Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 05:10:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524464.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_SRR10524464 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524464.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 05:10:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524464.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,138,028
Mapped reads	1,052,804 / 92.51%
Unmapped reads	85,224 / 7.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,409 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	37,842 / 3.33%
Duplication rate	2.78%
Clipped reads	1,051,693 / 92.41%

2.2. ACGT Content

Number/percentage of A's	15,579,157 / 25.54%
Number/percentage of C's	11,773,739 / 19.3%
Number/percentage of T's	19,128,413 / 31.36%
Number/percentage of G's	14,511,456 / 23.79%
Number/percentage of N's	1,316 / 0%
GC Percentage	43.09%

2.3. Coverage

Mean	0.0197

Standard Deviation	0.1998

2.4. Mapping Quality

Mean Mapping Quality	45.33

2.5. Mismatches and indels

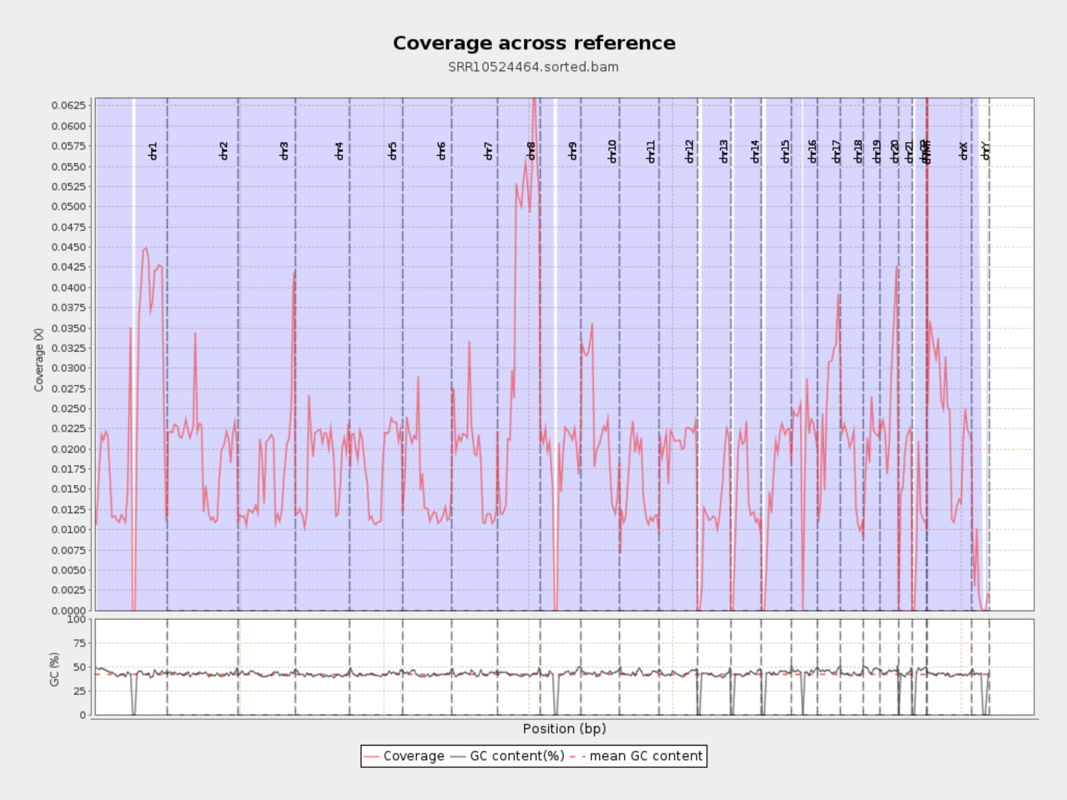
General error rate	0.48%
Mismatches	284,650
Insertions	4,728
Mapped reads with at least one insertion	0.45%
Deletions	11,420
Mapped reads with at least one deletion	1.08%
Homopolymer indels	41.44%

2.6. Chromosome stats

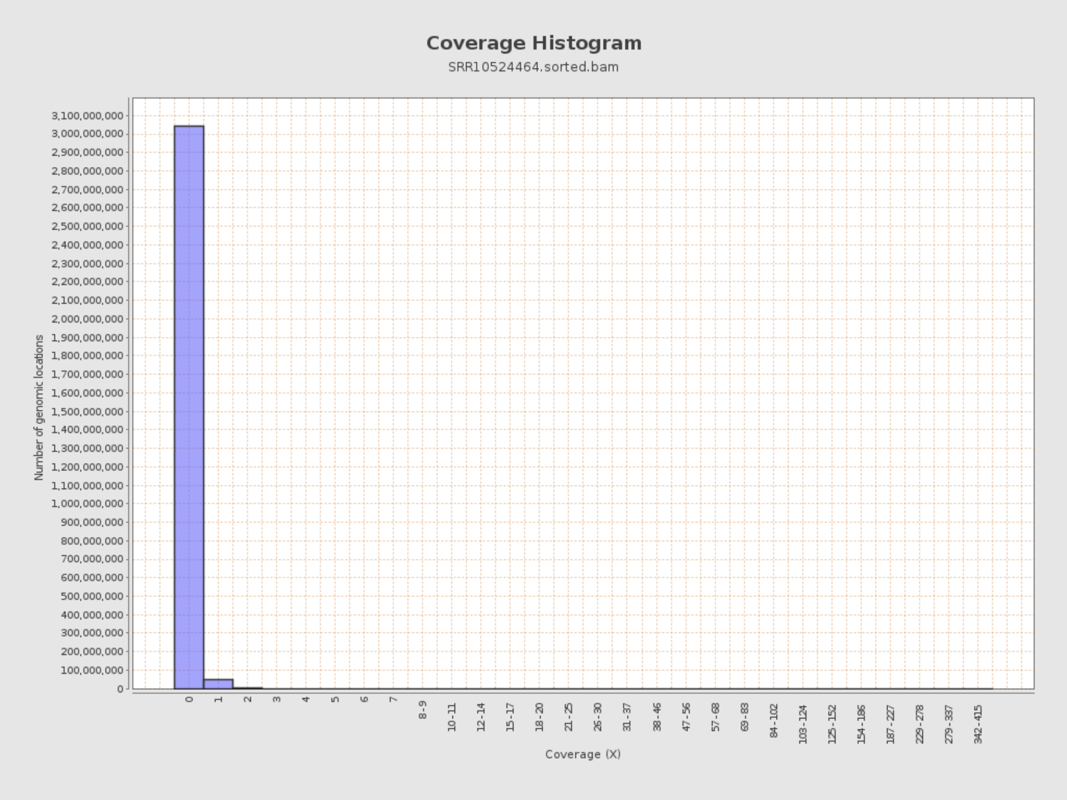
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6016809	0.0241	0.3453
chr2	243199373	4854029	0.02	0.2205
chr3	198022430	3327706	0.0168	0.1406
chr4	191154276	3481801	0.0182	0.1574
chr5	180915260	3344889	0.0185	0.1471
chr6	171115067	2655538	0.0155	0.1622
chr7	159138663	2990268	0.0188	0.2457

chr8	146364022	5723907	0.0391	0.2365
chr9	141213431	2543669	0.018	0.1766
chr10	135534747	3177061	0.0234	0.2068
chr11	135006516	2037857	0.0151	0.1834
chr12	133851895	2823109	0.0211	0.1567
chr13	115169878	1384548	0.012	0.1195
chr14	107349540	1445469	0.0135	0.126
chr15	102531392	1615733	0.0158	0.138
chr16	90354753	1910386	0.0211	0.1641
chr17	81195210	2104756	0.0259	0.1794
chr18	78077248	1403568	0.018	0.2674
chr19	59128983	1224465	0.0207	0.2547
chr20	63025520	1720608	0.0273	0.18
chr21	48129895	827355	0.0172	0.1477
chr22	51304566	503011	0.0098	0.1063
chrMT	16571	9285	0.5603	0.8753
chrX	155270560	3702415	0.0238	0.1812
chrY	59373566	185333	0.0031	0.0871

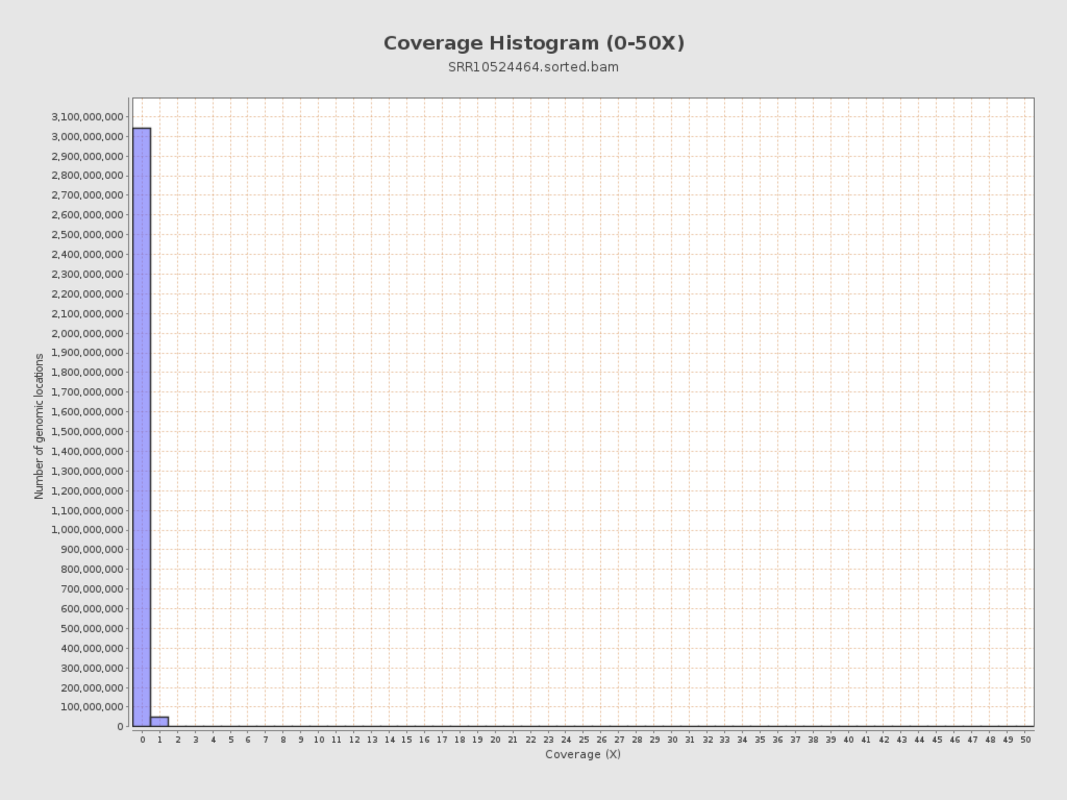
3. Results : Coverage across reference



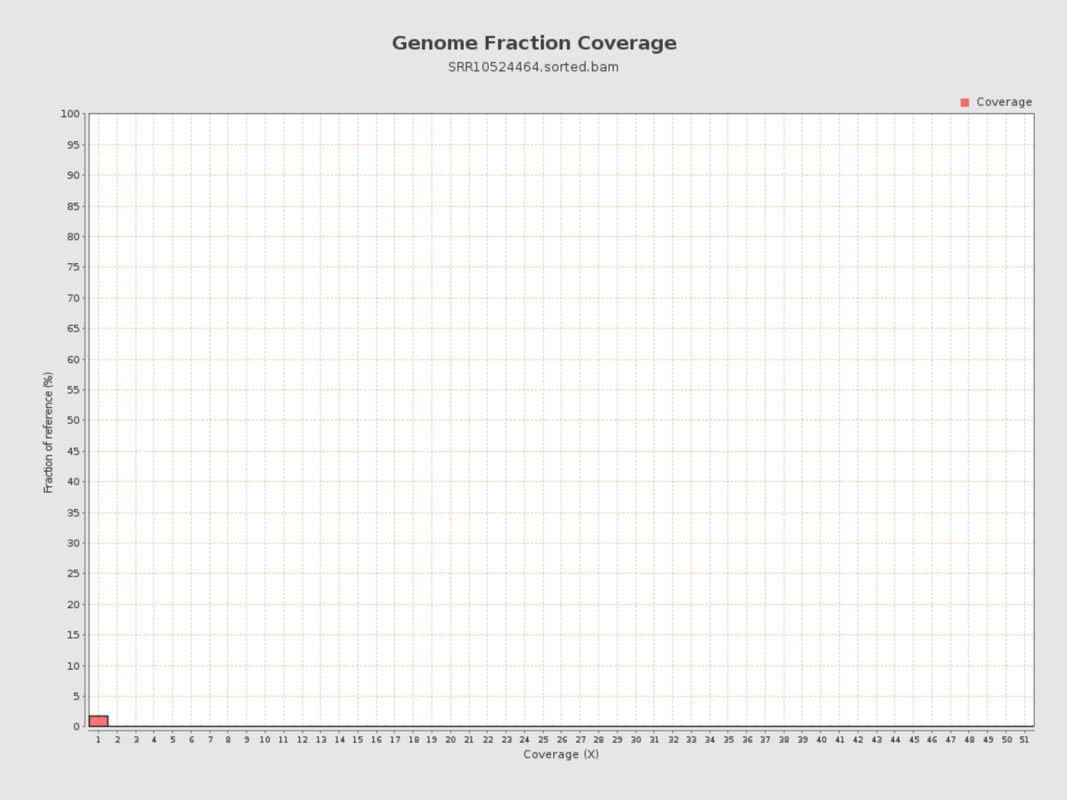
4. Results : Coverage Histogram



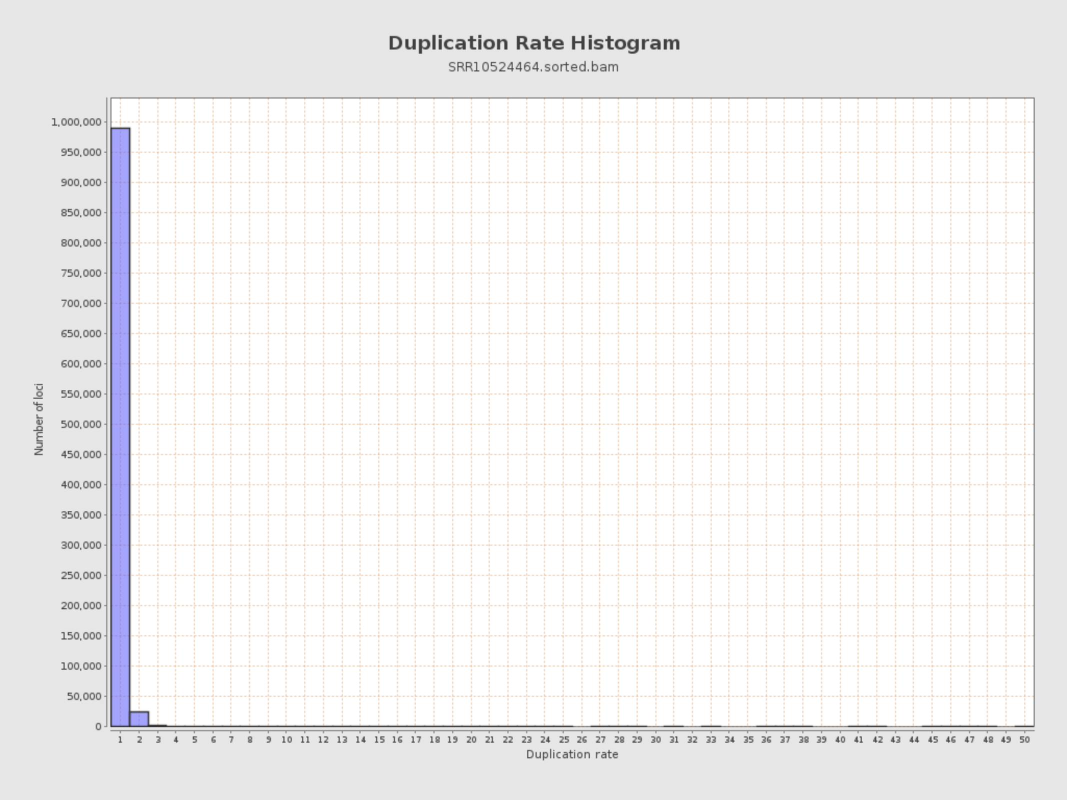
5. Results : Coverage Histogram (0-50X)



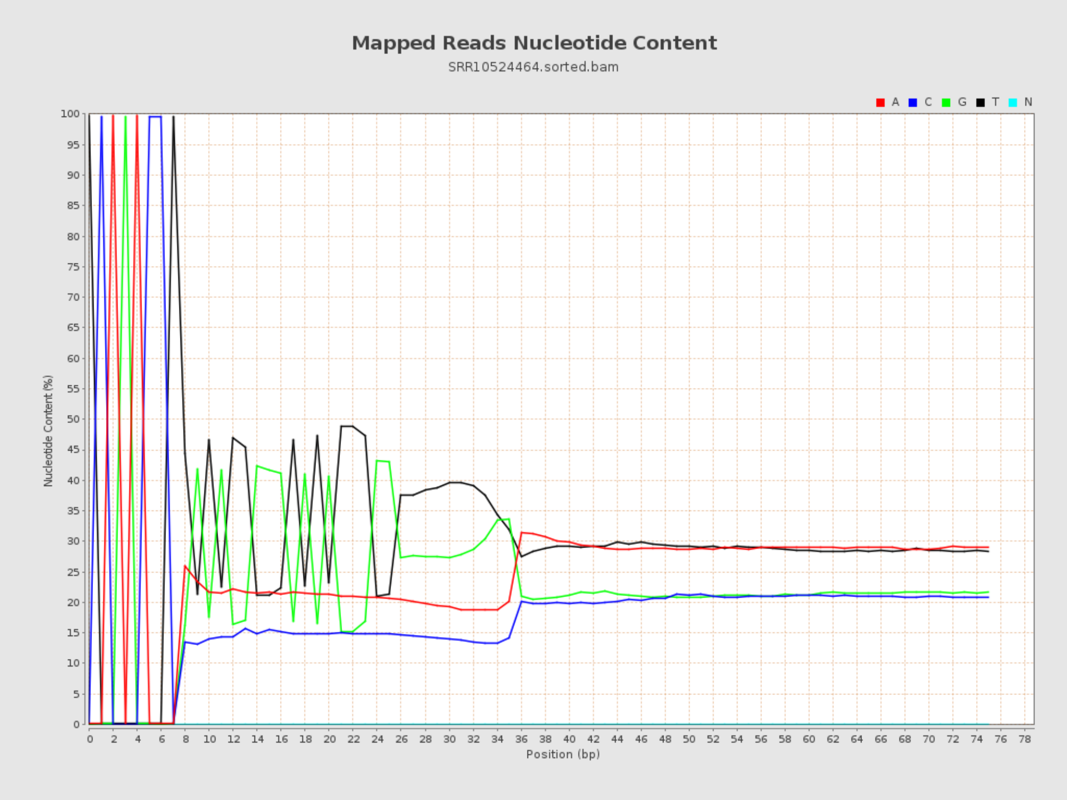
6. Results : Genome Fraction Coverage



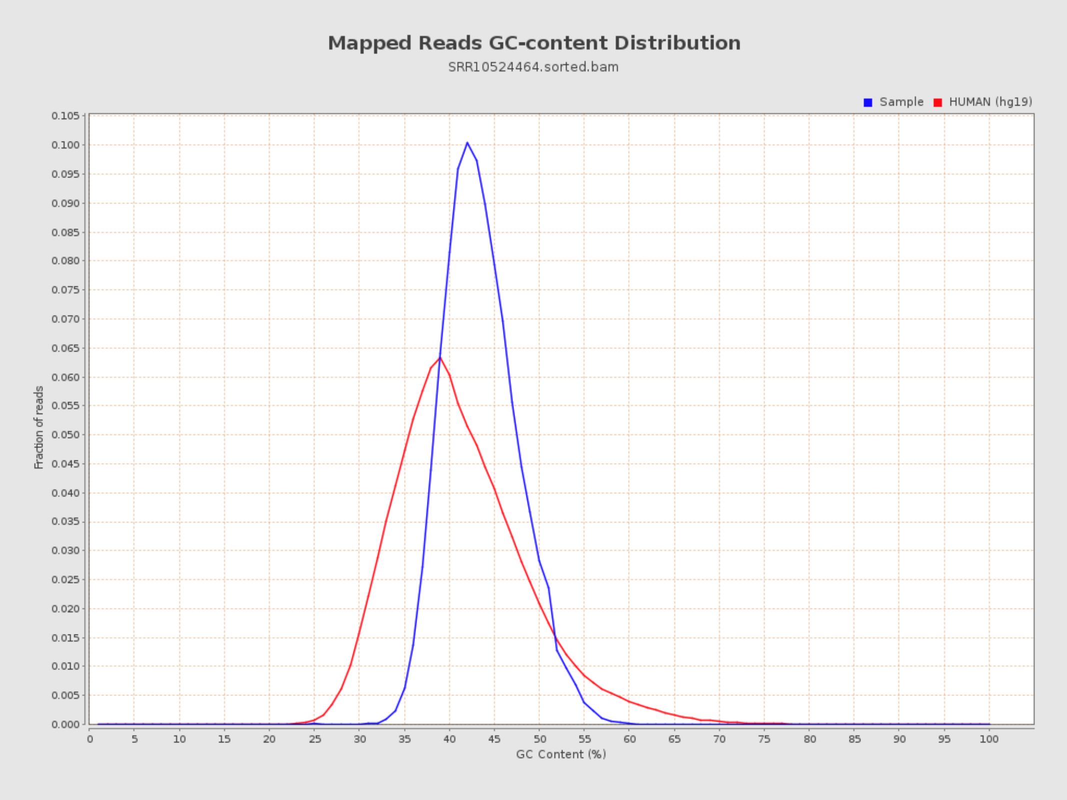
7. Results : Duplication Rate Histogram



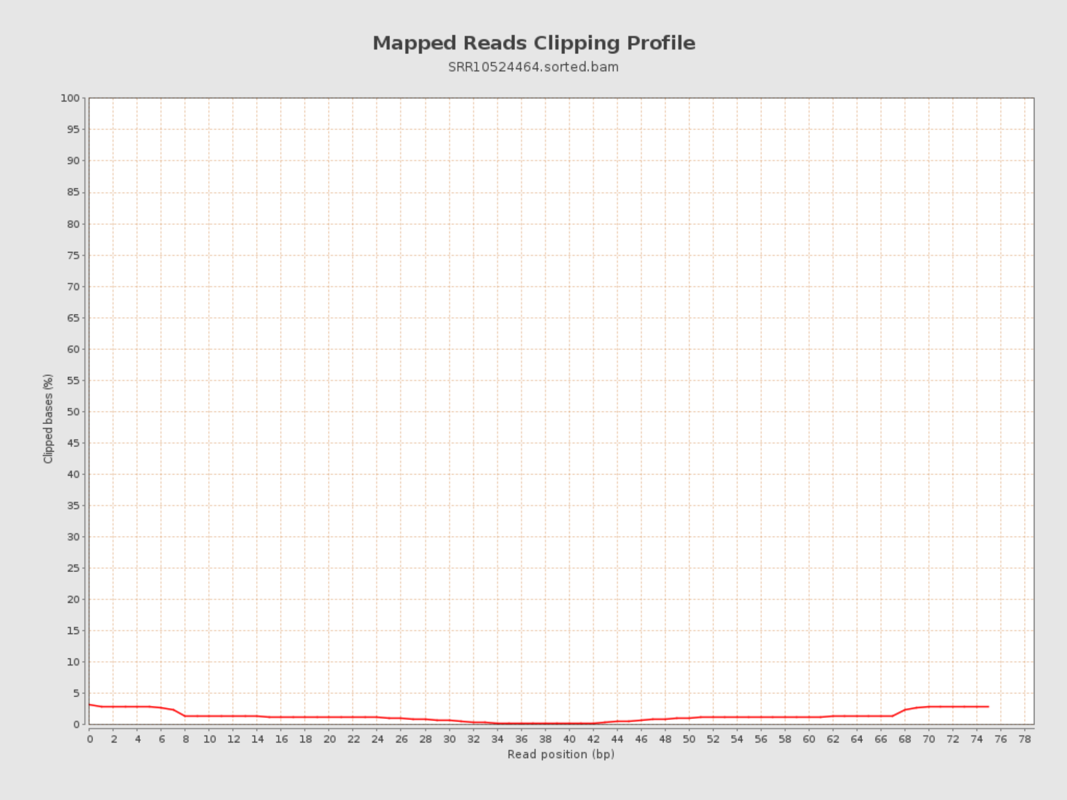
8. Results : Mapped Reads Nucleotide Content



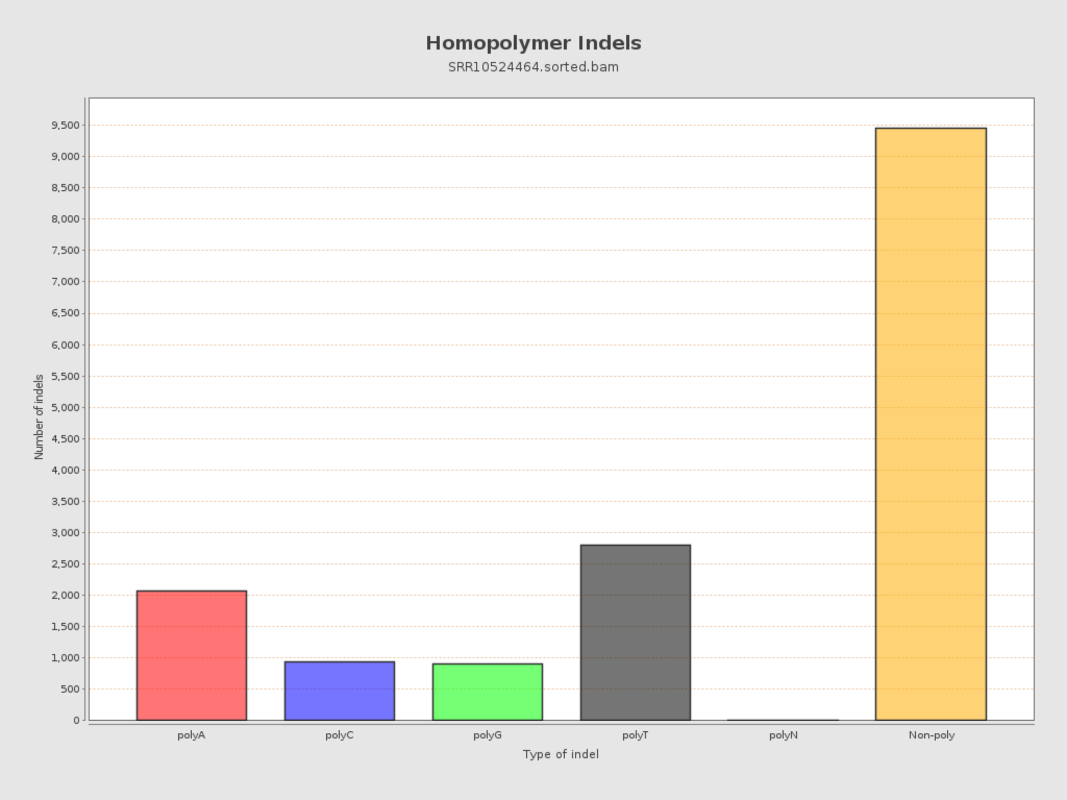
9. Results : Mapped Reads GC-content Distribution



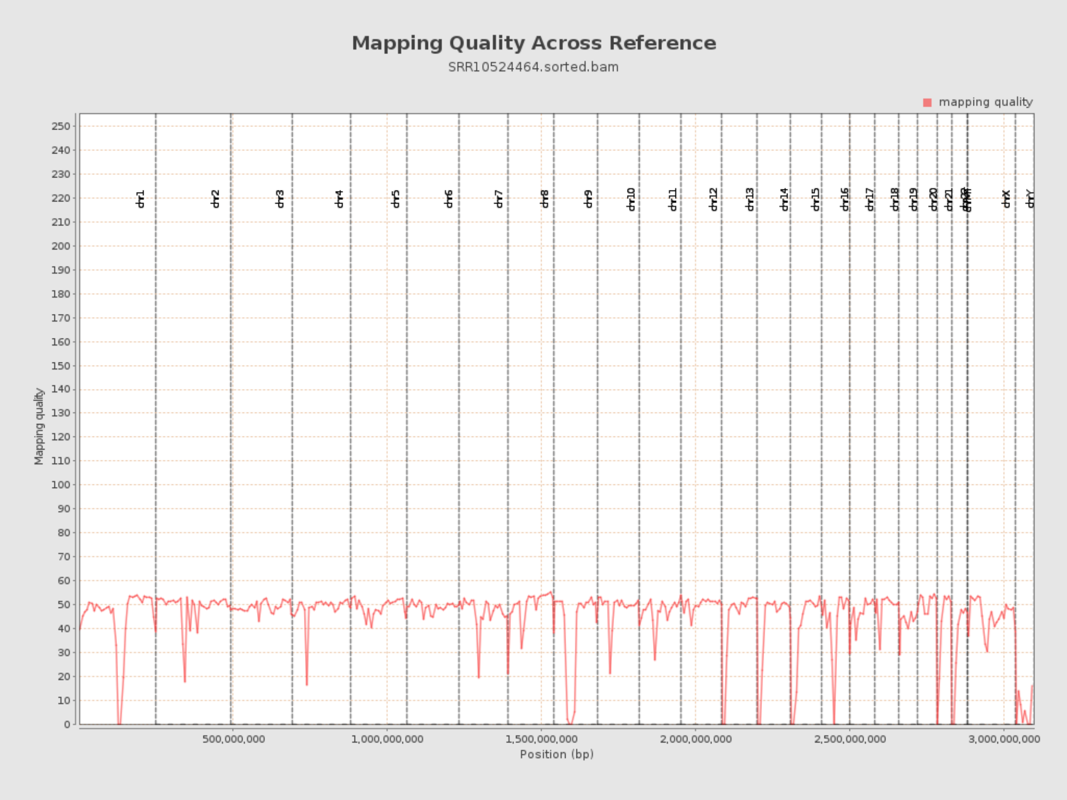
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram