Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 18:14:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819055.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_SRR1819055 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819055.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 18:14:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819055.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,605,992
Mapped reads	1,426,020 / 88.79%
Unmapped reads	179,972 / 11.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,058 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	37,174 / 2.31%
Duplication rate	2.02%
Clipped reads	1,431,143 / 89.11%

2.2. ACGT Content

Number/percentage of A's	20,920,714 / 25.46%
Number/percentage of C's	15,253,899 / 18.56%
Number/percentage of T's	25,113,233 / 30.56%
Number/percentage of G's	20,879,420 / 25.41%
Number/percentage of N's	1,721 / 0%
GC Percentage	43.97%

2.3. Coverage

Mean	0.0265

Standard Deviation	0.2142

2.4. Mapping Quality

Mean Mapping Quality	44.73

2.5. Mismatches and indels

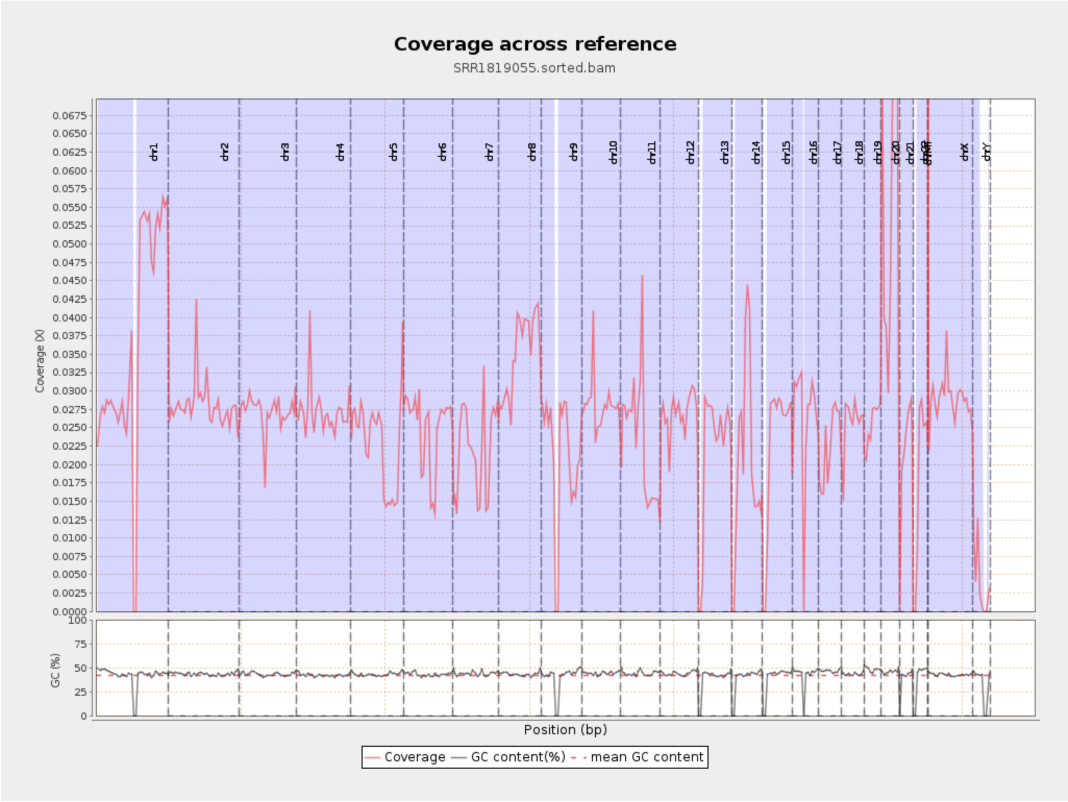
General error rate	0.48%
Mismatches	388,388
Insertions	4,013
Mapped reads with at least one insertion	0.28%
Deletions	12,330
Mapped reads with at least one deletion	0.86%
Homopolymer indels	43.06%

2.6. Chromosome stats

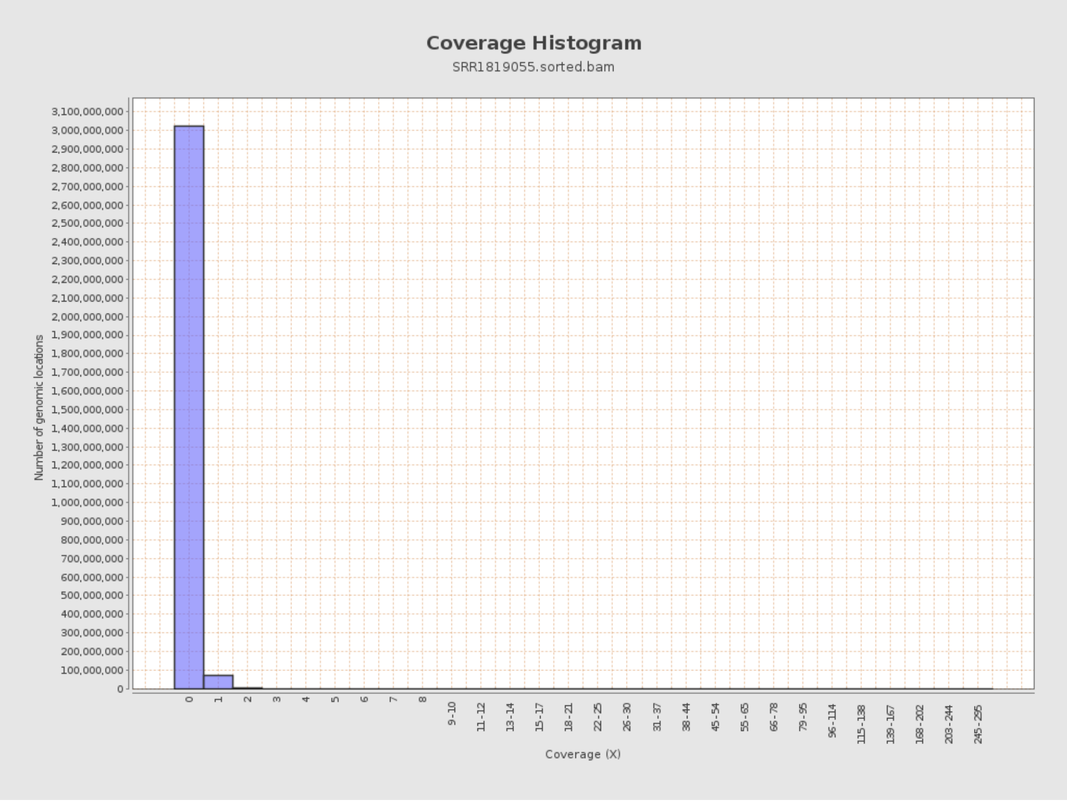
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9107786	0.0365	0.3186
chr2	243199373	6839764	0.0281	0.2359
chr3	198022430	5370242	0.0271	0.1776
chr4	191154276	5195908	0.0272	0.1896
chr5	180915260	4131060	0.0228	0.165
chr6	171115067	4250440	0.0248	0.1788
chr7	159138663	3516725	0.0221	0.1909

chr8	146364022	5132575	0.0351	0.2263
chr9	141213431	2957938	0.0209	0.2123
chr10	135534747	3807722	0.0281	0.2234
chr11	135006516	3184940	0.0236	0.214
chr12	133851895	3603547	0.0269	0.1801
chr13	115169878	2504589	0.0217	0.1575
chr14	107349540	2219708	0.0207	0.1645
chr15	102531392	2320363	0.0226	0.1622
chr16	90354753	2350779	0.026	0.1856
chr17	81195210	1818082	0.0224	0.1683
chr18	78077248	1983277	0.0254	0.386
chr19	59128983	1509188	0.0255	0.2319
chr20	63025520	3657006	0.058	0.2706
chr21	48129895	1050800	0.0218	0.1749
chr22	51304566	944424	0.0184	0.1468
chrMT	16571	2323	0.1402	0.3641
chrX	155270560	4495905	0.029	0.1994
chrY	59373566	235044	0.004	0.098

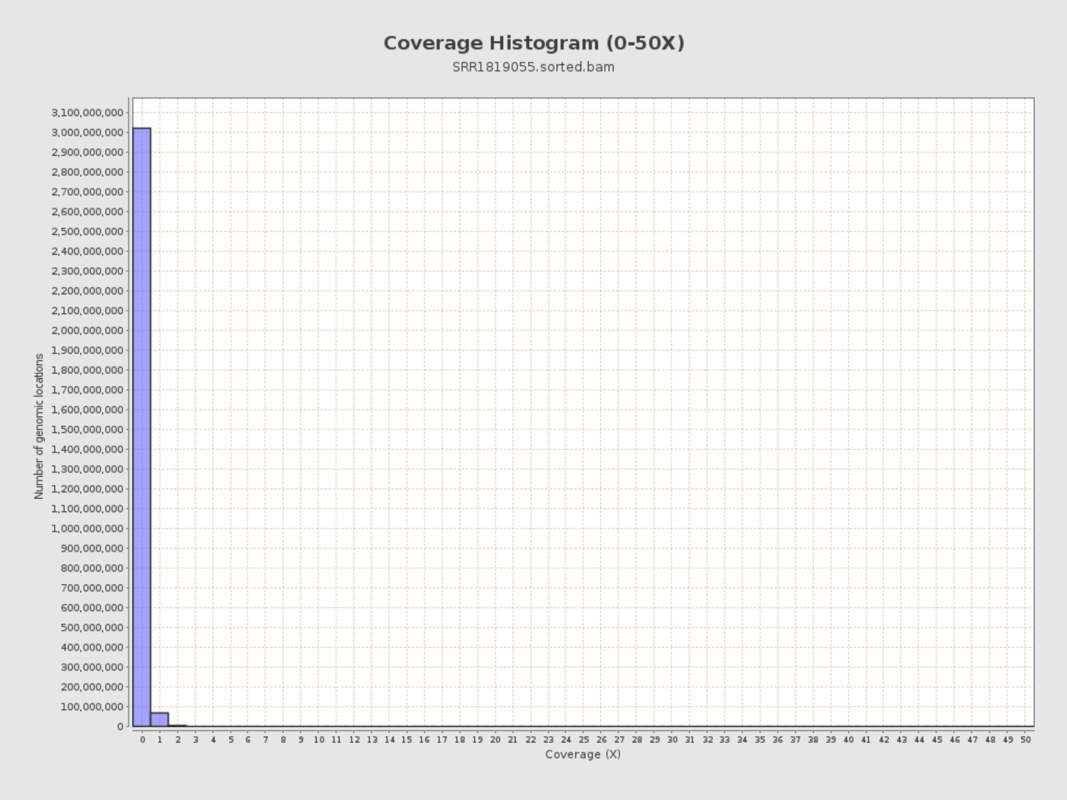
3. Results : Coverage across reference



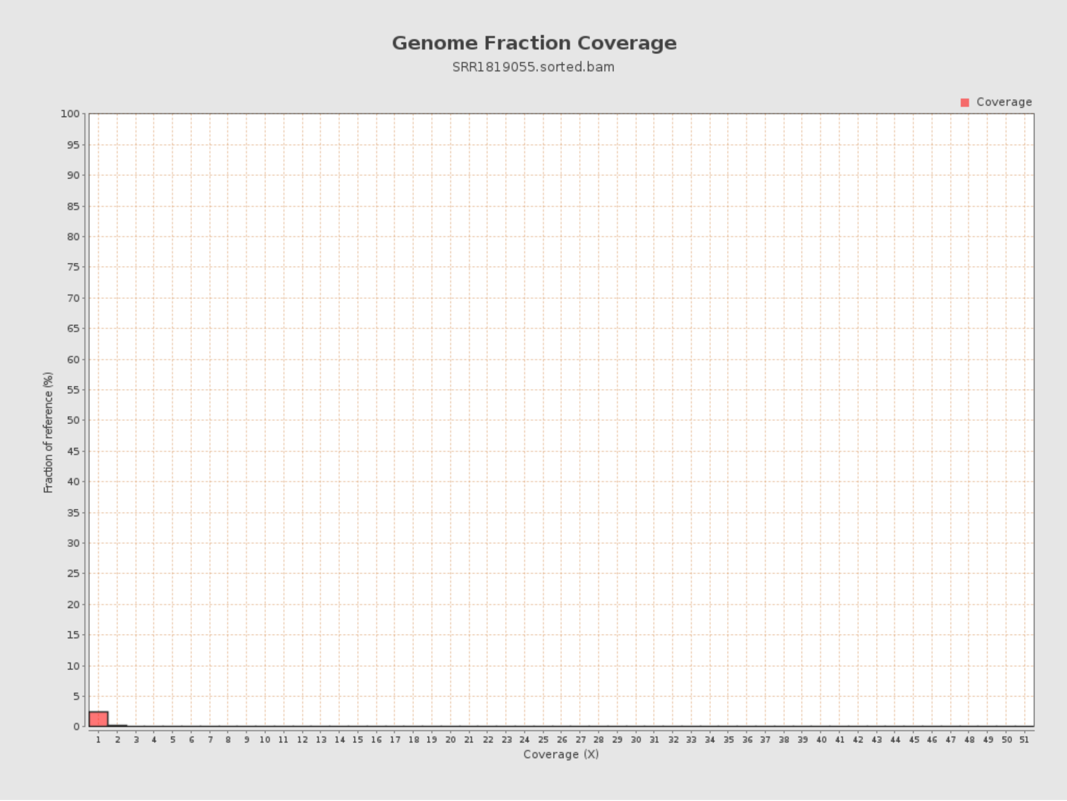
4. Results : Coverage Histogram



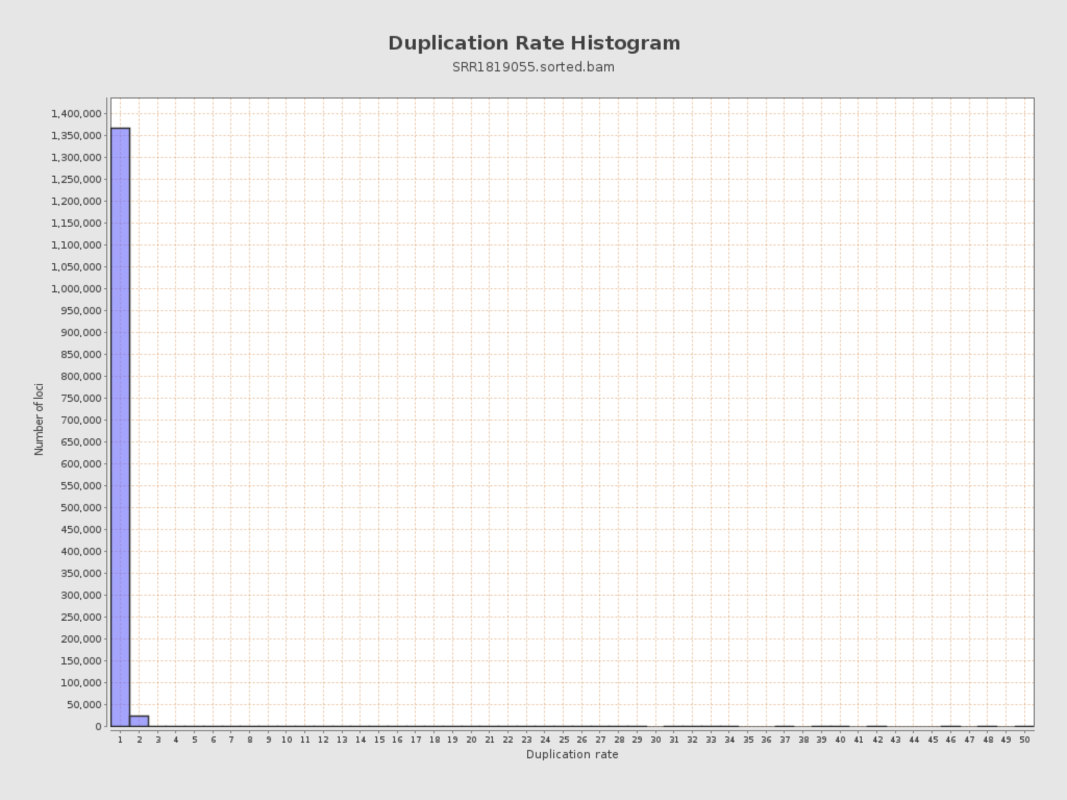
5. Results : Coverage Histogram (0-50X)



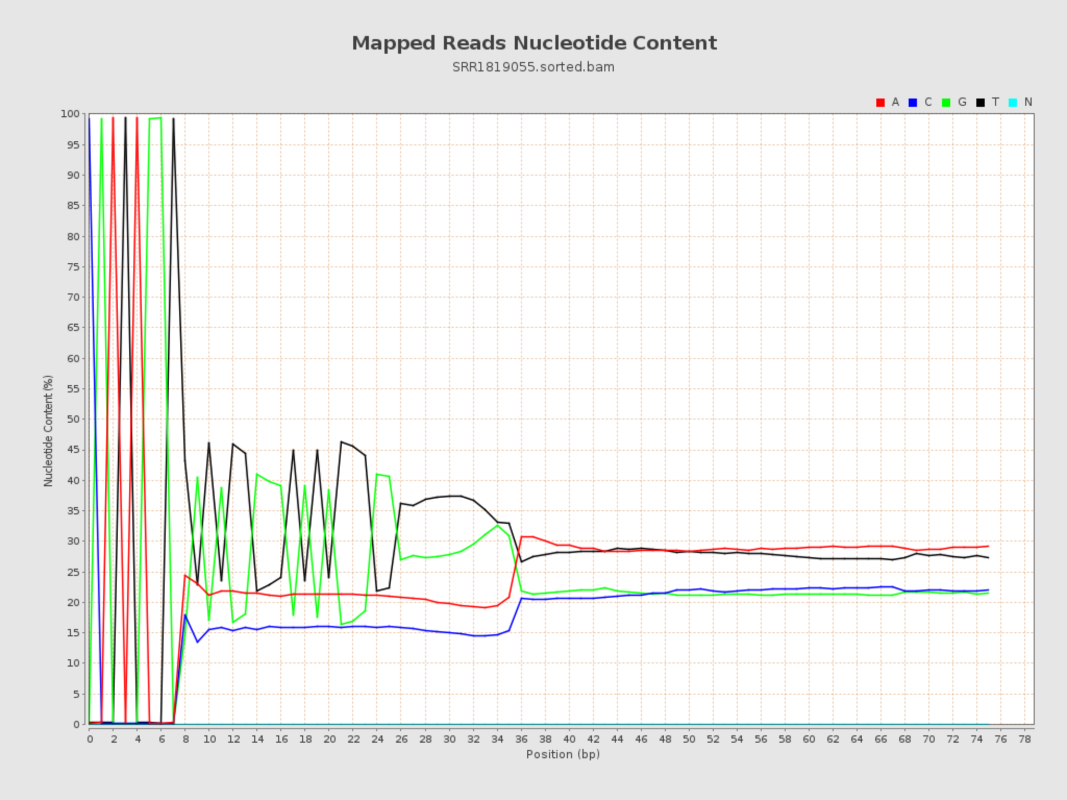
6. Results : Genome Fraction Coverage



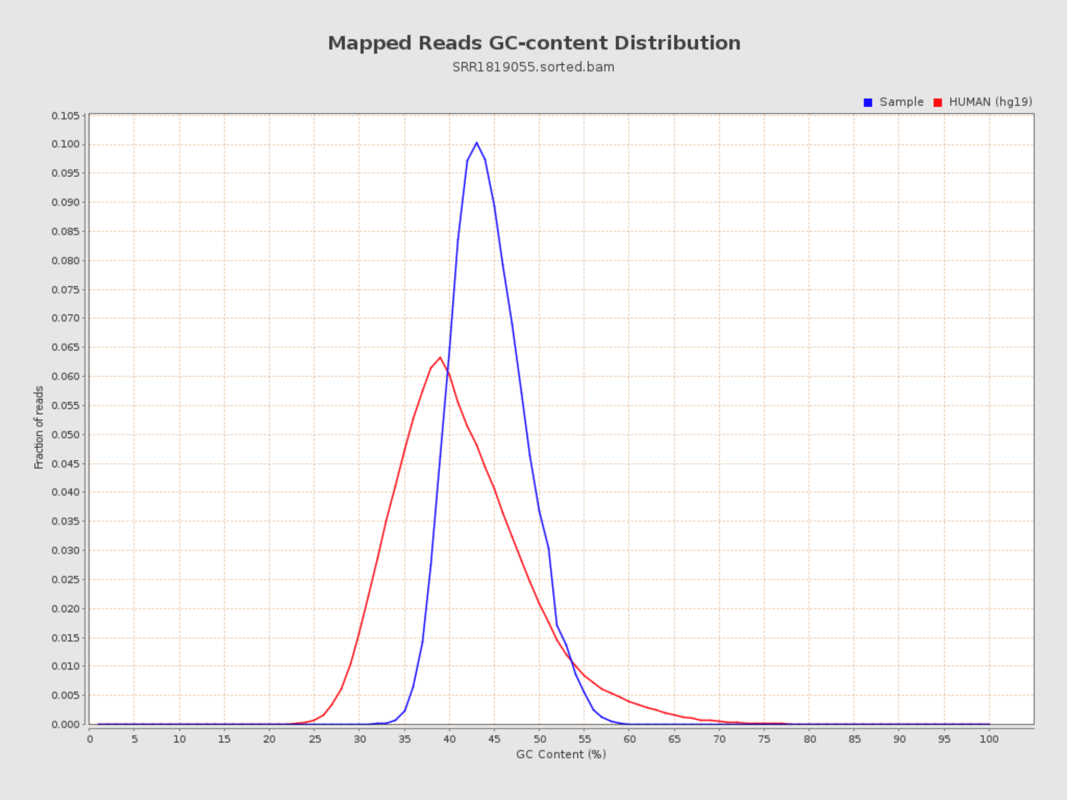
7. Results : Duplication Rate Histogram



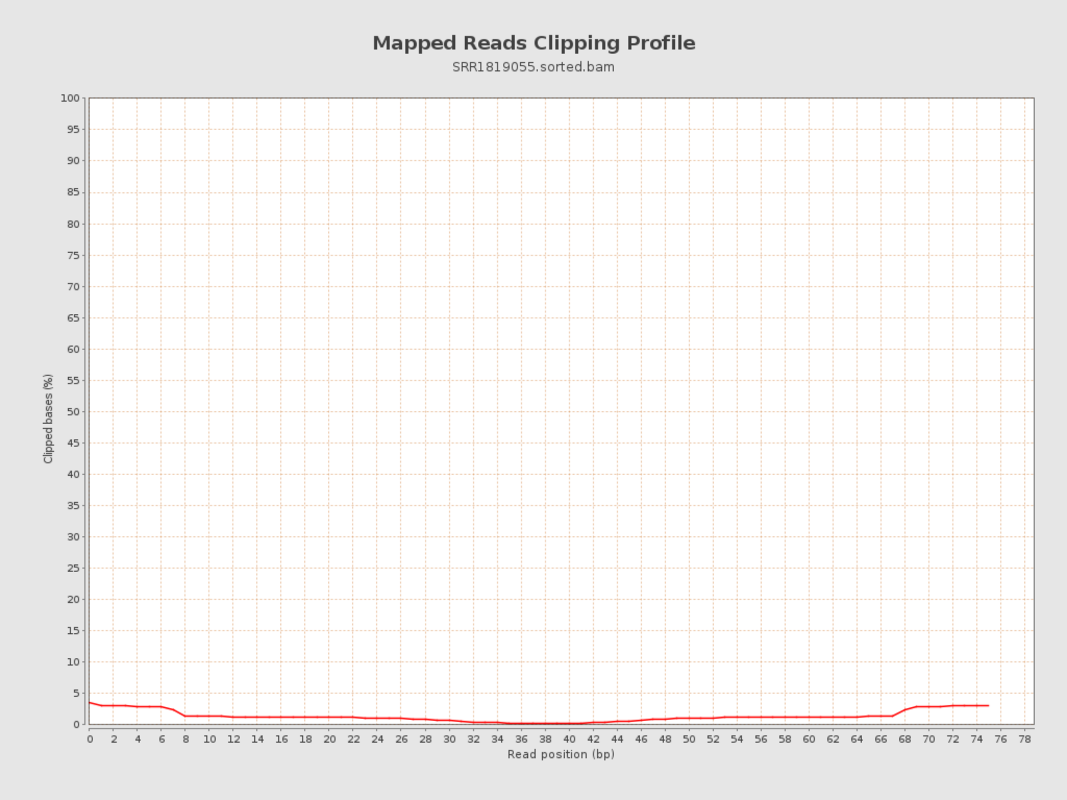
8. Results : Mapped Reads Nucleotide Content



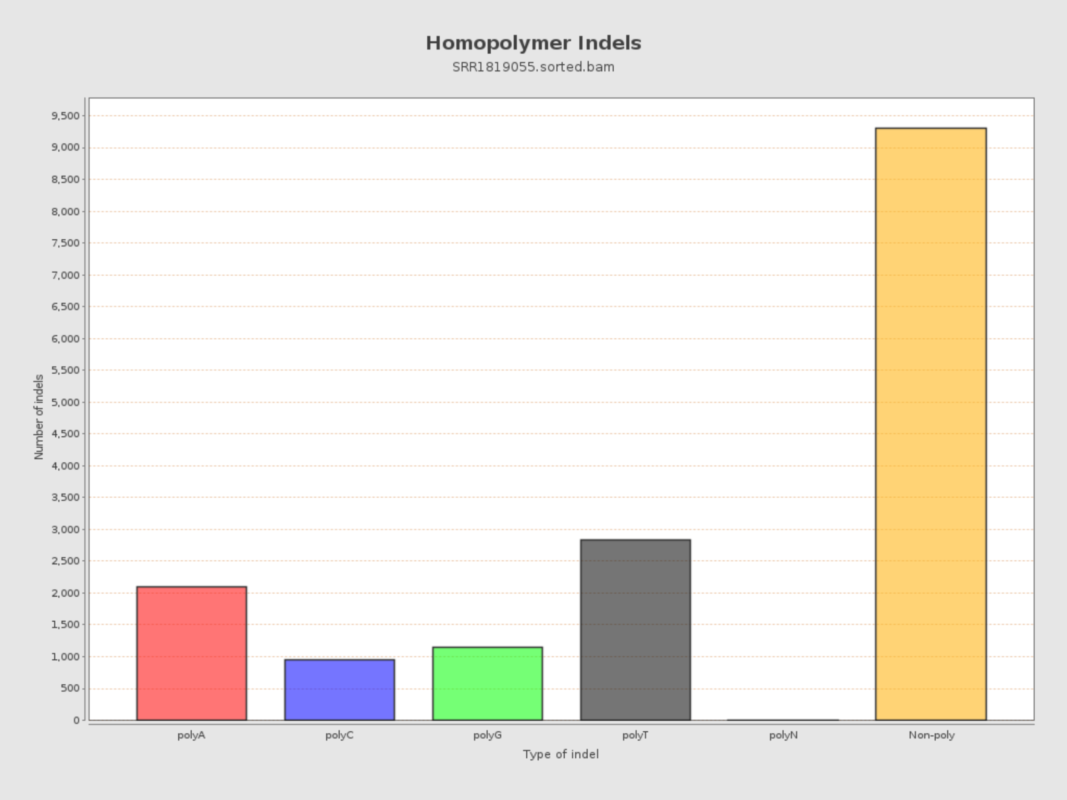
9. Results : Mapped Reads GC-content Distribution



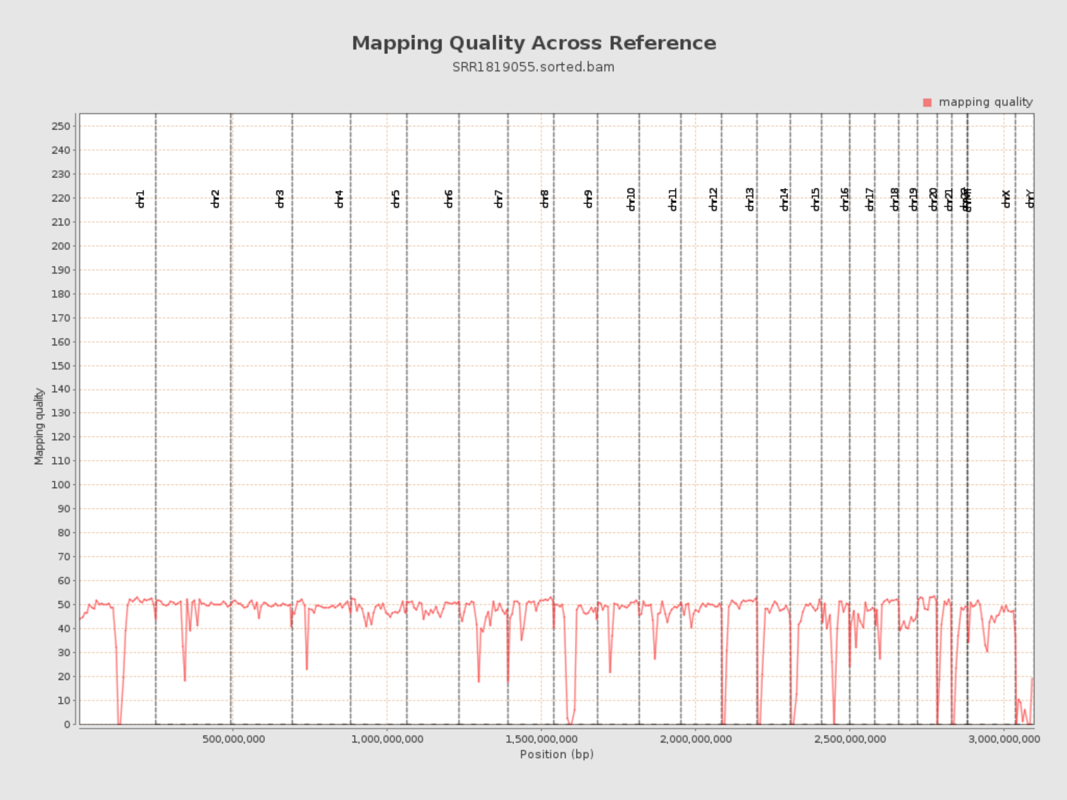
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram