

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 21:11:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236113.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_SRR6236113 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236113.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 21:11:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236113.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,979,741
Mapped reads	3,284,423 / 82.53%
Unmapped reads	695,318 / 17.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,945 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	259,523 / 6.52%
Duplication rate	6.28%
Clipped reads	1,657,873 / 41.66%

2.2. ACGT Content

Number/percentage of A's	57,236,701 / 26.84%
Number/percentage of C's	38,387,912 / 18%
Number/percentage of T's	68,151,985 / 31.95%
Number/percentage of G's	49,388,319 / 23.16%
Number/percentage of N's	119,130 / 0.06%
GC Percentage	41.15%

2.3. Coverage

Mean	0.0689

Standard Deviation	0.6188
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2.4. Mapping Quality

Mean Mapping Quality	44.92
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2.5. Mismatches and indels

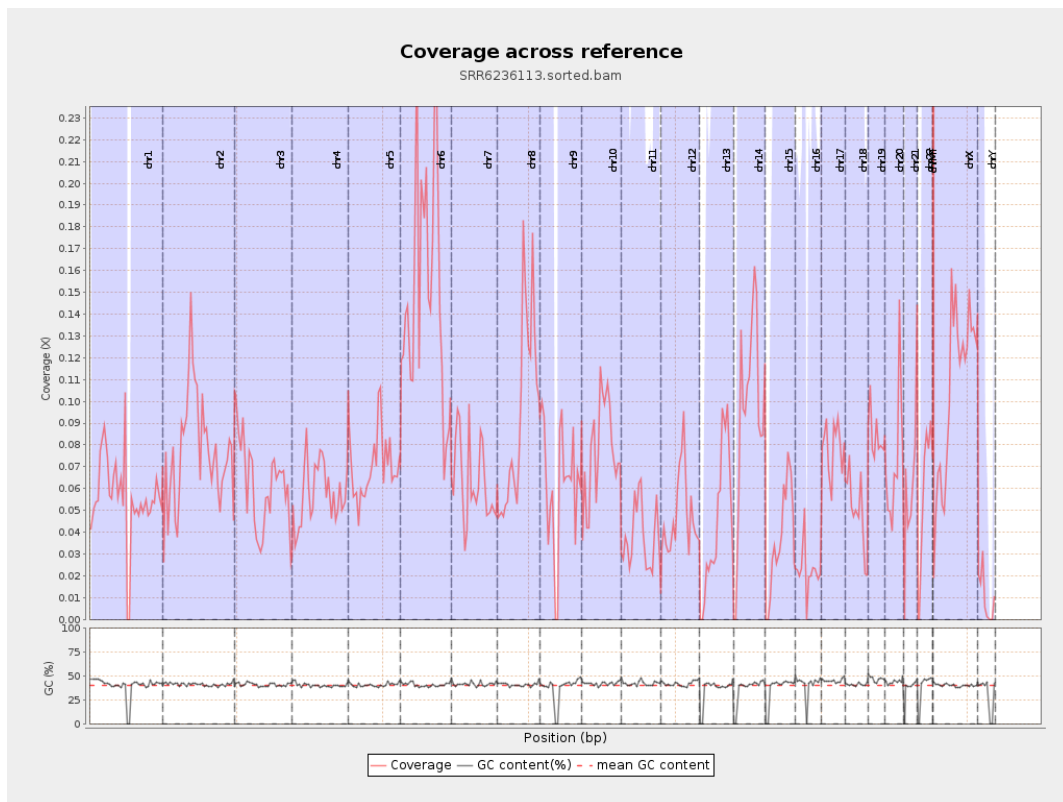
General error rate	0.86%
Mismatches	1,803,175
Insertions	14,960
Mapped reads with at least one insertion	0.45%
Deletions	67,471
Mapped reads with at least one deletion	2.03%
Homopolymer indels	45.59%

2.6. Chromosome stats

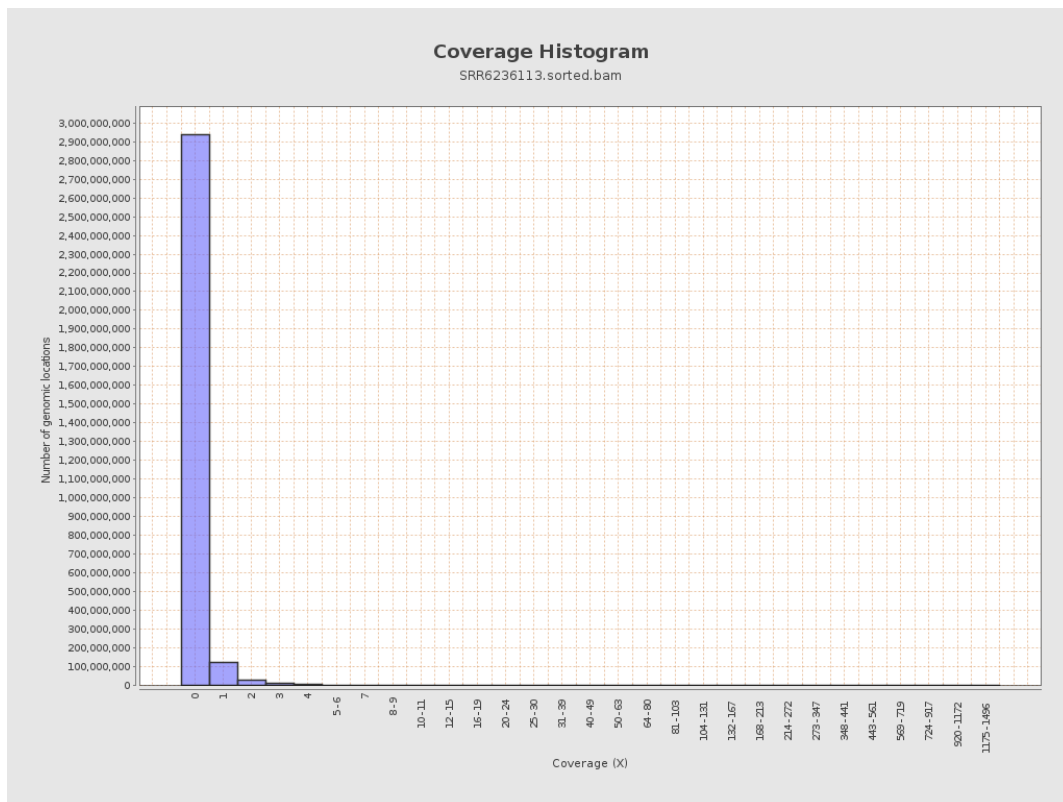
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	13944503	0.0559	1.2071
chr2	243199373	18783560	0.0772	0.6785
chr3	198022430	12179880	0.0615	0.3159
chr4	191154276	11083850	0.058	0.3512
chr5	180915260	12745332	0.0704	0.3433
chr6	171115067	25789680	0.1507	0.9781
chr7	159138663	10063711	0.0632	0.7198

chr8	146364022	13738180	0.0939	0.6314
chr9	141213431	8655047	0.0613	0.5149
chr10	135534747	10425807	0.0769	0.4722
chr11	135006516	5083039	0.0377	0.414
chr12	133851895	6387863	0.0477	0.2937
chr13	115169878	5138392	0.0446	0.2712
chr14	107349540	10295442	0.0959	0.4287
chr15	102531392	3755944	0.0366	0.2642
chr16	90354753	2011965	0.0223	0.2932
chr17	81195210	6469360	0.0797	0.444
chr18	78077248	3905949	0.05	1.0153
chr19	59128983	4980319	0.0842	0.7338
chr20	63025520	4619185	0.0733	0.3554
chr21	48129895	3050494	0.0634	0.3628
chr22	51304566	2952334	0.0575	0.305
chrMT	16571	271801	16.4022	9.5352
chrX	155270560	16454291	0.106	0.488
chrY	59373566	615186	0.0104	0.2245

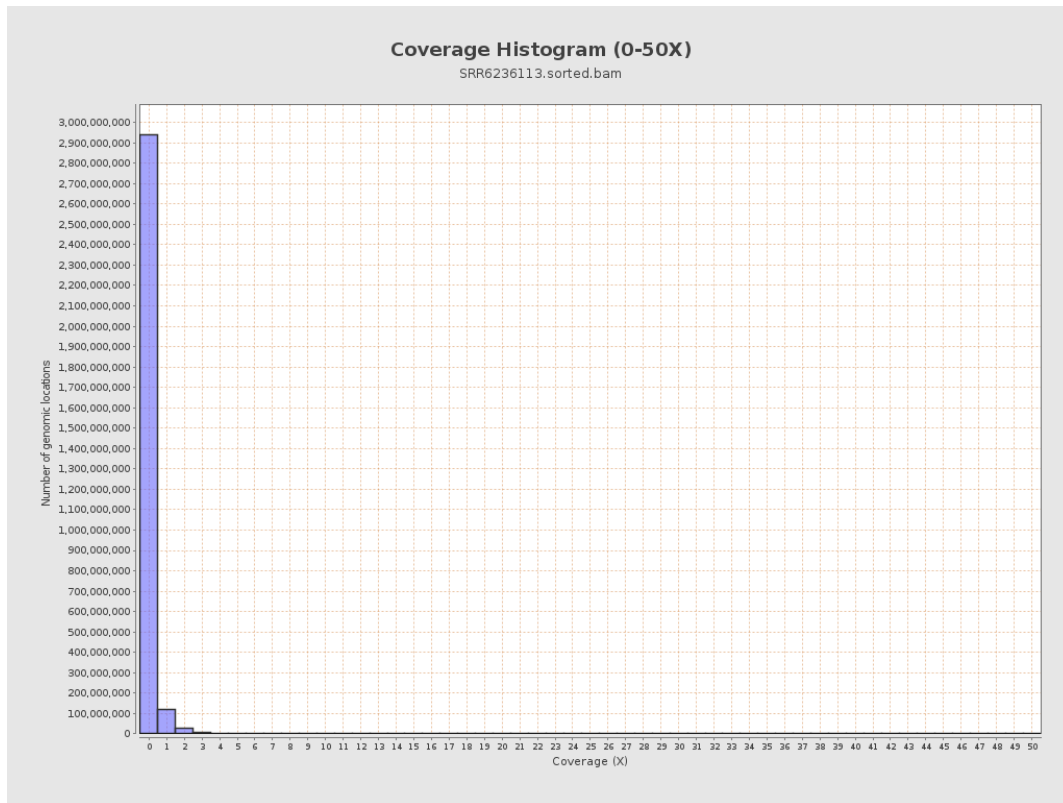
3. Results : Coverage across reference



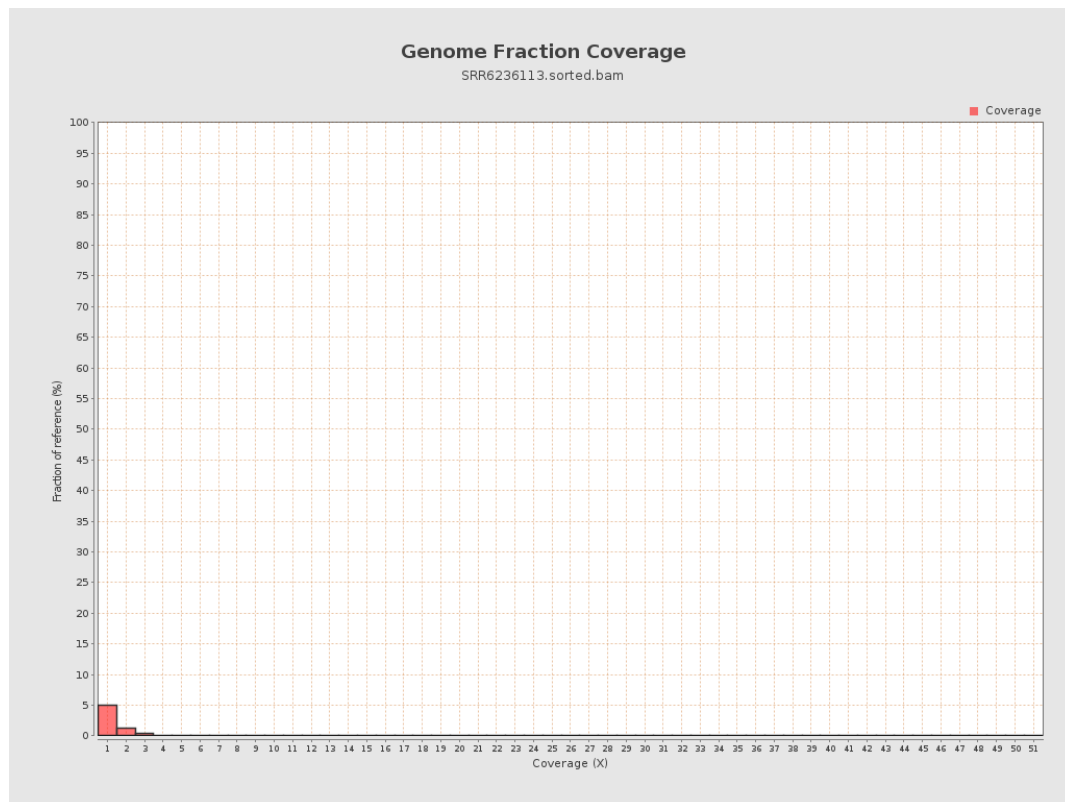
4. Results : Coverage Histogram



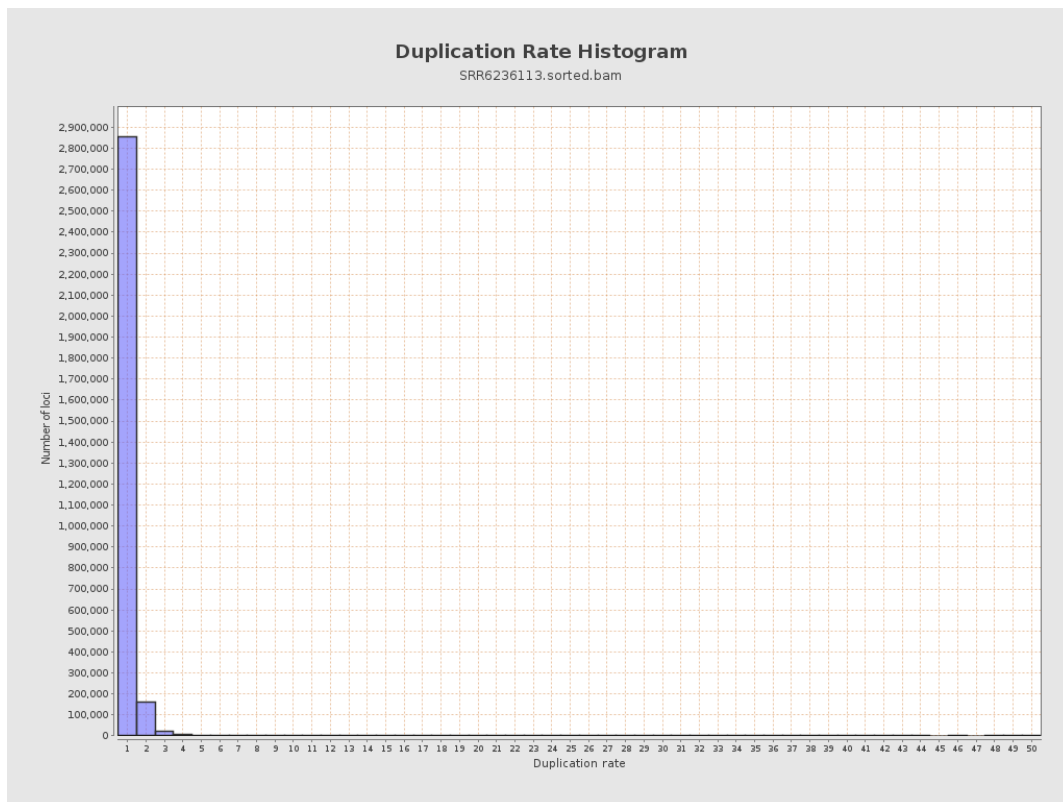
5. Results : Coverage Histogram (0-50X)



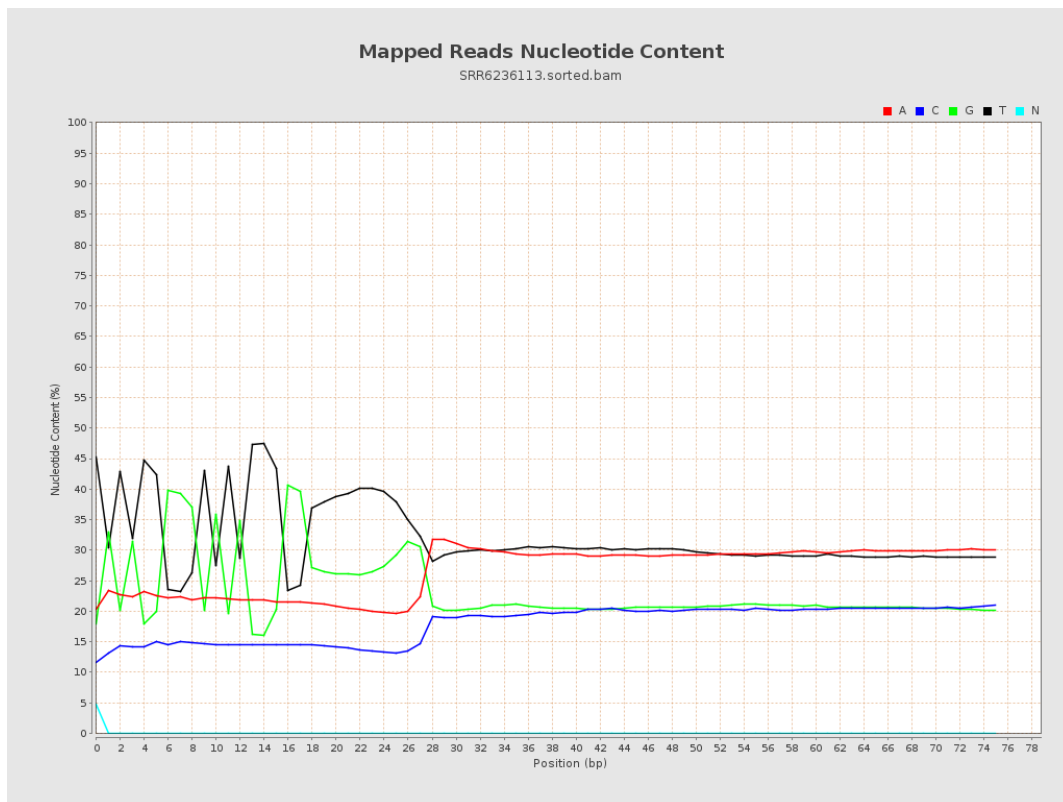
6. Results : Genome Fraction Coverage



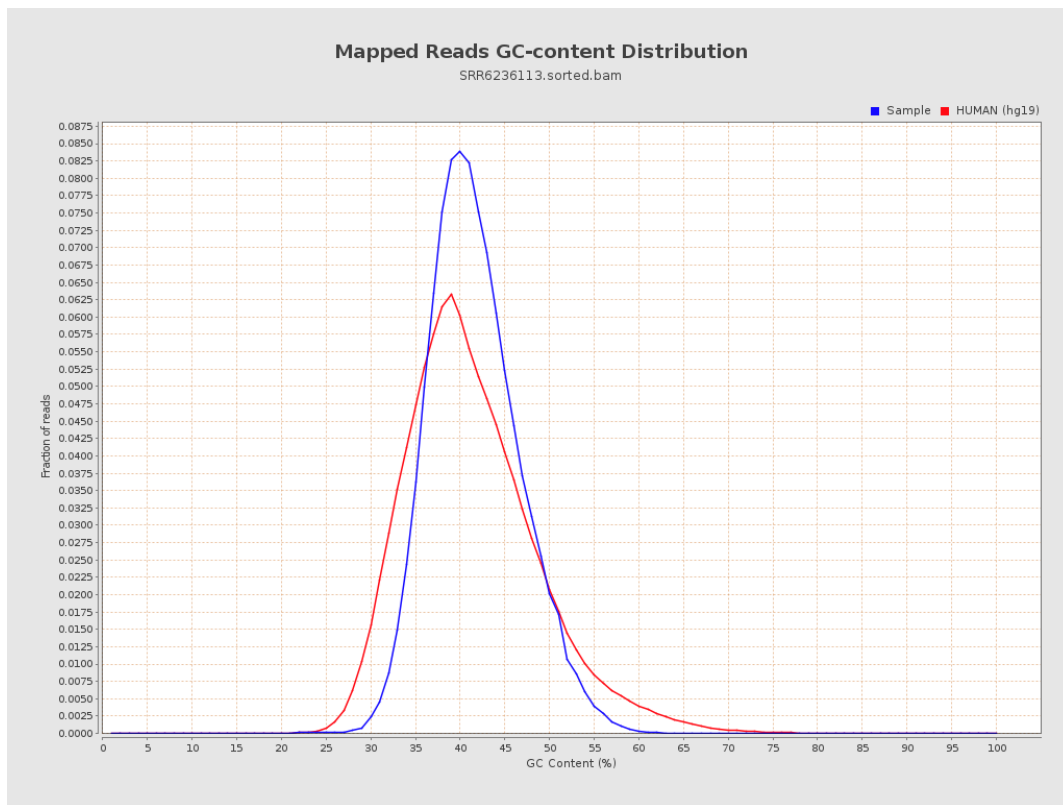
7. Results : Duplication Rate Histogram



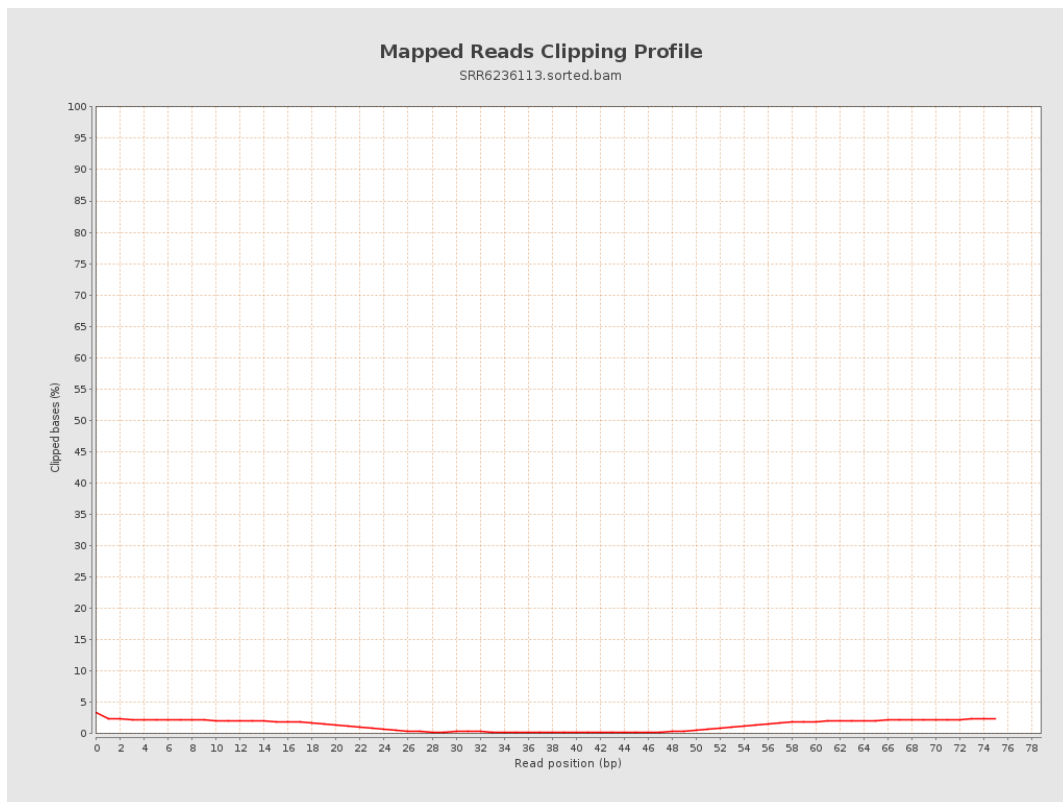
8. Results : Mapped Reads Nucleotide Content



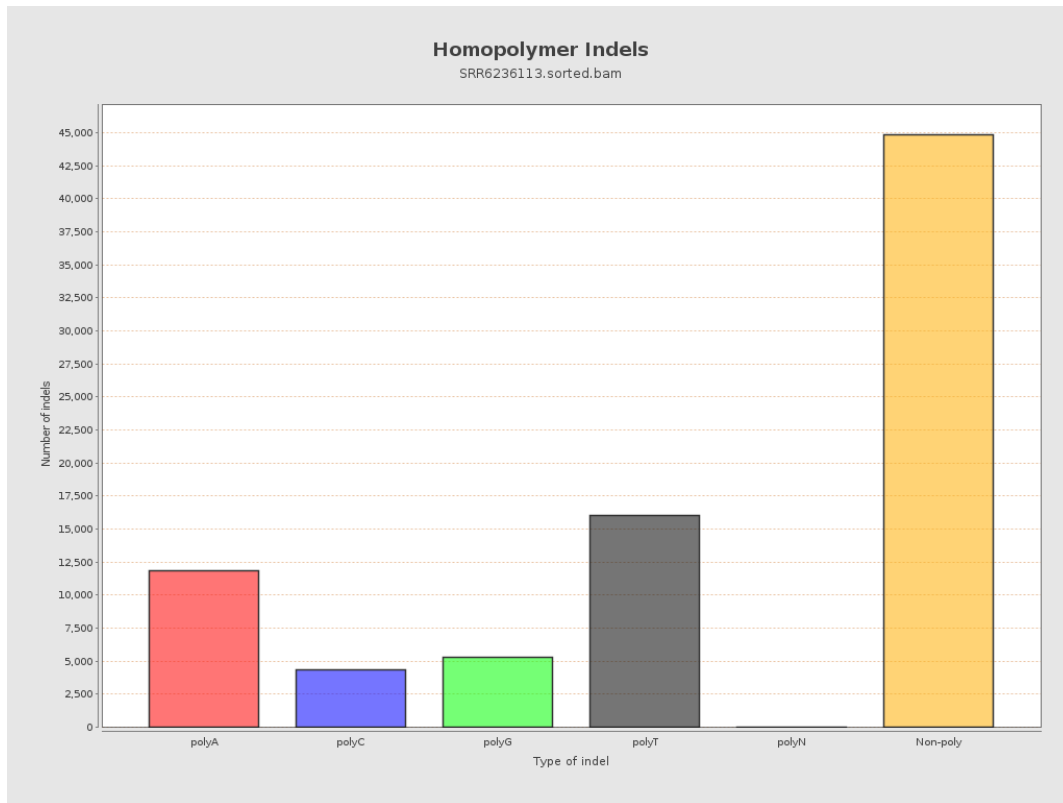
9. Results : Mapped Reads GC-content Distribution



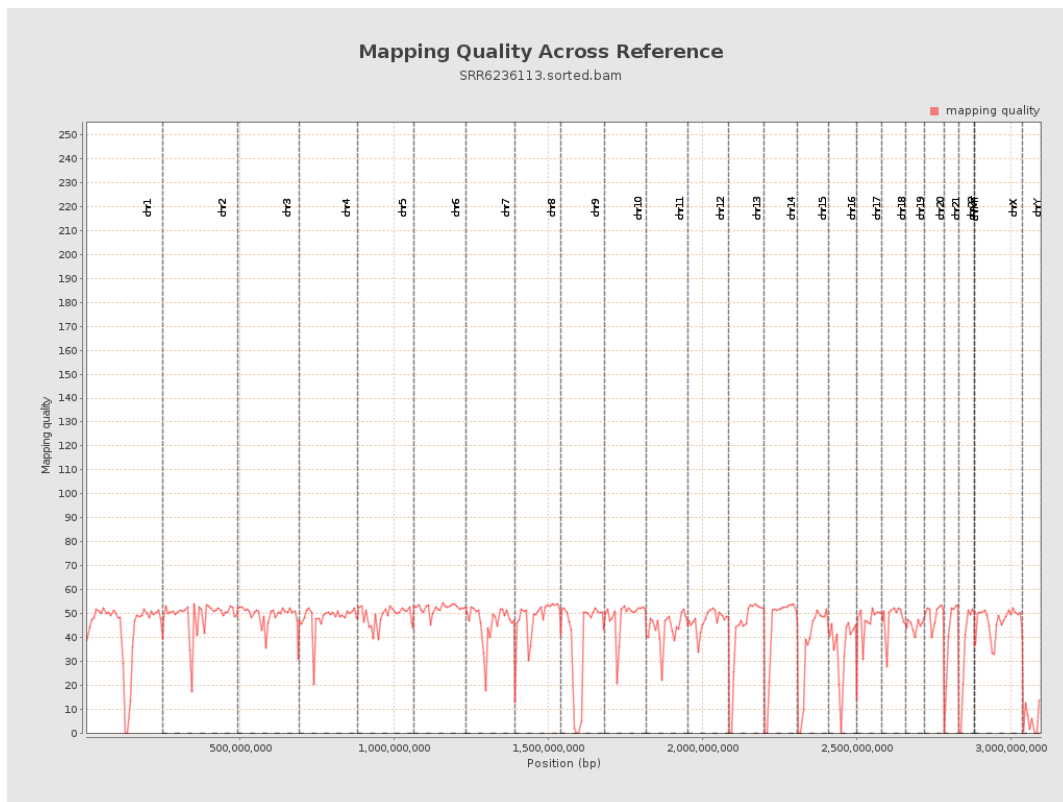
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

