Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 02:07:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717040.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_SRR9717040 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717040.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 02:07:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717040.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,230,669
Mapped reads	7,634,299 / 92.75%
Unmapped reads	596,370 / 7.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	218,183 / 2.65%
Read min/max/mean length	30 / 101 / 101.95
Duplicated reads (estimated)	557,712 / 6.78%
Duplication rate	5.21%
Clipped reads	7,844,514 / 95.31%

2.2. ACGT Content

Number/percentage of A's	143,104,378 / 25.19%
Number/percentage of C's	118,357,445 / 20.83%
Number/percentage of T's	167,894,821 / 29.55%
Number/percentage of G's	138,665,058 / 24.41%
Number/percentage of N's	65,102 / 0.01%
GC Percentage	45.24%

2.3. Coverage

Mean	0.1836

Standard Deviation	1.2339

2.4. Mapping Quality

Mean Mapping Quality	44.83

2.5. Mismatches and indels

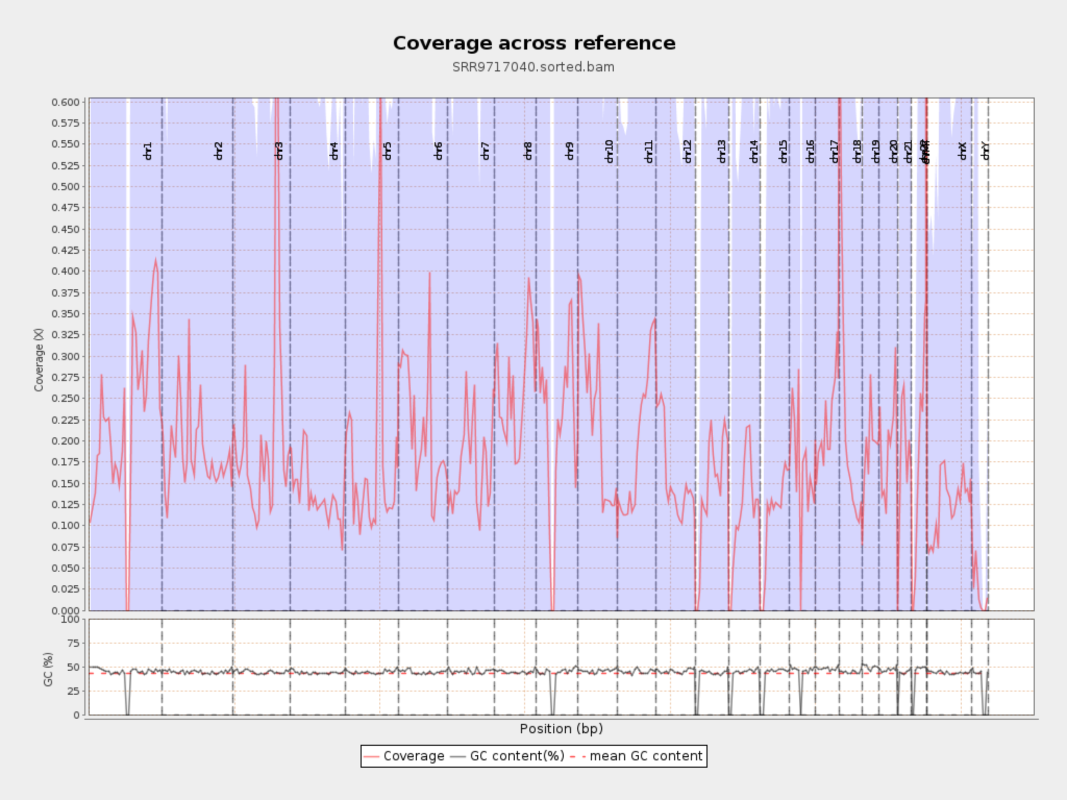
General error rate	0.77%
Mismatches	4,266,071
Insertions	46,749
Mapped reads with at least one insertion	0.6%
Deletions	115,013
Mapped reads with at least one deletion	1.48%
Homopolymer indels	40.78%

2.6. Chromosome stats

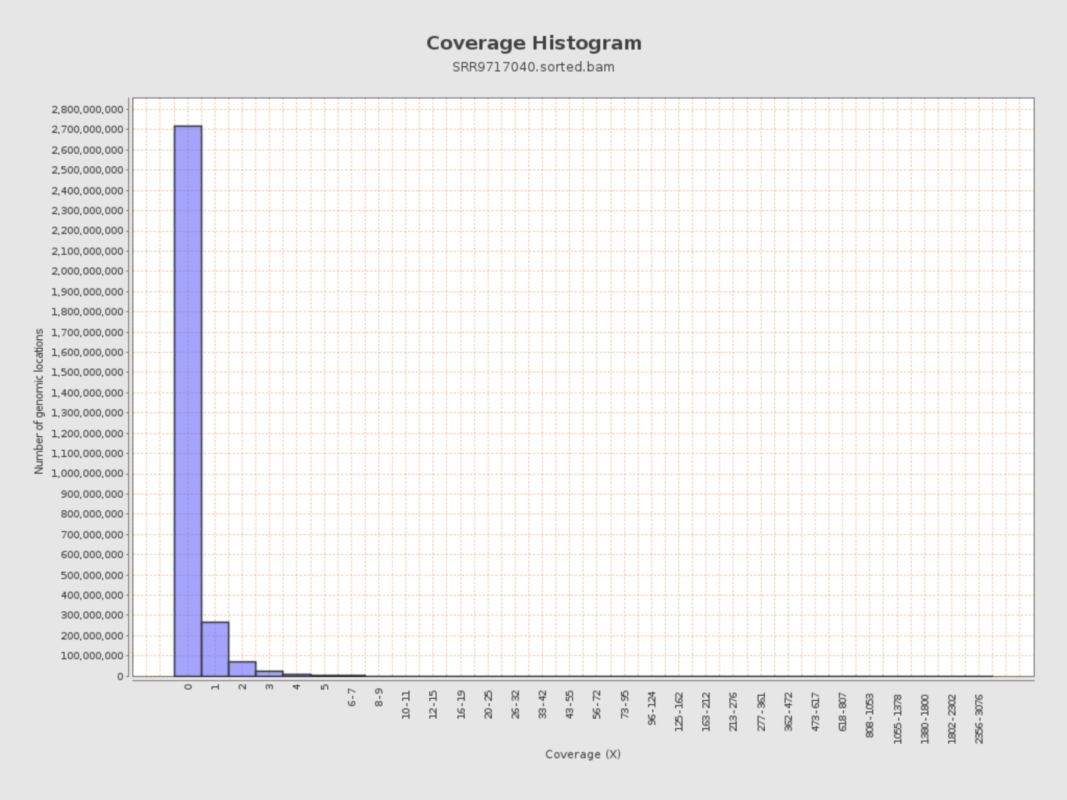
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	56657027	0.2273	1.8016
chr2	243199373	45539972	0.1873	2.197
chr3	198022430	41035287	0.2072	0.6844
chr4	191154276	25967902	0.1358	0.6623
chr5	180915260	31895069	0.1763	0.6182
chr6	171115067	37117897	0.2169	0.8896
chr7	159138663	27655047	0.1738	1.8563

chr8	146364022	38519289	0.2632	1.6419
chr9	141213431	31301040	0.2217	1.1508
chr10	135534747	31519856	0.2326	1.2433
chr11	135006516	26806600	0.1986	0.9867
chr12	133851895	20968710	0.1567	0.5634
chr13	115169878	16538227	0.1436	0.5225
chr14	107349540	12629295	0.1176	0.598
chr15	102531392	11305743	0.1103	0.4709
chr16	90354753	15121897	0.1674	0.7145
chr17	81195210	17987248	0.2215	0.8334
chr18	78077248	17496333	0.2241	1.8712
chr19	59128983	11475697	0.1941	1.6595
chr20	63025520	12419744	0.1971	0.7285
chr21	48129895	8480705	0.1762	0.6907
chr22	51304566	8552896	0.1667	0.6065
chrMT	16571	561718	33.8977	22.9941
chrX	155270560	19420296	0.1251	0.681
chrY	59373566	1316486	0.0222	0.6292

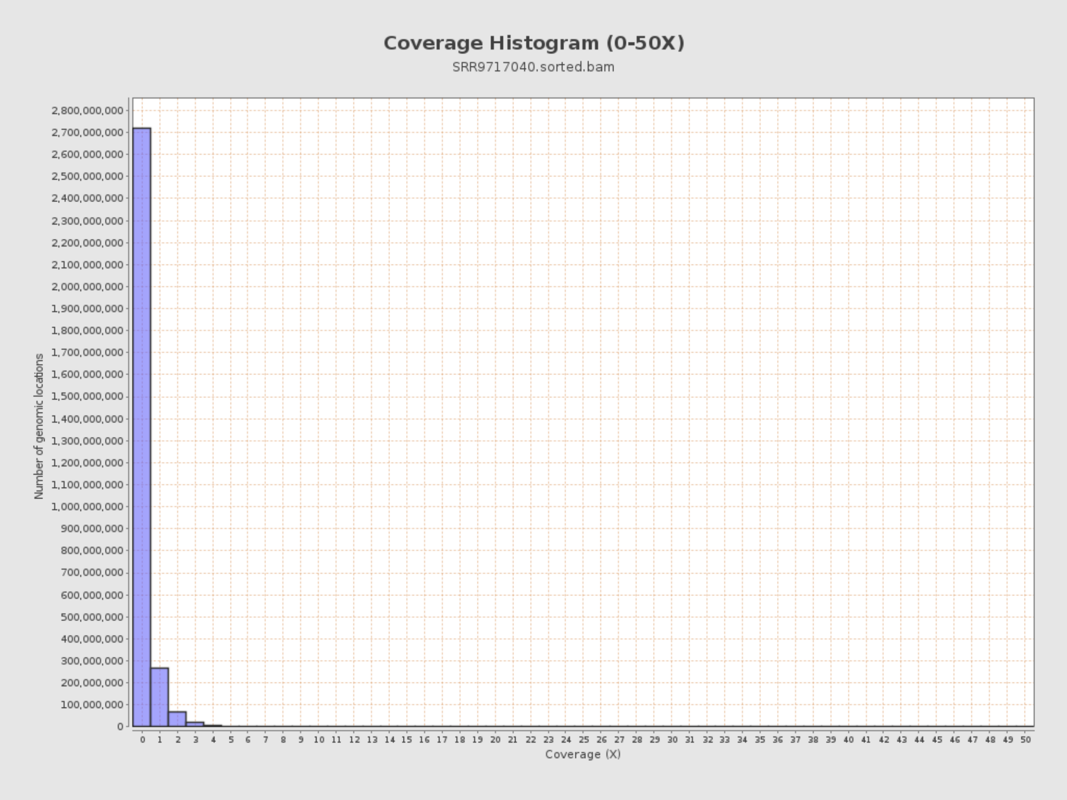
3. Results : Coverage across reference



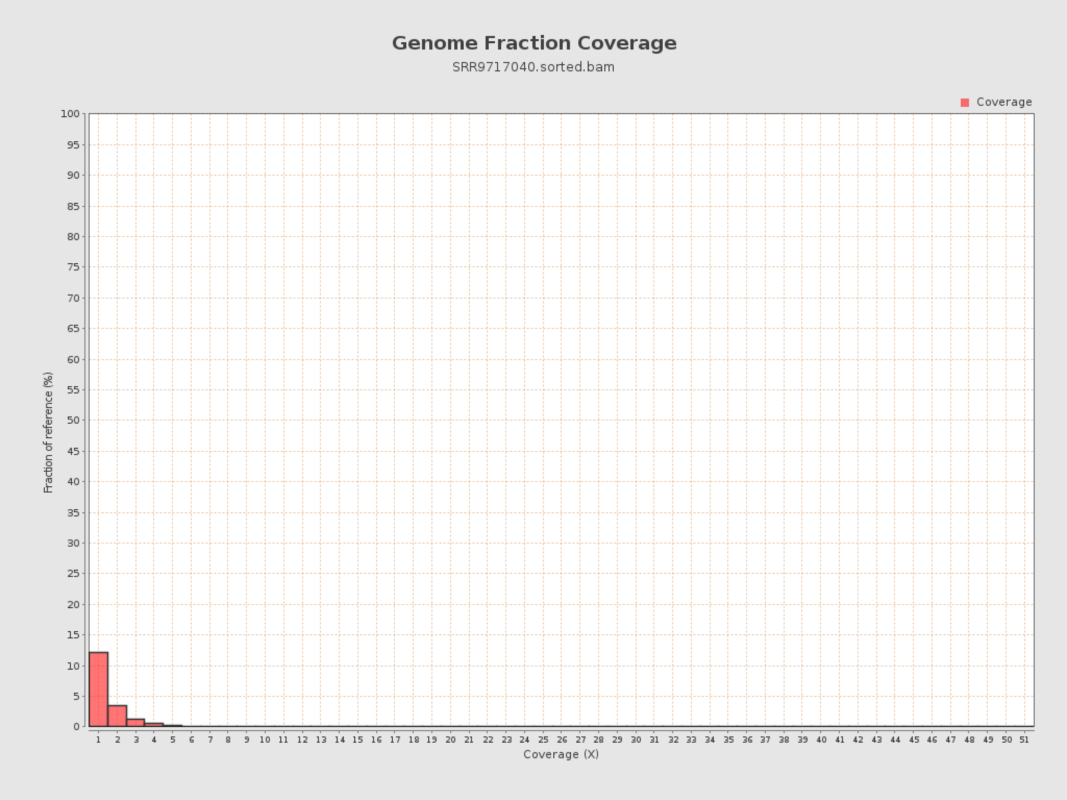
4. Results : Coverage Histogram



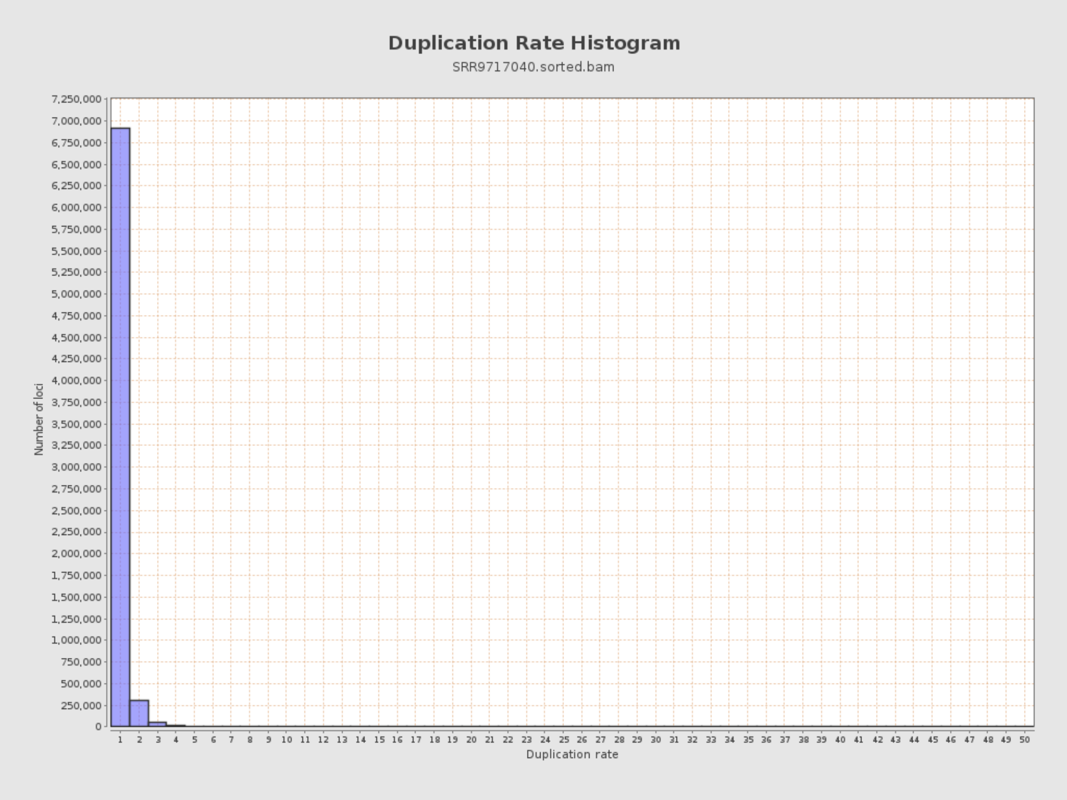
5. Results : Coverage Histogram (0-50X)



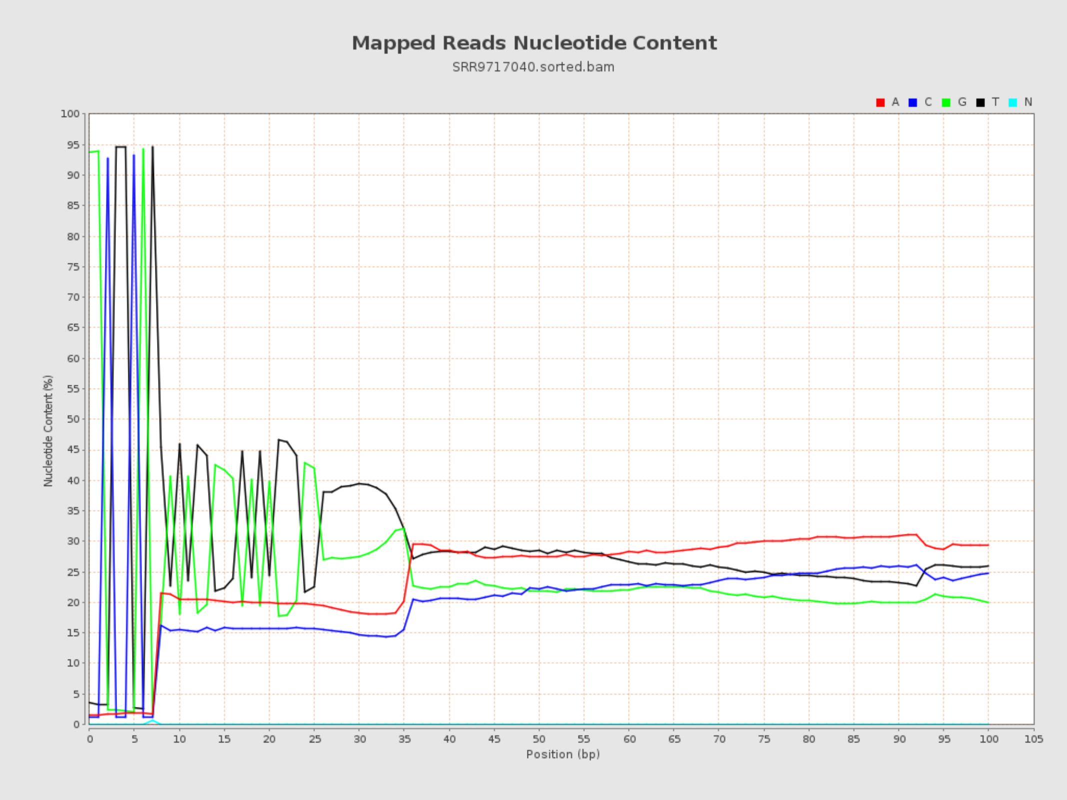
6. Results : Genome Fraction Coverage



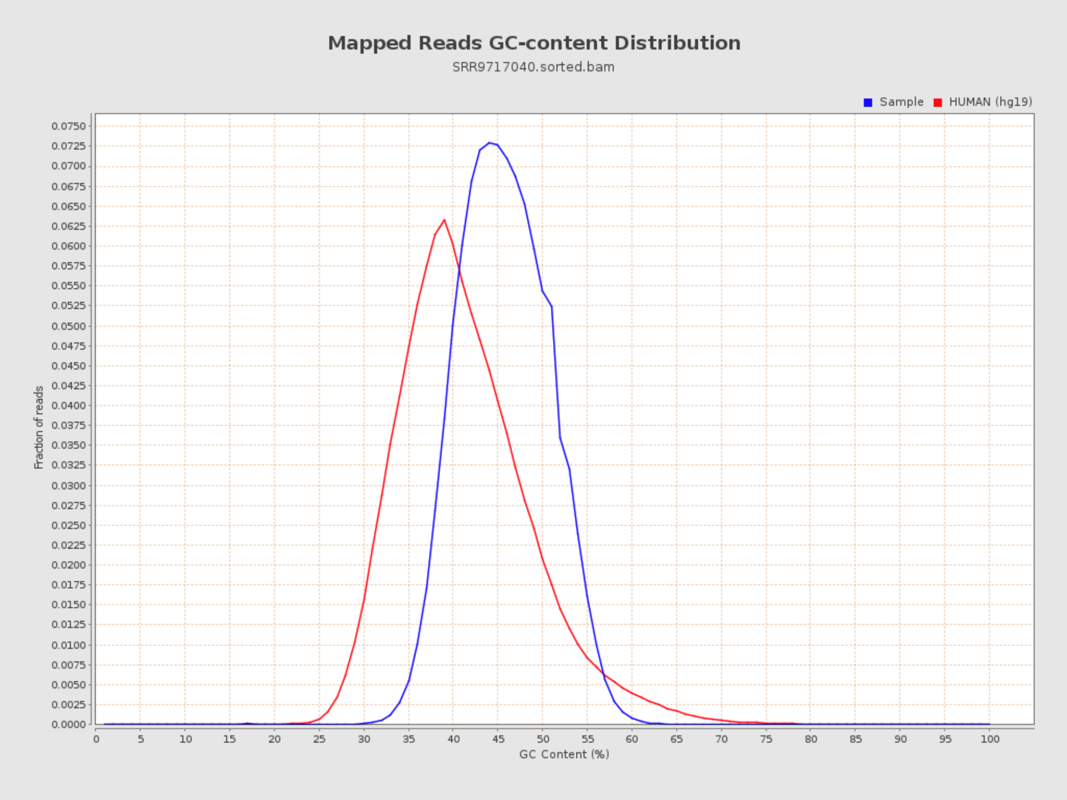
7. Results : Duplication Rate Histogram



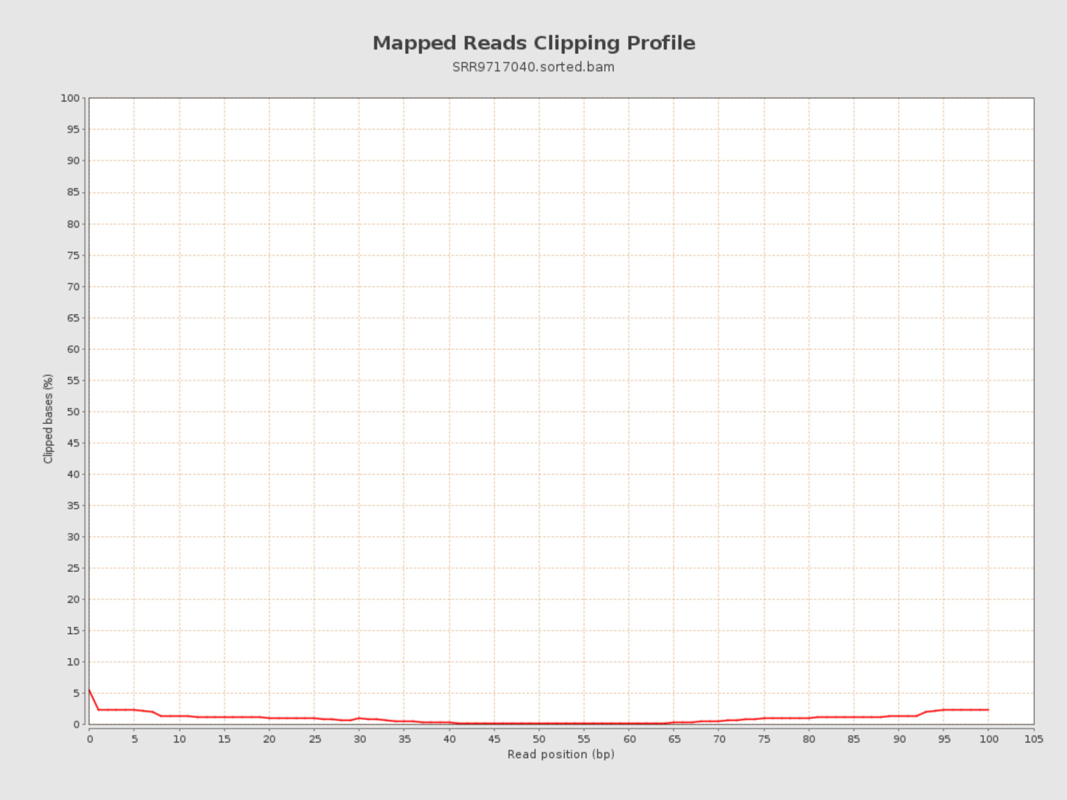
8. Results : Mapped Reads Nucleotide Content



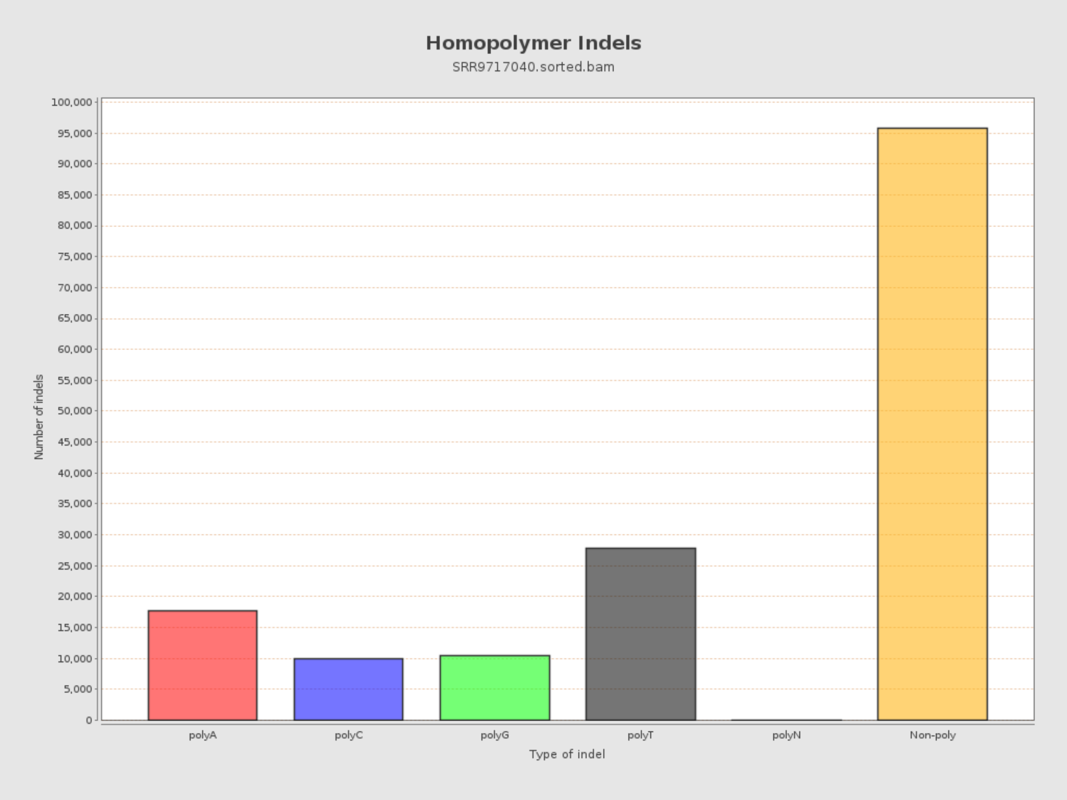
9. Results : Mapped Reads GC-content Distribution



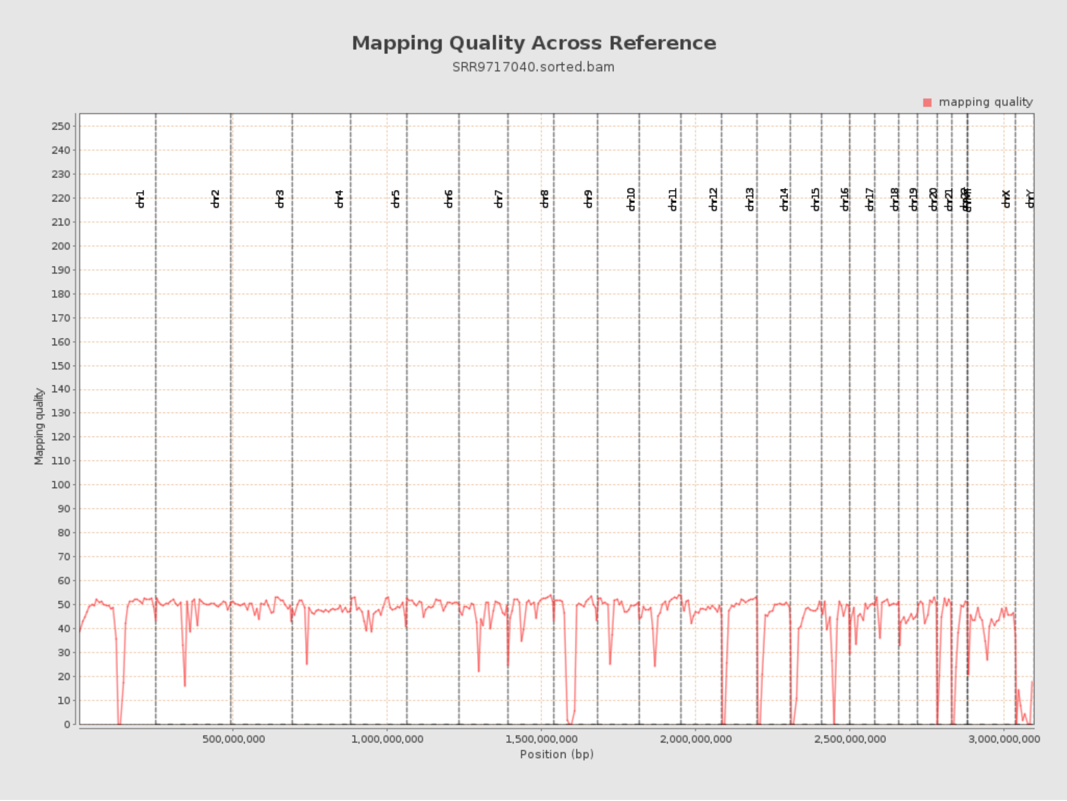
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram