Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/19 23:37:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1506019.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_SRR1506019 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1506019.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 19 23:37:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1506019.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,910,305
Mapped reads	2,893,279 / 73.99%
Unmapped reads	1,017,026 / 26.01%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	146 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	145,051 / 3.71%
Duplication rate	3.82%
Clipped reads	428,568 / 10.96%

2.2. ACGT Content

Number/percentage of A's	39,798,490 / 29.54%
Number/percentage of C's	27,479,106 / 20.4%
Number/percentage of T's	39,149,746 / 29.06%
Number/percentage of G's	27,859,812 / 20.68%
Number/percentage of N's	437,669 / 0.32%
GC Percentage	41.08%

2.3. Coverage

Mean	0.0435

Standard Deviation	0.417

2.4. Mapping Quality

Mean Mapping Quality	44.27

2.5. Mismatches and indels

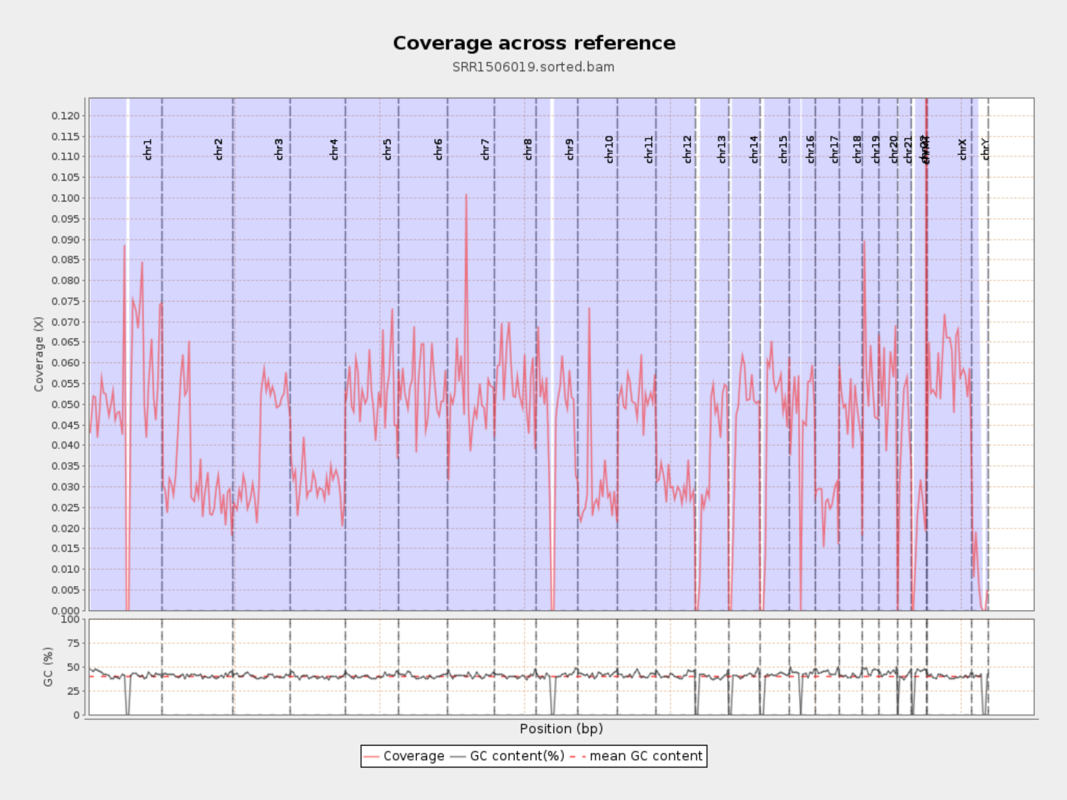
General error rate	0.8%
Mismatches	1,074,746
Insertions	5,975
Mapped reads with at least one insertion	0.21%
Deletions	20,000
Mapped reads with at least one deletion	0.69%
Homopolymer indels	45.82%

2.6. Chromosome stats

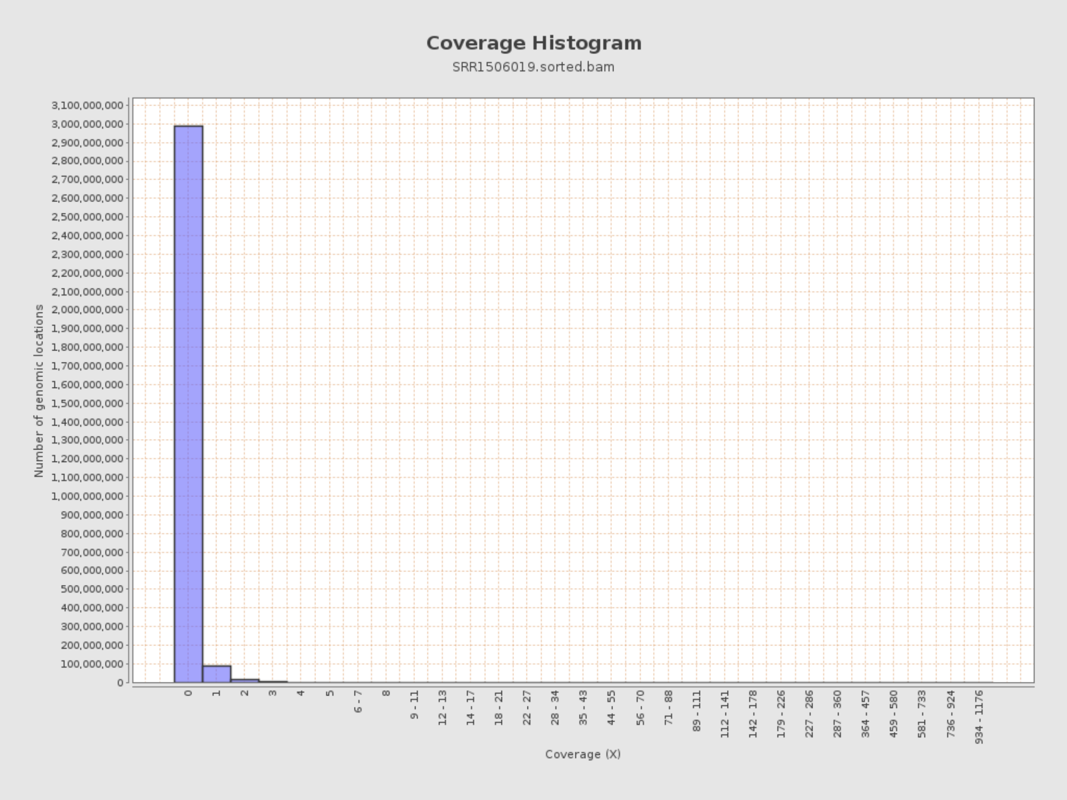
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13169978	0.0528	0.8541
chr2	243199373	8094284	0.0333	0.3332
chr3	198022430	8055634	0.0407	0.2426
chr4	191154276	5817901	0.0304	0.2142
chr5	180915260	9581077	0.053	0.281
chr6	171115067	9241807	0.054	0.3423
chr7	159138663	8478299	0.0533	0.647

chr8	146364022	8155949	0.0557	0.5003
chr9	141213431	6434492	0.0456	0.3259
chr10	135534747	3955420	0.0292	0.4042
chr11	135006516	6942024	0.0514	0.3532
chr12	133851895	4023086	0.0301	0.2235
chr13	115169878	4140587	0.036	0.2252
chr14	107349540	4726808	0.044	0.3949
chr15	102531392	4542634	0.0443	0.2514
chr16	90354753	4235087	0.0469	0.2896
chr17	81195210	2136879	0.0263	0.2117
chr18	78077248	3815936	0.0489	0.5234
chr19	59128983	3359115	0.0568	0.6054
chr20	63025520	3473786	0.0551	0.2855
chr21	48129895	1952736	0.0406	0.2582
chr22	51304566	925133	0.018	0.1594
chrMT	16571	25721	1.5522	1.6293
chrX	155270560	9072838	0.0584	0.3236
chrY	59373566	395198	0.0067	0.1255

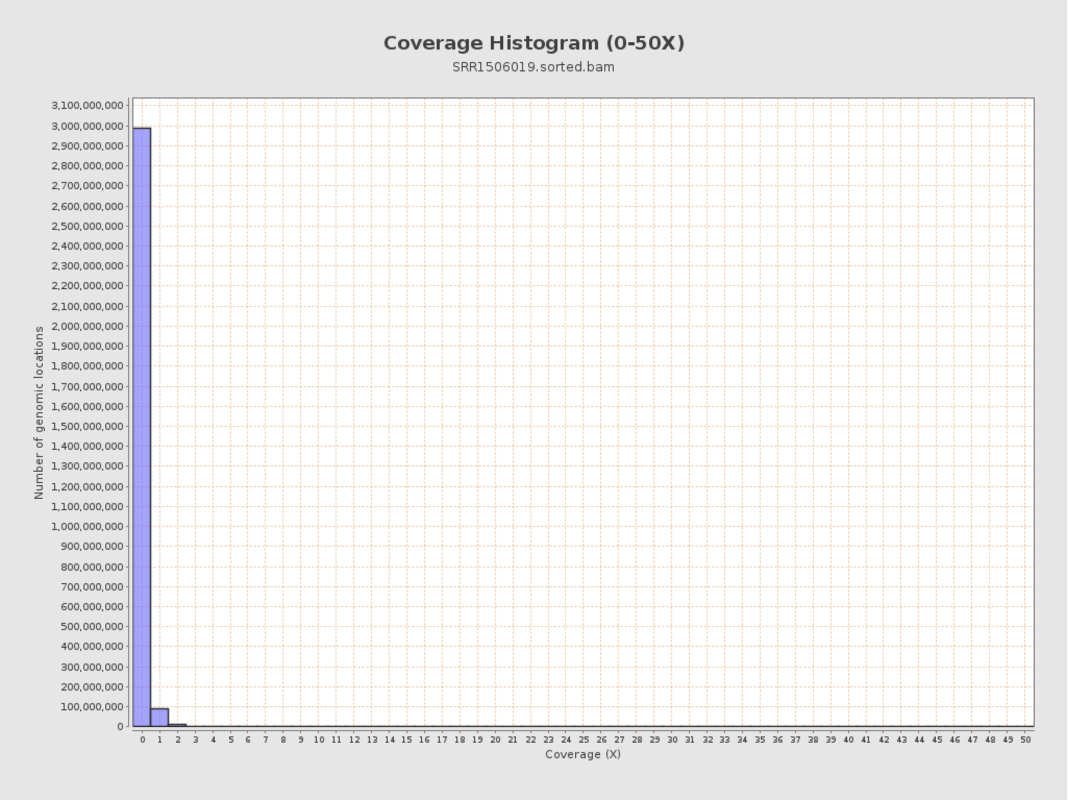
3. Results : Coverage across reference



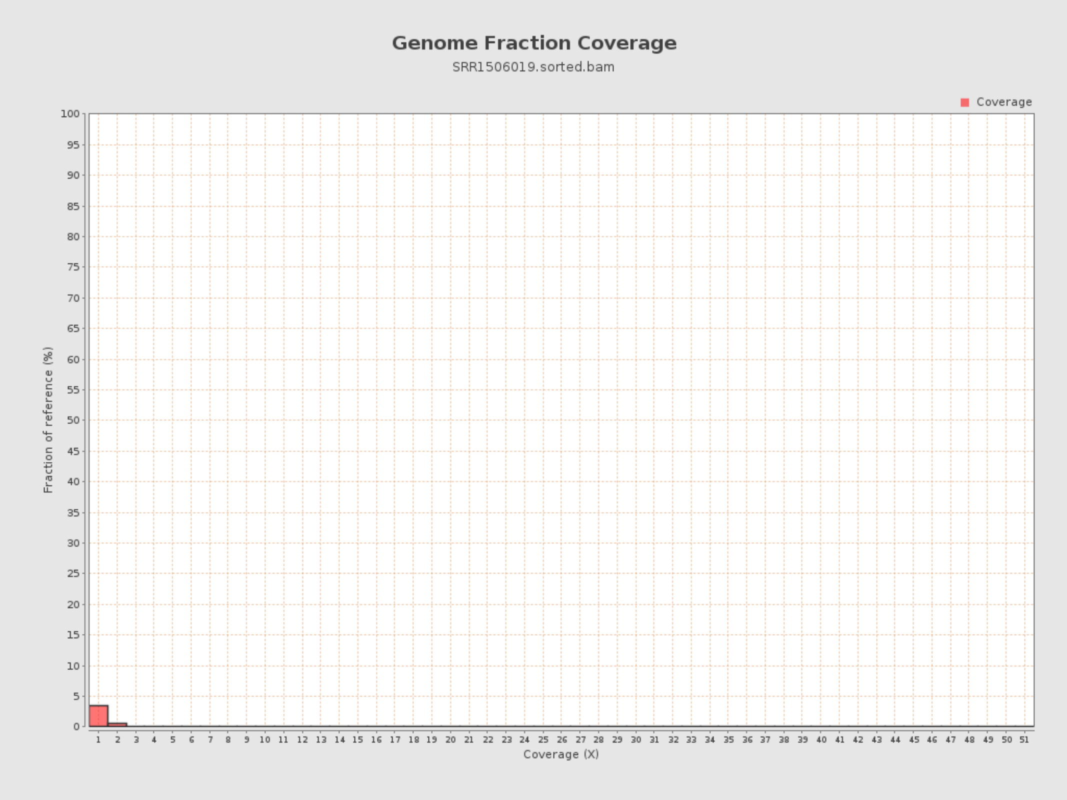
4. Results : Coverage Histogram



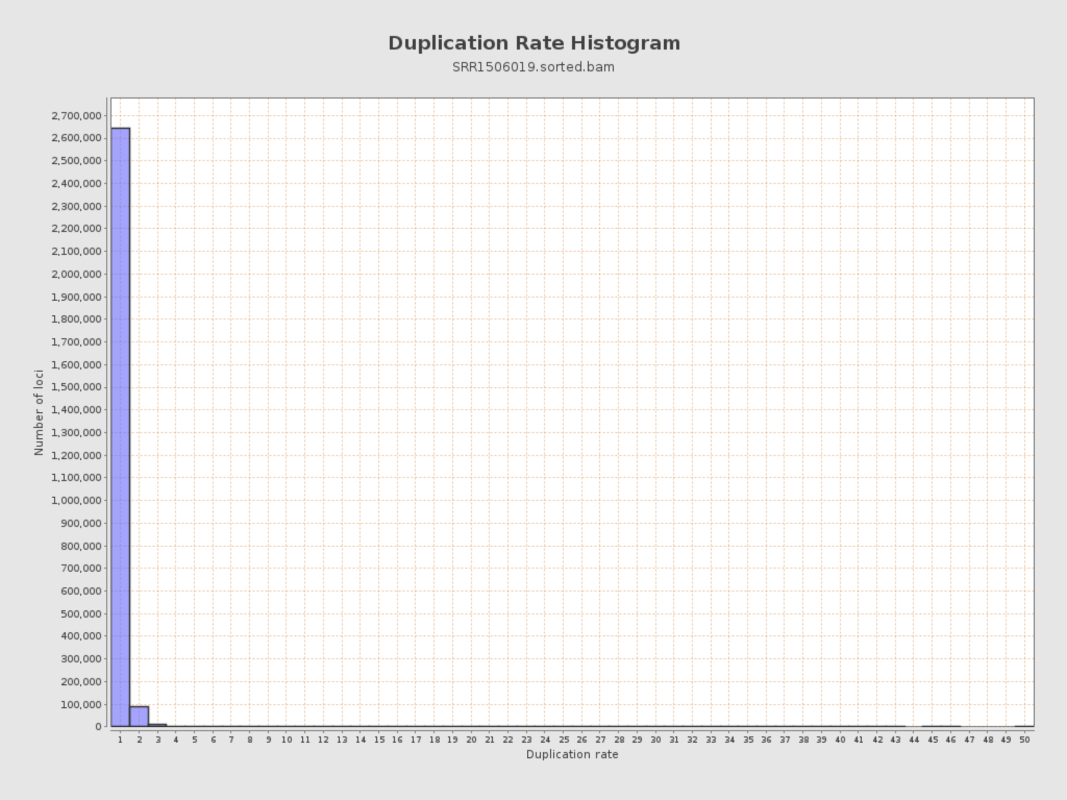
5. Results : Coverage Histogram (0-50X)



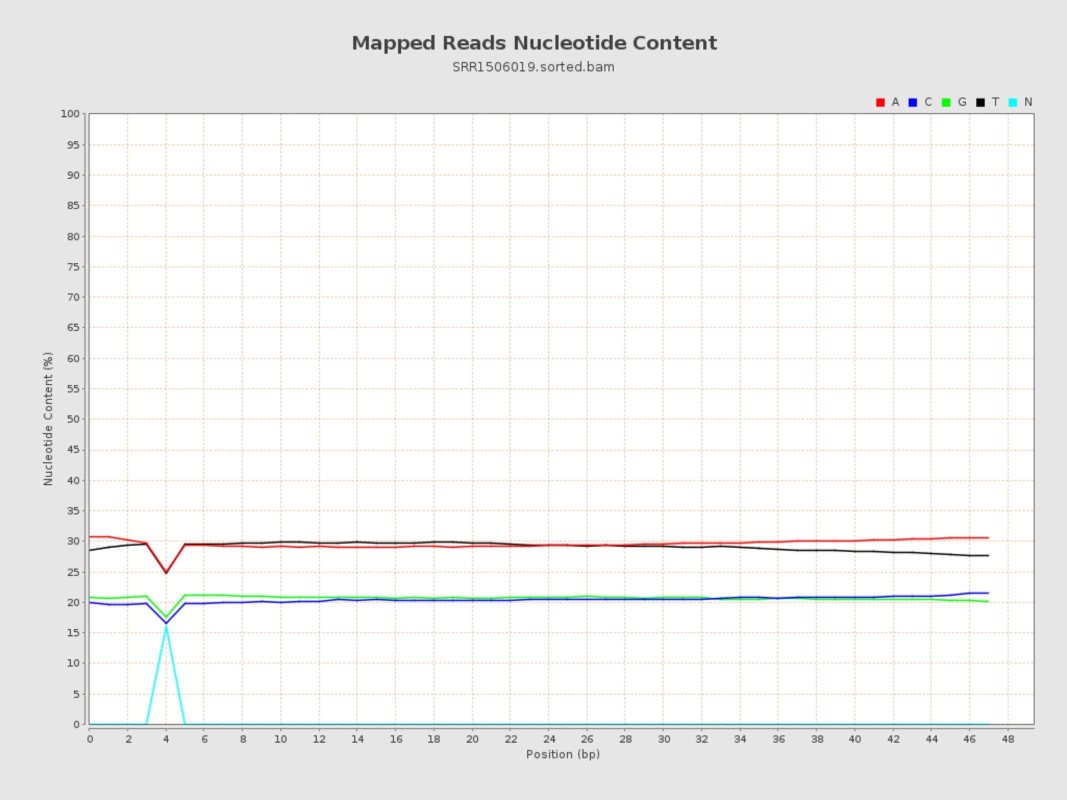
6. Results : Genome Fraction Coverage



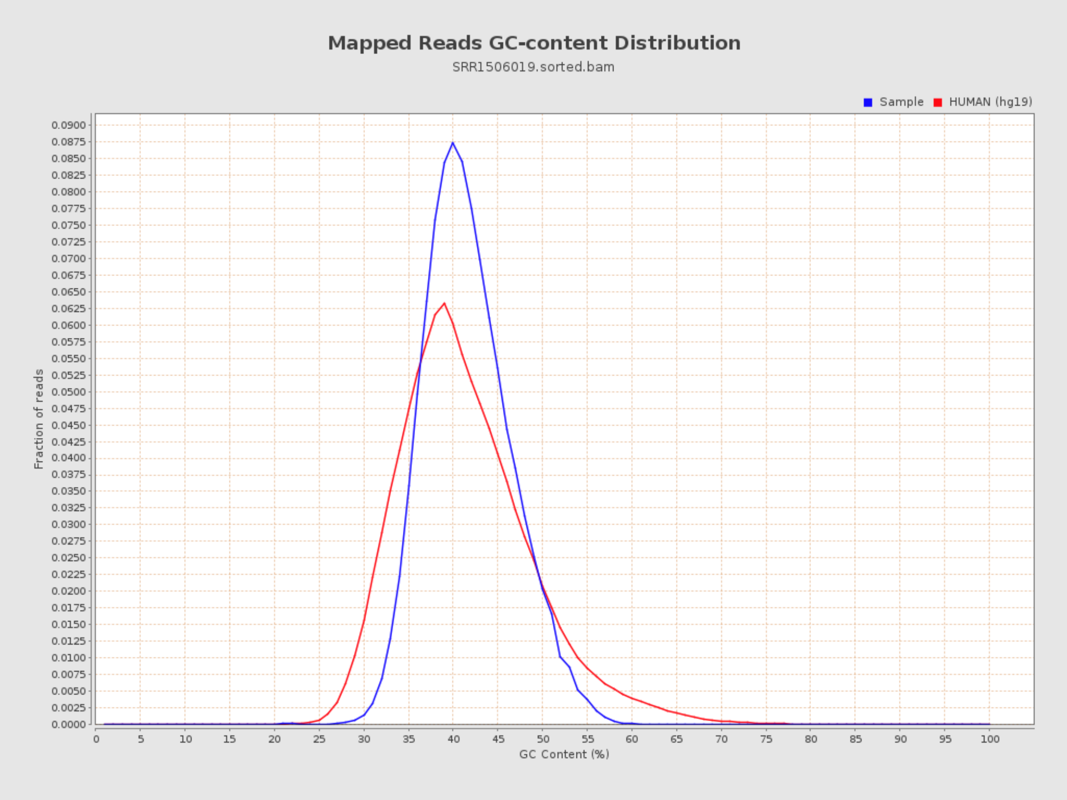
7. Results : Duplication Rate Histogram



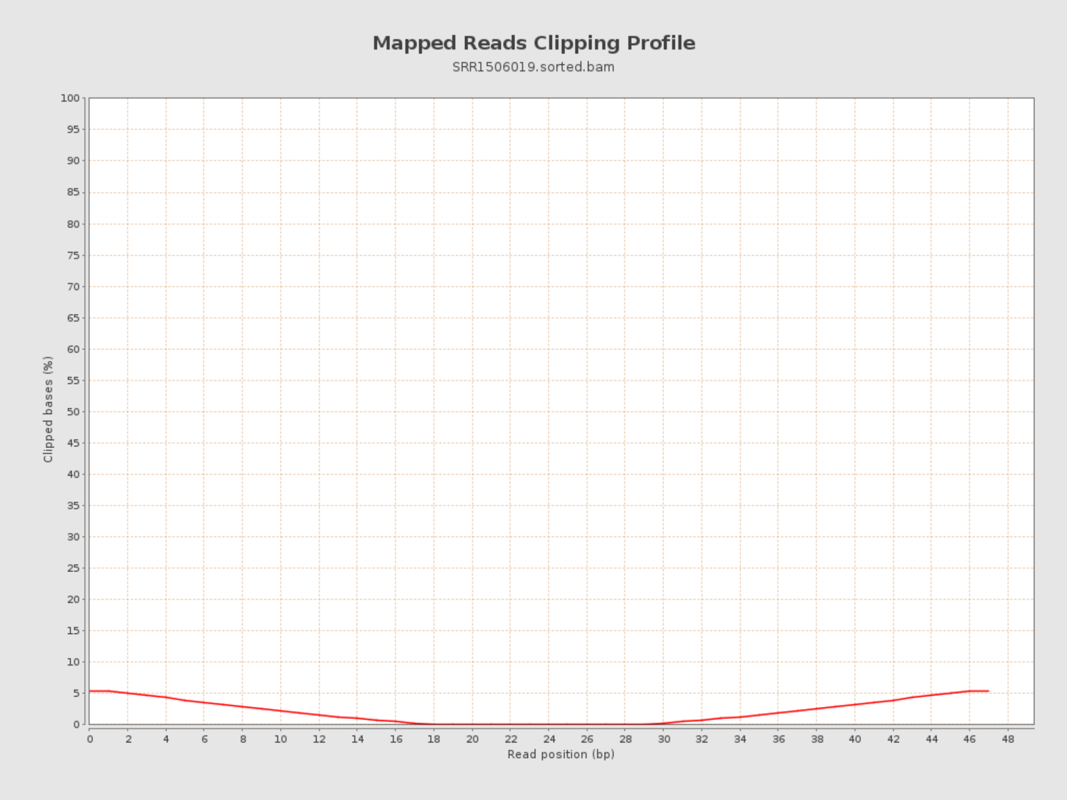
8. Results : Mapped Reads Nucleotide Content



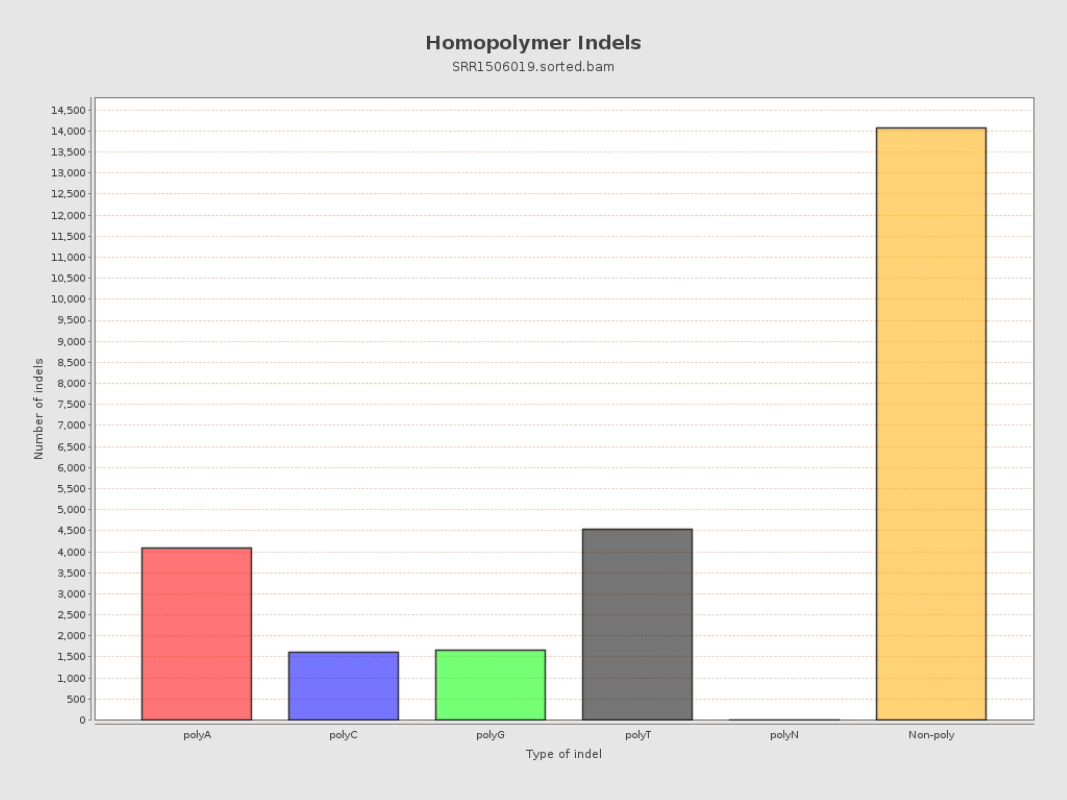
9. Results : Mapped Reads GC-content Distribution



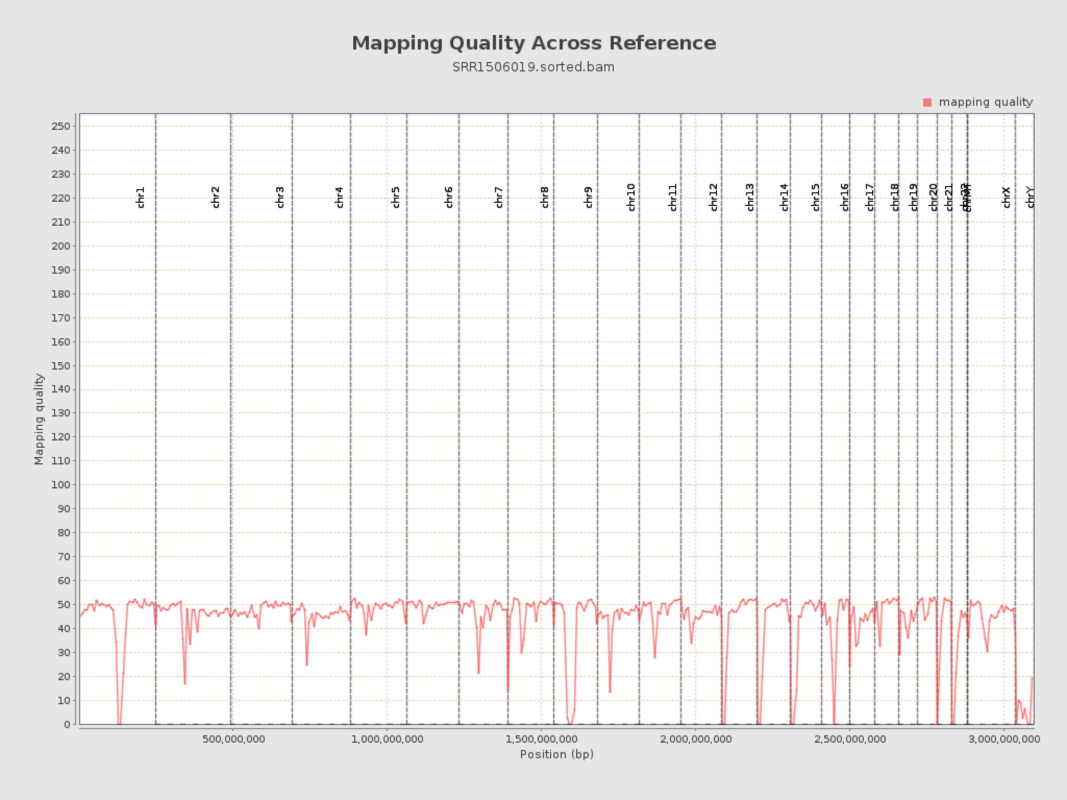
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram