

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 06:06:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008667.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_SRR6008667 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008667.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 06:05:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008667.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,812,913
Mapped reads	1,514,017 / 83.51%
Unmapped reads	298,896 / 16.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,481 / 0.74%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	89,285 / 4.92%
Duplication rate	4.84%
Clipped reads	731,072 / 40.33%

2.2. ACGT Content

Number/percentage of A's	27,202,032 / 27.32%
Number/percentage of C's	18,137,658 / 18.21%
Number/percentage of T's	31,724,996 / 31.86%
Number/percentage of G's	22,470,569 / 22.57%
Number/percentage of N's	42,845 / 0.04%
GC Percentage	40.78%

2.3. Coverage

Mean	0.0322

Standard Deviation	0.3092
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2.4. Mapping Quality

Mean Mapping Quality	46.21
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2.5. Mismatches and indels

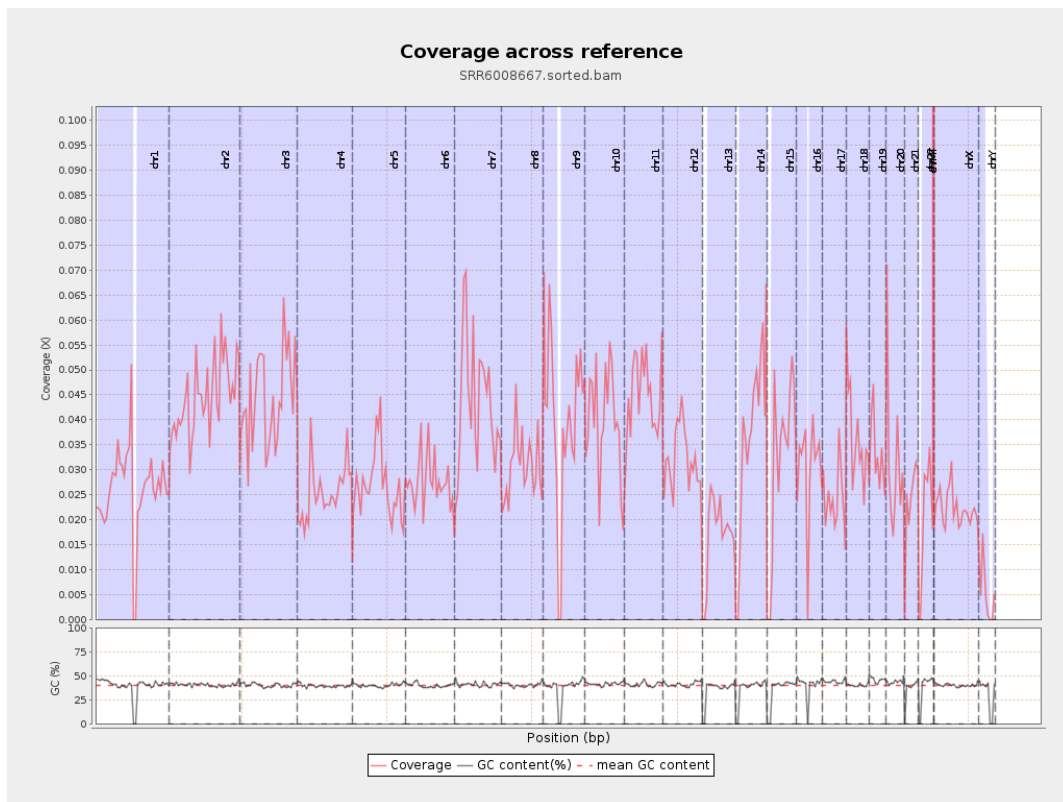
General error rate	0.87%
Mismatches	850,834
Insertions	7,931
Mapped reads with at least one insertion	0.52%
Deletions	29,264
Mapped reads with at least one deletion	1.91%
Homopolymer indels	47.62%

2.6. Chromosome stats

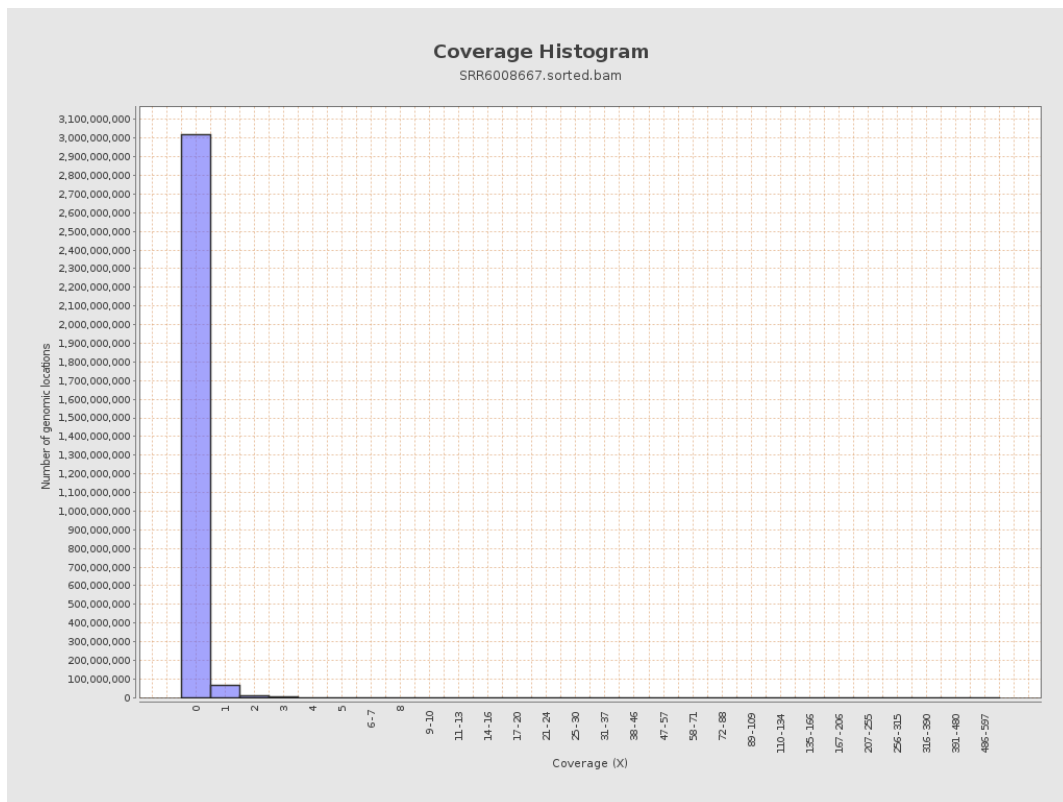
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6494460	0.0261	0.5337
chr2	243199373	10809141	0.0444	0.3626
chr3	198022430	8736094	0.0441	0.2544
chr4	191154276	4858196	0.0254	0.2201
chr5	180915260	4860802	0.0269	0.1976
chr6	171115067	4716308	0.0276	0.237
chr7	159138663	7001362	0.044	0.4326

chr8	146364022	4454970	0.0304	0.3328
chr9	141213431	5536480	0.0392	0.299
chr10	135534747	5397910	0.0398	0.3163
chr11	135006516	6074486	0.045	0.3265
chr12	133851895	4284510	0.032	0.222
chr13	115169878	1919231	0.0167	0.1553
chr14	107349540	3846313	0.0358	0.2378
chr15	102531392	3301205	0.0322	0.2185
chr16	90354753	2754324	0.0305	0.2216
chr17	81195210	1933330	0.0238	0.2108
chr18	78077248	2802029	0.0359	0.4637
chr19	59128983	1964560	0.0332	0.3723
chr20	63025520	1914910	0.0304	0.2163
chr21	48129895	1144563	0.0238	0.2046
chr22	51304566	1022889	0.0199	0.1682
chrMT	16571	54257	3.2742	2.9116
chrX	155270560	3451132	0.0222	0.1998
chrY	59373566	292537	0.0049	0.1377

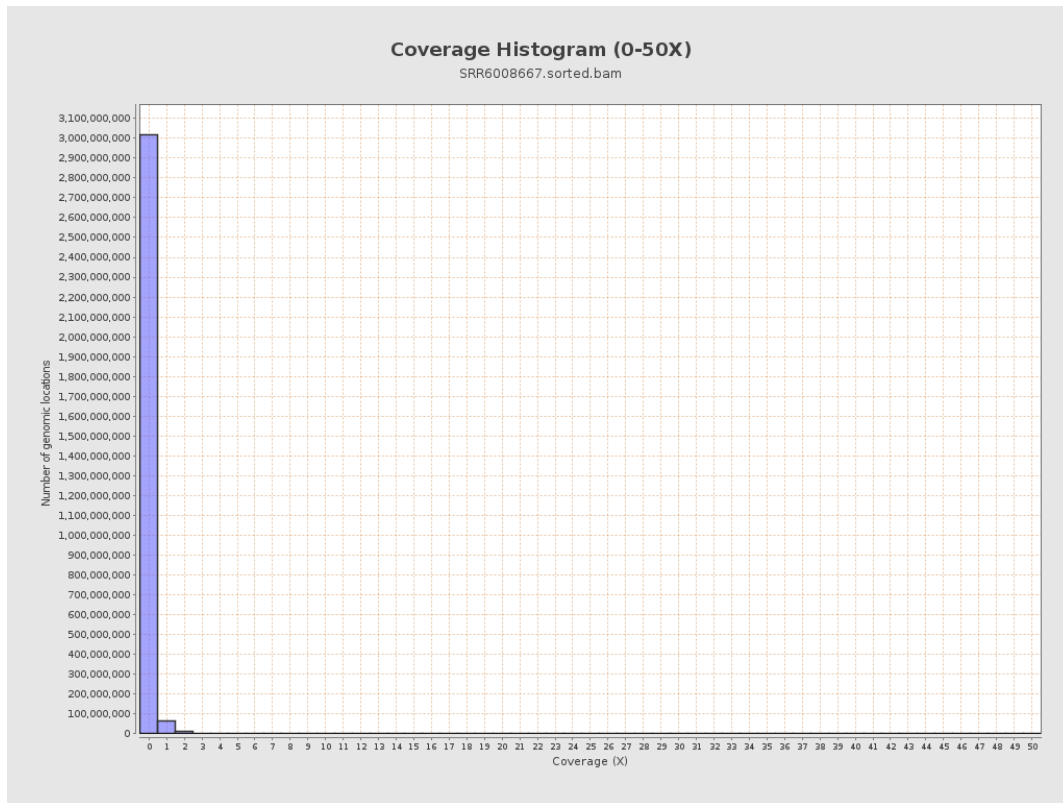
3. Results : Coverage across reference



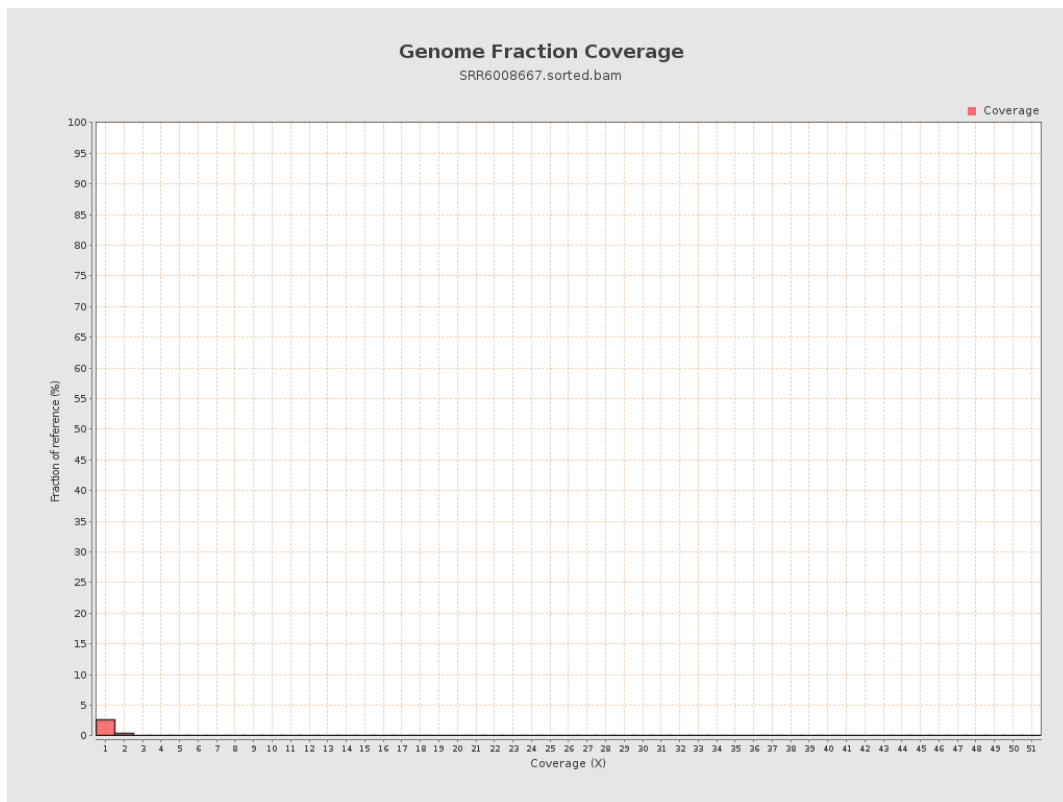
4. Results : Coverage Histogram



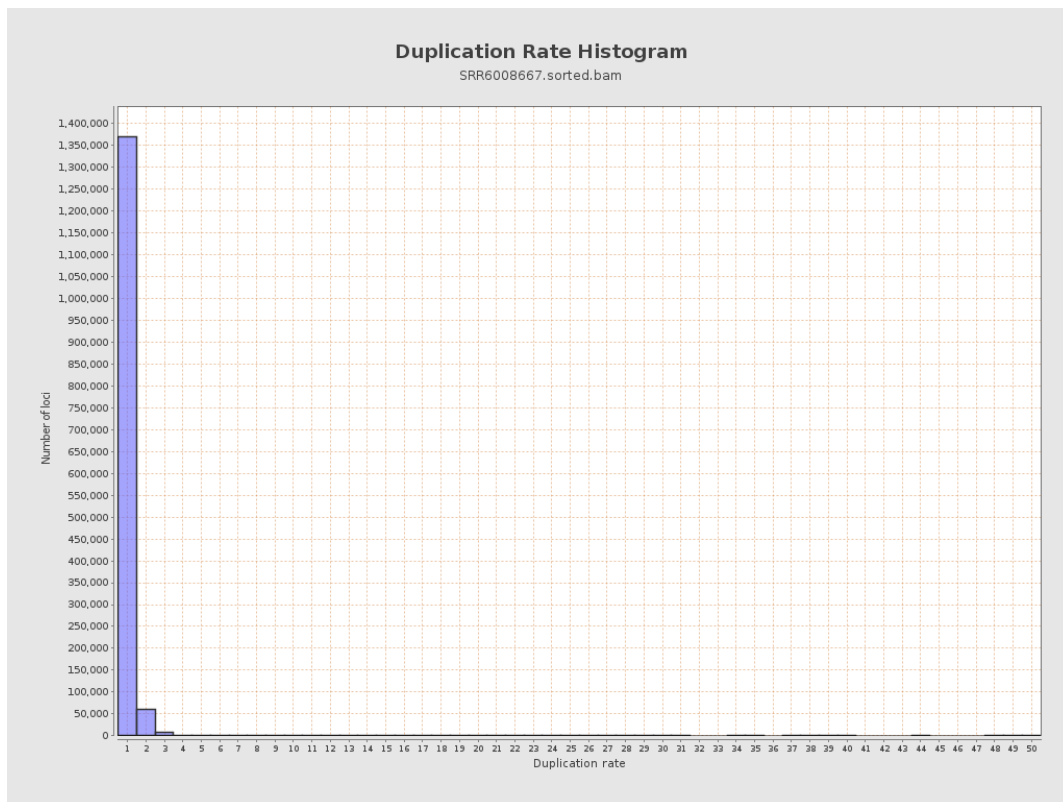
5. Results : Coverage Histogram (0-50X)



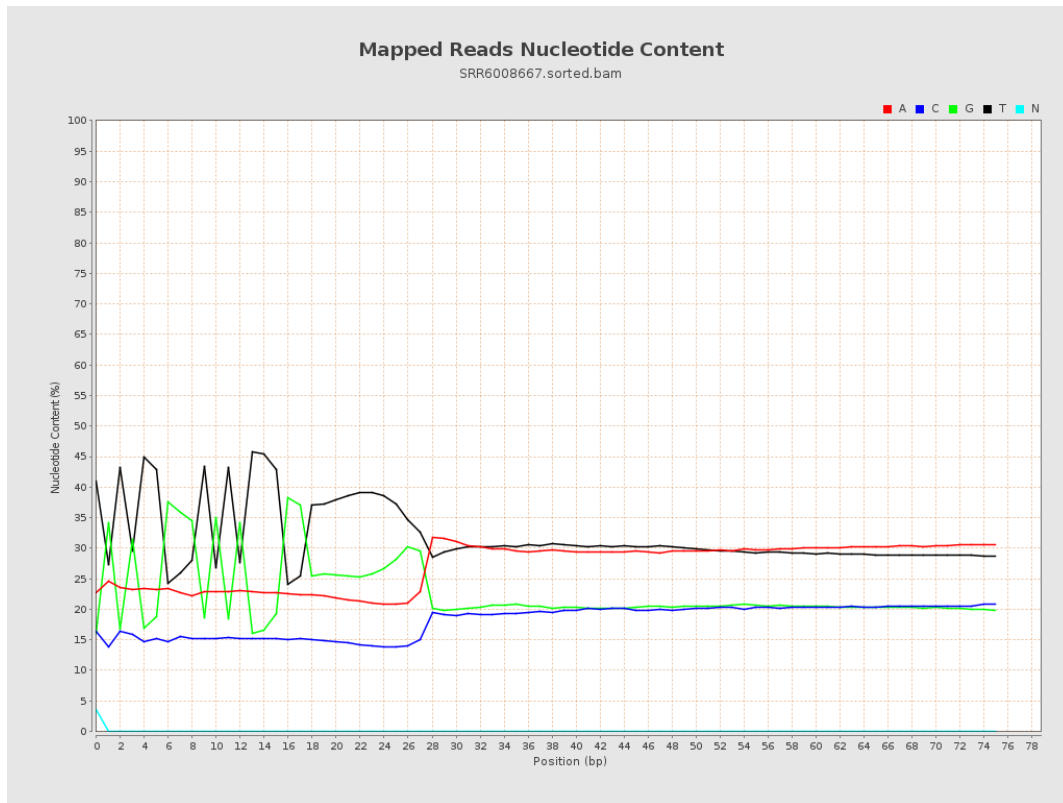
6. Results : Genome Fraction Coverage



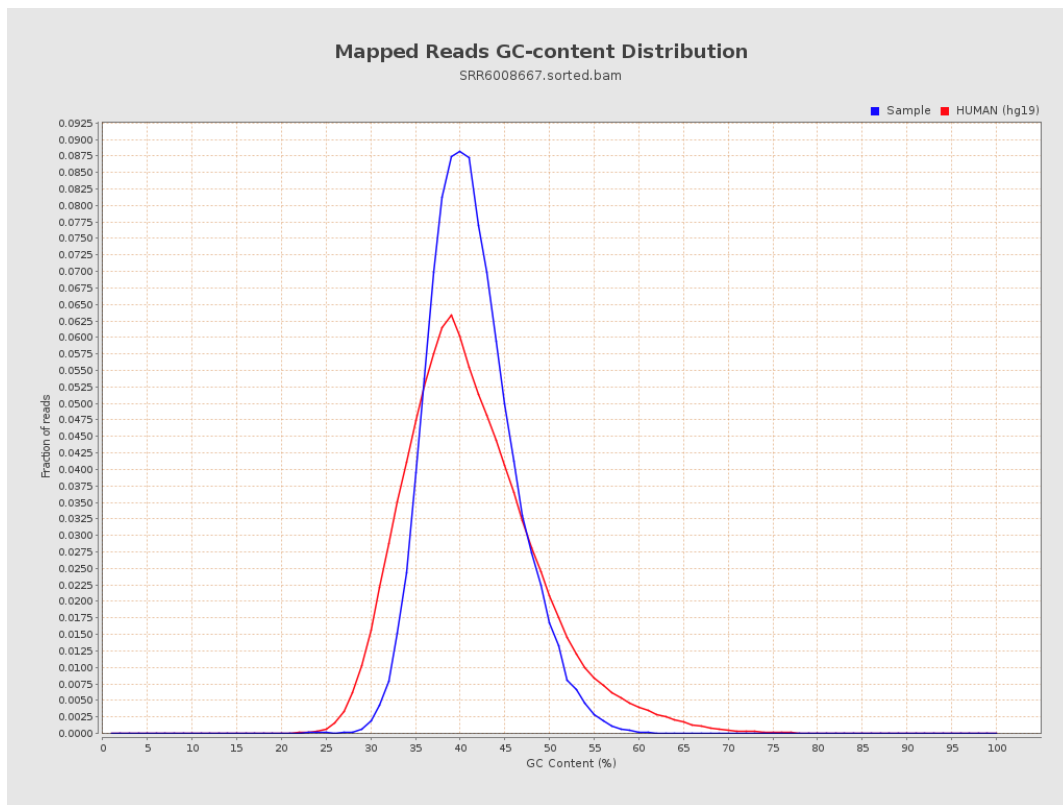
7. Results : Duplication Rate Histogram



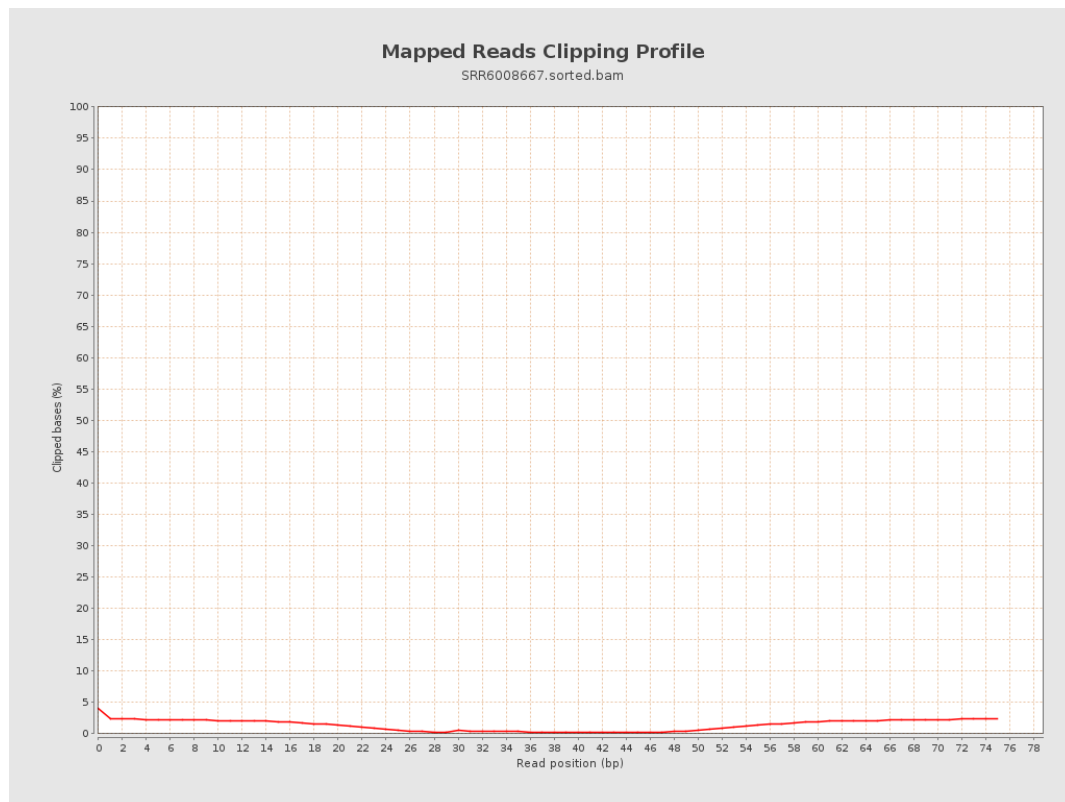
8. Results : Mapped Reads Nucleotide Content



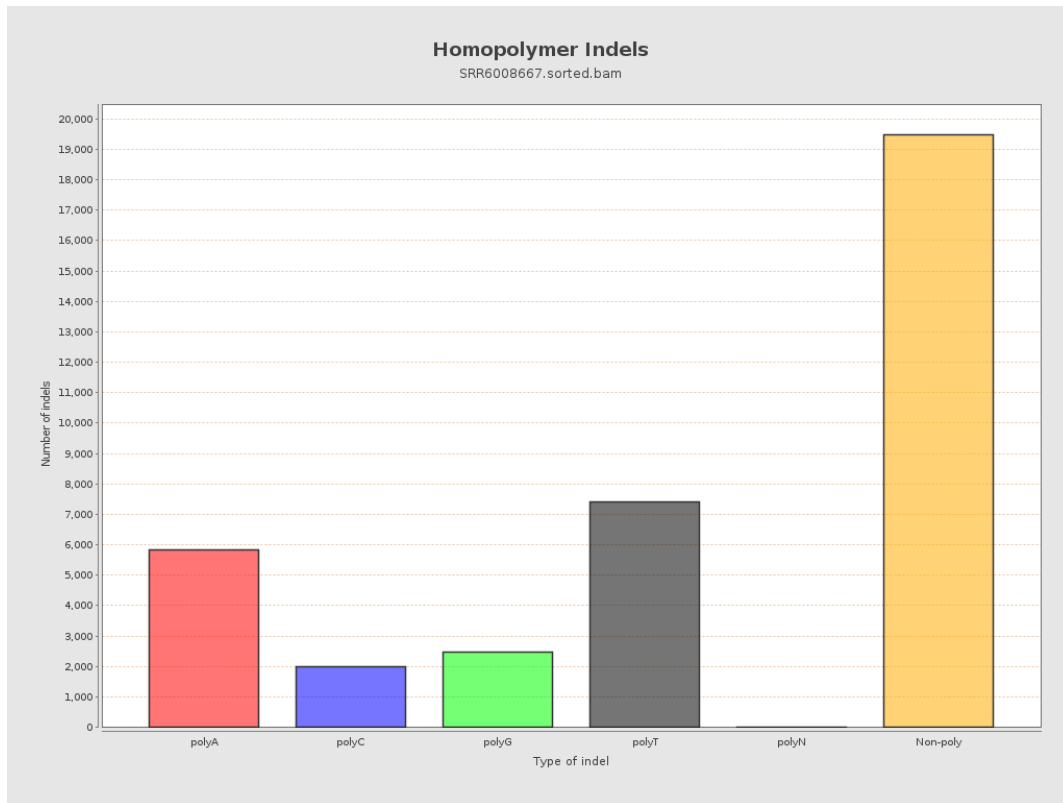
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

