Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 18:30:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524739.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_SRR10524739 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524739.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 18:30:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524739.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,650,748
Mapped reads	1,504,832 / 91.16%
Unmapped reads	145,916 / 8.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,803 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	62,583 / 3.79%
Duplication rate	3.17%
Clipped reads	1,507,199 / 91.3%

2.2. ACGT Content

Number/percentage of A's	20,564,288 / 24%
Number/percentage of C's	15,677,085 / 18.3%
Number/percentage of T's	27,921,046 / 32.59%
Number/percentage of G's	21,512,286 / 25.11%
Number/percentage of N's	9,901 / 0.01%
GC Percentage	43.4%

2.3. Coverage

Mean	0.0277

Standard Deviation	0.2519

2.4. Mapping Quality

Mean Mapping Quality	44.53

2.5. Mismatches and indels

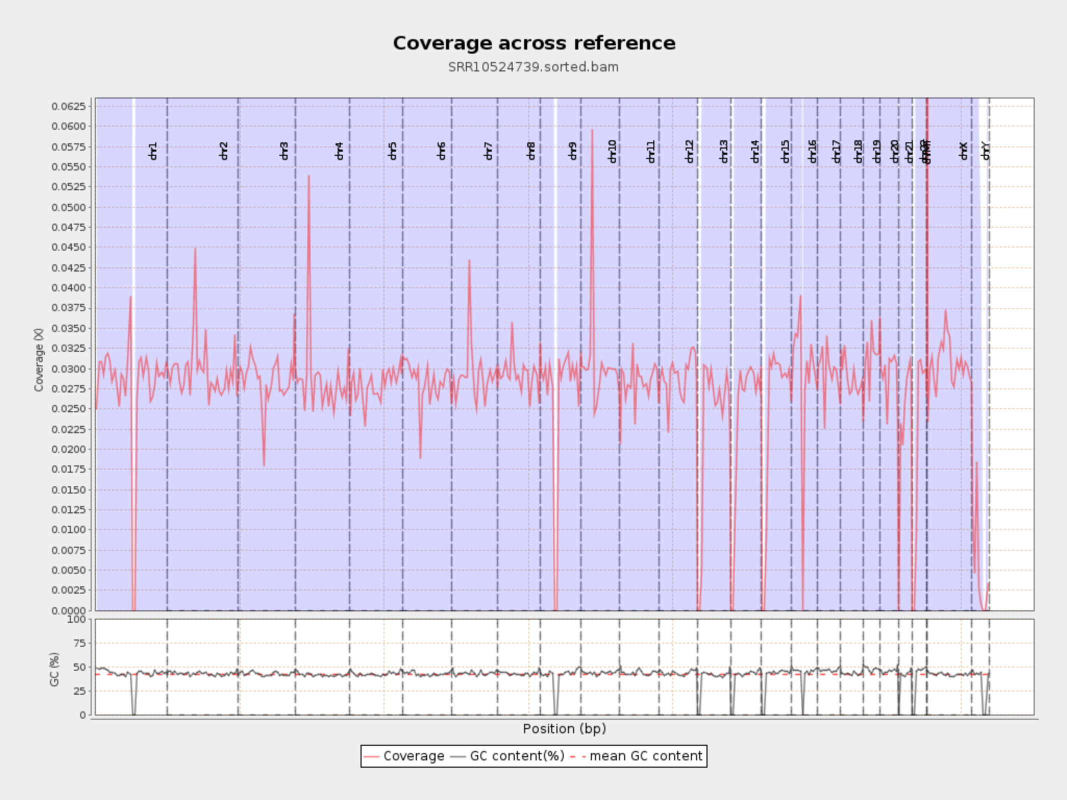
General error rate	0.52%
Mismatches	433,421
Insertions	6,040
Mapped reads with at least one insertion	0.4%
Deletions	17,151
Mapped reads with at least one deletion	1.13%
Homopolymer indels	42.96%

2.6. Chromosome stats

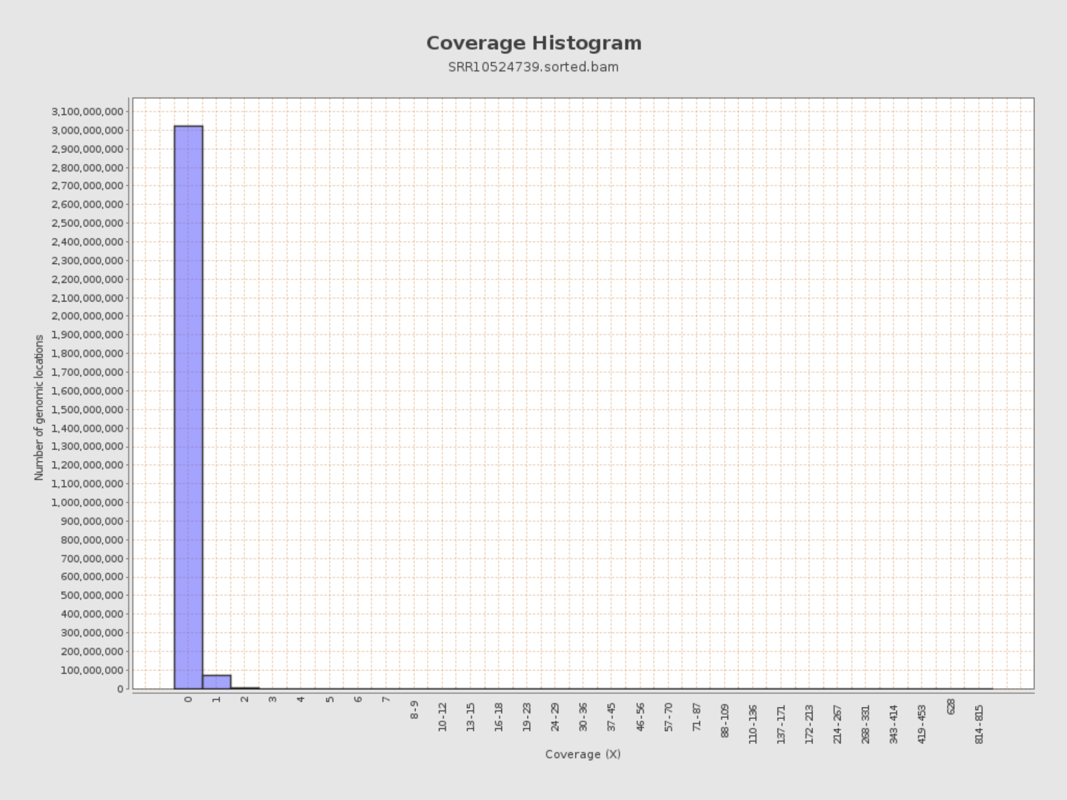
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6888149	0.0276	0.3568
chr2	243199373	7230590	0.0297	0.3974
chr3	198022430	5645675	0.0285	0.1889
chr4	191154276	5507114	0.0288	0.2173
chr5	180915260	5086778	0.0281	0.1842
chr6	171115067	4853943	0.0284	0.2065
chr7	159138663	4670510	0.0293	0.2947

chr8	146364022	4291453	0.0293	0.2311
chr9	141213431	3700172	0.0262	0.2202
chr10	135534747	4193116	0.0309	0.3013
chr11	135006516	3845497	0.0285	0.2176
chr12	133851895	3887311	0.029	0.1904
chr13	115169878	2653098	0.023	0.1664
chr14	107349540	2547028	0.0237	0.175
chr15	102531392	2489132	0.0243	0.1732
chr16	90354753	2600190	0.0288	0.205
chr17	81195210	2402891	0.0296	0.2022
chr18	78077248	2246447	0.0288	0.3396
chr19	59128983	1858516	0.0314	0.3014
chr20	63025520	1845946	0.0293	0.1962
chr21	48129895	1143530	0.0238	0.1909
chr22	51304566	1064566	0.0207	0.1608
chrMT	16571	11650	0.703	1.0035
chrX	155270560	4753930	0.0306	0.2089
chrY	59373566	294903	0.005	0.152

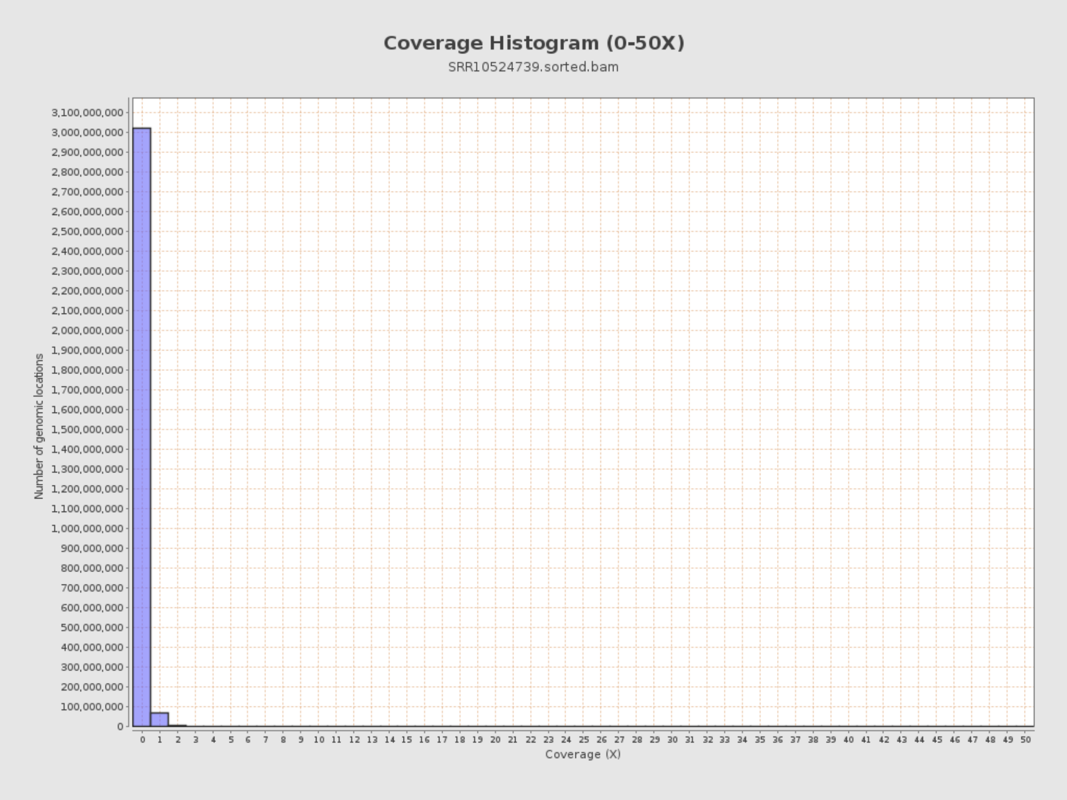
3. Results : Coverage across reference



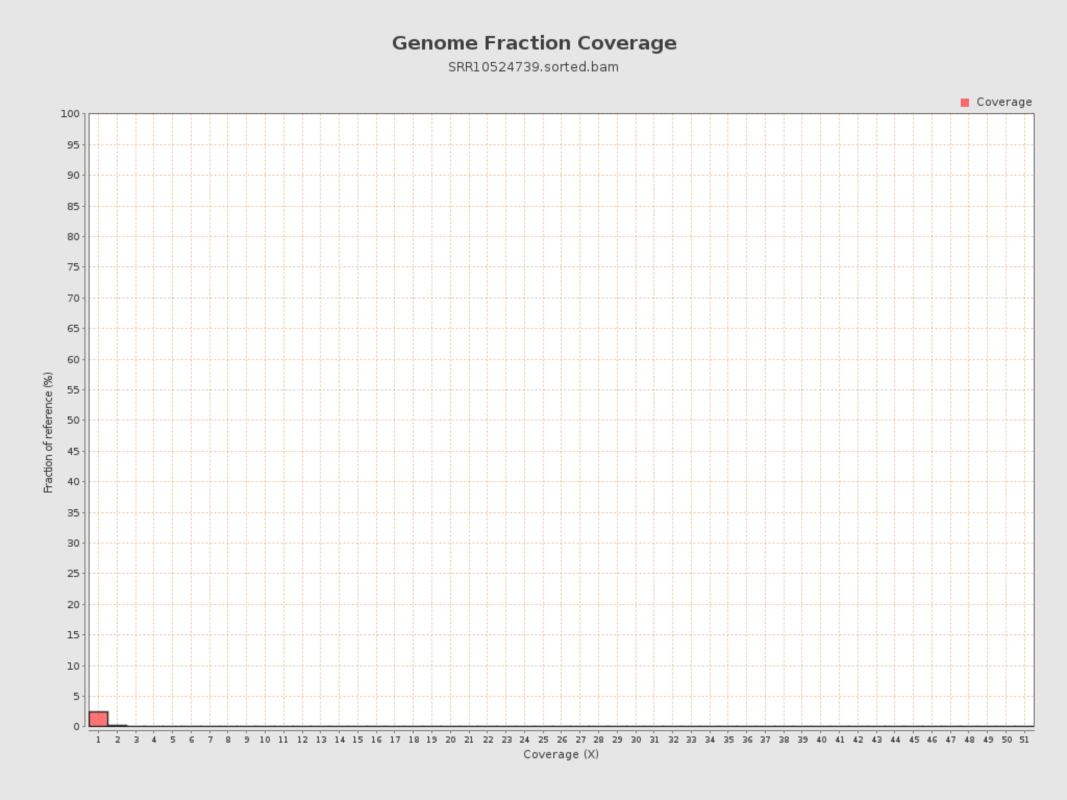
4. Results : Coverage Histogram



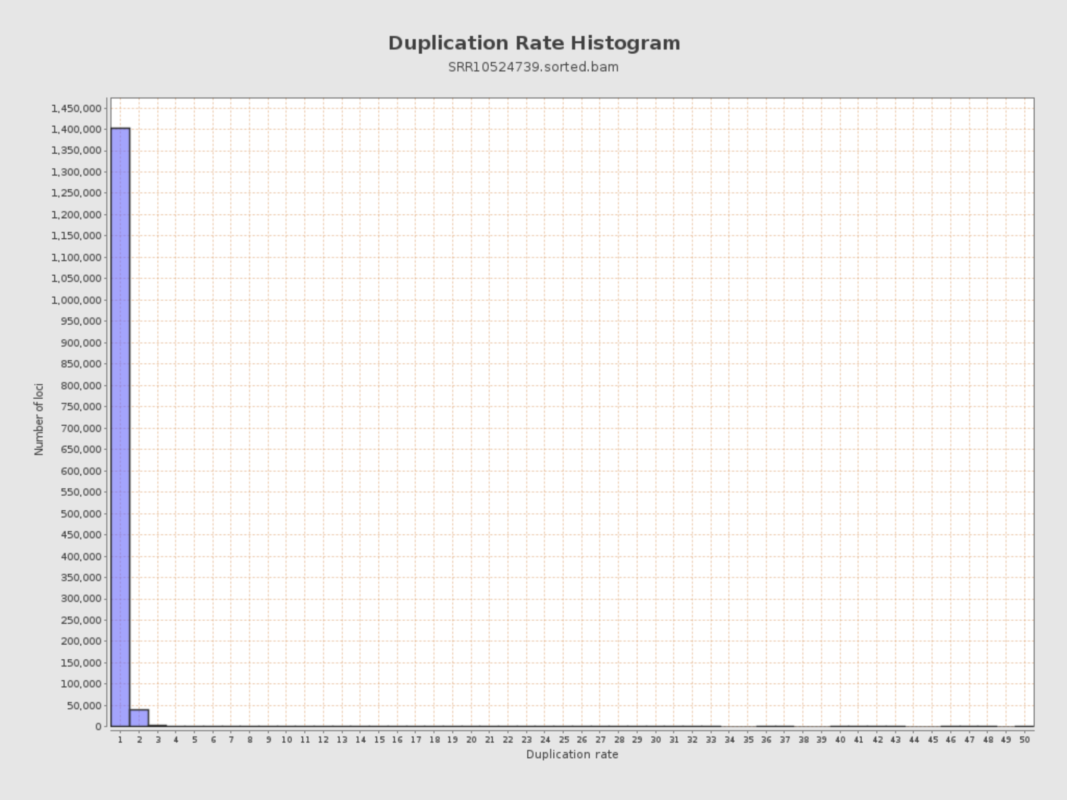
5. Results : Coverage Histogram (0-50X)



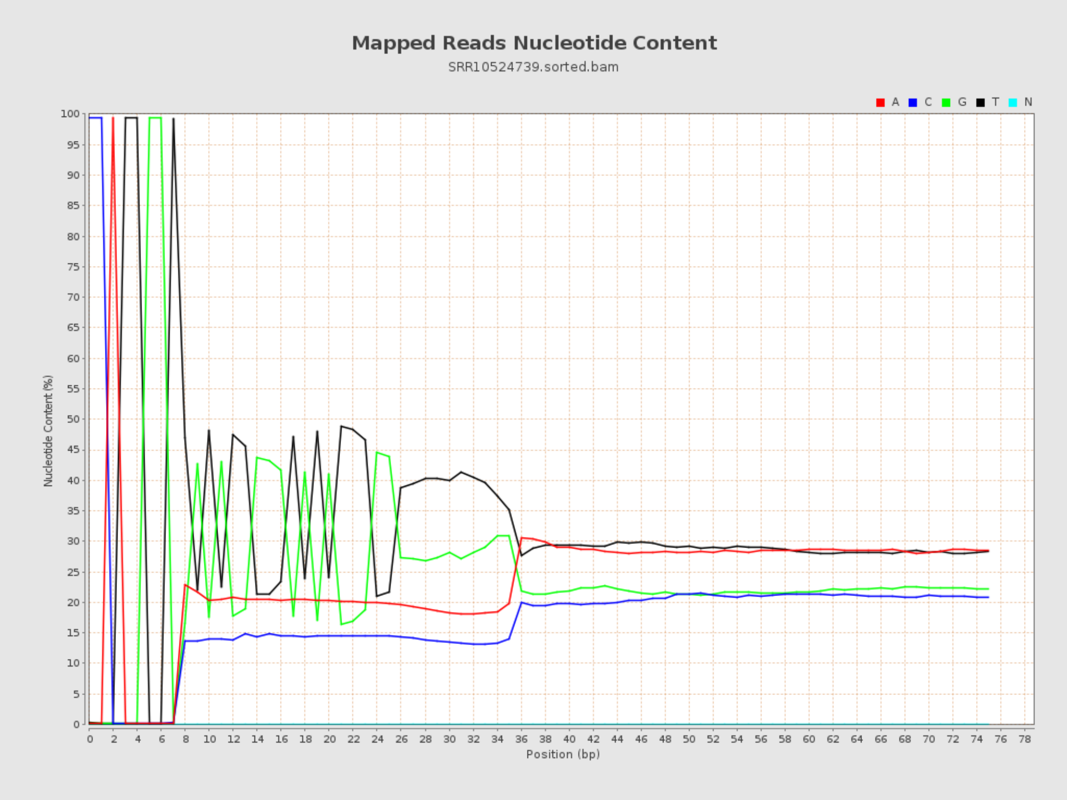
6. Results : Genome Fraction Coverage



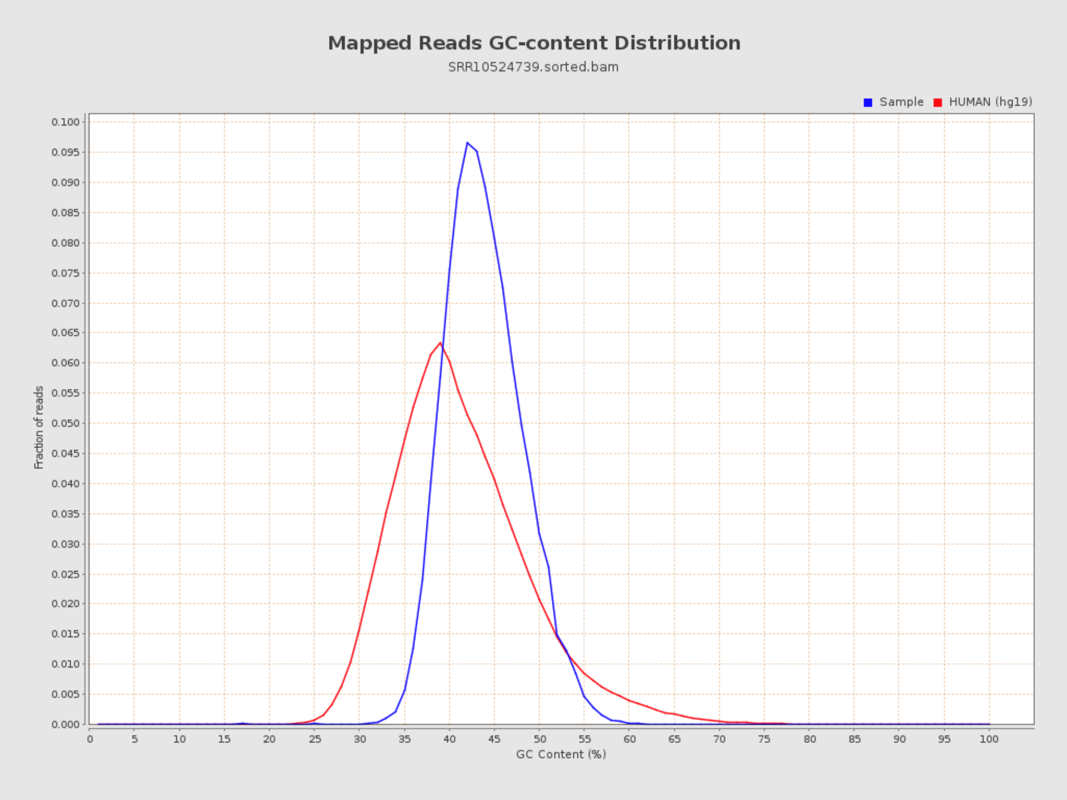
7. Results : Duplication Rate Histogram



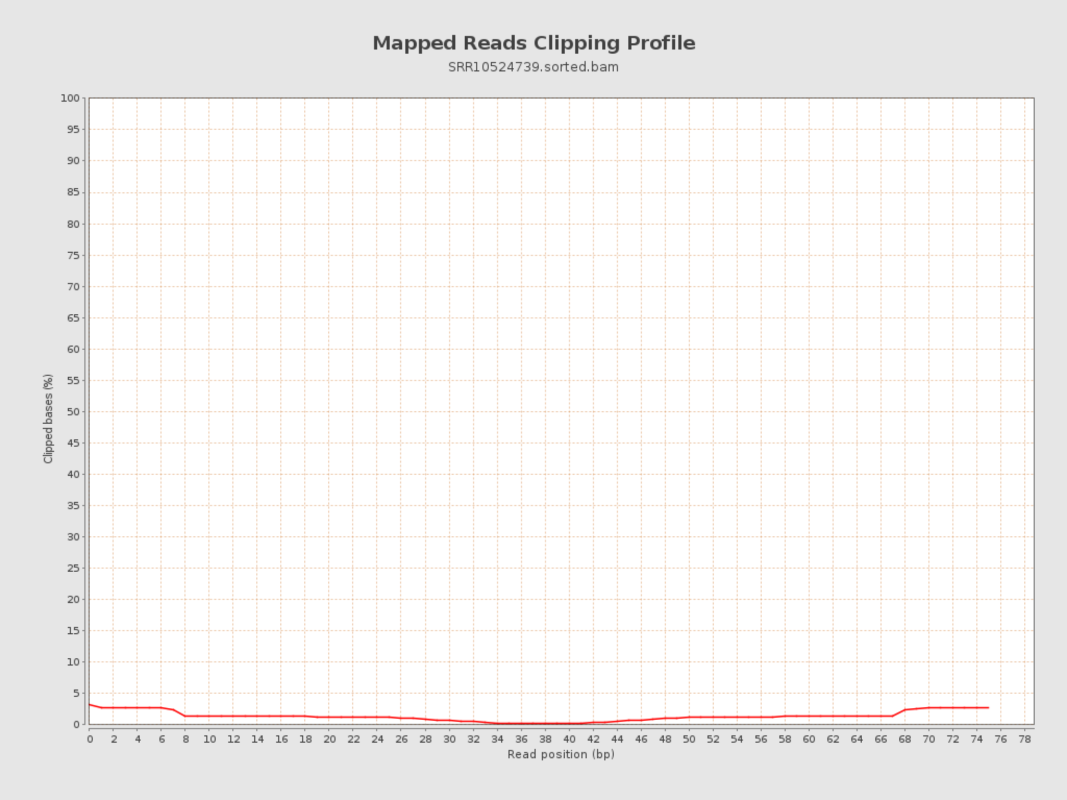
8. Results : Mapped Reads Nucleotide Content



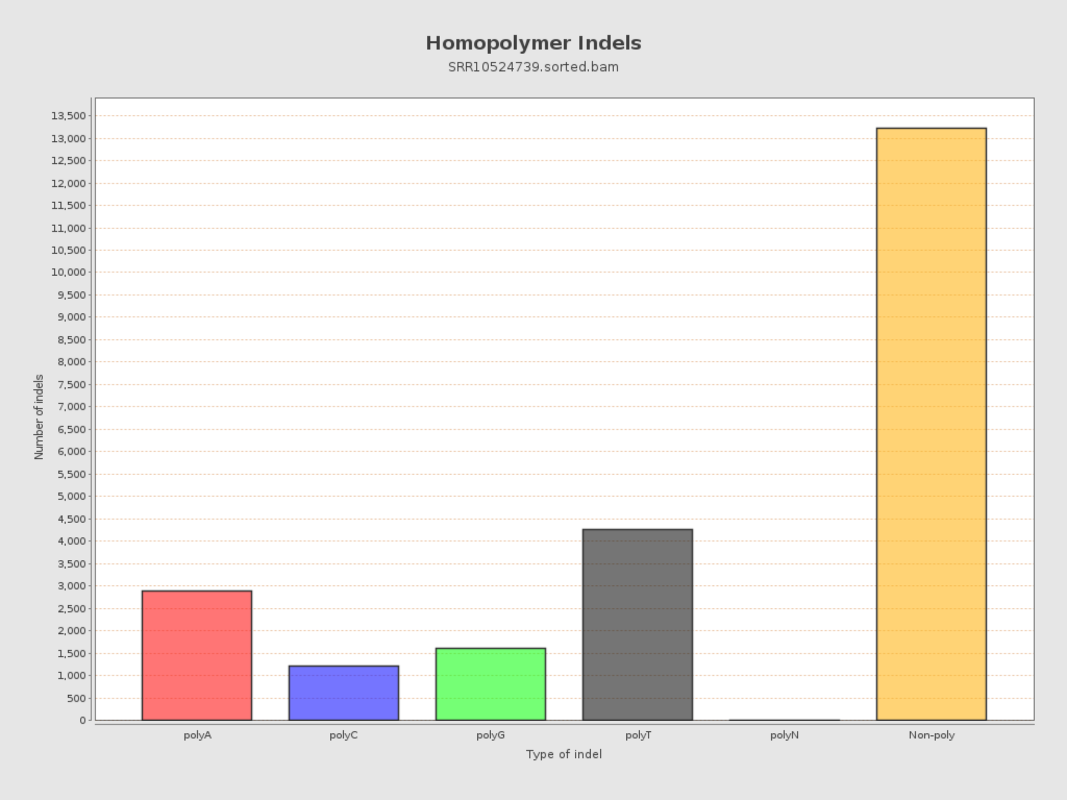
9. Results : Mapped Reads GC-content Distribution



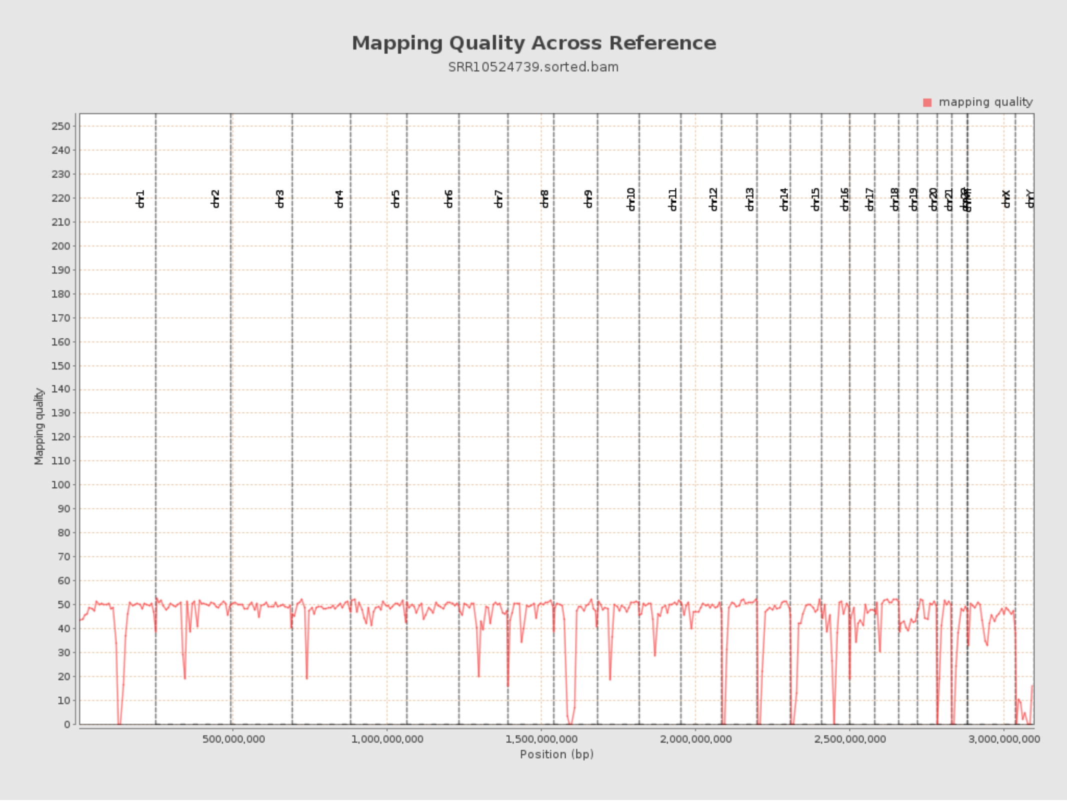
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram