

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 22:04:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231717.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_SRR6231717 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231717.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 22:04:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231717.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	712,776
Mapped reads	288,197 / 40.43%
Unmapped reads	424,579 / 59.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,904 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	19,671 / 2.76%
Duplication rate	5.62%
Clipped reads	173,071 / 24.28%

2.2. ACGT Content

Number/percentage of A's	5,000,270 / 27.98%
Number/percentage of C's	2,893,524 / 16.19%
Number/percentage of T's	6,132,692 / 34.31%
Number/percentage of G's	3,845,396 / 21.52%
Number/percentage of N's	854 / 0%
GC Percentage	37.71%

2.3. Coverage

Mean	0.0058

Standard Deviation	0.122
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2.4. Mapping Quality

Mean Mapping Quality	45.17
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2.5. Mismatches and indels

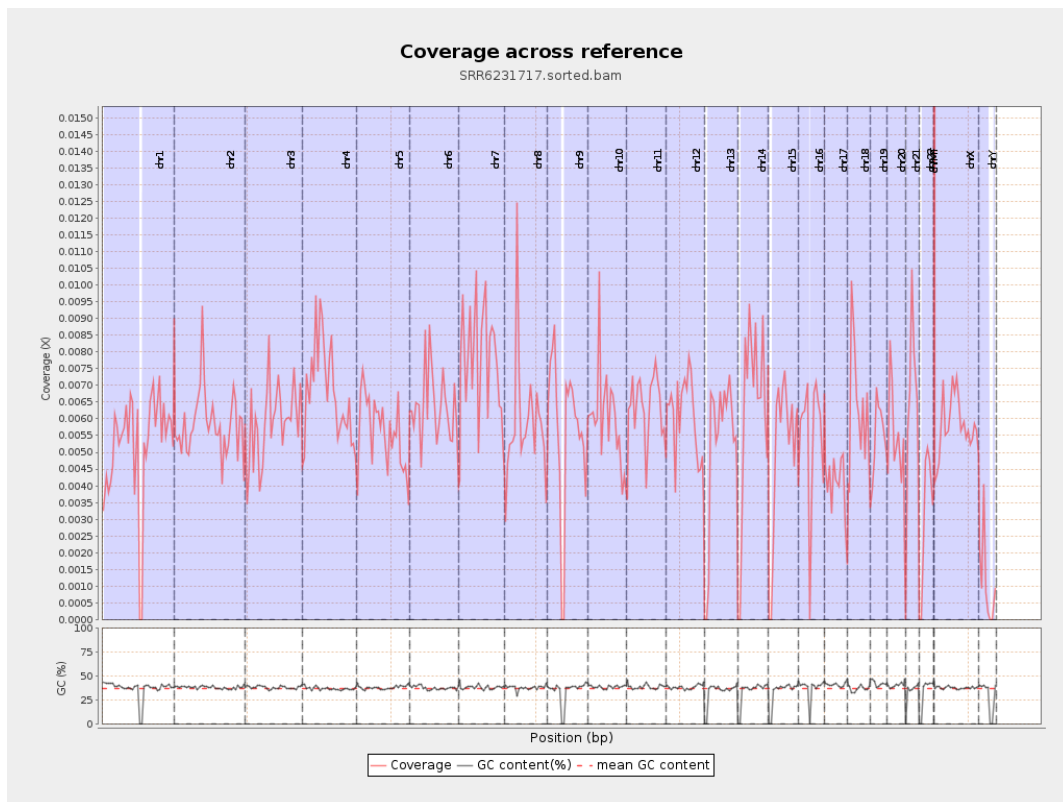
General error rate	1.06%
Mismatches	185,140
Insertions	1,773
Mapped reads with at least one insertion	0.61%
Deletions	9,909
Mapped reads with at least one deletion	3.36%
Homopolymer indels	42.11%

2.6. Chromosome stats

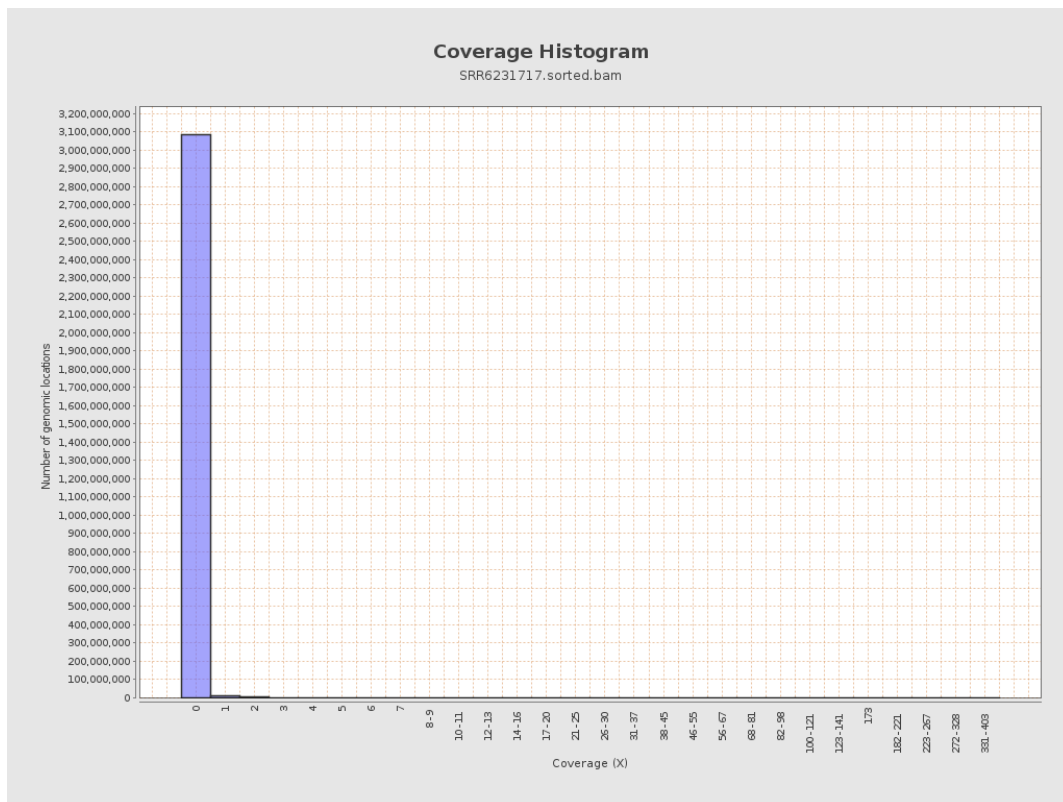
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	1304533	0.0052	0.1098
chr2	243199373	1419878	0.0058	0.1103
chr3	198022430	1171532	0.0059	0.0925
chr4	191154276	1294431	0.0068	0.1027
chr5	180915260	1027099	0.0057	0.0923
chr6	171115067	1090775	0.0064	0.1082
chr7	159138663	1237861	0.0078	0.1267

chr8	146364022	858960	0.0059	0.2566
chr9	141213431	797793	0.0056	0.1021
chr10	135534747	810595	0.006	0.0991
chr11	135006516	859320	0.0064	0.1003
chr12	133851895	814396	0.0061	0.1072
chr13	115169878	594819	0.0052	0.09
chr14	107349540	669047	0.0062	0.0978
chr15	102531392	518337	0.0051	0.1038
chr16	90354753	485770	0.0054	0.0906
chr17	81195210	328265	0.004	0.077
chr18	78077248	486882	0.0062	0.3084
chr19	59128983	323721	0.0055	0.0945
chr20	63025520	344562	0.0055	0.089
chr21	48129895	312978	0.0065	0.1
chr22	51304566	164140	0.0032	0.0661
chrMT	16571	6193	0.3737	0.6913
chrX	155270560	903504	0.0058	0.0948
chrY	59373566	64740	0.0011	0.0433

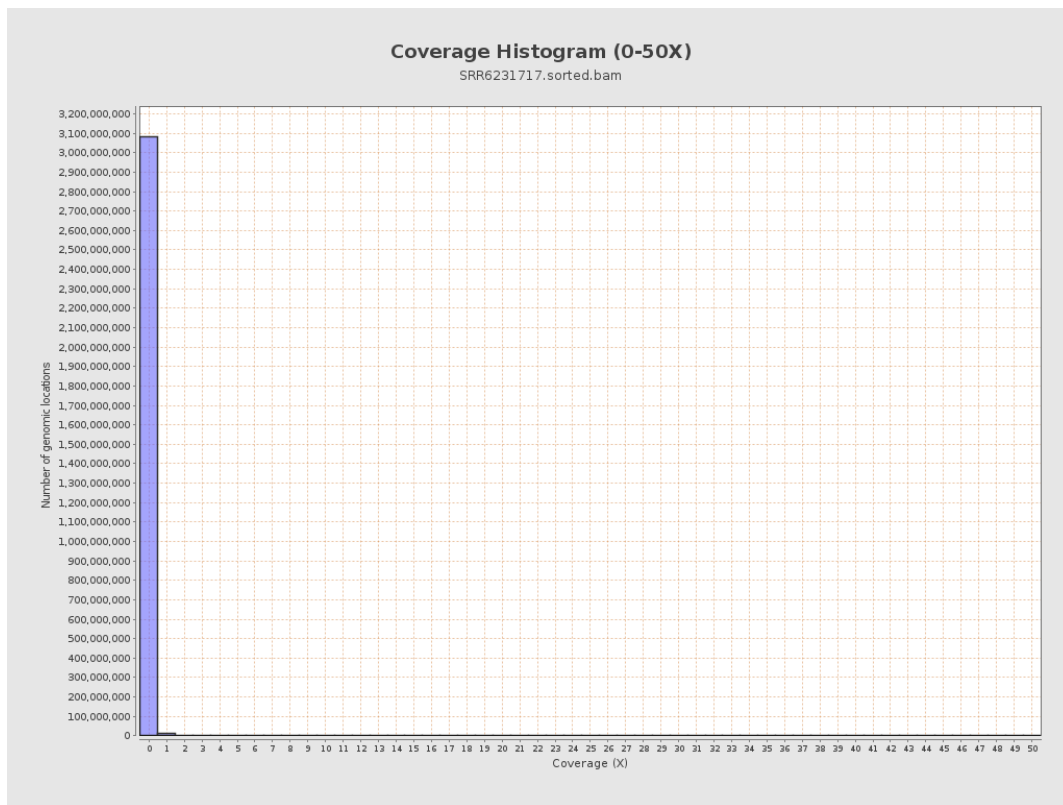
3. Results : Coverage across reference



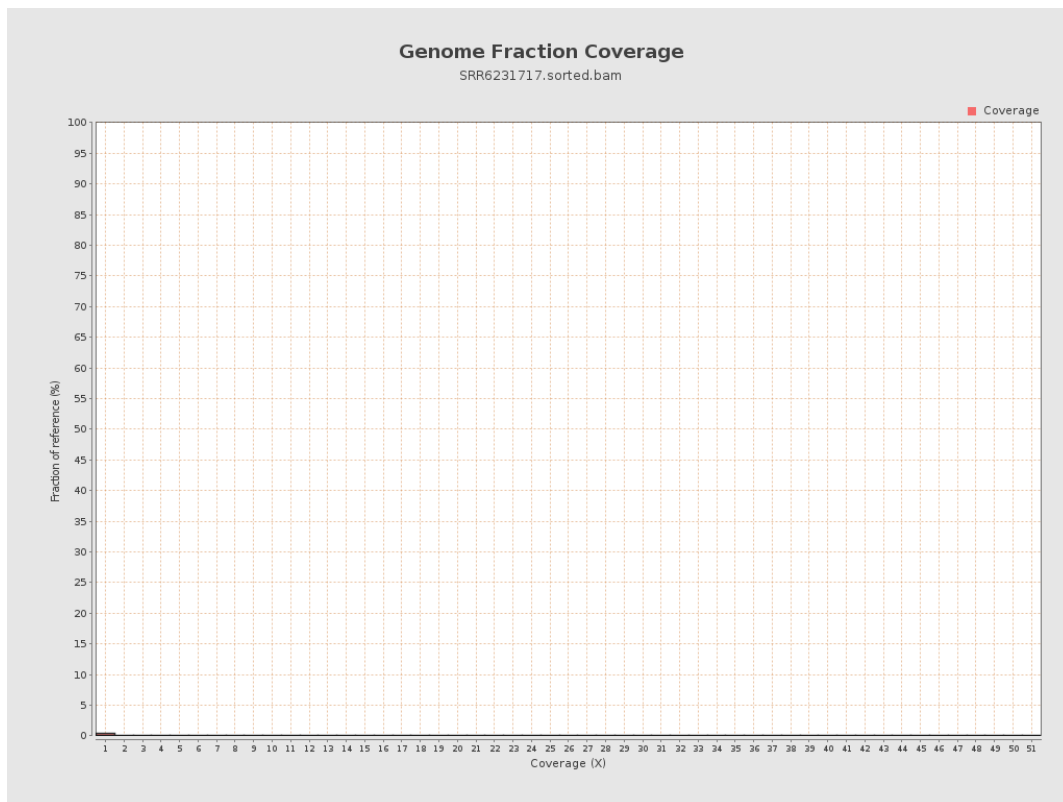
4. Results : Coverage Histogram



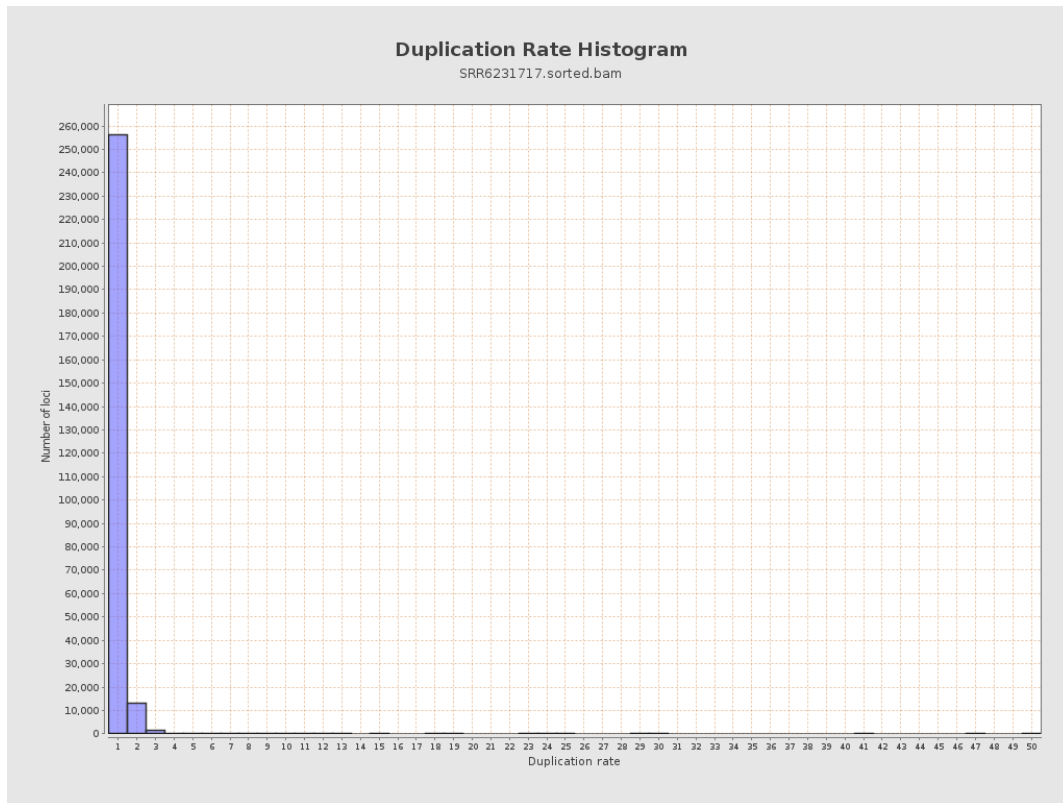
5. Results : Coverage Histogram (0-50X)



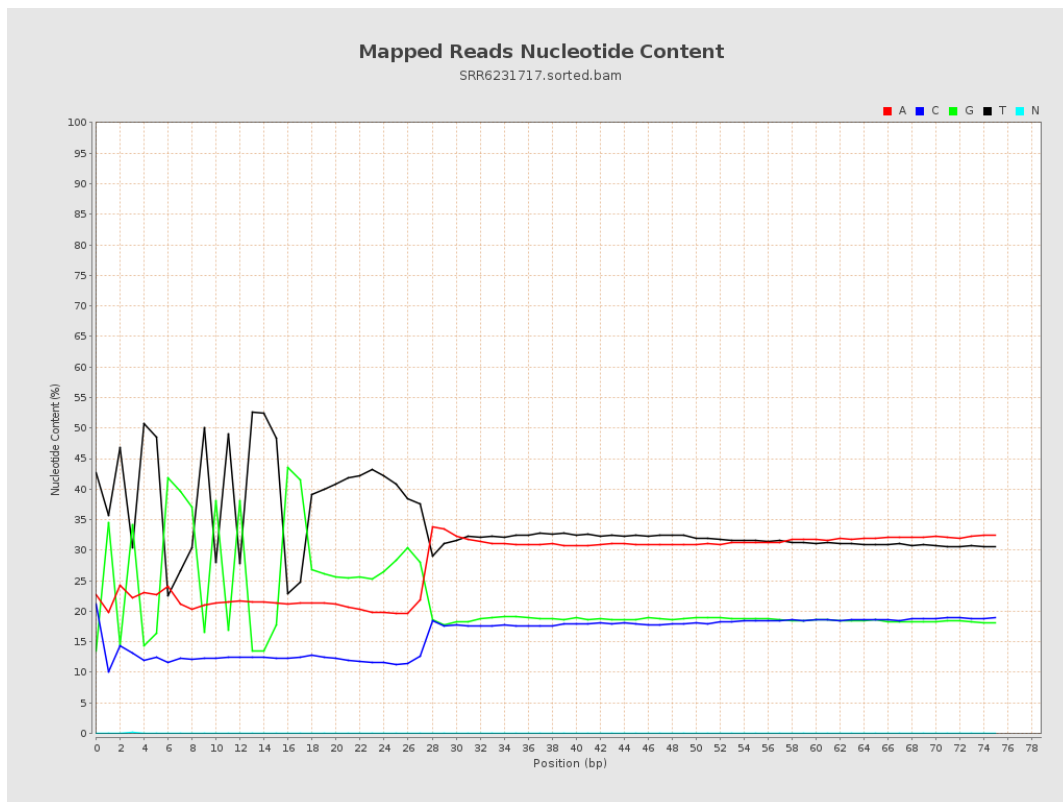
6. Results : Genome Fraction Coverage



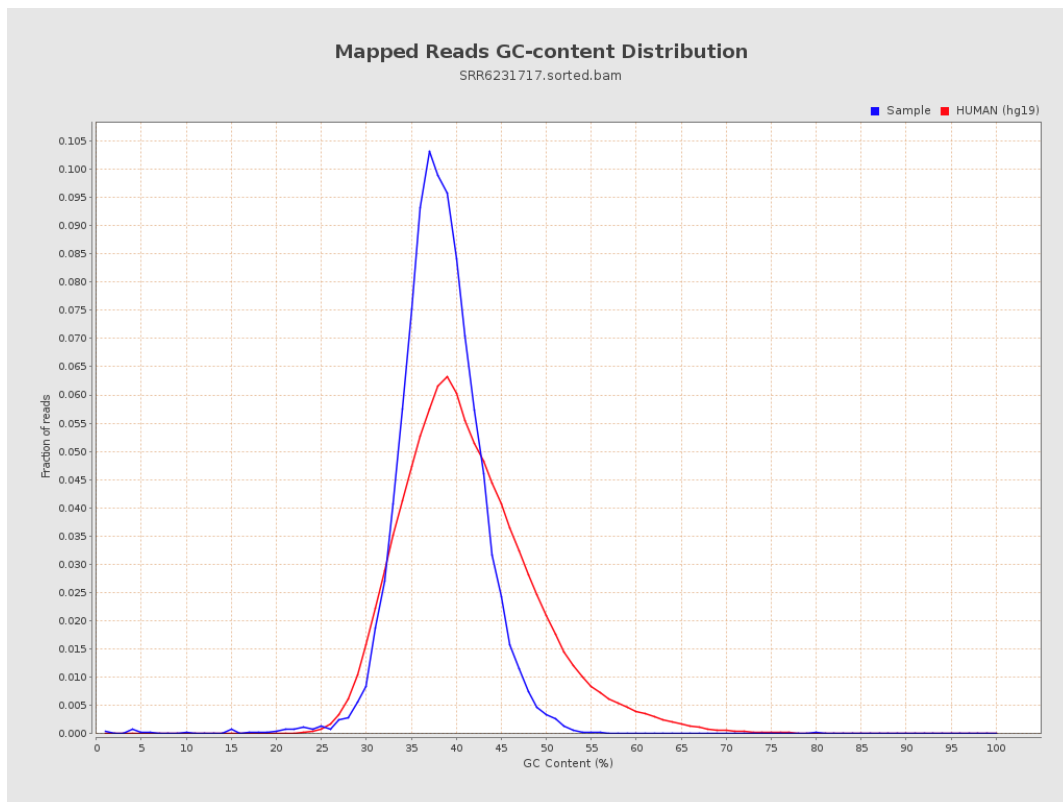
7. Results : Duplication Rate Histogram



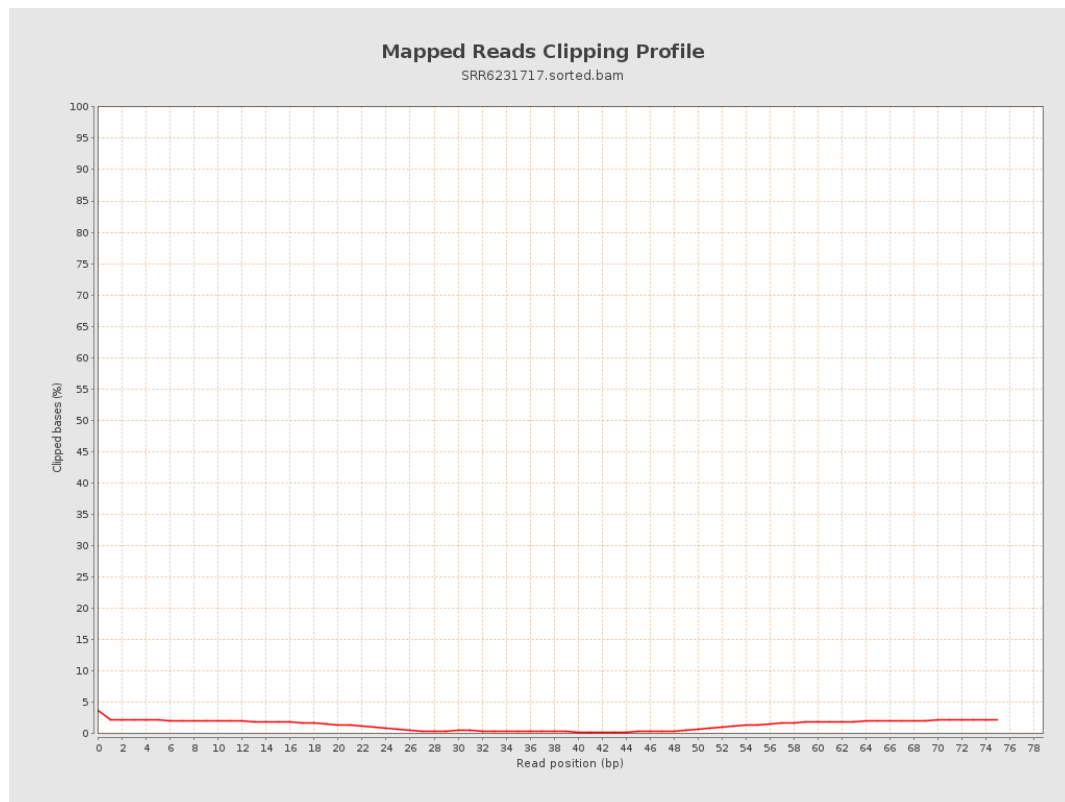
8. Results : Mapped Reads Nucleotide Content



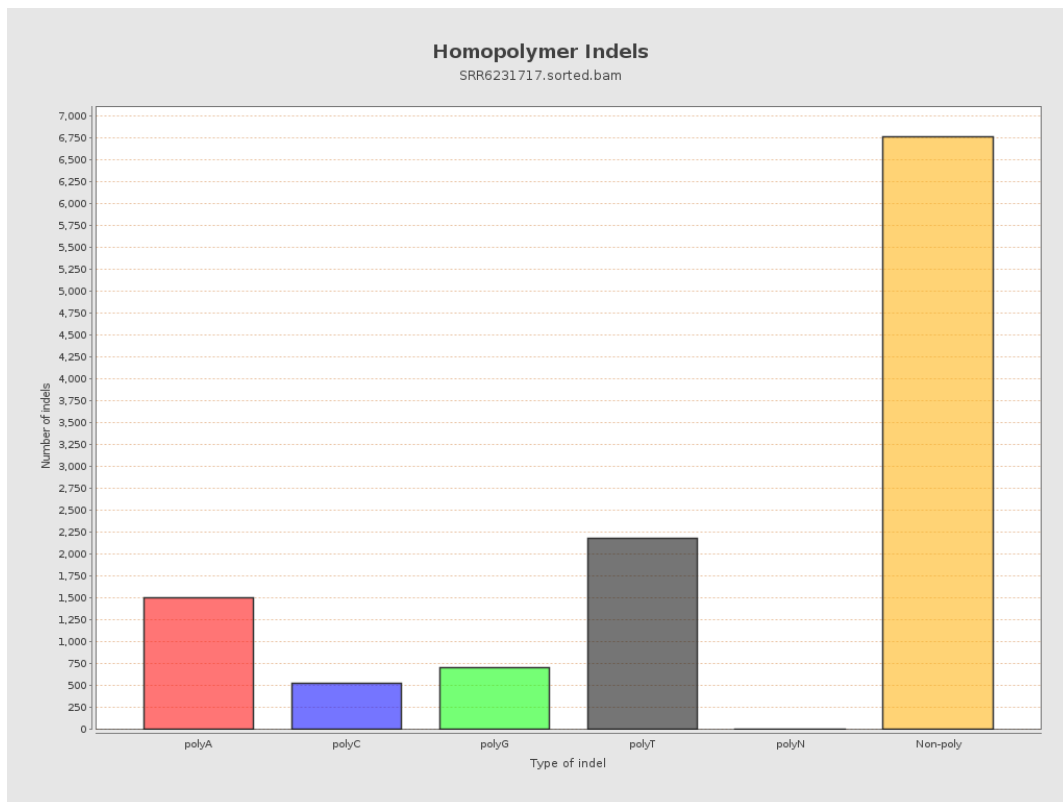
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

