

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 19:17:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230359.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_SRR6230359 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230359.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 19:17:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230359.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,656,057
Mapped reads	1,498,698 / 90.5%
Unmapped reads	157,359 / 9.5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,599 / 0.7%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	54,915 / 3.32%
Duplication rate	2.89%
Clipped reads	623,237 / 37.63%

2.2. ACGT Content

Number/percentage of A's	29,449,910 / 29.11%
Number/percentage of C's	18,639,133 / 18.42%
Number/percentage of T's	32,051,073 / 31.68%
Number/percentage of G's	20,985,510 / 20.74%
Number/percentage of N's	50,543 / 0.05%
GC Percentage	39.16%

2.3. Coverage

Mean	0.0327

Standard Deviation	0.301
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2.4. Mapping Quality

Mean Mapping Quality	47.07
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2.5. Mismatches and indels

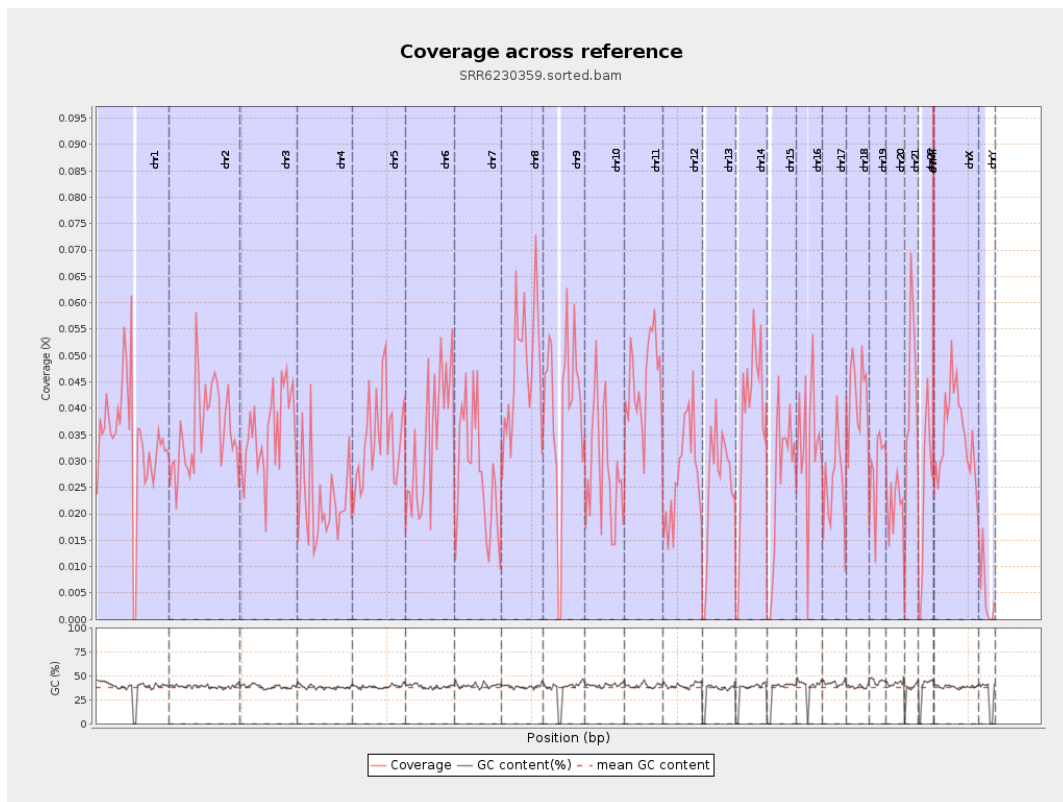
General error rate	0.87%
Mismatches	867,401
Insertions	8,664
Mapped reads with at least one insertion	0.57%
Deletions	27,184
Mapped reads with at least one deletion	1.79%
Homopolymer indels	46.26%

2.6. Chromosome stats

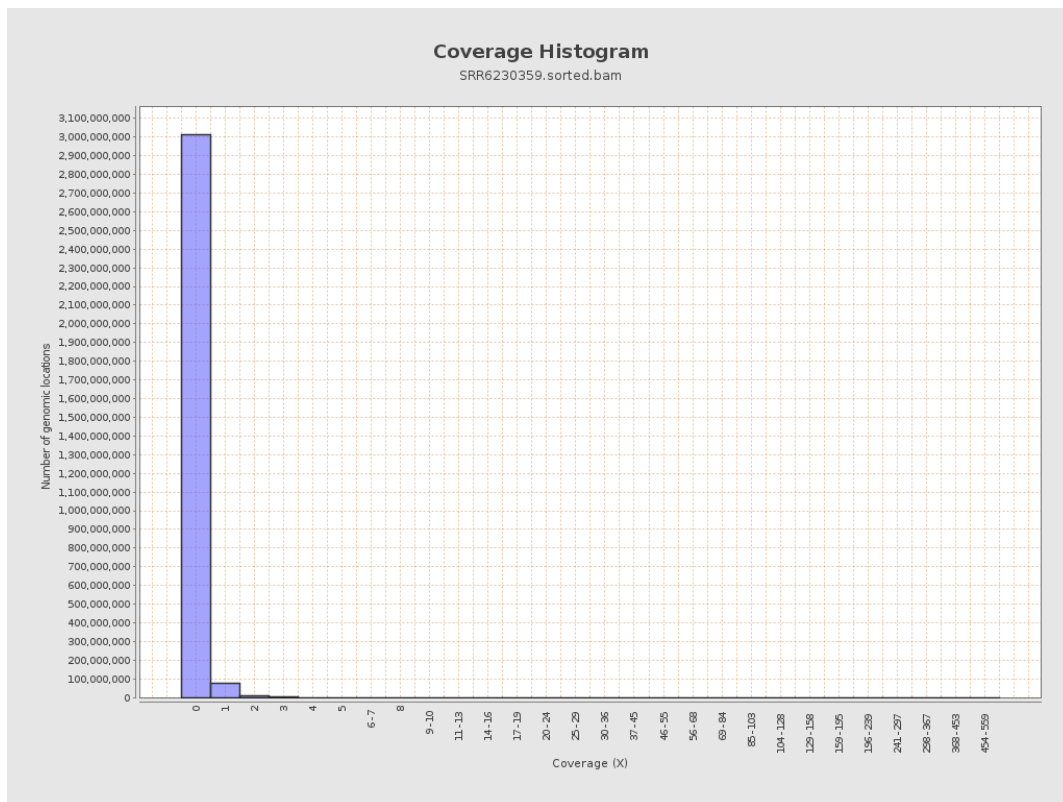
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8437695	0.0339	0.5081
chr2	243199373	8677805	0.0357	0.322
chr3	198022430	7051540	0.0356	0.2158
chr4	191154276	4259009	0.0223	0.1944
chr5	180915260	6143717	0.034	0.2105
chr6	171115067	5805253	0.0339	0.2214
chr7	159138663	4520661	0.0284	0.3003

chr8	146364022	6997447	0.0478	0.4492
chr9	141213431	5692425	0.0403	0.2989
chr10	135534747	3884120	0.0287	0.2914
chr11	135006516	6055780	0.0449	0.3168
chr12	133851895	3728430	0.0279	0.1932
chr13	115169878	2923775	0.0254	0.1811
chr14	107349540	4018145	0.0374	0.2289
chr15	102531392	2627869	0.0256	0.1813
chr16	90354753	3019620	0.0334	0.2589
chr17	81195210	2046957	0.0252	0.1957
chr18	78077248	3341779	0.0428	0.5653
chr19	59128983	1696860	0.0287	0.3758
chr20	63025520	1359164	0.0216	0.1791
chr21	48129895	1993059	0.0414	0.2504
chr22	51304566	1206609	0.0235	0.1731
chrMT	16571	4229	0.2552	0.5144
chrX	155270560	5436175	0.035	0.2335
chrY	59373566	293285	0.0049	0.1346

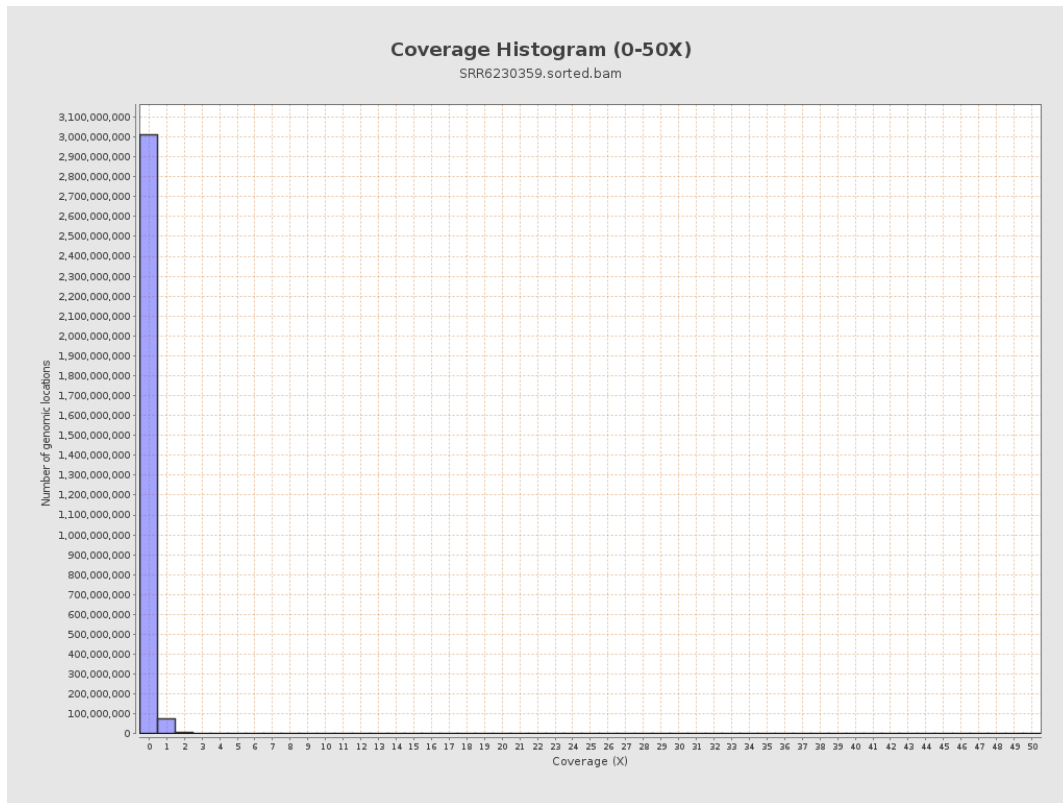
3. Results : Coverage across reference



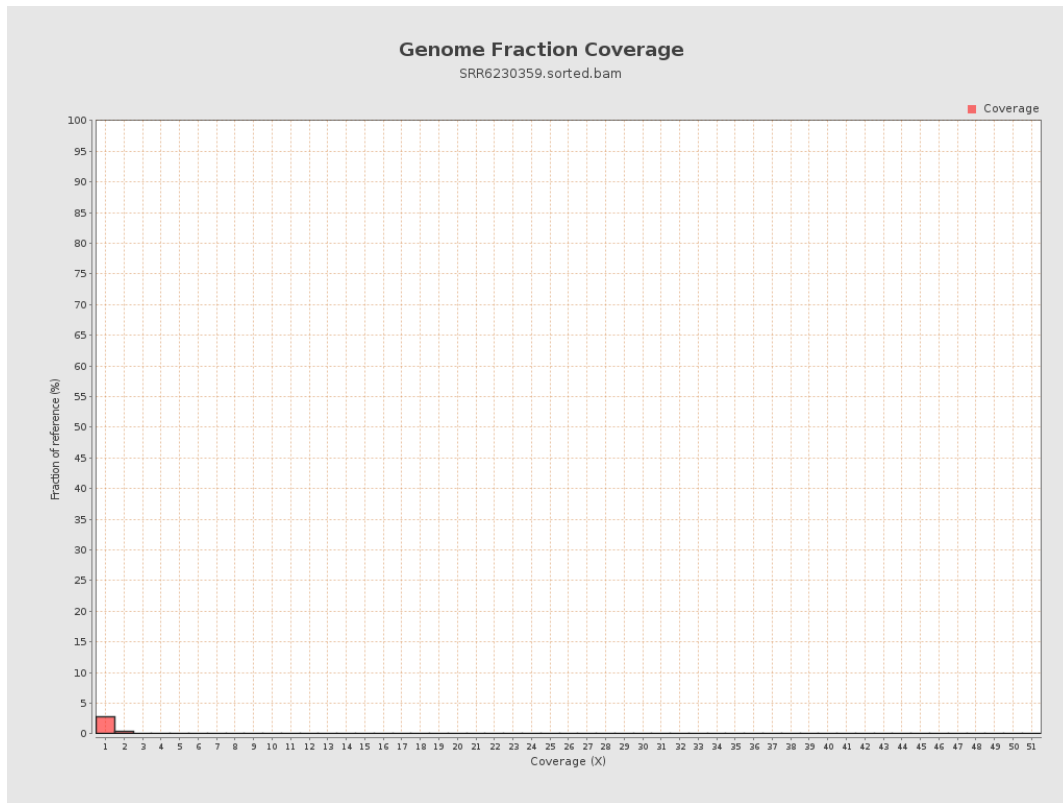
4. Results : Coverage Histogram



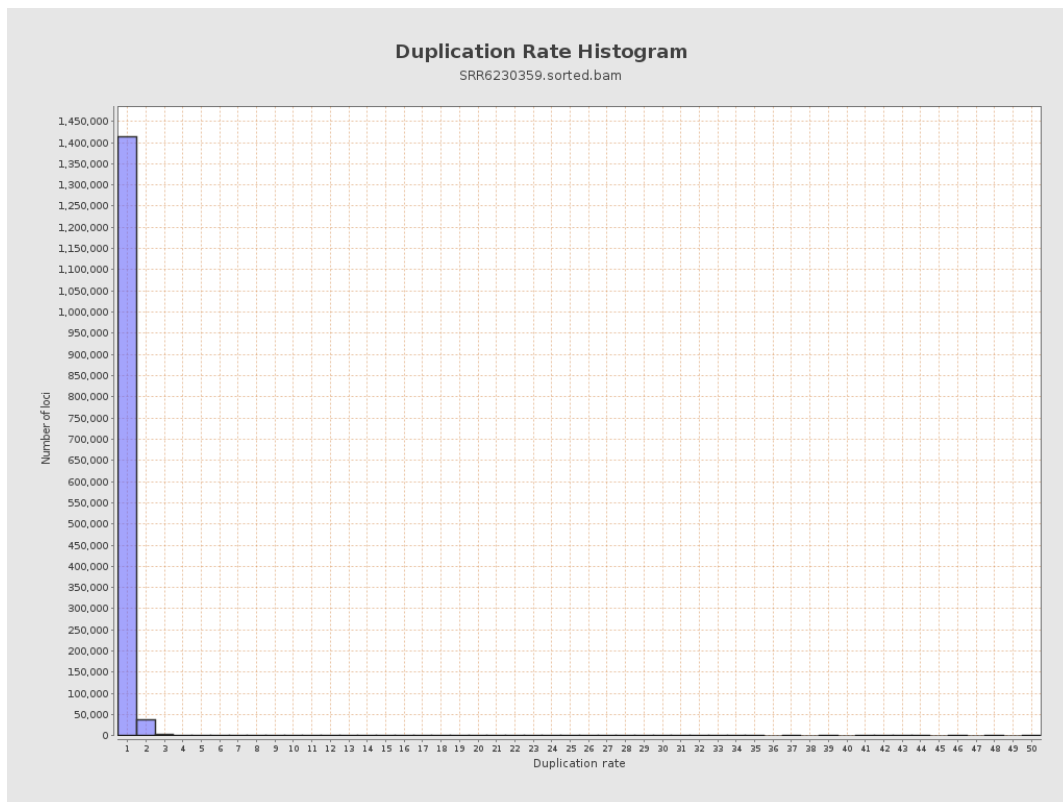
5. Results : Coverage Histogram (0-50X)



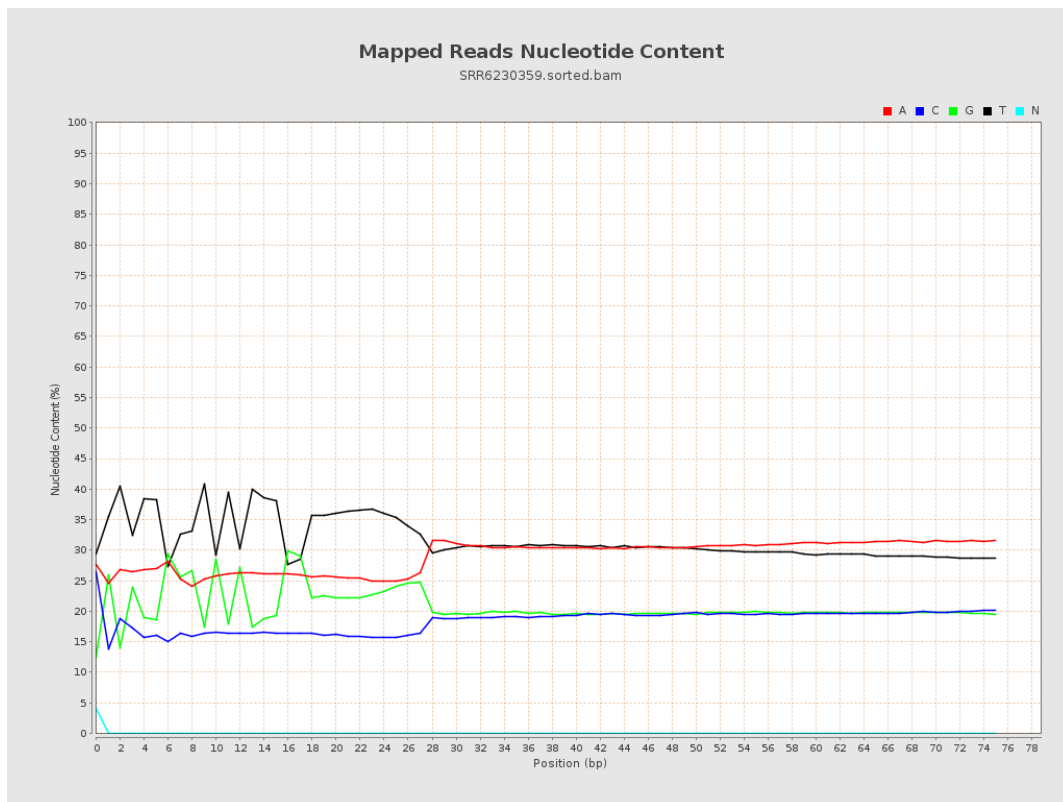
6. Results : Genome Fraction Coverage



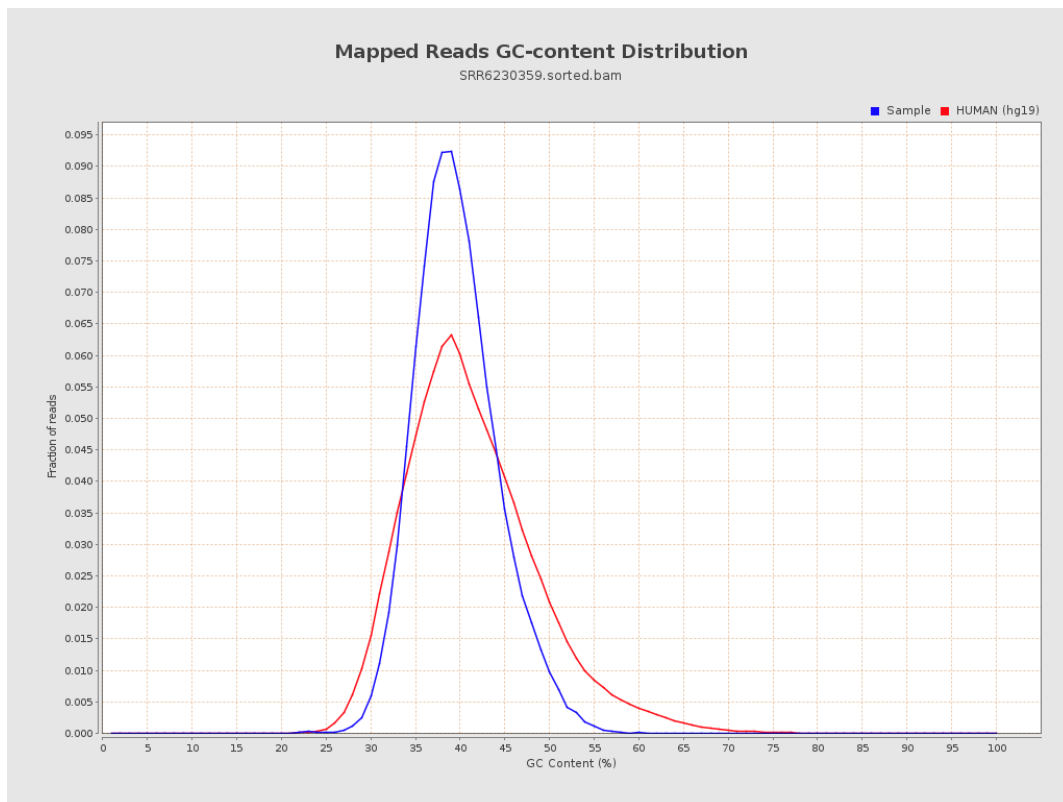
7. Results : Duplication Rate Histogram



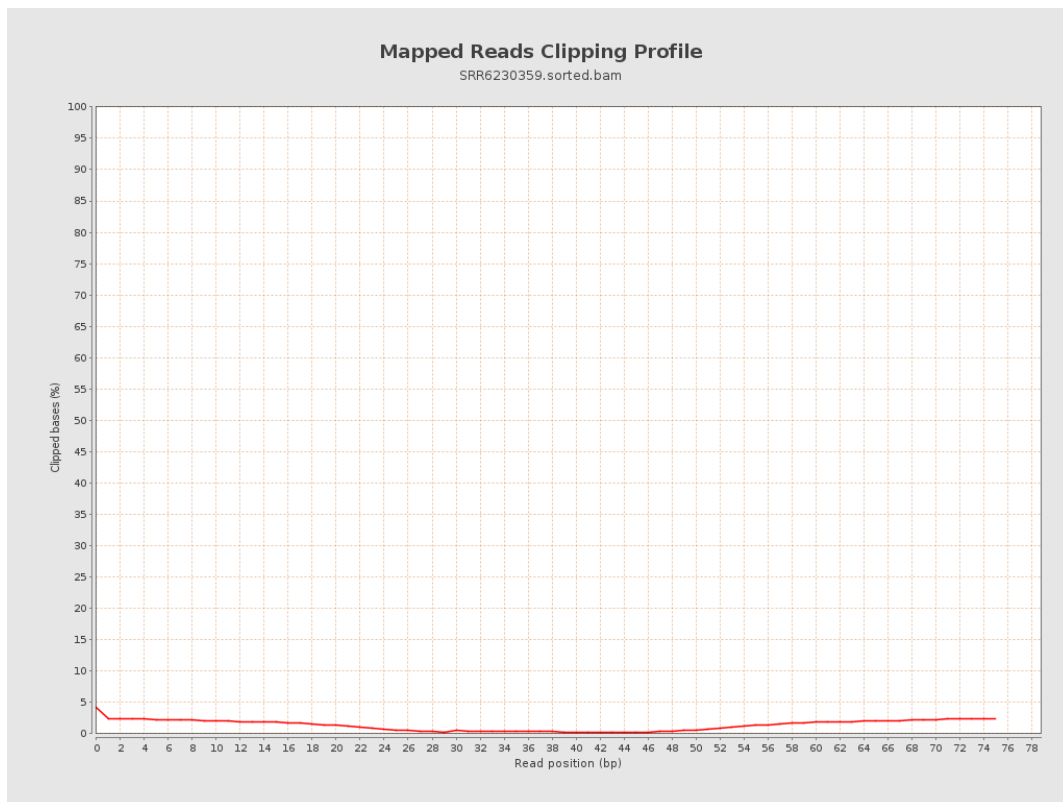
8. Results : Mapped Reads Nucleotide Content



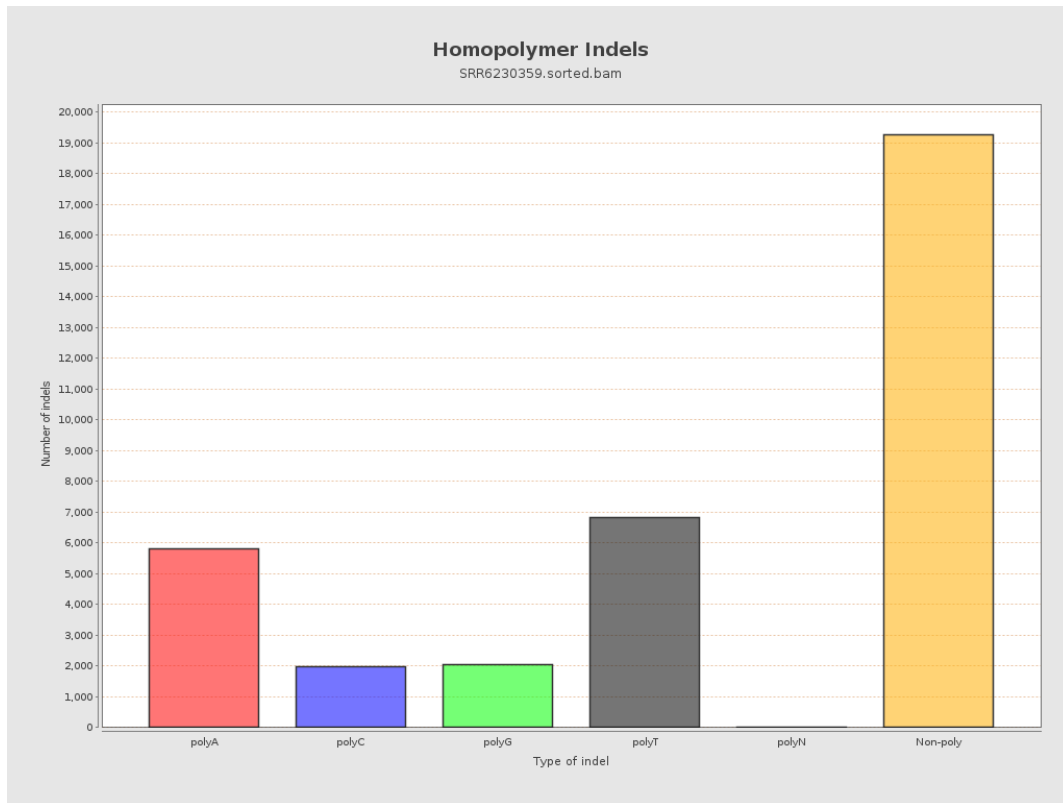
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

