Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 06:18:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818901.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_SRR1818901 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818901.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 06:18:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818901.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,710,911
Mapped reads	1,678,476 / 98.1%
Unmapped reads	32,435 / 1.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,531 / 1.38%
Read min/max/mean length	30 / 101 / 101.53
Duplicated reads (estimated)	250,298 / 14.63%
Duplication rate	11.71%
Clipped reads	1,693,302 / 98.97%

2.2. ACGT Content

Number/percentage of A's	44,214,212 / 28.44%
Number/percentage of C's	33,180,948 / 21.34%
Number/percentage of T's	44,249,802 / 28.46%
Number/percentage of G's	33,828,515 / 21.76%
Number/percentage of N's	2,509 / 0%
GC Percentage	43.1%

2.3. Coverage

Mean	0.0503

Standard Deviation	0.6722

2.4. Mapping Quality

Mean Mapping Quality	49.32

2.5. Mismatches and indels

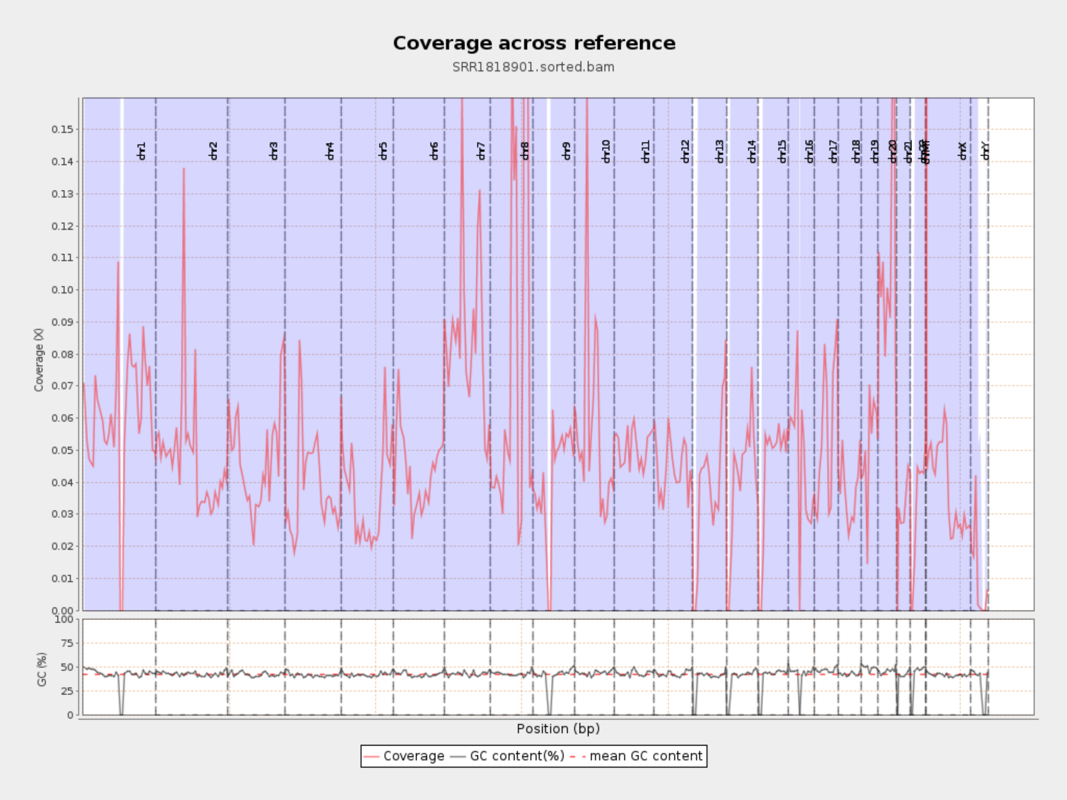
General error rate	0.63%
Mismatches	929,336
Insertions	22,239
Mapped reads with at least one insertion	1.29%
Deletions	45,657
Mapped reads with at least one deletion	2.65%
Homopolymer indels	39.96%

2.6. Chromosome stats

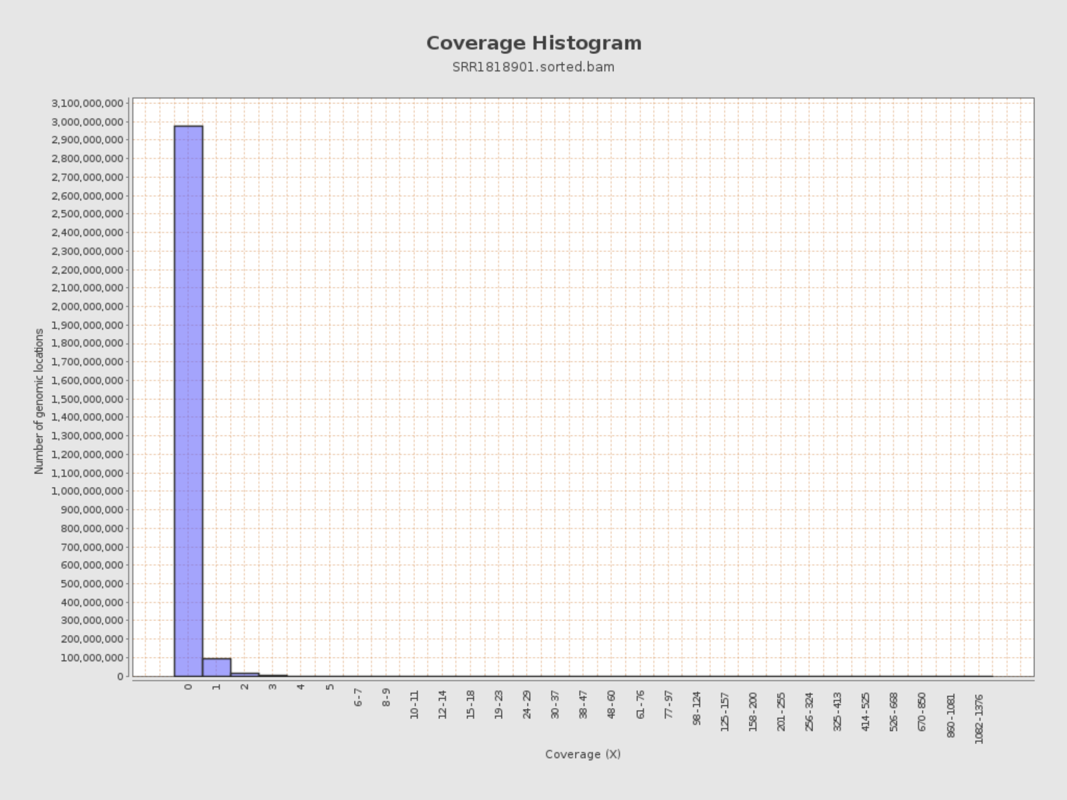
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15129679	0.0607	1.0245
chr2	243199373	11716567	0.0482	0.8403
chr3	198022430	9417898	0.0476	0.2719
chr4	191154276	7479778	0.0391	0.3721
chr5	180915260	6657834	0.0368	0.2493
chr6	171115067	7379241	0.0431	0.2879
chr7	159138663	13686312	0.086	1.5631

chr8	146364022	12915276	0.0882	0.5434
chr9	141213431	5762144	0.0408	0.6203
chr10	135534747	7554158	0.0557	1.0694
chr11	135006516	6858357	0.0508	0.3793
chr12	133851895	5996472	0.0448	0.2612
chr13	115169878	4446484	0.0386	0.2381
chr14	107349540	4487290	0.0418	0.2805
chr15	102531392	4397235	0.0429	0.2549
chr16	90354753	4156717	0.046	0.5705
chr17	81195210	4435775	0.0546	0.454
chr18	78077248	2903851	0.0372	0.6473
chr19	59128983	3009413	0.0509	0.8941
chr20	63025520	7143770	0.1133	0.4644
chr21	48129895	1512105	0.0314	0.3084
chr22	51304566	1557440	0.0304	0.2296
chrMT	16571	363793	21.9536	14.3959
chrX	155270560	5976286	0.0385	0.3212
chrY	59373566	624627	0.0105	0.7335

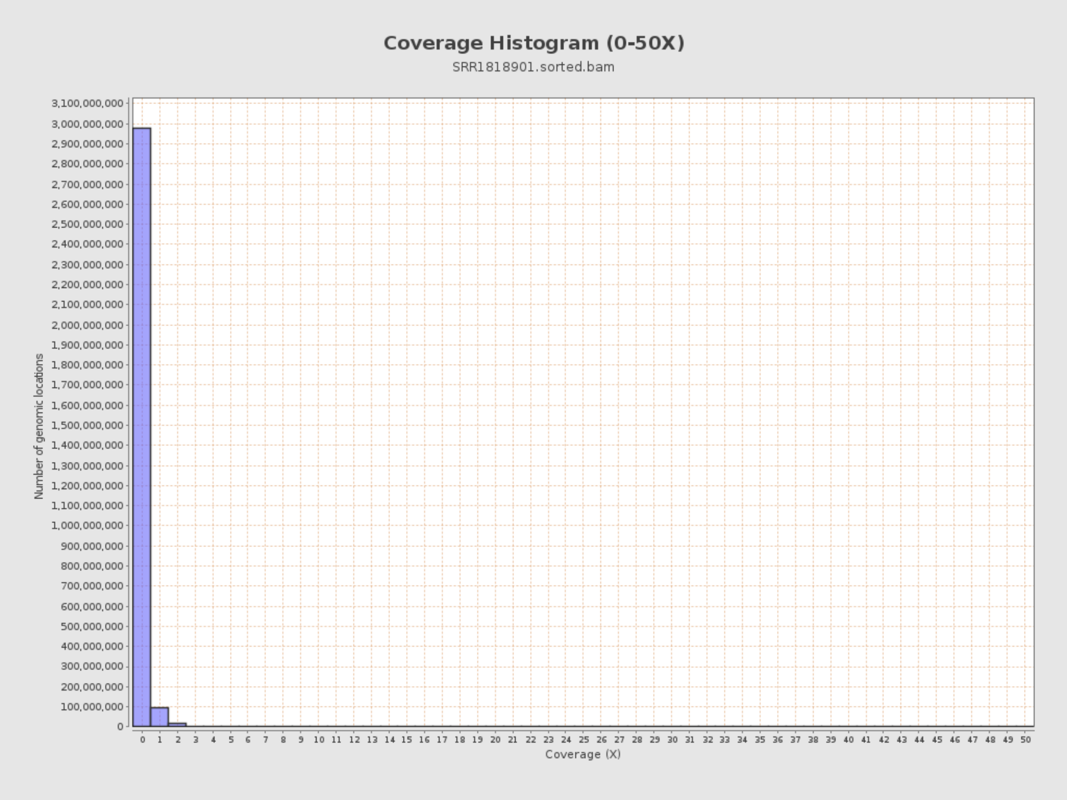
3. Results : Coverage across reference



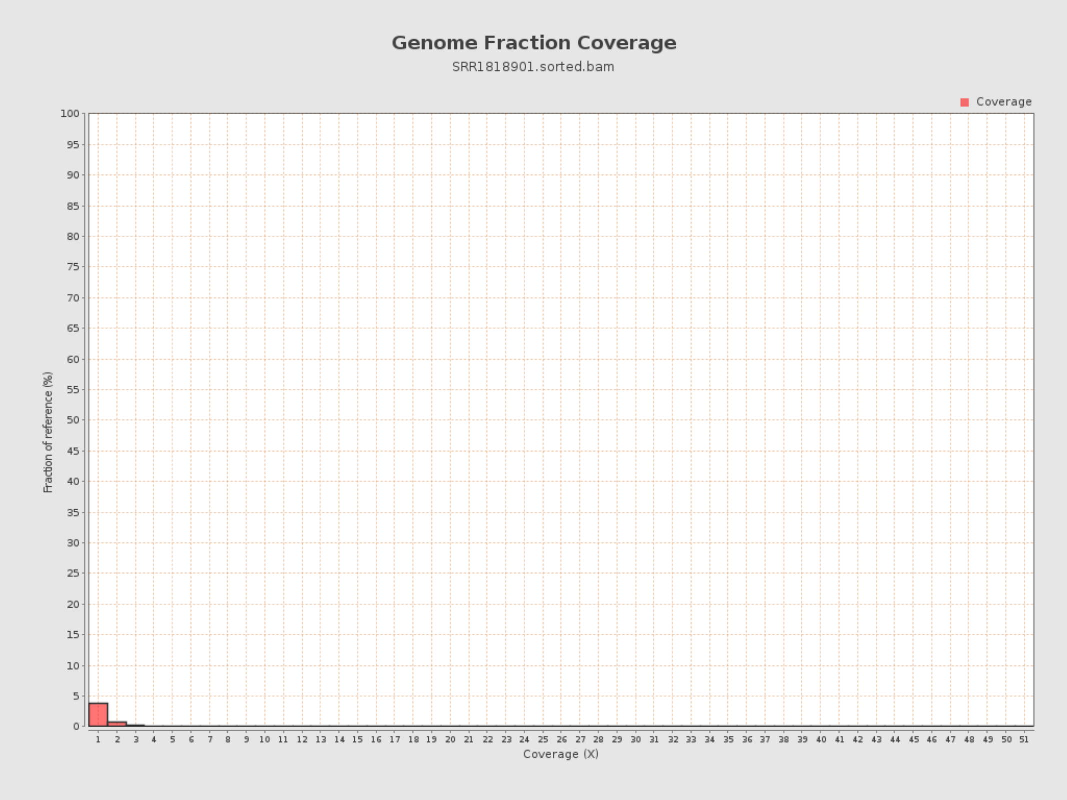
4. Results : Coverage Histogram



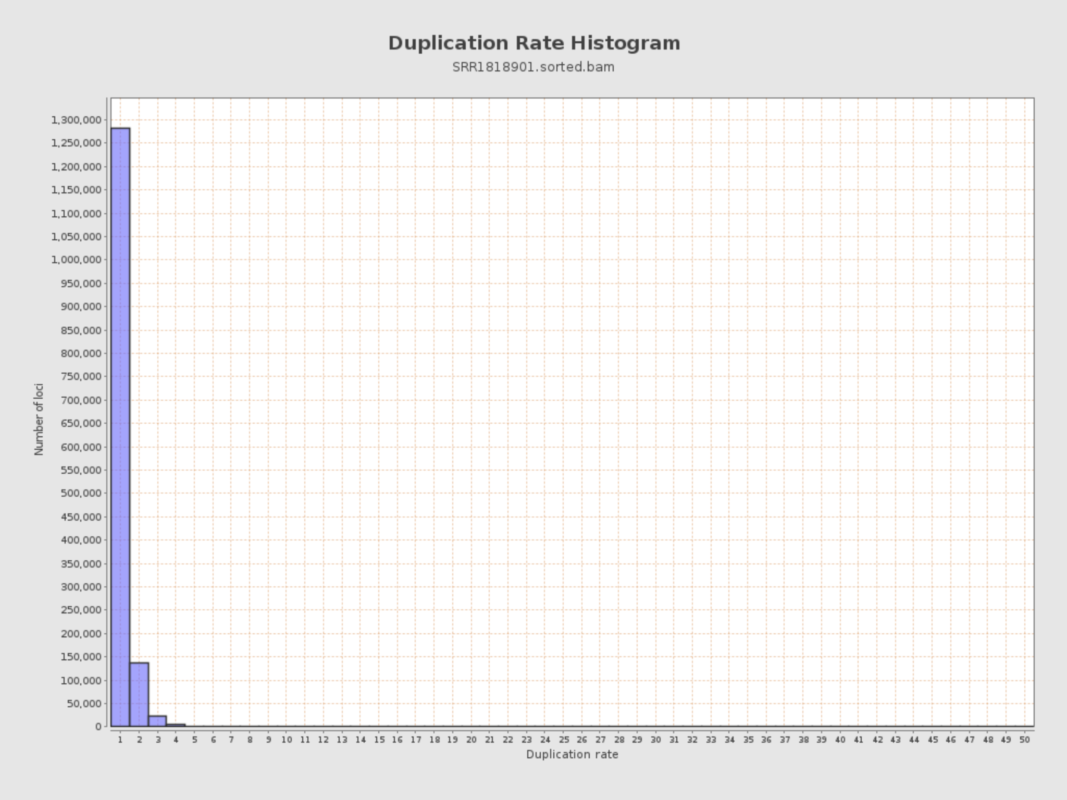
5. Results : Coverage Histogram (0-50X)



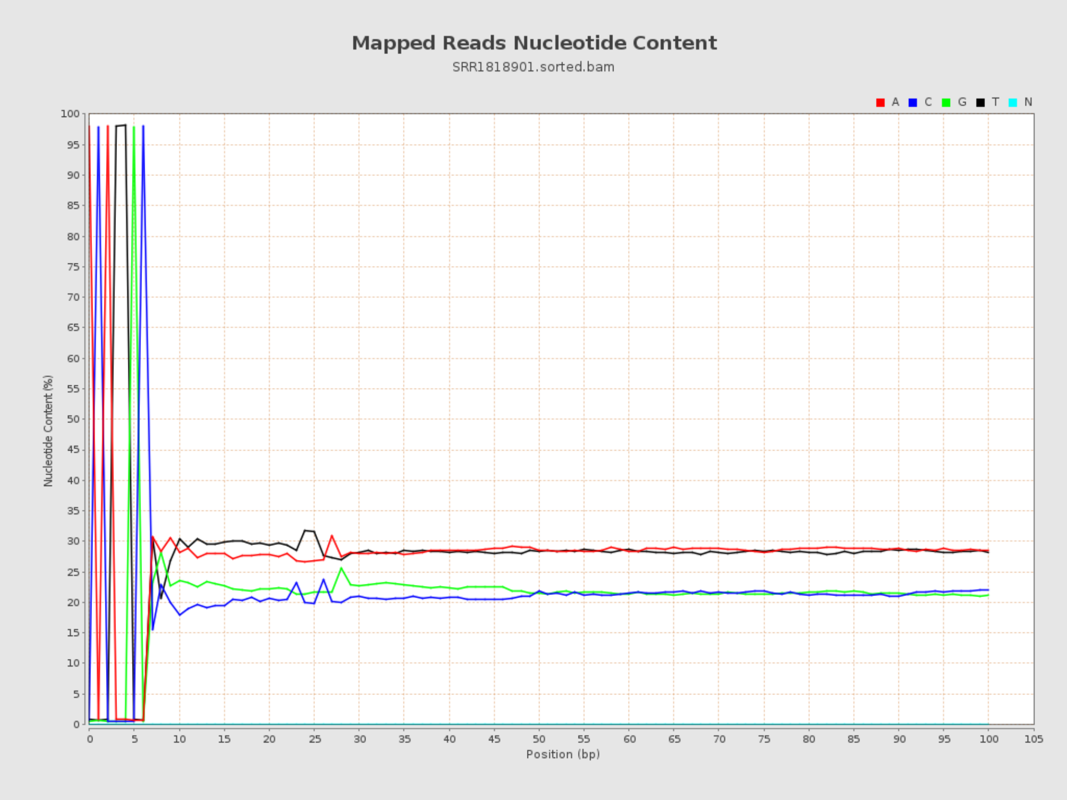
6. Results : Genome Fraction Coverage



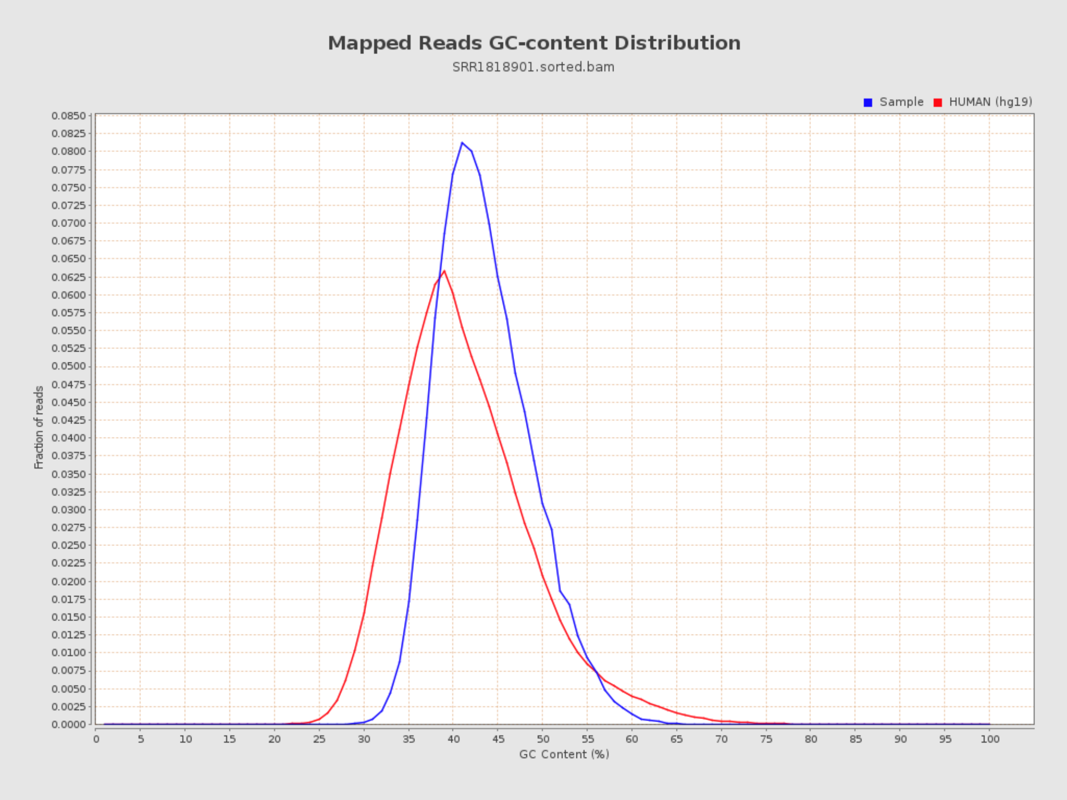
7. Results : Duplication Rate Histogram



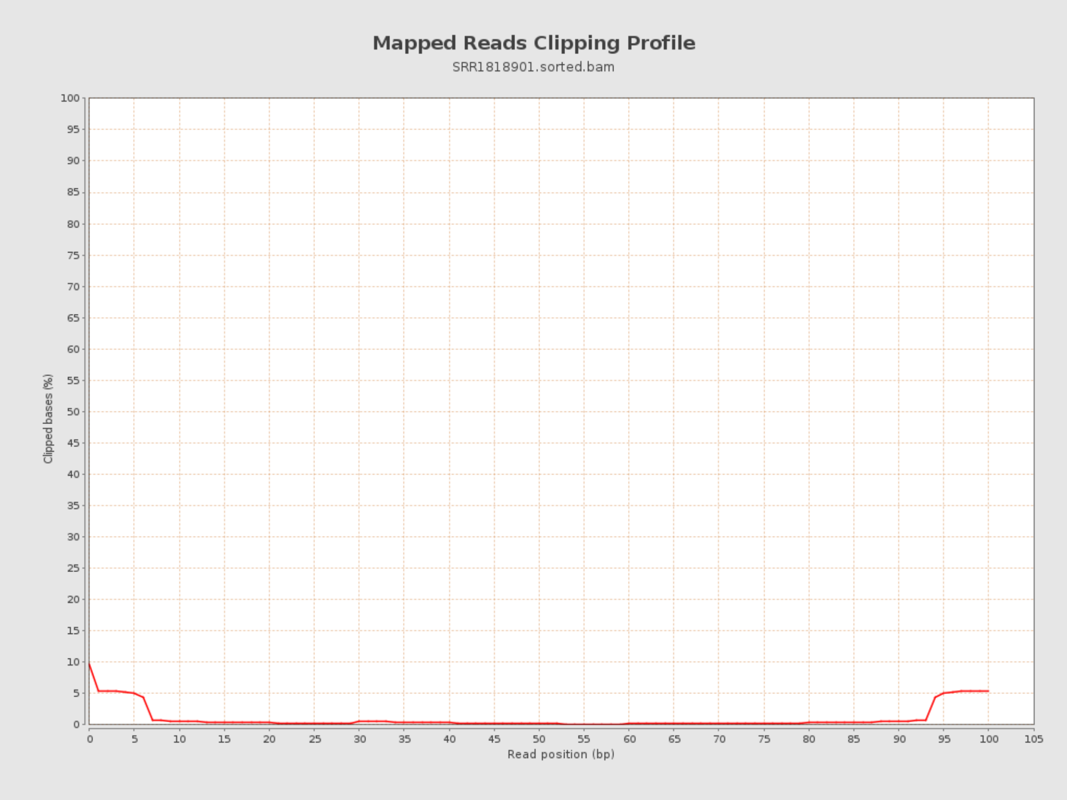
8. Results : Mapped Reads Nucleotide Content



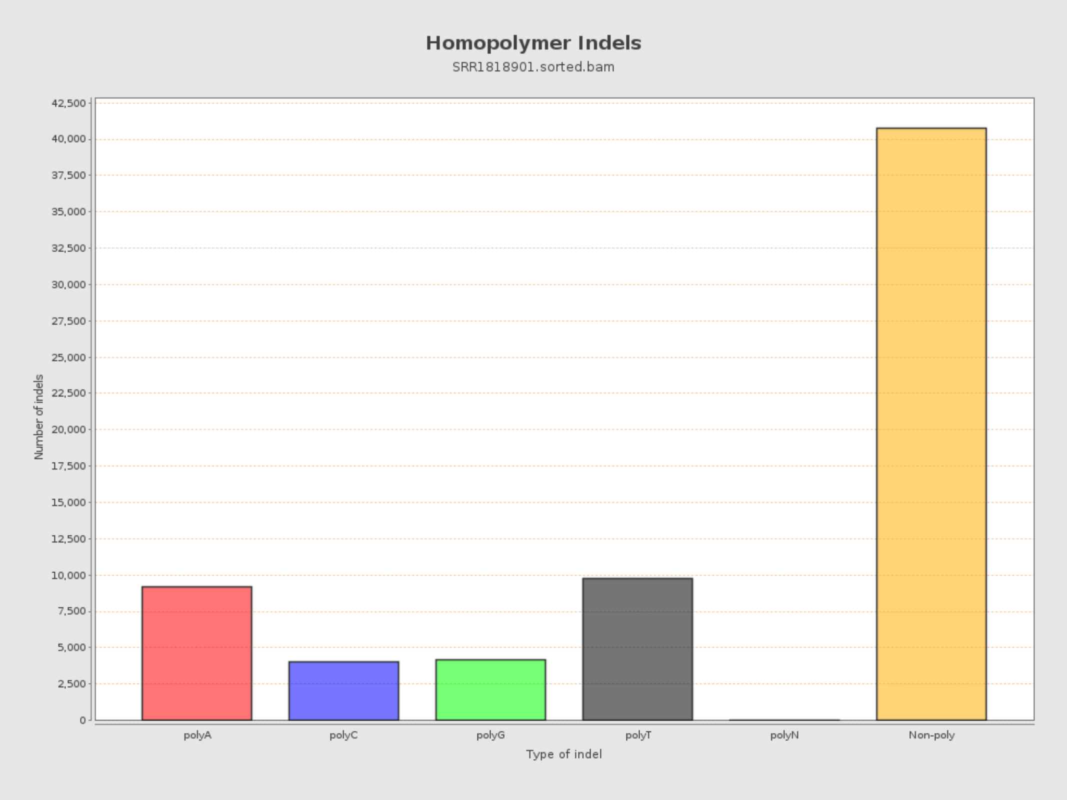
9. Results : Mapped Reads GC-content Distribution



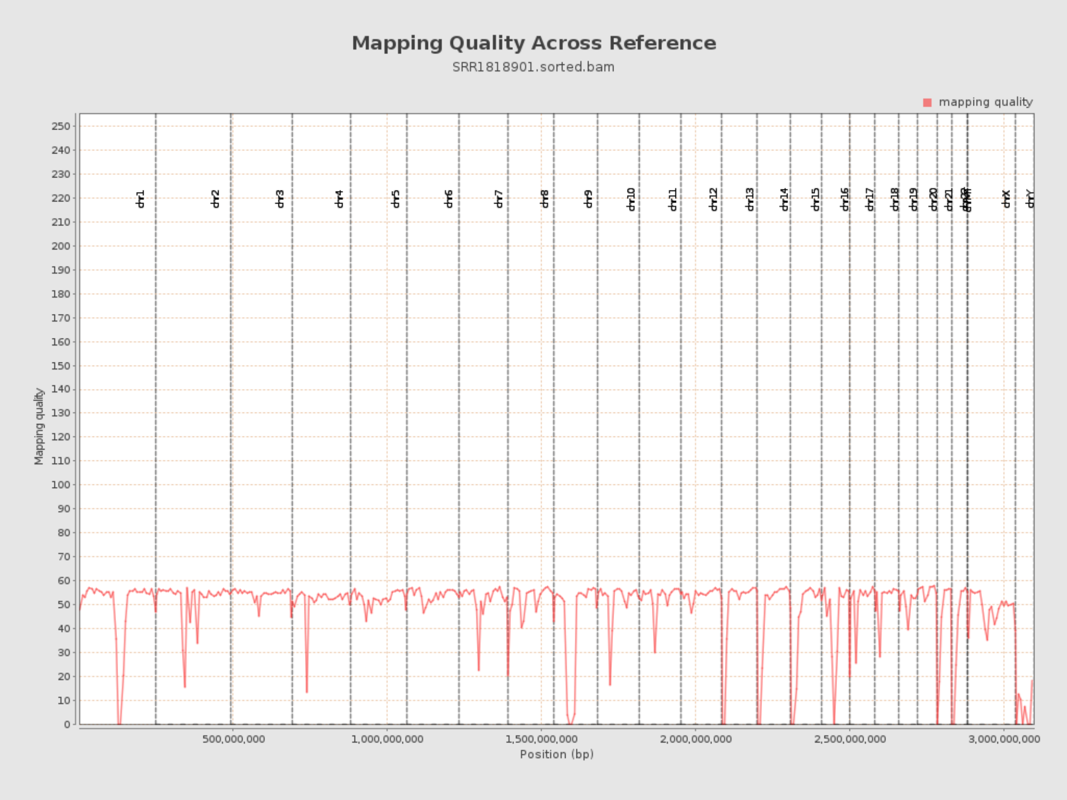
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram