Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/19 01:16:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR536763.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_SRR536763 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR536763.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Mar 19 01:16:34 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR536763.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	22,948,608
Mapped reads	22,381,330 / 97.53%
Unmapped reads	567,278 / 2.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	550 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	248,709 / 1.08%
Duplication rate	1.1%
Clipped reads	282,976 / 1.23%

2.2. ACGT Content

Number/percentage of A's	339,236,108 / 30.39%
Number/percentage of C's	217,270,141 / 19.46%
Number/percentage of T's	337,612,816 / 30.24%
Number/percentage of G's	222,281,713 / 19.91%
Number/percentage of N's	39,190 / 0%
GC Percentage	39.37%

2.3. Coverage

Mean	0.3607

Standard Deviation	0.7086

2.4. Mapping Quality

Mean Mapping Quality	46.33

2.5. Mismatches and indels

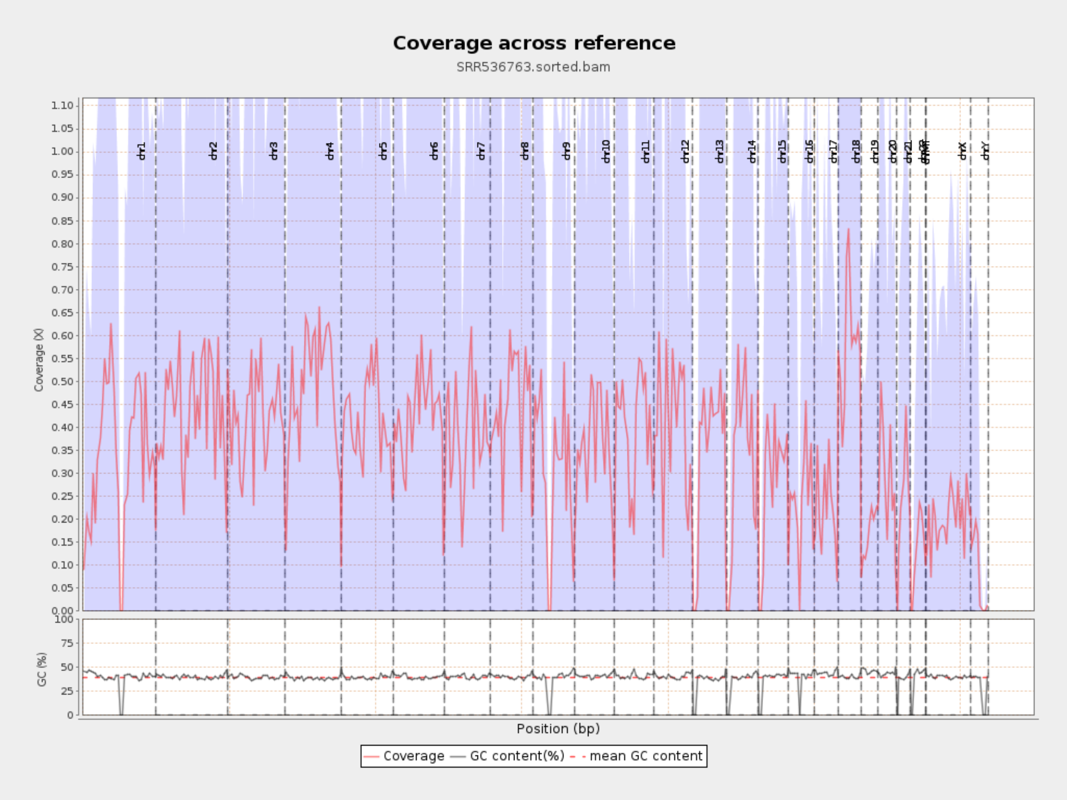
General error rate	0.22%
Mismatches	2,317,689
Insertions	68,296
Mapped reads with at least one insertion	0.3%
Deletions	60,483
Mapped reads with at least one deletion	0.27%
Homopolymer indels	48.68%

2.6. Chromosome stats

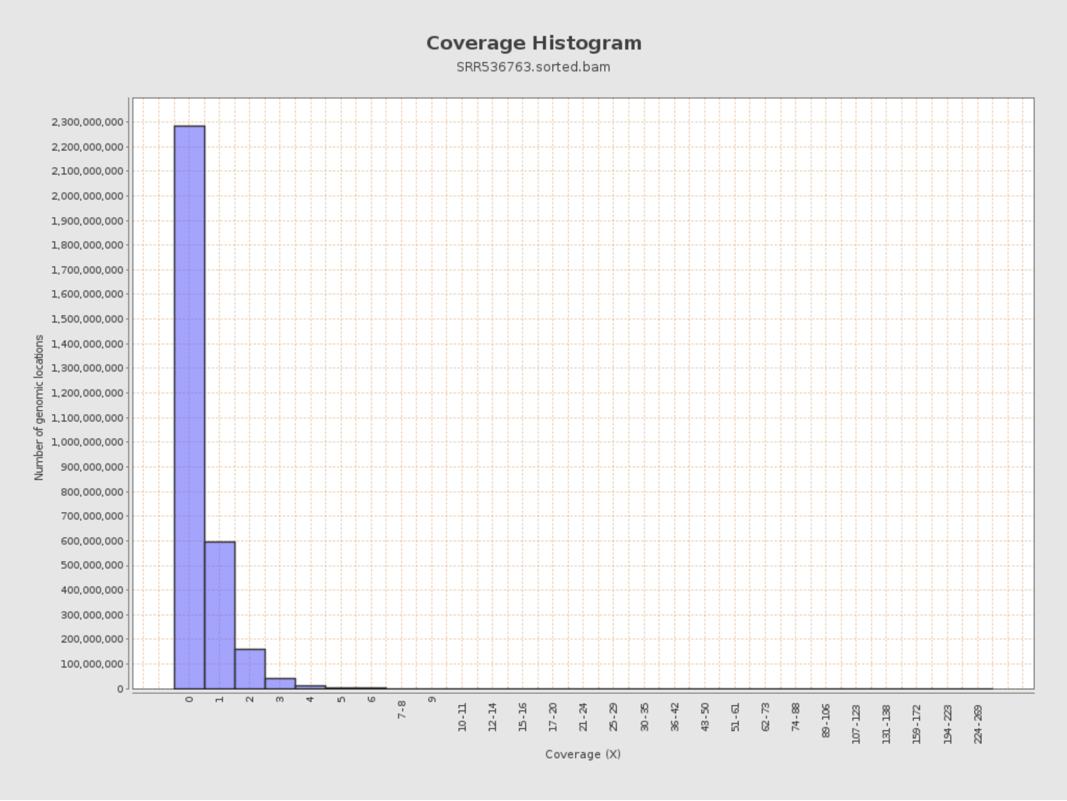
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	83875529	0.3365	0.6973
chr2	243199373	105997325	0.4358	0.7686
chr3	198022430	83836836	0.4234	0.7492
chr4	191154276	93418708	0.4887	0.8137
chr5	180915260	75076012	0.415	0.7403
chr6	171115067	73742271	0.431	0.7563
chr7	159138663	61111530	0.384	0.7253

chr8	146364022	65364720	0.4466	0.7762
chr9	141213431	43669885	0.3092	0.6557
chr10	135534747	49293710	0.3637	0.6942
chr11	135006516	53254766	0.3945	0.7427
chr12	133851895	54485416	0.4071	0.7465
chr13	115169878	40682594	0.3532	0.6973
chr14	107349540	35136856	0.3273	0.6793
chr15	102531392	28638930	0.2793	0.6288
chr16	90354753	21370333	0.2365	0.5694
chr17	81195210	18496183	0.2278	0.5484
chr18	78077248	45723129	0.5856	0.9139
chr19	59128983	10057696	0.1701	0.4659
chr20	63025520	18838391	0.2989	0.6399
chr21	48129895	11567565	0.2403	0.5945
chr22	51304566	6824922	0.133	0.4265
chrMT	16571	2371	0.1431	0.4056
chrX	155270560	31130546	0.2005	0.5099
chrY	59373566	4945872	0.0833	0.3406

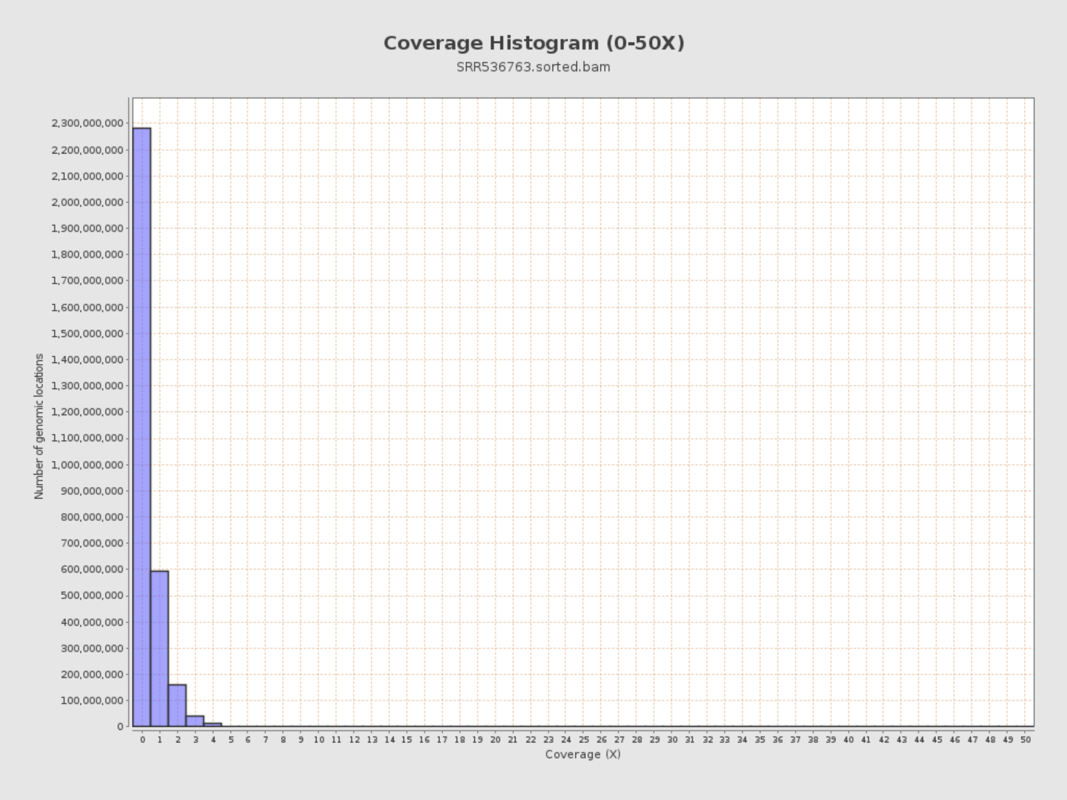
3. Results : Coverage across reference



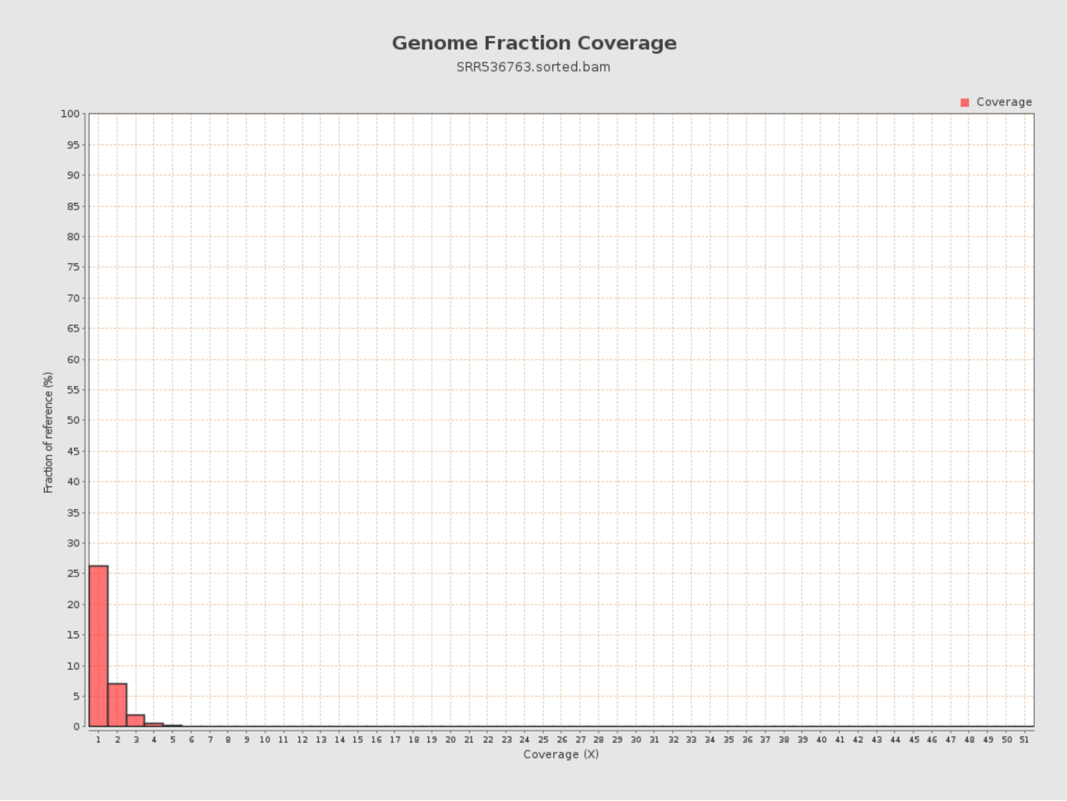
4. Results : Coverage Histogram



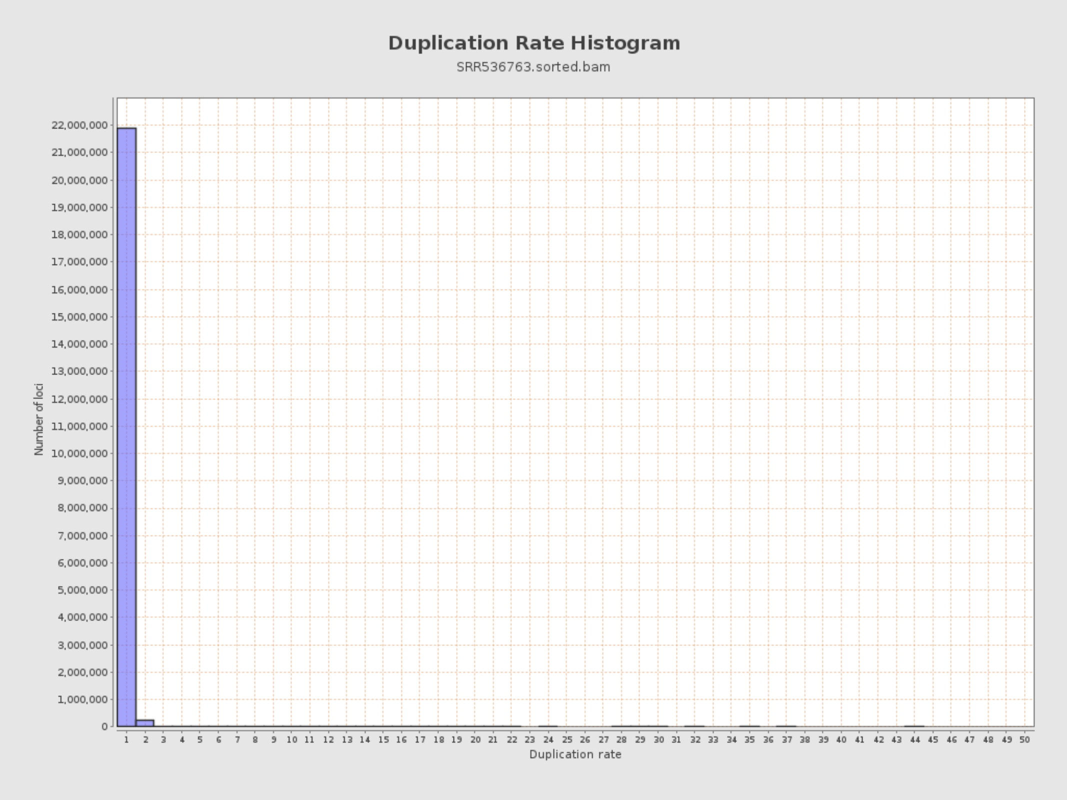
5. Results : Coverage Histogram (0-50X)



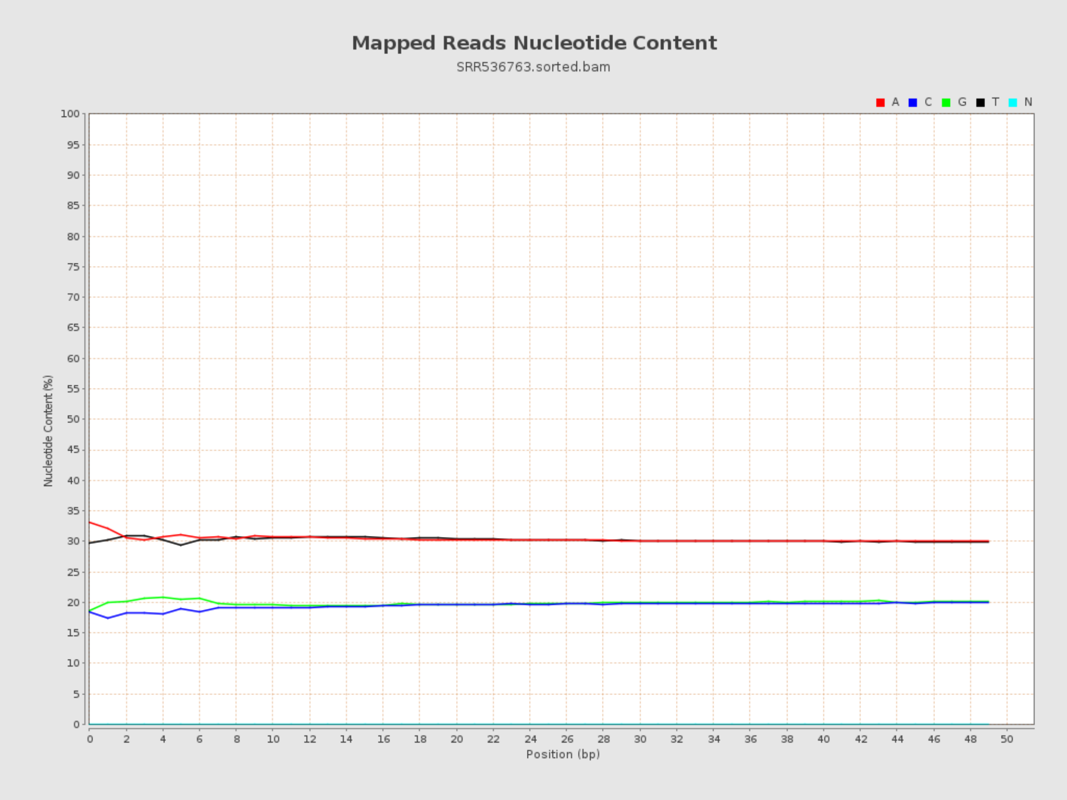
6. Results : Genome Fraction Coverage



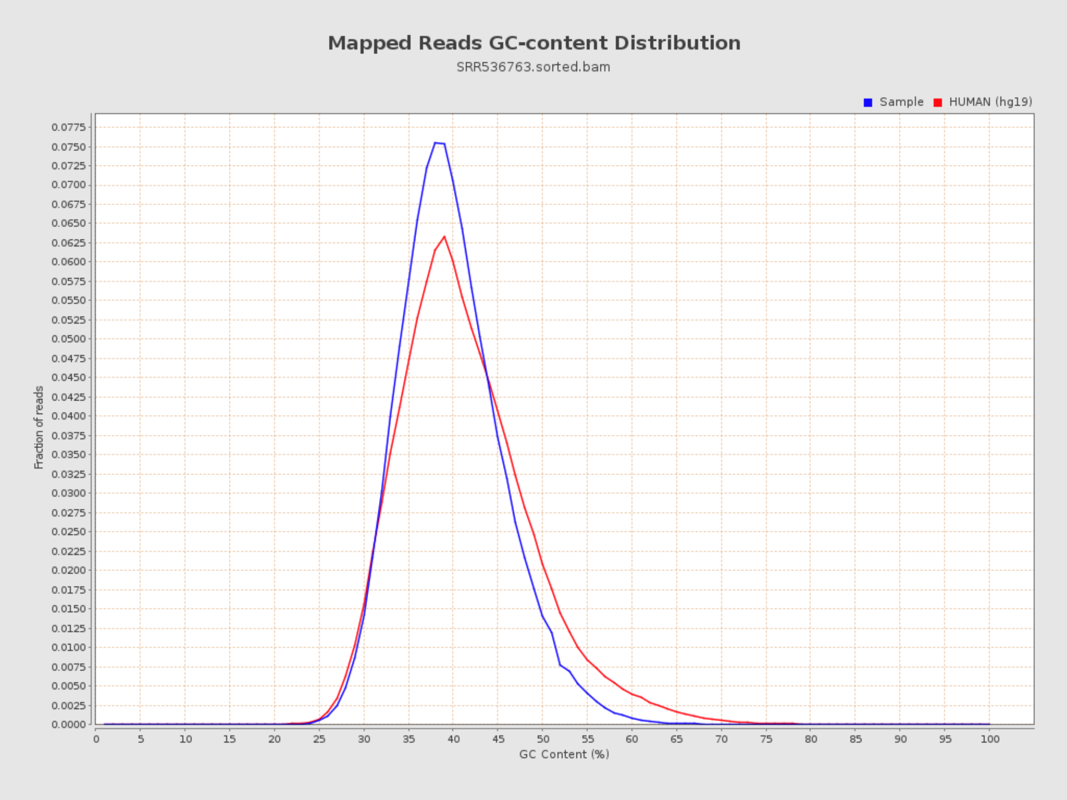
7. Results : Duplication Rate Histogram



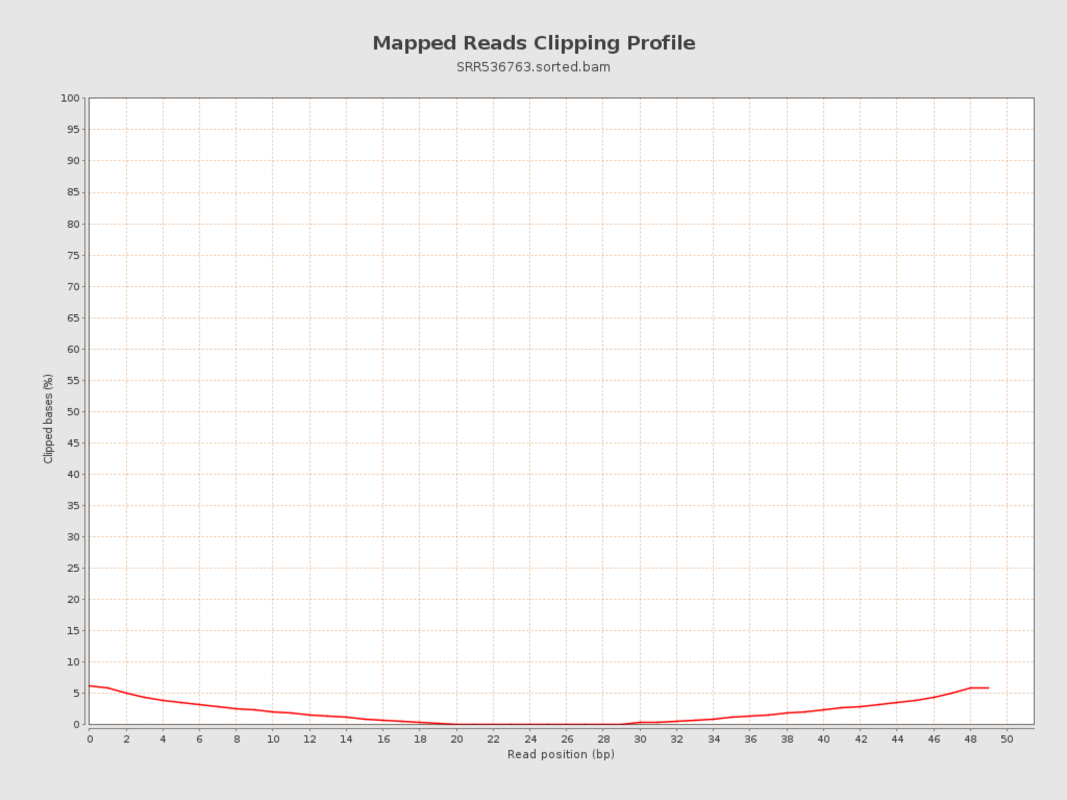
8. Results : Mapped Reads Nucleotide Content



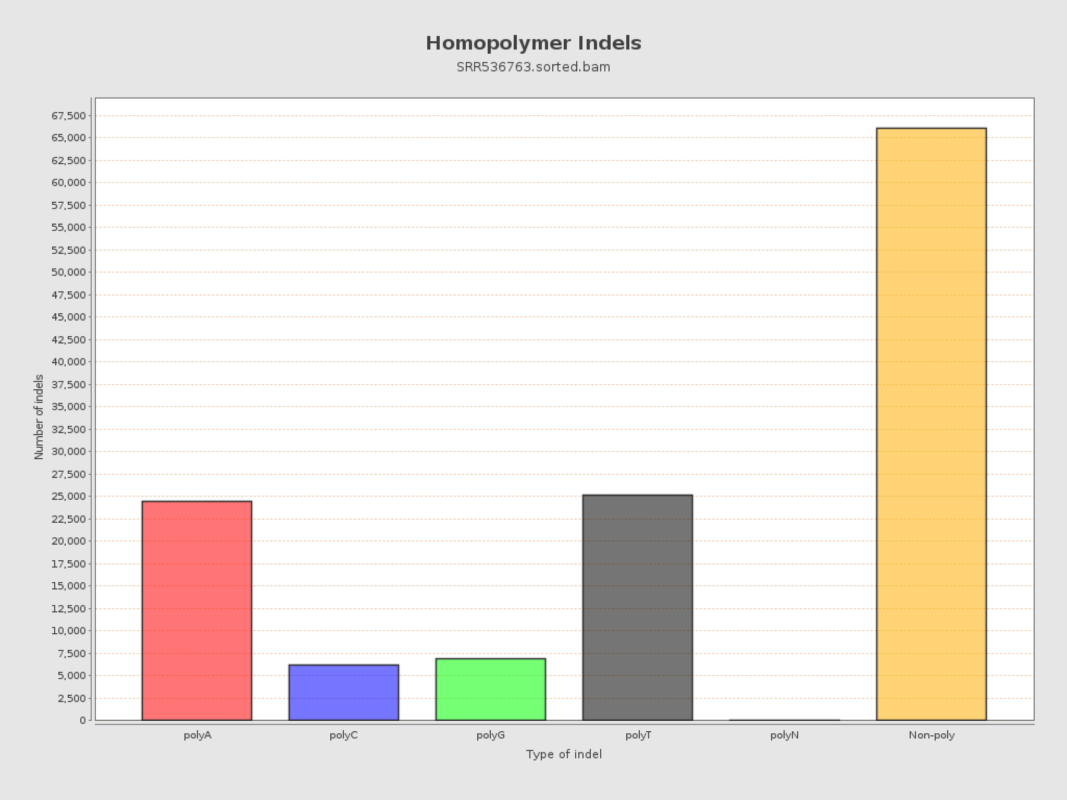
9. Results : Mapped Reads GC-content Distribution



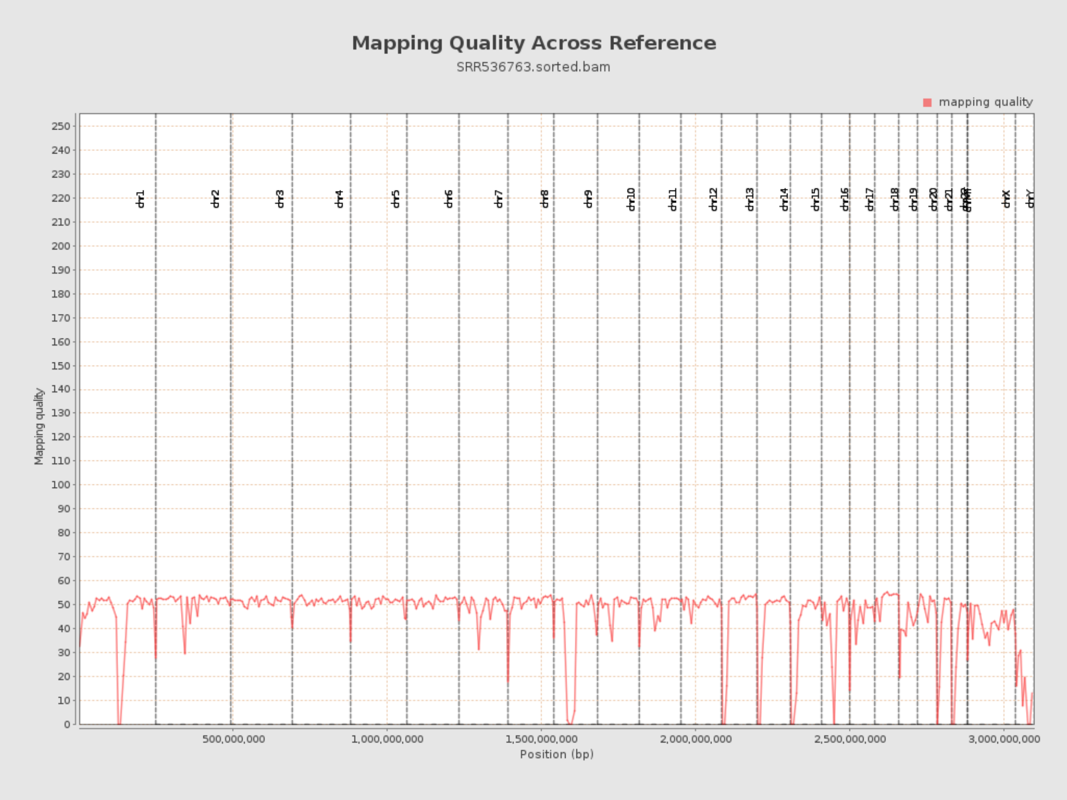
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram