Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 21:56:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818845.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_SRR1818845 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818845.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 21:56:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818845.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,848,706
Mapped reads	1,824,484 / 98.69%
Unmapped reads	24,222 / 1.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,628 / 1.55%
Read min/max/mean length	30 / 101 / 101.6
Duplicated reads (estimated)	426,099 / 23.05%
Duplication rate	20.12%
Clipped reads	1,831,346 / 99.06%

2.2. ACGT Content

Number/percentage of A's	49,659,741 / 29.39%
Number/percentage of C's	35,694,014 / 21.13%
Number/percentage of T's	46,757,193 / 27.67%
Number/percentage of G's	36,848,872 / 21.81%
Number/percentage of N's	2,423 / 0%
GC Percentage	42.93%

2.3. Coverage

Mean	0.0546

Standard Deviation	0.6329

2.4. Mapping Quality

Mean Mapping Quality	49.37

2.5. Mismatches and indels

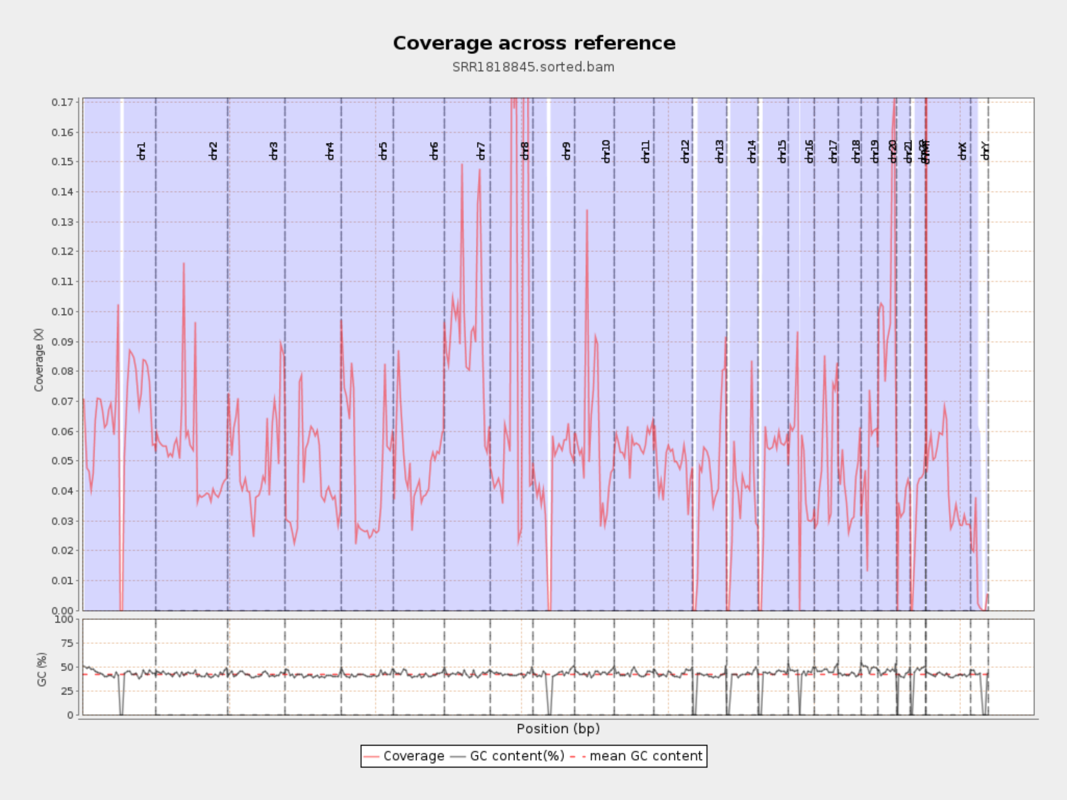
General error rate	0.64%
Mismatches	1,026,344
Insertions	24,583
Mapped reads with at least one insertion	1.31%
Deletions	54,756
Mapped reads with at least one deletion	2.93%
Homopolymer indels	39.98%

2.6. Chromosome stats

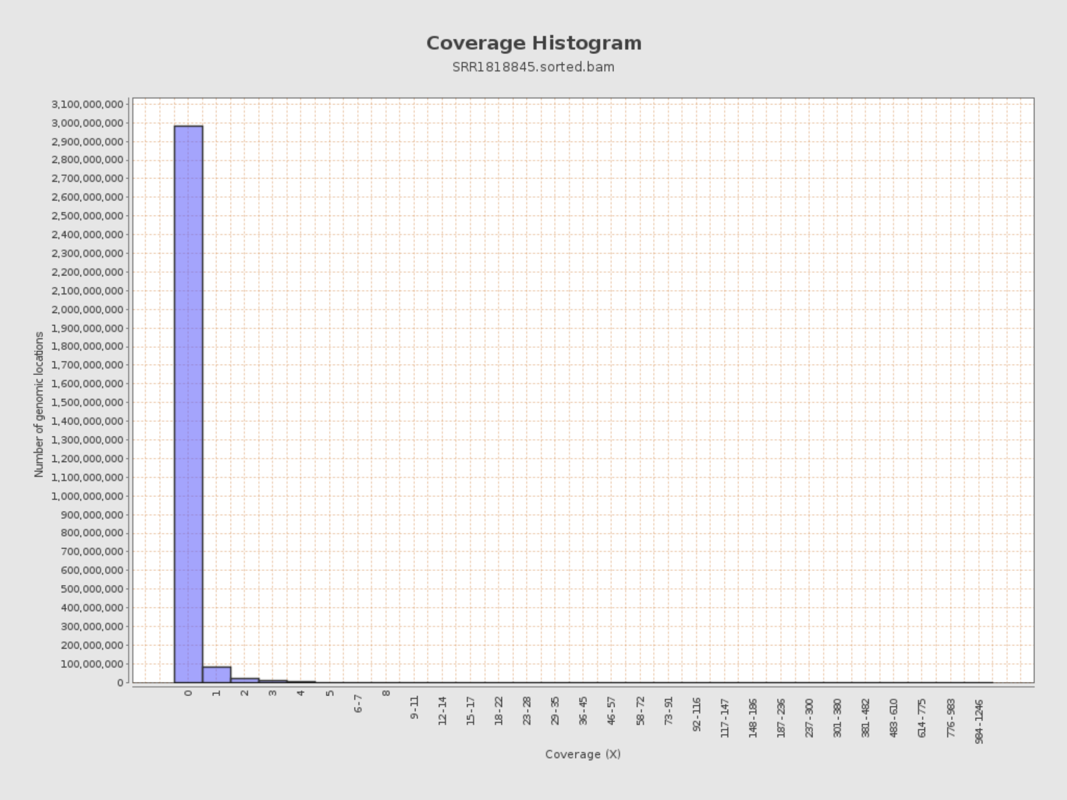
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16031492	0.0643	0.9731
chr2	243199373	12640505	0.052	0.8683
chr3	198022430	10463992	0.0528	0.314
chr4	191154276	8459488	0.0443	0.3839
chr5	180915260	8578898	0.0474	0.3112
chr6	171115067	8360200	0.0489	0.3412
chr7	159138663	14977369	0.0941	1.3301

chr8	146364022	15184170	0.1037	0.5535
chr9	141213431	6172211	0.0437	0.5074
chr10	135534747	7770875	0.0573	0.8536
chr11	135006516	7519193	0.0557	0.3993
chr12	133851895	6479451	0.0484	0.3007
chr13	115169878	5190018	0.0451	0.2881
chr14	107349540	4048478	0.0377	0.2962
chr15	102531392	4710886	0.0459	0.2936
chr16	90354753	4248426	0.047	0.6821
chr17	81195210	4235338	0.0522	0.4043
chr18	78077248	3227264	0.0413	0.6183
chr19	59128983	2945334	0.0498	0.8643
chr20	63025520	7021472	0.1114	0.5001
chr21	48129895	1633463	0.0339	0.318
chr22	51304566	1603160	0.0312	0.2717
chrMT	16571	201309	12.1483	8.1997
chrX	155270560	6743397	0.0434	0.3367
chrY	59373566	621997	0.0105	0.7838

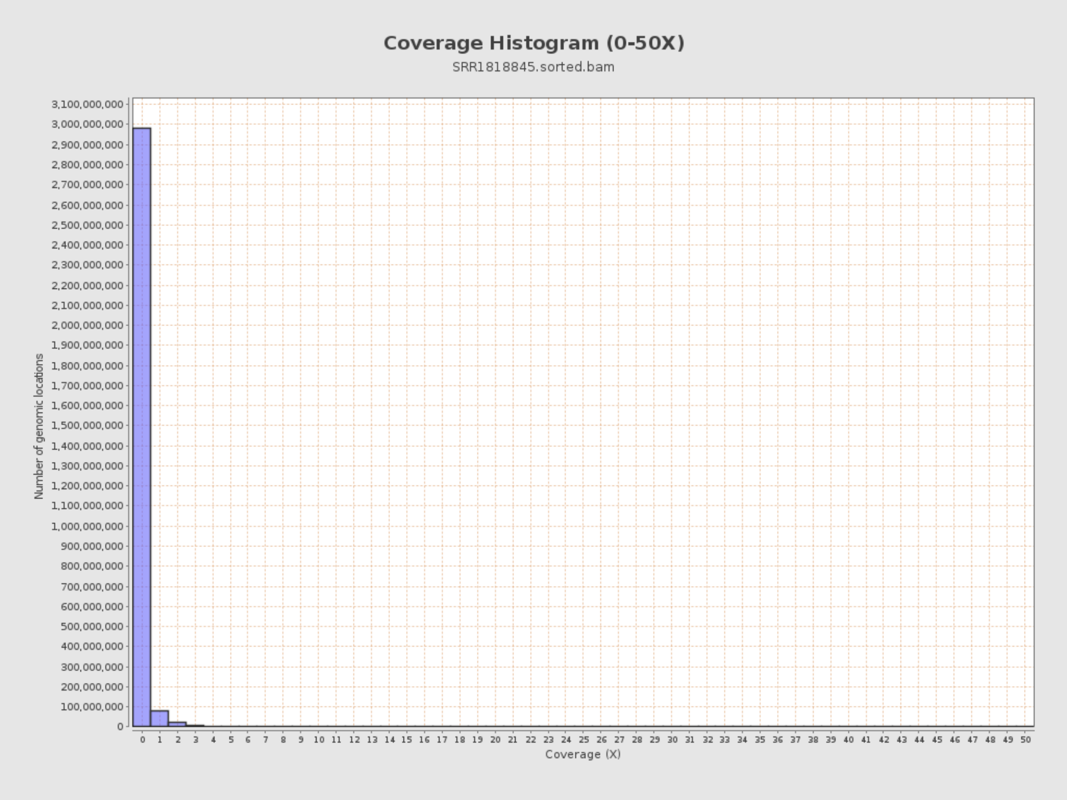
3. Results : Coverage across reference



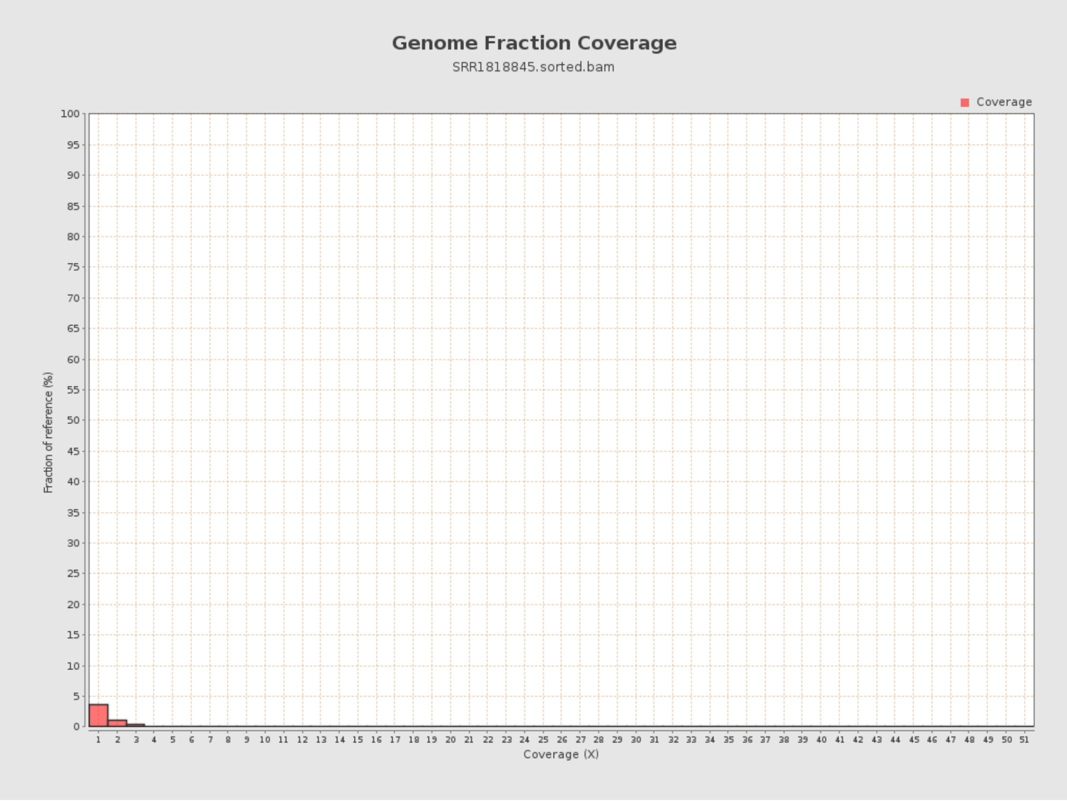
4. Results : Coverage Histogram



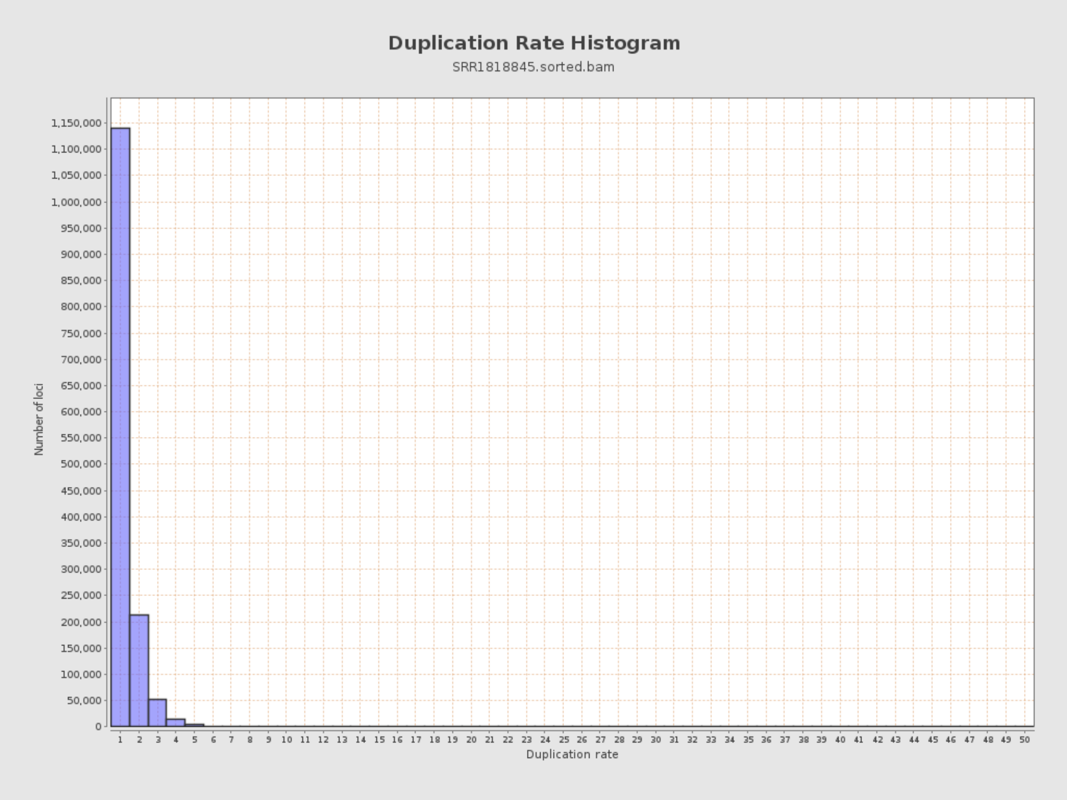
5. Results : Coverage Histogram (0-50X)



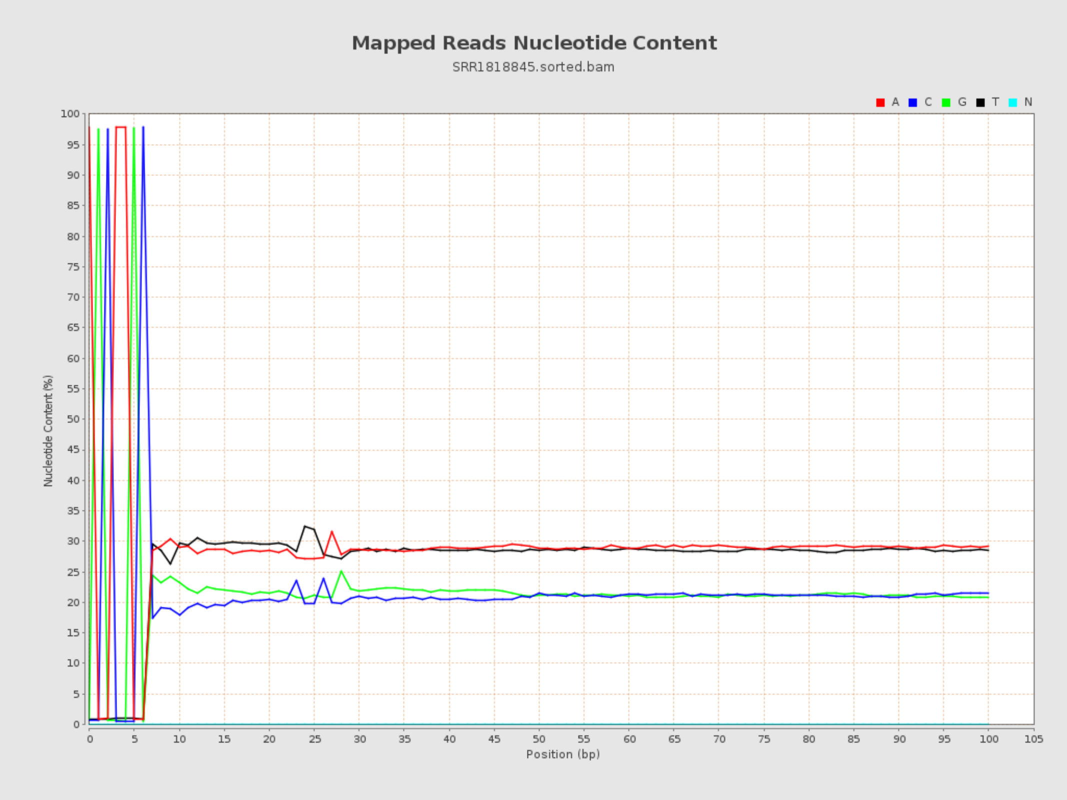
6. Results : Genome Fraction Coverage



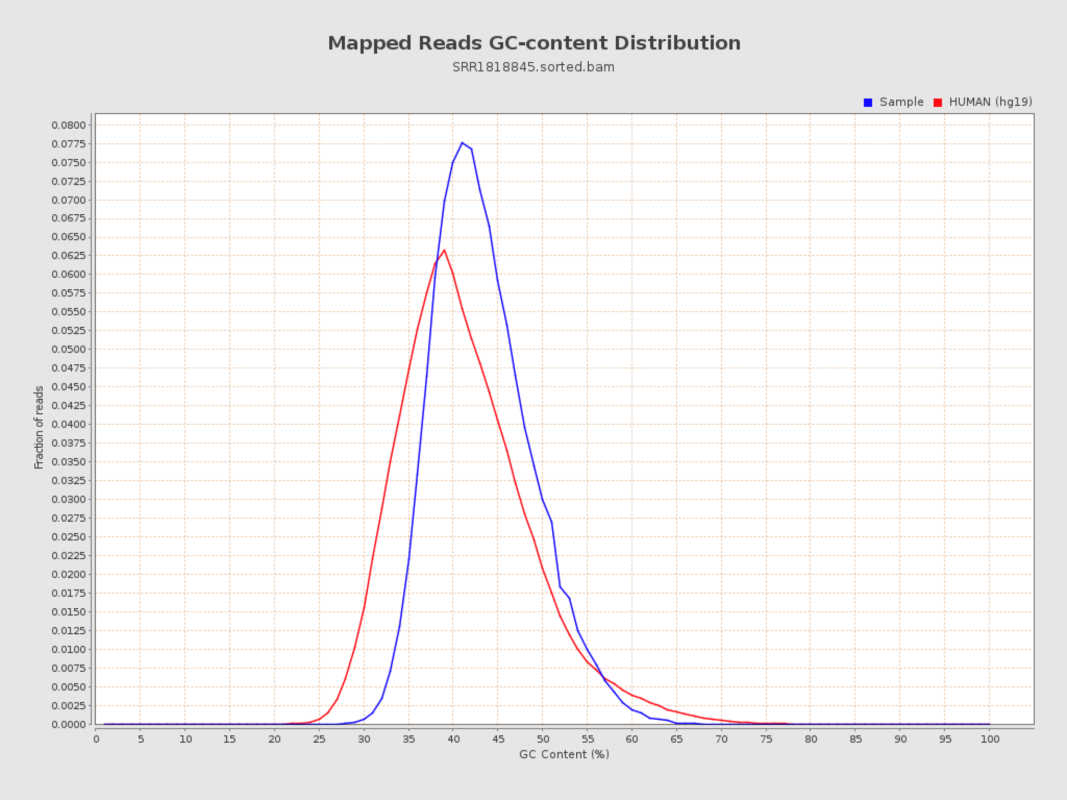
7. Results : Duplication Rate Histogram



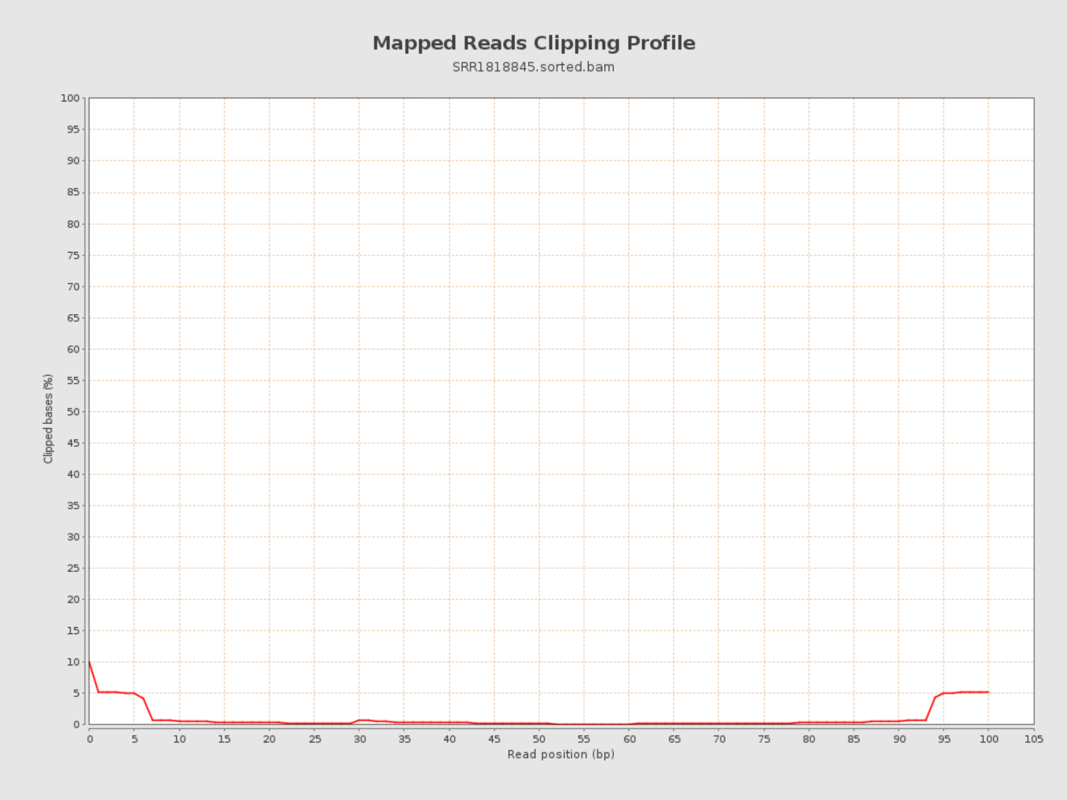
8. Results : Mapped Reads Nucleotide Content



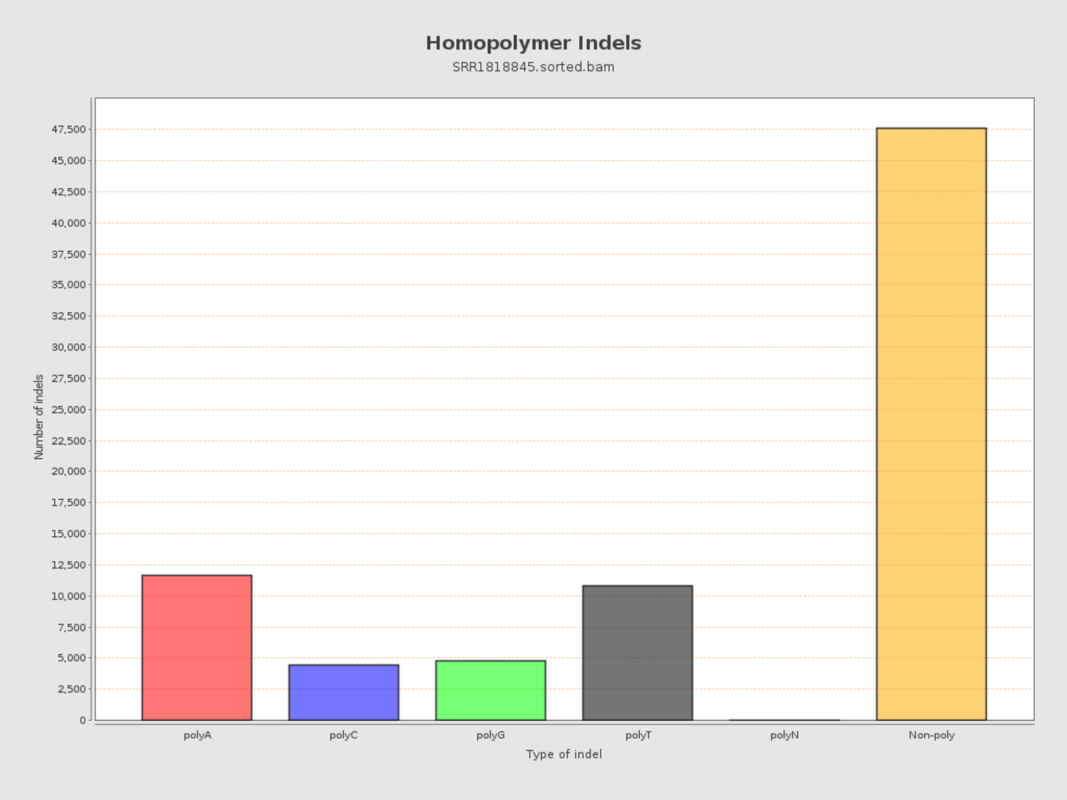
9. Results : Mapped Reads GC-content Distribution



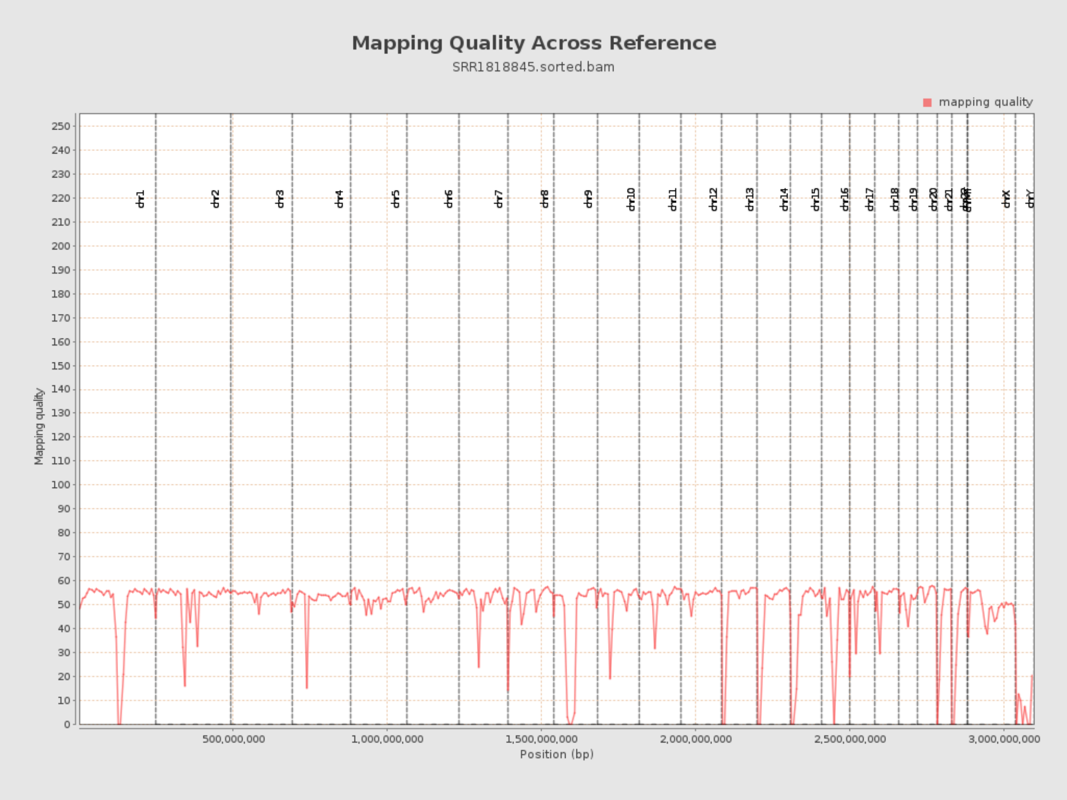
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram