

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 17:39:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068963.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_SRR6068963 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068963.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 17:39:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068963.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,840,331
Mapped reads	2,359,291 / 83.06%
Unmapped reads	481,040 / 16.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,999 / 0.49%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	99,413 / 3.5%
Duplication rate	3.25%
Clipped reads	1,130,323 / 39.8%

2.2. ACGT Content

Number/percentage of A's	42,208,268 / 27.22%
Number/percentage of C's	26,925,562 / 17.36%
Number/percentage of T's	51,316,723 / 33.09%
Number/percentage of G's	34,248,775 / 22.08%
Number/percentage of N's	378,853 / 0.24%
GC Percentage	39.45%

2.3. Coverage

Mean	0.0501

Standard Deviation	0.4523
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2.4. Mapping Quality

Mean Mapping Quality	45.98
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2.5. Mismatches and indels

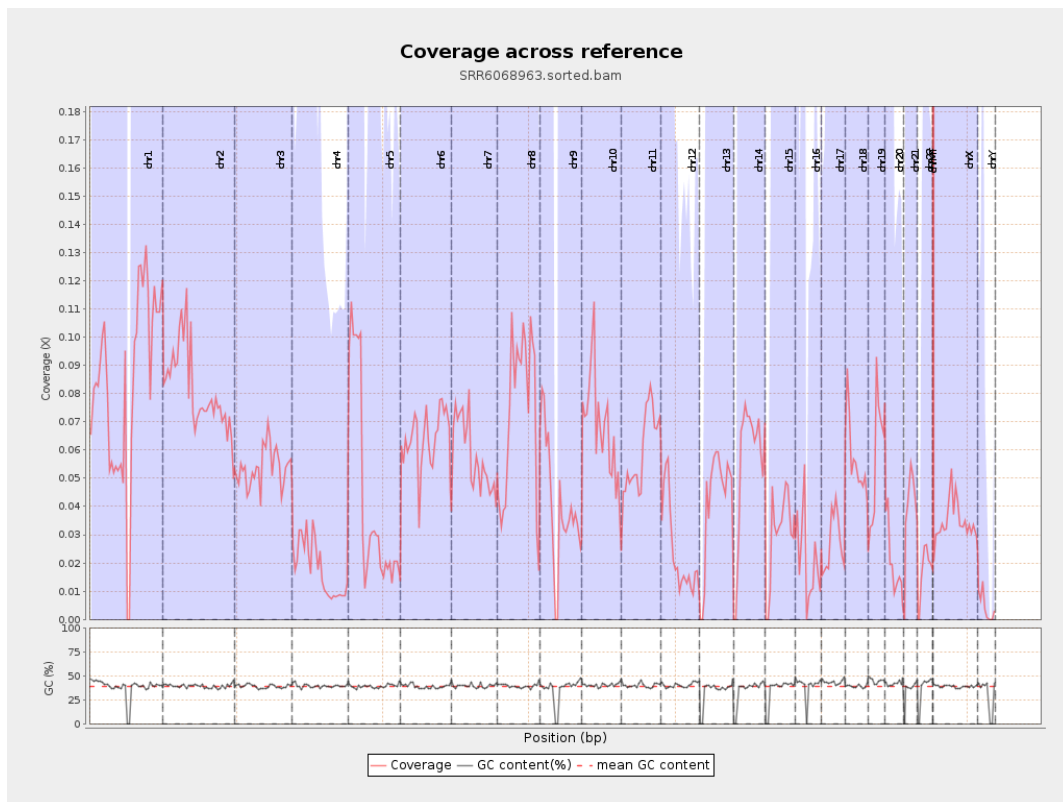
General error rate	0.98%
Mismatches	1,499,791
Insertions	13,327
Mapped reads with at least one insertion	0.56%
Deletions	39,150
Mapped reads with at least one deletion	1.64%
Homopolymer indels	49.16%

2.6. Chromosome stats

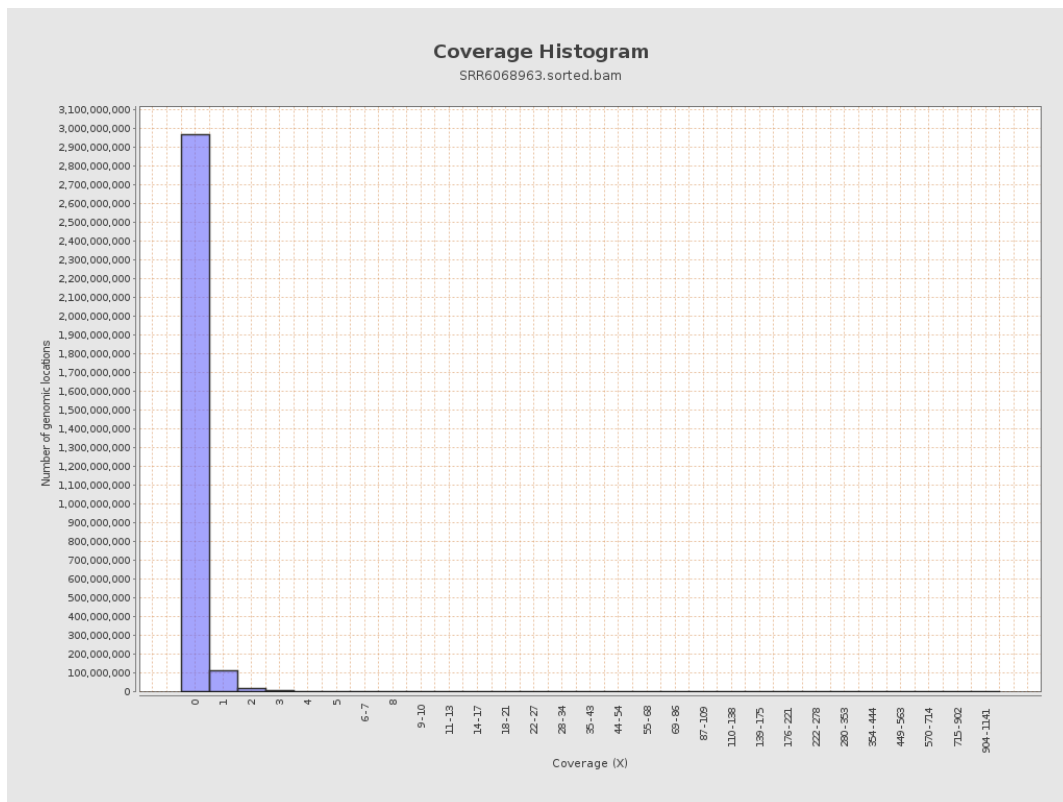
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	20902815	0.0839	1.026
chr2	243199373	19742662	0.0812	0.4714
chr3	198022430	10629717	0.0537	0.2744
chr4	191154276	3415320	0.0179	0.1679
chr5	180915260	7680668	0.0425	0.243
chr6	171115067	11010558	0.0643	0.3428
chr7	159138663	9180157	0.0577	0.5383

chr8	146364022	10698116	0.0731	0.5081
chr9	141213431	5697732	0.0403	0.3378
chr10	135534747	9214592	0.068	0.5295
chr11	135006516	7993692	0.0592	0.4139
chr12	133851895	3199450	0.0239	0.1826
chr13	115169878	4894517	0.0425	0.236
chr14	107349540	5994172	0.0558	0.2886
chr15	102531392	3092207	0.0302	0.1986
chr16	90354753	1850860	0.0205	0.1991
chr17	81195210	2220073	0.0273	0.2122
chr18	78077248	4475034	0.0573	0.6562
chr19	59128983	3394740	0.0574	0.5856
chr20	63025520	1256737	0.0199	0.1827
chr21	48129895	1911784	0.0397	0.2455
chr22	51304566	869358	0.0169	0.1471
chrMT	16571	157682	9.5155	6.3349
chrX	155270560	5390924	0.0347	0.244
chrY	59373566	268613	0.0045	0.1032

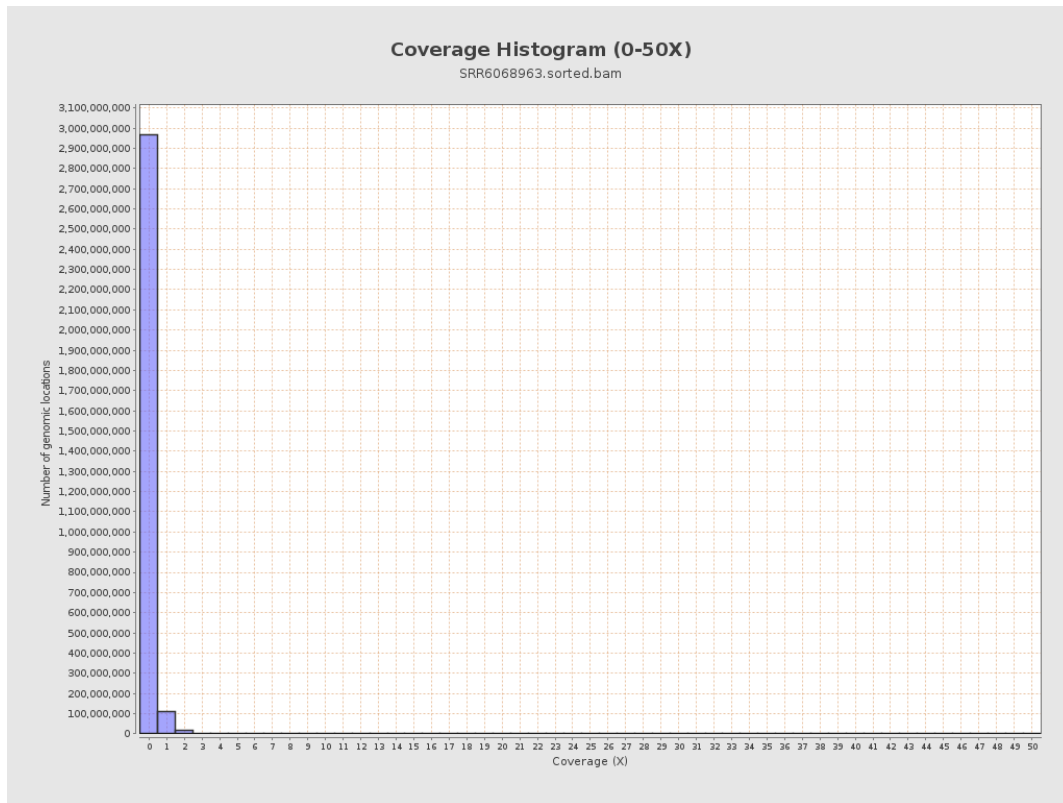
3. Results : Coverage across reference



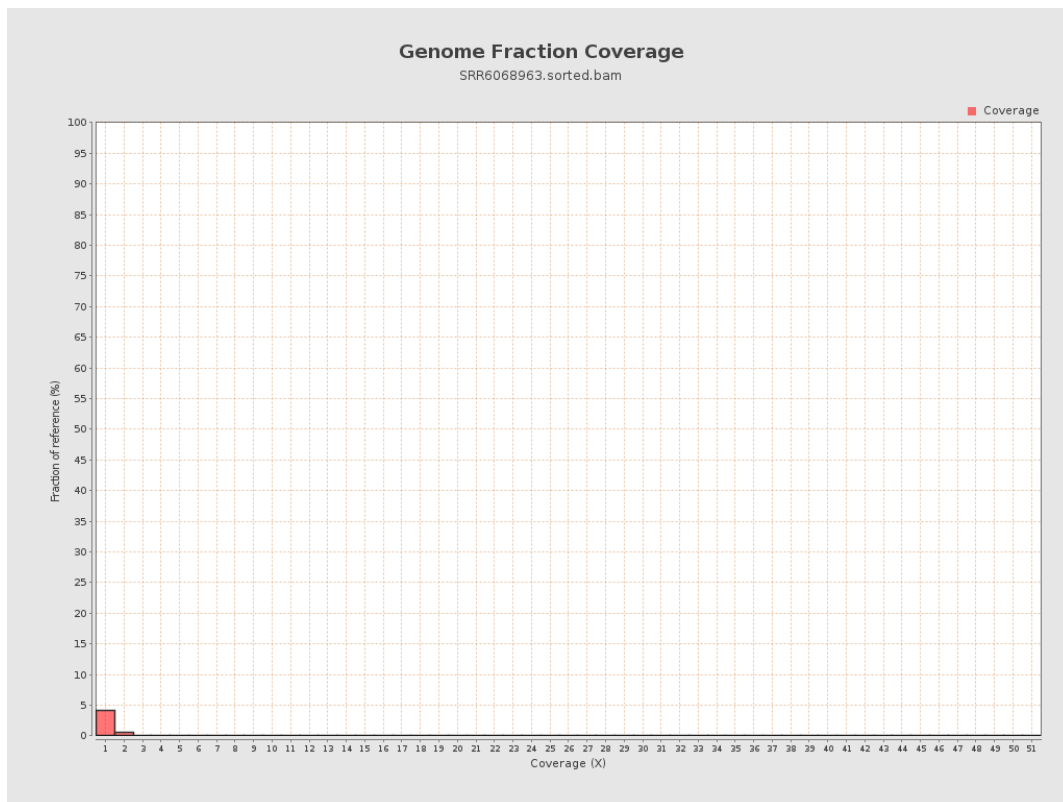
4. Results : Coverage Histogram



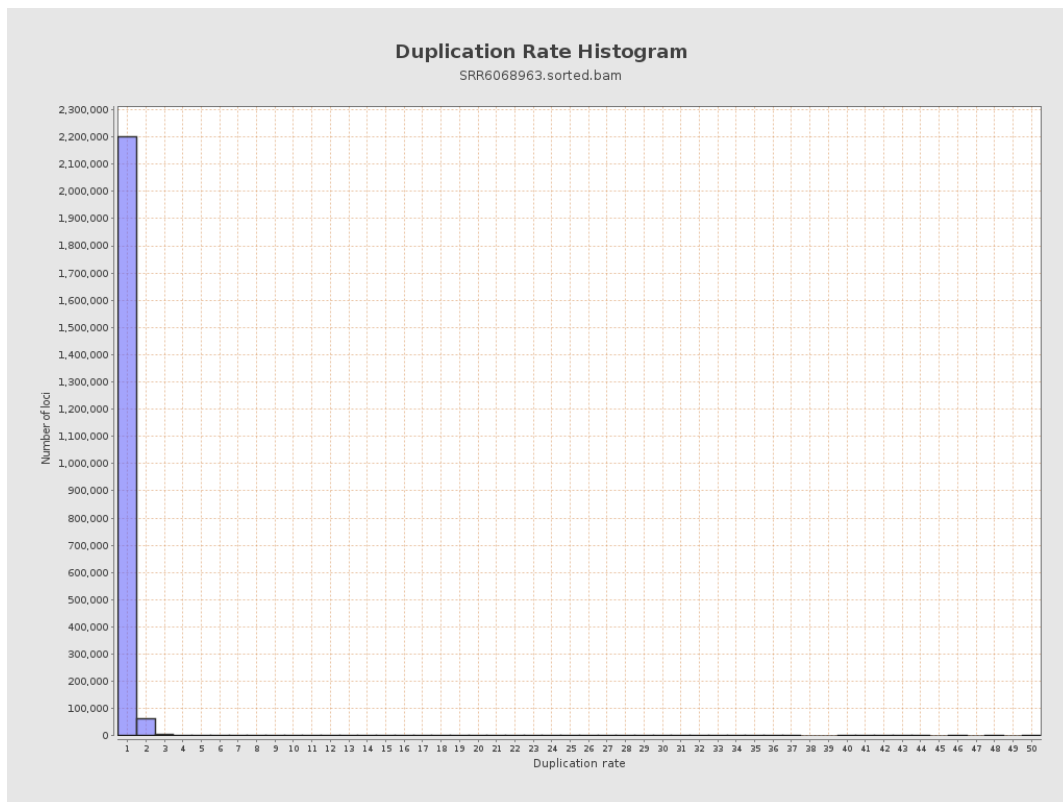
5. Results : Coverage Histogram (0-50X)



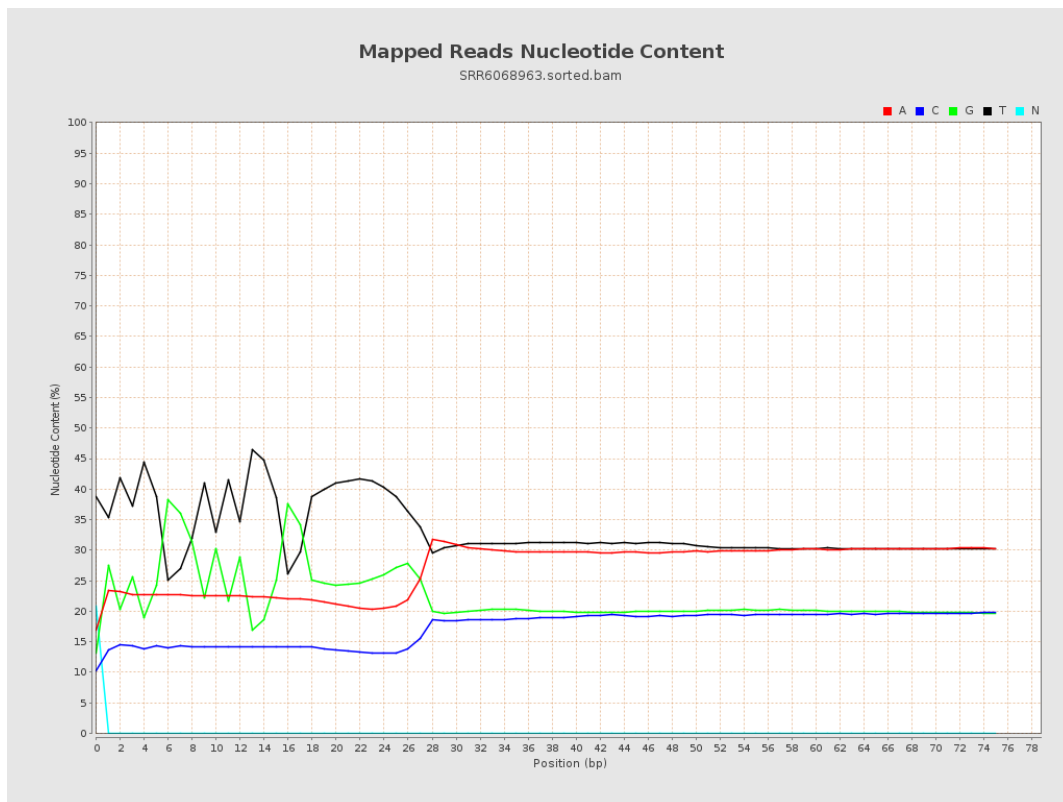
6. Results : Genome Fraction Coverage



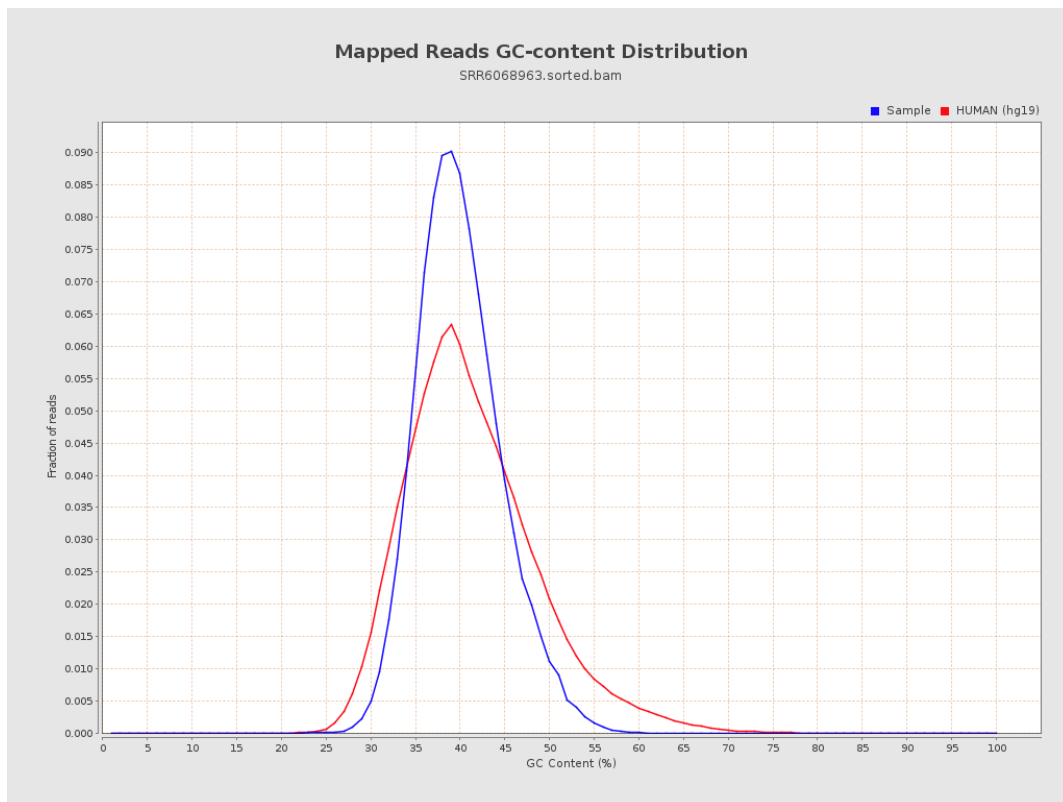
7. Results : Duplication Rate Histogram



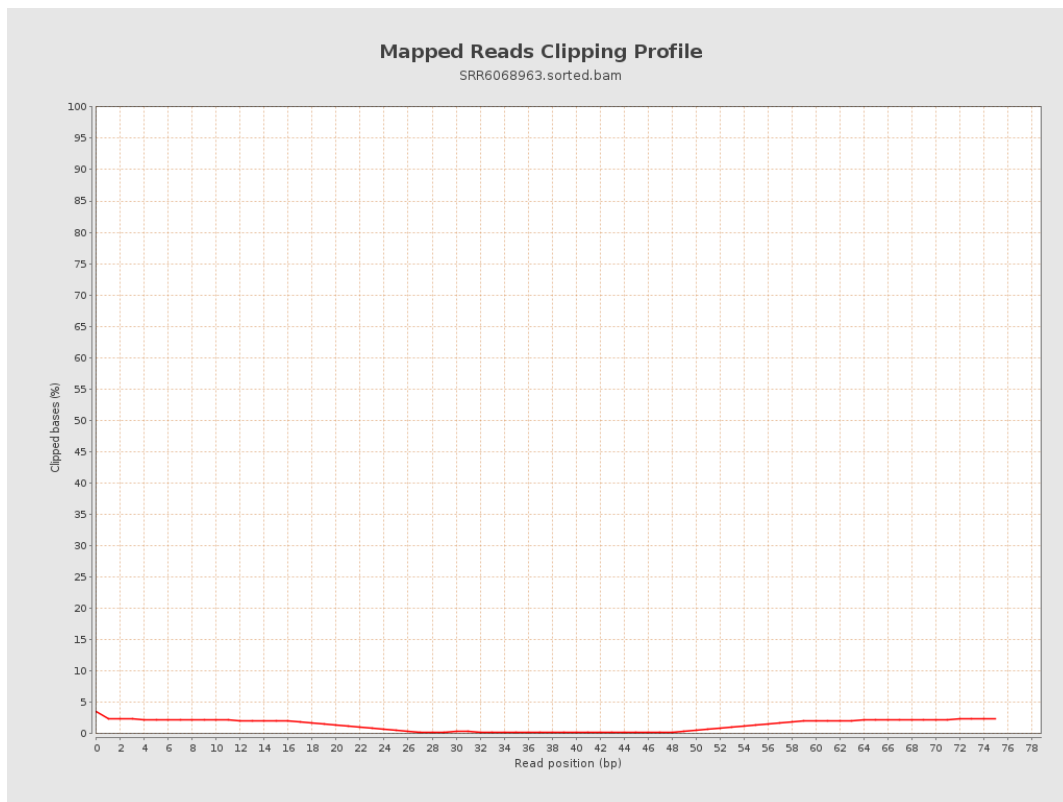
8. Results : Mapped Reads Nucleotide Content



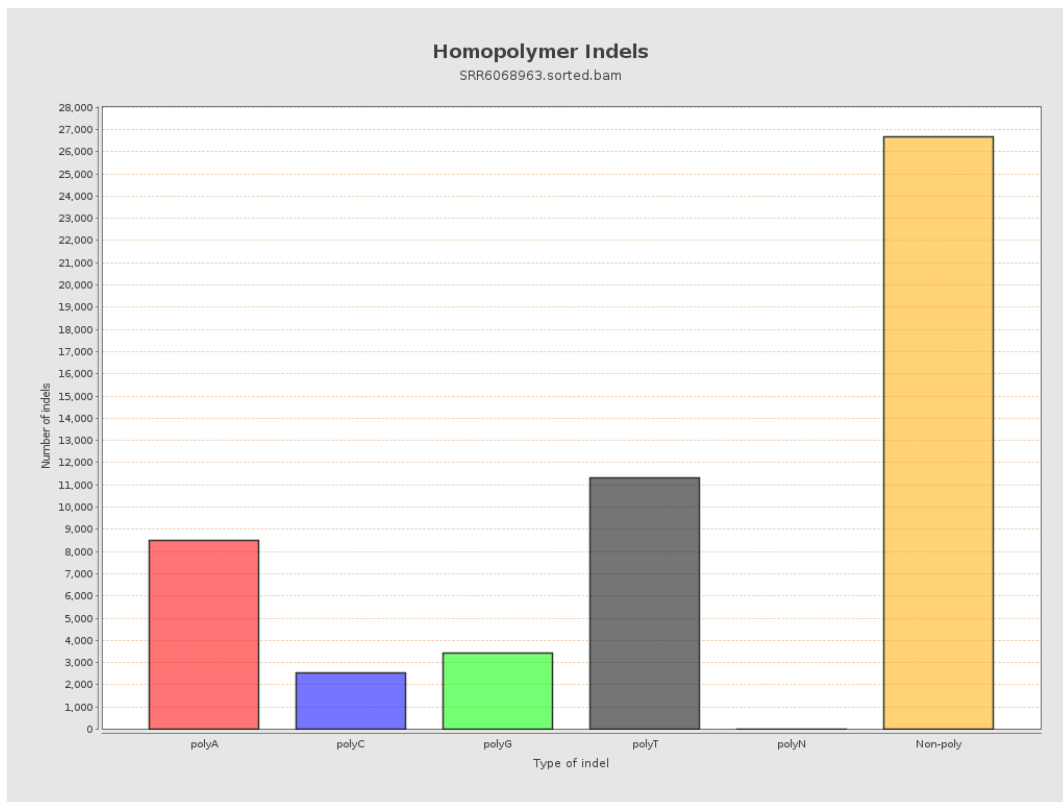
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

