

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 02:34:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240017.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_SRR6240017 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240017.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 02:34:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240017.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,558,544
Mapped reads	1,221,393 / 78.37%
Unmapped reads	337,151 / 21.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,720 / 0.24%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	130,075 / 8.35%
Duplication rate	8.15%
Clipped reads	905,469 / 58.1%

2.2. ACGT Content

Number/percentage of A's	19,453,307 / 26.8%
Number/percentage of C's	11,814,722 / 16.28%
Number/percentage of T's	23,828,854 / 32.83%
Number/percentage of G's	17,440,272 / 24.03%
Number/percentage of N's	46,807 / 0.06%
GC Percentage	40.31%

2.3. Coverage

Mean	0.0235

Standard Deviation	0.2678
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2.4. Mapping Quality

Mean Mapping Quality	43.76
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2.5. Mismatches and indels

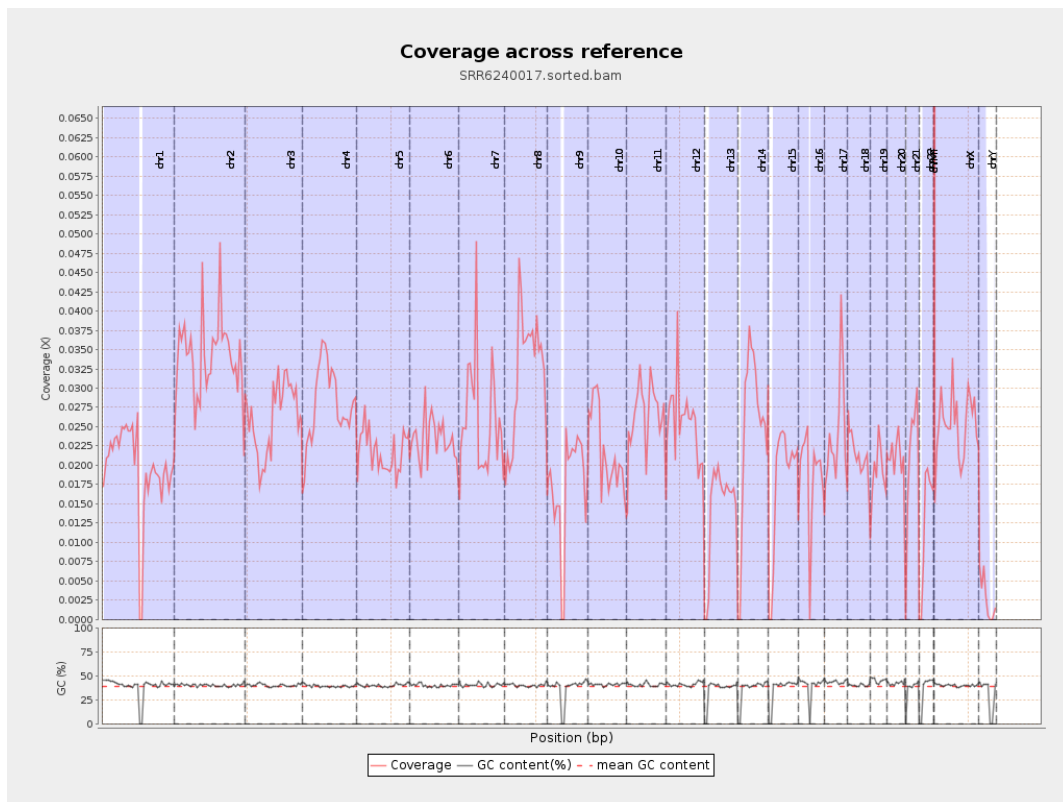
General error rate	1.06%
Mismatches	763,021
Insertions	5,386
Mapped reads with at least one insertion	0.44%
Deletions	25,653
Mapped reads with at least one deletion	2.07%
Homopolymer indels	51.21%

2.6. Chromosome stats

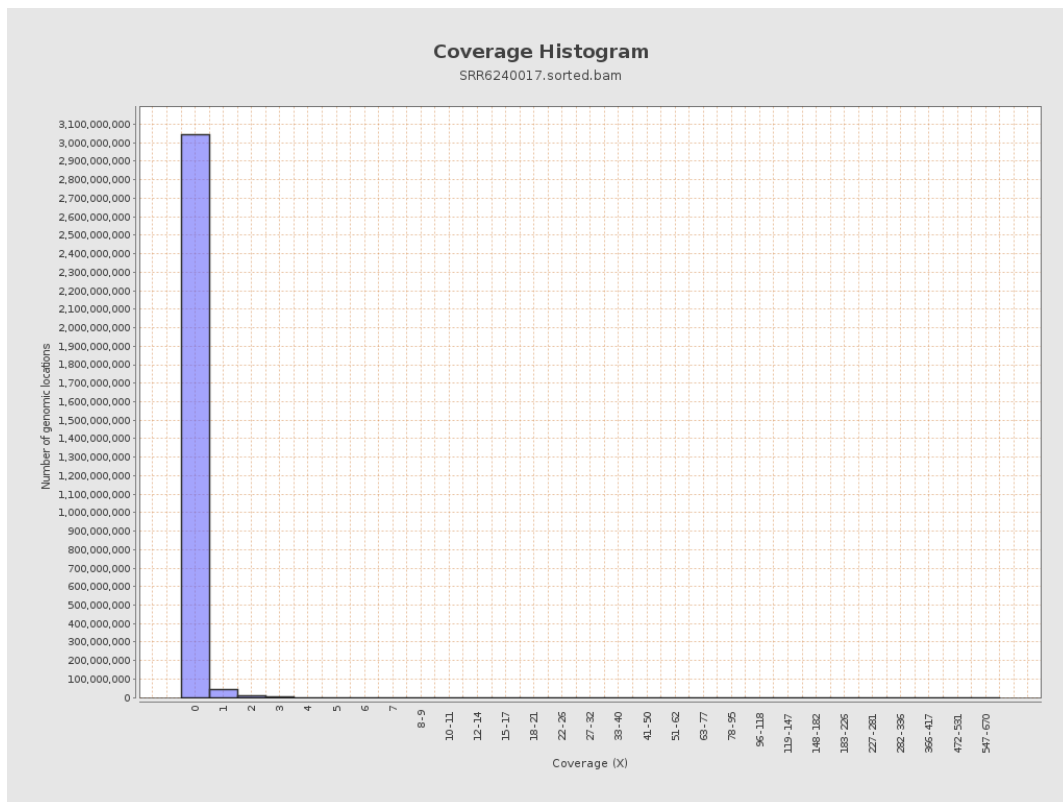
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4877542	0.0196	0.2689
chr2	243199373	8311933	0.0342	0.3339
chr3	198022430	5182410	0.0262	0.2272
chr4	191154276	5336707	0.0279	0.2348
chr5	180915260	3944355	0.0218	0.2005
chr6	171115067	3984227	0.0233	0.2265
chr7	159138663	4123087	0.0259	0.5515

chr8	146364022	4689110	0.032	0.3426
chr9	141213431	2424962	0.0172	0.2249
chr10	135534747	2964752	0.0219	0.2124
chr11	135006516	3610474	0.0267	0.2755
chr12	133851895	3426948	0.0256	0.2087
chr13	115169878	1644546	0.0143	0.1628
chr14	107349540	2681228	0.025	0.2133
chr15	102531392	1822435	0.0178	0.2009
chr16	90354753	1649476	0.0183	0.1774
chr17	81195210	1963933	0.0242	0.2221
chr18	78077248	1665705	0.0213	0.3218
chr19	59128983	1150432	0.0195	0.2323
chr20	63025520	1313264	0.0208	0.2018
chr21	48129895	1027357	0.0213	0.1999
chr22	51304566	659595	0.0129	0.1453
chrMT	16571	60121	3.6281	4.9719
chrX	155270560	3953570	0.0255	0.2332
chrY	59373566	159442	0.0027	0.0683

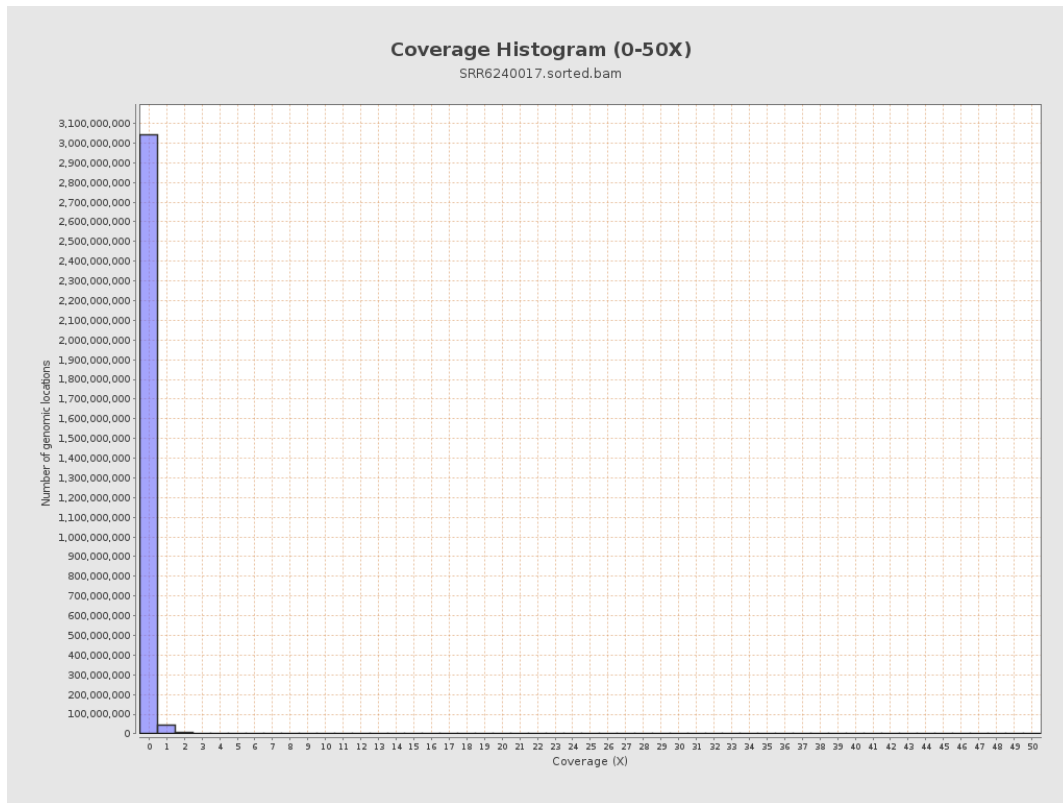
3. Results : Coverage across reference



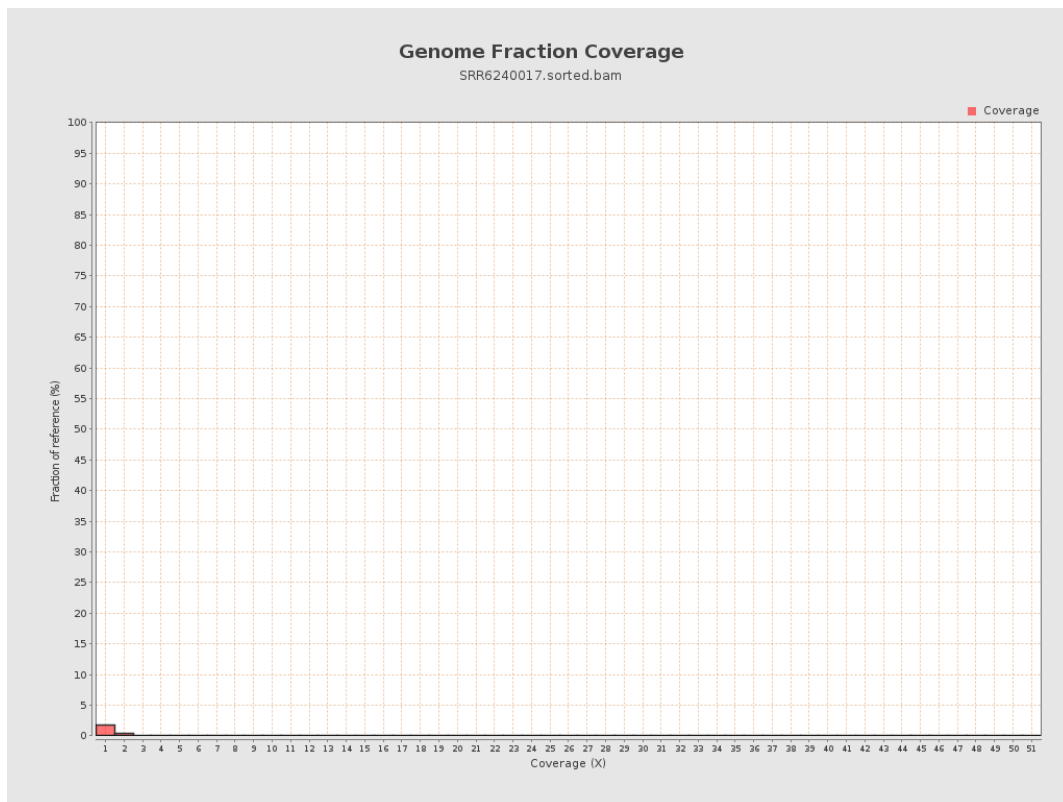
4. Results : Coverage Histogram



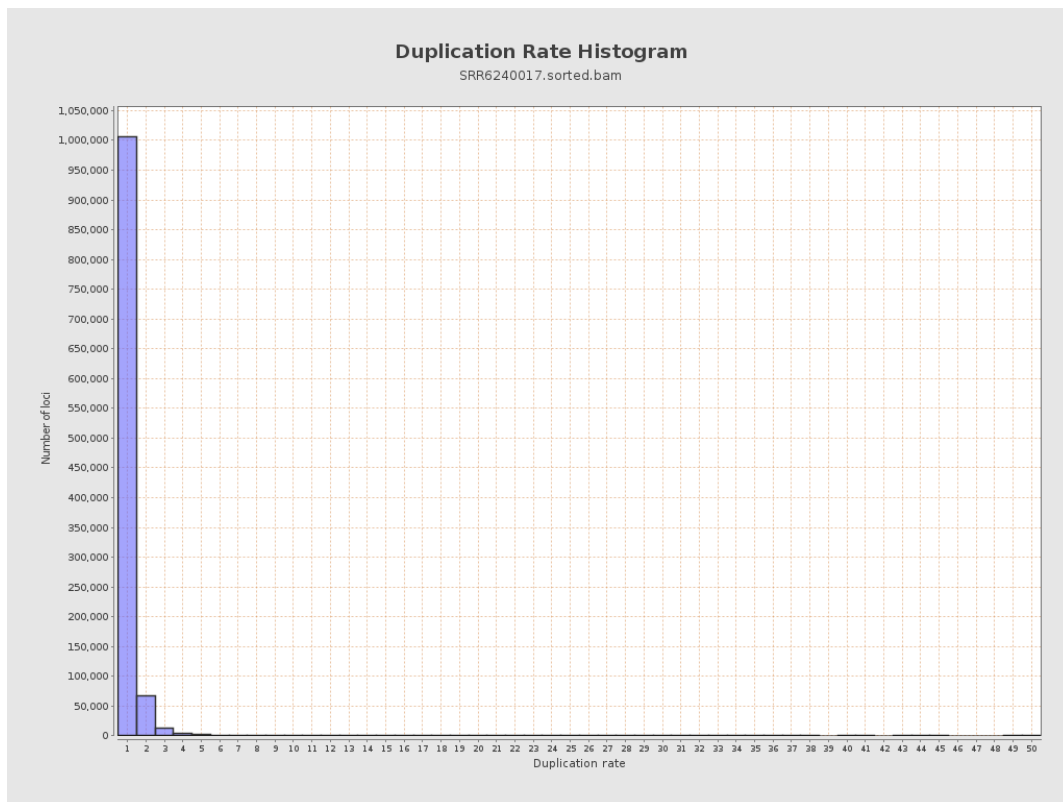
5. Results : Coverage Histogram (0-50X)



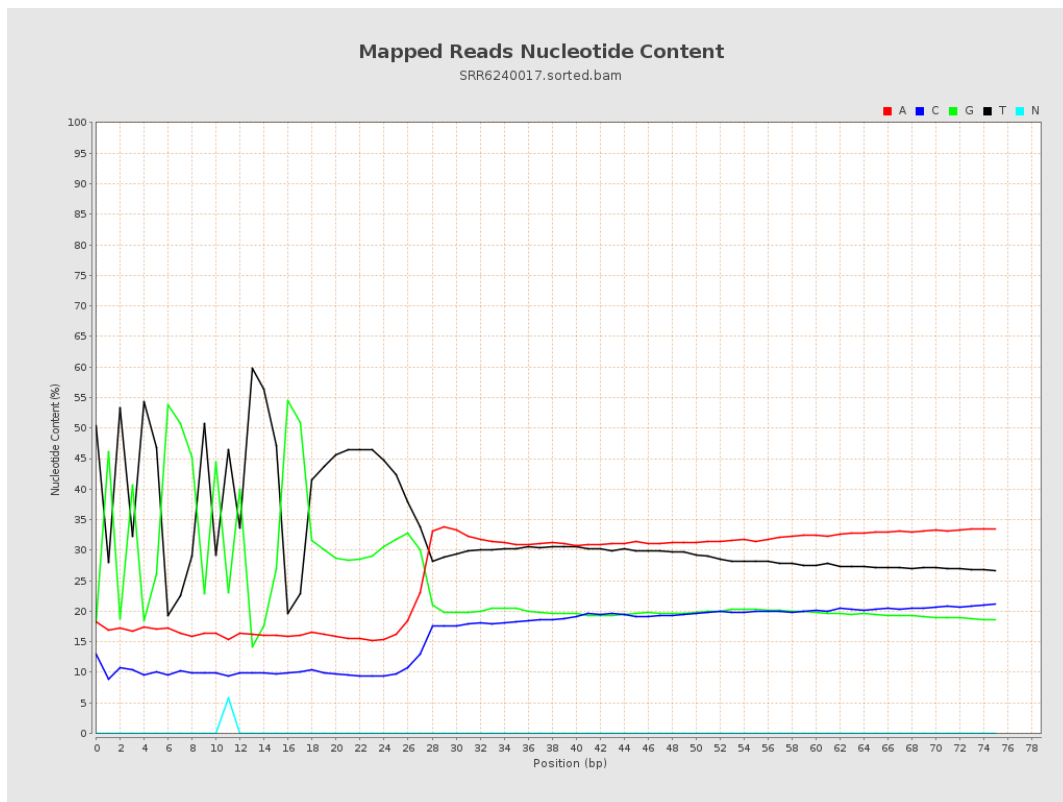
6. Results : Genome Fraction Coverage



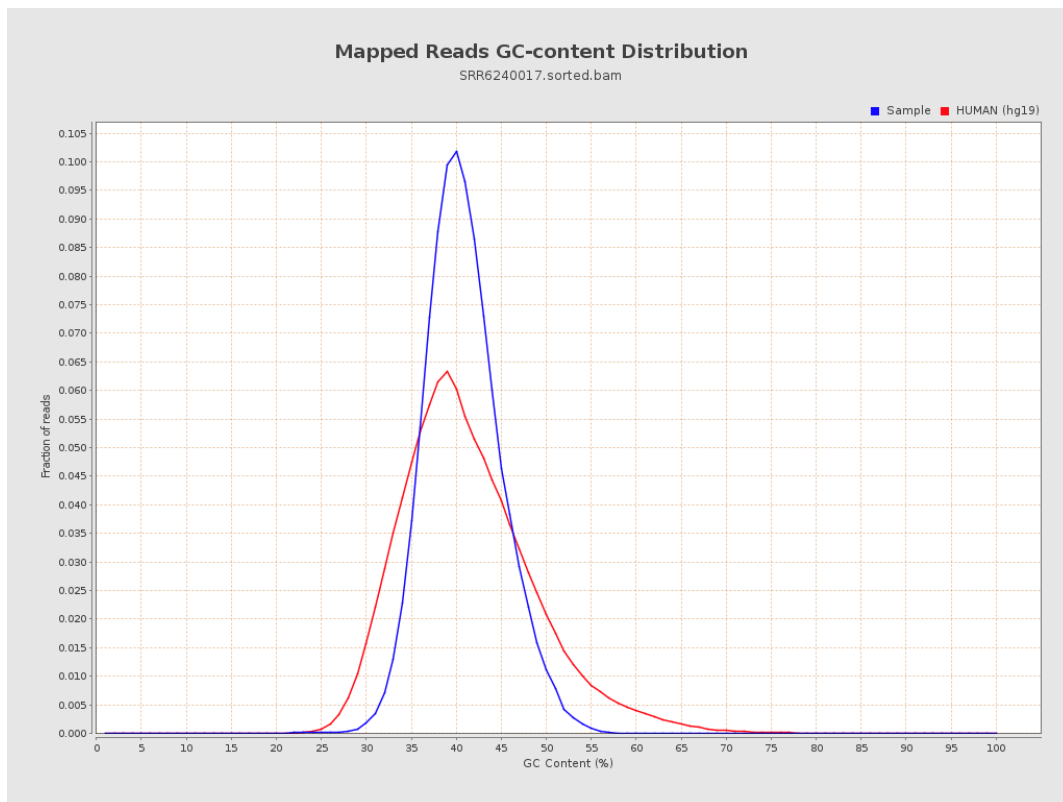
7. Results : Duplication Rate Histogram



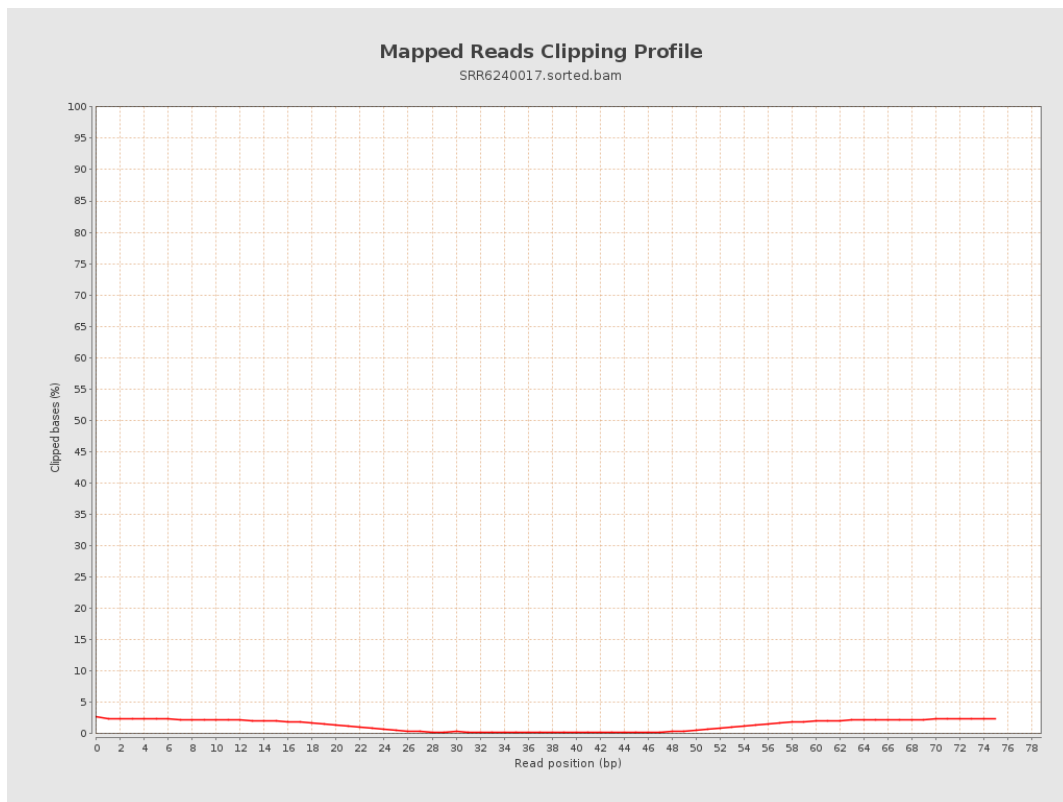
8. Results : Mapped Reads Nucleotide Content



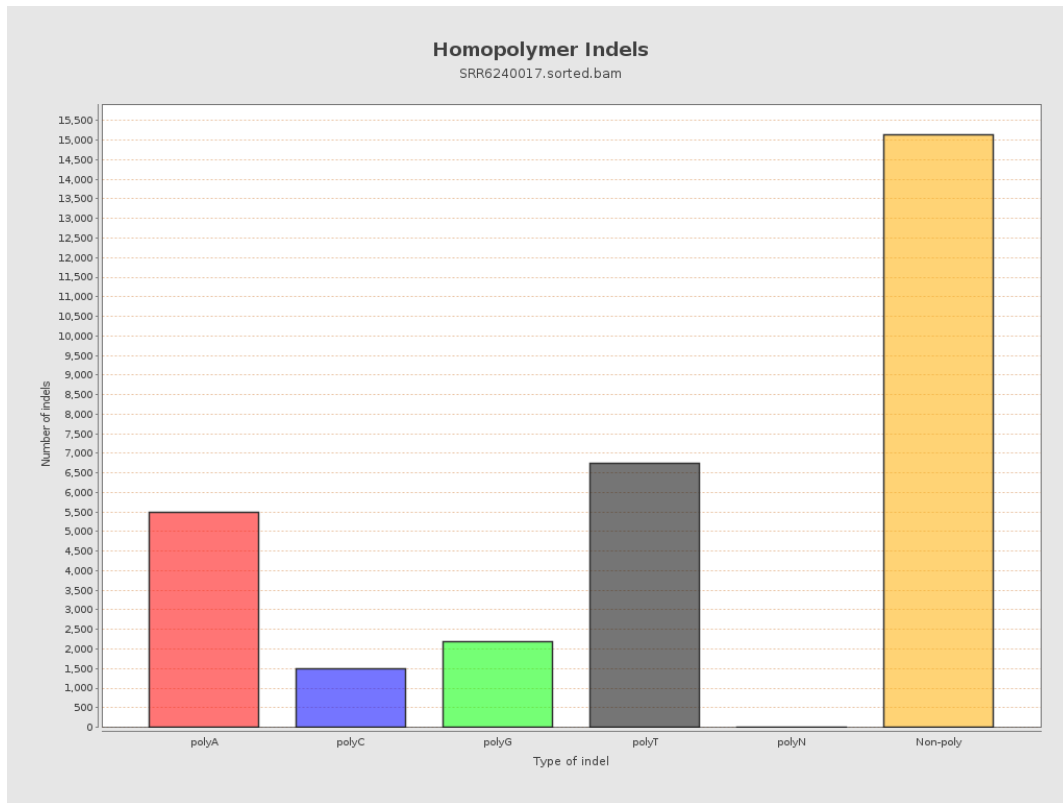
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

