Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 12:13:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080664.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_SRR3080664 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080664.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 12:13:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080664.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,455,949
Mapped reads	1,335,163 / 91.7%
Unmapped reads	120,786 / 8.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,338 / 0.85%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	44,947 / 3.09%
Duplication rate	2.9%
Clipped reads	578,606 / 39.74%

2.2. ACGT Content

Number/percentage of A's	24,417,728 / 27.31%
Number/percentage of C's	16,872,126 / 18.87%
Number/percentage of T's	27,883,688 / 31.18%
Number/percentage of G's	20,245,906 / 22.64%
Number/percentage of N's	4,064 / 0%
GC Percentage	41.51%

2.3. Coverage

Mean	0.0289

Standard Deviation	0.2305

2.4. Mapping Quality

Mean Mapping Quality	45.68

2.5. Mismatches and indels

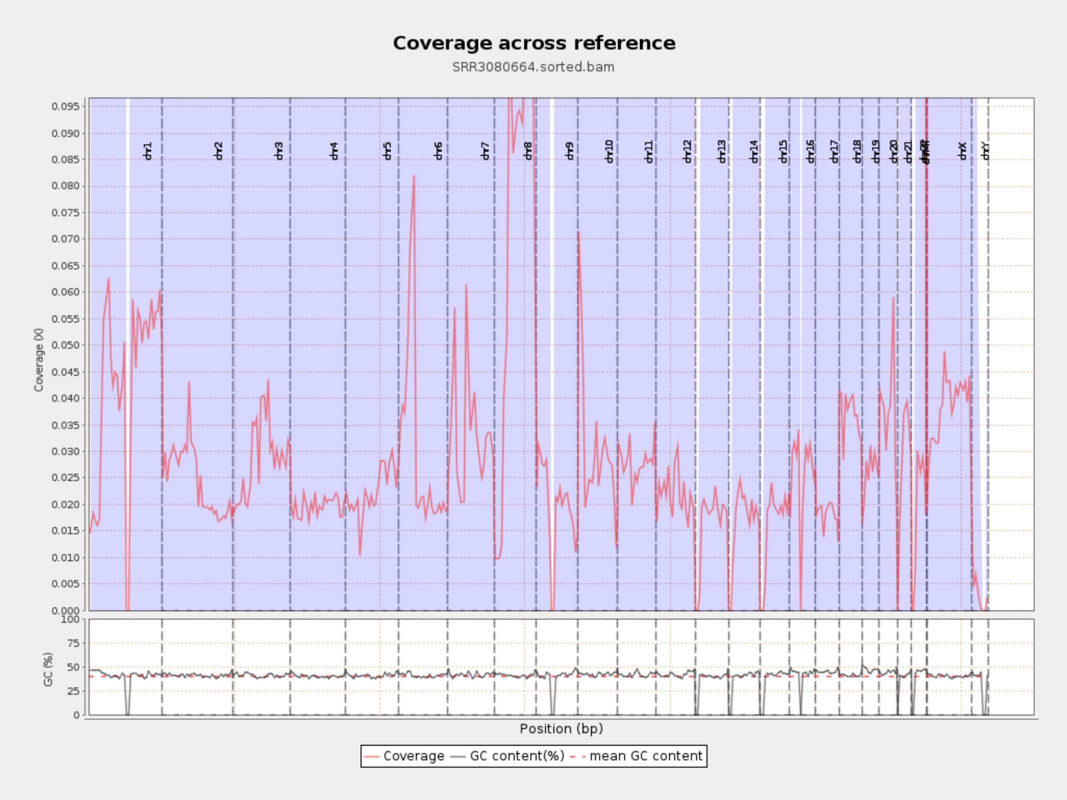
General error rate	0.68%
Mismatches	596,404
Insertions	6,763
Mapped reads with at least one insertion	0.5%
Deletions	20,742
Mapped reads with at least one deletion	1.54%
Homopolymer indels	48%

2.6. Chromosome stats

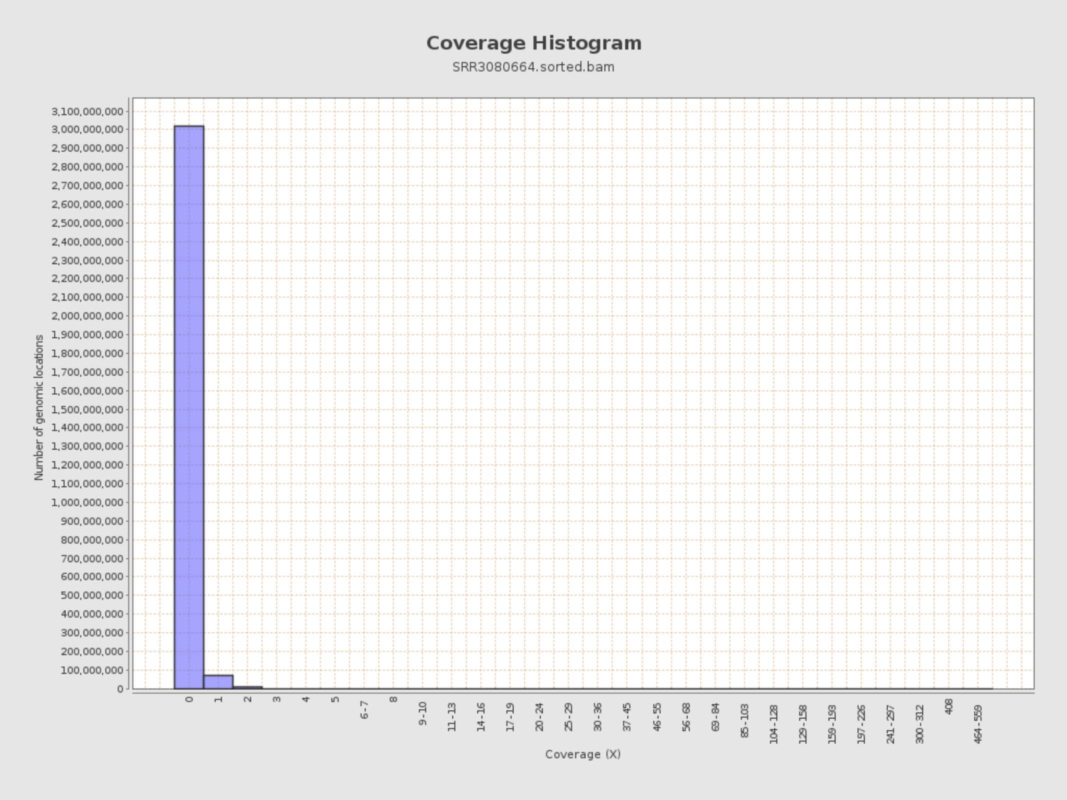
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10531488	0.0423	0.2784
chr2	243199373	5989450	0.0246	0.3148
chr3	198022430	5700051	0.0288	0.1881
chr4	191154276	3752067	0.0196	0.1593
chr5	180915260	4045124	0.0224	0.1647
chr6	171115067	5344737	0.0312	0.2275
chr7	159138663	5435328	0.0342	0.395

chr8	146364022	10675296	0.0729	0.3285
chr9	141213431	2760542	0.0195	0.1809
chr10	135534747	4261871	0.0314	0.2101
chr11	135006516	3747967	0.0278	0.2222
chr12	133851895	2903782	0.0217	0.1648
chr13	115169878	1848917	0.0161	0.1404
chr14	107349540	1794488	0.0167	0.1485
chr15	102531392	1640730	0.016	0.1468
chr16	90354753	2330511	0.0258	0.1814
chr17	81195210	1471922	0.0181	0.1514
chr18	78077248	2900548	0.0371	0.2602
chr19	59128983	1544778	0.0261	0.2004
chr20	63025520	2383838	0.0378	0.2188
chr21	48129895	1347059	0.028	0.1913
chr22	51304566	950896	0.0185	0.1505
chrMT	16571	17774	1.0726	1.1967
chrX	155270560	5898213	0.038	0.2243
chrY	59373566	180100	0.003	0.0665

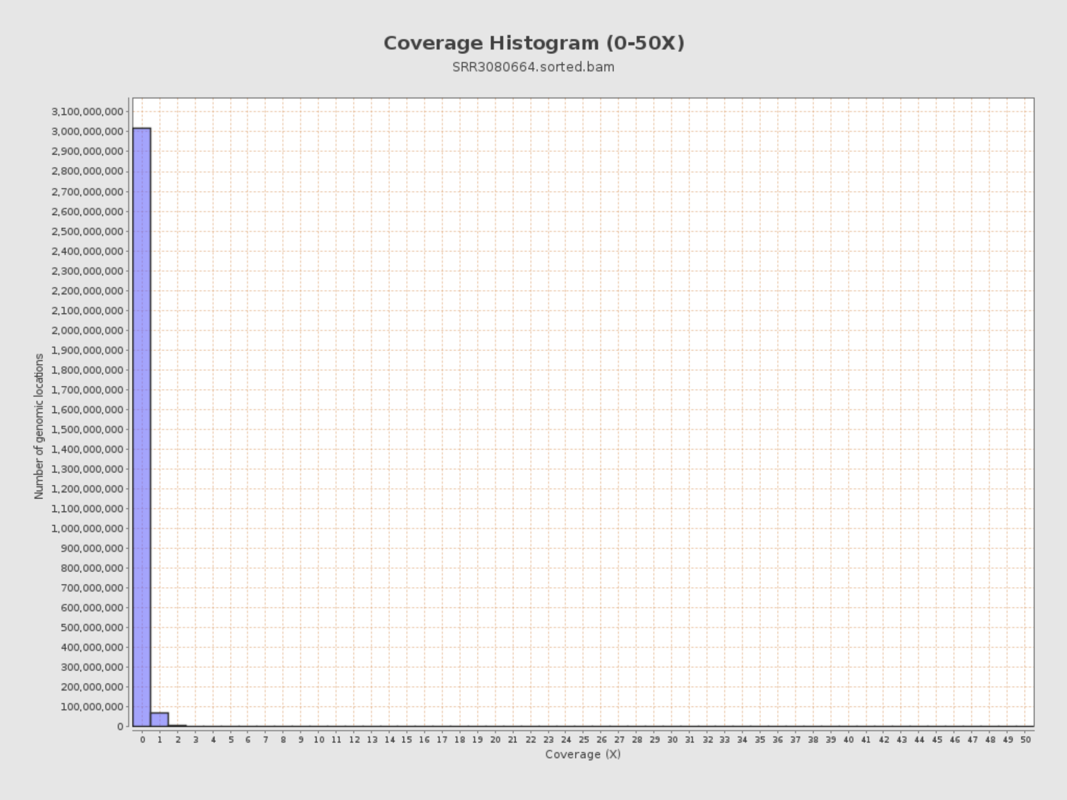
3. Results : Coverage across reference



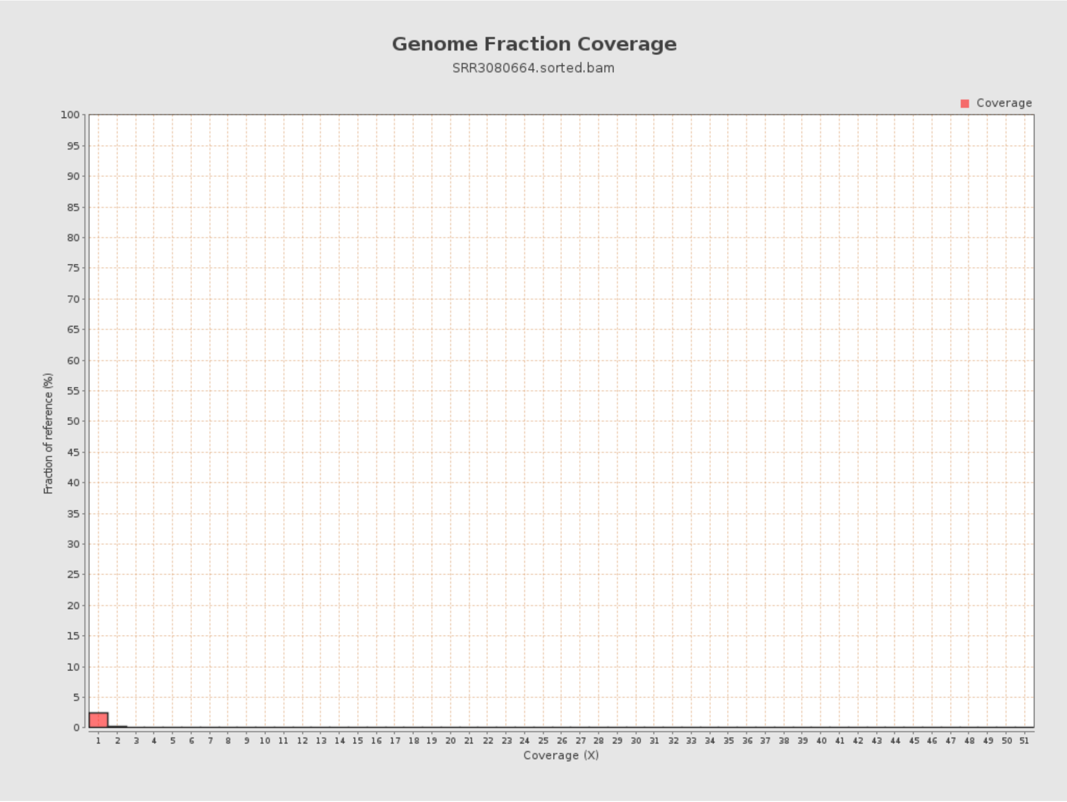
4. Results : Coverage Histogram



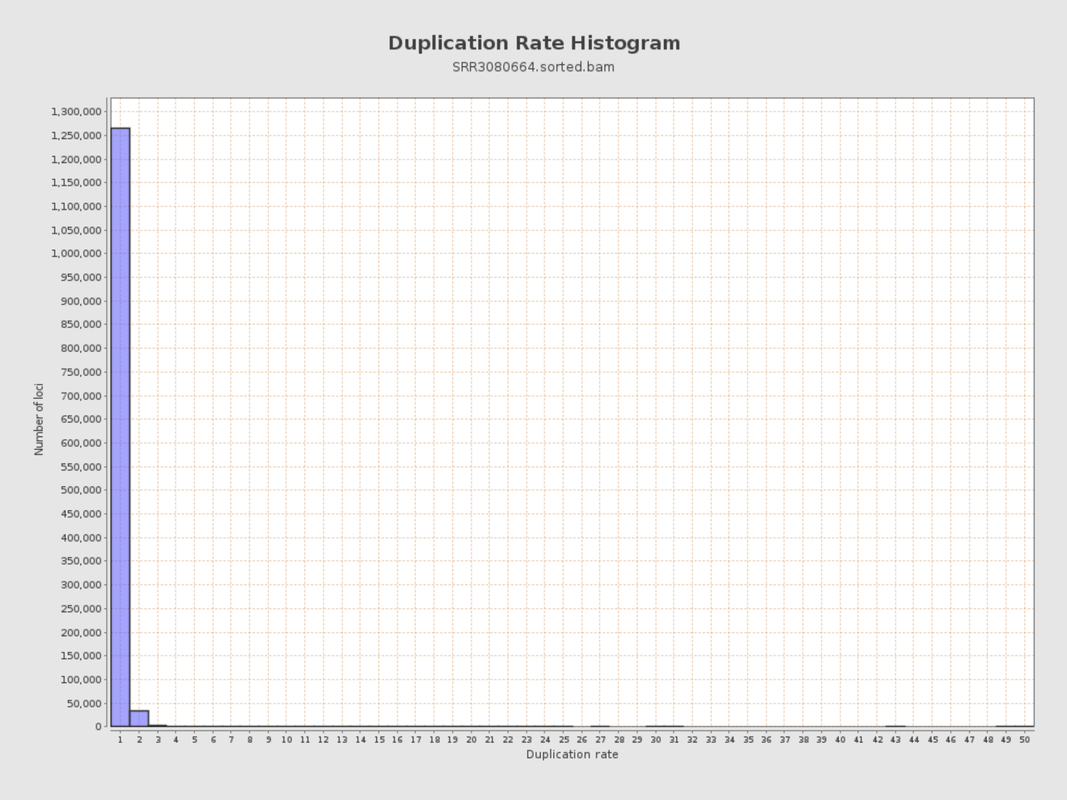
5. Results : Coverage Histogram (0-50X)



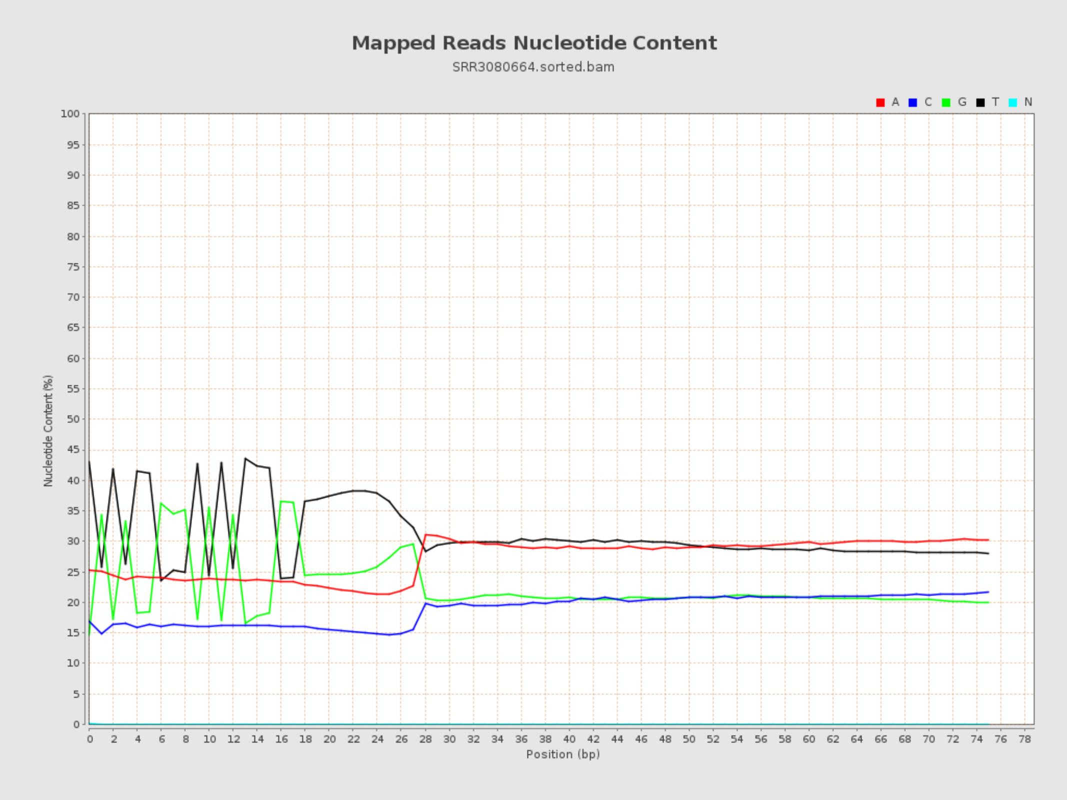
6. Results : Genome Fraction Coverage



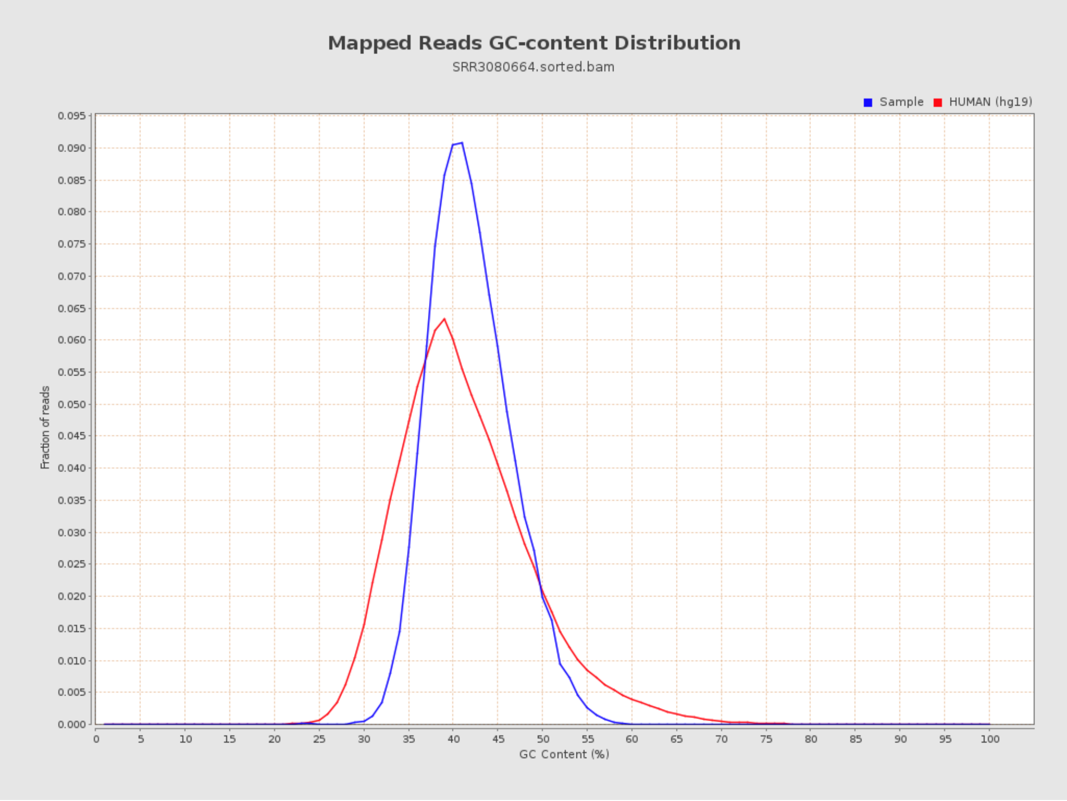
7. Results : Duplication Rate Histogram



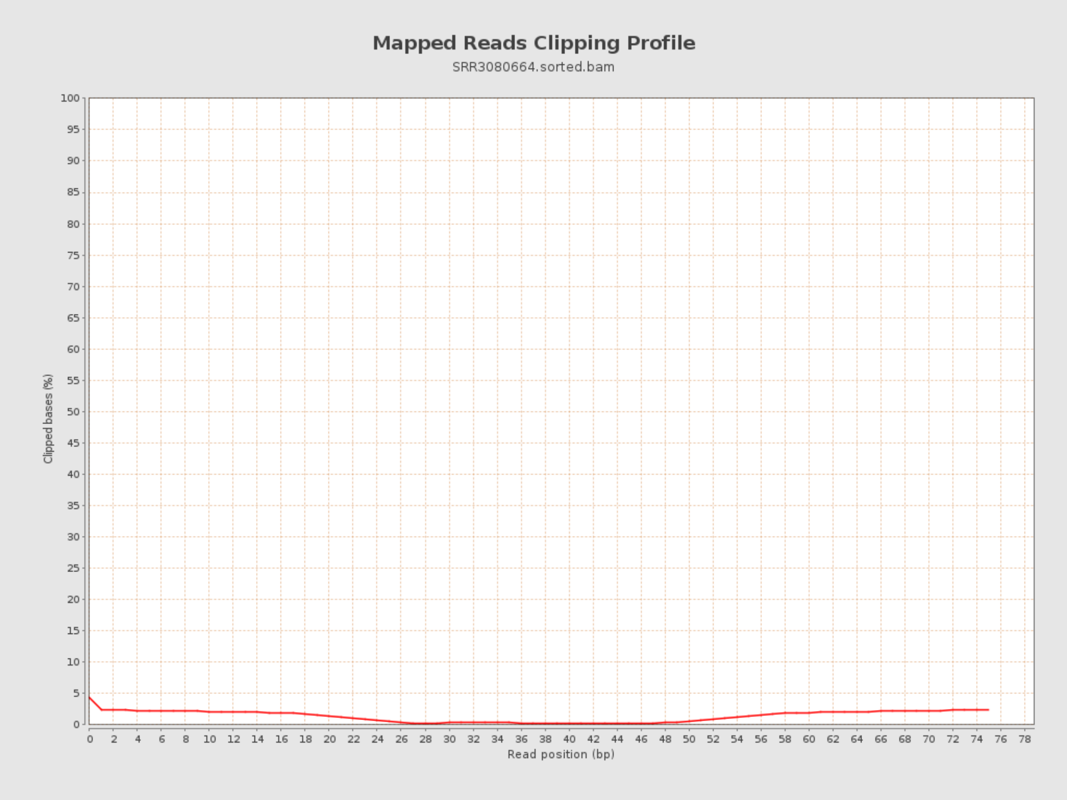
8. Results : Mapped Reads Nucleotide Content



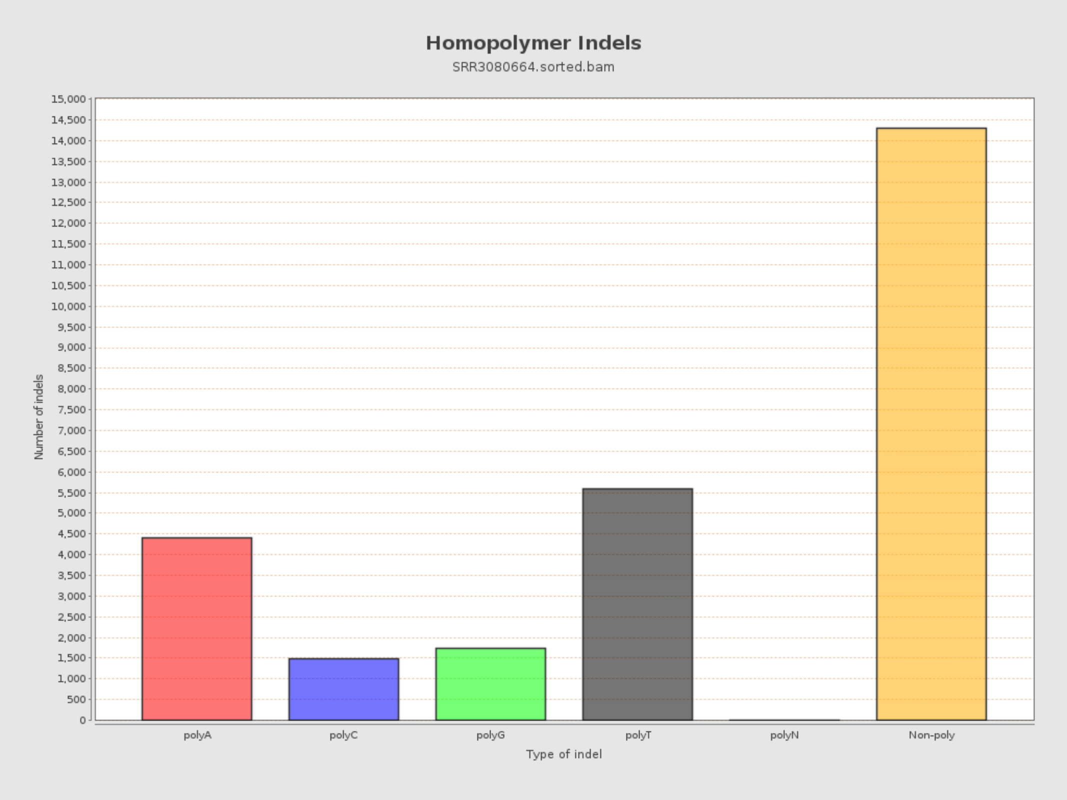
9. Results : Mapped Reads GC-content Distribution



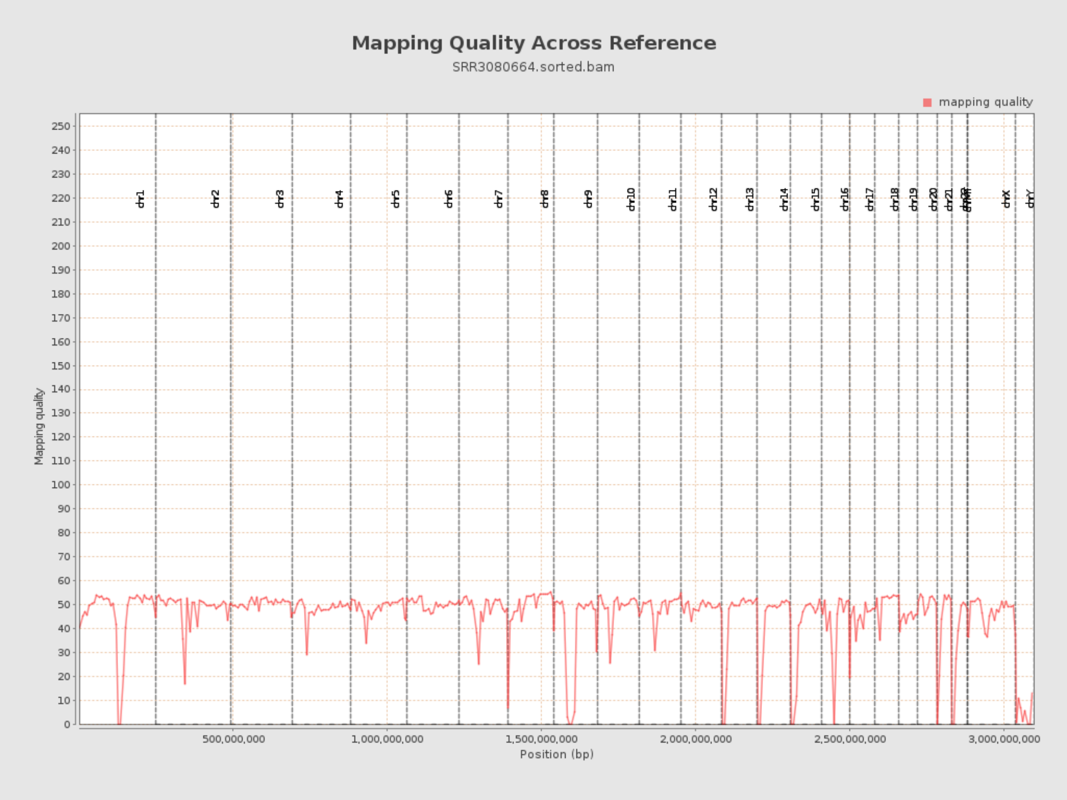
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram