

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 20:43:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236103.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_SRR6236103 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236103.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 20:43:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236103.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,339,722
Mapped reads	799,916 / 59.71%
Unmapped reads	539,806 / 40.29%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,748 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	33,234 / 2.48%
Duplication rate	3.66%
Clipped reads	391,005 / 29.19%

2.2. ACGT Content

Number/percentage of A's	14,403,836 / 27.66%
Number/percentage of C's	9,058,860 / 17.4%
Number/percentage of T's	17,097,090 / 32.83%
Number/percentage of G's	11,485,137 / 22.06%
Number/percentage of N's	26,287 / 0.05%
GC Percentage	39.45%

2.3. Coverage

Mean	0.0168

Standard Deviation	0.1701
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2.4. Mapping Quality

Mean Mapping Quality	44.93
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2.5. Mismatches and indels

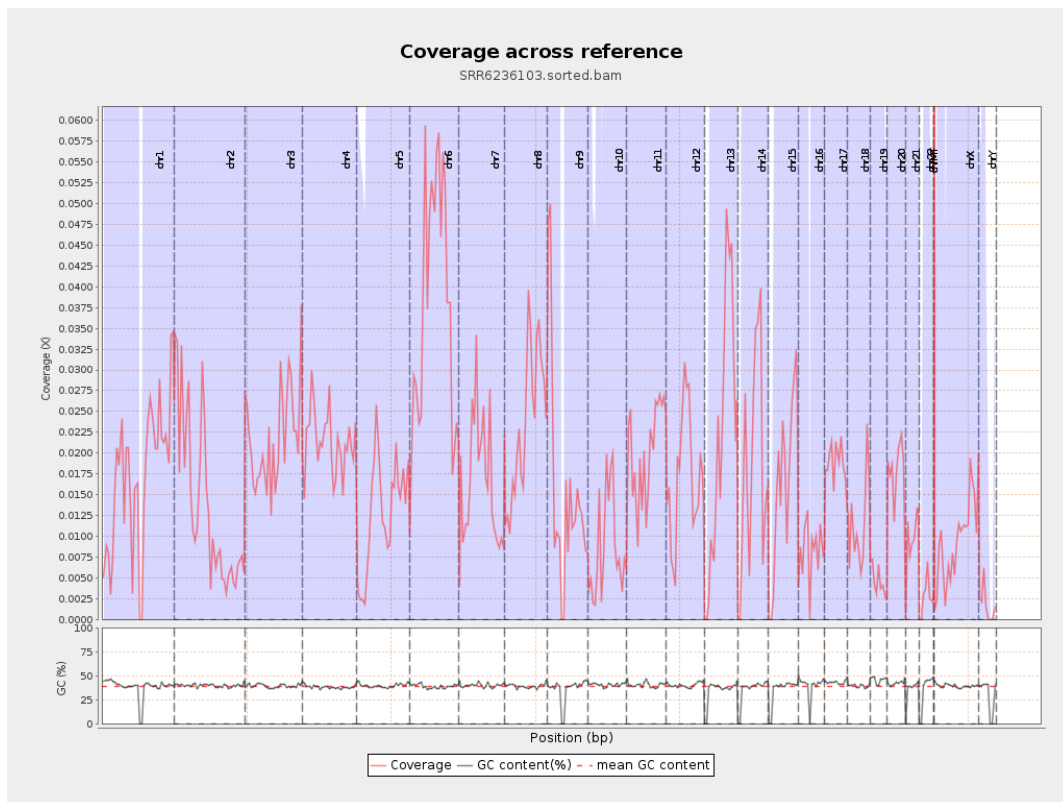
General error rate	0.82%
Mismatches	417,939
Insertions	3,560
Mapped reads with at least one insertion	0.44%
Deletions	15,451
Mapped reads with at least one deletion	1.91%
Homopolymer indels	47.06%

2.6. Chromosome stats

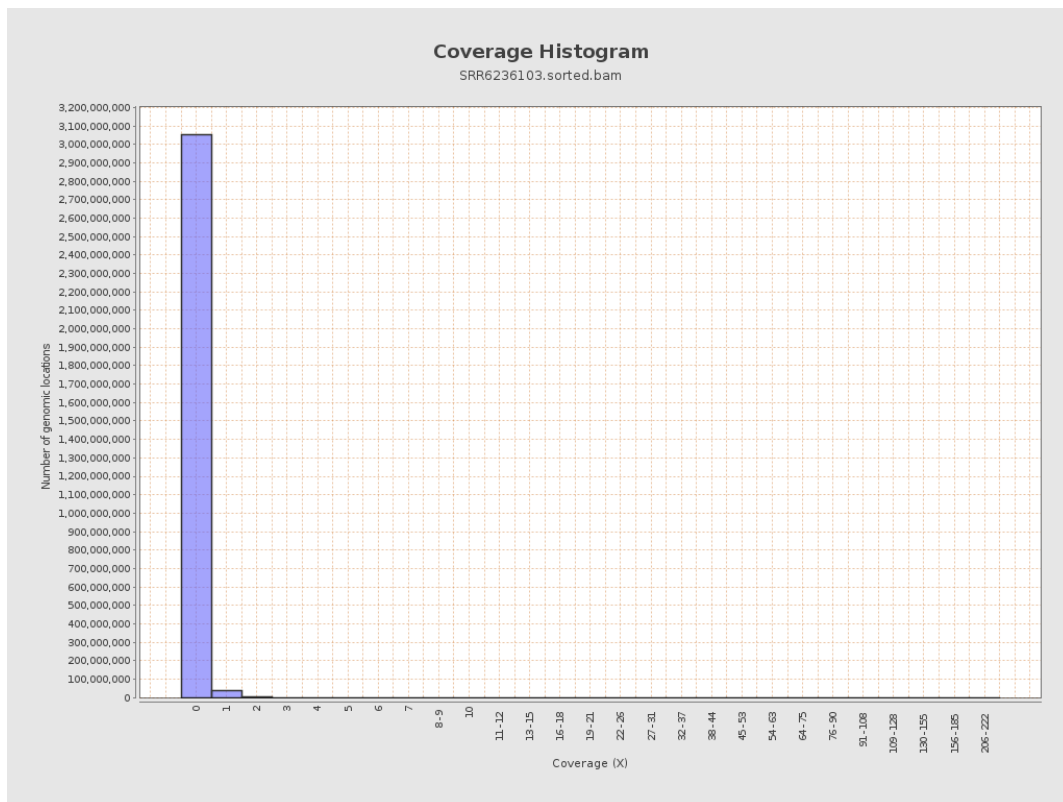
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4255518	0.0171	0.1704
chr2	243199373	3293925	0.0135	0.1705
chr3	198022430	4283941	0.0216	0.1637
chr4	191154276	4076267	0.0213	0.1656
chr5	180915260	2351959	0.013	0.1271
chr6	171115067	6482069	0.0379	0.2547
chr7	159138663	2644215	0.0166	0.2517

chr8	146364022	3431499	0.0234	0.2267
chr9	141213431	2197831	0.0156	0.1662
chr10	135534747	1174179	0.0087	0.1282
chr11	135006516	2721888	0.0202	0.1632
chr12	133851895	2284728	0.0171	0.1472
chr13	115169878	2528799	0.022	0.1657
chr14	107349540	1915615	0.0178	0.1518
chr15	102531392	1699376	0.0166	0.144
chr16	90354753	730304	0.0081	0.1058
chr17	81195210	1524961	0.0188	0.1643
chr18	78077248	872351	0.0112	0.2227
chr19	59128983	269025	0.0045	0.1138
chr20	63025520	1121666	0.0178	0.1489
chr21	48129895	463847	0.0096	0.1147
chr22	51304566	149017	0.0029	0.0585
chrMT	16571	63986	3.8613	2.8195
chrX	155270560	1457240	0.0094	0.1114
chrY	59373566	103975	0.0018	0.058

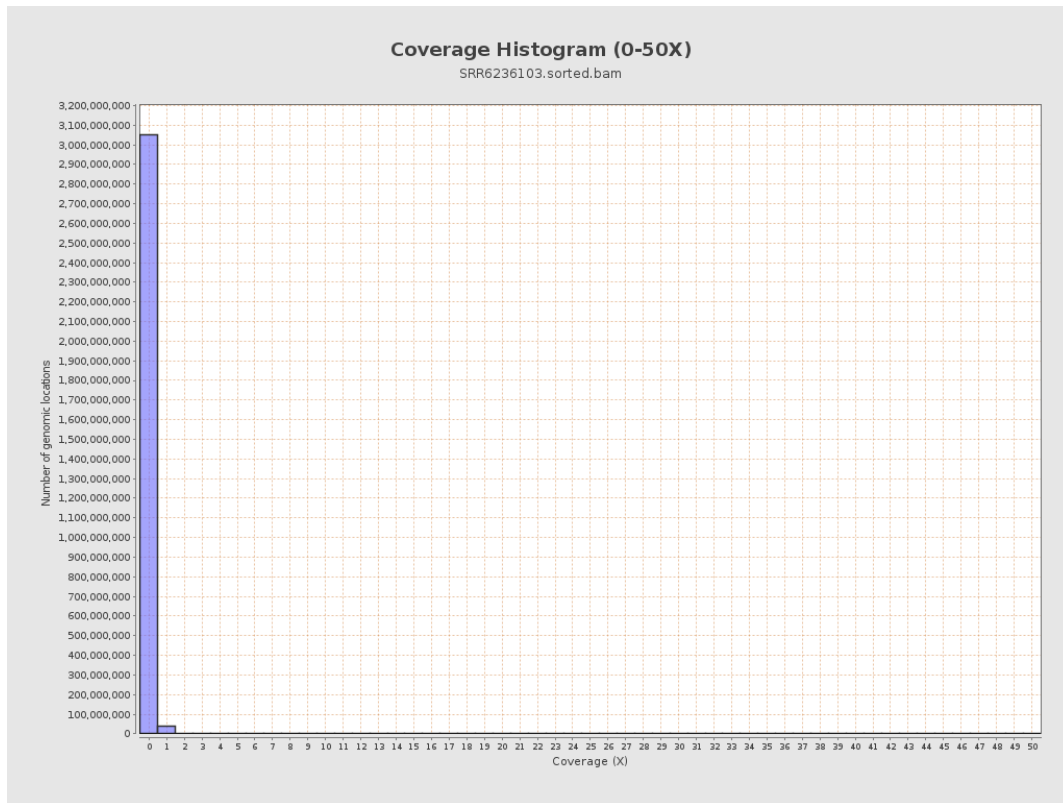
3. Results : Coverage across reference



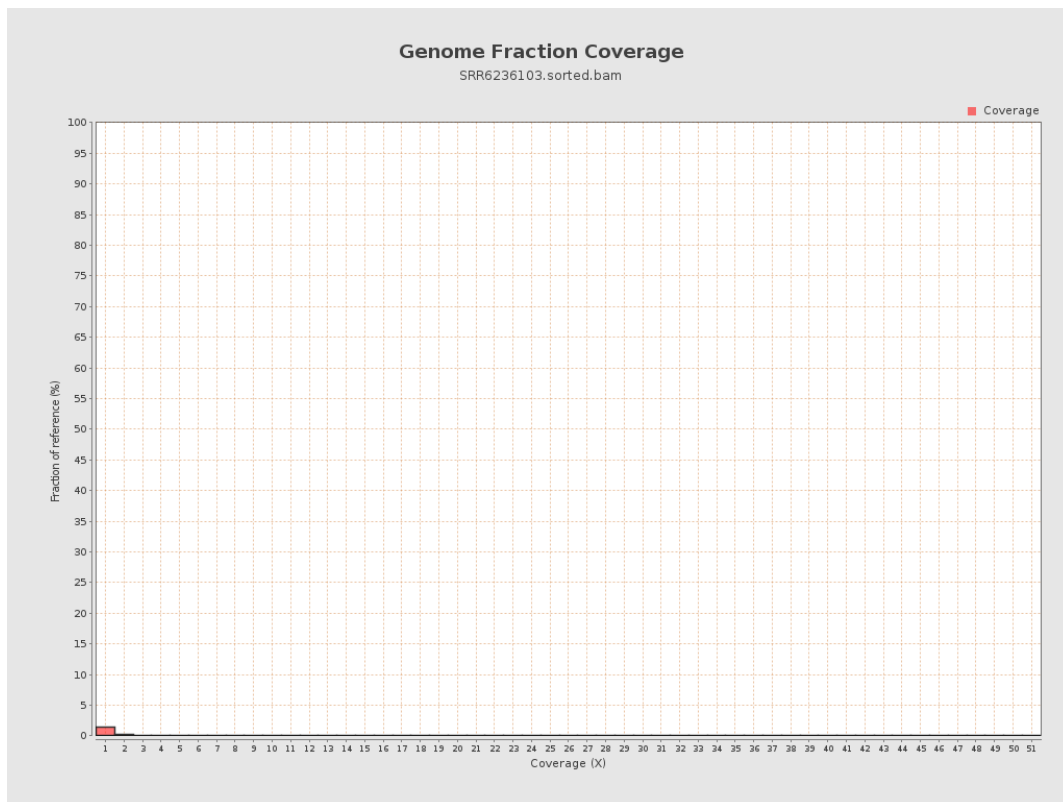
4. Results : Coverage Histogram



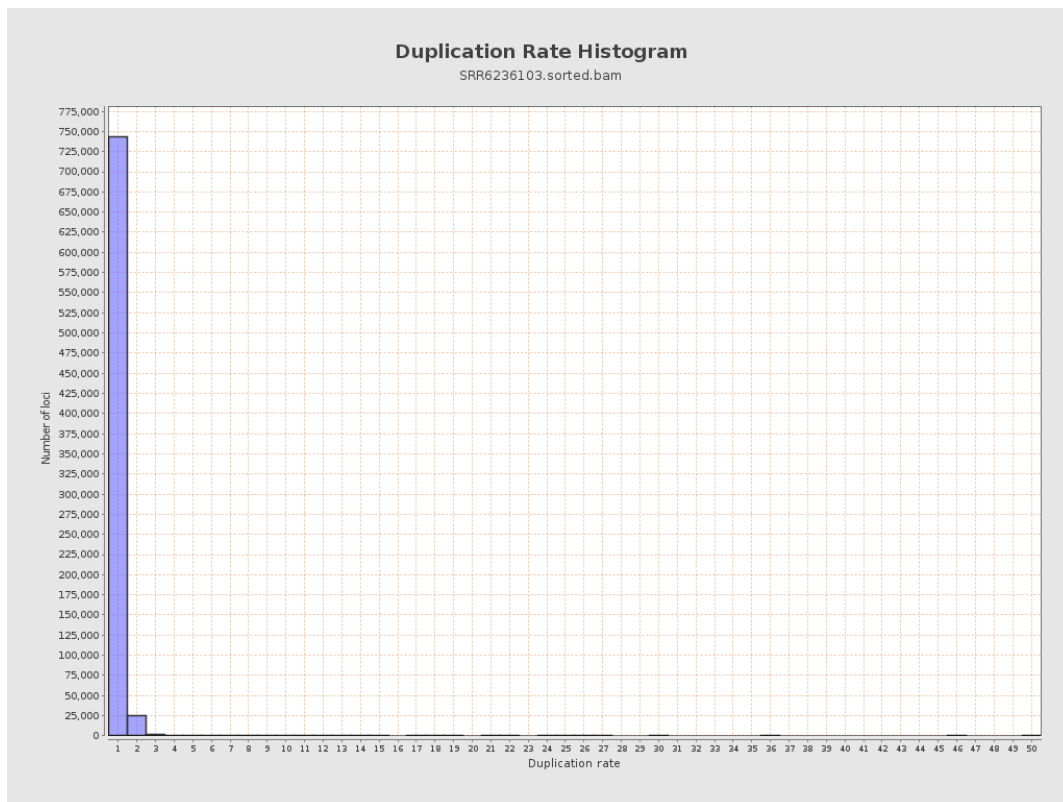
5. Results : Coverage Histogram (0-50X)



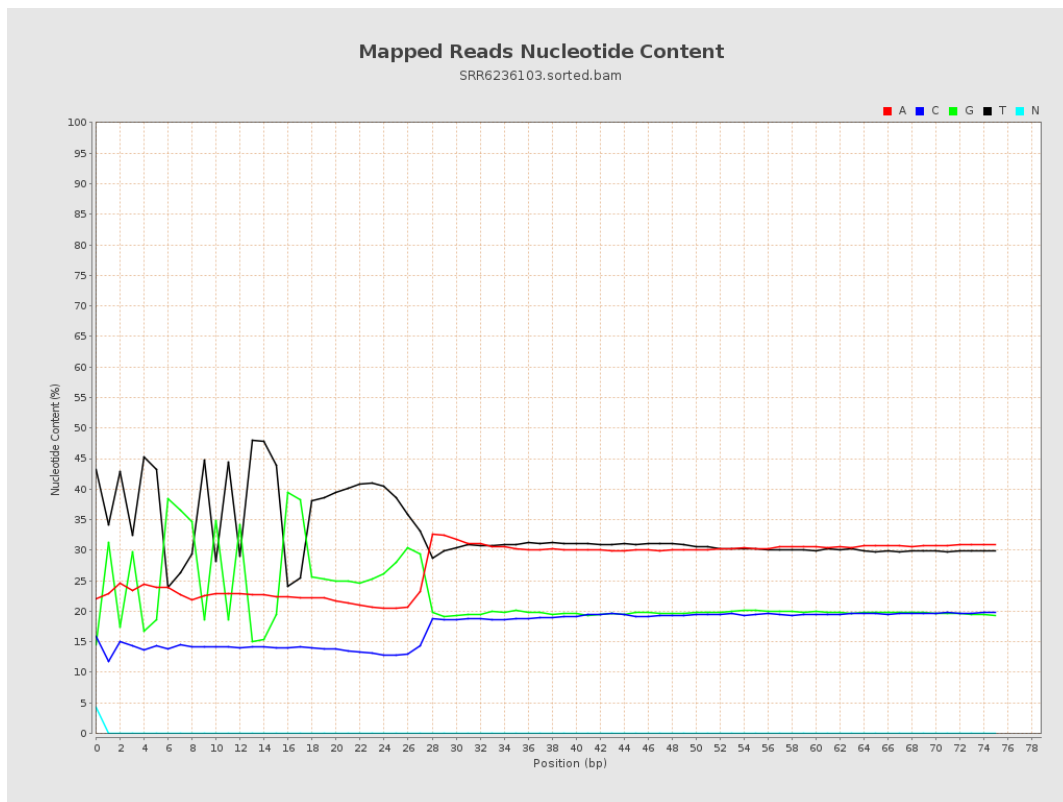
6. Results : Genome Fraction Coverage



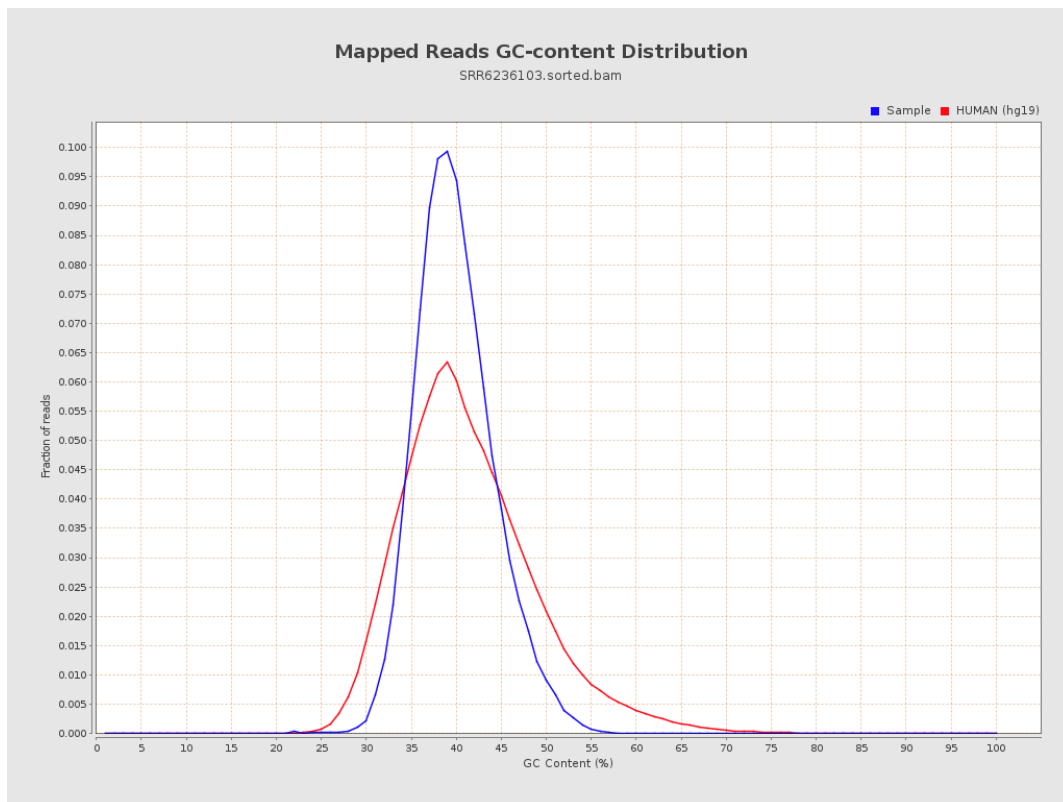
7. Results : Duplication Rate Histogram



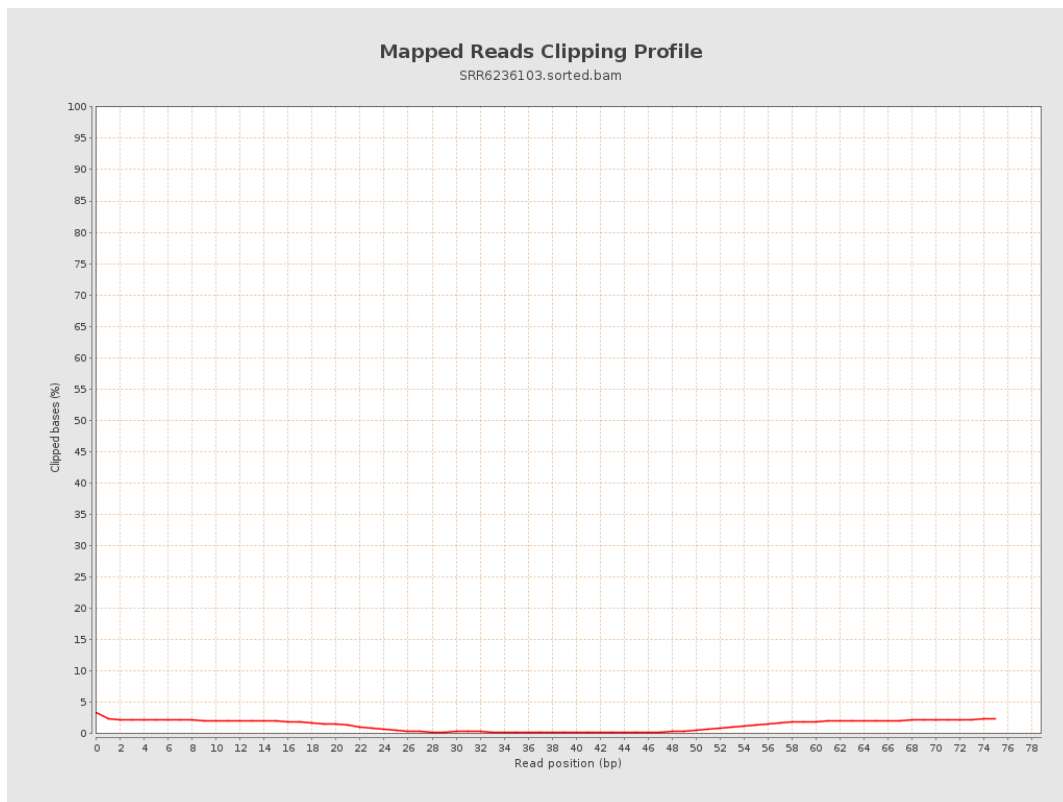
8. Results : Mapped Reads Nucleotide Content



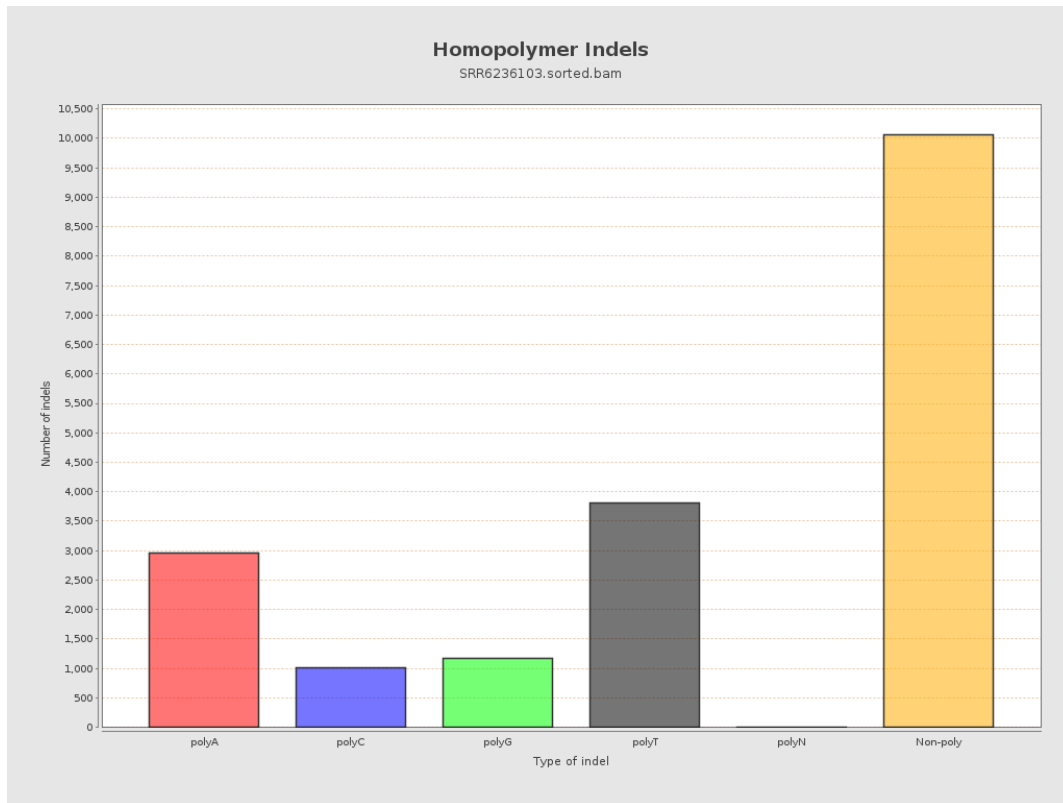
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

