Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 01:20:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717023.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_SRR9717023 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717023.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 01:20:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717023.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,452,398
Mapped reads	1,317,368 / 90.7%
Unmapped reads	135,030 / 9.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,769 / 0.4%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	32,436 / 2.23%
Duplication rate	1.87%
Clipped reads	1,322,845 / 91.08%

2.2. ACGT Content

Number/percentage of A's	17,862,534 / 23.72%
Number/percentage of C's	15,204,583 / 20.19%
Number/percentage of T's	22,899,320 / 30.41%
Number/percentage of G's	19,327,384 / 25.67%
Number/percentage of N's	1,700 / 0%
GC Percentage	45.86%

2.3. Coverage

Mean	0.0243

Standard Deviation	0.2049

2.4. Mapping Quality

Mean Mapping Quality	44.52

2.5. Mismatches and indels

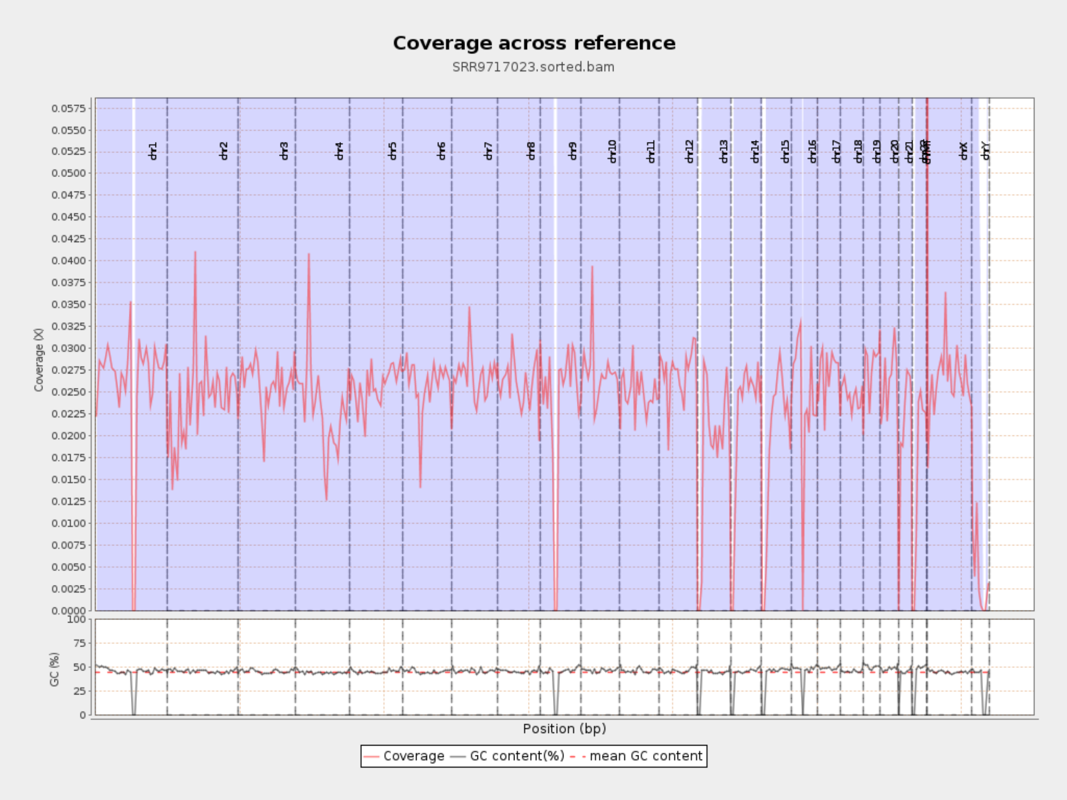
General error rate	0.51%
Mismatches	375,539
Insertions	3,646
Mapped reads with at least one insertion	0.28%
Deletions	10,963
Mapped reads with at least one deletion	0.83%
Homopolymer indels	41.77%

2.6. Chromosome stats

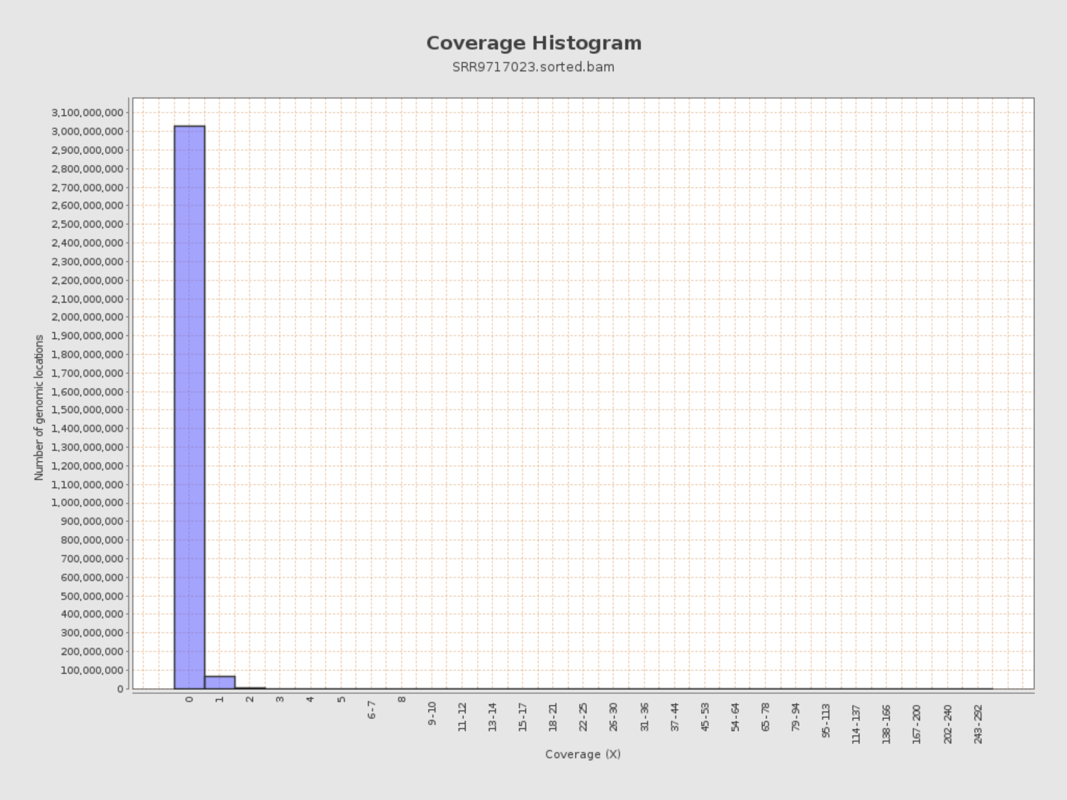
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6487790	0.026	0.2899
chr2	243199373	5883370	0.0242	0.2344
chr3	198022430	5125866	0.0259	0.1734
chr4	191154276	4465327	0.0234	0.1771
chr5	180915260	4675348	0.0258	0.1734
chr6	171115067	4418275	0.0258	0.1807
chr7	159138663	4272760	0.0268	0.2303

chr8	146364022	3797225	0.0259	0.1957
chr9	141213431	3311560	0.0235	0.2145
chr10	135534747	3684777	0.0272	0.2172
chr11	135006516	3376991	0.025	0.1996
chr12	133851895	3641450	0.0272	0.179
chr13	115169878	2125894	0.0185	0.1457
chr14	107349540	2313583	0.0216	0.1684
chr15	102531392	1964895	0.0192	0.1488
chr16	90354753	2152649	0.0238	0.177
chr17	81195210	2201741	0.0271	0.183
chr18	78077248	1920042	0.0246	0.3317
chr19	59128983	1650990	0.0279	0.2385
chr20	63025520	1644069	0.0261	0.1793
chr21	48129895	1020485	0.0212	0.1742
chr22	51304566	841420	0.0164	0.1384
chrMT	16571	8776	0.5296	0.7888
chrX	155270560	4108938	0.0265	0.1923
chrY	59373566	220075	0.0037	0.0915

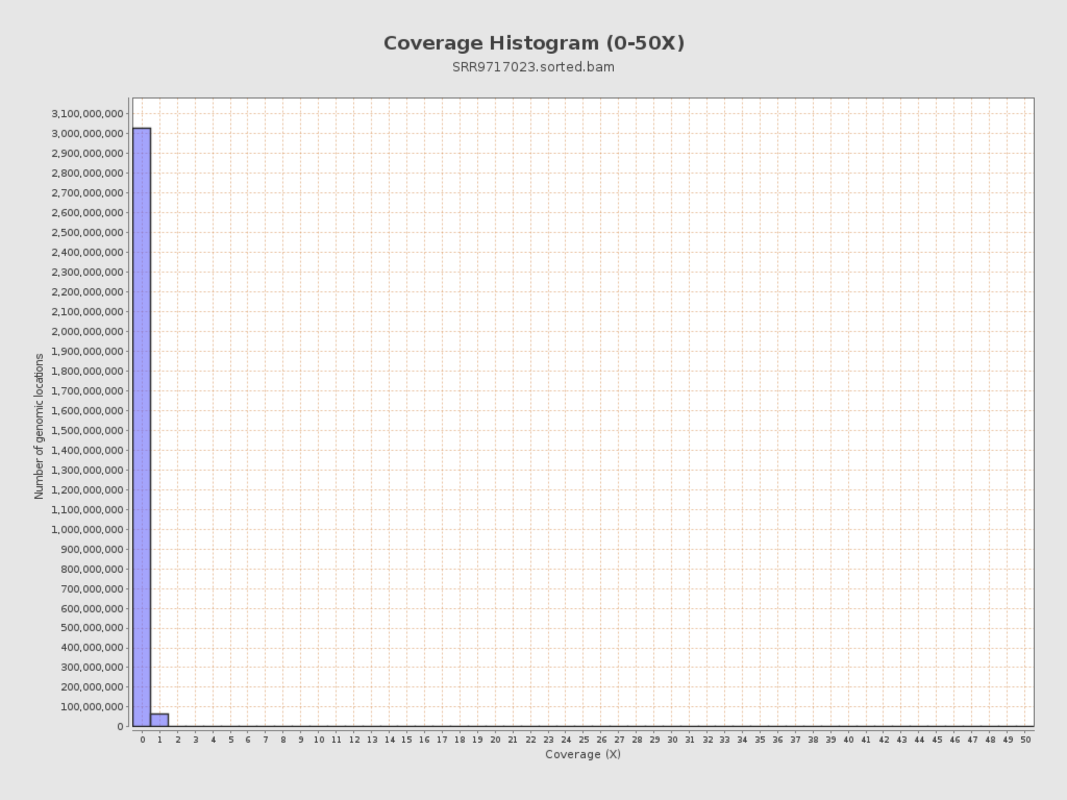
3. Results : Coverage across reference



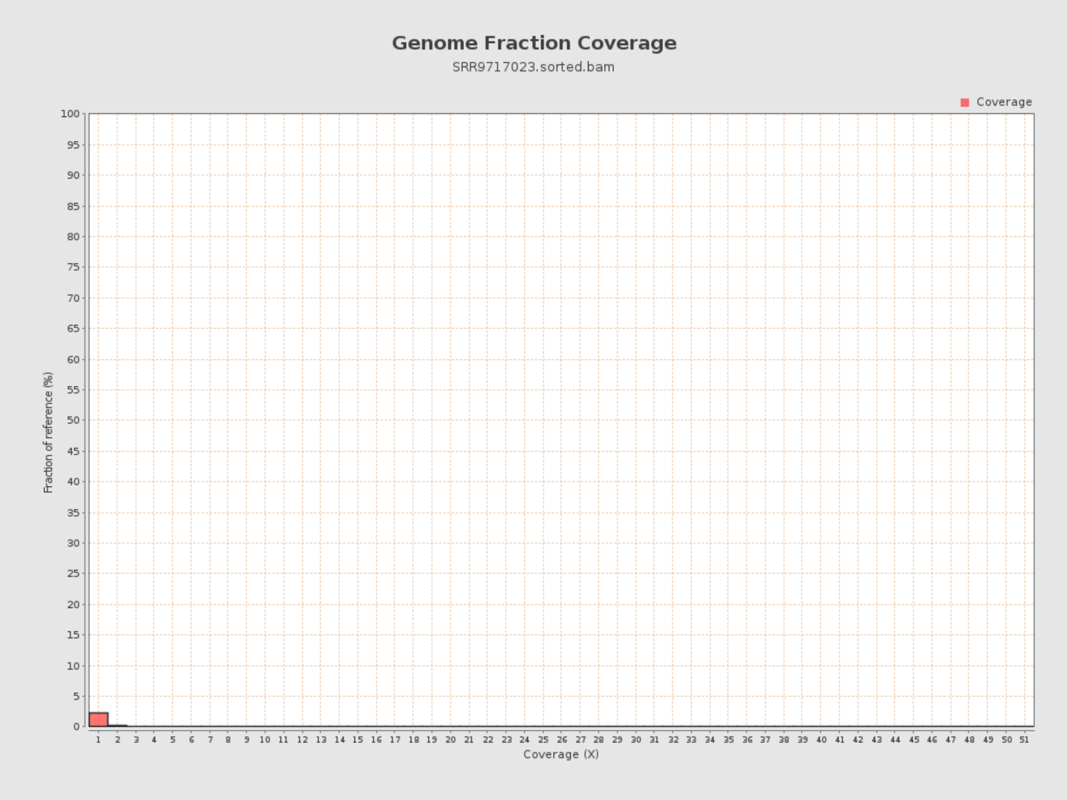
4. Results : Coverage Histogram



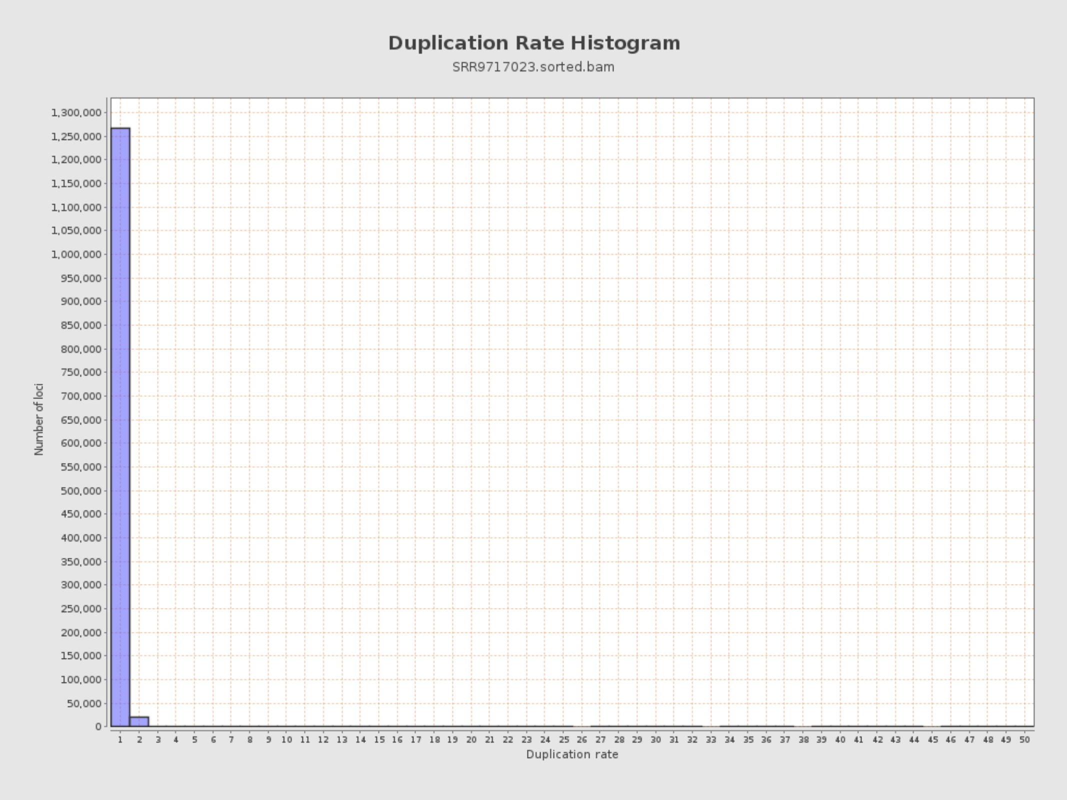
5. Results : Coverage Histogram (0-50X)



6. Results : Genome Fraction Coverage



7. Results : Duplication Rate Histogram



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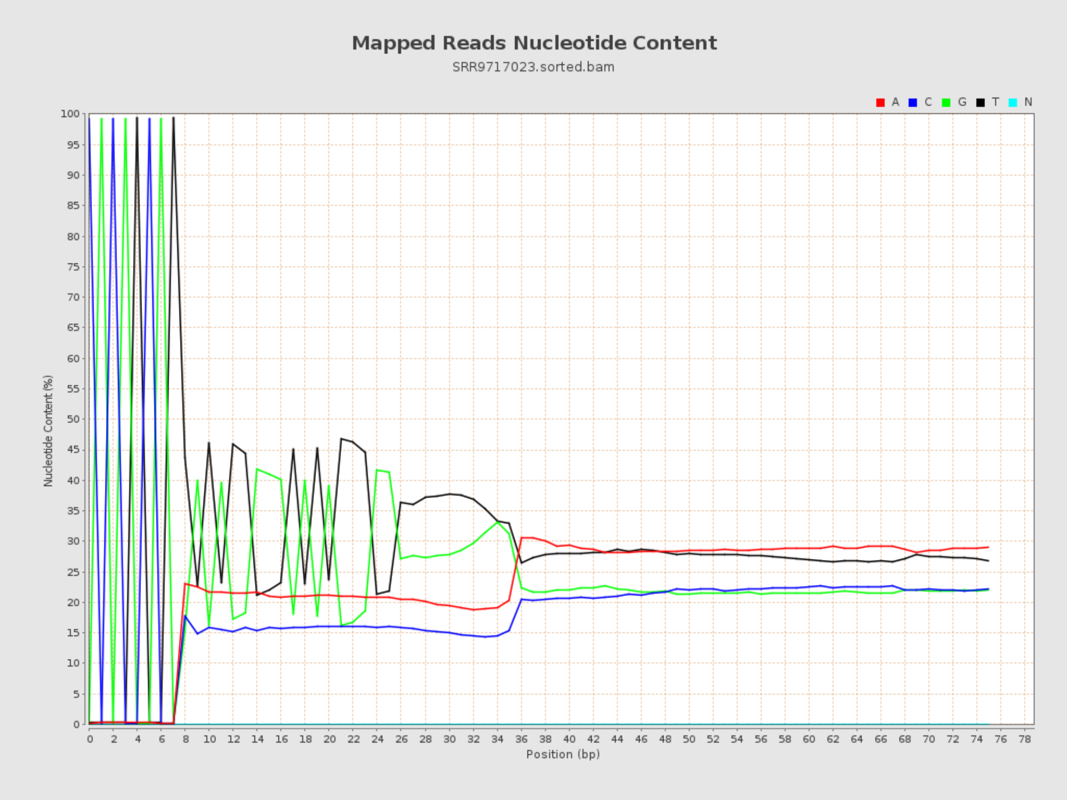
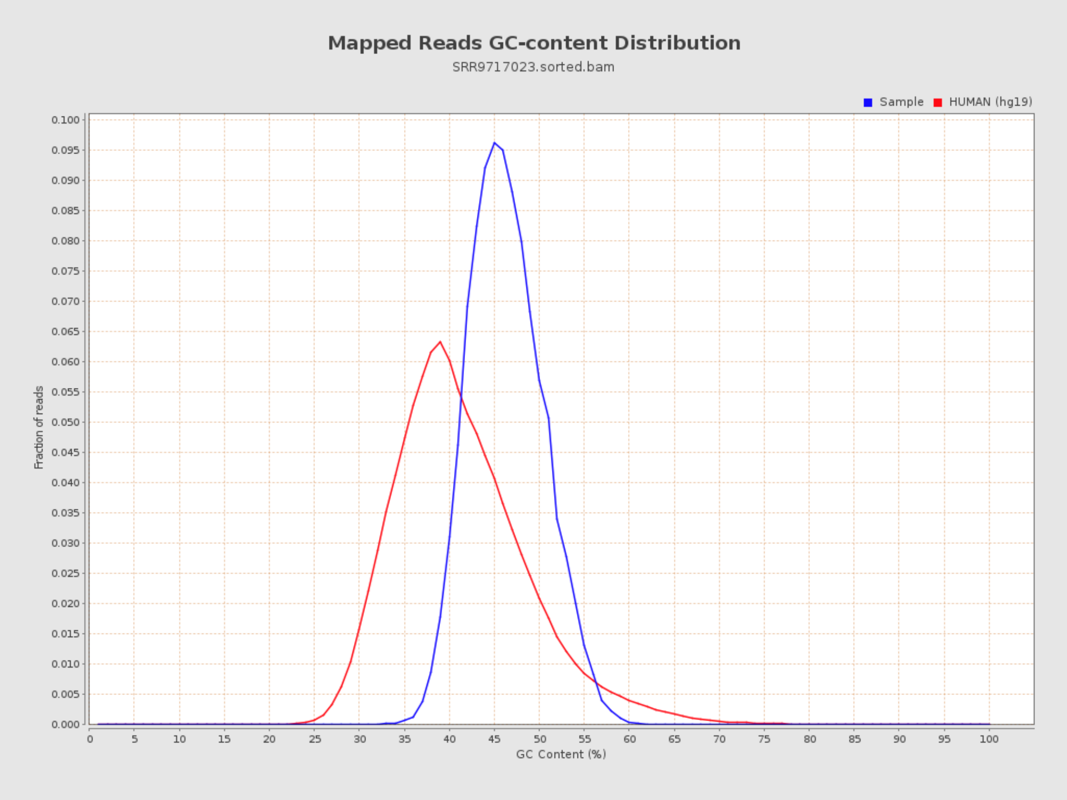
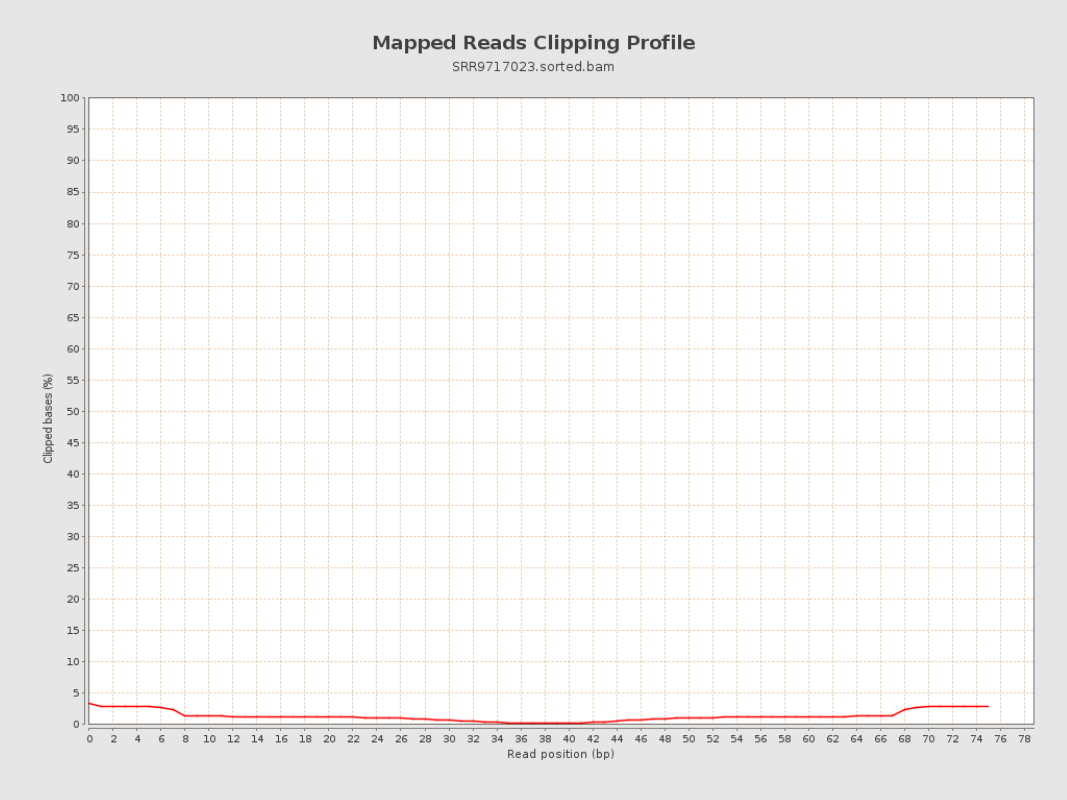
8. Results : Mapped Reads Nucleotide Content



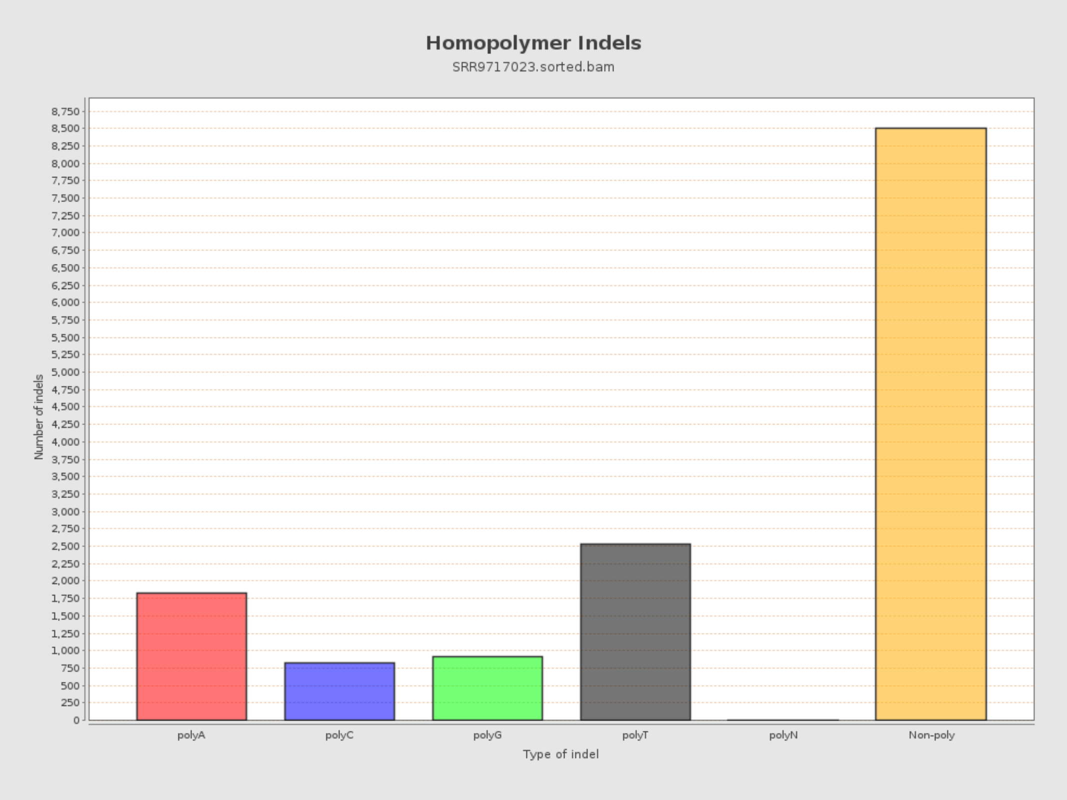
9. Results : Mapped Reads GC-content Distribution



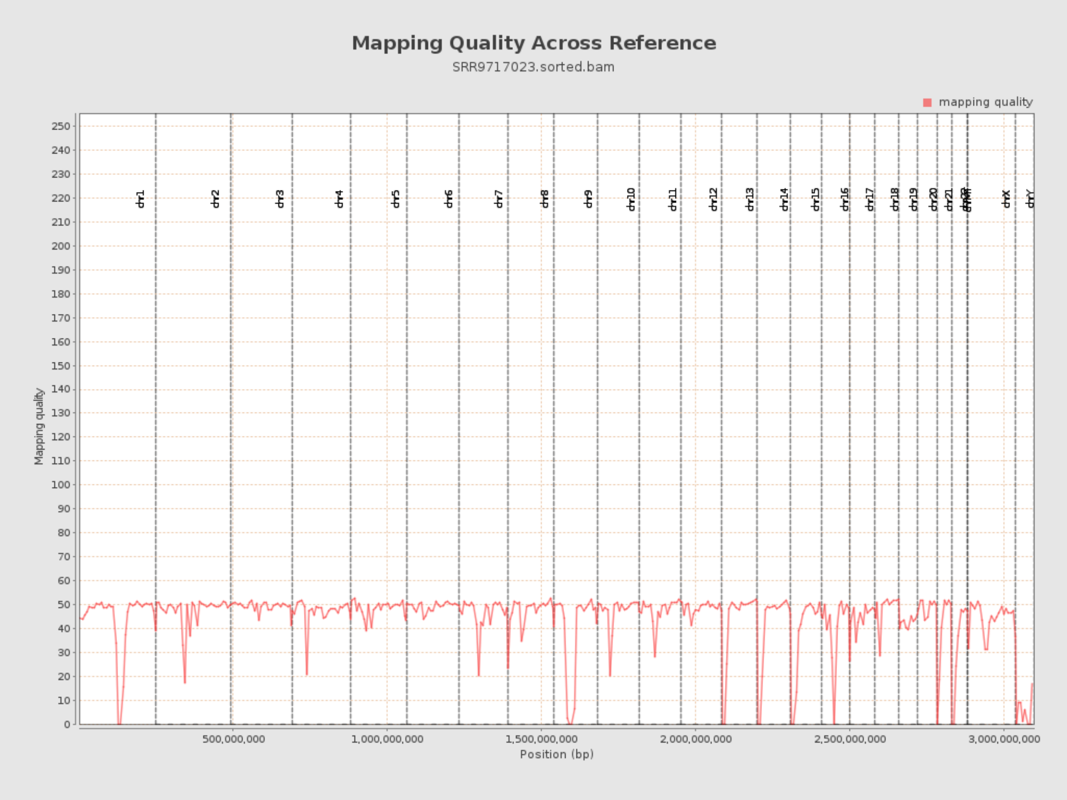
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram