

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 05:14:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004159.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_SRR6004159 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004159.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 05:14:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004159.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,335,745
Mapped reads	1,146,668 / 85.84%
Unmapped reads	189,077 / 14.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,519 / 0.71%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	36,053 / 2.7%
Duplication rate	2.45%
Clipped reads	557,356 / 41.73%

2.2. ACGT Content

Number/percentage of A's	21,790,125 / 28.85%
Number/percentage of C's	13,608,023 / 18.02%
Number/percentage of T's	23,936,420 / 31.69%
Number/percentage of G's	16,181,898 / 21.42%
Number/percentage of N's	14,089 / 0.02%
GC Percentage	39.44%

2.3. Coverage

Mean	0.0244

Standard Deviation	0.2607
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2.4. Mapping Quality

Mean Mapping Quality	45.32
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2.5. Mismatches and indels

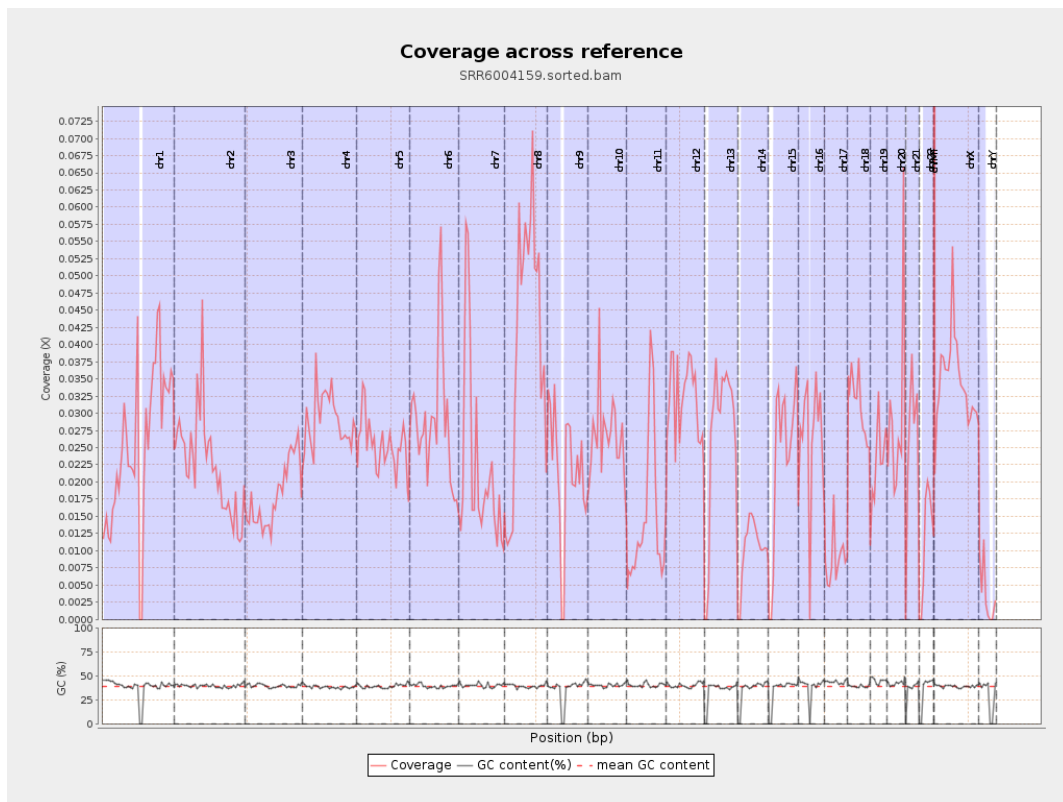
General error rate	1.01%
Mismatches	751,126
Insertions	5,888
Mapped reads with at least one insertion	0.51%
Deletions	29,265
Mapped reads with at least one deletion	2.51%
Homopolymer indels	43.68%

2.6. Chromosome stats

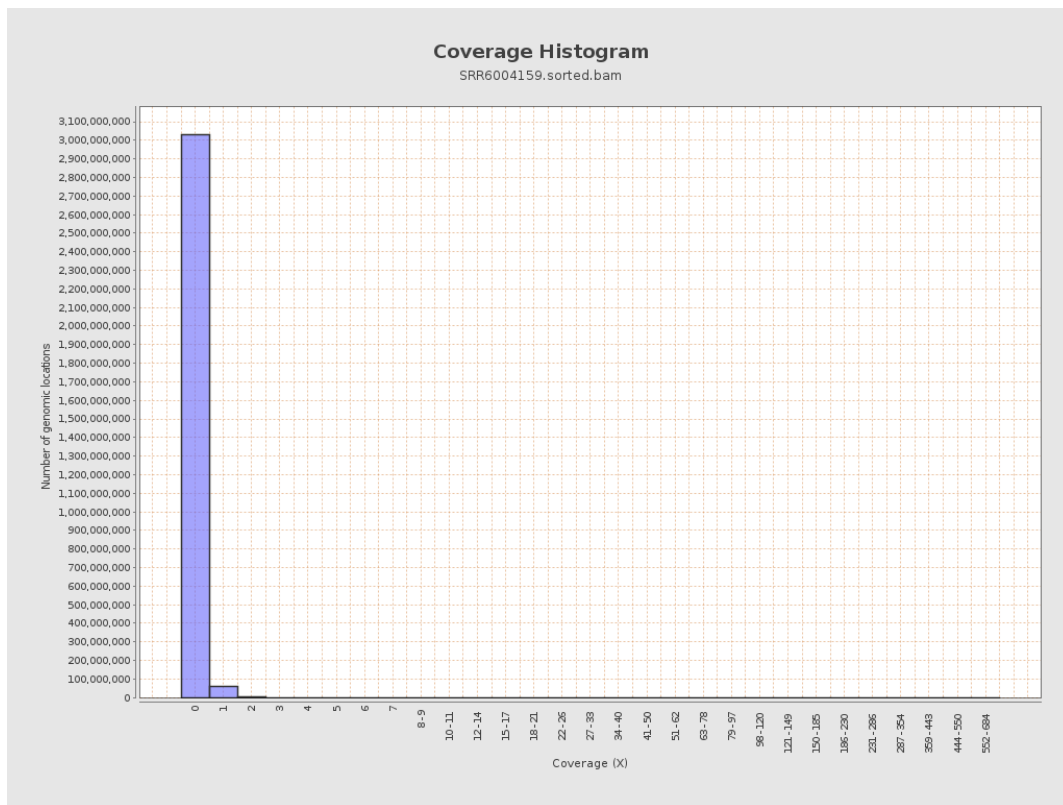
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6318035	0.0253	0.5116
chr2	243199373	5395861	0.0222	0.236
chr3	198022430	3578374	0.0181	0.1445
chr4	191154276	5519345	0.0289	0.1947
chr5	180915260	4587407	0.0254	0.1739
chr6	171115067	4914819	0.0287	0.1985
chr7	159138663	3503219	0.022	0.2412

chr8	146364022	5934940	0.0405	0.4619
chr9	141213431	3067526	0.0217	0.2271
chr10	135534747	3597289	0.0265	0.2464
chr11	135006516	1951052	0.0145	0.146
chr12	133851895	4299644	0.0321	0.1959
chr13	115169878	3058127	0.0266	0.1751
chr14	107349540	1115740	0.0104	0.123
chr15	102531392	2440622	0.0238	0.1656
chr16	90354753	2353121	0.026	0.1939
chr17	81195210	711412	0.0088	0.1041
chr18	78077248	2438023	0.0312	0.3914
chr19	59128983	1384229	0.0234	0.3416
chr20	63025520	1896346	0.0301	0.1927
chr21	48129895	1277521	0.0265	0.1868
chr22	51304566	609058	0.0119	0.1158
chrMT	16571	19450	1.1737	1.3883
chrX	155270560	5396327	0.0348	0.2182
chrY	59373566	212965	0.0036	0.0947

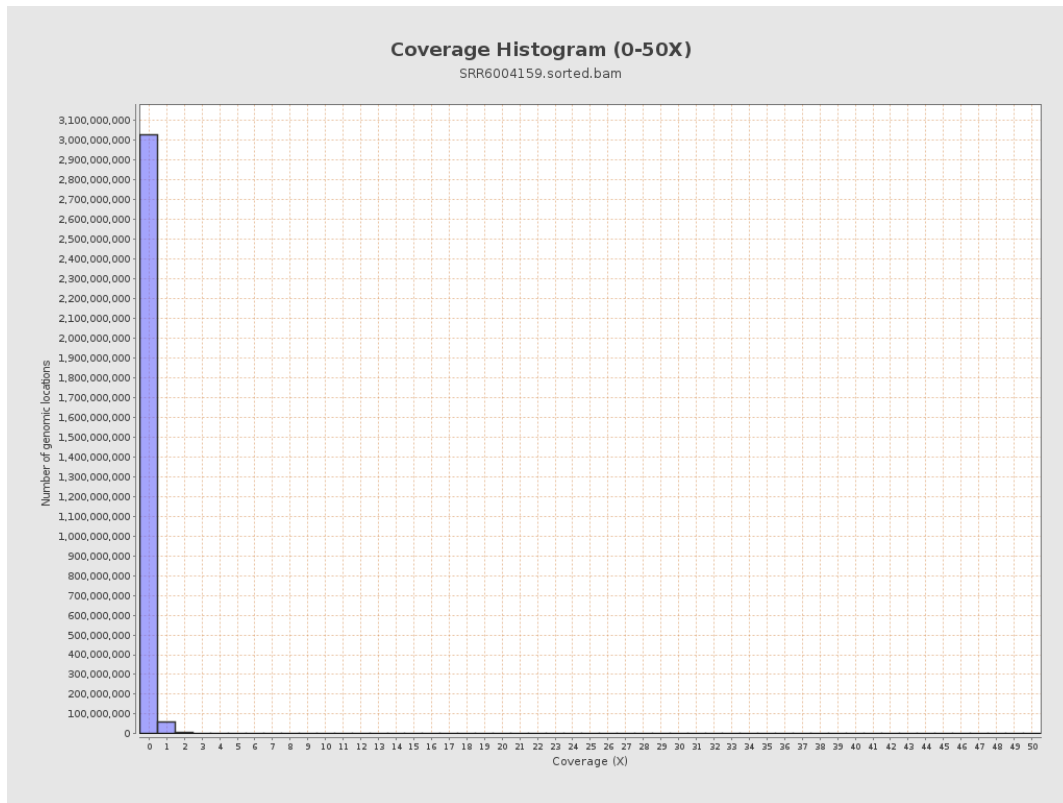
3. Results : Coverage across reference



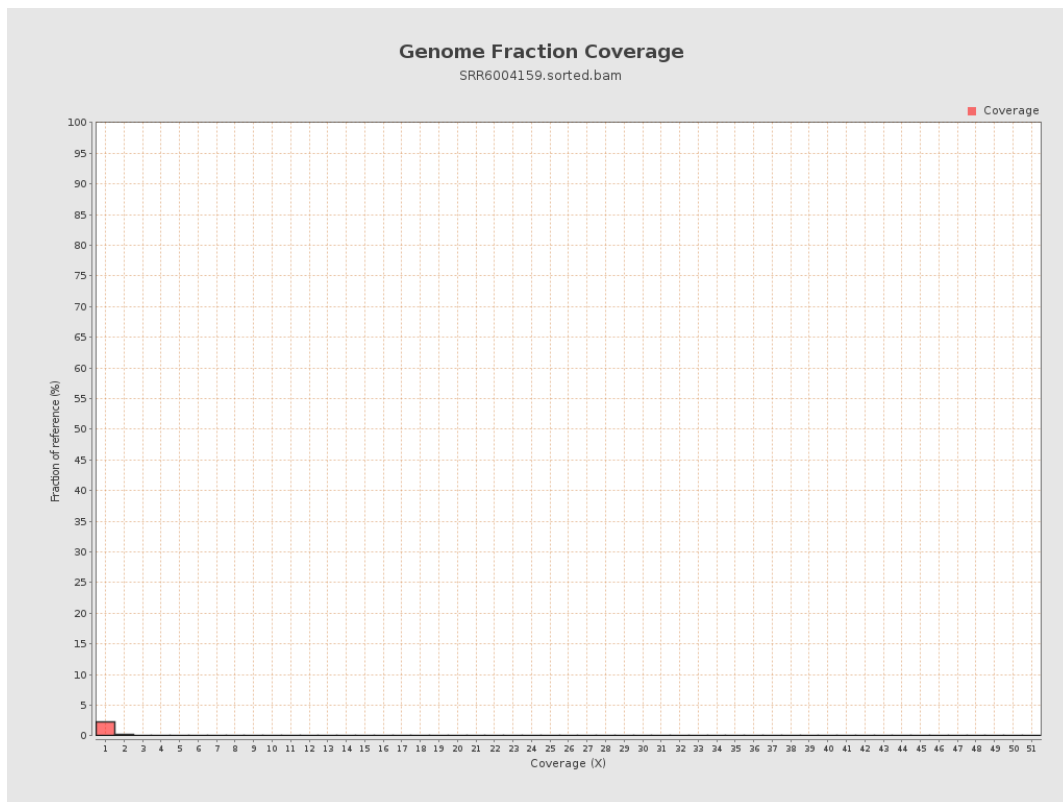
4. Results : Coverage Histogram



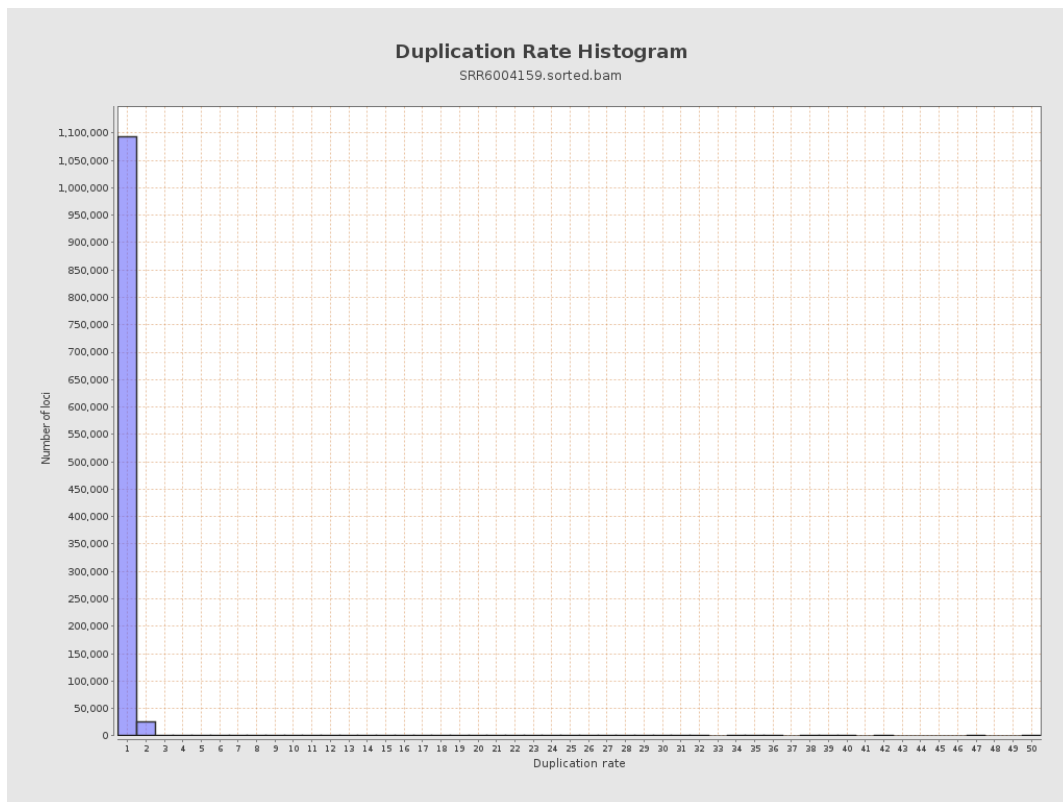
5. Results : Coverage Histogram (0-50X)



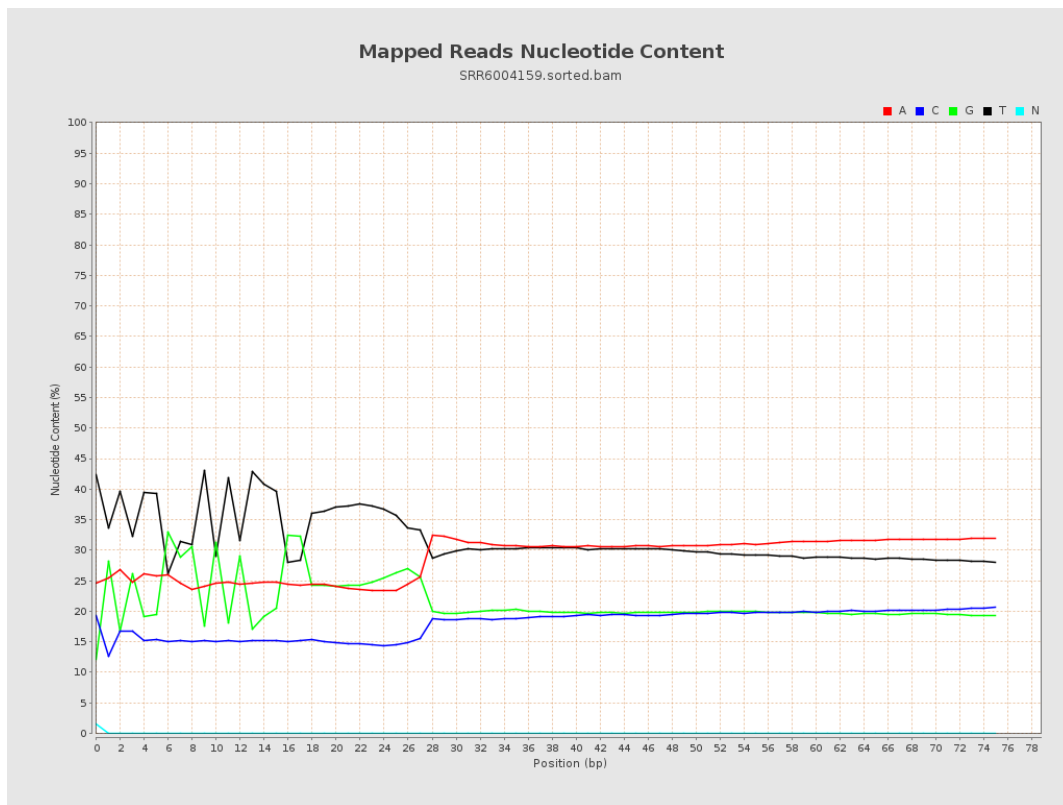
6. Results : Genome Fraction Coverage



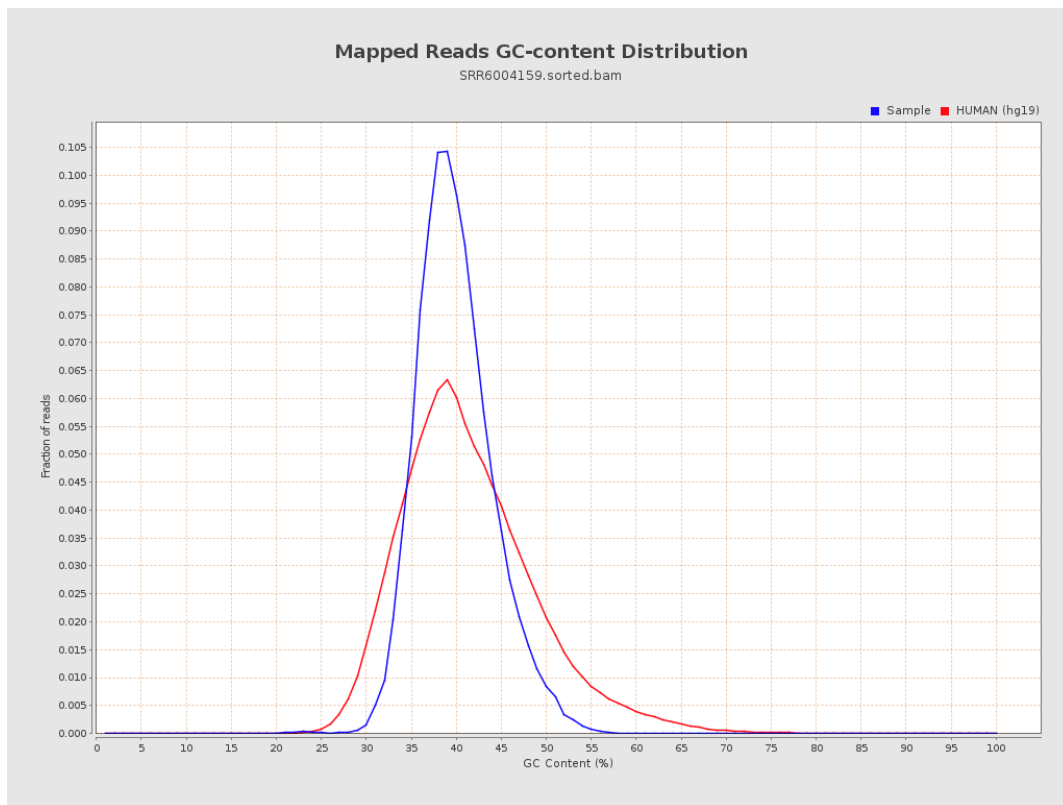
7. Results : Duplication Rate Histogram



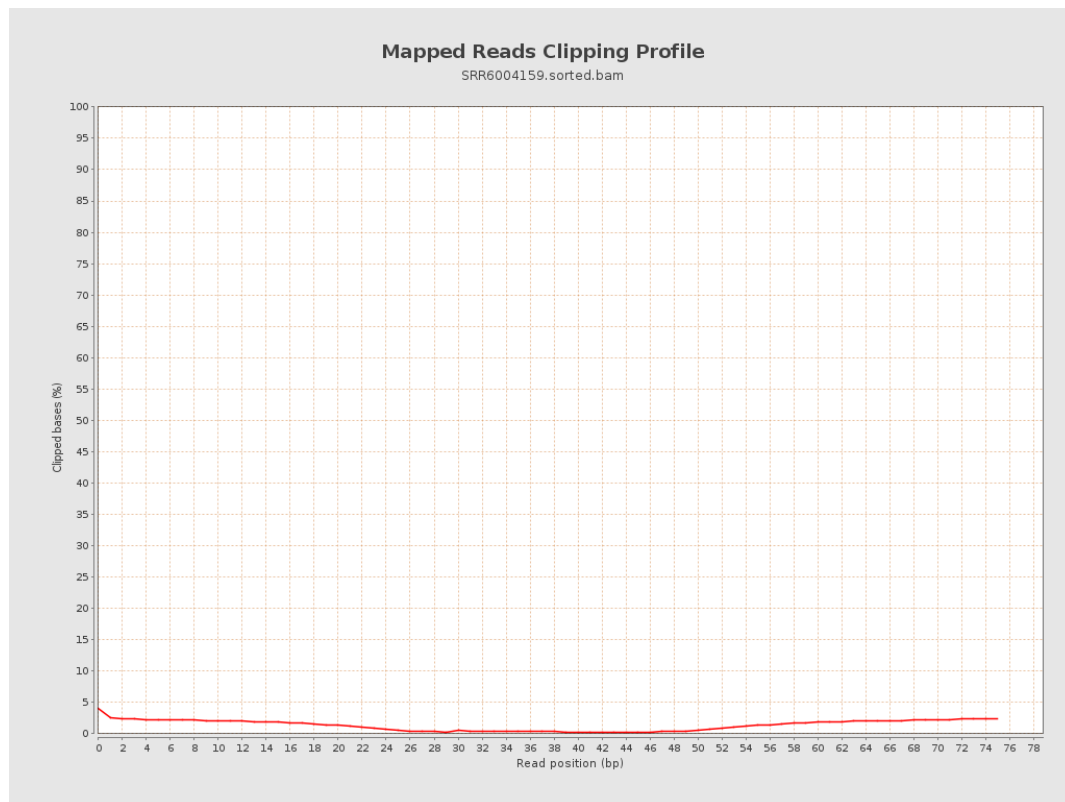
8. Results : Mapped Reads Nucleotide Content



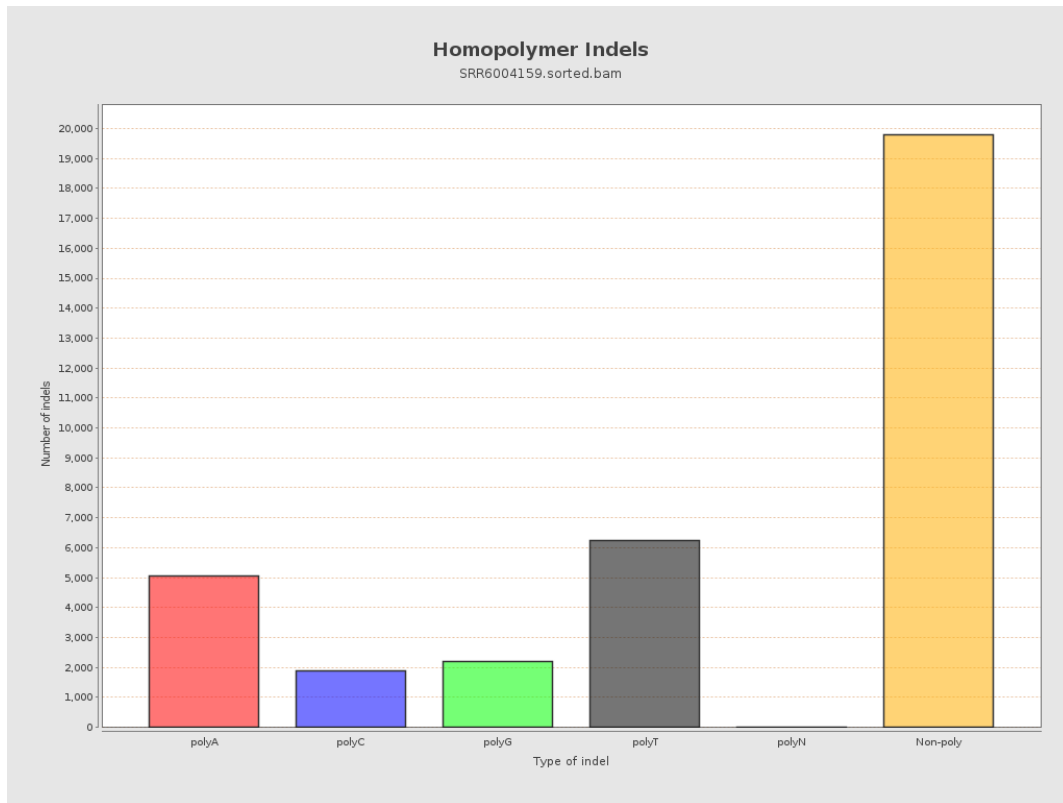
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

