Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 04:36:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524445.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_SRR10524445 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524445.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 04:36:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524445.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,083,027
Mapped reads	2,864,808 / 92.92%
Unmapped reads	218,219 / 7.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,642 / 0.22%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	198,694 / 6.44%
Duplication rate	5.28%
Clipped reads	2,868,045 / 93.03%

2.2. ACGT Content

Number/percentage of A's	40,225,028 / 24.03%
Number/percentage of C's	33,929,746 / 20.27%
Number/percentage of T's	53,645,642 / 32.05%
Number/percentage of G's	39,583,175 / 23.65%
Number/percentage of N's	3,308 / 0%
GC Percentage	43.92%

2.3. Coverage

Mean	0.0541

Standard Deviation	0.441

2.4. Mapping Quality

Mean Mapping Quality	46.03

2.5. Mismatches and indels

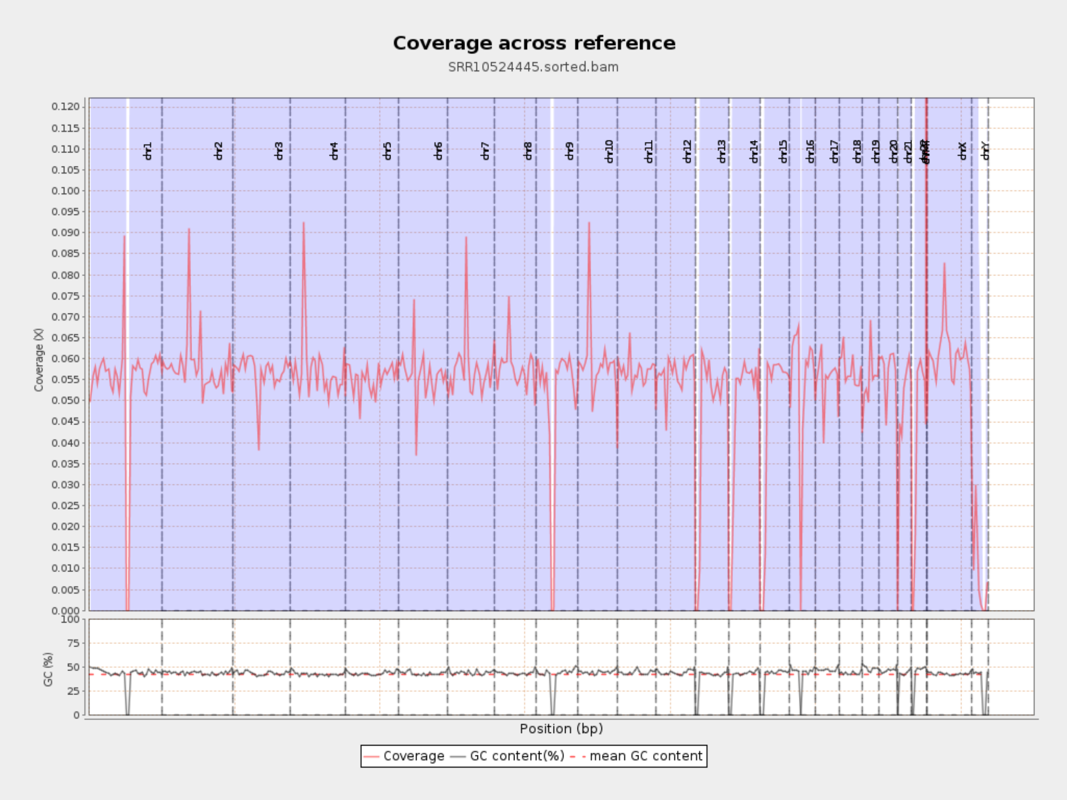
General error rate	0.47%
Mismatches	767,686
Insertions	9,067
Mapped reads with at least one insertion	0.32%
Deletions	30,796
Mapped reads with at least one deletion	1.07%
Homopolymer indels	45.2%

2.6. Chromosome stats

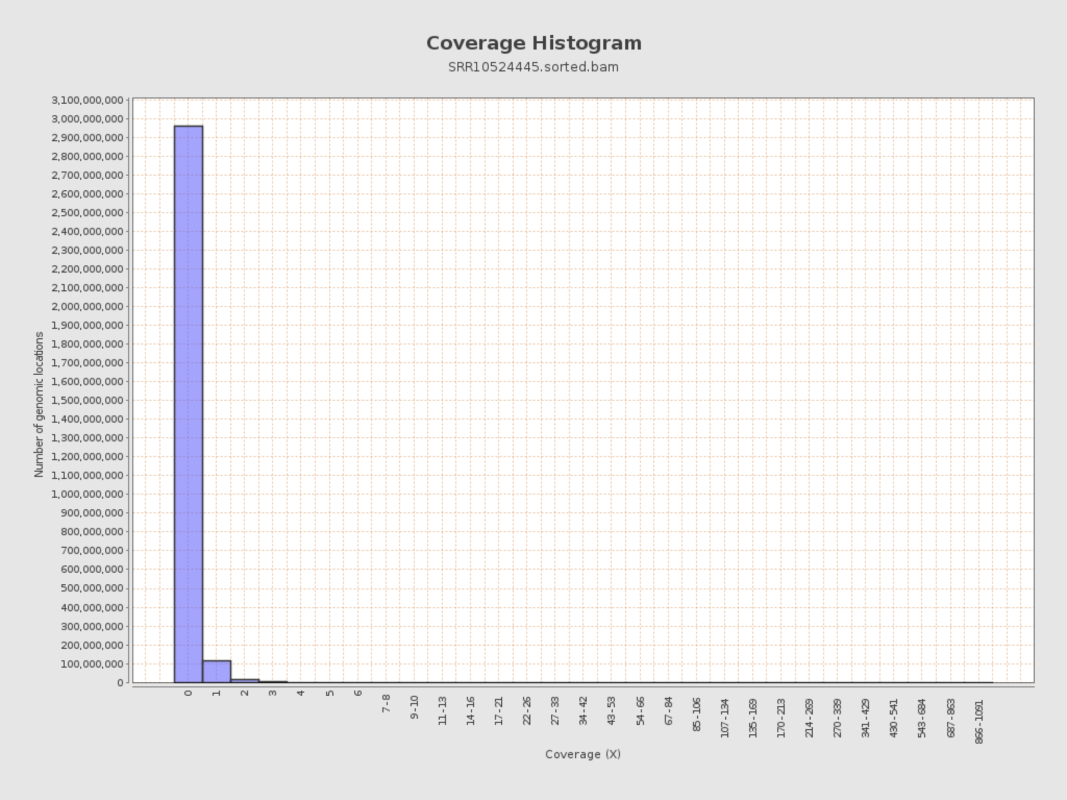
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13468146	0.054	0.813
chr2	243199373	14186973	0.0583	0.5006
chr3	198022430	11228573	0.0567	0.2842
chr4	191154276	10956080	0.0573	0.3333
chr5	180915260	10002294	0.0553	0.2815
chr6	171115067	9605143	0.0561	0.3634
chr7	159138663	9188319	0.0577	0.6043

chr8	146364022	8464117	0.0578	0.4202
chr9	141213431	7020508	0.0497	0.3847
chr10	135534747	8034936	0.0593	0.4253
chr11	135006516	7663683	0.0568	0.4445
chr12	133851895	7582186	0.0566	0.2893
chr13	115169878	5341440	0.0464	0.2589
chr14	107349540	4975072	0.0463	0.2649
chr15	102531392	4721156	0.046	0.2732
chr16	90354753	4932389	0.0546	0.308
chr17	81195210	4462963	0.055	0.31
chr18	78077248	4471705	0.0573	0.7247
chr19	59128983	3269538	0.0553	0.5872
chr20	63025520	3587323	0.0569	0.2936
chr21	48129895	2265005	0.0471	0.2875
chr22	51304566	1994882	0.0389	0.2334
chrMT	16571	19581	1.1816	1.3503
chrX	155270560	9481392	0.0611	0.3517
chrY	59373566	516363	0.0087	0.2137

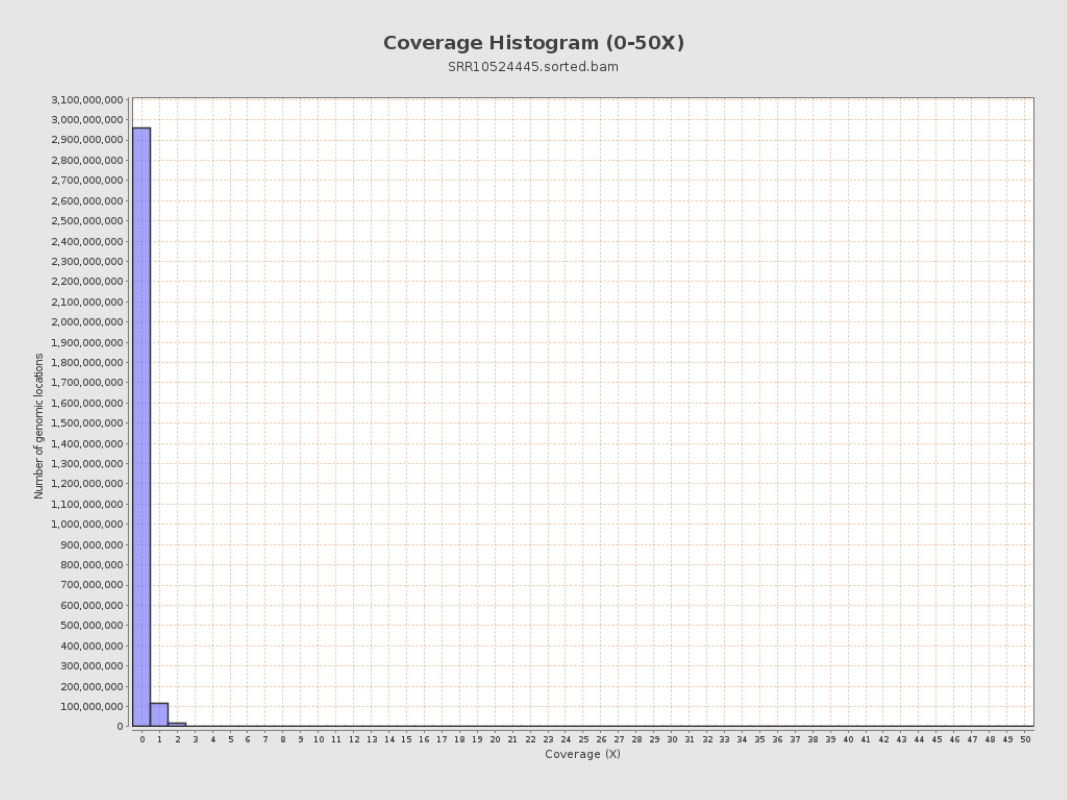
3. Results : Coverage across reference



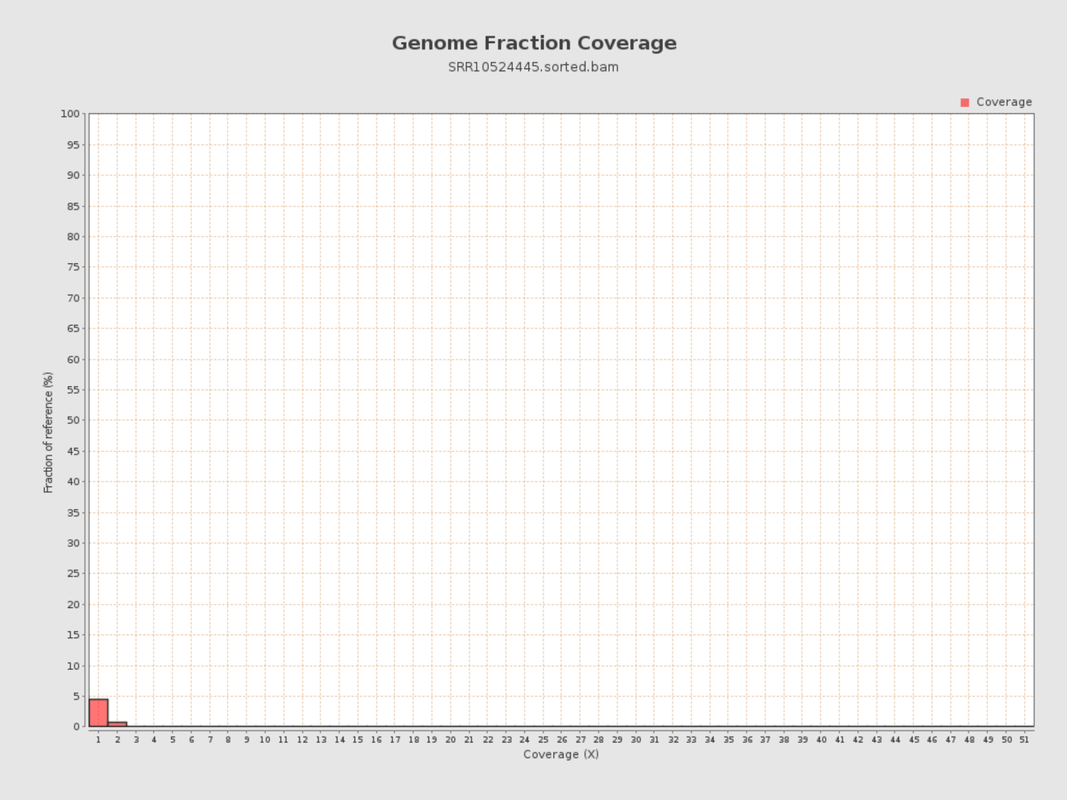
4. Results : Coverage Histogram



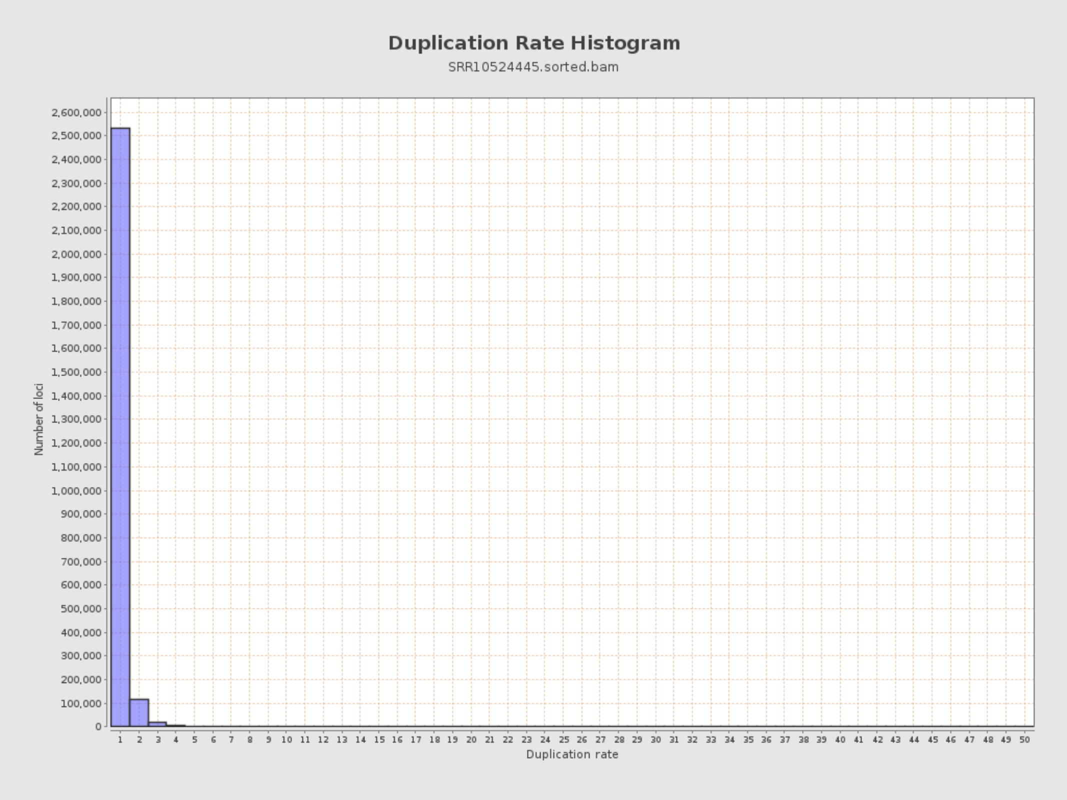
5. Results : Coverage Histogram (0-50X)



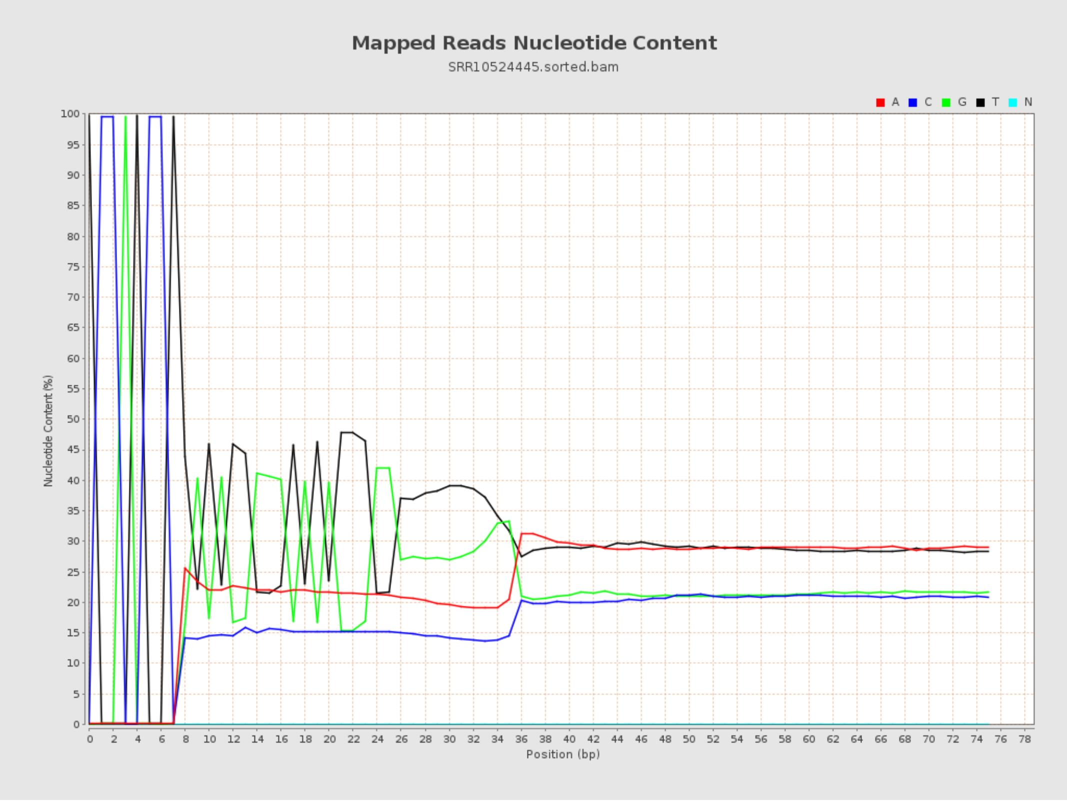
6. Results : Genome Fraction Coverage



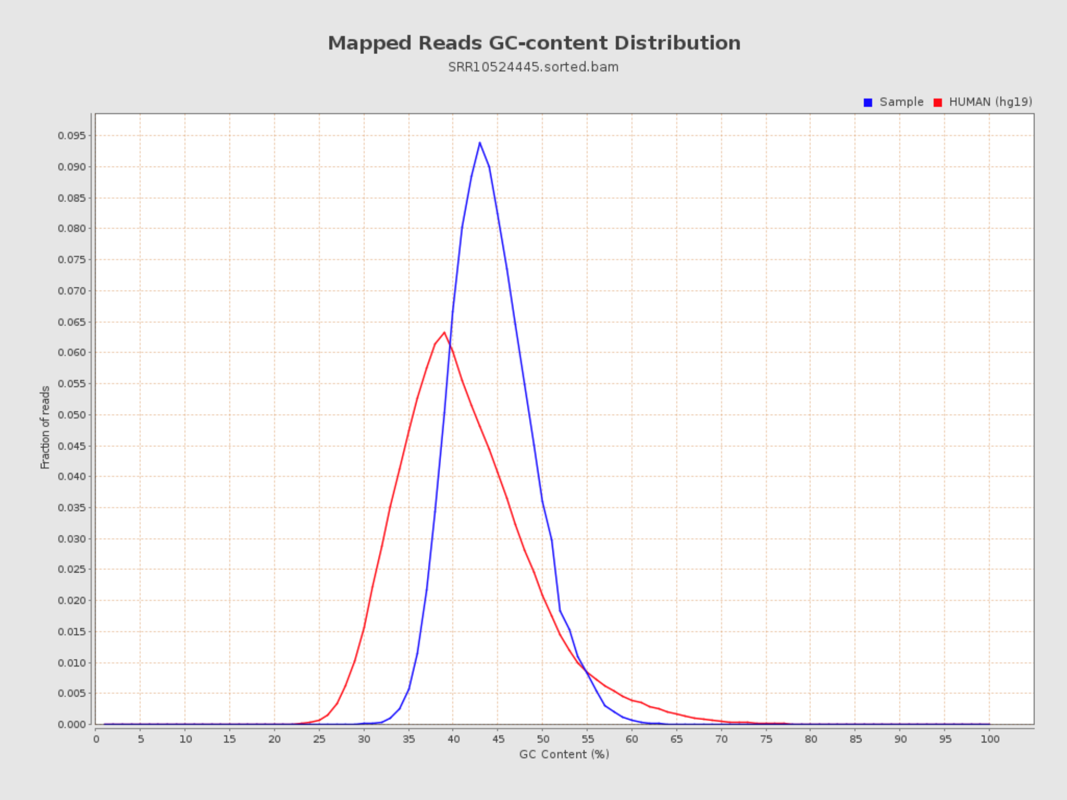
7. Results : Duplication Rate Histogram



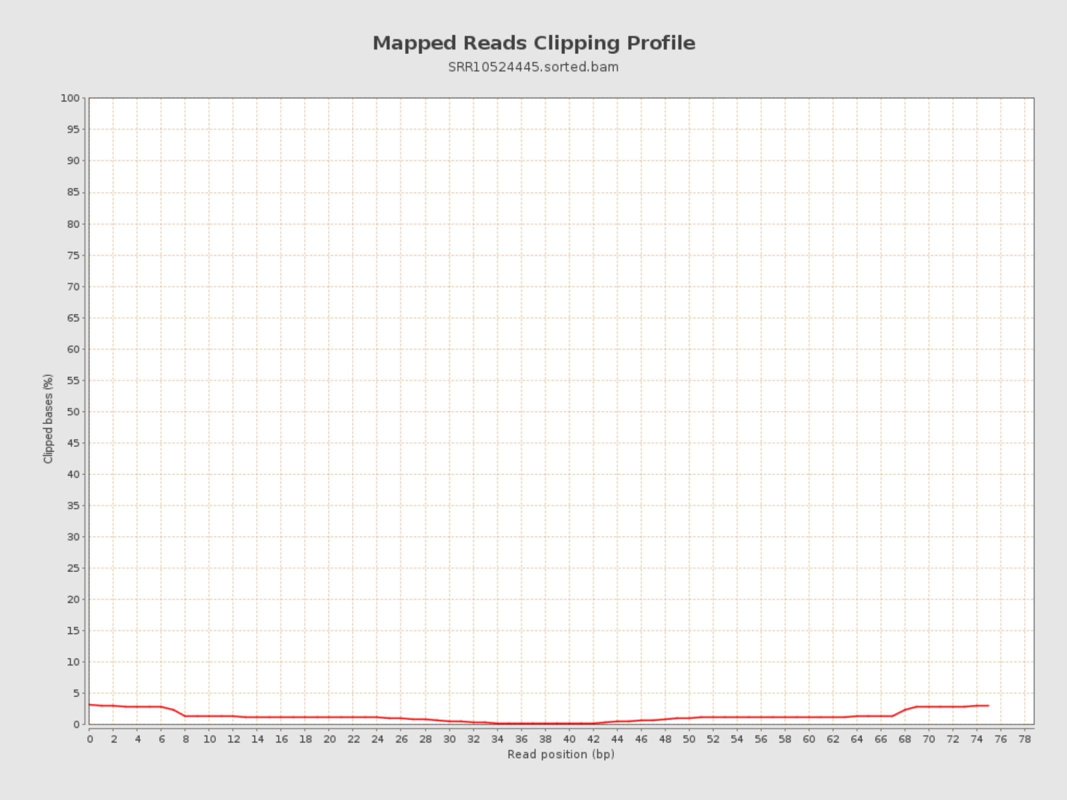
8. Results : Mapped Reads Nucleotide Content



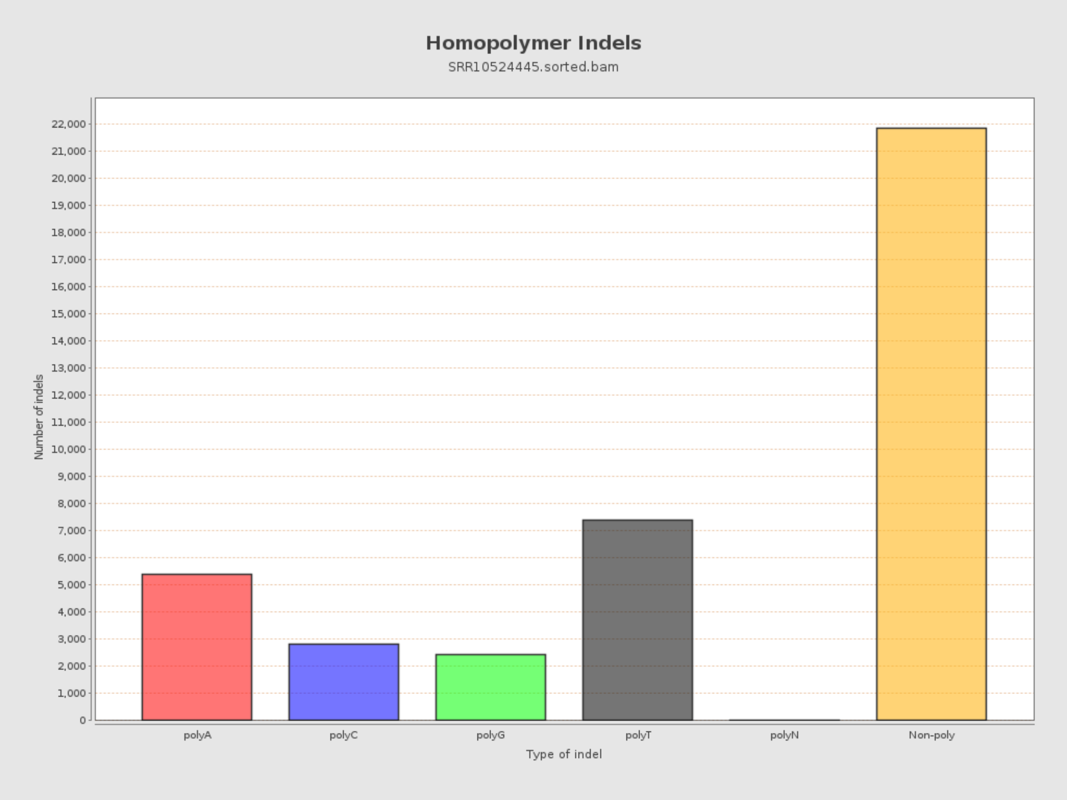
9. Results : Mapped Reads GC-content Distribution



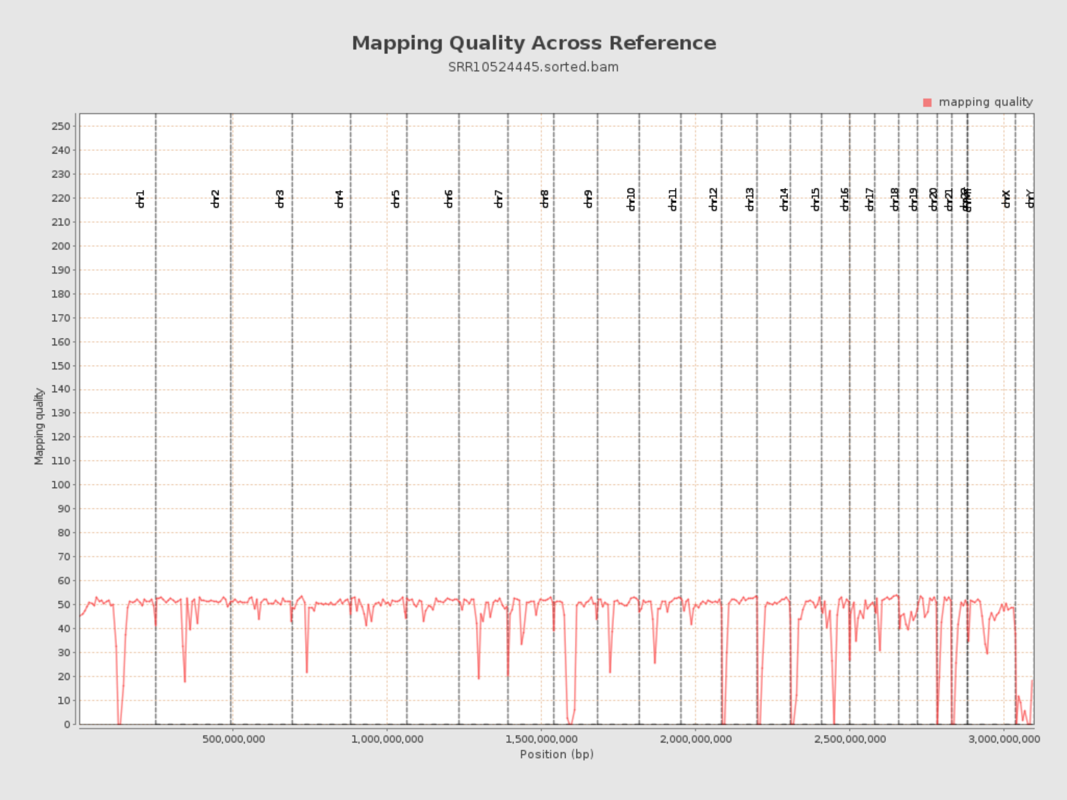
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram