Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 13:47:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818804.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_SRR1818804 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818804.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 13:47:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818804.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,285,550
Mapped reads	1,247,242 / 97.02%
Unmapped reads	38,308 / 2.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,370 / 0.65%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	429,541 / 33.41%
Duplication rate	30.03%
Clipped reads	1,245,621 / 96.89%

2.2. ACGT Content

Number/percentage of A's	24,404,456 / 28.8%
Number/percentage of C's	18,703,572 / 22.07%
Number/percentage of T's	23,725,907 / 28%
Number/percentage of G's	17,900,078 / 21.12%
Number/percentage of N's	5,540 / 0.01%
GC Percentage	43.2%

2.3. Coverage

Mean	0.0274

Standard Deviation	0.3741

2.4. Mapping Quality

Mean Mapping Quality	47.6

2.5. Mismatches and indels

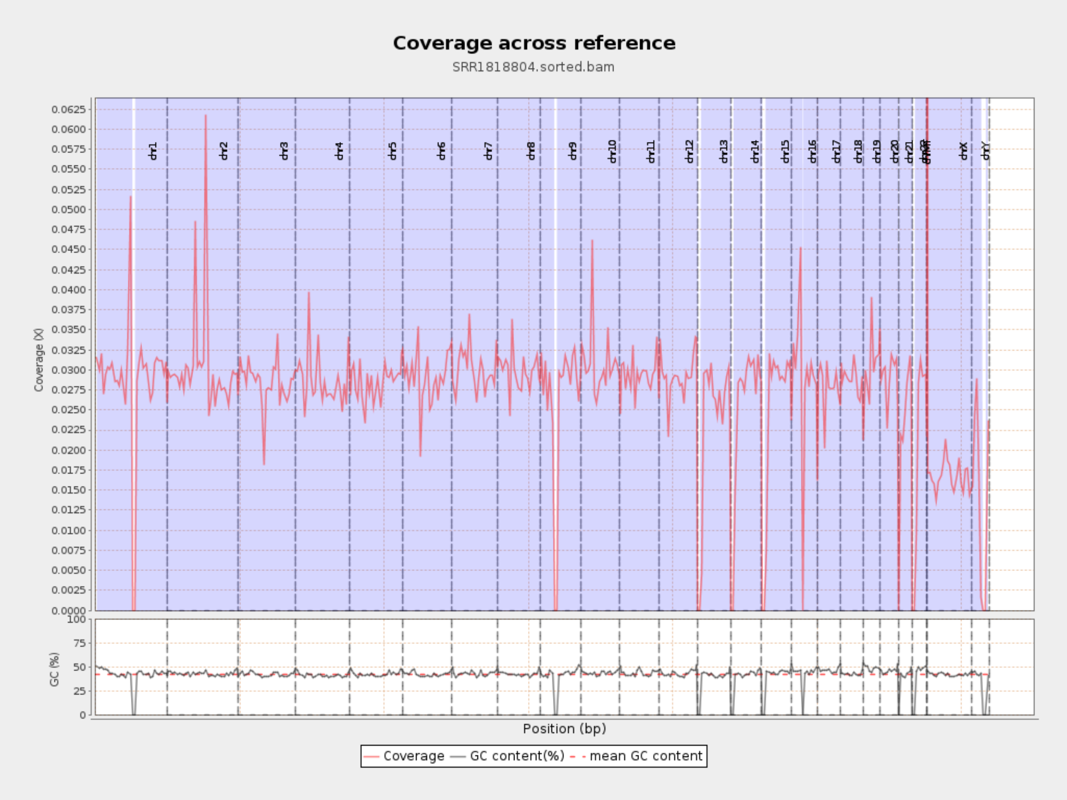
General error rate	0.55%
Mismatches	445,901
Insertions	10,866
Mapped reads with at least one insertion	0.86%
Deletions	21,075
Mapped reads with at least one deletion	1.67%
Homopolymer indels	39.35%

2.6. Chromosome stats

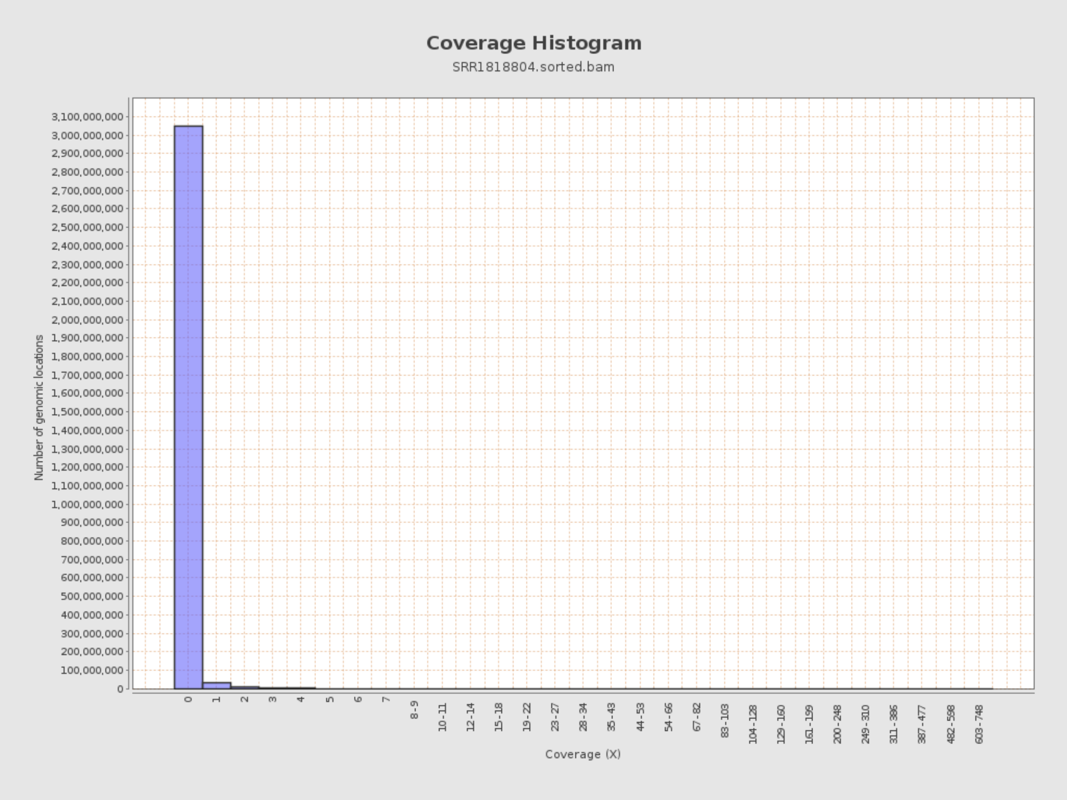
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7117806	0.0286	0.5792
chr2	243199373	7382080	0.0304	0.5789
chr3	198022430	5627056	0.0284	0.263
chr4	191154276	5481041	0.0287	0.3085
chr5	180915260	5143586	0.0284	0.2752
chr6	171115067	4969346	0.029	0.2989
chr7	159138663	4779091	0.03	0.3317

chr8	146364022	4375914	0.0299	0.298
chr9	141213431	3664498	0.026	0.3019
chr10	135534747	4183752	0.0309	0.4213
chr11	135006516	3976493	0.0295	0.2964
chr12	133851895	3907739	0.0292	0.2935
chr13	115169878	2661739	0.0231	0.2391
chr14	107349540	2654903	0.0247	0.2917
chr15	102531392	2479081	0.0242	0.246
chr16	90354753	2574665	0.0285	0.4359
chr17	81195210	2269076	0.0279	0.2805
chr18	78077248	2252964	0.0289	0.367
chr19	59128983	1806325	0.0305	0.4946
chr20	63025520	1832672	0.0291	0.285
chr21	48129895	1129204	0.0235	0.2643
chr22	51304566	1031465	0.0201	0.2458
chrMT	16571	46295	2.7937	3.1772
chrX	155270560	2608132	0.0168	0.2322
chrY	59373566	820141	0.0138	0.6587

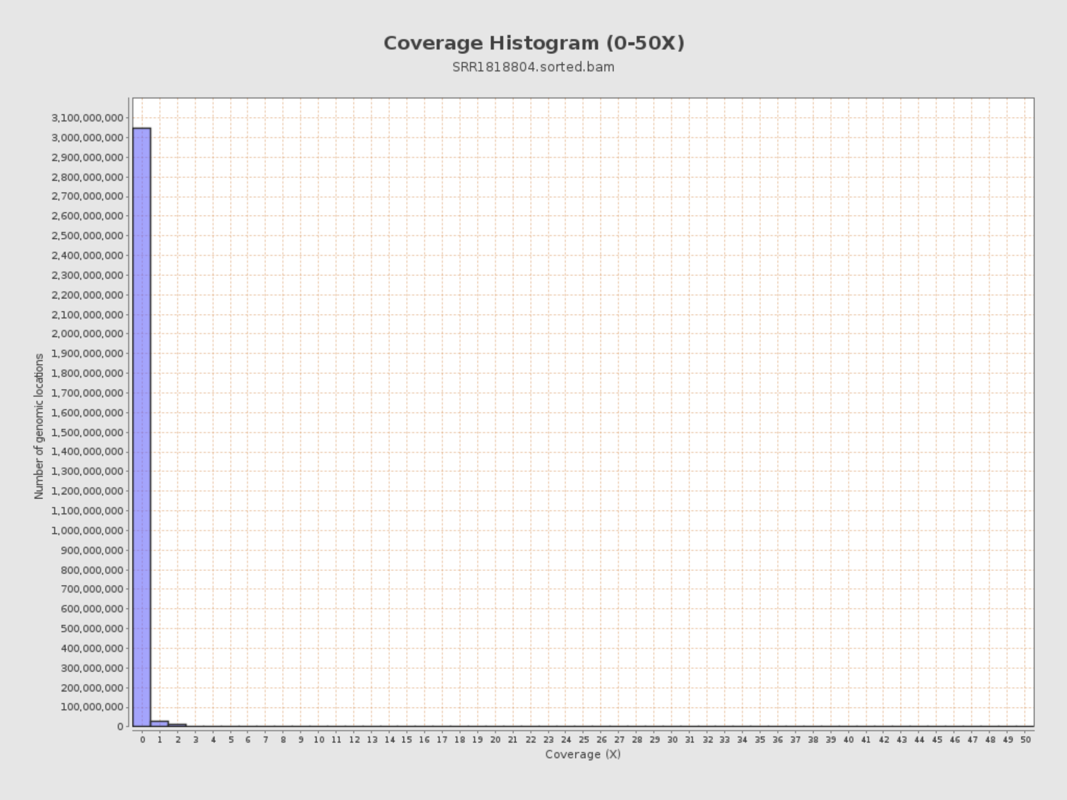
3. Results : Coverage across reference



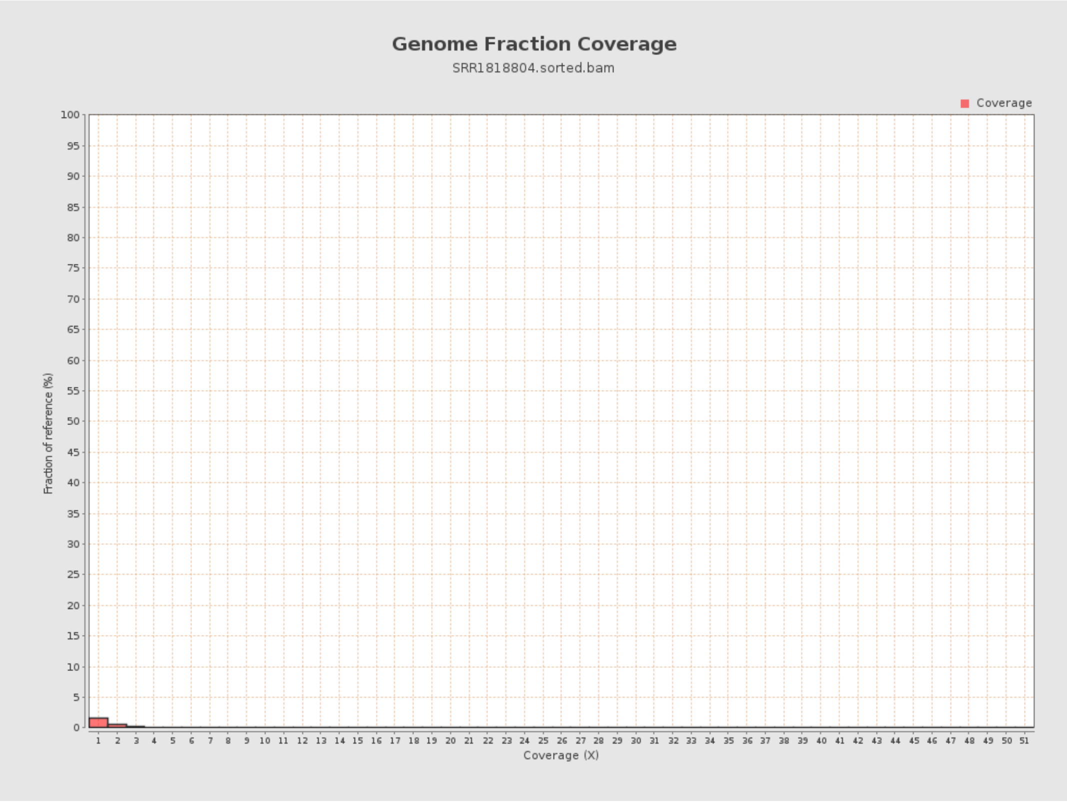
4. Results : Coverage Histogram



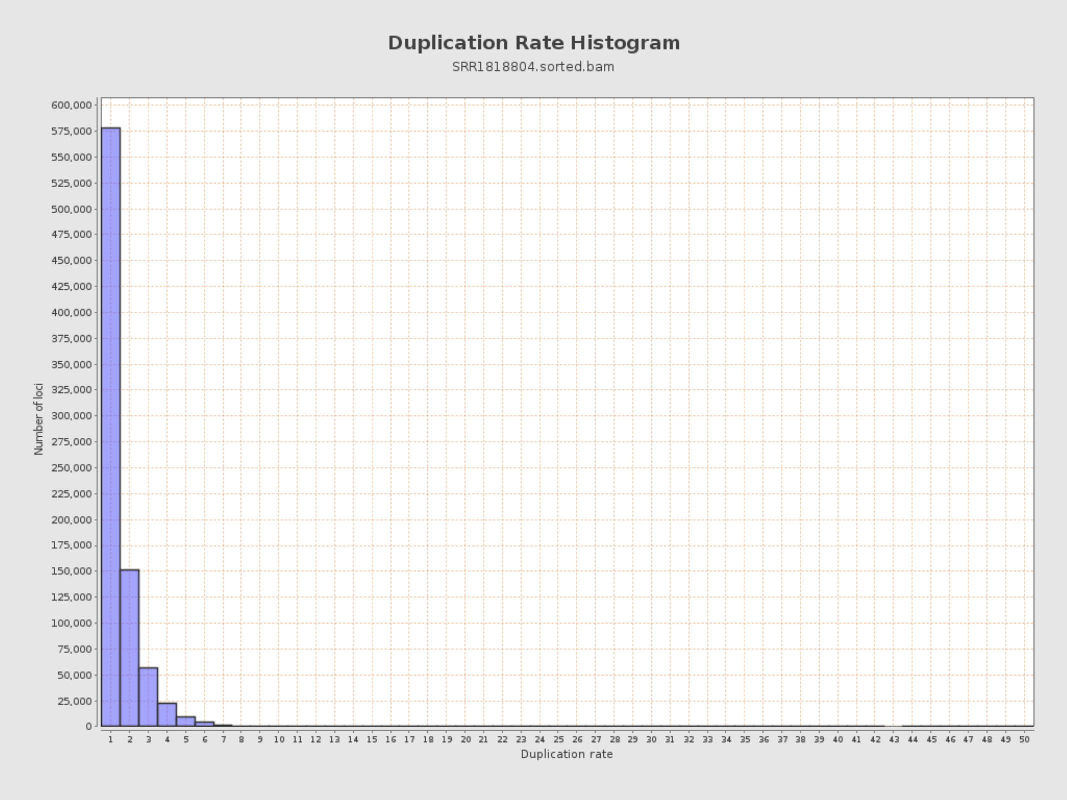
5. Results : Coverage Histogram (0-50X)



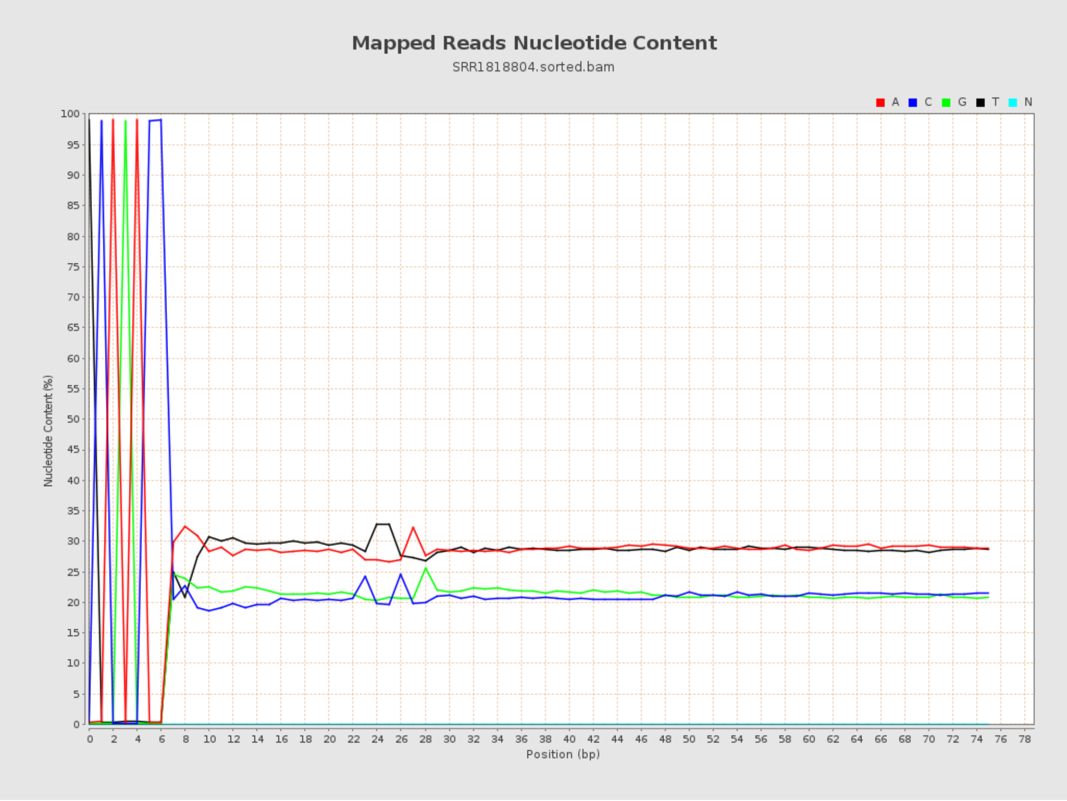
6. Results : Genome Fraction Coverage



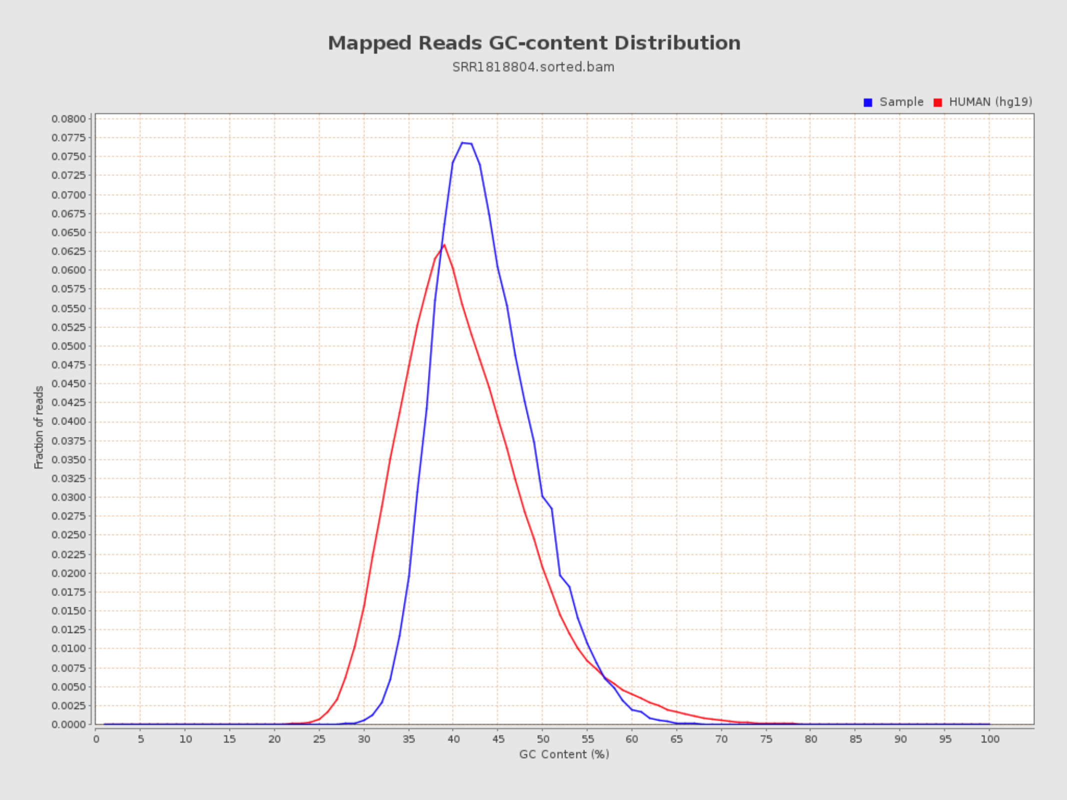
7. Results : Duplication Rate Histogram



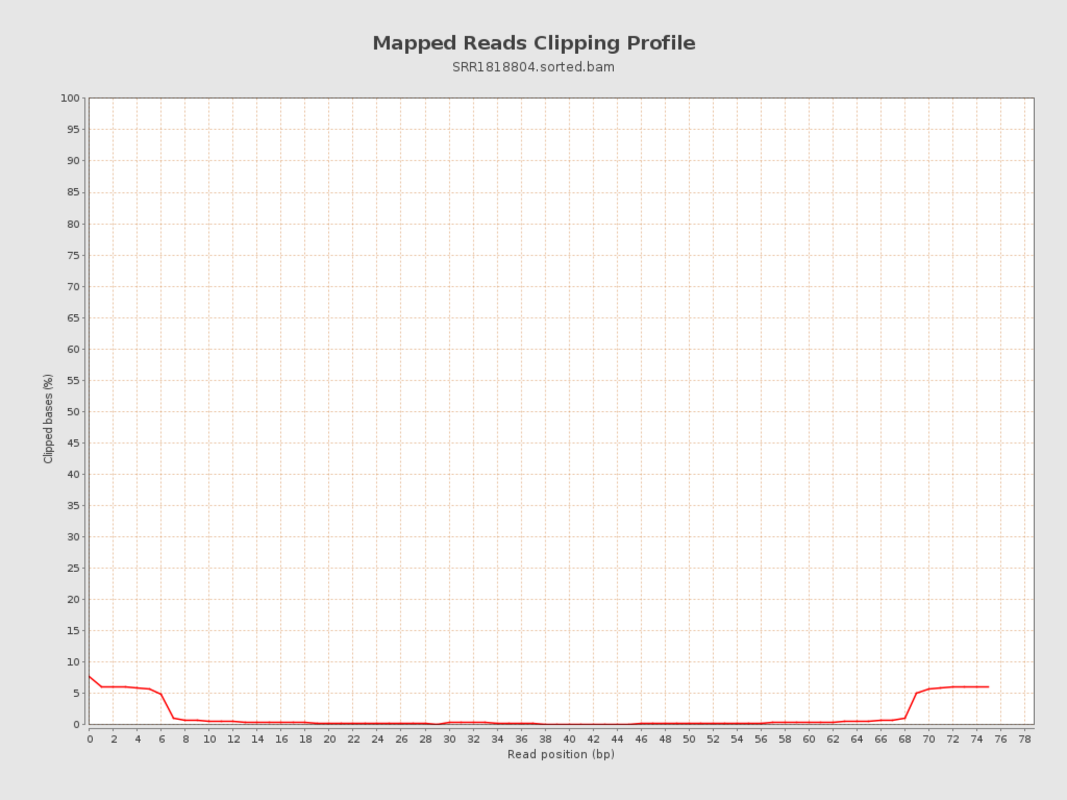
8. Results : Mapped Reads Nucleotide Content



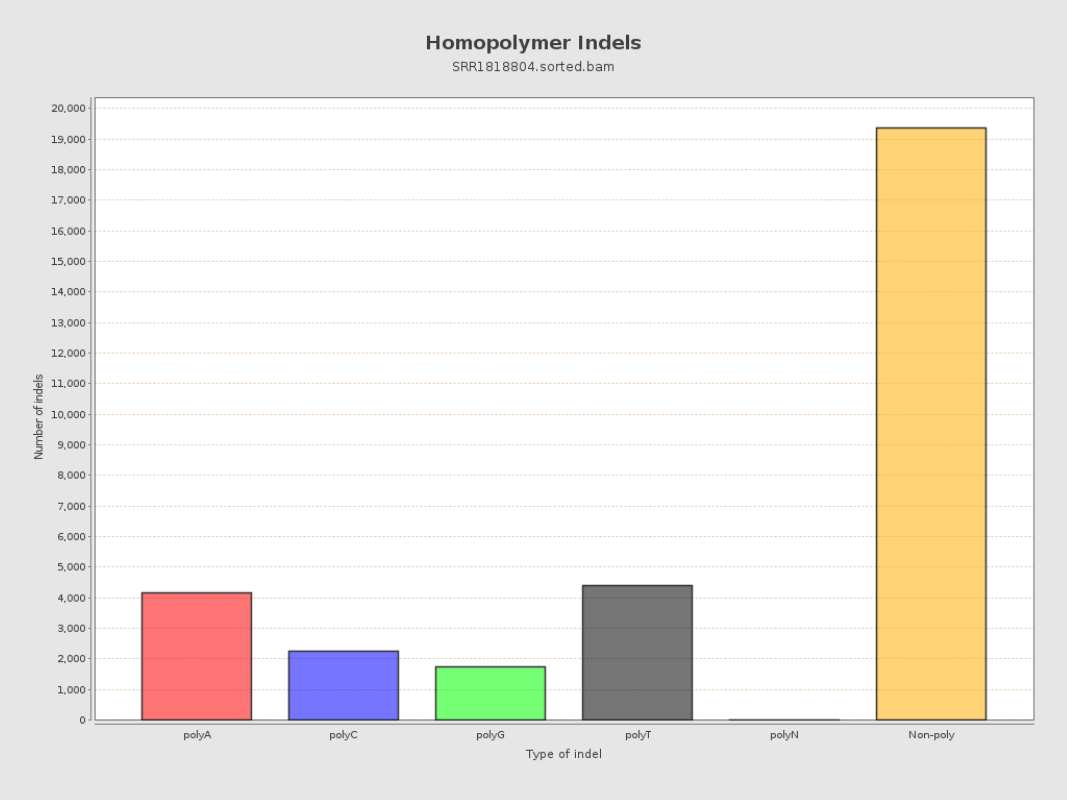
9. Results : Mapped Reads GC-content Distribution



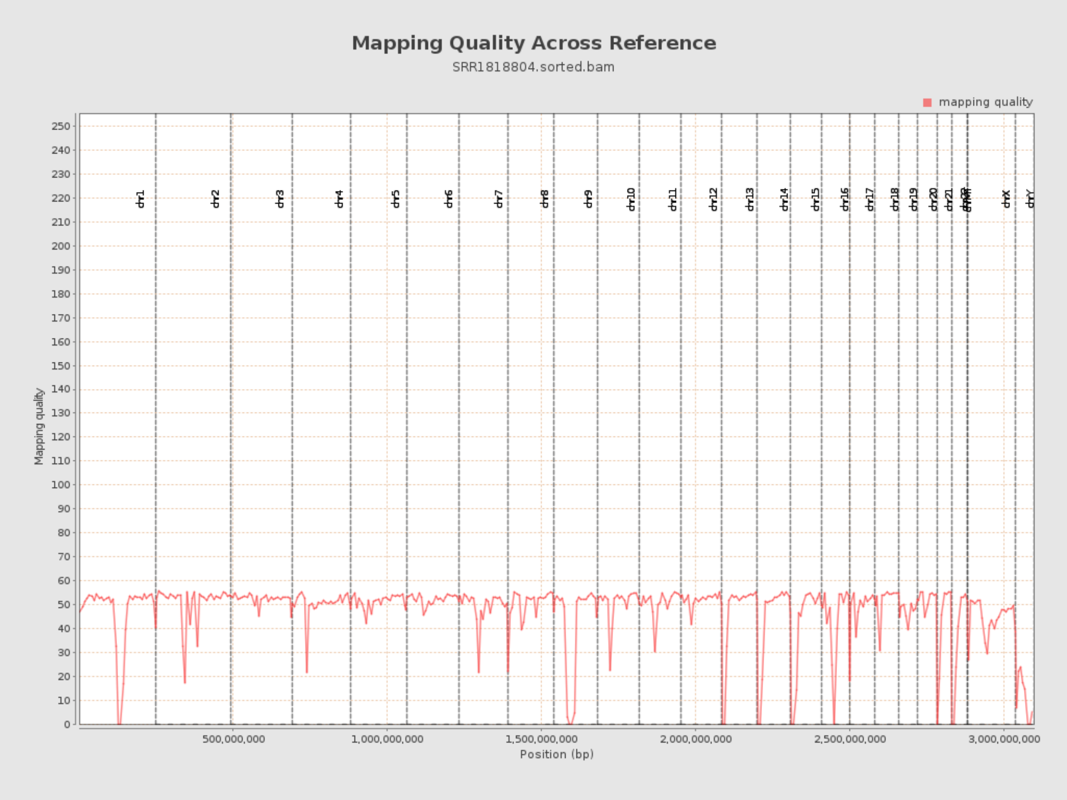
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram