Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 05:33:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818893.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_SRR1818893 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818893.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 05:32:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818893.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,325,451
Mapped reads	1,296,364 / 97.81%
Unmapped reads	29,087 / 2.19%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,967 / 1.51%
Read min/max/mean length	30 / 101 / 101.58
Duplicated reads (estimated)	226,757 / 17.11%
Duplication rate	14.25%
Clipped reads	1,307,240 / 98.63%

2.2. ACGT Content

Number/percentage of A's	34,206,485 / 28.54%
Number/percentage of C's	25,205,093 / 21.03%
Number/percentage of T's	34,365,400 / 28.68%
Number/percentage of G's	26,058,898 / 21.75%
Number/percentage of N's	1,896 / 0%
GC Percentage	42.78%

2.3. Coverage

Mean	0.0387

Standard Deviation	0.5283

2.4. Mapping Quality

Mean Mapping Quality	49.23

2.5. Mismatches and indels

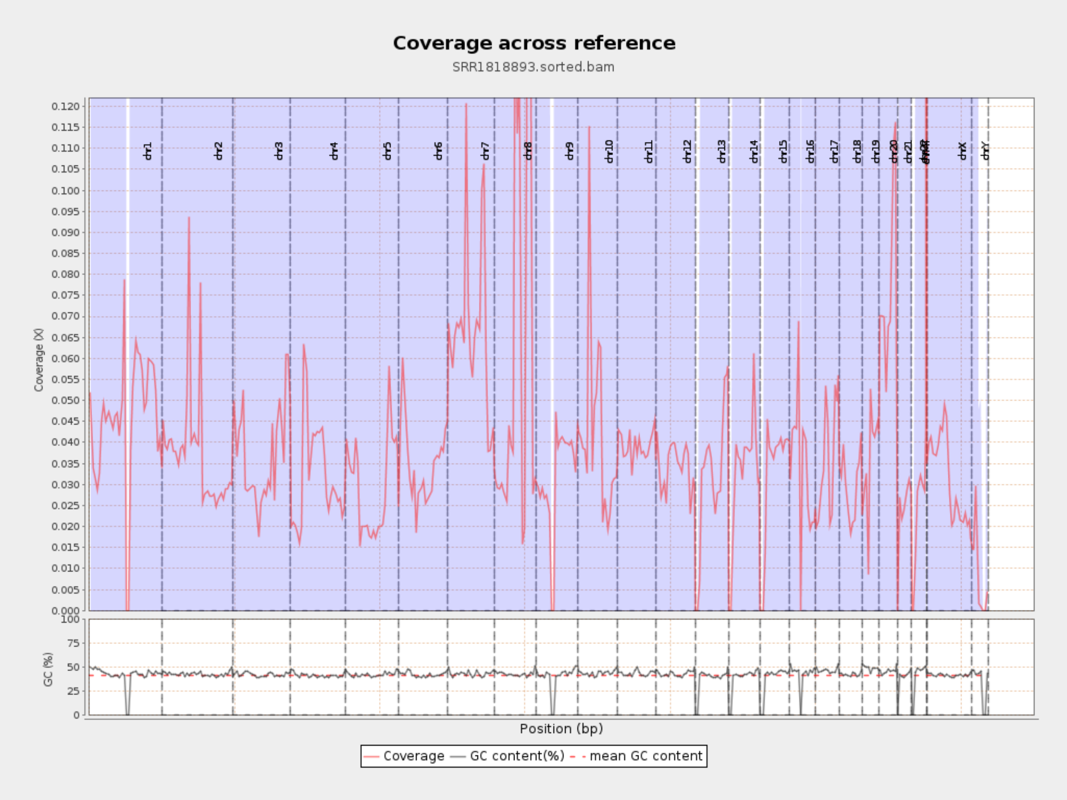
General error rate	0.67%
Mismatches	750,610
Insertions	19,018
Mapped reads with at least one insertion	1.42%
Deletions	39,299
Mapped reads with at least one deletion	2.96%
Homopolymer indels	39.65%

2.6. Chromosome stats

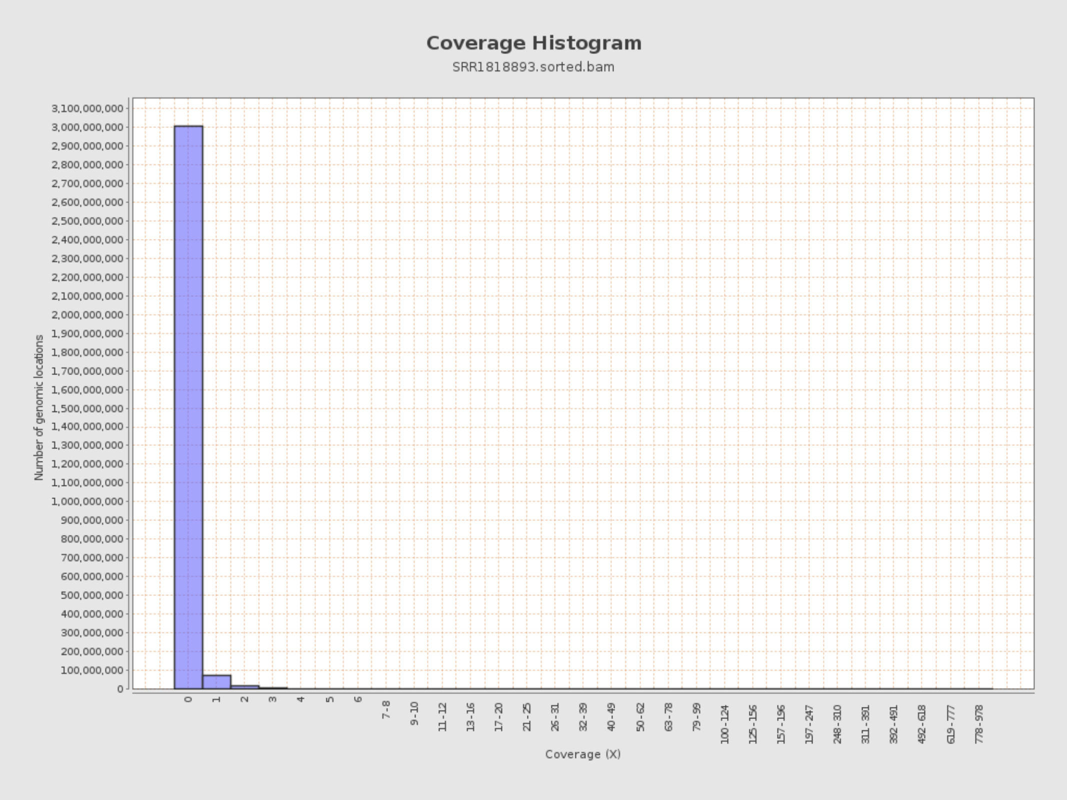
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11355300	0.0456	0.7865
chr2	243199373	9141908	0.0376	0.8033
chr3	198022430	7337079	0.0371	0.2416
chr4	191154276	6044648	0.0316	0.3182
chr5	180915260	5301036	0.0293	0.2341
chr6	171115067	5917894	0.0346	0.2547
chr7	159138663	10766325	0.0677	1.1195

chr8	146364022	10356172	0.0708	0.4114
chr9	141213431	4409116	0.0312	0.4086
chr10	135534747	5697762	0.042	0.7504
chr11	135006516	5293956	0.0392	0.3046
chr12	133851895	4611272	0.0345	0.2357
chr13	115169878	3613331	0.0314	0.2197
chr14	107349540	3497708	0.0326	0.2549
chr15	102531392	3302283	0.0322	0.2275
chr16	90354753	3012879	0.0333	0.5507
chr17	81195210	2931758	0.0361	0.3121
chr18	78077248	2313070	0.0296	0.479
chr19	59128983	2100282	0.0355	0.6371
chr20	63025520	4872127	0.0773	0.3786
chr21	48129895	1165223	0.0242	0.2522
chr22	51304566	1098514	0.0214	0.212
chrMT	16571	377992	22.8105	14.3467
chrX	155270560	4925614	0.0317	0.267
chrY	59373566	472518	0.008	0.6309

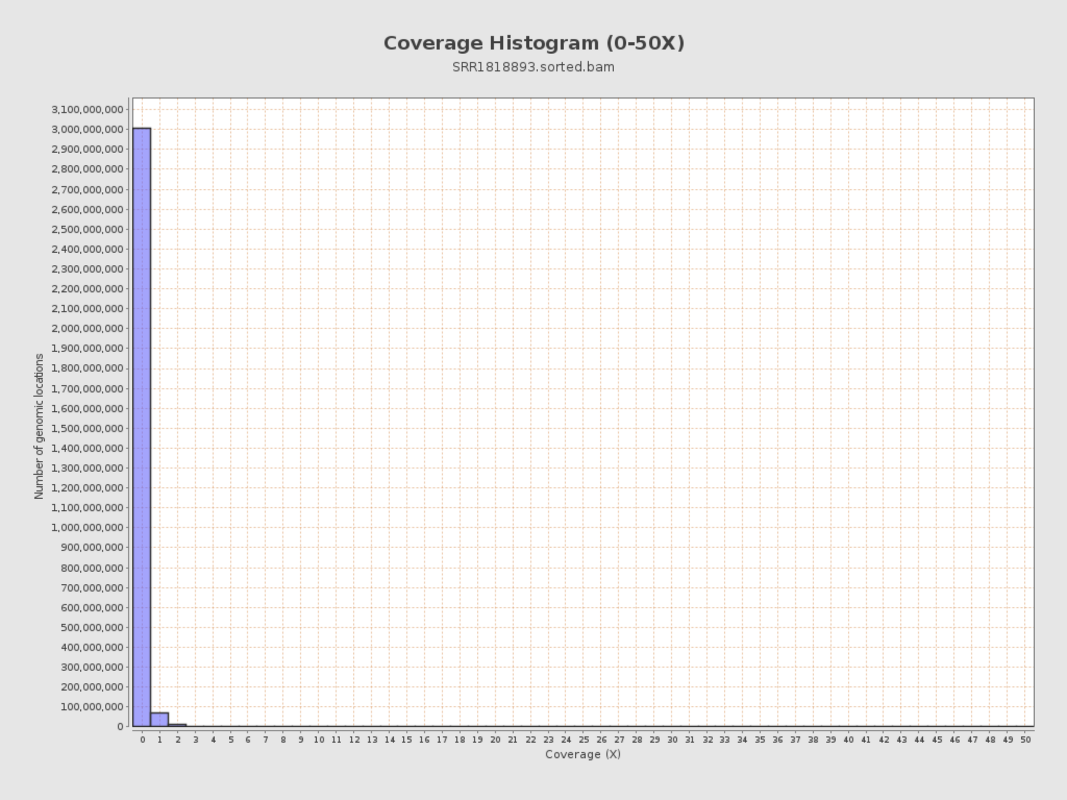
3. Results : Coverage across reference



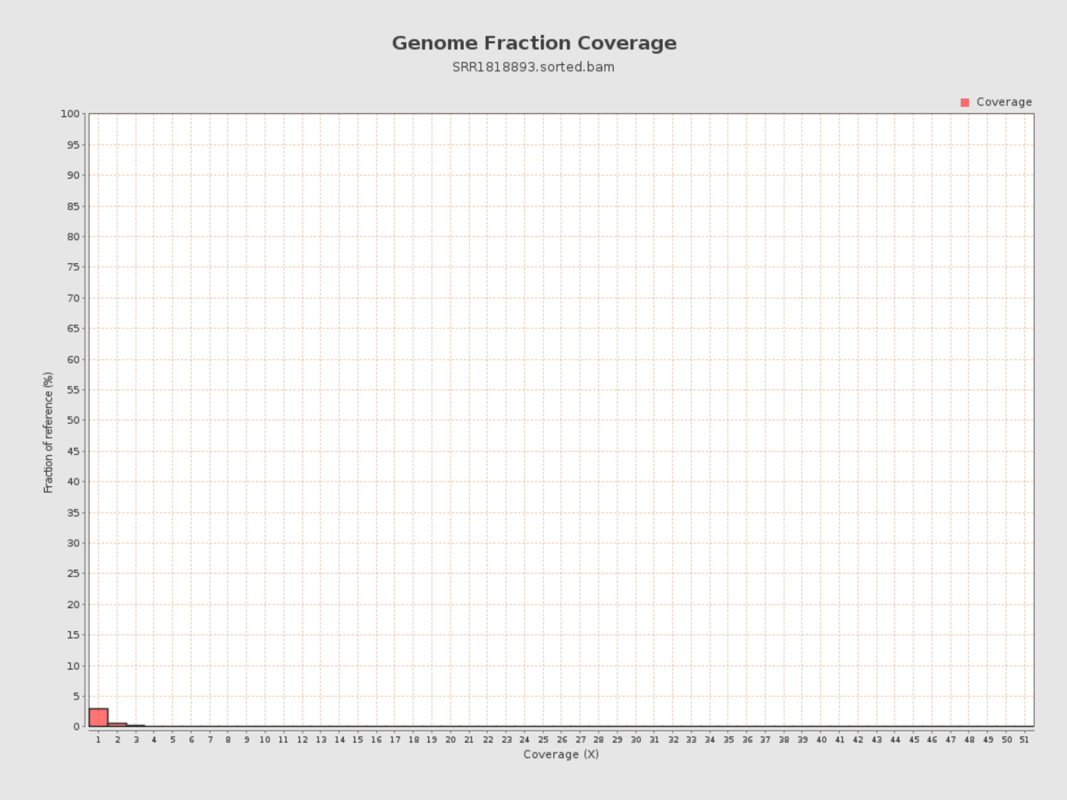
4. Results : Coverage Histogram



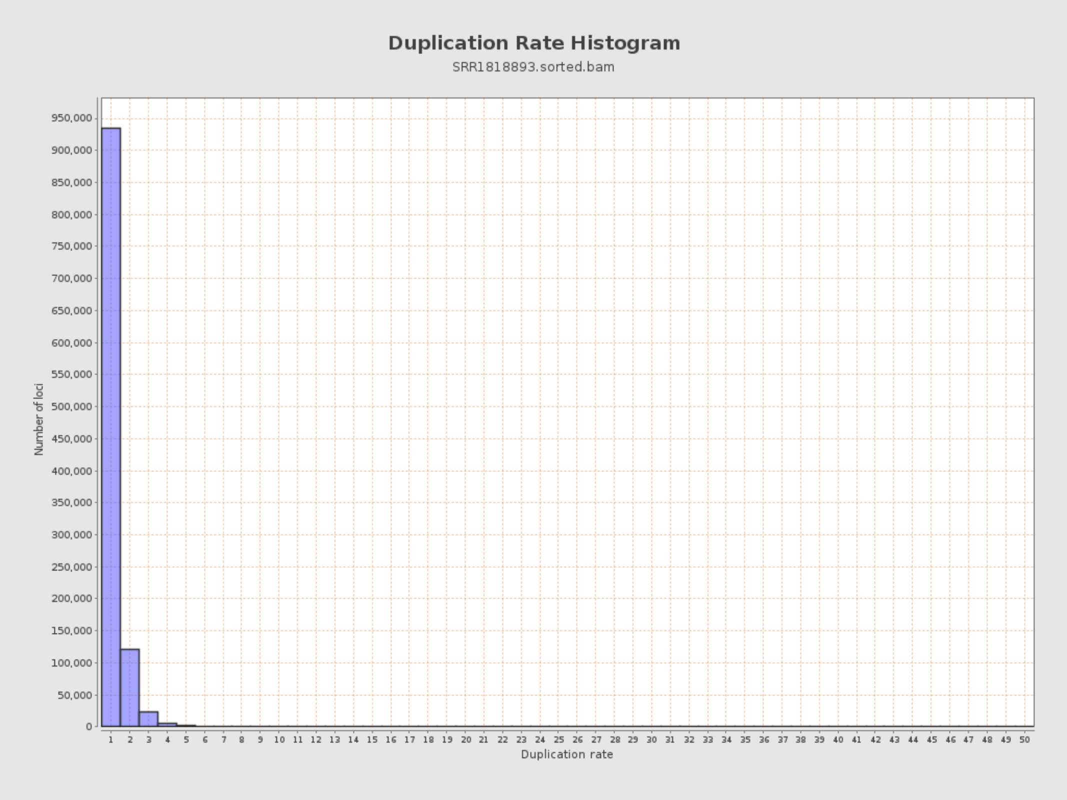
5. Results : Coverage Histogram (0-50X)



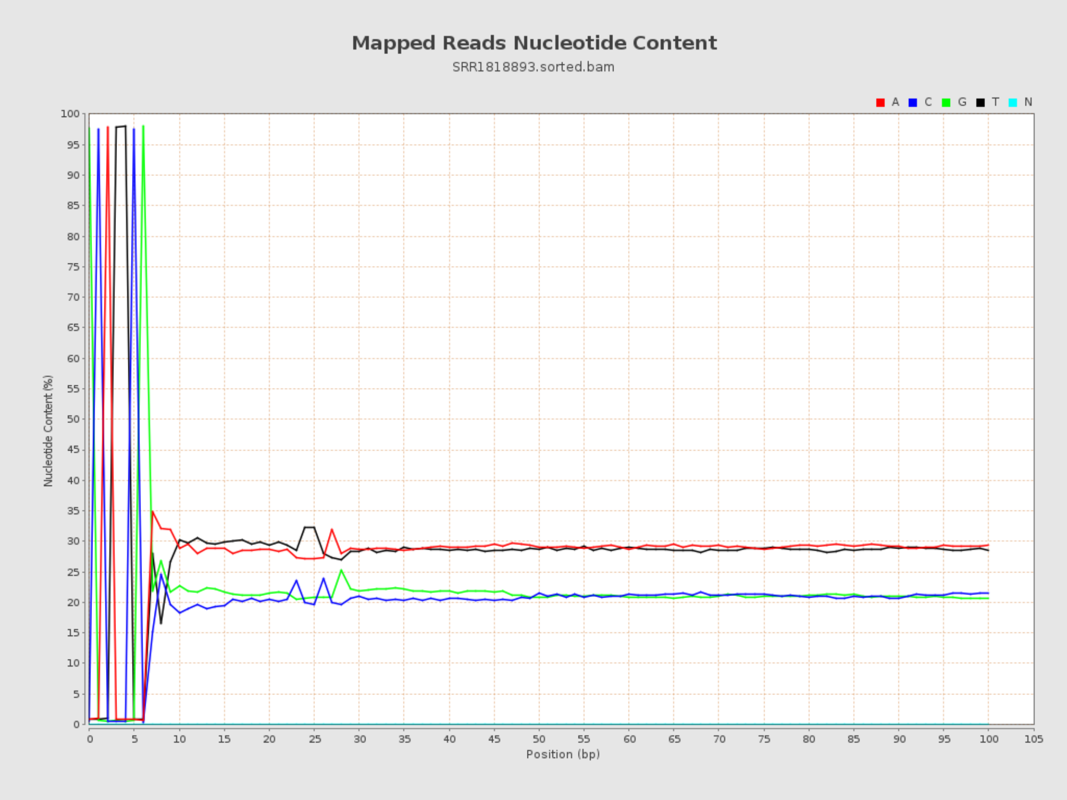
6. Results : Genome Fraction Coverage



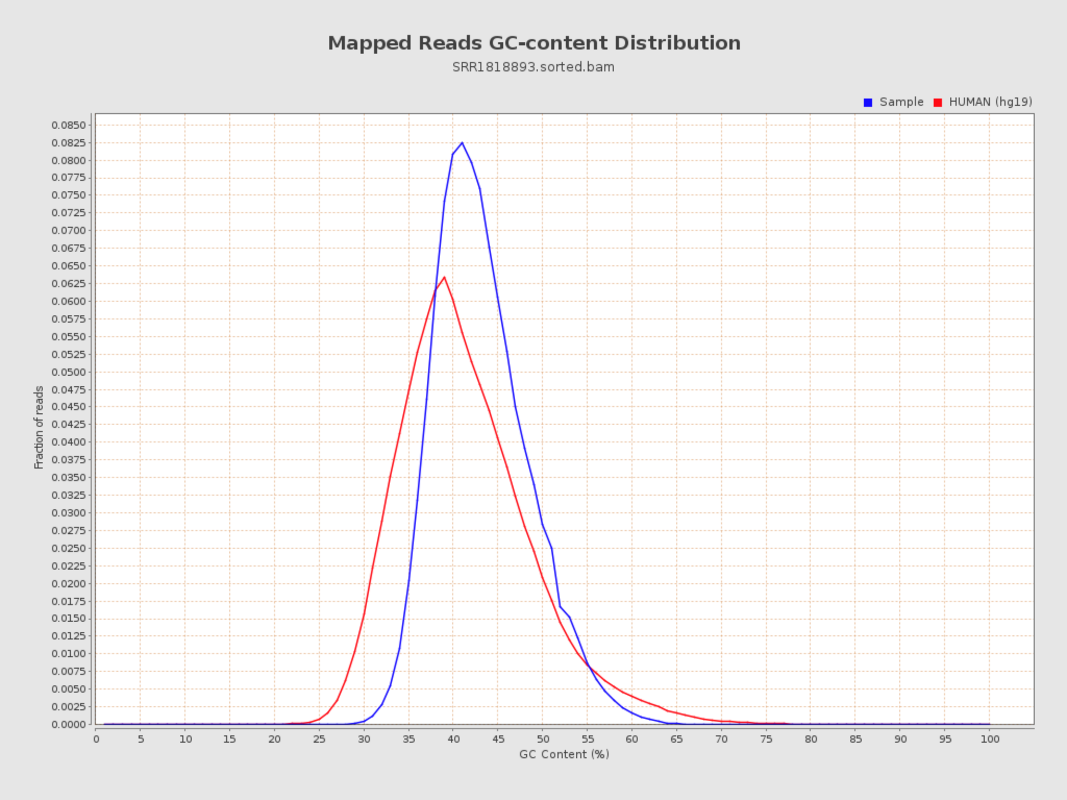
7. Results : Duplication Rate Histogram



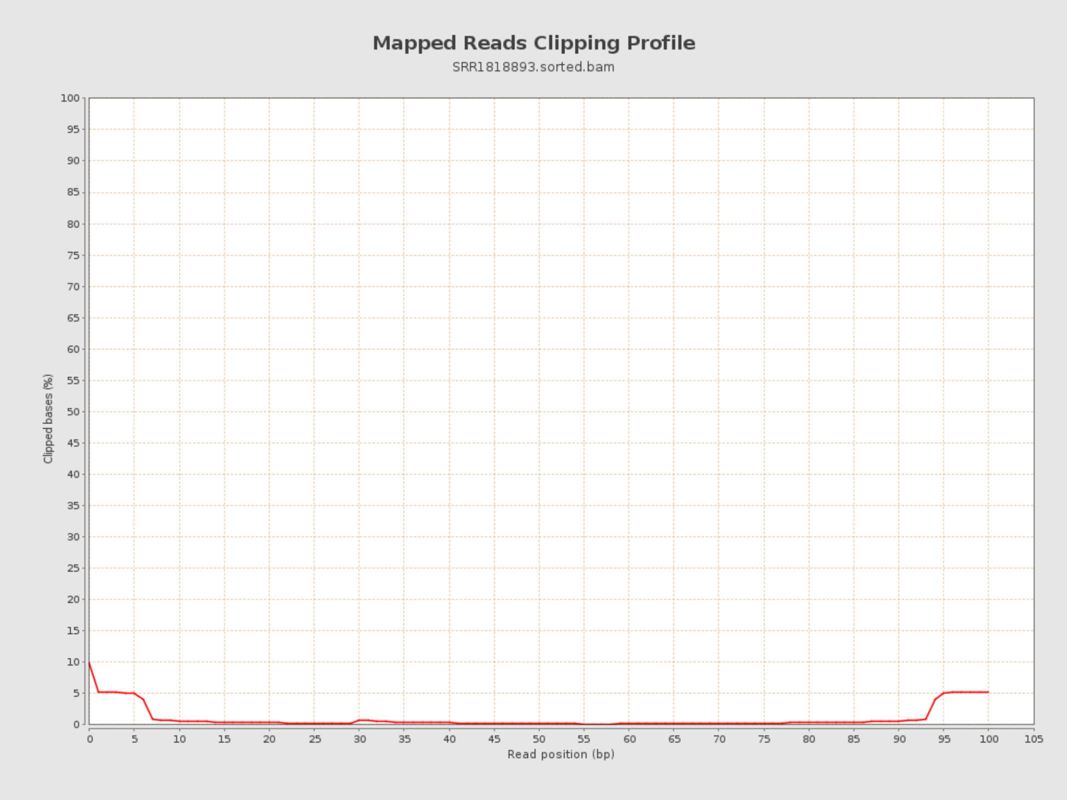
8. Results : Mapped Reads Nucleotide Content



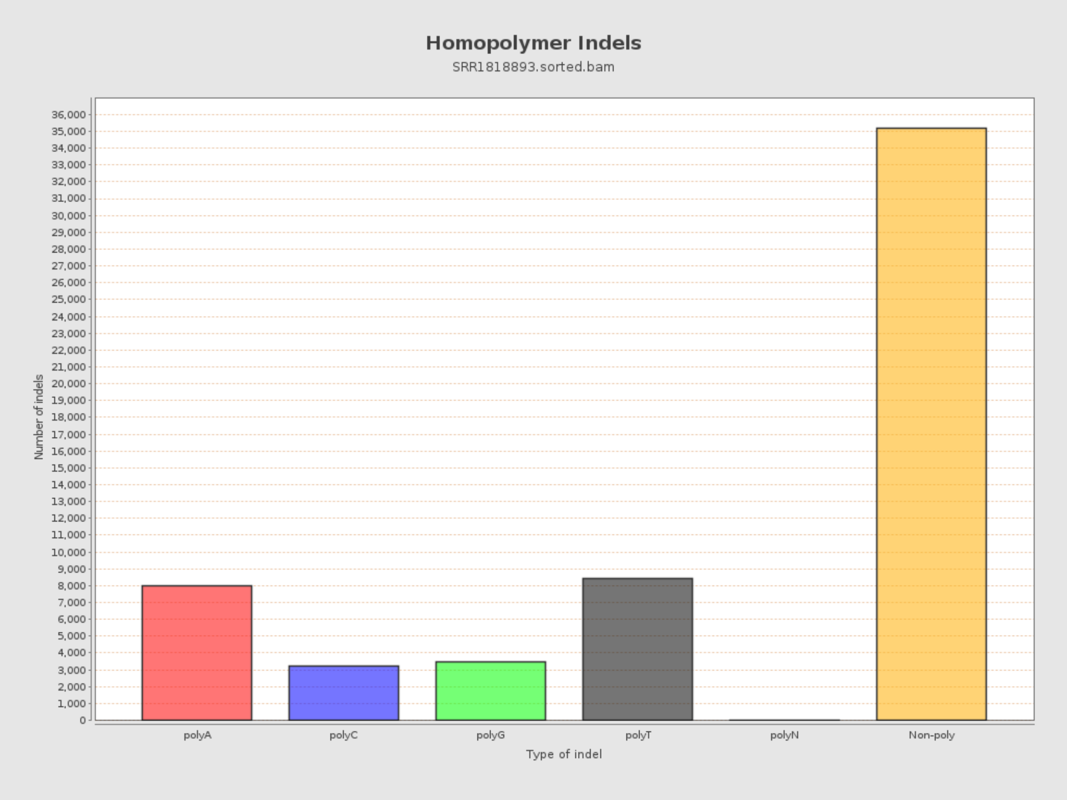
9. Results : Mapped Reads GC-content Distribution



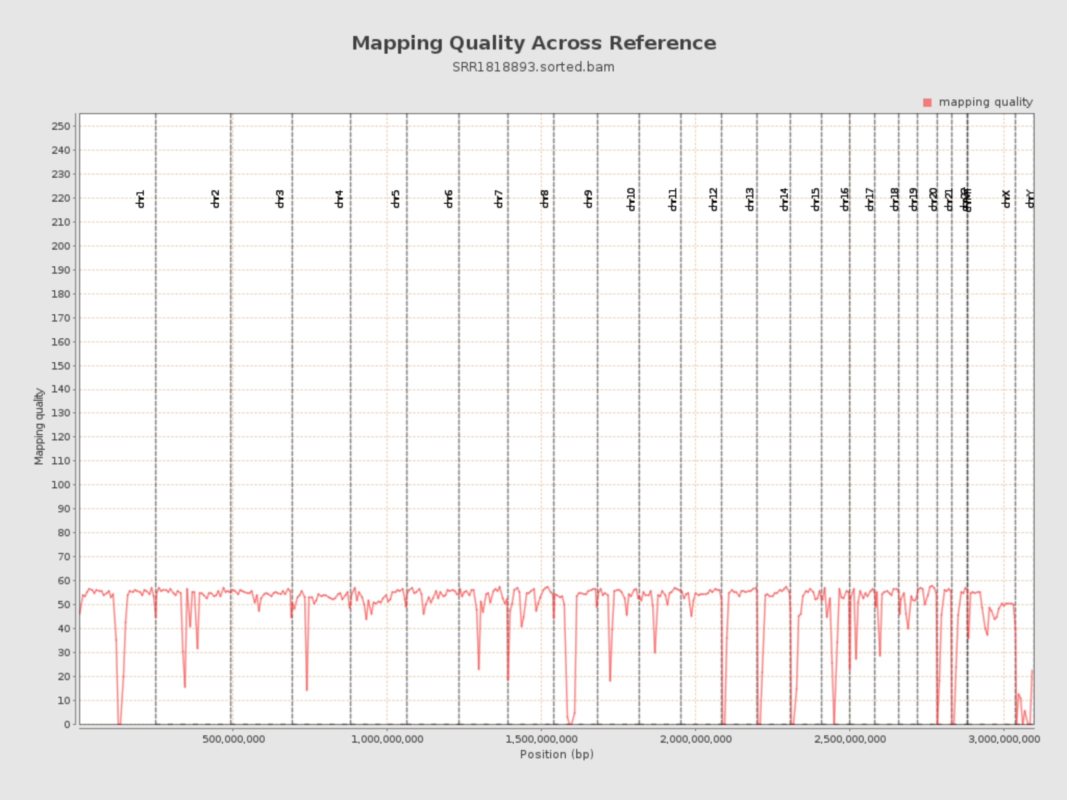
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram