Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 02:59:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818874.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_SRR1818874 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818874.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 02:59:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818874.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,988,287
Mapped reads	1,957,249 / 98.44%
Unmapped reads	31,038 / 1.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	31,369 / 1.58%
Read min/max/mean length	30 / 101 / 101.61
Duplicated reads (estimated)	546,735 / 27.5%
Duplication rate	24.25%
Clipped reads	1,974,369 / 99.3%

2.2. ACGT Content

Number/percentage of A's	52,594,365 / 29.05%
Number/percentage of C's	39,085,212 / 21.59%
Number/percentage of T's	51,295,783 / 28.34%
Number/percentage of G's	38,054,725 / 21.02%
Number/percentage of N's	2,663 / 0%
GC Percentage	42.61%

2.3. Coverage

Mean	0.0585

Standard Deviation	0.6895

2.4. Mapping Quality

Mean Mapping Quality	49.33

2.5. Mismatches and indels

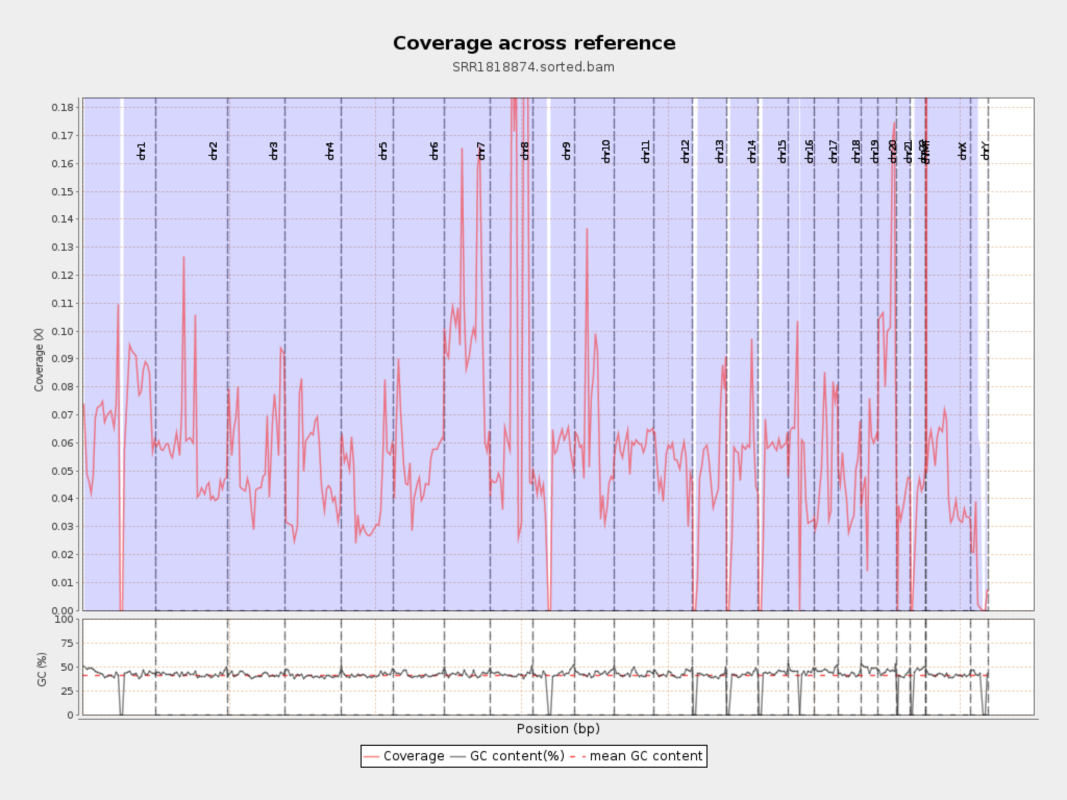
General error rate	0.65%
Mismatches	1,106,776
Insertions	24,596
Mapped reads with at least one insertion	1.22%
Deletions	59,901
Mapped reads with at least one deletion	2.99%
Homopolymer indels	41.64%

2.6. Chromosome stats

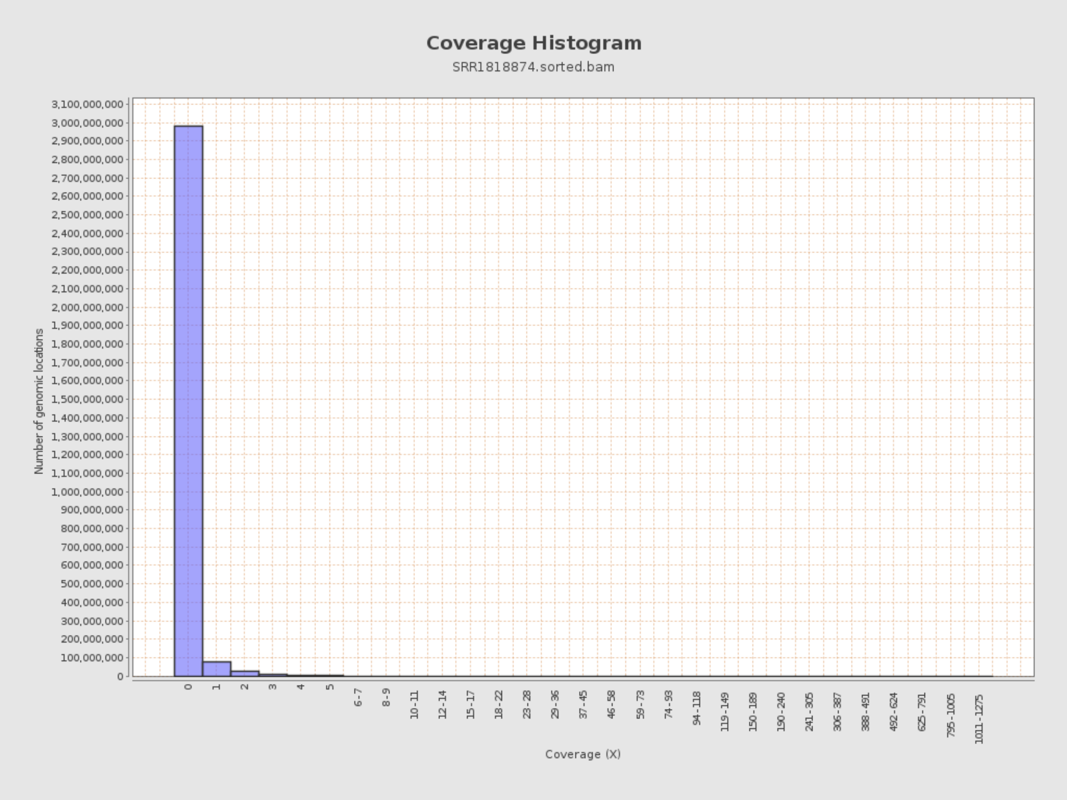
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17179826	0.0689	1.0407
chr2	243199373	13646214	0.0561	1.0013
chr3	198022430	11355169	0.0573	0.3463
chr4	191154276	9180418	0.048	0.407
chr5	180915260	7911328	0.0437	0.3267
chr6	171115067	8971590	0.0524	0.3646
chr7	159138663	16298466	0.1024	1.4691

chr8	146364022	15978839	0.1092	0.6114
chr9	141213431	6743559	0.0478	0.5467
chr10	135534747	8413933	0.0621	0.88
chr11	135006516	8058059	0.0597	0.4205
chr12	133851895	6967077	0.0521	0.3331
chr13	115169878	5487925	0.0477	0.3148
chr14	107349540	5317461	0.0495	0.347
chr15	102531392	5014729	0.0489	0.3166
chr16	90354753	4541865	0.0503	0.7588
chr17	81195210	4436518	0.0546	0.426
chr18	78077248	3505563	0.0449	0.6245
chr19	59128983	3073526	0.052	0.8538
chr20	63025520	7336483	0.1164	0.533
chr21	48129895	1772734	0.0368	0.3324
chr22	51304566	1619648	0.0316	0.283
chrMT	16571	275798	16.6434	10.8702
chrX	155270560	7410144	0.0477	0.375
chrY	59373566	650798	0.011	0.8645

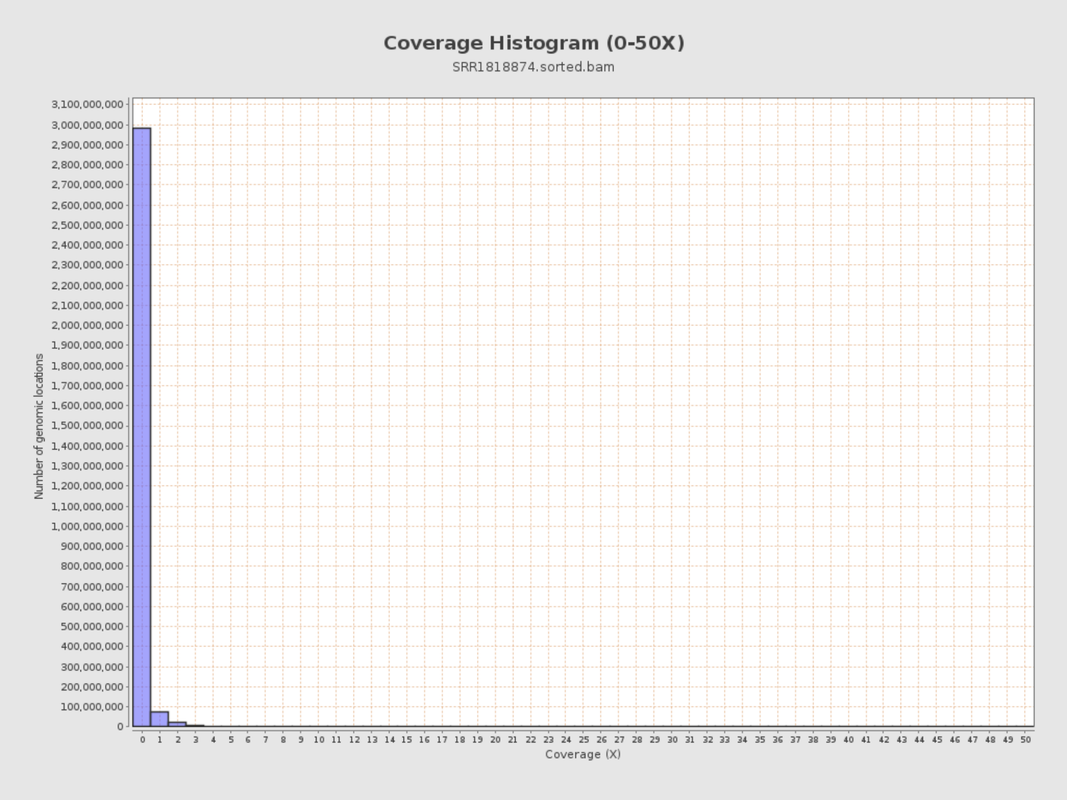
3. Results : Coverage across reference



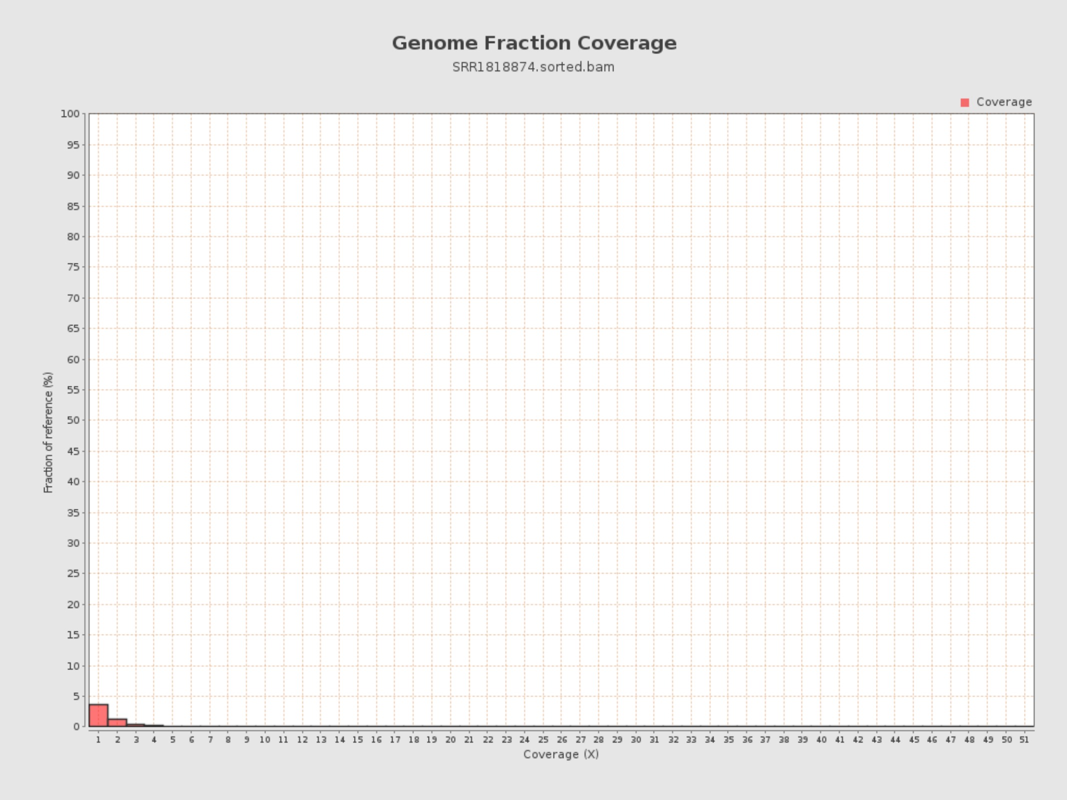
4. Results : Coverage Histogram



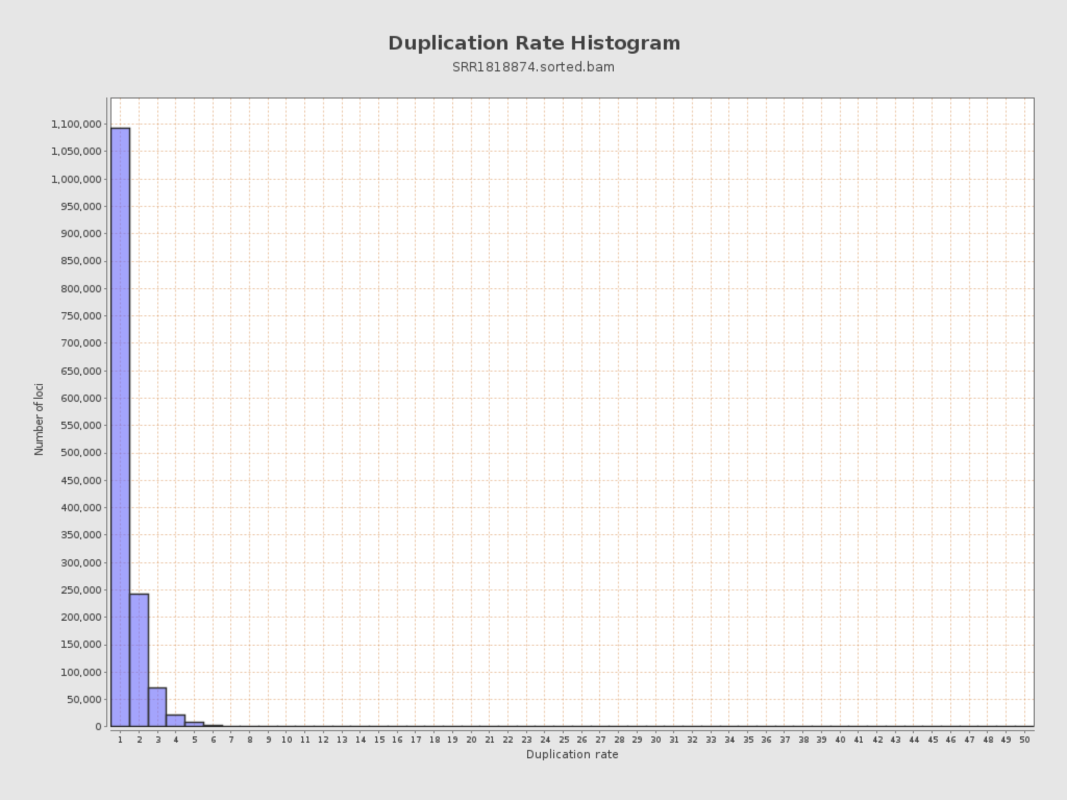
5. Results : Coverage Histogram (0-50X)



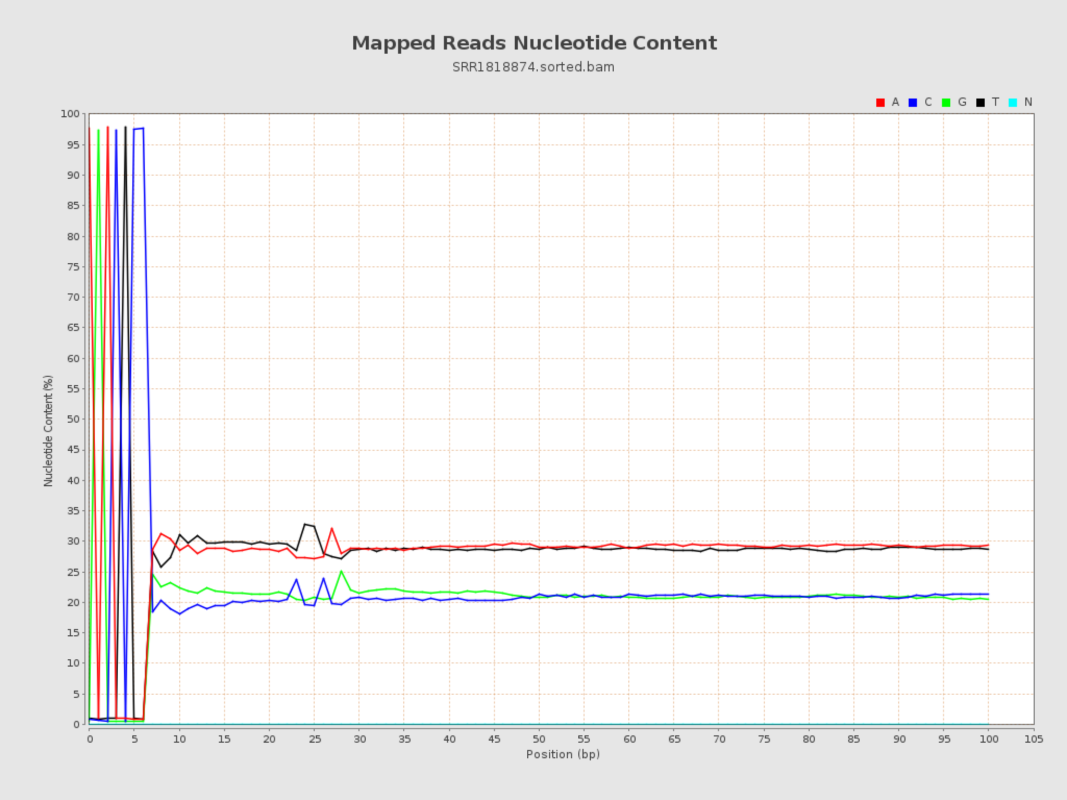
6. Results : Genome Fraction Coverage



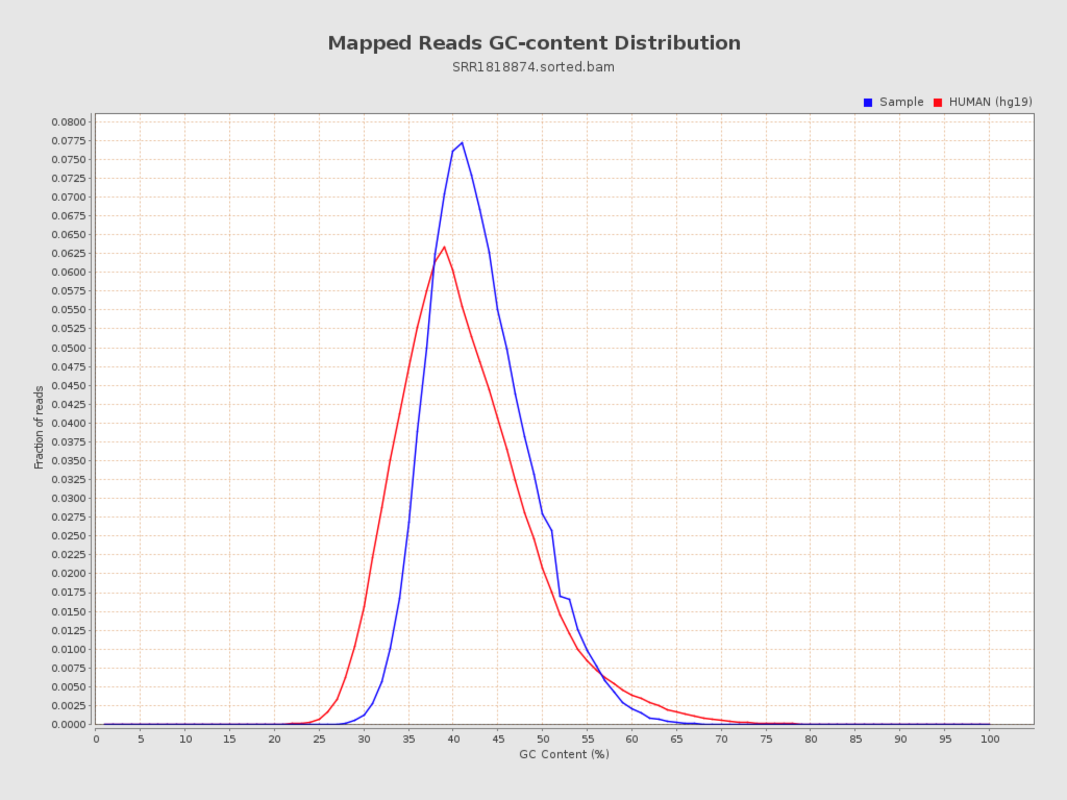
7. Results : Duplication Rate Histogram



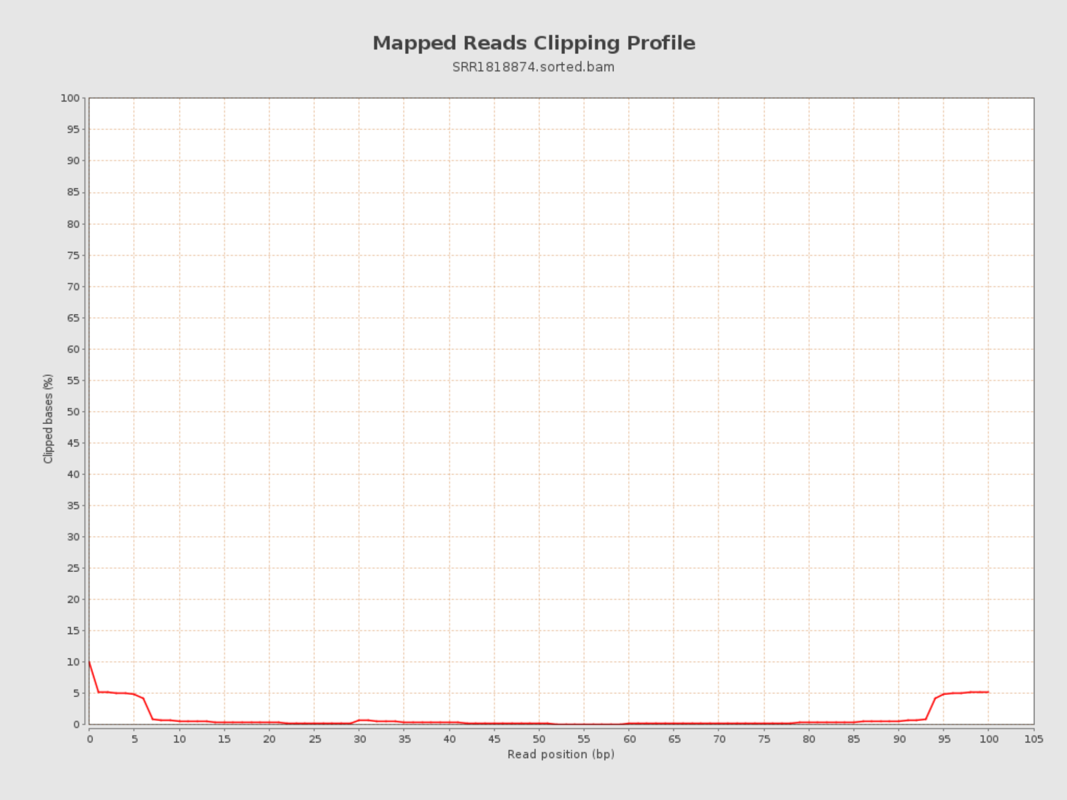
8. Results : Mapped Reads Nucleotide Content



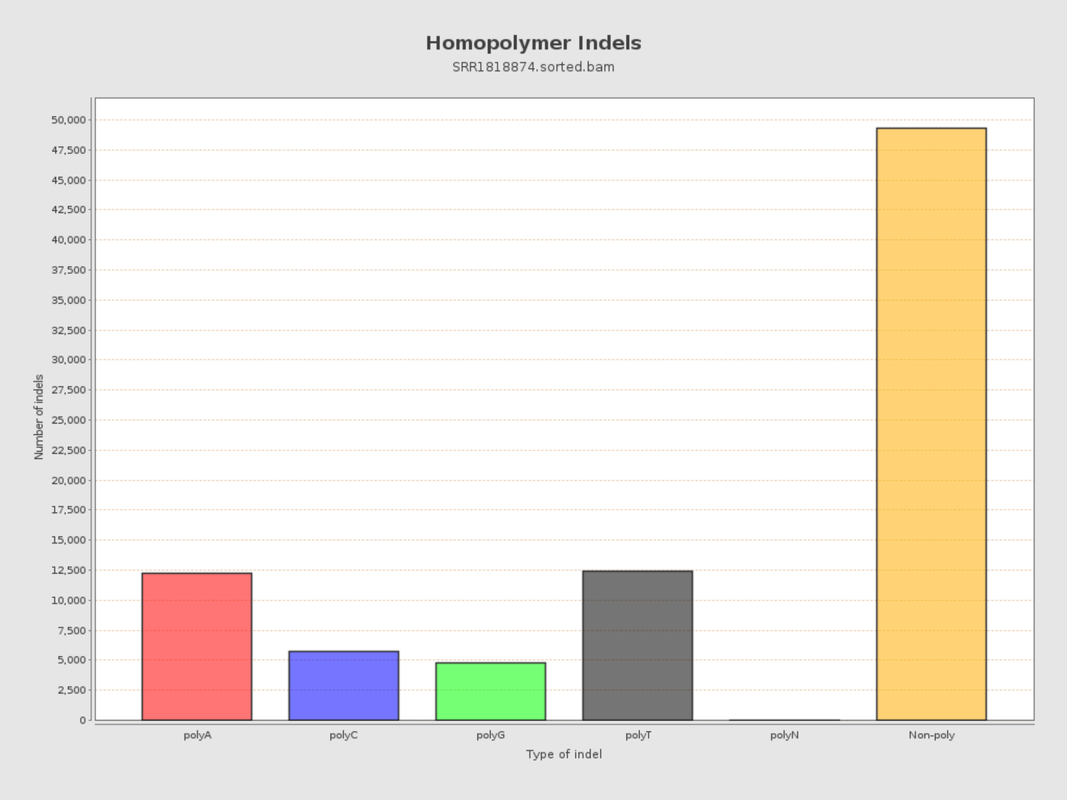
9. Results : Mapped Reads GC-content Distribution



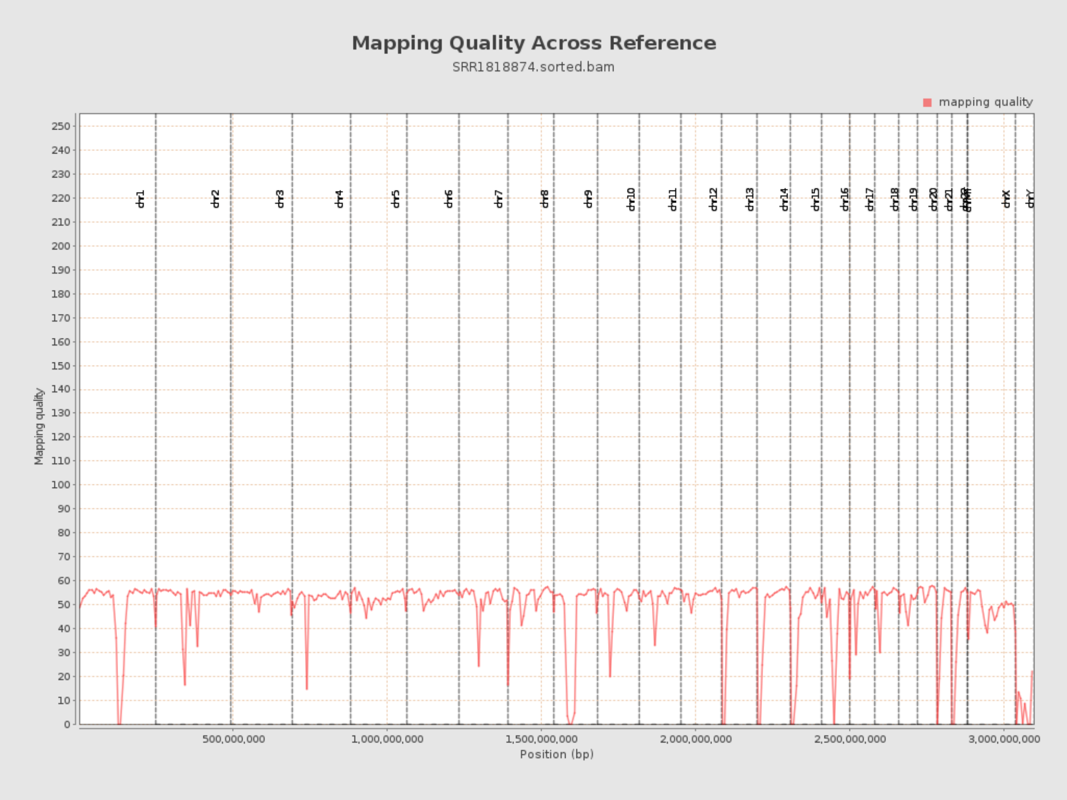
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram