

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/06/25 06:32:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504745.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_SRR504745 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504745.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jun 25 06:32:37 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504745.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,843,854
Mapped reads	1,680,648 / 91.15%
Unmapped reads	163,206 / 8.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	32 / 32 / 32
Duplicated reads (estimated)	150,164 / 8.14%
Duplication rate	6.37%
Clipped reads	2,604 / 0.14%

2.2. ACGT Content

Number/percentage of A's	15,403,365 / 28.64%
Number/percentage of C's	10,913,771 / 20.3%
Number/percentage of T's	16,334,109 / 30.37%
Number/percentage of G's	11,123,940 / 20.69%
Number/percentage of N's	343 / 0%
GC Percentage	40.98%

2.3. Coverage

Mean	0.0174
Standard Deviation	0.3911

2.4. Mapping Quality

Mean Mapping Quality	6.31
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2.5. Mismatches and indels

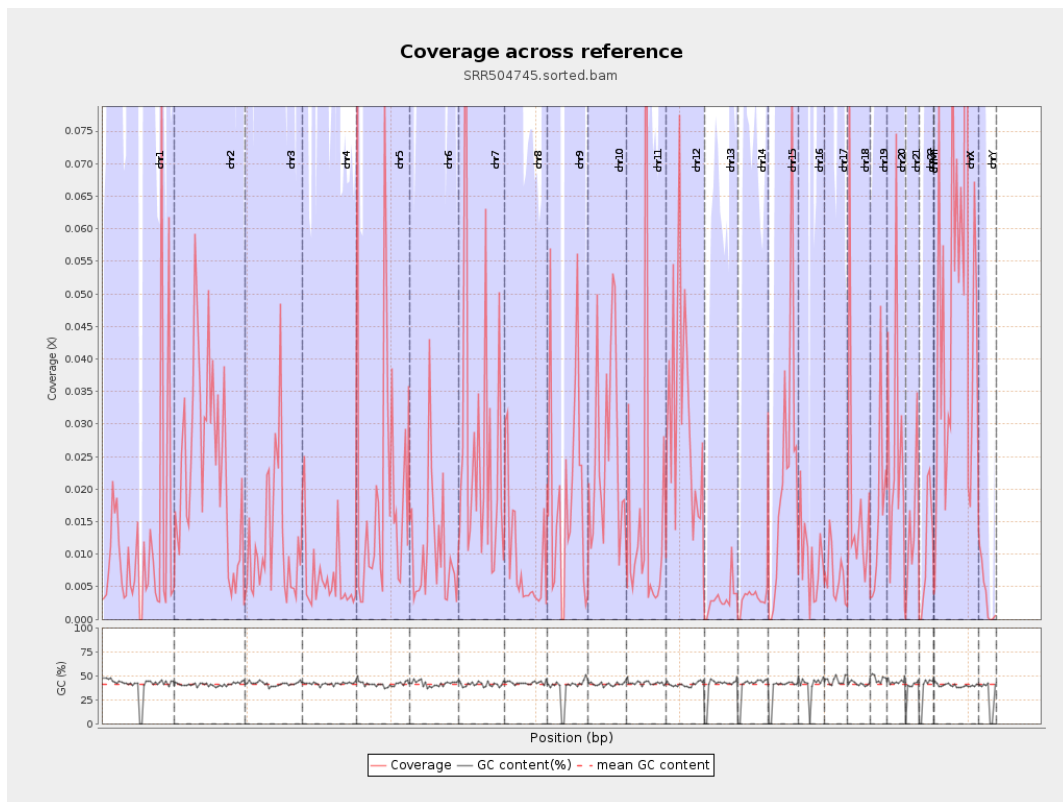
General error rate	0.05%
Mismatches	24,717

2.6. Chromosome stats

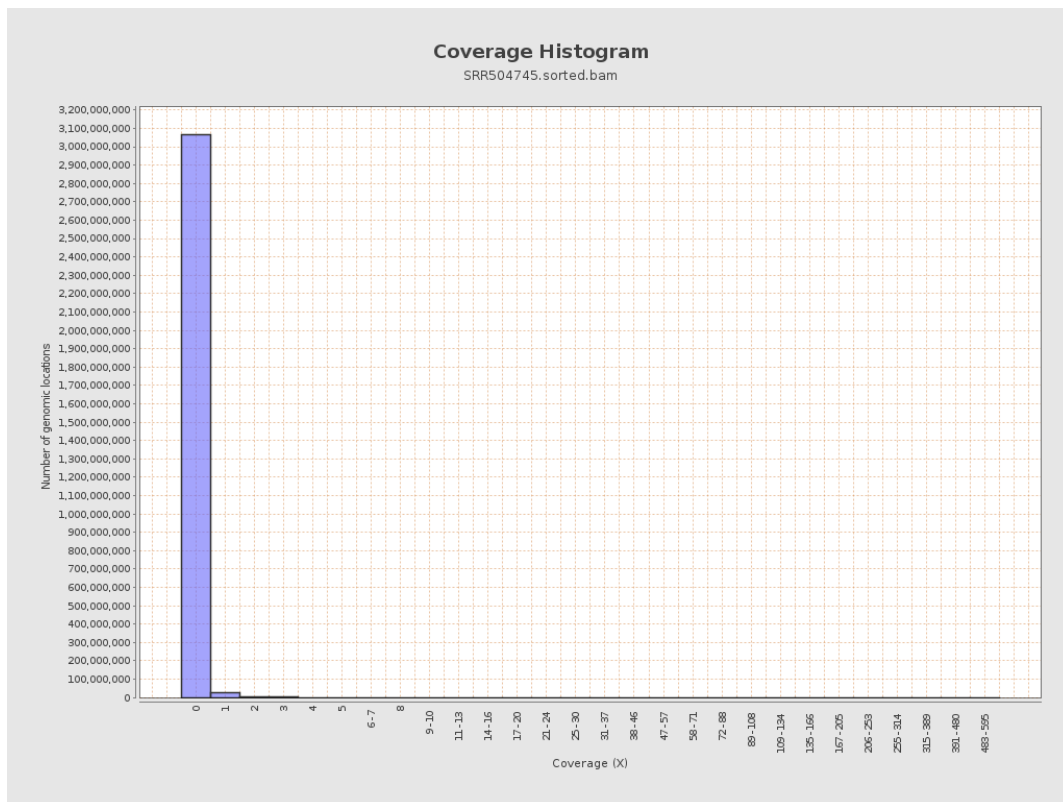
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	2831506	0.0114	0.3435
chr2	243199373	5776470	0.0238	0.2411
chr3	198022430	2390272	0.0121	0.3071
chr4	191154276	1221810	0.0064	0.151
chr5	180915260	3119154	0.0172	0.4074
chr6	171115067	1847268	0.0108	0.222
chr7	159138663	4145364	0.026	0.6772
chr8	146364022	1317070	0.009	0.2278
chr9	141213431	2644120	0.0187	0.2209
chr10	135534747	3549710	0.0262	0.276
chr11	135006516	2284556	0.0169	0.8709
chr12	133851895	4251278	0.0318	0.3302
chr13	115169878	364676	0.0032	0.0962
chr14	107349540	363236	0.0034	0.0706
chr15	102531392	2256840	0.022	0.289

chr16	90354753	803430	0.0089	0.2461
chr17	81195210	548998	0.0068	0.1149
chr18	78077248	1526762	0.0196	0.4449
chr19	59128983	978718	0.0166	0.3063
chr20	63025520	1691100	0.0268	0.4248
chr21	48129895	709028	0.0147	0.1624
chr22	51304566	533718	0.0104	0.1514
chrMT	16571	64	0.0039	0.062
chrX	155270560	8402914	0.0541	0.8078
chrY	59373566	217466	0.0037	0.0787

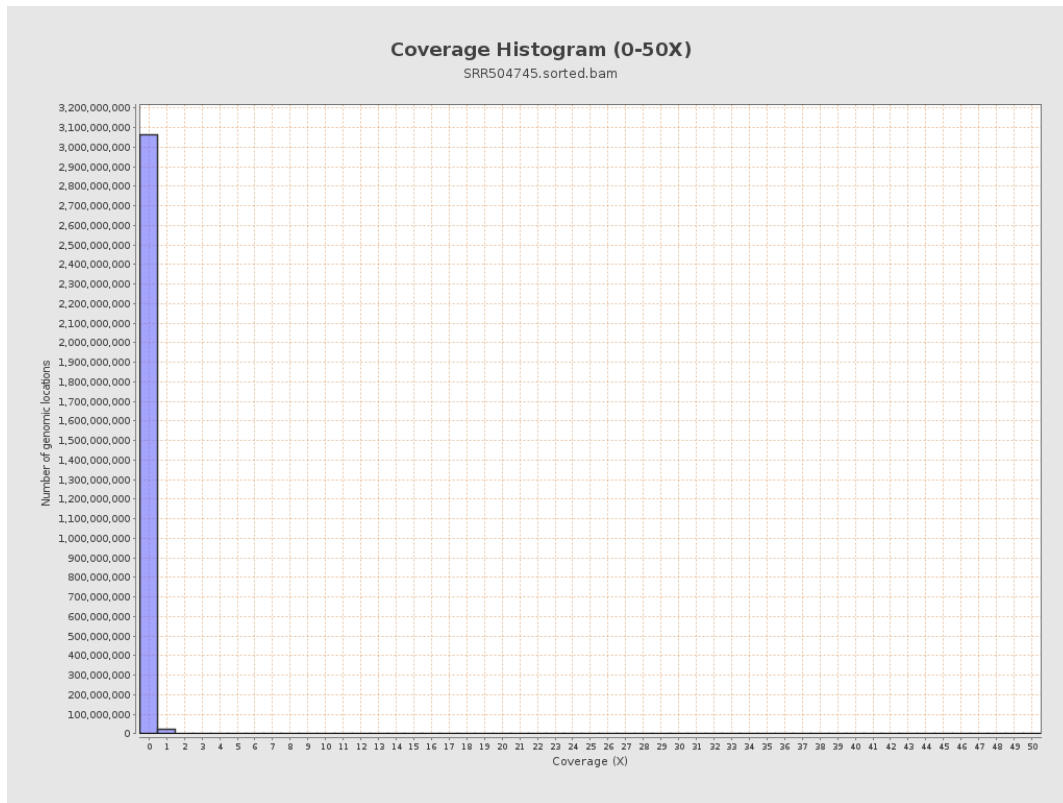
3. Results : Coverage across reference



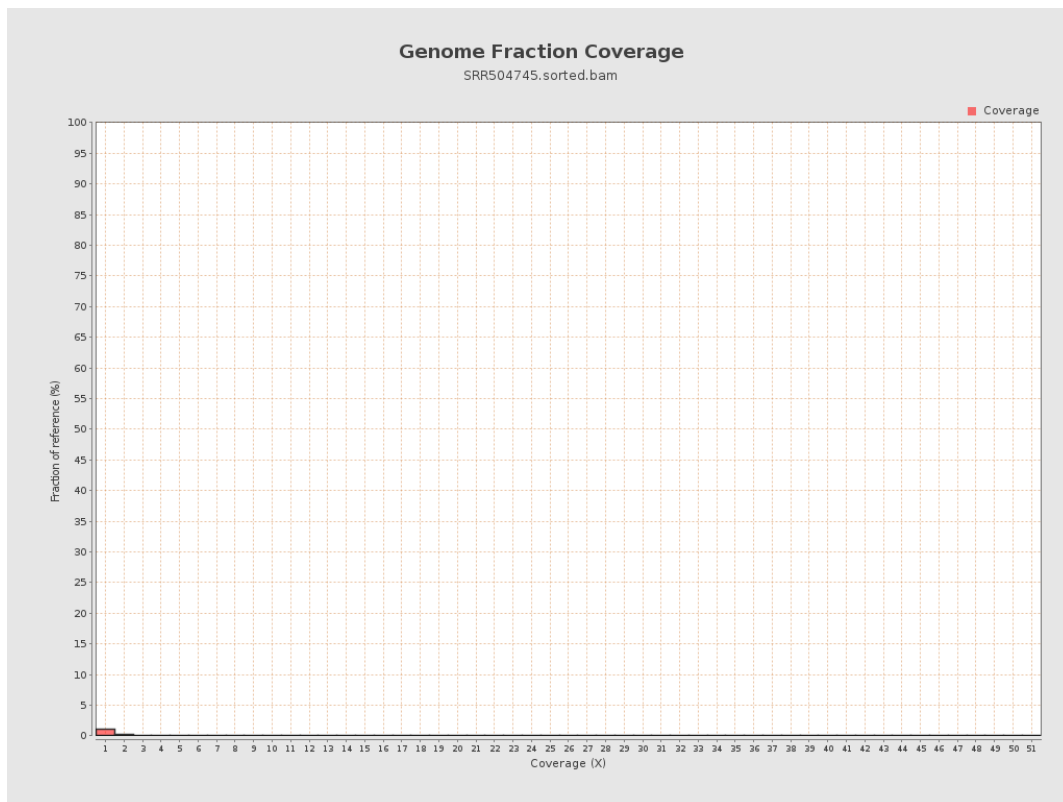
4. Results : Coverage Histogram



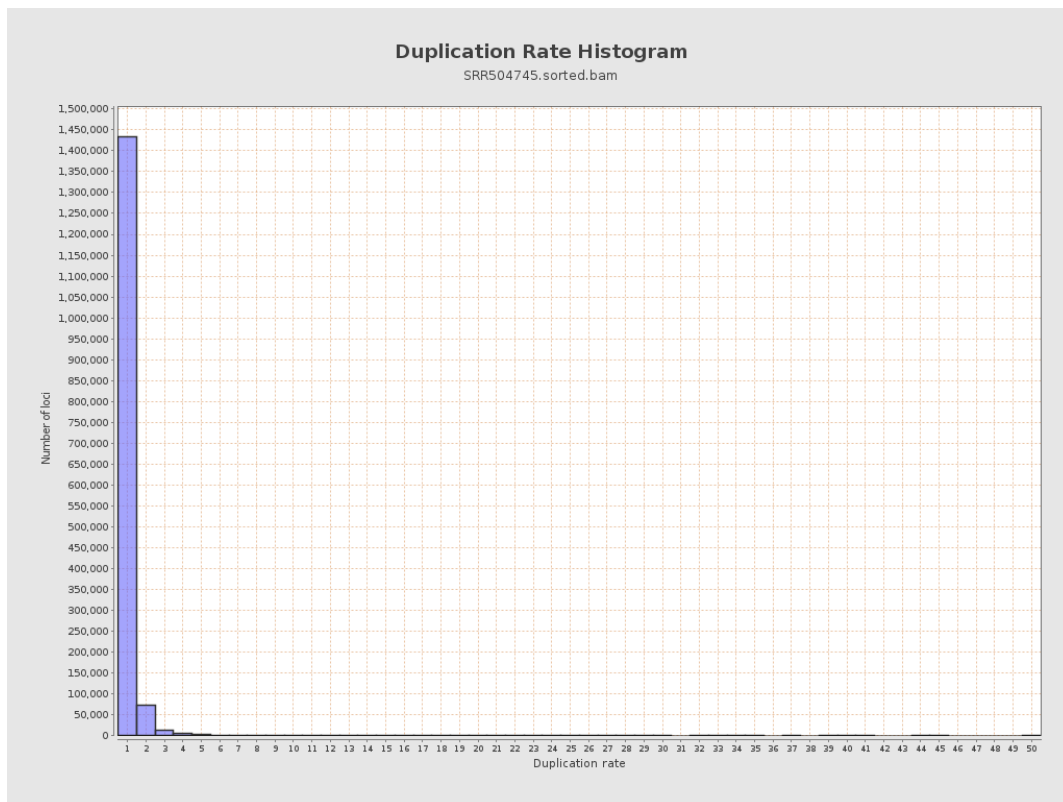
5. Results : Coverage Histogram (0-50X)



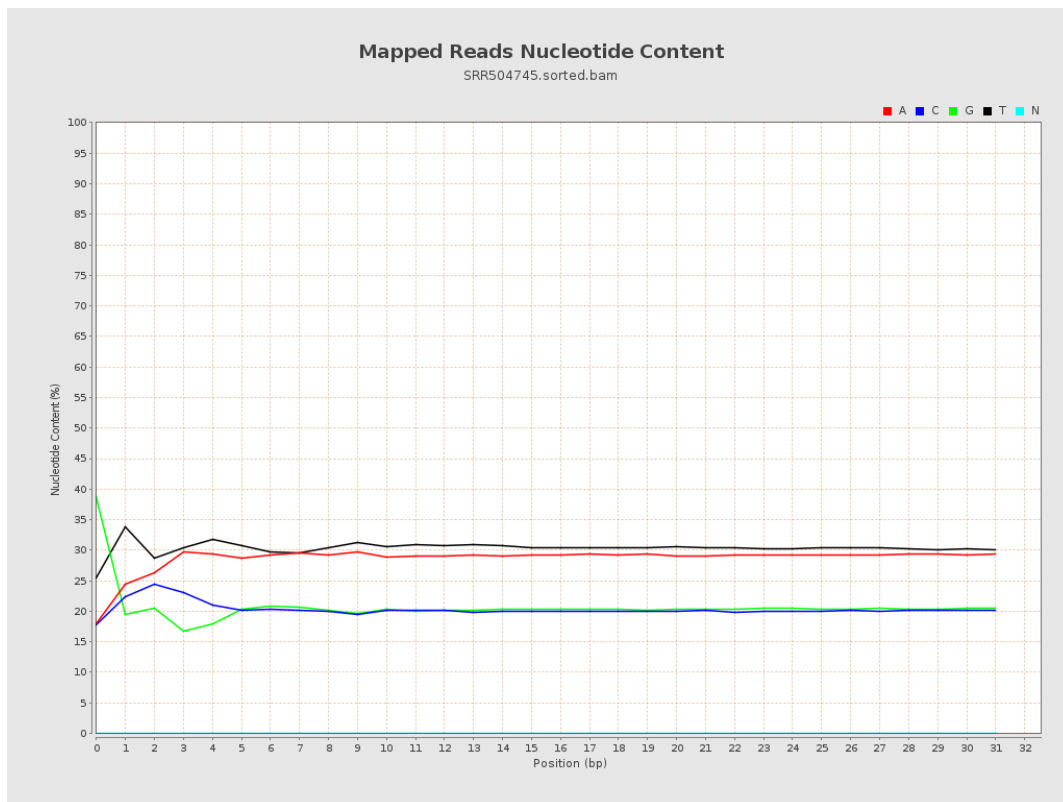
6. Results : Genome Fraction Coverage



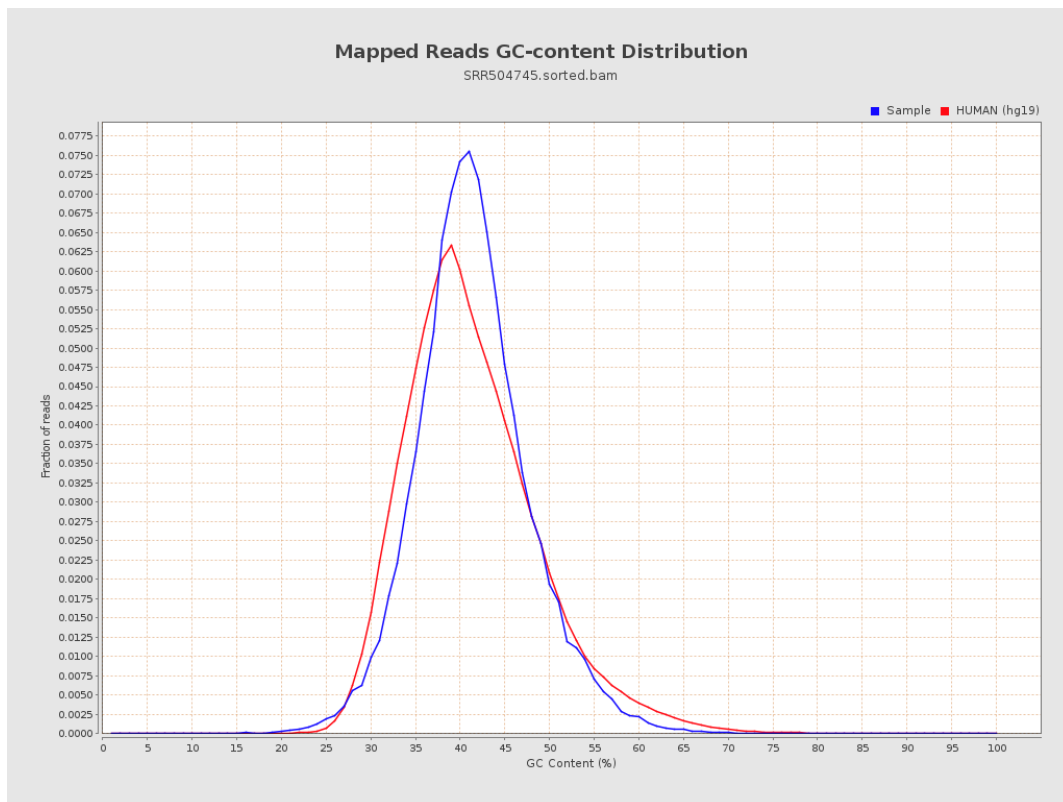
7. Results : Duplication Rate Histogram



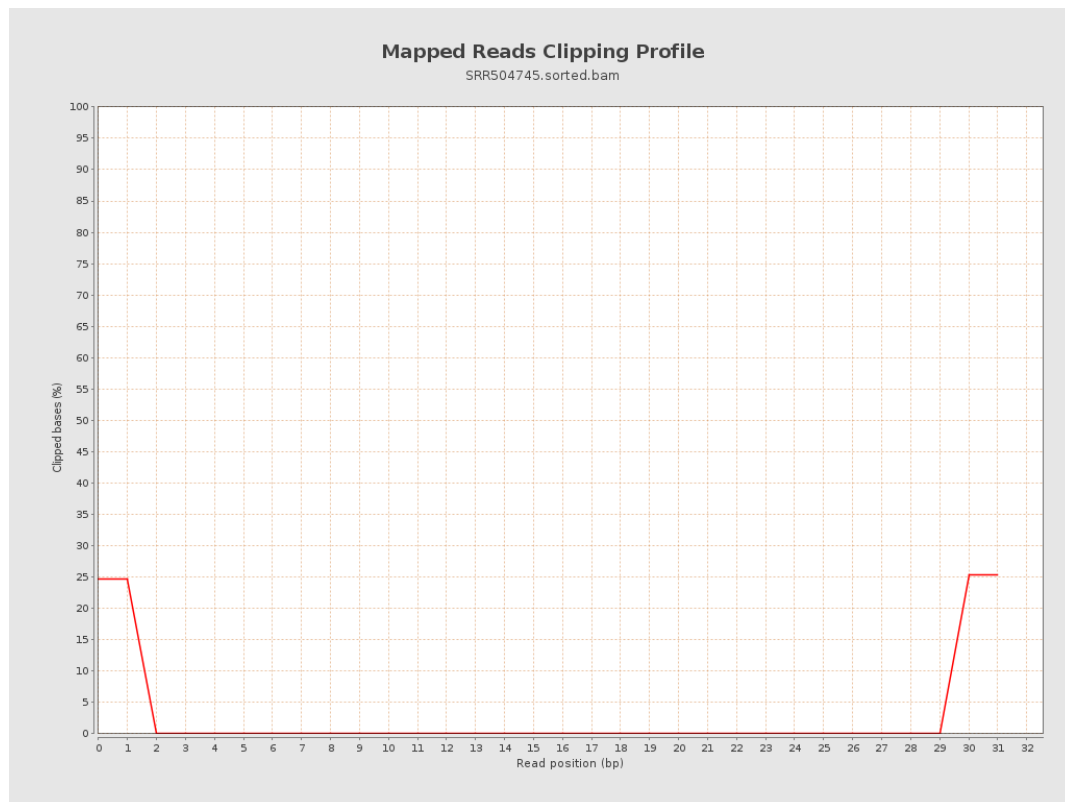
8. Results : Mapped Reads Nucleotide Content



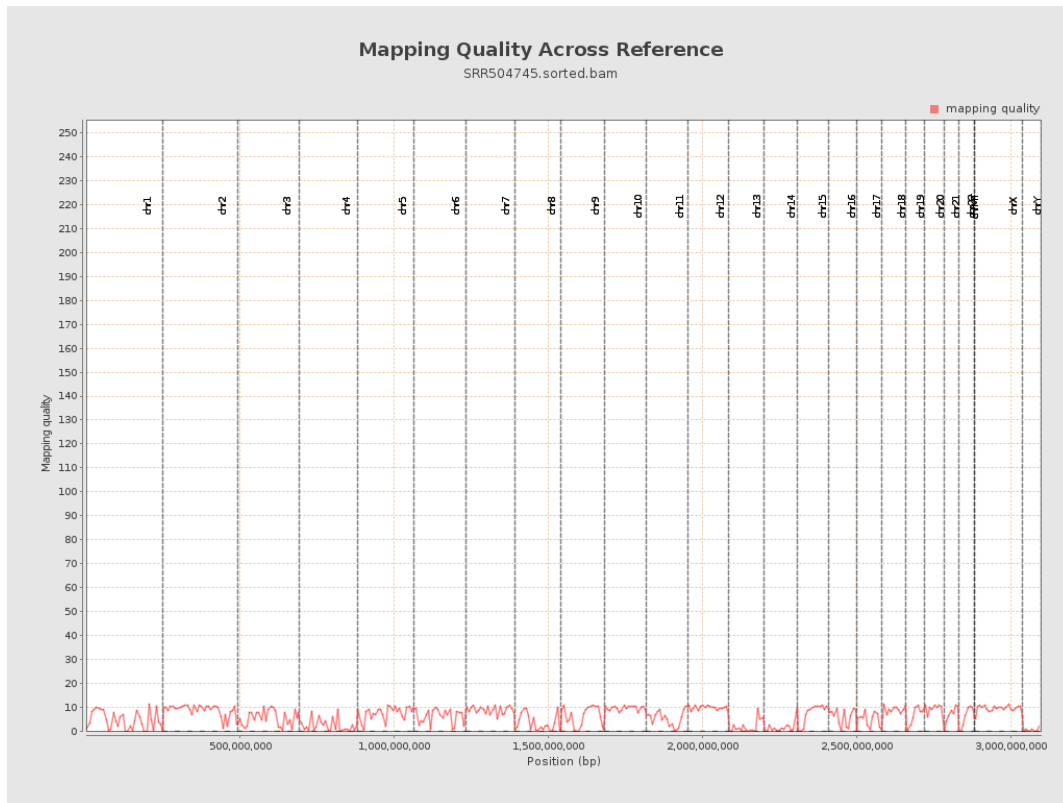
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Mapping Quality Across Reference



12. Results : Mapping Quality Histogram

