Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 04:06:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524433.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_SRR10524433 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524433.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 04:06:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524433.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,145,979
Mapped reads	1,055,819 / 92.13%
Unmapped reads	90,160 / 7.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,948 / 0.34%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	37,050 / 3.23%
Duplication rate	2.68%
Clipped reads	1,056,605 / 92.2%

2.2. ACGT Content

Number/percentage of A's	15,445,078 / 25.08%
Number/percentage of C's	11,814,286 / 19.19%
Number/percentage of T's	19,508,126 / 31.68%
Number/percentage of G's	14,810,053 / 24.05%
Number/percentage of N's	1,243 / 0%
GC Percentage	43.24%

2.3. Coverage

Mean	0.0199

Standard Deviation	0.2066

2.4. Mapping Quality

Mean Mapping Quality	45.67

2.5. Mismatches and indels

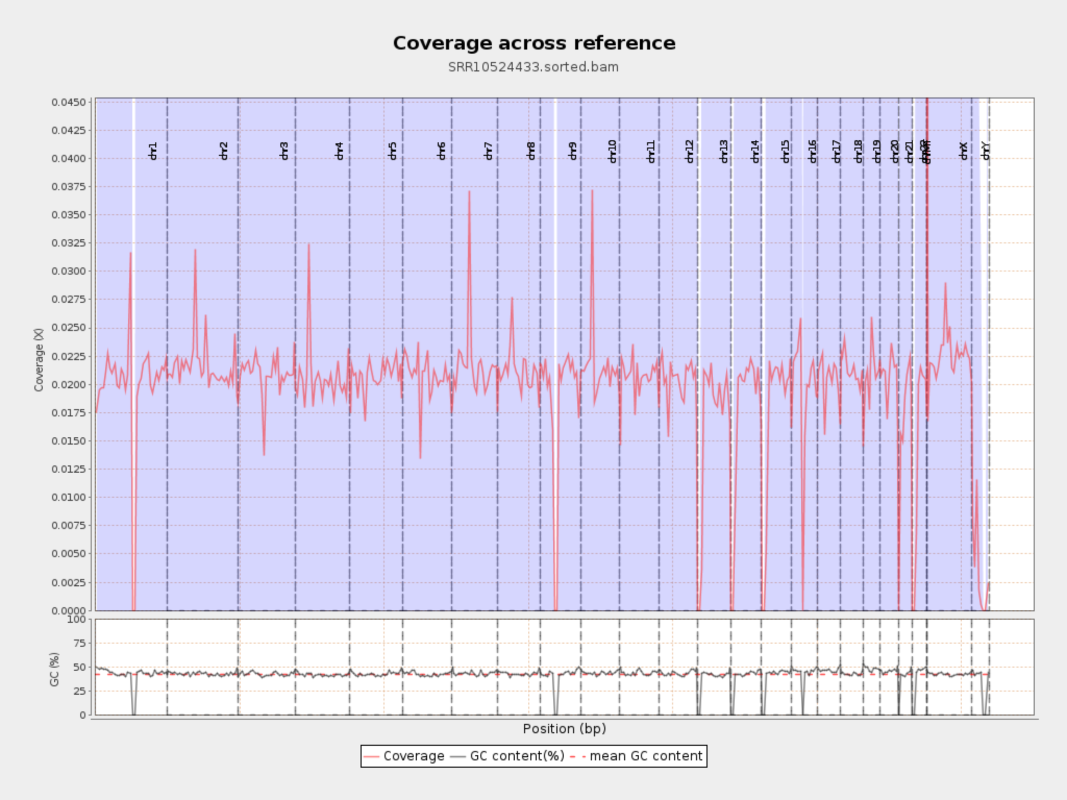
General error rate	0.52%
Mismatches	308,563
Insertions	5,110
Mapped reads with at least one insertion	0.48%
Deletions	12,894
Mapped reads with at least one deletion	1.21%
Homopolymer indels	42.01%

2.6. Chromosome stats

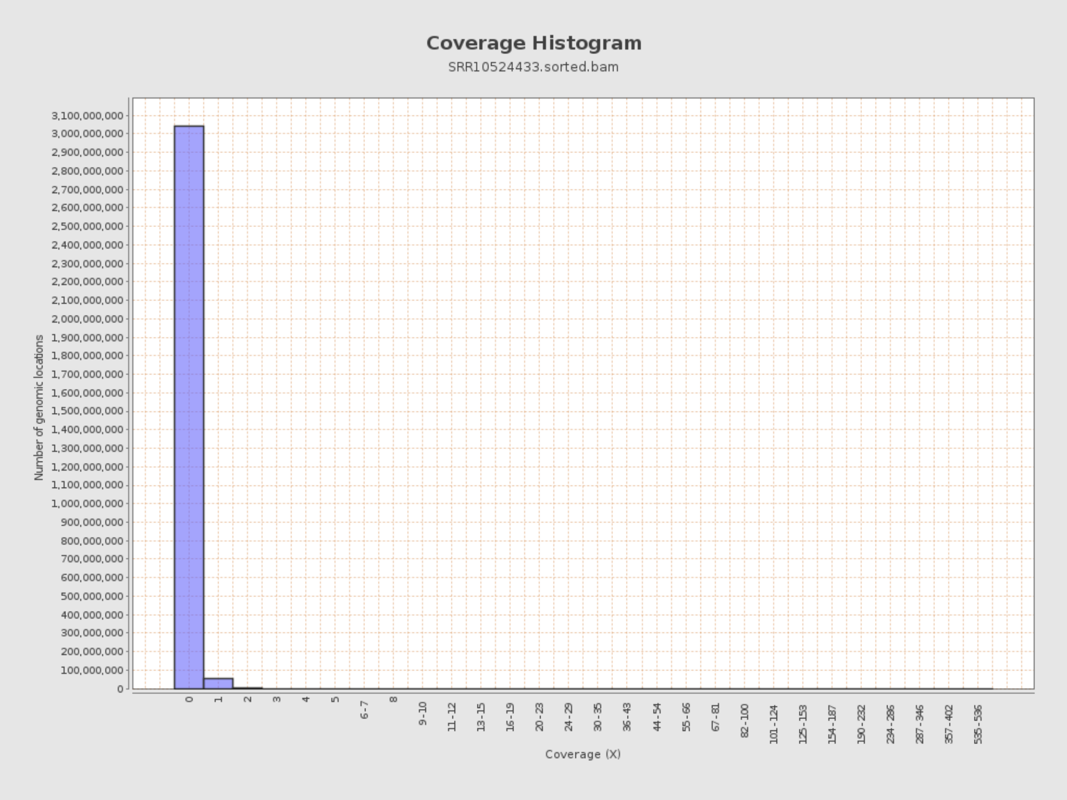
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4914542	0.0197	0.3211
chr2	243199373	5270414	0.0217	0.2781
chr3	198022430	4130196	0.0209	0.1548
chr4	191154276	3945030	0.0206	0.1648
chr5	180915260	3775901	0.0209	0.1544
chr6	171115067	3550116	0.0207	0.1694
chr7	159138663	3480383	0.0219	0.295

chr8	146364022	3113843	0.0213	0.2297
chr9	141213431	2606208	0.0185	0.1759
chr10	135534747	2960969	0.0218	0.2056
chr11	135006516	2806963	0.0208	0.1785
chr12	133851895	2737071	0.0204	0.1543
chr13	115169878	1884225	0.0164	0.1377
chr14	107349540	1846987	0.0172	0.1453
chr15	102531392	1724962	0.0168	0.139
chr16	90354753	1718861	0.019	0.156
chr17	81195210	1660367	0.0204	0.1581
chr18	78077248	1665142	0.0213	0.2887
chr19	59128983	1247323	0.0211	0.2472
chr20	63025520	1308581	0.0208	0.1559
chr21	48129895	814616	0.0169	0.1525
chr22	51304566	727962	0.0142	0.1276
chrMT	16571	5387	0.3251	0.625
chrX	155270560	3507025	0.0226	0.1698
chrY	59373566	196402	0.0033	0.1003

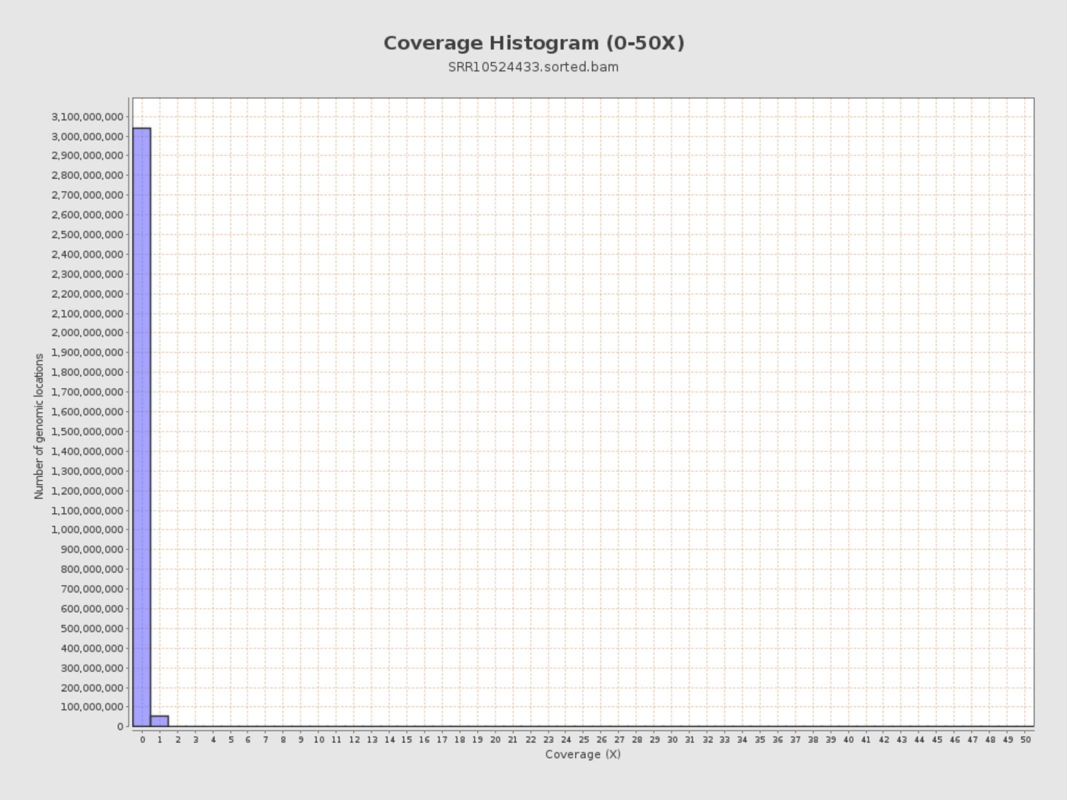
3. Results : Coverage across reference



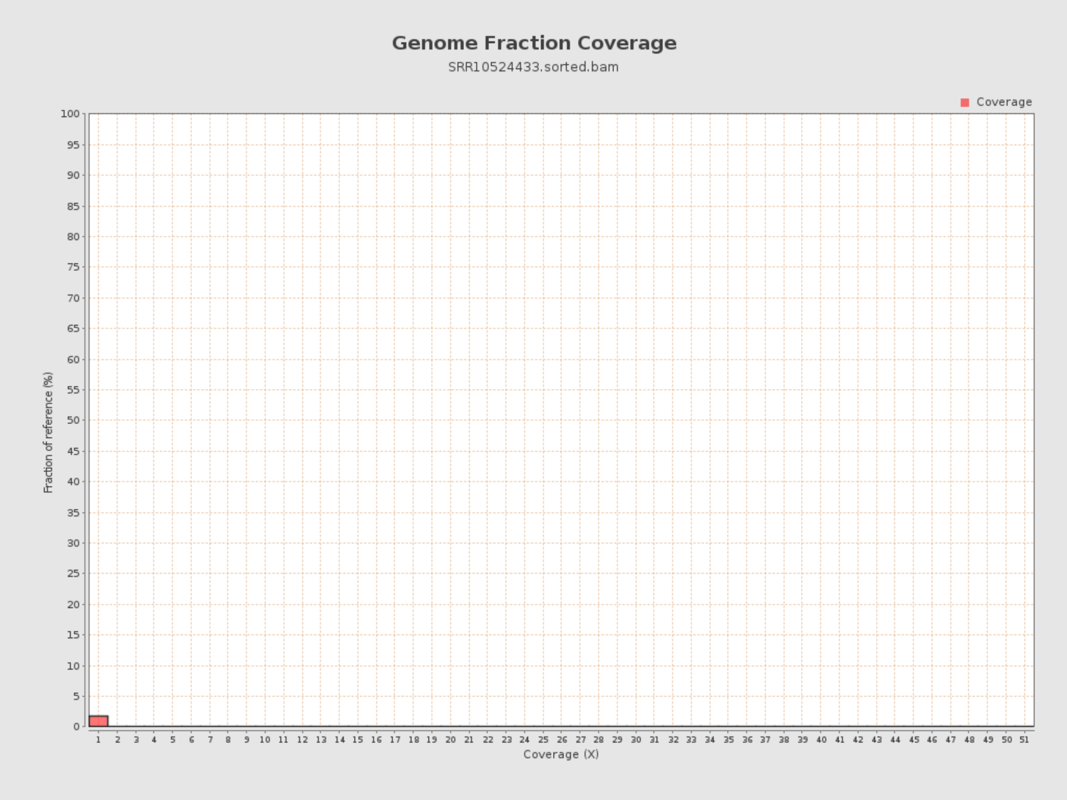
4. Results : Coverage Histogram



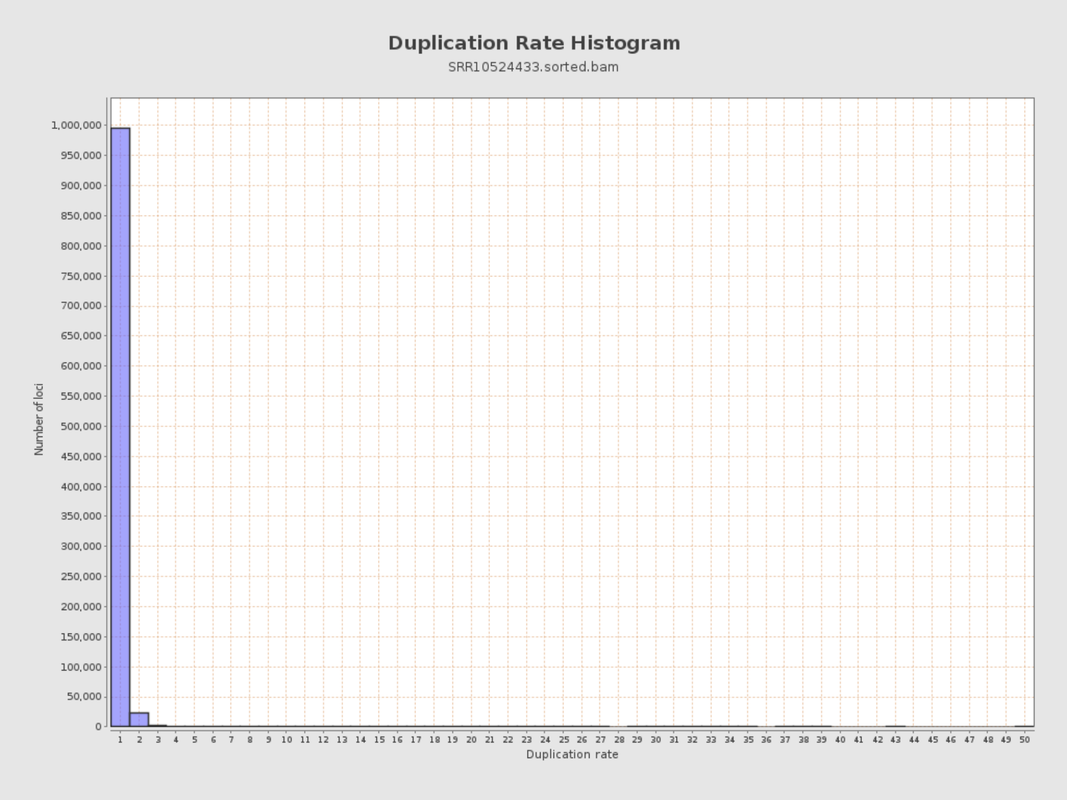
5. Results : Coverage Histogram (0-50X)



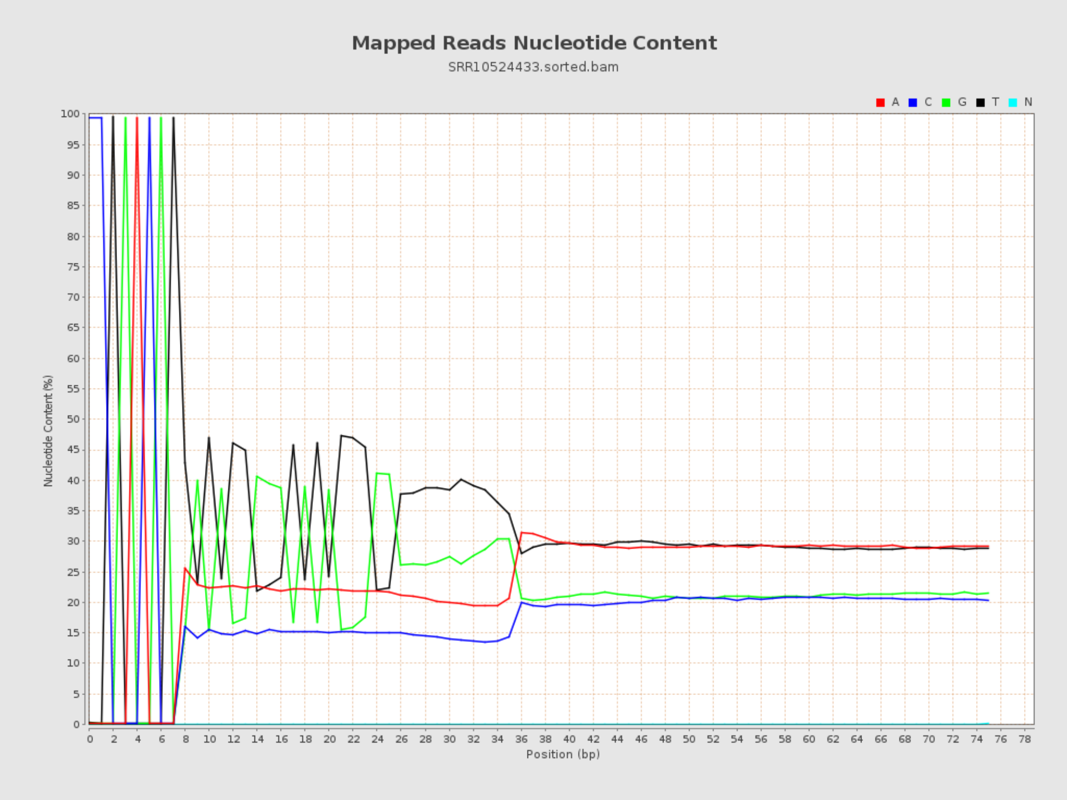
6. Results : Genome Fraction Coverage



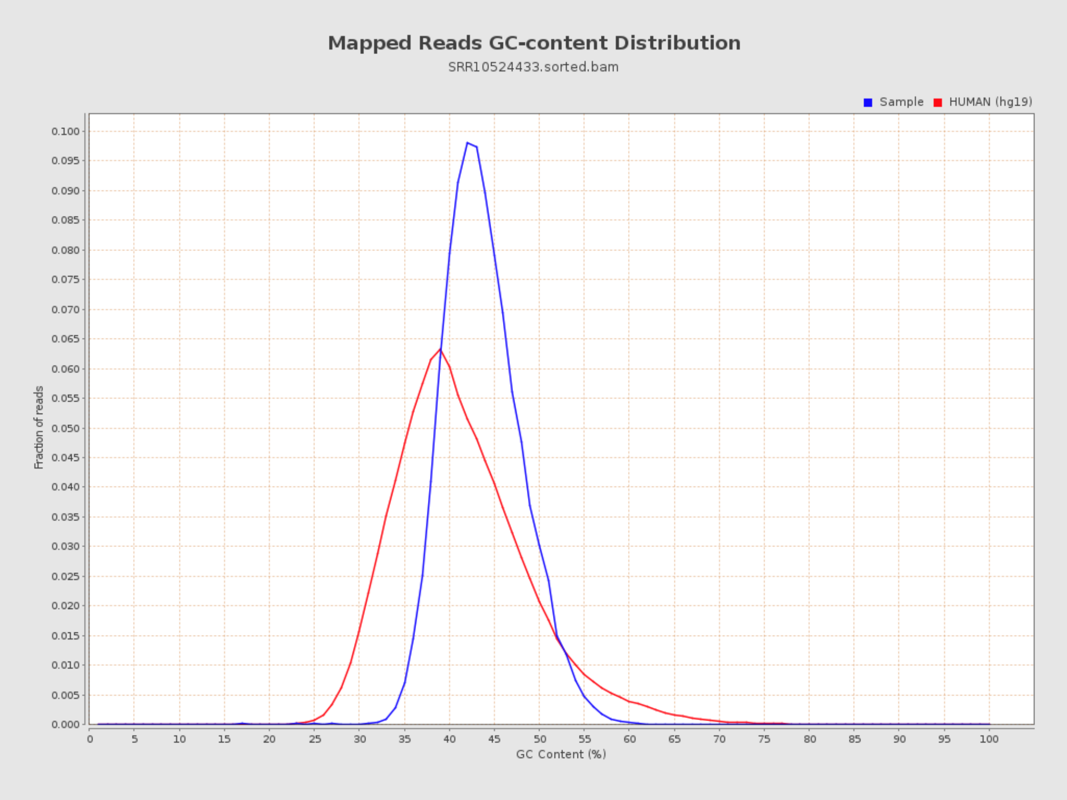
7. Results : Duplication Rate Histogram



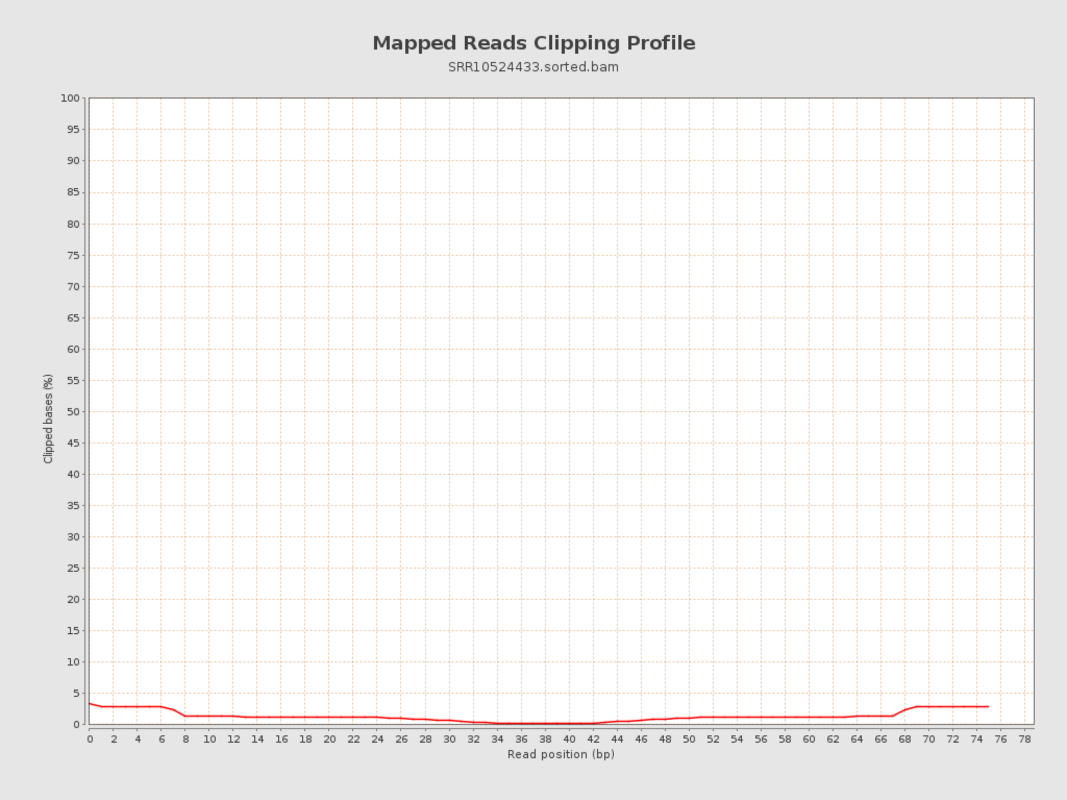
8. Results : Mapped Reads Nucleotide Content



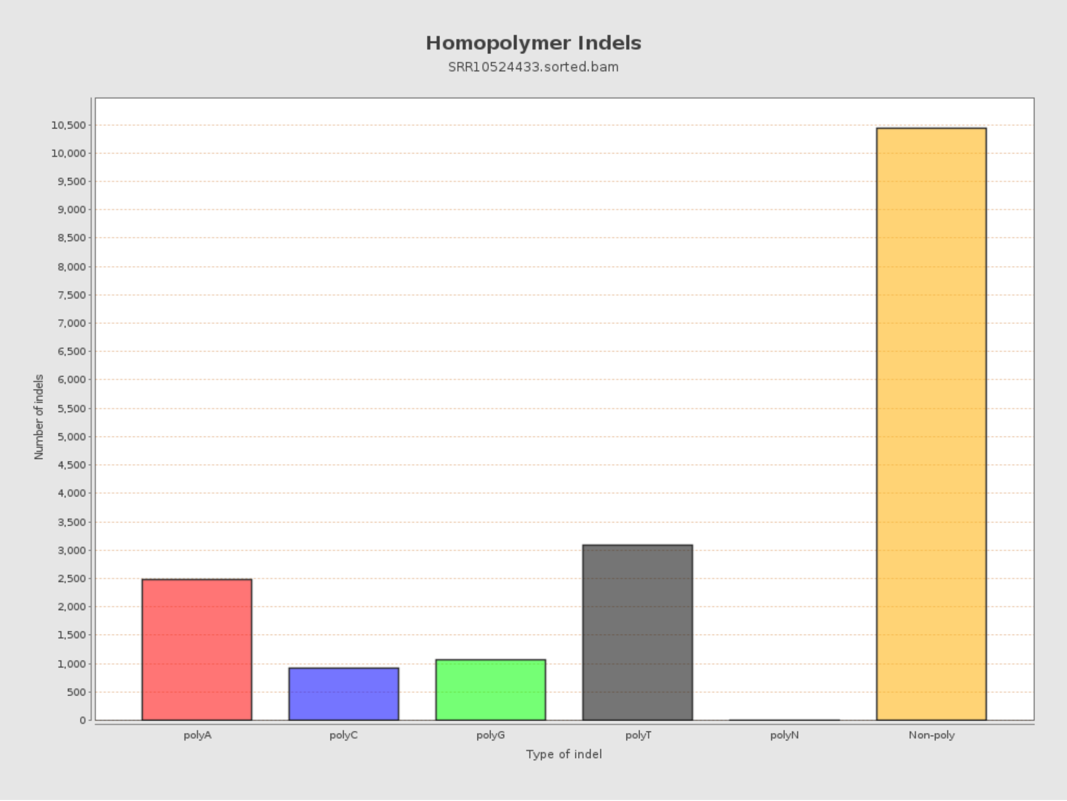
9. Results : Mapped Reads GC-content Distribution



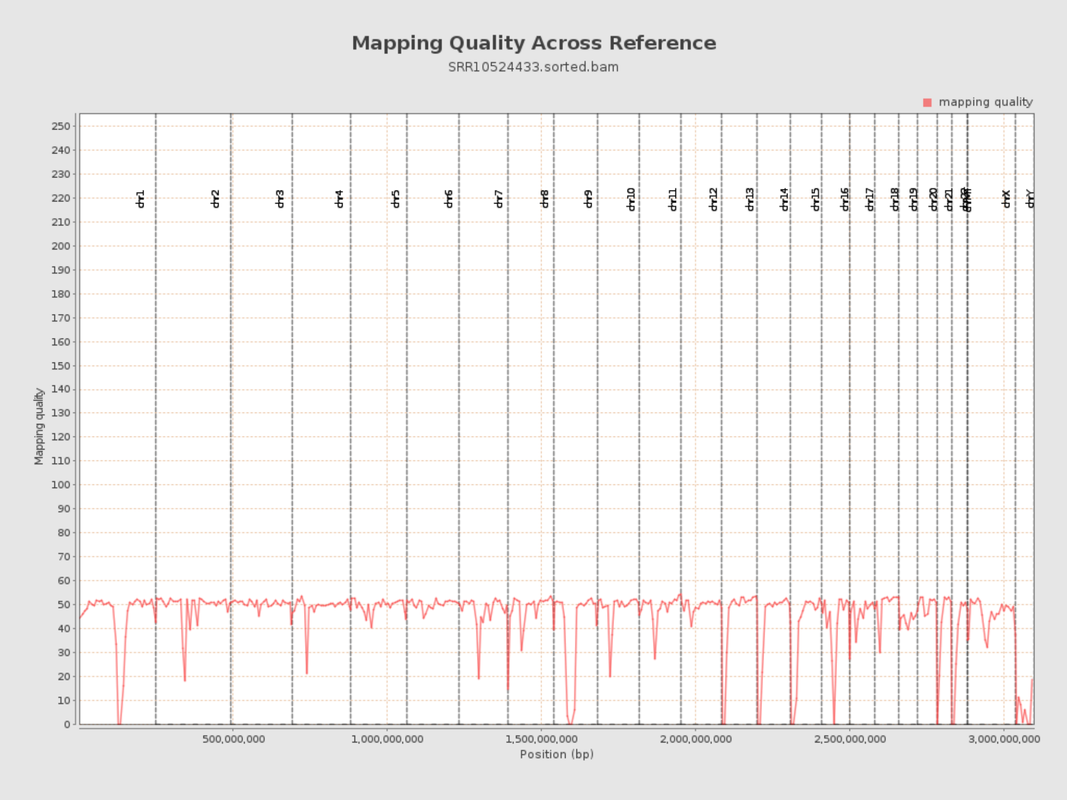
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram