Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 00:36:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524363.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_SRR10524363 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524363.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 00:36:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524363.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,118,833
Mapped reads	1,032,193 / 92.26%
Unmapped reads	86,640 / 7.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,174 / 0.46%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	48,645 / 4.35%
Duplication rate	3.73%
Clipped reads	1,033,359 / 92.36%

2.2. ACGT Content

Number/percentage of A's	16,301,224 / 26.47%
Number/percentage of C's	12,114,718 / 19.67%
Number/percentage of T's	18,170,452 / 29.5%
Number/percentage of G's	14,991,017 / 24.34%
Number/percentage of N's	9,045 / 0.01%
GC Percentage	44.01%

2.3. Coverage

Mean	0.0199

Standard Deviation	0.198

2.4. Mapping Quality

Mean Mapping Quality	45.7

2.5. Mismatches and indels

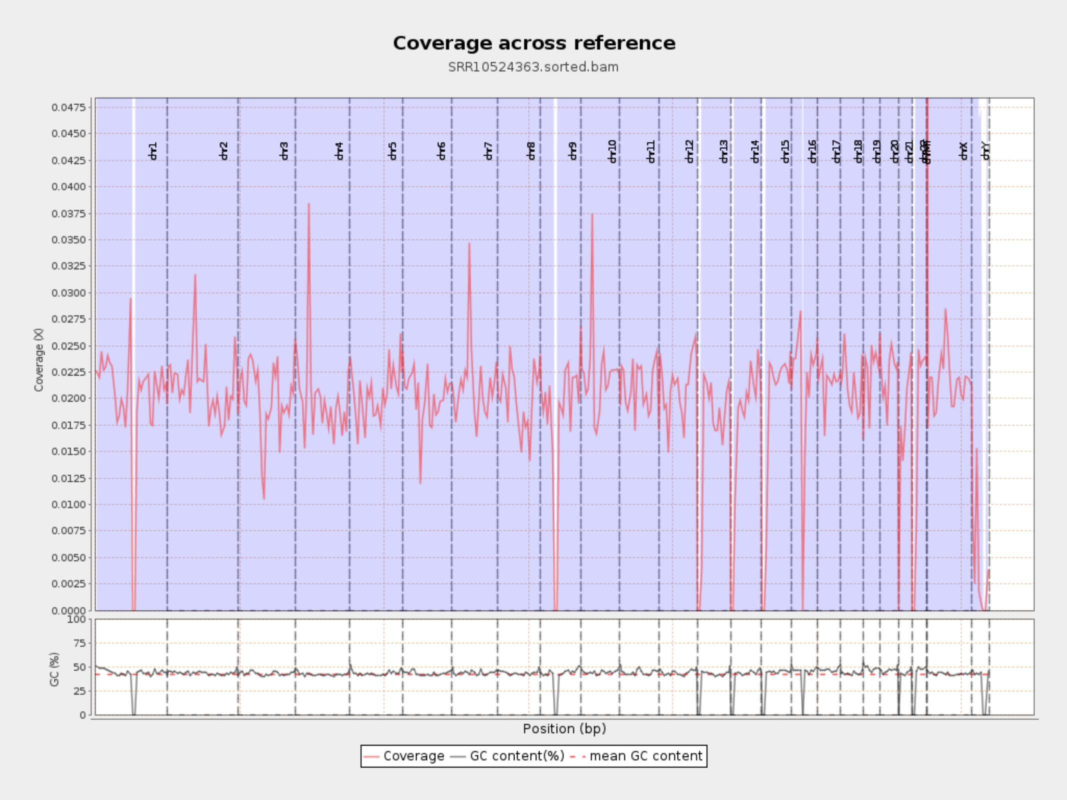
General error rate	0.52%
Mismatches	311,595
Insertions	5,287
Mapped reads with at least one insertion	0.51%
Deletions	10,847
Mapped reads with at least one deletion	1.04%
Homopolymer indels	41.54%

2.6. Chromosome stats

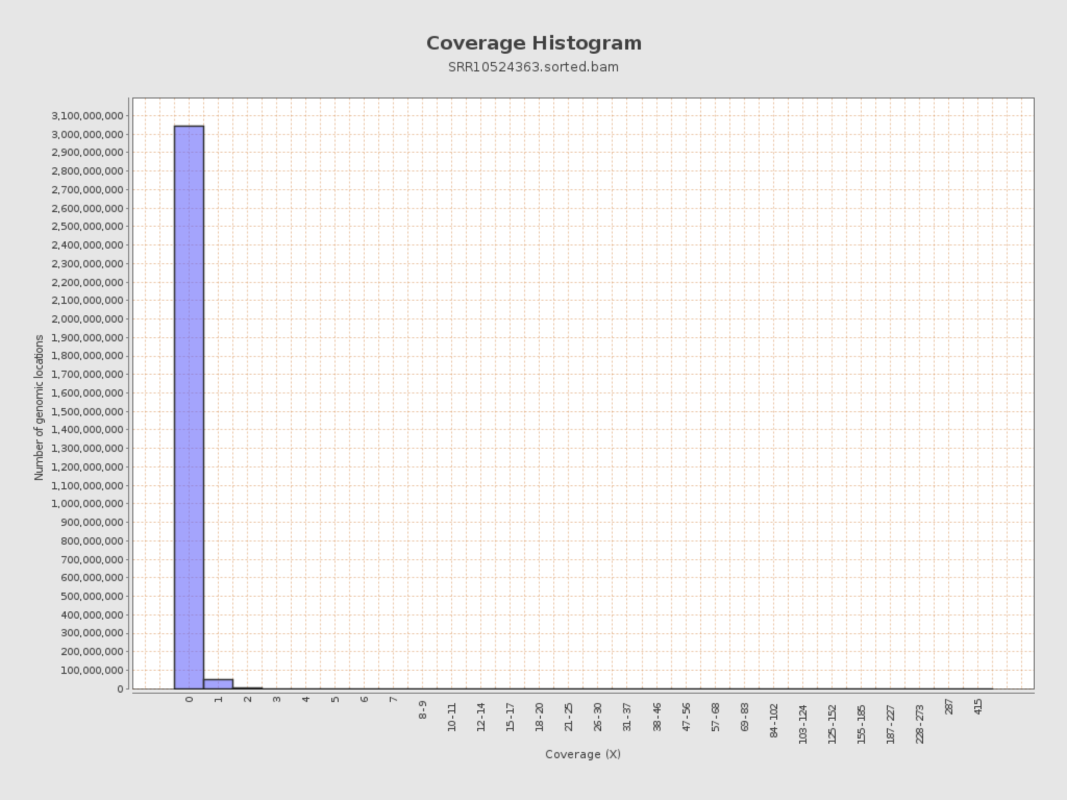
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4986479	0.02	0.2662
chr2	243199373	5186843	0.0213	0.2528
chr3	198022430	3959038	0.02	0.1561
chr4	191154276	3856274	0.0202	0.1806
chr5	180915260	3696416	0.0204	0.1588
chr6	171115067	3445192	0.0201	0.1618
chr7	159138663	3395082	0.0213	0.2563

chr8	146364022	2912434	0.0199	0.2057
chr9	141213431	2523421	0.0179	0.1723
chr10	135534747	3037212	0.0224	0.2168
chr11	135006516	2872927	0.0213	0.1889
chr12	133851895	2828550	0.0211	0.1633
chr13	115169878	1869058	0.0162	0.1415
chr14	107349540	1870643	0.0174	0.1502
chr15	102531392	1851935	0.0181	0.1488
chr16	90354753	1891737	0.0209	0.1714
chr17	81195210	1758387	0.0217	0.1723
chr18	78077248	1639964	0.021	0.3052
chr19	59128983	1338584	0.0226	0.2254
chr20	63025520	1395464	0.0221	0.1717
chr21	48129895	840494	0.0175	0.1697
chr22	51304566	844274	0.0165	0.146
chrMT	16571	5787	0.3492	0.6464
chrX	155270560	3364000	0.0217	0.1707
chrY	59373566	233701	0.0039	0.1423

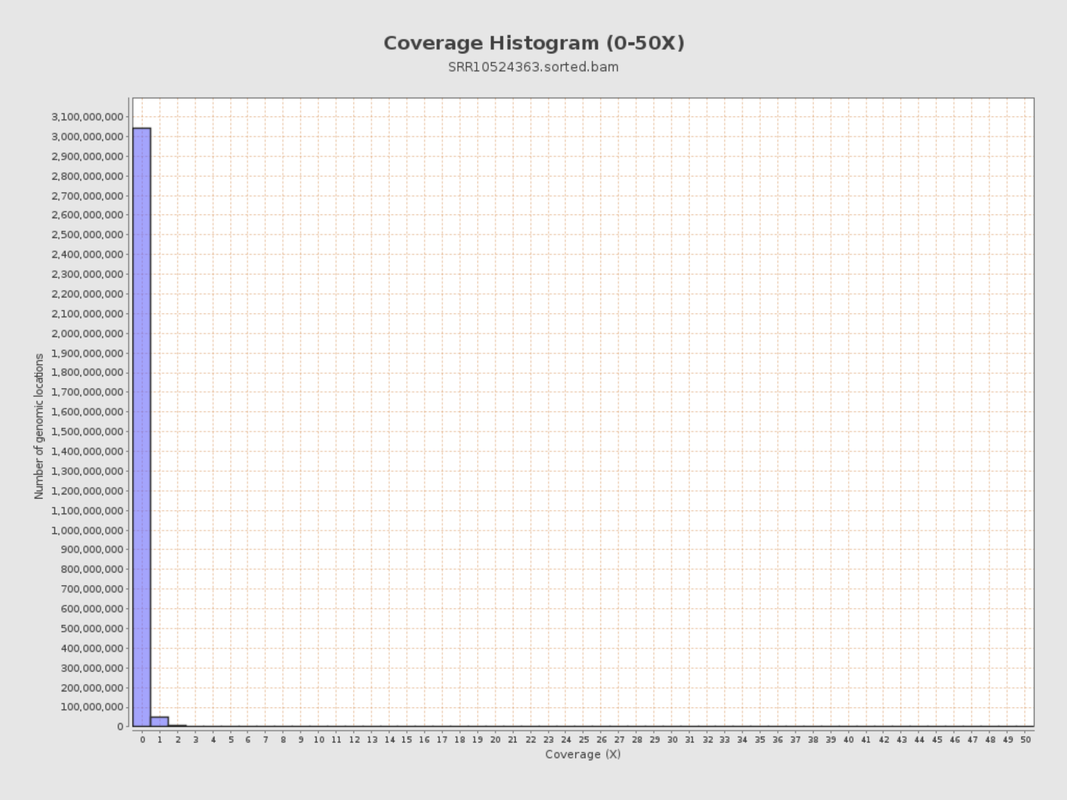
3. Results : Coverage across reference



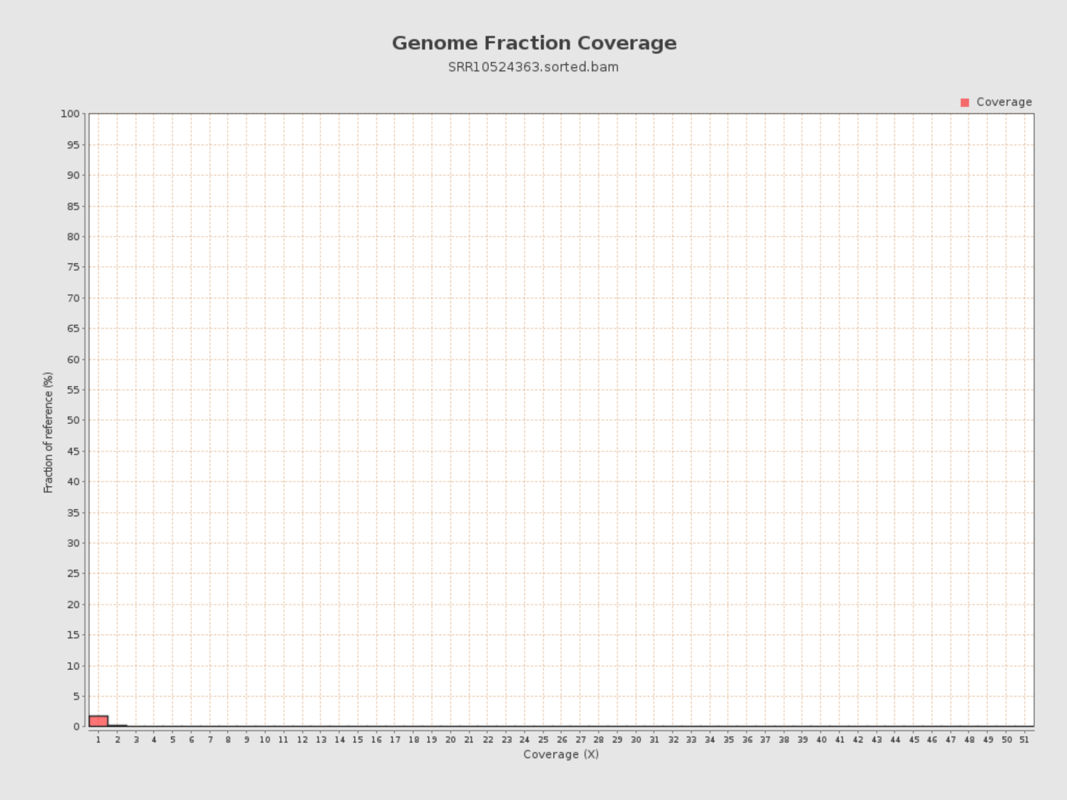
4. Results : Coverage Histogram



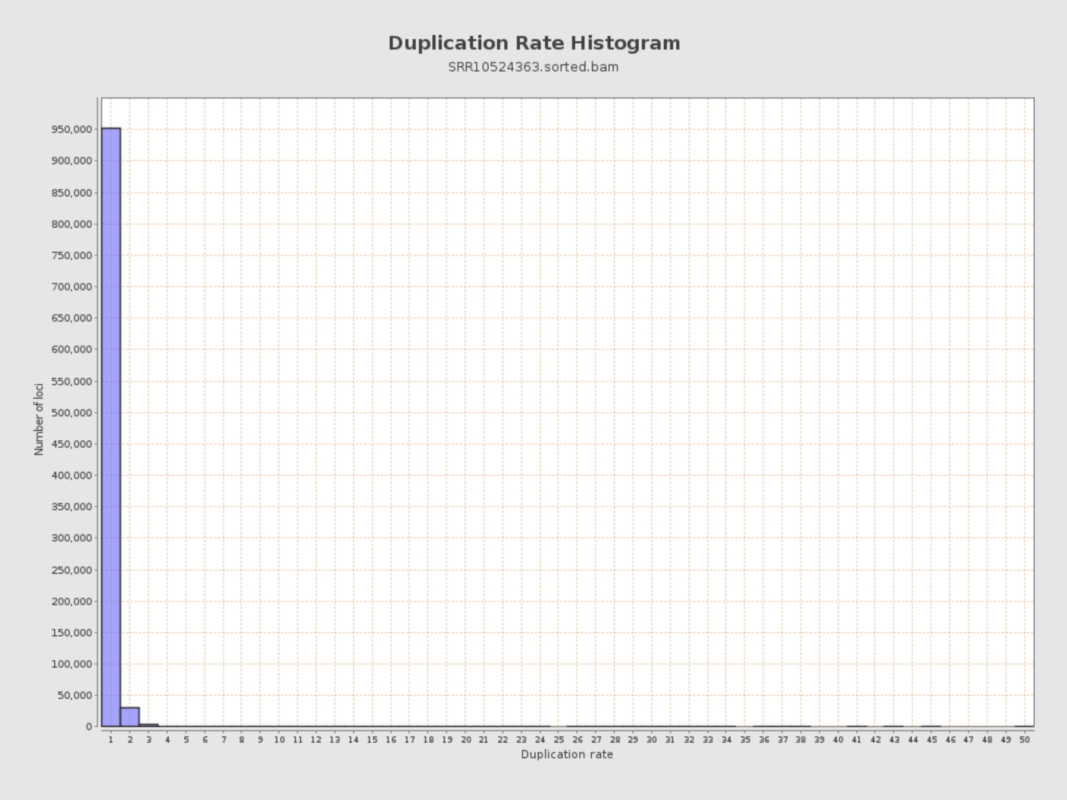
5. Results : Coverage Histogram (0-50X)



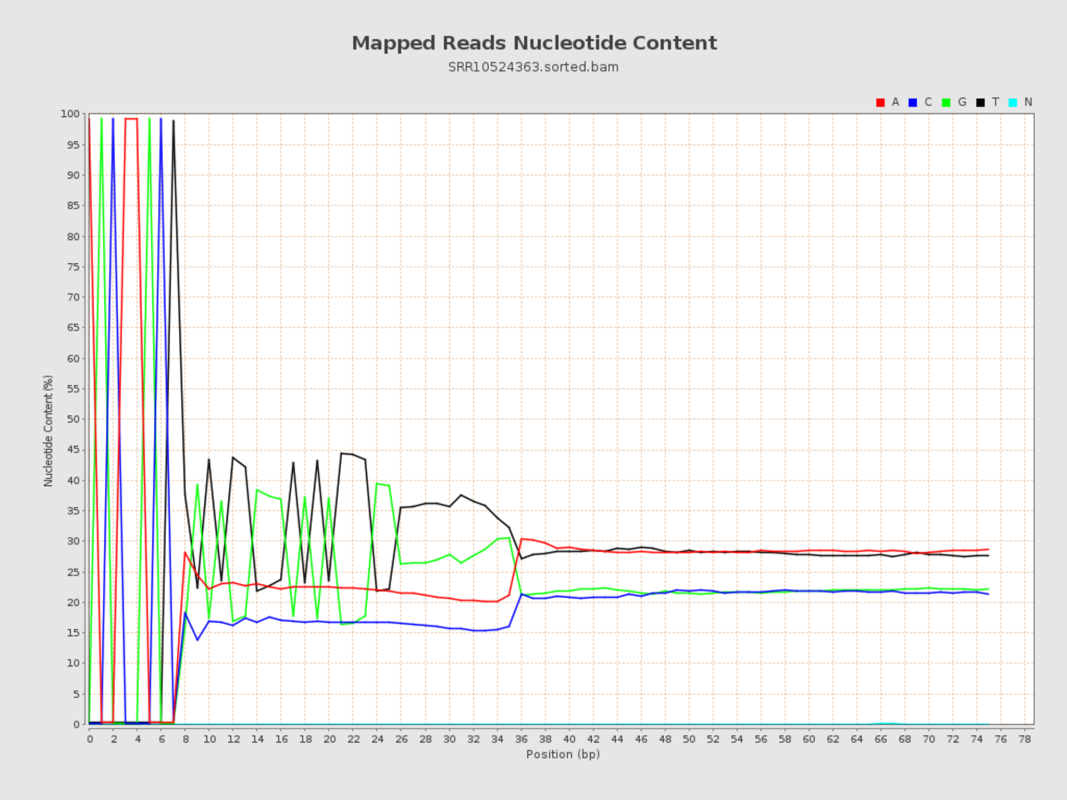
6. Results : Genome Fraction Coverage



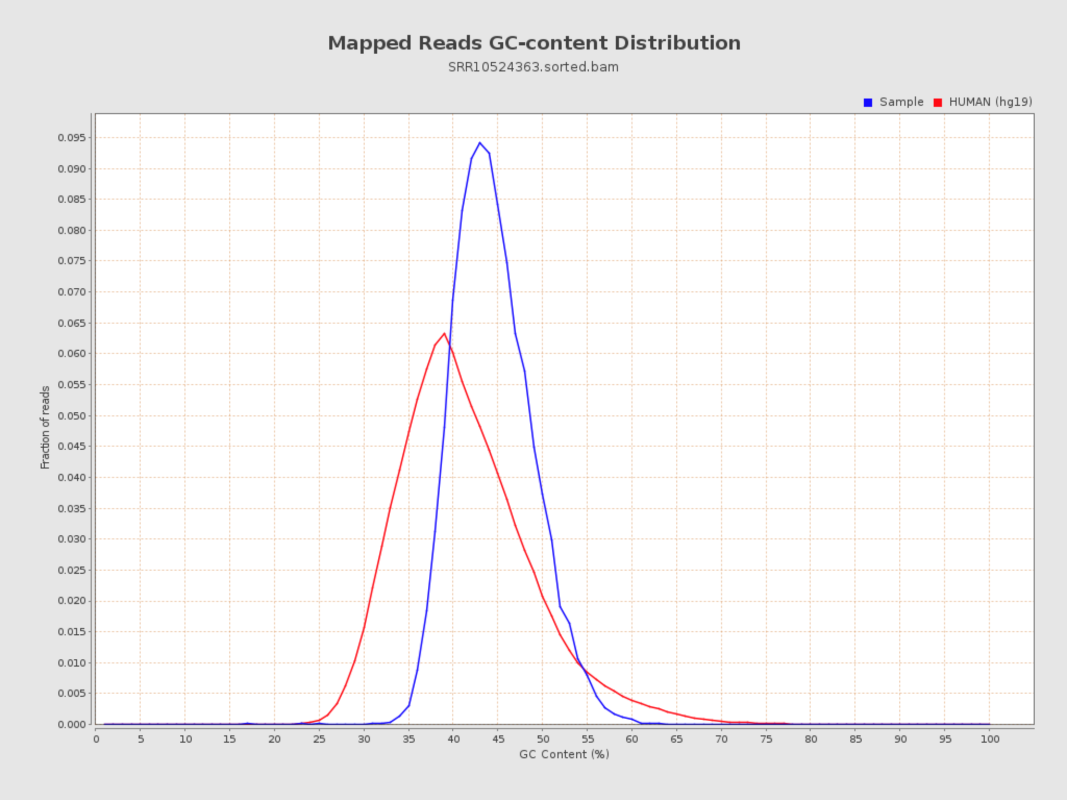
7. Results : Duplication Rate Histogram



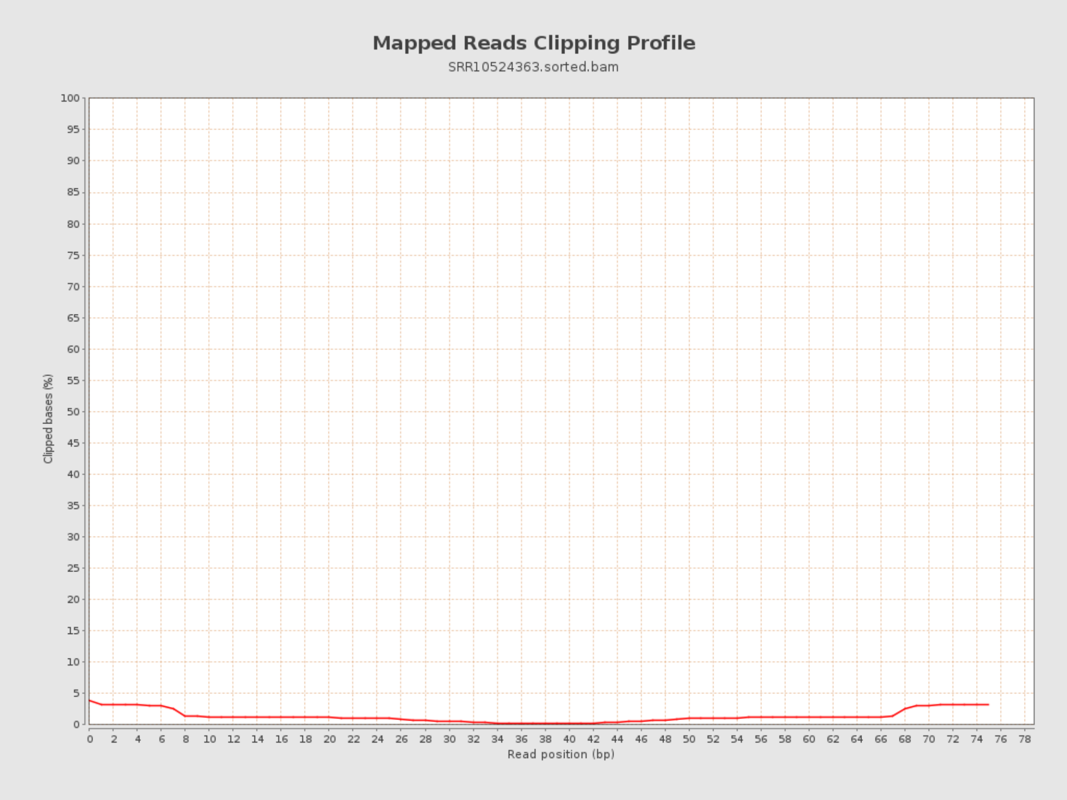
8. Results : Mapped Reads Nucleotide Content



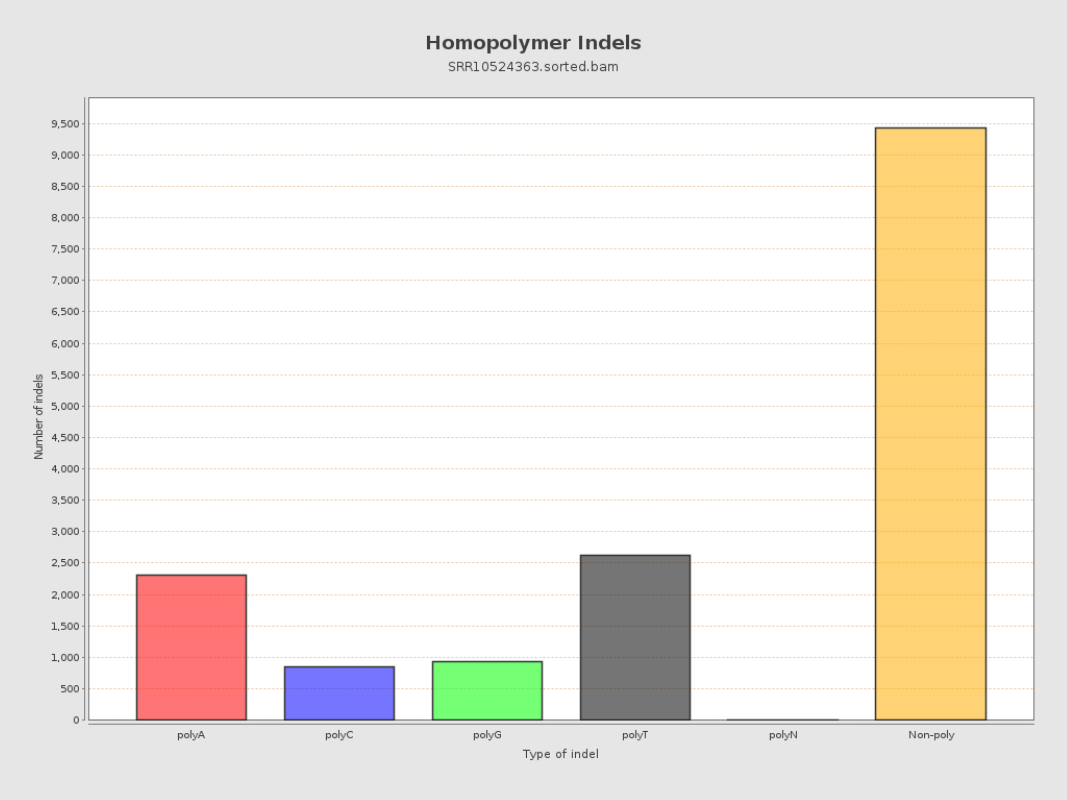
9. Results : Mapped Reads GC-content Distribution



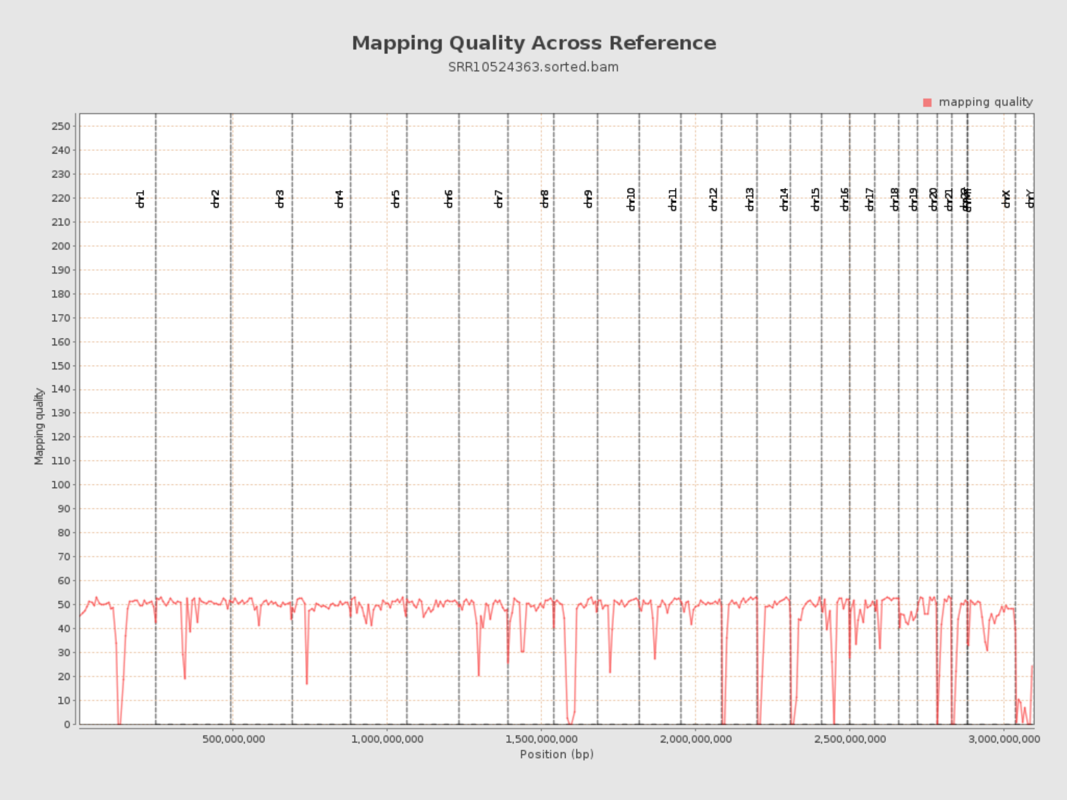
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram