

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 05:17:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524466.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_SRR10524466 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524466.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 05:17:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524466.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,221,867
Mapped reads	1,111,524 / 90.97%
Unmapped reads	110,343 / 9.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,851 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	58,416 / 4.78%
Duplication rate	4.17%
Clipped reads	1,111,438 / 90.96%

2.2. ACGT Content

Number/percentage of A's	16,511,524 / 25.53%
Number/percentage of C's	11,817,313 / 18.27%
Number/percentage of T's	21,114,428 / 32.65%
Number/percentage of G's	15,225,125 / 23.54%
Number/percentage of N's	1,424 / 0%
GC Percentage	41.82%

2.3. Coverage

Mean	0.0209

Standard Deviation	0.2301
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2.4. Mapping Quality

Mean Mapping Quality	45.86
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2.5. Mismatches and indels

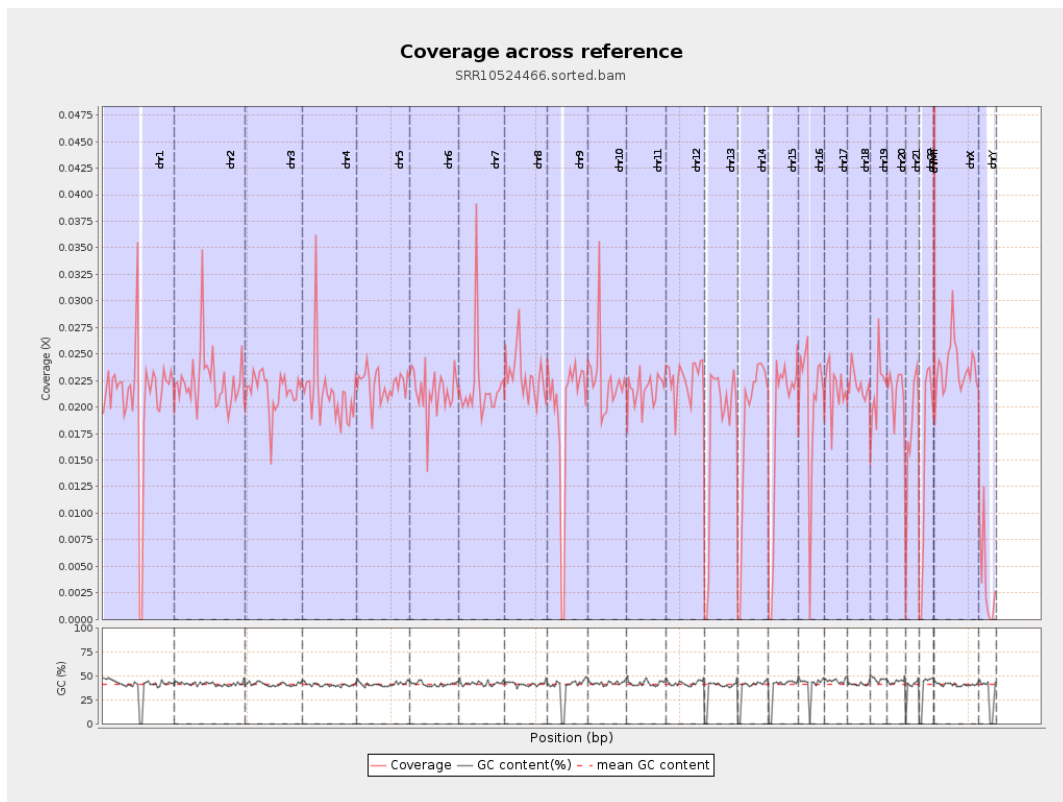
General error rate	0.52%
Mismatches	328,223
Insertions	5,525
Mapped reads with at least one insertion	0.49%
Deletions	13,208
Mapped reads with at least one deletion	1.18%
Homopolymer indels	44.25%

2.6. Chromosome stats

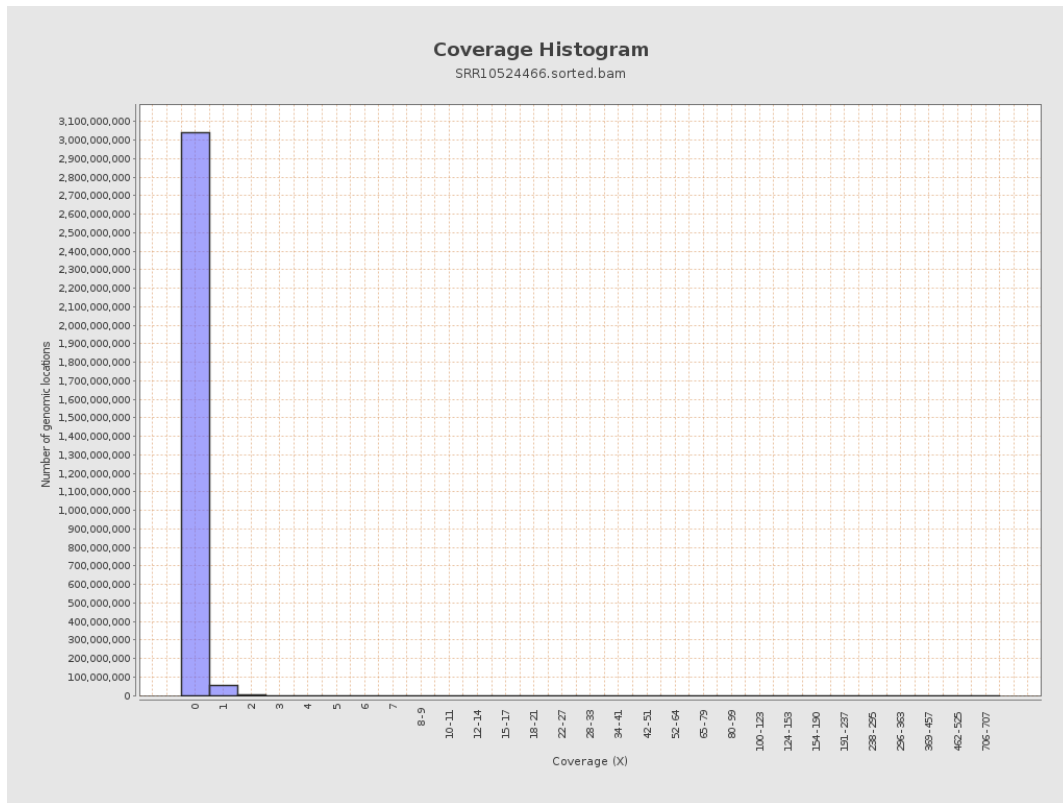
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5172474	0.0208	0.3679
chr2	243199373	5467360	0.0225	0.3354
chr3	198022430	4262532	0.0215	0.1616
chr4	191154276	4072088	0.0213	0.1793
chr5	180915260	4006180	0.0221	0.1645
chr6	171115067	3677623	0.0215	0.1766
chr7	159138663	3485506	0.0219	0.2973

chr8	146364022	3365448	0.023	0.2994
chr9	141213431	2756347	0.0195	0.189
chr10	135534747	3055358	0.0225	0.2078
chr11	135006516	2925560	0.0217	0.1963
chr12	133851895	3024508	0.0226	0.168
chr13	115169878	2048093	0.0178	0.1482
chr14	107349540	1996694	0.0186	0.1531
chr15	102531392	1869981	0.0182	0.1494
chr16	90354753	1837343	0.0203	0.1679
chr17	81195210	1765732	0.0217	0.1683
chr18	78077248	1722464	0.0221	0.3232
chr19	59128983	1291248	0.0218	0.2621
chr20	63025520	1341922	0.0213	0.1646
chr21	48129895	853541	0.0177	0.1579
chr22	51304566	786131	0.0153	0.136
chrMT	16571	4596	0.2774	0.5827
chrX	155270560	3686433	0.0237	0.1838
chrY	59373566	215457	0.0036	0.112

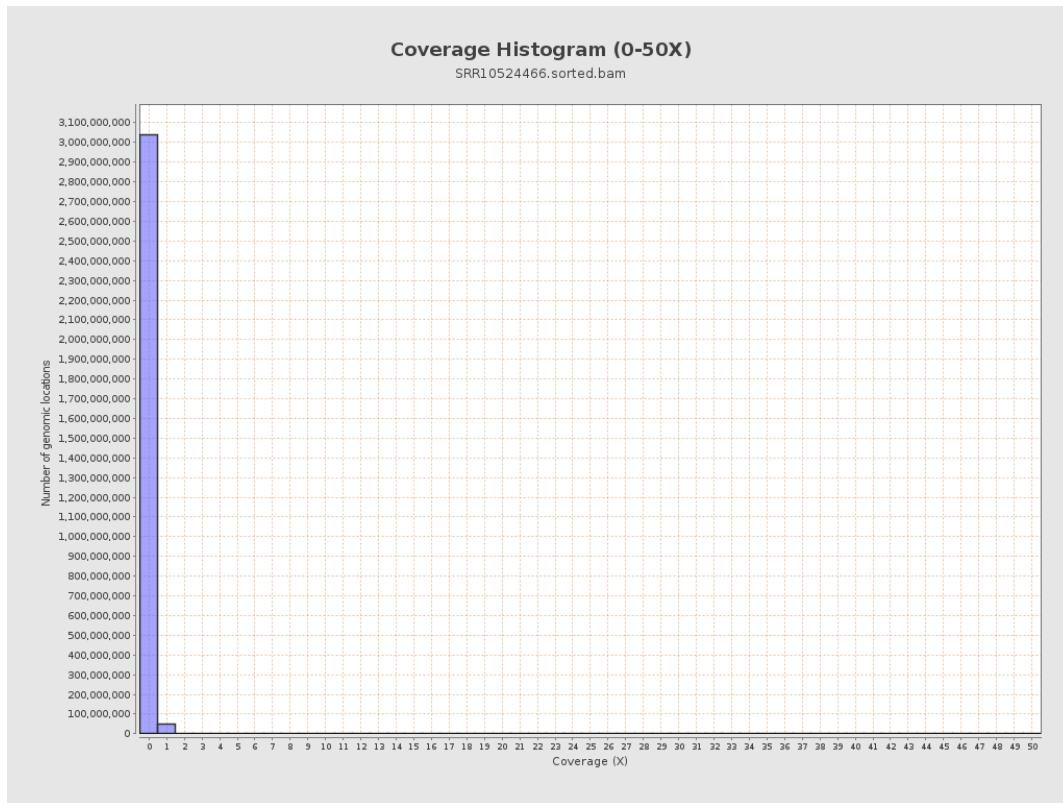
3. Results : Coverage across reference



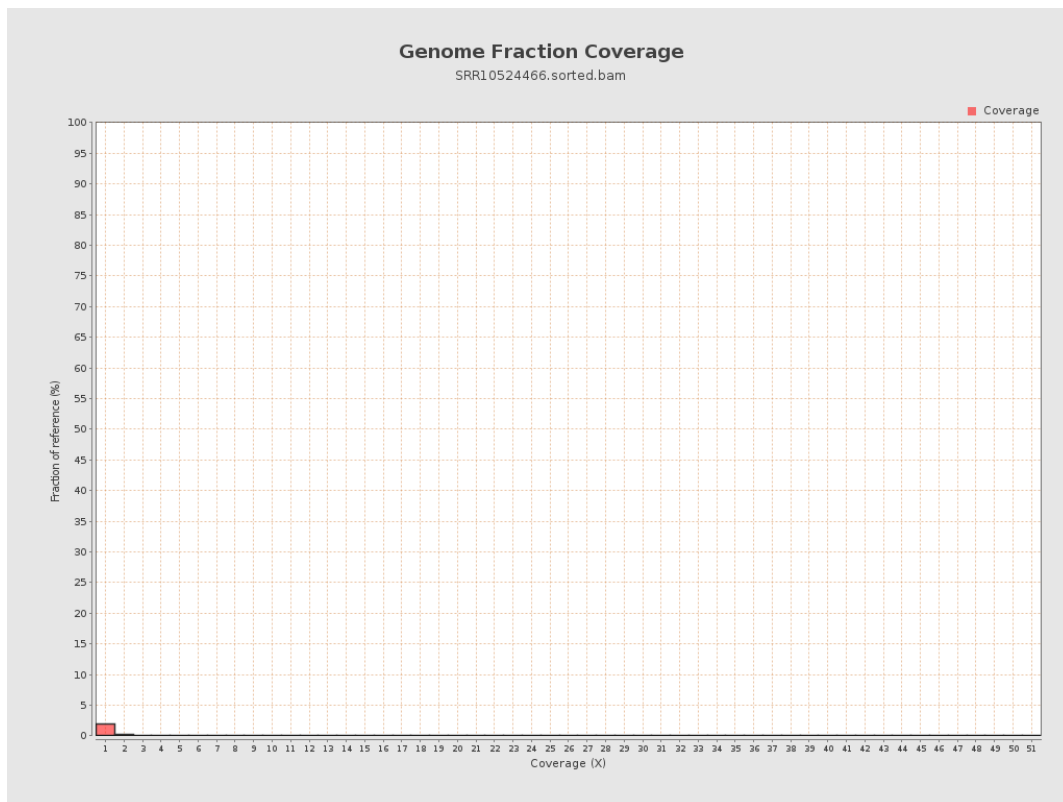
4. Results : Coverage Histogram



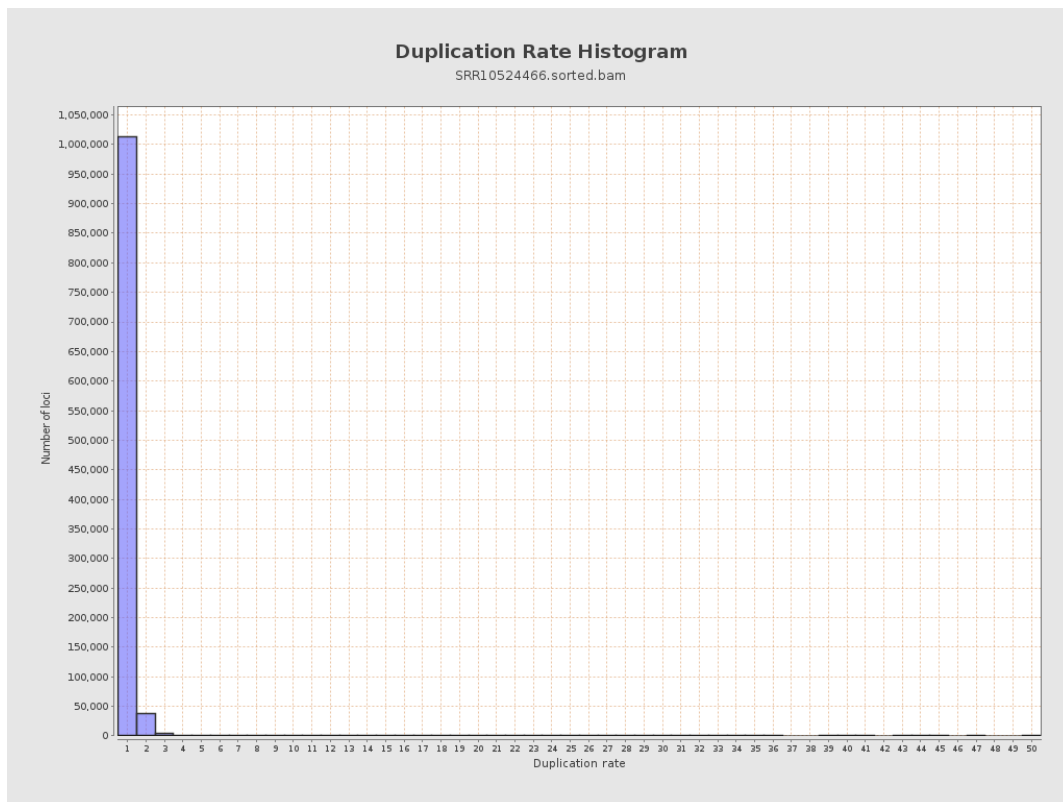
5. Results : Coverage Histogram (0-50X)



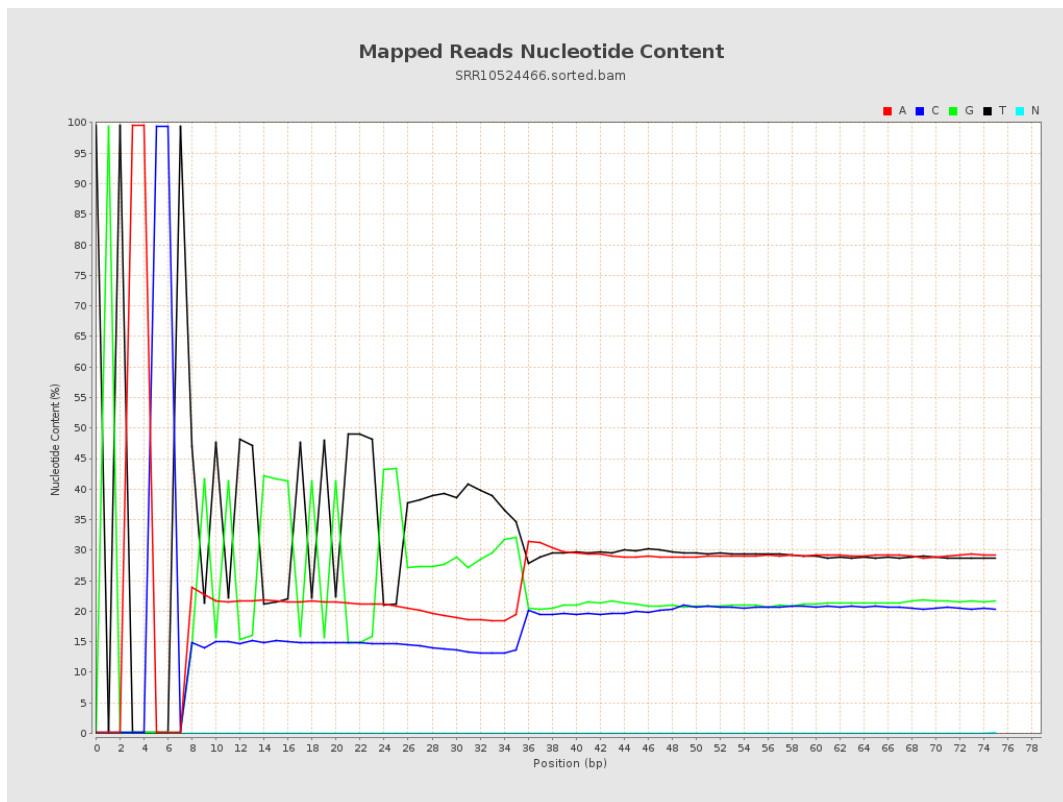
6. Results : Genome Fraction Coverage



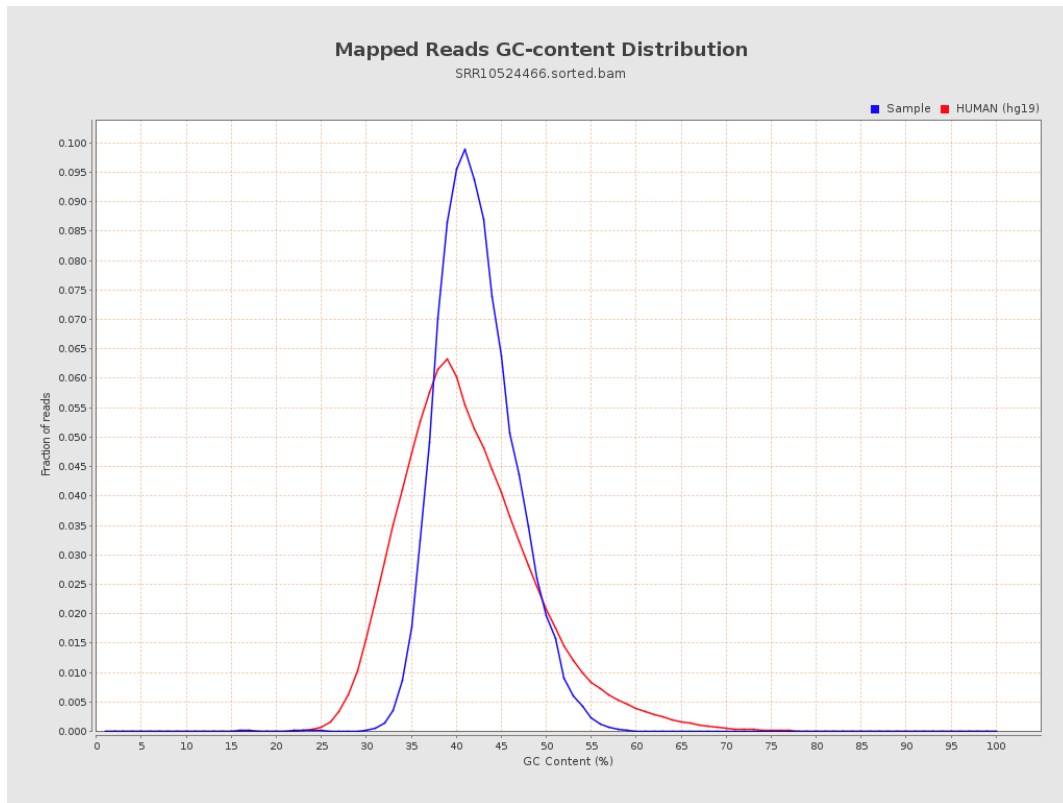
7. Results : Duplication Rate Histogram



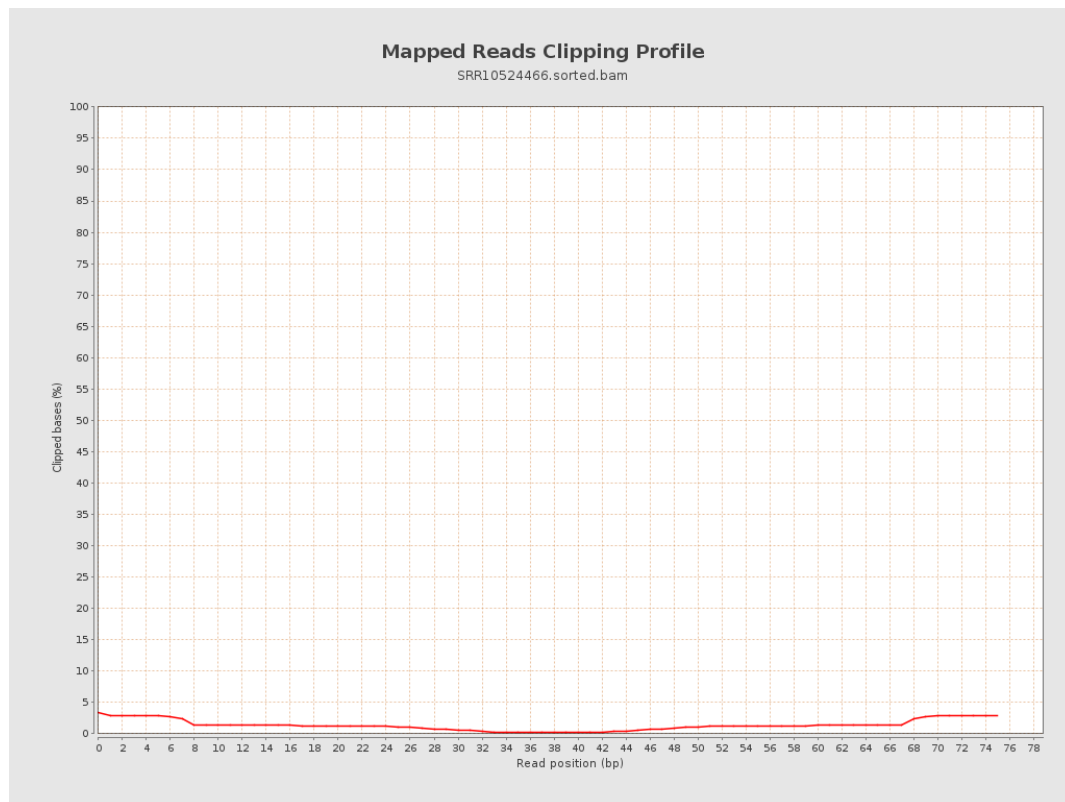
8. Results : Mapped Reads Nucleotide Content



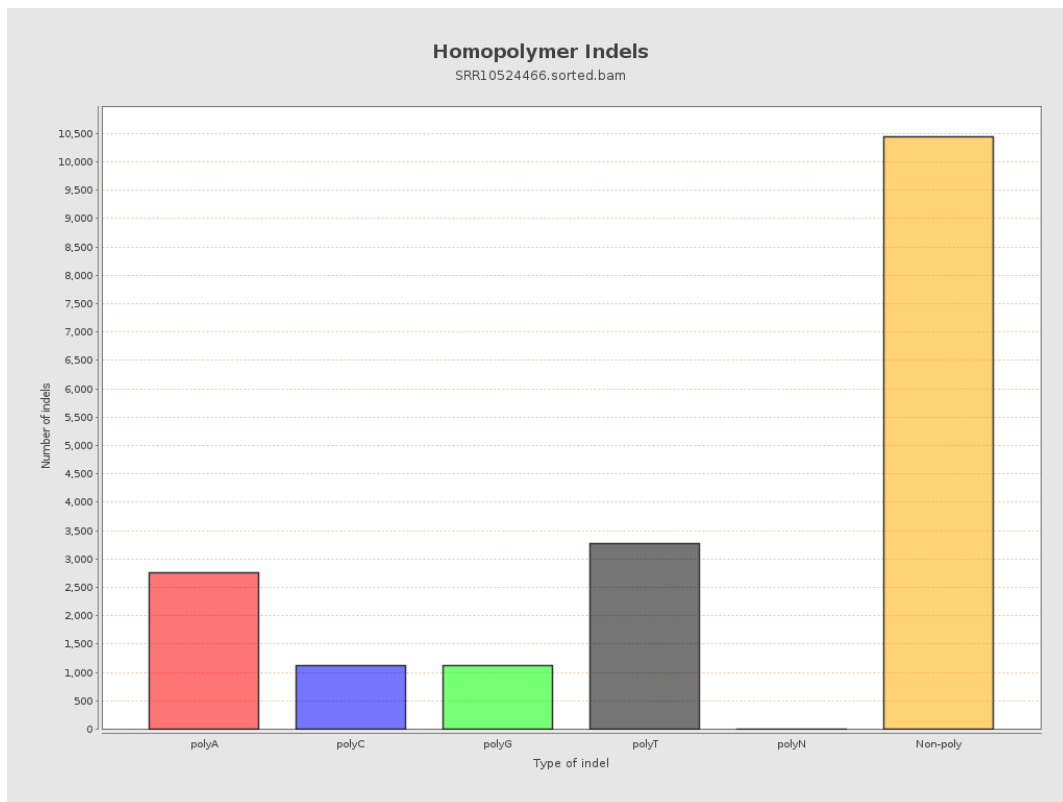
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

