Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 03:16:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818876.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_SRR1818876 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818876.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 03:16:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818876.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,581,806
Mapped reads	2,416,093 / 93.58%
Unmapped reads	165,713 / 6.42%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	37,414 / 1.45%
Read min/max/mean length	30 / 101 / 101.56
Duplicated reads (estimated)	745,799 / 28.89%
Duplication rate	26.32%
Clipped reads	2,441,974 / 94.58%

2.2. ACGT Content

Number/percentage of A's	64,853,080 / 29.03%
Number/percentage of C's	46,941,437 / 21.01%
Number/percentage of T's	64,427,391 / 28.84%
Number/percentage of G's	47,149,103 / 21.11%
Number/percentage of N's	3,213 / 0%
GC Percentage	42.12%

2.3. Coverage

Mean	0.0722

Standard Deviation	0.856

2.4. Mapping Quality

Mean Mapping Quality	49.35

2.5. Mismatches and indels

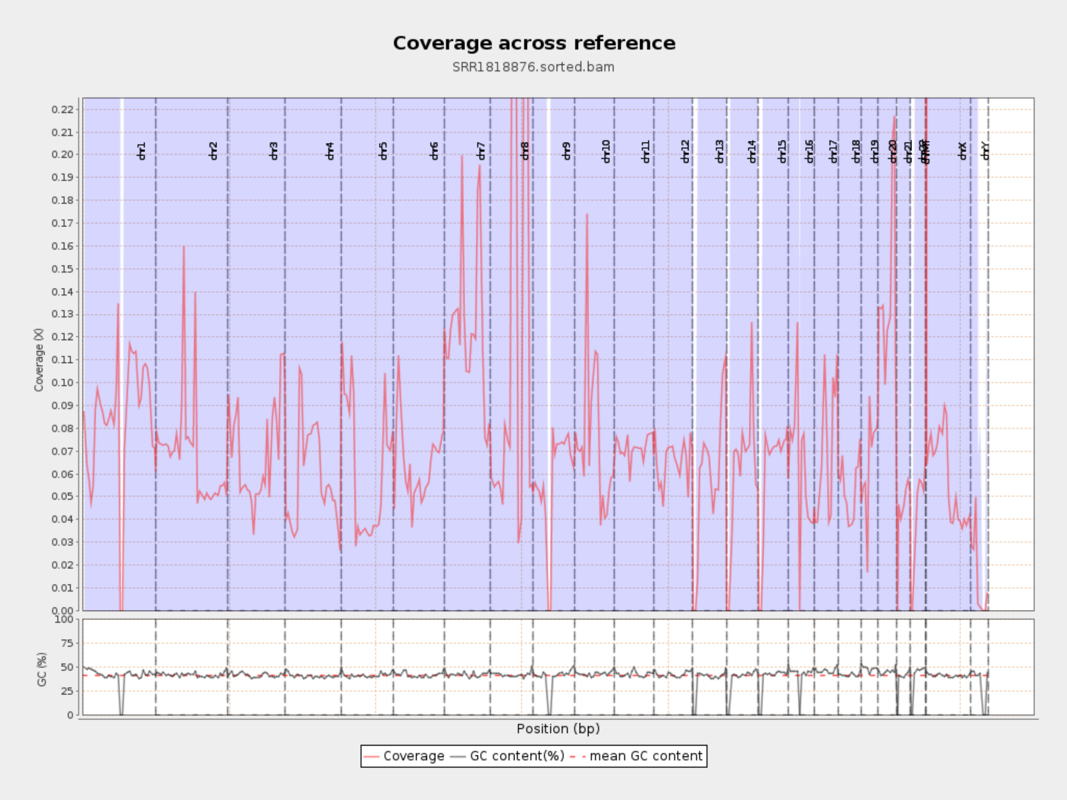
General error rate	0.64%
Mismatches	1,343,894
Insertions	34,440
Mapped reads with at least one insertion	1.37%
Deletions	73,183
Mapped reads with at least one deletion	2.96%
Homopolymer indels	39.68%

2.6. Chromosome stats

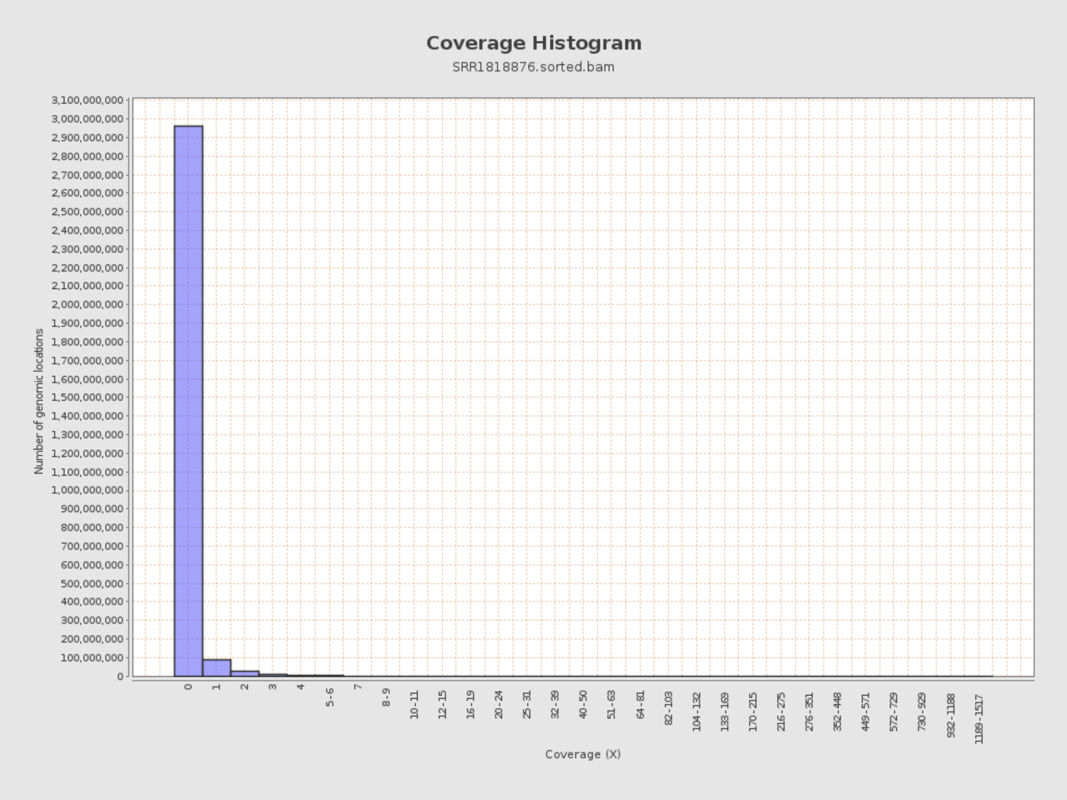
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20949116	0.084	1.279
chr2	243199373	16754246	0.0689	1.3562
chr3	198022430	13774333	0.0696	0.3997
chr4	191154276	11250740	0.0589	0.5251
chr5	180915260	11259342	0.0622	0.4099
chr6	171115067	11028308	0.0644	0.4298
chr7	159138663	19724014	0.1239	1.7403

chr8	146364022	20012090	0.1367	0.7133
chr9	141213431	8123330	0.0575	0.6611
chr10	135534747	10203981	0.0753	1.1214
chr11	135006516	9639535	0.0714	0.4931
chr12	133851895	8784484	0.0656	0.3951
chr13	115169878	6807735	0.0591	0.3662
chr14	107349540	6632847	0.0618	0.4214
chr15	102531392	6082447	0.0593	0.3762
chr16	90354753	5578161	0.0617	0.9668
chr17	81195210	5559338	0.0685	0.5082
chr18	78077248	4164370	0.0533	0.7573
chr19	59128983	3801875	0.0643	1.1134
chr20	63025520	9159608	0.1453	0.6384
chr21	48129895	2146855	0.0446	0.4128
chr22	51304566	1988092	0.0388	0.3481
chrMT	16571	239936	14.4793	9.3917
chrX	155270560	9019371	0.0581	0.4505
chrY	59373566	832871	0.014	1.1145

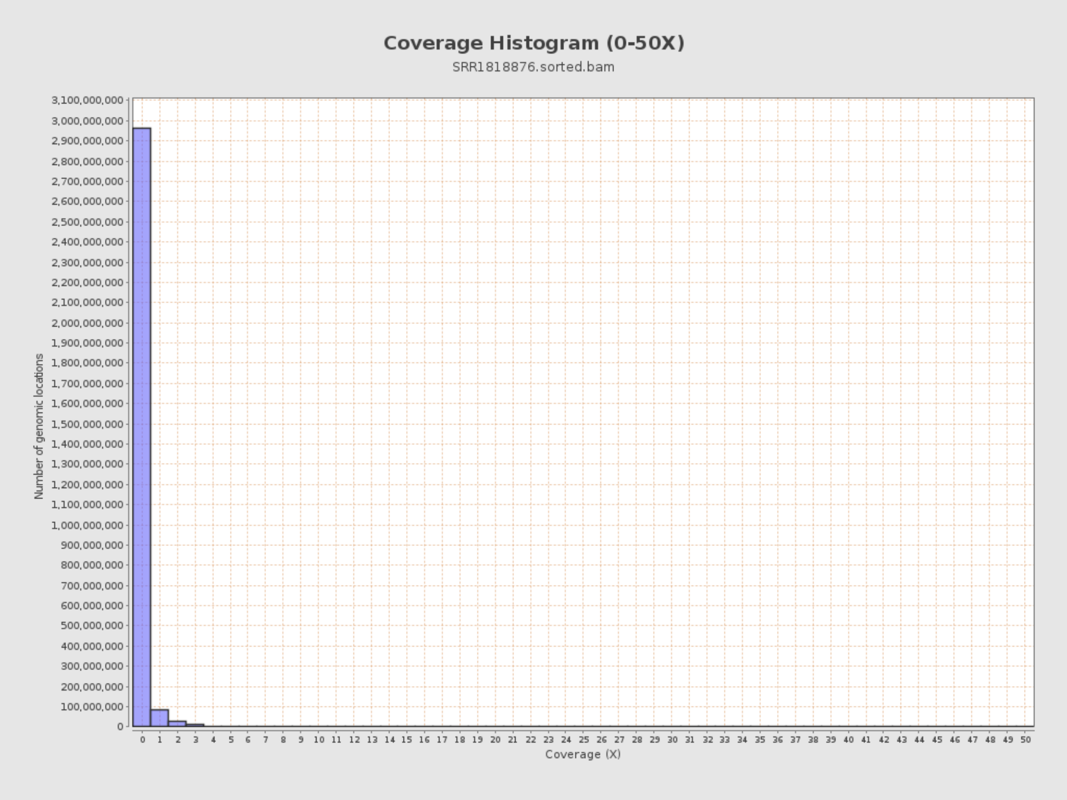
3. Results : Coverage across reference



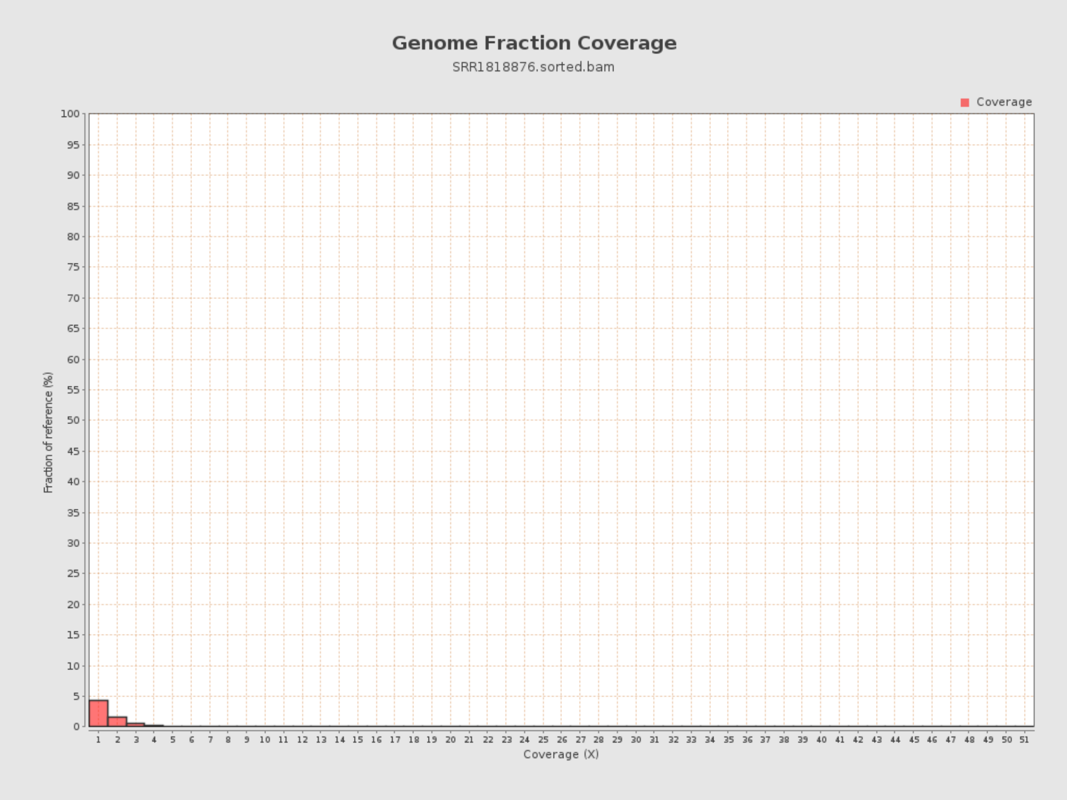
4. Results : Coverage Histogram



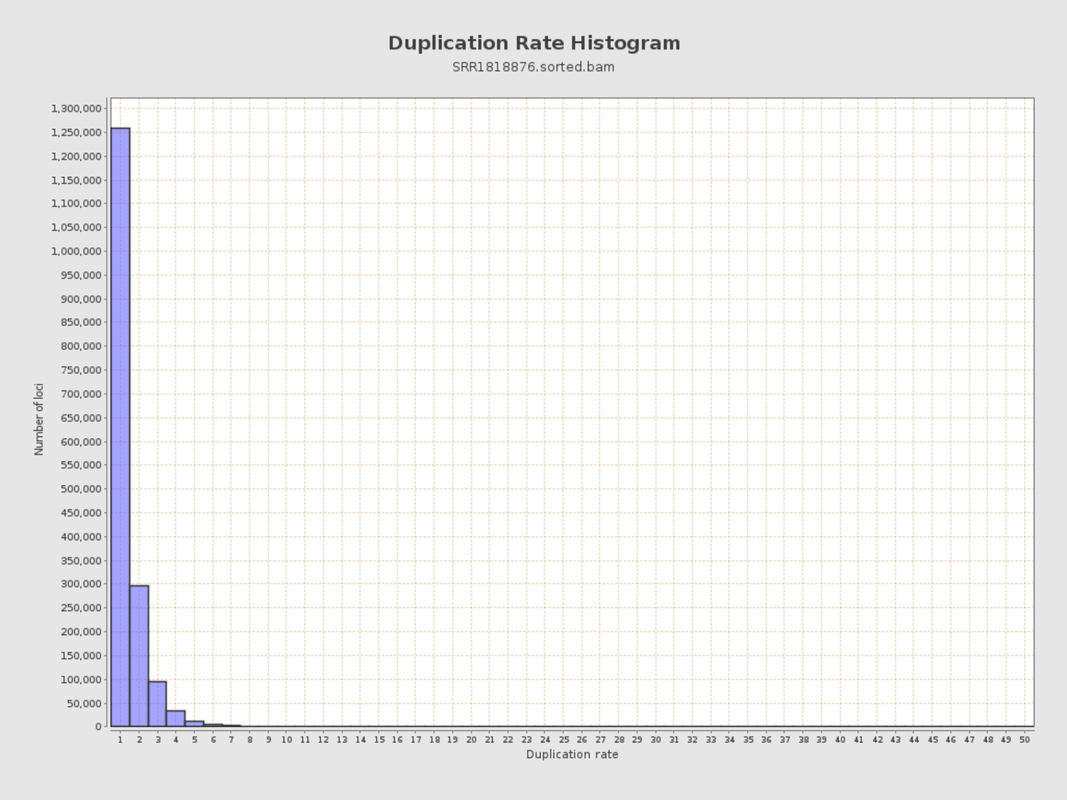
5. Results : Coverage Histogram (0-50X)



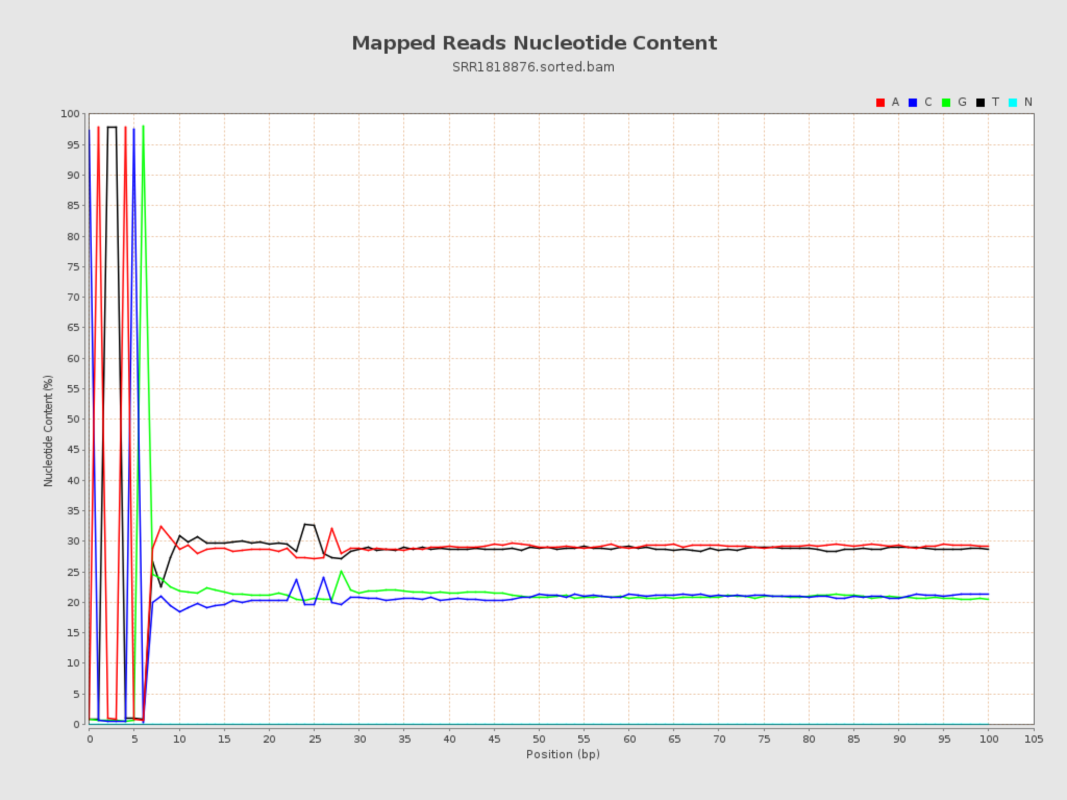
6. Results : Genome Fraction Coverage



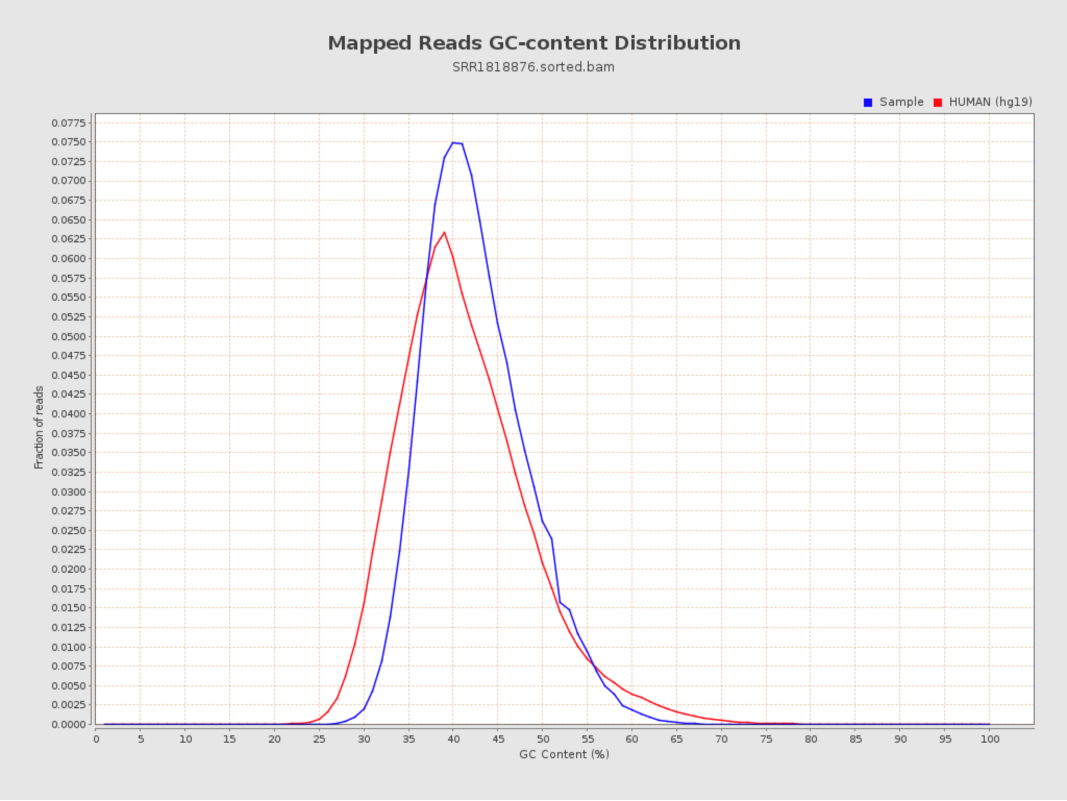
7. Results : Duplication Rate Histogram



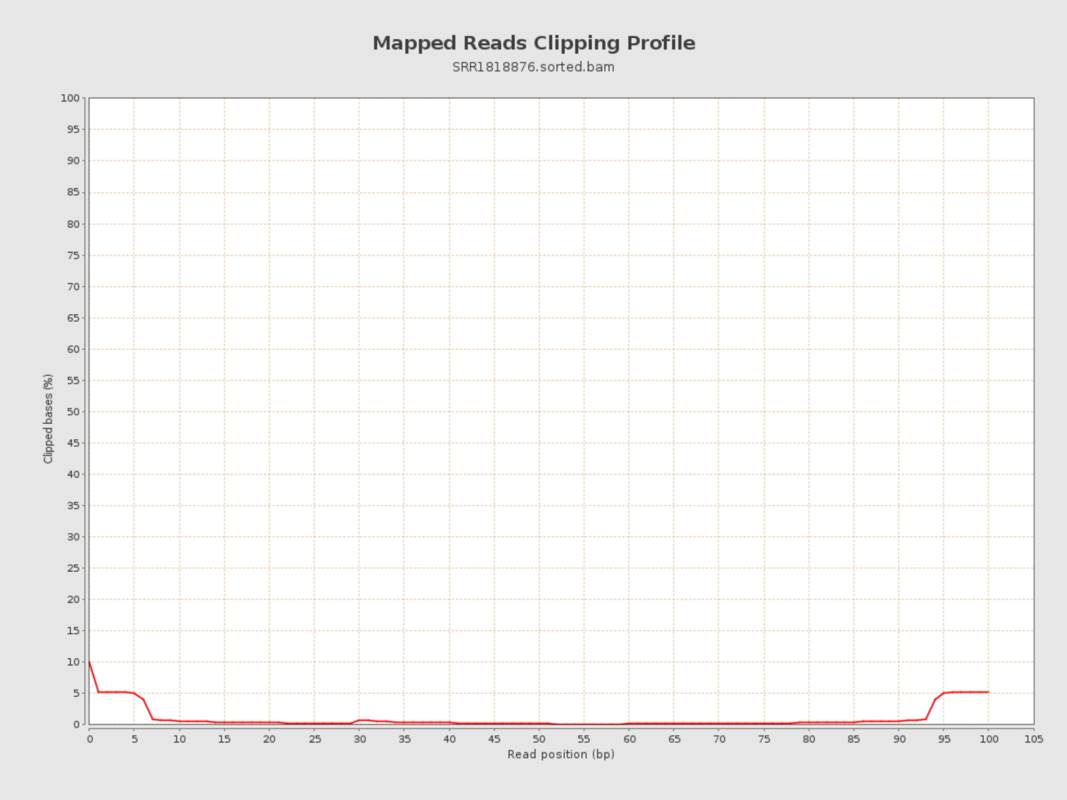
8. Results : Mapped Reads Nucleotide Content



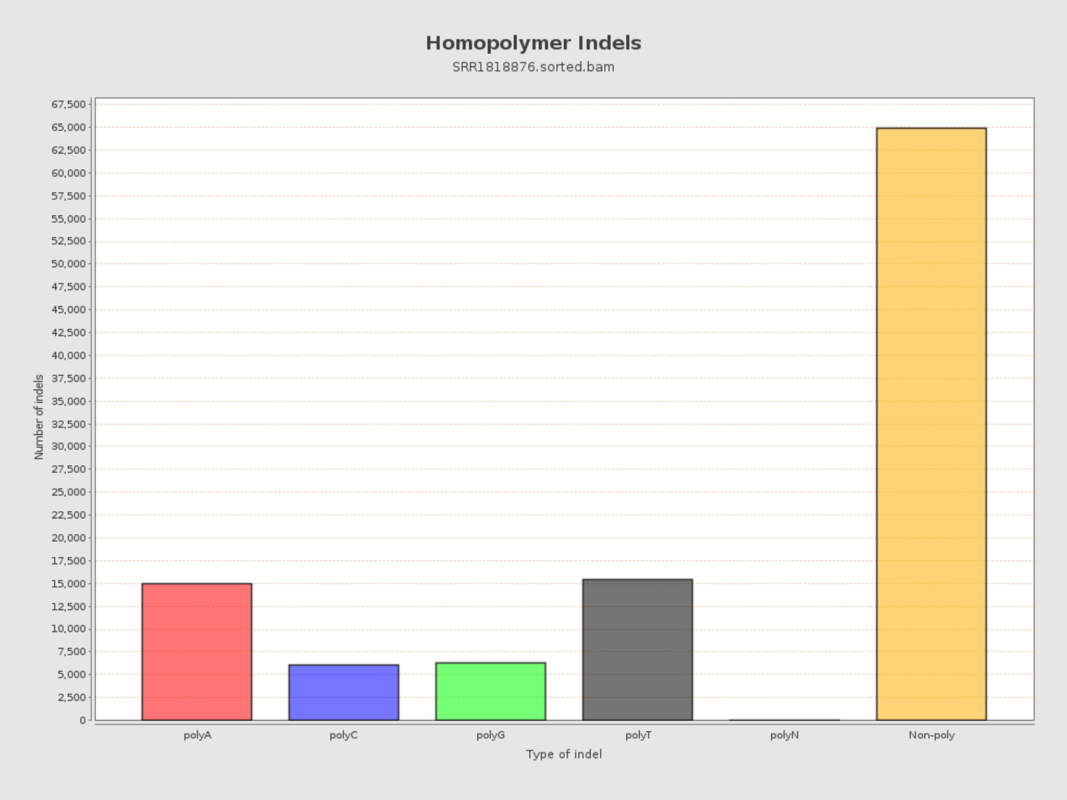
9. Results : Mapped Reads GC-content Distribution



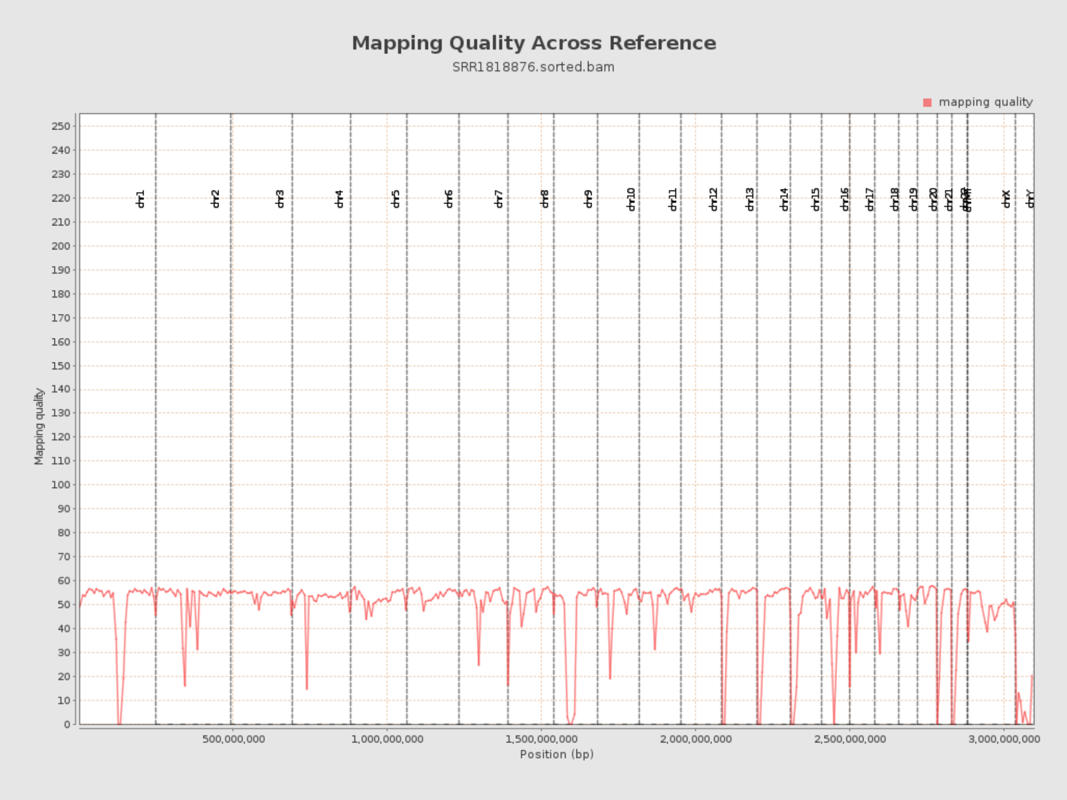
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram