Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 08:53:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524943.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_SRR10524943 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524943.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 08:53:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524943.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,263,336
Mapped reads	1,170,430 / 92.65%
Unmapped reads	92,906 / 7.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,077 / 0.24%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	31,689 / 2.51%
Duplication rate	1.84%
Clipped reads	1,169,751 / 92.59%

2.2. ACGT Content

Number/percentage of A's	16,733,126 / 24.41%
Number/percentage of C's	12,100,747 / 17.65%
Number/percentage of T's	22,384,275 / 32.66%
Number/percentage of G's	17,324,281 / 25.27%
Number/percentage of N's	800 / 0%
GC Percentage	42.93%

2.3. Coverage

Mean	0.0221

Standard Deviation	0.229

2.4. Mapping Quality

Mean Mapping Quality	44.76

2.5. Mismatches and indels

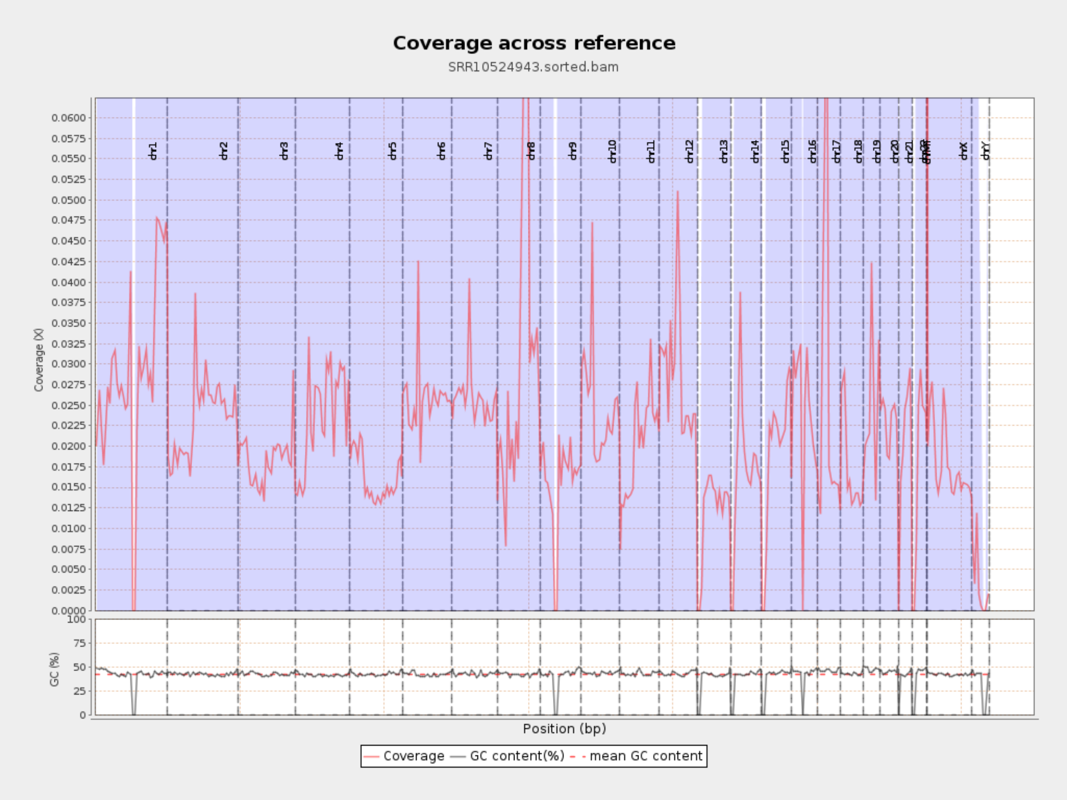
General error rate	0.5%
Mismatches	331,317
Insertions	4,698
Mapped reads with at least one insertion	0.4%
Deletions	12,983
Mapped reads with at least one deletion	1.1%
Homopolymer indels	44.48%

2.6. Chromosome stats

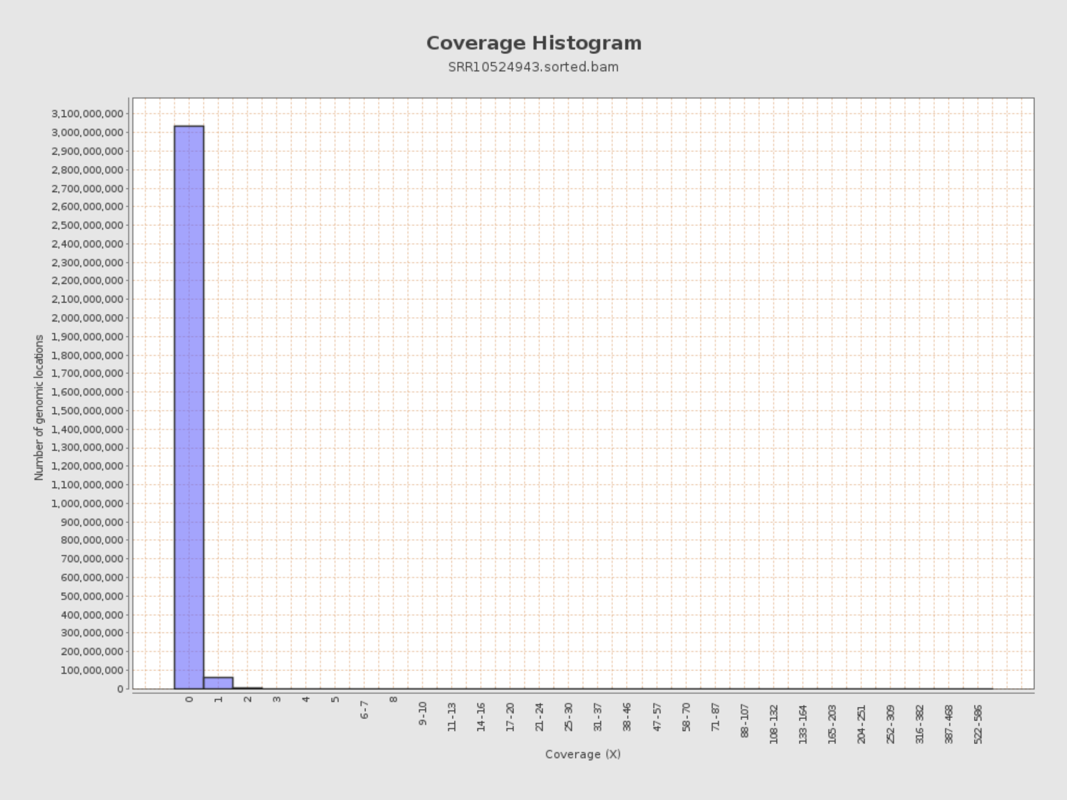
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7176708	0.0288	0.4347
chr2	243199373	5726742	0.0235	0.2418
chr3	198022430	3656298	0.0185	0.1442
chr4	191154276	4561766	0.0239	0.1785
chr5	180915260	2913961	0.0161	0.1368
chr6	171115067	4433882	0.0259	0.2355
chr7	159138663	4157168	0.0261	0.2898

chr8	146364022	4997113	0.0341	0.24
chr9	141213431	2170607	0.0154	0.1835
chr10	135534747	3388264	0.025	0.2345
chr11	135006516	2757657	0.0204	0.2009
chr12	133851895	3841927	0.0287	0.1808
chr13	115169878	1378135	0.012	0.1183
chr14	107349540	1833269	0.0171	0.1436
chr15	102531392	1948951	0.019	0.1567
chr16	90354753	2148392	0.0238	0.1709
chr17	81195210	2257492	0.0278	0.2592
chr18	78077248	1360567	0.0174	0.2831
chr19	59128983	1486882	0.0251	0.2766
chr20	63025520	1435698	0.0228	0.1637
chr21	48129895	990230	0.0206	0.1654
chr22	51304566	906343	0.0177	0.1398
chrMT	16571	6218	0.3752	0.6799
chrX	155270560	2834973	0.0183	0.1642
chrY	59373566	196109	0.0033	0.092

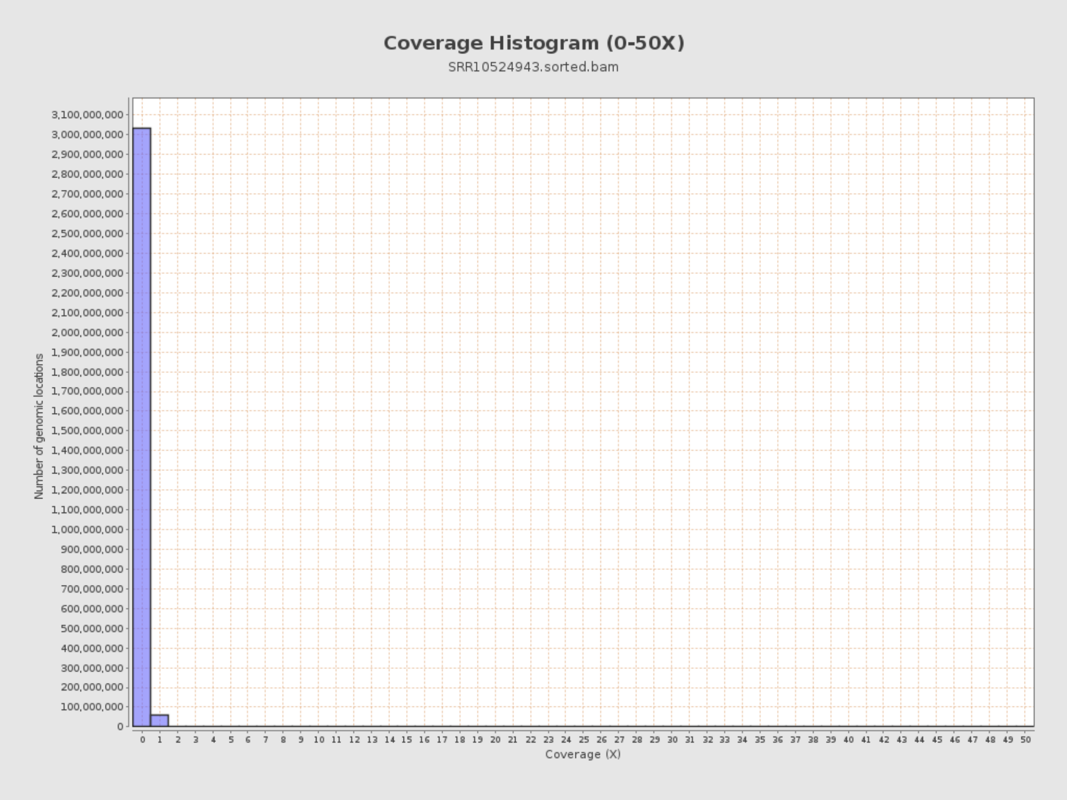
3. Results : Coverage across reference



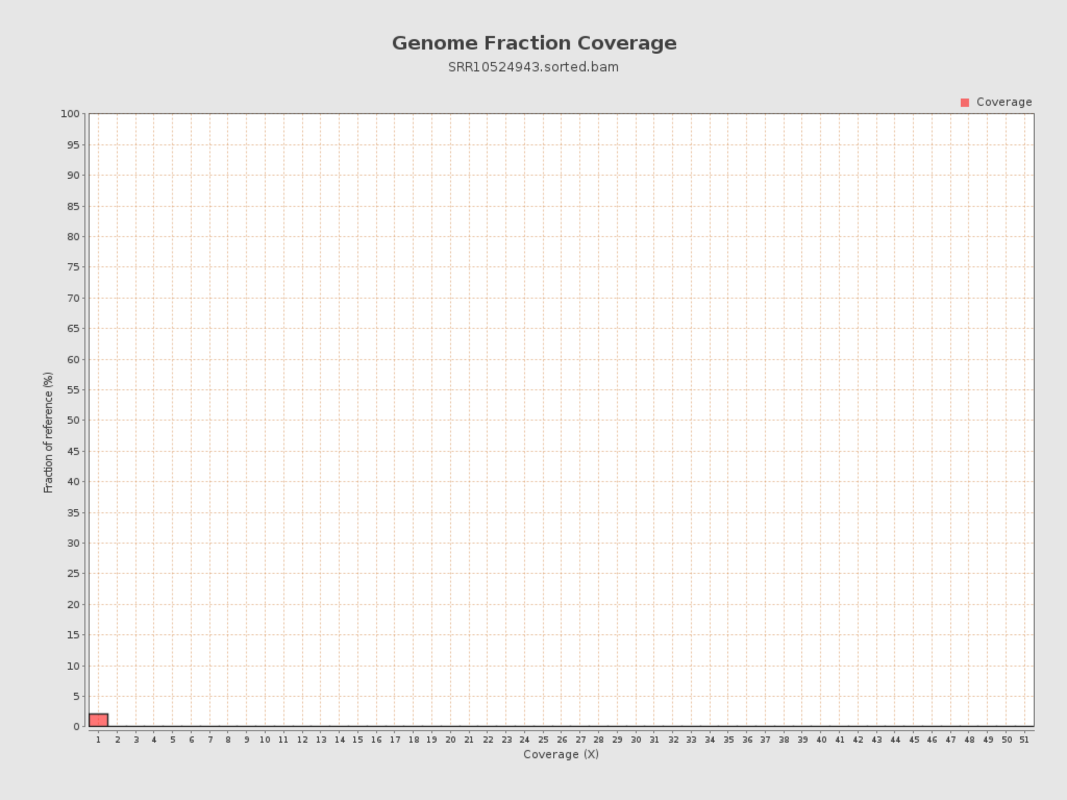
4. Results : Coverage Histogram



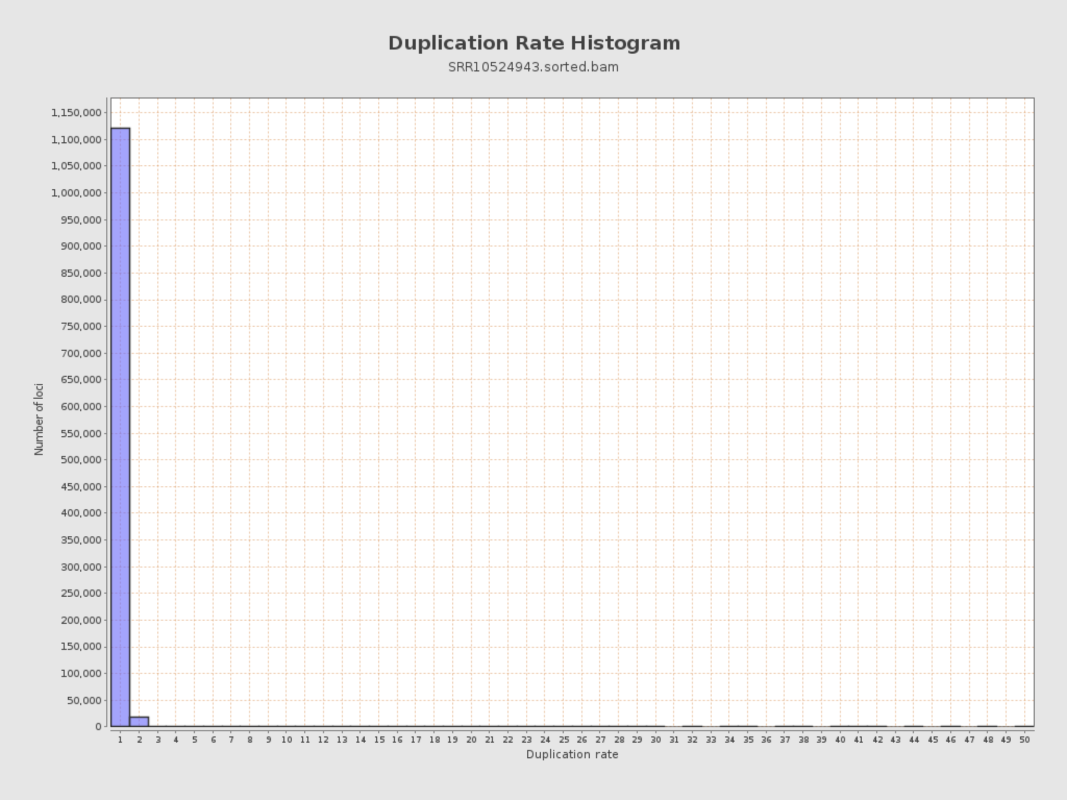
5. Results : Coverage Histogram (0-50X)



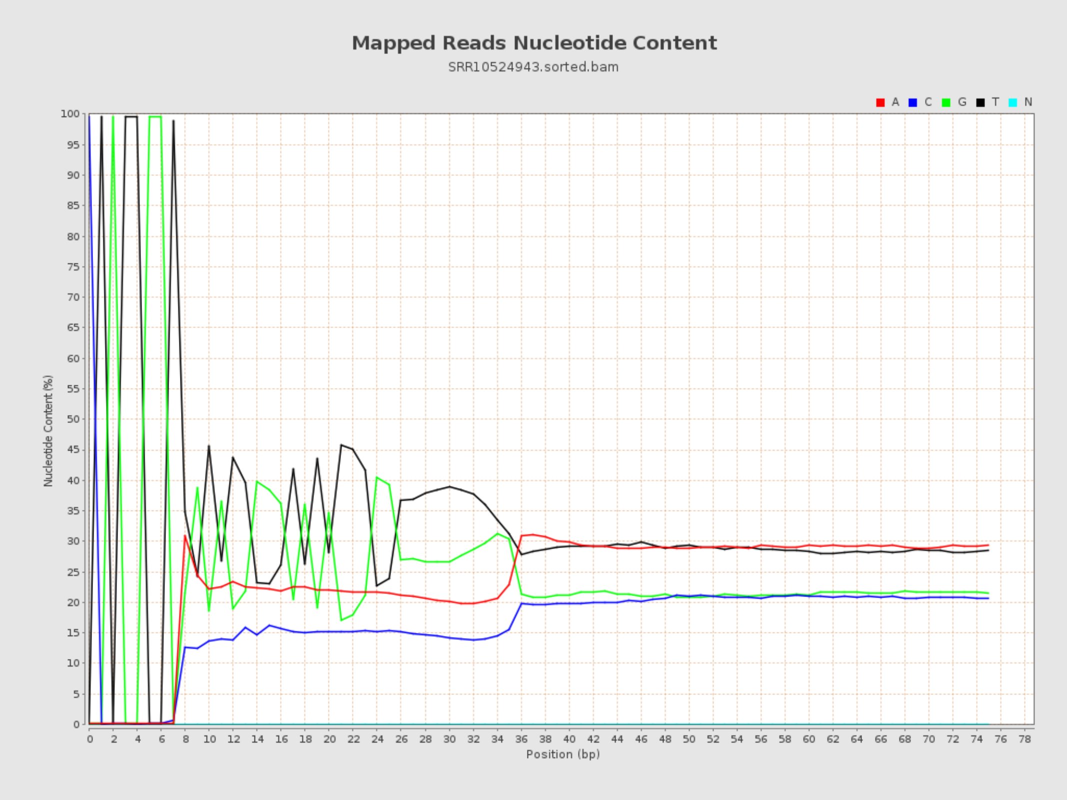
6. Results : Genome Fraction Coverage



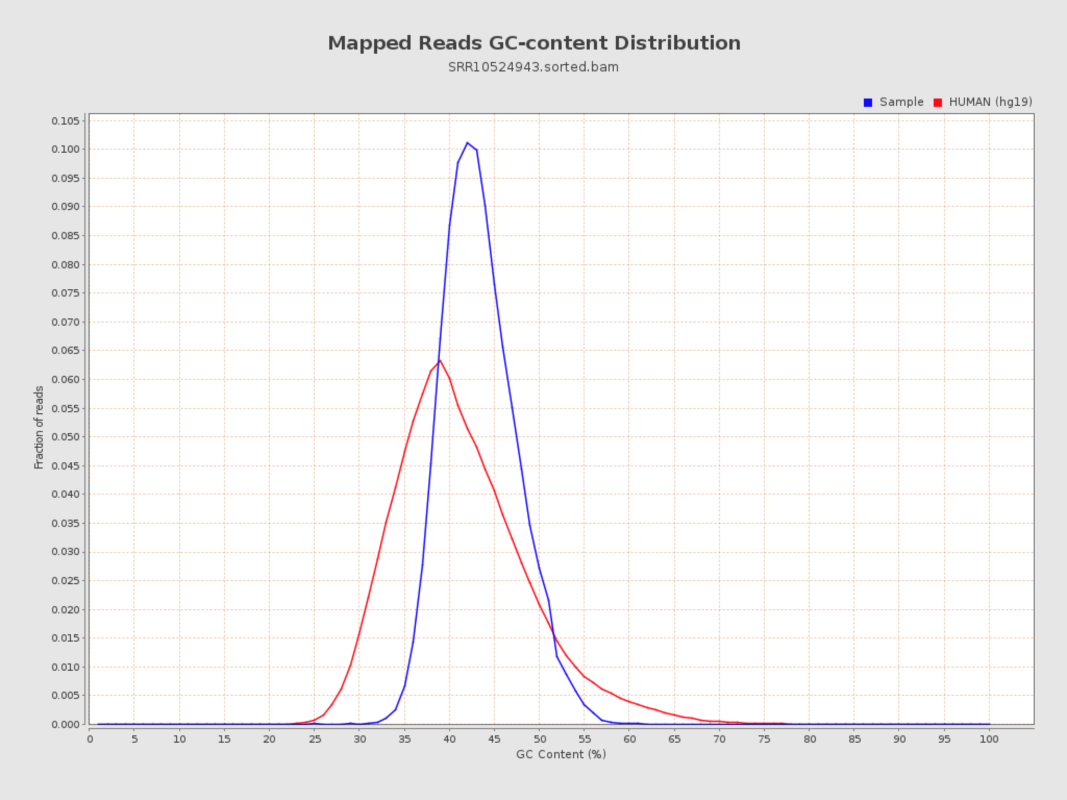
7. Results : Duplication Rate Histogram



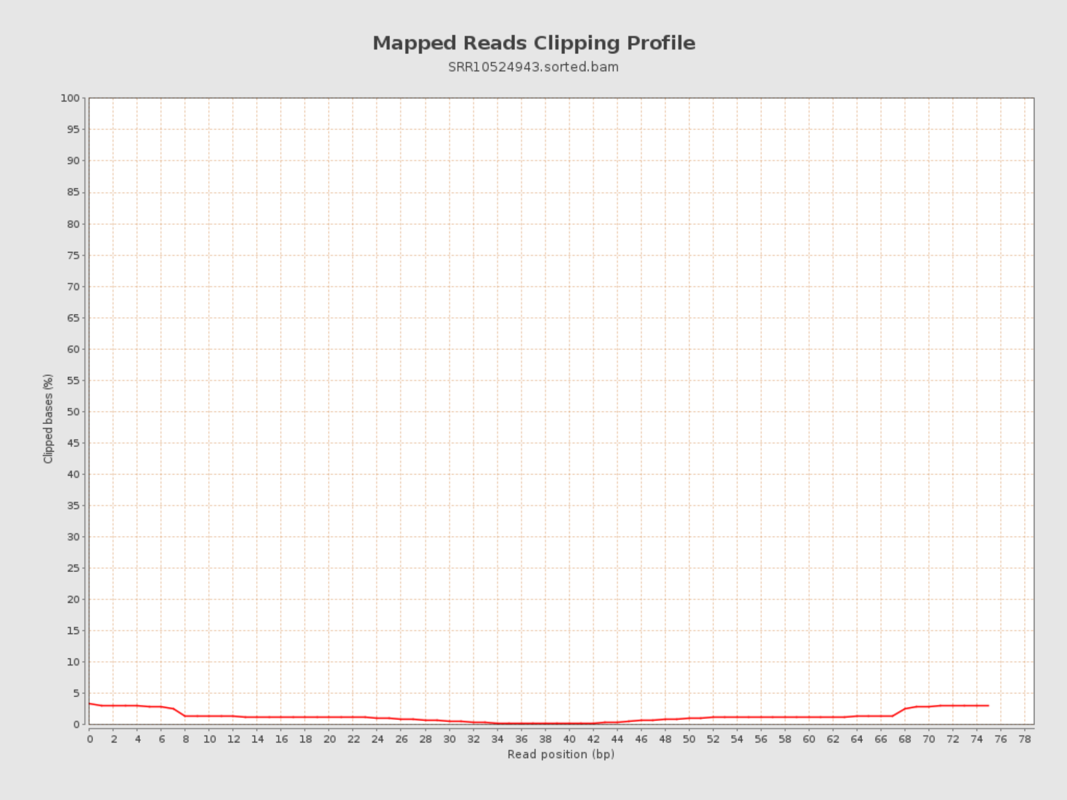
8. Results : Mapped Reads Nucleotide Content



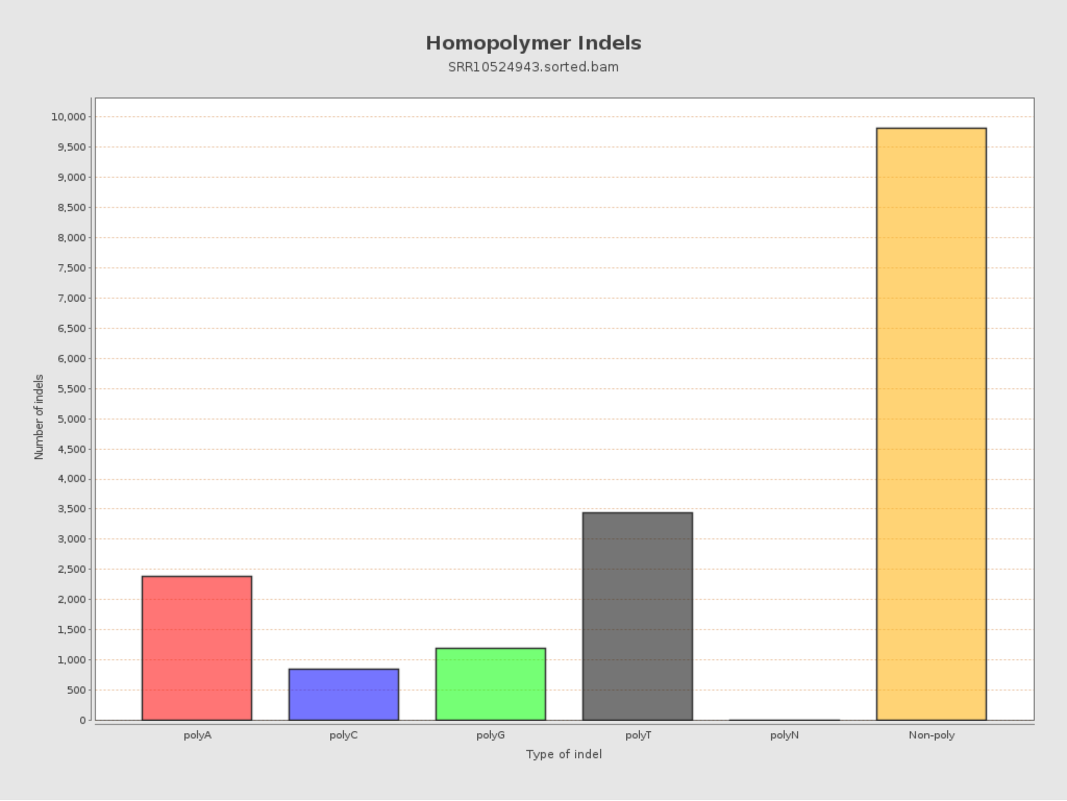
9. Results : Mapped Reads GC-content Distribution



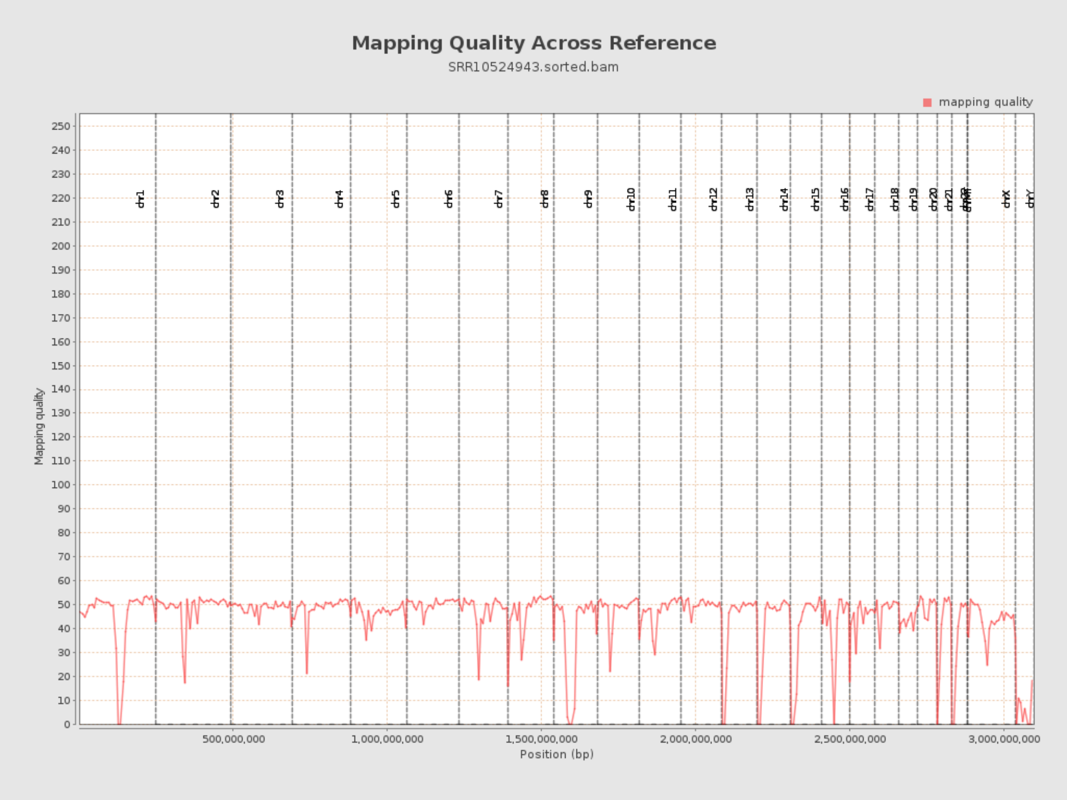
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram