

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 18:38:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230345.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_SRR6230345 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230345.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 18:38:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230345.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,487,774
Mapped reads	1,282,801 / 86.22%
Unmapped reads	204,973 / 13.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,180 / 0.68%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	37,697 / 2.53%
Duplication rate	1.94%
Clipped reads	466,272 / 31.34%

2.2. ACGT Content

Number/percentage of A's	26,433,316 / 29.8%
Number/percentage of C's	16,810,841 / 18.95%
Number/percentage of T's	26,902,920 / 30.33%
Number/percentage of G's	18,501,723 / 20.86%
Number/percentage of N's	43,479 / 0.05%
GC Percentage	39.81%

2.3. Coverage

Mean	0.0287

Standard Deviation	0.3415
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2.4. Mapping Quality

Mean Mapping Quality	46.57
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2.5. Mismatches and indels

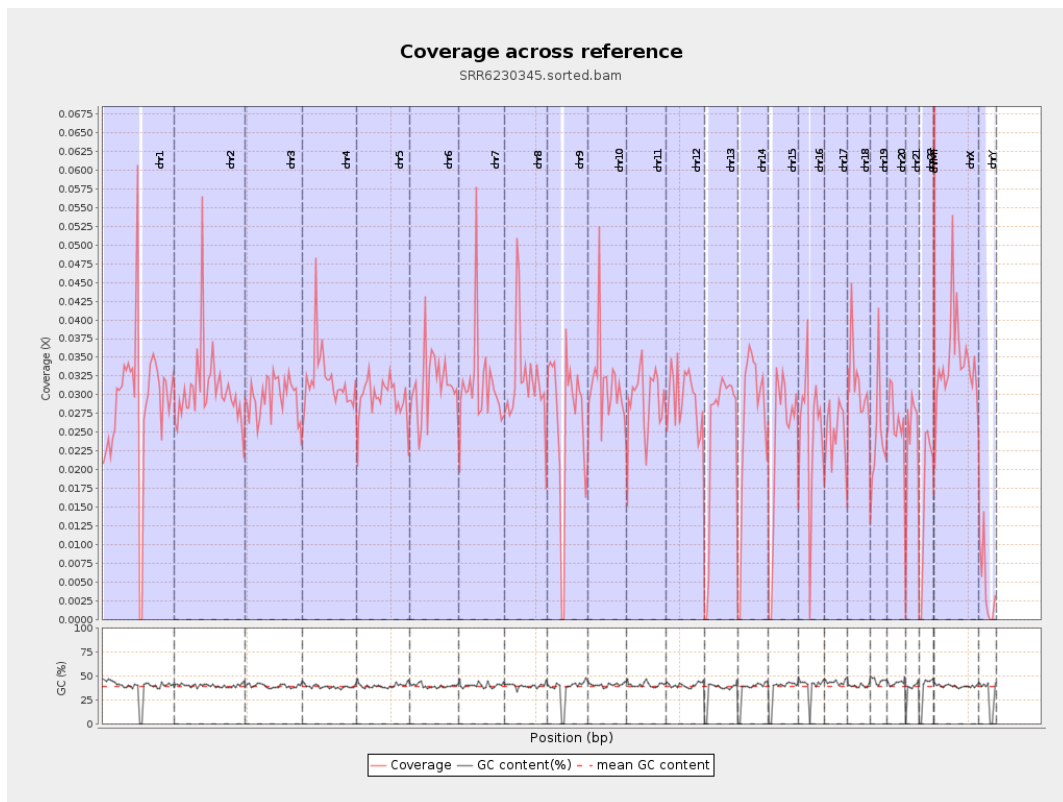
General error rate	0.98%
Mismatches	852,387
Insertions	8,145
Mapped reads with at least one insertion	0.63%
Deletions	28,349
Mapped reads with at least one deletion	2.18%
Homopolymer indels	46.2%

2.6. Chromosome stats

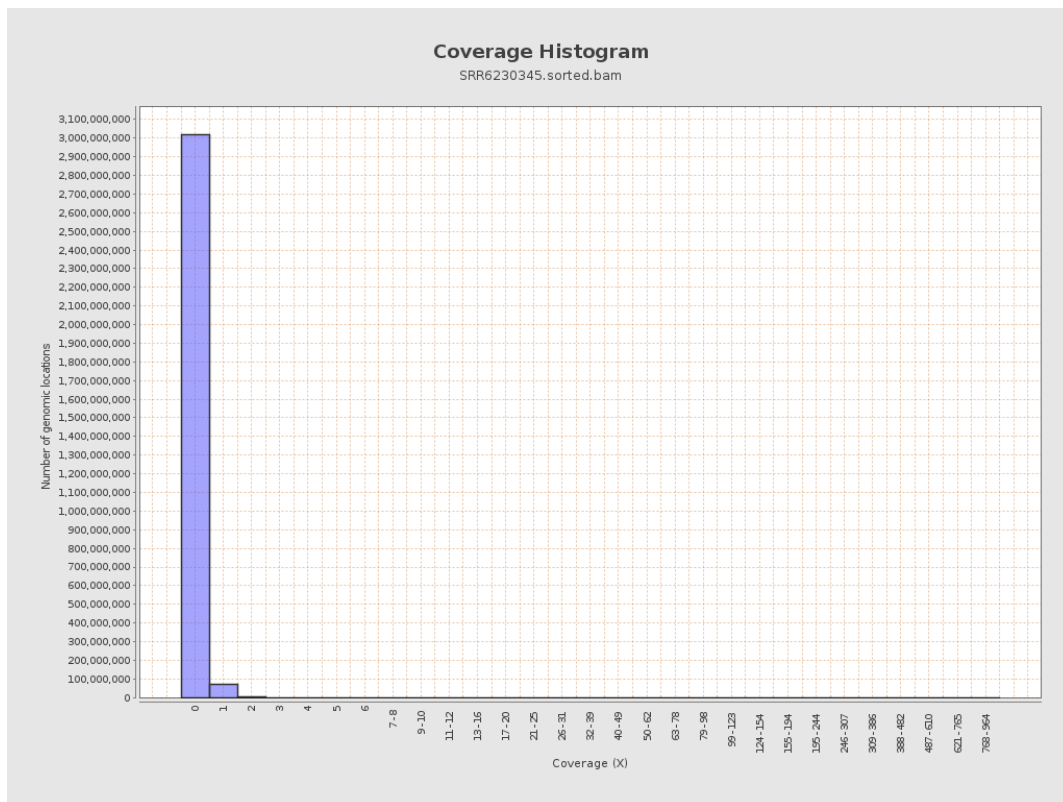
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7185444	0.0288	0.6842
chr2	243199373	7430716	0.0306	0.3082
chr3	198022430	5877497	0.0297	0.1844
chr4	191154276	6076436	0.0318	0.2106
chr5	180915260	5385933	0.0298	0.1865
chr6	171115067	5350241	0.0313	0.2194
chr7	159138663	4987114	0.0313	0.3757

chr8	146364022	4680917	0.032	0.6503
chr9	141213431	3754605	0.0266	0.2855
chr10	135534747	4244302	0.0313	0.2948
chr11	135006516	3984286	0.0295	0.2963
chr12	133851895	3943486	0.0295	0.1883
chr13	115169878	2885923	0.0251	0.1698
chr14	107349540	2856680	0.0266	0.1874
chr15	102531392	2458496	0.024	0.1664
chr16	90354753	2249198	0.0249	0.1993
chr17	81195210	2015843	0.0248	0.1989
chr18	78077248	2459307	0.0315	0.5846
chr19	59128983	1462456	0.0247	0.3754
chr20	63025520	1670884	0.0265	0.1853
chr21	48129895	1159727	0.0241	0.1867
chr22	51304566	856361	0.0167	0.1373
chrMT	16571	143311	8.6483	6.7089
chrX	155270560	5360239	0.0345	0.2242
chrY	59373566	260175	0.0044	0.1172

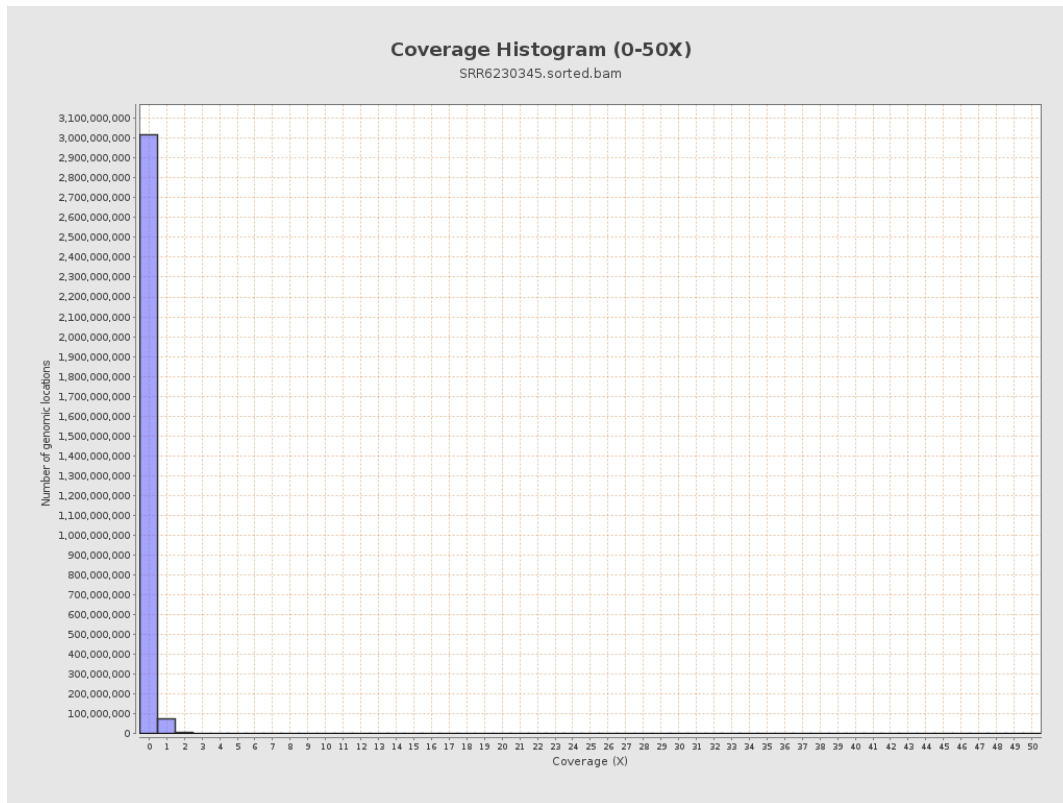
3. Results : Coverage across reference



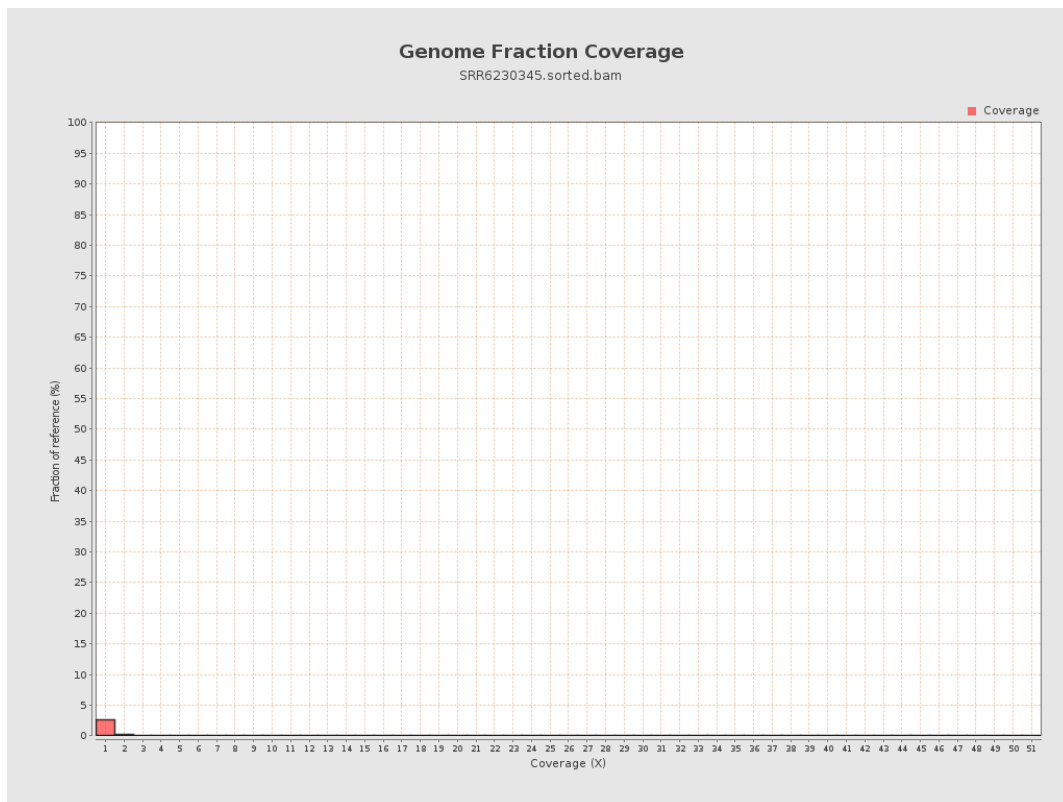
4. Results : Coverage Histogram



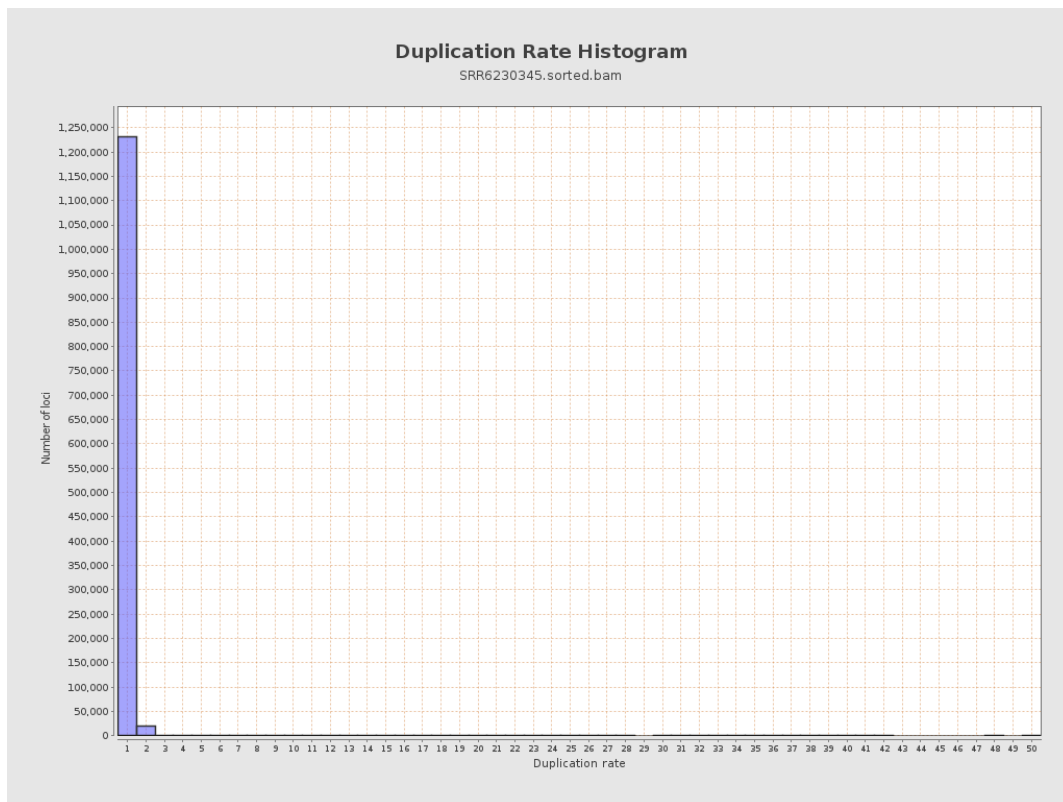
5. Results : Coverage Histogram (0-50X)



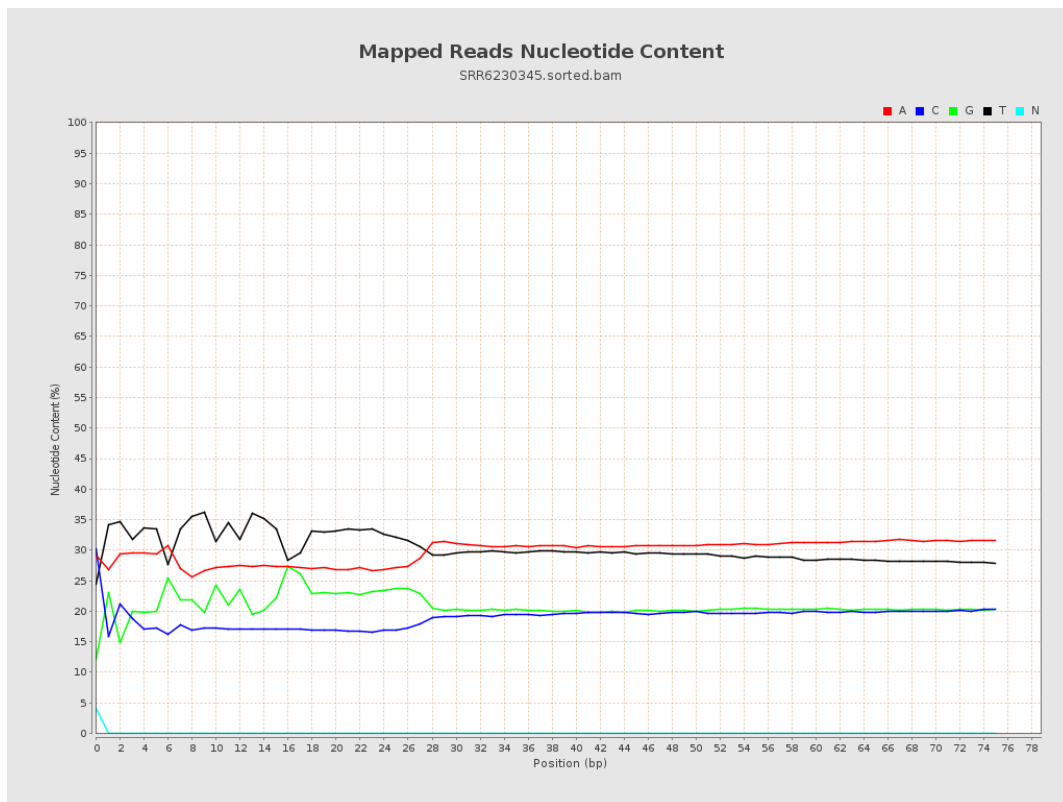
6. Results : Genome Fraction Coverage



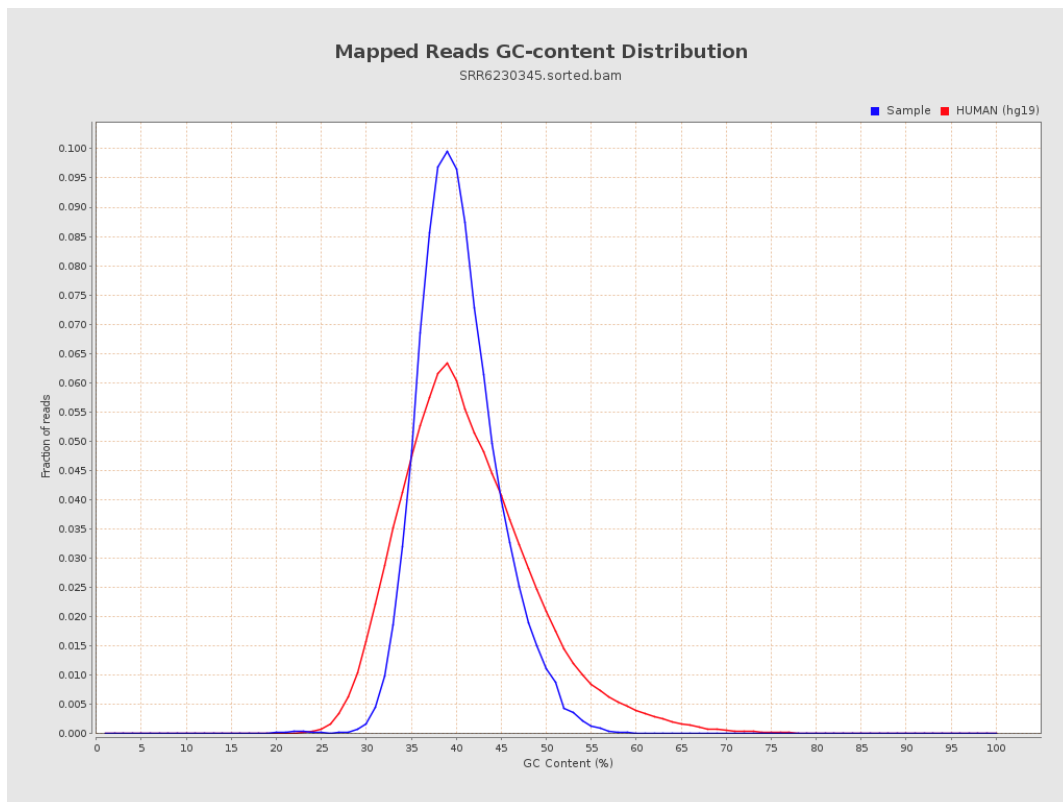
7. Results : Duplication Rate Histogram



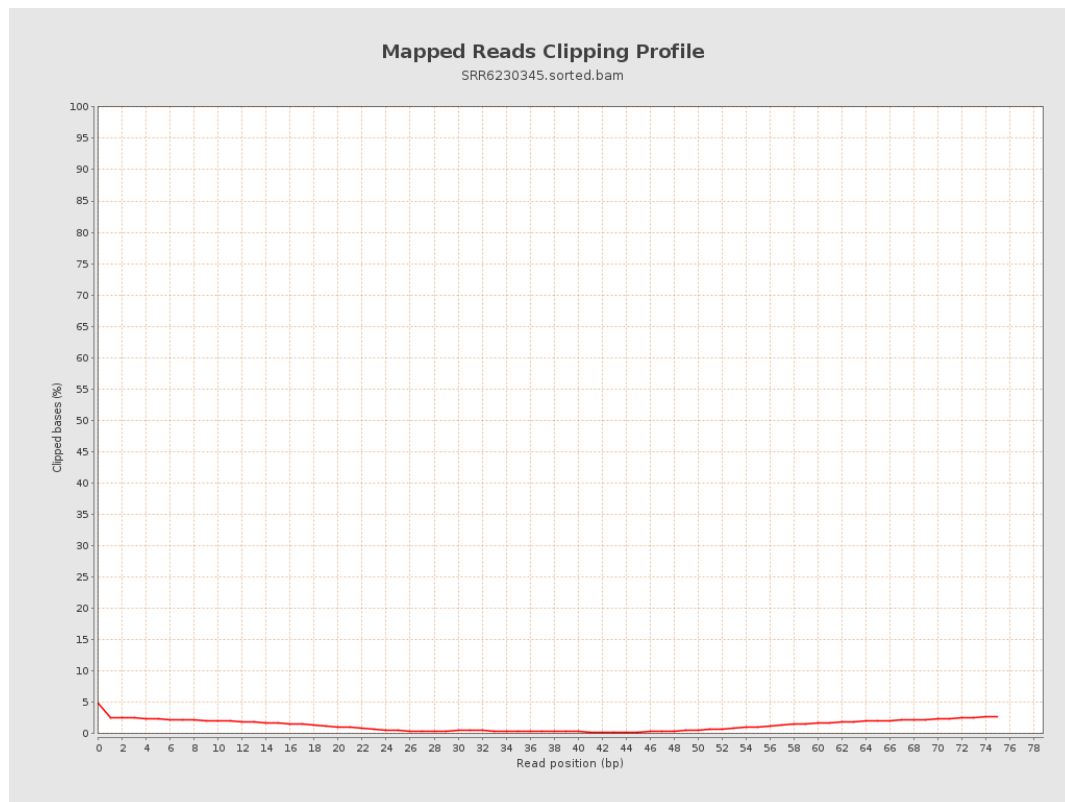
8. Results : Mapped Reads Nucleotide Content



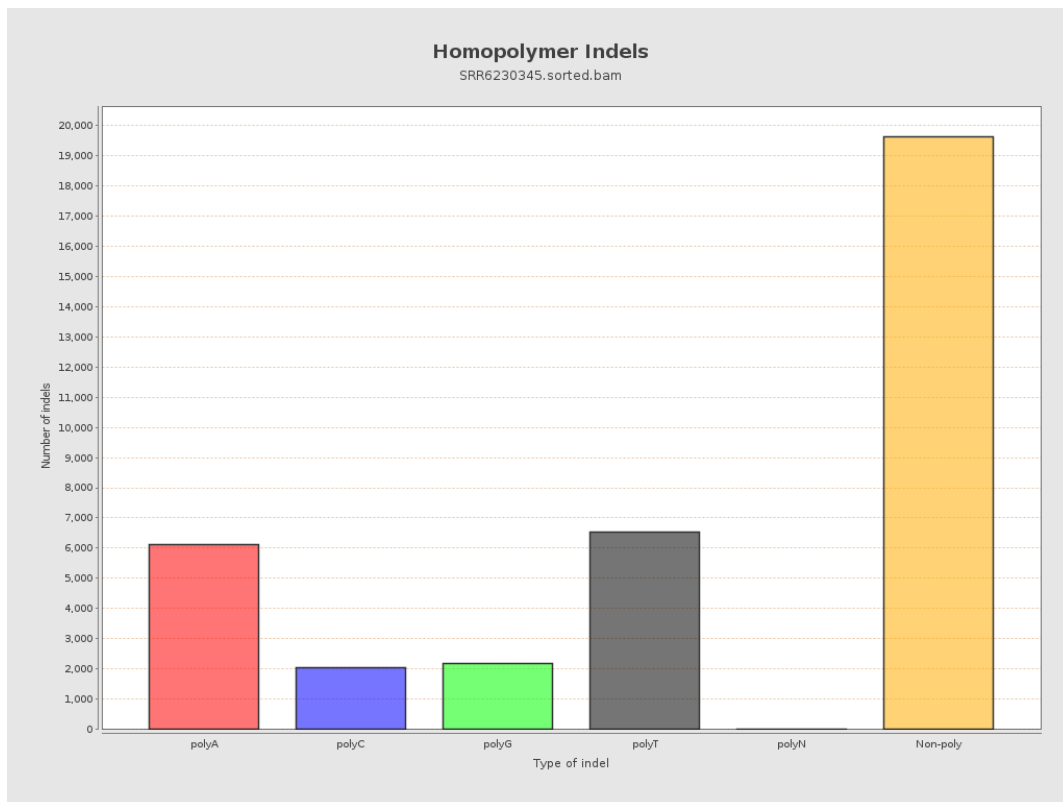
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

