Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 22:10:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524825.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_SRR10524825 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524825.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 22:10:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524825.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,480,100
Mapped reads	1,344,832 / 90.86%
Unmapped reads	135,268 / 9.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,347 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	46,130 / 3.12%
Duplication rate	2.61%
Clipped reads	1,345,445 / 90.9%

2.2. ACGT Content

Number/percentage of A's	18,316,857 / 23.9%
Number/percentage of C's	14,826,447 / 19.34%
Number/percentage of T's	24,099,056 / 31.44%
Number/percentage of G's	19,391,683 / 25.3%
Number/percentage of N's	8,425 / 0.01%
GC Percentage	44.65%

2.3. Coverage

Mean	0.0248

Standard Deviation	0.2203

2.4. Mapping Quality

Mean Mapping Quality	44.61

2.5. Mismatches and indels

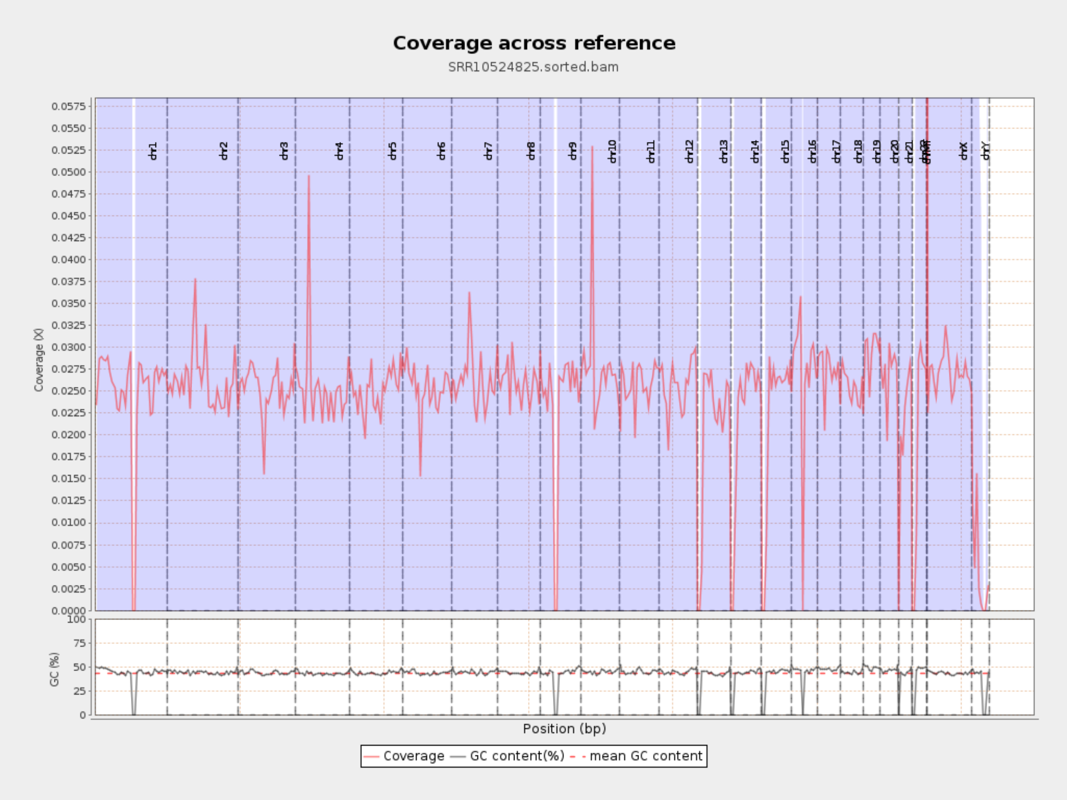
General error rate	0.52%
Mismatches	386,514
Insertions	6,036
Mapped reads with at least one insertion	0.45%
Deletions	14,778
Mapped reads with at least one deletion	1.09%
Homopolymer indels	41.1%

2.6. Chromosome stats

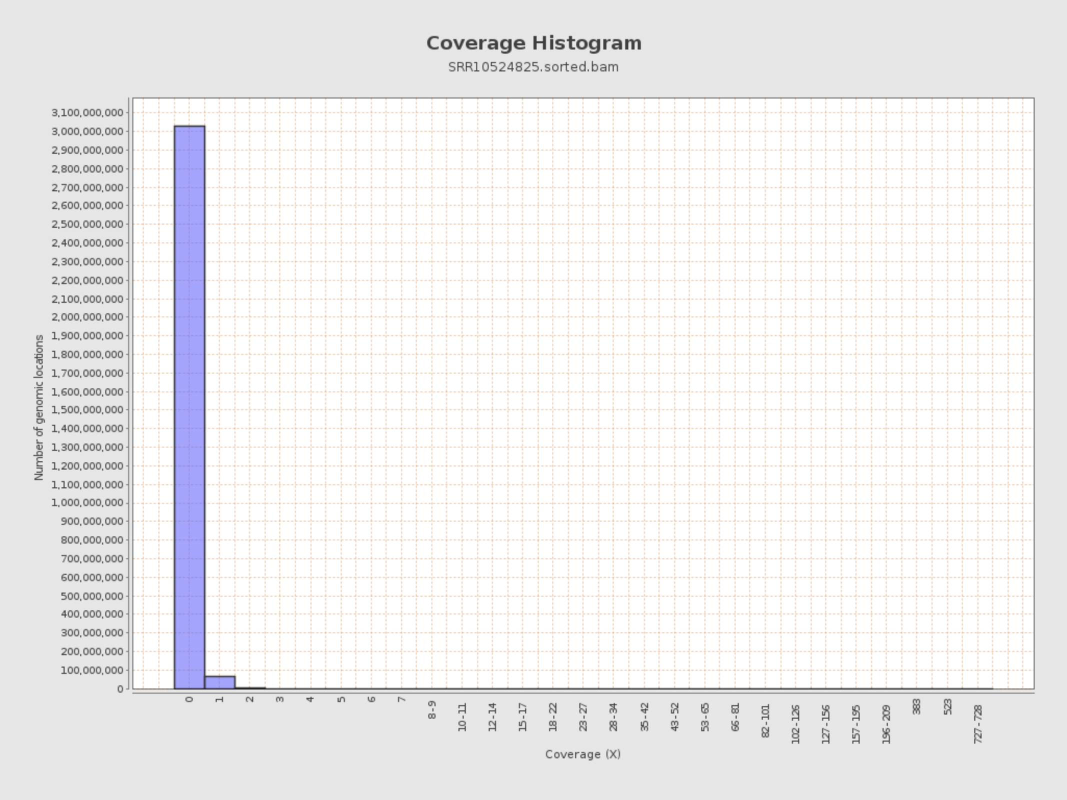
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6129233	0.0246	0.2369
chr2	243199373	6370870	0.0262	0.3613
chr3	198022430	4987006	0.0252	0.1751
chr4	191154276	4892274	0.0256	0.2049
chr5	180915260	4562240	0.0252	0.1734
chr6	171115067	4337659	0.0253	0.1907
chr7	159138663	4192946	0.0263	0.2549

chr8	146364022	3794981	0.0259	0.1983
chr9	141213431	3272591	0.0232	0.1932
chr10	135534747	3769713	0.0278	0.2832
chr11	135006516	3490156	0.0259	0.2026
chr12	133851895	3437167	0.0257	0.1775
chr13	115169878	2346322	0.0204	0.1568
chr14	107349540	2320707	0.0216	0.1633
chr15	102531392	2202937	0.0215	0.1632
chr16	90354753	2401404	0.0266	0.1974
chr17	81195210	2225801	0.0274	0.1903
chr18	78077248	1992462	0.0255	0.297
chr19	59128983	1738748	0.0294	0.2334
chr20	63025520	1689006	0.0268	0.1915
chr21	48129895	1017290	0.0211	0.1753
chr22	51304566	1003289	0.0196	0.1544
chrMT	16571	11587	0.6992	1.0373
chrX	155270560	4213820	0.0271	0.1917
chrY	59373566	266164	0.0045	0.1302

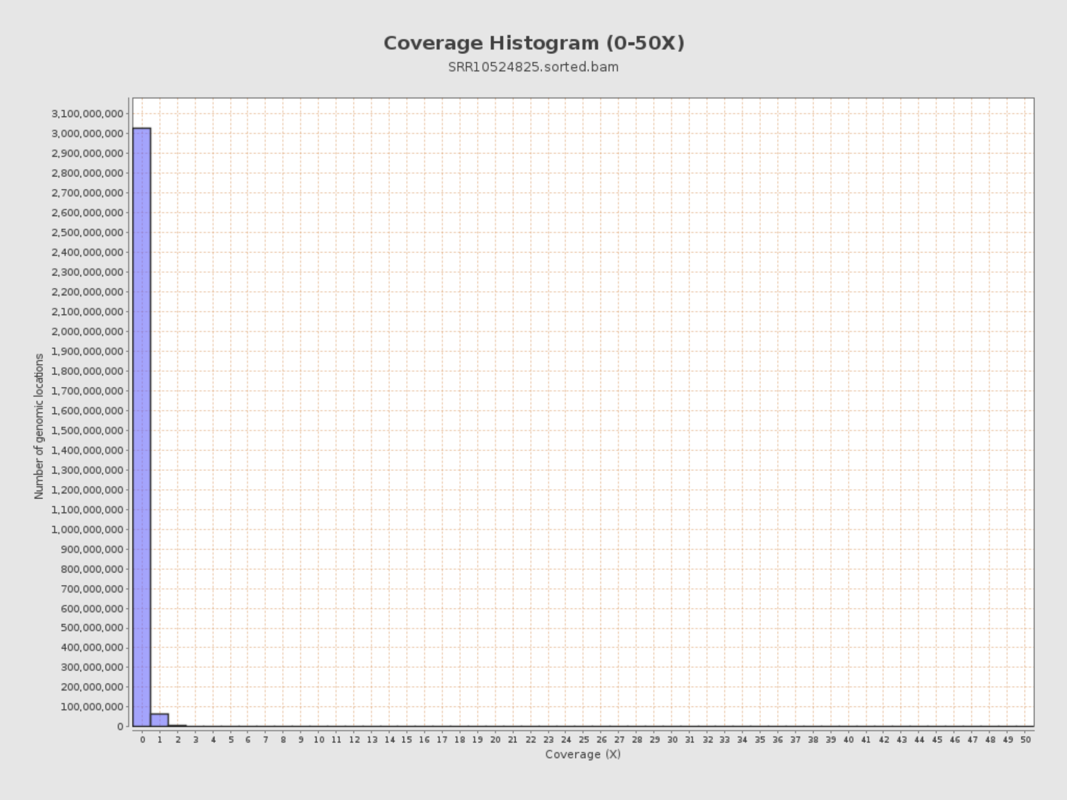
3. Results : Coverage across reference



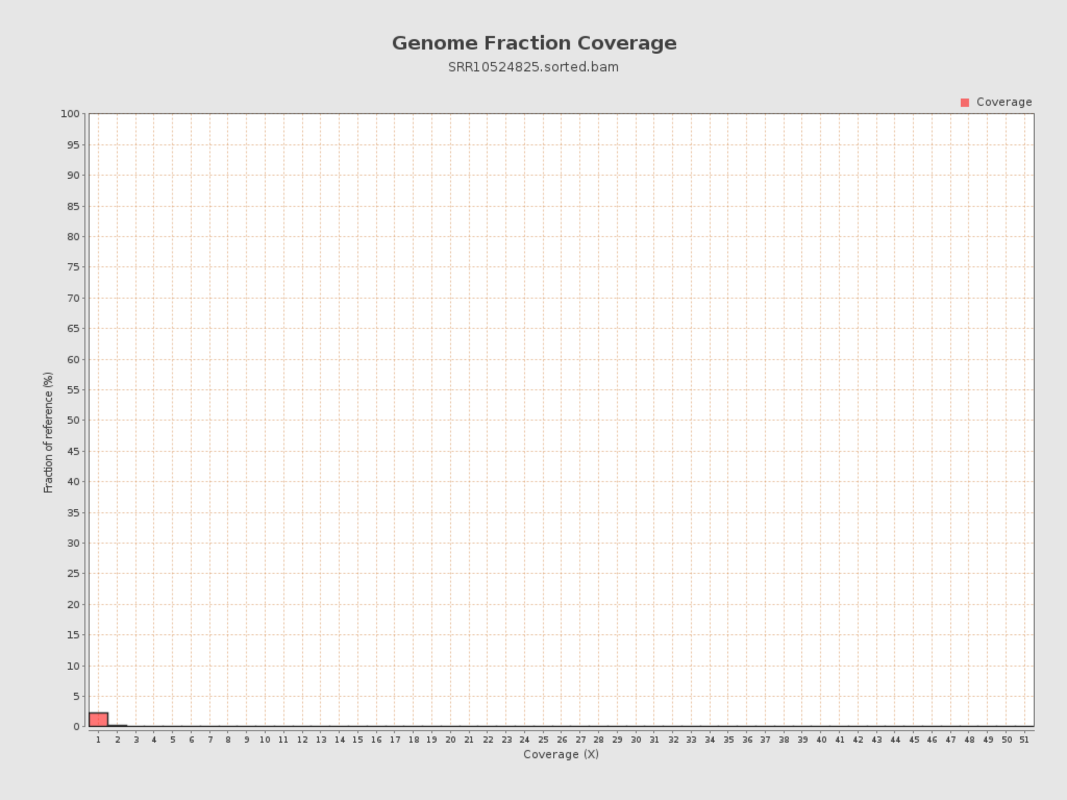
4. Results : Coverage Histogram



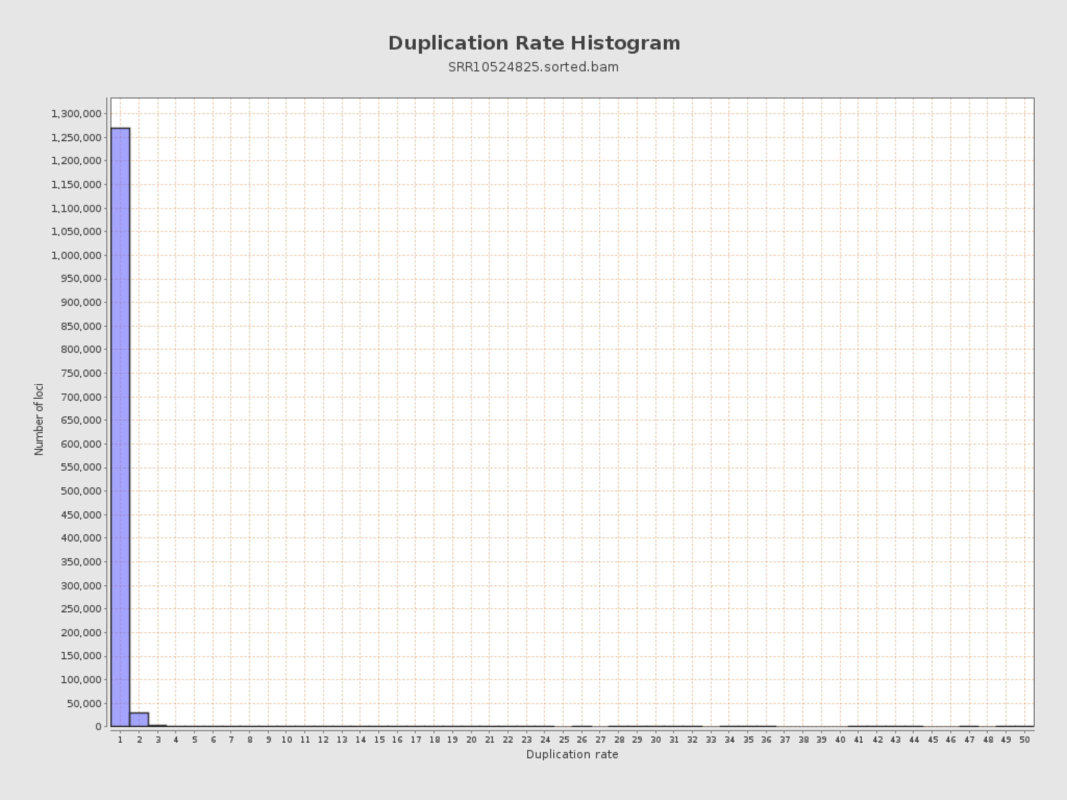
5. Results : Coverage Histogram (0-50X)



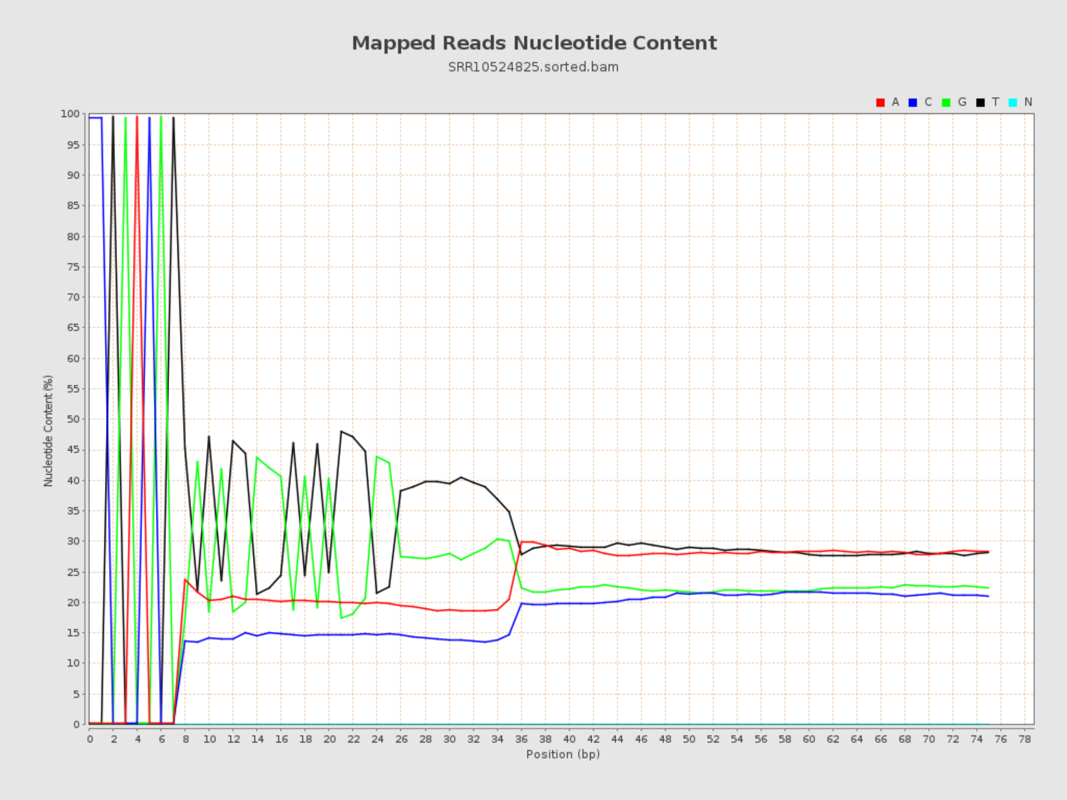
6. Results : Genome Fraction Coverage



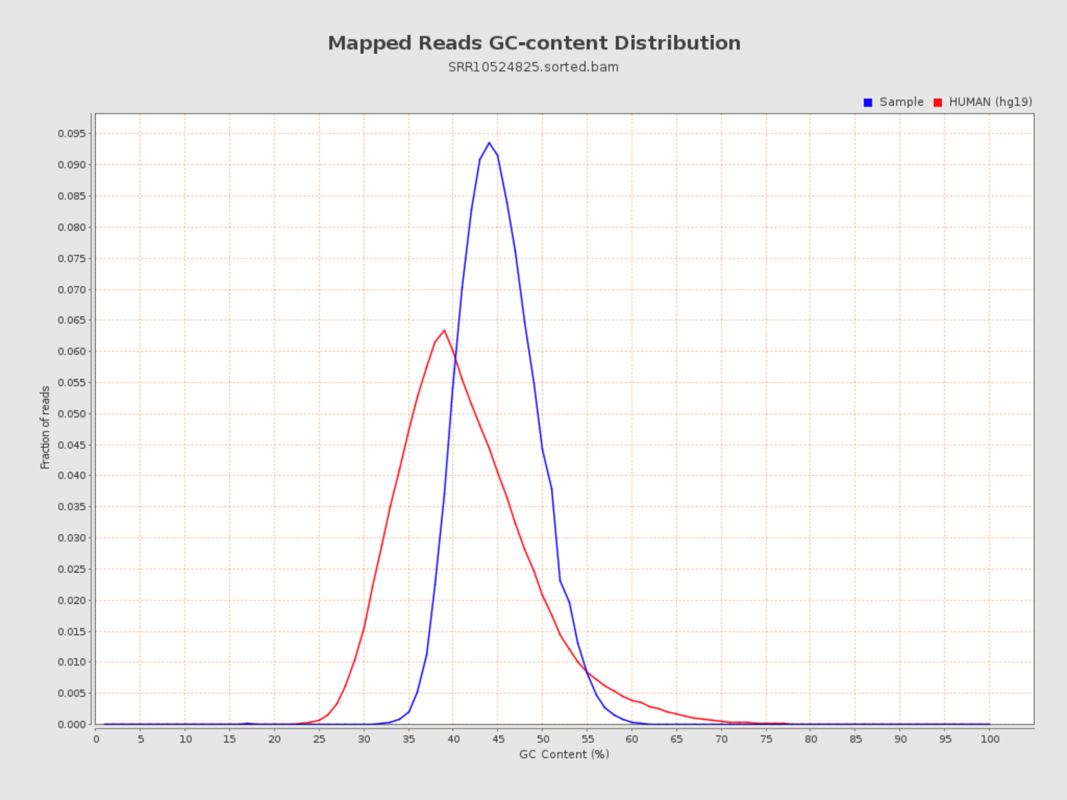
7. Results : Duplication Rate Histogram



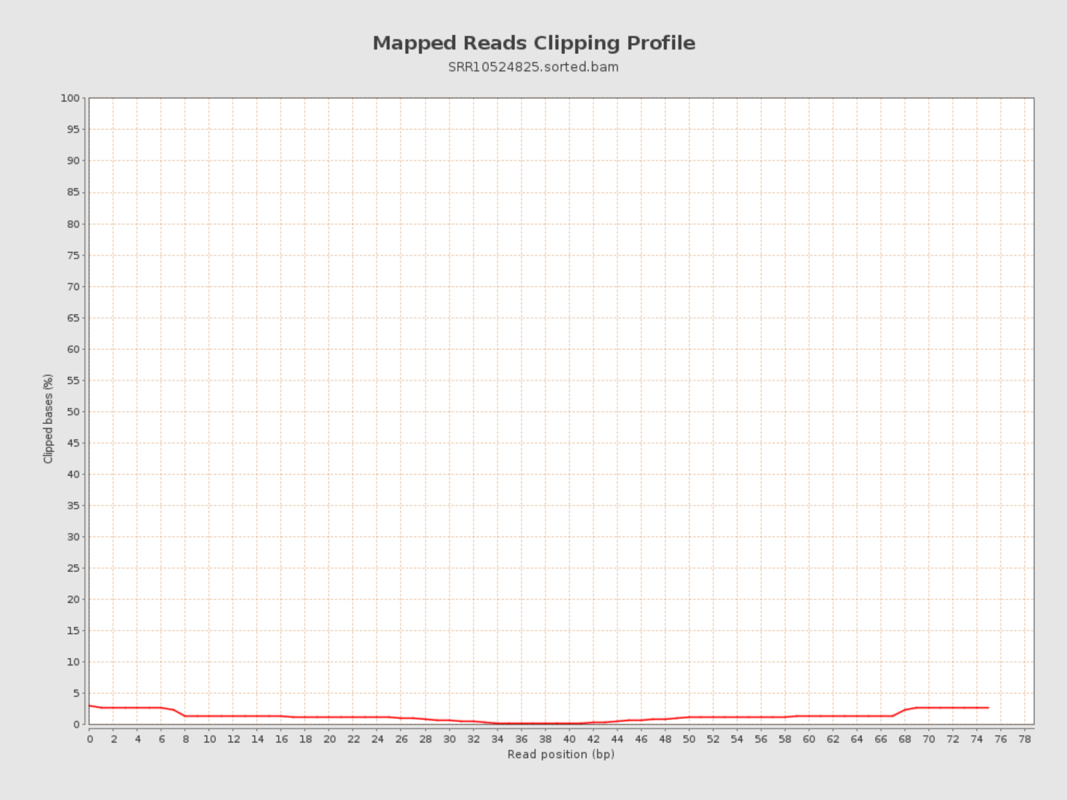
8. Results : Mapped Reads Nucleotide Content



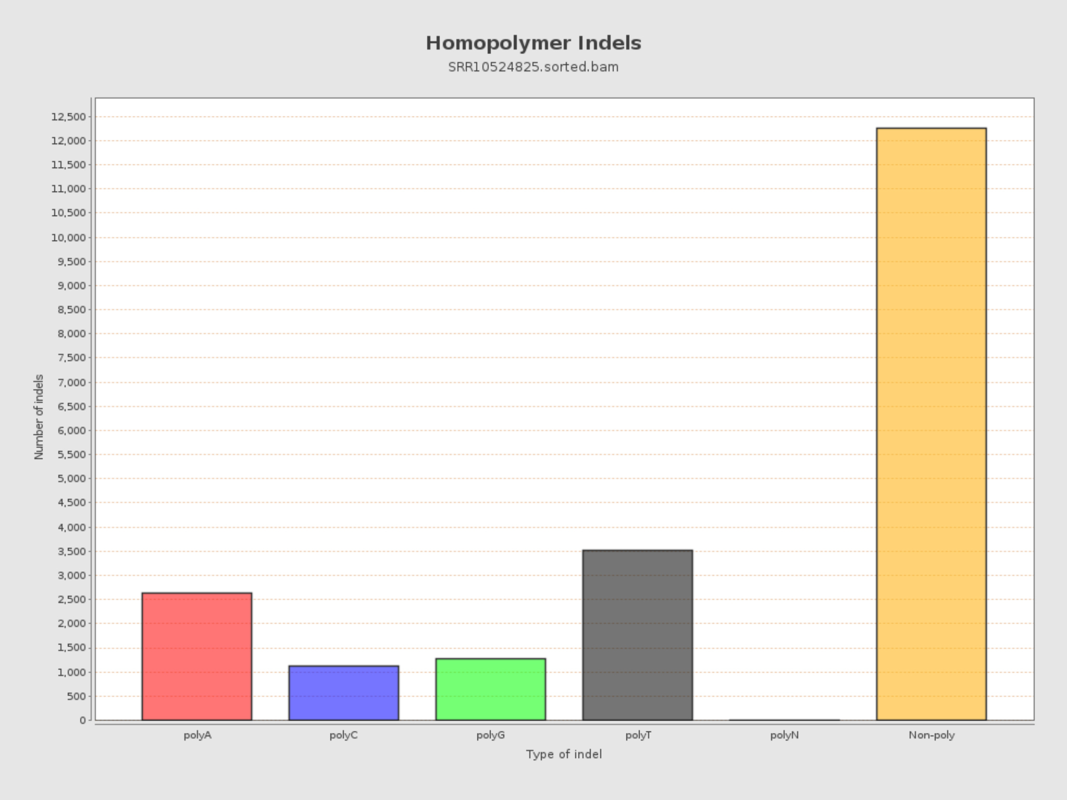
9. Results : Mapped Reads GC-content Distribution



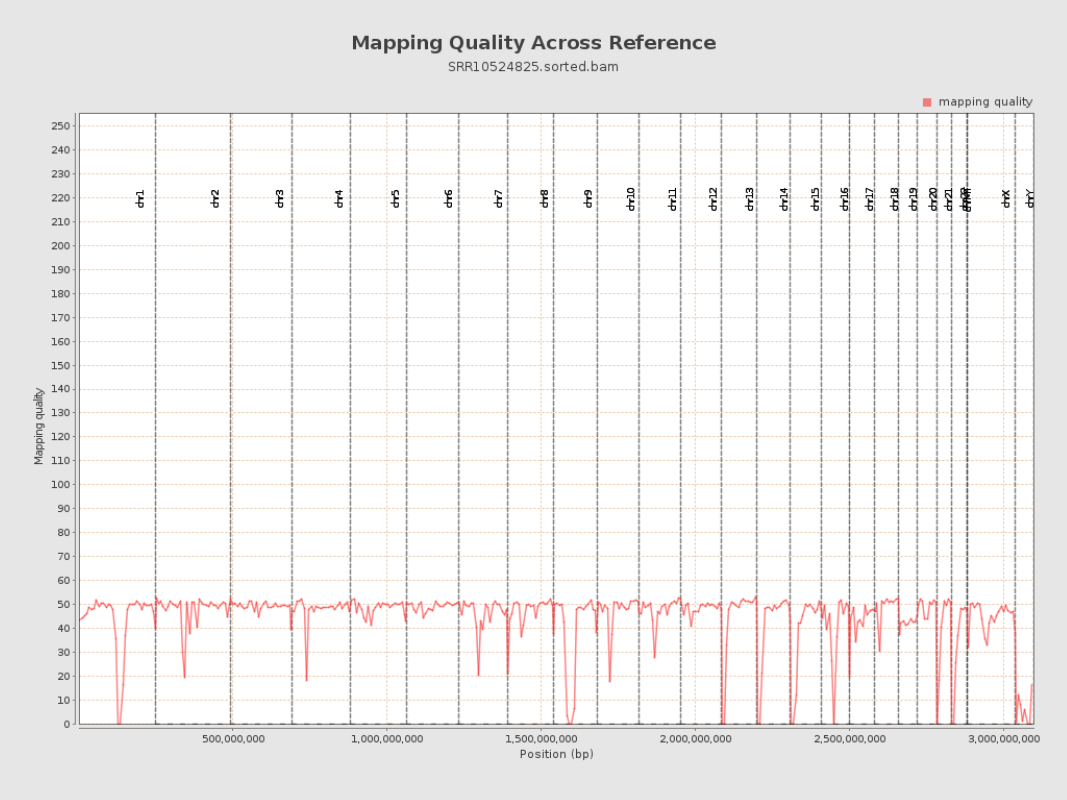
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram