Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 09:58:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524953.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_SRR10524953 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524953.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 09:58:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524953.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,549,806
Mapped reads	1,444,320 / 93.19%
Unmapped reads	105,486 / 6.81%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,441 / 0.22%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	43,065 / 2.78%
Duplication rate	2.16%
Clipped reads	1,444,588 / 93.21%

2.2. ACGT Content

Number/percentage of A's	21,154,644 / 25.02%
Number/percentage of C's	16,446,125 / 19.45%
Number/percentage of T's	26,193,700 / 30.98%
Number/percentage of G's	20,759,644 / 24.55%
Number/percentage of N's	934 / 0%
GC Percentage	44%

2.3. Coverage

Mean	0.0273

Standard Deviation	0.2449

2.4. Mapping Quality

Mean Mapping Quality	44.82

2.5. Mismatches and indels

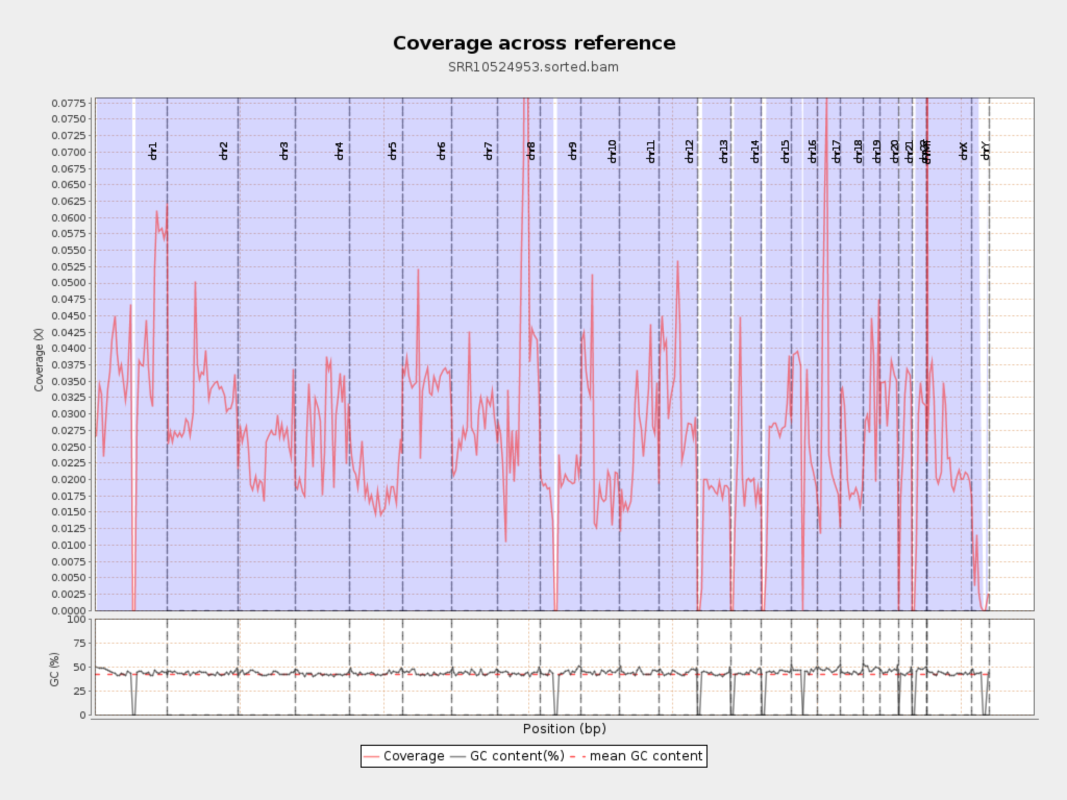
General error rate	0.49%
Mismatches	407,959
Insertions	5,113
Mapped reads with at least one insertion	0.35%
Deletions	16,212
Mapped reads with at least one deletion	1.11%
Homopolymer indels	43.89%

2.6. Chromosome stats

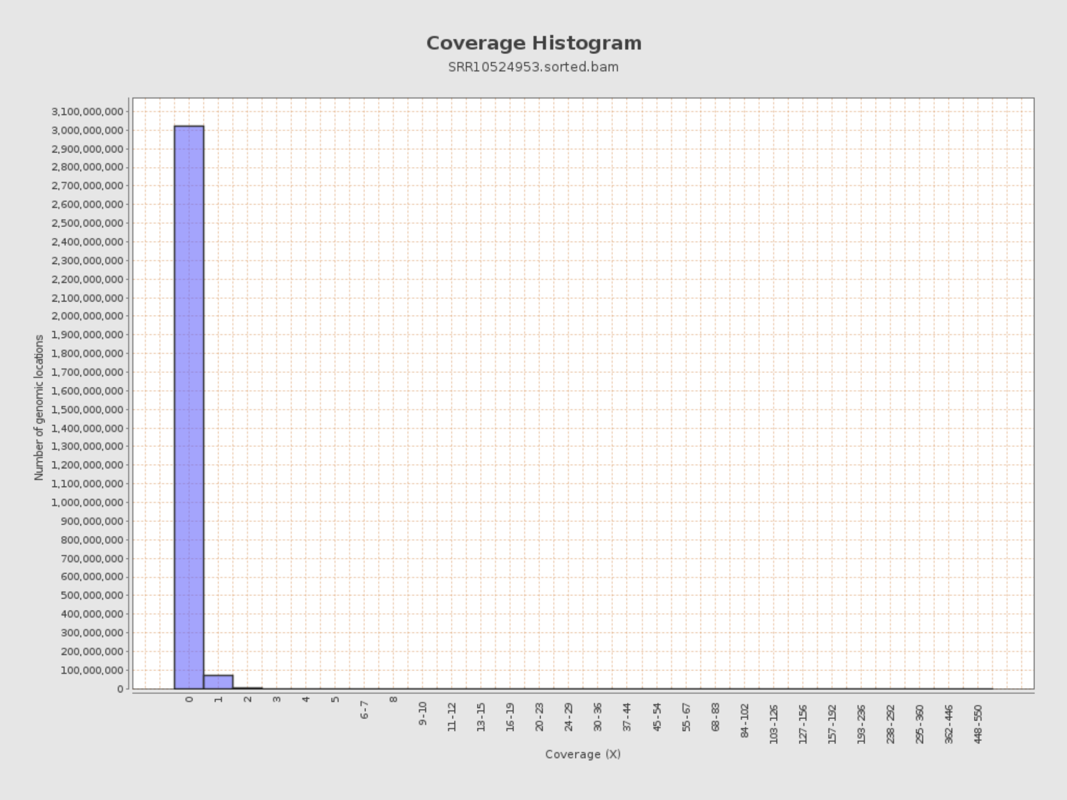
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9362626	0.0376	0.4347
chr2	243199373	7805377	0.0321	0.2817
chr3	198022430	4940522	0.0249	0.172
chr4	191154276	5303165	0.0277	0.1891
chr5	180915260	3438556	0.019	0.1515
chr6	171115067	6083613	0.0356	0.272
chr7	159138663	4513273	0.0284	0.2939

chr8	146364022	5848177	0.04	0.2757
chr9	141213431	2483663	0.0176	0.1868
chr10	135534747	3379521	0.0249	0.2482
chr11	135006516	3526385	0.0261	0.2218
chr12	133851895	4530231	0.0338	0.1999
chr13	115169878	1799015	0.0156	0.1365
chr14	107349540	1973869	0.0184	0.1506
chr15	102531392	2417369	0.0236	0.1739
chr16	90354753	2518694	0.0279	0.187
chr17	81195210	2483628	0.0306	0.2688
chr18	78077248	1682631	0.0216	0.2858
chr19	59128983	1955511	0.0331	0.2883
chr20	63025520	2138273	0.0339	0.1998
chr21	48129895	1293758	0.0269	0.1812
chr22	51304566	1113522	0.0217	0.1578
chrMT	16571	4792	0.2892	0.5793
chrX	155270560	3765644	0.0243	0.1898
chrY	59373566	221038	0.0037	0.0899

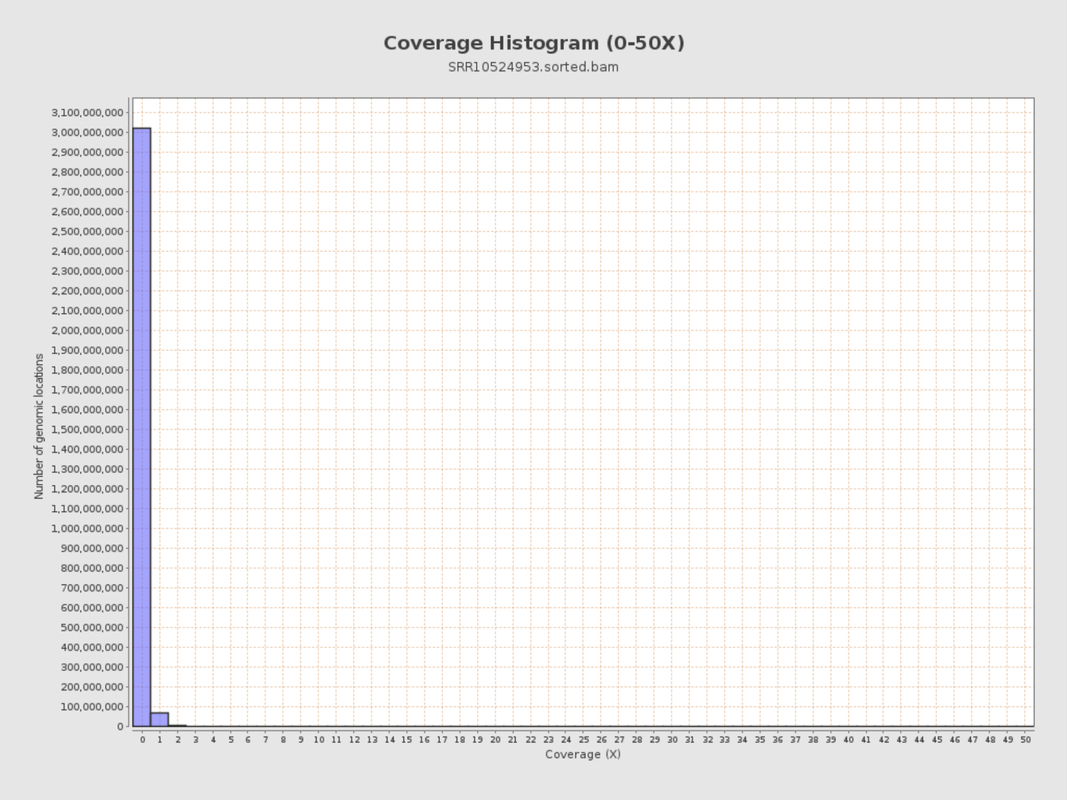
3. Results : Coverage across reference



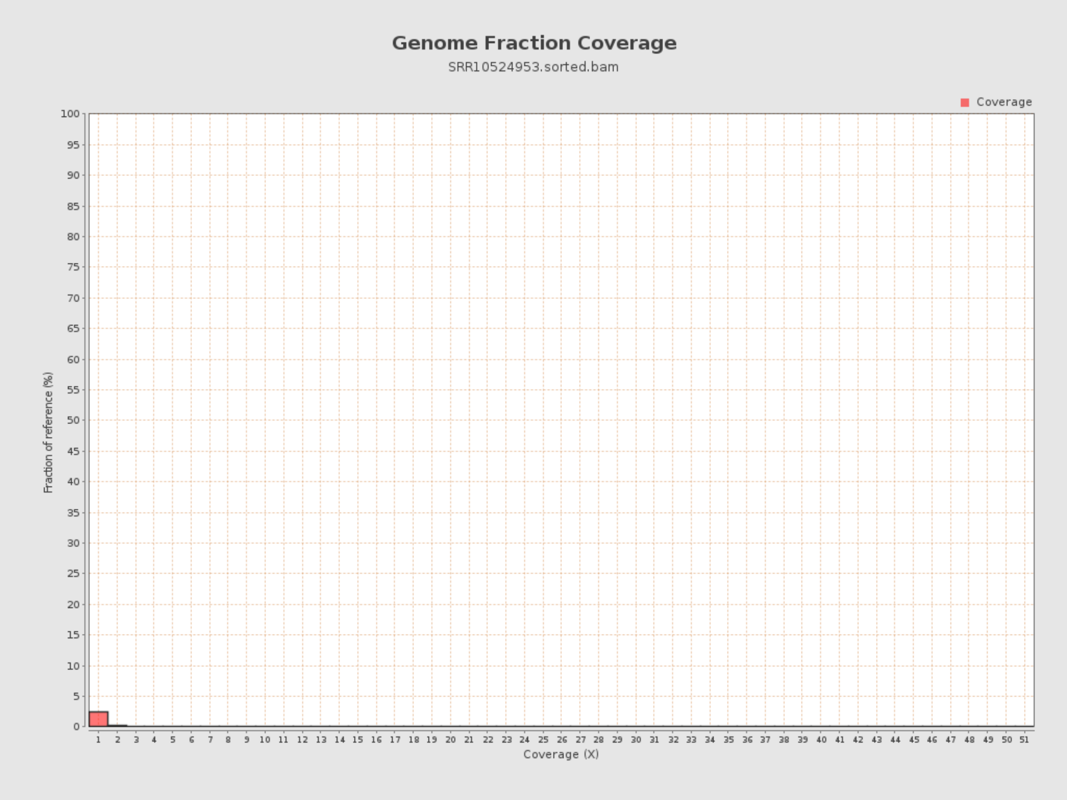
4. Results : Coverage Histogram



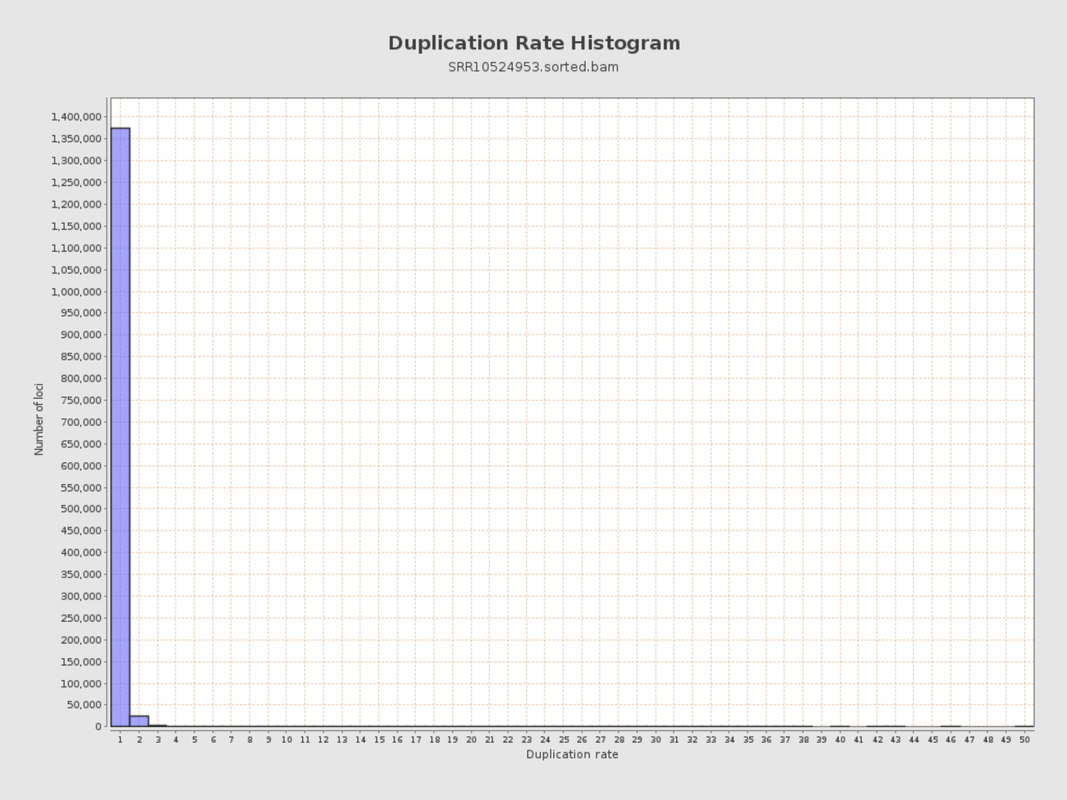
5. Results : Coverage Histogram (0-50X)



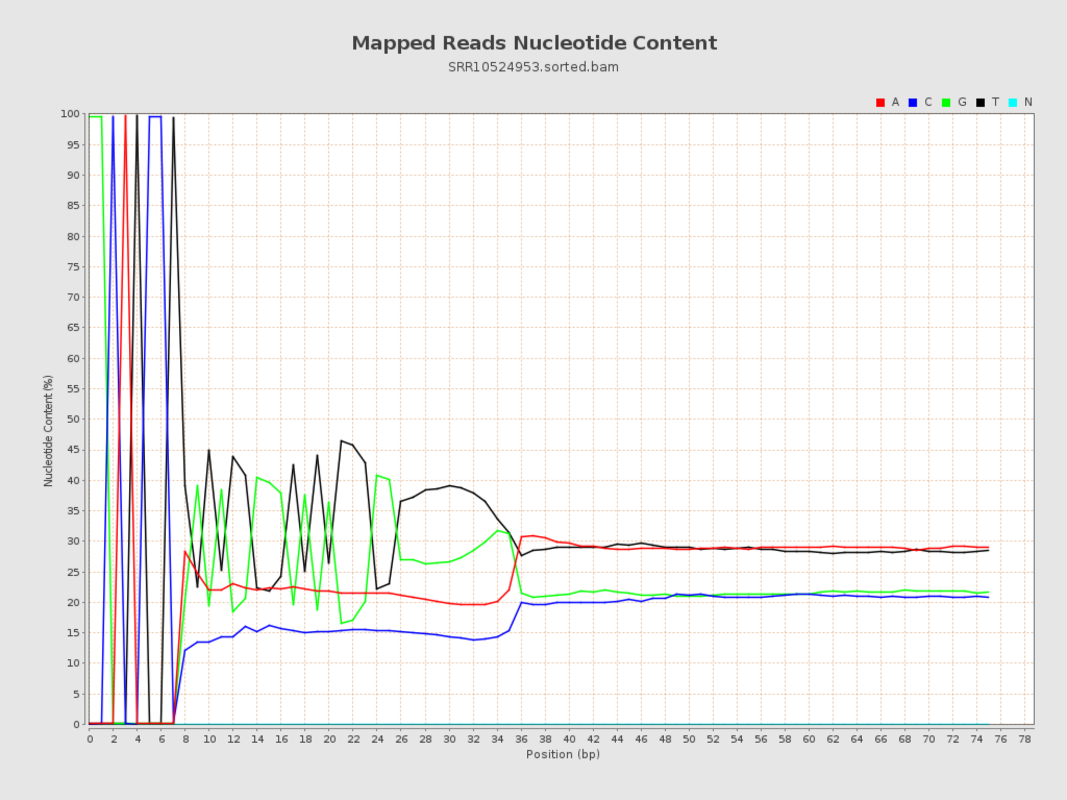
6. Results : Genome Fraction Coverage



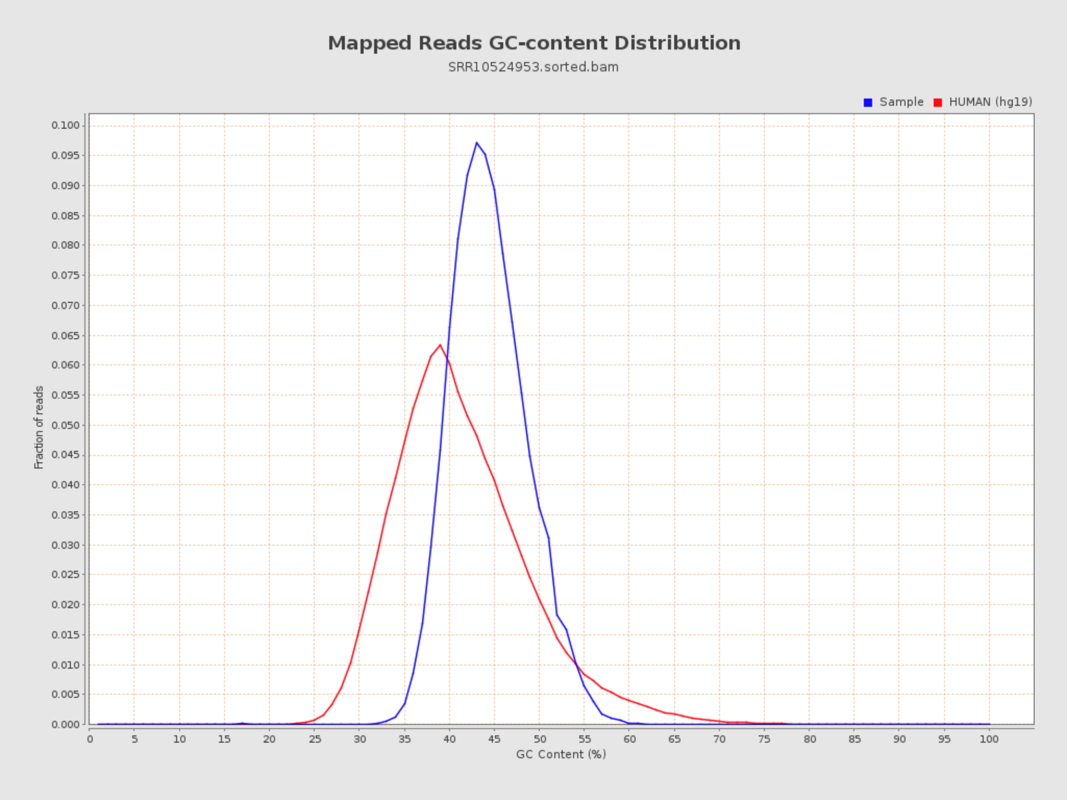
7. Results : Duplication Rate Histogram



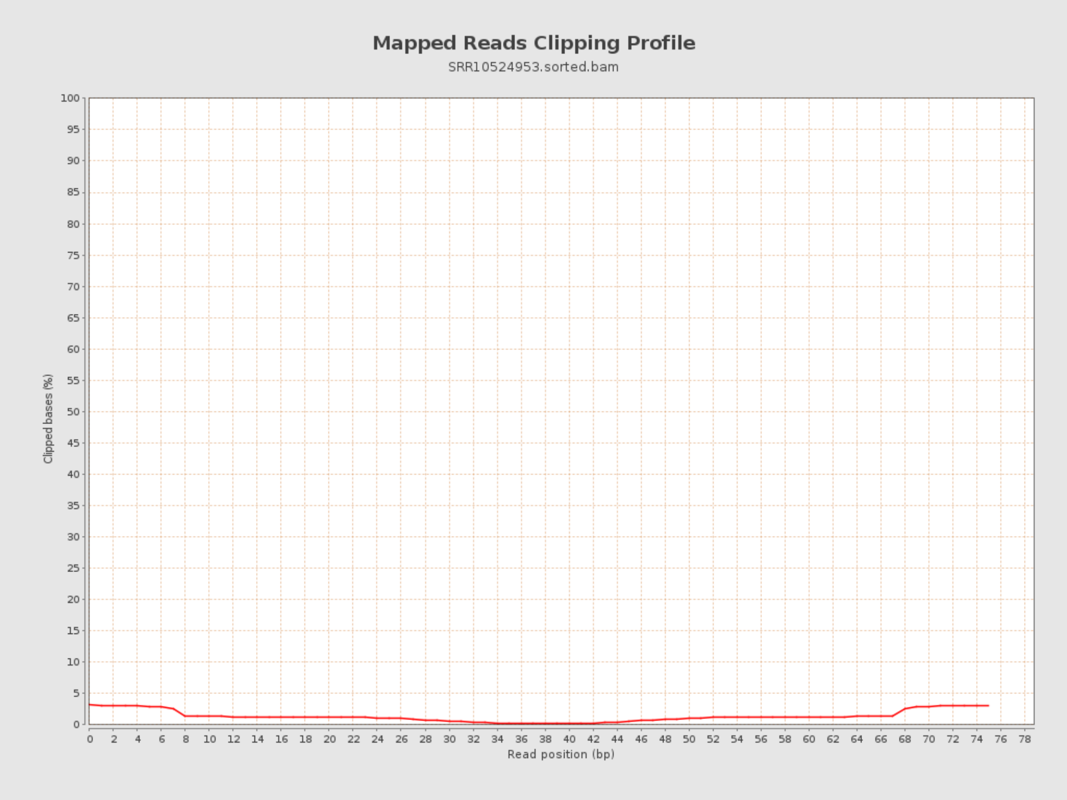
8. Results : Mapped Reads Nucleotide Content



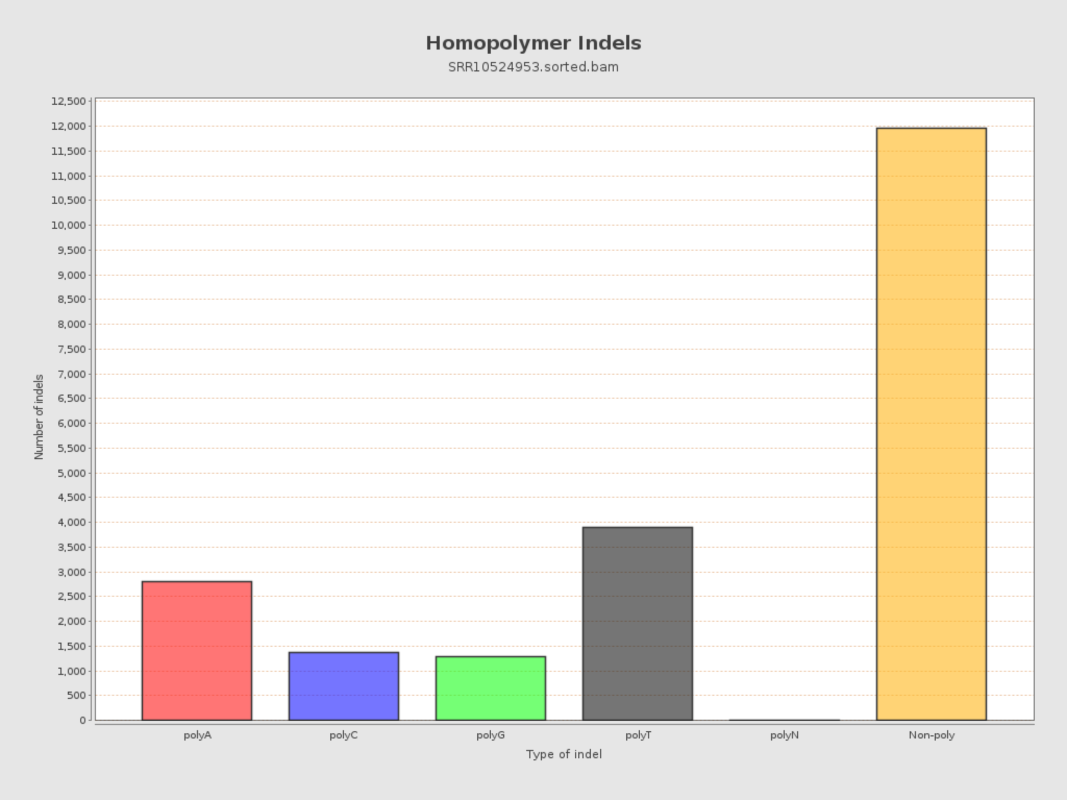
9. Results : Mapped Reads GC-content Distribution



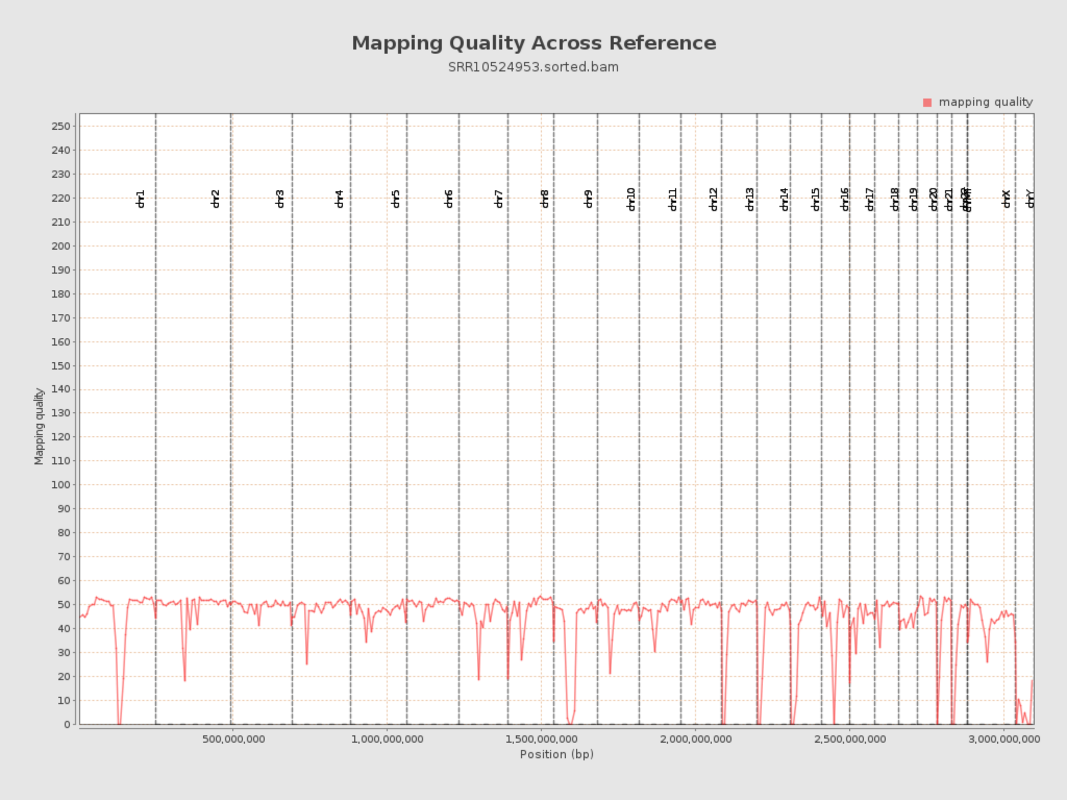
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram