Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 19:21:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524510.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_SRR10524510 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524510.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 19:21:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524510.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,693,531
Mapped reads	4,305,939 / 91.74%
Unmapped reads	387,592 / 8.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,191 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	631,540 / 13.46%
Duplication rate	9.92%
Clipped reads	4,312,932 / 91.89%

2.2. ACGT Content

Number/percentage of A's	62,580,784 / 24.77%
Number/percentage of C's	47,690,256 / 18.88%
Number/percentage of T's	80,864,587 / 32.01%
Number/percentage of G's	61,464,651 / 24.33%
Number/percentage of N's	3,781 / 0%
GC Percentage	43.21%

2.3. Coverage

Mean	0.0816

Standard Deviation	0.7442

2.4. Mapping Quality

Mean Mapping Quality	45

2.5. Mismatches and indels

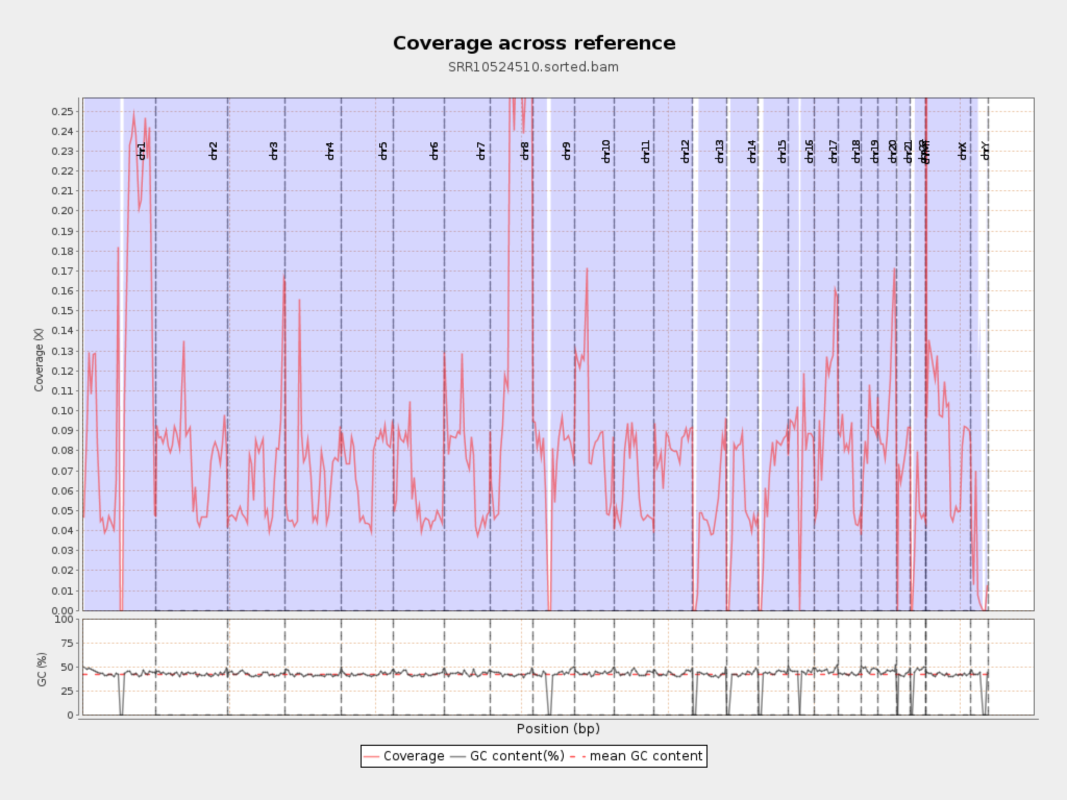
General error rate	0.53%
Mismatches	1,287,660
Insertions	20,211
Mapped reads with at least one insertion	0.47%
Deletions	46,295
Mapped reads with at least one deletion	1.07%
Homopolymer indels	41.07%

2.6. Chromosome stats

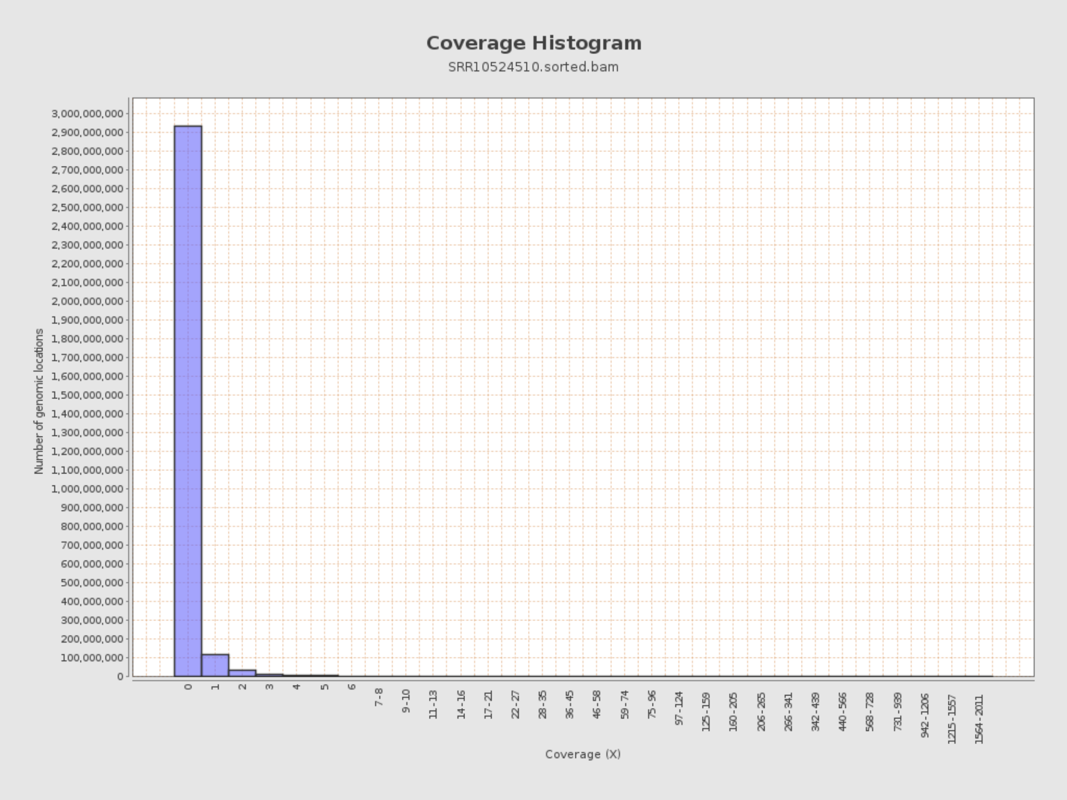
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	31294442	0.1256	1.6017
chr2	243199373	19088964	0.0785	0.902
chr3	198022430	13087205	0.0661	0.3713
chr4	191154276	12547423	0.0656	0.5746
chr5	180915260	13060628	0.0722	0.391
chr6	171115067	10249544	0.0599	0.451
chr7	159138663	11870274	0.0746	0.8012

chr8	146364022	27793652	0.1899	0.8503
chr9	141213431	10255216	0.0726	0.522
chr10	135534747	12669927	0.0935	0.8383
chr11	135006516	8228710	0.061	0.5498
chr12	133851895	10985438	0.0821	0.4192
chr13	115169878	5275125	0.0458	0.3189
chr14	107349540	5673357	0.0528	0.3421
chr15	102531392	6299823	0.0614	0.3539
chr16	90354753	7413945	0.0821	0.4525
chr17	81195210	8500965	0.1047	0.5209
chr18	78077248	5642720	0.0723	1.0402
chr19	59128983	5060447	0.0856	1.0179
chr20	63025520	6885163	0.1092	0.5067
chr21	48129895	3425280	0.0712	0.5306
chr22	51304566	2013690	0.0392	0.2866
chrMT	16571	53244	3.2131	3.115
chrX	155270560	14279942	0.092	0.4864
chrY	59373566	1027233	0.0173	0.5882

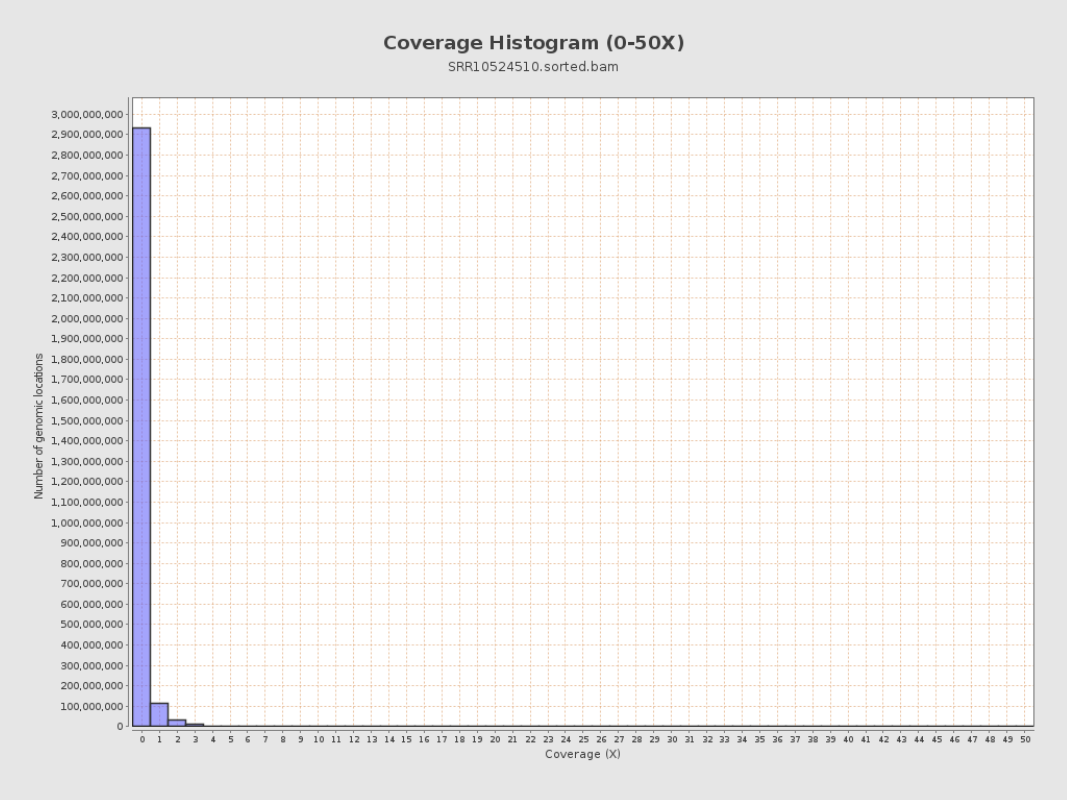
3. Results : Coverage across reference



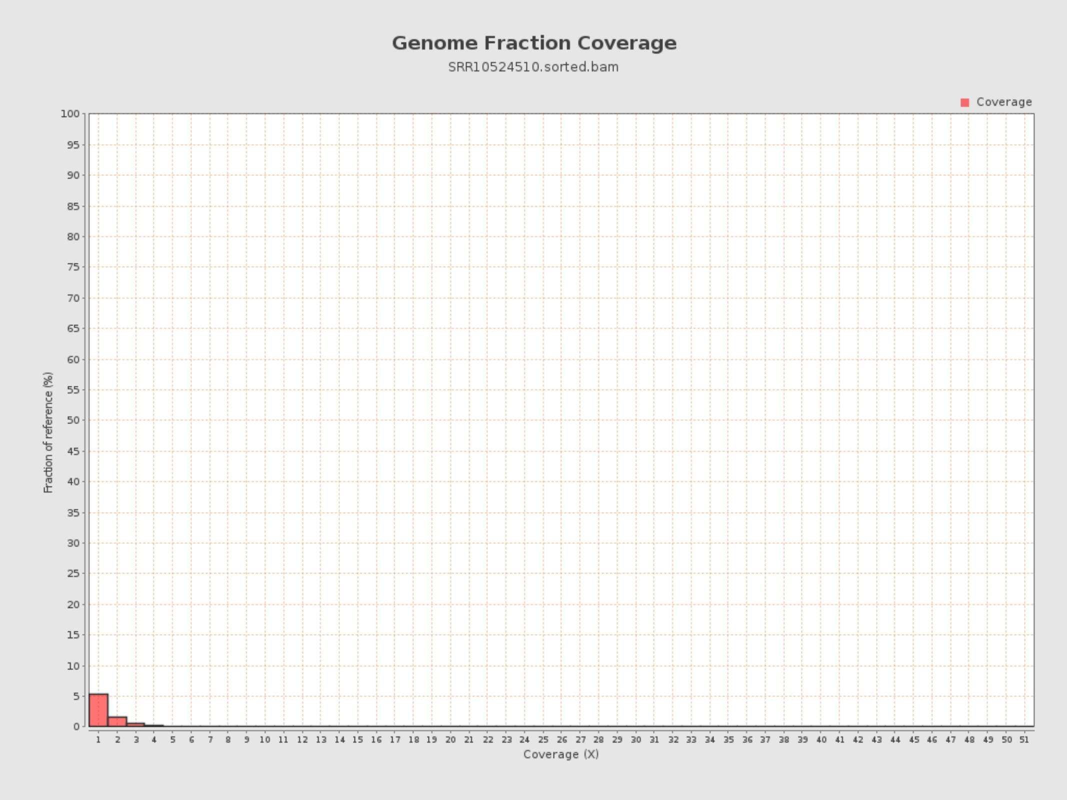
4. Results : Coverage Histogram



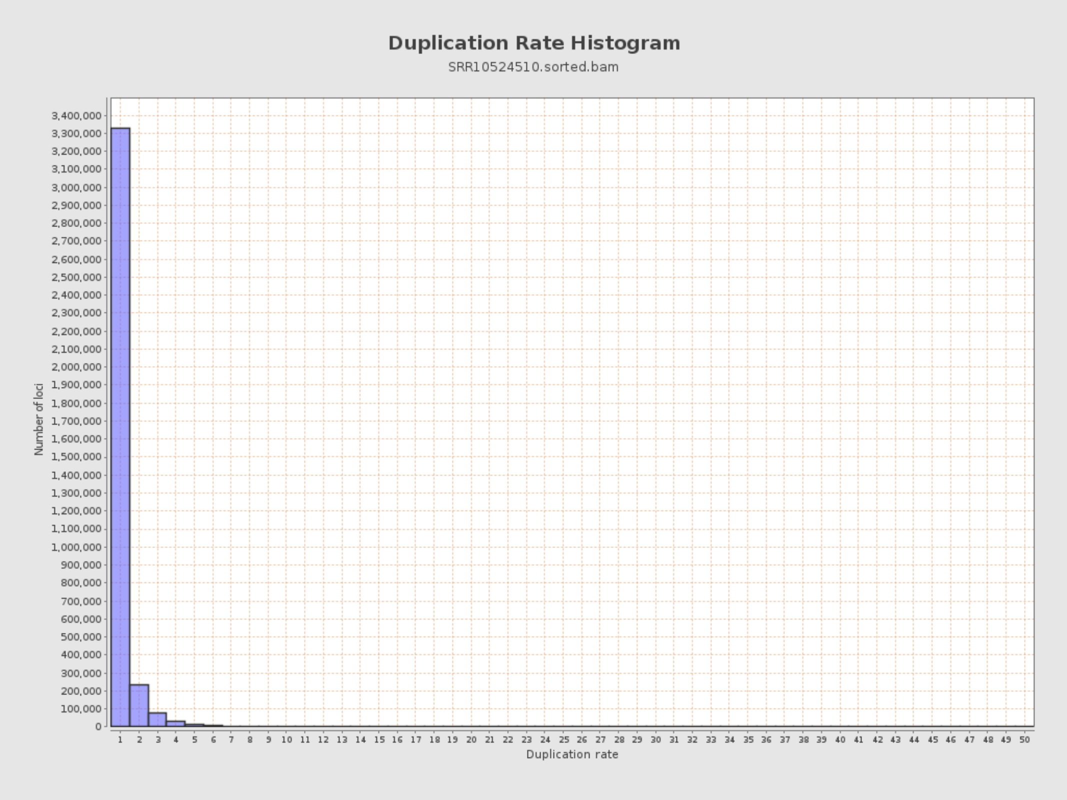
5. Results : Coverage Histogram (0-50X)



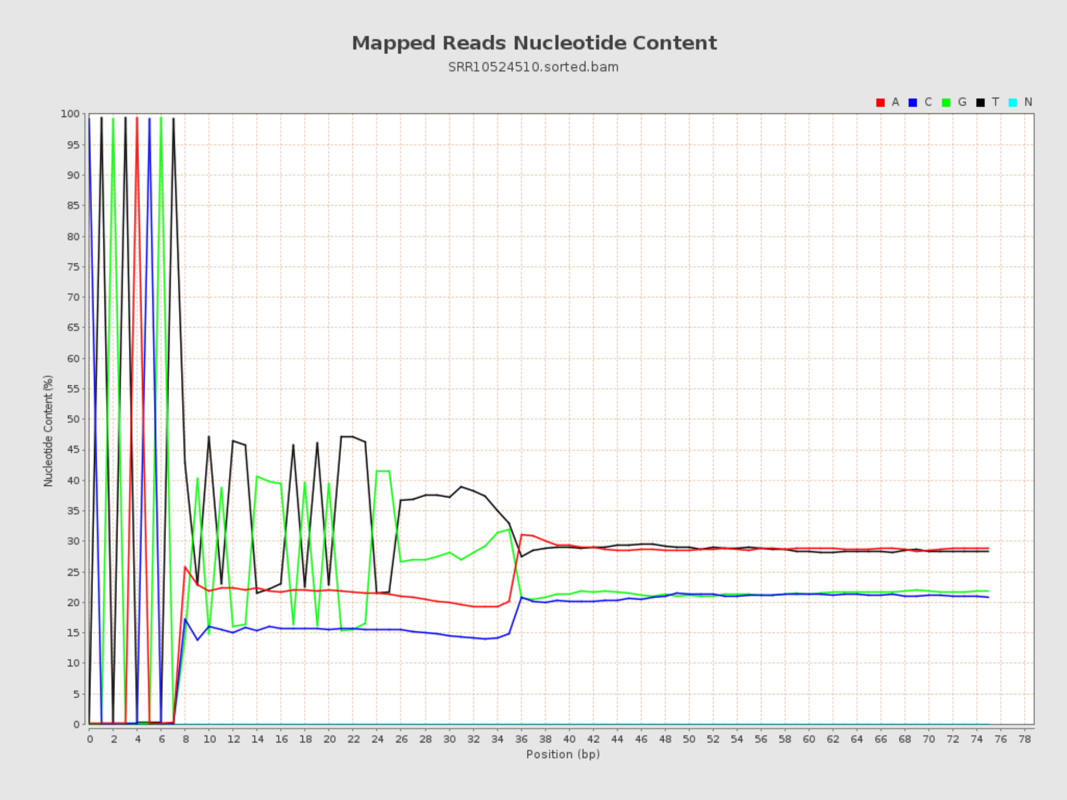
6. Results : Genome Fraction Coverage



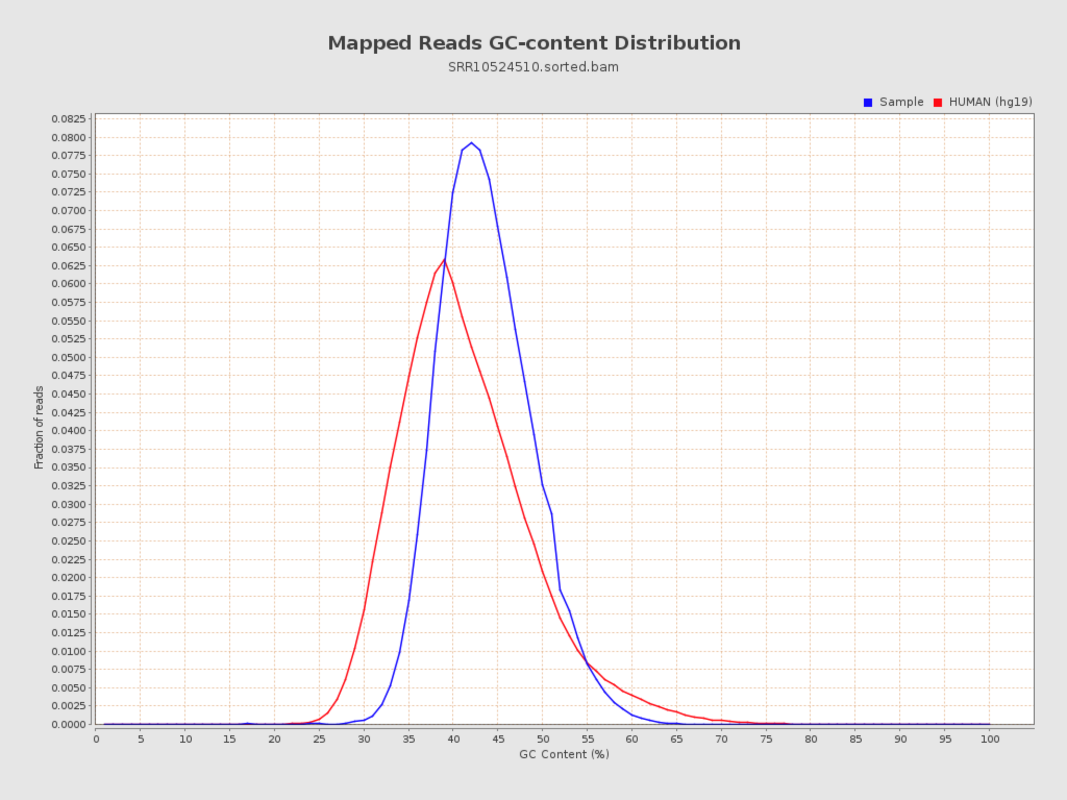
7. Results : Duplication Rate Histogram



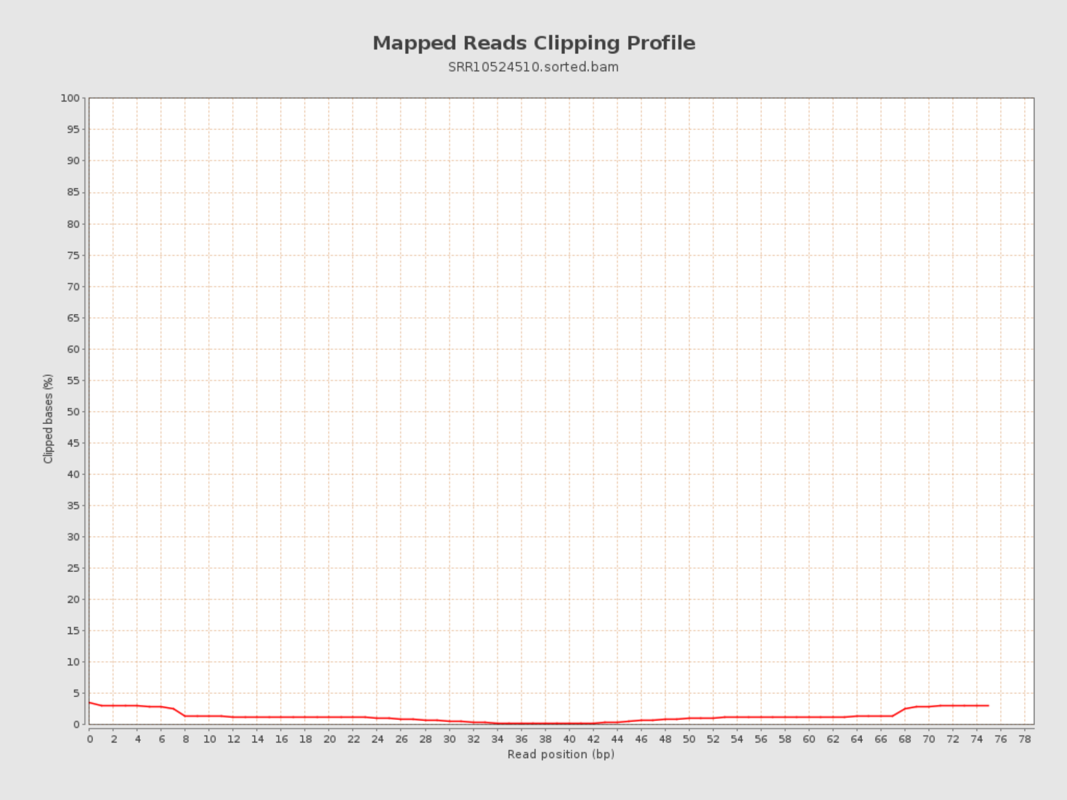
8. Results : Mapped Reads Nucleotide Content



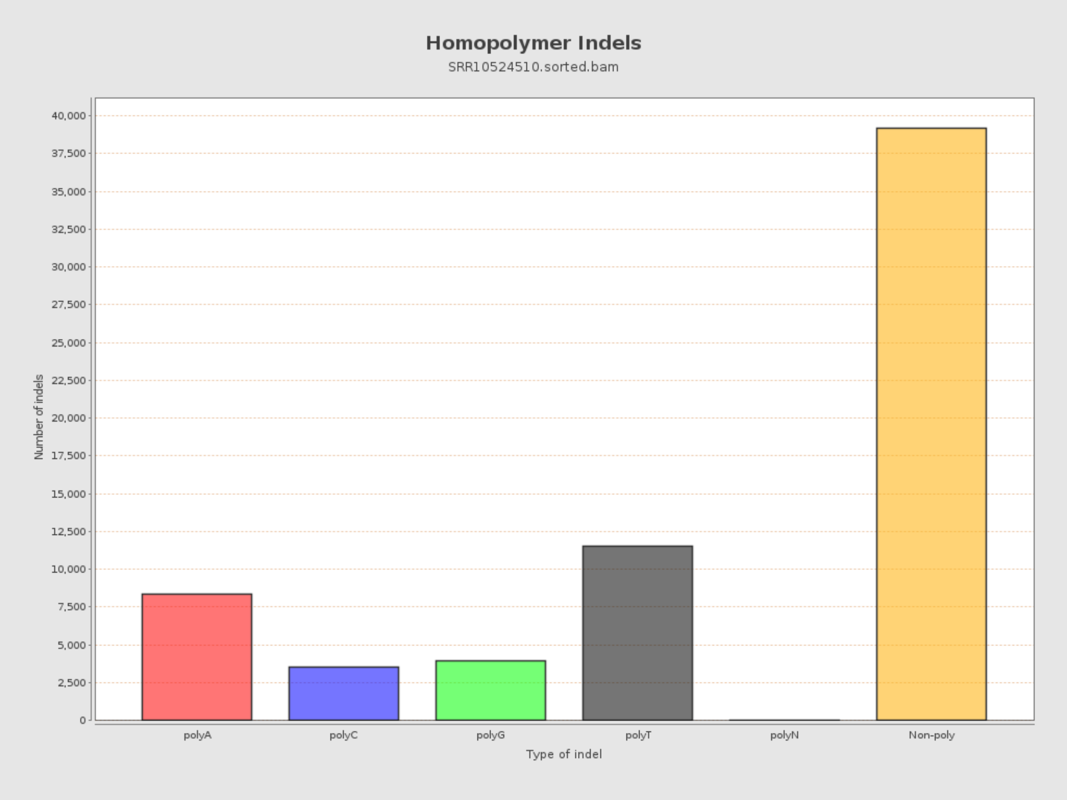
9. Results : Mapped Reads GC-content Distribution



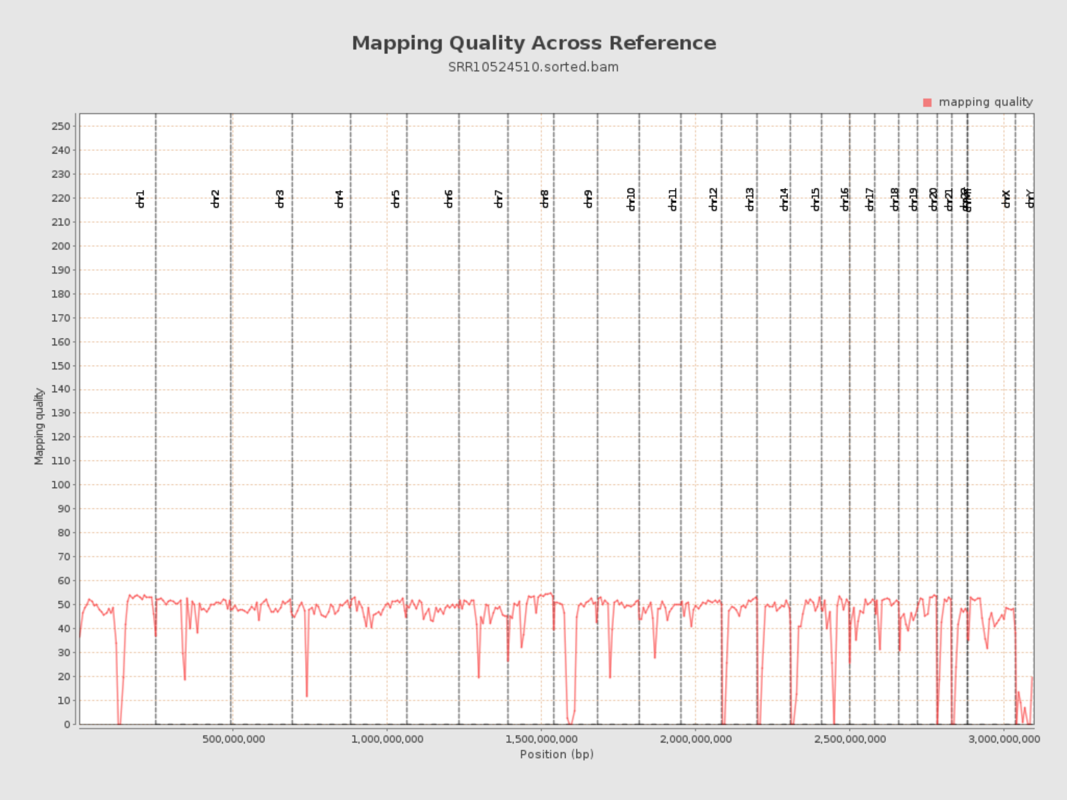
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram