

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 11:49:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008794.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_SRR6008794 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008794.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 11:49:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008794.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,406,342
Mapped reads	1,161,035 / 82.56%
Unmapped reads	245,307 / 17.44%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,340 / 0.81%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	99,703 / 7.09%
Duplication rate	6.97%
Clipped reads	590,805 / 42.01%

2.2. ACGT Content

Number/percentage of A's	20,217,675 / 26.68%
Number/percentage of C's	13,998,403 / 18.47%
Number/percentage of T's	23,954,061 / 31.61%
Number/percentage of G's	17,582,773 / 23.2%
Number/percentage of N's	33,914 / 0.04%
GC Percentage	41.67%

2.3. Coverage

Mean	0.0245

Standard Deviation	0.2741
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2.4. Mapping Quality

Mean Mapping Quality	45.14
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2.5. Mismatches and indels

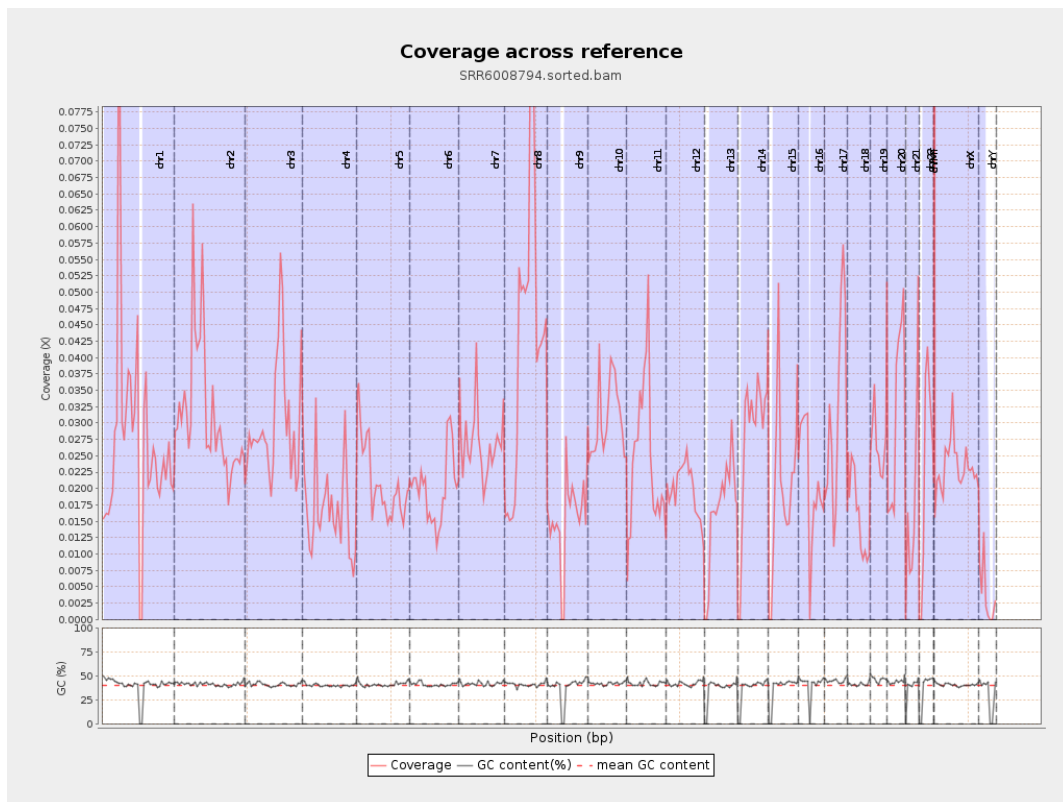
General error rate	0.86%
Mismatches	638,368
Insertions	5,341
Mapped reads with at least one insertion	0.46%
Deletions	19,511
Mapped reads with at least one deletion	1.66%
Homopolymer indels	45.87%

2.6. Chromosome stats

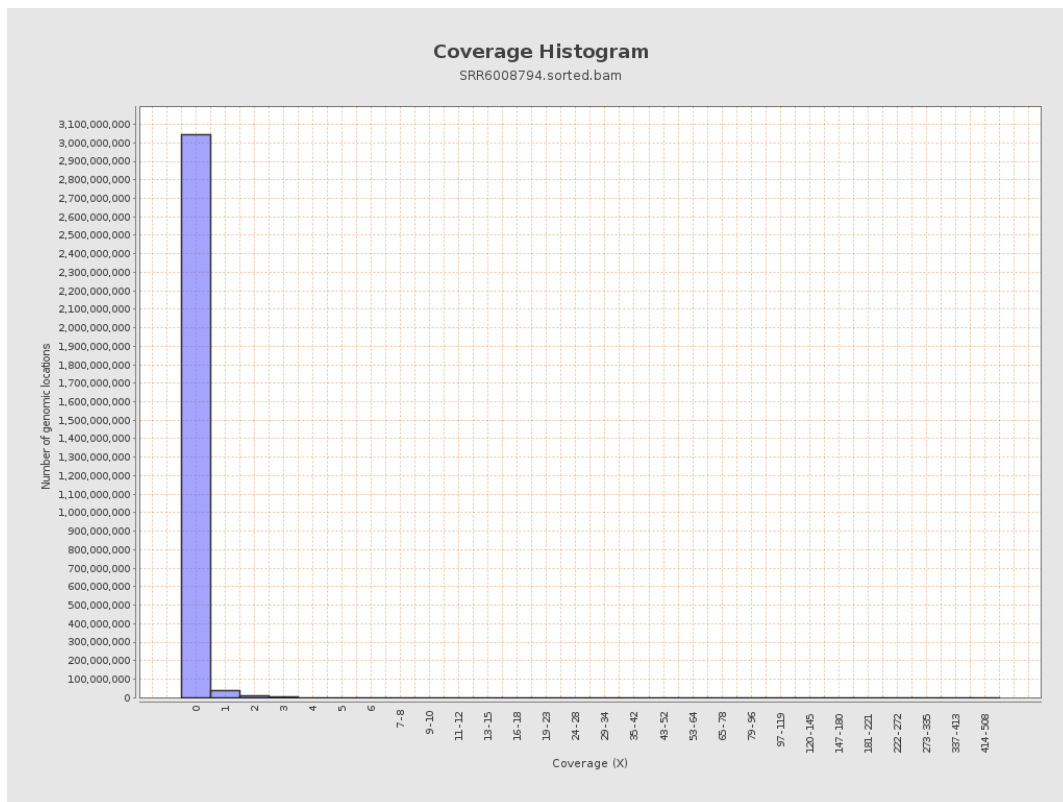
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6654316	0.0267	0.4264
chr2	243199373	7604428	0.0313	0.336
chr3	198022430	5924320	0.0299	0.2304
chr4	191154276	3261983	0.0171	0.1884
chr5	180915260	3775237	0.0209	0.1912
chr6	171115067	3401757	0.0199	0.1966
chr7	159138663	4307609	0.0271	0.3088

chr8	146364022	6394817	0.0437	0.4105
chr9	141213431	2149704	0.0152	0.2254
chr10	135534747	4174401	0.0308	0.2682
chr11	135006516	3363805	0.0249	0.3202
chr12	133851895	2657948	0.0199	0.1857
chr13	115169878	1929704	0.0168	0.1704
chr14	107349540	2952495	0.0275	0.2243
chr15	102531392	2055861	0.0201	0.1904
chr16	90354753	1871016	0.0207	0.1982
chr17	81195210	2558666	0.0315	0.2726
chr18	78077248	1224654	0.0157	0.3626
chr19	59128983	1637776	0.0277	0.3092
chr20	63025520	1978576	0.0314	0.2404
chr21	48129895	885209	0.0184	0.1888
chr22	51304566	1208070	0.0235	0.2034
chrMT	16571	10505	0.6339	1.0673
chrX	155270560	3616540	0.0233	0.2198
chrY	59373566	220901	0.0037	0.1272

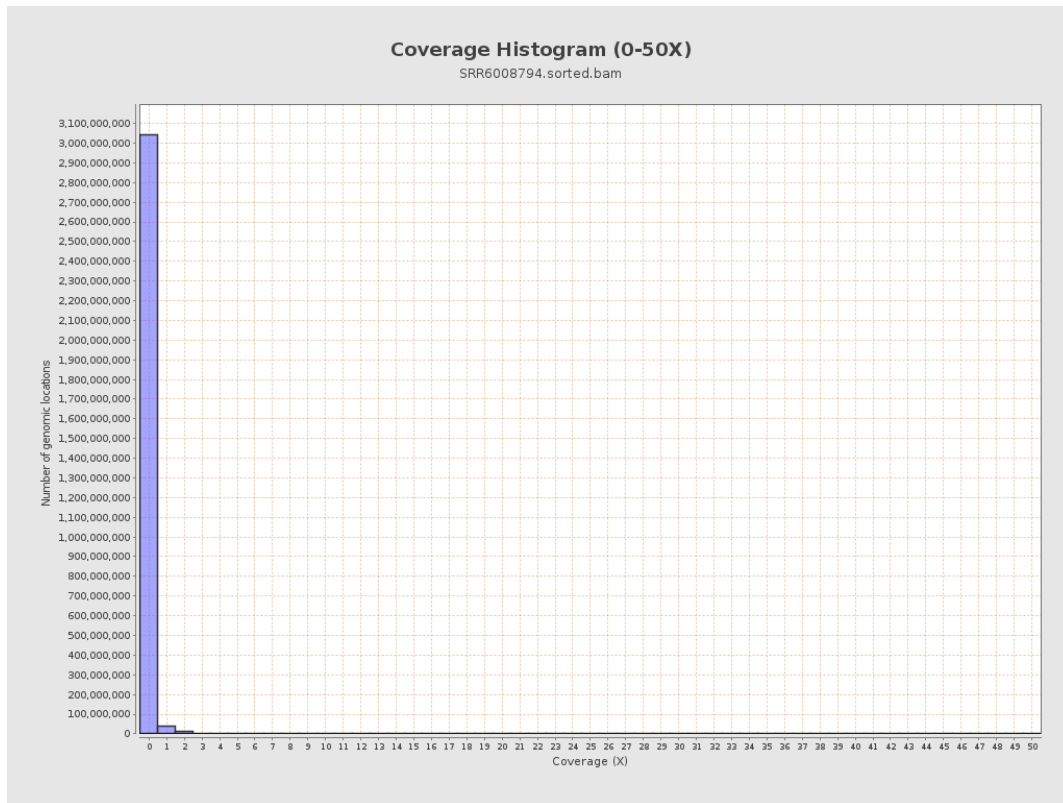
3. Results : Coverage across reference



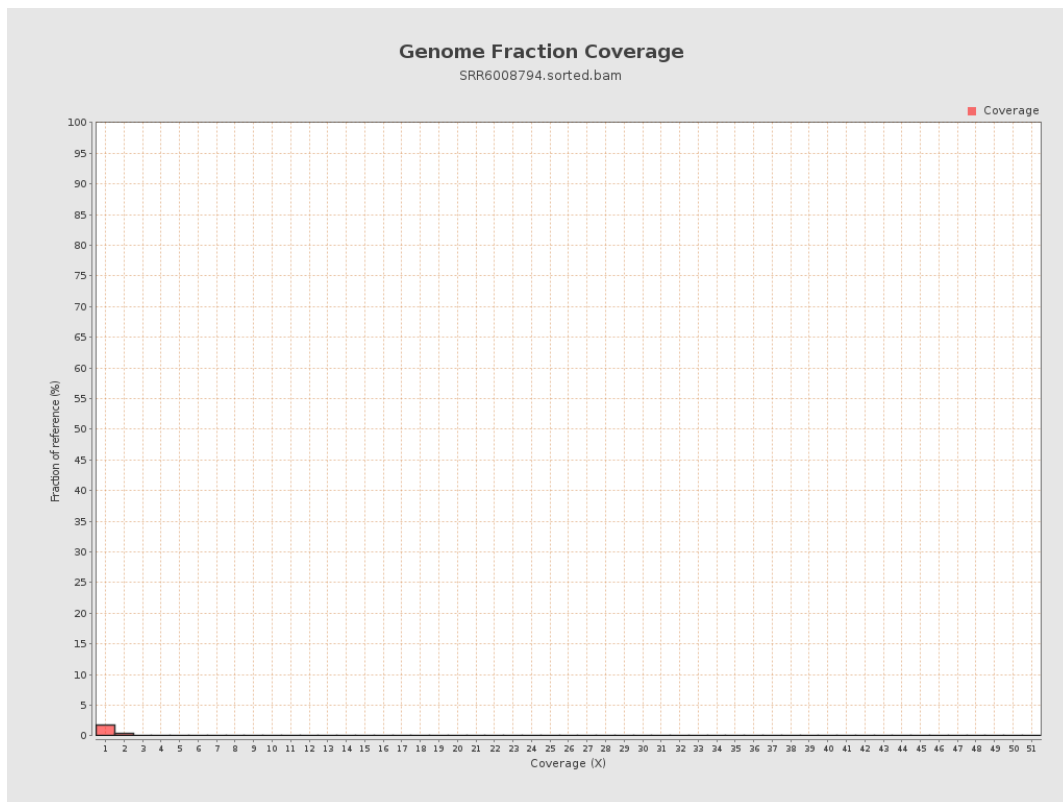
4. Results : Coverage Histogram



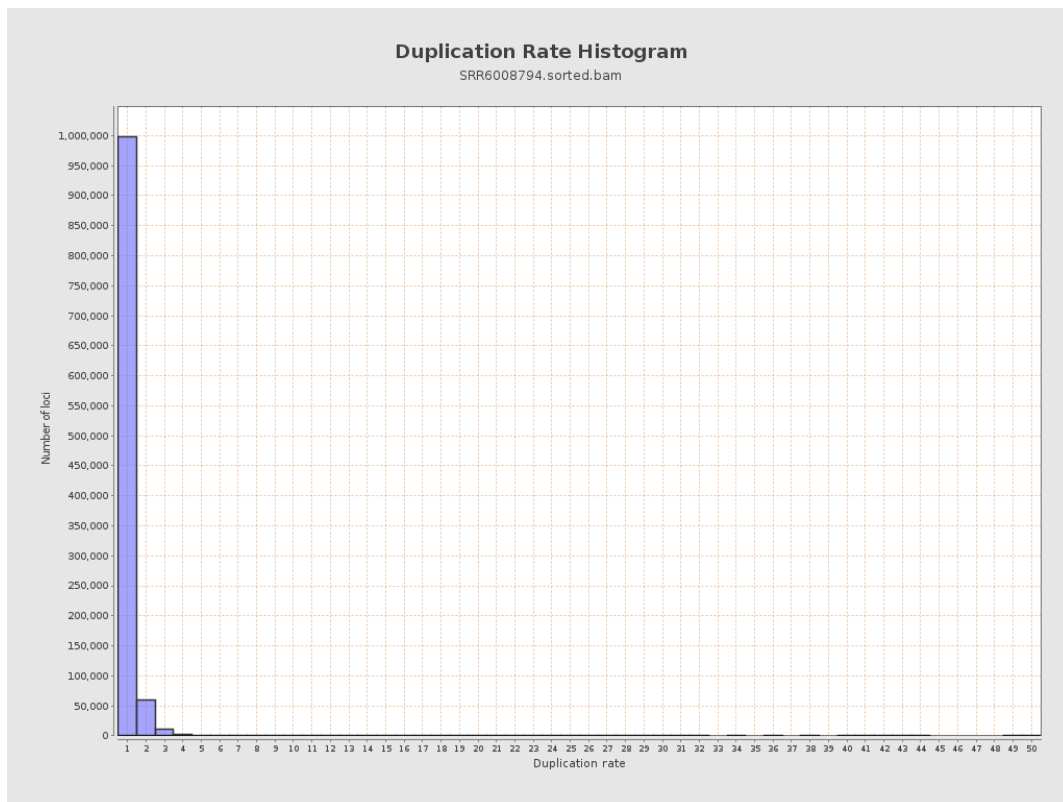
5. Results : Coverage Histogram (0-50X)



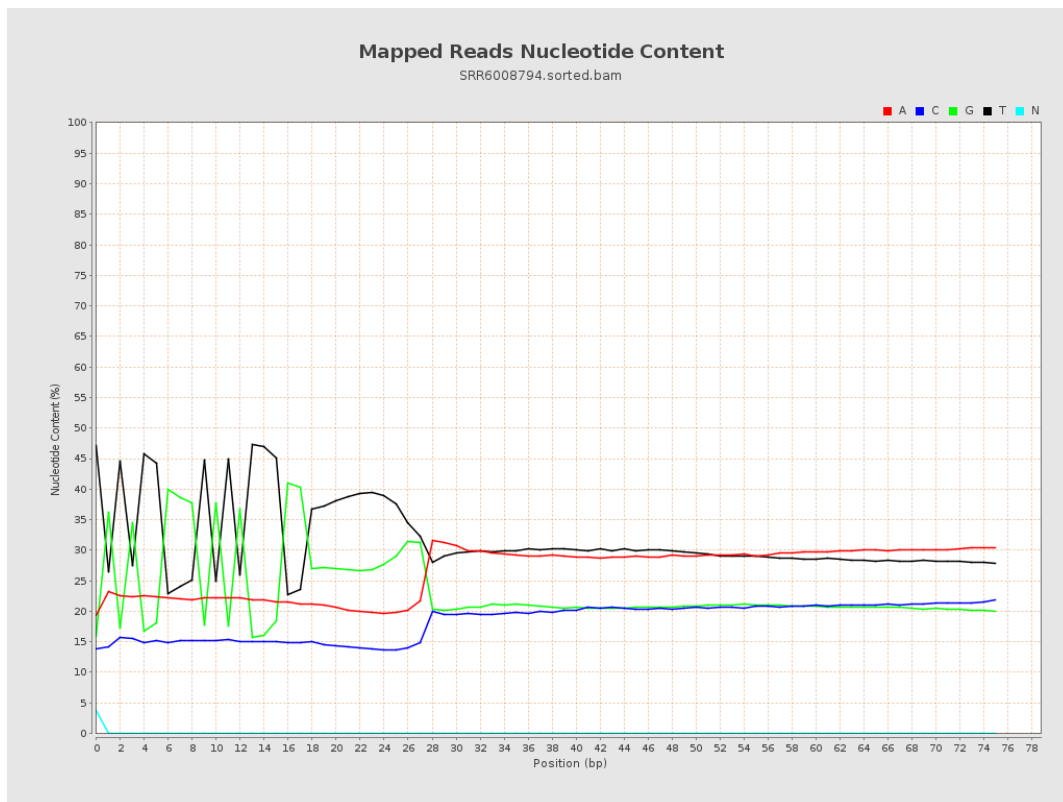
6. Results : Genome Fraction Coverage



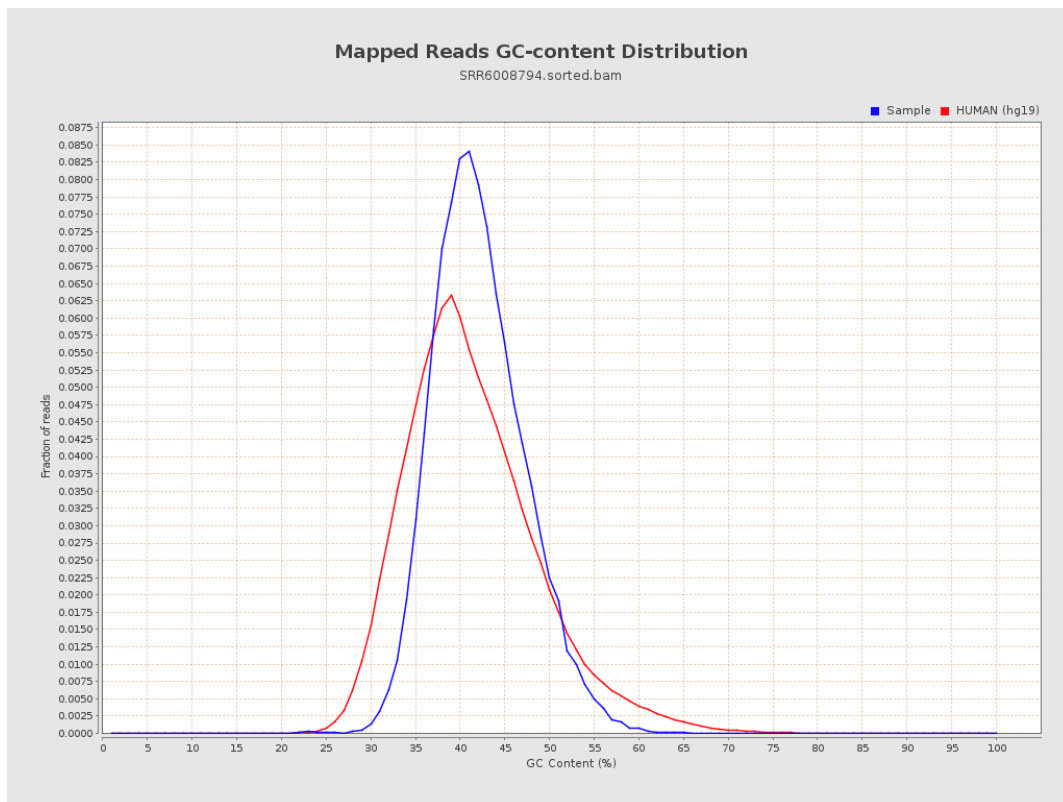
7. Results : Duplication Rate Histogram



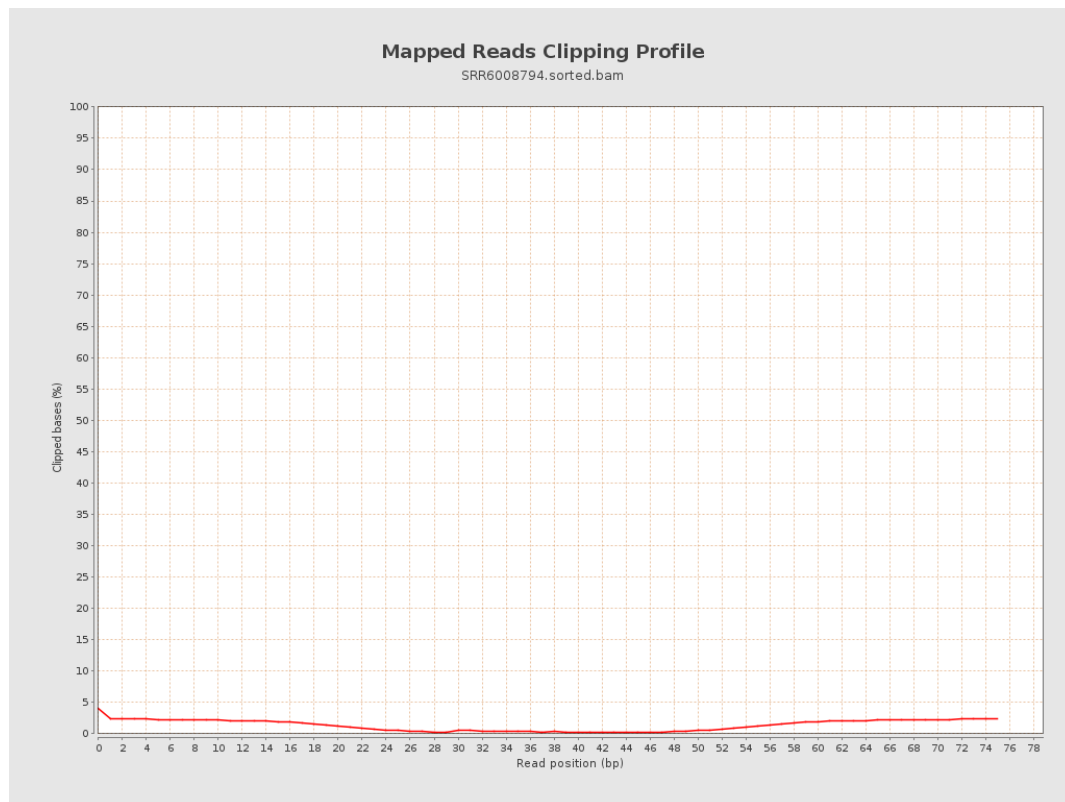
8. Results : Mapped Reads Nucleotide Content



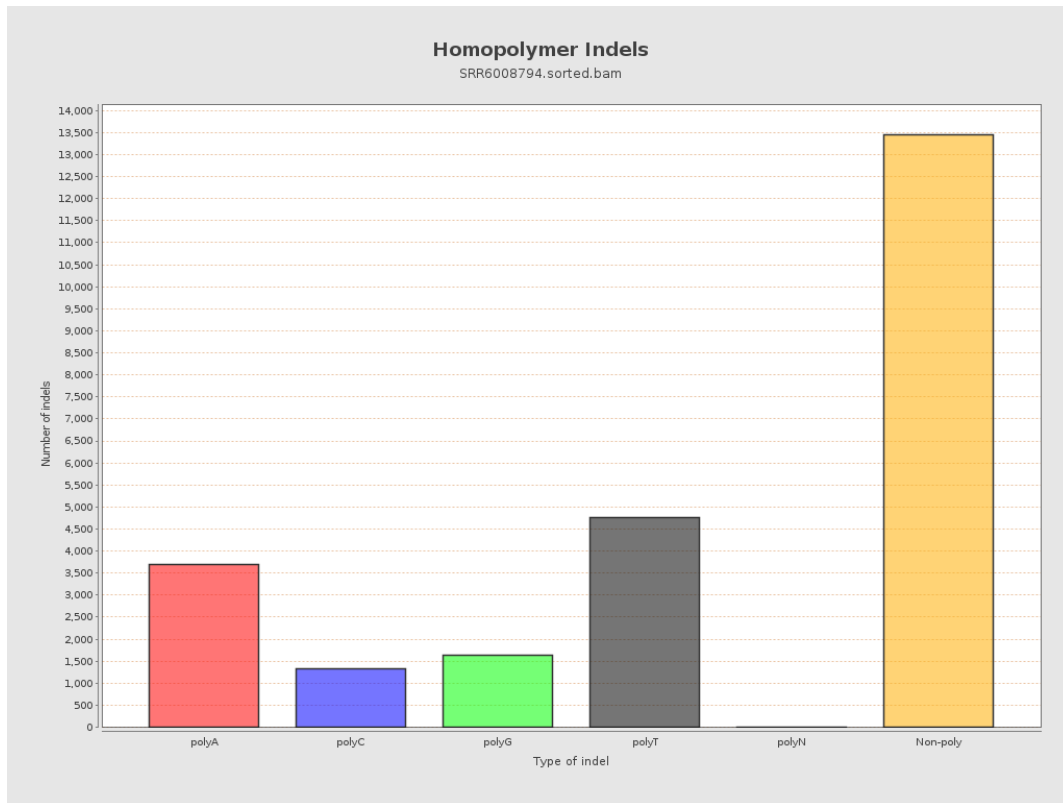
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

