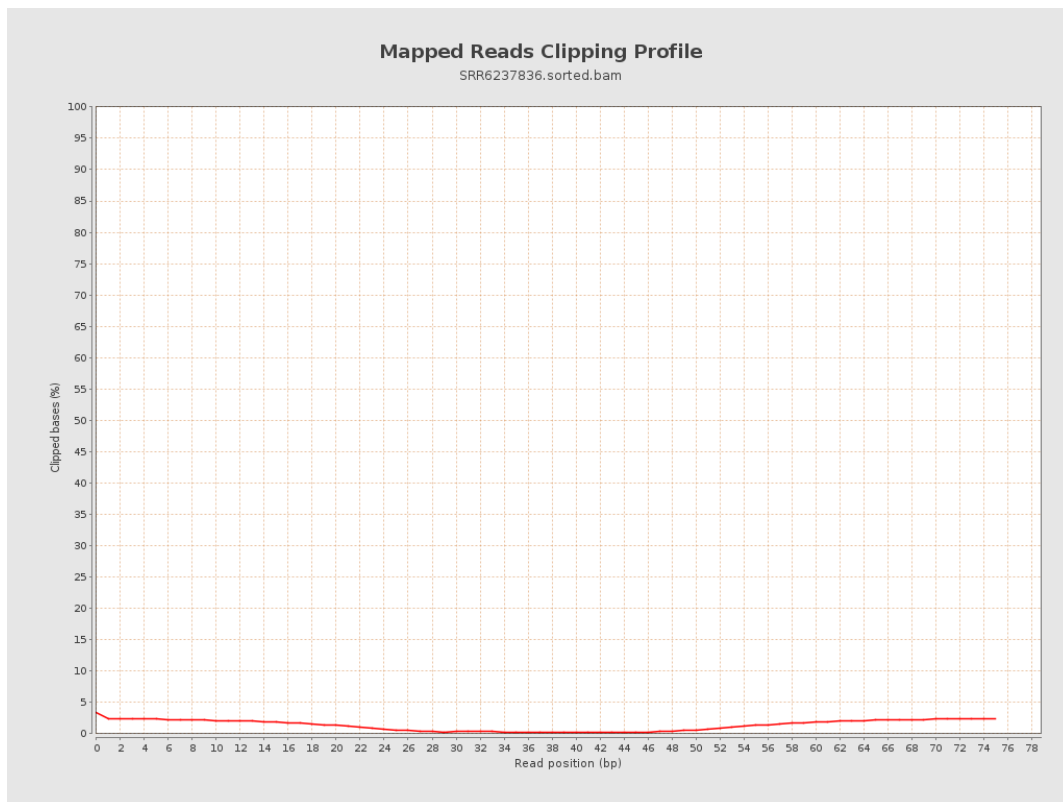
8. Results : Mapped Reads Nucleotide Content



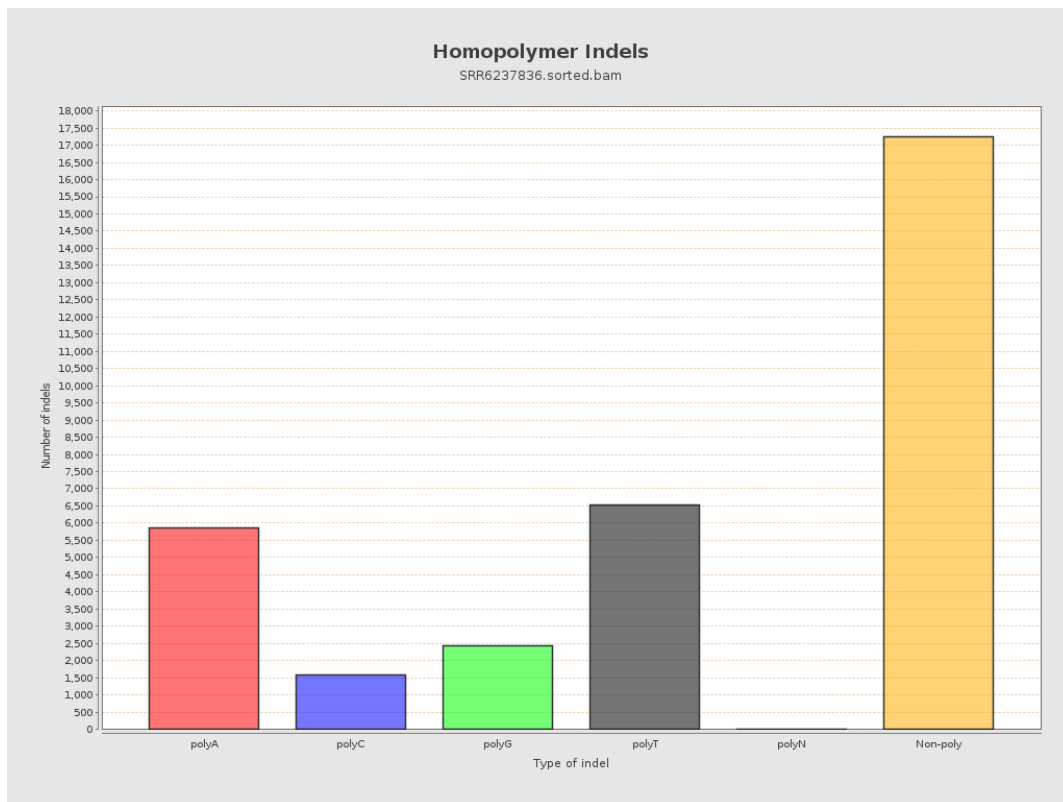
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

