Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 17:42:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081037.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_SRR3081037 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081037.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 17:42:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081037.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,762,117
Mapped reads	1,881,932 / 68.13%
Unmapped reads	880,185 / 31.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,203 / 0.33%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	59,557 / 2.16%
Duplication rate	2.51%
Clipped reads	1,017,497 / 36.84%

2.2. ACGT Content

Number/percentage of A's	33,489,963 / 28.1%
Number/percentage of C's	22,924,679 / 19.24%
Number/percentage of T's	35,931,513 / 30.15%
Number/percentage of G's	26,830,386 / 22.51%
Number/percentage of N's	1,496 / 0%
GC Percentage	41.75%

2.3. Coverage

Mean	0.0385

Standard Deviation	0.3031

2.4. Mapping Quality

Mean Mapping Quality	45.78

2.5. Mismatches and indels

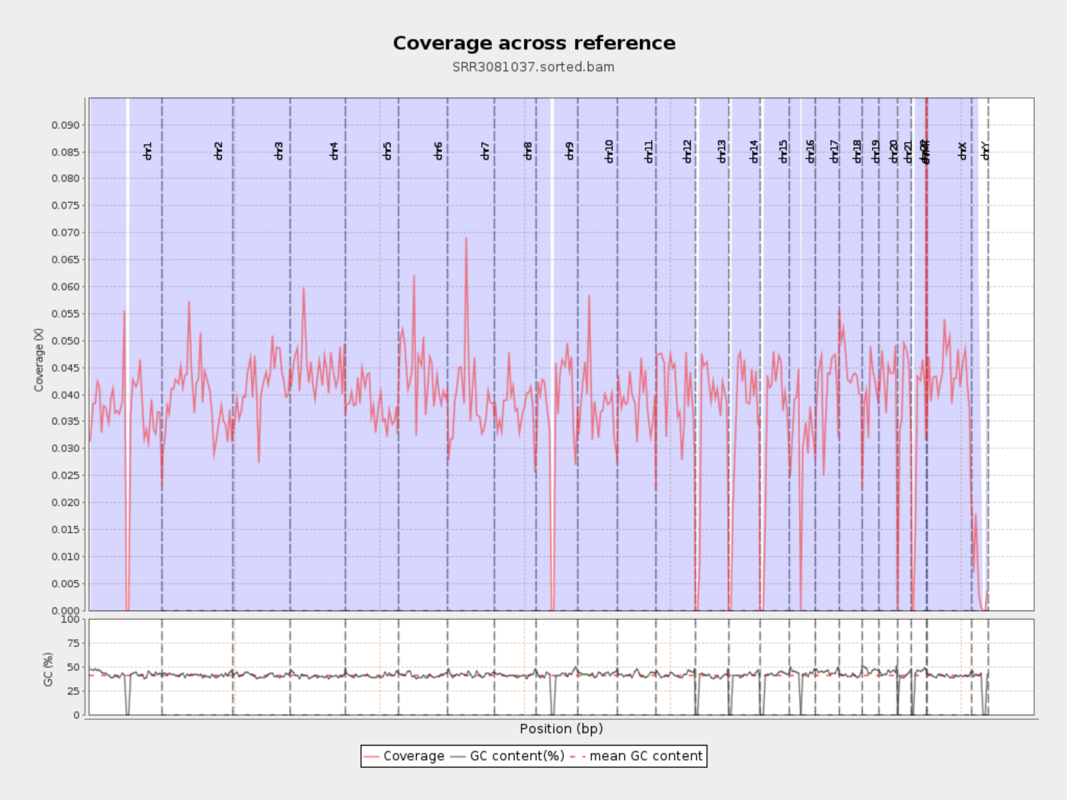
General error rate	0.79%
Mismatches	926,232
Insertions	7,894
Mapped reads with at least one insertion	0.42%
Deletions	24,017
Mapped reads with at least one deletion	1.26%
Homopolymer indels	46.9%

2.6. Chromosome stats

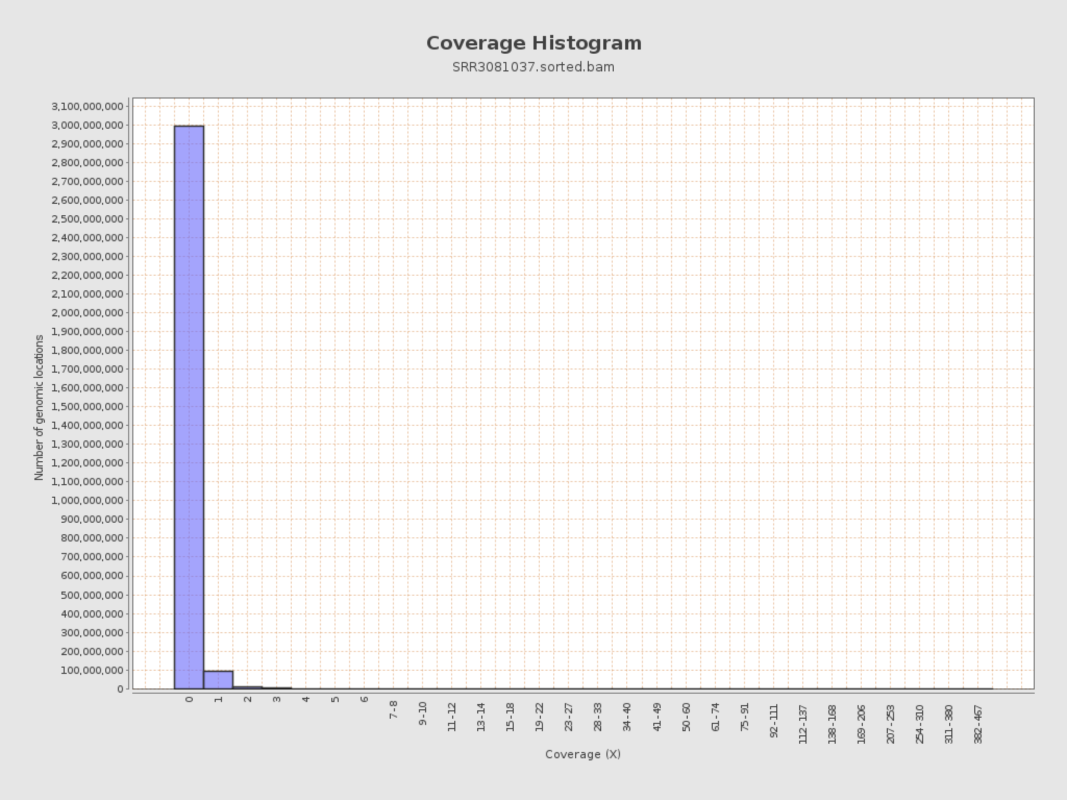
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8891369	0.0357	0.4624
chr2	243199373	9597918	0.0395	0.312
chr3	198022430	8239676	0.0416	0.2258
chr4	191154276	8594999	0.045	0.2509
chr5	180915260	6921807	0.0383	0.2172
chr6	171115067	7535125	0.044	0.309
chr7	159138663	6350310	0.0399	0.4612

chr8	146364022	5515200	0.0377	0.3046
chr9	141213431	5165030	0.0366	0.2854
chr10	135534747	5212697	0.0385	0.2809
chr11	135006516	5245875	0.0389	0.2801
chr12	133851895	5500038	0.0411	0.2266
chr13	115169878	3985427	0.0346	0.2055
chr14	107349540	3742332	0.0349	0.221
chr15	102531392	3499073	0.0341	0.2123
chr16	90354753	2858115	0.0316	0.2202
chr17	81195210	3309252	0.0408	0.2509
chr18	78077248	3537898	0.0453	0.5401
chr19	59128983	2373349	0.0401	0.347
chr20	63025520	2733935	0.0434	0.2372
chr21	48129895	1790902	0.0372	0.2297
chr22	51304566	1523307	0.0297	0.1908
chrMT	16571	28734	1.734	1.5908
chrX	155270560	6739886	0.0434	0.2543
chrY	59373566	327702	0.0055	0.1297

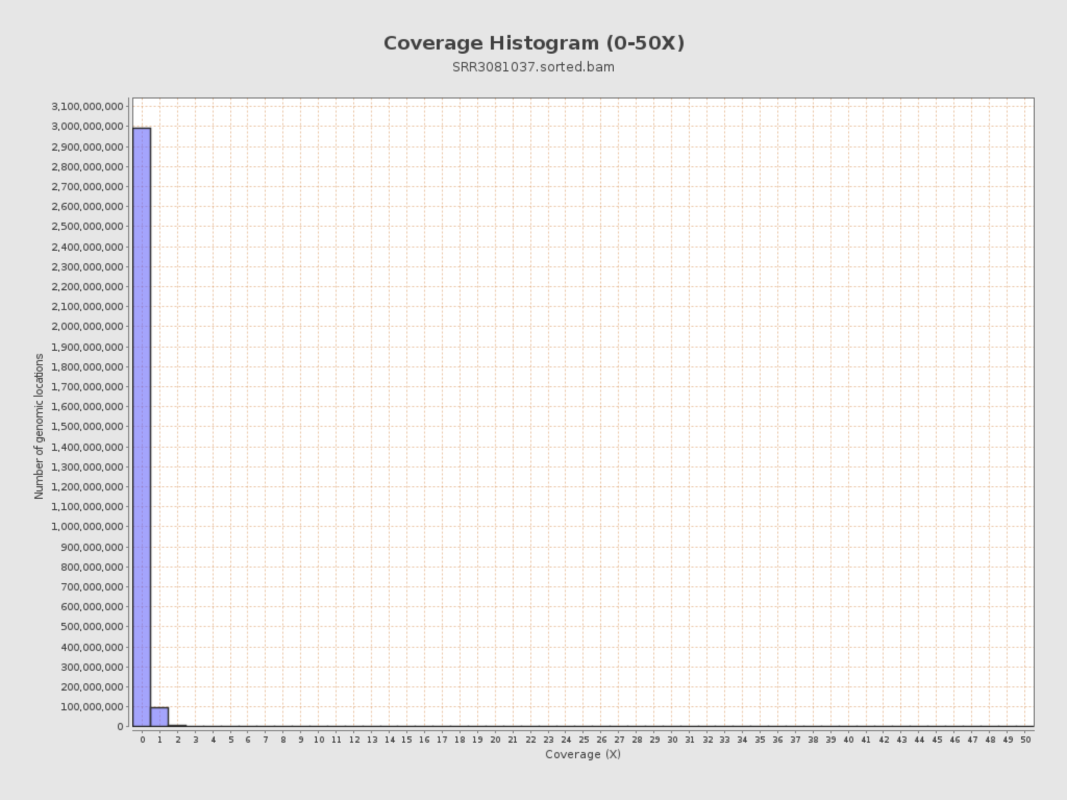
3. Results : Coverage across reference



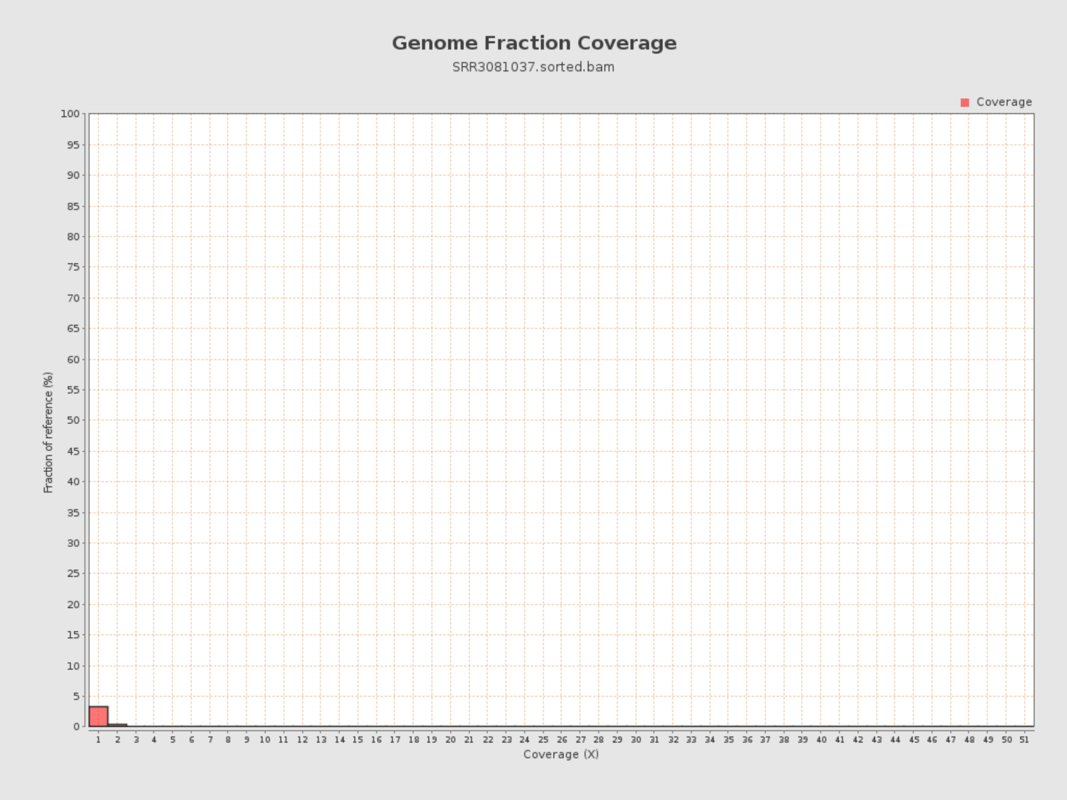
4. Results : Coverage Histogram



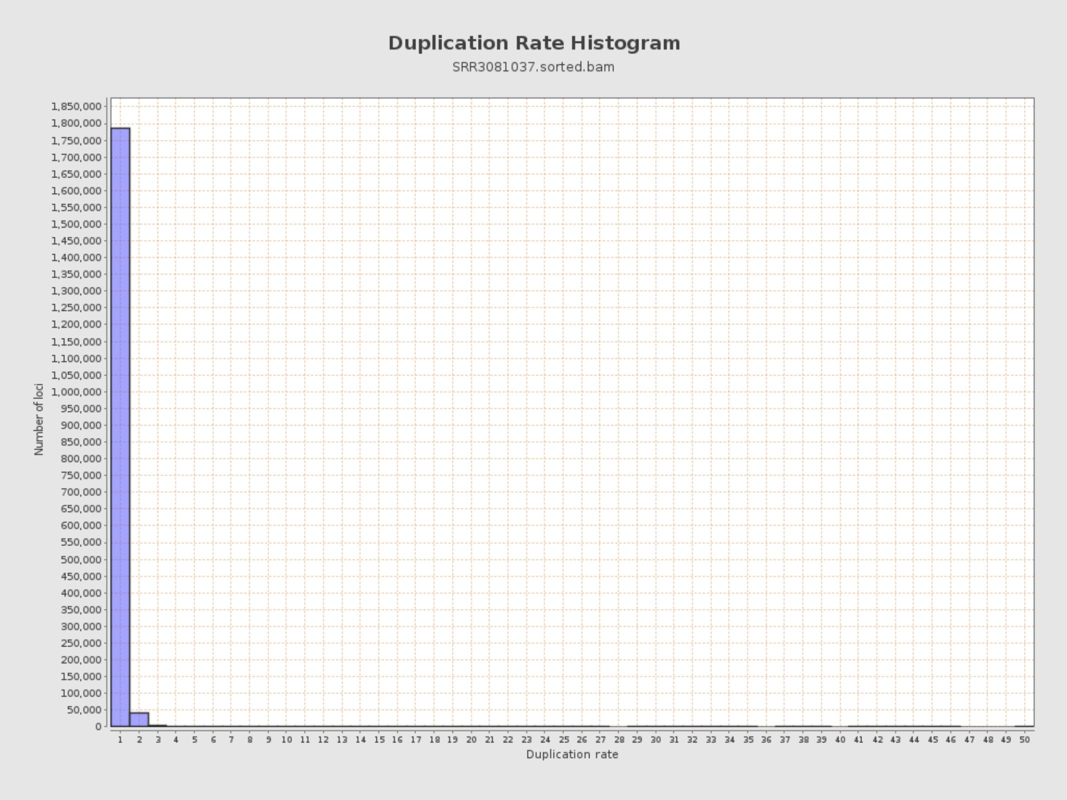
5. Results : Coverage Histogram (0-50X)



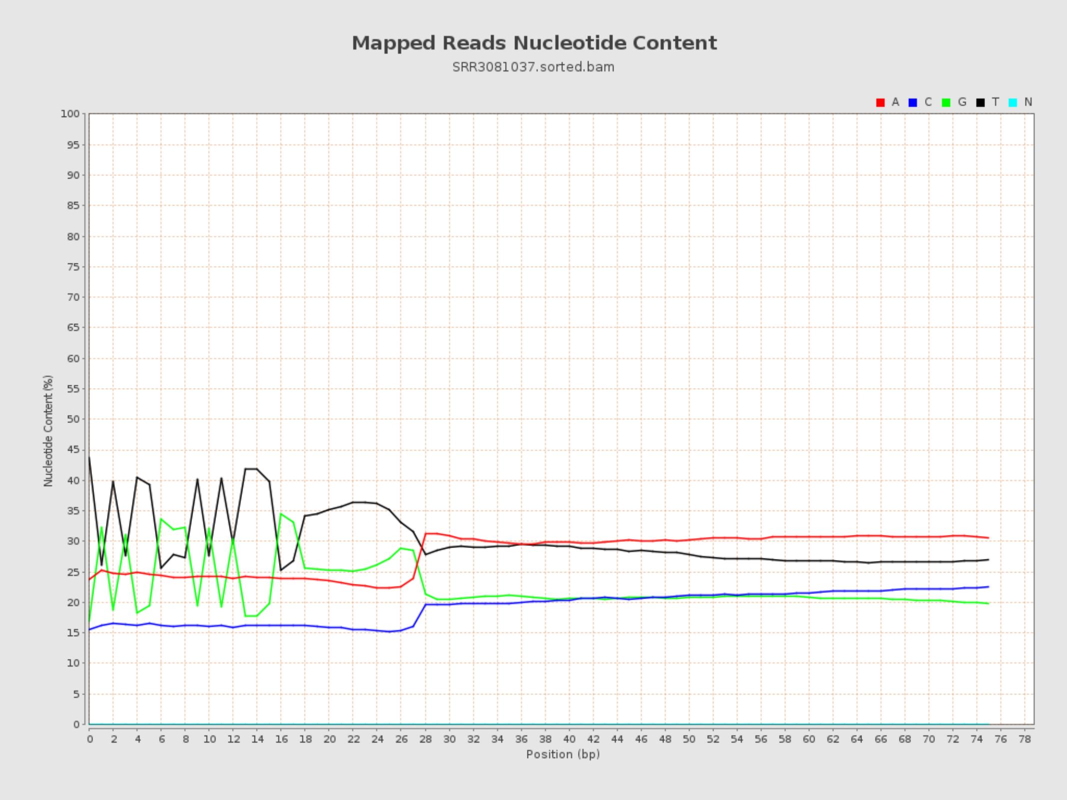
6. Results : Genome Fraction Coverage



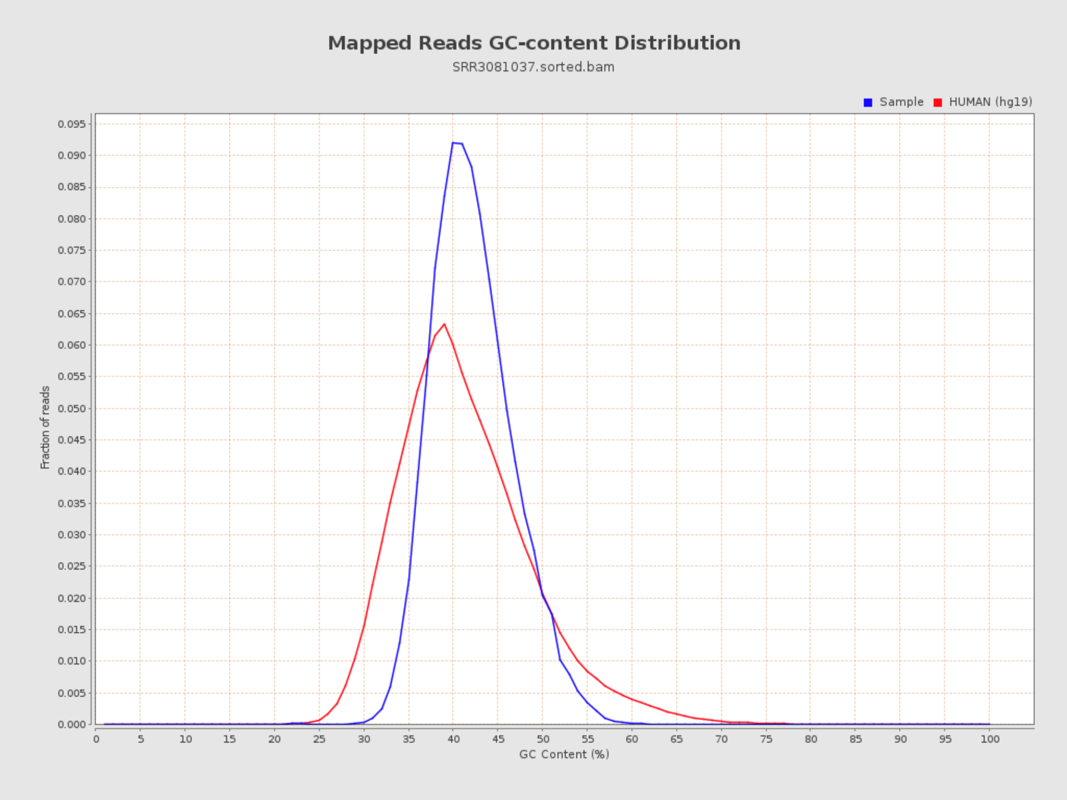
7. Results : Duplication Rate Histogram



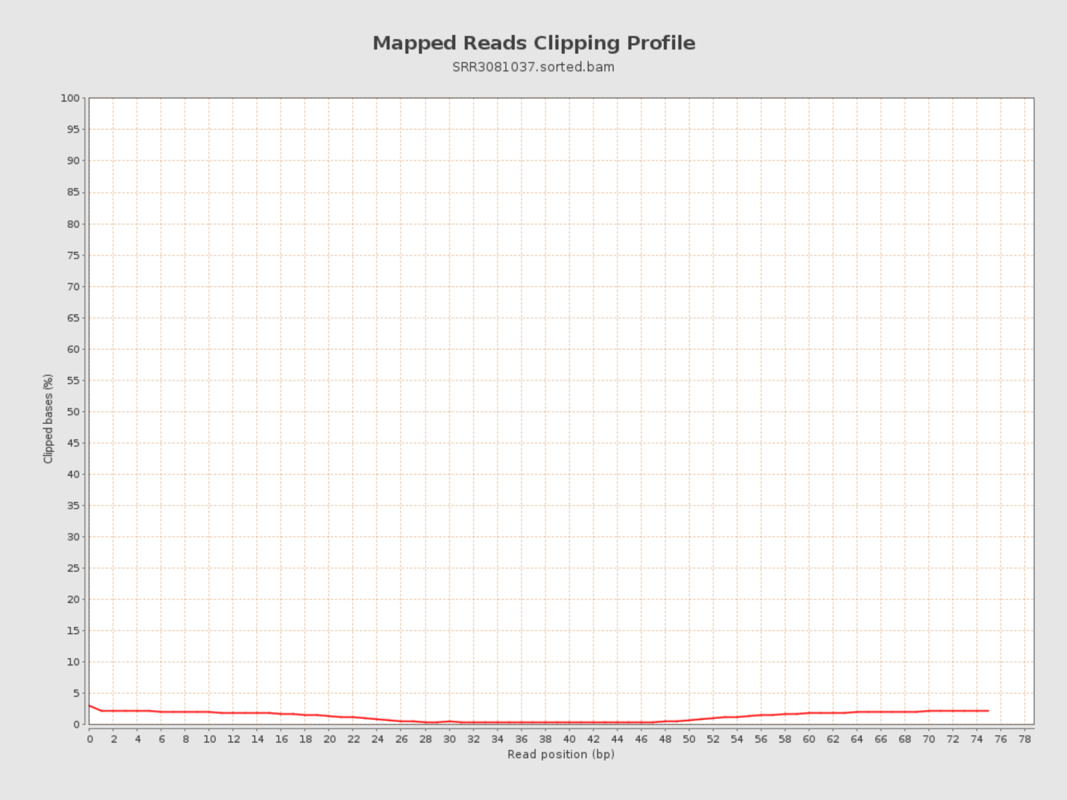
8. Results : Mapped Reads Nucleotide Content



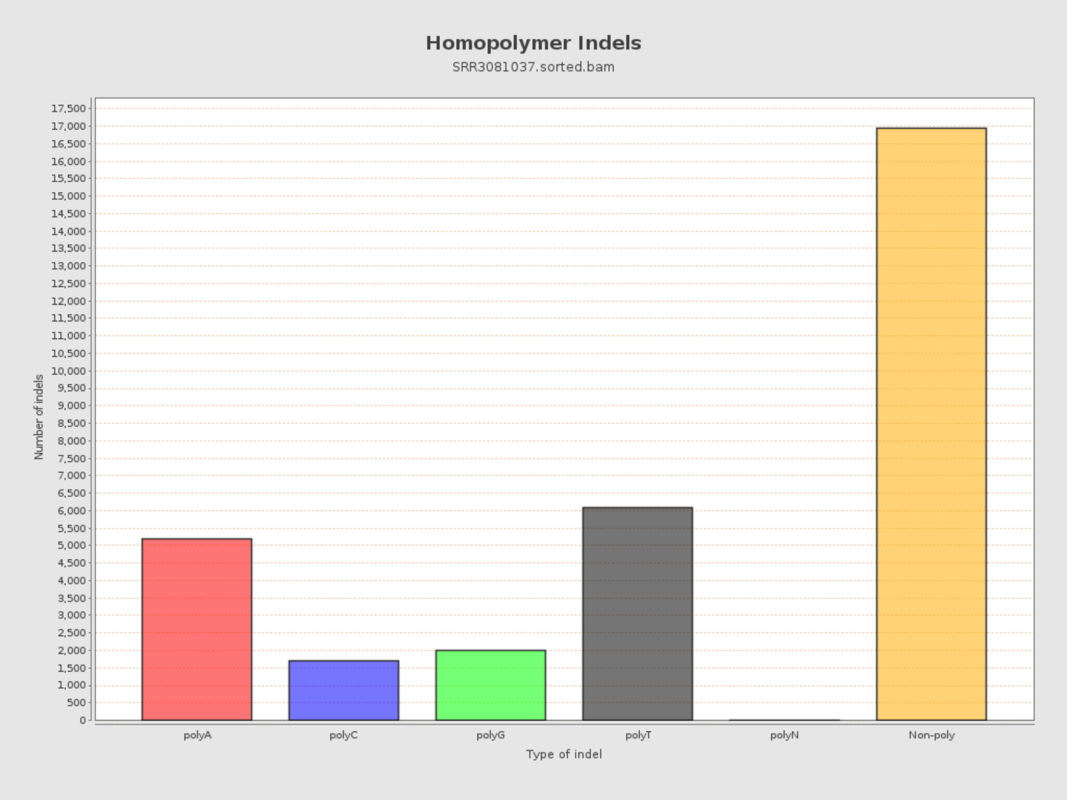
9. Results : Mapped Reads GC-content Distribution



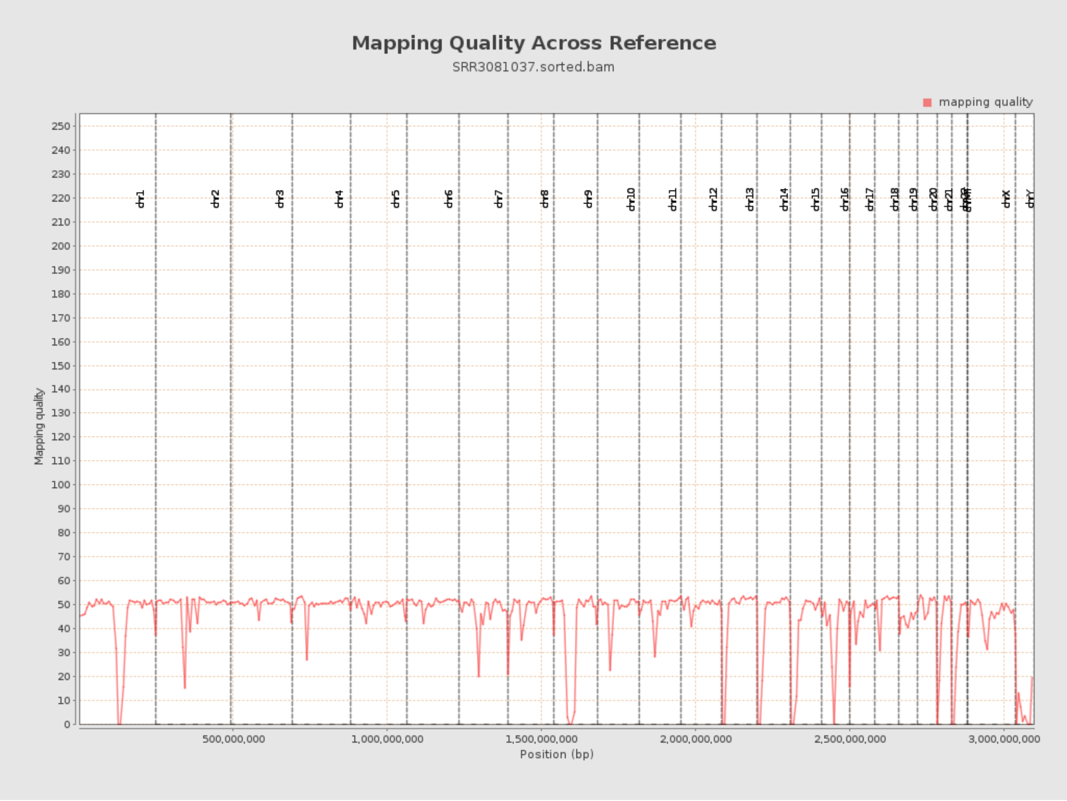
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram