

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 12:20:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008806.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_SRR6008806 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008806.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 12:20:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008806.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,272,521
Mapped reads	1,086,800 / 85.41%
Unmapped reads	185,721 / 14.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,773 / 1%
Read min/max/mean length	30 / 76 / 76.35
Duplicated reads (estimated)	112,278 / 8.82%
Duplication rate	7.88%
Clipped reads	528,533 / 41.53%

2.2. ACGT Content

Number/percentage of A's	19,176,387 / 26.77%
Number/percentage of C's	13,947,871 / 19.47%
Number/percentage of T's	21,942,590 / 30.64%
Number/percentage of G's	16,446,963 / 22.96%
Number/percentage of N's	107,101 / 0.15%
GC Percentage	42.44%

2.3. Coverage

Mean	0.0231

Standard Deviation	0.3318
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2.4. Mapping Quality

Mean Mapping Quality	44.08
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2.5. Mismatches and indels

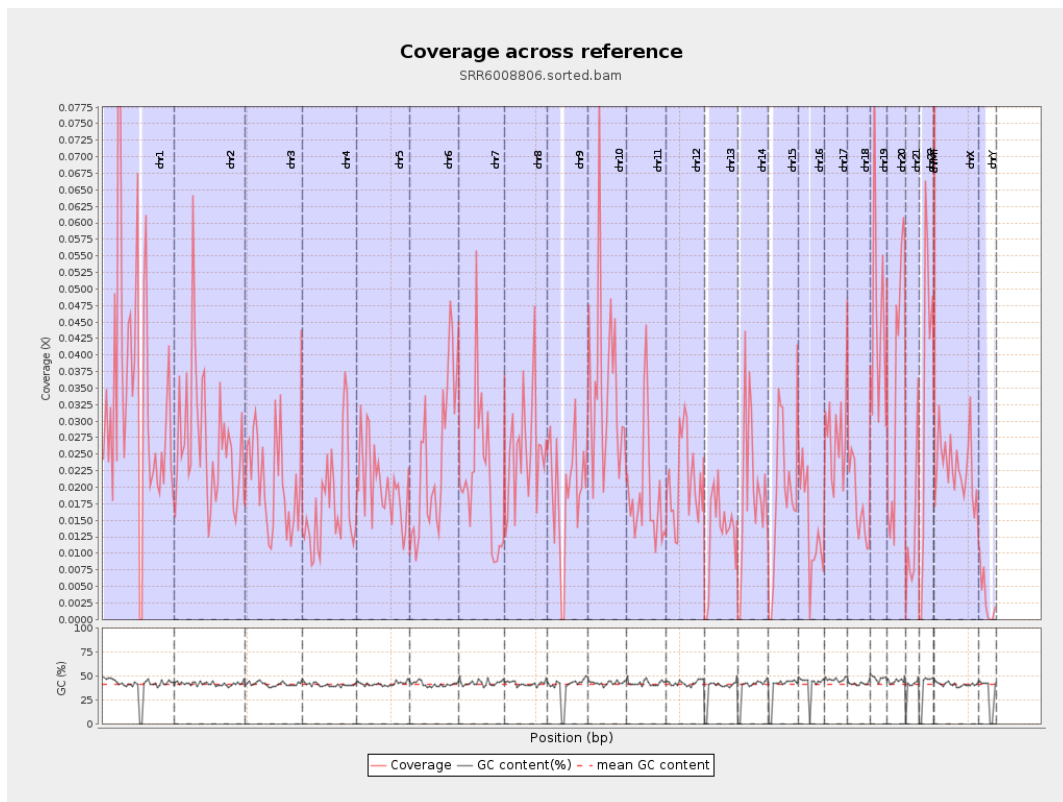
General error rate	0.9%
Mismatches	636,268
Insertions	5,258
Mapped reads with at least one insertion	0.48%
Deletions	21,067
Mapped reads with at least one deletion	1.92%
Homopolymer indels	44.07%

2.6. Chromosome stats

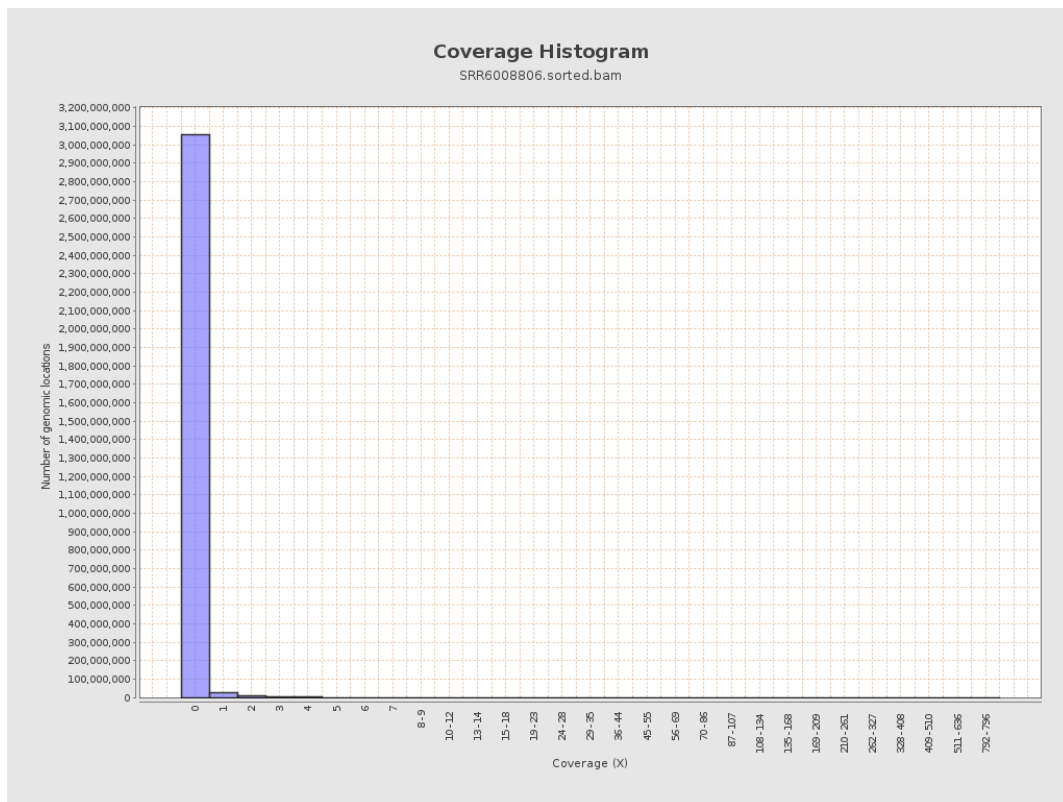
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8232681	0.033	0.6054
chr2	243199373	6514275	0.0268	0.4244
chr3	198022430	4111690	0.0208	0.2264
chr4	191154276	3328414	0.0174	0.2064
chr5	180915260	3692369	0.0204	0.2195
chr6	171115067	4141712	0.0242	0.2673
chr7	159138663	3333235	0.0209	0.4774

chr8	146364022	3749914	0.0256	0.3203
chr9	141213431	2709987	0.0192	0.2479
chr10	135534747	4788452	0.0353	0.4353
chr11	135006516	2608217	0.0193	0.2246
chr12	133851895	2800727	0.0209	0.2238
chr13	115169878	1478405	0.0128	0.1768
chr14	107349540	2051239	0.0191	0.2183
chr15	102531392	1929811	0.0188	0.21
chr16	90354753	1286409	0.0142	0.2159
chr17	81195210	2248741	0.0277	0.2642
chr18	78077248	1352972	0.0173	0.3164
chr19	59128983	2686708	0.0454	0.4692
chr20	63025520	2208851	0.035	0.2946
chr21	48129895	662304	0.0138	0.1826
chr22	51304566	1826307	0.0356	0.2995
chrMT	16571	156147	9.4229	7.0631
chrX	155270560	3574101	0.023	0.2368
chrY	59373566	184077	0.0031	0.0944

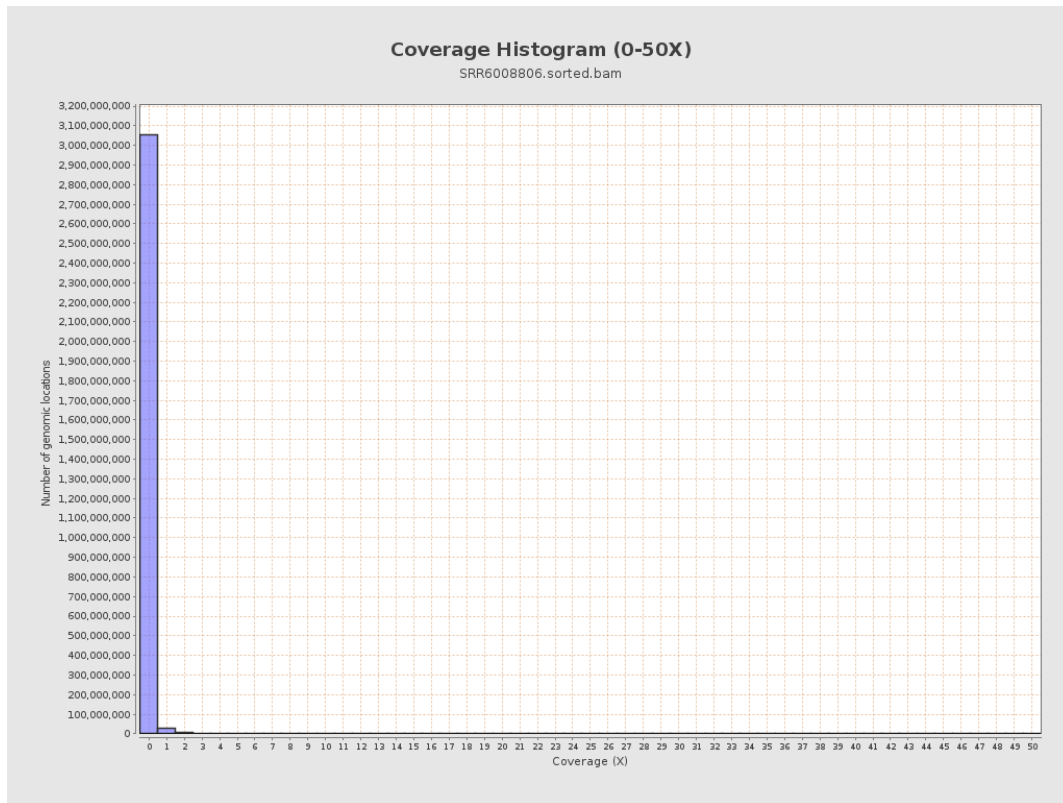
3. Results : Coverage across reference



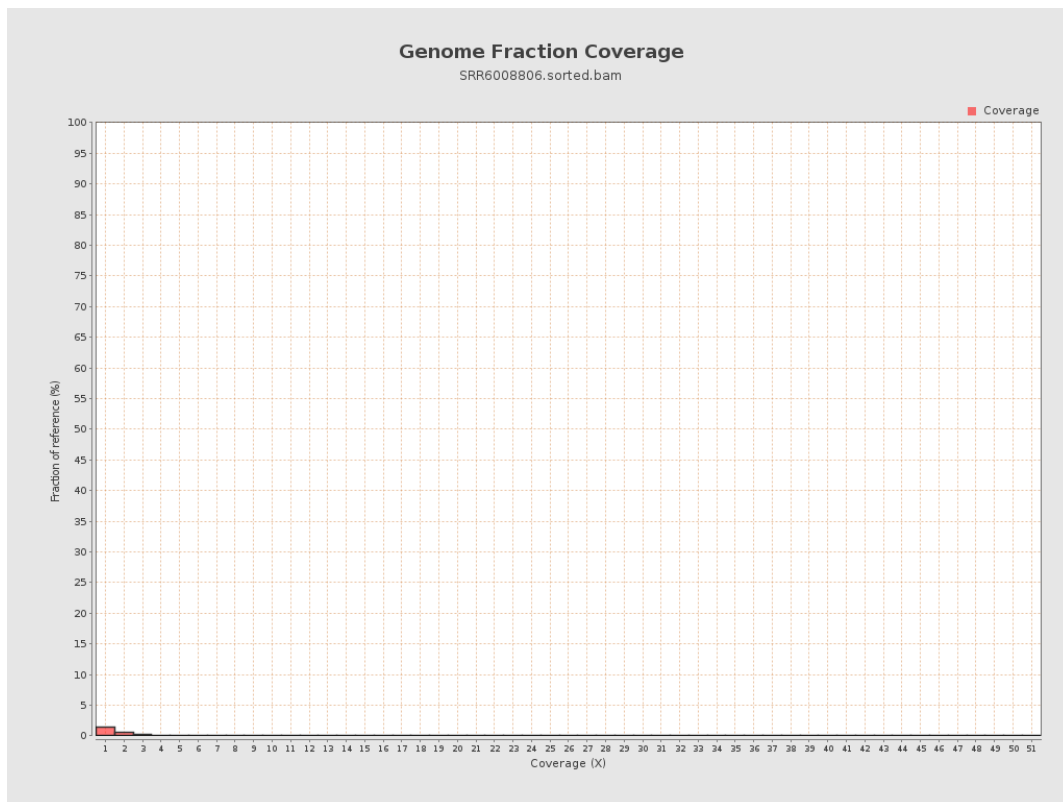
4. Results : Coverage Histogram



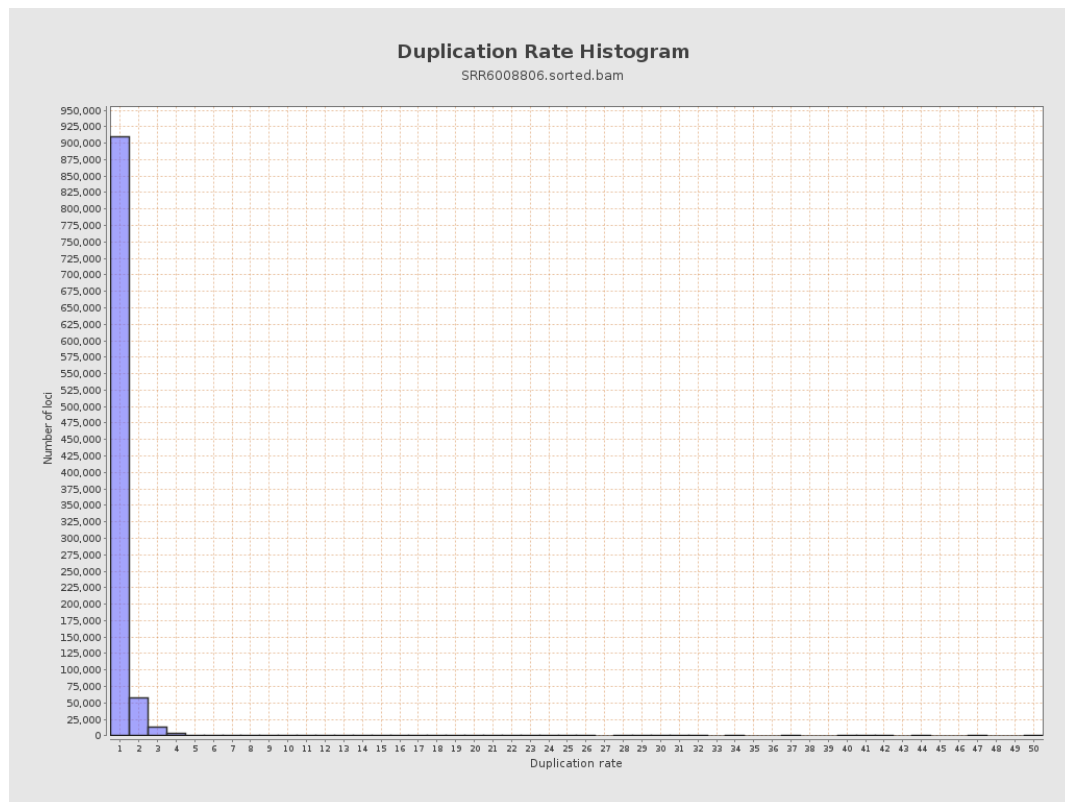
5. Results : Coverage Histogram (0-50X)



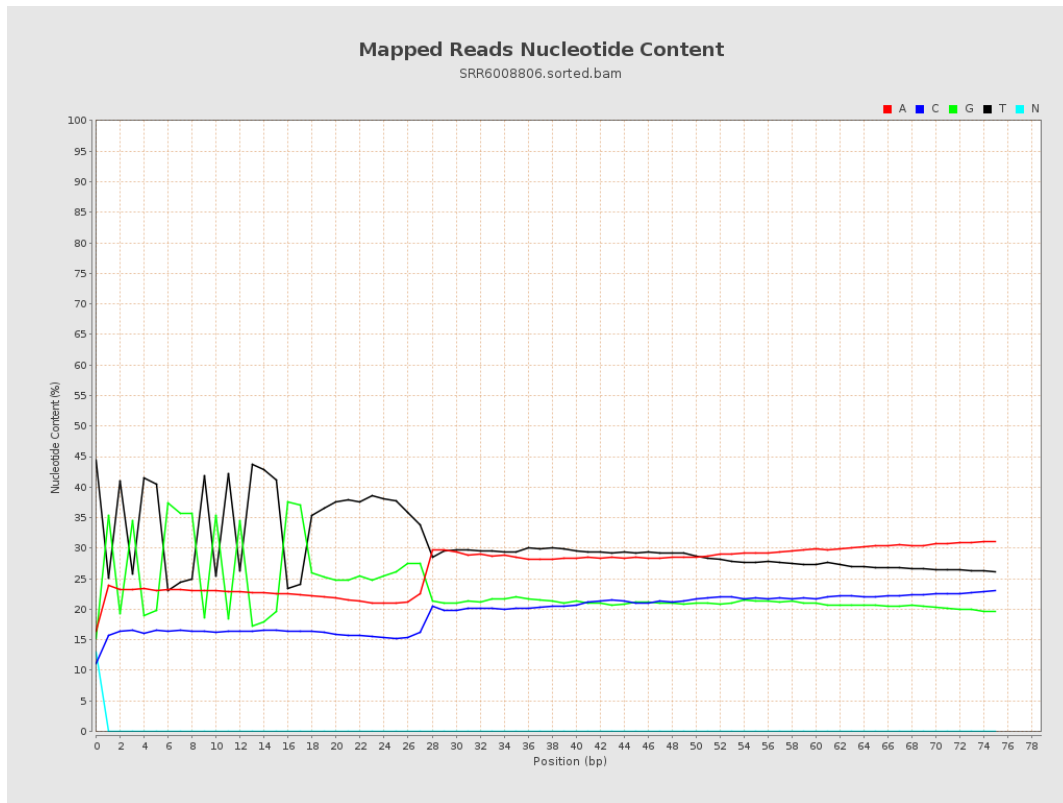
6. Results : Genome Fraction Coverage



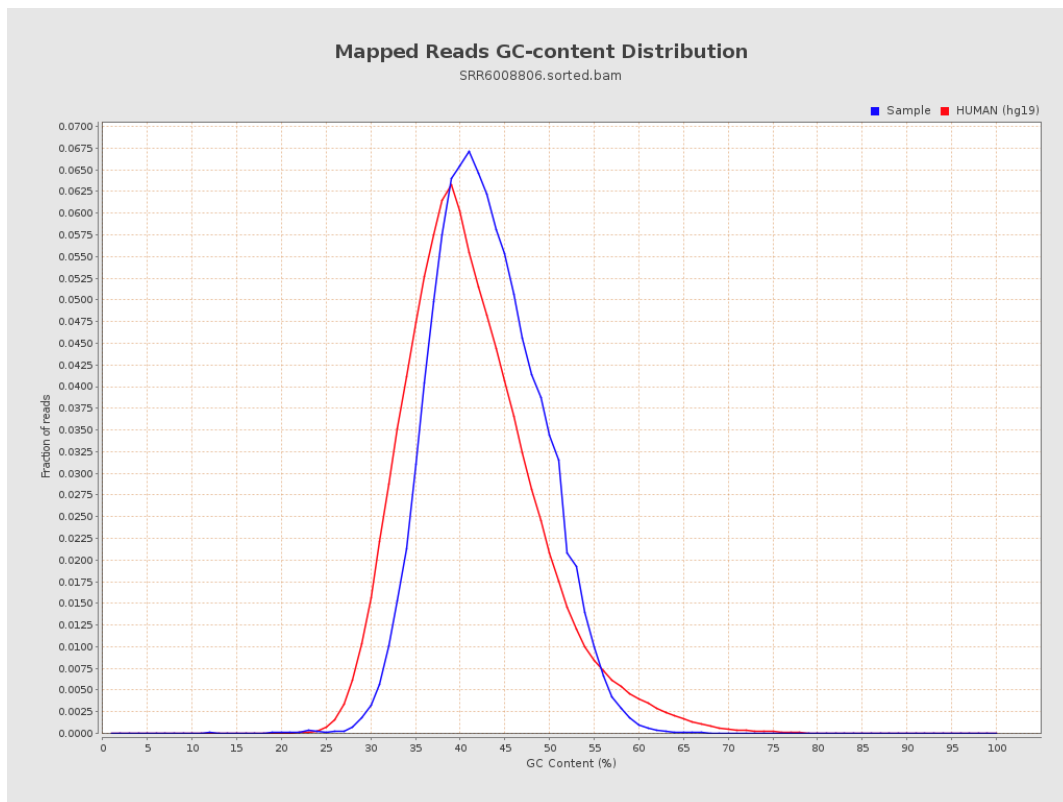
7. Results : Duplication Rate Histogram



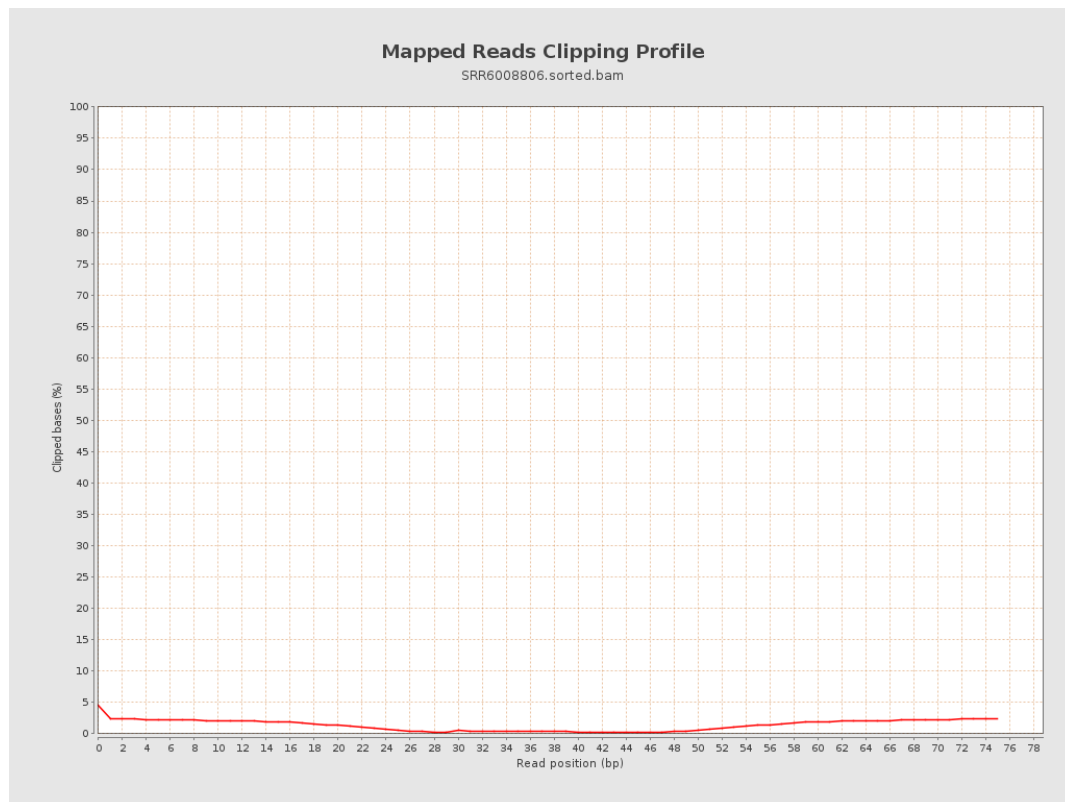
8. Results : Mapped Reads Nucleotide Content



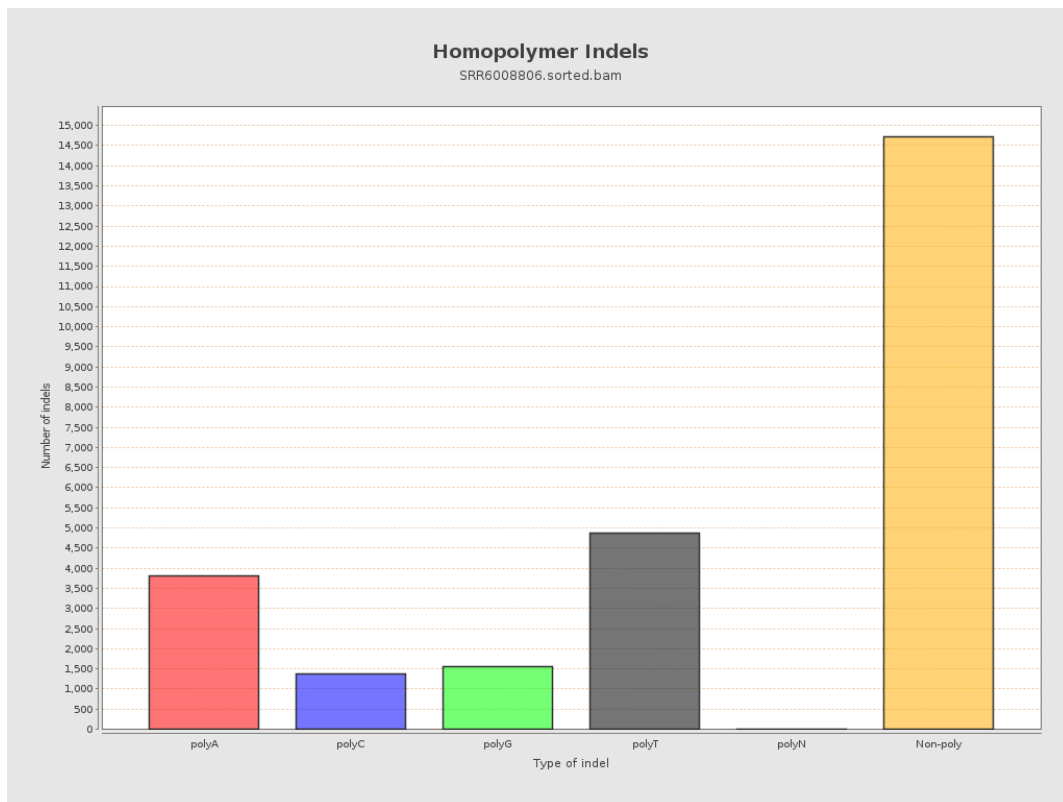
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

