Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 15:12:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2971294.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_SRR2971294 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2971294.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 15:12:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2971294.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,901,804
Mapped reads	14,693,137 / 86.93%
Unmapped reads	2,208,667 / 13.07%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	1,339,754 / 7.93%
Duplication rate	7.3%
Clipped reads	1,219,307 / 7.21%

2.2. ACGT Content

Number/percentage of A's	169,370,363 / 29.18%
Number/percentage of C's	117,751,127 / 20.29%
Number/percentage of T's	172,311,564 / 29.69%
Number/percentage of G's	120,992,255 / 20.85%
Number/percentage of N's	9,945 / 0%
GC Percentage	41.13%

2.3. Coverage

Mean	0.1875
Standard Deviation	1.8182

2.4. Mapping Quality

Mean Mapping Quality	40.6

2.5. Mismatches and indels

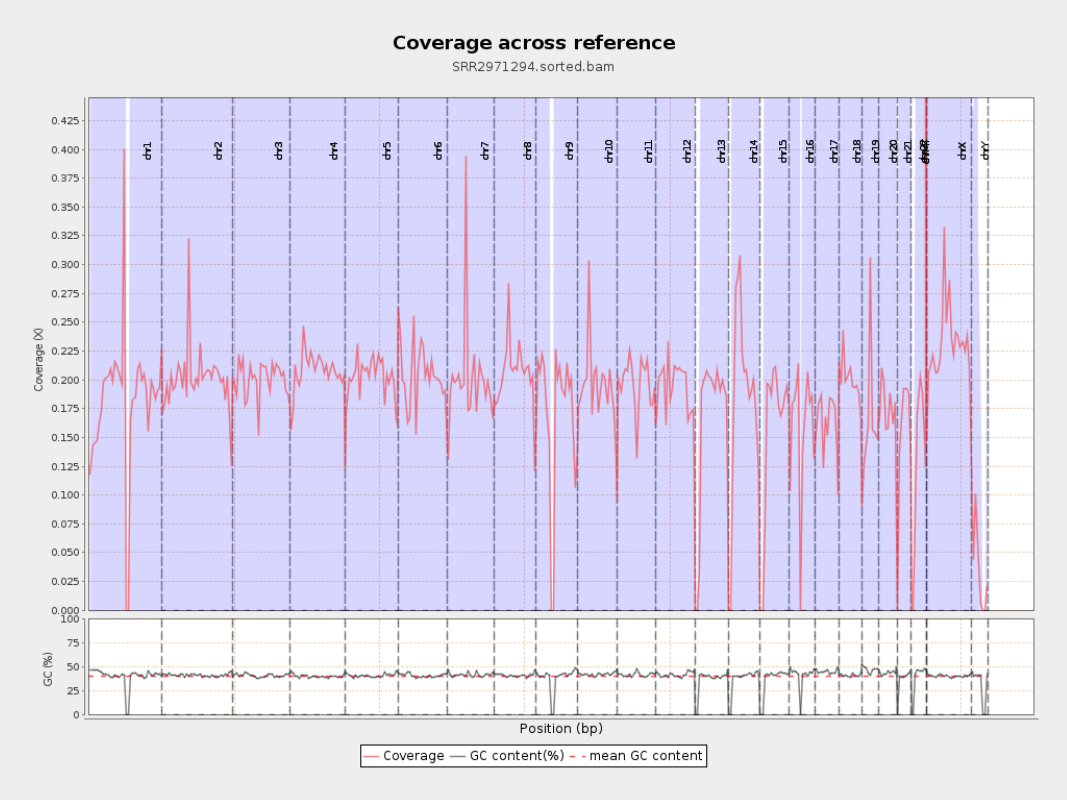
General error rate	0.27%
Mismatches	1,564,543
Insertions	17,081
Mapped reads with at least one insertion	0.12%
Deletions	39,153
Mapped reads with at least one deletion	0.27%
Homopolymer indels	40.58%

2.6. Chromosome stats

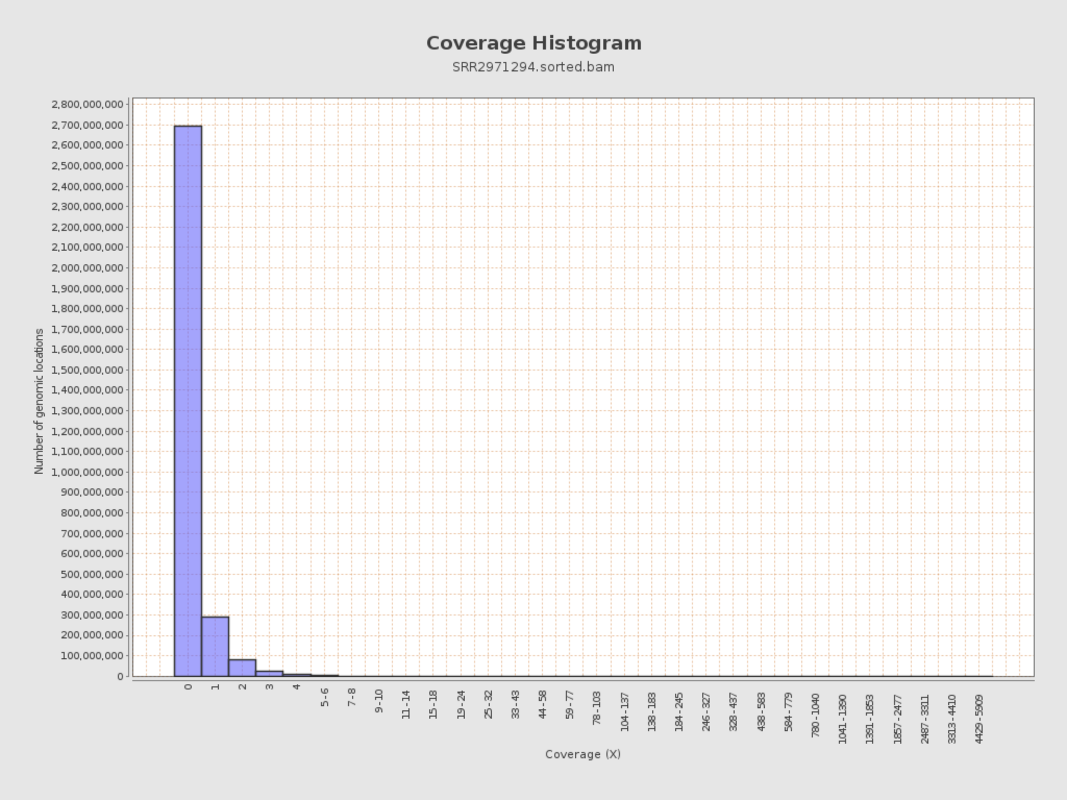
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	45256390	0.1816	4.4272
chr2	243199373	48949805	0.2013	1.3026
chr3	198022430	39782634	0.2009	0.6263
chr4	191154276	39690428	0.2076	0.7034
chr5	180915260	36684920	0.2028	0.6664
chr6	171115067	34979087	0.2044	0.8391
chr7	159138663	32160663	0.2021	2.3727
chr8	146364022	30059460	0.2054	2.1429

chr9	141213431	24064348	0.1704	1.3092
chr10	135534747	26546096	0.1959	1.3134
chr11	135006516	26333253	0.1951	1.2711
chr12	133851895	25942325	0.1938	0.691
chr13	115169878	18793145	0.1632	0.532
chr14	107349540	19703749	0.1835	0.9022
chr15	102531392	15803198	0.1541	0.5462
chr16	90354753	14421471	0.1596	0.774
chr17	81195210	13117381	0.1616	0.6968
chr18	78077248	15671932	0.2007	3.3562
chr19	59128983	9886645	0.1672	3.9009
chr20	63025520	10942400	0.1736	0.6612
chr21	48129895	7409233	0.1539	0.7258
chr22	51304566	6351126	0.1238	0.4624
chrMT	16571	93892	5.666	5.805
chrX	155270560	35764903	0.2303	0.9346
chrY	59373566	2077947	0.035	0.4163

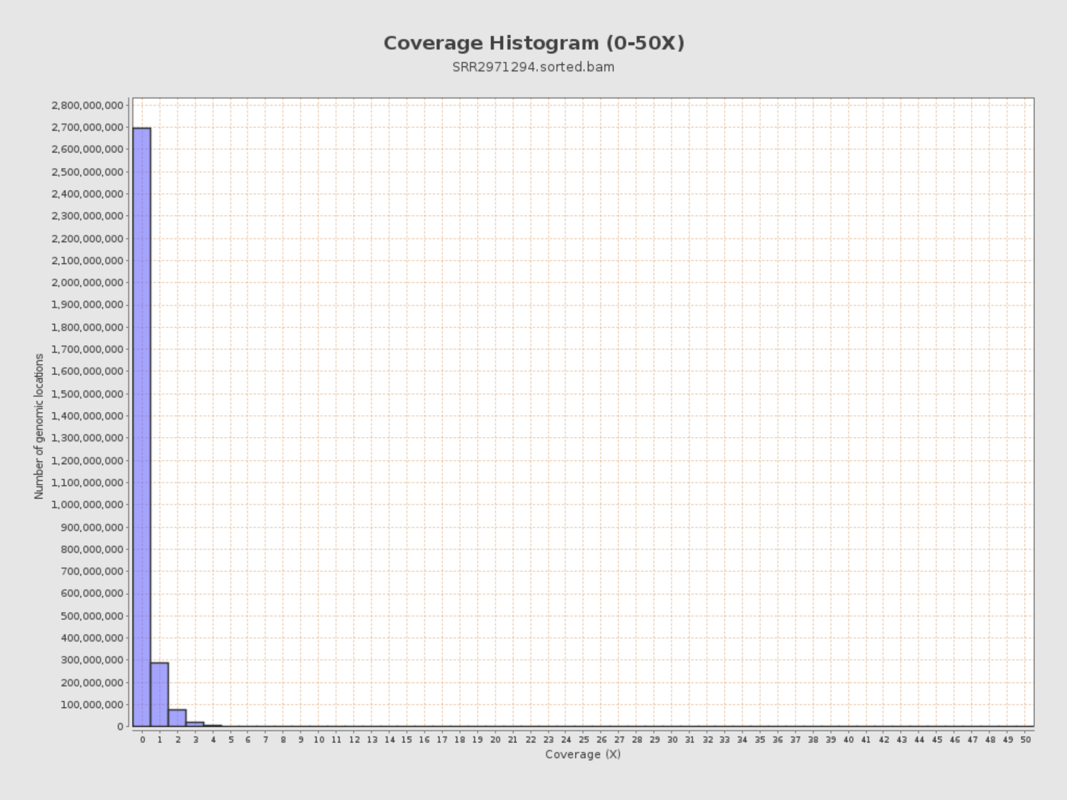
3. Results : Coverage across reference



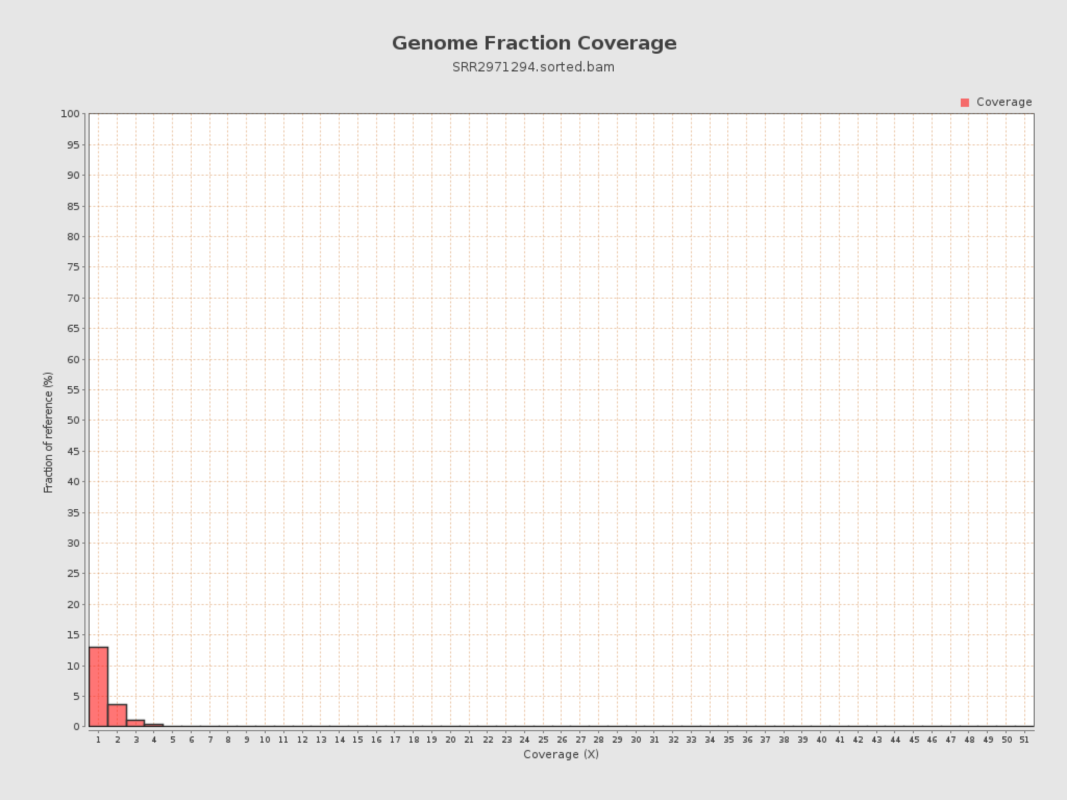
4. Results : Coverage Histogram



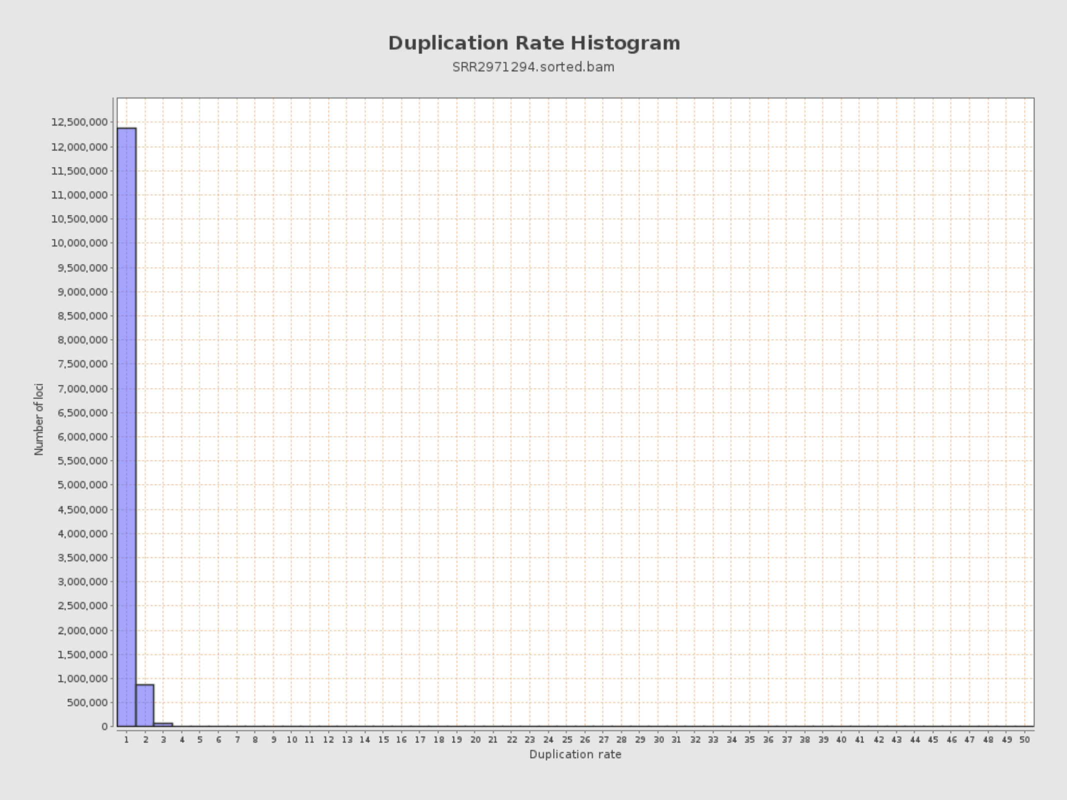
5. Results : Coverage Histogram (0-50X)



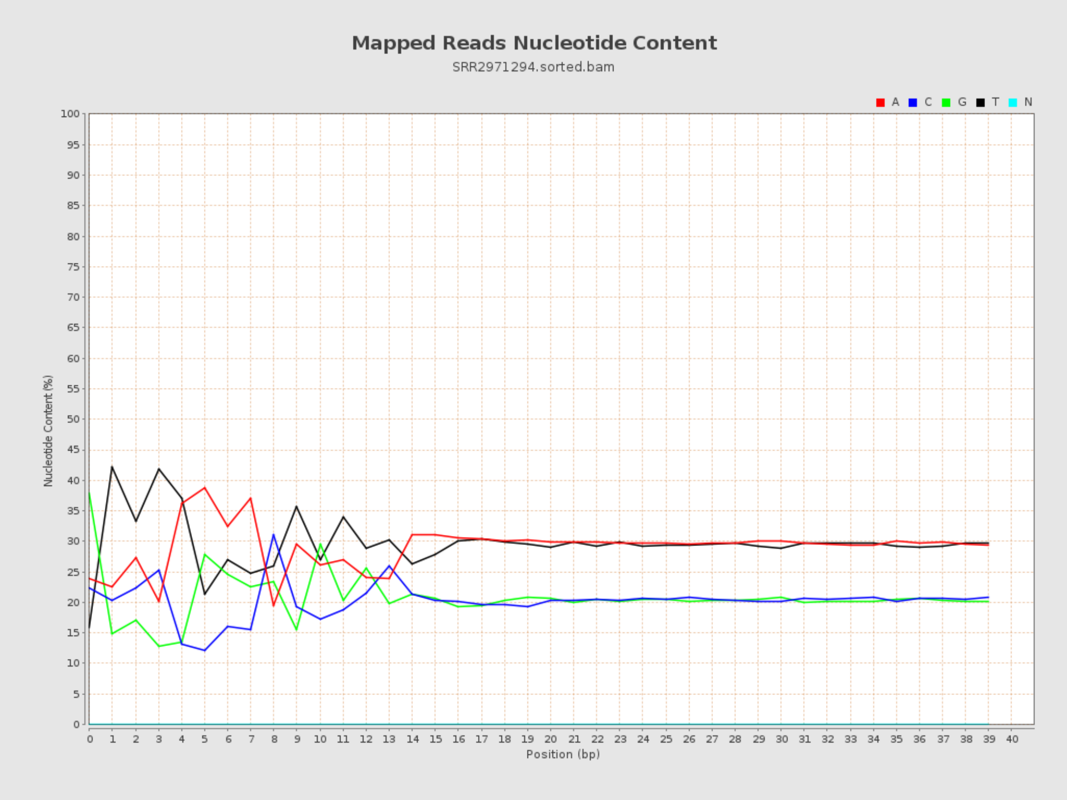
6. Results : Genome Fraction Coverage



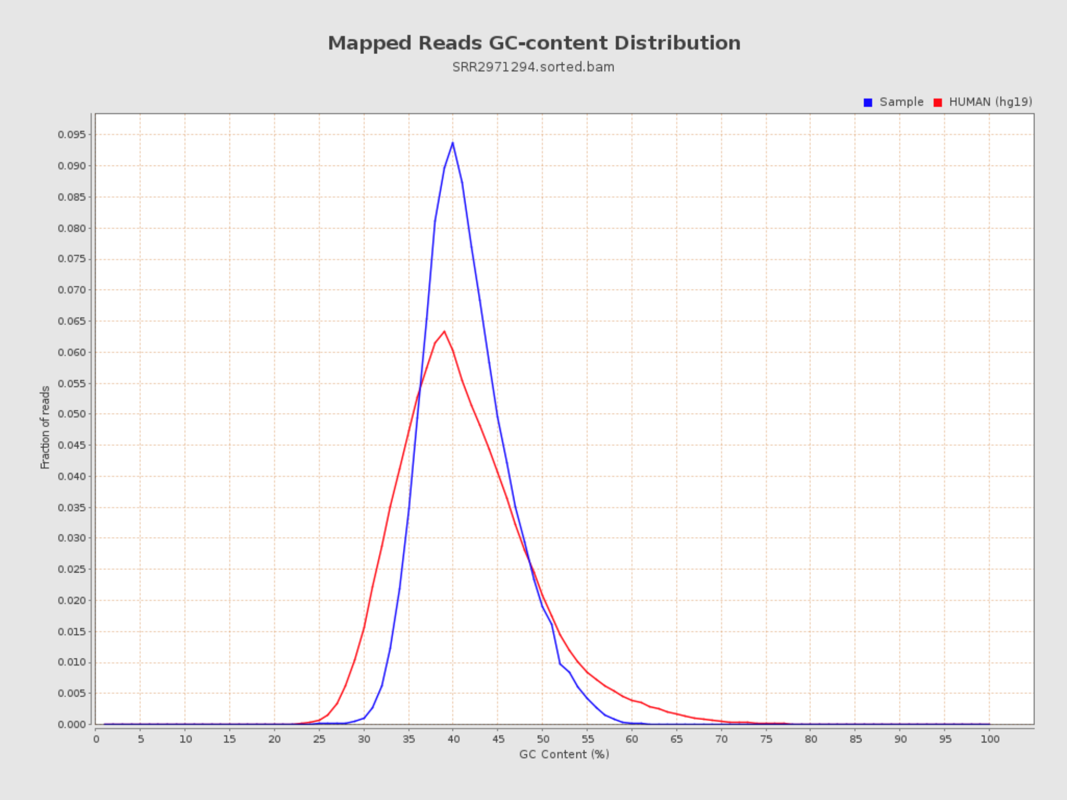
7. Results : Duplication Rate Histogram



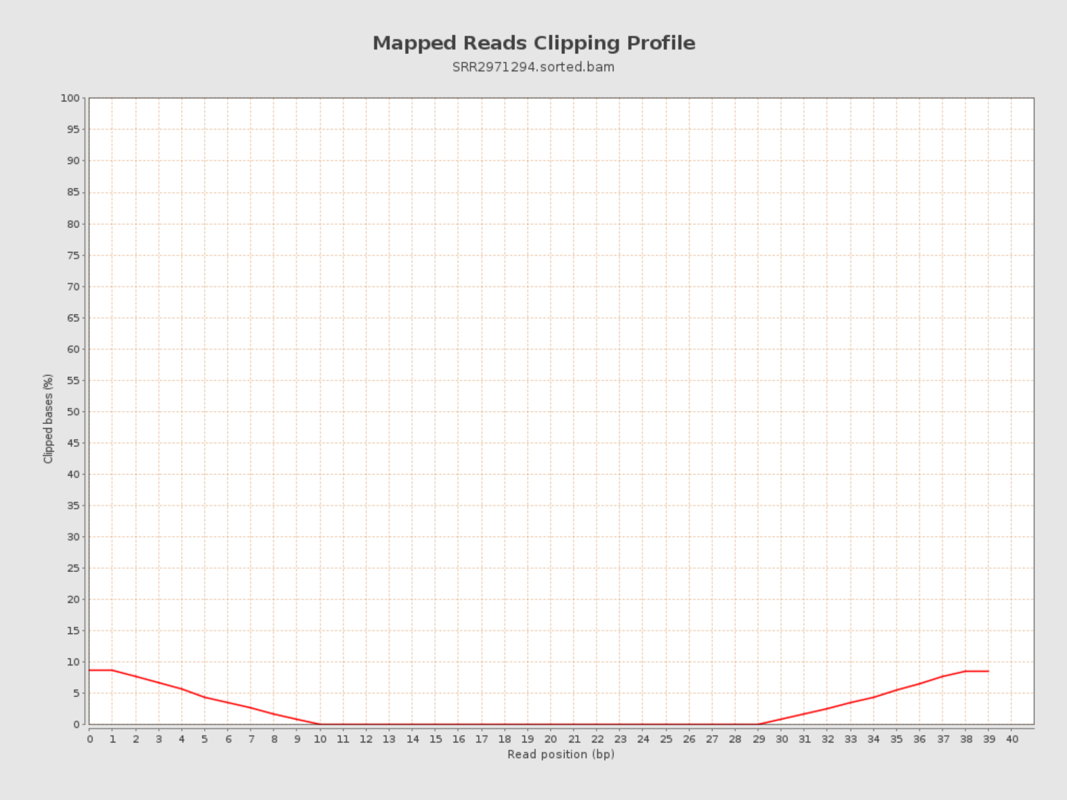
8. Results : Mapped Reads Nucleotide Content



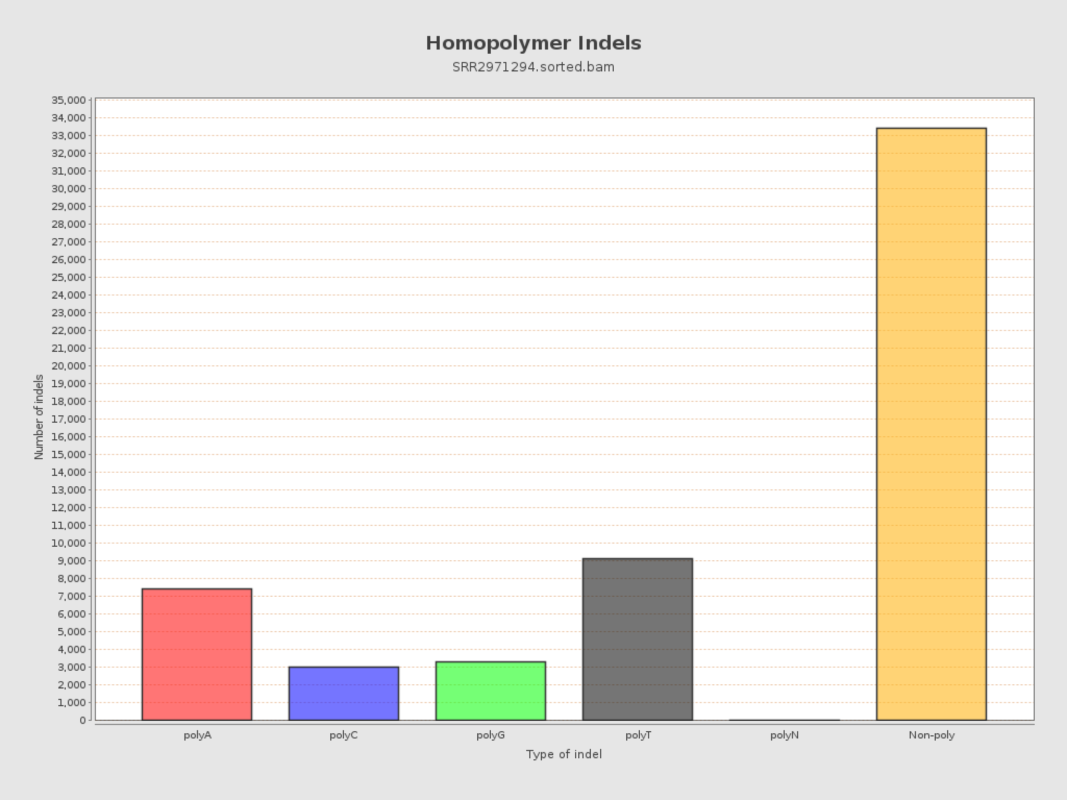
9. Results : Mapped Reads GC-content Distribution



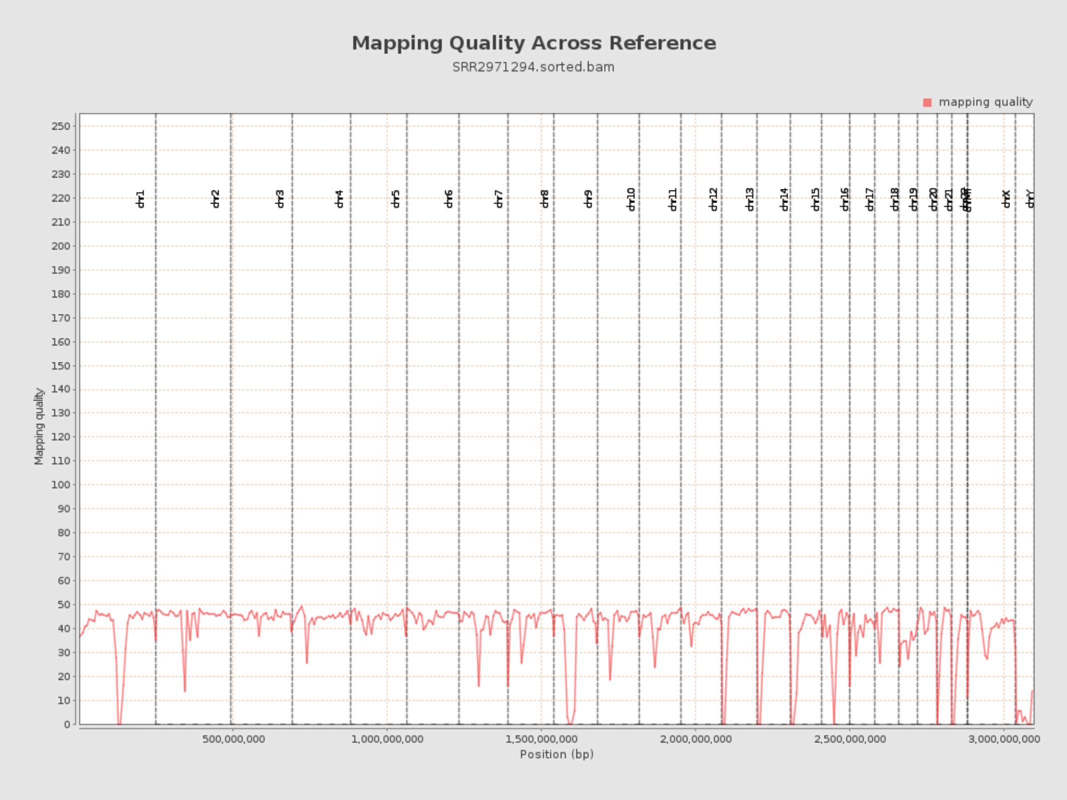
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram