

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/20 02:57:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1506326.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_SRR1506326 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1506326.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 20 02:57:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1506326.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,040,817
Mapped reads	9,221,932 / 65.68%
Unmapped reads	4,818,885 / 34.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	183,965 / 1.31%
Read min/max/mean length	30 / 94 / 94.47
Duplicated reads (estimated)	1,894,282 / 13.49%
Duplication rate	12.99%
Clipped reads	5,324,056 / 37.92%

2.2. ACGT Content

Number/percentage of A's	201,327,354 / 27.28%
Number/percentage of C's	141,124,472 / 19.12%
Number/percentage of T's	214,123,375 / 29.01%
Number/percentage of G's	181,256,697 / 24.56%
Number/percentage of N's	168,749 / 0.02%
GC Percentage	43.68%

2.3. Coverage

Mean	0.2385

Standard Deviation	1.6992
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2.4. Mapping Quality

Mean Mapping Quality	47.89
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2.5. Mismatches and indels

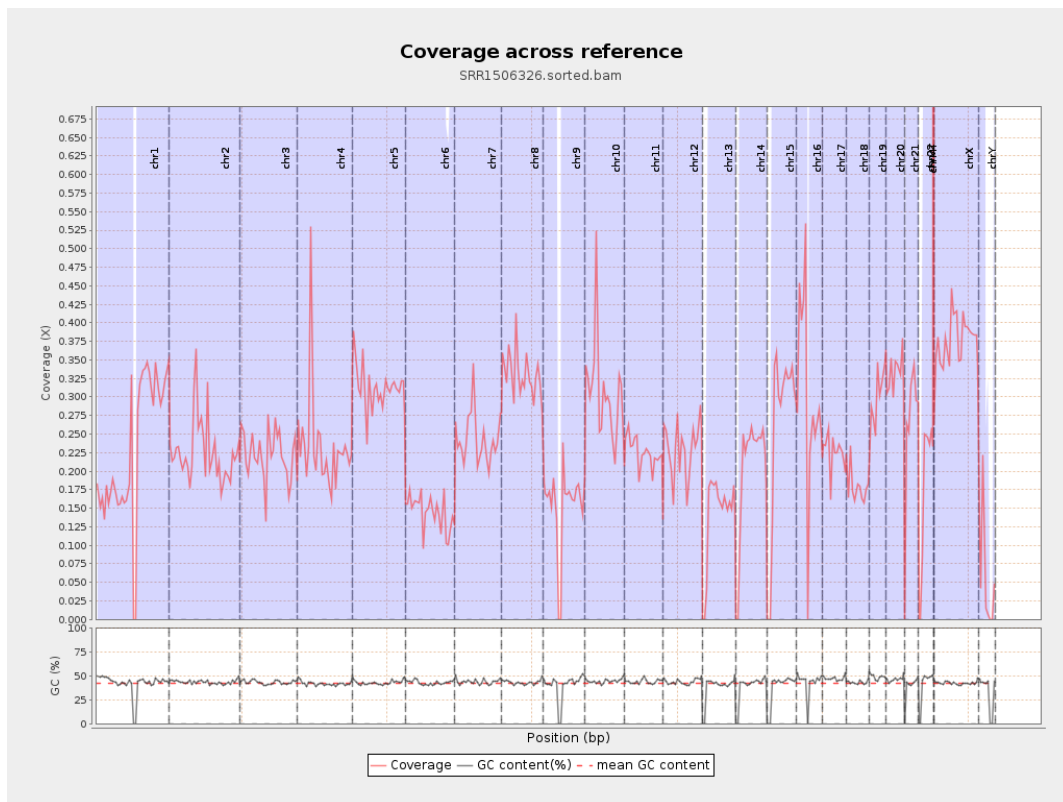
General error rate	0.77%
Mismatches	5,551,416
Insertions	61,325
Mapped reads with at least one insertion	0.65%
Deletions	149,761
Mapped reads with at least one deletion	1.59%
Homopolymer indels	42.35%

2.6. Chromosome stats

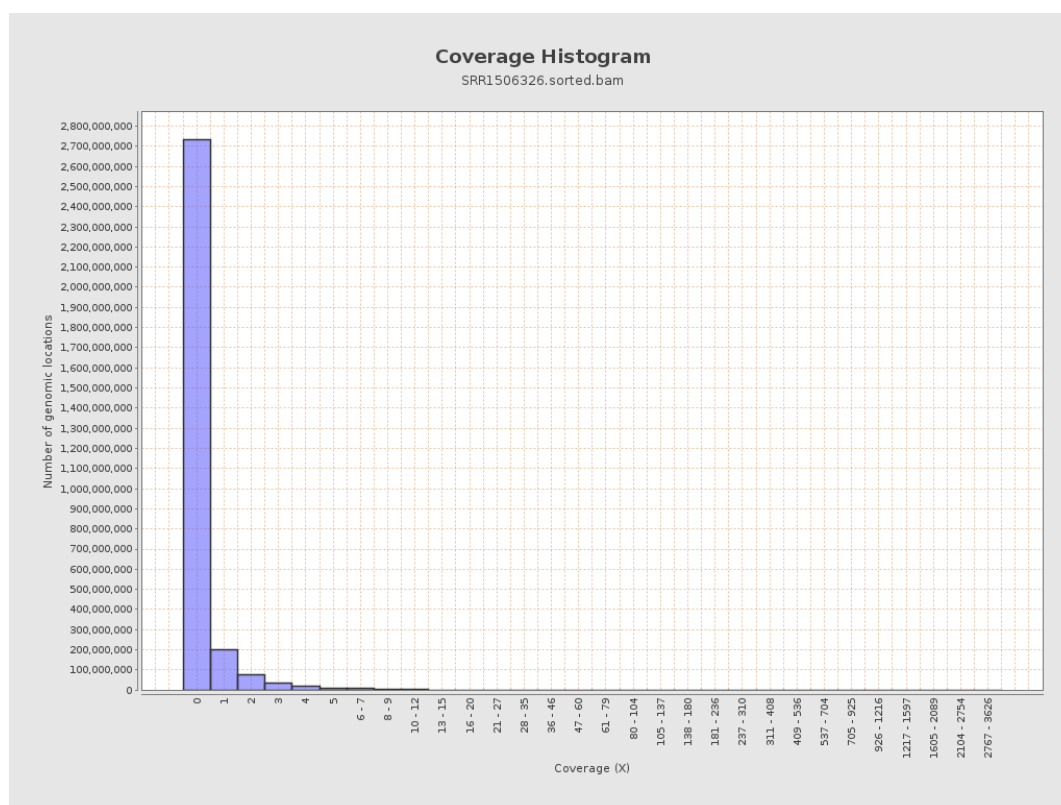
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	56765742	0.2277	3.187
chr2	243199373	54753653	0.2251	1.7481
chr3	198022430	43968668	0.222	0.8476
chr4	191154276	44223312	0.2313	1.4932
chr5	180915260	56606558	0.3129	1.024
chr6	171115067	24646280	0.144	0.7454
chr7	159138663	38619596	0.2427	2.0435

chr8	146364022	48412551	0.3308	2.3511
chr9	141213431	21411578	0.1516	1.543
chr10	135534747	41517879	0.3063	2.1196
chr11	135006516	30358532	0.2249	1.3673
chr12	133851895	30634589	0.2289	0.9222
chr13	115169878	16084332	0.1397	0.6507
chr14	107349540	21750338	0.2026	0.9605
chr15	102531392	26965066	0.263	0.9528
chr16	90354753	27505163	0.3044	1.266
chr17	81195210	18208898	0.2243	1.0809
chr18	78077248	13968369	0.1789	2.457
chr19	59128983	17756974	0.3003	2.3317
chr20	63025520	21031748	0.3337	1.1927
chr21	48129895	12829703	0.2666	1.4143
chr22	51304566	8788968	0.1713	0.8015
chrMT	16571	92208	5.5644	6.4334
chrX	155270560	58231752	0.375	1.2977
chrY	59373566	3178165	0.0535	2.0769

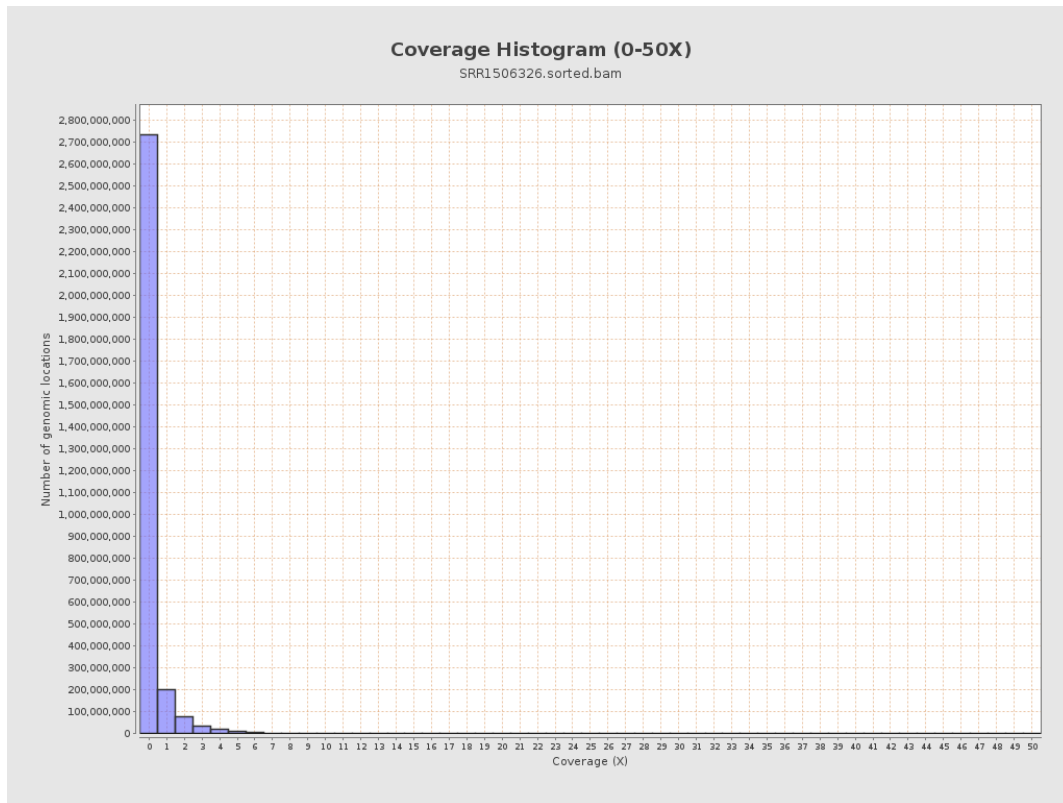
3. Results : Coverage across reference



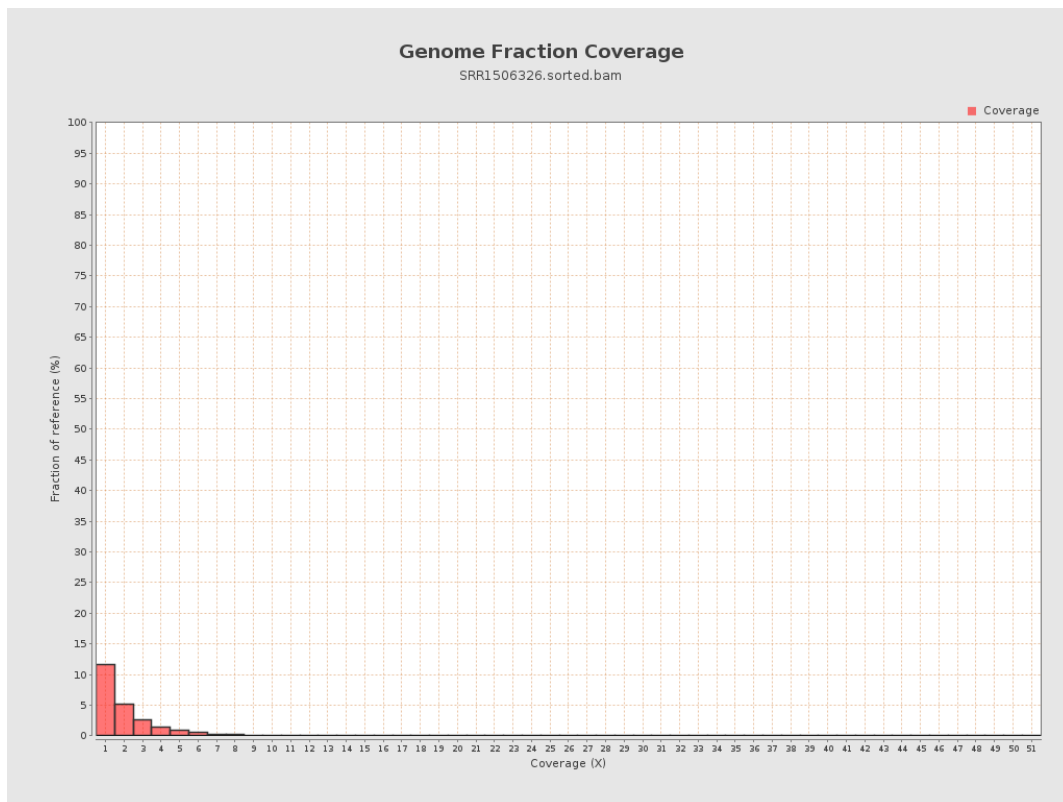
4. Results : Coverage Histogram



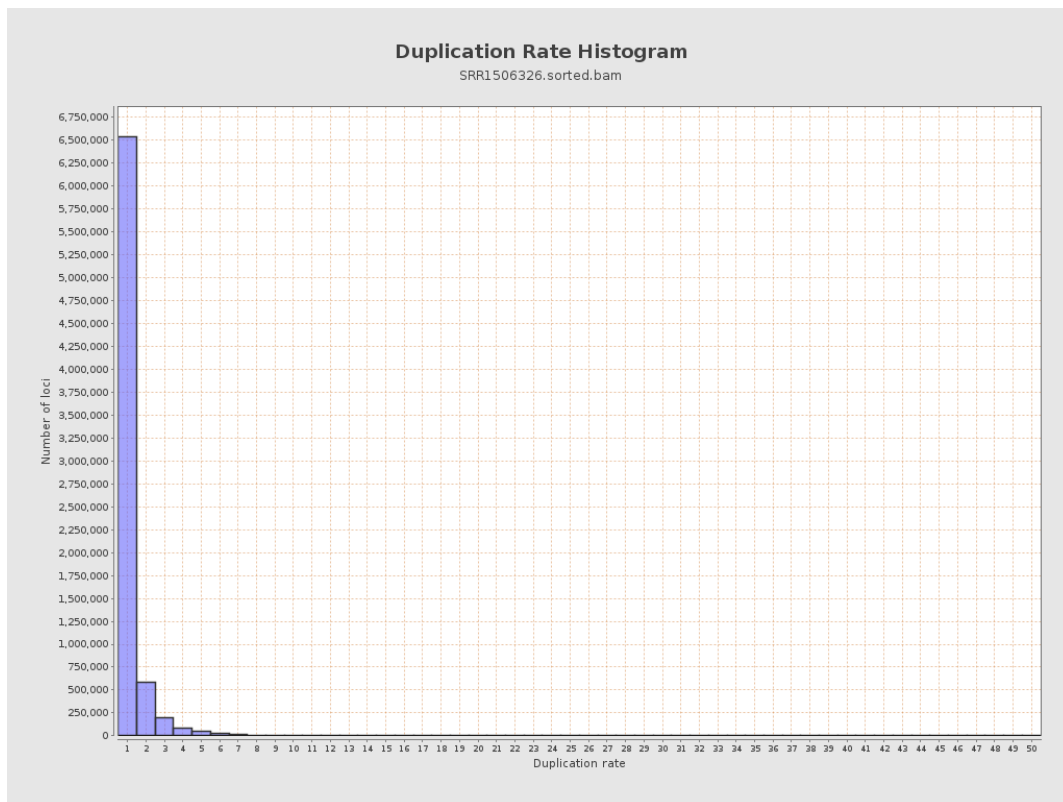
5. Results : Coverage Histogram (0-50X)



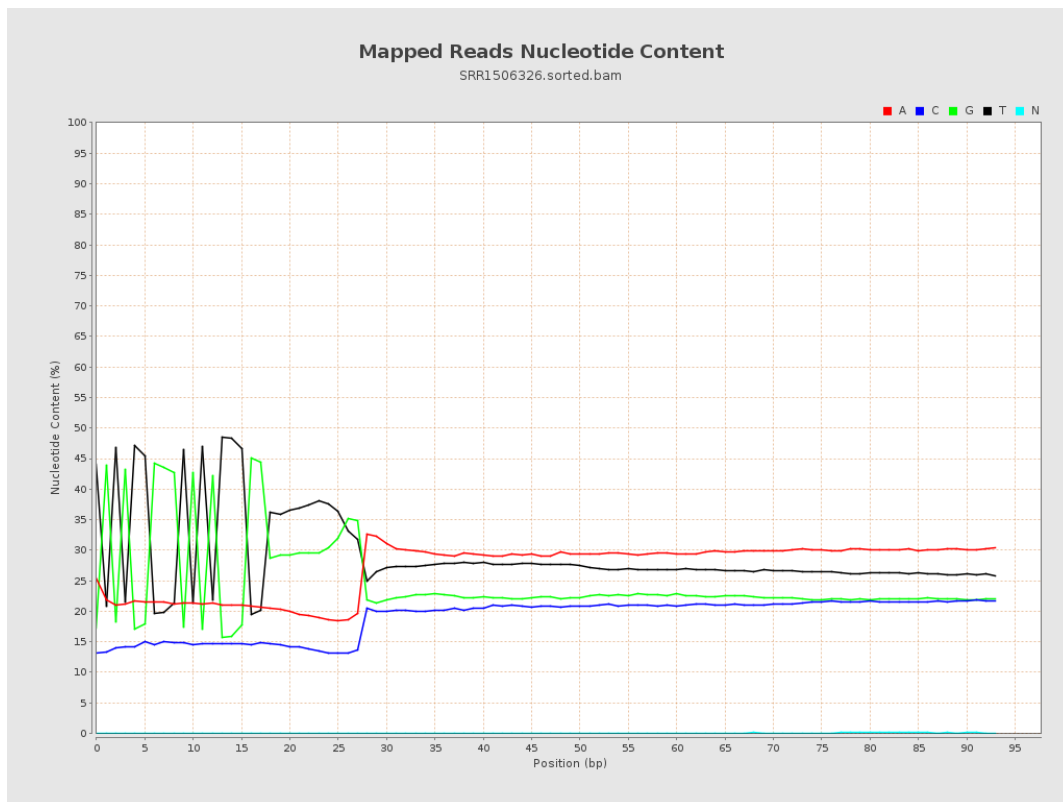
6. Results : Genome Fraction Coverage



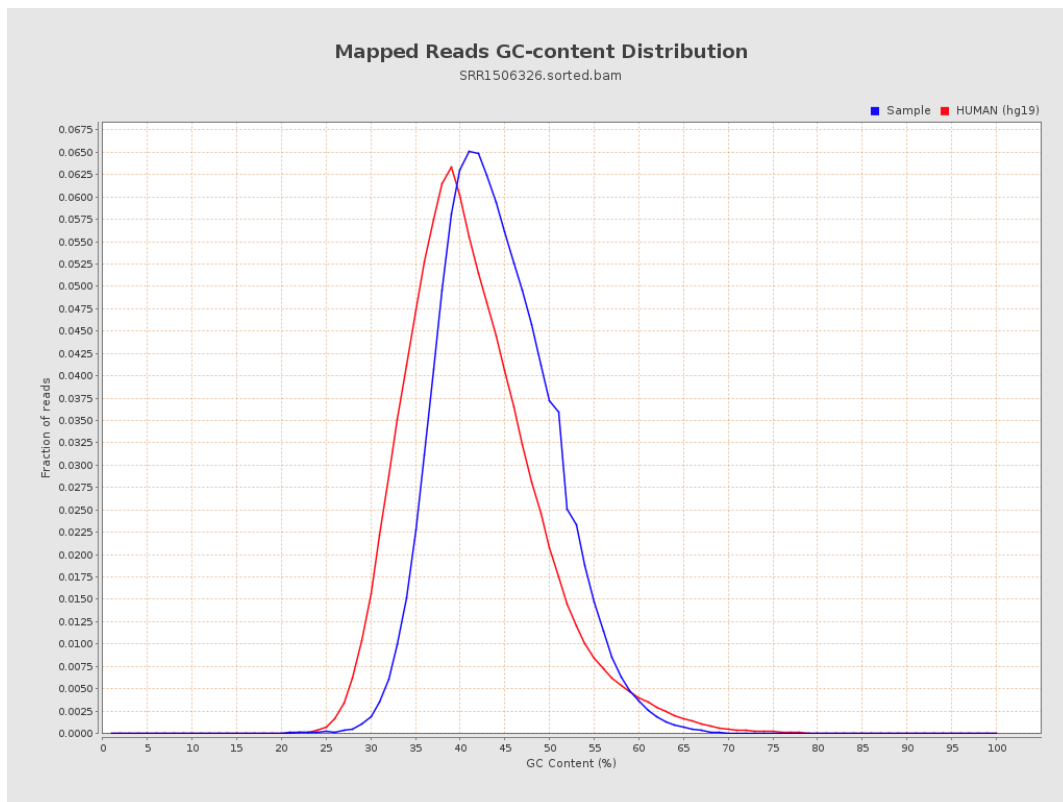
7. Results : Duplication Rate Histogram



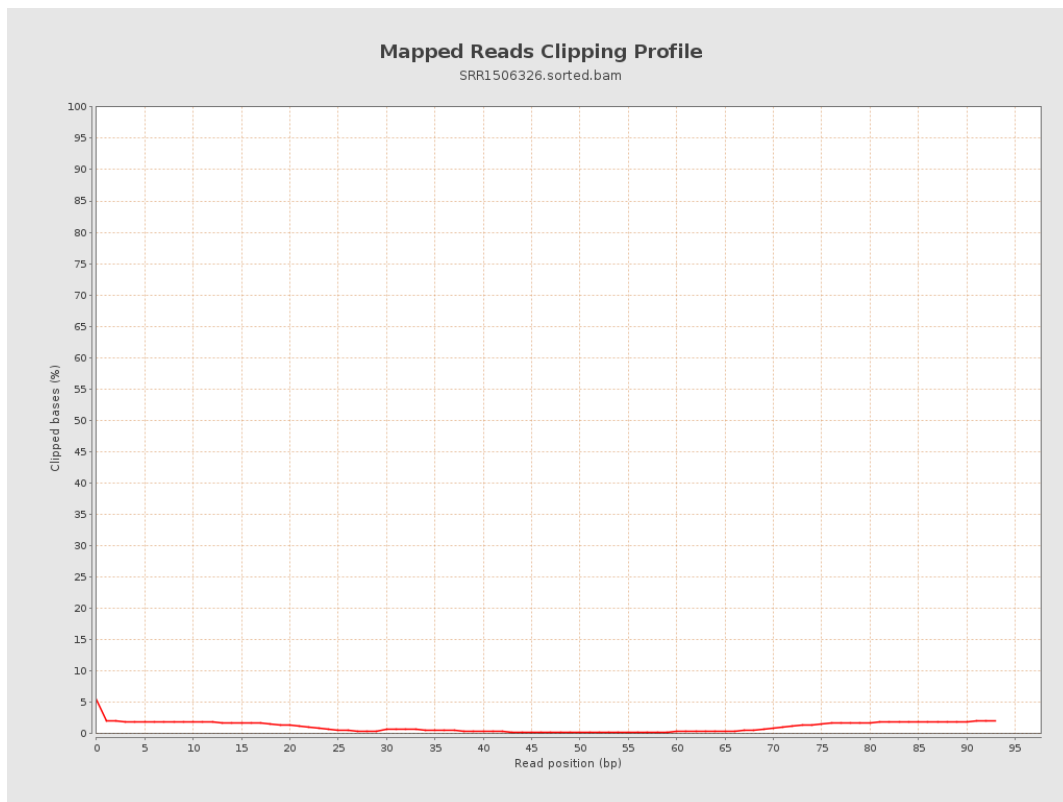
8. Results : Mapped Reads Nucleotide Content



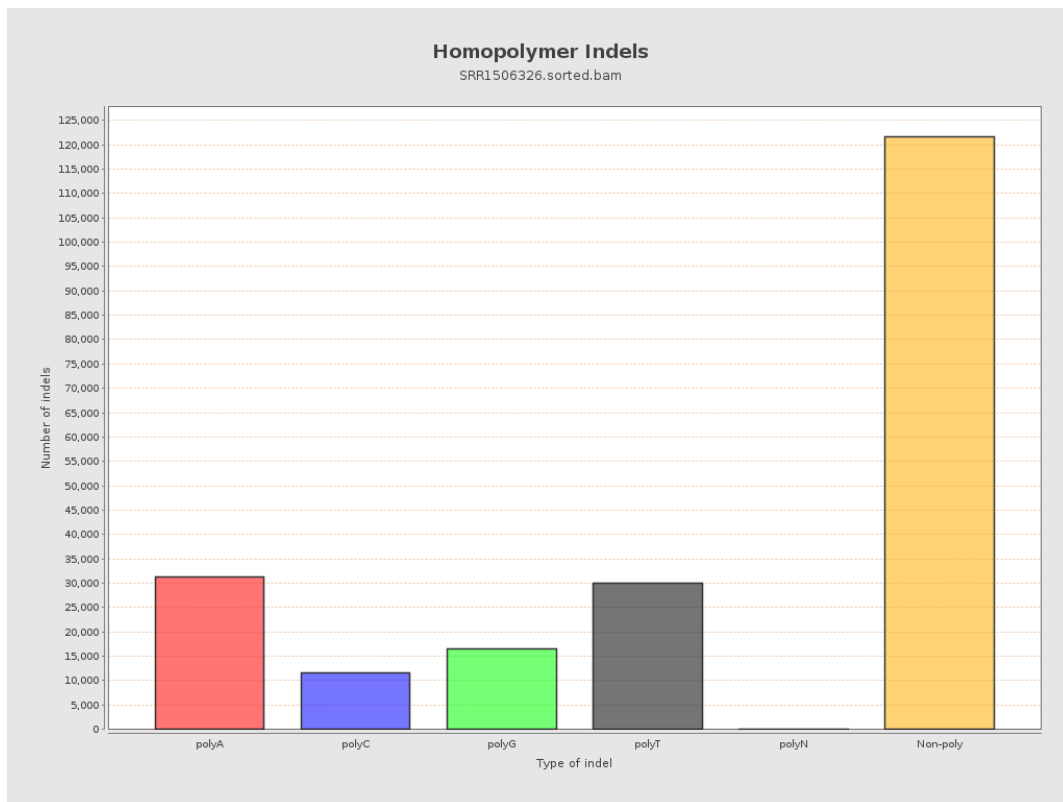
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

