Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 22:52:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524844.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_SRR10524844 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524844.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 22:52:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524844.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	909,944
Mapped reads	821,944 / 90.33%
Unmapped reads	88,000 / 9.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,584 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	20,044 / 2.2%
Duplication rate	1.77%
Clipped reads	823,371 / 90.49%

2.2. ACGT Content

Number/percentage of A's	12,363,553 / 26%
Number/percentage of C's	8,936,140 / 18.79%
Number/percentage of T's	15,230,811 / 32.03%
Number/percentage of G's	11,015,916 / 23.17%
Number/percentage of N's	976 / 0%
GC Percentage	41.96%

2.3. Coverage

Mean	0.0154

Standard Deviation	0.1727

2.4. Mapping Quality

Mean Mapping Quality	44.98

2.5. Mismatches and indels

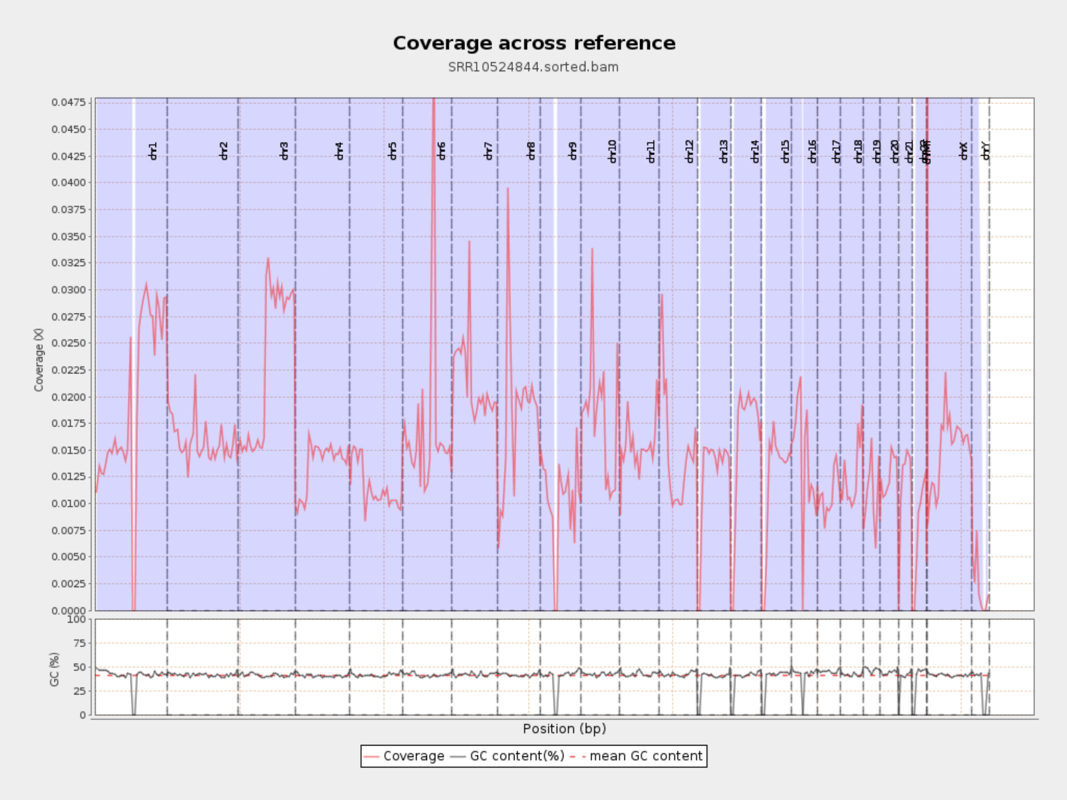
General error rate	0.53%
Mismatches	245,715
Insertions	3,577
Mapped reads with at least one insertion	0.43%
Deletions	10,200
Mapped reads with at least one deletion	1.23%
Homopolymer indels	42.24%

2.6. Chromosome stats

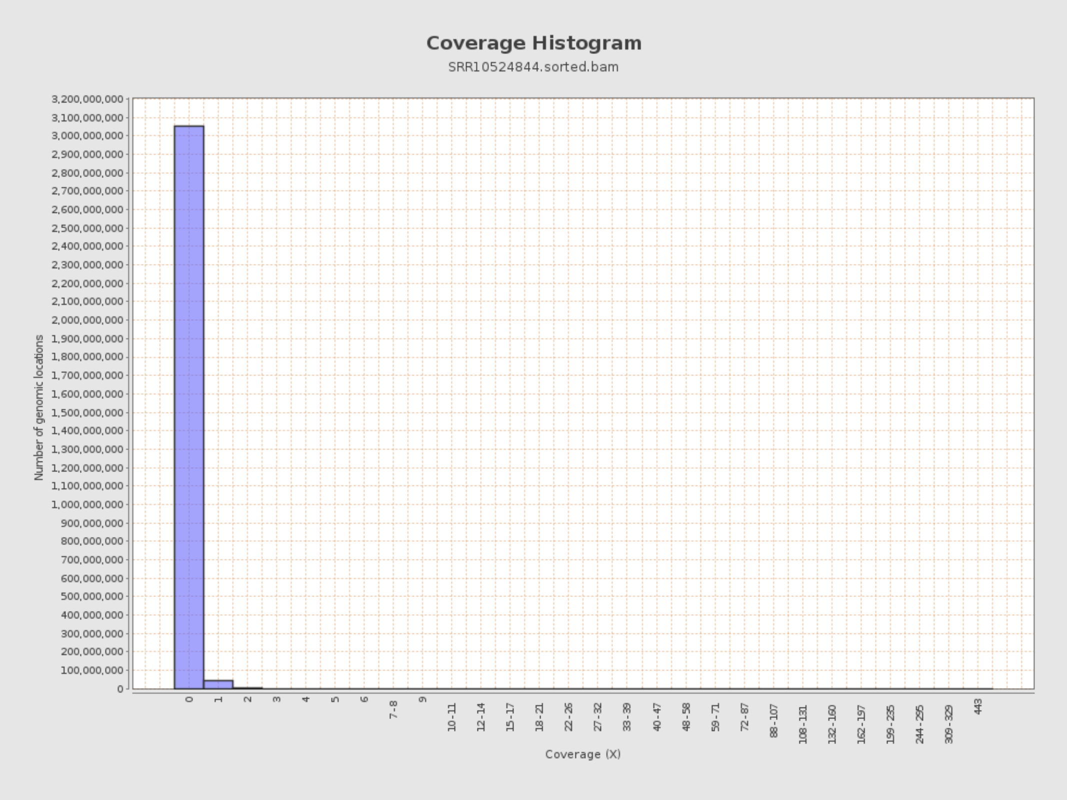
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4847949	0.0195	0.2676
chr2	243199373	3843495	0.0158	0.2232
chr3	198022430	4535663	0.0229	0.1586
chr4	191154276	2624573	0.0137	0.1268
chr5	180915260	2097608	0.0116	0.1126
chr6	171115067	3033733	0.0177	0.1491
chr7	159138663	3419818	0.0215	0.2851

chr8	146364022	2699313	0.0184	0.1768
chr9	141213431	1443327	0.0102	0.1235
chr10	135534747	2469173	0.0182	0.1893
chr11	135006516	2074228	0.0154	0.1489
chr12	133851895	2039616	0.0152	0.1302
chr13	115169878	1453378	0.0126	0.1175
chr14	107349540	1696867	0.0158	0.1325
chr15	102531392	1234584	0.012	0.1165
chr16	90354753	1261914	0.014	0.132
chr17	81195210	882864	0.0109	0.1117
chr18	78077248	977246	0.0125	0.204
chr19	59128983	649692	0.011	0.1969
chr20	63025520	790117	0.0125	0.1183
chr21	48129895	577038	0.012	0.1169
chr22	51304566	380000	0.0074	0.0895
chrMT	16571	51696	3.1197	2.3539
chrX	155270560	2348136	0.0151	0.1353
chrY	59373566	131706	0.0022	0.0708

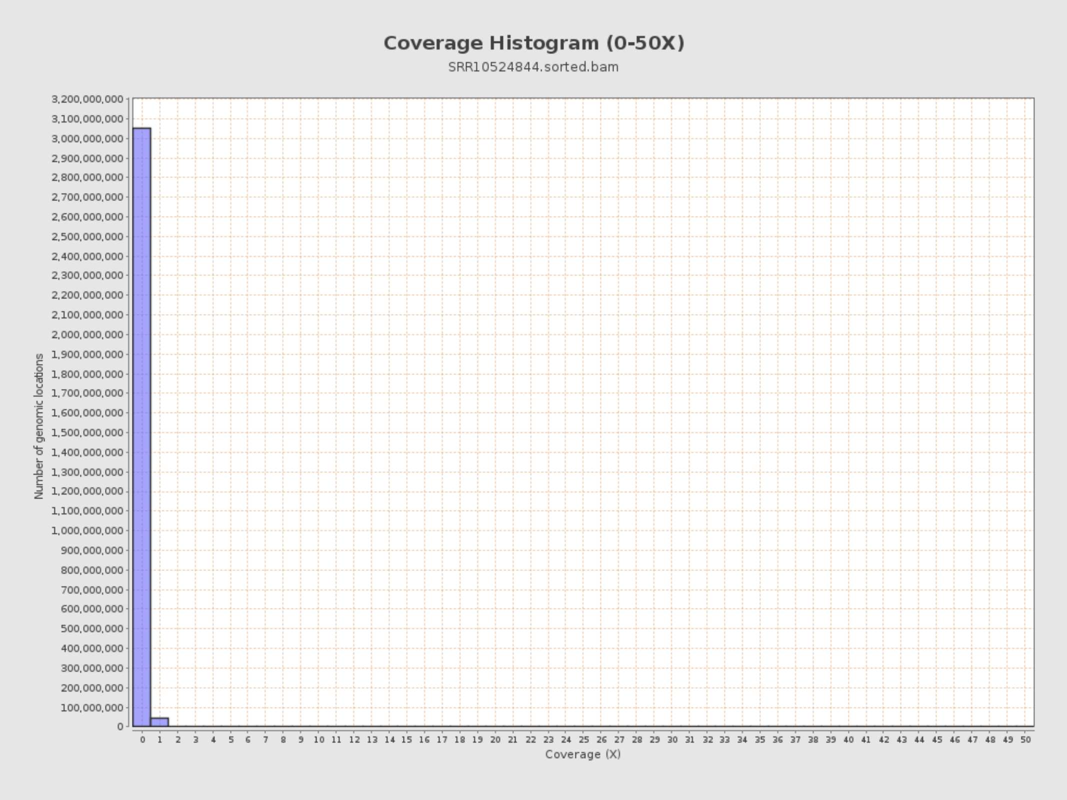
3. Results : Coverage across reference



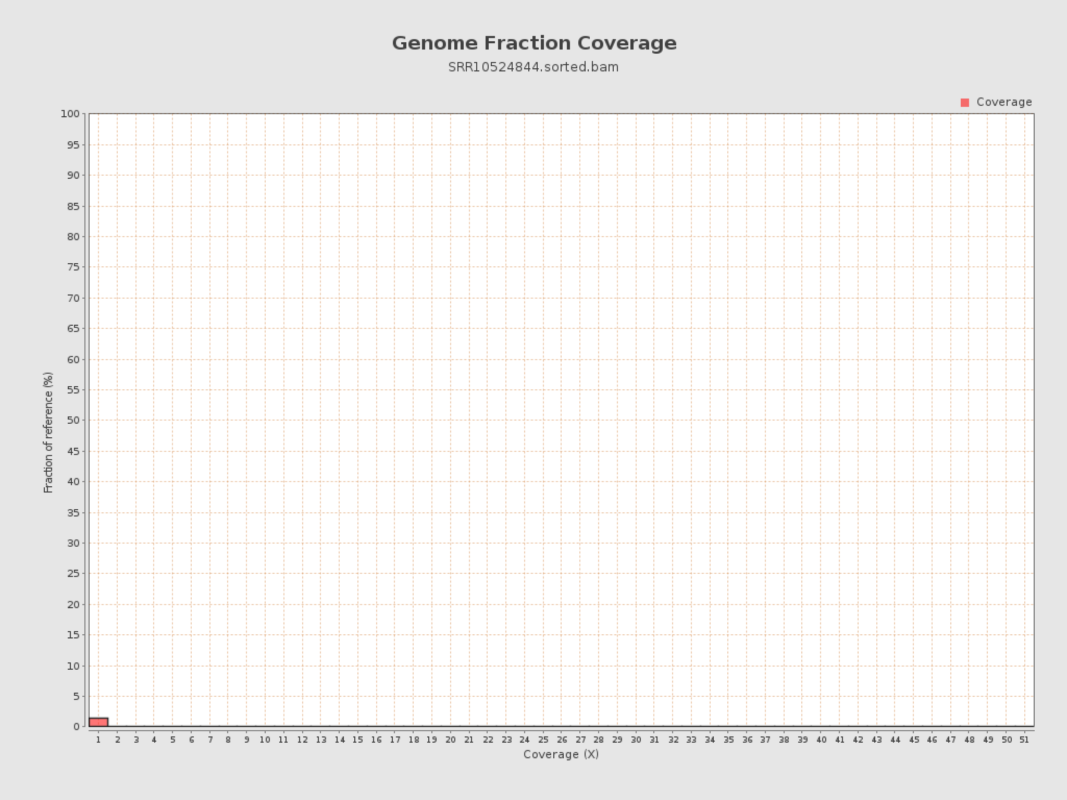
4. Results : Coverage Histogram



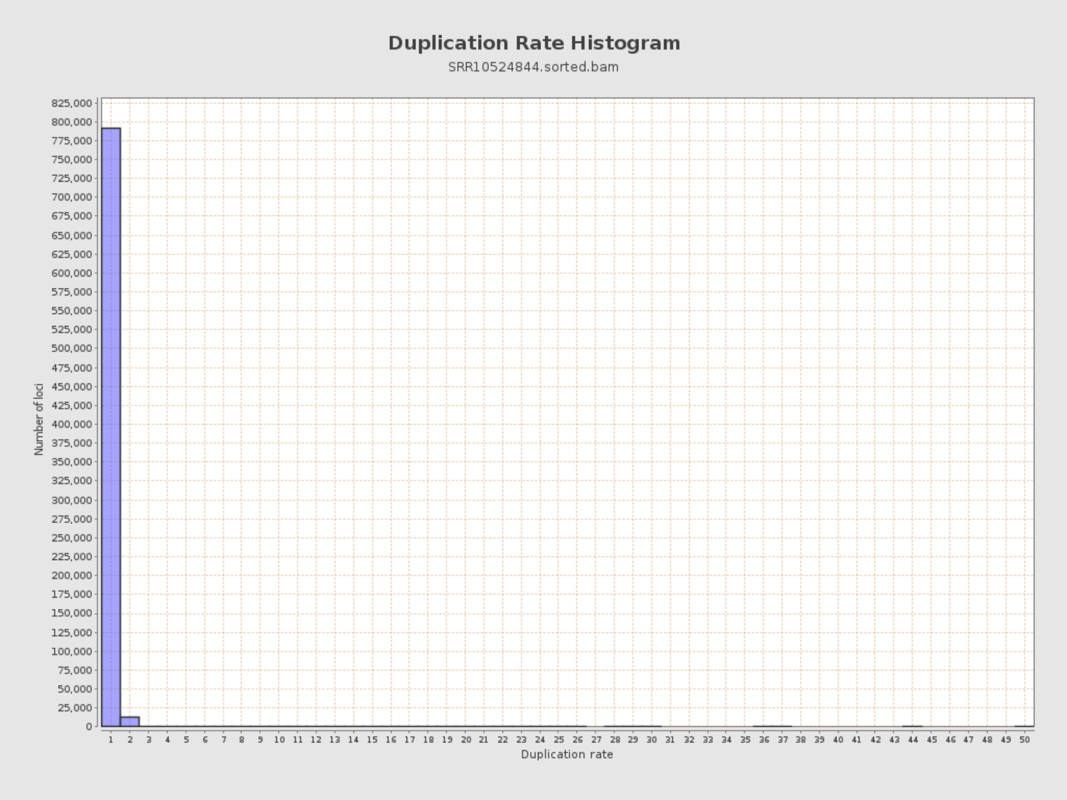
5. Results : Coverage Histogram (0-50X)



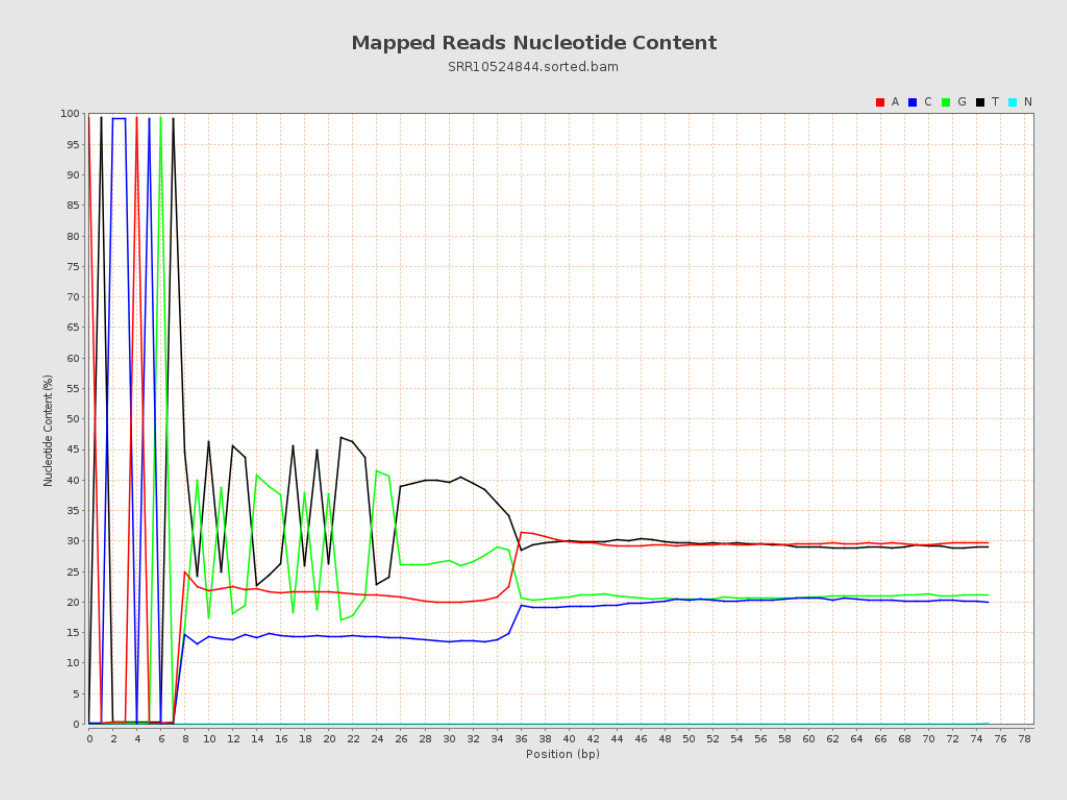
6. Results : Genome Fraction Coverage



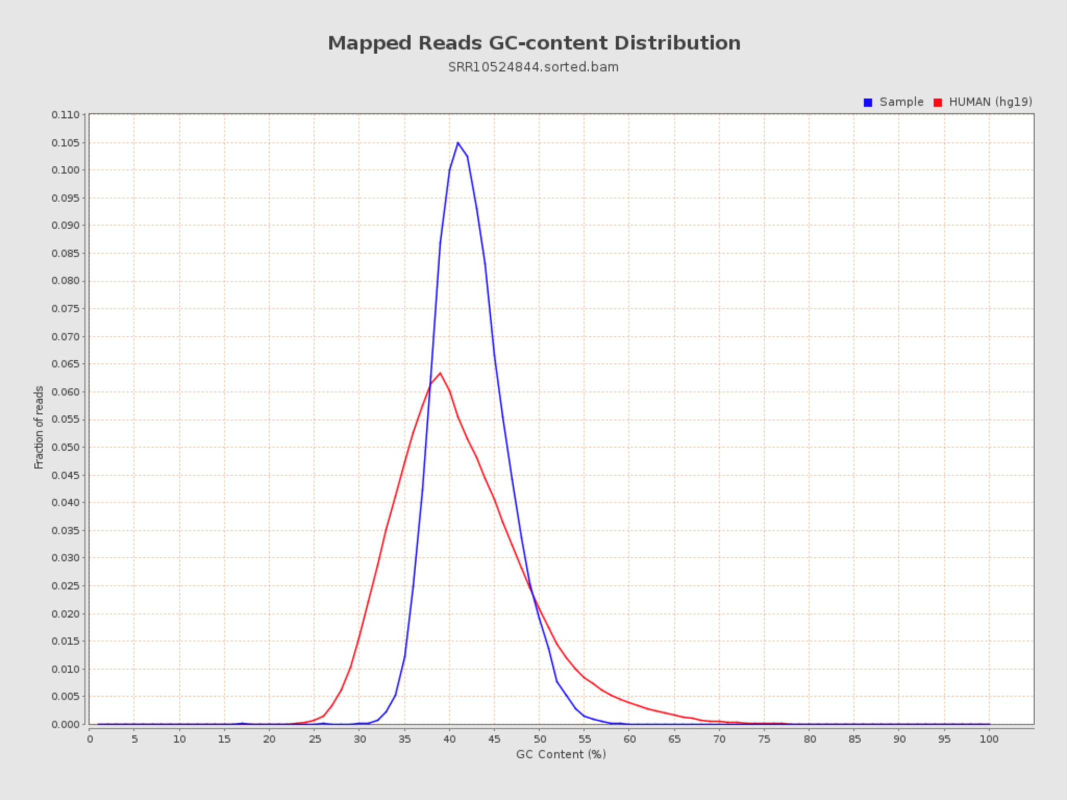
7. Results : Duplication Rate Histogram



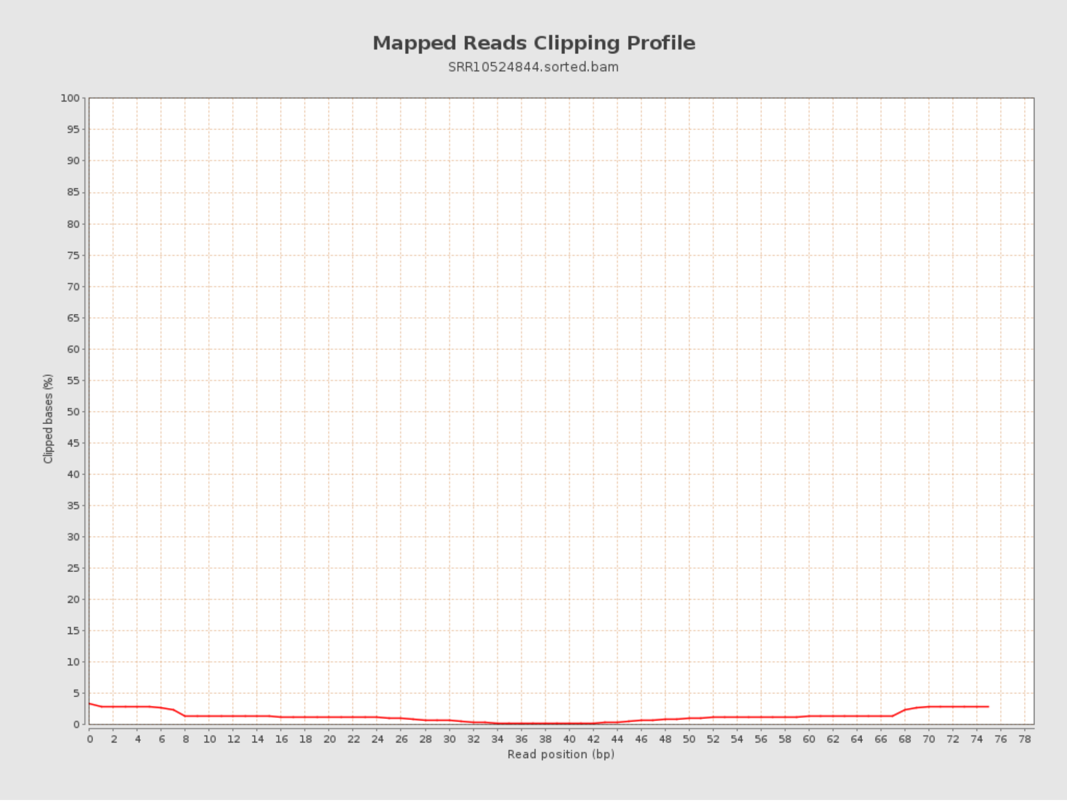
8. Results : Mapped Reads Nucleotide Content



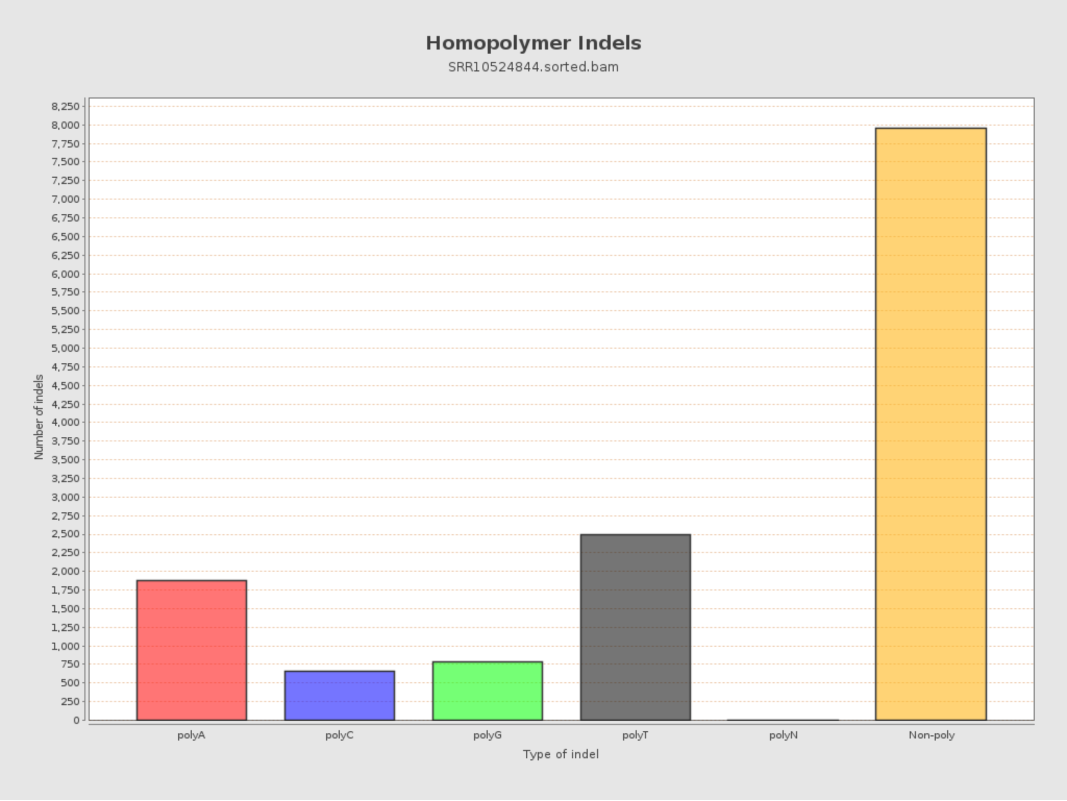
9. Results : Mapped Reads GC-content Distribution



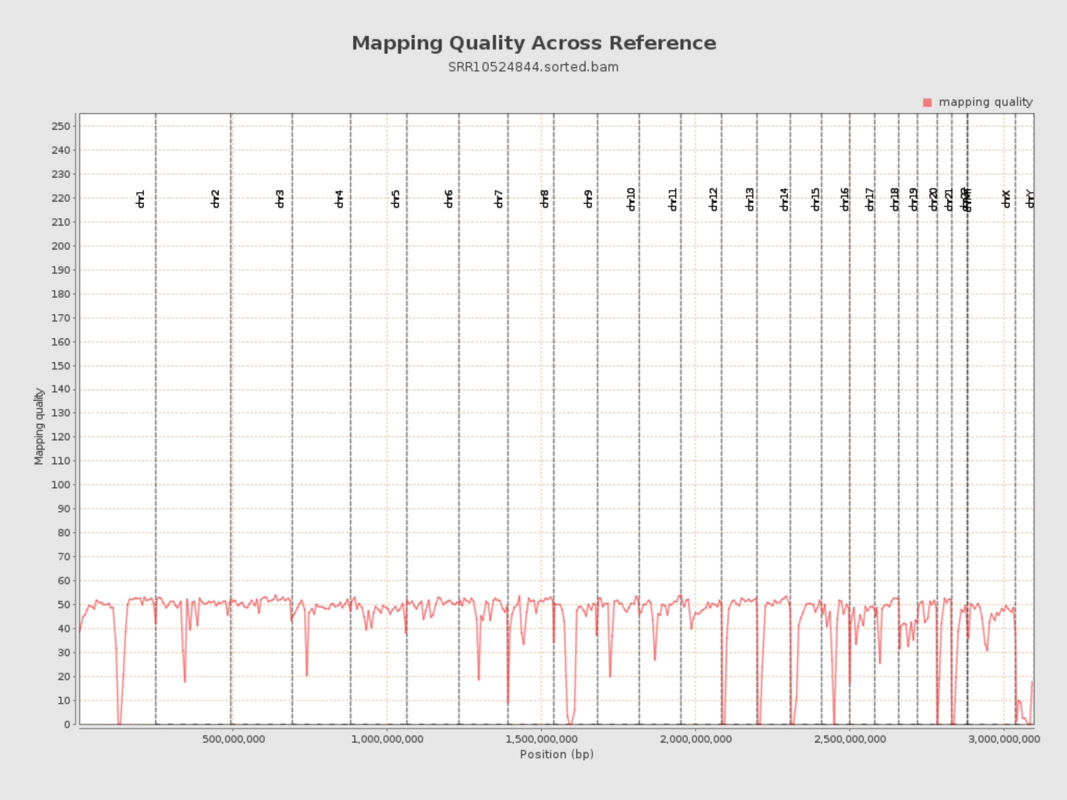
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram