

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 13:07:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008825.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_SRR6008825 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008825.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 13:07:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008825.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,892,292
Mapped reads	736,373 / 38.91%
Unmapped reads	1,155,919 / 61.09%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,960 / 0.42%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	36,550 / 1.93%
Duplication rate	3.75%
Clipped reads	361,662 / 19.11%

2.2. ACGT Content

Number/percentage of A's	13,278,553 / 27.56%
Number/percentage of C's	9,166,087 / 19.02%
Number/percentage of T's	14,967,171 / 31.06%
Number/percentage of G's	10,717,438 / 22.24%
Number/percentage of N's	58,516 / 0.12%
GC Percentage	41.26%

2.3. Coverage

Mean	0.0156

Standard Deviation	0.2322
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2.4. Mapping Quality

Mean Mapping Quality	44.39
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2.5. Mismatches and indels

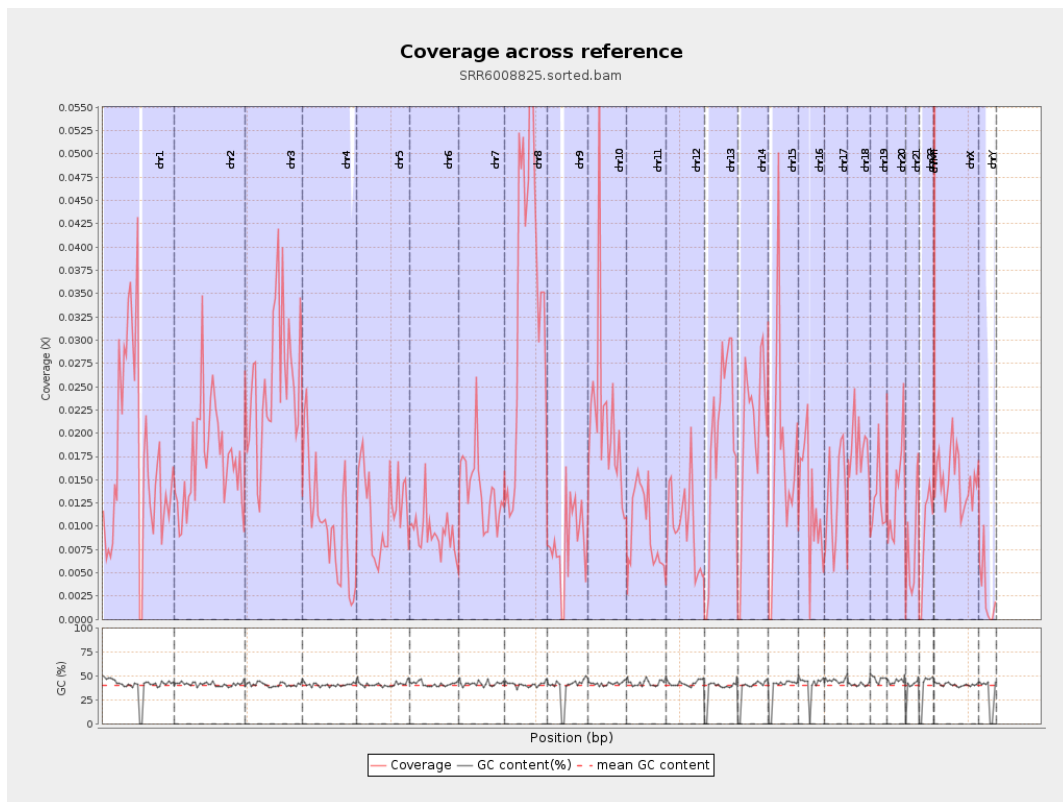
General error rate	0.92%
Mismatches	438,284
Insertions	3,534
Mapped reads with at least one insertion	0.47%
Deletions	14,322
Mapped reads with at least one deletion	1.92%
Homopolymer indels	44.04%

2.6. Chromosome stats

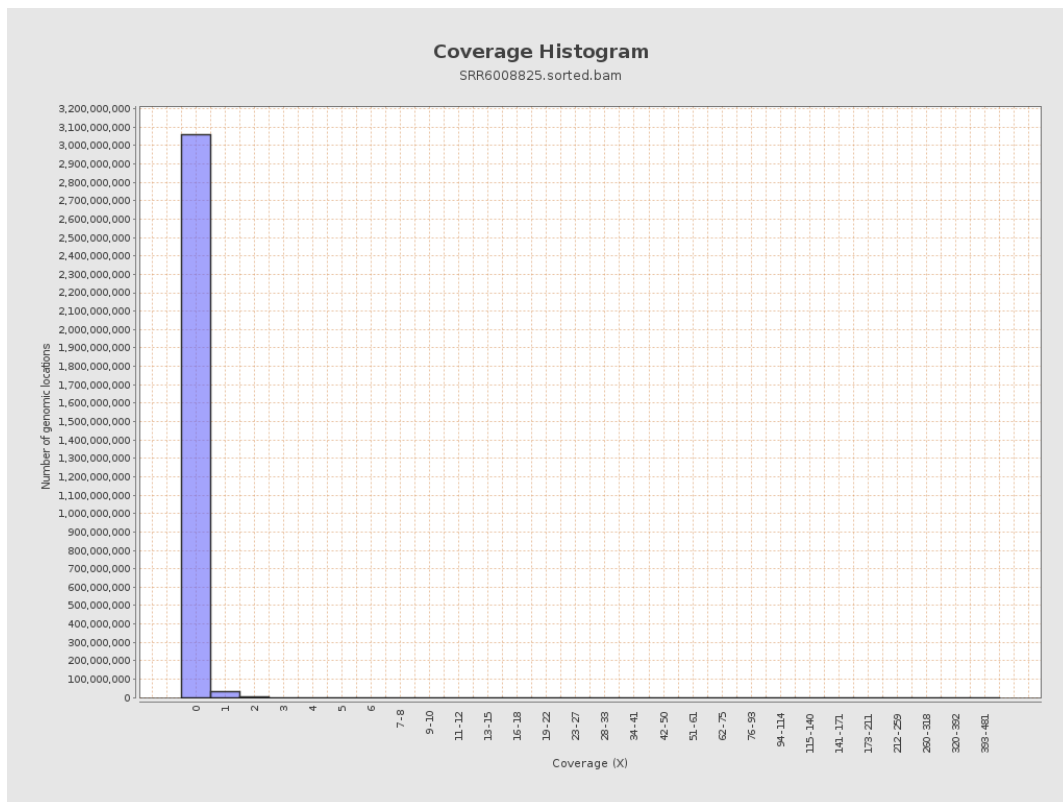
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4267265	0.0171	0.416
chr2	243199373	4162517	0.0171	0.2224
chr3	198022430	5079489	0.0257	0.2023
chr4	191154276	1947368	0.0102	0.125
chr5	180915260	2136951	0.0118	0.1288
chr6	171115067	1587930	0.0093	0.1257
chr7	159138663	2227553	0.014	0.2049

chr8	146364022	5087774	0.0348	0.3666
chr9	141213431	1162490	0.0082	0.136
chr10	135534747	2899843	0.0214	0.4199
chr11	135006516	1322462	0.0098	0.1348
chr12	133851895	1353515	0.0101	0.1274
chr13	115169878	2214144	0.0192	0.1654
chr14	107349540	2147686	0.02	0.1749
chr15	102531392	1703082	0.0166	0.1518
chr16	90354753	1110195	0.0123	0.1698
chr17	81195210	1054487	0.013	0.1591
chr18	78077248	1436378	0.0184	0.274
chr19	59128983	783844	0.0133	0.2674
chr20	63025520	881789	0.014	0.1422
chr21	48129895	376130	0.0078	0.1426
chr22	51304566	492362	0.0096	0.1141
chrMT	16571	263774	15.9178	10.3662
chrX	155270560	2349308	0.0151	0.1583
chrY	59373566	164966	0.0028	0.1265

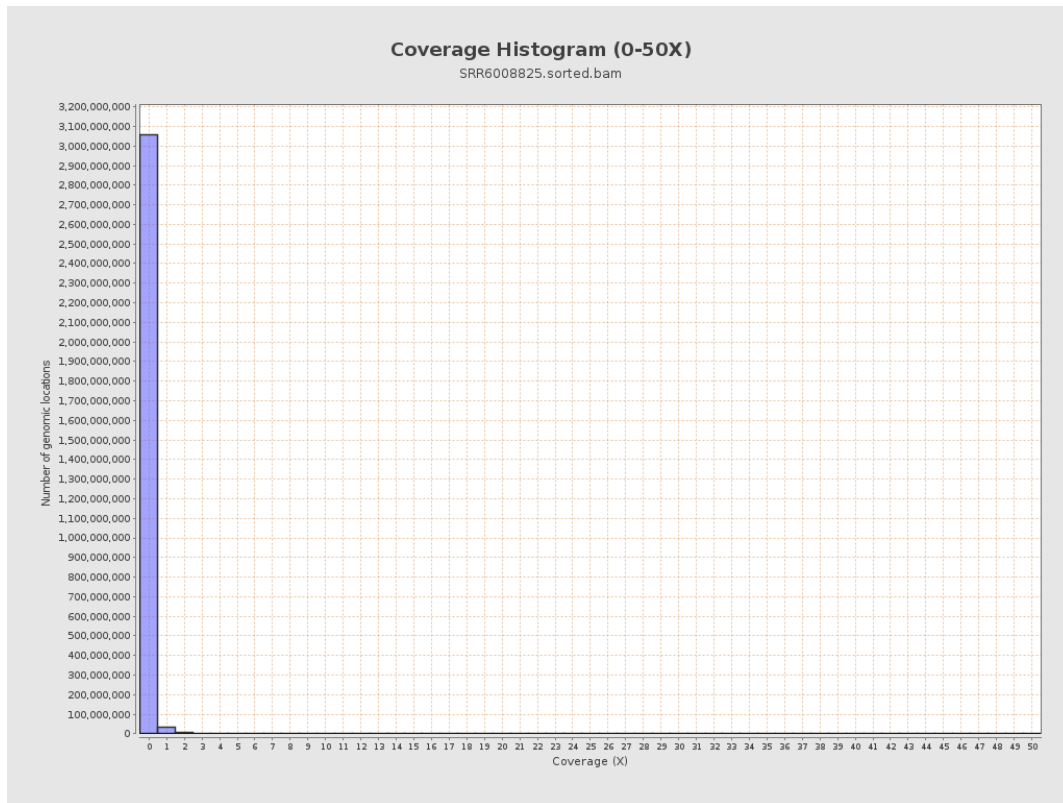
3. Results : Coverage across reference



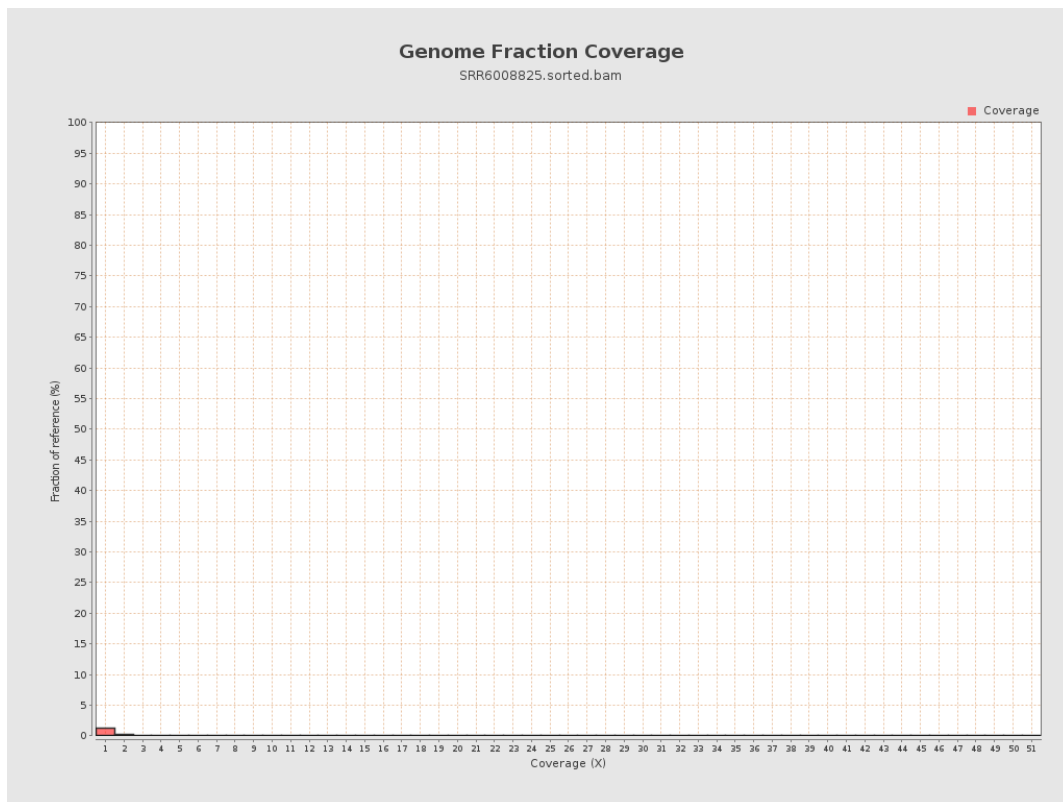
4. Results : Coverage Histogram



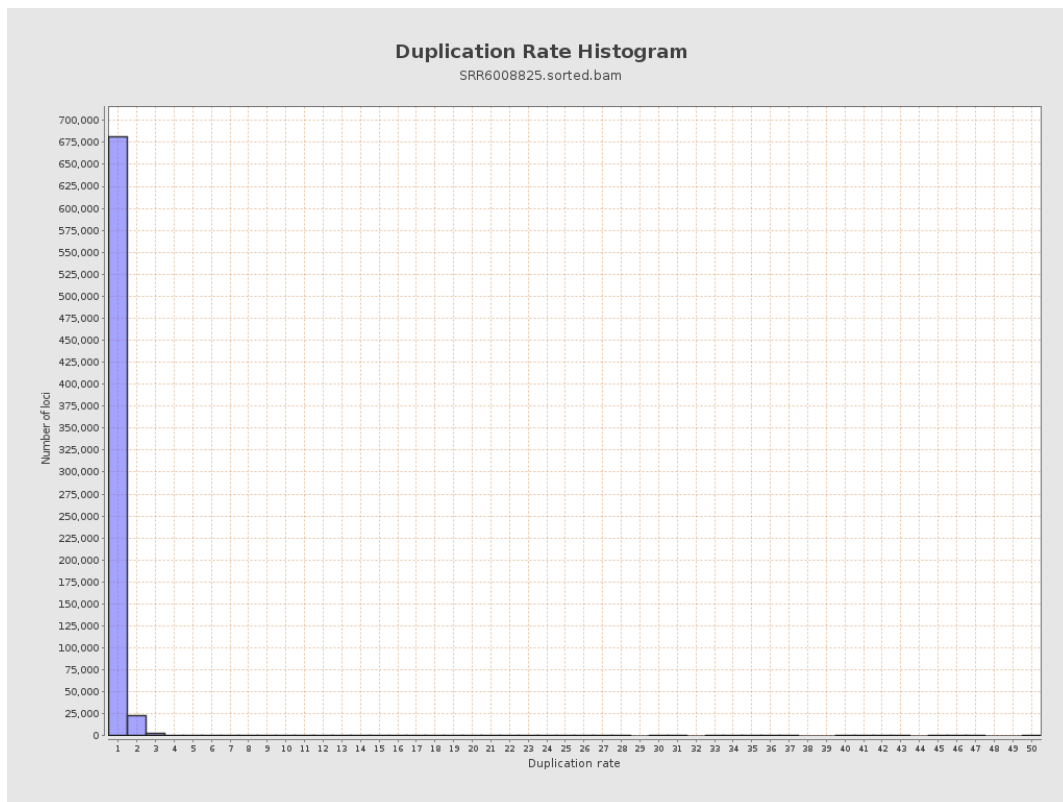
5. Results : Coverage Histogram (0-50X)



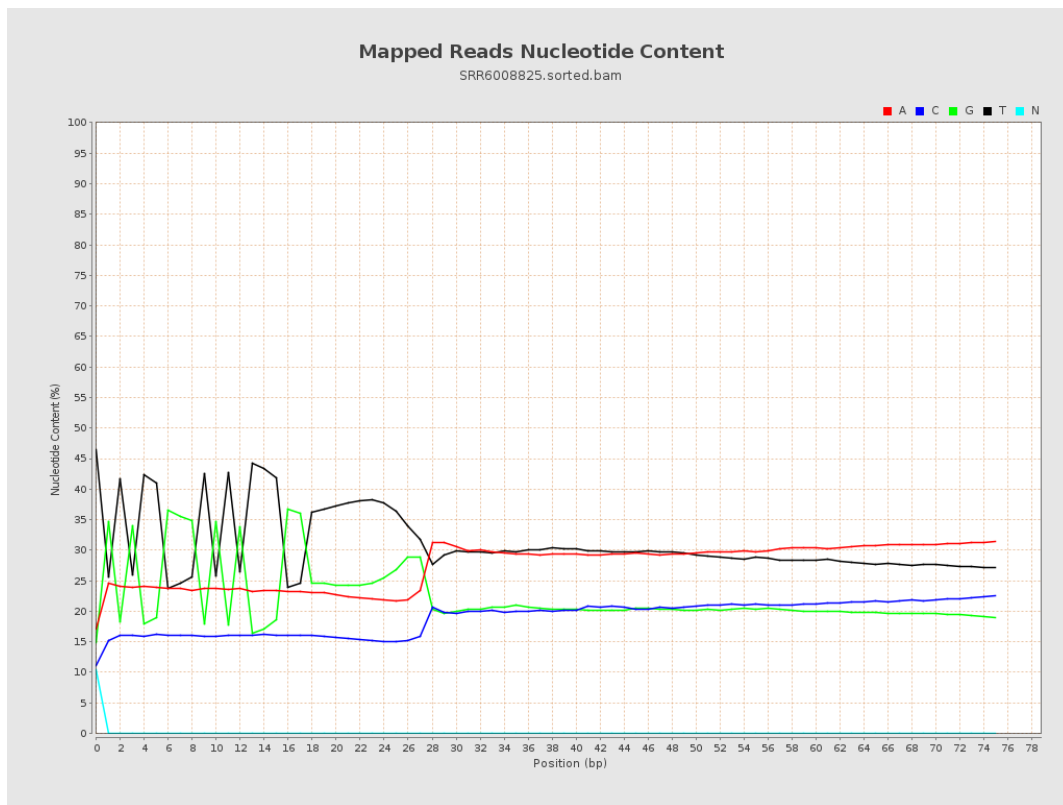
6. Results : Genome Fraction Coverage



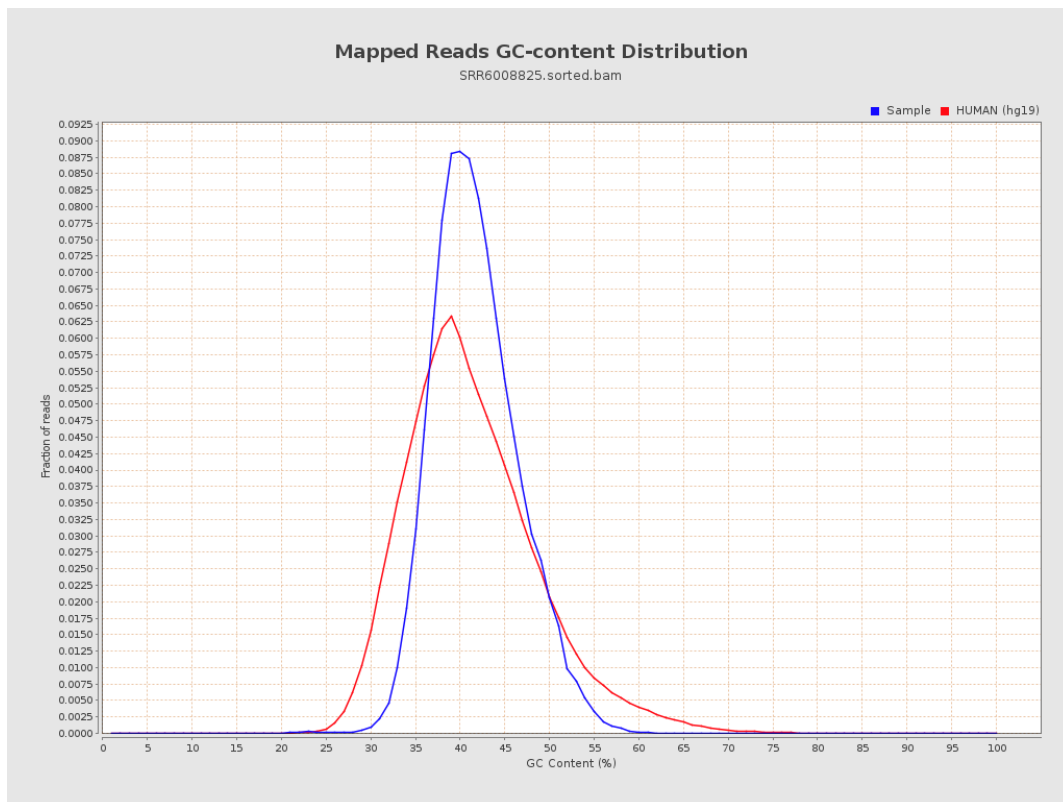
7. Results : Duplication Rate Histogram



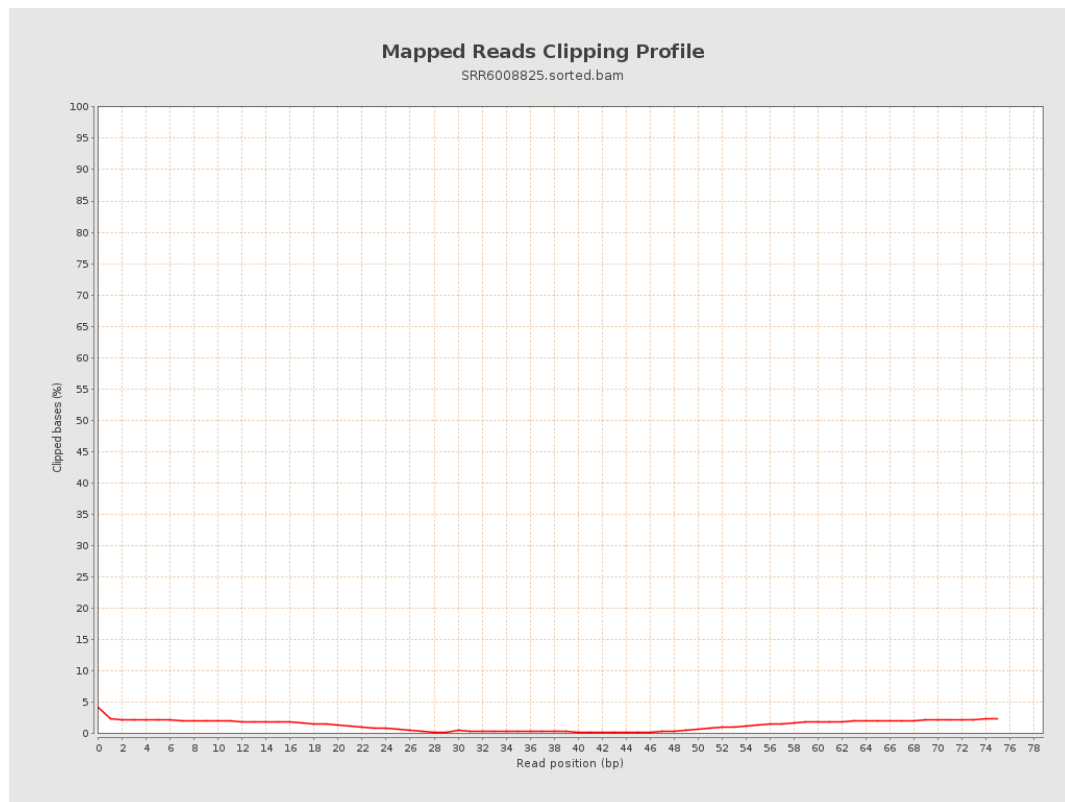
8. Results : Mapped Reads Nucleotide Content



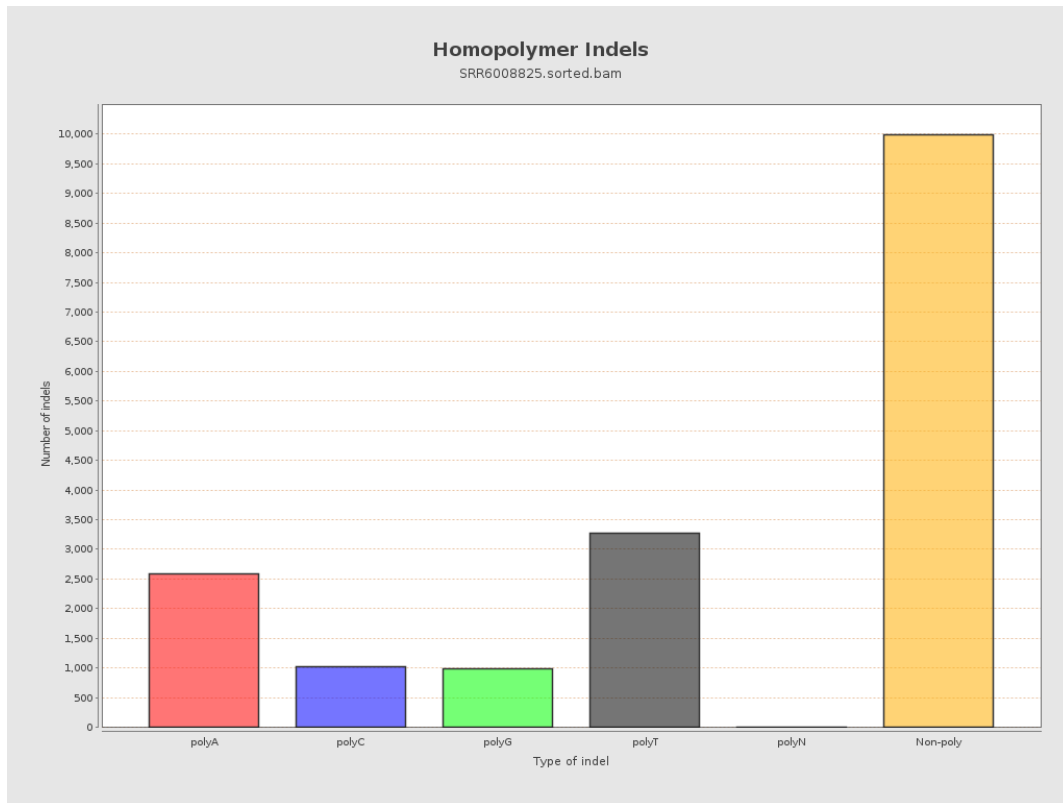
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

