Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 02:47:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818873.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_SRR1818873 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818873.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 02:47:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818873.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,177,745
Mapped reads	2,113,395 / 97.05%
Unmapped reads	64,350 / 2.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	34,549 / 1.59%
Read min/max/mean length	30 / 101 / 101.61
Duplicated reads (estimated)	589,539 / 27.07%
Duplication rate	24.07%
Clipped reads	2,133,429 / 97.97%

2.2. ACGT Content

Number/percentage of A's	55,545,476 / 28.42%
Number/percentage of C's	41,353,913 / 21.16%
Number/percentage of T's	56,358,293 / 28.83%
Number/percentage of G's	42,217,419 / 21.6%
Number/percentage of N's	3,090 / 0%
GC Percentage	42.75%

2.3. Coverage

Mean	0.0632

Standard Deviation	0.7467

2.4. Mapping Quality

Mean Mapping Quality	49.37

2.5. Mismatches and indels

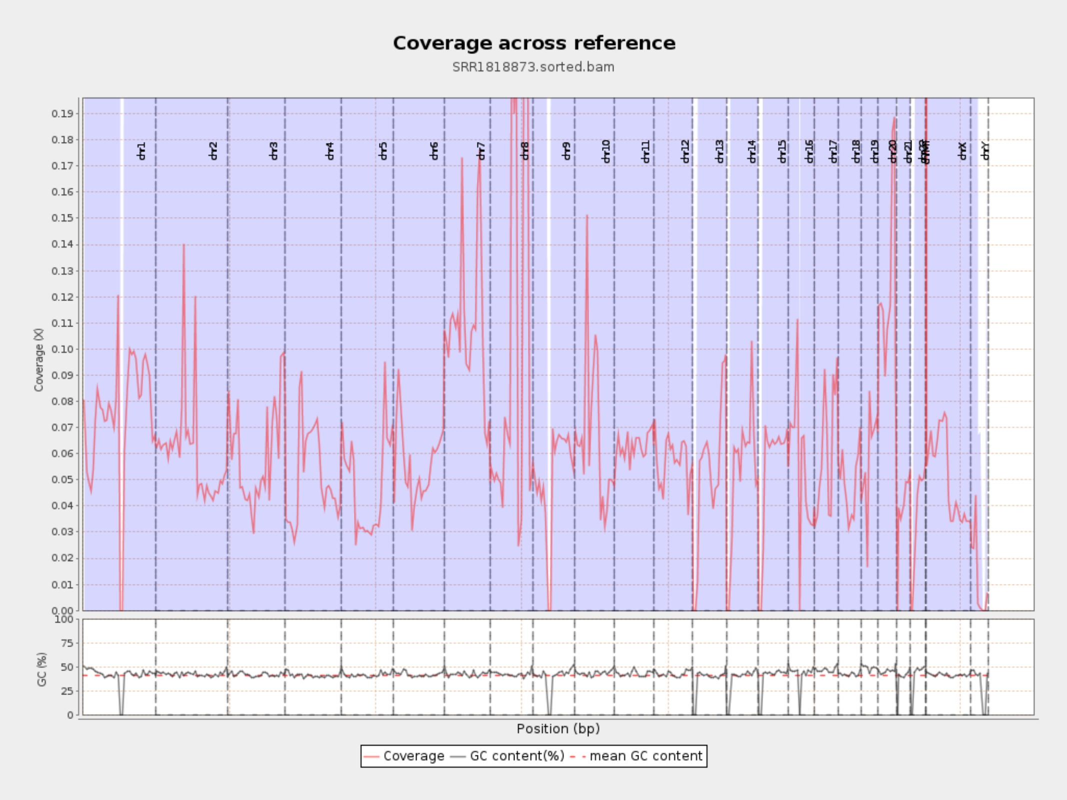
General error rate	0.64%
Mismatches	1,187,587
Insertions	25,328
Mapped reads with at least one insertion	1.16%
Deletions	64,204
Mapped reads with at least one deletion	2.97%
Homopolymer indels	40.94%

2.6. Chromosome stats

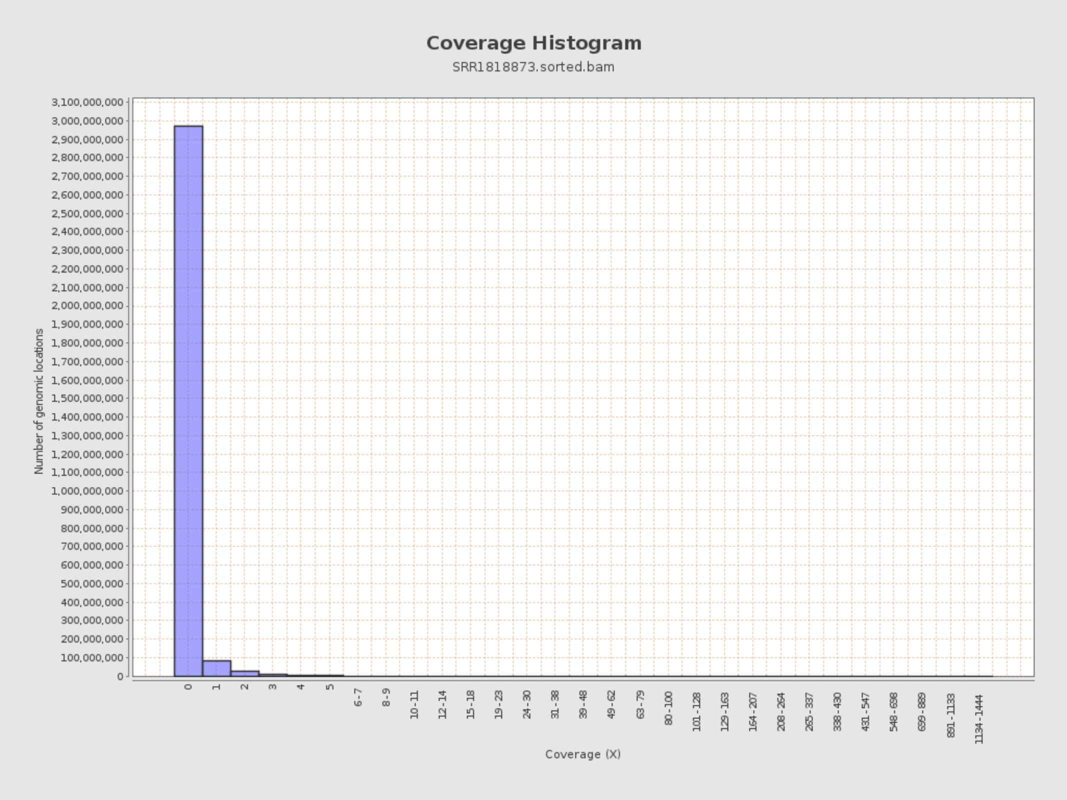
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18531885	0.0744	1.1844
chr2	243199373	14847247	0.061	1.1182
chr3	198022430	11871341	0.0599	0.3546
chr4	191154276	9890784	0.0517	0.4348
chr5	180915260	8691220	0.048	0.3391
chr6	171115067	9600625	0.0561	0.3862
chr7	159138663	17396968	0.1093	1.4929

chr8	146364022	17424850	0.1191	0.6396
chr9	141213431	7161033	0.0507	0.5751
chr10	135534747	9012450	0.0665	0.9695
chr11	135006516	8482809	0.0628	0.4396
chr12	133851895	7667855	0.0573	0.349
chr13	115169878	6069721	0.0527	0.3299
chr14	107349540	5788472	0.0539	0.3608
chr15	102531392	5423337	0.0529	0.3305
chr16	90354753	4916123	0.0544	0.8143
chr17	81195210	4888179	0.0602	0.457
chr18	78077248	3793680	0.0486	0.6608
chr19	59128983	3432054	0.058	1.0524
chr20	63025520	8051600	0.1278	0.5598
chr21	48129895	1908603	0.0397	0.346
chr22	51304566	1766126	0.0344	0.3024
chrMT	16571	331444	20.0014	12.3358
chrX	155270560	7923824	0.051	0.3995
chrY	59373566	730373	0.0123	0.9558

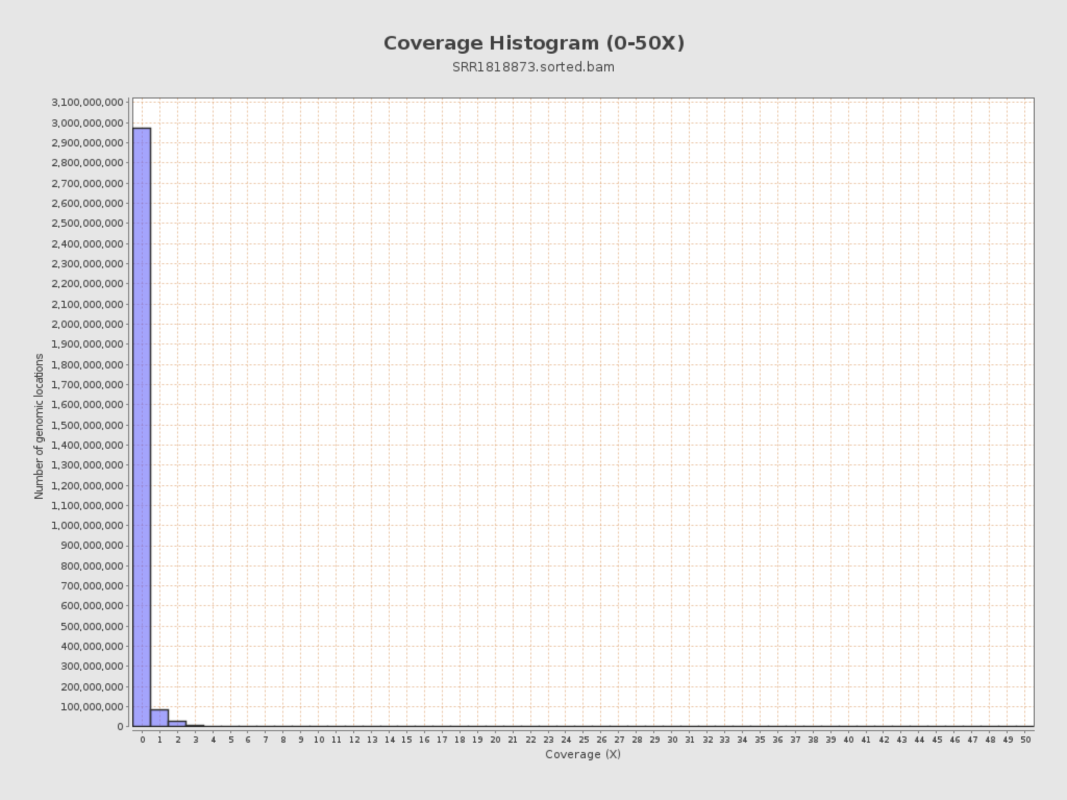
3. Results : Coverage across reference



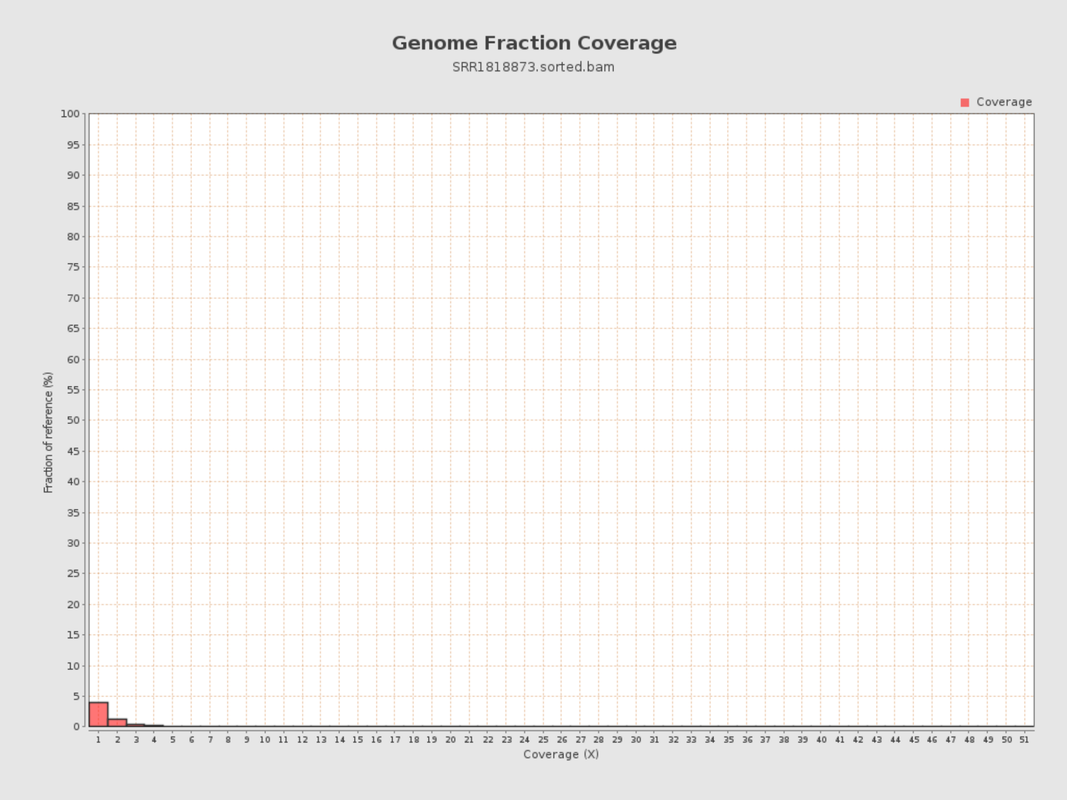
4. Results : Coverage Histogram



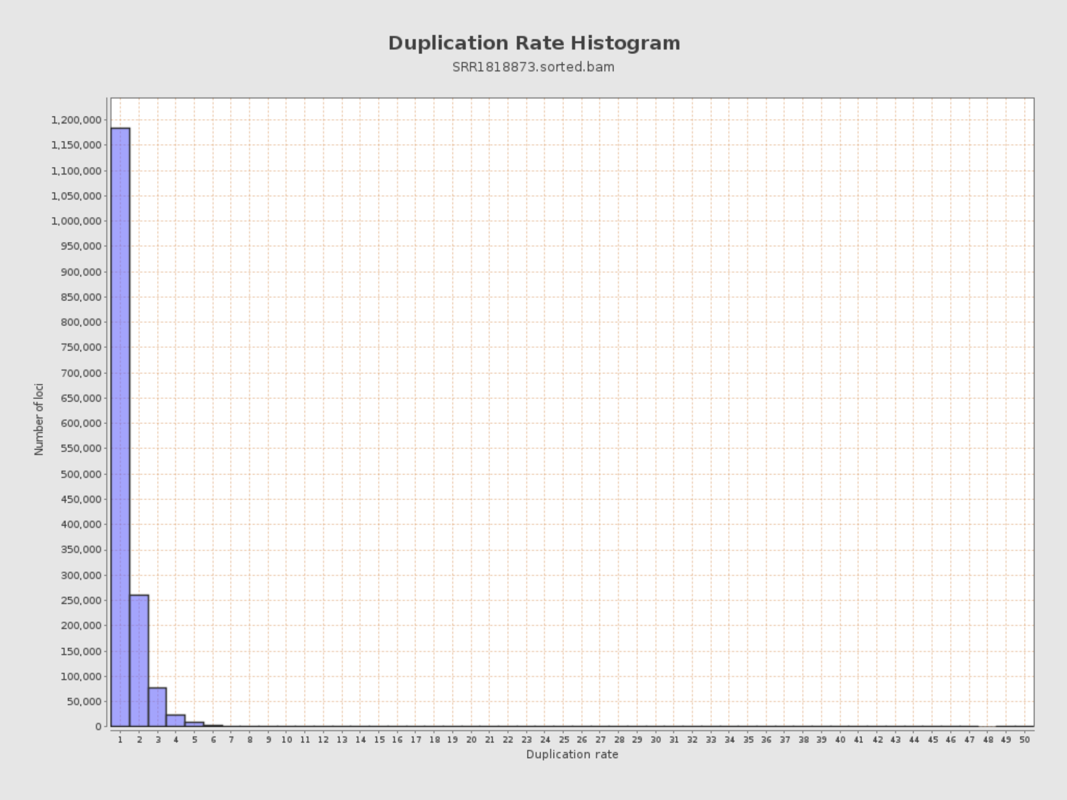
5. Results : Coverage Histogram (0-50X)



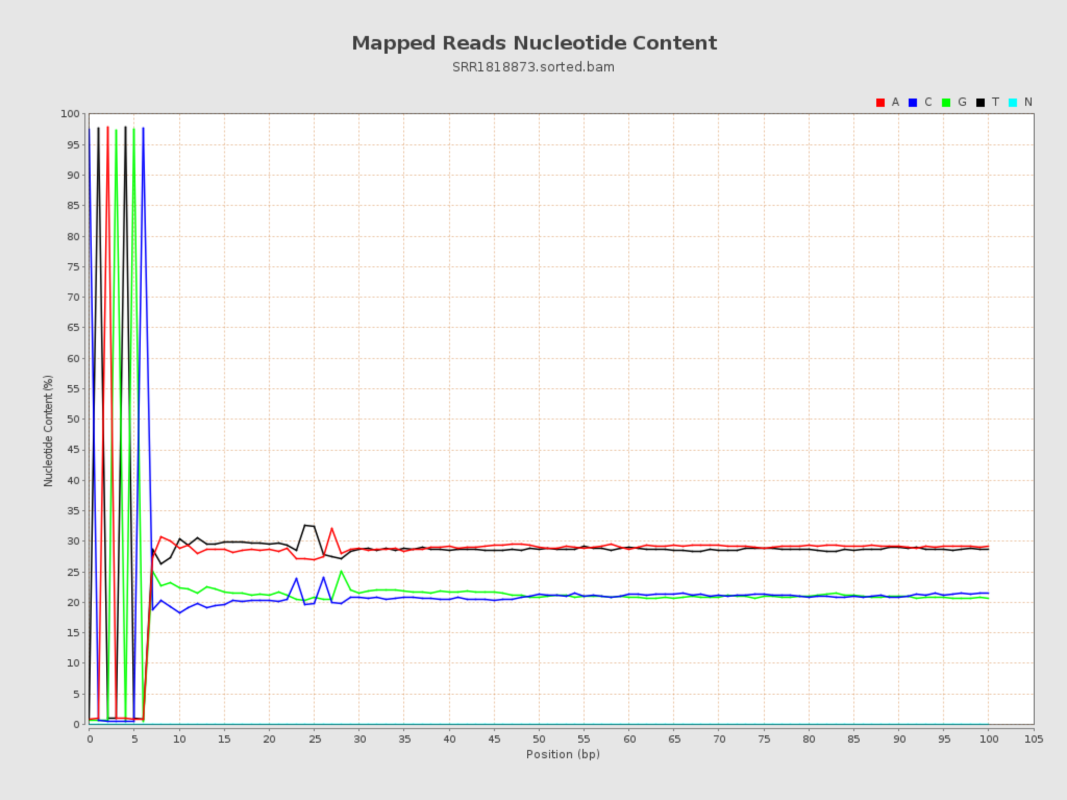
6. Results : Genome Fraction Coverage



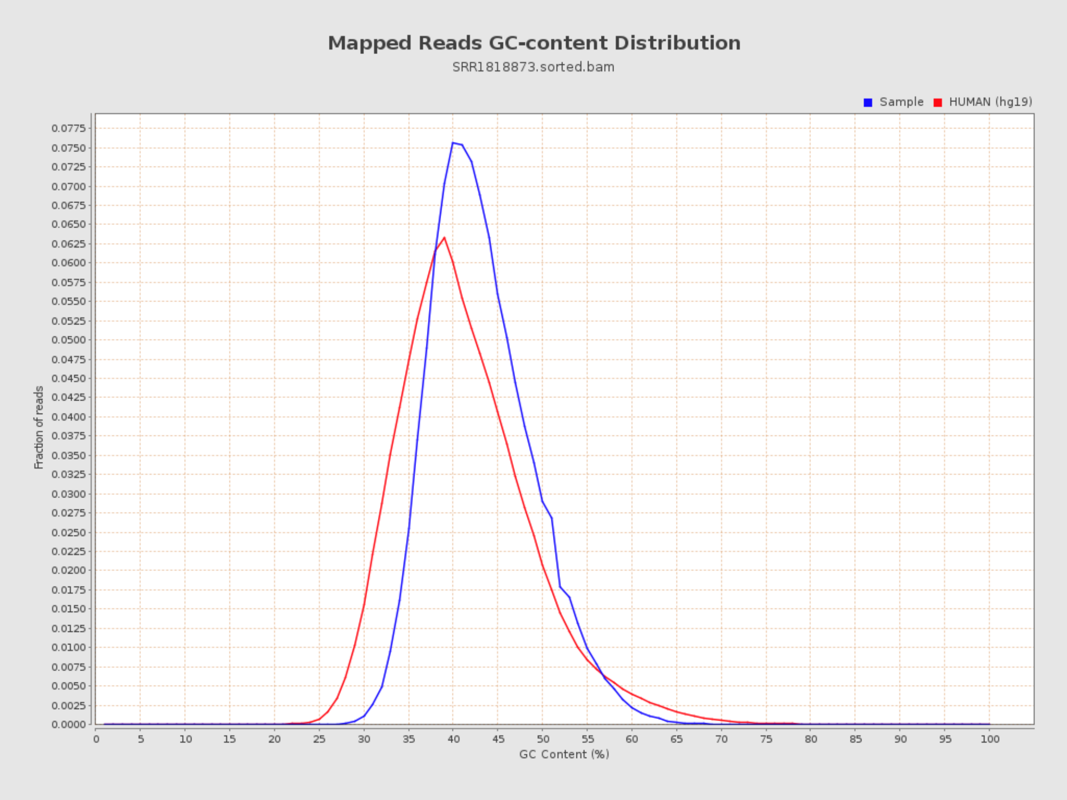
7. Results : Duplication Rate Histogram



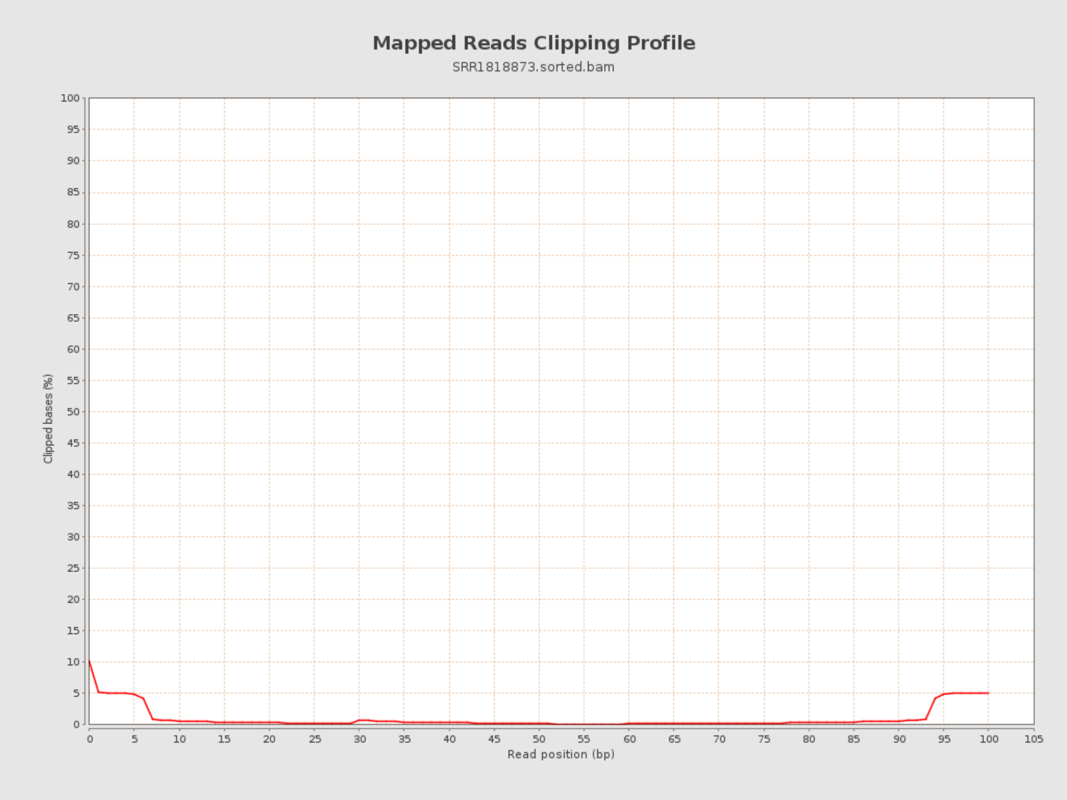
8. Results : Mapped Reads Nucleotide Content



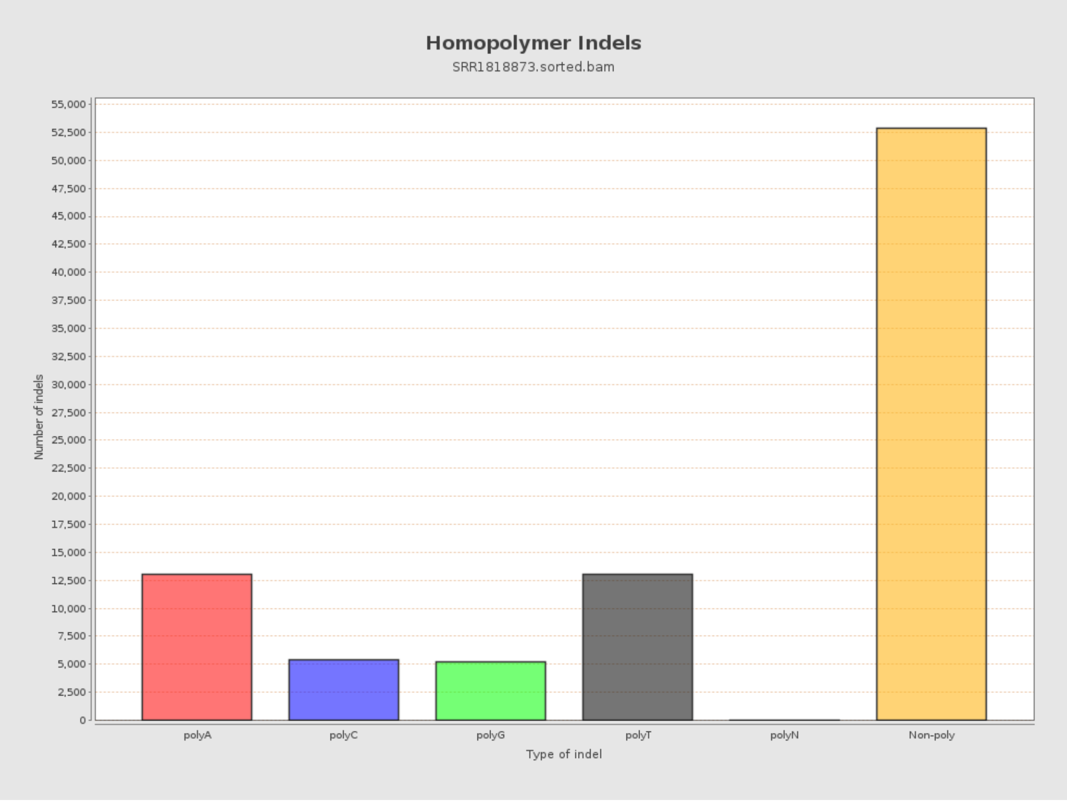
9. Results : Mapped Reads GC-content Distribution



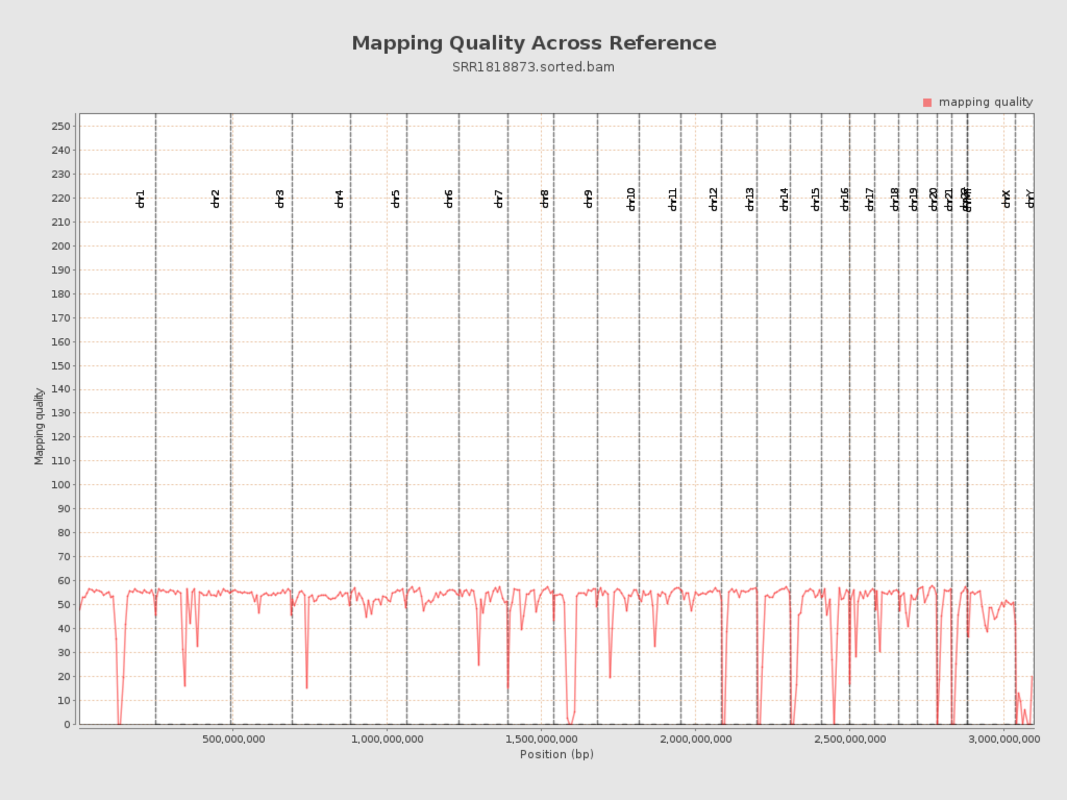
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram