

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 16:54:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013226.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_SRR6013226 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013226.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 16:54:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013226.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,499,868
Mapped reads	3,133,867 / 89.54%
Unmapped reads	366,001 / 10.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,299 / 0.52%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	151,717 / 4.33%
Duplication rate	3.54%
Clipped reads	1,489,384 / 42.56%

2.2. ACGT Content

Number/percentage of A's	56,614,377 / 27.48%
Number/percentage of C's	37,339,869 / 18.13%
Number/percentage of T's	65,680,273 / 31.89%
Number/percentage of G's	46,352,283 / 22.5%
Number/percentage of N's	2,794 / 0%
GC Percentage	40.63%

2.3. Coverage

Mean	0.0666

Standard Deviation	0.6228
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2.4. Mapping Quality

Mean Mapping Quality	45.14
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2.5. Mismatches and indels

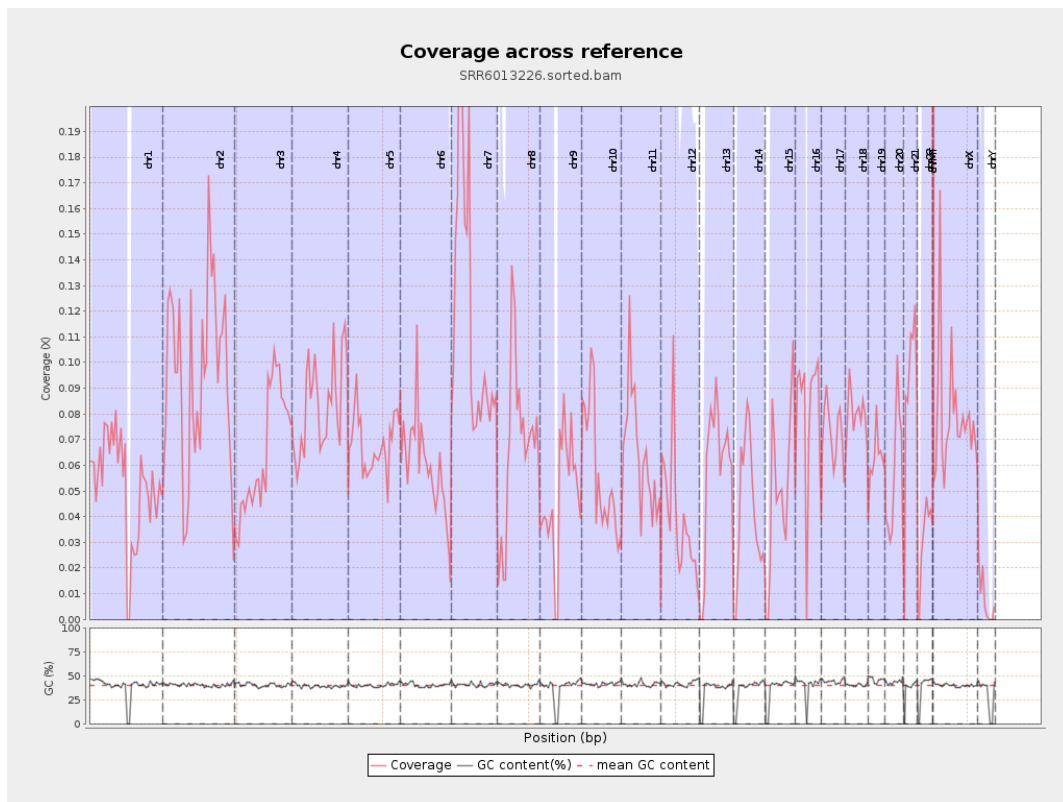
General error rate	0.74%
Mismatches	1,492,860
Insertions	14,468
Mapped reads with at least one insertion	0.46%
Deletions	50,250
Mapped reads with at least one deletion	1.59%
Homopolymer indels	46.06%

2.6. Chromosome stats

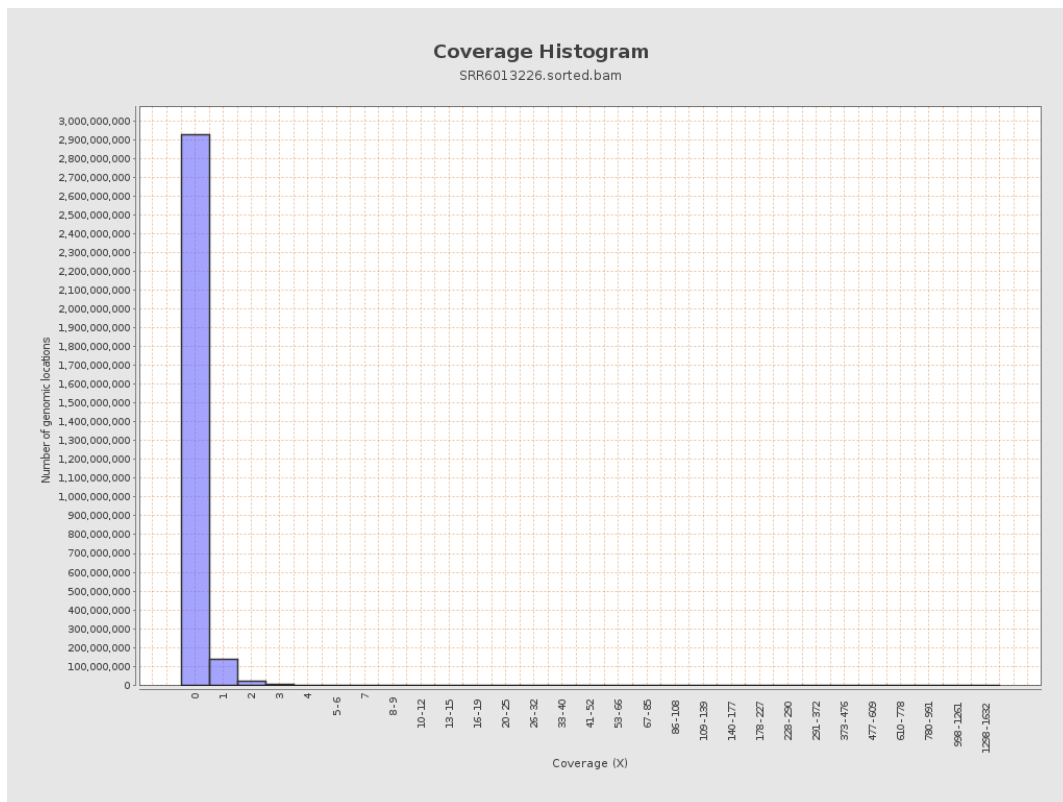
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	12962033	0.052	0.7105
chr2	243199373	23046303	0.0948	0.7525
chr3	198022430	12942637	0.0654	0.2989
chr4	191154276	15824113	0.0828	0.3548
chr5	180915260	12360510	0.0683	0.3128
chr6	171115067	10260572	0.06	0.5319
chr7	159138663	18659302	0.1173	1.7576

chr8	146364022	9810406	0.067	0.6951
chr9	141213431	6858004	0.0486	0.4782
chr10	135534747	7711282	0.0569	0.4585
chr11	135006516	8571694	0.0635	0.4096
chr12	133851895	5209649	0.0389	0.2488
chr13	115169878	6769251	0.0588	0.286
chr14	107349540	4598157	0.0428	0.2857
chr15	102531392	5224585	0.051	0.2749
chr16	90354753	7094312	0.0785	0.3692
chr17	81195210	5945955	0.0732	0.4058
chr18	78077248	6268173	0.0803	0.8344
chr19	59128983	3741029	0.0633	0.6473
chr20	63025520	3543978	0.0562	0.2976
chr21	48129895	4400316	0.0914	0.399
chr22	51304566	1568306	0.0306	0.2019
chrMT	16571	30979	1.8695	1.8346
chrX	155270560	12217881	0.0787	0.4115
chrY	59373566	456512	0.0077	0.1551

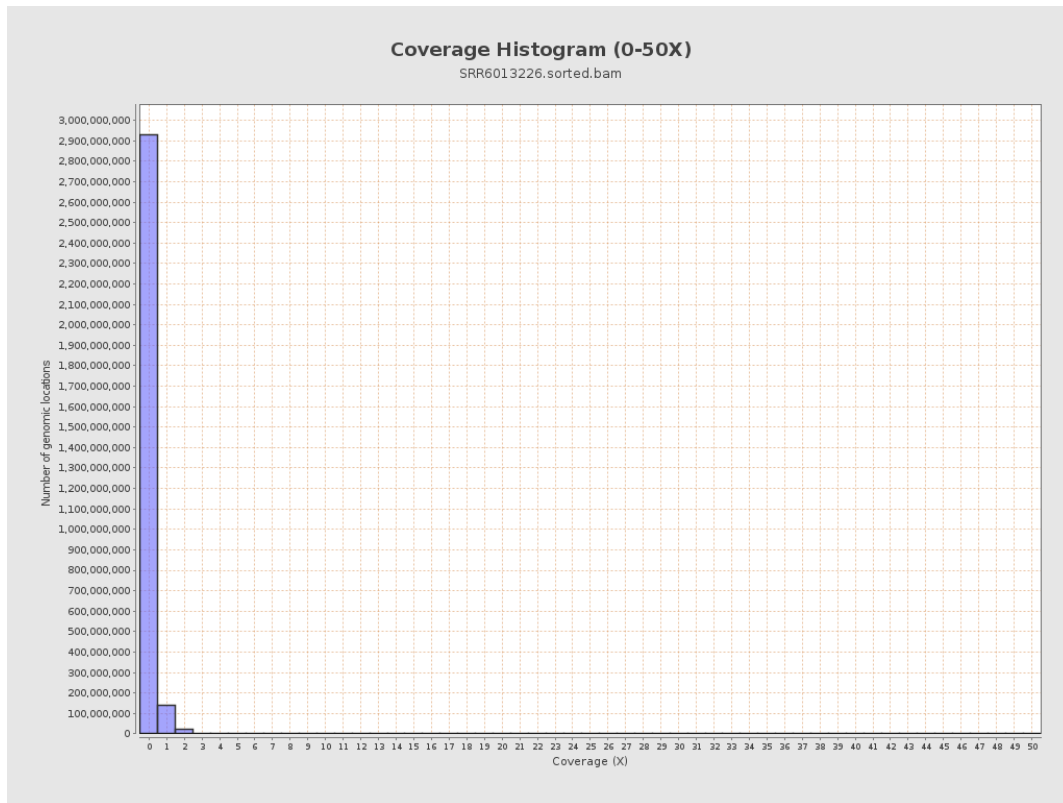
3. Results : Coverage across reference



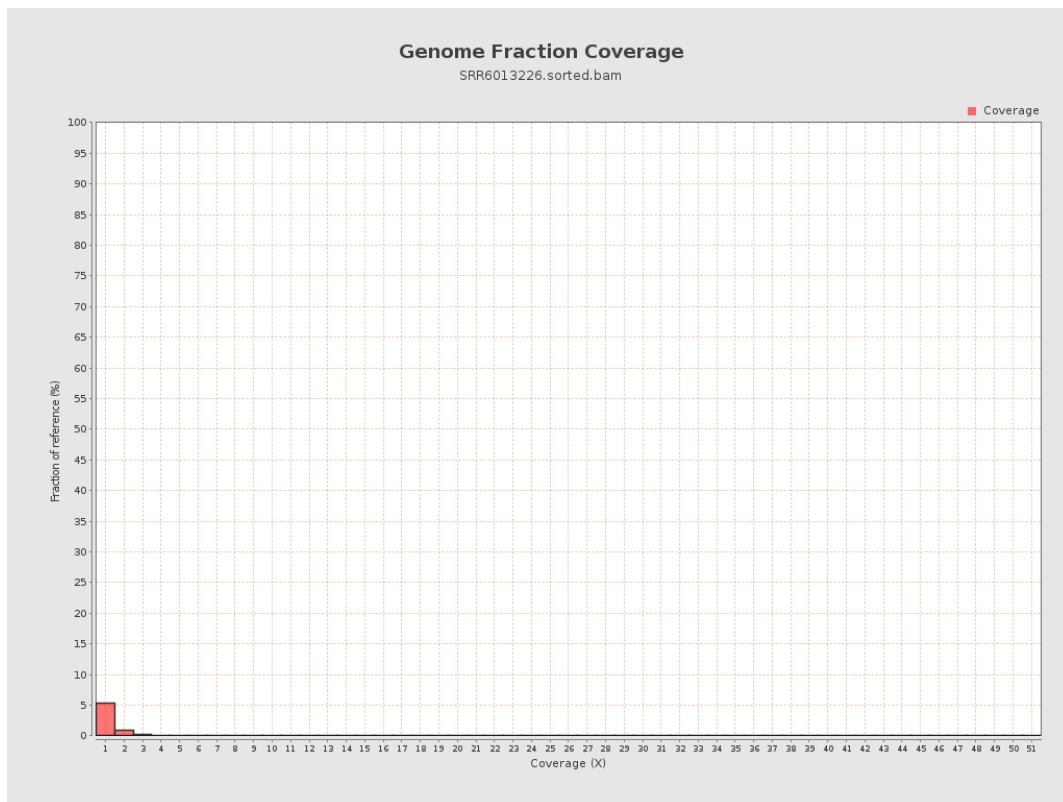
4. Results : Coverage Histogram



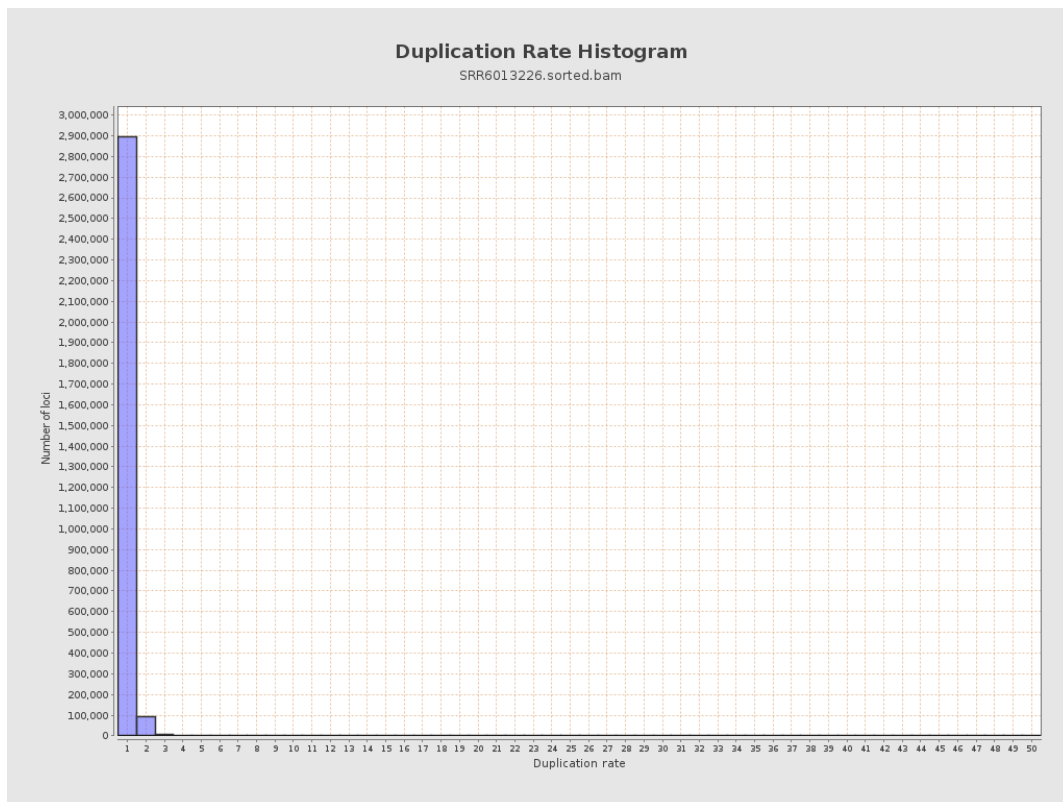
5. Results : Coverage Histogram (0-50X)



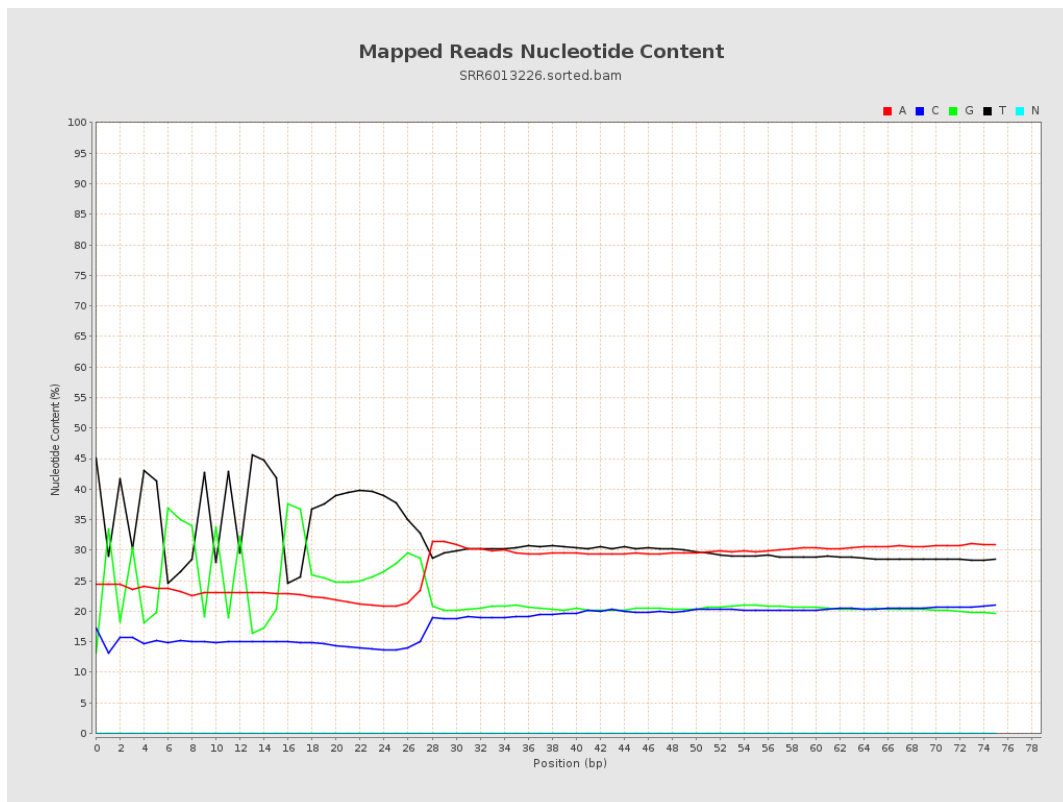
6. Results : Genome Fraction Coverage



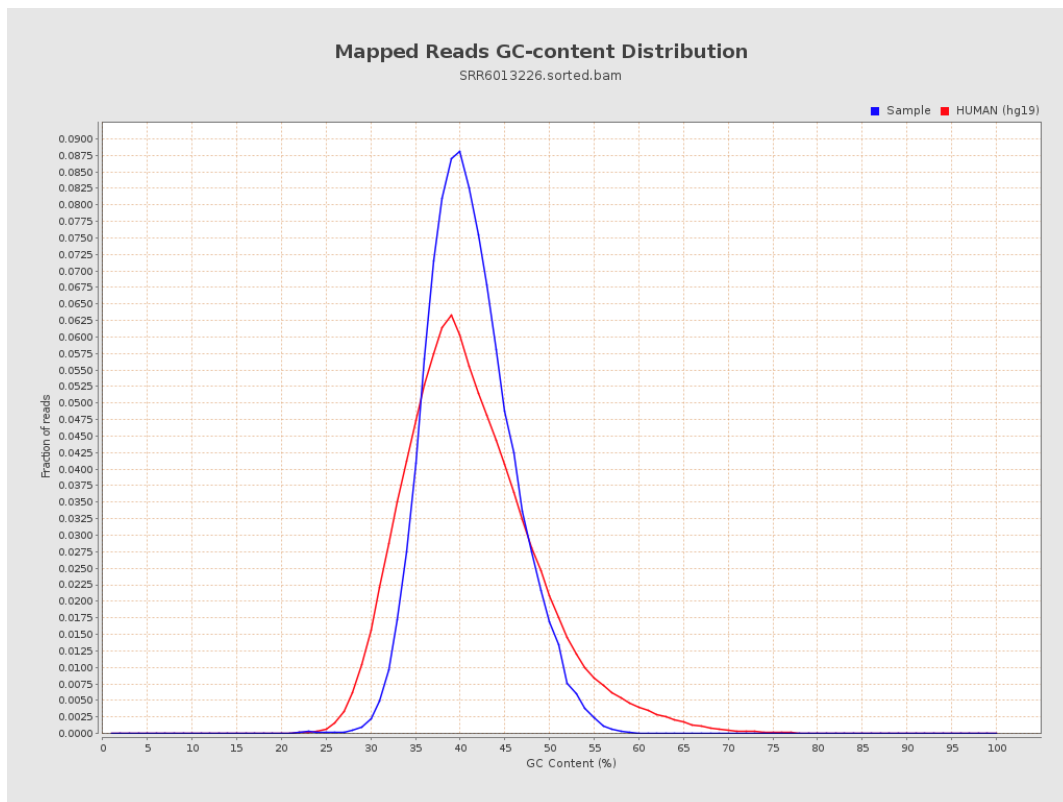
7. Results : Duplication Rate Histogram



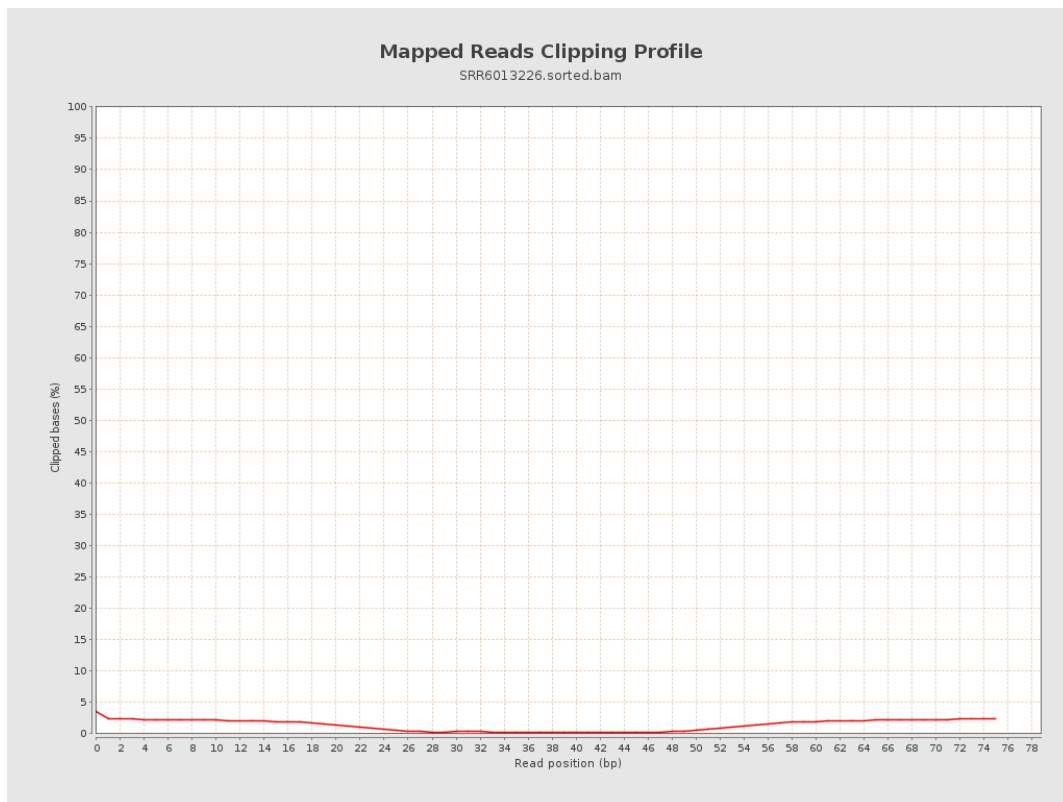
8. Results : Mapped Reads Nucleotide Content



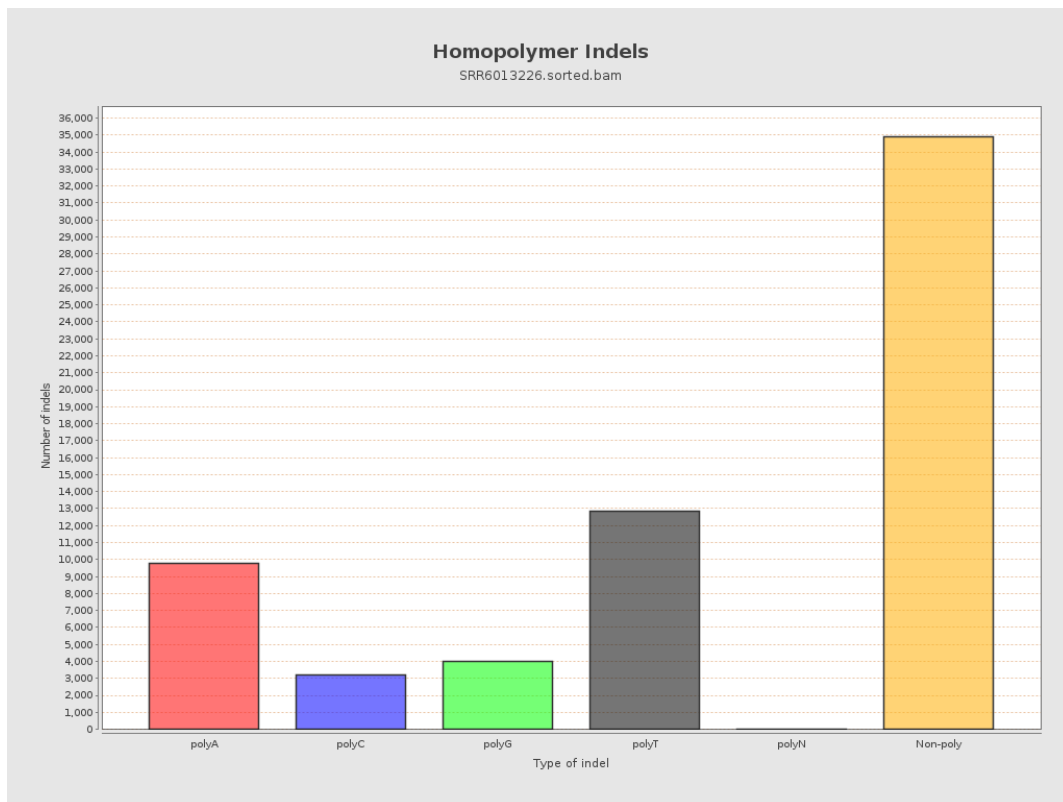
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

