Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 23:05:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524330.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_SRR10524330 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524330.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 23:05:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524330.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,070,989
Mapped reads	976,929 / 91.22%
Unmapped reads	94,060 / 8.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,928 / 0.37%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	25,780 / 2.41%
Duplication rate	1.87%
Clipped reads	978,694 / 91.38%

2.2. ACGT Content

Number/percentage of A's	14,126,623 / 24.96%
Number/percentage of C's	11,204,265 / 19.8%
Number/percentage of T's	17,624,817 / 31.15%
Number/percentage of G's	13,622,259 / 24.07%
Number/percentage of N's	7,921 / 0.01%
GC Percentage	43.87%

2.3. Coverage

Mean	0.0183

Standard Deviation	0.1937

2.4. Mapping Quality

Mean Mapping Quality	44.03

2.5. Mismatches and indels

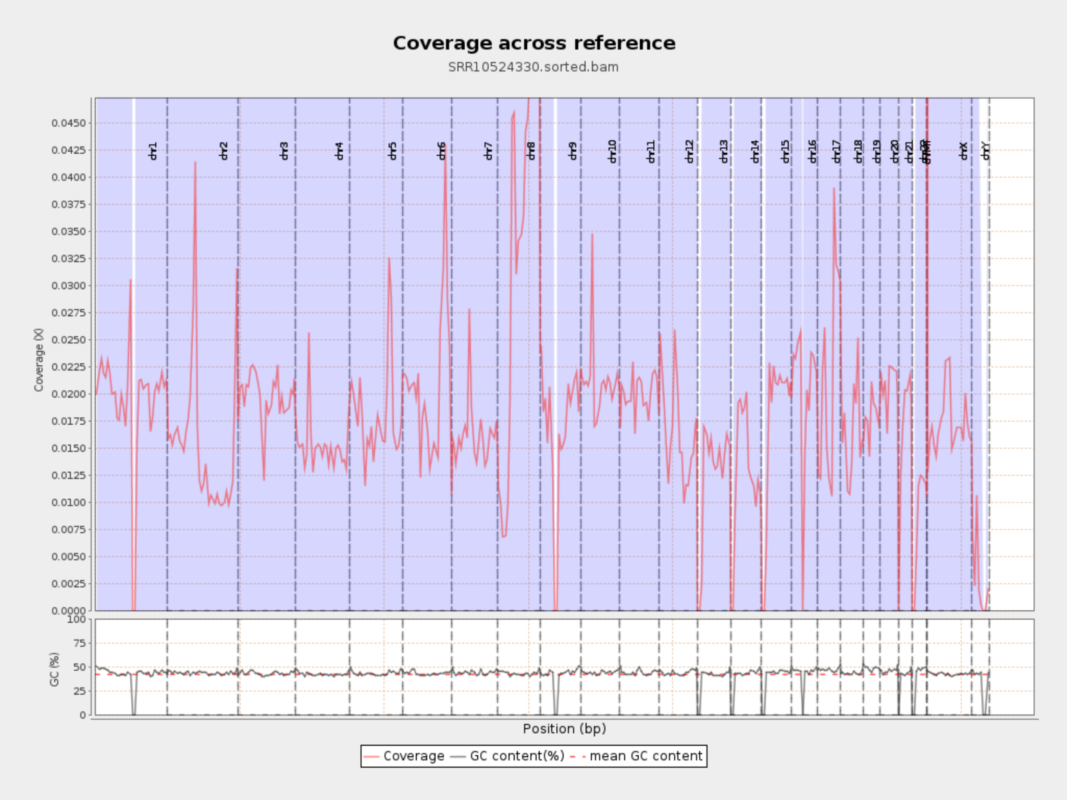
General error rate	0.52%
Mismatches	287,150
Insertions	3,794
Mapped reads with at least one insertion	0.39%
Deletions	9,287
Mapped reads with at least one deletion	0.94%
Homopolymer indels	41.82%

2.6. Chromosome stats

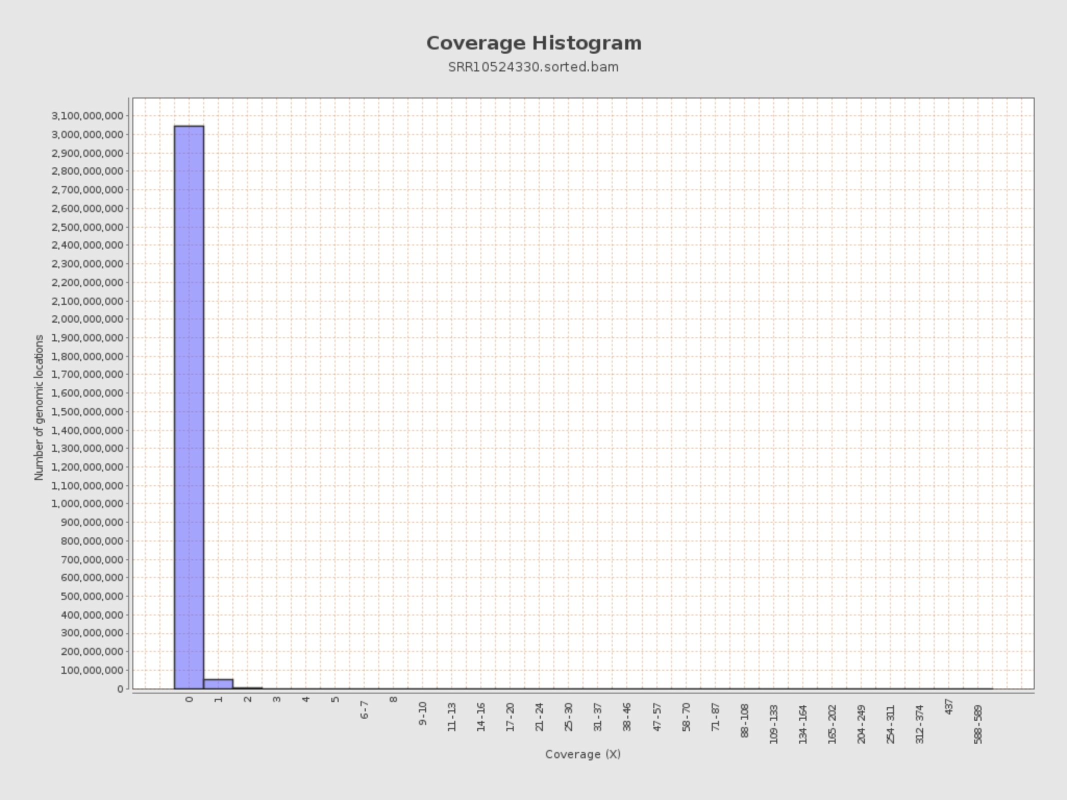
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4802192	0.0193	0.3207
chr2	243199373	3692299	0.0152	0.2682
chr3	198022430	3899956	0.0197	0.1478
chr4	191154276	2914442	0.0152	0.1452
chr5	180915260	3278162	0.0181	0.1421
chr6	171115067	3546713	0.0207	0.1606
chr7	159138663	2598630	0.0163	0.223

chr8	146364022	5782255	0.0395	0.2479
chr9	141213431	2338018	0.0166	0.1569
chr10	135534747	2880542	0.0213	0.1932
chr11	135006516	2716795	0.0201	0.1753
chr12	133851895	2205983	0.0165	0.1369
chr13	115169878	1423239	0.0124	0.1174
chr14	107349540	1357539	0.0126	0.1214
chr15	102531392	1745114	0.017	0.1382
chr16	90354753	1807526	0.02	0.1536
chr17	81195210	1774568	0.0219	0.1641
chr18	78077248	1299371	0.0166	0.2451
chr19	59128983	1058946	0.0179	0.2256
chr20	63025520	1324386	0.021	0.1577
chr21	48129895	809104	0.0168	0.1443
chr22	51304566	431934	0.0084	0.0982
chrMT	16571	42262	2.5504	2.3243
chrX	155270560	2702113	0.0174	0.1496
chrY	59373566	168883	0.0028	0.095

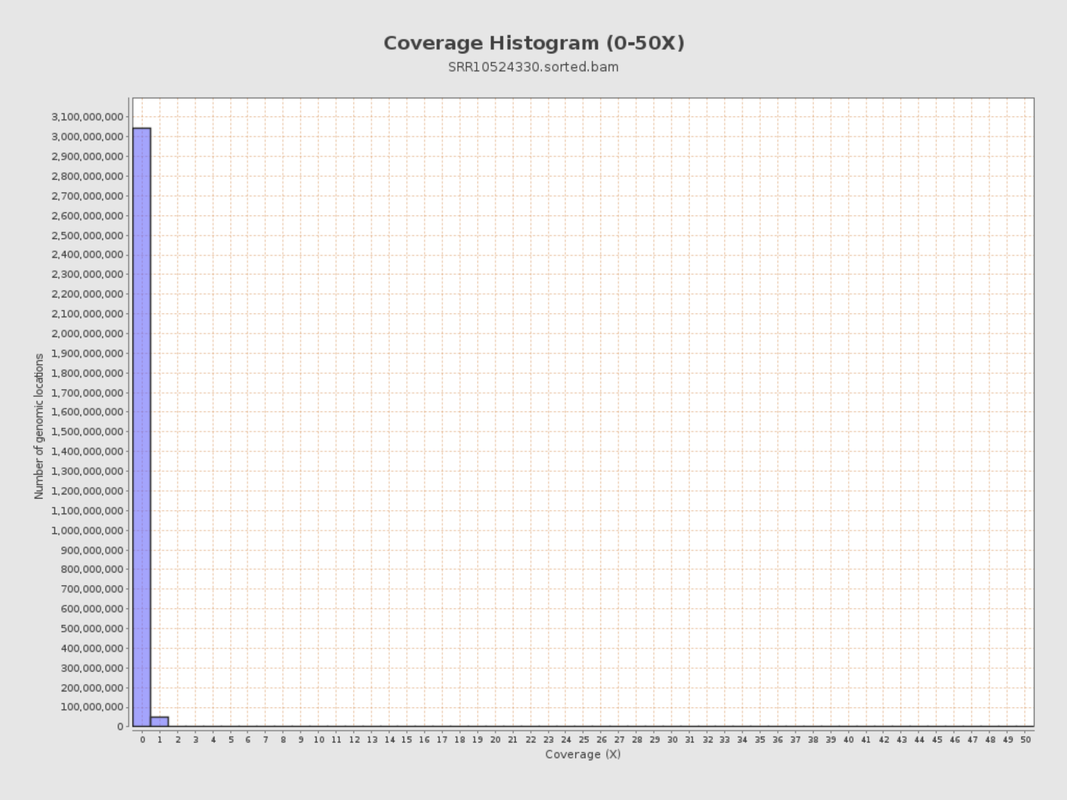
3. Results : Coverage across reference



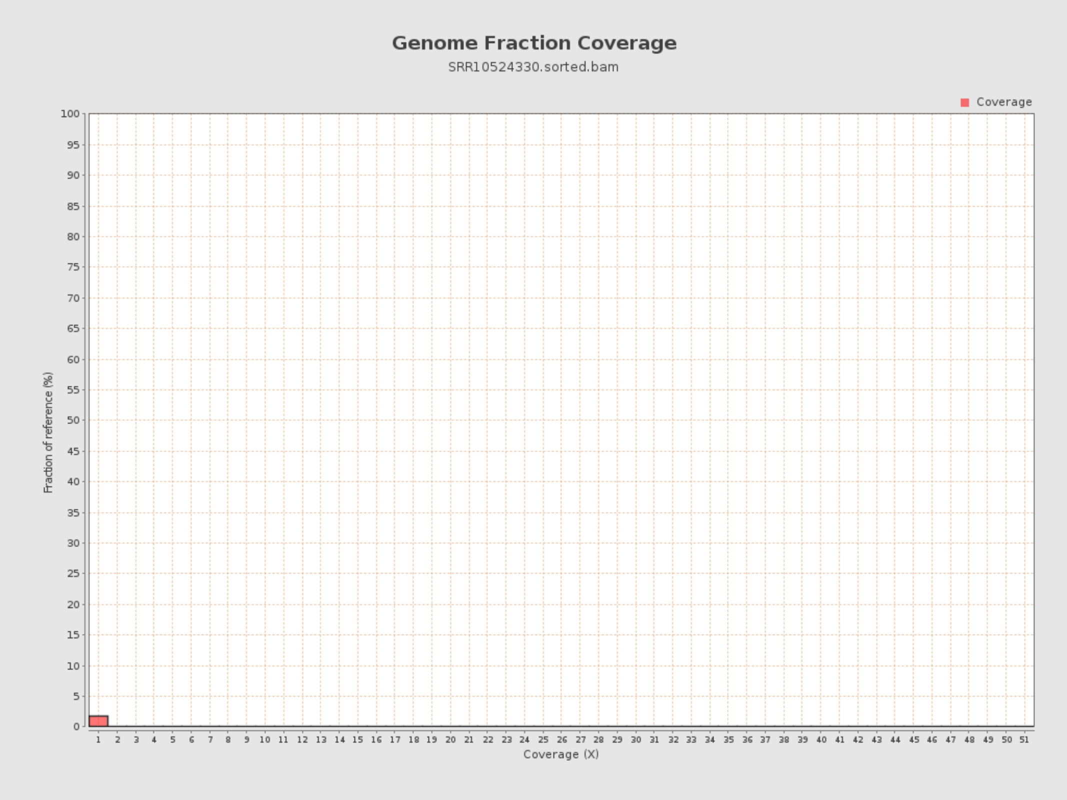
4. Results : Coverage Histogram



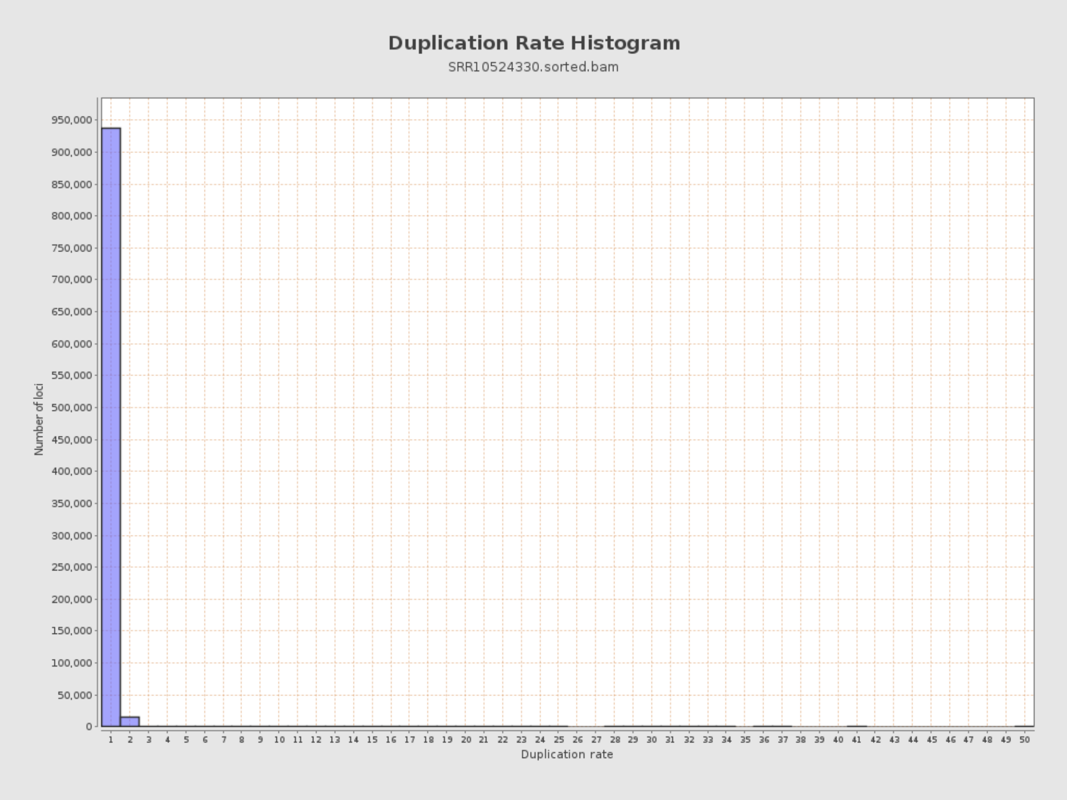
5. Results : Coverage Histogram (0-50X)



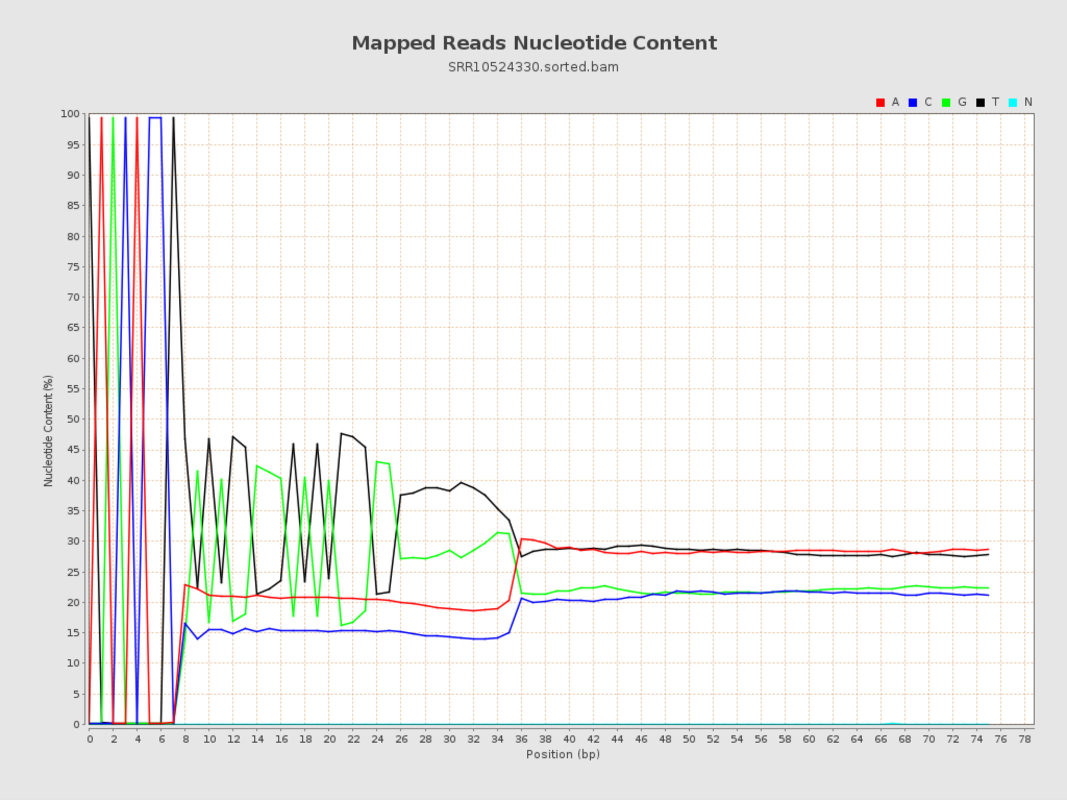
6. Results : Genome Fraction Coverage



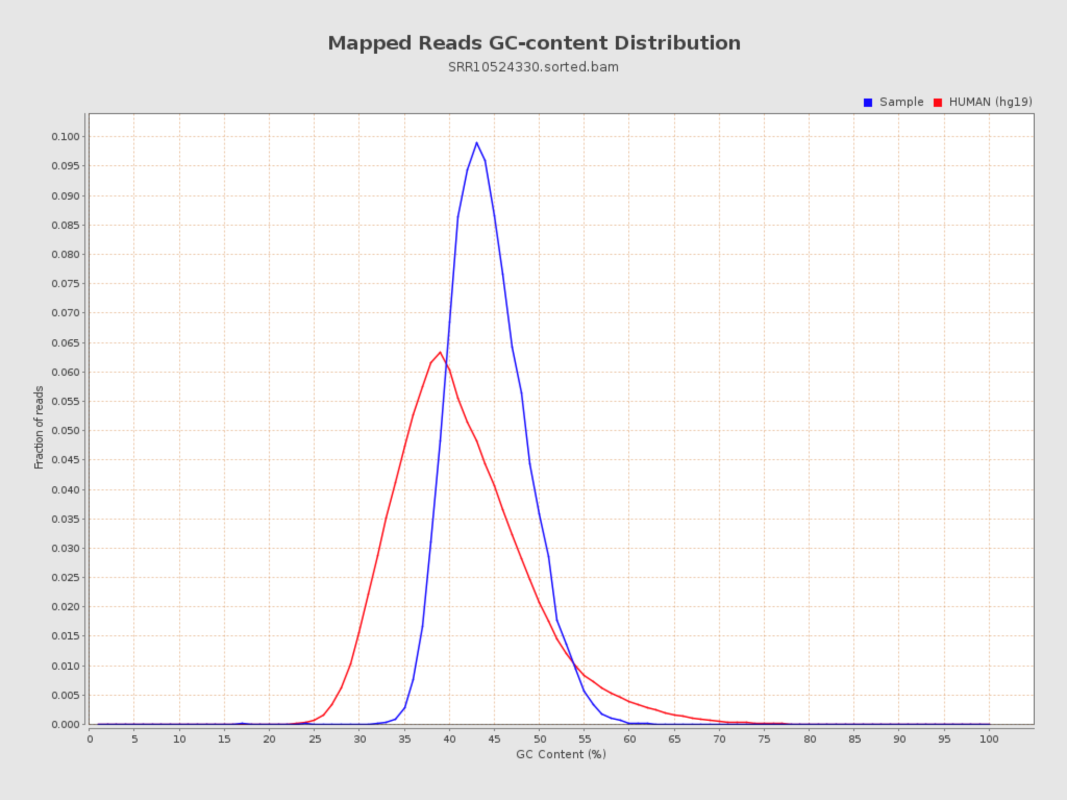
7. Results : Duplication Rate Histogram



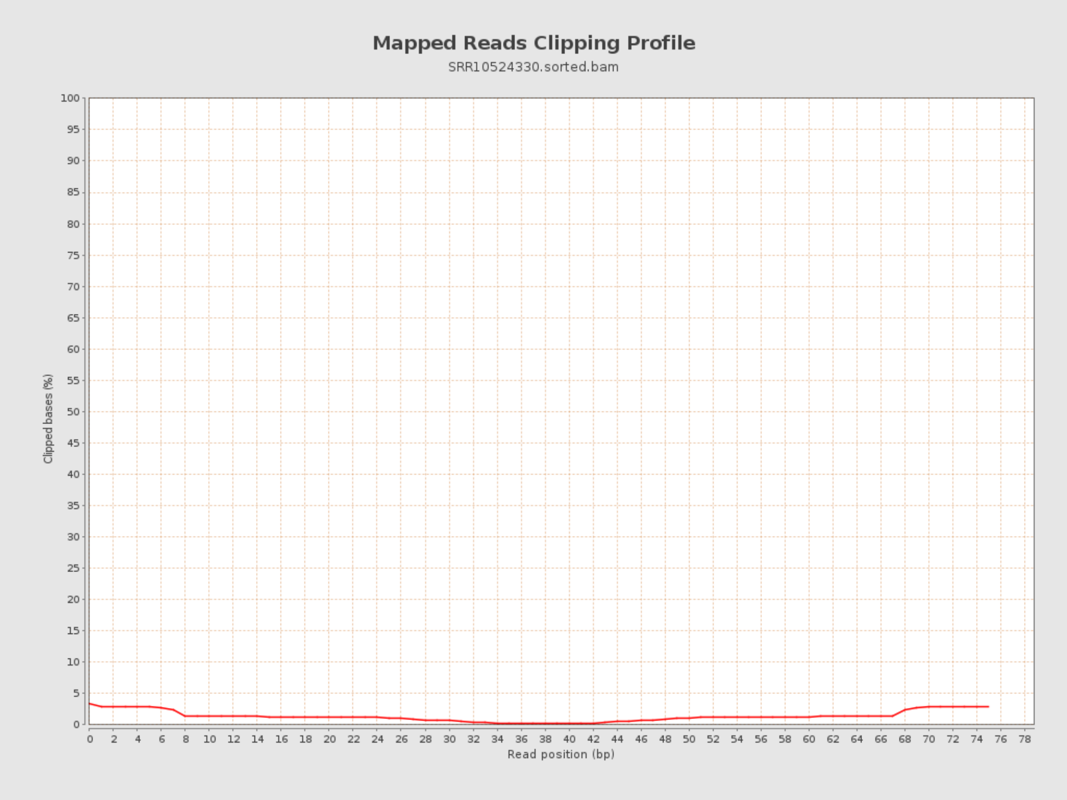
8. Results : Mapped Reads Nucleotide Content



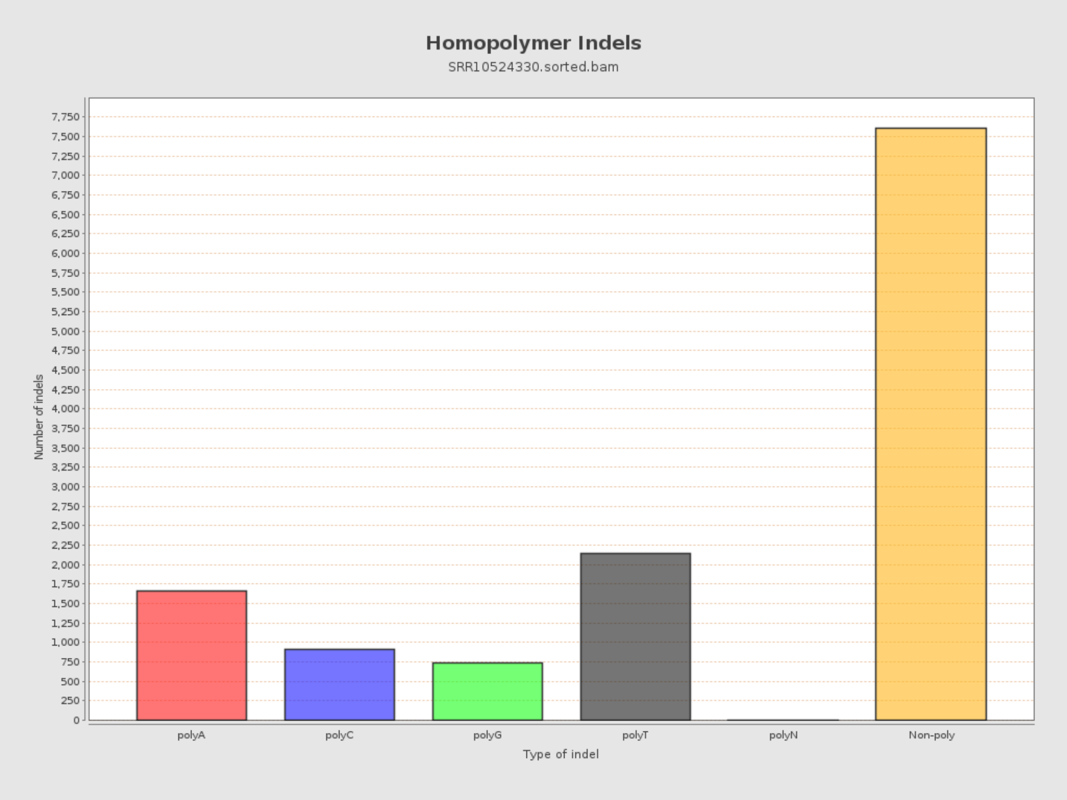
9. Results : Mapped Reads GC-content Distribution



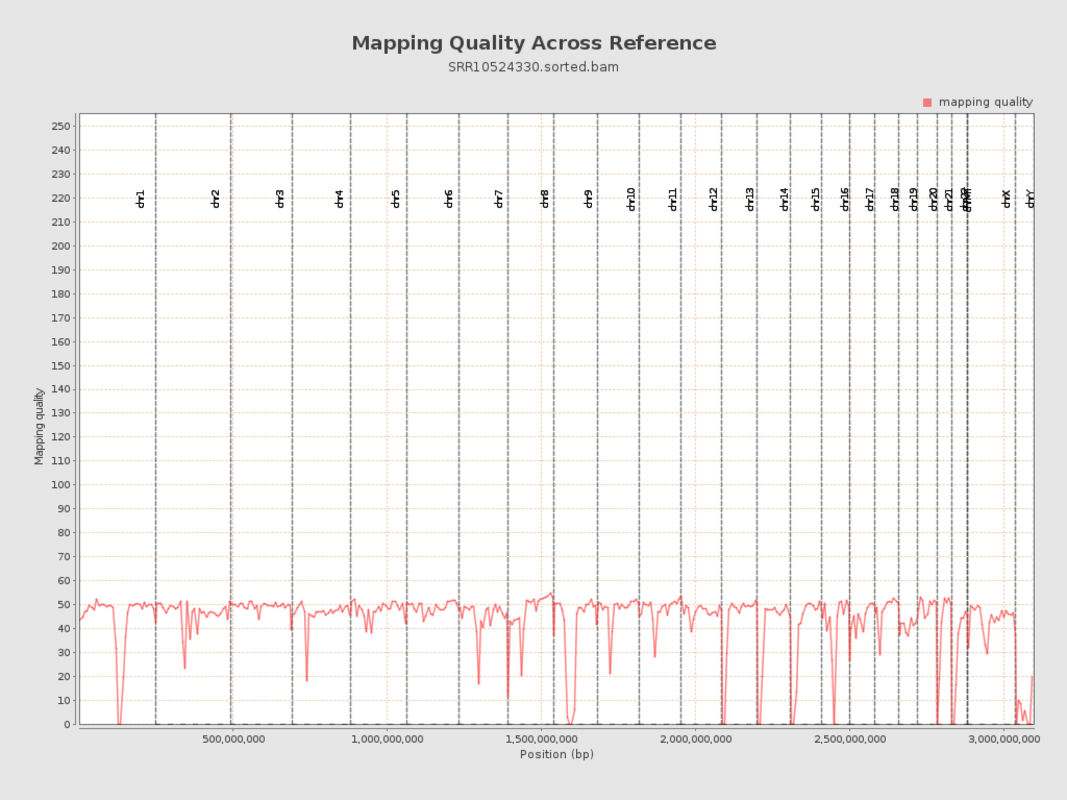
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram