

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 04:16:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240054.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_SRR6240054 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240054.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 04:16:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240054.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,777,255
Mapped reads	3,136,044 / 83.02%
Unmapped reads	641,211 / 16.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,556 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	354,081 / 9.37%
Duplication rate	9.05%
Clipped reads	2,009,940 / 53.21%

2.2. ACGT Content

Number/percentage of A's	52,584,688 / 27.12%
Number/percentage of C's	33,849,898 / 17.46%
Number/percentage of T's	63,045,250 / 32.51%
Number/percentage of G's	44,295,867 / 22.84%
Number/percentage of N's	122,941 / 0.06%
GC Percentage	40.3%

2.3. Coverage

Mean	0.0627

Standard Deviation	0.5566
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	45.03
----------------------	-------

2.5. Mismatches and indels

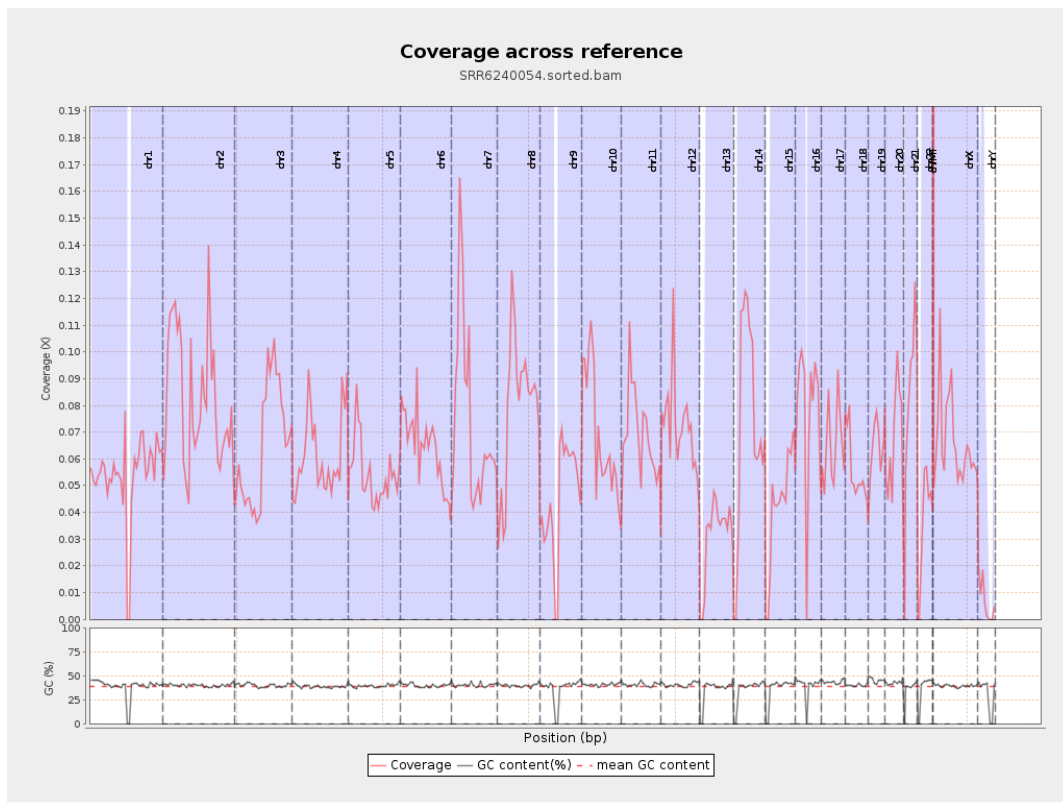
General error rate	0.99%
Mismatches	1,902,333
Insertions	13,707
Mapped reads with at least one insertion	0.43%
Deletions	61,291
Mapped reads with at least one deletion	1.93%
Homopolymer indels	49.16%

2.6. Chromosome stats

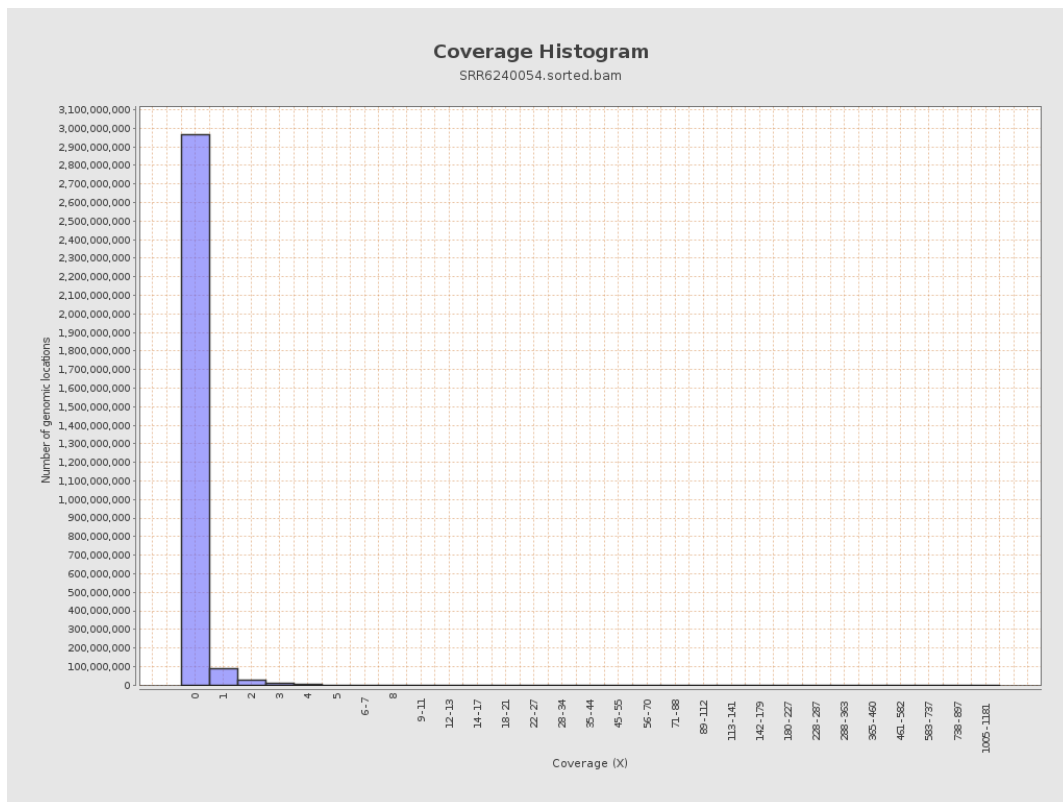
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	13385757	0.0537	0.8837
chr2	243199373	19955885	0.0821	0.6787
chr3	198022430	12839328	0.0648	0.3599
chr4	191154276	11766936	0.0616	0.3618
chr5	180915260	9861022	0.0545	0.3367
chr6	171115067	10982216	0.0642	0.5
chr7	159138663	11583119	0.0728	0.8745

chr8	146364022	11661155	0.0797	0.8144
chr9	141213431	6421161	0.0455	0.4858
chr10	135534747	9376121	0.0692	0.4923
chr11	135006516	9298453	0.0689	0.5283
chr12	133851895	9641281	0.072	0.3846
chr13	115169878	3638441	0.0316	0.247
chr14	107349540	8076693	0.0752	0.4069
chr15	102531392	4309722	0.042	0.3087
chr16	90354753	6847813	0.0758	0.4009
chr17	81195210	5322298	0.0655	0.4035
chr18	78077248	4377788	0.0561	0.8601
chr19	59128983	3836709	0.0649	0.6531
chr20	63025520	4255699	0.0675	0.3773
chr21	48129895	3984491	0.0828	0.4302
chr22	51304566	1847849	0.036	0.2573
chrMT	16571	57080	3.4446	3.3913
chrX	155270560	10269931	0.0661	0.4187
chrY	59373566	407167	0.0069	0.1305

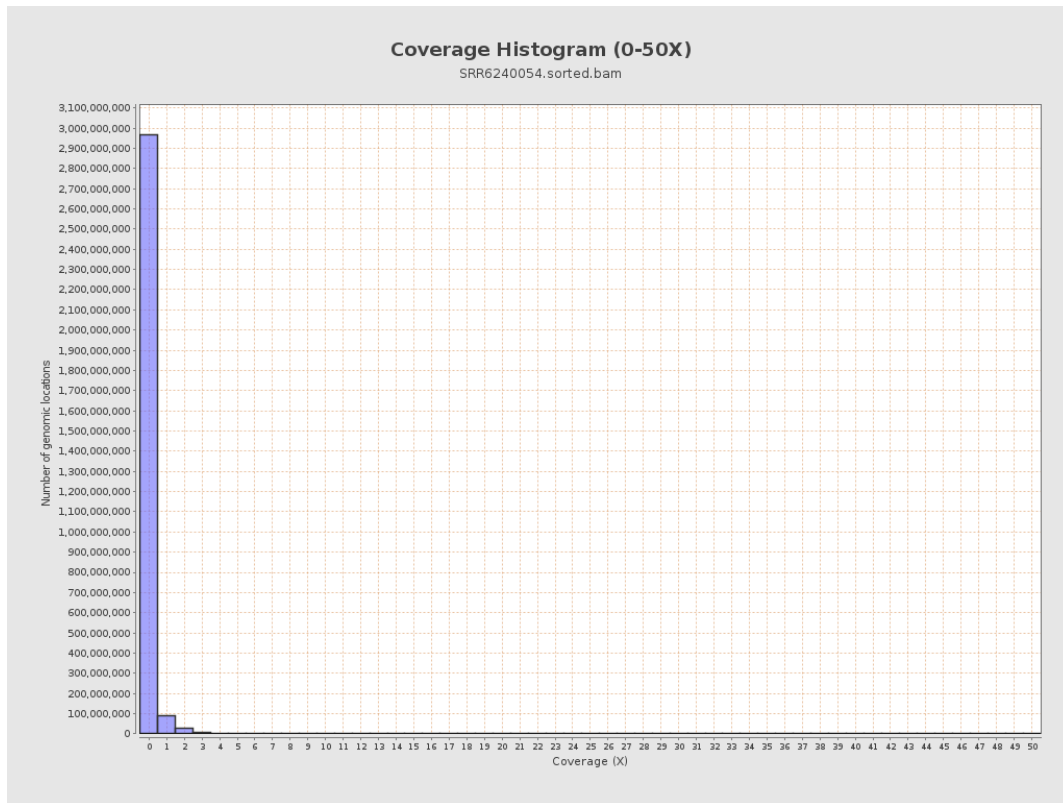
3. Results : Coverage across reference



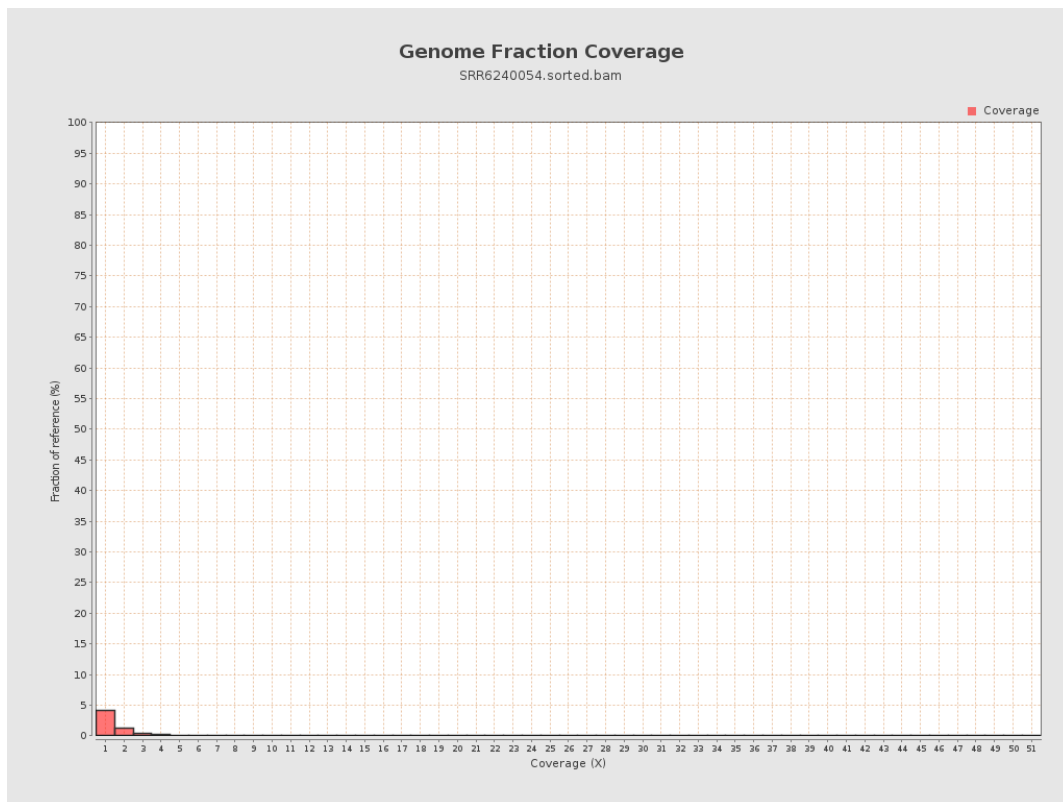
4. Results : Coverage Histogram



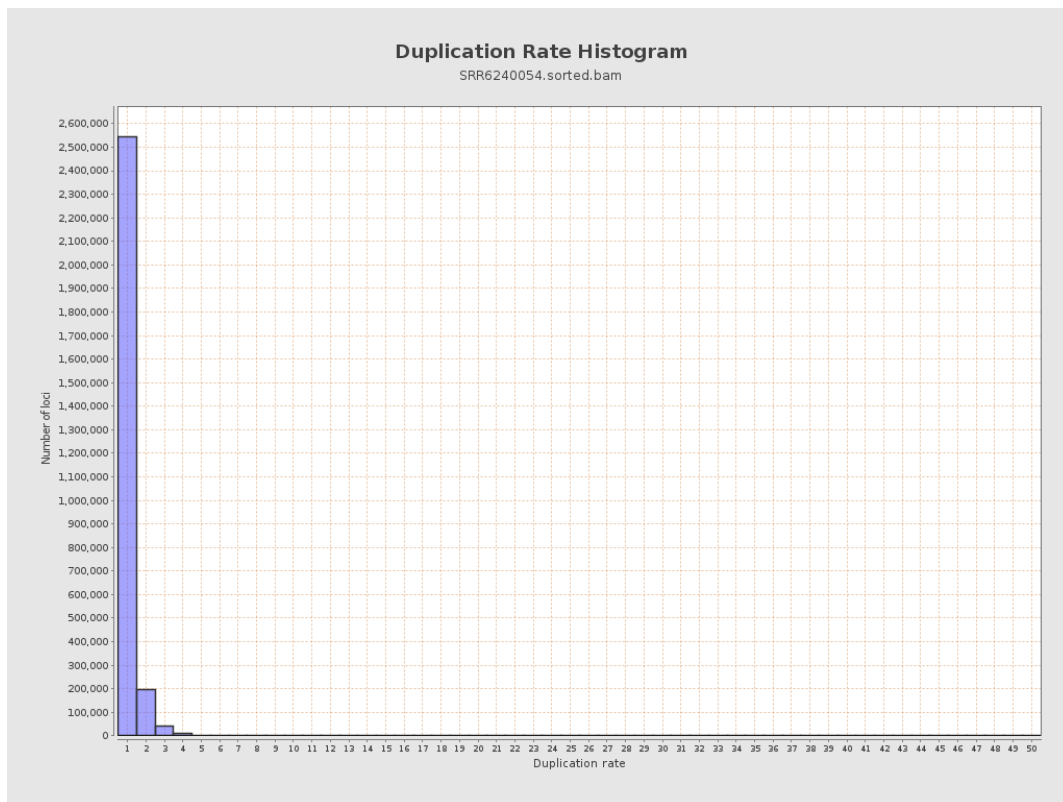
5. Results : Coverage Histogram (0-50X)



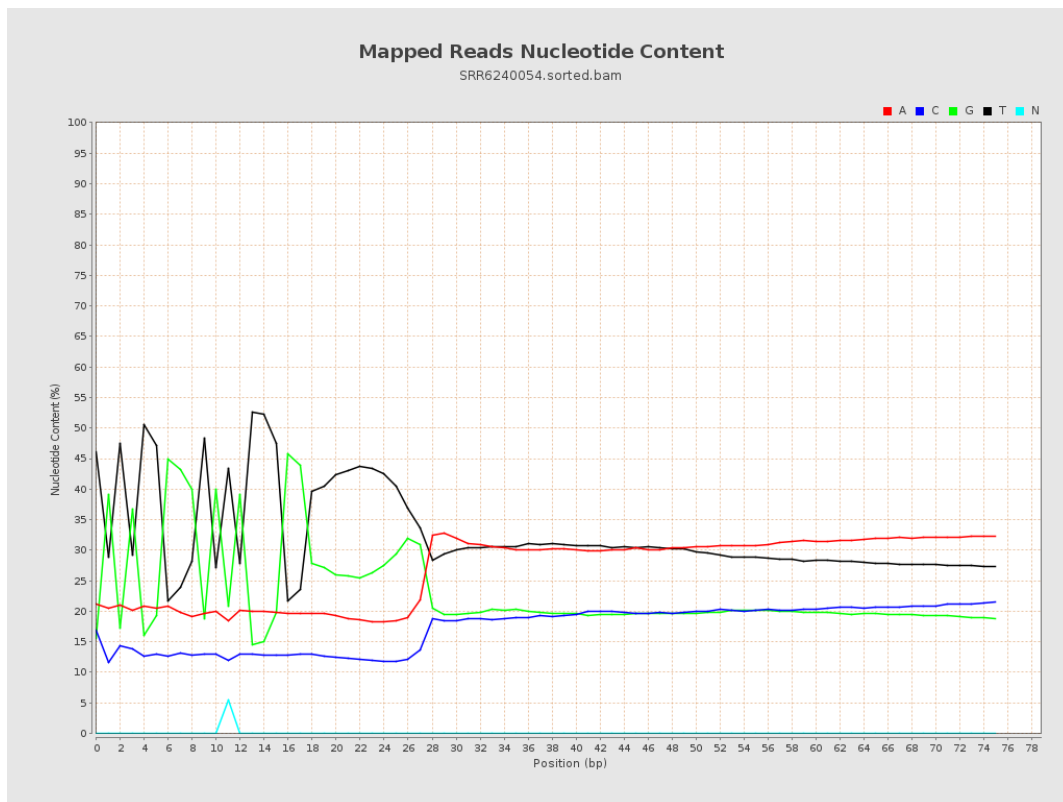
6. Results : Genome Fraction Coverage



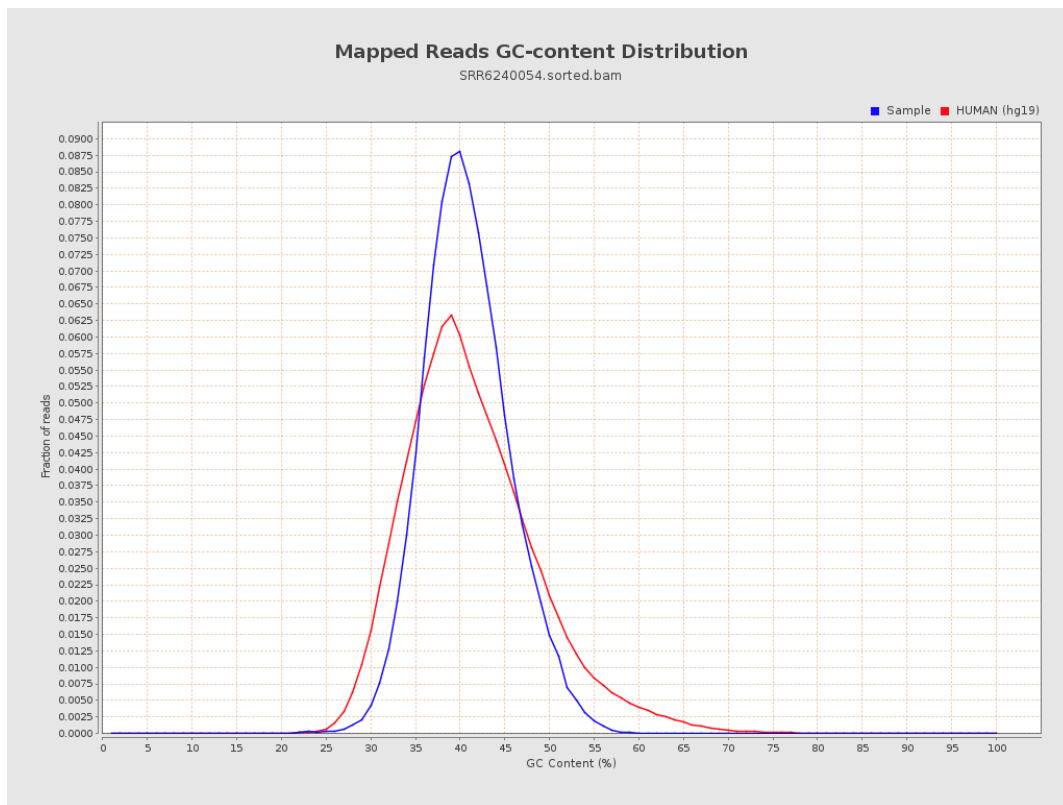
7. Results : Duplication Rate Histogram



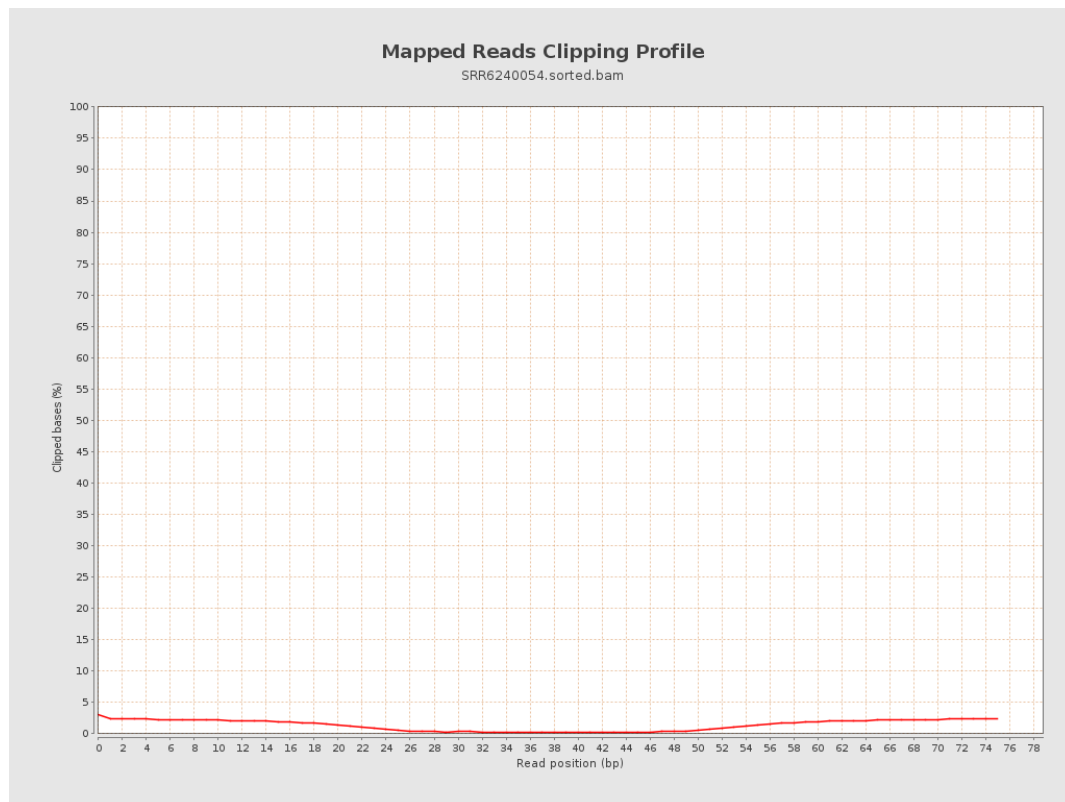
8. Results : Mapped Reads Nucleotide Content



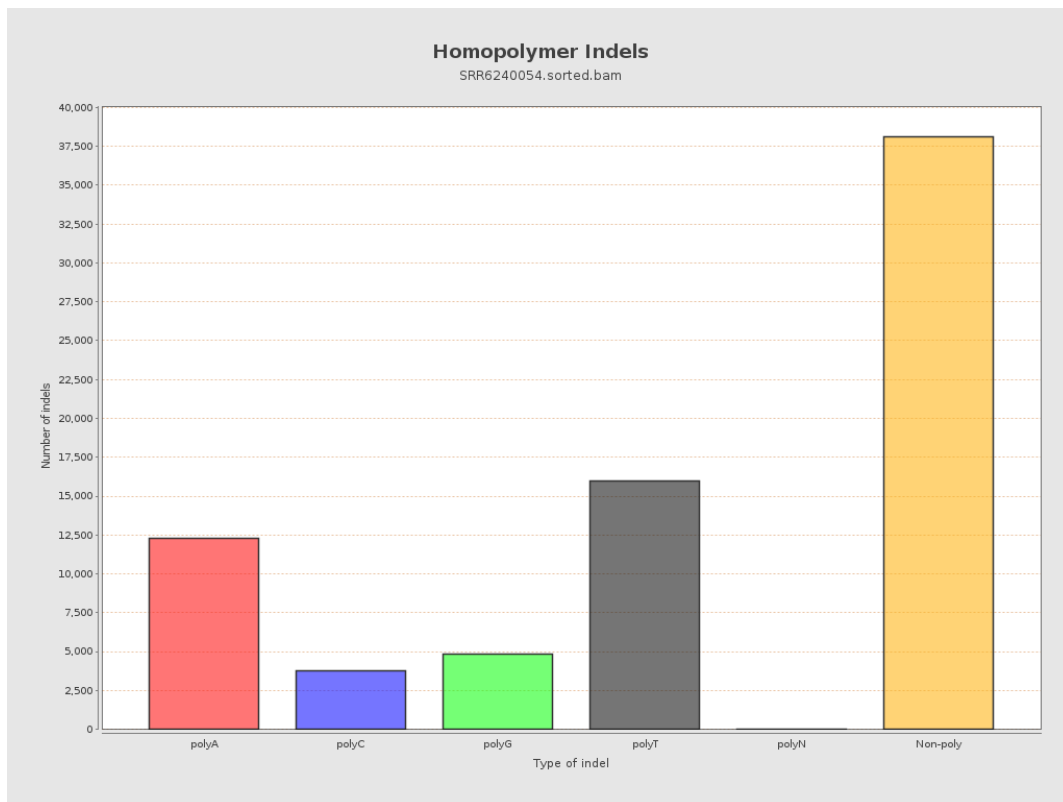
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

