Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 23:38:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818853.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_SRR1818853 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818853.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 23:38:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818853.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,509,284
Mapped reads	1,474,916 / 97.72%
Unmapped reads	34,368 / 2.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,332 / 1.55%
Read min/max/mean length	30 / 101 / 101.59
Duplicated reads (estimated)	313,314 / 20.76%
Duplication rate	18.48%
Clipped reads	1,489,055 / 98.66%

2.2. ACGT Content

Number/percentage of A's	39,692,536 / 29.08%
Number/percentage of C's	28,654,152 / 21%
Number/percentage of T's	39,652,209 / 29.05%
Number/percentage of G's	28,479,324 / 20.87%
Number/percentage of N's	1,980 / 0%
GC Percentage	41.86%

2.3. Coverage

Mean	0.0441

Standard Deviation	0.5053

2.4. Mapping Quality

Mean Mapping Quality	49.32

2.5. Mismatches and indels

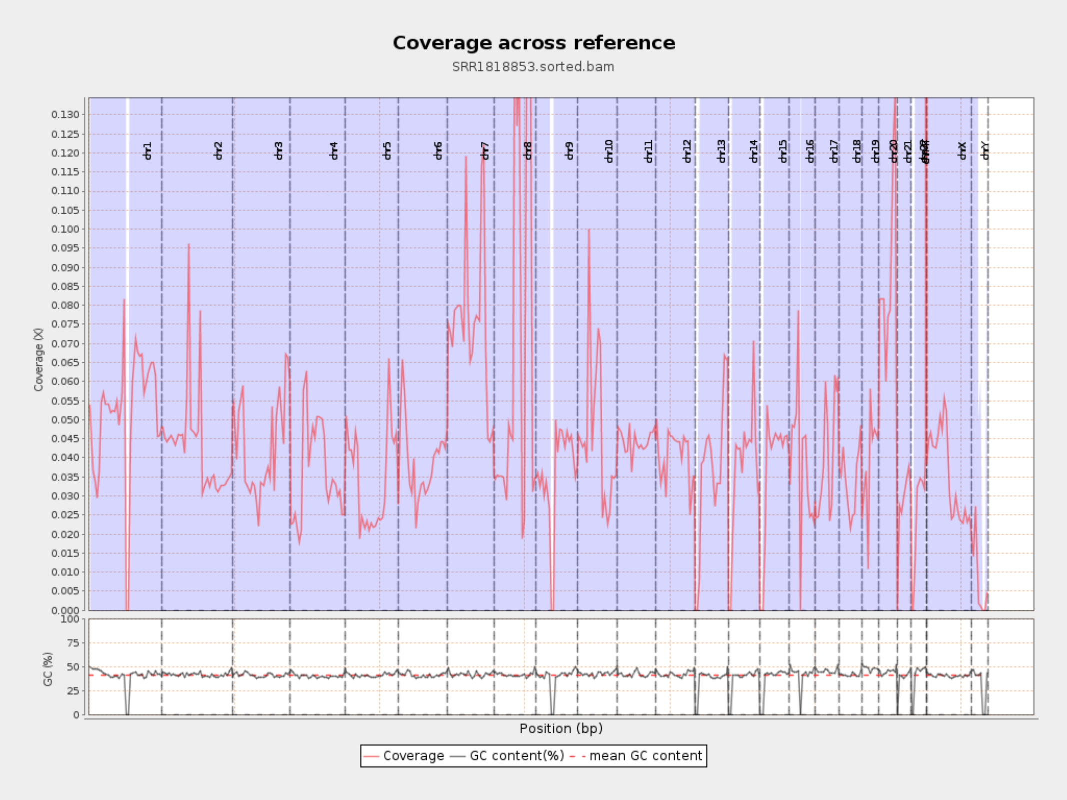
General error rate	0.63%
Mismatches	816,309
Insertions	19,424
Mapped reads with at least one insertion	1.28%
Deletions	44,382
Mapped reads with at least one deletion	2.94%
Homopolymer indels	40.79%

2.6. Chromosome stats

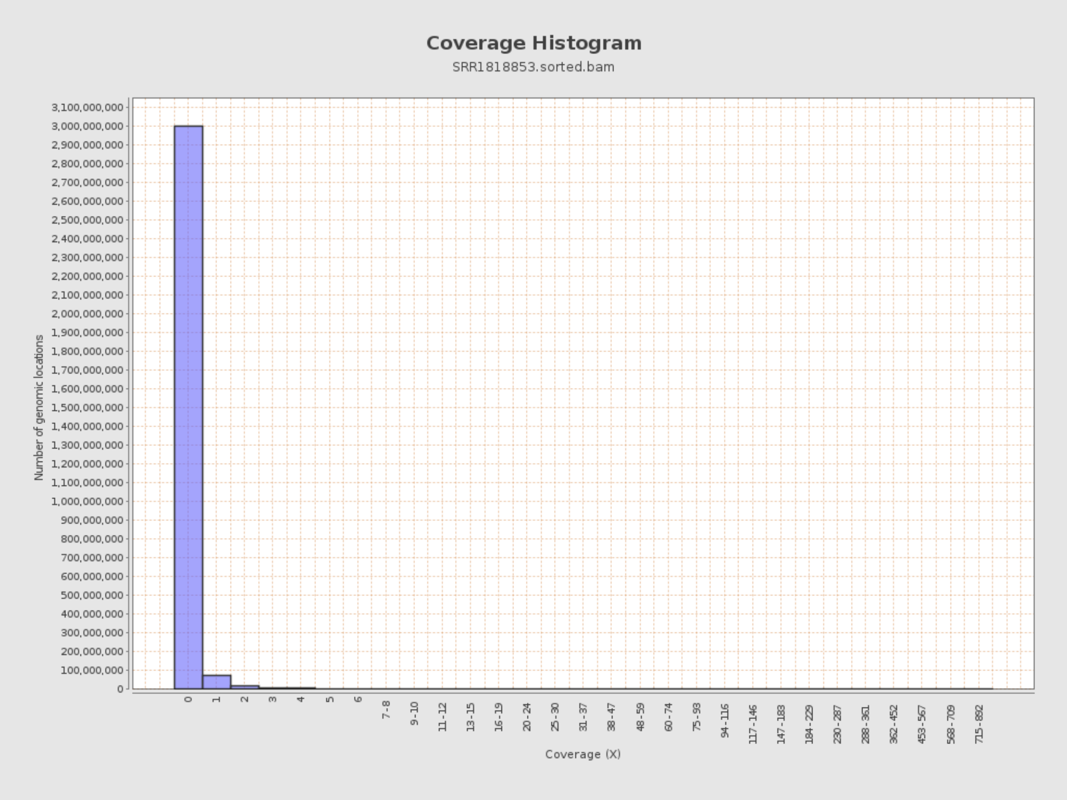
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12837194	0.0515	0.7531
chr2	243199373	10498452	0.0432	0.7301
chr3	198022430	8546024	0.0432	0.2743
chr4	191154276	6875688	0.036	0.3093
chr5	180915260	6209346	0.0343	0.2573
chr6	171115067	6667074	0.039	0.2836
chr7	159138663	12211798	0.0767	1.0423

chr8	146364022	11801495	0.0806	0.4668
chr9	141213431	4999911	0.0354	0.419
chr10	135534747	6254463	0.0461	0.6525
chr11	135006516	5983025	0.0443	0.3366
chr12	133851895	5474610	0.0409	0.2676
chr13	115169878	4253728	0.0369	0.2531
chr14	107349540	3981389	0.0371	0.2767
chr15	102531392	3809239	0.0372	0.252
chr16	90354753	3434157	0.038	0.5267
chr17	81195210	3318285	0.0409	0.3261
chr18	78077248	2657051	0.034	0.4568
chr19	59128983	2297924	0.0389	0.6073
chr20	63025520	5589246	0.0887	0.4157
chr21	48129895	1356154	0.0282	0.2455
chr22	51304566	1209317	0.0236	0.2284
chrMT	16571	253213	15.2805	10.0048
chrX	155270560	5585543	0.036	0.2945
chrY	59373566	461758	0.0078	0.5548

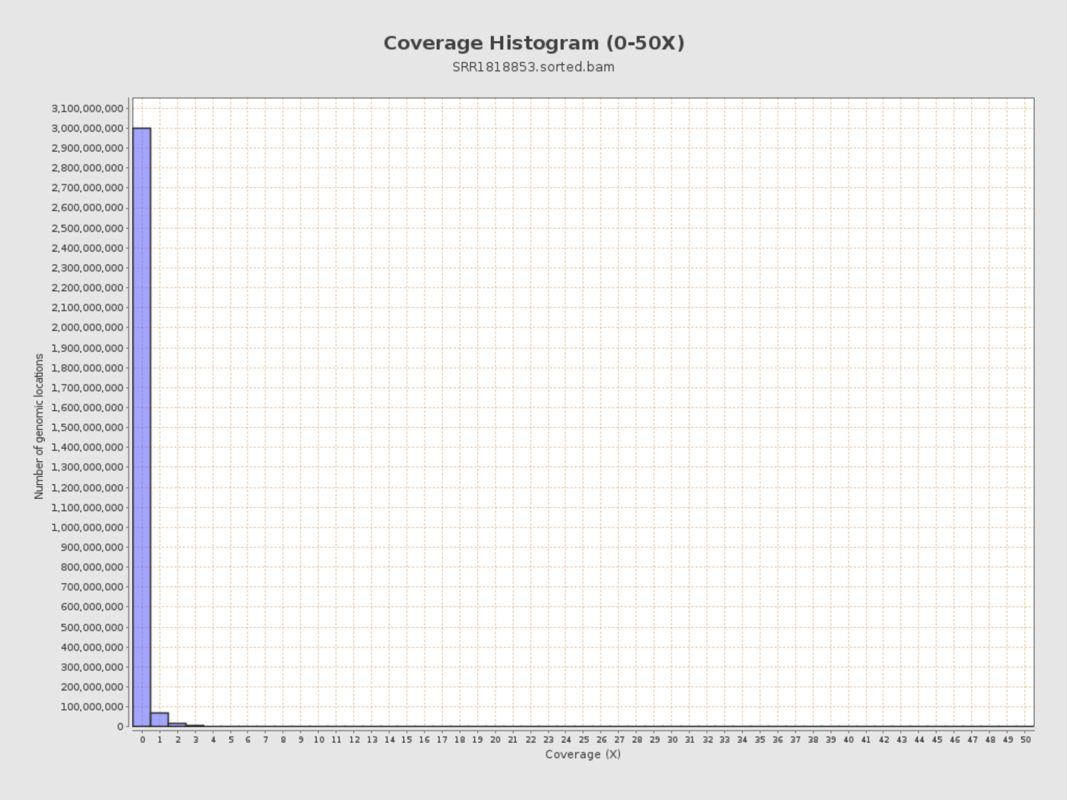
3. Results : Coverage across reference



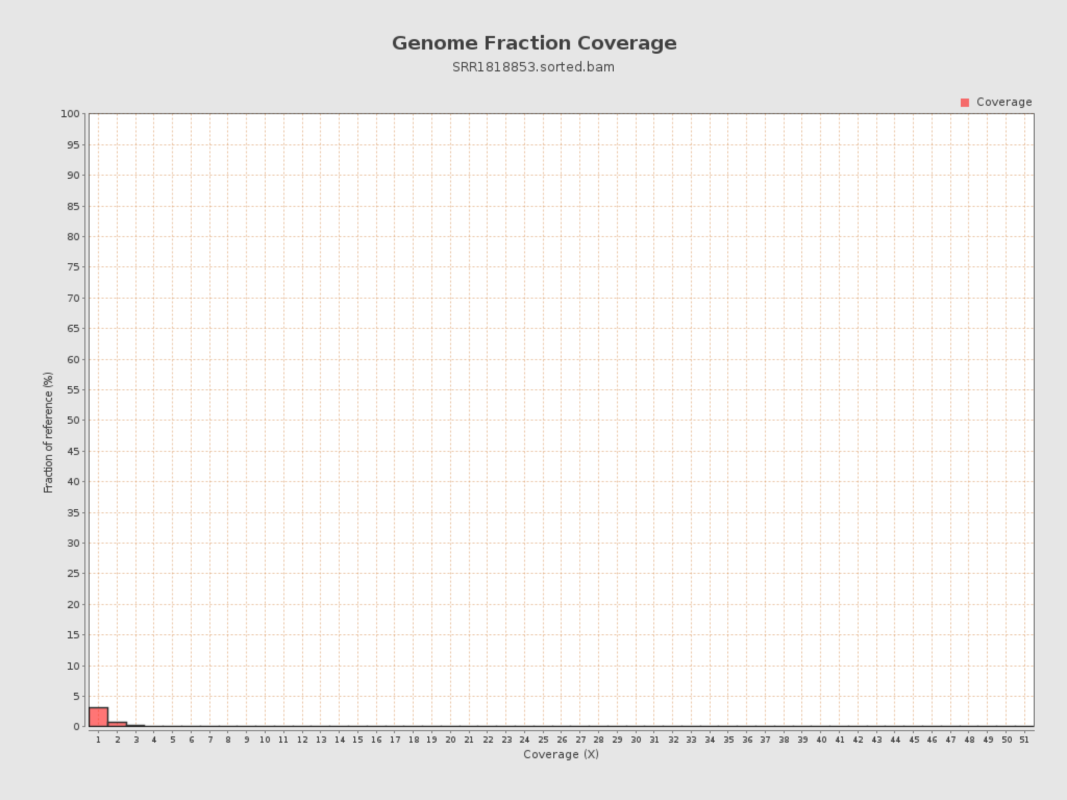
4. Results : Coverage Histogram



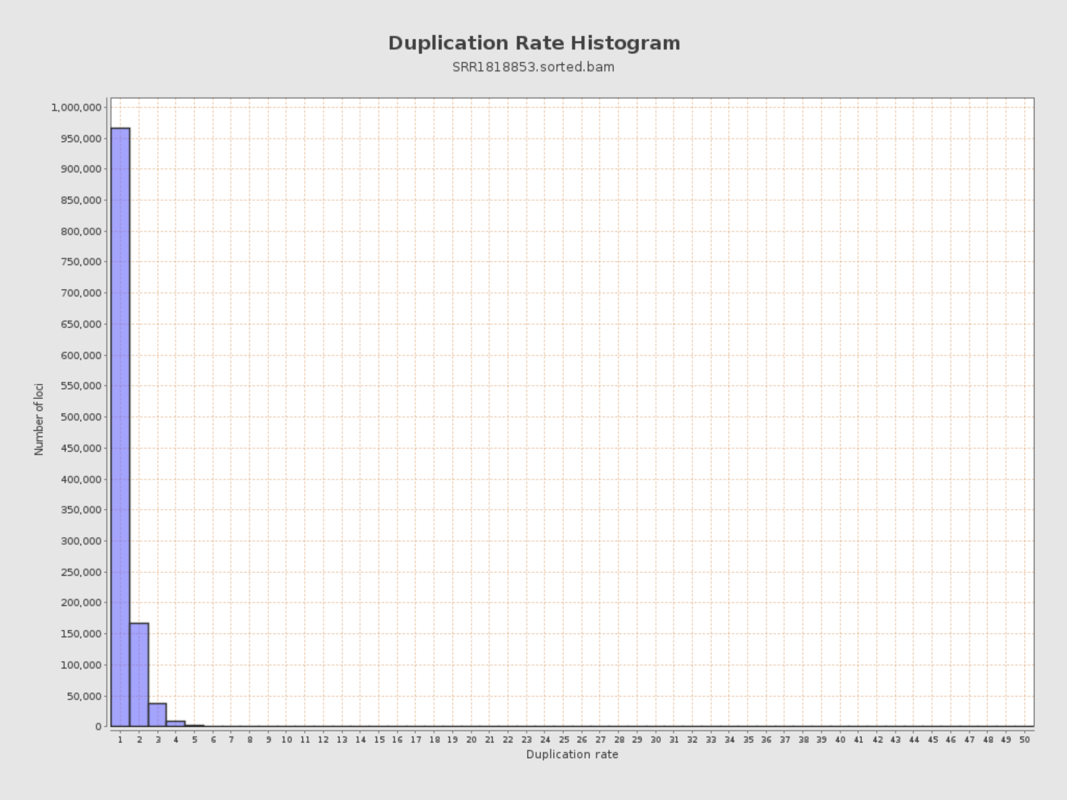
5. Results : Coverage Histogram (0-50X)



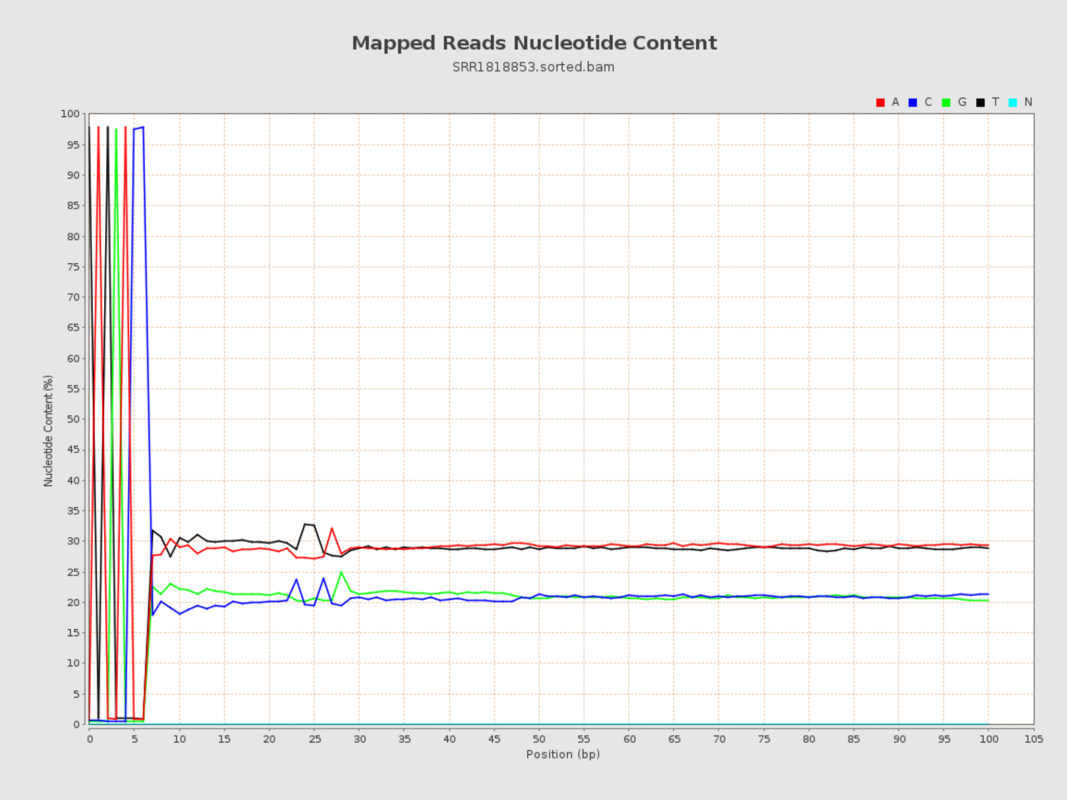
6. Results : Genome Fraction Coverage



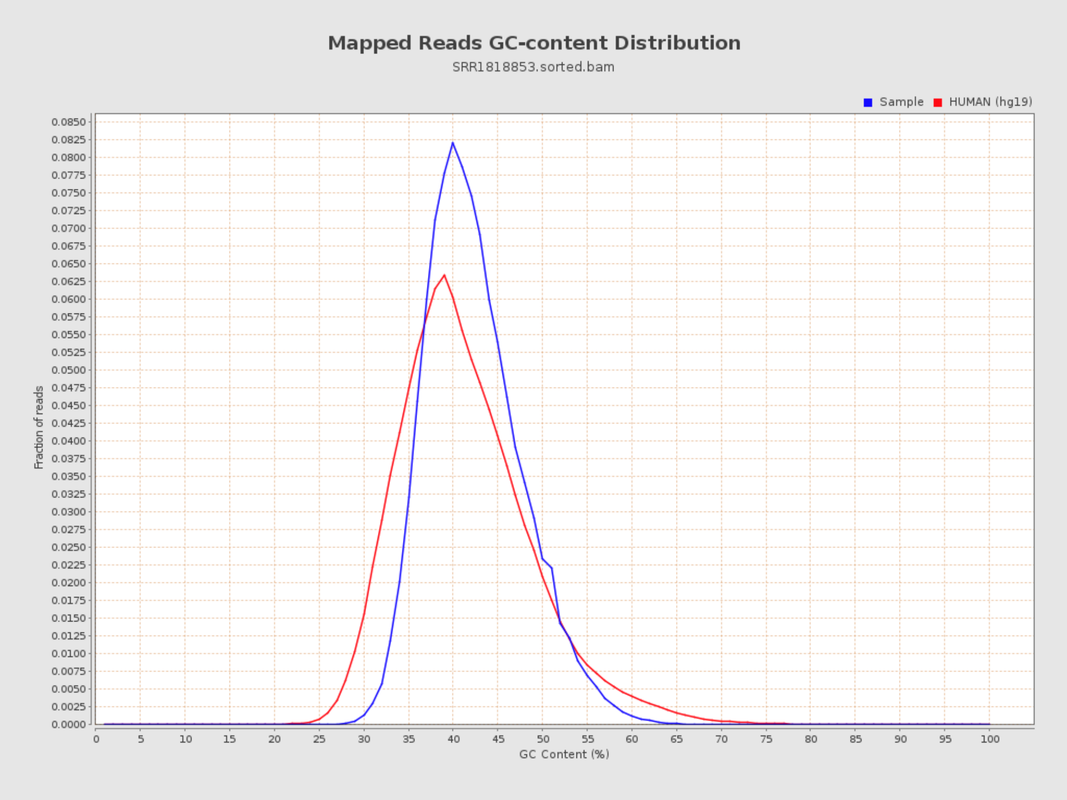
7. Results : Duplication Rate Histogram



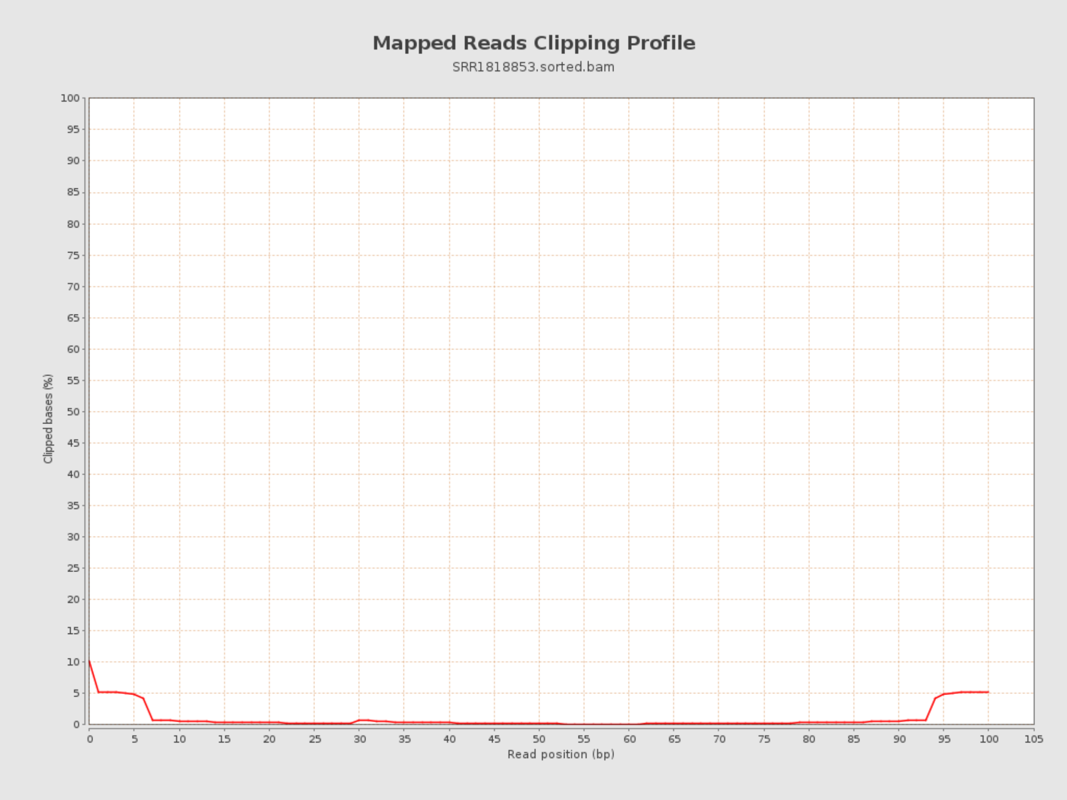
8. Results : Mapped Reads Nucleotide Content



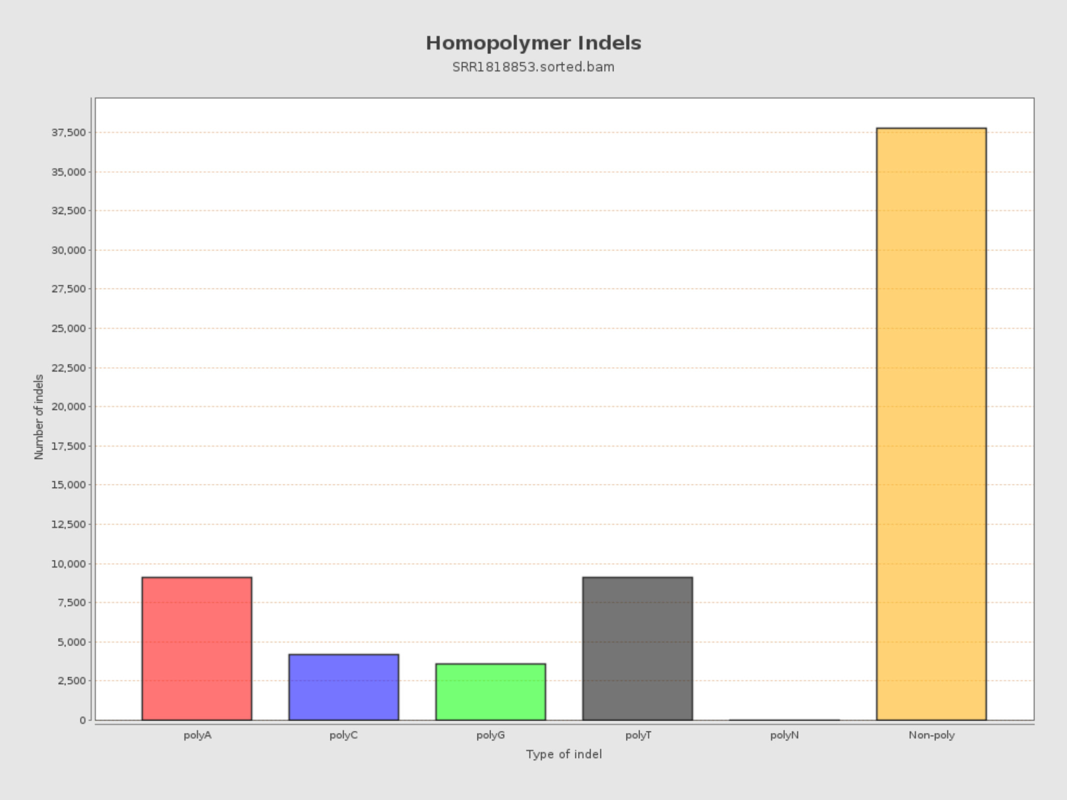
9. Results : Mapped Reads GC-content Distribution



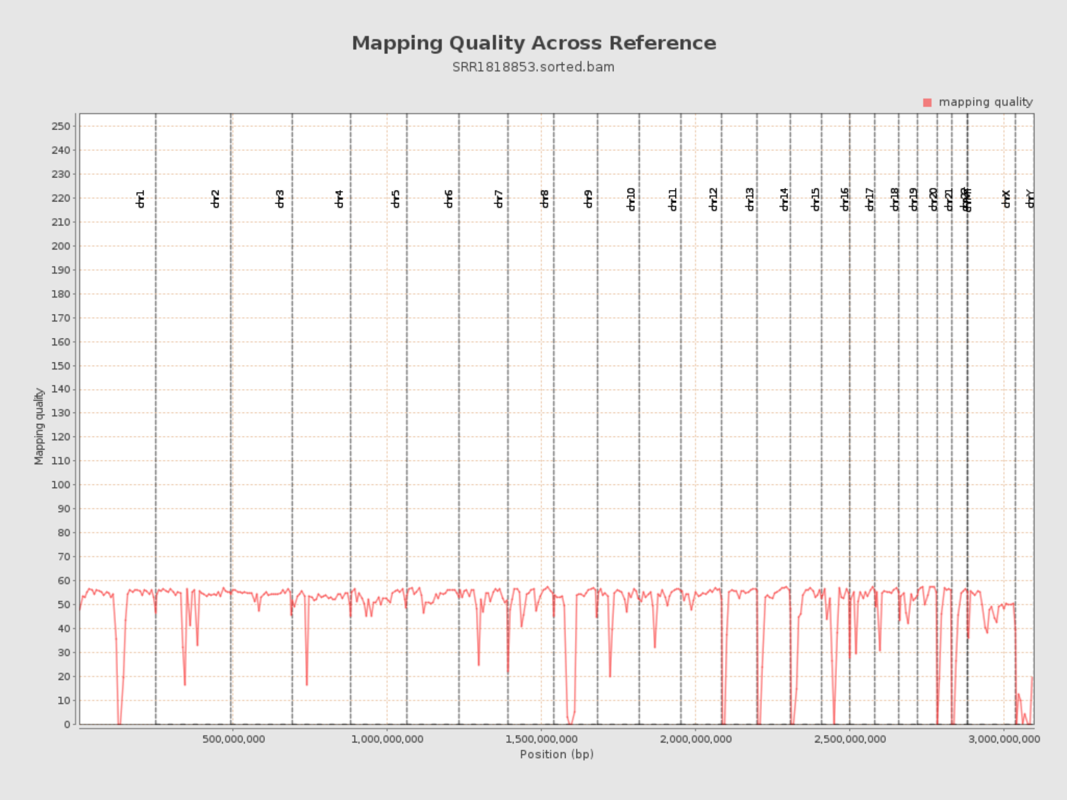
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram