

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 02:00:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717039.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_SRR9717039 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717039.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 02:00:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717039.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,350,440
Mapped reads	1,201,627 / 88.98%
Unmapped reads	148,813 / 11.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	32,764 / 2.43%
Read min/max/mean length	30 / 101 / 101.87
Duplicated reads (estimated)	26,140 / 1.94%
Duplication rate	1.48%
Clipped reads	1,232,624 / 91.28%

2.2. ACGT Content

Number/percentage of A's	23,392,332 / 26.54%
Number/percentage of C's	18,031,320 / 20.45%
Number/percentage of T's	26,346,204 / 29.89%
Number/percentage of G's	20,372,827 / 23.11%
Number/percentage of N's	10,132 / 0.01%
GC Percentage	43.57%

2.3. Coverage

Mean	0.0285

Standard Deviation	0.2376
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2.4. Mapping Quality

Mean Mapping Quality	45.04
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2.5. Mismatches and indels

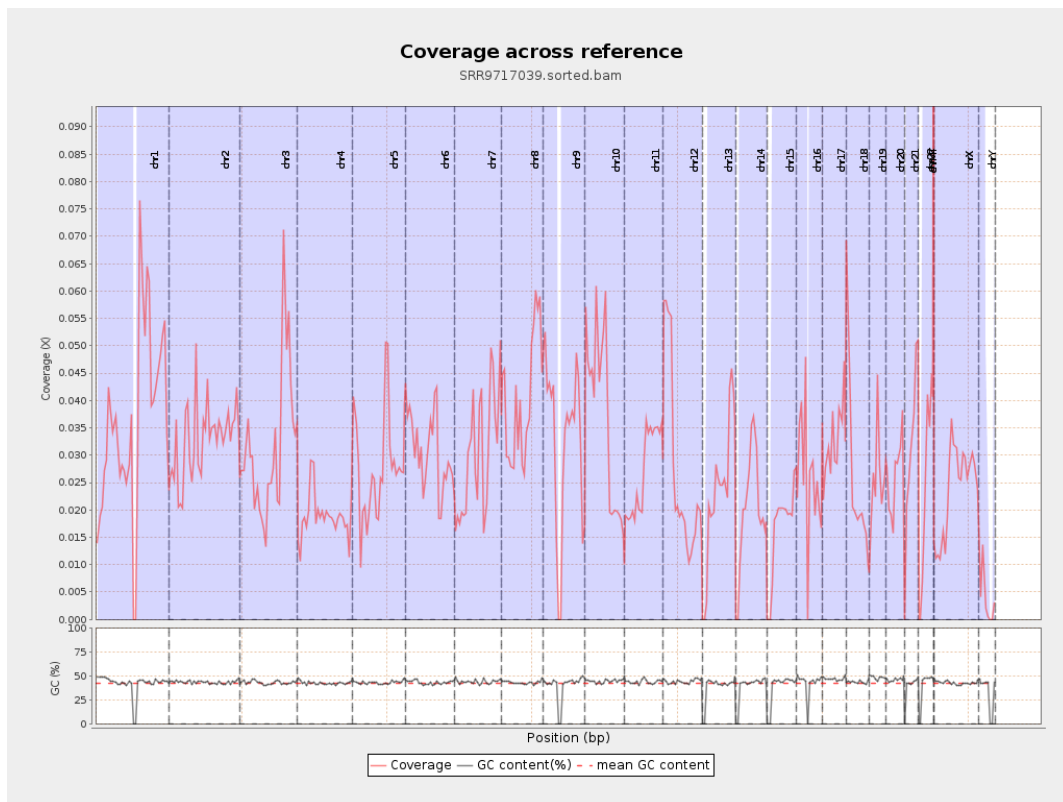
General error rate	0.74%
Mismatches	634,774
Insertions	7,919
Mapped reads with at least one insertion	0.65%
Deletions	17,876
Mapped reads with at least one deletion	1.47%
Homopolymer indels	38.17%

2.6. Chromosome stats

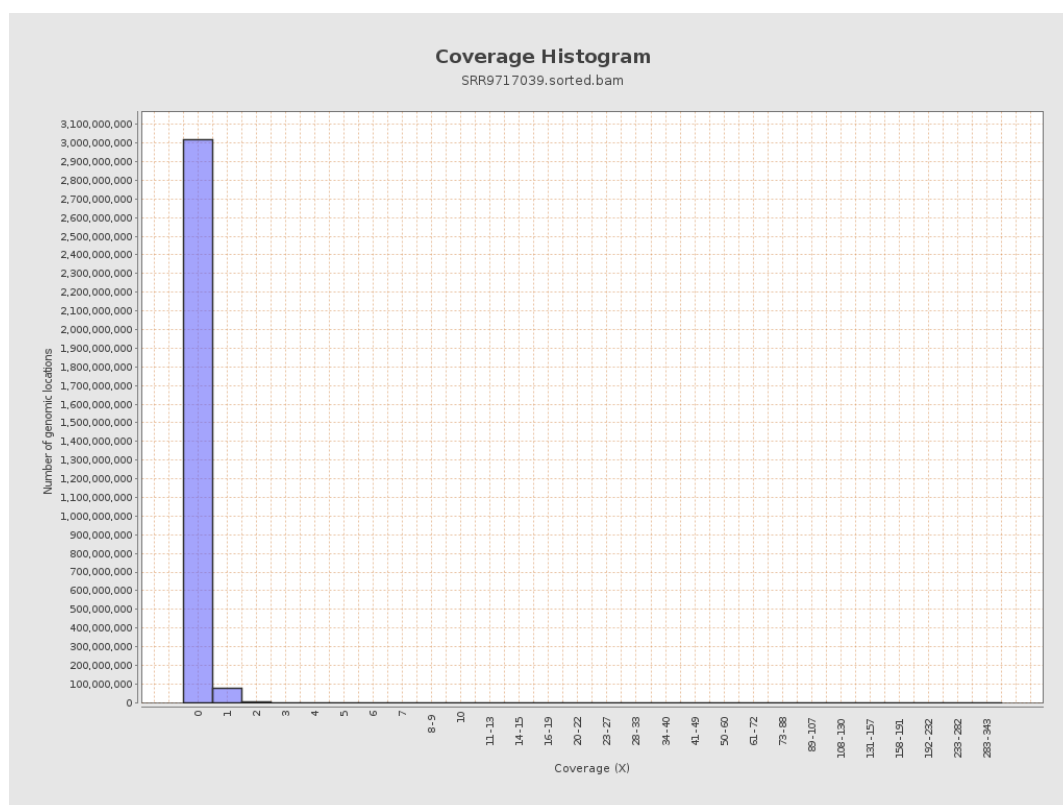
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9055887	0.0363	0.3346
chr2	243199373	8002254	0.0329	0.3301
chr3	198022430	6216709	0.0314	0.1911
chr4	191154276	3565481	0.0187	0.1601
chr5	180915260	4965189	0.0274	0.1778
chr6	171115067	5275648	0.0308	0.1983
chr7	159138663	4846442	0.0305	0.3061

chr8	146364022	5927050	0.0405	0.2924
chr9	141213431	4560404	0.0323	0.2333
chr10	135534747	5098954	0.0376	0.2962
chr11	135006516	3647681	0.027	0.2196
chr12	133851895	3560348	0.0266	0.1764
chr13	115169878	2728655	0.0237	0.1645
chr14	107349540	2164711	0.0202	0.165
chr15	102531392	1703817	0.0166	0.1428
chr16	90354753	2329028	0.0258	0.1884
chr17	81195210	2644188	0.0326	0.2071
chr18	78077248	2024401	0.0259	0.3063
chr19	59128983	1541932	0.0261	0.2723
chr20	63025520	1631702	0.0259	0.1776
chr21	48129895	1528983	0.0318	0.1996
chr22	51304566	1218416	0.0237	0.1666
chrMT	16571	3130	0.1889	0.5586
chrX	155270560	3702214	0.0238	0.1823
chrY	59373566	240414	0.004	0.1226

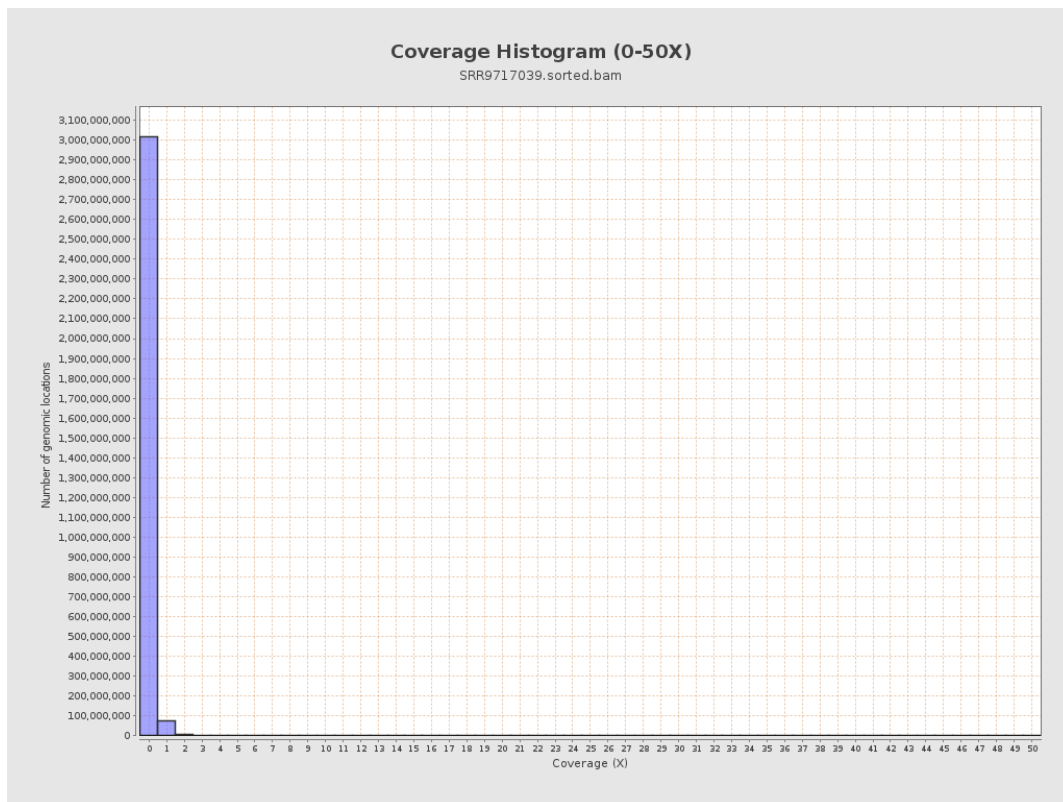
3. Results : Coverage across reference



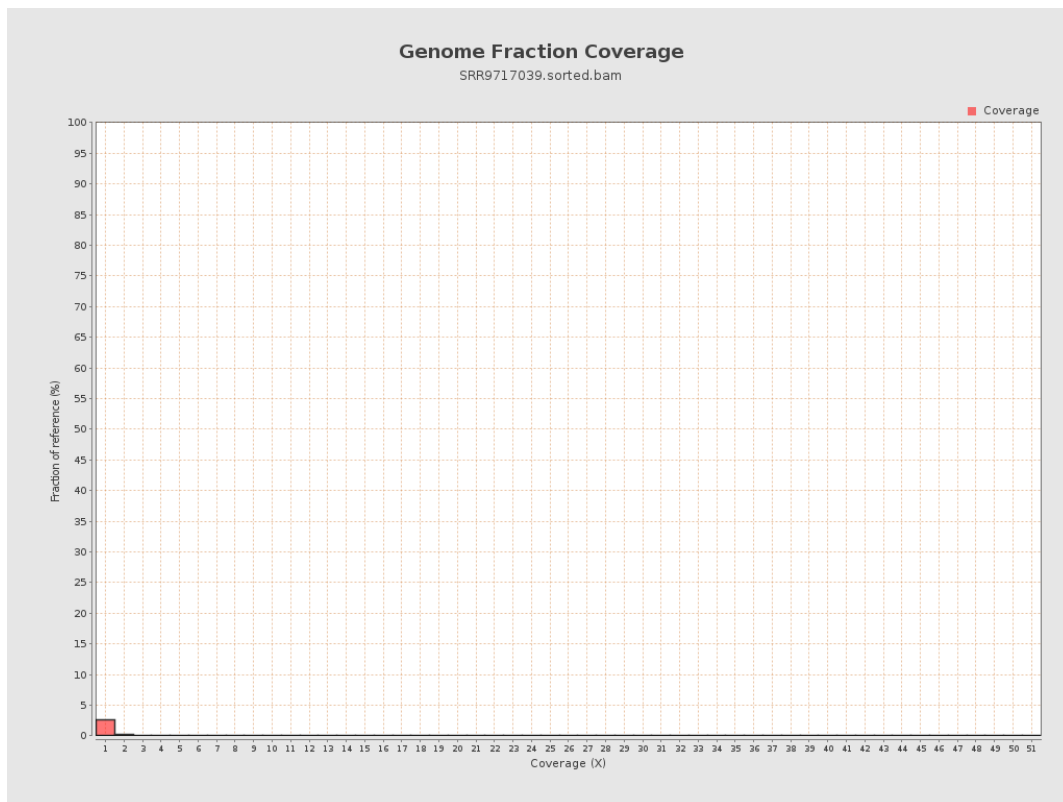
4. Results : Coverage Histogram



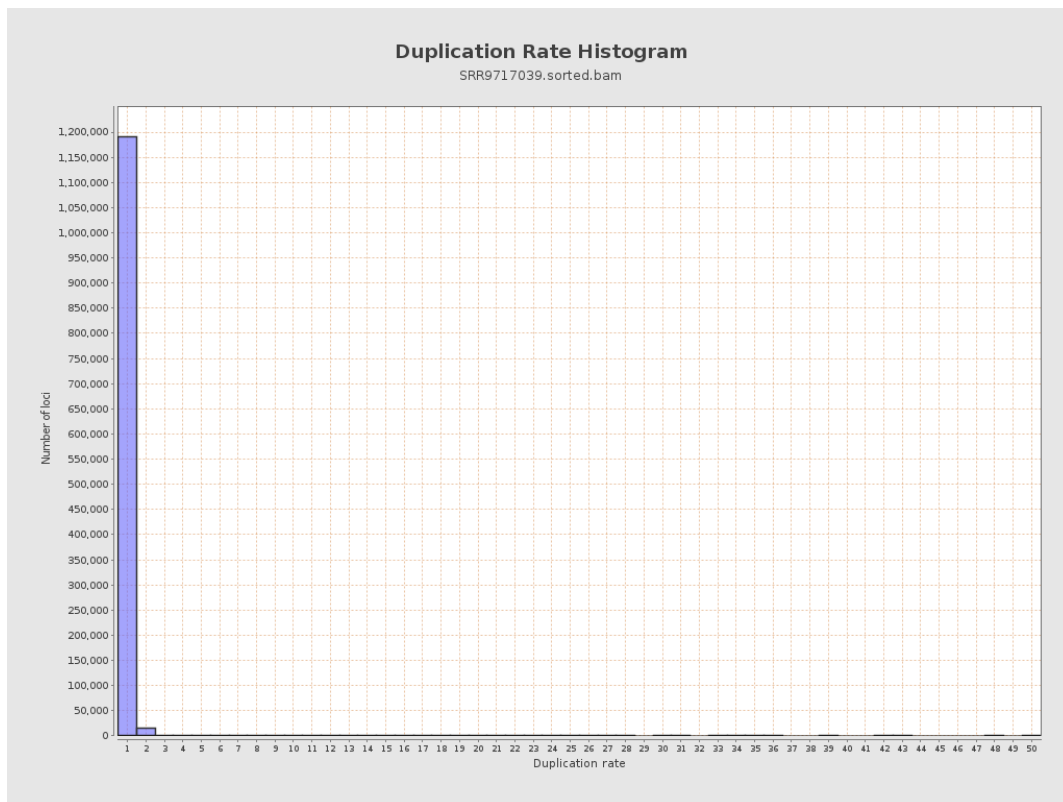
5. Results : Coverage Histogram (0-50X)



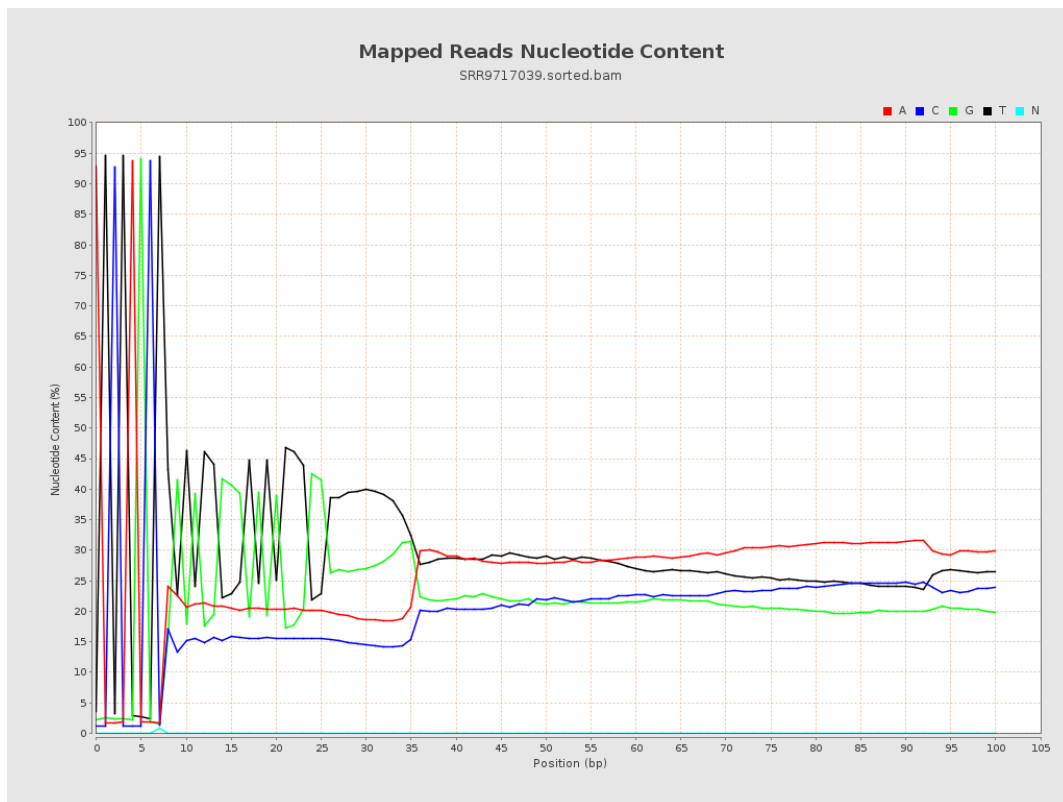
6. Results : Genome Fraction Coverage



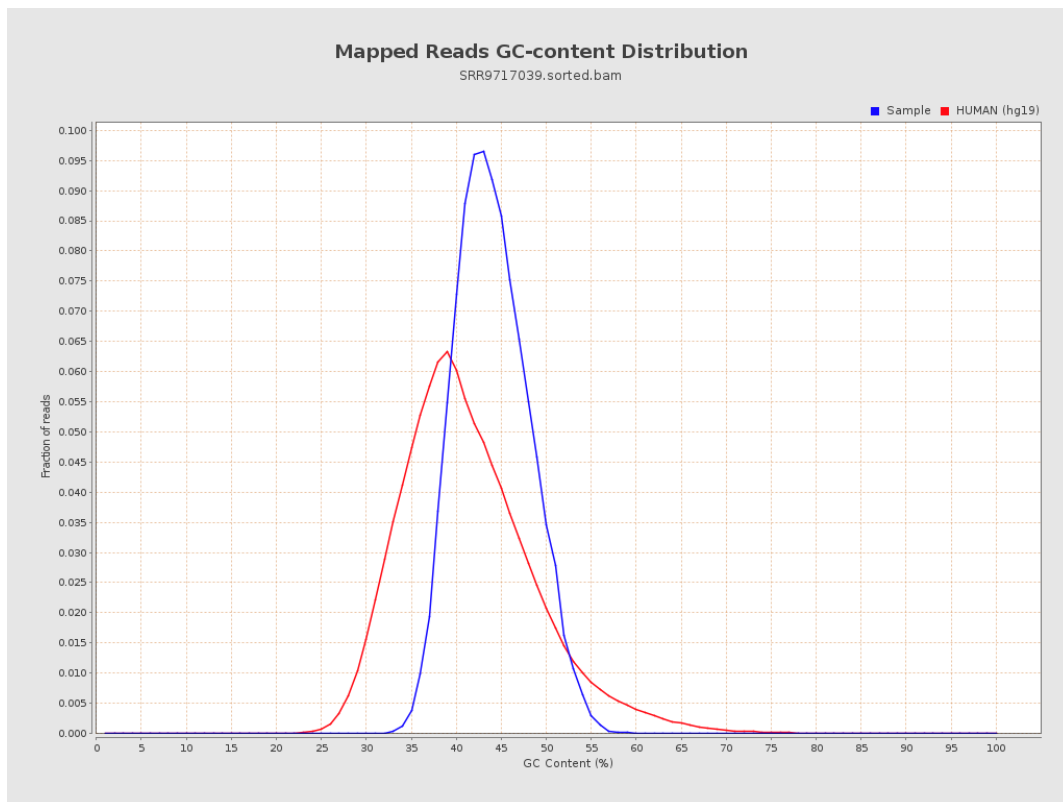
7. Results : Duplication Rate Histogram



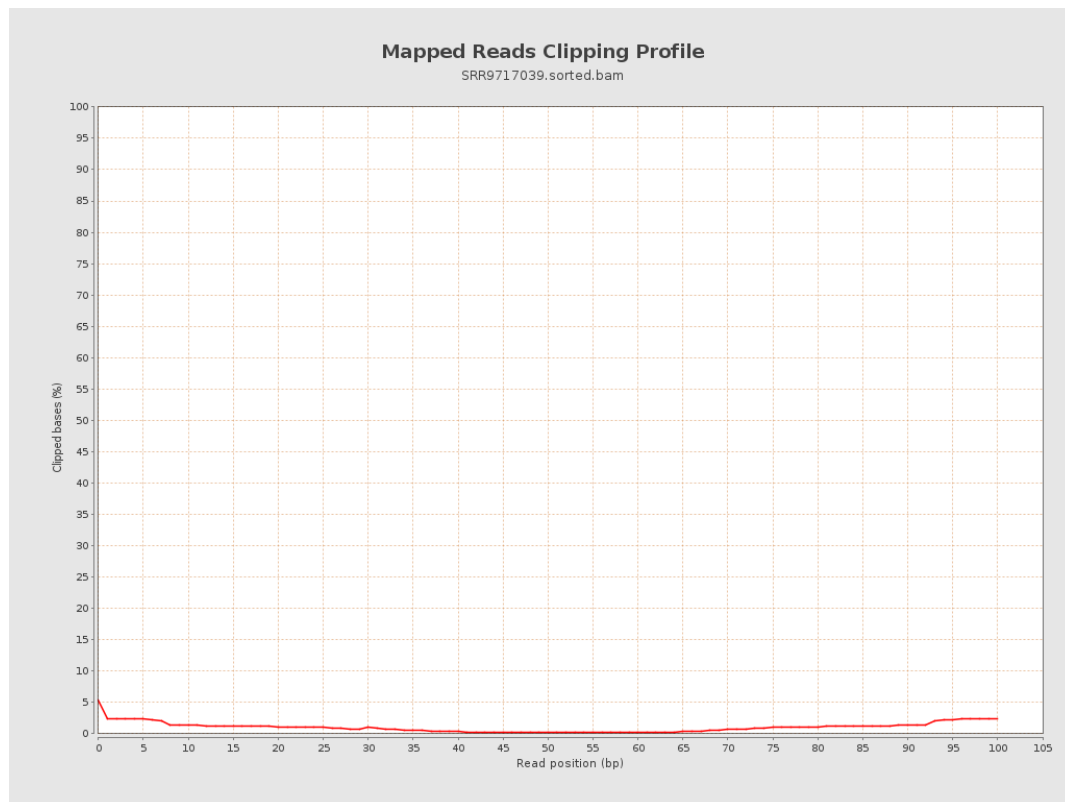
8. Results : Mapped Reads Nucleotide Content



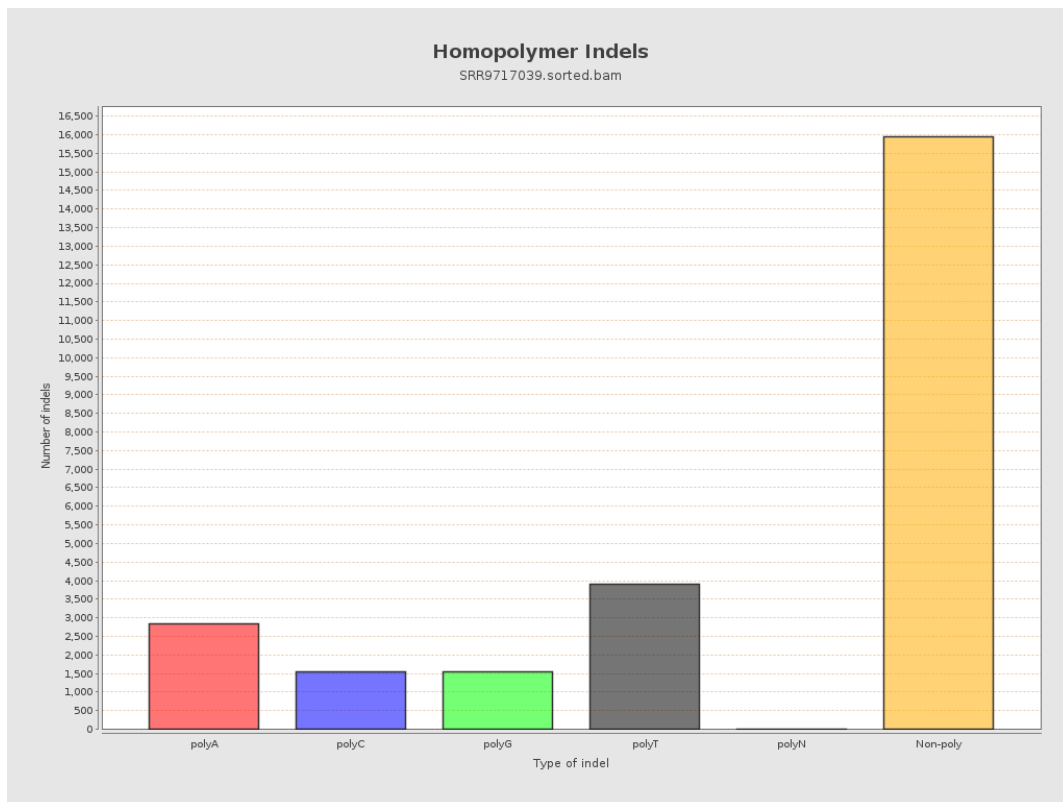
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

