Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 16:06:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819021.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_SRR1819021 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819021.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 16:06:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819021.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,069,551
Mapped reads	1,996,315 / 96.46%
Unmapped reads	73,236 / 3.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	32,451 / 1.57%
Read min/max/mean length	30 / 101 / 101.6
Duplicated reads (estimated)	942,137 / 45.52%
Duplication rate	37.83%
Clipped reads	1,990,480 / 96.18%

2.2. ACGT Content

Number/percentage of A's	54,004,670 / 29.26%
Number/percentage of C's	36,872,355 / 19.98%
Number/percentage of T's	53,044,277 / 28.74%
Number/percentage of G's	40,650,083 / 22.02%
Number/percentage of N's	9,039 / 0%
GC Percentage	42%

2.3. Coverage

Mean	0.0597

Standard Deviation	0.7671

2.4. Mapping Quality

Mean Mapping Quality	48.97

2.5. Mismatches and indels

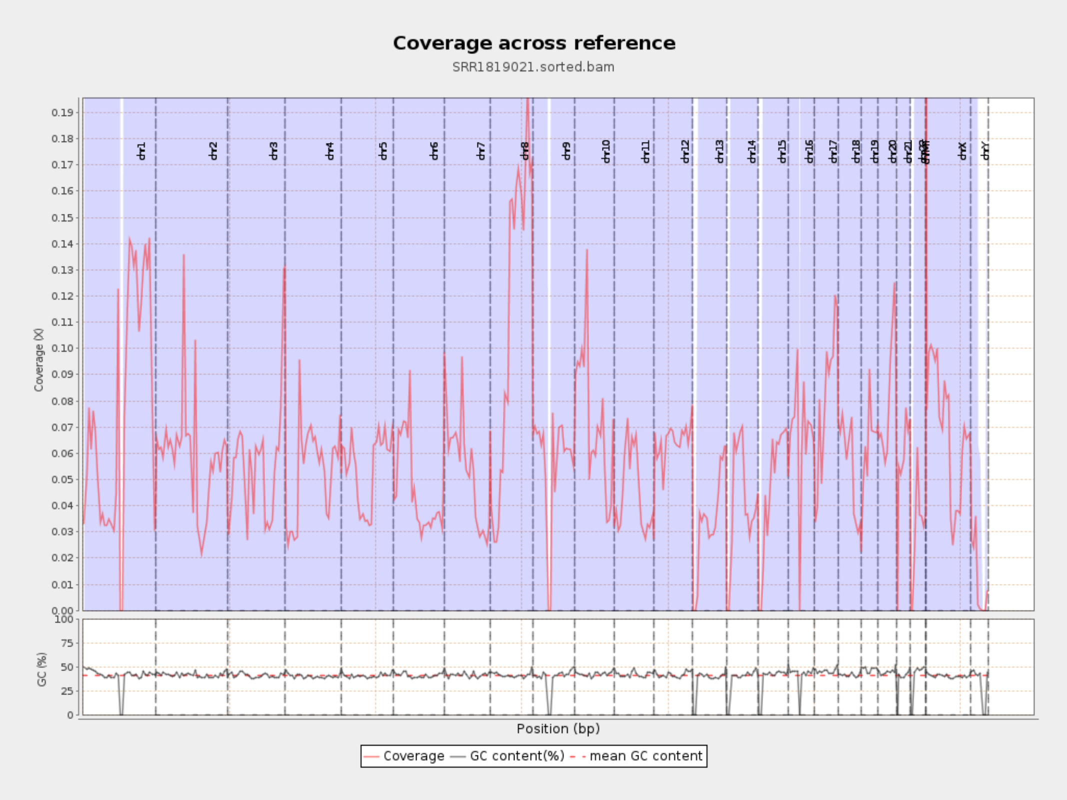
General error rate	0.7%
Mismatches	1,218,602
Insertions	33,321
Mapped reads with at least one insertion	1.63%
Deletions	61,742
Mapped reads with at least one deletion	3.03%
Homopolymer indels	40.98%

2.6. Chromosome stats

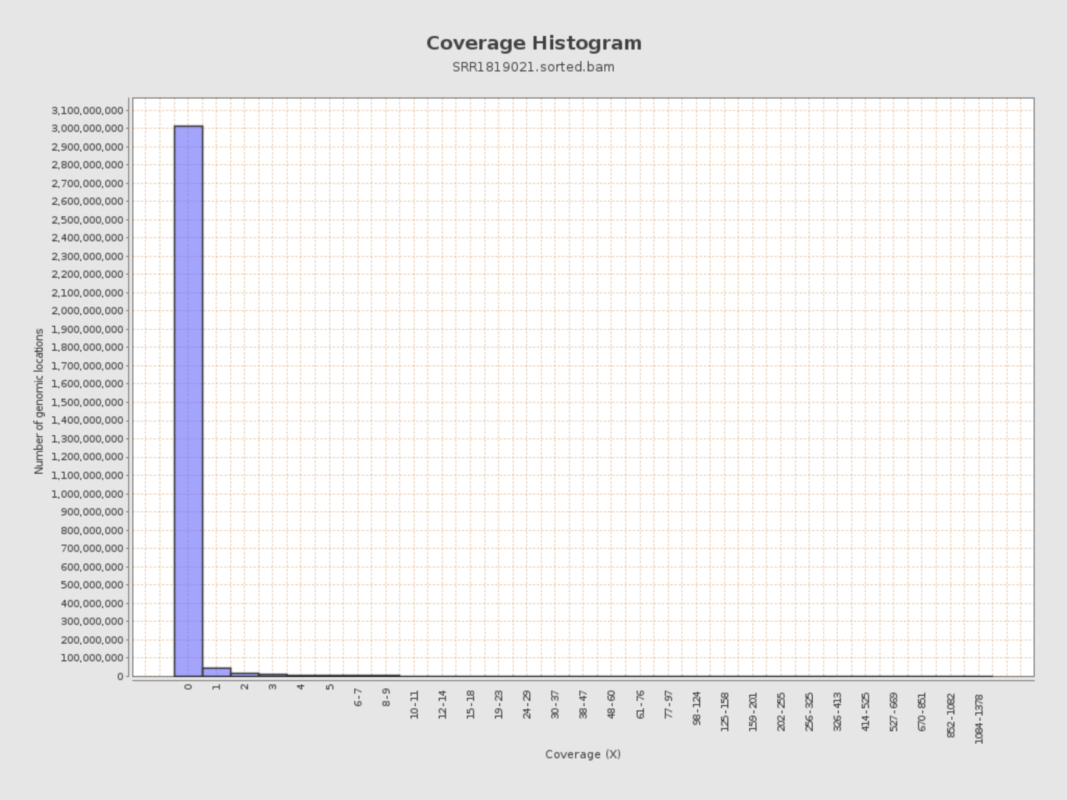
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18908415	0.0759	1.3469
chr2	243199373	14398364	0.0592	1.1481
chr3	198022430	10956642	0.0553	0.4533
chr4	191154276	10214938	0.0534	0.5381
chr5	180915260	9878288	0.0546	0.4673
chr6	171115067	7907456	0.0462	0.4942
chr7	159138663	8607652	0.0541	0.8304

chr8	146364022	16852793	0.1151	0.729
chr9	141213431	7936178	0.0562	0.6709
chr10	135534747	9712137	0.0717	0.9444
chr11	135006516	6037581	0.0447	0.5066
chr12	133851895	8686274	0.0649	0.5116
chr13	115169878	3917728	0.034	0.3558
chr14	107349540	4429702	0.0413	0.4257
chr15	102531392	4696252	0.0458	0.4166
chr16	90354753	5919317	0.0655	0.9384
chr17	81195210	6514148	0.0802	0.6276
chr18	78077248	4331345	0.0555	0.7812
chr19	59128983	3765623	0.0637	1.1829
chr20	63025520	5187030	0.0823	0.6009
chr21	48129895	2763935	0.0574	0.5318
chr22	51304566	1514360	0.0295	0.3701
chrMT	16571	24836	1.4988	2.7124
chrX	155270560	10850808	0.0699	0.5775
chrY	59373566	685497	0.0115	0.8213

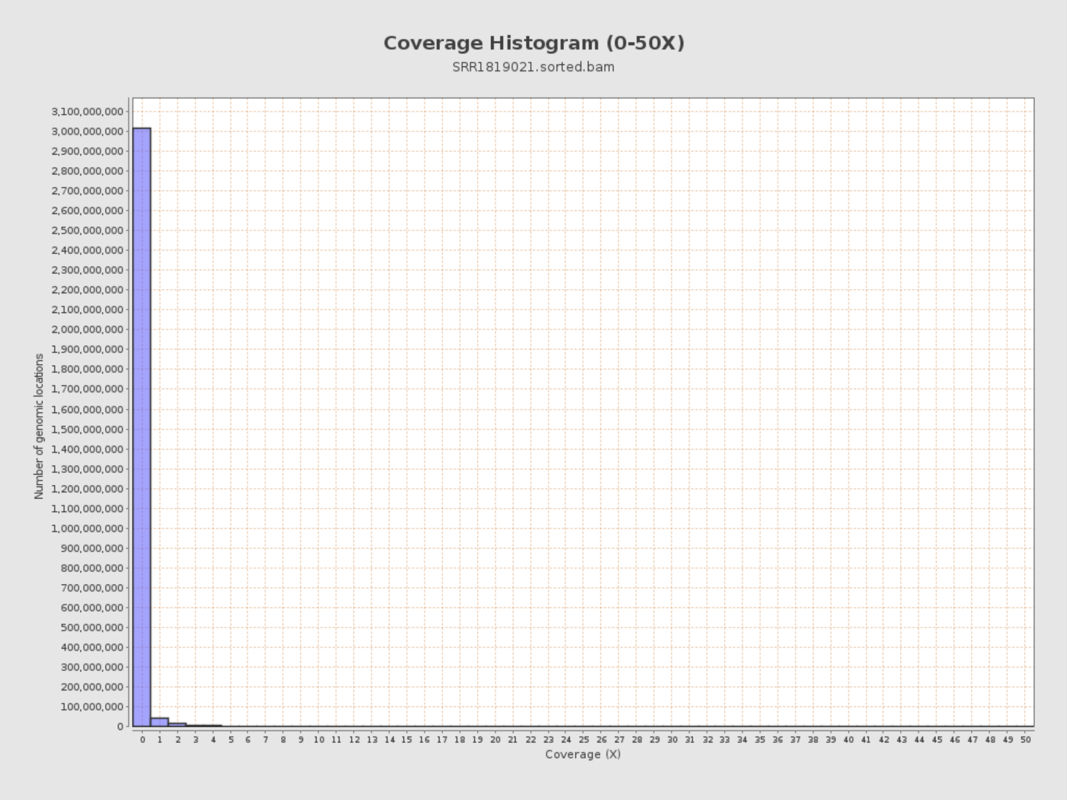
3. Results : Coverage across reference



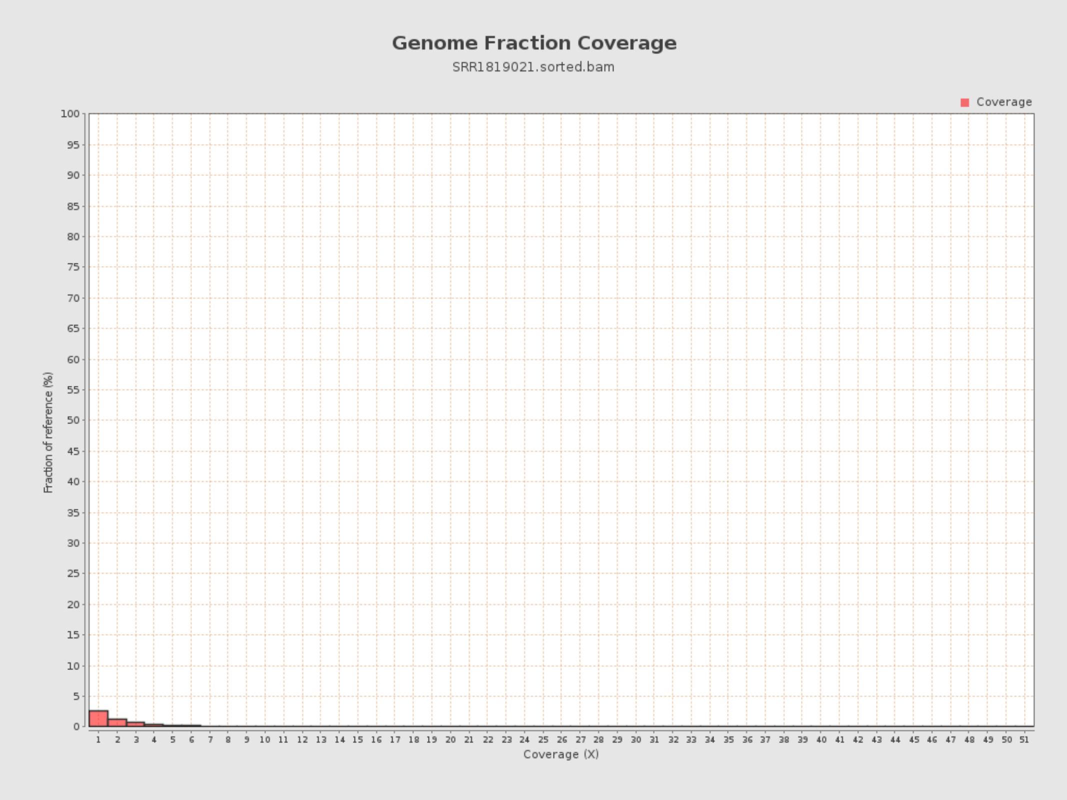
4. Results : Coverage Histogram



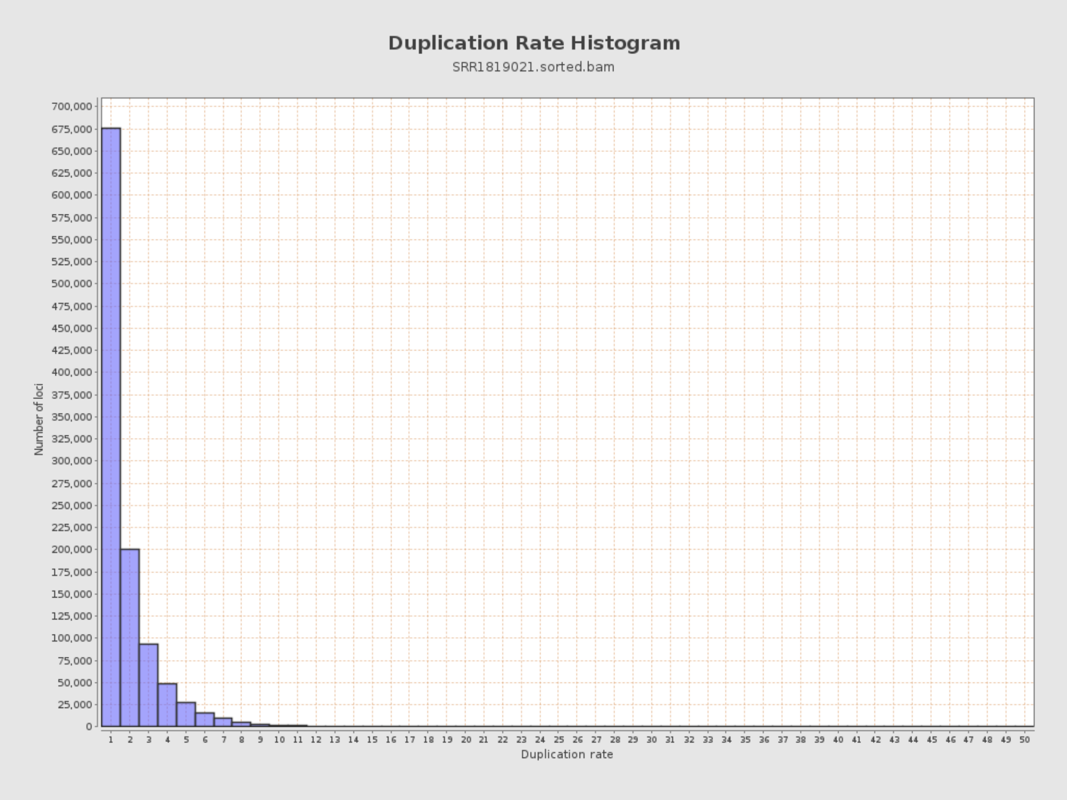
5. Results : Coverage Histogram (0-50X)



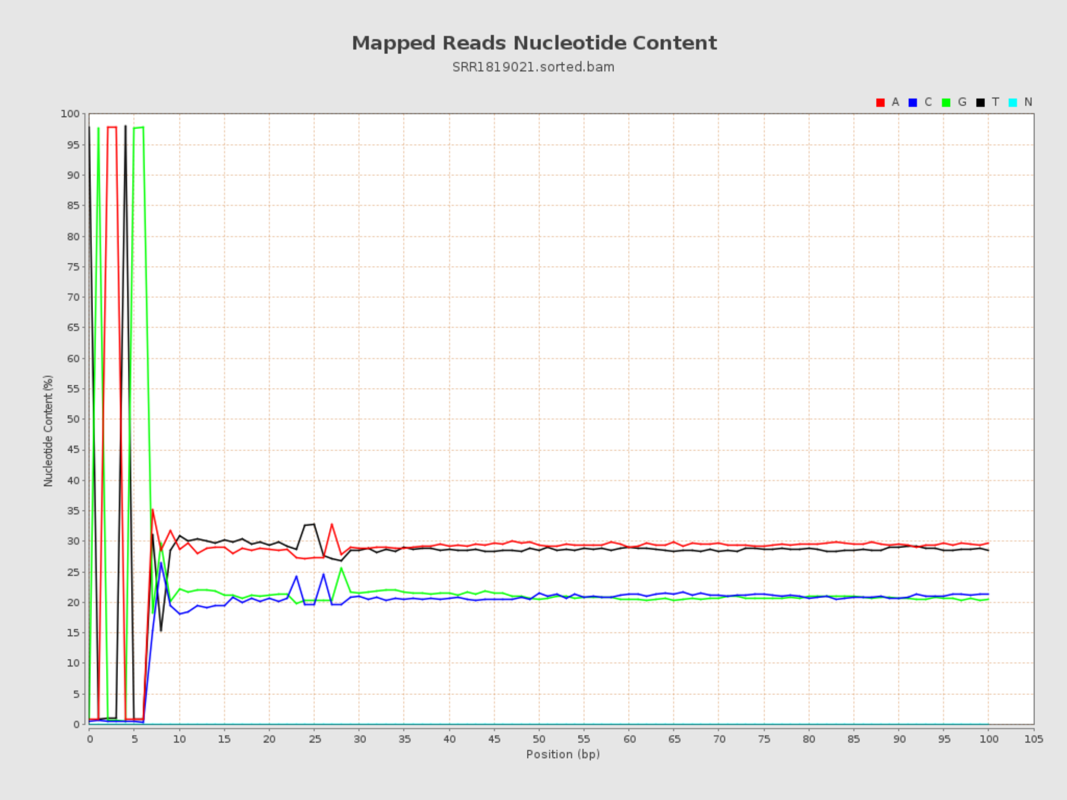
6. Results : Genome Fraction Coverage



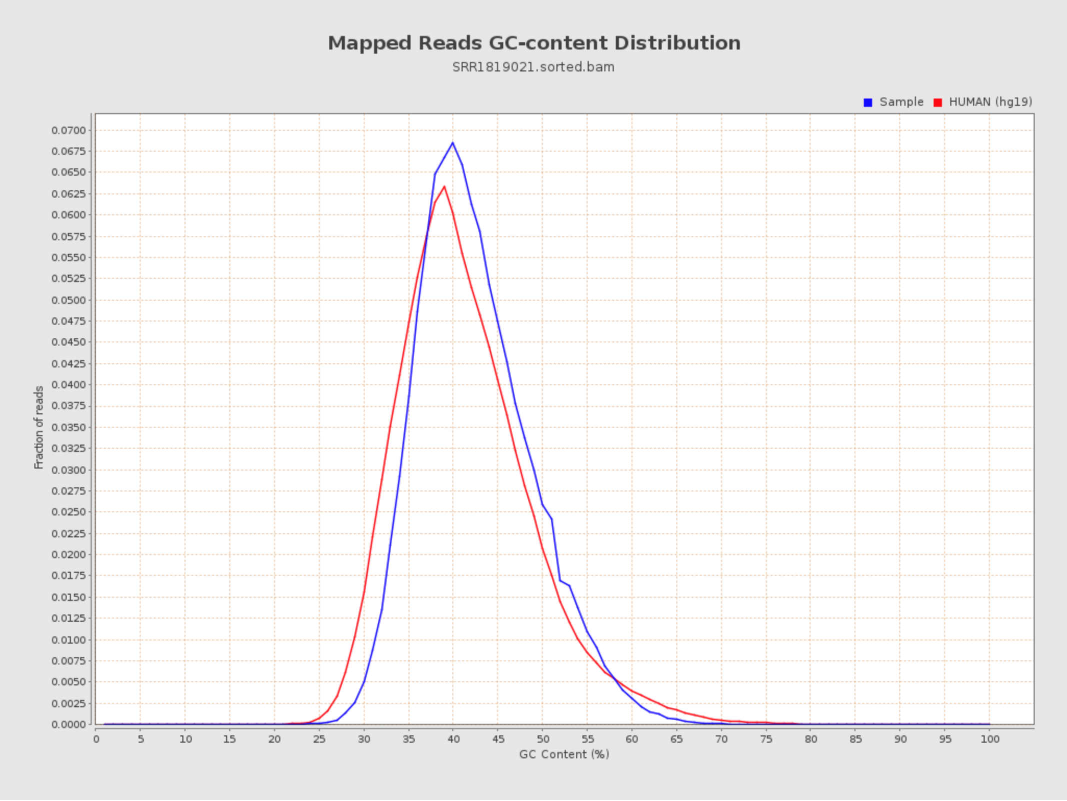
7. Results : Duplication Rate Histogram



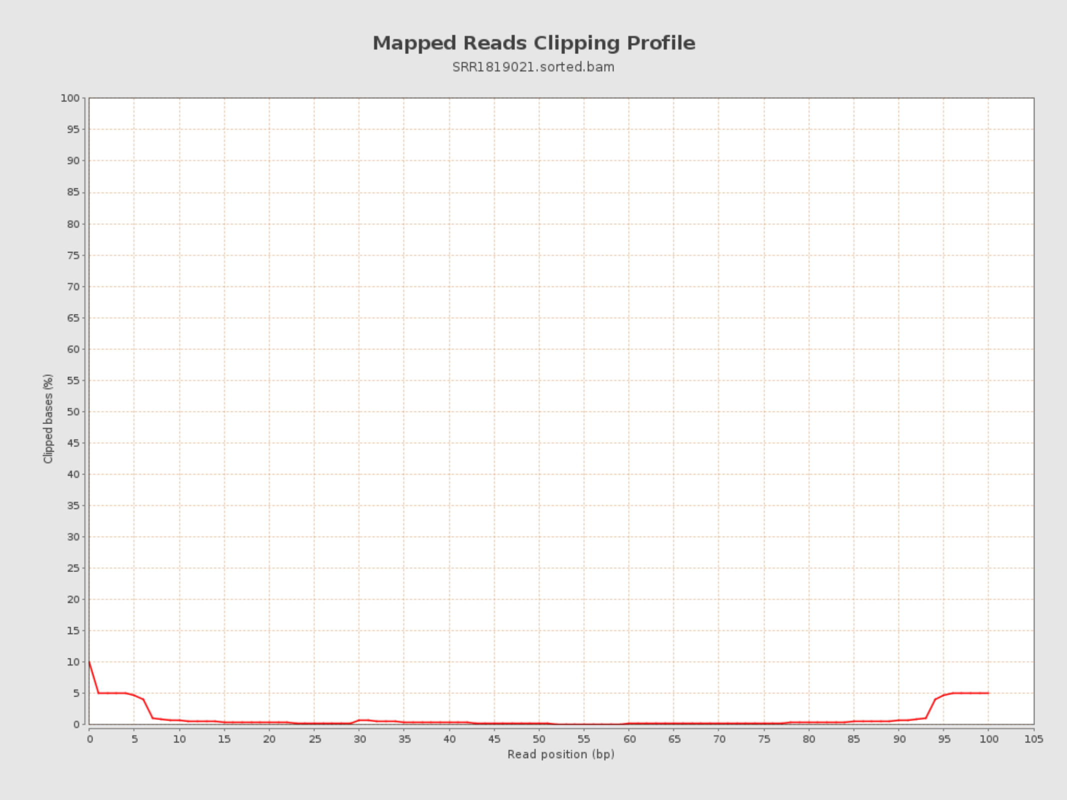
8. Results : Mapped Reads Nucleotide Content



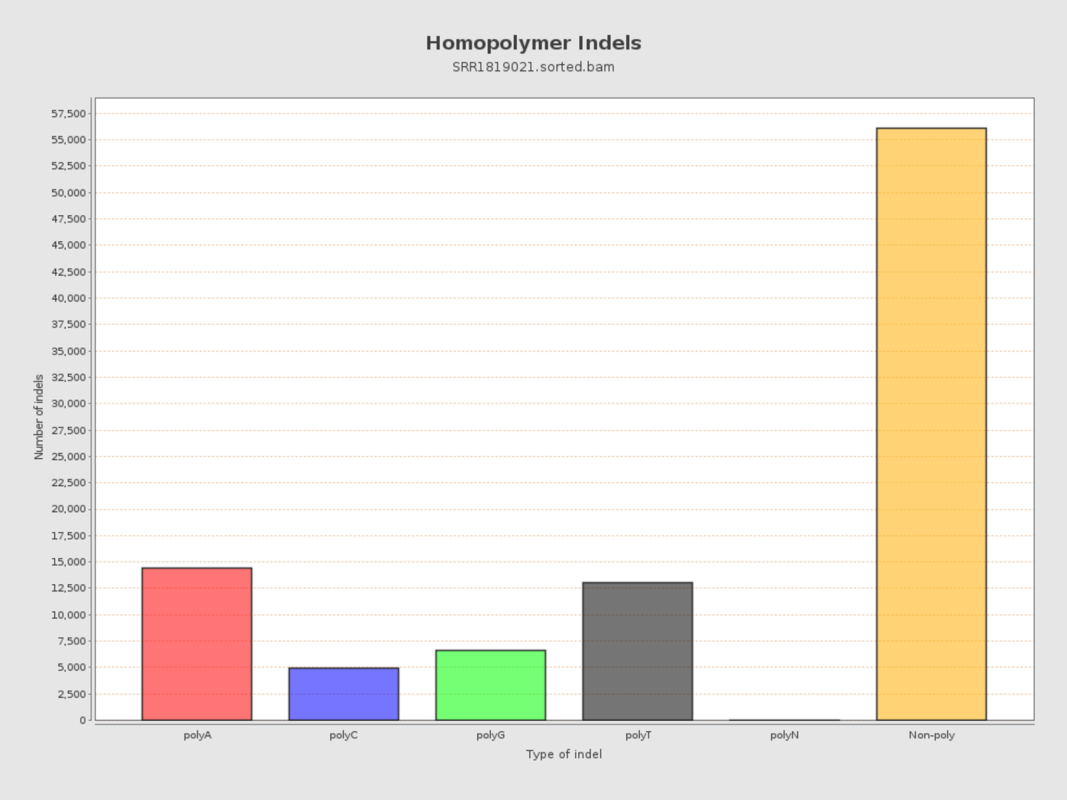
9. Results : Mapped Reads GC-content Distribution



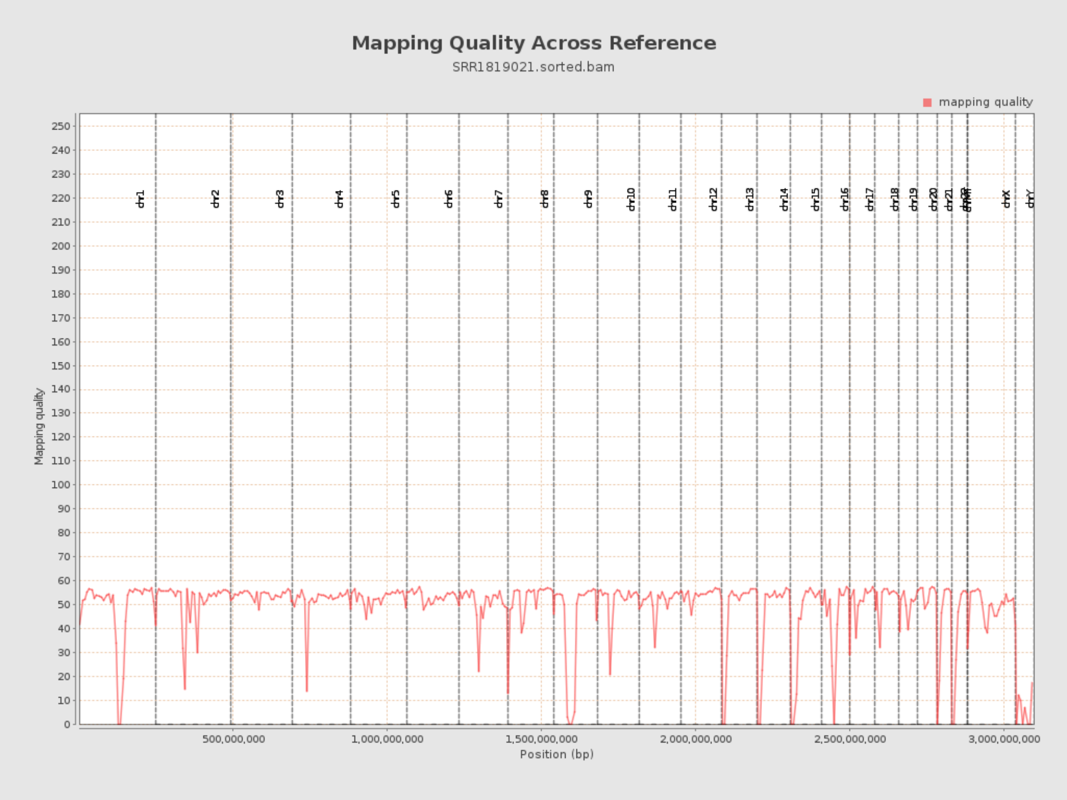
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram