Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 21:16:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524290.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_SRR10524290 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524290.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 21:16:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524290.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,153,462
Mapped reads	1,065,236 / 92.35%
Unmapped reads	88,226 / 7.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,003 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	31,451 / 2.73%
Duplication rate	2.12%
Clipped reads	1,066,094 / 92.43%

2.2. ACGT Content

Number/percentage of A's	15,899,886 / 25.37%
Number/percentage of C's	11,569,106 / 18.46%
Number/percentage of T's	20,246,502 / 32.31%
Number/percentage of G's	14,945,590 / 23.85%
Number/percentage of N's	8,441 / 0.01%
GC Percentage	42.31%

2.3. Coverage

Mean	0.0203

Standard Deviation	0.2193

2.4. Mapping Quality

Mean Mapping Quality	46.4

2.5. Mismatches and indels

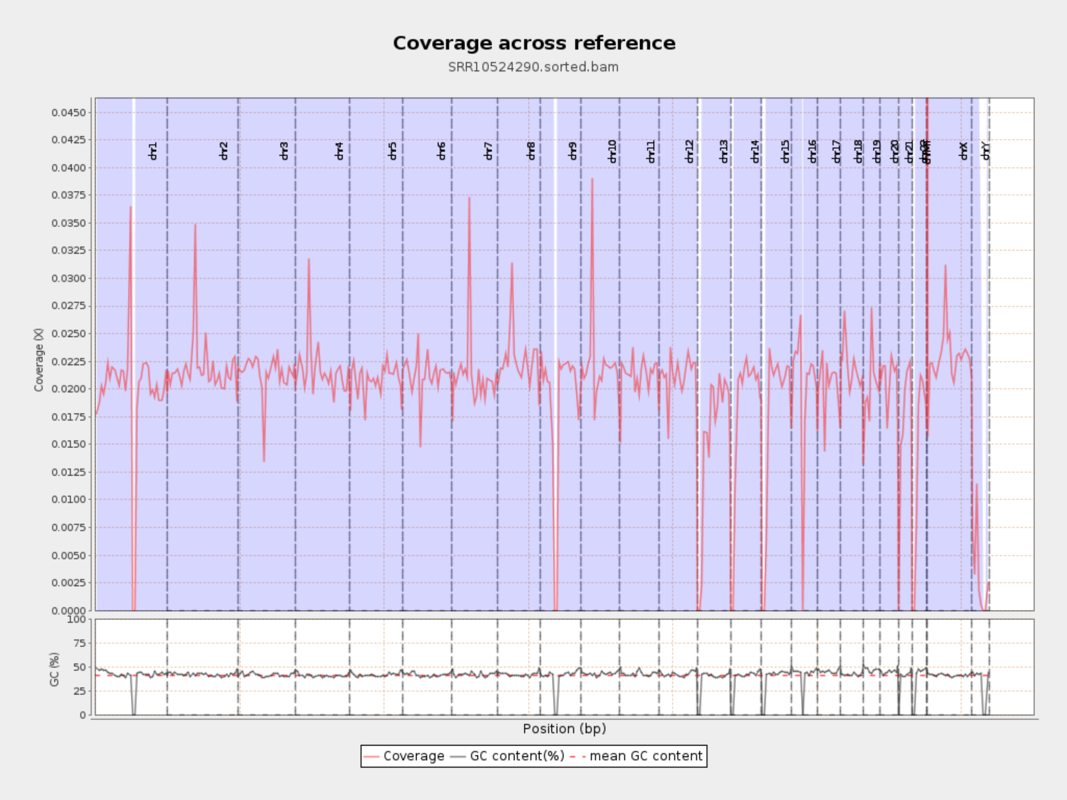
General error rate	0.51%
Mismatches	308,797
Insertions	4,317
Mapped reads with at least one insertion	0.4%
Deletions	12,255
Mapped reads with at least one deletion	1.14%
Homopolymer indels	43.98%

2.6. Chromosome stats

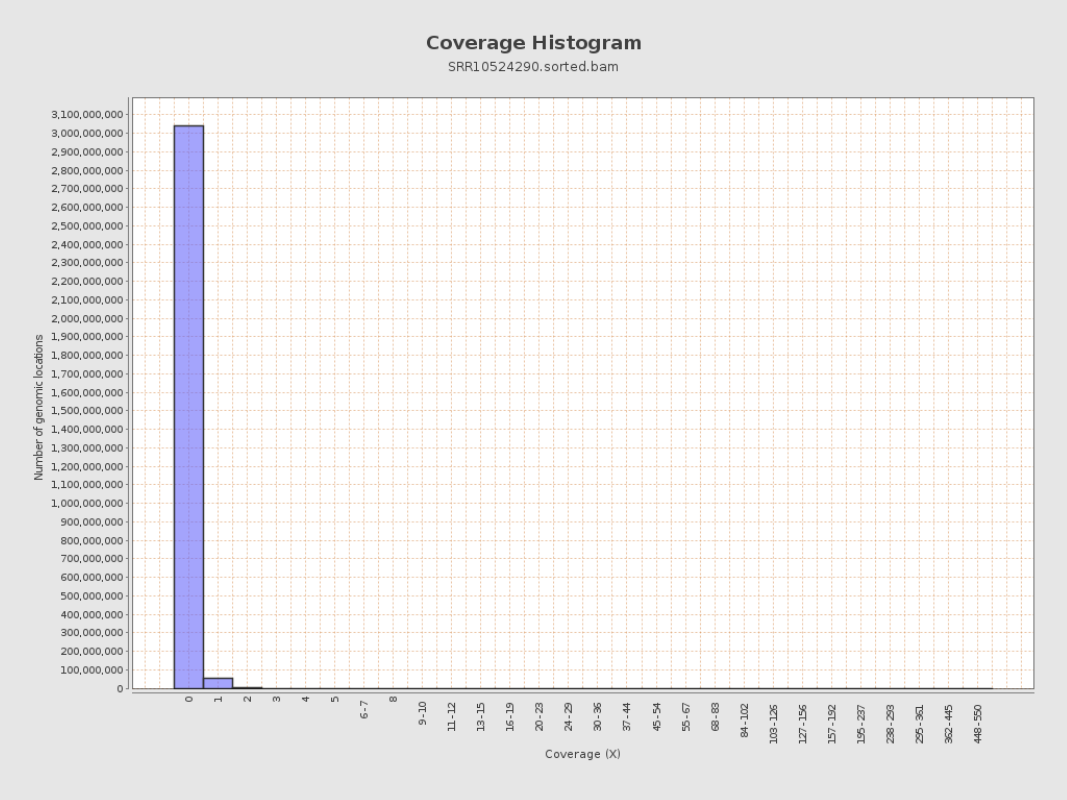
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4922108	0.0197	0.4078
chr2	243199373	5337791	0.0219	0.2291
chr3	198022430	4248451	0.0215	0.1545
chr4	191154276	4152342	0.0217	0.166
chr5	180915260	3799039	0.021	0.1537
chr6	171115067	3645657	0.0213	0.1631
chr7	159138663	3410764	0.0214	0.2885

chr8	146364022	3324863	0.0227	0.2116
chr9	141213431	2640225	0.0187	0.1943
chr10	135534747	3025169	0.0223	0.2105
chr11	135006516	2887124	0.0214	0.2042
chr12	133851895	2844646	0.0213	0.1578
chr13	115169878	1775856	0.0154	0.1312
chr14	107349540	1911681	0.0178	0.148
chr15	102531392	1788833	0.0174	0.1402
chr16	90354753	1791858	0.0198	0.1618
chr17	81195210	1652293	0.0203	0.1611
chr18	78077248	1718907	0.022	0.3729
chr19	59128983	1203676	0.0204	0.2944
chr20	63025520	1313140	0.0208	0.1544
chr21	48129895	830465	0.0173	0.1531
chr22	51304566	704019	0.0137	0.1231
chrMT	16571	9783	0.5904	0.8138
chrX	155270560	3562620	0.0229	0.1785
chrY	59373566	187790	0.0032	0.0947

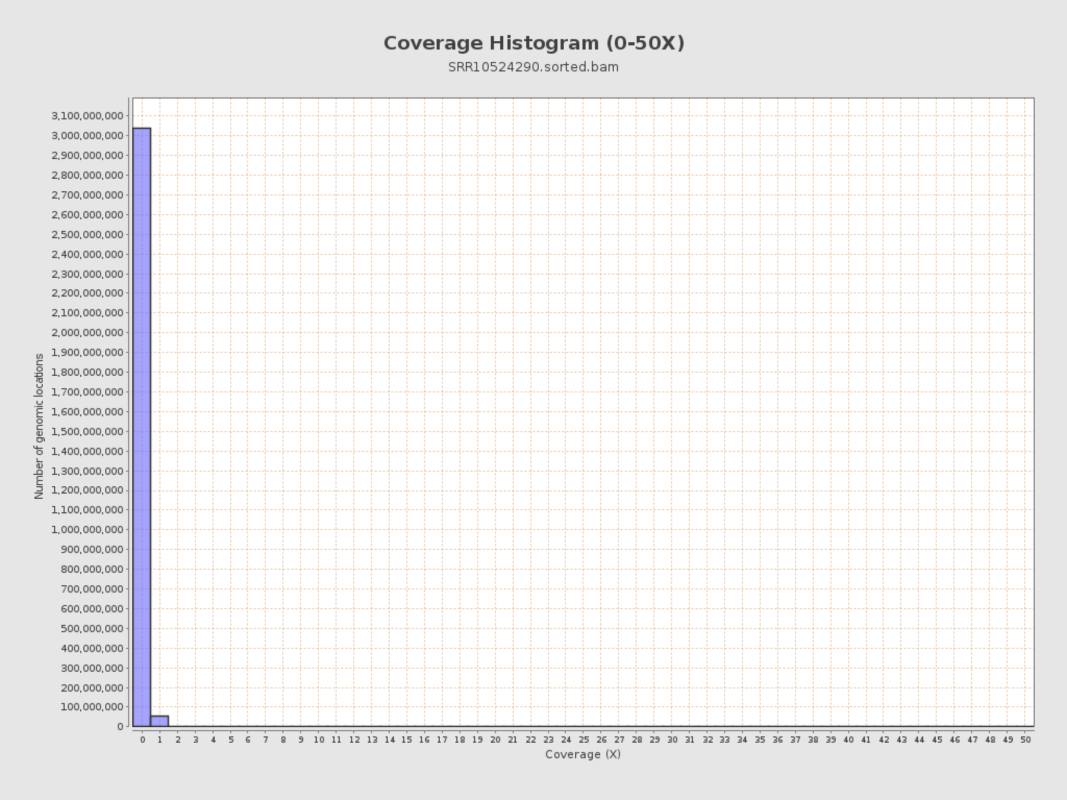
3. Results : Coverage across reference



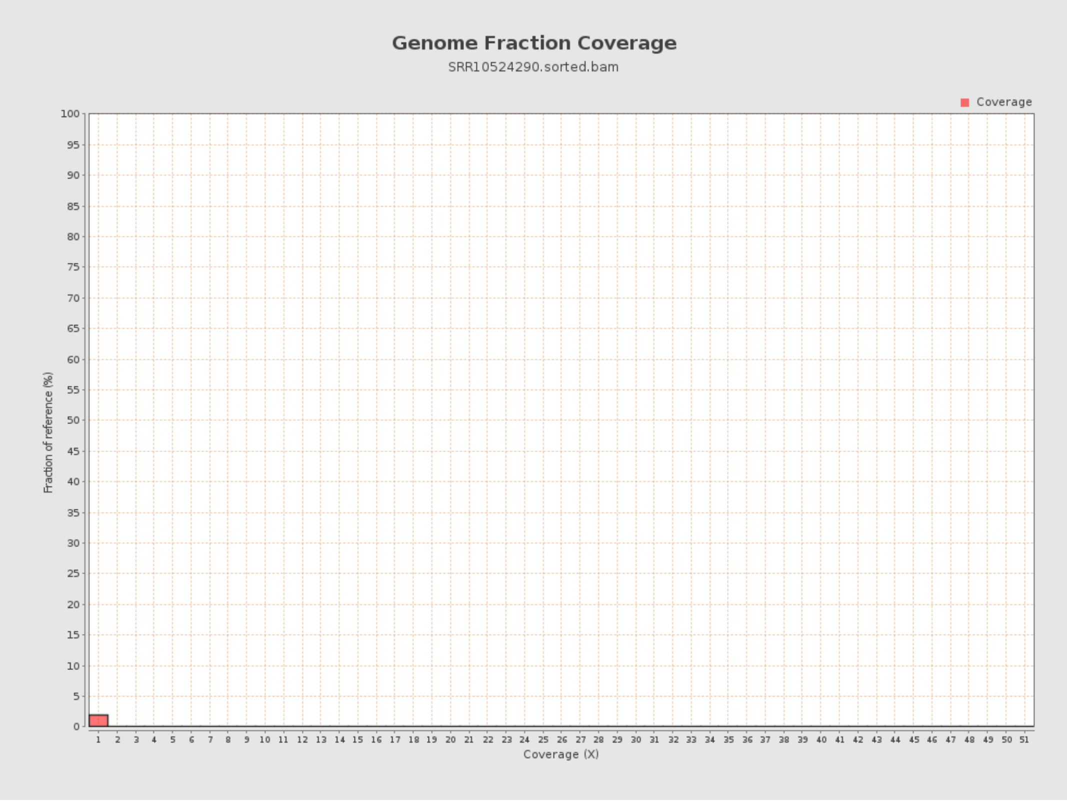
4. Results : Coverage Histogram



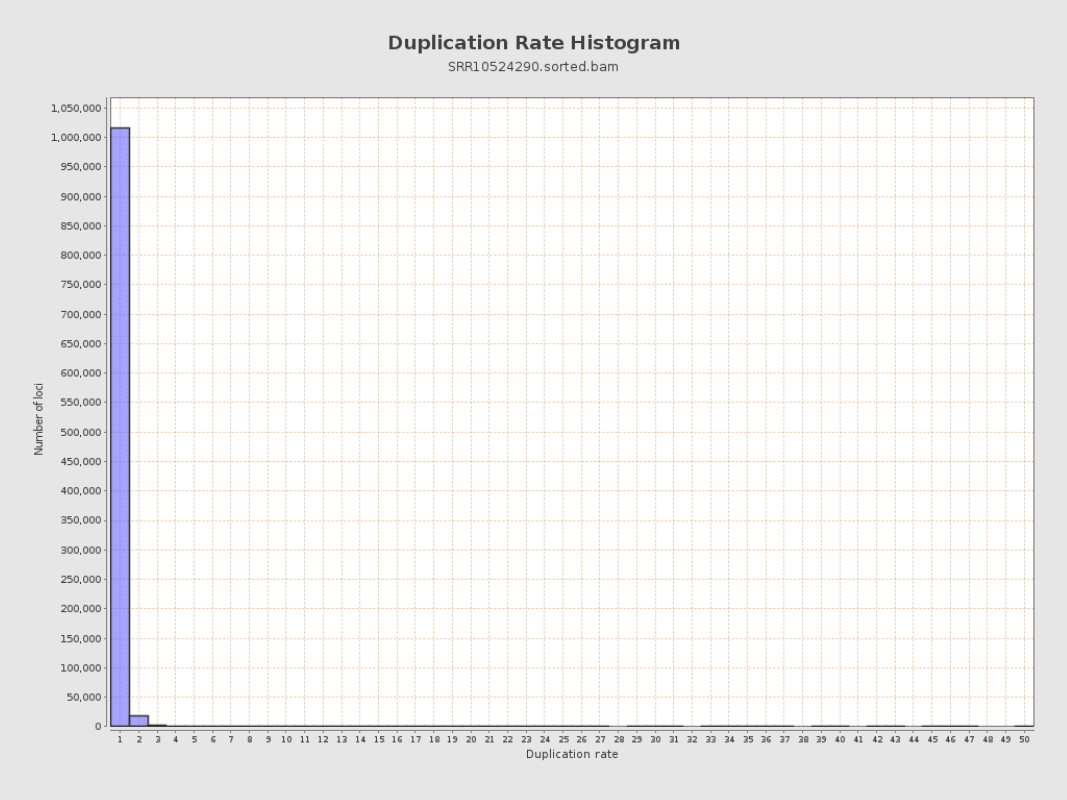
5. Results : Coverage Histogram (0-50X)



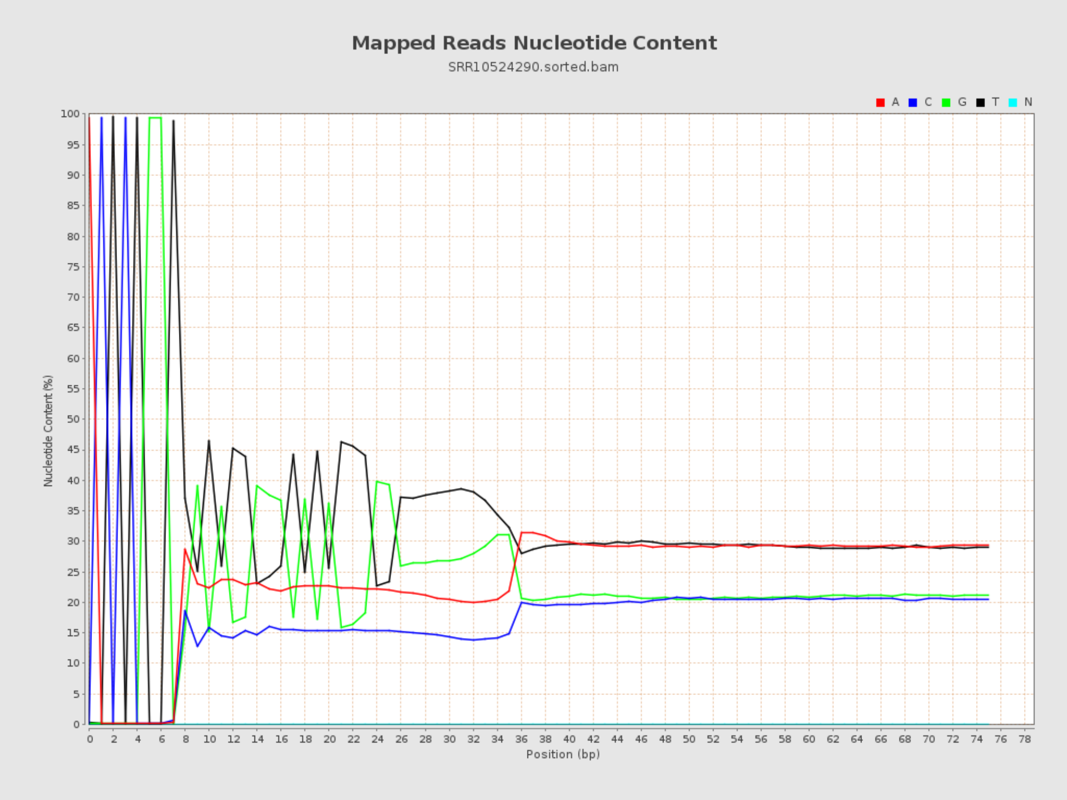
6. Results : Genome Fraction Coverage



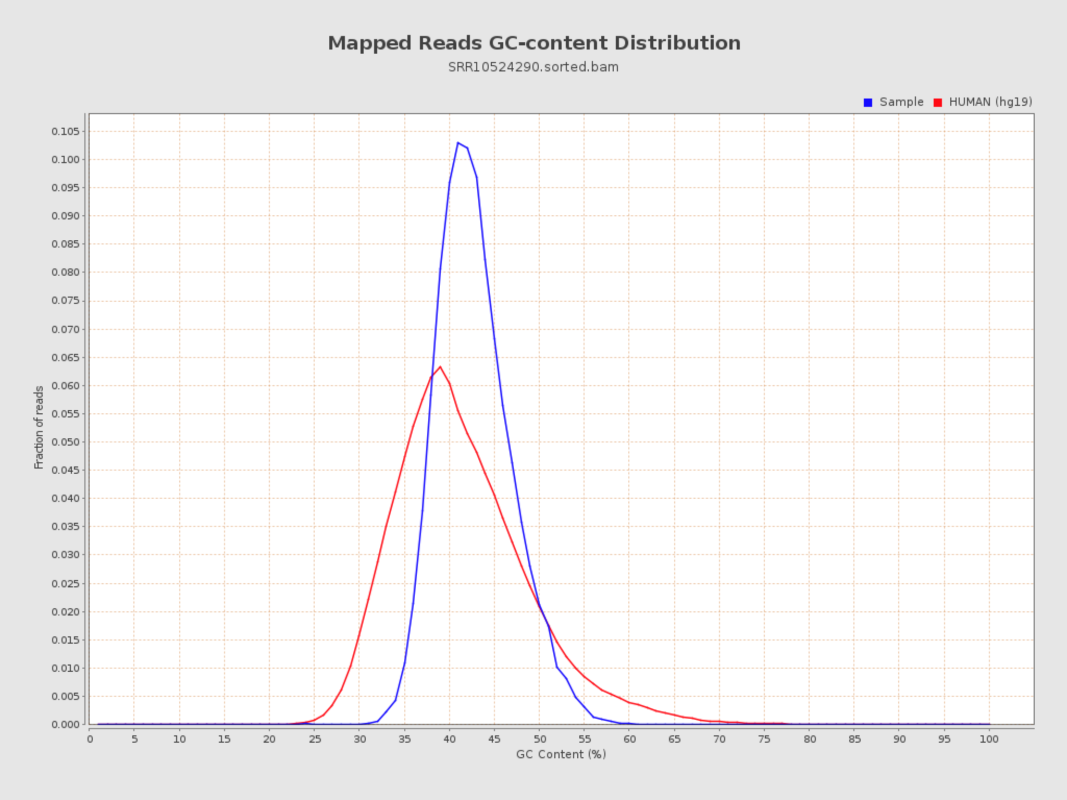
7. Results : Duplication Rate Histogram



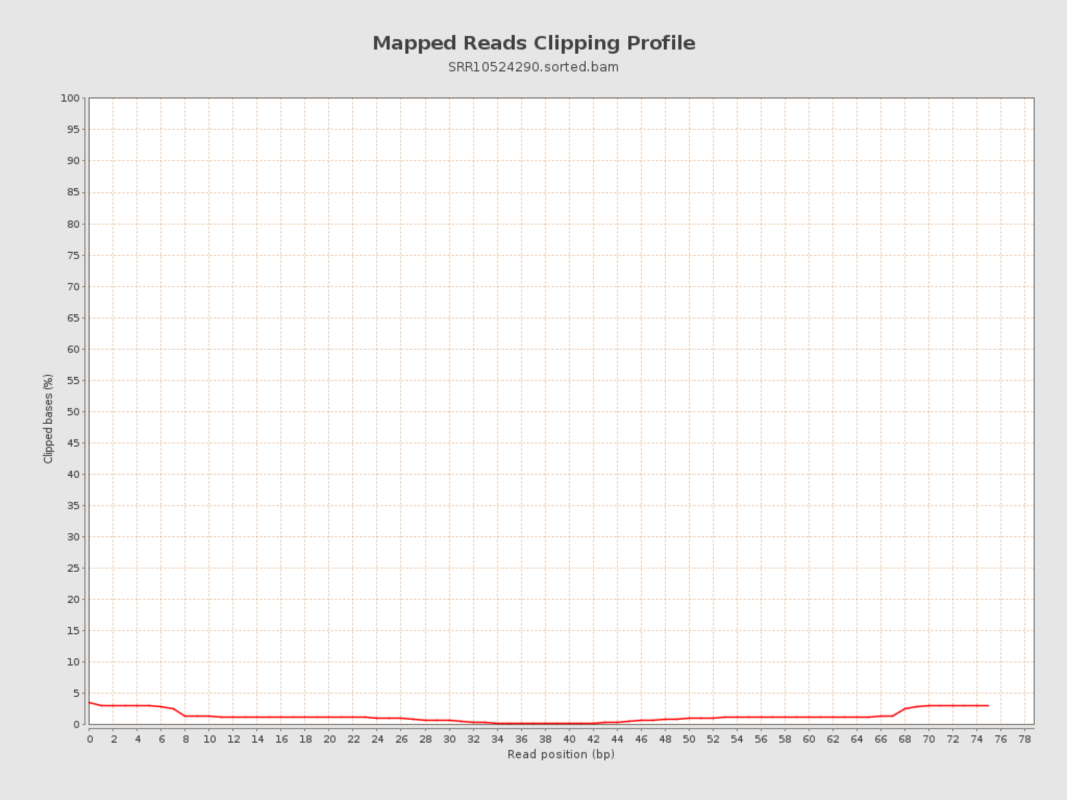
8. Results : Mapped Reads Nucleotide Content



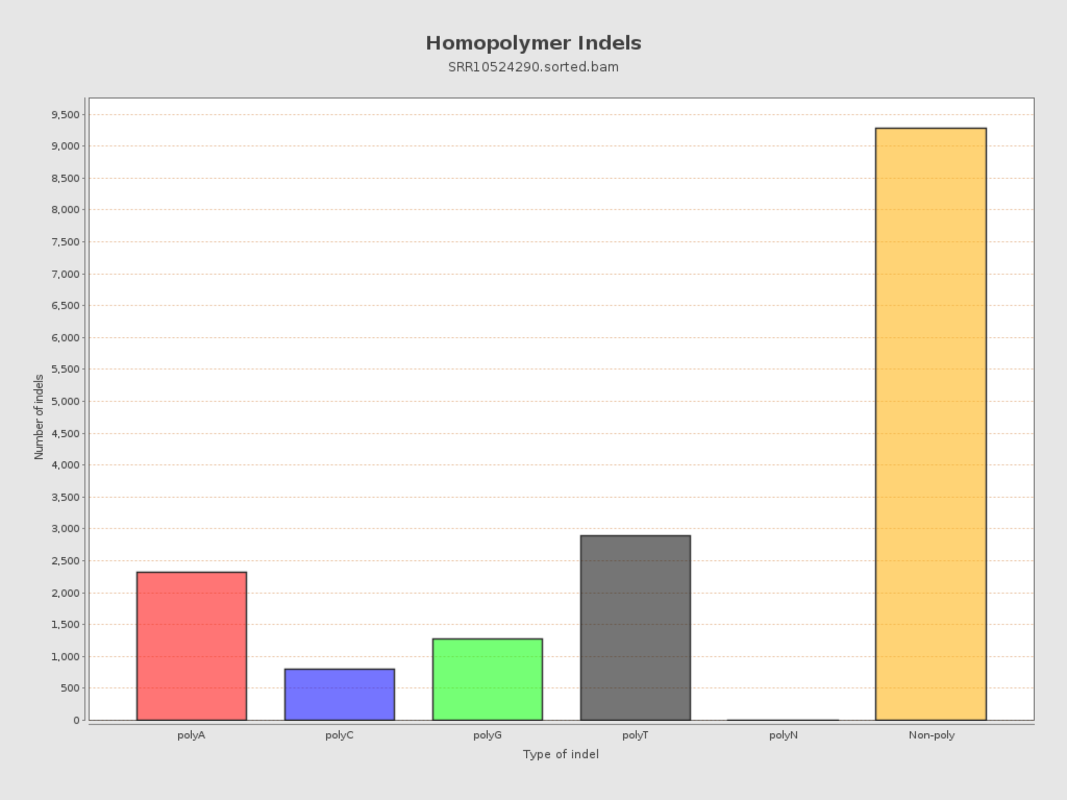
9. Results : Mapped Reads GC-content Distribution



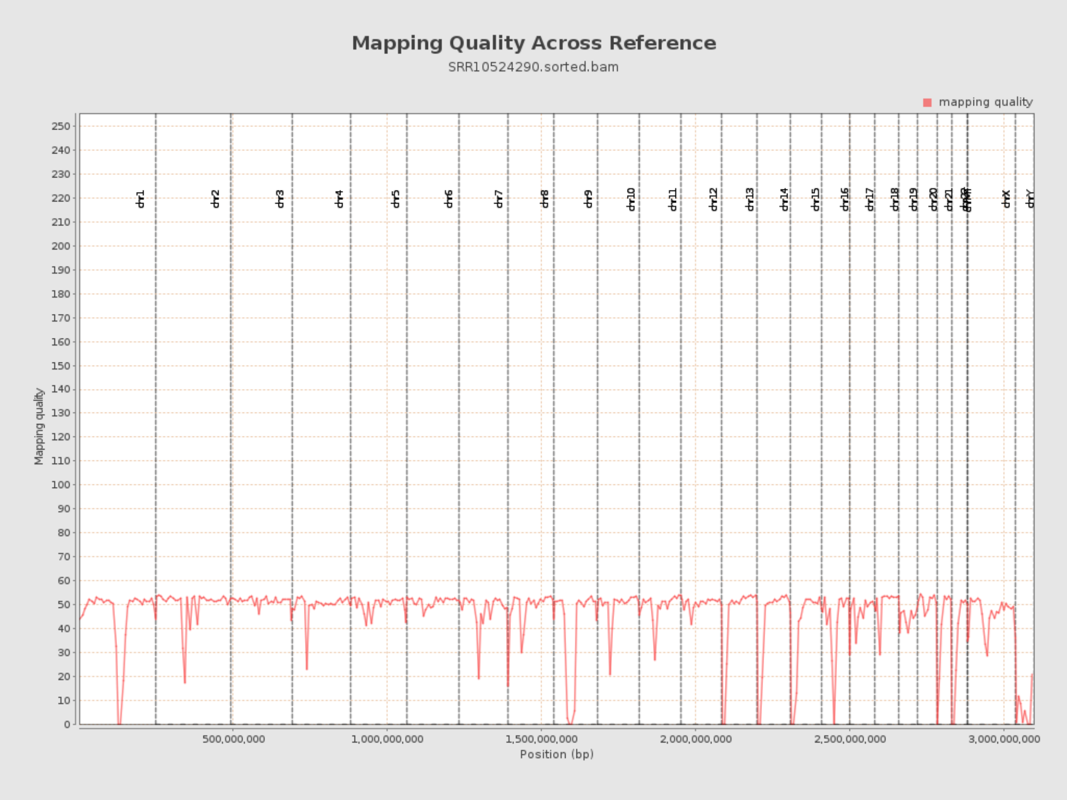
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram