

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 14:45:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068174.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_SRR6068174 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068174.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 14:45:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068174.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,632,856
Mapped reads	4,906,969 / 87.11%
Unmapped reads	725,887 / 12.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,541 / 0.51%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	562,311 / 9.98%
Duplication rate	9.22%
Clipped reads	2,646,365 / 46.98%

2.2. ACGT Content

Number/percentage of A's	80,223,470 / 25.56%
Number/percentage of C's	56,670,318 / 18.06%
Number/percentage of T's	101,934,907 / 32.48%
Number/percentage of G's	75,004,201 / 23.9%
Number/percentage of N's	35,449 / 0.01%
GC Percentage	41.95%

2.3. Coverage

Mean	0.1014

Standard Deviation	1.3279
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2.4. Mapping Quality

Mean Mapping Quality	44.05
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2.5. Mismatches and indels

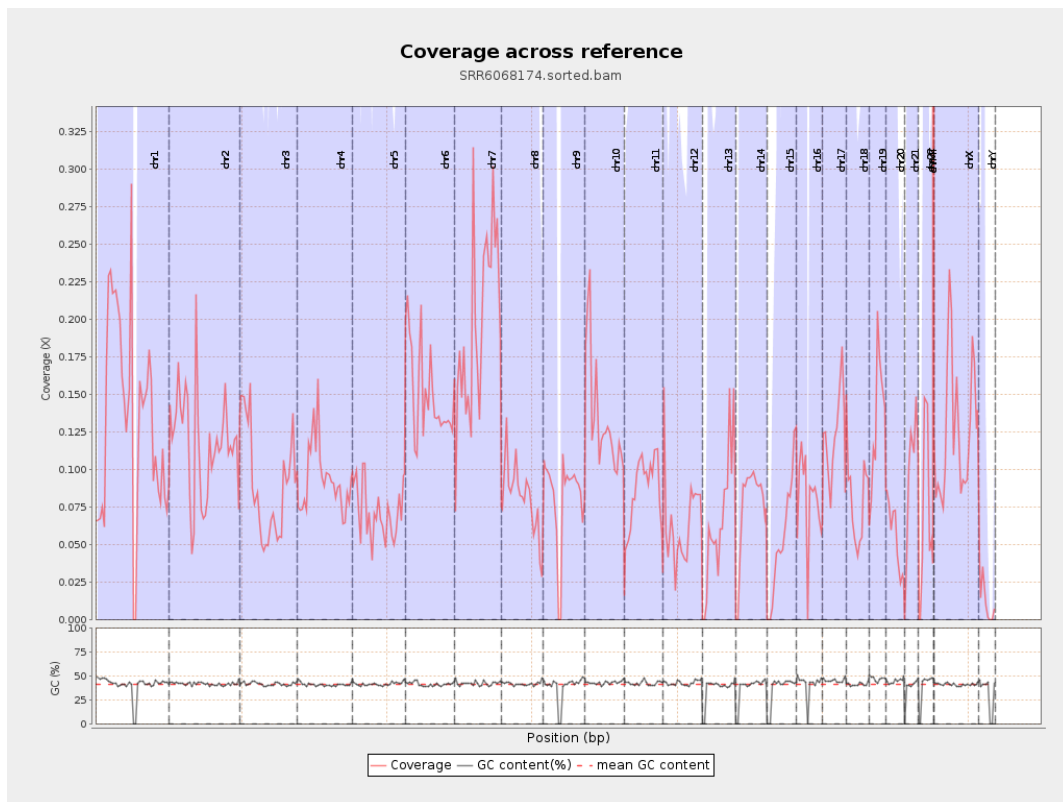
General error rate	0.58%
Mismatches	1,784,431
Insertions	19,142
Mapped reads with at least one insertion	0.39%
Deletions	79,535
Mapped reads with at least one deletion	1.6%
Homopolymer indels	44.19%

2.6. Chromosome stats

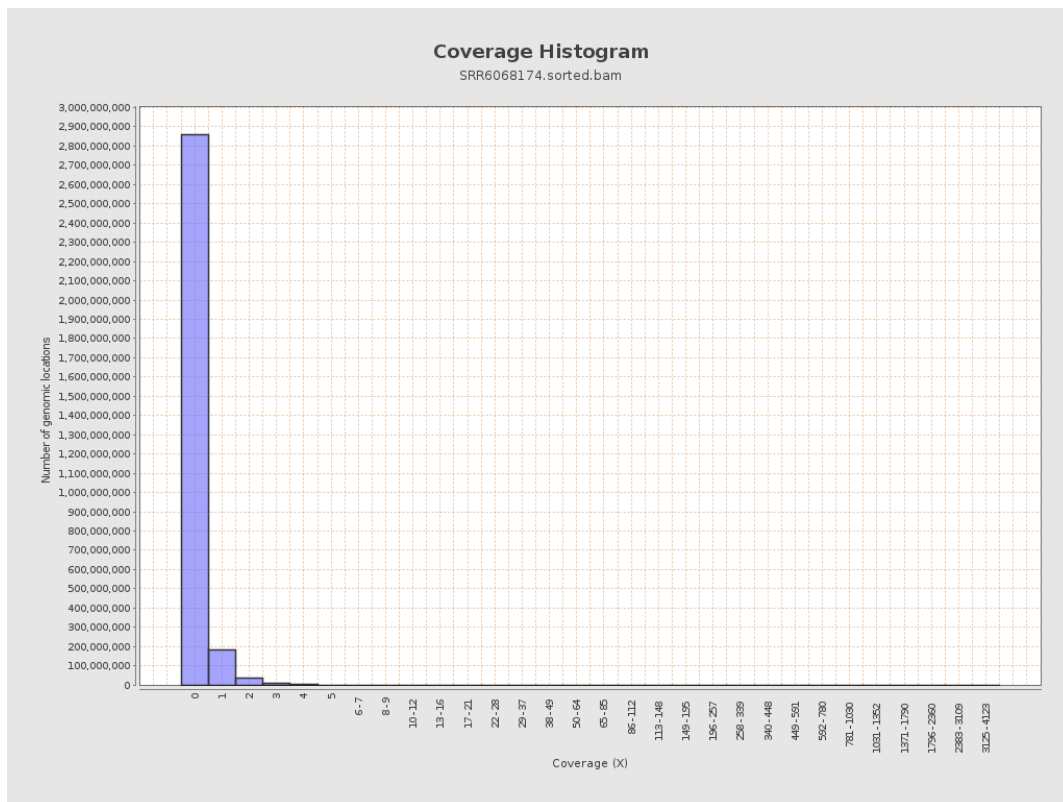
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	33361815	0.1338	3.2814
chr2	243199373	28384622	0.1167	1.7355
chr3	198022430	17793855	0.0899	0.3923
chr4	191154276	17835099	0.0933	0.4237
chr5	180915260	12964671	0.0717	0.3556
chr6	171115067	25816662	0.1509	0.7954
chr7	159138663	31610042	0.1986	2.3635

chr8	146364022	11864555	0.0811	0.7405
chr9	141213431	11371332	0.0805	0.8459
chr10	135534747	18294679	0.135	0.7649
chr11	135006516	11518467	0.0853	0.6393
chr12	133851895	8640129	0.0645	0.4164
chr13	115169878	7619823	0.0662	0.3823
chr14	107349540	7987099	0.0744	0.4971
chr15	102531392	5539318	0.054	0.4143
chr16	90354753	7219067	0.0799	0.4442
chr17	81195210	9934973	0.1224	0.5267
chr18	78077248	6100359	0.0781	1.4549
chr19	59128983	7947037	0.1344	2.0554
chr20	63025520	3498618	0.0555	0.367
chr21	48129895	4591517	0.0954	0.4267
chr22	51304566	3414920	0.0666	0.3236
chrMT	16571	152569	9.207	5.593
chrX	155270560	19823121	0.1277	0.6568
chrY	59373566	722586	0.0122	0.32

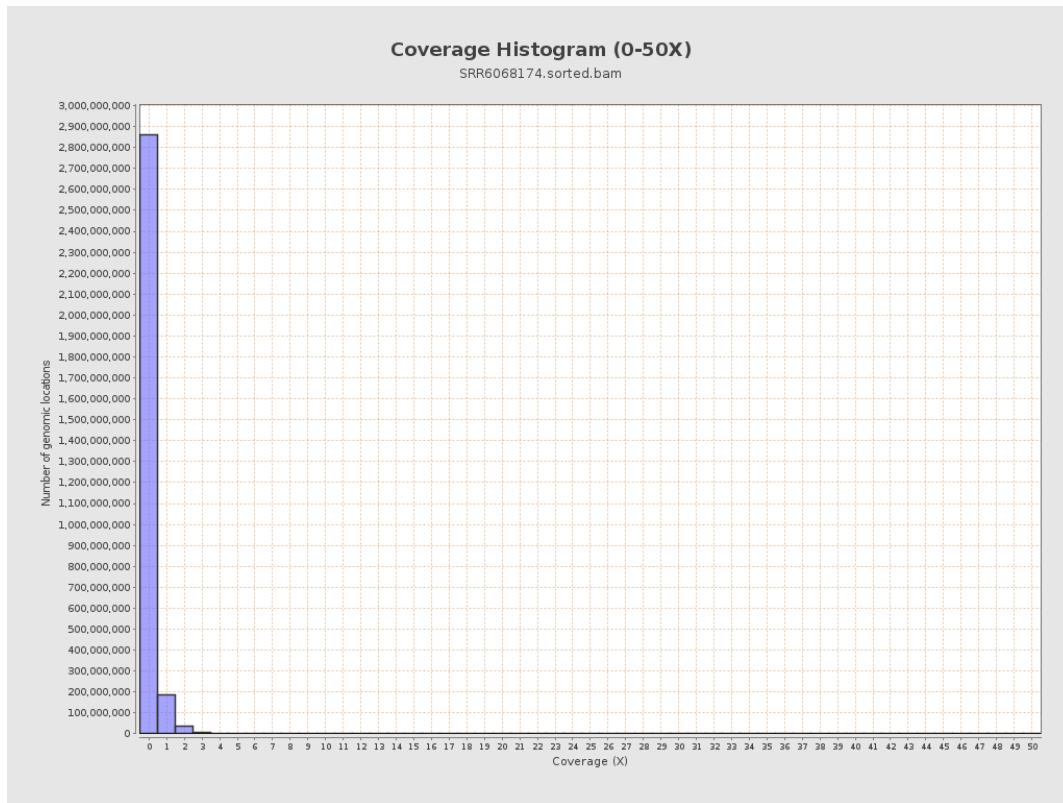
3. Results : Coverage across reference



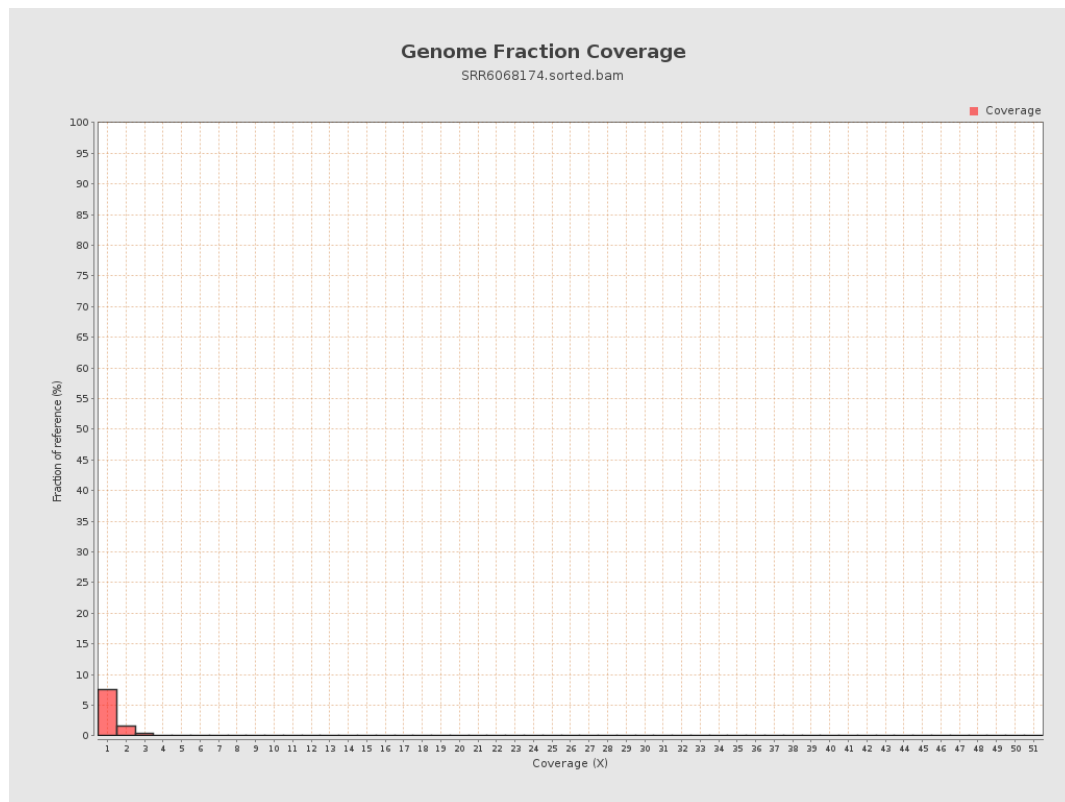
4. Results : Coverage Histogram



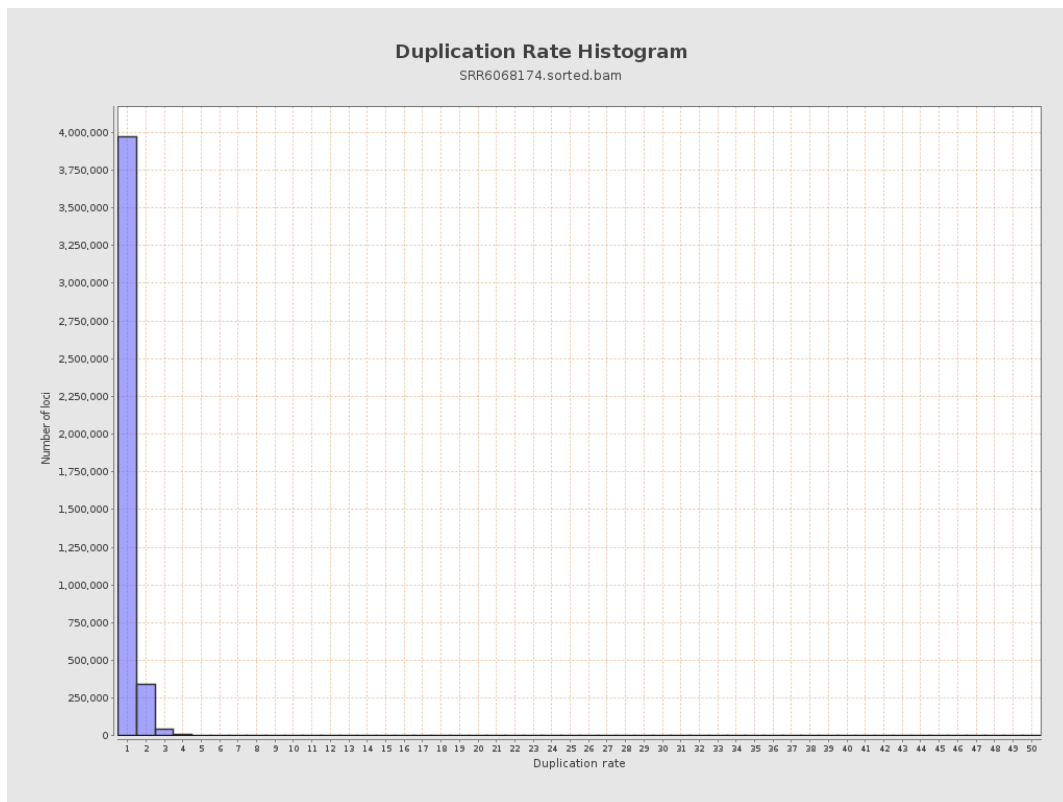
5. Results : Coverage Histogram (0-50X)



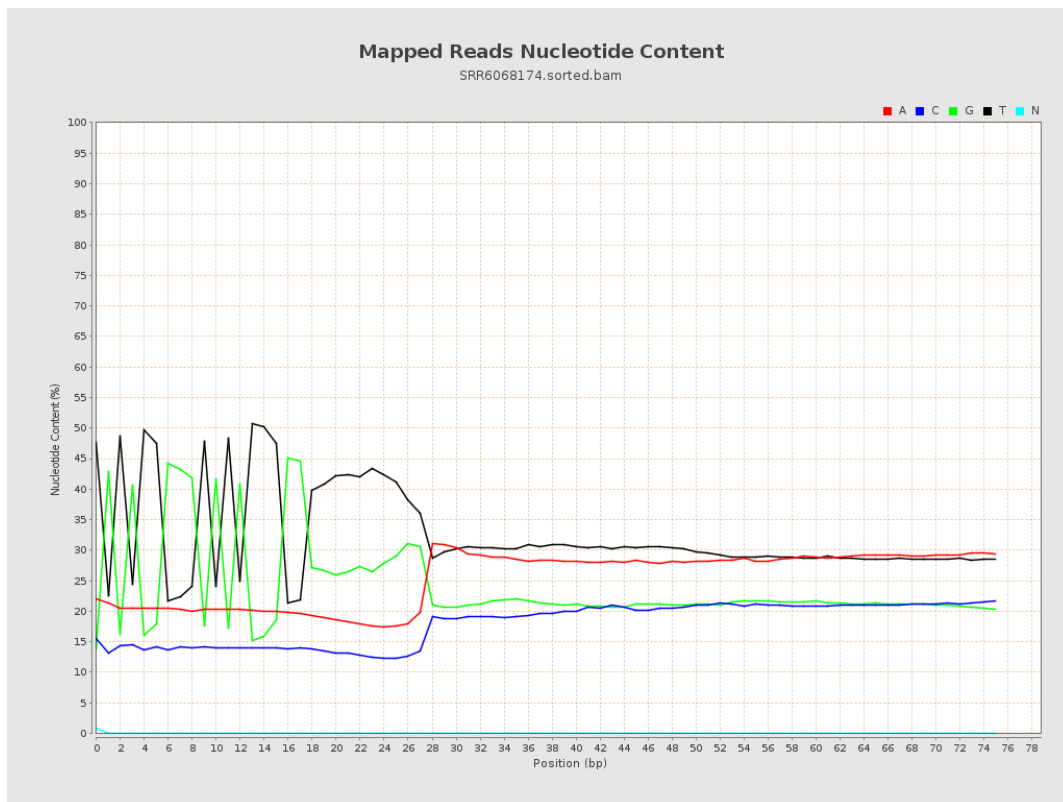
6. Results : Genome Fraction Coverage



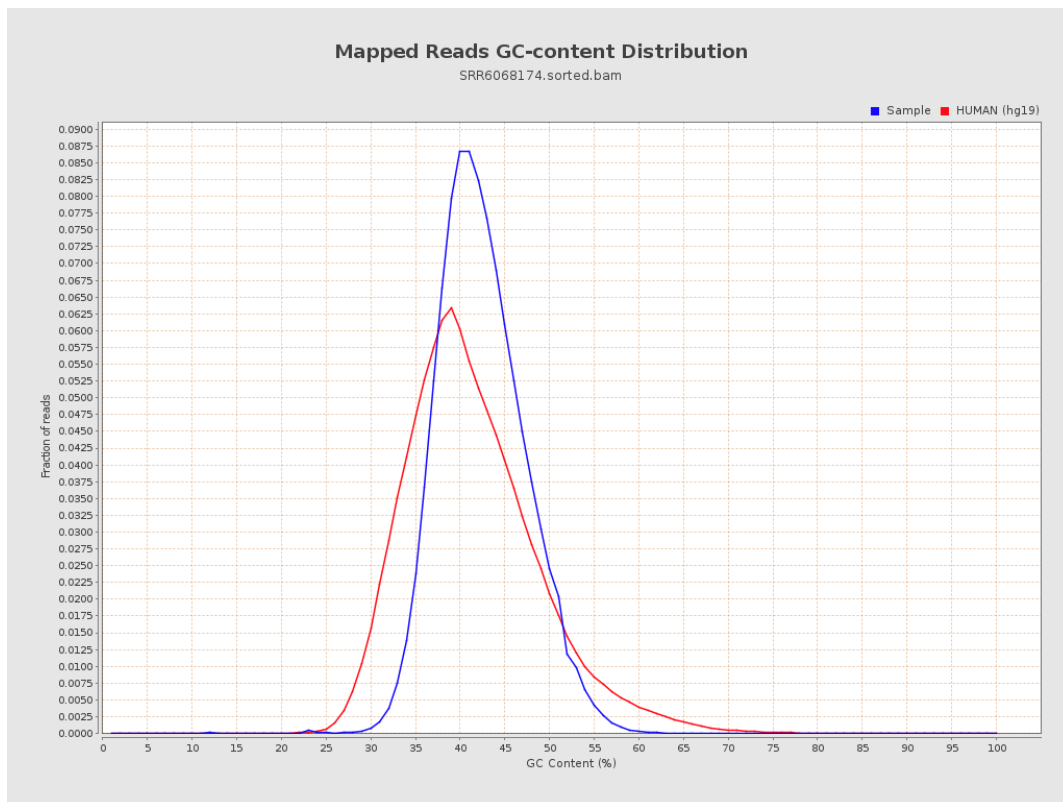
7. Results : Duplication Rate Histogram



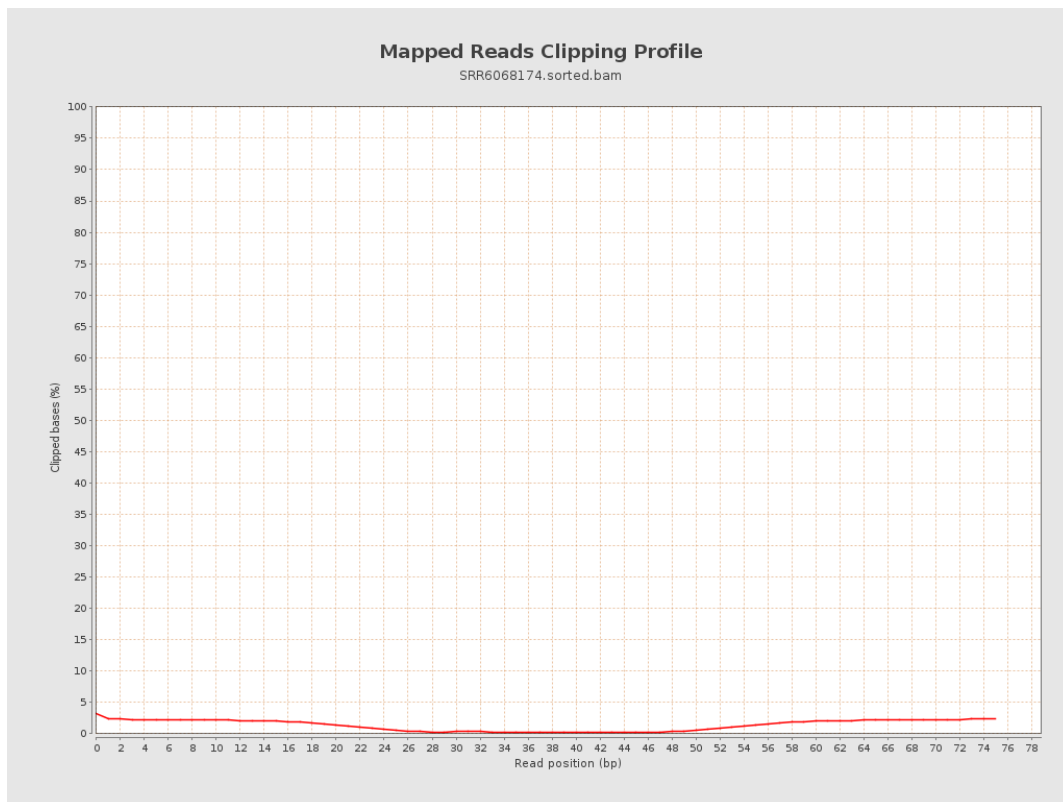
8. Results : Mapped Reads Nucleotide Content



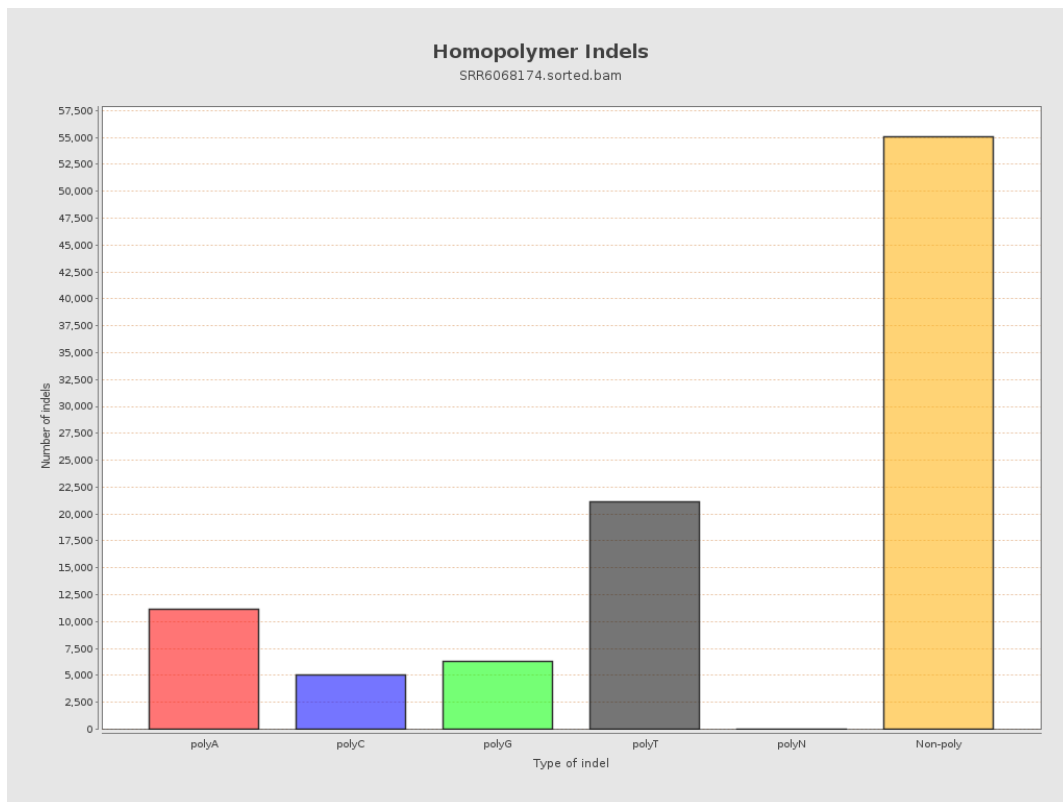
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

