

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 14:10:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013173.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_SRR6013173 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013173.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 14:10:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013173.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,259,086
Mapped reads	2,065,004 / 91.41%
Unmapped reads	194,082 / 8.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,074 / 0.62%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	52,383 / 2.32%
Duplication rate	1.85%
Clipped reads	1,019,141 / 45.11%

2.2. ACGT Content

Number/percentage of A's	37,014,357 / 27.39%
Number/percentage of C's	26,369,800 / 19.52%
Number/percentage of T's	40,466,851 / 29.95%
Number/percentage of G's	31,240,994 / 23.12%
Number/percentage of N's	32,927 / 0.02%
GC Percentage	42.64%

2.3. Coverage

Mean	0.0437

Standard Deviation	0.3254
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2.4. Mapping Quality

Mean Mapping Quality	43.64
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2.5. Mismatches and indels

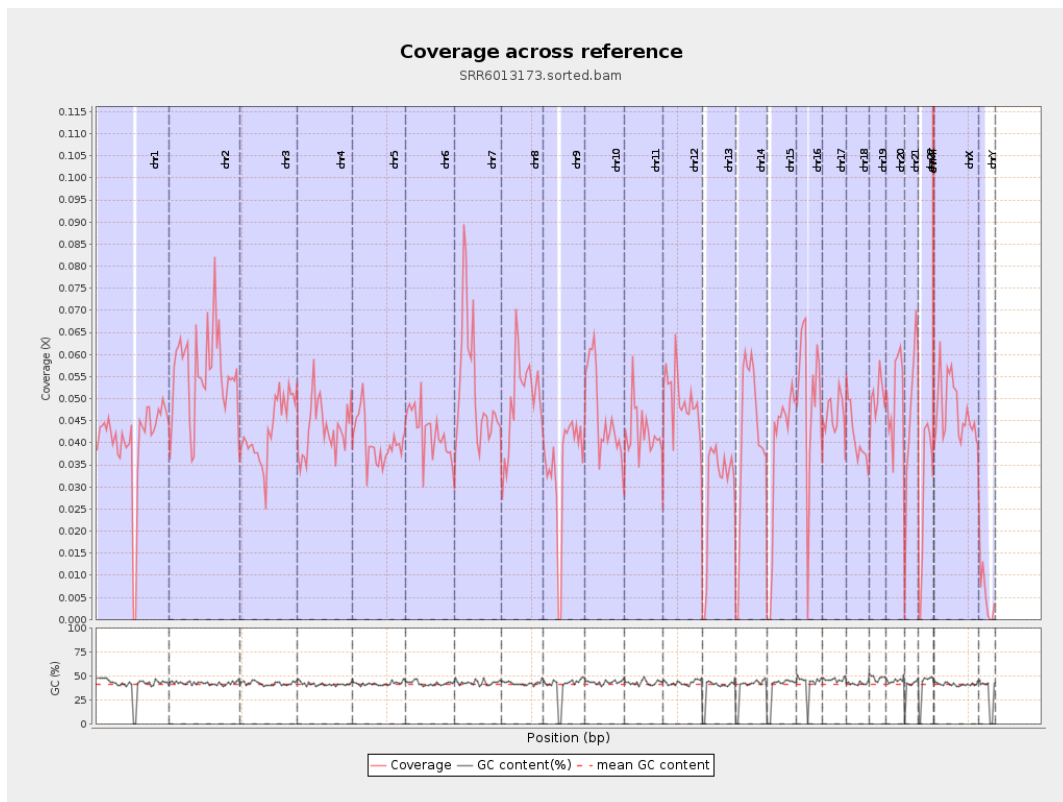
General error rate	0.76%
Mismatches	1,013,602
Insertions	9,468
Mapped reads with at least one insertion	0.45%
Deletions	28,400
Mapped reads with at least one deletion	1.36%
Homopolymer indels	45.56%

2.6. Chromosome stats

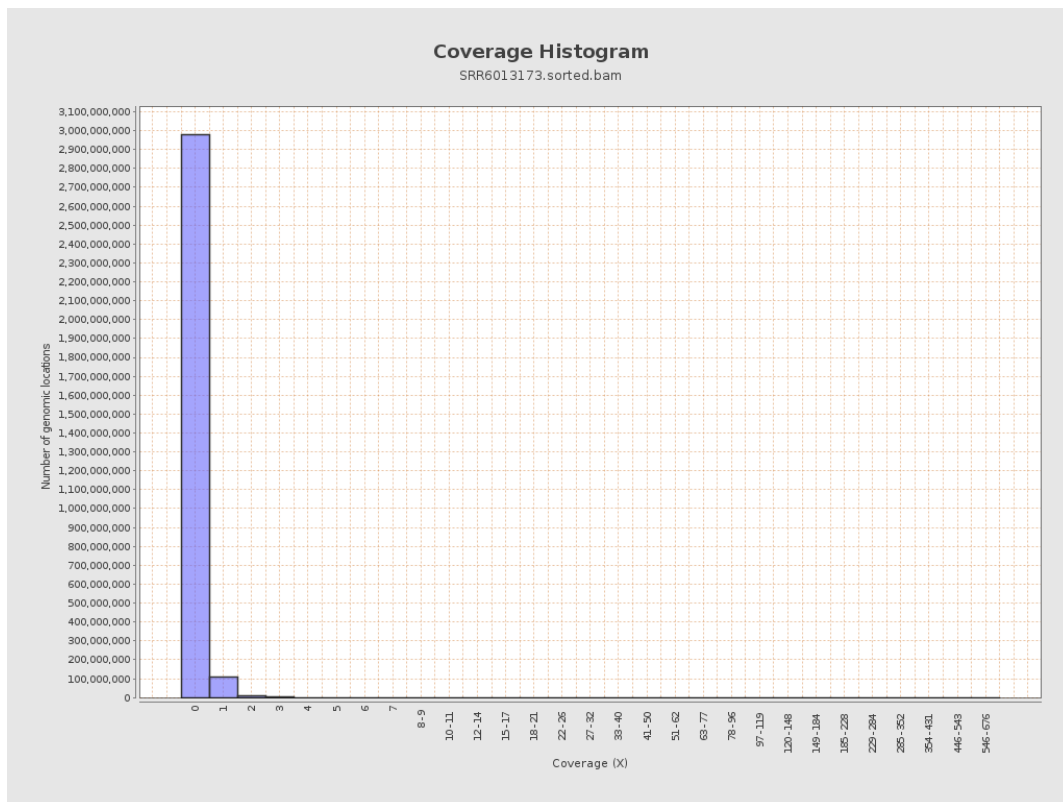
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10063286	0.0404	0.3802
chr2	243199373	13516398	0.0556	0.4424
chr3	198022430	8494490	0.0429	0.2271
chr4	191154276	8236843	0.0431	0.2322
chr5	180915260	7273604	0.0402	0.2214
chr6	171115067	7221196	0.0422	0.2709
chr7	159138663	8320218	0.0523	0.587

chr8	146364022	7264258	0.0496	0.3196
chr9	141213431	4877609	0.0345	0.2677
chr10	135534747	6331209	0.0467	0.3193
chr11	135006516	5716309	0.0423	0.2726
chr12	133851895	6654823	0.0497	0.2502
chr13	115169878	3387935	0.0294	0.1913
chr14	107349540	4467470	0.0416	0.2421
chr15	102531392	3865644	0.0377	0.2308
chr16	90354753	4597463	0.0509	0.2825
chr17	81195210	3739204	0.0461	0.2475
chr18	78077248	3237296	0.0415	0.4718
chr19	59128983	2971756	0.0503	0.3443
chr20	63025520	3168403	0.0503	0.2513
chr21	48129895	2248150	0.0467	0.254
chr22	51304566	1473118	0.0287	0.1864
chrMT	16571	408361	24.6431	21.6202
chrX	155270560	7311425	0.0471	0.2548
chrY	59373566	327896	0.0055	0.1014

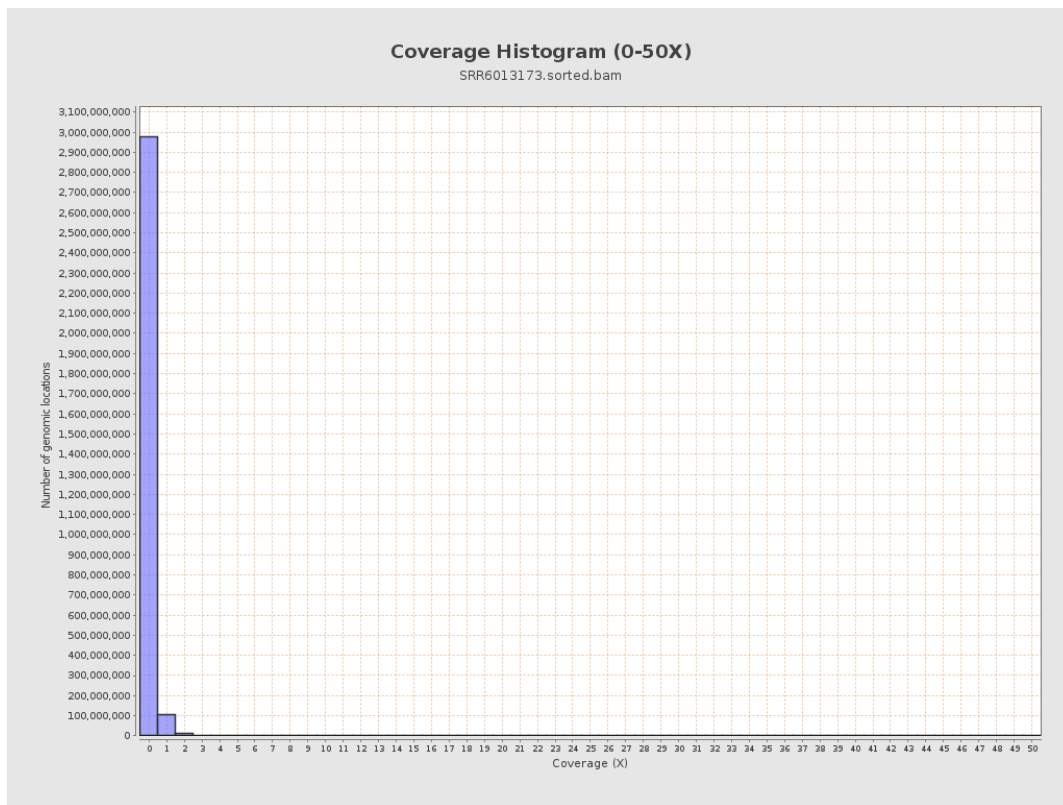
3. Results : Coverage across reference



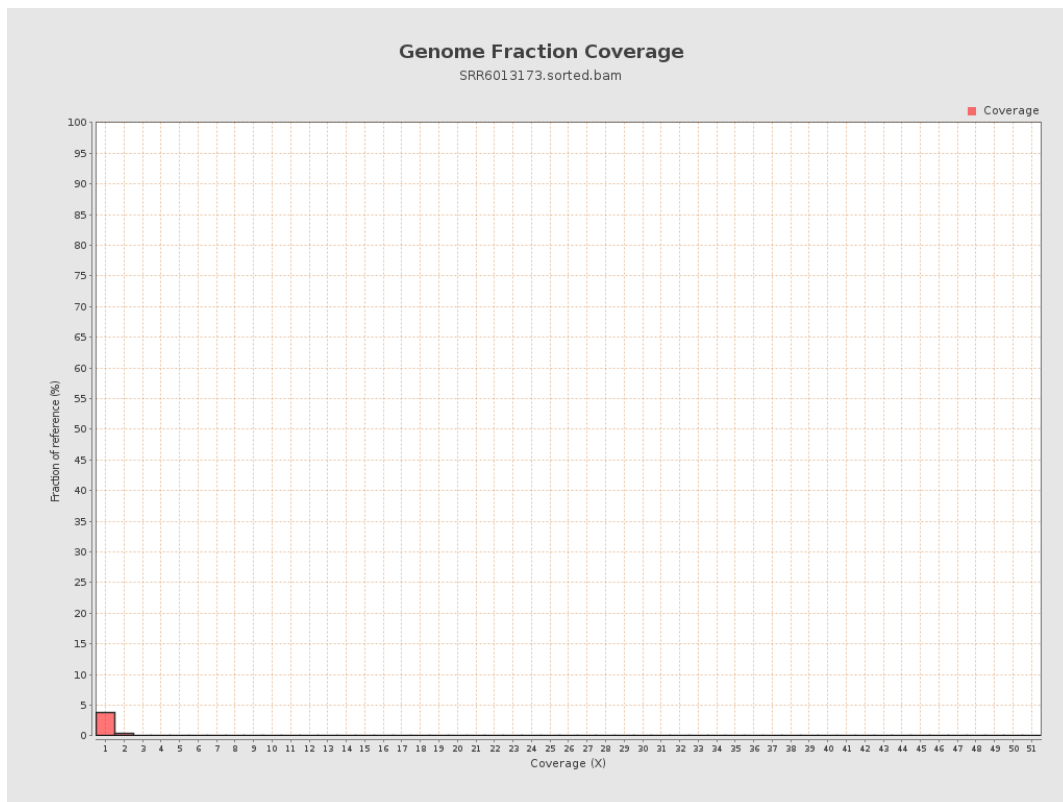
4. Results : Coverage Histogram



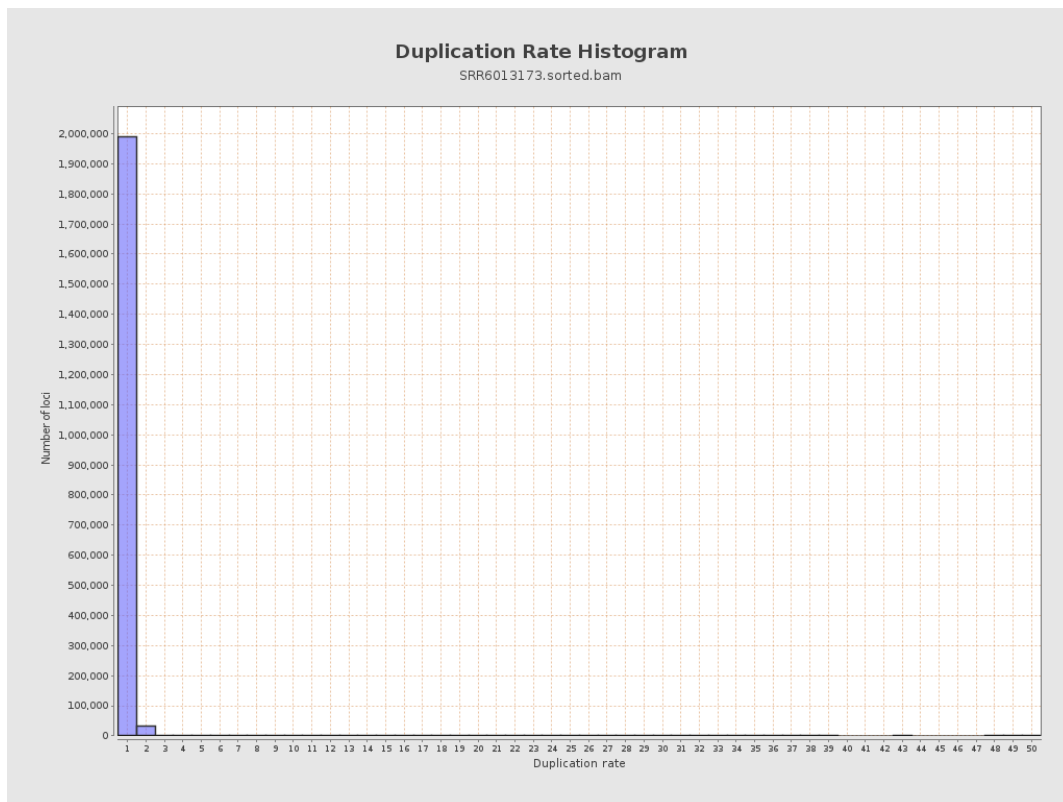
5. Results : Coverage Histogram (0-50X)



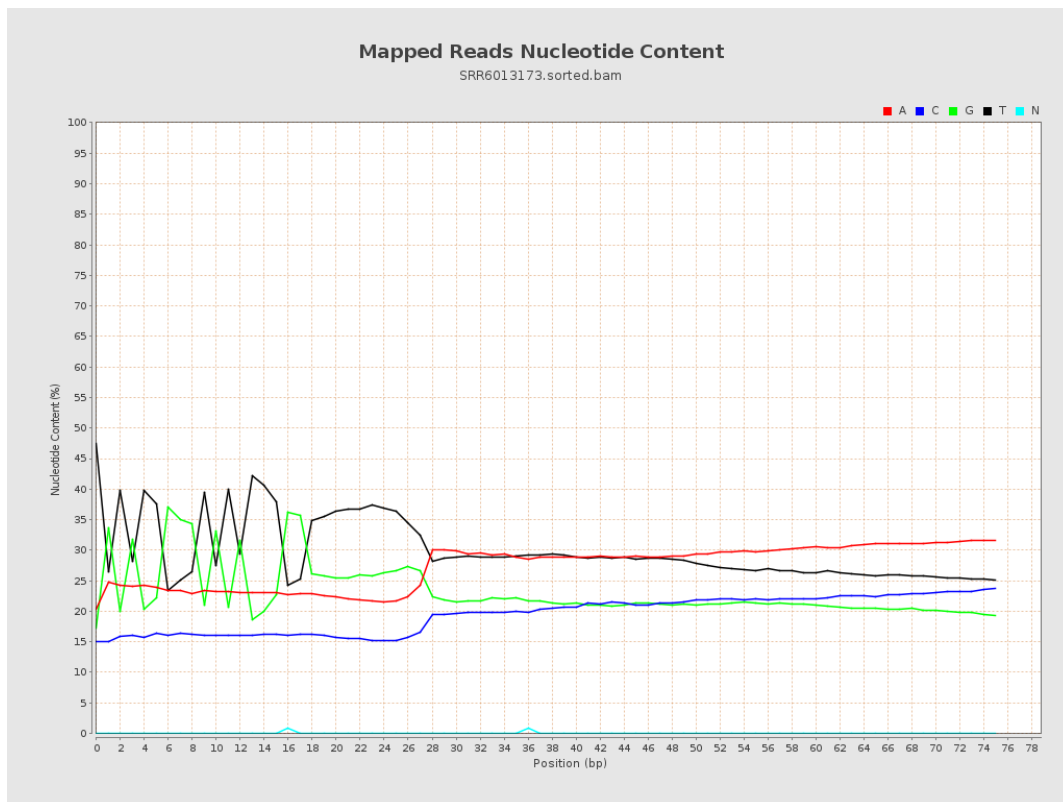
6. Results : Genome Fraction Coverage



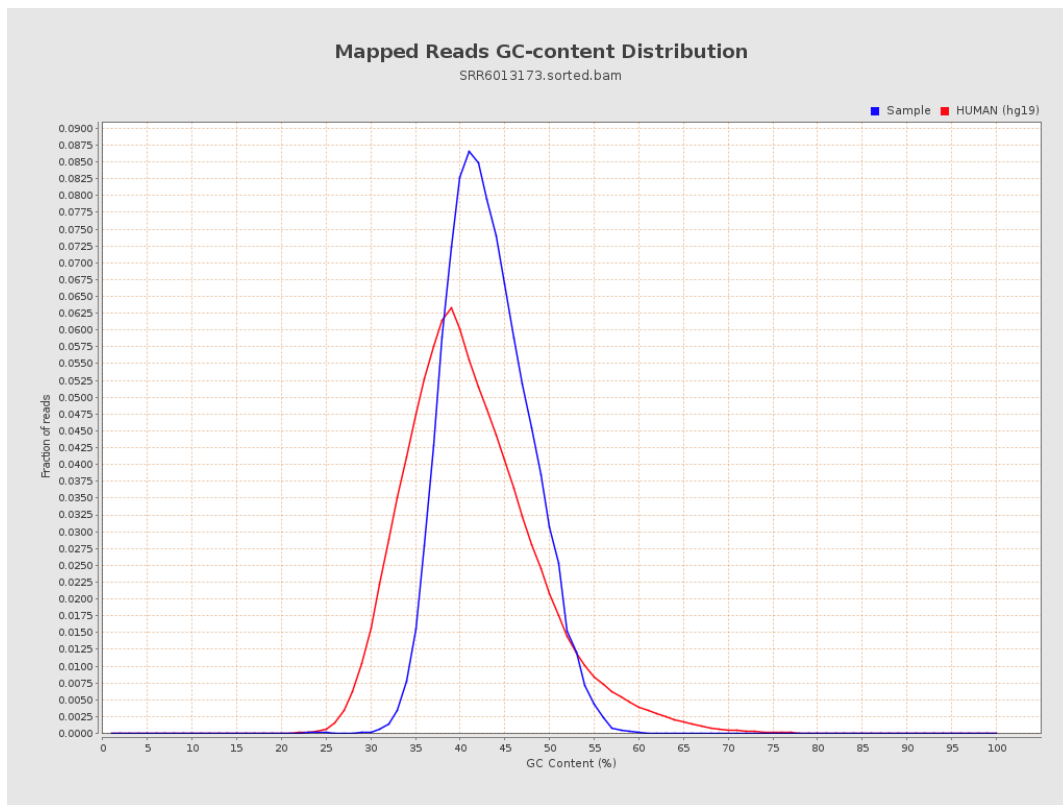
7. Results : Duplication Rate Histogram



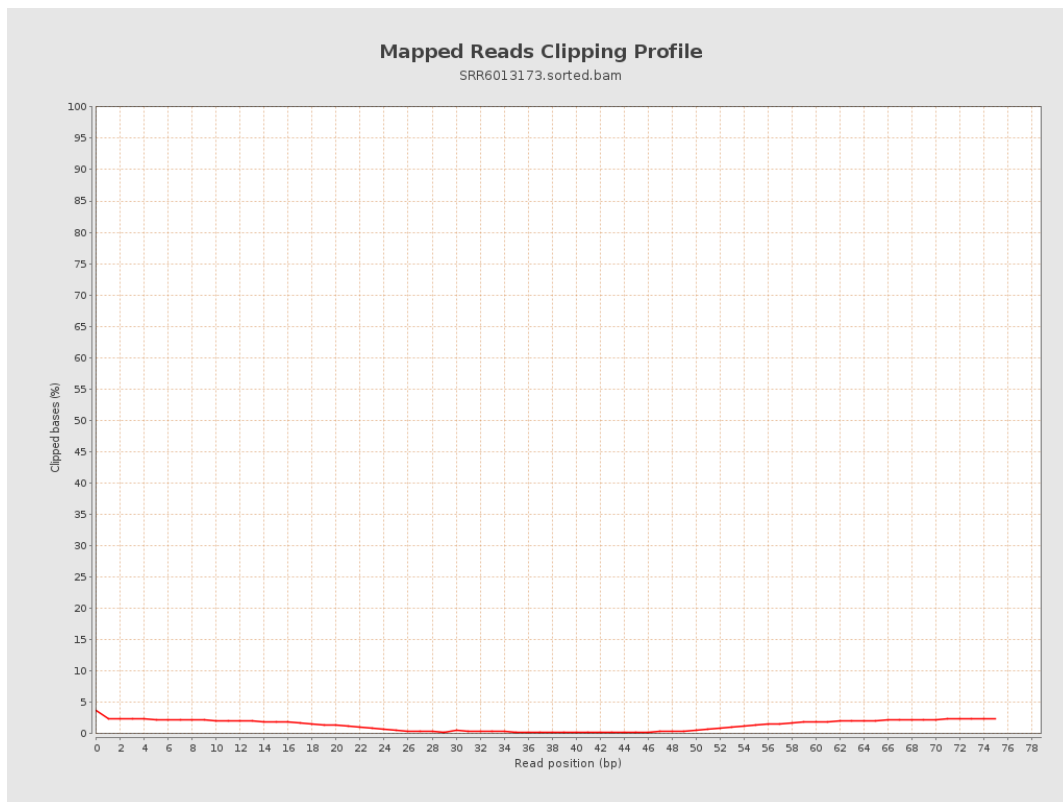
8. Results : Mapped Reads Nucleotide Content



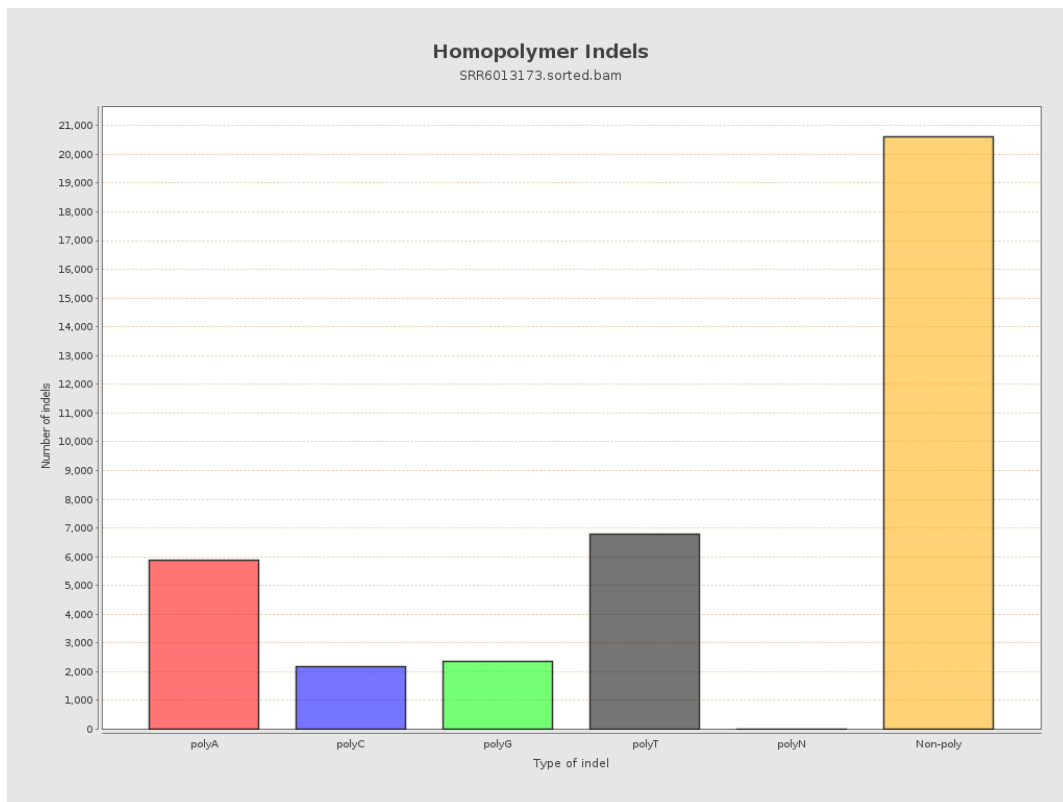
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

