Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 18:35:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524447.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_SRR10524447 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524447.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 18:35:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524447.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,707,892
Mapped reads	5,260,823 / 92.17%
Unmapped reads	447,069 / 7.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,102 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	586,999 / 10.28%
Duplication rate	8.02%
Clipped reads	5,255,498 / 92.07%

2.2. ACGT Content

Number/percentage of A's	78,396,268 / 25.58%
Number/percentage of C's	51,598,346 / 16.84%
Number/percentage of T's	98,512,680 / 32.15%
Number/percentage of G's	77,922,198 / 25.43%
Number/percentage of N's	6,117 / 0%
GC Percentage	42.27%

2.3. Coverage

Mean	0.099

Standard Deviation	0.7928

2.4. Mapping Quality

Mean Mapping Quality	45.47

2.5. Mismatches and indels

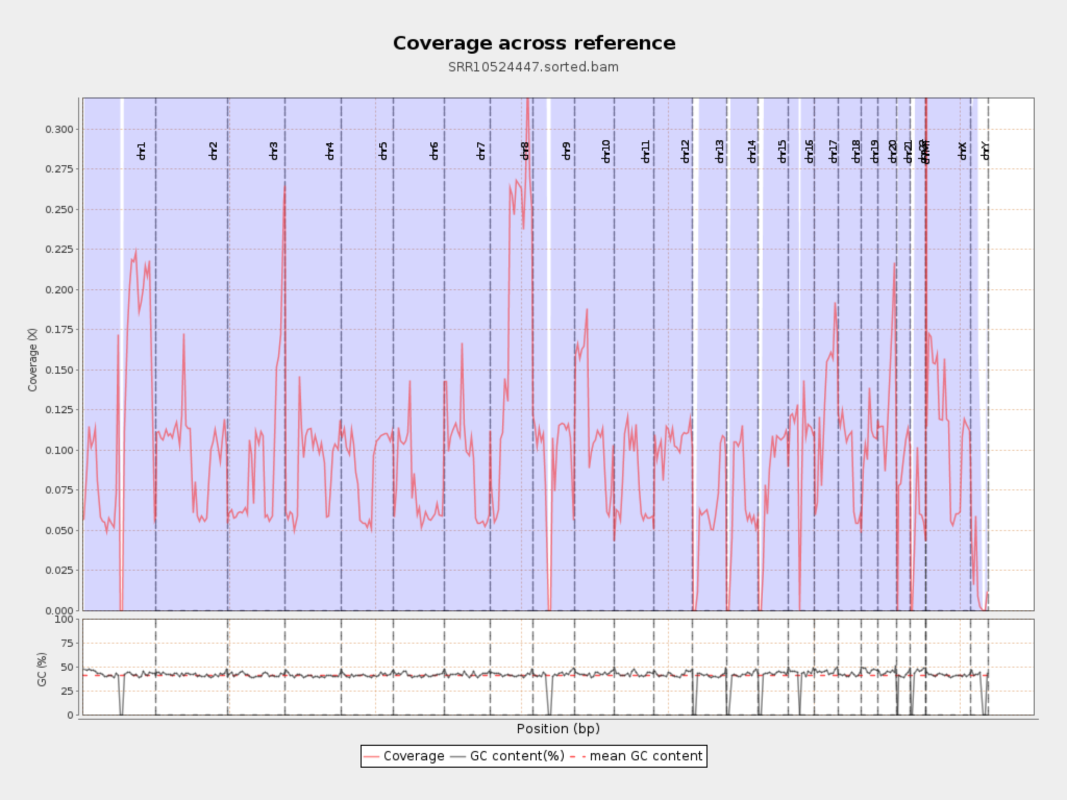
General error rate	0.48%
Mismatches	1,426,830
Insertions	20,487
Mapped reads with at least one insertion	0.39%
Deletions	56,845
Mapped reads with at least one deletion	1.07%
Homopolymer indels	43.53%

2.6. Chromosome stats

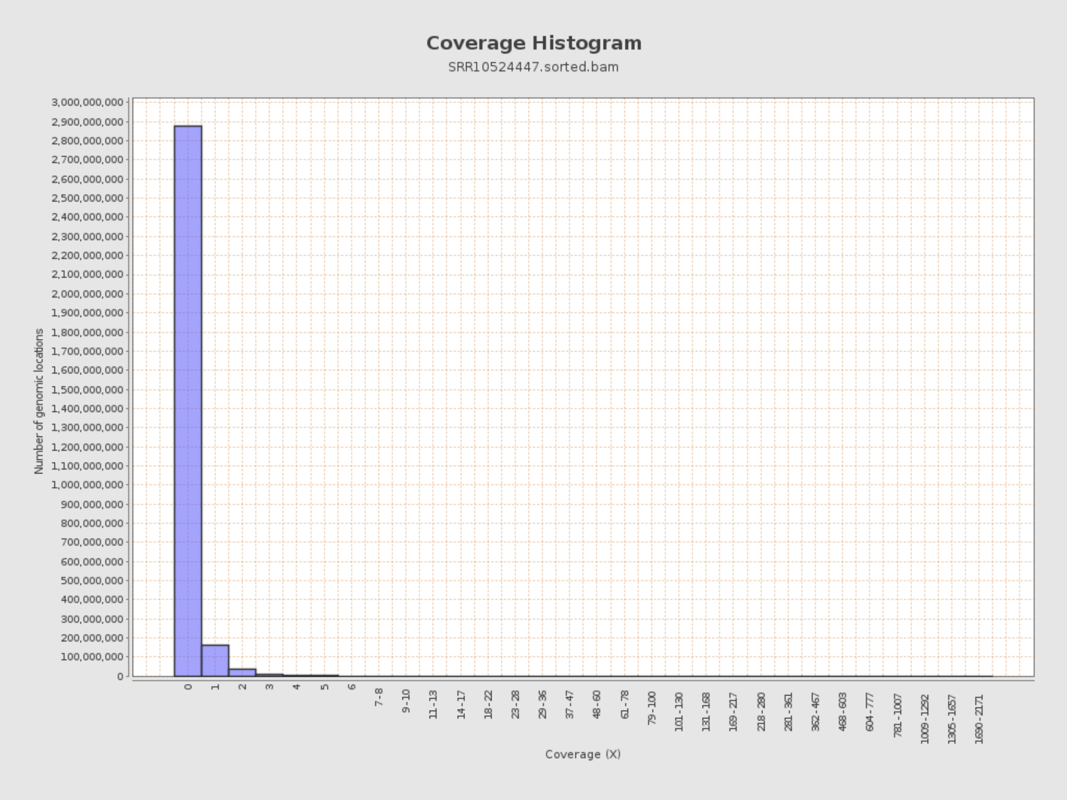
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	29773367	0.1195	1.61
chr2	243199373	24241486	0.0997	0.9002
chr3	198022430	18583961	0.0938	0.4217
chr4	191154276	17349521	0.0908	0.527
chr5	180915260	16480265	0.0911	0.4112
chr6	171115067	13121361	0.0767	0.5831
chr7	159138663	15101982	0.0949	1.0596

chr8	146364022	28197657	0.1927	0.7932
chr9	141213431	12983695	0.0919	0.656
chr10	135534747	15895706	0.1173	0.7889
chr11	135006516	10564689	0.0783	0.7757
chr12	133851895	14164504	0.1058	0.4435
chr13	115169878	6909187	0.06	0.338
chr14	107349540	7190079	0.067	0.3662
chr15	102531392	8051231	0.0785	0.4173
chr16	90354753	9465867	0.1048	0.4999
chr17	81195210	10577781	0.1303	0.5447
chr18	78077248	7285871	0.0933	1.3343
chr19	59128983	6207110	0.105	1.0939
chr20	63025520	8740713	0.1387	0.5185
chr21	48129895	4166389	0.0866	0.475
chr22	51304566	2492899	0.0486	0.2959
chrMT	16571	163946	9.8935	6.7962
chrX	155270560	17829582	0.1148	0.5805
chrY	59373566	993497	0.0167	0.4257

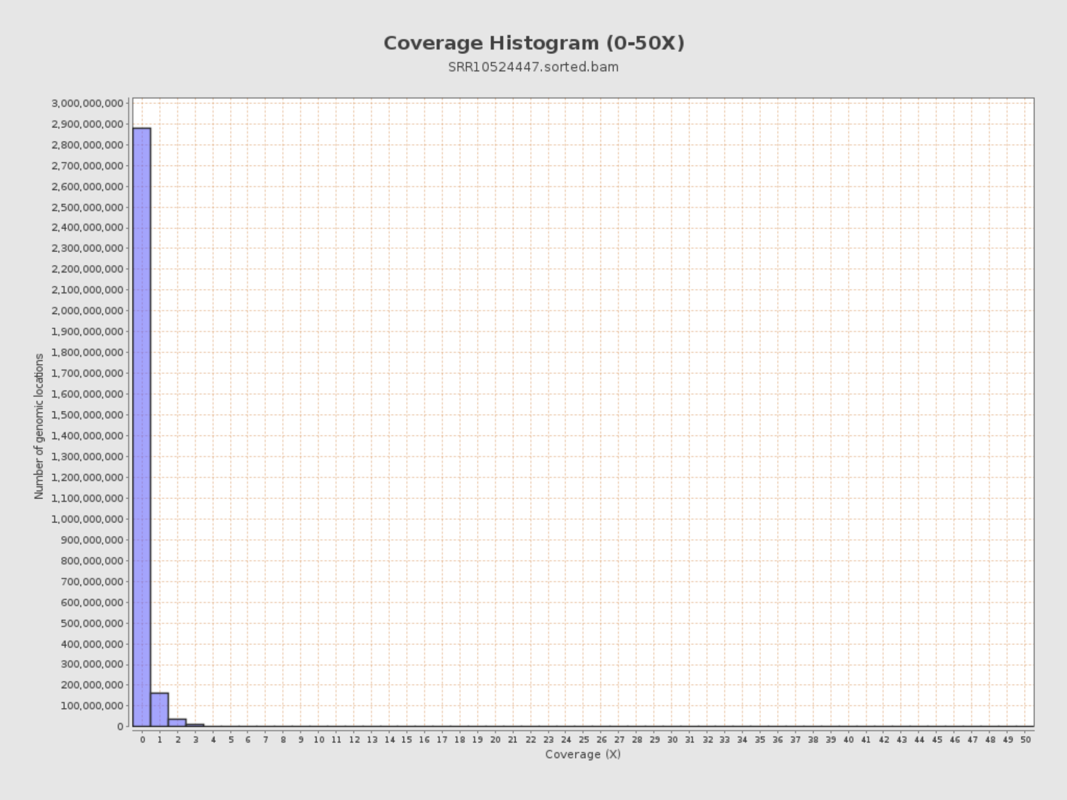
3. Results : Coverage across reference



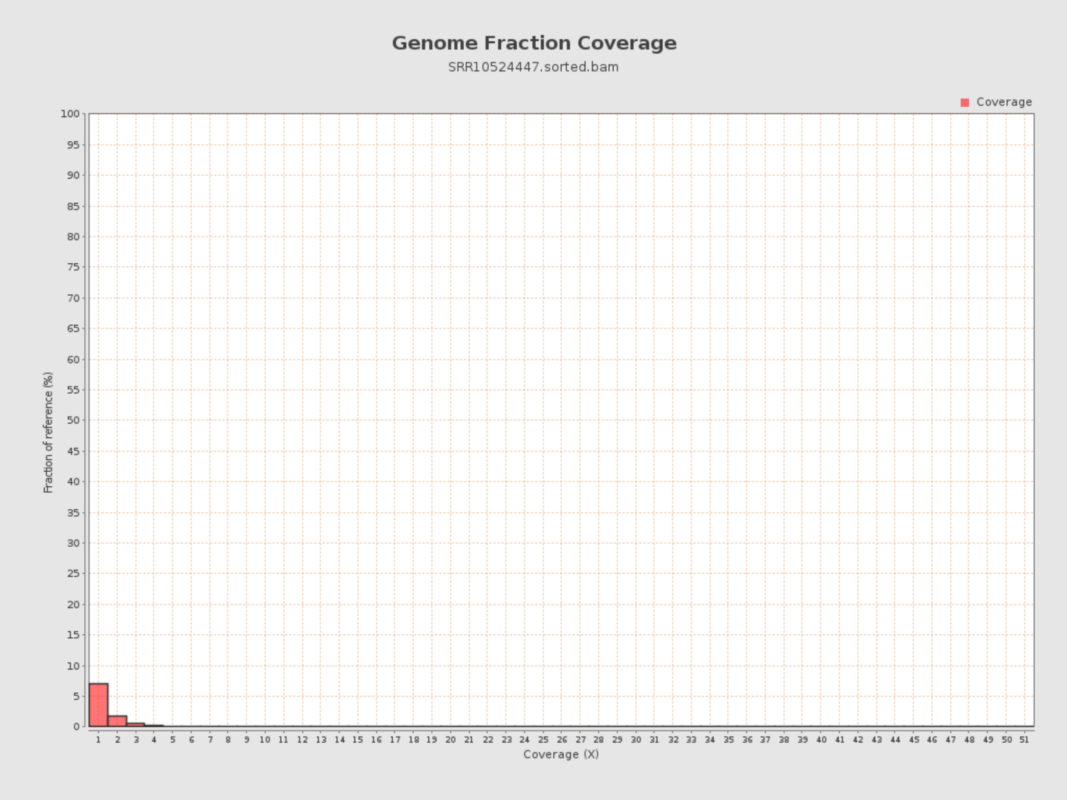
4. Results : Coverage Histogram



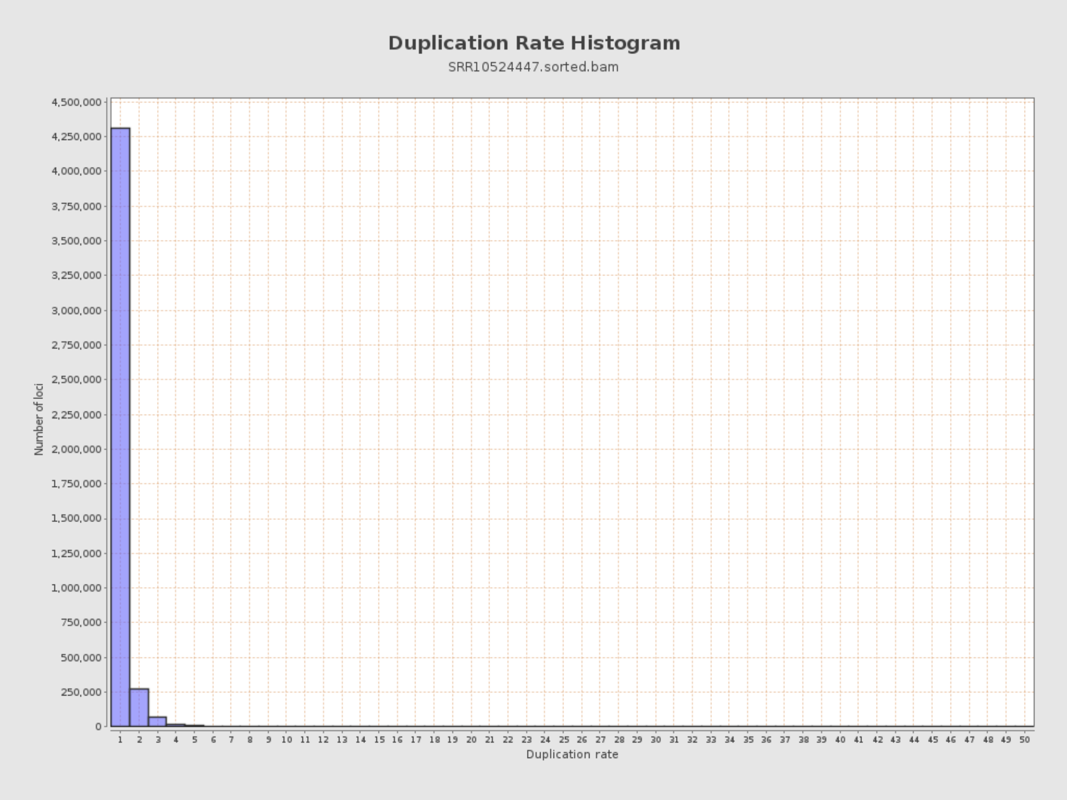
5. Results : Coverage Histogram (0-50X)



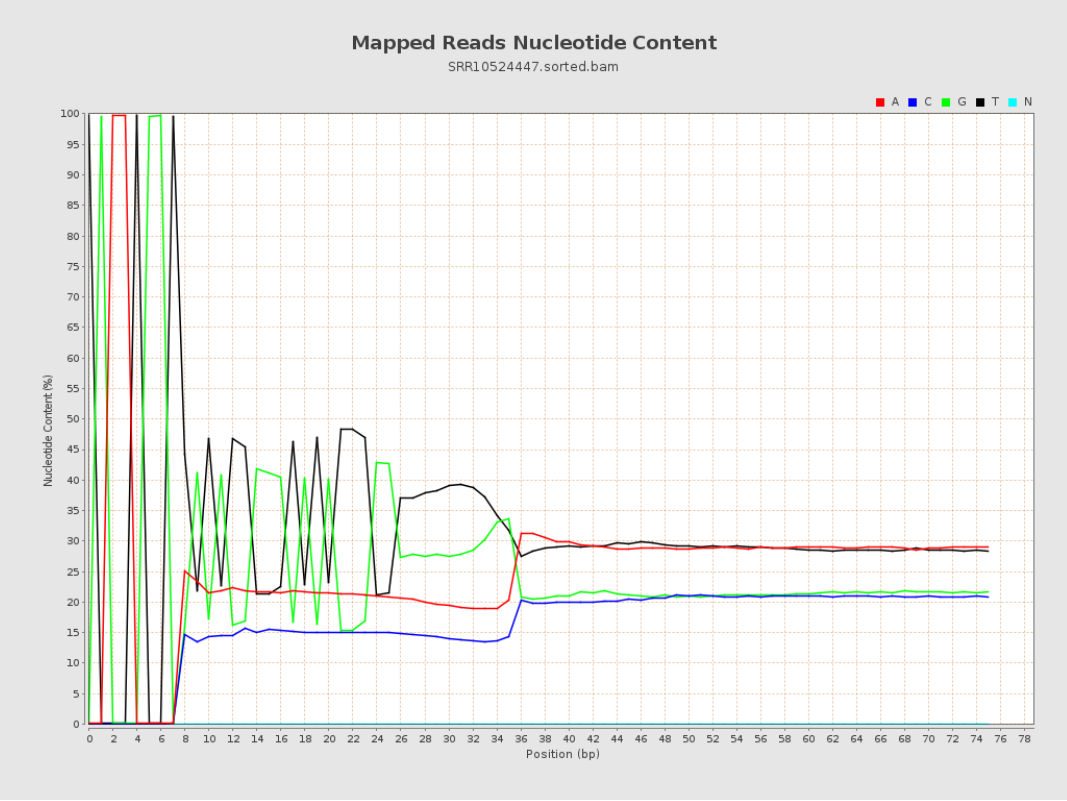
6. Results : Genome Fraction Coverage



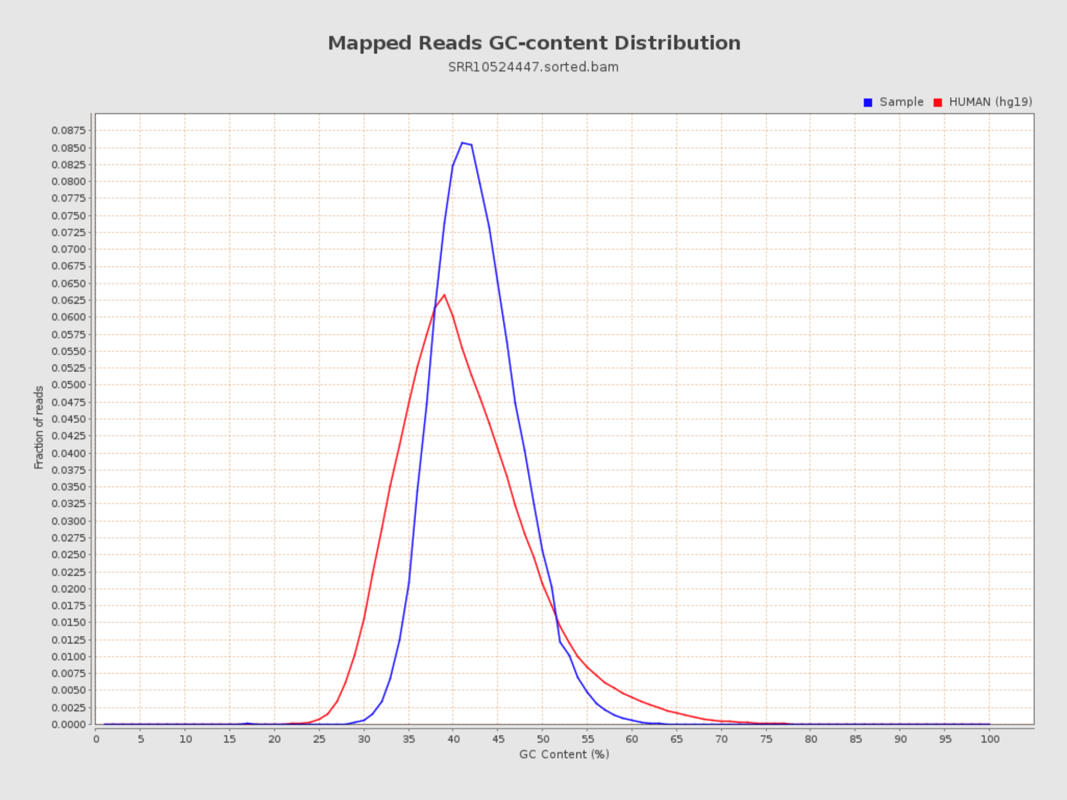
7. Results : Duplication Rate Histogram



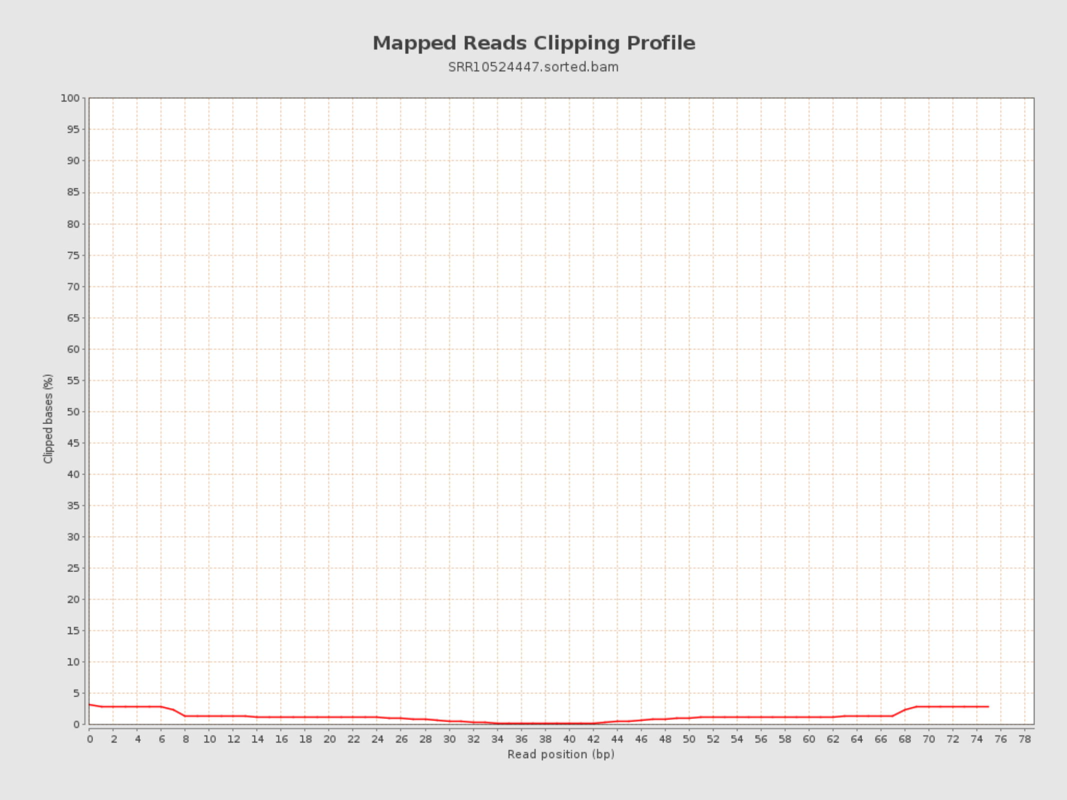
8. Results : Mapped Reads Nucleotide Content



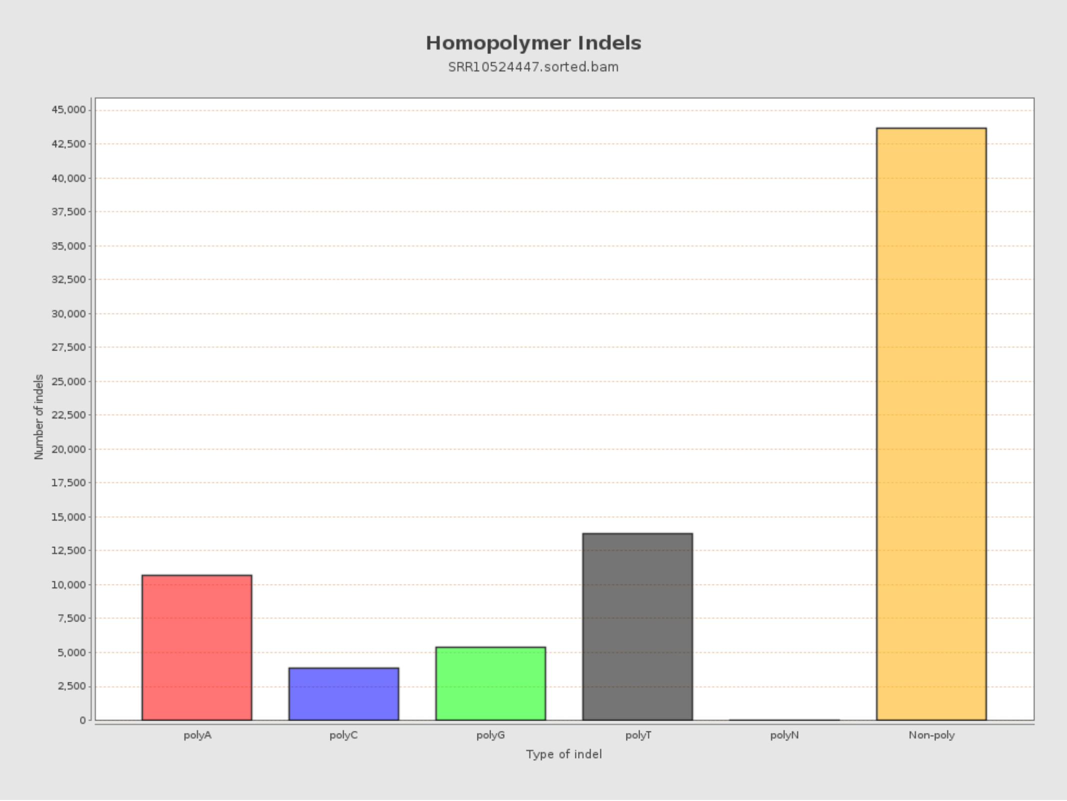
9. Results : Mapped Reads GC-content Distribution



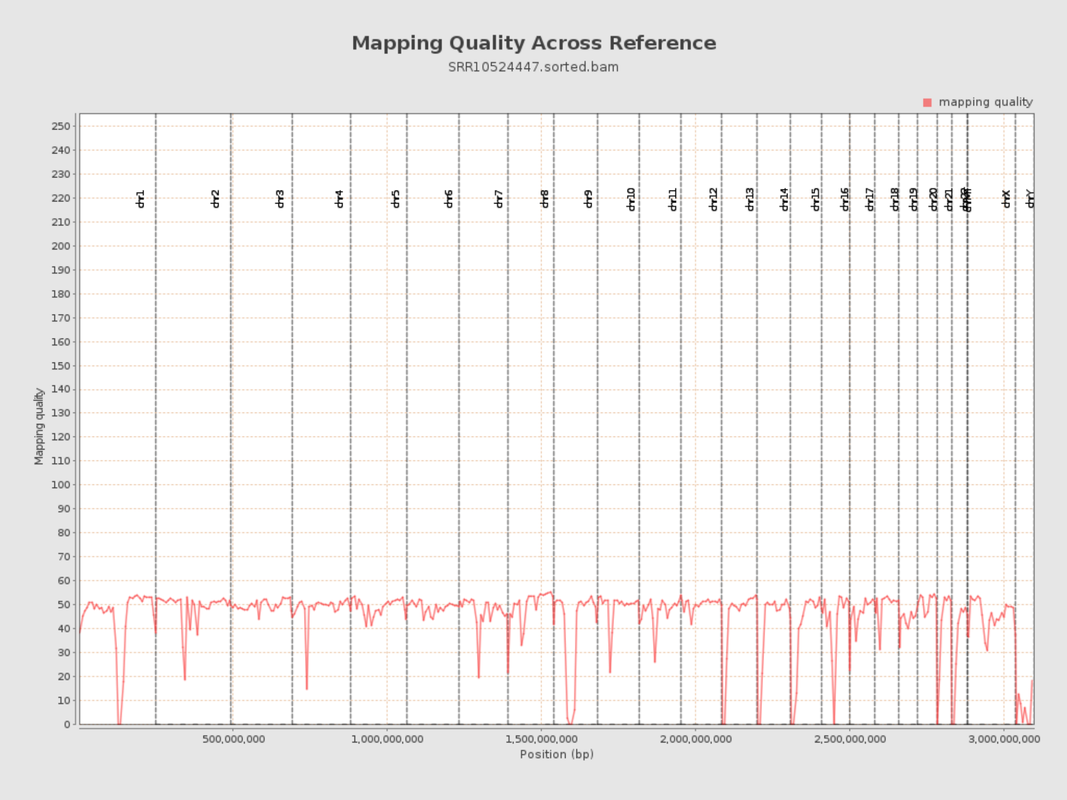
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram