Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 12:16:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524994.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_SRR10524994 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524994.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 12:16:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524994.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,995,191
Mapped reads	2,728,594 / 91.1%
Unmapped reads	266,597 / 8.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,761 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	204,358 / 6.82%
Duplication rate	5.64%
Clipped reads	2,736,733 / 91.37%

2.2. ACGT Content

Number/percentage of A's	38,605,446 / 23.87%
Number/percentage of C's	33,641,799 / 20.8%
Number/percentage of T's	51,196,074 / 31.65%
Number/percentage of G's	38,299,751 / 23.68%
Number/percentage of N's	1,678 / 0%
GC Percentage	44.48%

2.3. Coverage

Mean	0.0523

Standard Deviation	0.4623

2.4. Mapping Quality

Mean Mapping Quality	45.92

2.5. Mismatches and indels

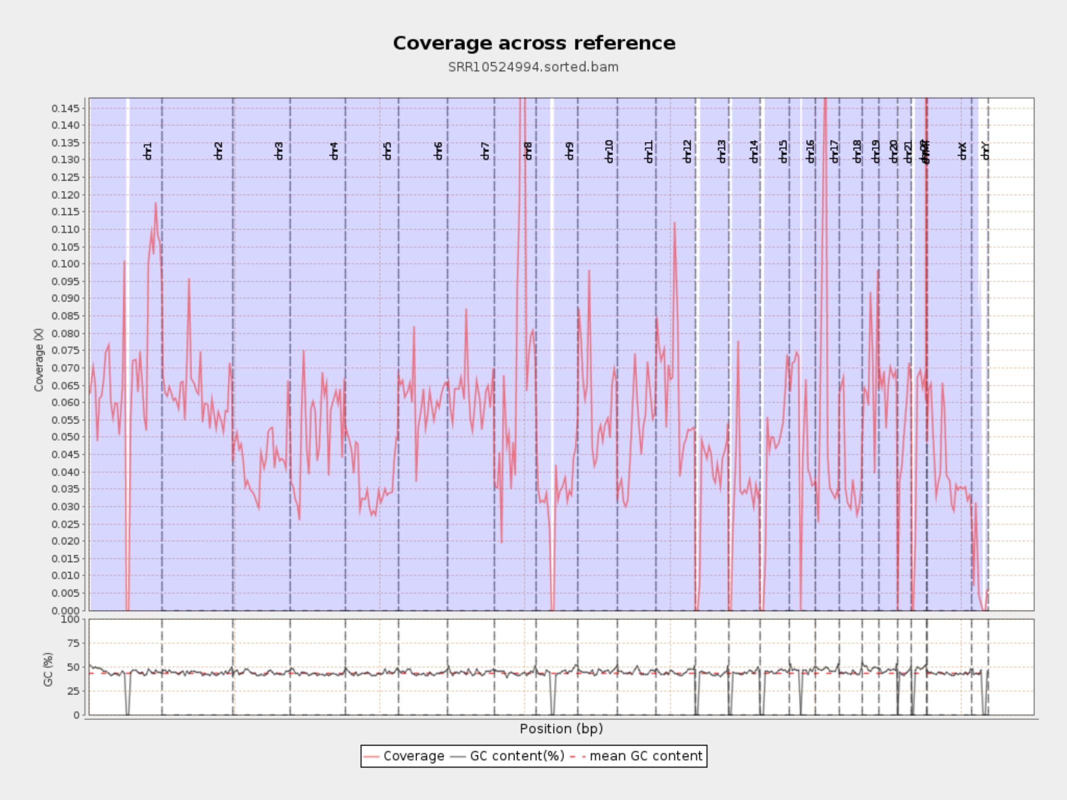
General error rate	0.49%
Mismatches	782,734
Insertions	9,455
Mapped reads with at least one insertion	0.34%
Deletions	28,758
Mapped reads with at least one deletion	1.05%
Homopolymer indels	45.86%

2.6. Chromosome stats

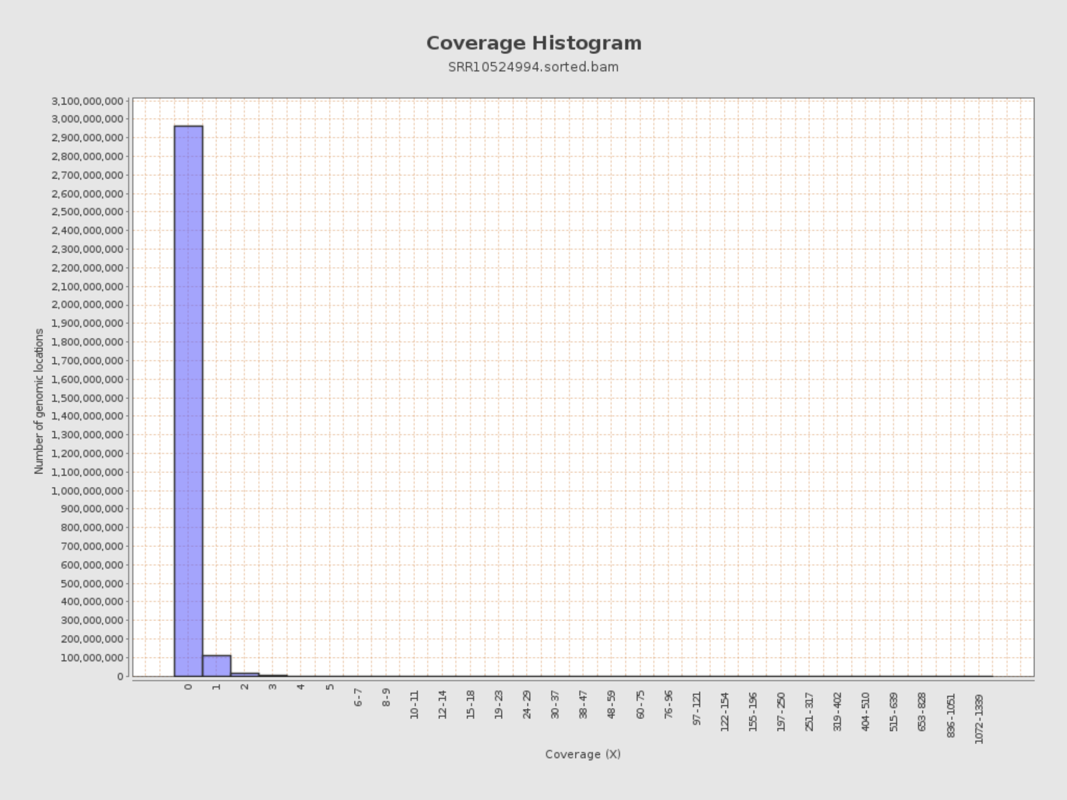
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17142068	0.0688	0.99
chr2	243199373	15190084	0.0625	0.5218
chr3	198022430	8613741	0.0435	0.2446
chr4	191154276	9936029	0.052	0.3195
chr5	180915260	6764171	0.0374	0.24
chr6	171115067	10442026	0.061	0.3947
chr7	159138663	9915454	0.0623	0.523

chr8	146364022	10786536	0.0737	0.5539
chr9	141213431	4423245	0.0313	0.3244
chr10	135534747	8262335	0.061	0.4606
chr11	135006516	6719200	0.0498	0.3911
chr12	133851895	8600859	0.0643	0.3053
chr13	115169878	4229542	0.0367	0.2302
chr14	107349540	3560940	0.0332	0.2236
chr15	102531392	4477221	0.0437	0.2461
chr16	90354753	4603920	0.051	0.2855
chr17	81195210	4959897	0.0611	0.4646
chr18	78077248	3153467	0.0404	0.571
chr19	59128983	4076273	0.0689	0.5321
chr20	63025520	4137703	0.0657	0.3106
chr21	48129895	2351649	0.0489	0.3041
chr22	51304566	2357874	0.046	0.2546
chrMT	16571	103585	6.251	4.5633
chrX	155270560	6483680	0.0418	0.2977
chrY	59373566	501040	0.0084	0.244

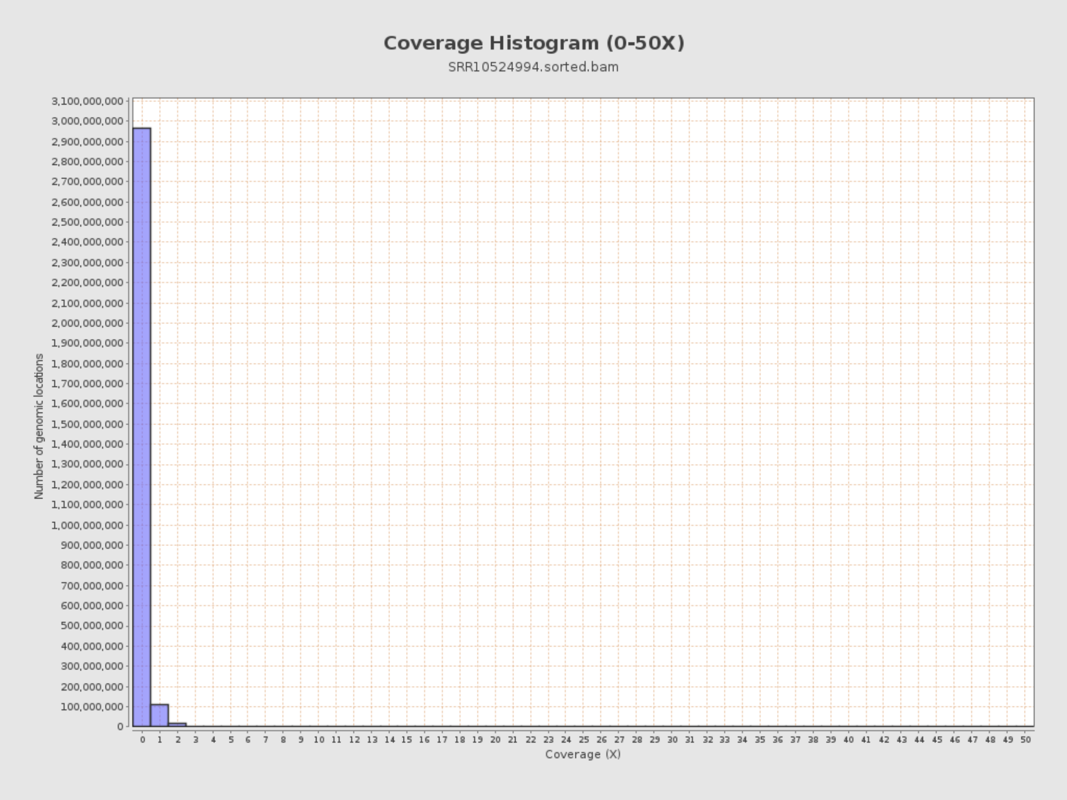
3. Results : Coverage across reference



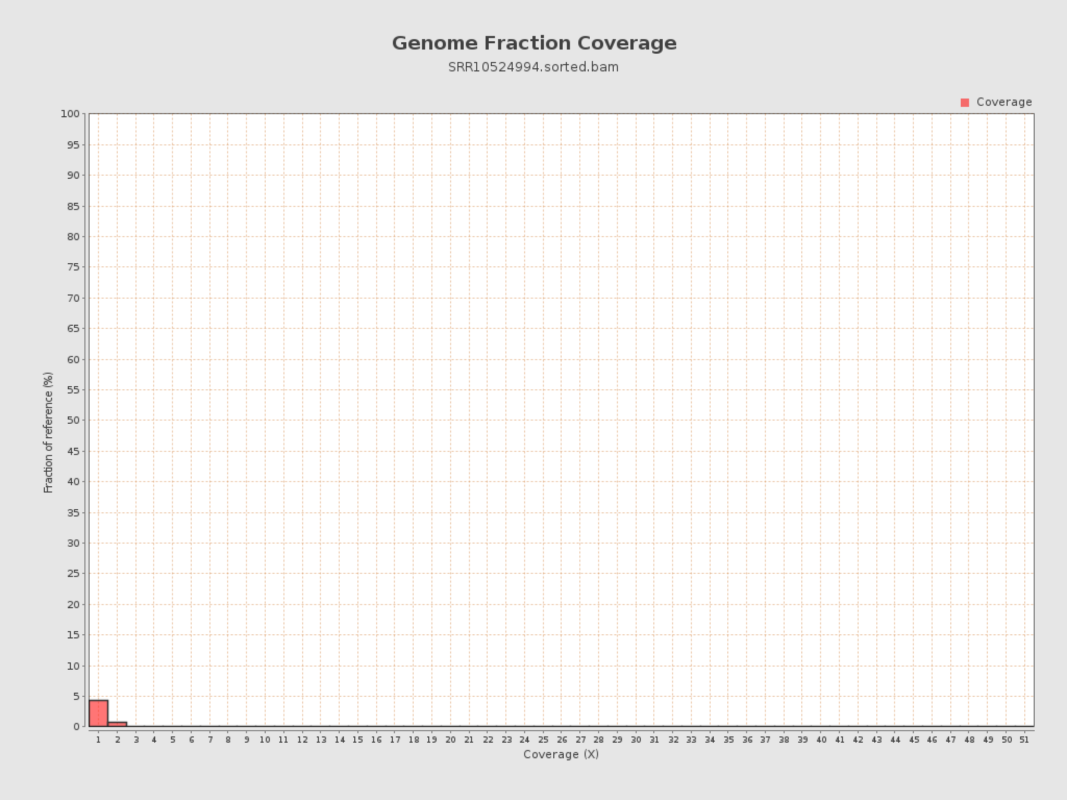
4. Results : Coverage Histogram



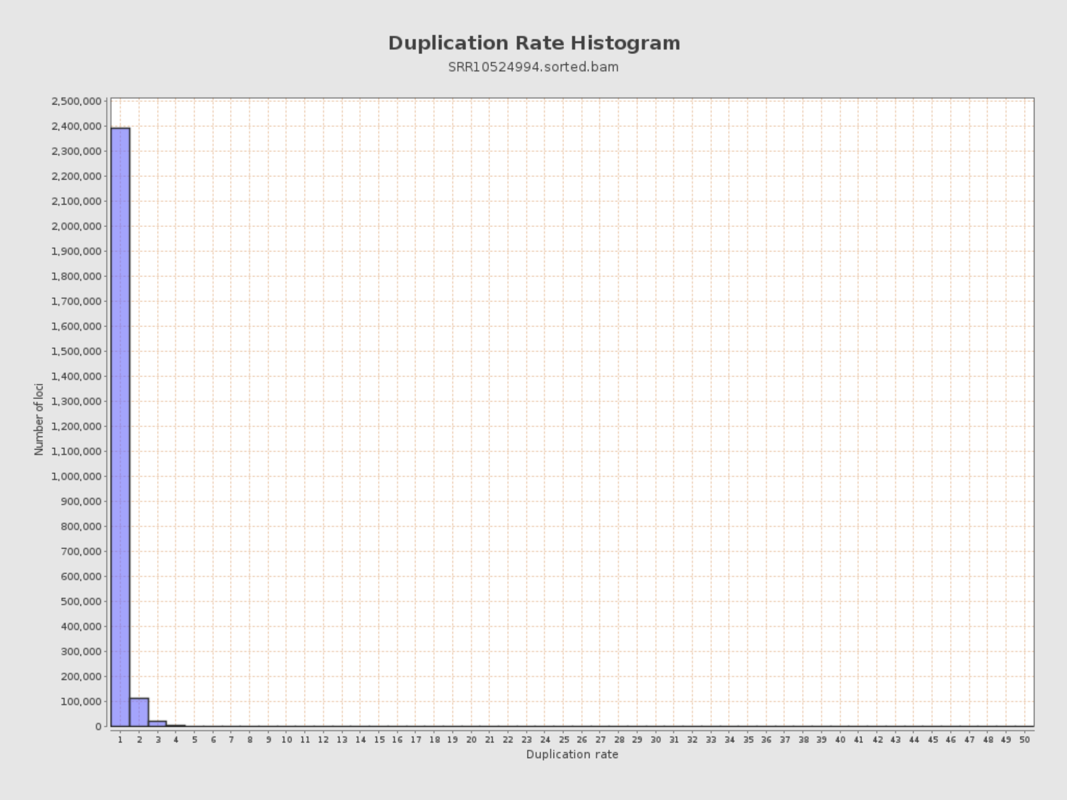
5. Results : Coverage Histogram (0-50X)



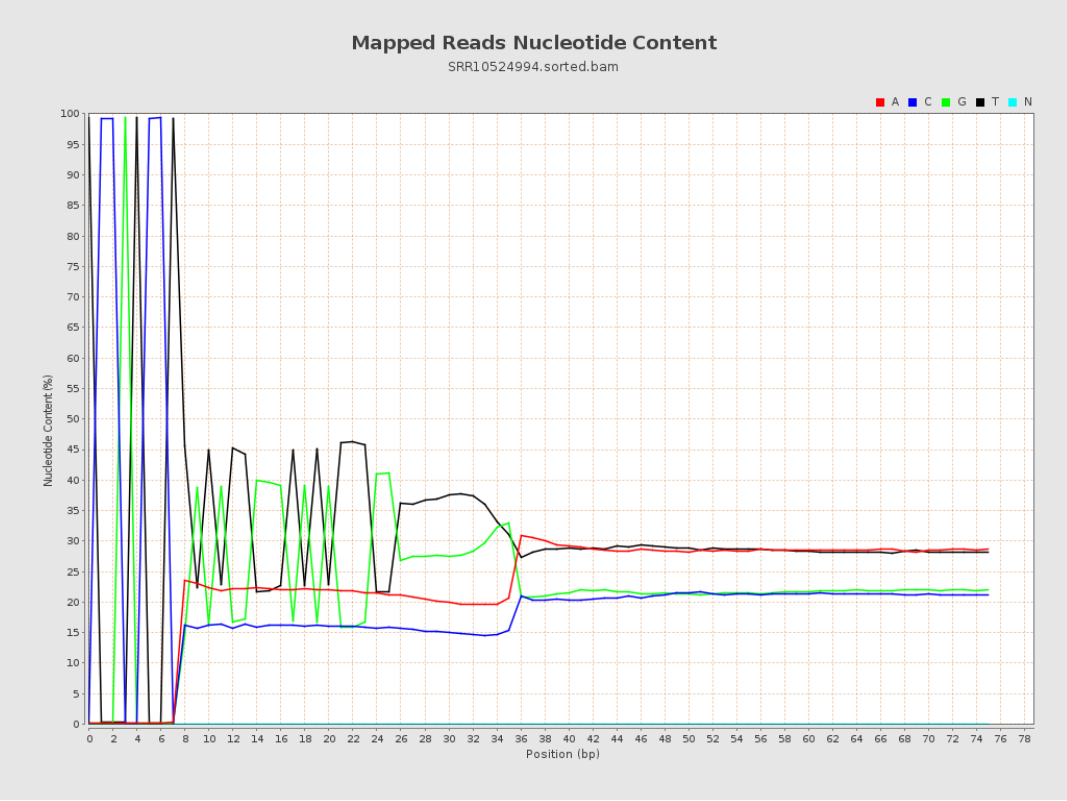
6. Results : Genome Fraction Coverage



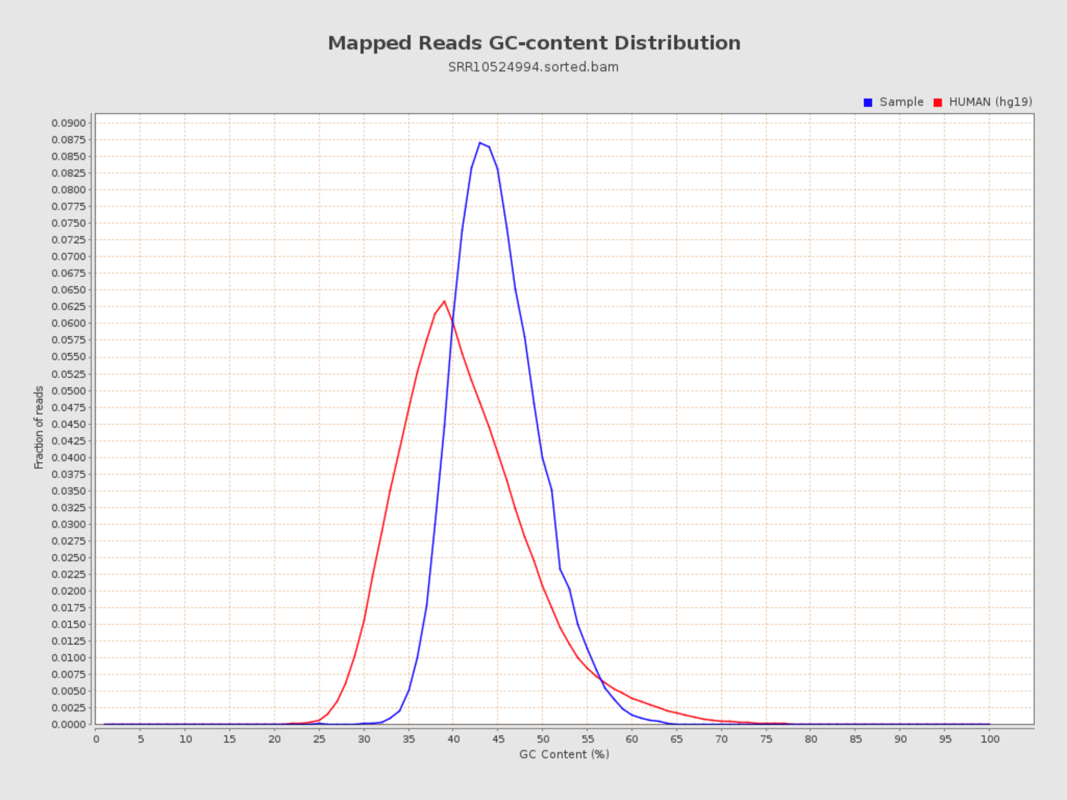
7. Results : Duplication Rate Histogram



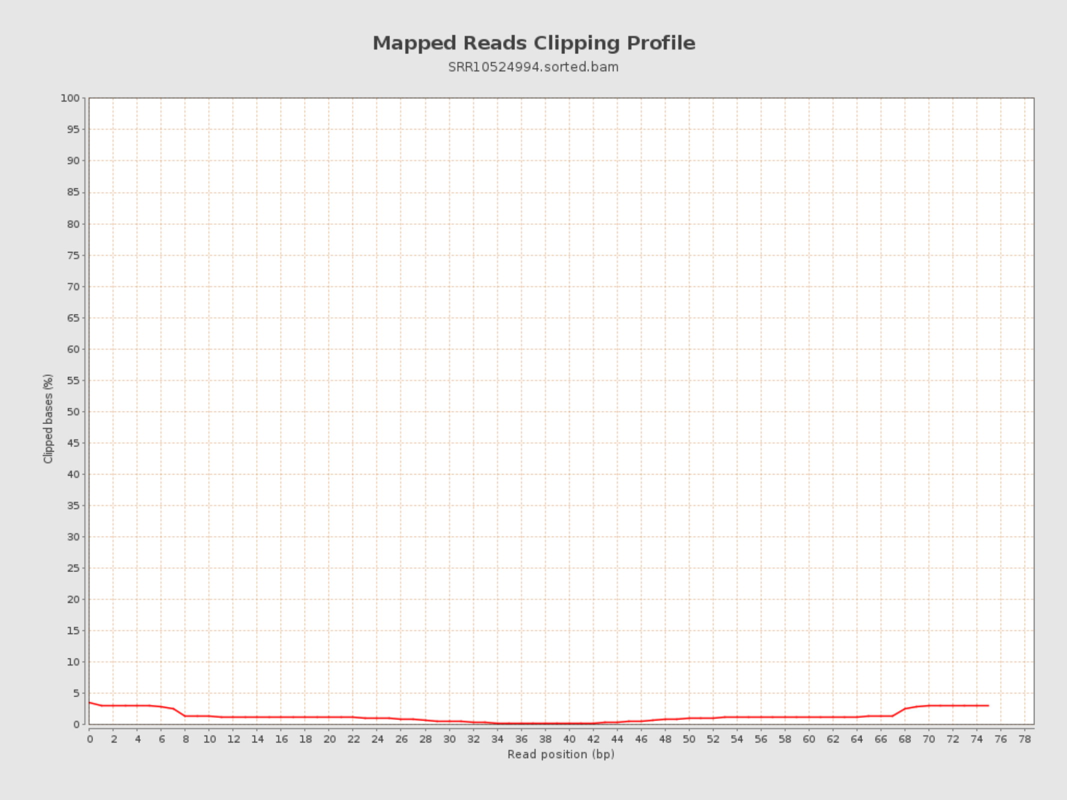
8. Results : Mapped Reads Nucleotide Content



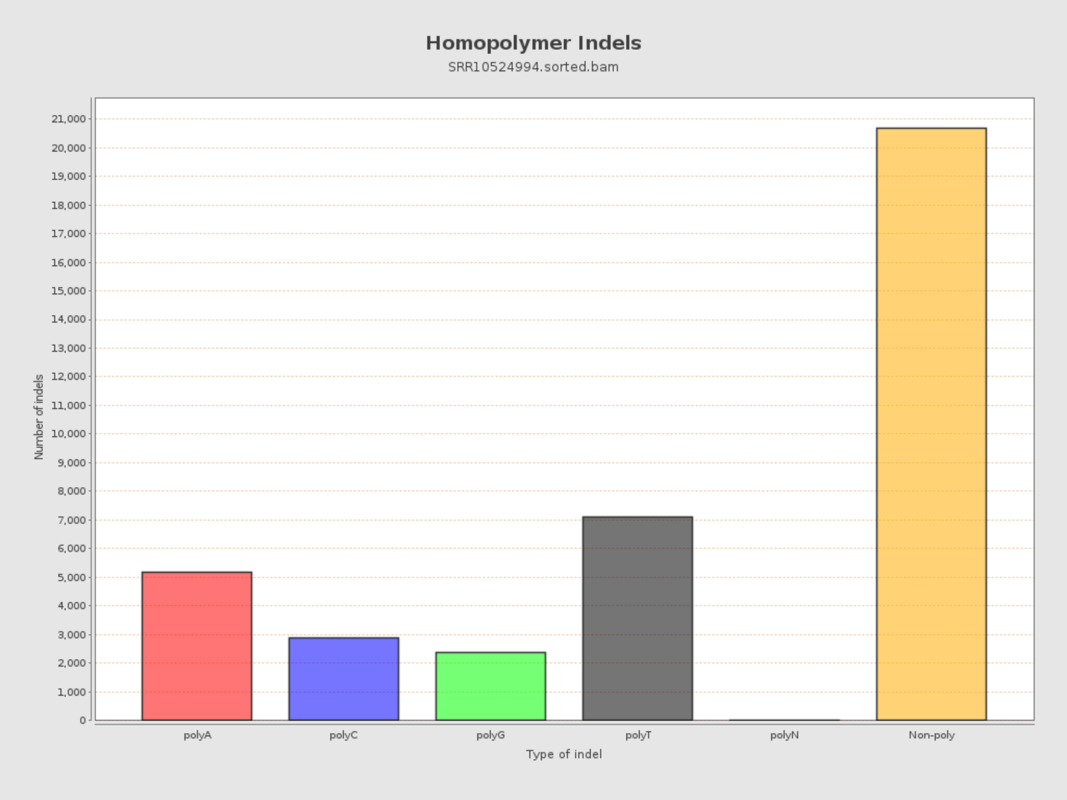
9. Results : Mapped Reads GC-content Distribution



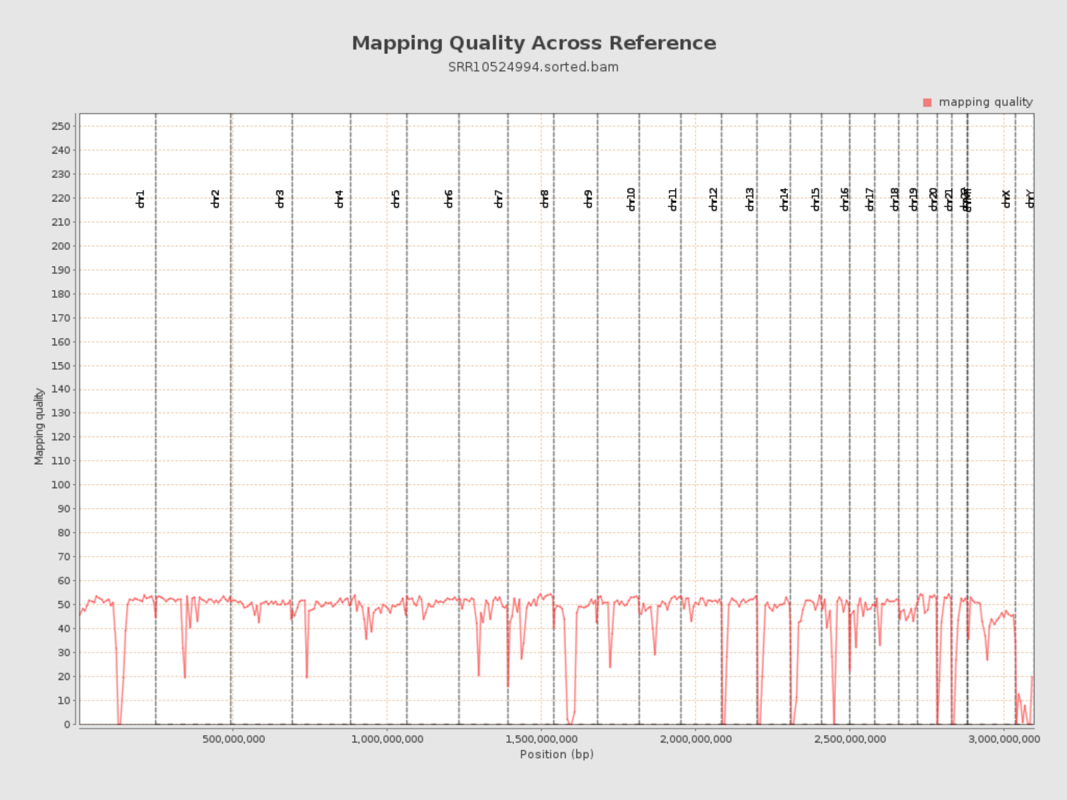
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram