Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 00:42:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524365.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_SRR10524365 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524365.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 00:42:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524365.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,257,991
Mapped reads	1,167,644 / 92.82%
Unmapped reads	90,347 / 7.18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,501 / 0.44%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	42,463 / 3.38%
Duplication rate	2.65%
Clipped reads	1,169,666 / 92.98%

2.2. ACGT Content

Number/percentage of A's	18,121,483 / 25.95%
Number/percentage of C's	14,153,645 / 20.27%
Number/percentage of T's	21,385,553 / 30.63%
Number/percentage of G's	16,149,566 / 23.13%
Number/percentage of N's	10,431 / 0.01%
GC Percentage	43.4%

2.3. Coverage

Mean	0.0226

Standard Deviation	0.2438

2.4. Mapping Quality

Mean Mapping Quality	45.64

2.5. Mismatches and indels

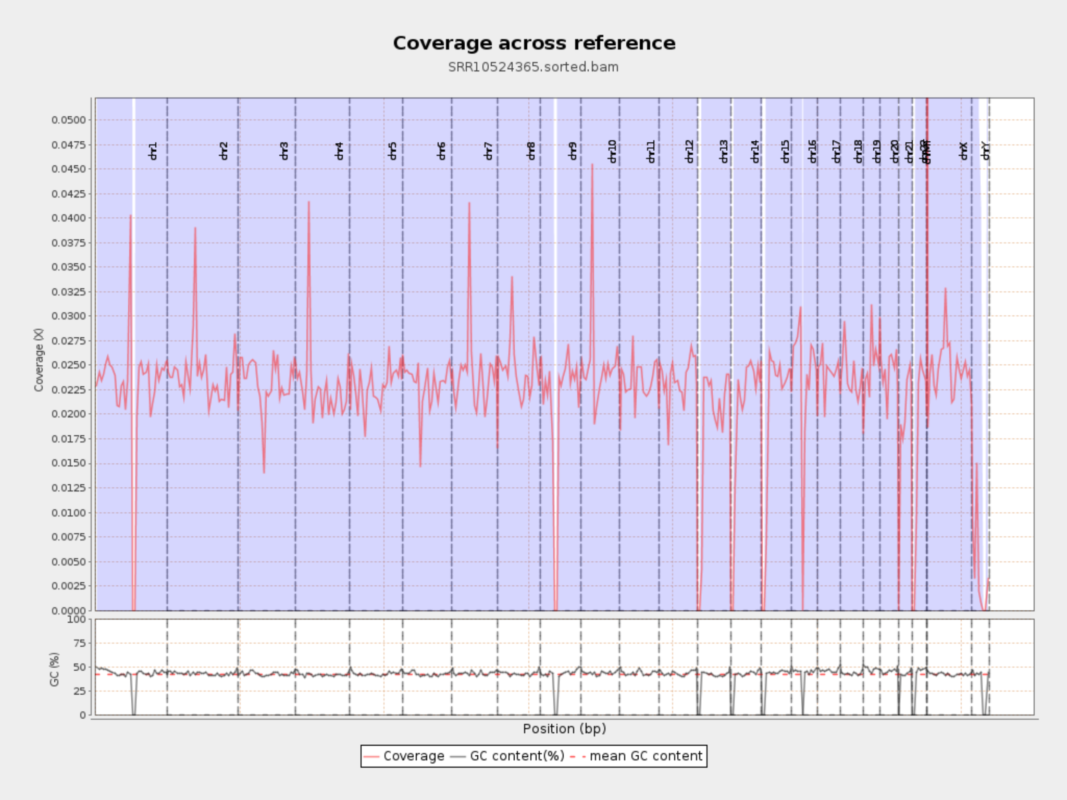
General error rate	0.52%
Mismatches	353,493
Insertions	5,560
Mapped reads with at least one insertion	0.47%
Deletions	12,961
Mapped reads with at least one deletion	1.1%
Homopolymer indels	42.52%

2.6. Chromosome stats

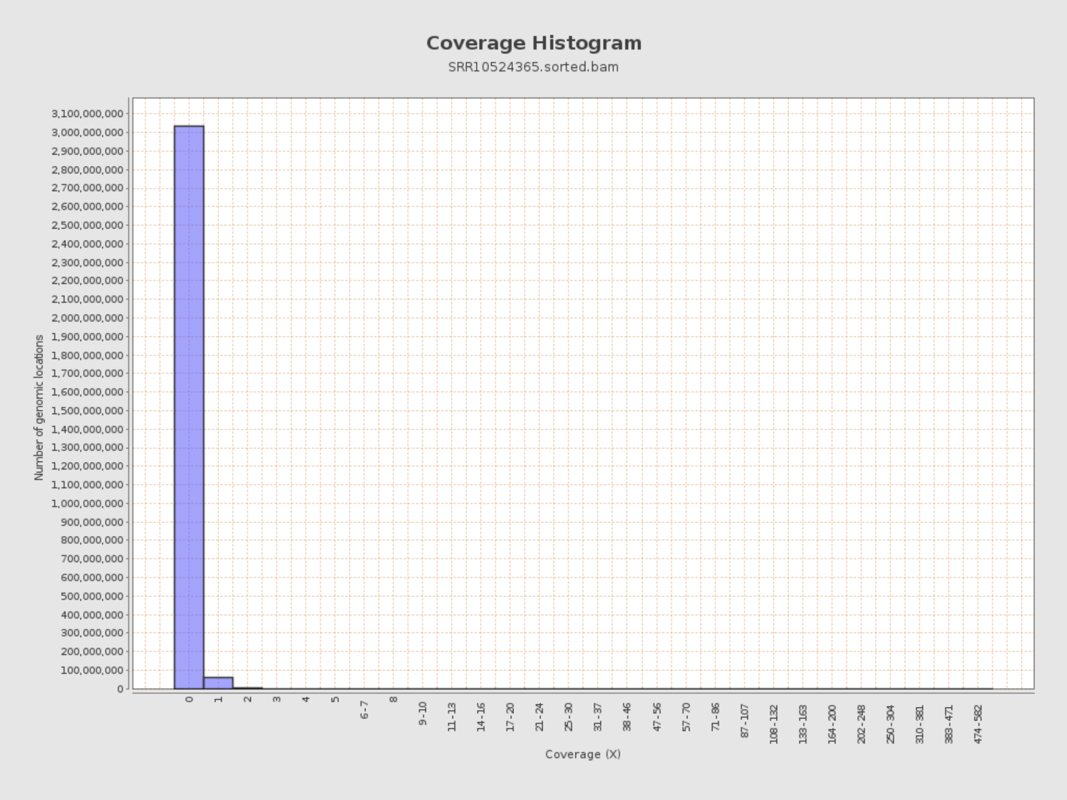
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5623113	0.0226	0.4589
chr2	243199373	5875588	0.0242	0.2886
chr3	198022430	4596887	0.0232	0.1645
chr4	191154276	4391624	0.023	0.189
chr5	180915260	4165466	0.023	0.1647
chr6	171115067	3949898	0.0231	0.1713
chr7	159138663	3876978	0.0244	0.3273

chr8	146364022	3610129	0.0247	0.2248
chr9	141213431	2933305	0.0208	0.1965
chr10	135534747	3411642	0.0252	0.2405
chr11	135006516	3176163	0.0235	0.2093
chr12	133851895	3160140	0.0236	0.1682
chr13	115169878	2107427	0.0183	0.1461
chr14	107349540	2117061	0.0197	0.1617
chr15	102531392	2019257	0.0197	0.1512
chr16	90354753	2097647	0.0232	0.1781
chr17	81195210	1973789	0.0243	0.1775
chr18	78077248	1866958	0.0239	0.3938
chr19	59128983	1485862	0.0251	0.3145
chr20	63025520	1537979	0.0244	0.1738
chr21	48129895	921981	0.0192	0.1778
chr22	51304566	859167	0.0167	0.1407
chrMT	16571	10246	0.6183	0.9447
chrX	155270560	3837521	0.0247	0.1849
chrY	59373566	235486	0.004	0.128

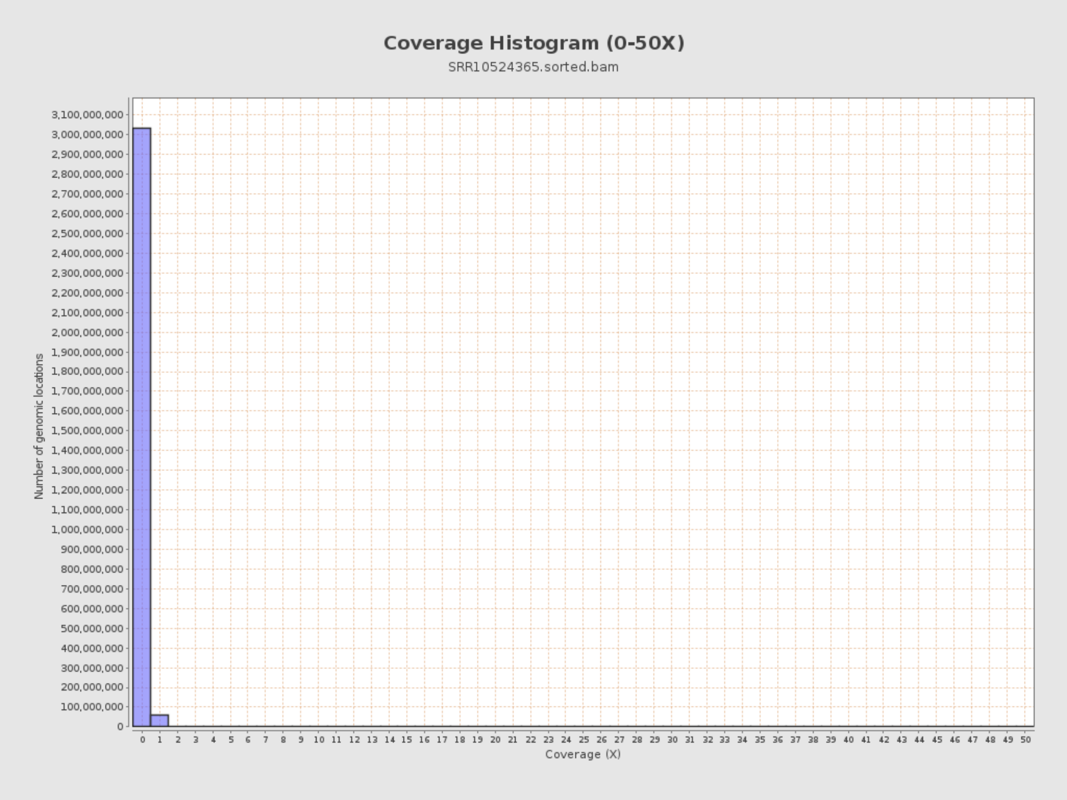
3. Results : Coverage across reference



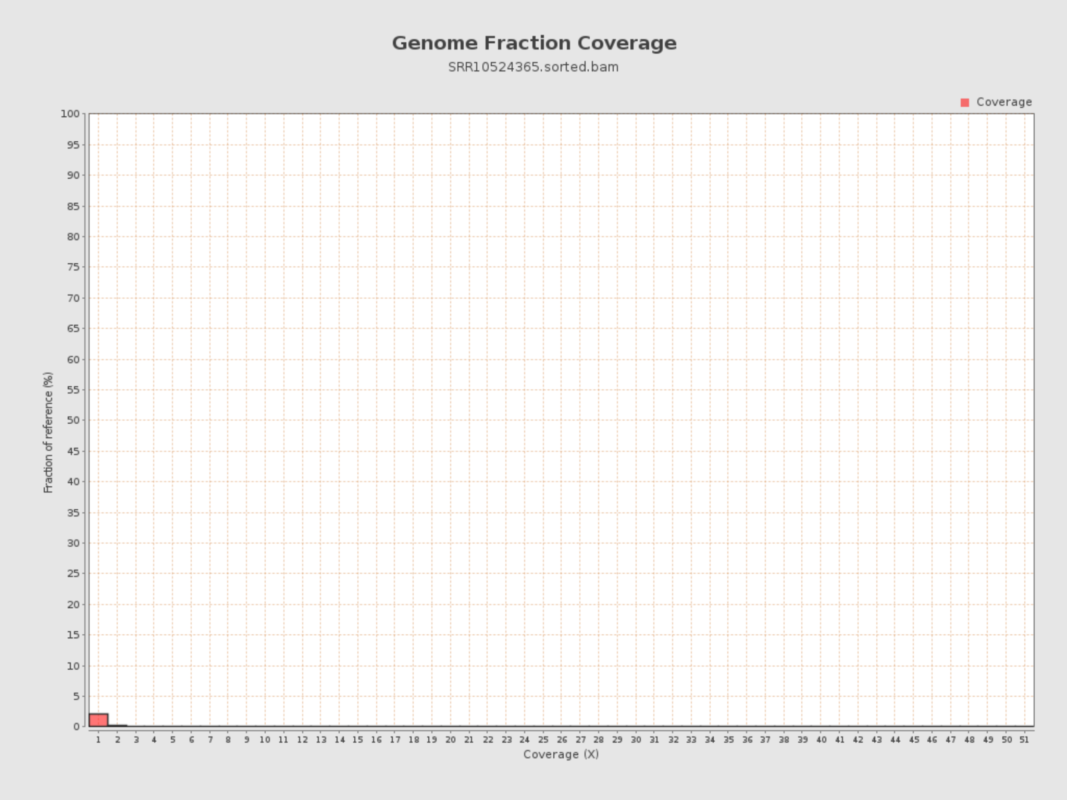
4. Results : Coverage Histogram



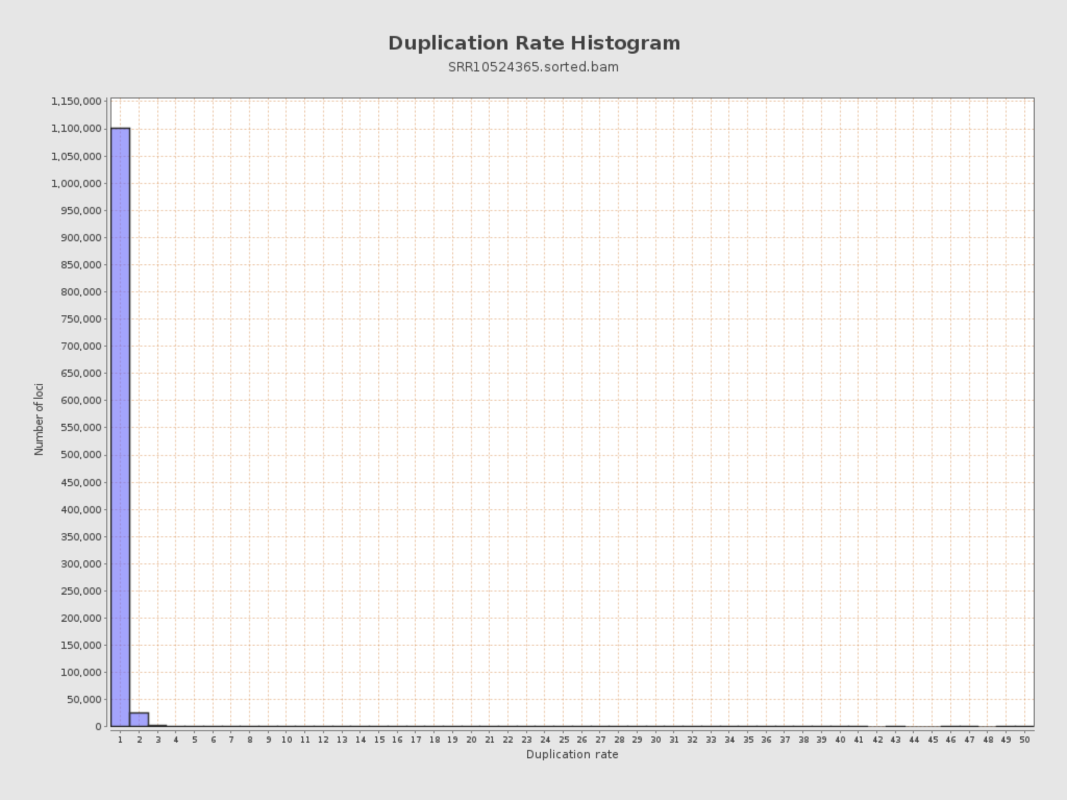
5. Results : Coverage Histogram (0-50X)



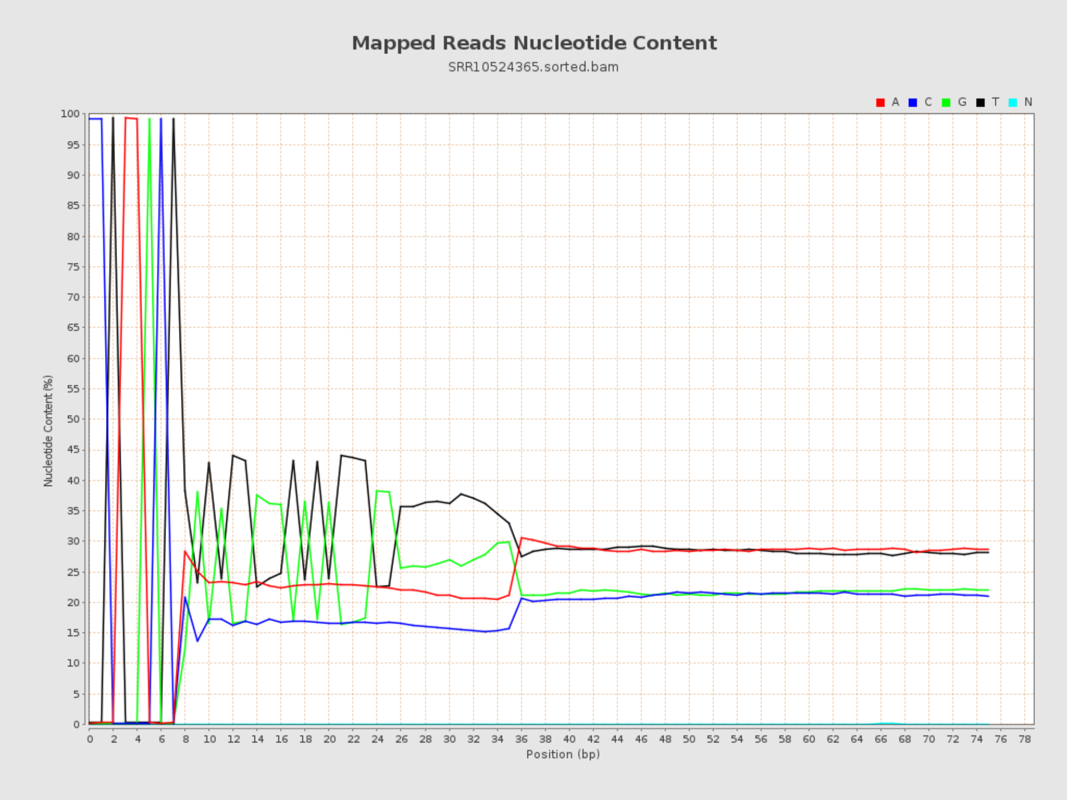
6. Results : Genome Fraction Coverage



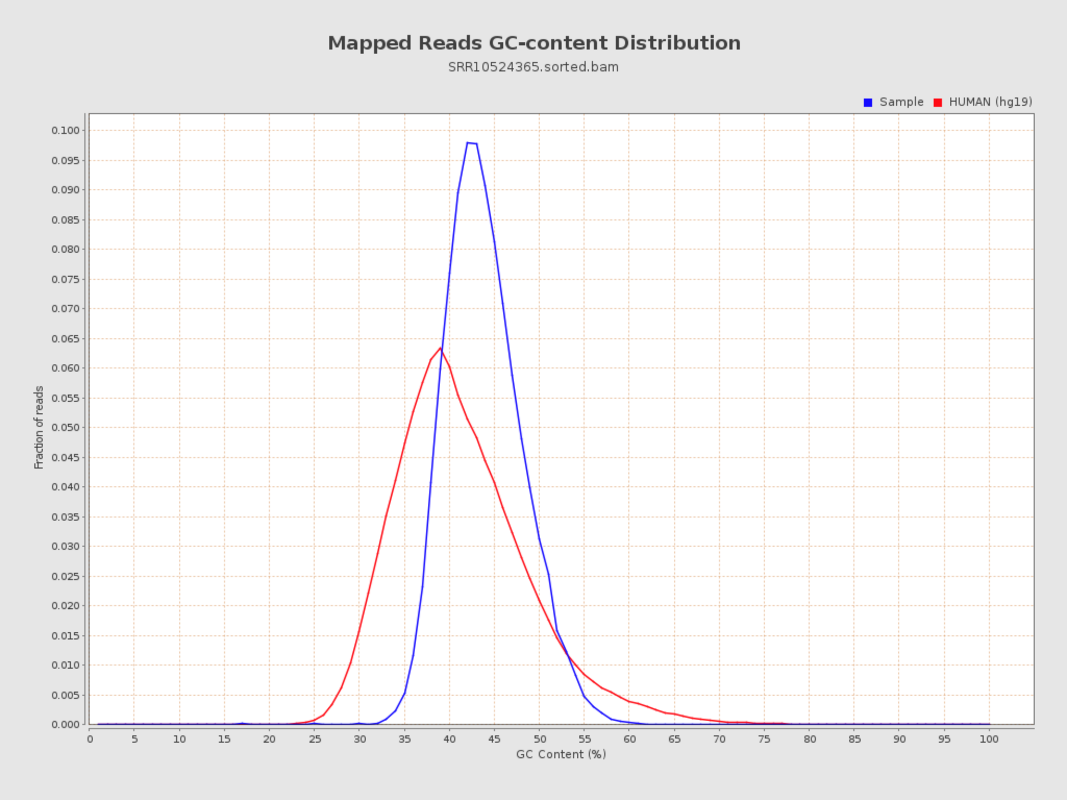
7. Results : Duplication Rate Histogram



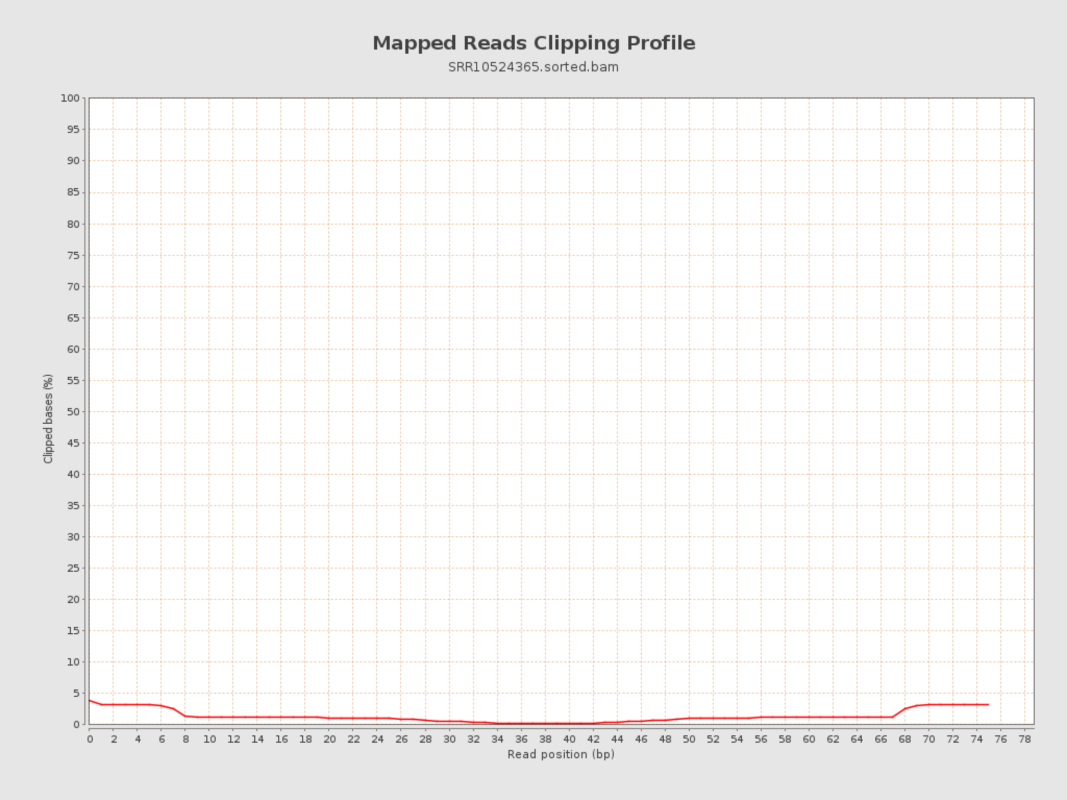
8. Results : Mapped Reads Nucleotide Content



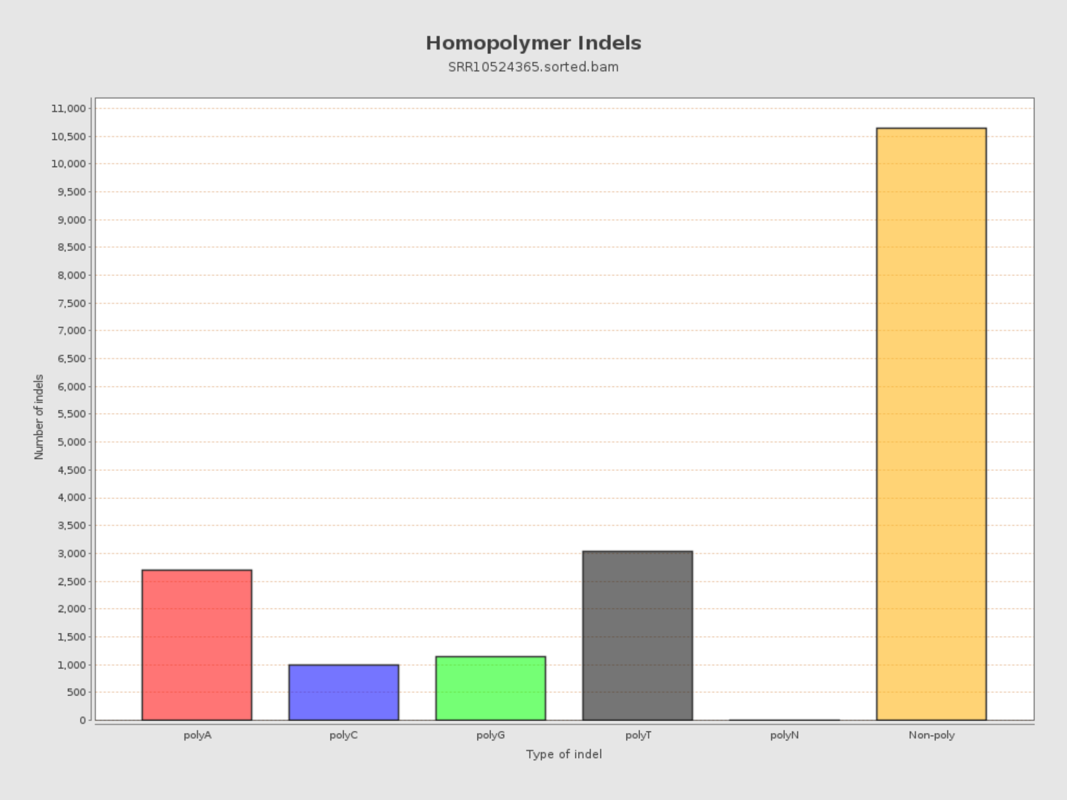
9. Results : Mapped Reads GC-content Distribution



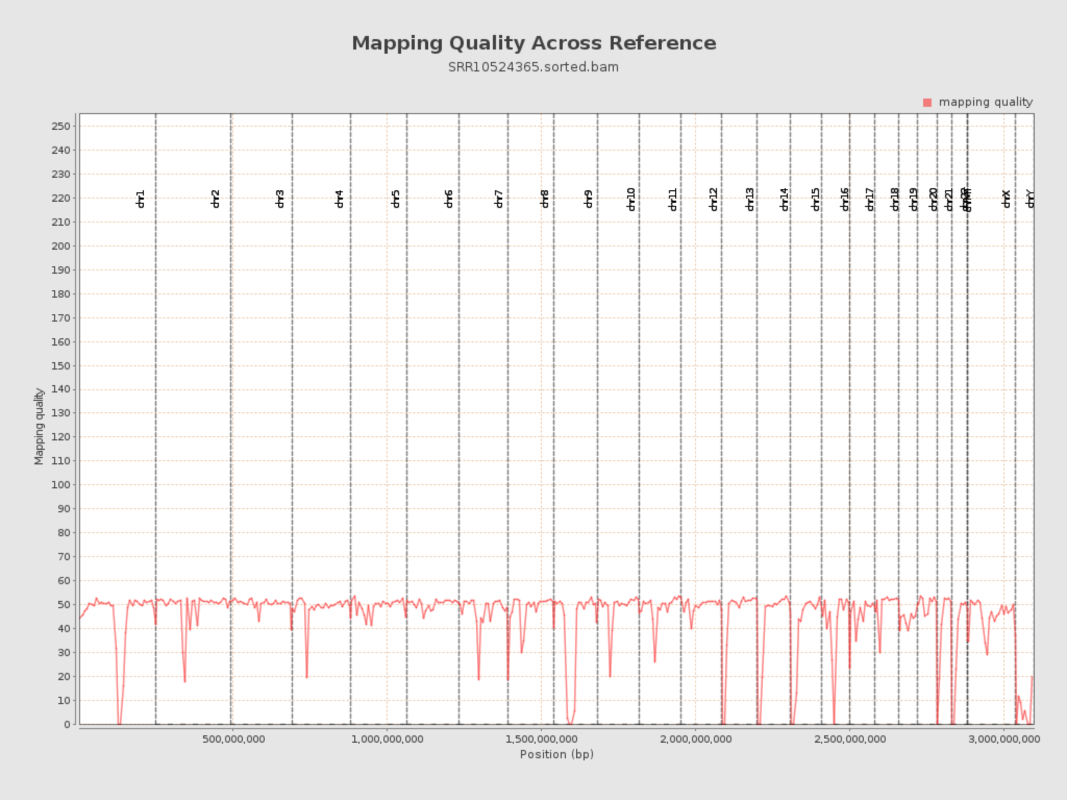
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram