

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/06/25 05:56:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504711.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_SRR504711 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504711.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jun 25 05:56:21 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504711.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,370,955
Mapped reads	2,139,336 / 90.23%
Unmapped reads	231,619 / 9.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	32 / 32 / 32
Duplicated reads (estimated)	232,384 / 9.8%
Duplication rate	7.32%
Clipped reads	3,266 / 0.14%

2.2. ACGT Content

Number/percentage of A's	19,919,275 / 29.1%
Number/percentage of C's	13,582,991 / 19.84%
Number/percentage of T's	21,226,983 / 31.01%
Number/percentage of G's	13,722,851 / 20.05%
Number/percentage of N's	120 / 0%
GC Percentage	39.89%

2.3. Coverage

Mean	0.0221
Standard Deviation	0.7334

2.4. Mapping Quality

Mean Mapping Quality	8.14
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2.5. Mismatches and indels

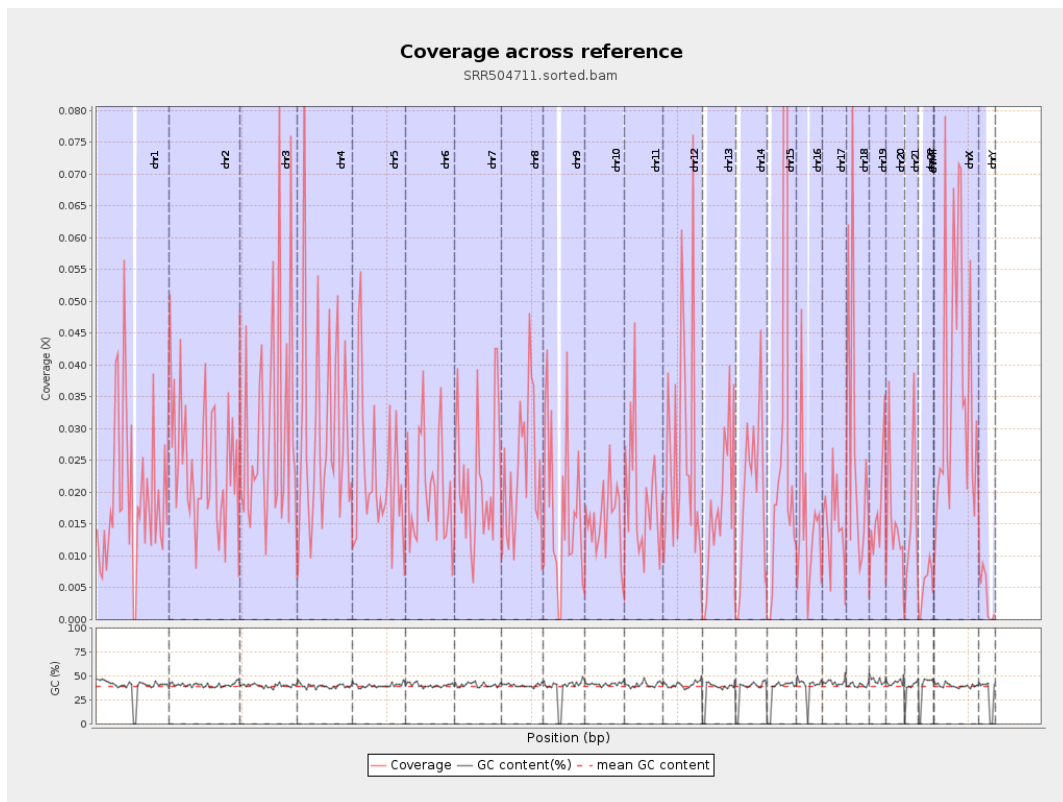
General error rate	0.04%
Mismatches	28,437

2.6. Chromosome stats

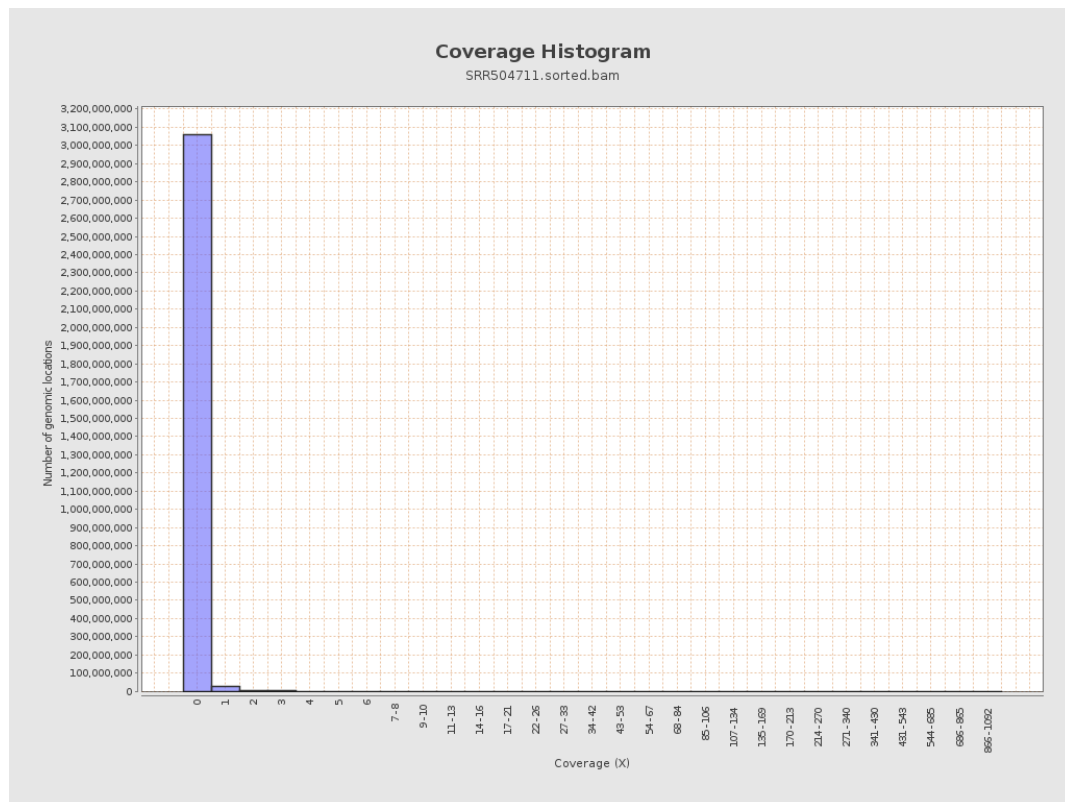
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4739834	0.019	0.2777
chr2	243199373	5915454	0.0243	0.3637
chr3	198022430	6022740	0.0304	0.5625
chr4	191154276	5751714	0.0301	0.5717
chr5	180915260	4091748	0.0226	0.3511
chr6	171115067	3482572	0.0204	0.2945
chr7	159138663	3518556	0.0221	0.3293
chr8	146364022	3379216	0.0231	0.3553
chr9	141213431	2516312	0.0178	0.29
chr10	135534747	2155808	0.0159	0.2184
chr11	135006516	2591578	0.0192	0.2798
chr12	133851895	3425572	0.0256	0.4587
chr13	115169878	1994552	0.0173	0.2999
chr14	107349540	2179240	0.0203	0.323
chr15	102531392	3219198	0.0314	3.4395

chr16	90354753	1350450	0.0149	0.2939
chr17	81195210	1205256	0.0148	0.2299
chr18	78077248	2145414	0.0275	0.6941
chr19	59128983	990688	0.0168	0.295
chr20	63025520	977218	0.0155	0.2755
chr21	48129895	695536	0.0145	0.2974
chr22	51304566	280032	0.0055	0.0949
chrMT	16571	96	0.0058	0.1029
chrX	155270560	5611598	0.0361	0.6184
chrY	59373566	211838	0.0036	0.0808

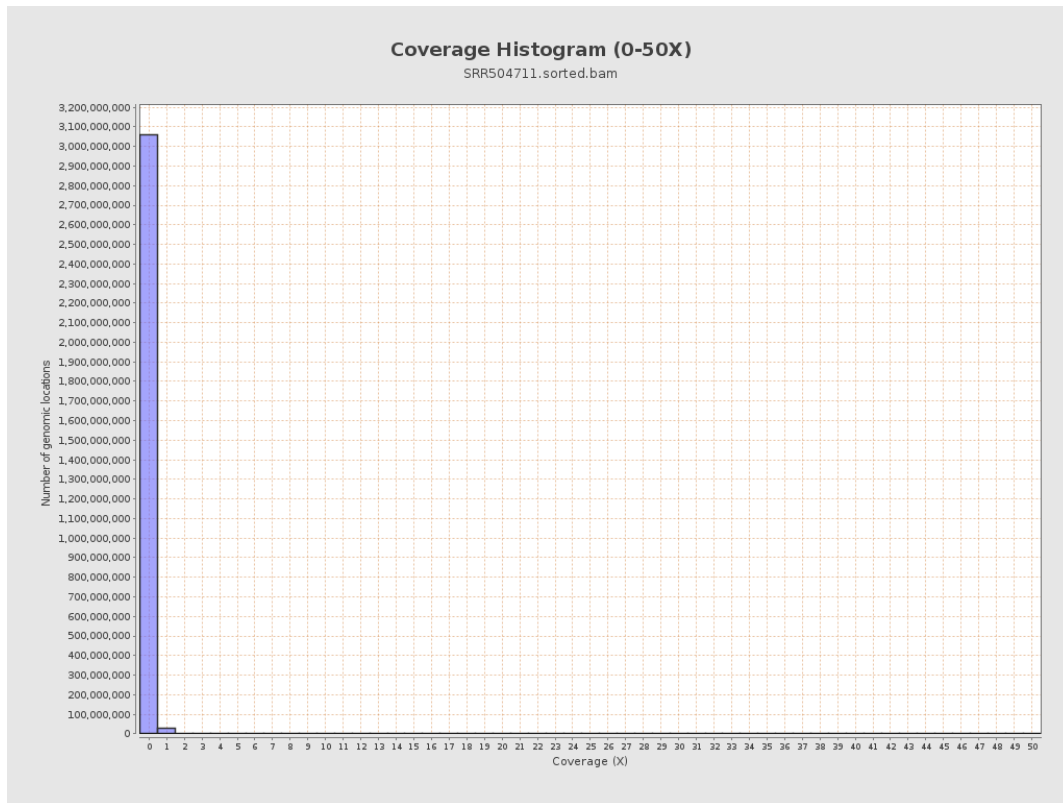
3. Results : Coverage across reference



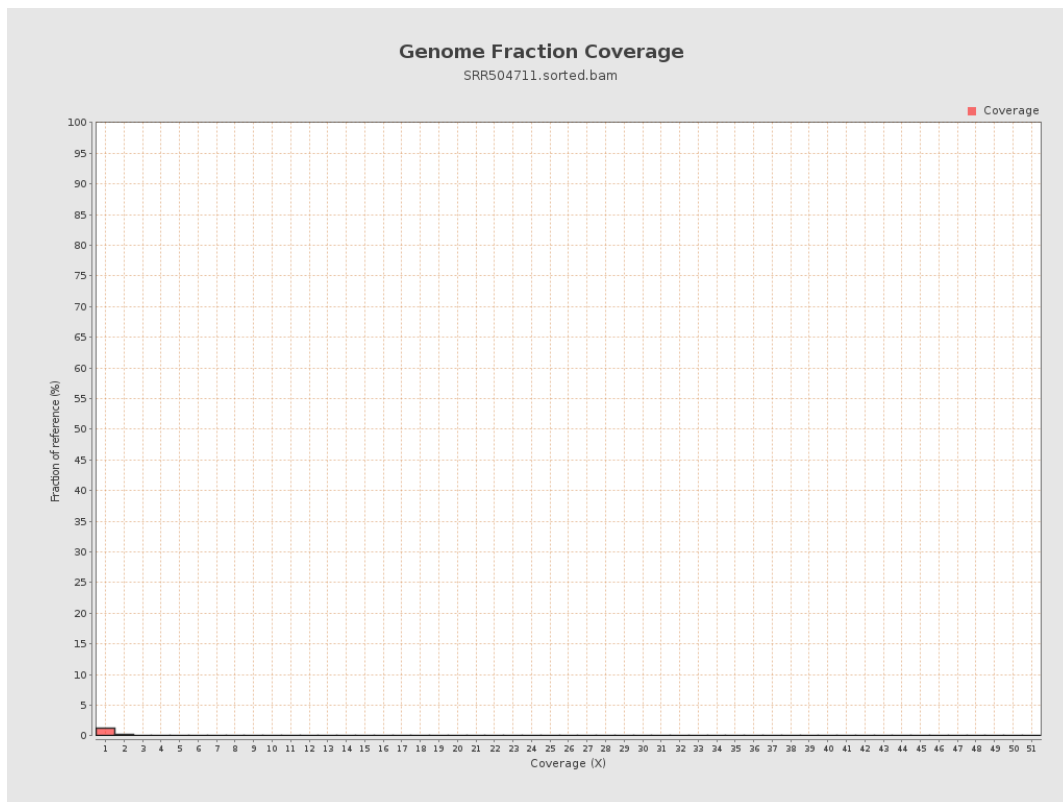
4. Results : Coverage Histogram



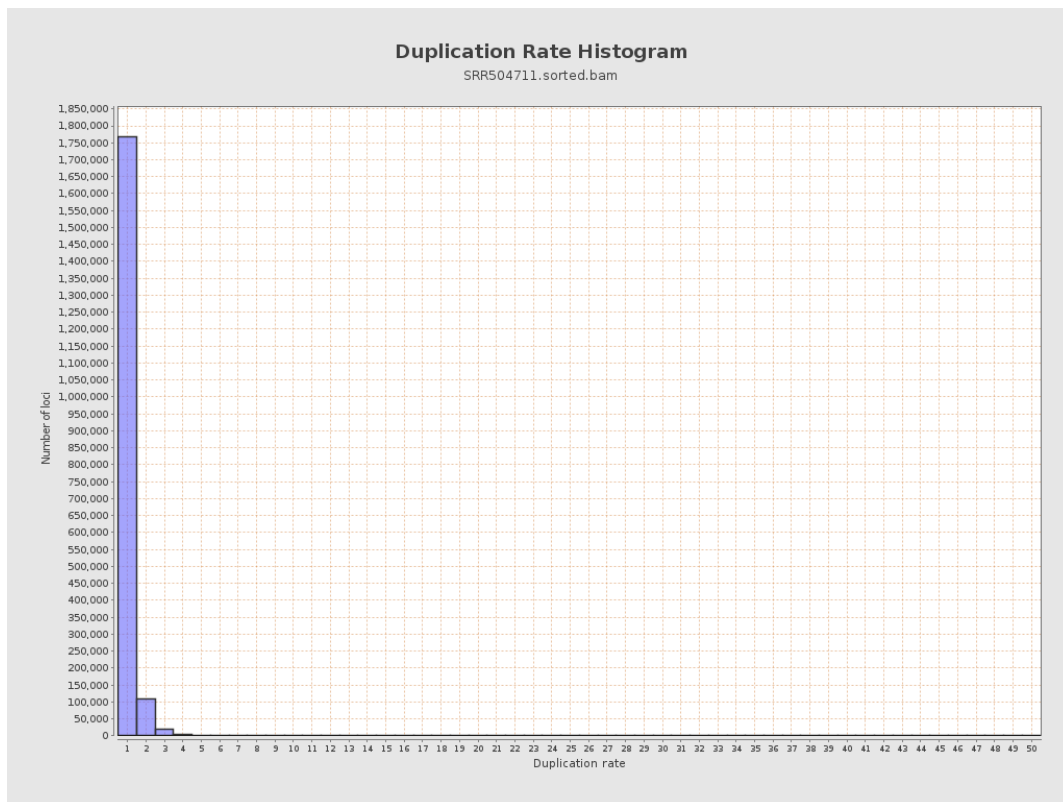
5. Results : Coverage Histogram (0-50X)



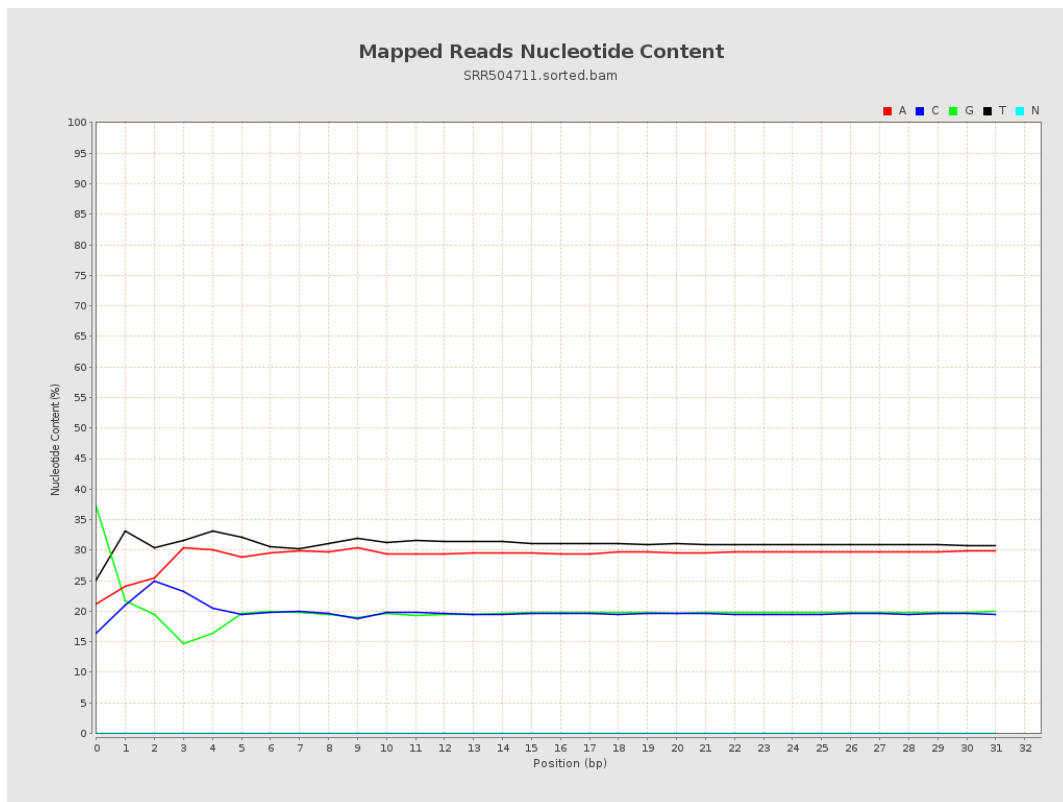
6. Results : Genome Fraction Coverage



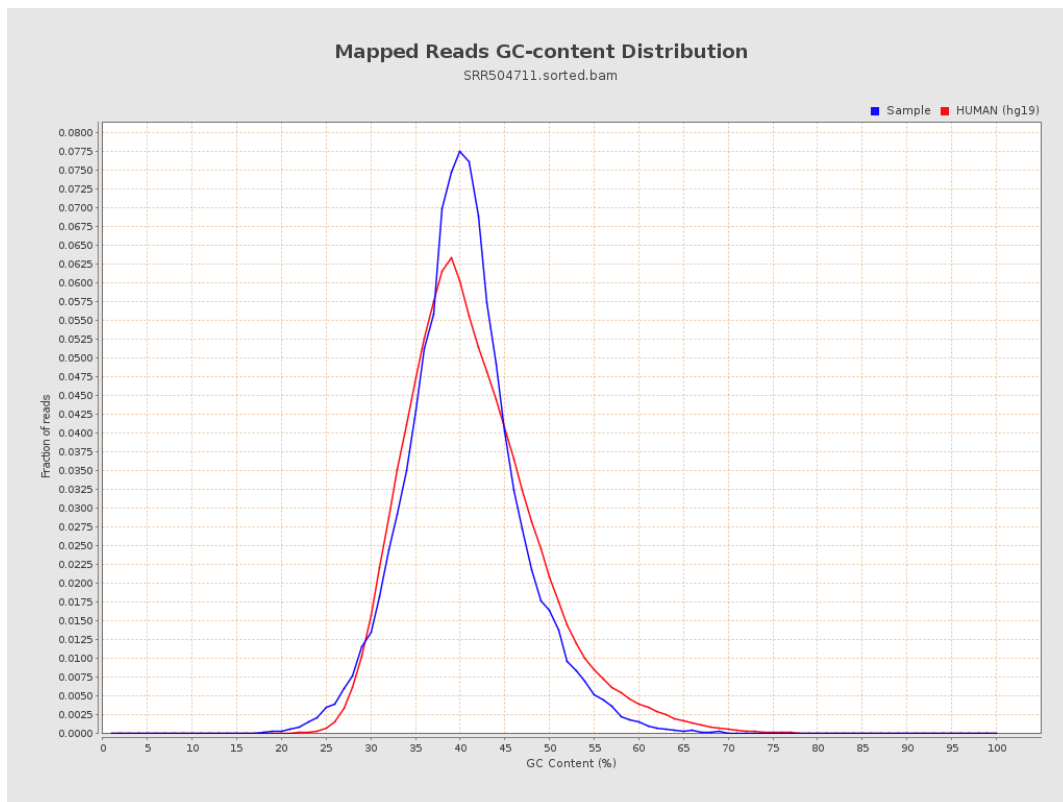
7. Results : Duplication Rate Histogram



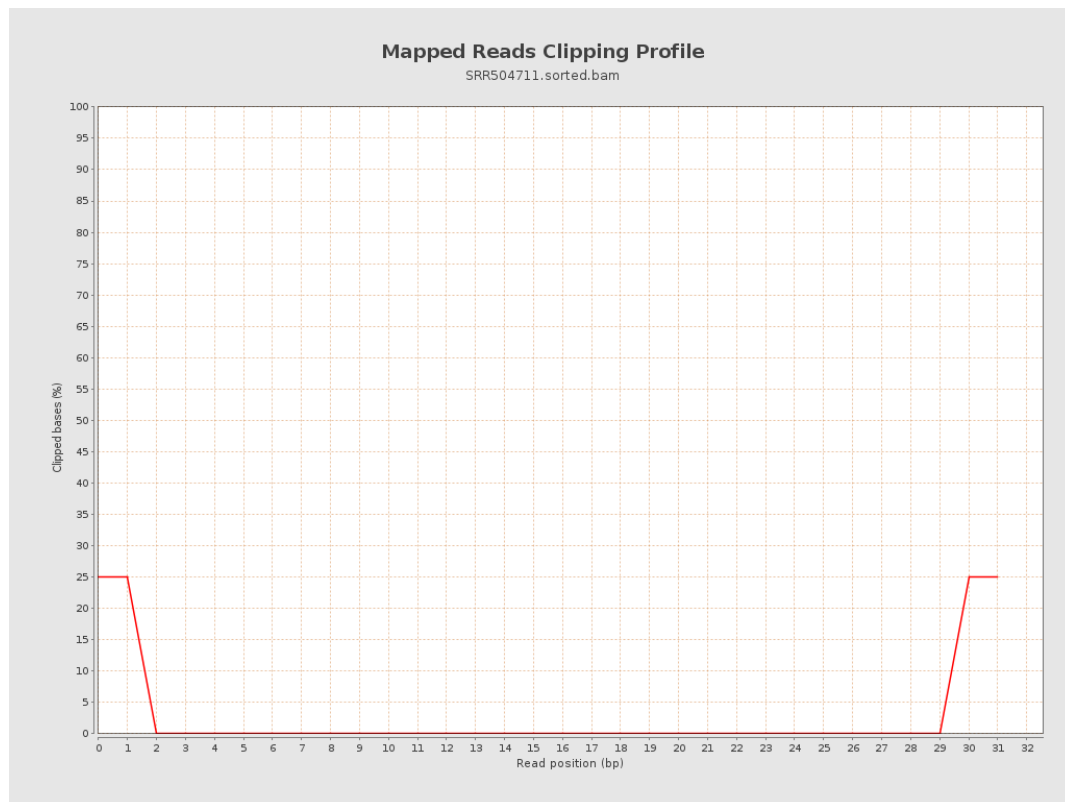
8. Results : Mapped Reads Nucleotide Content



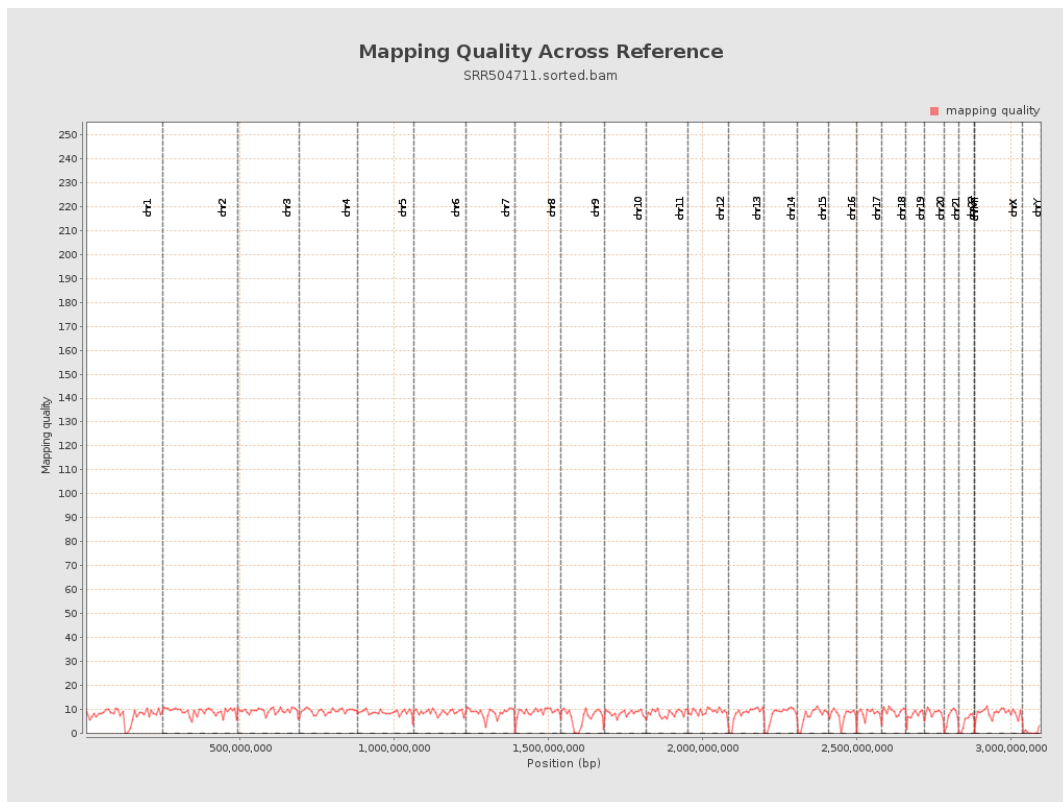
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Mapping Quality Across Reference



12. Results : Mapping Quality Histogram

