

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 16:31:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234107.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_SRR6234107 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234107.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 16:31:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234107.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,535,940
Mapped reads	6,098,091 / 93.3%
Unmapped reads	437,849 / 6.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	41,438 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	623,443 / 9.54%
Duplication rate	4.78%
Clipped reads	2,556,804 / 39.12%

2.2. ACGT Content

Number/percentage of A's	109,697,993 / 26.7%
Number/percentage of C's	76,442,416 / 18.61%
Number/percentage of T's	119,380,946 / 29.06%
Number/percentage of G's	105,221,748 / 25.61%
Number/percentage of N's	88,450 / 0.02%
GC Percentage	44.22%

2.3. Coverage

Mean	0.1328

Standard Deviation	32.4917
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2.4. Mapping Quality

Mean Mapping Quality	42.93
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2.5. Mismatches and indels

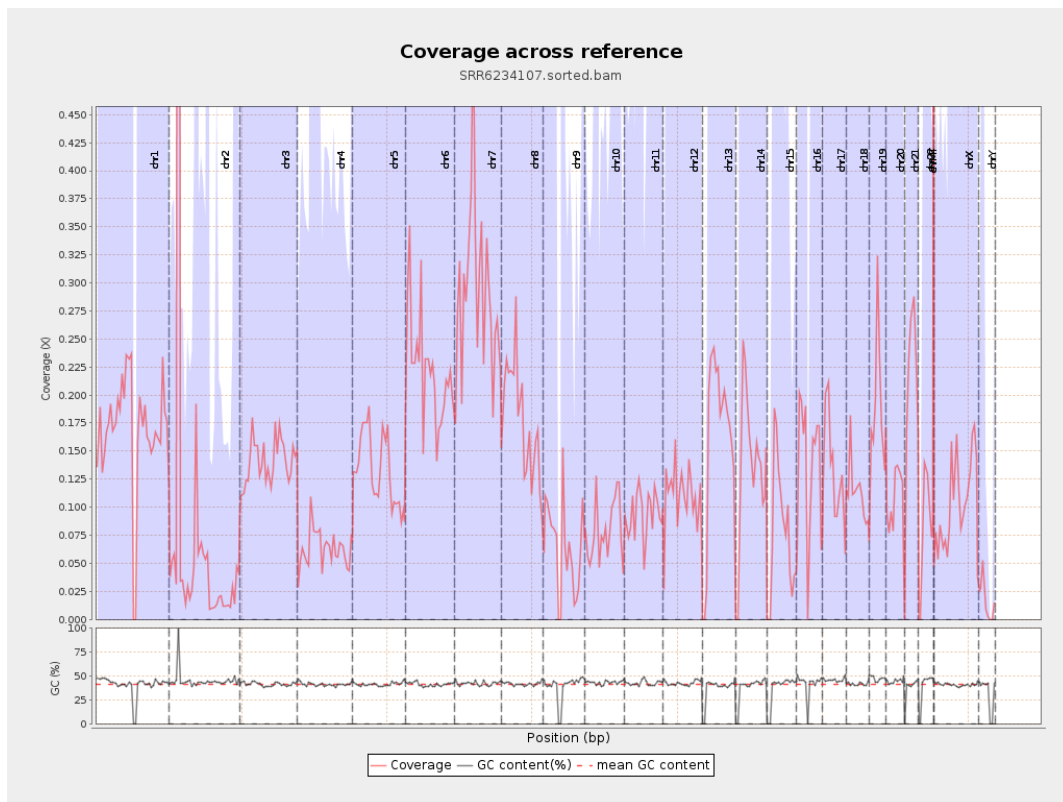
General error rate	0.7%
Mismatches	2,820,712
Insertions	29,039
Mapped reads with at least one insertion	0.47%
Deletions	94,946
Mapped reads with at least one deletion	1.54%
Homopolymer indels	45.72%

2.6. Chromosome stats

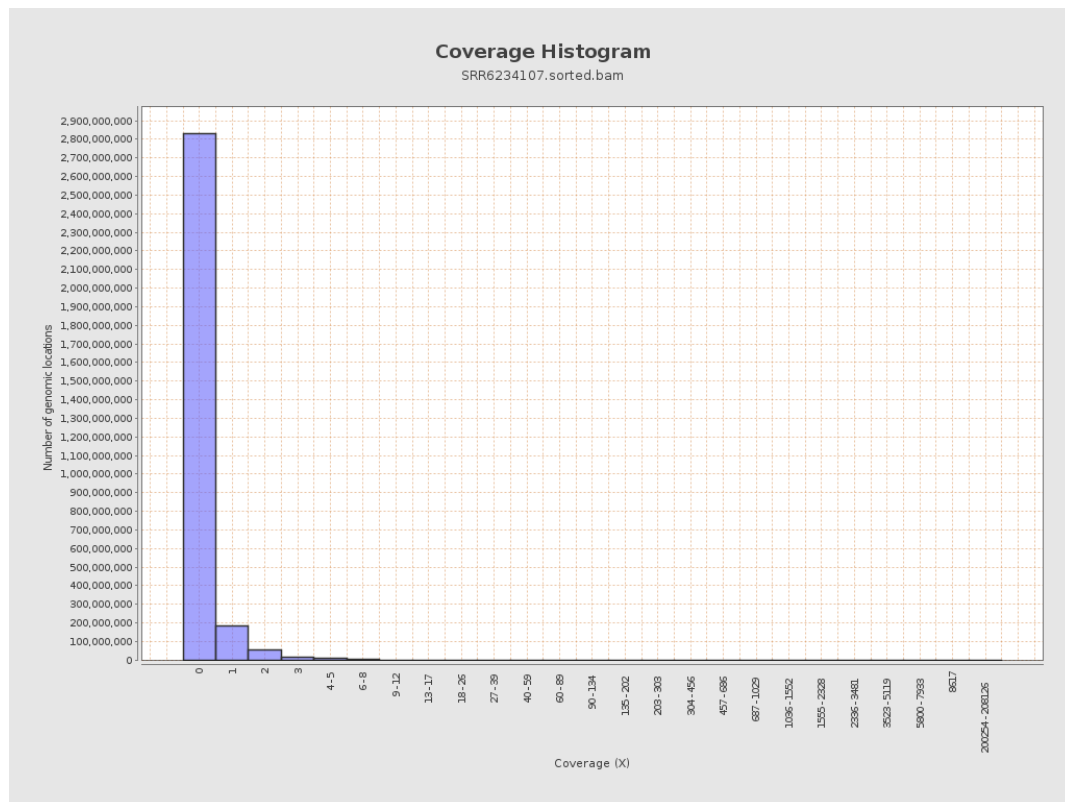
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	42046251	0.1687	2.2544
chr2	243199373	25350342	0.1042	115.8155
chr3	198022430	27904302	0.1409	0.5167
chr4	191154276	11987310	0.0627	0.3967
chr5	180915260	24194186	0.1337	0.5303
chr6	171115067	37785321	0.2208	1.069
chr7	159138663	46628641	0.293	4.264

chr8	146364022	25909529	0.177	1.2867
chr9	141213431	9053628	0.0641	0.9566
chr10	135534747	10701051	0.079	0.74
chr11	135006516	12539873	0.0929	0.9812
chr12	133851895	14691169	0.1098	0.4867
chr13	115169878	18531750	0.1609	0.5591
chr14	107349540	14485654	0.1349	0.76
chr15	102531392	8175241	0.0797	0.407
chr16	90354753	12411011	0.1374	0.7123
chr17	81195210	10504158	0.1294	0.6692
chr18	78077248	8918128	0.1142	2.5674
chr19	59128983	11249909	0.1903	1.4644
chr20	63025520	6739469	0.1069	0.5073
chr21	48129895	10029207	0.2084	0.7378
chr22	51304566	4085042	0.0796	0.3853
chrMT	16571	12078	0.7289	1.14
chrX	155270560	16101671	0.1037	0.6549
chrY	59373566	951246	0.016	0.3029

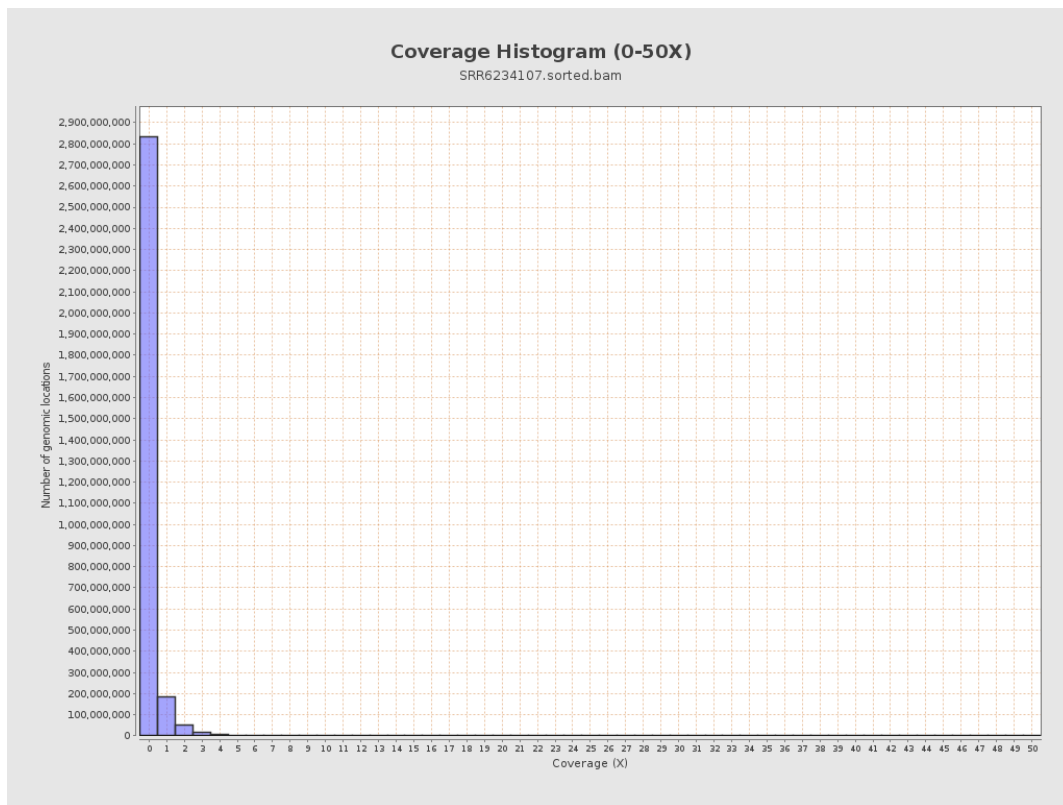
3. Results : Coverage across reference



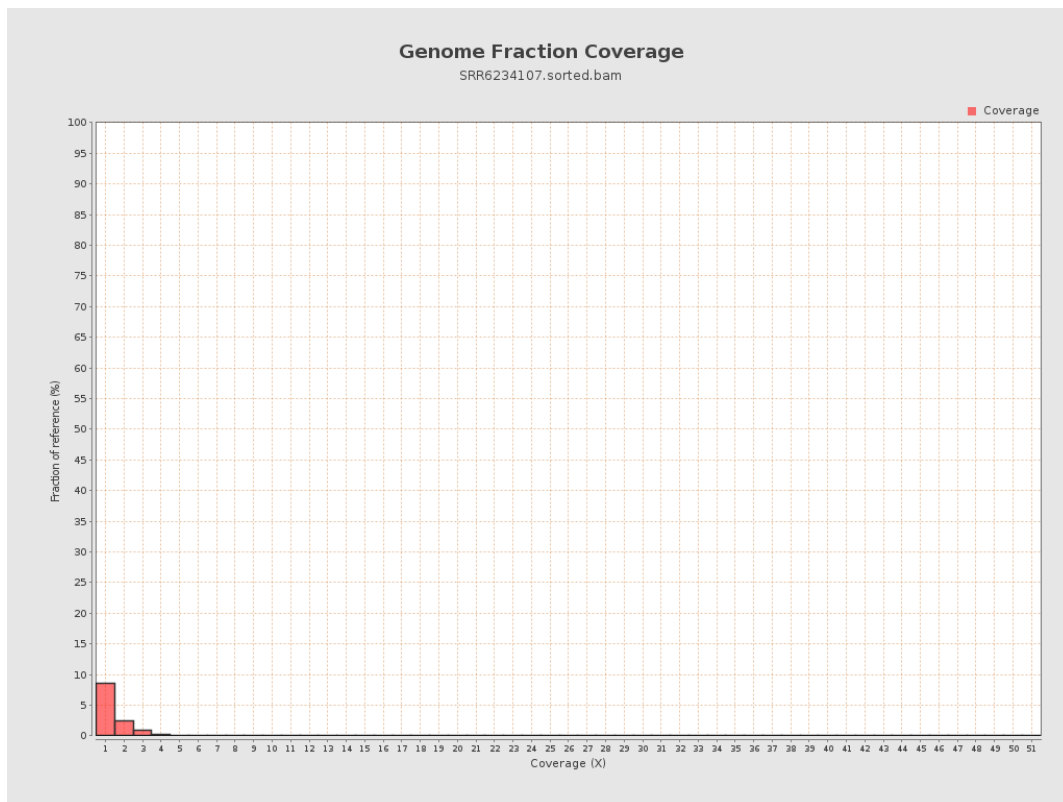
4. Results : Coverage Histogram



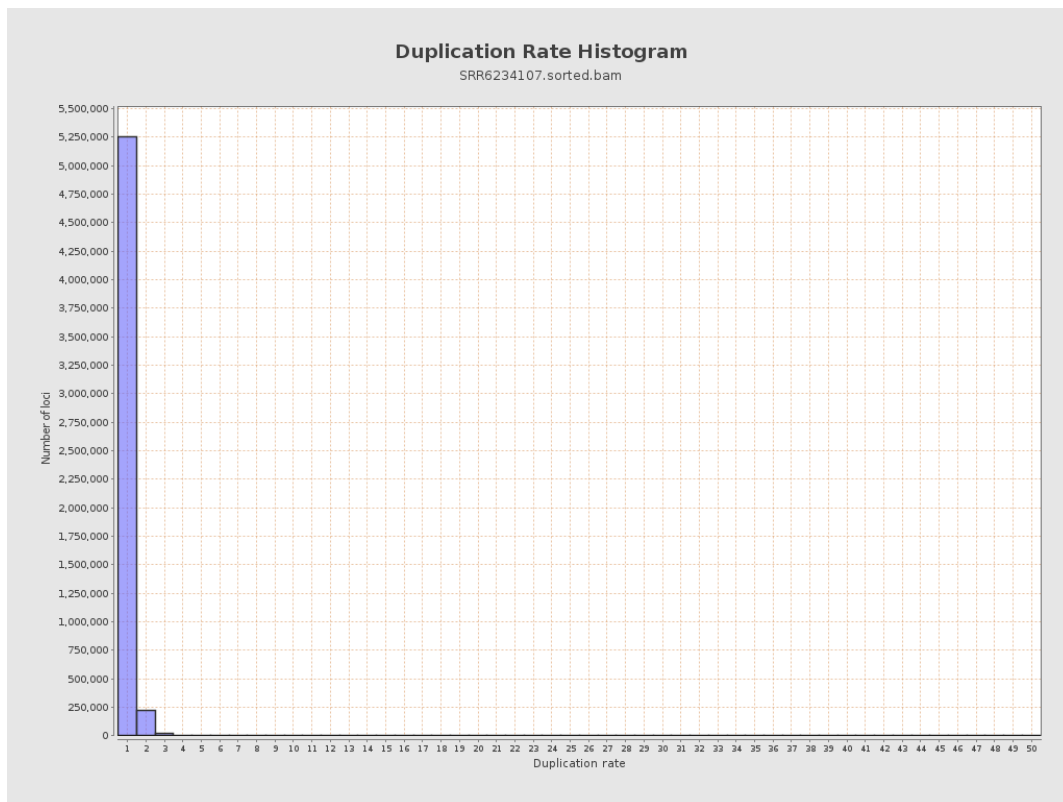
5. Results : Coverage Histogram (0-50X)



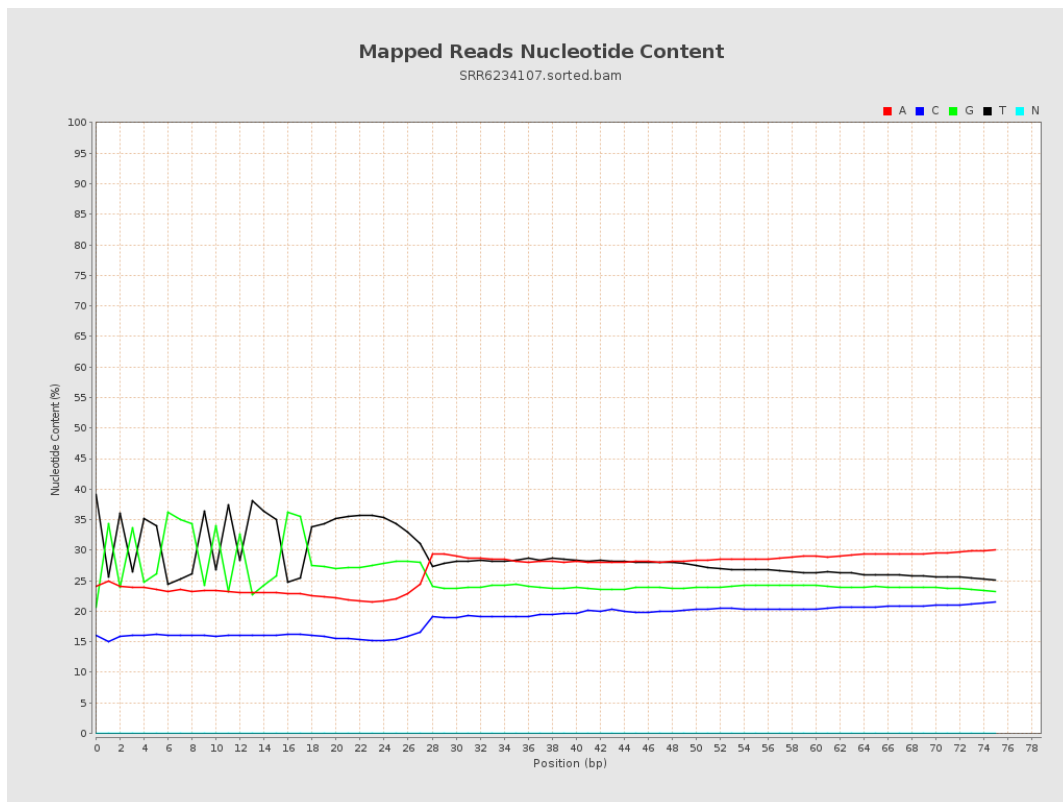
6. Results : Genome Fraction Coverage



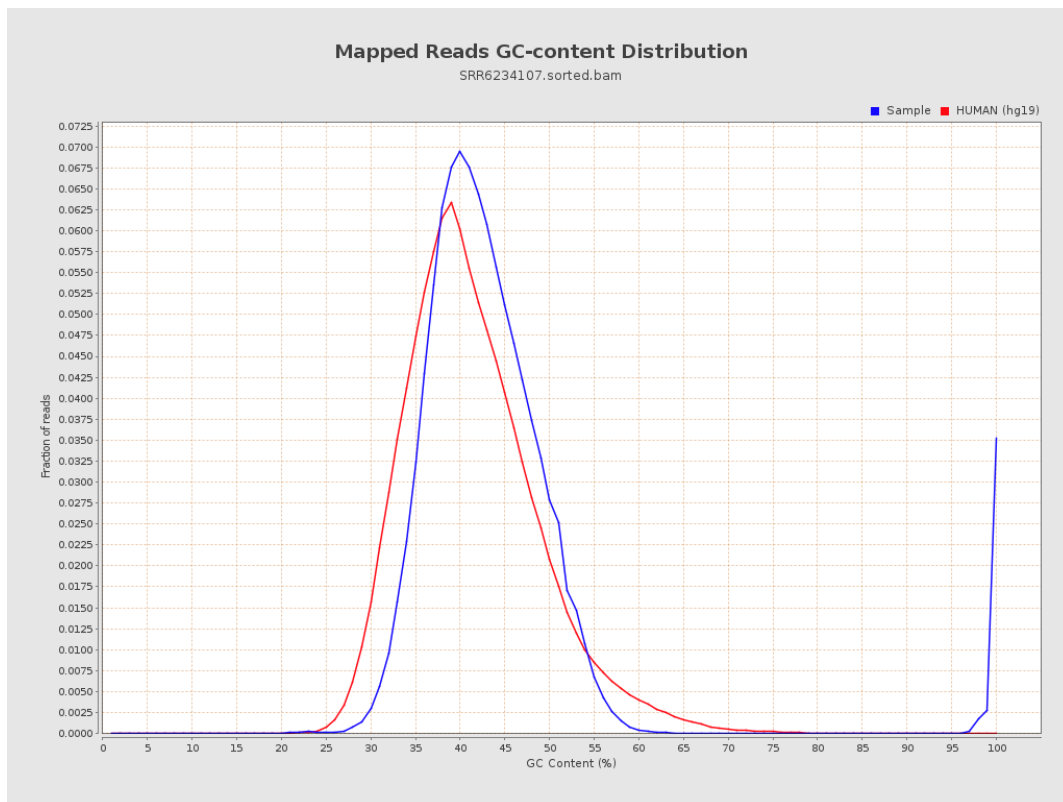
7. Results : Duplication Rate Histogram



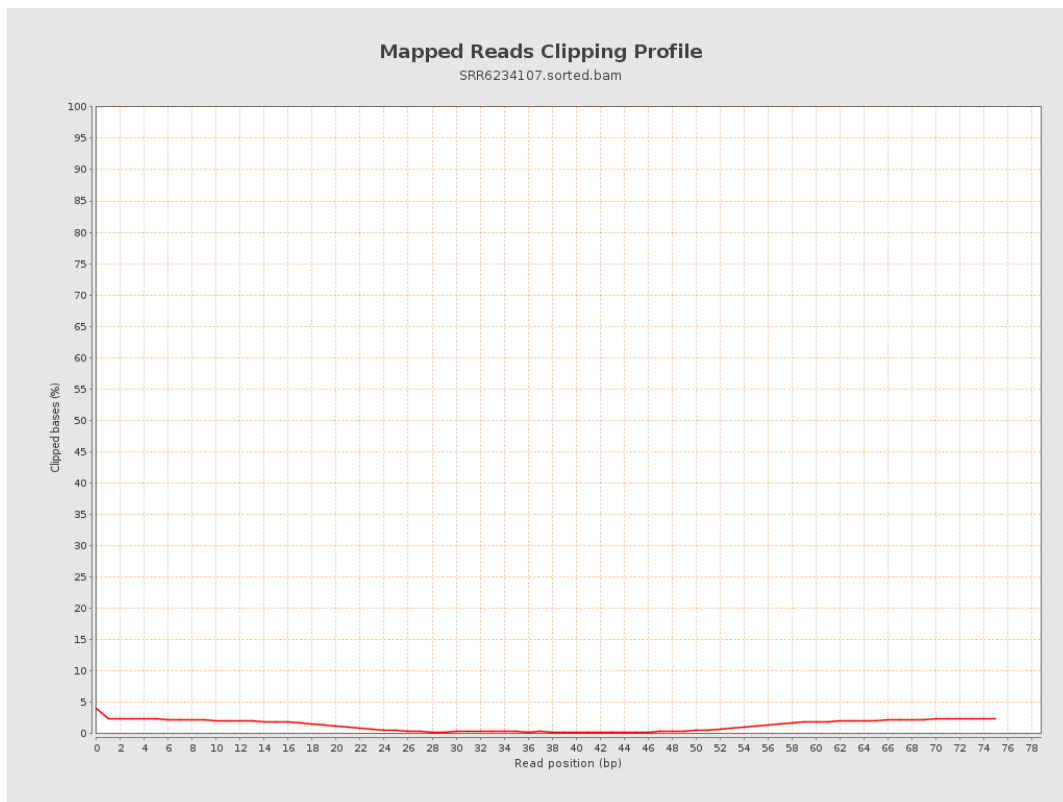
8. Results : Mapped Reads Nucleotide Content



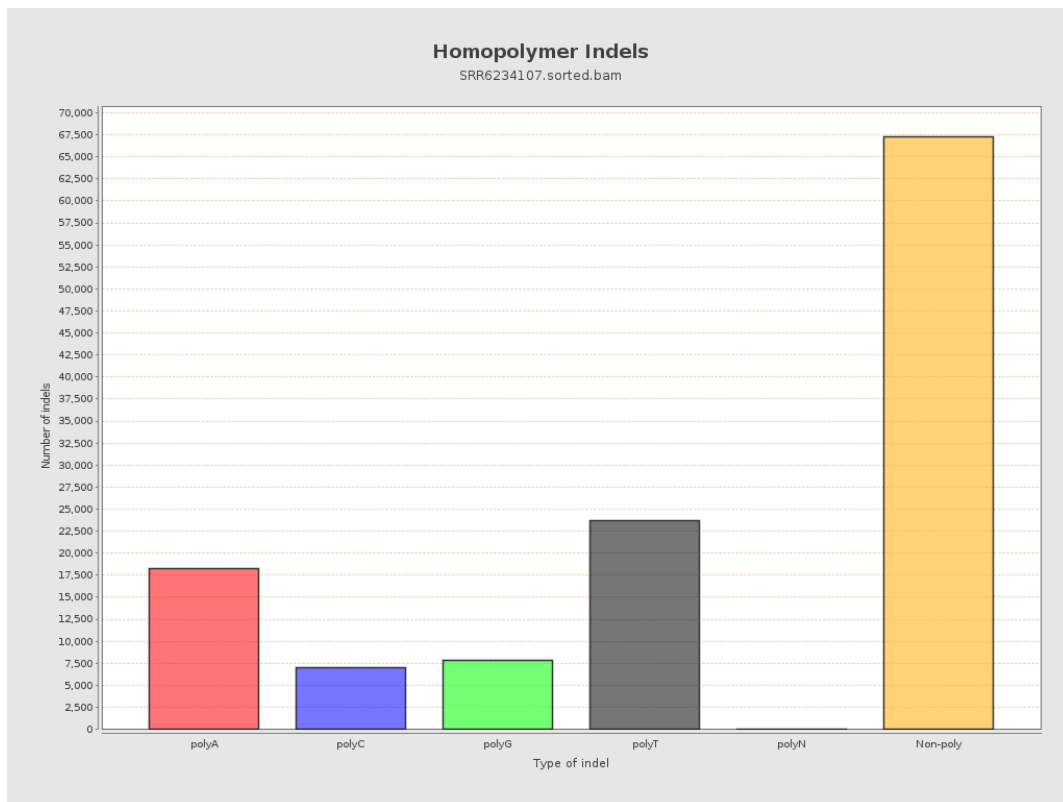
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

