

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 13:40:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234068.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_SRR6234068 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234068.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 13:40:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234068.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	785,688
Mapped reads	605,956 / 77.12%
Unmapped reads	179,732 / 22.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,513 / 0.83%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	44,497 / 5.66%
Duplication rate	6.05%
Clipped reads	326,650 / 41.58%

2.2. ACGT Content

Number/percentage of A's	10,805,549 / 27.83%
Number/percentage of C's	6,557,325 / 16.89%
Number/percentage of T's	13,135,567 / 33.83%
Number/percentage of G's	8,327,073 / 21.45%
Number/percentage of N's	2,046 / 0.01%
GC Percentage	38.33%

2.3. Coverage

Mean	0.0126

Standard Deviation	0.2142
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2.4. Mapping Quality

Mean Mapping Quality	45.53
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2.5. Mismatches and indels

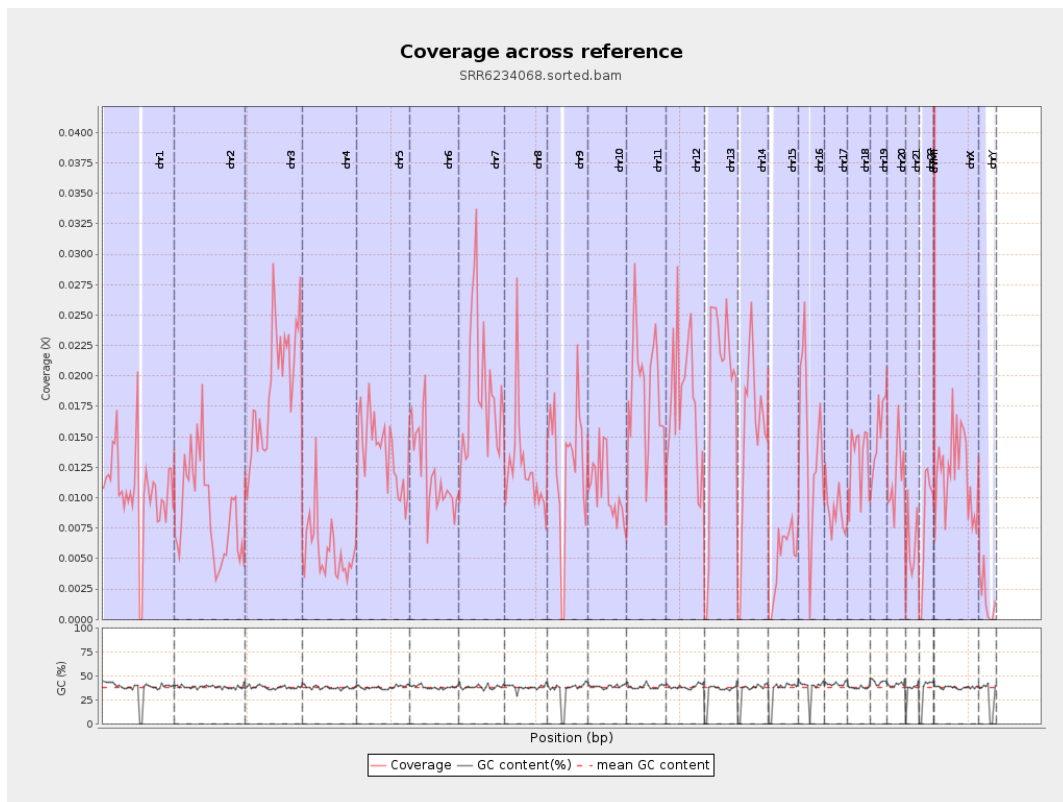
General error rate	0.83%
Mismatches	318,314
Insertions	3,098
Mapped reads with at least one insertion	0.51%
Deletions	14,805
Mapped reads with at least one deletion	2.41%
Homopolymer indels	42.84%

2.6. Chromosome stats

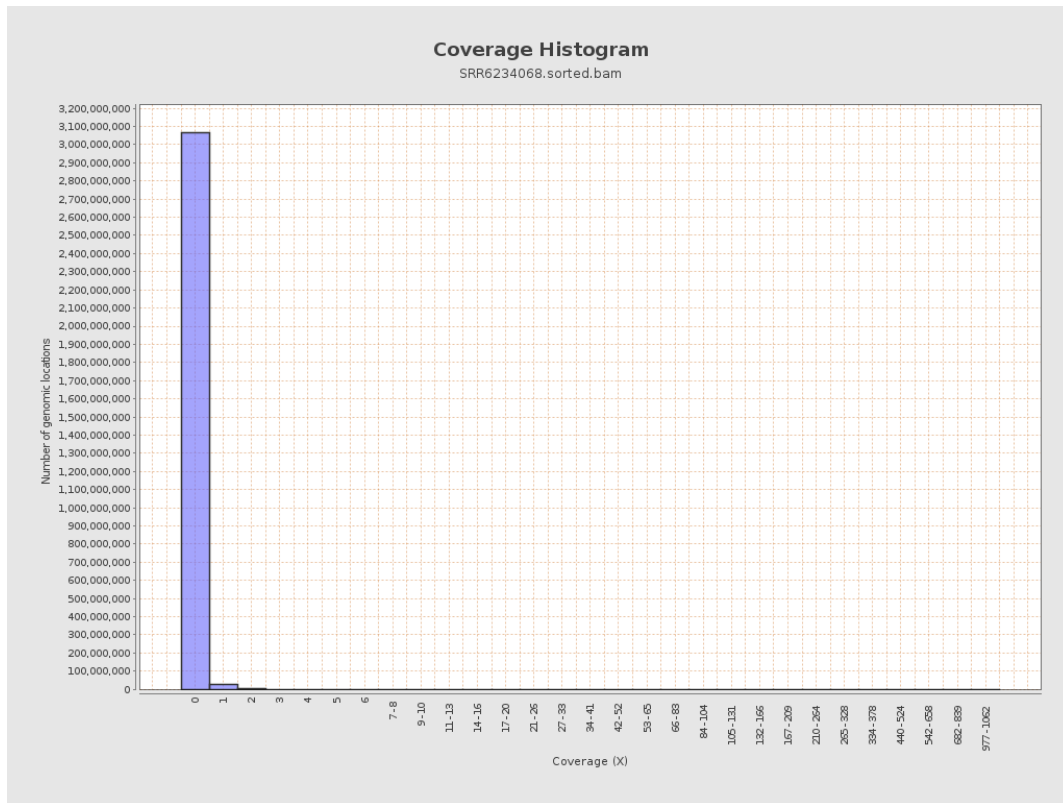
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	2620859	0.0105	0.2457
chr2	243199373	2139881	0.0088	0.1763
chr3	198022430	3797889	0.0192	0.1704
chr4	191154276	1087702	0.0057	0.0965
chr5	180915260	2486471	0.0137	0.1448
chr6	171115067	2064214	0.0121	0.1407
chr7	159138663	2980500	0.0187	0.255

chr8	146364022	1819880	0.0124	0.6243
chr9	141213431	1802666	0.0128	0.1522
chr10	135534747	1435099	0.0106	0.1501
chr11	135006516	2549931	0.0189	0.194
chr12	133851895	2406632	0.018	0.1675
chr13	115169878	2171764	0.0189	0.1717
chr14	107349540	1655244	0.0154	0.1559
chr15	102531392	510022	0.005	0.0845
chr16	90354753	1254285	0.0139	0.1496
chr17	81195210	721361	0.0089	0.1186
chr18	78077248	1025165	0.0131	0.2511
chr19	59128983	907185	0.0153	0.1814
chr20	63025520	736570	0.0117	0.1347
chr21	48129895	291171	0.006	0.096
chr22	51304566	410231	0.008	0.1059
chrMT	16571	14061	0.8485	1.1845
chrX	155270560	1864866	0.012	0.14
chrY	59373566	100007	0.0017	0.0506

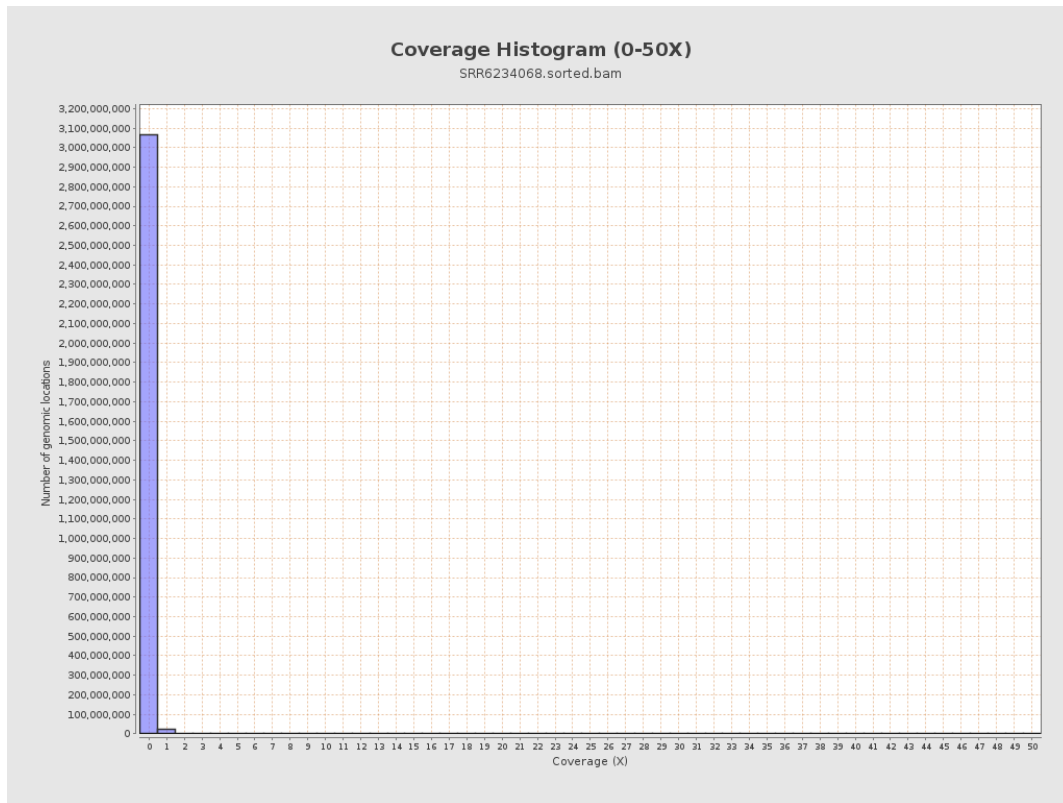
3. Results : Coverage across reference



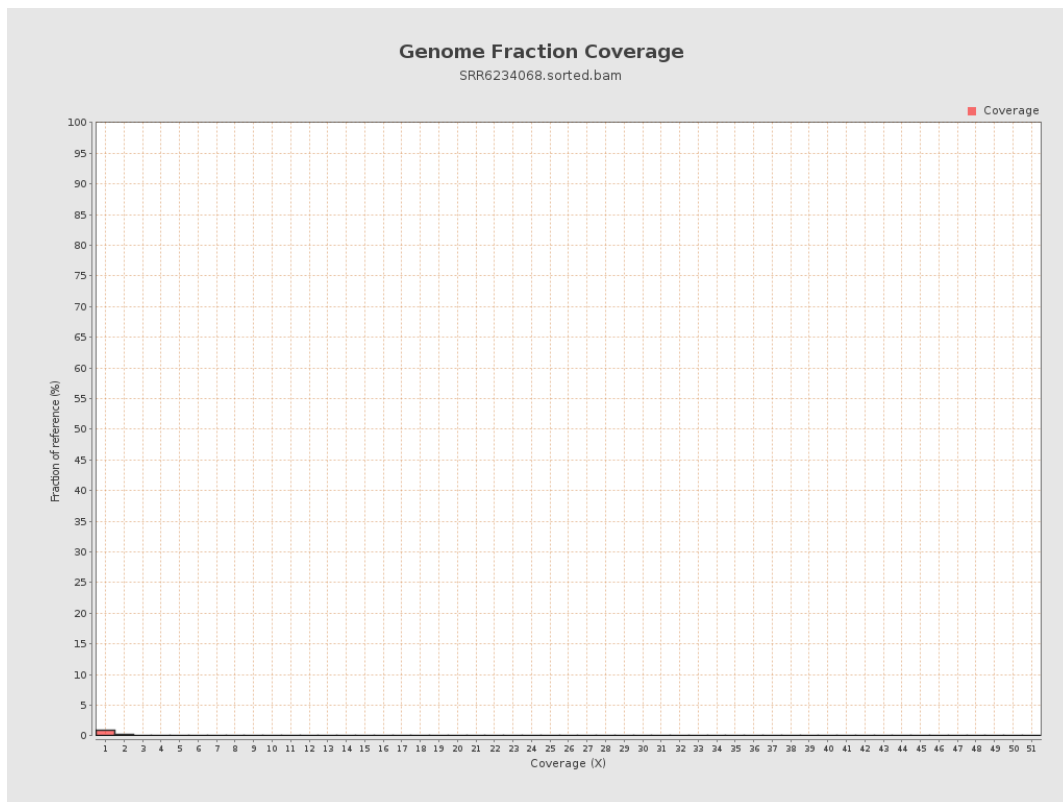
4. Results : Coverage Histogram



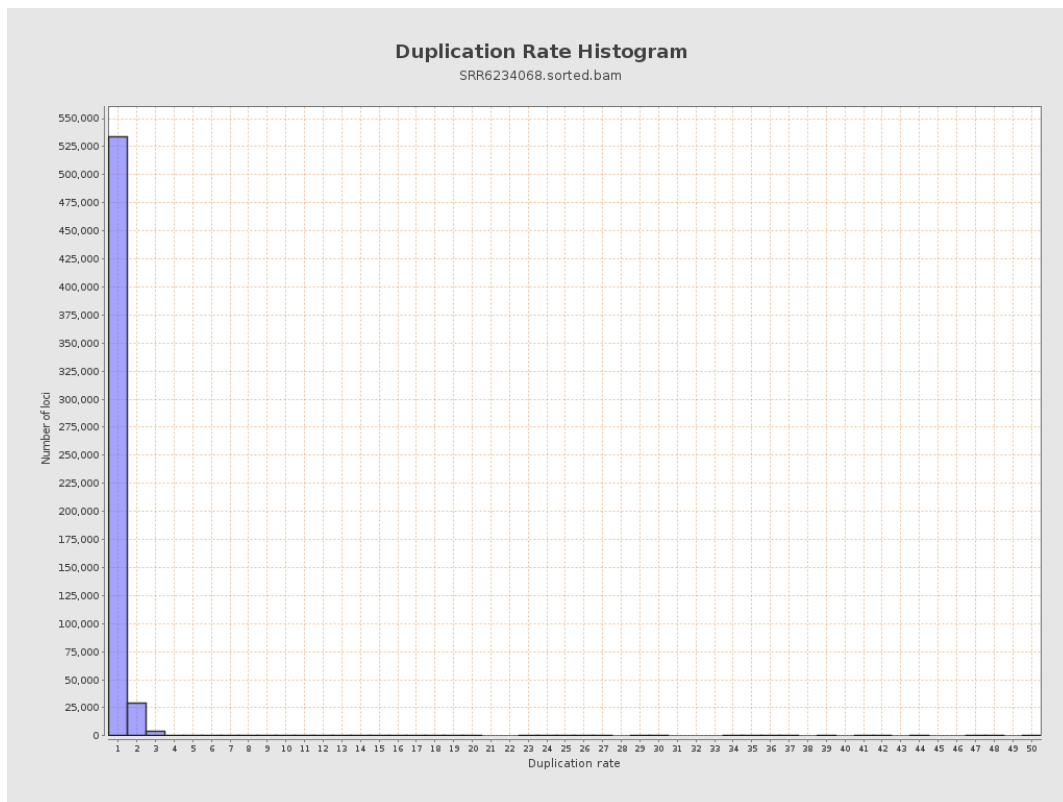
5. Results : Coverage Histogram (0-50X)



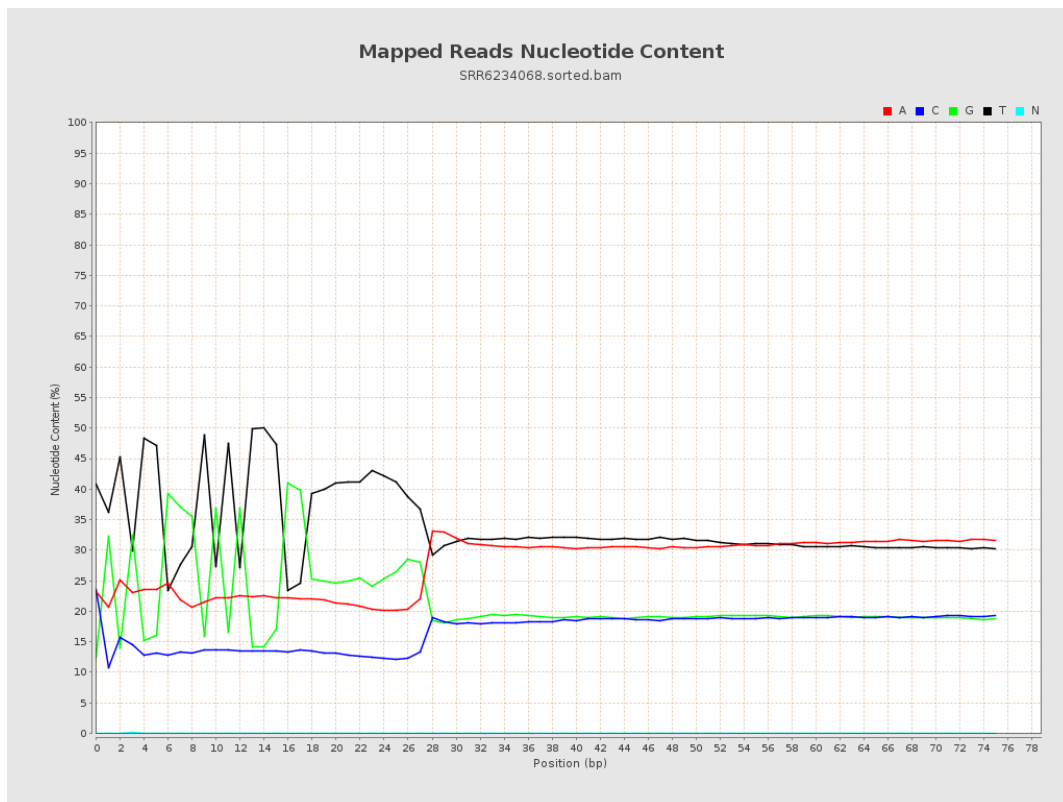
6. Results : Genome Fraction Coverage



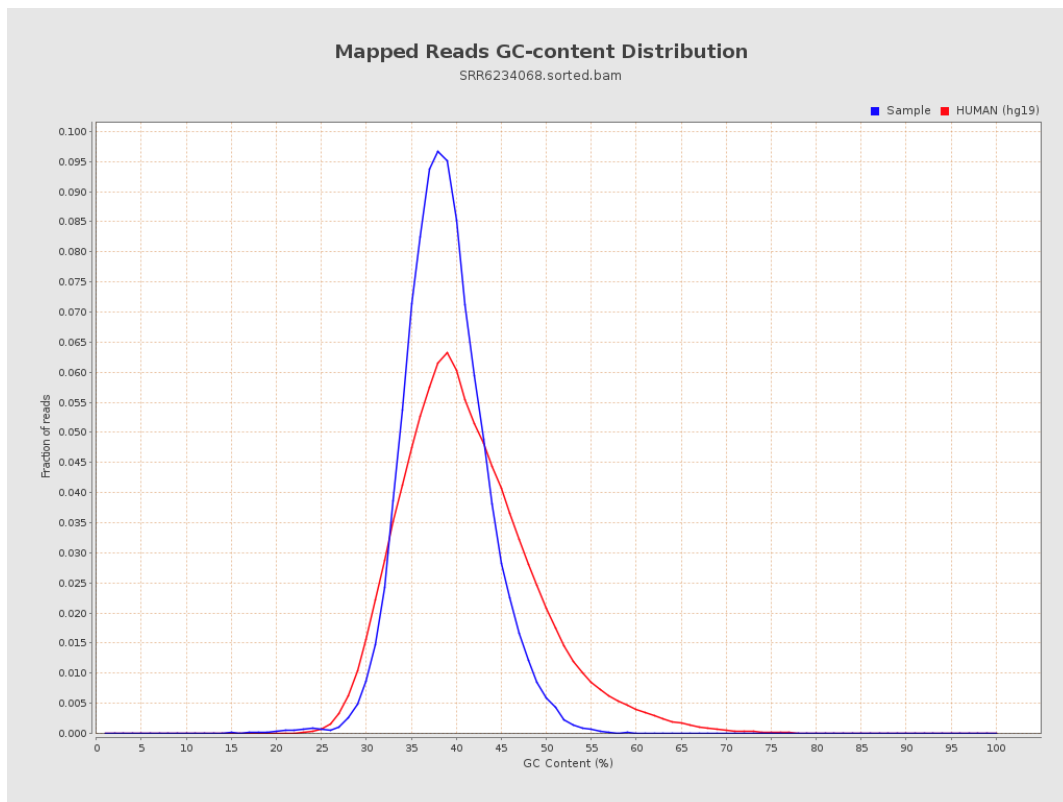
7. Results : Duplication Rate Histogram



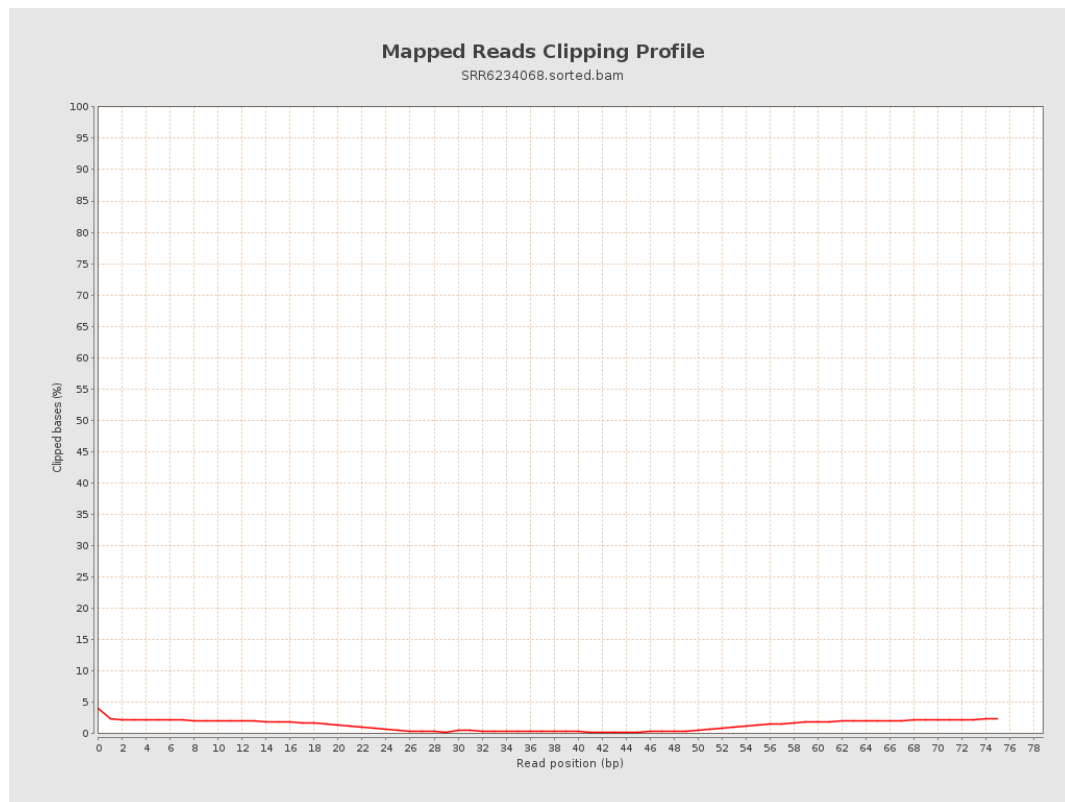
8. Results : Mapped Reads Nucleotide Content



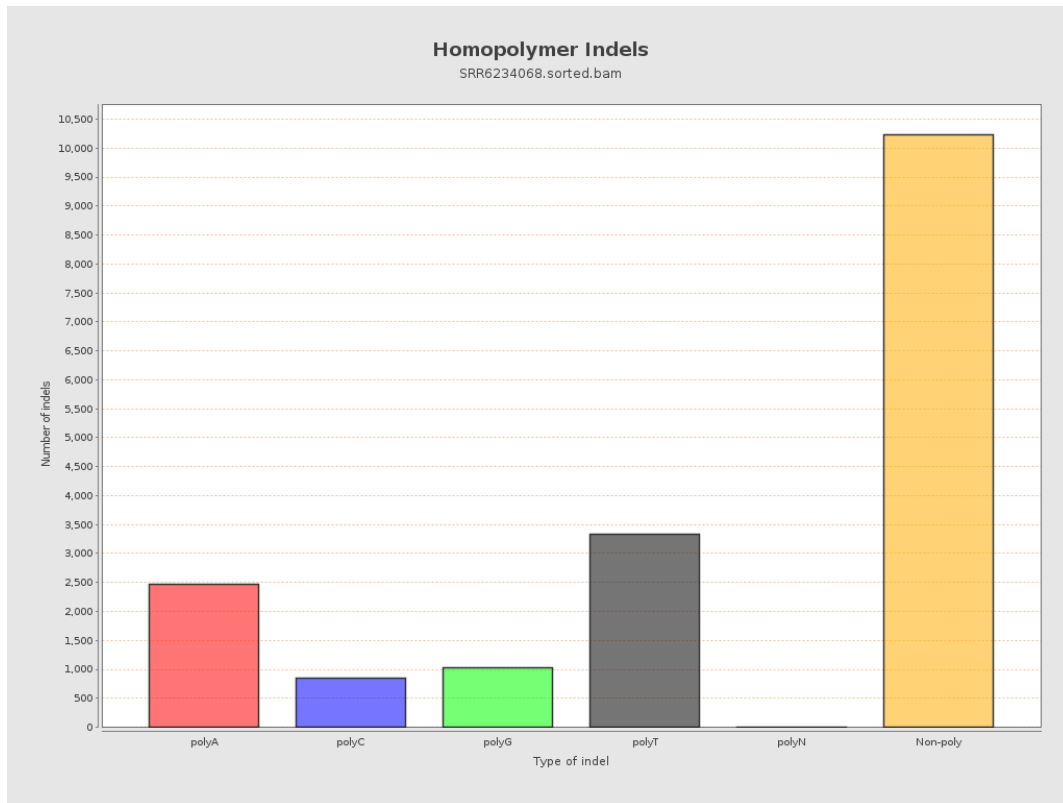
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

