Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 04:07:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818882.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_SRR1818882 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818882.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 04:07:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818882.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	880,850
Mapped reads	869,276 / 98.69%
Unmapped reads	11,574 / 1.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,692 / 1.55%
Read min/max/mean length	30 / 101 / 101.6
Duplicated reads (estimated)	114,171 / 12.96%
Duplication rate	10.71%
Clipped reads	877,115 / 99.58%

2.2. ACGT Content

Number/percentage of A's	22,195,399 / 27.6%
Number/percentage of C's	17,229,152 / 21.42%
Number/percentage of T's	23,236,724 / 28.89%
Number/percentage of G's	17,764,743 / 22.09%
Number/percentage of N's	1,134 / 0%
GC Percentage	43.51%

2.3. Coverage

Mean	0.026

Standard Deviation	0.3268

2.4. Mapping Quality

Mean Mapping Quality	49.16

2.5. Mismatches and indels

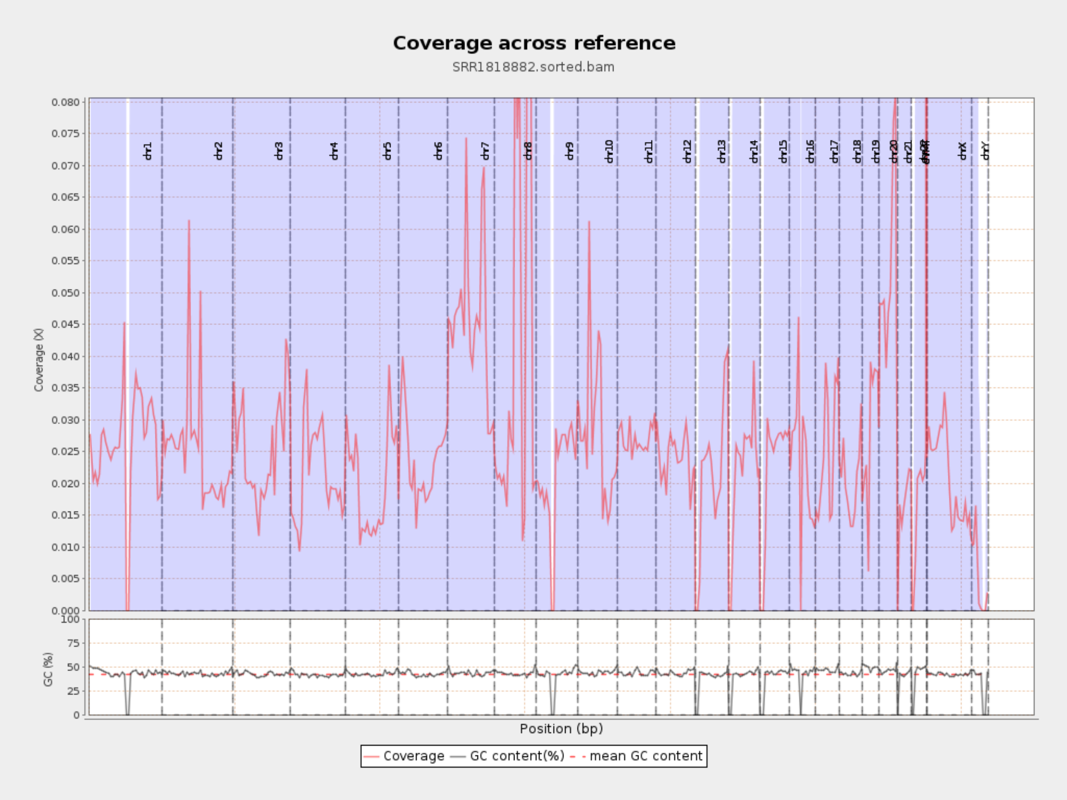
General error rate	0.64%
Mismatches	485,732
Insertions	10,252
Mapped reads with at least one insertion	1.14%
Deletions	25,828
Mapped reads with at least one deletion	2.9%
Homopolymer indels	40.92%

2.6. Chromosome stats

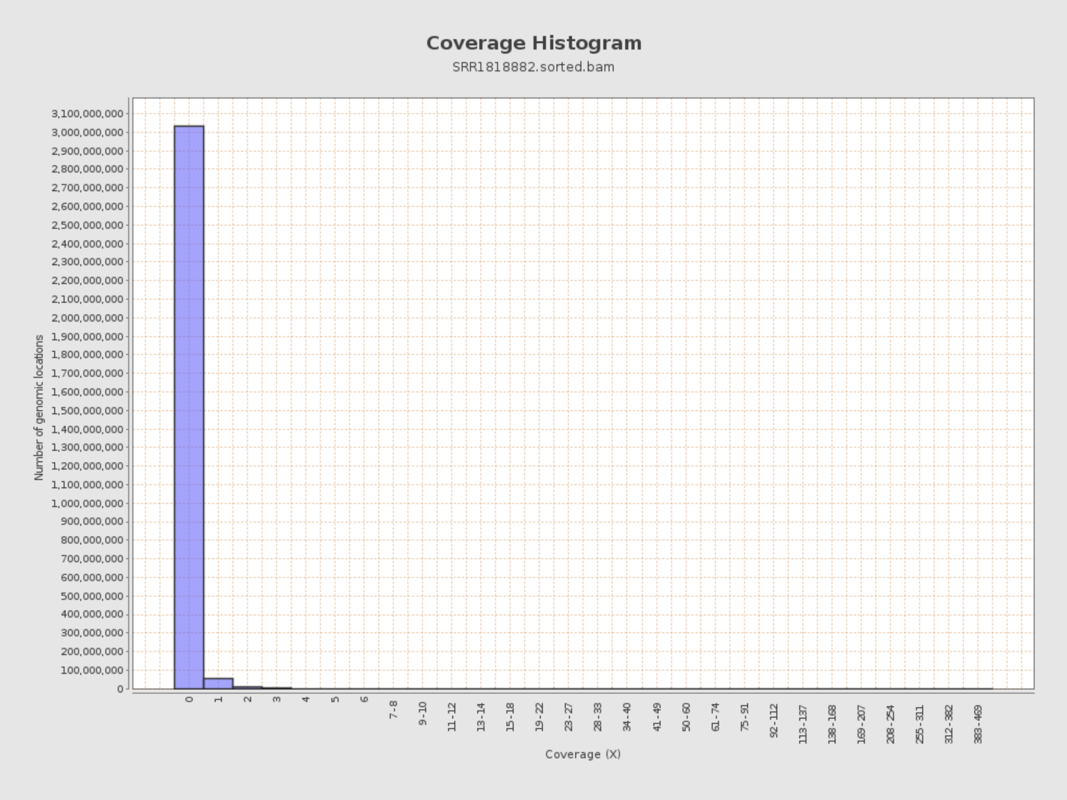
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6478111	0.026	0.3951
chr2	243199373	6131209	0.0252	0.4935
chr3	198022430	5043830	0.0255	0.1881
chr4	191154276	4024453	0.0211	0.2057
chr5	180915260	3619931	0.02	0.1756
chr6	171115067	4026399	0.0235	0.193
chr7	159138663	7362169	0.0463	0.6821

chr8	146364022	7056992	0.0482	0.3099
chr9	141213431	2955793	0.0209	0.2823
chr10	135534747	3803612	0.0281	0.4416
chr11	135006516	3636736	0.0269	0.2311
chr12	133851895	3248910	0.0243	0.1857
chr13	115169878	2450249	0.0213	0.1707
chr14	107349540	2358073	0.022	0.1881
chr15	102531392	2284465	0.0223	0.1749
chr16	90354753	2057139	0.0228	0.3716
chr17	81195210	2082007	0.0256	0.2285
chr18	78077248	1577230	0.0202	0.3315
chr19	59128983	1655827	0.028	0.3531
chr20	63025520	3430656	0.0544	0.2933
chr21	48129895	795525	0.0165	0.1716
chr22	51304566	765175	0.0149	0.1647
chrMT	16571	37271	2.2492	2.1893
chrX	155270560	3302104	0.0213	0.2056
chrY	59373566	295071	0.005	0.4043

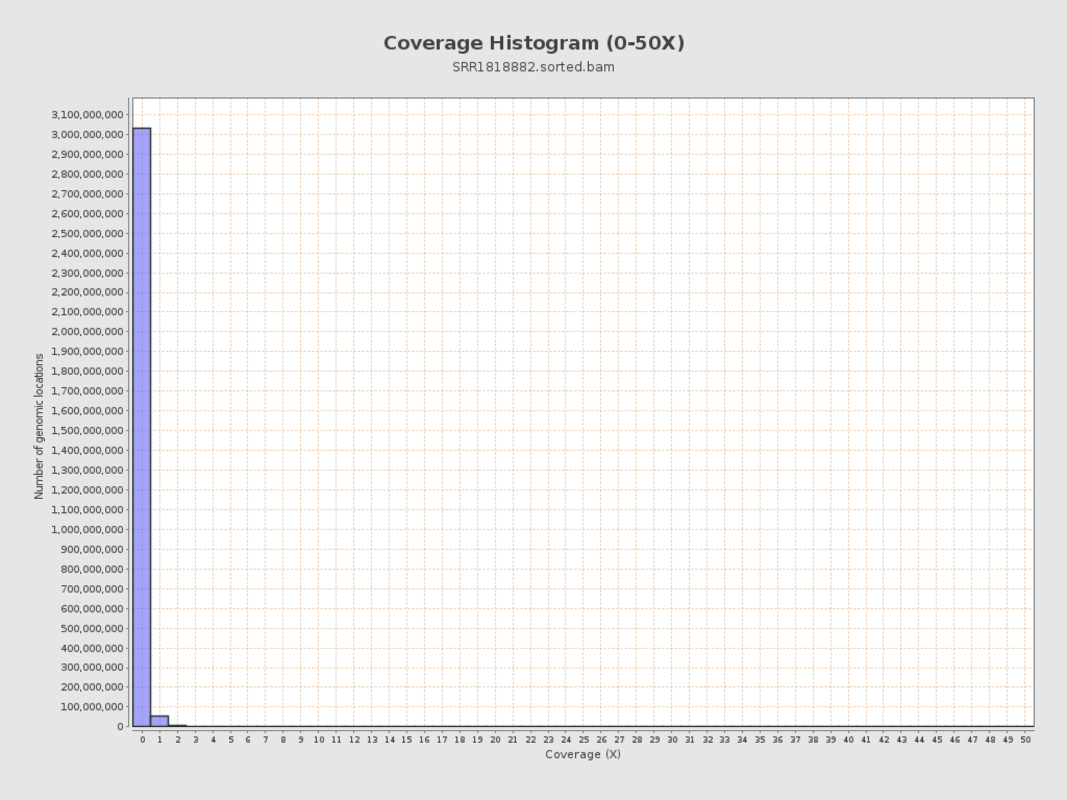
3. Results : Coverage across reference



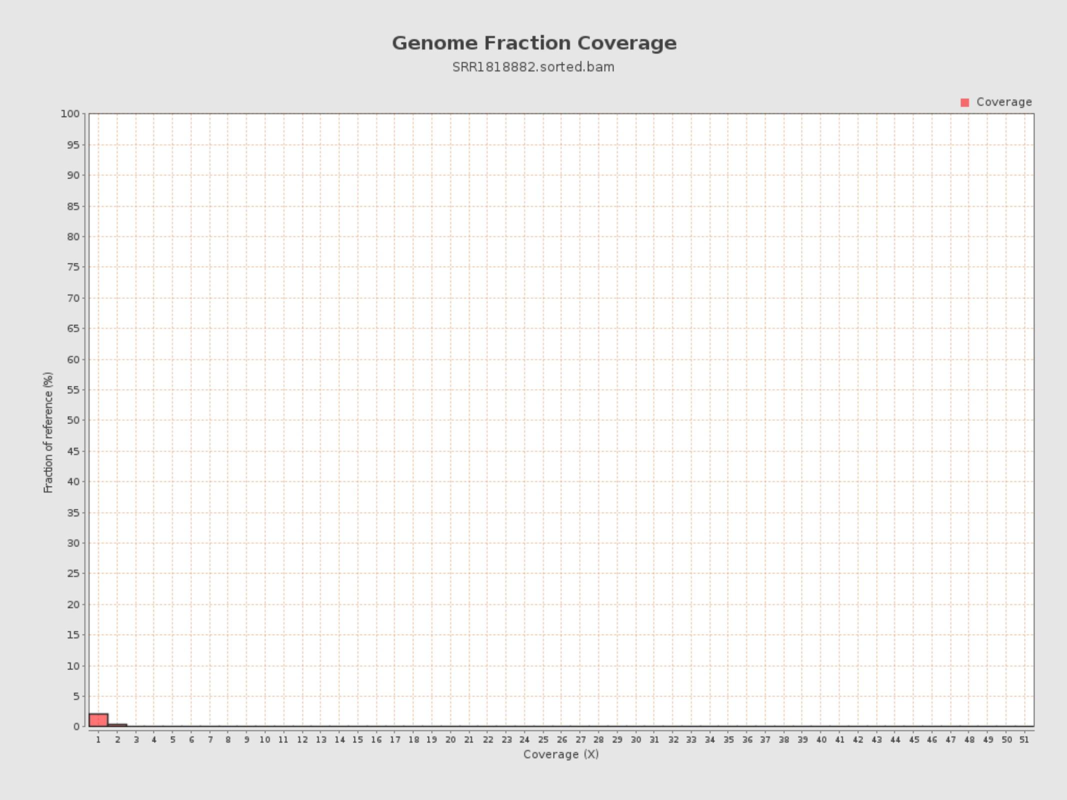
4. Results : Coverage Histogram



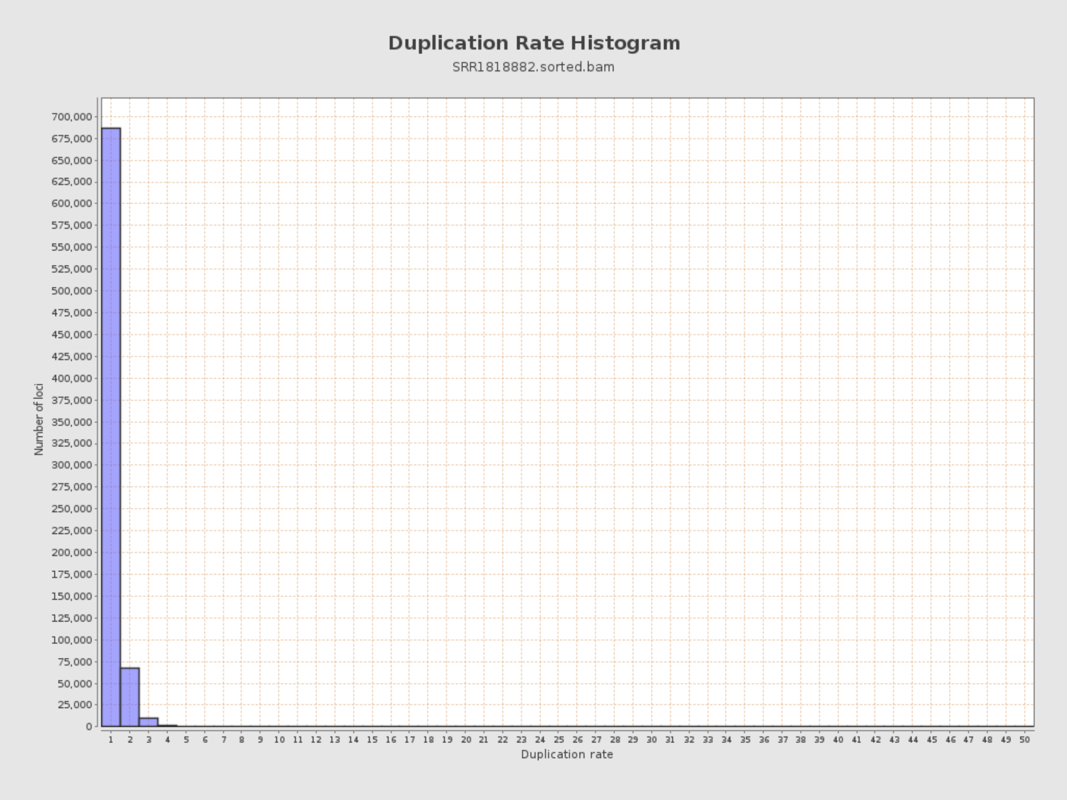
5. Results : Coverage Histogram (0-50X)



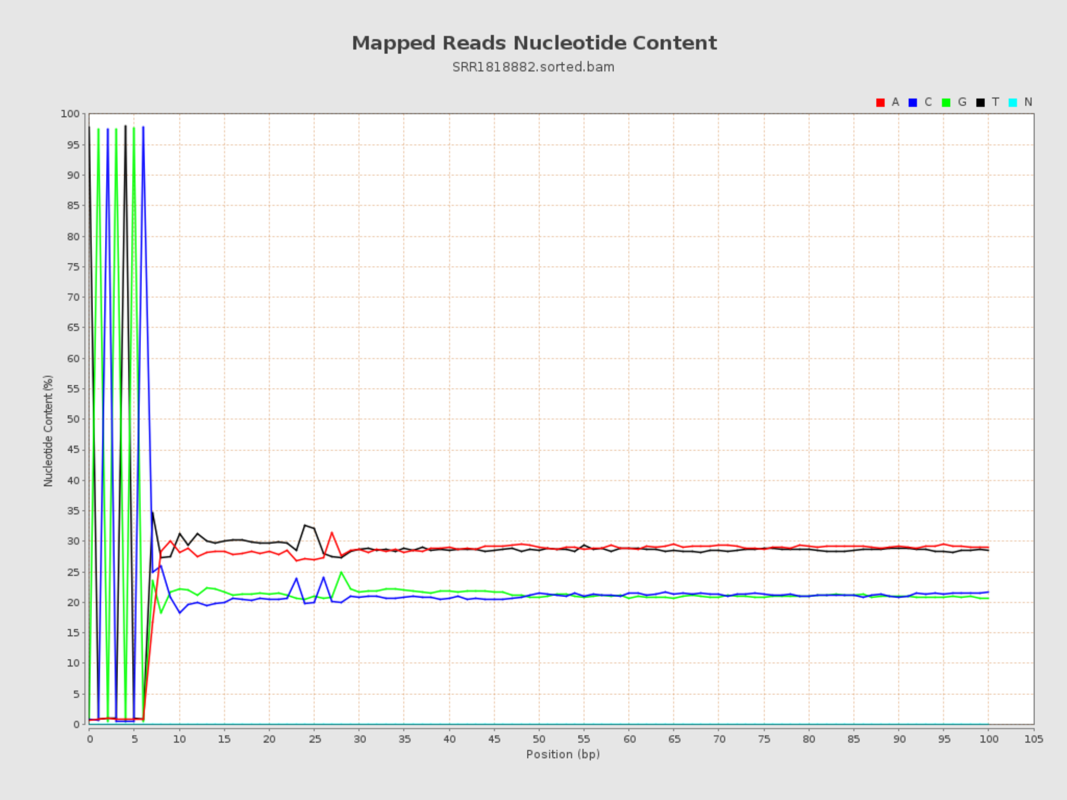
6. Results : Genome Fraction Coverage



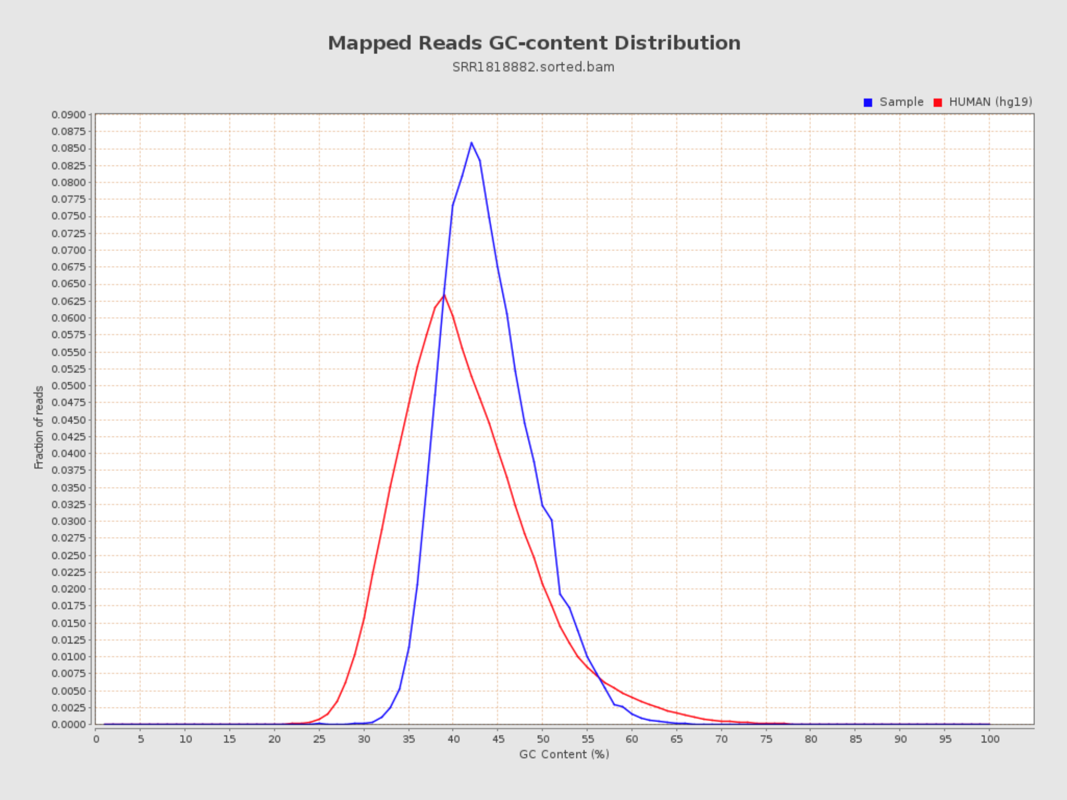
7. Results : Duplication Rate Histogram



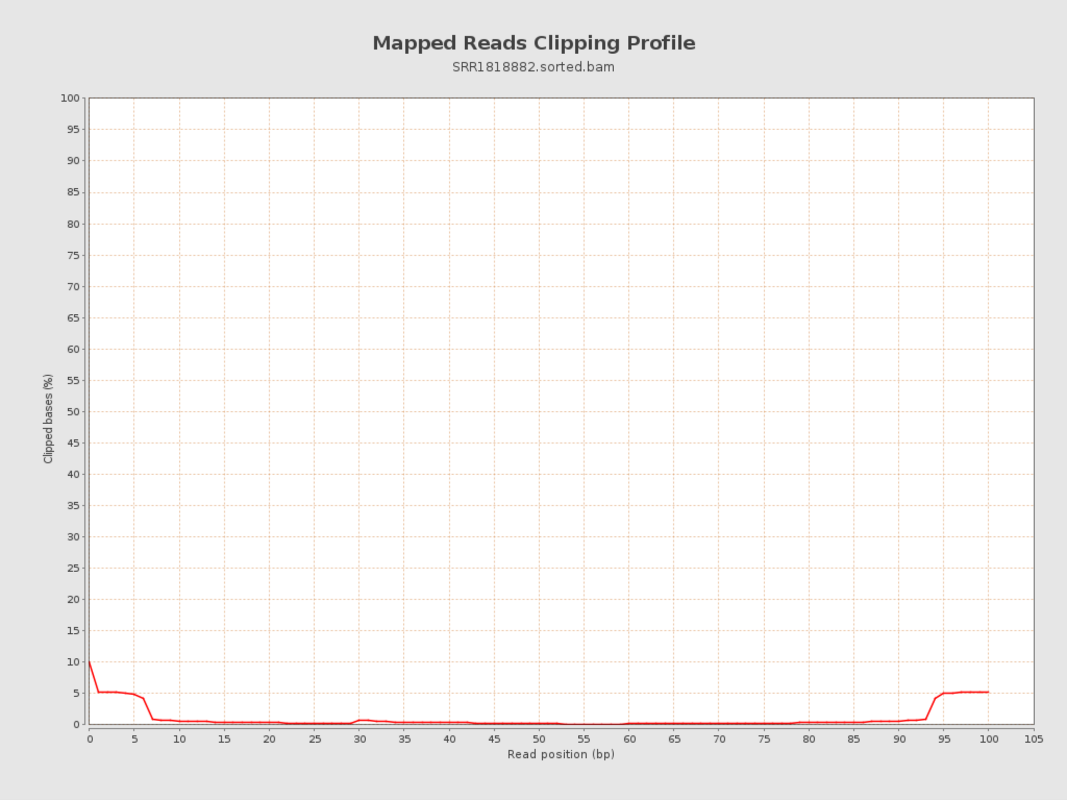
8. Results : Mapped Reads Nucleotide Content



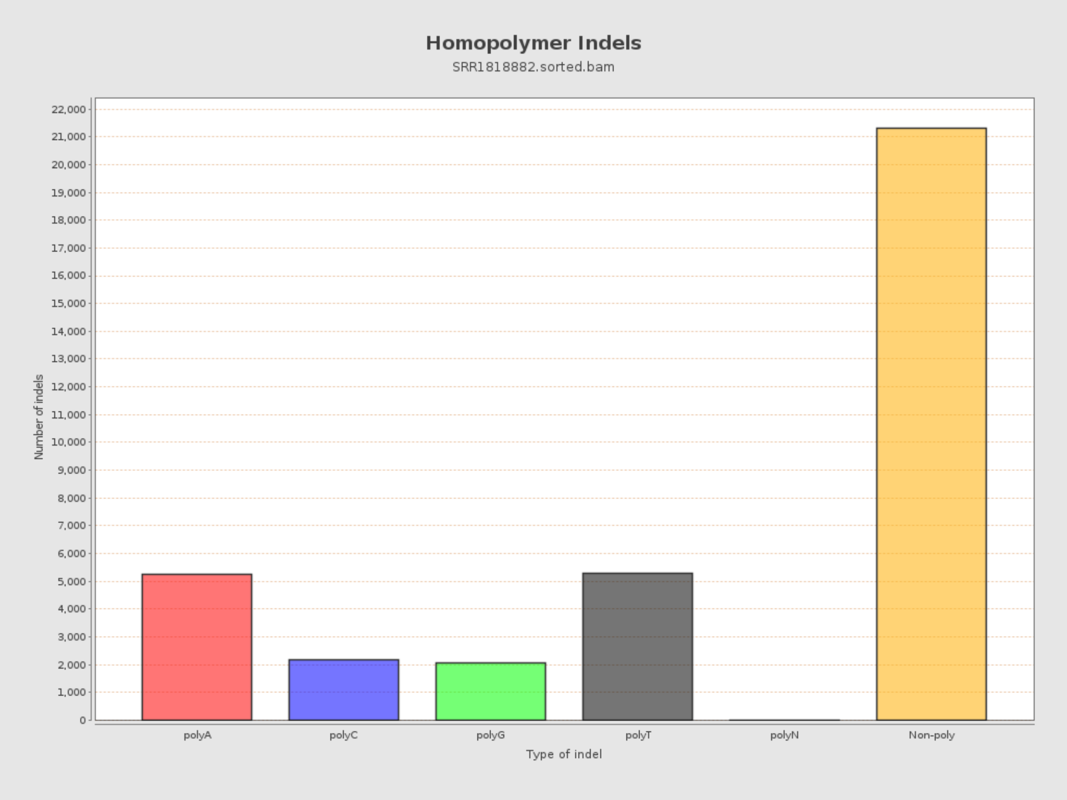
9. Results : Mapped Reads GC-content Distribution



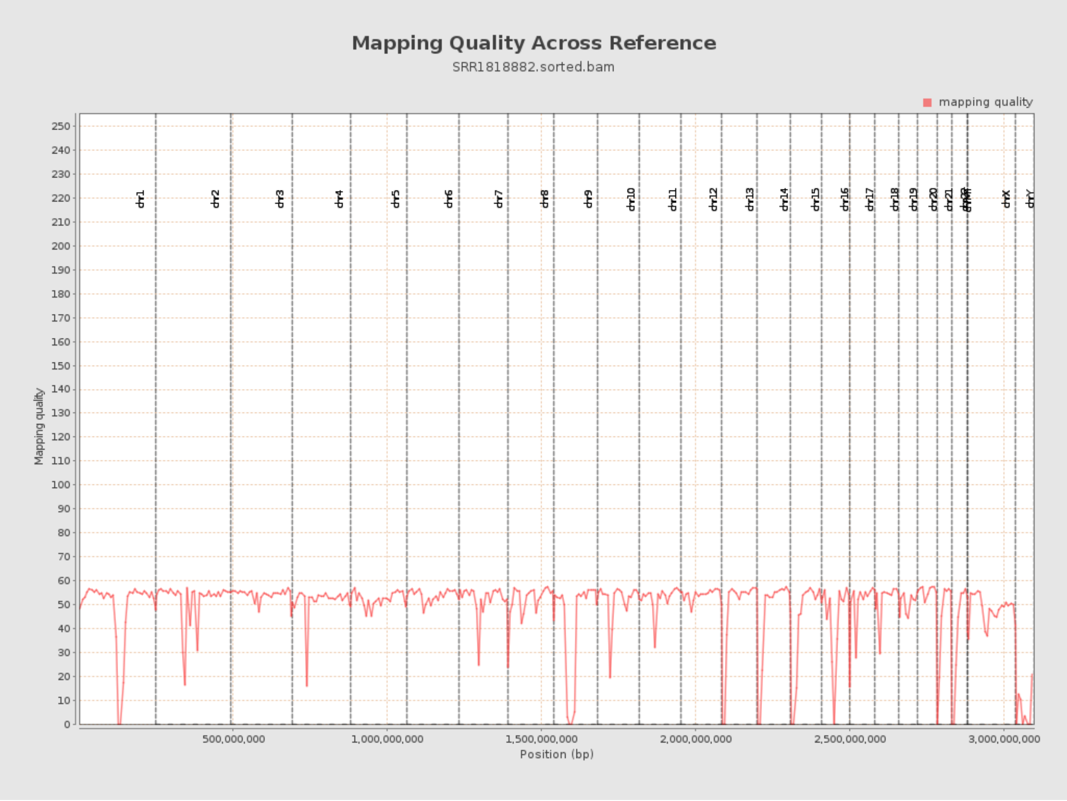
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram