Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 00:31:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524361.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_SRR10524361 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524361.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 00:31:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524361.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,261,535
Mapped reads	2,074,472 / 91.73%
Unmapped reads	187,063 / 8.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,019 / 0.44%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	134,498 / 5.95%
Duplication rate	4.87%
Clipped reads	2,077,484 / 91.86%

2.2. ACGT Content

Number/percentage of A's	28,580,247 / 23.59%
Number/percentage of C's	25,090,490 / 20.71%
Number/percentage of T's	38,639,807 / 31.89%
Number/percentage of G's	28,823,739 / 23.79%
Number/percentage of N's	16,806 / 0.01%
GC Percentage	44.5%

2.3. Coverage

Mean	0.0391

Standard Deviation	0.3804

2.4. Mapping Quality

Mean Mapping Quality	44.98

2.5. Mismatches and indels

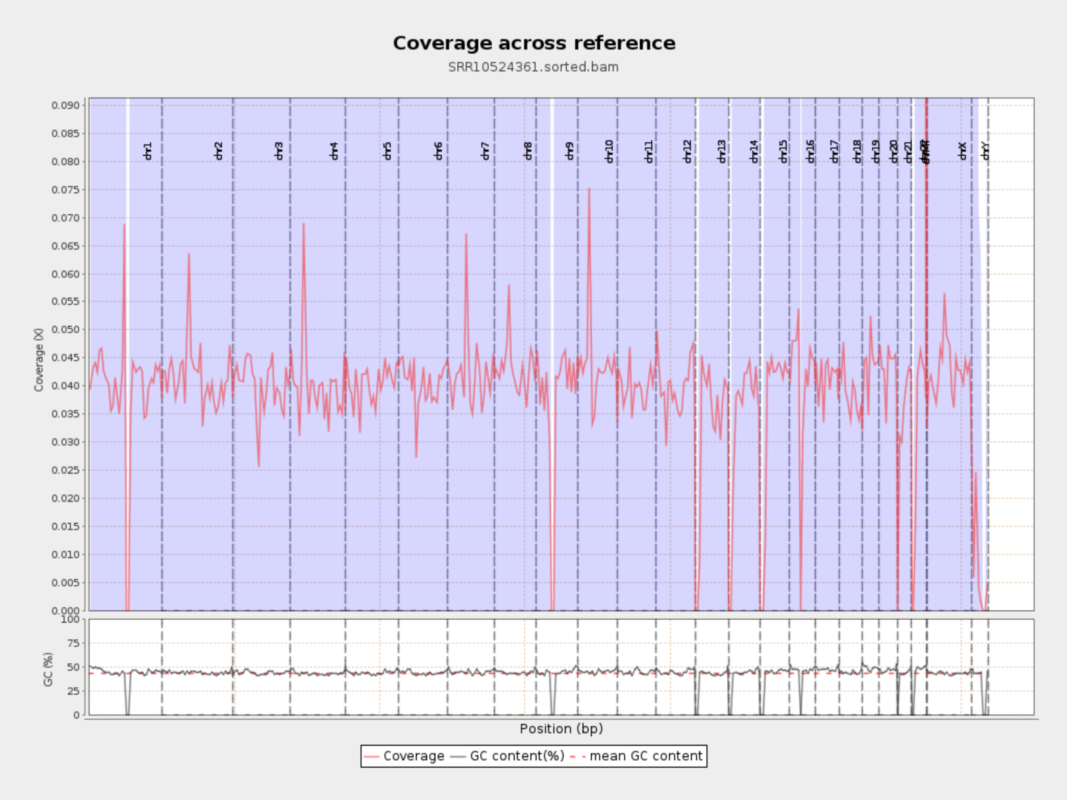
General error rate	0.53%
Mismatches	630,373
Insertions	8,967
Mapped reads with at least one insertion	0.43%
Deletions	21,991
Mapped reads with at least one deletion	1.05%
Homopolymer indels	42.18%

2.6. Chromosome stats

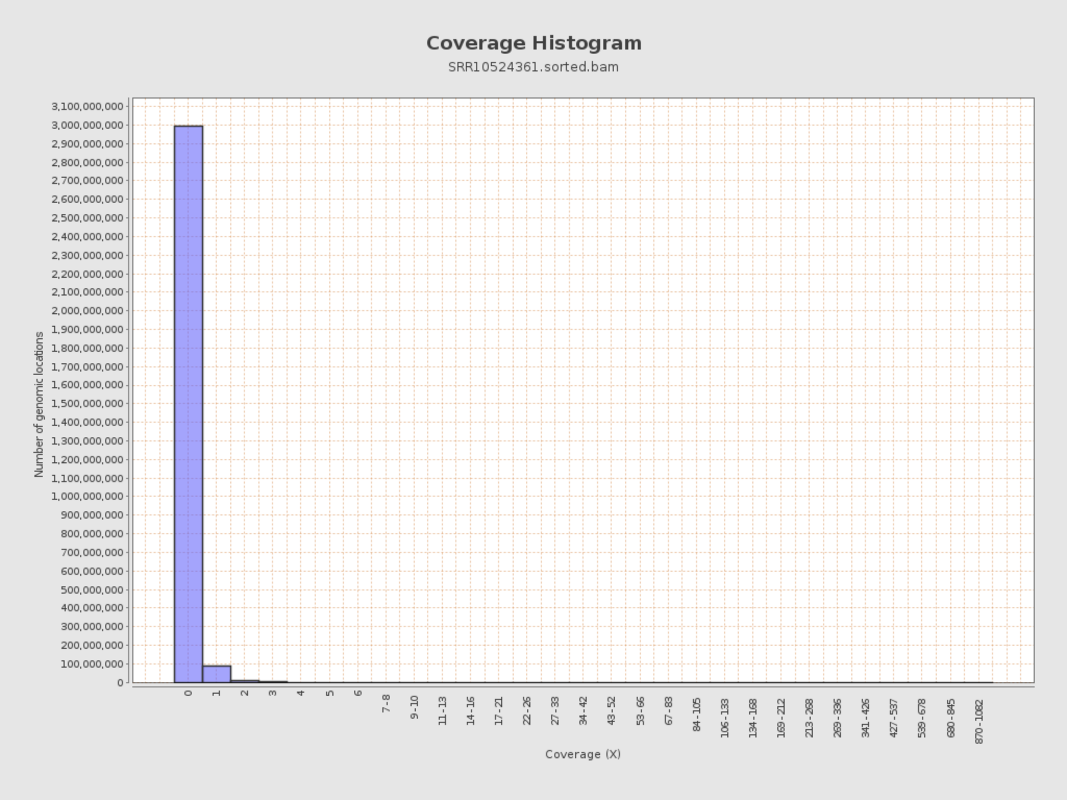
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9786997	0.0393	0.7603
chr2	243199373	10181741	0.0419	0.5097
chr3	198022430	7935710	0.0401	0.2334
chr4	191154276	7666577	0.0401	0.276
chr5	180915260	7295760	0.0403	0.2331
chr6	171115067	6941209	0.0406	0.2553
chr7	159138663	6717602	0.0422	0.4551

chr8	146364022	6308639	0.0431	0.333
chr9	141213431	5147114	0.0364	0.3129
chr10	135534747	5960879	0.044	0.3647
chr11	135006516	5370006	0.0398	0.3154
chr12	133851895	5346526	0.0399	0.2397
chr13	115169878	3717455	0.0323	0.2092
chr14	107349540	3596892	0.0335	0.2317
chr15	102531392	3559325	0.0347	0.2179
chr16	90354753	3691691	0.0409	0.2567
chr17	81195210	3355500	0.0413	0.2547
chr18	78077248	3034193	0.0389	0.5964
chr19	59128983	2588816	0.0438	0.4974
chr20	63025520	2729099	0.0433	0.2493
chr21	48129895	1622066	0.0337	0.2495
chr22	51304566	1542944	0.0301	0.2045
chrMT	16571	41140	2.4827	2.2323
chrX	155270560	6642240	0.0428	0.2706
chrY	59373566	405416	0.0068	0.1947

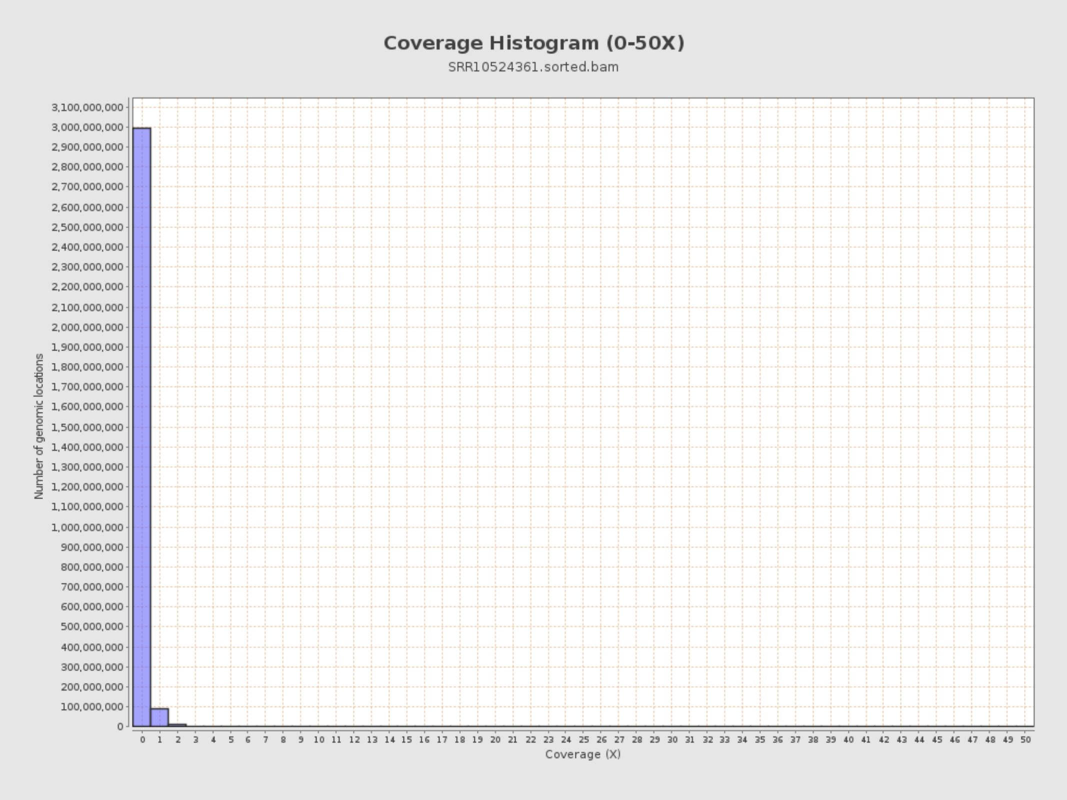
3. Results : Coverage across reference



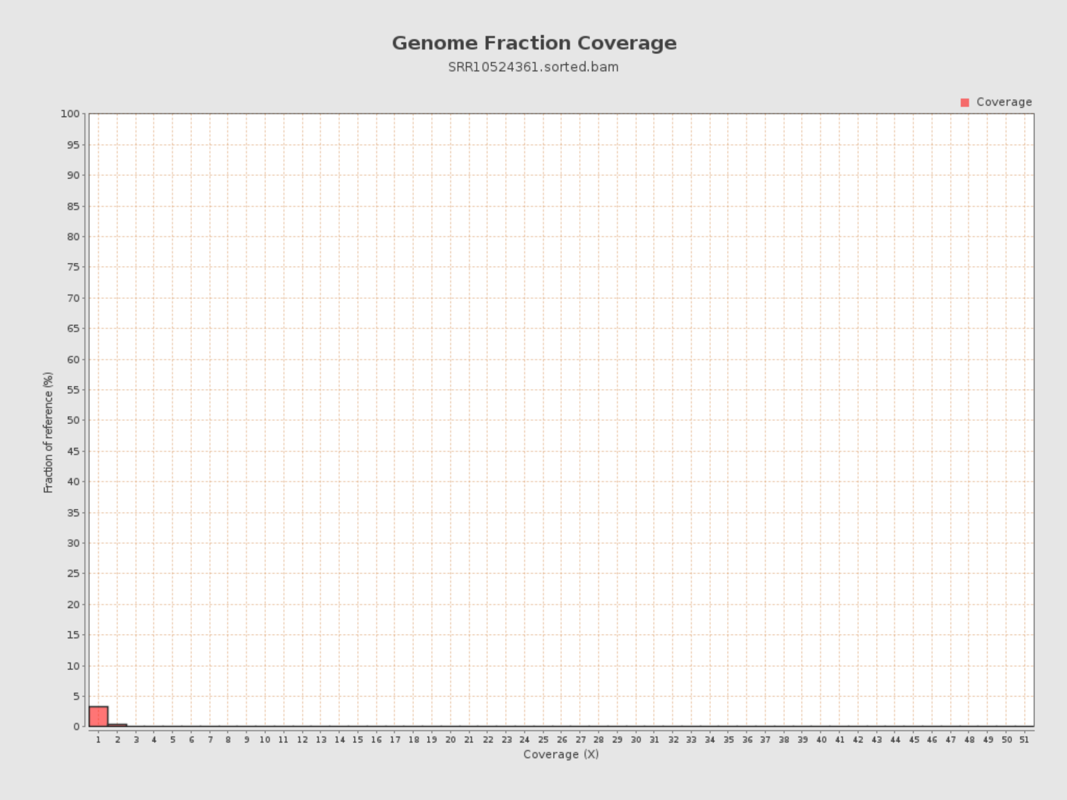
4. Results : Coverage Histogram



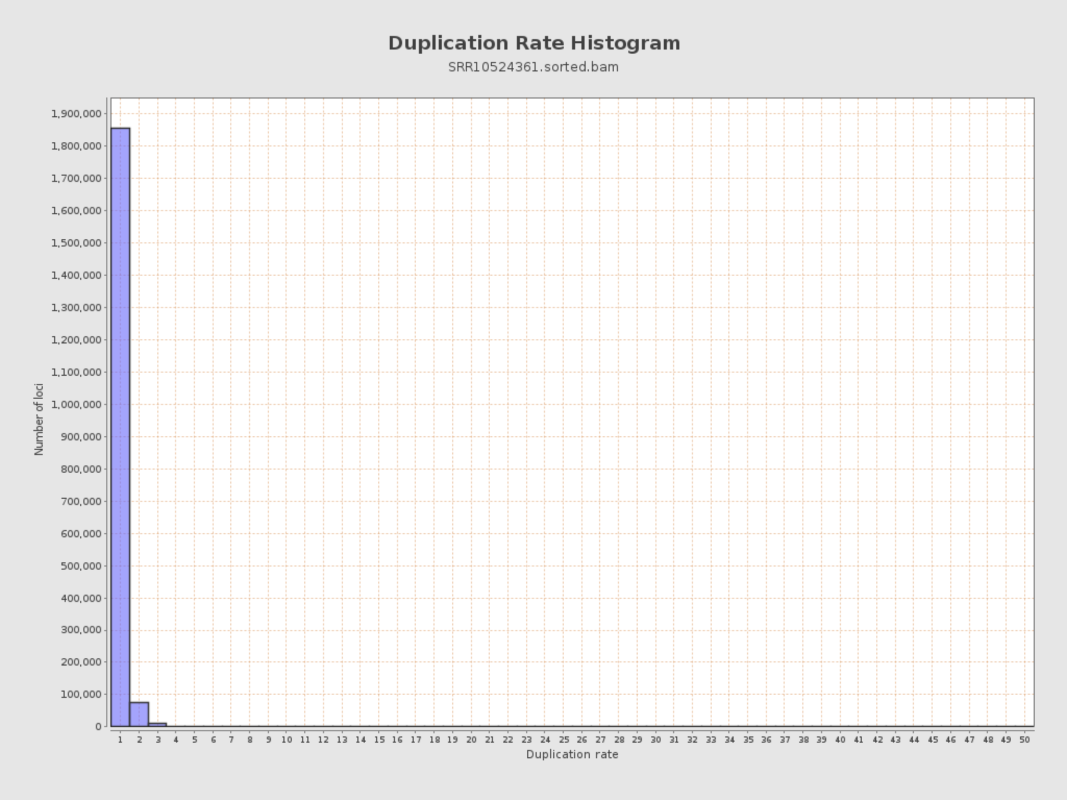
5. Results : Coverage Histogram (0-50X)



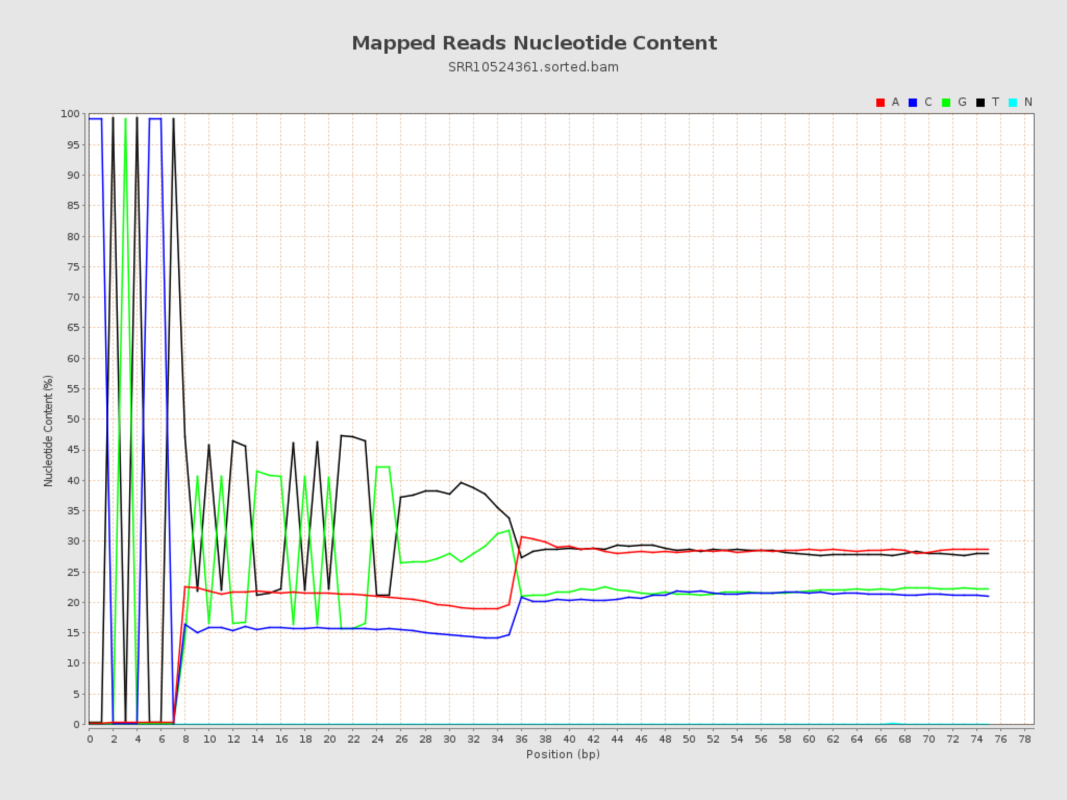
6. Results : Genome Fraction Coverage



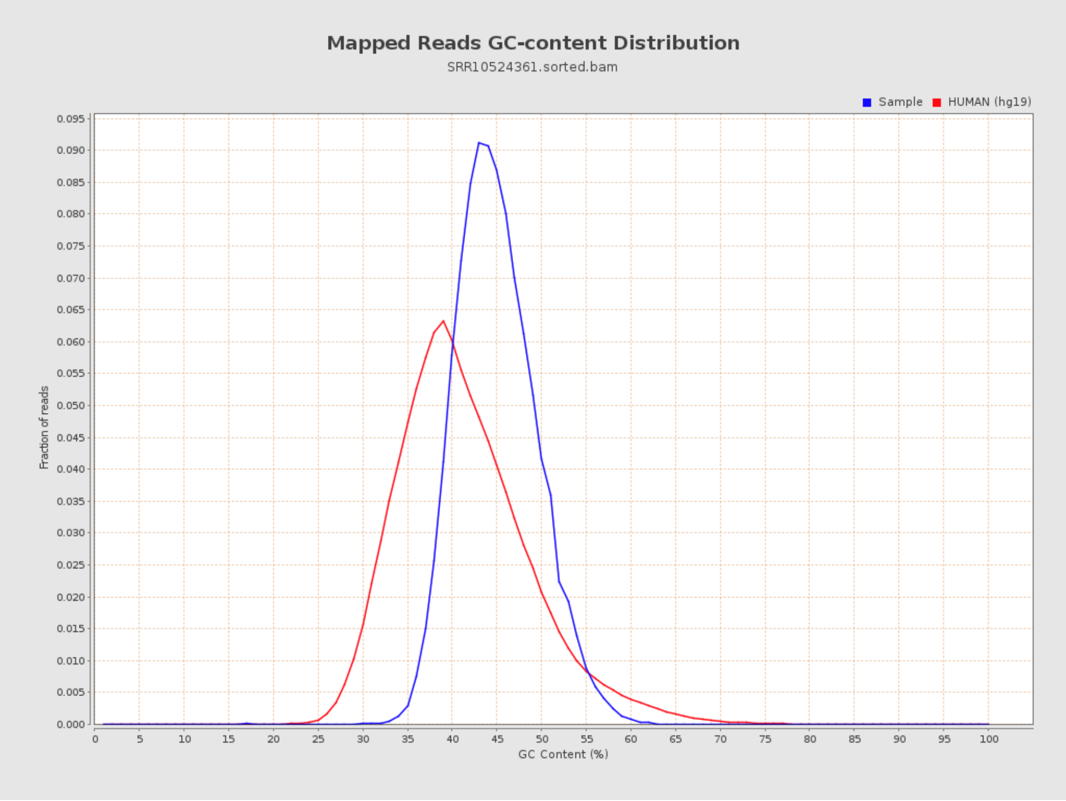
7. Results : Duplication Rate Histogram



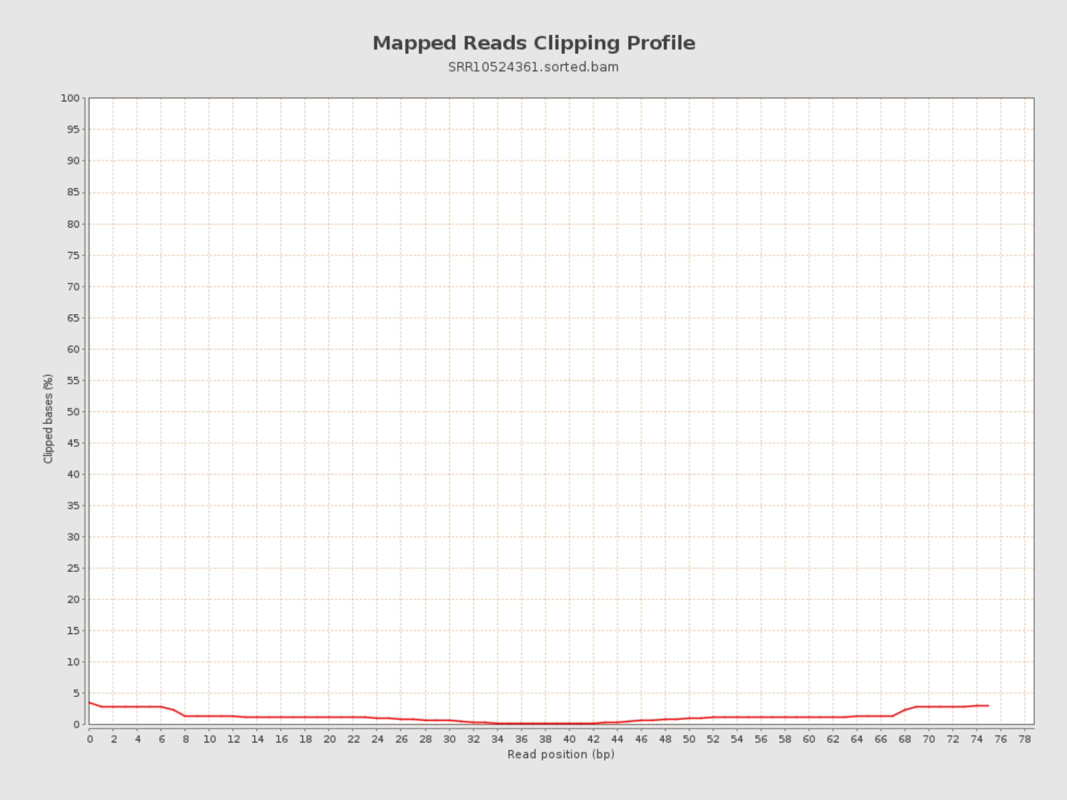
8. Results : Mapped Reads Nucleotide Content



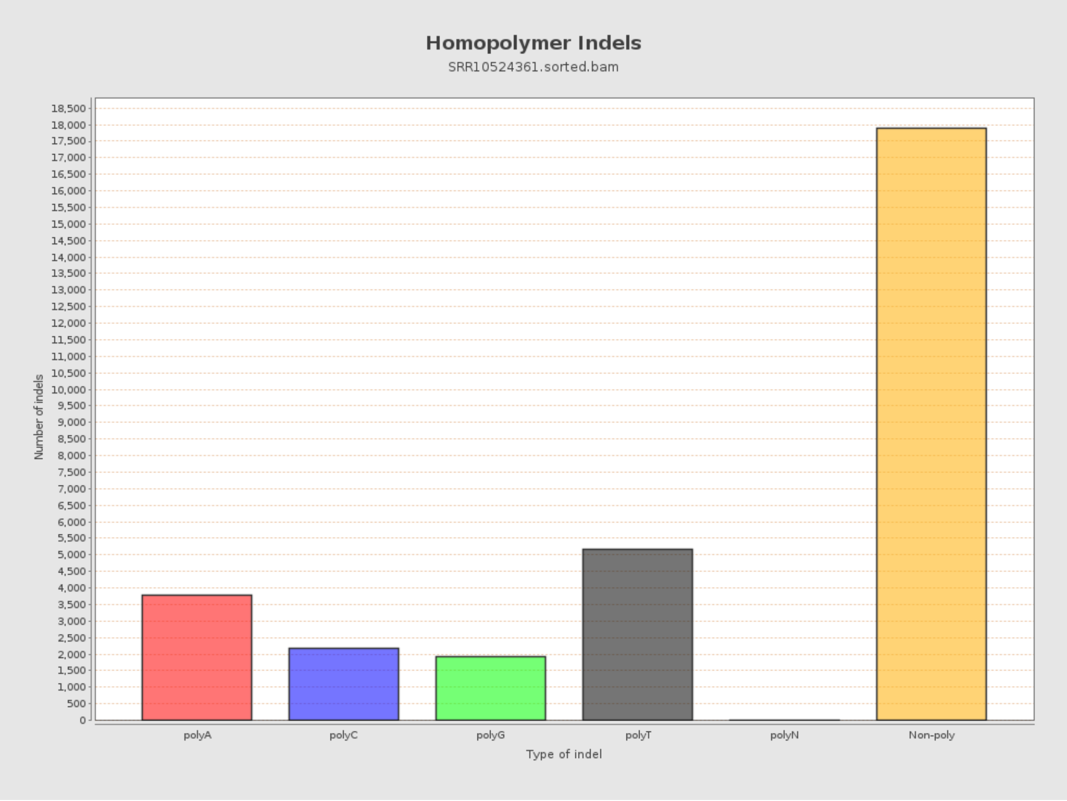
9. Results : Mapped Reads GC-content Distribution



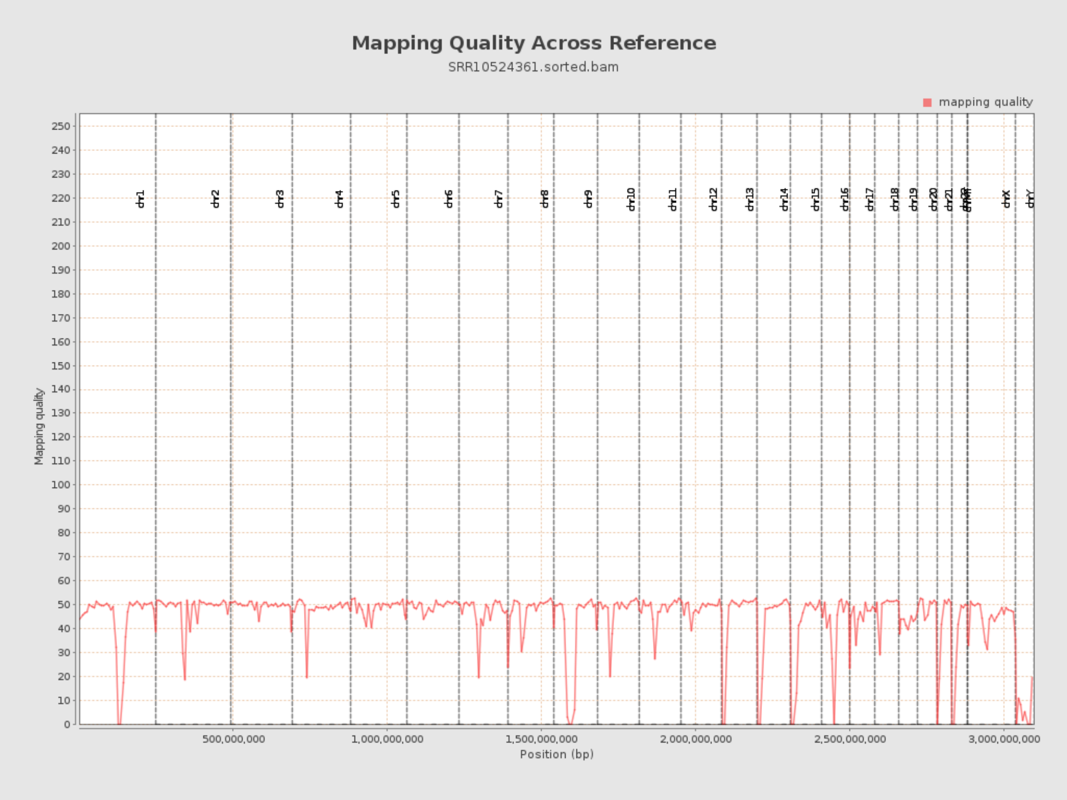
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram