

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 12:46:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008817.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_SRR6008817 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008817.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 12:46:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008817.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,049,763
Mapped reads	1,600,695 / 78.09%
Unmapped reads	449,068 / 21.91%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,406 / 0.56%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	69,111 / 3.37%
Duplication rate	3.29%
Clipped reads	921,337 / 44.95%

2.2. ACGT Content

Number/percentage of A's	30,461,117 / 29.88%
Number/percentage of C's	17,108,095 / 16.78%
Number/percentage of T's	31,232,081 / 30.64%
Number/percentage of G's	23,102,104 / 22.66%
Number/percentage of N's	28,620 / 0.03%
GC Percentage	39.45%

2.3. Coverage

Mean	0.0329

Standard Deviation	0.2563
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2.4. Mapping Quality

Mean Mapping Quality	47.15
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2.5. Mismatches and indels

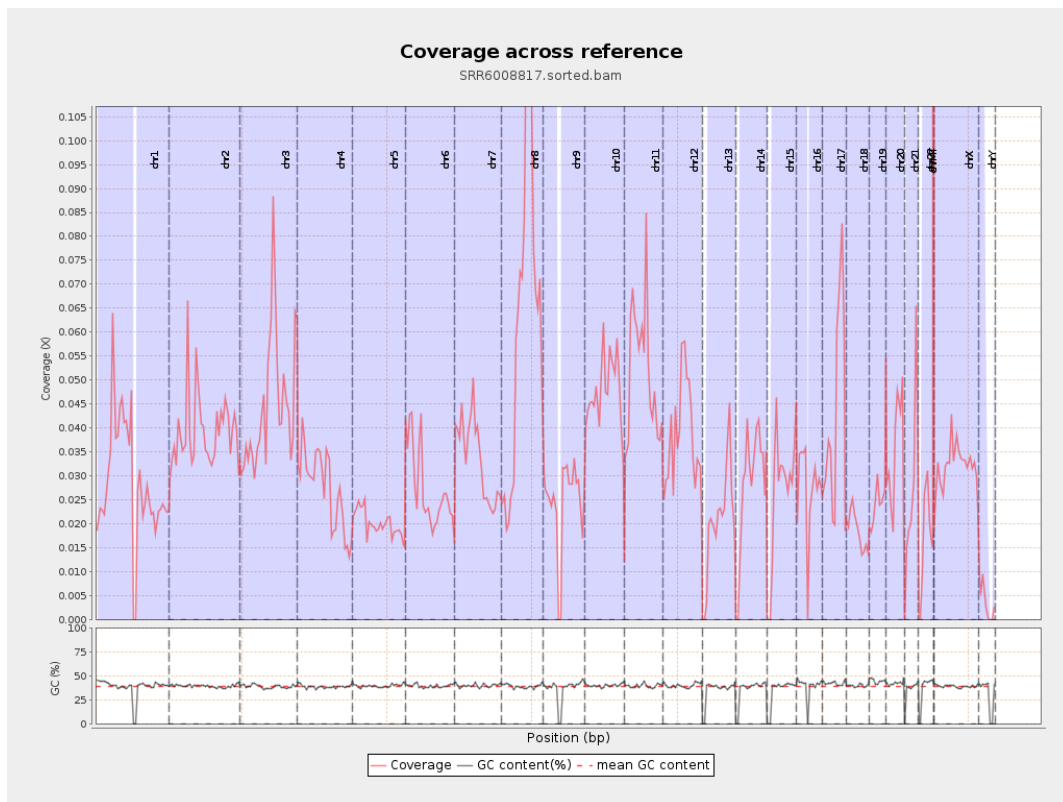
General error rate	1.08%
Mismatches	1,090,149
Insertions	7,929
Mapped reads with at least one insertion	0.49%
Deletions	40,026
Mapped reads with at least one deletion	2.47%
Homopolymer indels	48.54%

2.6. Chromosome stats

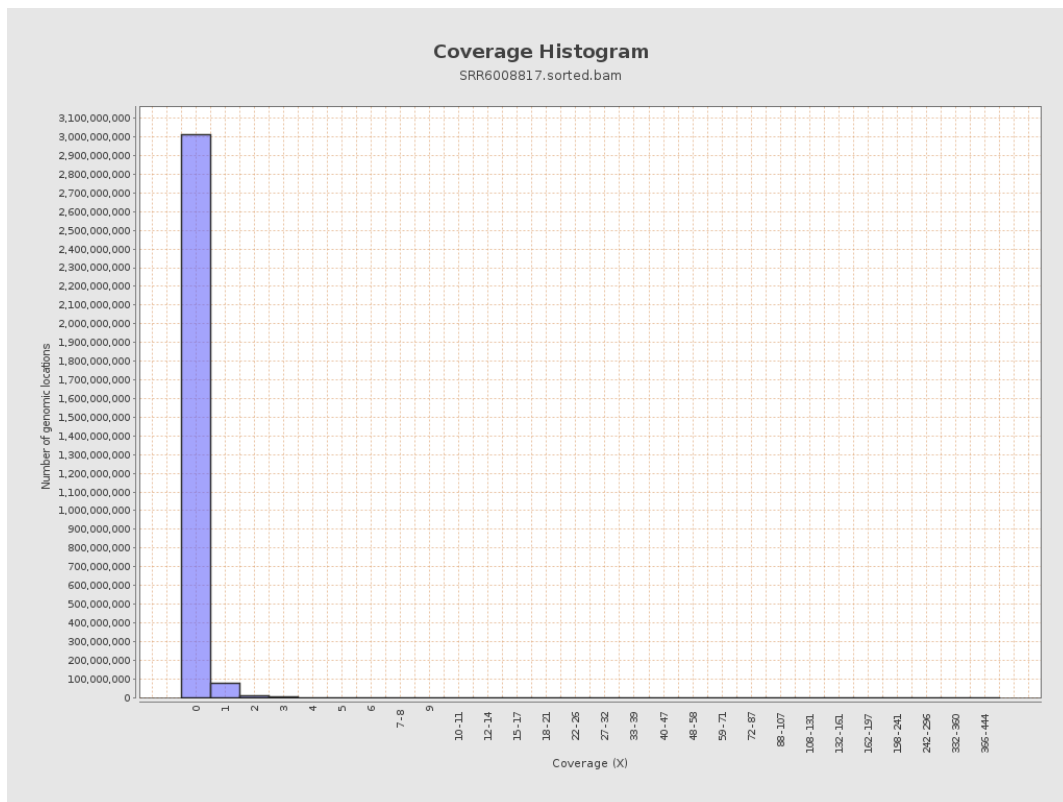
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7097364	0.0285	0.3227
chr2	243199373	9584361	0.0394	0.2756
chr3	198022430	8801500	0.0444	0.2507
chr4	191154276	5207752	0.0272	0.1962
chr5	180915260	3624907	0.02	0.1686
chr6	171115067	4665619	0.0273	0.223
chr7	159138663	5350980	0.0336	0.3279

chr8	146364022	9115723	0.0623	0.4009
chr9	141213431	3416866	0.0242	0.209
chr10	135534747	6535357	0.0482	0.2877
chr11	135006516	6932854	0.0514	0.3259
chr12	133851895	5150824	0.0385	0.2309
chr13	115169878	2367135	0.0206	0.1724
chr14	107349540	3016295	0.0281	0.1995
chr15	102531392	2720632	0.0265	0.1939
chr16	90354753	2481395	0.0275	0.2082
chr17	81195210	3472448	0.0428	0.2732
chr18	78077248	1446898	0.0185	0.2888
chr19	59128983	1480801	0.025	0.2259
chr20	63025520	2195405	0.0348	0.2226
chr21	48129895	1298201	0.027	0.1969
chr22	51304566	826521	0.0161	0.1479
chrMT	16571	30722	1.854	2.8801
chrX	155270560	4969509	0.032	0.2238
chrY	59373566	203723	0.0034	0.0798

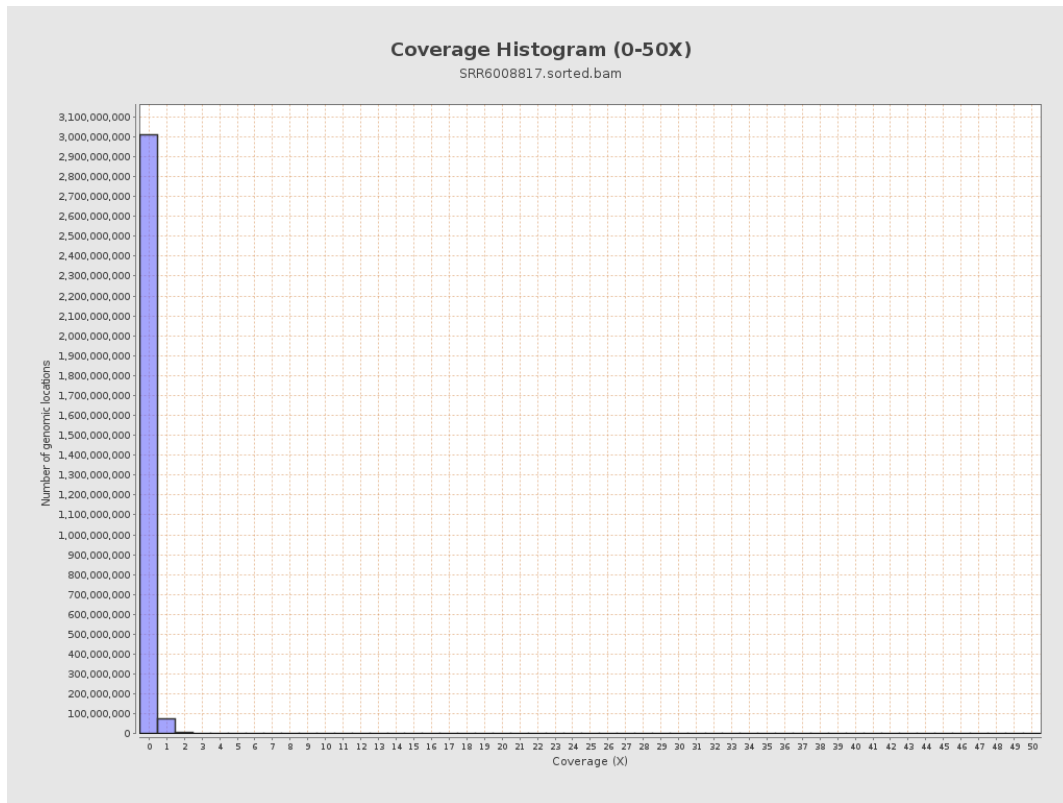
3. Results : Coverage across reference



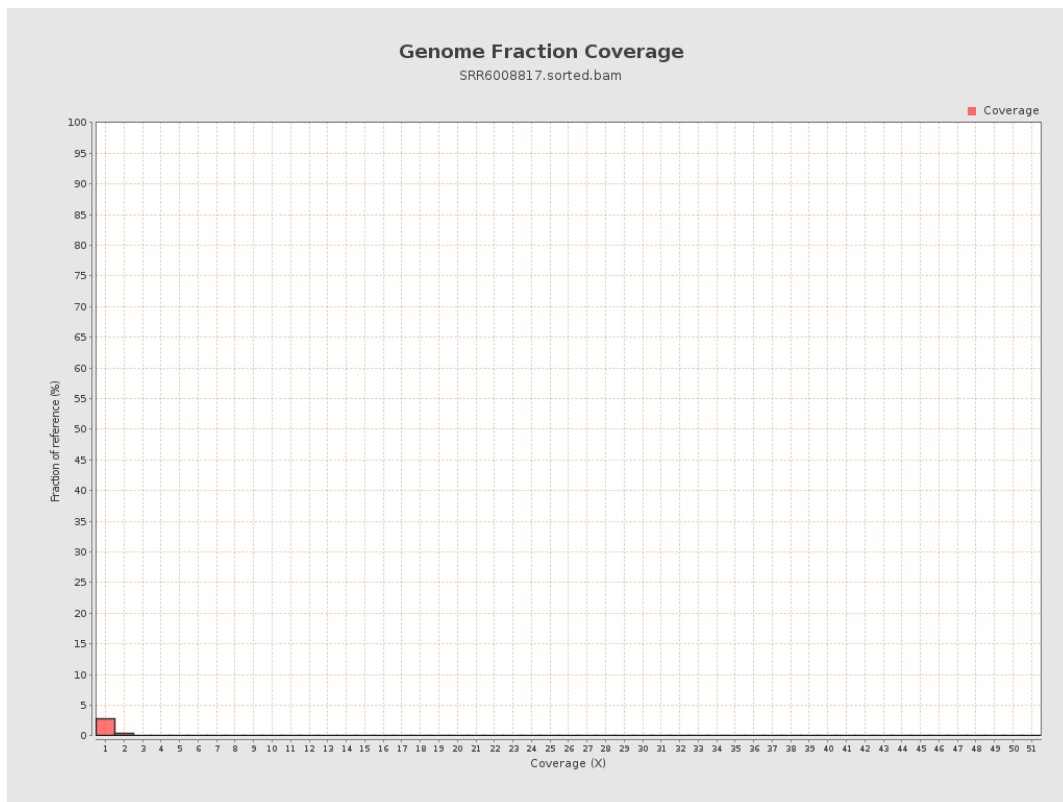
4. Results : Coverage Histogram



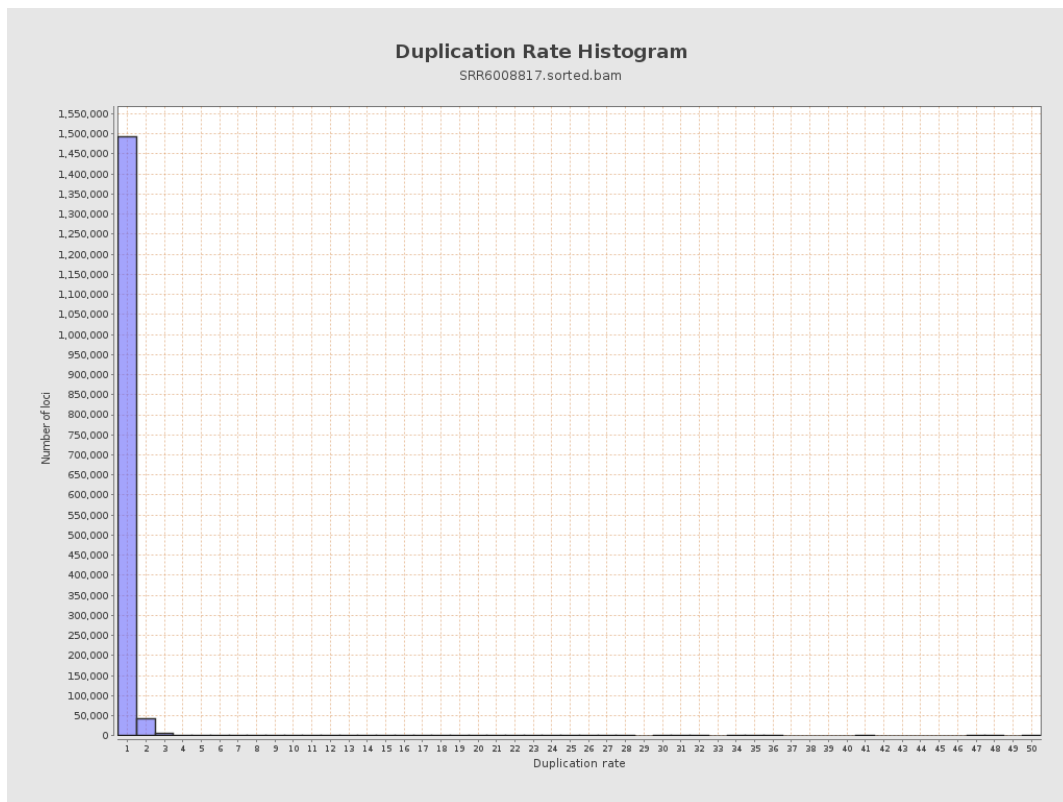
5. Results : Coverage Histogram (0-50X)



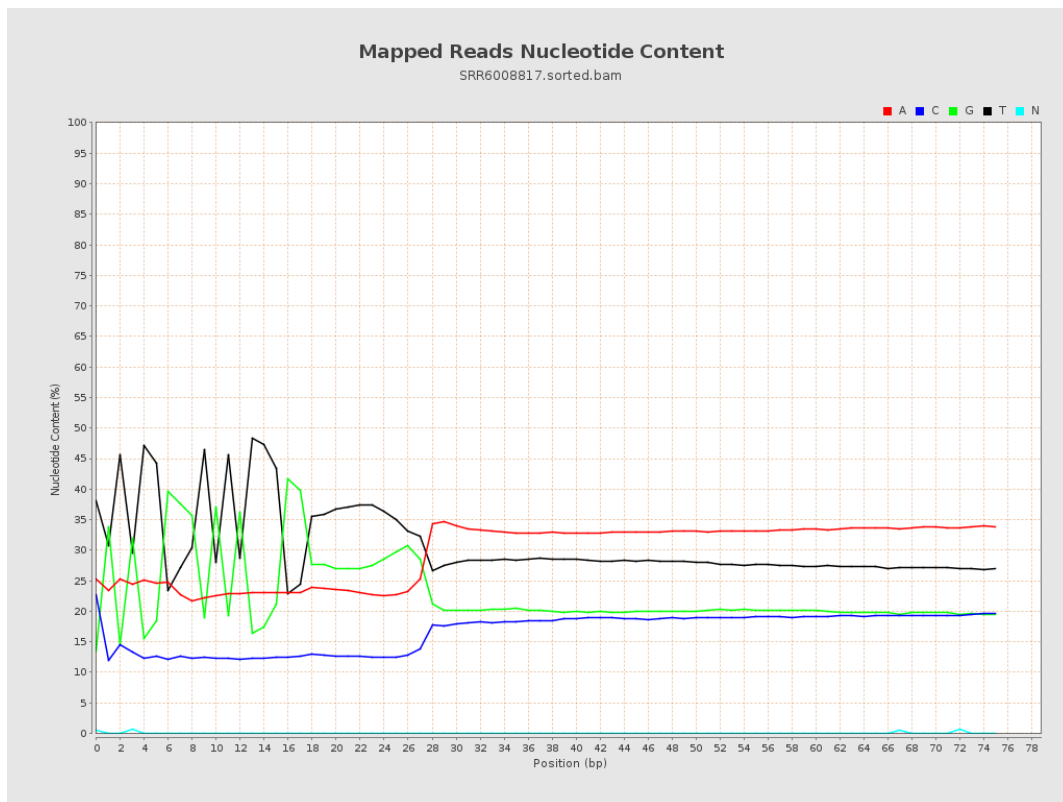
6. Results : Genome Fraction Coverage



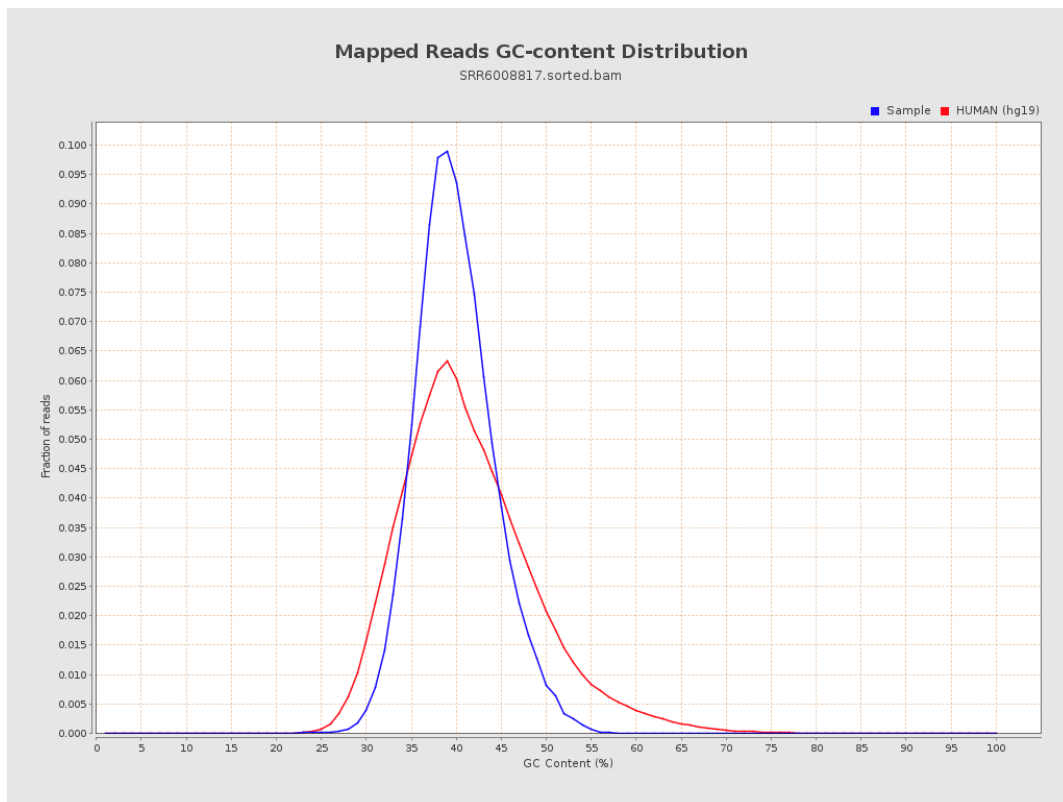
7. Results : Duplication Rate Histogram



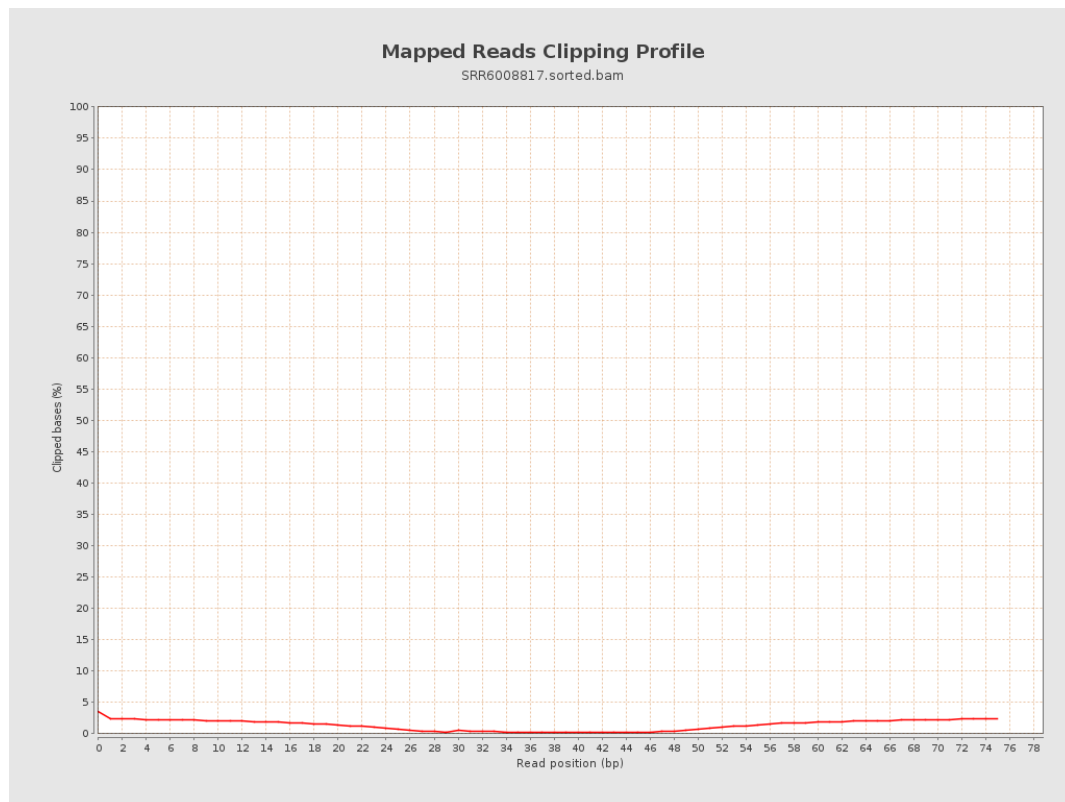
8. Results : Mapped Reads Nucleotide Content



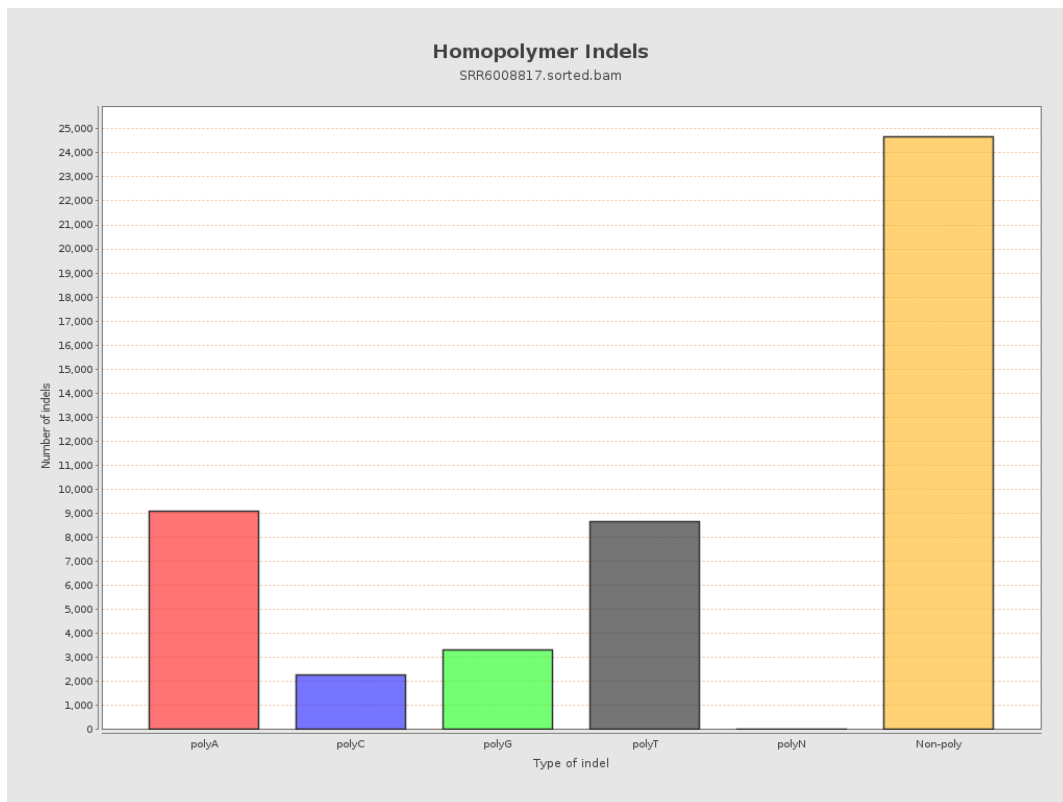
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

