

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 07:37:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237824.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_SRR6237824 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237824.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 07:37:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237824.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,760,358
Mapped reads	1,488,110 / 84.53%
Unmapped reads	272,248 / 15.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,720 / 0.84%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	248,712 / 14.13%
Duplication rate	11.55%
Clipped reads	733,392 / 41.66%

2.2. ACGT Content

Number/percentage of A's	26,500,450 / 27.18%
Number/percentage of C's	18,112,646 / 18.58%
Number/percentage of T's	30,689,775 / 31.48%
Number/percentage of G's	22,048,501 / 22.61%
Number/percentage of N's	150,133 / 0.15%
GC Percentage	41.19%

2.3. Coverage

Mean	0.0315

Standard Deviation	0.4074
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2.4. Mapping Quality

Mean Mapping Quality	45.52
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2.5. Mismatches and indels

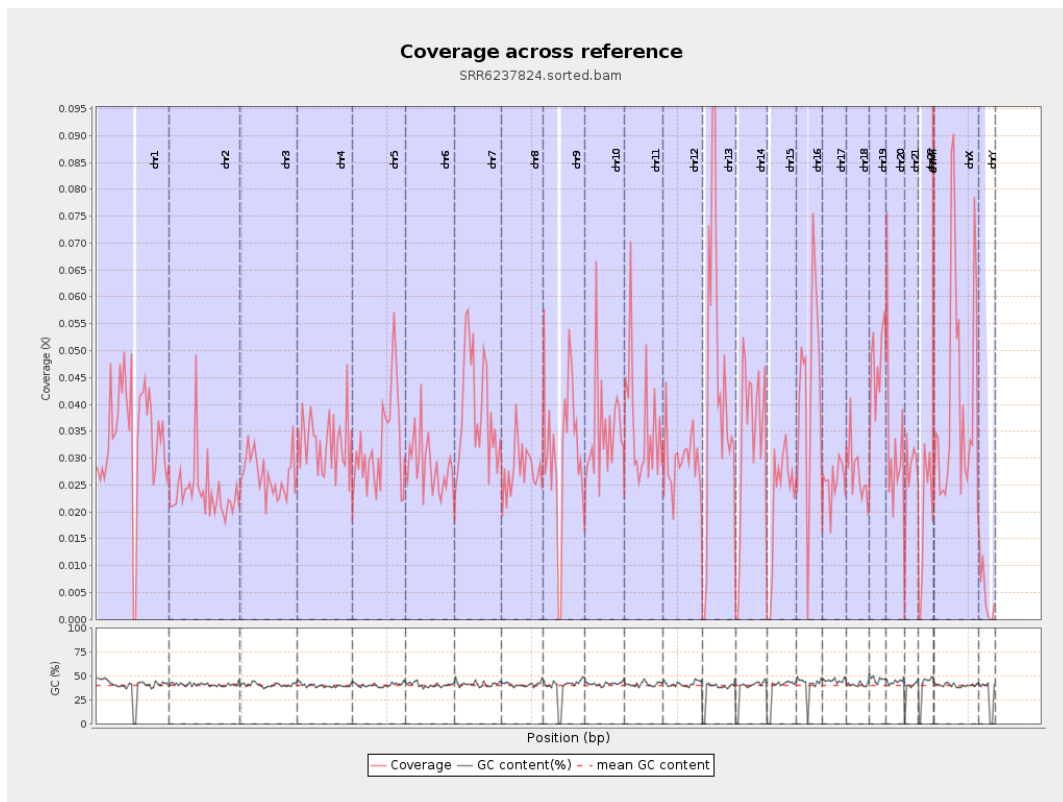
General error rate	0.86%
Mismatches	822,072
Insertions	6,820
Mapped reads with at least one insertion	0.45%
Deletions	22,970
Mapped reads with at least one deletion	1.53%
Homopolymer indels	46.99%

2.6. Chromosome stats

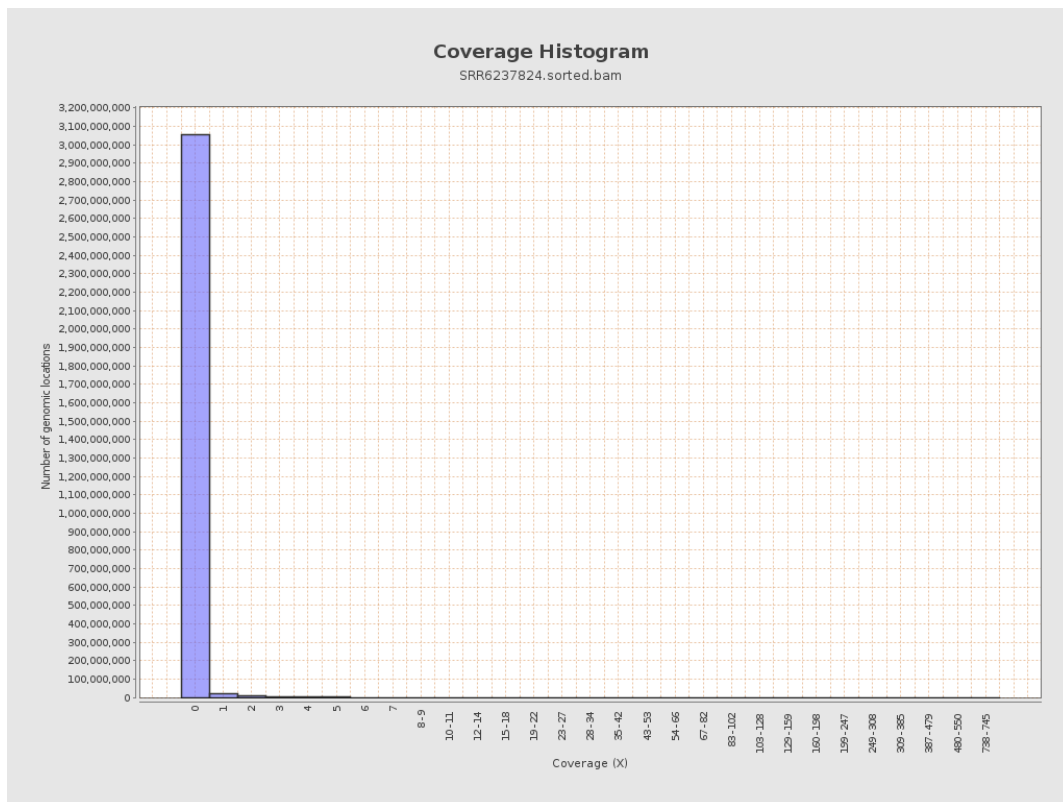
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8446785	0.0339	0.5545
chr2	243199373	5757260	0.0237	0.4531
chr3	198022430	5321386	0.0269	0.3193
chr4	191154276	6271428	0.0328	0.3545
chr5	180915260	5861650	0.0324	0.3551
chr6	171115067	4866285	0.0284	0.3566
chr7	159138663	6183518	0.0389	0.514

chr8	146364022	4065343	0.0278	0.3815
chr9	141213431	4262640	0.0302	0.3618
chr10	135534747	4742580	0.035	0.4466
chr11	135006516	4845601	0.0359	0.3962
chr12	133851895	3944864	0.0295	0.3441
chr13	115169878	4921052	0.0427	0.4181
chr14	107349540	3659040	0.0341	0.3753
chr15	102531392	2288341	0.0223	0.2885
chr16	90354753	3962698	0.0439	0.4239
chr17	81195210	2087660	0.0257	0.3093
chr18	78077248	2142154	0.0274	0.5322
chr19	59128983	2794254	0.0473	0.5399
chr20	63025520	2035804	0.0323	0.3571
chr21	48129895	1288096	0.0268	0.3139
chr22	51304566	973024	0.019	0.2658
chrMT	16571	139139	8.3965	7.0647
chrX	155270560	6413871	0.0413	0.4089
chrY	59373566	266602	0.0045	0.115

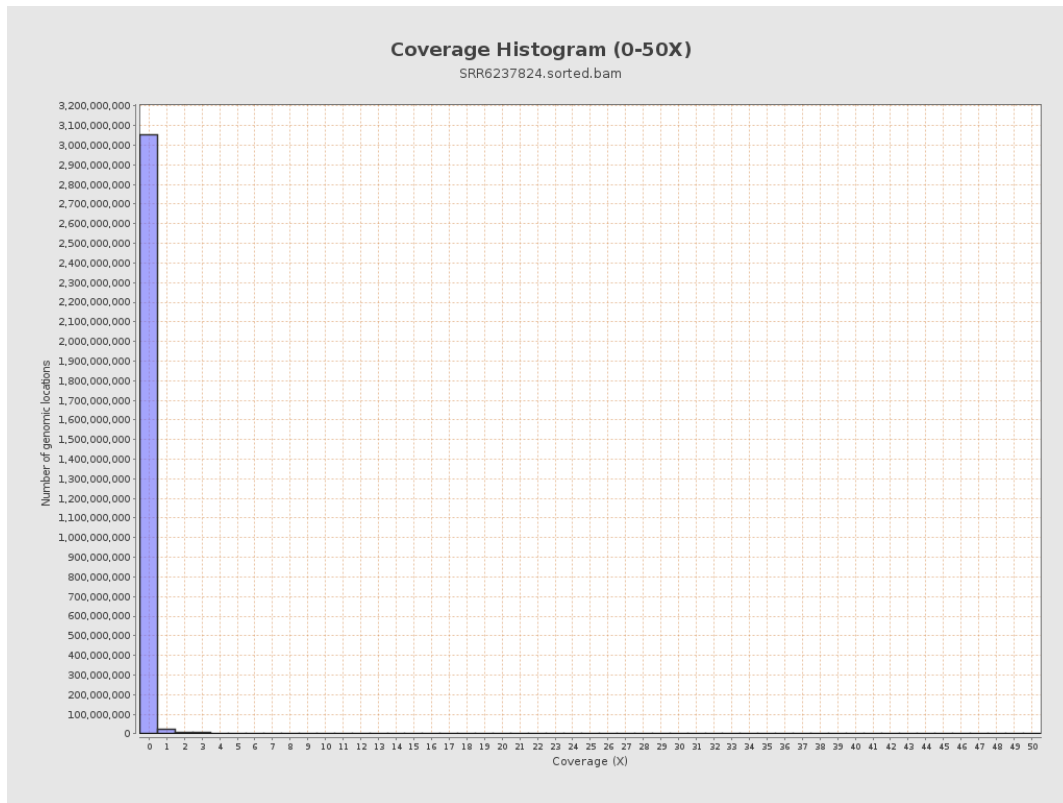
3. Results : Coverage across reference



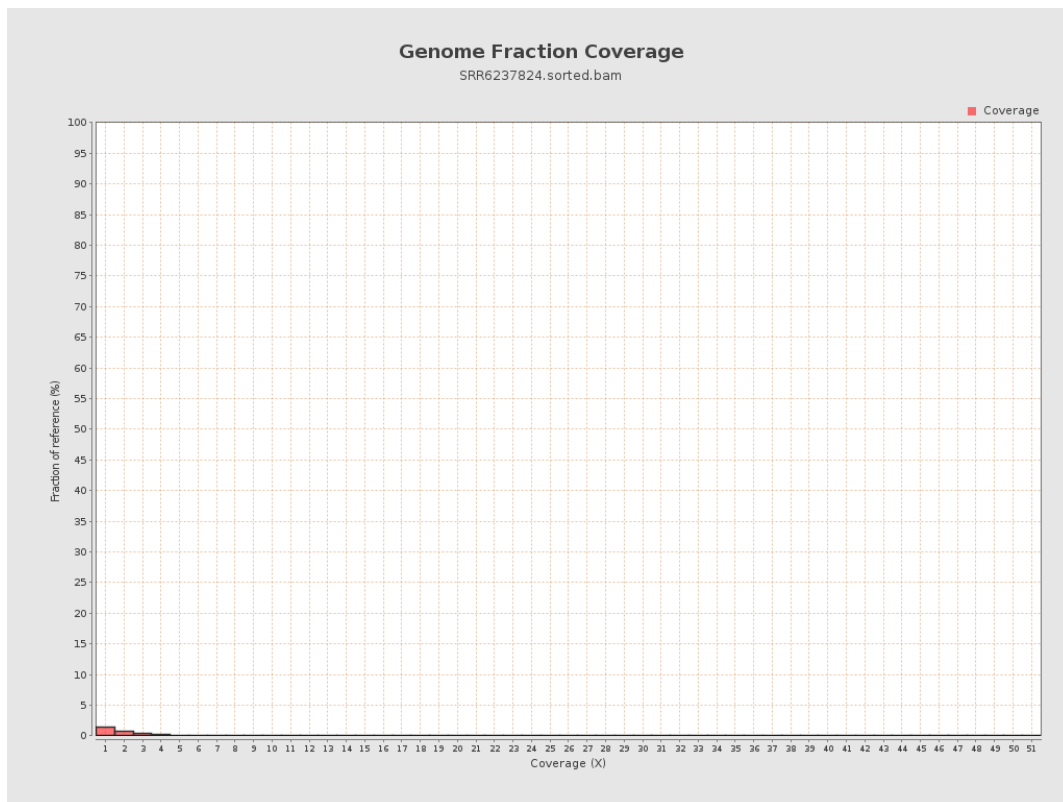
4. Results : Coverage Histogram



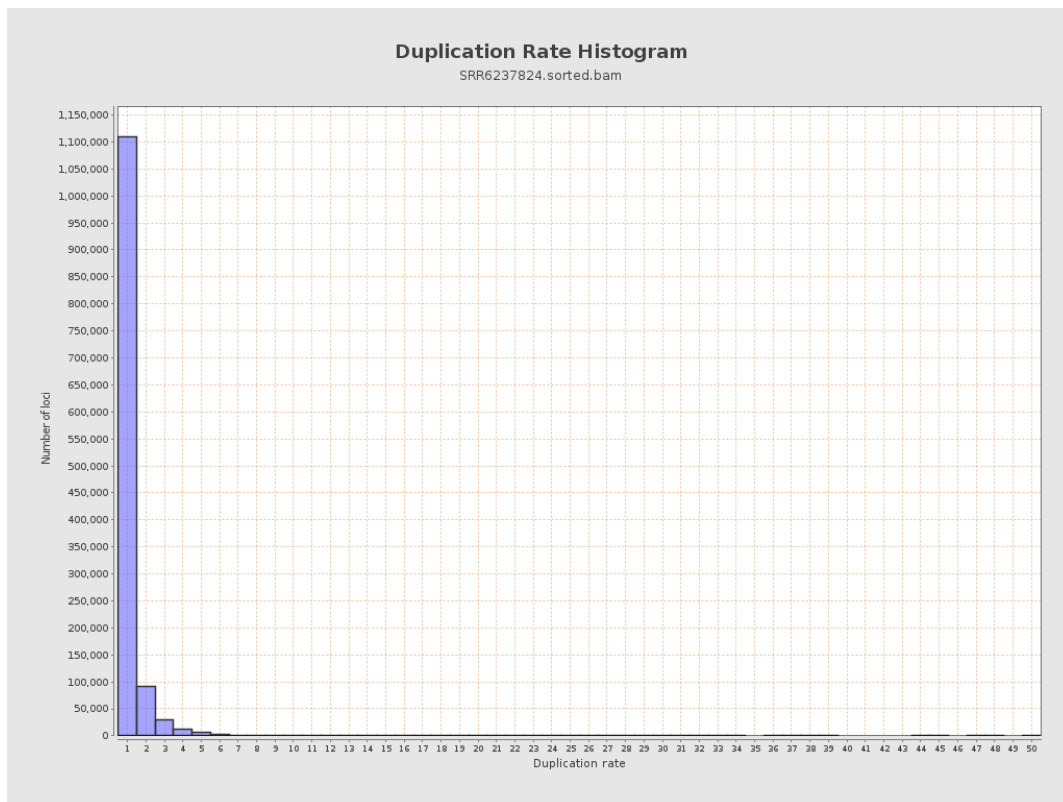
5. Results : Coverage Histogram (0-50X)



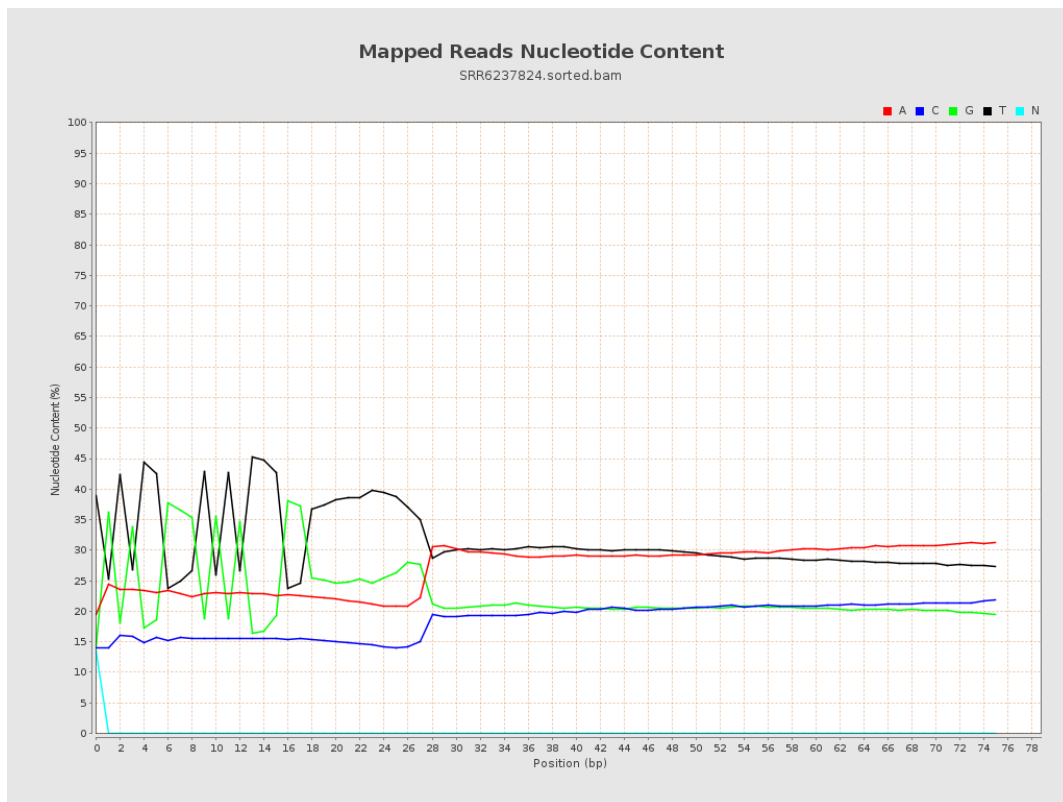
6. Results : Genome Fraction Coverage



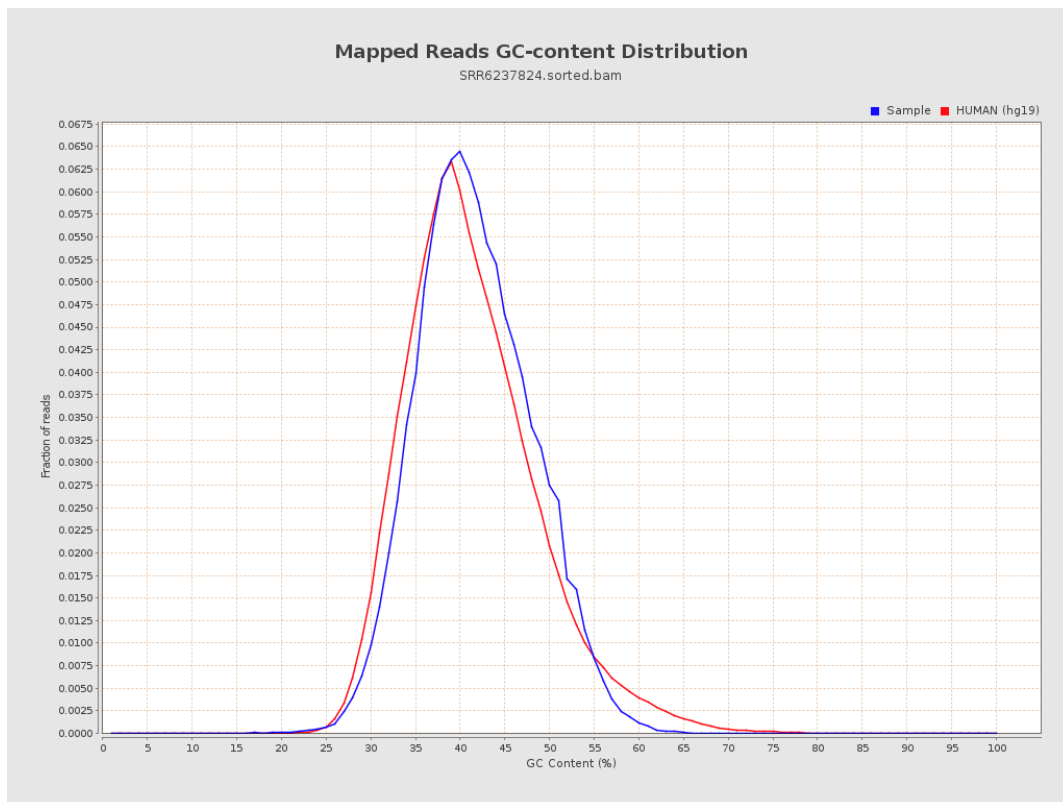
7. Results : Duplication Rate Histogram



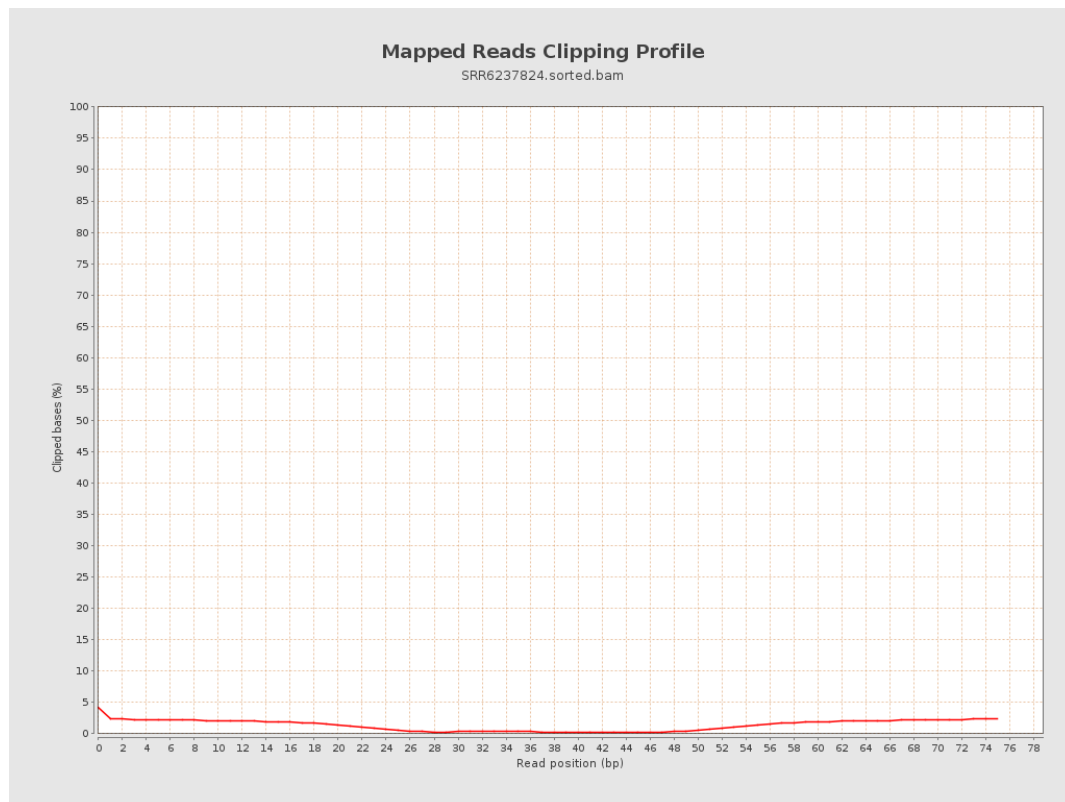
8. Results : Mapped Reads Nucleotide Content



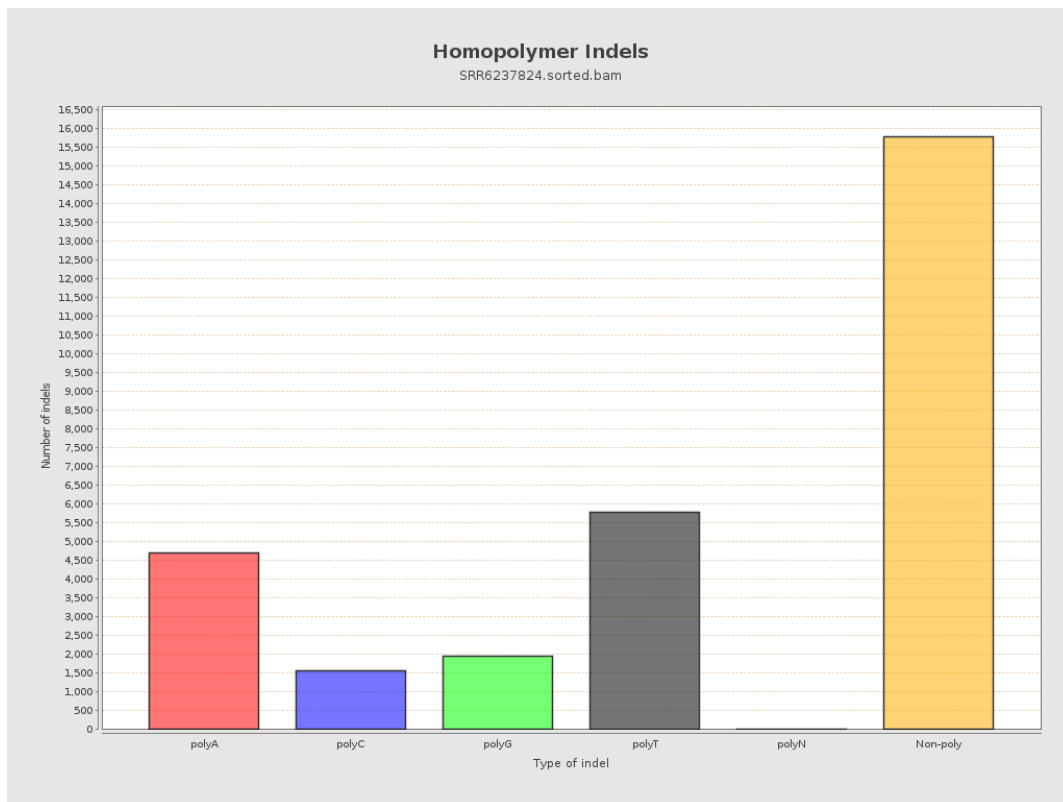
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

