Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 16:12:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524680.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_SRR10524680 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524680.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 16:12:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524680.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,882,917
Mapped reads	1,744,277 / 92.64%
Unmapped reads	138,640 / 7.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,160 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	86,128 / 4.57%
Duplication rate	3.71%
Clipped reads	1,749,468 / 92.91%

2.2. ACGT Content

Number/percentage of A's	27,011,143 / 26.13%
Number/percentage of C's	19,434,031 / 18.8%
Number/percentage of T's	31,267,577 / 30.25%
Number/percentage of G's	25,642,028 / 24.81%
Number/percentage of N's	14,285 / 0.01%
GC Percentage	43.61%

2.3. Coverage

Mean	0.0334

Standard Deviation	0.3189

2.4. Mapping Quality

Mean Mapping Quality	46.01

2.5. Mismatches and indels

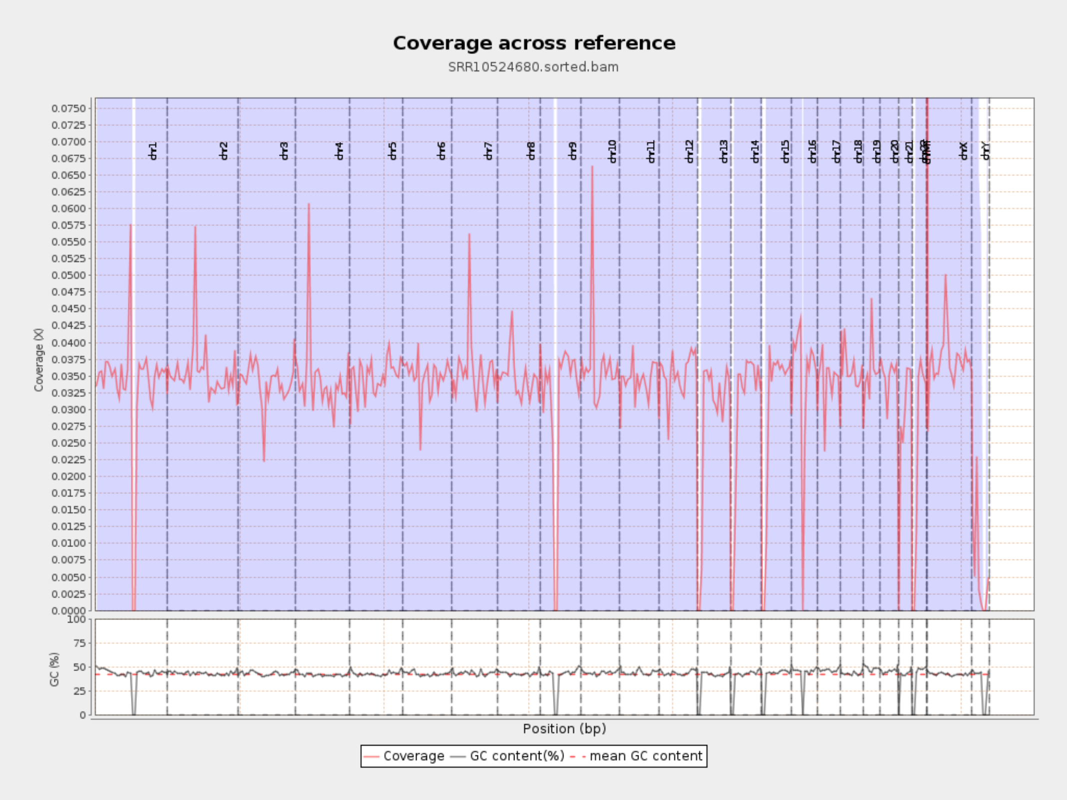
General error rate	0.51%
Mismatches	512,628
Insertions	6,884
Mapped reads with at least one insertion	0.39%
Deletions	19,439
Mapped reads with at least one deletion	1.11%
Homopolymer indels	43.01%

2.6. Chromosome stats

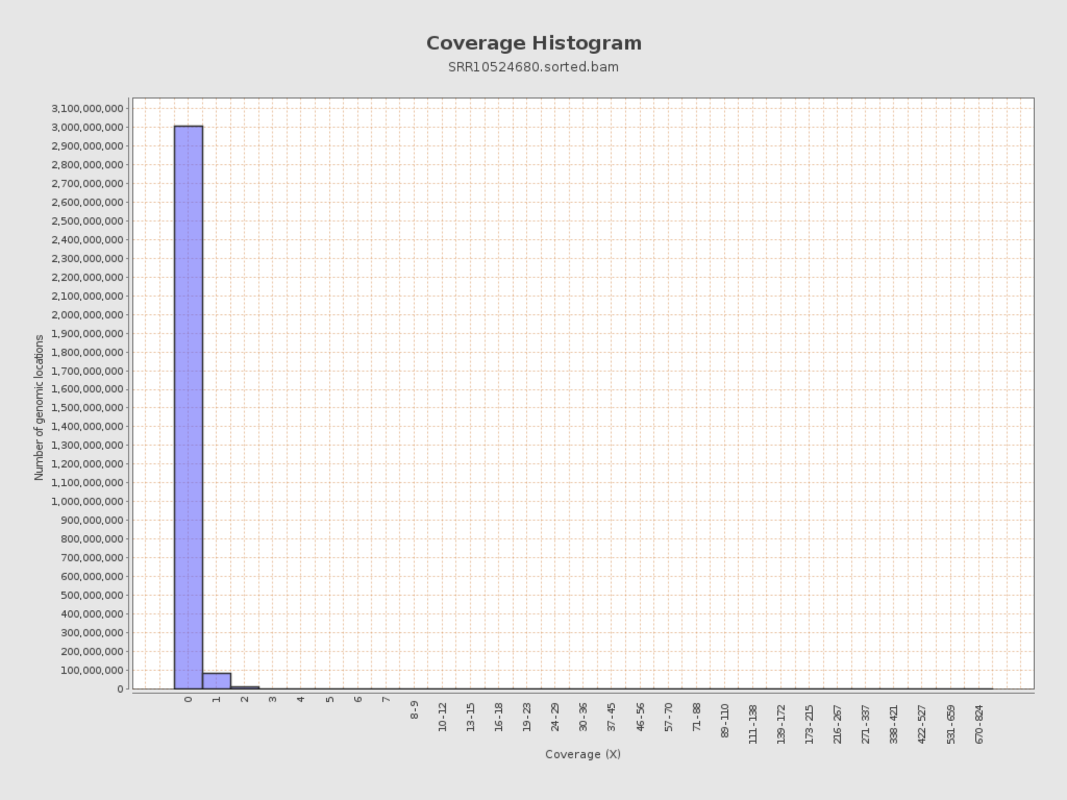
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8326329	0.0334	0.5799
chr2	243199373	8671366	0.0357	0.4292
chr3	198022430	6724579	0.034	0.2036
chr4	191154276	6616773	0.0346	0.2463
chr5	180915260	6353102	0.0351	0.2093
chr6	171115067	5974372	0.0349	0.2303
chr7	159138663	5711752	0.0359	0.3793

chr8	146364022	5102733	0.0349	0.3584
chr9	141213431	4421245	0.0313	0.2652
chr10	135534747	4996917	0.0369	0.3296
chr11	135006516	4664949	0.0346	0.27
chr12	133851895	4726256	0.0353	0.2111
chr13	115169878	3203407	0.0278	0.1861
chr14	107349540	3134024	0.0292	0.1947
chr15	102531392	3010580	0.0294	0.1919
chr16	90354753	3063121	0.0339	0.221
chr17	81195210	2774946	0.0342	0.2181
chr18	78077248	2811987	0.036	0.4826
chr19	59128983	2126133	0.036	0.4191
chr20	63025520	2190871	0.0348	0.213
chr21	48129895	1361396	0.0283	0.2203
chr22	51304566	1239629	0.0242	0.1736
chrMT	16571	14571	0.8793	1.1874
chrX	155270560	5818249	0.0375	0.2404
chrY	59373566	361089	0.0061	0.2105

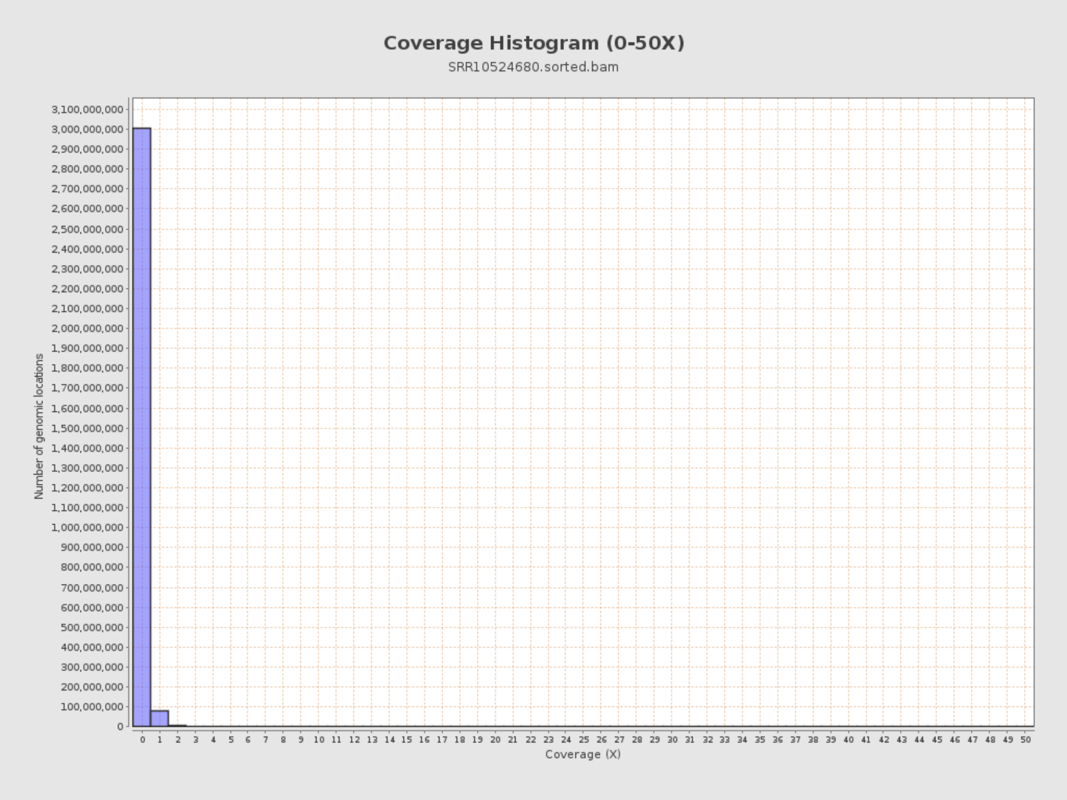
3. Results : Coverage across reference



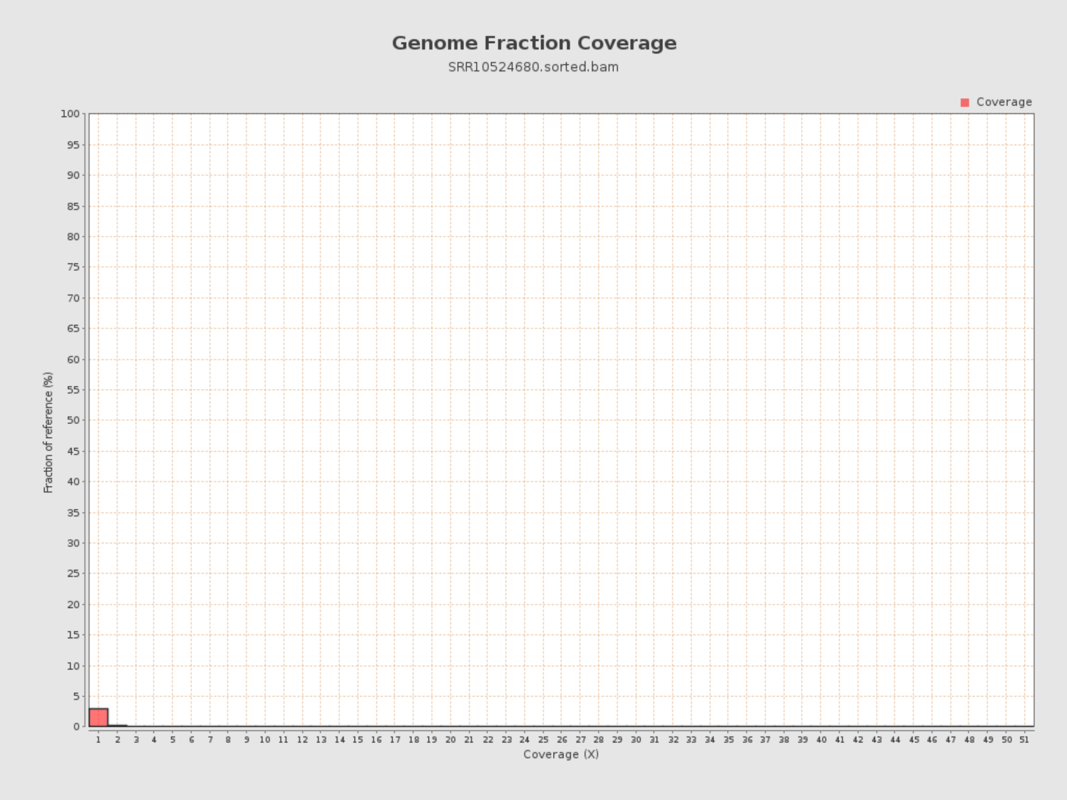
4. Results : Coverage Histogram



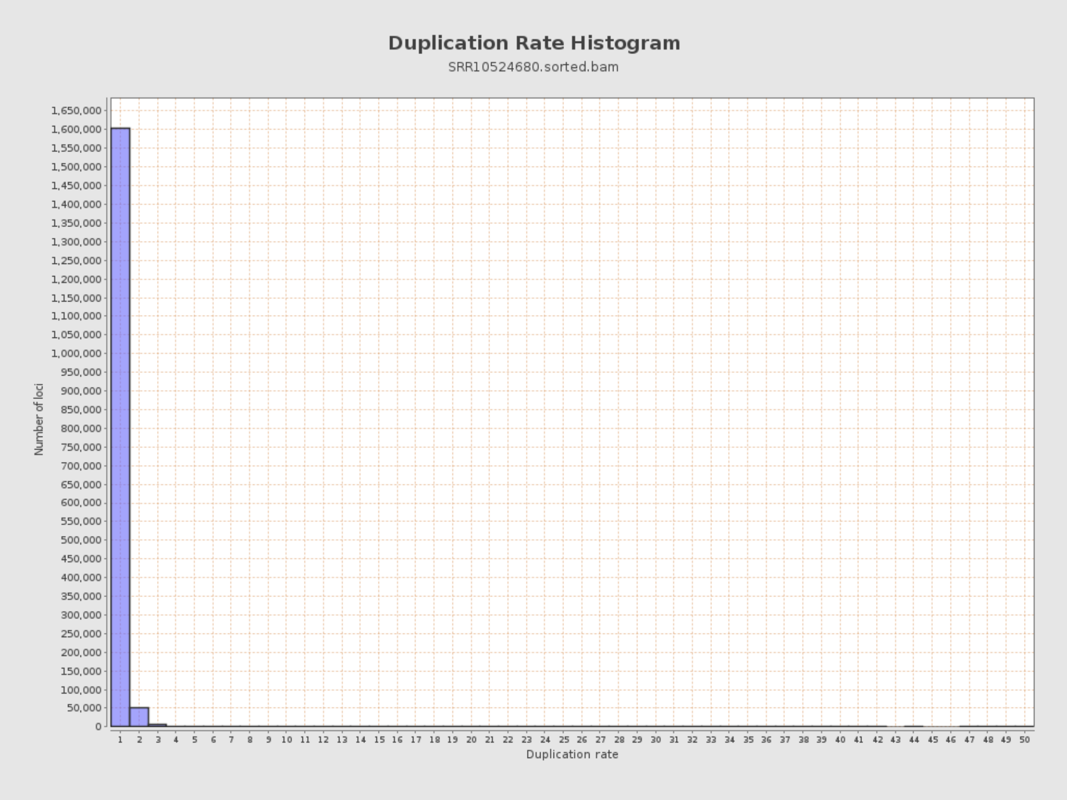
5. Results : Coverage Histogram (0-50X)



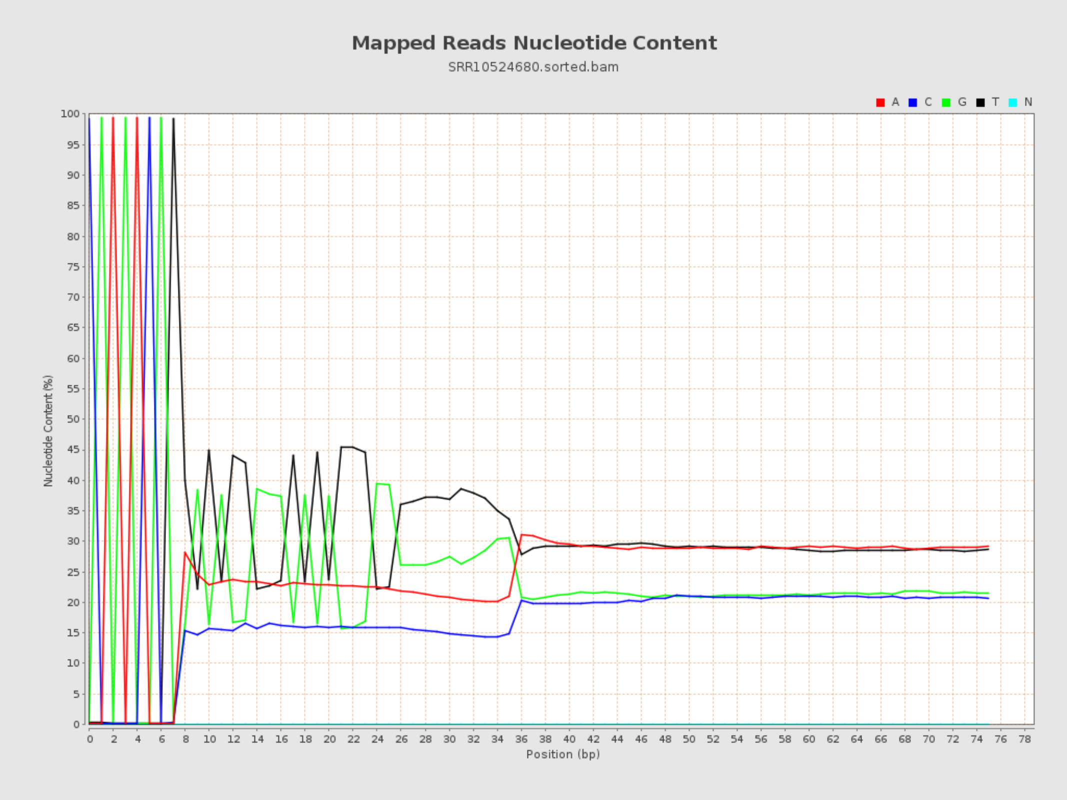
6. Results : Genome Fraction Coverage



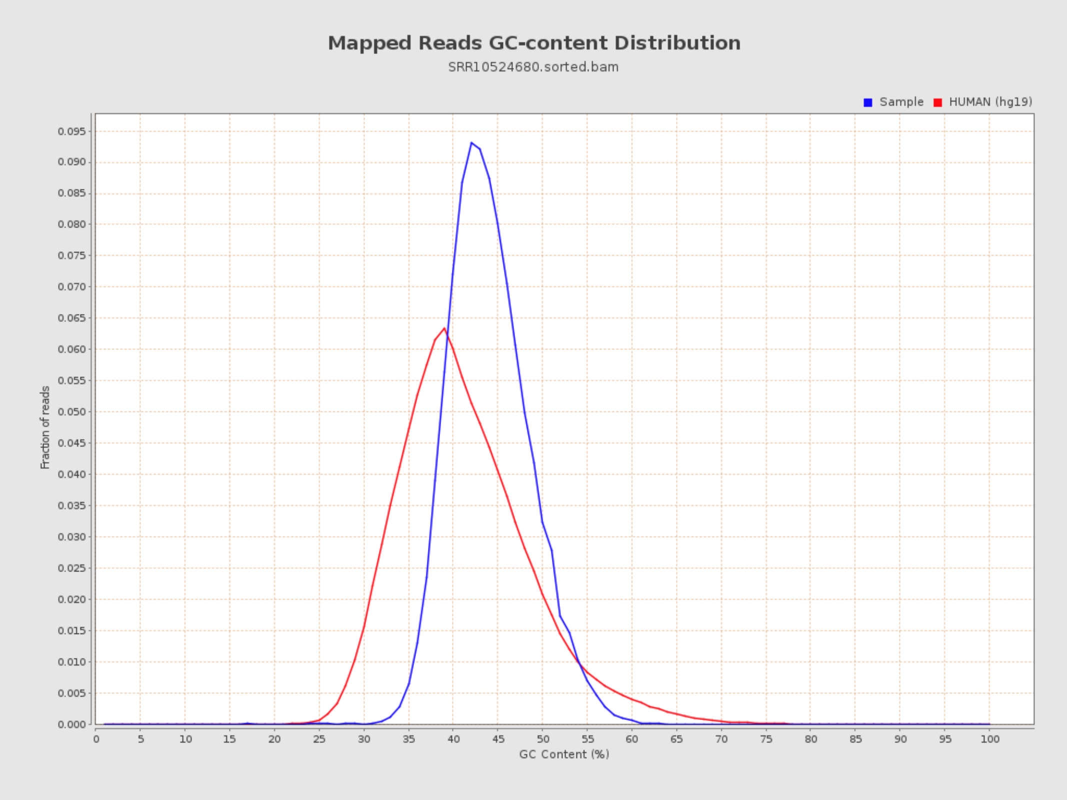
7. Results : Duplication Rate Histogram



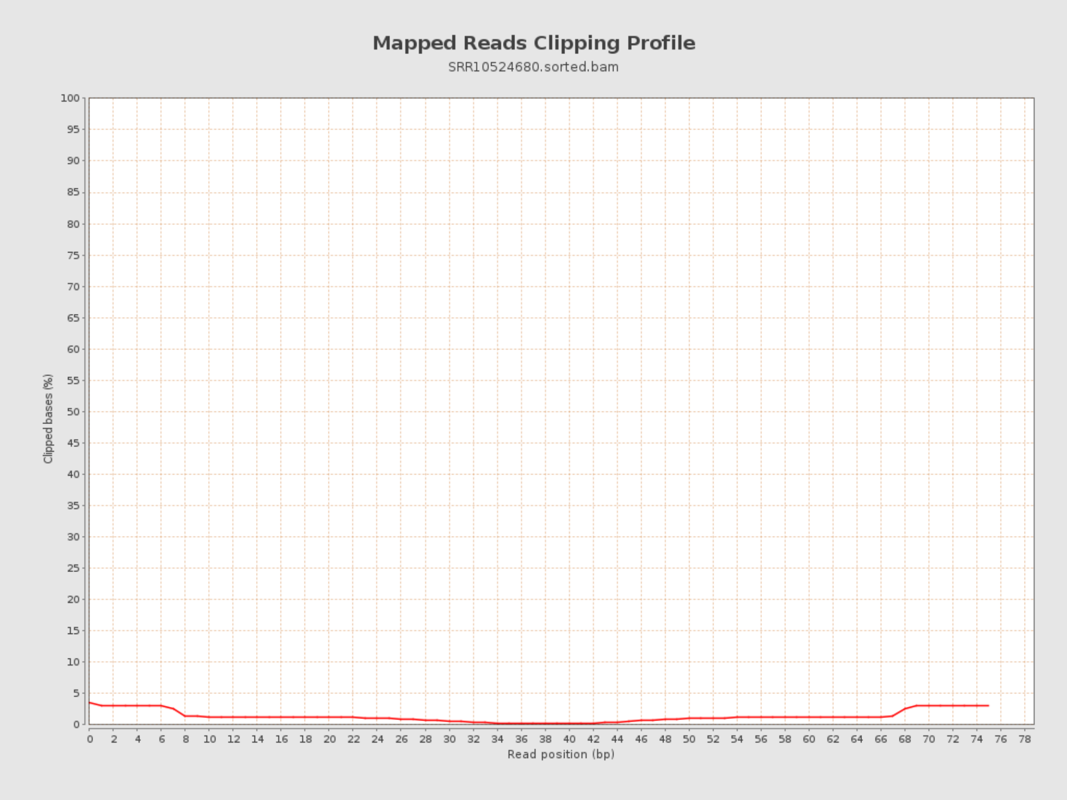
8. Results : Mapped Reads Nucleotide Content



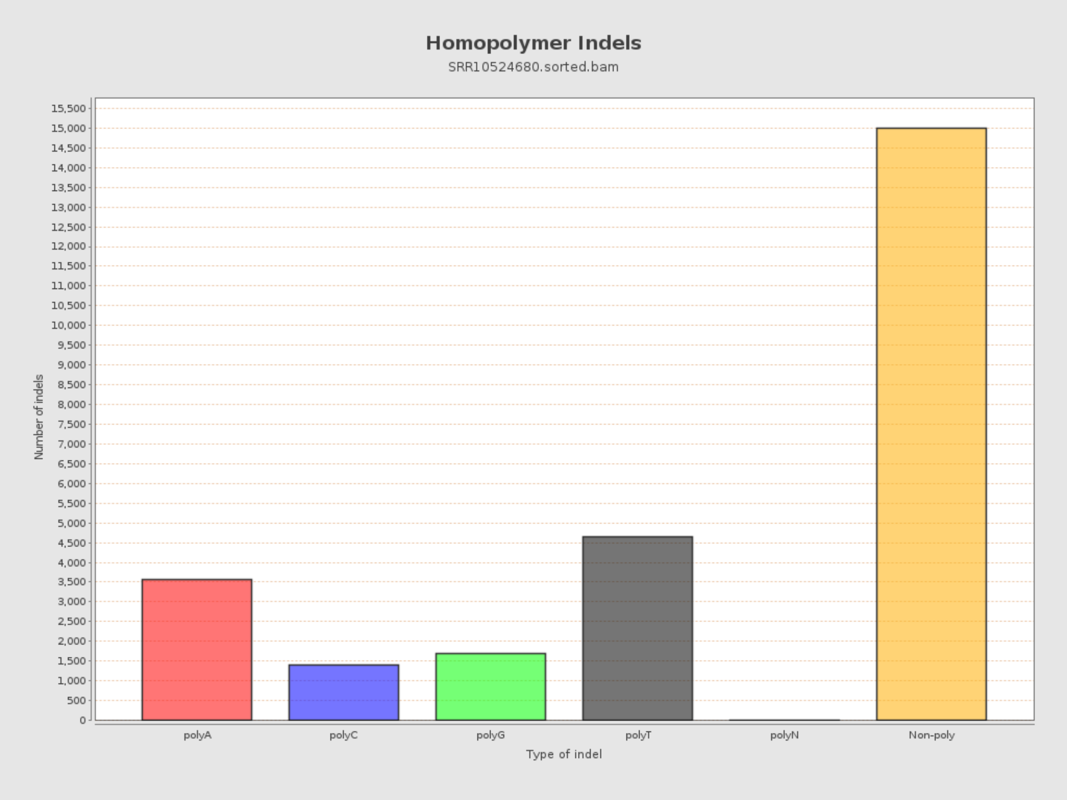
9. Results : Mapped Reads GC-content Distribution



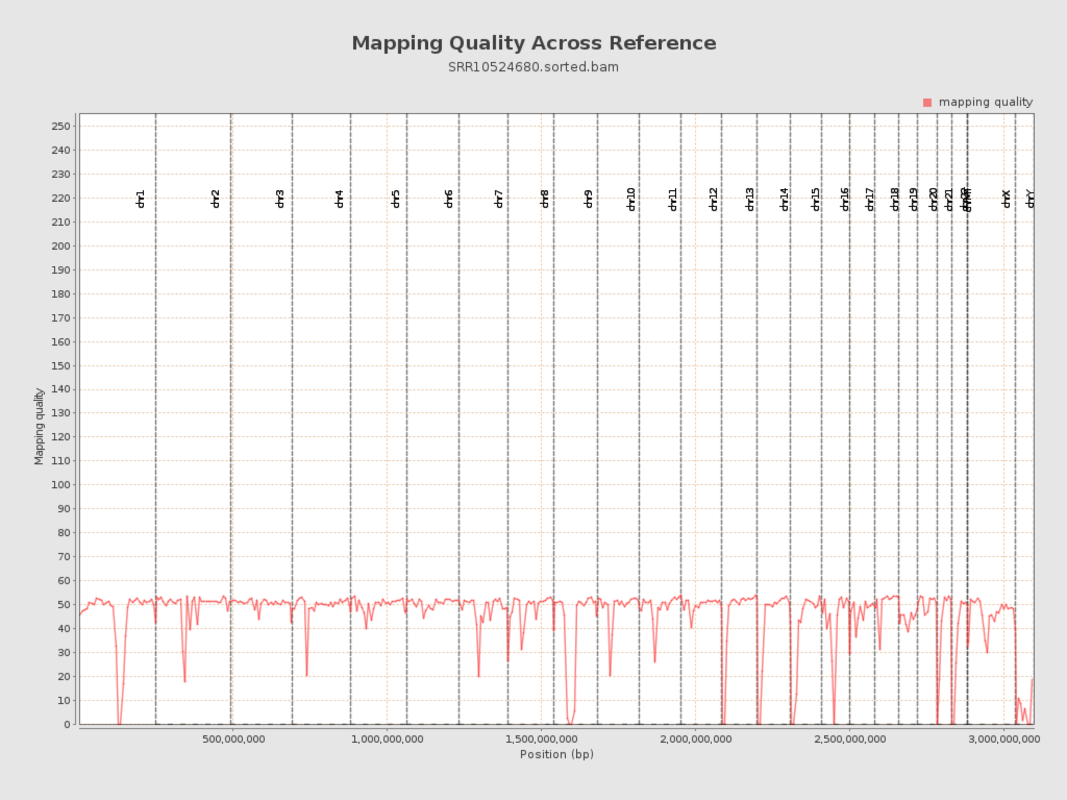
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram