

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 03:10:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063573.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_SRR6063573 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063573.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 03:10:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063573.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,844,736
Mapped reads	2,588,186 / 90.98%
Unmapped reads	256,550 / 9.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,921 / 0.88%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	131,066 / 4.61%
Duplication rate	4.11%
Clipped reads	1,190,982 / 41.87%

2.2. ACGT Content

Number/percentage of A's	51,247,599 / 29.58%
Number/percentage of C's	32,076,592 / 18.51%
Number/percentage of T's	54,583,815 / 31.5%
Number/percentage of G's	35,352,241 / 20.4%
Number/percentage of N's	5,032 / 0%
GC Percentage	38.92%

2.3. Coverage

Mean	0.056

Standard Deviation	0.47
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2.4. Mapping Quality

Mean Mapping Quality	45.56
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2.5. Mismatches and indels

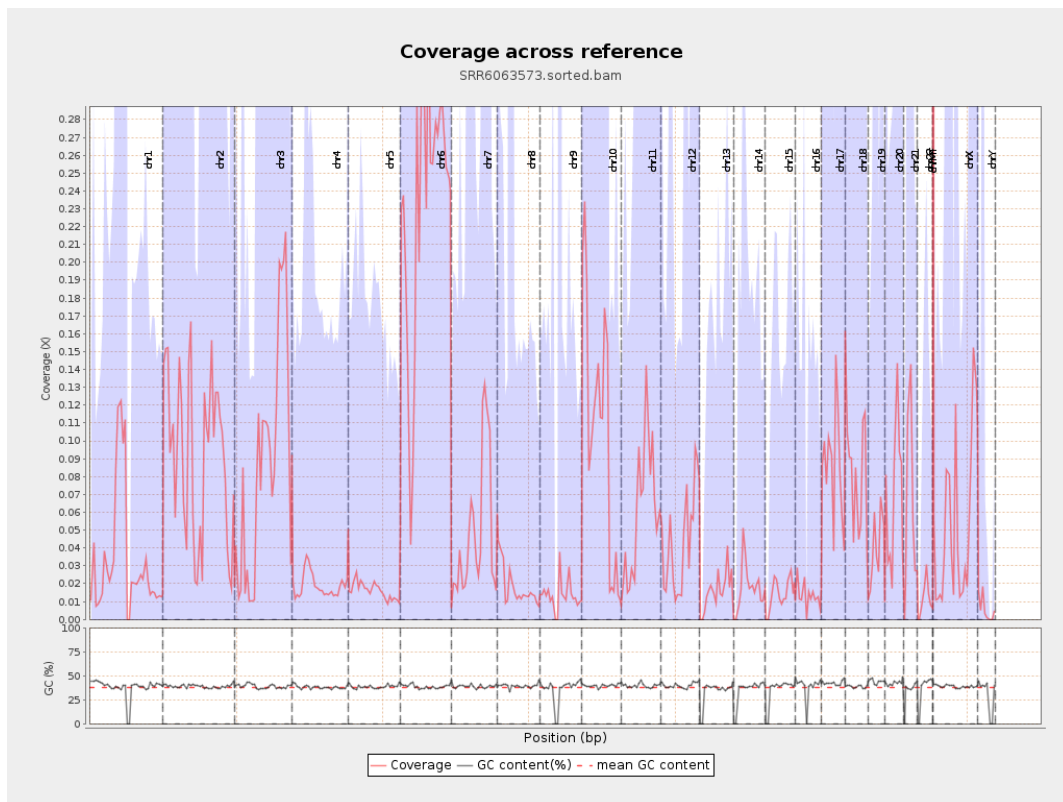
General error rate	0.82%
Mismatches	1,397,411
Insertions	12,325
Mapped reads with at least one insertion	0.47%
Deletions	46,554
Mapped reads with at least one deletion	1.78%
Homopolymer indels	46.13%

2.6. Chromosome stats

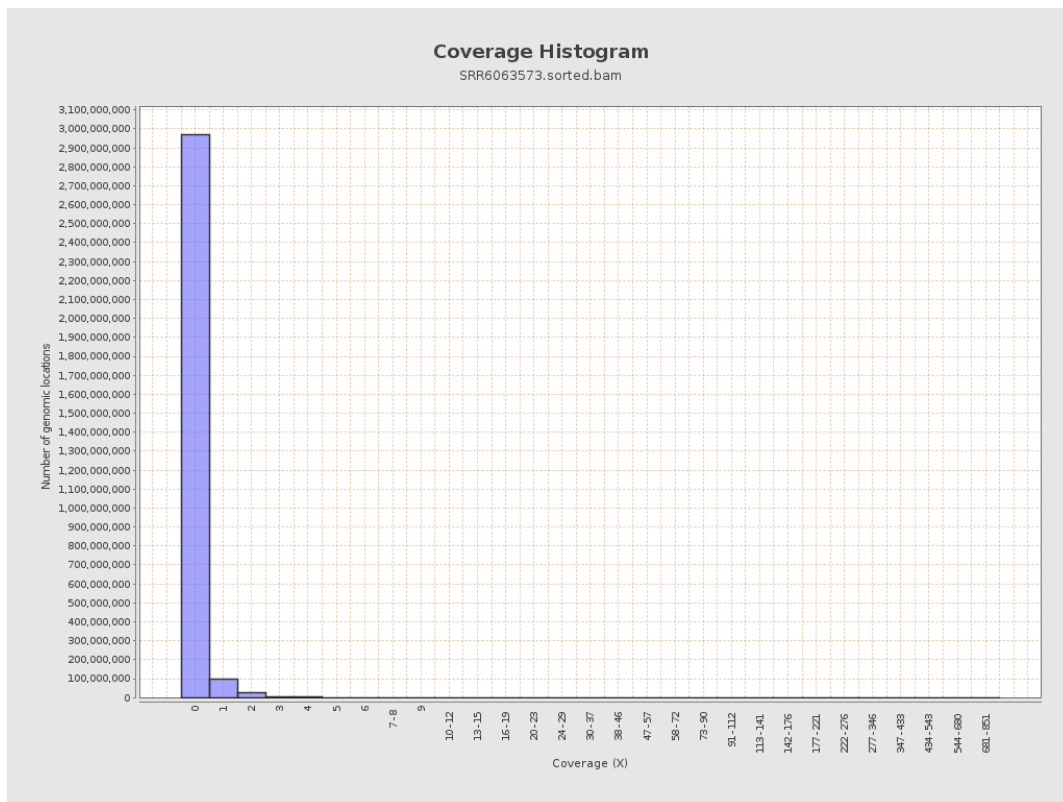
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8108049	0.0325	0.7461
chr2	243199373	22487206	0.0925	0.6302
chr3	198022430	17079039	0.0862	0.3695
chr4	191154276	3619633	0.0189	0.1838
chr5	180915260	3005144	0.0166	0.165
chr6	171115067	40013216	0.2338	1.0125
chr7	159138663	7544076	0.0474	0.371

chr8	146364022	2616884	0.0179	0.5187
chr9	141213431	1918975	0.0136	0.2986
chr10	135534747	14223234	0.1049	0.5054
chr11	135006516	8259223	0.0612	0.3415
chr12	133851895	5630844	0.0421	0.2678
chr13	115169878	1901419	0.0165	0.1592
chr14	107349540	1969529	0.0183	0.1737
chr15	102531392	1436879	0.014	0.1462
chr16	90354753	1198314	0.0133	0.1531
chr17	81195210	7105154	0.0875	0.3888
chr18	78077248	6469807	0.0829	0.5176
chr19	59128983	2305668	0.039	0.5459
chr20	63025520	4442780	0.0705	0.3364
chr21	48129895	2924230	0.0608	0.319
chr22	51304566	609851	0.0119	0.132
chrMT	16571	32490	1.9607	2.3003
chrX	155270560	8103427	0.0522	0.3122
chrY	59373566	337533	0.0057	0.2155

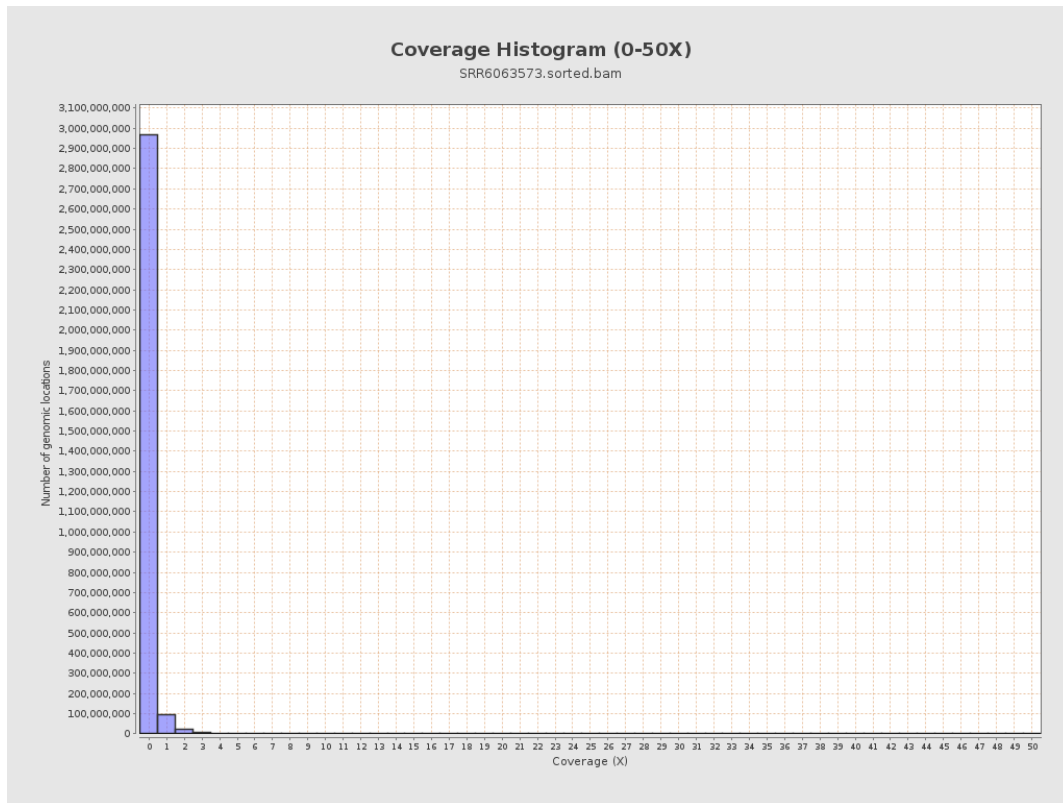
3. Results : Coverage across reference



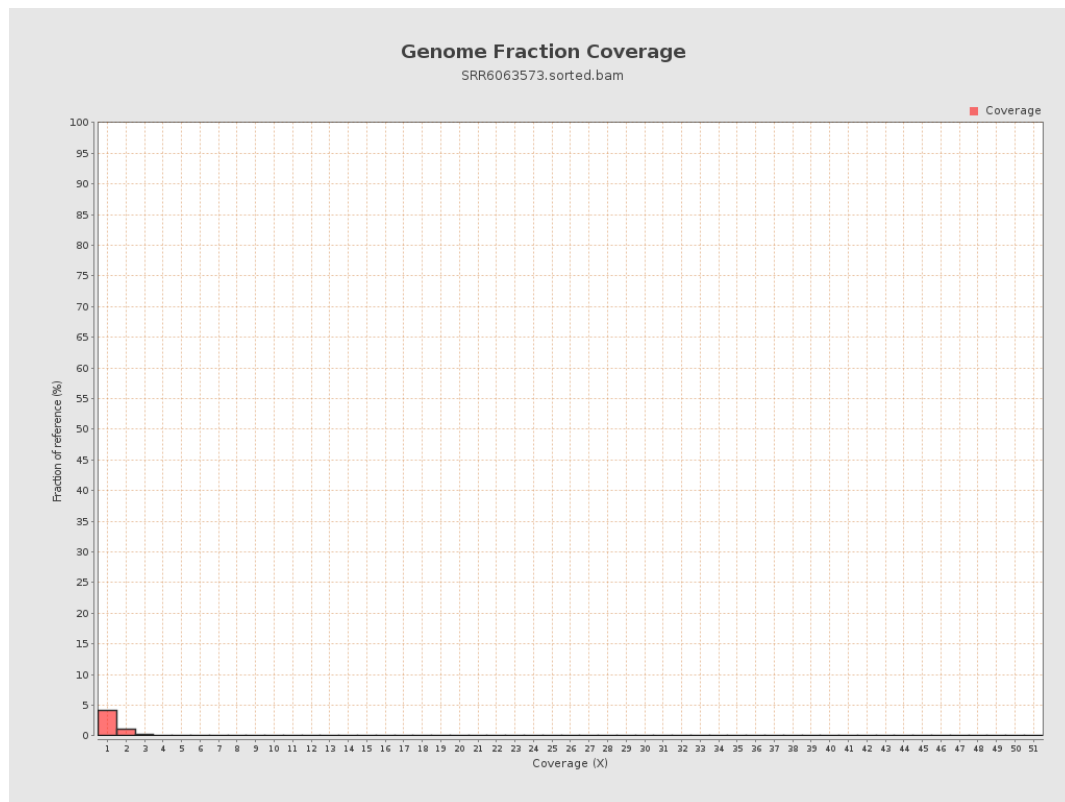
4. Results : Coverage Histogram



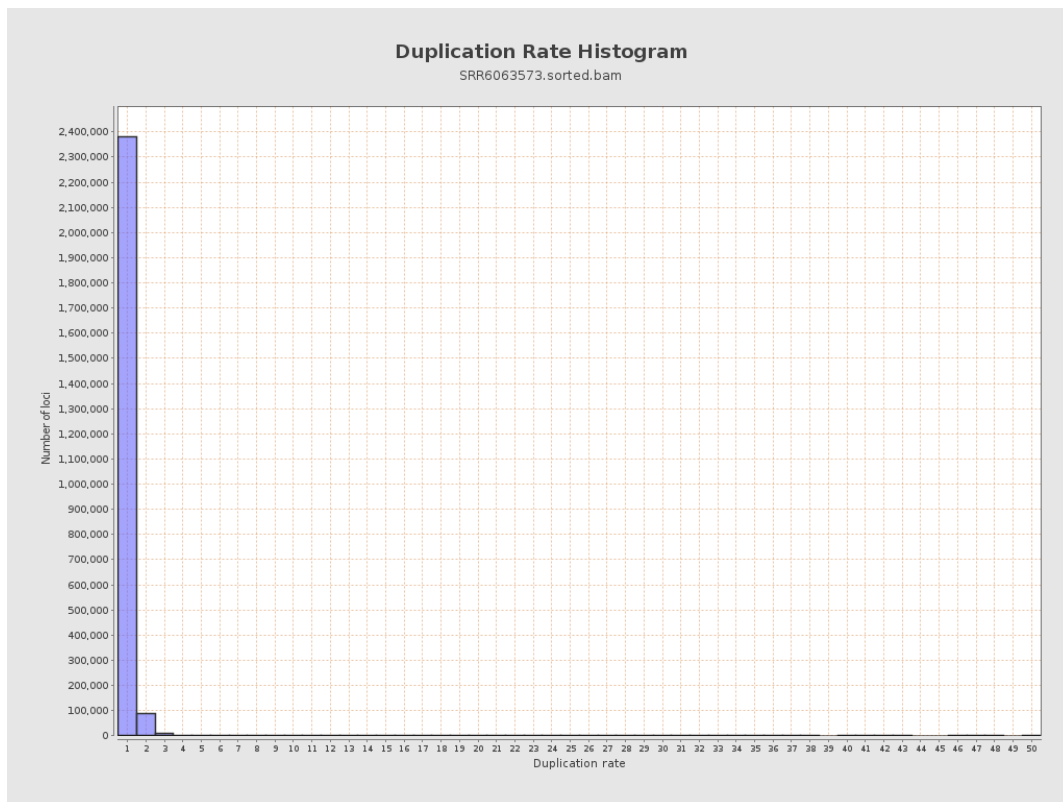
5. Results : Coverage Histogram (0-50X)



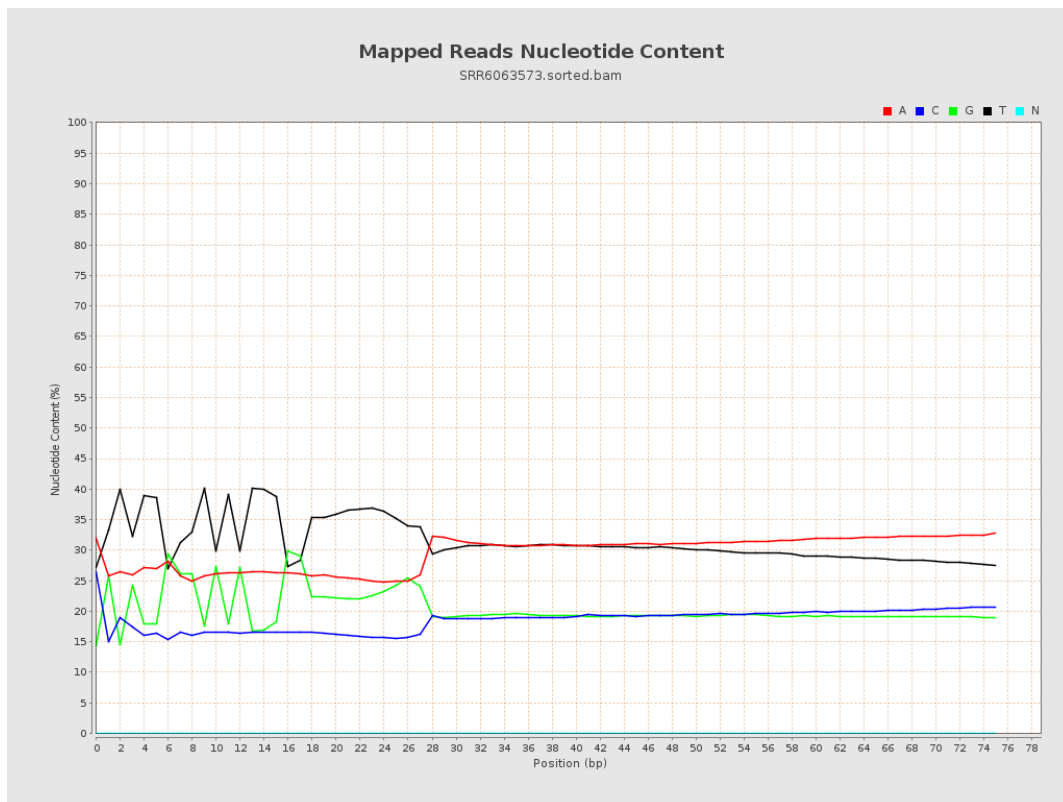
6. Results : Genome Fraction Coverage



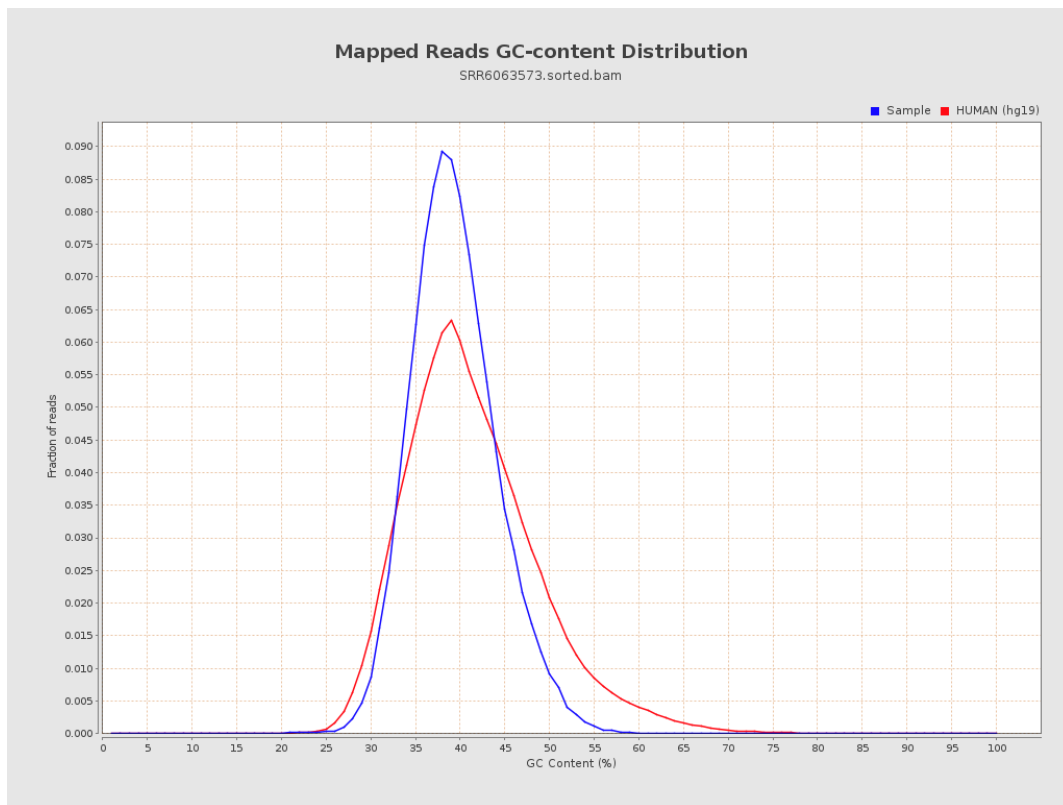
7. Results : Duplication Rate Histogram



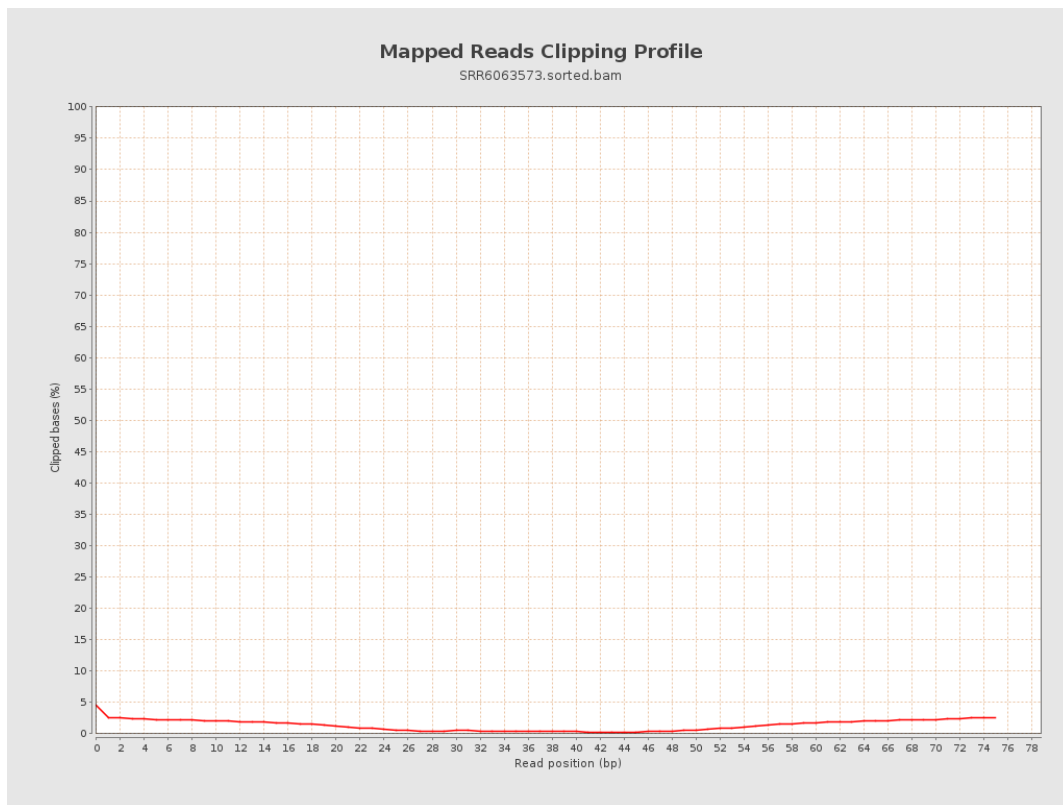
8. Results : Mapped Reads Nucleotide Content



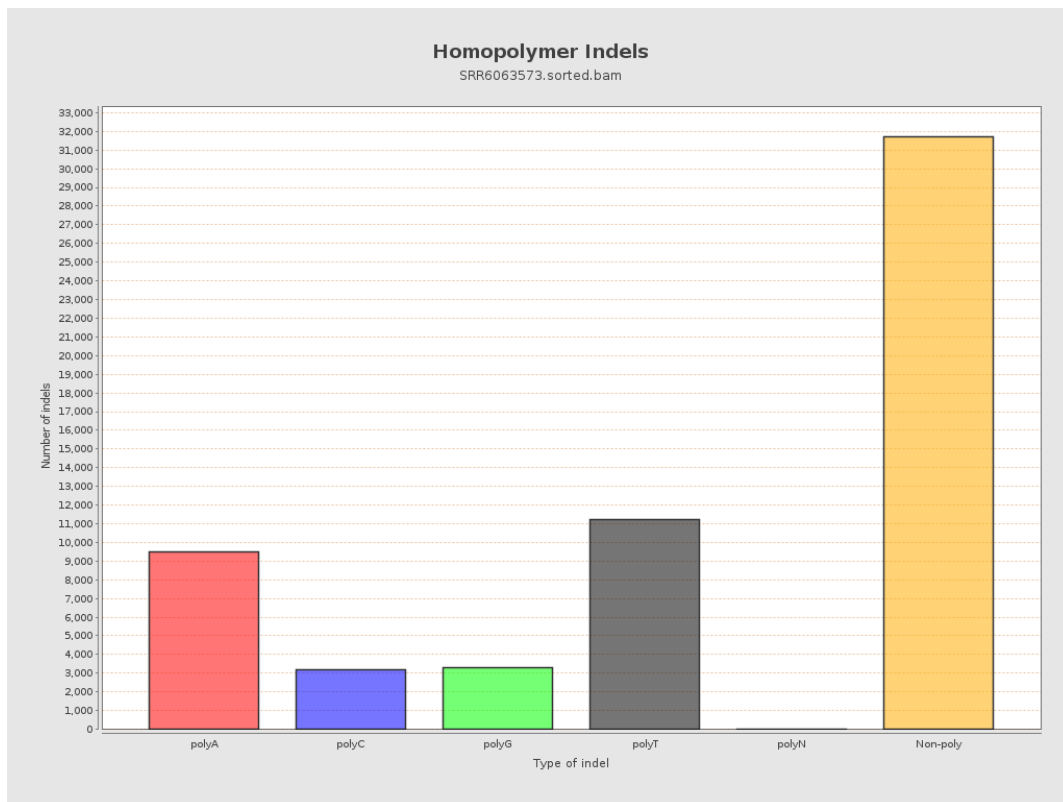
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

