Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 01:57:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717038.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_SRR9717038 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717038.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 01:57:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717038.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,769,600
Mapped reads	1,534,458 / 86.71%
Unmapped reads	235,142 / 13.29%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,564 / 0.43%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	41,610 / 2.35%
Duplication rate	1.92%
Clipped reads	1,537,806 / 86.9%

2.2. ACGT Content

Number/percentage of A's	23,000,018 / 26.39%
Number/percentage of C's	16,534,859 / 18.97%
Number/percentage of T's	26,525,584 / 30.43%
Number/percentage of G's	21,093,422 / 24.2%
Number/percentage of N's	1,240 / 0%
GC Percentage	43.17%

2.3. Coverage

Mean	0.0282

Standard Deviation	0.2534

2.4. Mapping Quality

Mean Mapping Quality	43.16

2.5. Mismatches and indels

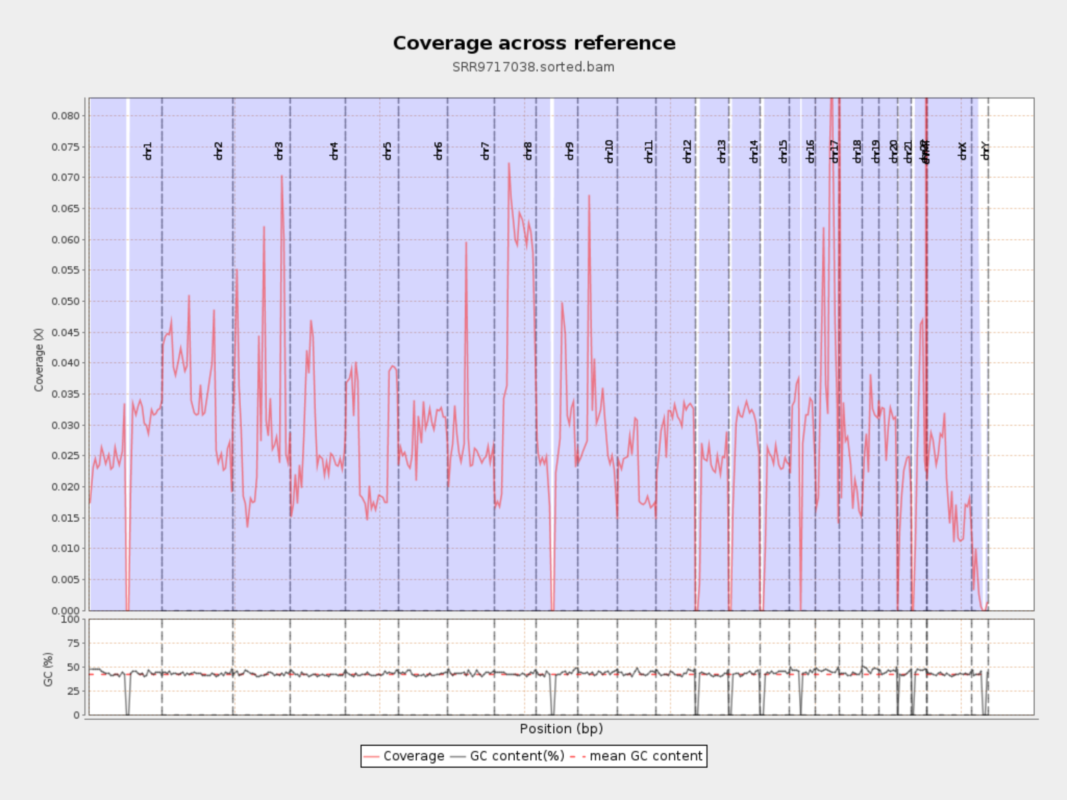
General error rate	0.52%
Mismatches	442,202
Insertions	6,937
Mapped reads with at least one insertion	0.45%
Deletions	16,690
Mapped reads with at least one deletion	1.08%
Homopolymer indels	39.6%

2.6. Chromosome stats

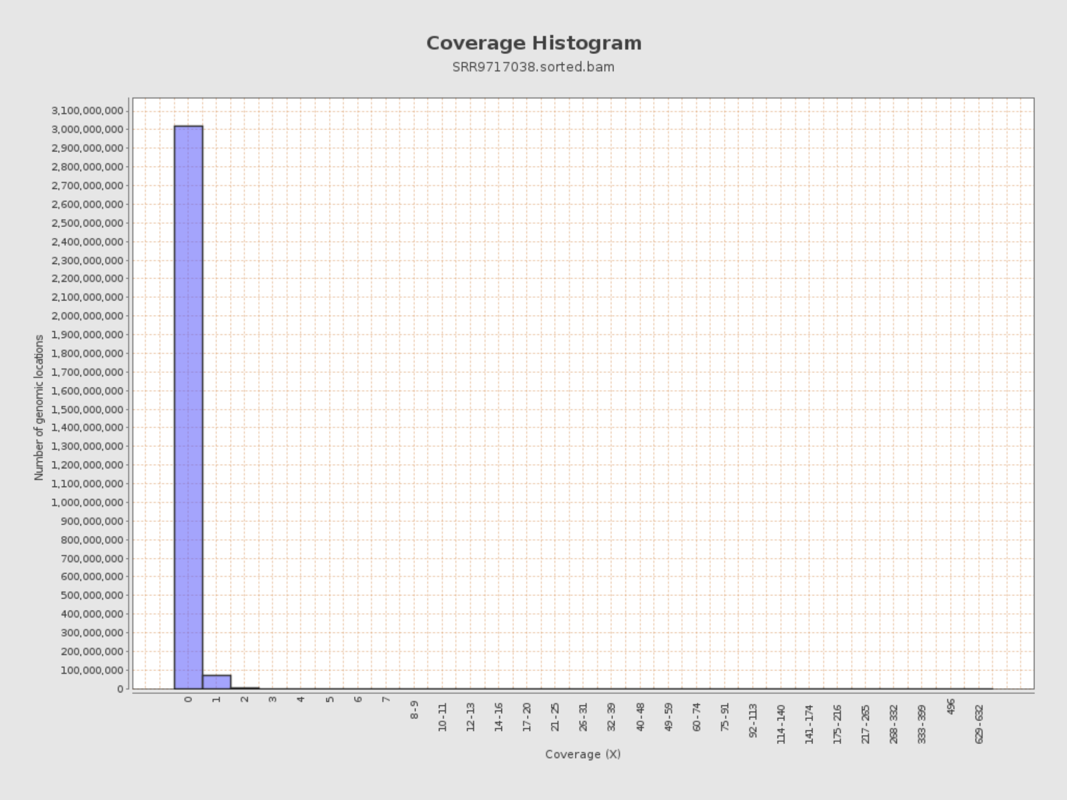
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6459601	0.0259	0.3003
chr2	243199373	8685686	0.0357	0.3478
chr3	198022430	6255990	0.0316	0.1996
chr4	191154276	5047226	0.0264	0.1823
chr5	180915260	4808907	0.0266	0.1768
chr6	171115067	4925367	0.0288	0.1999
chr7	159138663	4355883	0.0274	0.4953

chr8	146364022	7203325	0.0492	0.2799
chr9	141213431	3613434	0.0256	0.2015
chr10	135534747	4142548	0.0306	0.3116
chr11	135006516	2962135	0.0219	0.1972
chr12	133851895	4073165	0.0304	0.1959
chr13	115169878	2371664	0.0206	0.1547
chr14	107349540	2829719	0.0264	0.181
chr15	102531392	2046833	0.02	0.157
chr16	90354753	2644235	0.0293	0.1941
chr17	81195210	3554230	0.0438	0.2372
chr18	78077248	2004722	0.0257	0.3053
chr19	59128983	1741360	0.0295	0.3062
chr20	63025520	1898713	0.0301	0.1925
chr21	48129895	898686	0.0187	0.1532
chr22	51304566	1239668	0.0242	0.1704
chrMT	16571	63551	3.8351	3.1438
chrX	155270560	3166652	0.0204	0.1772
chrY	59373566	188273	0.0032	0.0828

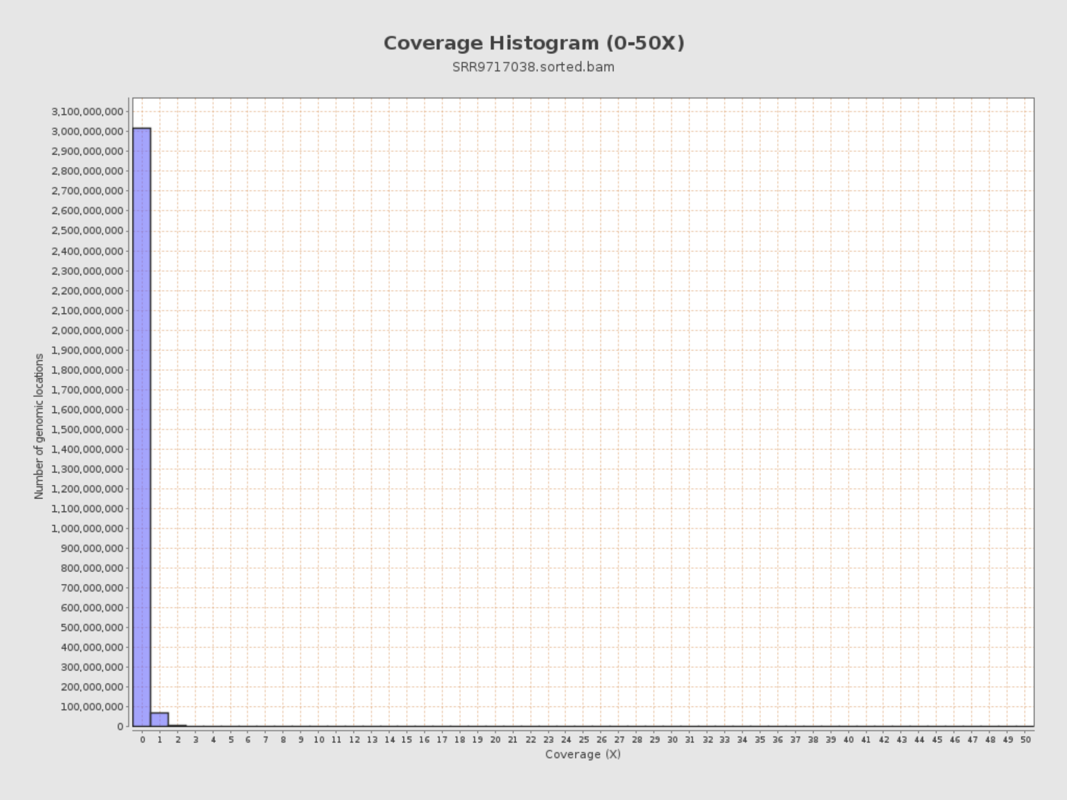
3. Results : Coverage across reference



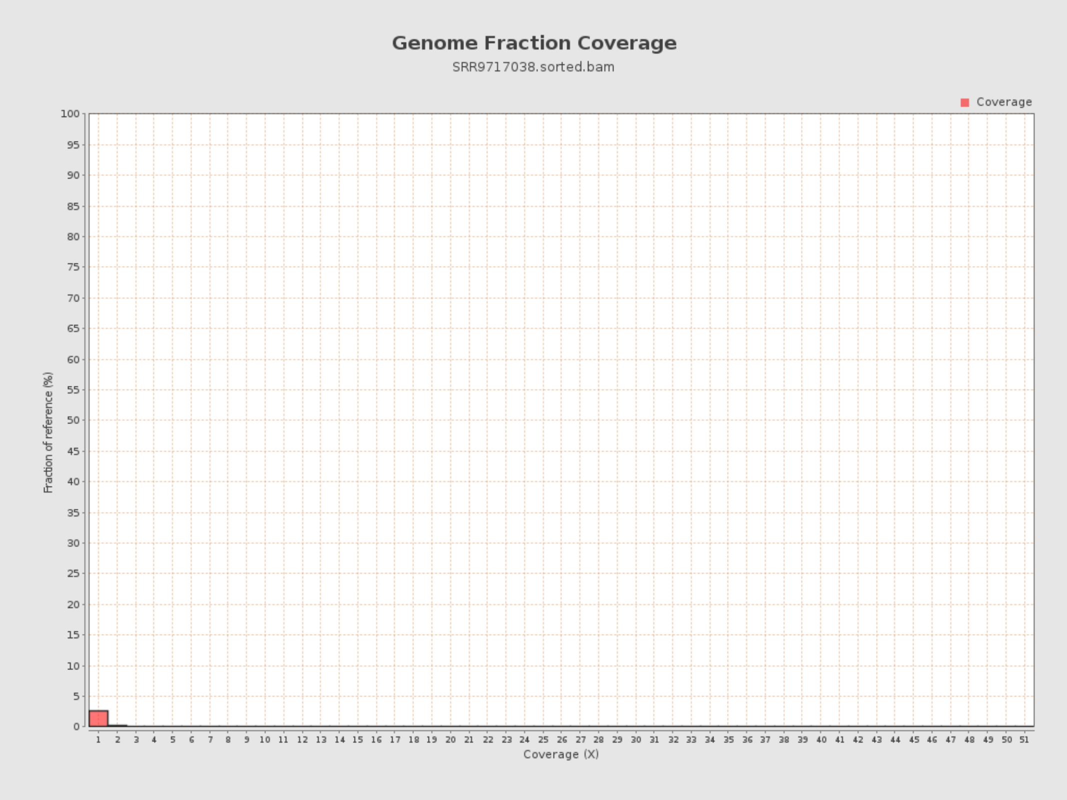
4. Results : Coverage Histogram



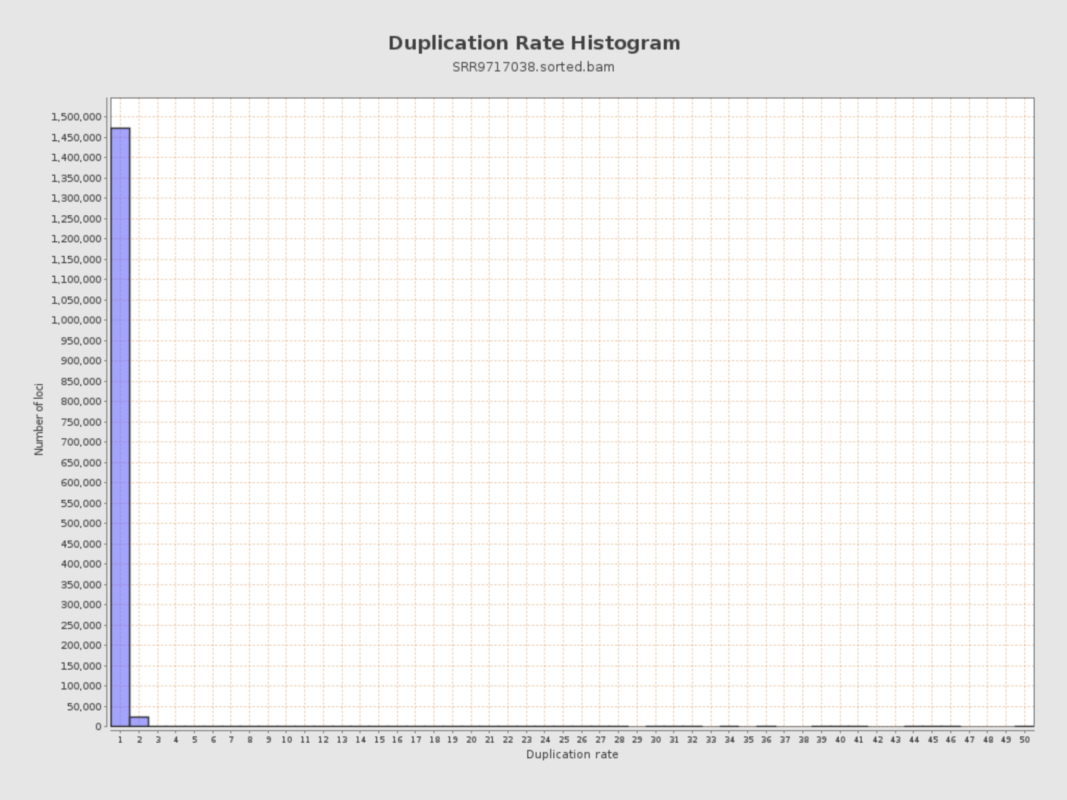
5. Results : Coverage Histogram (0-50X)



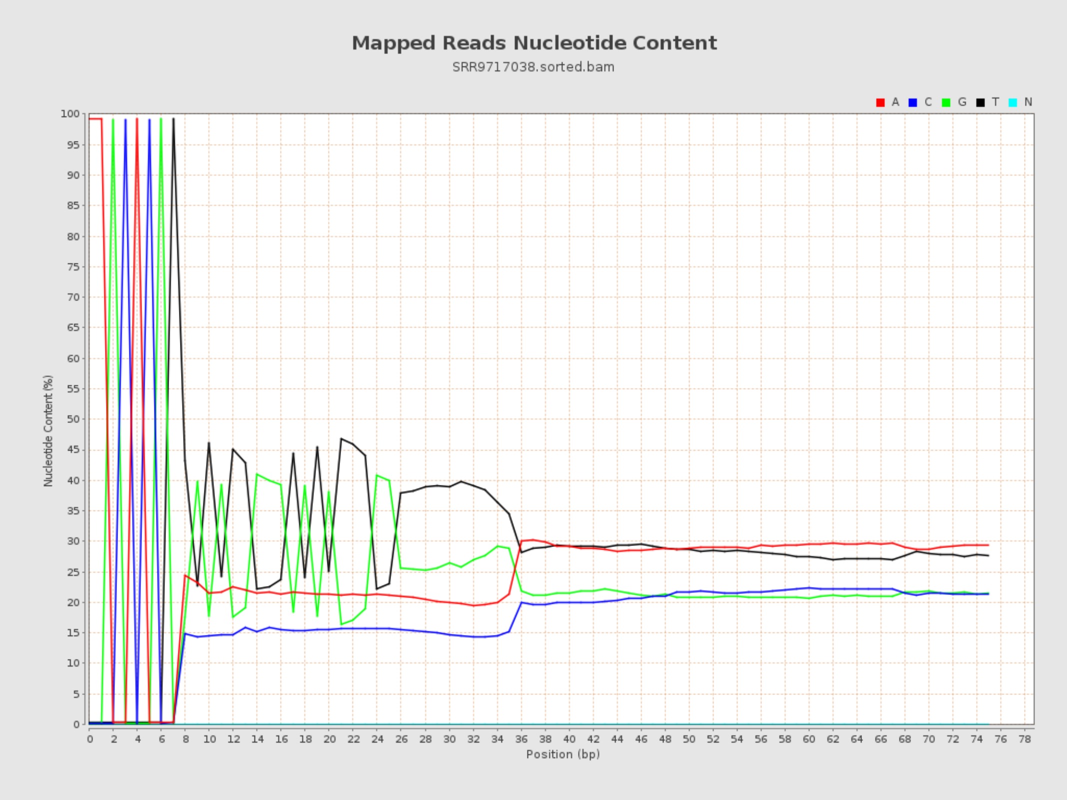
6. Results : Genome Fraction Coverage



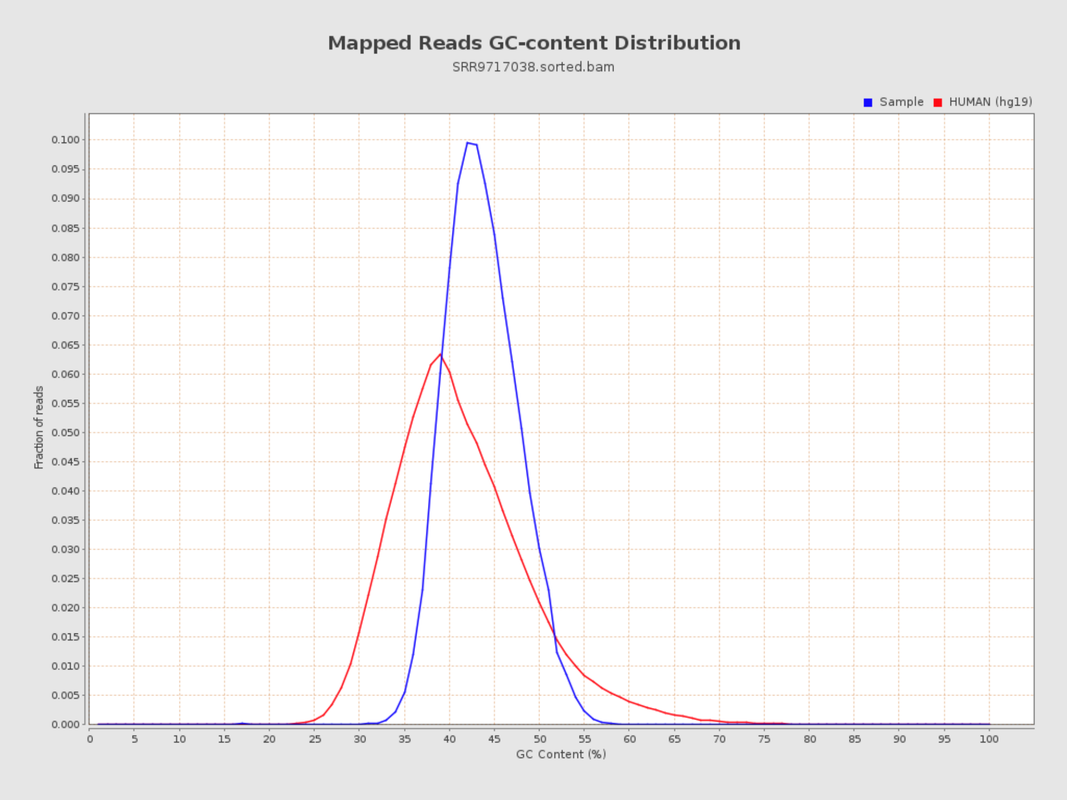
7. Results : Duplication Rate Histogram



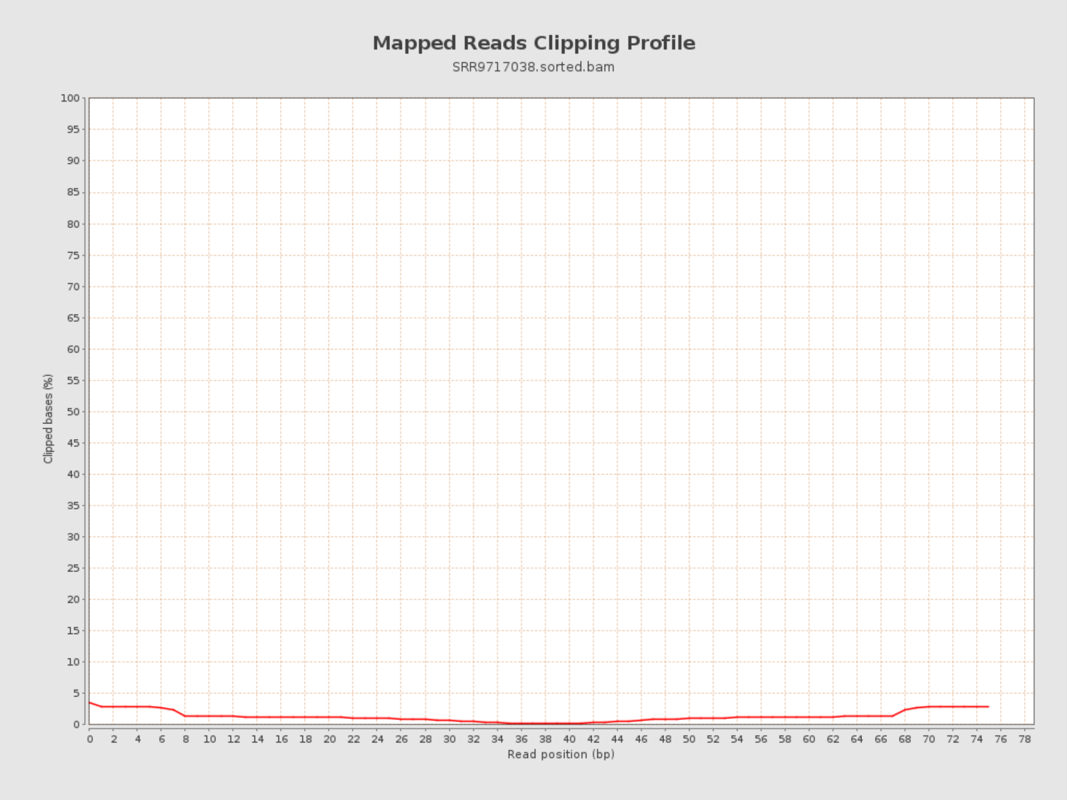
8. Results : Mapped Reads Nucleotide Content



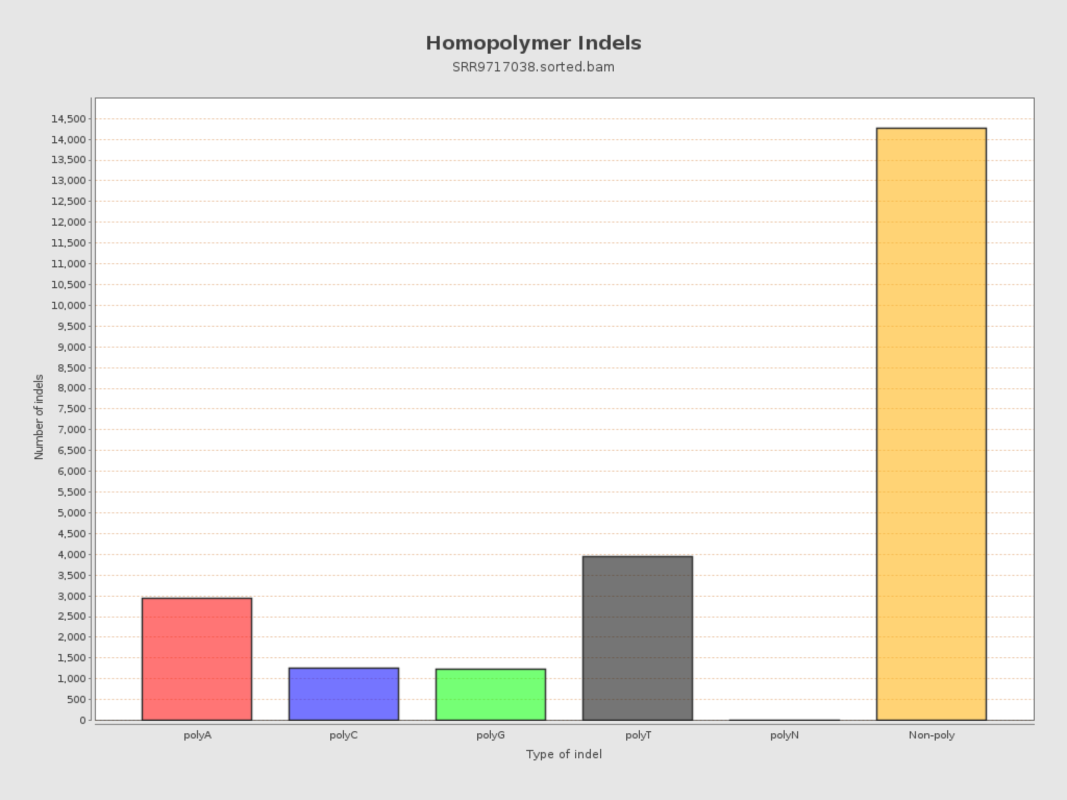
9. Results : Mapped Reads GC-content Distribution



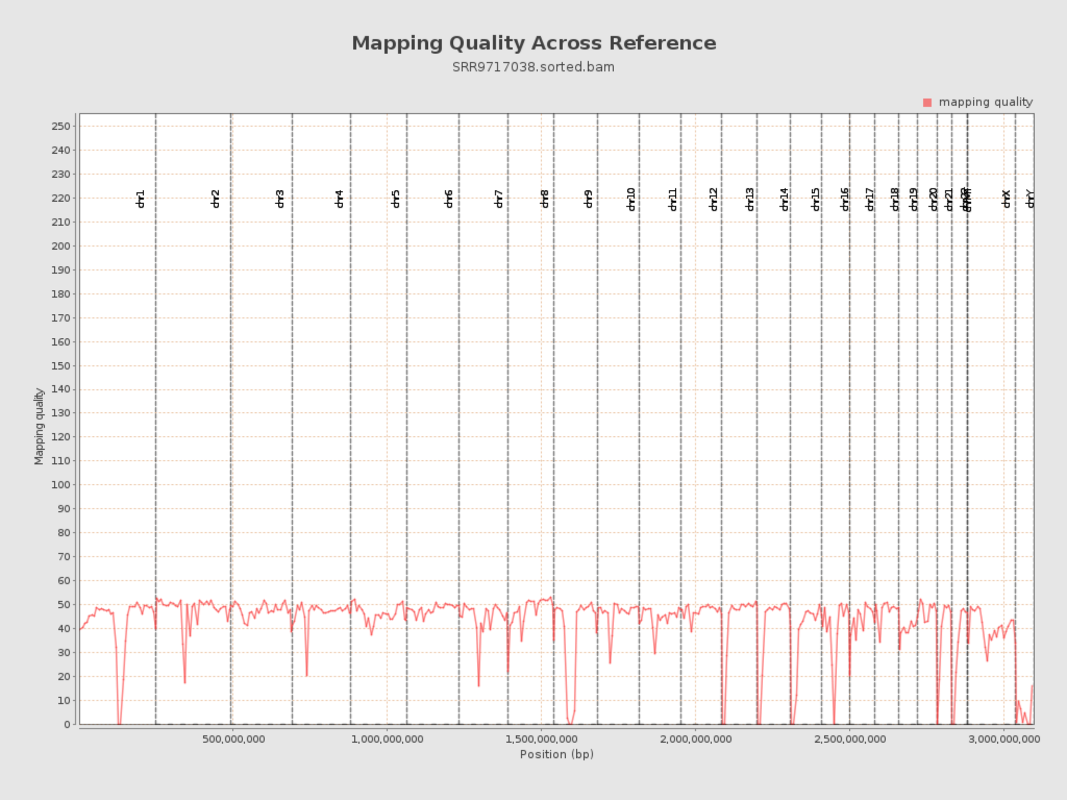
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram