

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/06/23 07:44:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504415.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_SRR504415 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504415.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Jun 23 07:44:45 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504415.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,241,719
Mapped reads	1,897,583 / 84.65%
Unmapped reads	344,136 / 15.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	32 / 32 / 32
Duplicated reads (estimated)	64,311 / 2.87%
Duplication rate	2.84%
Clipped reads	3,083 / 0.14%

2.2. ACGT Content

Number/percentage of A's	17,551,426 / 28.91%
Number/percentage of C's	12,237,019 / 20.15%
Number/percentage of T's	18,688,118 / 30.78%
Number/percentage of G's	12,239,780 / 20.16%
Number/percentage of N's	147 / 0%
GC Percentage	40.31%

2.3. Coverage

Mean	0.0196
Standard Deviation	0.2429

2.4. Mapping Quality

Mean Mapping Quality	8.38
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2.5. Mismatches and indels

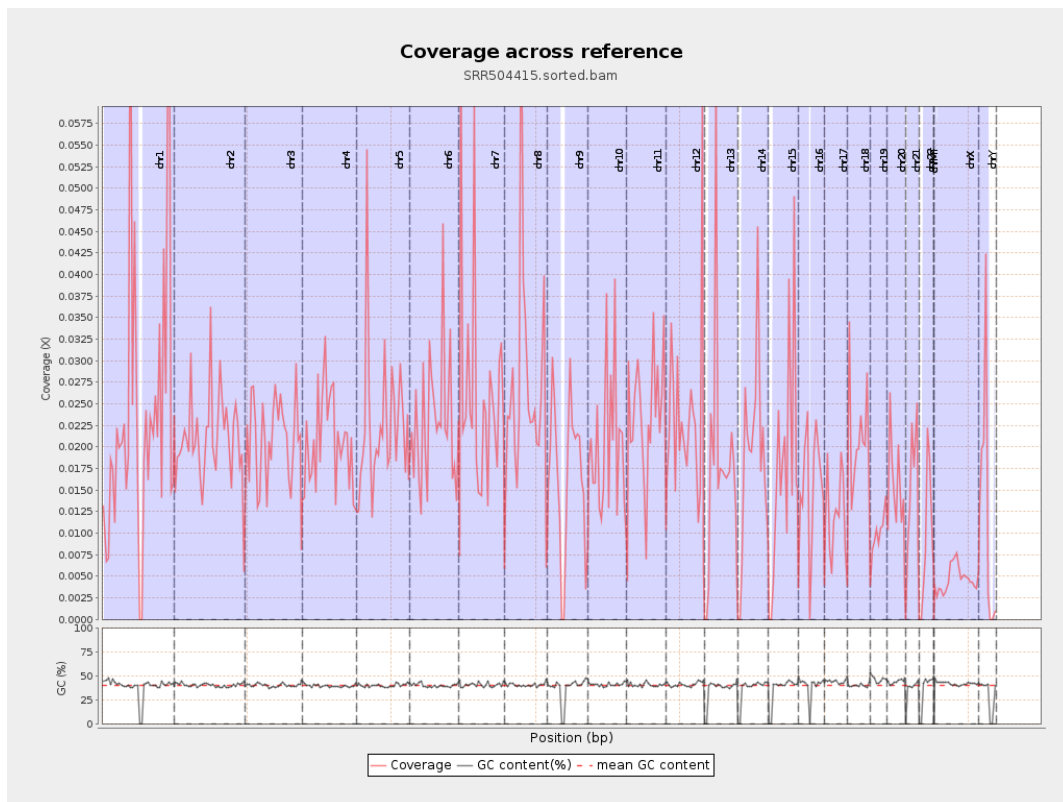
General error rate	0.05%
Mismatches	28,695

2.6. Chromosome stats

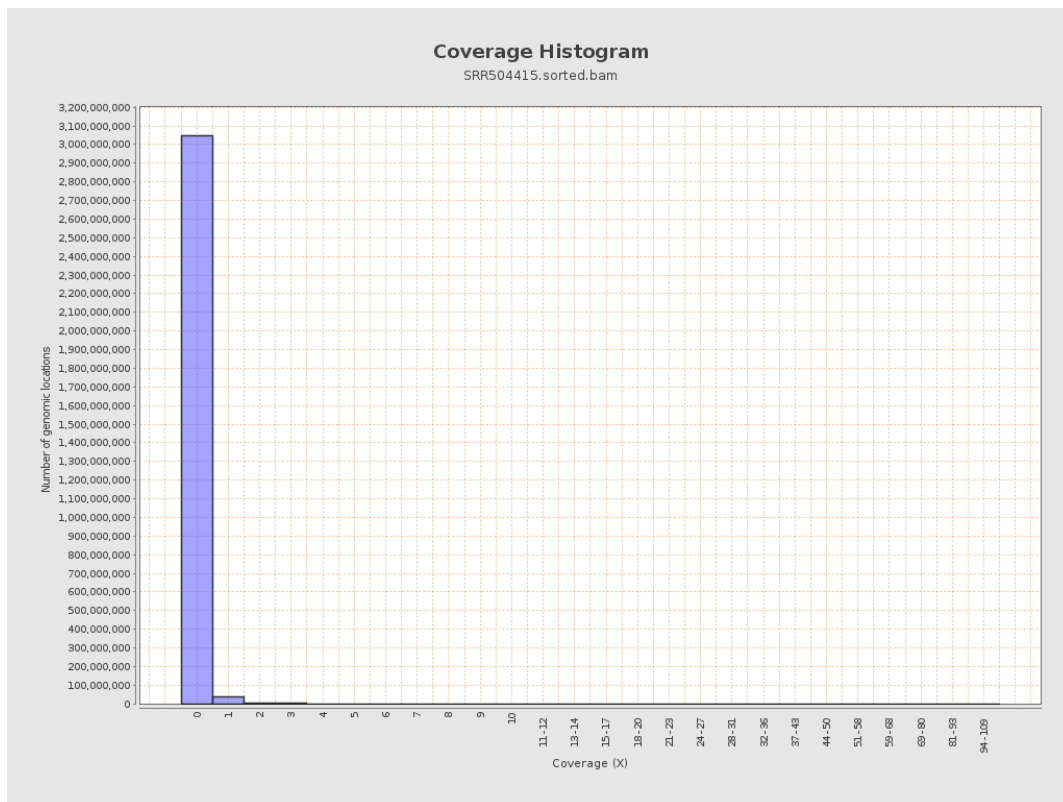
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5855356	0.0235	0.4085
chr2	243199373	5139370	0.0211	0.1793
chr3	198022430	4174684	0.0211	0.1781
chr4	191154276	3898544	0.0204	0.1798
chr5	180915260	4091234	0.0226	0.2235
chr6	171115067	3879144	0.0227	0.2193
chr7	159138663	4276824	0.0269	0.3406
chr8	146364022	3913880	0.0267	0.3465
chr9	141213431	2366614	0.0168	0.1648
chr10	135534747	2689226	0.0198	0.2147
chr11	135006516	3208196	0.0238	0.2264
chr12	133851895	3175930	0.0237	0.3262
chr13	115169878	2029980	0.0176	0.2437
chr14	107349540	1976824	0.0184	0.2449
chr15	102531392	1798104	0.0175	0.291

chr16	90354753	1368204	0.0151	0.168
chr17	81195210	978600	0.0121	0.1255
chr18	78077248	1675952	0.0215	0.2197
chr19	59128983	594162	0.01	0.1122
chr20	63025520	964734	0.0153	0.1581
chr21	48129895	707644	0.0147	0.1601
chr22	51304566	477268	0.0093	0.1185
chrMT	16571	0	0	0
chrX	155270560	734338	0.0047	0.0747
chrY	59373566	741678	0.0125	0.1529

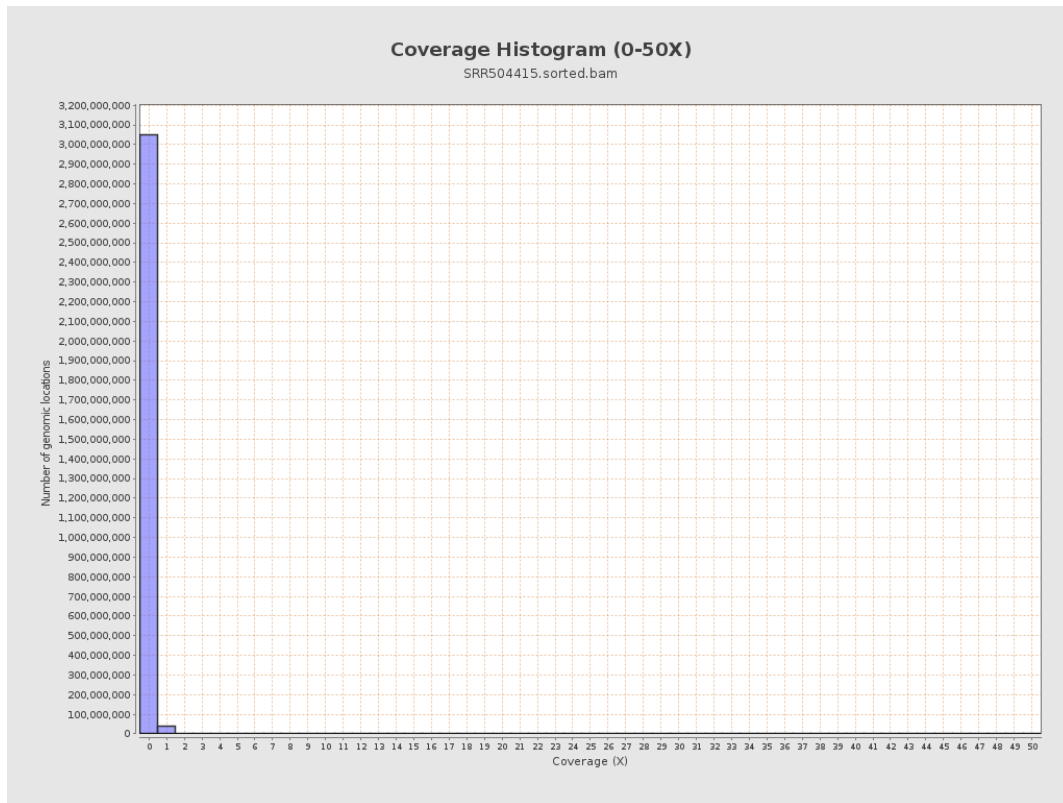
3. Results : Coverage across reference



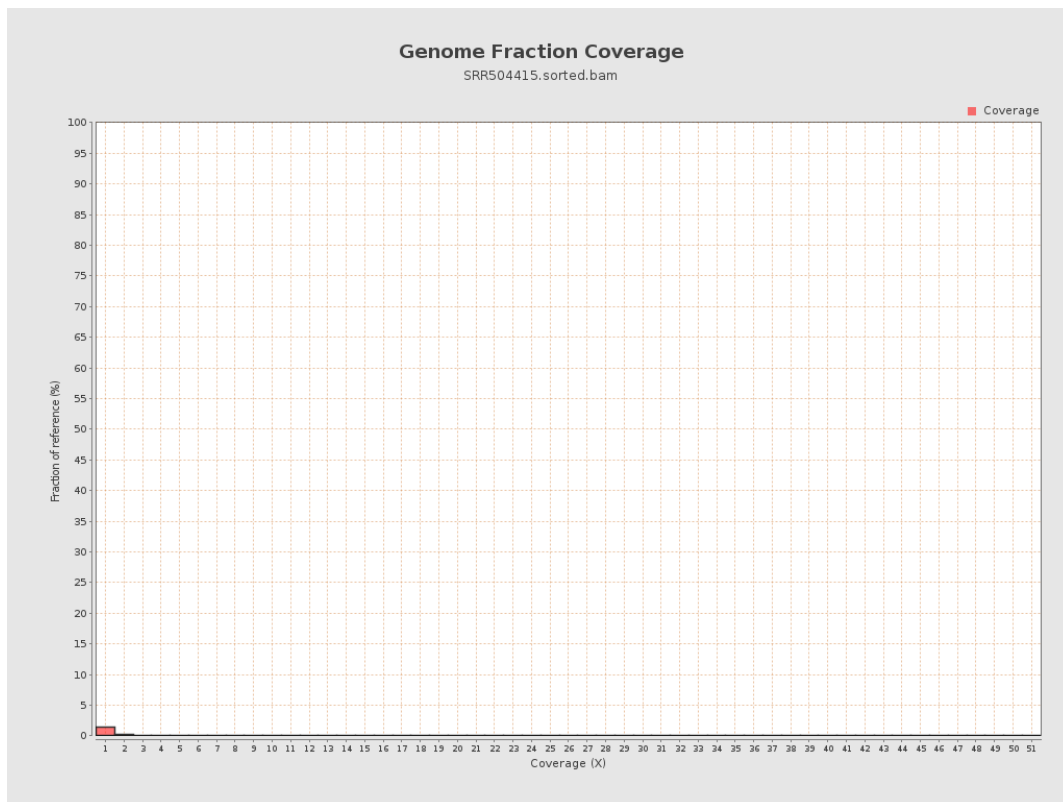
4. Results : Coverage Histogram



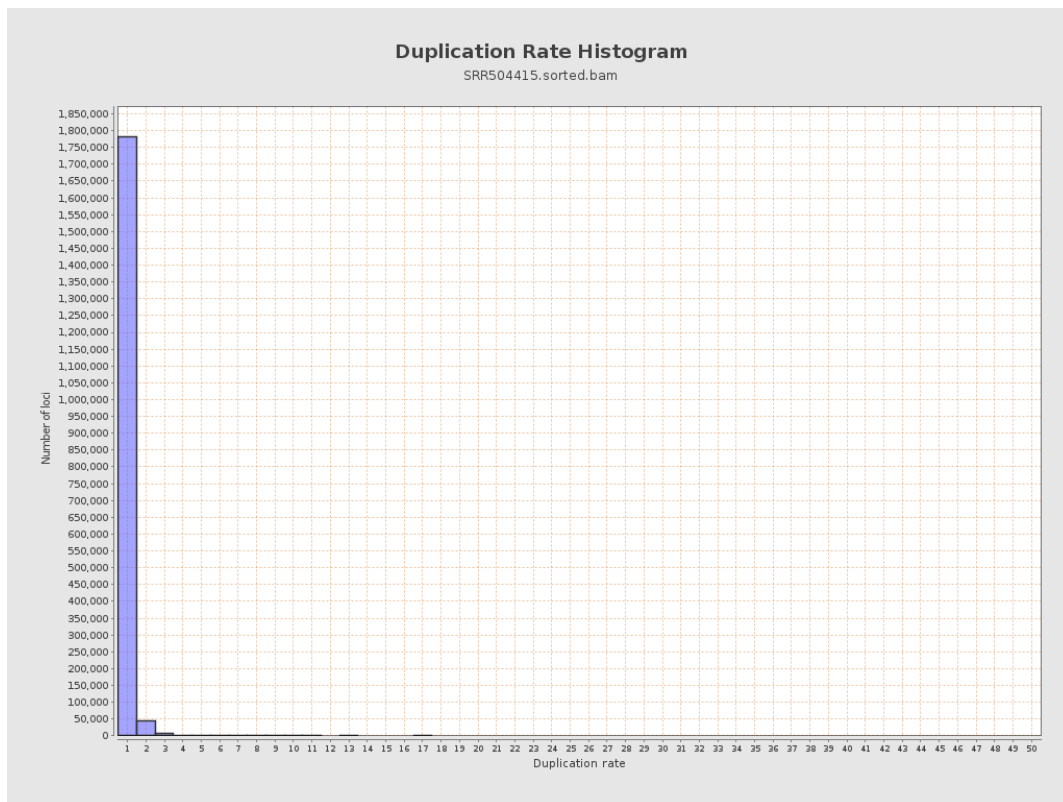
5. Results : Coverage Histogram (0-50X)



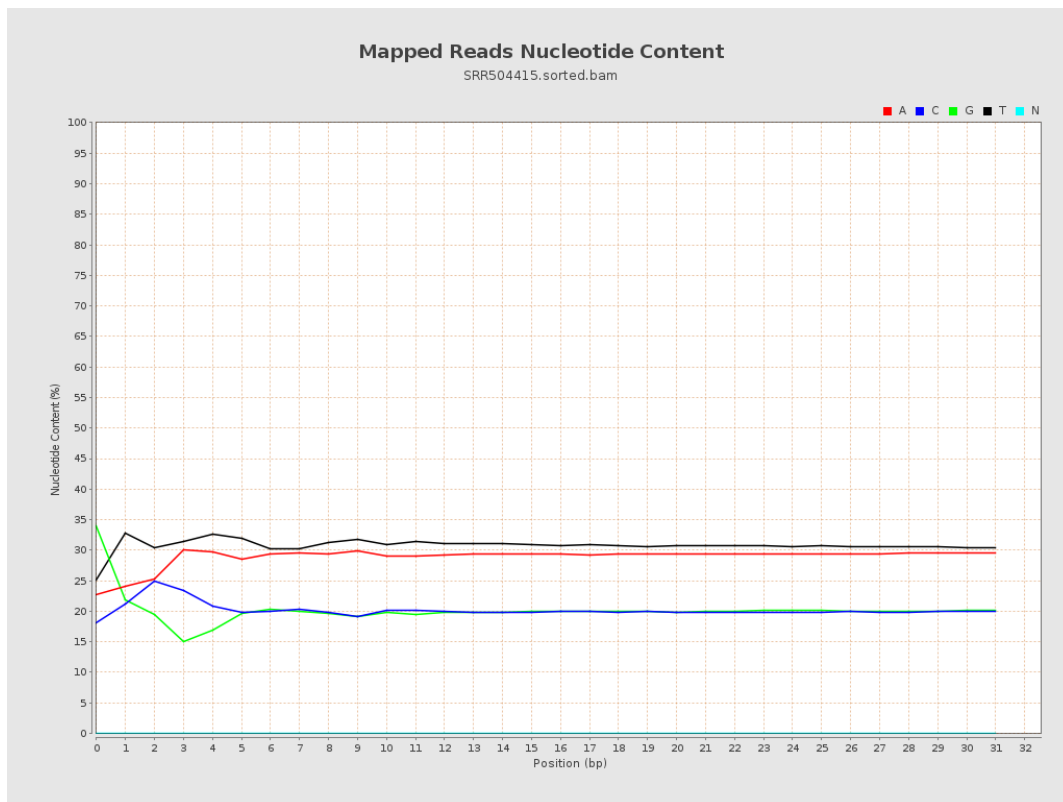
6. Results : Genome Fraction Coverage



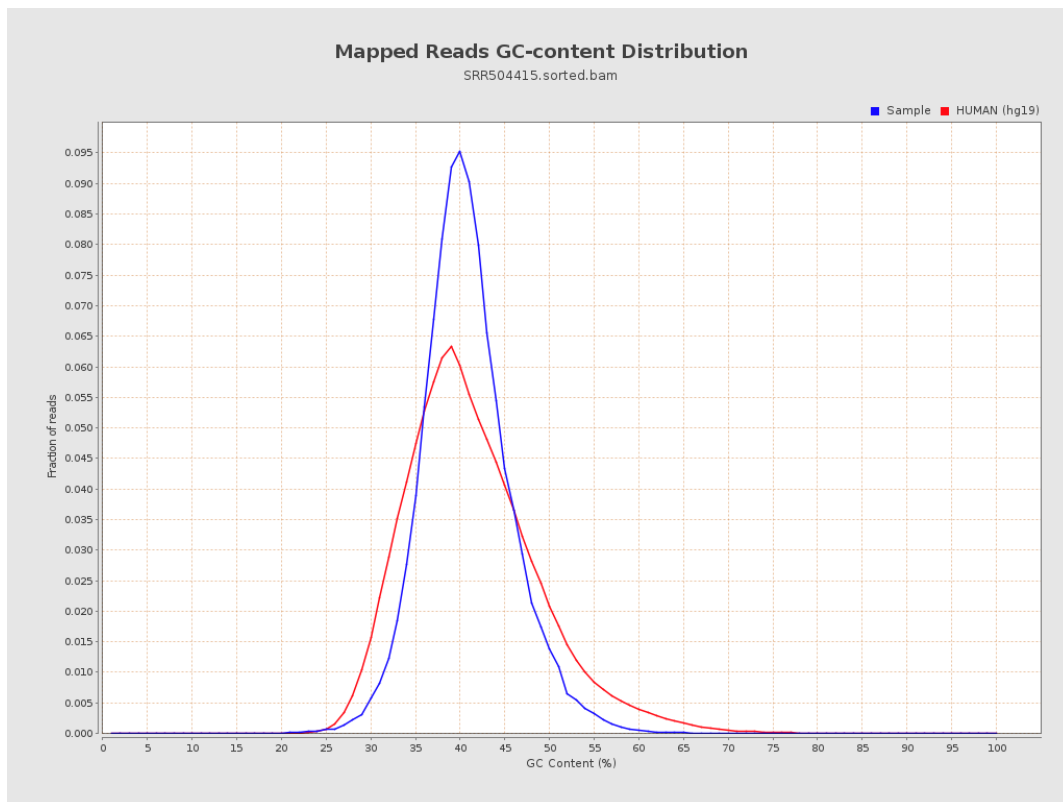
7. Results : Duplication Rate Histogram



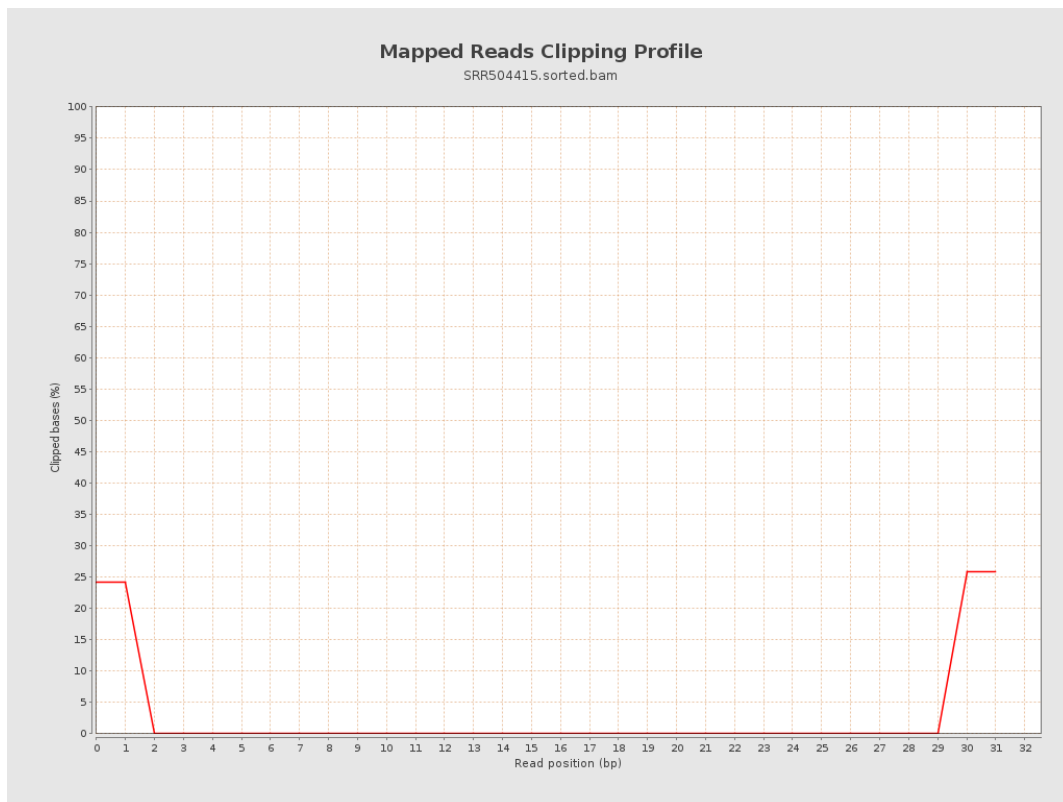
8. Results : Mapped Reads Nucleotide Content



9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Mapping Quality Across Reference



12. Results : Mapping Quality Histogram

