

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 01:48:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237311.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_SRR6237311 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237311.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 01:48:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237311.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,446,044
Mapped reads	2,028,367 / 82.92%
Unmapped reads	417,677 / 17.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,932 / 0.69%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	158,960 / 6.5%
Duplication rate	6.19%
Clipped reads	953,931 / 39%

2.2. ACGT Content

Number/percentage of A's	36,545,417 / 27.23%
Number/percentage of C's	24,634,575 / 18.35%
Number/percentage of T's	42,723,871 / 31.83%
Number/percentage of G's	30,317,687 / 22.59%
Number/percentage of N's	2,132 / 0%
GC Percentage	40.94%

2.3. Coverage

Mean	0.0434

Standard Deviation	0.4338
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2.4. Mapping Quality

Mean Mapping Quality	42.45
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2.5. Mismatches and indels

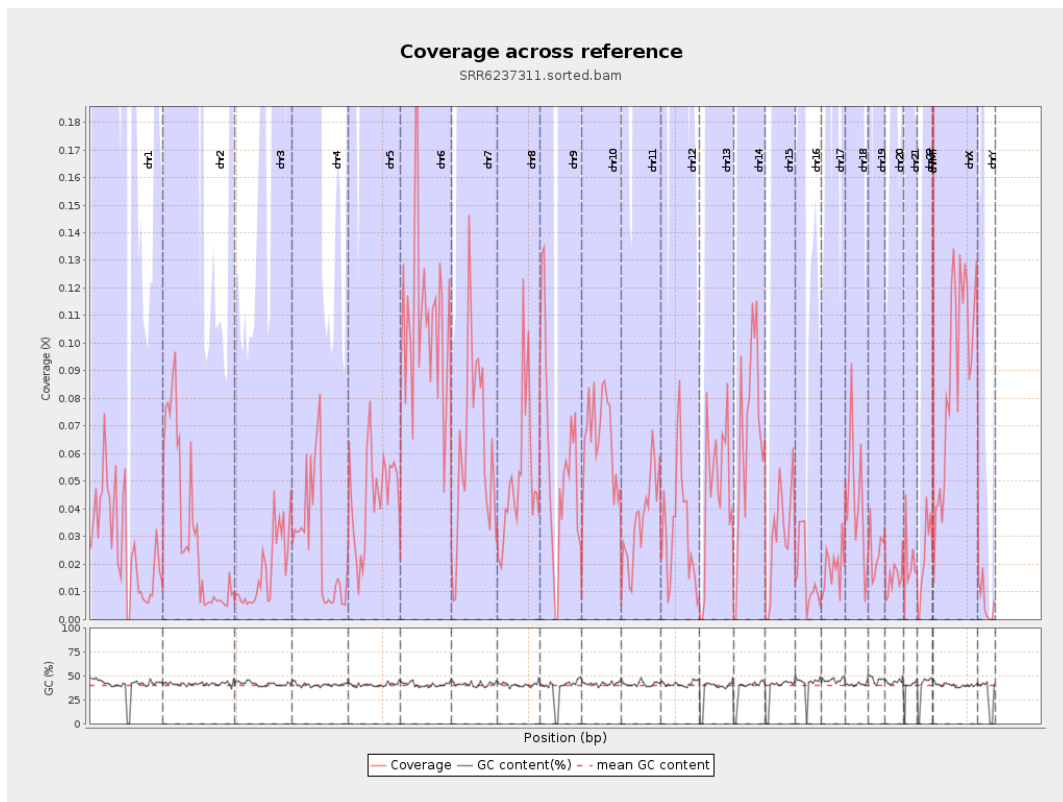
General error rate	0.8%
Mismatches	1,059,151
Insertions	9,587
Mapped reads with at least one insertion	0.47%
Deletions	30,884
Mapped reads with at least one deletion	1.51%
Homopolymer indels	47.26%

2.6. Chromosome stats

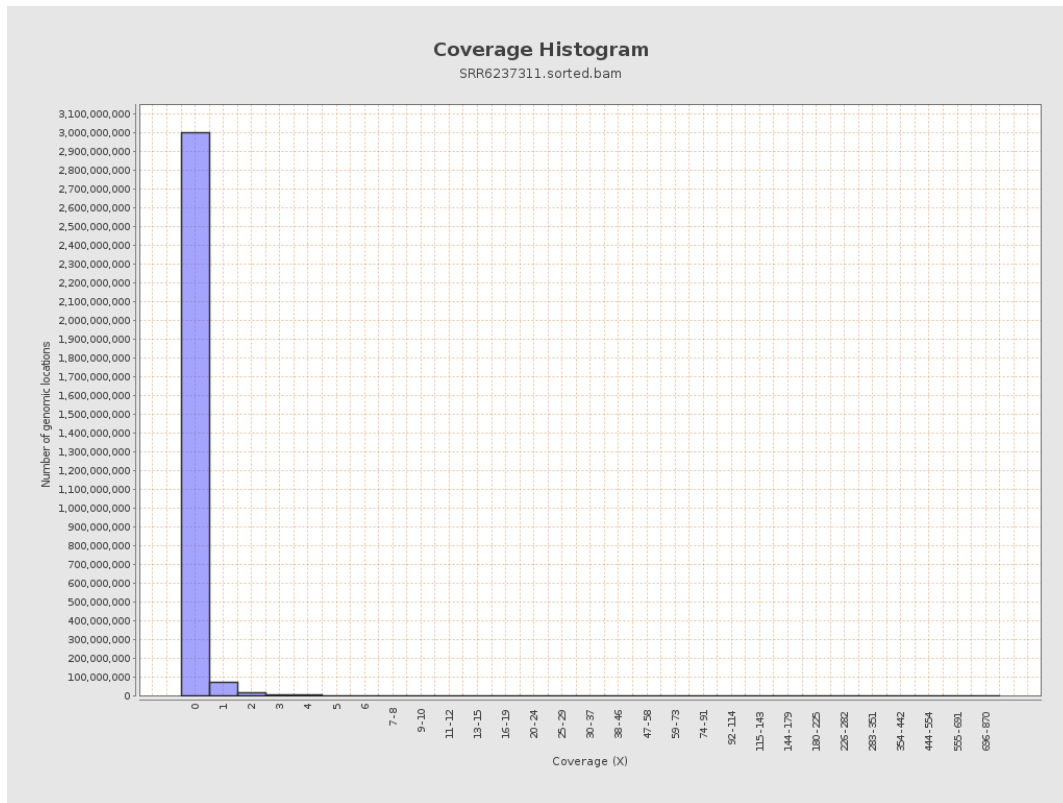
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6721487	0.027	0.305
chr2	243199373	7569874	0.0311	0.4521
chr3	198022430	3543252	0.0179	0.1734
chr4	191154276	5336732	0.0279	0.264
chr5	180915260	7971671	0.0441	0.2748
chr6	171115067	18630388	0.1089	0.7276
chr7	159138663	9823129	0.0617	0.9409

chr8	146364022	7425681	0.0507	0.549
chr9	141213431	7897941	0.0559	0.4163
chr10	135534747	8925833	0.0659	0.4377
chr11	135006516	4981887	0.0369	0.3511
chr12	133851895	4388282	0.0328	0.2437
chr13	115169878	5444367	0.0473	0.2853
chr14	107349540	7170913	0.0668	0.3644
chr15	102531392	3192335	0.0311	0.2412
chr16	90354753	1414384	0.0157	0.2063
chr17	81195210	1514987	0.0187	0.197
chr18	78077248	3482209	0.0446	0.7213
chr19	59128983	1441946	0.0244	0.3143
chr20	63025520	914755	0.0145	0.1856
chr21	48129895	1013574	0.0211	0.2299
chr22	51304566	1187555	0.0231	0.1978
chrMT	16571	215532	13.0066	8.7964
chrX	155270560	13692943	0.0882	0.4301
chrY	59373566	375422	0.0063	0.17

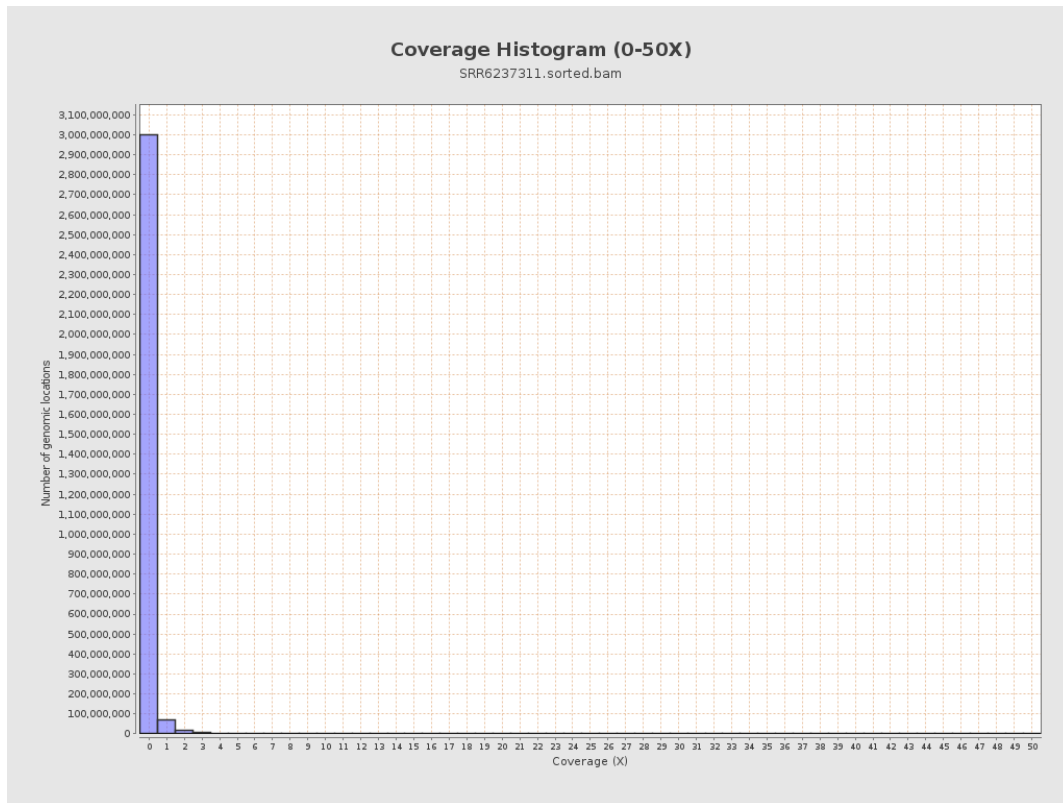
3. Results : Coverage across reference



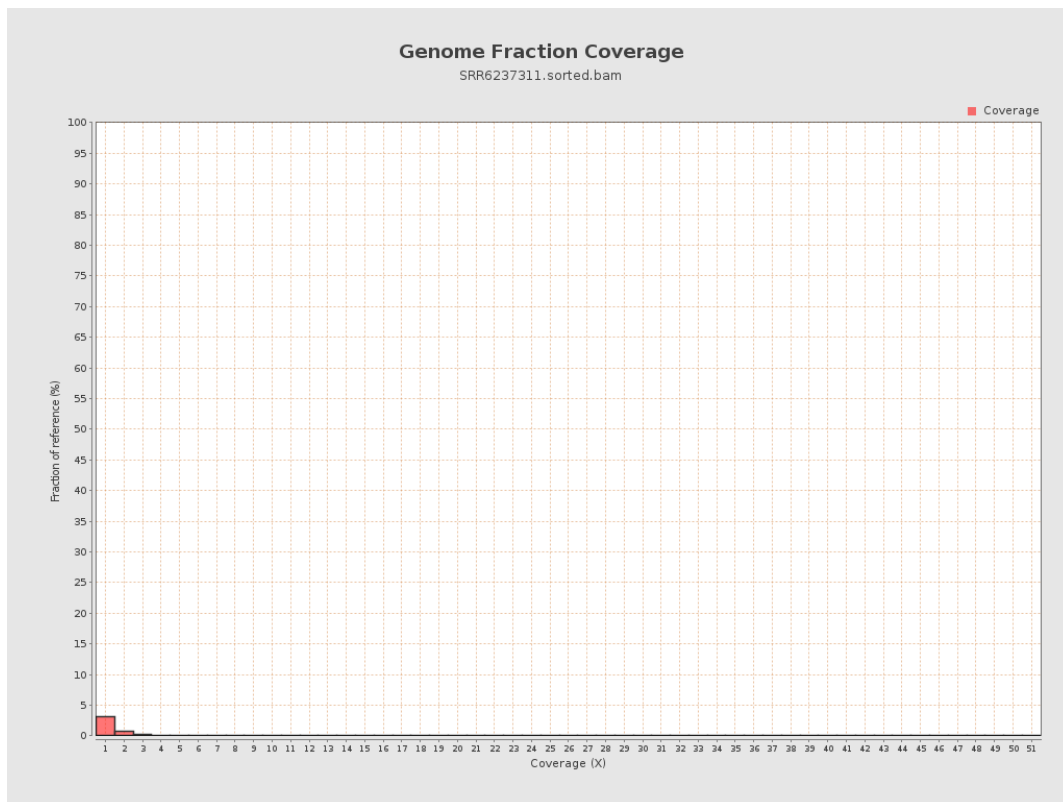
4. Results : Coverage Histogram



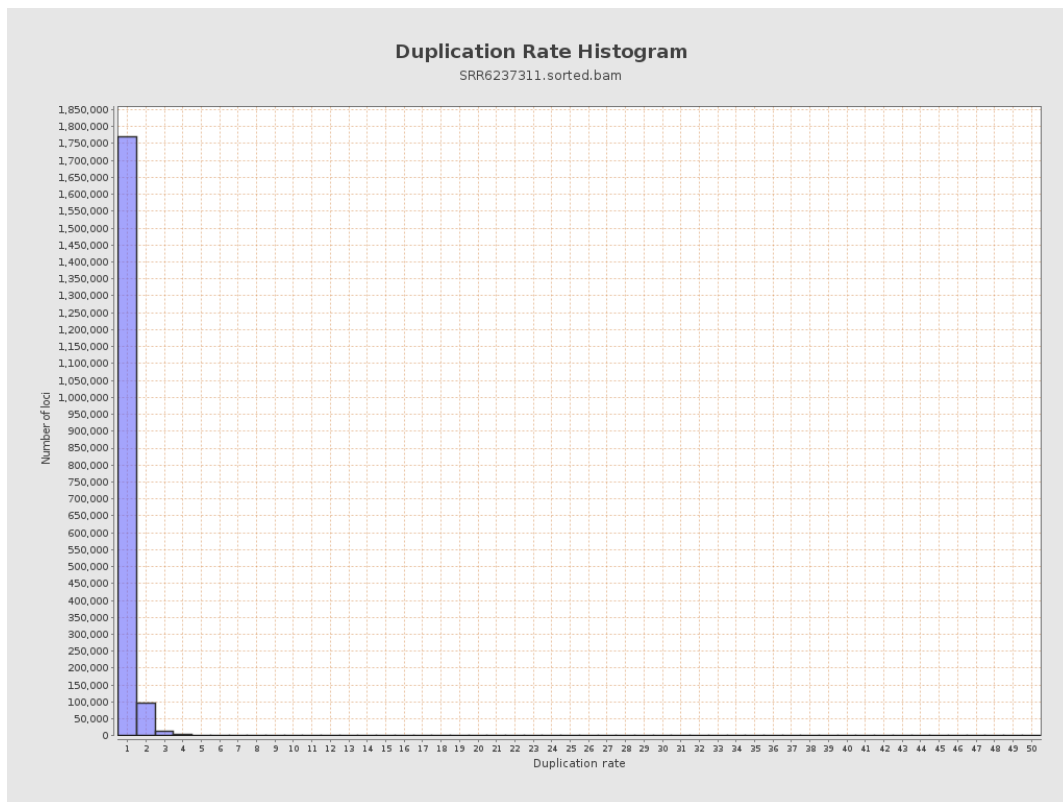
5. Results : Coverage Histogram (0-50X)



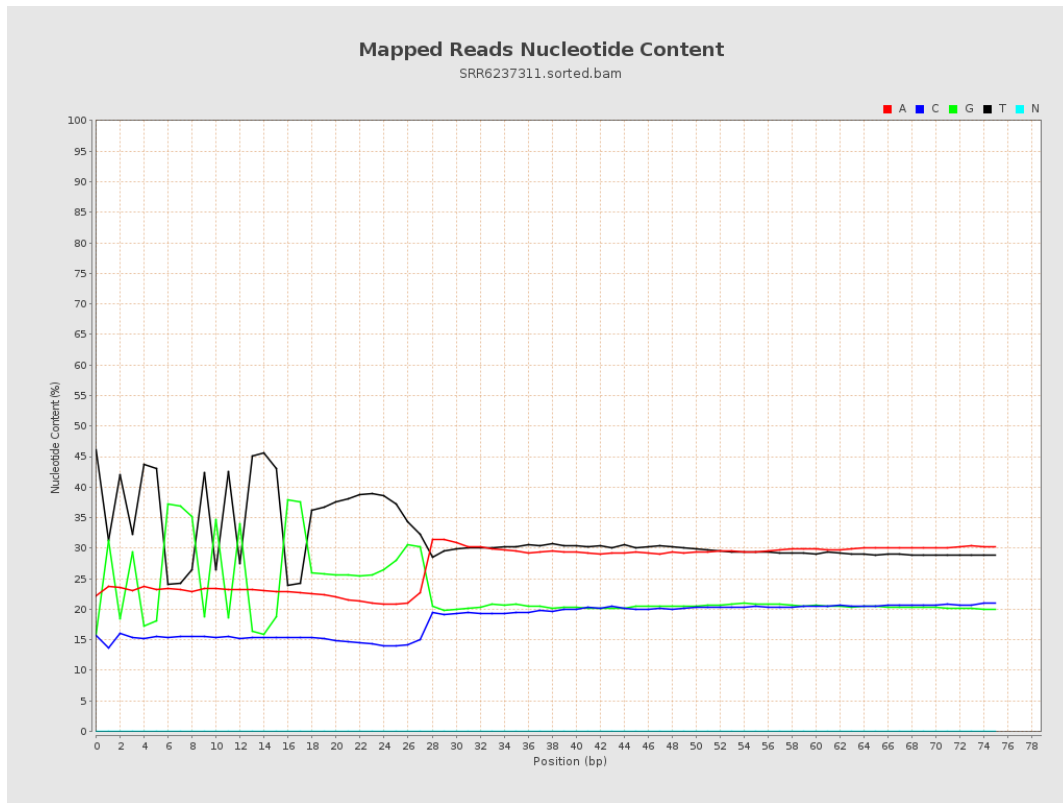
6. Results : Genome Fraction Coverage



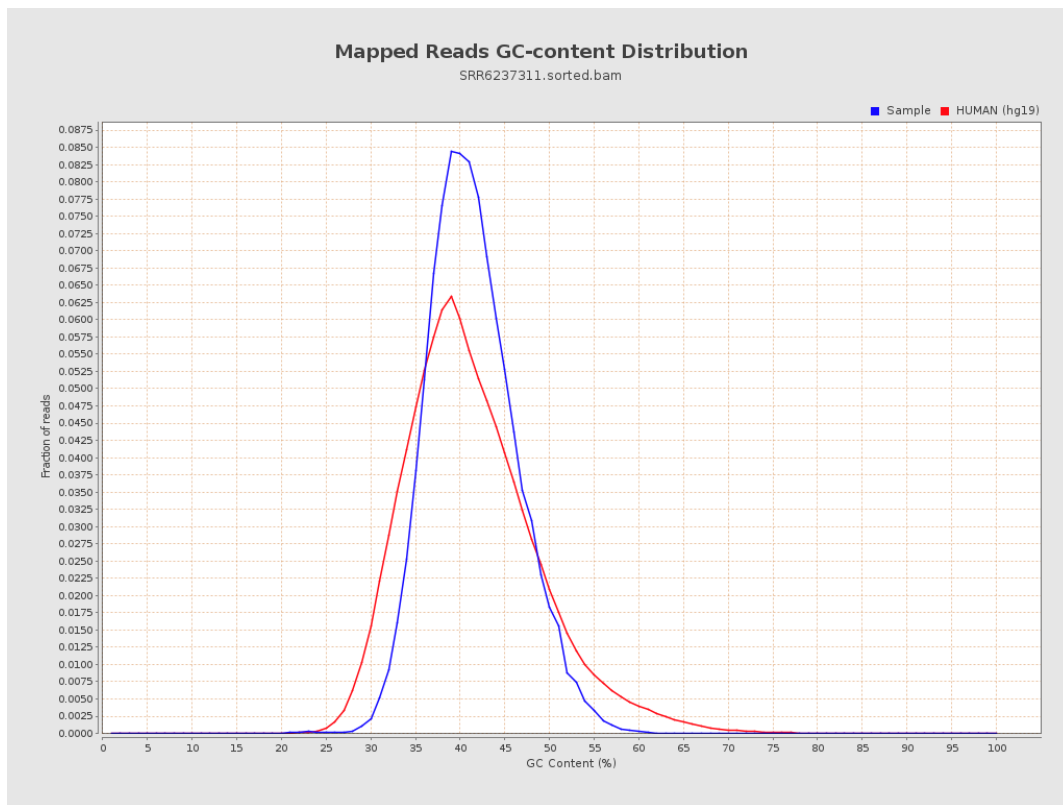
7. Results : Duplication Rate Histogram



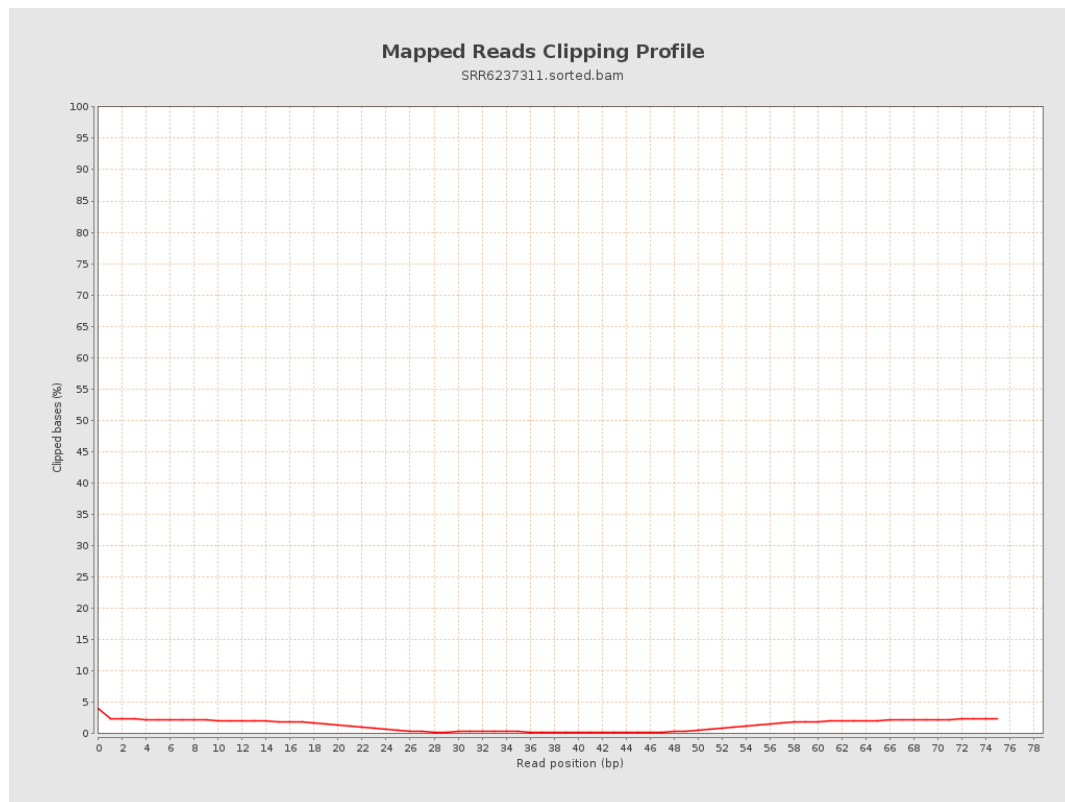
8. Results : Mapped Reads Nucleotide Content



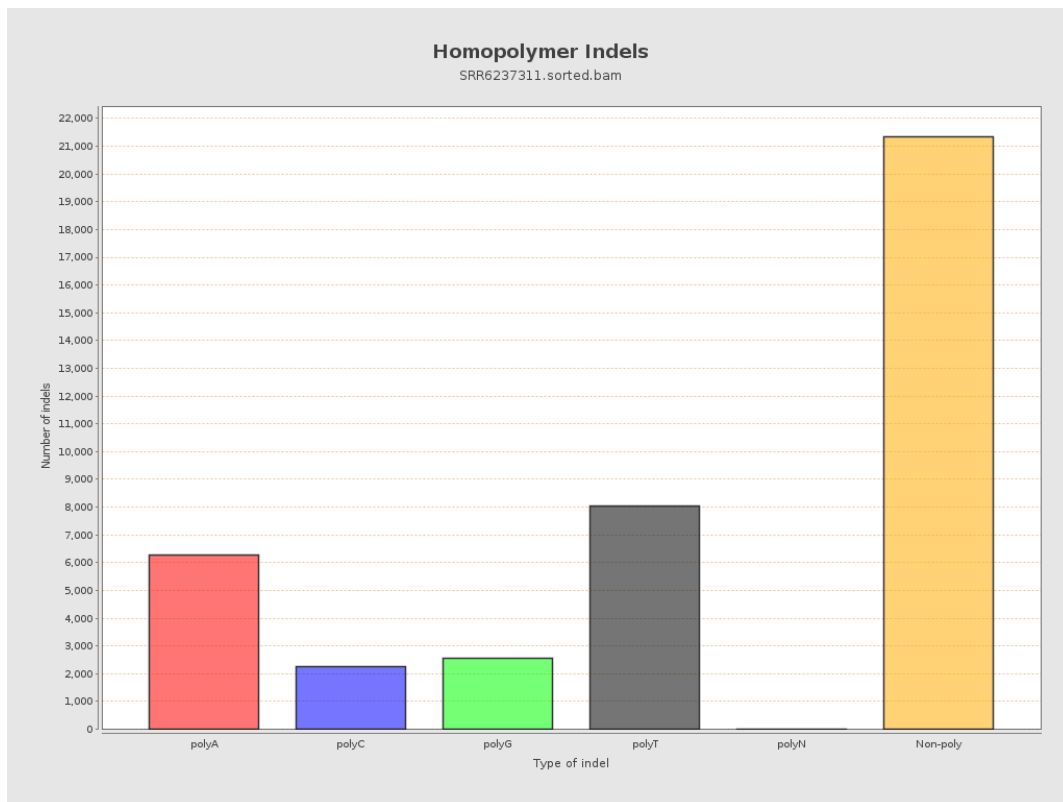
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

