Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 10:00:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080824.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_SRR3080824 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080824.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 10:00:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080824.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,151,281
Mapped reads	1,850,260 / 86.01%
Unmapped reads	301,021 / 13.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,795 / 0.87%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	104,666 / 4.87%
Duplication rate	3.42%
Clipped reads	860,568 / 40%

2.2. ACGT Content

Number/percentage of A's	33,508,647 / 27.14%
Number/percentage of C's	23,749,813 / 19.23%
Number/percentage of T's	36,758,320 / 29.77%
Number/percentage of G's	29,441,129 / 23.84%
Number/percentage of N's	17,058 / 0.01%
GC Percentage	43.08%

2.3. Coverage

Mean	0.0399

Standard Deviation	0.7284

2.4. Mapping Quality

Mean Mapping Quality	40.64

2.5. Mismatches and indels

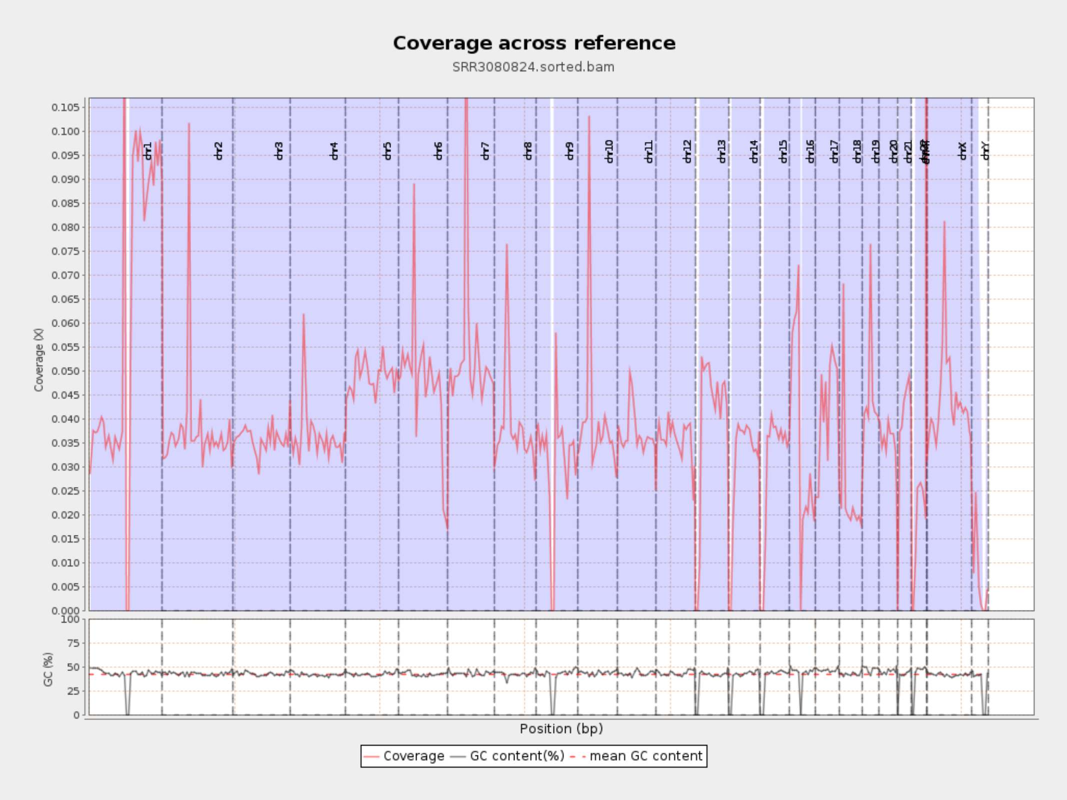
General error rate	0.94%
Mismatches	1,135,268
Insertions	11,675
Mapped reads with at least one insertion	0.62%
Deletions	24,951
Mapped reads with at least one deletion	1.33%
Homopolymer indels	43.24%

2.6. Chromosome stats

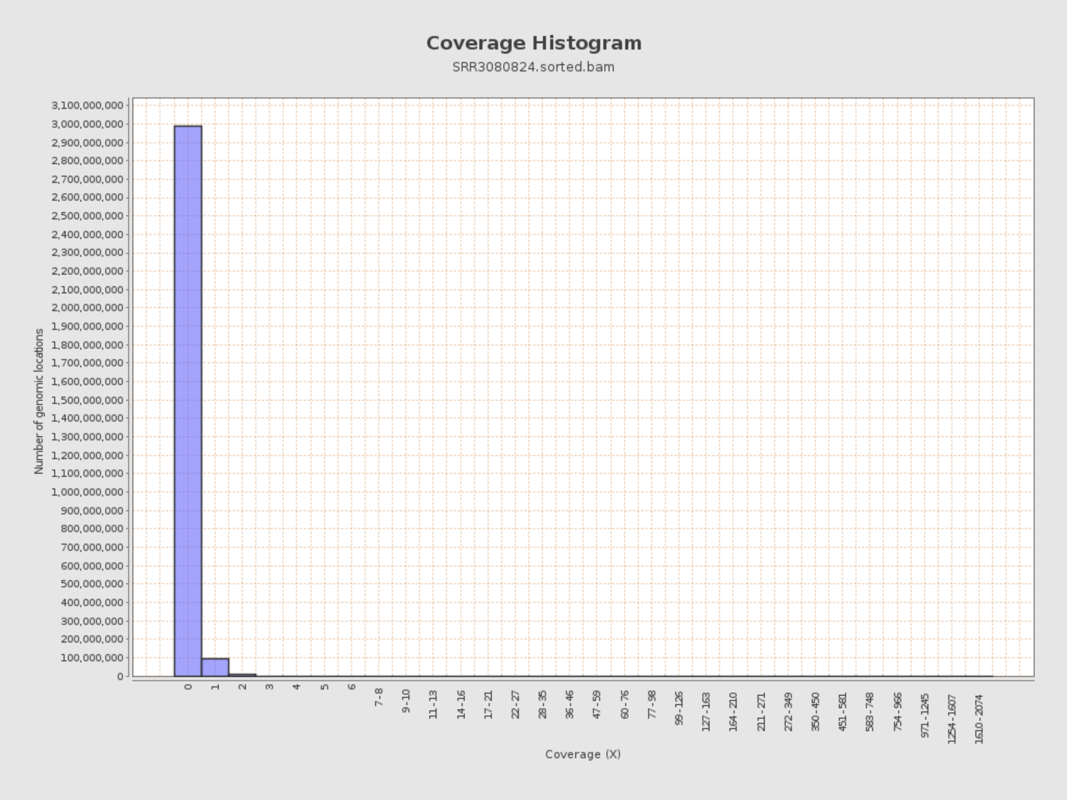
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15142719	0.0608	1.6867
chr2	243199373	9162080	0.0377	0.531
chr3	198022430	7050038	0.0356	0.2109
chr4	191154276	6951094	0.0364	0.2516
chr5	180915260	8853766	0.0489	0.254
chr6	171115067	8138584	0.0476	0.4888
chr7	159138663	8648399	0.0543	1.1419

chr8	146364022	5619402	0.0384	1.2805
chr9	141213431	4380524	0.031	0.4694
chr10	135534747	5374277	0.0397	0.5716
chr11	135006516	4995804	0.037	0.4113
chr12	133851895	4794508	0.0358	0.2252
chr13	115169878	4513392	0.0392	0.2193
chr14	107349540	3254351	0.0303	0.2588
chr15	102531392	3073541	0.03	0.2027
chr16	90354753	3191958	0.0353	0.2911
chr17	81195210	3432277	0.0423	0.2955
chr18	78077248	1953515	0.025	1.1458
chr19	59128983	2682060	0.0454	1.1459
chr20	63025520	2236456	0.0355	0.2666
chr21	48129895	1868115	0.0388	0.2563
chr22	51304566	888657	0.0173	0.1404
chrMT	16571	45674	2.7563	2.3198
chrX	155270560	6854220	0.0441	0.3113
chrY	59373566	413455	0.007	0.218

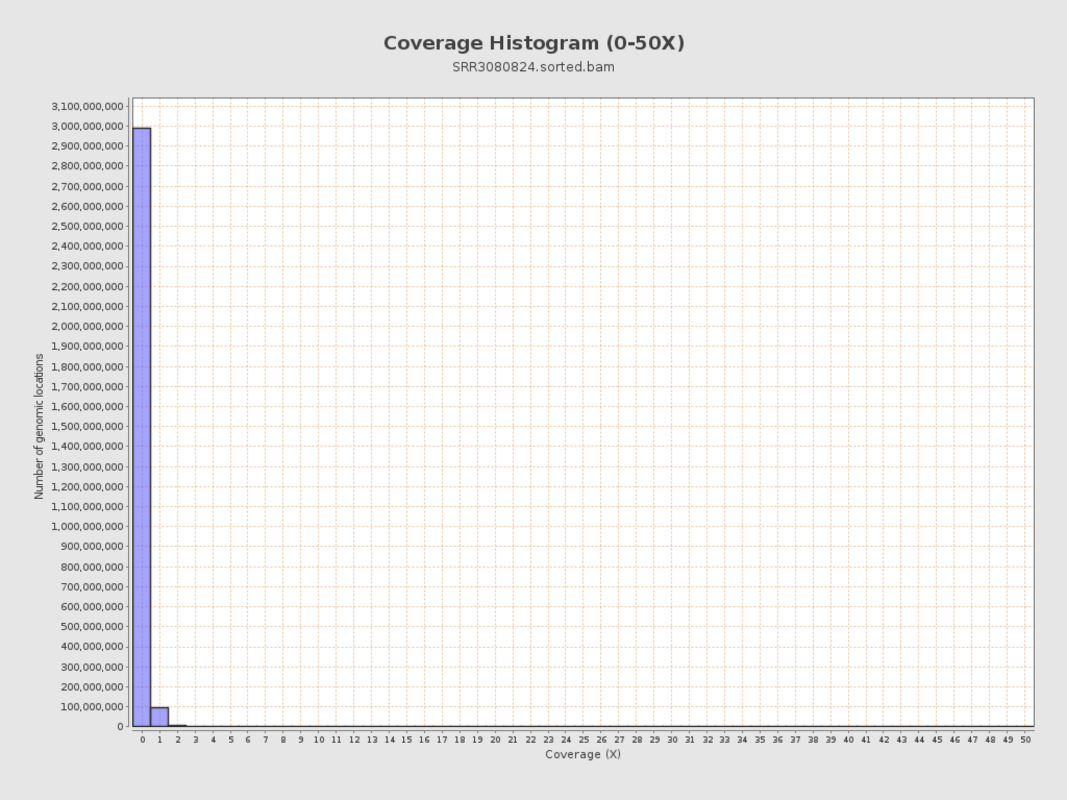
3. Results : Coverage across reference



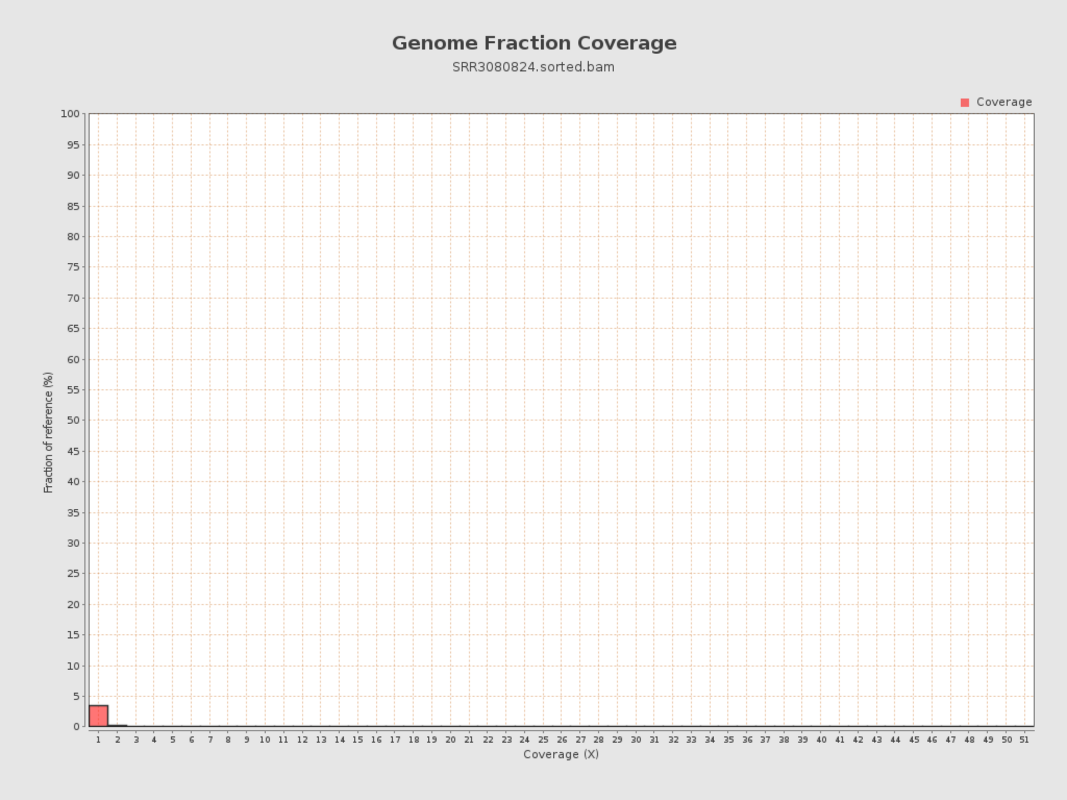
4. Results : Coverage Histogram



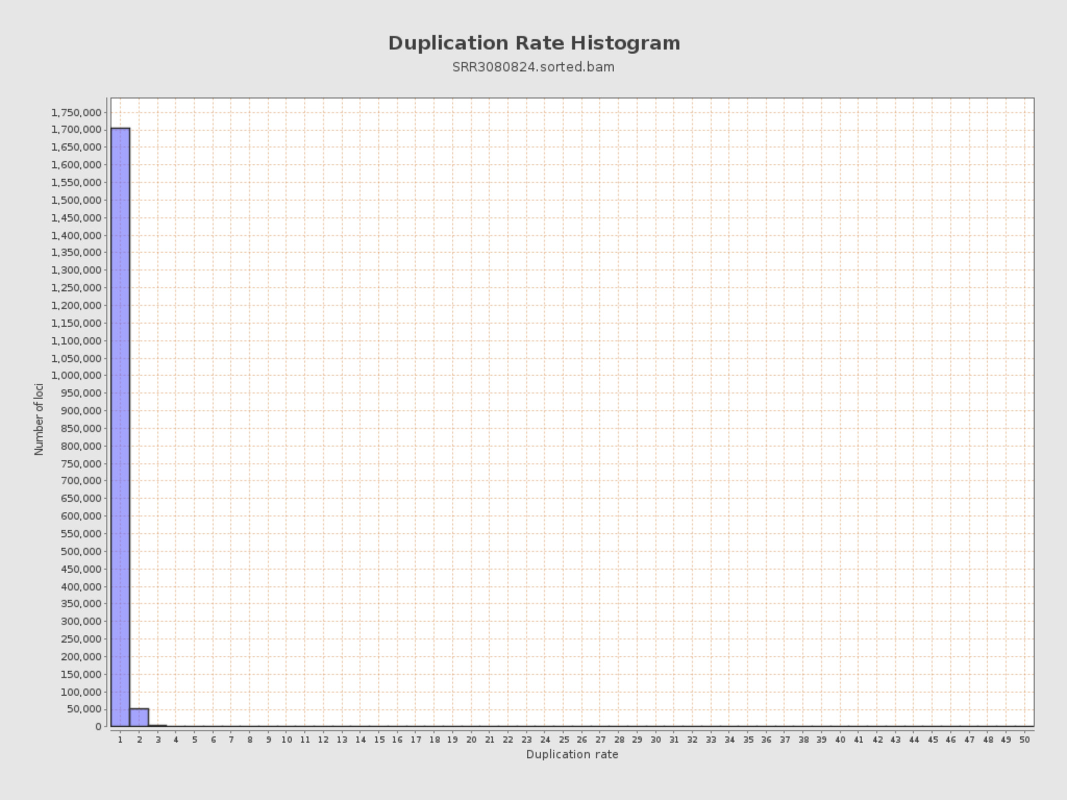
5. Results : Coverage Histogram (0-50X)



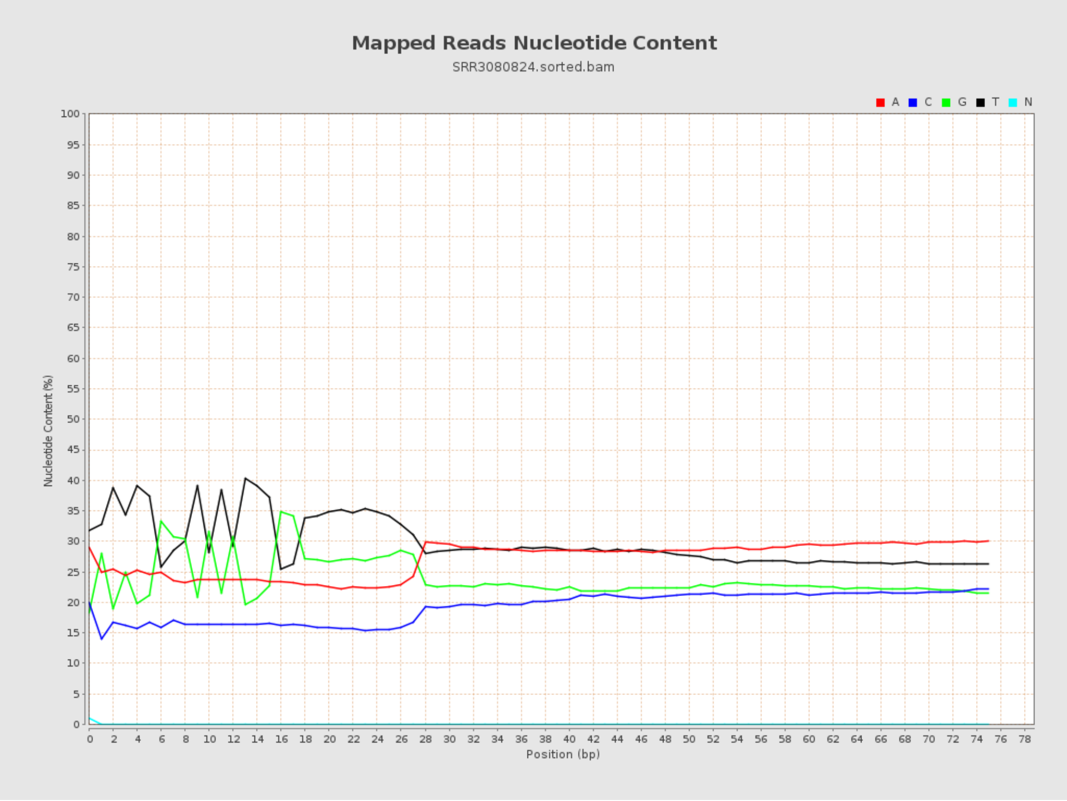
6. Results : Genome Fraction Coverage



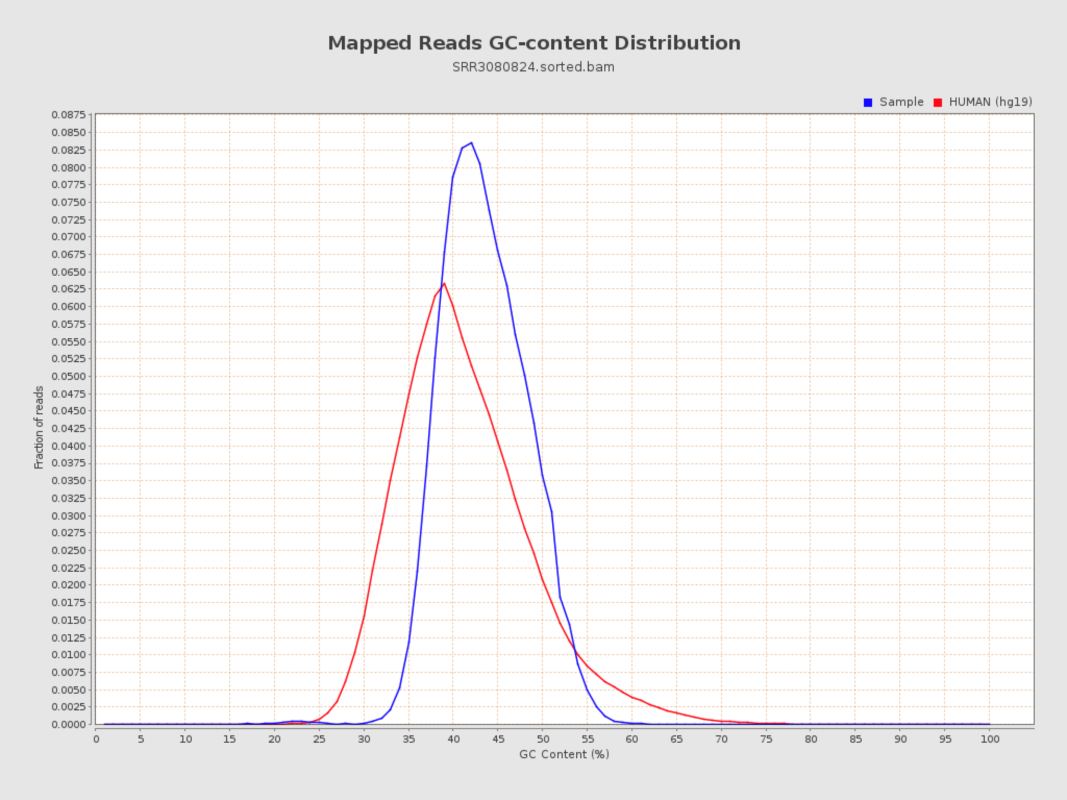
7. Results : Duplication Rate Histogram



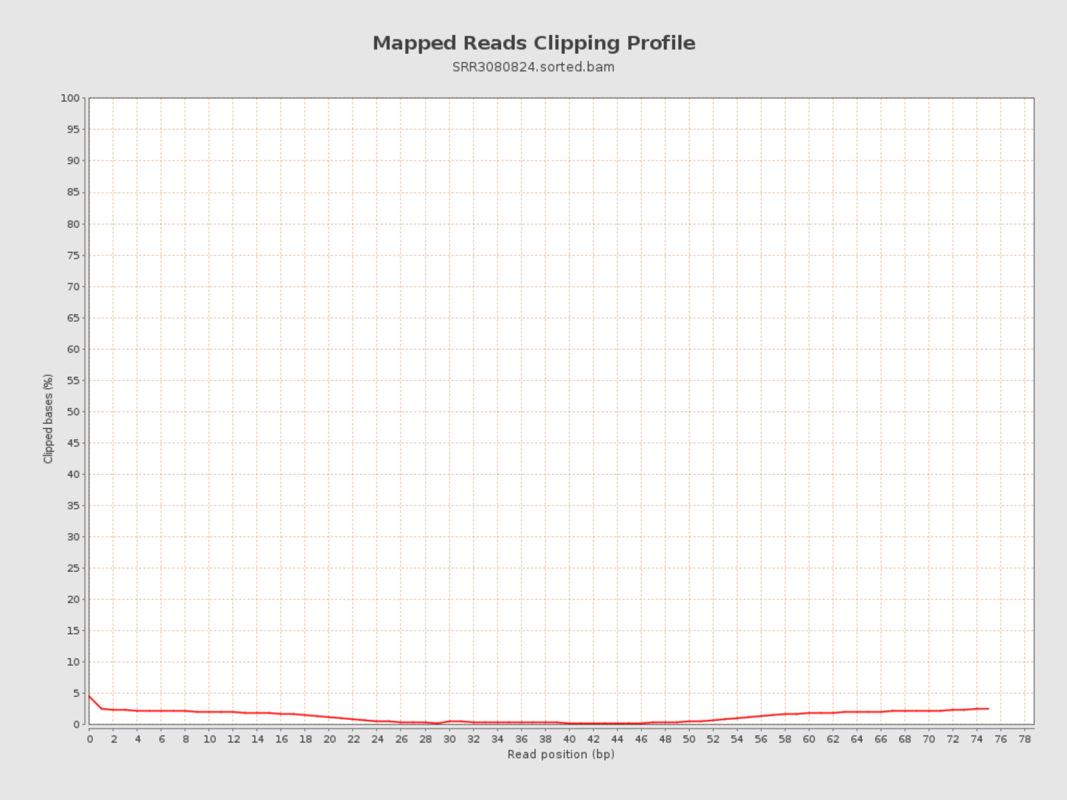
8. Results : Mapped Reads Nucleotide Content



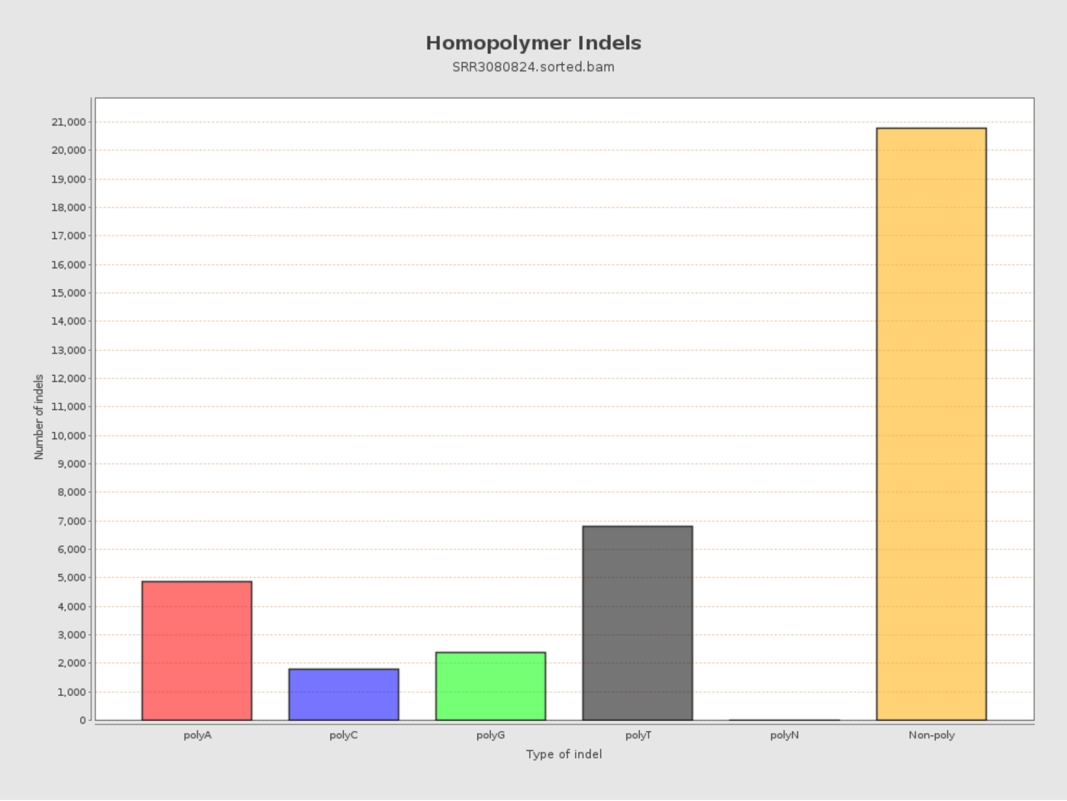
9. Results : Mapped Reads GC-content Distribution



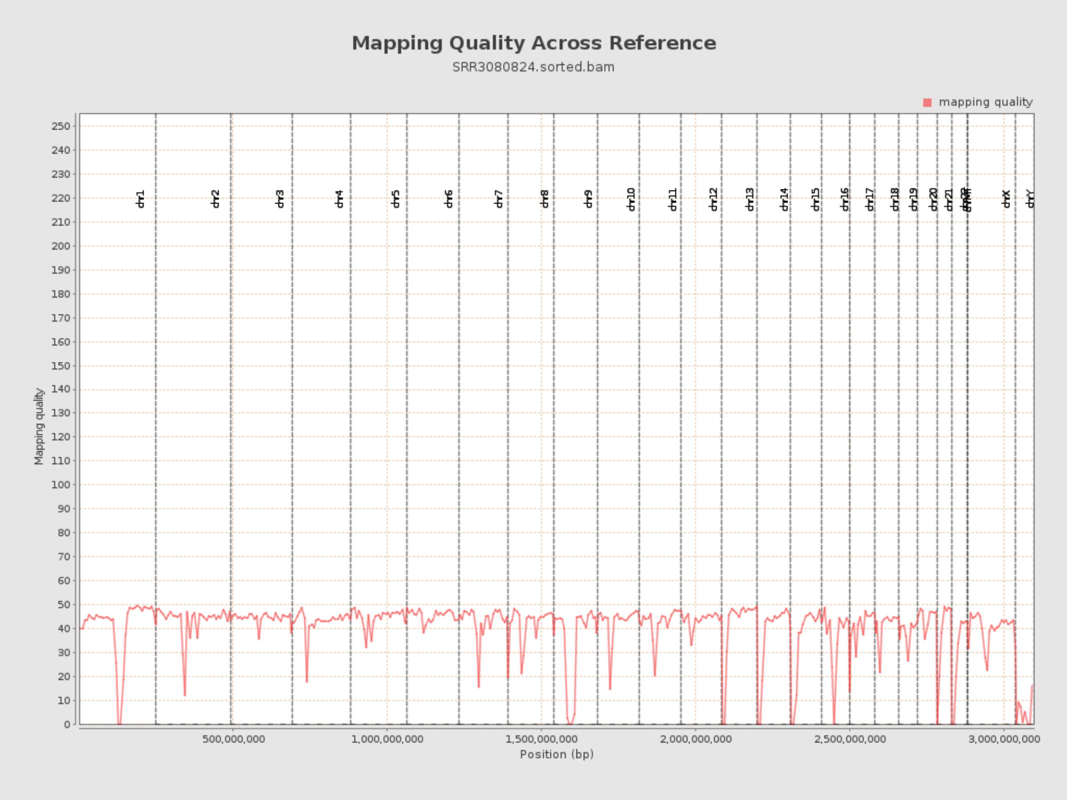
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram