

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 20:14:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004004.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_SRR6004004 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004004.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 20:14:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004004.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,508,092
Mapped reads	1,175,261 / 77.93%
Unmapped reads	332,831 / 22.07%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,116 / 0.67%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	97,210 / 6.45%
Duplication rate	6.85%
Clipped reads	636,404 / 42.2%

2.2. ACGT Content

Number/percentage of A's	20,064,414 / 26.47%
Number/percentage of C's	14,604,200 / 19.27%
Number/percentage of T's	23,335,913 / 30.79%
Number/percentage of G's	17,773,698 / 23.45%
Number/percentage of N's	14,739 / 0.02%
GC Percentage	42.72%

2.3. Coverage

Mean	0.0245

Standard Deviation	0.2606
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2.4. Mapping Quality

Mean Mapping Quality	44.84
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2.5. Mismatches and indels

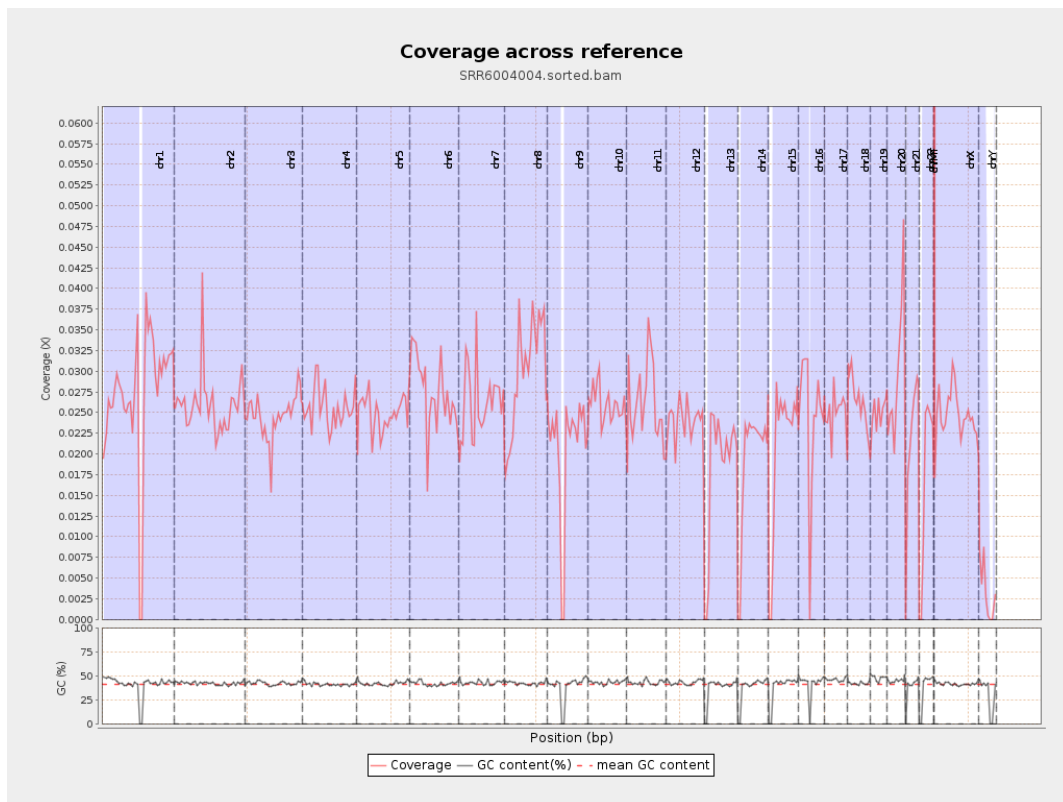
General error rate	0.96%
Mismatches	717,028
Insertions	5,820
Mapped reads with at least one insertion	0.49%
Deletions	25,100
Mapped reads with at least one deletion	2.11%
Homopolymer indels	47.22%

2.6. Chromosome stats

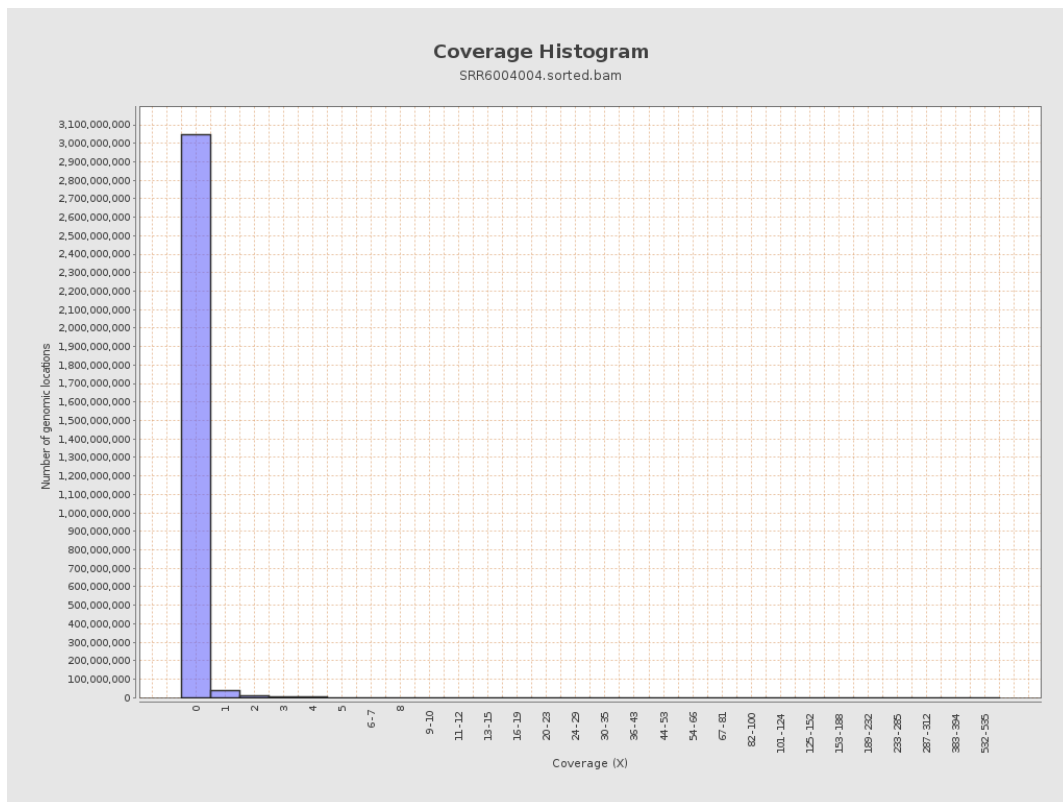
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6776892	0.0272	0.346
chr2	243199373	6319507	0.026	0.3373
chr3	198022430	4876004	0.0246	0.2184
chr4	191154276	4892636	0.0256	0.2241
chr5	180915260	4510689	0.0249	0.2185
chr6	171115067	4689555	0.0274	0.2482
chr7	159138663	4178099	0.0263	0.3276

chr8	146364022	4409131	0.0301	0.2818
chr9	141213431	2911810	0.0206	0.2334
chr10	135534747	3529607	0.026	0.2433
chr11	135006516	3550743	0.0263	0.2682
chr12	133851895	3216711	0.024	0.2147
chr13	115169878	2112048	0.0183	0.1876
chr14	107349540	2053414	0.0191	0.2046
chr15	102531392	2116401	0.0206	0.2012
chr16	90354753	2186722	0.0242	0.2249
chr17	81195210	2021428	0.0249	0.2319
chr18	78077248	2072790	0.0265	0.3714
chr19	59128983	1474306	0.0249	0.2888
chr20	63025520	1880206	0.0298	0.2476
chr21	48129895	1055046	0.0219	0.2124
chr22	51304566	876119	0.0171	0.1834
chrMT	16571	81478	4.9169	4.5197
chrX	155270560	3852290	0.0248	0.2251
chrY	59373566	190681	0.0032	0.0787

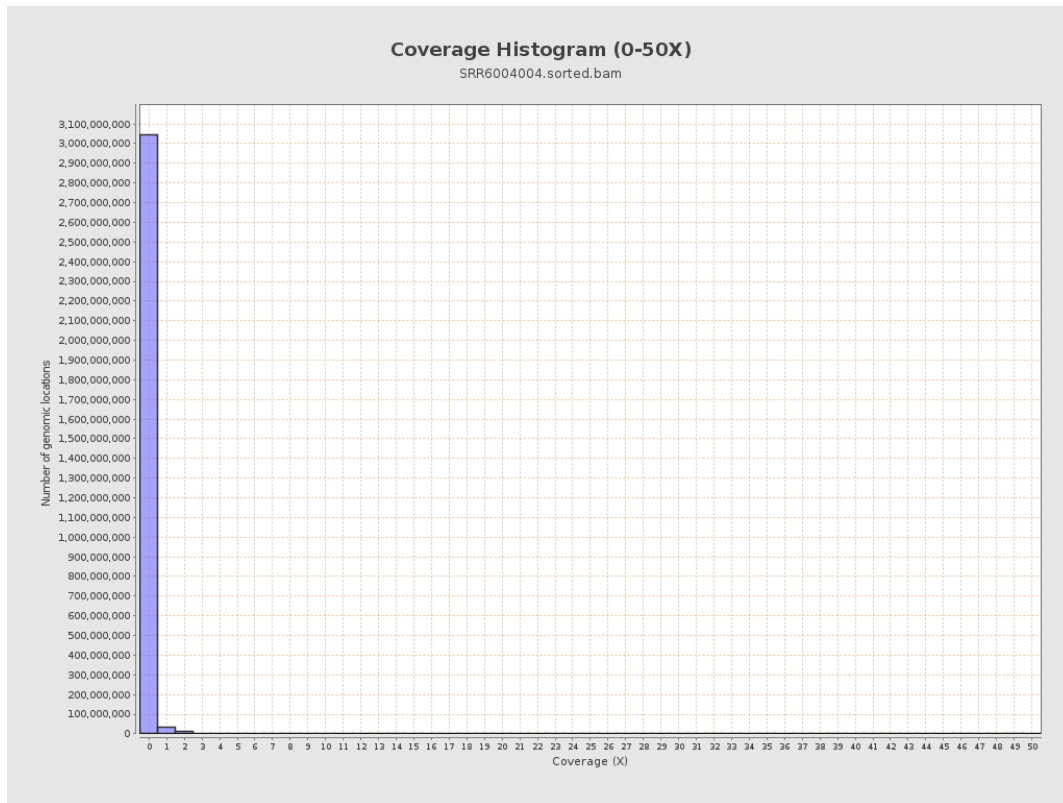
3. Results : Coverage across reference



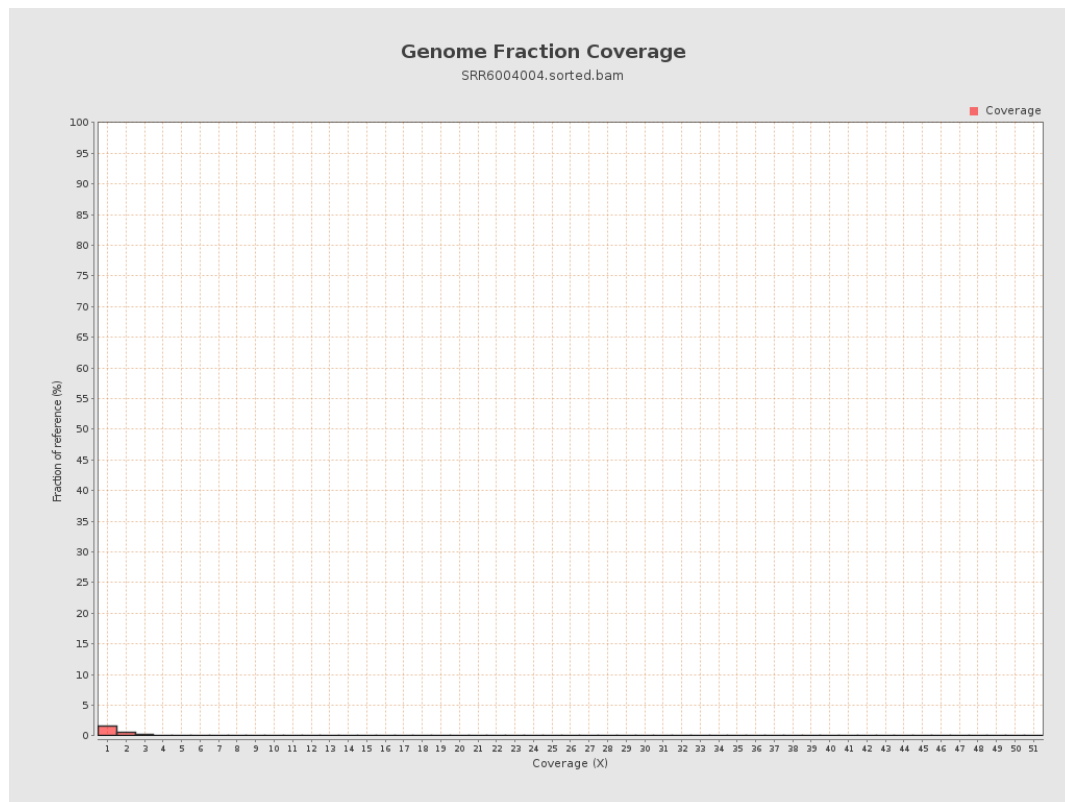
4. Results : Coverage Histogram



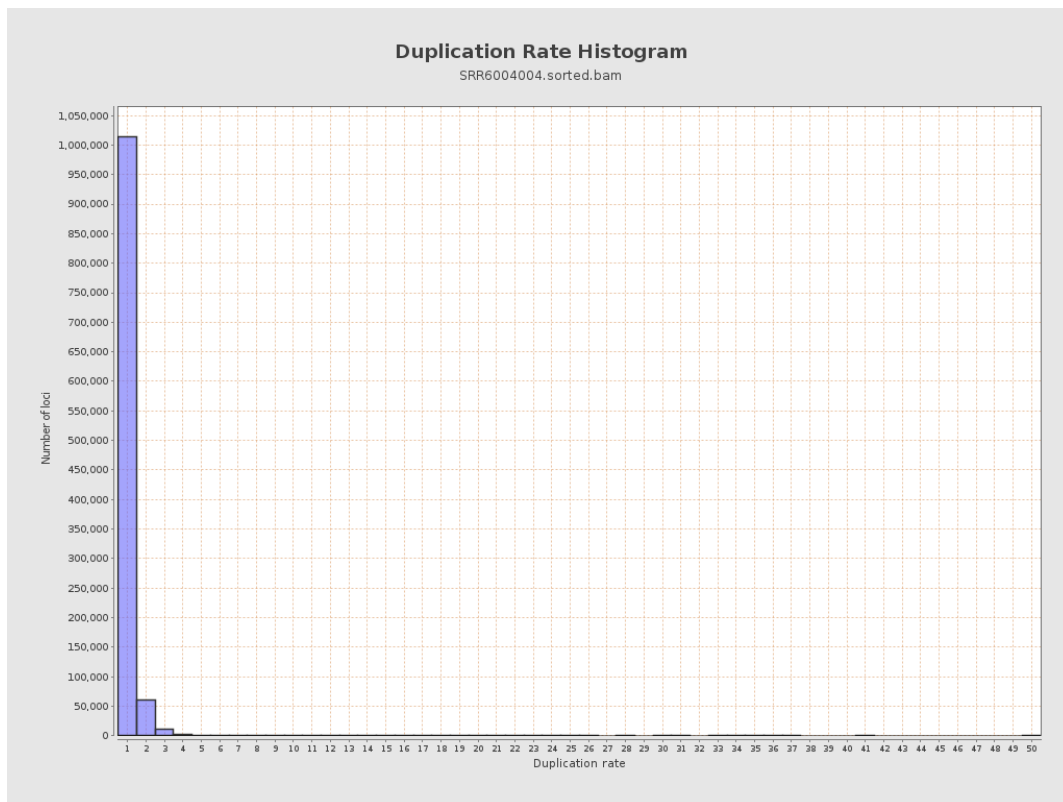
5. Results : Coverage Histogram (0-50X)



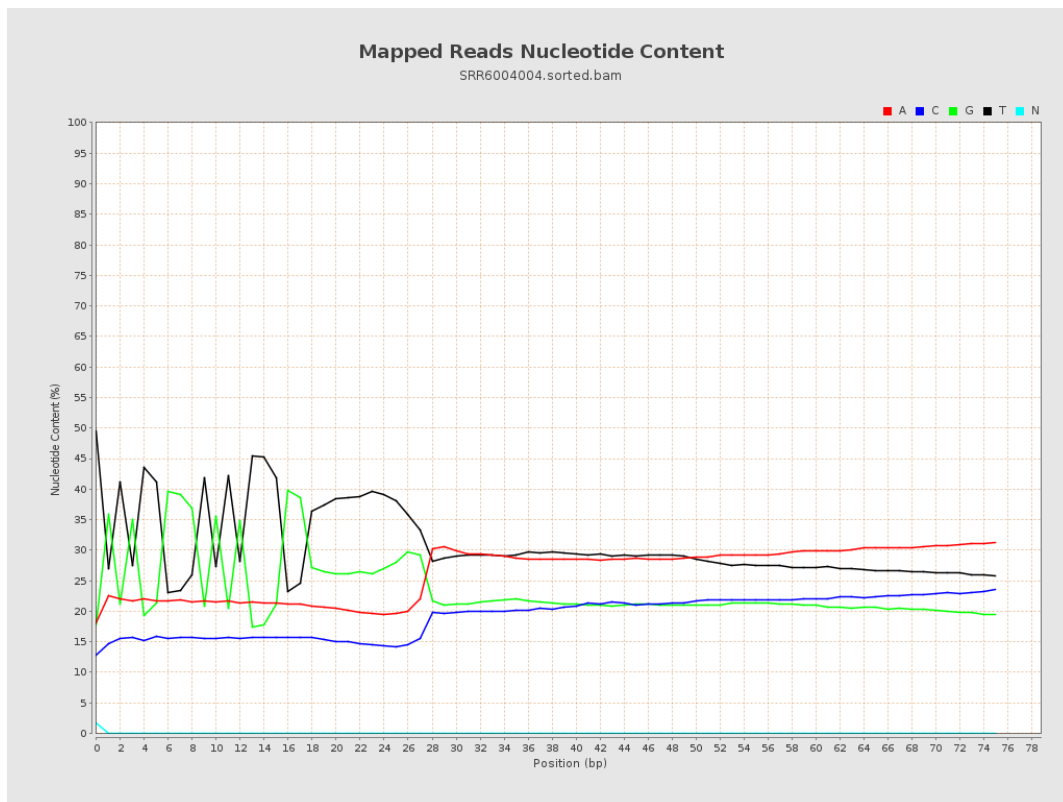
6. Results : Genome Fraction Coverage



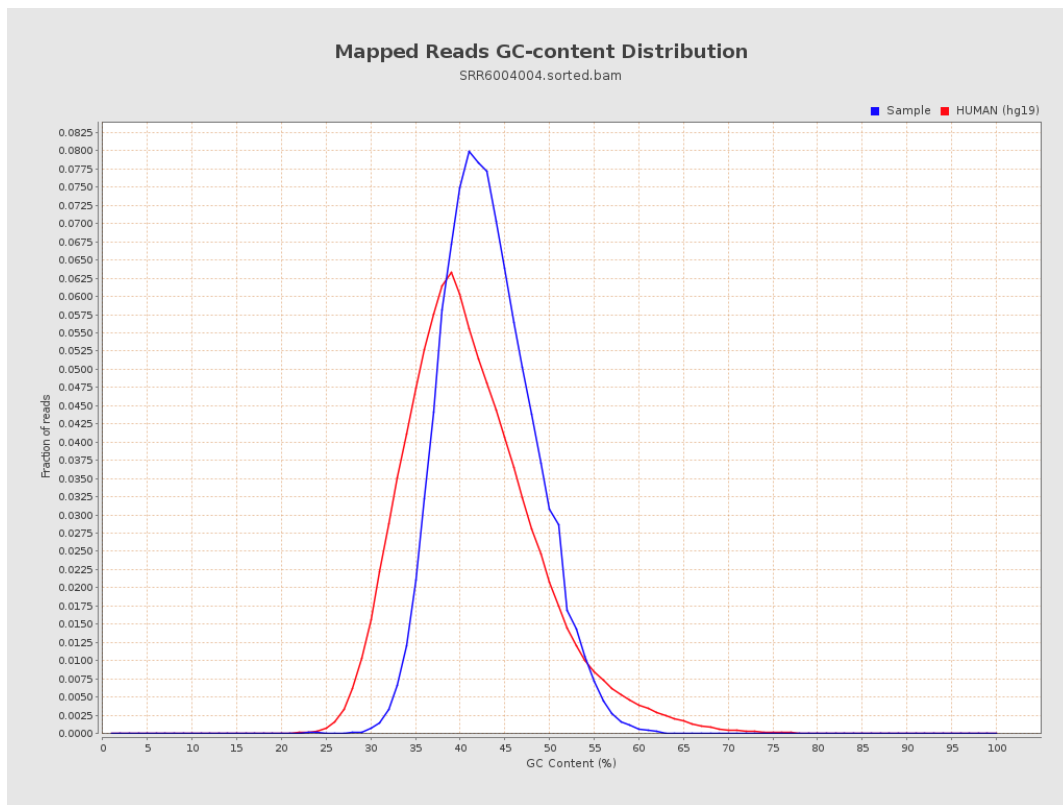
7. Results : Duplication Rate Histogram



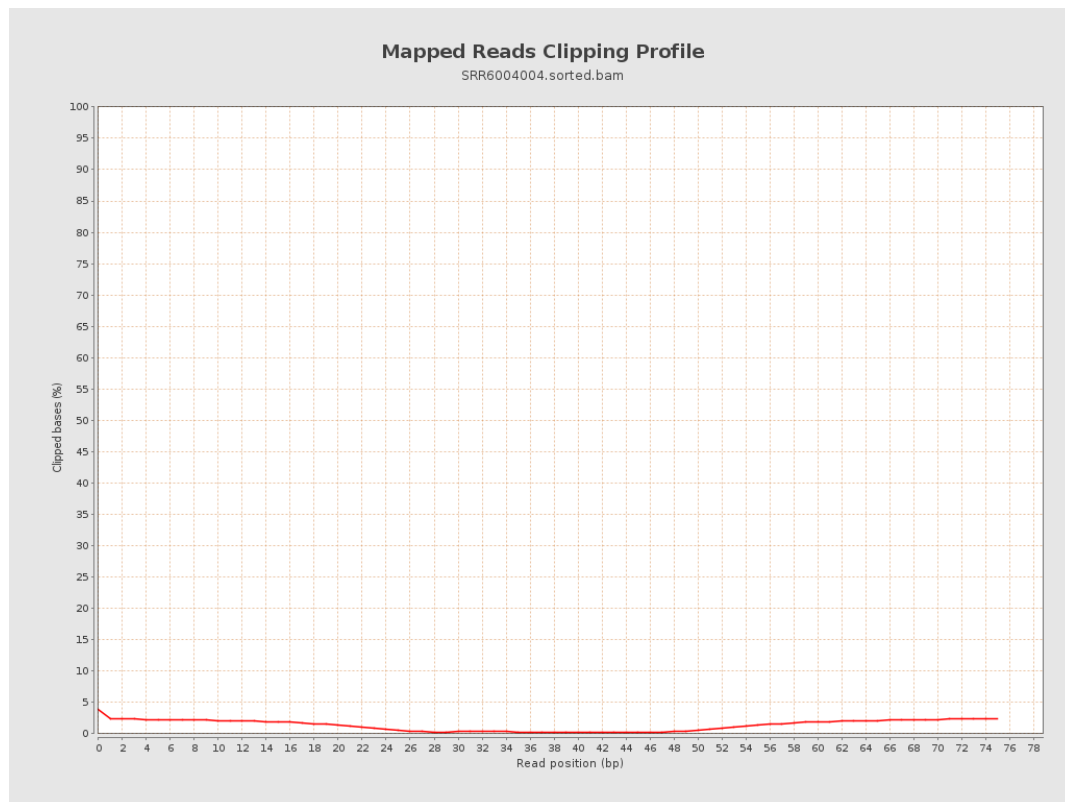
8. Results : Mapped Reads Nucleotide Content



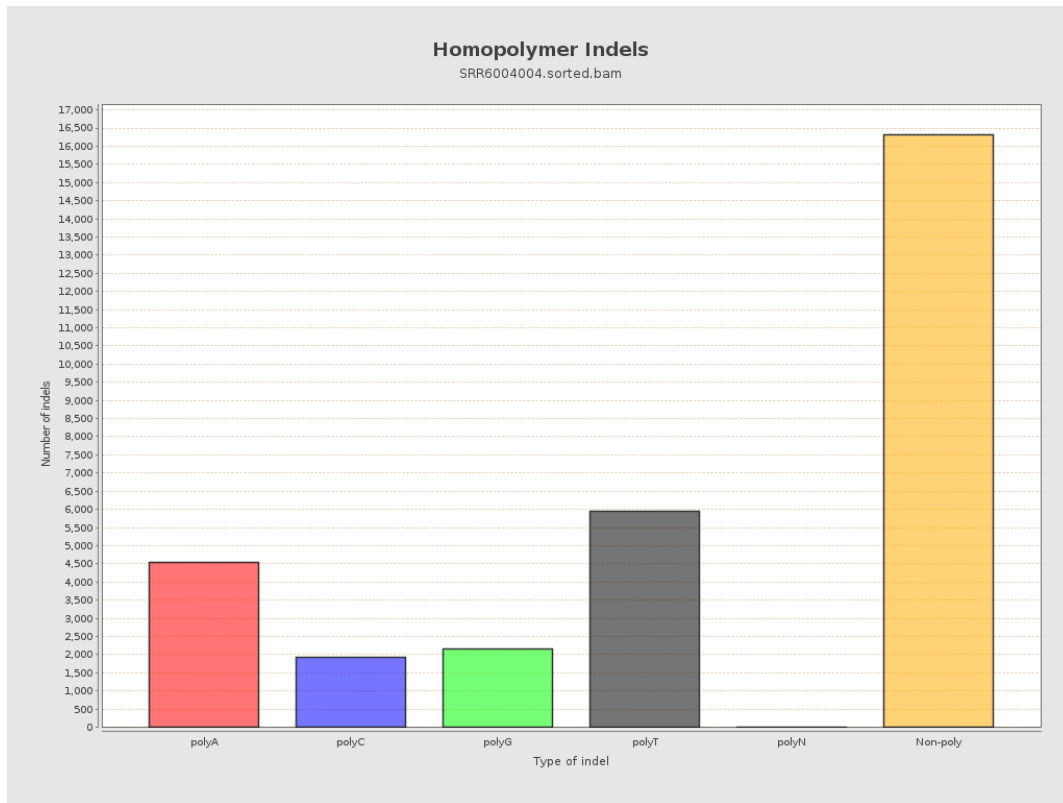
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

