Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 11:24:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524975.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_SRR10524975 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524975.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 11:24:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524975.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,103,553
Mapped reads	2,827,244 / 91.1%
Unmapped reads	276,309 / 8.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,280 / 0.2%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	169,594 / 5.46%
Duplication rate	4.58%
Clipped reads	2,823,135 / 90.96%

2.2. ACGT Content

Number/percentage of A's	40,422,267 / 24.66%
Number/percentage of C's	32,908,398 / 20.08%
Number/percentage of T's	52,880,478 / 32.26%
Number/percentage of G's	37,713,257 / 23.01%
Number/percentage of N's	1,858 / 0%
GC Percentage	43.08%

2.3. Coverage

Mean	0.053

Standard Deviation	0.4127

2.4. Mapping Quality

Mean Mapping Quality	45.74

2.5. Mismatches and indels

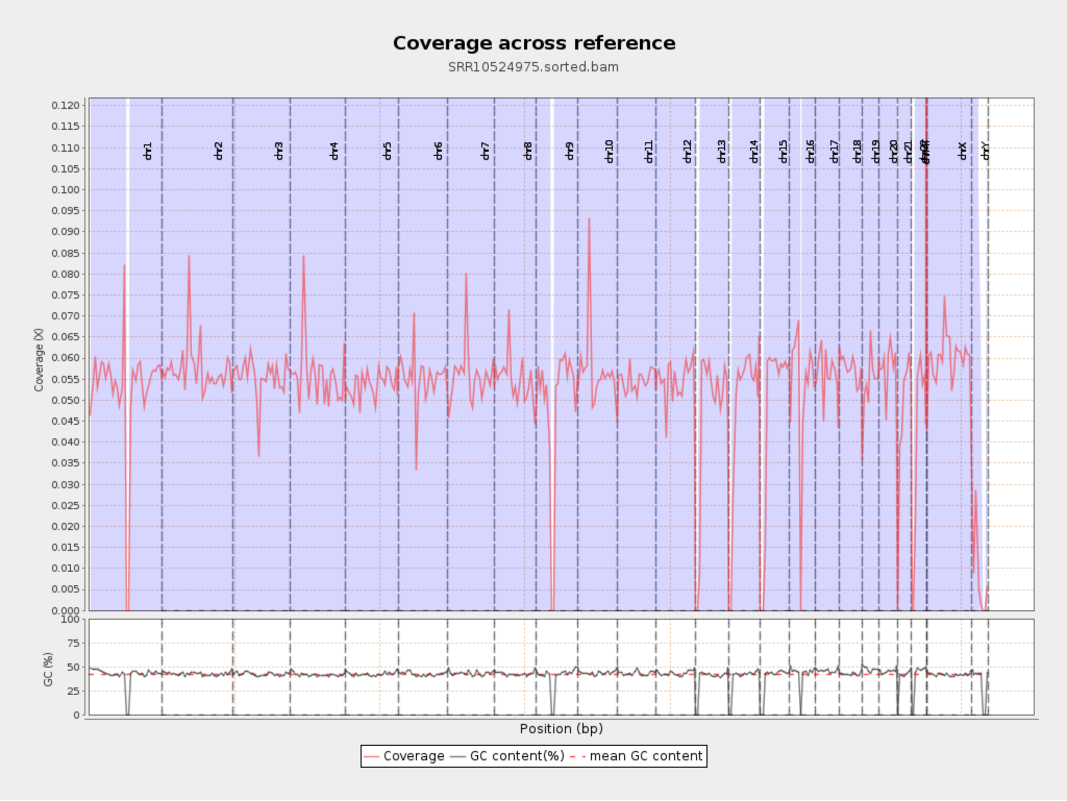
General error rate	0.51%
Mismatches	805,659
Insertions	13,070
Mapped reads with at least one insertion	0.46%
Deletions	30,426
Mapped reads with at least one deletion	1.07%
Homopolymer indels	41.8%

2.6. Chromosome stats

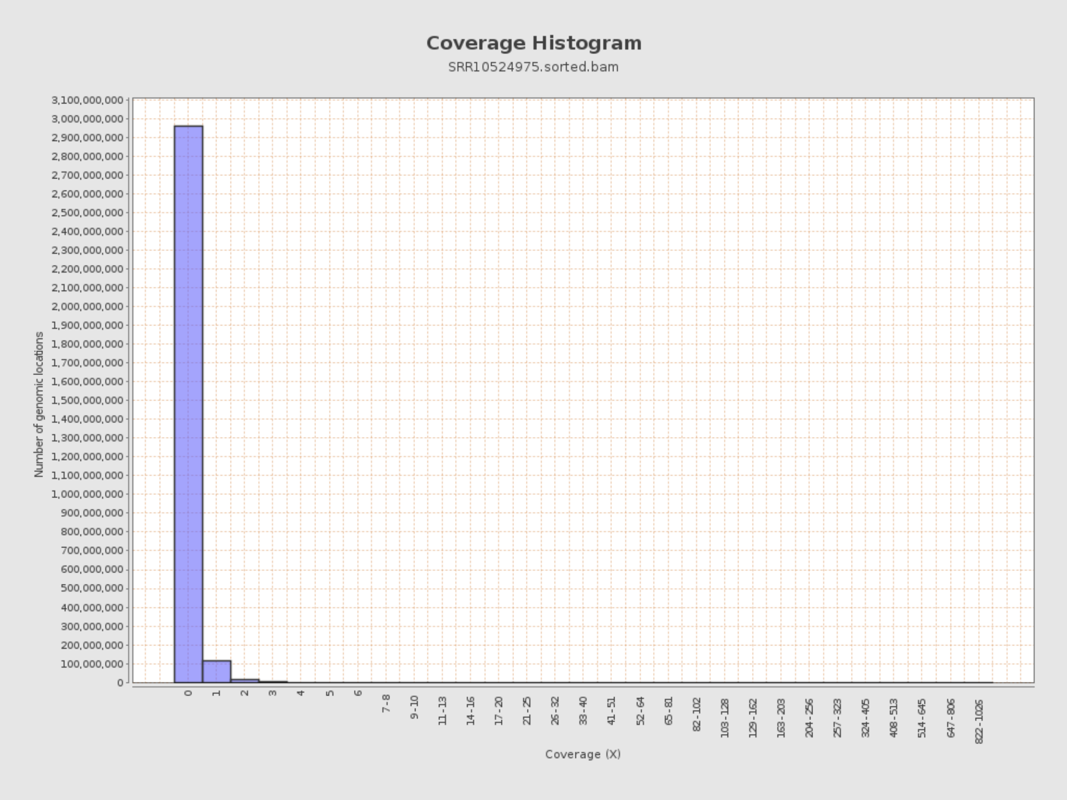
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13023734	0.0523	0.7472
chr2	243199373	13990551	0.0575	0.4893
chr3	198022430	11001003	0.0556	0.281
chr4	191154276	10671484	0.0558	0.3296
chr5	180915260	9733890	0.0538	0.2745
chr6	171115067	9465173	0.0553	0.3576
chr7	159138663	8903228	0.0559	0.5113

chr8	146364022	8014293	0.0548	0.43
chr9	141213431	6873101	0.0487	0.3511
chr10	135534747	7740494	0.0571	0.4265
chr11	135006516	7376460	0.0546	0.4055
chr12	133851895	7322923	0.0547	0.28
chr13	115169878	5252627	0.0456	0.2529
chr14	107349540	5050709	0.047	0.2658
chr15	102531392	4837183	0.0472	0.2817
chr16	90354753	4796927	0.0531	0.2921
chr17	81195210	4537384	0.0559	0.3262
chr18	78077248	4500568	0.0576	0.6044
chr19	59128983	3239025	0.0548	0.5032
chr20	63025520	3613128	0.0573	0.2911
chr21	48129895	2230870	0.0464	0.2864
chr22	51304566	1993487	0.0389	0.23
chrMT	16571	8837	0.5333	0.8865
chrX	155270560	9310221	0.06	0.3271
chrY	59373566	490962	0.0083	0.2164

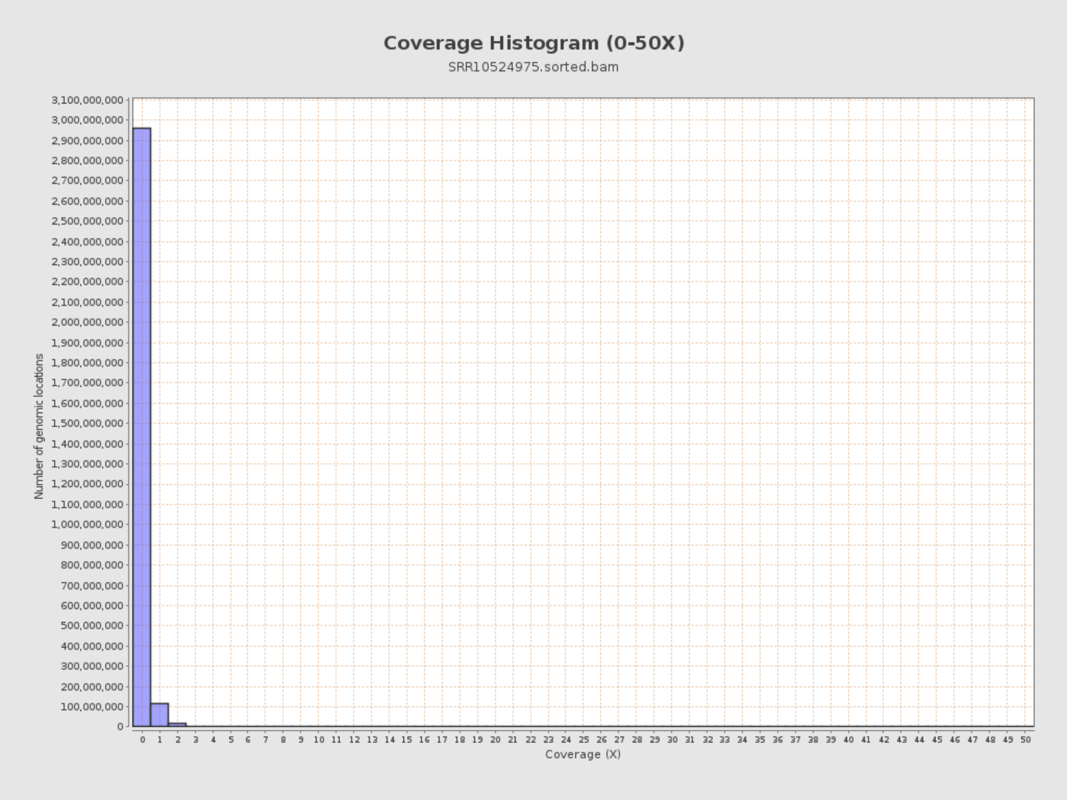
3. Results : Coverage across reference



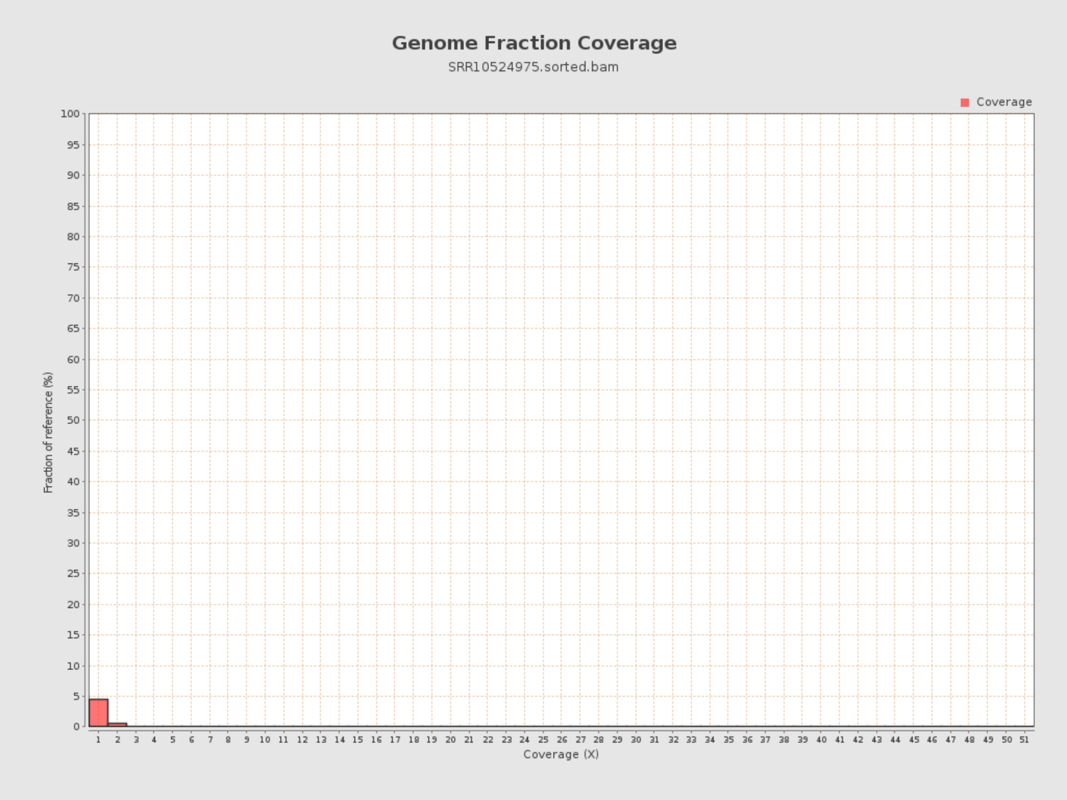
4. Results : Coverage Histogram



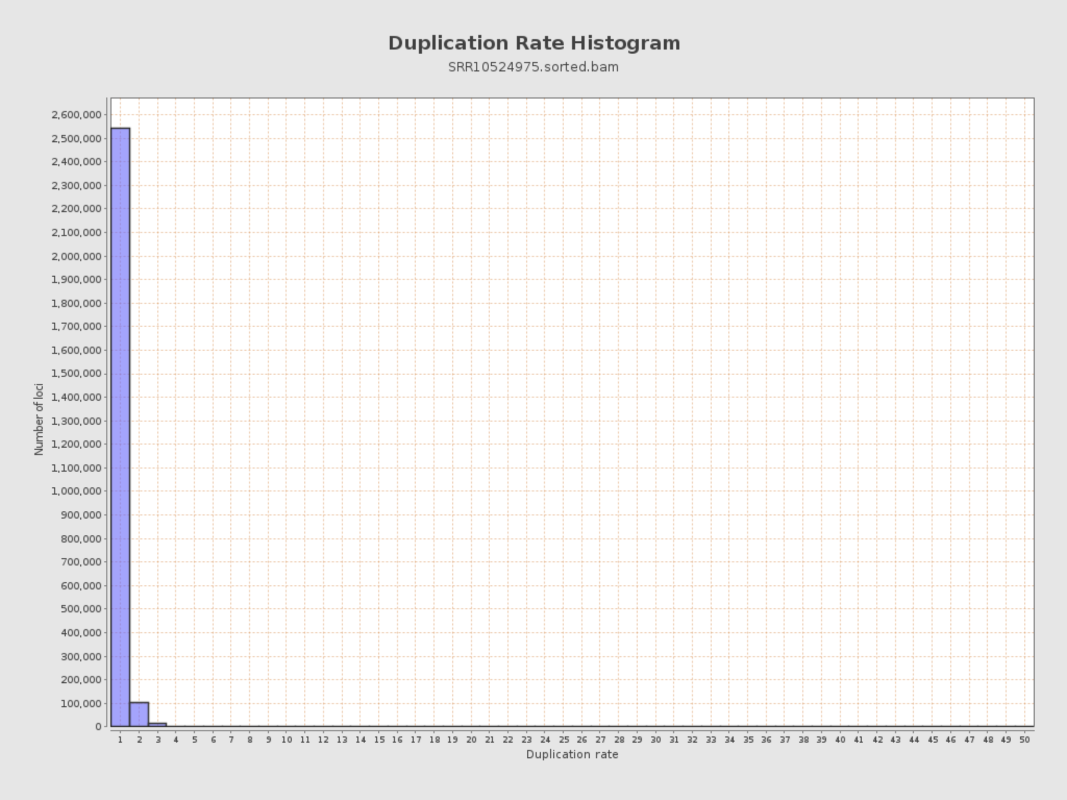
5. Results : Coverage Histogram (0-50X)



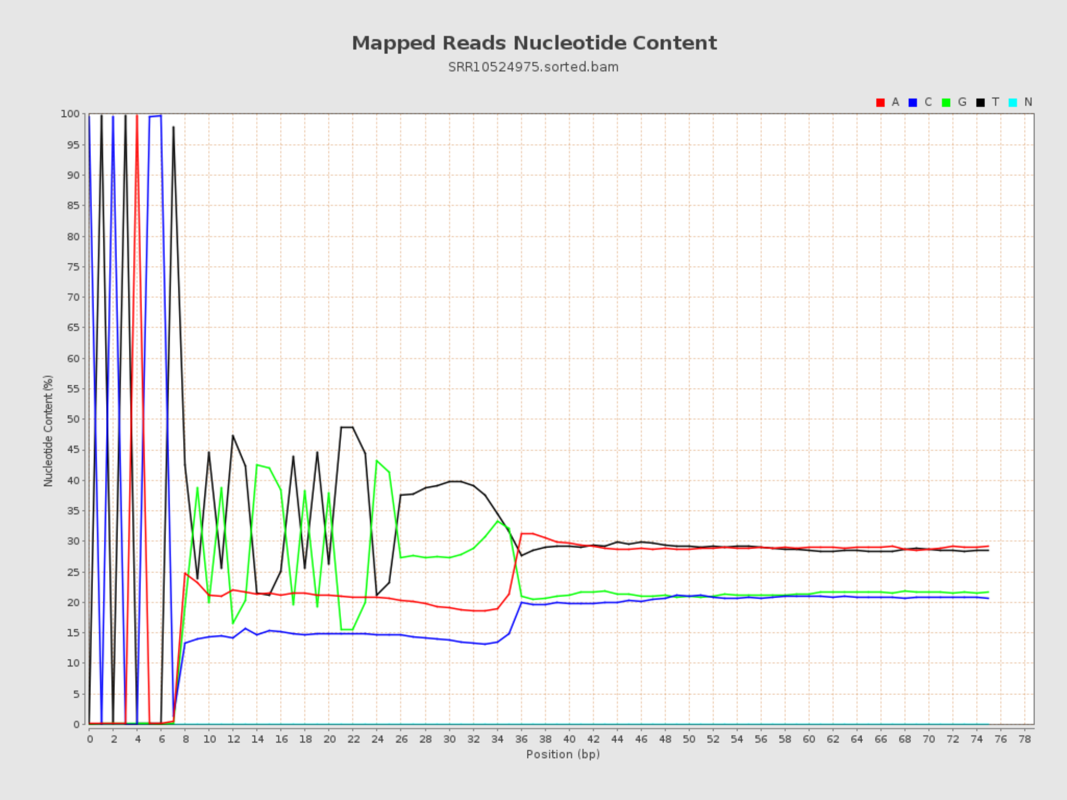
6. Results : Genome Fraction Coverage



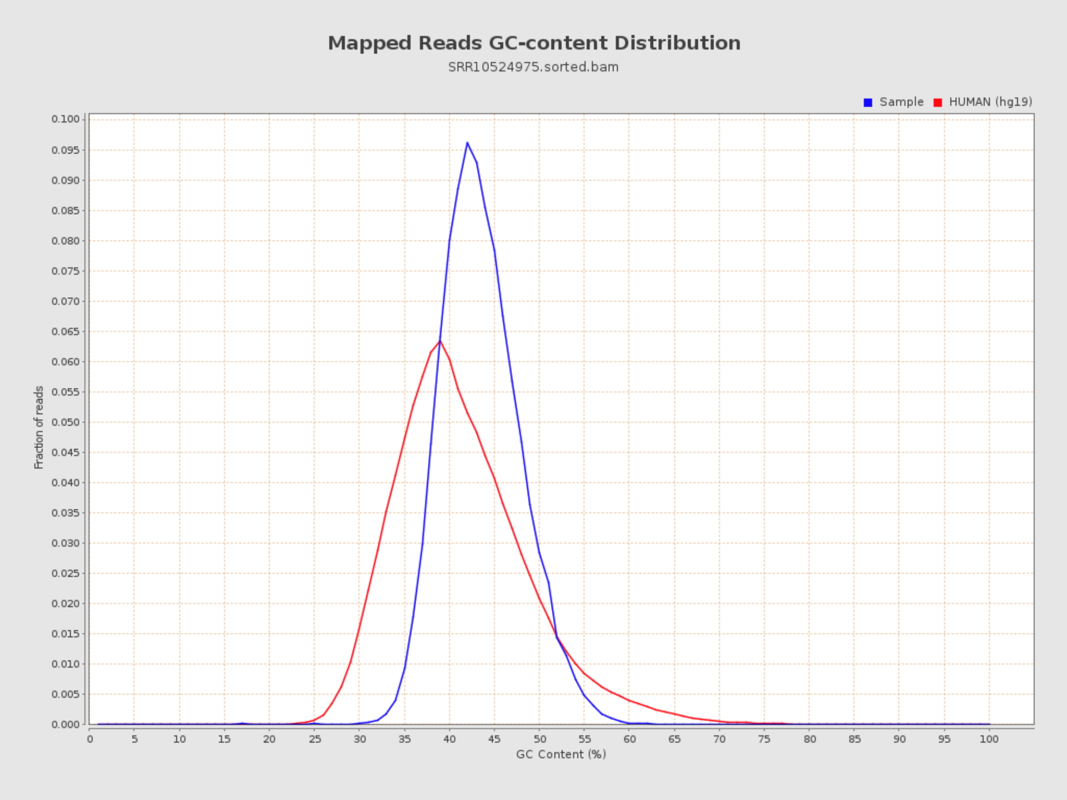
7. Results : Duplication Rate Histogram



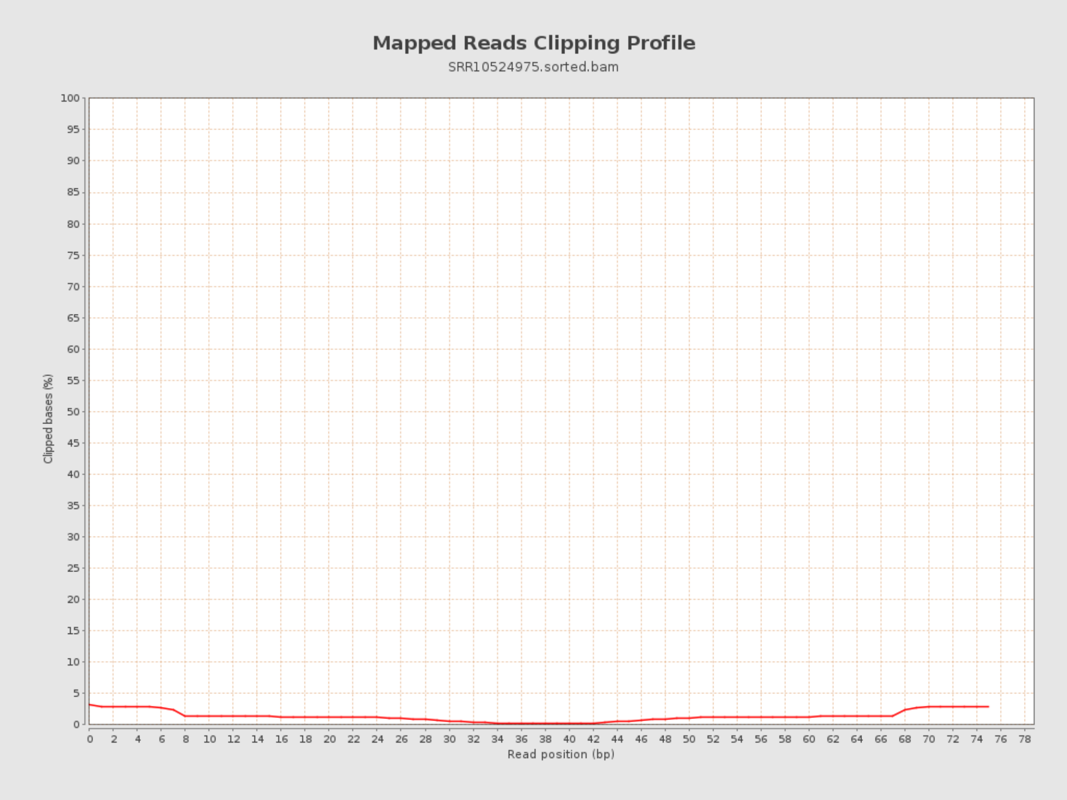
8. Results : Mapped Reads Nucleotide Content



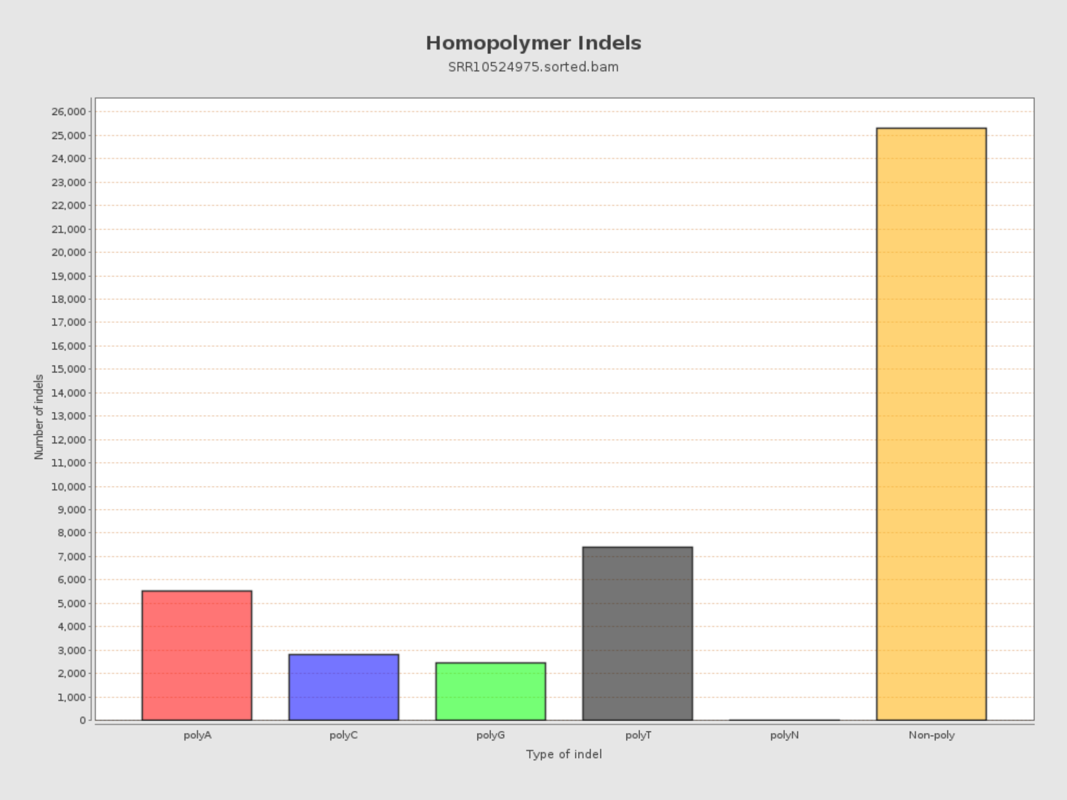
9. Results : Mapped Reads GC-content Distribution



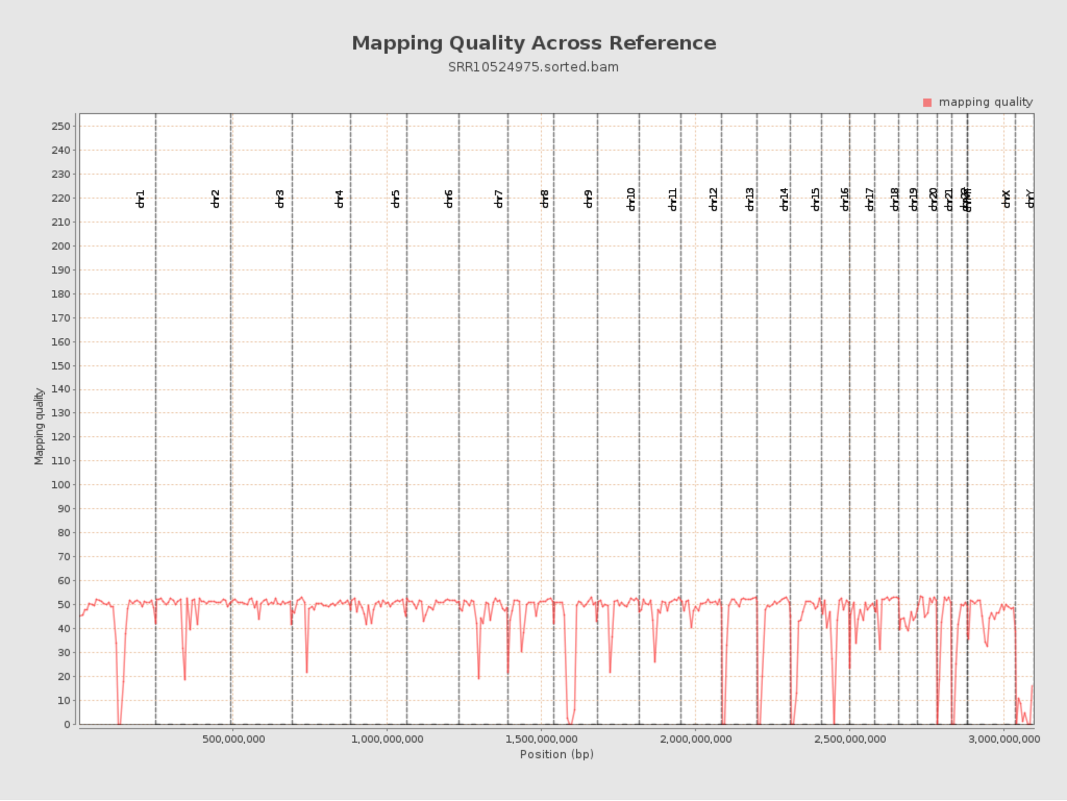
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram