

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/06/25 06:44:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504757.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_SRR504757 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504757.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jun 25 06:44:58 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504757.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,773,875
Mapped reads	1,605,270 / 90.5%
Unmapped reads	168,605 / 9.5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	32 / 32 / 32
Duplicated reads (estimated)	426,455 / 24.04%
Duplication rate	12.34%
Clipped reads	2,514 / 0.14%

2.2. ACGT Content

Number/percentage of A's	14,626,482 / 28.48%
Number/percentage of C's	10,380,470 / 20.21%
Number/percentage of T's	16,084,783 / 31.32%
Number/percentage of G's	10,271,539 / 20%
Number/percentage of N's	338 / 0%
GC Percentage	40.21%

2.3. Coverage

Mean	0.0166
Standard Deviation	1.273

2.4. Mapping Quality

Mean Mapping Quality	7.42
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2.5. Mismatches and indels

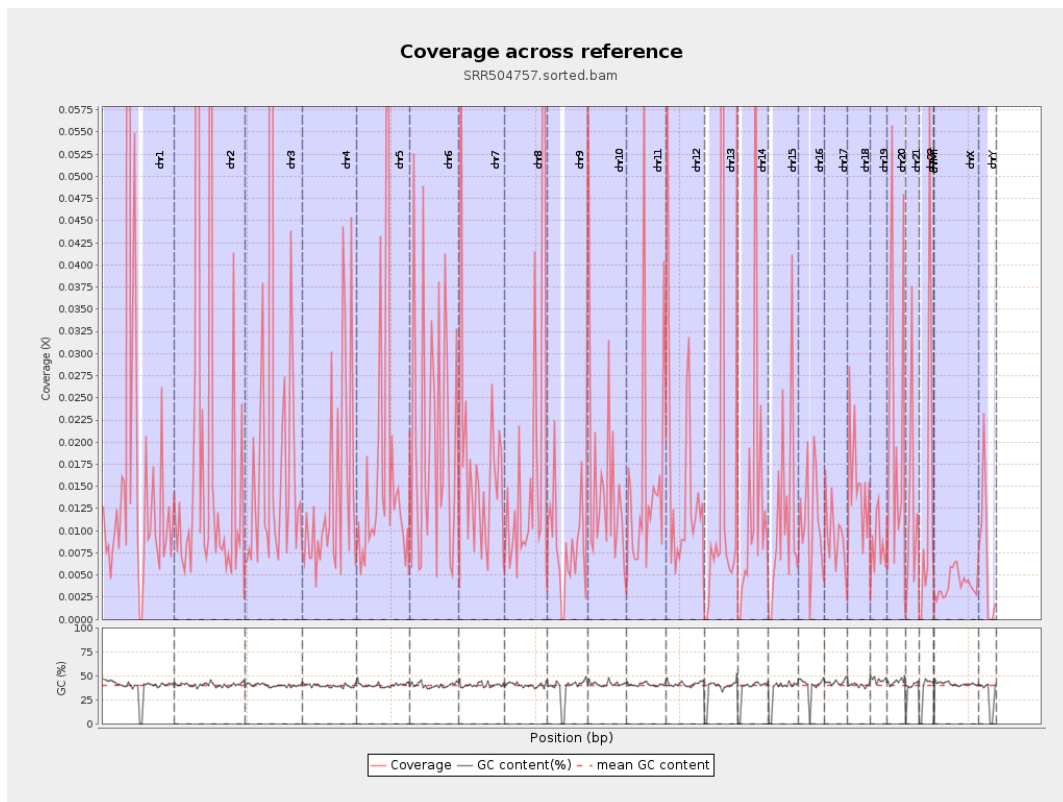
General error rate	0.05%
Mismatches	27,224

2.6. Chromosome stats

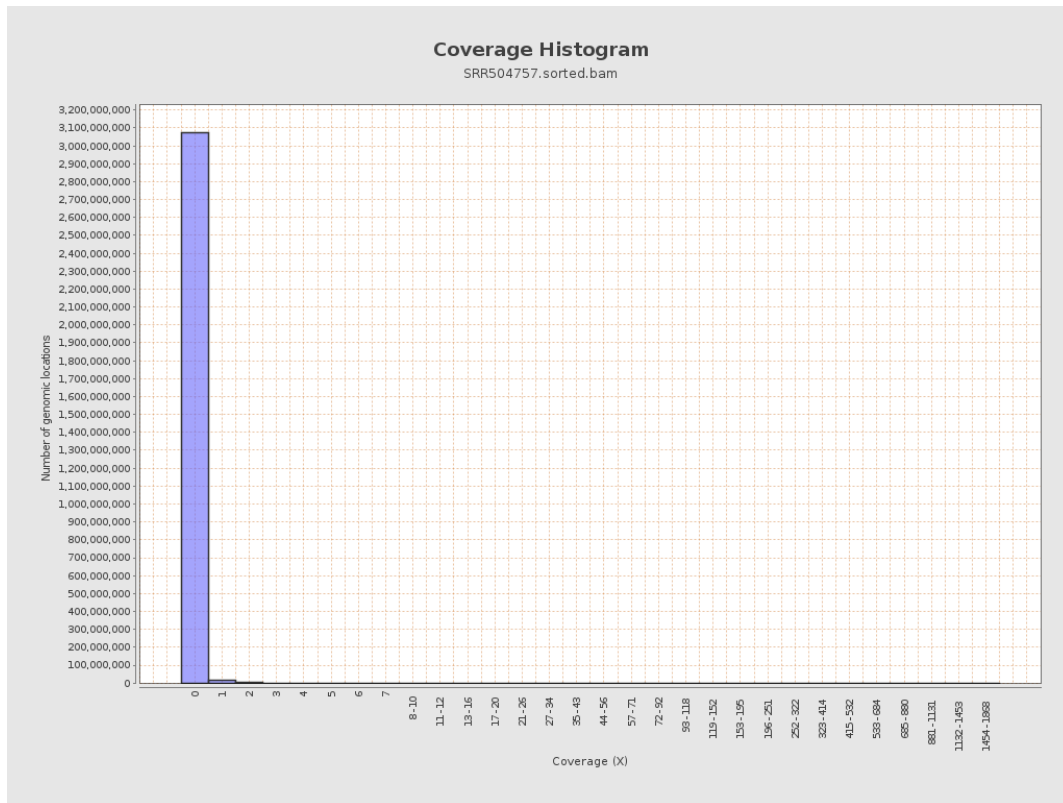
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5780534	0.0232	1.6303
chr2	243199373	4802780	0.0197	1.3575
chr3	198022430	6682224	0.0337	4.0493
chr4	191154276	2712498	0.0142	0.3611
chr5	180915260	3041794	0.0168	0.5872
chr6	171115067	3532642	0.0206	0.4767
chr7	159138663	2835248	0.0178	0.4701
chr8	146364022	2623064	0.0179	0.6073
chr9	141213431	1222306	0.0087	0.1799
chr10	135534747	1978994	0.0146	0.4297
chr11	135006516	2169872	0.0161	0.4612
chr12	133851895	2197626	0.0164	0.6087
chr13	115169878	1855600	0.0161	1.4647
chr14	107349540	1477780	0.0138	0.4666
chr15	102531392	1149350	0.0112	0.3128

chr16	90354753	988116	0.0109	0.1928
chr17	81195210	771956	0.0095	0.1879
chr18	78077248	1209816	0.0155	0.2735
chr19	59128983	505592	0.0086	0.1712
chr20	63025520	1478046	0.0235	0.6307
chr21	48129895	634666	0.0132	0.3047
chr22	51304566	649986	0.0127	0.4212
chrMT	16571	0	0	0
chrX	155270560	631156	0.0041	0.0829
chrY	59373566	431966	0.0073	0.1583

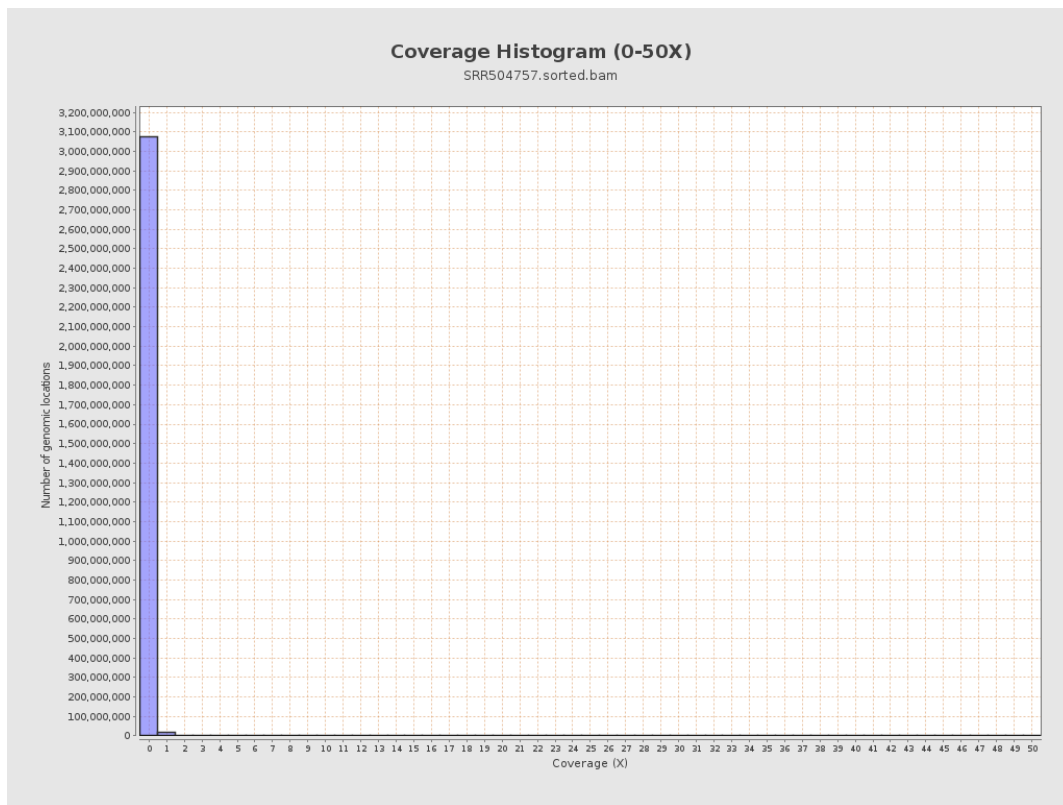
3. Results : Coverage across reference



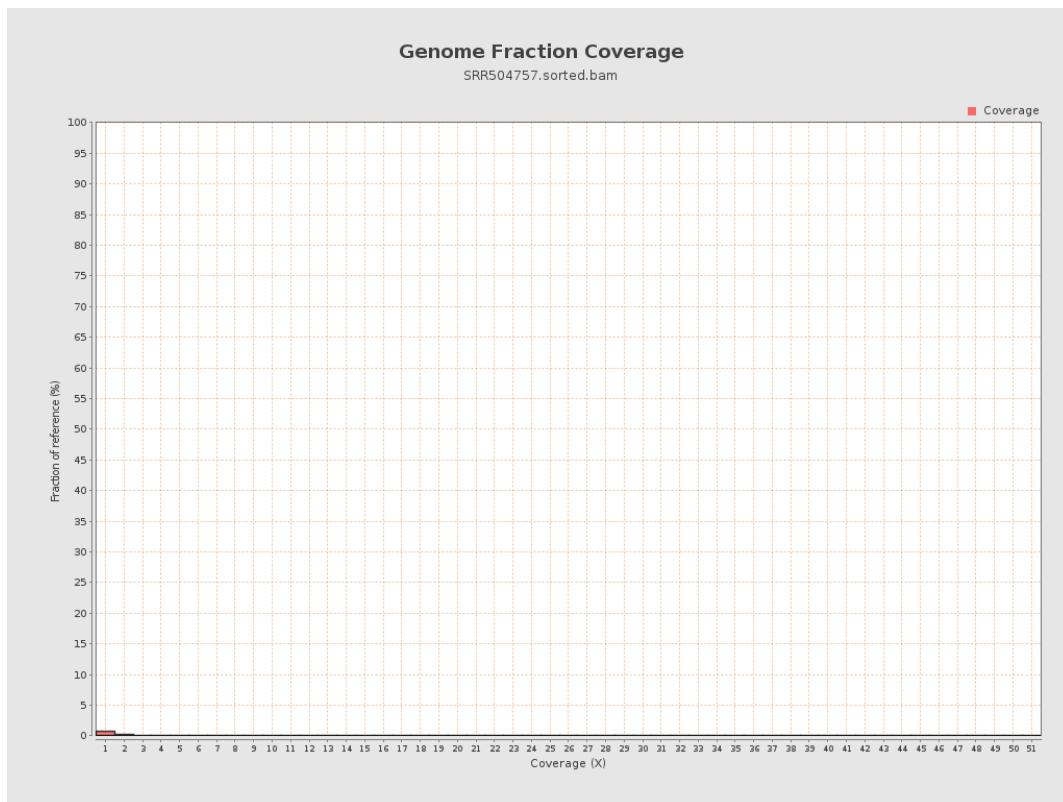
4. Results : Coverage Histogram



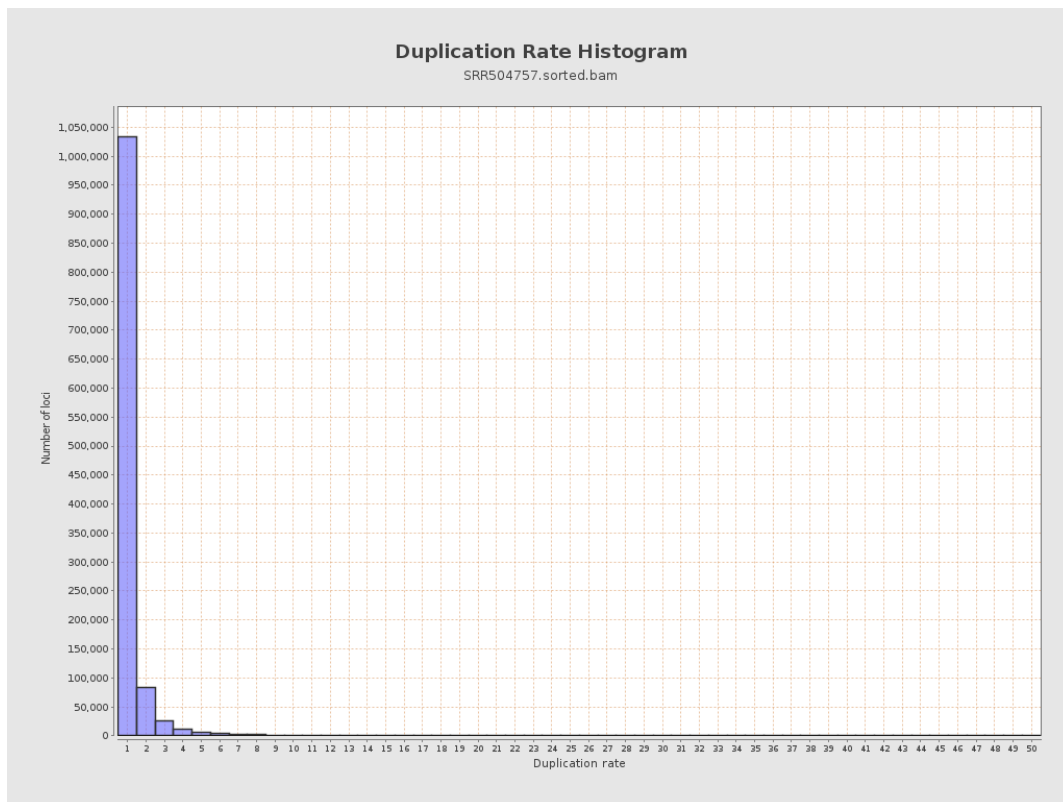
5. Results : Coverage Histogram (0-50X)



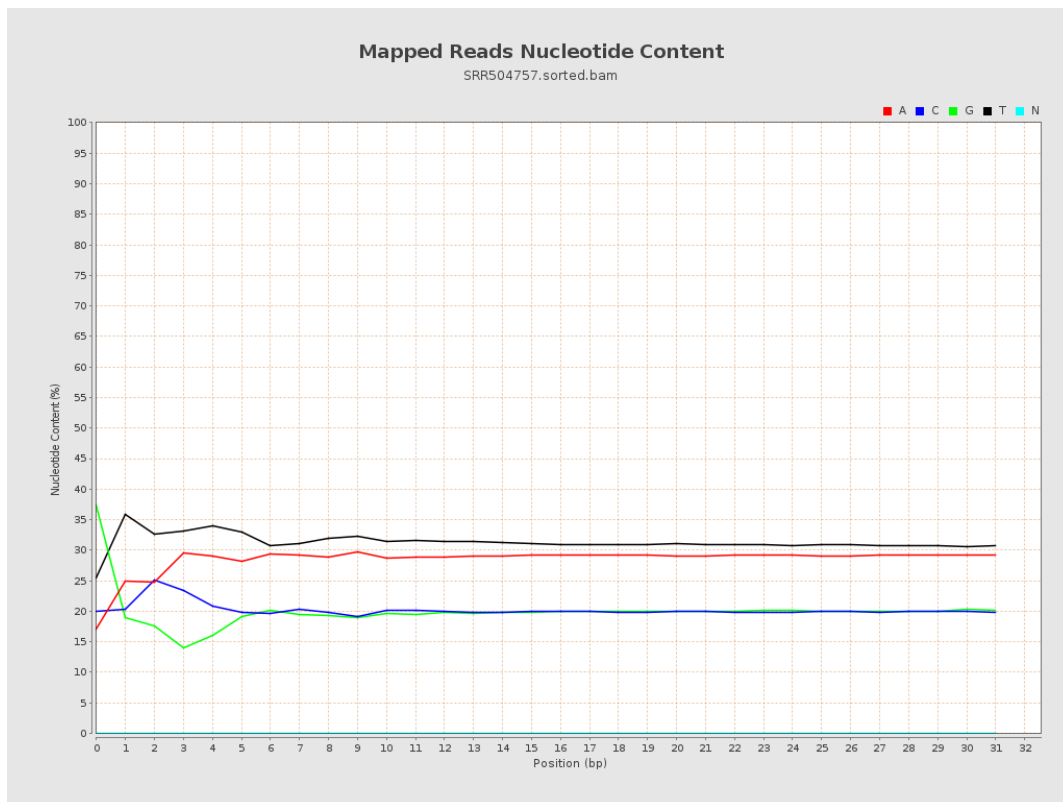
6. Results : Genome Fraction Coverage



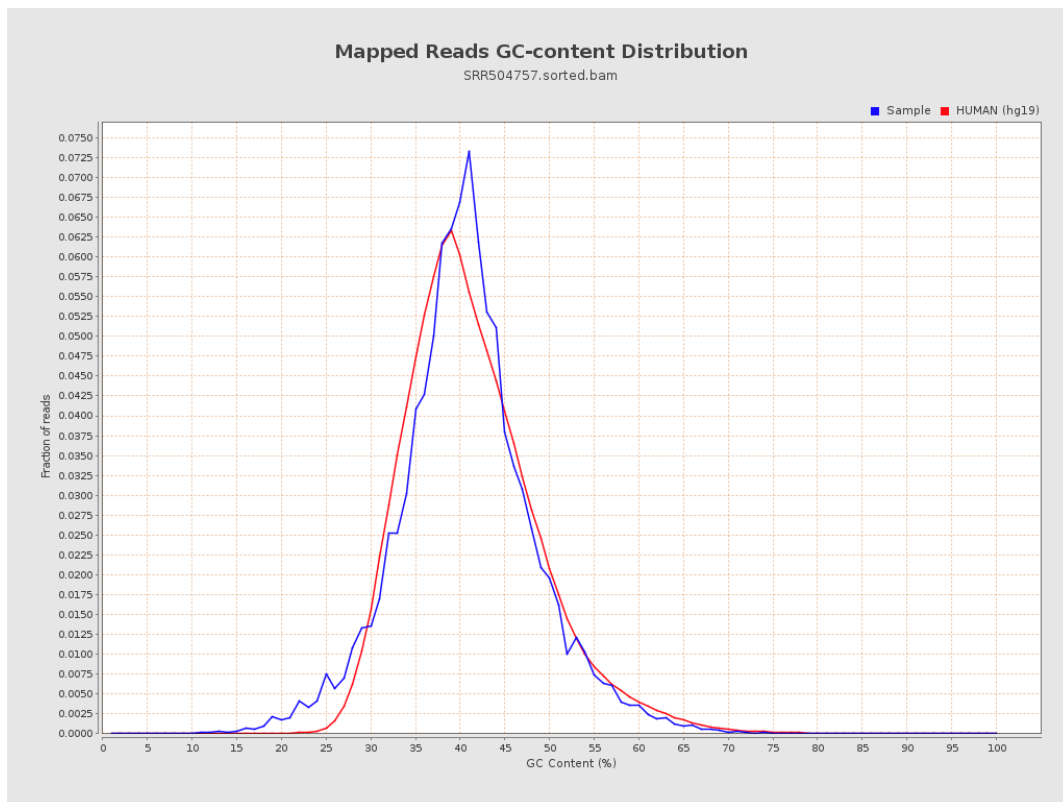
7. Results : Duplication Rate Histogram



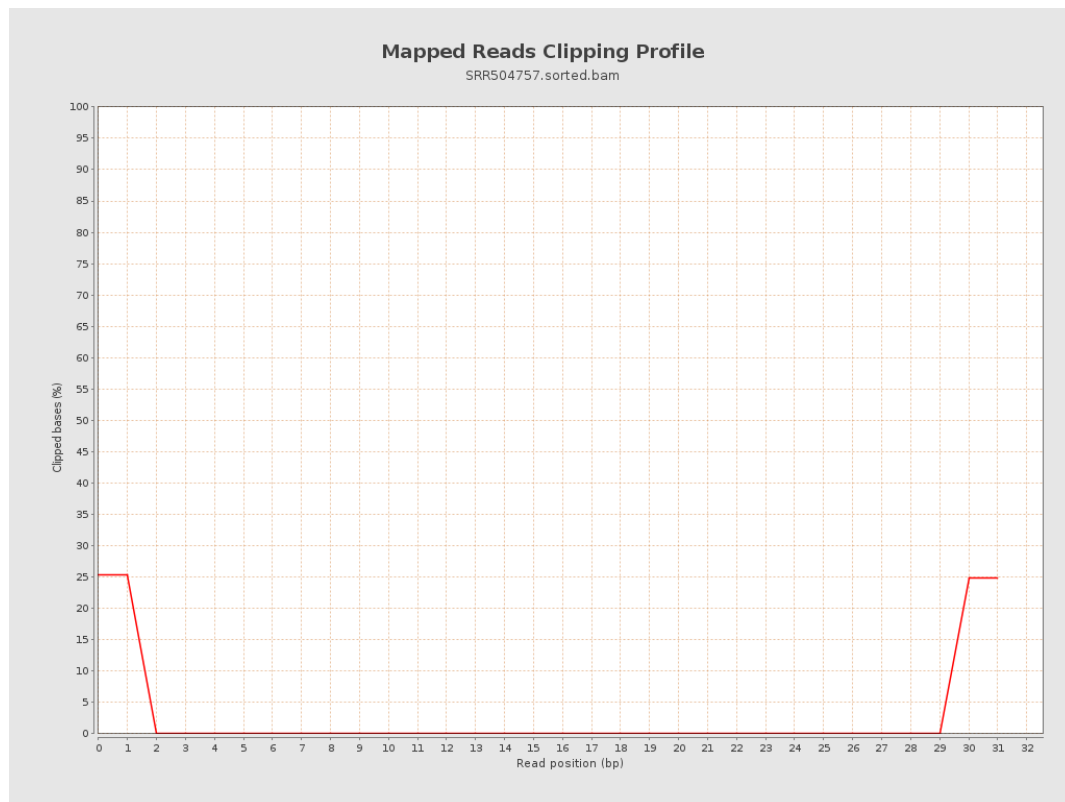
8. Results : Mapped Reads Nucleotide Content



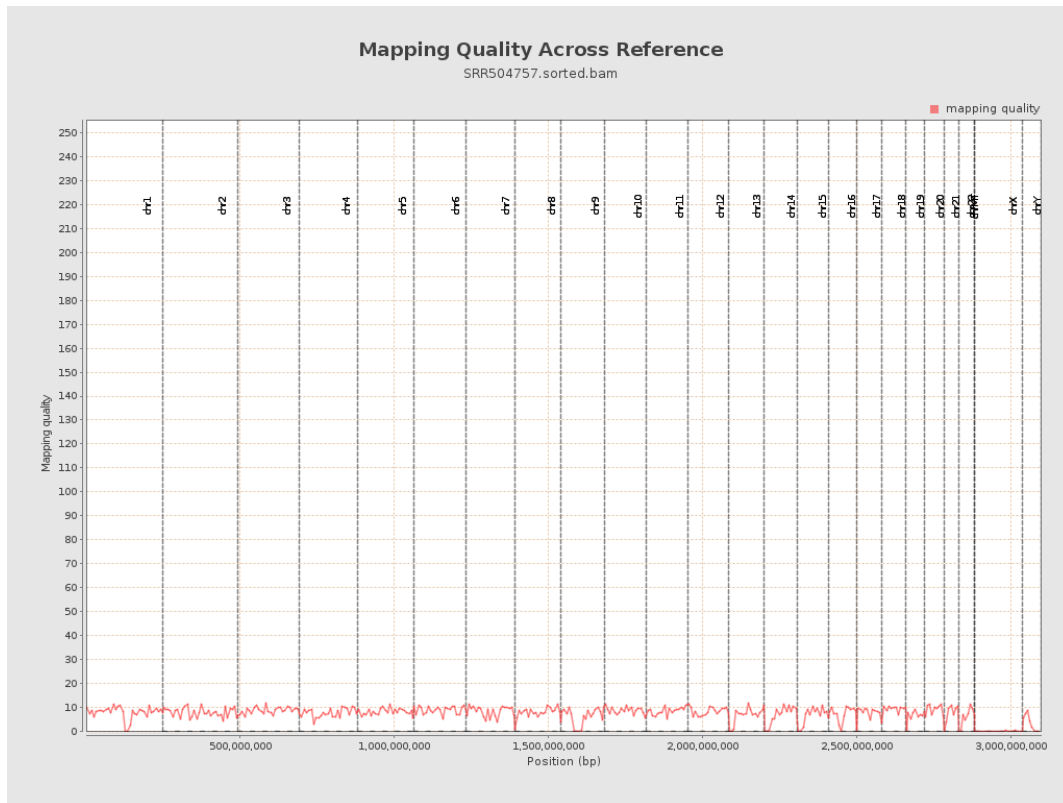
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Mapping Quality Across Reference



12. Results : Mapping Quality Histogram

