Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/19 01:42:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1163164.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_SRR1163164 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1163164.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 19 01:42:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1163164.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	63,023,376
Mapped reads	60,869,083 / 96.58%
Unmapped reads	2,154,293 / 3.42%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	677,506 / 1.08%
Read min/max/mean length	30 / 100 / 100.44
Duplicated reads (estimated)	32,658,692 / 51.82%
Duplication rate	48.8%
Clipped reads	3,701,679 / 5.87%

2.2. ACGT Content

Number/percentage of A's	1,569,172,491 / 25.93%
Number/percentage of C's	1,458,983,883 / 24.11%
Number/percentage of T's	1,593,061,356 / 26.33%
Number/percentage of G's	1,427,188,712 / 23.59%
Number/percentage of N's	2,775,460 / 0.05%
GC Percentage	47.7%

2.3. Coverage

Mean	1.9551

Standard Deviation	18.6383

2.4. Mapping Quality

Mean Mapping Quality	49.41

2.5. Mismatches and indels

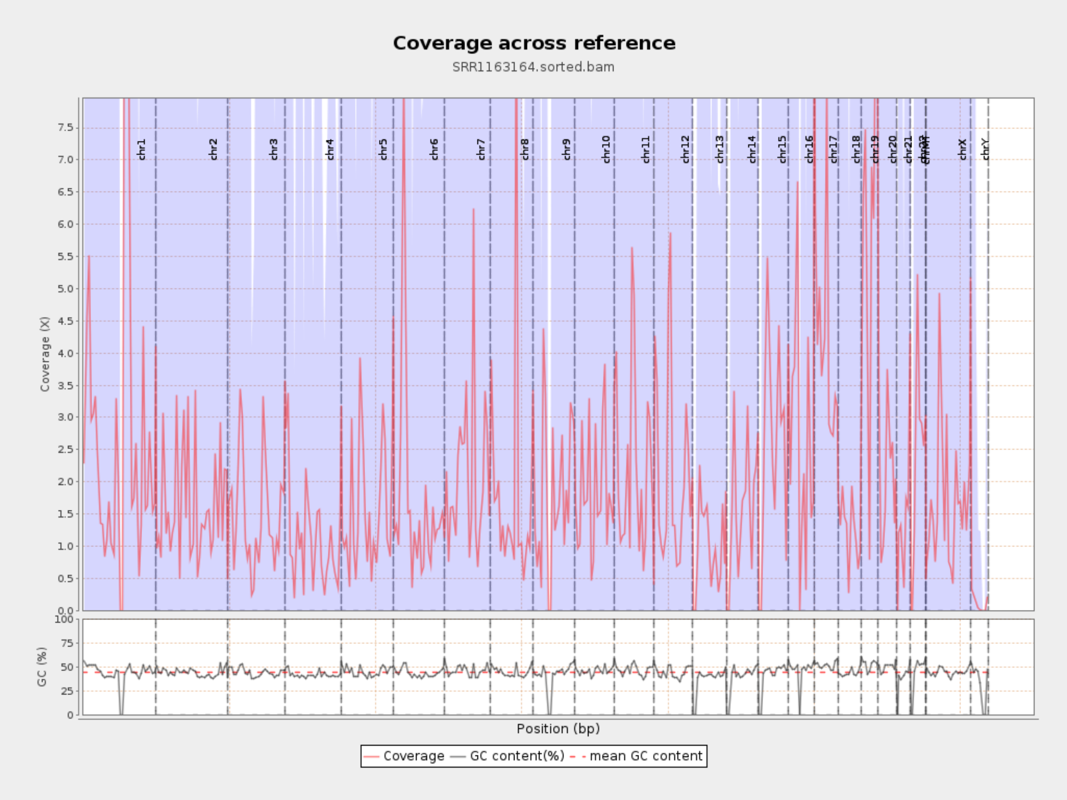
General error rate	0.91%
Mismatches	54,145,328
Insertions	437,015
Mapped reads with at least one insertion	0.71%
Deletions	569,099
Mapped reads with at least one deletion	0.92%
Homopolymer indels	45.62%

2.6. Chromosome stats

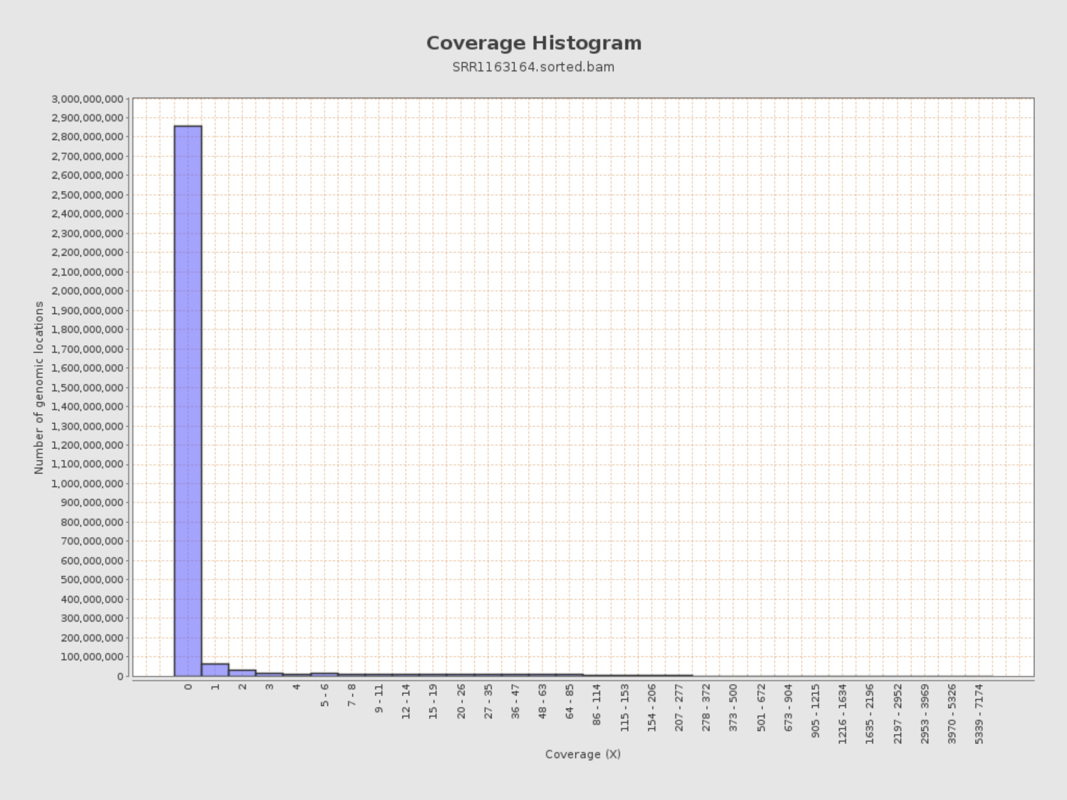
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	684158937	2.7449	22.5345
chr2	243199373	398515290	1.6386	15.2875
chr3	198022430	295171901	1.4906	13.4175
chr4	191154276	213822907	1.1186	13.7789
chr5	180915260	291631616	1.612	21.5019
chr6	171115067	291801057	1.7053	15.6573
chr7	159138663	334297794	2.1007	20.5342

chr8	146364022	267027990	1.8244	28.9263
chr9	141213431	248265377	1.7581	15.3856
chr10	135534747	251295430	1.8541	18.2122
chr11	135006516	304065539	2.2522	17.6549
chr12	133851895	295593403	2.2084	16.9567
chr13	115169878	112355640	0.9756	11.0974
chr14	107349540	167973159	1.5647	13.5511
chr15	102531392	263272749	2.5677	20.0138
chr16	90354753	234507274	2.5954	19.3371
chr17	81195210	345204961	4.2515	27.4391
chr18	78077248	98901569	1.2667	12.3989
chr19	59128983	359453954	6.0791	34.1172
chr20	63025520	128874683	2.0448	16.7142
chr21	48129895	69329322	1.4405	15.9785
chr22	51304566	121445337	2.3671	17.8599
chrMT	16571	8045	0.4855	0.8844
chrX	155270560	268579424	1.7298	16.2237
chrY	59373566	6776165	0.1141	9.8568

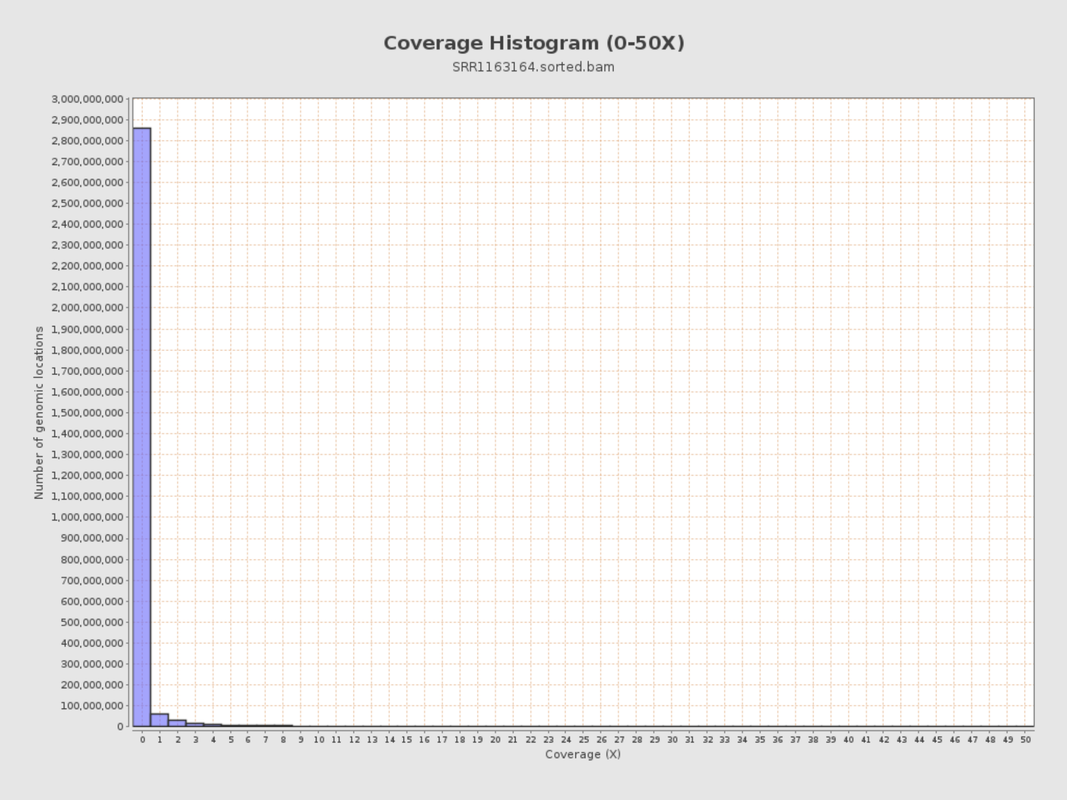
3. Results : Coverage across reference



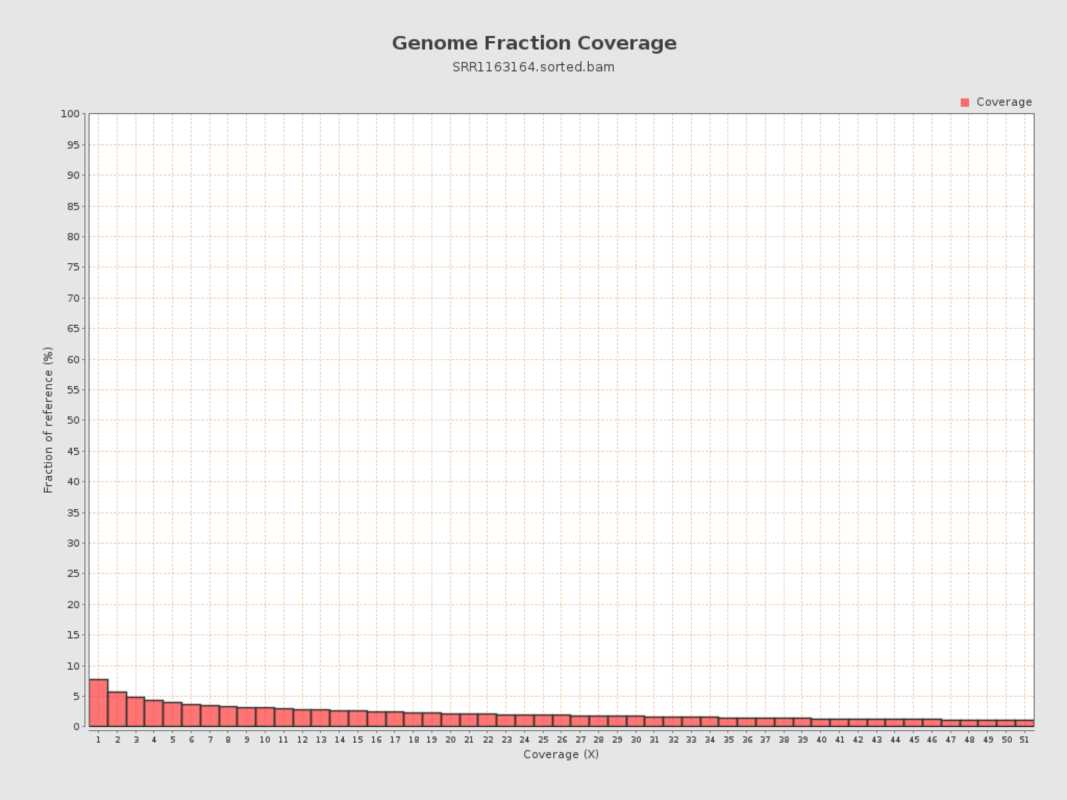
4. Results : Coverage Histogram



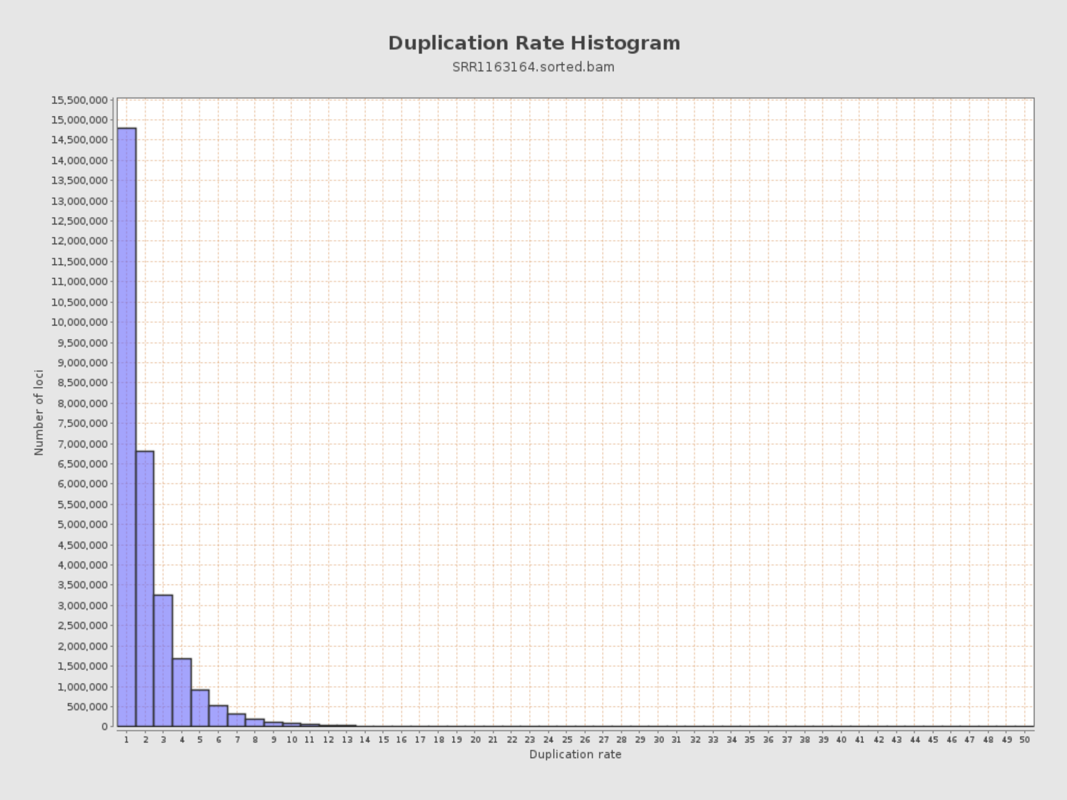
5. Results : Coverage Histogram (0-50X)



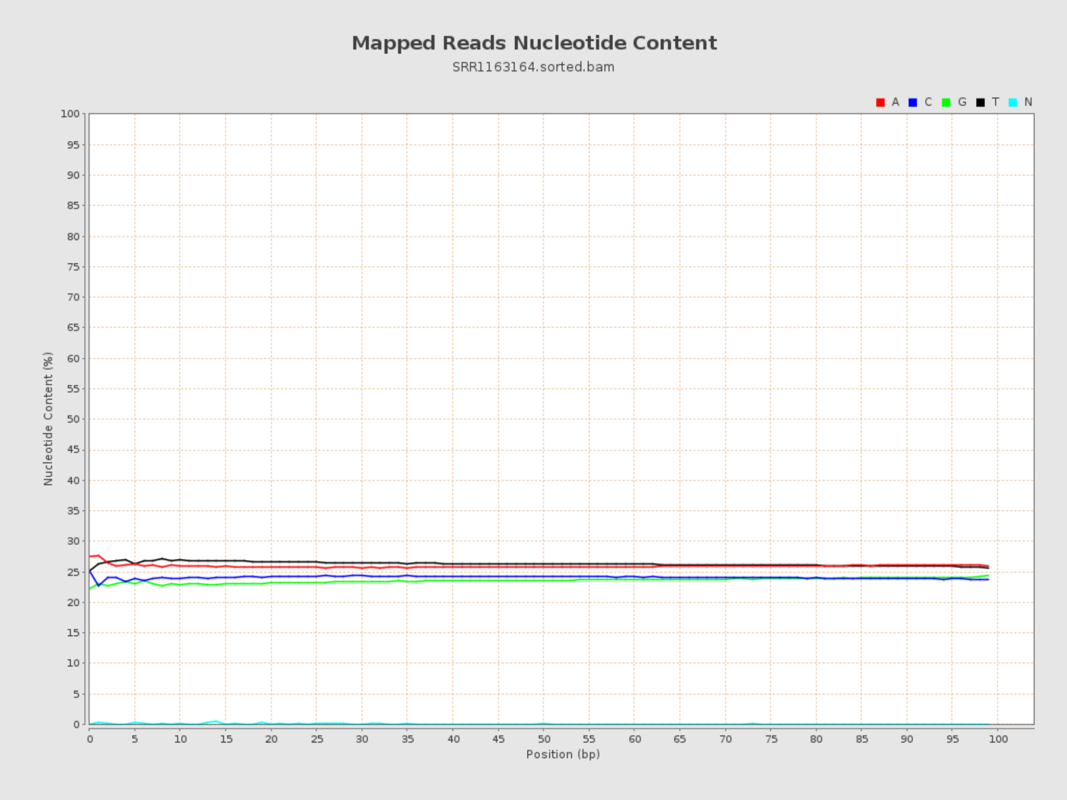
6. Results : Genome Fraction Coverage



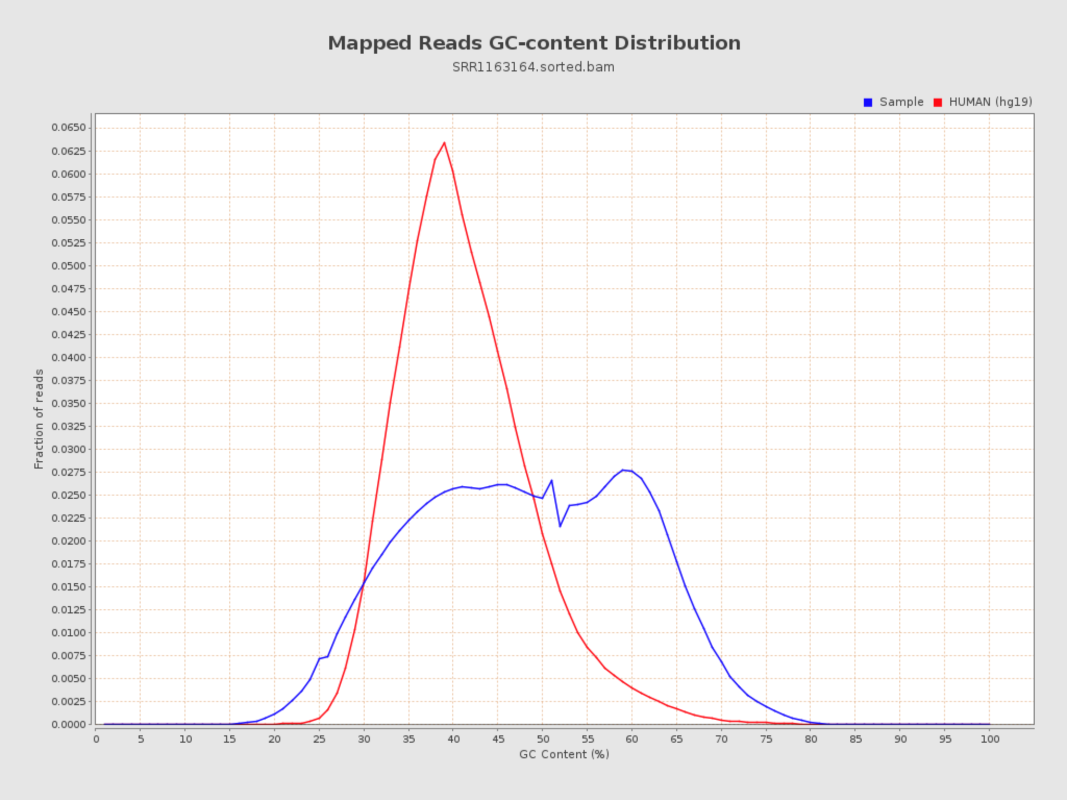
7. Results : Duplication Rate Histogram



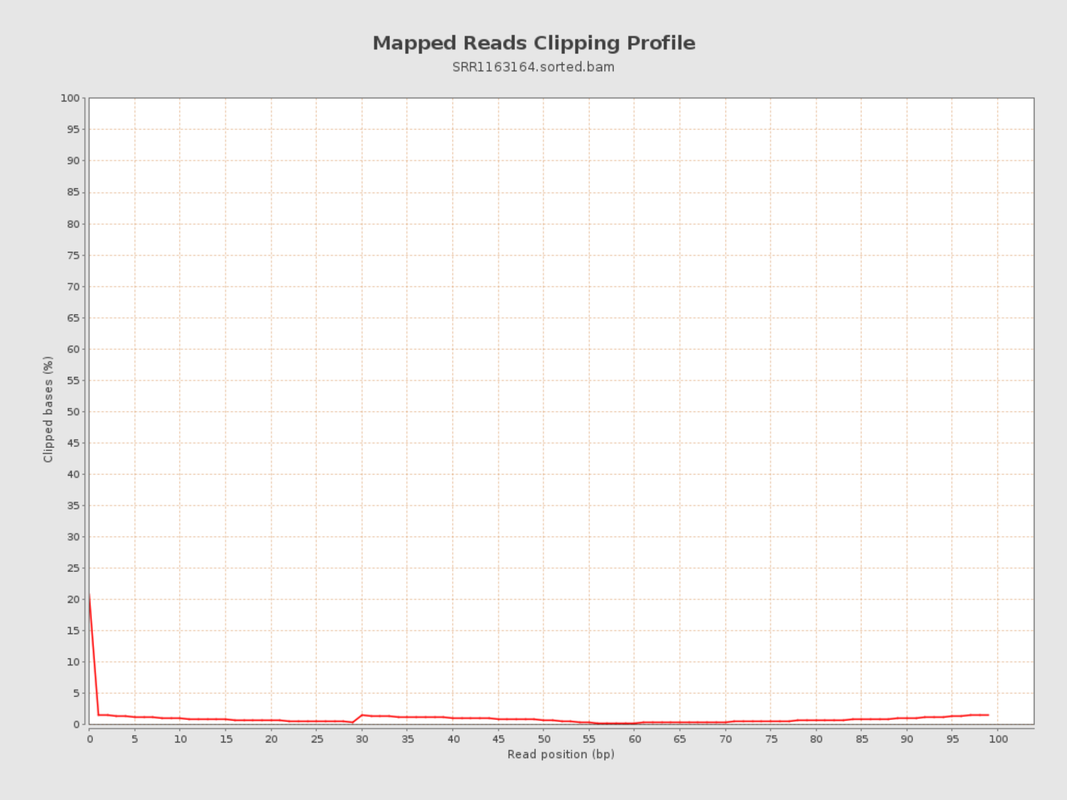
8. Results : Mapped Reads Nucleotide Content



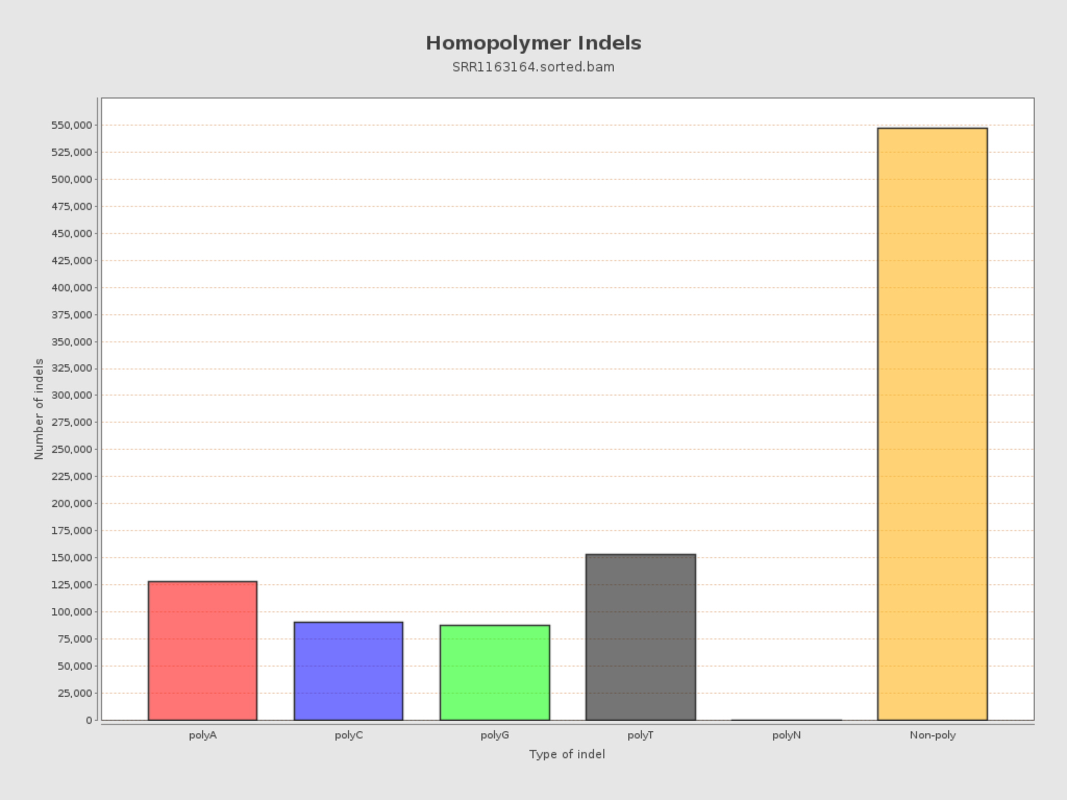
9. Results : Mapped Reads GC-content Distribution



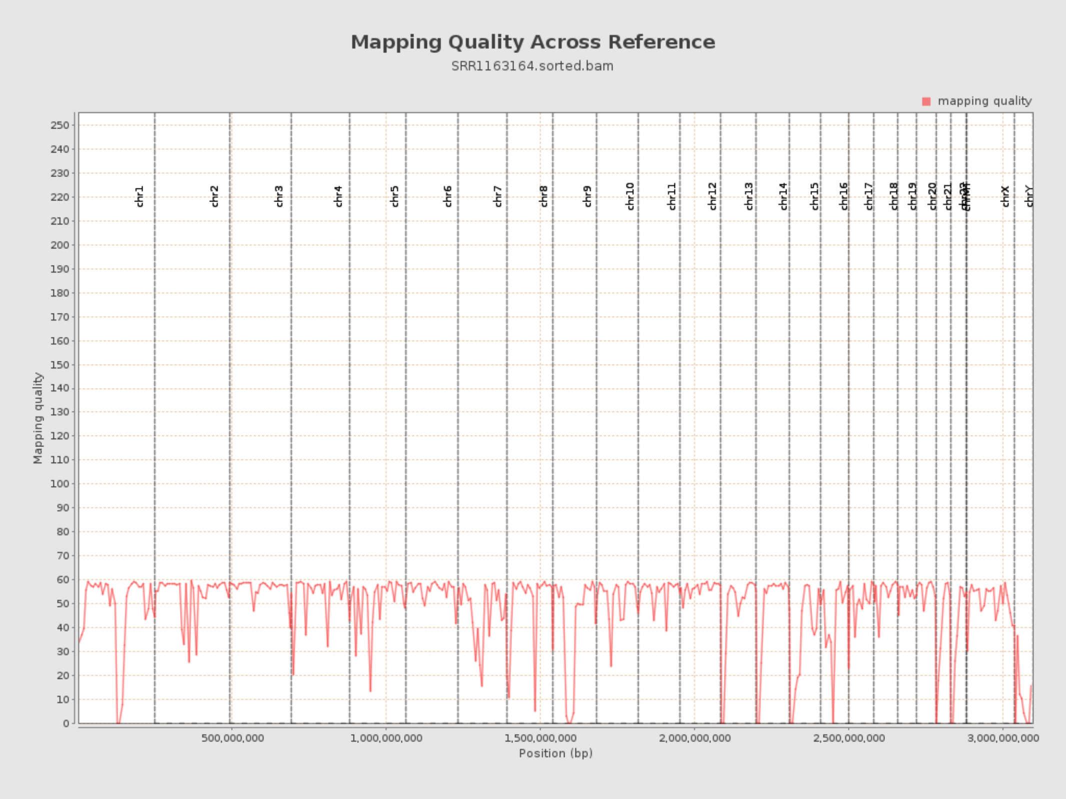
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram