

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 20:57:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004017.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_SRR6004017 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004017.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 20:57:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004017.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,961,974
Mapped reads	1,809,228 / 92.21%
Unmapped reads	152,746 / 7.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,126 / 0.57%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	58,372 / 2.98%
Duplication rate	2.61%
Clipped reads	731,642 / 37.29%

2.2. ACGT Content

Number/percentage of A's	34,892,067 / 28.43%
Number/percentage of C's	22,872,757 / 18.64%
Number/percentage of T's	38,490,782 / 31.36%
Number/percentage of G's	26,443,703 / 21.55%
Number/percentage of N's	21,538 / 0.02%
GC Percentage	40.19%

2.3. Coverage

Mean	0.0397

Standard Deviation	0.3025
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2.4. Mapping Quality

Mean Mapping Quality	46.26
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2.5. Mismatches and indels

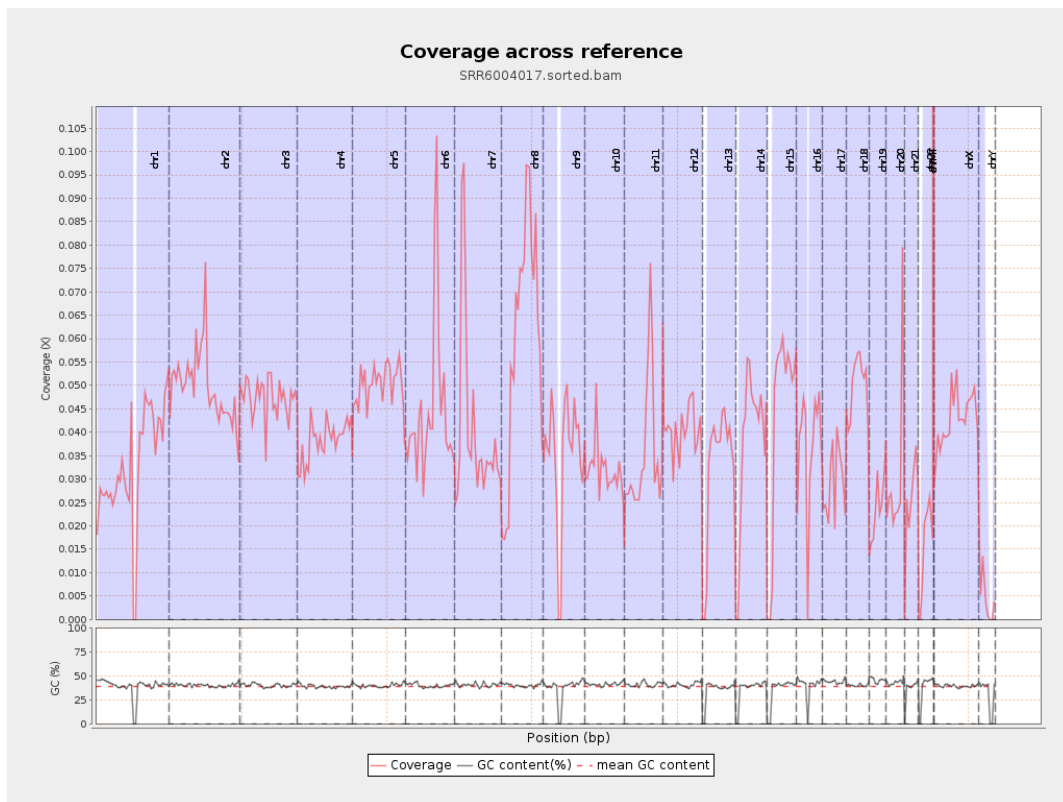
General error rate	0.86%
Mismatches	1,033,387
Insertions	8,798
Mapped reads with at least one insertion	0.48%
Deletions	29,398
Mapped reads with at least one deletion	1.61%
Homopolymer indels	47.08%

2.6. Chromosome stats

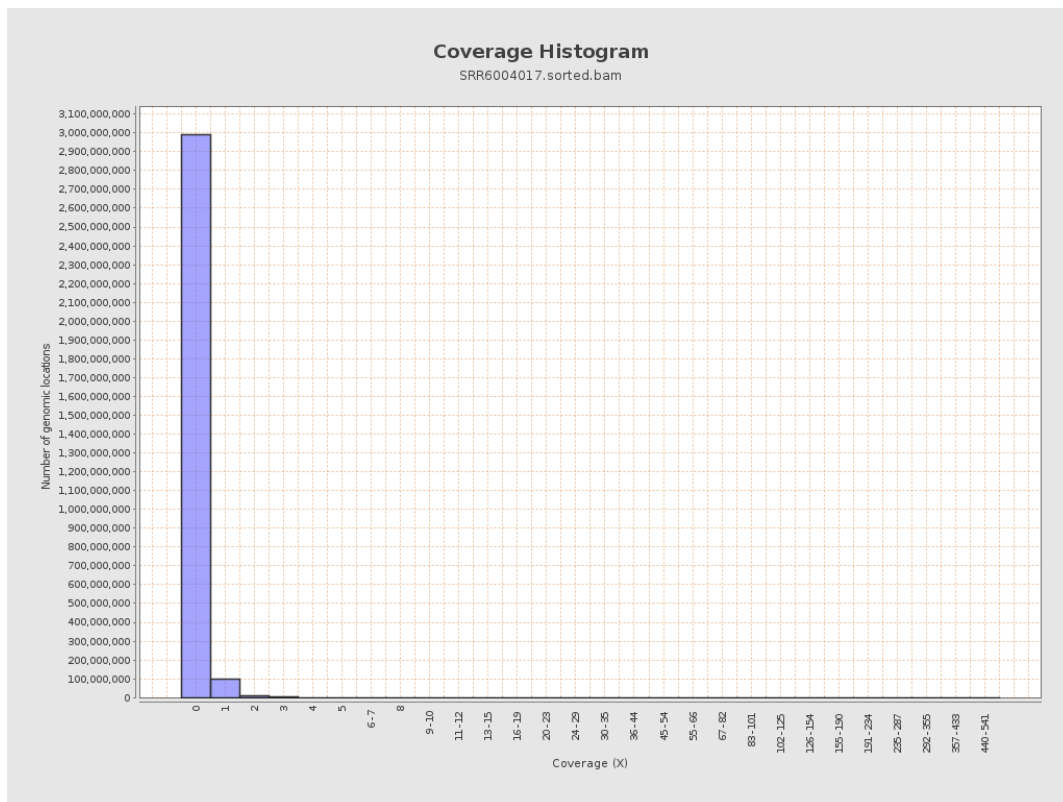
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8230392	0.033	0.4724
chr2	243199373	12102304	0.0498	0.3656
chr3	198022430	9370608	0.0473	0.2406
chr4	191154276	7285615	0.0381	0.2328
chr5	180915260	9102269	0.0503	0.2506
chr6	171115067	7655971	0.0447	0.2504
chr7	159138663	6560291	0.0412	0.3605

chr8	146364022	8722014	0.0596	0.4281
chr9	141213431	4968609	0.0352	0.2875
chr10	135534747	4336148	0.032	0.2884
chr11	135006516	4813946	0.0357	0.2402
chr12	133851895	5409445	0.0404	0.2279
chr13	115169878	3681654	0.032	0.2056
chr14	107349540	4079226	0.038	0.2302
chr15	102531392	4450565	0.0434	0.235
chr16	90354753	3346363	0.037	0.2304
chr17	81195210	2376317	0.0293	0.1961
chr18	78077248	3915836	0.0502	0.4899
chr19	59128983	1423696	0.0241	0.3545
chr20	63025520	2015622	0.032	0.2054
chr21	48129895	1220025	0.0253	0.2017
chr22	51304566	791629	0.0154	0.1351
chrMT	16571	17689	1.0675	1.1937
chrX	155270560	6623634	0.0427	0.2416
chrY	59373566	272841	0.0046	0.11

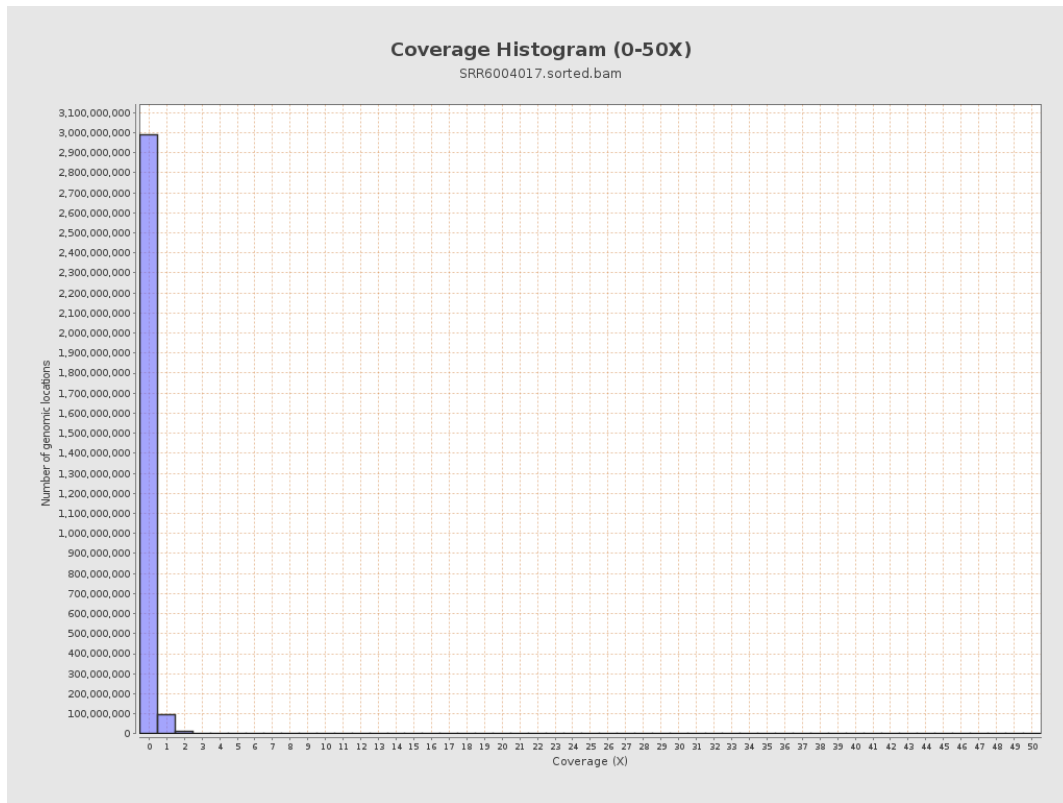
3. Results : Coverage across reference



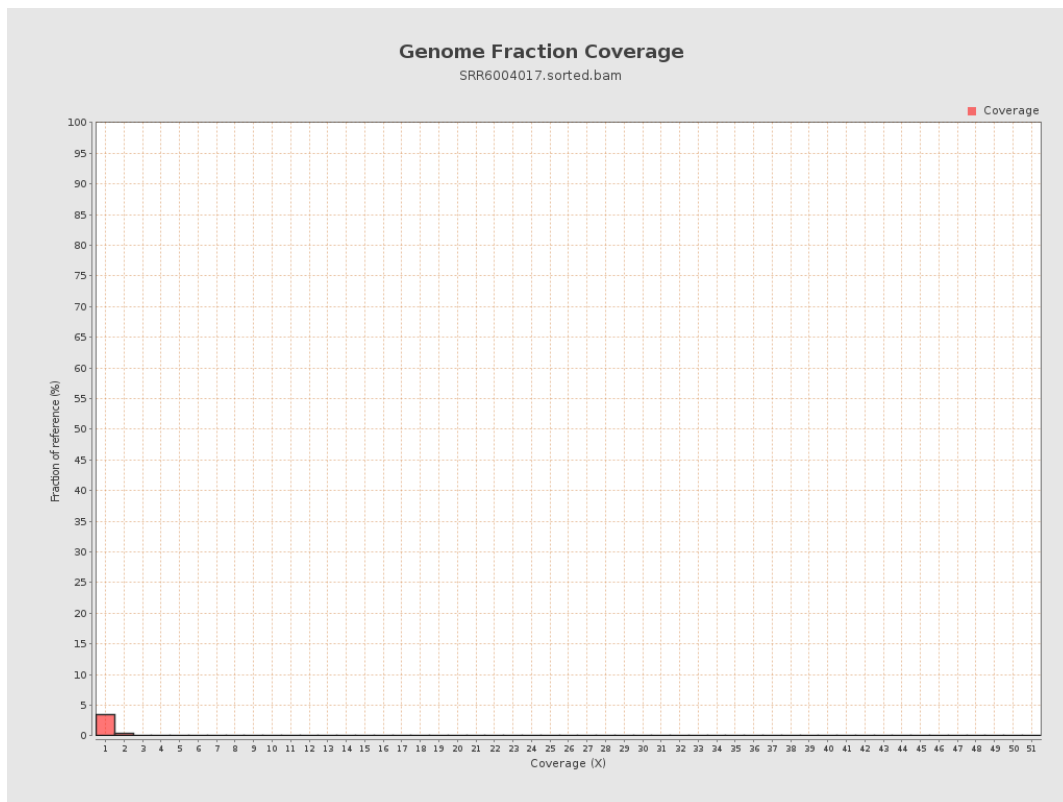
4. Results : Coverage Histogram



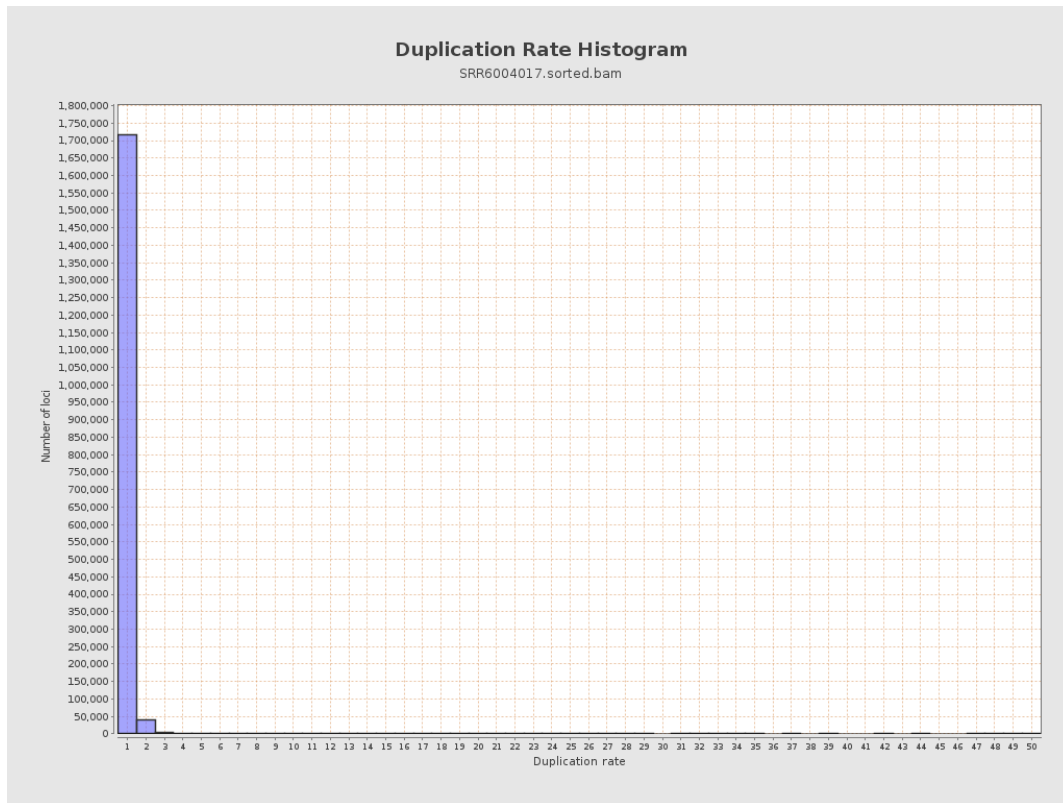
5. Results : Coverage Histogram (0-50X)



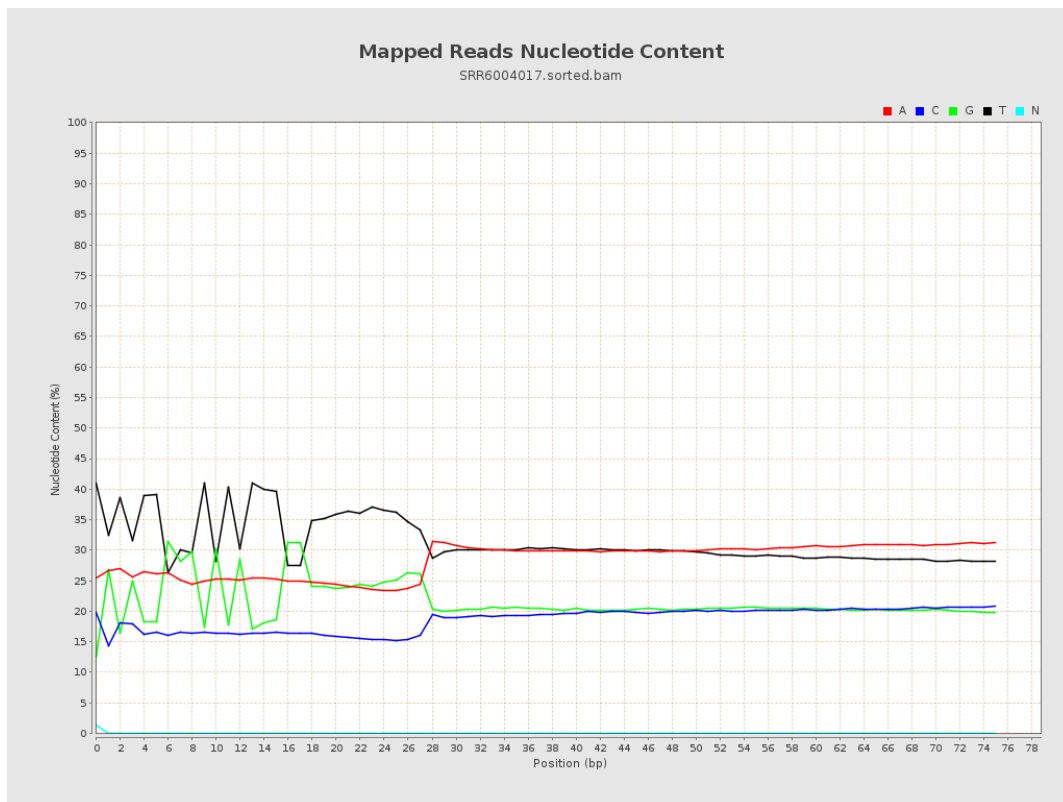
6. Results : Genome Fraction Coverage



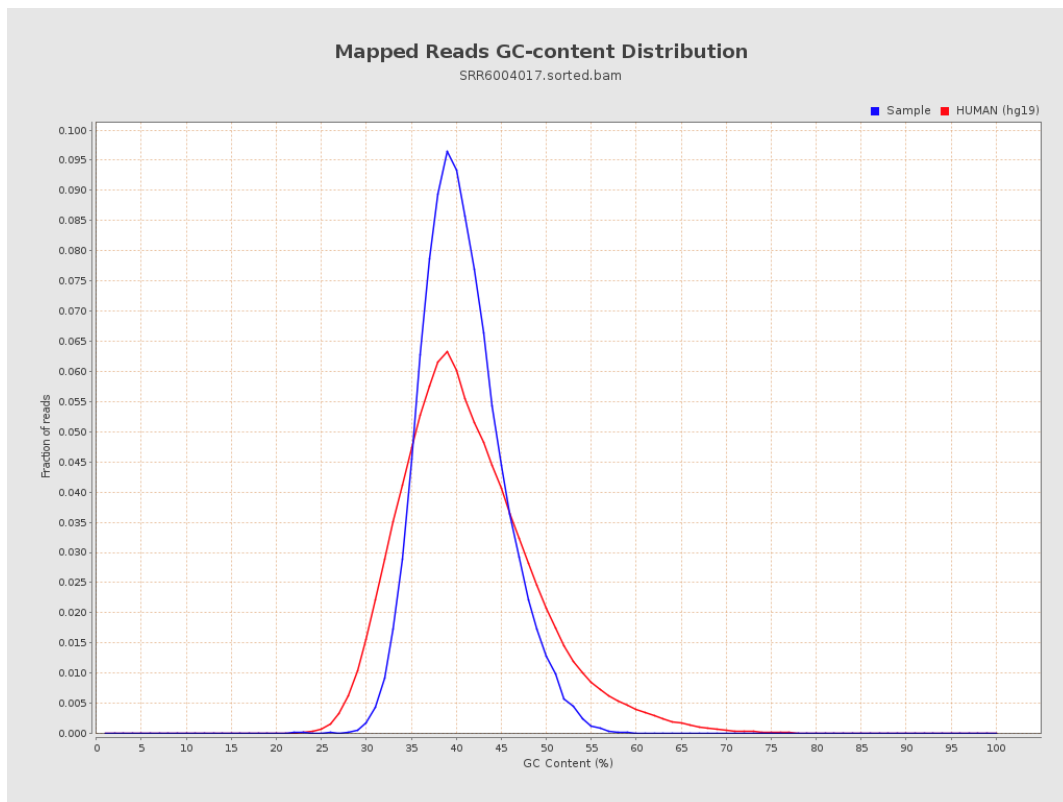
7. Results : Duplication Rate Histogram



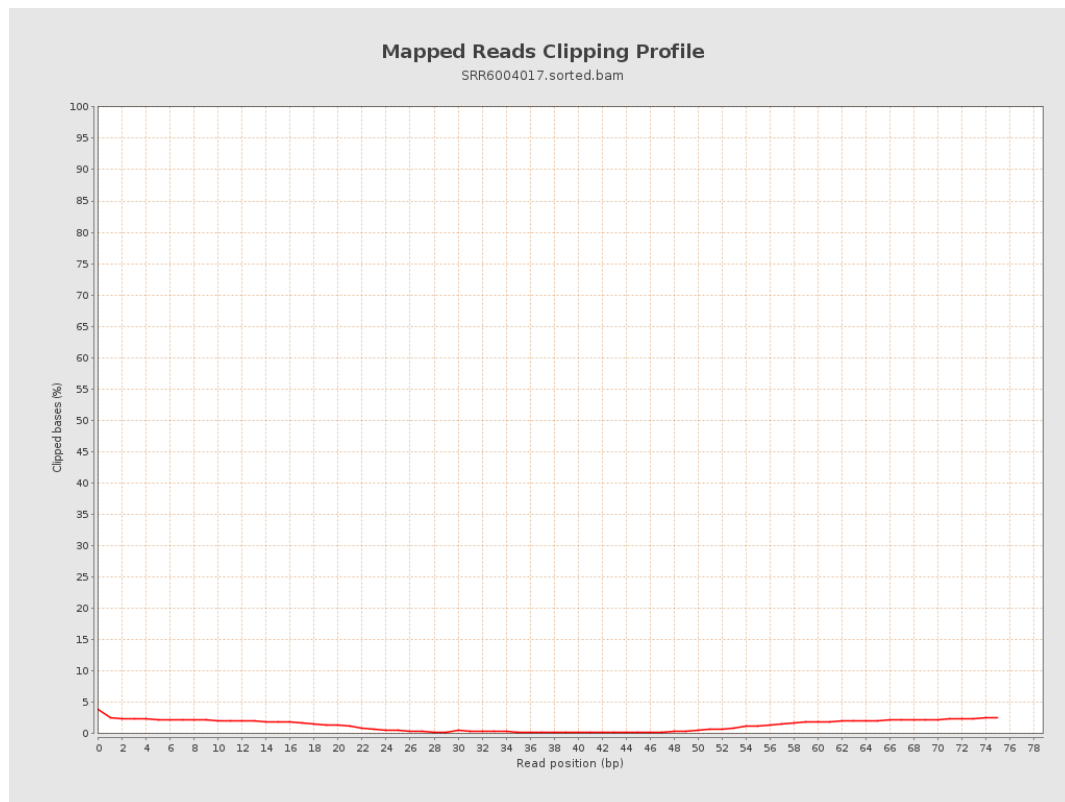
8. Results : Mapped Reads Nucleotide Content



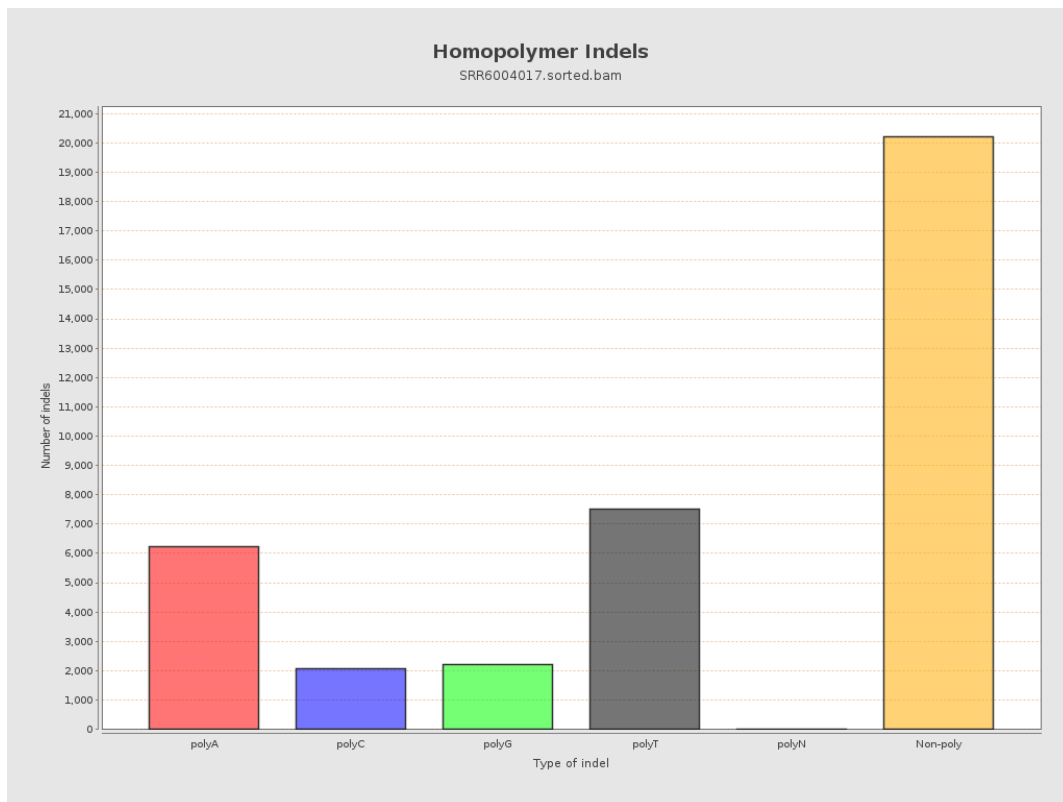
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

