Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 02:16:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083652.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_SRR3083652 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083652.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 02:16:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083652.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,250,211
Mapped reads	1,886,071 / 83.82%
Unmapped reads	364,140 / 16.18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,963 / 0.58%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	49,291 / 2.19%
Duplication rate	2.11%
Clipped reads	1,242,773 / 55.23%

2.2. ACGT Content

Number/percentage of A's	34,188,498 / 29.57%
Number/percentage of C's	22,515,861 / 19.48%
Number/percentage of T's	33,918,825 / 29.34%
Number/percentage of G's	24,965,991 / 21.6%
Number/percentage of N's	15,438 / 0.01%
GC Percentage	41.07%

2.3. Coverage

Mean	0.0374

Standard Deviation	0.3077

2.4. Mapping Quality

Mean Mapping Quality	45.21

2.5. Mismatches and indels

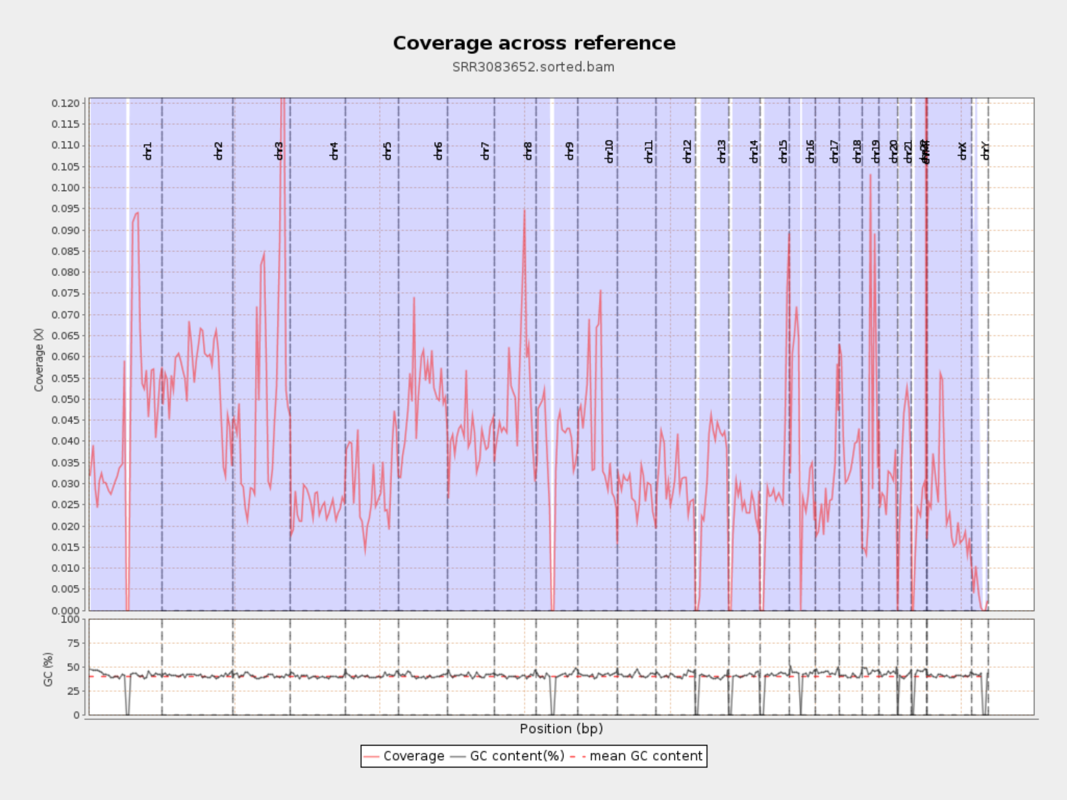
General error rate	0.81%
Mismatches	919,529
Insertions	7,906
Mapped reads with at least one insertion	0.42%
Deletions	22,892
Mapped reads with at least one deletion	1.2%
Homopolymer indels	46.3%

2.6. Chromosome stats

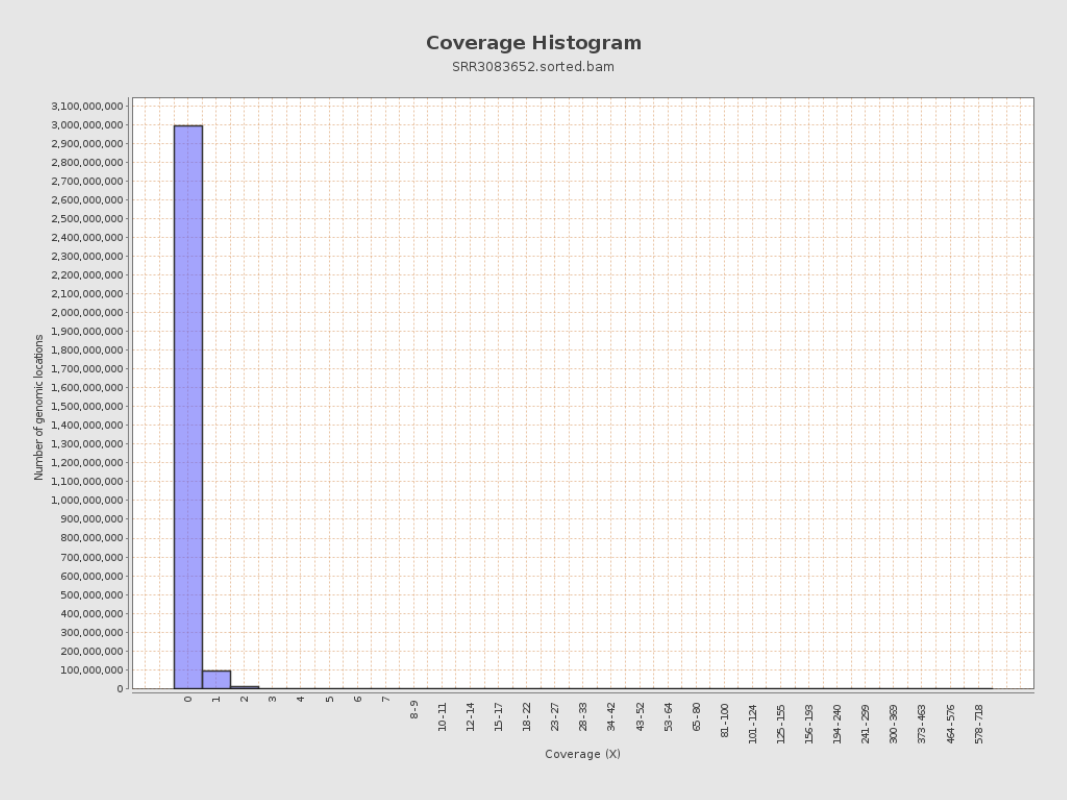
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10808286	0.0434	0.6394
chr2	243199373	13452803	0.0553	0.3009
chr3	198022430	10395637	0.0525	0.2536
chr4	191154276	4664490	0.0244	0.1717
chr5	180915260	5435426	0.03	0.1887
chr6	171115067	8700730	0.0508	0.2878
chr7	159138663	6526468	0.041	0.3605

chr8	146364022	7549038	0.0516	0.4144
chr9	141213431	5240537	0.0371	0.2376
chr10	135534747	6026576	0.0445	0.3478
chr11	135006516	3789533	0.0281	0.2017
chr12	133851895	4089240	0.0306	0.1915
chr13	115169878	3576520	0.0311	0.1903
chr14	107349540	2324988	0.0217	0.162
chr15	102531392	3010548	0.0294	0.187
chr16	90354753	3493015	0.0387	0.2248
chr17	81195210	2320818	0.0286	0.1888
chr18	78077248	3100874	0.0397	0.3293
chr19	59128983	2495622	0.0422	0.4493
chr20	63025520	1837859	0.0292	0.1893
chr21	48129895	1741082	0.0362	0.2106
chr22	51304566	981513	0.0191	0.1493
chrMT	16571	13720	0.828	1.0335
chrX	155270560	3862010	0.0249	0.178
chrY	59373566	203243	0.0034	0.0715

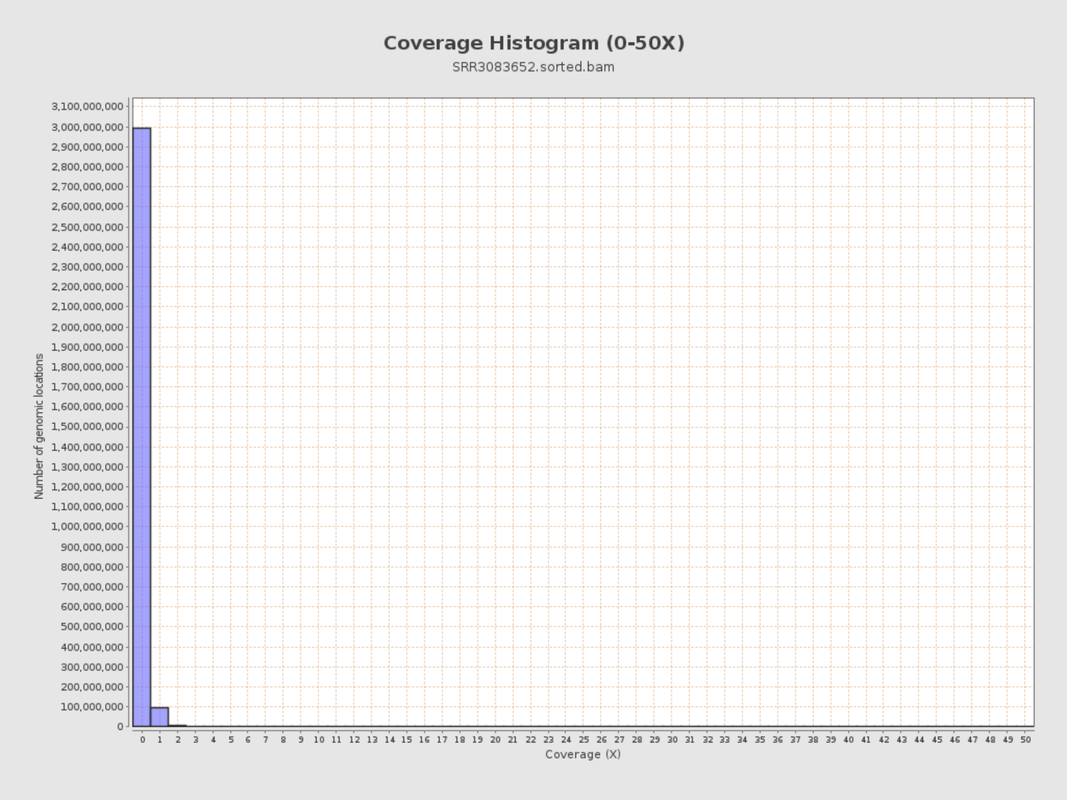
3. Results : Coverage across reference



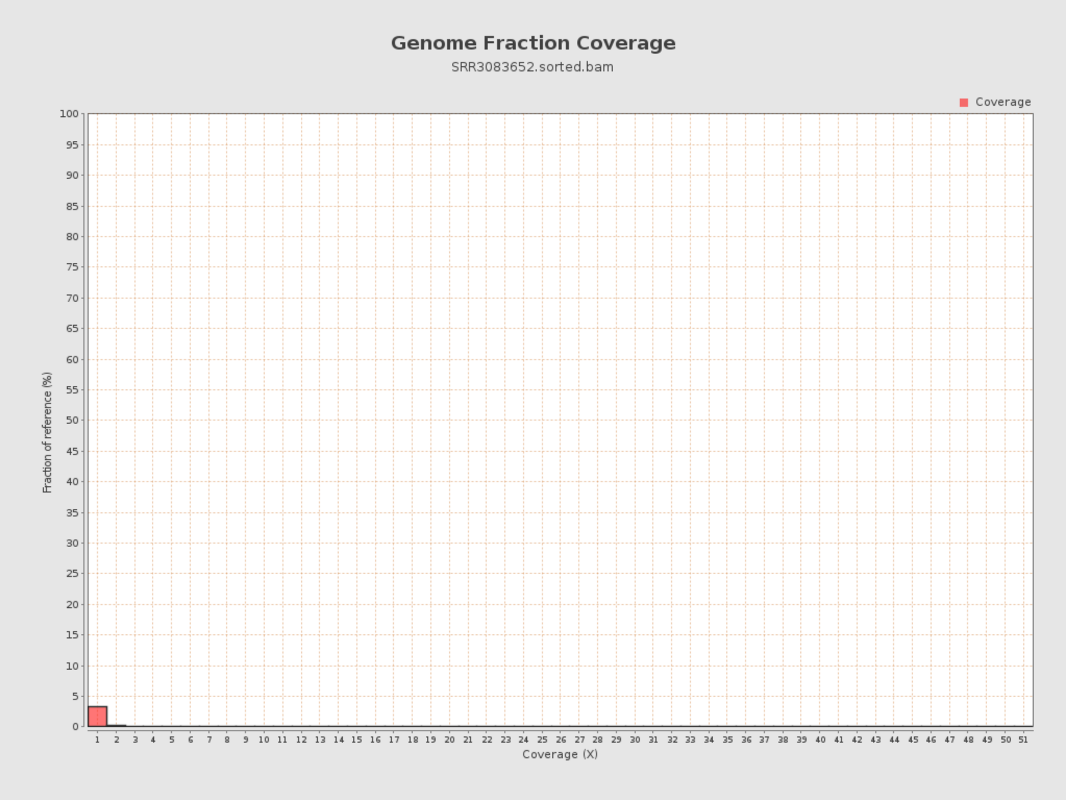
4. Results : Coverage Histogram



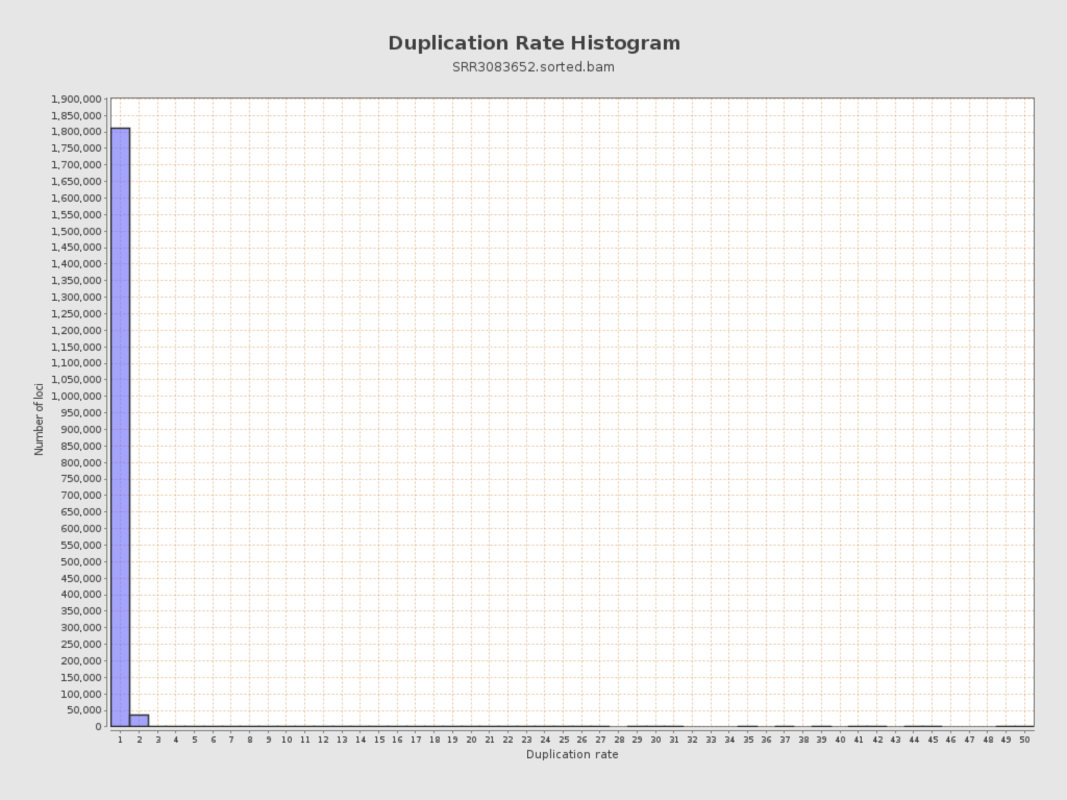
5. Results : Coverage Histogram (0-50X)



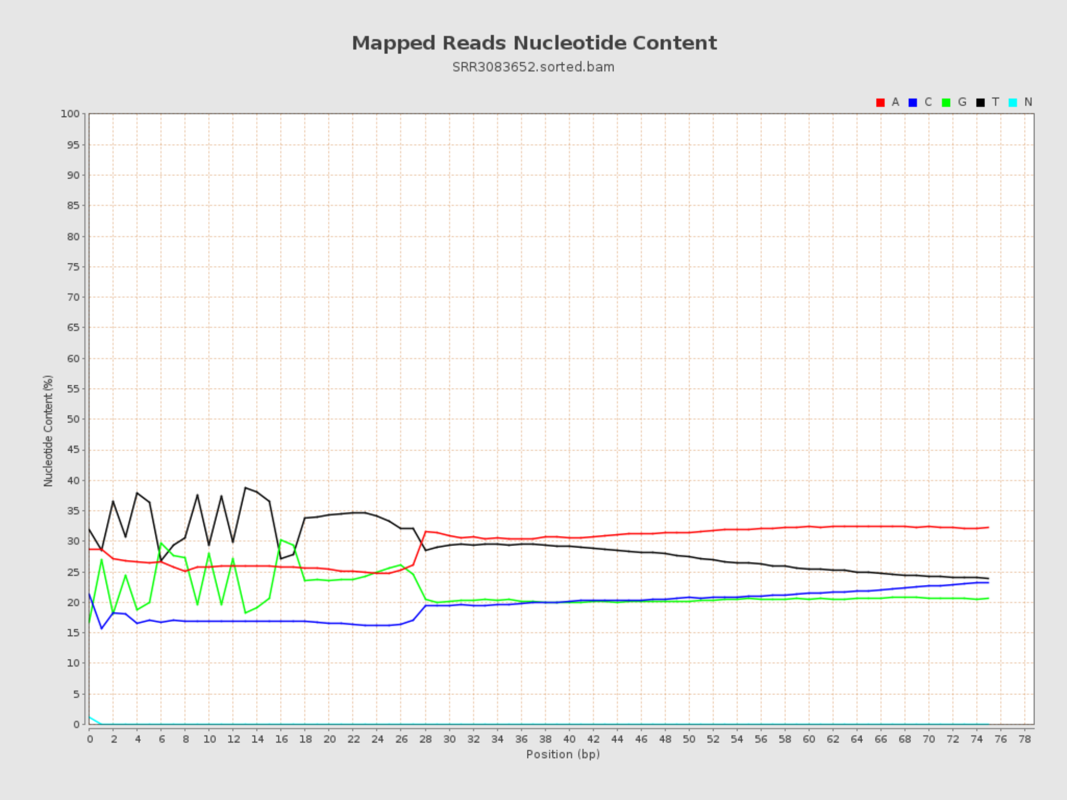
6. Results : Genome Fraction Coverage



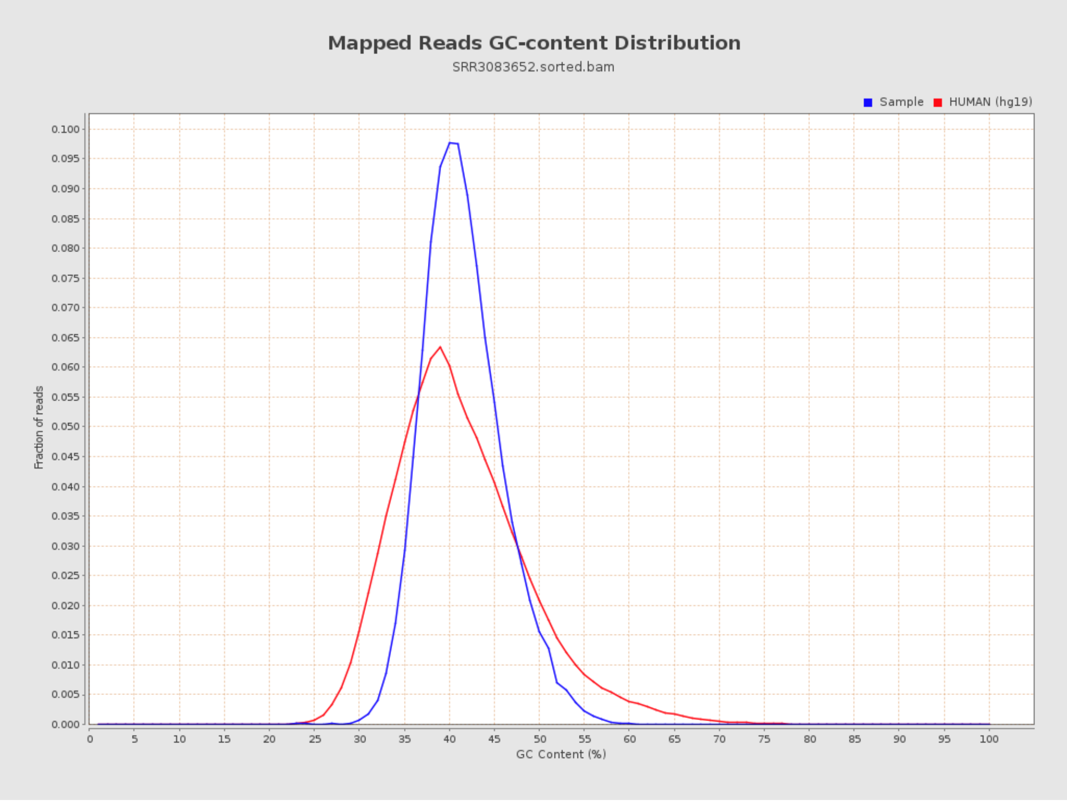
7. Results : Duplication Rate Histogram



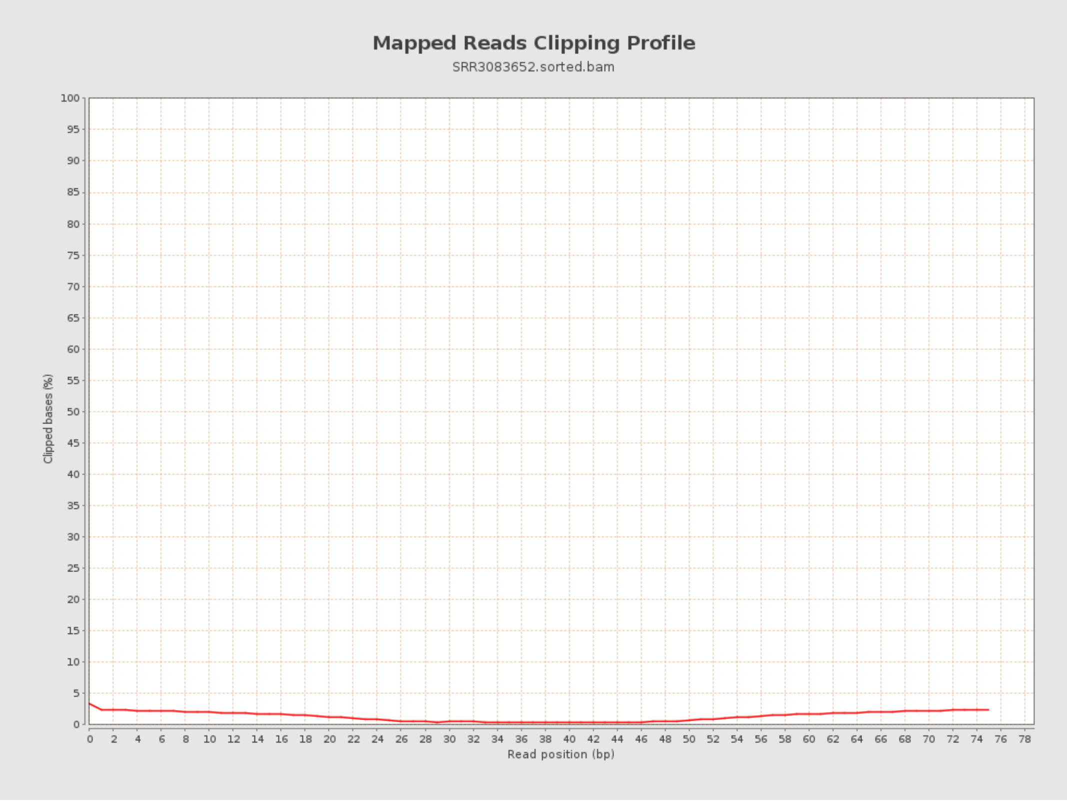
8. Results : Mapped Reads Nucleotide Content



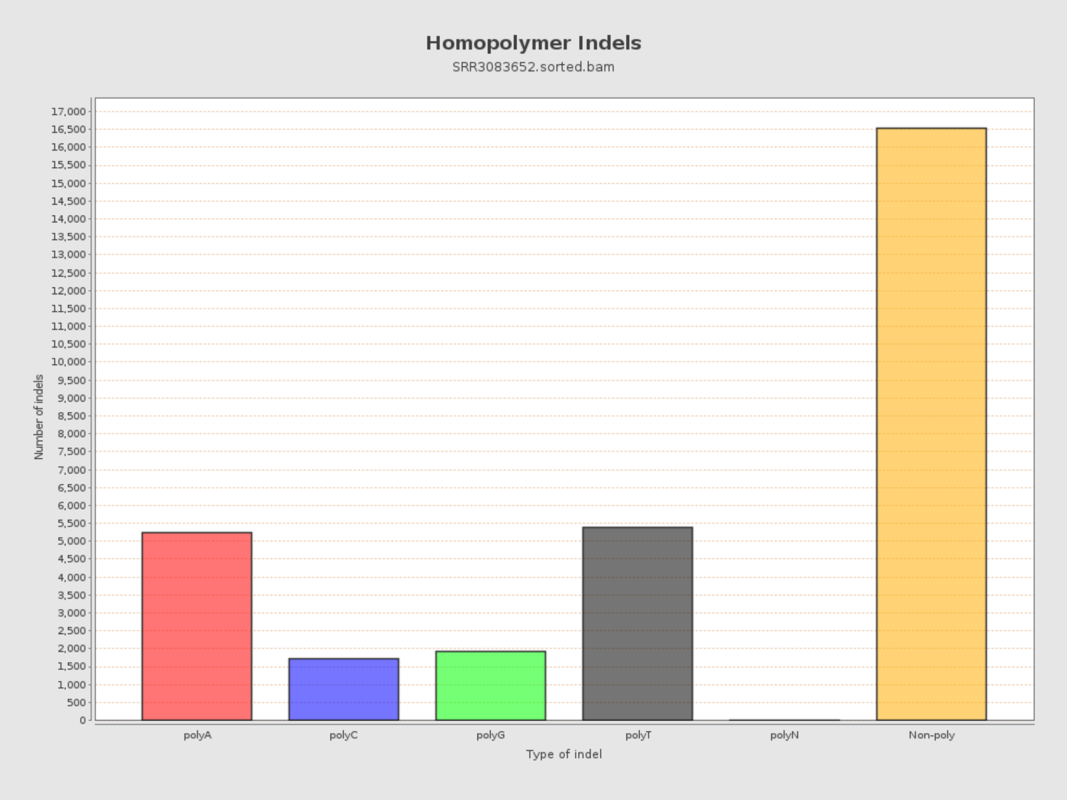
9. Results : Mapped Reads GC-content Distribution



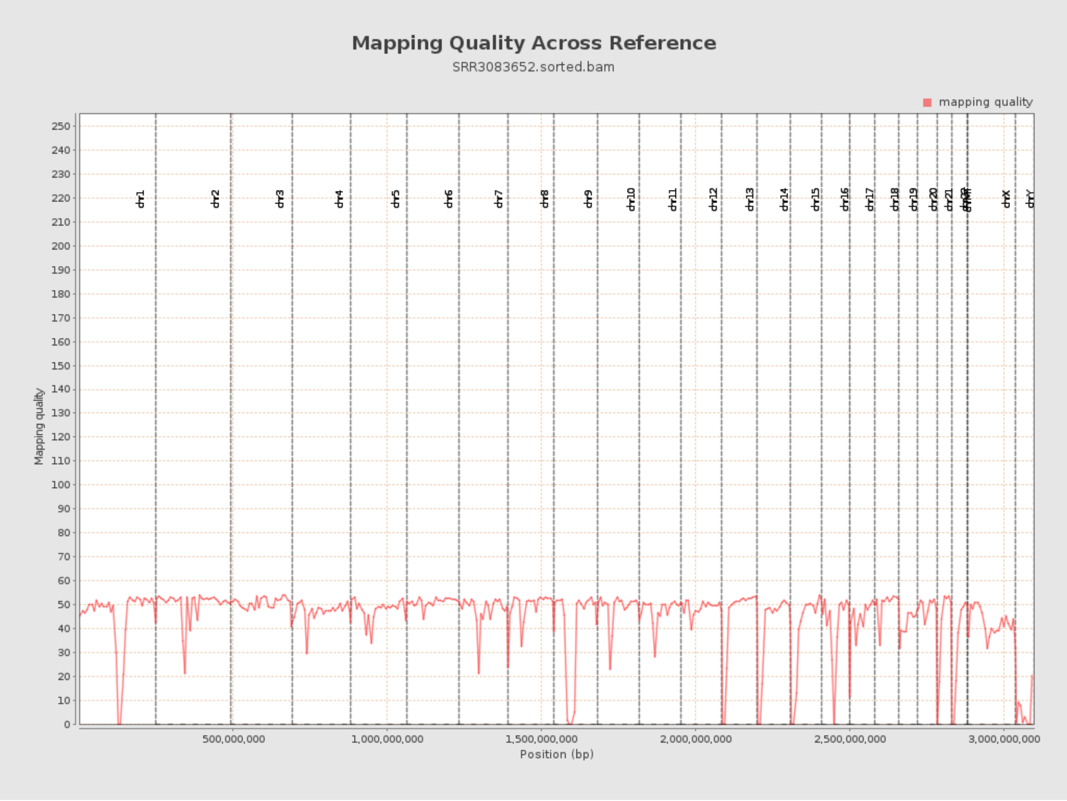
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram