Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 18:44:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524744.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_SRR10524744 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524744.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 18:44:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524744.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,011,172
Mapped reads	1,847,367 / 91.86%
Unmapped reads	163,805 / 8.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,284 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	73,075 / 3.63%
Duplication rate	2.83%
Clipped reads	1,853,857 / 92.18%

2.2. ACGT Content

Number/percentage of A's	27,721,772 / 25.89%
Number/percentage of C's	19,396,254 / 18.11%
Number/percentage of T's	33,261,771 / 31.06%
Number/percentage of G's	26,695,470 / 24.93%
Number/percentage of N's	2,209 / 0%
GC Percentage	43.05%

2.3. Coverage

Mean	0.0346

Standard Deviation	0.3405

2.4. Mapping Quality

Mean Mapping Quality	44.99

2.5. Mismatches and indels

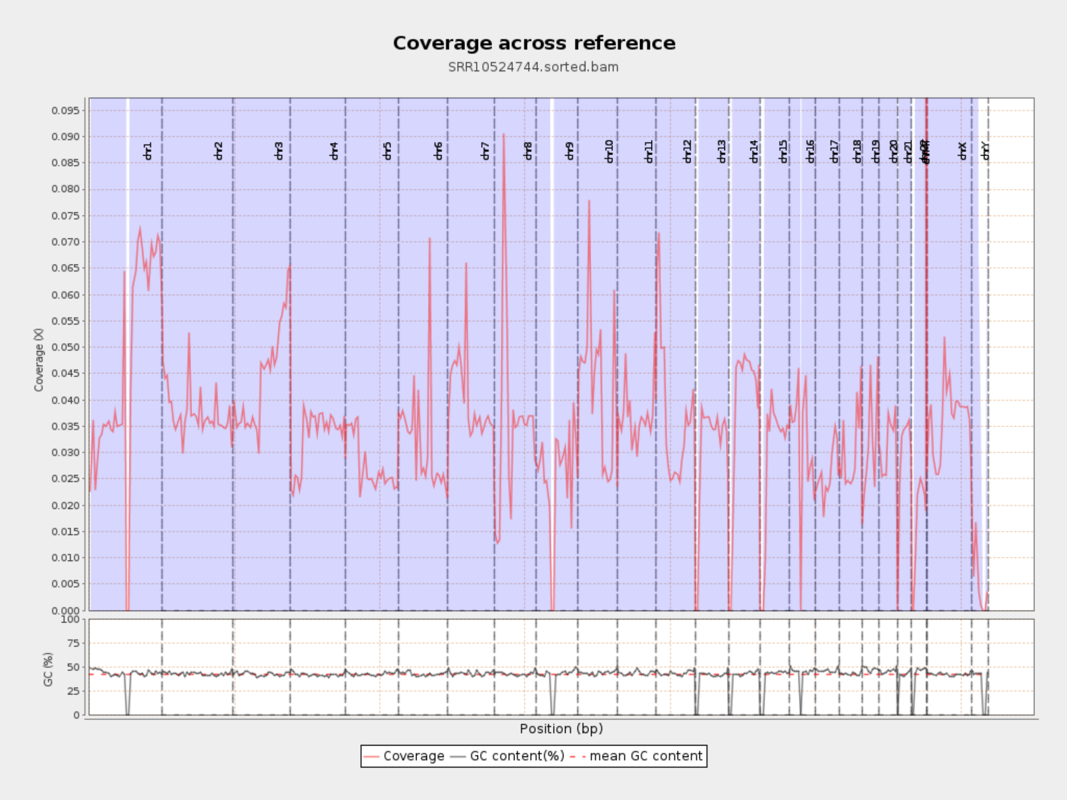
General error rate	0.51%
Mismatches	537,083
Insertions	6,683
Mapped reads with at least one insertion	0.36%
Deletions	22,100
Mapped reads with at least one deletion	1.19%
Homopolymer indels	44.09%

2.6. Chromosome stats

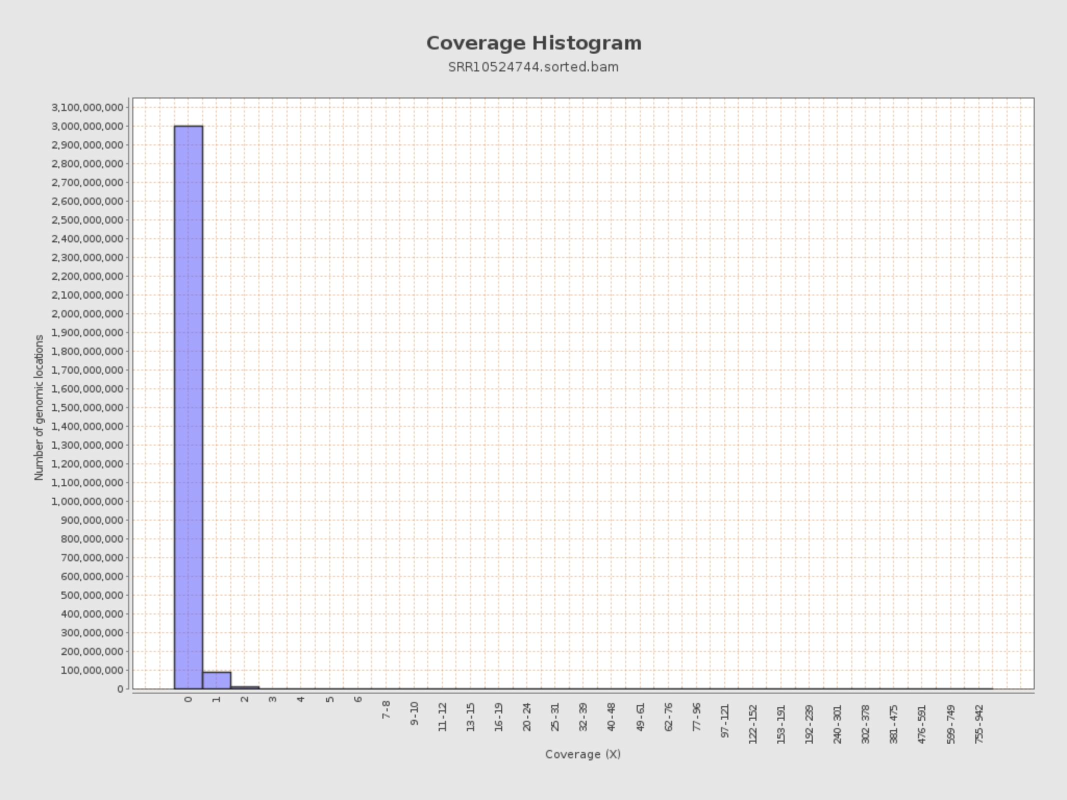
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11522250	0.0462	0.6747
chr2	243199373	9170862	0.0377	0.4351
chr3	198022430	8682367	0.0438	0.2347
chr4	191154276	6314818	0.033	0.2109
chr5	180915260	4985161	0.0276	0.1819
chr6	171115067	5516460	0.0322	0.231
chr7	159138663	6454479	0.0406	0.5015

chr8	146364022	5117649	0.035	0.3166
chr9	141213431	3571074	0.0253	0.2386
chr10	135534747	5872825	0.0433	0.3808
chr11	135006516	4987388	0.0369	0.2723
chr12	133851895	4956955	0.037	0.2167
chr13	115169878	3523405	0.0306	0.1923
chr14	107349540	4072077	0.0379	0.2179
chr15	102531392	2950380	0.0288	0.1886
chr16	90354753	2835288	0.0314	0.2231
chr17	81195210	2105487	0.0259	0.1823
chr18	78077248	2350326	0.0301	0.4751
chr19	59128983	1893899	0.032	0.4677
chr20	63025520	1978189	0.0314	0.1977
chr21	48129895	1407943	0.0293	0.1997
chr22	51304566	833863	0.0163	0.1394
chrMT	16571	22563	1.3616	1.3872
chrX	155270560	5675254	0.0366	0.2337
chrY	59373566	311874	0.0053	0.1492

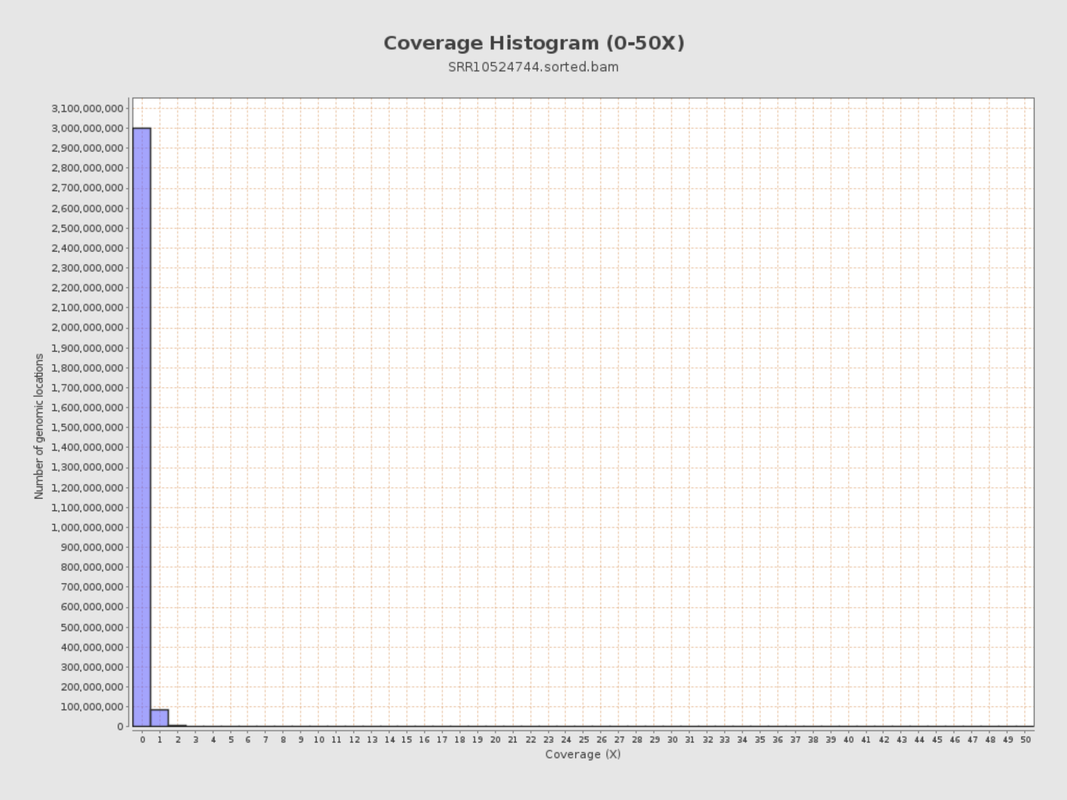
3. Results : Coverage across reference



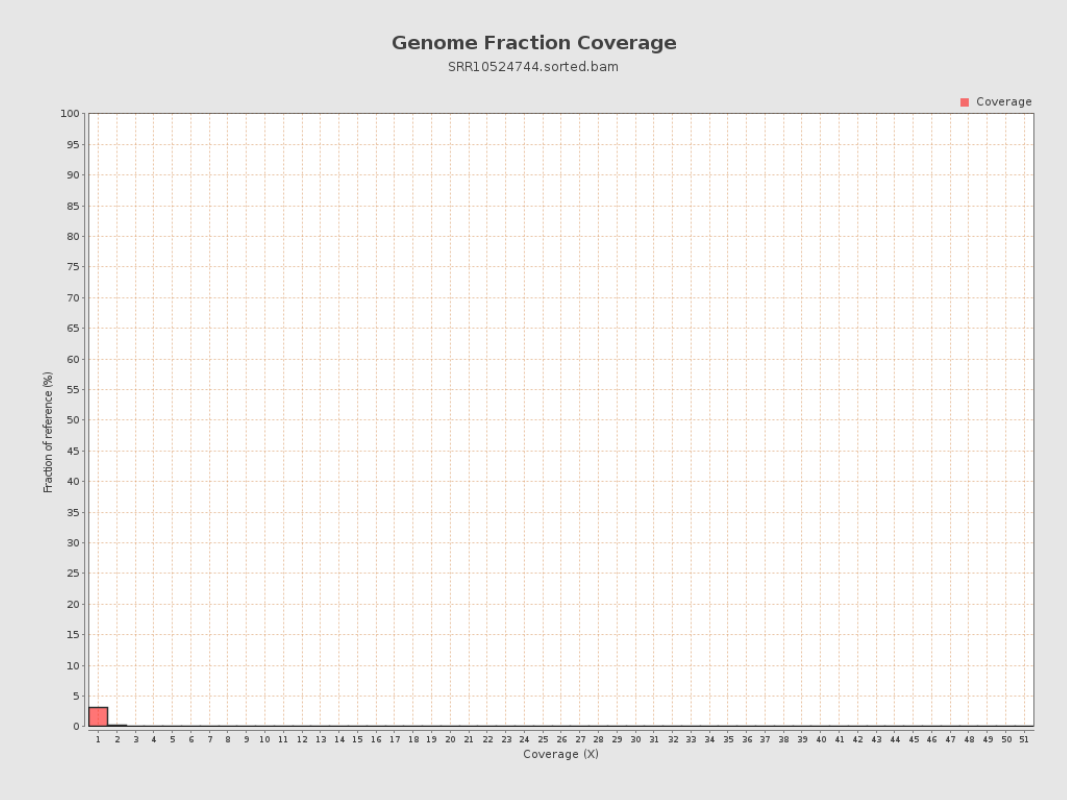
4. Results : Coverage Histogram



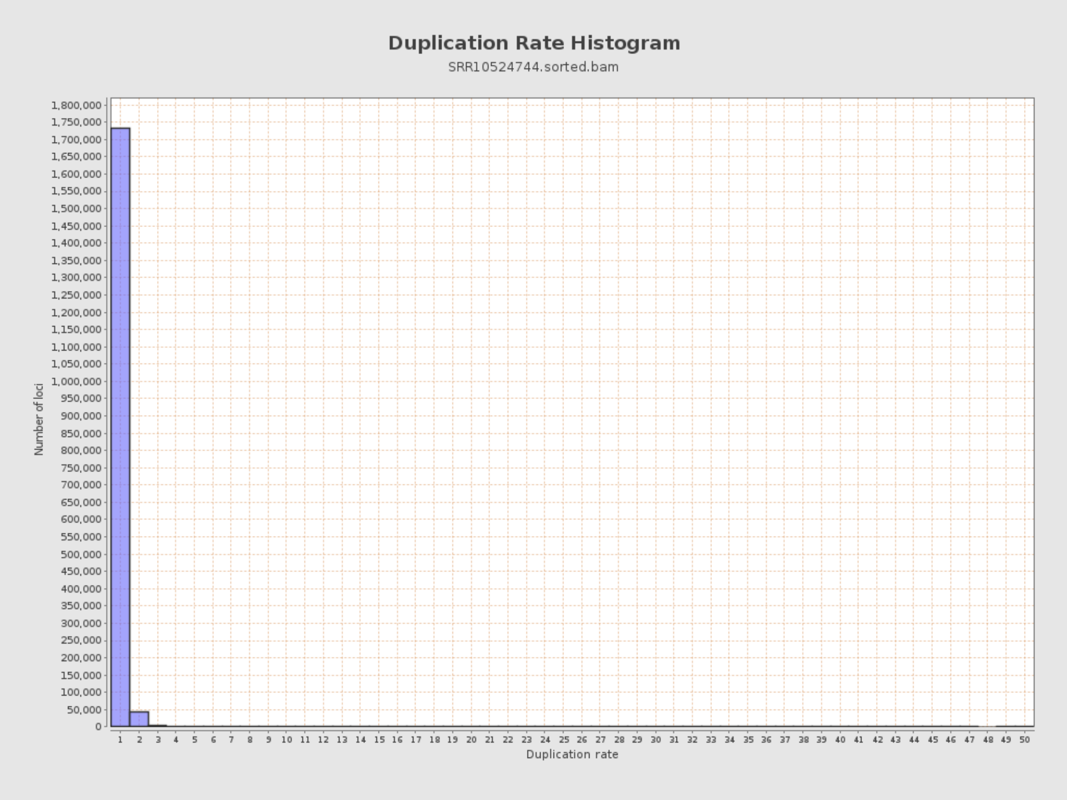
5. Results : Coverage Histogram (0-50X)



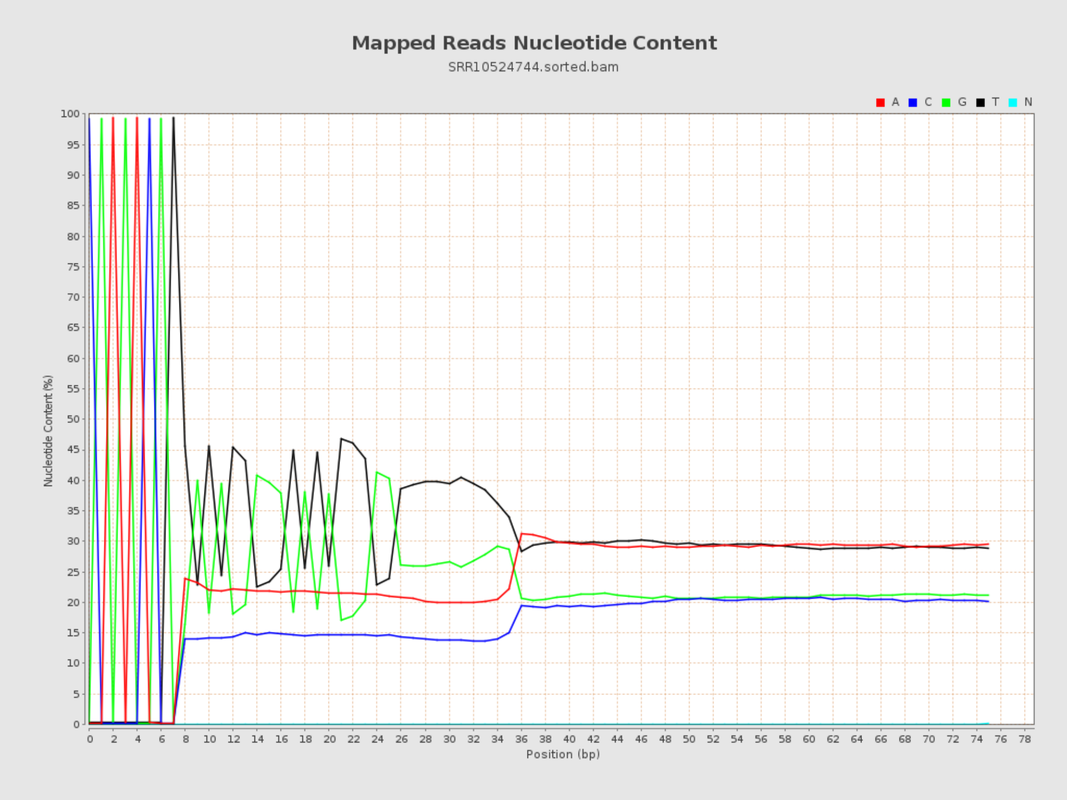
6. Results : Genome Fraction Coverage



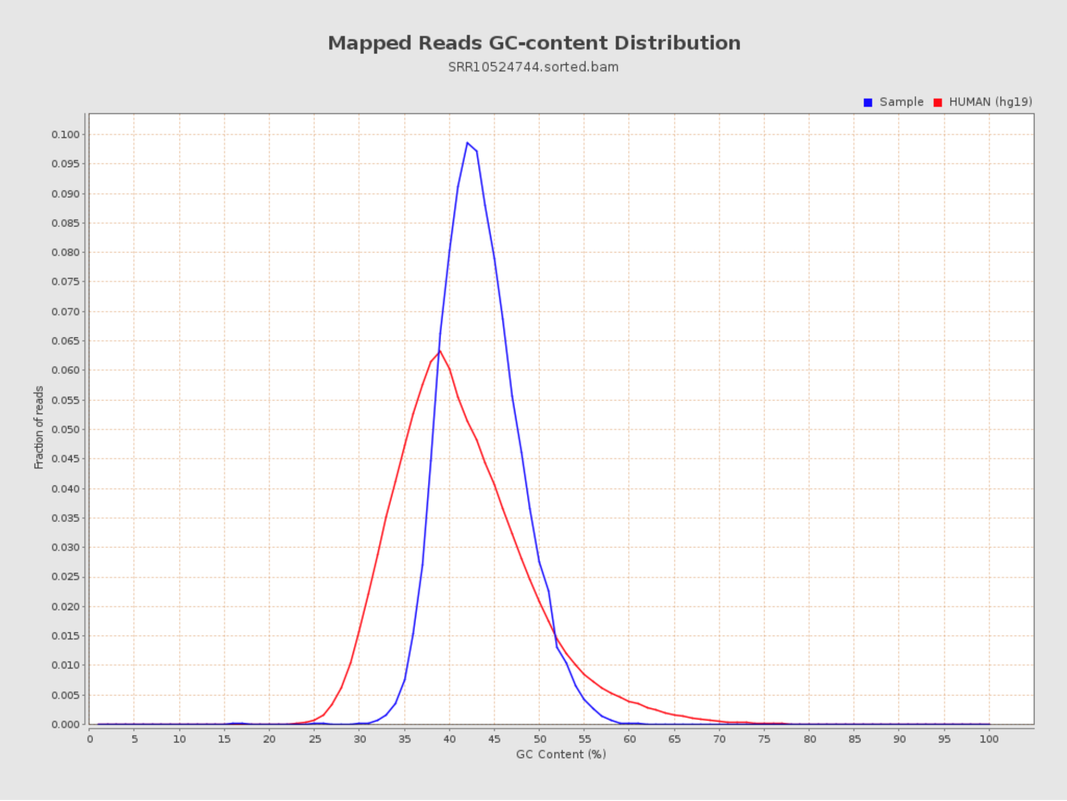
7. Results : Duplication Rate Histogram



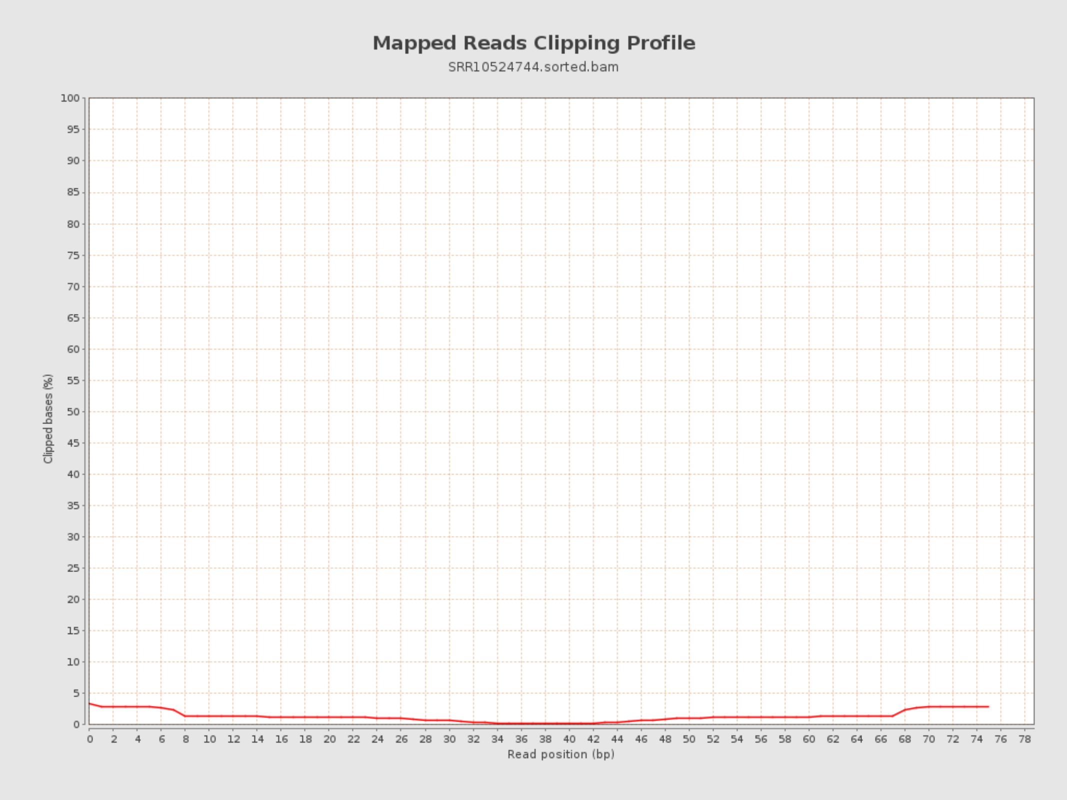
8. Results : Mapped Reads Nucleotide Content



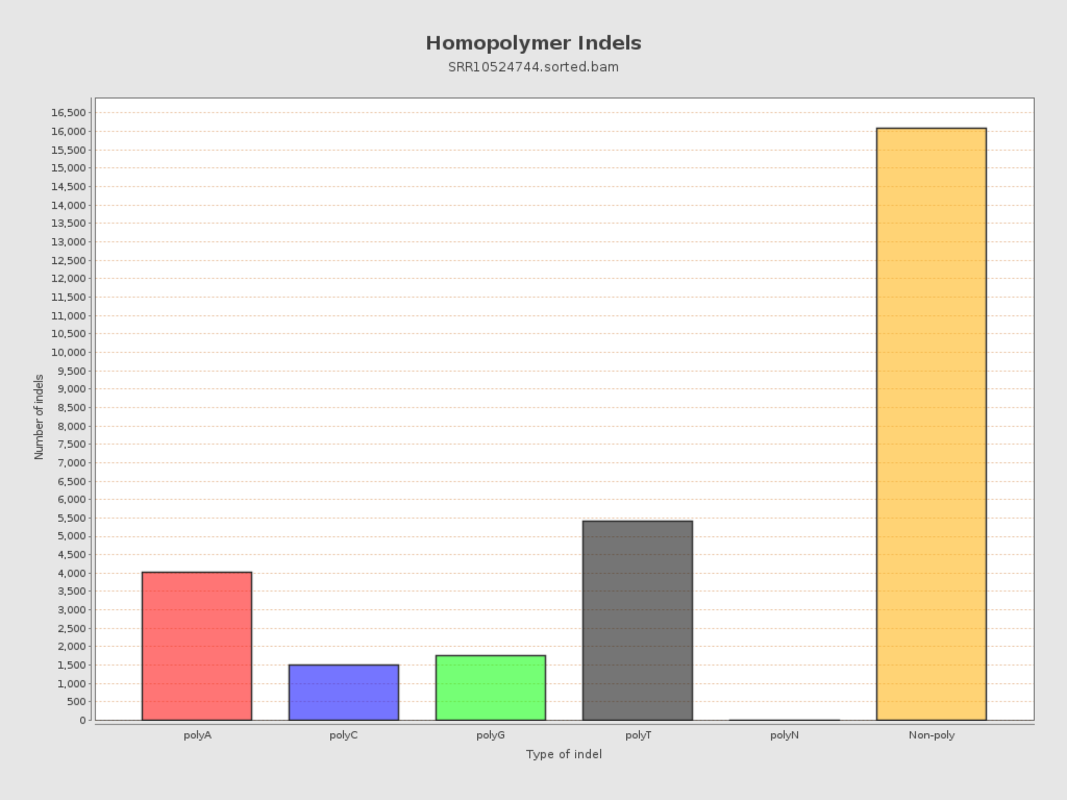
9. Results : Mapped Reads GC-content Distribution



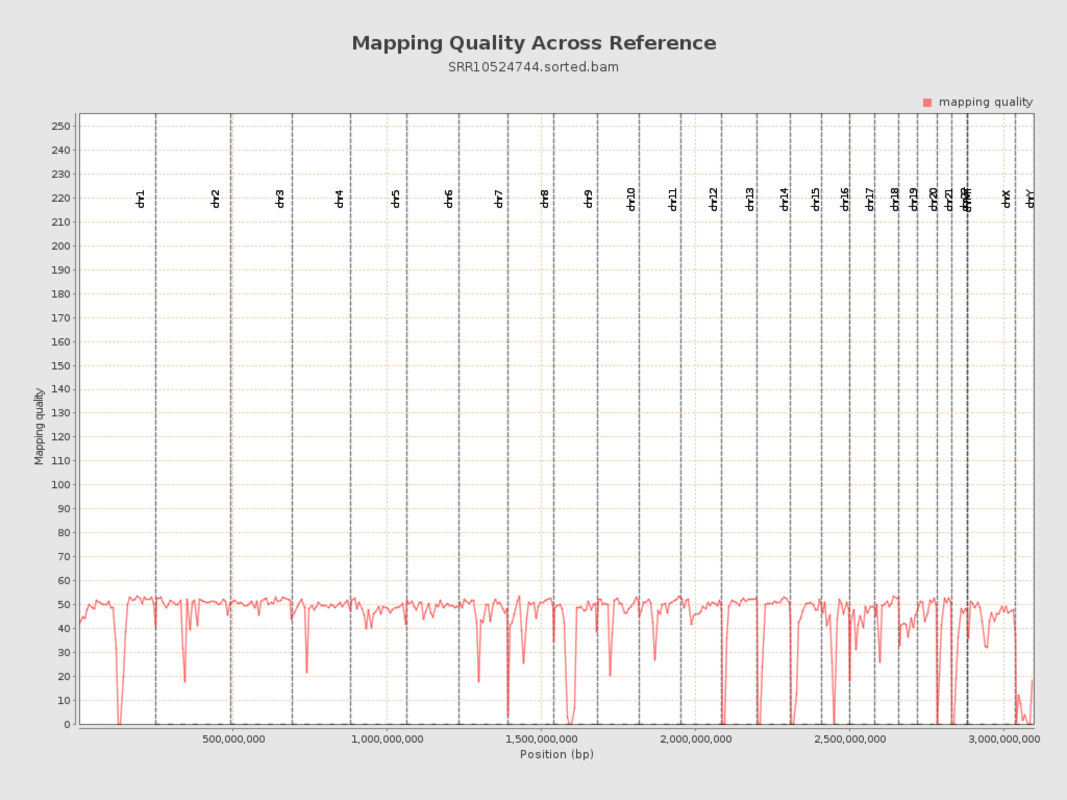
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram