Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 05:38:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818894.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_SRR1818894 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818894.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 05:38:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818894.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,463,187
Mapped reads	1,442,856 / 98.61%
Unmapped reads	20,331 / 1.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,159 / 1.45%
Read min/max/mean length	30 / 101 / 101.55
Duplicated reads (estimated)	268,255 / 18.33%
Duplication rate	15.53%
Clipped reads	1,461,502 / 99.88%

2.2. ACGT Content

Number/percentage of A's	38,806,723 / 29.08%
Number/percentage of C's	28,675,675 / 21.49%
Number/percentage of T's	37,737,243 / 28.28%
Number/percentage of G's	28,224,663 / 21.15%
Number/percentage of N's	2,028 / 0%
GC Percentage	42.64%

2.3. Coverage

Mean	0.0431

Standard Deviation	0.5534

2.4. Mapping Quality

Mean Mapping Quality	49.18

2.5. Mismatches and indels

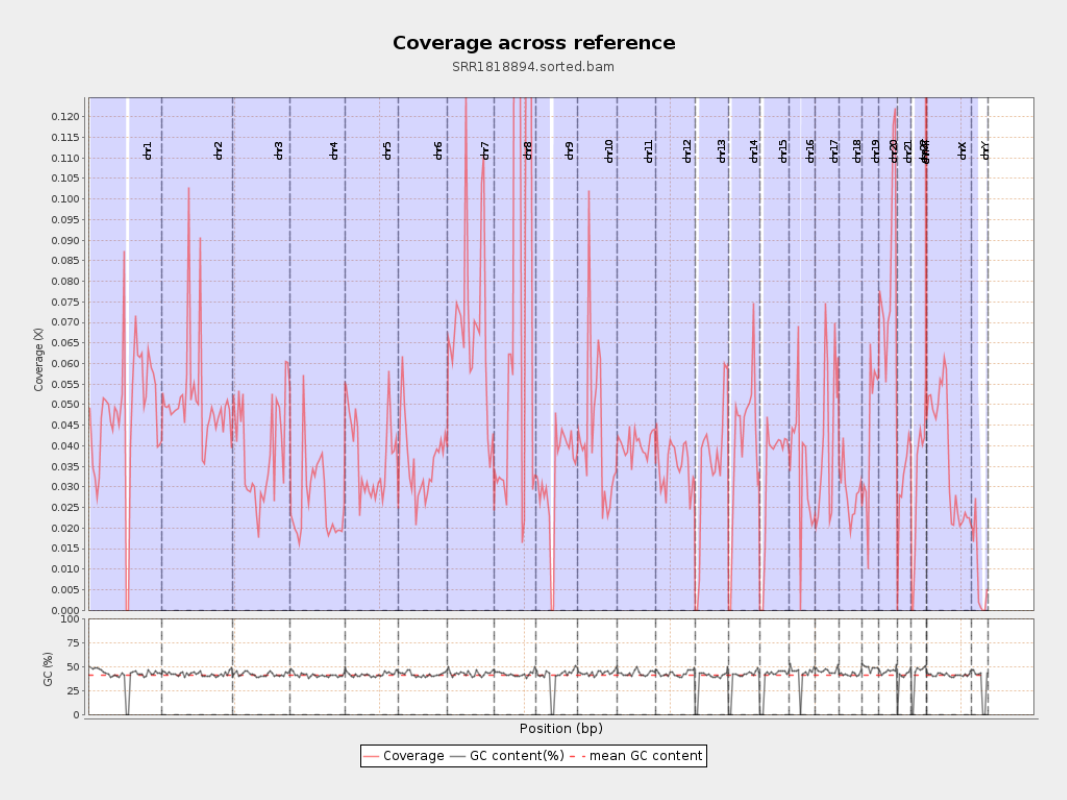
General error rate	0.64%
Mismatches	807,207
Insertions	16,867
Mapped reads with at least one insertion	1.12%
Deletions	44,066
Mapped reads with at least one deletion	2.98%
Homopolymer indels	42.26%

2.6. Chromosome stats

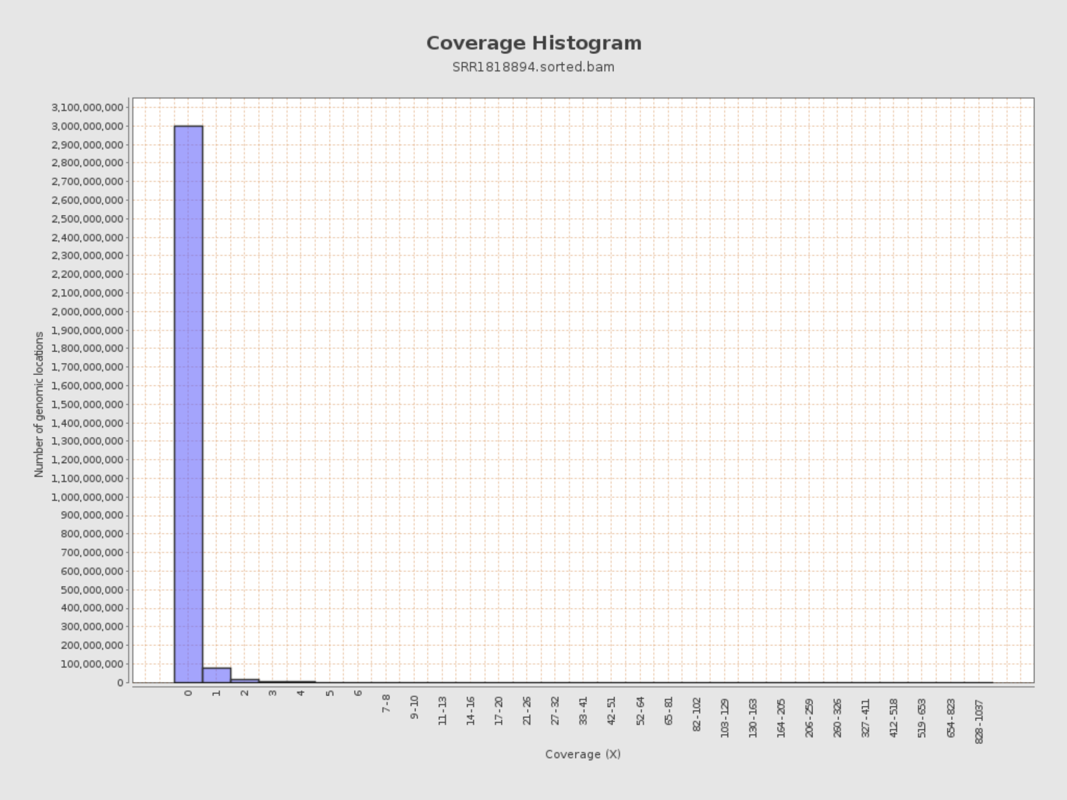
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11790337	0.0473	0.8512
chr2	243199373	12453698	0.0512	0.8349
chr3	198022430	7693600	0.0389	0.2524
chr4	191154276	5006763	0.0262	0.2914
chr5	180915260	6703165	0.0371	0.2641
chr6	171115067	6152235	0.036	0.2769
chr7	159138663	11088857	0.0697	1.193

chr8	146364022	14350499	0.098	0.5136
chr9	141213431	4546595	0.0322	0.4237
chr10	135534747	5765308	0.0425	0.6816
chr11	135006516	5458860	0.0404	0.3234
chr12	133851895	4768040	0.0356	0.2444
chr13	115169878	4039096	0.0351	0.2397
chr14	107349540	4304363	0.0401	0.2841
chr15	102531392	3412948	0.0333	0.2324
chr16	90354753	3086335	0.0342	0.5789
chr17	81195210	3507915	0.0432	0.3464
chr18	78077248	2238237	0.0287	0.487
chr19	59128983	2521296	0.0426	0.7229
chr20	63025520	5133640	0.0815	0.3949
chr21	48129895	1506445	0.0313	0.2598
chr22	51304566	1493585	0.0291	0.2375
chrMT	16571	162306	9.7946	6.3911
chrX	155270560	5844923	0.0376	0.2999
chrY	59373566	504372	0.0085	0.6417

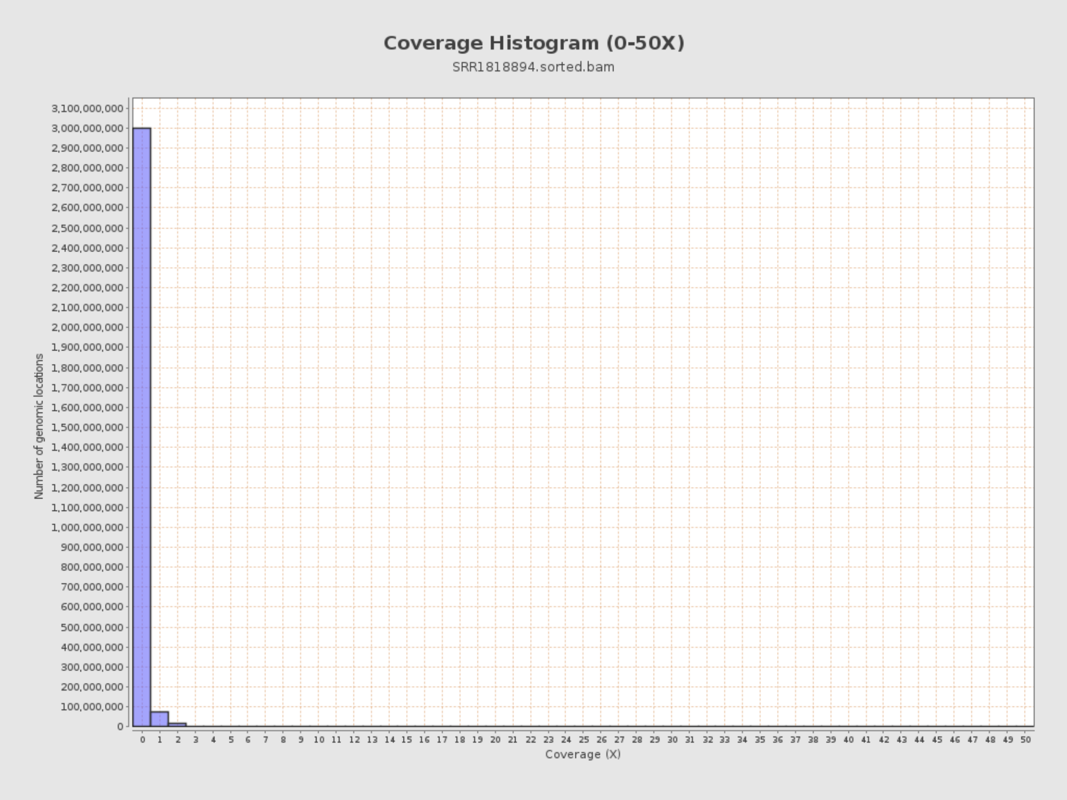
3. Results : Coverage across reference



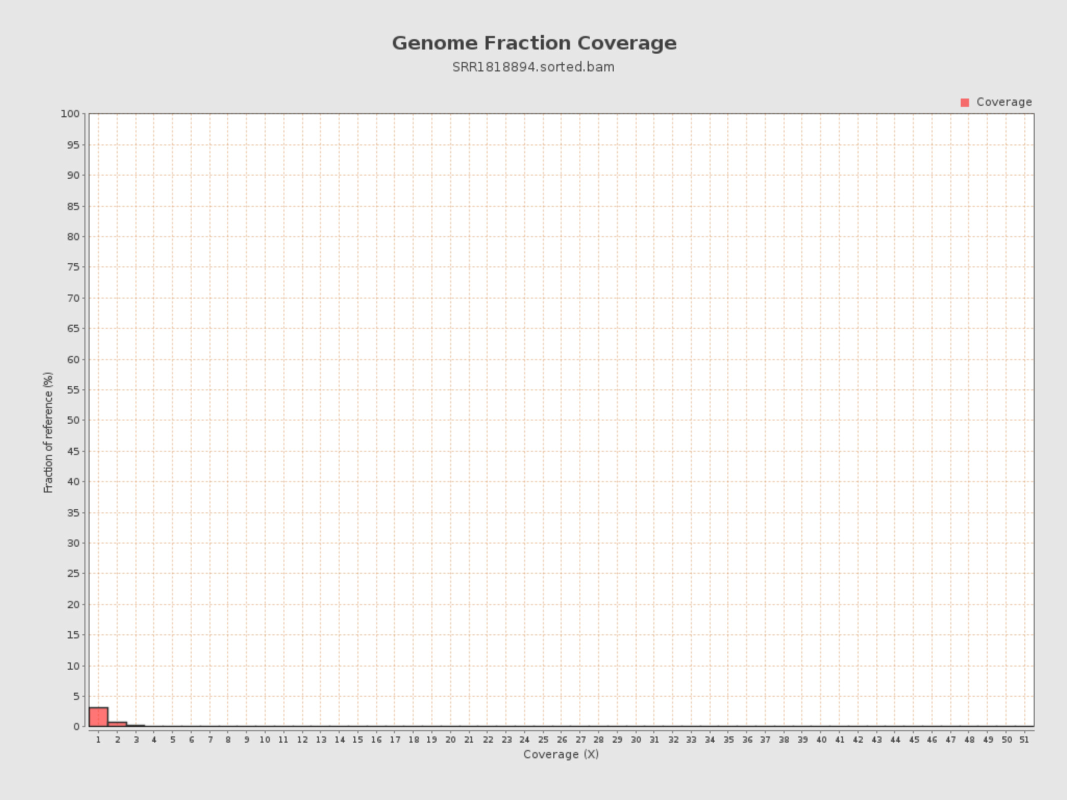
4. Results : Coverage Histogram



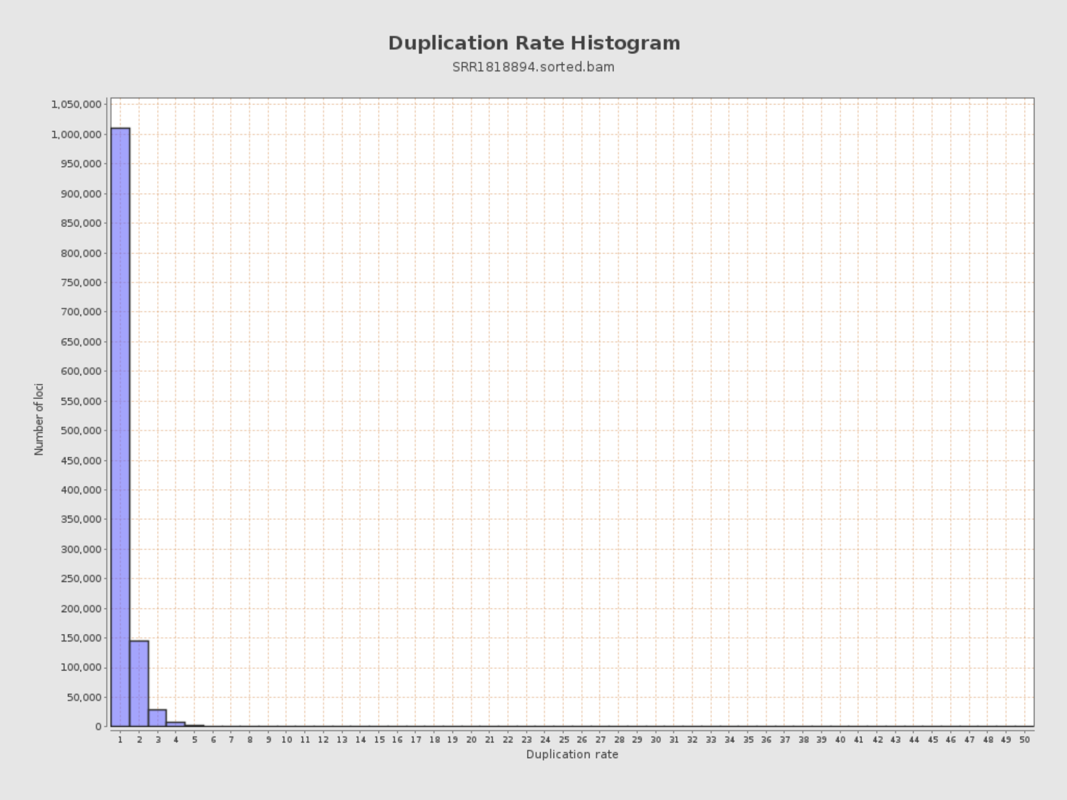
5. Results : Coverage Histogram (0-50X)



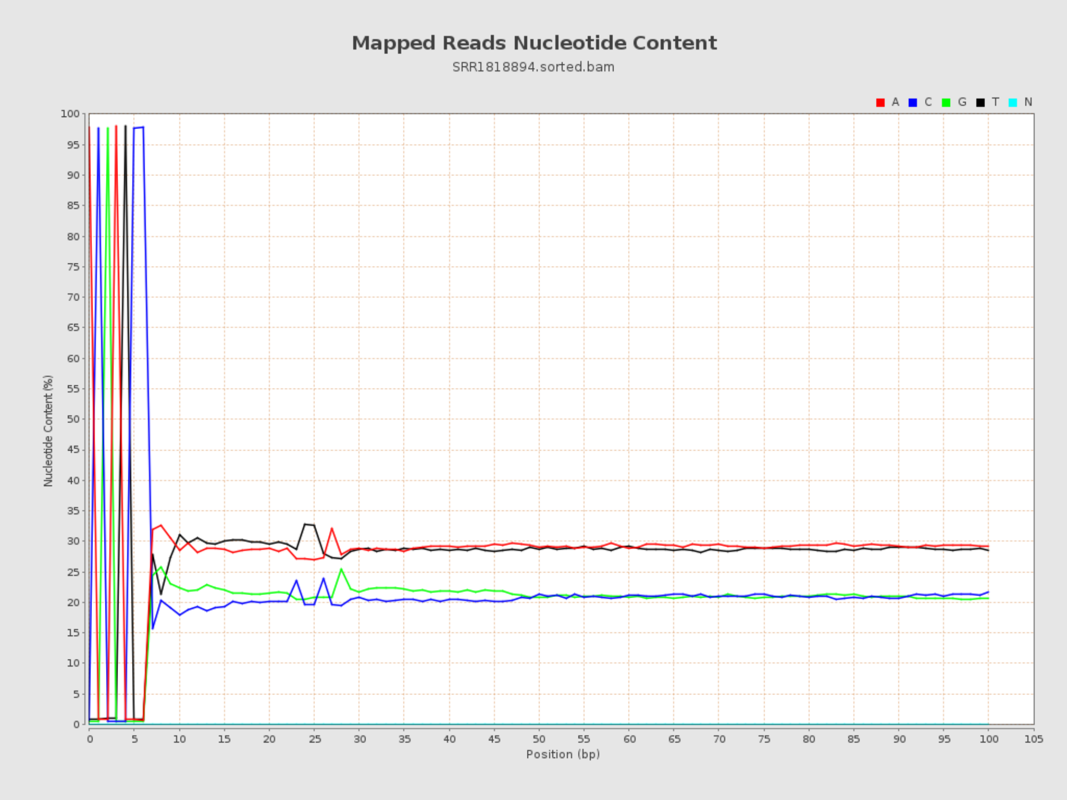
6. Results : Genome Fraction Coverage



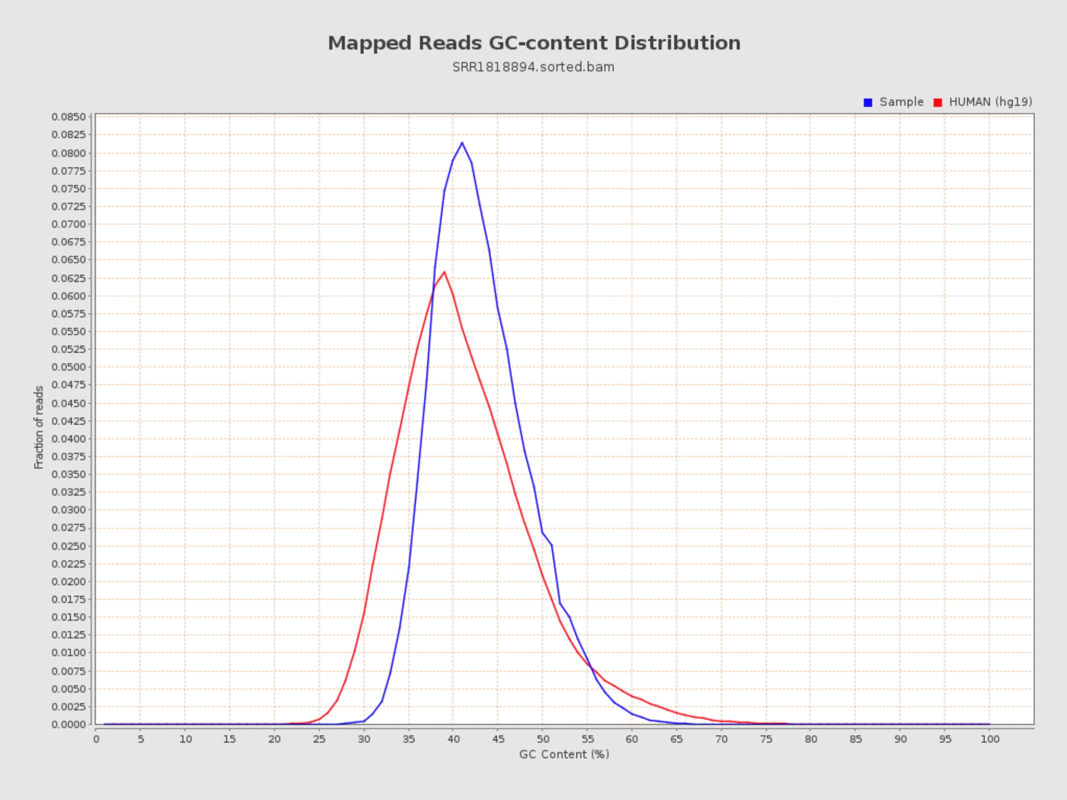
7. Results : Duplication Rate Histogram



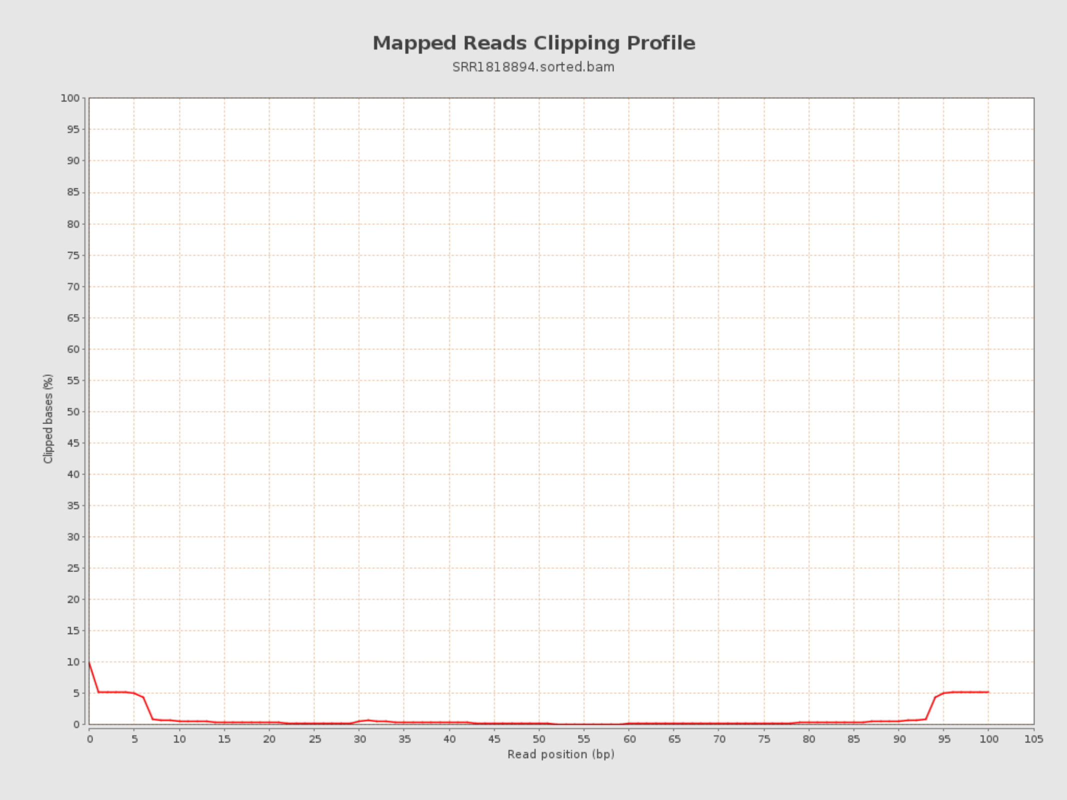
8. Results : Mapped Reads Nucleotide Content



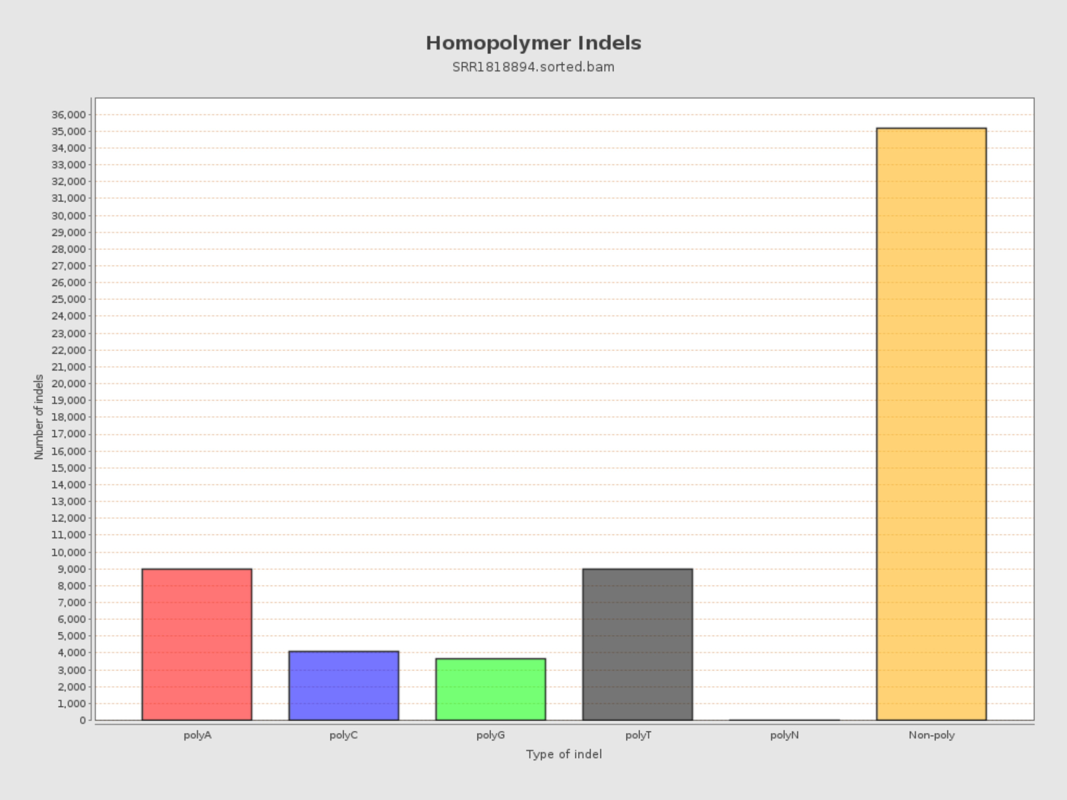
9. Results : Mapped Reads GC-content Distribution



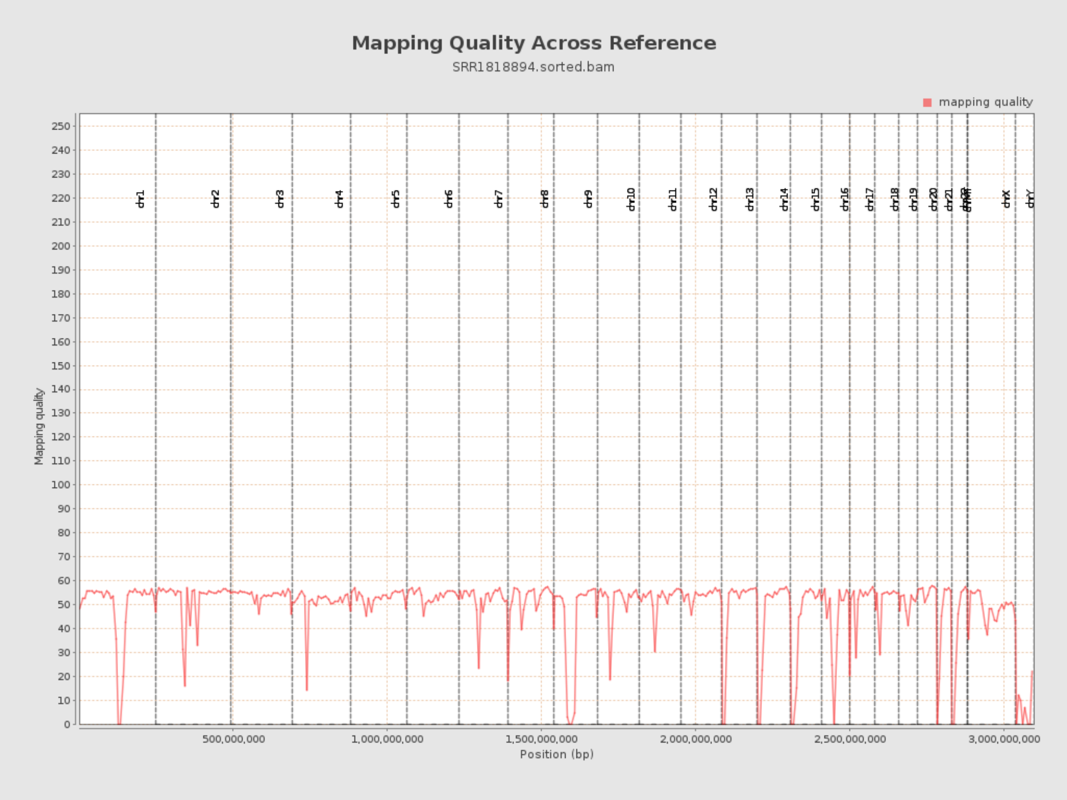
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram