Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 05:49:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818896.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_SRR1818896 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818896.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 05:49:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818896.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,387,818
Mapped reads	1,325,693 / 95.52%
Unmapped reads	62,125 / 4.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,718 / 1.49%
Read min/max/mean length	30 / 101 / 101.57
Duplicated reads (estimated)	232,045 / 16.72%
Duplication rate	14.45%
Clipped reads	1,339,392 / 96.51%

2.2. ACGT Content

Number/percentage of A's	35,715,265 / 29.16%
Number/percentage of C's	25,718,747 / 21%
Number/percentage of T's	35,507,143 / 28.99%
Number/percentage of G's	25,522,731 / 20.84%
Number/percentage of N's	1,803 / 0%
GC Percentage	41.84%

2.3. Coverage

Mean	0.0396

Standard Deviation	0.5151

2.4. Mapping Quality

Mean Mapping Quality	49.13

2.5. Mismatches and indels

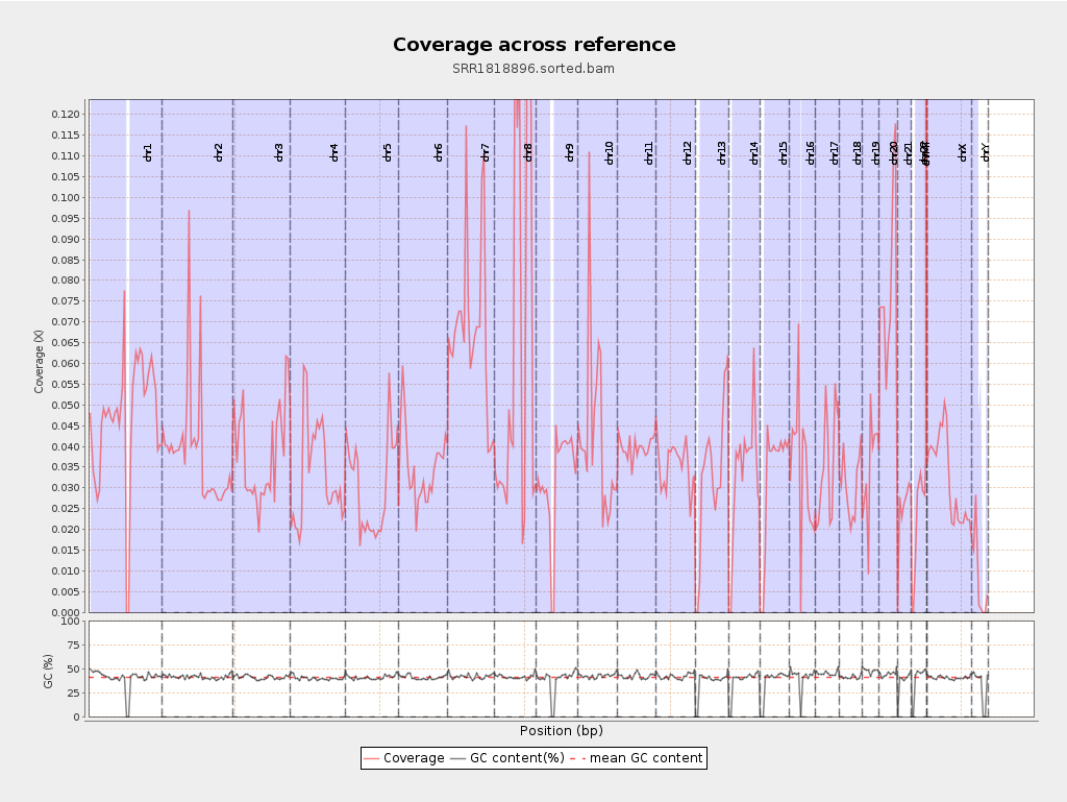
General error rate	0.66%
Mismatches	760,573
Insertions	18,042
Mapped reads with at least one insertion	1.31%
Deletions	40,693
Mapped reads with at least one deletion	3%
Homopolymer indels	40.2%

2.6. Chromosome stats

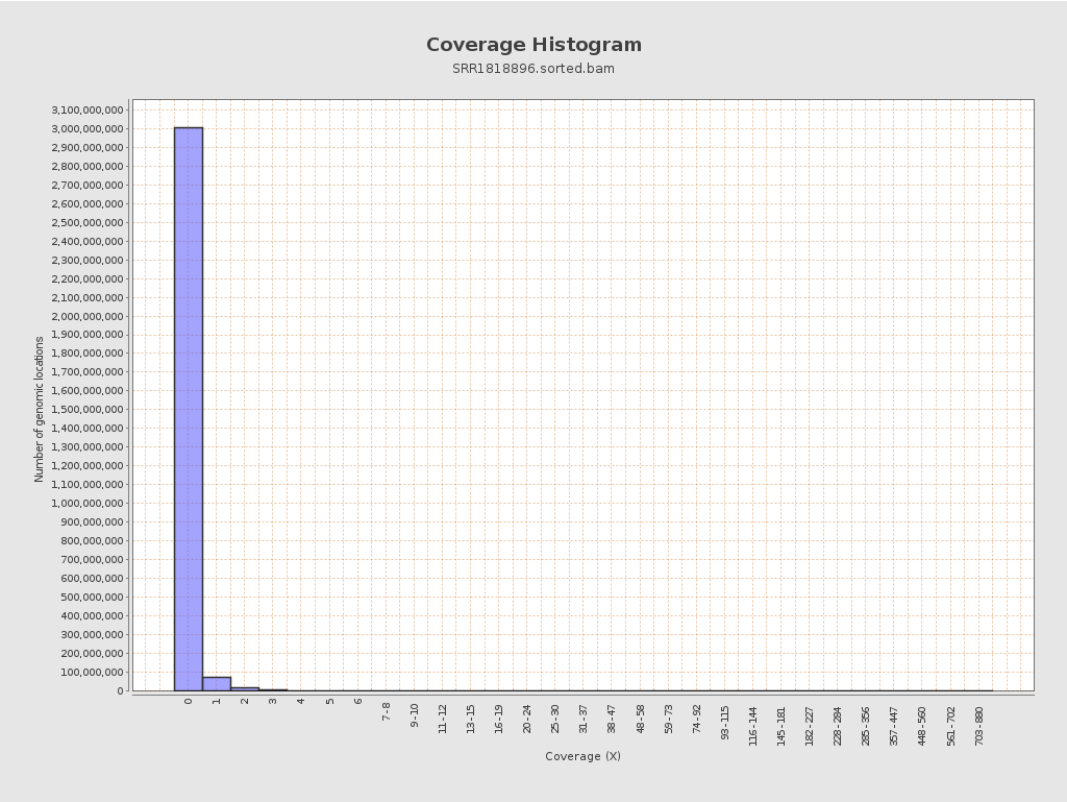
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	11574493	0.0464	0.7537
chr2	243199373	9399967	0.0387	0.7769
chr3	198022430	7582374	0.0383	0.245
chr4	191154276	6285566	0.0329	0.314
chr5	180915260	5431800	0.03	0.2293
chr6	171115067	5970676	0.0349	0.2556
chr7	159138663	10986654	0.069	1.0866

chr8	146364022	10781927	0.0737	0.4236
chr9	141213431	4507008	0.0319	0.4228
chr10	135534747	5746510	0.0424	0.772
chr11	135006516	5358128	0.0397	0.2953
chr12	133851895	4778628	0.0357	0.2414
chr13	115169878	3789048	0.0329	0.2249
chr14	107349540	3568368	0.0332	0.2484
chr15	102531392	3355558	0.0327	0.2307
chr16	90354753	3051814	0.0338	0.5288
chr17	81195210	2946051	0.0363	0.3053
chr18	78077248	2387787	0.0306	0.4782
chr19	59128983	2049789	0.0347	0.5905
chr20	63025520	4965194	0.0788	0.3746
chr21	48129895	1201499	0.025	0.2435
chr22	51304566	1100306	0.0214	0.2032
chrMT	16571	207231	12.5056	8.3257
chrX	155270560	5047434	0.0325	0.2687
chrY	59373566	471885	0.0079	0.6239

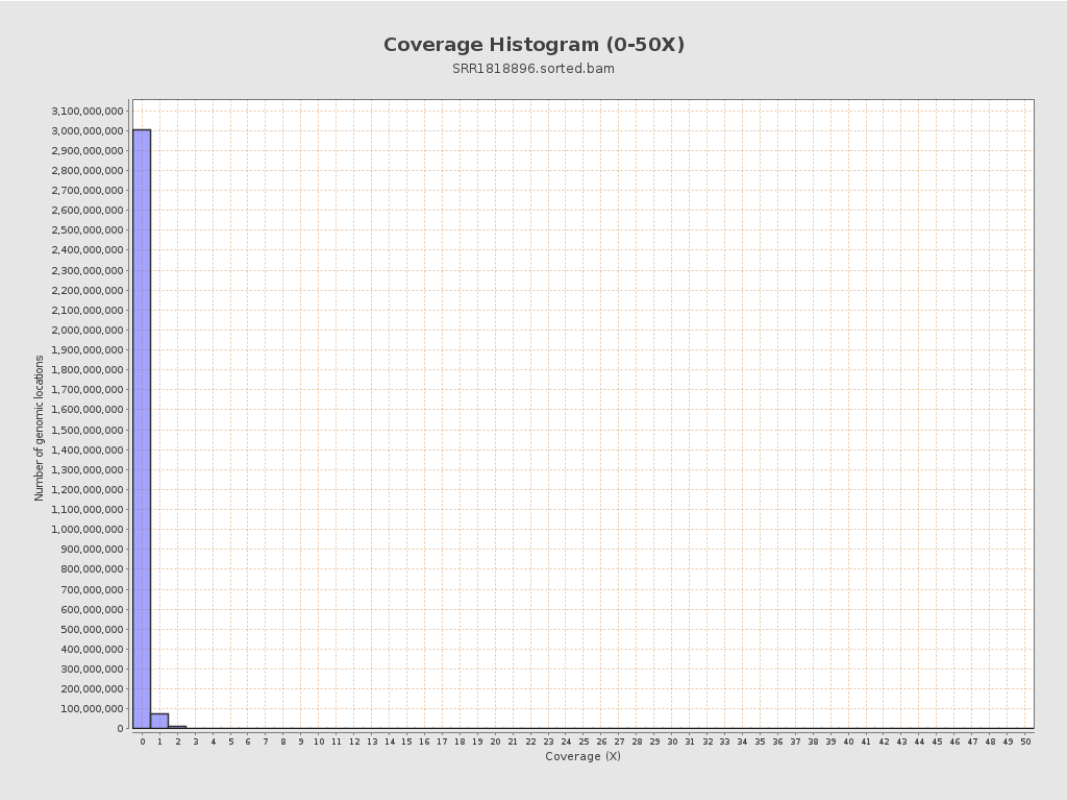
3. Results : Coverage across reference



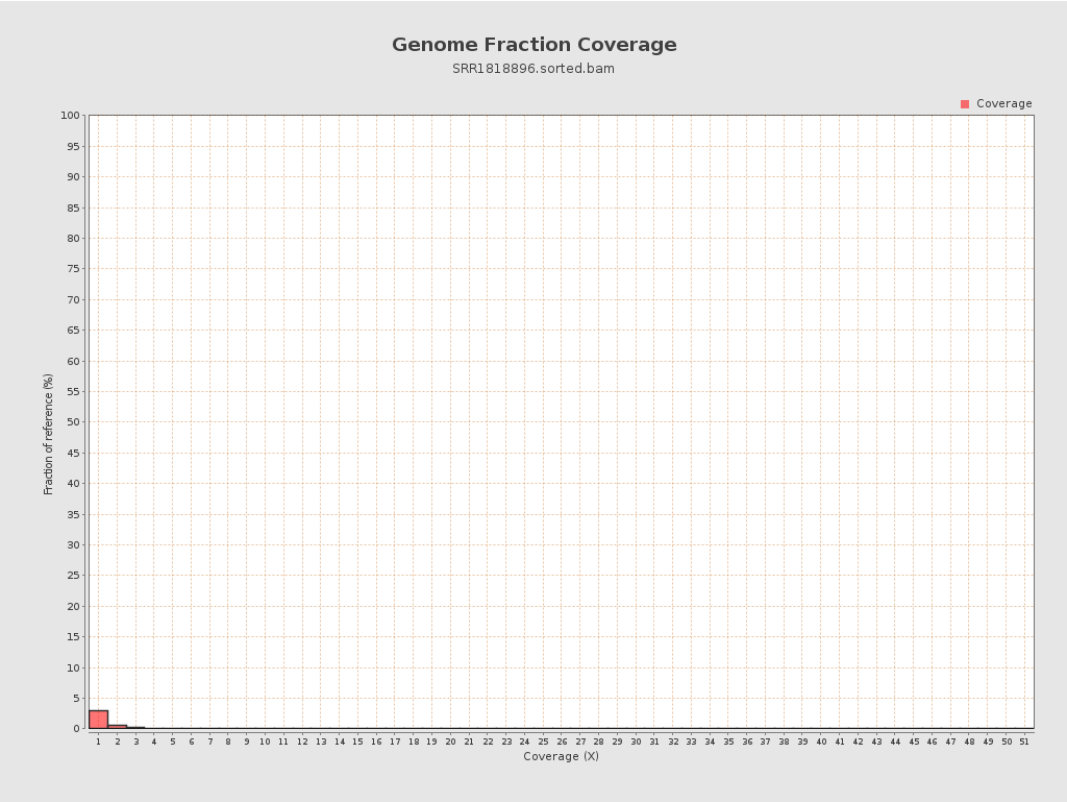
4. Results : Coverage Histogram



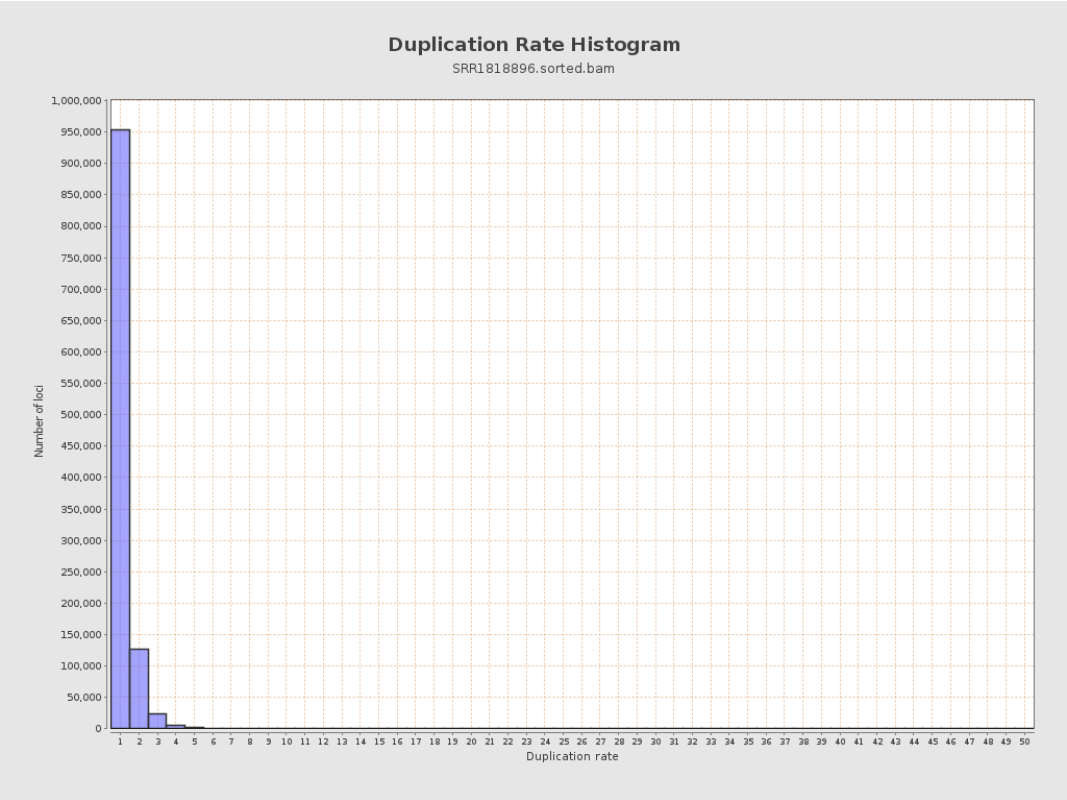
5. Results : Coverage Histogram (0-50X)



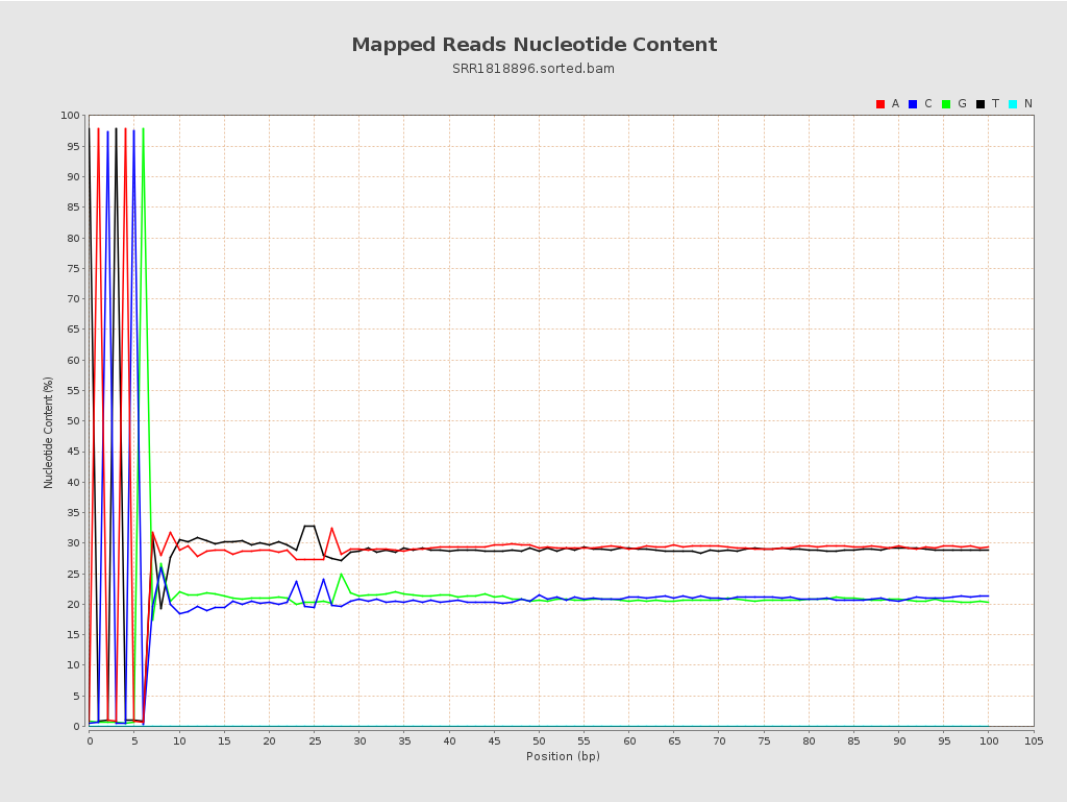
6. Results : Genome Fraction Coverage



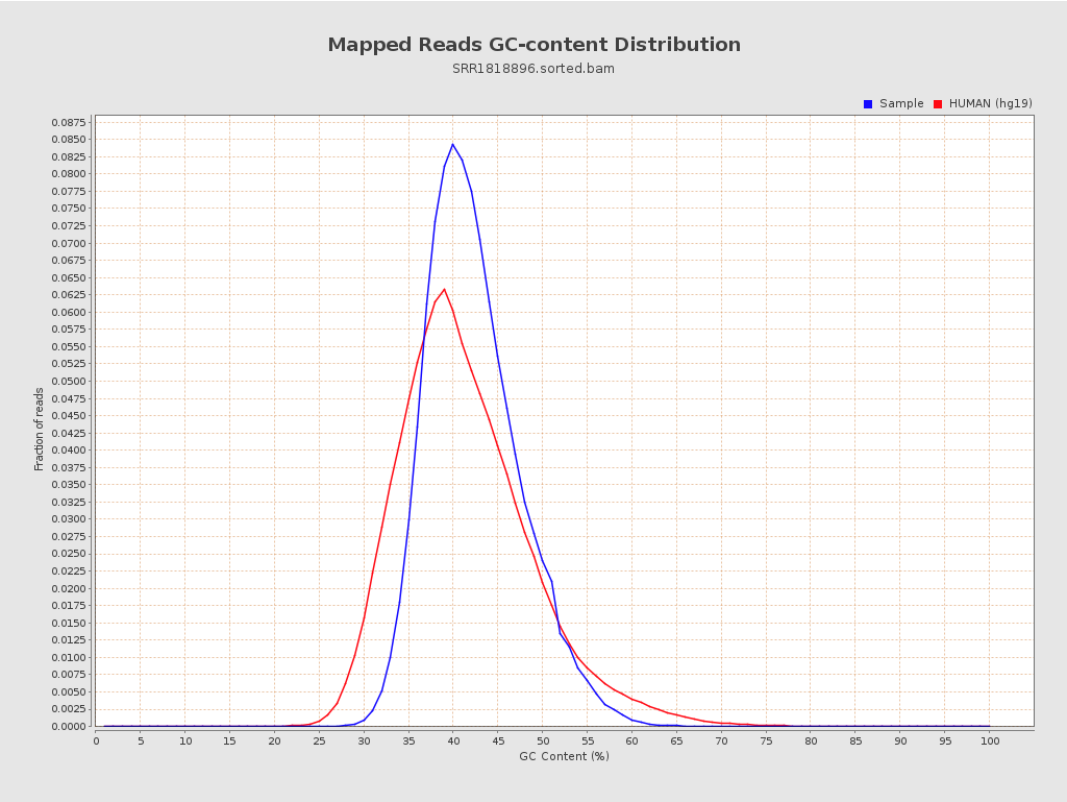
7. Results : Duplication Rate Histogram



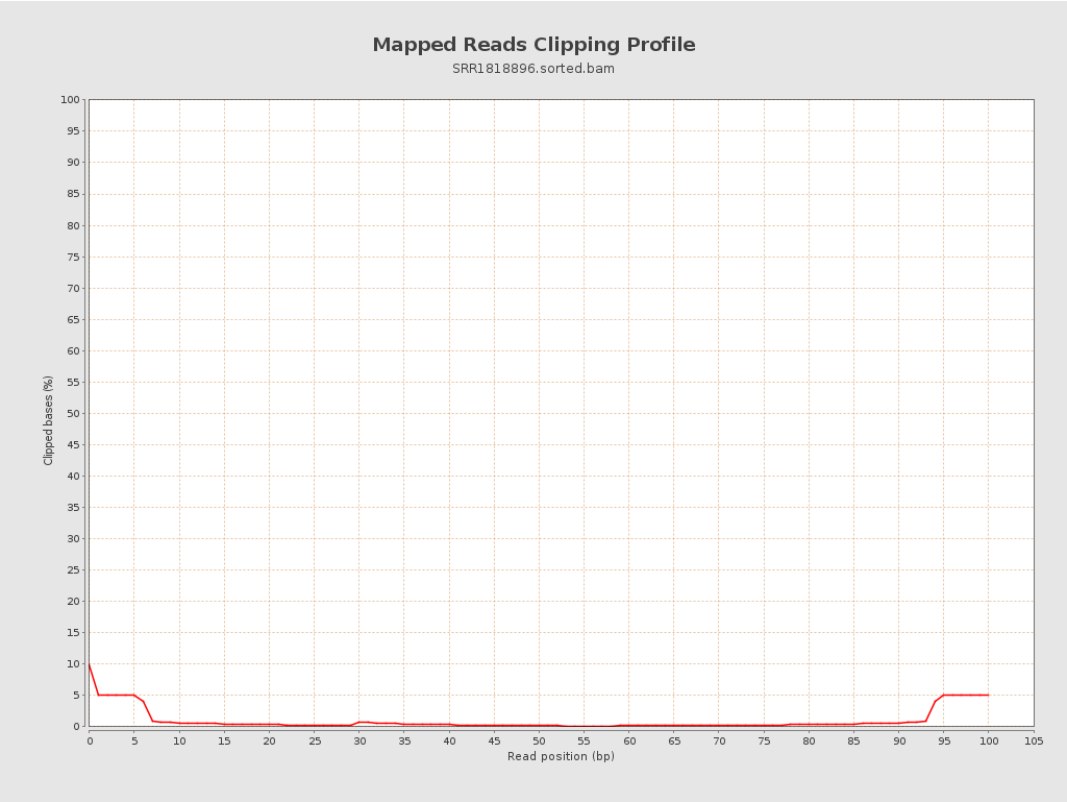
8. Results : Mapped Reads Nucleotide Content



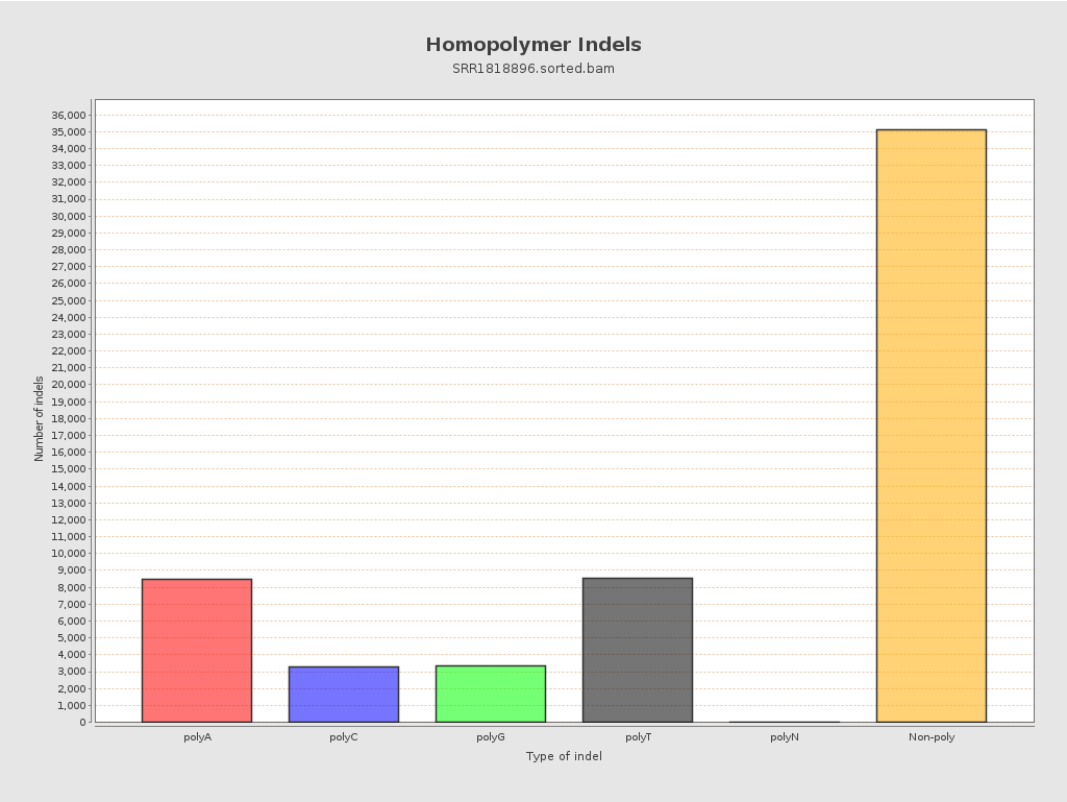
9. Results : Mapped Reads GC-content Distribution



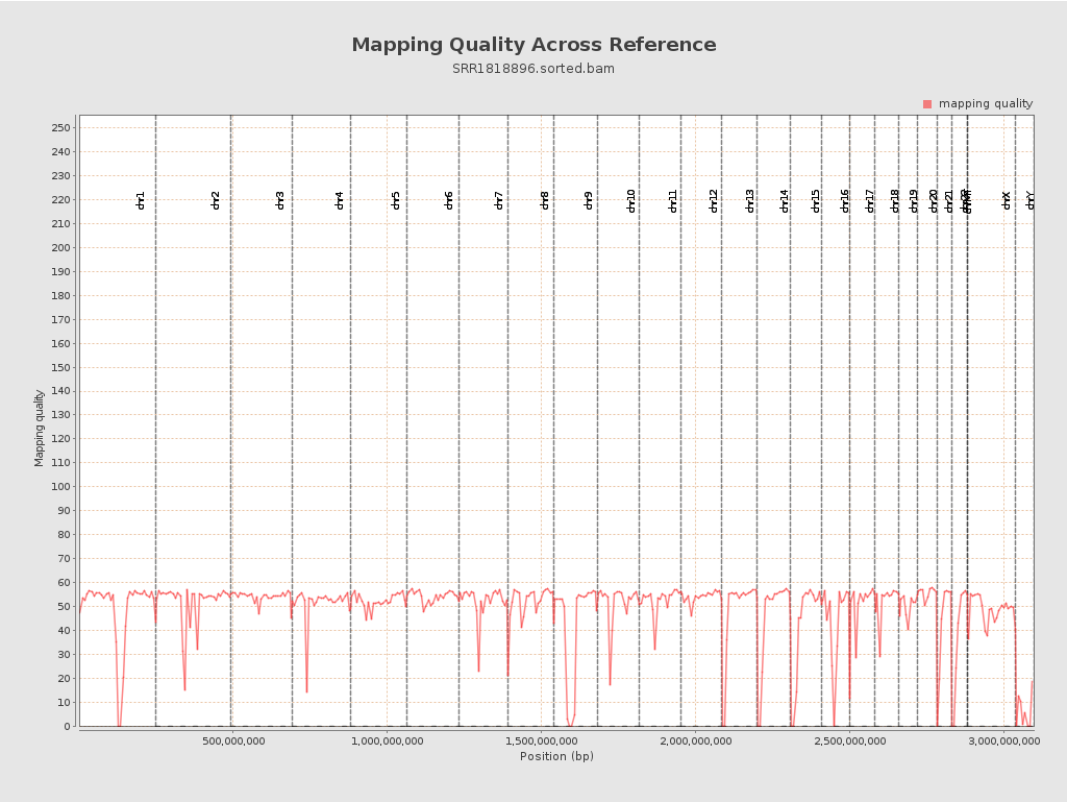
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram