Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 01:09:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717019.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_SRR9717019 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717019.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 01:09:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717019.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,141,702
Mapped reads	2,038,393 / 95.18%
Unmapped reads	103,309 / 4.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	40,224 / 1.88%
Read min/max/mean length	30 / 101 / 101.68
Duplicated reads (estimated)	121,079 / 5.65%
Duplication rate	4.59%
Clipped reads	2,074,823 / 96.88%

2.2. ACGT Content

Number/percentage of A's	39,472,202 / 24.6%
Number/percentage of C's	33,700,742 / 21%
Number/percentage of T's	47,384,644 / 29.53%
Number/percentage of G's	39,901,239 / 24.87%
Number/percentage of N's	6,176 / 0%
GC Percentage	45.87%

2.3. Coverage

Mean	0.0519

Standard Deviation	0.4345

2.4. Mapping Quality

Mean Mapping Quality	46.6

2.5. Mismatches and indels

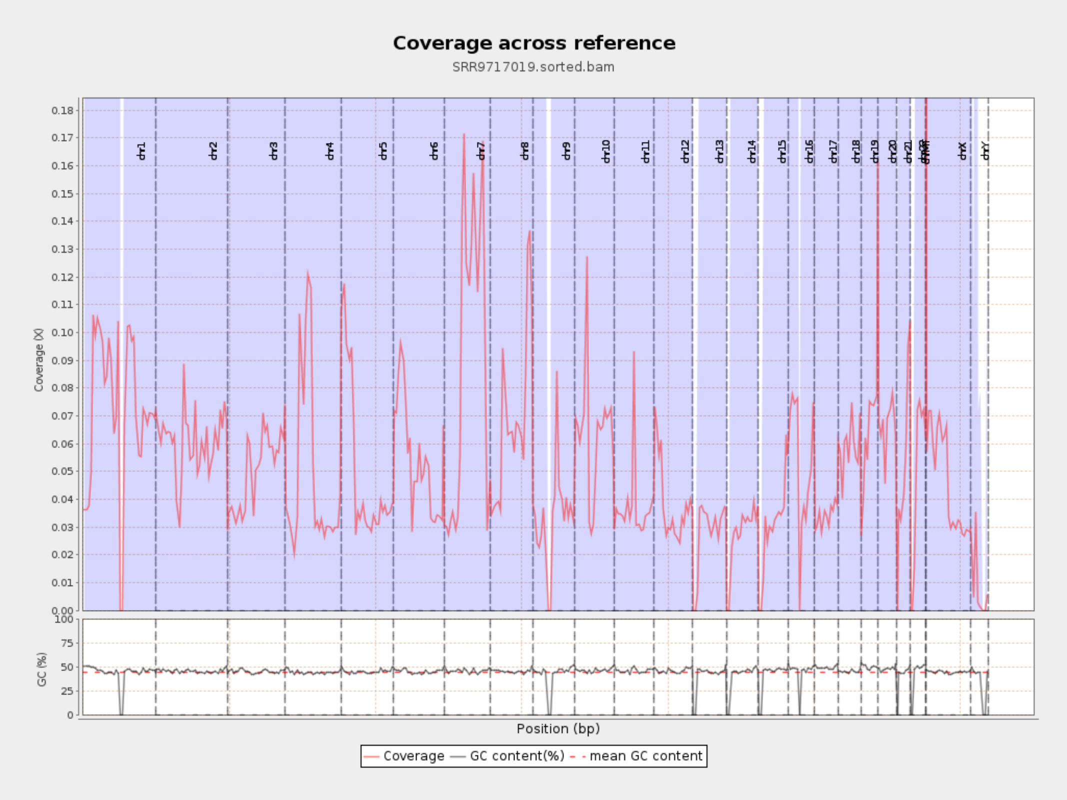
General error rate	0.66%
Mismatches	1,017,420
Insertions	13,957
Mapped reads with at least one insertion	0.67%
Deletions	30,126
Mapped reads with at least one deletion	1.45%
Homopolymer indels	38.54%

2.6. Chromosome stats

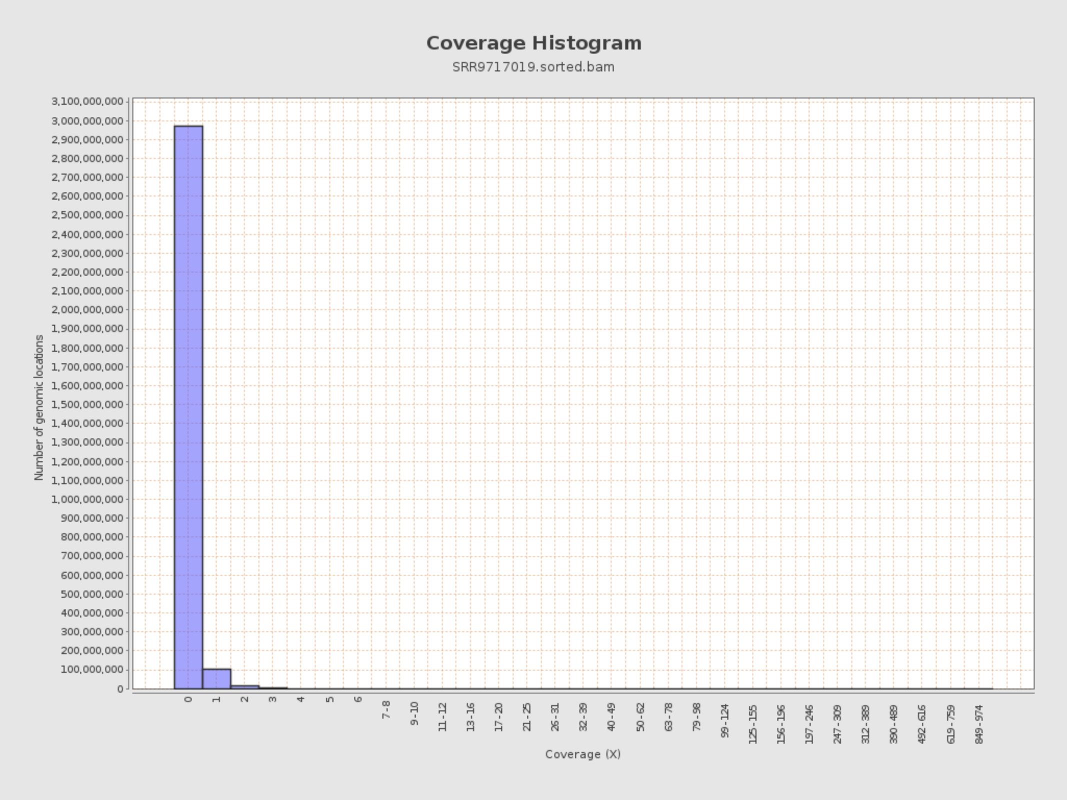
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18158471	0.0729	0.8682
chr2	243199373	14774908	0.0608	0.4249
chr3	198022430	9936965	0.0502	0.2745
chr4	191154276	9336225	0.0488	0.4029
chr5	180915260	9065454	0.0501	0.2747
chr6	171115067	9262888	0.0541	0.2991
chr7	159138663	14157679	0.089	0.6445

chr8	146364022	10139073	0.0693	0.4327
chr9	141213431	4668477	0.0331	0.2764
chr10	135534747	8595741	0.0634	0.6004
chr11	135006516	5057475	0.0375	0.3174
chr12	133851895	5234279	0.0391	0.2387
chr13	115169878	3199021	0.0278	0.1984
chr14	107349540	2899188	0.027	0.2177
chr15	102531392	2987482	0.0291	0.2057
chr16	90354753	4725131	0.0523	0.3014
chr17	81195210	2763488	0.034	0.2545
chr18	78077248	4569489	0.0585	0.4332
chr19	59128983	3949146	0.0668	0.6165
chr20	63025520	4197374	0.0666	0.3381
chr21	48129895	2565659	0.0533	0.3591
chr22	51304566	2488961	0.0485	0.2833
chrMT	16571	68195	4.1153	3.8788
chrX	155270560	7218348	0.0465	0.2839
chrY	59373566	508933	0.0086	0.3515

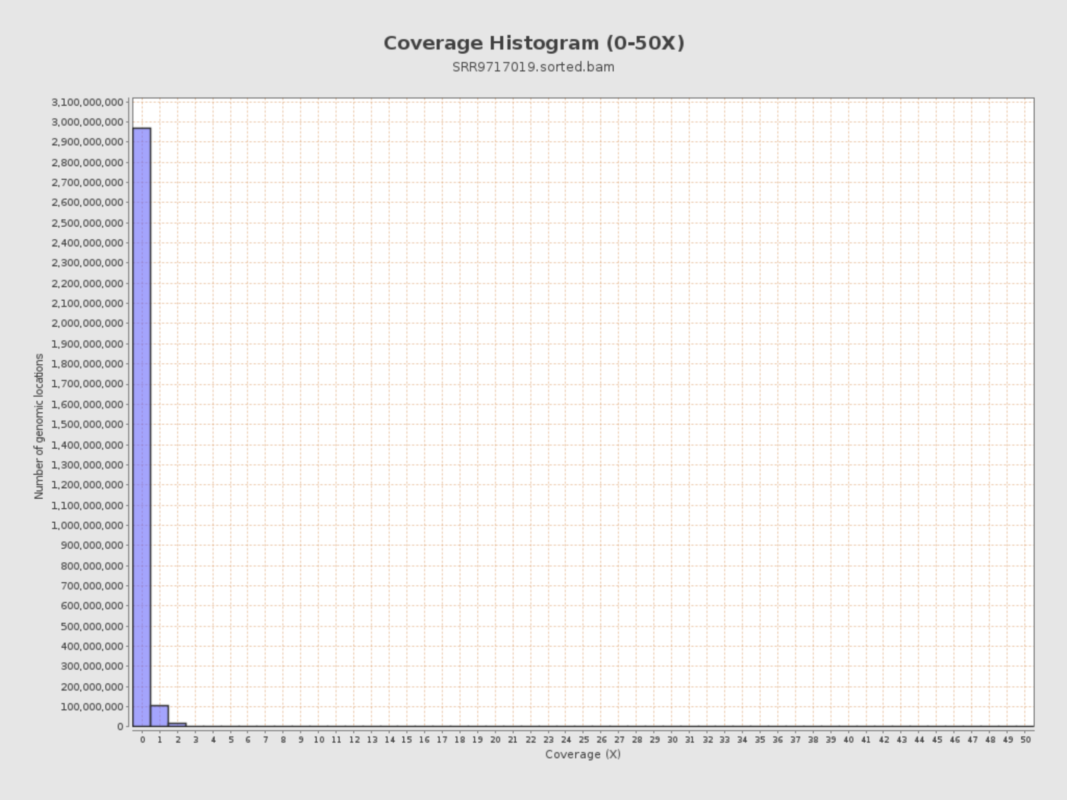
3. Results : Coverage across reference



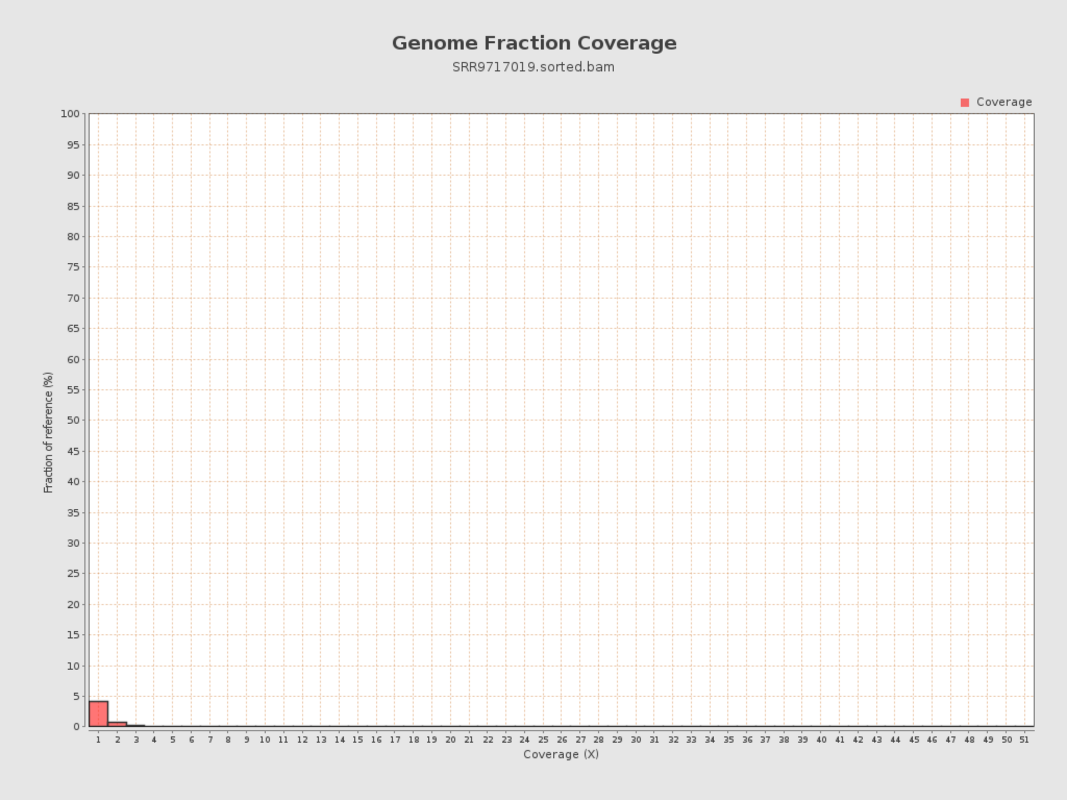
4. Results : Coverage Histogram



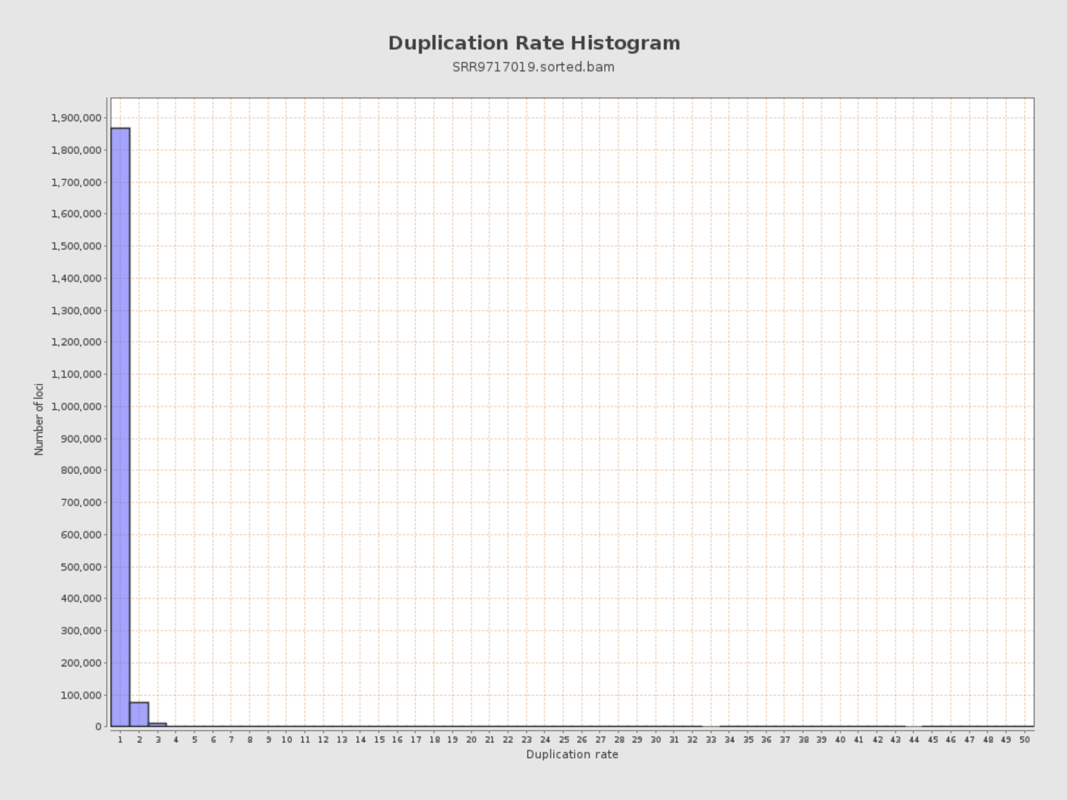
5. Results : Coverage Histogram (0-50X)



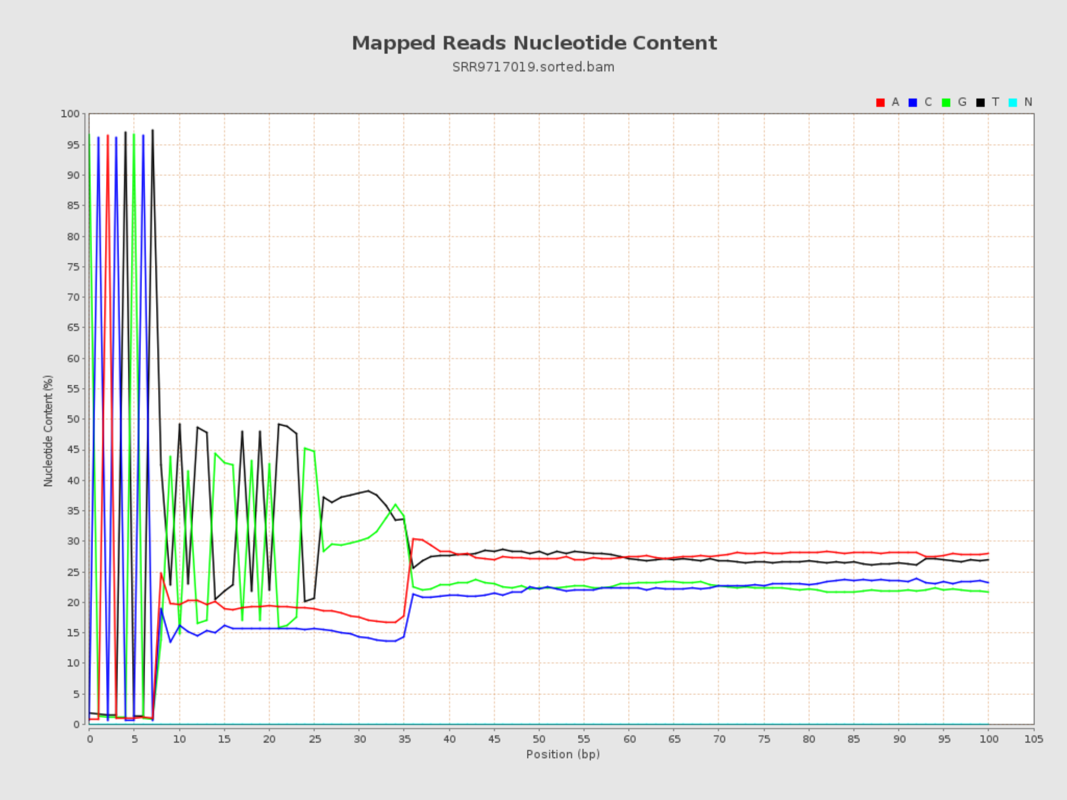
6. Results : Genome Fraction Coverage



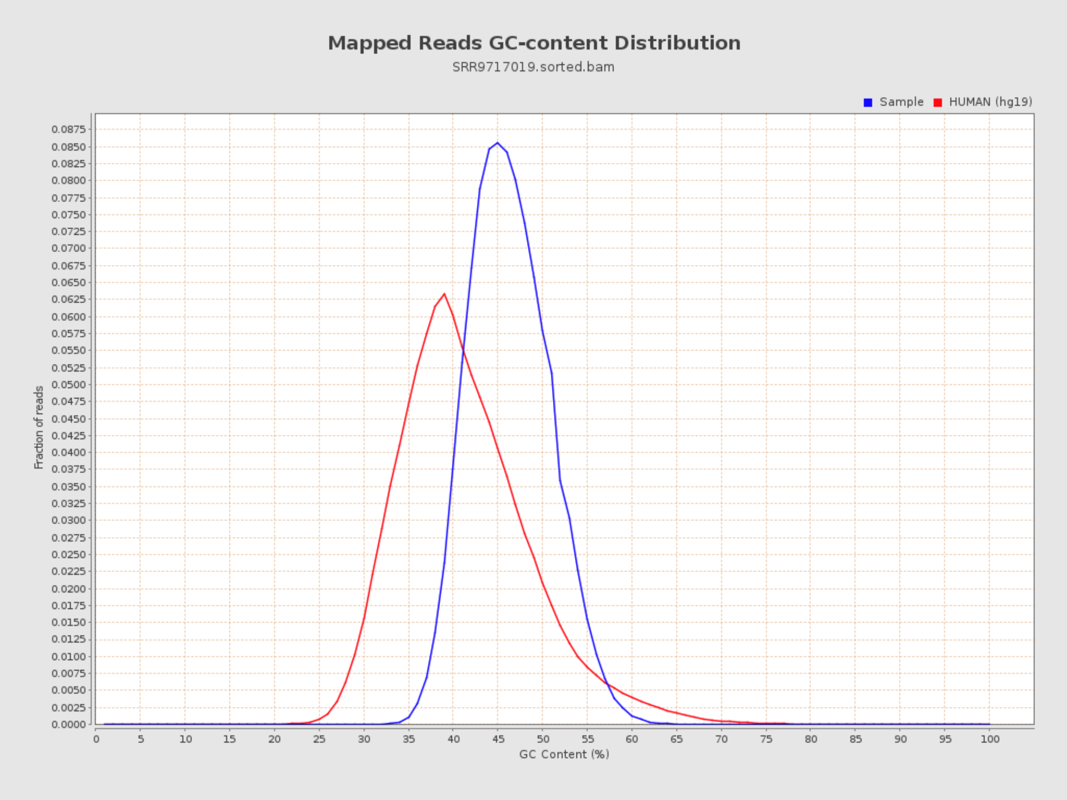
7. Results : Duplication Rate Histogram



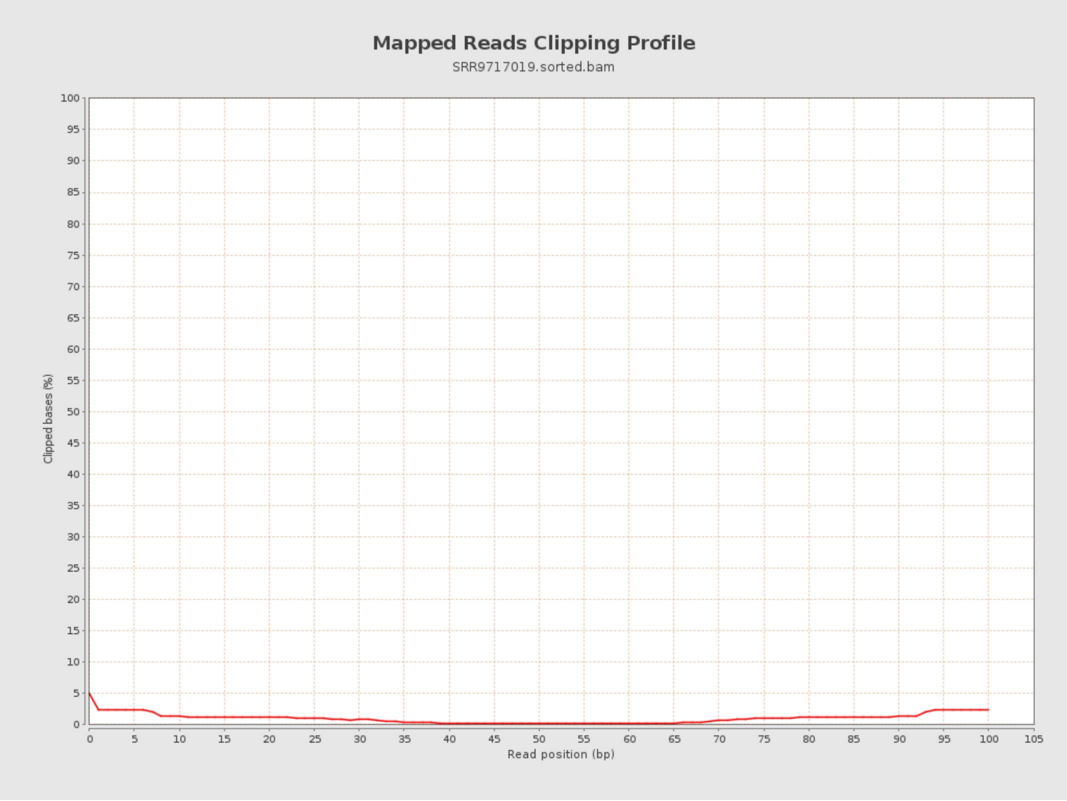
8. Results : Mapped Reads Nucleotide Content



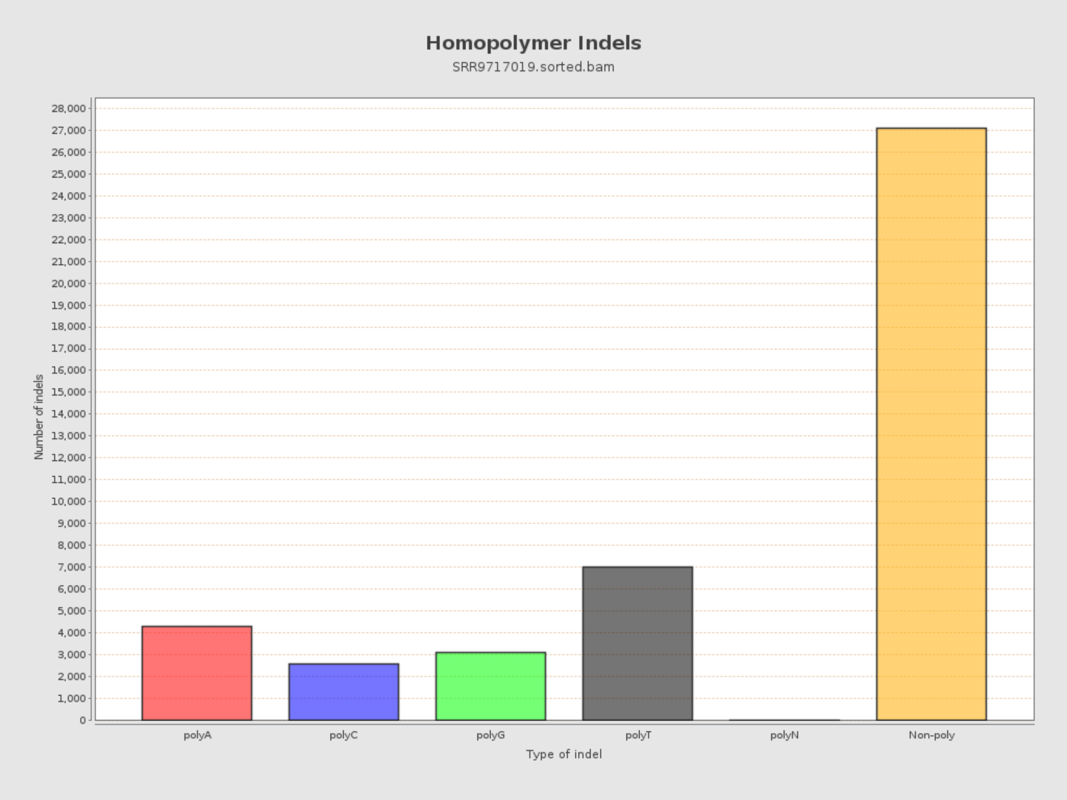
9. Results : Mapped Reads GC-content Distribution



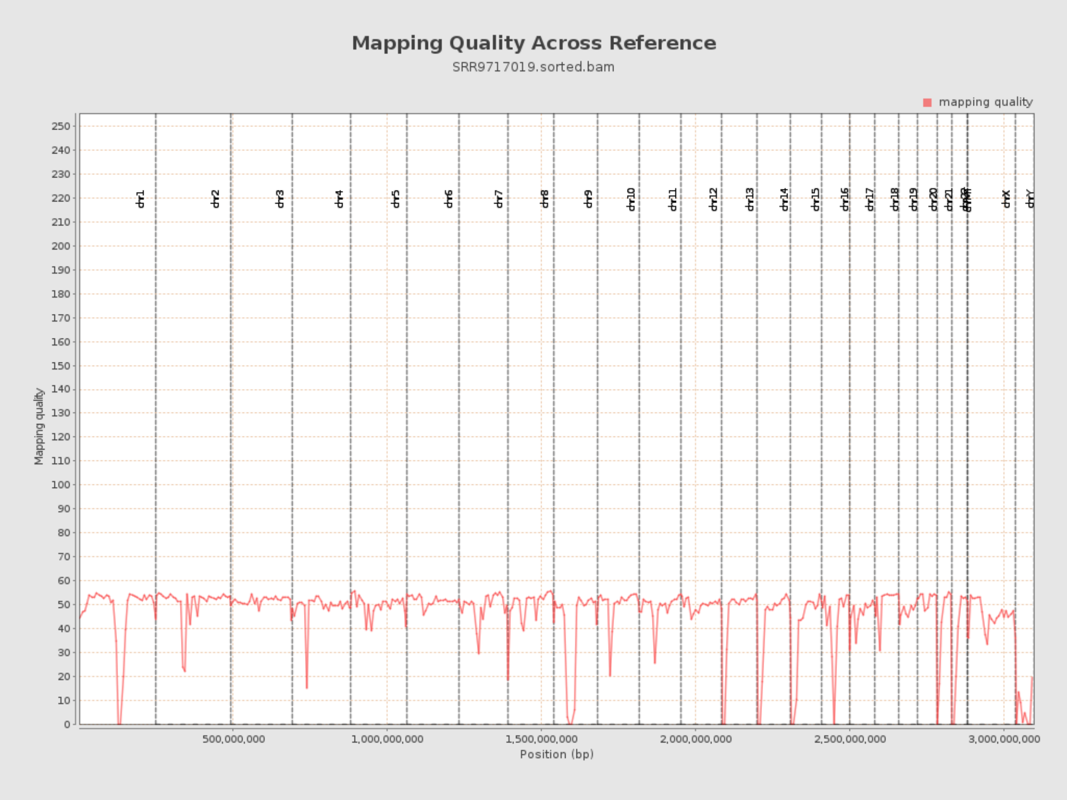
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram