Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/19 01:39:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR536764.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_SRR536764 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR536764.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Mar 19 01:39:03 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR536764.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	21,223,508
Mapped reads	20,717,106 / 97.61%
Unmapped reads	506,402 / 2.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	519 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	211,412 / 1%
Duplication rate	1.01%
Clipped reads	258,078 / 1.22%

2.2. ACGT Content

Number/percentage of A's	314,518,533 / 30.43%
Number/percentage of C's	200,195,520 / 19.37%
Number/percentage of T's	313,959,545 / 30.38%
Number/percentage of G's	204,750,368 / 19.81%
Number/percentage of N's	36,571 / 0%
GC Percentage	39.18%

2.3. Coverage

Mean	0.3339

Standard Deviation	0.6745

2.4. Mapping Quality

Mean Mapping Quality	46.41

2.5. Mismatches and indels

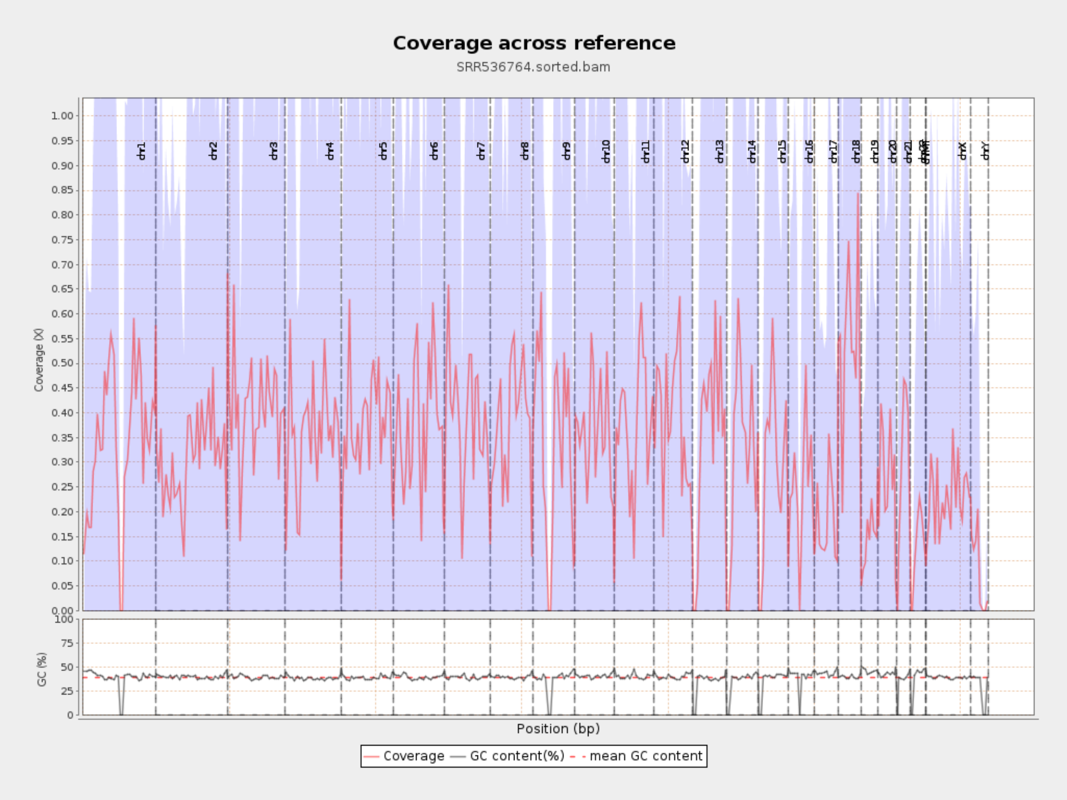
General error rate	0.21%
Mismatches	2,111,282
Insertions	64,816
Mapped reads with at least one insertion	0.31%
Deletions	57,200
Mapped reads with at least one deletion	0.28%
Homopolymer indels	48.85%

2.6. Chromosome stats

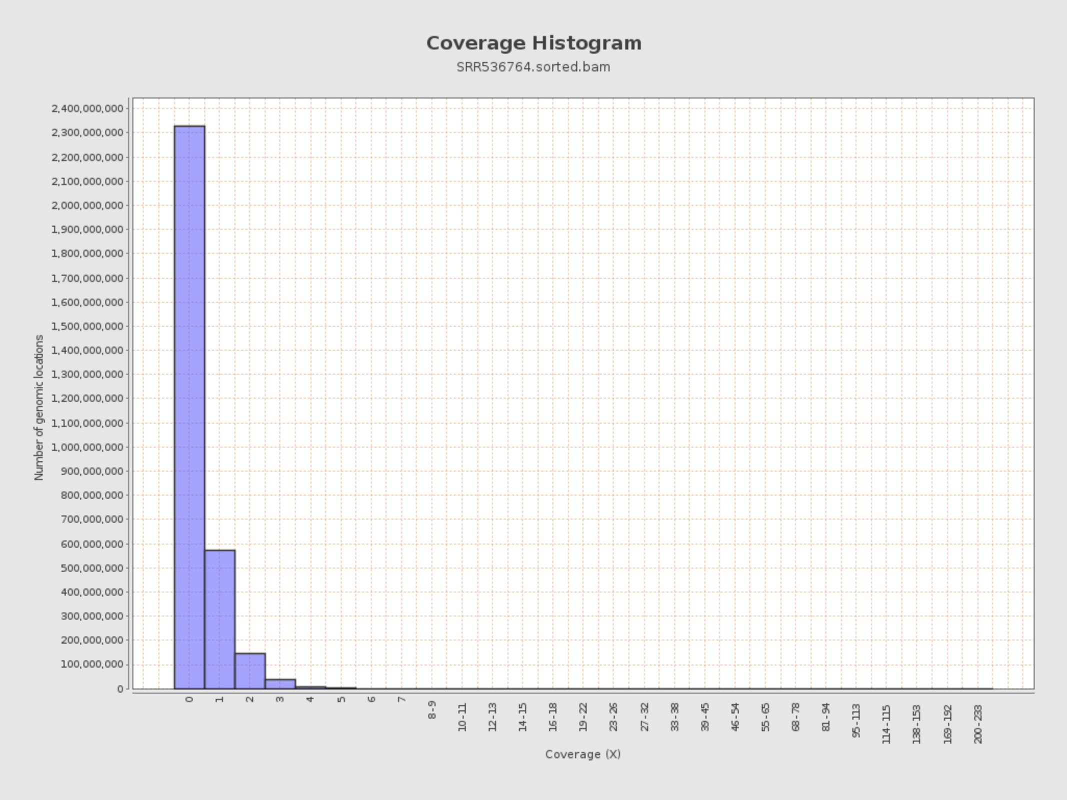
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	85556493	0.3433	0.6918
chr2	243199373	74646467	0.3069	0.6344
chr3	198022430	81360628	0.4109	0.7374
chr4	191154276	68392940	0.3578	0.6824
chr5	180915260	67723622	0.3743	0.6992
chr6	171115067	64799743	0.3787	0.7083
chr7	159138663	61493500	0.3864	0.7254

chr8	146364022	56369381	0.3851	0.7137
chr9	141213431	48542042	0.3437	0.6976
chr10	135534747	49892677	0.3681	0.6945
chr11	135006516	50528713	0.3743	0.7226
chr12	133851895	51231405	0.3827	0.7178
chr13	115169878	40667121	0.3531	0.6931
chr14	107349540	35074516	0.3267	0.6724
chr15	102531392	29739239	0.2901	0.6321
chr16	90354753	22083545	0.2444	0.5697
chr17	81195210	15069200	0.1856	0.4974
chr18	78077248	42688529	0.5467	0.8623
chr19	59128983	8844630	0.1496	0.4336
chr20	63025520	17886708	0.2838	0.614
chr21	48129895	13796819	0.2867	0.6486
chr22	51304566	6717185	0.1309	0.414
chrMT	16571	1496	0.0903	0.2967
chrX	155270560	35757220	0.2303	0.5425
chrY	59373566	4693064	0.079	0.3308

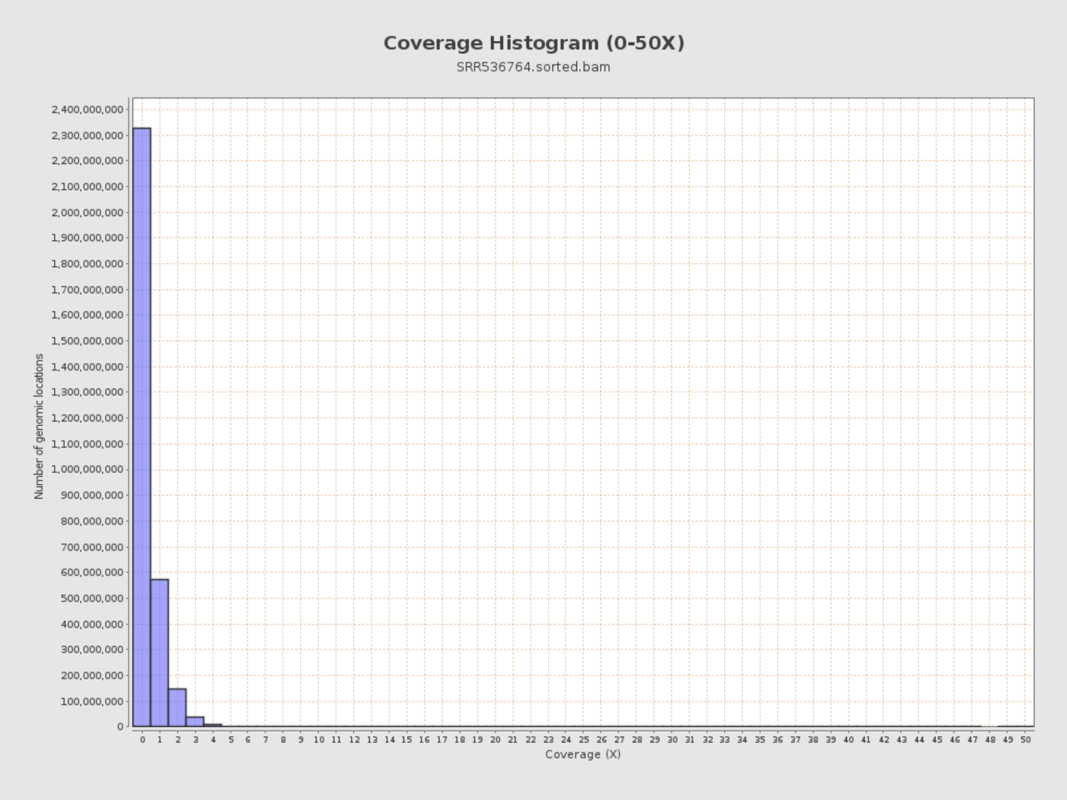
3. Results : Coverage across reference



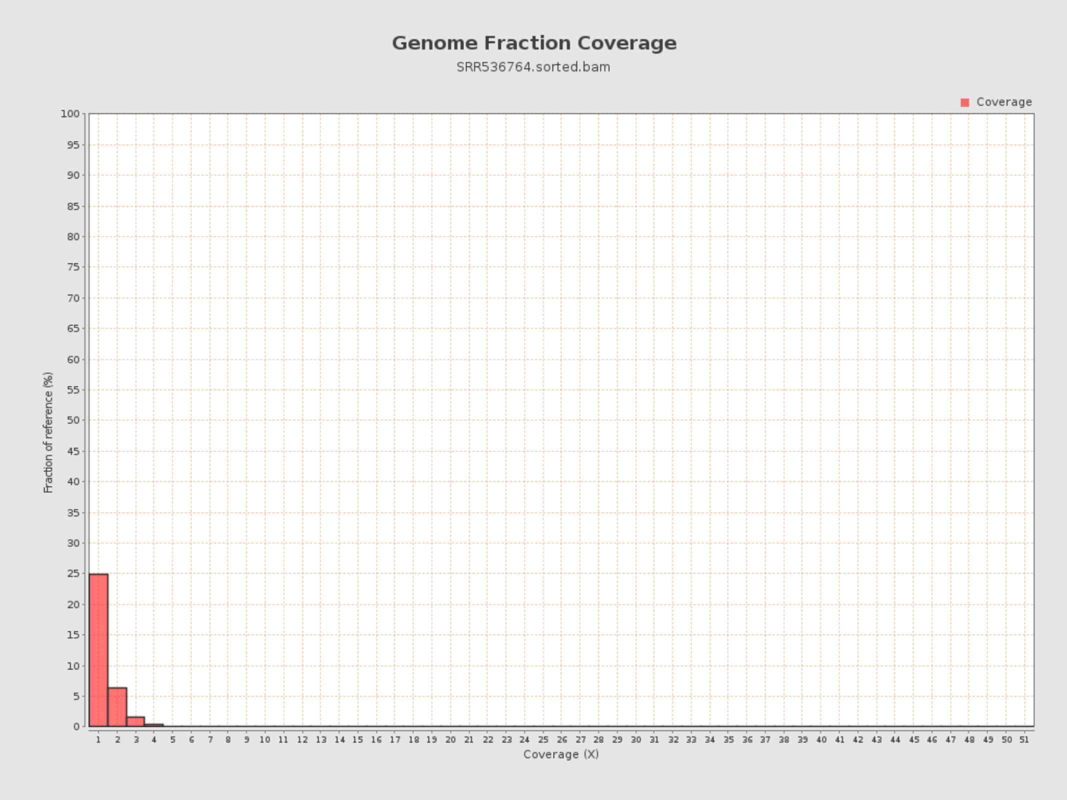
4. Results : Coverage Histogram



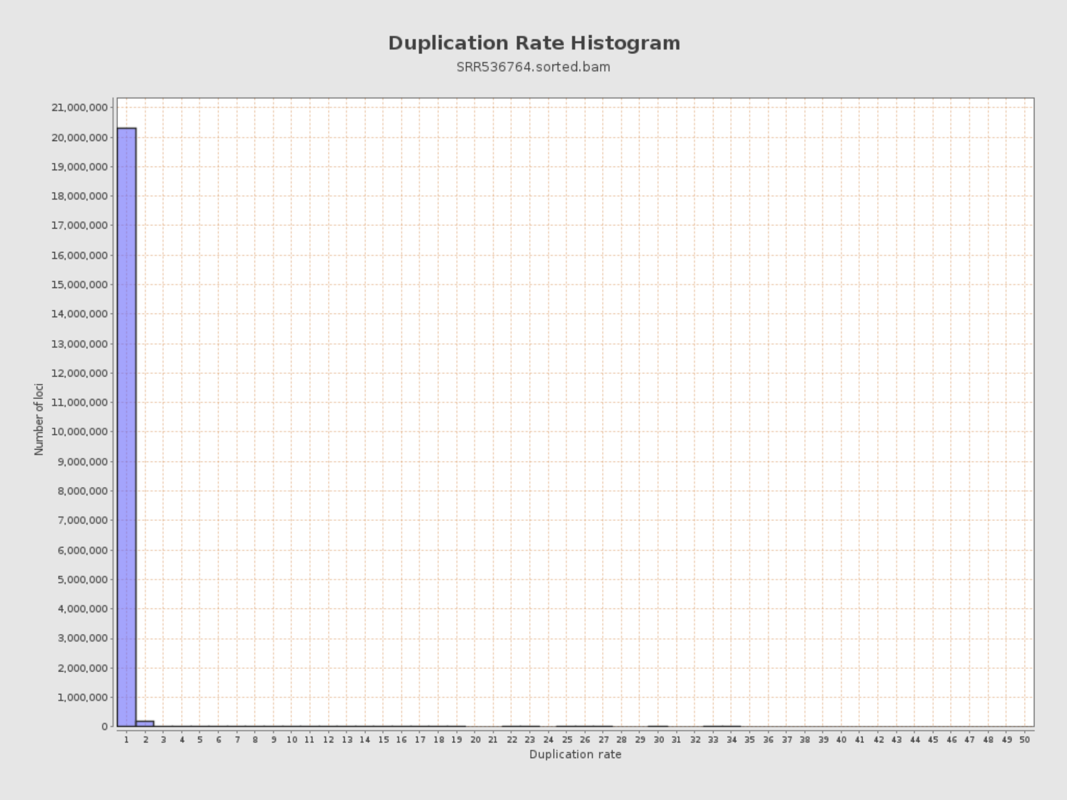
5. Results : Coverage Histogram (0-50X)



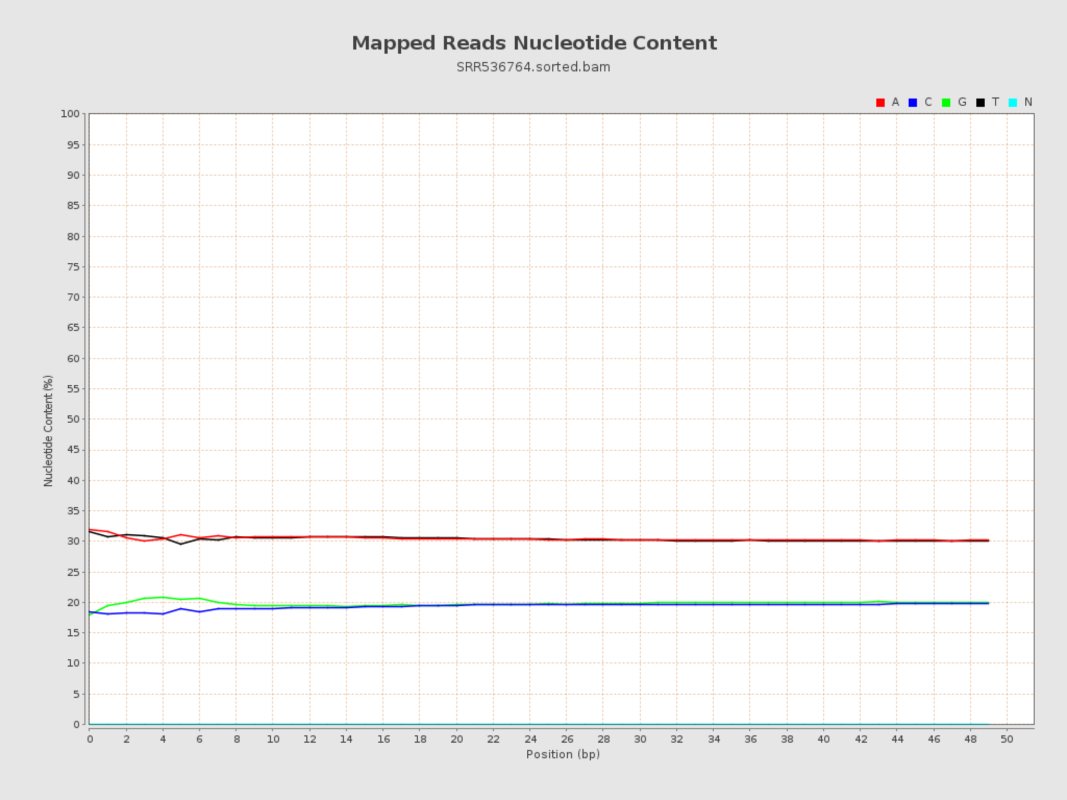
6. Results : Genome Fraction Coverage



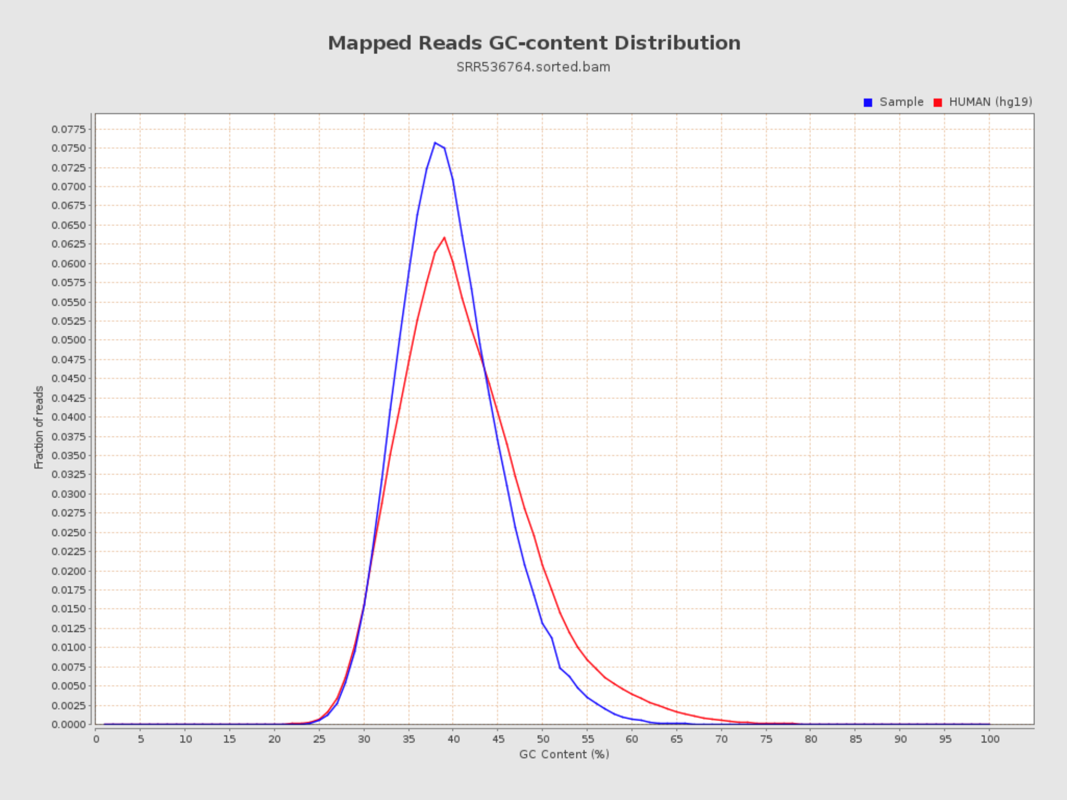
7. Results : Duplication Rate Histogram



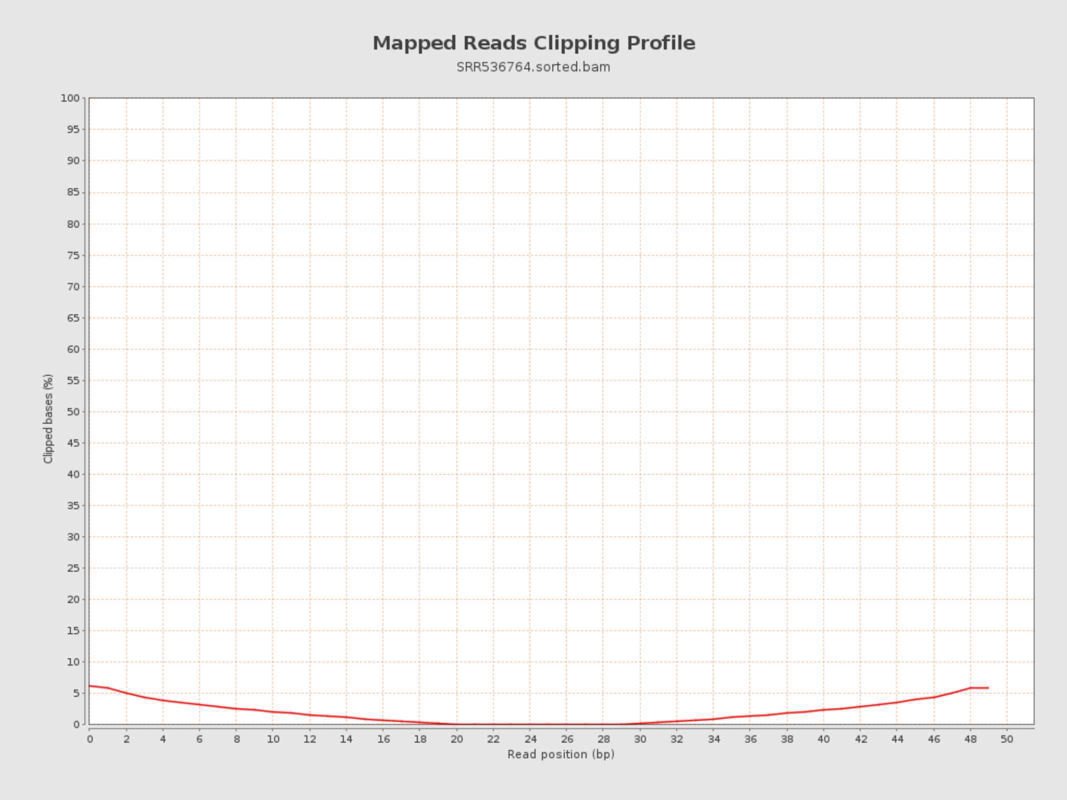
8. Results : Mapped Reads Nucleotide Content



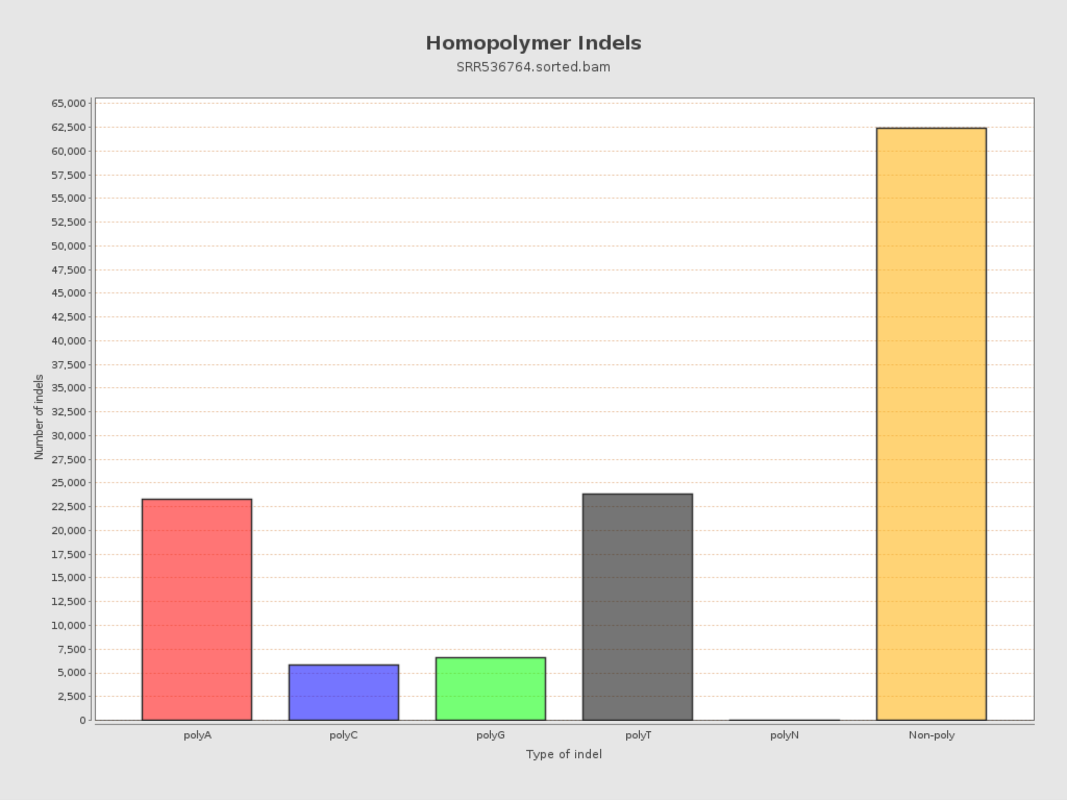
9. Results : Mapped Reads GC-content Distribution



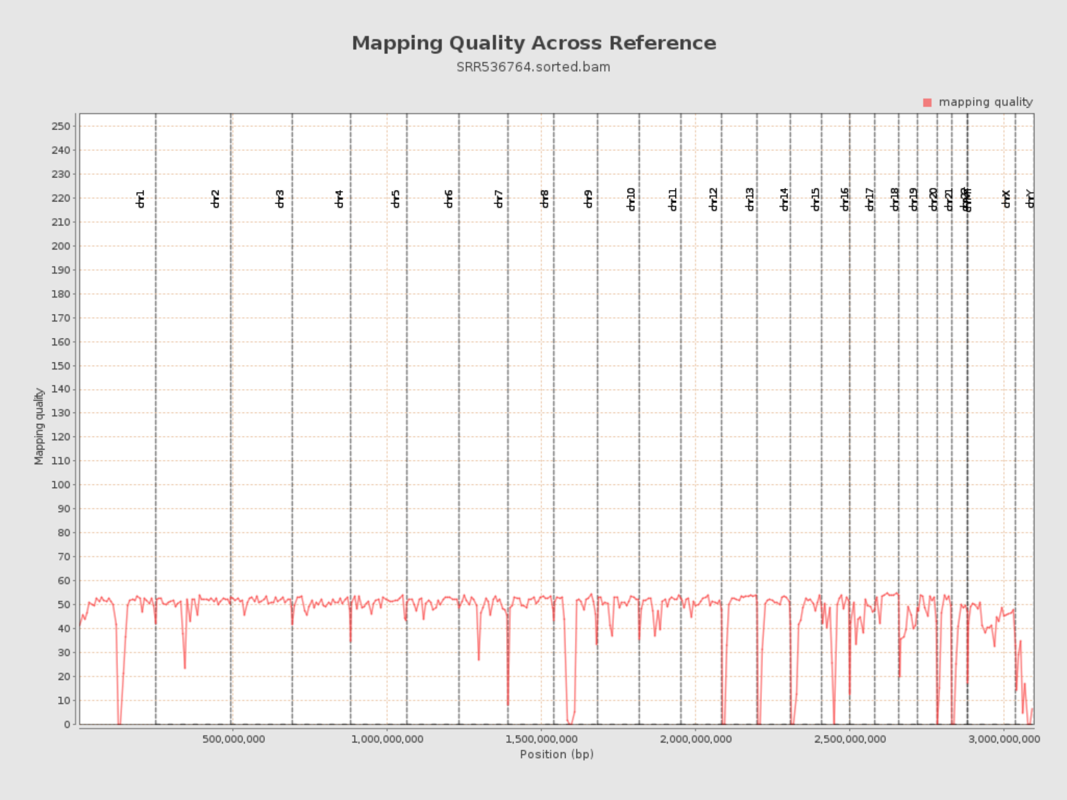
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram