Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 23:46:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818854.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_SRR1818854 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818854.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 23:46:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818854.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	895,951
Mapped reads	842,150 / 94%
Unmapped reads	53,801 / 6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,013 / 1.45%
Read min/max/mean length	30 / 101 / 101.57
Duplicated reads (estimated)	79,383 / 8.86%
Duplication rate	7.32%
Clipped reads	844,310 / 94.24%

2.2. ACGT Content

Number/percentage of A's	21,229,244 / 27.21%
Number/percentage of C's	16,232,917 / 20.81%
Number/percentage of T's	22,853,593 / 29.29%
Number/percentage of G's	17,698,581 / 22.69%
Number/percentage of N's	1,065 / 0%
GC Percentage	43.49%

2.3. Coverage

Mean	0.0252

Standard Deviation	0.3286

2.4. Mapping Quality

Mean Mapping Quality	49.25

2.5. Mismatches and indels

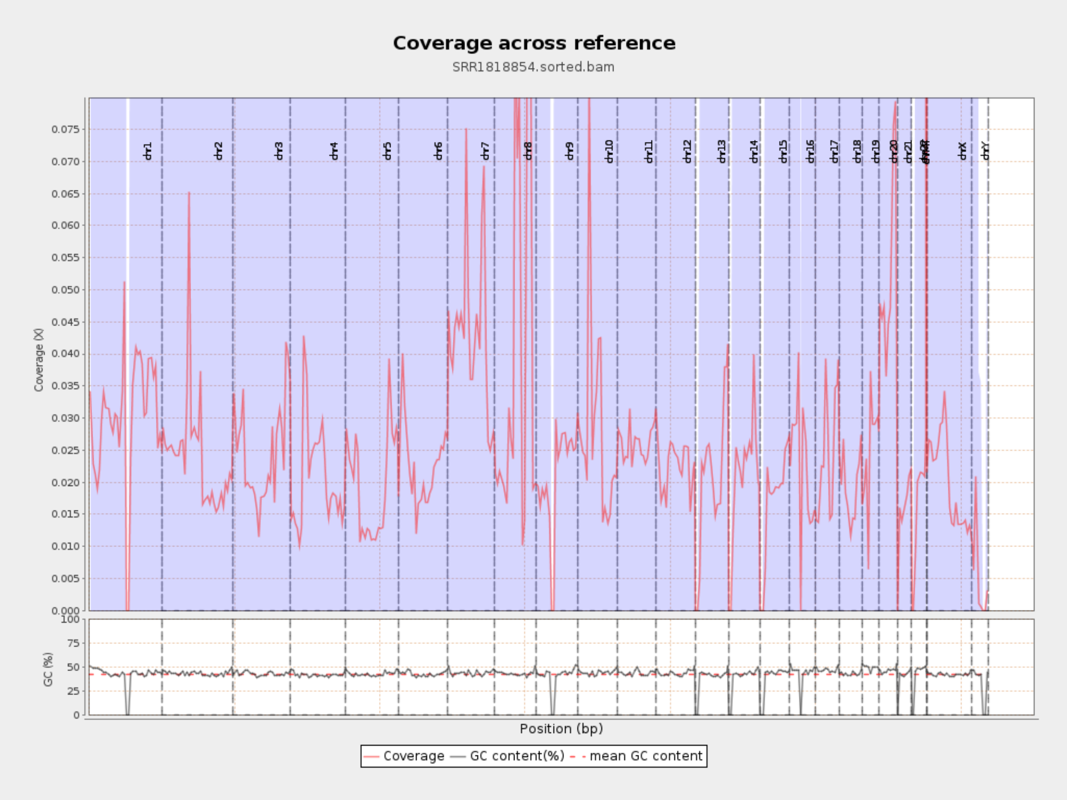
General error rate	0.63%
Mismatches	467,125
Insertions	10,894
Mapped reads with at least one insertion	1.25%
Deletions	22,691
Mapped reads with at least one deletion	2.63%
Homopolymer indels	41.4%

2.6. Chromosome stats

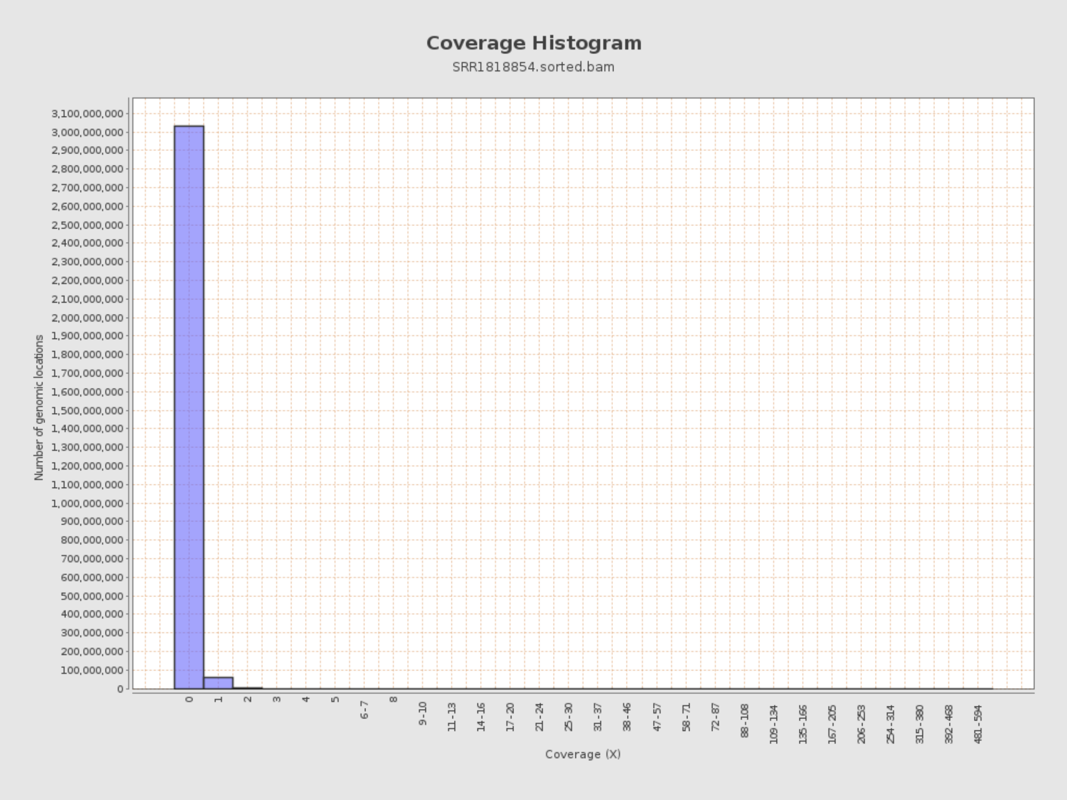
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7472687	0.03	0.4908
chr2	243199373	5882830	0.0242	0.3795
chr3	198022430	4821499	0.0243	0.181
chr4	191154276	3900686	0.0204	0.2086
chr5	180915260	3505436	0.0194	0.1585
chr6	171115067	3849766	0.0225	0.1831
chr7	159138663	6975681	0.0438	0.6823

chr8	146364022	6708281	0.0458	0.3048
chr9	141213431	2896472	0.0205	0.3028
chr10	135534747	3795663	0.028	0.5339
chr11	135006516	3509127	0.026	0.2321
chr12	133851895	3038397	0.0227	0.1704
chr13	115169878	2357880	0.0205	0.1607
chr14	107349540	2246502	0.0209	0.1737
chr15	102531392	1727577	0.0168	0.1448
chr16	90354753	2003497	0.0222	0.2525
chr17	81195210	2019682	0.0249	0.2586
chr18	78077248	1502398	0.0192	0.3404
chr19	59128983	1458575	0.0247	0.4868
chr20	63025520	3313878	0.0526	0.2729
chr21	48129895	762871	0.0159	0.1725
chr22	51304566	767731	0.015	0.142
chrMT	16571	95358	5.7545	4.6077
chrX	155270560	3150504	0.0203	0.1995
chrY	59373566	297756	0.005	0.3334

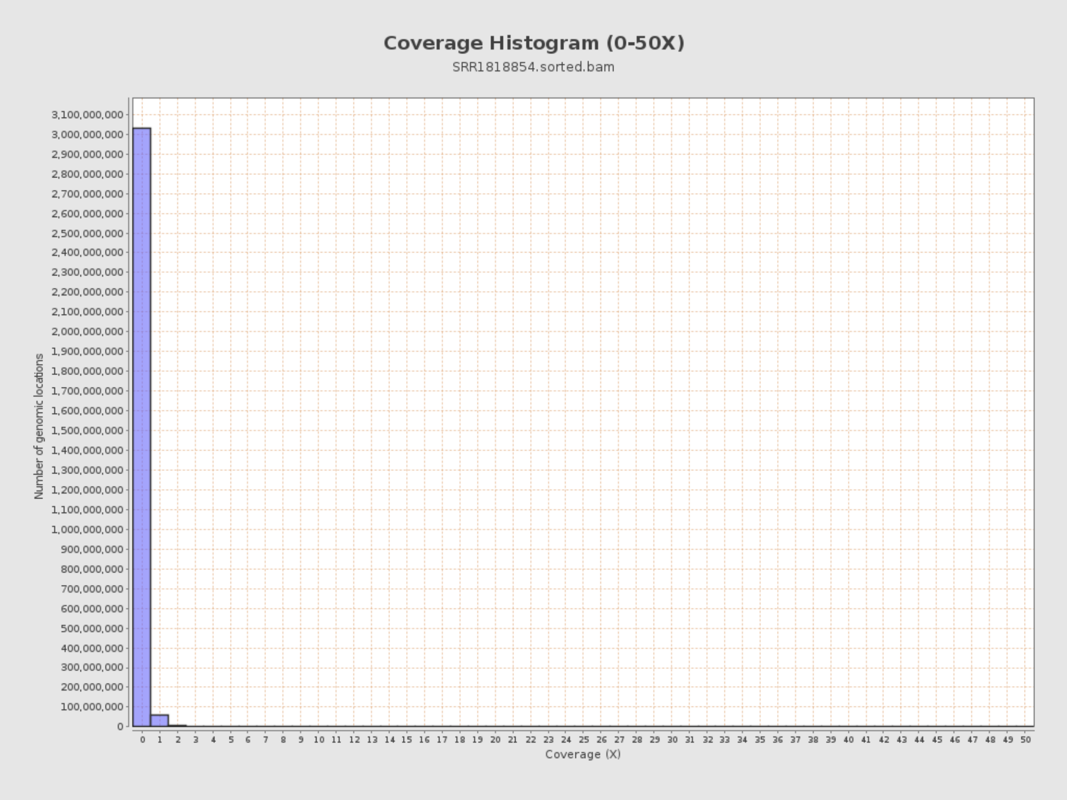
3. Results : Coverage across reference



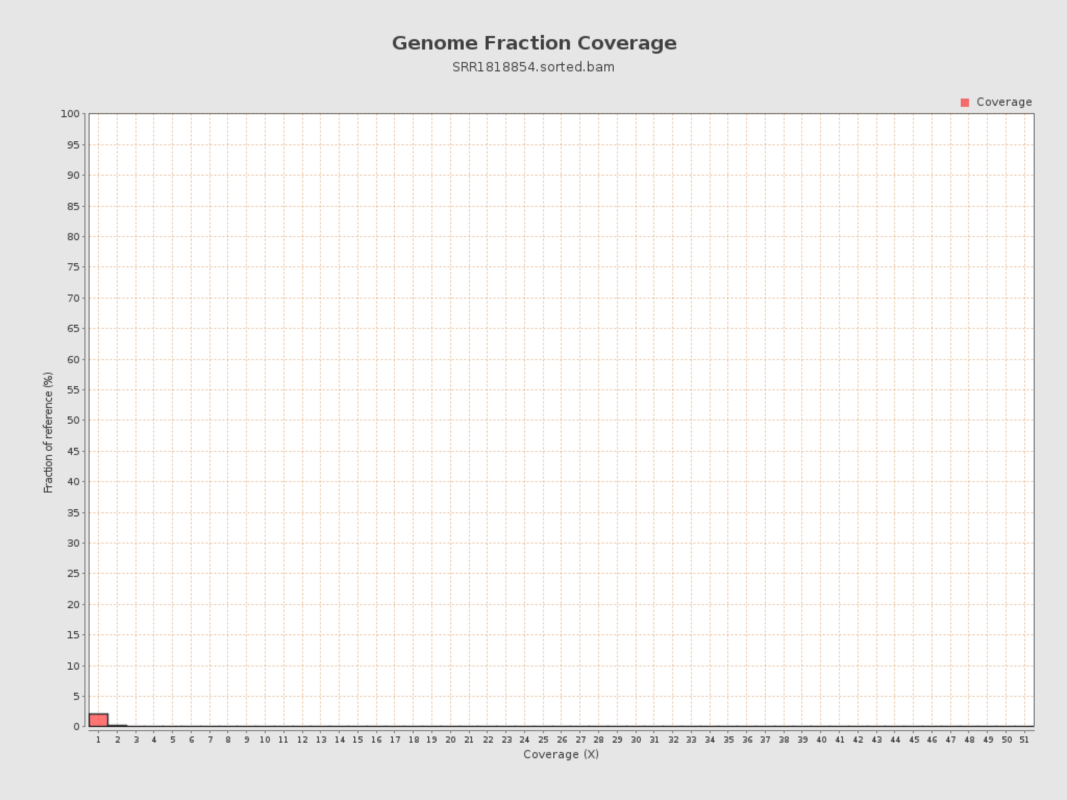
4. Results : Coverage Histogram



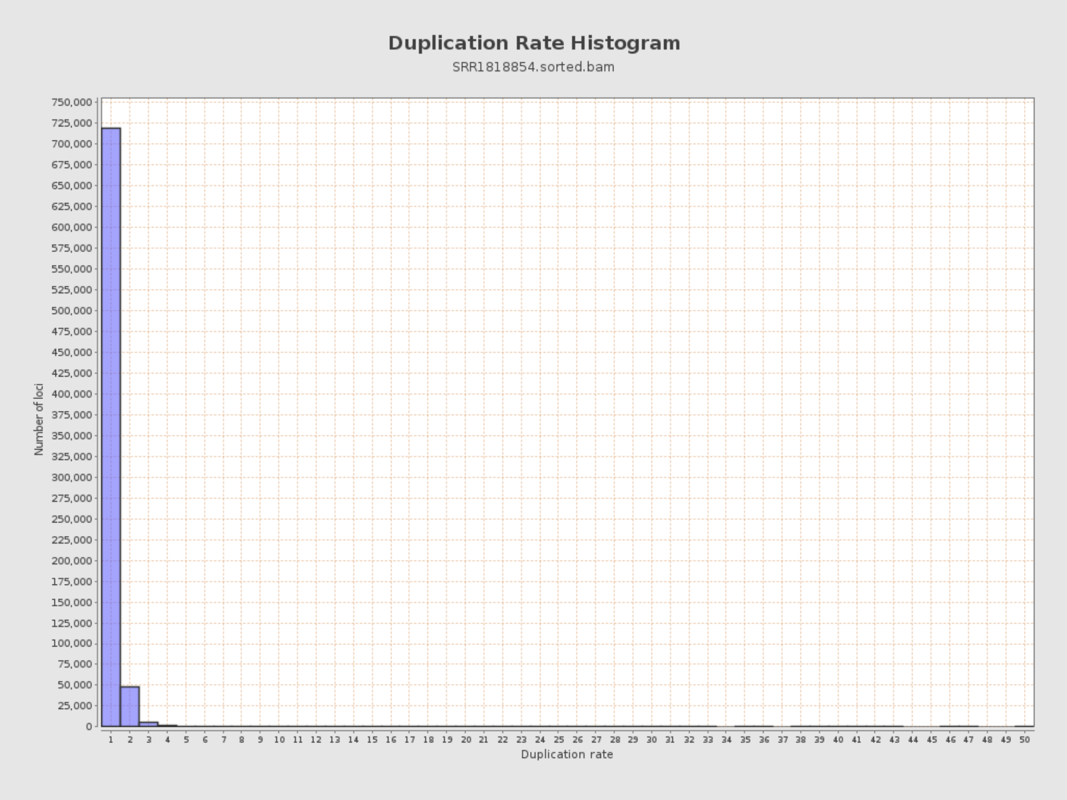
5. Results : Coverage Histogram (0-50X)



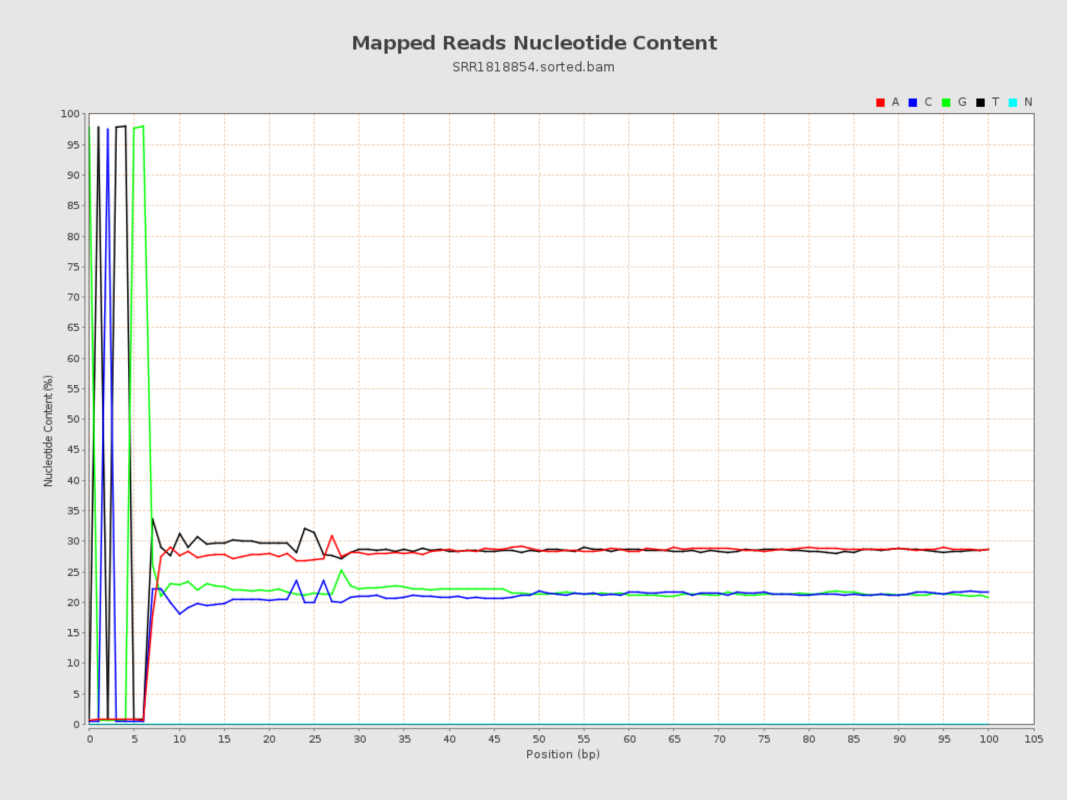
6. Results : Genome Fraction Coverage



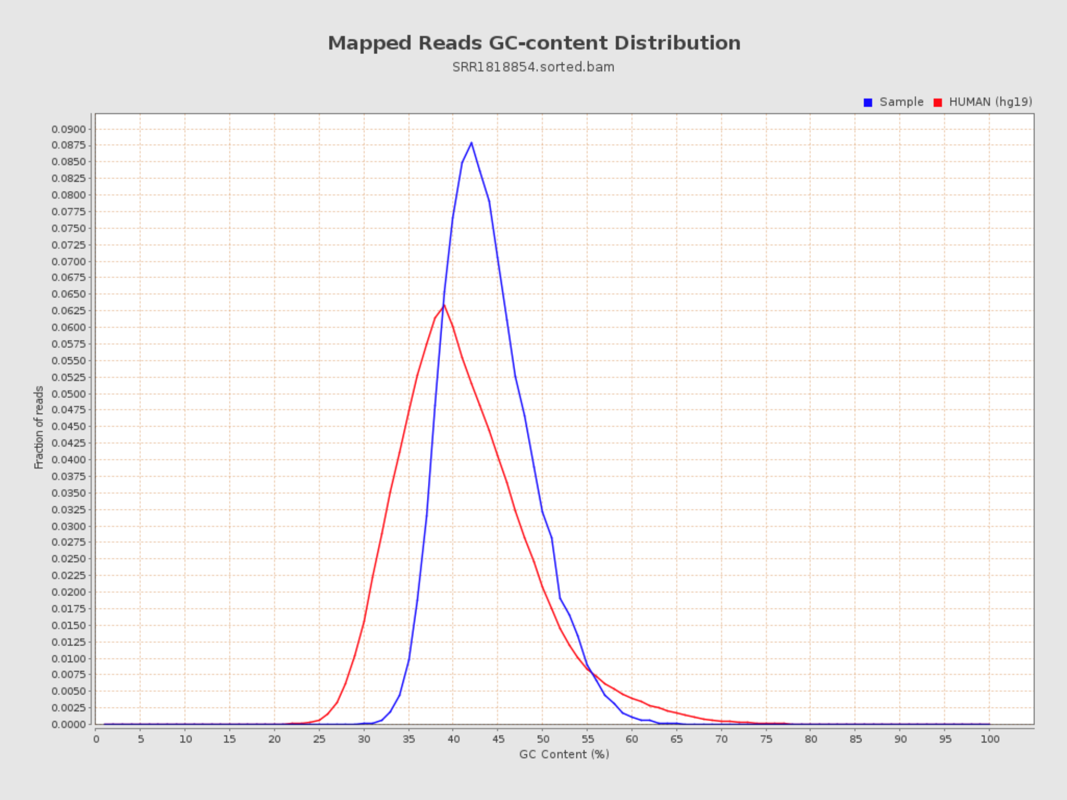
7. Results : Duplication Rate Histogram



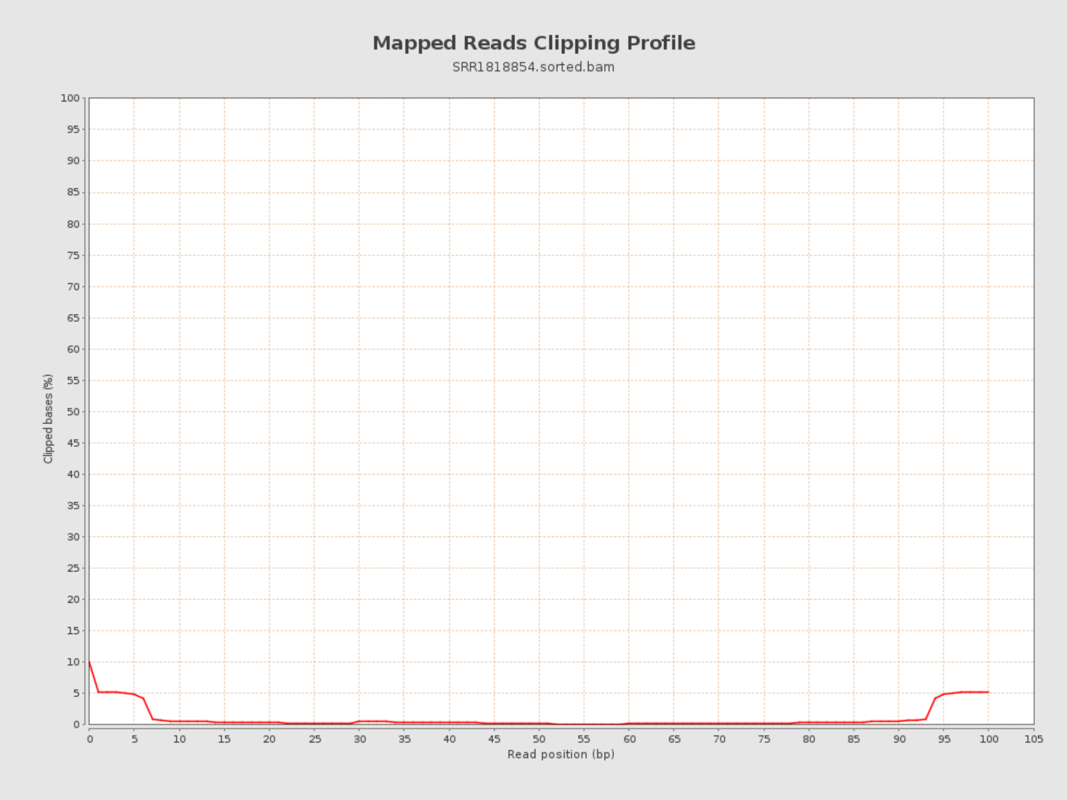
8. Results : Mapped Reads Nucleotide Content



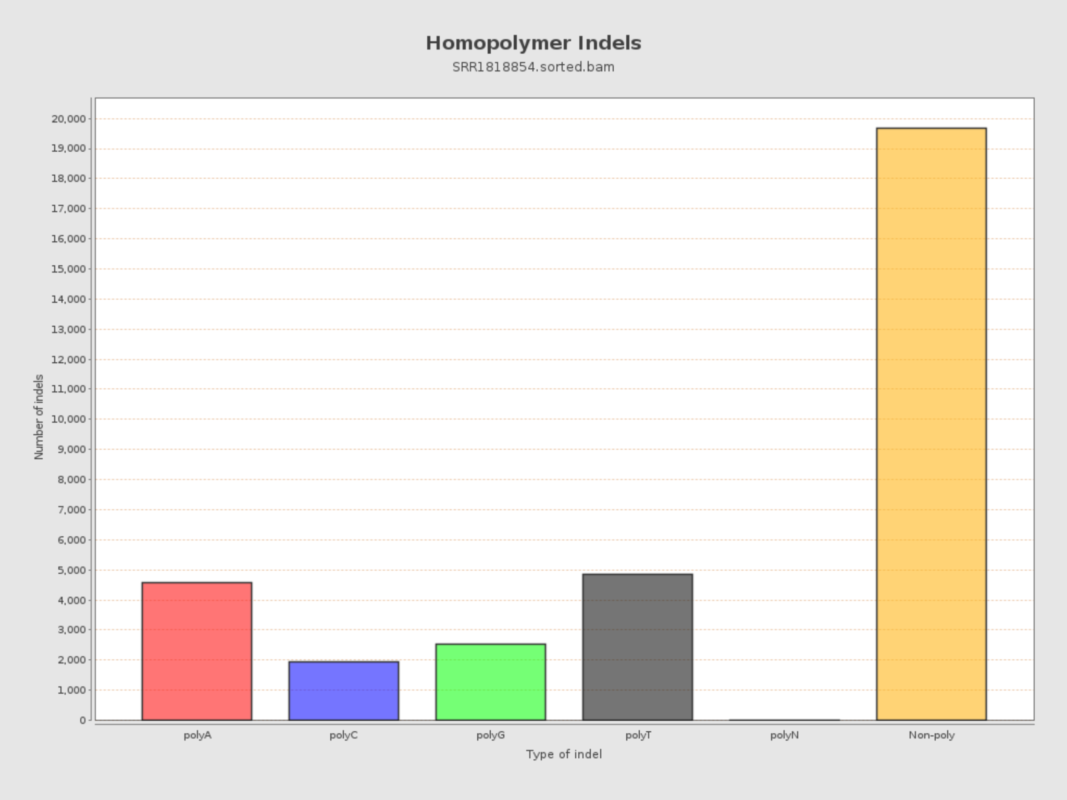
9. Results : Mapped Reads GC-content Distribution



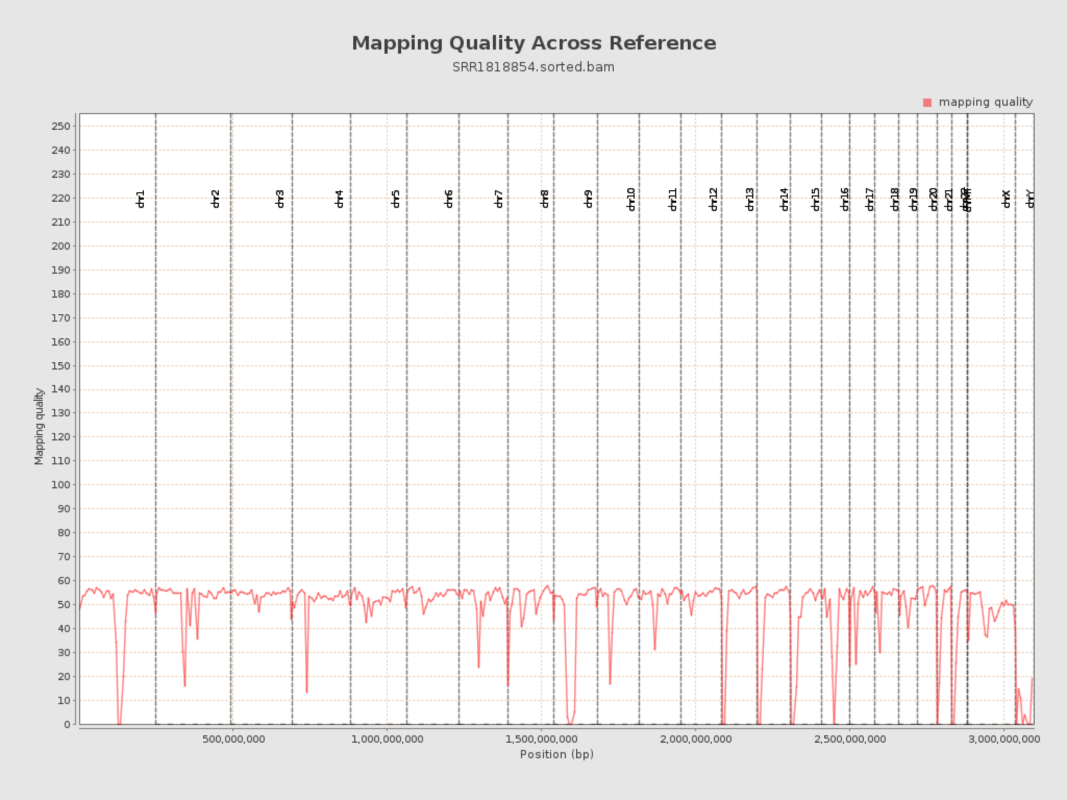
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram