Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 21:24:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2971320.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_SRR2971320 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2971320.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 21:24:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2971320.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	93,057,651
Mapped reads	72,420,823 / 77.82%
Unmapped reads	20,636,828 / 22.18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	11,078,470 / 11.9%
Duplication rate	11.92%
Clipped reads	6,665,813 / 7.16%

2.2. ACGT Content

Number/percentage of A's	818,613,323 / 28.62%
Number/percentage of C's	602,731,304 / 21.07%
Number/percentage of T's	827,294,799 / 28.92%
Number/percentage of G's	611,709,835 / 21.38%
Number/percentage of N's	146,972 / 0.01%
GC Percentage	42.46%

2.3. Coverage

Mean	0.9241
Standard Deviation	6.6047

2.4. Mapping Quality

Mean Mapping Quality	40.43

2.5. Mismatches and indels

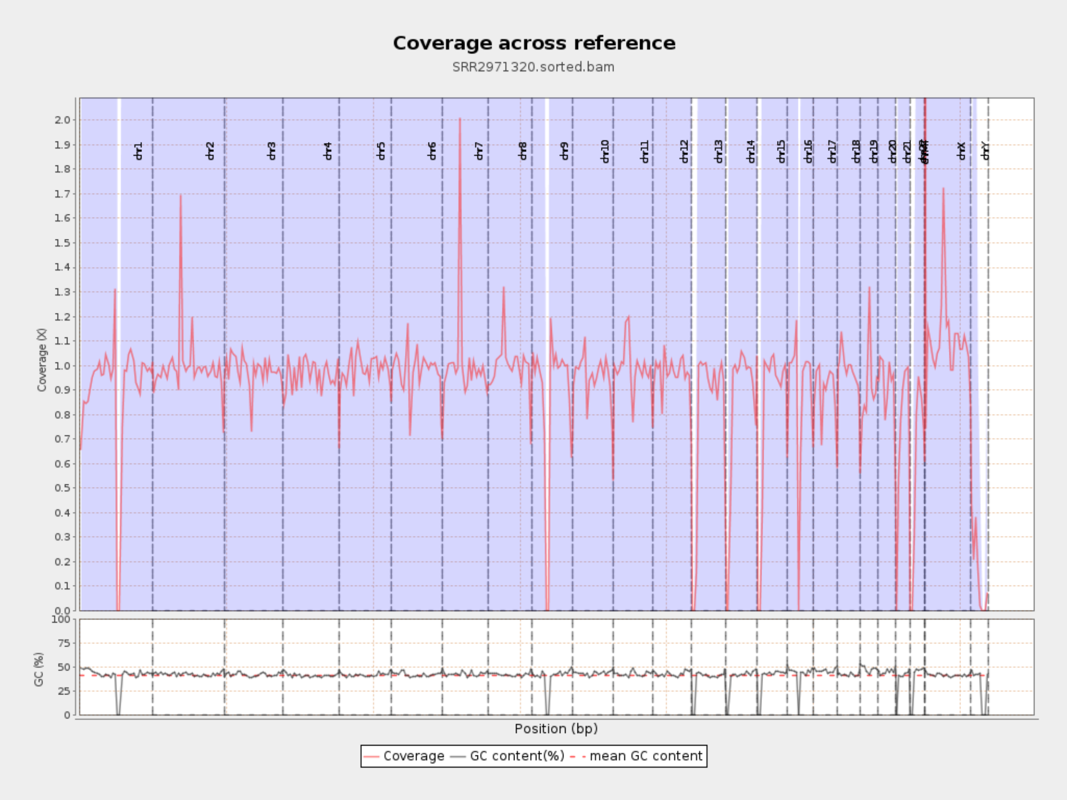
General error rate	0.32%
Mismatches	9,033,593
Insertions	104,678
Mapped reads with at least one insertion	0.14%
Deletions	222,899
Mapped reads with at least one deletion	0.31%
Homopolymer indels	39.76%

2.6. Chromosome stats

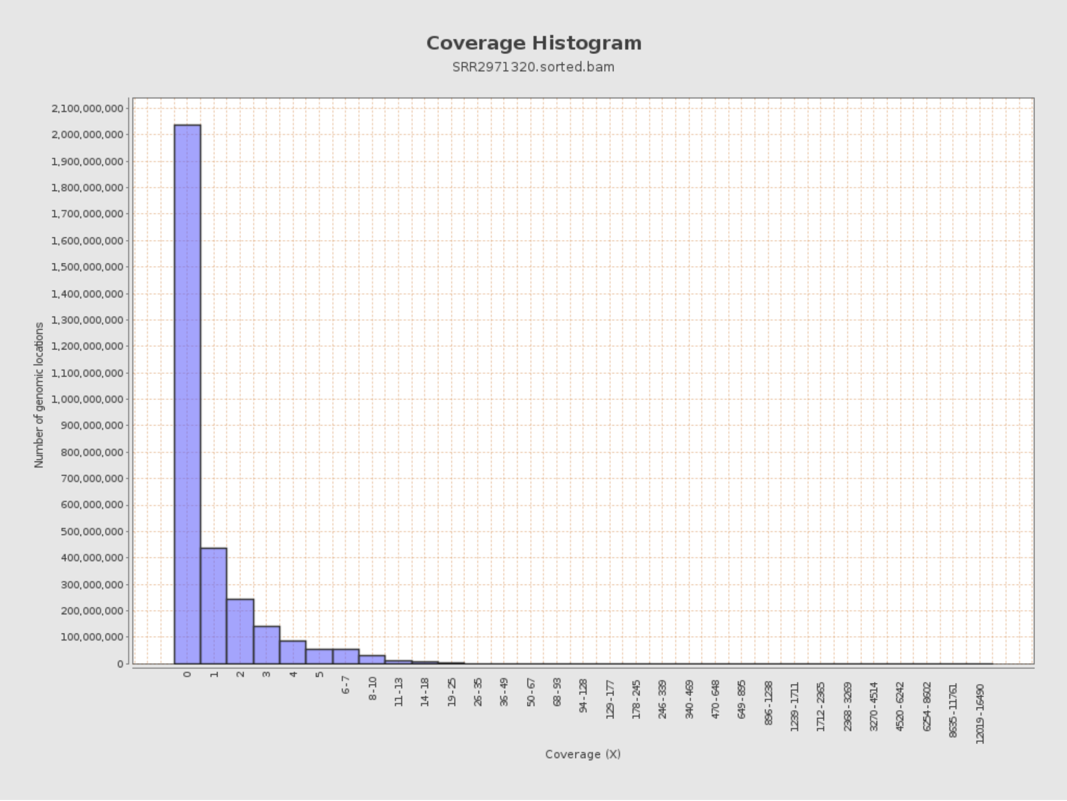
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	224312114	0.8999	8.9409
chr2	243199373	243032256	0.9993	7.0594
chr3	198022430	194152708	0.9805	2.1935
chr4	191154276	184234745	0.9638	2.2969
chr5	180915260	178069478	0.9843	2.4322
chr6	171115067	168515262	0.9848	3.496
chr7	159138663	161114449	1.0124	13.2801
chr8	146364022	146332297	0.9998	5.4997

chr9	141213431	120971273	0.8567	7.5786
chr10	135534747	130575679	0.9634	3.8396
chr11	135006516	132919234	0.9845	11.4977
chr12	133851895	129787757	0.9696	2.7163
chr13	115169878	91819338	0.7973	1.8253
chr14	107349540	87839780	0.8183	5.1802
chr15	102531392	82155958	0.8013	2.0015
chr16	90354753	78141855	0.8648	3.58
chr17	81195210	72158132	0.8887	3.8795
chr18	78077248	77185022	0.9886	15.6498
chr19	59128983	53195122	0.8996	9.9248
chr20	63025520	58132868	0.9224	2.4579
chr21	48129895	36089379	0.7498	3.2573
chr22	51304566	29659139	0.5781	3.0632
chrMT	16571	287432	17.3455	18.1626
chrX	155270560	171237669	1.1028	4.9991
chrY	59373566	8861260	0.1492	1.3479

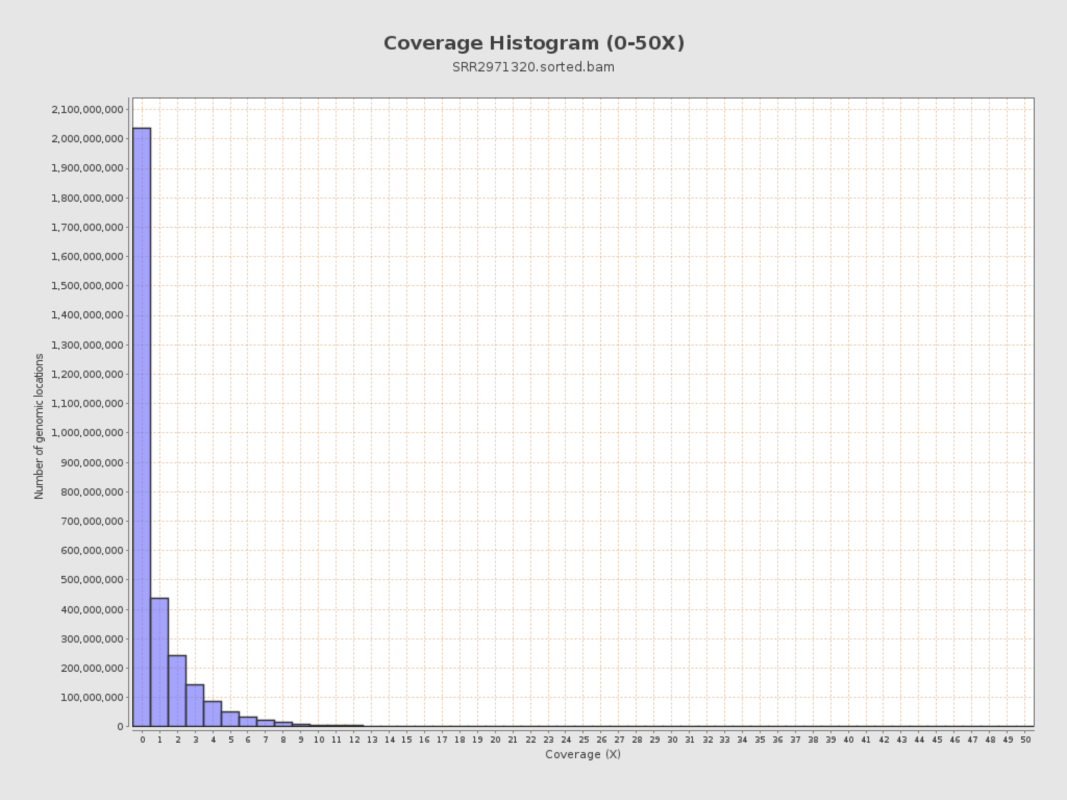
3. Results : Coverage across reference



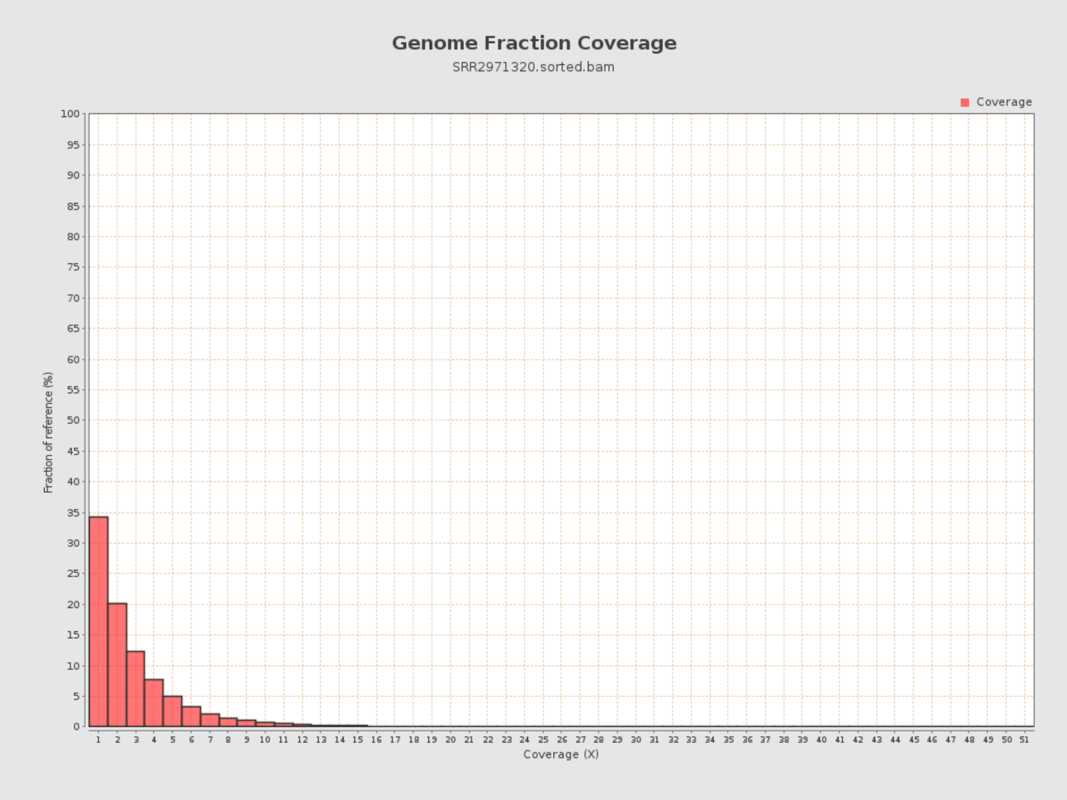
4. Results : Coverage Histogram



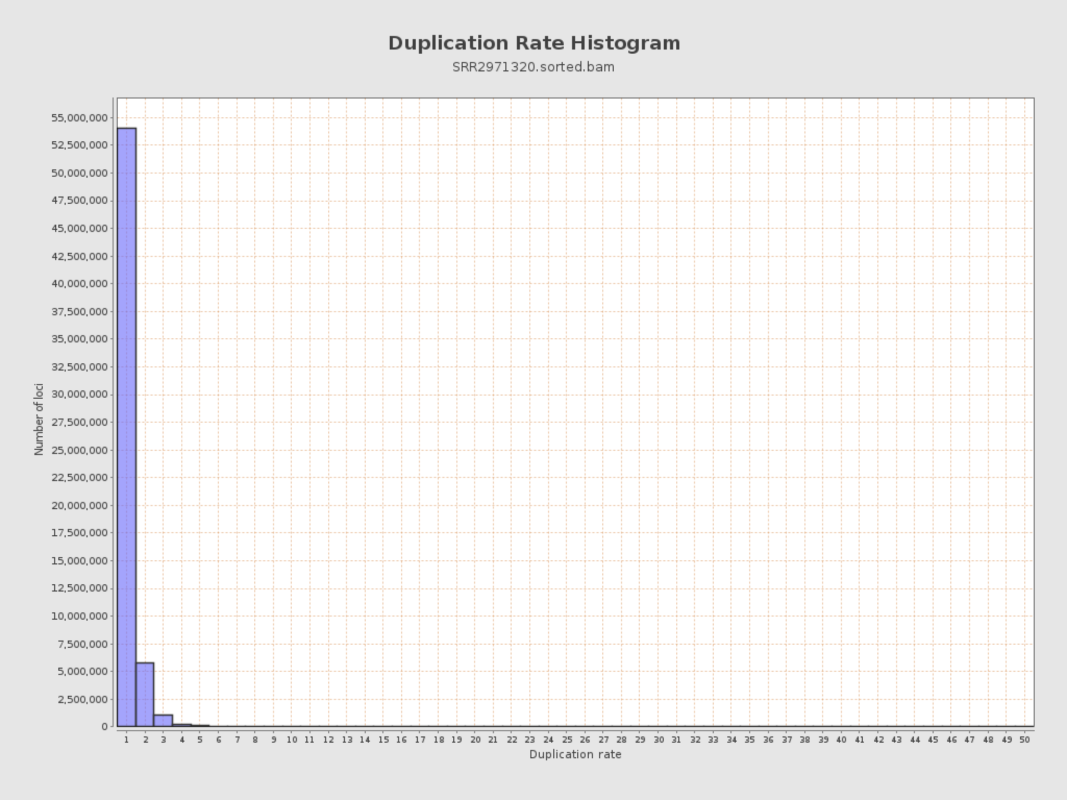
5. Results : Coverage Histogram (0-50X)



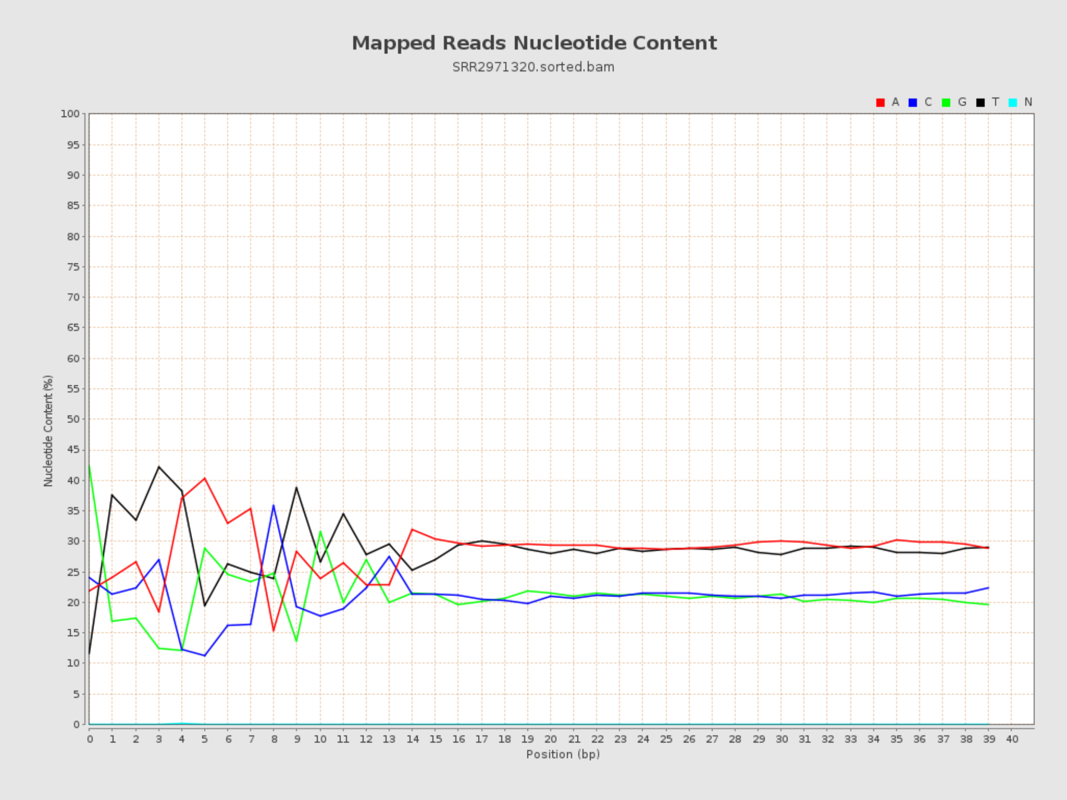
6. Results : Genome Fraction Coverage



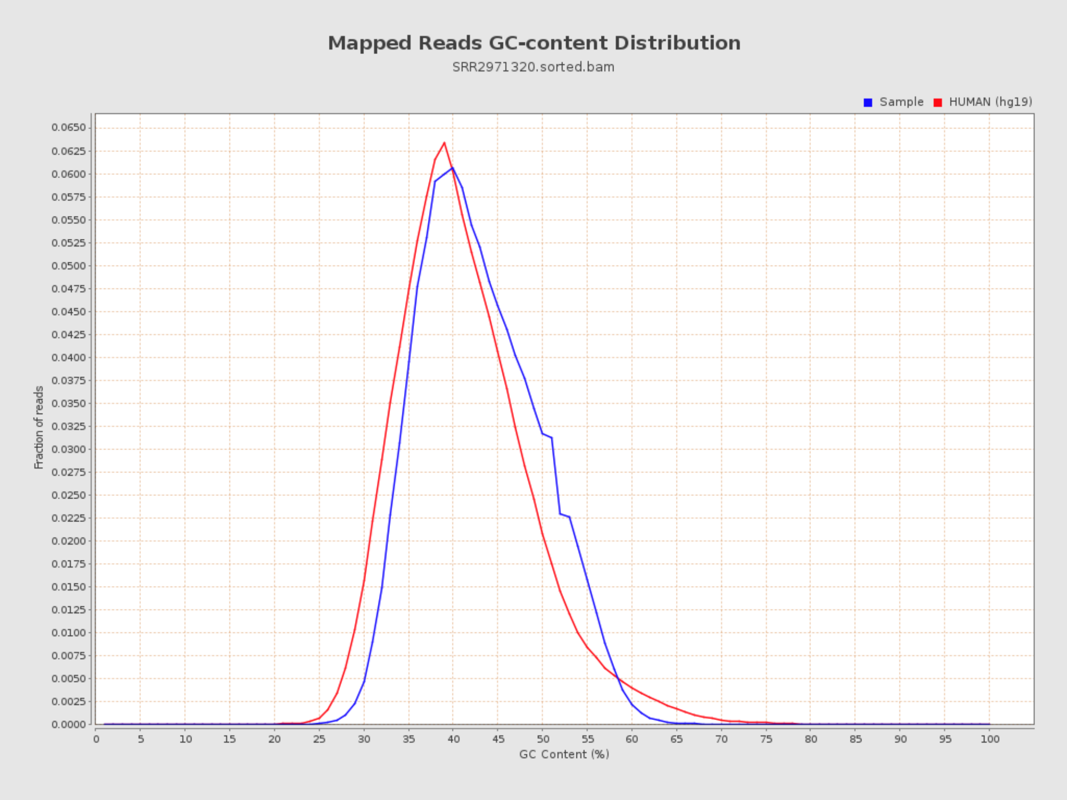
7. Results : Duplication Rate Histogram



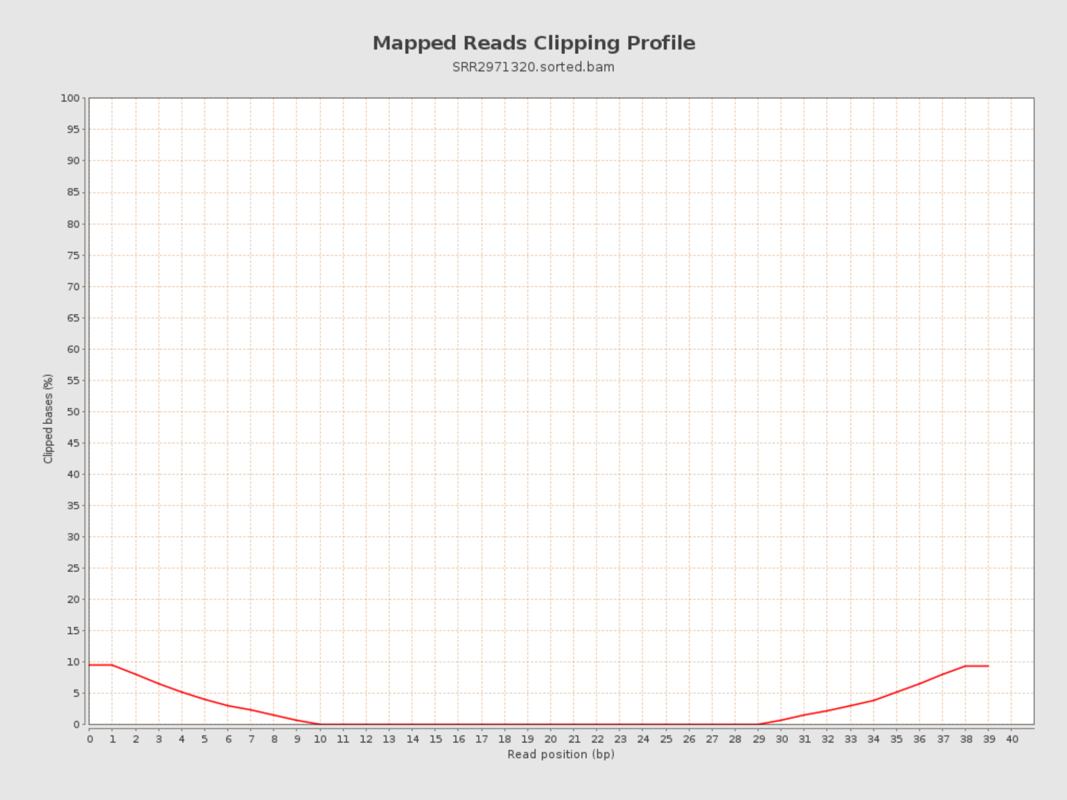
8. Results : Mapped Reads Nucleotide Content



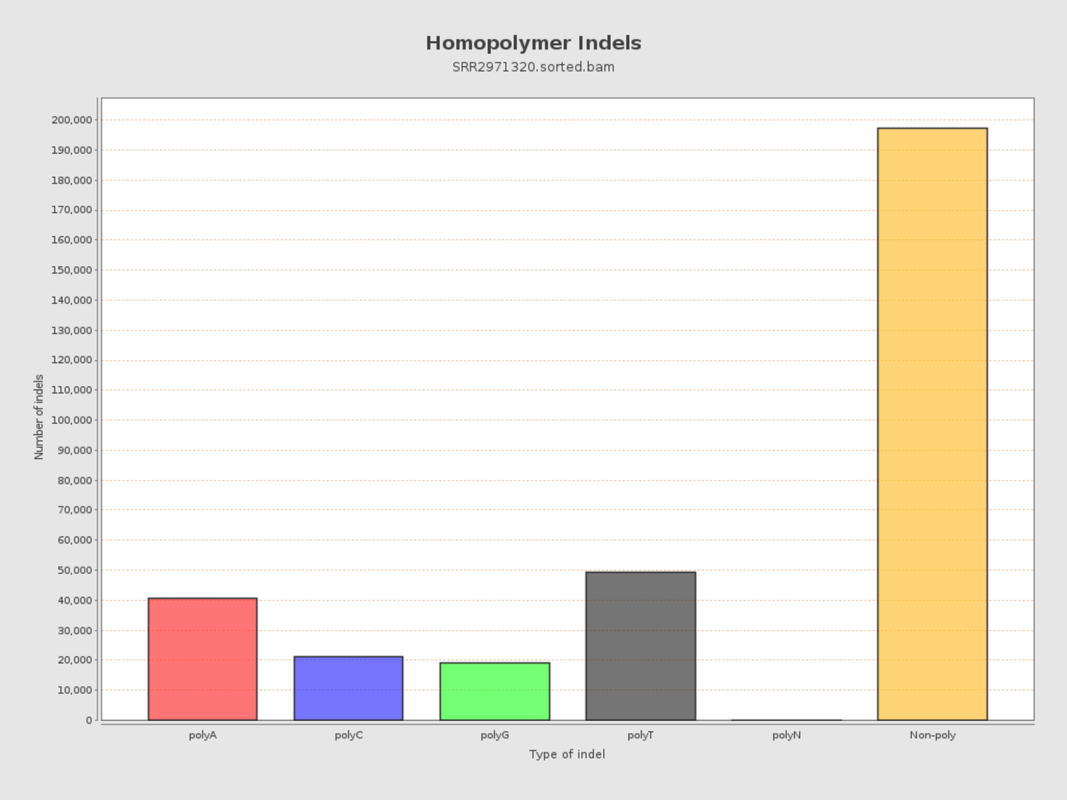
9. Results : Mapped Reads GC-content Distribution



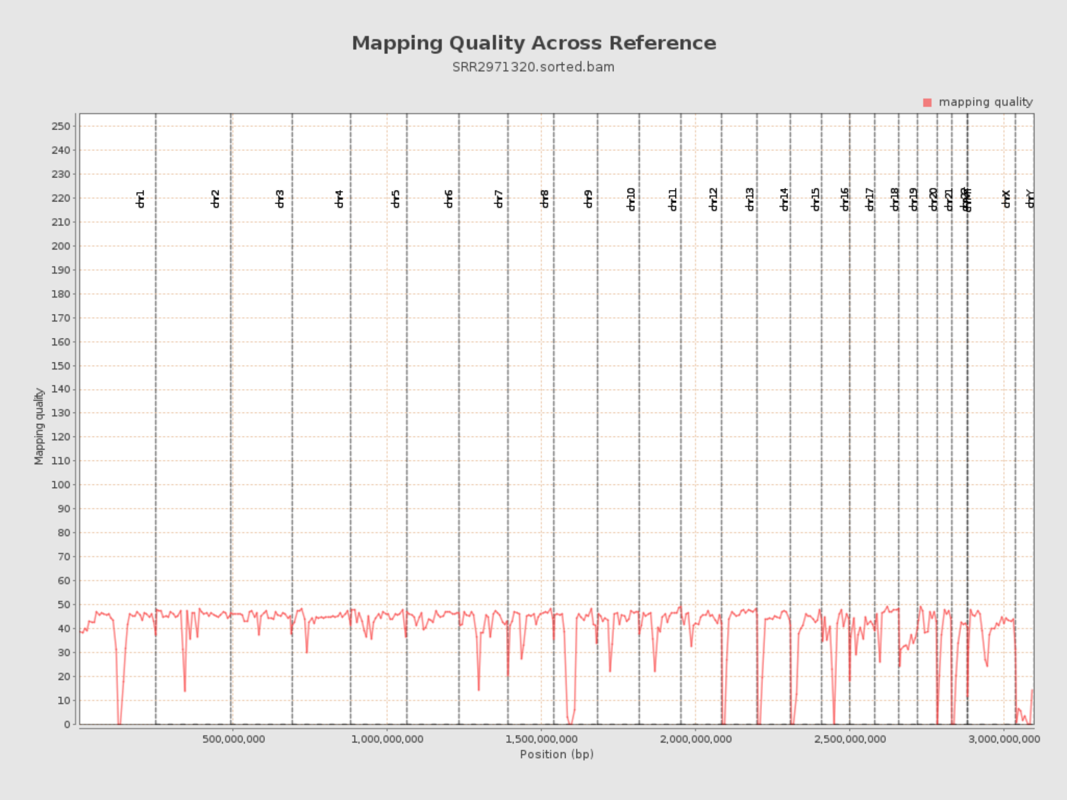
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram