

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 05:37:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237788.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_SRR6237788 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237788.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 05:37:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237788.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	621,625
Mapped reads	458,382 / 73.74%
Unmapped reads	163,243 / 26.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,214 / 0.52%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	9,350 / 1.5%
Duplication rate	1.73%
Clipped reads	252,344 / 40.59%

2.2. ACGT Content

Number/percentage of A's	8,594,948 / 29.37%
Number/percentage of C's	5,075,946 / 17.35%
Number/percentage of T's	9,097,926 / 31.09%
Number/percentage of G's	6,465,756 / 22.1%
Number/percentage of N's	25,843 / 0.09%
GC Percentage	39.44%

2.3. Coverage

Mean	0.0095

Standard Deviation	0.1208
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2.4. Mapping Quality

Mean Mapping Quality	46.9
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2.5. Mismatches and indels

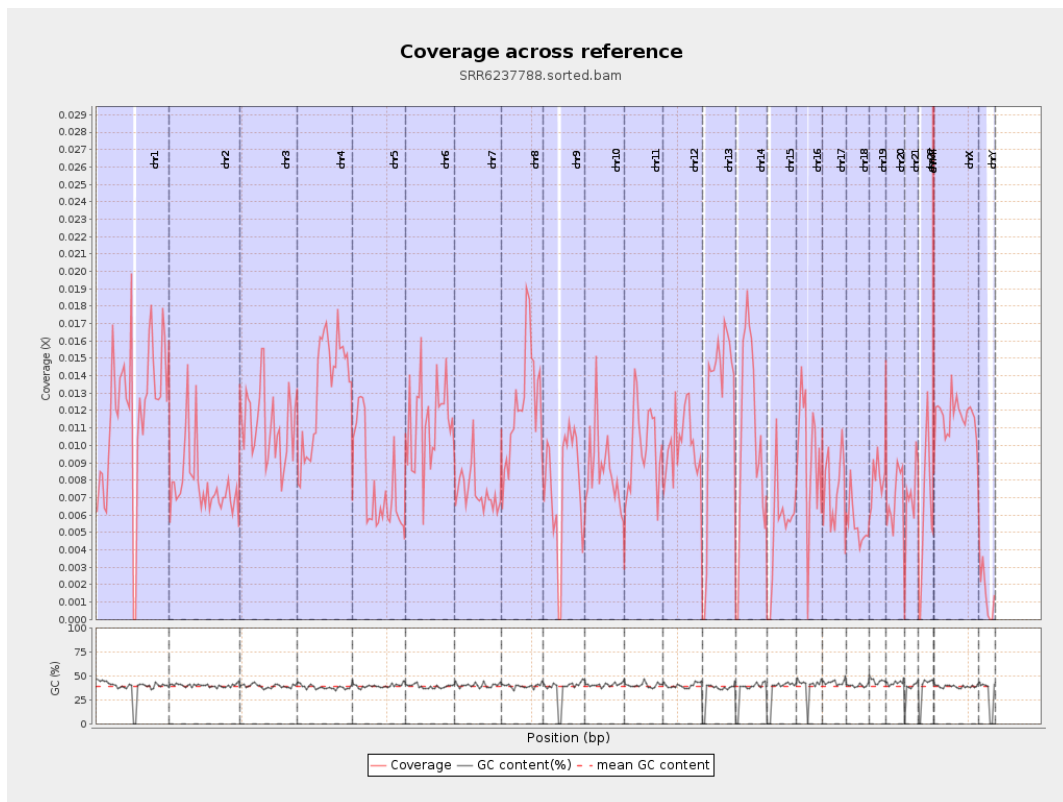
General error rate	0.97%
Mismatches	280,982
Insertions	2,351
Mapped reads with at least one insertion	0.51%
Deletions	10,725
Mapped reads with at least one deletion	2.3%
Homopolymer indels	47.91%

2.6. Chromosome stats

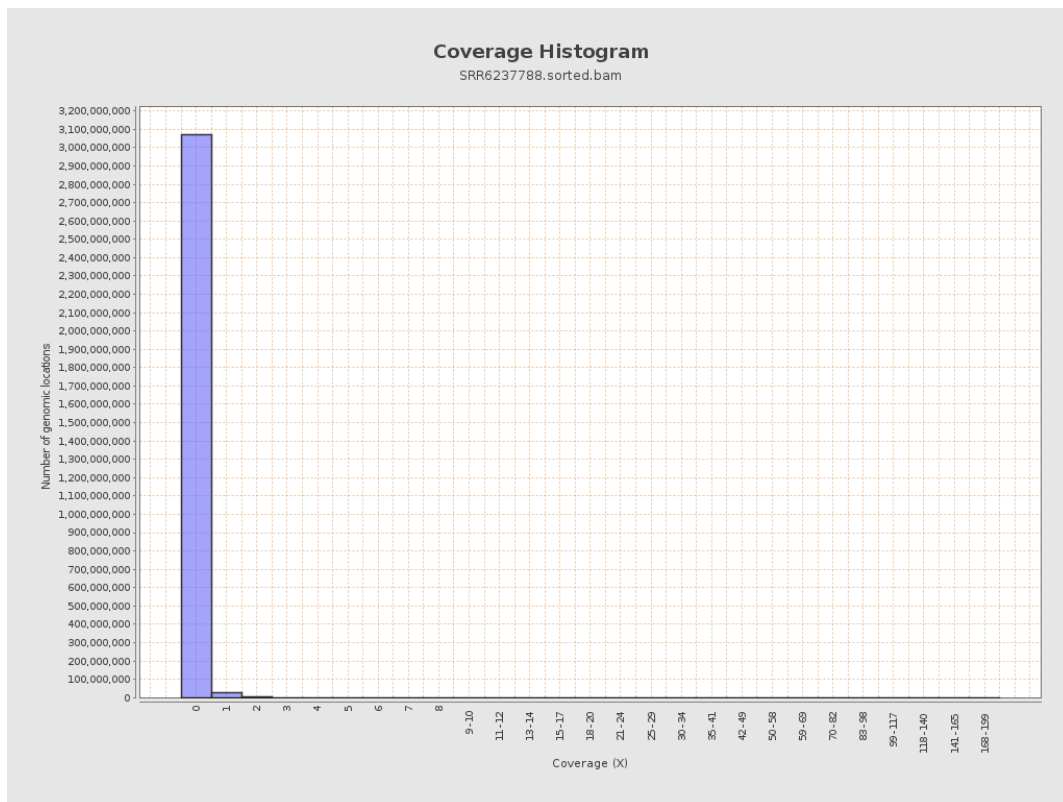
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	2954568	0.0119	0.1992
chr2	243199373	1879982	0.0077	0.1051
chr3	198022430	2230505	0.0113	0.1117
chr4	191154276	2530087	0.0132	0.1219
chr5	180915260	1404748	0.0078	0.0927
chr6	171115067	1940293	0.0113	0.115
chr7	159138663	1173815	0.0074	0.1123

chr8	146364022	1783653	0.0122	0.168
chr9	141213431	1084493	0.0077	0.1002
chr10	135534747	1164522	0.0086	0.1131
chr11	135006516	1339665	0.0099	0.1159
chr12	133851895	1336392	0.01	0.1054
chr13	115169878	1431422	0.0124	0.1176
chr14	107349540	1133253	0.0106	0.1097
chr15	102531392	543098	0.0053	0.0768
chr16	90354753	850810	0.0094	0.1033
chr17	81195210	593264	0.0073	0.096
chr18	78077248	426736	0.0055	0.1292
chr19	59128983	491732	0.0083	0.1245
chr20	63025520	437731	0.0069	0.0886
chr21	48129895	336386	0.007	0.0893
chr22	51304566	308440	0.006	0.0811
chrMT	16571	15934	0.9616	1.2266
chrX	155270560	1797581	0.0116	0.1154
chrY	59373566	87905	0.0015	0.0438

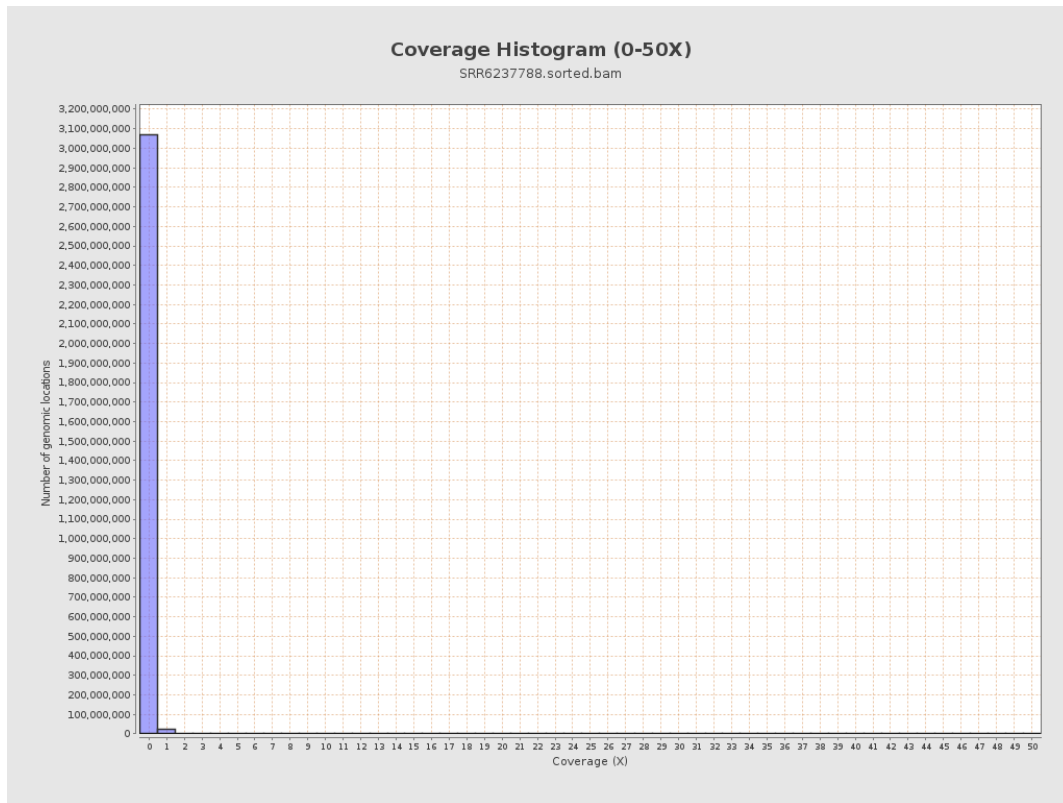
3. Results : Coverage across reference



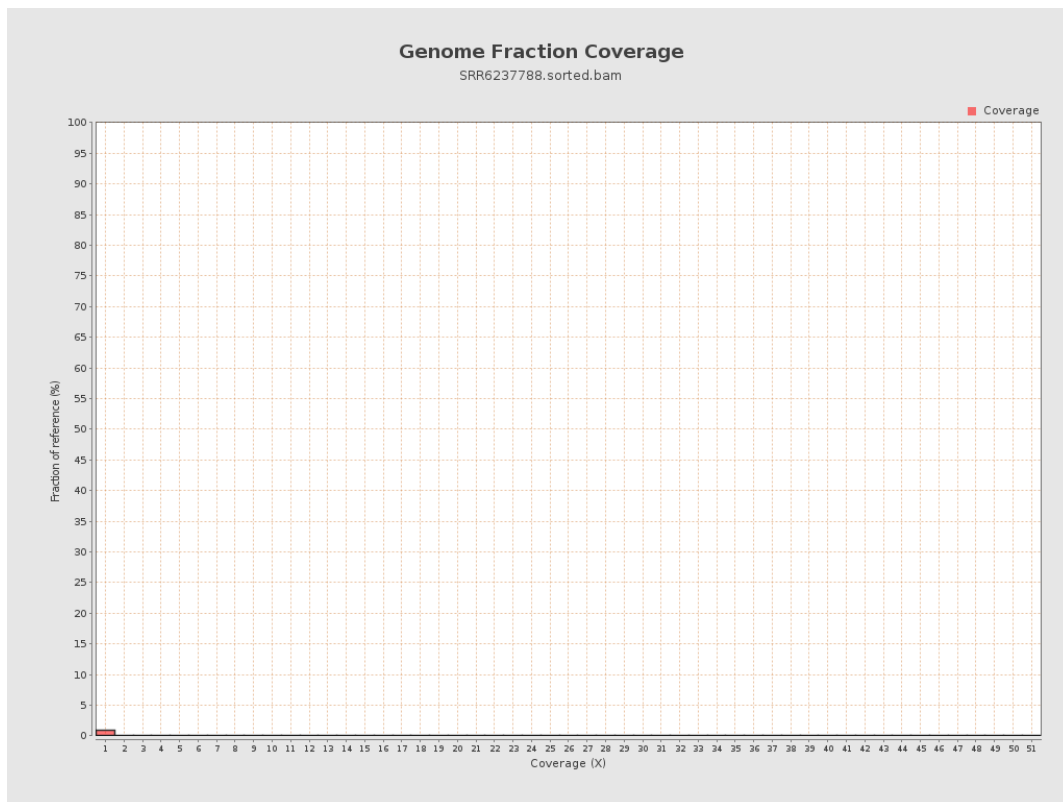
4. Results : Coverage Histogram



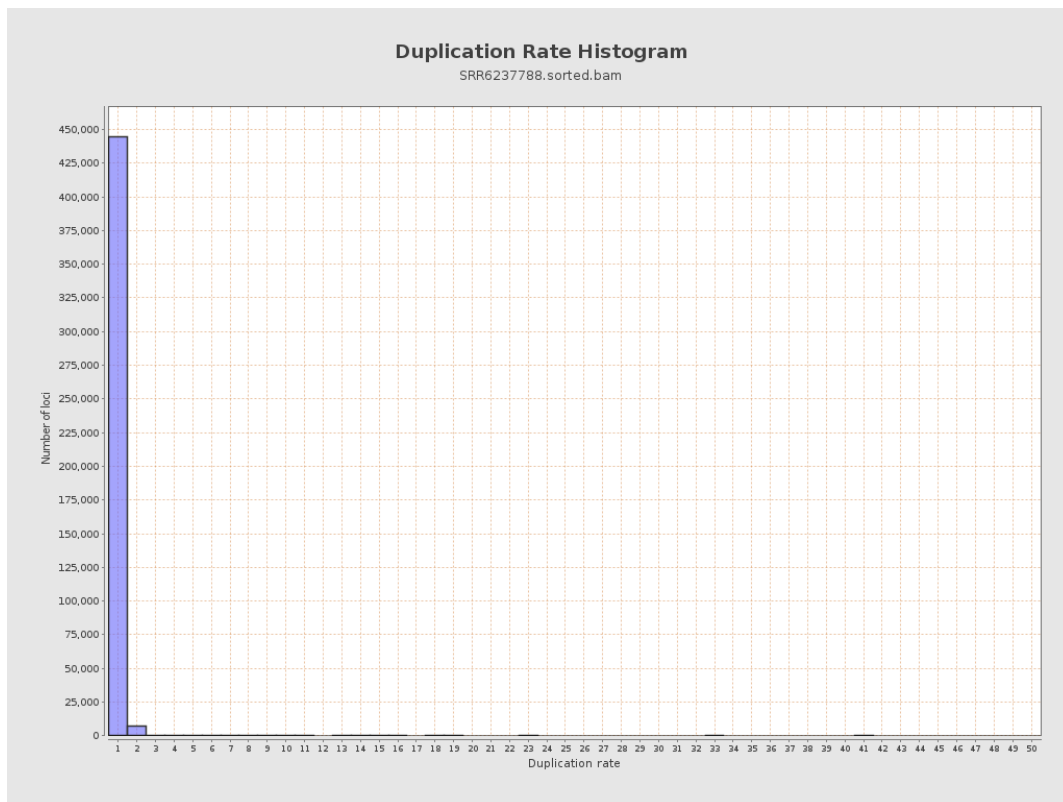
5. Results : Coverage Histogram (0-50X)



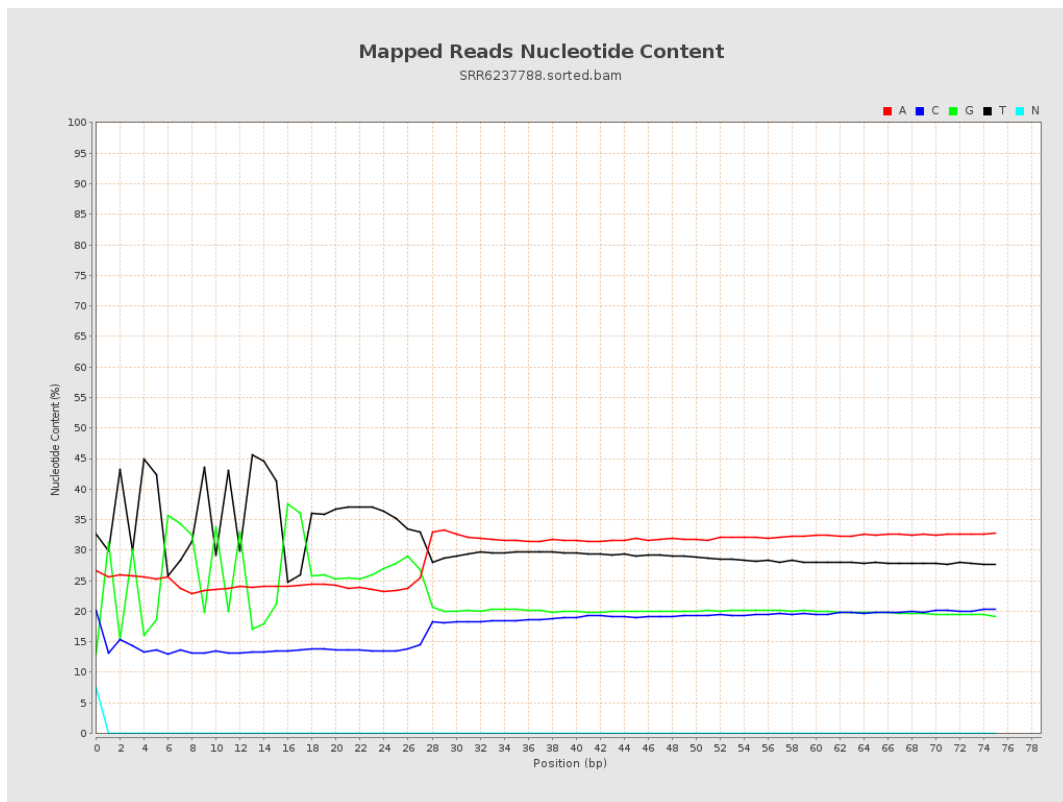
6. Results : Genome Fraction Coverage



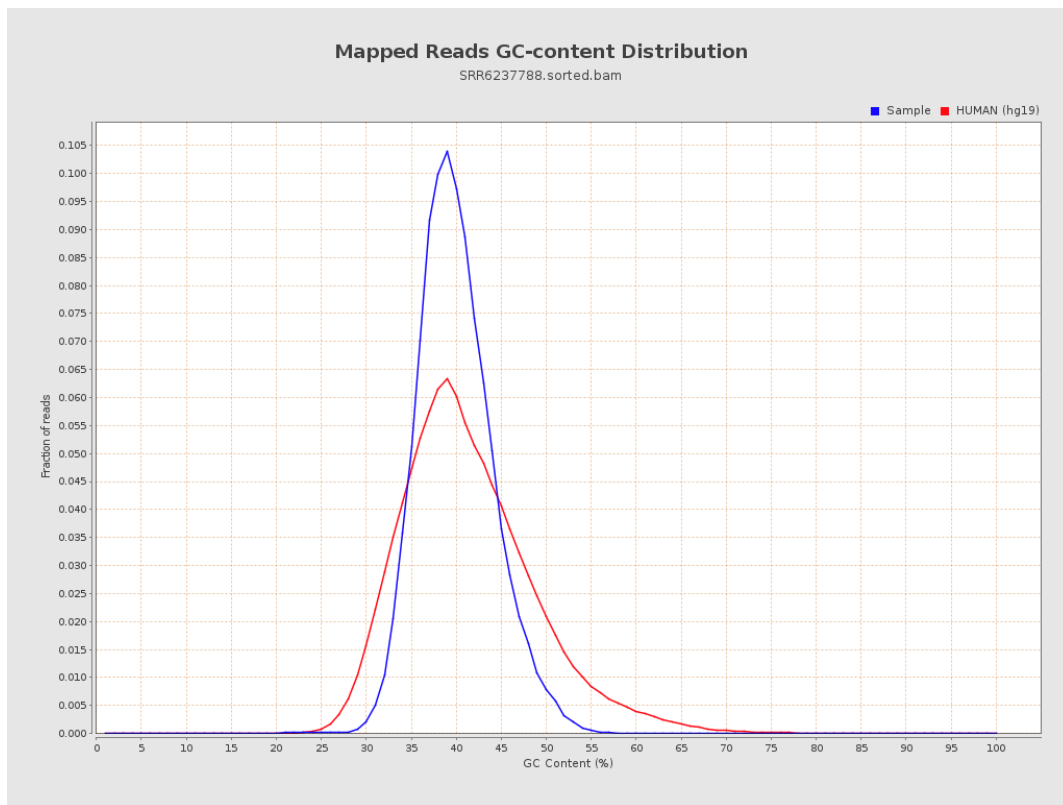
7. Results : Duplication Rate Histogram



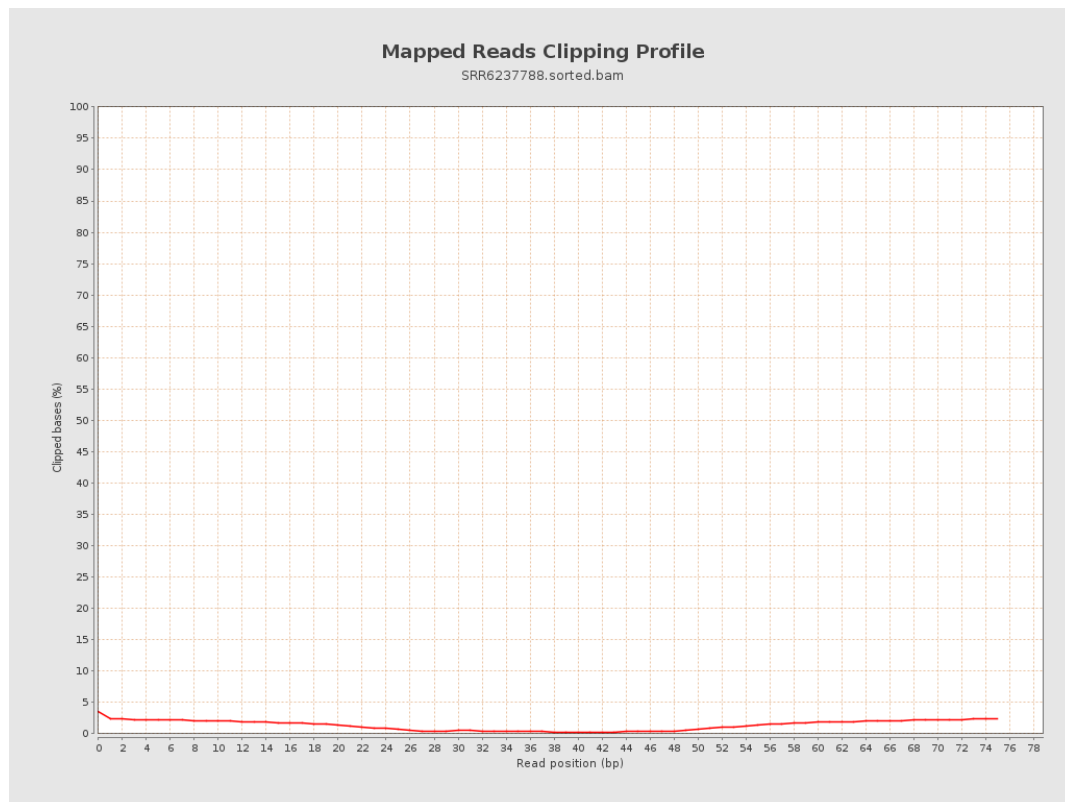
8. Results : Mapped Reads Nucleotide Content



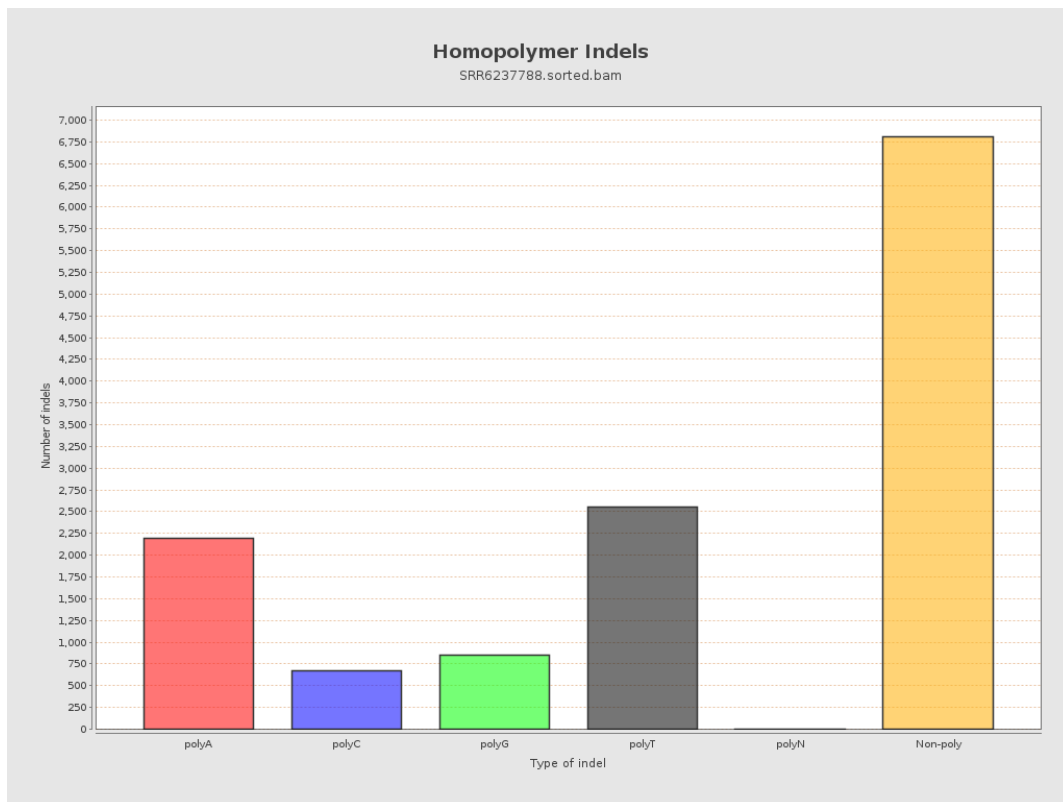
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

