

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 16:00:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013208.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_SRR6013208 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013208.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 16:00:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013208.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,326,035
Mapped reads	2,054,150 / 88.31%
Unmapped reads	271,885 / 11.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,188 / 0.7%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	114,283 / 4.91%
Duplication rate	4.26%
Clipped reads	829,894 / 35.68%

2.2. ACGT Content

Number/percentage of A's	39,813,265 / 28.59%
Number/percentage of C's	25,249,237 / 18.13%
Number/percentage of T's	44,847,341 / 32.21%
Number/percentage of G's	29,291,746 / 21.04%
Number/percentage of N's	30,667 / 0.02%
GC Percentage	39.17%

2.3. Coverage

Mean	0.045

Standard Deviation	0.4752
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	42.36
----------------------	-------

2.5. Mismatches and indels

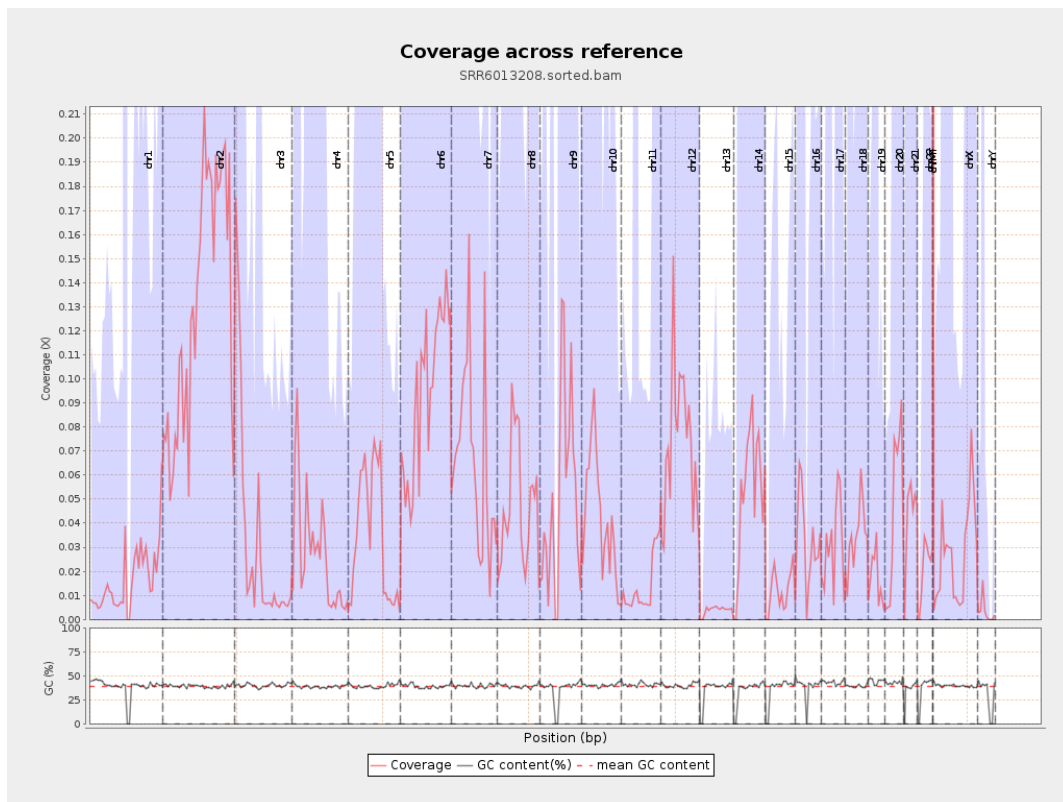
General error rate	0.8%
Mismatches	1,088,529
Insertions	10,542
Mapped reads with at least one insertion	0.51%
Deletions	33,154
Mapped reads with at least one deletion	1.6%
Homopolymer indels	47.11%

2.6. Chromosome stats

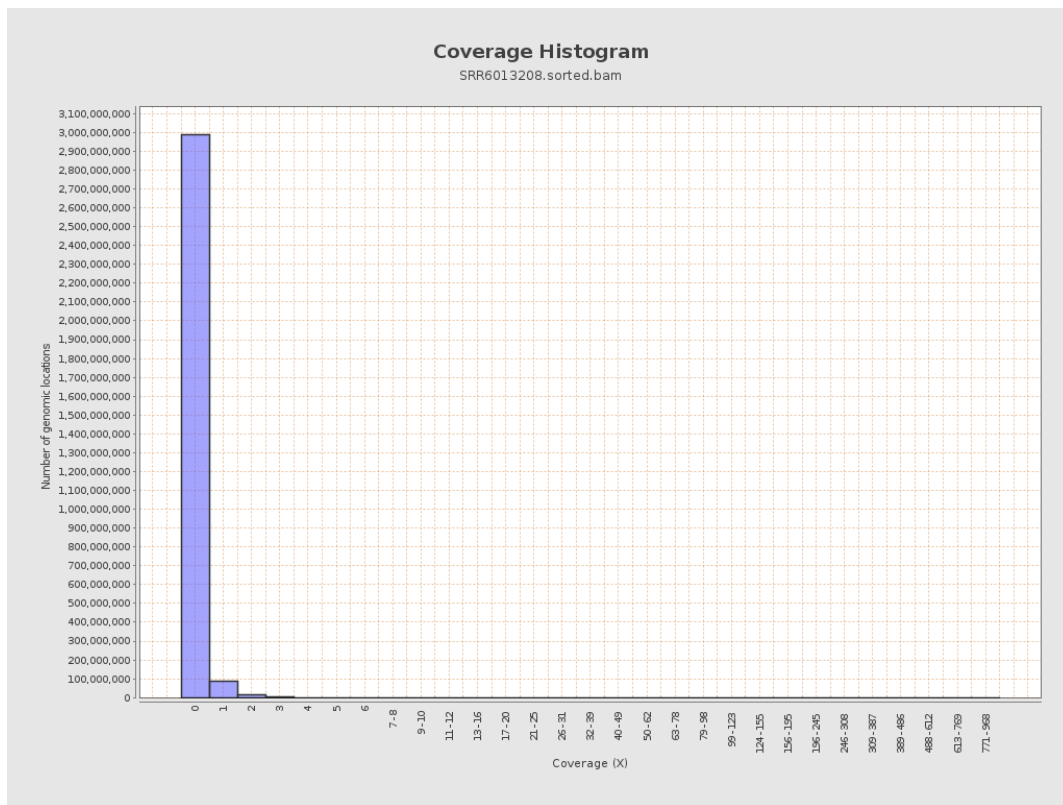
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4162178	0.0167	0.6384
chr2	243199373	31842162	0.1309	0.6148
chr3	198022430	6330439	0.032	0.2198
chr4	191154276	5392172	0.0282	0.2602
chr5	180915260	6289502	0.0348	0.2298
chr6	171115067	16287086	0.0952	0.4685
chr7	159138663	10549172	0.0663	1.25

chr8	146364022	6929043	0.0473	0.3716
chr9	141213431	7260036	0.0514	0.4089
chr10	135534747	5752394	0.0424	0.4838
chr11	135006516	1828297	0.0135	0.1929
chr12	133851895	9786269	0.0731	0.3353
chr13	115169878	444550	0.0039	0.0791
chr14	107349540	5664680	0.0528	0.2991
chr15	102531392	1241486	0.0121	0.1328
chr16	90354753	2886430	0.0319	0.2484
chr17	81195210	2592784	0.0319	0.2216
chr18	78077248	2710463	0.0347	0.6591
chr19	59128983	1007220	0.017	0.4611
chr20	63025520	2876719	0.0456	0.2661
chr21	48129895	1966755	0.0409	0.2892
chr22	51304566	1046685	0.0204	0.1641
chrMT	16571	37067	2.2369	2.051
chrX	155270560	4196935	0.027	0.2292
chrY	59373566	209395	0.0035	0.1723

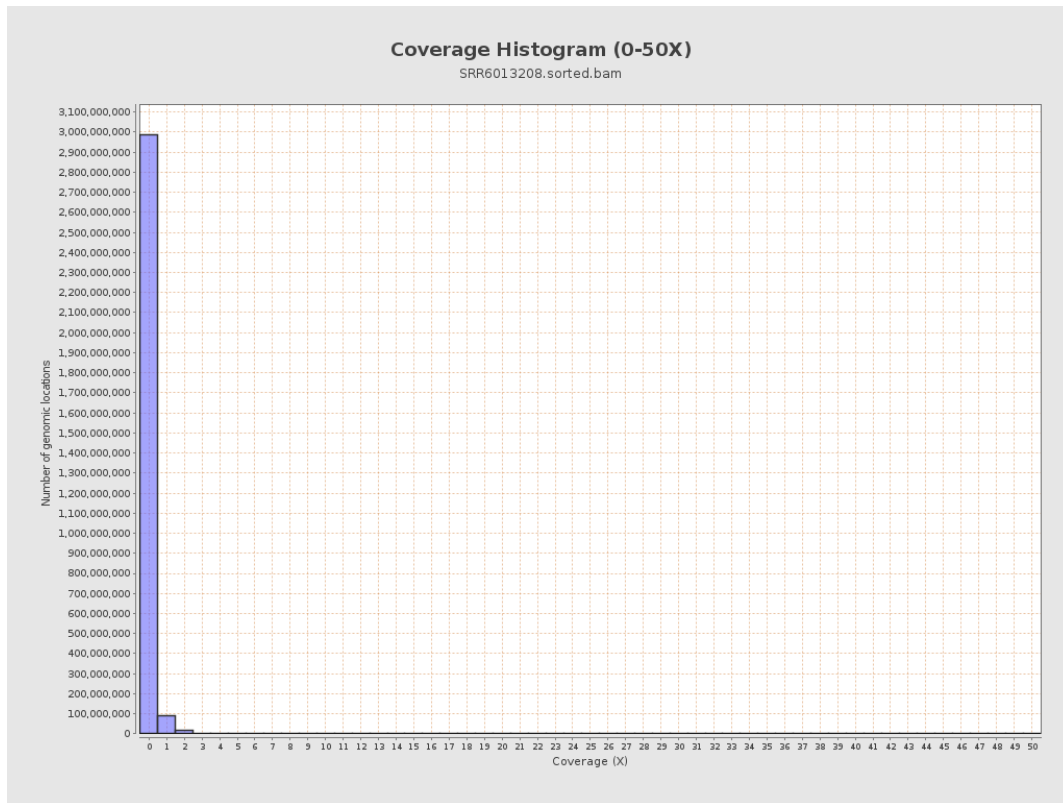
3. Results : Coverage across reference



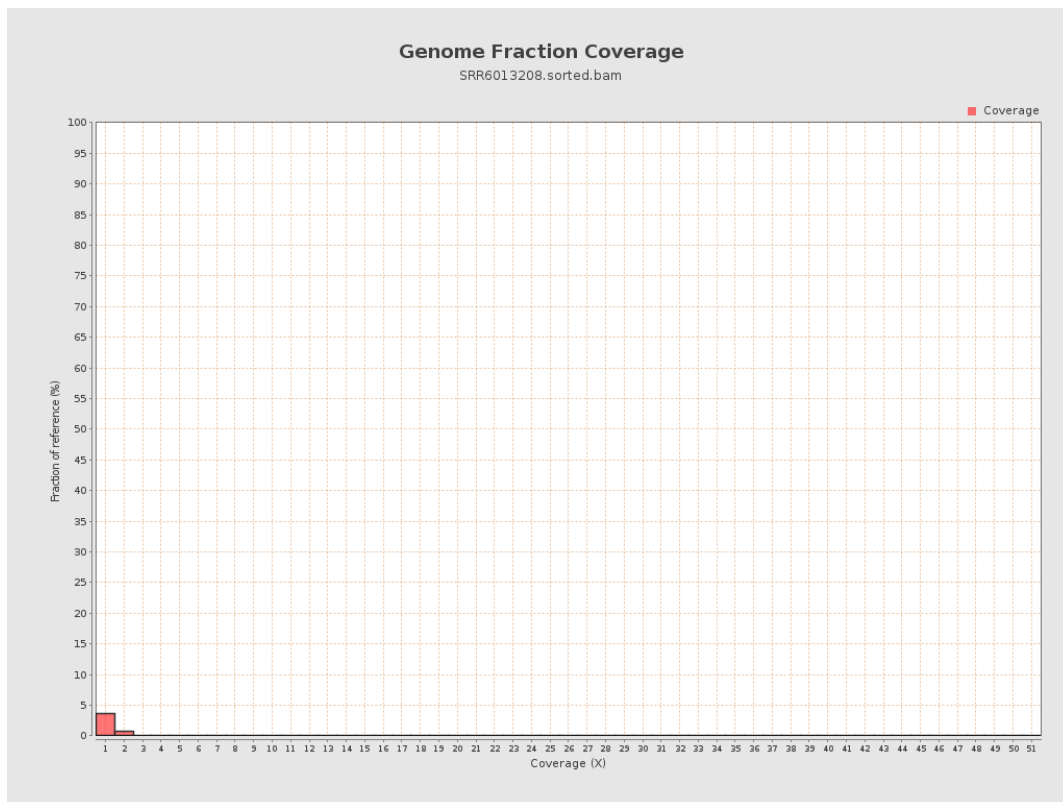
4. Results : Coverage Histogram



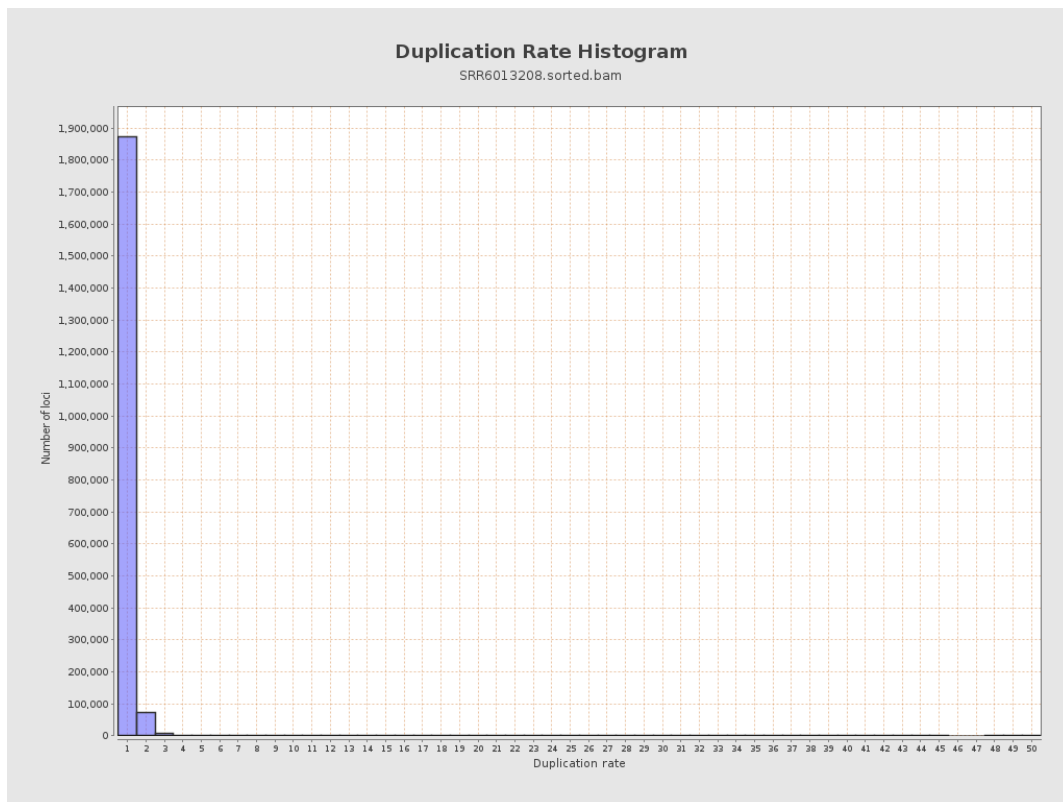
5. Results : Coverage Histogram (0-50X)



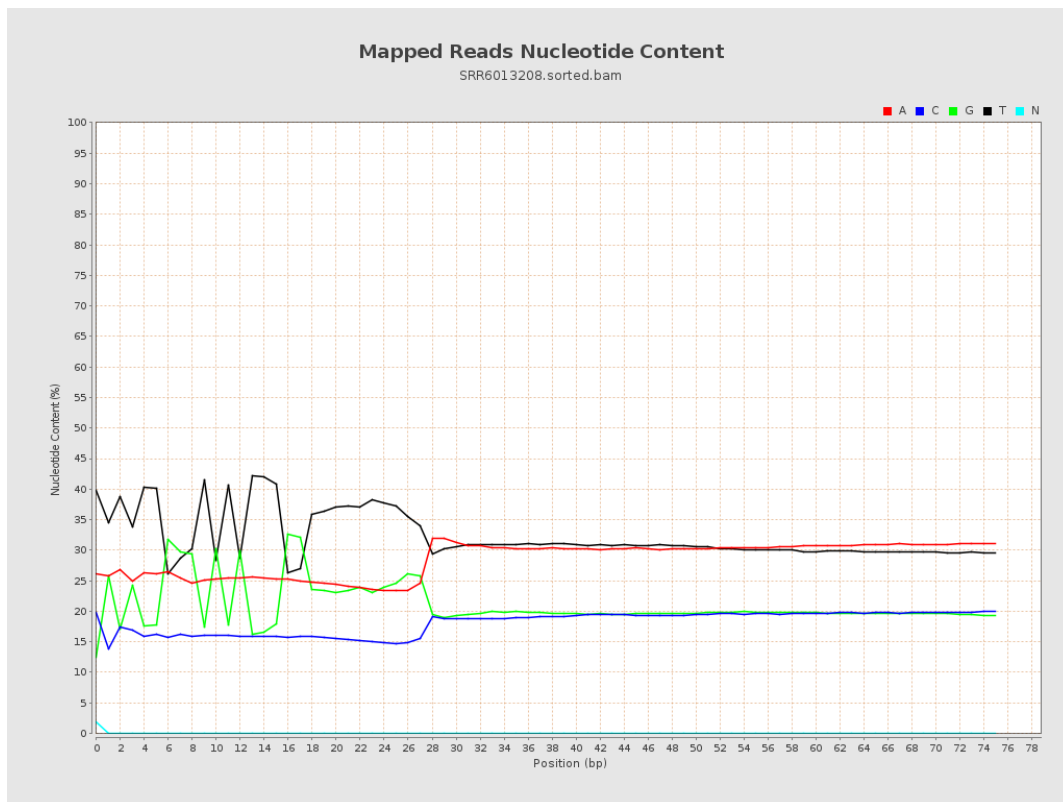
6. Results : Genome Fraction Coverage



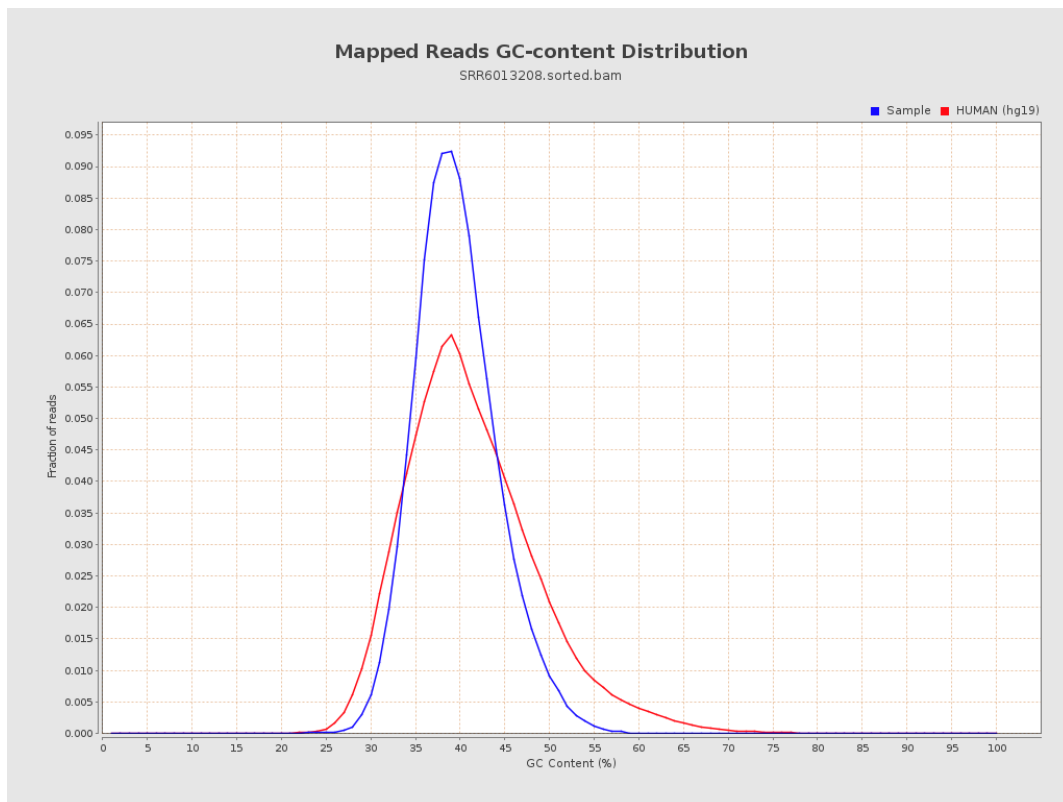
7. Results : Duplication Rate Histogram



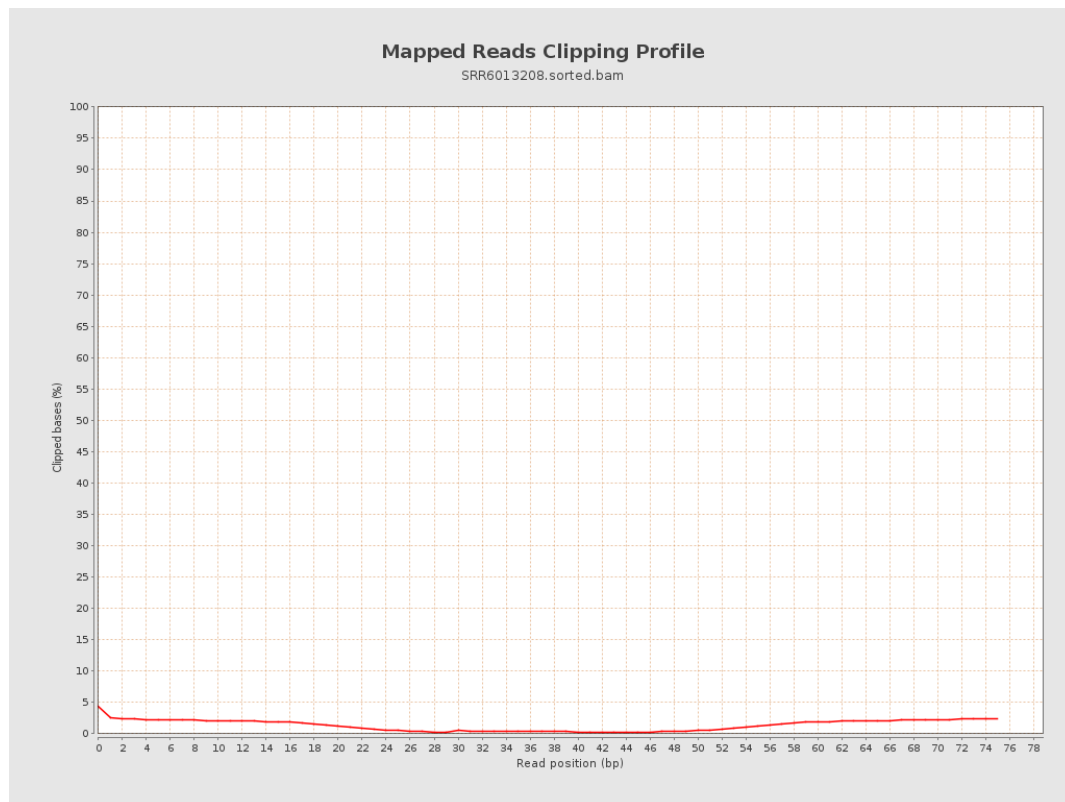
8. Results : Mapped Reads Nucleotide Content



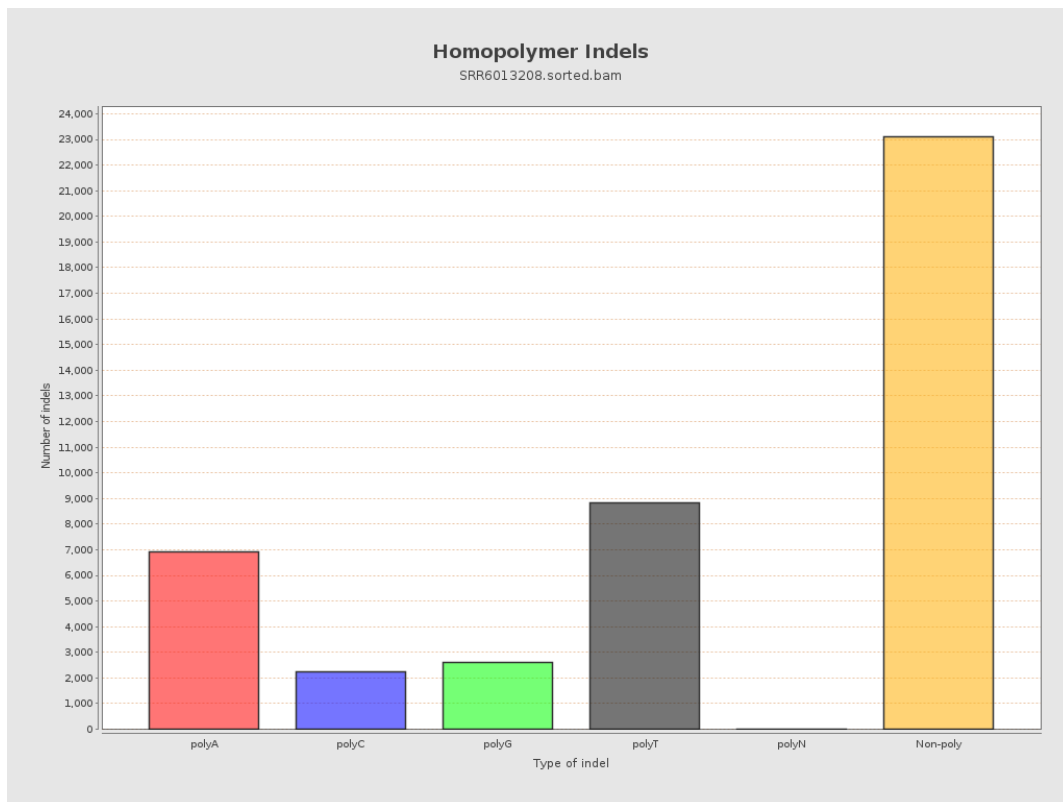
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

