Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 12:31:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524599.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_SRR10524599 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524599.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 12:31:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524599.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,232,319
Mapped reads	1,148,676 / 93.21%
Unmapped reads	83,643 / 6.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,468 / 0.2%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	38,385 / 3.11%
Duplication rate	2.61%
Clipped reads	1,147,600 / 93.13%

2.2. ACGT Content

Number/percentage of A's	16,024,405 / 23.95%
Number/percentage of C's	12,392,637 / 18.52%
Number/percentage of T's	21,501,137 / 32.13%
Number/percentage of G's	17,002,092 / 25.41%
Number/percentage of N's	350 / 0%
GC Percentage	43.92%

2.3. Coverage

Mean	0.0216

Standard Deviation	0.2029

2.4. Mapping Quality

Mean Mapping Quality	45.44

2.5. Mismatches and indels

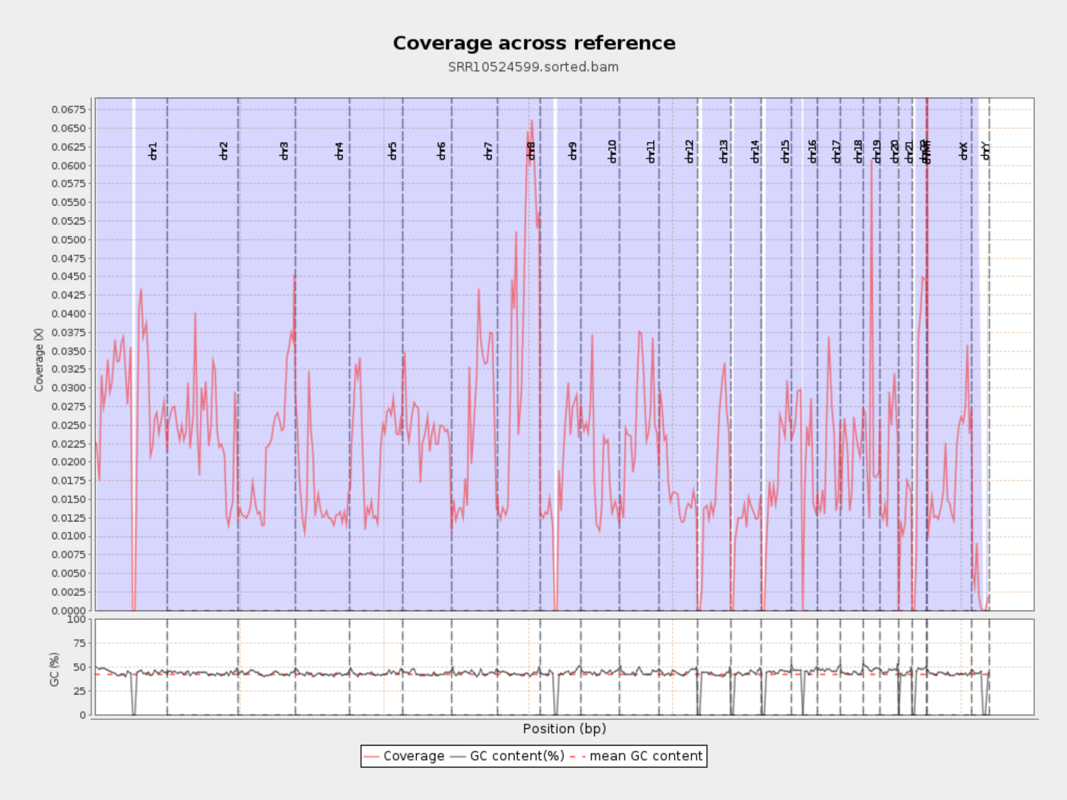
General error rate	0.48%
Mismatches	314,237
Insertions	4,340
Mapped reads with at least one insertion	0.38%
Deletions	12,595
Mapped reads with at least one deletion	1.09%
Homopolymer indels	44.45%

2.6. Chromosome stats

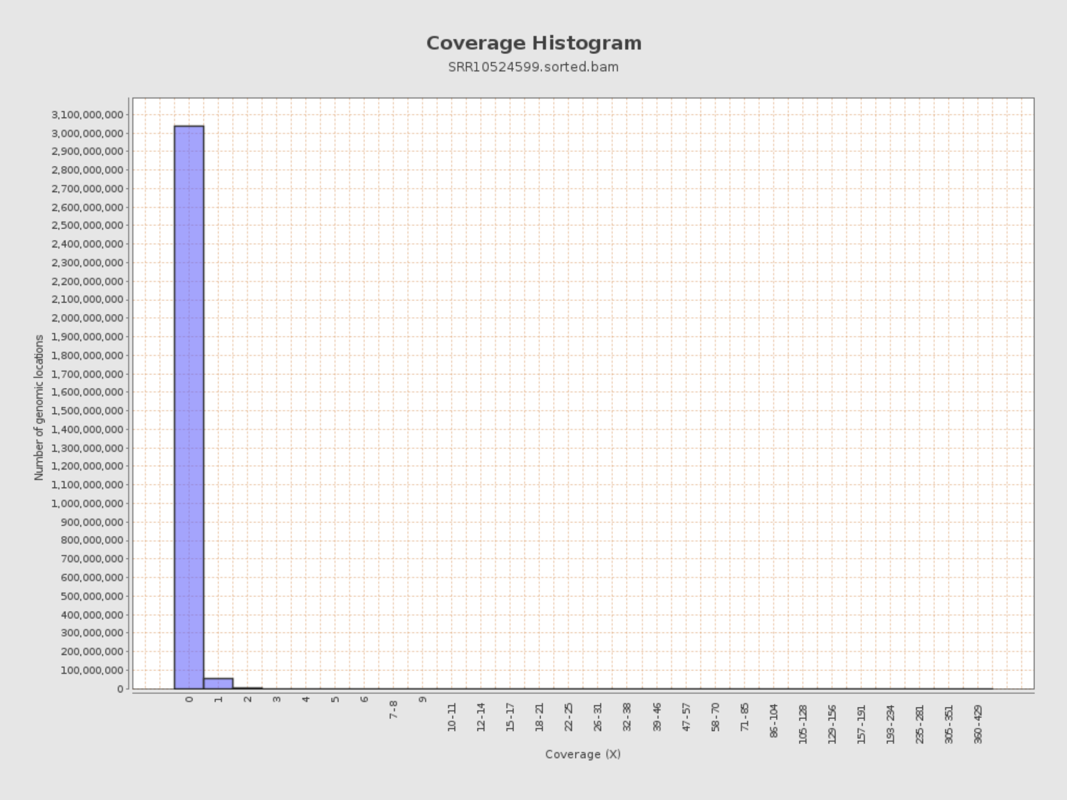
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7052682	0.0283	0.3348
chr2	243199373	5952235	0.0245	0.2316
chr3	198022430	4154071	0.021	0.1567
chr4	191154276	3002082	0.0157	0.1508
chr5	180915260	4055500	0.0224	0.1614
chr6	171115067	4210371	0.0246	0.1785
chr7	159138663	3971452	0.025	0.2513

chr8	146364022	5649842	0.0386	0.2638
chr9	141213431	2505639	0.0177	0.1854
chr10	135534747	2698732	0.0199	0.1979
chr11	135006516	3428357	0.0254	0.2051
chr12	133851895	2278133	0.017	0.1436
chr13	115169878	1959386	0.017	0.1427
chr14	107349540	1212822	0.0113	0.1195
chr15	102531392	1773889	0.0173	0.1458
chr16	90354753	1890107	0.0209	0.1612
chr17	81195210	1648376	0.0203	0.1559
chr18	78077248	1629057	0.0209	0.267
chr19	59128983	1468339	0.0248	0.2488
chr20	63025520	1310578	0.0208	0.1578
chr21	48129895	600367	0.0125	0.1298
chr22	51304566	1426319	0.0278	0.1809
chrMT	16571	5628	0.3396	0.6306
chrX	155270560	2903273	0.0187	0.163
chrY	59373566	154602	0.0026	0.0777

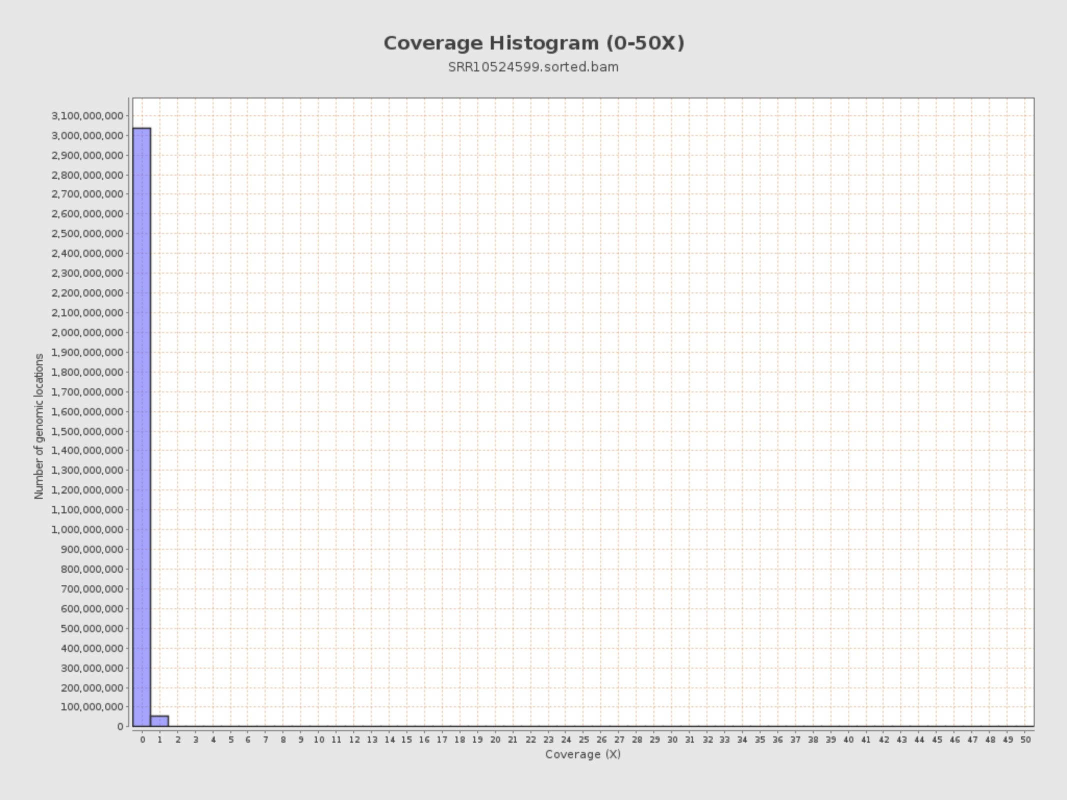
3. Results : Coverage across reference



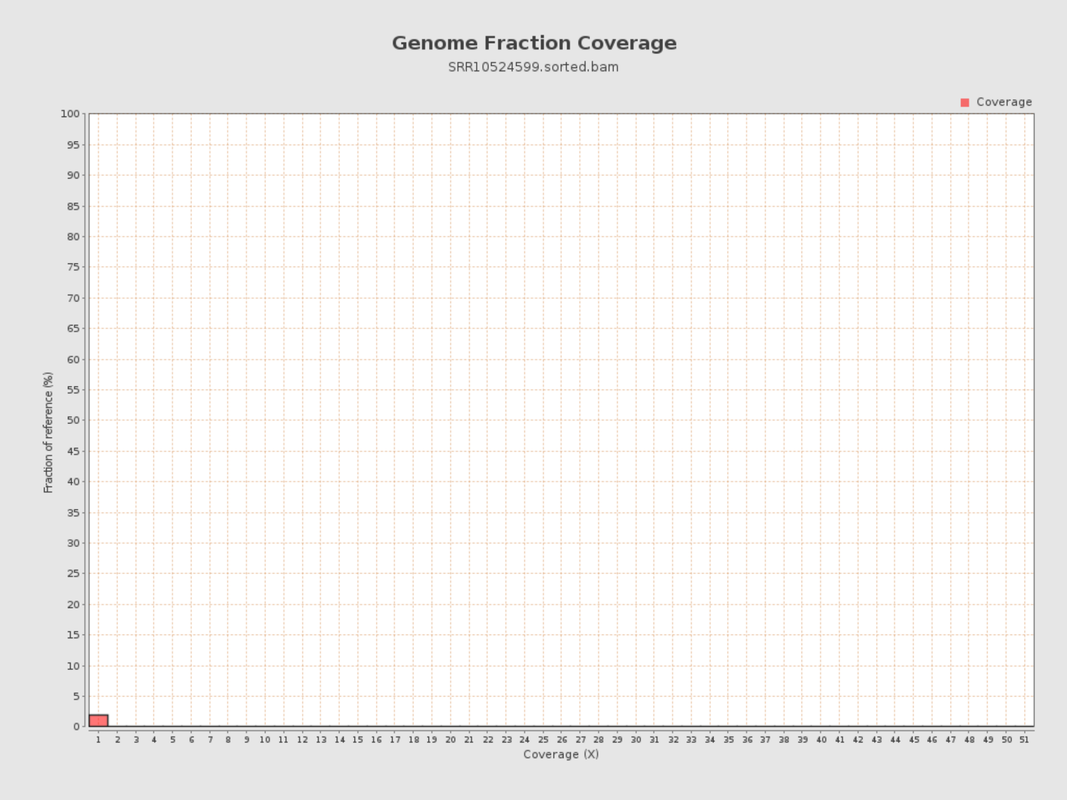
4. Results : Coverage Histogram



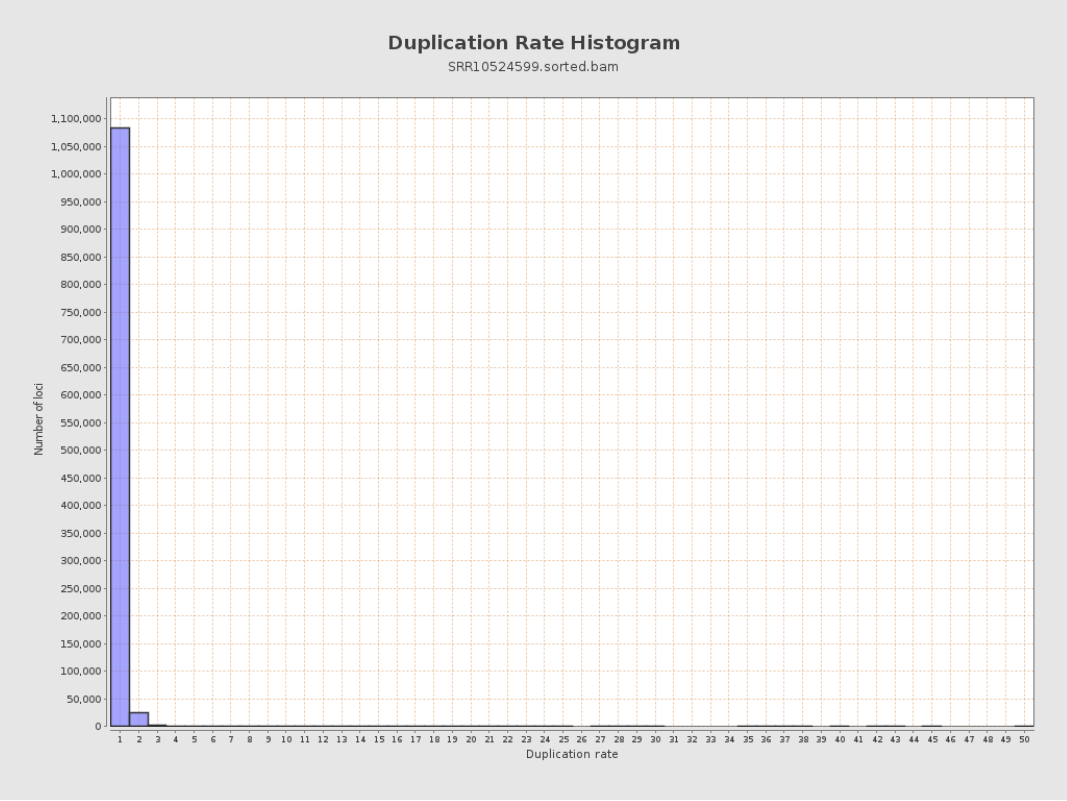
5. Results : Coverage Histogram (0-50X)



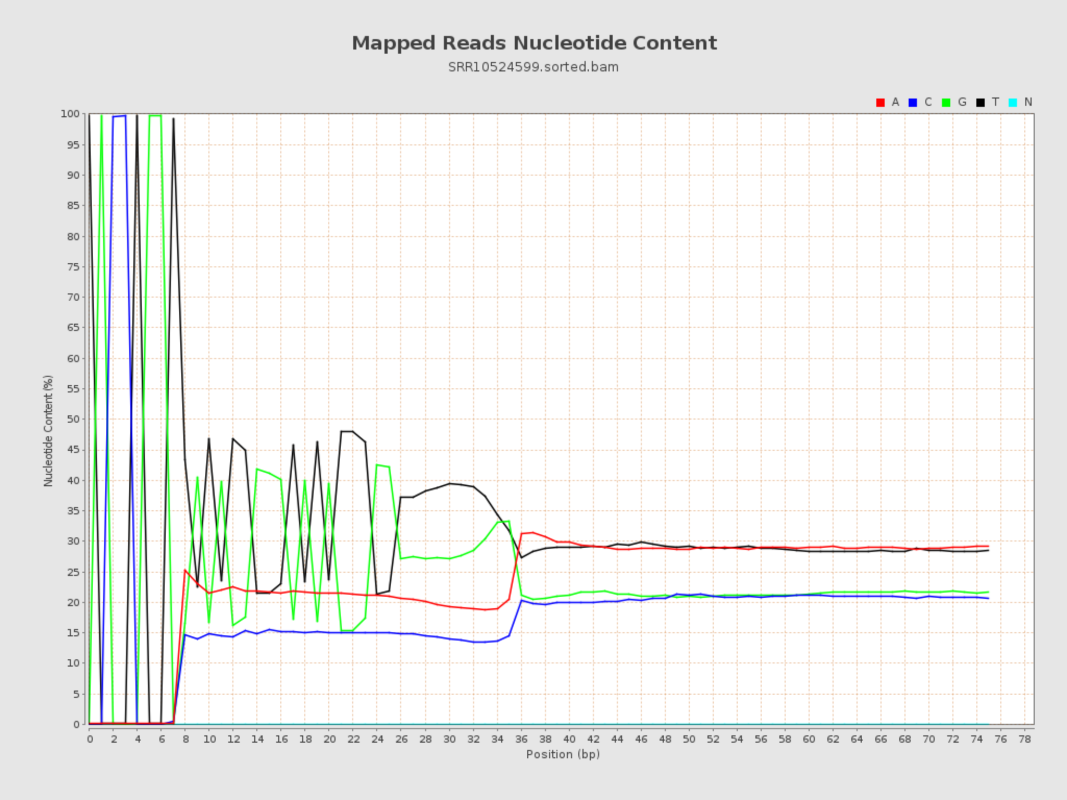
6. Results : Genome Fraction Coverage



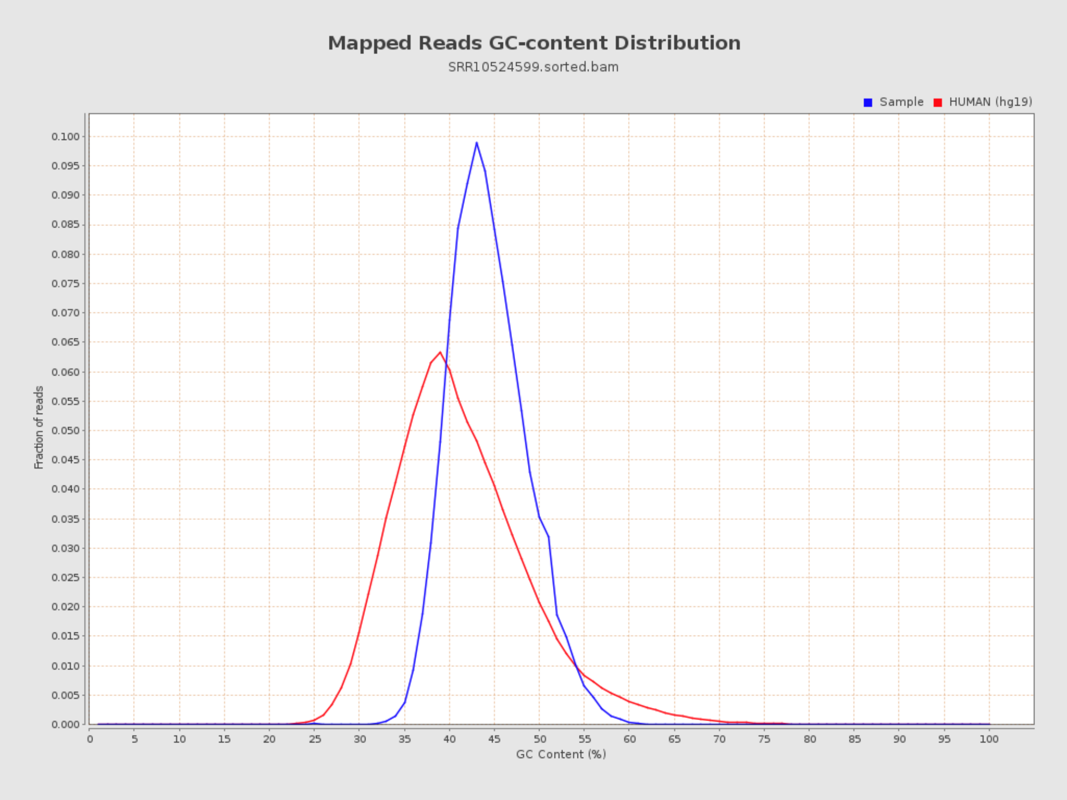
7. Results : Duplication Rate Histogram



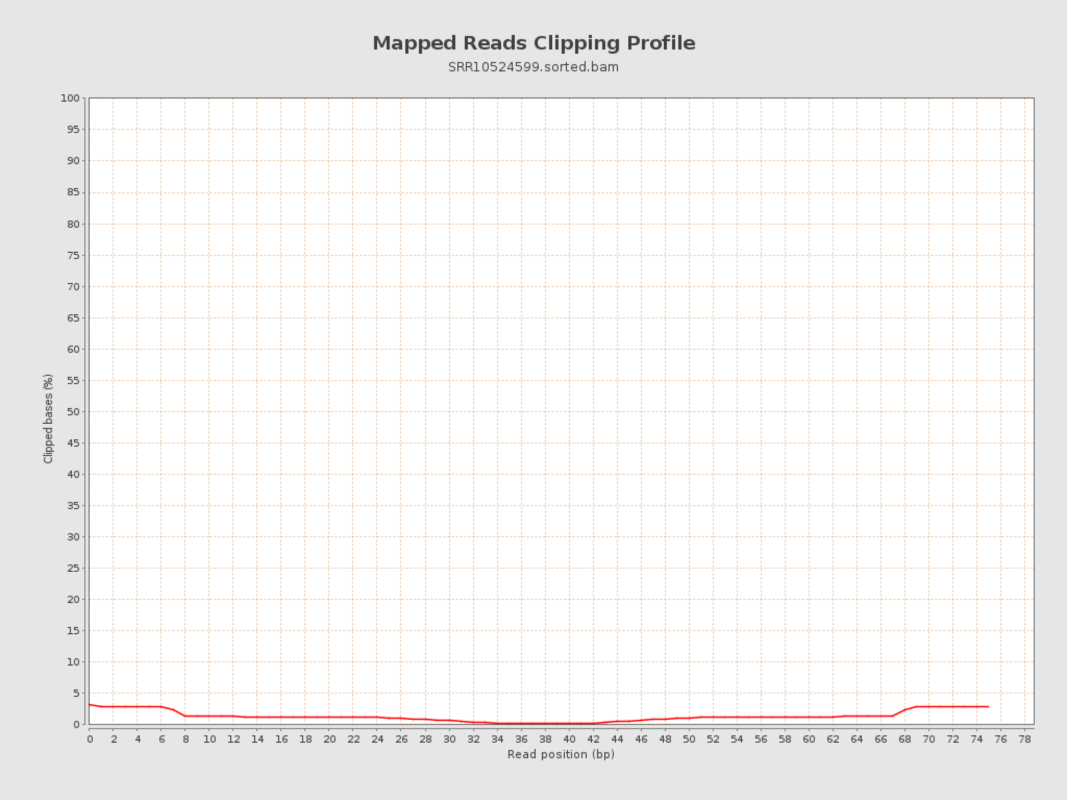
8. Results : Mapped Reads Nucleotide Content



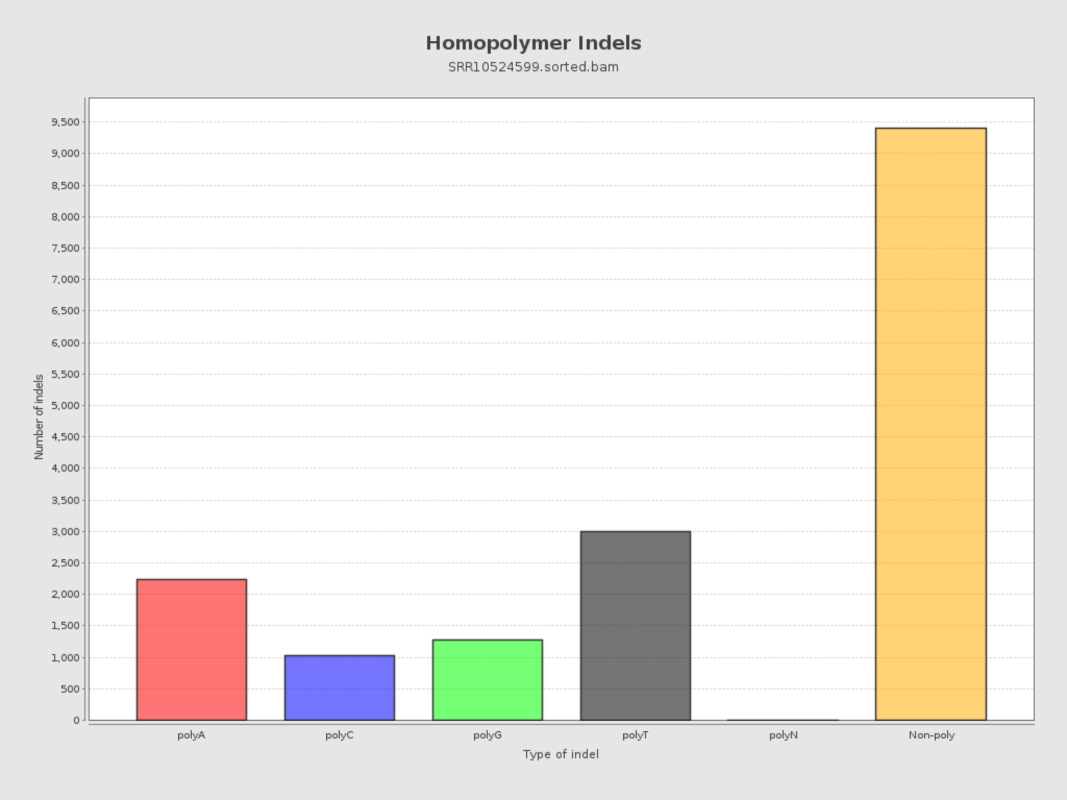
9. Results : Mapped Reads GC-content Distribution



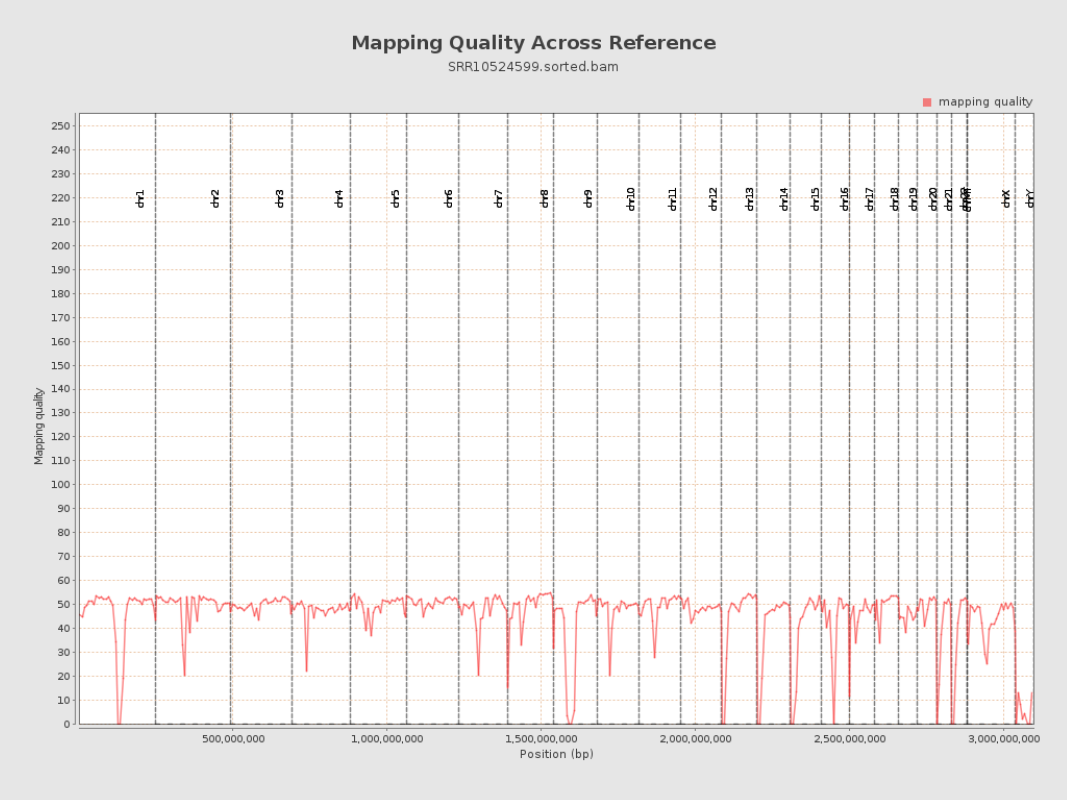
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram