Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 18:08:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524729.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_SRR10524729 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524729.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 18:08:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524729.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,692,665
Mapped reads	1,545,448 / 91.3%
Unmapped reads	147,217 / 8.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,709 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	67,233 / 3.97%
Duplication rate	3.32%
Clipped reads	1,549,310 / 91.53%

2.2. ACGT Content

Number/percentage of A's	20,579,387 / 23.23%
Number/percentage of C's	17,895,815 / 20.2%
Number/percentage of T's	28,743,391 / 32.45%
Number/percentage of G's	21,344,188 / 24.1%
Number/percentage of N's	10,875 / 0.01%
GC Percentage	44.3%

2.3. Coverage

Mean	0.0286

Standard Deviation	0.2573

2.4. Mapping Quality

Mean Mapping Quality	44.58

2.5. Mismatches and indels

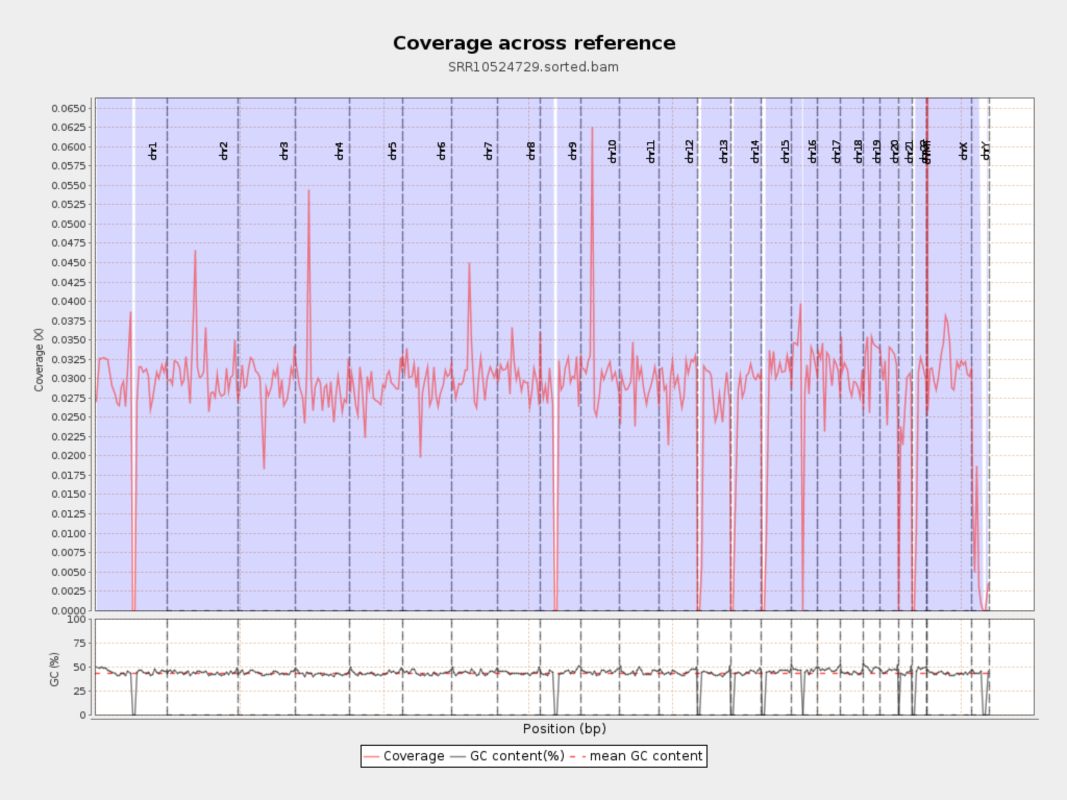
General error rate	0.52%
Mismatches	449,996
Insertions	5,464
Mapped reads with at least one insertion	0.35%
Deletions	17,211
Mapped reads with at least one deletion	1.11%
Homopolymer indels	44.75%

2.6. Chromosome stats

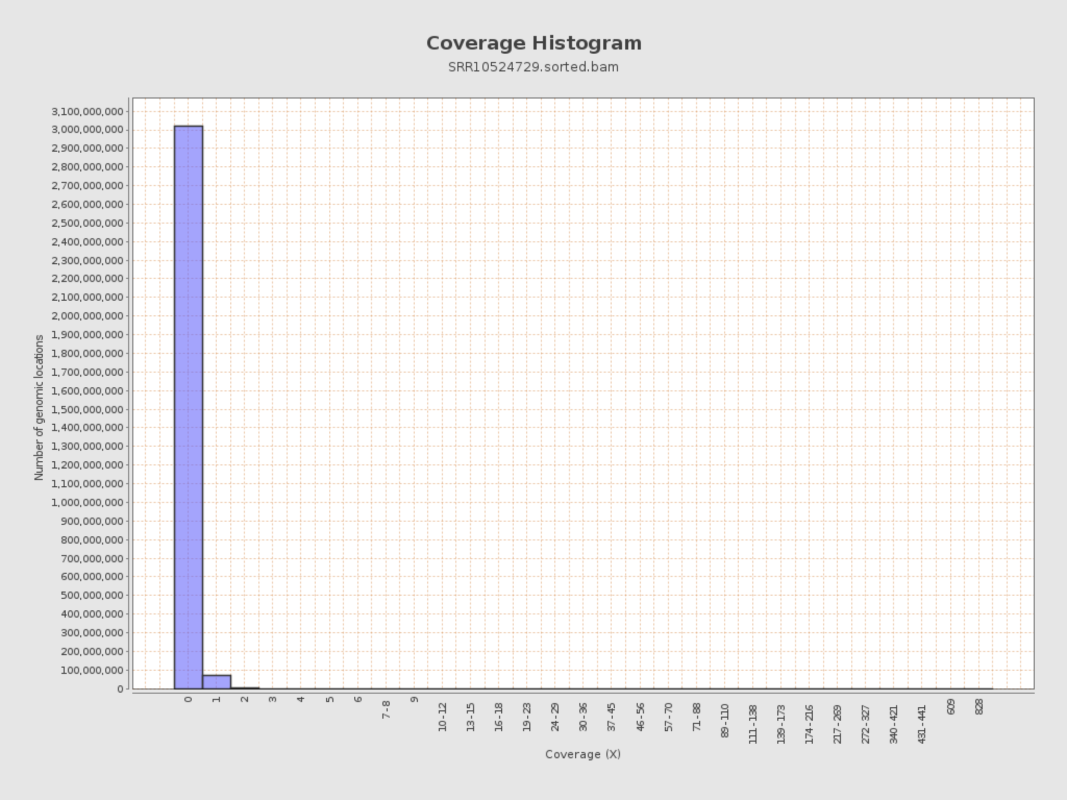
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7062594	0.0283	0.353
chr2	243199373	7496897	0.0308	0.4088
chr3	198022430	5787245	0.0292	0.1911
chr4	191154276	5627337	0.0294	0.2224
chr5	180915260	5202949	0.0288	0.1881
chr6	171115067	5040557	0.0295	0.2086
chr7	159138663	4881594	0.0307	0.3069

chr8	146364022	4419043	0.0302	0.2385
chr9	141213431	3740419	0.0265	0.2232
chr10	135534747	4330020	0.0319	0.307
chr11	135006516	3985765	0.0295	0.2323
chr12	133851895	3990545	0.0298	0.1943
chr13	115169878	2733558	0.0237	0.1706
chr14	107349540	2669554	0.0249	0.1802
chr15	102531392	2621532	0.0256	0.1794
chr16	90354753	2703189	0.0299	0.2127
chr17	81195210	2538788	0.0313	0.206
chr18	78077248	2337232	0.0299	0.3629
chr19	59128983	1943534	0.0329	0.2908
chr20	63025520	1960780	0.0311	0.2062
chr21	48129895	1164548	0.0242	0.1934
chr22	51304566	1101590	0.0215	0.1636
chrMT	16571	28088	1.695	1.5924
chrX	155270560	4921051	0.0317	0.2117
chrY	59373566	312945	0.0053	0.149

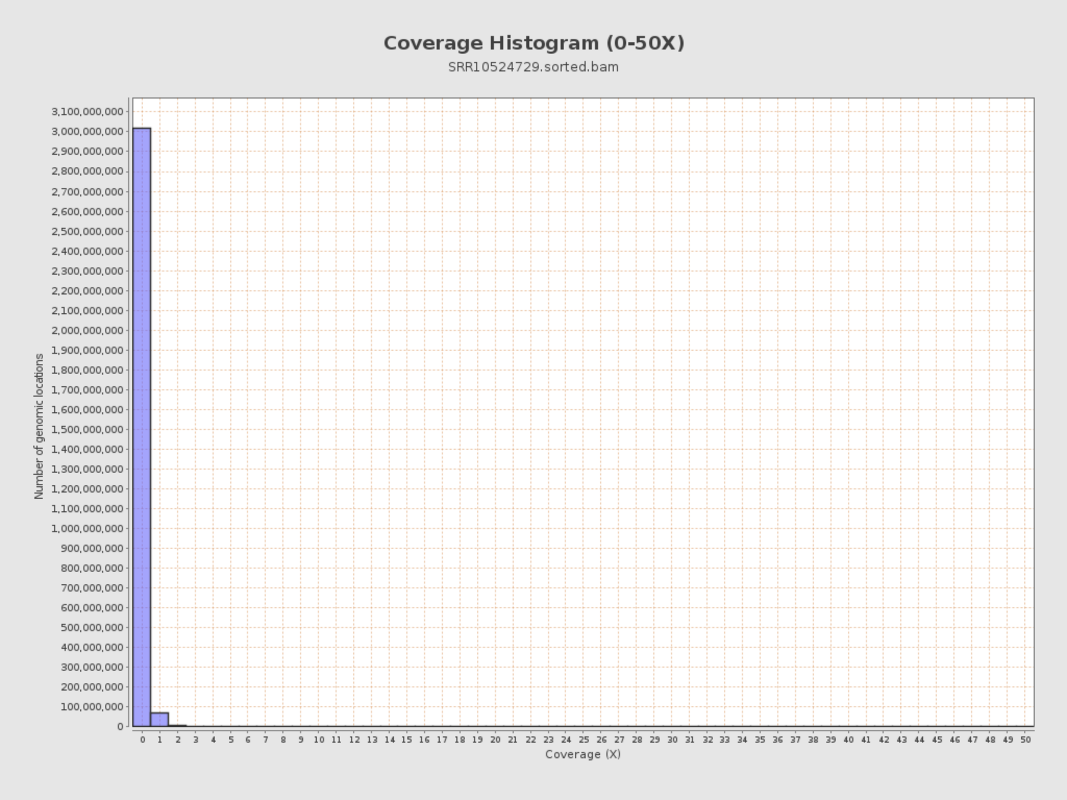
3. Results : Coverage across reference



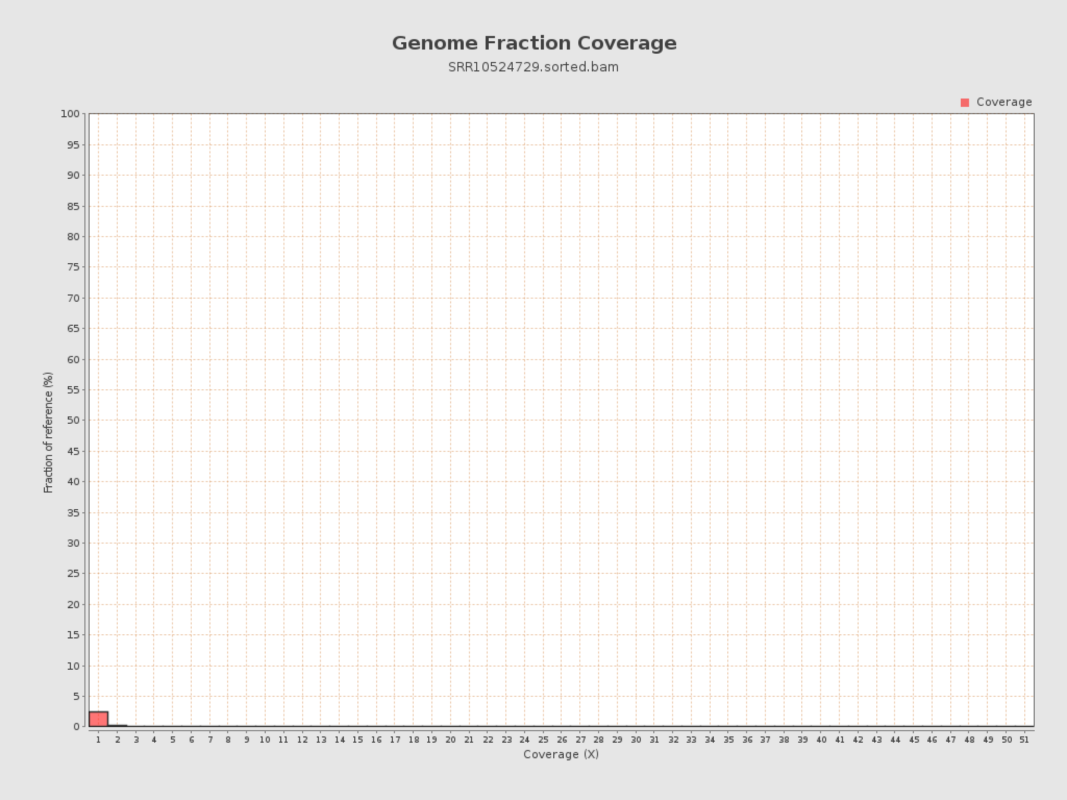
4. Results : Coverage Histogram



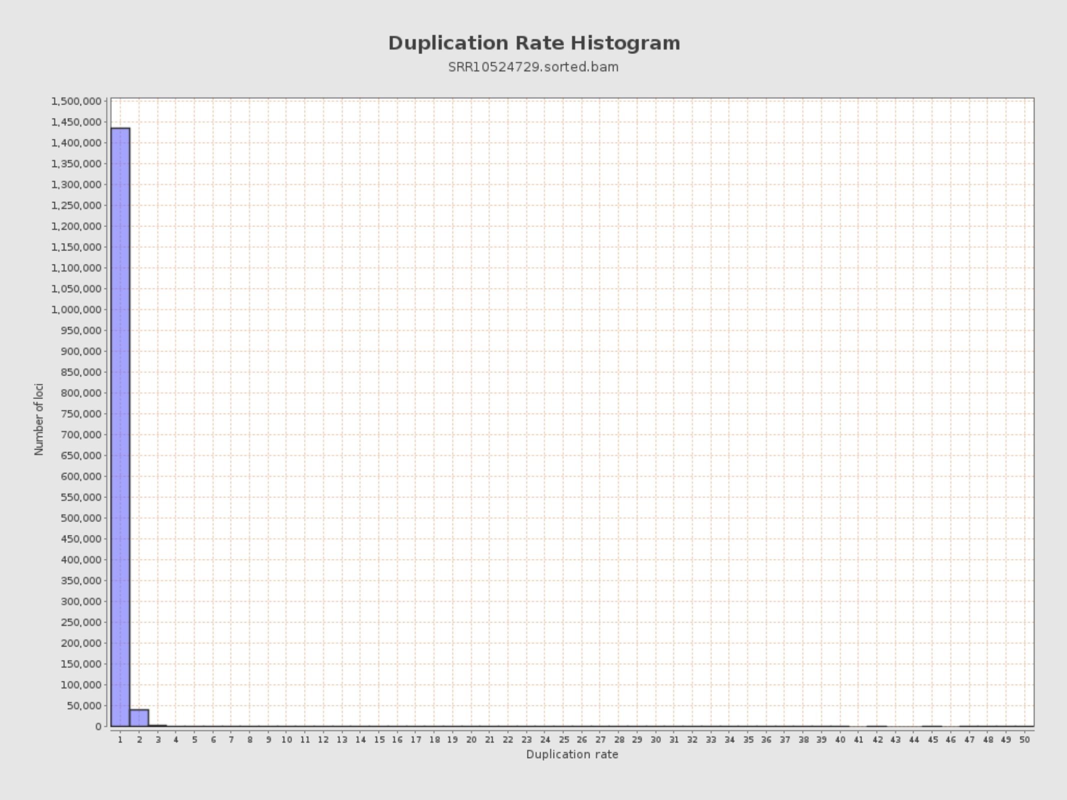
5. Results : Coverage Histogram (0-50X)



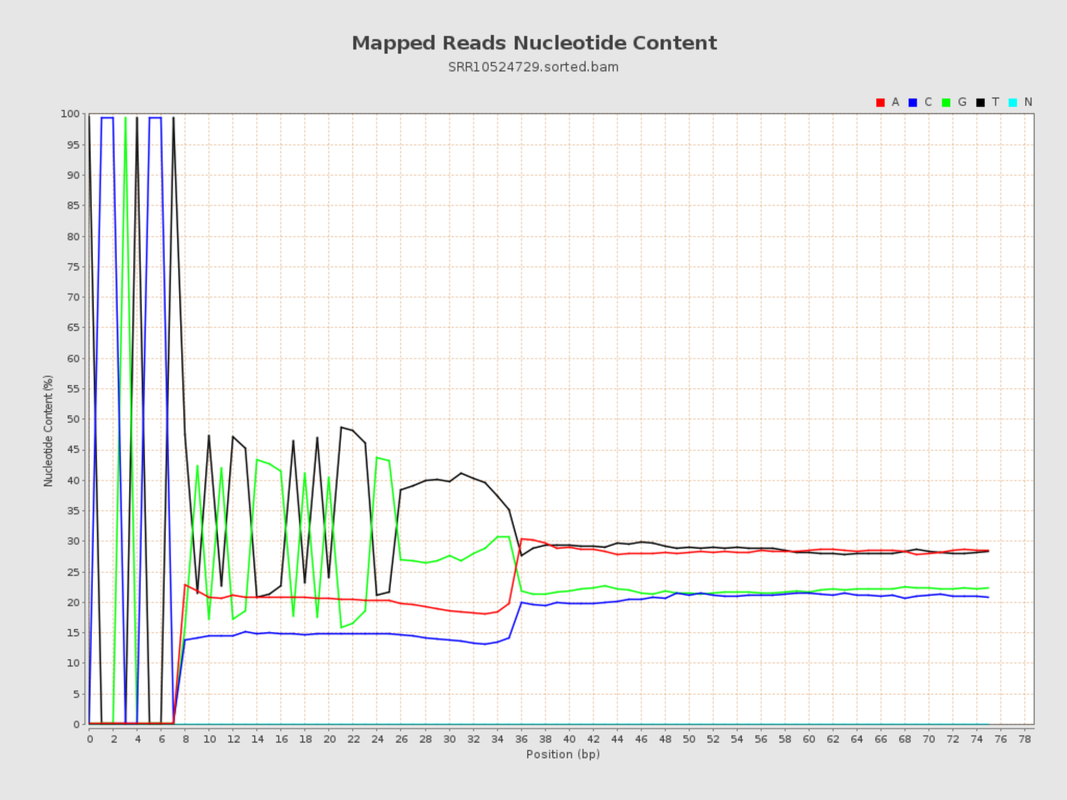
6. Results : Genome Fraction Coverage



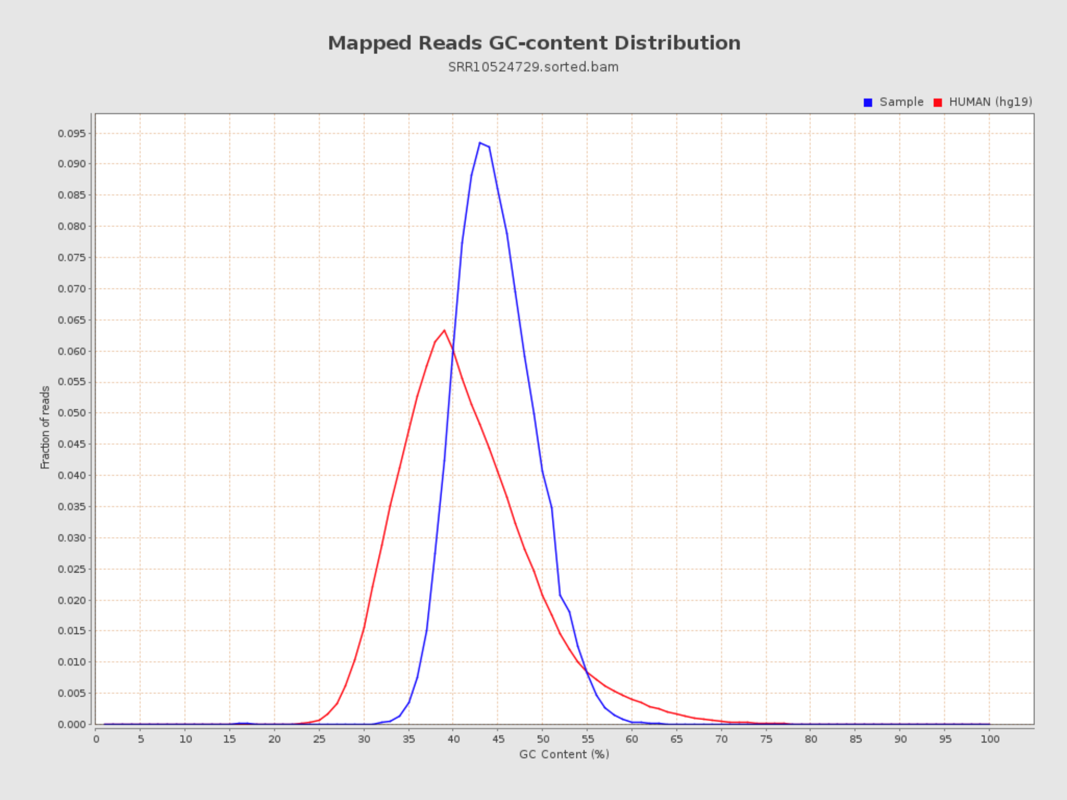
7. Results : Duplication Rate Histogram



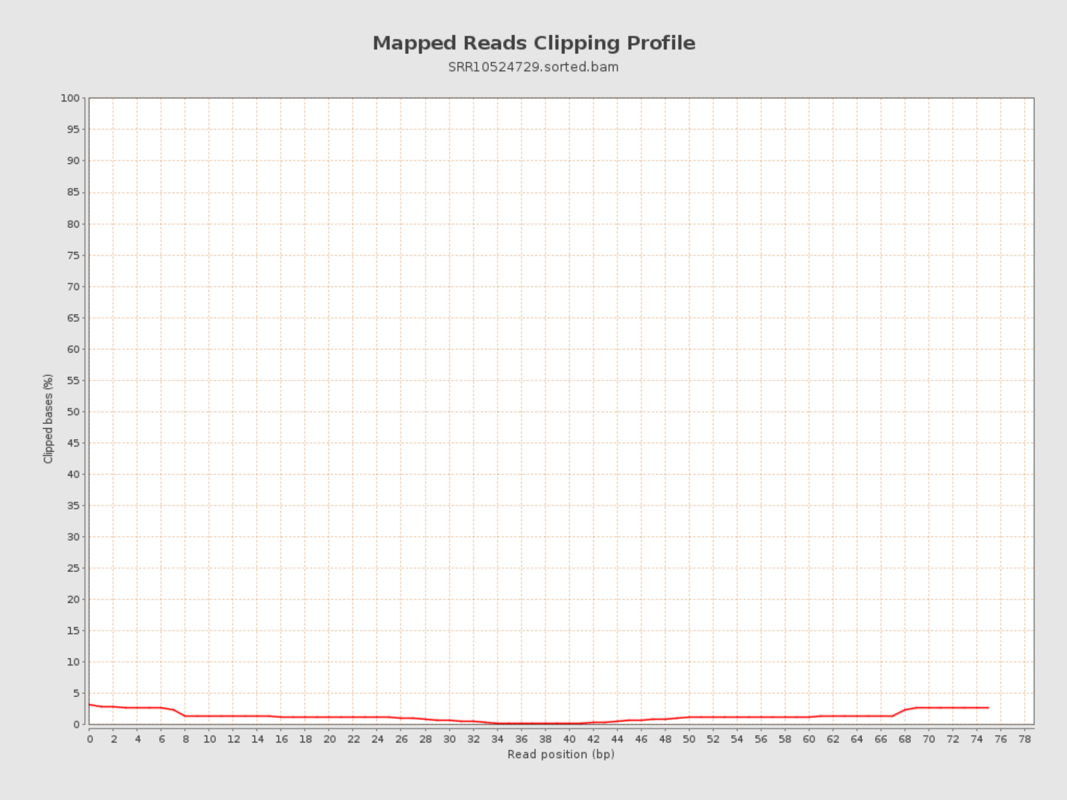
8. Results : Mapped Reads Nucleotide Content



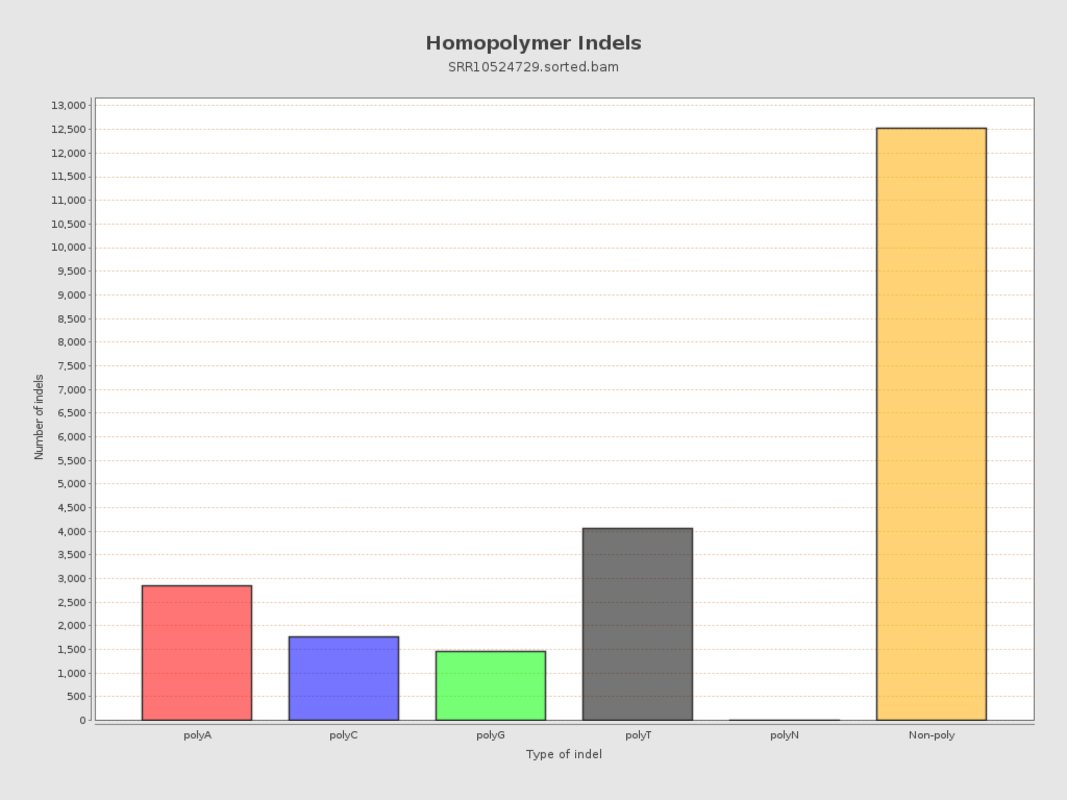
9. Results : Mapped Reads GC-content Distribution



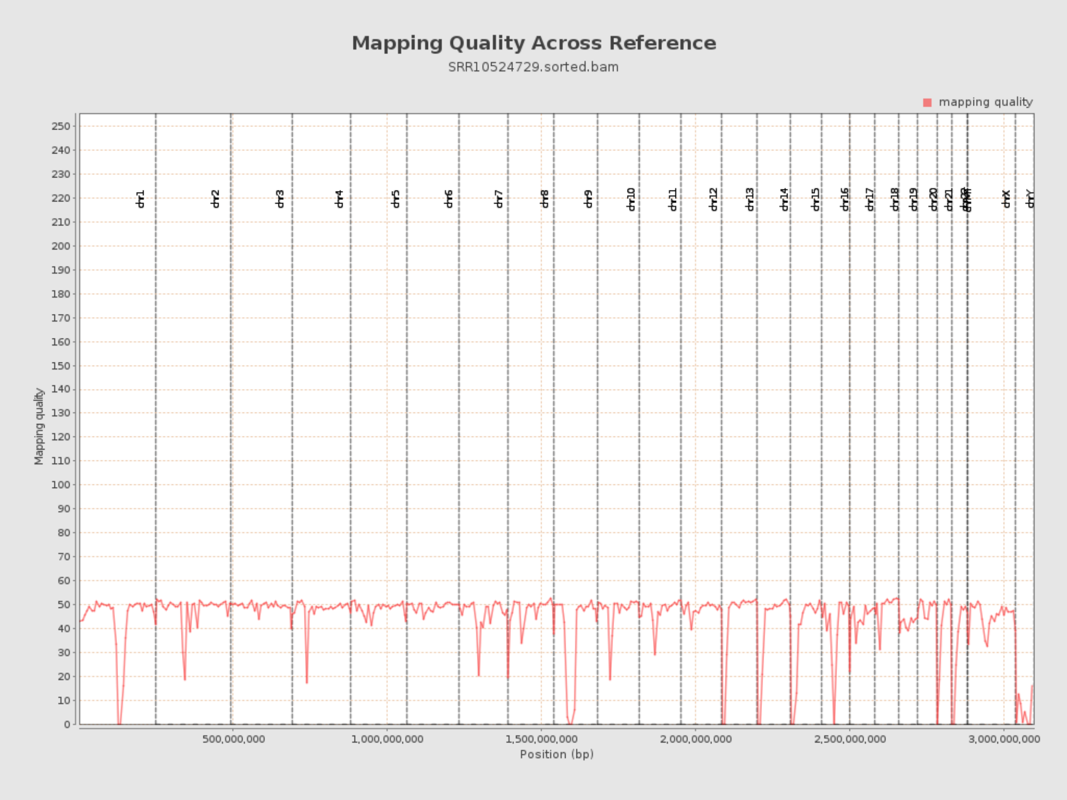
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram