Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 05:10:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818890.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_SRR1818890 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818890.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 05:10:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818890.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,717,020
Mapped reads	1,694,552 / 98.69%
Unmapped reads	22,468 / 1.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,338 / 1.42%
Read min/max/mean length	30 / 101 / 101.54
Duplicated reads (estimated)	290,710 / 16.93%
Duplication rate	14.17%
Clipped reads	1,700,615 / 99.04%

2.2. ACGT Content

Number/percentage of A's	43,416,388 / 27.67%
Number/percentage of C's	33,220,638 / 21.17%
Number/percentage of T's	44,872,725 / 28.6%
Number/percentage of G's	35,403,508 / 22.56%
Number/percentage of N's	2,219 / 0%
GC Percentage	43.73%

2.3. Coverage

Mean	0.0507

Standard Deviation	0.6363

2.4. Mapping Quality

Mean Mapping Quality	49.34

2.5. Mismatches and indels

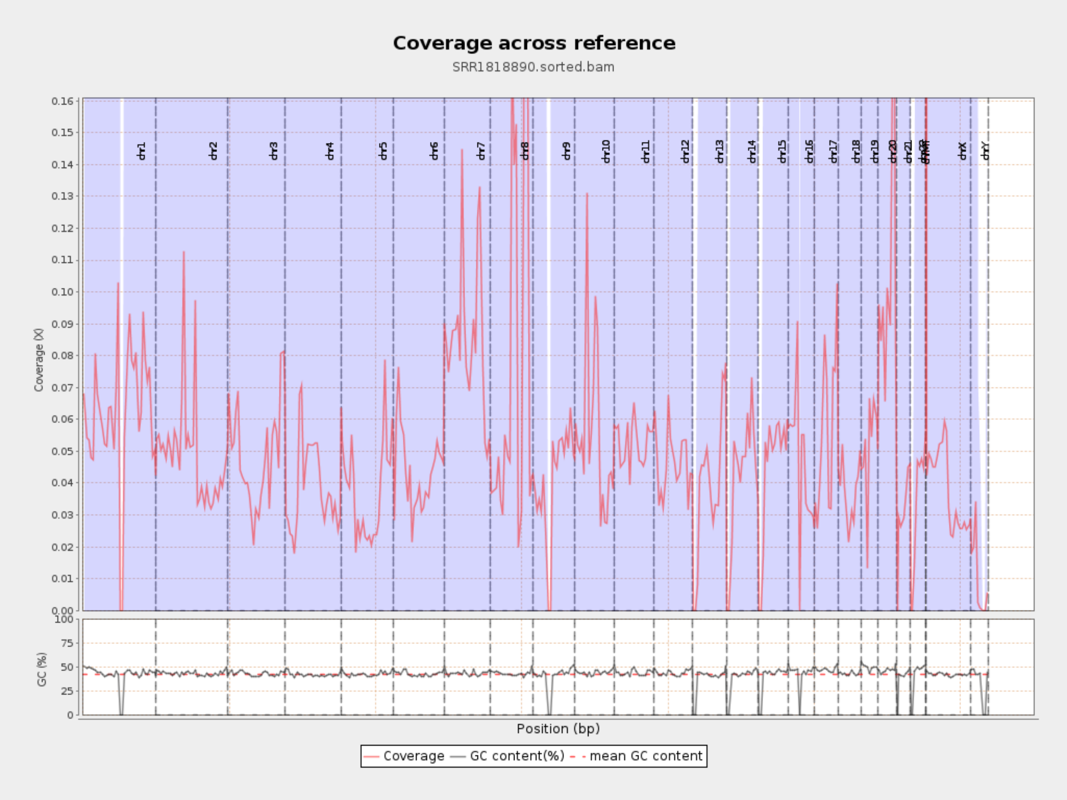
General error rate	0.64%
Mismatches	941,752
Insertions	23,021
Mapped reads with at least one insertion	1.31%
Deletions	50,054
Mapped reads with at least one deletion	2.88%
Homopolymer indels	40.94%

2.6. Chromosome stats

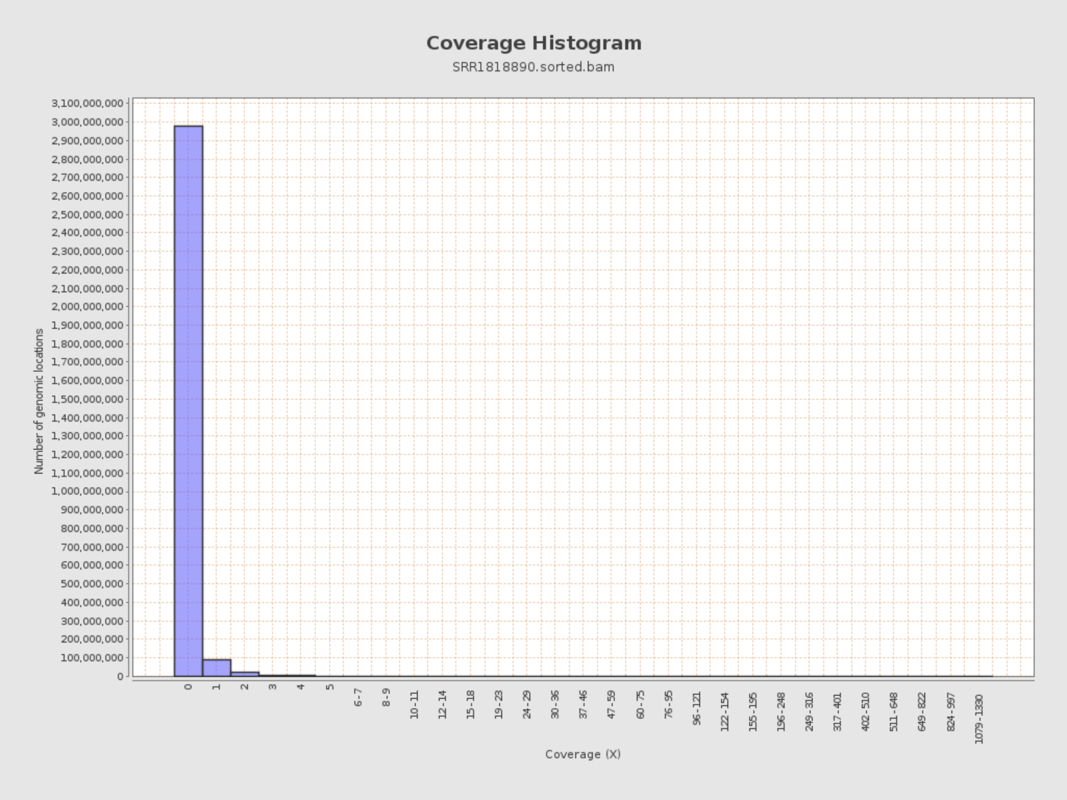
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15507105	0.0622	0.9814
chr2	243199373	11954032	0.0492	0.927
chr3	198022430	9615607	0.0486	0.2787
chr4	191154276	7436547	0.0389	0.3501
chr5	180915260	6882955	0.038	0.2651
chr6	171115067	7460593	0.0436	0.3015
chr7	159138663	13645657	0.0857	1.3531

chr8	146364022	13033848	0.0891	0.515
chr9	141213431	5704711	0.0404	0.5053
chr10	135534747	7486794	0.0552	0.9041
chr11	135006516	7089293	0.0525	0.3612
chr12	133851895	6258721	0.0468	0.2772
chr13	115169878	4519134	0.0392	0.247
chr14	107349540	4617526	0.043	0.2858
chr15	102531392	4454287	0.0434	0.2627
chr16	90354753	4162043	0.0461	0.6836
chr17	81195210	4477946	0.0552	0.3894
chr18	78077248	2903348	0.0372	0.6115
chr19	59128983	3018691	0.0511	0.8848
chr20	63025520	6834972	0.1084	0.4657
chr21	48129895	1513786	0.0315	0.2784
chr22	51304566	1651728	0.0322	0.2685
chrMT	16571	269560	16.267	10.8935
chrX	155270560	5934952	0.0382	0.3124
chrY	59373566	581177	0.0098	0.7765

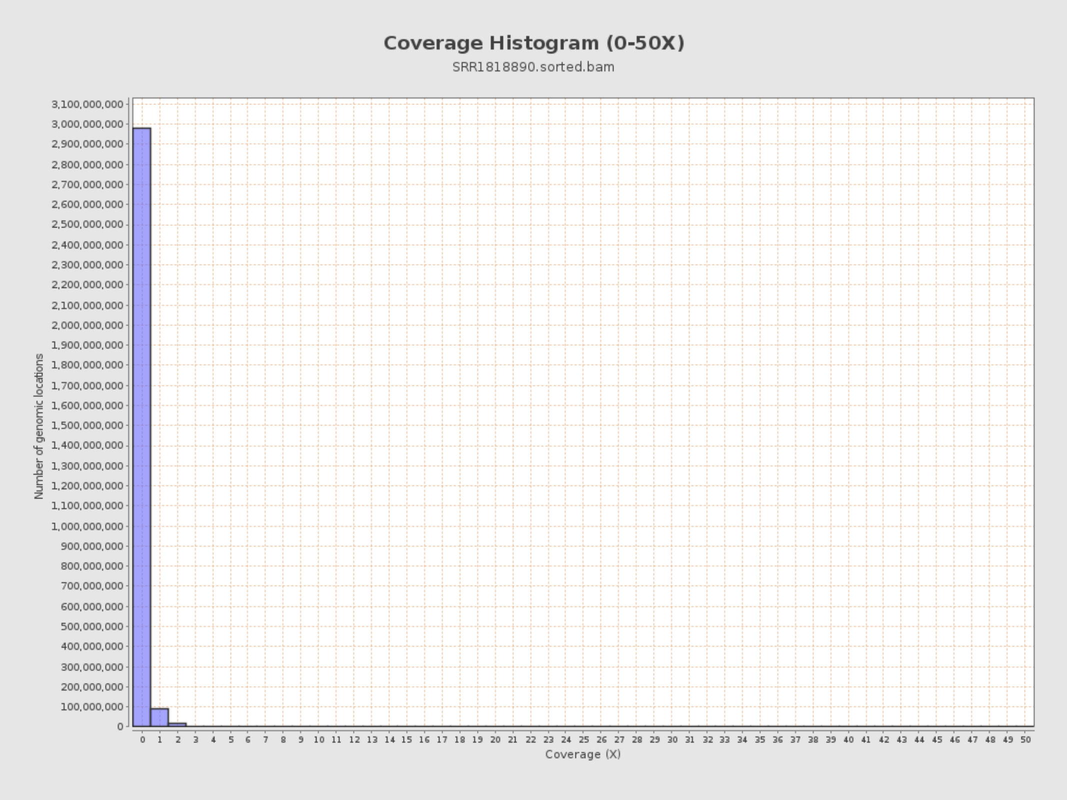
3. Results : Coverage across reference



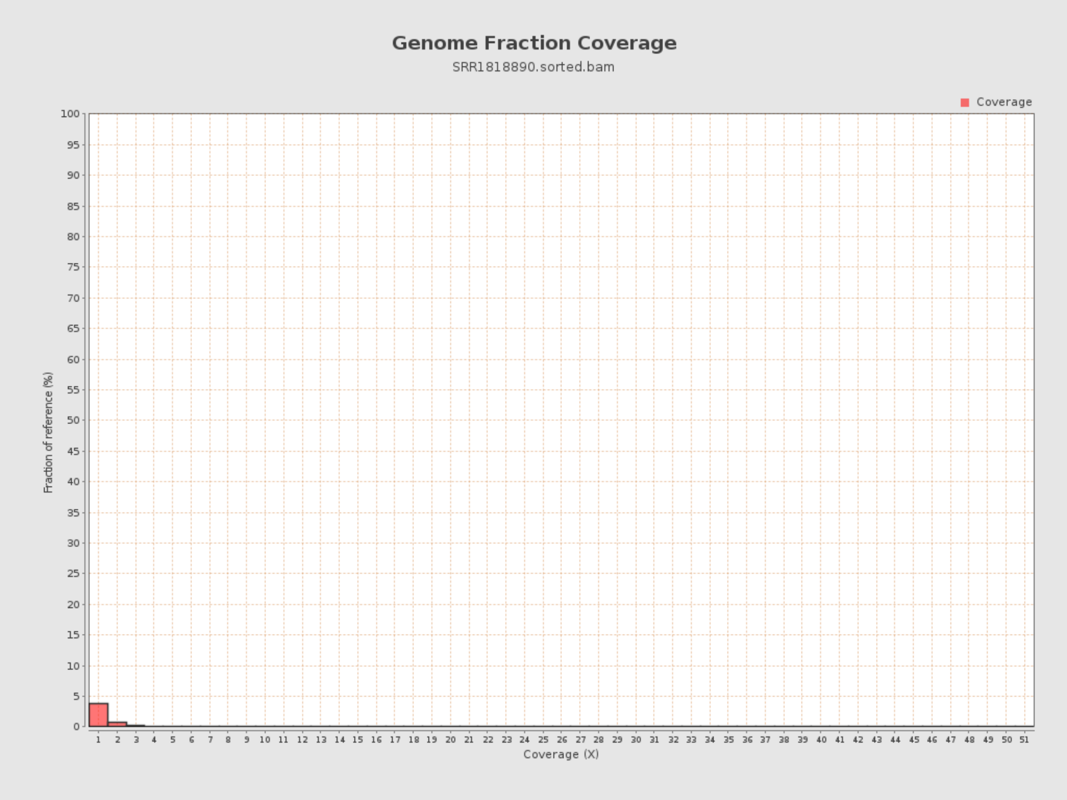
4. Results : Coverage Histogram



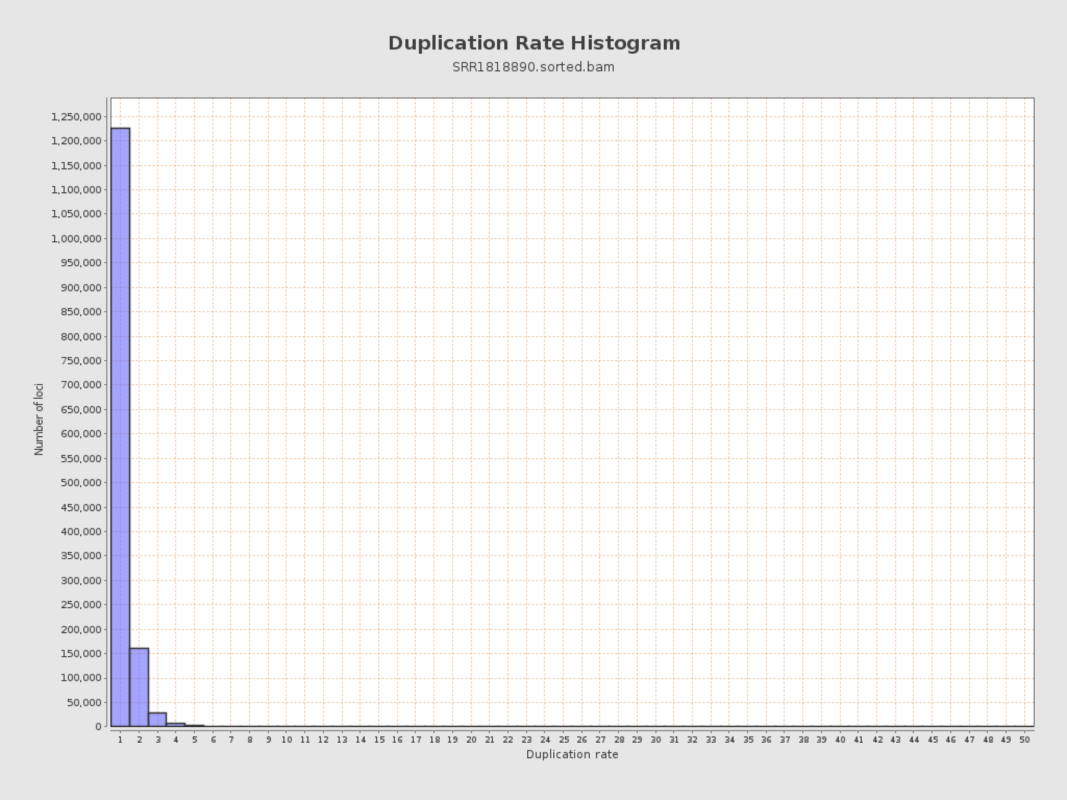
5. Results : Coverage Histogram (0-50X)



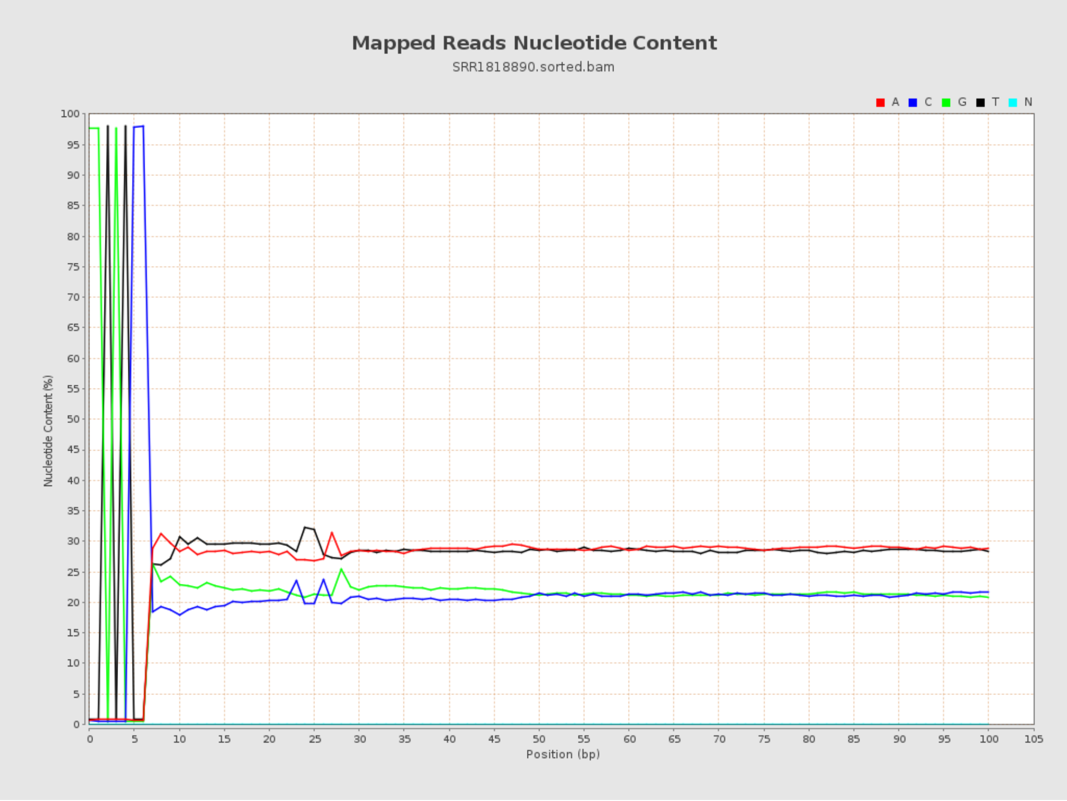
6. Results : Genome Fraction Coverage



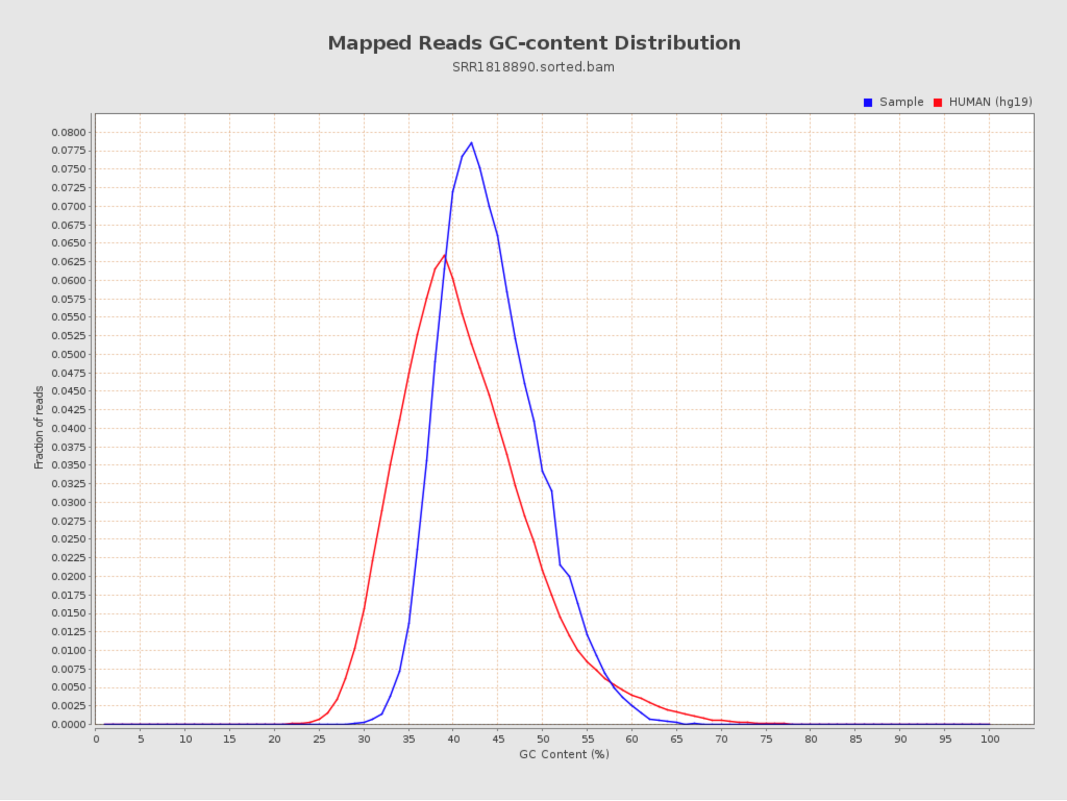
7. Results : Duplication Rate Histogram



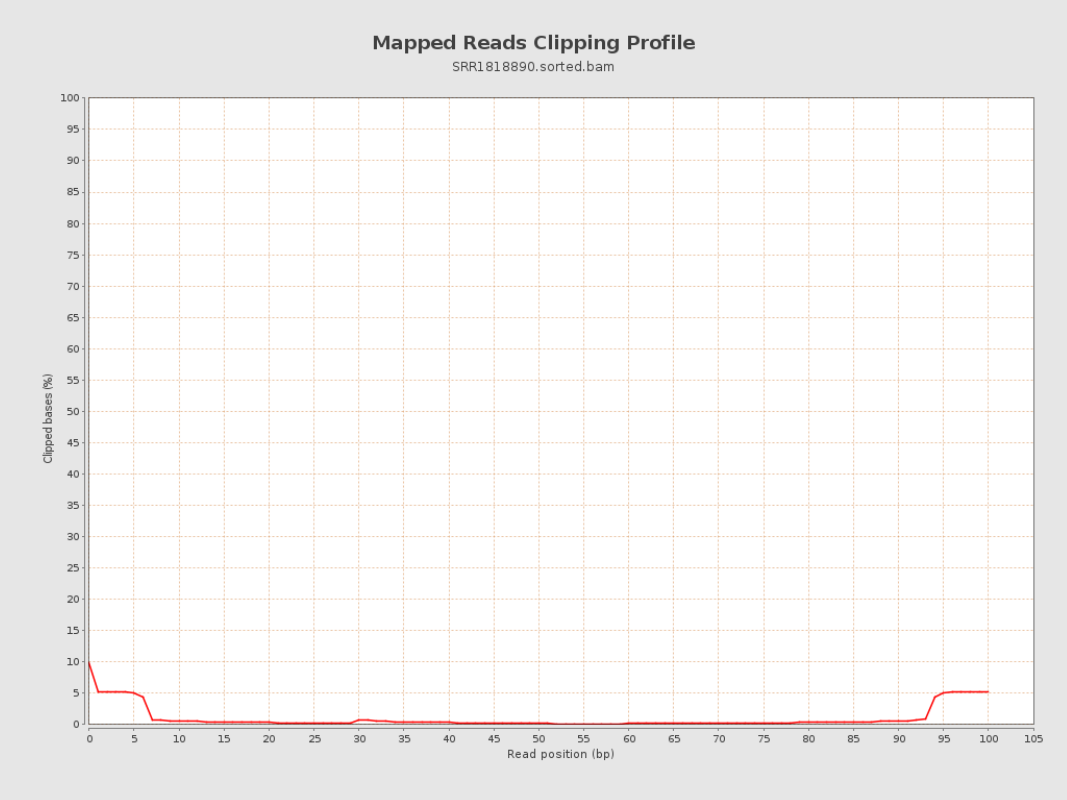
8. Results : Mapped Reads Nucleotide Content



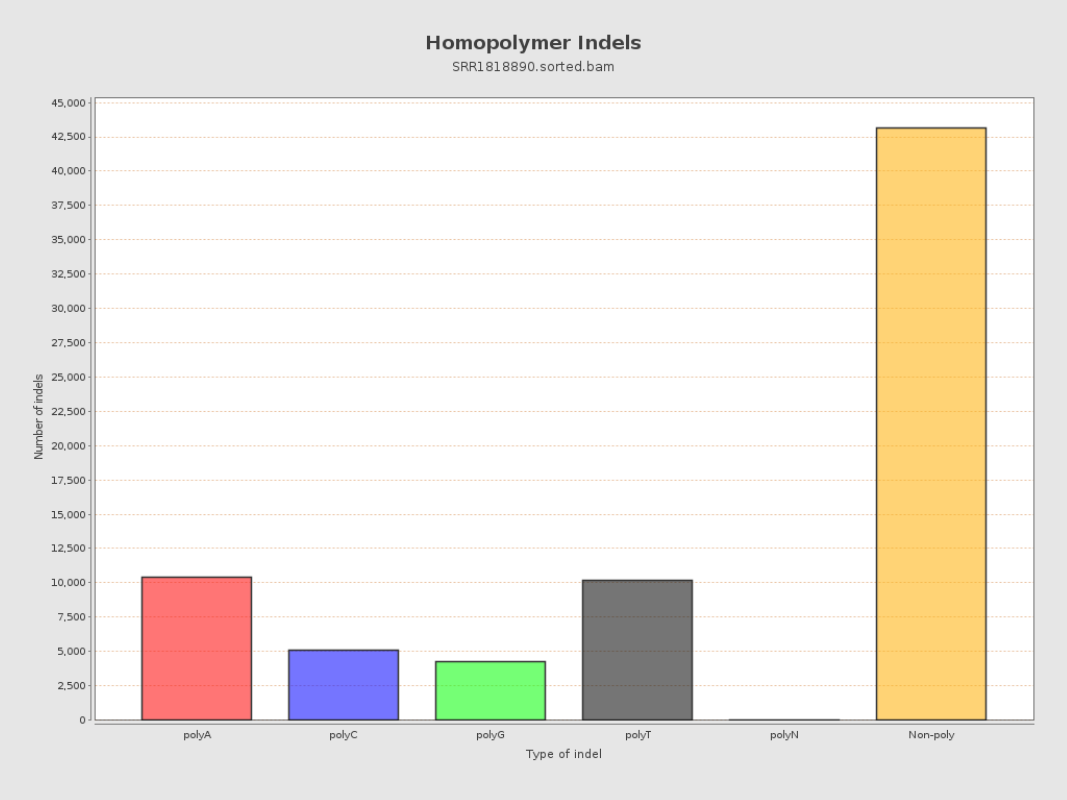
9. Results : Mapped Reads GC-content Distribution



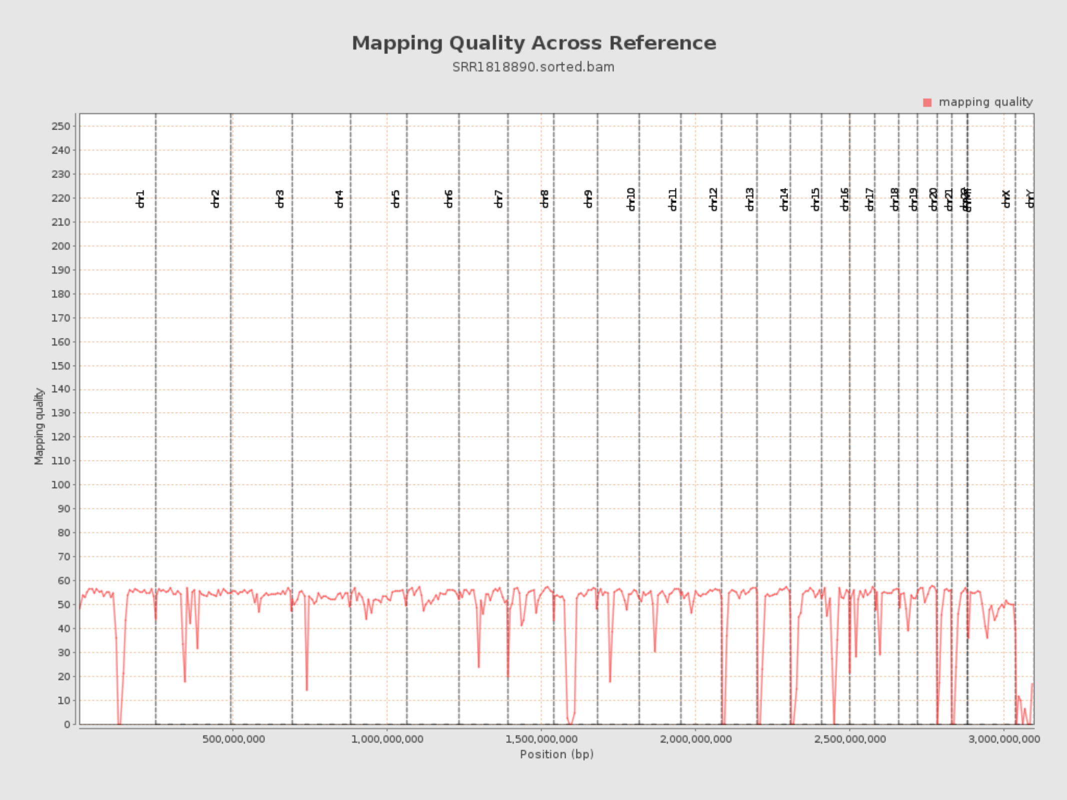
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram