Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 18:38:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818830.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_SRR1818830 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818830.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 18:38:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818830.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,929,026
Mapped reads	1,887,805 / 97.86%
Unmapped reads	41,221 / 2.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	39,839 / 2.07%
Read min/max/mean length	30 / 101 / 101.81
Duplicated reads (estimated)	335,398 / 17.39%
Duplication rate	14.86%
Clipped reads	1,902,507 / 98.63%

2.2. ACGT Content

Number/percentage of A's	50,645,801 / 28.96%
Number/percentage of C's	36,939,747 / 21.12%
Number/percentage of T's	49,990,799 / 28.58%
Number/percentage of G's	37,319,935 / 21.34%
Number/percentage of N's	2,706 / 0%
GC Percentage	42.46%

2.3. Coverage

Mean	0.0565

Standard Deviation	0.5575

2.4. Mapping Quality

Mean Mapping Quality	49.63

2.5. Mismatches and indels

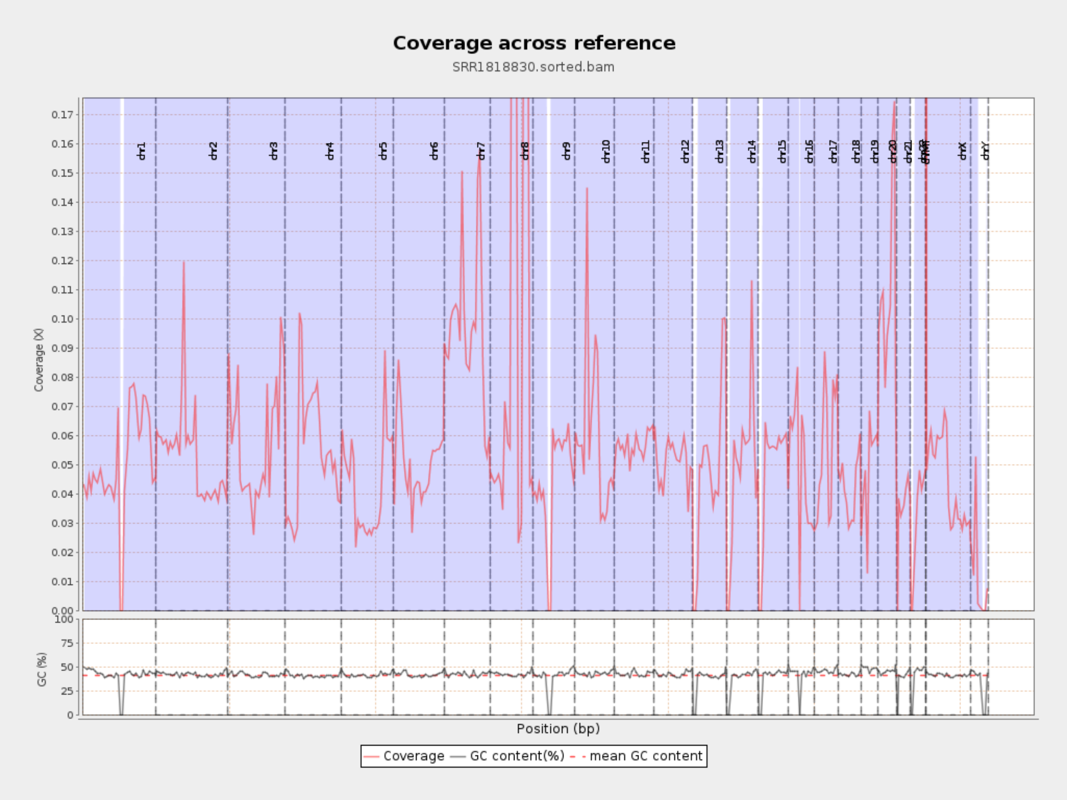
General error rate	0.61%
Mismatches	1,013,916
Insertions	22,859
Mapped reads with at least one insertion	1.18%
Deletions	48,536
Mapped reads with at least one deletion	2.52%
Homopolymer indels	41.4%

2.6. Chromosome stats

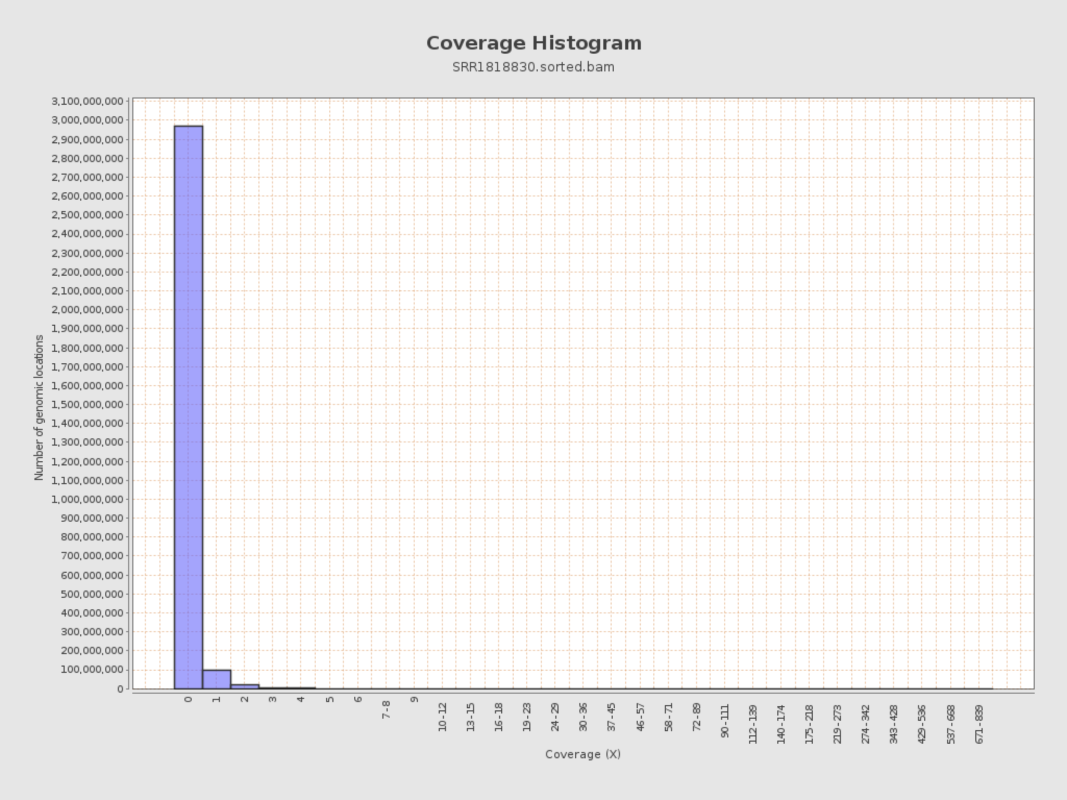
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12542489	0.0503	0.674
chr2	243199373	12950375	0.0533	0.6632
chr3	198022430	11416028	0.0577	0.3068
chr4	191154276	10505683	0.055	0.4432
chr5	180915260	7756102	0.0429	0.2671
chr6	171115067	8624145	0.0504	0.3136
chr7	159138663	15477708	0.0973	1.3069

chr8	146364022	17959371	0.1227	0.5894
chr9	141213431	6301183	0.0446	0.5197
chr10	135534747	8041455	0.0593	0.7609
chr11	135006516	7629679	0.0565	0.3854
chr12	133851895	6878469	0.0514	0.2911
chr13	115169878	5646913	0.049	0.282
chr14	107349540	5339580	0.0497	0.3011
chr15	102531392	4834129	0.0471	0.2757
chr16	90354753	4328861	0.0479	0.4366
chr17	81195210	4396361	0.0541	0.4472
chr18	78077248	3295979	0.0422	0.5568
chr19	59128983	2852739	0.0482	0.6074
chr20	63025520	7207267	0.1144	0.4689
chr21	48129895	1702829	0.0354	0.3438
chr22	51304566	1562627	0.0305	0.2359
chrMT	16571	142397	8.5931	5.99
chrX	155270560	6909287	0.0445	0.3215
chrY	59373566	692461	0.0117	0.7955

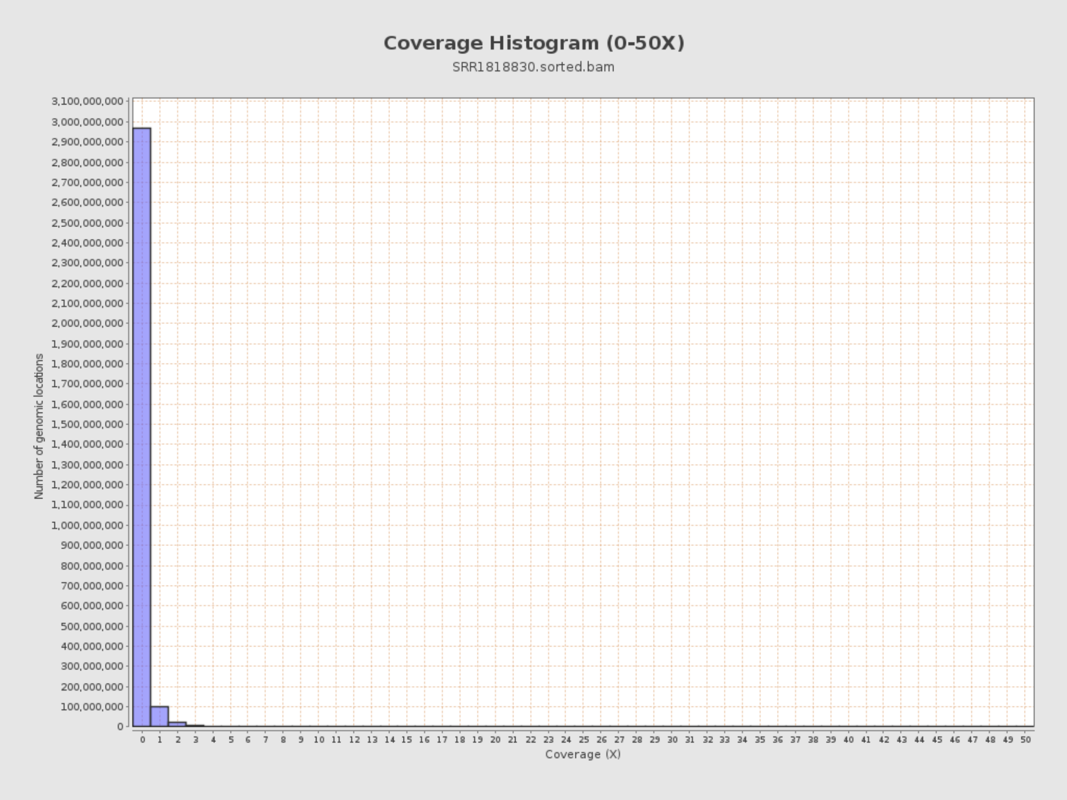
3. Results : Coverage across reference



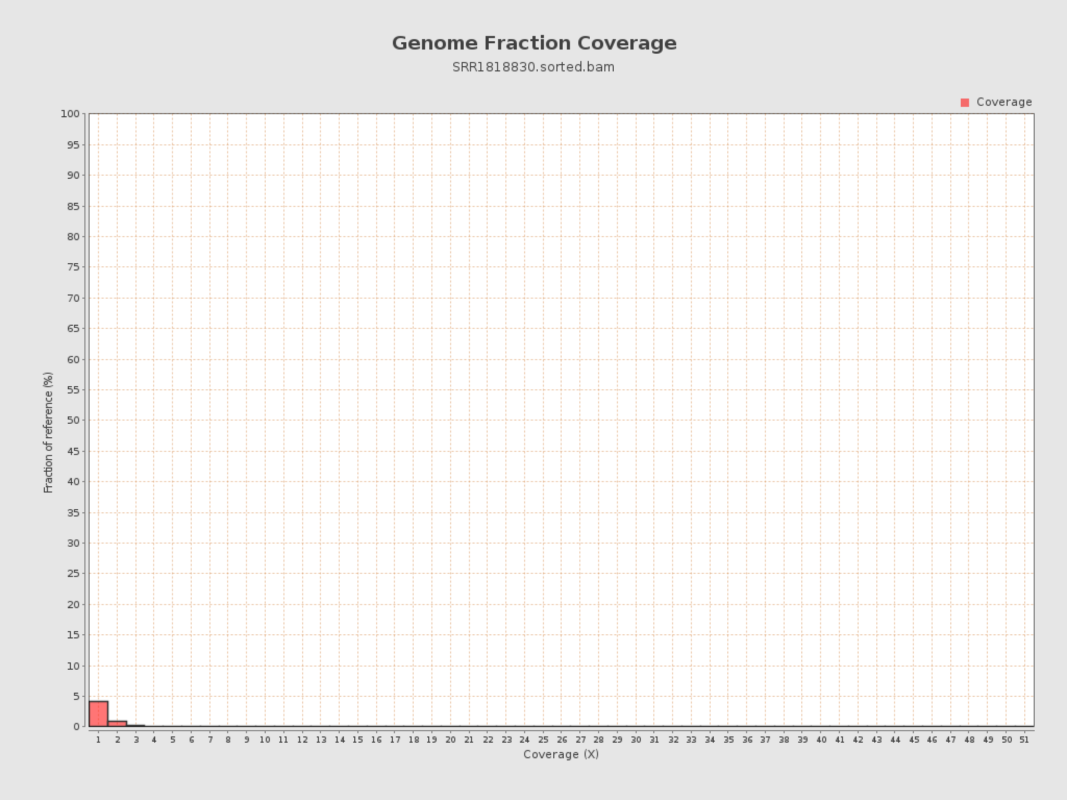
4. Results : Coverage Histogram



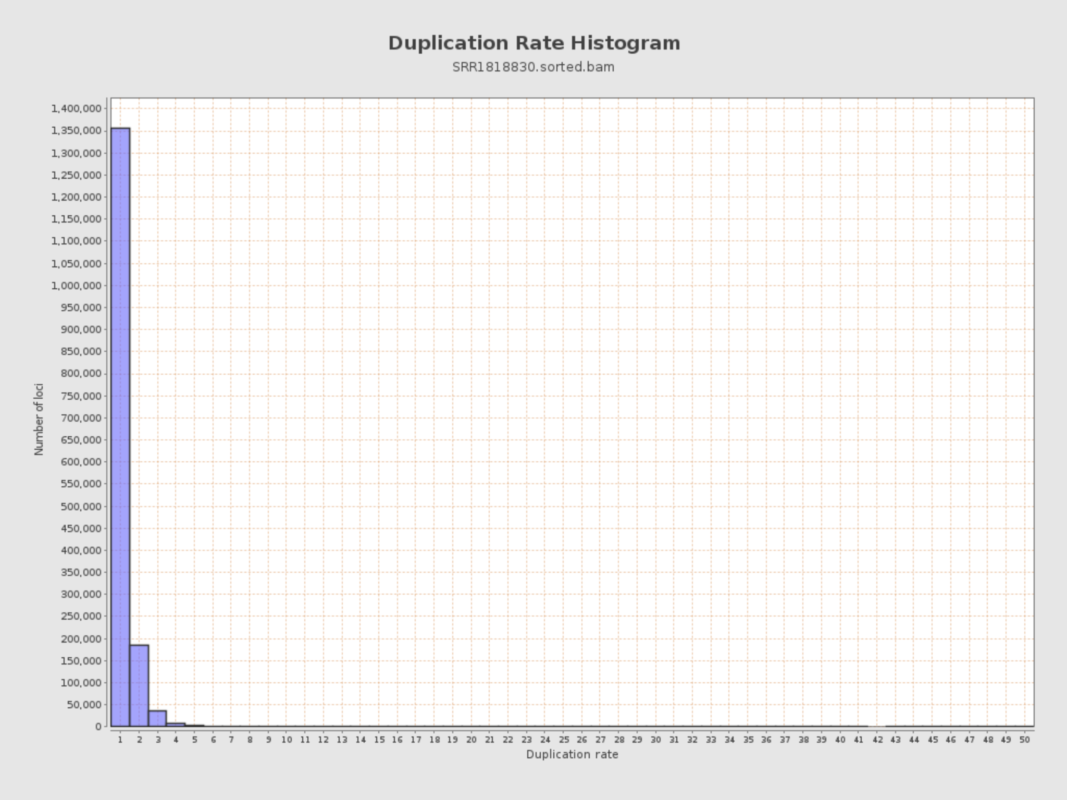
5. Results : Coverage Histogram (0-50X)



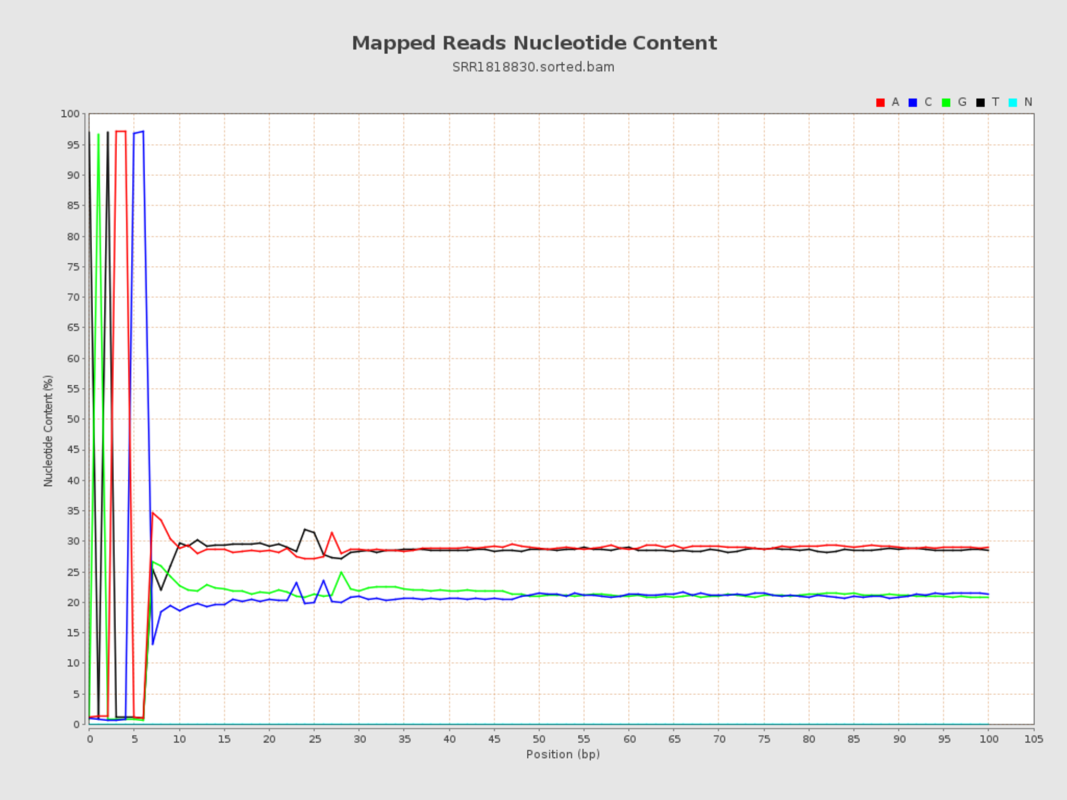
6. Results : Genome Fraction Coverage



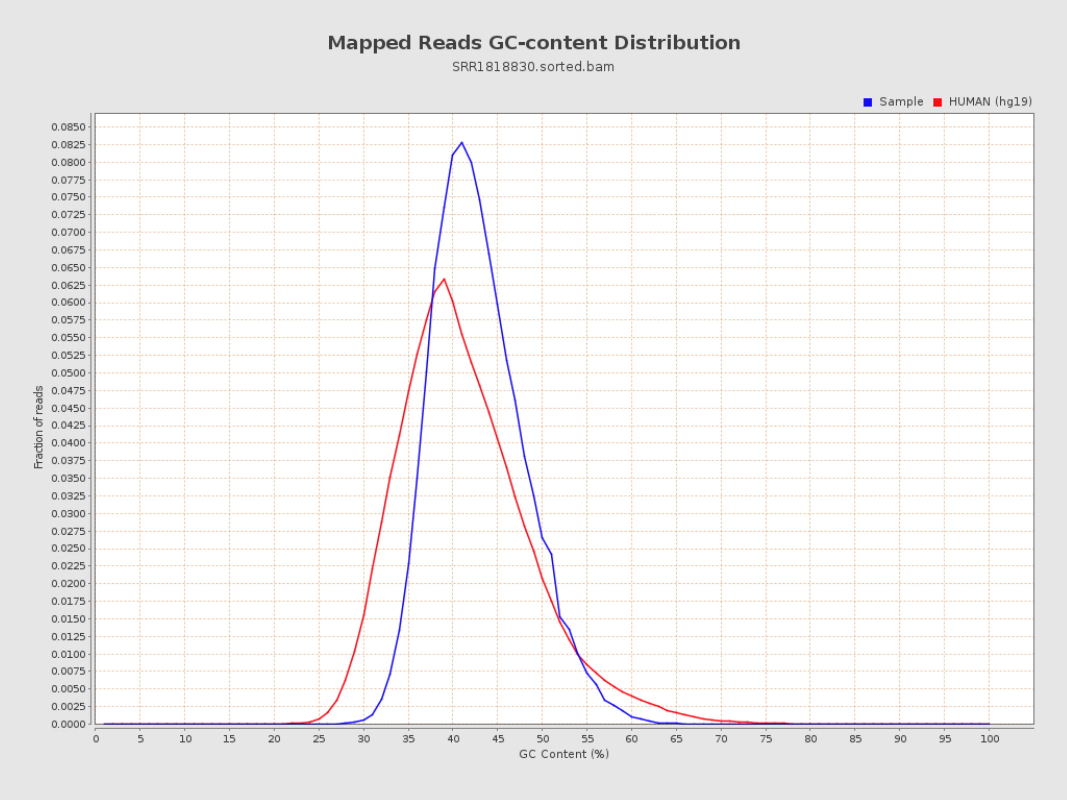
7. Results : Duplication Rate Histogram



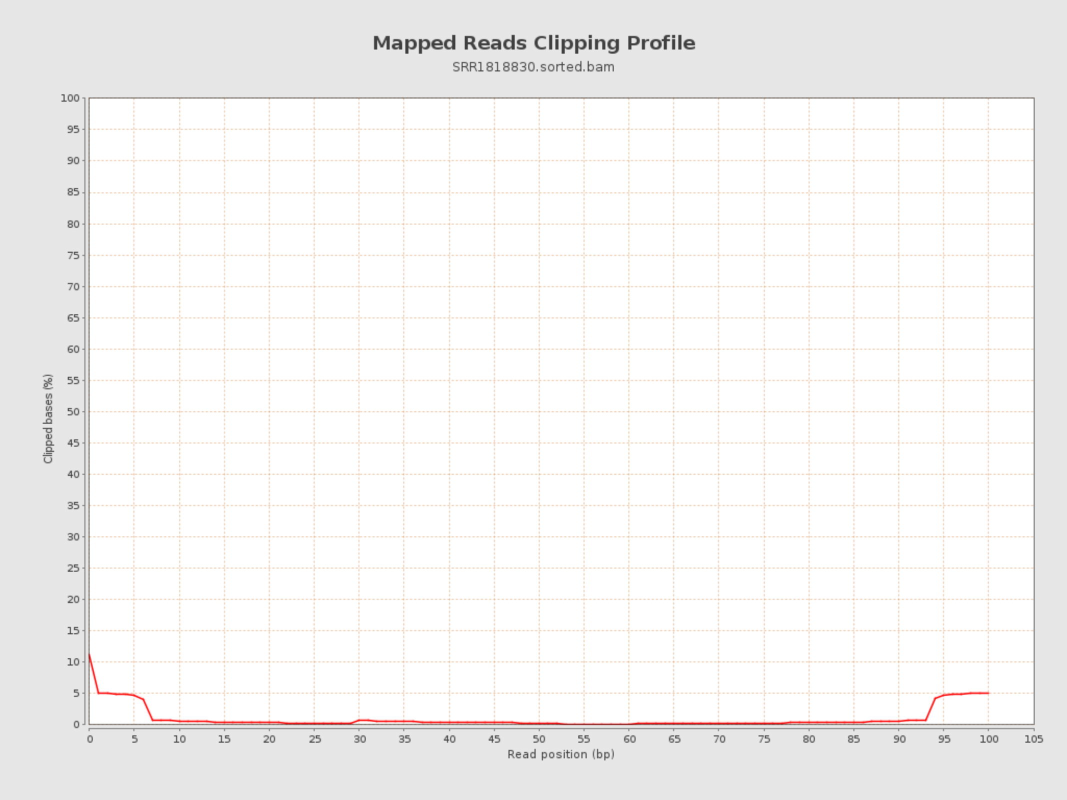
8. Results : Mapped Reads Nucleotide Content



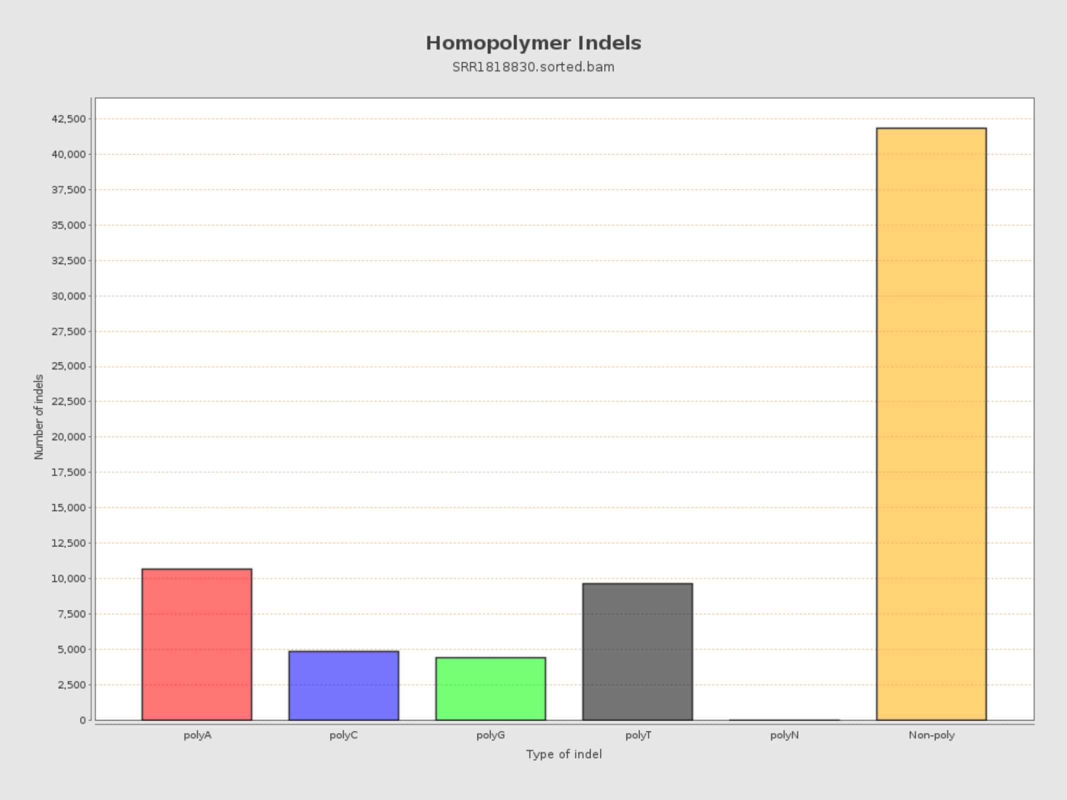
9. Results : Mapped Reads GC-content Distribution



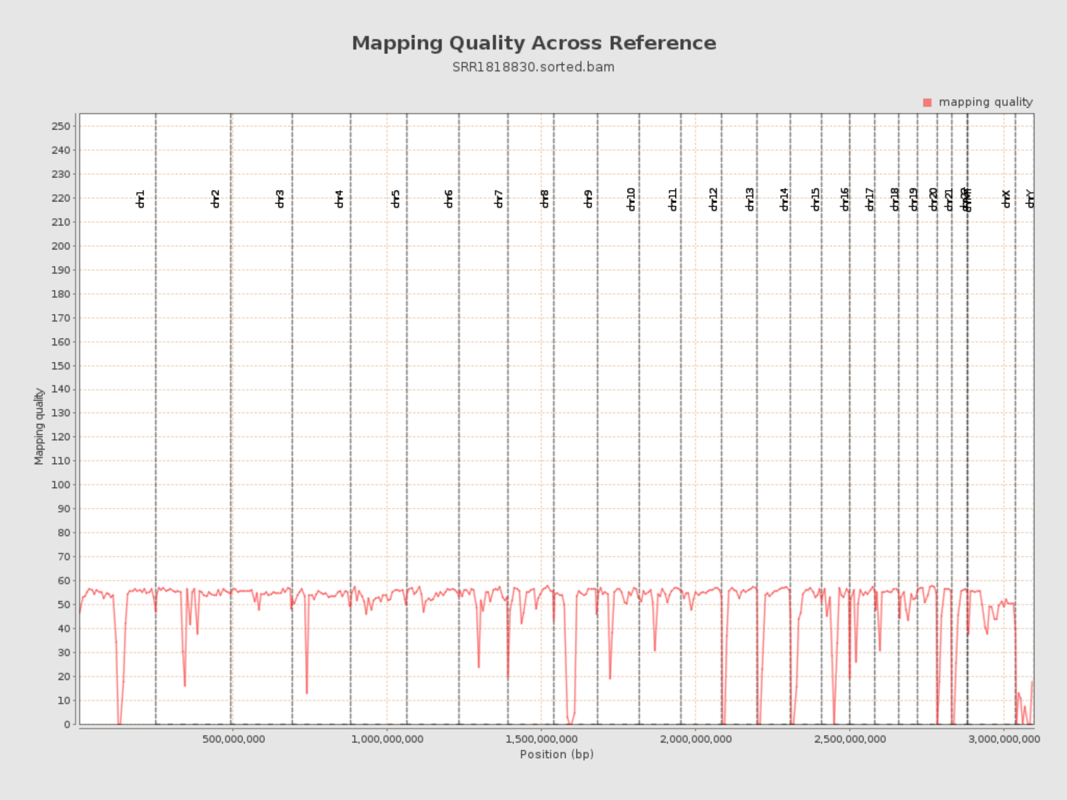
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram