

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/06/25 06:07:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504717.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_SRR504717 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504717.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jun 25 06:07:53 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504717.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,051,590
Mapped reads	1,834,675 / 89.43%
Unmapped reads	216,915 / 10.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	32 / 32 / 32
Duplicated reads (estimated)	414,231 / 20.19%
Duplication rate	14.48%
Clipped reads	2,924 / 0.14%

2.2. ACGT Content

Number/percentage of A's	16,925,823 / 28.83%
Number/percentage of C's	11,529,366 / 19.64%
Number/percentage of T's	18,692,238 / 31.84%
Number/percentage of G's	11,556,223 / 19.69%
Number/percentage of N's	102 / 0%
GC Percentage	39.33%

2.3. Coverage

Mean	0.019
Standard Deviation	0.7312

2.4. Mapping Quality

Mean Mapping Quality	6.65
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2.5. Mismatches and indels

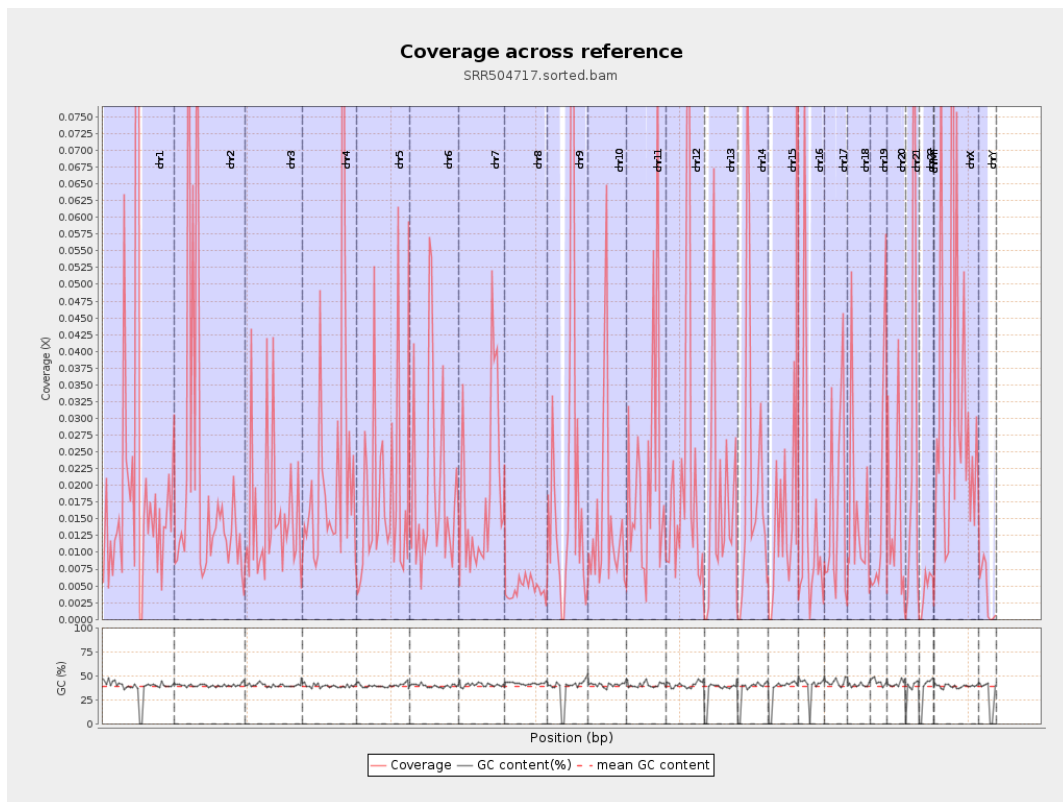
General error rate	0.06%
Mismatches	33,027

2.6. Chromosome stats

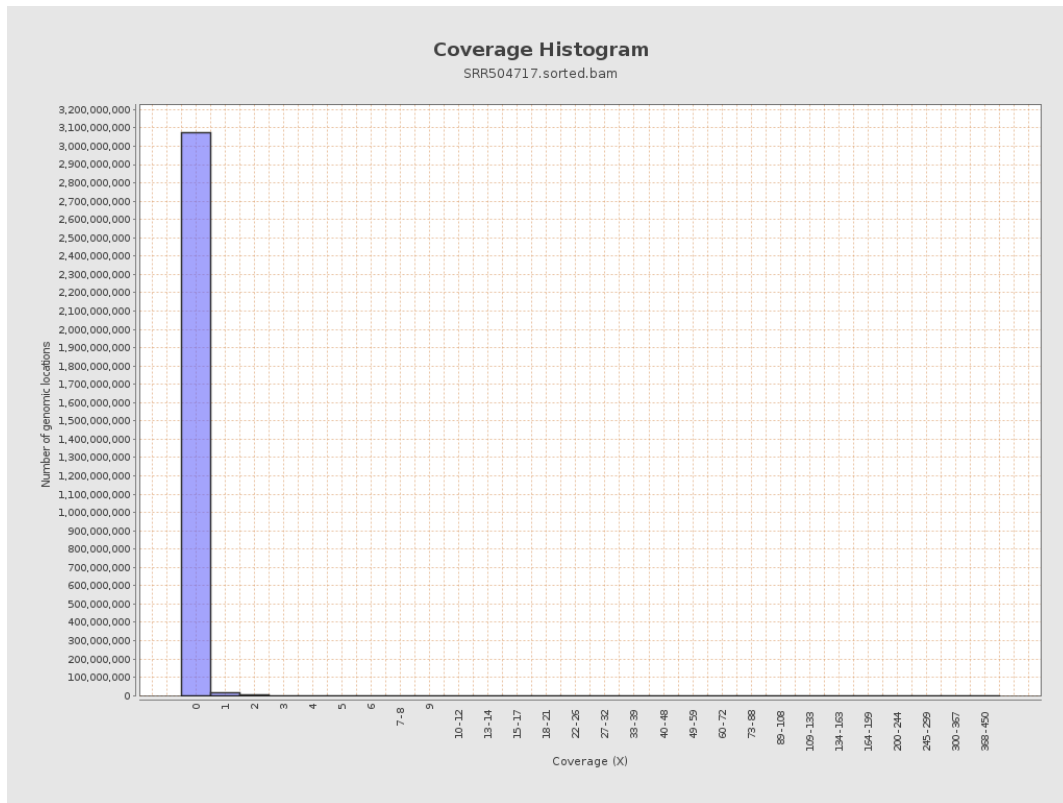
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5485822	0.022	1.1431
chr2	243199373	5039320	0.0207	0.7852
chr3	198022430	3085356	0.0156	0.3206
chr4	191154276	4368954	0.0229	0.7978
chr5	180915260	3345160	0.0185	0.5226
chr6	171115067	3357914	0.0196	0.4127
chr7	159138663	2875170	0.0181	0.4112
chr8	146364022	670384	0.0046	0.1186
chr9	141213431	3040992	0.0215	1.08
chr10	135534747	1907260	0.0141	0.4945
chr11	135006516	2961494	0.0219	0.6024
chr12	133851895	2989078	0.0223	0.8513
chr13	115169878	1952428	0.017	0.3909
chr14	107349540	2237282	0.0208	0.8324
chr15	102531392	2566424	0.025	1.3324

chr16	90354753	1208396	0.0134	0.7281
chr17	81195210	1394742	0.0172	0.4373
chr18	78077248	1198318	0.0153	0.4321
chr19	59128983	973656	0.0165	0.6369
chr20	63025520	968958	0.0154	0.3679
chr21	48129895	1262198	0.0262	1.3202
chr22	51304566	224162	0.0044	0.0928
chrMT	16571	32	0.0019	0.0439
chrX	155270560	5353236	0.0345	0.8649
chrY	59373566	237016	0.004	0.1366

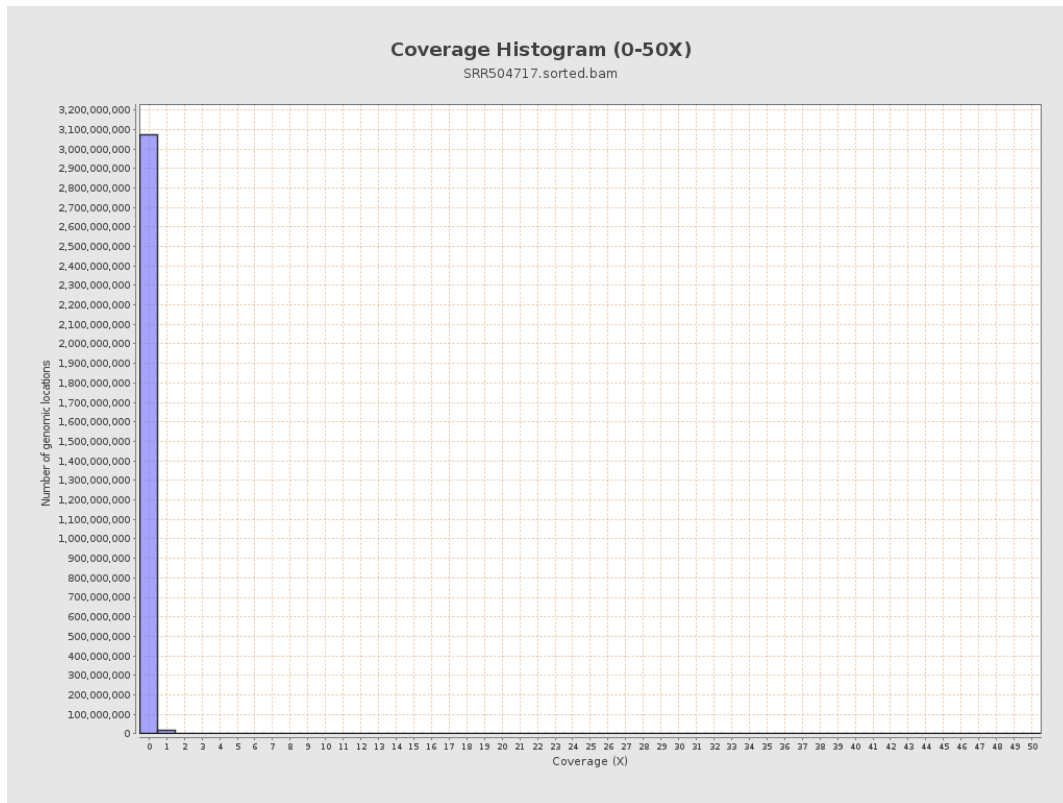
3. Results : Coverage across reference



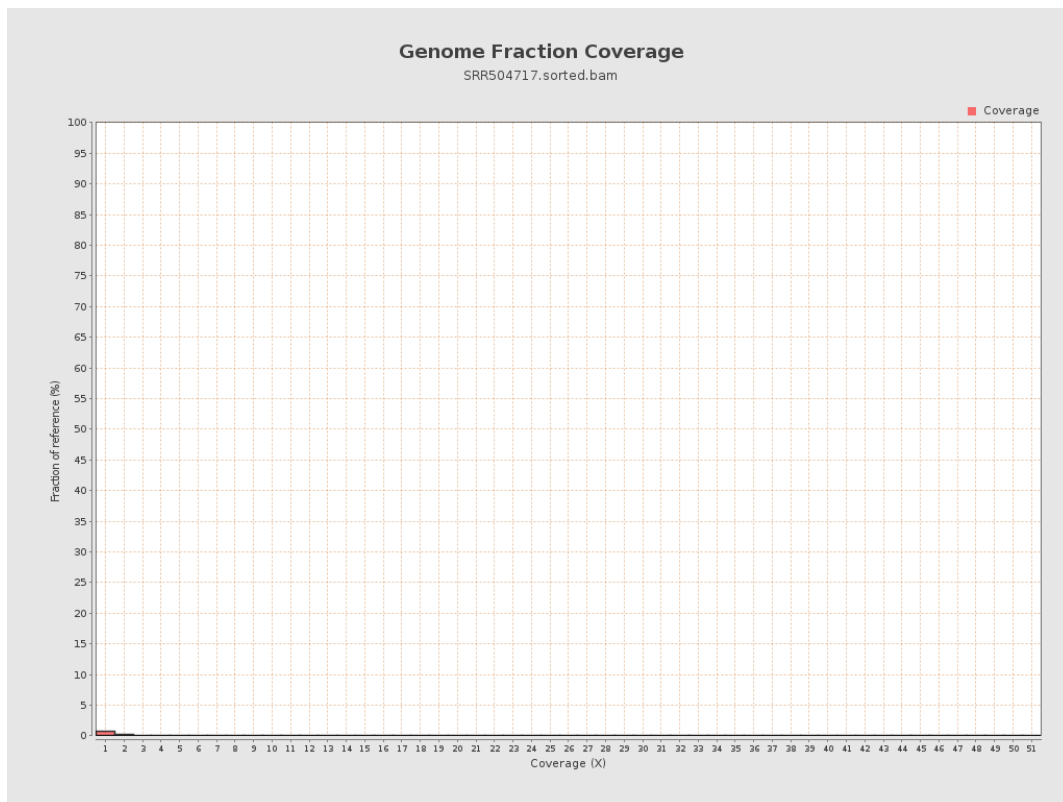
4. Results : Coverage Histogram



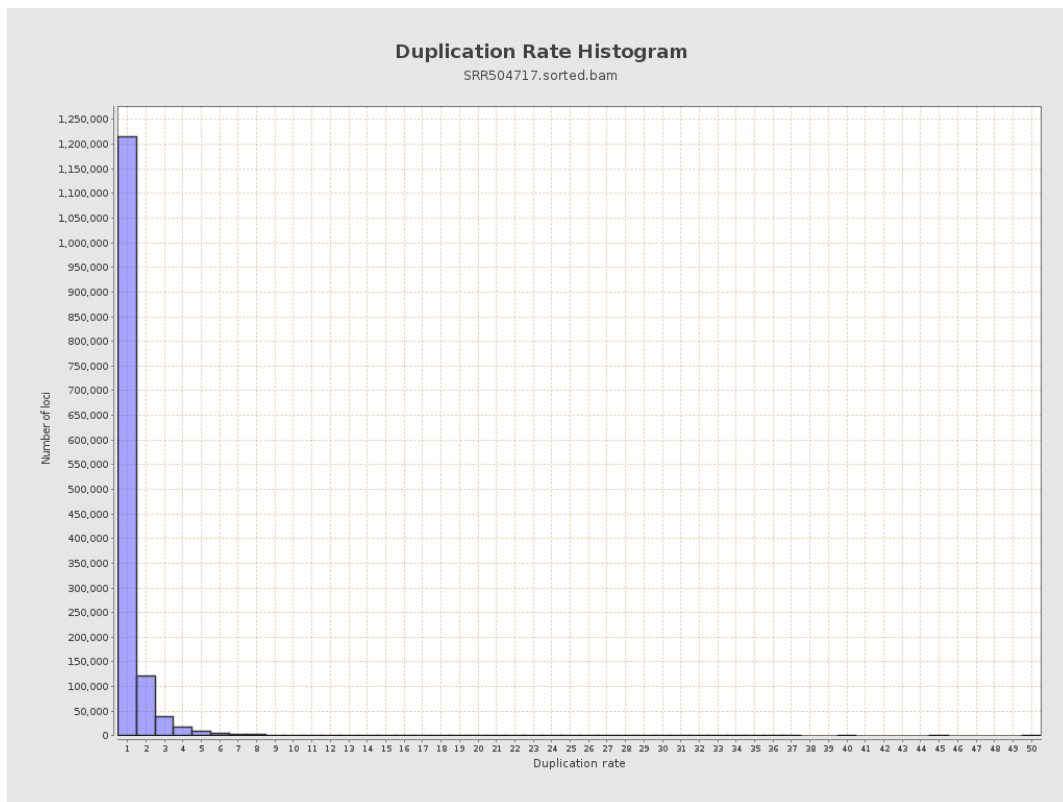
5. Results : Coverage Histogram (0-50X)



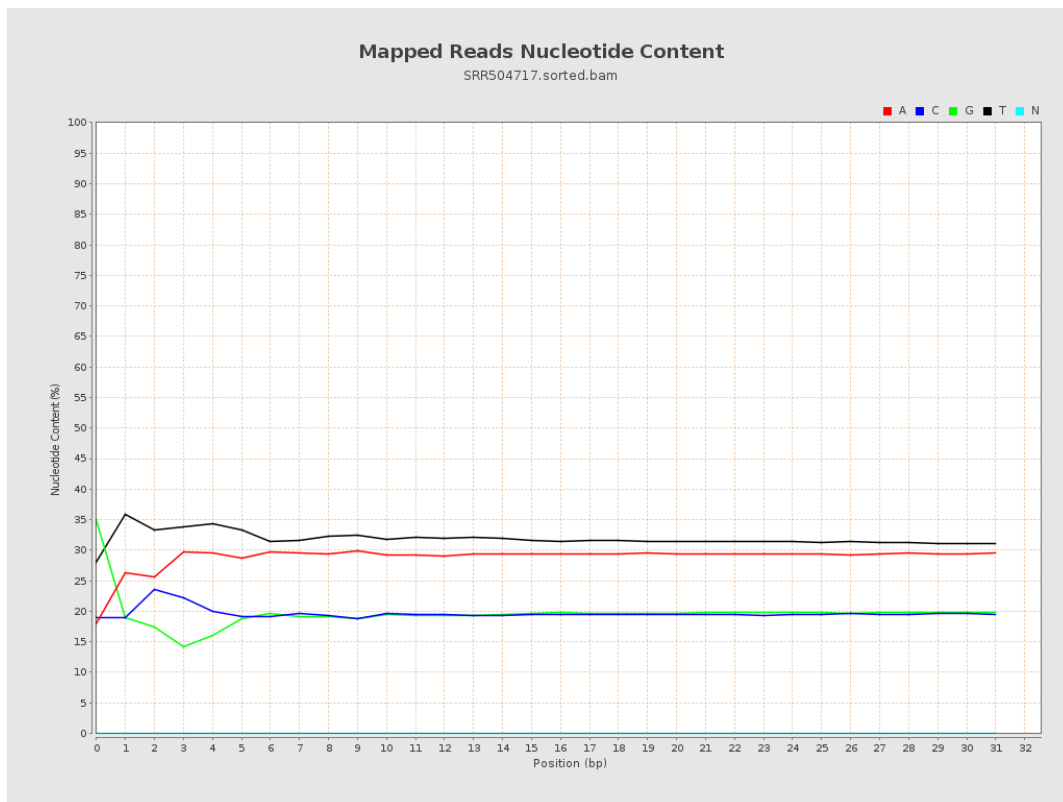
6. Results : Genome Fraction Coverage



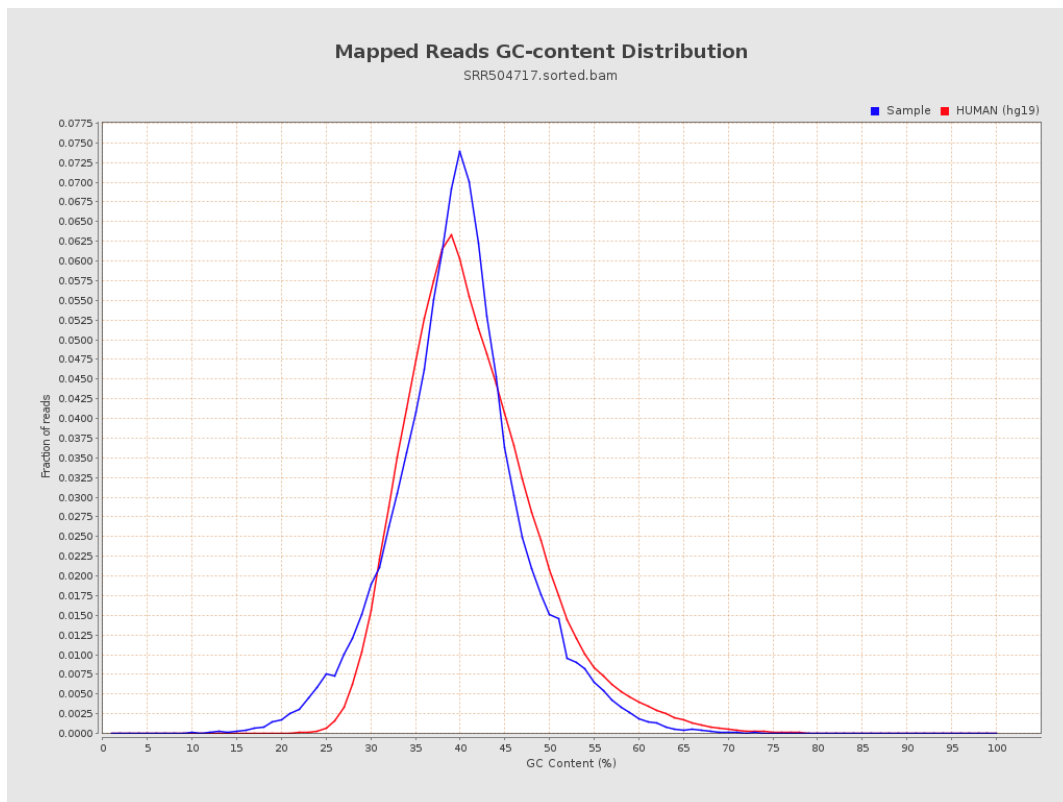
7. Results : Duplication Rate Histogram



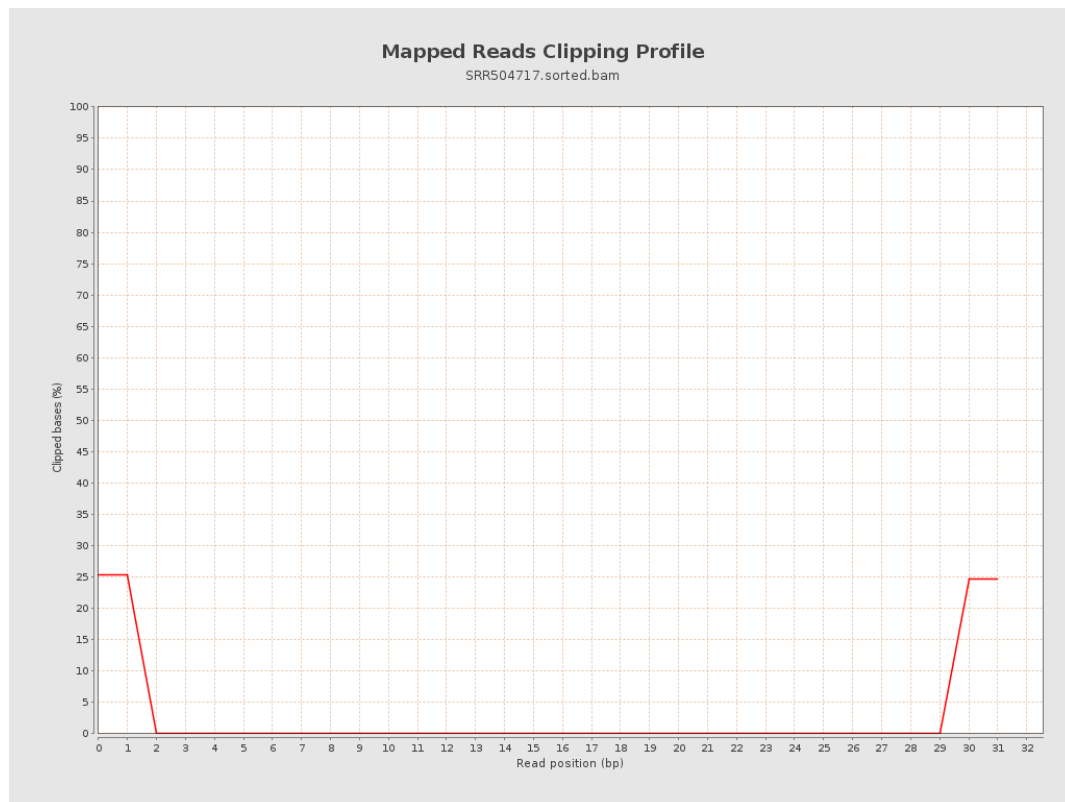
8. Results : Mapped Reads Nucleotide Content



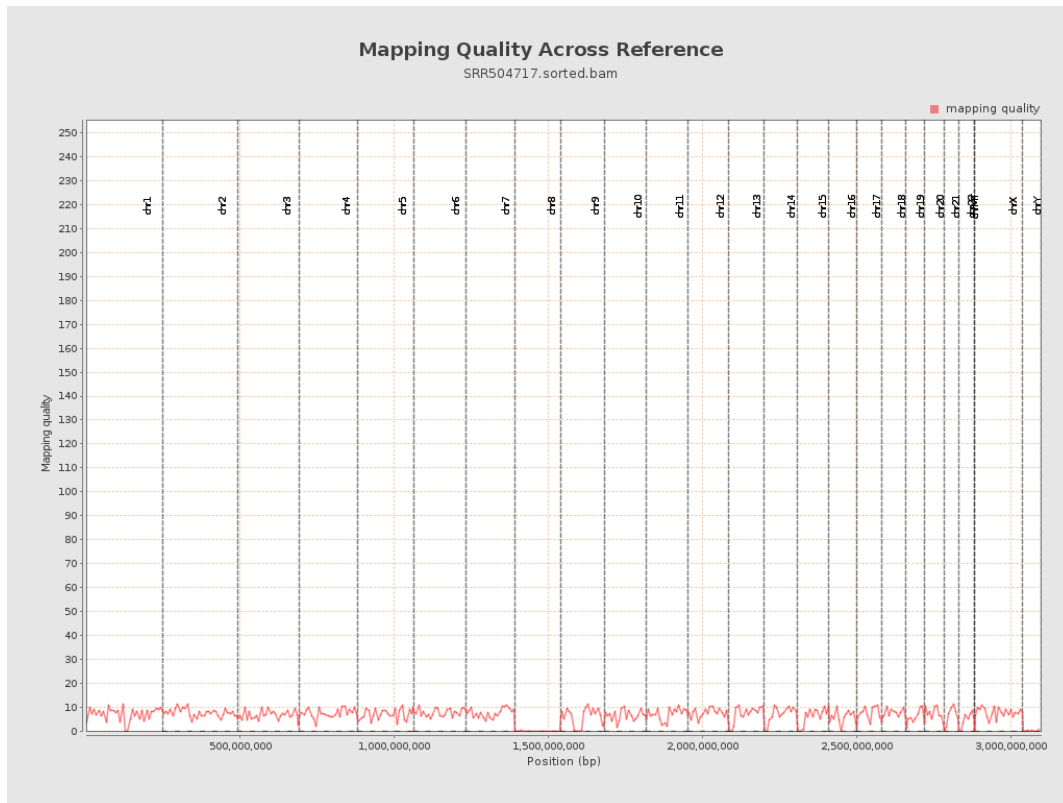
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Mapping Quality Across Reference



12. Results : Mapping Quality Histogram

