

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 12:39:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008814.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_SRR6008814 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008814.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 12:39:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008814.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,719,648
Mapped reads	1,664,192 / 61.19%
Unmapped reads	1,055,456 / 38.81%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,745 / 0.28%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	95,355 / 3.51%
Duplication rate	4.32%
Clipped reads	1,090,751 / 40.11%

2.2. ACGT Content

Number/percentage of A's	29,544,949 / 28.94%
Number/percentage of C's	16,909,094 / 16.56%
Number/percentage of T's	31,740,113 / 31.09%
Number/percentage of G's	23,862,303 / 23.37%
Number/percentage of N's	28,724 / 0.03%
GC Percentage	39.94%

2.3. Coverage

Mean	0.033

Standard Deviation	0.2717
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2.4. Mapping Quality

Mean Mapping Quality	46
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2.5. Mismatches and indels

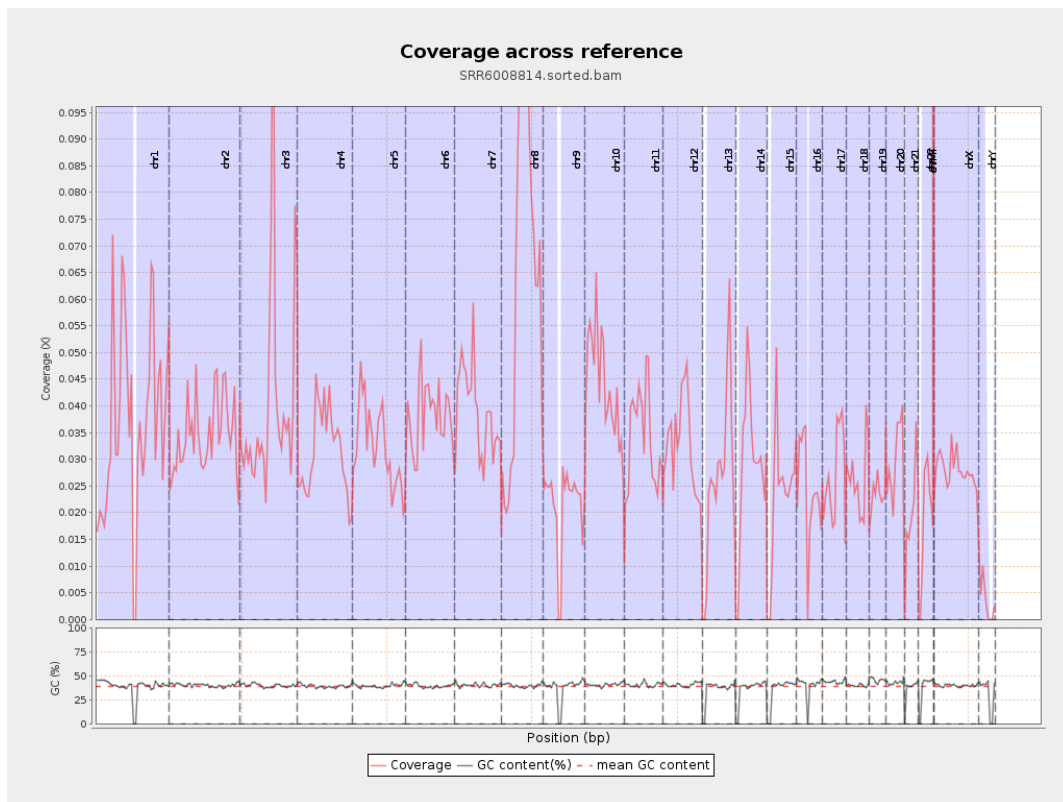
General error rate	1.17%
Mismatches	1,186,255
Insertions	7,720
Mapped reads with at least one insertion	0.46%
Deletions	41,726
Mapped reads with at least one deletion	2.48%
Homopolymer indels	48.93%

2.6. Chromosome stats

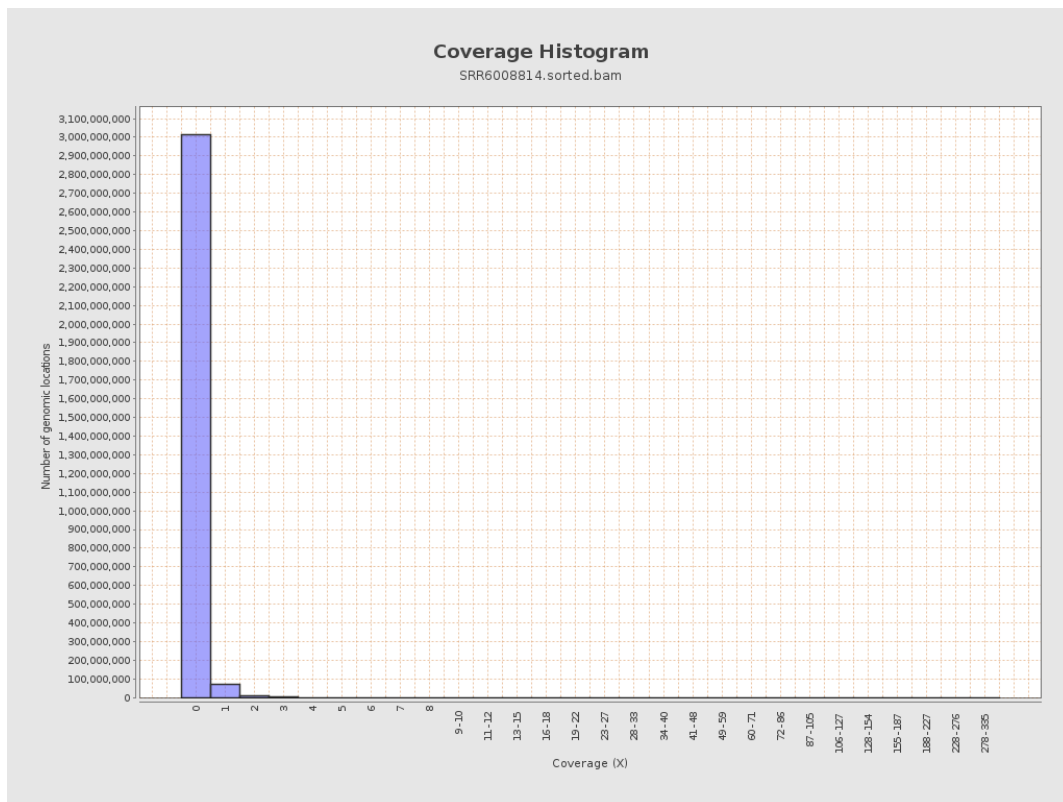
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9146771	0.0367	0.3498
chr2	243199373	8433975	0.0347	0.2922
chr3	198022430	8018048	0.0405	0.255
chr4	191154276	5991576	0.0313	0.2182
chr5	180915260	5848471	0.0323	0.2215
chr6	171115067	6512357	0.0381	0.2835
chr7	159138663	6262504	0.0394	0.4132

chr8	146364022	9439709	0.0645	0.3708
chr9	141213431	2999269	0.0212	0.2145
chr10	135534747	5987198	0.0442	0.3468
chr11	135006516	4567343	0.0338	0.264
chr12	133851895	4355402	0.0325	0.2237
chr13	115169878	3033069	0.0263	0.2068
chr14	107349540	3094573	0.0288	0.2118
chr15	102531392	2387333	0.0233	0.1941
chr16	90354753	2166876	0.024	0.2035
chr17	81195210	2158837	0.0266	0.2146
chr18	78077248	2036881	0.0261	0.3255
chr19	59128983	1408641	0.0238	0.2346
chr20	63025520	1860388	0.0295	0.2119
chr21	48129895	965320	0.0201	0.1811
chr22	51304566	914612	0.0178	0.1594
chrMT	16571	34902	2.1062	2.8923
chrX	155270560	4310493	0.0278	0.217
chrY	59373566	213855	0.0036	0.0801

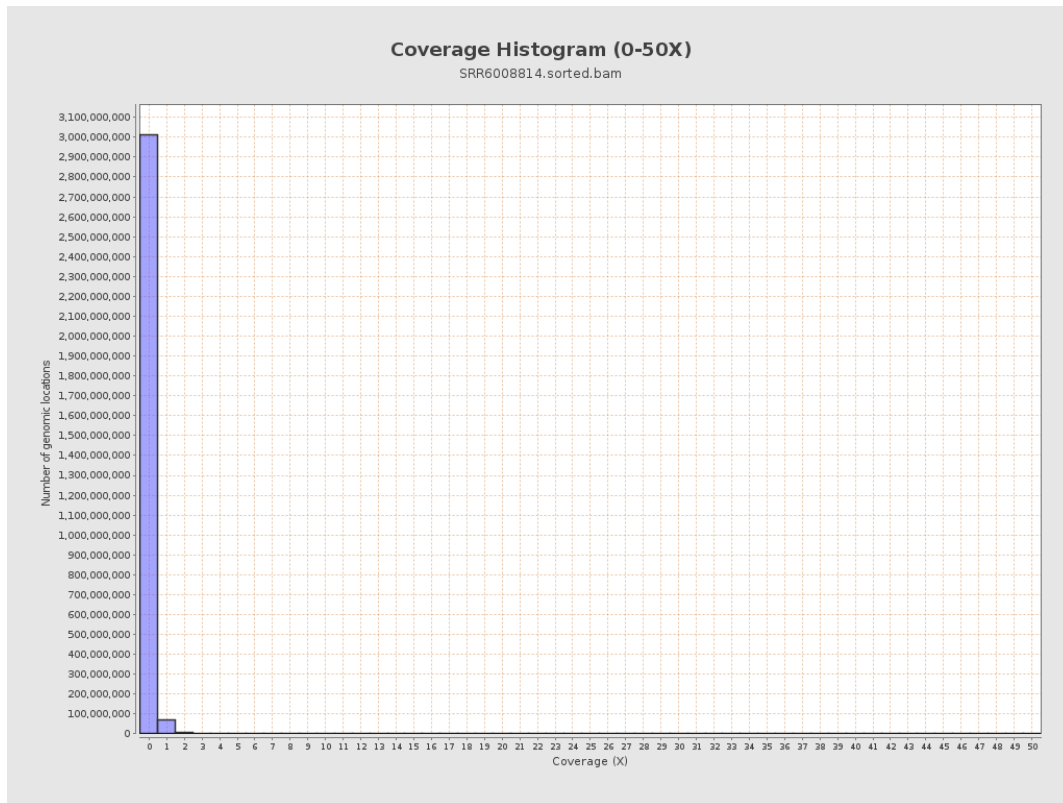
3. Results : Coverage across reference



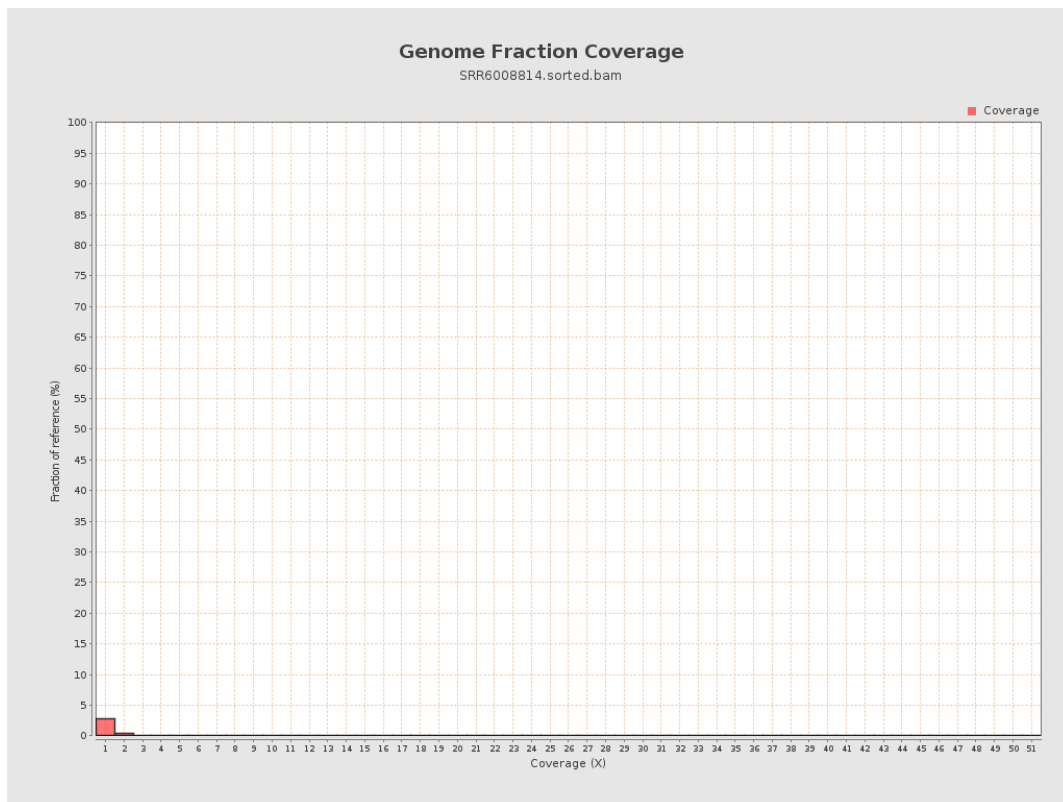
4. Results : Coverage Histogram



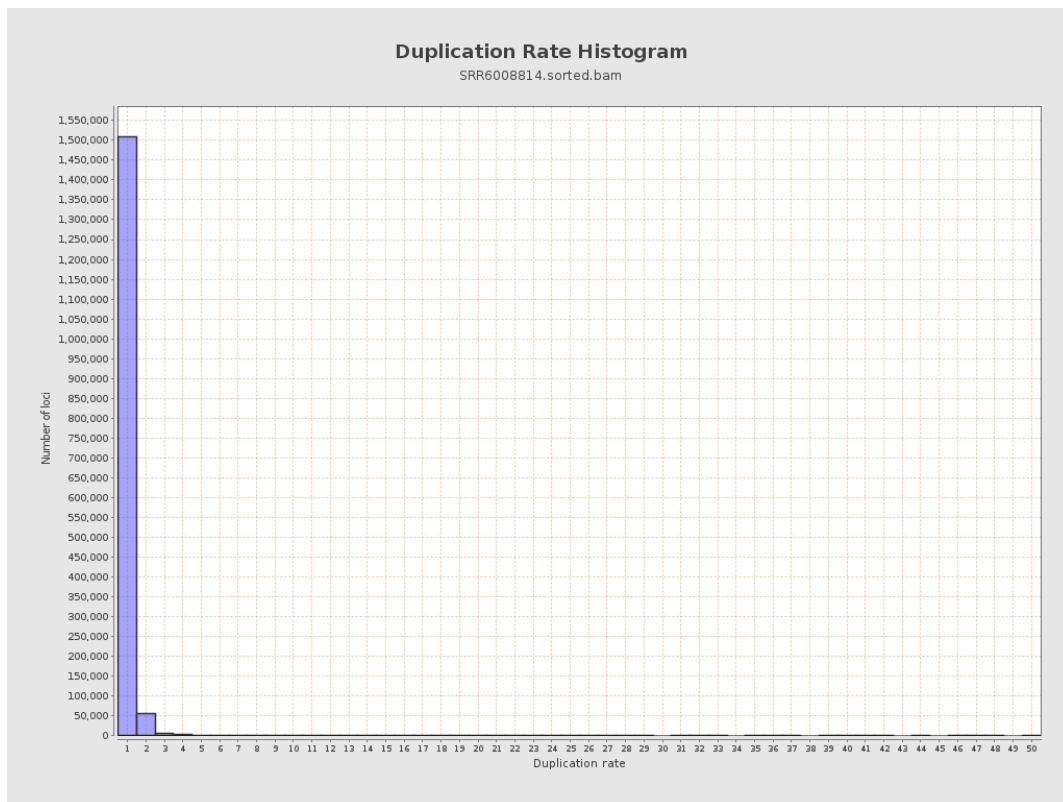
5. Results : Coverage Histogram (0-50X)



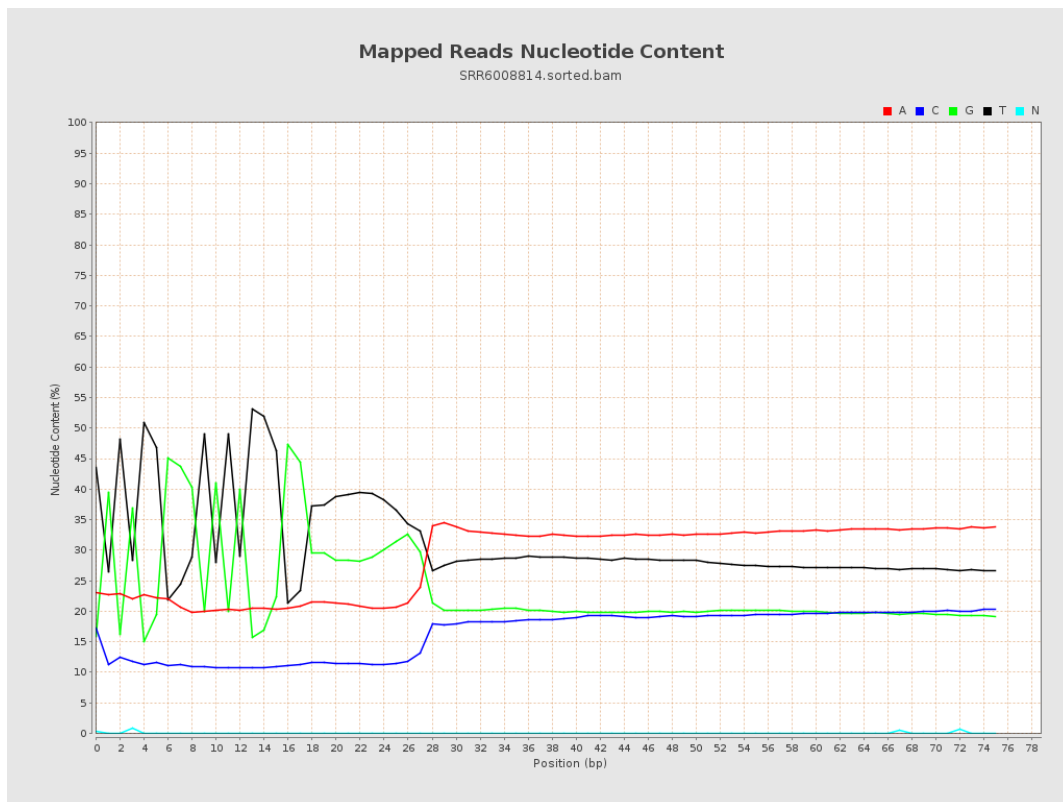
6. Results : Genome Fraction Coverage



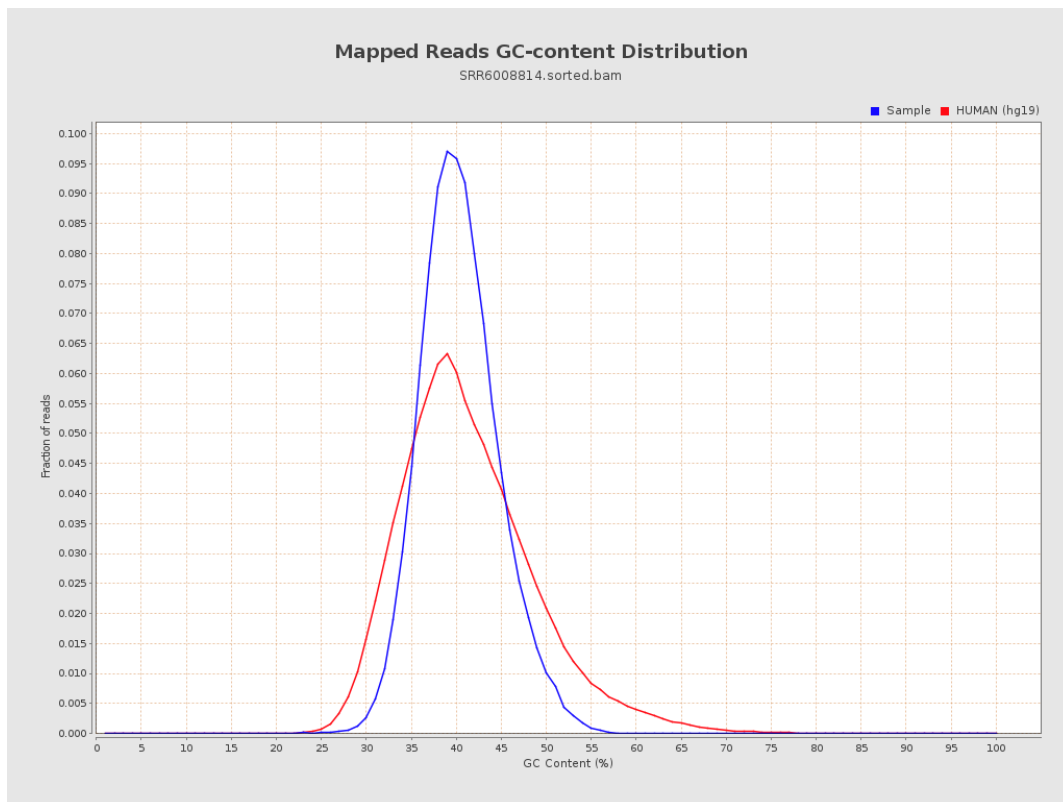
7. Results : Duplication Rate Histogram



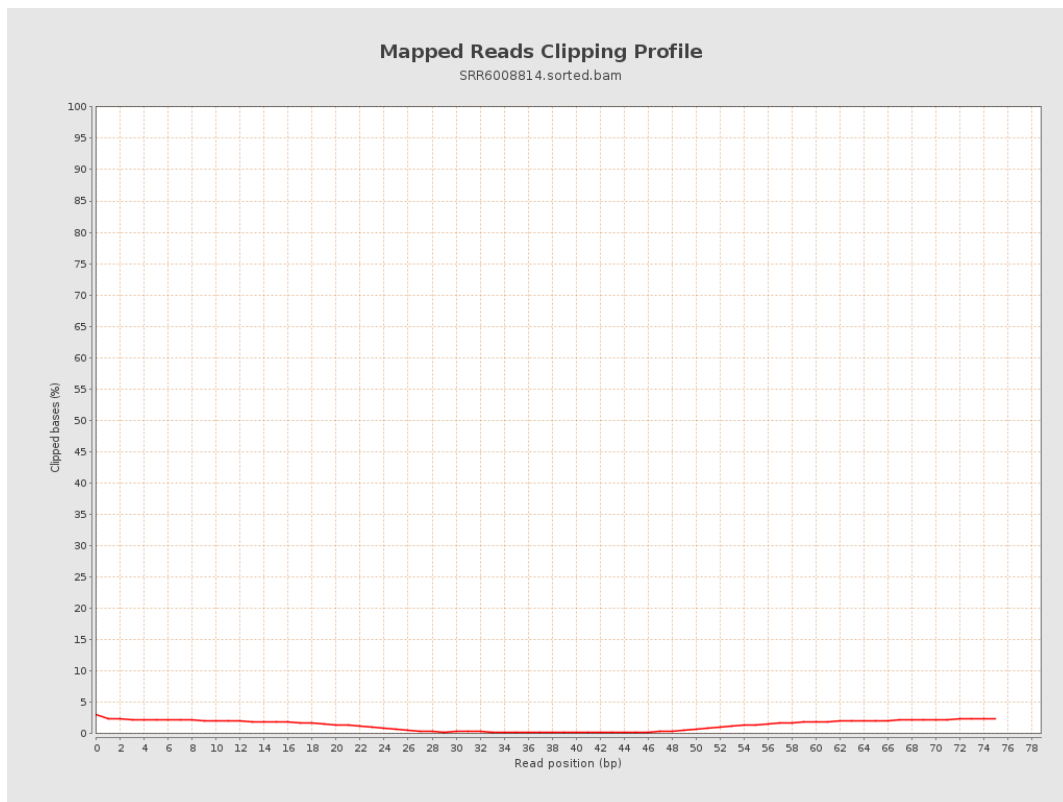
8. Results : Mapped Reads Nucleotide Content



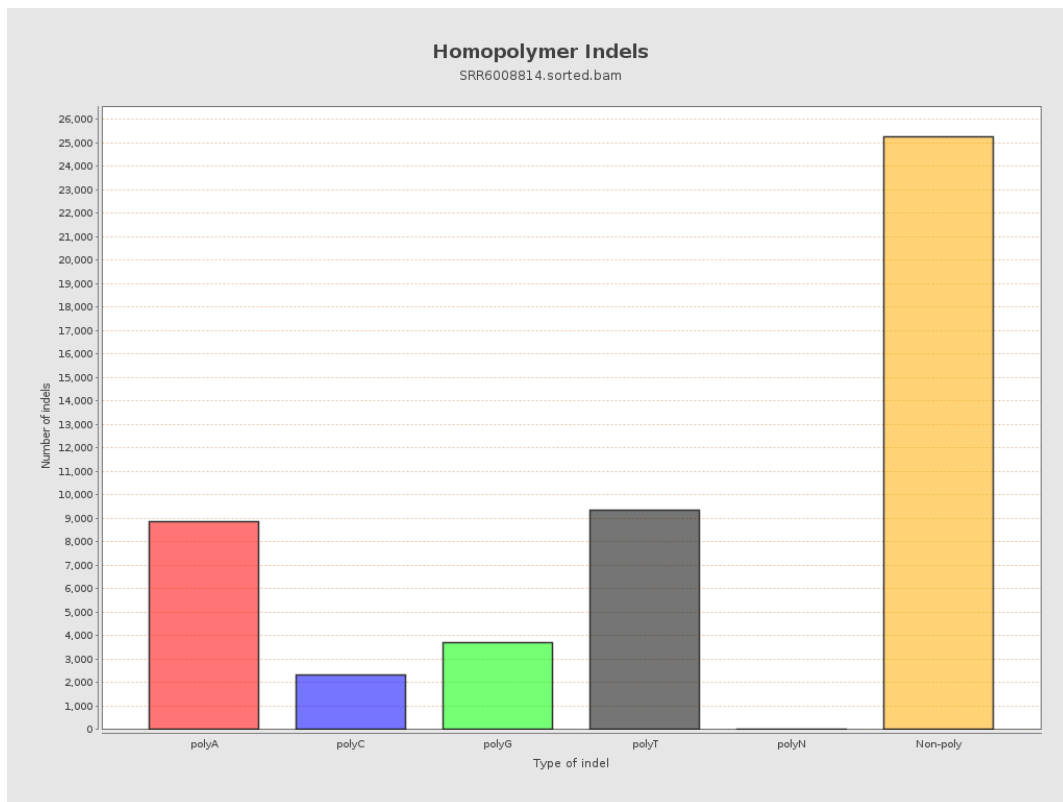
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

