Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 01:09:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081183.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_SRR3081183 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081183.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 01:09:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081183.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,720,544
Mapped reads	1,508,520 / 87.68%
Unmapped reads	212,024 / 12.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,879 / 1.1%
Read min/max/mean length	30 / 76 / 76.38
Duplicated reads (estimated)	58,519 / 3.4%
Duplication rate	2.27%
Clipped reads	731,888 / 42.54%

2.2. ACGT Content

Number/percentage of A's	27,872,055 / 27.82%
Number/percentage of C's	19,344,773 / 19.31%
Number/percentage of T's	29,273,802 / 29.22%
Number/percentage of G's	23,661,349 / 23.62%
Number/percentage of N's	28,922 / 0.03%
GC Percentage	42.93%

2.3. Coverage

Mean	0.0324

Standard Deviation	0.4538

2.4. Mapping Quality

Mean Mapping Quality	42.57

2.5. Mismatches and indels

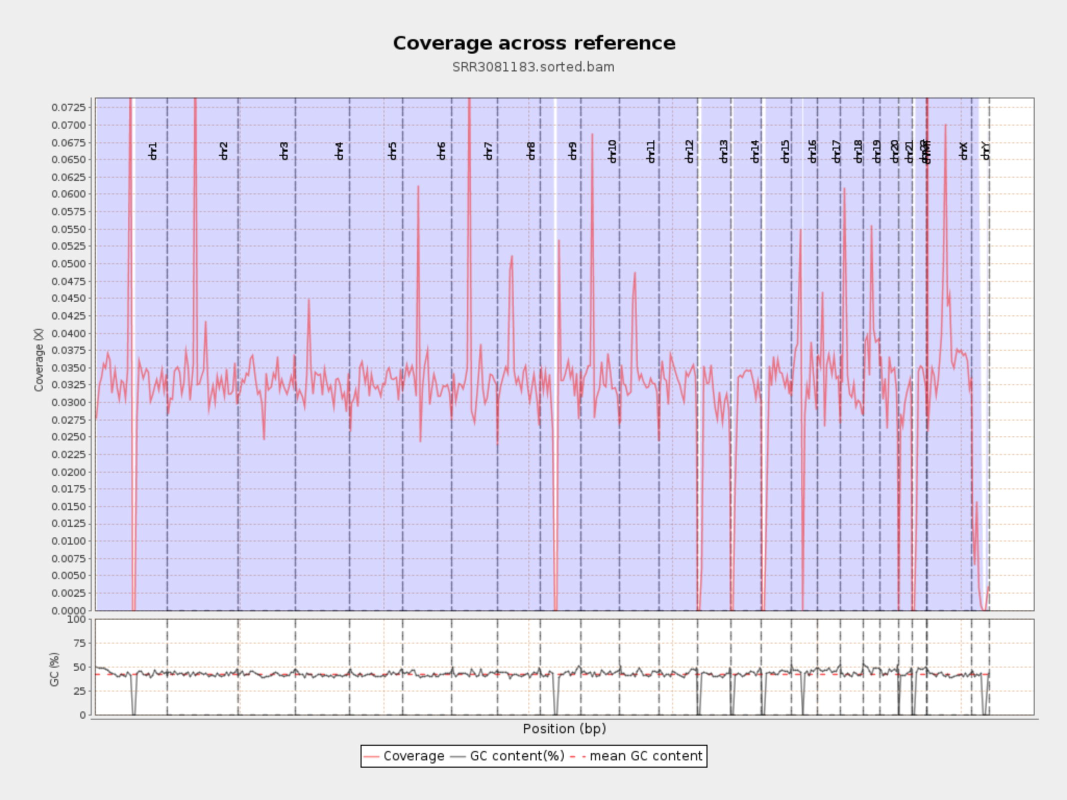
General error rate	0.9%
Mismatches	887,841
Insertions	8,937
Mapped reads with at least one insertion	0.59%
Deletions	20,615
Mapped reads with at least one deletion	1.35%
Homopolymer indels	43.11%

2.6. Chromosome stats

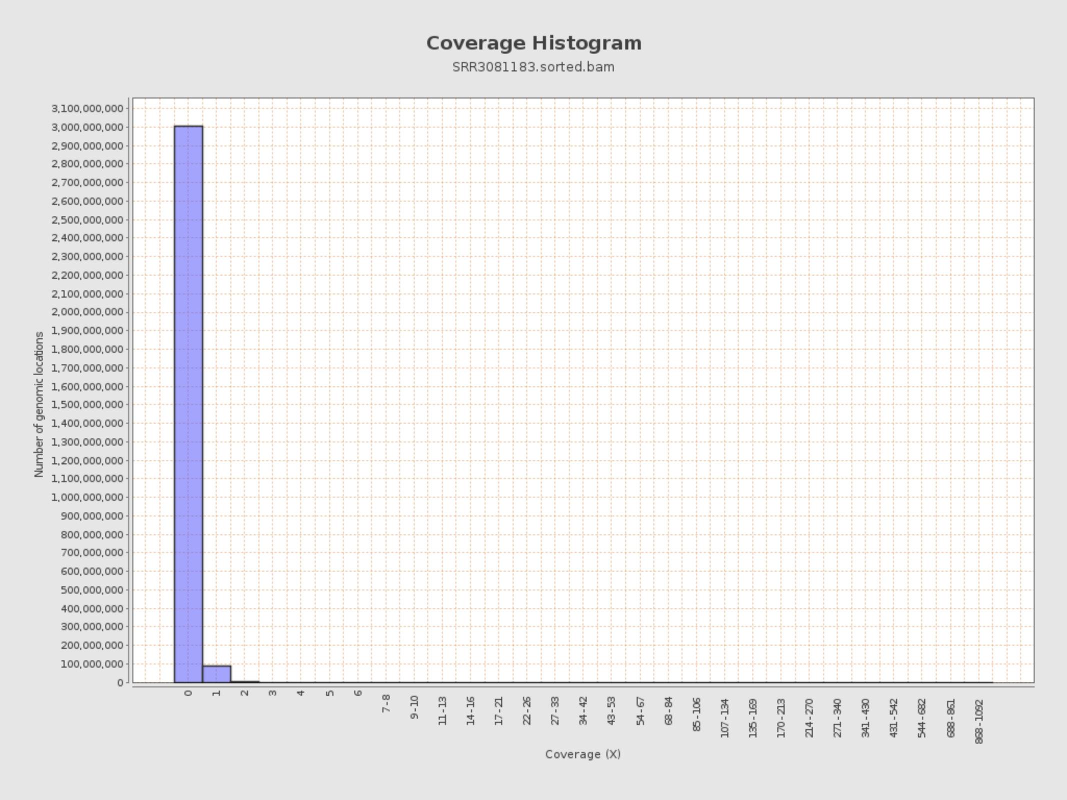
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8104356	0.0325	0.9646
chr2	243199373	8425796	0.0346	0.4682
chr3	198022430	6489110	0.0328	0.1917
chr4	191154276	6270054	0.0328	0.2067
chr5	180915260	5922583	0.0327	0.1974
chr6	171115067	5774831	0.0337	0.35
chr7	159138663	5554170	0.0349	0.6945

chr8	146364022	5043425	0.0345	0.4505
chr9	141213431	4274493	0.0303	0.4048
chr10	135534747	4717731	0.0348	0.3823
chr11	135006516	4640264	0.0344	0.4385
chr12	133851895	4482357	0.0335	0.206
chr13	115169878	2984679	0.0259	0.1685
chr14	107349540	3003082	0.028	0.2265
chr15	102531392	2827375	0.0276	0.1888
chr16	90354753	2942876	0.0326	0.2593
chr17	81195210	2846209	0.0351	0.2785
chr18	78077248	2684594	0.0344	0.8599
chr19	59128983	2373284	0.0401	0.6532
chr20	63025520	2050915	0.0325	0.2057
chr21	48129895	1312211	0.0273	0.2128
chr22	51304566	1215229	0.0237	0.1605
chrMT	16571	35207	2.1246	1.9086
chrX	155270560	5945090	0.0383	0.2848
chrY	59373566	295714	0.005	0.1287

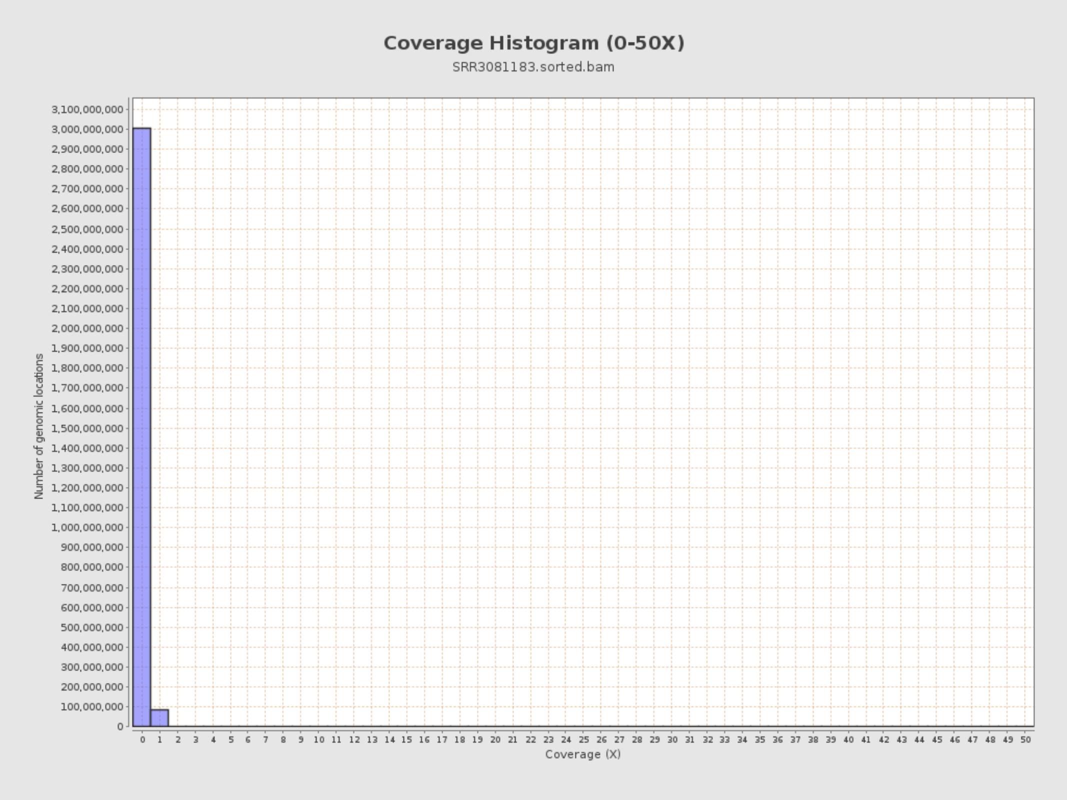
3. Results : Coverage across reference



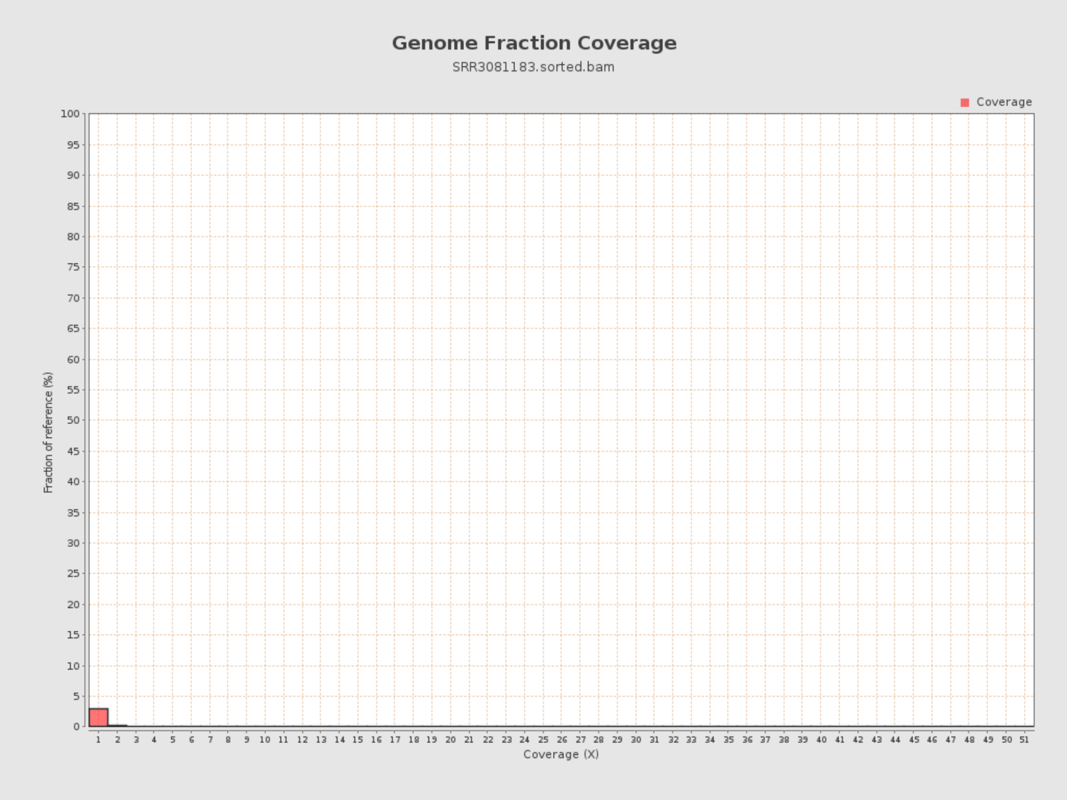
4. Results : Coverage Histogram



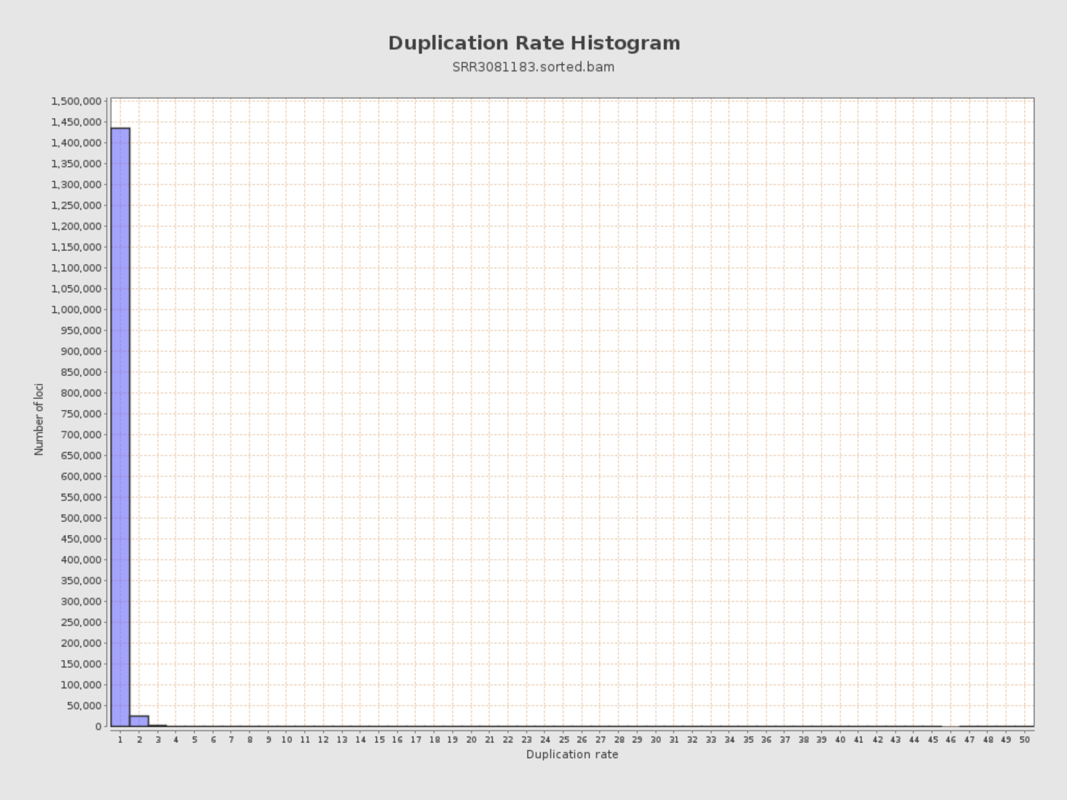
5. Results : Coverage Histogram (0-50X)



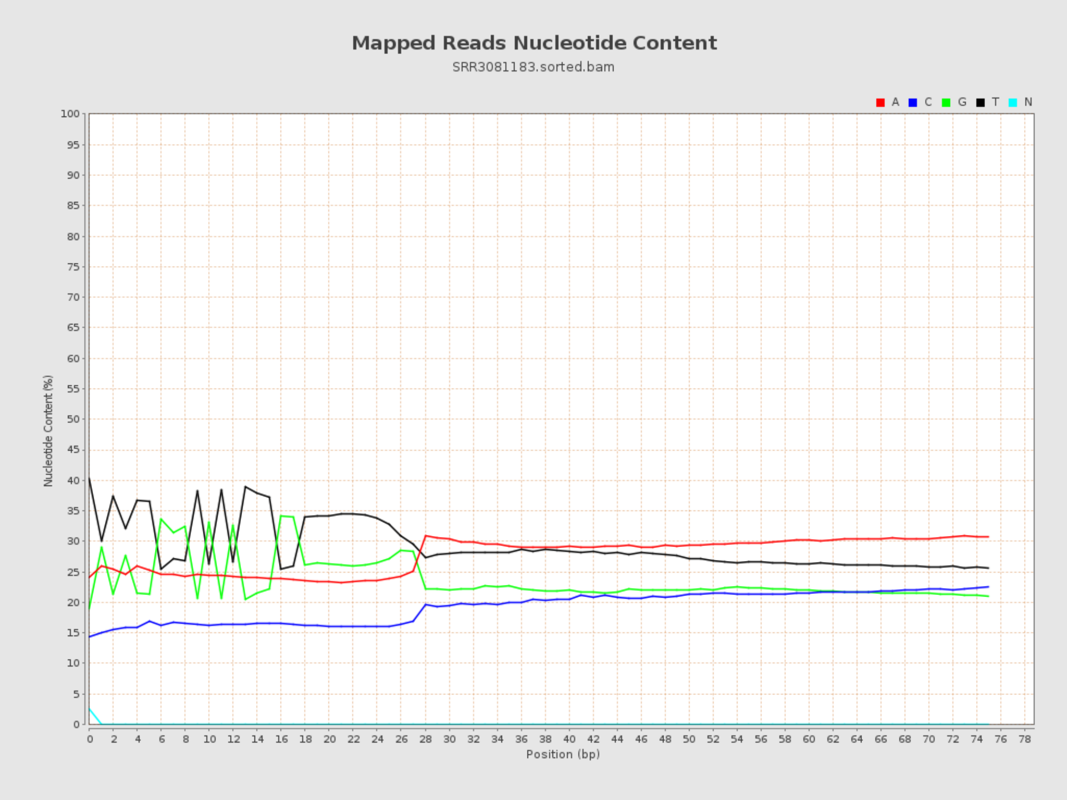
6. Results : Genome Fraction Coverage



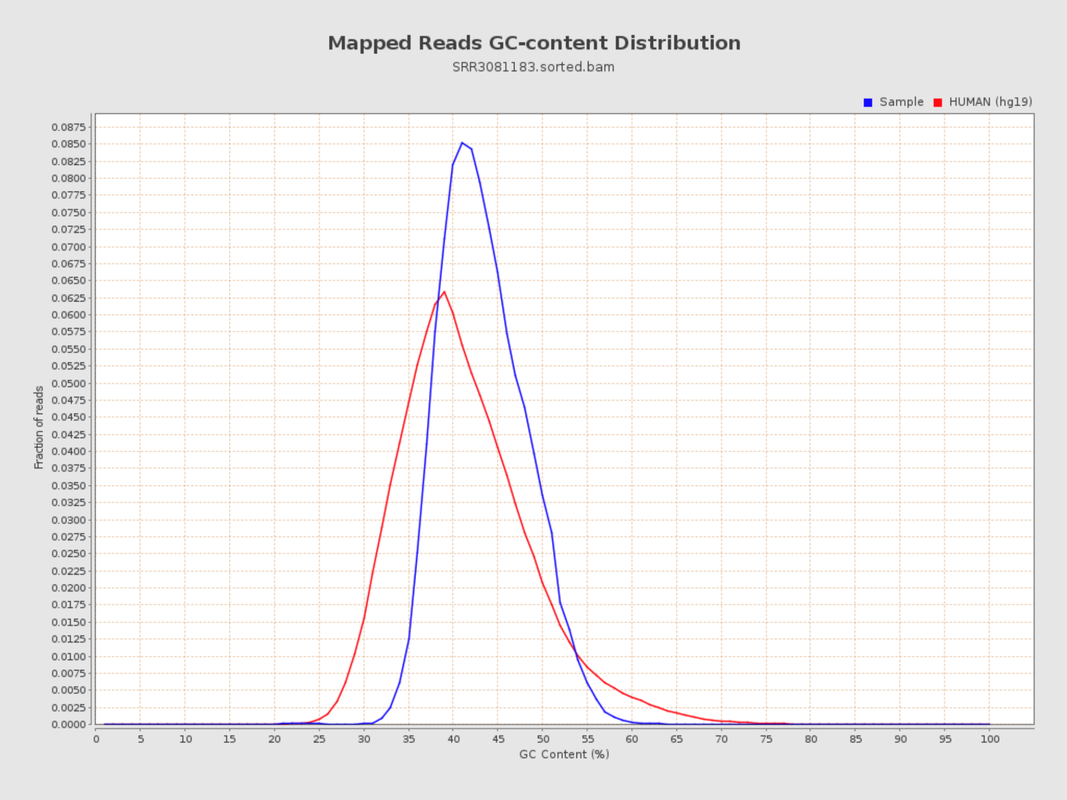
7. Results : Duplication Rate Histogram



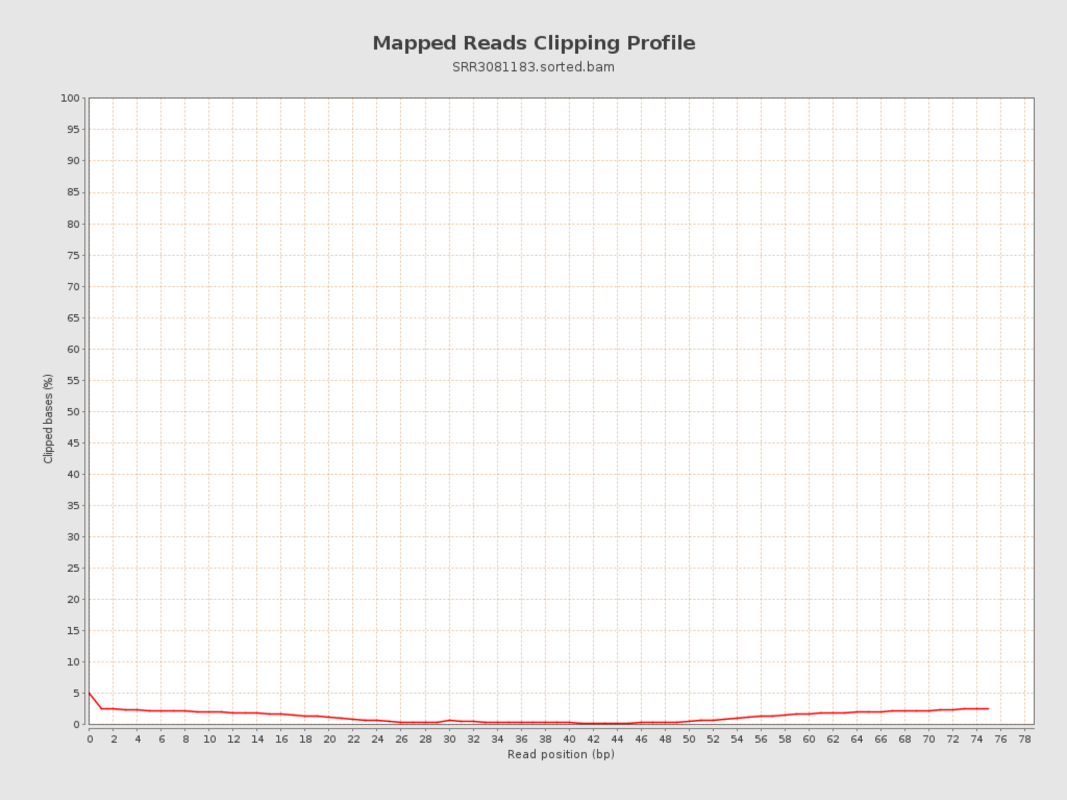
8. Results : Mapped Reads Nucleotide Content



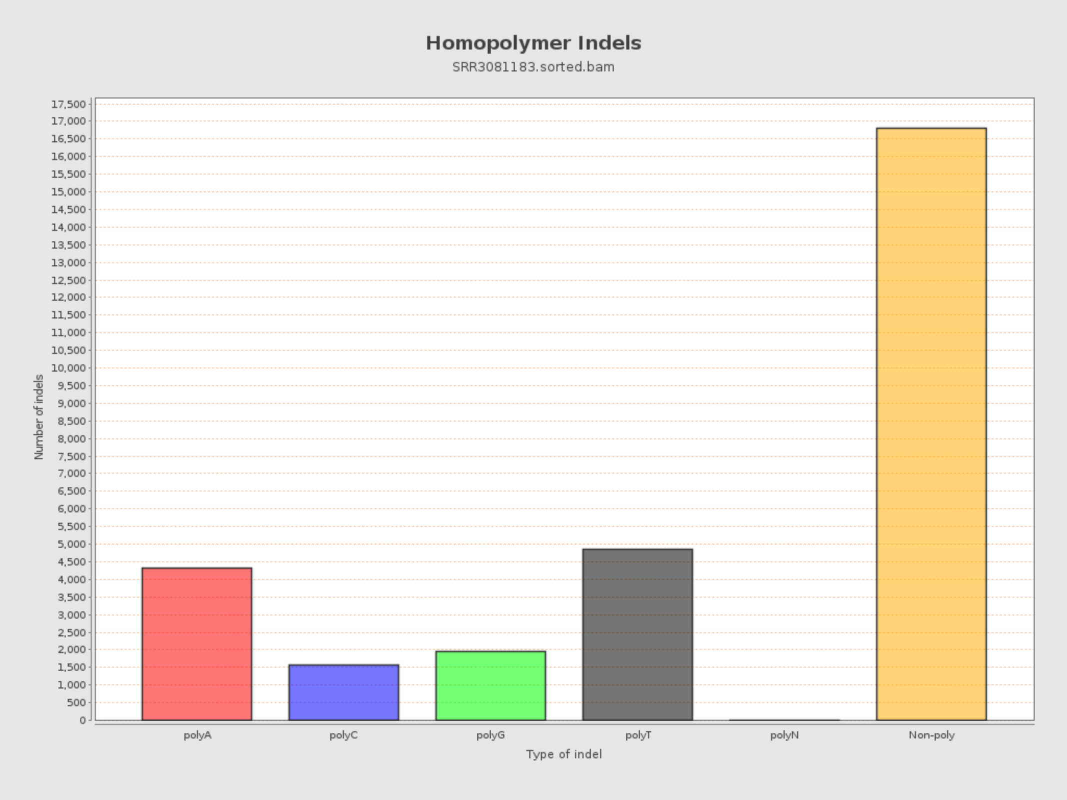
9. Results : Mapped Reads GC-content Distribution



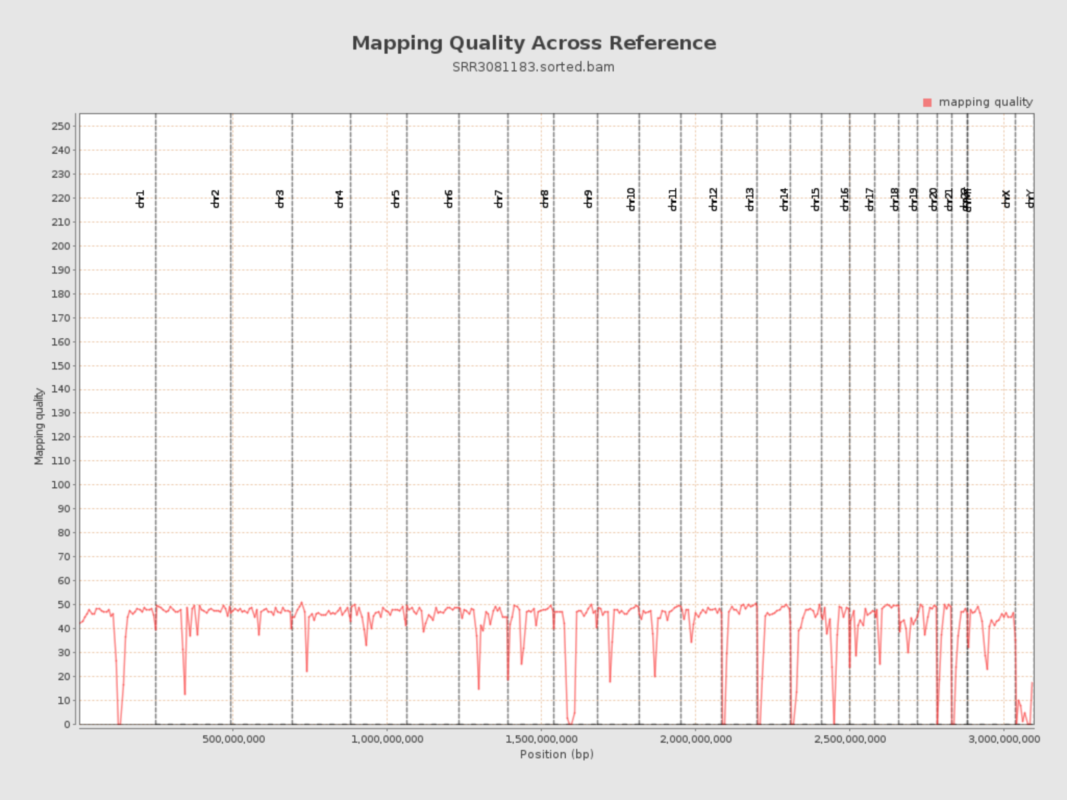
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram