Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 20:50:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525164.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_SRR10525164 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525164.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 20:50:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525164.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,379,499
Mapped reads	2,171,421 / 91.26%
Unmapped reads	208,078 / 8.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,238 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	88,756 / 3.73%
Duplication rate	2.97%
Clipped reads	2,171,691 / 91.27%

2.2. ACGT Content

Number/percentage of A's	32,228,501 / 25.53%
Number/percentage of C's	23,204,153 / 18.38%
Number/percentage of T's	40,704,270 / 32.25%
Number/percentage of G's	30,089,389 / 23.84%
Number/percentage of N's	3,168 / 0%
GC Percentage	42.22%

2.3. Coverage

Mean	0.0408

Standard Deviation	0.3647

2.4. Mapping Quality

Mean Mapping Quality	44.85

2.5. Mismatches and indels

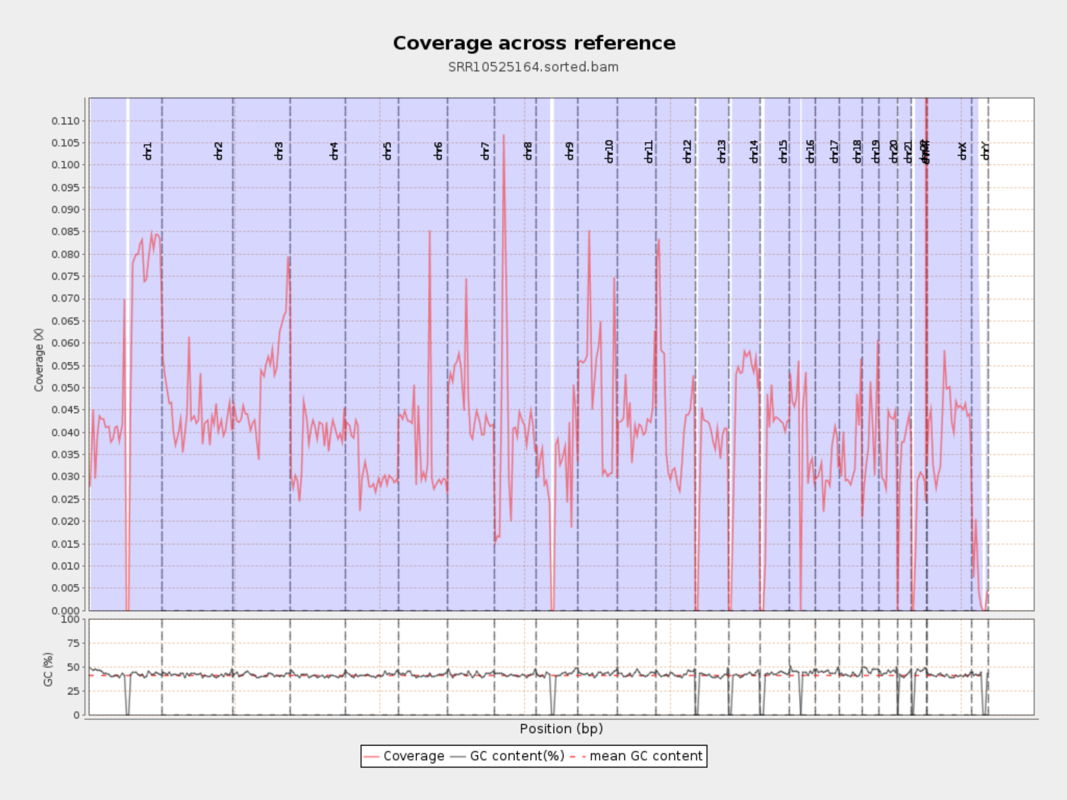
General error rate	0.52%
Mismatches	642,211
Insertions	9,908
Mapped reads with at least one insertion	0.45%
Deletions	25,349
Mapped reads with at least one deletion	1.16%
Homopolymer indels	40.92%

2.6. Chromosome stats

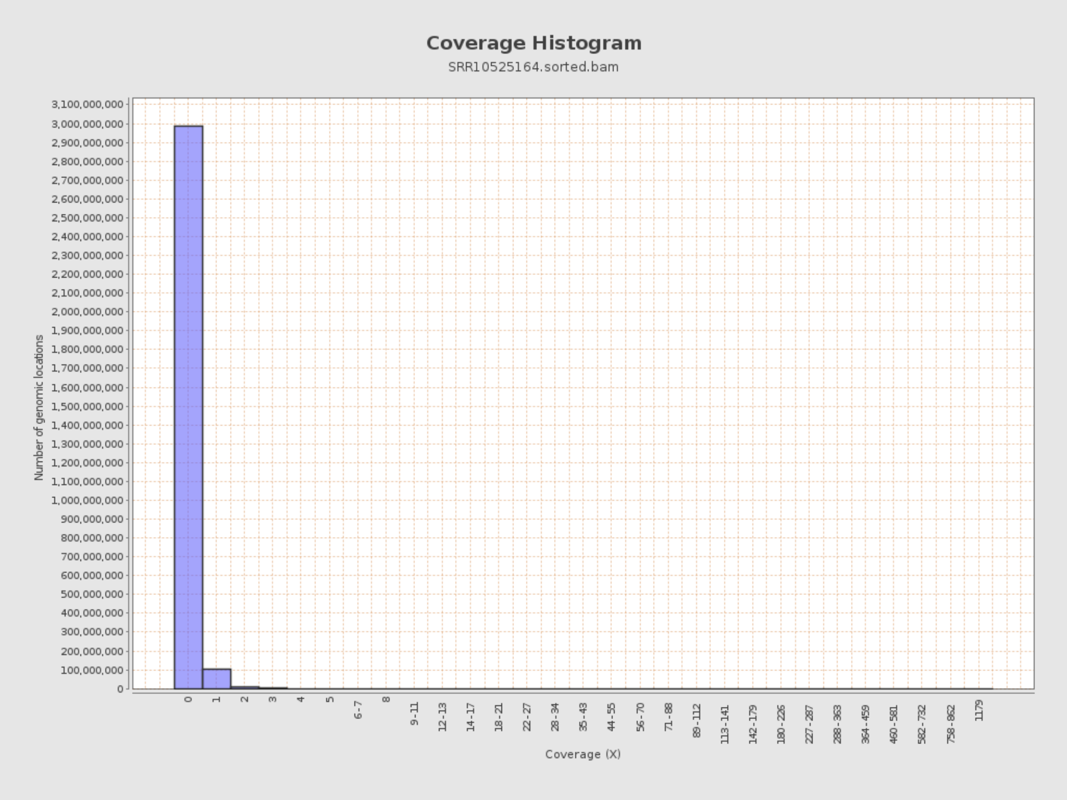
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13735133	0.0551	0.6684
chr2	243199373	10648250	0.0438	0.5315
chr3	198022430	10182227	0.0514	0.2566
chr4	191154276	7245666	0.0379	0.2316
chr5	180915260	5795911	0.032	0.1987
chr6	171115067	6468594	0.0378	0.2536
chr7	159138663	7578105	0.0476	0.541

chr8	146364022	5932883	0.0405	0.3234
chr9	141213431	4259253	0.0302	0.2632
chr10	135534747	6931580	0.0511	0.391
chr11	135006516	5831030	0.0432	0.2965
chr12	133851895	5888884	0.044	0.238
chr13	115169878	4006755	0.0348	0.2135
chr14	107349540	4878092	0.0454	0.2479
chr15	102531392	3582056	0.0349	0.2157
chr16	90354753	3514978	0.0389	0.2447
chr17	81195210	2589764	0.0319	0.2109
chr18	78077248	2790363	0.0357	0.523
chr19	59128983	2332926	0.0395	0.4579
chr20	63025520	2350650	0.0373	0.2196
chr21	48129895	1657163	0.0344	0.2202
chr22	51304566	1065541	0.0208	0.1597
chrMT	16571	50154	3.0266	2.3047
chrX	155270560	6579409	0.0424	0.2554
chrY	59373566	374457	0.0063	0.168

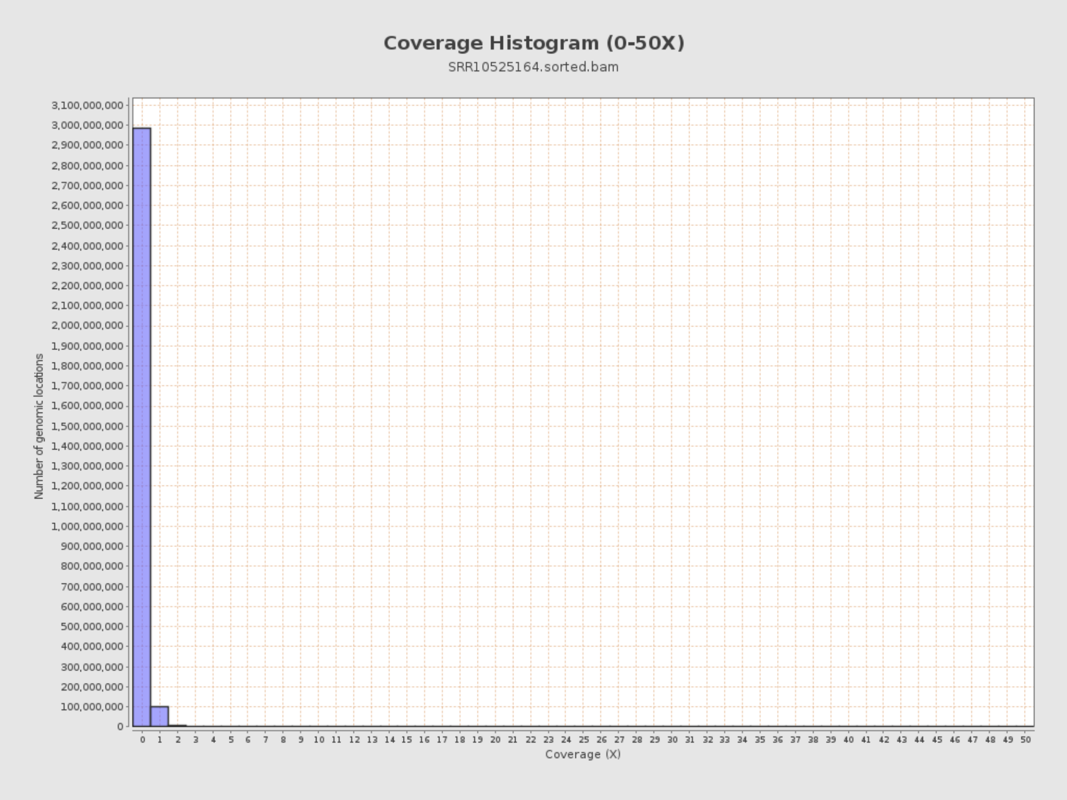
3. Results : Coverage across reference



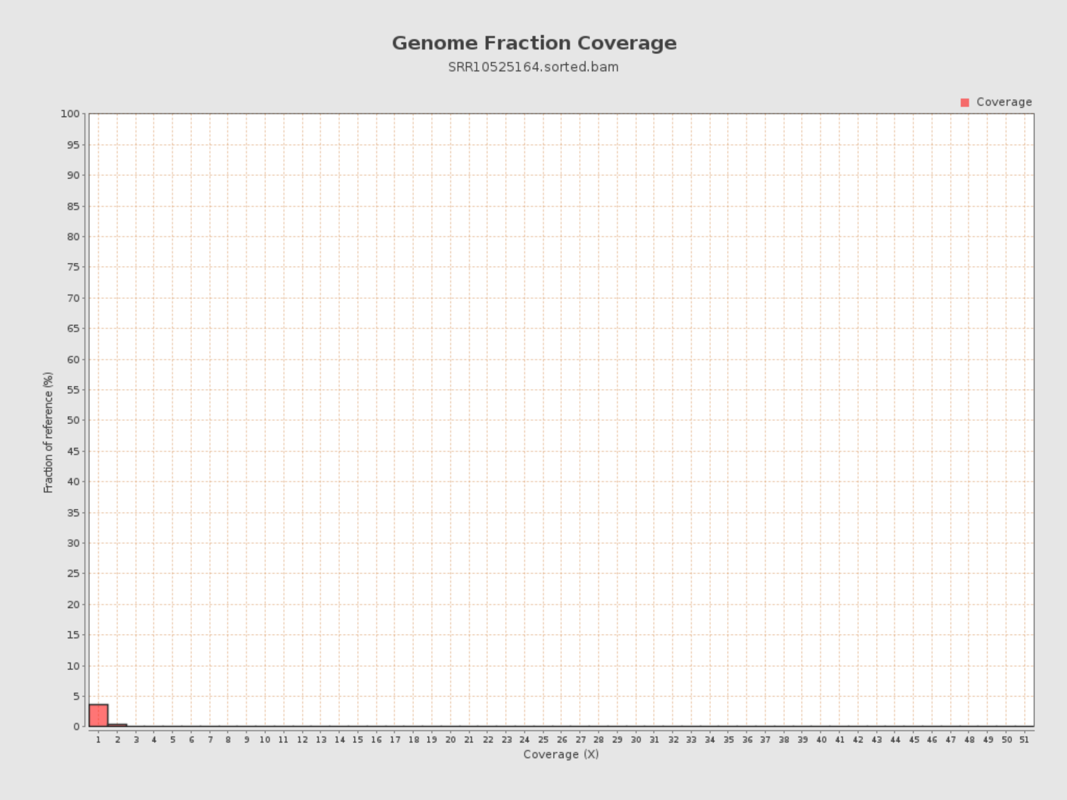
4. Results : Coverage Histogram



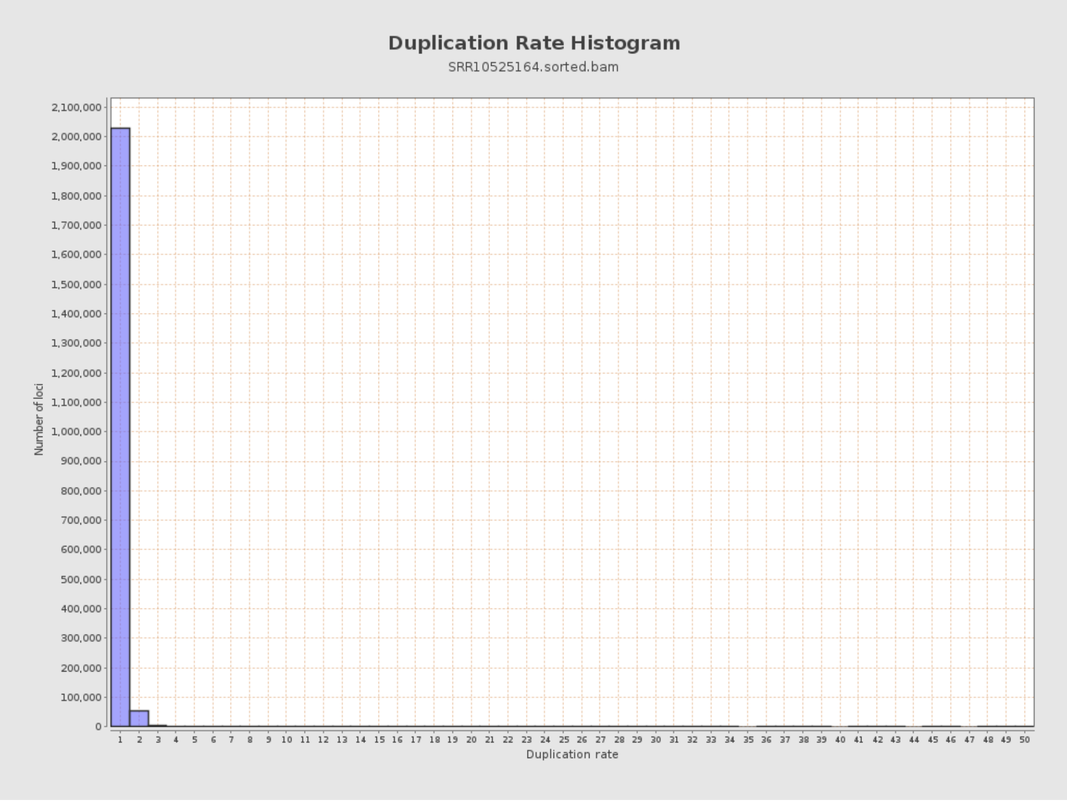
5. Results : Coverage Histogram (0-50X)



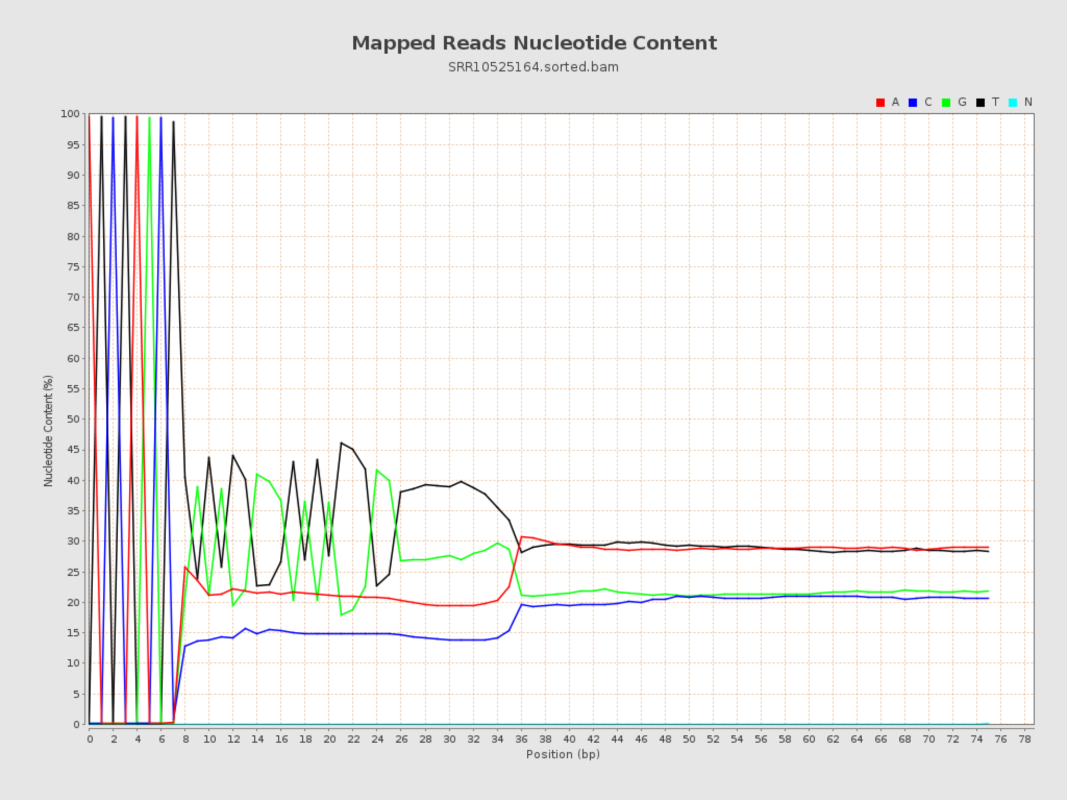
6. Results : Genome Fraction Coverage



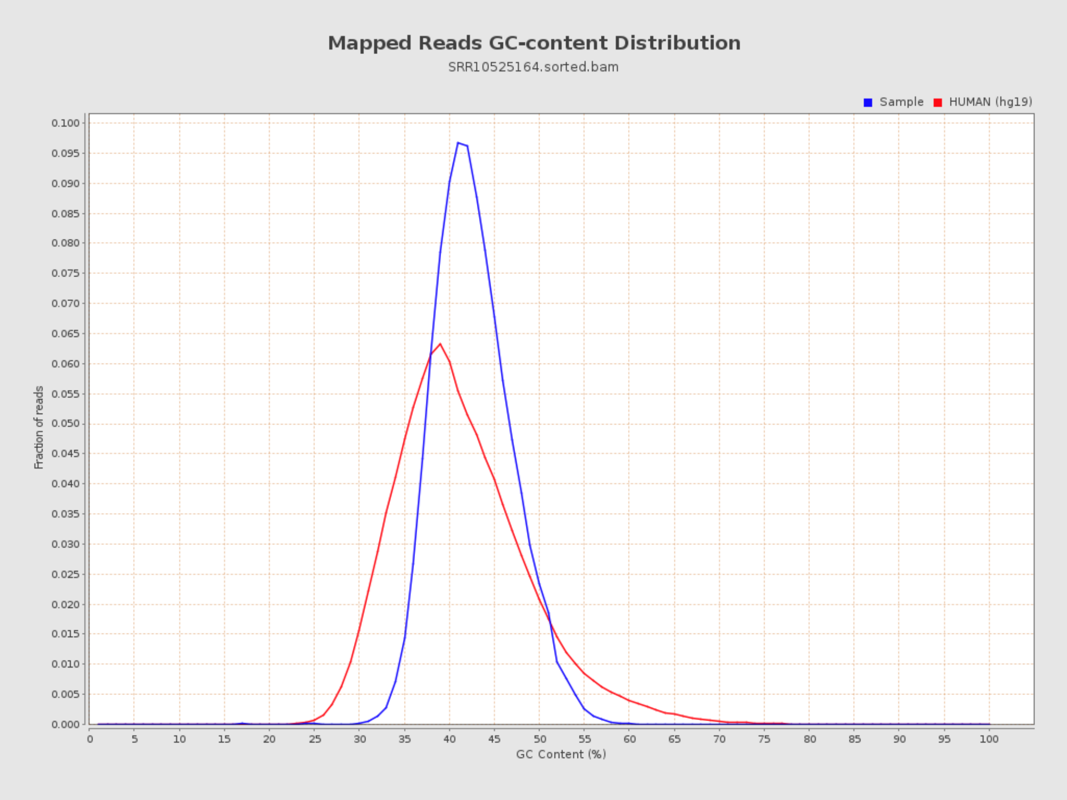
7. Results : Duplication Rate Histogram



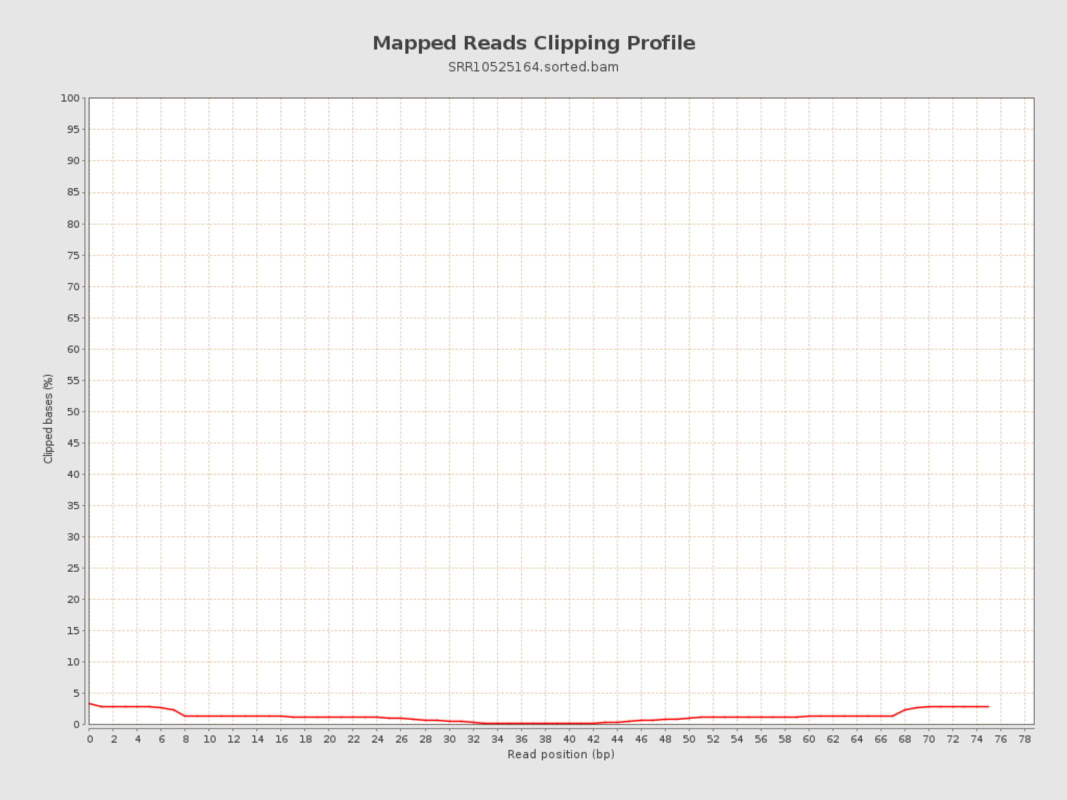
8. Results : Mapped Reads Nucleotide Content



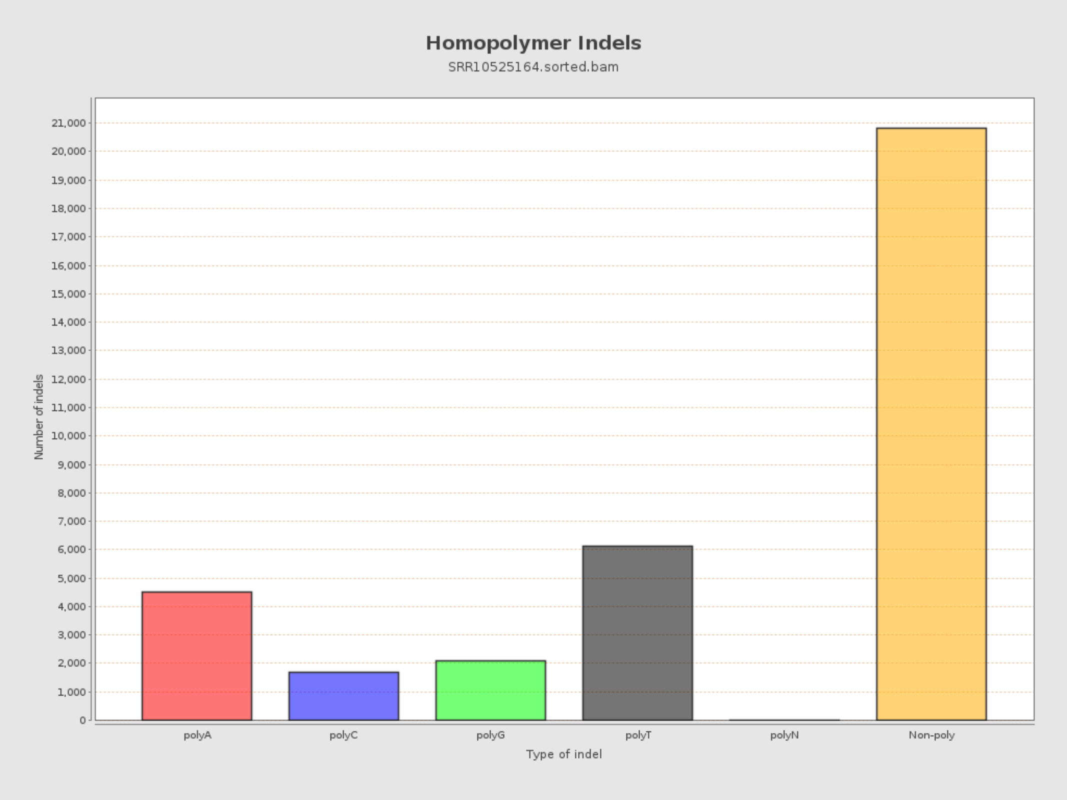
9. Results : Mapped Reads GC-content Distribution



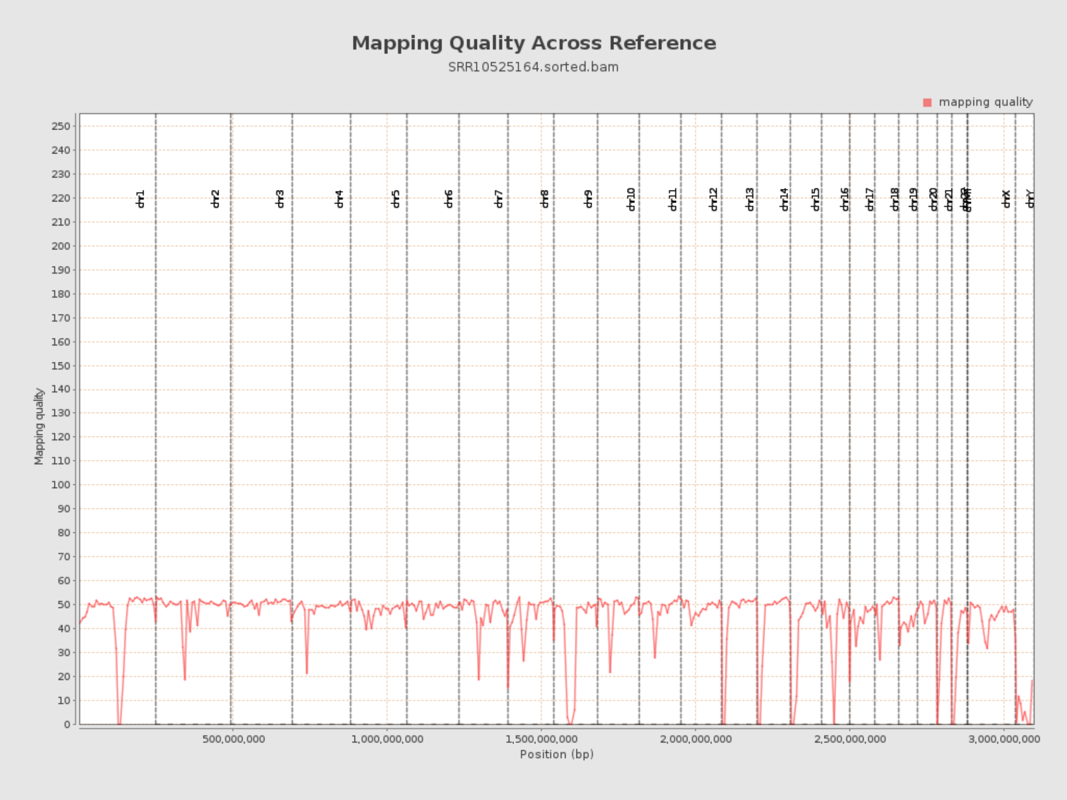
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram