Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.2-dev
2024/08/28 23:00:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524847.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_SRR10524847 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524847.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 23:00:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524847.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,531,744
Mapped reads	1,403,304 / 91.61%
Unmapped reads	128,440 / 8.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,551 / 0.56%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	38,814 / 2.53%
Duplication rate	1.83%
Clipped reads	1,408,068 / 91.93%

2.2. ACGT Content

Number/percentage of A's	21,532,266 / 26.36%
Number/percentage of C's	14,252,536 / 17.45%
Number/percentage of T's	25,761,452 / 31.54%
Number/percentage of G's	20,119,187 / 24.63%
Number/percentage of N's	10,591 / 0.01%
GC Percentage	42.08%

2.3. Coverage

Mean	0.0264

Standard Deviation	0.2726

2.4. Mapping Quality

Mean Mapping Quality	44.65

2.5. Mismatches and indels

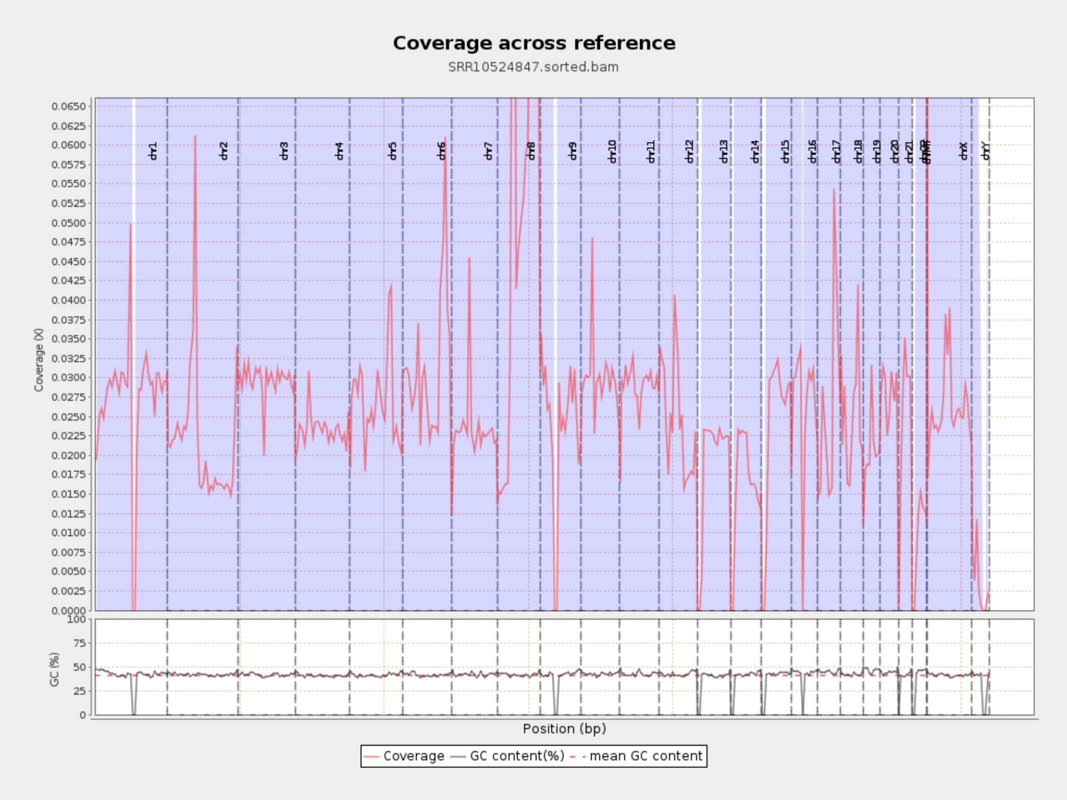
General error rate	0.5%
Mismatches	397,939
Insertions	5,691
Mapped reads with at least one insertion	0.4%
Deletions	16,114
Mapped reads with at least one deletion	1.14%
Homopolymer indels	42.99%

2.6. Chromosome stats

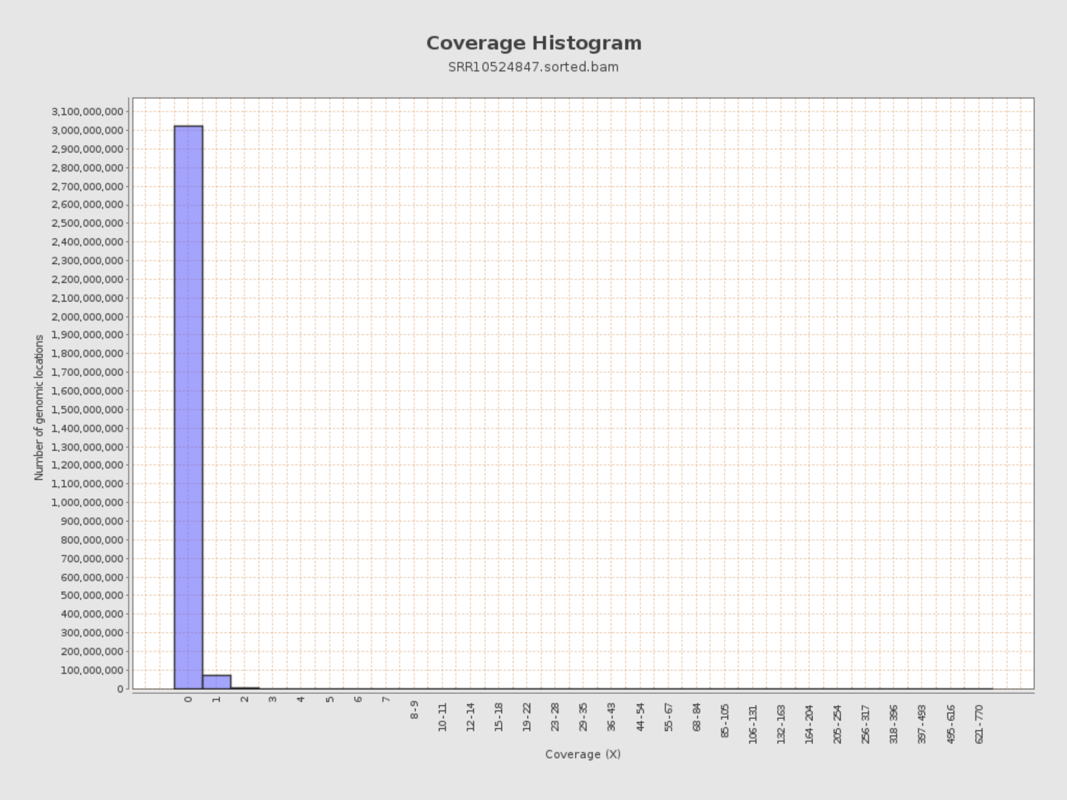
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6805098	0.0273	0.5474
chr2	243199373	5294113	0.0218	0.2697
chr3	198022430	5871415	0.0297	0.1825
chr4	191154276	4450040	0.0233	0.1743
chr5	180915260	4943794	0.0273	0.1757
chr6	171115067	5325470	0.0311	0.2053
chr7	159138663	3761013	0.0236	0.359

chr8	146364022	8841802	0.0604	0.3682
chr9	141213431	3369090	0.0239	0.2299
chr10	135534747	4067877	0.03	0.2503
chr11	135006516	3916167	0.029	0.2343
chr12	133851895	3257600	0.0243	0.1712
chr13	115169878	2160758	0.0188	0.1455
chr14	107349540	1724852	0.0161	0.1431
chr15	102531392	2433363	0.0237	0.1654
chr16	90354753	2352856	0.026	0.1831
chr17	81195210	2182543	0.0269	0.1945
chr18	78077248	1969052	0.0252	0.4013
chr19	59128983	1234703	0.0209	0.3597
chr20	63025520	1741419	0.0276	0.18
chr21	48129895	1188801	0.0247	0.1799
chr22	51304566	491582	0.0096	0.1036
chrMT	16571	3222	0.1944	0.434
chrX	155270560	4109234	0.0265	0.1997
chrY	59373566	205020	0.0035	0.095

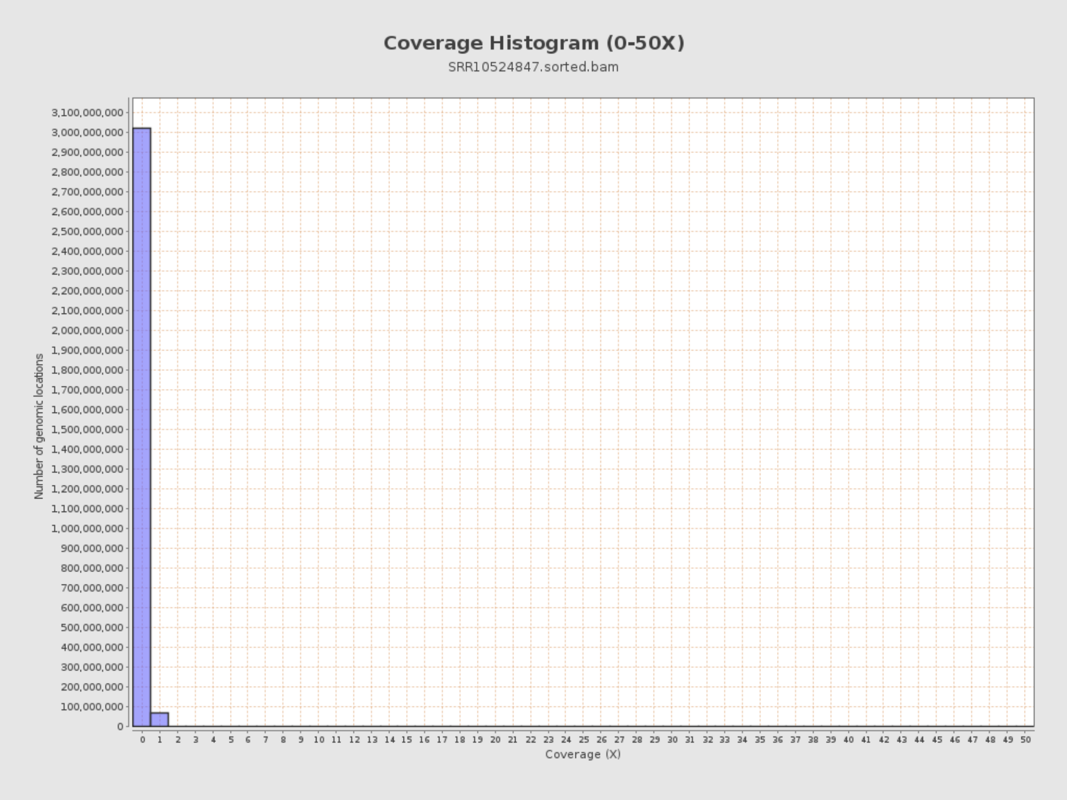
3. Results : Coverage across reference



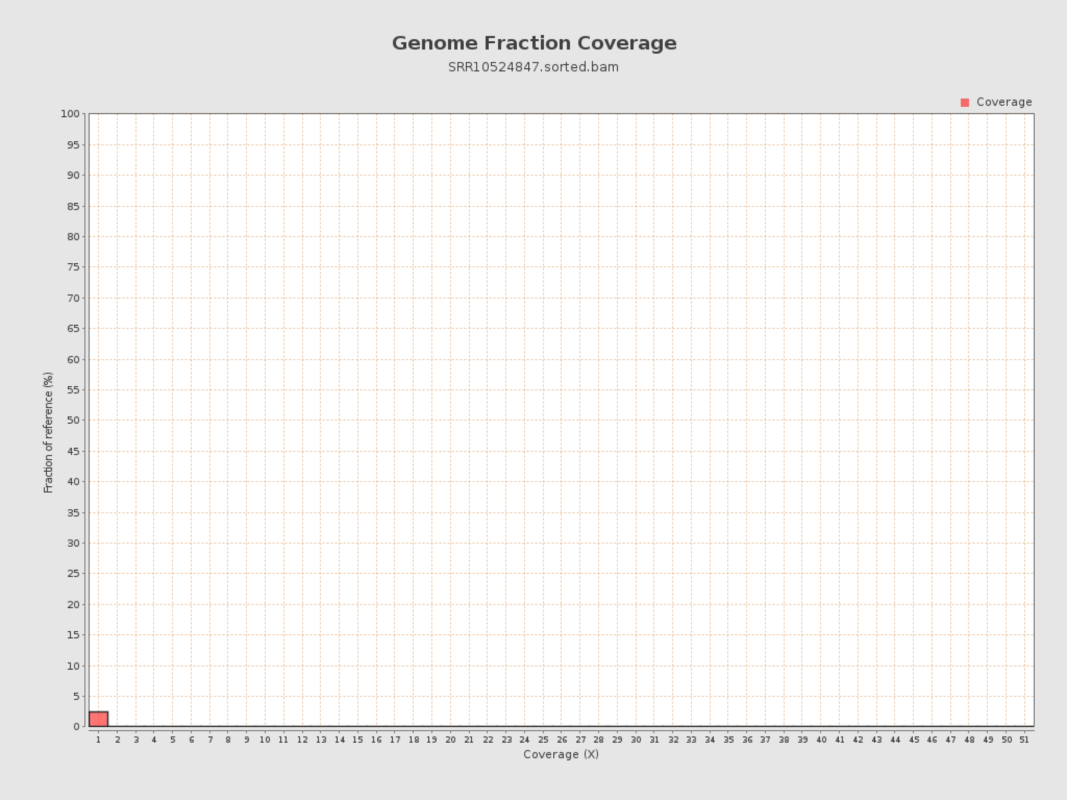
4. Results : Coverage Histogram



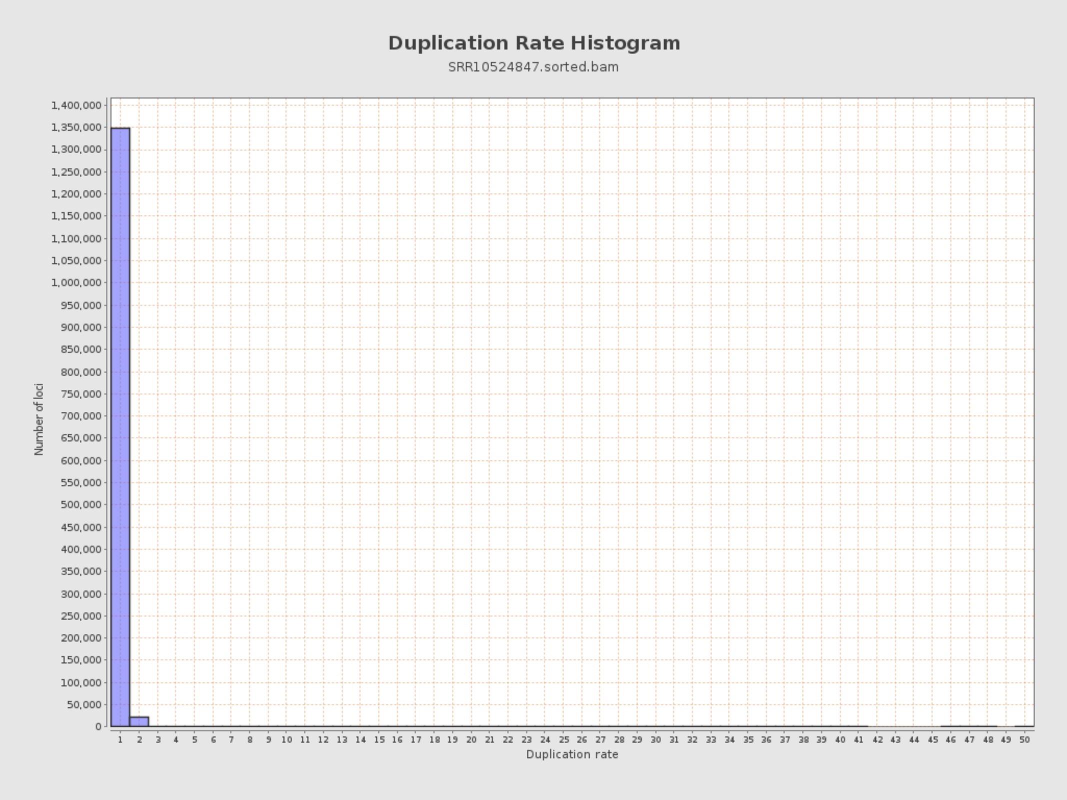
5. Results : Coverage Histogram (0-50X)



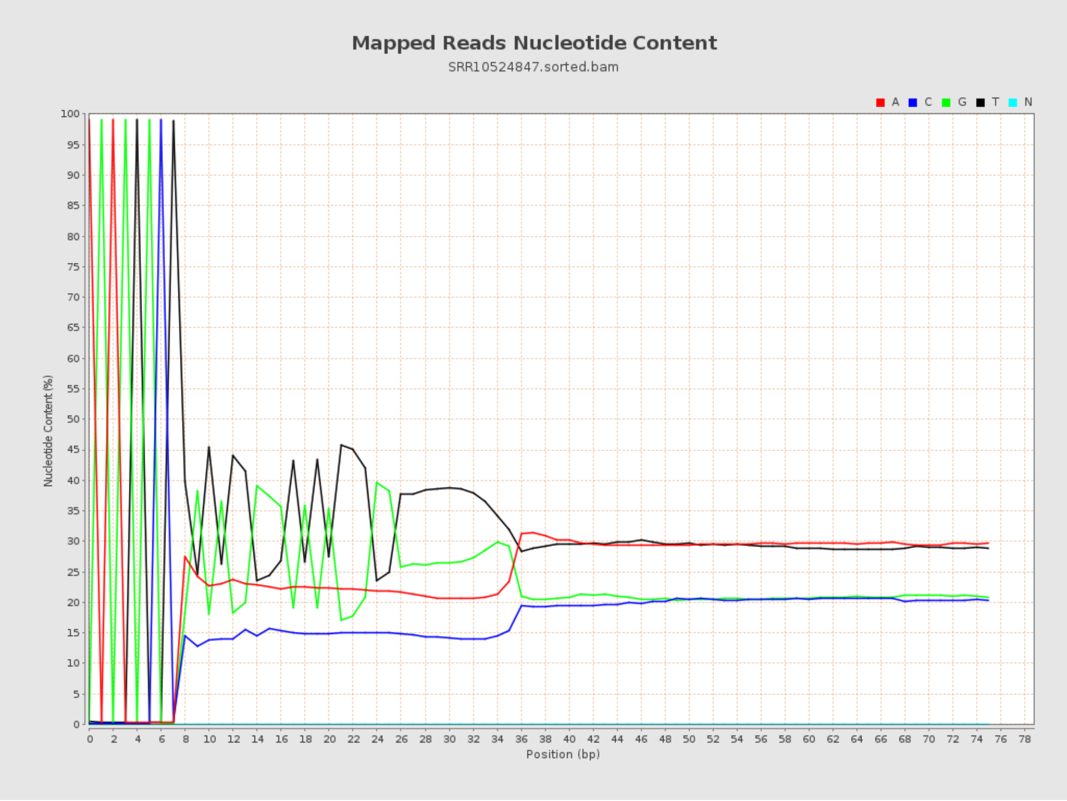
6. Results : Genome Fraction Coverage



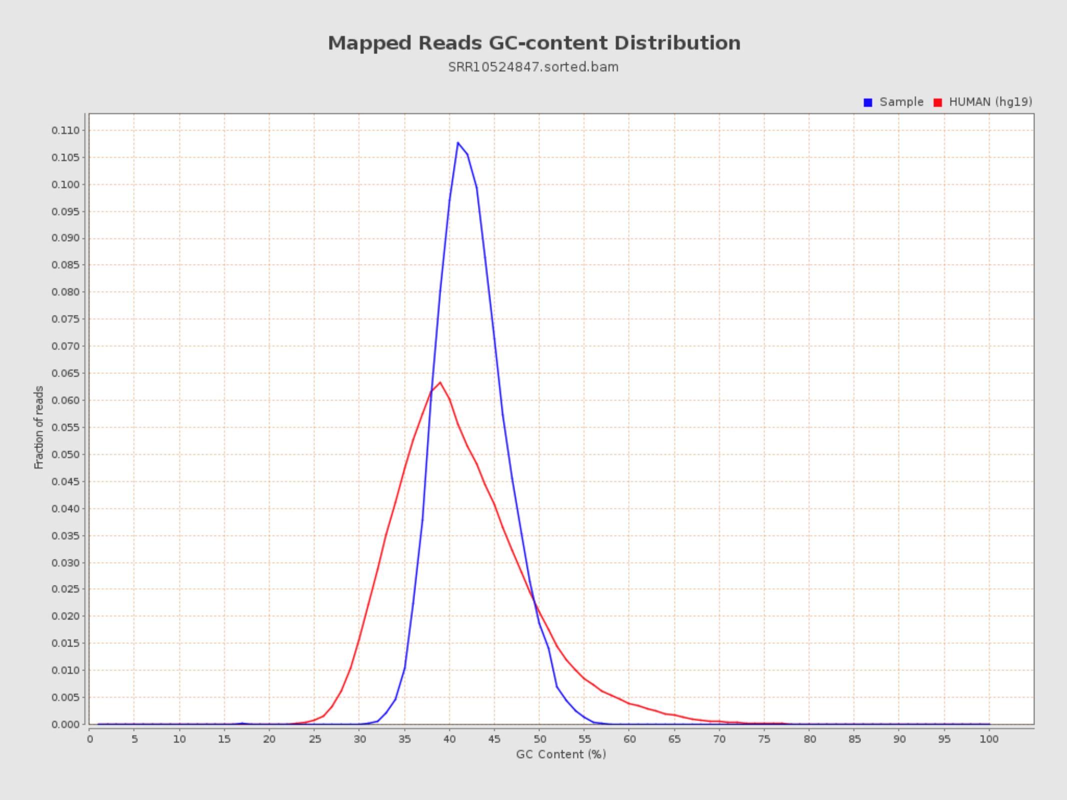
7. Results : Duplication Rate Histogram



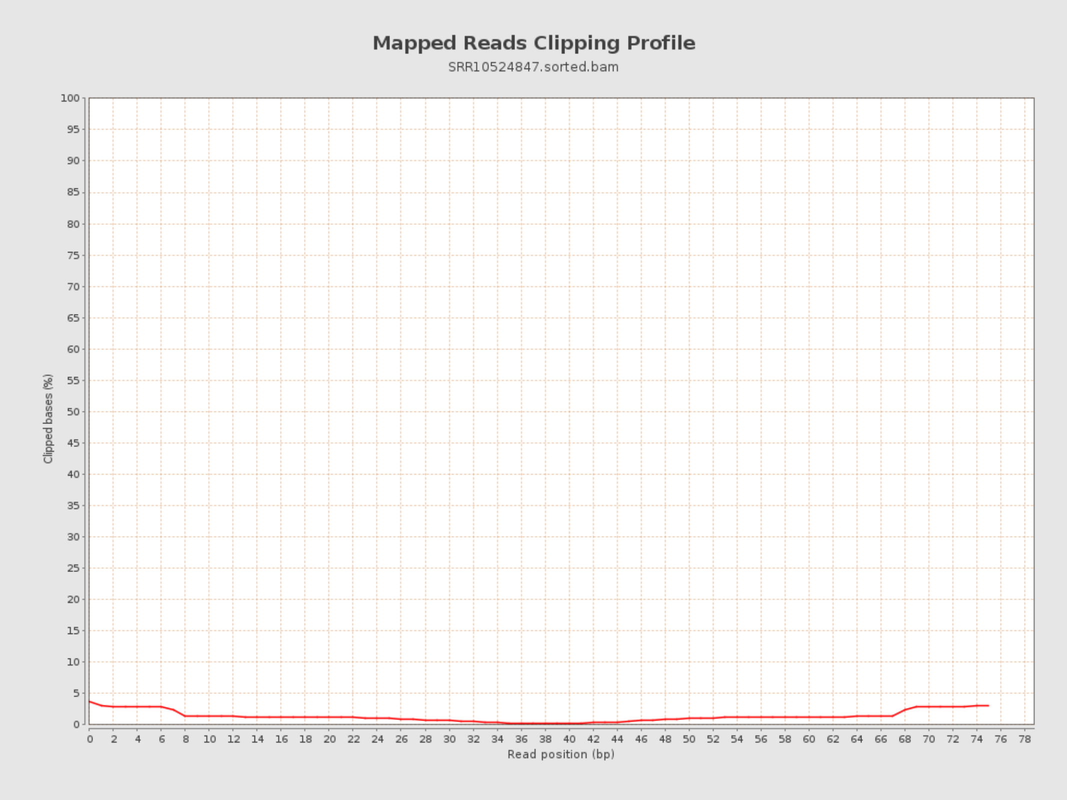
8. Results : Mapped Reads Nucleotide Content



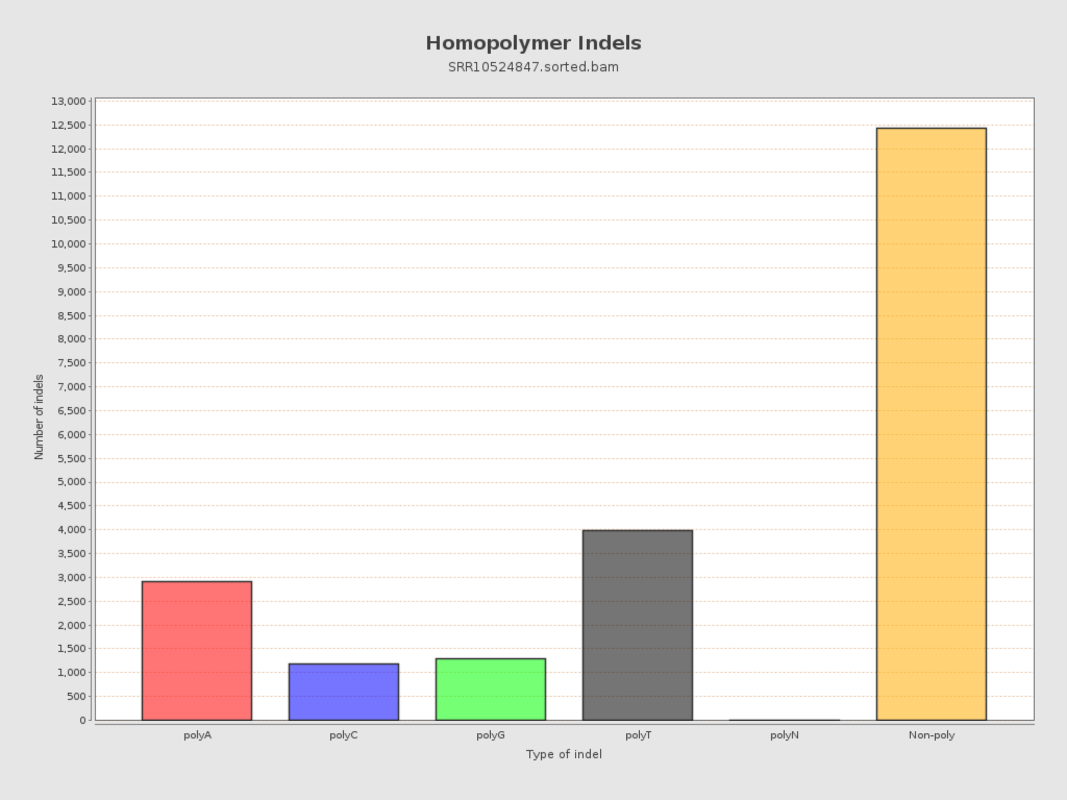
9. Results : Mapped Reads GC-content Distribution



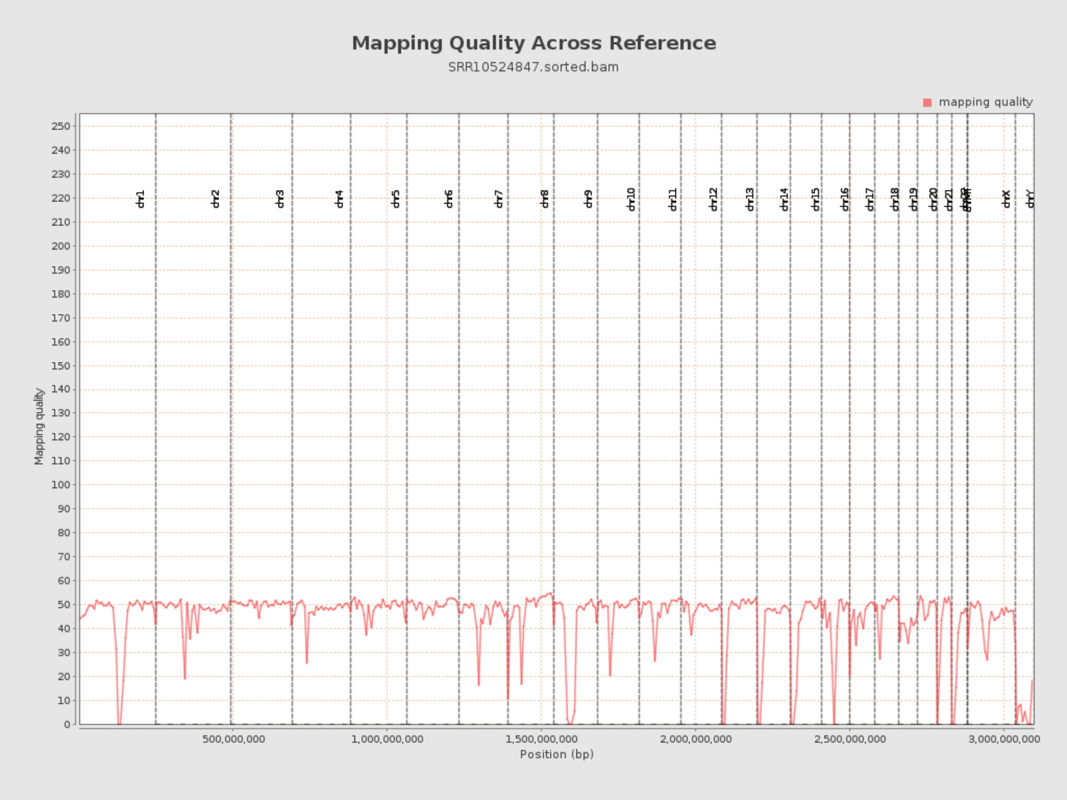
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram