

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 07:28:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237821.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_SRR6237821 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237821.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 07:28:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237821.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,149,294
Mapped reads	266,682 / 12.41%
Unmapped reads	1,882,612 / 87.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,748 / 0.13%
Read min/max/mean length	30 / 76 / 76.04
Duplicated reads (estimated)	33,912 / 1.58%
Duplication rate	8.38%
Clipped reads	172,835 / 8.04%

2.2. ACGT Content

Number/percentage of A's	4,264,540 / 27.93%
Number/percentage of C's	2,756,041 / 18.05%
Number/percentage of T's	4,882,292 / 31.97%
Number/percentage of G's	3,347,234 / 21.92%
Number/percentage of N's	20,756 / 0.14%
GC Percentage	39.97%

2.3. Coverage

Mean	0.0049

Standard Deviation	0.1382
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2.4. Mapping Quality

Mean Mapping Quality	37.12
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2.5. Mismatches and indels

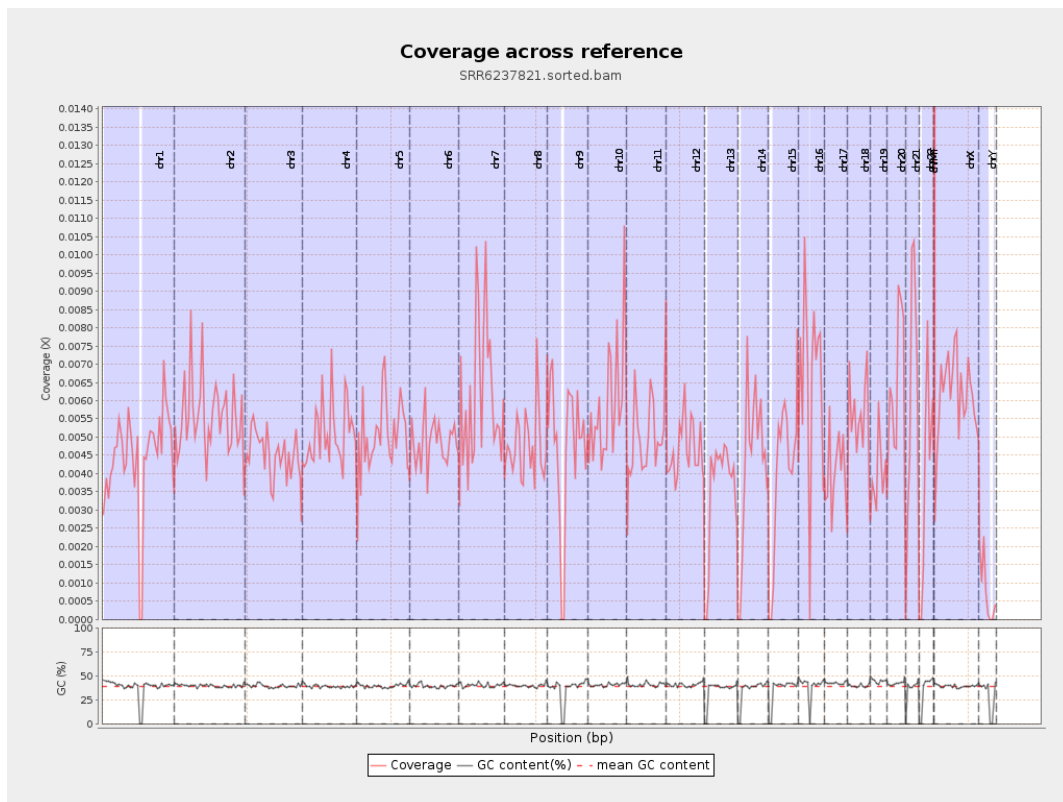
General error rate	1.51%
Mismatches	225,242
Insertions	3,410
Mapped reads with at least one insertion	1.25%
Deletions	5,870
Mapped reads with at least one deletion	2.14%
Homopolymer indels	38.8%

2.6. Chromosome stats

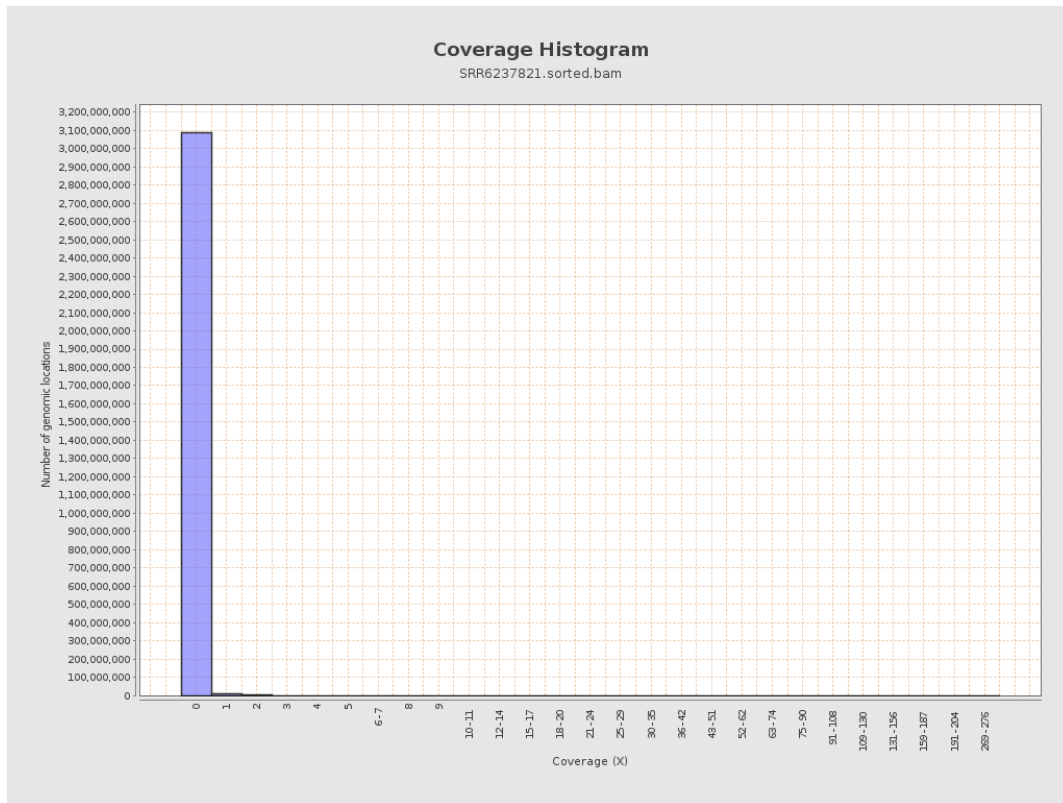
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	1102736	0.0044	0.1408
chr2	243199373	1353165	0.0056	0.1857
chr3	198022430	898265	0.0045	0.1249
chr4	191154276	974982	0.0051	0.1285
chr5	180915260	924972	0.0051	0.144
chr6	171115067	828538	0.0048	0.1192
chr7	159138663	982828	0.0062	0.1736

chr8	146364022	697306	0.0048	0.1047
chr9	141213431	668477	0.0047	0.1085
chr10	135534747	798178	0.0059	0.1183
chr11	135006516	656842	0.0049	0.1196
chr12	133851895	621424	0.0046	0.1316
chr13	115169878	405101	0.0035	0.0893
chr14	107349540	462815	0.0043	0.1054
chr15	102531392	412236	0.004	0.1348
chr16	90354753	581426	0.0064	0.1162
chr17	81195210	325289	0.004	0.1214
chr18	78077248	441451	0.0057	0.1511
chr19	59128983	236449	0.004	0.0932
chr20	63025520	408093	0.0065	0.1958
chr21	48129895	290103	0.006	0.1271
chr22	51304566	205801	0.004	0.1669
chrMT	16571	5358	0.3233	0.7227
chrX	155270560	952807	0.0061	0.1932
chrY	59373566	46298	0.0008	0.0345

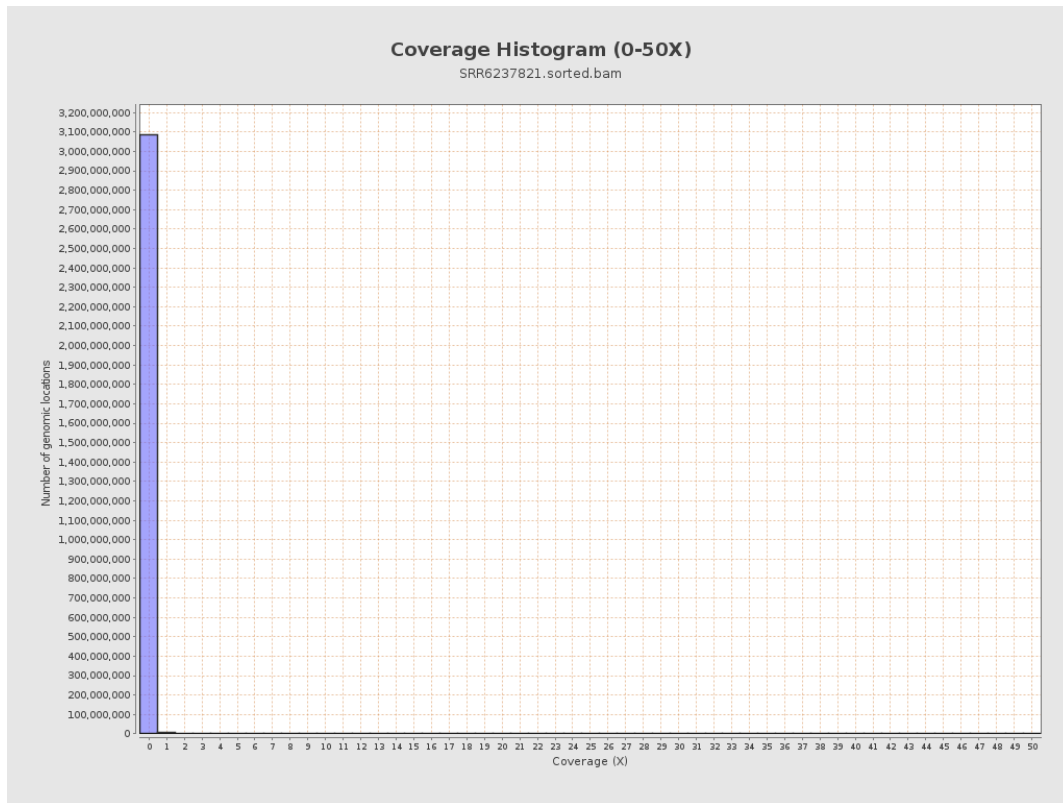
3. Results : Coverage across reference



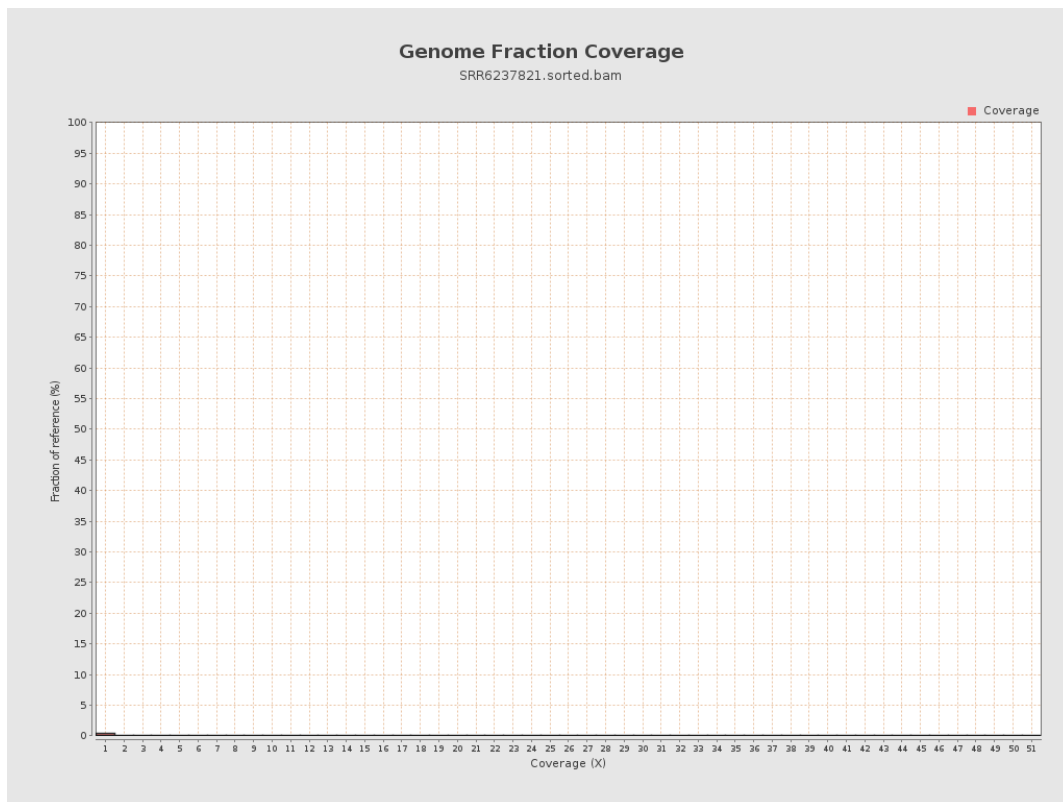
4. Results : Coverage Histogram



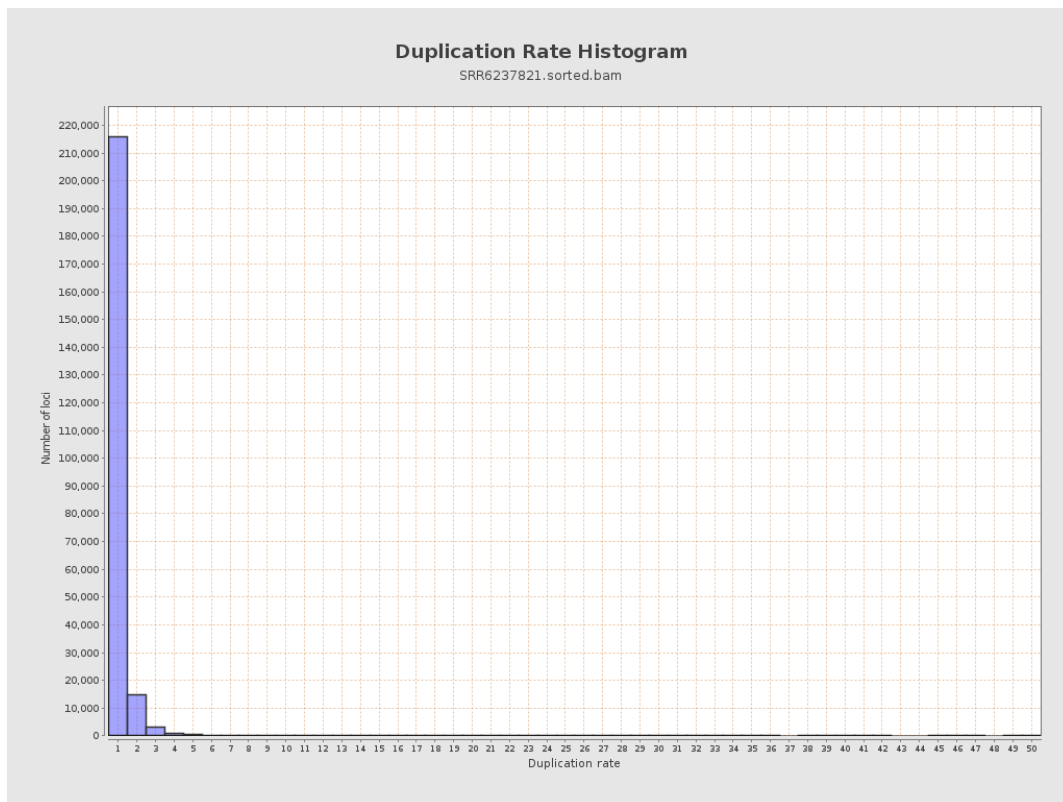
5. Results : Coverage Histogram (0-50X)



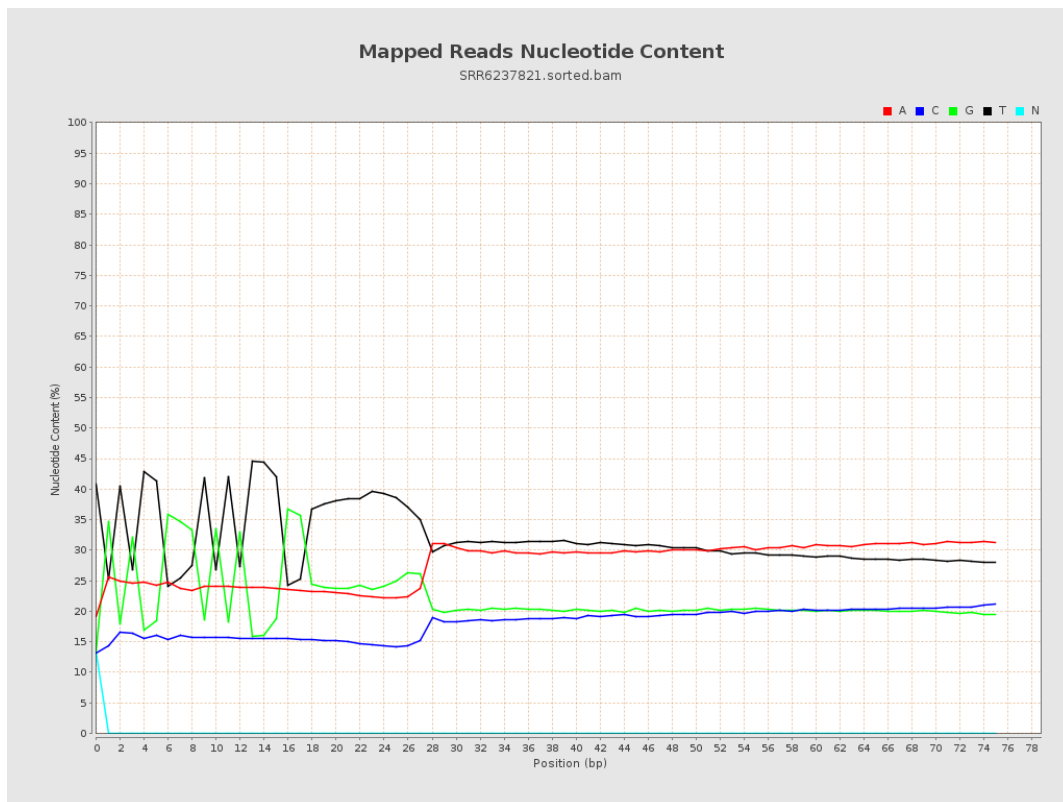
6. Results : Genome Fraction Coverage



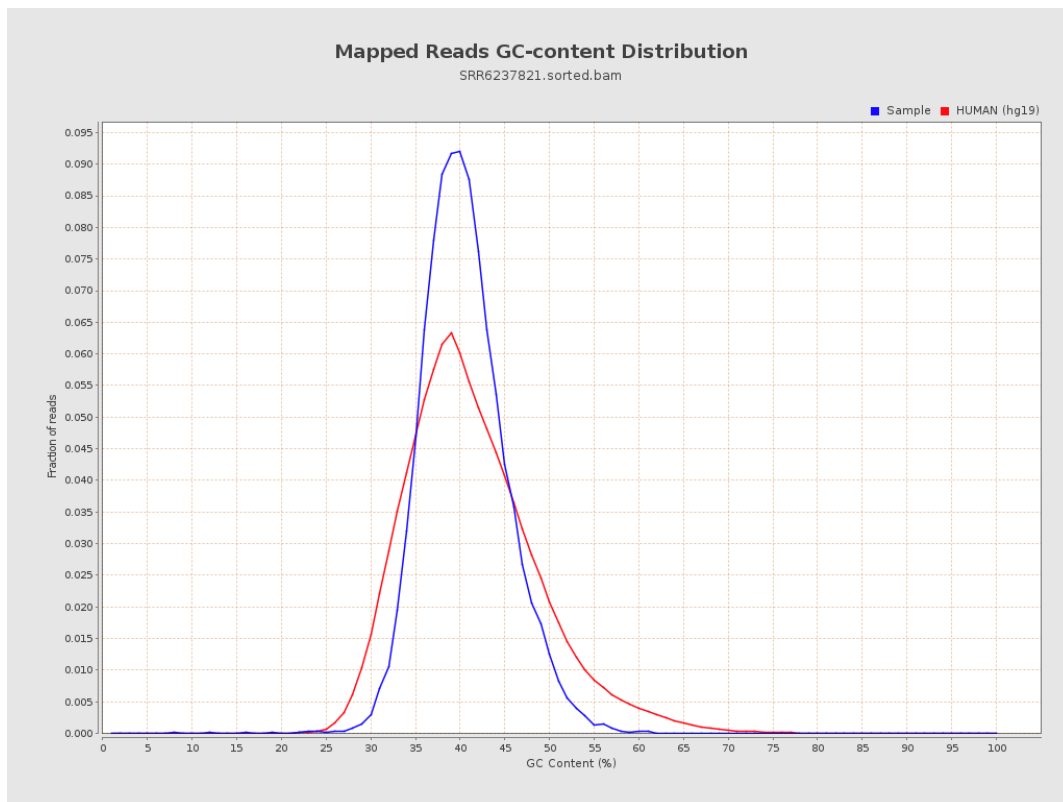
7. Results : Duplication Rate Histogram



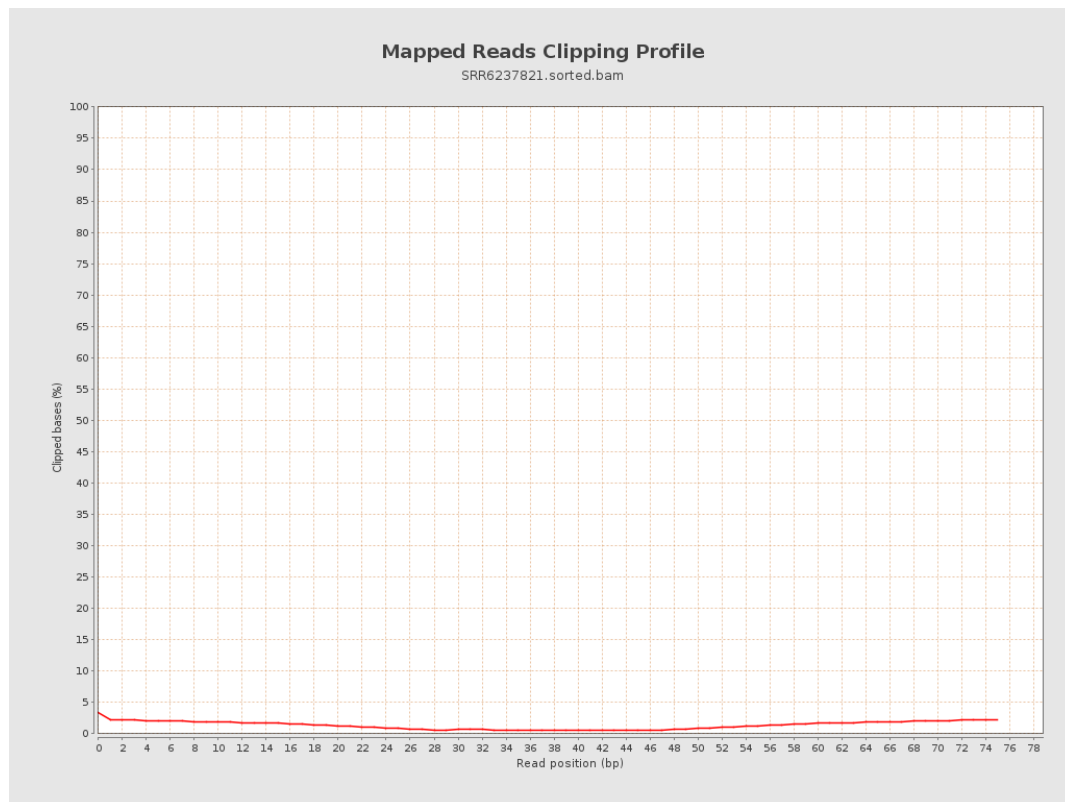
8. Results : Mapped Reads Nucleotide Content



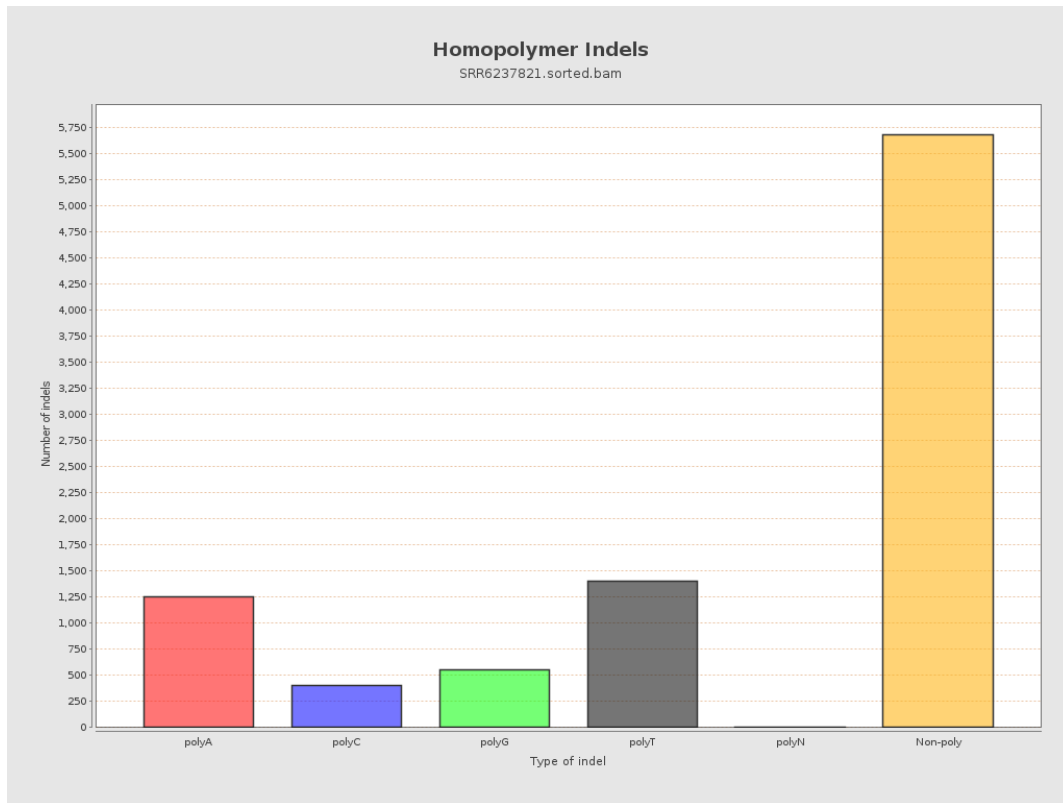
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

