Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 20:49:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818840.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_SRR1818840 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818840.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 20:49:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818840.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,847,684
Mapped reads	1,824,056 / 98.72%
Unmapped reads	23,628 / 1.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,867 / 1.56%
Read min/max/mean length	30 / 101 / 101.6
Duplicated reads (estimated)	435,170 / 23.55%
Duplication rate	20.37%
Clipped reads	1,835,140 / 99.32%

2.2. ACGT Content

Number/percentage of A's	48,044,280 / 28.48%
Number/percentage of C's	35,563,311 / 21.08%
Number/percentage of T's	48,470,762 / 28.73%
Number/percentage of G's	36,618,039 / 21.71%
Number/percentage of N's	2,289 / 0%
GC Percentage	42.79%

2.3. Coverage

Mean	0.0545

Standard Deviation	0.6844

2.4. Mapping Quality

Mean Mapping Quality	49.35

2.5. Mismatches and indels

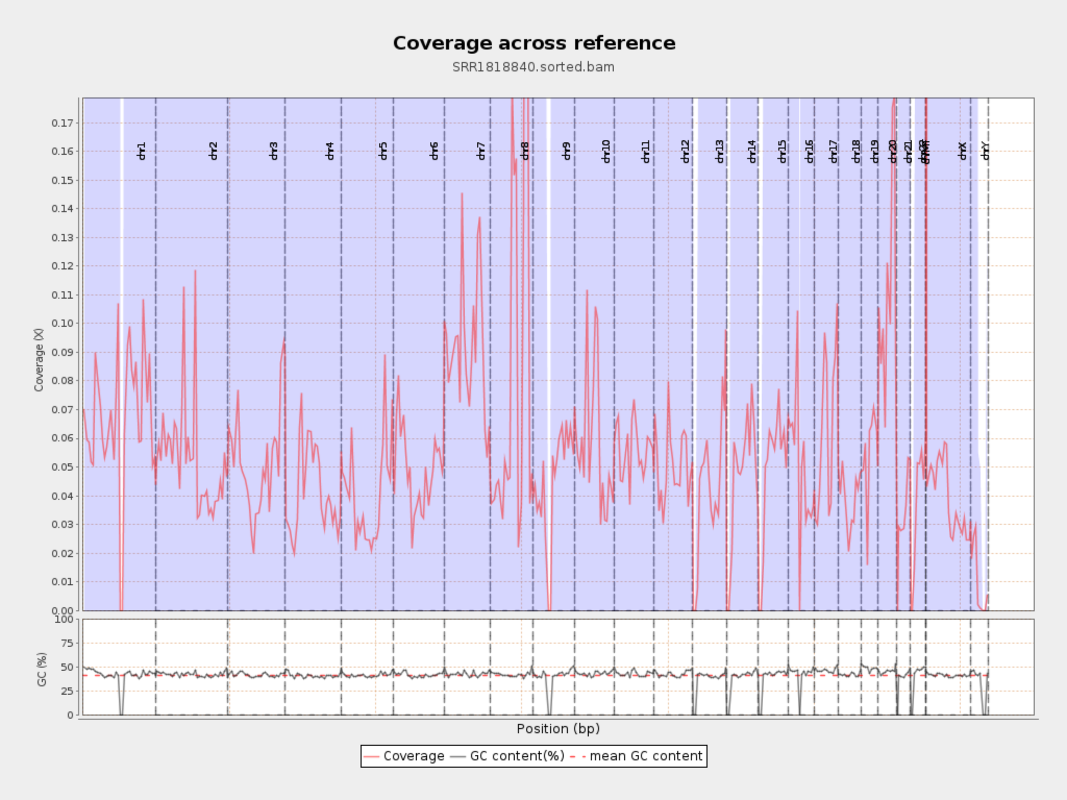
General error rate	0.63%
Mismatches	998,405
Insertions	26,104
Mapped reads with at least one insertion	1.37%
Deletions	54,035
Mapped reads with at least one deletion	2.89%
Homopolymer indels	41.31%

2.6. Chromosome stats

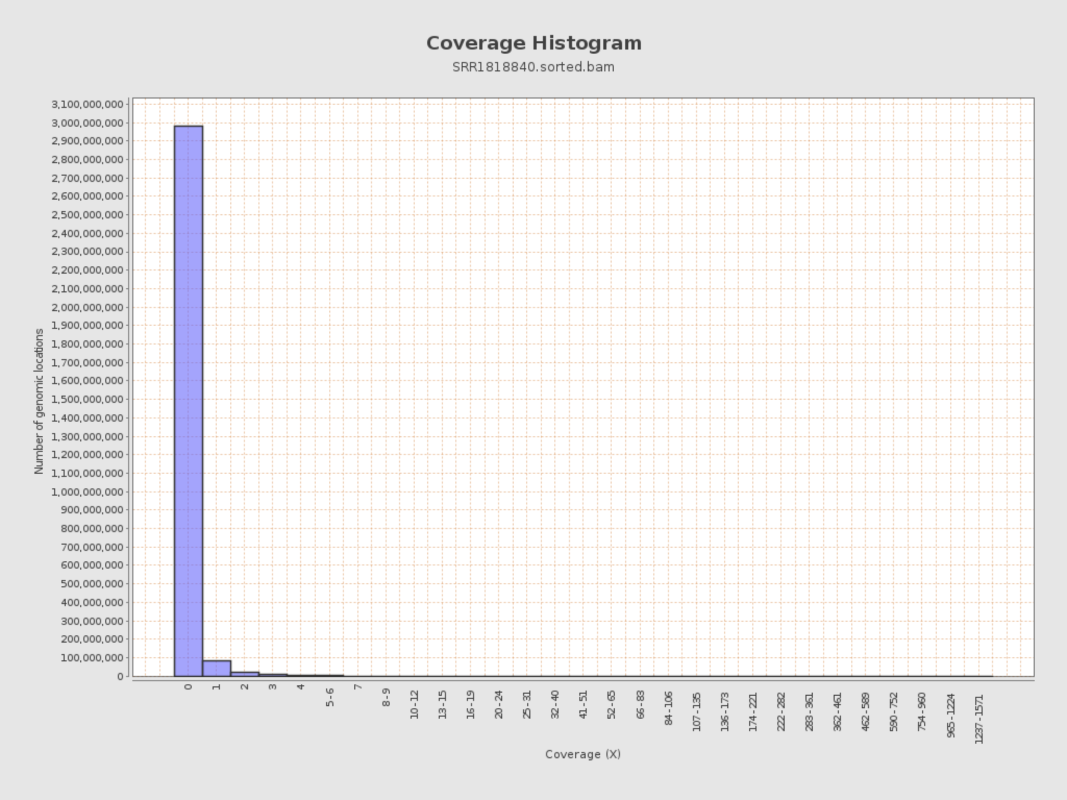
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16754314	0.0672	0.8485
chr2	243199373	12920023	0.0531	1.2718
chr3	198022430	10188043	0.0514	0.3114
chr4	191154276	7953849	0.0416	0.3945
chr5	180915260	7393840	0.0409	0.323
chr6	171115067	8307447	0.0485	0.3473
chr7	159138663	14613948	0.0918	1.3079

chr8	146364022	13914189	0.0951	0.5306
chr9	141213431	6286749	0.0445	0.5007
chr10	135534747	7891129	0.0582	0.8769
chr11	135006516	7586357	0.0562	0.3865
chr12	133851895	6823877	0.051	0.3158
chr13	115169878	4851777	0.0421	0.2797
chr14	107349540	5166360	0.0481	0.3431
chr15	102531392	4876573	0.0476	0.2964
chr16	90354753	4488183	0.0497	0.9553
chr17	81195210	4978130	0.0613	0.4085
chr18	78077248	3030556	0.0388	0.5361
chr19	59128983	3217669	0.0544	0.8099
chr20	63025520	7276766	0.1155	0.5142
chr21	48129895	1618152	0.0336	0.2797
chr22	51304566	1813076	0.0353	0.3182
chrMT	16571	142338	8.5896	6.1497
chrX	155270560	6128579	0.0395	0.3318
chrY	59373566	585880	0.0099	1.0739

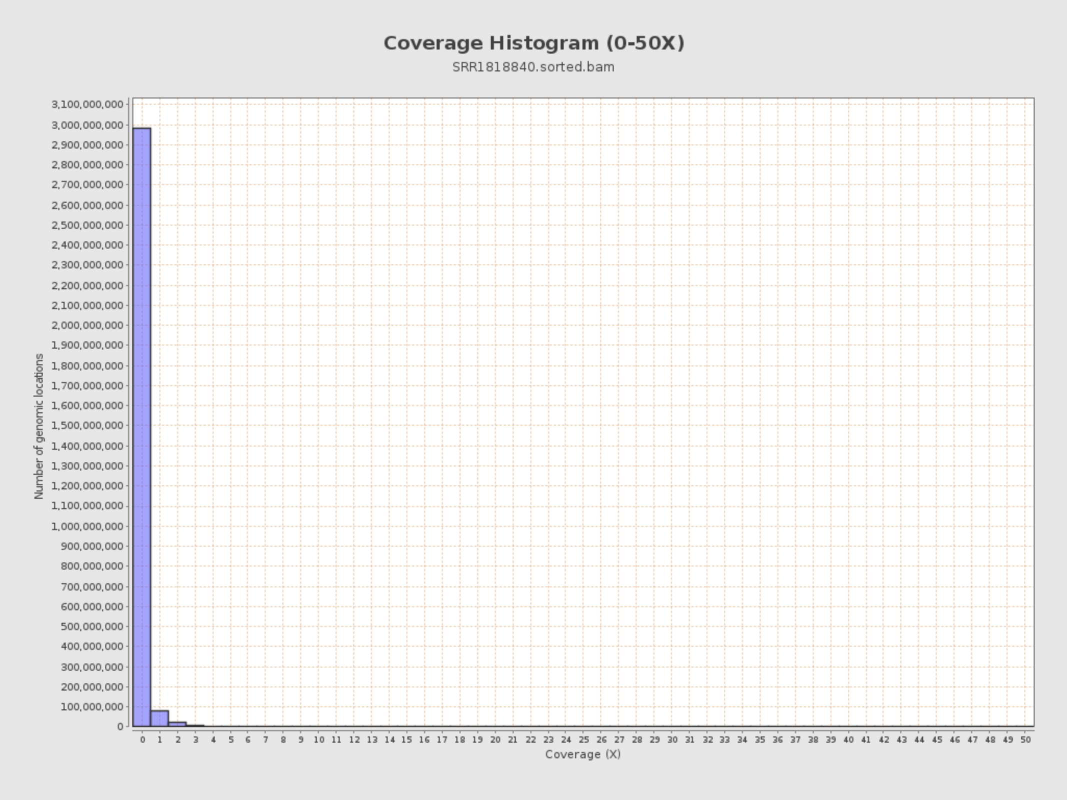
3. Results : Coverage across reference



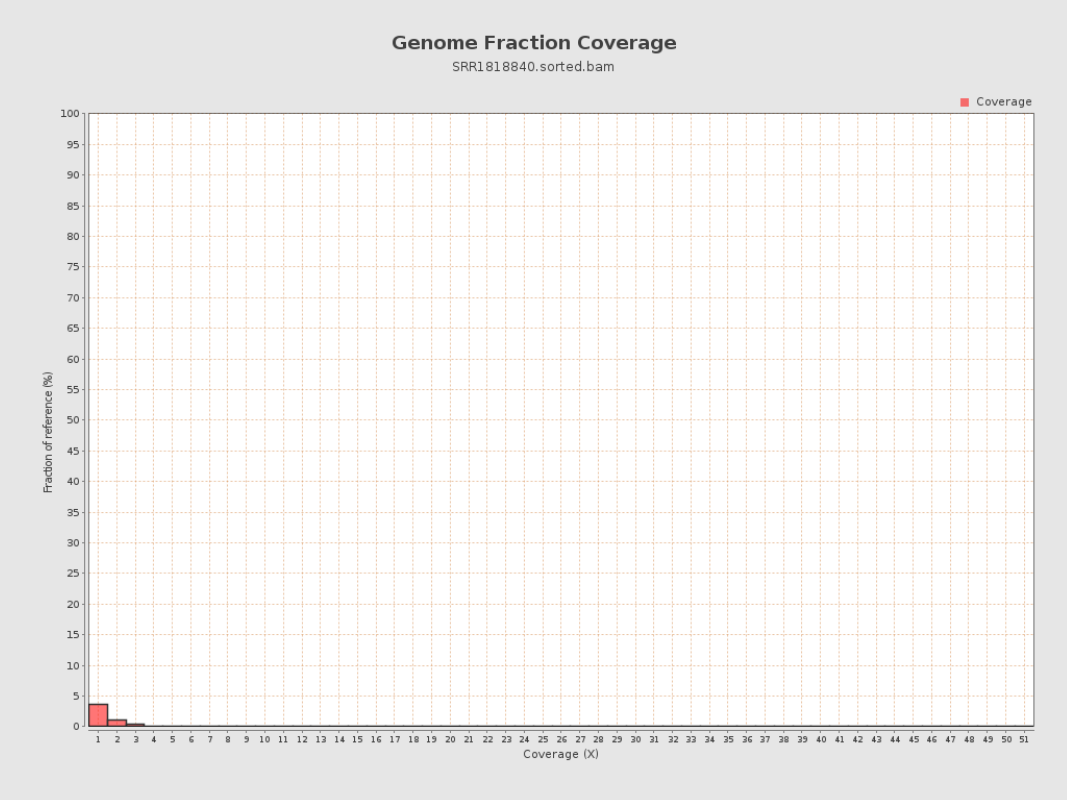
4. Results : Coverage Histogram



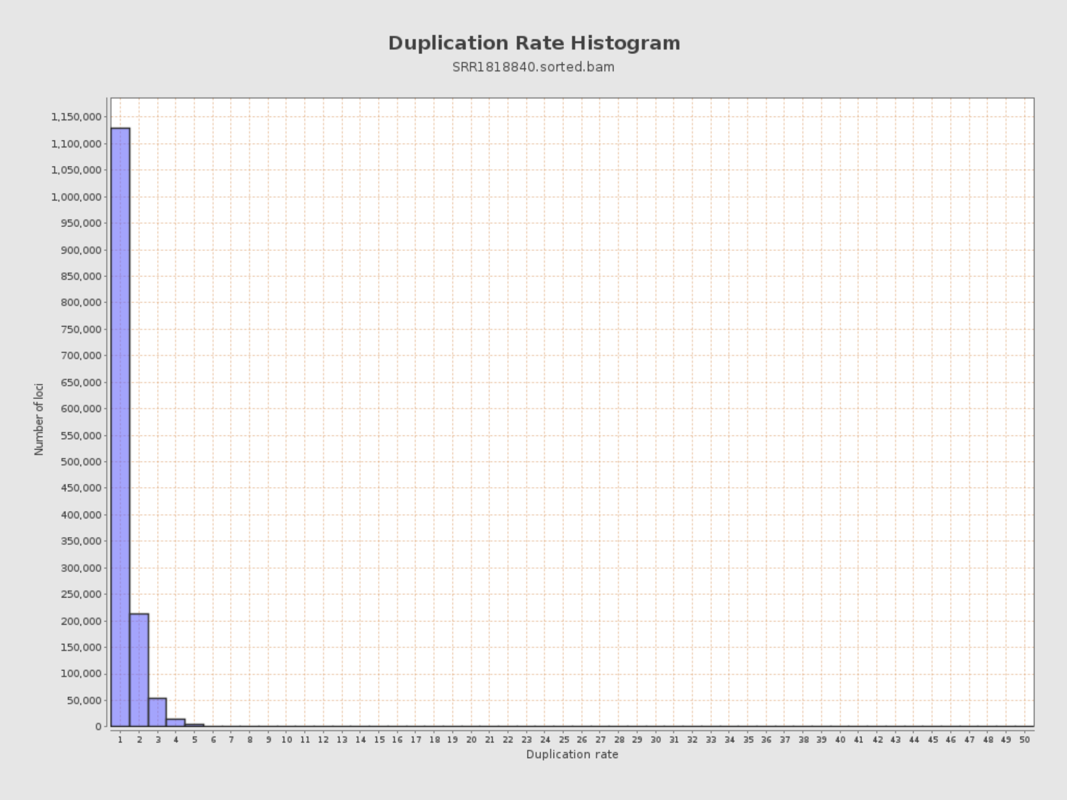
5. Results : Coverage Histogram (0-50X)



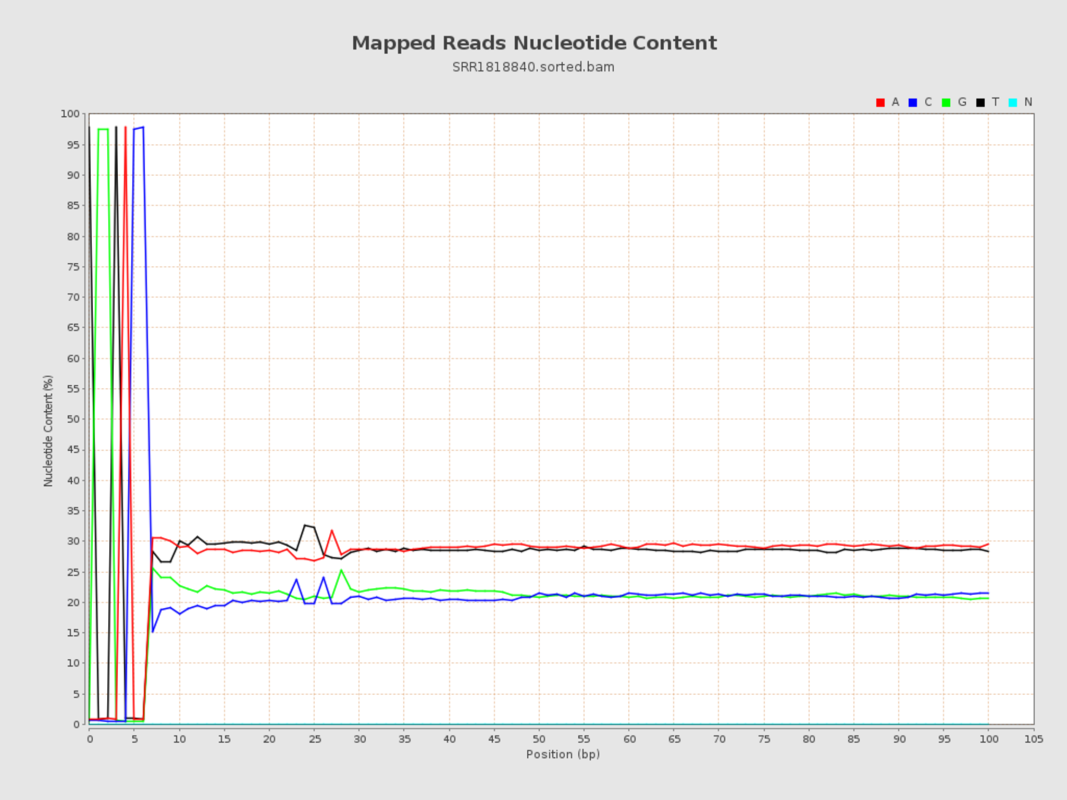
6. Results : Genome Fraction Coverage



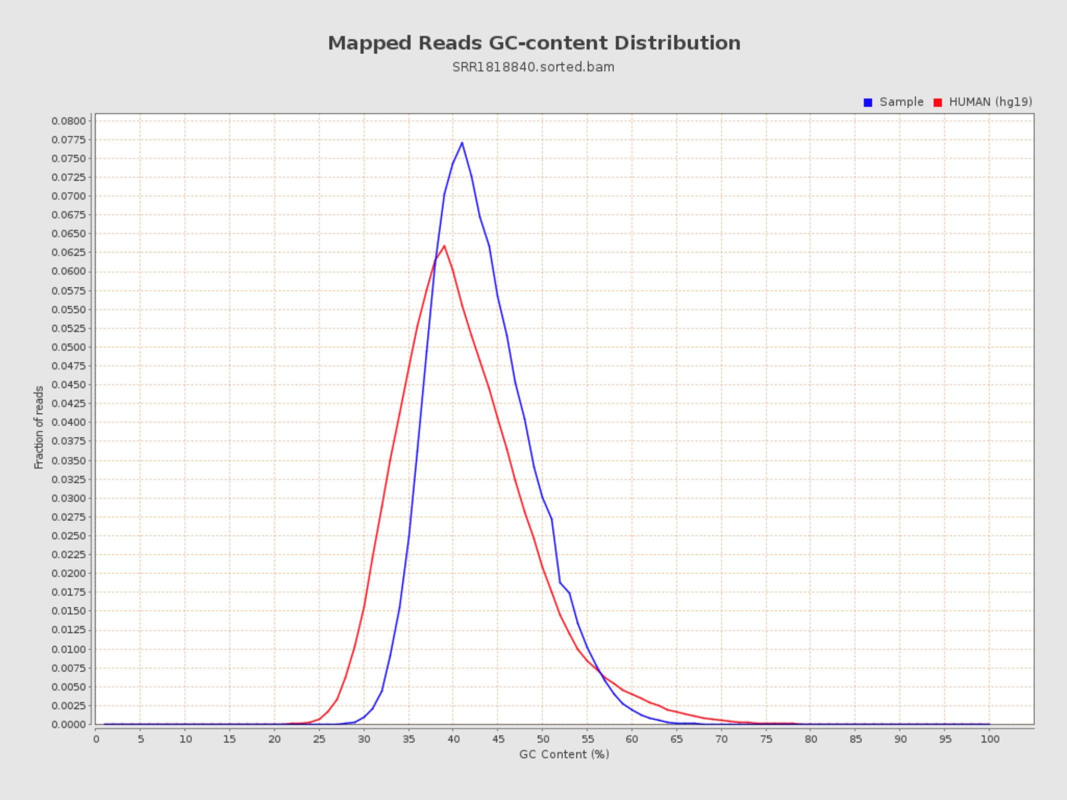
7. Results : Duplication Rate Histogram



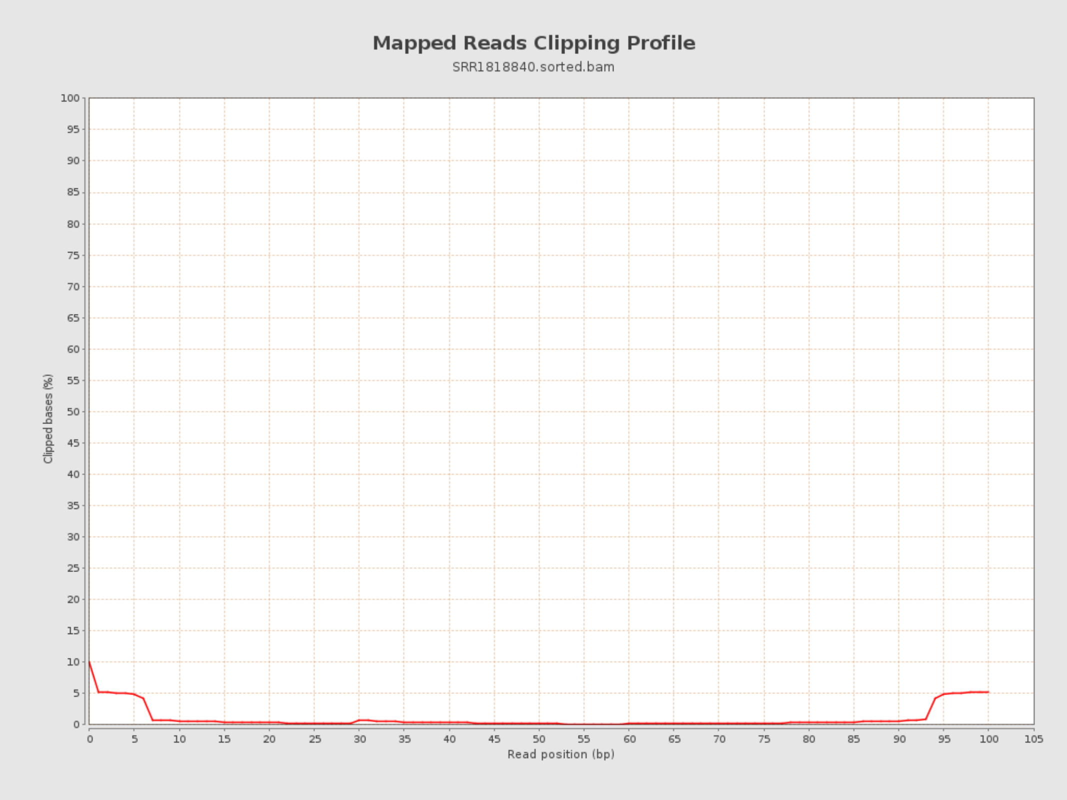
8. Results : Mapped Reads Nucleotide Content



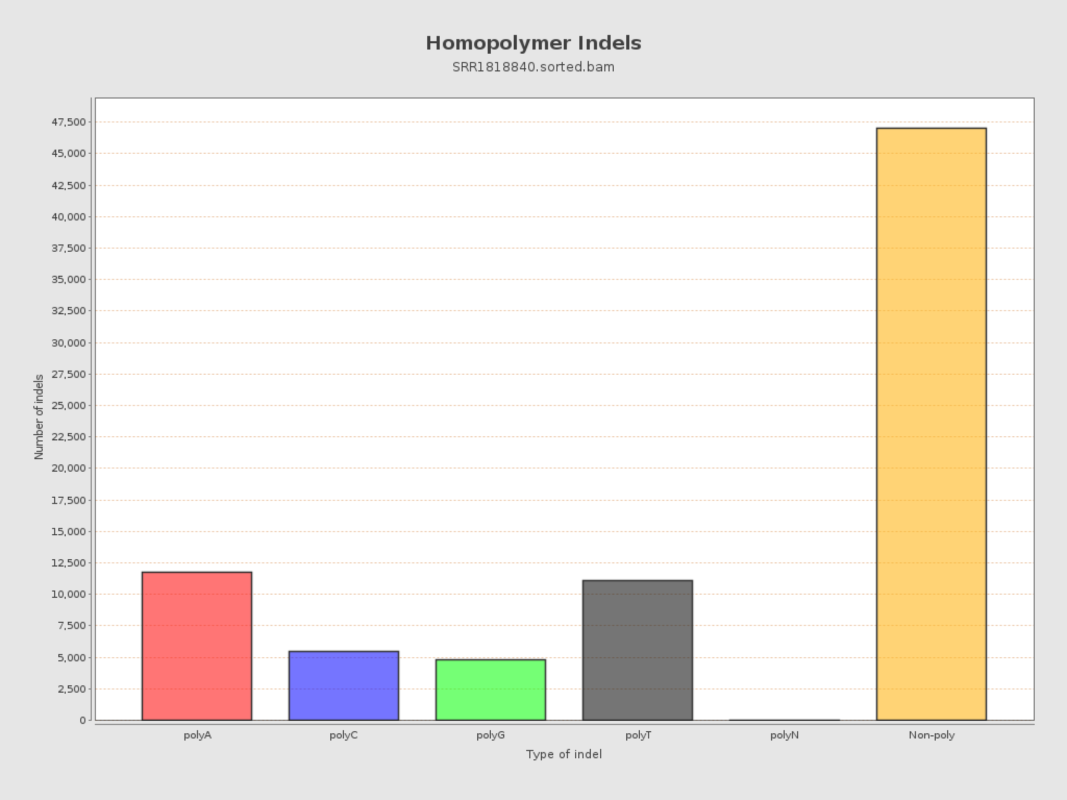
9. Results : Mapped Reads GC-content Distribution



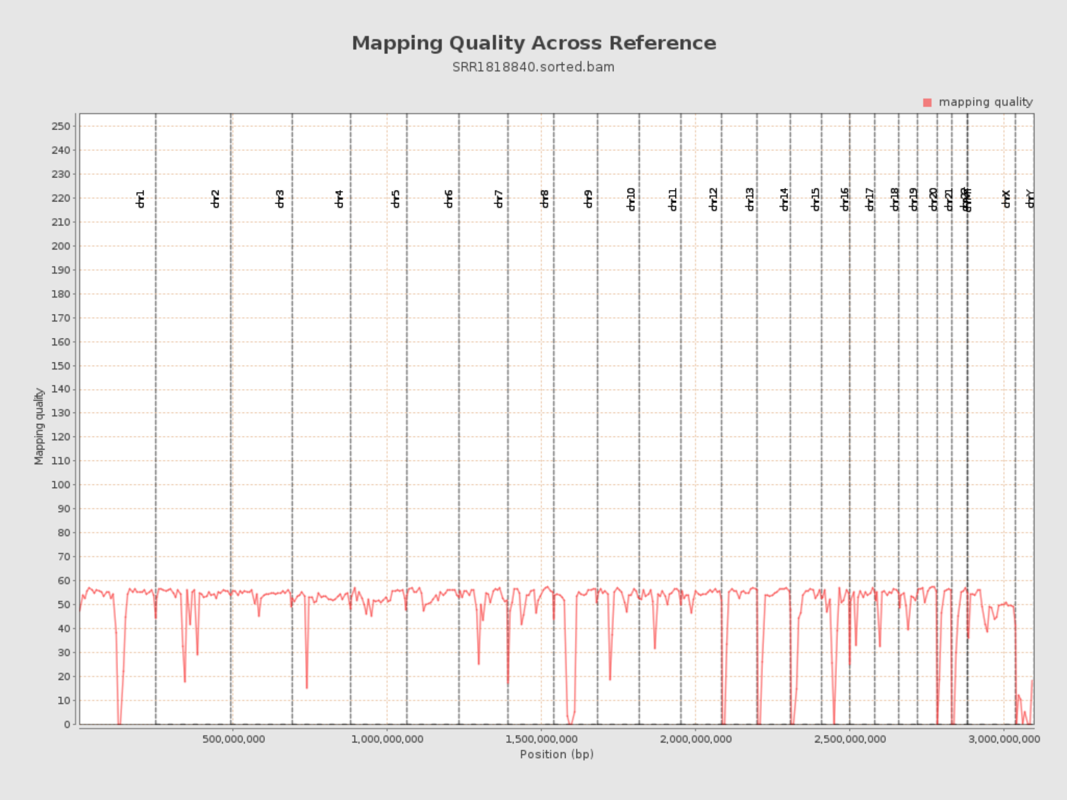
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram