Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 22:49:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524324.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_SRR10524324 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524324.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 22:49:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524324.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,162,533
Mapped reads	1,065,436 / 91.65%
Unmapped reads	97,097 / 8.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,095 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	26,654 / 2.29%
Duplication rate	1.81%
Clipped reads	1,066,011 / 91.7%

2.2. ACGT Content

Number/percentage of A's	15,704,879 / 25.57%
Number/percentage of C's	12,615,733 / 20.54%
Number/percentage of T's	18,628,509 / 30.33%
Number/percentage of G's	14,468,893 / 23.55%
Number/percentage of N's	8,260 / 0.01%
GC Percentage	44.09%

2.3. Coverage

Mean	0.0198

Standard Deviation	0.1971

2.4. Mapping Quality

Mean Mapping Quality	43.7

2.5. Mismatches and indels

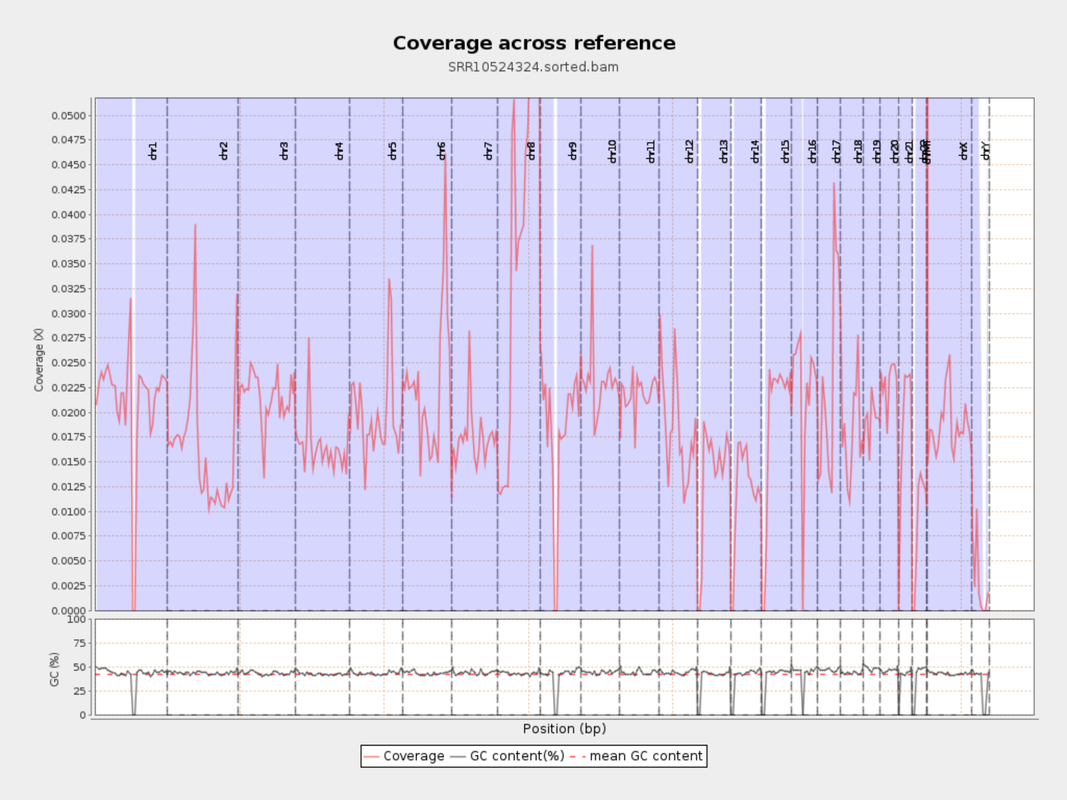
General error rate	0.52%
Mismatches	307,432
Insertions	4,591
Mapped reads with at least one insertion	0.43%
Deletions	9,799
Mapped reads with at least one deletion	0.91%
Homopolymer indels	41.33%

2.6. Chromosome stats

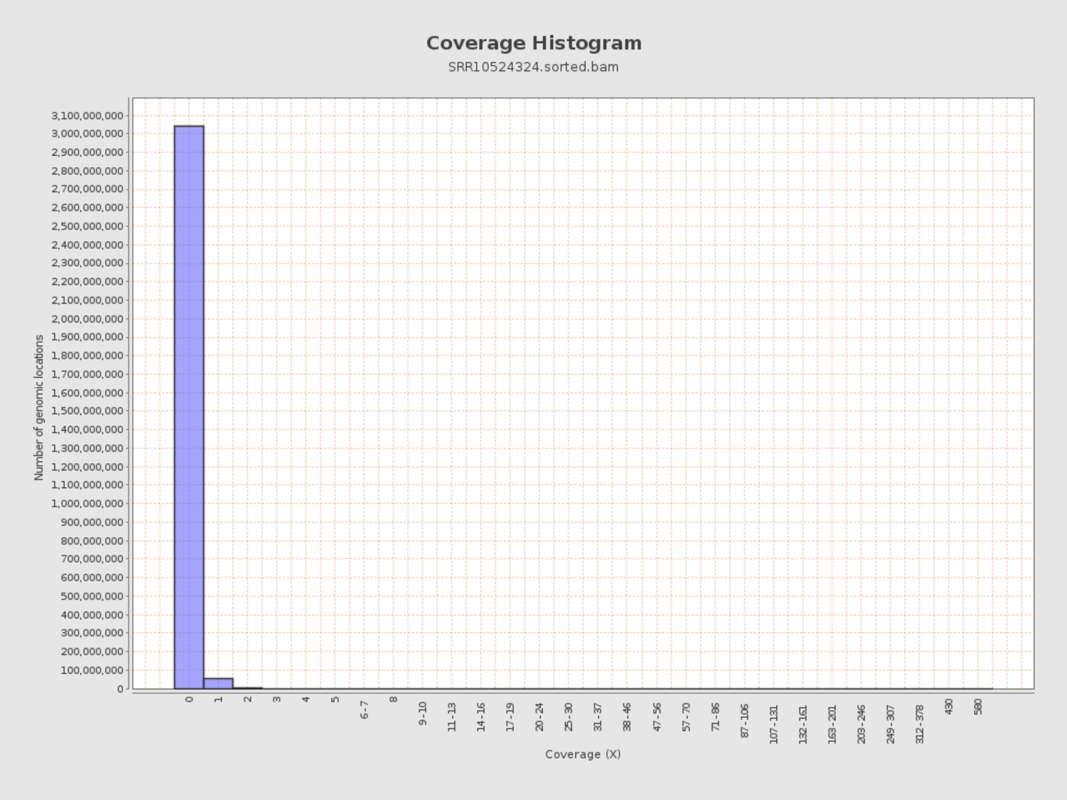
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5246343	0.021	0.321
chr2	243199373	3955829	0.0163	0.2668
chr3	198022430	4273072	0.0216	0.1566
chr4	191154276	3166825	0.0166	0.1472
chr5	180915260	3605912	0.0199	0.1498
chr6	171115067	3845280	0.0225	0.1678
chr7	159138663	2789297	0.0175	0.2217

chr8	146364022	6335405	0.0433	0.2555
chr9	141213431	2563840	0.0182	0.1621
chr10	135534747	3145222	0.0232	0.1998
chr11	135006516	2956177	0.0219	0.1775
chr12	133851895	2447330	0.0183	0.1454
chr13	115169878	1546717	0.0134	0.1228
chr14	107349540	1277298	0.0119	0.1183
chr15	102531392	1911671	0.0186	0.1479
chr16	90354753	1977783	0.0219	0.163
chr17	81195210	1912155	0.0236	0.1715
chr18	78077248	1421804	0.0182	0.2412
chr19	59128983	1142638	0.0193	0.2381
chr20	63025520	1436788	0.0228	0.162
chr21	48129895	897309	0.0186	0.1512
chr22	51304566	462747	0.009	0.1003
chrMT	16571	34472	2.0803	1.9161
chrX	155270560	2921323	0.0188	0.1544
chrY	59373566	168790	0.0028	0.0844

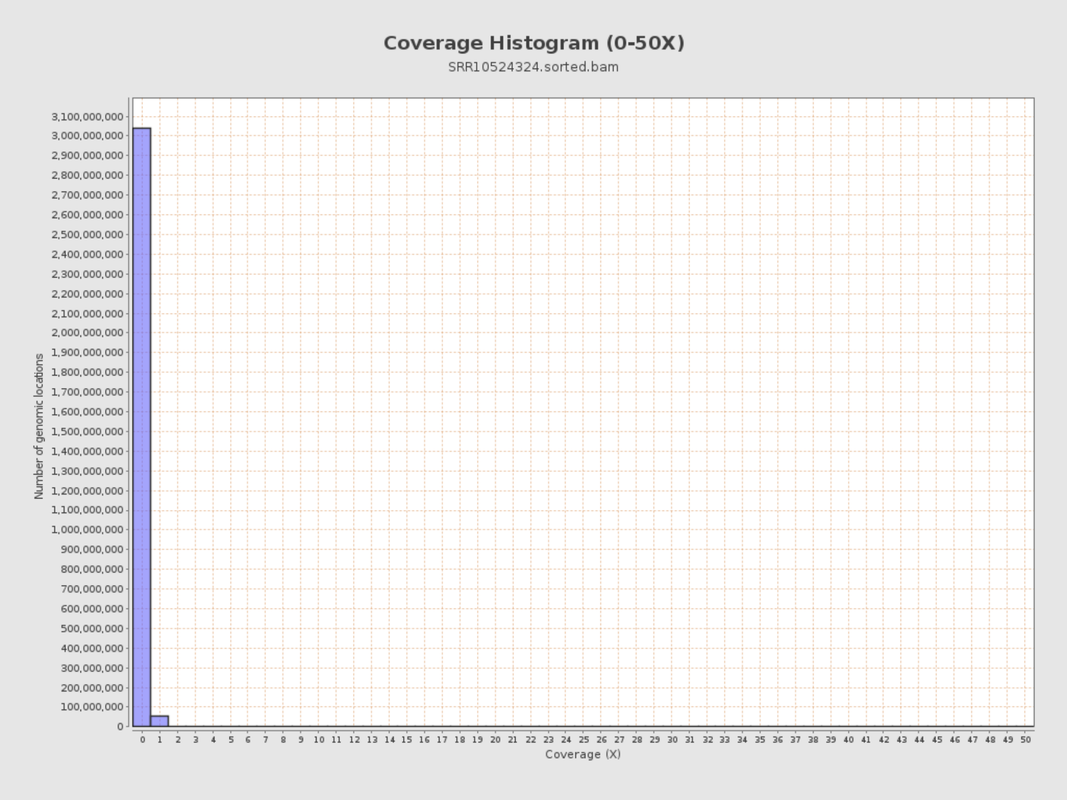
3. Results : Coverage across reference



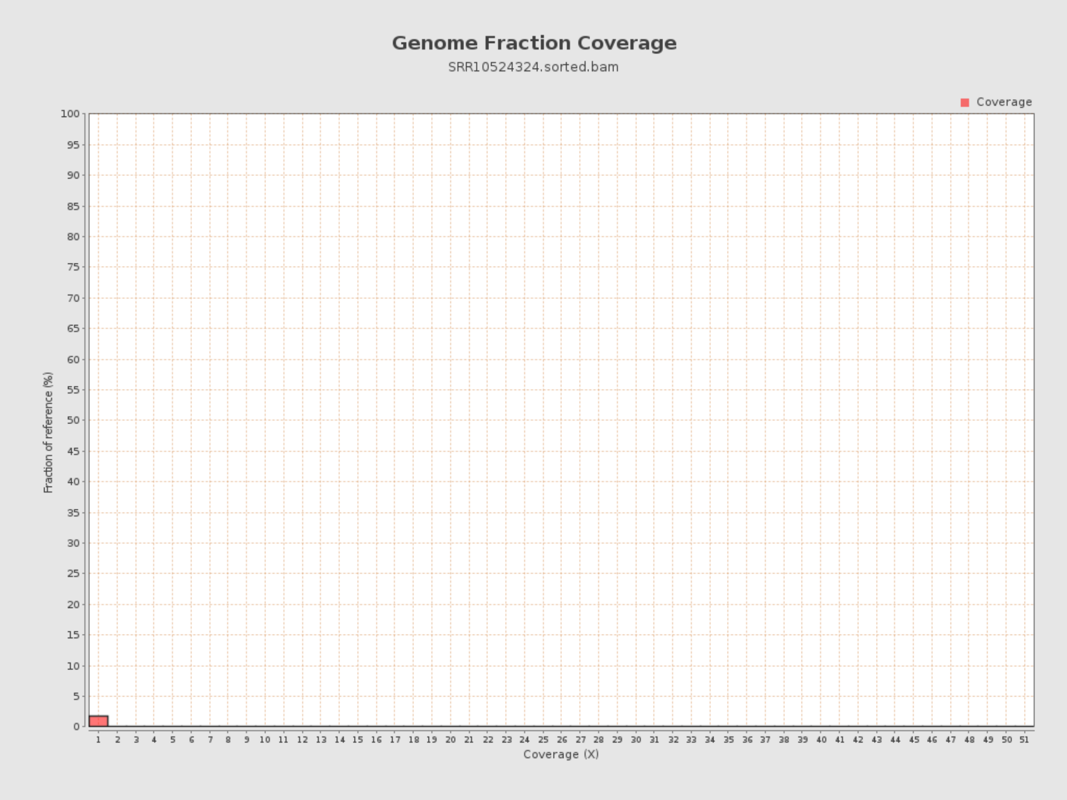
4. Results : Coverage Histogram



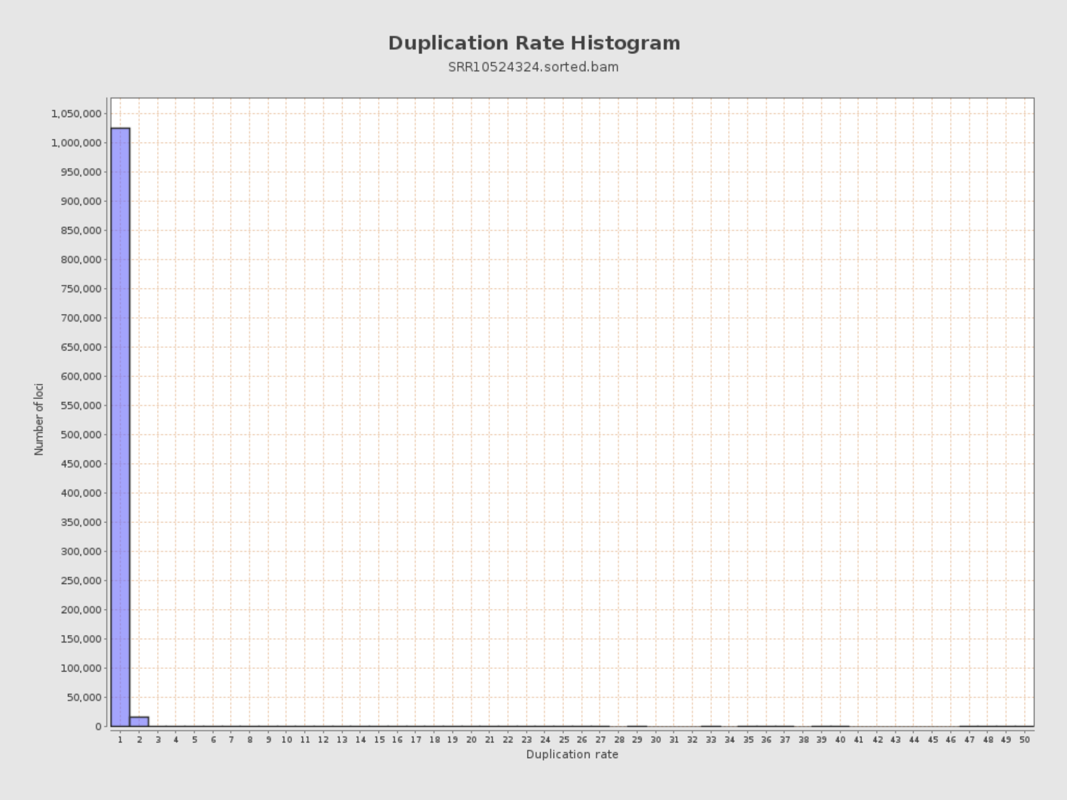
5. Results : Coverage Histogram (0-50X)



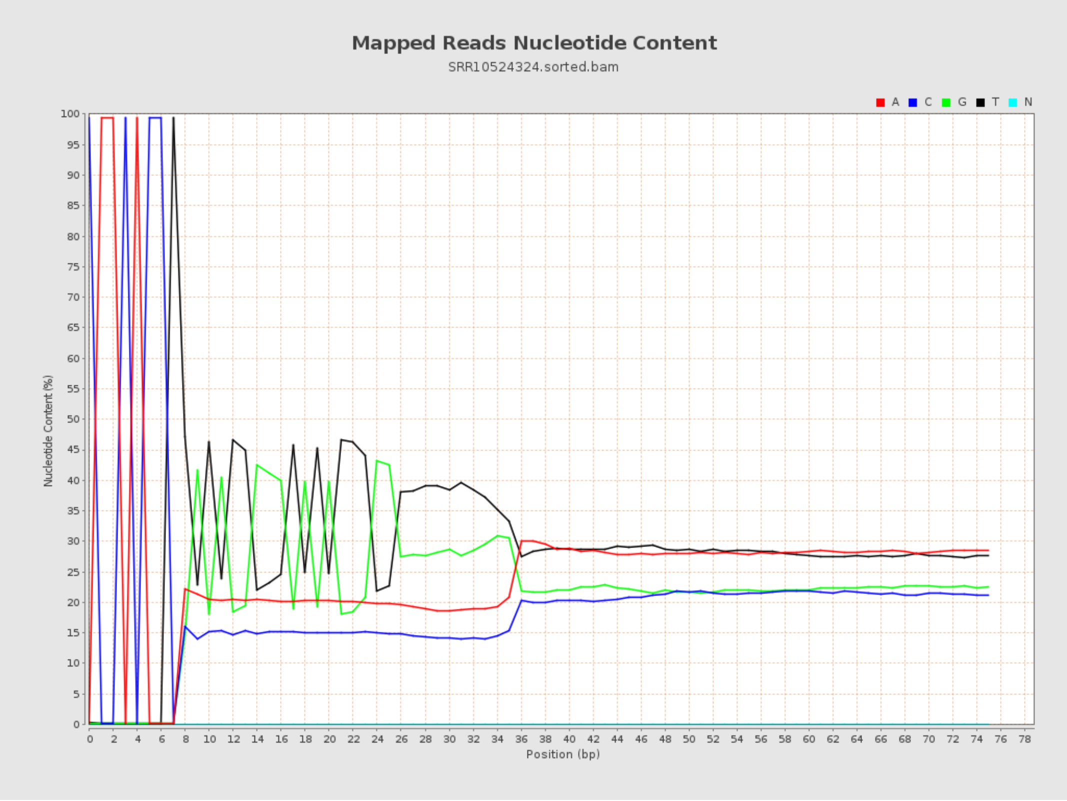
6. Results : Genome Fraction Coverage



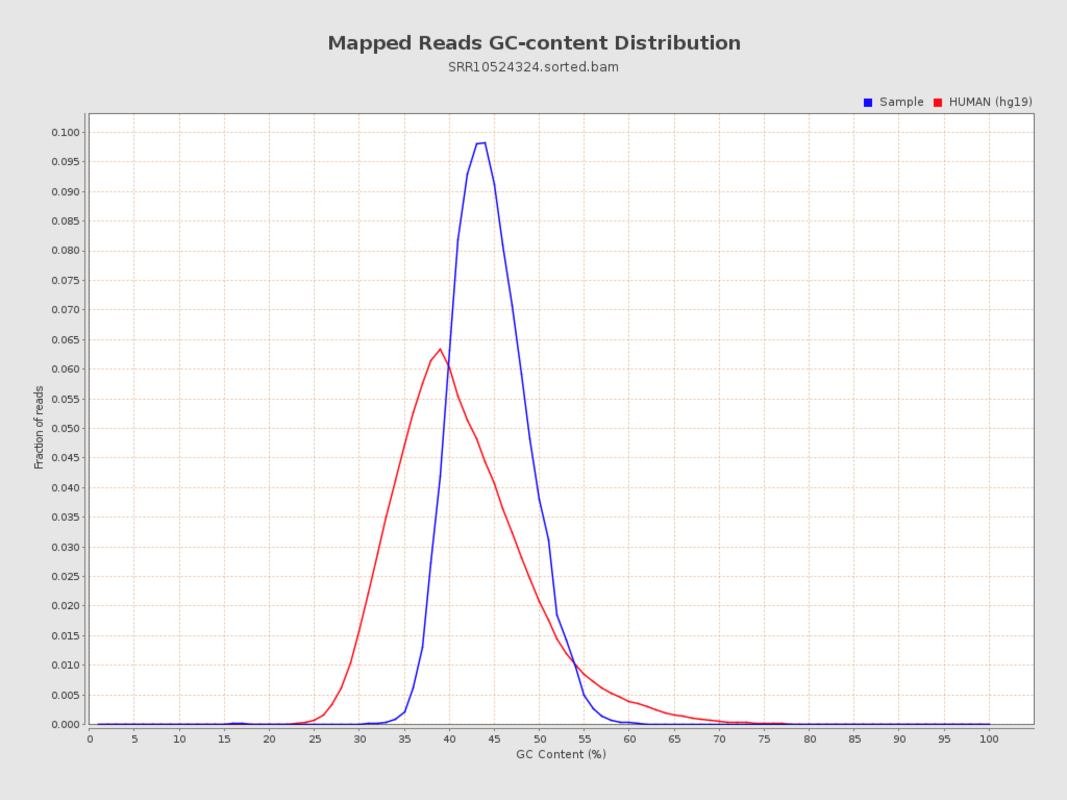
7. Results : Duplication Rate Histogram



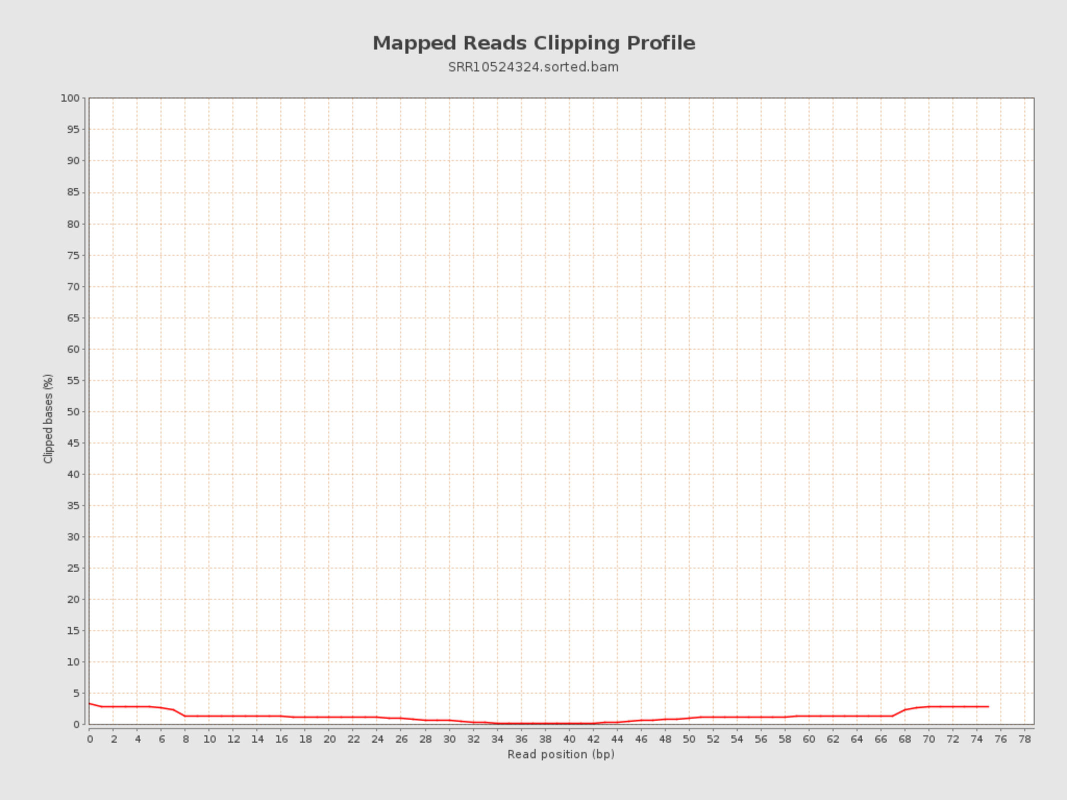
8. Results : Mapped Reads Nucleotide Content



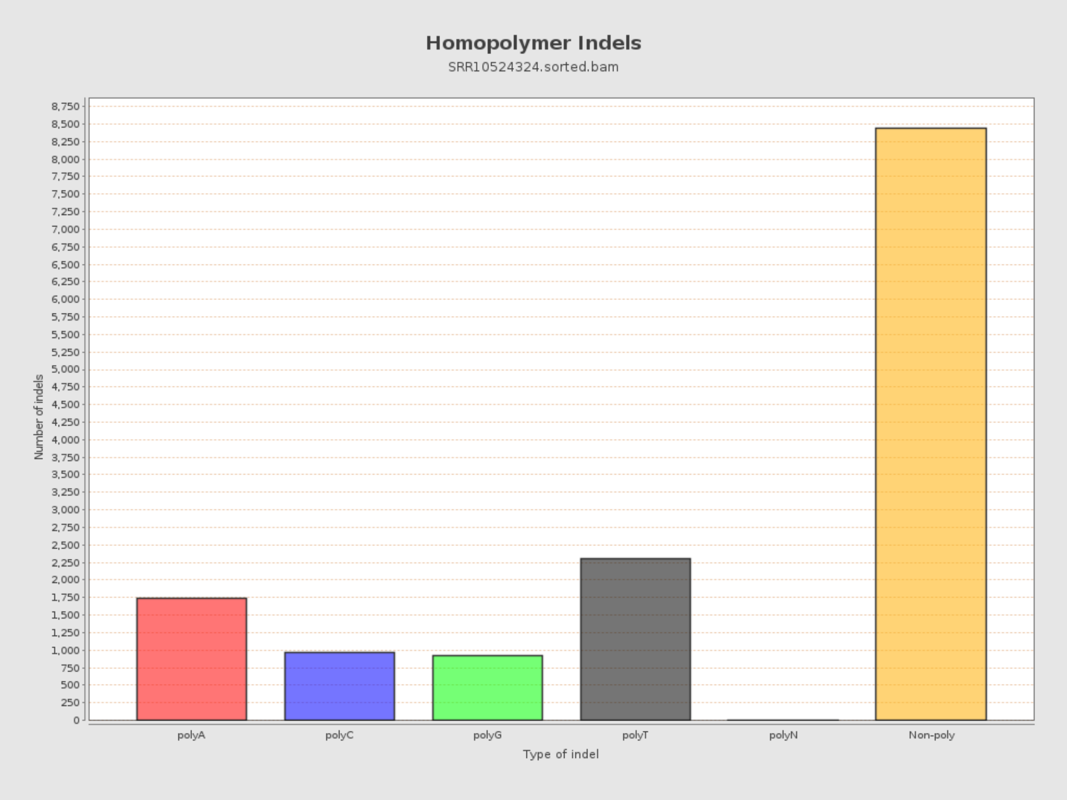
9. Results : Mapped Reads GC-content Distribution



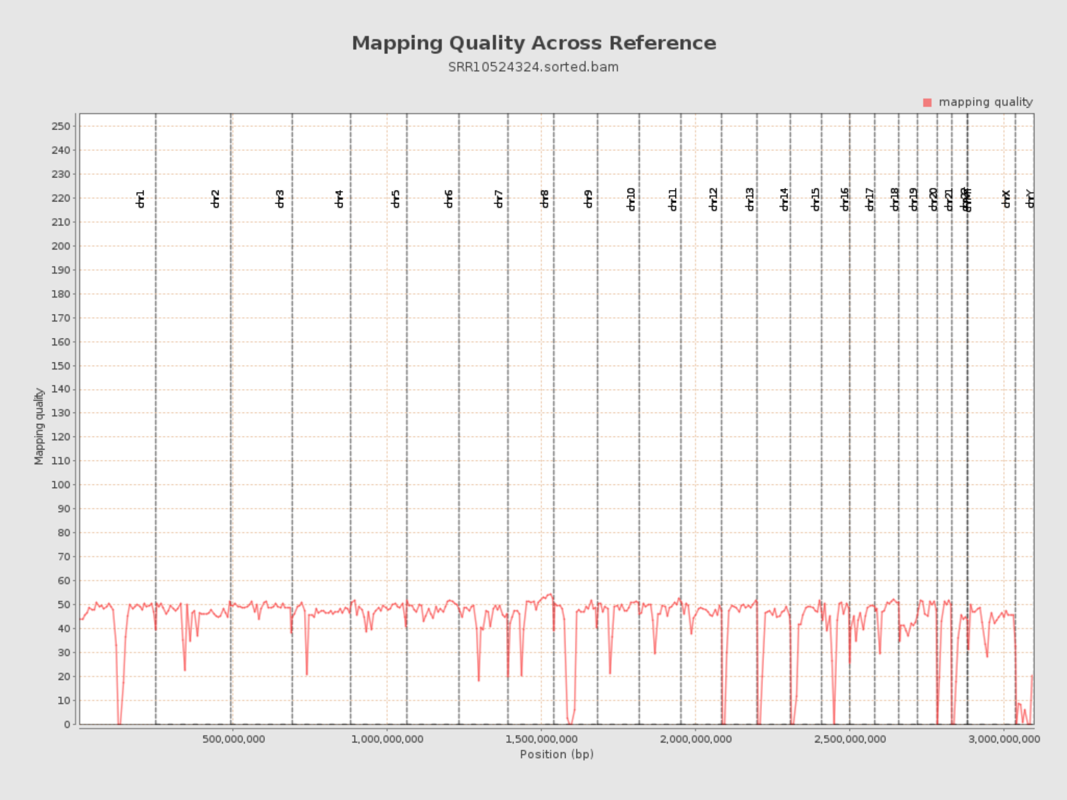
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram