Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 03:45:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524425.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_SRR10524425 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524425.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 03:45:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524425.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,162,552
Mapped reads	1,982,397 / 91.67%
Unmapped reads	180,155 / 8.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,092 / 0.37%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	107,952 / 4.99%
Duplication rate	4.06%
Clipped reads	1,987,619 / 91.91%

2.2. ACGT Content

Number/percentage of A's	29,096,222 / 24.7%
Number/percentage of C's	23,149,276 / 19.65%
Number/percentage of T's	34,853,188 / 29.59%
Number/percentage of G's	30,671,988 / 26.04%
Number/percentage of N's	12,300 / 0.01%
GC Percentage	45.7%

2.3. Coverage

Mean	0.0381

Standard Deviation	0.3656

2.4. Mapping Quality

Mean Mapping Quality	45.26

2.5. Mismatches and indels

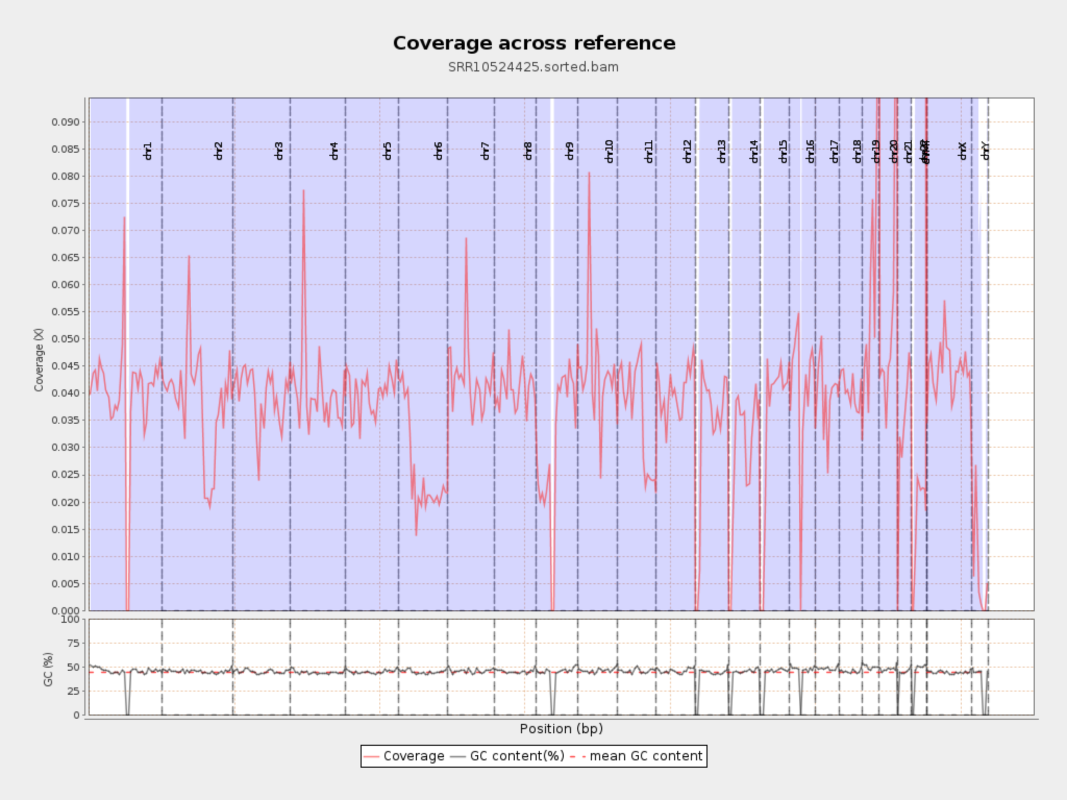
General error rate	0.52%
Mismatches	600,673
Insertions	7,148
Mapped reads with at least one insertion	0.36%
Deletions	20,441
Mapped reads with at least one deletion	1.02%
Homopolymer indels	43.87%

2.6. Chromosome stats

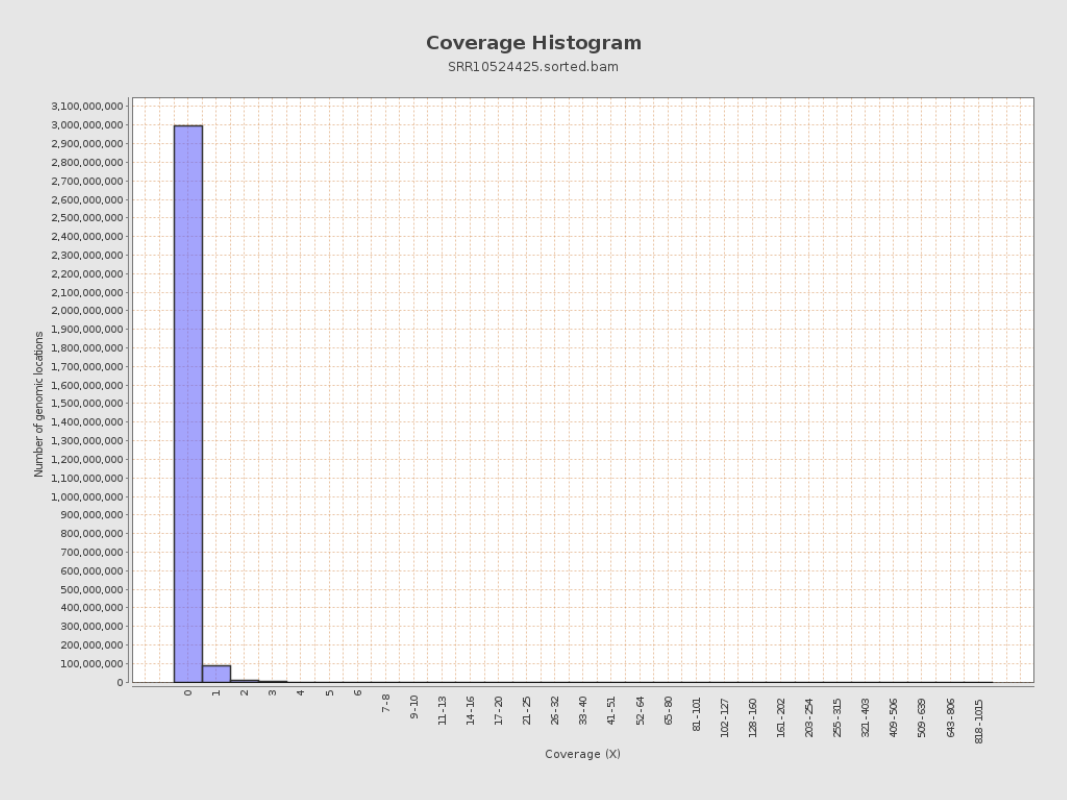
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9880175	0.0396	0.7764
chr2	243199373	9386932	0.0386	0.4109
chr3	198022430	7838926	0.0396	0.2253
chr4	191154276	7719915	0.0404	0.2976
chr5	180915260	7253198	0.0401	0.2273
chr6	171115067	4428905	0.0259	0.1962
chr7	159138663	6848773	0.043	0.4885

chr8	146364022	6003631	0.041	0.2823
chr9	141213431	4254757	0.0301	0.2421
chr10	135534747	5979285	0.0441	0.4037
chr11	135006516	4933037	0.0365	0.2713
chr12	133851895	5414271	0.0404	0.2355
chr13	115169878	3755188	0.0326	0.2056
chr14	107349540	3105961	0.0289	0.199
chr15	102531392	3554207	0.0347	0.2135
chr16	90354753	3709662	0.0411	0.2471
chr17	81195210	3202930	0.0394	0.2542
chr18	78077248	3164007	0.0405	0.4668
chr19	59128983	3863766	0.0653	0.5276
chr20	63025520	3725930	0.0591	0.3002
chr21	48129895	1622690	0.0337	0.2595
chr22	51304566	828190	0.0161	0.1447
chrMT	16571	13545	0.8174	1.1224
chrX	155270560	6907889	0.0445	0.261
chrY	59373566	419827	0.0071	0.2372

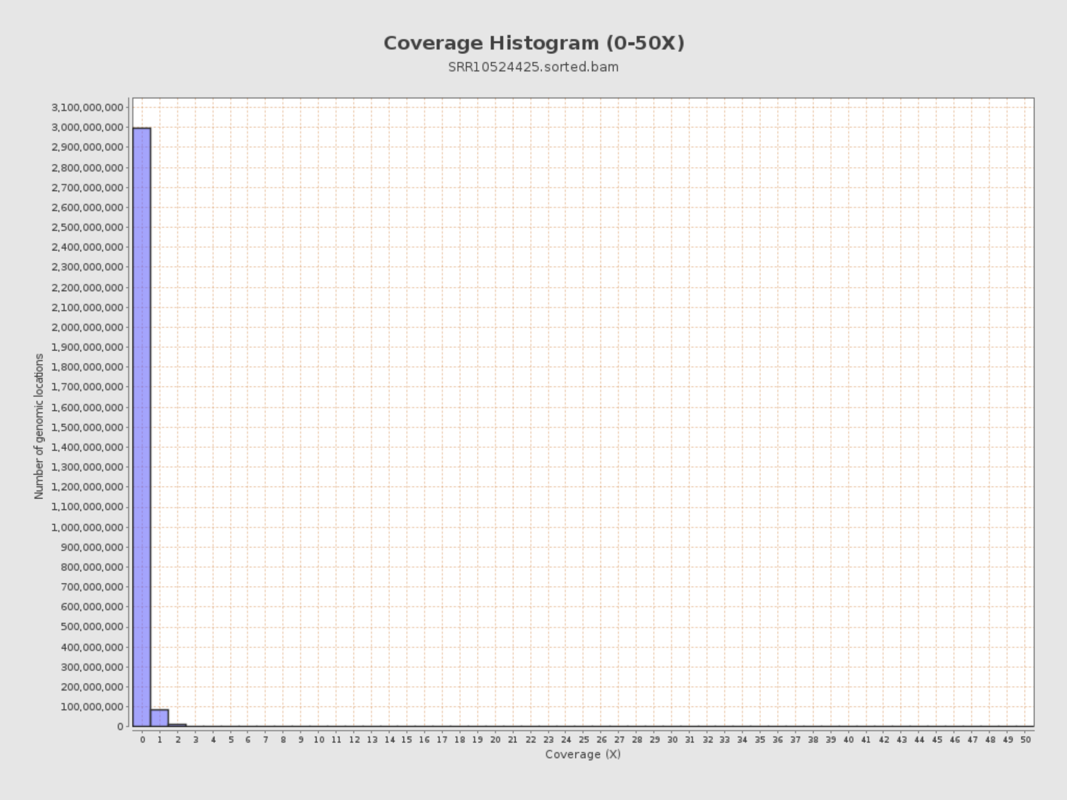
3. Results : Coverage across reference



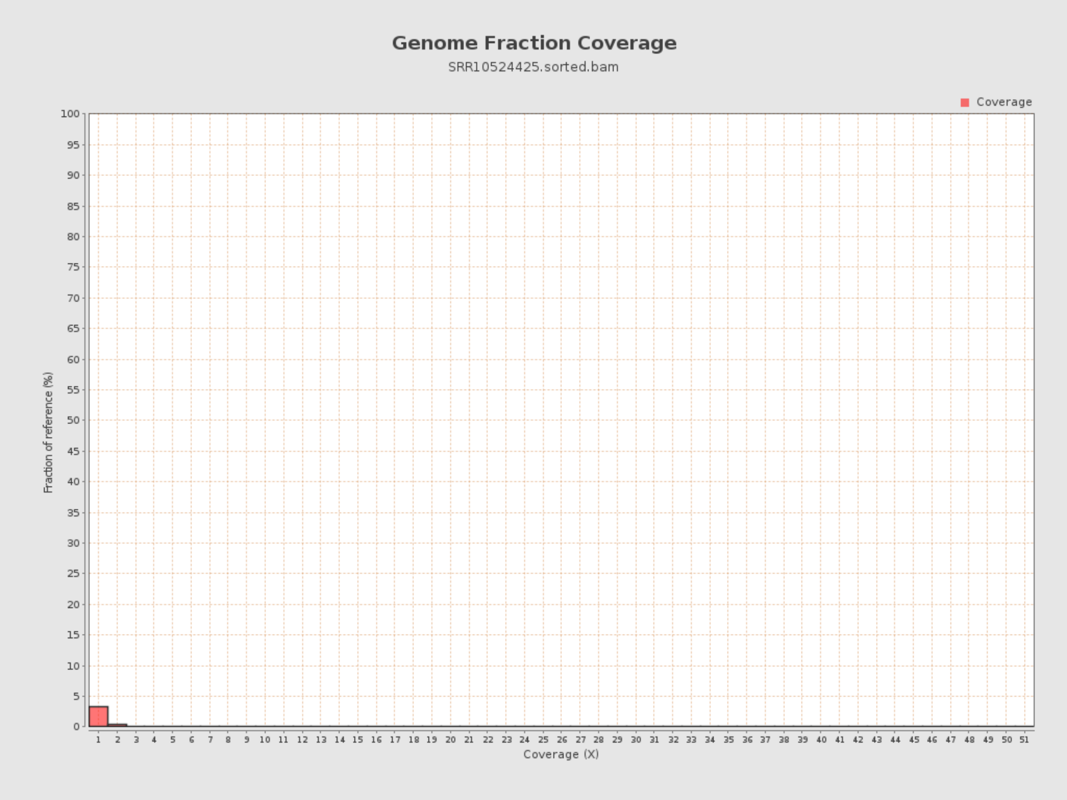
4. Results : Coverage Histogram



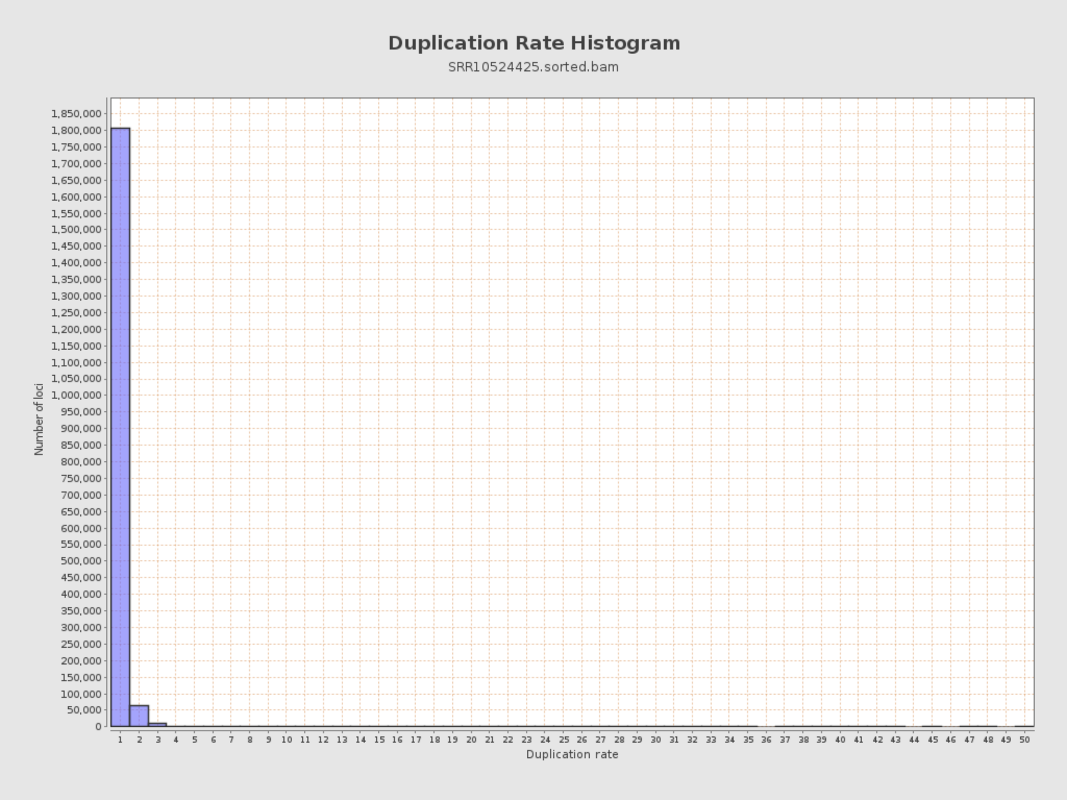
5. Results : Coverage Histogram (0-50X)



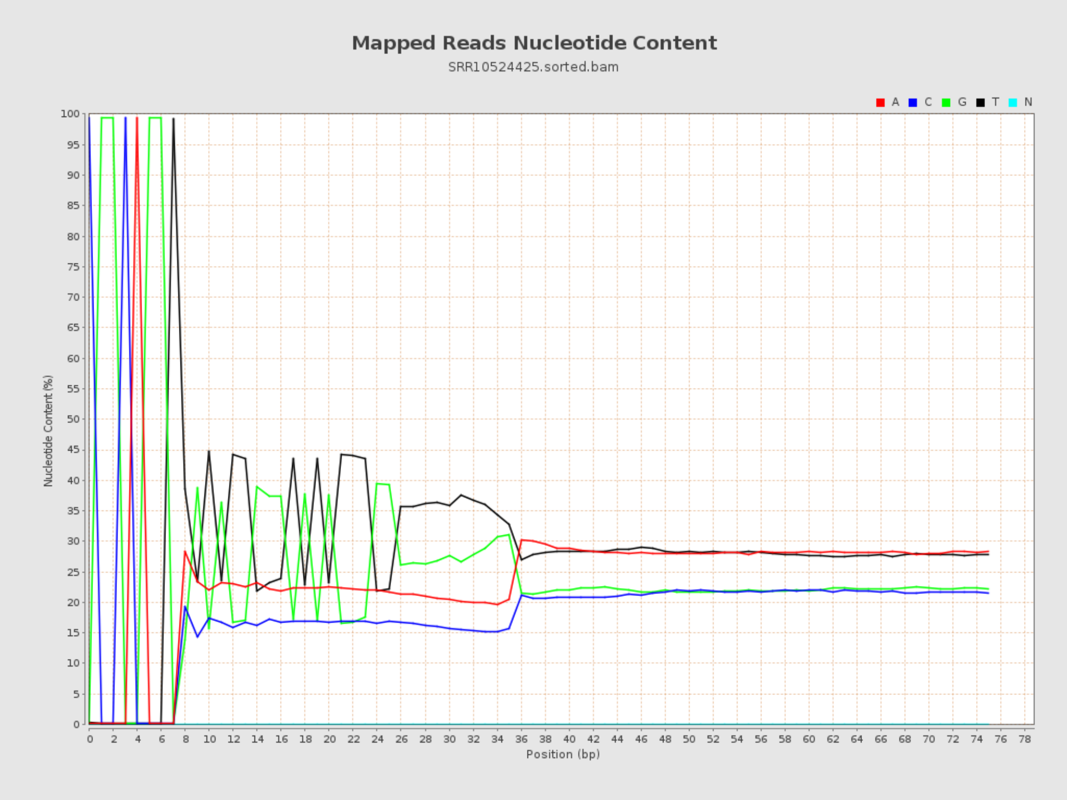
6. Results : Genome Fraction Coverage



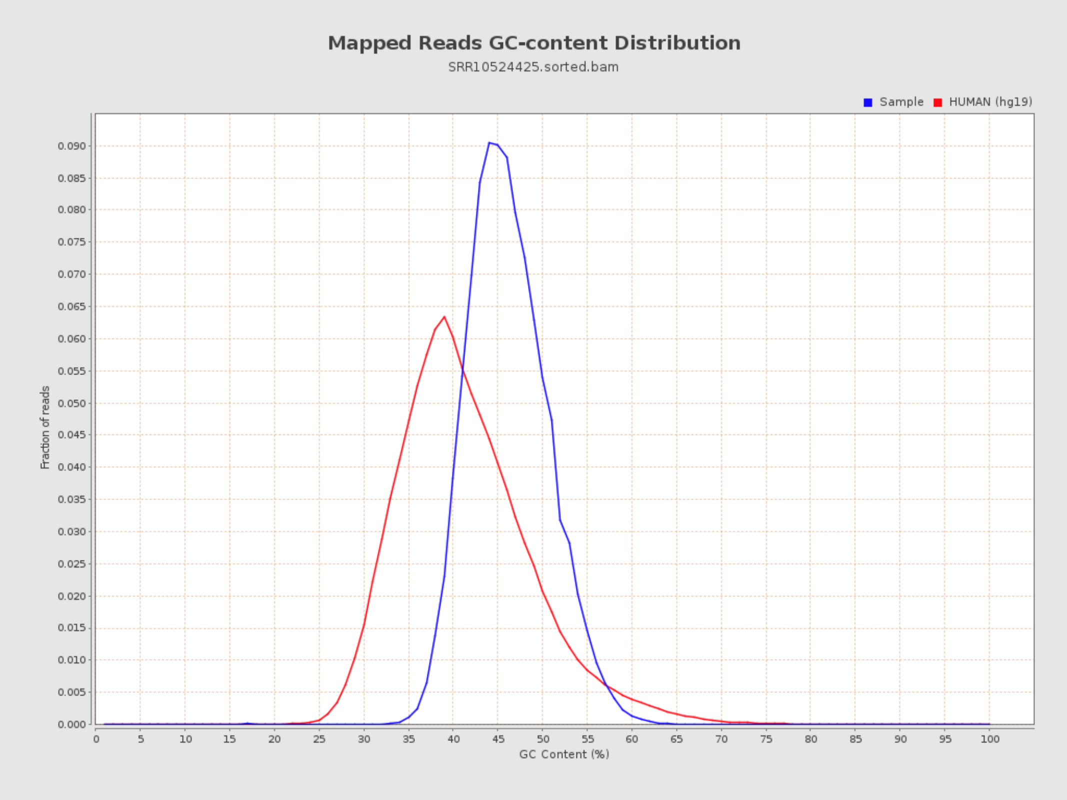
7. Results : Duplication Rate Histogram



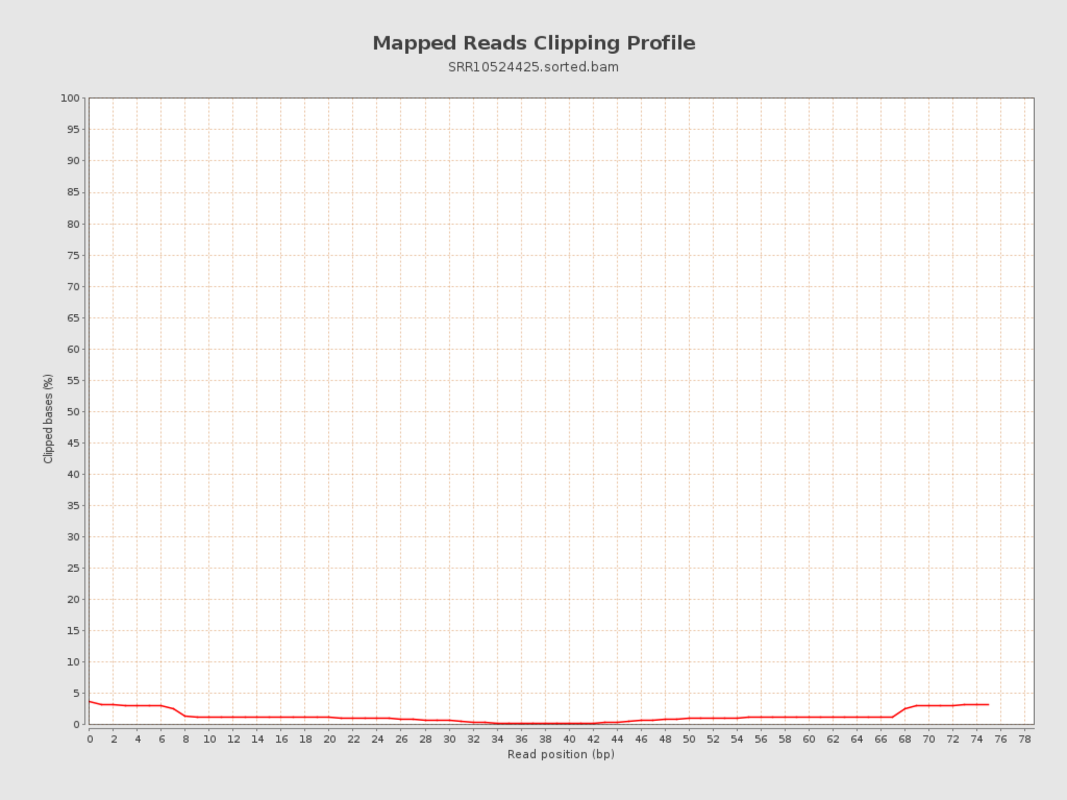
8. Results : Mapped Reads Nucleotide Content



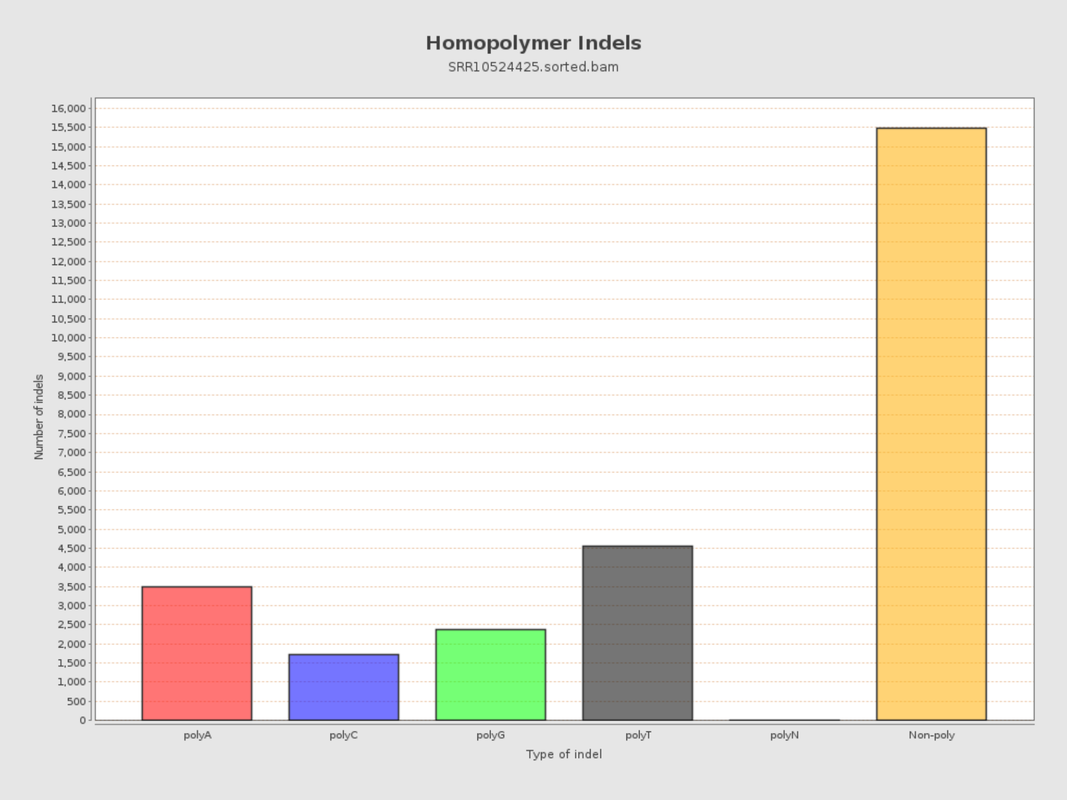
9. Results : Mapped Reads GC-content Distribution



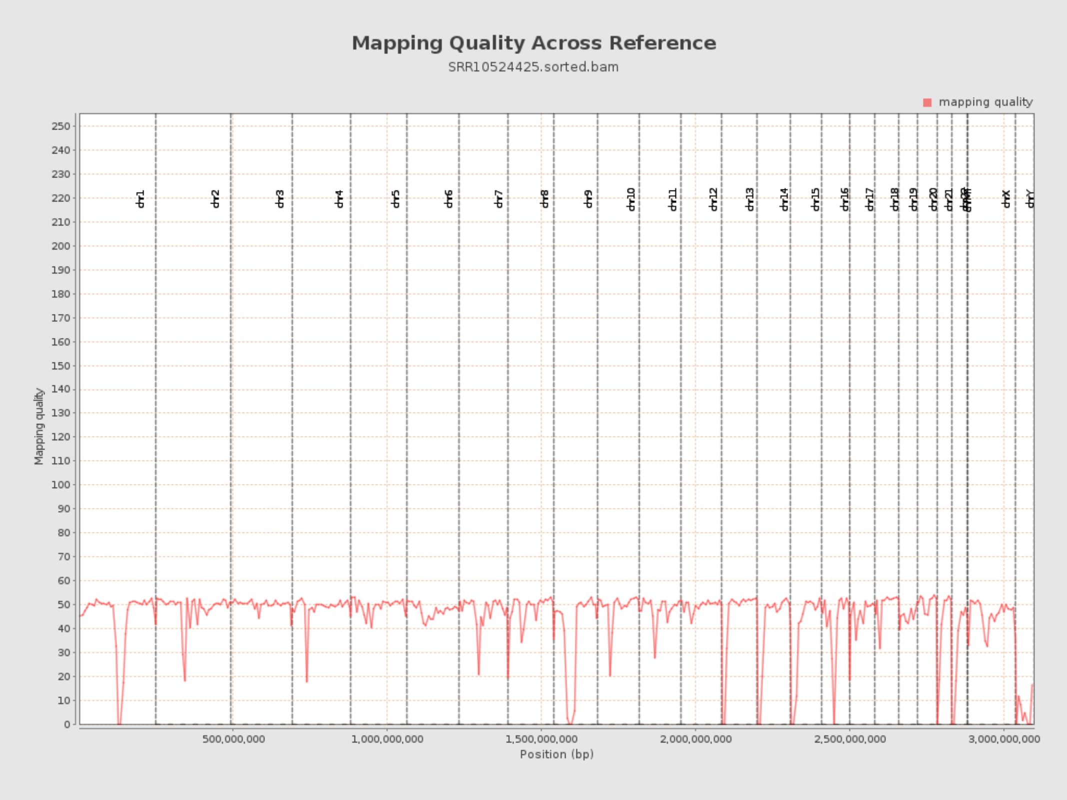
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram