Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 23:09:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2971322.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_SRR2971322 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2971322.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 23:09:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2971322.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	73,411,052
Mapped reads	63,776,737 / 86.88%
Unmapped reads	9,634,315 / 13.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	10,351,204 / 14.1%
Duplication rate	13.46%
Clipped reads	3,927,563 / 5.35%

2.2. ACGT Content

Number/percentage of A's	750,292,841 / 29.67%
Number/percentage of C's	508,485,074 / 20.11%
Number/percentage of T's	754,271,035 / 29.83%
Number/percentage of G's	515,361,299 / 20.38%
Number/percentage of N's	71,658 / 0%
GC Percentage	40.49%

2.3. Coverage

Mean	0.8169
Standard Deviation	4.8463

2.4. Mapping Quality

Mean Mapping Quality	43.6

2.5. Mismatches and indels

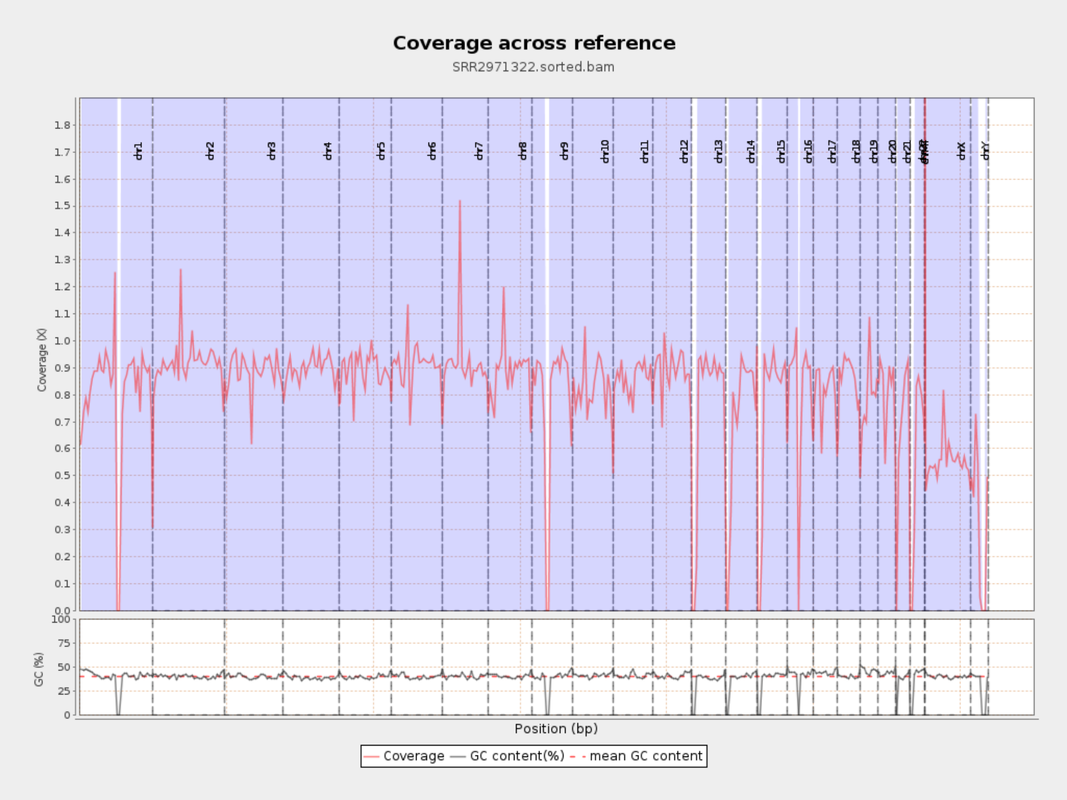
General error rate	0.27%
Mismatches	6,717,199
Insertions	77,057
Mapped reads with at least one insertion	0.12%
Deletions	234,659
Mapped reads with at least one deletion	0.37%
Homopolymer indels	46.39%

2.6. Chromosome stats

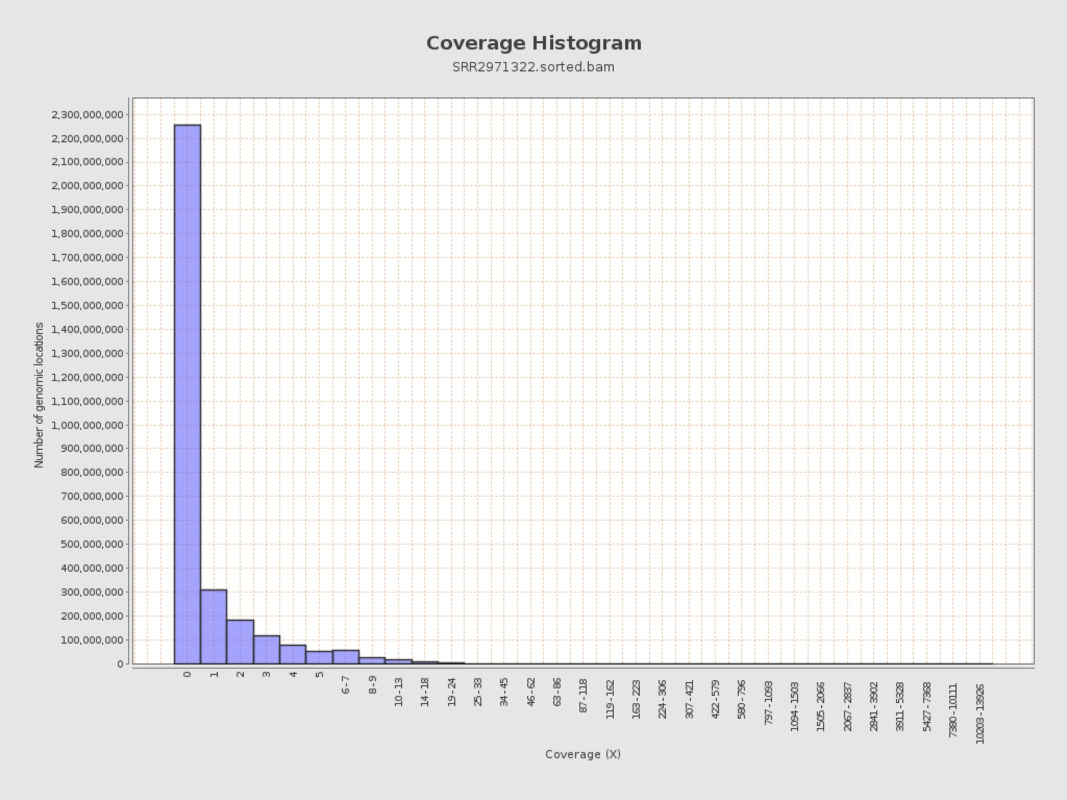
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	200972734	0.8063	9.7018
chr2	243199373	224641551	0.9237	4.3366
chr3	198022430	175821394	0.8879	2.1342
chr4	191154276	172002682	0.8998	2.2734
chr5	180915260	160933480	0.8896	2.2436
chr6	171115067	156976821	0.9174	3.3986
chr7	159138663	146545212	0.9209	8.7794
chr8	146364022	129873304	0.8873	6.8844

chr9	141213431	108751750	0.7701	3.923
chr10	135534747	112811464	0.8323	3.342
chr11	135006516	115659877	0.8567	4.0988
chr12	133851895	119434389	0.8923	2.3743
chr13	115169878	86249842	0.7489	1.9054
chr14	107349540	74639366	0.6953	2.8028
chr15	102531392	74099872	0.7227	1.8951
chr16	90354753	71140023	0.7873	2.4815
chr17	81195210	65354719	0.8049	2.5638
chr18	78077248	67808396	0.8685	8.0556
chr19	59128983	46554998	0.7873	7.9502
chr20	63025520	51243584	0.8131	2.2579
chr21	48129895	32764803	0.6808	2.5522
chr22	51304566	28375866	0.5531	2.149
chrMT	16571	50569	3.0517	3.5858
chrX	155270560	86185927	0.5551	2.7402
chrY	59373566	19886971	0.3349	2.5244

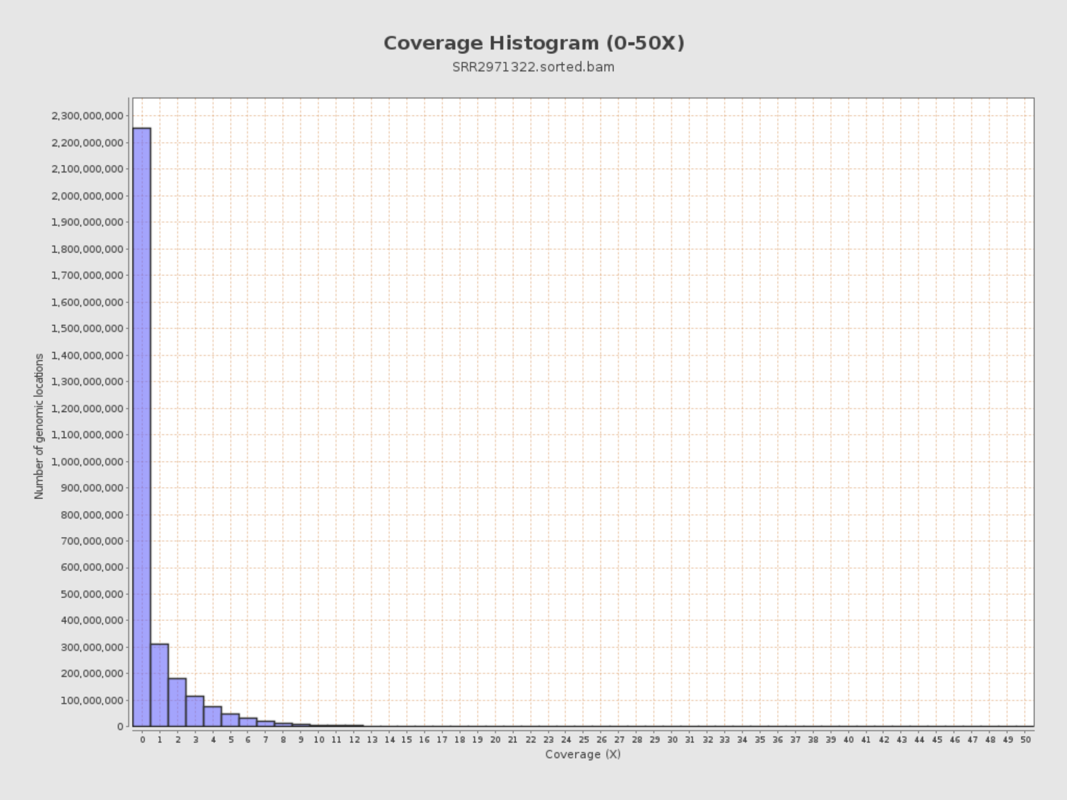
3. Results : Coverage across reference



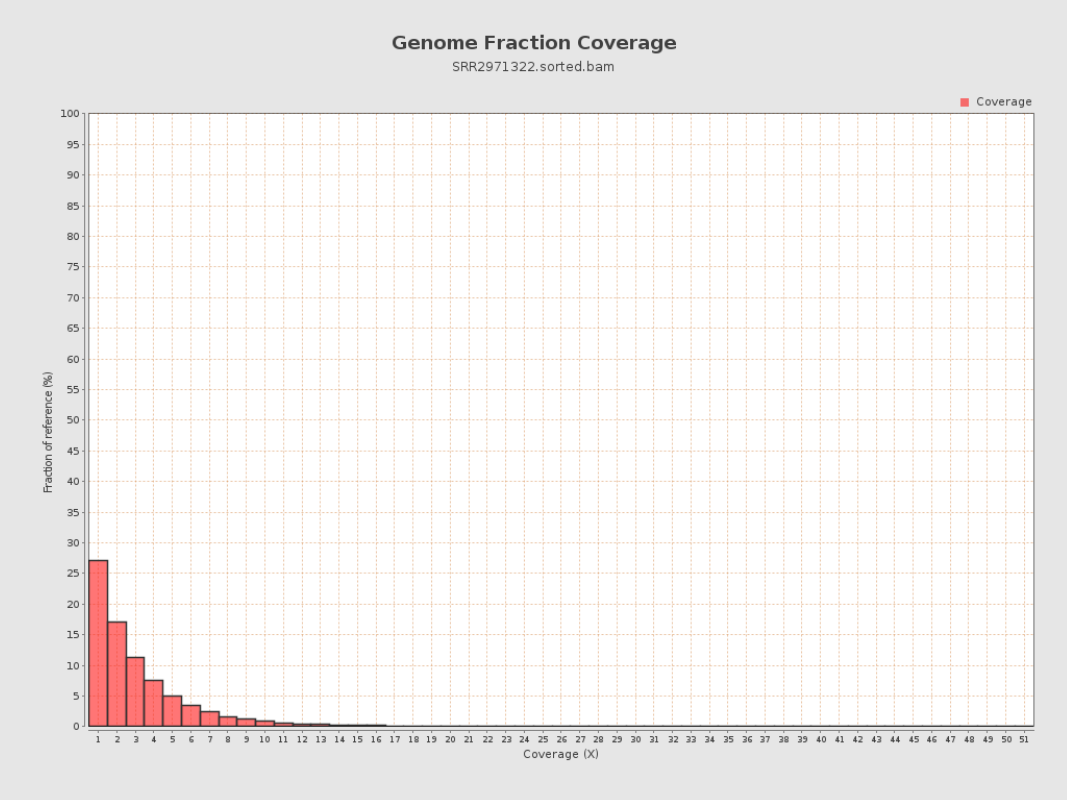
4. Results : Coverage Histogram



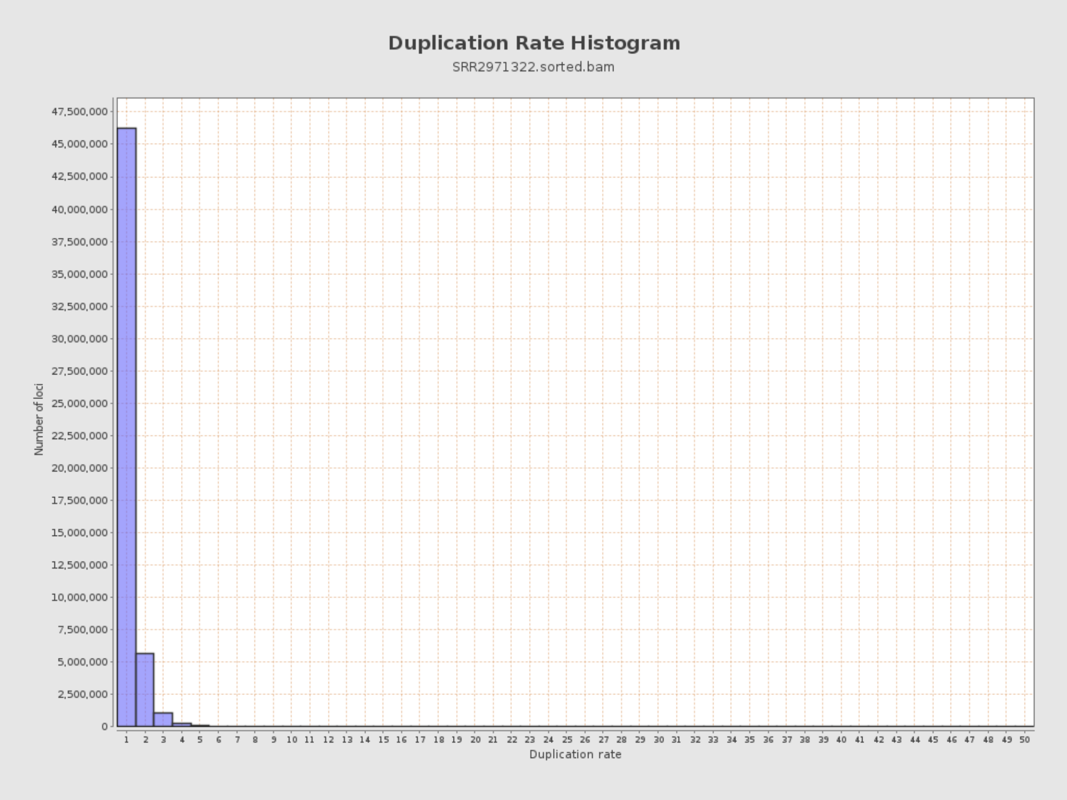
5. Results : Coverage Histogram (0-50X)



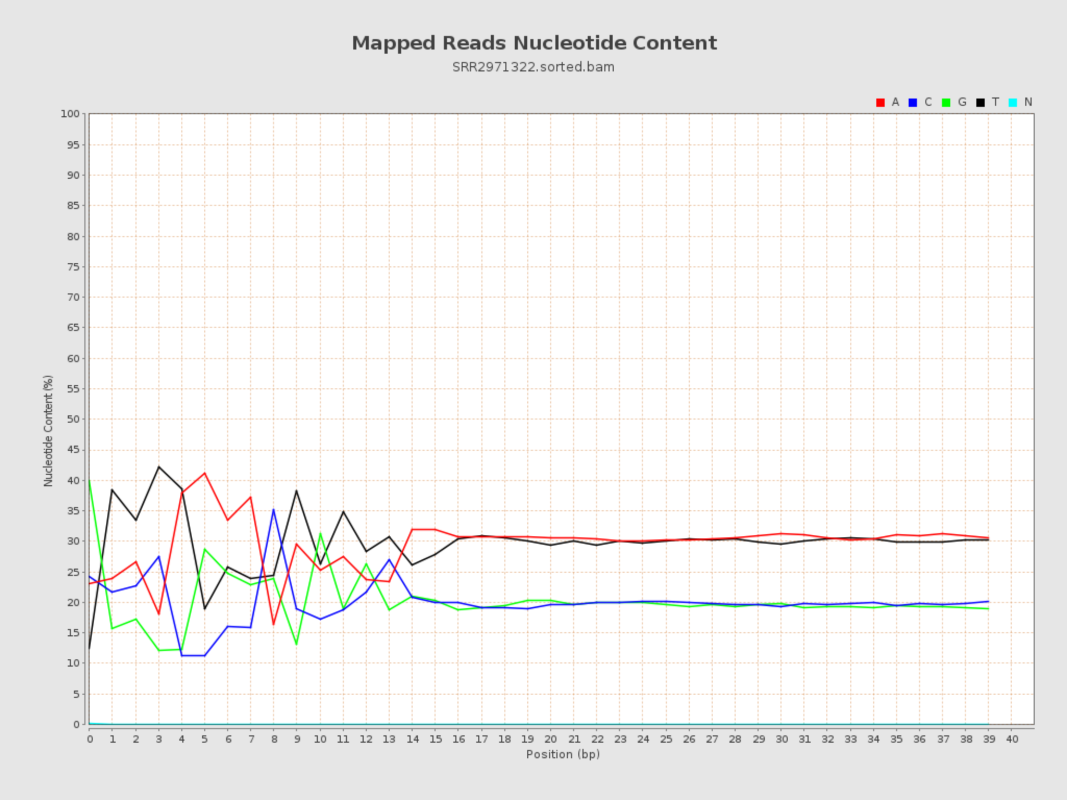
6. Results : Genome Fraction Coverage



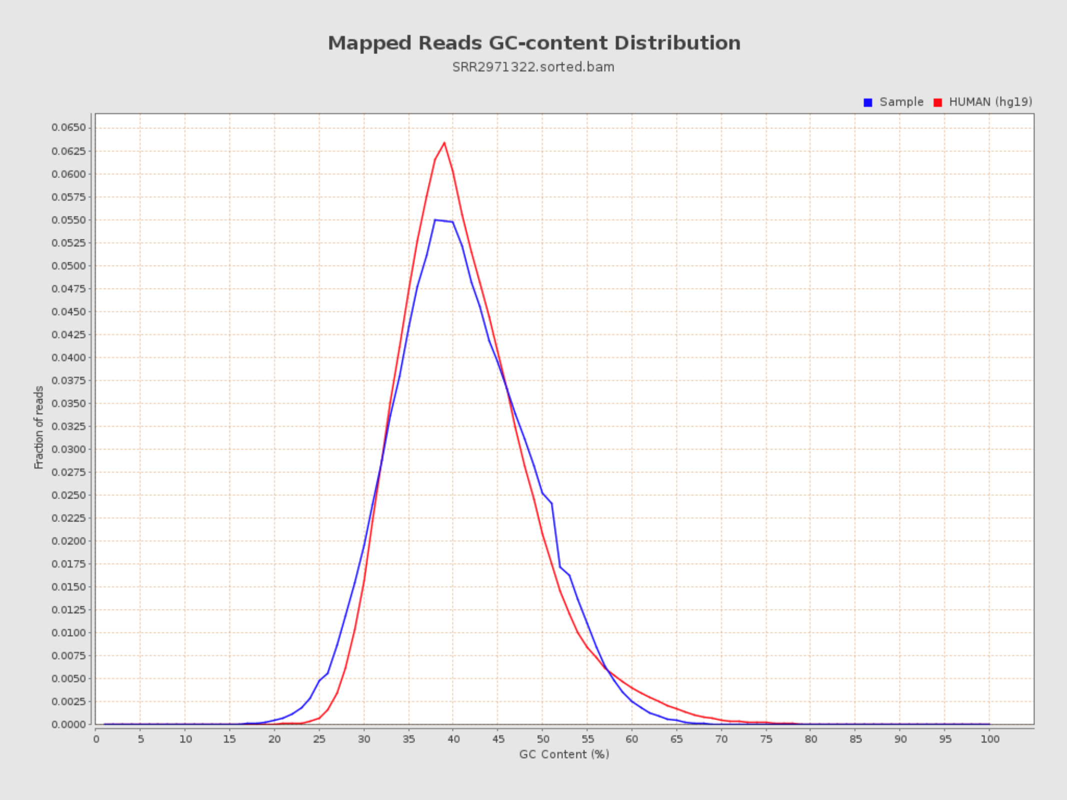
7. Results : Duplication Rate Histogram



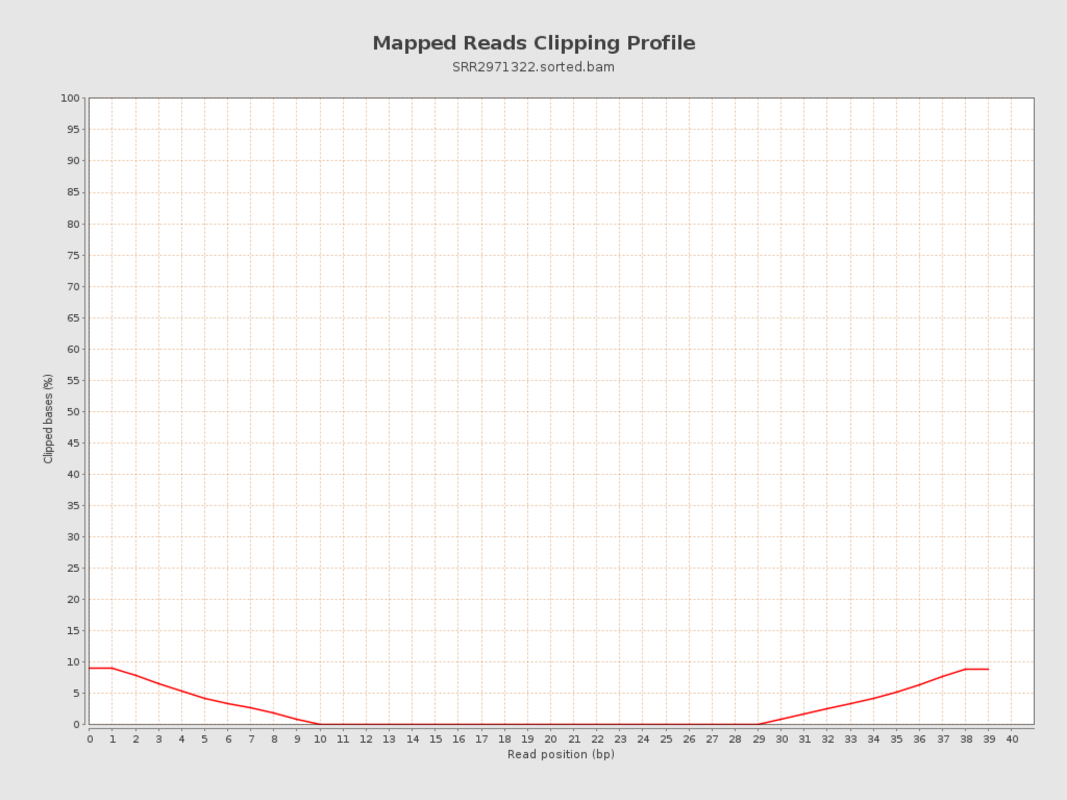
8. Results : Mapped Reads Nucleotide Content



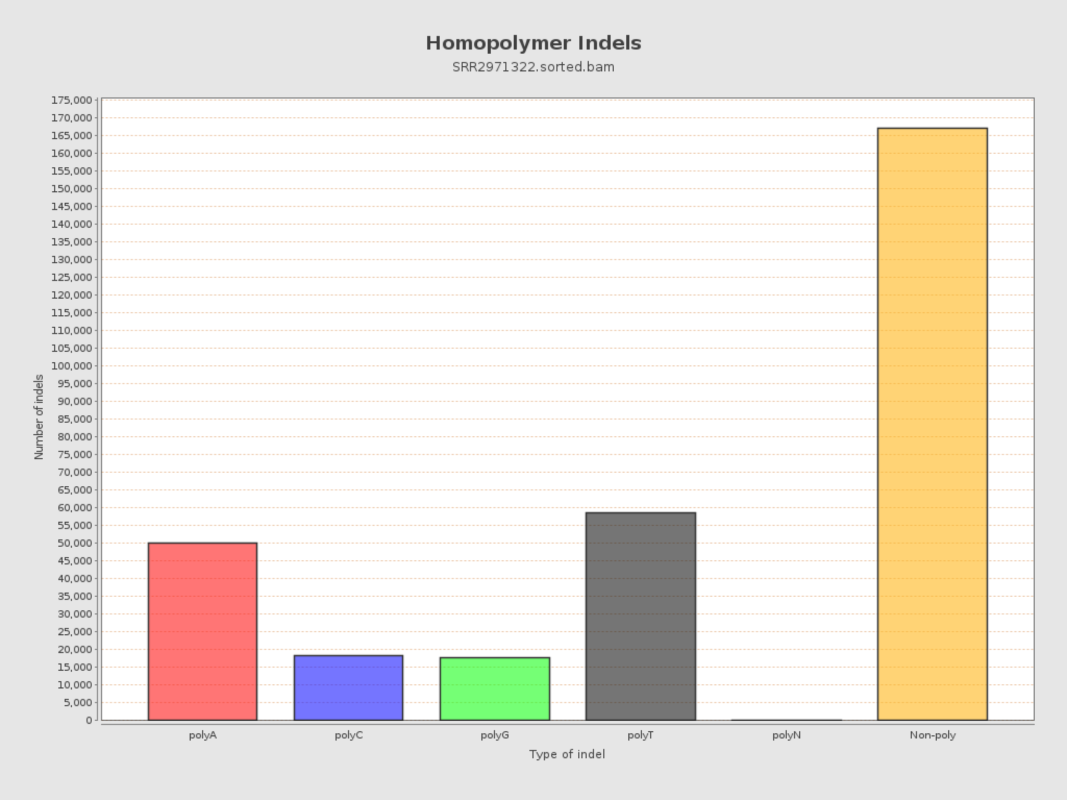
9. Results : Mapped Reads GC-content Distribution



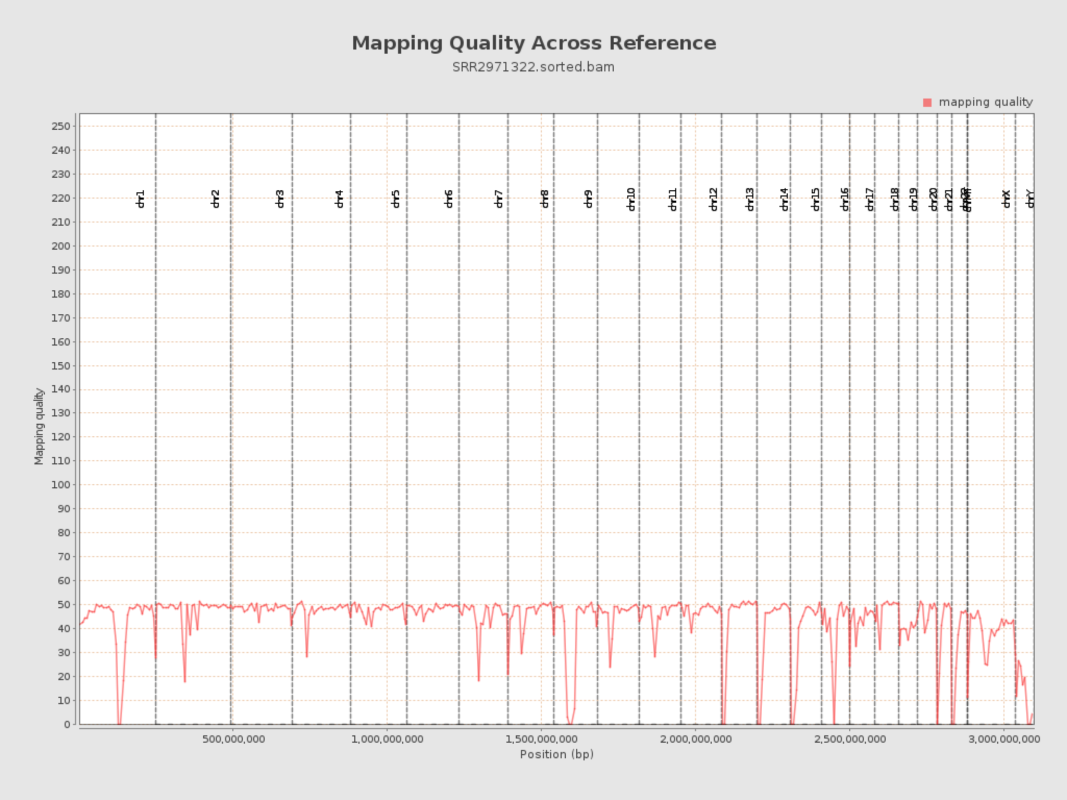
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram