Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 09:50:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081917.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_SRR3081917 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081917.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 09:50:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081917.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,177,354
Mapped reads	2,009,009 / 92.27%
Unmapped reads	168,345 / 7.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,435 / 0.66%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	62,814 / 2.88%
Duplication rate	2.38%
Clipped reads	756,964 / 34.77%

2.2. ACGT Content

Number/percentage of A's	39,011,329 / 28.34%
Number/percentage of C's	25,831,916 / 18.77%
Number/percentage of T's	42,876,773 / 31.15%
Number/percentage of G's	29,927,106 / 21.74%
Number/percentage of N's	1,564 / 0%
GC Percentage	40.51%

2.3. Coverage

Mean	0.0445

Standard Deviation	0.3474

2.4. Mapping Quality

Mean Mapping Quality	46.25

2.5. Mismatches and indels

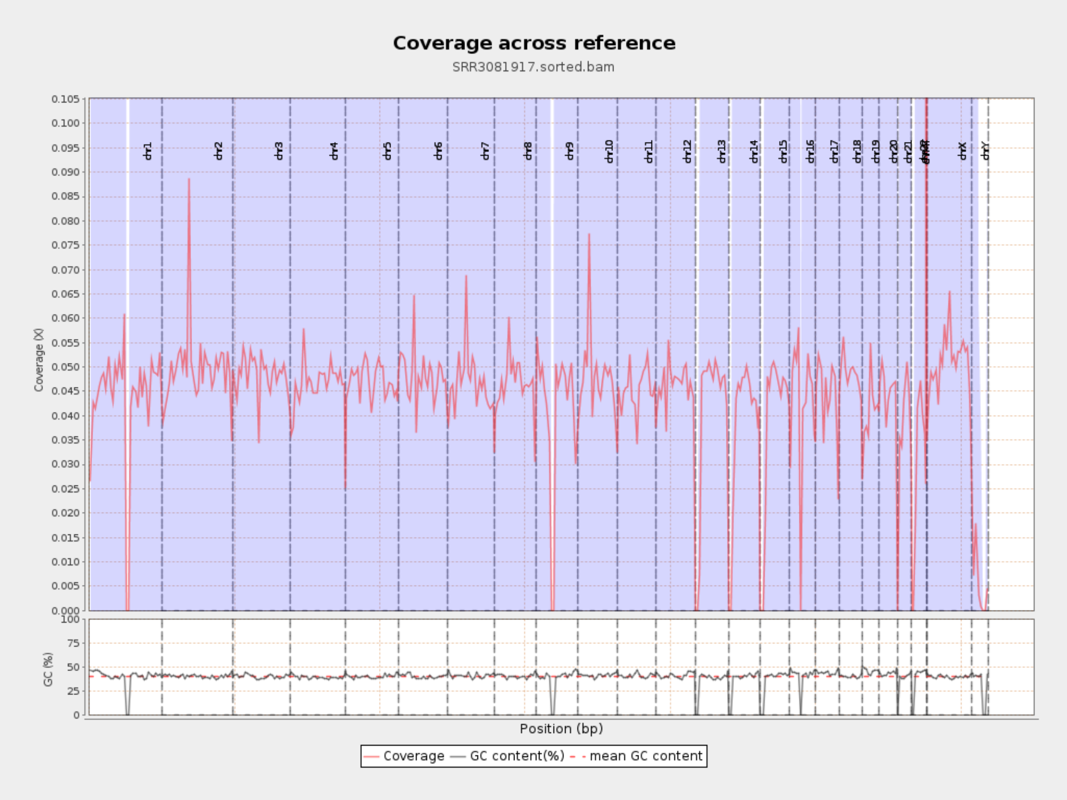
General error rate	0.86%
Mismatches	1,167,818
Insertions	11,224
Mapped reads with at least one insertion	0.55%
Deletions	32,421
Mapped reads with at least one deletion	1.6%
Homopolymer indels	47.71%

2.6. Chromosome stats

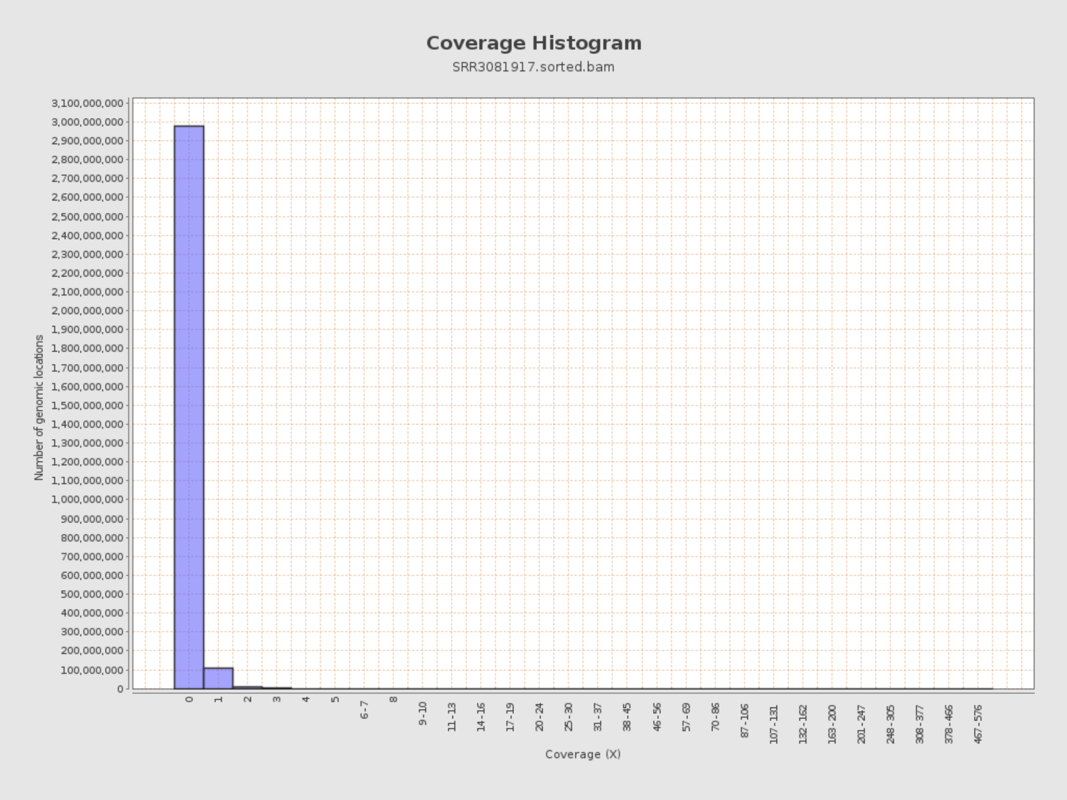
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10861753	0.0436	0.5133
chr2	243199373	12140088	0.0499	0.4506
chr3	198022430	9607270	0.0485	0.2454
chr4	191154276	8926409	0.0467	0.2544
chr5	180915260	8515253	0.0471	0.2407
chr6	171115067	8261294	0.0483	0.2846
chr7	159138663	7502854	0.0471	0.4547

chr8	146364022	6807702	0.0465	0.4516
chr9	141213431	5737163	0.0406	0.3364
chr10	135534747	6524984	0.0481	0.3789
chr11	135006516	6108718	0.0452	0.314
chr12	133851895	6176762	0.0461	0.2406
chr13	115169878	4599241	0.0399	0.2215
chr14	107349540	4029119	0.0375	0.229
chr15	102531392	3948270	0.0385	0.2226
chr16	90354753	3873530	0.0429	0.2584
chr17	81195210	3539313	0.0436	0.253
chr18	78077248	3821856	0.0489	0.6294
chr19	59128983	2431569	0.0411	0.4433
chr20	63025520	2820942	0.0448	0.24
chr21	48129895	1766839	0.0367	0.2268
chr22	51304566	1464826	0.0286	0.1866
chrMT	16571	10992	0.6633	0.8839
chrX	155270560	7879413	0.0507	0.2708
chrY	59373566	345371	0.0058	0.1385

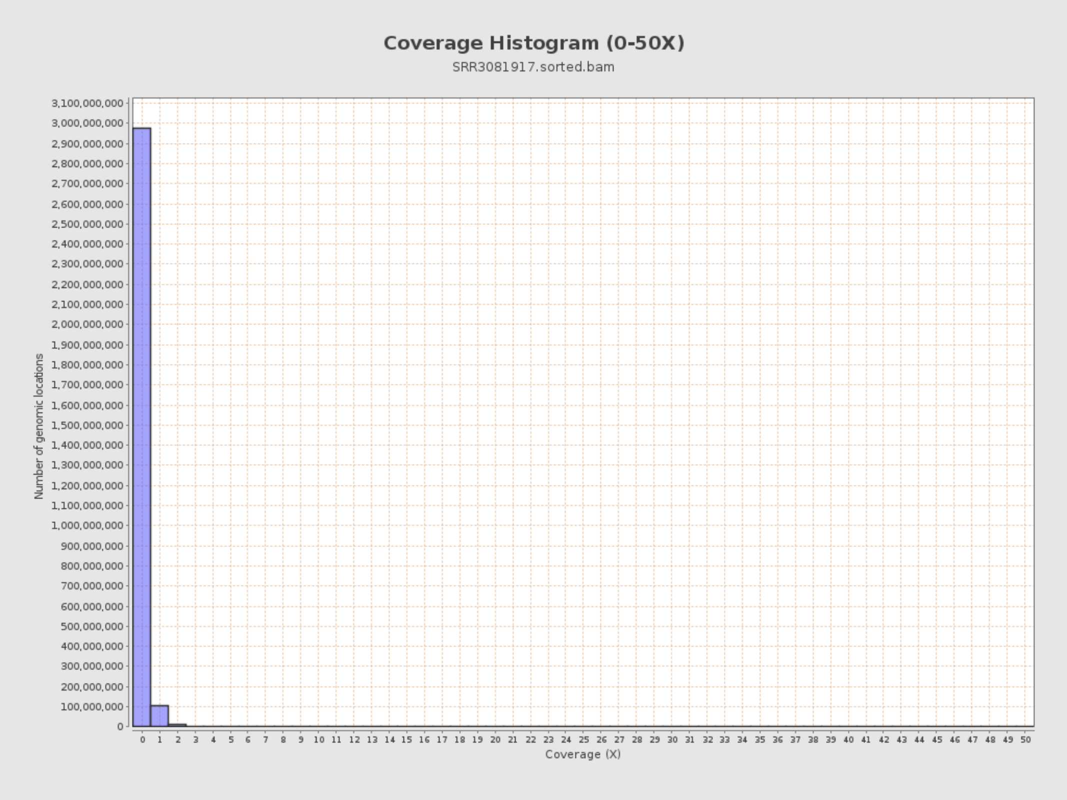
3. Results : Coverage across reference



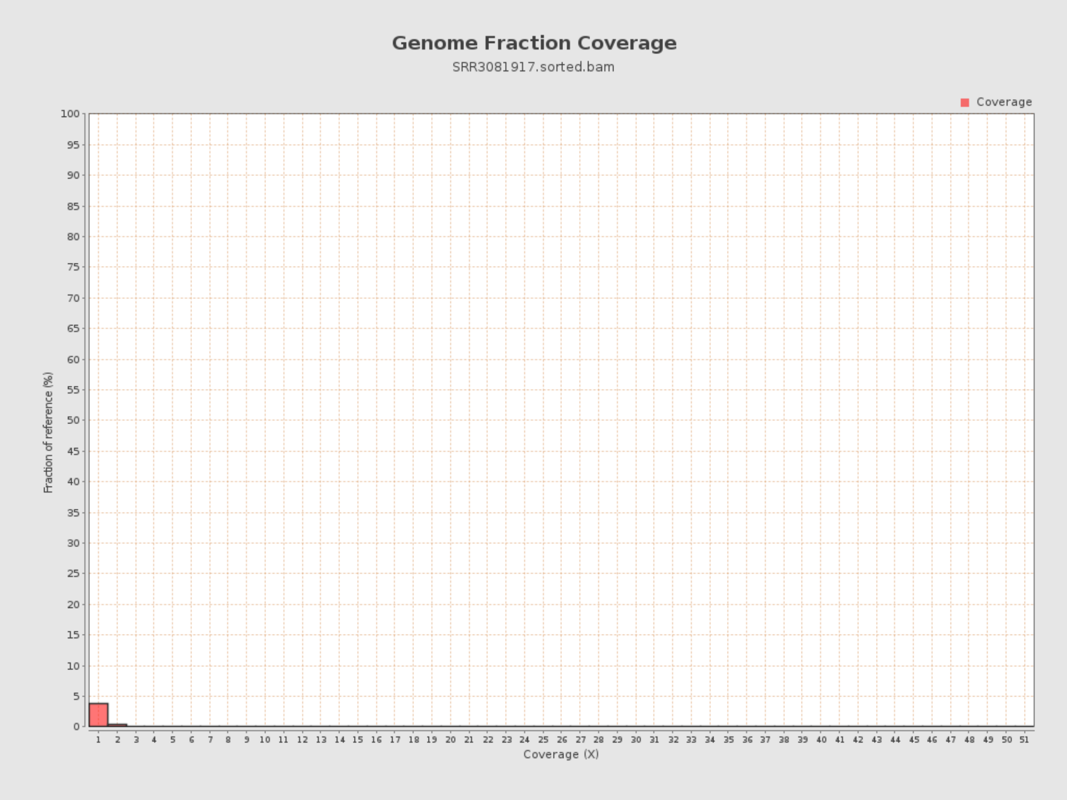
4. Results : Coverage Histogram



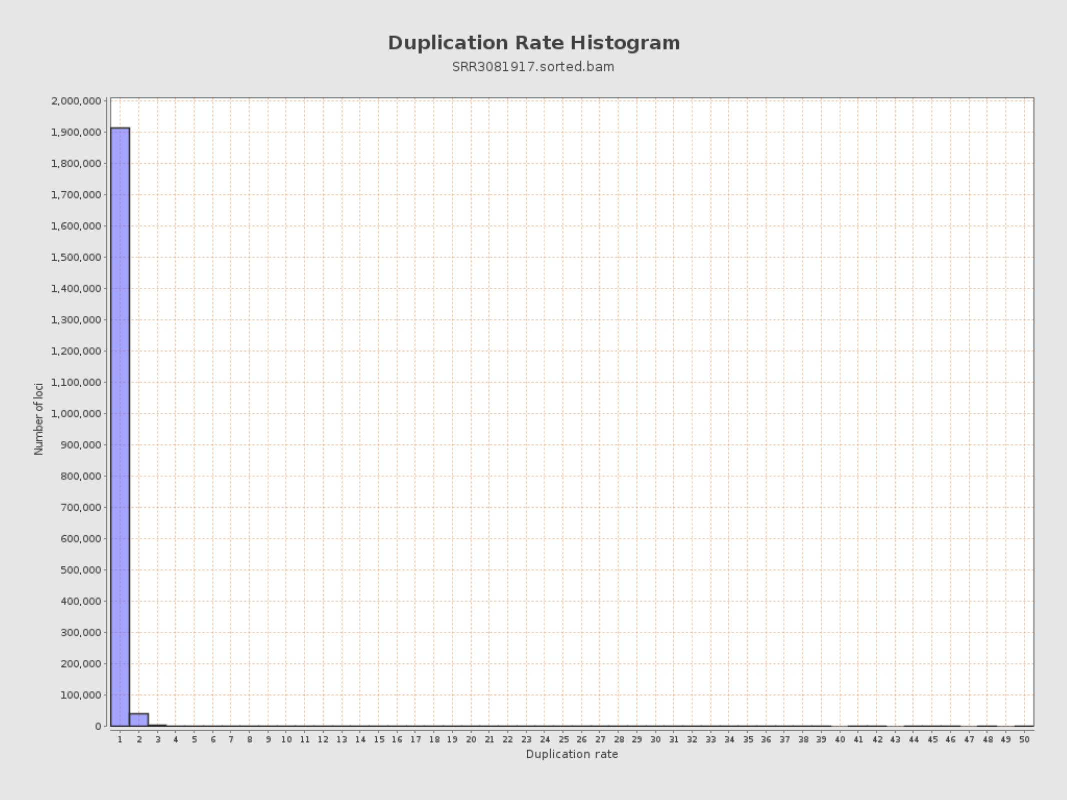
5. Results : Coverage Histogram (0-50X)



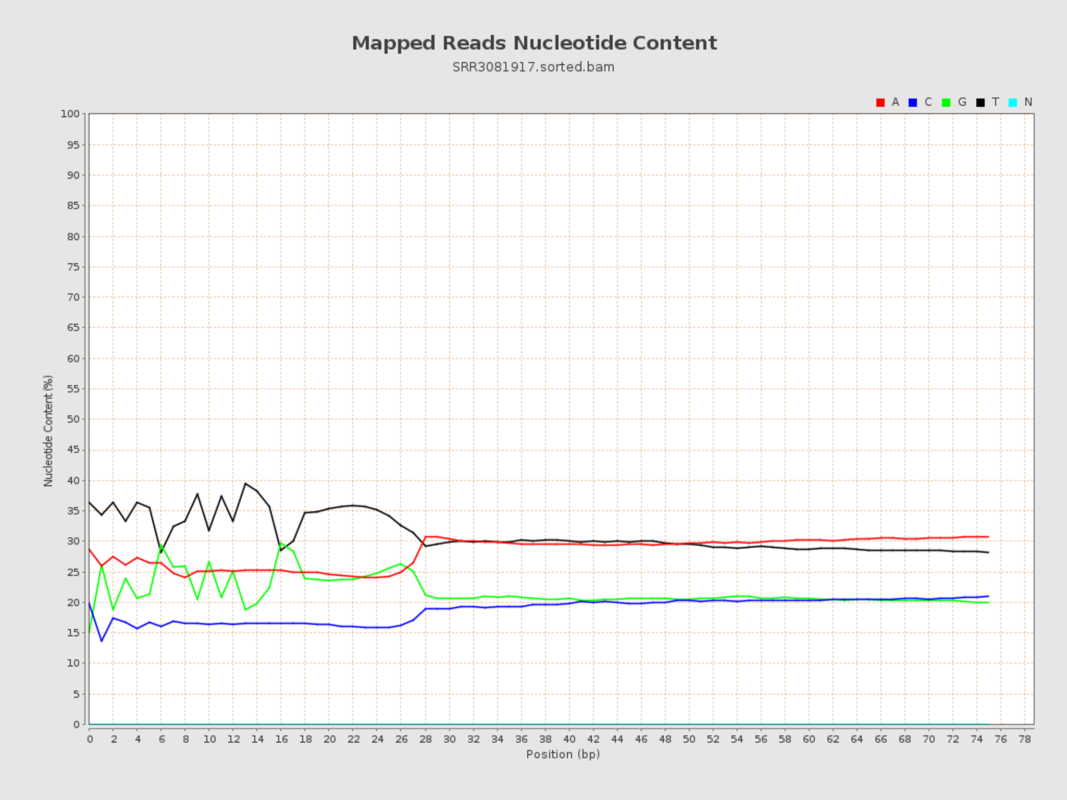
6. Results : Genome Fraction Coverage



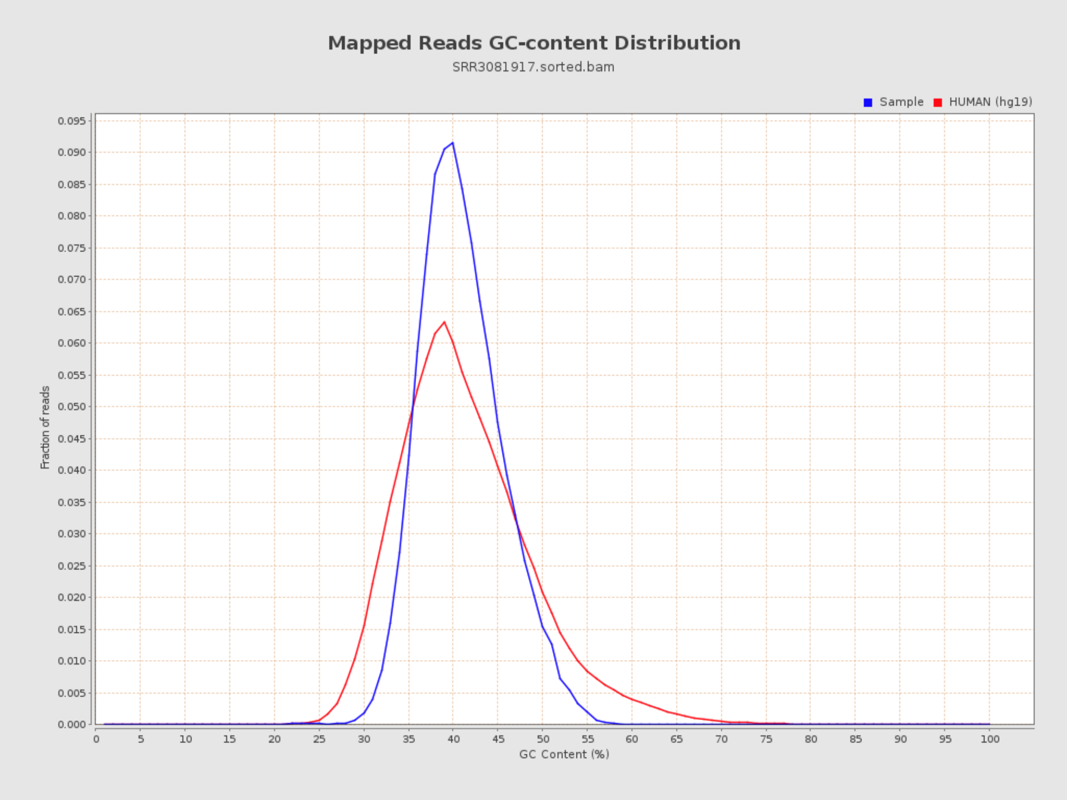
7. Results : Duplication Rate Histogram



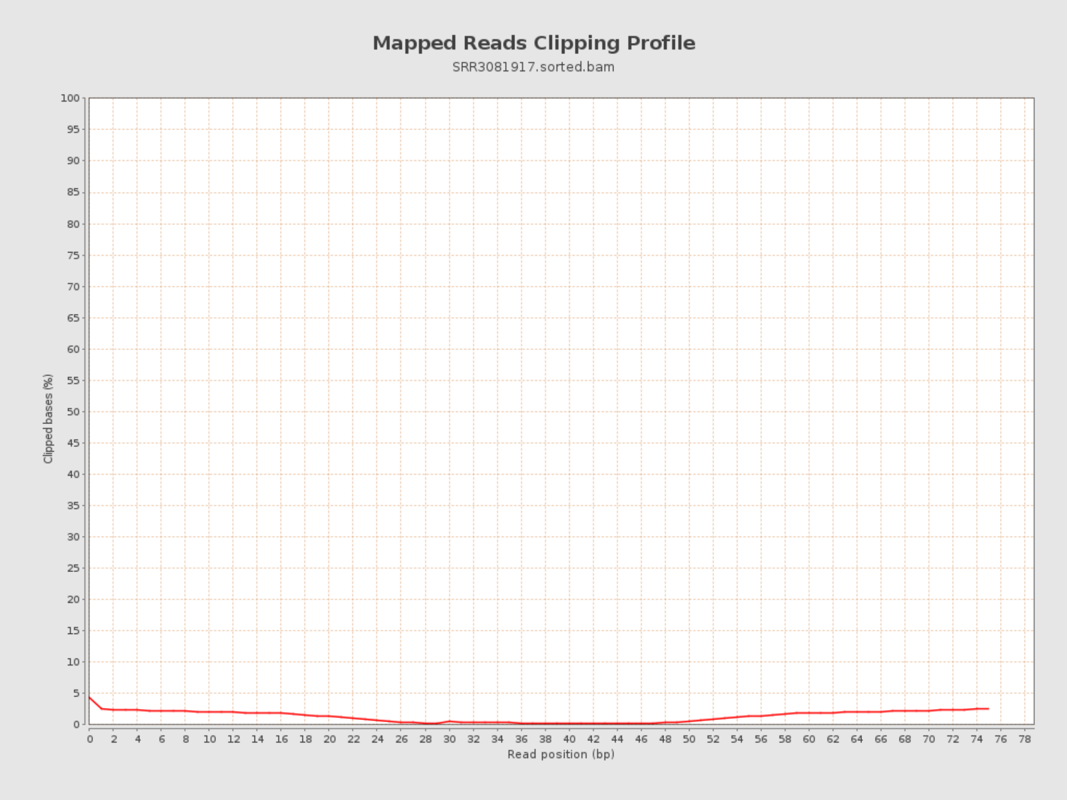
8. Results : Mapped Reads Nucleotide Content



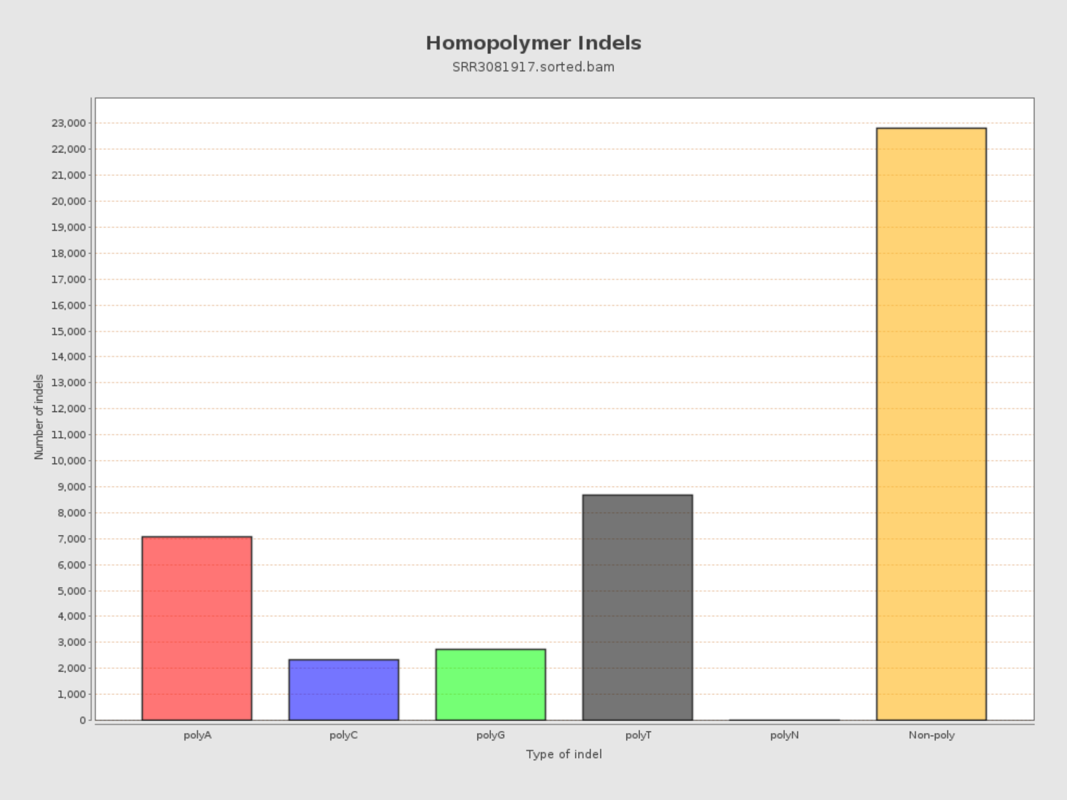
9. Results : Mapped Reads GC-content Distribution



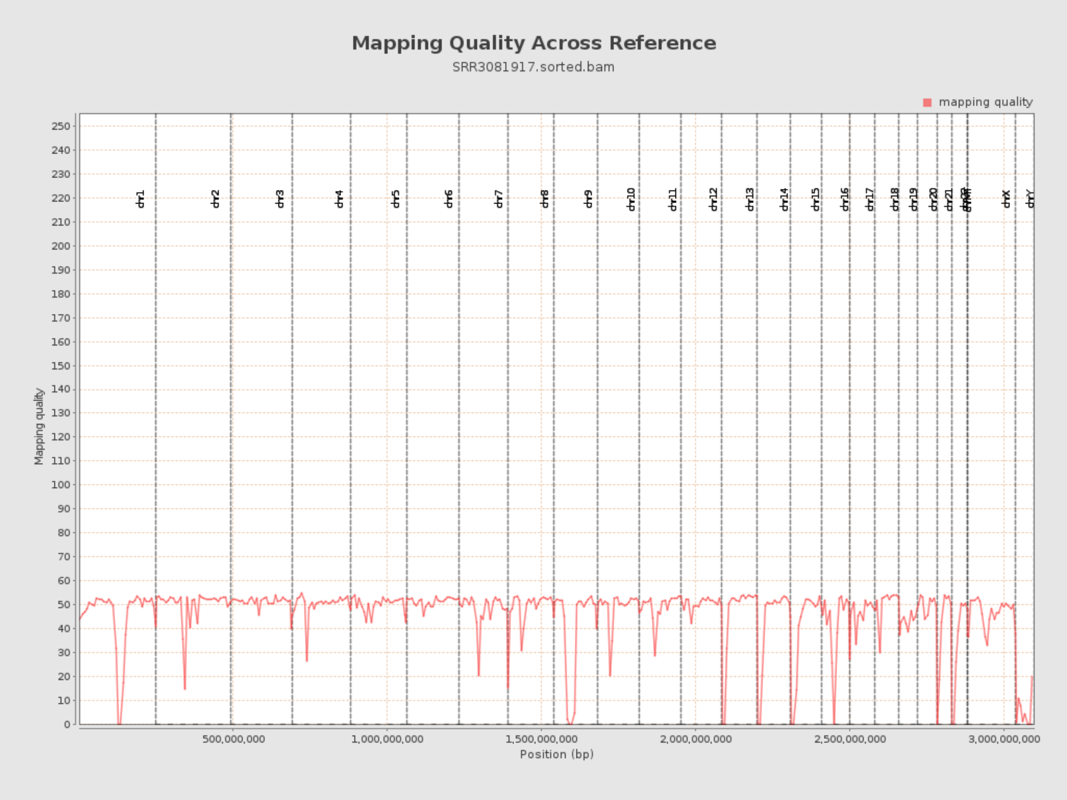
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram