

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 12:53:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008820.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_SRR6008820 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008820.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 12:53:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008820.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,344,817
Mapped reads	1,294,928 / 29.8%
Unmapped reads	3,049,889 / 70.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,029 / 0.16%
Read min/max/mean length	30 / 76 / 76.05
Duplicated reads (estimated)	96,392 / 2.22%
Duplication rate	5.96%
Clipped reads	871,917 / 20.07%

2.2. ACGT Content

Number/percentage of A's	22,766,146 / 28.99%
Number/percentage of C's	13,883,645 / 17.68%
Number/percentage of T's	23,575,514 / 30.02%
Number/percentage of G's	18,299,785 / 23.3%
Number/percentage of N's	19,140 / 0.02%
GC Percentage	40.97%

2.3. Coverage

Mean	0.0254

Standard Deviation	0.2556
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2.4. Mapping Quality

Mean Mapping Quality	46.6
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2.5. Mismatches and indels

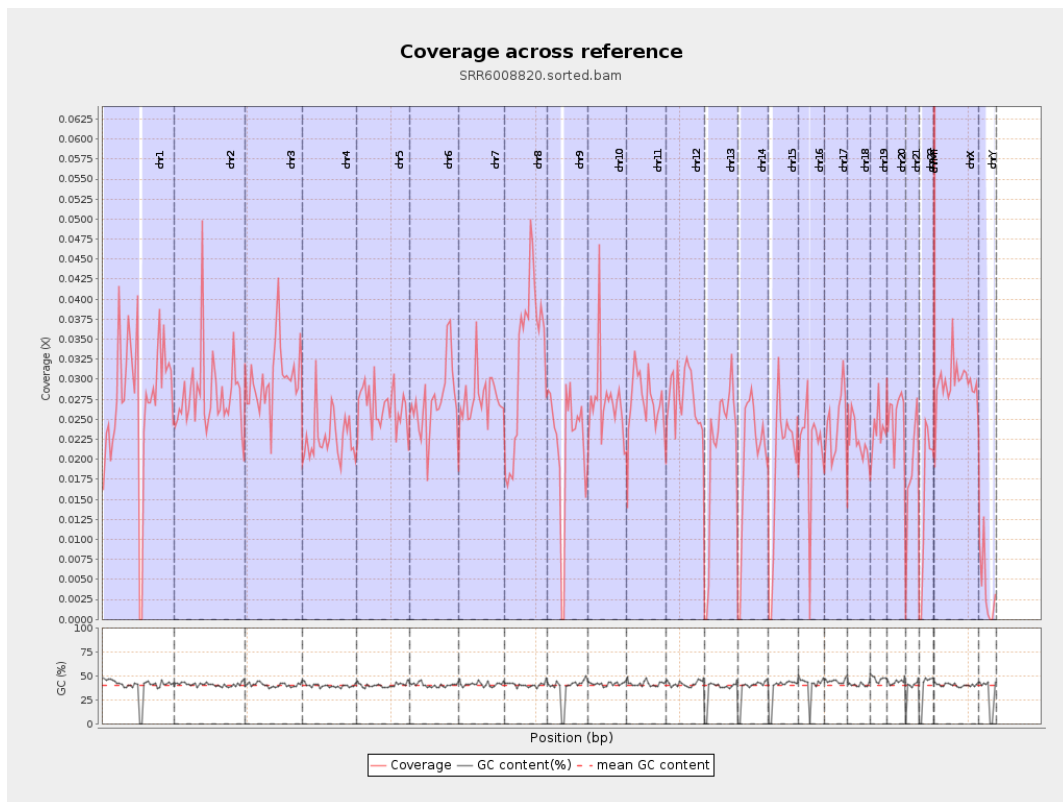
General error rate	0.97%
Mismatches	752,673
Insertions	5,342
Mapped reads with at least one insertion	0.41%
Deletions	23,300
Mapped reads with at least one deletion	1.78%
Homopolymer indels	47.18%

2.6. Chromosome stats

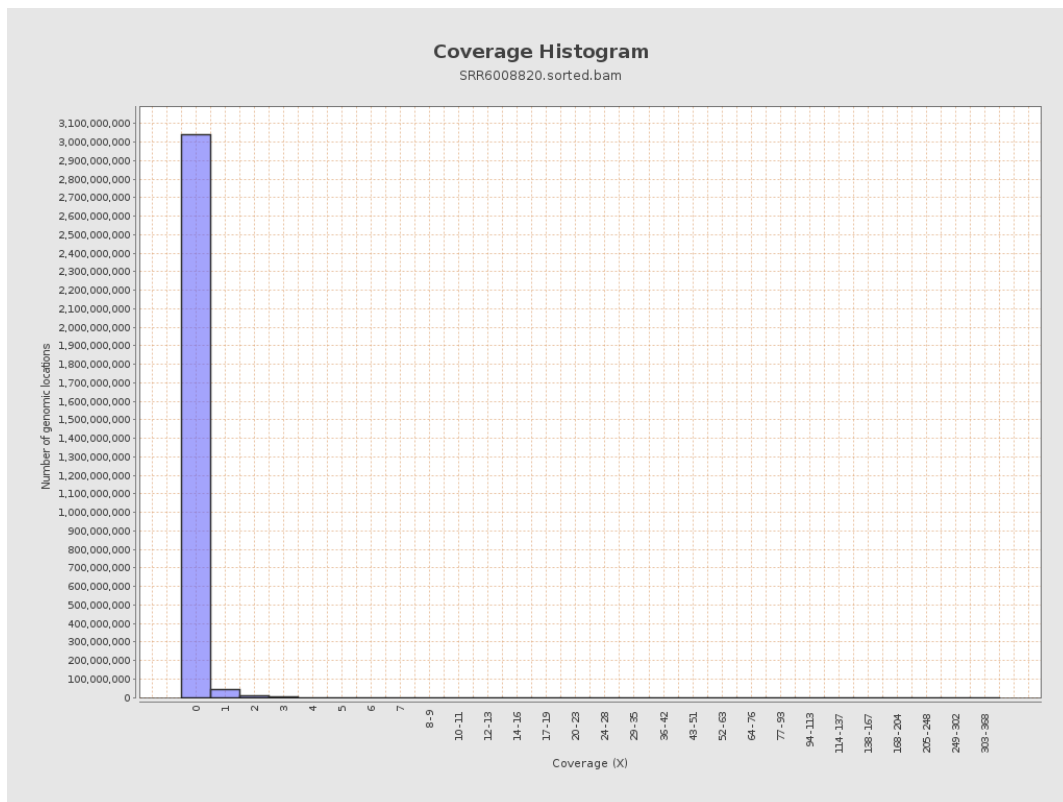
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6816015	0.0273	0.366
chr2	243199373	6807812	0.028	0.2973
chr3	198022430	5968530	0.0301	0.2284
chr4	191154276	4346138	0.0227	0.2047
chr5	180915260	4817812	0.0266	0.2146
chr6	171115067	4634140	0.0271	0.2326
chr7	159138663	4406878	0.0277	0.2834

chr8	146364022	4755879	0.0325	0.332
chr9	141213431	3099616	0.0219	0.2455
chr10	135534747	3681573	0.0272	0.275
chr11	135006516	3688040	0.0273	0.2509
chr12	133851895	3714387	0.0277	0.22
chr13	115169878	2470605	0.0215	0.1931
chr14	107349540	2181882	0.0203	0.1909
chr15	102531392	1994690	0.0195	0.1816
chr16	90354753	1929343	0.0214	0.2074
chr17	81195210	1967191	0.0242	0.2157
chr18	78077248	1747881	0.0224	0.3541
chr19	59128983	1412760	0.0239	0.2666
chr20	63025520	1594107	0.0253	0.2102
chr21	48129895	892915	0.0186	0.1886
chr22	51304566	819477	0.016	0.1638
chrMT	16571	24407	1.4729	1.9437
chrX	155270560	4581648	0.0295	0.2375
chrY	59373566	227543	0.0038	0.1091

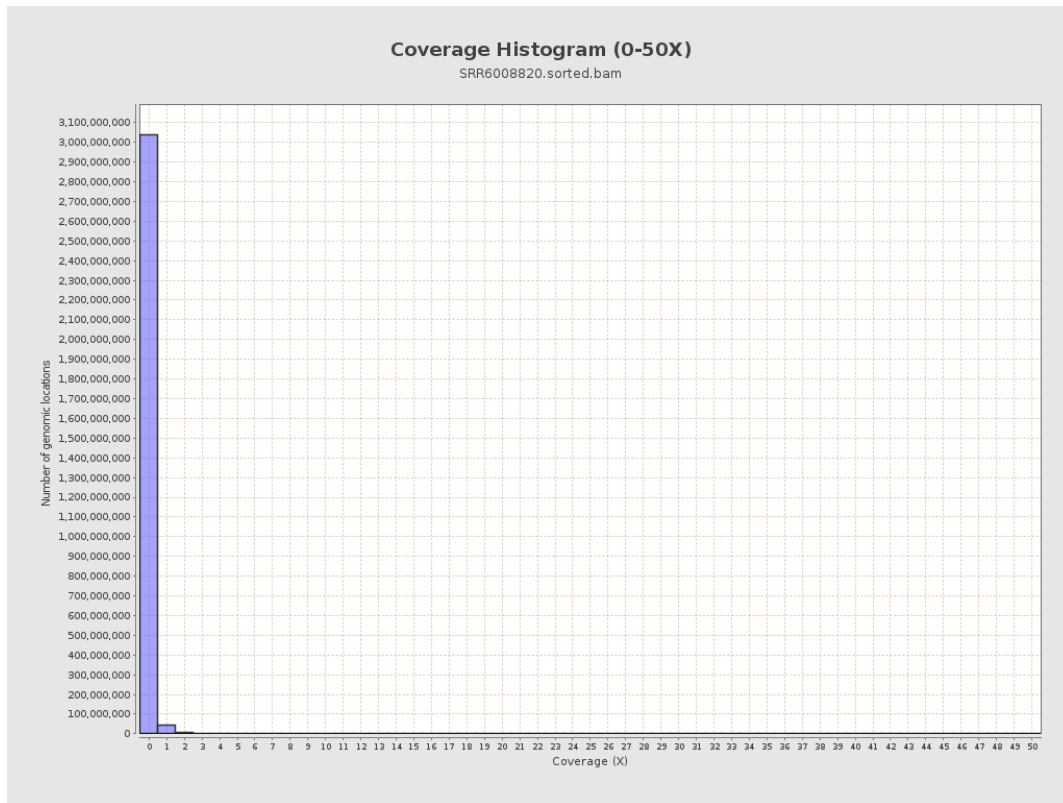
3. Results : Coverage across reference



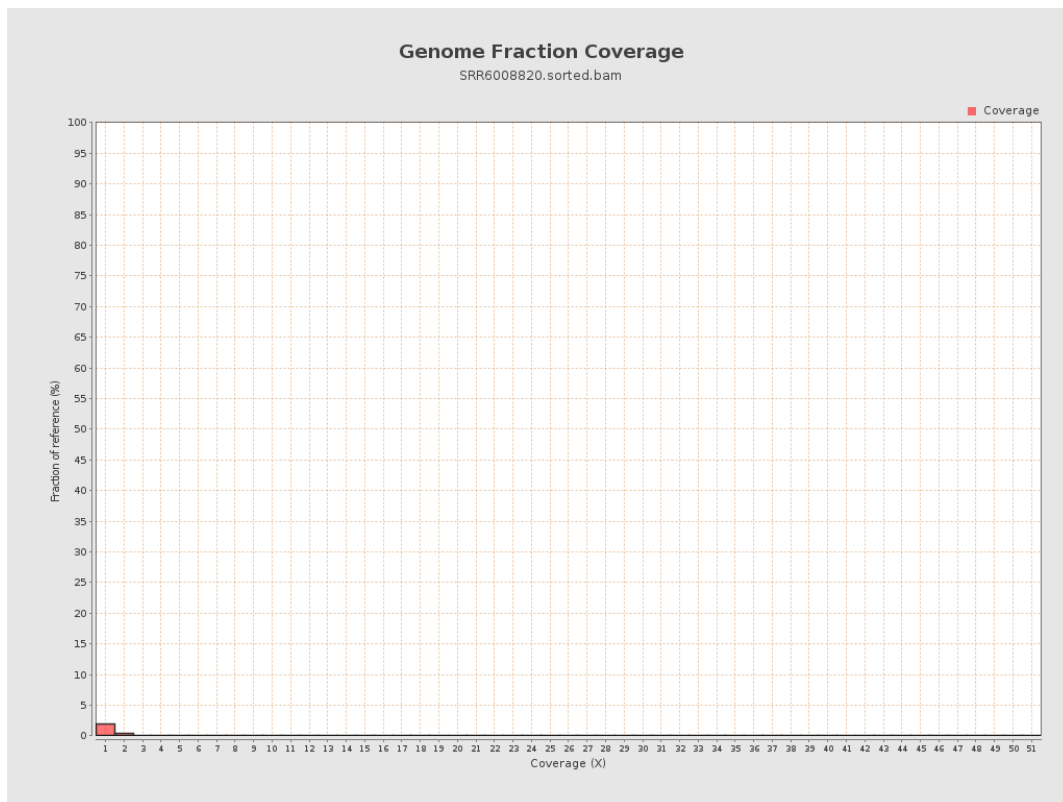
4. Results : Coverage Histogram



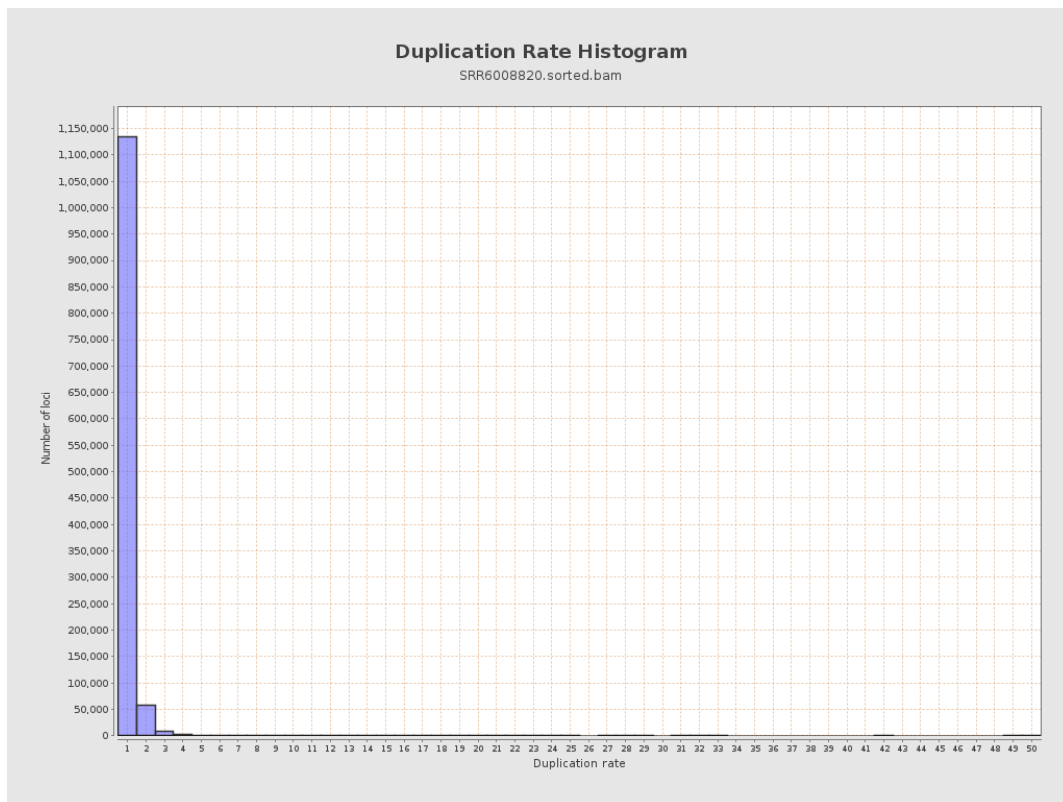
5. Results : Coverage Histogram (0-50X)



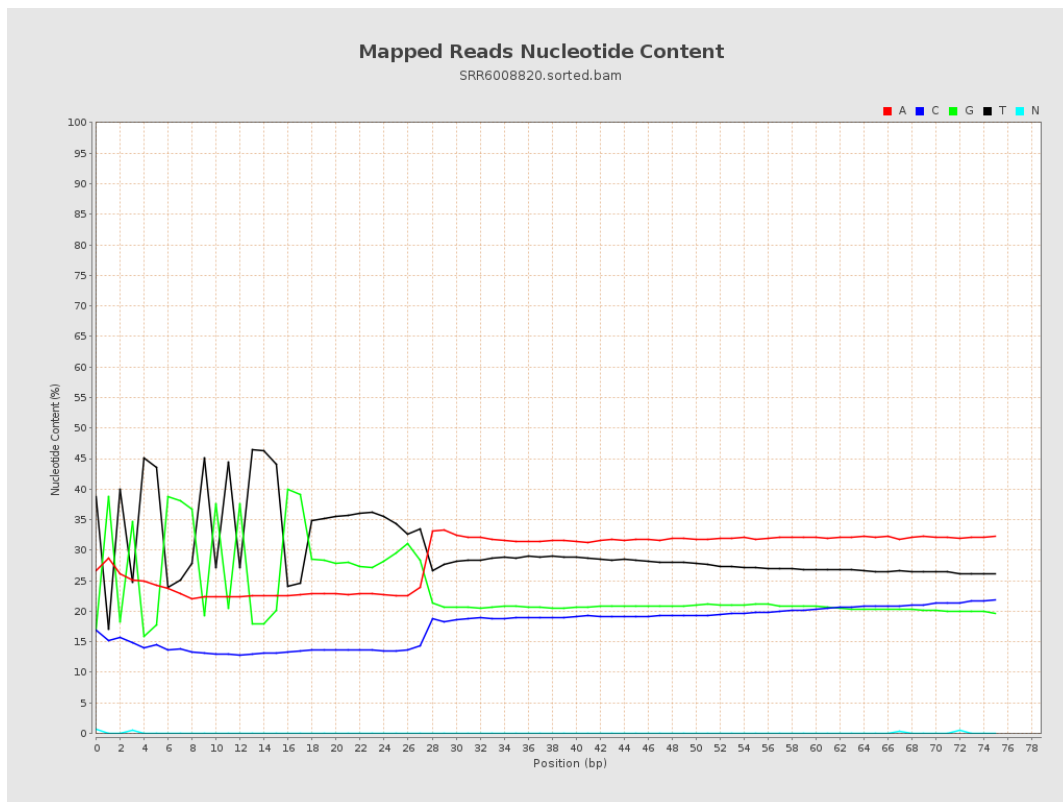
6. Results : Genome Fraction Coverage



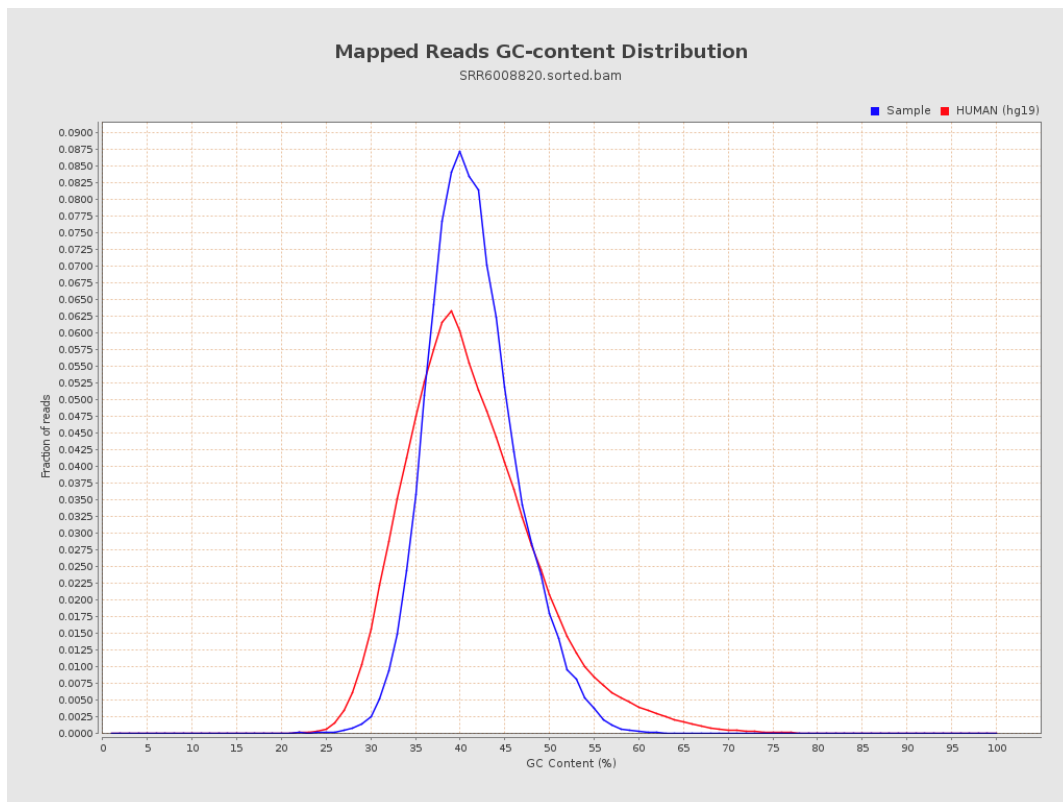
7. Results : Duplication Rate Histogram



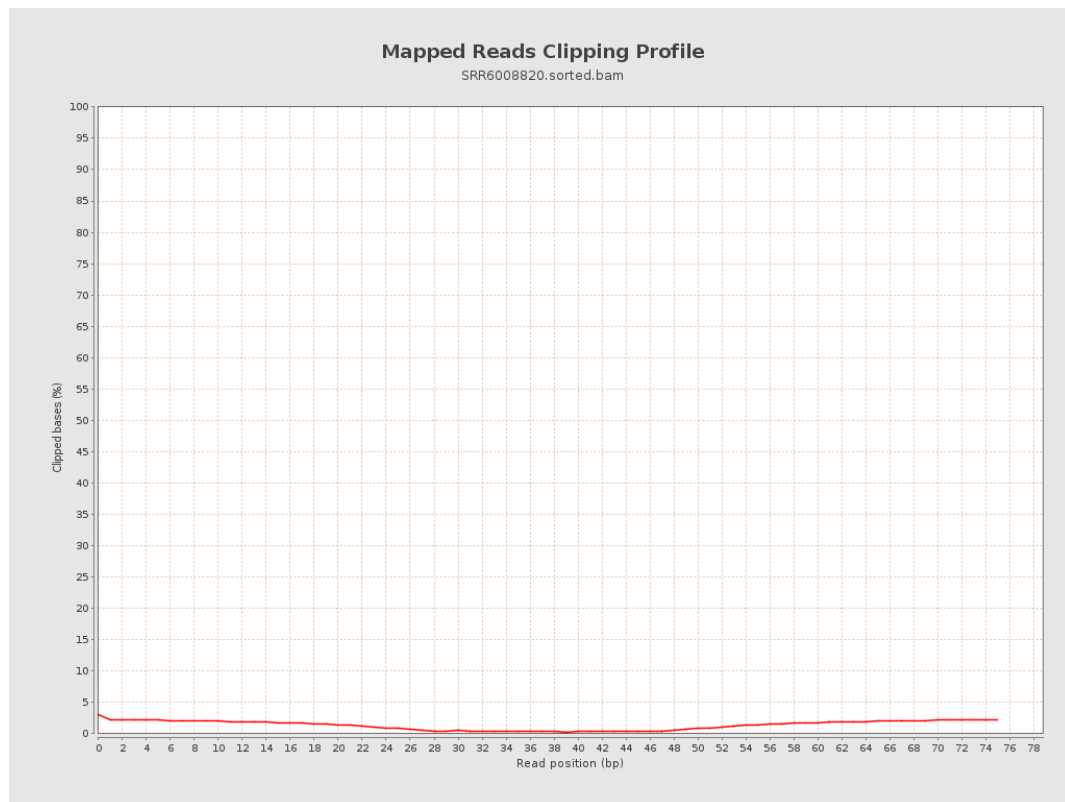
8. Results : Mapped Reads Nucleotide Content



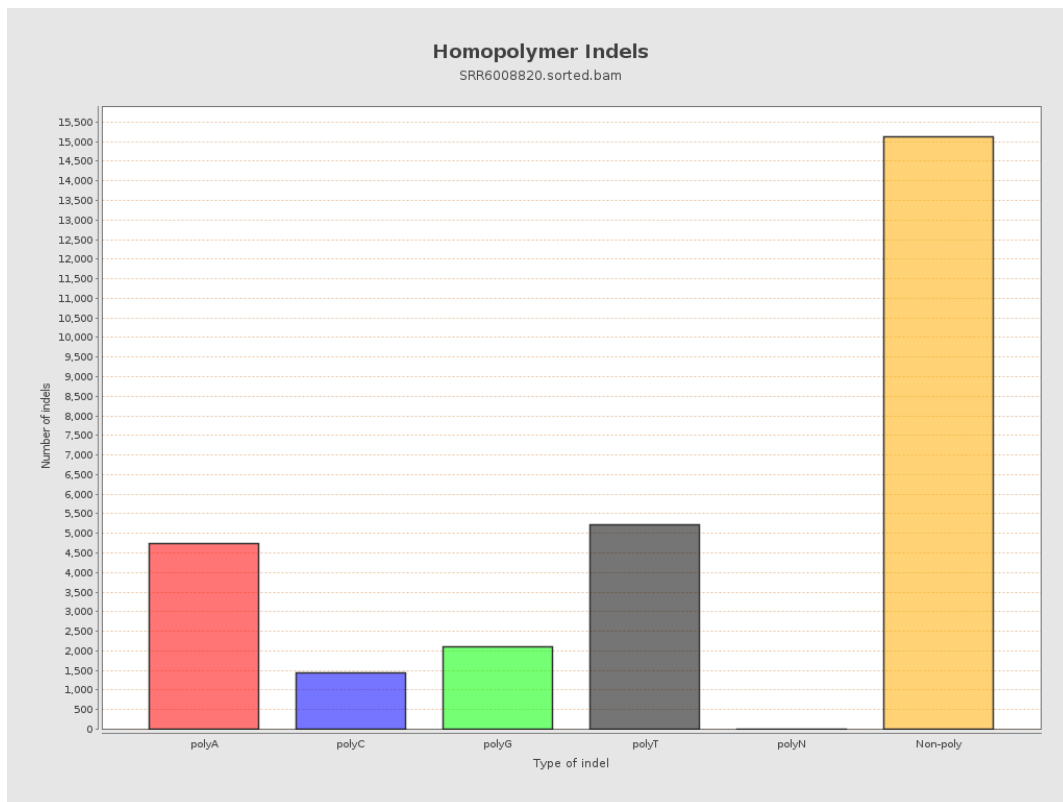
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

