Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 10:34:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524553.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_SRR10524553 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524553.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 10:34:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524553.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,280,535
Mapped reads	2,086,297 / 91.48%
Unmapped reads	194,238 / 8.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,062 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	111,034 / 4.87%
Duplication rate	4.01%
Clipped reads	2,087,177 / 91.52%

2.2. ACGT Content

Number/percentage of A's	29,732,966 / 24.56%
Number/percentage of C's	24,640,680 / 20.35%
Number/percentage of T's	38,975,555 / 32.19%
Number/percentage of G's	27,730,899 / 22.9%
Number/percentage of N's	1,906 / 0%
GC Percentage	43.25%

2.3. Coverage

Mean	0.0391

Standard Deviation	0.3558

2.4. Mapping Quality

Mean Mapping Quality	44.94

2.5. Mismatches and indels

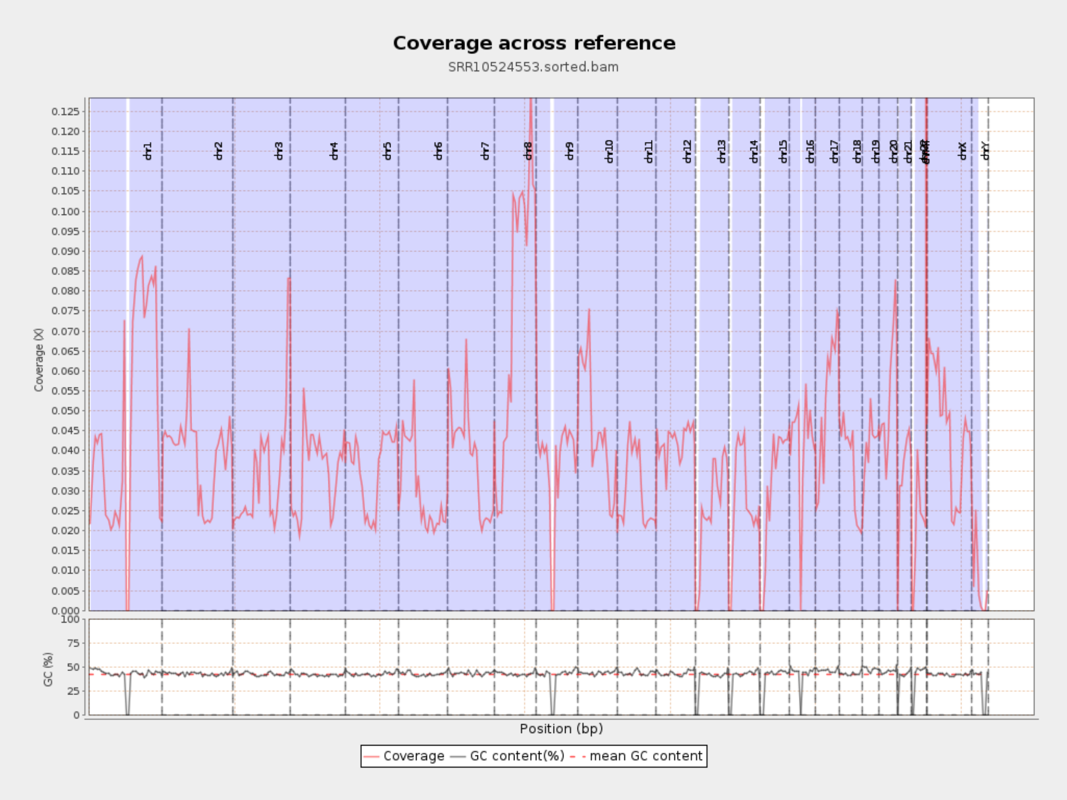
General error rate	0.52%
Mismatches	616,603
Insertions	9,171
Mapped reads with at least one insertion	0.44%
Deletions	23,364
Mapped reads with at least one deletion	1.11%
Homopolymer indels	42.8%

2.6. Chromosome stats

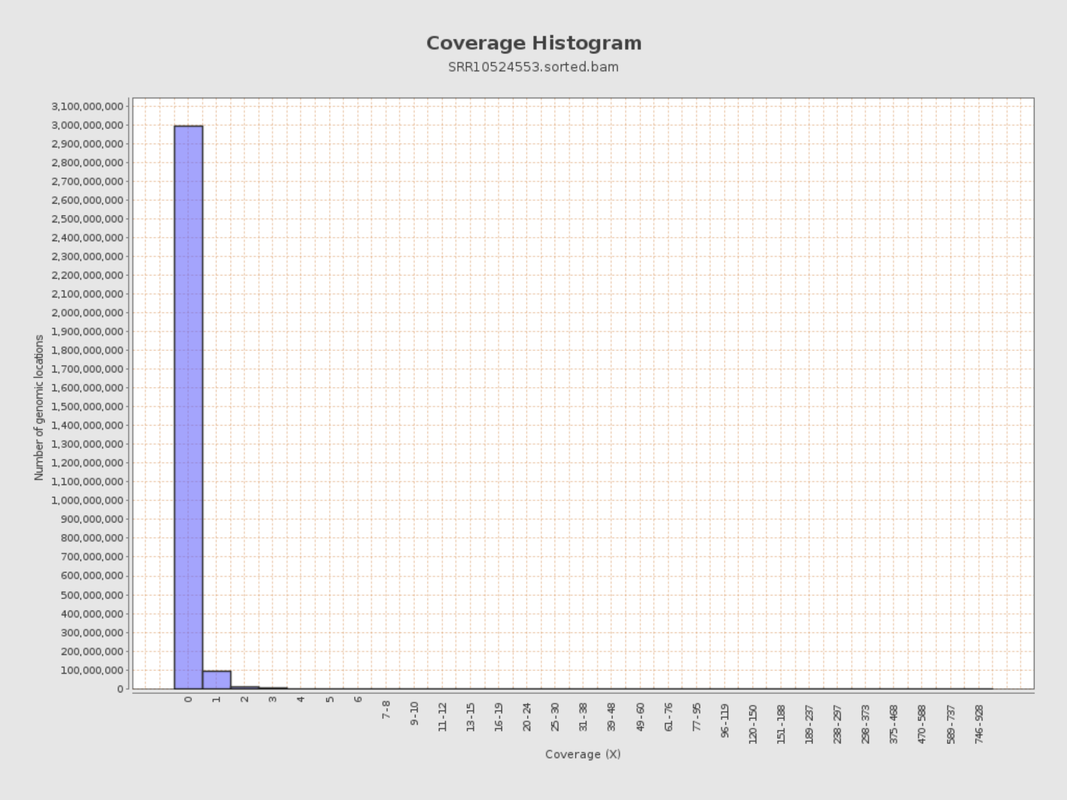
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12002048	0.0482	0.7003
chr2	243199373	9618724	0.0396	0.422
chr3	198022430	6636500	0.0335	0.2098
chr4	191154276	6688966	0.035	0.2512
chr5	180915260	6503838	0.0359	0.2153
chr6	171115067	5178183	0.0303	0.2663
chr7	159138663	6130089	0.0385	0.4371

chr8	146364022	11161375	0.0763	0.3802
chr9	141213431	5052897	0.0358	0.2922
chr10	135534747	6281012	0.0463	0.3606
chr11	135006516	4079737	0.0302	0.3123
chr12	133851895	5669627	0.0424	0.2338
chr13	115169878	2960197	0.0257	0.1817
chr14	107349540	2884101	0.0269	0.1914
chr15	102531392	3155885	0.0308	0.2035
chr16	90354753	3780514	0.0418	0.2491
chr17	81195210	4314216	0.0531	0.278
chr18	78077248	2841451	0.0364	0.5525
chr19	59128983	2453992	0.0415	0.4587
chr20	63025520	3439321	0.0546	0.268
chr21	48129895	1653677	0.0344	0.2356
chr22	51304566	1004268	0.0196	0.1569
chrMT	16571	50777	3.0642	2.3456
chrX	155270560	7163703	0.0461	0.274
chrY	59373566	415272	0.007	0.2051

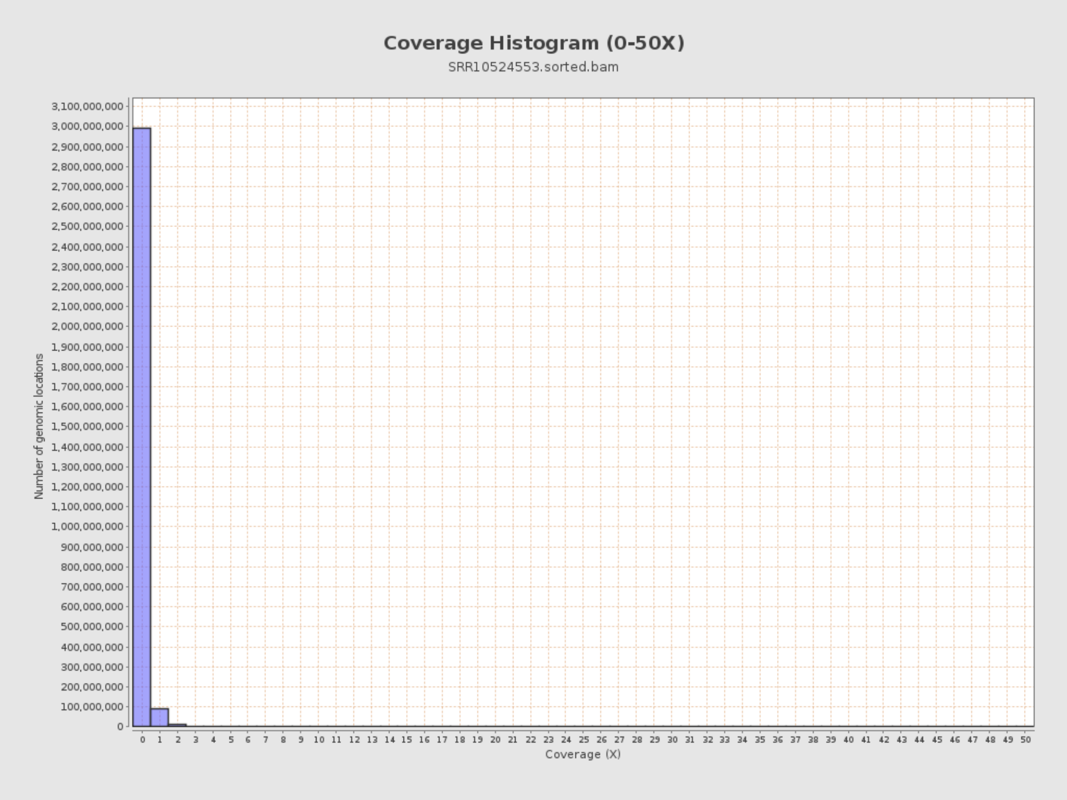
3. Results : Coverage across reference



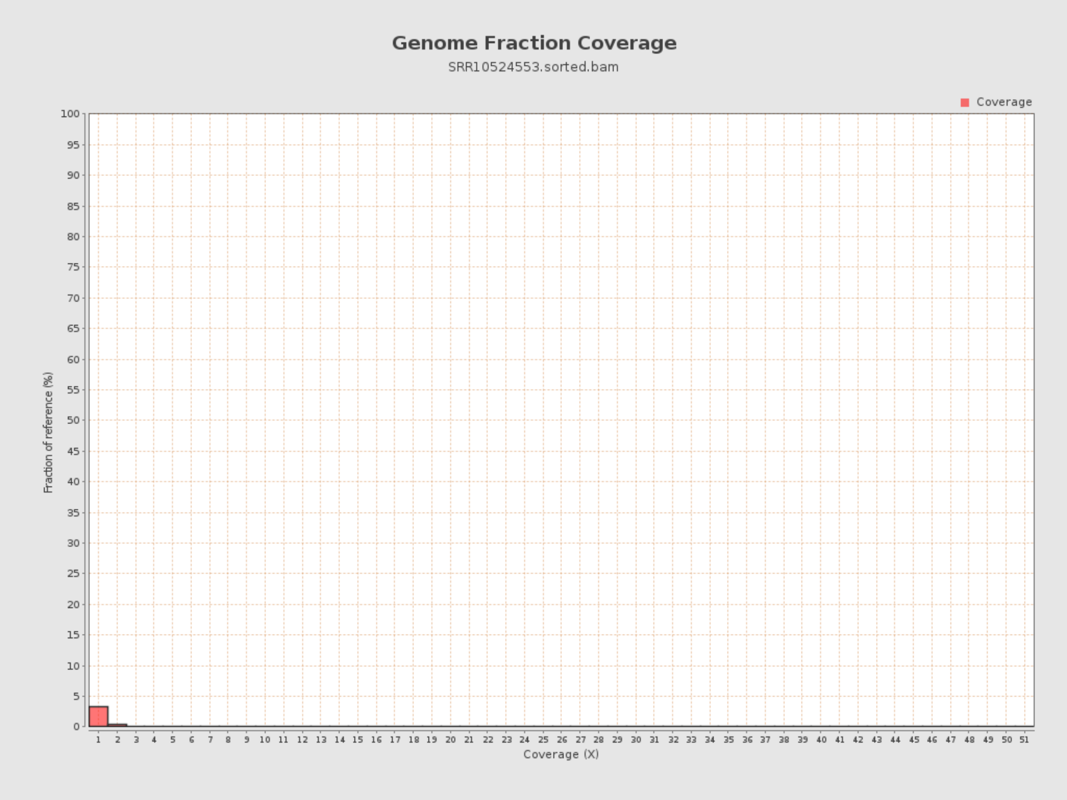
4. Results : Coverage Histogram



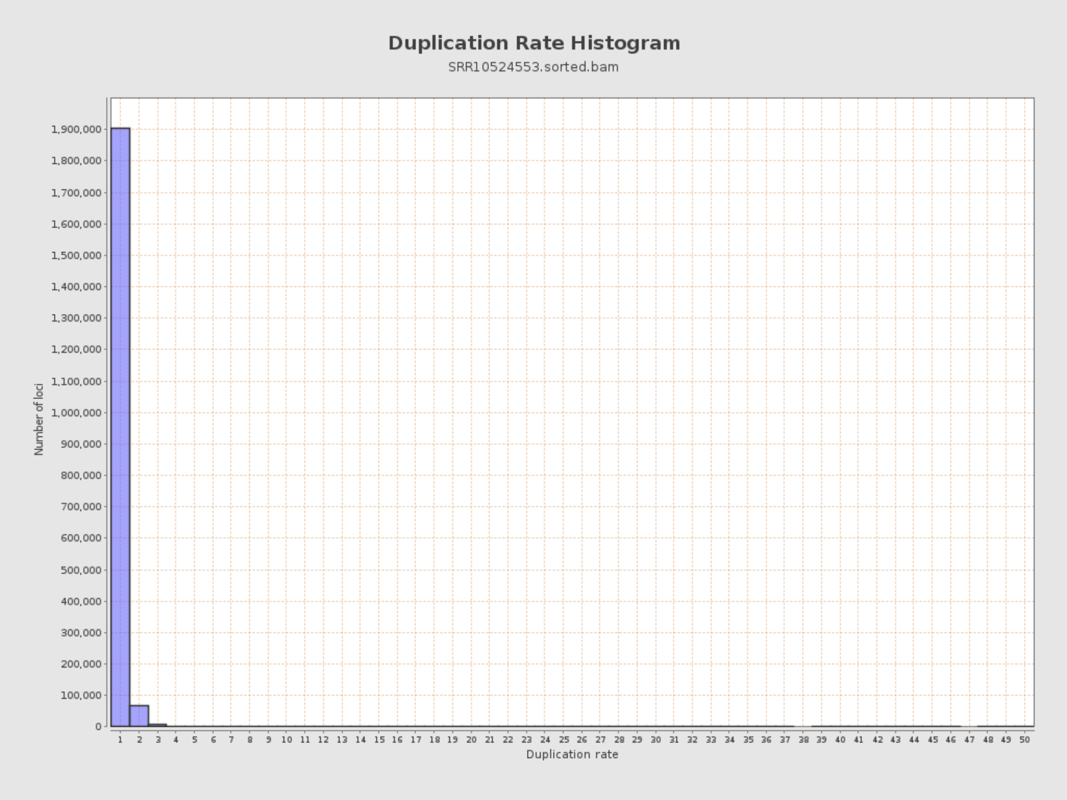
5. Results : Coverage Histogram (0-50X)



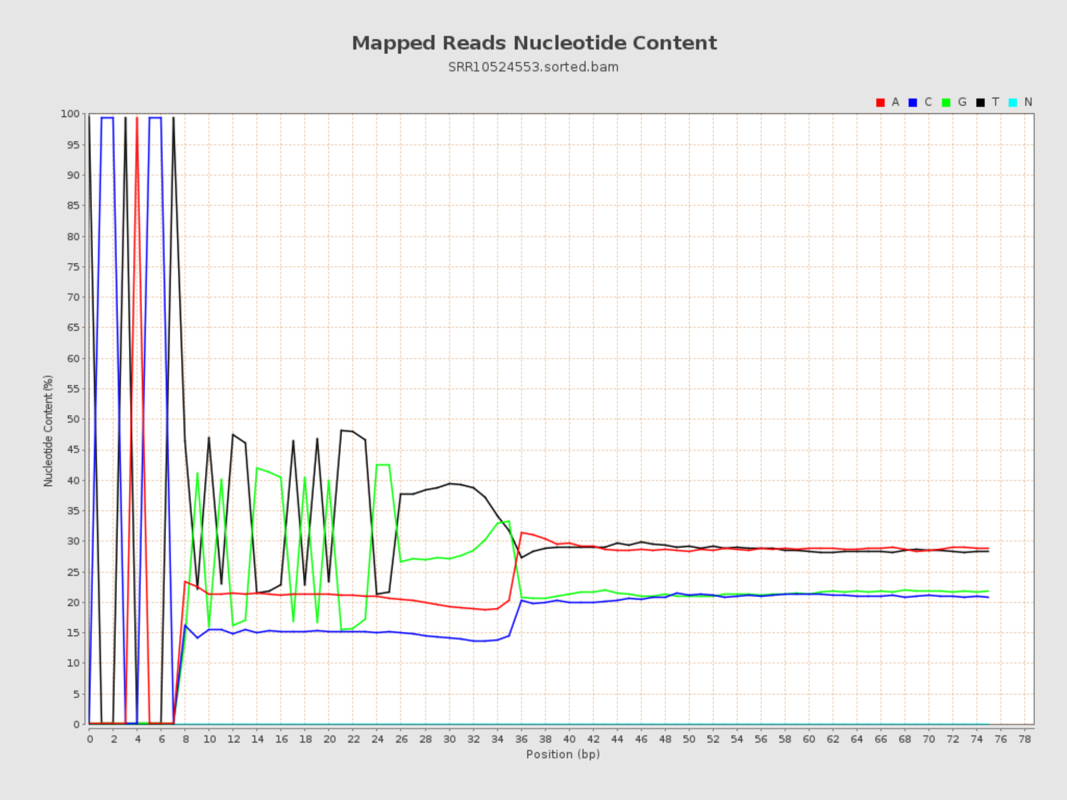
6. Results : Genome Fraction Coverage



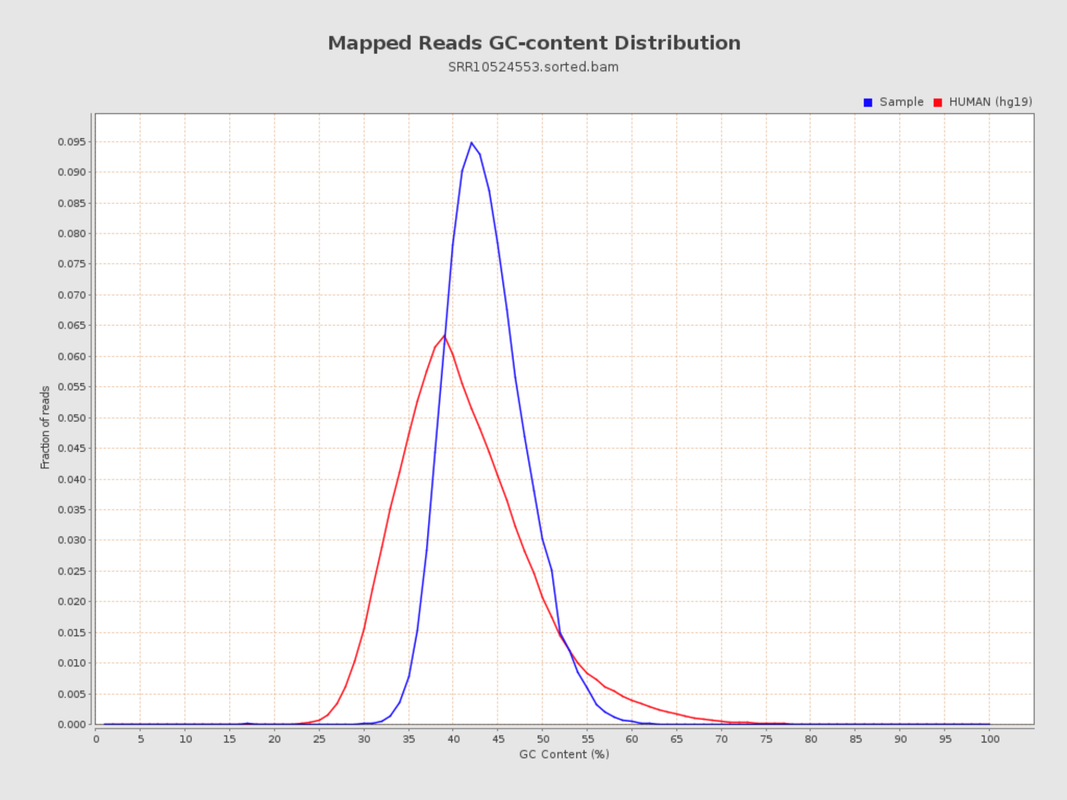
7. Results : Duplication Rate Histogram



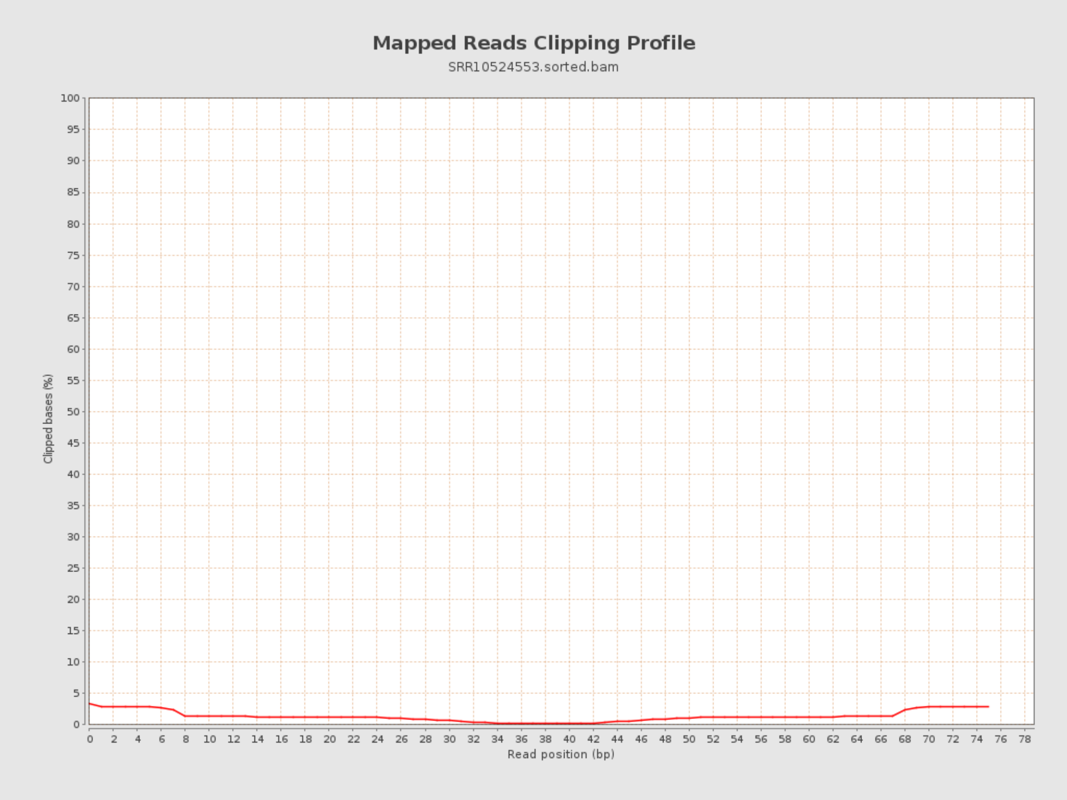
8. Results : Mapped Reads Nucleotide Content



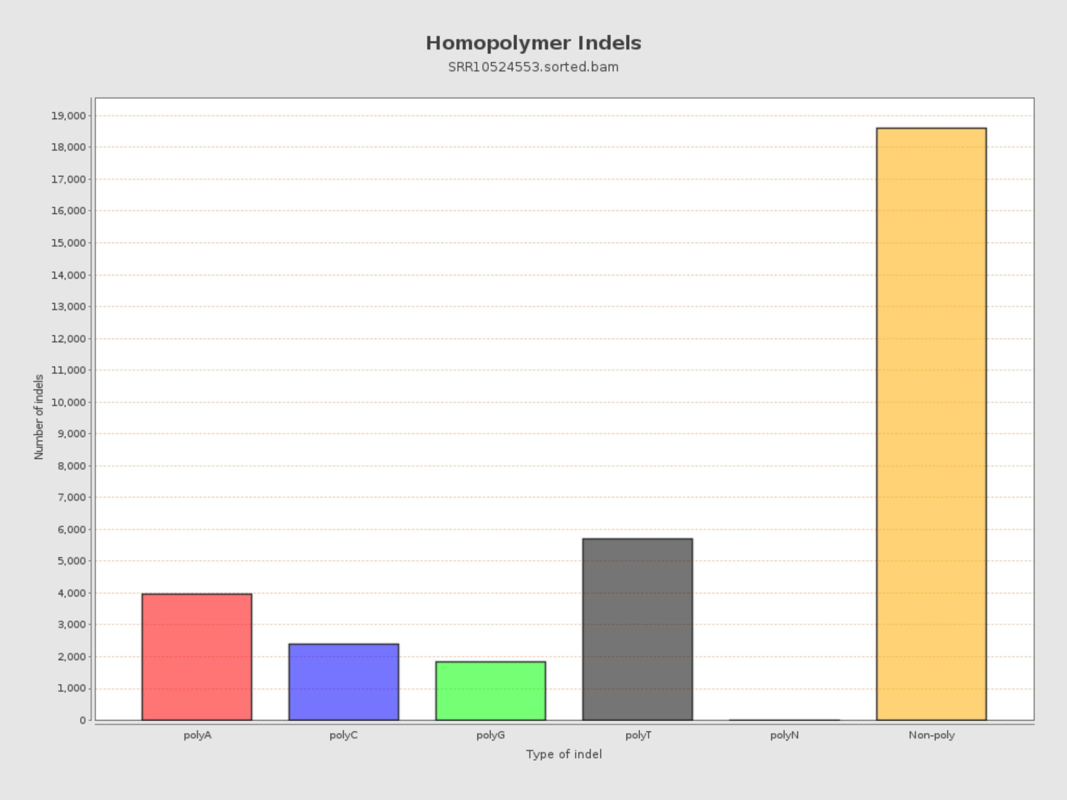
9. Results : Mapped Reads GC-content Distribution



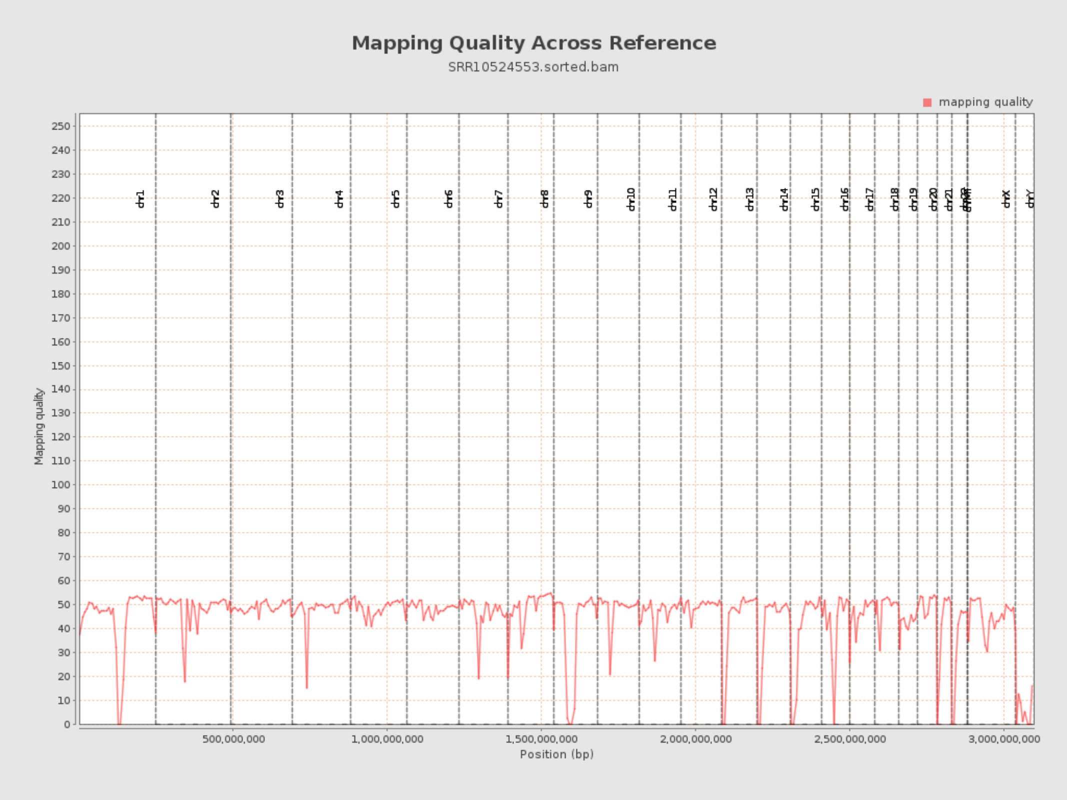
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram