Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 05:24:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717089.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_SRR9717089 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717089.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 05:24:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717089.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,415,489
Mapped reads	3,145,684 / 92.1%
Unmapped reads	269,805 / 7.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	52,321 / 1.53%
Read min/max/mean length	30 / 101 / 101.56
Duplicated reads (estimated)	205,047 / 6%
Duplication rate	4.3%
Clipped reads	3,191,467 / 93.44%

2.2. ACGT Content

Number/percentage of A's	62,111,332 / 24.99%
Number/percentage of C's	45,873,391 / 18.46%
Number/percentage of T's	79,727,053 / 32.08%
Number/percentage of G's	60,828,762 / 24.47%
Number/percentage of N's	14,805 / 0.01%
GC Percentage	42.93%

2.3. Coverage

Mean	0.0803

Standard Deviation	0.8367

2.4. Mapping Quality

Mean Mapping Quality	45.22

2.5. Mismatches and indels

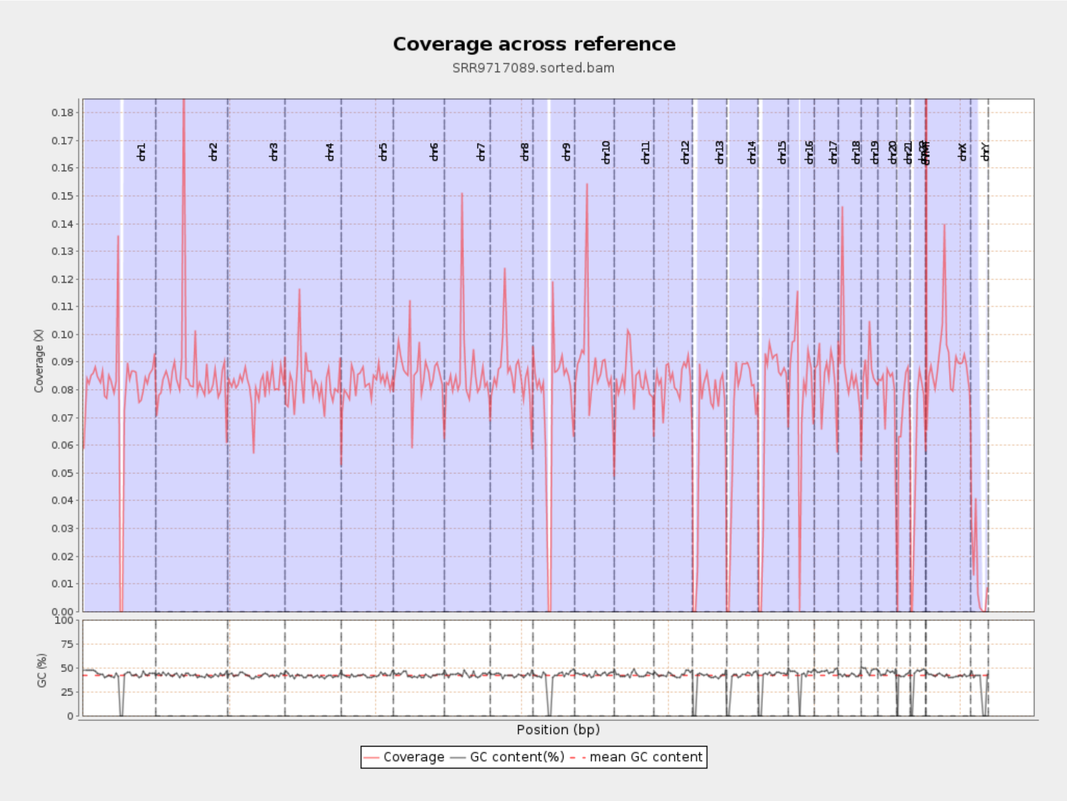
General error rate	0.85%
Mismatches	2,054,000
Insertions	24,481
Mapped reads with at least one insertion	0.77%
Deletions	62,930
Mapped reads with at least one deletion	1.97%
Homopolymer indels	43.78%

2.6. Chromosome stats

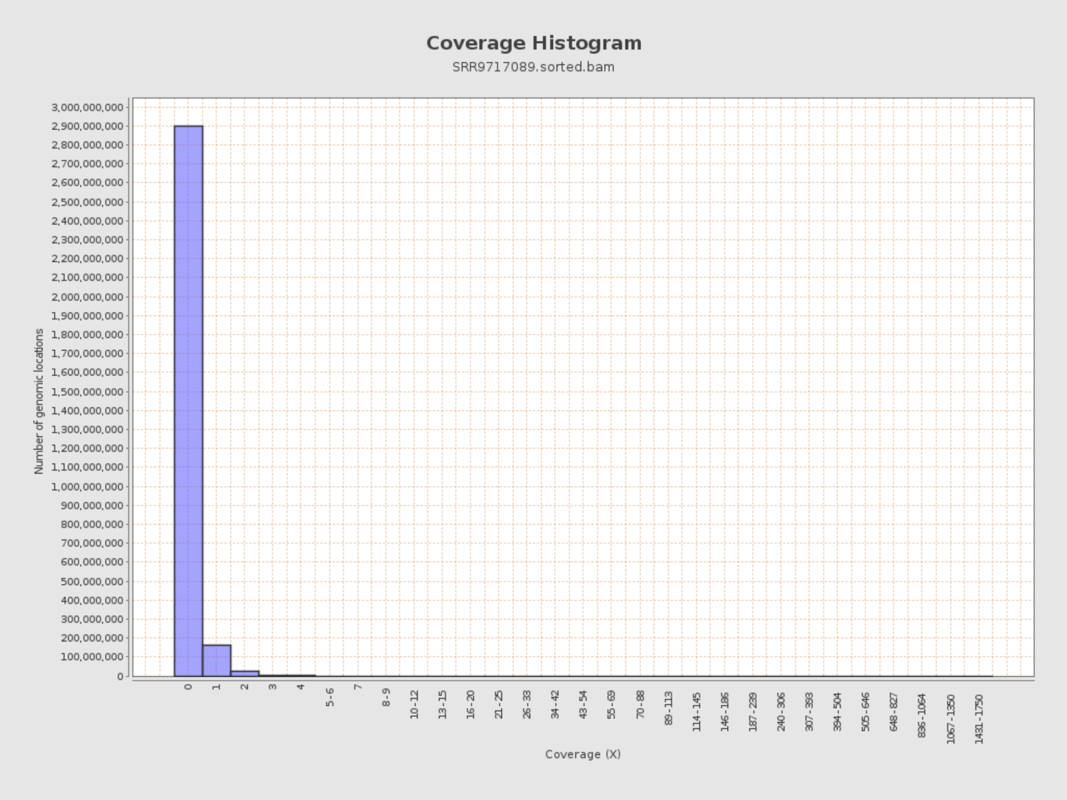
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19728306	0.0792	1.3445
chr2	243199373	21076364	0.0867	1.2376
chr3	198022430	16124257	0.0814	0.3524
chr4	191154276	15839809	0.0829	0.4258
chr5	180915260	14942189	0.0826	0.3667
chr6	171115067	14825667	0.0866	0.514
chr7	159138663	13695974	0.0861	1.0862

chr8	146364022	12567215	0.0859	1.1552
chr9	141213431	10605114	0.0751	0.9277
chr10	135534747	12093530	0.0892	0.7821
chr11	135006516	11238485	0.0832	0.856
chr12	133851895	11170371	0.0835	0.3739
chr13	115169878	7716958	0.067	0.3121
chr14	107349540	7571446	0.0705	0.5349
chr15	102531392	7428500	0.0725	0.3429
chr16	90354753	7166194	0.0793	0.447
chr17	81195210	6910931	0.0851	0.4249
chr18	78077248	7027559	0.09	1.8717
chr19	59128983	5057021	0.0855	1.0268
chr20	63025520	5049563	0.0801	0.4018
chr21	48129895	3269094	0.0679	0.3684
chr22	51304566	2881776	0.0562	0.2891
chrMT	16571	19353	1.1679	1.3591
chrX	155270560	13958328	0.0899	0.6176
chrY	59373566	702202	0.0118	0.3382

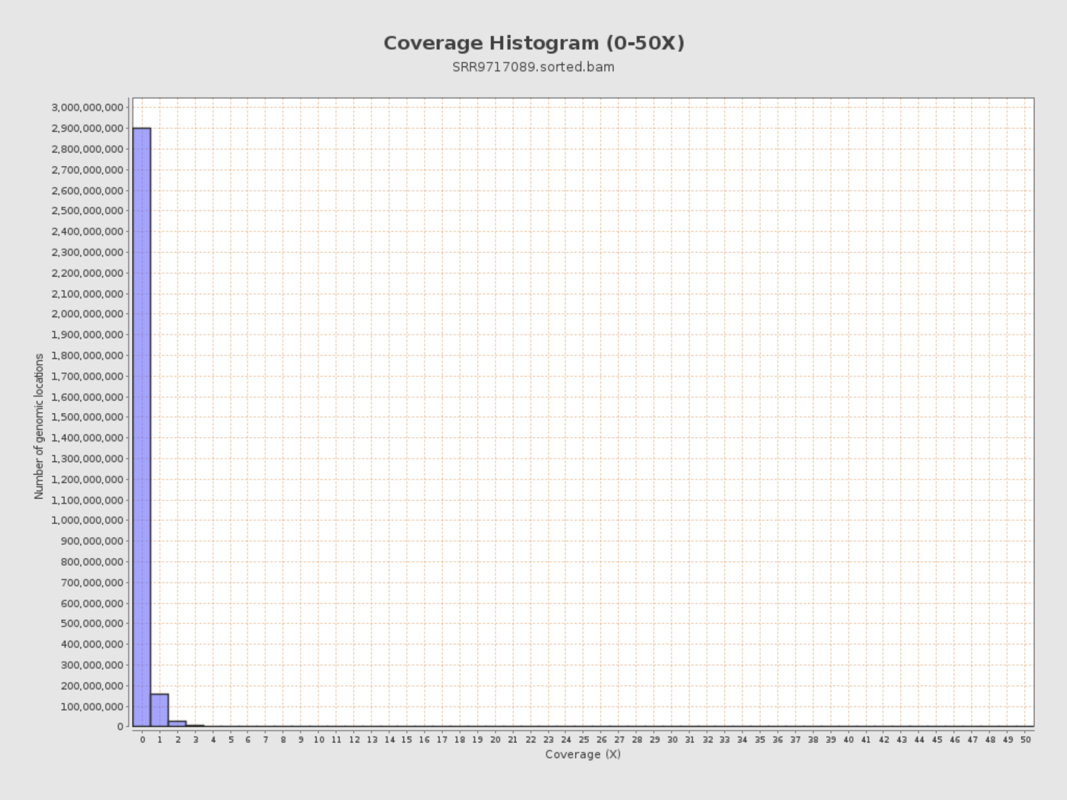
3. Results : Coverage across reference



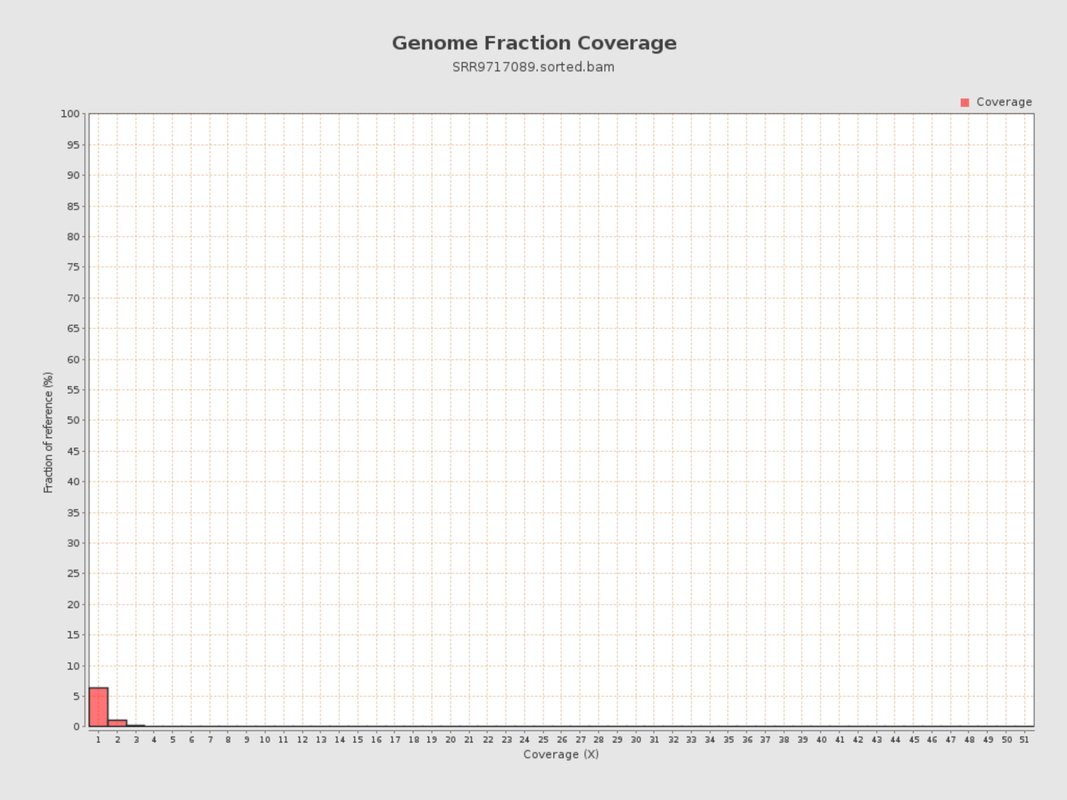
4. Results : Coverage Histogram



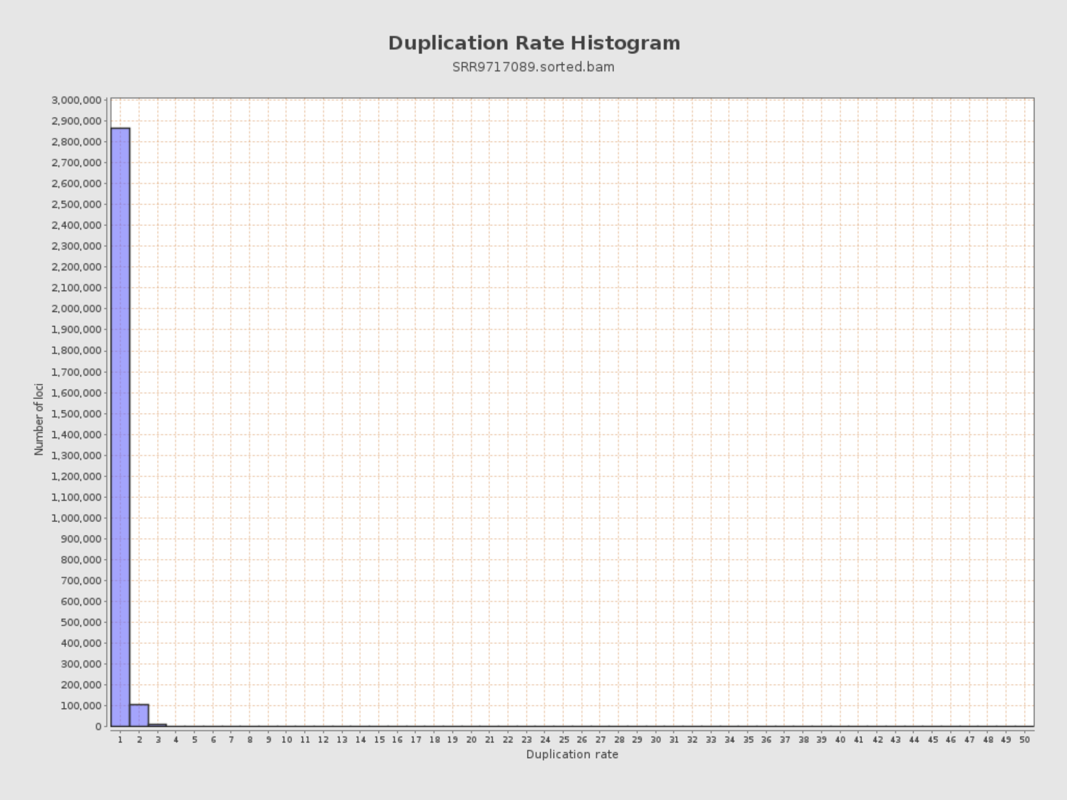
5. Results : Coverage Histogram (0-50X)



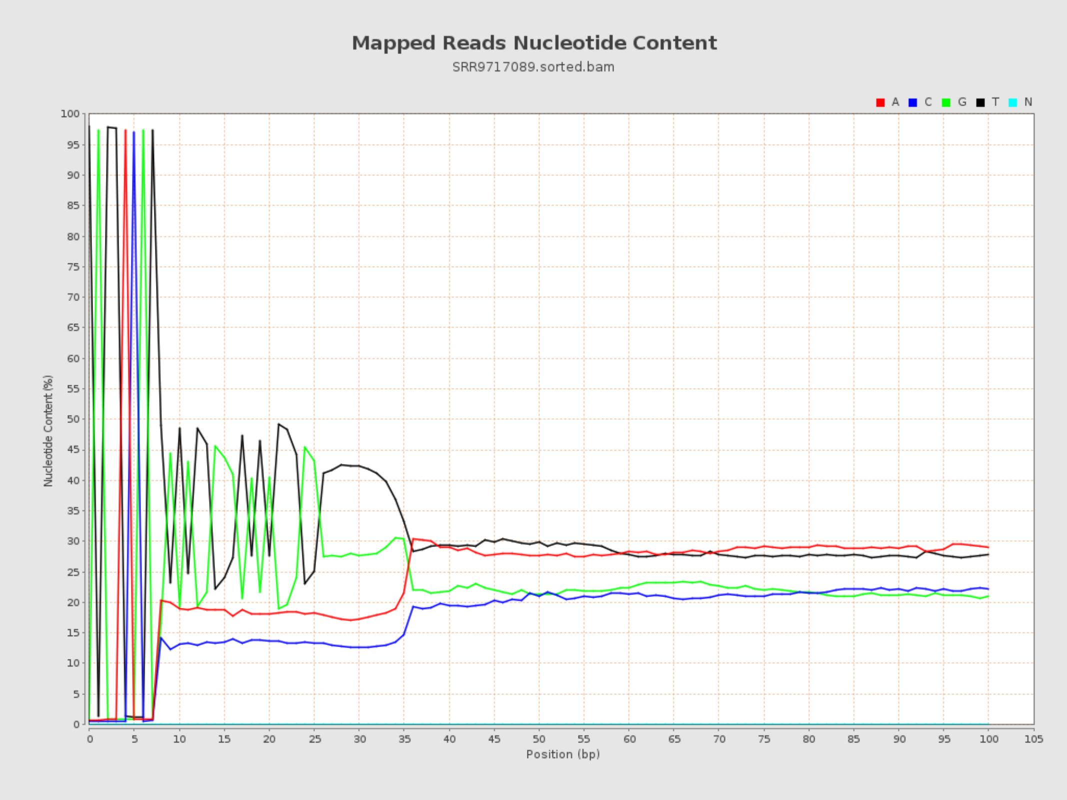
6. Results : Genome Fraction Coverage



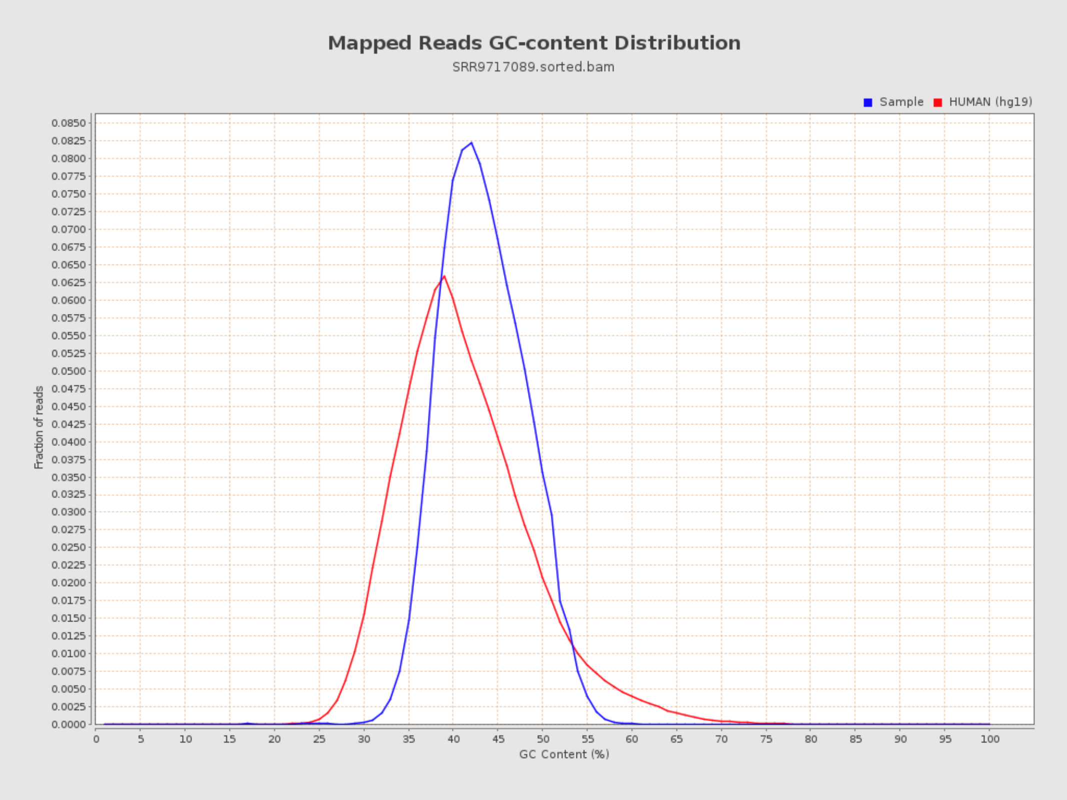
7. Results : Duplication Rate Histogram



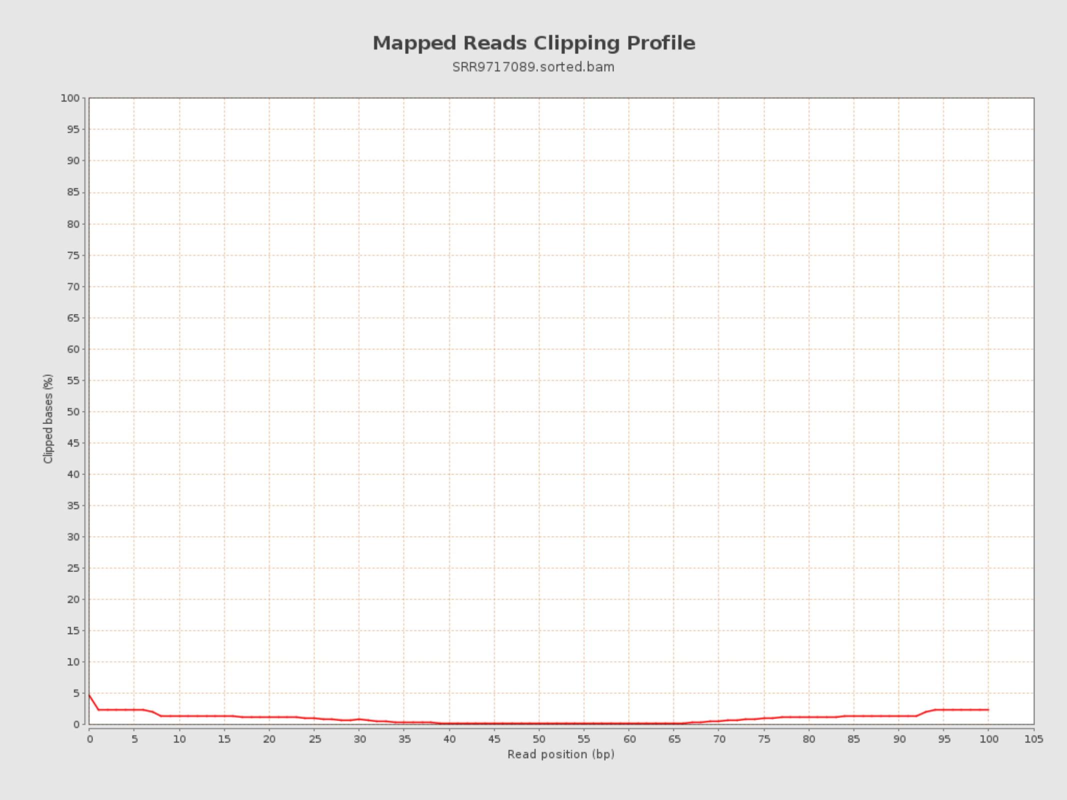
8. Results : Mapped Reads Nucleotide Content



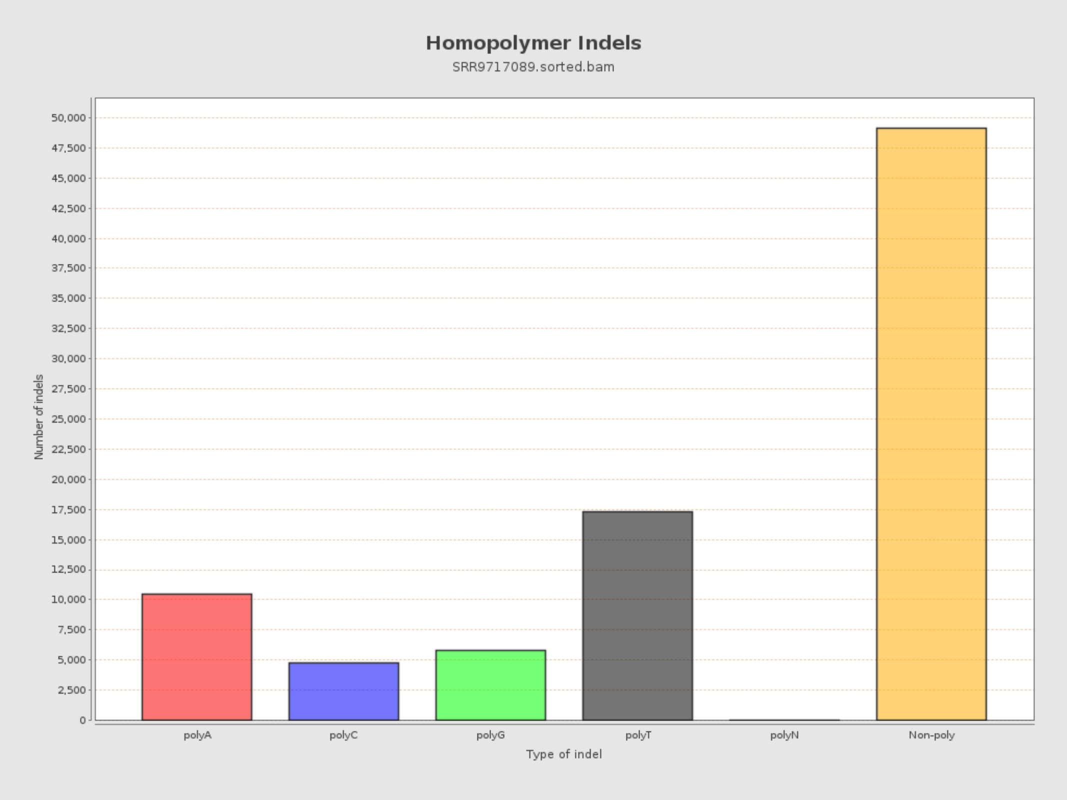
9. Results : Mapped Reads GC-content Distribution



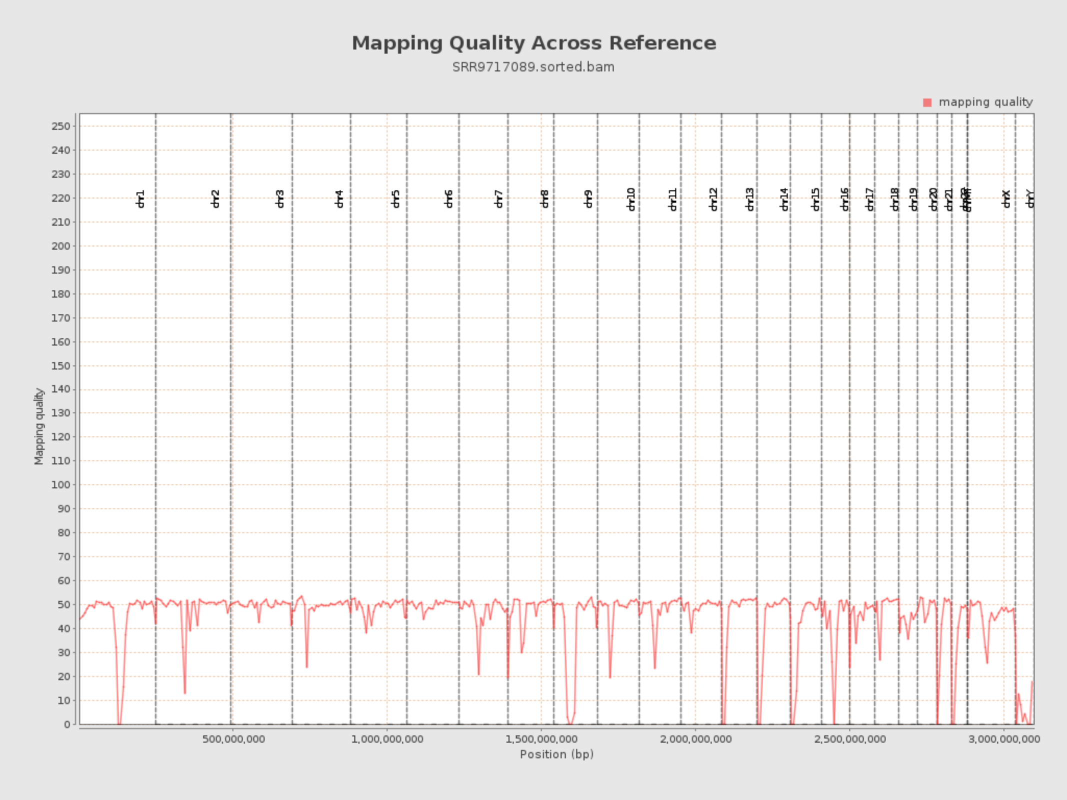
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram