

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 05:08:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004157.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_SRR6004157 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004157.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 05:08:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004157.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,535,212
Mapped reads	2,149,069 / 84.77%
Unmapped reads	386,143 / 15.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,173 / 0.68%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	95,858 / 3.78%
Duplication rate	3.39%
Clipped reads	1,028,114 / 40.55%

2.2. ACGT Content

Number/percentage of A's	38,691,283 / 27.29%
Number/percentage of C's	26,564,072 / 18.73%
Number/percentage of T's	44,260,436 / 31.22%
Number/percentage of G's	32,253,021 / 22.75%
Number/percentage of N's	21,886 / 0.02%
GC Percentage	41.48%

2.3. Coverage

Mean	0.0458

Standard Deviation	0.4201
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2.4. Mapping Quality

Mean Mapping Quality	45.28
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2.5. Mismatches and indels

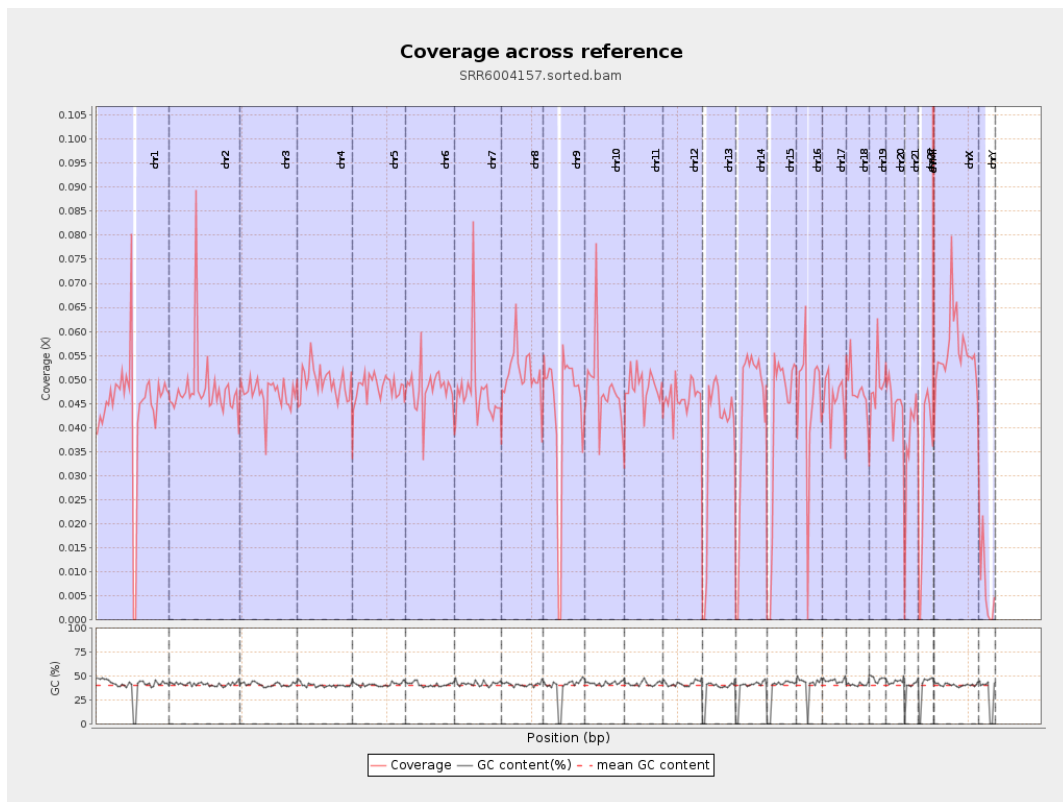
General error rate	0.9%
Mismatches	1,255,993
Insertions	10,460
Mapped reads with at least one insertion	0.48%
Deletions	32,161
Mapped reads with at least one deletion	1.48%
Homopolymer indels	46.73%

2.6. Chromosome stats

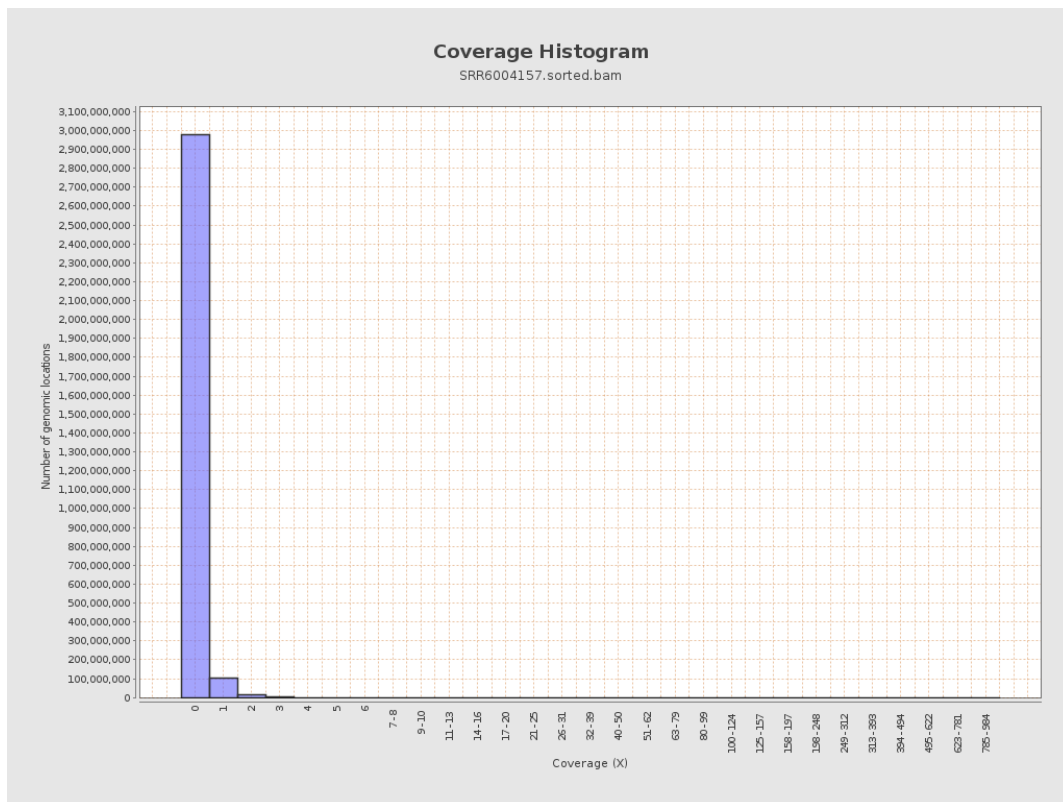
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	11026471	0.0442	0.8155
chr2	243199373	11663736	0.048	0.4691
chr3	198022430	9298684	0.047	0.2459
chr4	191154276	9431073	0.0493	0.2641
chr5	180915260	8772432	0.0485	0.253
chr6	171115067	8221208	0.048	0.2915
chr7	159138663	7573208	0.0476	0.6028

chr8	146364022	7482041	0.0511	0.4935
chr9	141213431	6171891	0.0437	0.3761
chr10	135534747	6516150	0.0481	0.3937
chr11	135006516	6512805	0.0482	0.3617
chr12	133851895	6170262	0.0461	0.2502
chr13	115169878	4321386	0.0375	0.2252
chr14	107349540	4644500	0.0433	0.263
chr15	102531392	4208249	0.041	0.2375
chr16	90354753	4102533	0.0454	0.2676
chr17	81195210	3684778	0.0454	0.2797
chr18	78077248	3760524	0.0482	0.6832
chr19	59128983	2889481	0.0489	0.5596
chr20	63025520	2827008	0.0449	0.2469
chr21	48129895	1753206	0.0364	0.2379
chr22	51304566	1564060	0.0305	0.198
chrMT	16571	185357	11.1856	6.24
chrX	155270560	8660614	0.0558	0.3097
chrY	59373566	401941	0.0068	0.1888

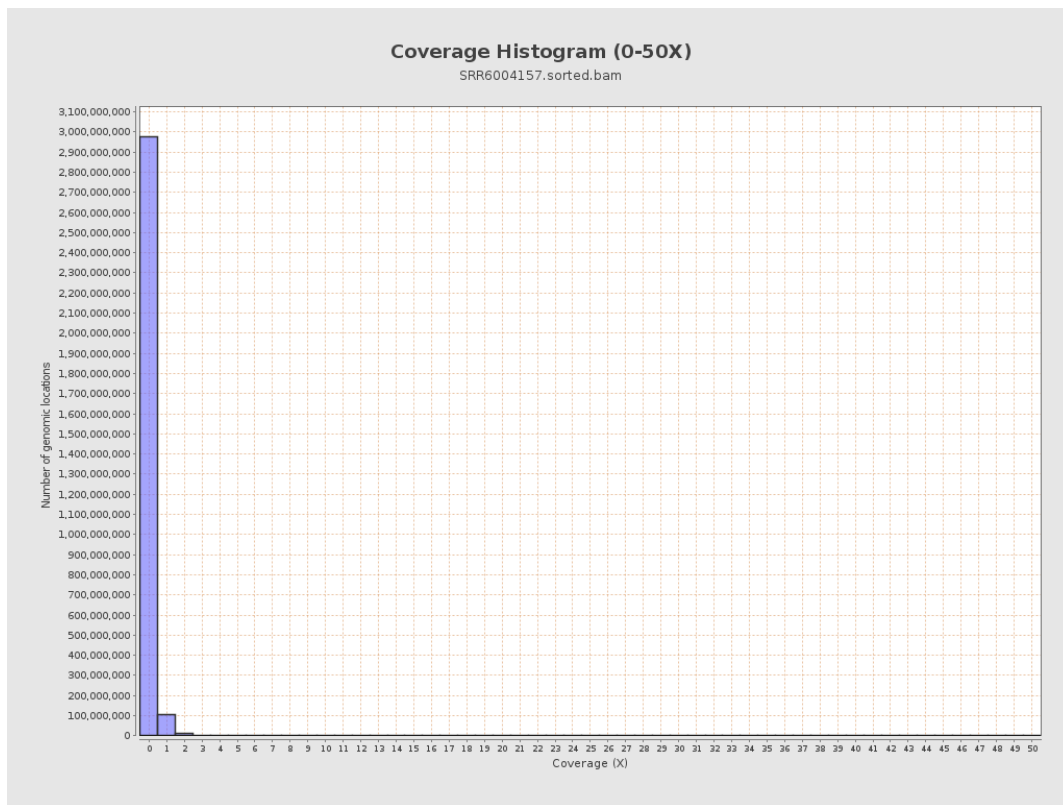
3. Results : Coverage across reference



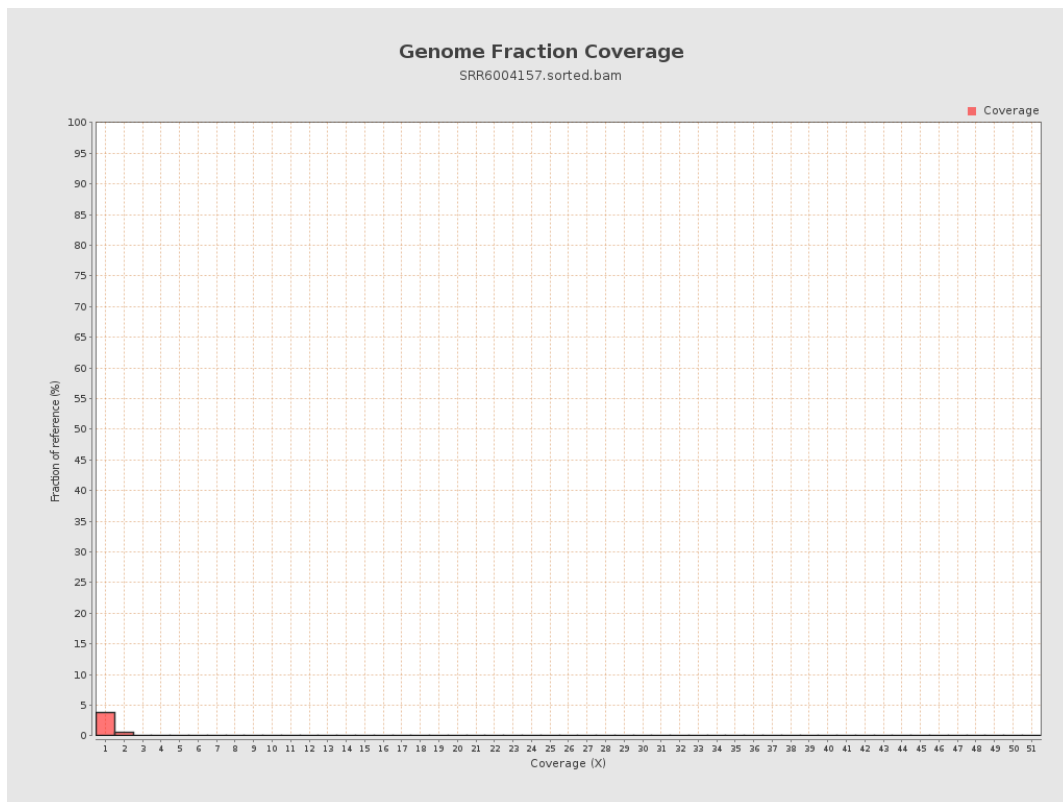
4. Results : Coverage Histogram



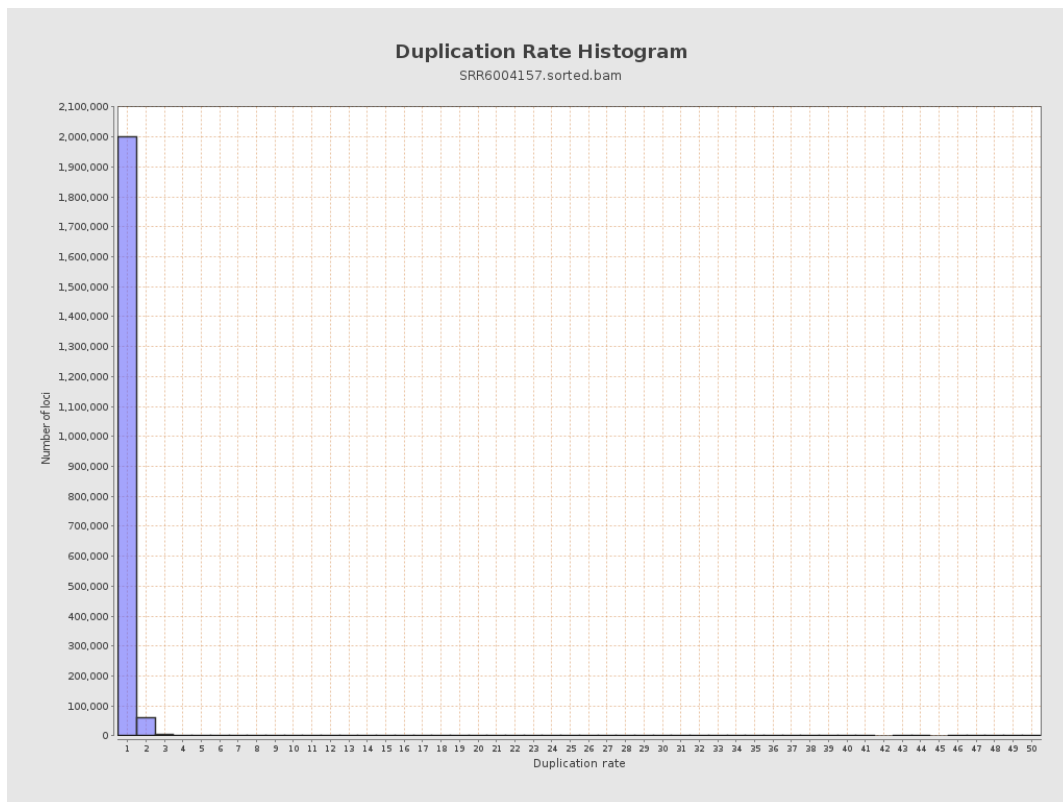
5. Results : Coverage Histogram (0-50X)



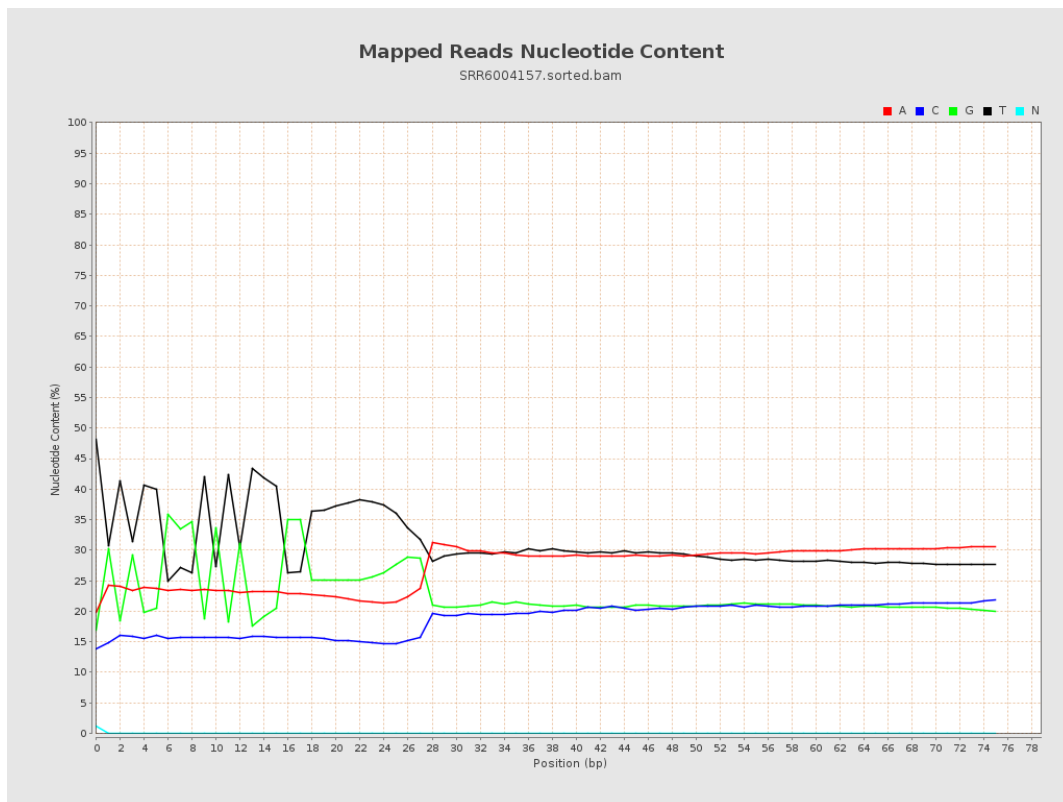
6. Results : Genome Fraction Coverage



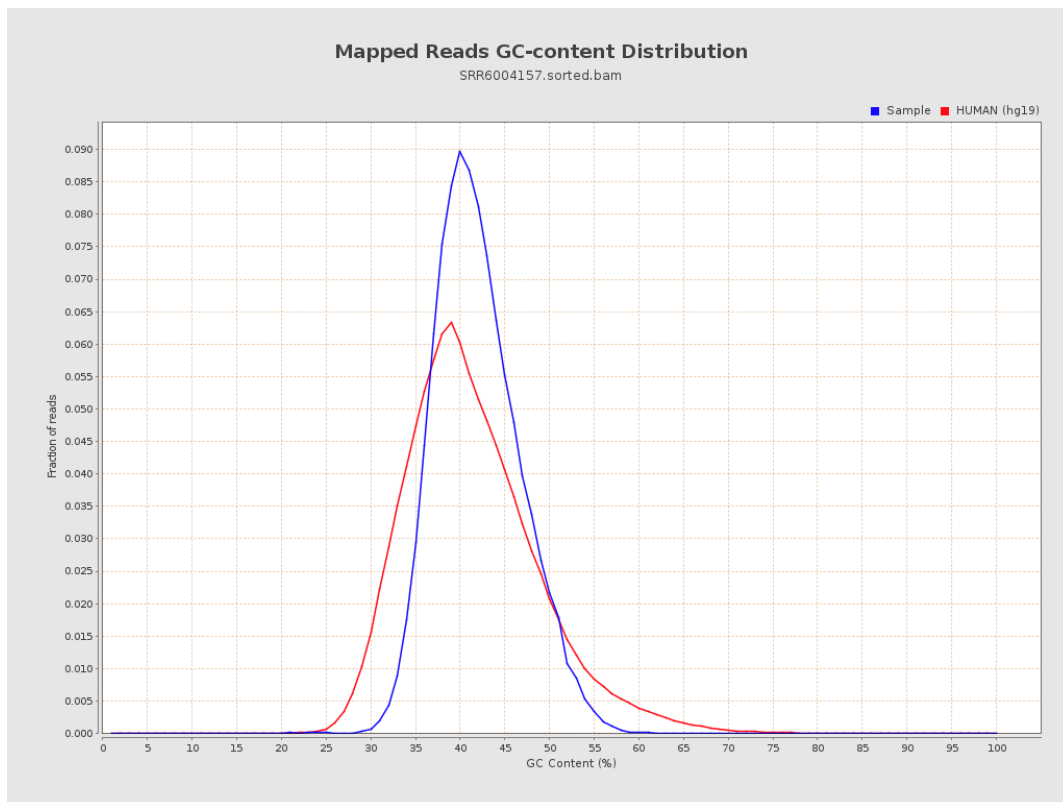
7. Results : Duplication Rate Histogram



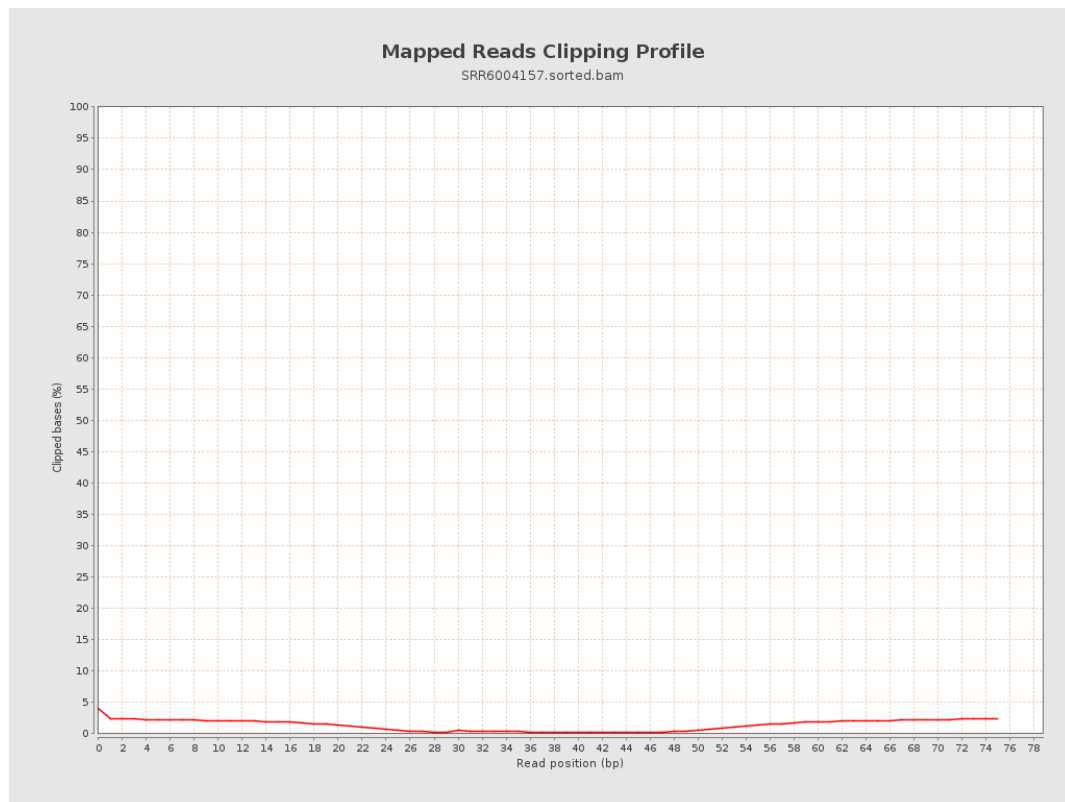
8. Results : Mapped Reads Nucleotide Content



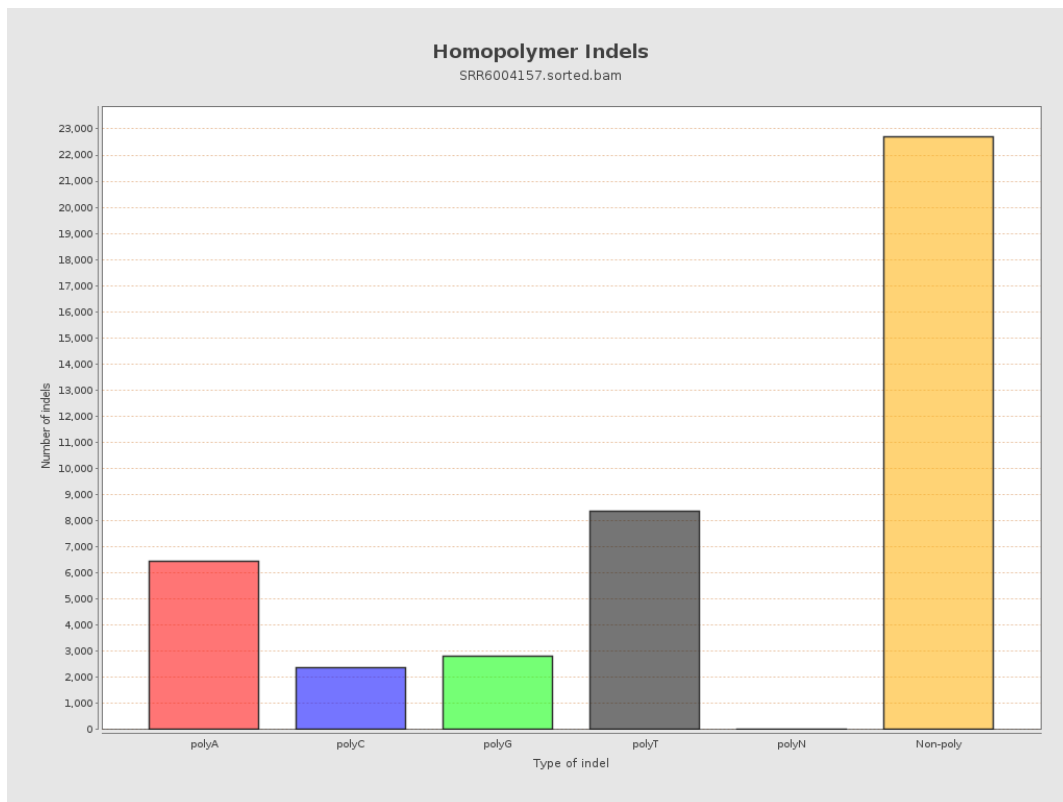
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

