

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 12:44:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008816.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_SRR6008816 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008816.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 12:44:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008816.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,671,411
Mapped reads	1,300,912 / 77.83%
Unmapped reads	370,499 / 22.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,143 / 0.37%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	43,736 / 2.62%
Duplication rate	2.56%
Clipped reads	815,888 / 48.81%

2.2. ACGT Content

Number/percentage of A's	23,226,335 / 28.74%
Number/percentage of C's	14,812,214 / 18.33%
Number/percentage of T's	23,884,882 / 29.55%
Number/percentage of G's	18,889,992 / 23.37%
Number/percentage of N's	13,468 / 0.02%
GC Percentage	41.7%

2.3. Coverage

Mean	0.0261

Standard Deviation	0.2345
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2.4. Mapping Quality

Mean Mapping Quality	44.87
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2.5. Mismatches and indels

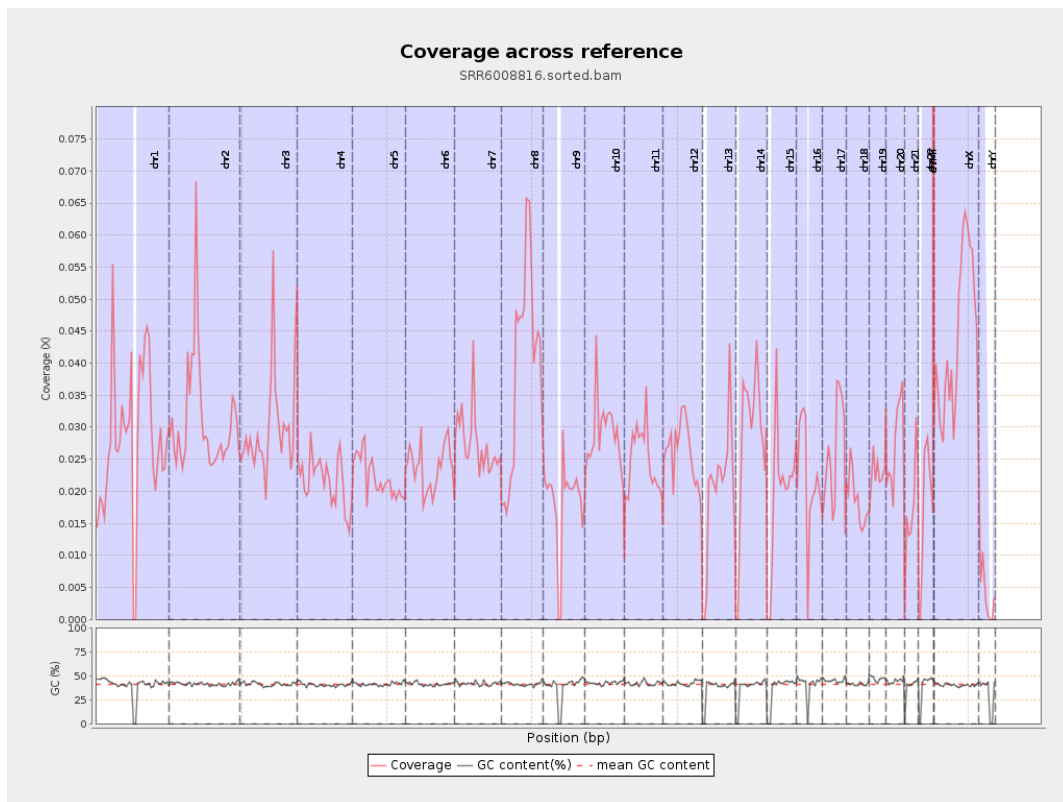
General error rate	0.95%
Mismatches	759,922
Insertions	6,684
Mapped reads with at least one insertion	0.51%
Deletions	31,718
Mapped reads with at least one deletion	2.41%
Homopolymer indels	48.09%

2.6. Chromosome stats

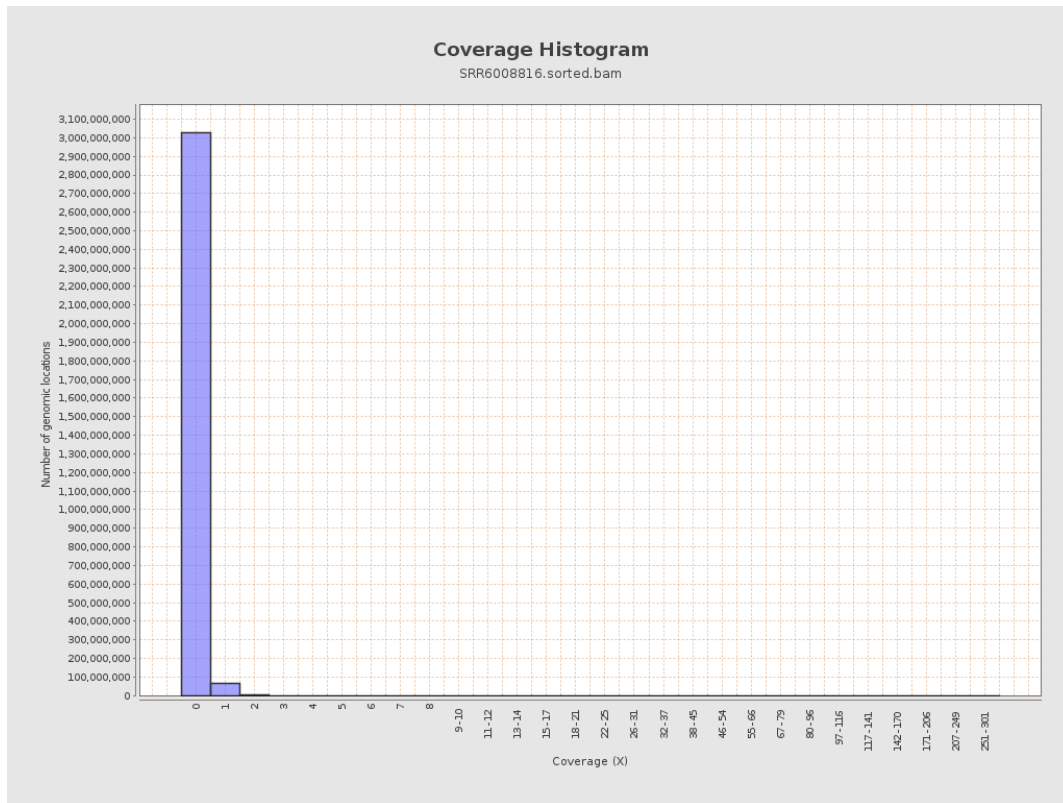
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6943883	0.0279	0.3056
chr2	243199373	7572307	0.0311	0.3011
chr3	198022430	5881444	0.0297	0.1969
chr4	191154276	4102546	0.0215	0.17
chr5	180915260	4003216	0.0221	0.1673
chr6	171115067	4058331	0.0237	0.1952
chr7	159138663	4394690	0.0276	0.3321

chr8	146364022	5736384	0.0392	0.258
chr9	141213431	2579775	0.0183	0.2186
chr10	135534747	3921354	0.0289	0.2425
chr11	135006516	3328666	0.0247	0.2614
chr12	133851895	3495773	0.0261	0.1846
chr13	115169878	2337089	0.0203	0.1646
chr14	107349540	2985986	0.0278	0.1933
chr15	102531392	2040304	0.0199	0.1613
chr16	90354753	2003842	0.0222	0.1798
chr17	81195210	2087499	0.0257	0.2208
chr18	78077248	1454584	0.0186	0.3559
chr19	59128983	1366476	0.0231	0.2212
chr20	63025520	1725586	0.0274	0.1891
chr21	48129895	826755	0.0172	0.1547
chr22	51304566	863768	0.0168	0.146
chrMT	16571	27606	1.6659	1.7632
chrX	155270560	6886189	0.0443	0.2492
chrY	59373566	252860	0.0043	0.0874

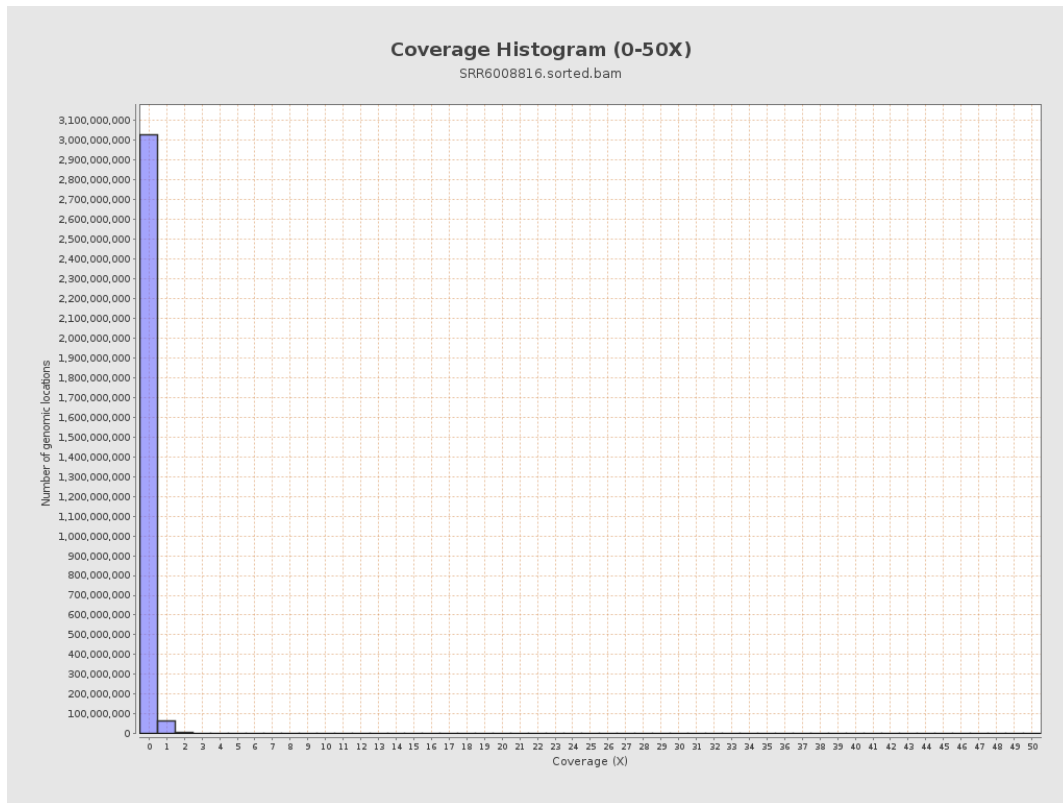
3. Results : Coverage across reference



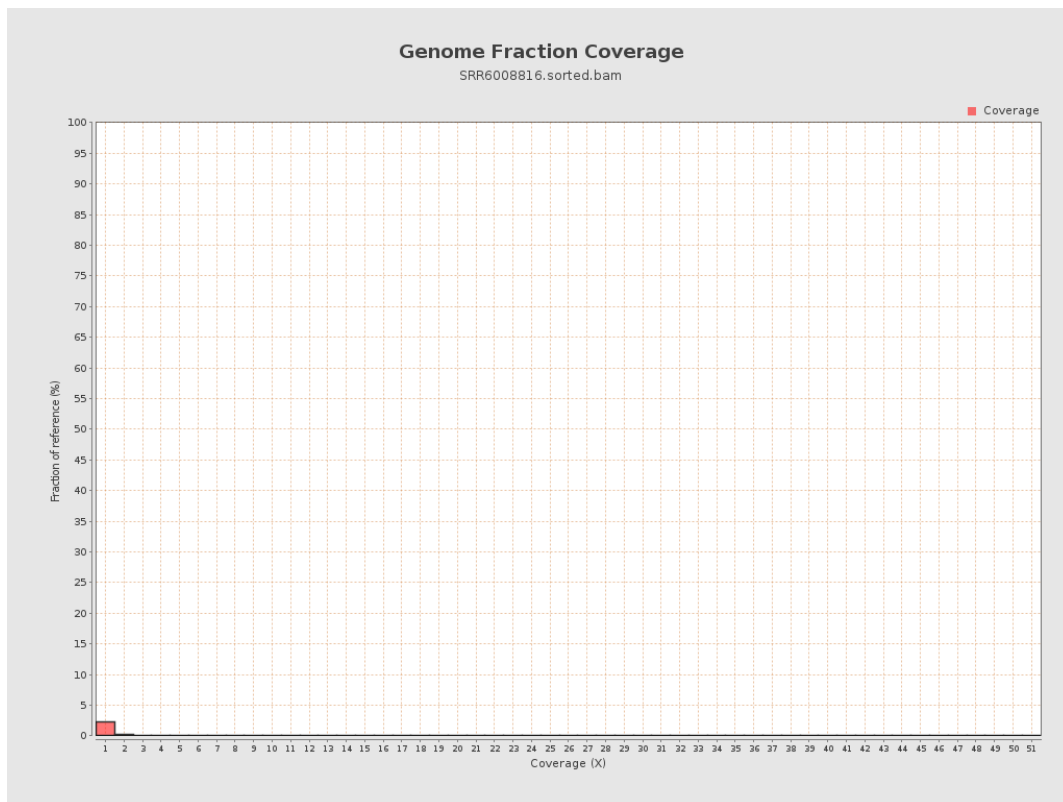
4. Results : Coverage Histogram



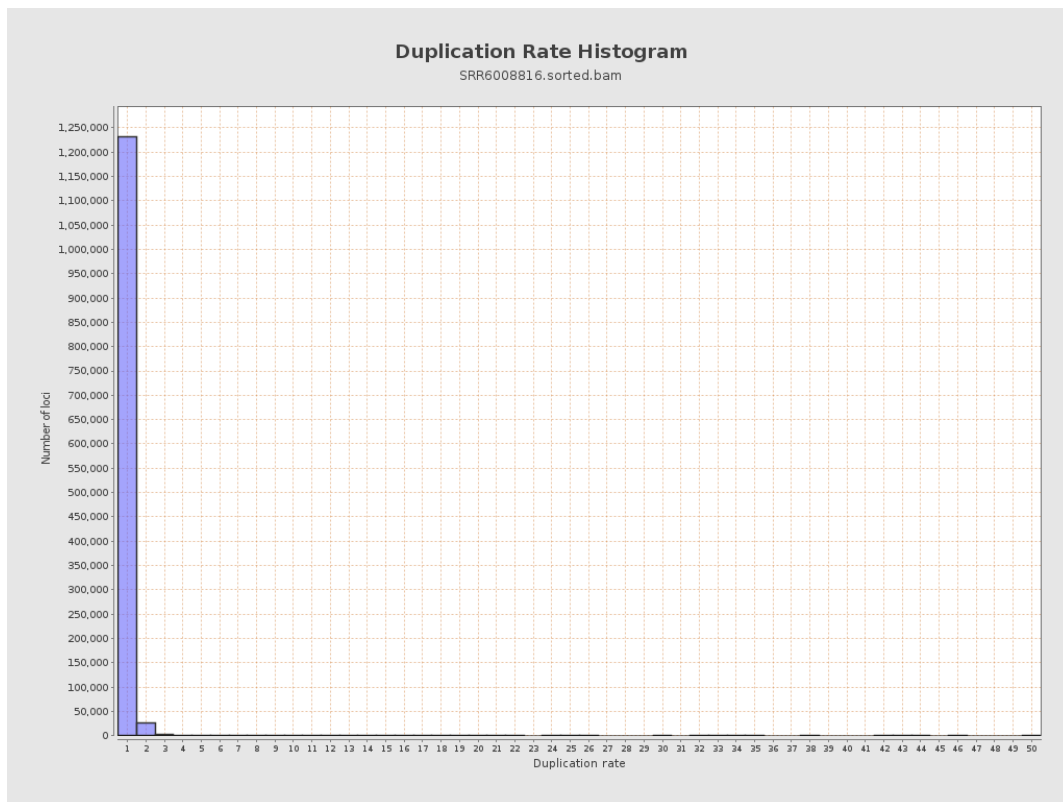
5. Results : Coverage Histogram (0-50X)



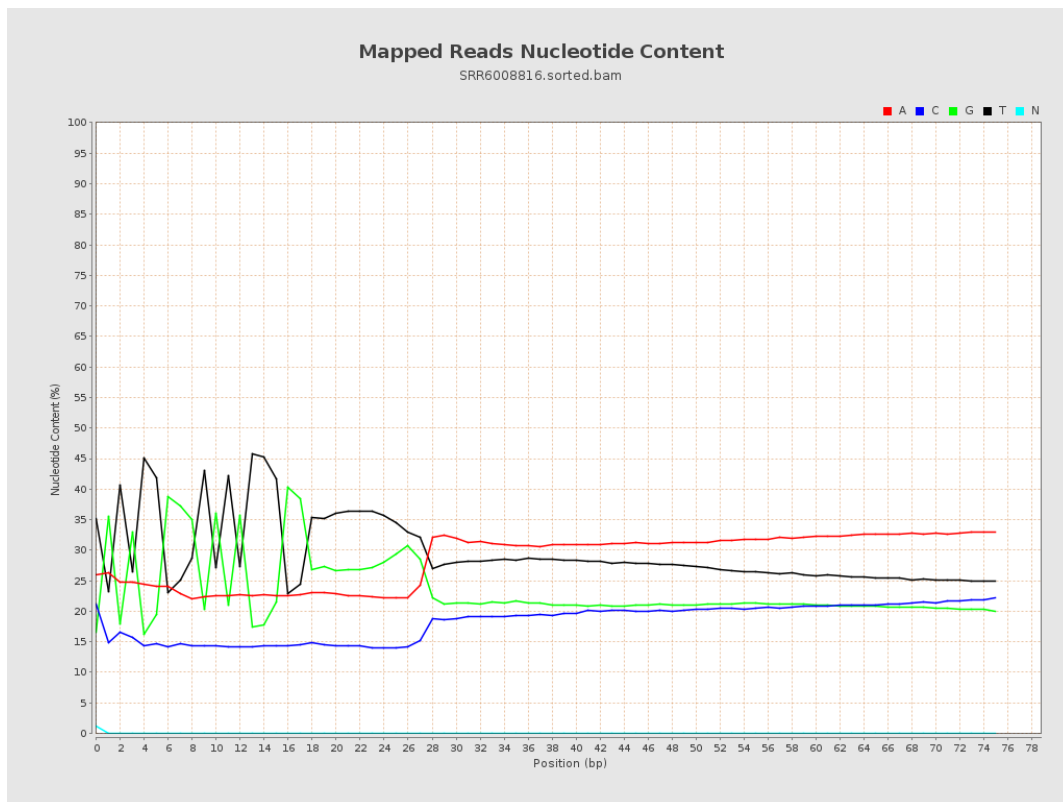
6. Results : Genome Fraction Coverage



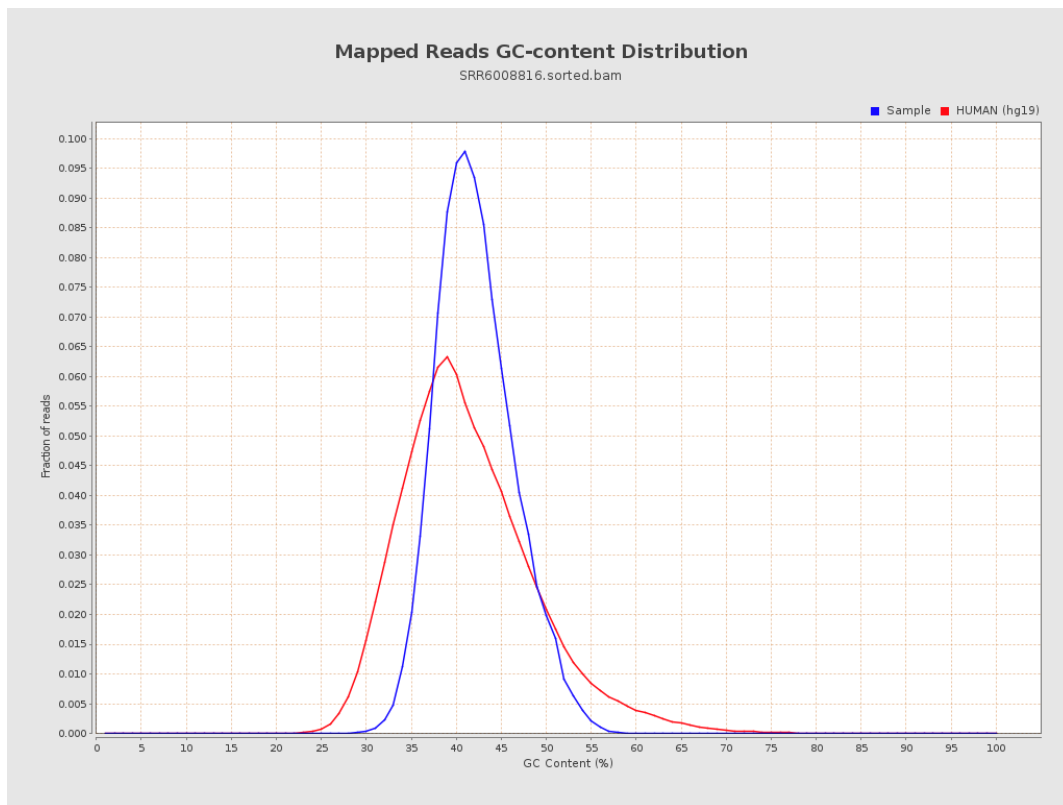
7. Results : Duplication Rate Histogram



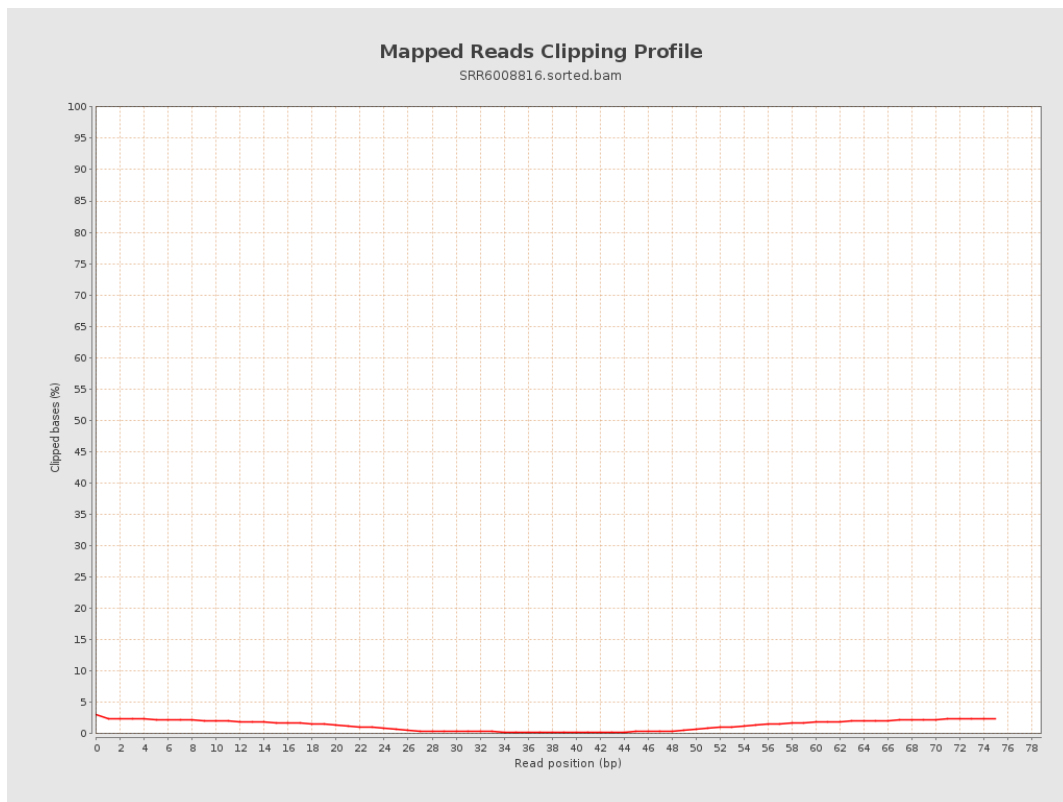
8. Results : Mapped Reads Nucleotide Content



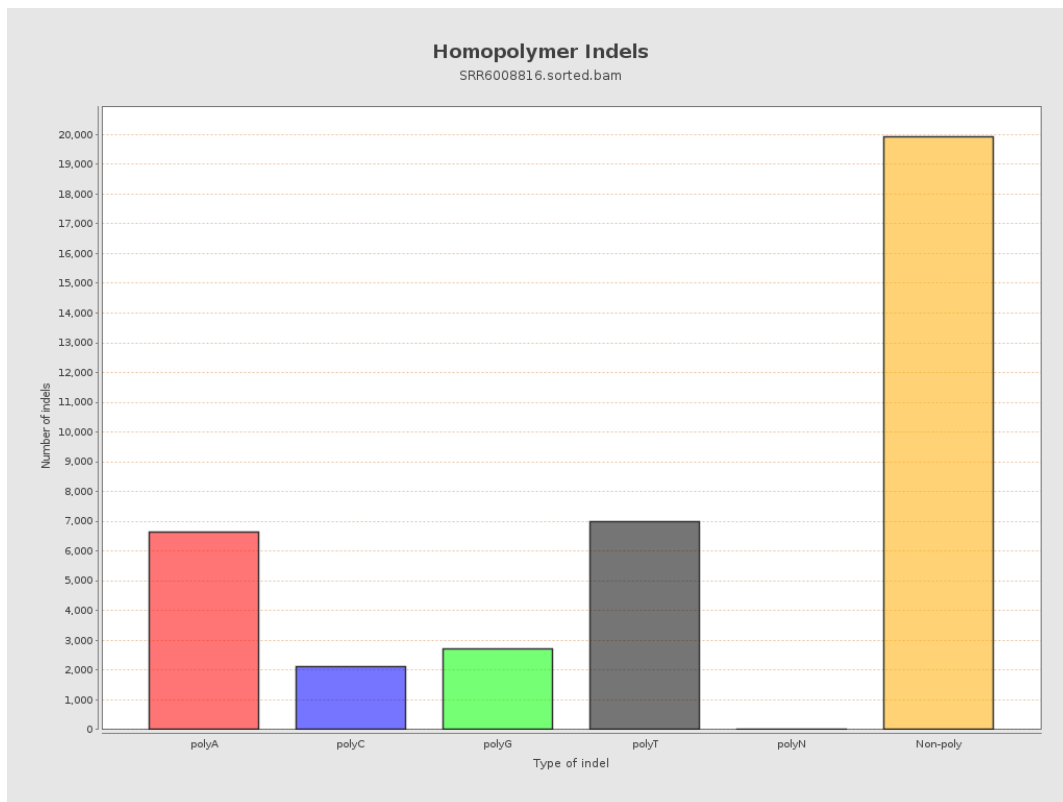
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

