Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 05:00:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081246.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_SRR3081246 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081246.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 05:00:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081246.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,394,569
Mapped reads	1,163,901 / 83.46%
Unmapped reads	230,668 / 16.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,794 / 1.06%
Read min/max/mean length	30 / 76 / 76.37
Duplicated reads (estimated)	29,291 / 2.1%
Duplication rate	1.67%
Clipped reads	594,304 / 42.62%

2.2. ACGT Content

Number/percentage of A's	22,312,142 / 29.25%
Number/percentage of C's	14,964,643 / 19.62%
Number/percentage of T's	21,936,730 / 28.76%
Number/percentage of G's	17,054,295 / 22.36%
Number/percentage of N's	5,113 / 0.01%
GC Percentage	41.98%

2.3. Coverage

Mean	0.0246

Standard Deviation	0.2818

2.4. Mapping Quality

Mean Mapping Quality	43.5

2.5. Mismatches and indels

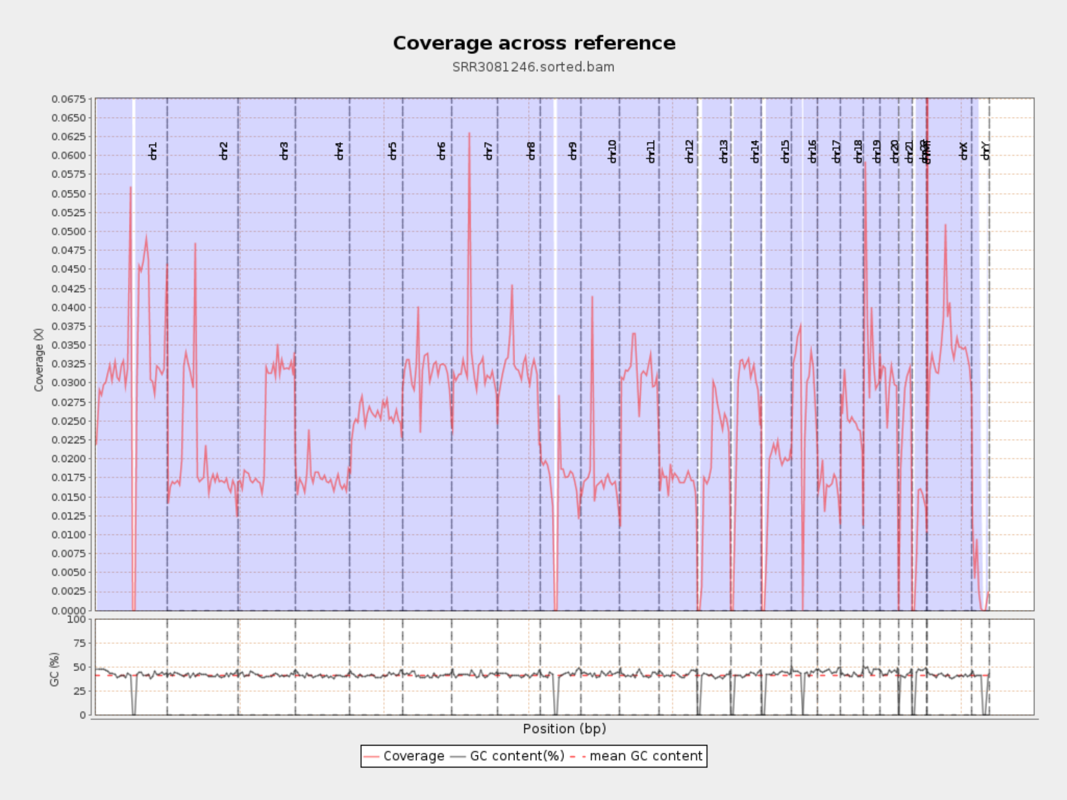
General error rate	0.93%
Mismatches	696,539
Insertions	6,236
Mapped reads with at least one insertion	0.53%
Deletions	16,005
Mapped reads with at least one deletion	1.36%
Homopolymer indels	44.1%

2.6. Chromosome stats

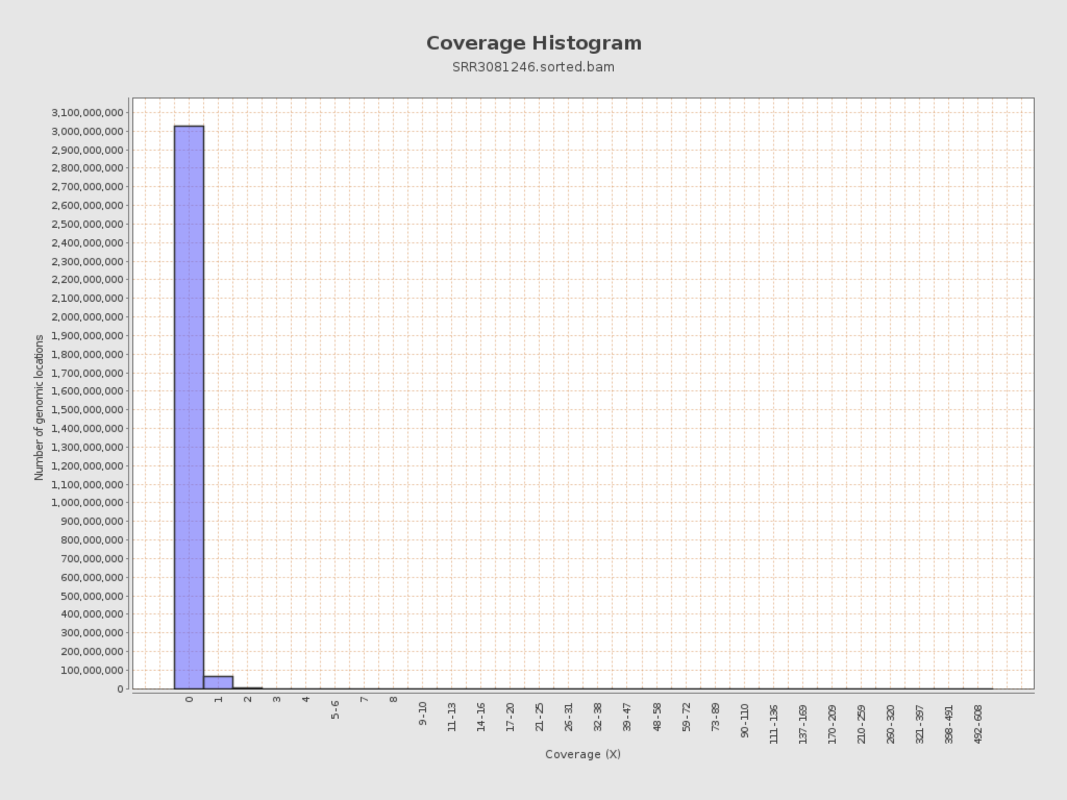
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8044484	0.0323	0.5566
chr2	243199373	4965531	0.0204	0.2834
chr3	198022430	4932155	0.0249	0.1659
chr4	191154276	3327153	0.0174	0.1429
chr5	180915260	4654937	0.0257	0.1685
chr6	171115067	5400445	0.0316	0.2177
chr7	159138663	5183046	0.0326	0.4696

chr8	146364022	4682097	0.032	0.3058
chr9	141213431	2296937	0.0163	0.2236
chr10	135534747	2438340	0.018	0.2387
chr11	135006516	4196330	0.0311	0.3267
chr12	133851895	2297725	0.0172	0.1402
chr13	115169878	2237789	0.0194	0.144
chr14	107349540	2766374	0.0258	0.1755
chr15	102531392	1700246	0.0166	0.1394
chr16	90354753	2543469	0.0281	0.1865
chr17	81195210	1327170	0.0163	0.1682
chr18	78077248	1987437	0.0255	0.375
chr19	59128983	2095635	0.0354	0.4029
chr20	63025520	1848456	0.0293	0.1803
chr21	48129895	1172965	0.0244	0.1719
chr22	51304566	542259	0.0106	0.1062
chrMT	16571	38235	2.3073	2.0703
chrX	155270560	5415722	0.0349	0.2194
chrY	59373566	204276	0.0034	0.0754

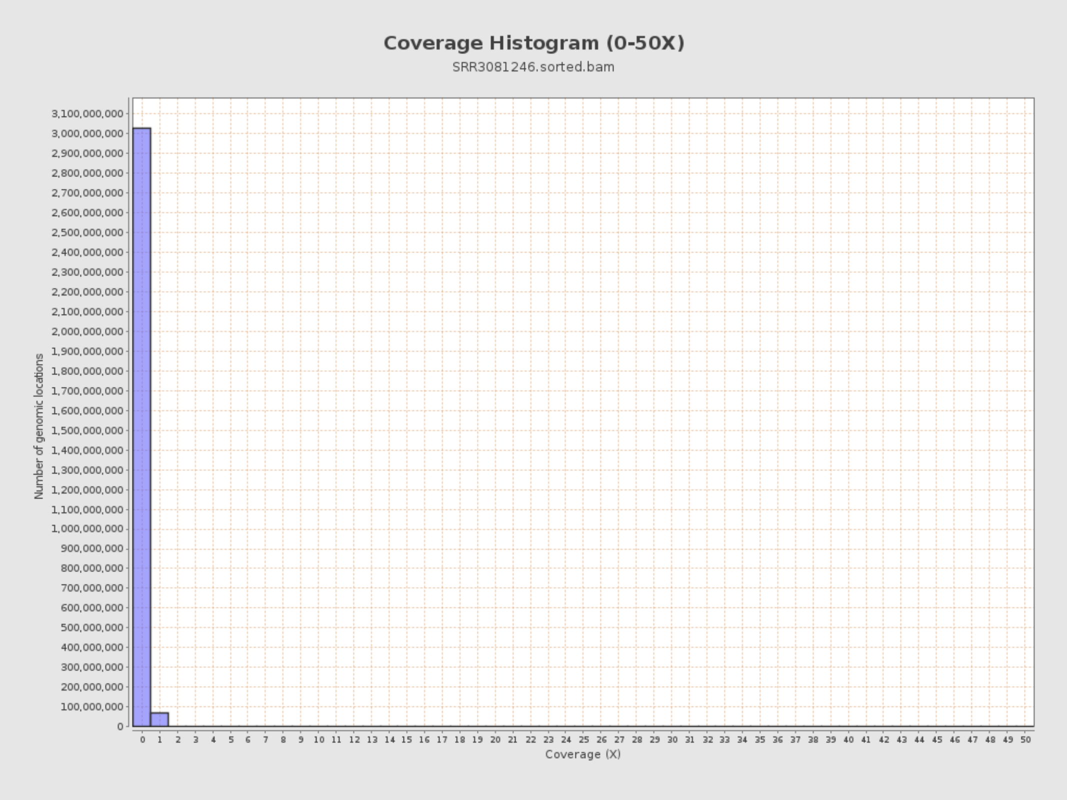
3. Results : Coverage across reference



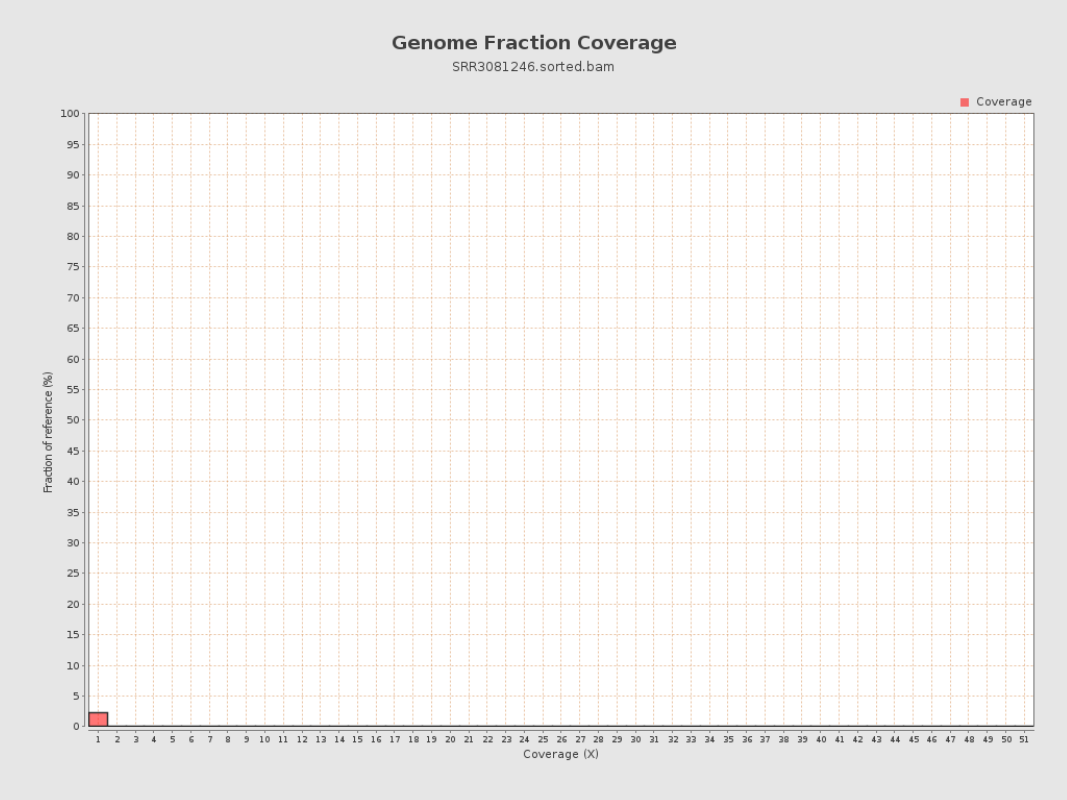
4. Results : Coverage Histogram



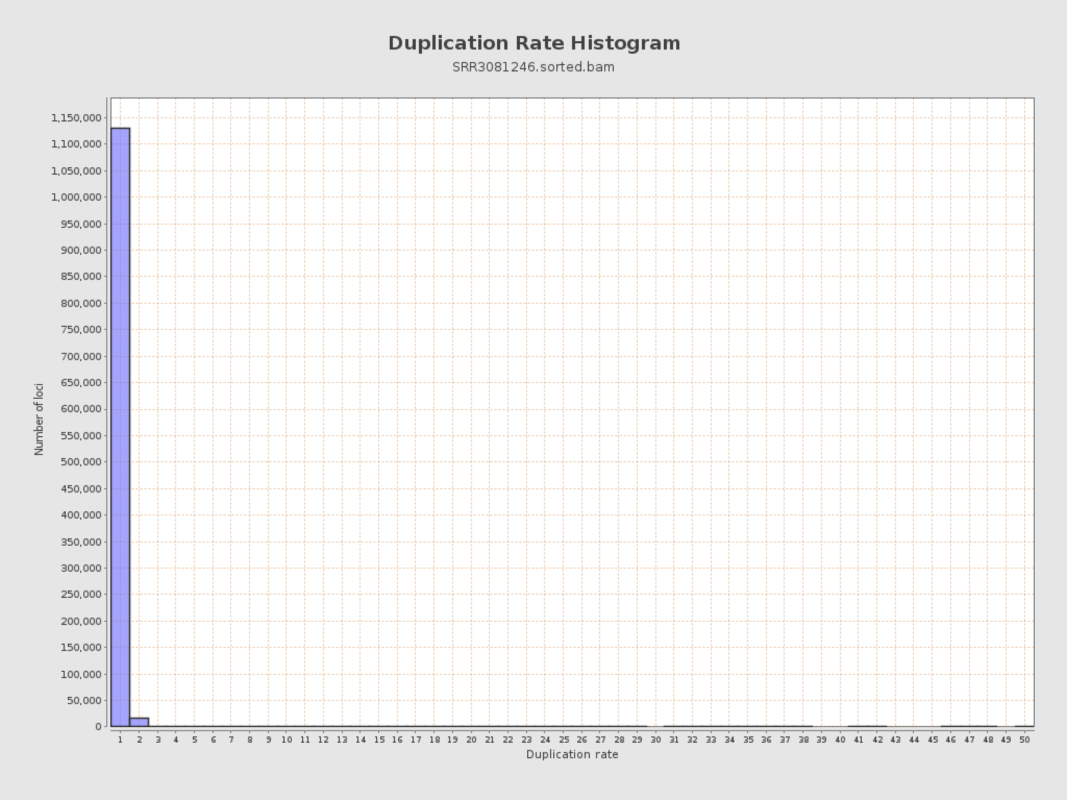
5. Results : Coverage Histogram (0-50X)



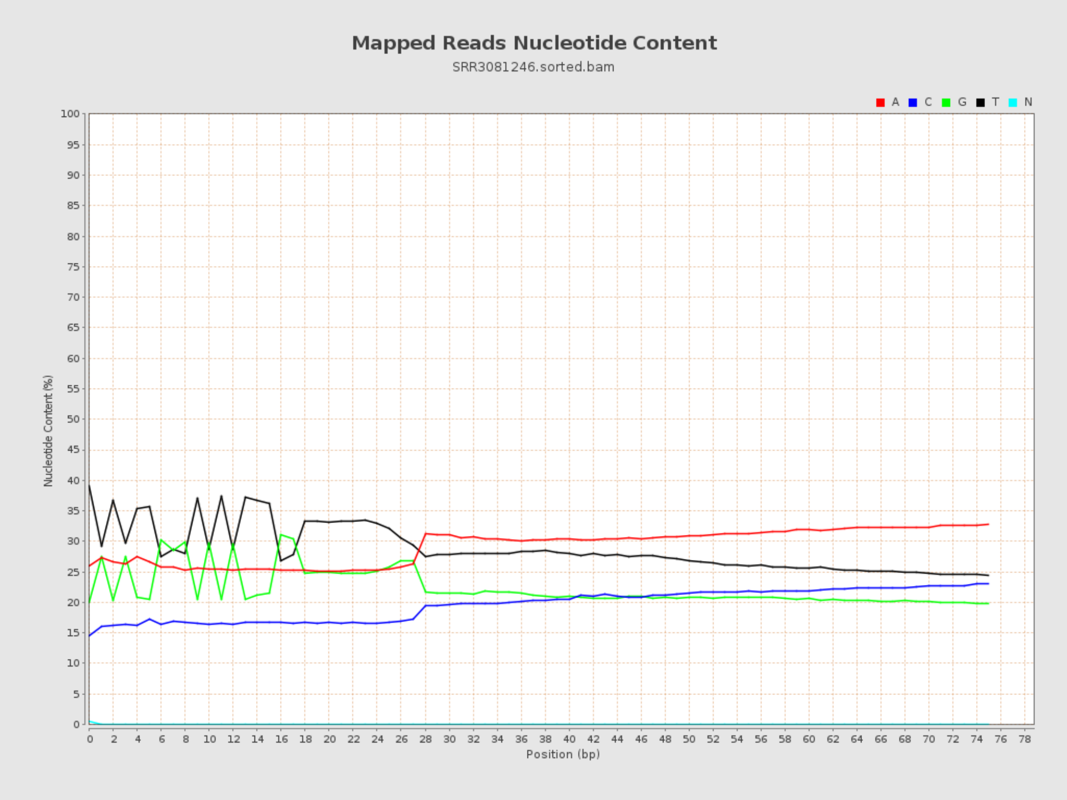
6. Results : Genome Fraction Coverage



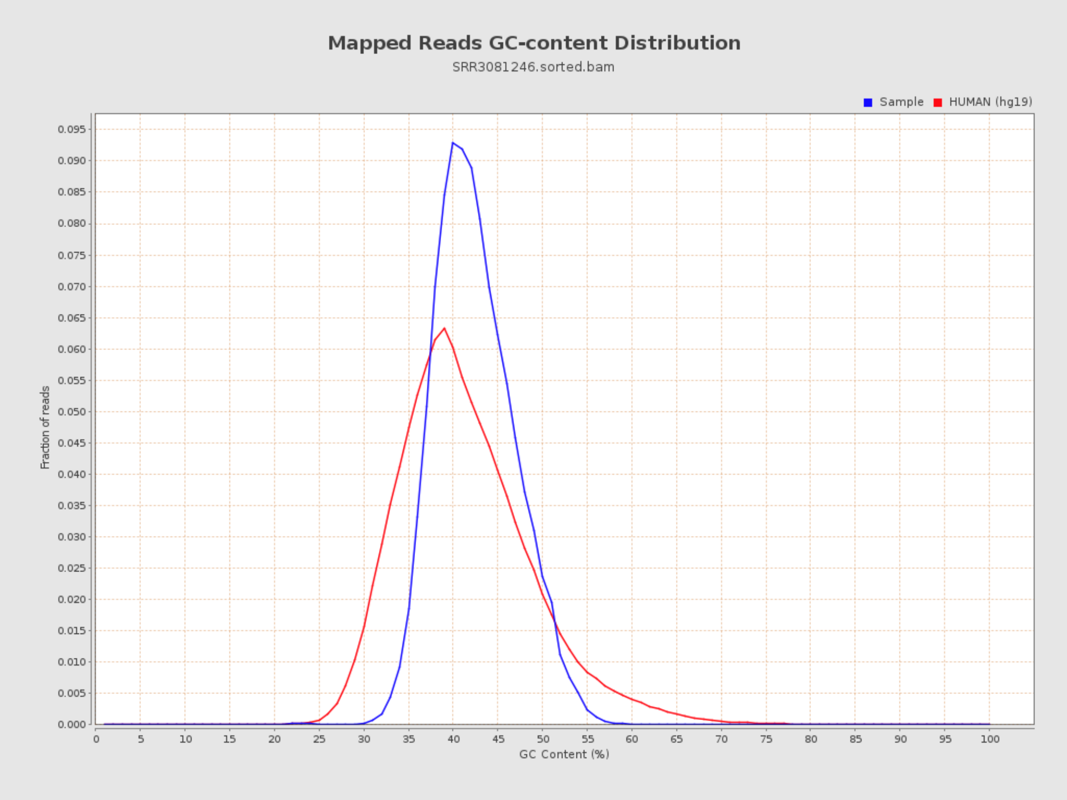
7. Results : Duplication Rate Histogram



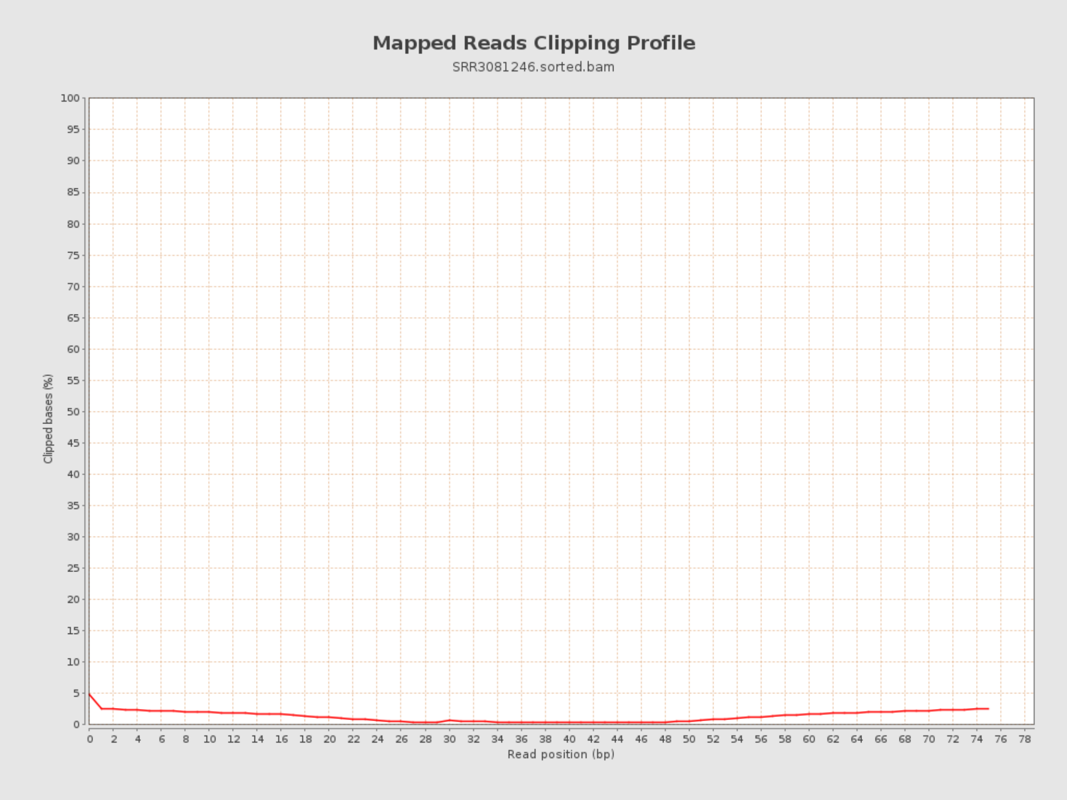
8. Results : Mapped Reads Nucleotide Content



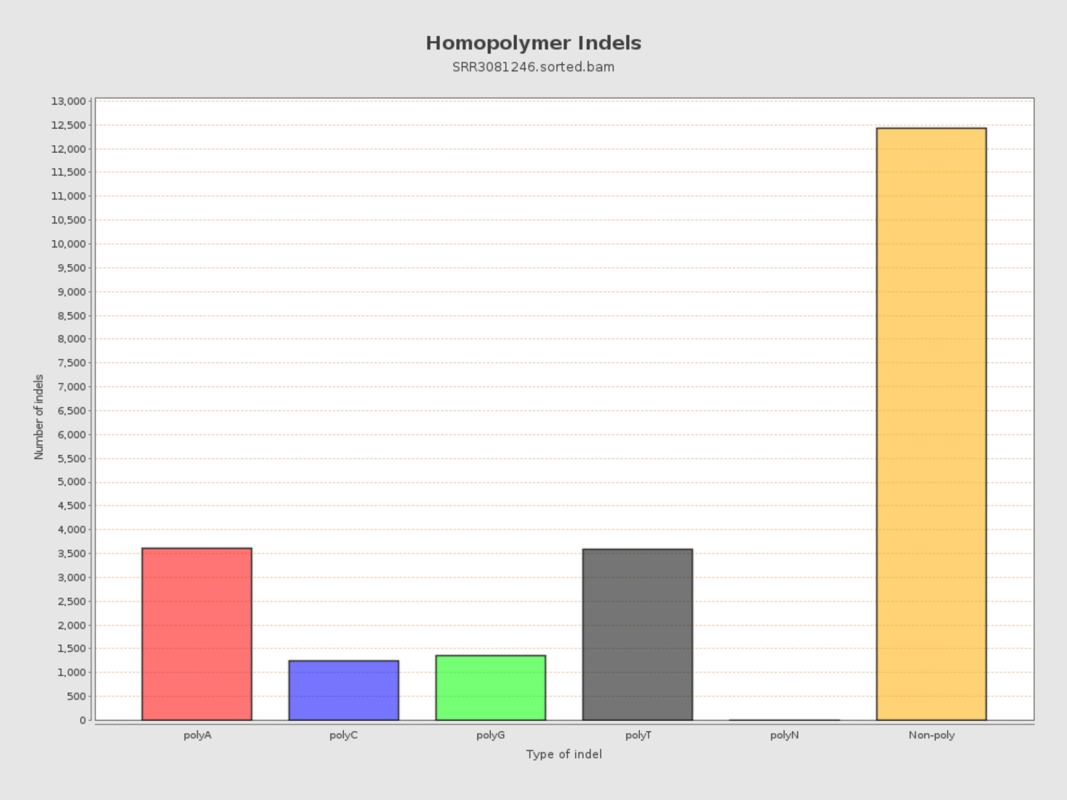
9. Results : Mapped Reads GC-content Distribution



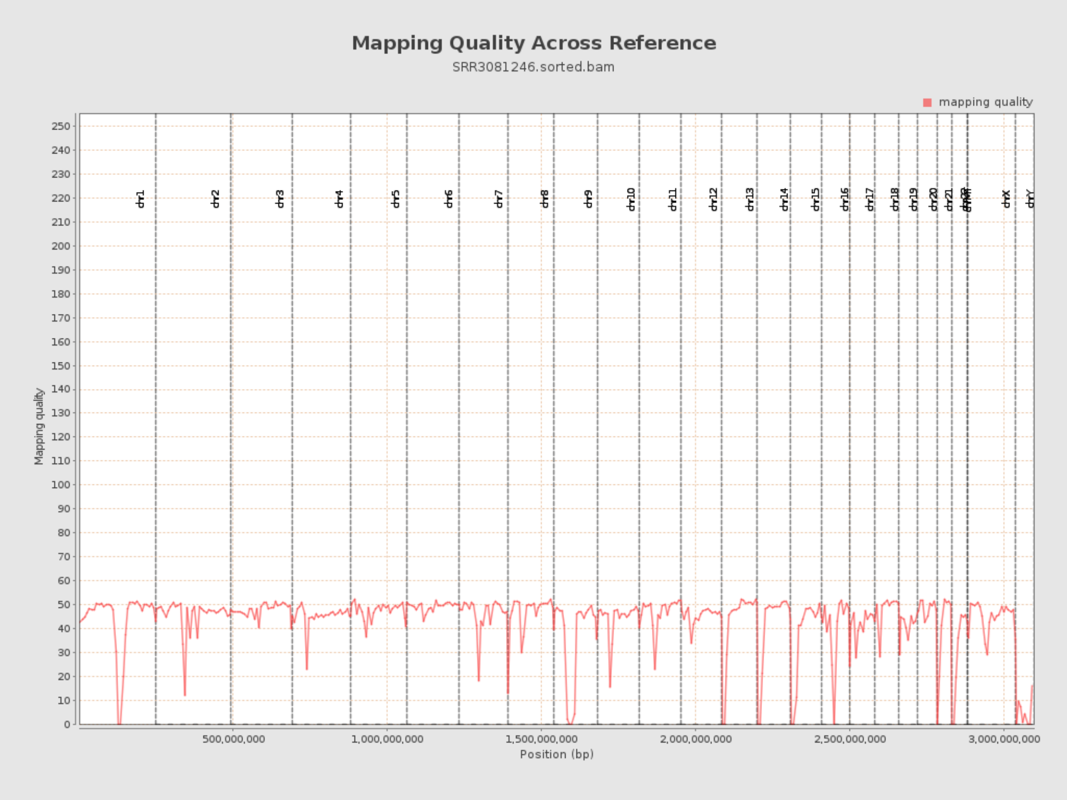
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram