Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 05:20:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818891.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_SRR1818891 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818891.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 05:20:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818891.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,177,382
Mapped reads	1,161,759 / 98.67%
Unmapped reads	15,623 / 1.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,353 / 1.39%
Read min/max/mean length	30 / 101 / 101.53
Duplicated reads (estimated)	175,057 / 14.87%
Duplication rate	12.24%
Clipped reads	1,167,421 / 99.15%

2.2. ACGT Content

Number/percentage of A's	30,489,957 / 28.36%
Number/percentage of C's	23,888,166 / 22.22%
Number/percentage of T's	29,668,295 / 27.59%
Number/percentage of G's	23,466,227 / 21.83%
Number/percentage of N's	1,572 / 0%
GC Percentage	44.04%

2.3. Coverage

Mean	0.0348

Standard Deviation	0.4737

2.4. Mapping Quality

Mean Mapping Quality	49.17

2.5. Mismatches and indels

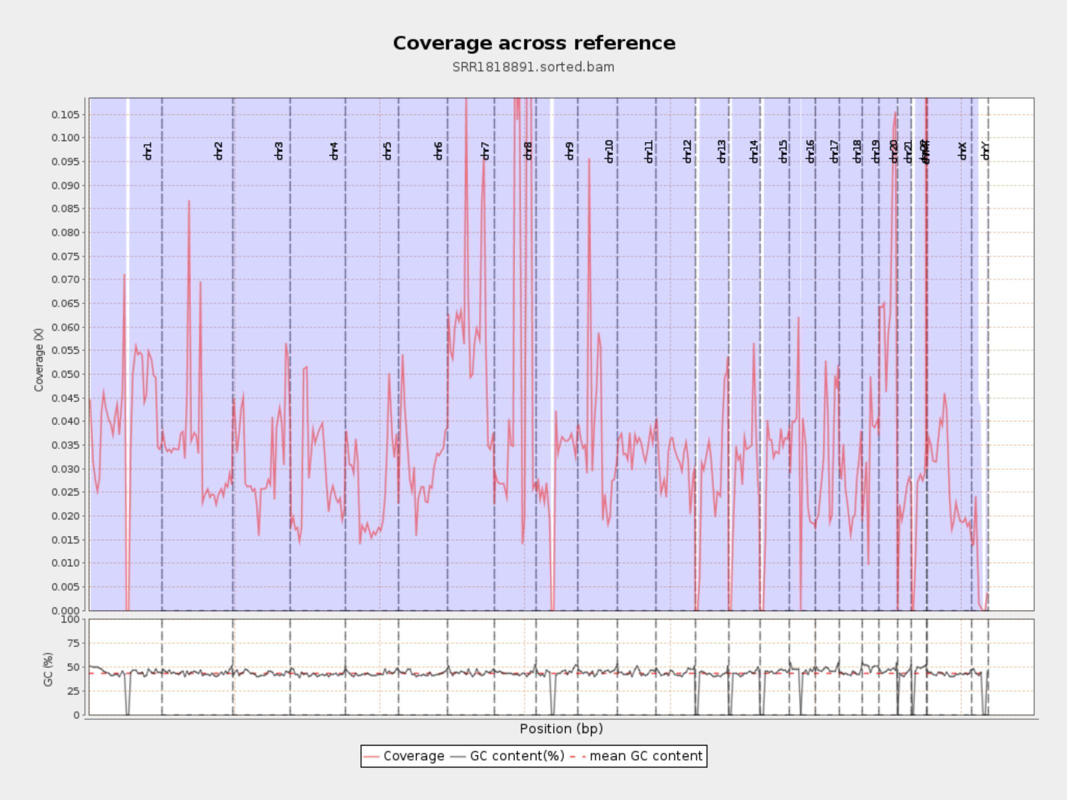
General error rate	0.66%
Mismatches	667,216
Insertions	14,766
Mapped reads with at least one insertion	1.22%
Deletions	34,899
Mapped reads with at least one deletion	2.93%
Homopolymer indels	41.26%

2.6. Chromosome stats

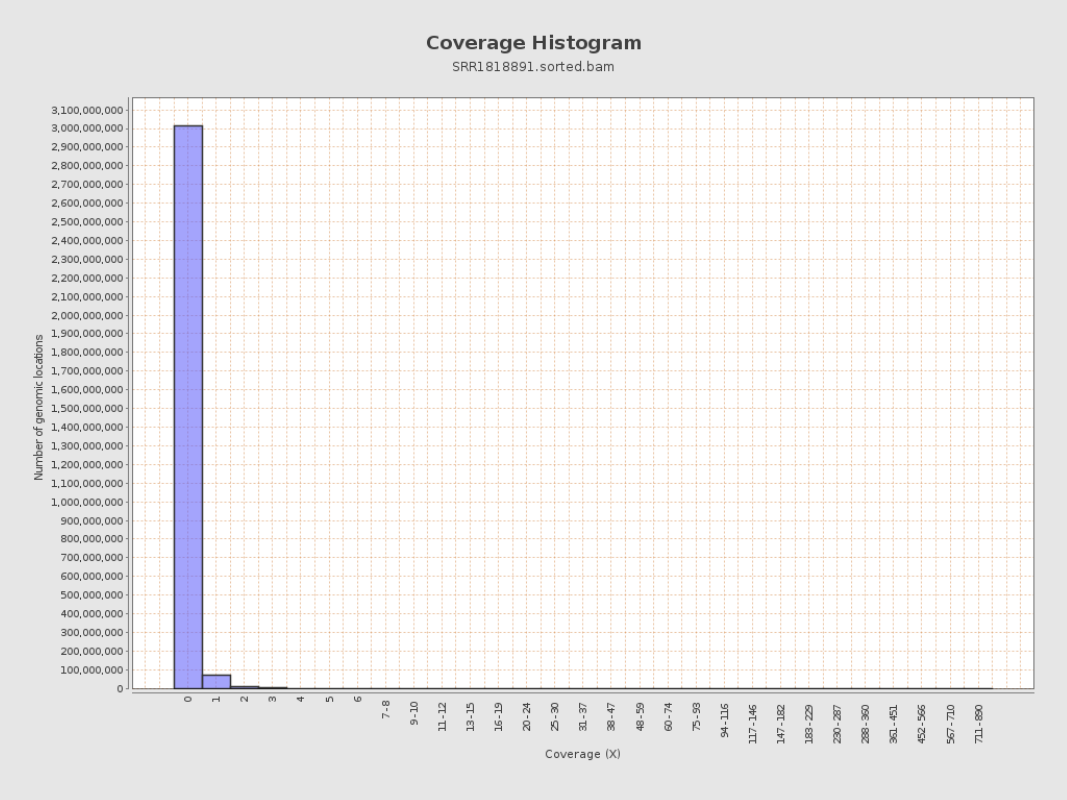
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10214055	0.041	0.7179
chr2	243199373	8226848	0.0338	0.7
chr3	198022430	6611558	0.0334	0.2214
chr4	191154276	5370189	0.0281	0.2699
chr5	180915260	4719630	0.0261	0.2081
chr6	171115067	5263773	0.0308	0.234
chr7	159138663	9593181	0.0603	1.0291

chr8	146364022	9323360	0.0637	0.3797
chr9	141213431	3990720	0.0283	0.3867
chr10	135534747	5044844	0.0372	0.6593
chr11	135006516	4718150	0.0349	0.2772
chr12	133851895	4182691	0.0312	0.2161
chr13	115169878	3231585	0.0281	0.2005
chr14	107349540	3156027	0.0294	0.2311
chr15	102531392	2989546	0.0292	0.2064
chr16	90354753	2747060	0.0304	0.4811
chr17	81195210	2760560	0.034	0.3031
chr18	78077248	2054580	0.0263	0.4224
chr19	59128983	1941341	0.0328	0.6111
chr20	63025520	4440793	0.0705	0.3457
chr21	48129895	1042756	0.0217	0.209
chr22	51304566	1018187	0.0198	0.1849
chrMT	16571	167478	10.1067	6.8043
chrX	155270560	4361076	0.0281	0.2424
chrY	59373566	413125	0.007	0.5403

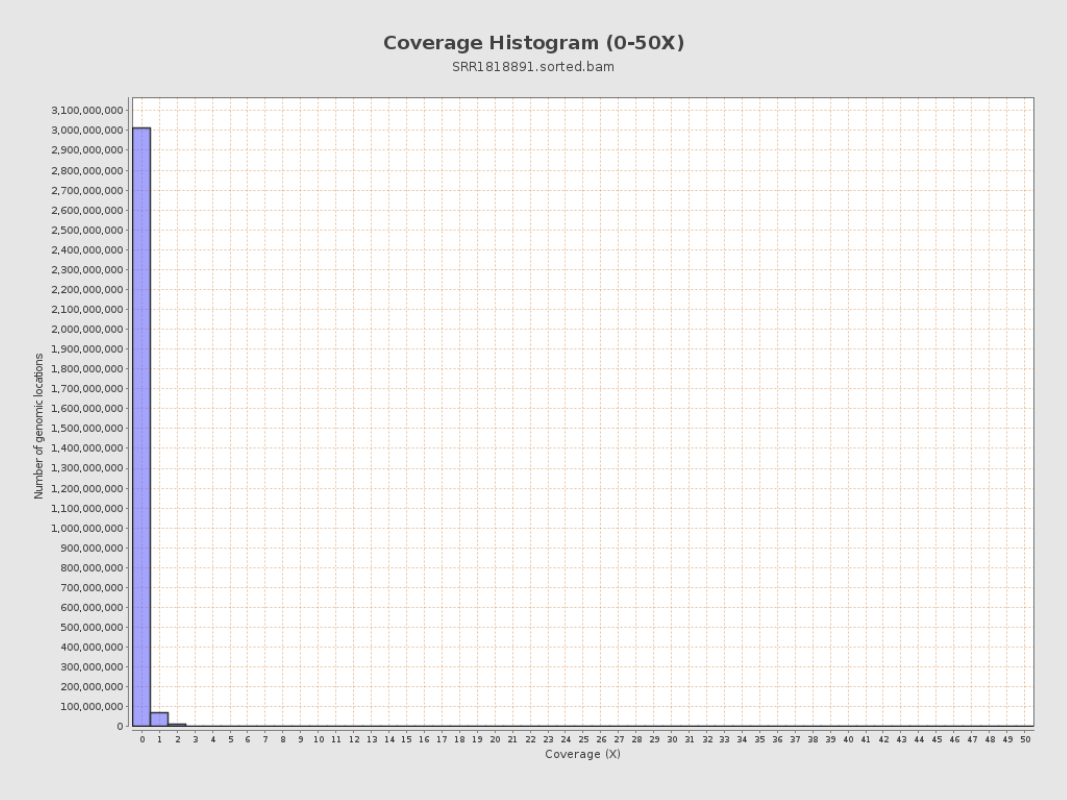
3. Results : Coverage across reference



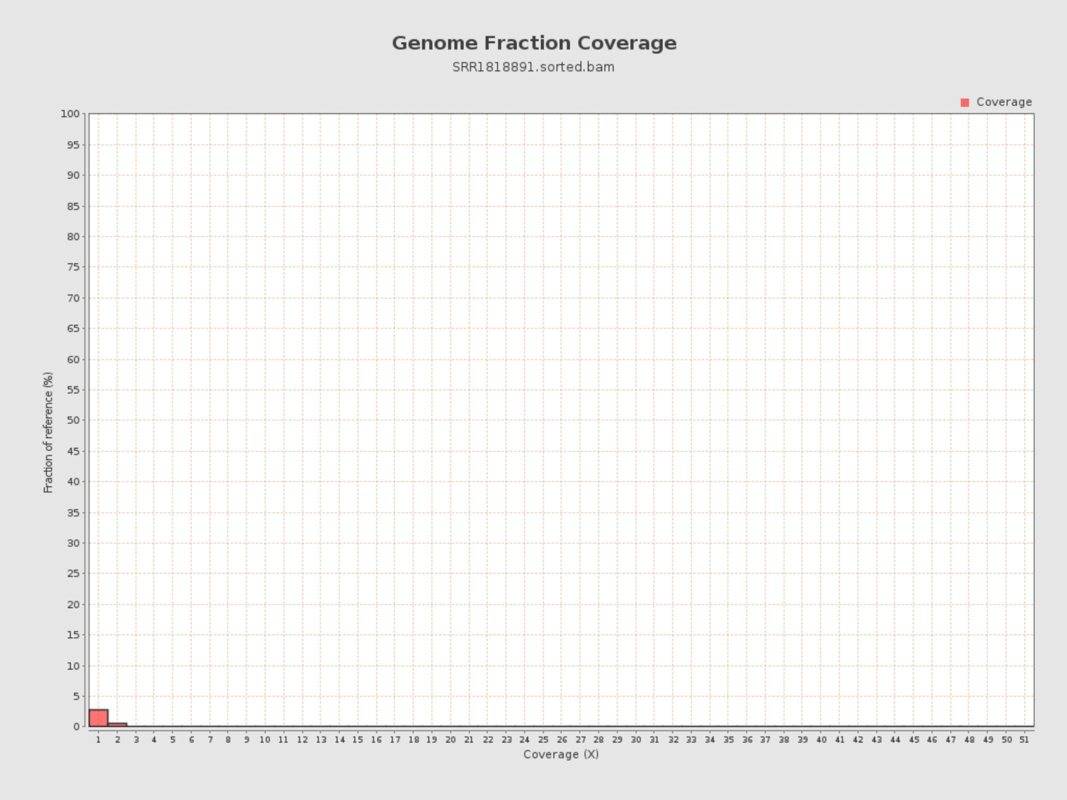
4. Results : Coverage Histogram



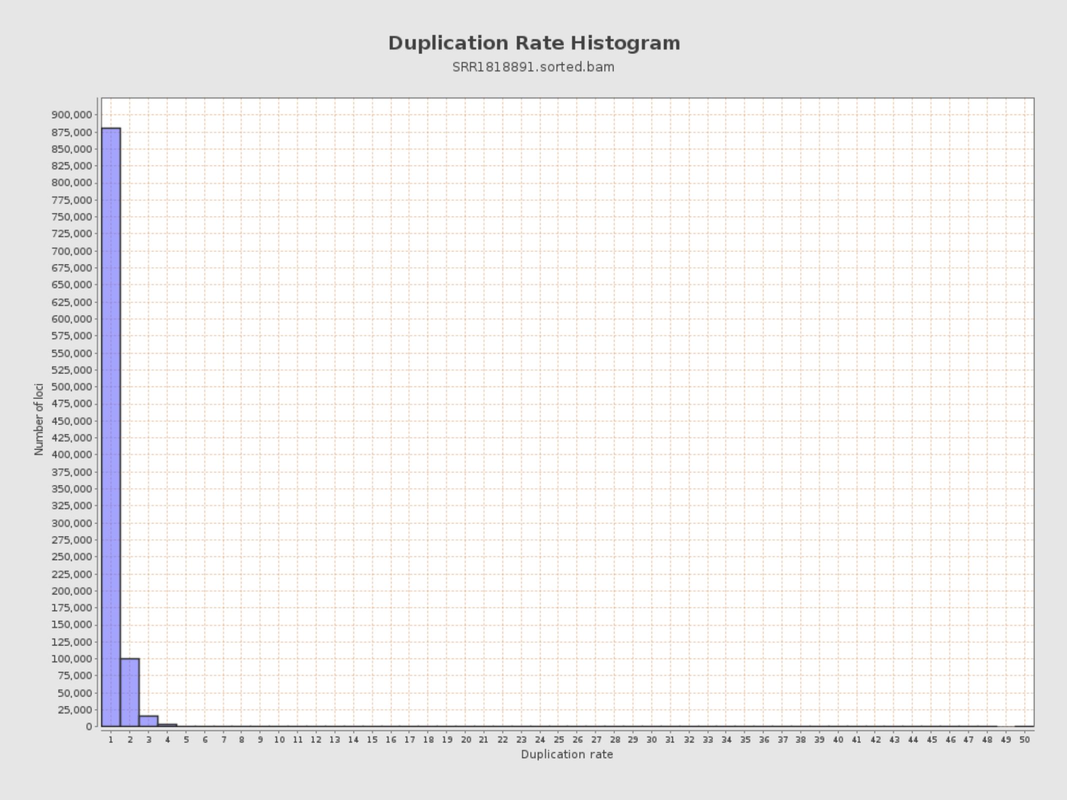
5. Results : Coverage Histogram (0-50X)



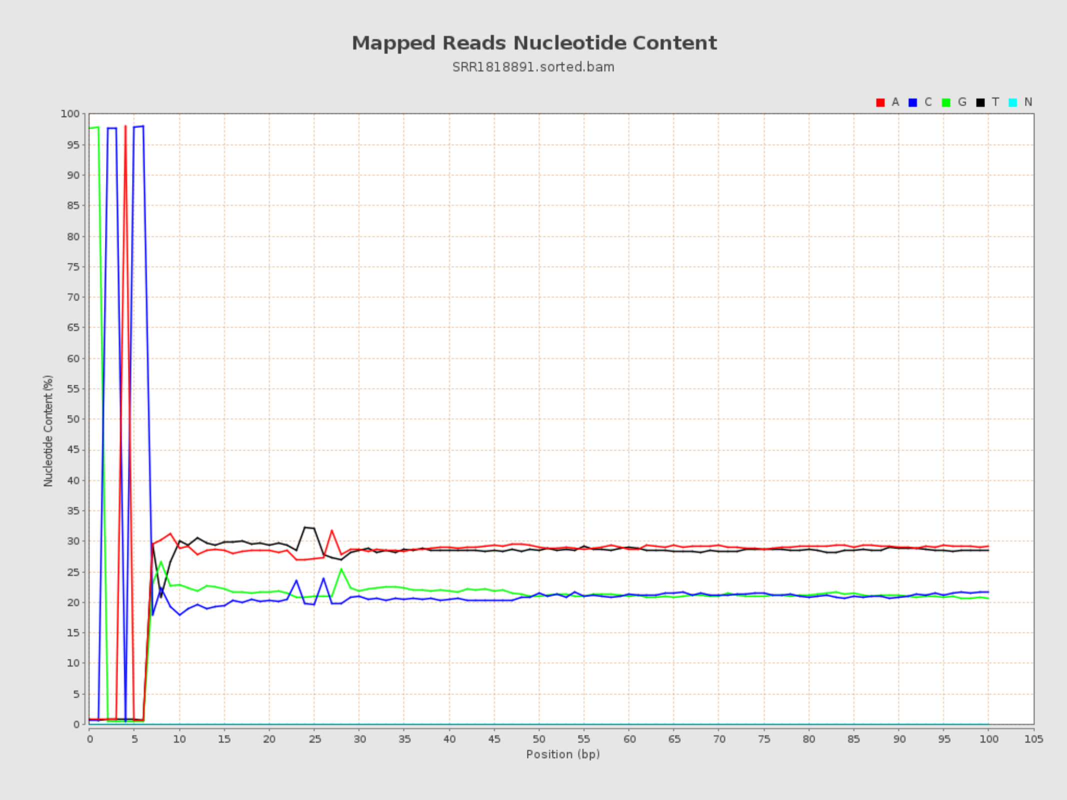
6. Results : Genome Fraction Coverage



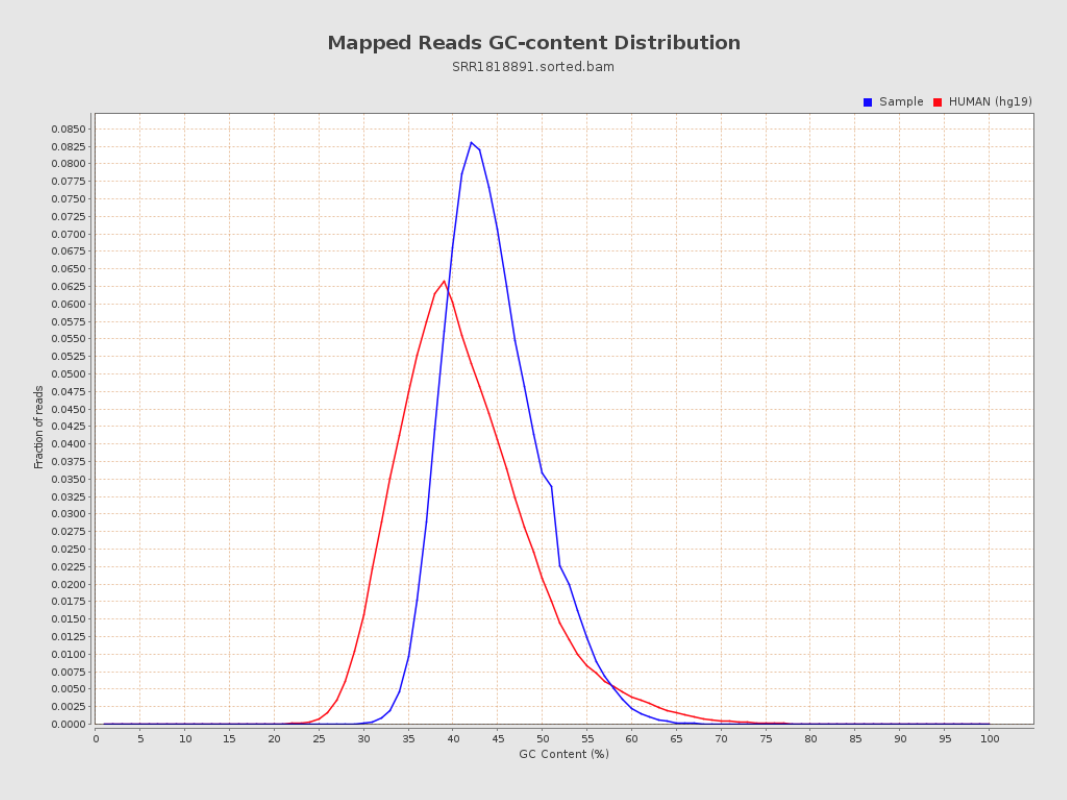
7. Results : Duplication Rate Histogram



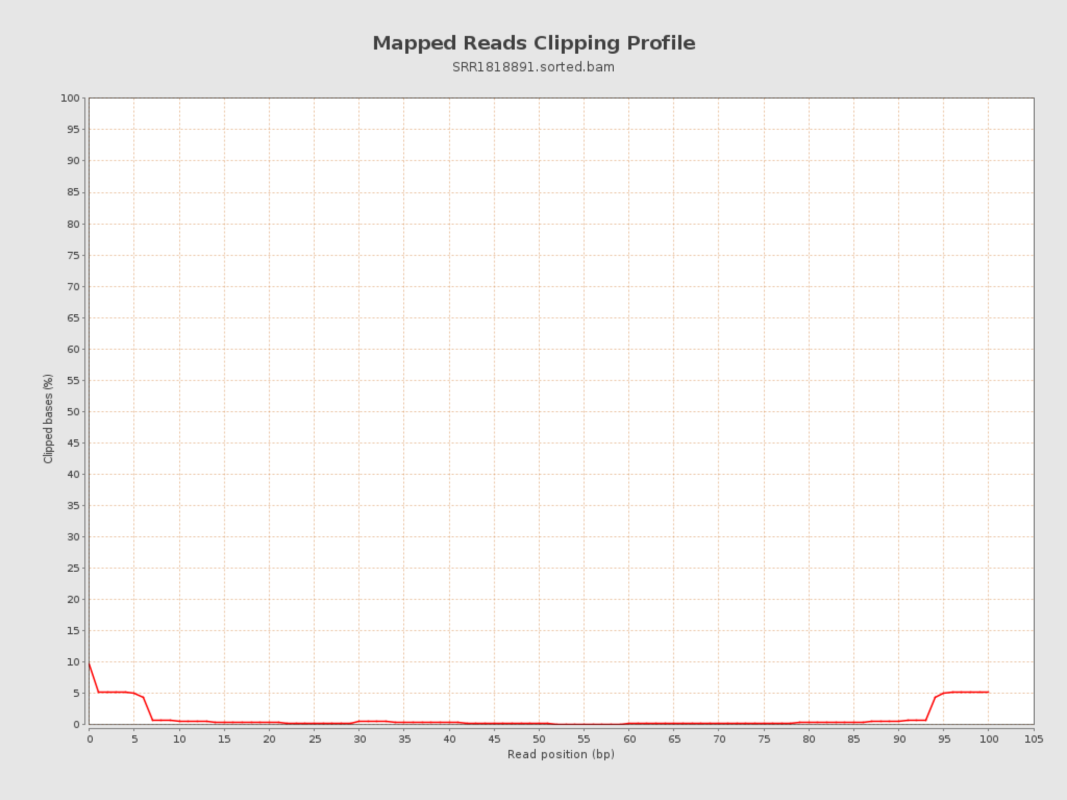
8. Results : Mapped Reads Nucleotide Content



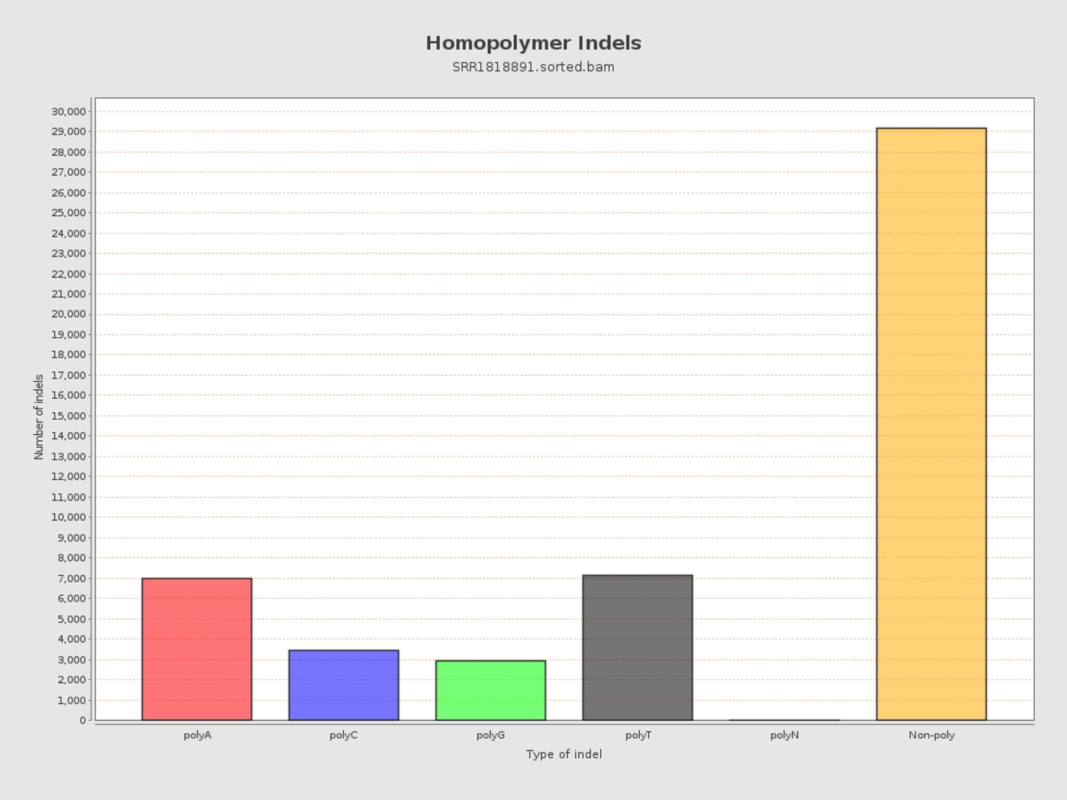
9. Results : Mapped Reads GC-content Distribution



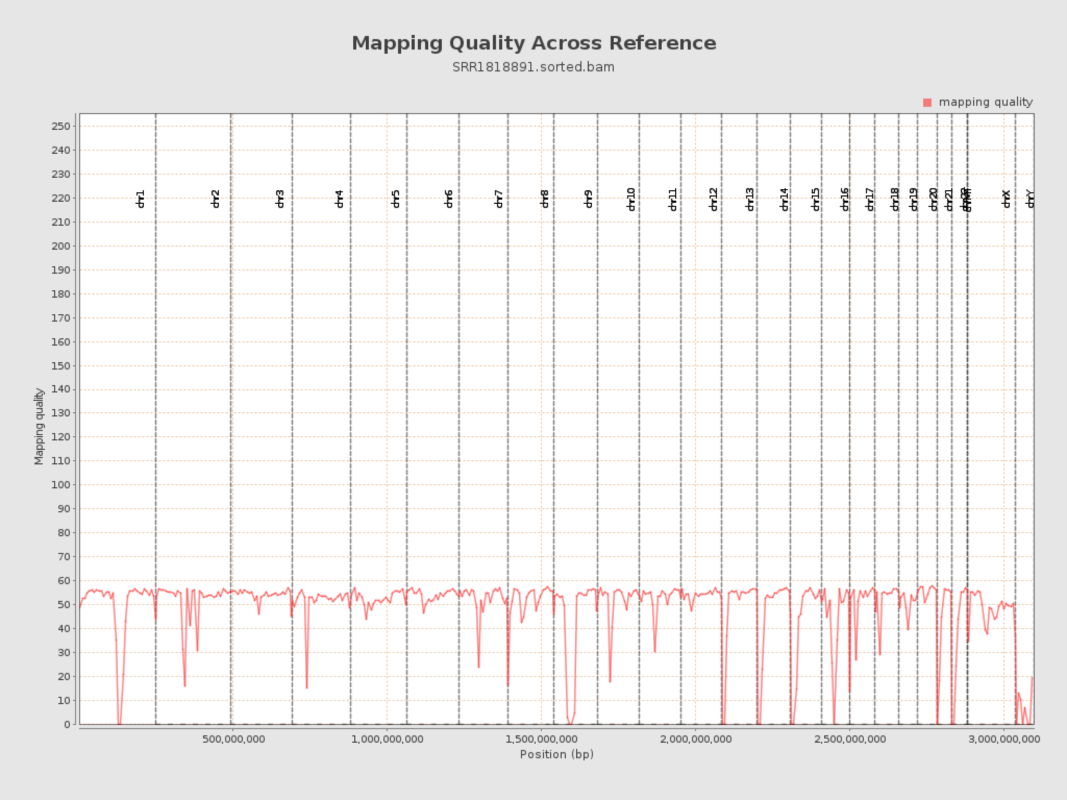
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram