Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 23:25:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524859.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_SRR10524859 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524859.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 23:25:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524859.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,896,970
Mapped reads	1,744,191 / 91.95%
Unmapped reads	152,779 / 8.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,371 / 0.55%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	54,345 / 2.86%
Duplication rate	2.06%
Clipped reads	1,749,619 / 92.23%

2.2. ACGT Content

Number/percentage of A's	26,751,357 / 26.23%
Number/percentage of C's	17,990,558 / 17.64%
Number/percentage of T's	32,051,929 / 31.42%
Number/percentage of G's	25,188,522 / 24.7%
Number/percentage of N's	14,541 / 0.01%
GC Percentage	42.33%

2.3. Coverage

Mean	0.033

Standard Deviation	0.3257

2.4. Mapping Quality

Mean Mapping Quality	44.61

2.5. Mismatches and indels

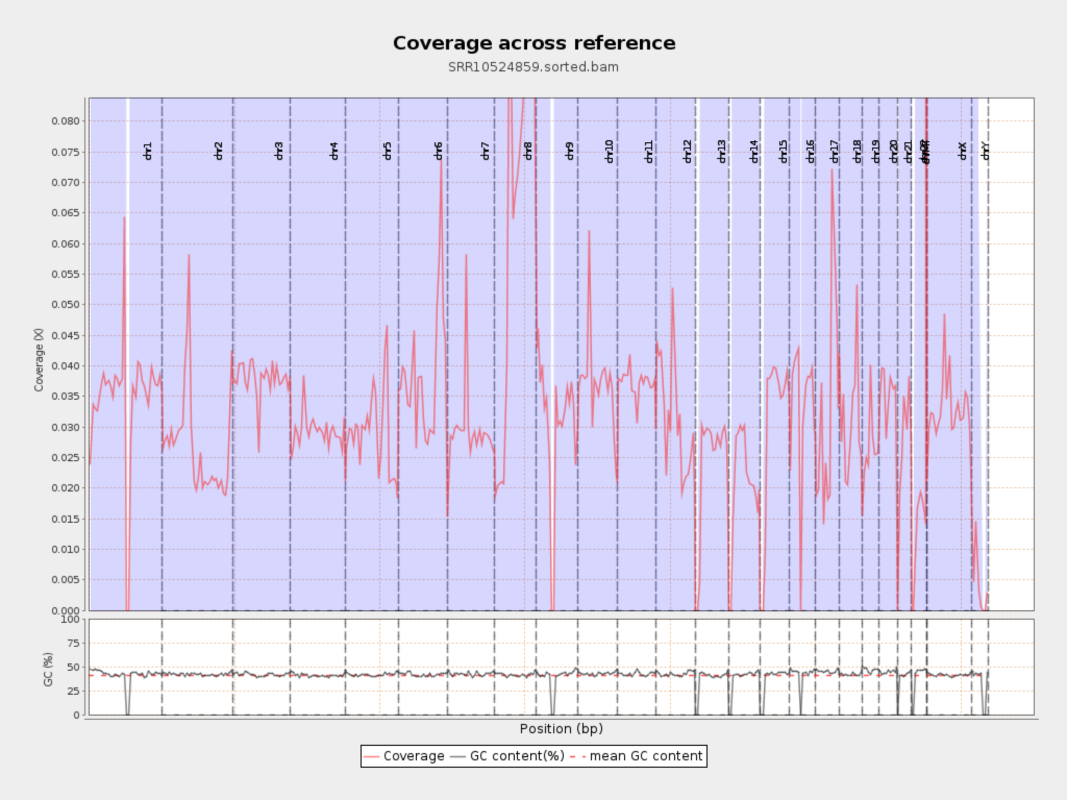
General error rate	0.49%
Mismatches	491,945
Insertions	6,970
Mapped reads with at least one insertion	0.4%
Deletions	19,331
Mapped reads with at least one deletion	1.1%
Homopolymer indels	42.88%

2.6. Chromosome stats

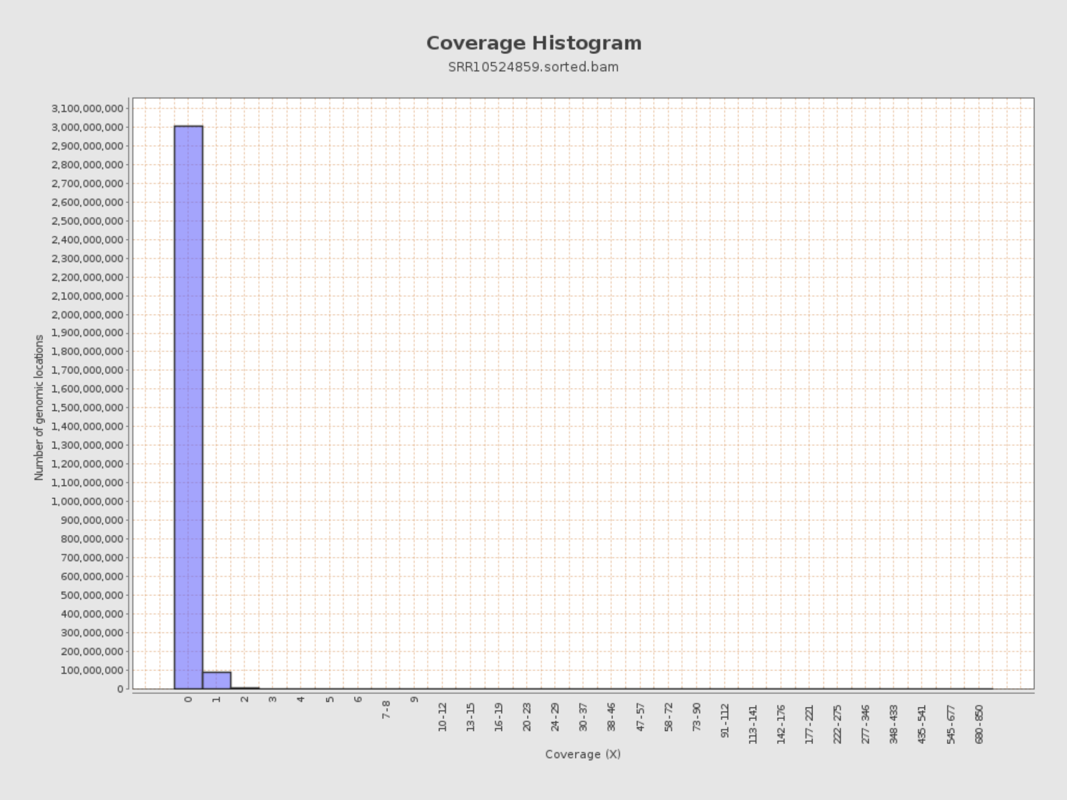
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8640383	0.0347	0.6598
chr2	243199373	6569136	0.027	0.3123
chr3	198022430	7501749	0.0379	0.2087
chr4	191154276	5598769	0.0293	0.2008
chr5	180915260	5324106	0.0294	0.1853
chr6	171115067	6571043	0.0384	0.237
chr7	159138663	4741462	0.0298	0.4492

chr8	146364022	11226348	0.0767	0.4289
chr9	141213431	4268045	0.0302	0.2803
chr10	135534747	5083204	0.0375	0.3107
chr11	135006516	4990917	0.037	0.2966
chr12	133851895	4217444	0.0315	0.1961
chr13	115169878	2723613	0.0236	0.1634
chr14	107349540	2196974	0.0205	0.1692
chr15	102531392	3095894	0.0302	0.1886
chr16	90354753	3037305	0.0336	0.2189
chr17	81195210	2659416	0.0328	0.2249
chr18	78077248	2487097	0.0319	0.4886
chr19	59128983	1585904	0.0268	0.4584
chr20	63025520	2215729	0.0352	0.204
chr21	48129895	1274892	0.0265	0.1913
chr22	51304566	637049	0.0124	0.1183
chrMT	16571	18840	1.1369	1.258
chrX	155270560	5103442	0.0329	0.2306
chrY	59373566	258526	0.0044	0.1074

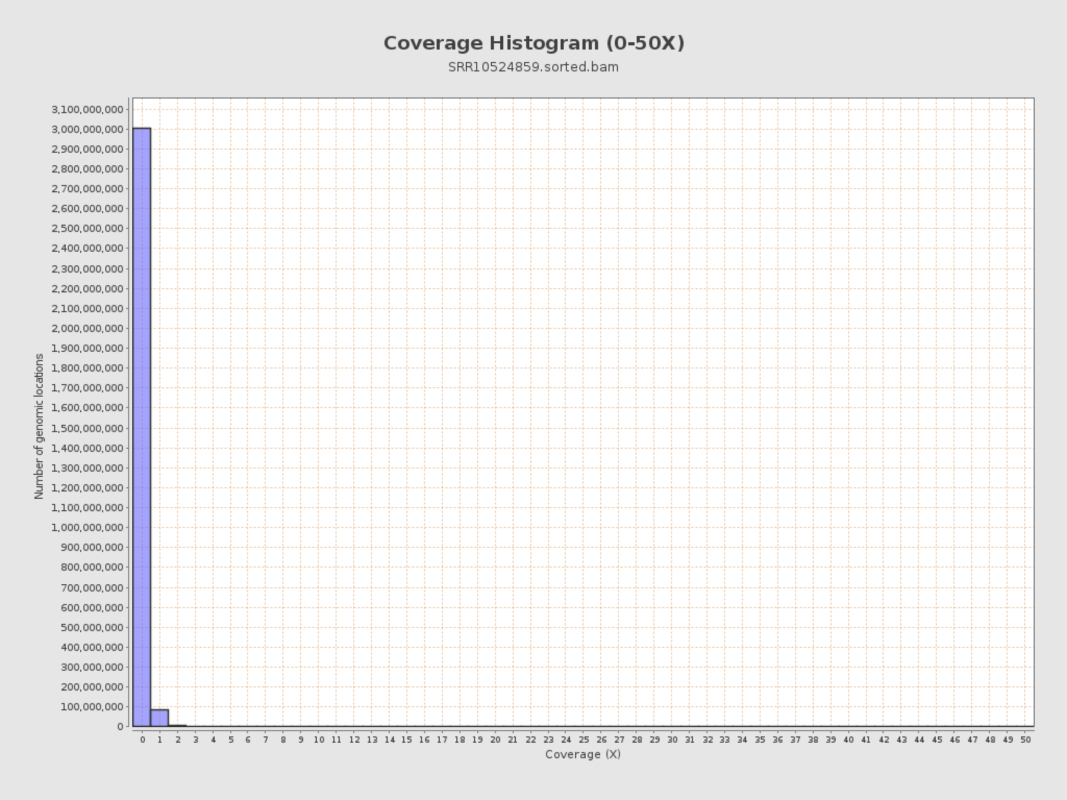
3. Results : Coverage across reference



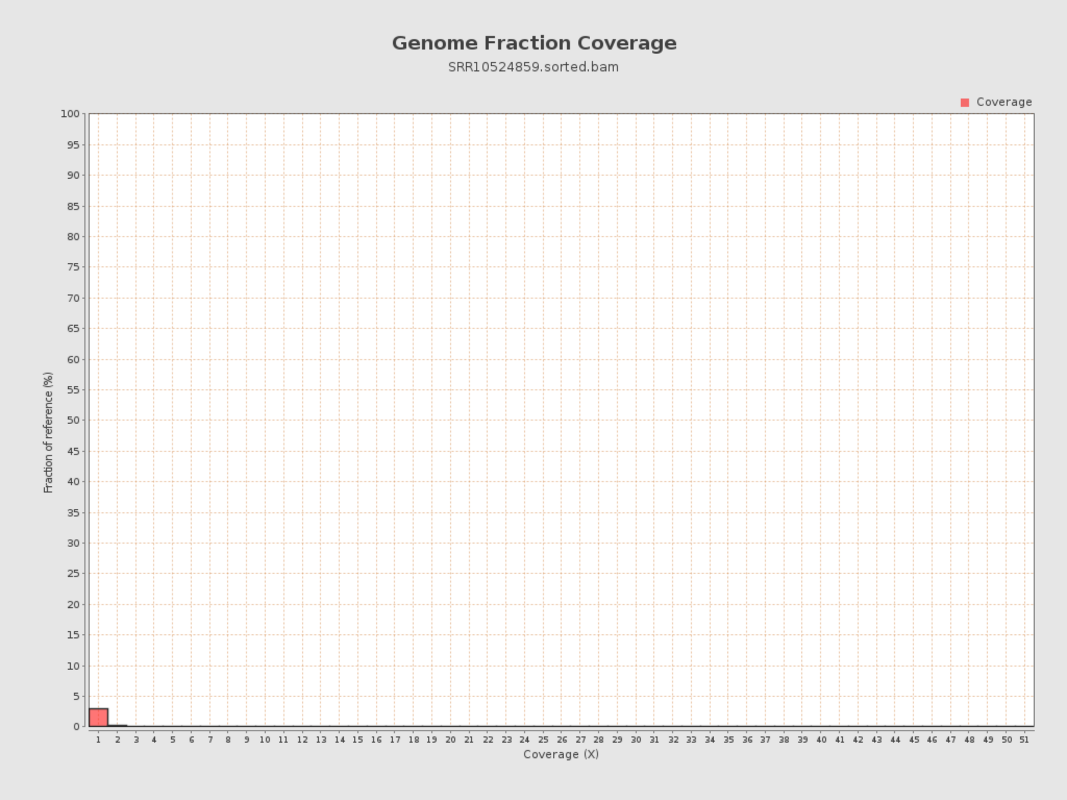
4. Results : Coverage Histogram



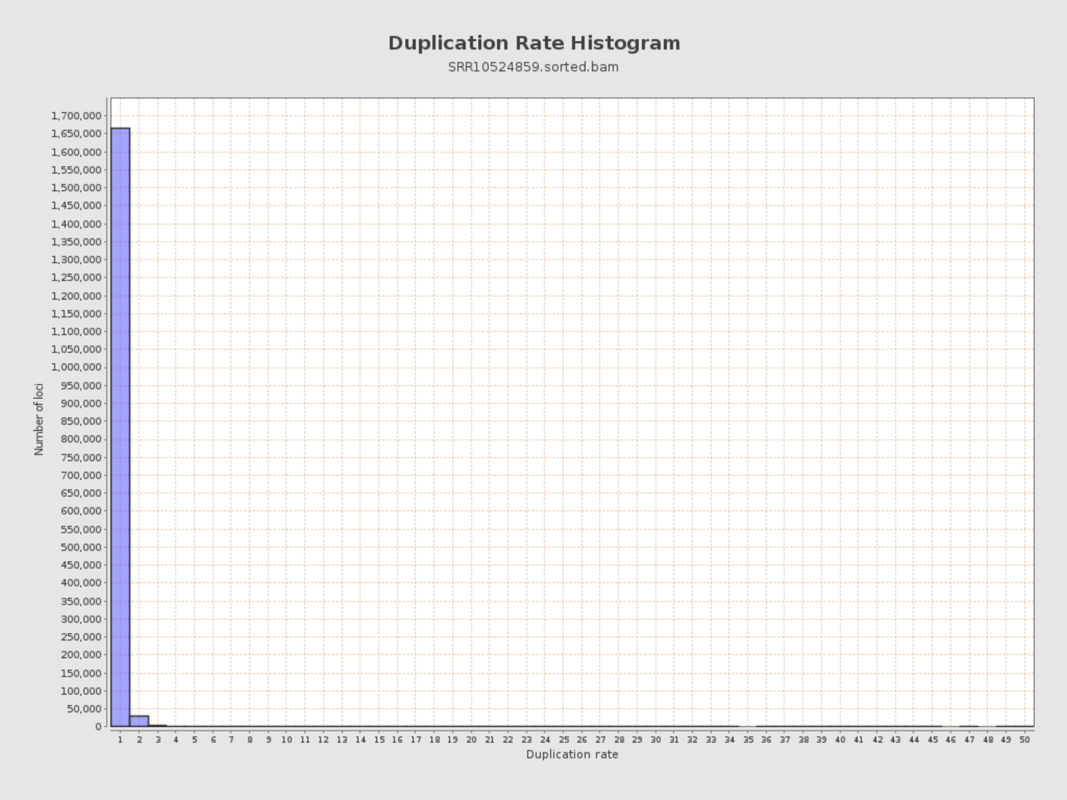
5. Results : Coverage Histogram (0-50X)



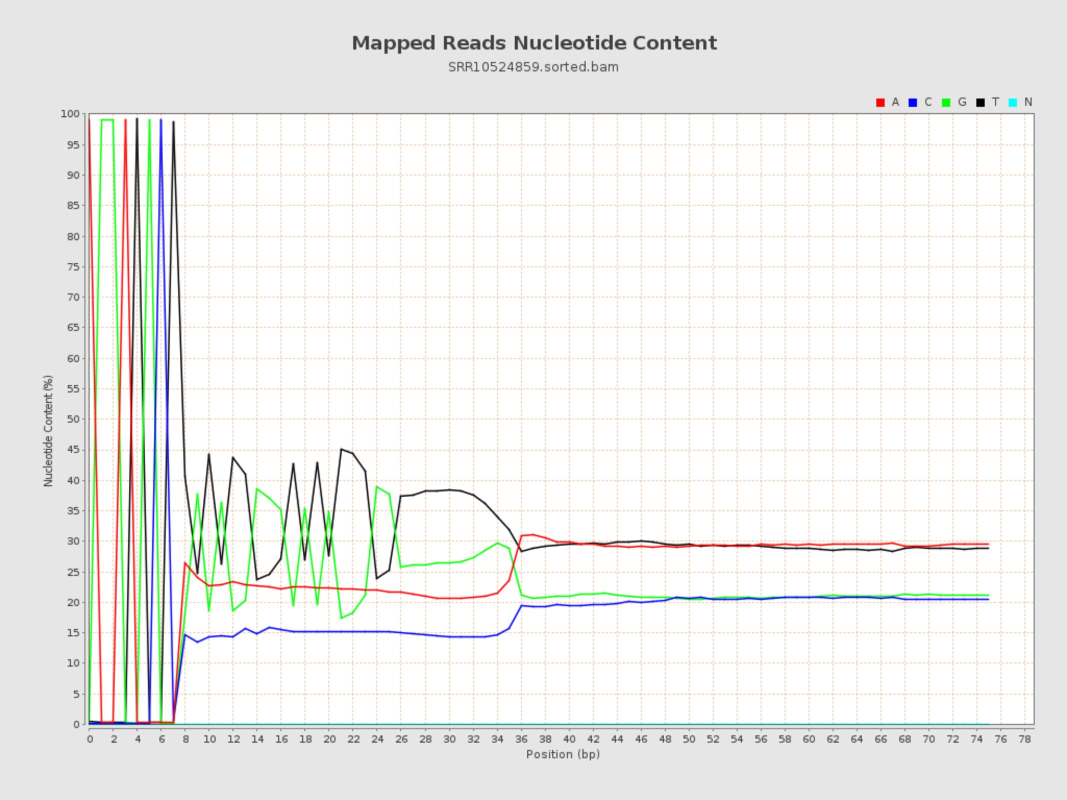
6. Results : Genome Fraction Coverage



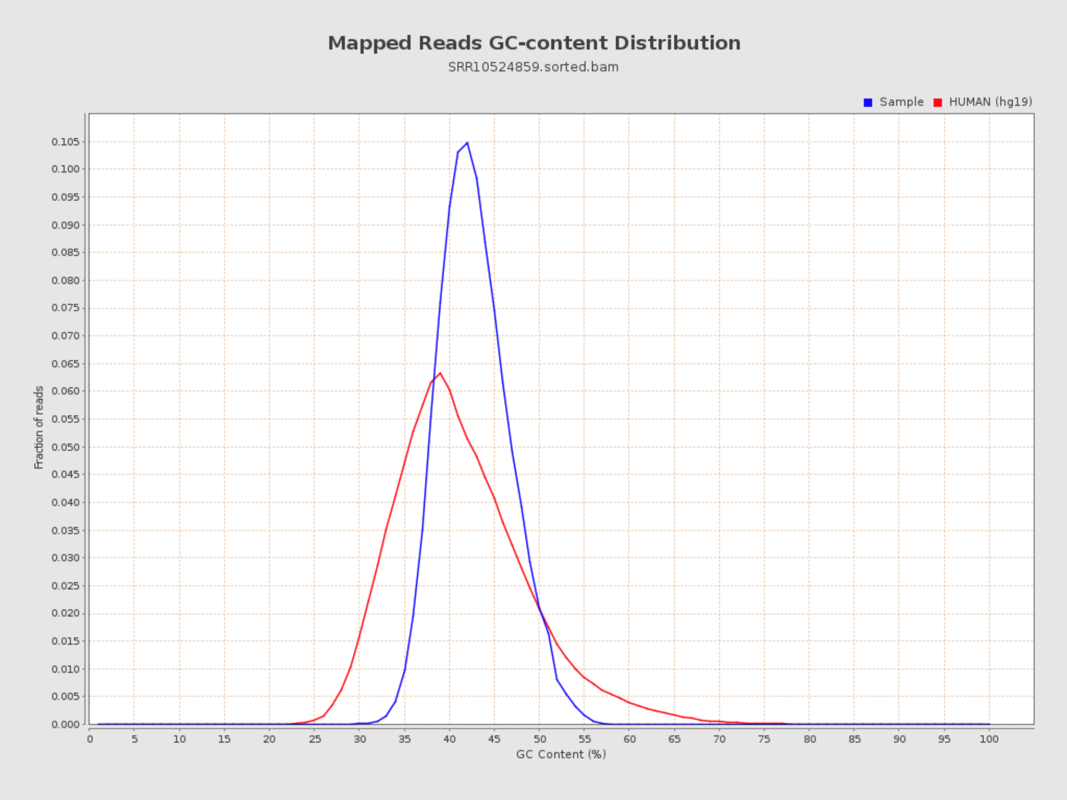
7. Results : Duplication Rate Histogram



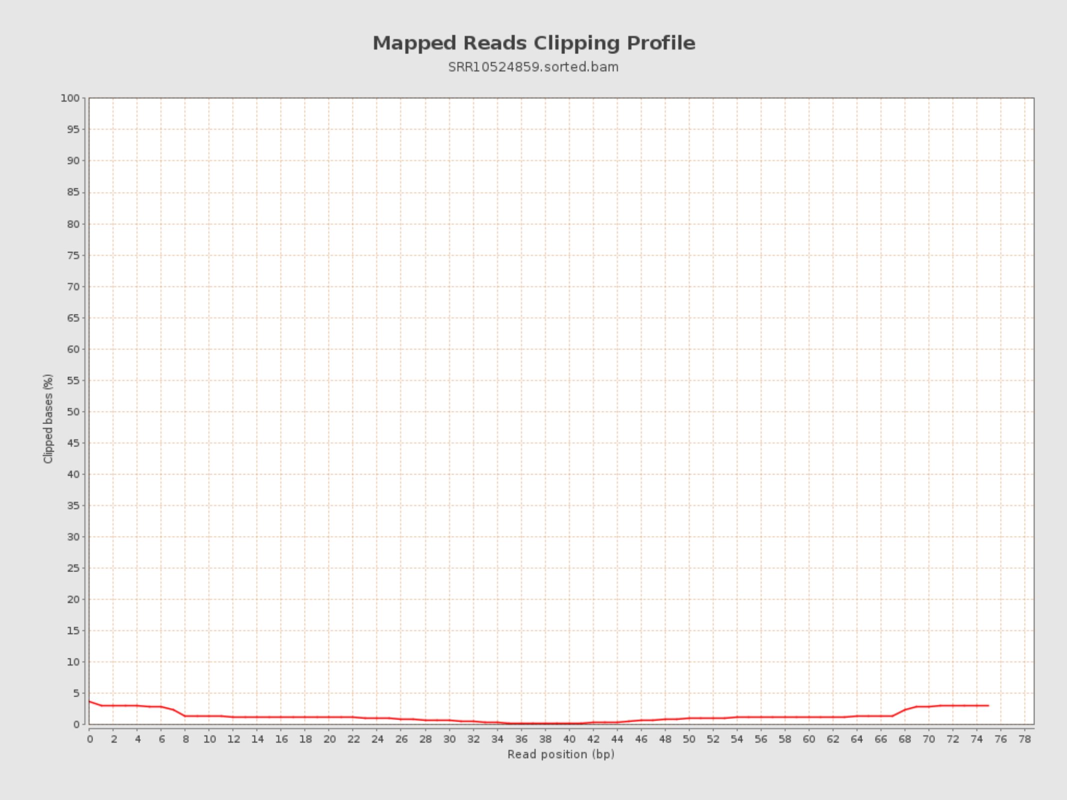
8. Results : Mapped Reads Nucleotide Content



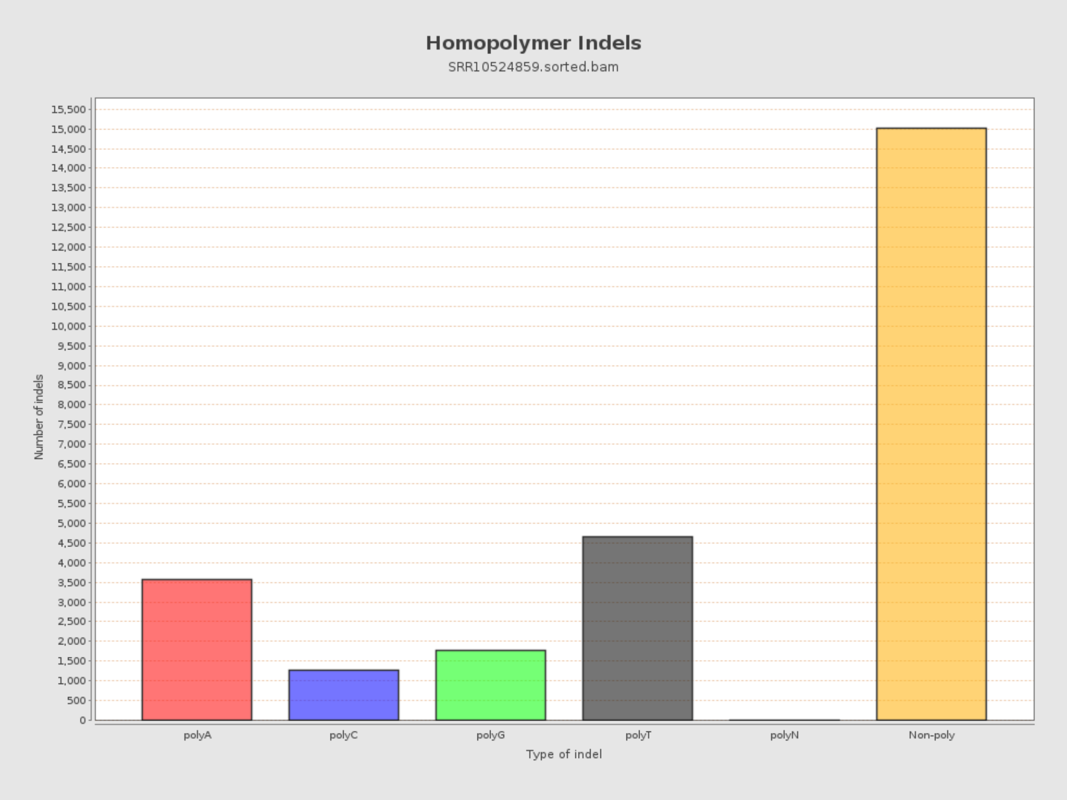
9. Results : Mapped Reads GC-content Distribution



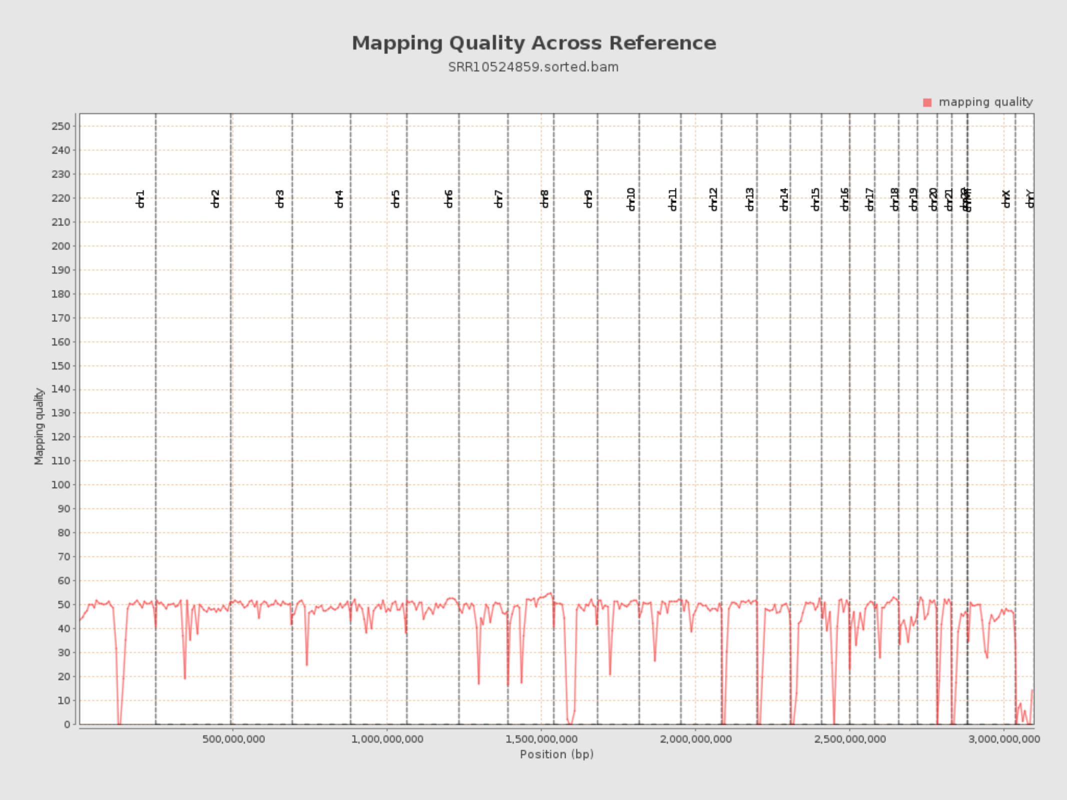
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram