Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 19:06:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524474.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_SRR10524474 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524474.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 19:06:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524474.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,767,783
Mapped reads	1,632,598 / 92.35%
Unmapped reads	135,185 / 7.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,058 / 0.23%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	67,261 / 3.8%
Duplication rate	3.12%
Clipped reads	1,632,174 / 92.33%

2.2. ACGT Content

Number/percentage of A's	23,951,333 / 25.05%
Number/percentage of C's	17,054,335 / 17.83%
Number/percentage of T's	31,244,155 / 32.67%
Number/percentage of G's	23,371,245 / 24.44%
Number/percentage of N's	1,902 / 0%
GC Percentage	42.28%

2.3. Coverage

Mean	0.0309

Standard Deviation	0.2801

2.4. Mapping Quality

Mean Mapping Quality	45.53

2.5. Mismatches and indels

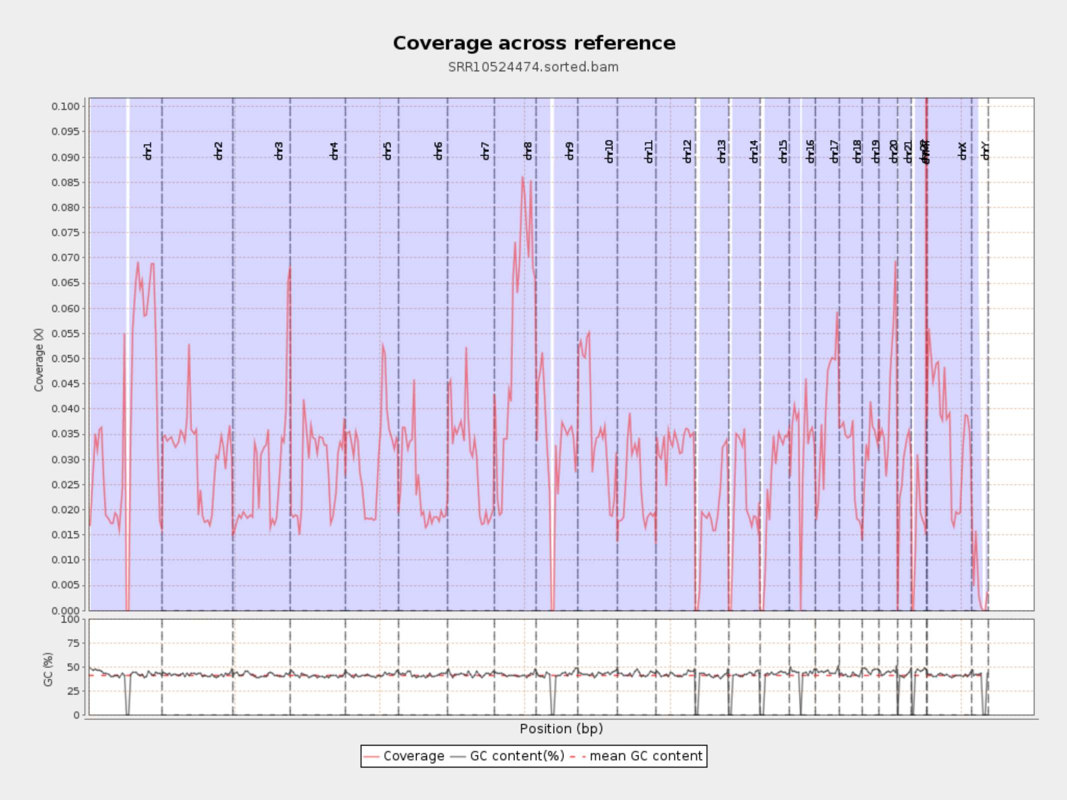
General error rate	0.47%
Mismatches	442,385
Insertions	6,301
Mapped reads with at least one insertion	0.38%
Deletions	17,797
Mapped reads with at least one deletion	1.08%
Homopolymer indels	43.28%

2.6. Chromosome stats

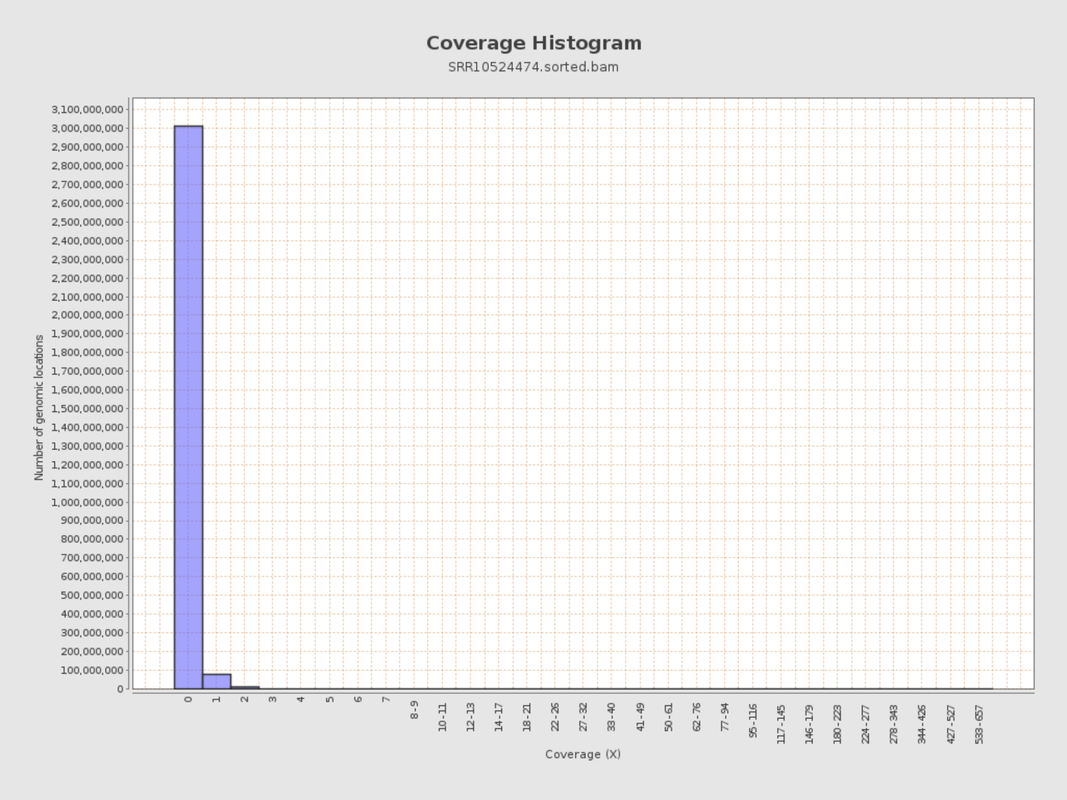
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9257587	0.0371	0.5133
chr2	243199373	7501533	0.0308	0.3147
chr3	198022430	5201260	0.0263	0.1796
chr4	191154276	5439751	0.0285	0.2058
chr5	180915260	5600719	0.031	0.1948
chr6	171115067	4142575	0.0242	0.2239
chr7	159138663	4874937	0.0306	0.3595

chr8	146364022	8143102	0.0556	0.3008
chr9	141213431	4523703	0.032	0.2515
chr10	135534747	5036739	0.0372	0.2772
chr11	135006516	3278276	0.0243	0.2568
chr12	133851895	4433375	0.0331	0.202
chr13	115169878	2160275	0.0188	0.1533
chr14	107349540	2299958	0.0214	0.1663
chr15	102531392	2529363	0.0247	0.1843
chr16	90354753	2973057	0.0329	0.2138
chr17	81195210	3277755	0.0404	0.235
chr18	78077248	2327372	0.0298	0.4162
chr19	59128983	1934666	0.0327	0.3704
chr20	63025520	2702650	0.0429	0.2335
chr21	48129895	1292362	0.0269	0.1929
chr22	51304566	777488	0.0152	0.1354
chrMT	16571	9928	0.5991	0.9132
chrX	155270560	5650611	0.0364	0.2386
chrY	59373566	284248	0.0048	0.1288

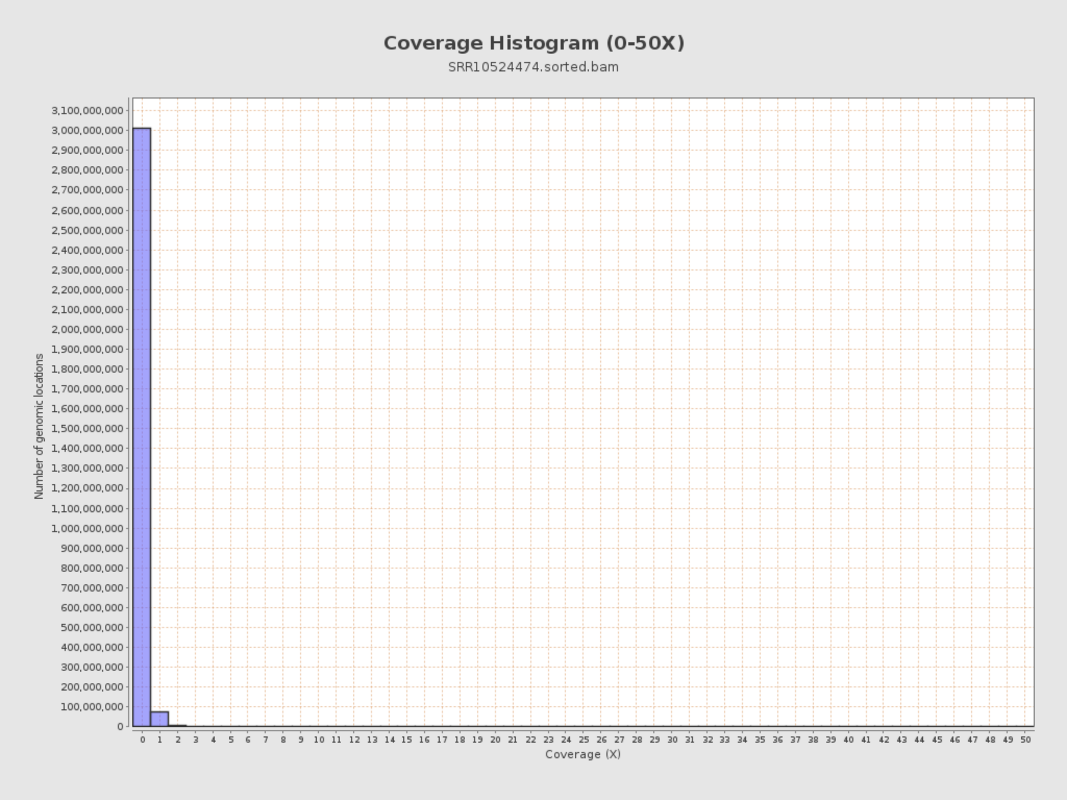
3. Results : Coverage across reference



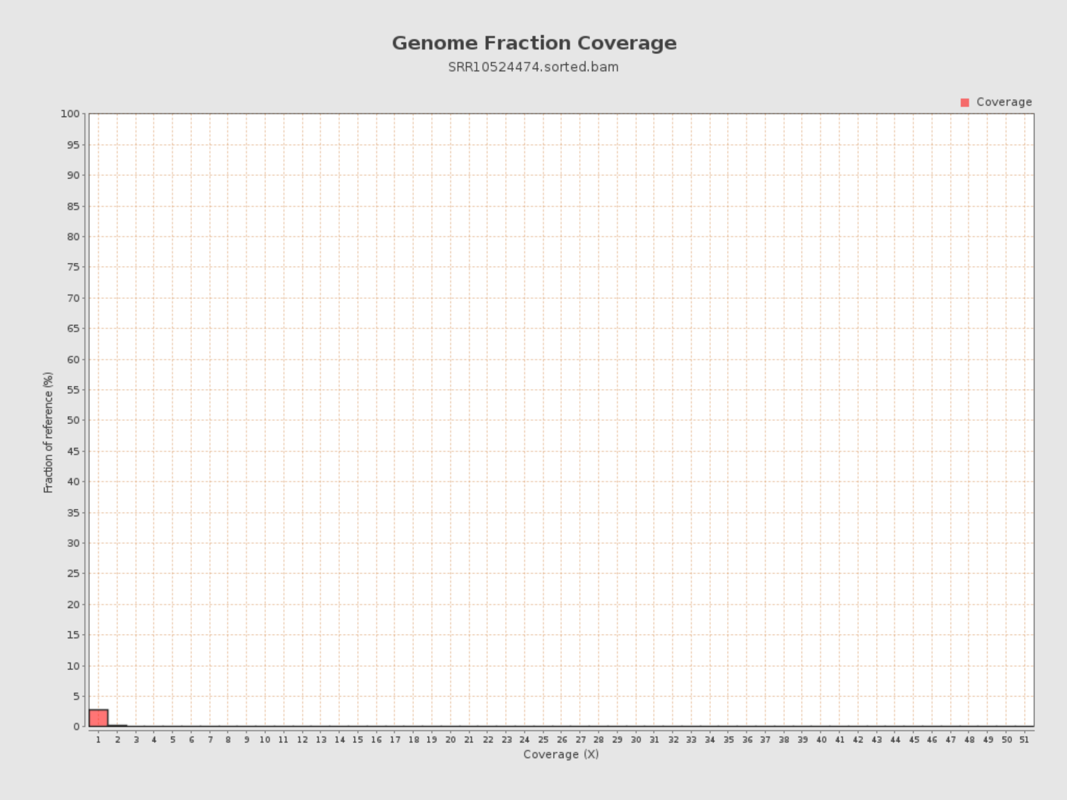
4. Results : Coverage Histogram



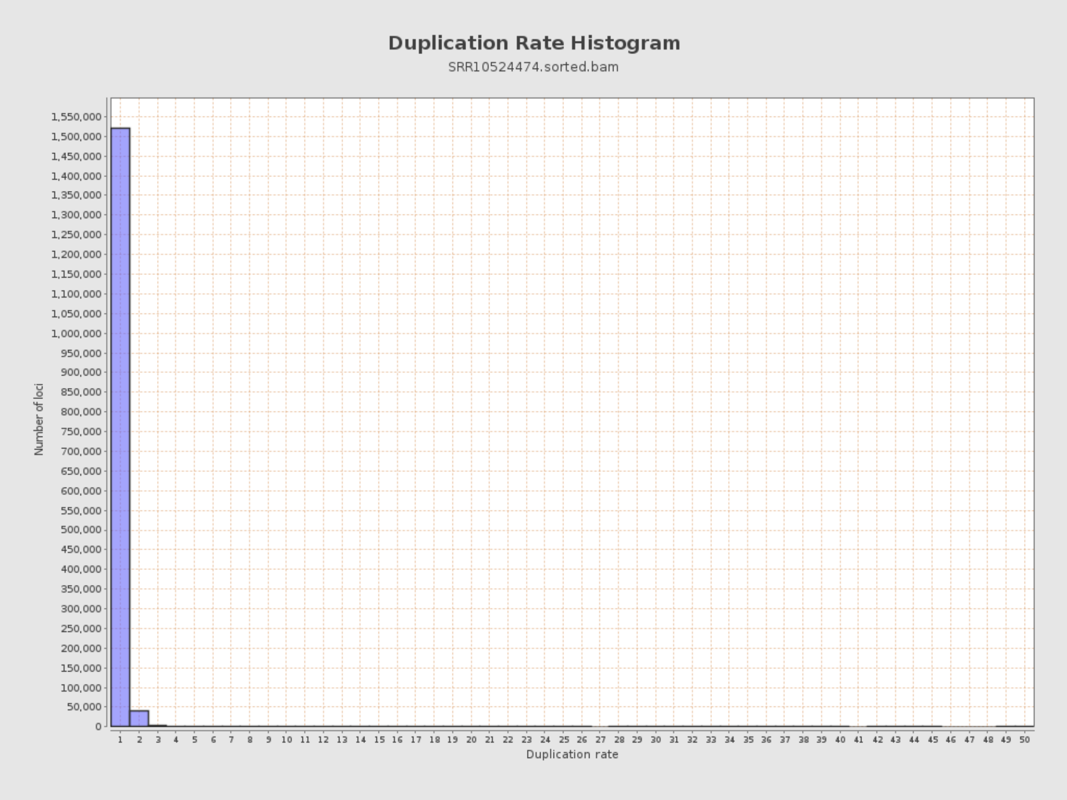
5. Results : Coverage Histogram (0-50X)



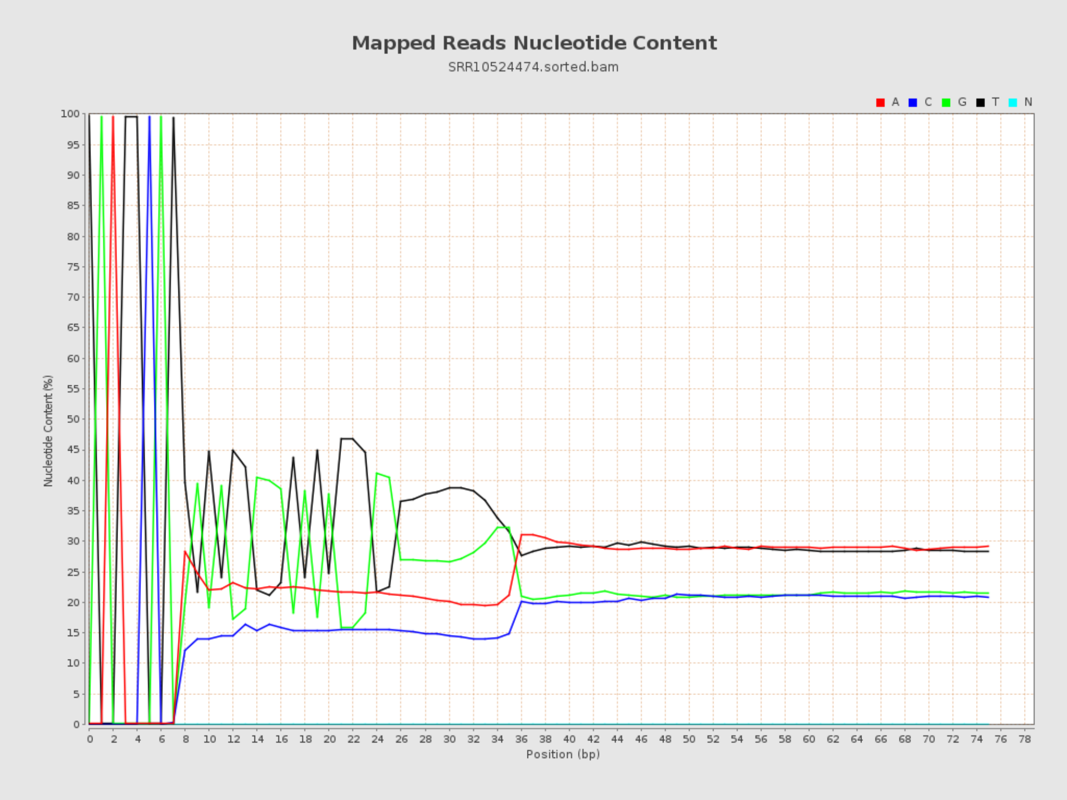
6. Results : Genome Fraction Coverage



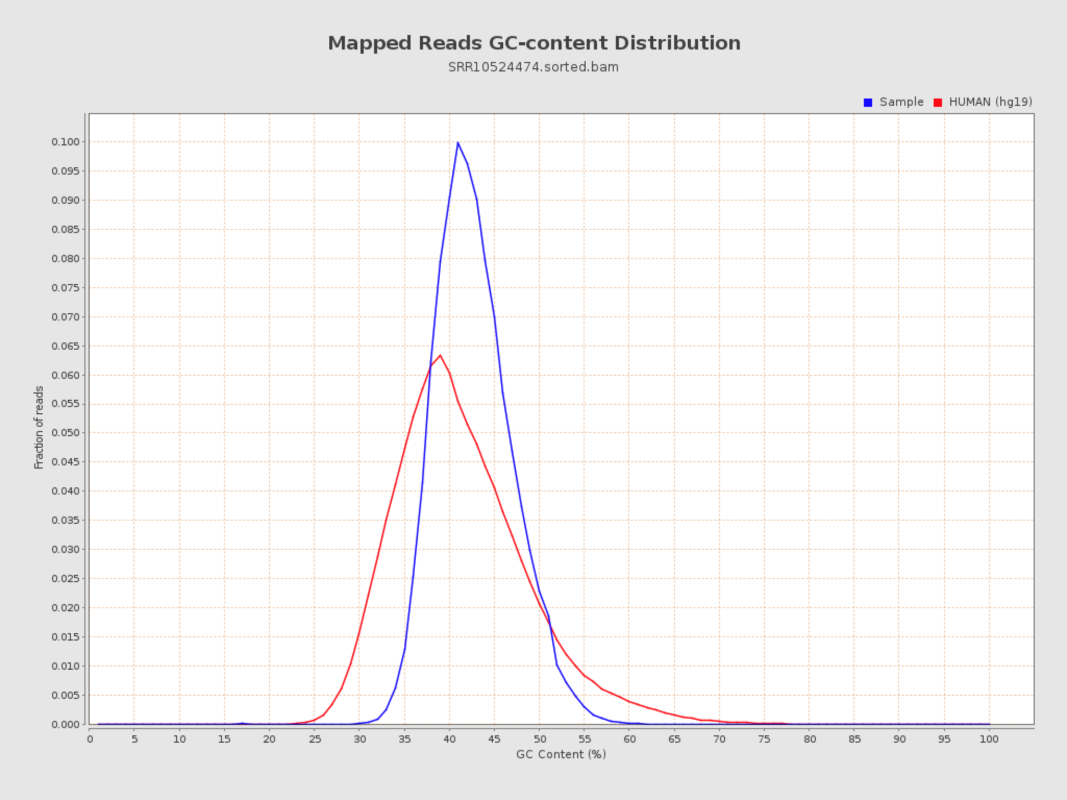
7. Results : Duplication Rate Histogram



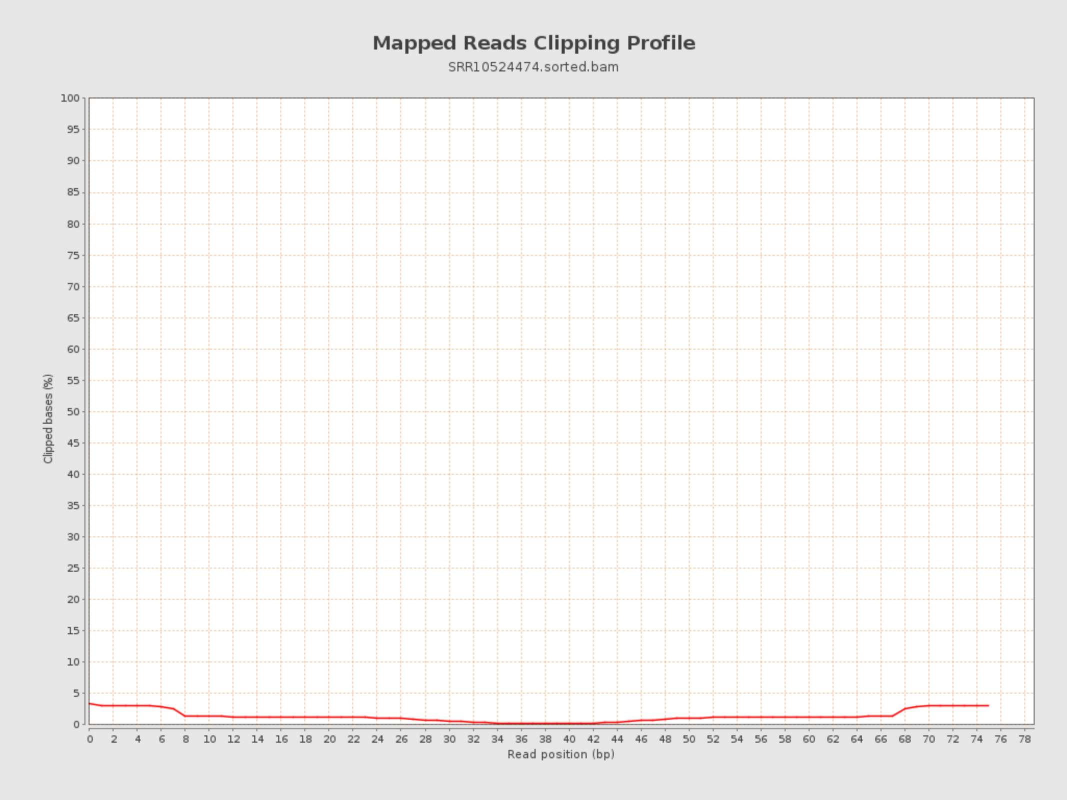
8. Results : Mapped Reads Nucleotide Content



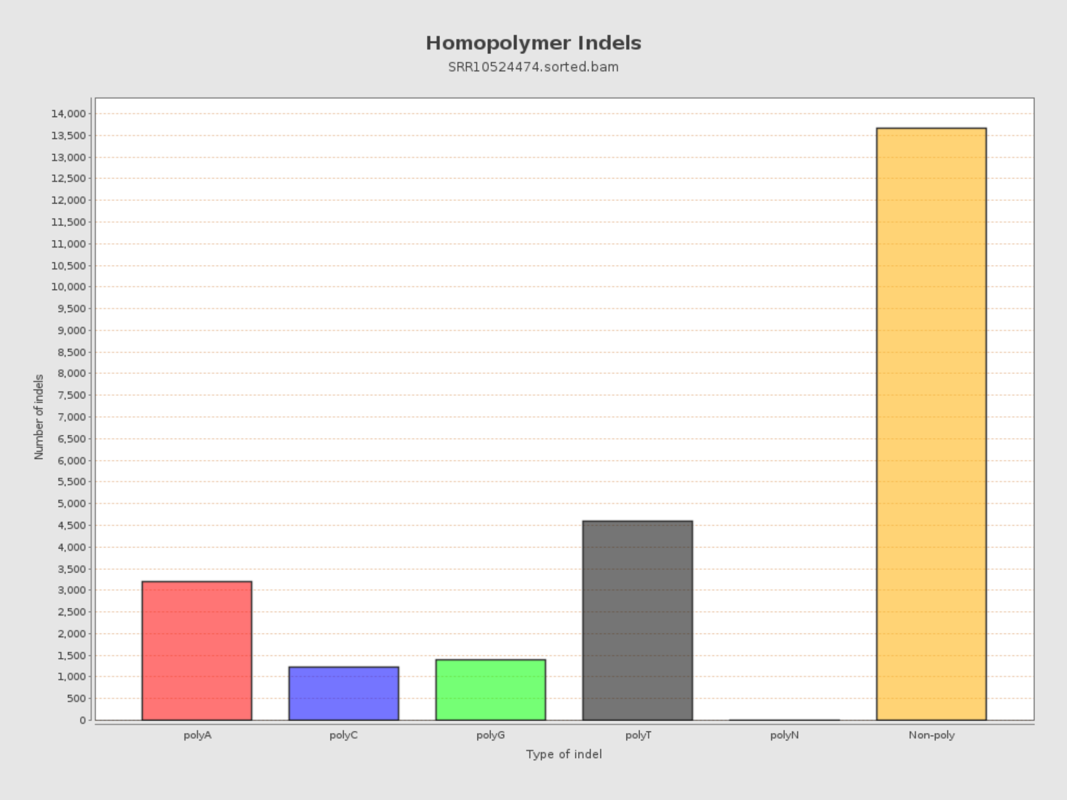
9. Results : Mapped Reads GC-content Distribution



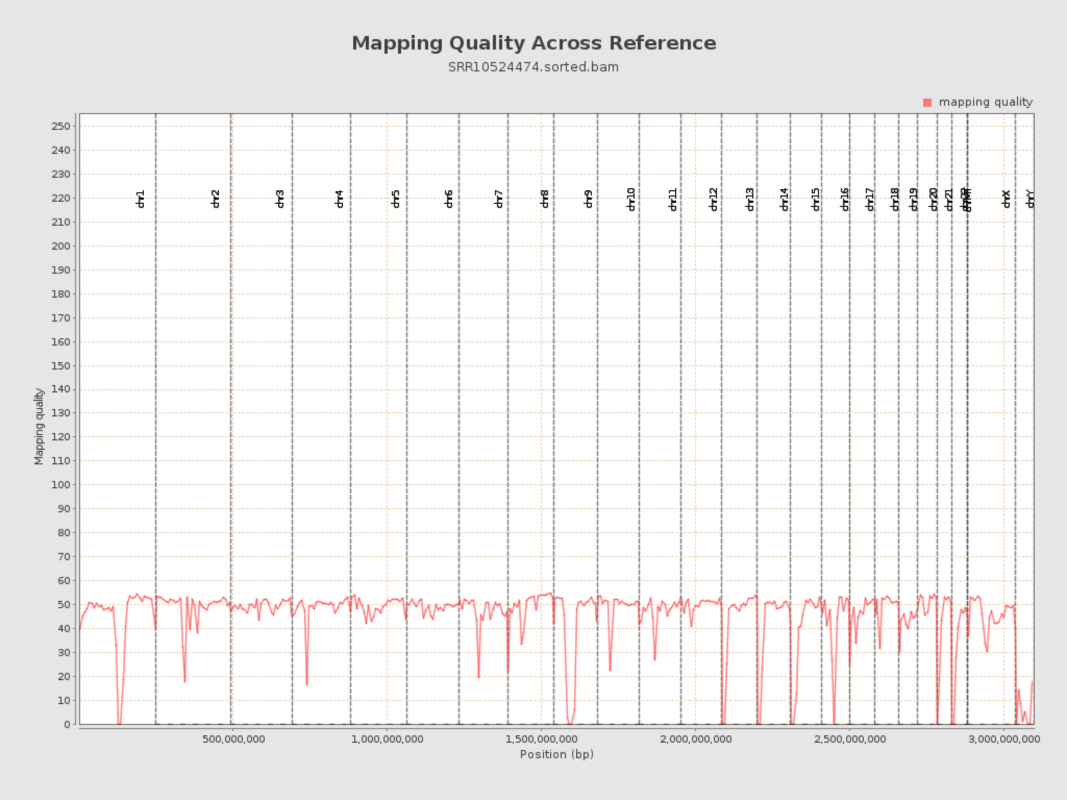
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram