

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 10:19:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231886.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_SRR6231886 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231886.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 10:19:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231886.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,565,233
Mapped reads	5,214,472 / 93.7%
Unmapped reads	350,761 / 6.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,768 / 0.55%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	506,515 / 9.1%
Duplication rate	4.11%
Clipped reads	2,124,831 / 38.18%

2.2. ACGT Content

Number/percentage of A's	93,466,337 / 26.47%
Number/percentage of C's	64,952,258 / 18.4%
Number/percentage of T's	101,939,414 / 28.87%
Number/percentage of G's	92,657,116 / 26.24%
Number/percentage of N's	77,849 / 0.02%
GC Percentage	44.64%

2.3. Coverage

Mean	0.1141

Standard Deviation	33.0495
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2.4. Mapping Quality

Mean Mapping Quality	44.21
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2.5. Mismatches and indels

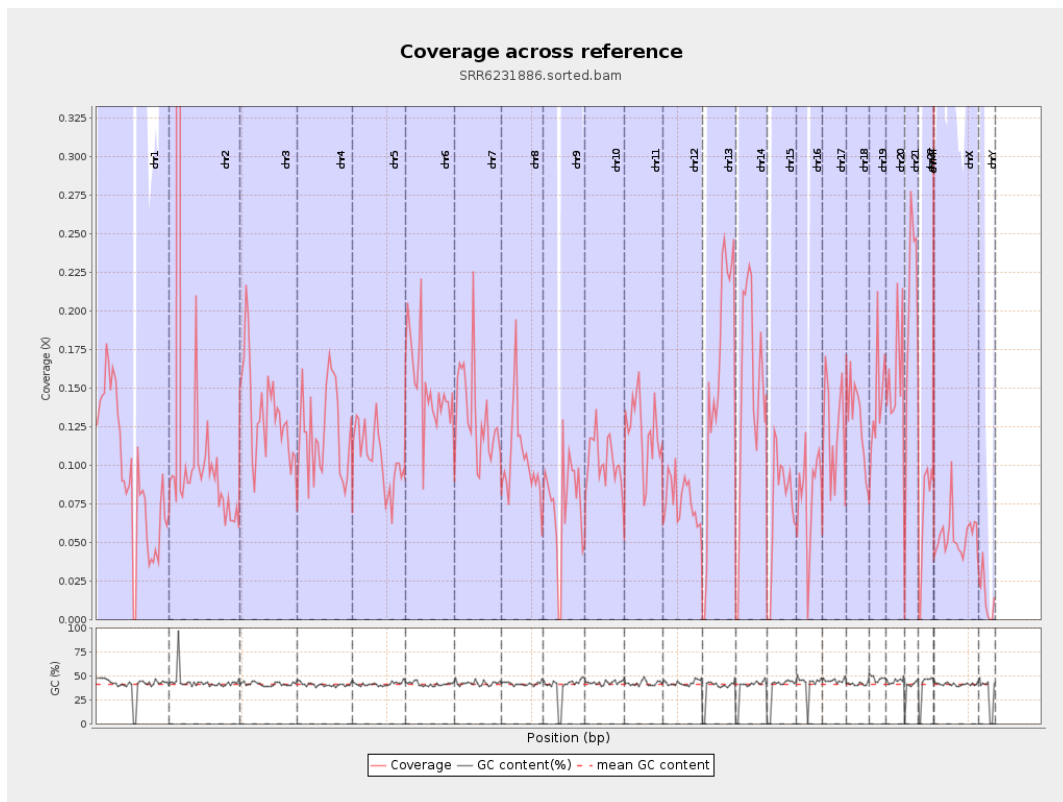
General error rate	0.69%
Mismatches	2,374,590
Insertions	25,498
Mapped reads with at least one insertion	0.48%
Deletions	79,092
Mapped reads with at least one deletion	1.5%
Homopolymer indels	45.85%

2.6. Chromosome stats

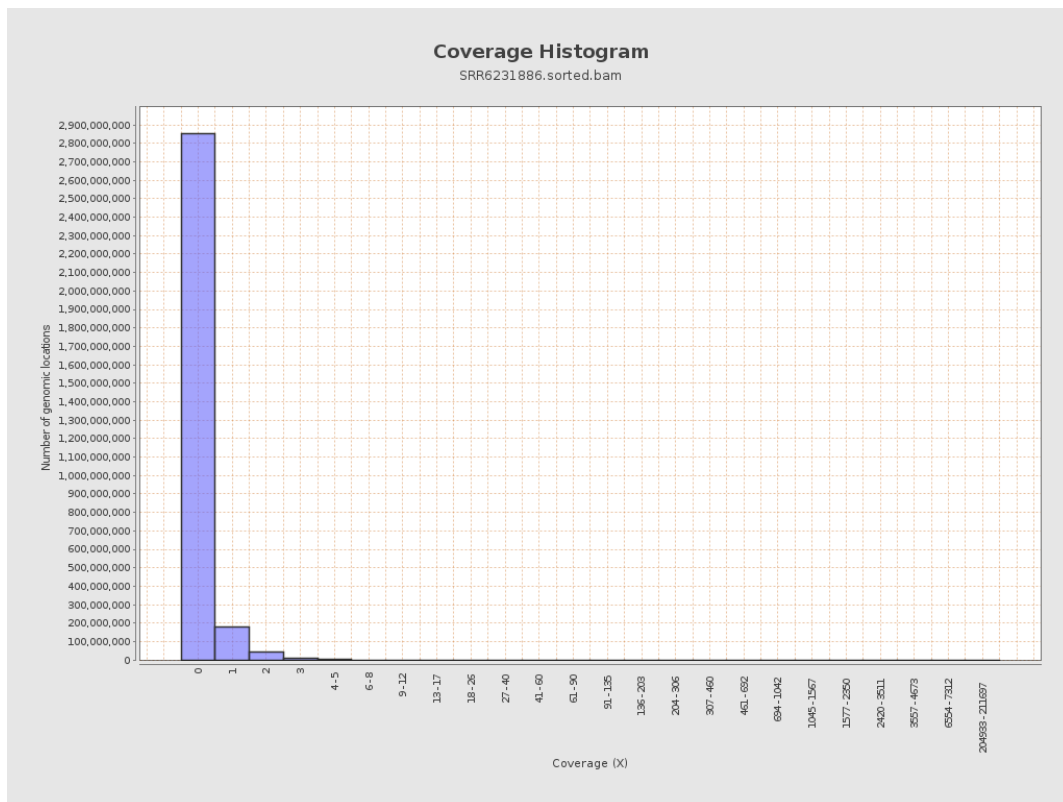
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	23135446	0.0928	1.2115
chr2	243199373	38793420	0.1595	117.8736
chr3	198022430	26551715	0.1341	0.4848
chr4	191154276	23220092	0.1215	0.5233
chr5	180915260	18976347	0.1049	0.4398
chr6	171115067	25749856	0.1505	0.7124
chr7	159138663	21121509	0.1327	1.6918

chr8	146364022	15154615	0.1035	1.2209
chr9	141213431	10552418	0.0747	0.8947
chr10	135534747	13983240	0.1032	0.6129
chr11	135006516	16185773	0.1199	1.3382
chr12	133851895	10328194	0.0772	0.3742
chr13	115169878	18092305	0.1571	0.5375
chr14	107349540	16001140	0.1491	0.6674
chr15	102531392	7714292	0.0752	0.3713
chr16	90354753	7403044	0.0819	0.5226
chr17	81195210	9719575	0.1197	0.7451
chr18	78077248	10102444	0.1294	1.9166
chr19	59128983	8366331	0.1415	0.8809
chr20	63025520	9962884	0.1581	0.5807
chr21	48129895	9405205	0.1954	0.6846
chr22	51304566	3471473	0.0677	0.3392
chrMT	16571	6098	0.368	0.7944
chrX	155270560	8417443	0.0542	0.5251
chrY	59373566	807018	0.0136	0.2573

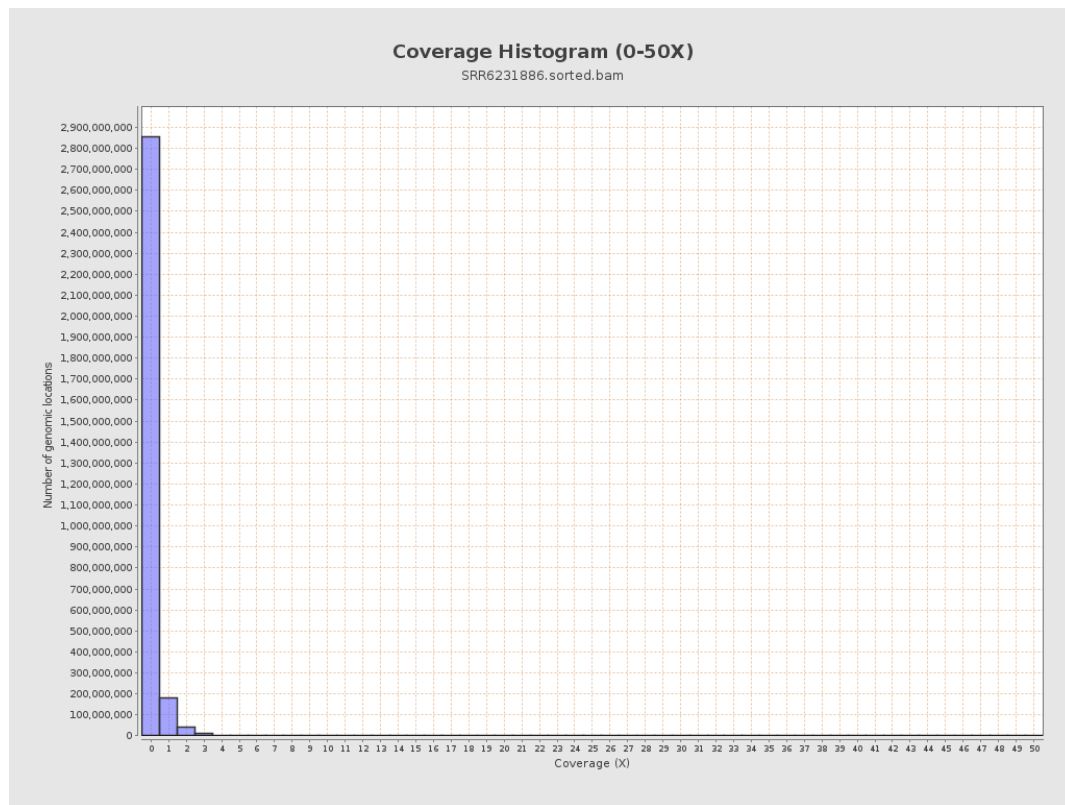
3. Results : Coverage across reference



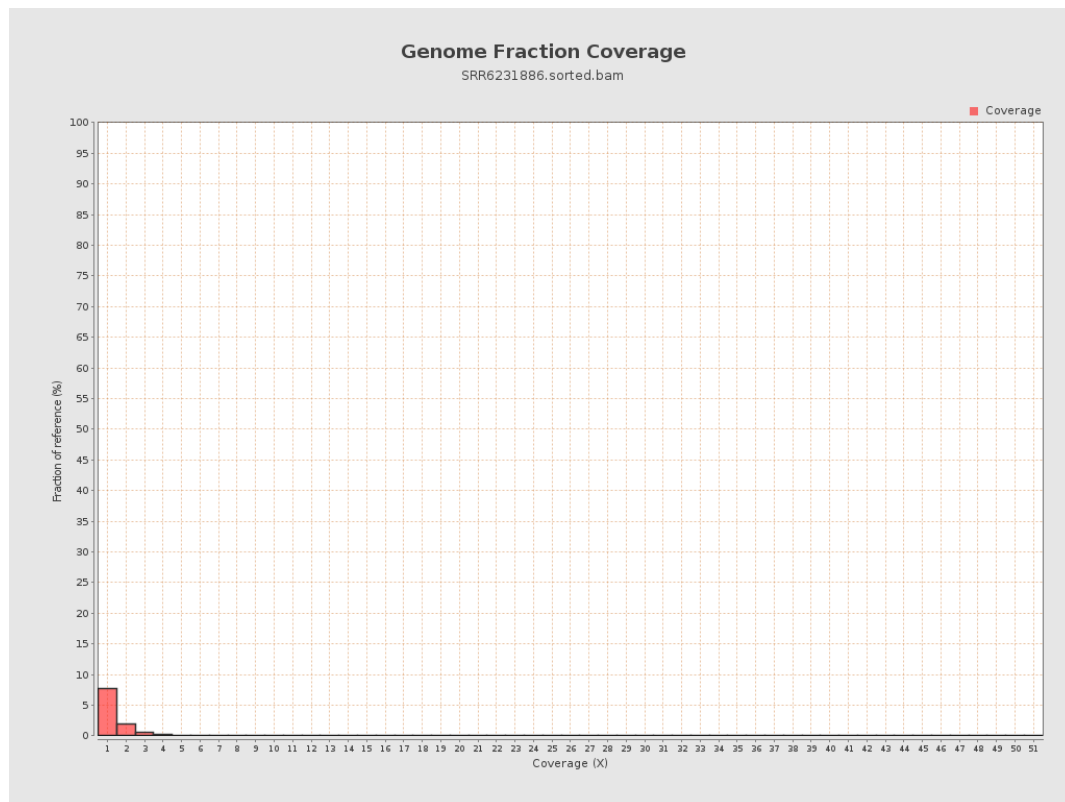
4. Results : Coverage Histogram



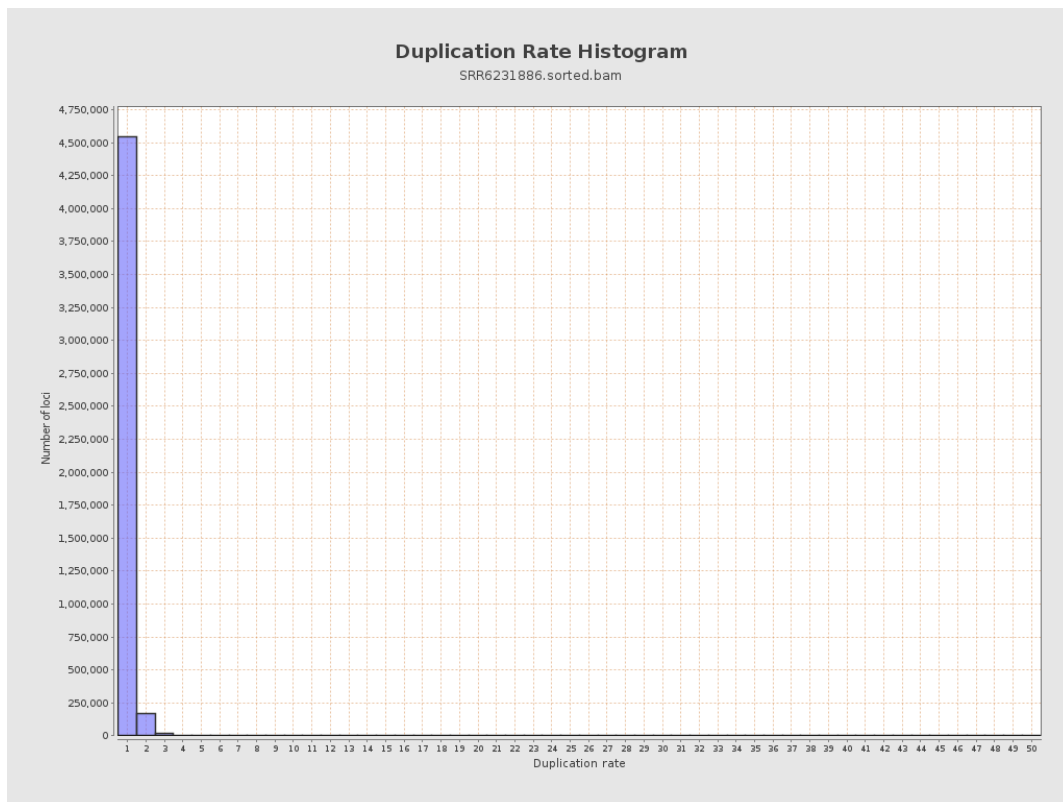
5. Results : Coverage Histogram (0-50X)



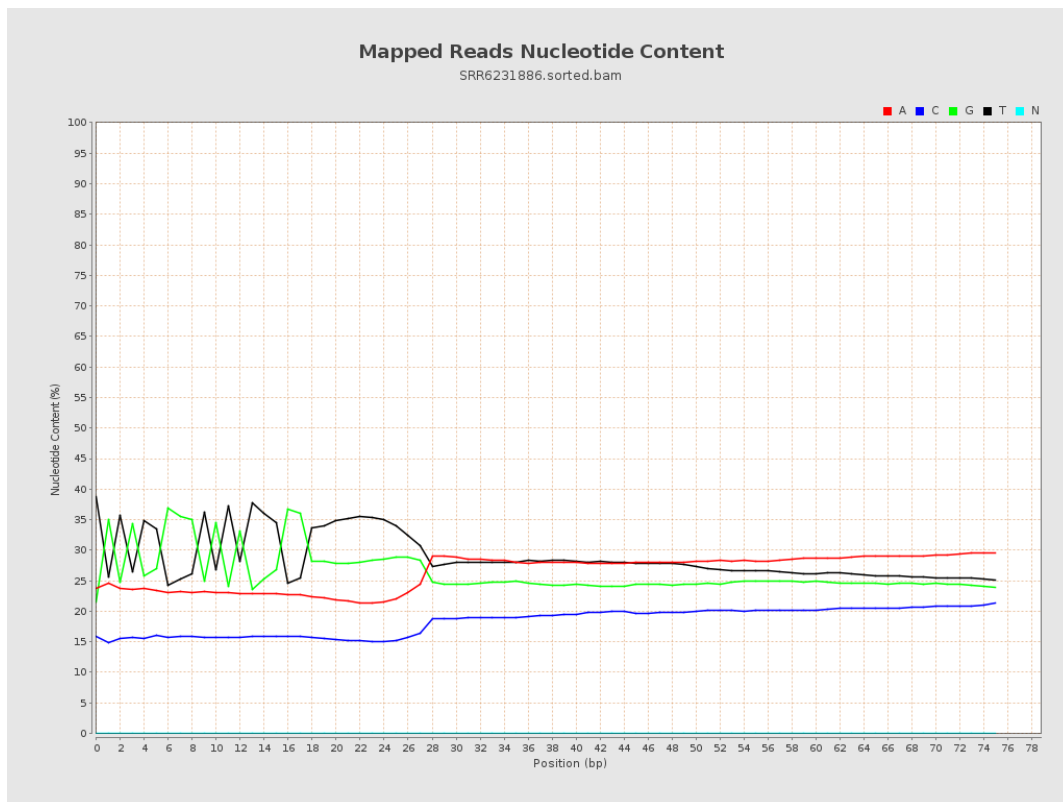
6. Results : Genome Fraction Coverage



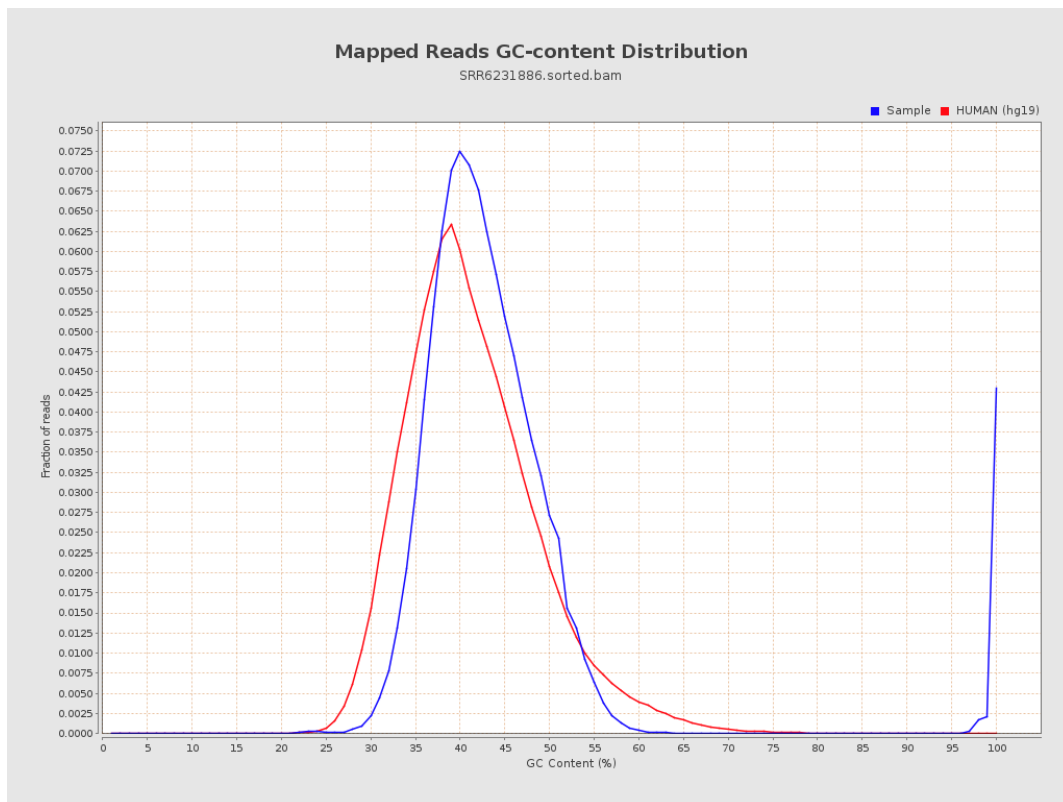
7. Results : Duplication Rate Histogram



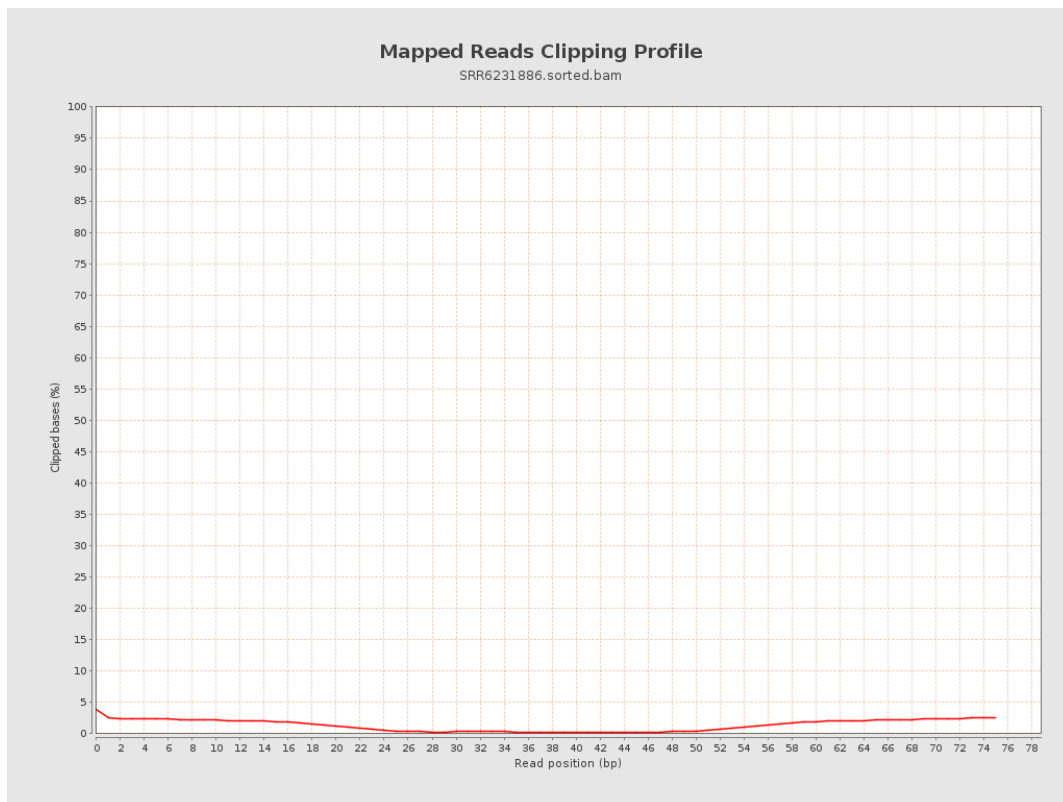
8. Results : Mapped Reads Nucleotide Content



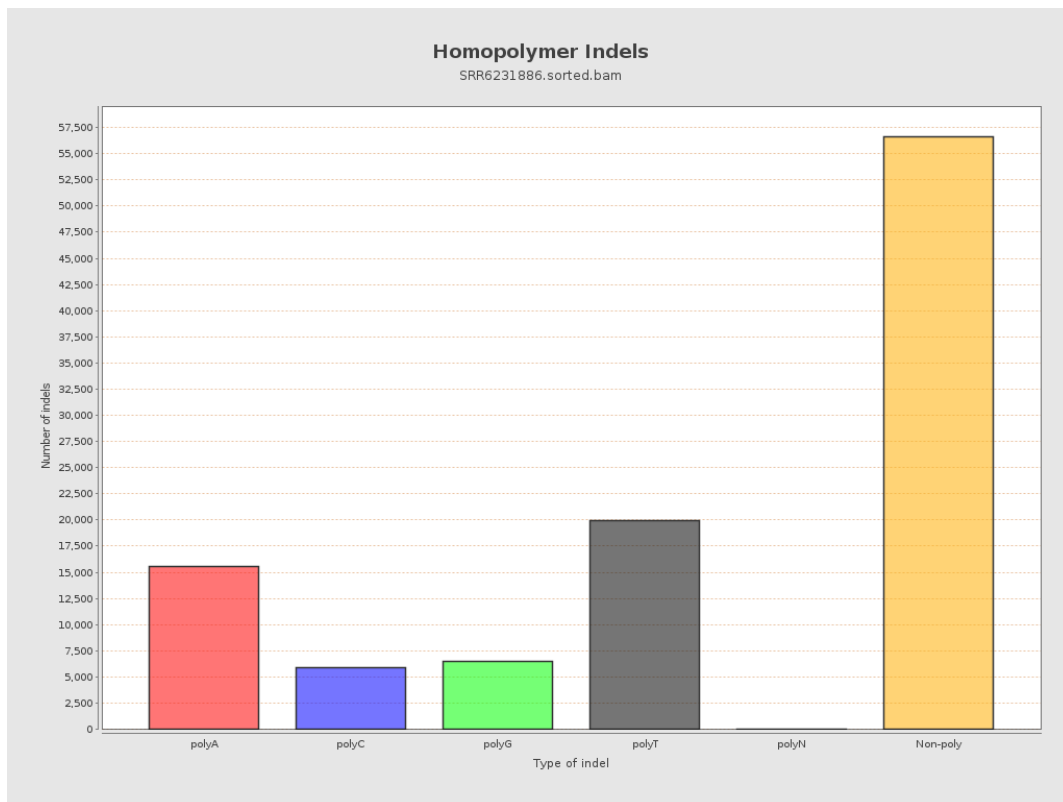
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

