Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 14:18:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819001.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_SRR1819001 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819001.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 14:18:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819001.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,127,079
Mapped reads	1,093,289 / 97%
Unmapped reads	33,790 / 3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,838 / 1.67%
Read min/max/mean length	30 / 101 / 101.64
Duplicated reads (estimated)	374,199 / 33.2%
Duplication rate	28.39%
Clipped reads	1,107,632 / 98.27%

2.2. ACGT Content

Number/percentage of A's	30,119,056 / 29.89%
Number/percentage of C's	22,314,730 / 22.14%
Number/percentage of T's	27,988,138 / 27.77%
Number/percentage of G's	20,347,985 / 20.19%
Number/percentage of N's	4,813 / 0%
GC Percentage	42.33%

2.3. Coverage

Mean	0.0326

Standard Deviation	0.4704

2.4. Mapping Quality

Mean Mapping Quality	49.09

2.5. Mismatches and indels

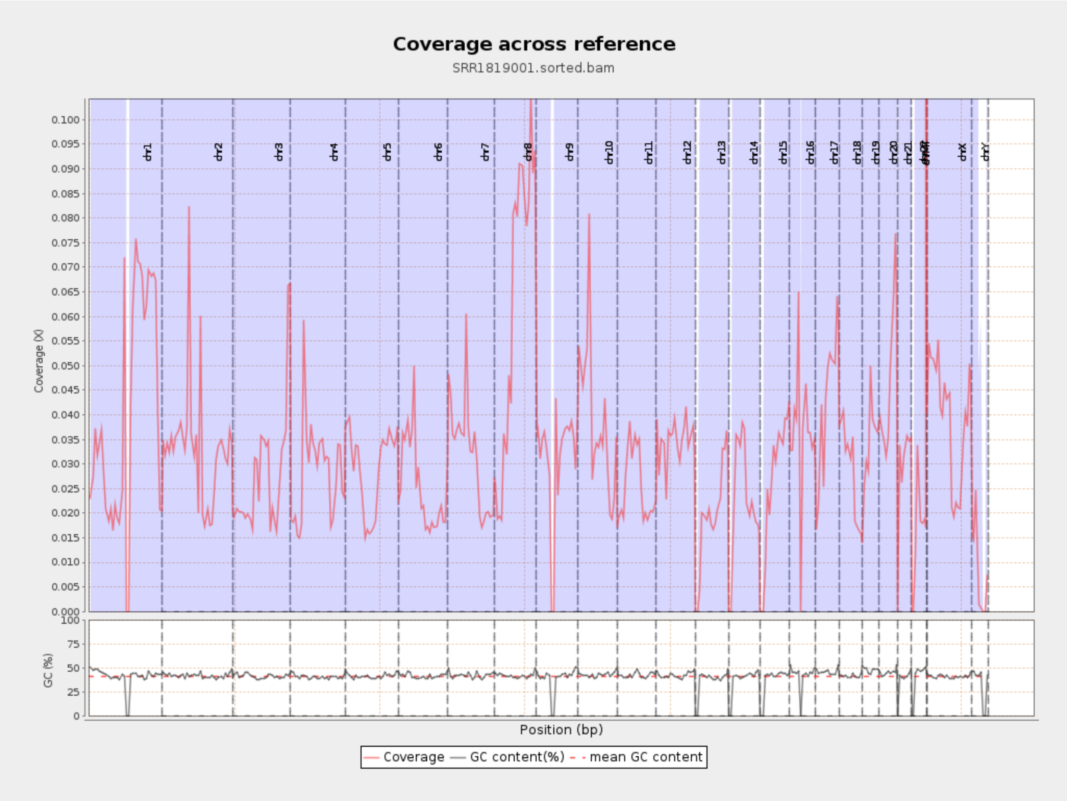
General error rate	0.72%
Mismatches	687,908
Insertions	16,641
Mapped reads with at least one insertion	1.47%
Deletions	33,414
Mapped reads with at least one deletion	2.99%
Homopolymer indels	40.86%

2.6. Chromosome stats

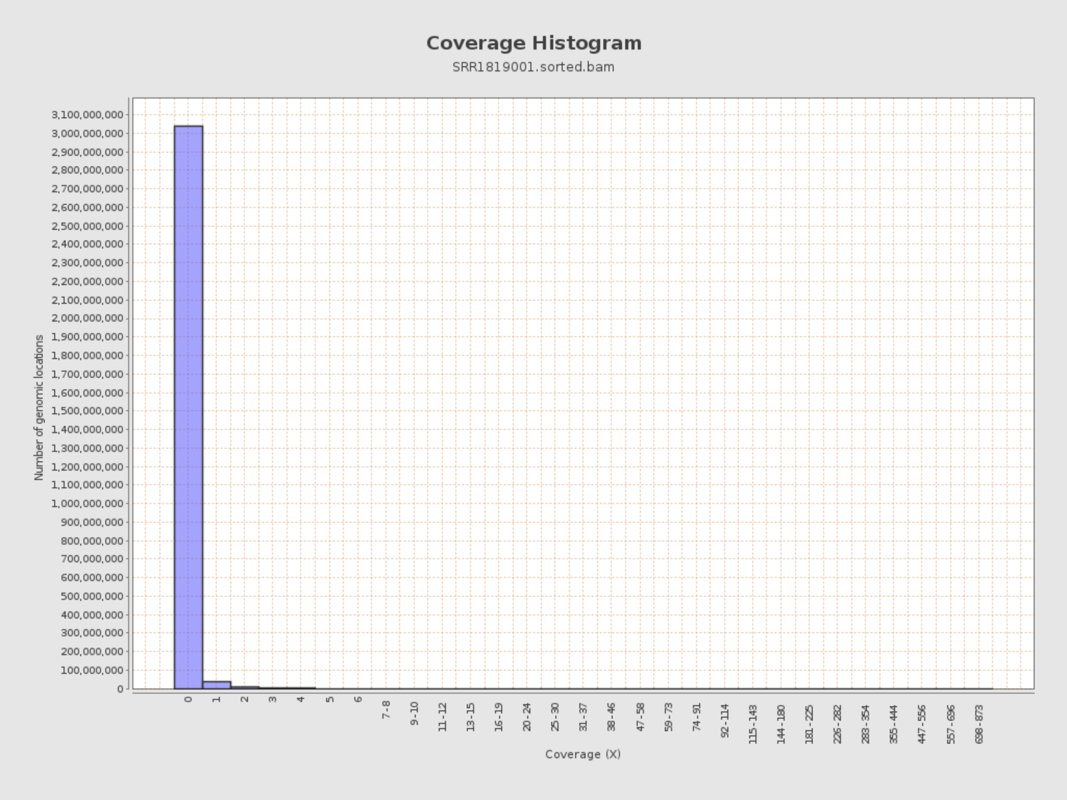
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10074287	0.0404	0.8071
chr2	243199373	8107541	0.0333	0.7572
chr3	198022430	5338786	0.027	0.2534
chr4	191154276	5387542	0.0282	0.3285
chr5	180915260	5253444	0.029	0.2732
chr6	171115067	4341405	0.0254	0.3027
chr7	159138663	5078106	0.0319	0.5247

chr8	146364022	9214273	0.063	0.4376
chr9	141213431	4329381	0.0307	0.3844
chr10	135534747	5255957	0.0388	0.5981
chr11	135006516	3458282	0.0256	0.3028
chr12	133851895	4641633	0.0347	0.2942
chr13	115169878	2253312	0.0196	0.2189
chr14	107349540	2453209	0.0229	0.2464
chr15	102531392	2662275	0.026	0.2505
chr16	90354753	3287748	0.0364	0.5704
chr17	81195210	3478772	0.0428	0.3646
chr18	78077248	2263956	0.029	0.477
chr19	59128983	2038347	0.0345	0.6362
chr20	63025520	2974939	0.0472	0.3646
chr21	48129895	1428140	0.0297	0.3045
chr22	51304566	810031	0.0158	0.2196
chrMT	16571	123175	7.4332	6.4462
chrX	155270560	6125710	0.0395	0.3561
chrY	59373566	458646	0.0077	0.5559

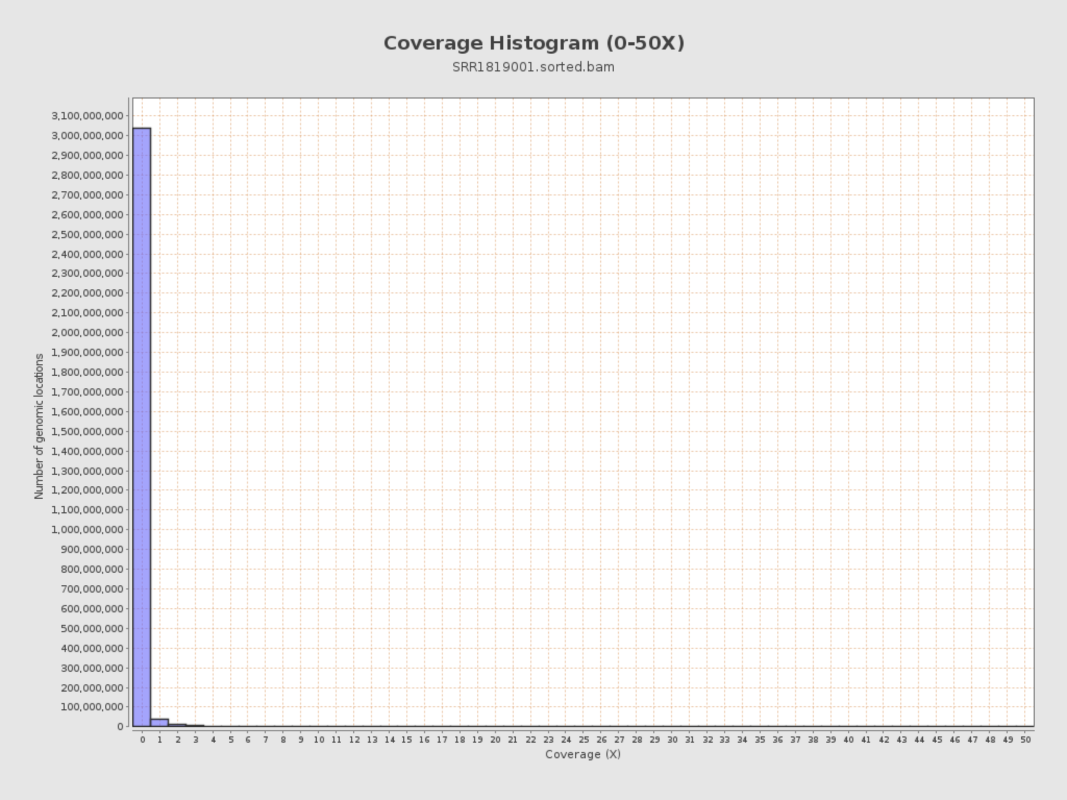
3. Results : Coverage across reference



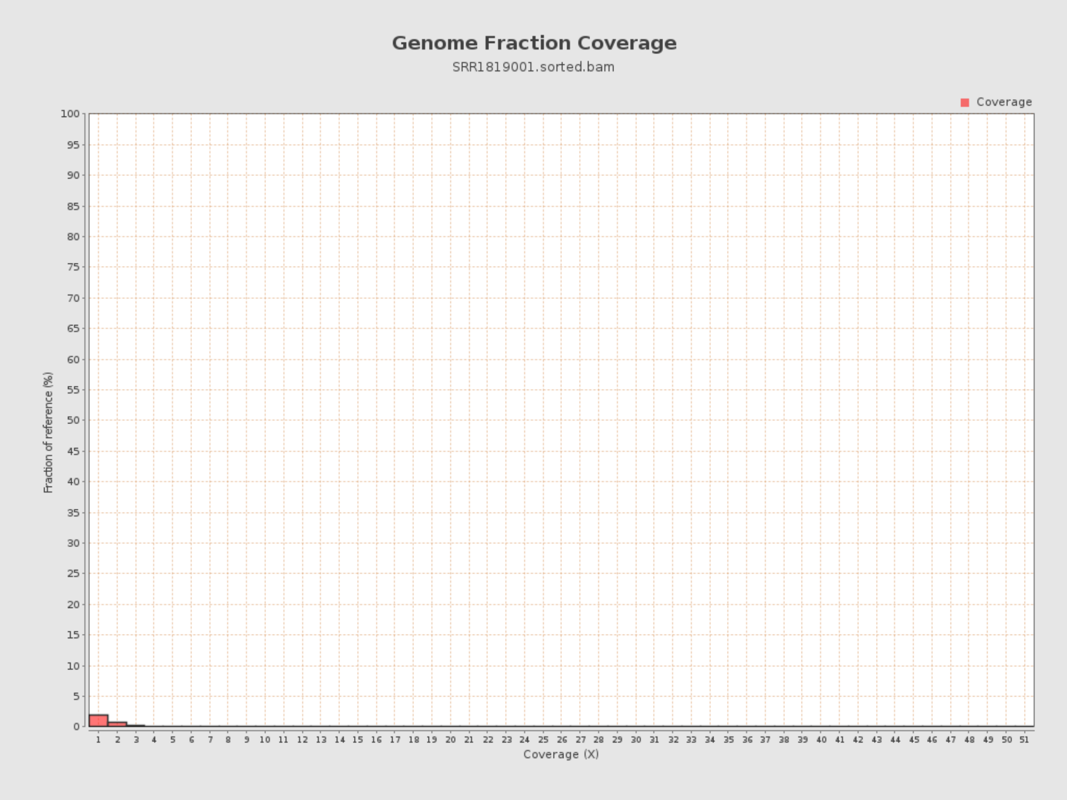
4. Results : Coverage Histogram



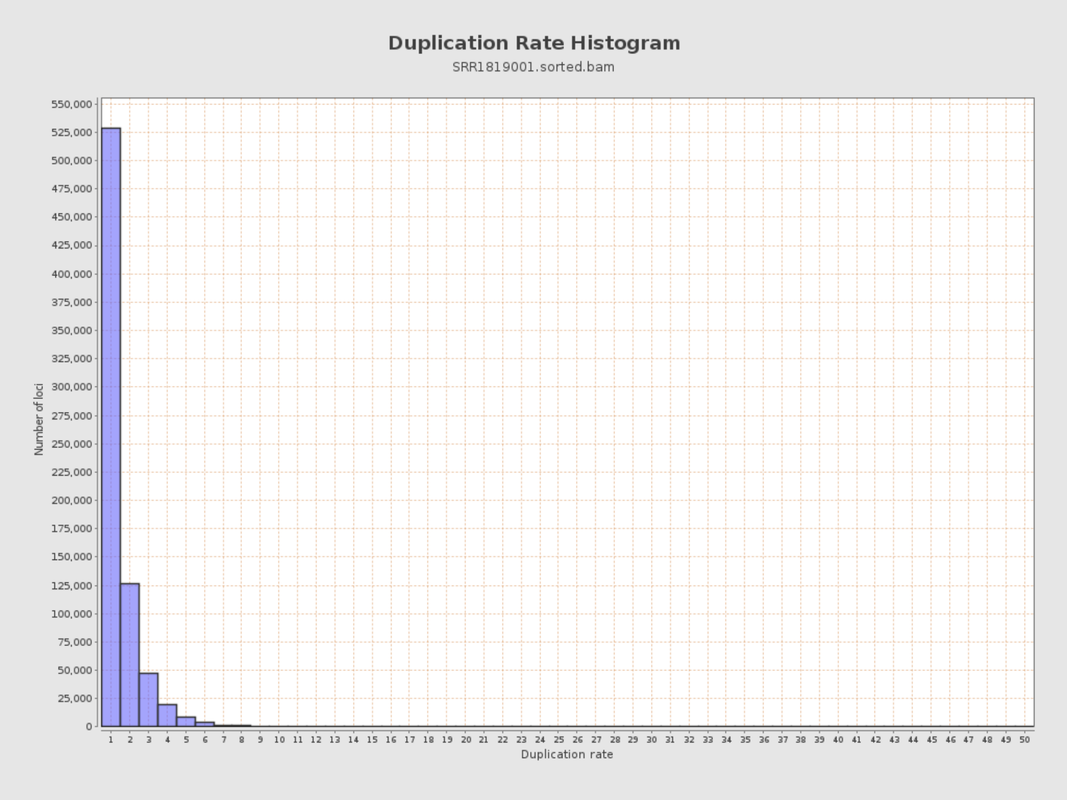
5. Results : Coverage Histogram (0-50X)



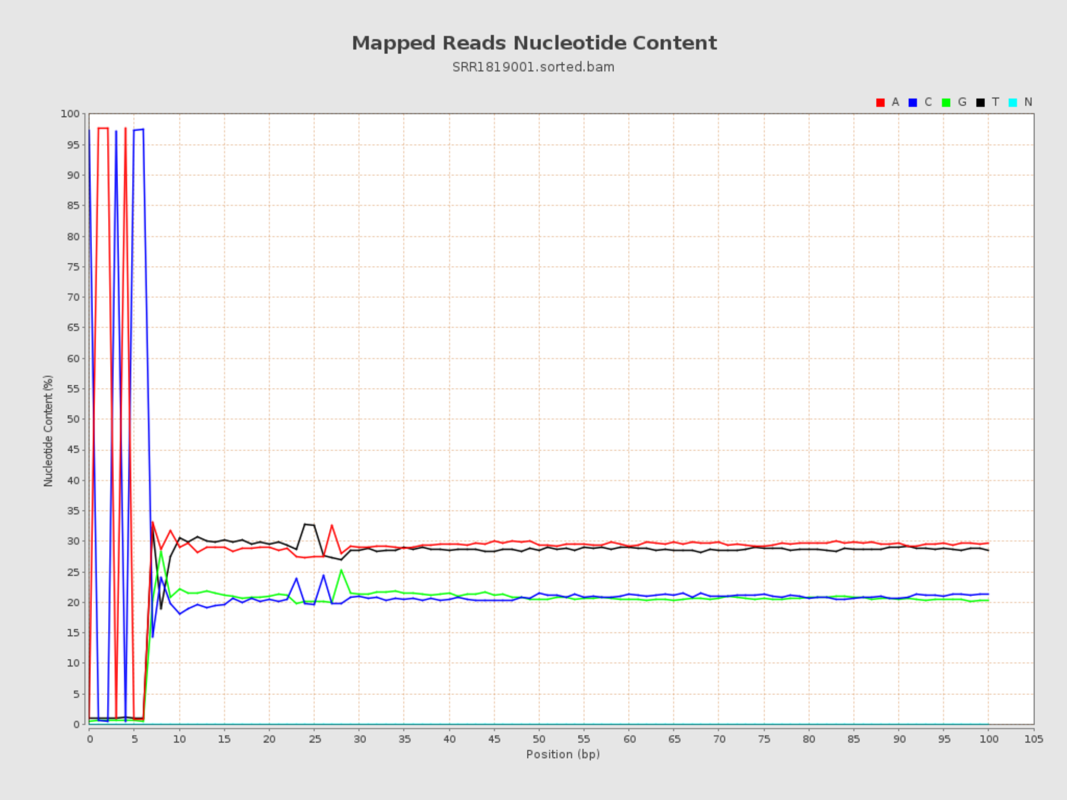
6. Results : Genome Fraction Coverage



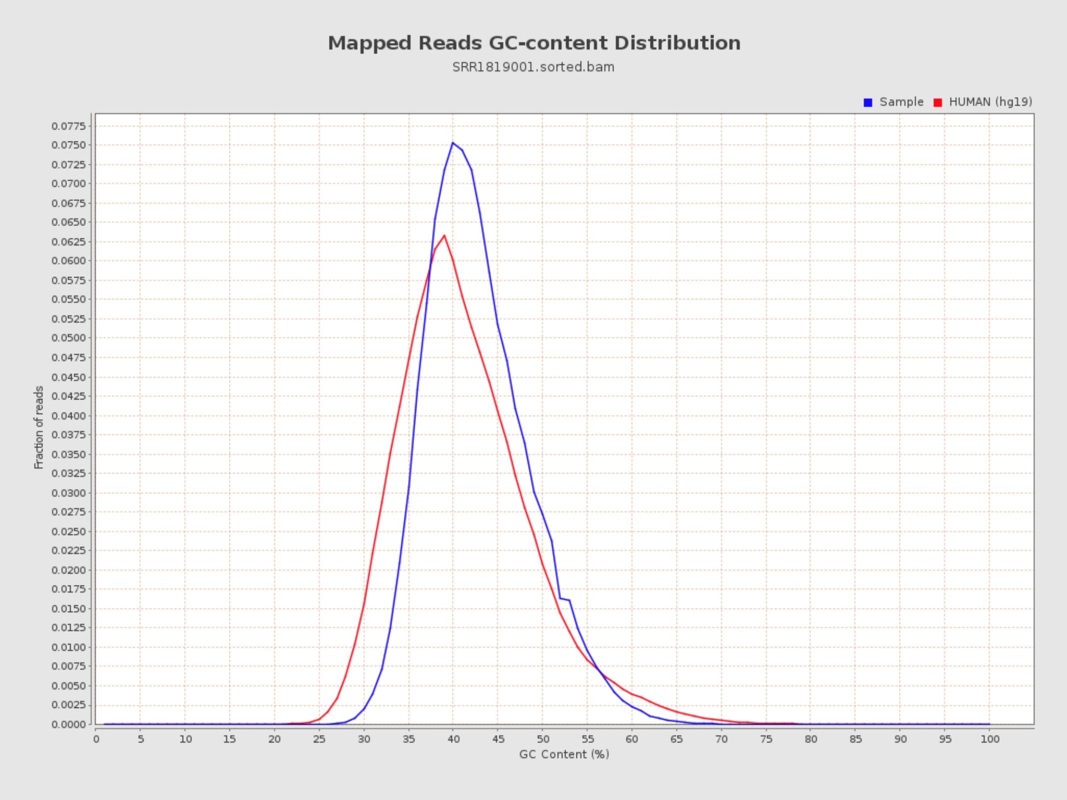
7. Results : Duplication Rate Histogram



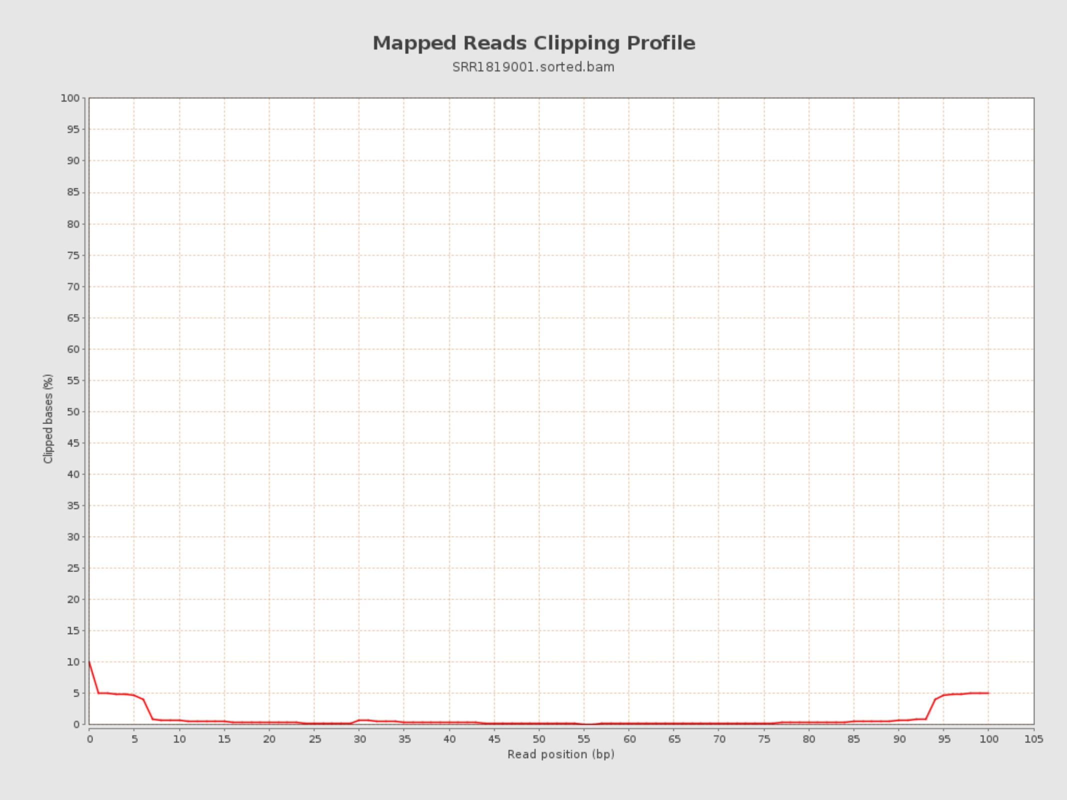
8. Results : Mapped Reads Nucleotide Content



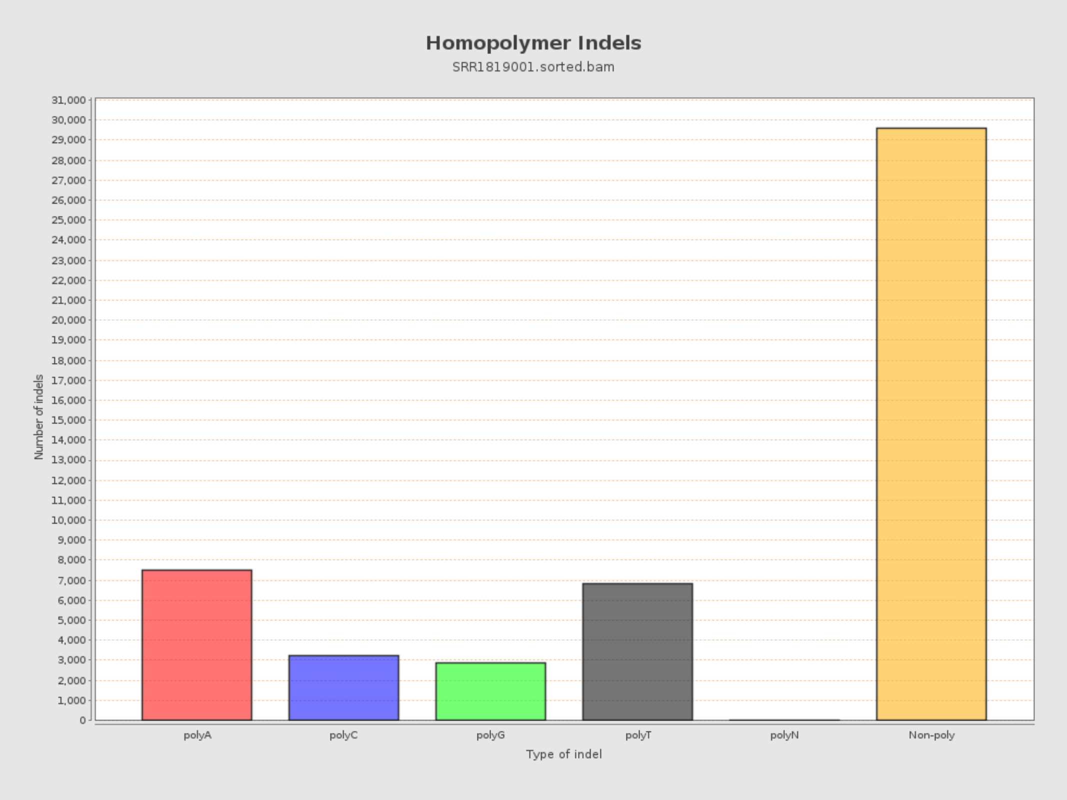
9. Results : Mapped Reads GC-content Distribution



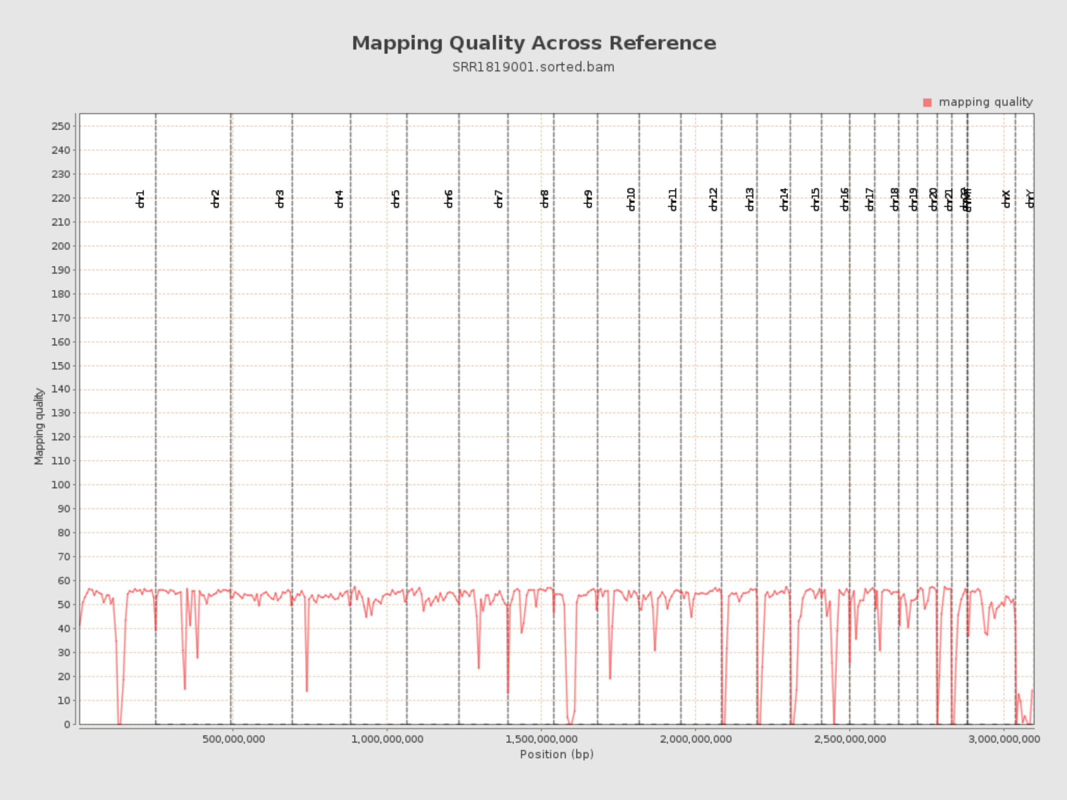
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram