

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/06/23 19:18:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504425.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_SRR504425 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504425.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Jun 23 19:18:02 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504425.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,210,994
Mapped reads	1,947,631 / 88.09%
Unmapped reads	263,363 / 11.91%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	32 / 32 / 32
Duplicated reads (estimated)	106,071 / 4.8%
Duplication rate	3.86%
Clipped reads	3,025 / 0.14%

2.2. ACGT Content

Number/percentage of A's	18,032,241 / 28.94%
Number/percentage of C's	12,524,052 / 20.1%
Number/percentage of T's	19,208,791 / 30.82%
Number/percentage of G's	12,552,916 / 20.14%
Number/percentage of N's	142 / 0%
GC Percentage	40.24%

2.3. Coverage

Mean	0.0201
Standard Deviation	0.3315

2.4. Mapping Quality

Mean Mapping Quality	8.42
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2.5. Mismatches and indels

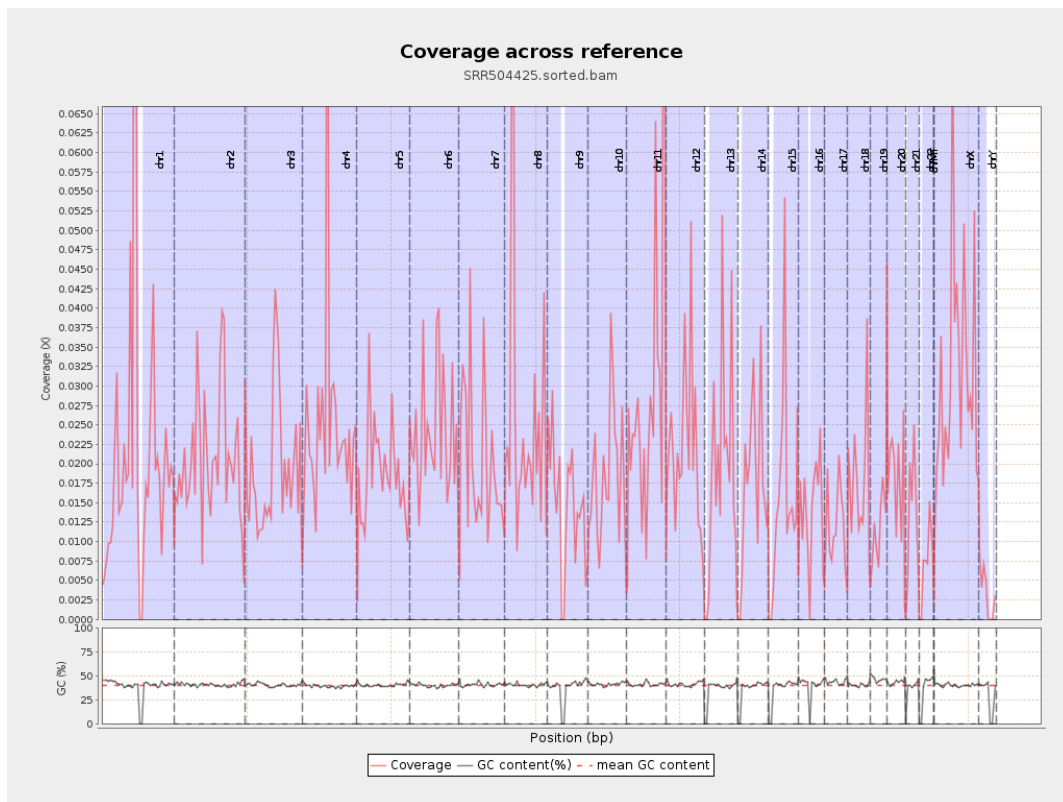
General error rate	0.04%
Mismatches	27,556

2.6. Chromosome stats

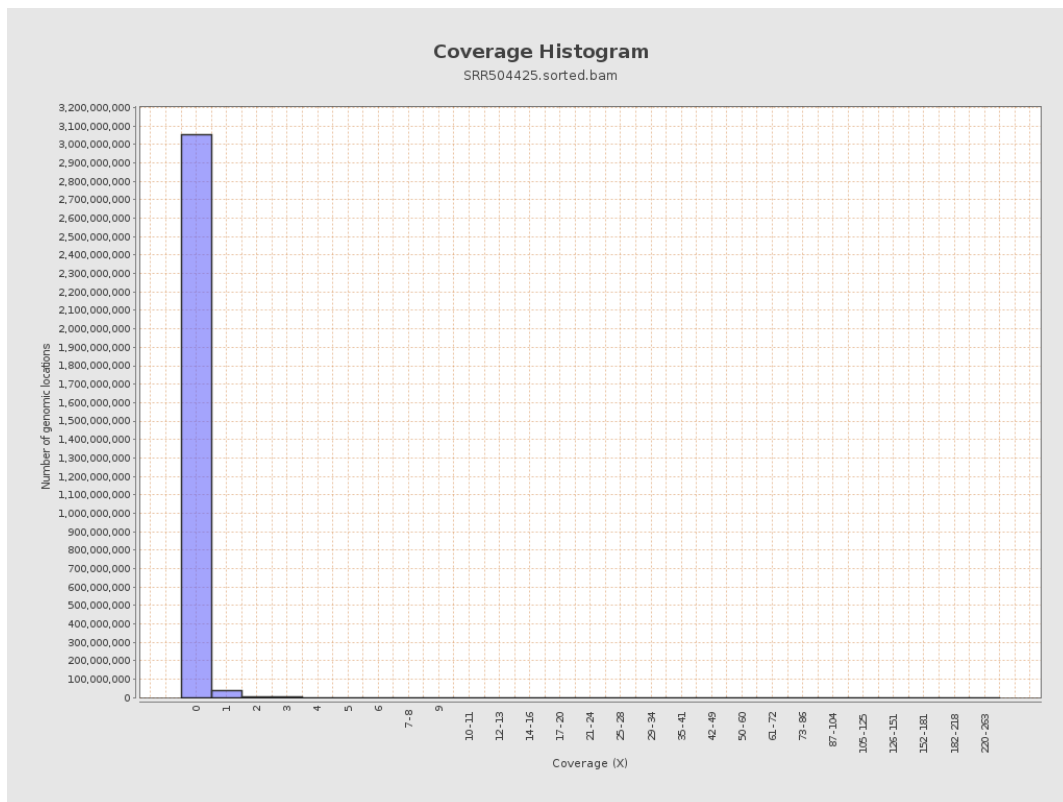
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5330986	0.0214	0.5112
chr2	243199373	5008830	0.0206	0.2464
chr3	198022430	3837920	0.0194	0.2118
chr4	191154276	4828390	0.0253	0.4995
chr5	180915260	3392032	0.0187	0.1823
chr6	171115067	4161308	0.0243	0.2614
chr7	159138663	3219182	0.0202	0.2557
chr8	146364022	3646920	0.0249	0.3694
chr9	141213431	2087998	0.0148	0.2011
chr10	135534747	2490166	0.0184	0.3376
chr11	135006516	4120372	0.0305	0.7359
chr12	133851895	2895806	0.0216	0.2564
chr13	115169878	2183938	0.019	0.3701
chr14	107349540	1859612	0.0173	0.1853
chr15	102531392	1593182	0.0155	0.2248

chr16	90354753	1231926	0.0136	0.1414
chr17	81195210	966066	0.0119	0.1336
chr18	78077248	1430416	0.0183	0.1917
chr19	59128983	742382	0.0126	0.1722
chr20	63025520	1150100	0.0182	0.1878
chr21	48129895	621184	0.0129	0.1497
chr22	51304566	364548	0.0071	0.1026
chrMT	16571	32	0.0019	0.0439
chrX	155270560	4959462	0.0319	0.3187
chrY	59373566	195384	0.0033	0.0655

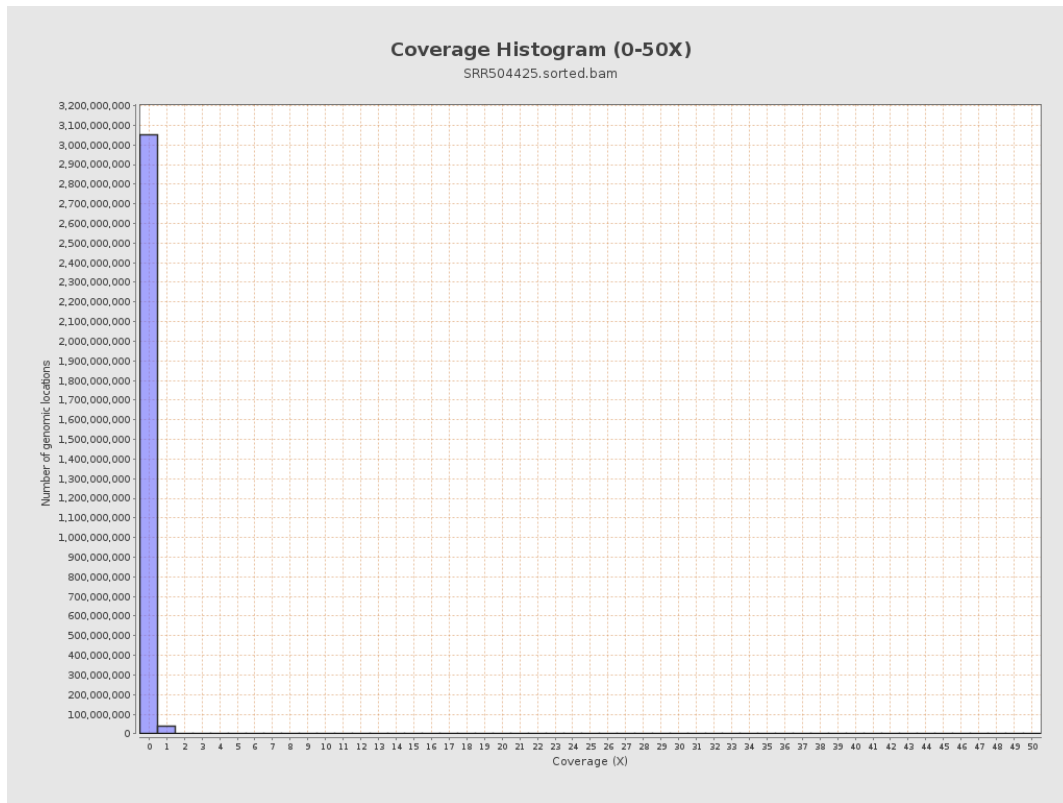
3. Results : Coverage across reference



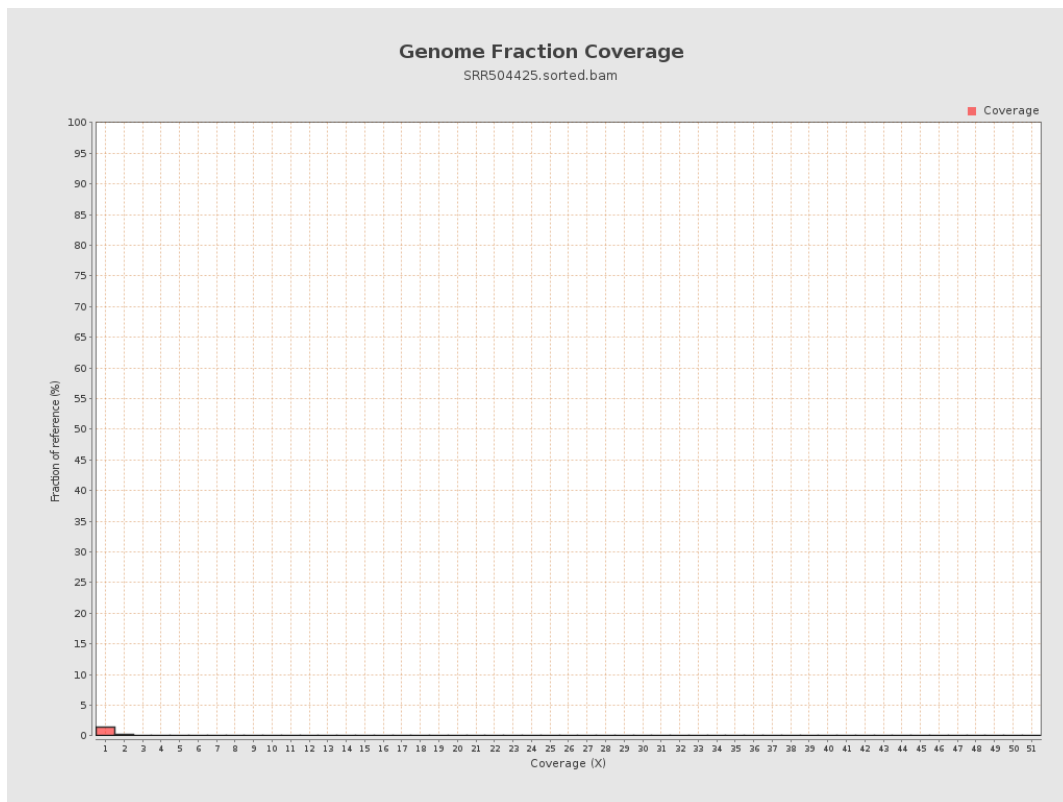
4. Results : Coverage Histogram



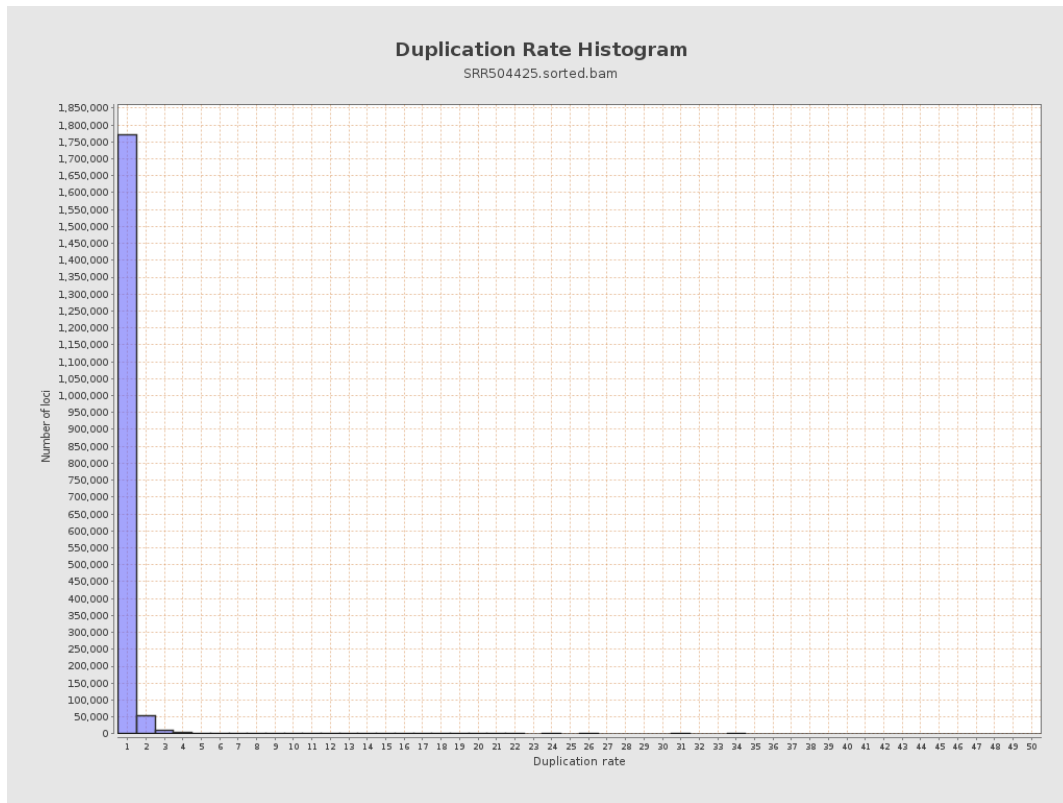
5. Results : Coverage Histogram (0-50X)



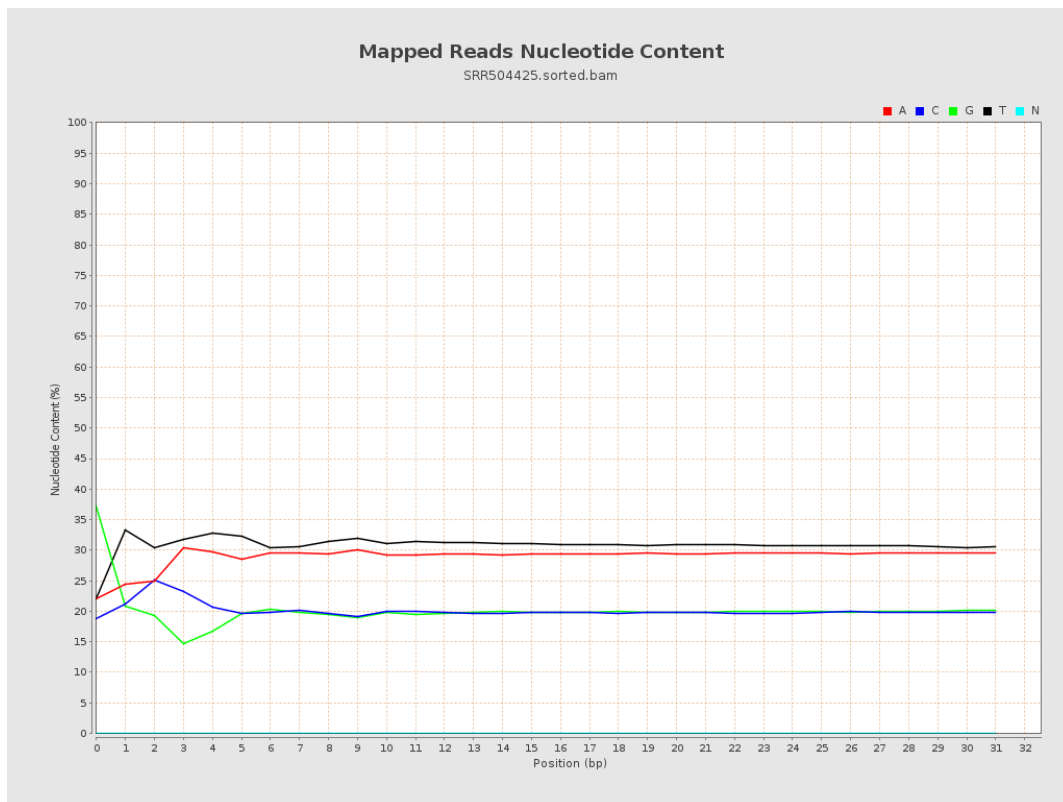
6. Results : Genome Fraction Coverage



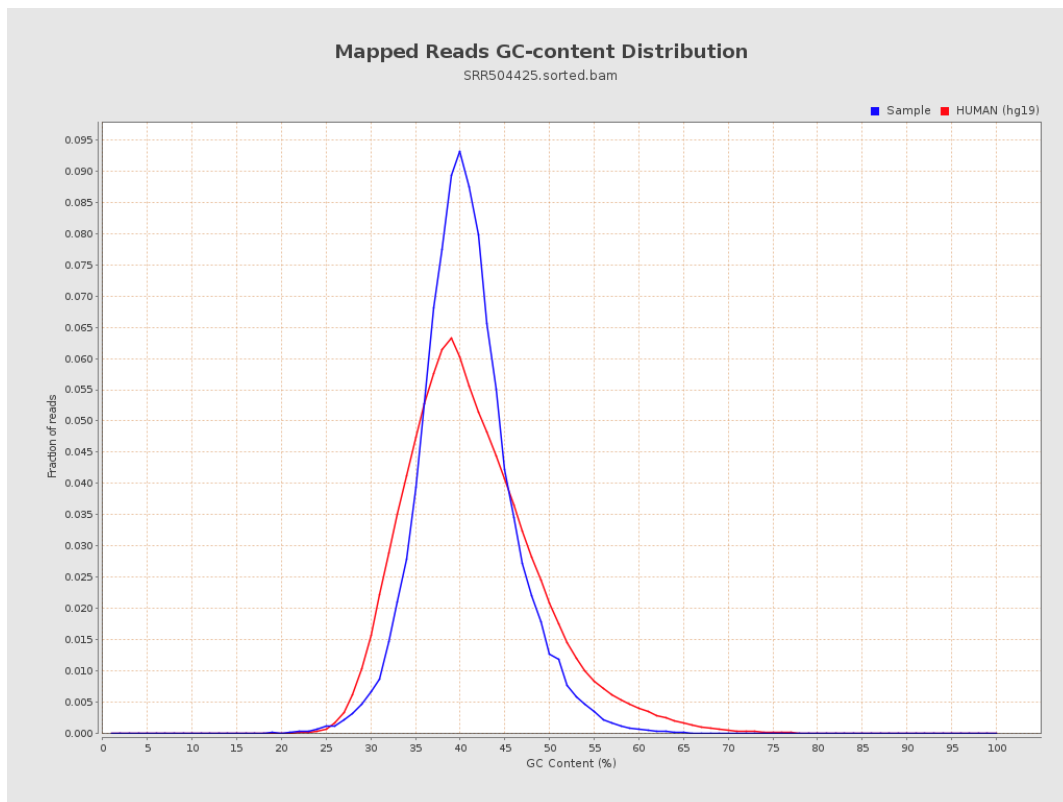
7. Results : Duplication Rate Histogram



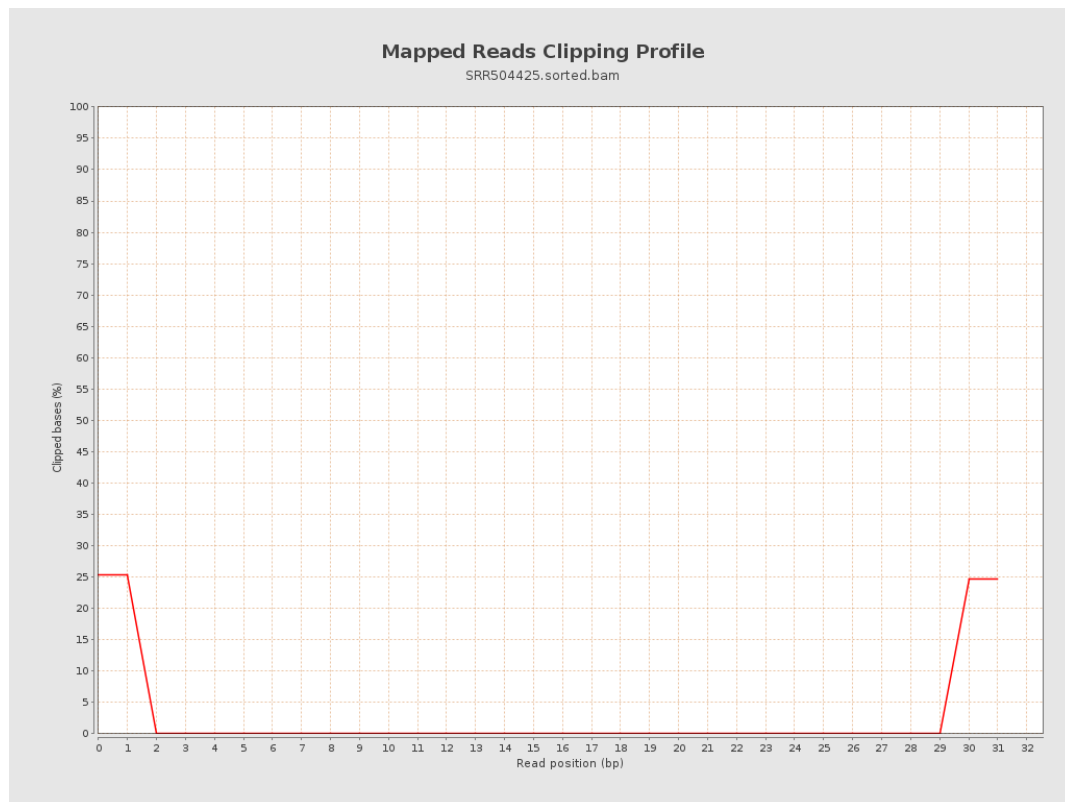
8. Results : Mapped Reads Nucleotide Content



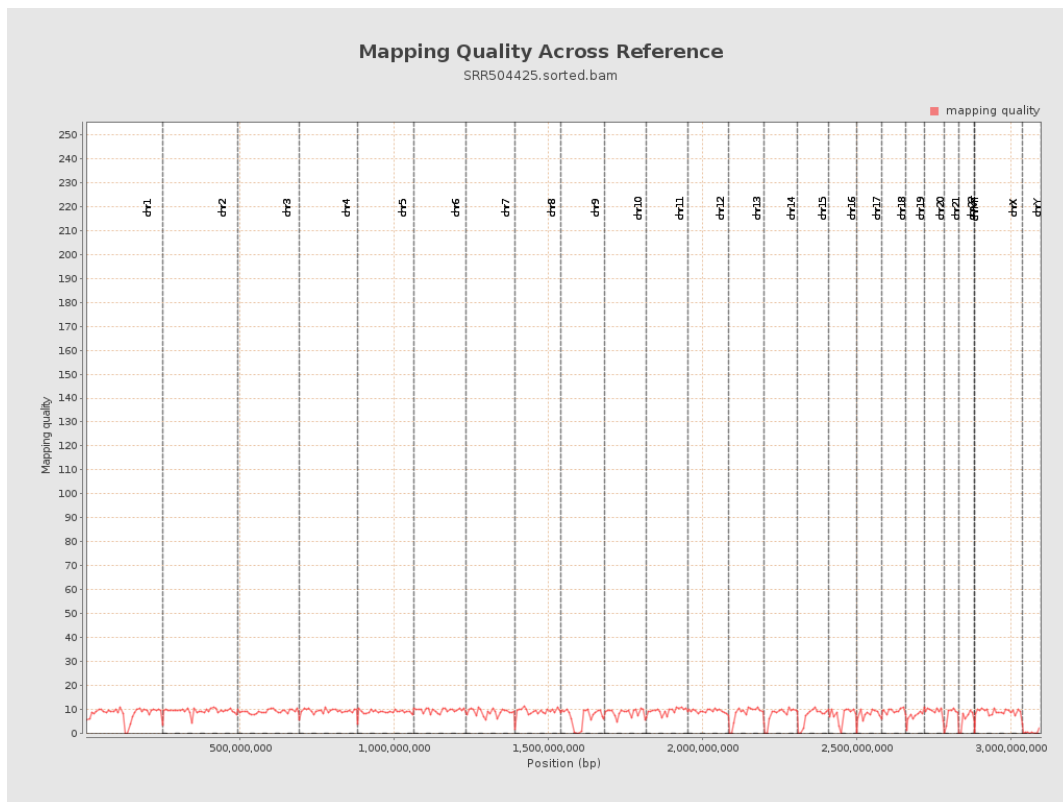
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Mapping Quality Across Reference



12. Results : Mapping Quality Histogram

