Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 00:22:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083622.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_SRR3083622 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083622.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 00:22:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083622.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,702,217
Mapped reads	1,552,031 / 91.18%
Unmapped reads	150,186 / 8.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,587 / 0.86%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	64,064 / 3.76%
Duplication rate	3.33%
Clipped reads	688,682 / 40.46%

2.2. ACGT Content

Number/percentage of A's	27,932,358 / 27.06%
Number/percentage of C's	19,180,934 / 18.58%
Number/percentage of T's	32,591,427 / 31.57%
Number/percentage of G's	23,517,190 / 22.78%
Number/percentage of N's	5,034 / 0%
GC Percentage	41.36%

2.3. Coverage

Mean	0.0334

Standard Deviation	0.3234

2.4. Mapping Quality

Mean Mapping Quality	45.74

2.5. Mismatches and indels

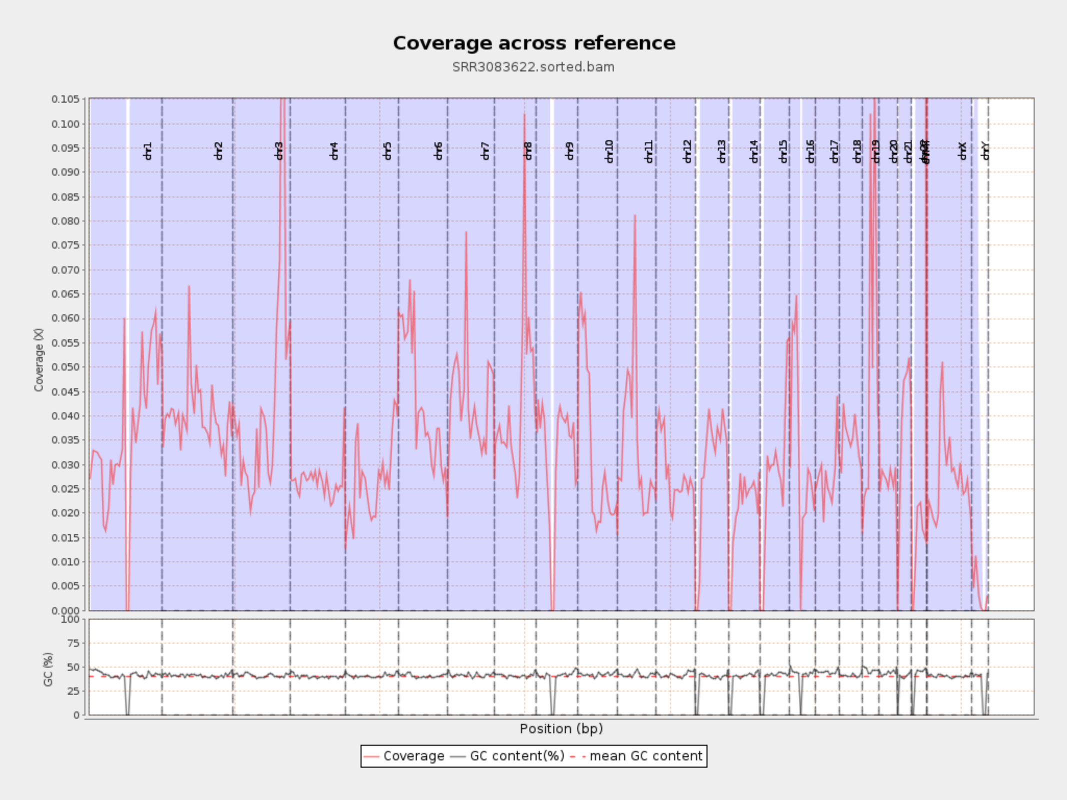
General error rate	0.74%
Mismatches	753,046
Insertions	7,652
Mapped reads with at least one insertion	0.49%
Deletions	24,125
Mapped reads with at least one deletion	1.54%
Homopolymer indels	48.48%

2.6. Chromosome stats

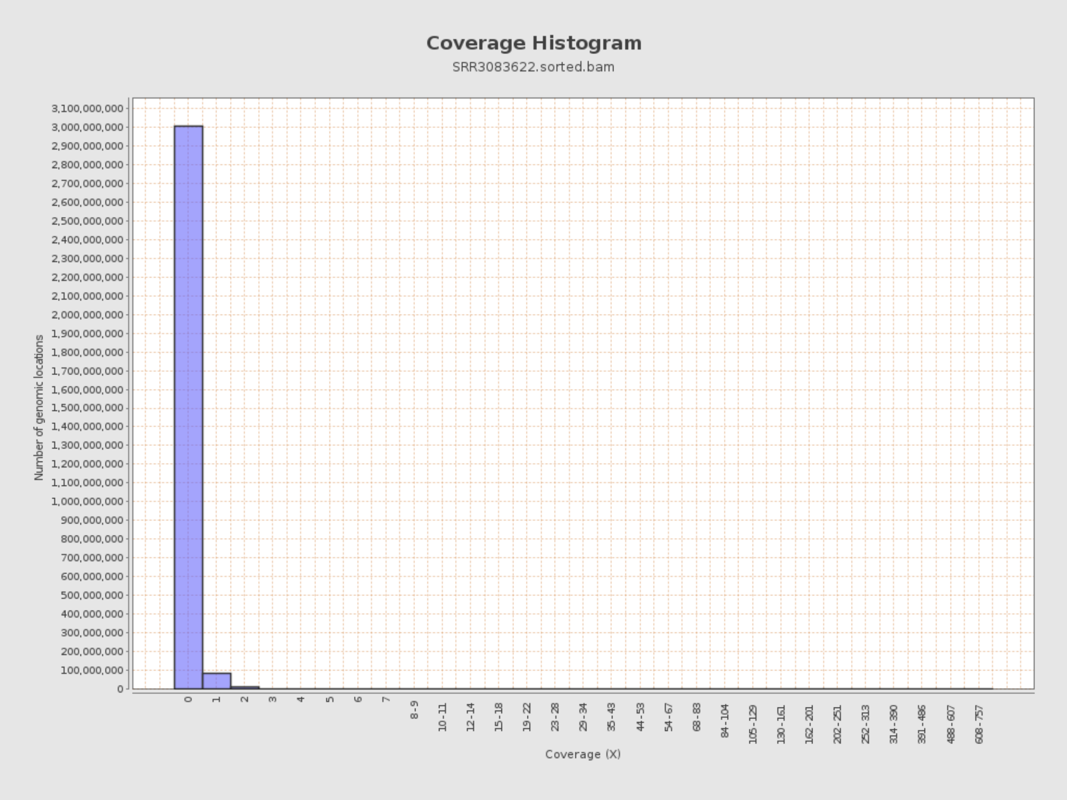
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8934766	0.0358	0.6446
chr2	243199373	9739576	0.04	0.3764
chr3	198022430	8682871	0.0438	0.235
chr4	191154276	5084856	0.0266	0.1865
chr5	180915260	4827192	0.0267	0.1815
chr6	171115067	7379356	0.0431	0.299
chr7	159138663	6989159	0.0439	0.5497

chr8	146364022	6297978	0.043	0.3359
chr9	141213431	4510006	0.0319	0.2386
chr10	135534747	4474192	0.033	0.2572
chr11	135006516	4565227	0.0338	0.2461
chr12	133851895	3747451	0.028	0.187
chr13	115169878	3377348	0.0293	0.1903
chr14	107349540	2168895	0.0202	0.1602
chr15	102531392	2811721	0.0274	0.1881
chr16	90354753	2946123	0.0326	0.2117
chr17	81195210	2258283	0.0278	0.1985
chr18	78077248	2743149	0.0351	0.379
chr19	59128983	3032585	0.0513	0.4413
chr20	63025520	1688913	0.0268	0.1848
chr21	48129895	1815655	0.0377	0.2206
chr22	51304566	686363	0.0134	0.1263
chrMT	16571	33805	2.04	1.8268
chrX	155270560	4256944	0.0274	0.1938
chrY	59373566	214145	0.0036	0.0854

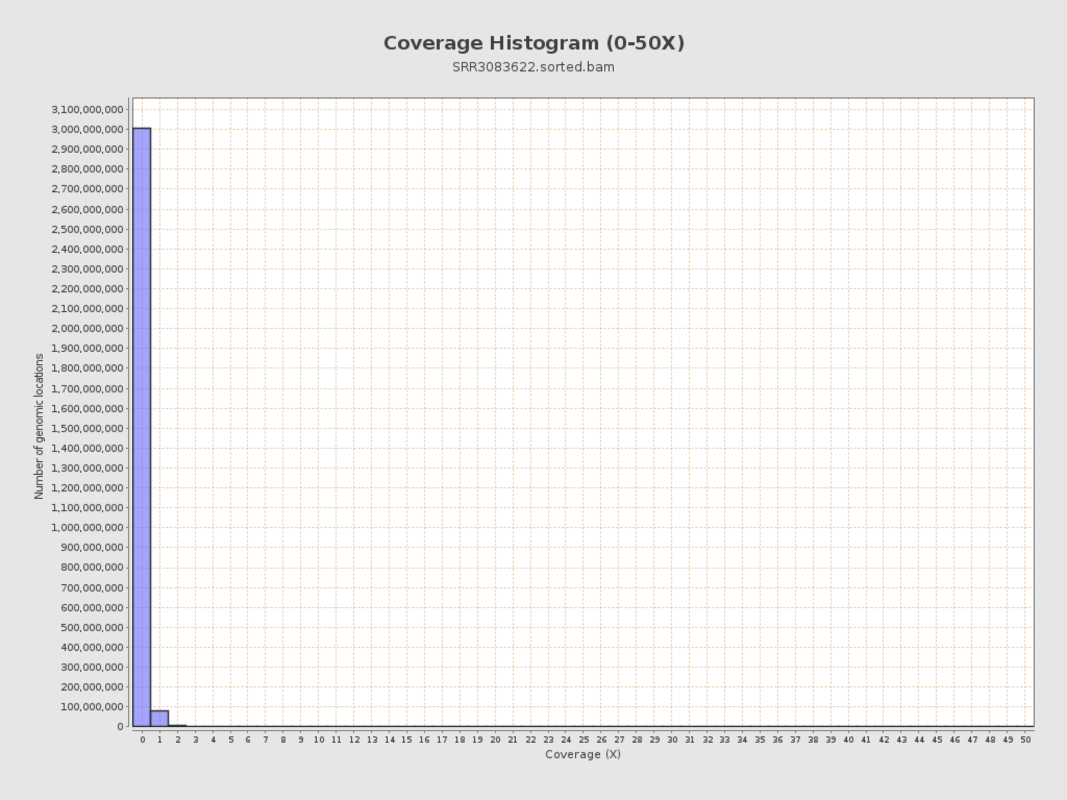
3. Results : Coverage across reference



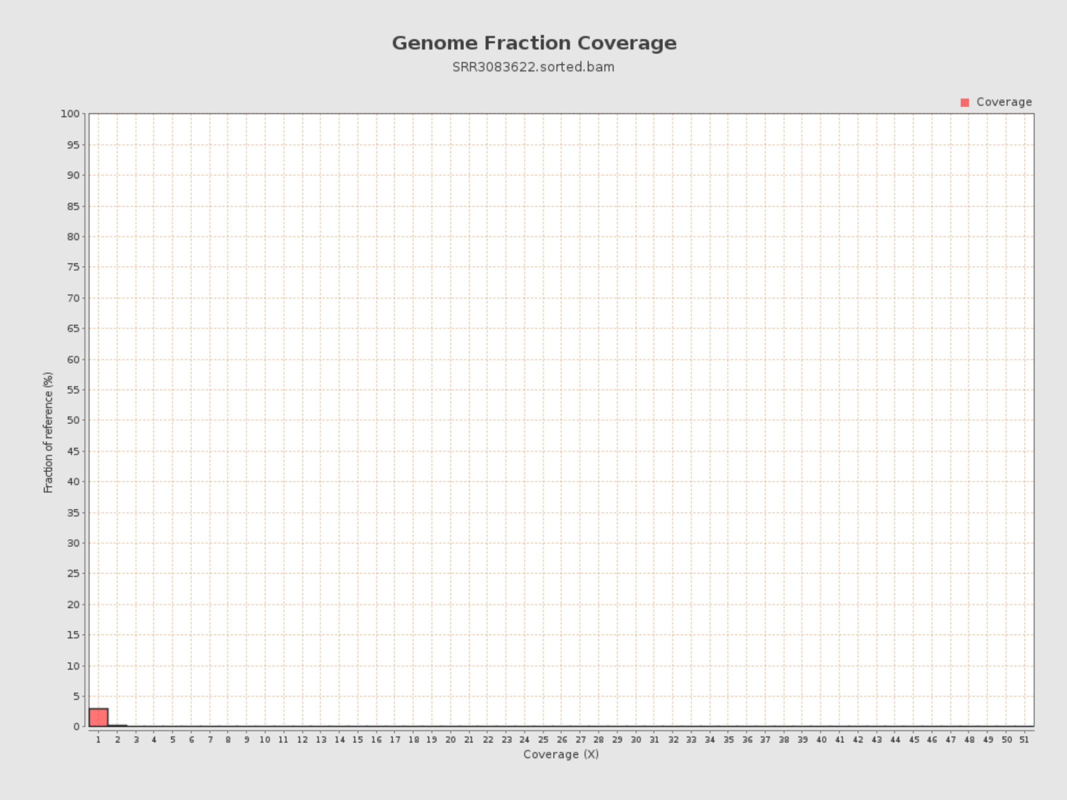
4. Results : Coverage Histogram



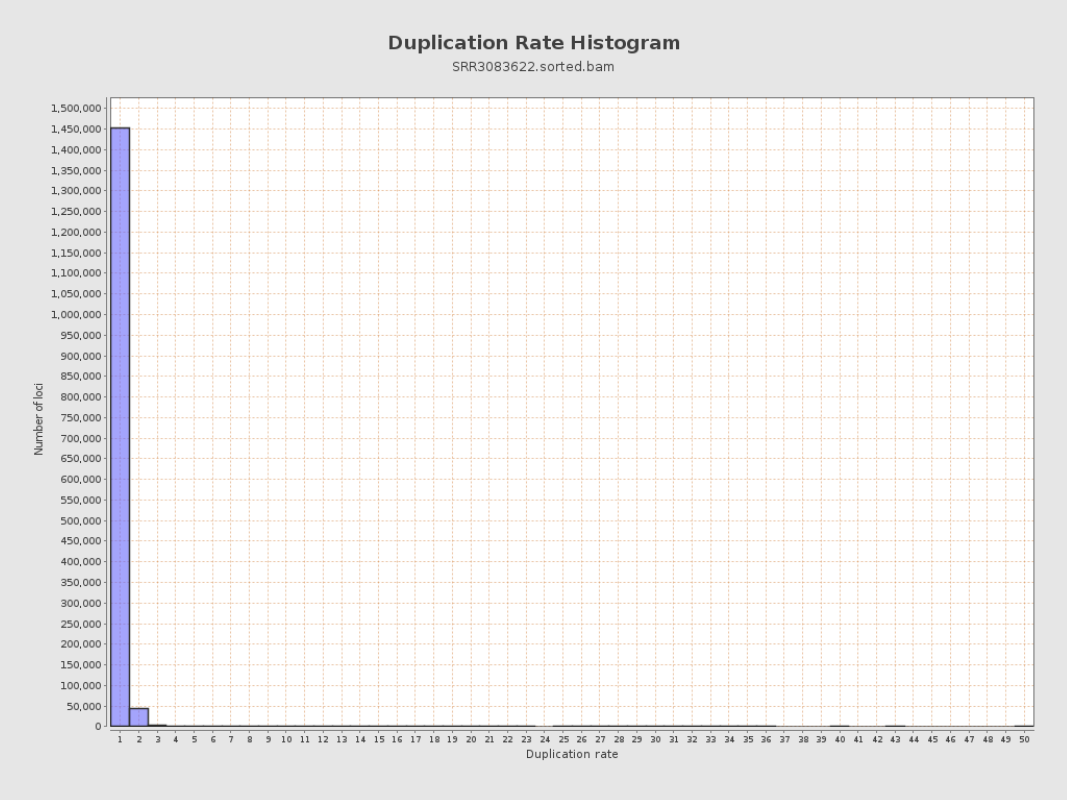
5. Results : Coverage Histogram (0-50X)



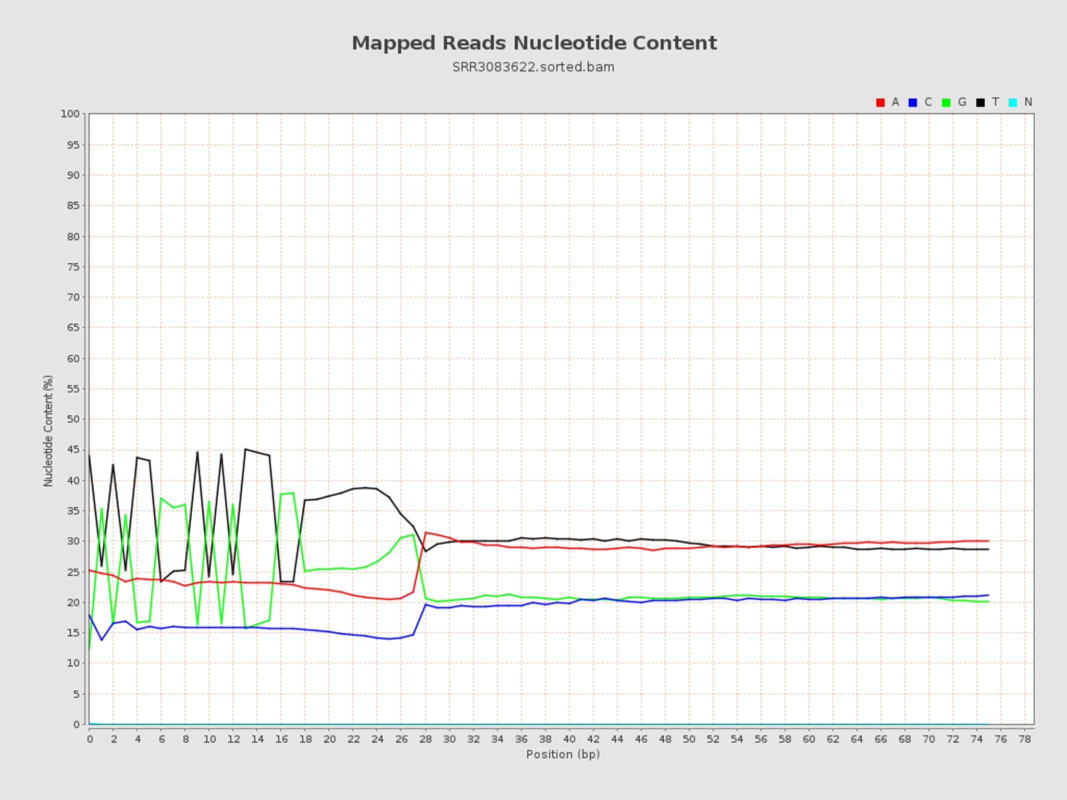
6. Results : Genome Fraction Coverage



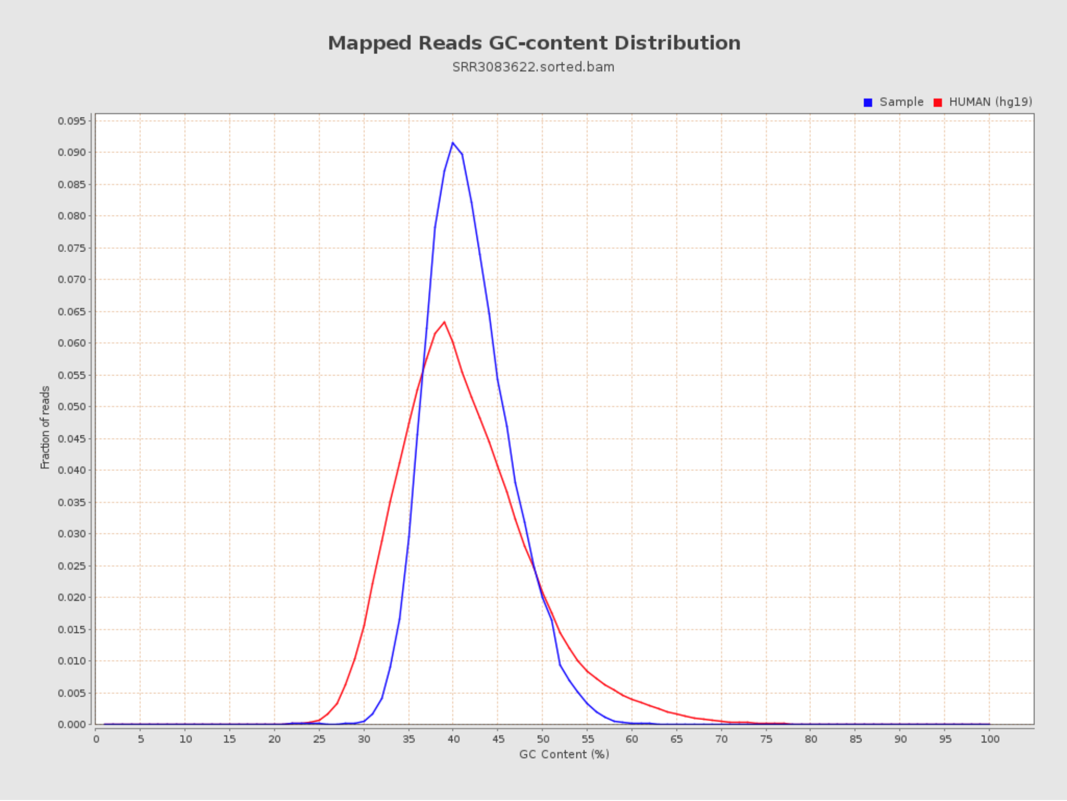
7. Results : Duplication Rate Histogram



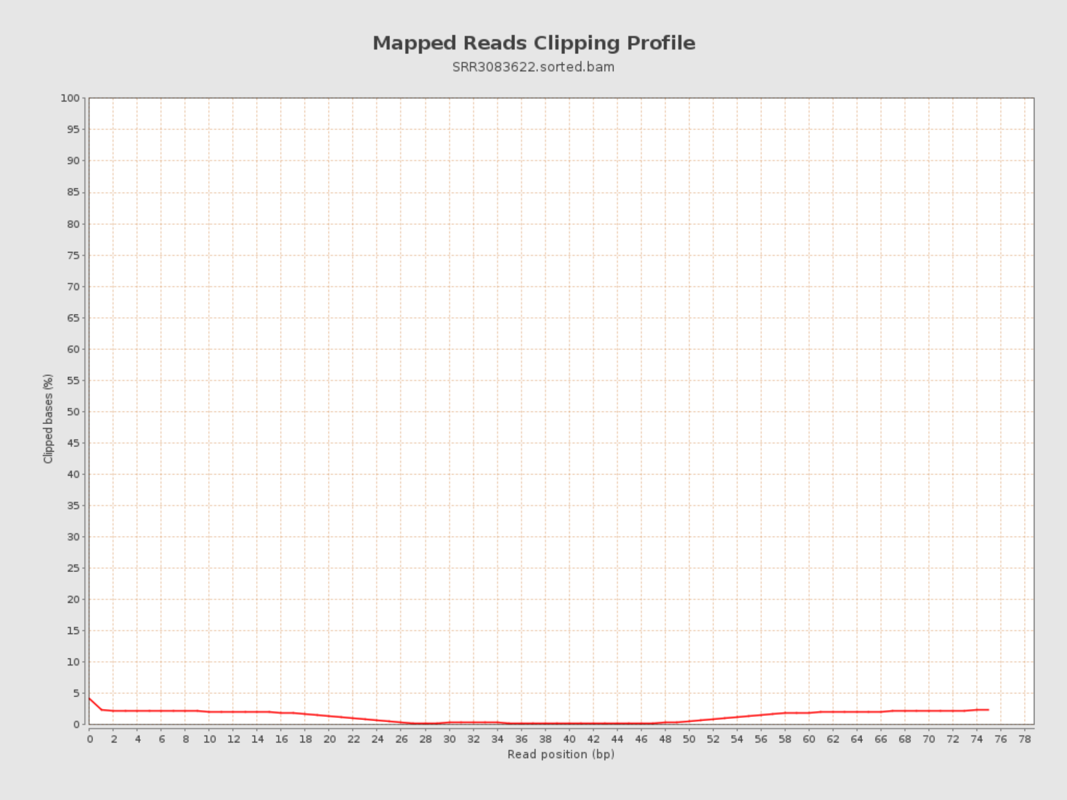
8. Results : Mapped Reads Nucleotide Content



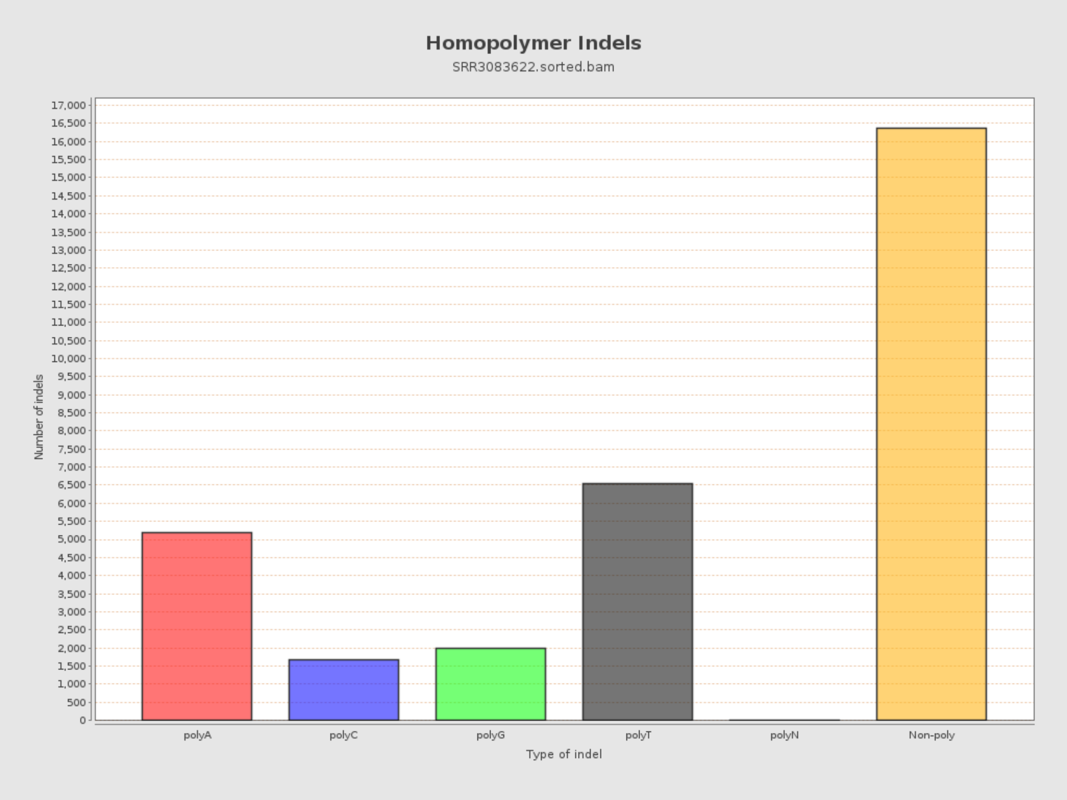
9. Results : Mapped Reads GC-content Distribution



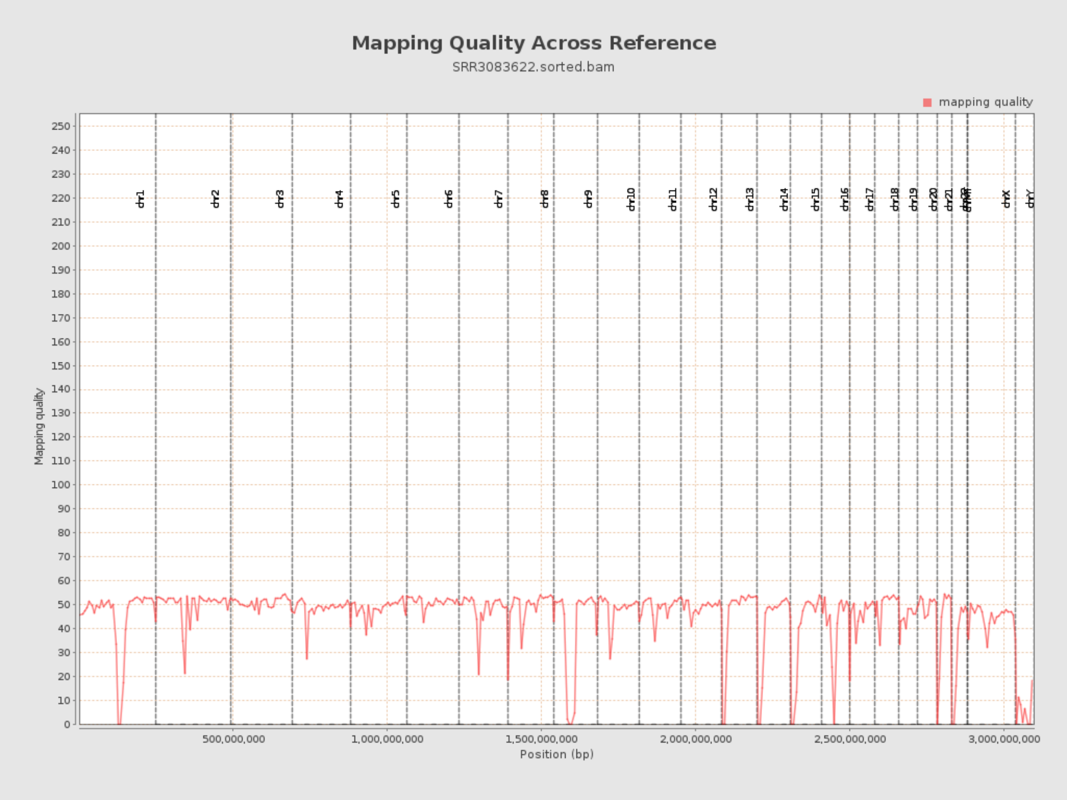
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram