Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/19 00:54:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1163163.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_SRR1163163 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1163163.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 19 00:54:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1163163.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	107,344,996
Mapped reads	103,759,043 / 96.66%
Unmapped reads	3,585,953 / 3.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,028,509 / 0.96%
Read min/max/mean length	30 / 100 / 100.4
Duplicated reads (estimated)	60,594,940 / 56.45%
Duplication rate	51.61%
Clipped reads	5,355,683 / 4.99%

2.2. ACGT Content

Number/percentage of A's	2,724,828,298 / 26.39%
Number/percentage of C's	2,432,479,190 / 23.56%
Number/percentage of T's	2,756,770,400 / 26.7%
Number/percentage of G's	2,405,674,088 / 23.3%
Number/percentage of N's	4,557,932 / 0.04%
GC Percentage	46.86%

2.3. Coverage

Mean	3.3356

Standard Deviation	32.3494

2.4. Mapping Quality

Mean Mapping Quality	49.33

2.5. Mismatches and indels

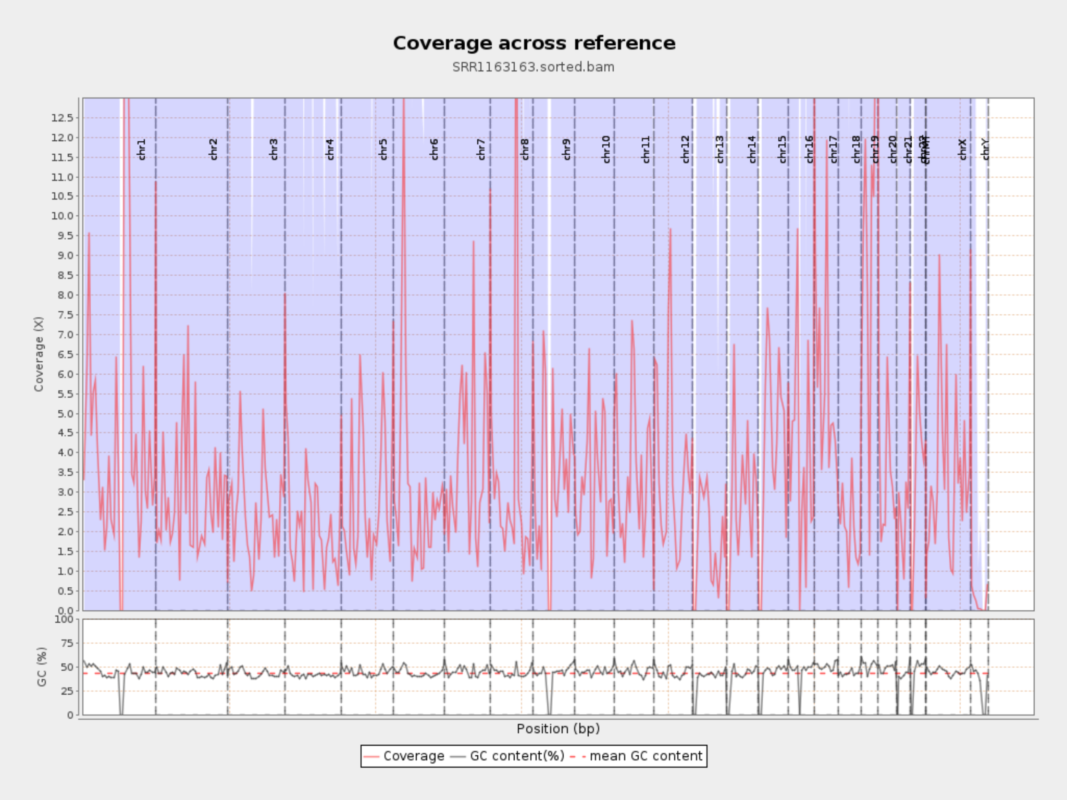
General error rate	0.73%
Mismatches	74,205,017
Insertions	744,148
Mapped reads with at least one insertion	0.71%
Deletions	778,551
Mapped reads with at least one deletion	0.74%
Homopolymer indels	46.63%

2.6. Chromosome stats

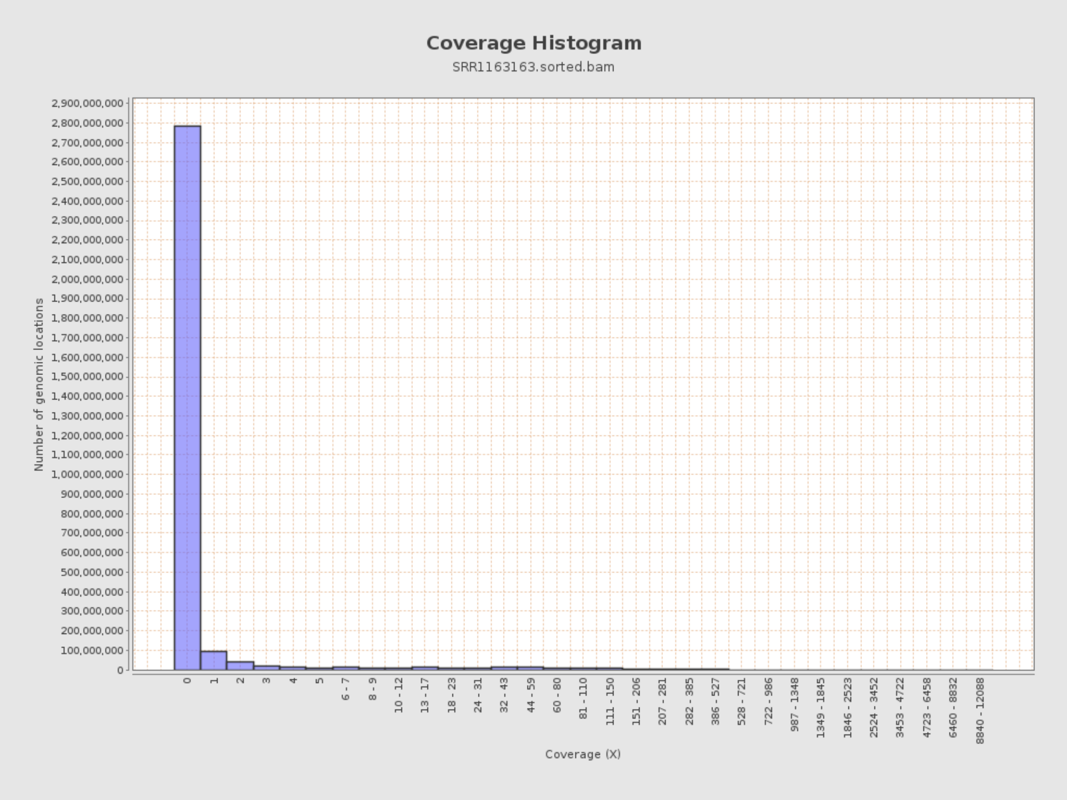
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1150377355	4.6153	38.0873
chr2	243199373	709607095	2.9178	26.7761
chr3	198022430	504451320	2.5474	22.1334
chr4	191154276	406549419	2.1268	23.7626
chr5	180915260	511065445	2.8249	36.6581
chr6	171115067	521079847	3.0452	27.6444
chr7	159138663	590746041	3.7121	37.6356

chr8	146364022	488754015	3.3393	56.5212
chr9	141213431	462568598	3.2757	28.8827
chr10	135534747	431368507	3.1827	29.1447
chr11	135006516	472797401	3.502	25.6682
chr12	133851895	503931972	3.7648	28.9228
chr13	115169878	201797823	1.7522	19.6805
chr14	107349540	301785352	2.8112	24.4963
chr15	102531392	420059946	4.0969	31.8117
chr16	90354753	345177960	3.8203	28.145
chr17	81195210	480872829	5.9224	39.4622
chr18	78077248	160847779	2.0601	20.2588
chr19	59128983	595229088	10.0666	58.3463
chr20	63025520	204264078	3.241	26.2711
chr21	48129895	132803823	2.7593	41.9152
chr22	51304566	175279429	3.4164	26.5103
chrMT	16571	4911	0.2964	0.6346
chrX	155270560	540623911	3.4818	32.6007
chrY	59373566	13881779	0.2338	18.0818

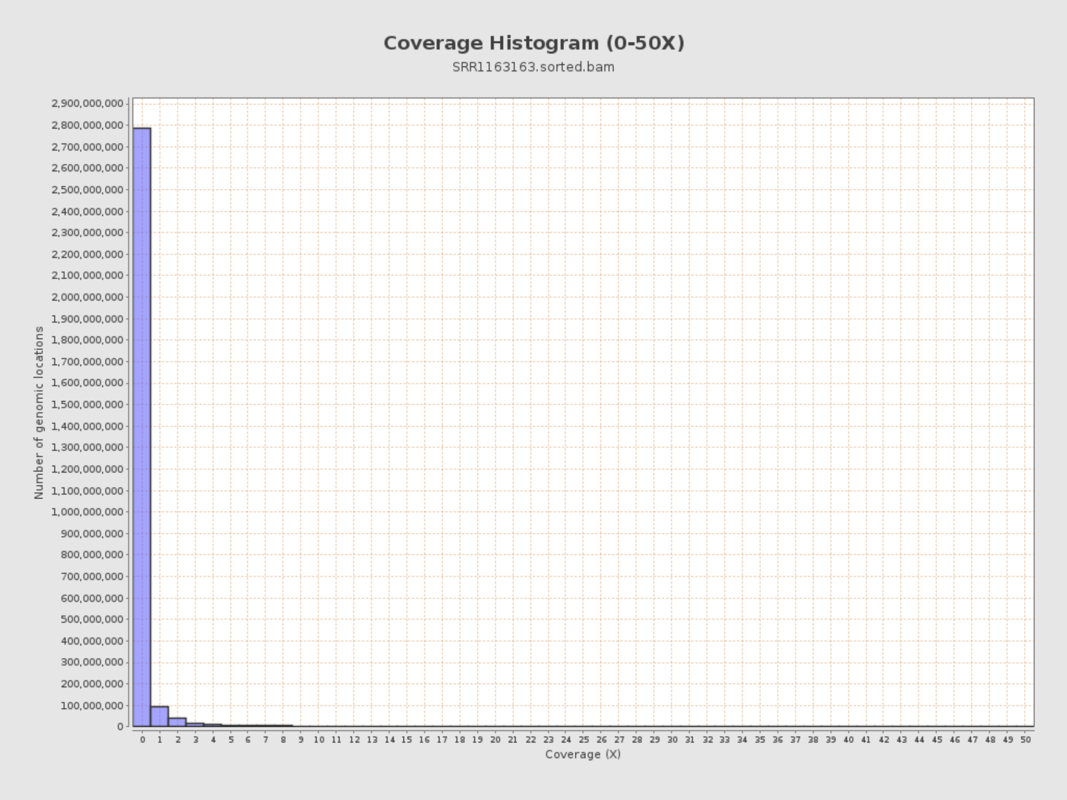
3. Results : Coverage across reference



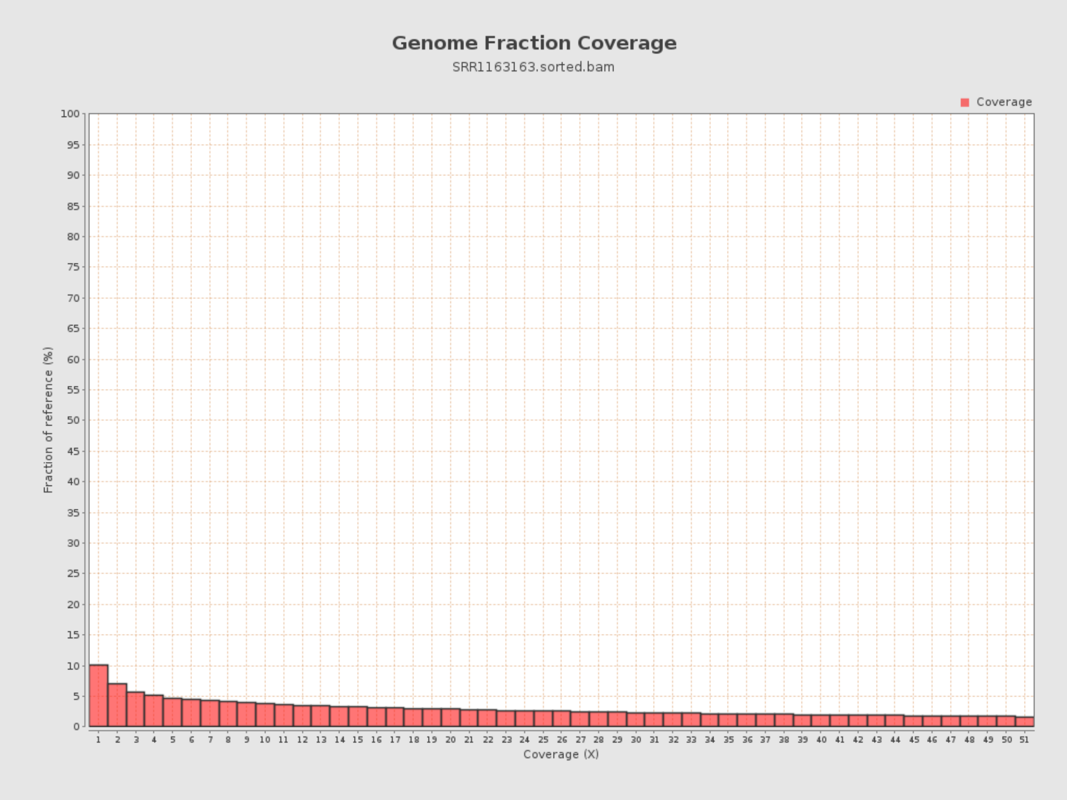
4. Results : Coverage Histogram



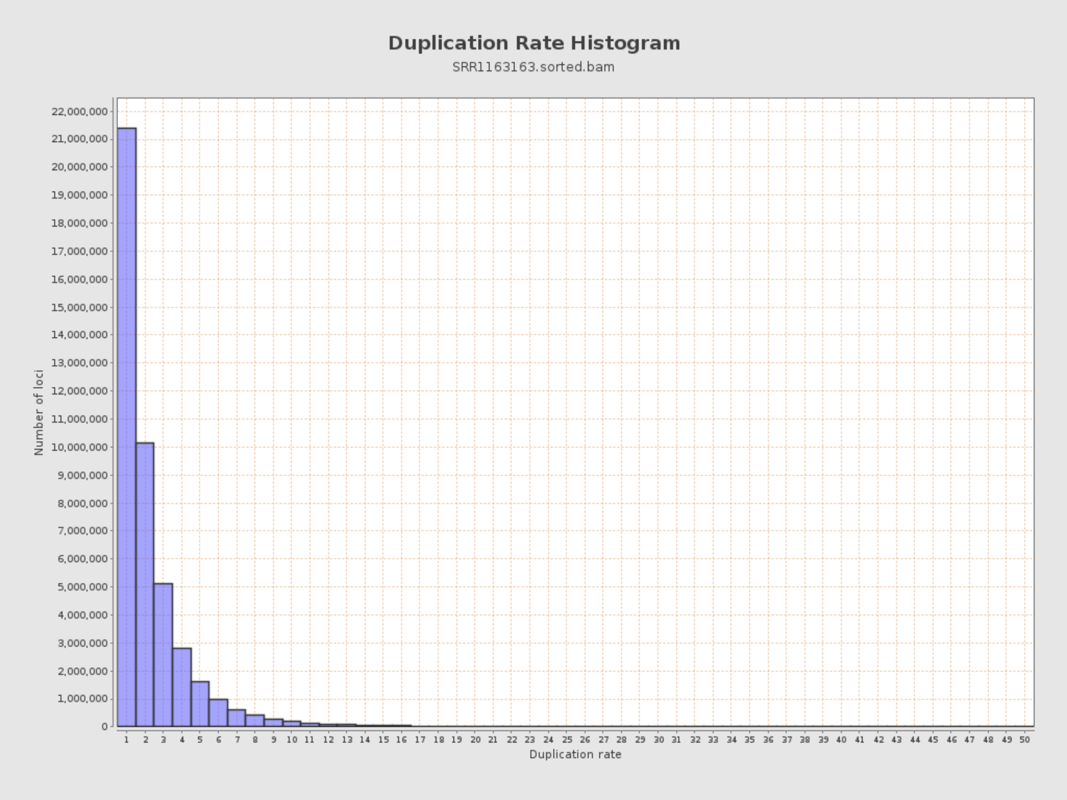
5. Results : Coverage Histogram (0-50X)



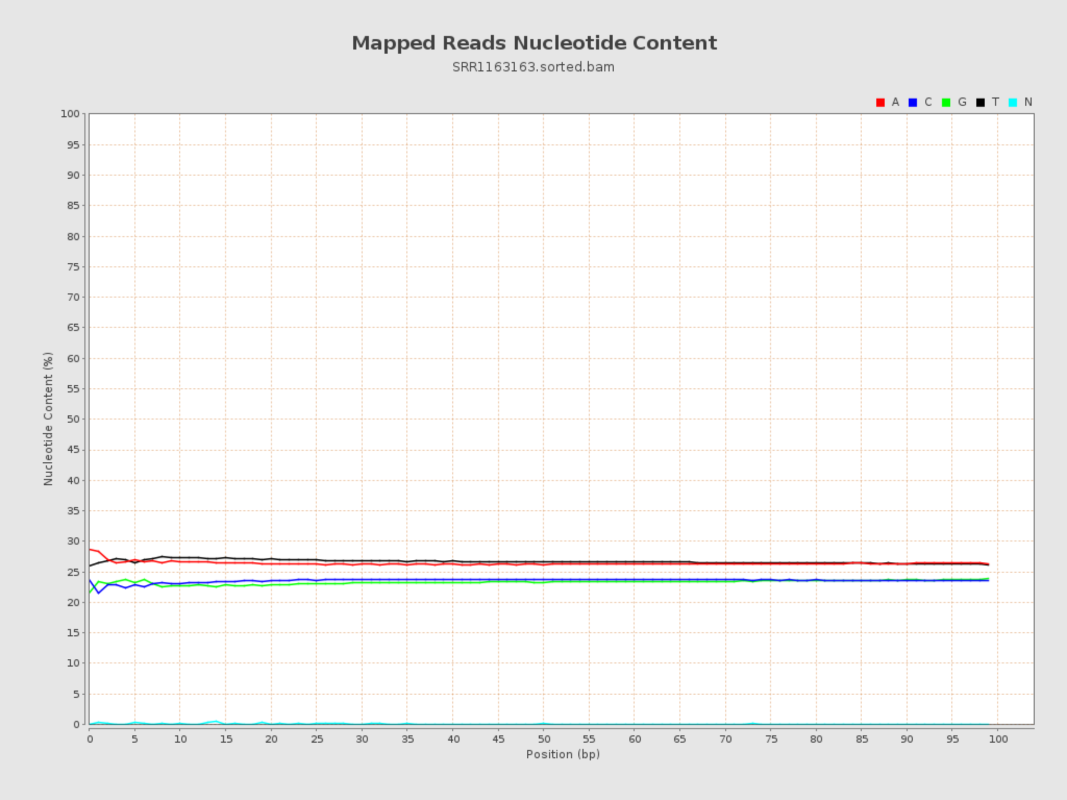
6. Results : Genome Fraction Coverage



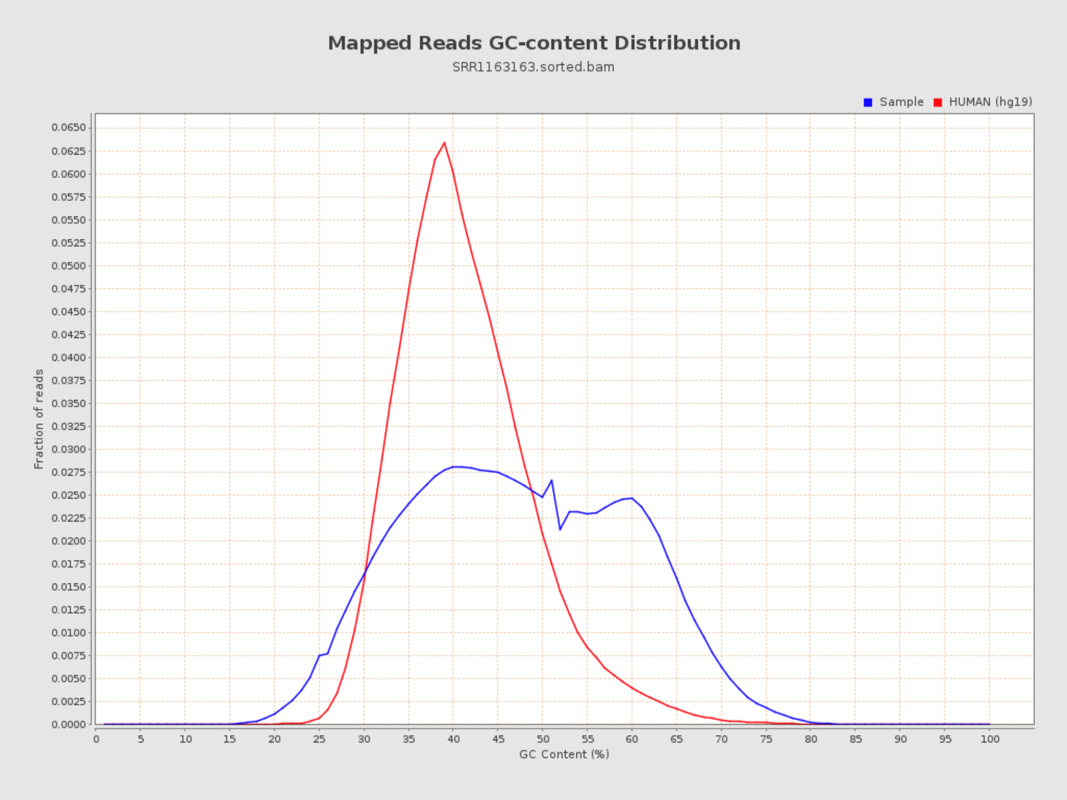
7. Results : Duplication Rate Histogram



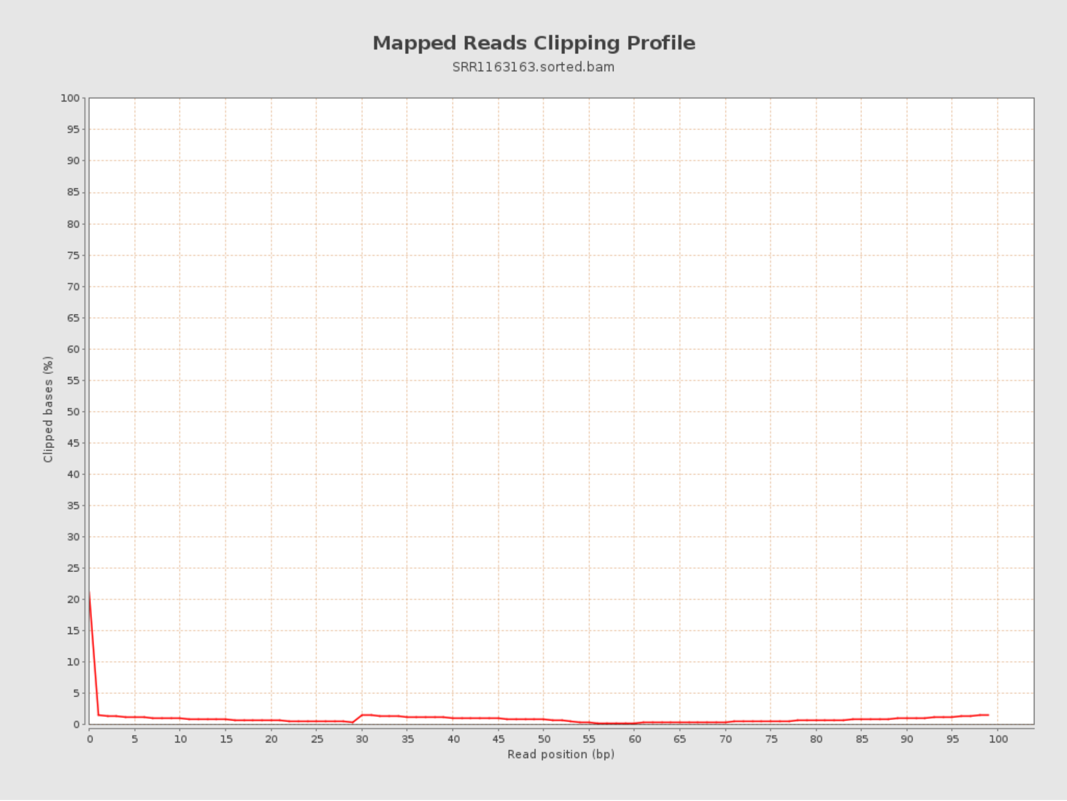
8. Results : Mapped Reads Nucleotide Content



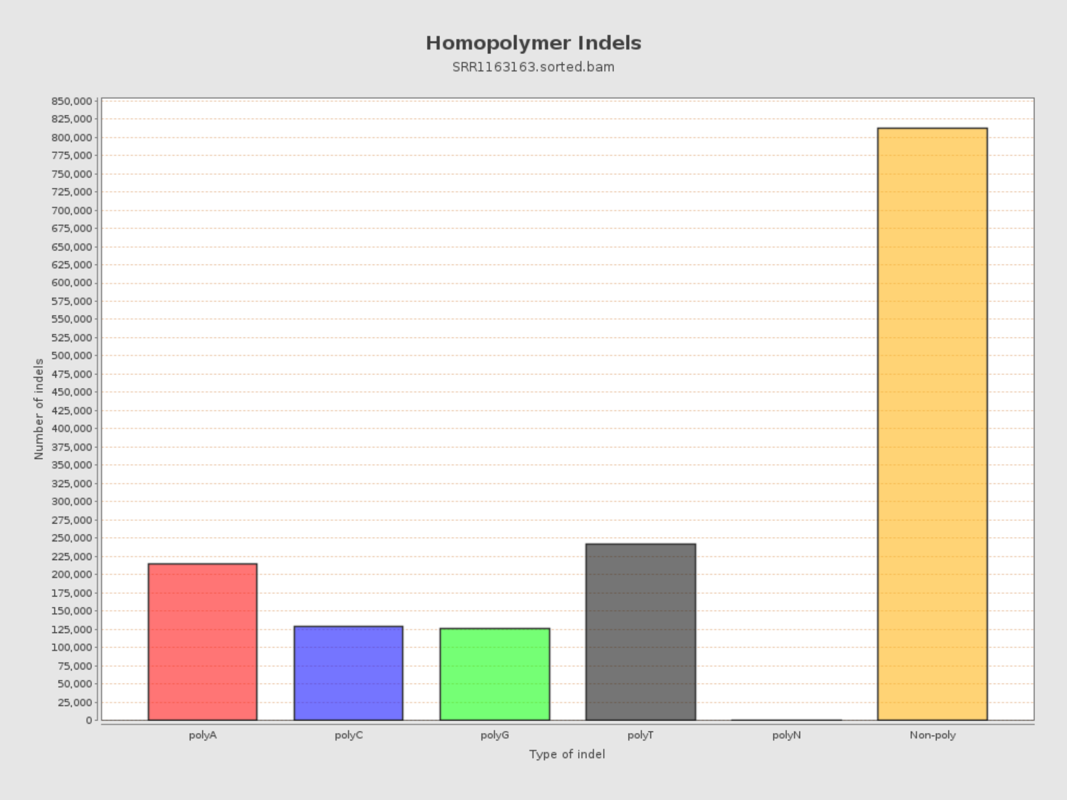
9. Results : Mapped Reads GC-content Distribution



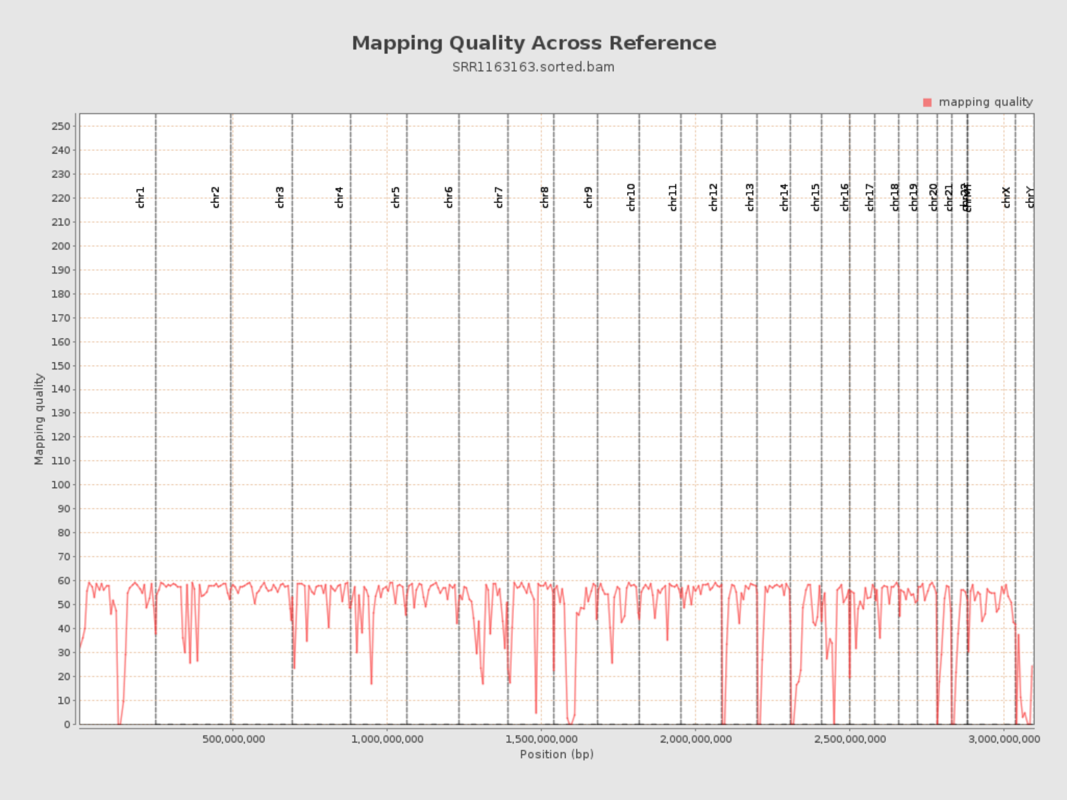
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram