

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 18:12:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013255.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_SRR6013255 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013255.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 18:12:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013255.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,194,850
Mapped reads	979,489 / 81.98%
Unmapped reads	215,361 / 18.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,805 / 0.57%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	72,441 / 6.06%
Duplication rate	6.36%
Clipped reads	559,049 / 46.79%

2.2. ACGT Content

Number/percentage of A's	16,915,343 / 27.16%
Number/percentage of C's	10,916,842 / 17.53%
Number/percentage of T's	20,522,707 / 32.95%
Number/percentage of G's	13,934,842 / 22.37%
Number/percentage of N's	713 / 0%
GC Percentage	39.9%

2.3. Coverage

Mean	0.0201

Standard Deviation	0.2276
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2.4. Mapping Quality

Mean Mapping Quality	46.38
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2.5. Mismatches and indels

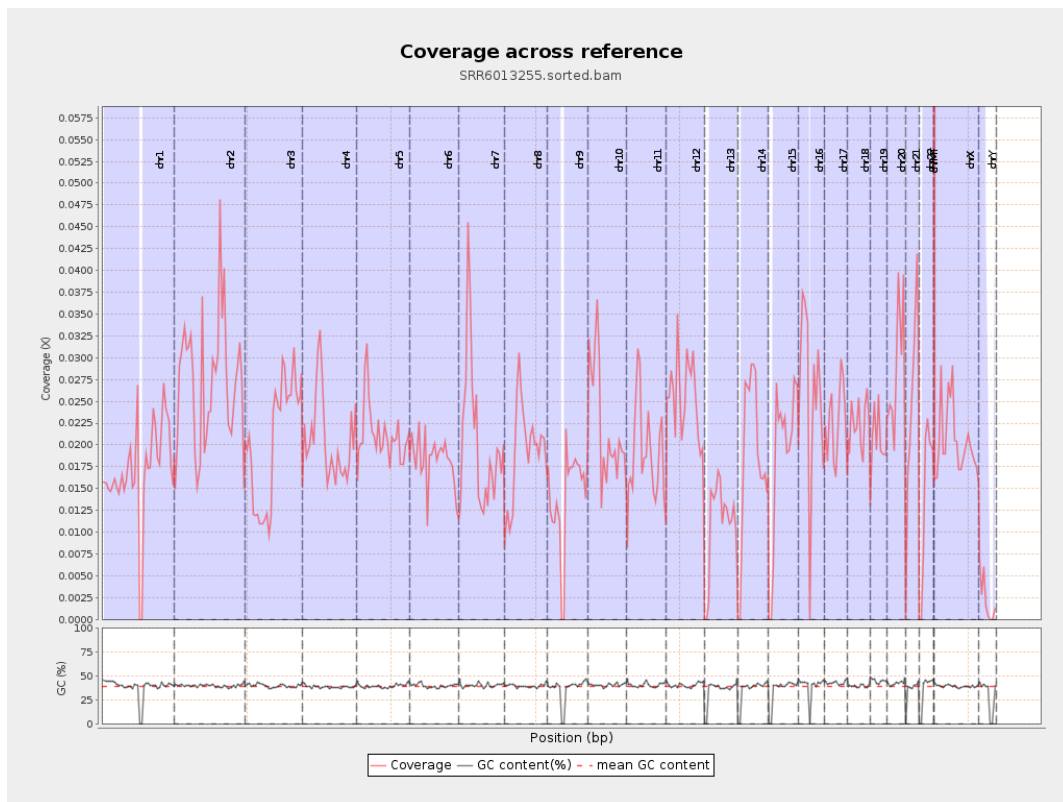
General error rate	0.82%
Mismatches	501,658
Insertions	4,396
Mapped reads with at least one insertion	0.45%
Deletions	19,468
Mapped reads with at least one deletion	1.96%
Homopolymer indels	47.42%

2.6. Chromosome stats

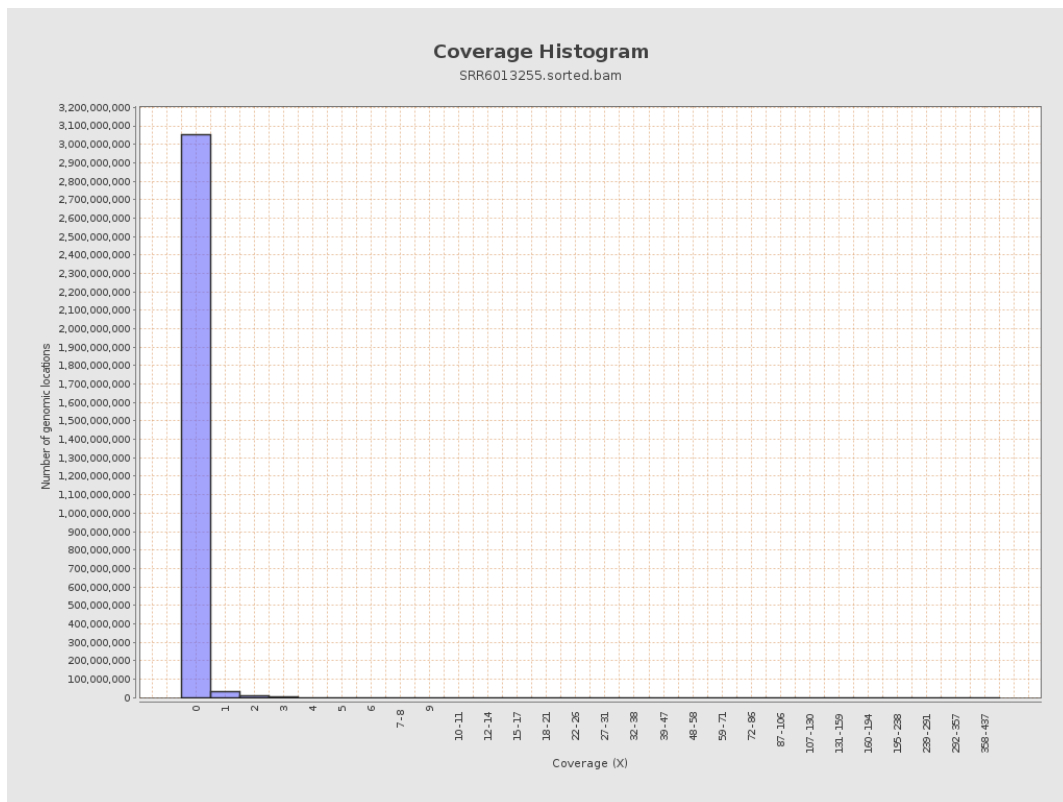
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4257163	0.0171	0.3275
chr2	243199373	6637743	0.0273	0.2901
chr3	198022430	4000097	0.0202	0.1859
chr4	191154276	3916228	0.0205	0.1907
chr5	180915260	3853904	0.0213	0.1923
chr6	171115067	3114687	0.0182	0.1914
chr7	159138663	3246094	0.0204	0.2377

chr8	146364022	2865819	0.0196	0.3156
chr9	141213431	1973379	0.014	0.1999
chr10	135534747	3026172	0.0223	0.2163
chr11	135006516	2582274	0.0191	0.2019
chr12	133851895	3413562	0.0255	0.2099
chr13	115169878	1263789	0.011	0.1373
chr14	107349540	2031471	0.0189	0.183
chr15	102531392	1933619	0.0189	0.1816
chr16	90354753	2310515	0.0256	0.2068
chr17	81195210	1842061	0.0227	0.1988
chr18	78077248	1743557	0.0223	0.2931
chr19	59128983	1231324	0.0208	0.2534
chr20	63025520	1797501	0.0285	0.2222
chr21	48129895	1209088	0.0251	0.2105
chr22	51304566	737106	0.0144	0.1522
chrMT	16571	20768	1.2533	1.6063
chrX	155270560	3185937	0.0205	0.1951
chrY	59373566	130038	0.0022	0.0597

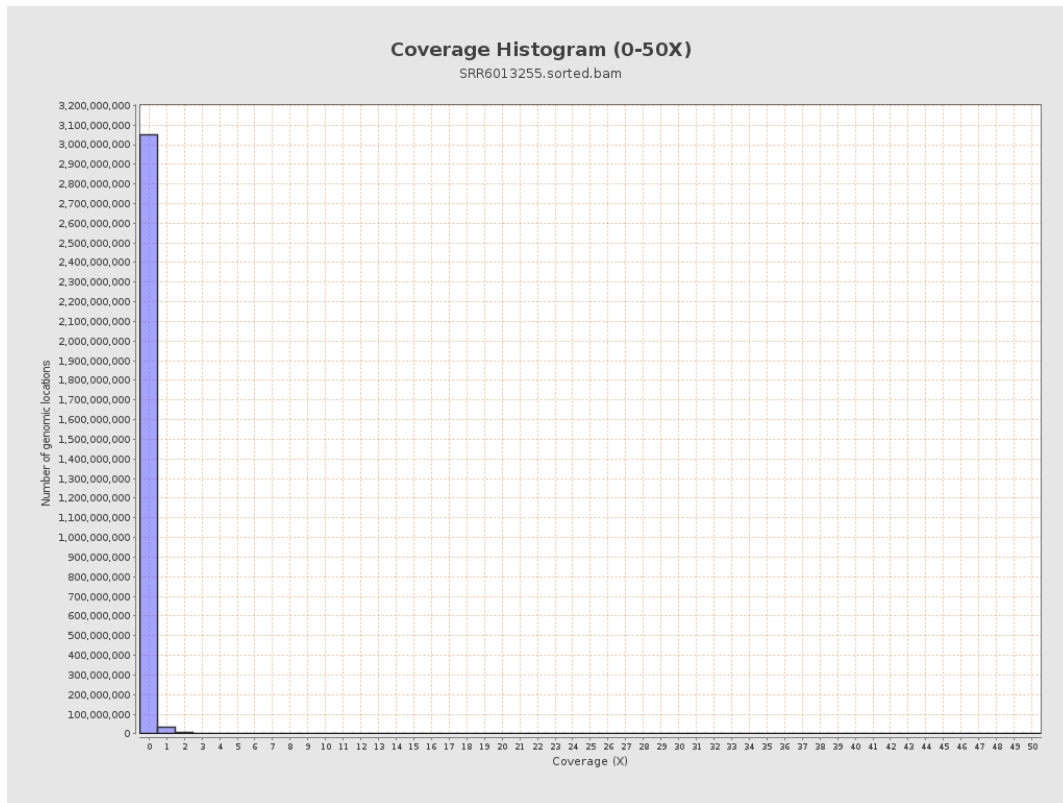
3. Results : Coverage across reference



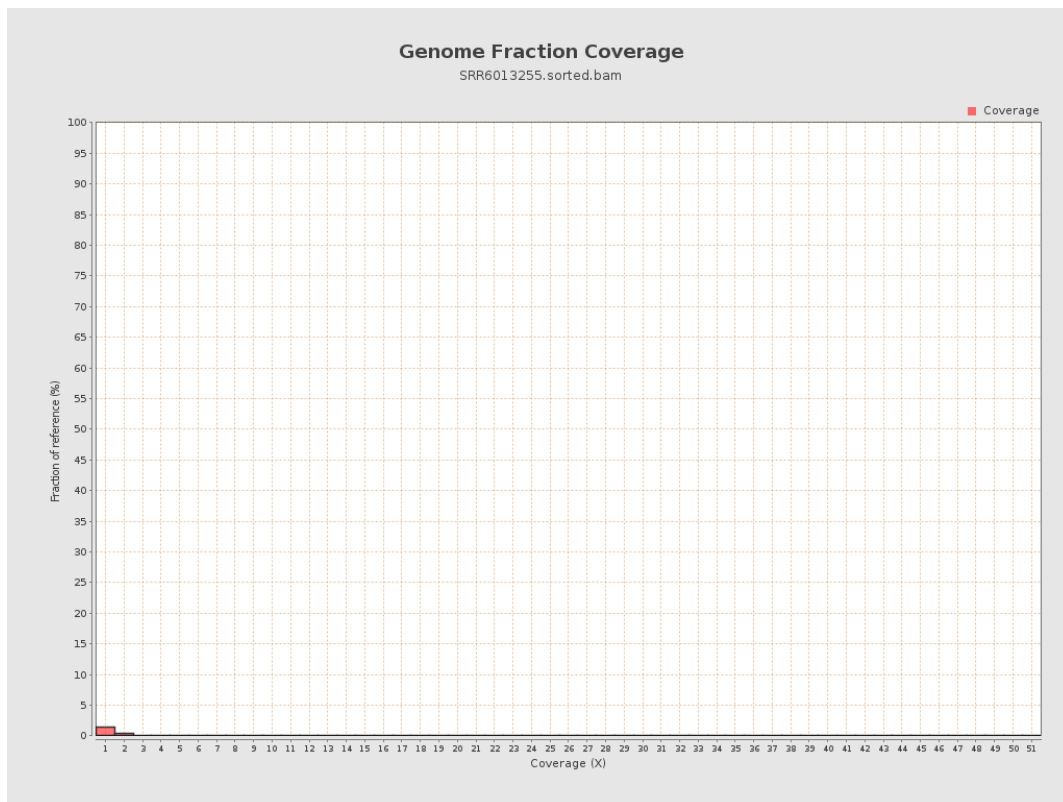
4. Results : Coverage Histogram



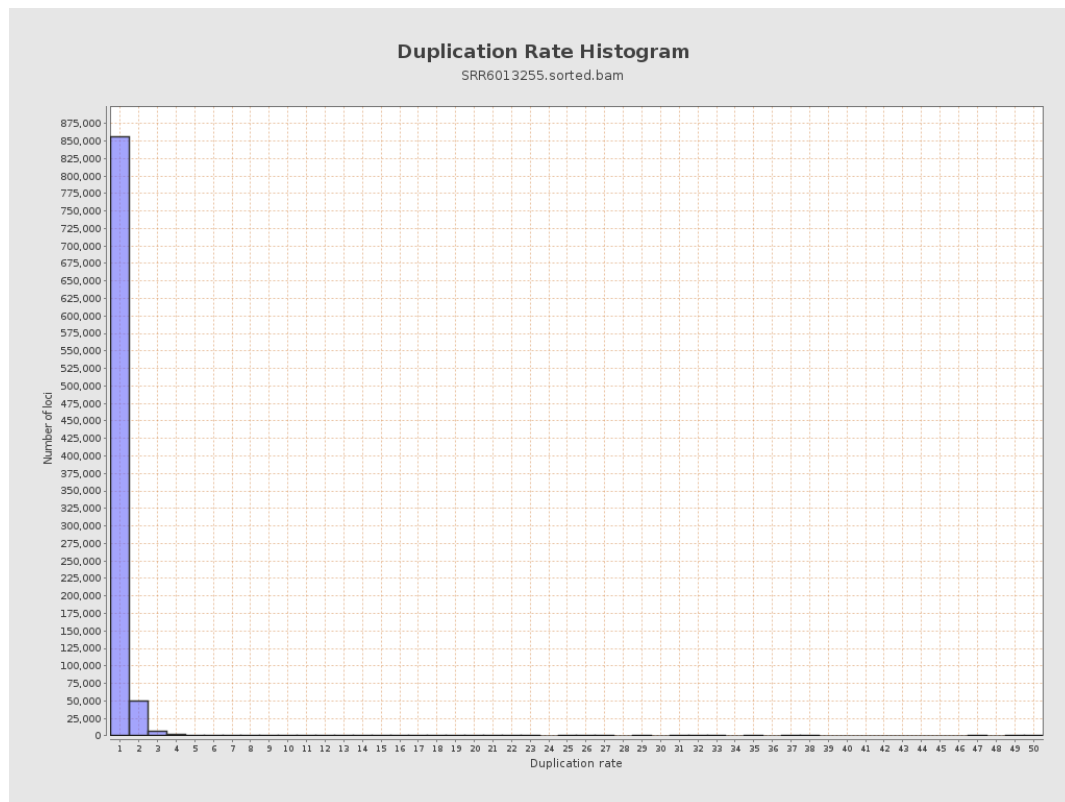
5. Results : Coverage Histogram (0-50X)



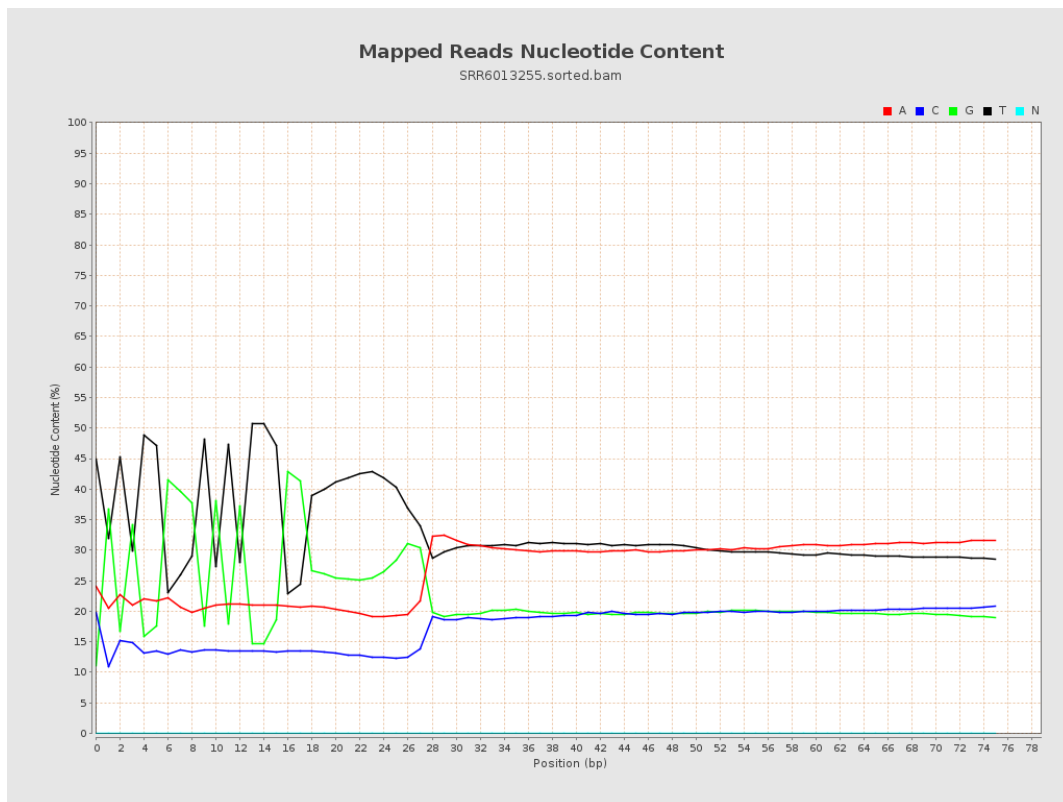
6. Results : Genome Fraction Coverage



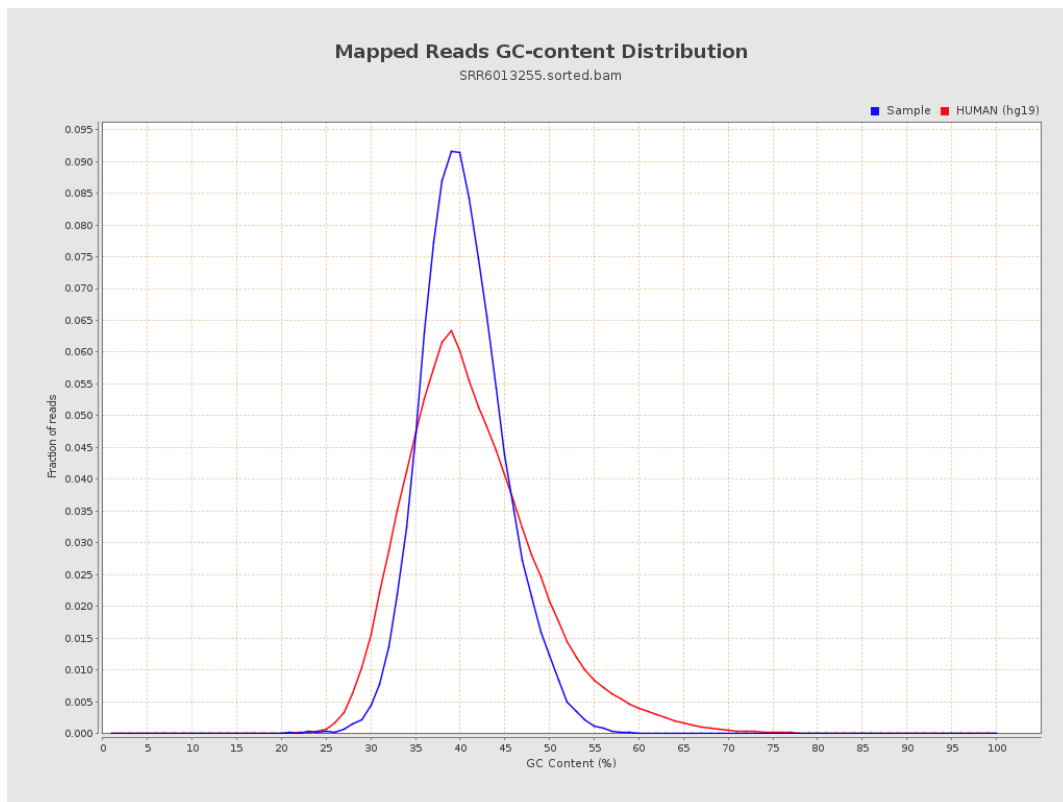
7. Results : Duplication Rate Histogram



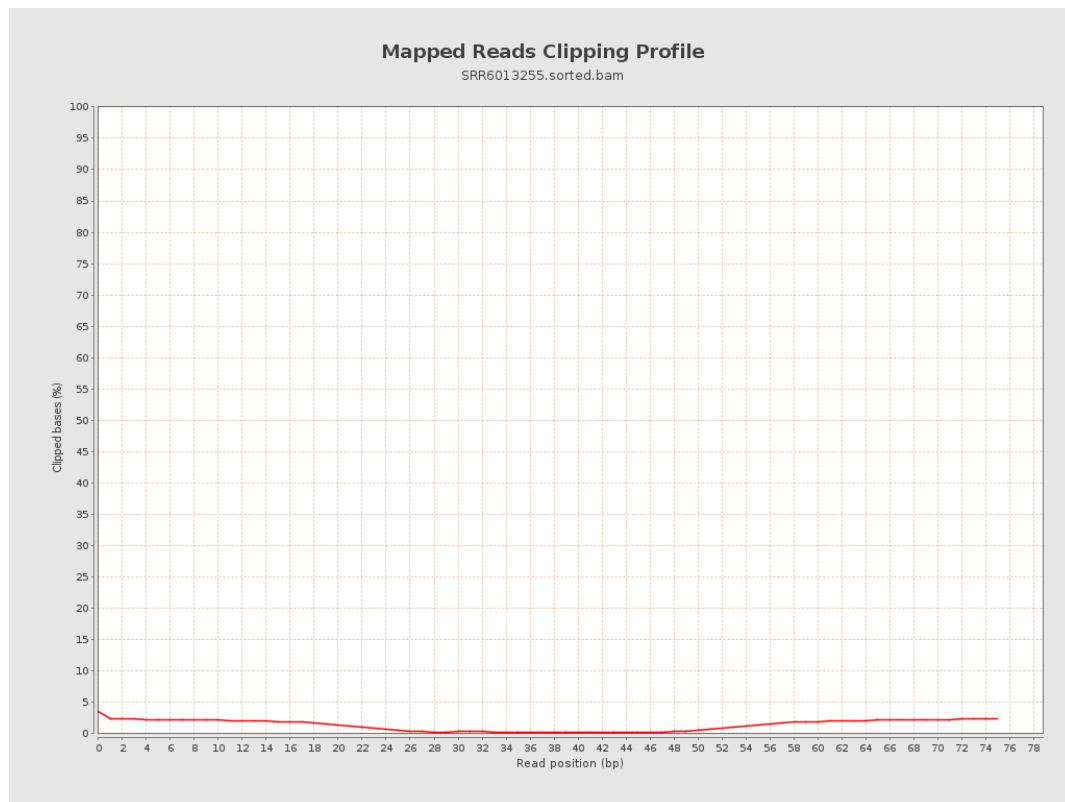
8. Results : Mapped Reads Nucleotide Content



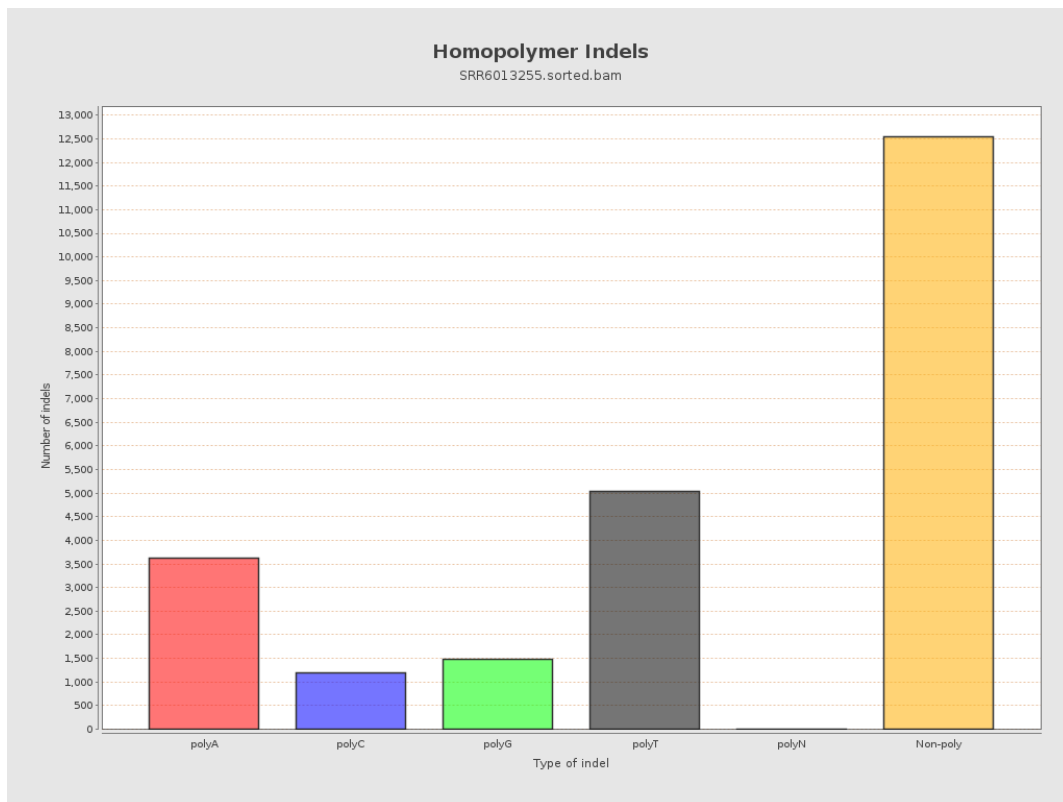
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

