Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 02:24:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083654.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_SRR3083654 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083654.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 02:24:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083654.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,551,627
Mapped reads	1,211,101 / 78.05%
Unmapped reads	340,526 / 21.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,051 / 0.52%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	26,187 / 1.69%
Duplication rate	1.63%
Clipped reads	630,056 / 40.61%

2.2. ACGT Content

Number/percentage of A's	23,527,181 / 30.06%
Number/percentage of C's	14,516,421 / 18.55%
Number/percentage of T's	22,829,185 / 29.17%
Number/percentage of G's	17,390,739 / 22.22%
Number/percentage of N's	10,689 / 0.01%
GC Percentage	40.76%

2.3. Coverage

Mean	0.0253

Standard Deviation	0.267

2.4. Mapping Quality

Mean Mapping Quality	45.38

2.5. Mismatches and indels

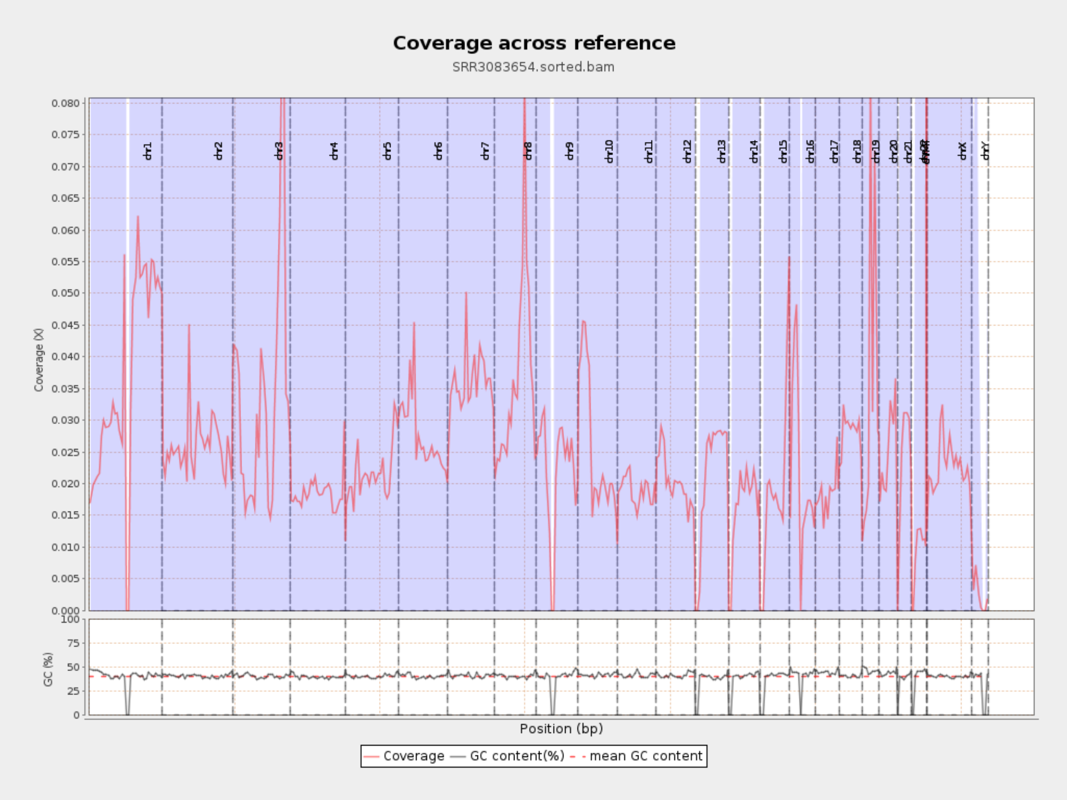
General error rate	0.9%
Mismatches	693,269
Insertions	5,725
Mapped reads with at least one insertion	0.47%
Deletions	16,393
Mapped reads with at least one deletion	1.34%
Homopolymer indels	46.68%

2.6. Chromosome stats

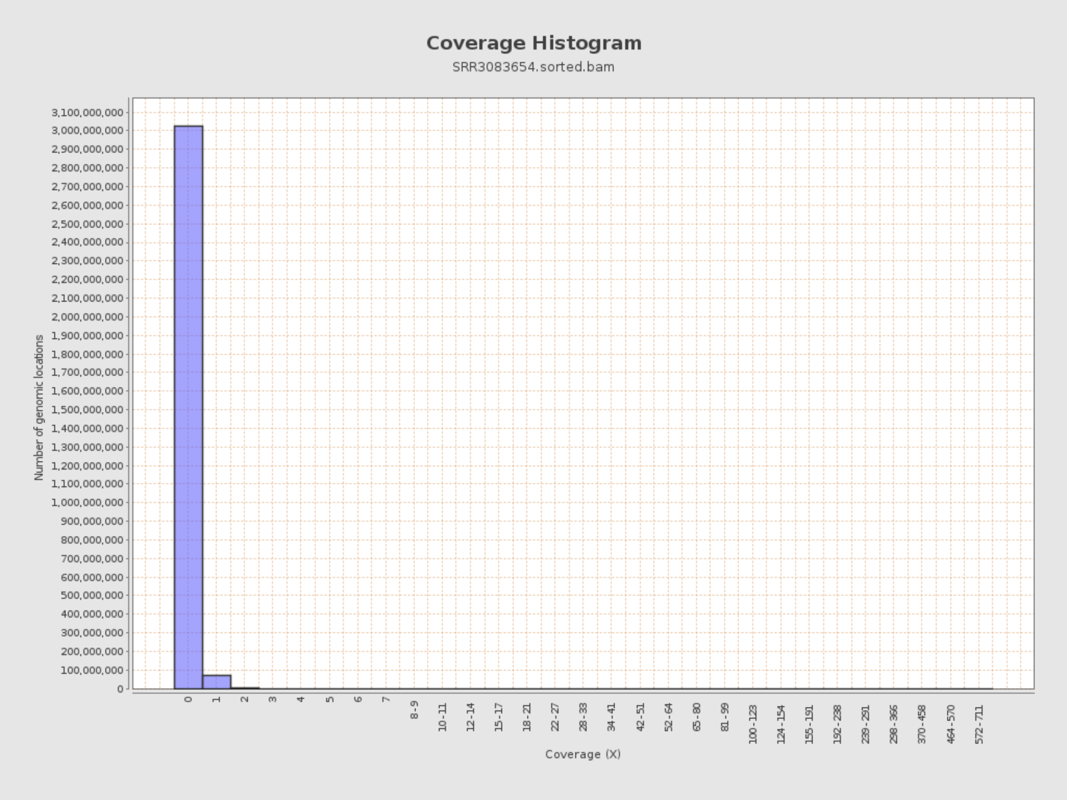
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9156098	0.0367	0.6393
chr2	243199373	6338545	0.0261	0.2252
chr3	198022430	6660955	0.0336	0.1939
chr4	191154276	3557493	0.0186	0.1443
chr5	180915260	3934669	0.0217	0.1545
chr6	171115067	4772837	0.0279	0.2011
chr7	159138663	5779523	0.0363	0.3619

chr8	146364022	5379667	0.0368	0.2965
chr9	141213431	3113692	0.022	0.1883
chr10	135534747	3556847	0.0262	0.2174
chr11	135006516	2545406	0.0189	0.1572
chr12	133851895	2697032	0.0201	0.1495
chr13	115169878	2441110	0.0212	0.1516
chr14	107349540	1745016	0.0163	0.1346
chr15	102531392	1886930	0.0184	0.1423
chr16	90354753	2021256	0.0224	0.1611
chr17	81195210	1499687	0.0185	0.1472
chr18	78077248	2211731	0.0283	0.2801
chr19	59128983	2155303	0.0365	0.3583
chr20	63025520	1593447	0.0253	0.1679
chr21	48129895	1127187	0.0234	0.1618
chr22	51304566	454851	0.0089	0.098
chrMT	16571	4199	0.2534	0.4808
chrX	155270560	3518707	0.0227	0.1614
chrY	59373566	148295	0.0025	0.0595

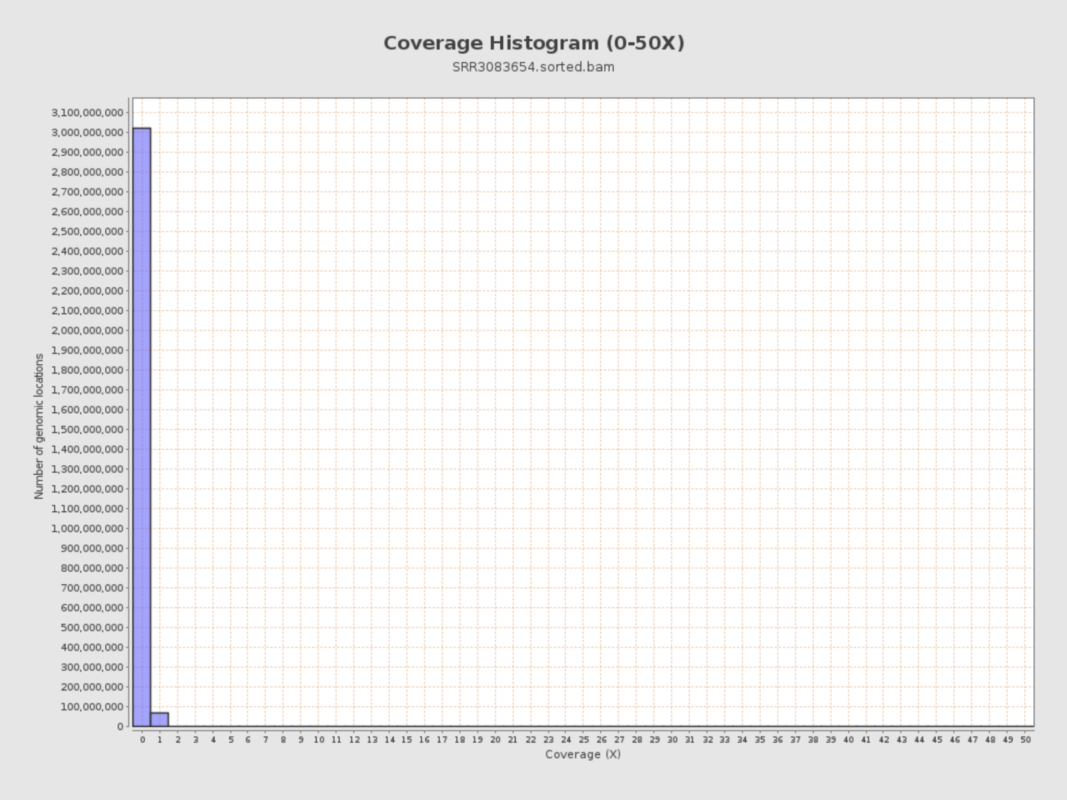
3. Results : Coverage across reference



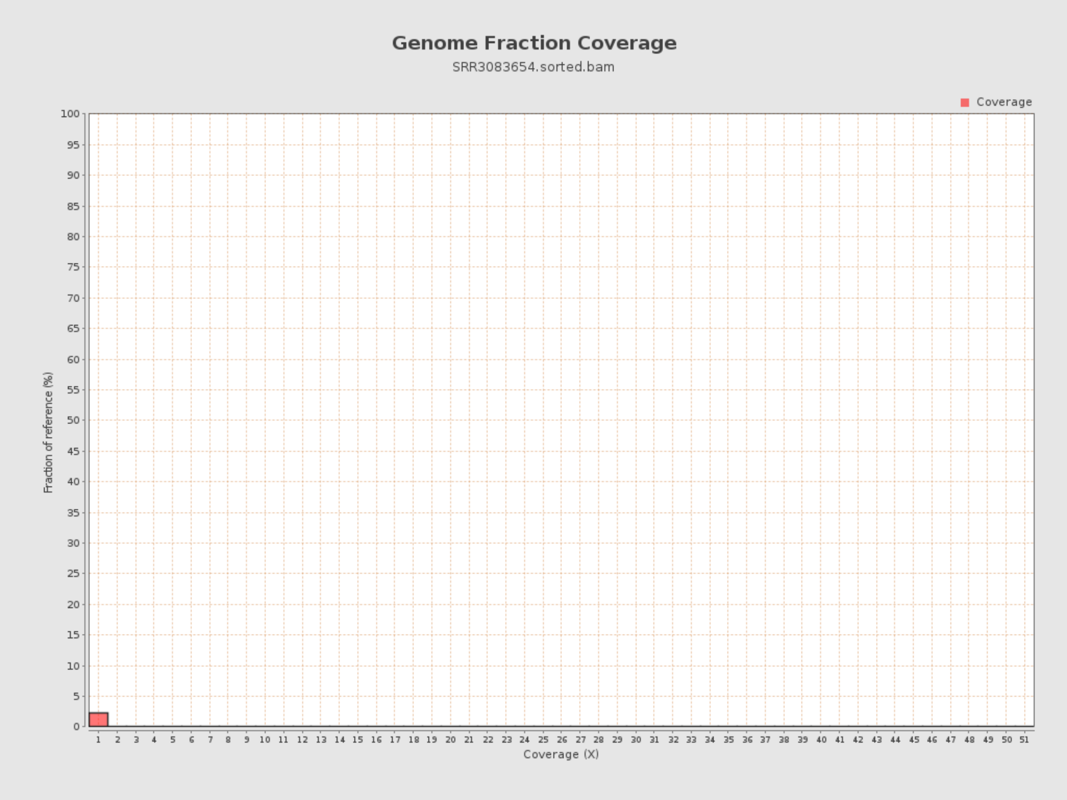
4. Results : Coverage Histogram



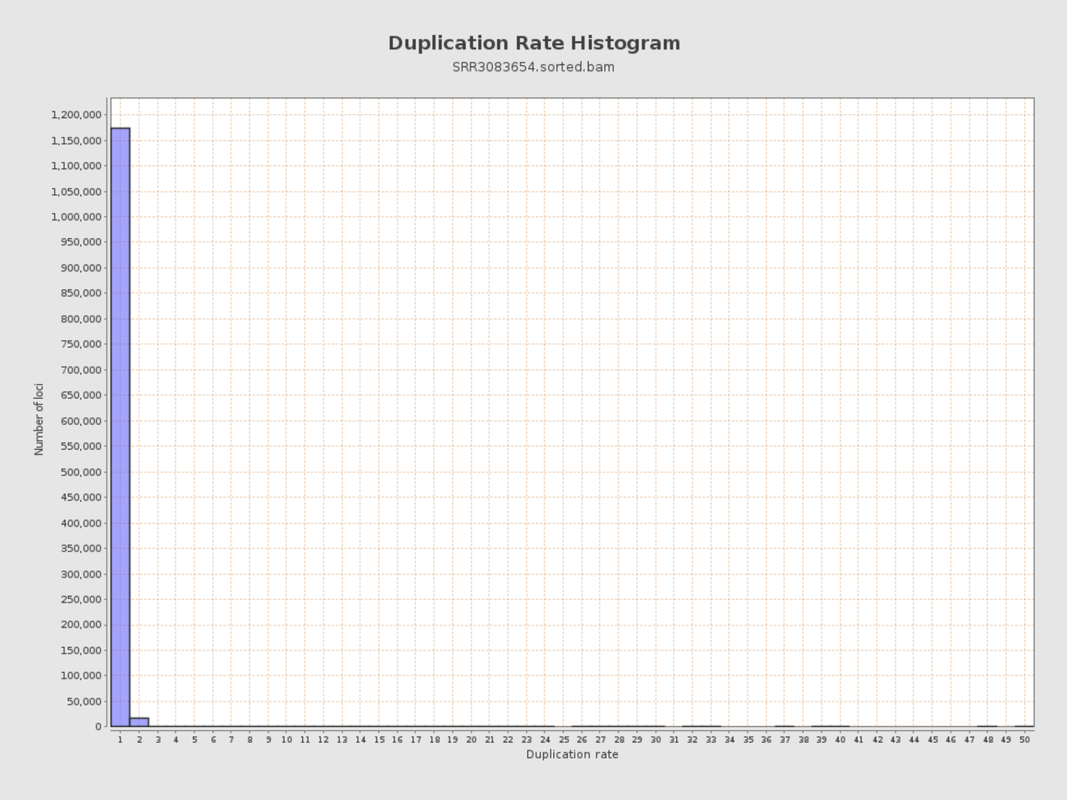
5. Results : Coverage Histogram (0-50X)



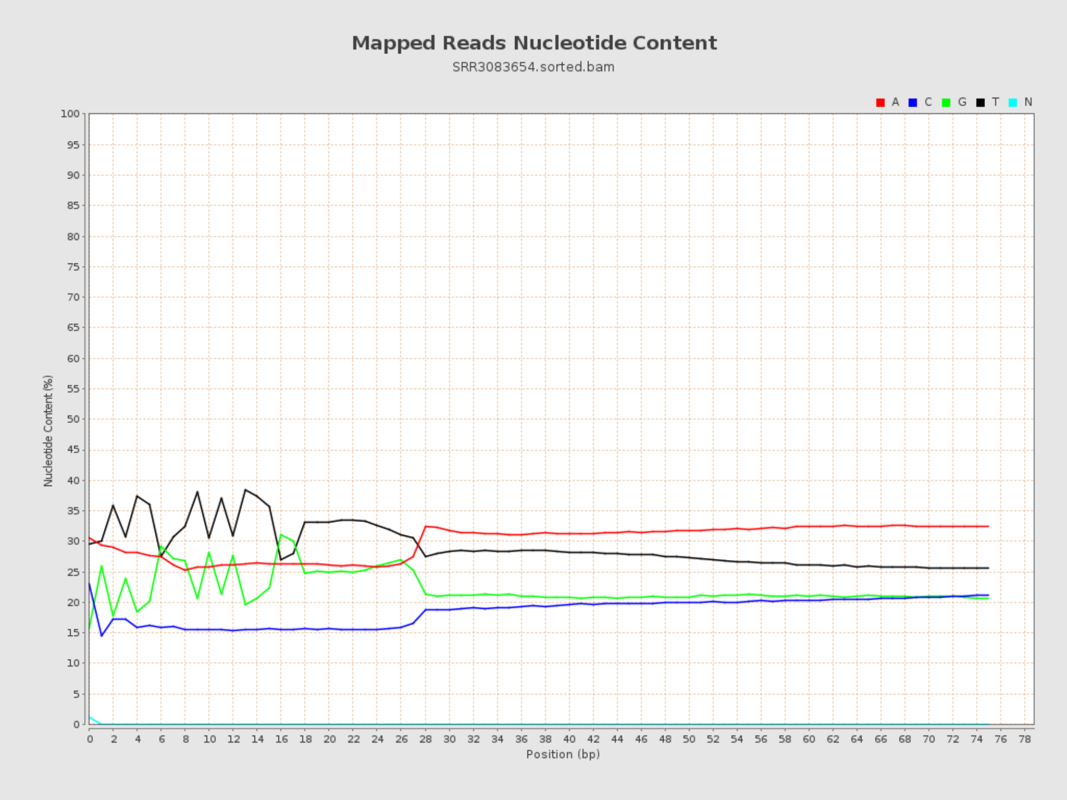
6. Results : Genome Fraction Coverage



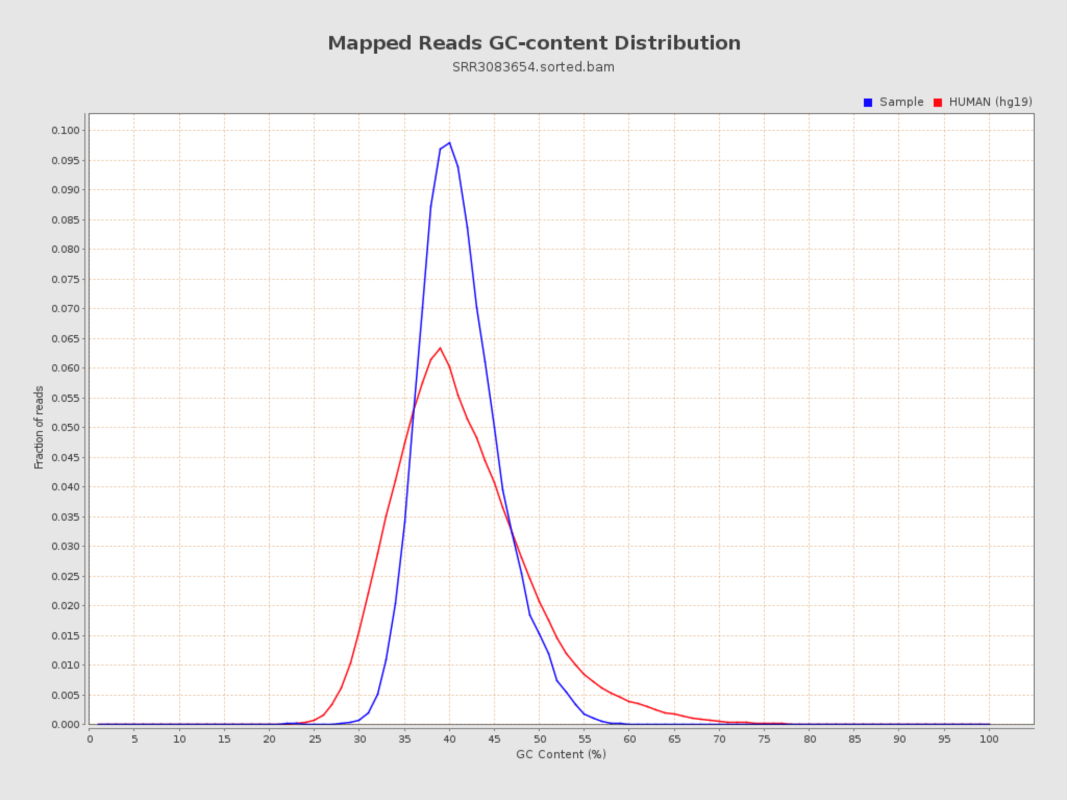
7. Results : Duplication Rate Histogram



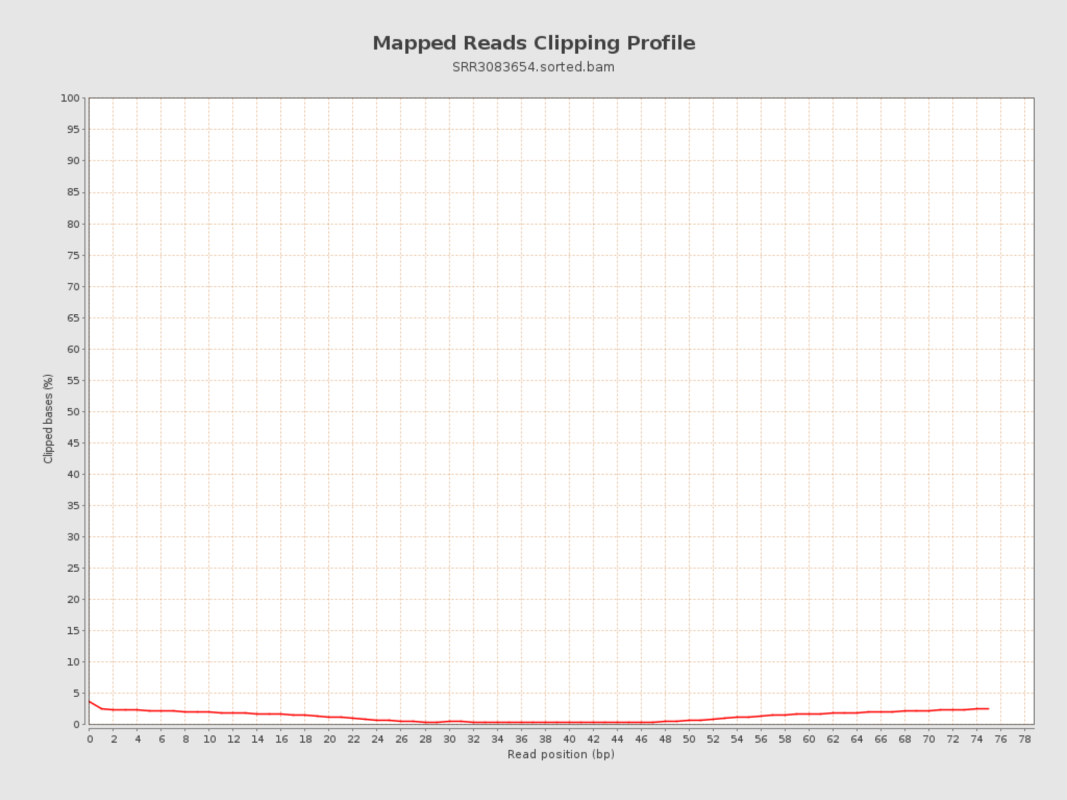
8. Results : Mapped Reads Nucleotide Content



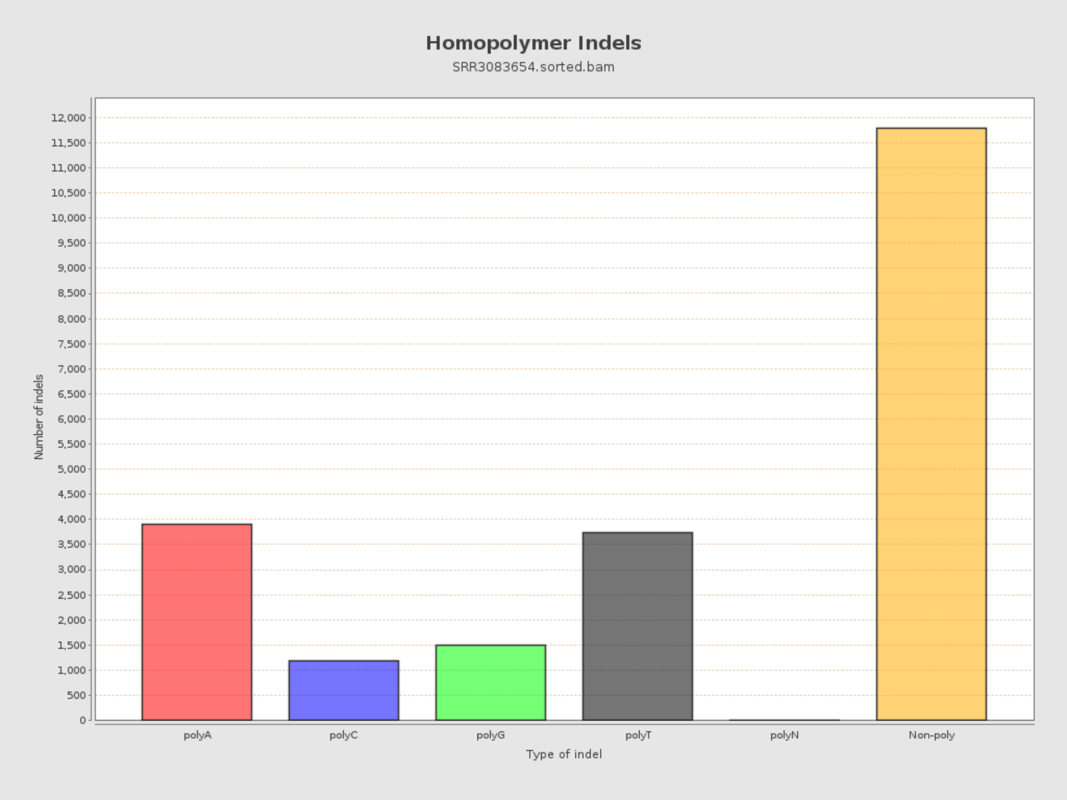
9. Results : Mapped Reads GC-content Distribution



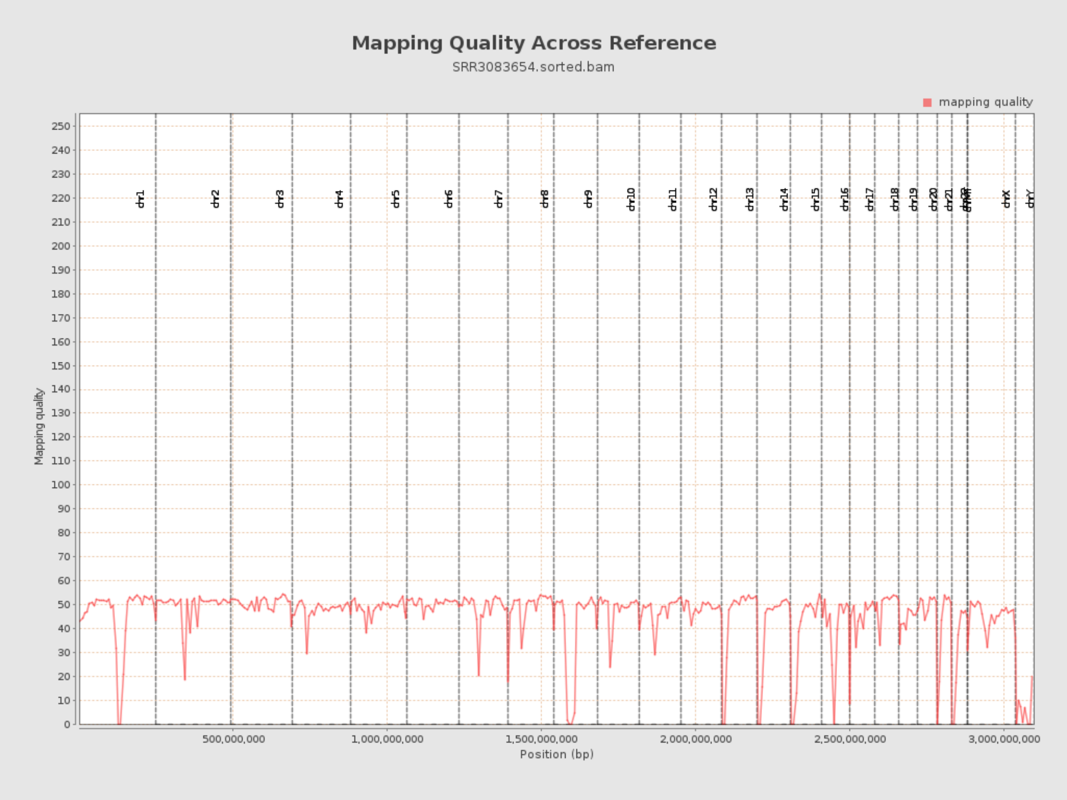
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram