

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 13:44:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234069.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_SRR6234069 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234069.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 13:44:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234069.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,581,169
Mapped reads	5,288,077 / 94.75%
Unmapped reads	293,092 / 5.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	37,767 / 0.68%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	575,879 / 10.32%
Duplication rate	8.86%
Clipped reads	2,721,909 / 48.77%

2.2. ACGT Content

Number/percentage of A's	88,657,394 / 25.91%
Number/percentage of C's	62,590,319 / 18.29%
Number/percentage of T's	110,128,481 / 32.18%
Number/percentage of G's	80,819,018 / 23.62%
Number/percentage of N's	33,512 / 0.01%
GC Percentage	41.9%

2.3. Coverage

Mean	0.1106

Standard Deviation	1.1428
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2.4. Mapping Quality

Mean Mapping Quality	45.7
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2.5. Mismatches and indels

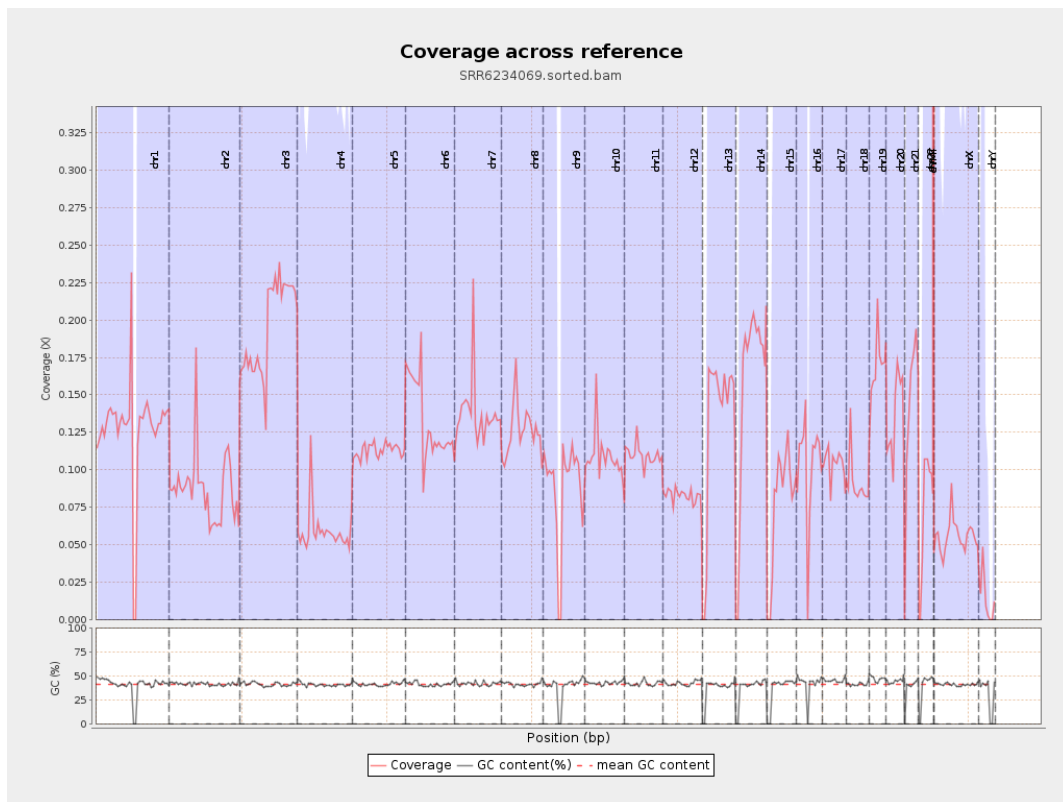
General error rate	0.55%
Mismatches	1,835,907
Insertions	22,379
Mapped reads with at least one insertion	0.42%
Deletions	75,388
Mapped reads with at least one deletion	1.41%
Homopolymer indels	43.88%

2.6. Chromosome stats

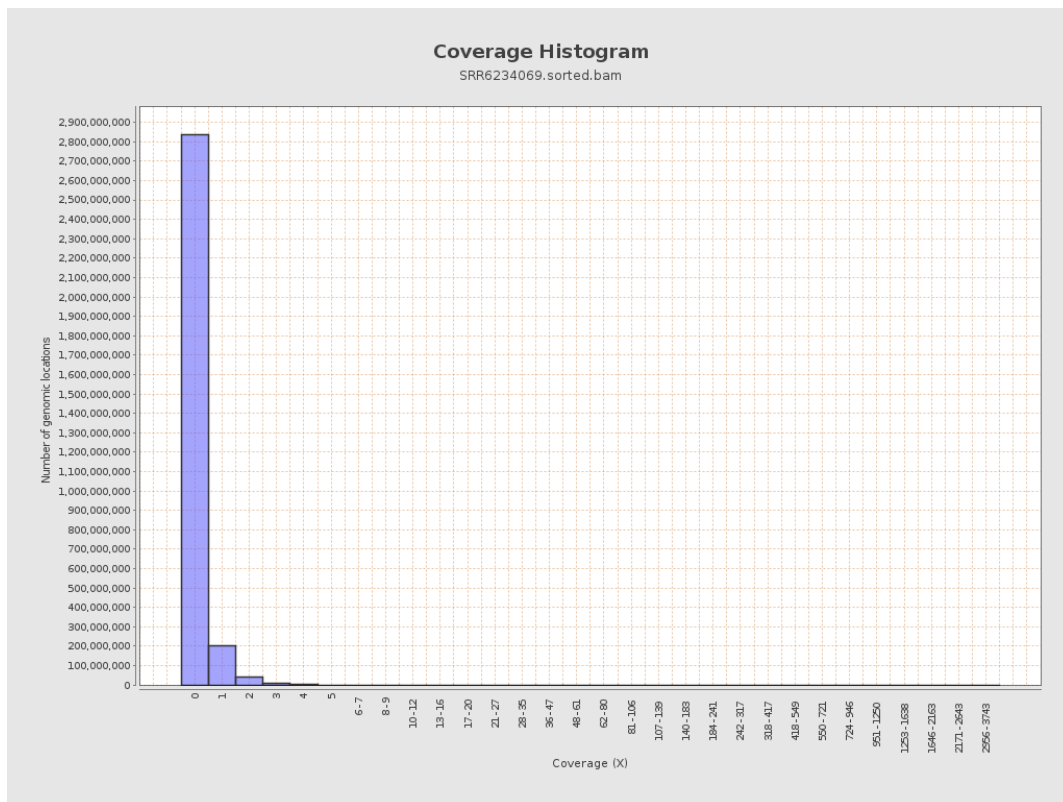
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	31646591	0.127	2.5584
chr2	243199373	21144947	0.0869	1.7636
chr3	198022430	38544866	0.1946	0.5602
chr4	191154276	11187744	0.0585	0.3999
chr5	180915260	20411019	0.1128	0.4413
chr6	171115067	22714625	0.1327	0.7487
chr7	159138663	21937794	0.1379	1.4516

chr8	146364022	18389317	0.1256	1.2211
chr9	141213431	12322304	0.0873	0.7223
chr10	135534747	14784827	0.1091	0.795
chr11	135006516	14701899	0.1089	0.8525
chr12	133851895	11033449	0.0824	0.3952
chr13	115169878	15144655	0.1315	0.5013
chr14	107349540	16715226	0.1557	0.5501
chr15	102531392	8045365	0.0785	0.3827
chr16	90354753	9353070	0.1035	0.5374
chr17	81195210	8379785	0.1032	0.5026
chr18	78077248	7138579	0.0914	1.9311
chr19	59128983	10062721	0.1702	1.3238
chr20	63025520	8529797	0.1353	0.5342
chr21	48129895	6849203	0.1423	0.5244
chr22	51304566	3657708	0.0713	0.3285
chrMT	16571	210484	12.7019	7.491
chrX	155270560	8651633	0.0557	0.4498
chrY	59373566	802203	0.0135	0.299

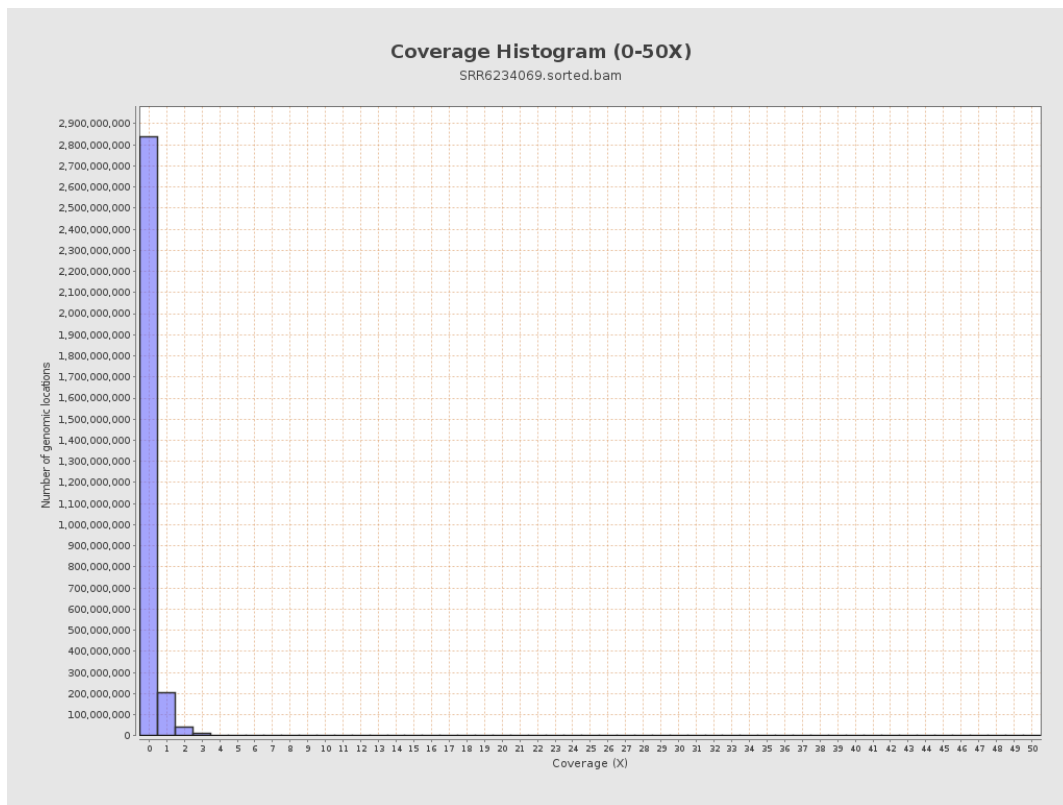
3. Results : Coverage across reference



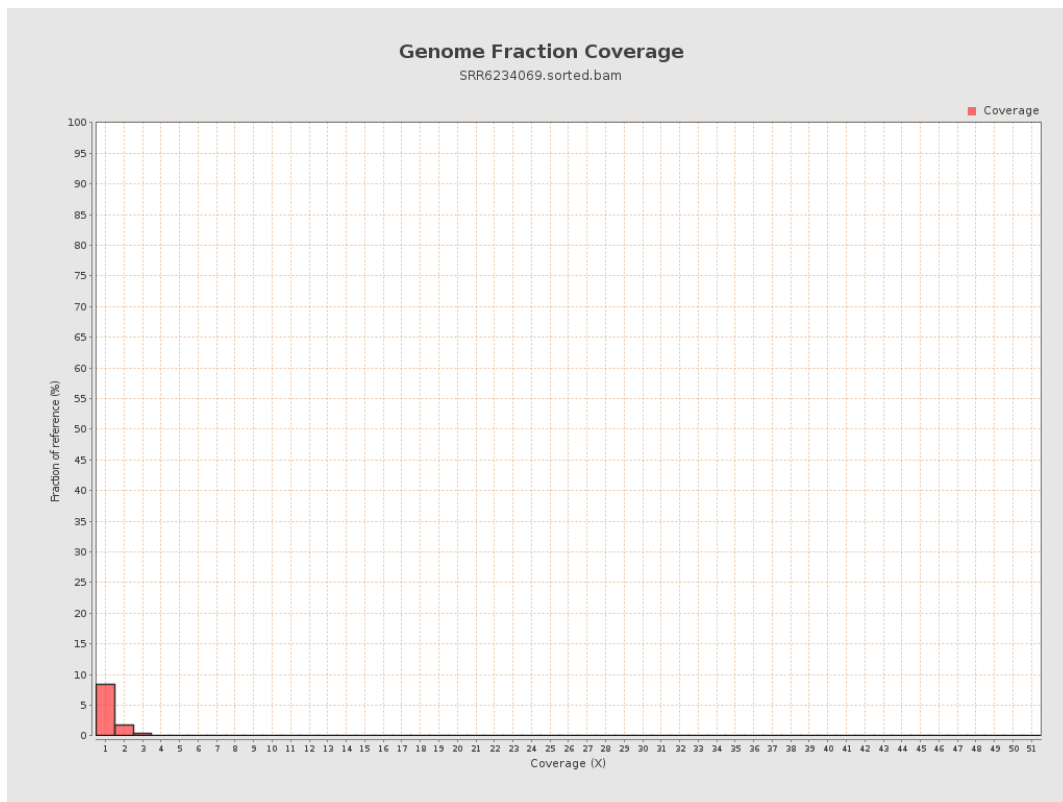
4. Results : Coverage Histogram



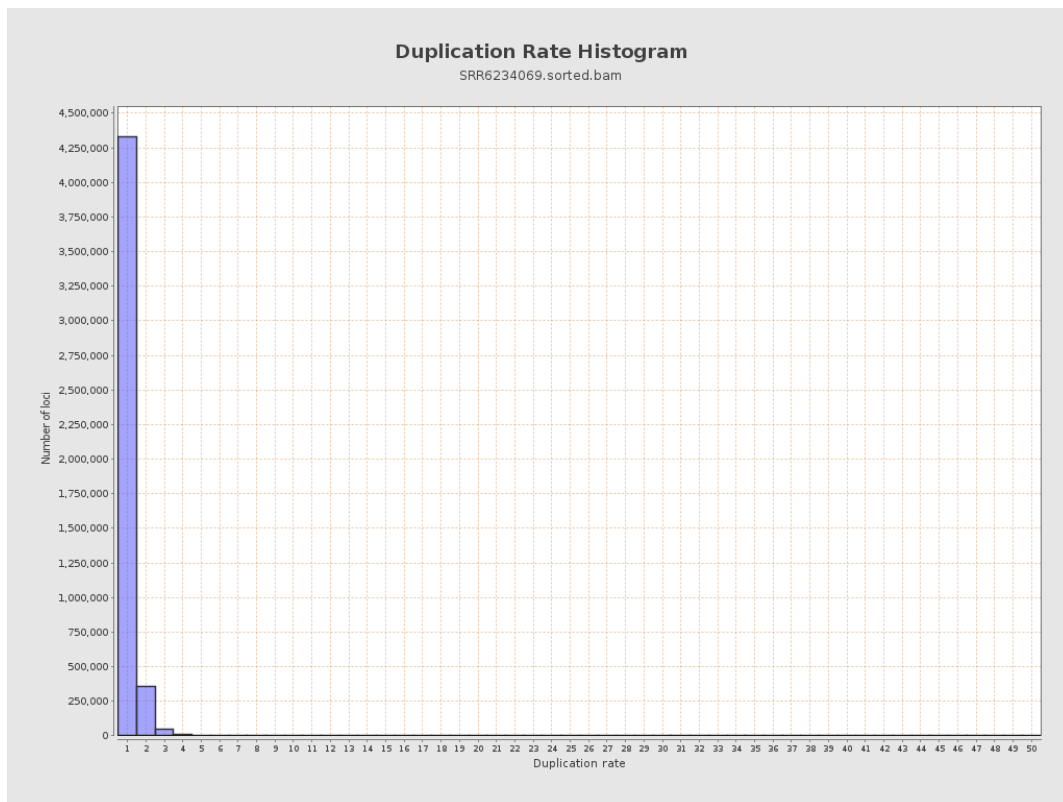
5. Results : Coverage Histogram (0-50X)



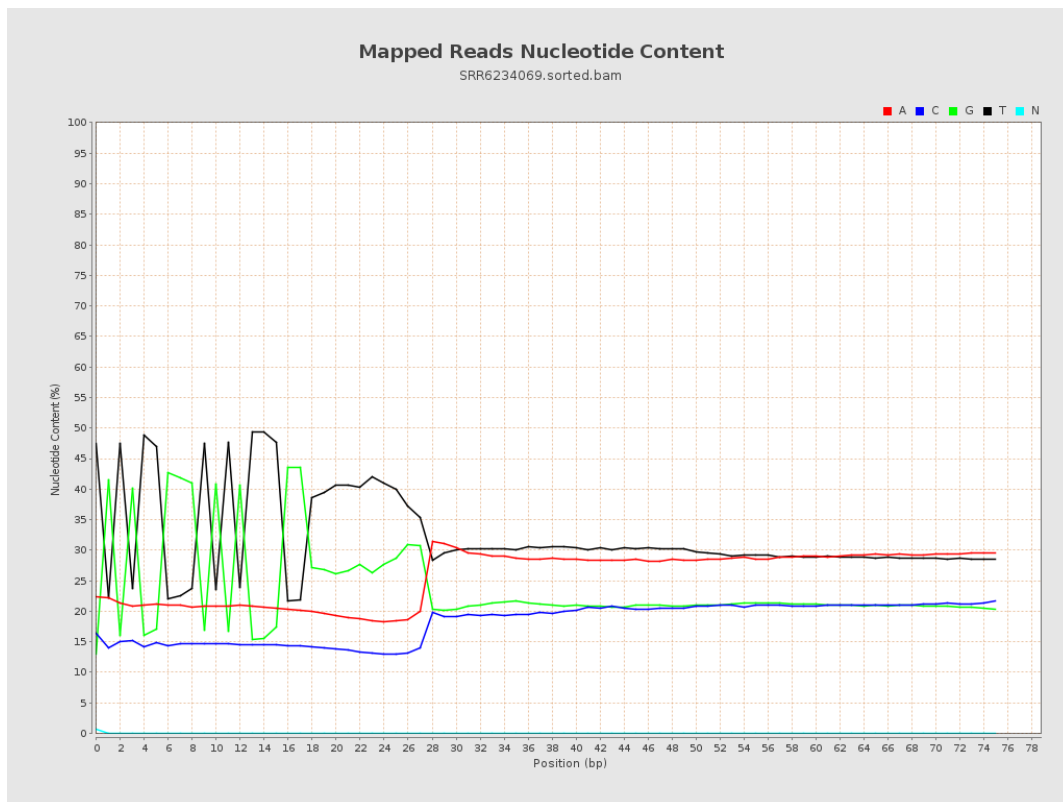
6. Results : Genome Fraction Coverage



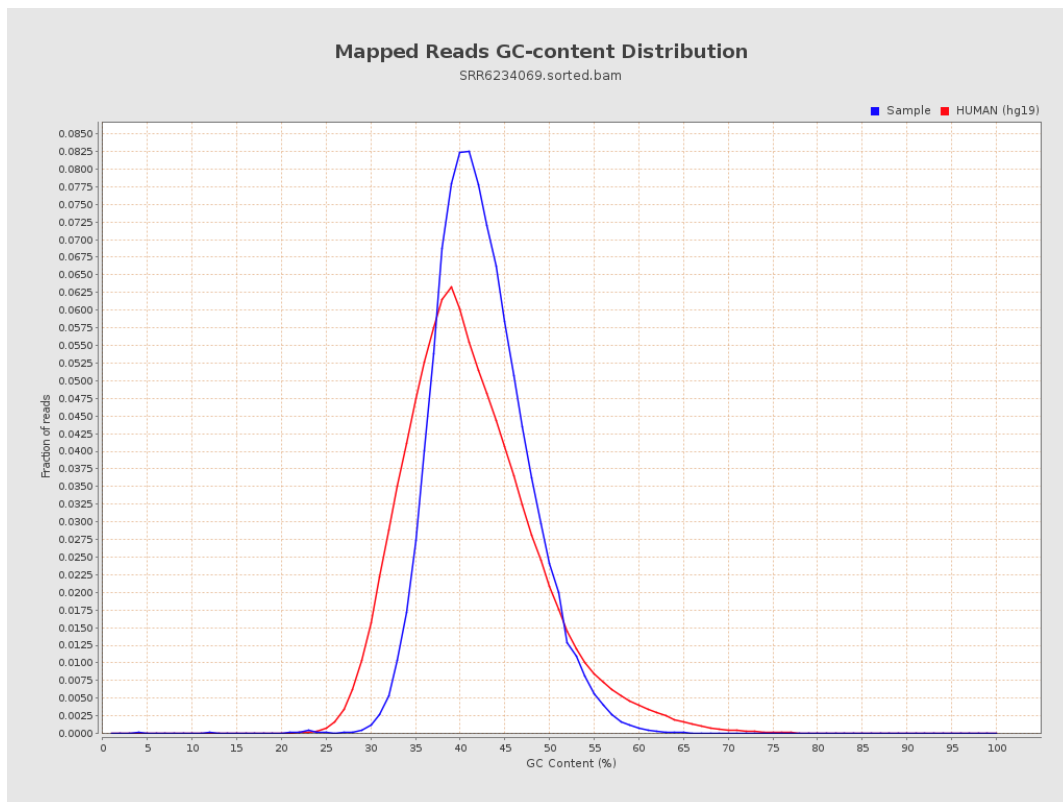
7. Results : Duplication Rate Histogram



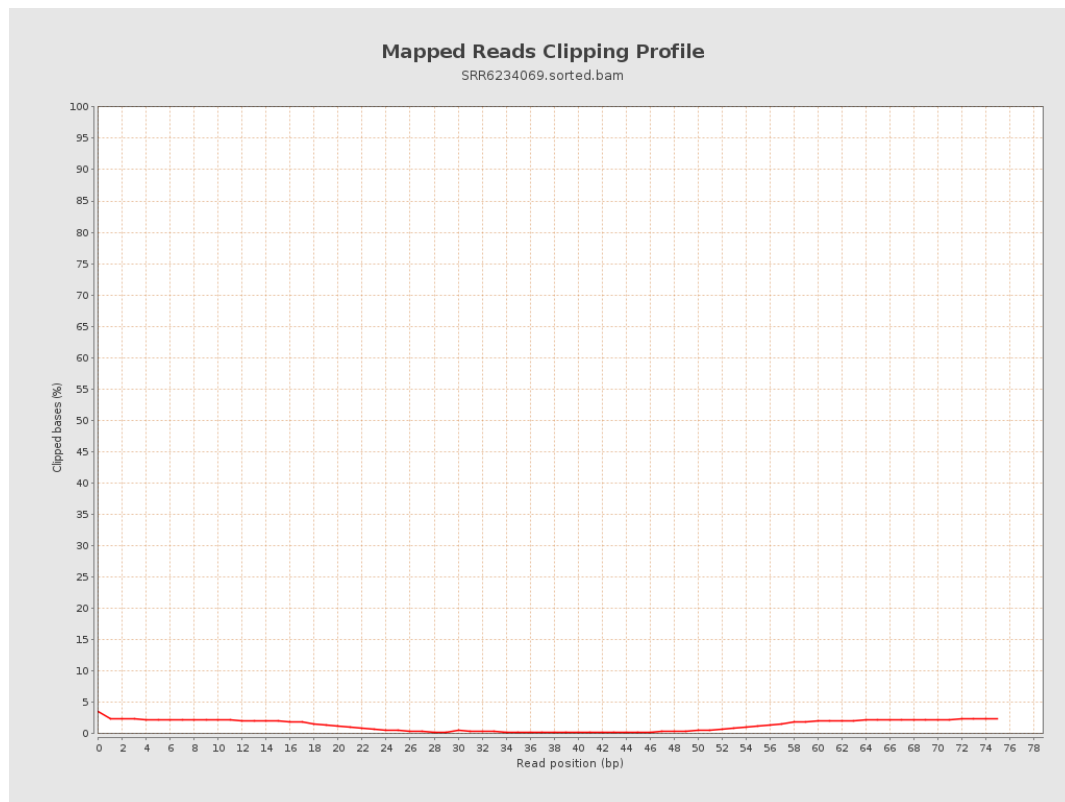
8. Results : Mapped Reads Nucleotide Content



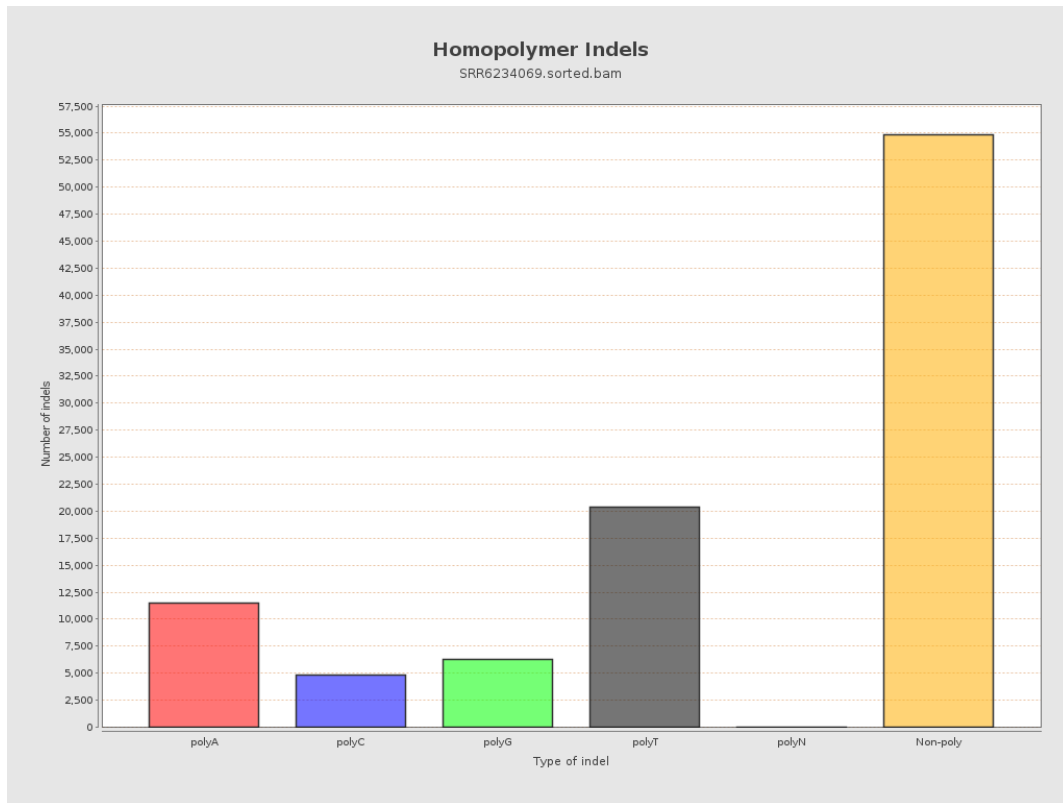
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

