

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 09:11:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068086.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_SRR6068086 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068086.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 09:11:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068086.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,361,874
Mapped reads	2,103,767 / 89.07%
Unmapped reads	258,107 / 10.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,500 / 0.91%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	209,893 / 8.89%
Duplication rate	7.95%
Clipped reads	981,533 / 41.56%

2.2. ACGT Content

Number/percentage of A's	38,352,041 / 27.49%
Number/percentage of C's	25,958,804 / 18.61%
Number/percentage of T's	44,074,951 / 31.6%
Number/percentage of G's	31,105,630 / 22.3%
Number/percentage of N's	3,030 / 0%
GC Percentage	40.91%

2.3. Coverage

Mean	0.0451

Standard Deviation	0.465
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2.4. Mapping Quality

Mean Mapping Quality	41.49
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2.5. Mismatches and indels

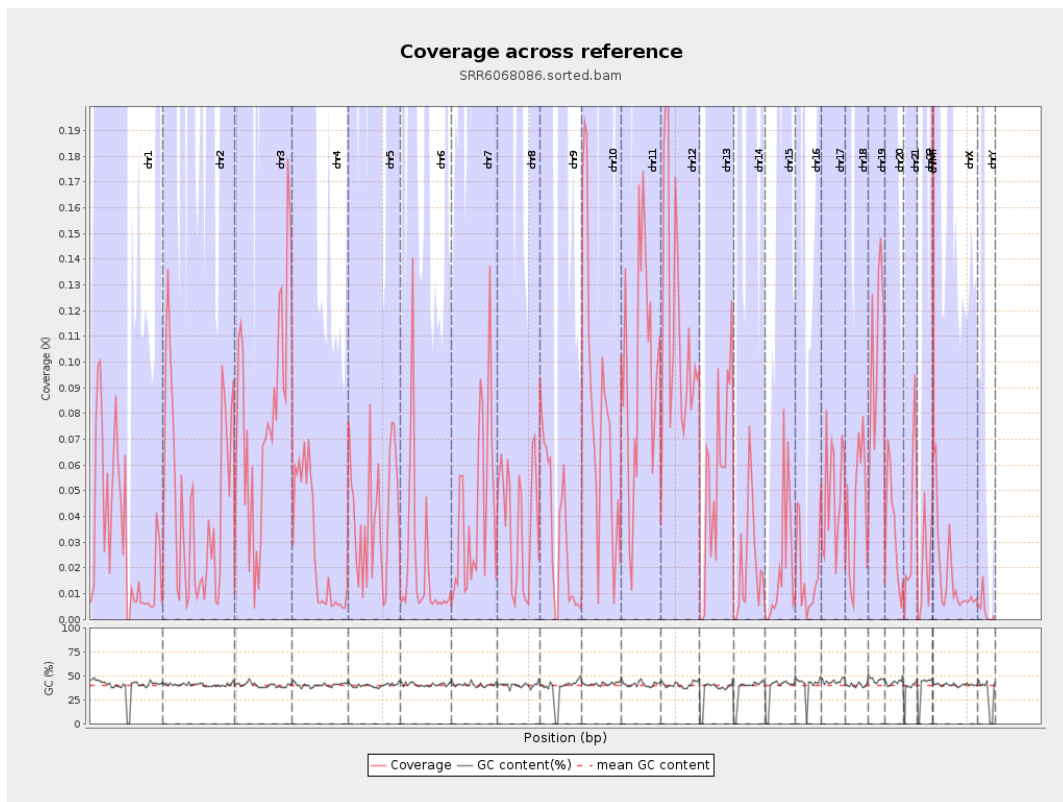
General error rate	0.78%
Mismatches	1,061,764
Insertions	11,063
Mapped reads with at least one insertion	0.52%
Deletions	39,012
Mapped reads with at least one deletion	1.83%
Homopolymer indels	46.95%

2.6. Chromosome stats

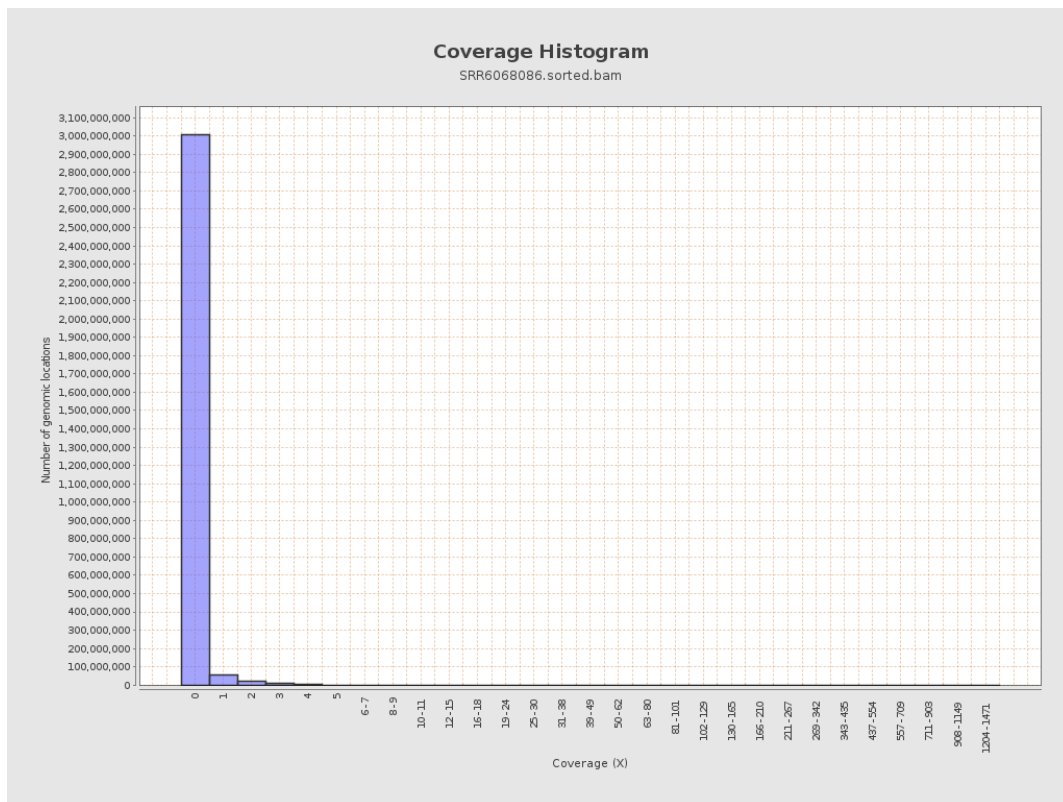
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7953772	0.0319	0.8255
chr2	243199373	10621863	0.0437	0.5396
chr3	198022430	15168835	0.0766	0.406
chr4	191154276	5200082	0.0272	0.2531
chr5	180915260	7288007	0.0403	0.2919
chr6	171115067	3501404	0.0205	0.2327
chr7	159138663	6547706	0.0411	0.3281

chr8	146364022	5639436	0.0385	0.8815
chr9	141213431	4630033	0.0328	0.3553
chr10	135534747	10883826	0.0803	0.4792
chr11	135006516	13066980	0.0968	0.5423
chr12	133851895	15568498	0.1163	0.511
chr13	115169878	6475458	0.0562	0.3487
chr14	107349540	2320381	0.0216	0.2448
chr15	102531392	2047254	0.02	0.2094
chr16	90354753	1598207	0.0177	0.2095
chr17	81195210	3908801	0.0481	0.3336
chr18	78077248	3297168	0.0422	0.463
chr19	59128983	5975833	0.1011	0.6813
chr20	63025520	2194664	0.0348	0.274
chr21	48129895	1847004	0.0384	0.2985
chr22	51304566	981422	0.0191	0.1936
chrMT	16571	15907	0.9599	1.6558
chrX	155270560	2592589	0.0167	0.2092
chrY	59373566	232765	0.0039	0.2011

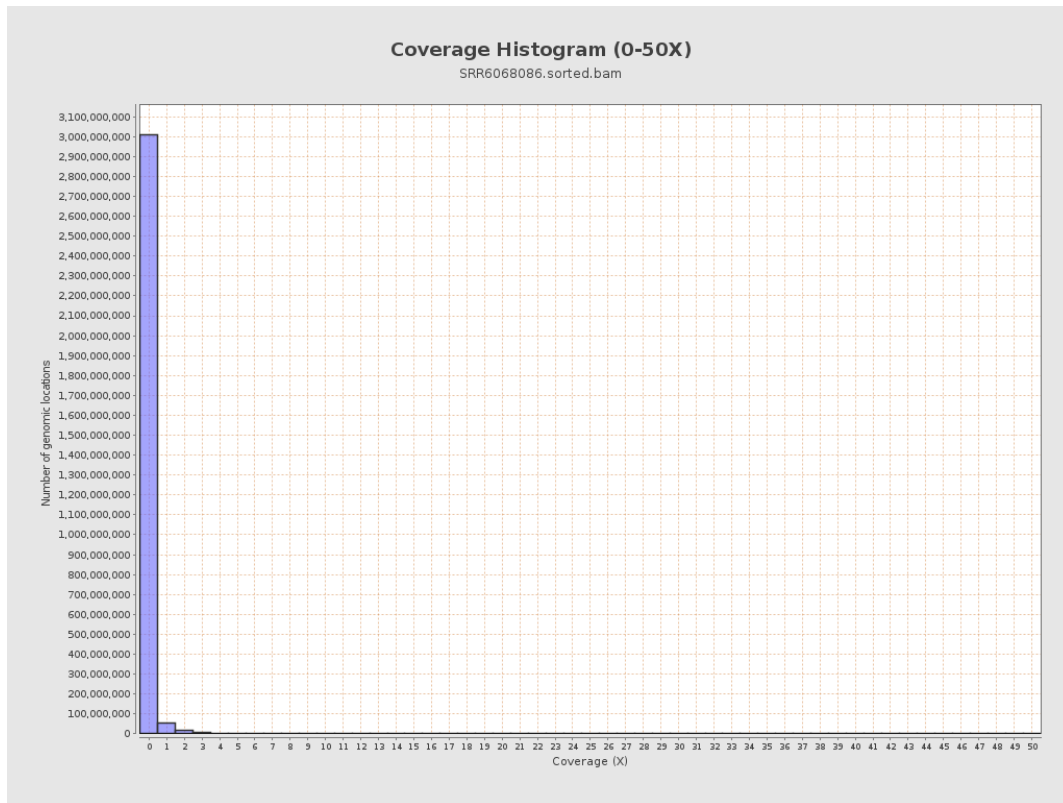
3. Results : Coverage across reference



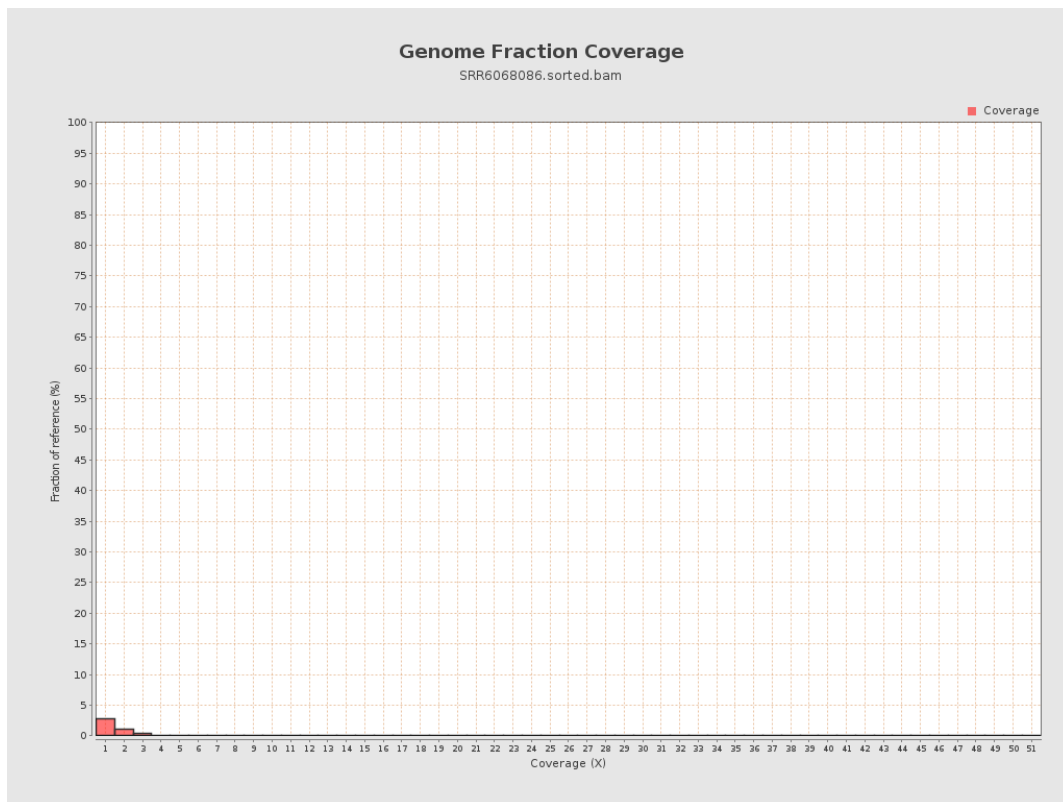
4. Results : Coverage Histogram



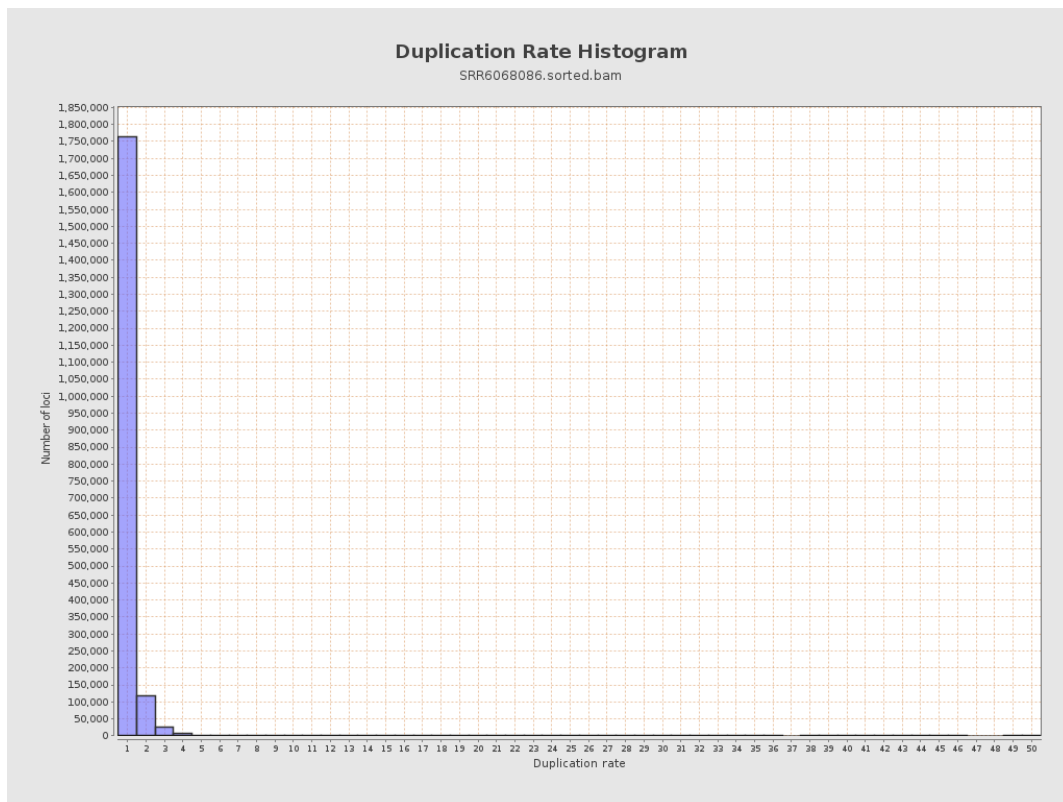
5. Results : Coverage Histogram (0-50X)



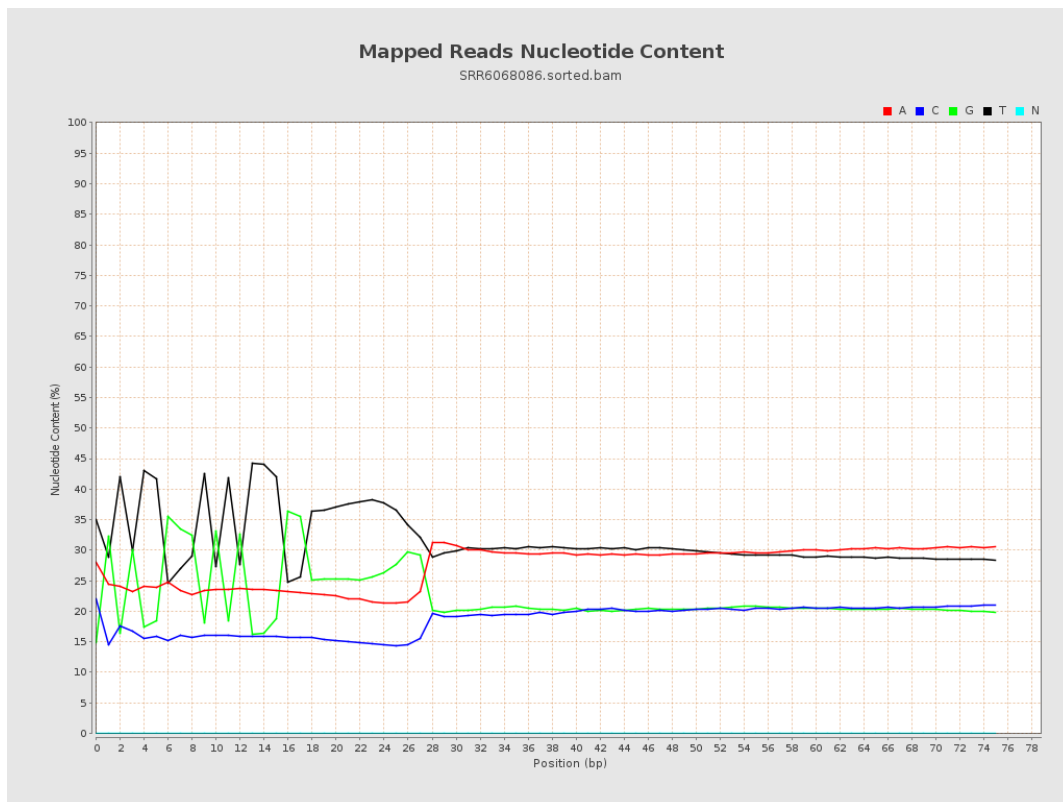
6. Results : Genome Fraction Coverage



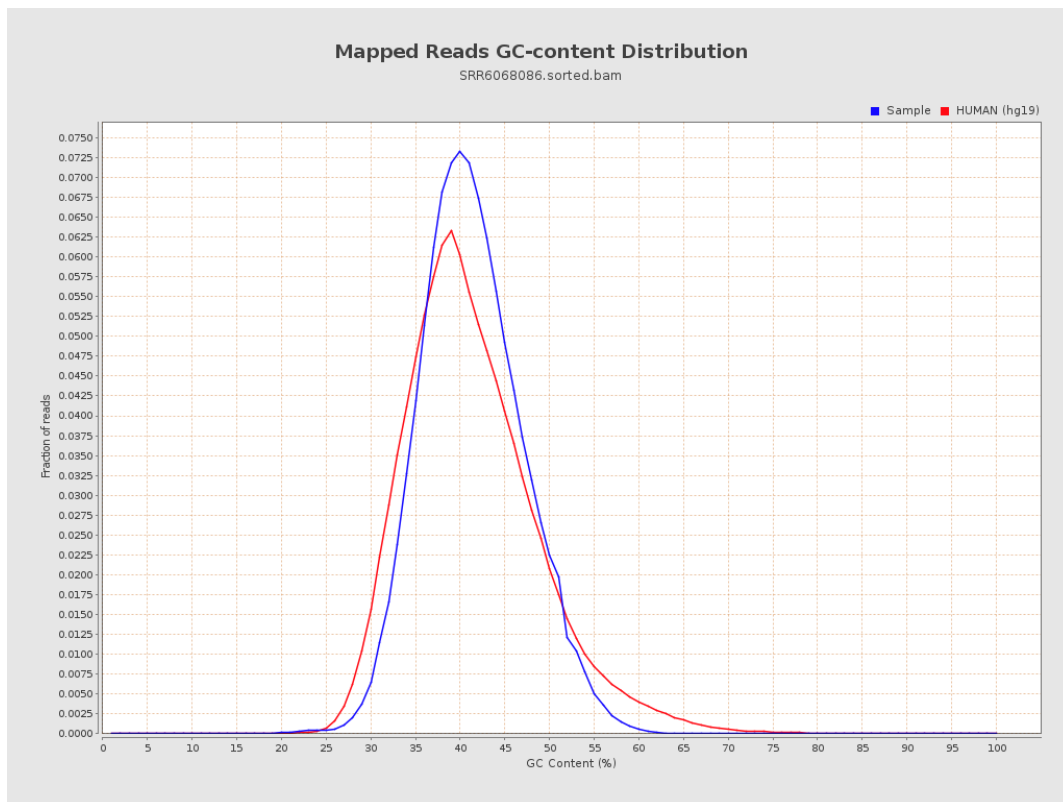
7. Results : Duplication Rate Histogram



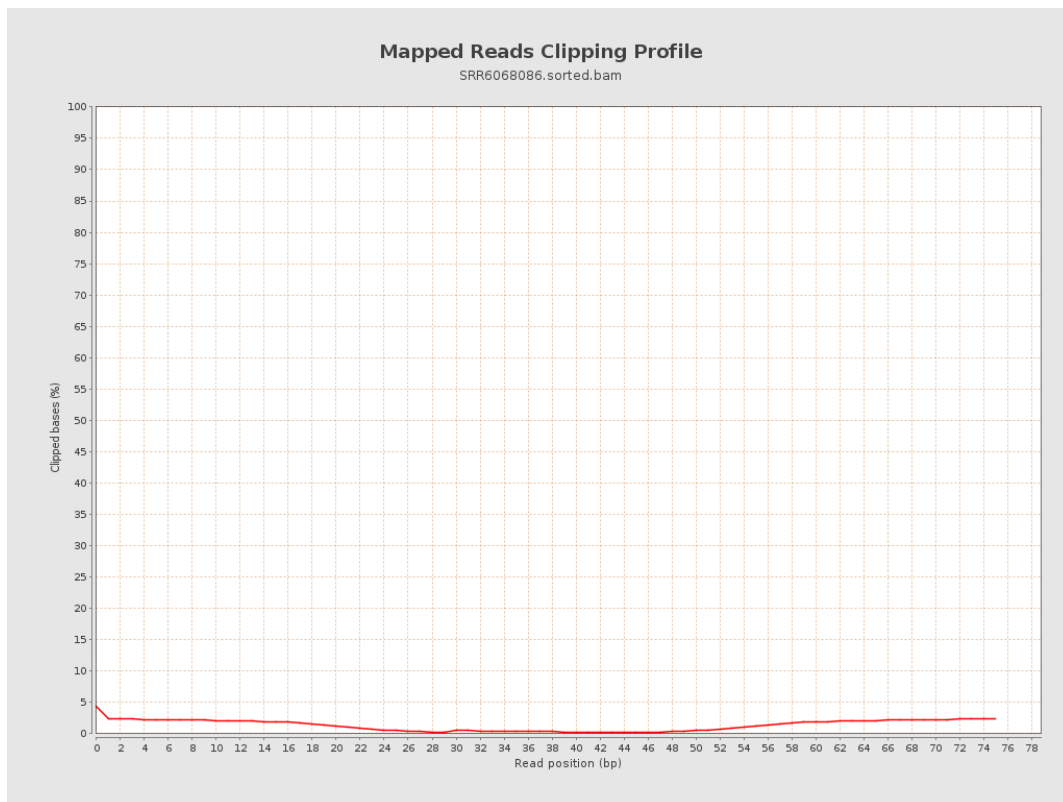
8. Results : Mapped Reads Nucleotide Content



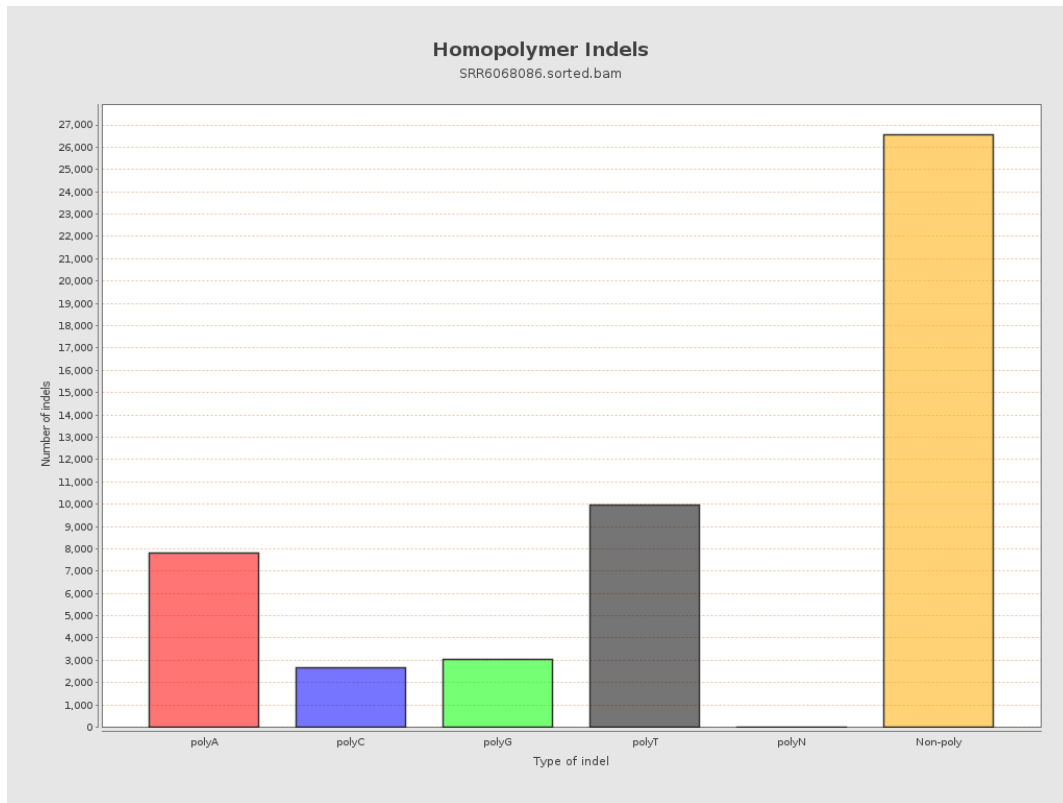
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

