Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 03:51:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818880.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_SRR1818880 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818880.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 03:51:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818880.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,715,584
Mapped reads	1,688,411 / 98.42%
Unmapped reads	27,173 / 1.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,570 / 1.32%
Read min/max/mean length	30 / 101 / 101.51
Duplicated reads (estimated)	286,399 / 16.69%
Duplication rate	13.82%
Clipped reads	1,704,797 / 99.37%

2.2. ACGT Content

Number/percentage of A's	43,448,720 / 27.78%
Number/percentage of C's	32,747,328 / 20.94%
Number/percentage of T's	44,819,643 / 28.65%
Number/percentage of G's	35,395,022 / 22.63%
Number/percentage of N's	2,295 / 0%
GC Percentage	43.57%

2.3. Coverage

Mean	0.0506

Standard Deviation	0.6433

2.4. Mapping Quality

Mean Mapping Quality	49.34

2.5. Mismatches and indels

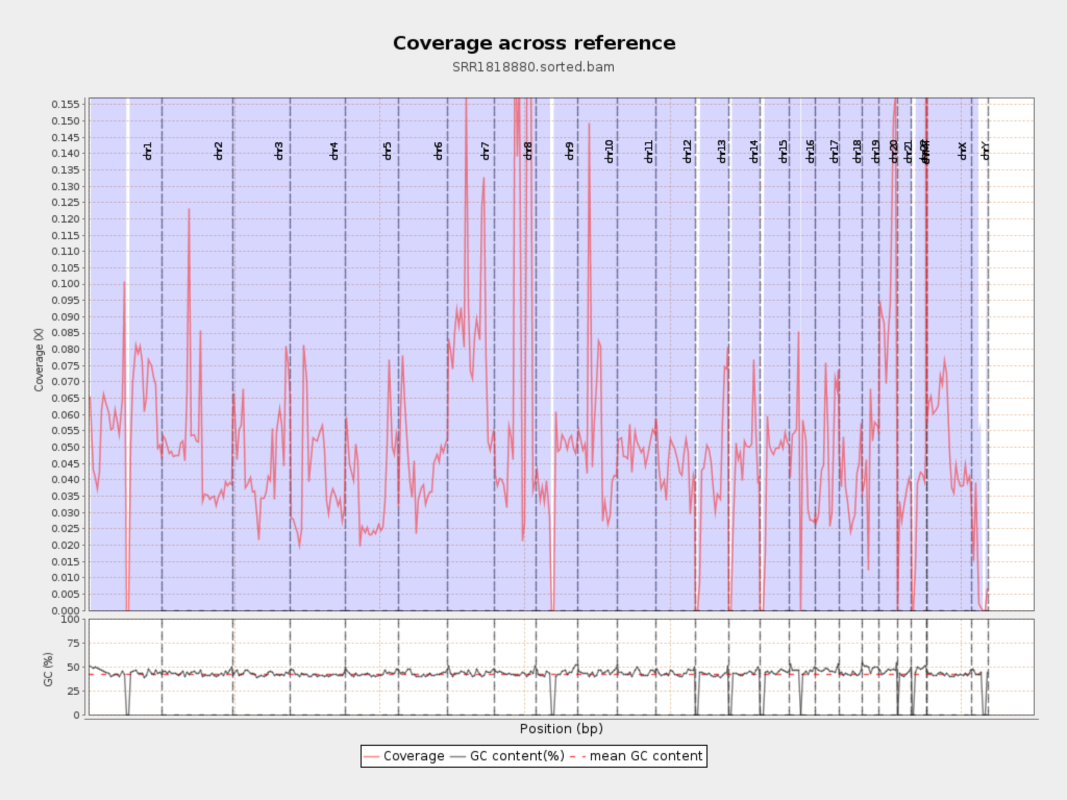
General error rate	0.63%
Mismatches	930,037
Insertions	19,069
Mapped reads with at least one insertion	1.09%
Deletions	48,420
Mapped reads with at least one deletion	2.8%
Homopolymer indels	42.36%

2.6. Chromosome stats

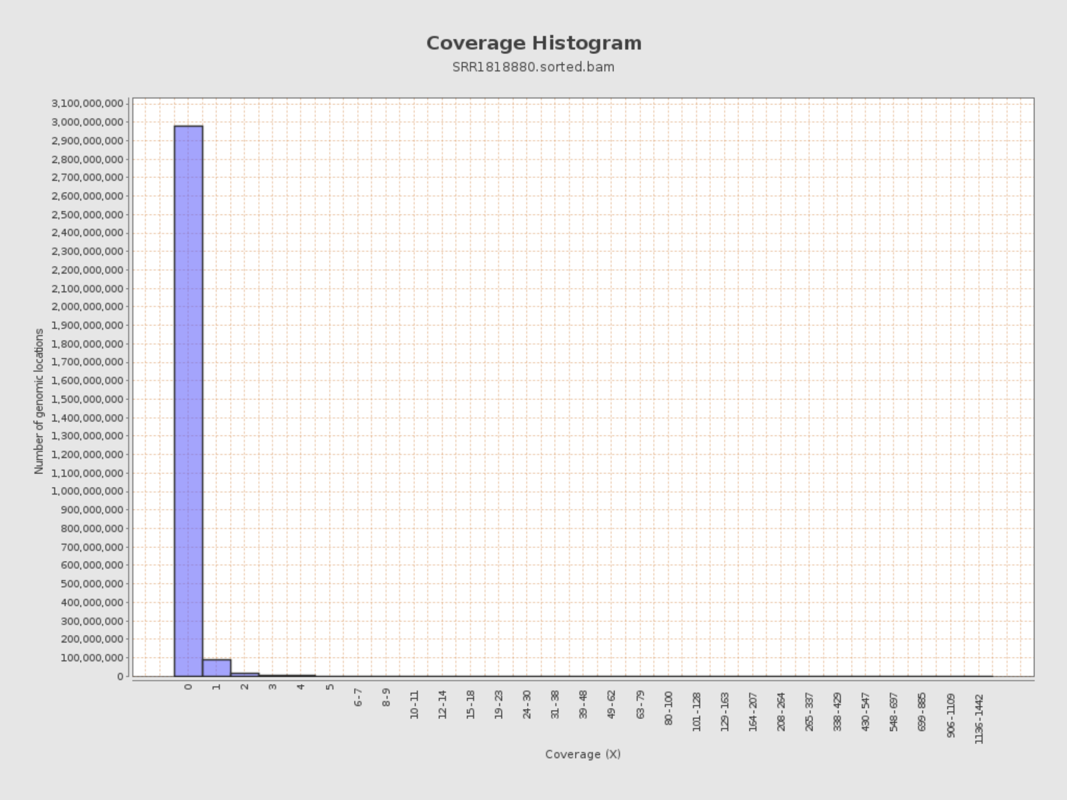
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14687360	0.0589	1.0104
chr2	243199373	11672294	0.048	0.7856
chr3	198022430	9447183	0.0477	0.2773
chr4	191154276	7674827	0.0401	0.3586
chr5	180915260	6810153	0.0376	0.259
chr6	171115067	7558879	0.0442	0.2972
chr7	159138663	13794950	0.0867	1.5262

chr8	146364022	13319721	0.091	0.5108
chr9	141213431	5757706	0.0408	0.5599
chr10	135534747	7353213	0.0543	0.9135
chr11	135006516	6775723	0.0502	0.3724
chr12	133851895	5964880	0.0446	0.2695
chr13	115169878	4684771	0.0407	0.2515
chr14	107349540	4553142	0.0424	0.2863
chr15	102531392	4263622	0.0416	0.2627
chr16	90354753	3870540	0.0428	0.5334
chr17	81195210	3939106	0.0485	0.4124
chr18	78077248	3000092	0.0384	0.6338
chr19	59128983	2780511	0.047	0.8859
chr20	63025520	6486471	0.1029	0.4456
chr21	48129895	1502641	0.0312	0.2804
chr22	51304566	1455240	0.0284	0.235
chrMT	16571	277492	16.7456	10.4487
chrX	155270560	8258519	0.0532	0.3672
chrY	59373566	620675	0.0105	0.6742

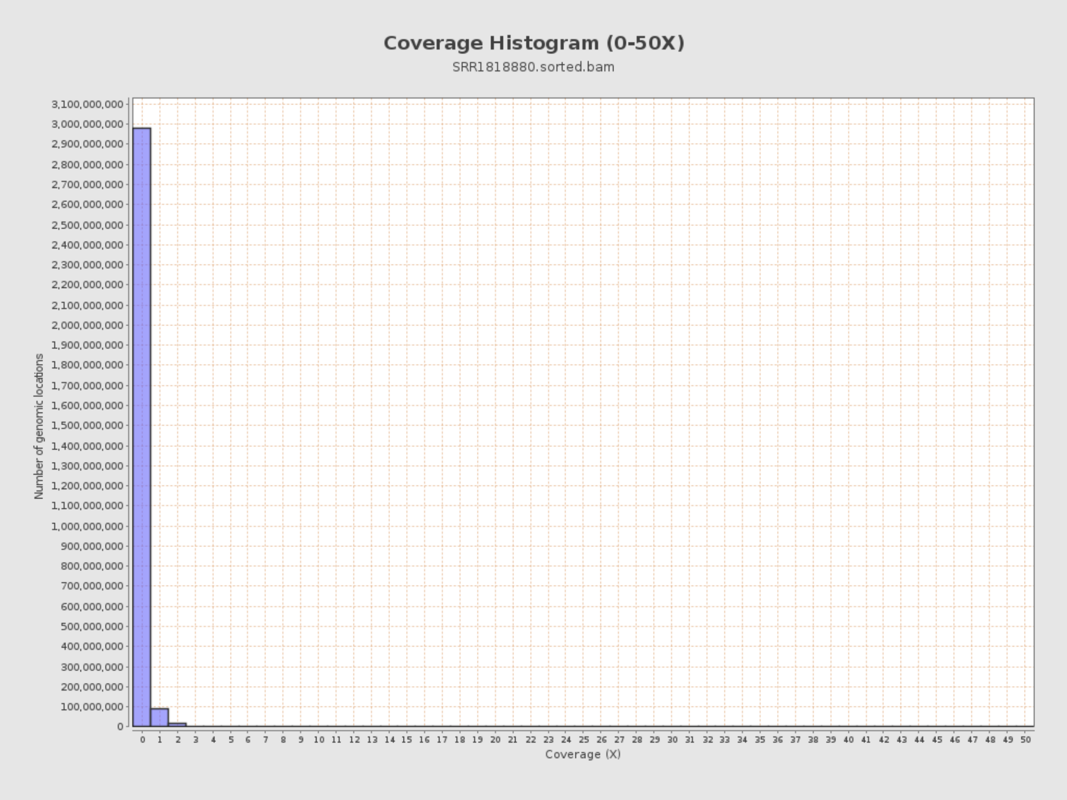
3. Results : Coverage across reference



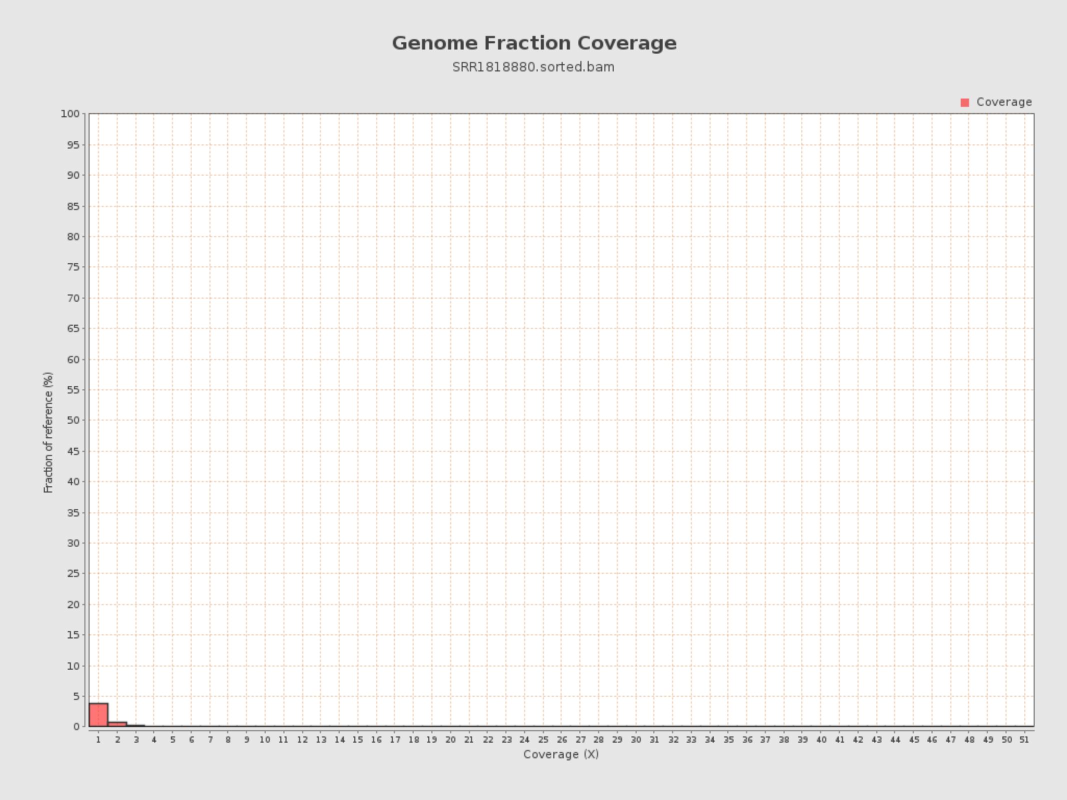
4. Results : Coverage Histogram



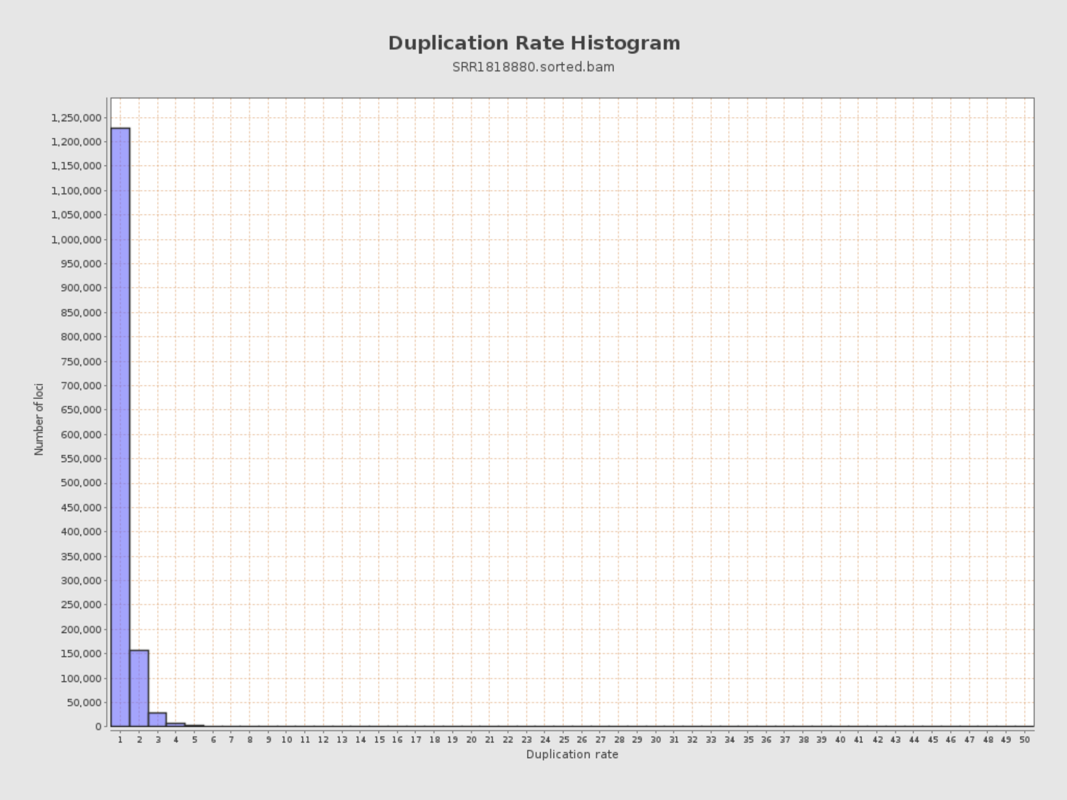
5. Results : Coverage Histogram (0-50X)



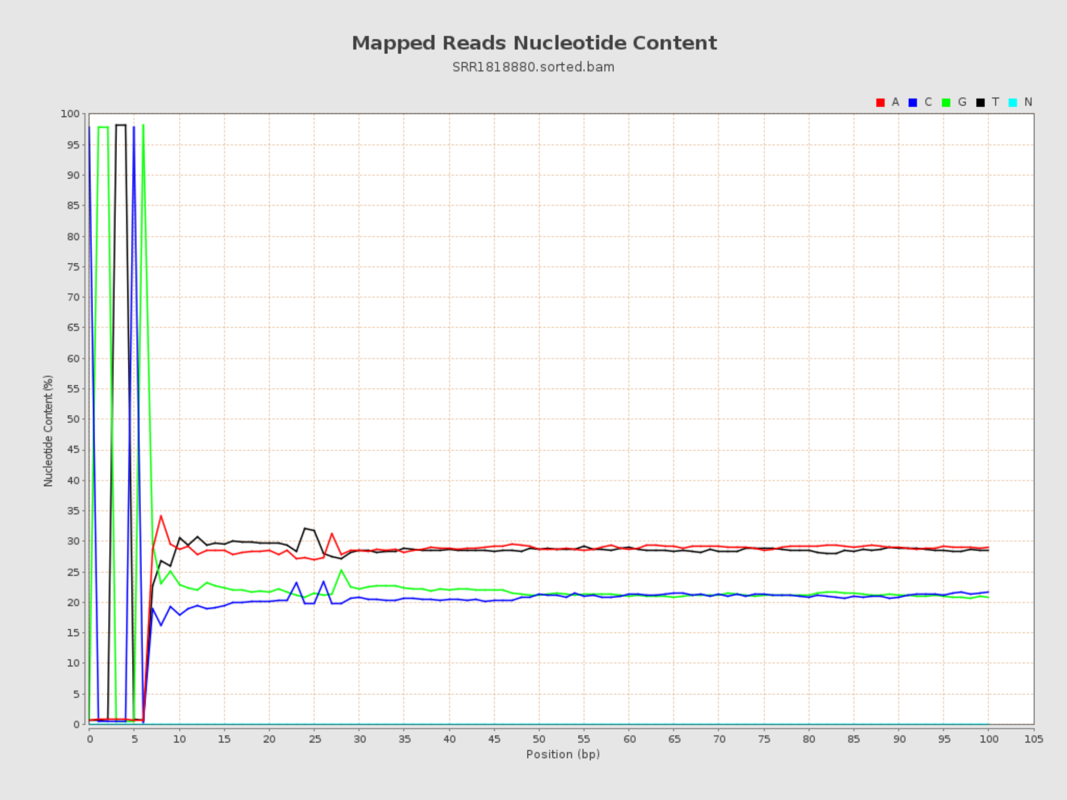
6. Results : Genome Fraction Coverage



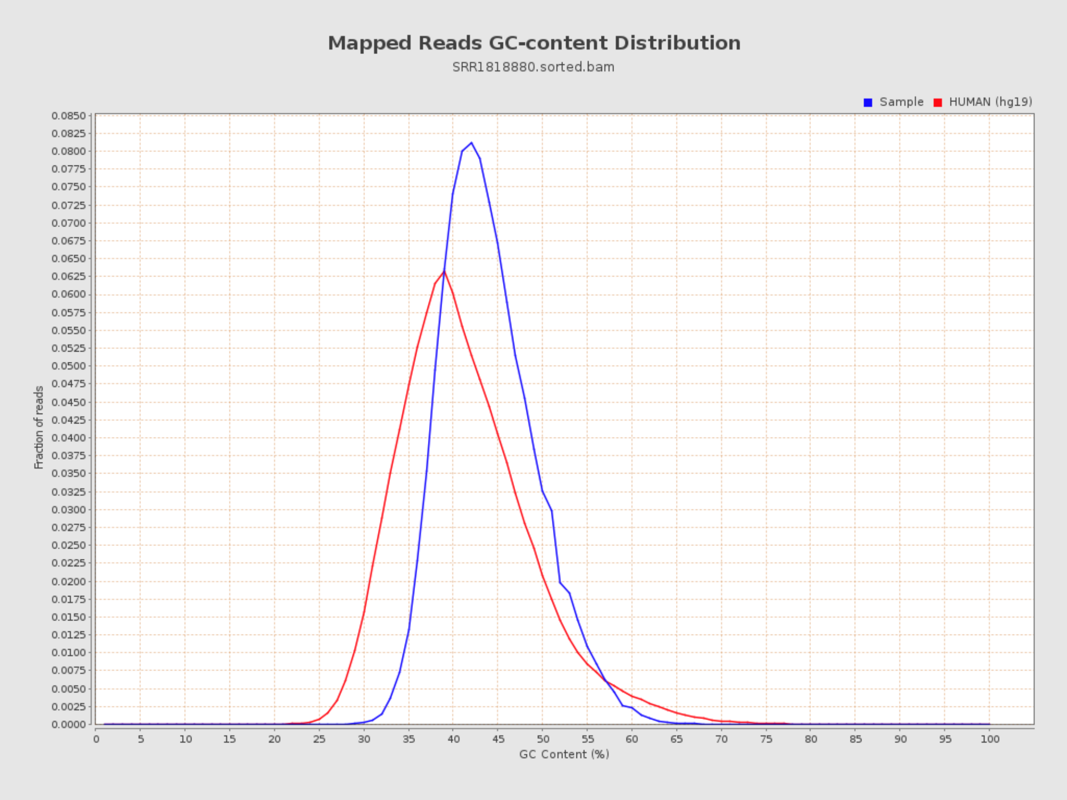
7. Results : Duplication Rate Histogram



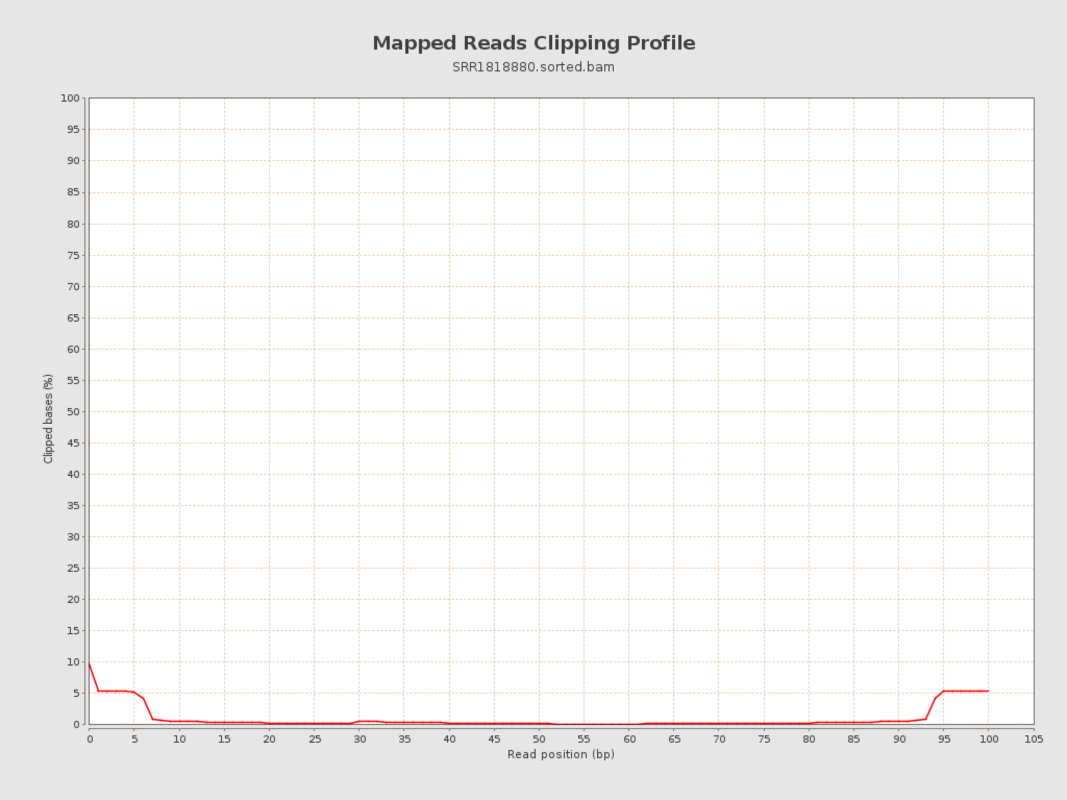
8. Results : Mapped Reads Nucleotide Content



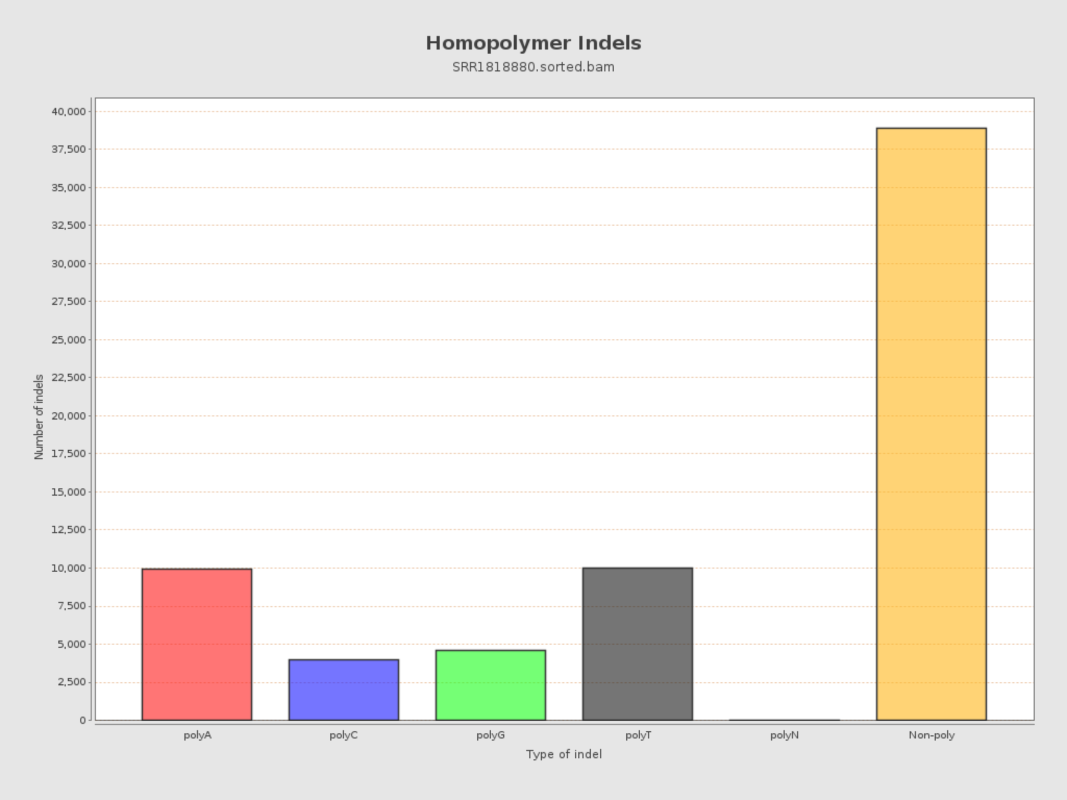
9. Results : Mapped Reads GC-content Distribution



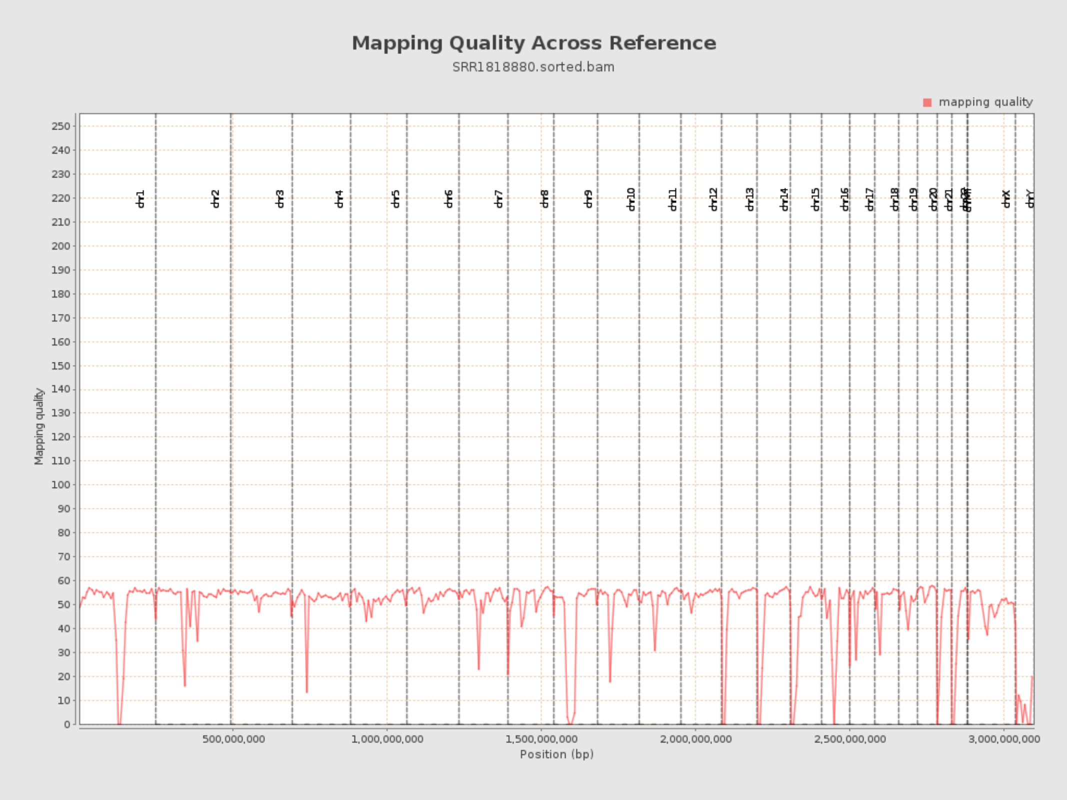
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram