Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 12:41:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818978.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_SRR1818978 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818978.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 12:41:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818978.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	719,578
Mapped reads	656,887 / 91.29%
Unmapped reads	62,691 / 8.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,904 / 1.52%
Read min/max/mean length	30 / 101 / 101.58
Duplicated reads (estimated)	192,288 / 26.72%
Duplication rate	24.74%
Clipped reads	661,974 / 91.99%

2.2. ACGT Content

Number/percentage of A's	17,440,143 / 28.73%
Number/percentage of C's	12,334,989 / 20.32%
Number/percentage of T's	17,595,777 / 28.99%
Number/percentage of G's	13,319,711 / 21.95%
Number/percentage of N's	2,891 / 0%
GC Percentage	42.27%

2.3. Coverage

Mean	0.0196

Standard Deviation	0.2757

2.4. Mapping Quality

Mean Mapping Quality	49.04

2.5. Mismatches and indels

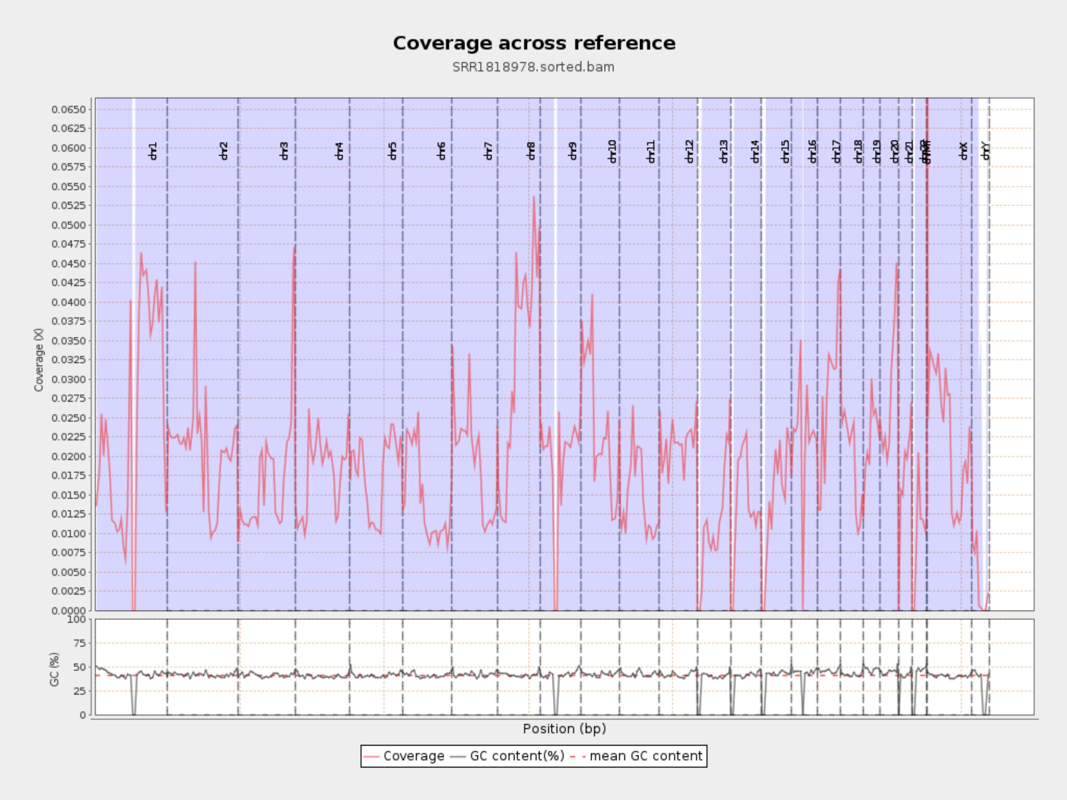
General error rate	0.67%
Mismatches	384,396
Insertions	9,539
Mapped reads with at least one insertion	1.41%
Deletions	20,141
Mapped reads with at least one deletion	3%
Homopolymer indels	42.56%

2.6. Chromosome stats

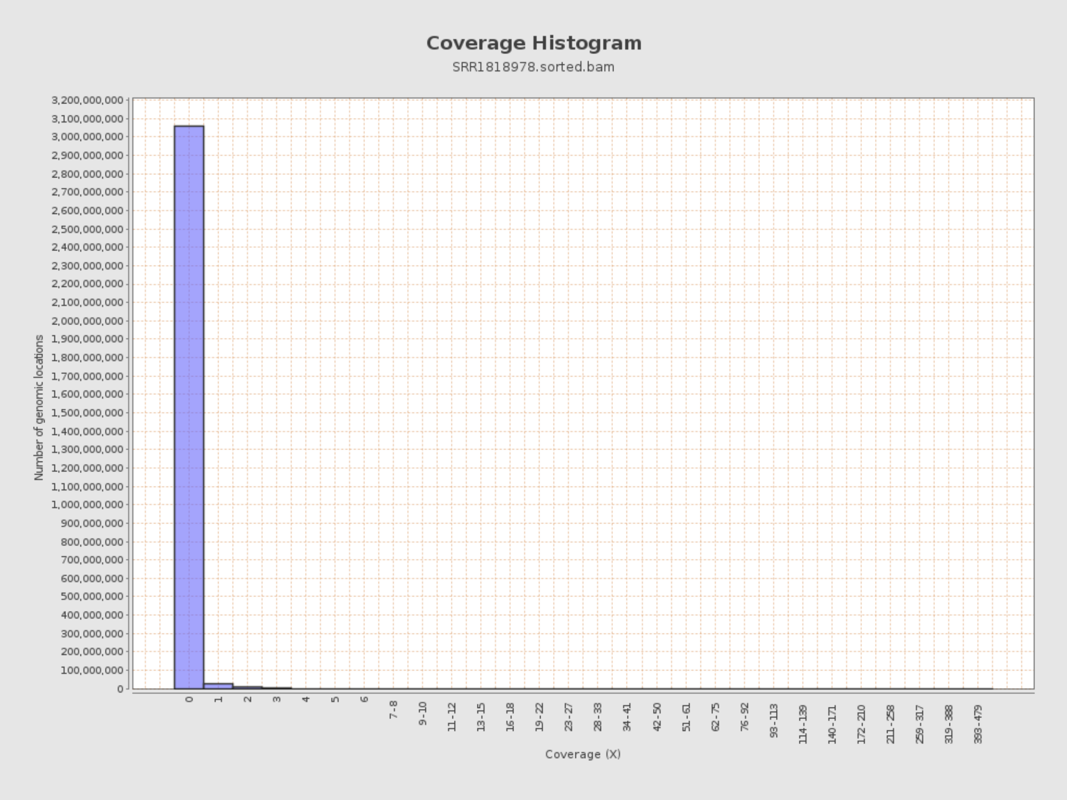
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6033808	0.0242	0.4555
chr2	243199373	5071048	0.0209	0.3687
chr3	198022430	3350086	0.0169	0.1903
chr4	191154276	3430842	0.0179	0.2056
chr5	180915260	3246199	0.0179	0.198
chr6	171115067	2467485	0.0144	0.189
chr7	159138663	3118248	0.0196	0.288

chr8	146364022	4787618	0.0327	0.2851
chr9	141213431	2705438	0.0192	0.2653
chr10	135534747	3307338	0.0244	0.3167
chr11	135006516	1977852	0.0147	0.1957
chr12	133851895	2896301	0.0216	0.2184
chr13	115169878	1255921	0.0109	0.1511
chr14	107349540	1477381	0.0138	0.1778
chr15	102531392	1490267	0.0145	0.1757
chr16	90354753	1991492	0.022	0.3153
chr17	81195210	2259604	0.0278	0.2615
chr18	78077248	1536063	0.0197	0.3073
chr19	59128983	1339939	0.0227	0.4161
chr20	63025520	1808427	0.0287	0.2581
chr21	48129895	863332	0.0179	0.2053
chr22	51304566	511536	0.01	0.1622
chrMT	16571	8141	0.4913	1.021
chrX	155270560	3587768	0.0231	0.2378
chrY	59373566	208881	0.0035	0.2648

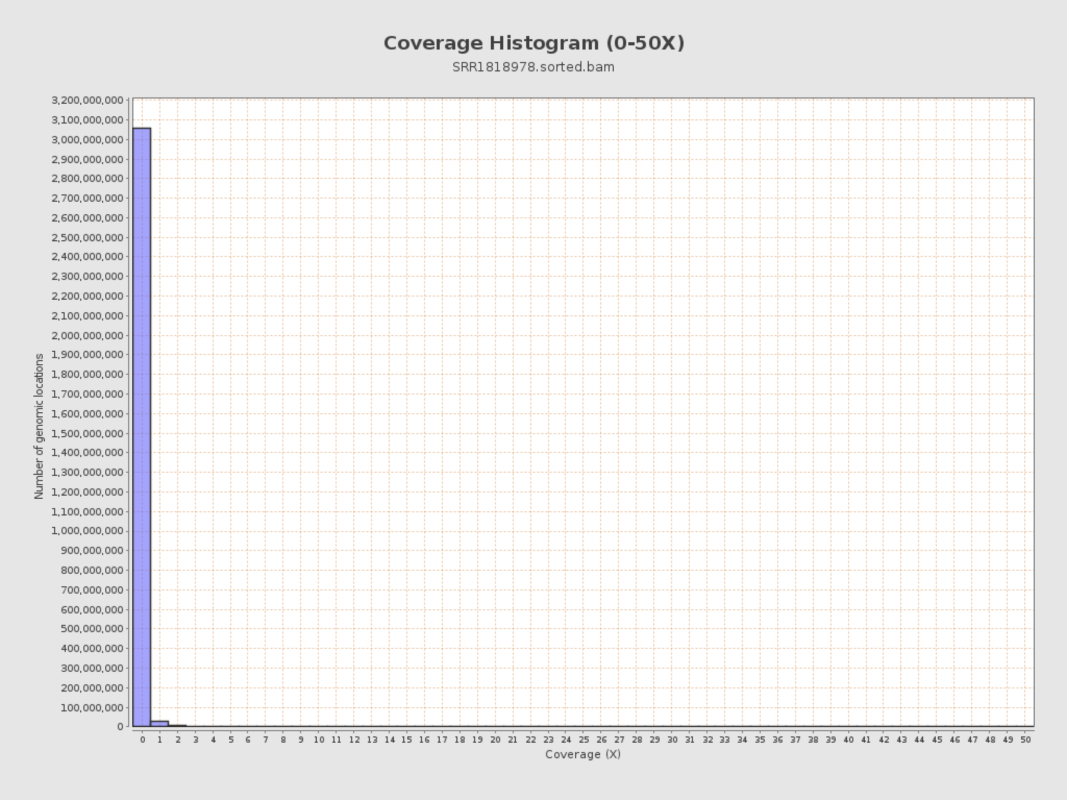
3. Results : Coverage across reference



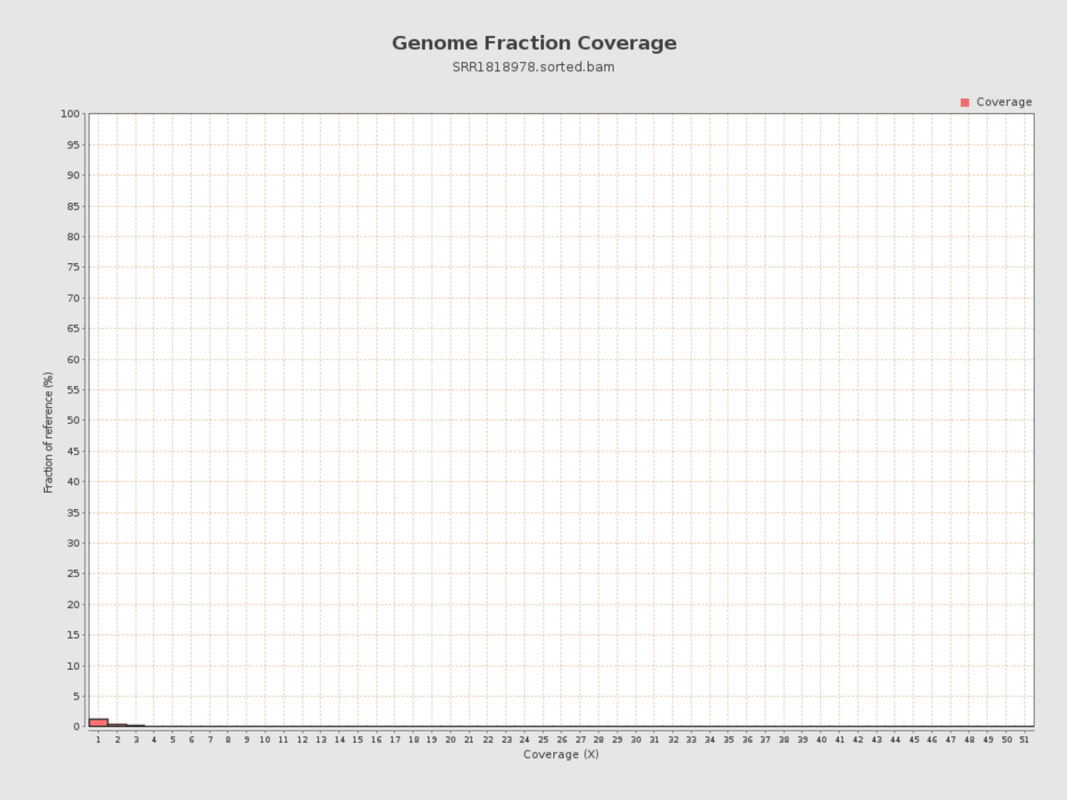
4. Results : Coverage Histogram



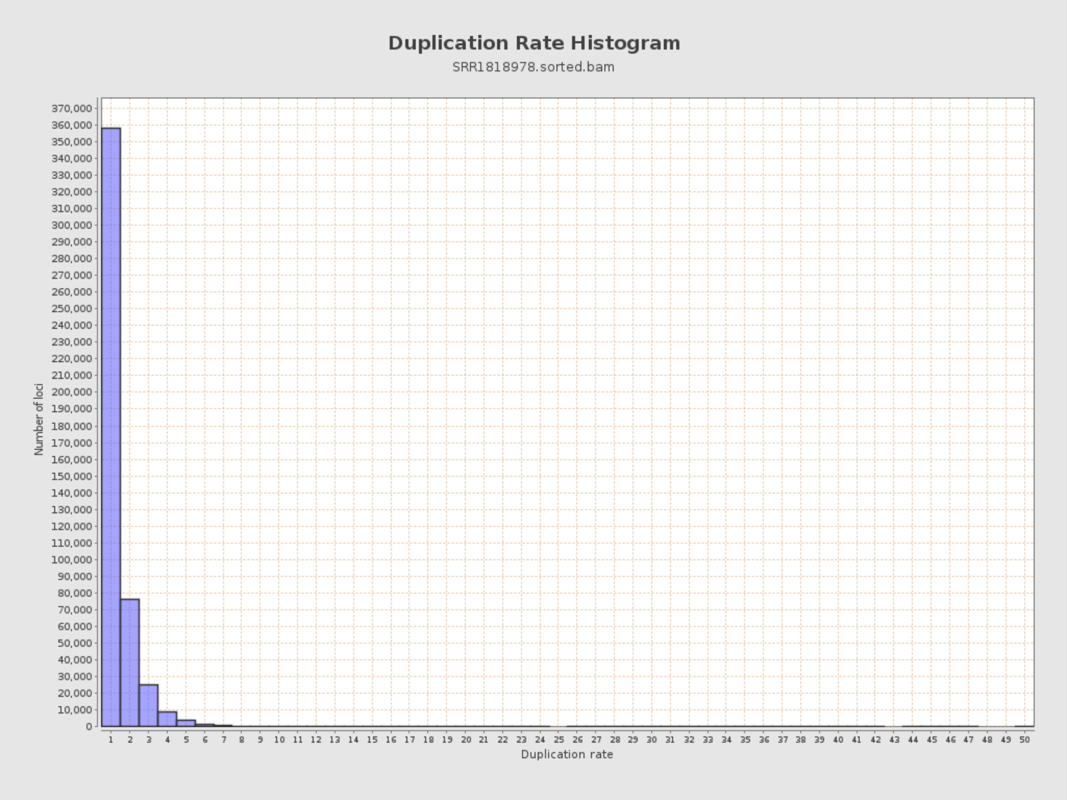
5. Results : Coverage Histogram (0-50X)



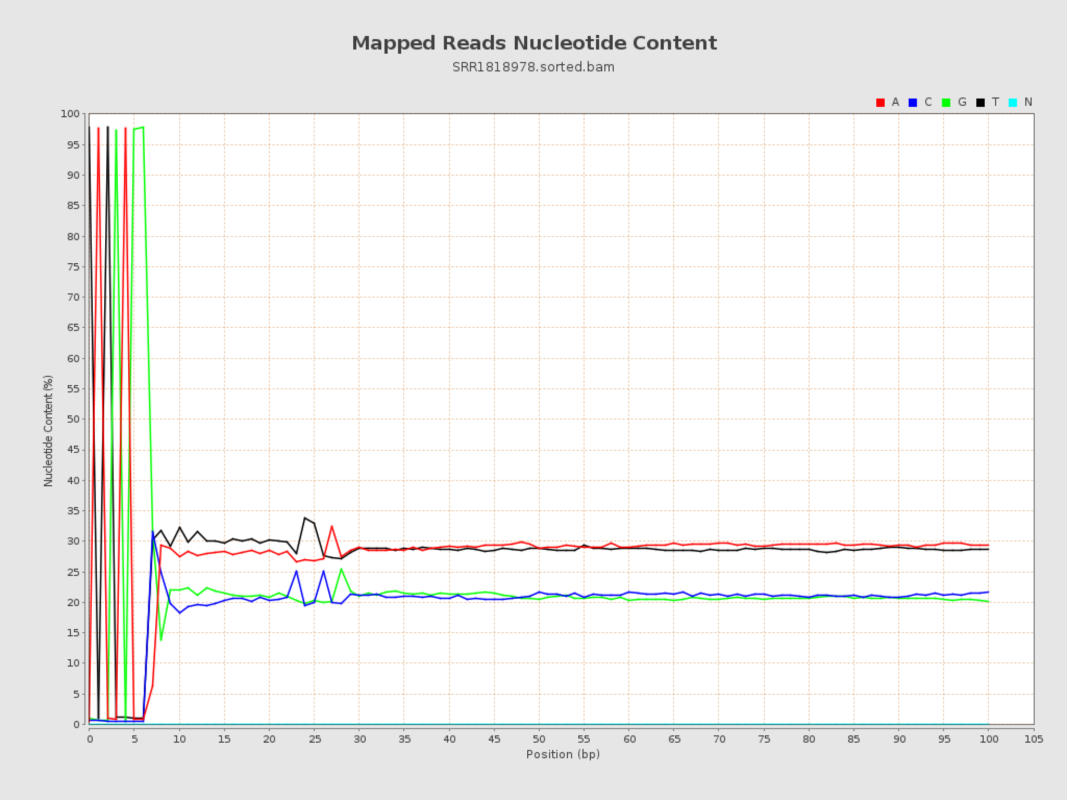
6. Results : Genome Fraction Coverage



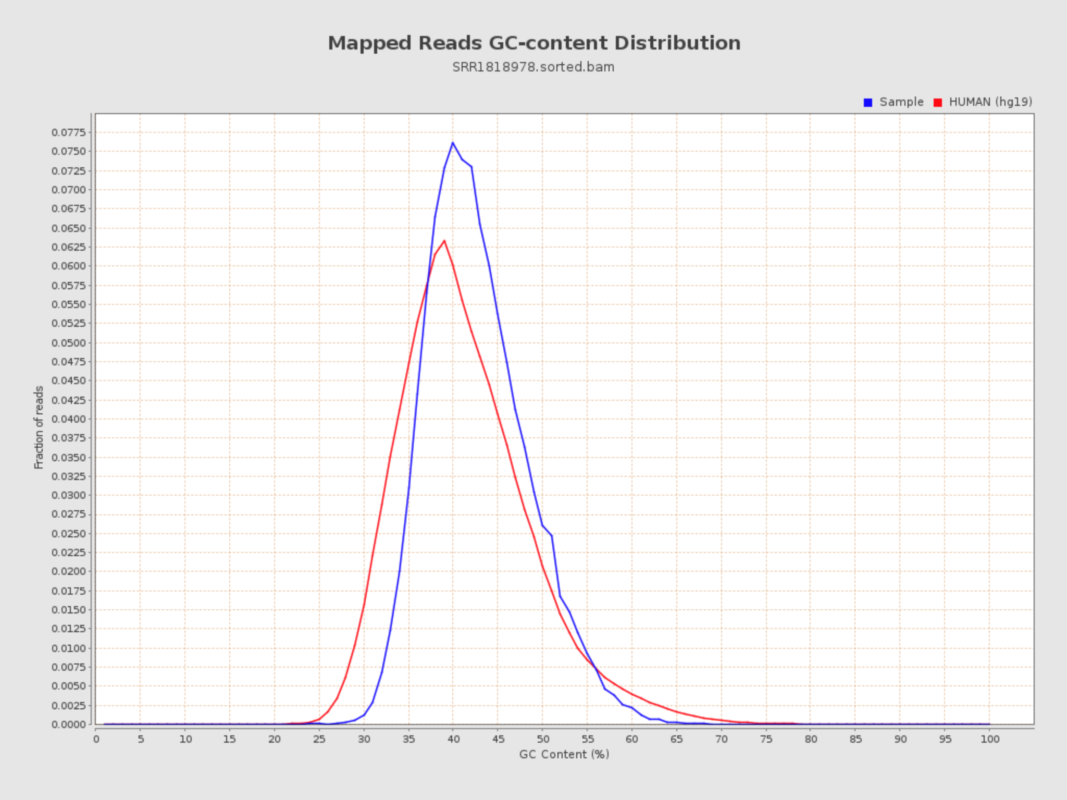
7. Results : Duplication Rate Histogram



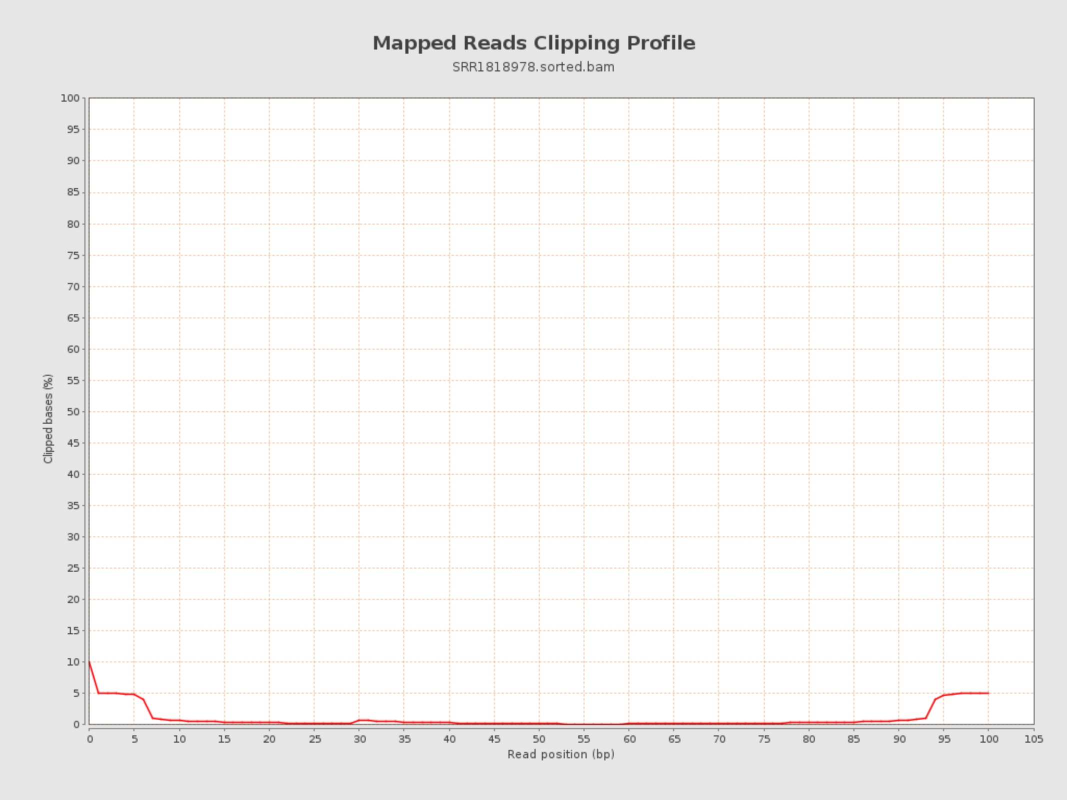
8. Results : Mapped Reads Nucleotide Content



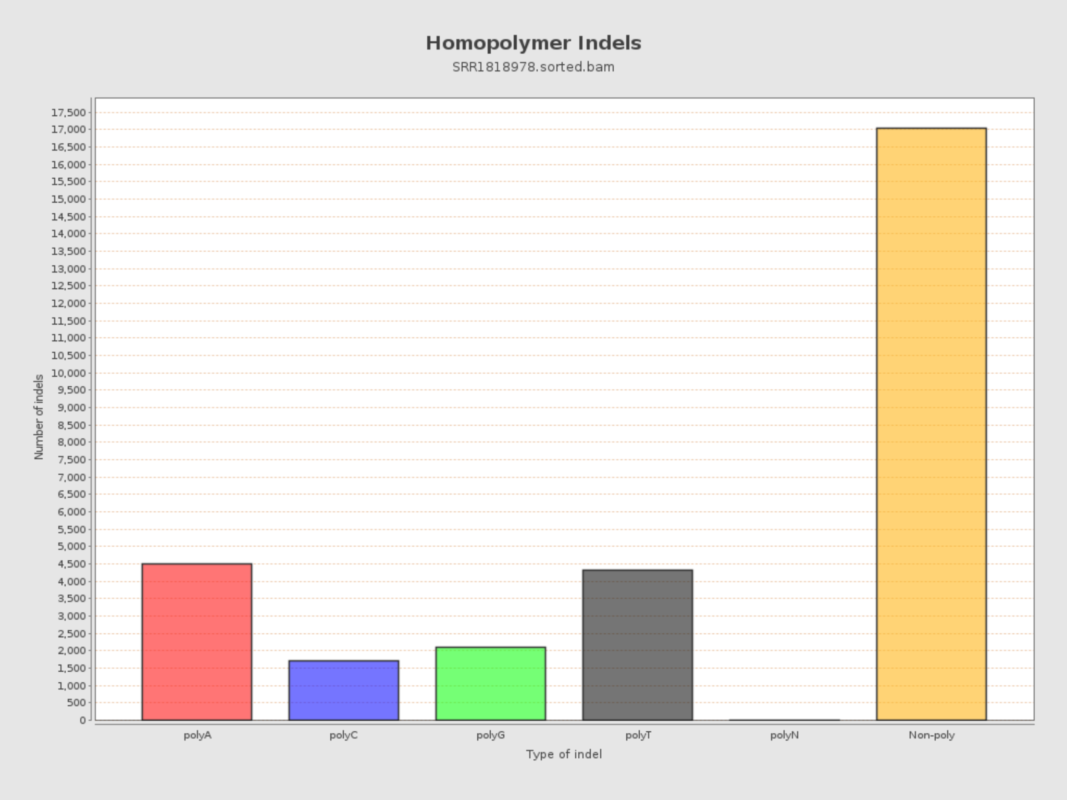
9. Results : Mapped Reads GC-content Distribution



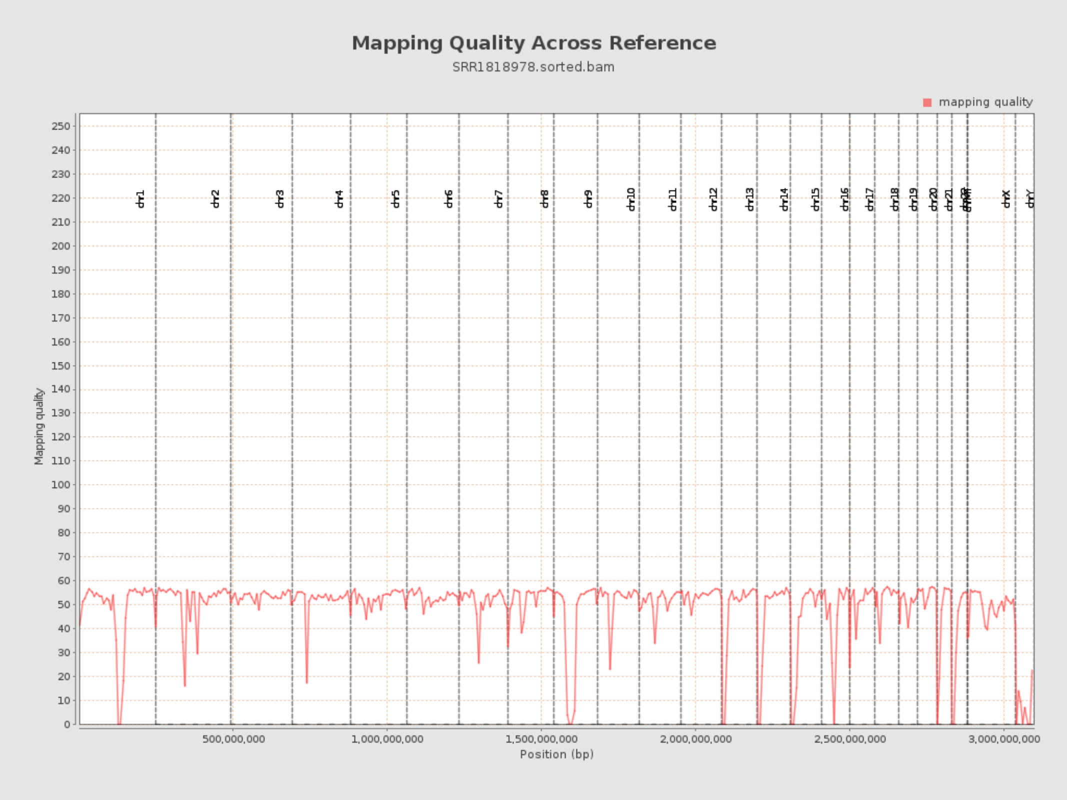
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram