Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 19:33:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524759.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_SRR10524759 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524759.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 19:33:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524759.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,644,288
Mapped reads	1,478,156 / 89.9%
Unmapped reads	166,132 / 10.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,933 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	53,431 / 3.25%
Duplication rate	2.77%
Clipped reads	1,478,659 / 89.93%

2.2. ACGT Content

Number/percentage of A's	21,303,564 / 25.32%
Number/percentage of C's	17,011,043 / 20.21%
Number/percentage of T's	25,763,733 / 30.62%
Number/percentage of G's	20,062,506 / 23.84%
Number/percentage of N's	10,303 / 0.01%
GC Percentage	44.06%

2.3. Coverage

Mean	0.0272

Standard Deviation	0.2314

2.4. Mapping Quality

Mean Mapping Quality	44.29

2.5. Mismatches and indels

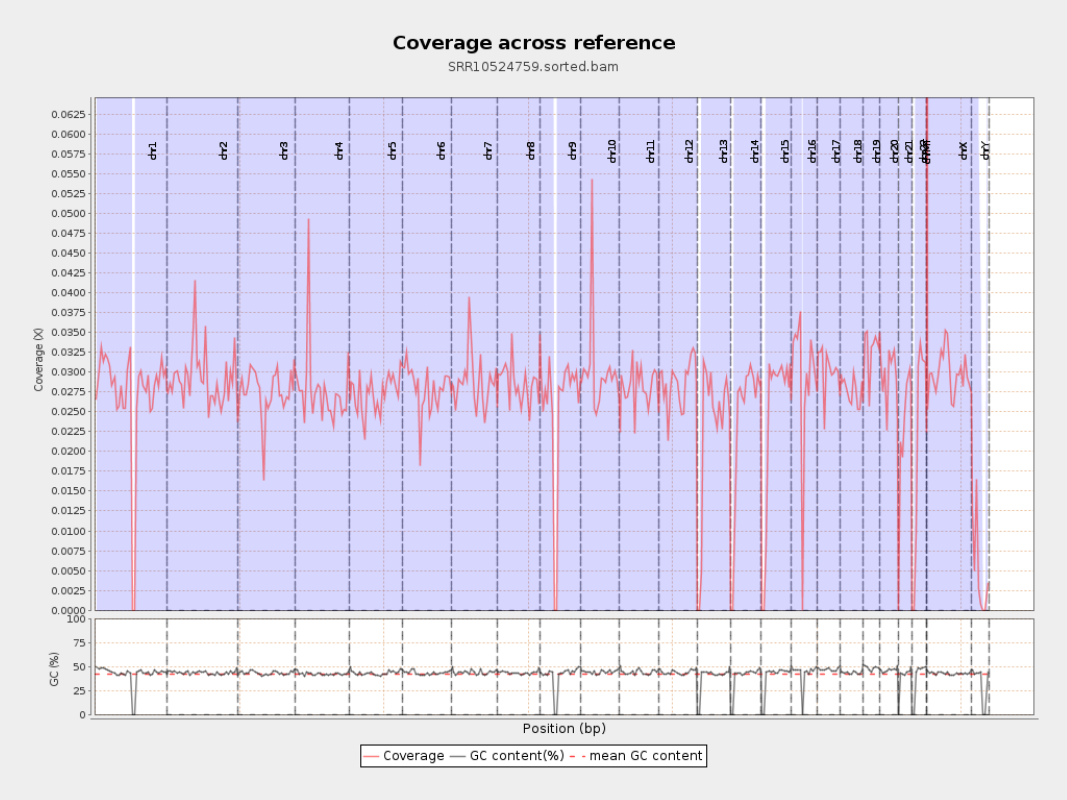
General error rate	0.52%
Mismatches	423,623
Insertions	6,408
Mapped reads with at least one insertion	0.43%
Deletions	16,138
Mapped reads with at least one deletion	1.08%
Homopolymer indels	41.59%

2.6. Chromosome stats

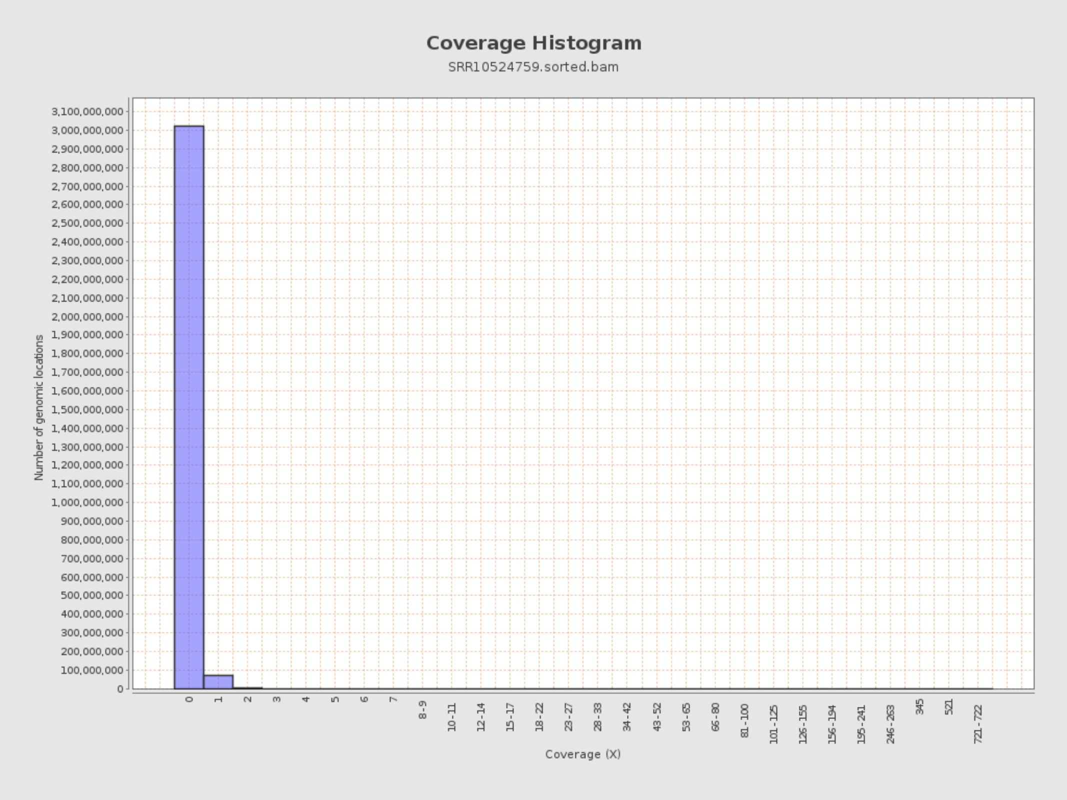
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6749668	0.0271	0.2677
chr2	243199373	7114467	0.0293	0.37
chr3	198022430	5440638	0.0275	0.1835
chr4	191154276	5317273	0.0278	0.2078
chr5	180915260	4966490	0.0275	0.1822
chr6	171115067	4777987	0.0279	0.2018
chr7	159138663	4595009	0.0289	0.2746

chr8	146364022	4172949	0.0285	0.2119
chr9	141213431	3570683	0.0253	0.2035
chr10	135534747	4097598	0.0302	0.276
chr11	135006516	3819471	0.0283	0.2188
chr12	133851895	3828598	0.0286	0.1892
chr13	115169878	2595459	0.0225	0.166
chr14	107349540	2534863	0.0236	0.1727
chr15	102531392	2457425	0.024	0.1735
chr16	90354753	2596186	0.0287	0.2053
chr17	81195210	2461576	0.0303	0.2002
chr18	78077248	2154756	0.0276	0.3015
chr19	59128983	1929476	0.0326	0.2588
chr20	63025520	1855874	0.0294	0.1992
chr21	48129895	1100641	0.0229	0.185
chr22	51304566	1105517	0.0215	0.164
chrMT	16571	17672	1.0664	1.3202
chrX	155270560	4631615	0.0298	0.2046
chrY	59373566	285022	0.0048	0.1322

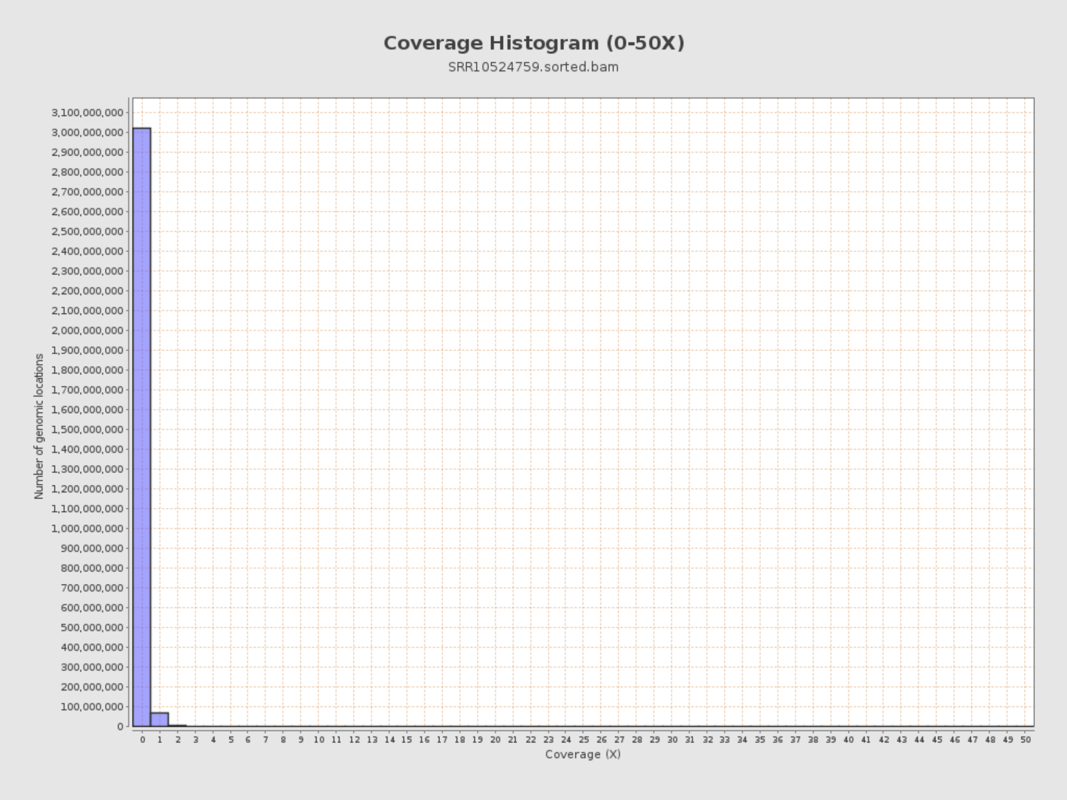
3. Results : Coverage across reference



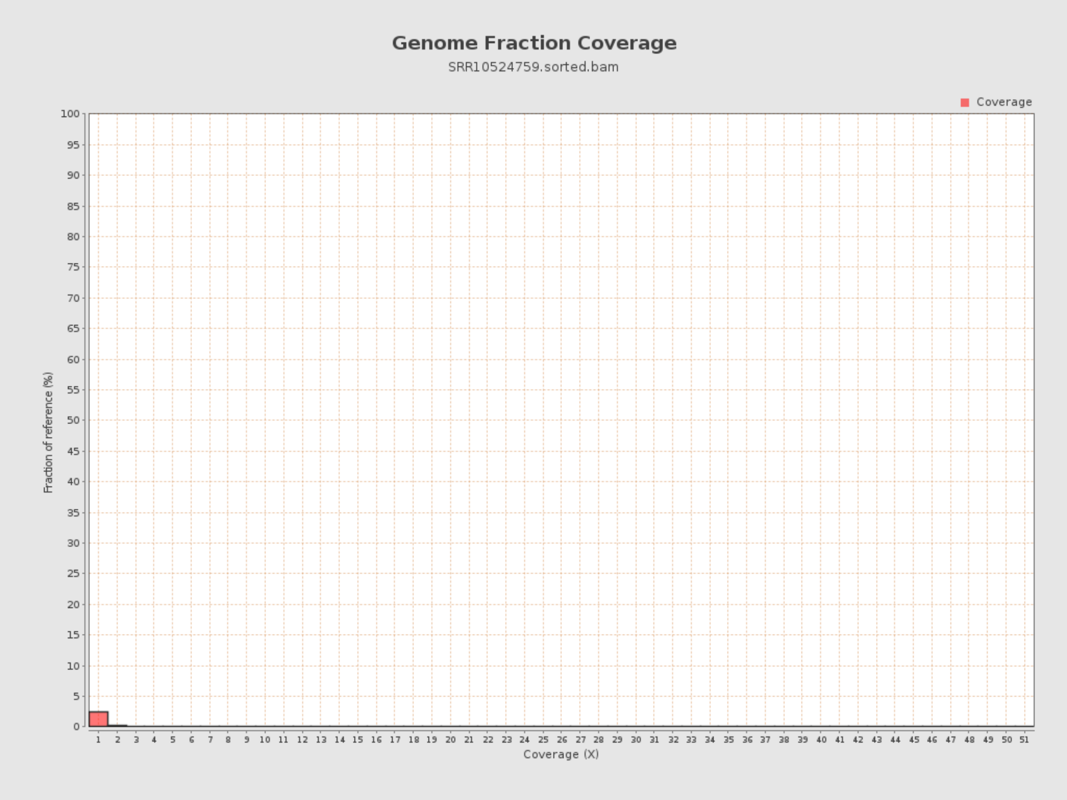
4. Results : Coverage Histogram



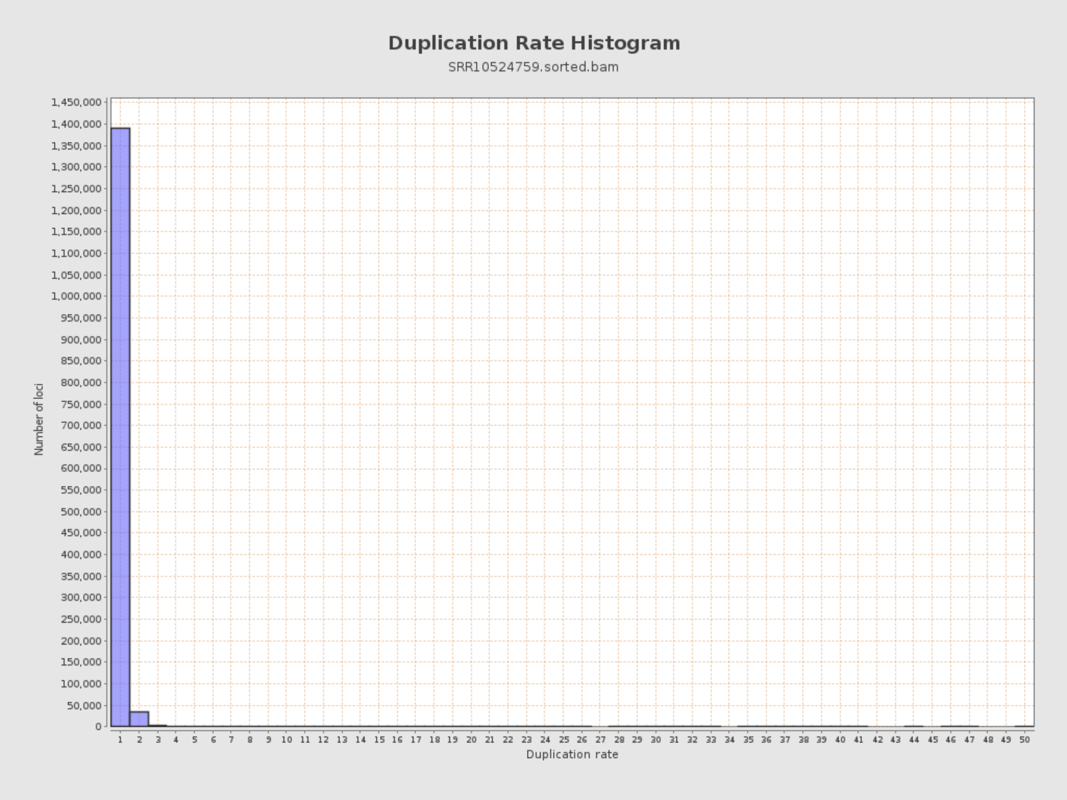
5. Results : Coverage Histogram (0-50X)



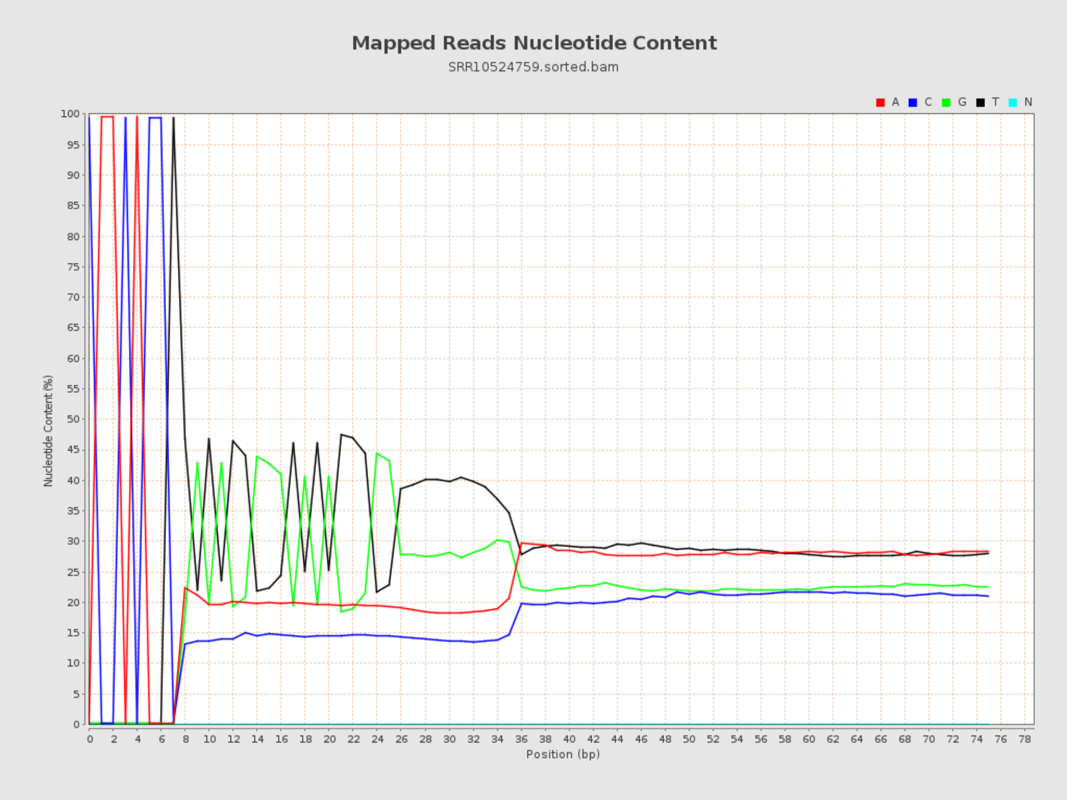
6. Results : Genome Fraction Coverage



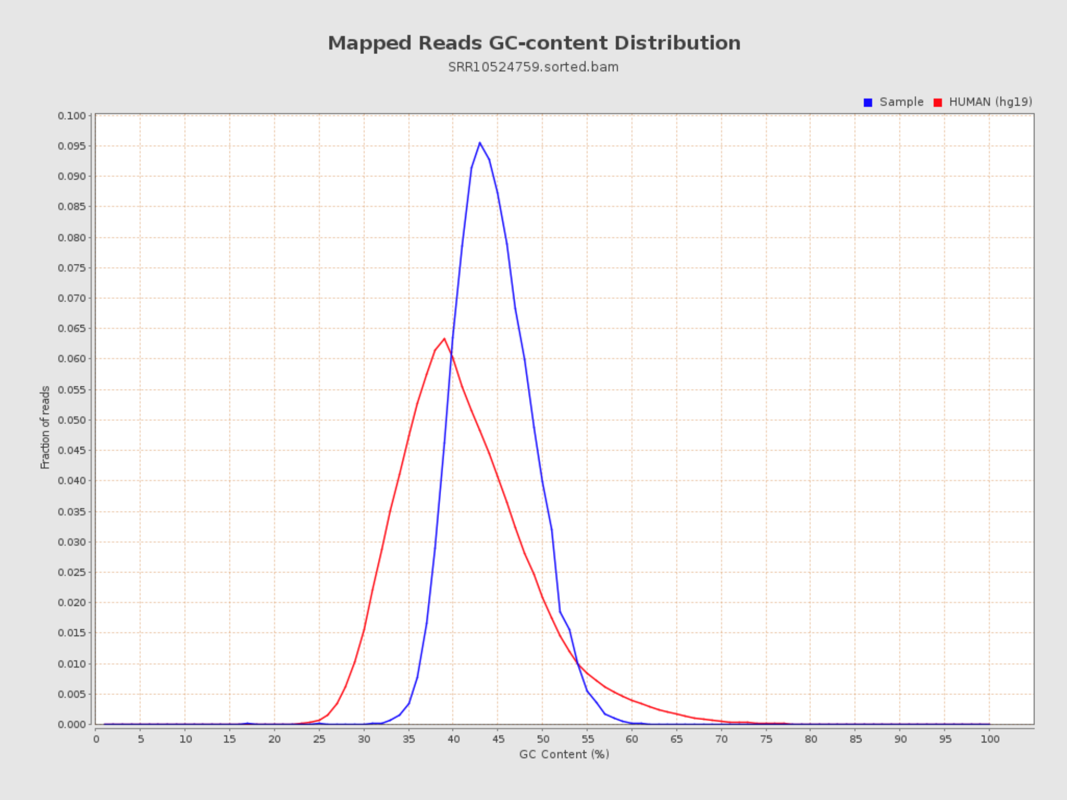
7. Results : Duplication Rate Histogram



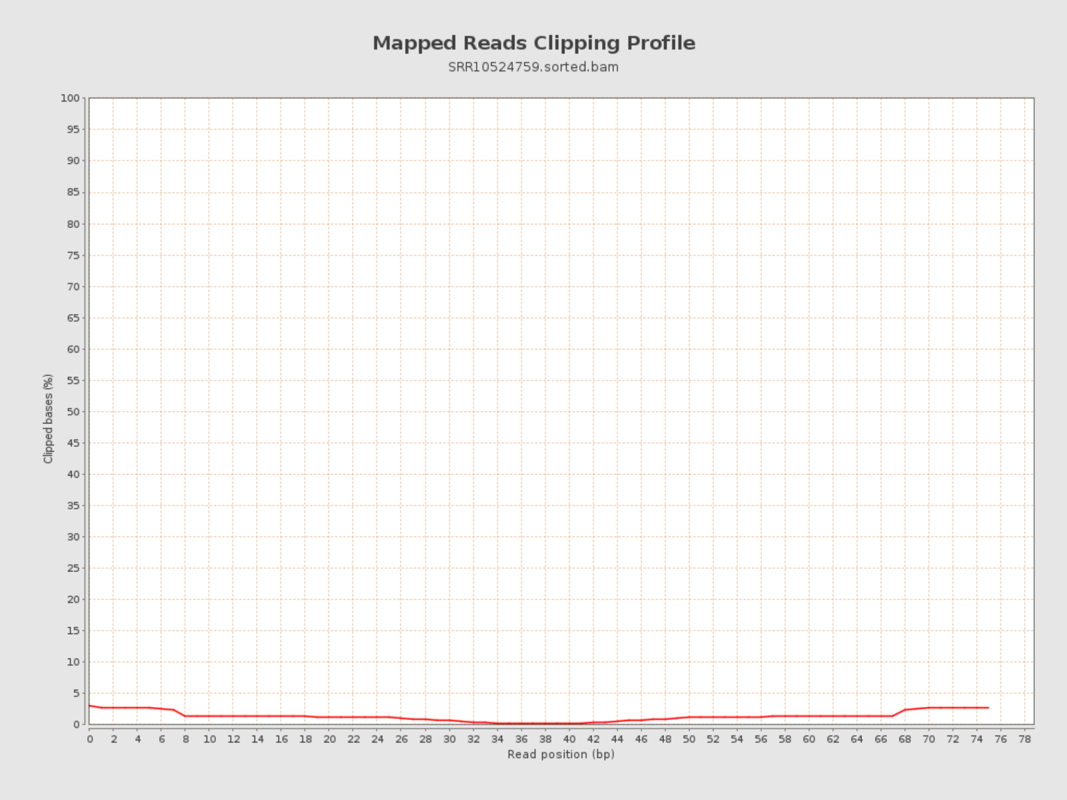
8. Results : Mapped Reads Nucleotide Content



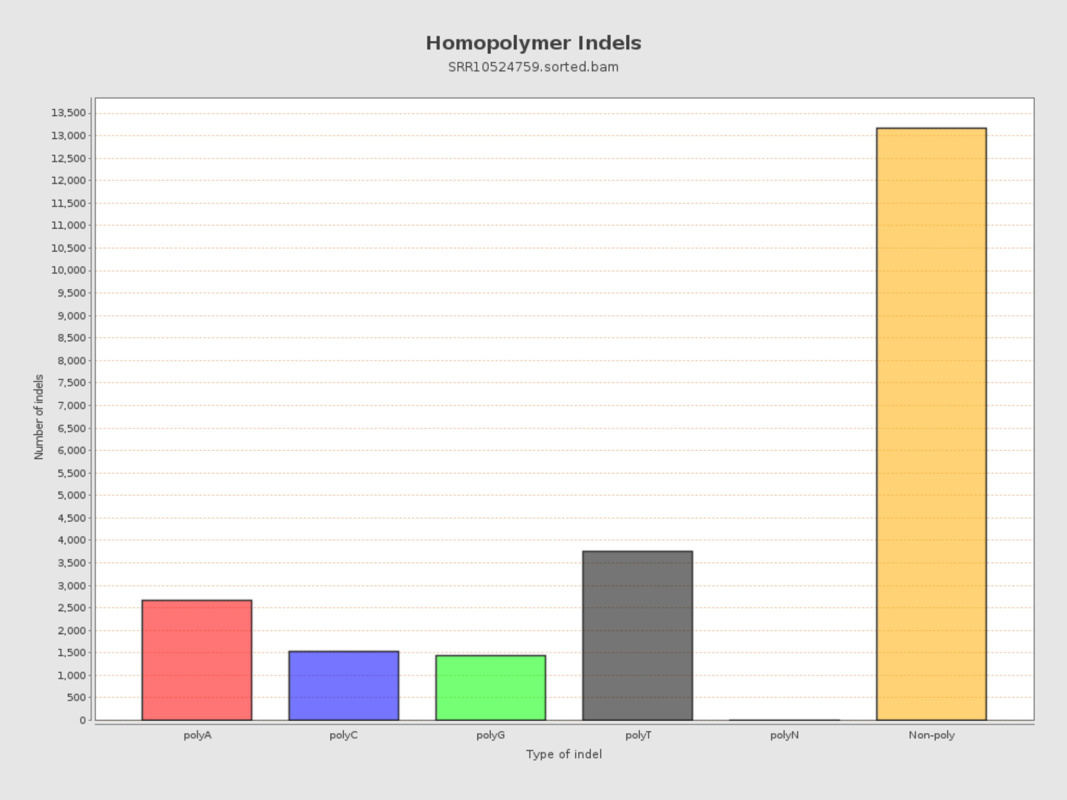
9. Results : Mapped Reads GC-content Distribution



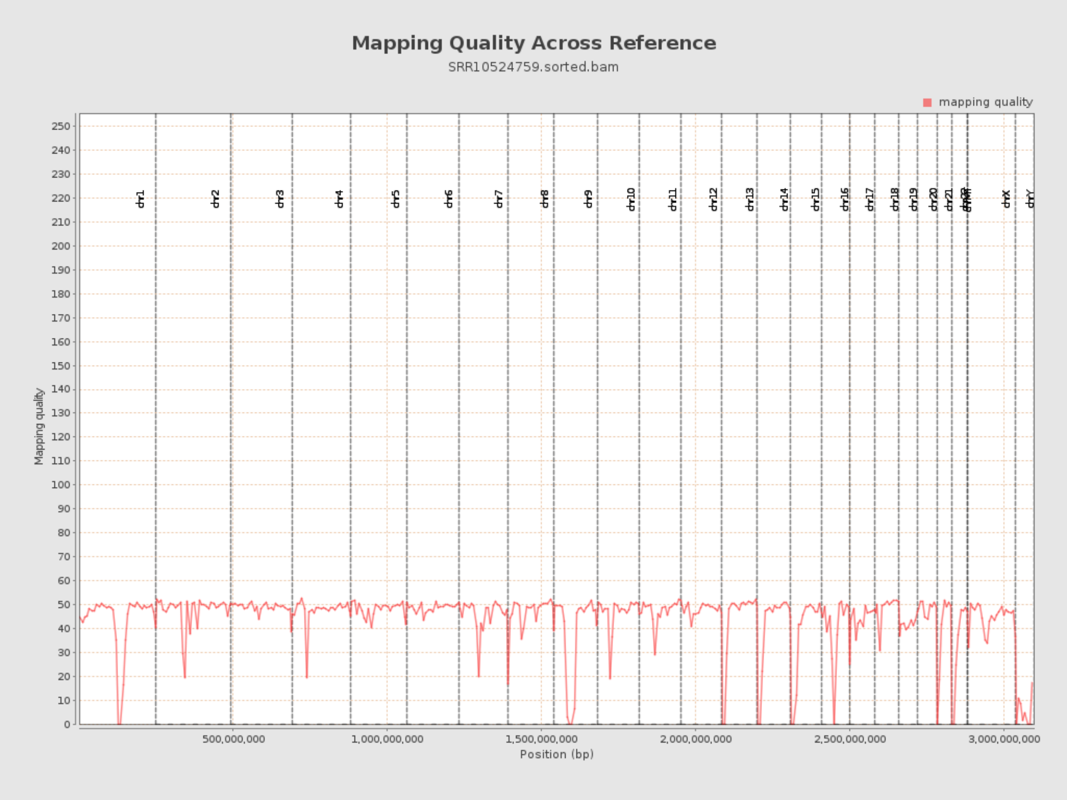
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram