Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 06:13:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081691.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_SRR3081691 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081691.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 06:13:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081691.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,051,883
Mapped reads	1,804,664 / 87.95%
Unmapped reads	247,219 / 12.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,320 / 0.8%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	91,550 / 4.46%
Duplication rate	4.07%
Clipped reads	789,583 / 38.48%

2.2. ACGT Content

Number/percentage of A's	33,812,236 / 28%
Number/percentage of C's	21,346,512 / 17.67%
Number/percentage of T's	39,316,463 / 32.55%
Number/percentage of G's	26,217,027 / 21.71%
Number/percentage of N's	82,971 / 0.07%
GC Percentage	39.38%

2.3. Coverage

Mean	0.039

Standard Deviation	0.3525

2.4. Mapping Quality

Mean Mapping Quality	47.25

2.5. Mismatches and indels

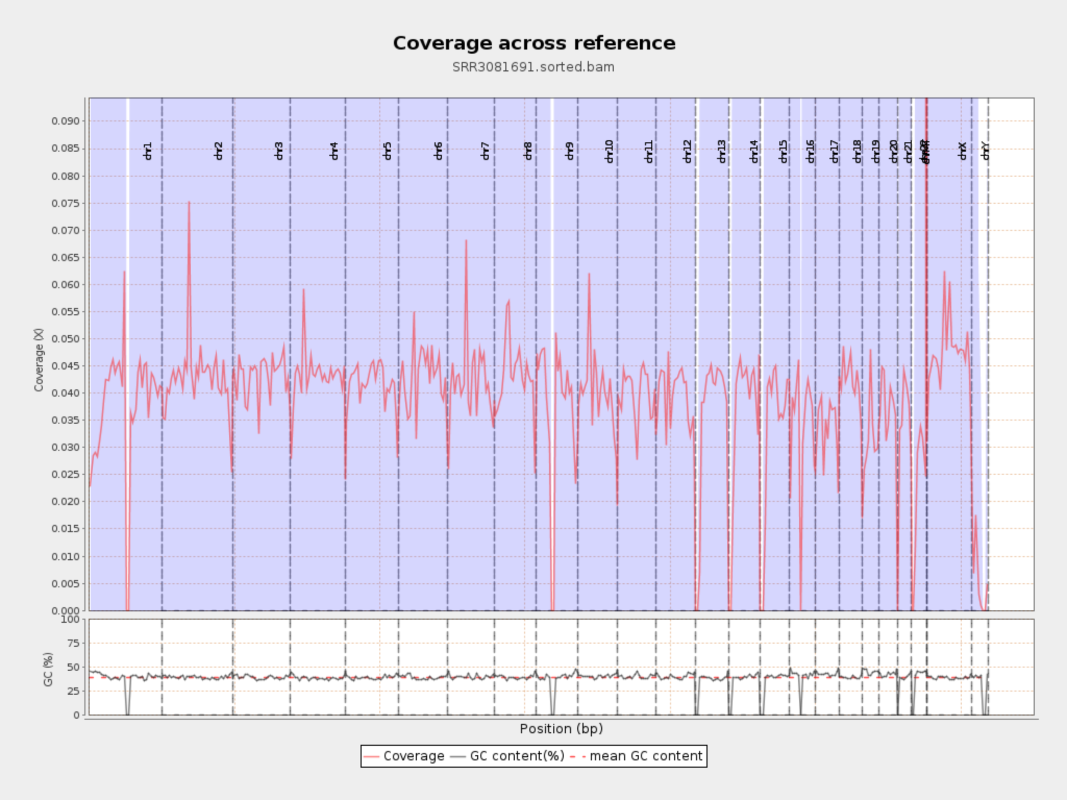
General error rate	0.9%
Mismatches	1,073,164
Insertions	10,612
Mapped reads with at least one insertion	0.58%
Deletions	27,523
Mapped reads with at least one deletion	1.51%
Homopolymer indels	49.22%

2.6. Chromosome stats

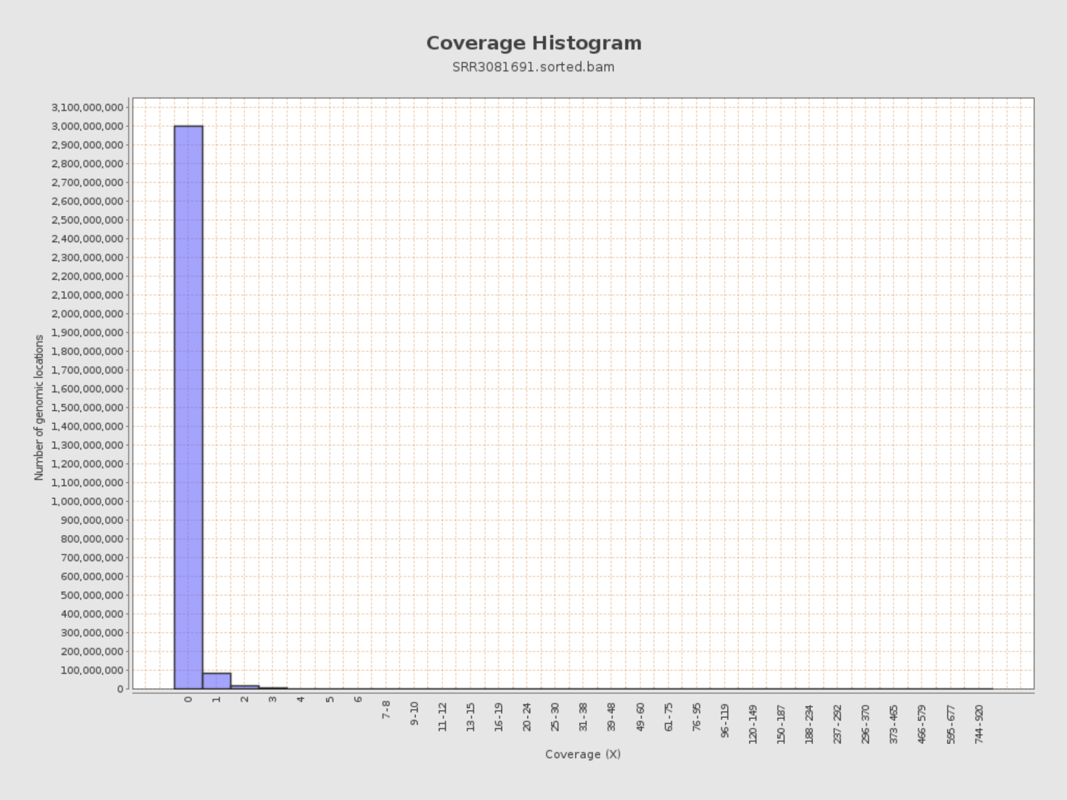
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9353568	0.0375	0.5146
chr2	243199373	10483296	0.0431	0.3974
chr3	198022430	8555158	0.0432	0.2455
chr4	191154276	8268139	0.0433	0.2645
chr5	180915260	7571598	0.0419	0.2423
chr6	171115067	7348045	0.0429	0.2904
chr7	159138663	6774241	0.0426	0.4831

chr8	146364022	6294942	0.043	0.6085
chr9	141213431	5184769	0.0367	0.346
chr10	135534747	5529774	0.0408	0.3376
chr11	135006516	5346733	0.0396	0.3067
chr12	133851895	5289566	0.0395	0.2389
chr13	115169878	3987846	0.0346	0.2191
chr14	107349540	3772548	0.0351	0.2342
chr15	102531392	3344798	0.0326	0.2132
chr16	90354753	3057995	0.0338	0.2333
chr17	81195210	2709772	0.0334	0.2417
chr18	78077248	3322185	0.0425	0.6161
chr19	59128983	1875404	0.0317	0.392
chr20	63025520	2354843	0.0374	0.2399
chr21	48129895	1608801	0.0334	0.2346
chr22	51304566	1083395	0.0211	0.169
chrMT	16571	17040	1.0283	1.2446
chrX	155270560	7361322	0.0474	0.283
chrY	59373566	324359	0.0055	0.1342

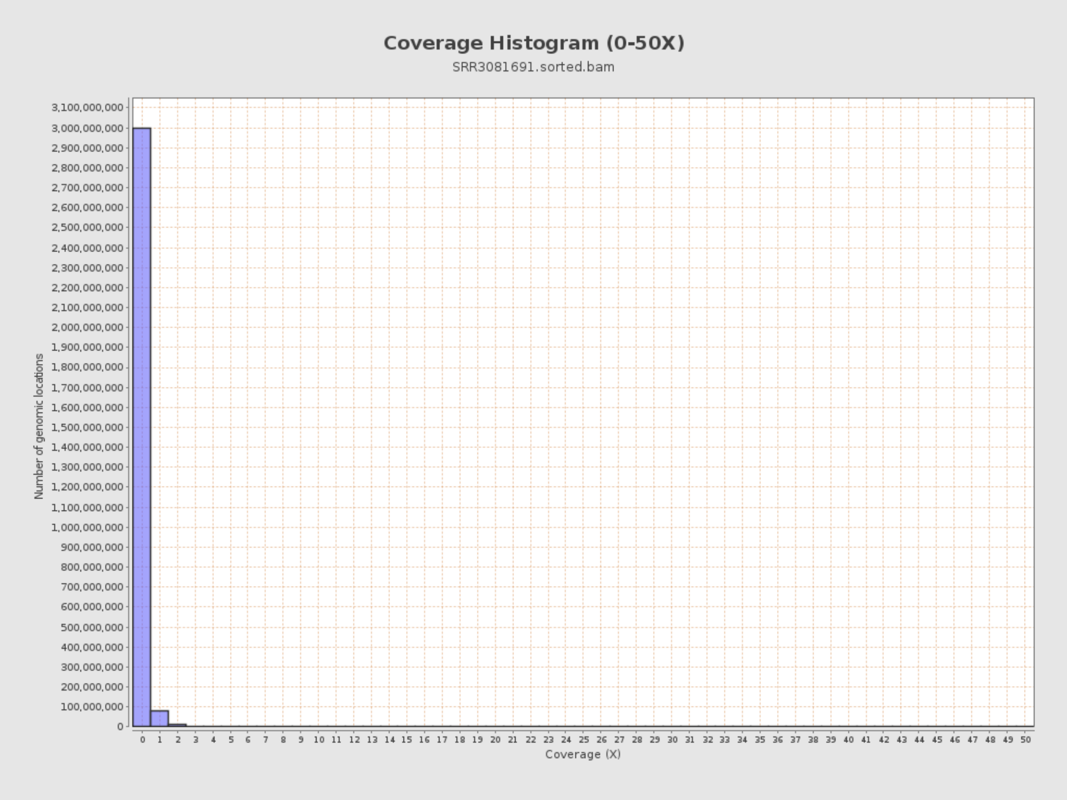
3. Results : Coverage across reference



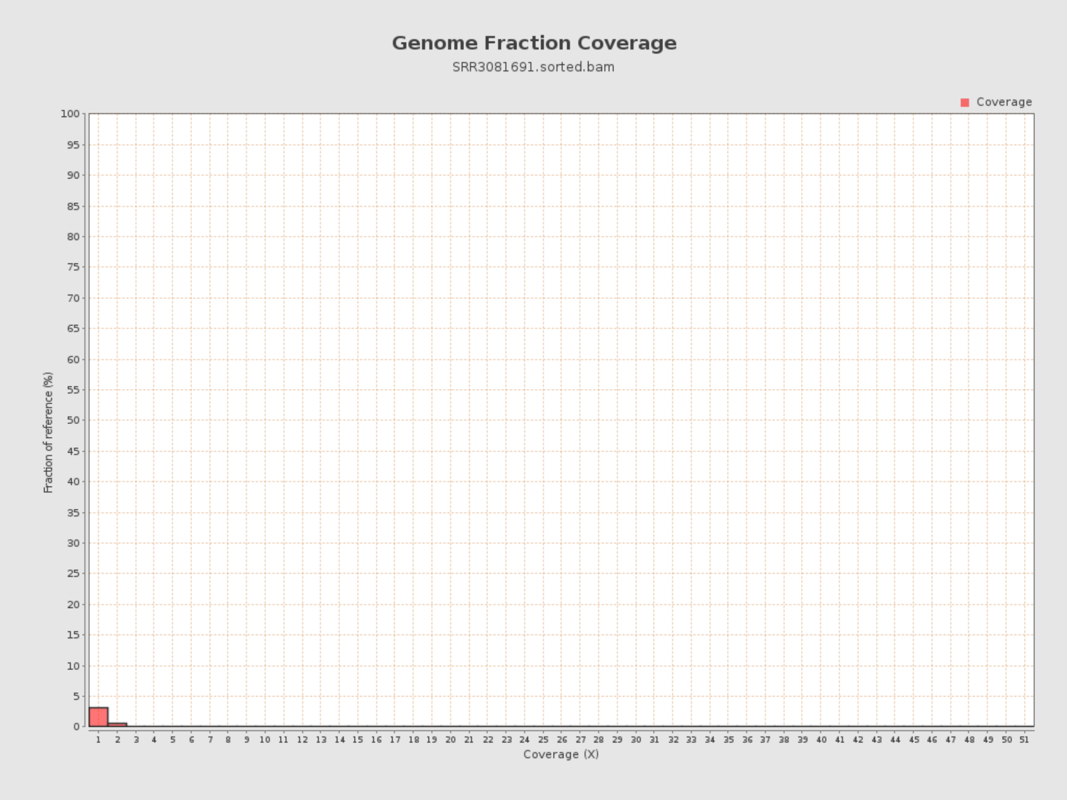
4. Results : Coverage Histogram



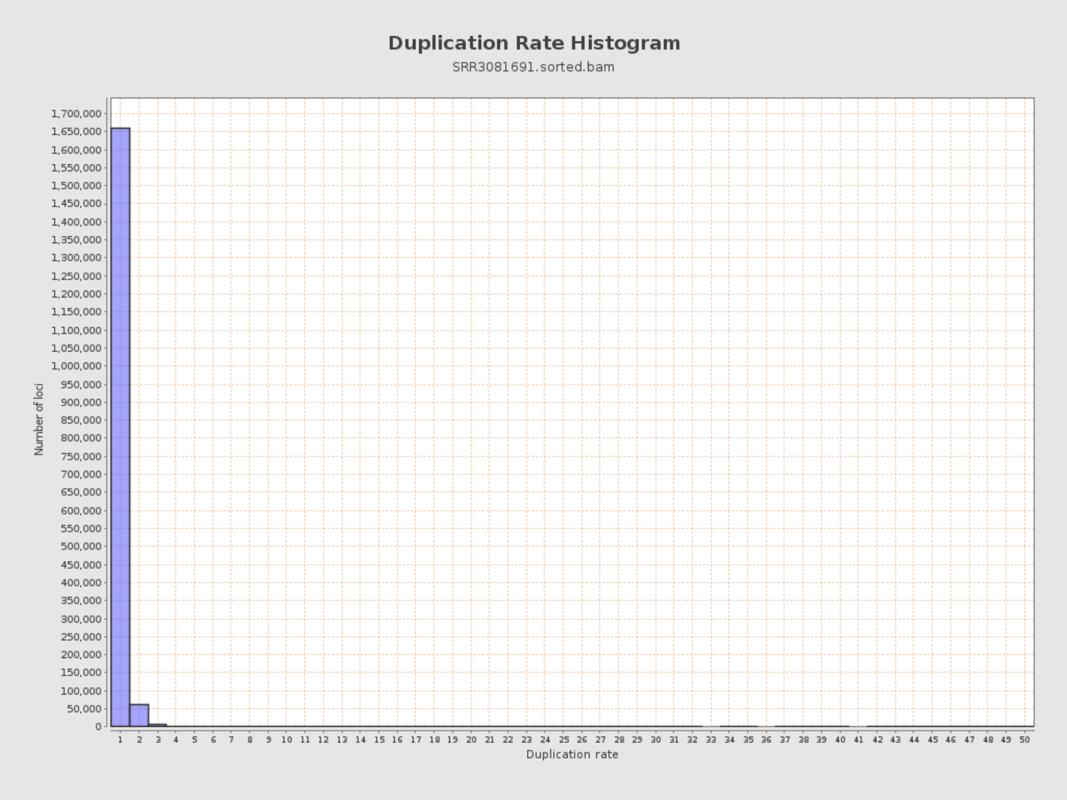
5. Results : Coverage Histogram (0-50X)



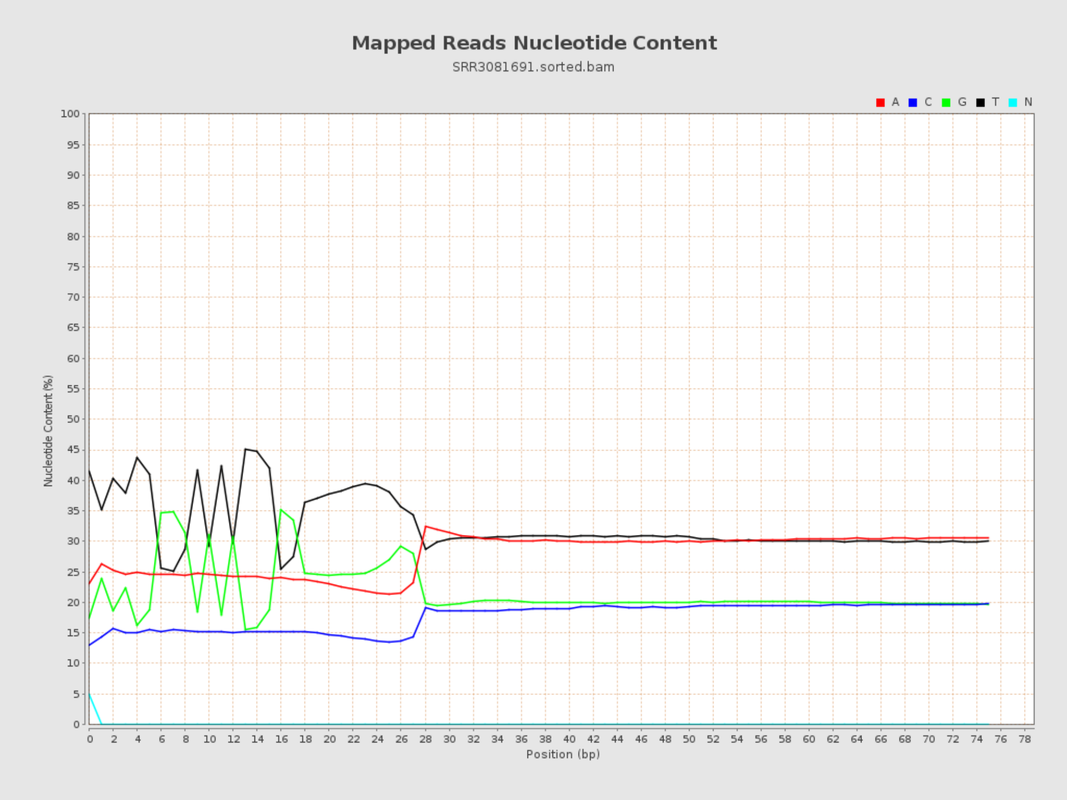
6. Results : Genome Fraction Coverage



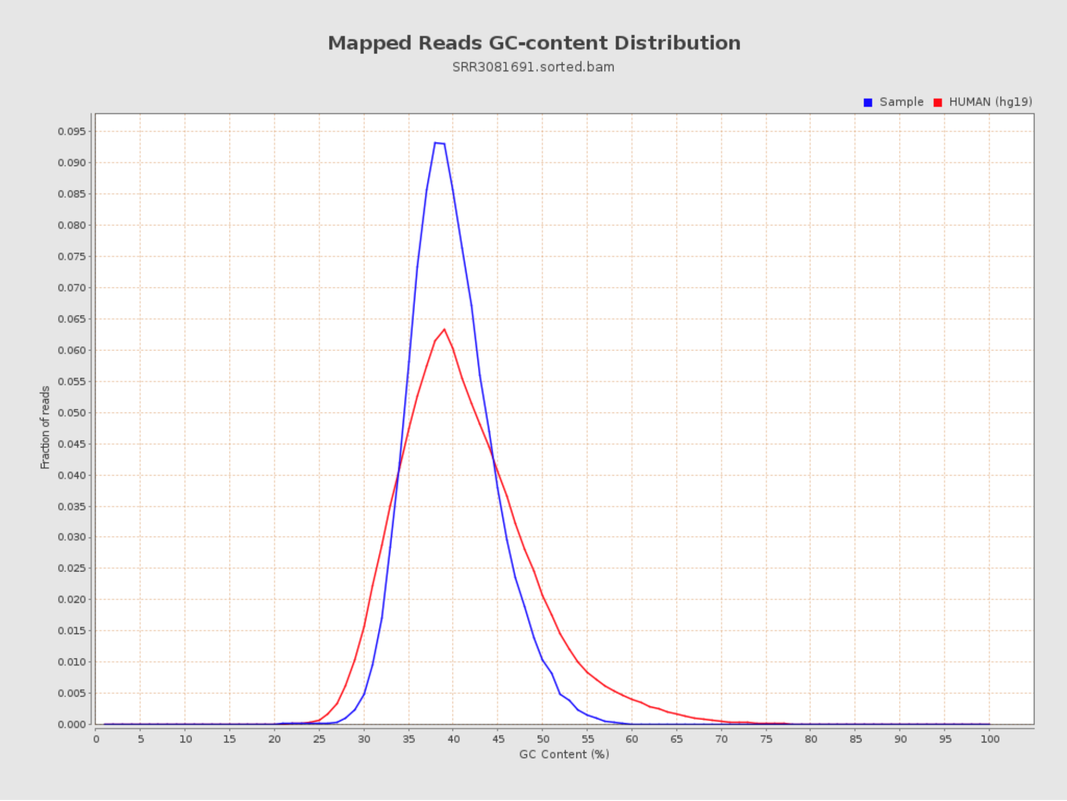
7. Results : Duplication Rate Histogram



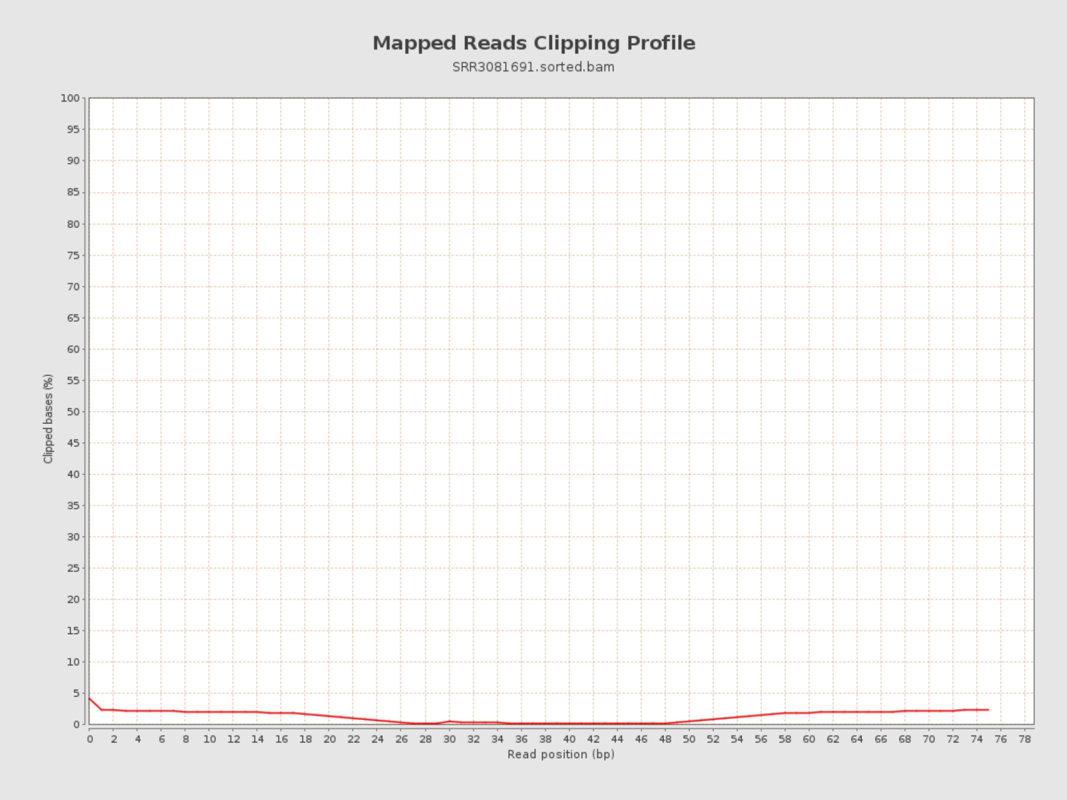
8. Results : Mapped Reads Nucleotide Content



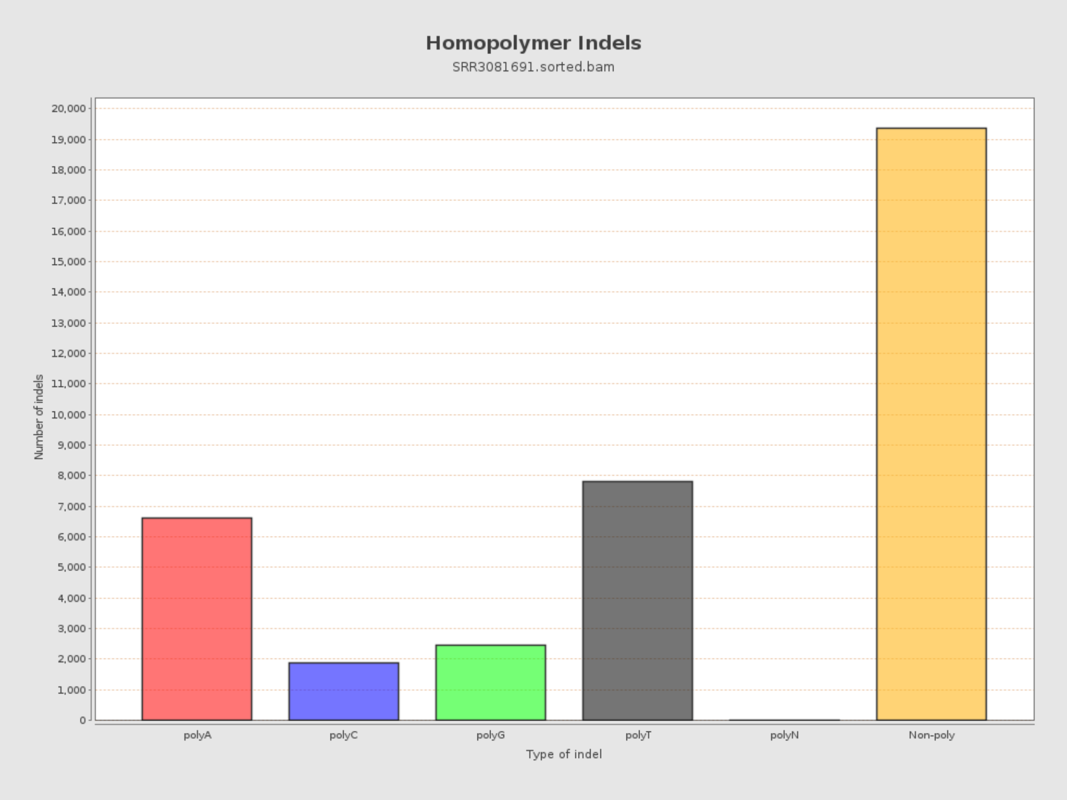
9. Results : Mapped Reads GC-content Distribution



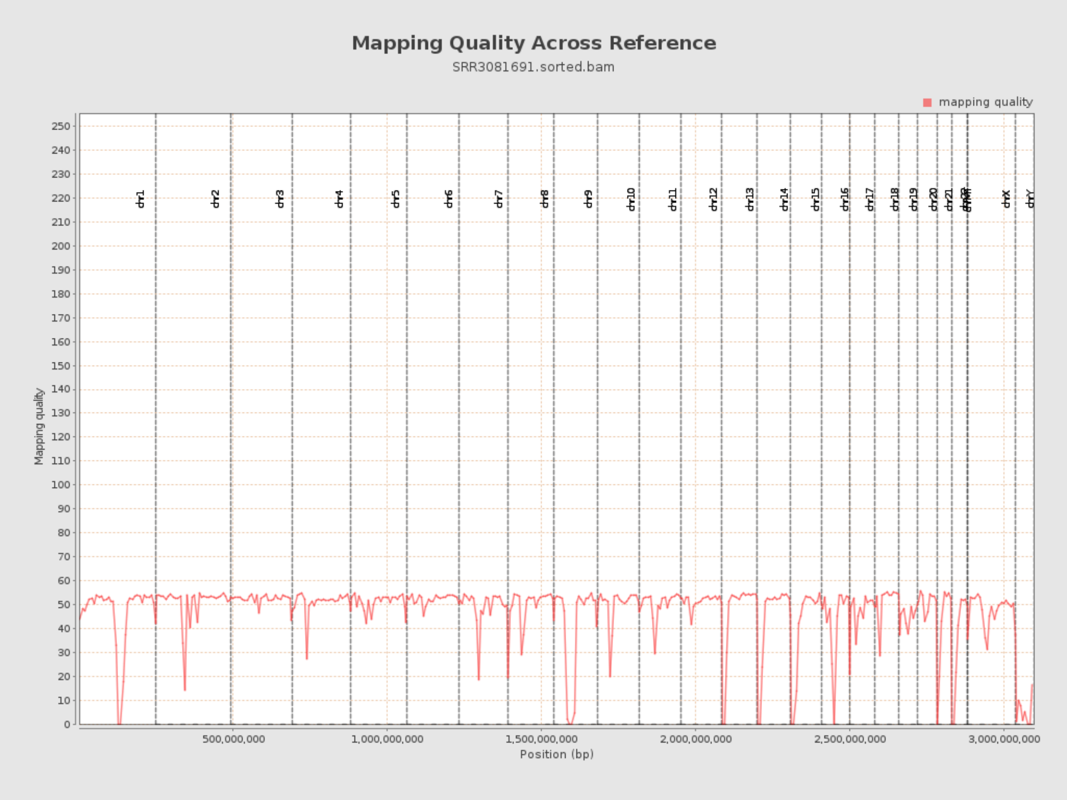
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram