

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 18:14:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234137.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_SRR6234137 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234137.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 18:14:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234137.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	791,897
Mapped reads	441,226 / 55.72%
Unmapped reads	350,671 / 44.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,771 / 0.22%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	12,106 / 1.53%
Duplication rate	2.26%
Clipped reads	287,059 / 36.25%

2.2. ACGT Content

Number/percentage of A's	7,293,647 / 27.13%
Number/percentage of C's	4,328,251 / 16.1%
Number/percentage of T's	8,840,329 / 32.89%
Number/percentage of G's	6,415,558 / 23.87%
Number/percentage of N's	4,422 / 0.02%
GC Percentage	39.97%

2.3. Coverage

Mean	0.0087

Standard Deviation	0.112
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2.4. Mapping Quality

Mean Mapping Quality	45.2
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2.5. Mismatches and indels

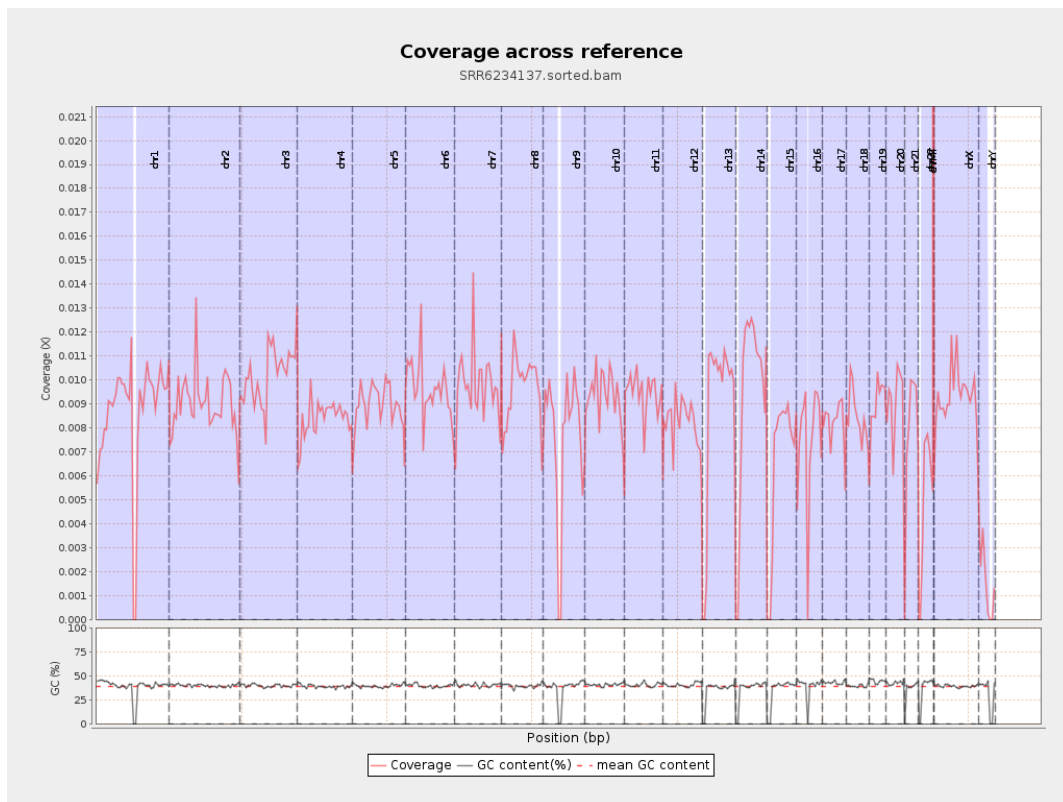
General error rate	1.03%
Mismatches	272,748
Insertions	2,184
Mapped reads with at least one insertion	0.49%
Deletions	9,595
Mapped reads with at least one deletion	2.14%
Homopolymer indels	46.71%

2.6. Chromosome stats

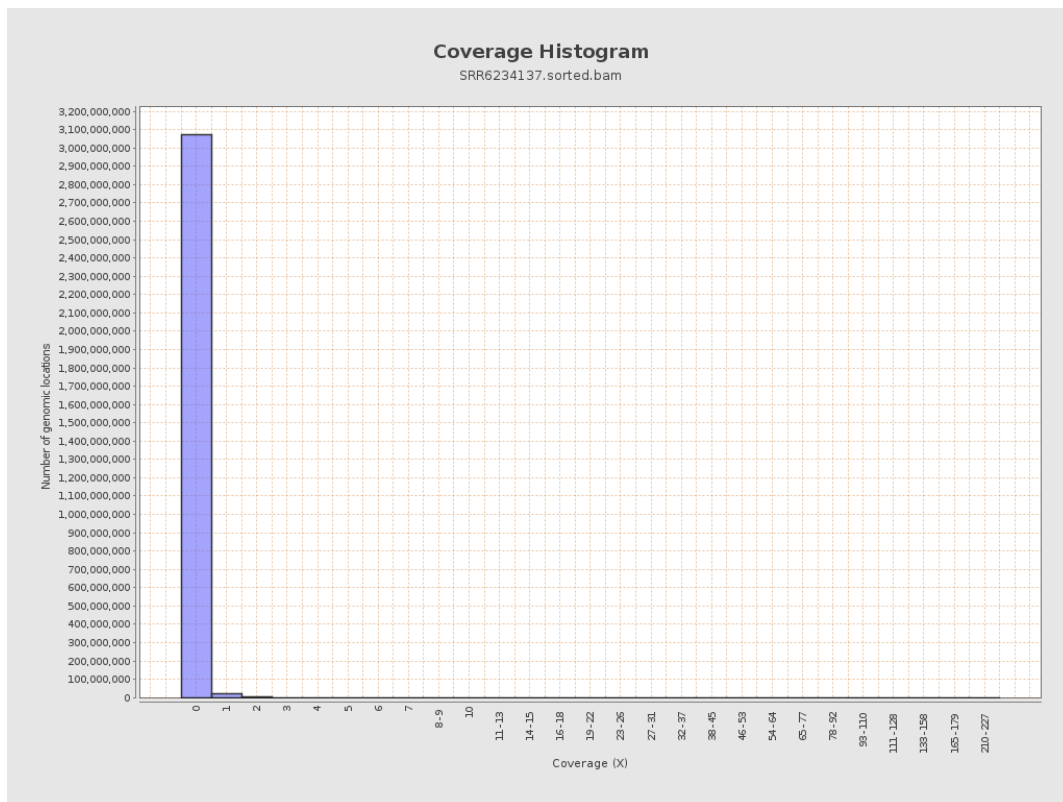
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	2161316	0.0087	0.1272
chr2	243199373	2192577	0.009	0.1195
chr3	198022430	2017588	0.0102	0.1074
chr4	191154276	1604345	0.0084	0.0982
chr5	180915260	1622713	0.009	0.1006
chr6	171115067	1643736	0.0096	0.1098
chr7	159138663	1561048	0.0098	0.1363

chr8	146364022	1405346	0.0096	0.1688
chr9	141213431	1082141	0.0077	0.0989
chr10	135534747	1270149	0.0094	0.108
chr11	135006516	1266965	0.0094	0.114
chr12	133851895	1106844	0.0083	0.0966
chr13	115169878	1008496	0.0088	0.0997
chr14	107349540	1009580	0.0094	0.1044
chr15	102531392	679691	0.0066	0.087
chr16	90354753	672565	0.0074	0.0918
chr17	81195210	658724	0.0081	0.0968
chr18	78077248	663441	0.0085	0.1467
chr19	59128983	534967	0.009	0.1103
chr20	63025520	561906	0.0089	0.1009
chr21	48129895	379551	0.0079	0.0941
chr22	51304566	249259	0.0049	0.0735
chrMT	16571	13457	0.8121	1.1254
chrX	155270560	1445134	0.0093	0.105
chrY	59373566	87432	0.0015	0.0431

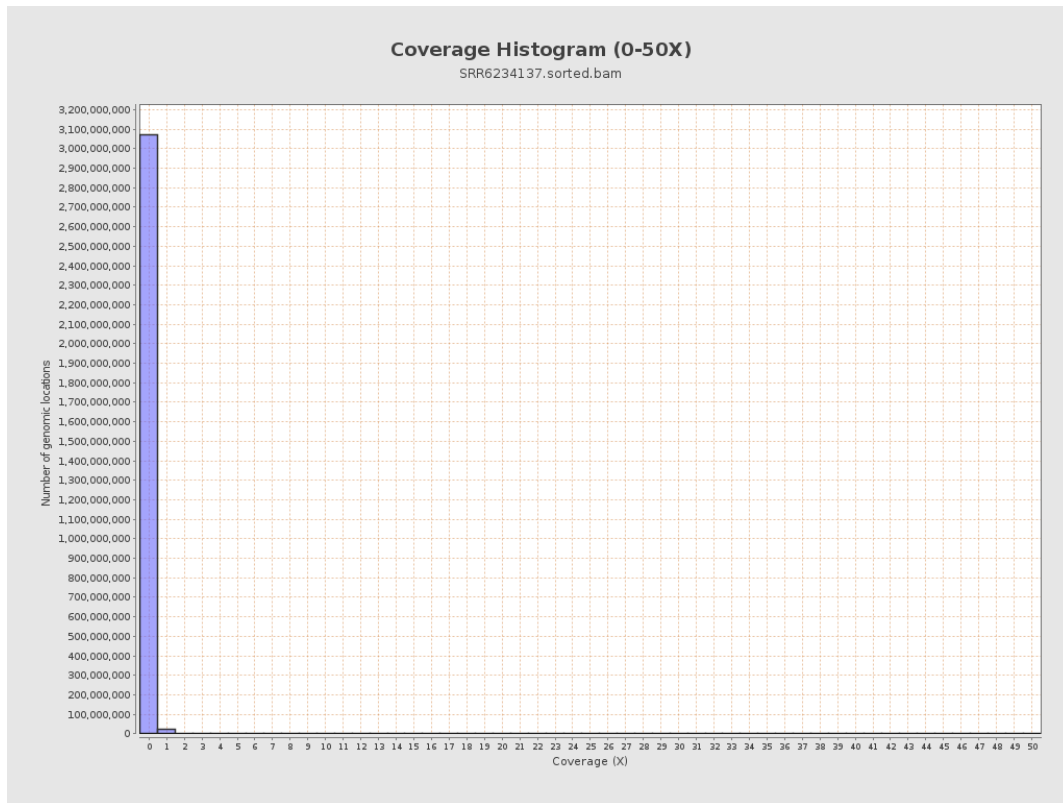
3. Results : Coverage across reference



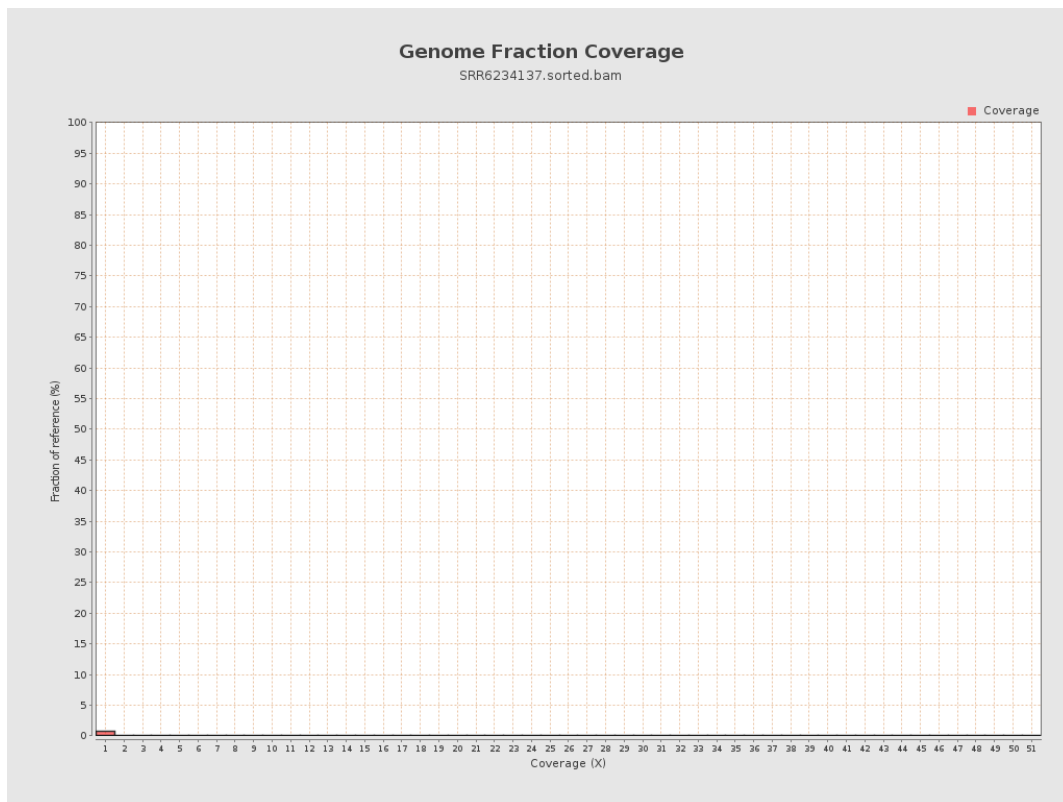
4. Results : Coverage Histogram



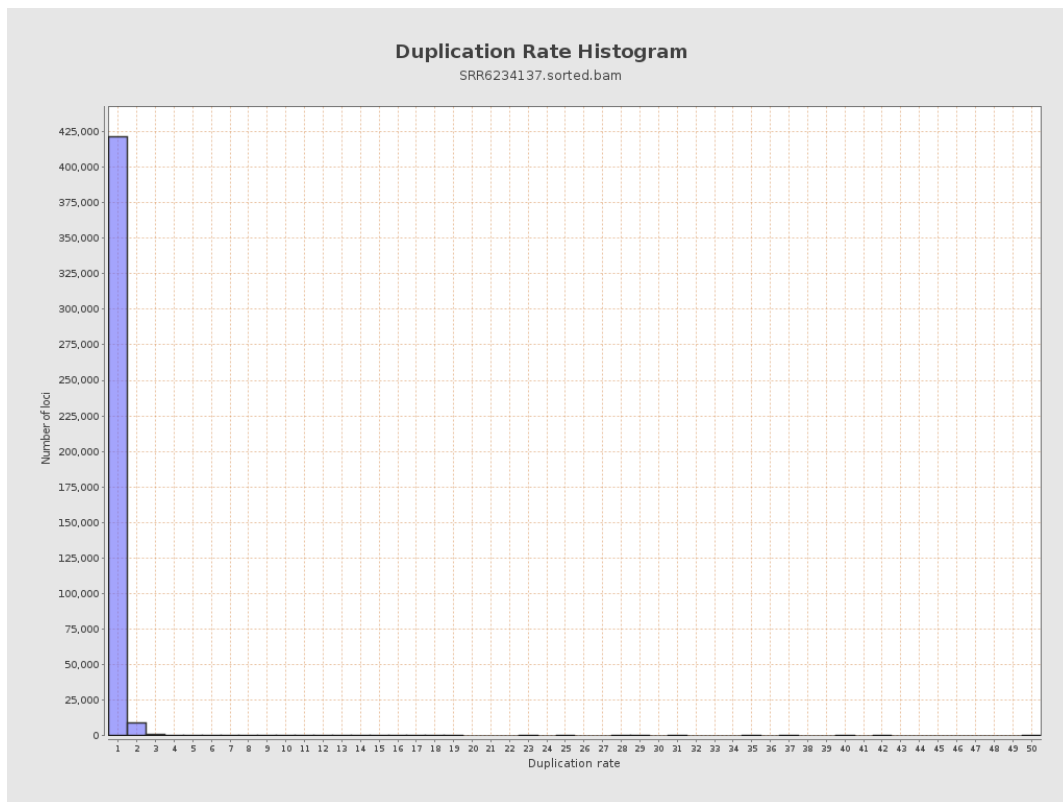
5. Results : Coverage Histogram (0-50X)



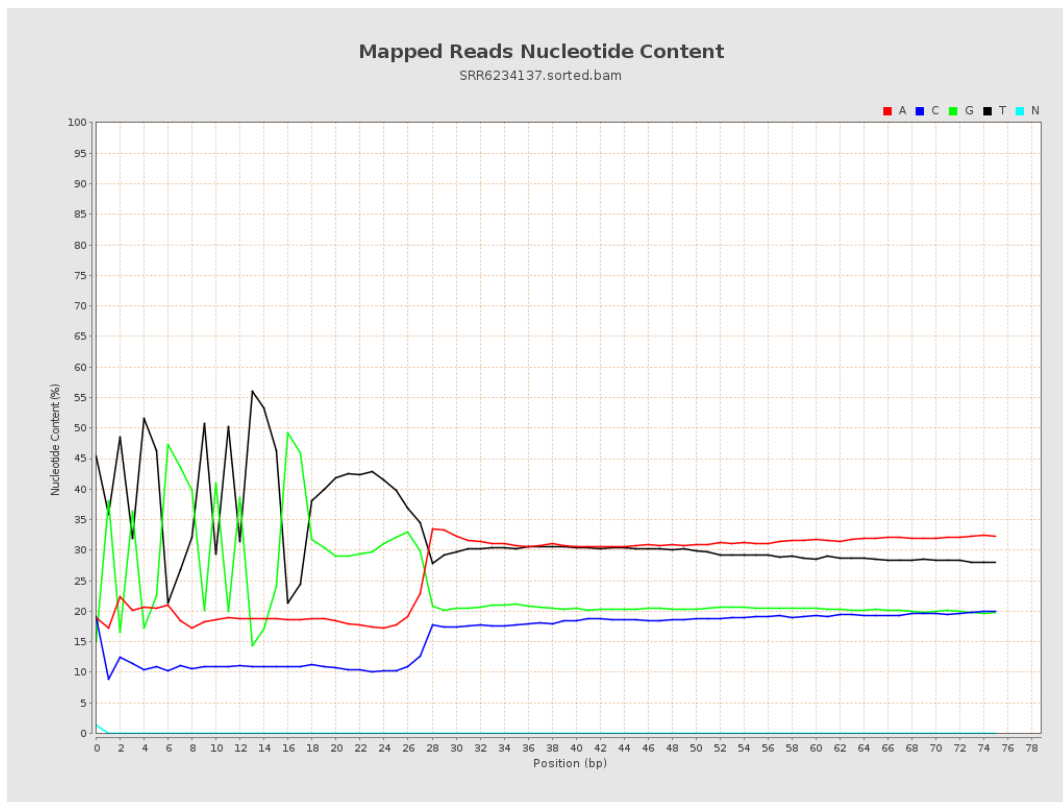
6. Results : Genome Fraction Coverage



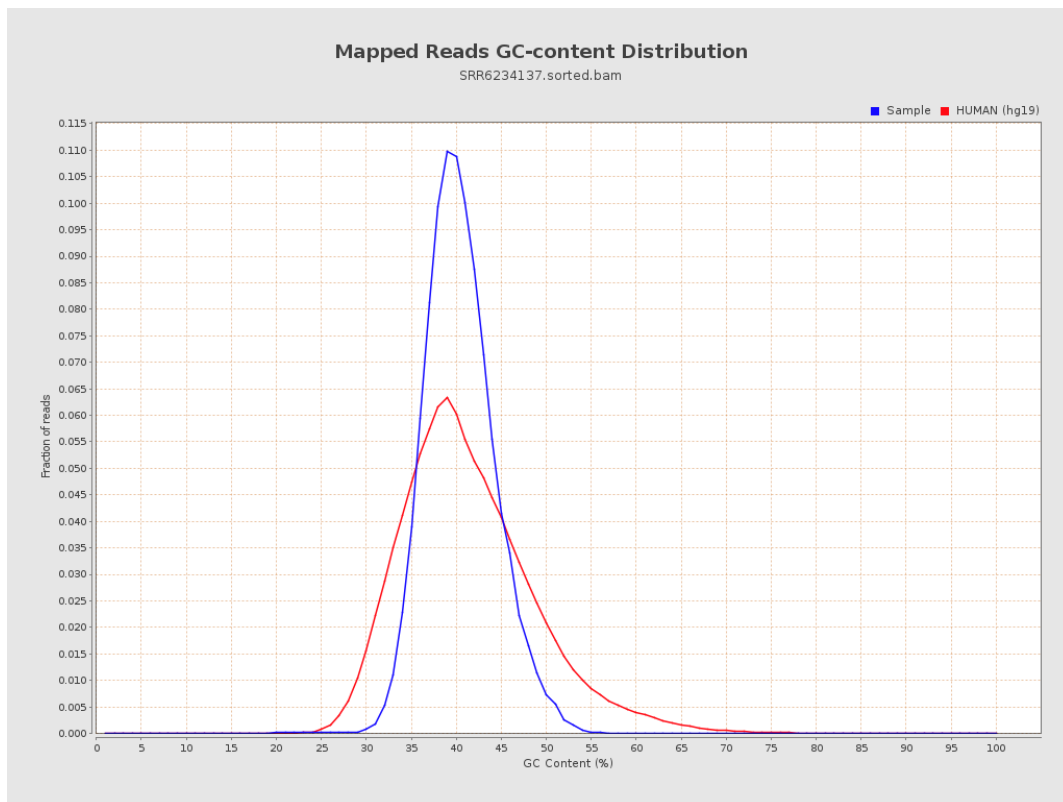
7. Results : Duplication Rate Histogram



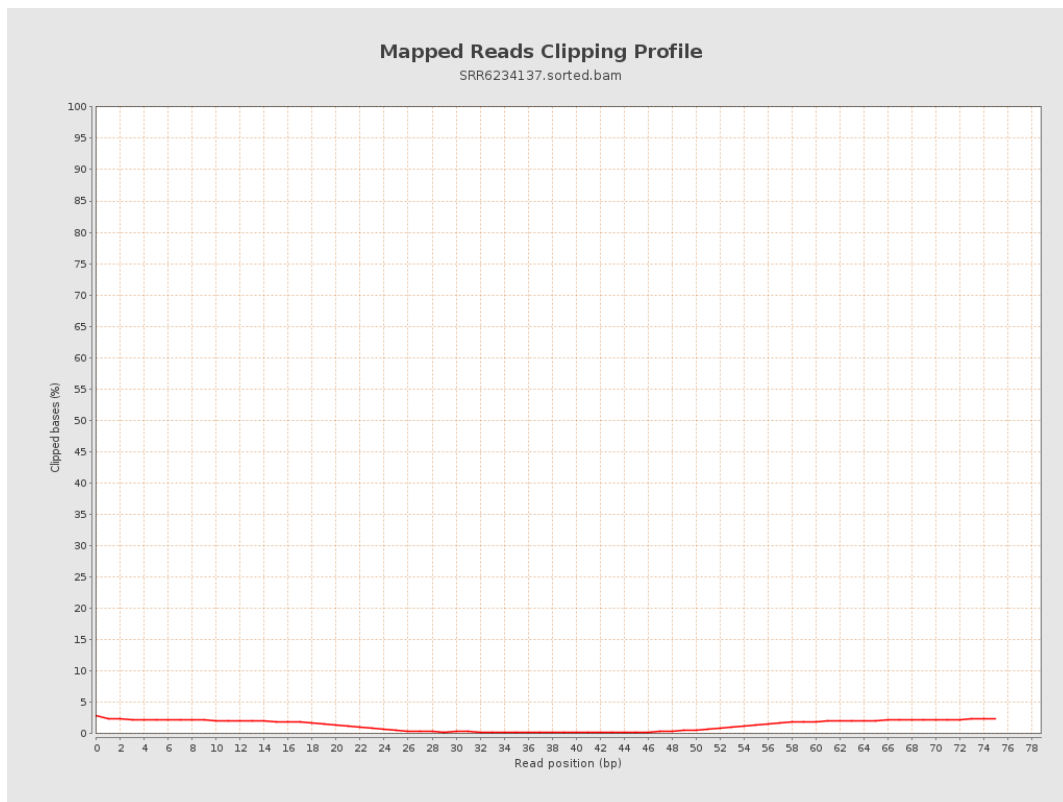
8. Results : Mapped Reads Nucleotide Content



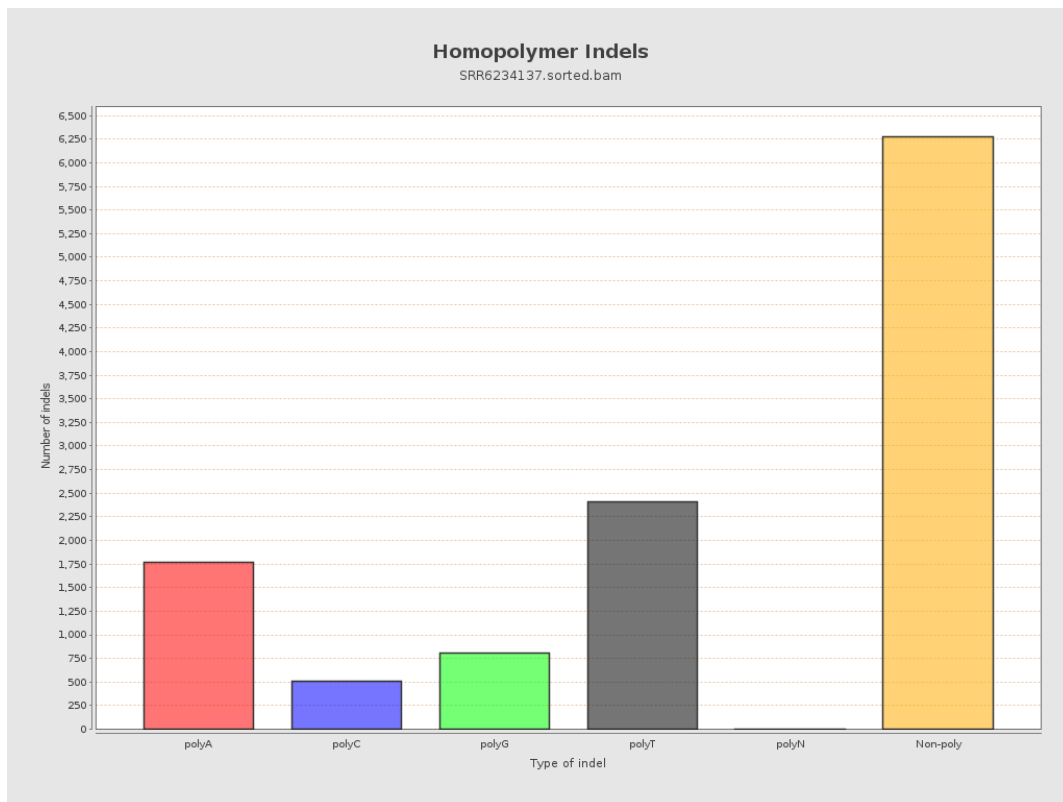
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

