

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/06/23 07:50:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504417.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_SRR504417 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504417.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Jun 23 07:50:24 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504417.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,217,180
Mapped reads	1,942,022 / 87.59%
Unmapped reads	275,158 / 12.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	32 / 32 / 32
Duplicated reads (estimated)	121,143 / 5.46%
Duplication rate	3.78%
Clipped reads	3,242 / 0.15%

2.2. ACGT Content

Number/percentage of A's	18,030,027 / 29.02%
Number/percentage of C's	12,327,723 / 19.84%
Number/percentage of T's	19,336,989 / 31.12%
Number/percentage of G's	12,443,316 / 20.03%
Number/percentage of N's	165 / 0%
GC Percentage	39.86%

2.3. Coverage

Mean	0.0201
Standard Deviation	0.4275

2.4. Mapping Quality

Mean Mapping Quality	8.23
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2.5. Mismatches and indels

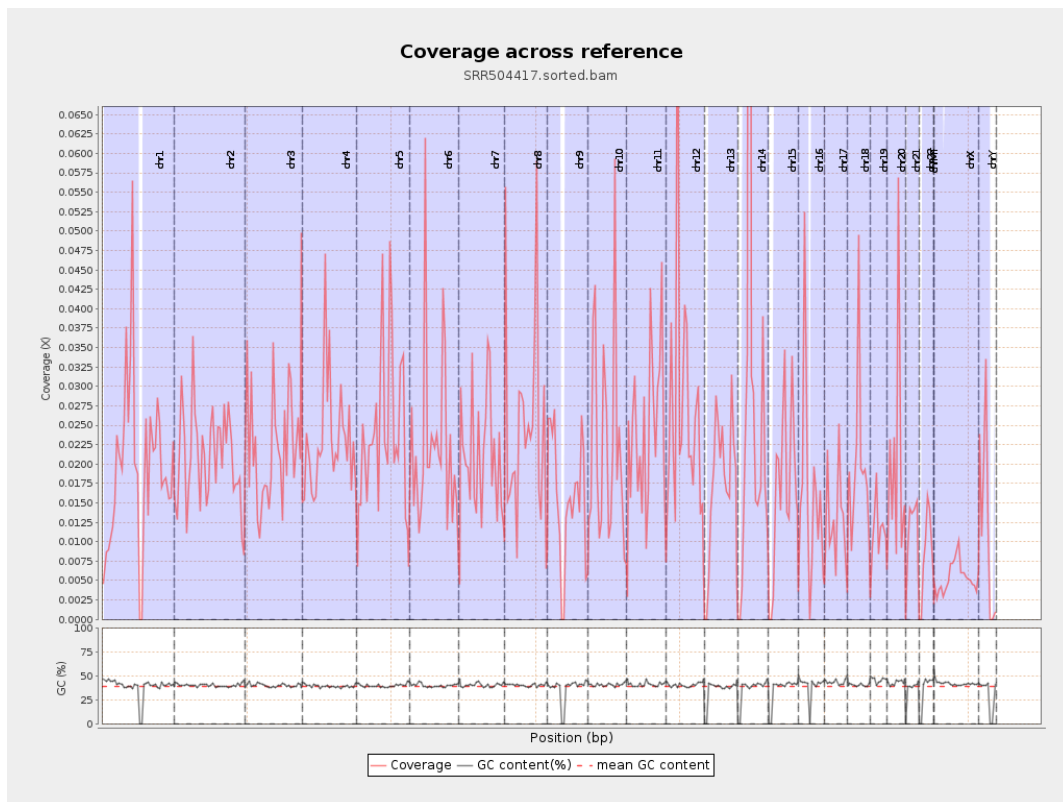
General error rate	0.05%
Mismatches	31,841

2.6. Chromosome stats

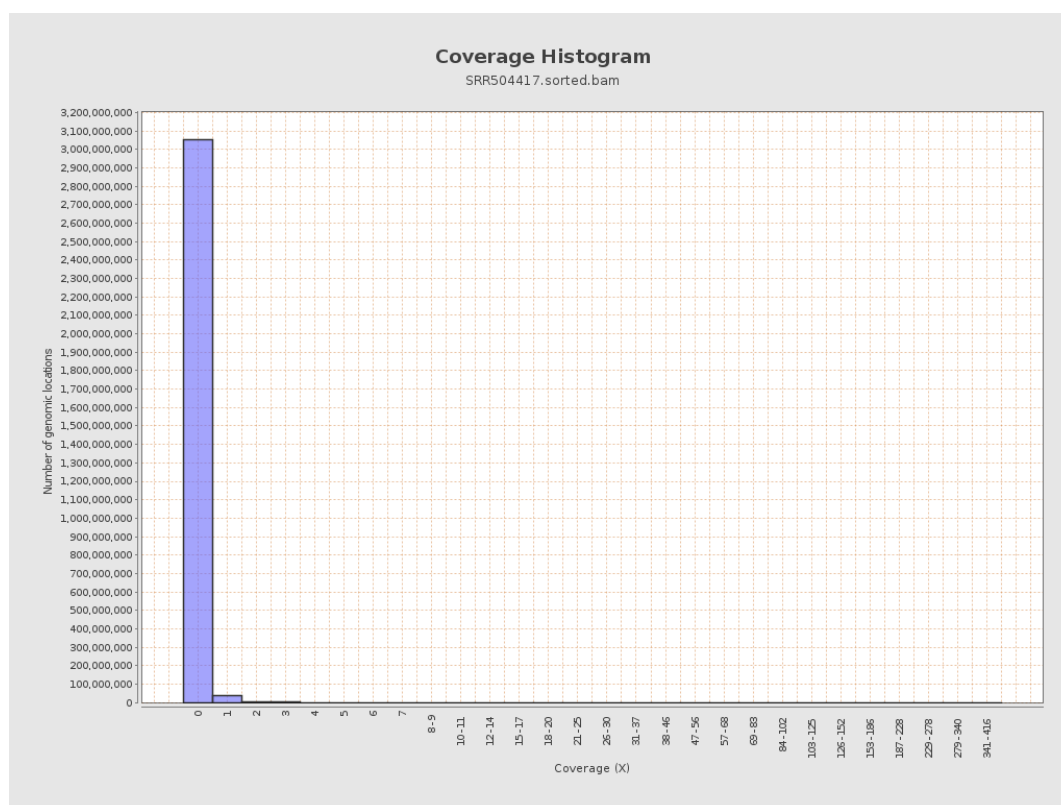
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4885176	0.0196	0.2282
chr2	243199373	5050480	0.0208	0.2031
chr3	198022430	4373128	0.0221	0.2304
chr4	191154276	4358174	0.0228	0.2063
chr5	180915260	4412928	0.0244	0.2935
chr6	171115067	3820260	0.0223	0.2812
chr7	159138663	3357986	0.0211	0.2617
chr8	146364022	3685812	0.0252	0.3362
chr9	141213431	2252892	0.016	0.1646
chr10	135534747	2985636	0.022	0.3245
chr11	135006516	3297246	0.0244	0.2472
chr12	133851895	3614946	0.027	0.4563
chr13	115169878	2046038	0.0178	0.2079
chr14	107349540	3812728	0.0355	1.8552
chr15	102531392	1726244	0.0168	0.182

chr16	90354753	1366208	0.0151	0.2416
chr17	81195210	1027312	0.0127	0.1519
chr18	78077248	1595056	0.0204	0.297
chr19	59128983	676750	0.0114	0.1812
chr20	63025520	1248686	0.0198	0.4693
chr21	48129895	542056	0.0113	0.125
chr22	51304566	431176	0.0084	0.1171
chrMT	16571	32	0.0019	0.0439
chrX	155270560	842622	0.0054	0.0935
chrY	59373566	728648	0.0123	0.2184

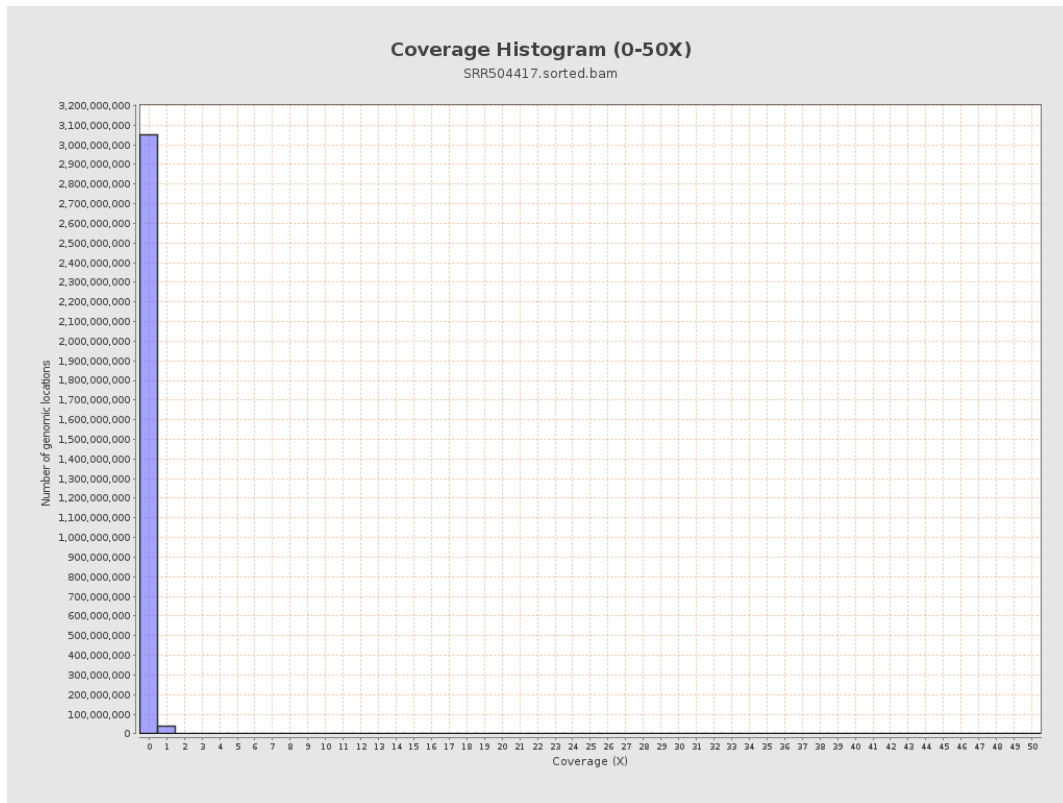
3. Results : Coverage across reference



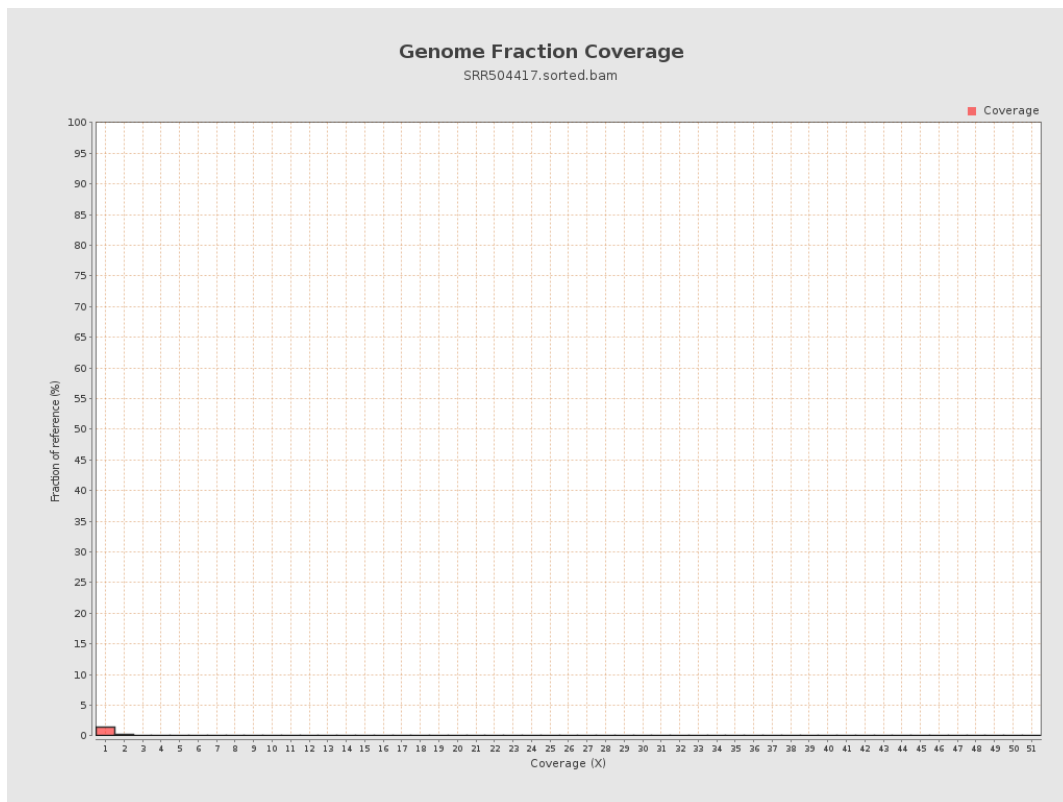
4. Results : Coverage Histogram



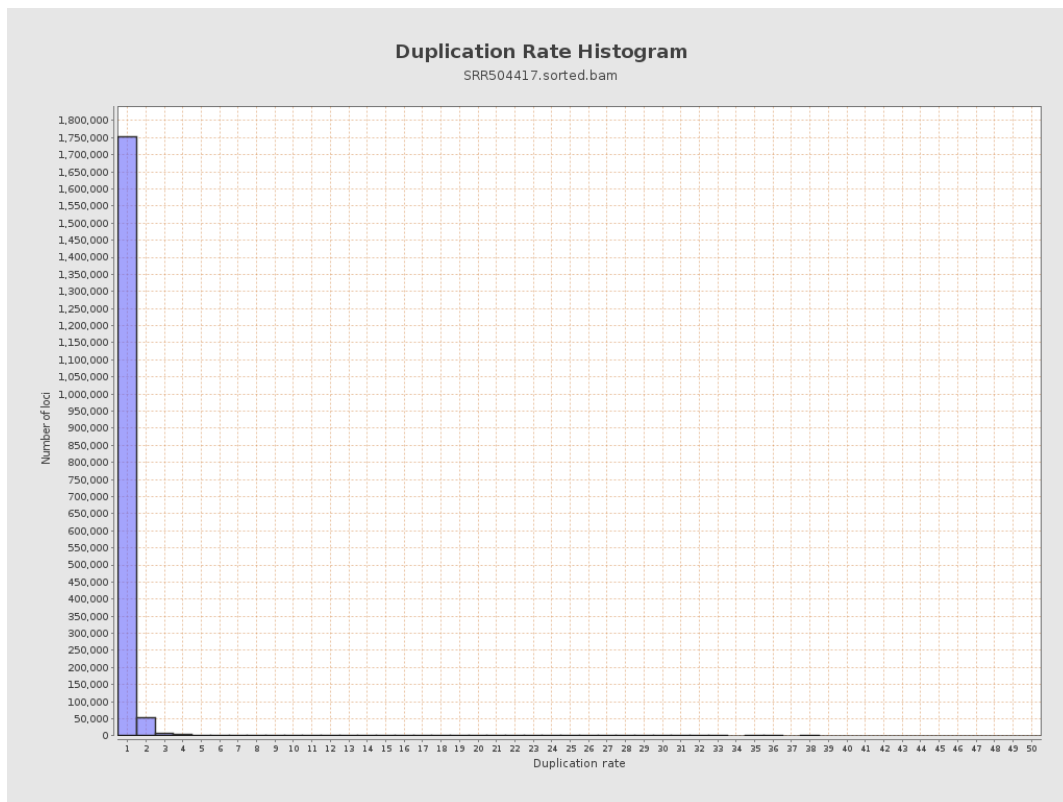
5. Results : Coverage Histogram (0-50X)



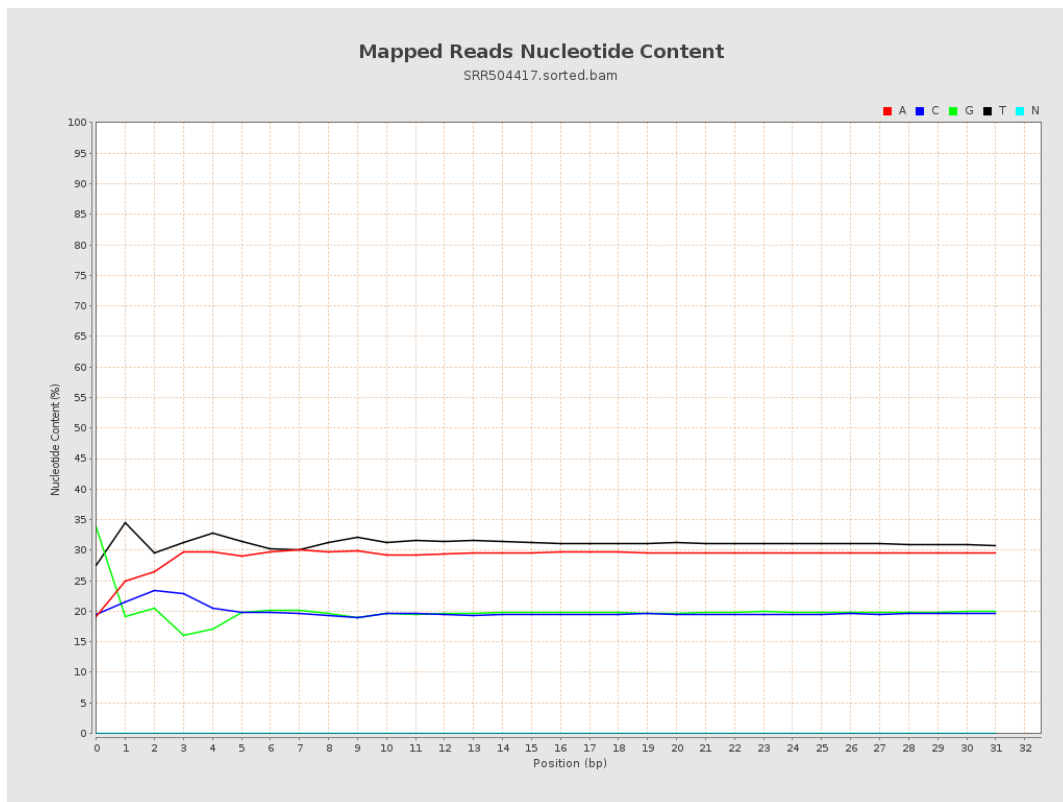
6. Results : Genome Fraction Coverage



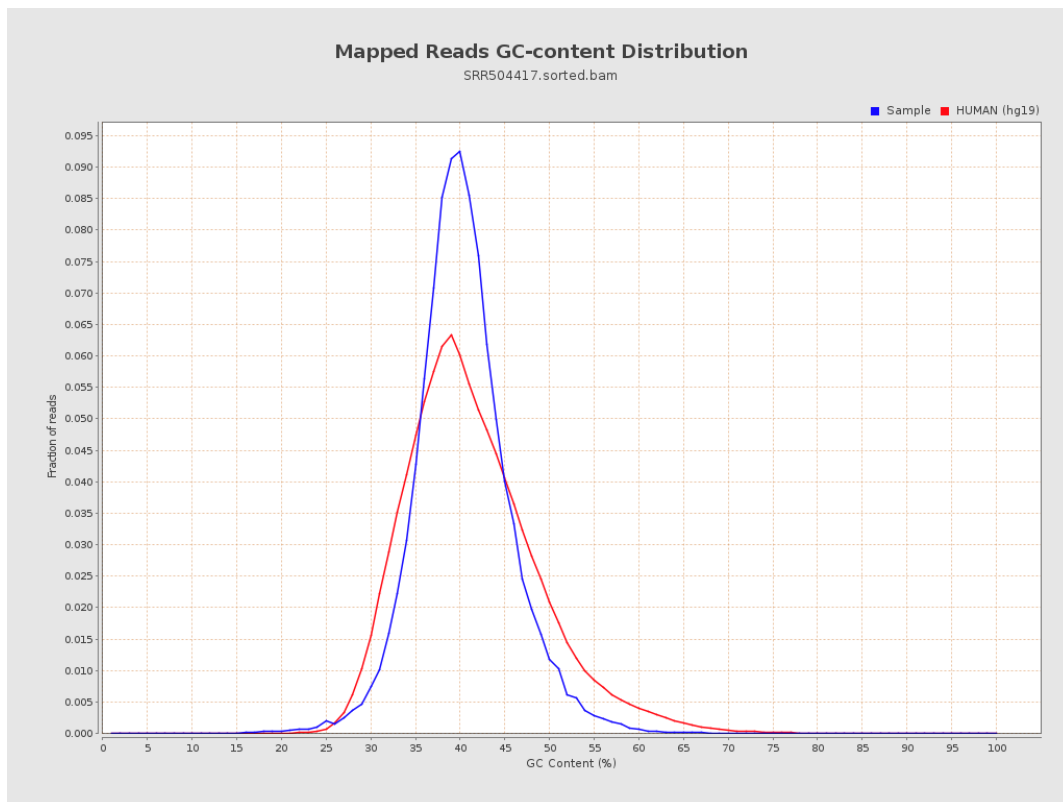
7. Results : Duplication Rate Histogram



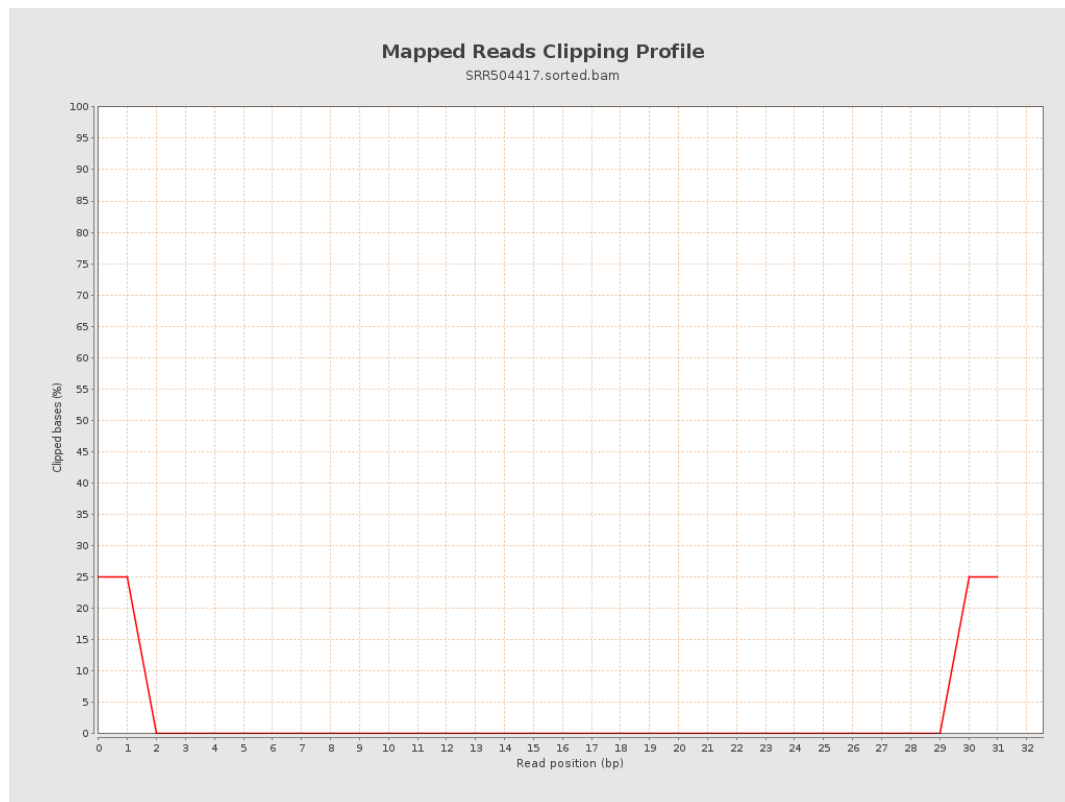
8. Results : Mapped Reads Nucleotide Content



9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Mapping Quality Across Reference



12. Results : Mapping Quality Histogram

