Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 16:29:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084832.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_SRR3084832 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084832.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 16:29:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084832.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,093,963
Mapped reads	990,217 / 90.52%
Unmapped reads	103,746 / 9.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,355 / 1.04%
Read min/max/mean length	30 / 76 / 76.36
Duplicated reads (estimated)	36,099 / 3.3%
Duplication rate	2.29%
Clipped reads	435,715 / 39.83%

2.2. ACGT Content

Number/percentage of A's	18,462,372 / 27.79%
Number/percentage of C's	12,565,141 / 18.91%
Number/percentage of T's	20,073,889 / 30.21%
Number/percentage of G's	15,329,784 / 23.07%
Number/percentage of N's	9,278 / 0.01%
GC Percentage	41.98%

2.3. Coverage

Mean	0.0215

Standard Deviation	0.3125

2.4. Mapping Quality

Mean Mapping Quality	43.17

2.5. Mismatches and indels

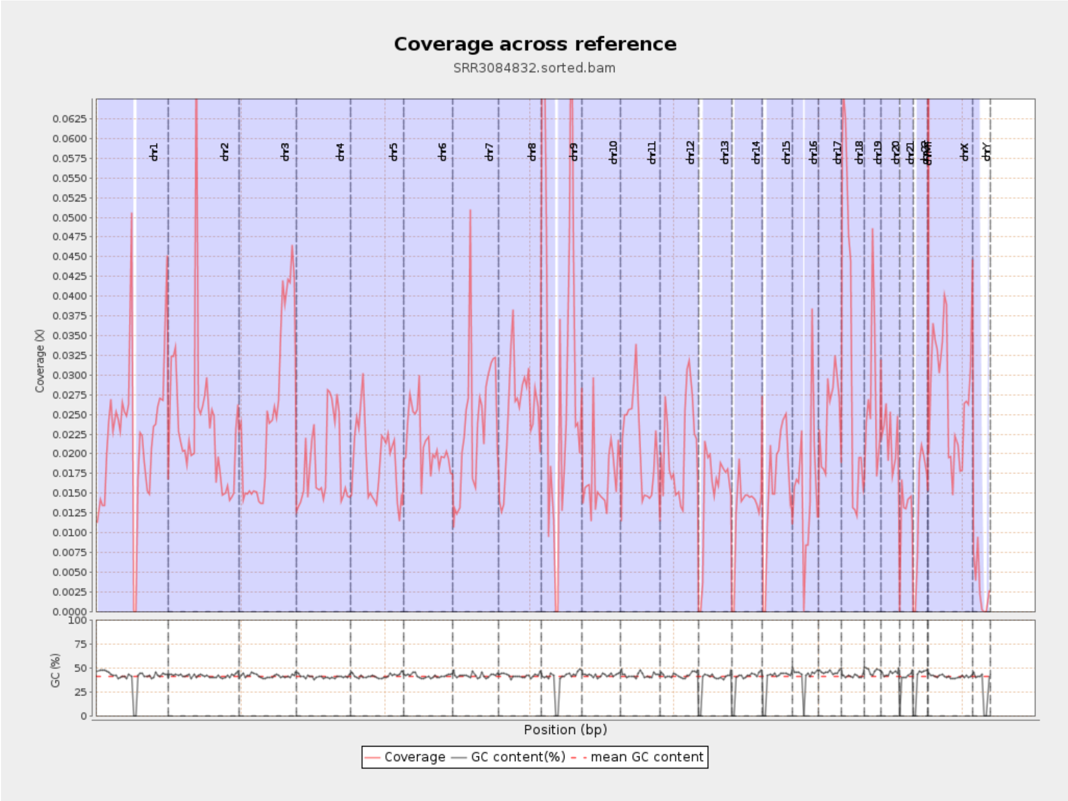
General error rate	0.87%
Mismatches	566,792
Insertions	6,180
Mapped reads with at least one insertion	0.62%
Deletions	13,975
Mapped reads with at least one deletion	1.39%
Homopolymer indels	44.22%

2.6. Chromosome stats

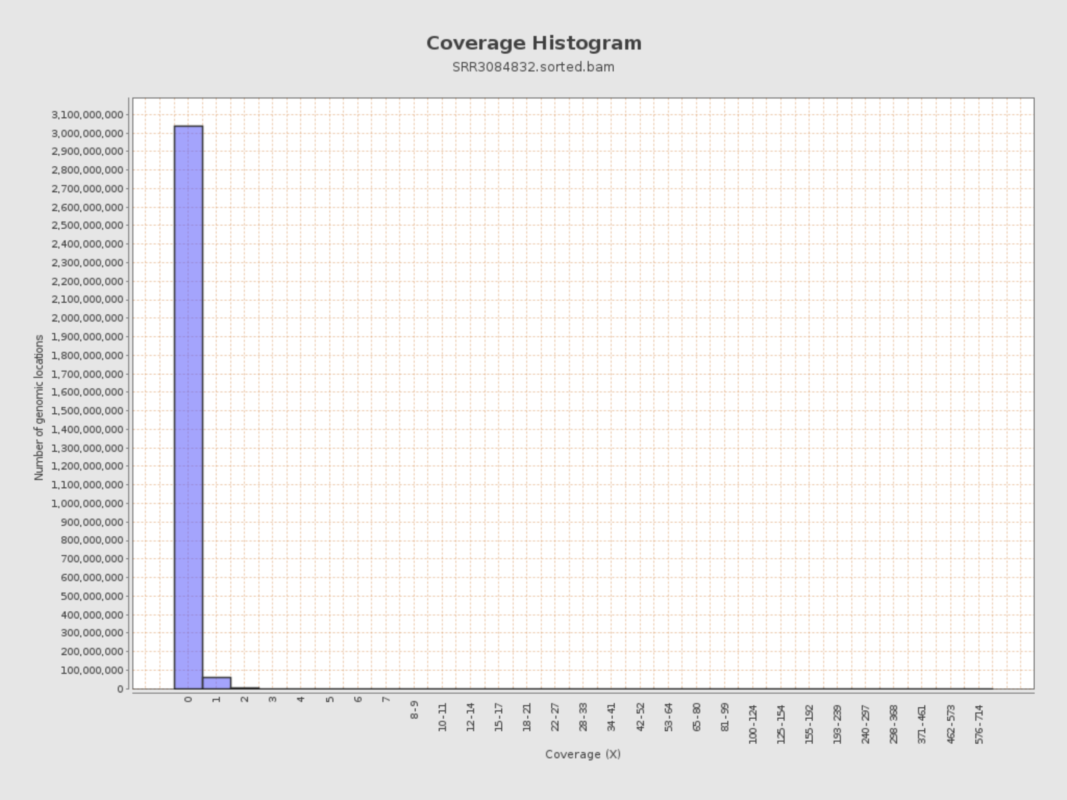
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5544096	0.0222	0.5933
chr2	243199373	5768219	0.0237	0.4291
chr3	198022430	4973257	0.0251	0.1665
chr4	191154276	3578092	0.0187	0.1463
chr5	180915260	3476753	0.0192	0.1553
chr6	171115067	3630966	0.0212	0.1682
chr7	159138663	3837529	0.0241	0.3716

chr8	146364022	3698428	0.0253	0.322
chr9	141213431	4485712	0.0318	0.3731
chr10	135534747	2279292	0.0168	0.2009
chr11	135006516	2864823	0.0212	0.3235
chr12	133851895	2783535	0.0208	0.1619
chr13	115169878	1709841	0.0148	0.1266
chr14	107349540	1371054	0.0128	0.1513
chr15	102531392	1645878	0.0161	0.1386
chr16	90354753	1405503	0.0156	0.1723
chr17	81195210	2011044	0.0248	0.191
chr18	78077248	2593799	0.0332	0.7093
chr19	59128983	1657835	0.028	0.3715
chr20	63025520	1383630	0.022	0.1708
chr21	48129895	612139	0.0127	0.1433
chr22	51304566	683741	0.0133	0.1194
chrMT	16571	25836	1.5591	1.5384
chrX	155270560	4260822	0.0274	0.2161
chrY	59373566	182525	0.0031	0.1081

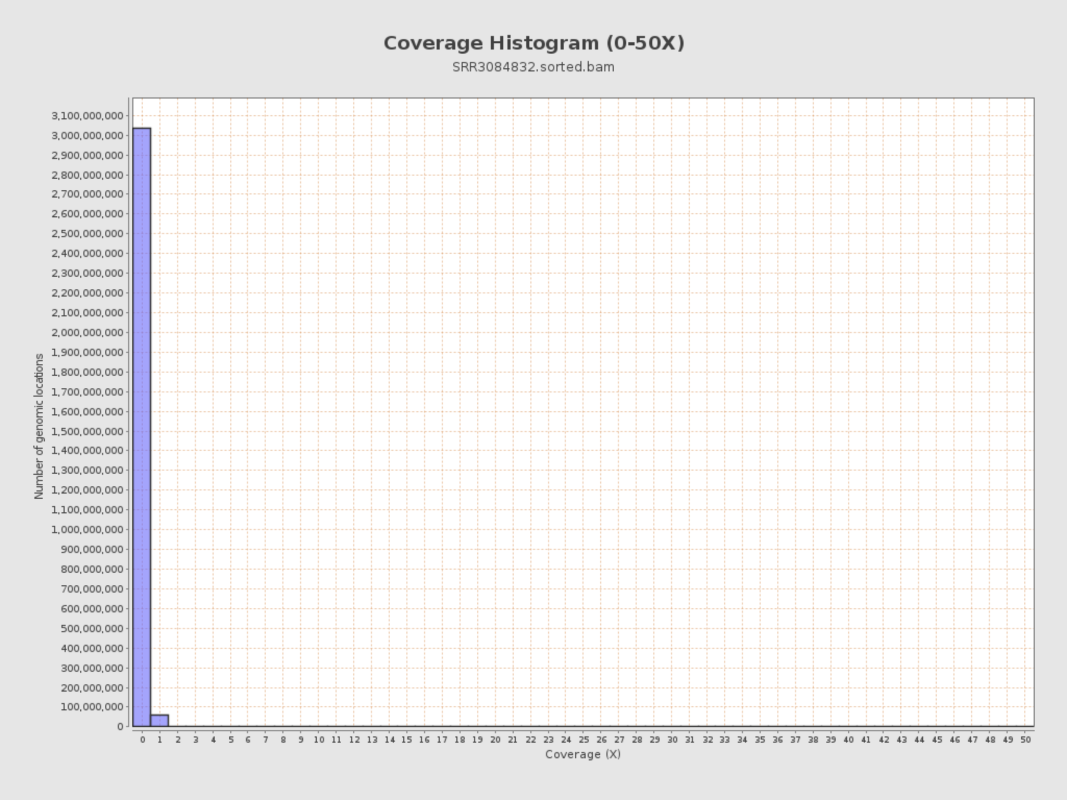
3. Results : Coverage across reference



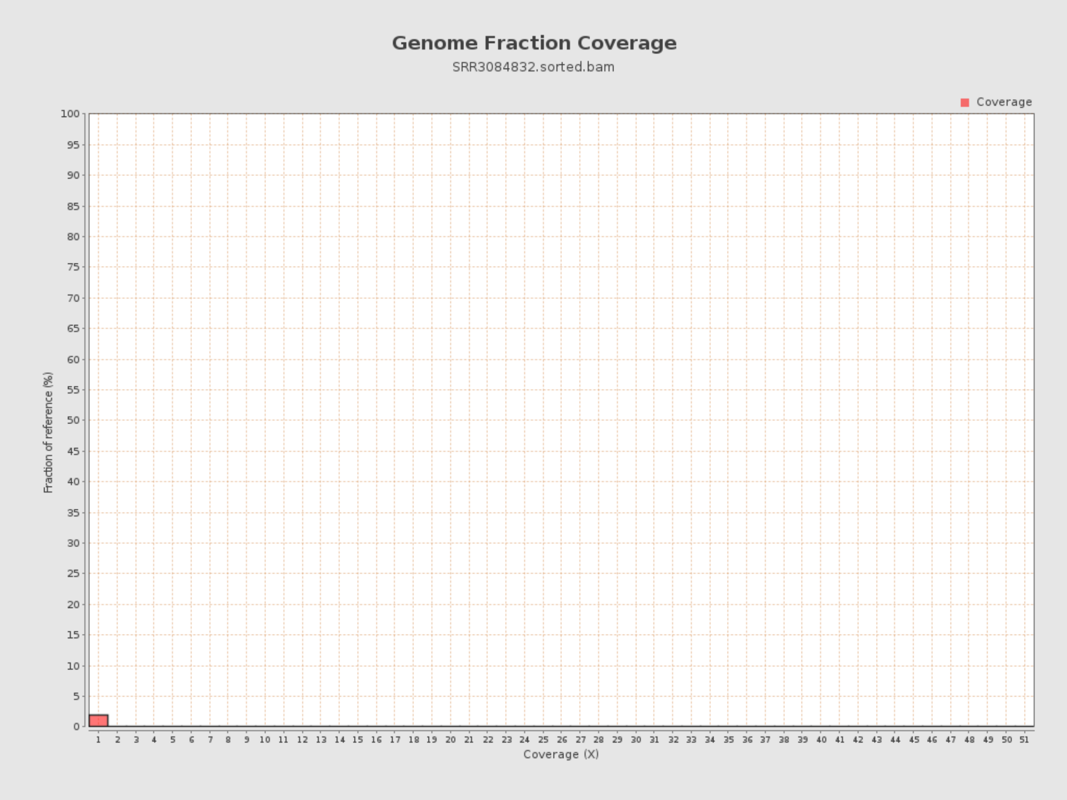
4. Results : Coverage Histogram



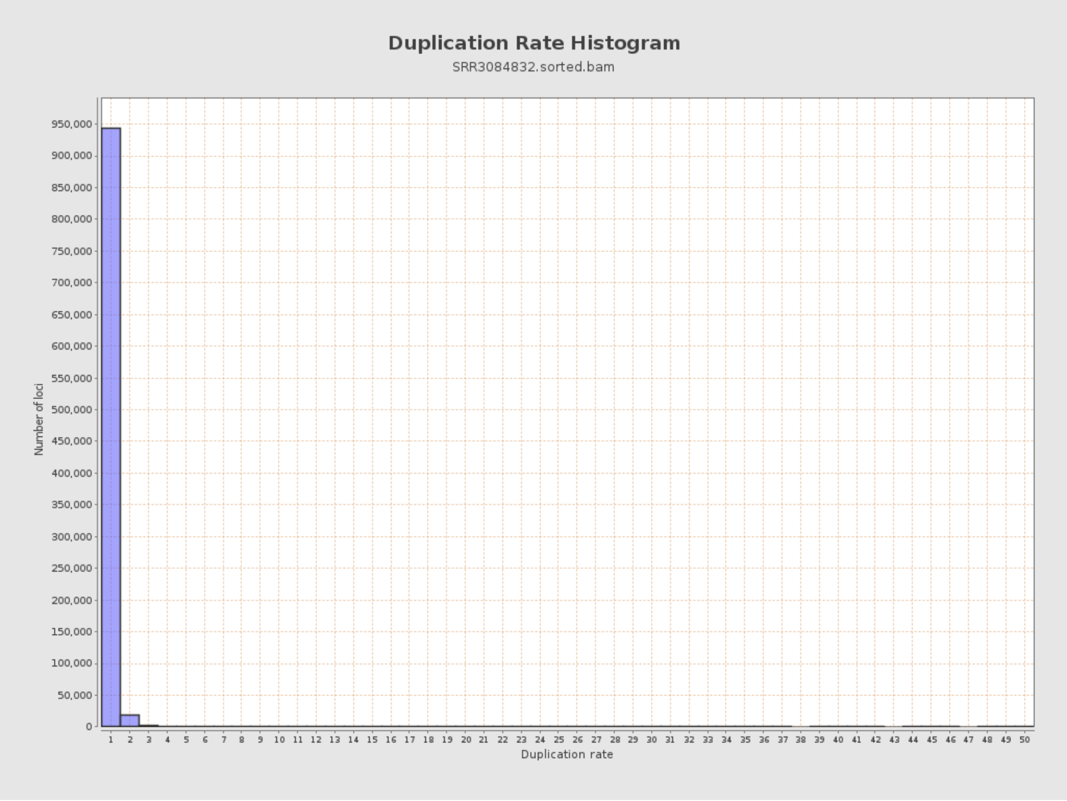
5. Results : Coverage Histogram (0-50X)



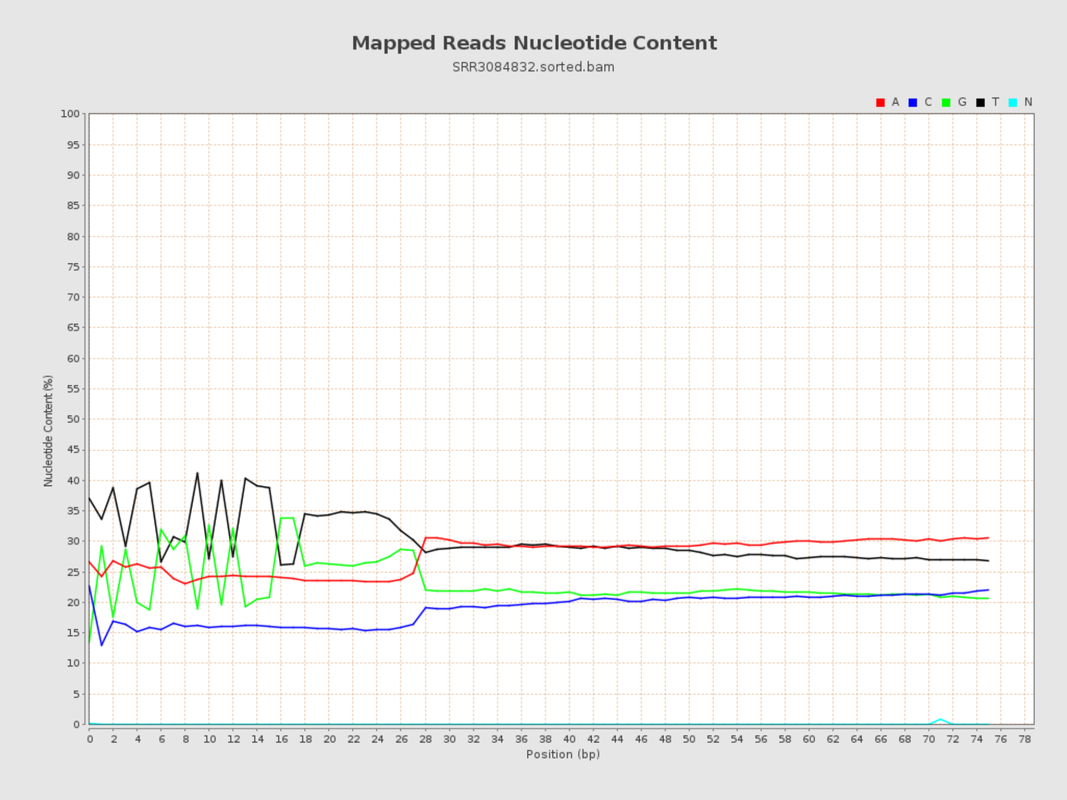
6. Results : Genome Fraction Coverage



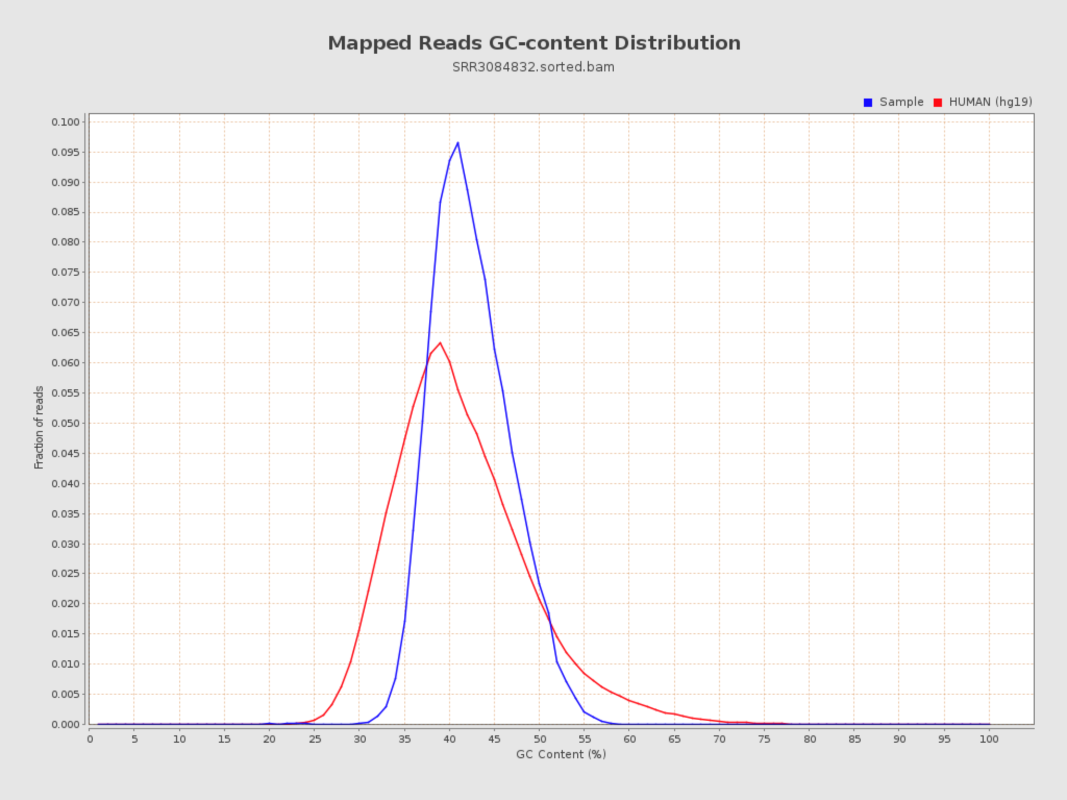
7. Results : Duplication Rate Histogram



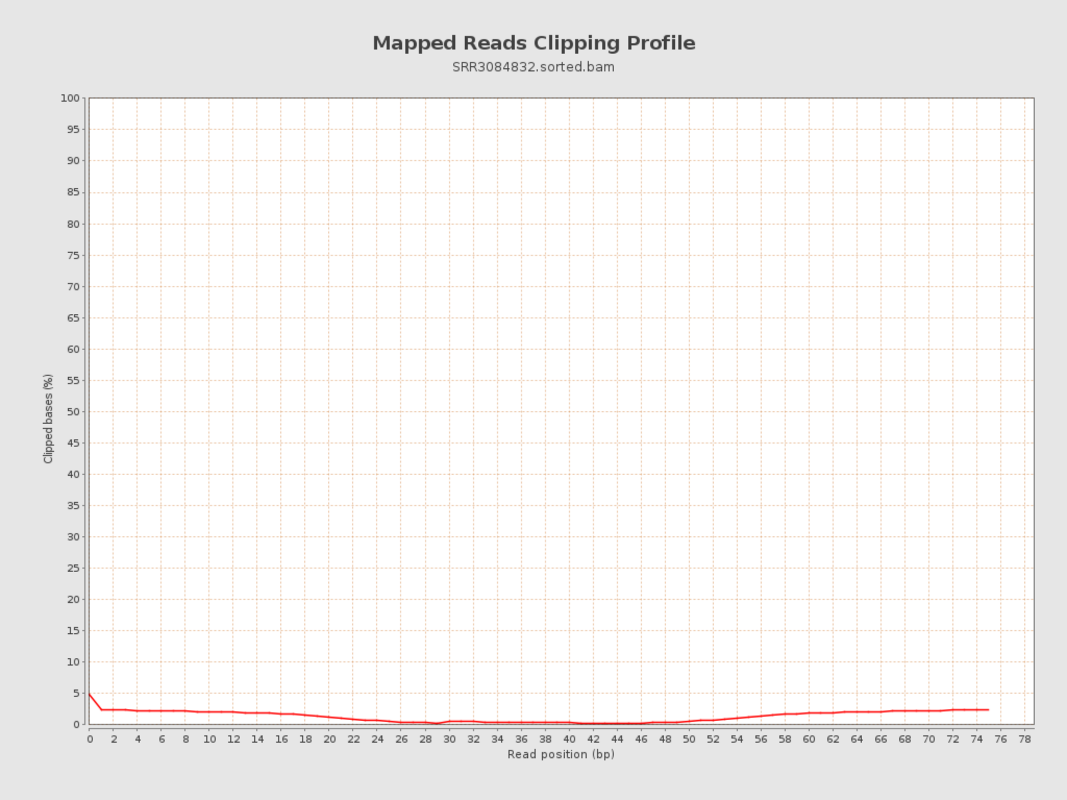
8. Results : Mapped Reads Nucleotide Content



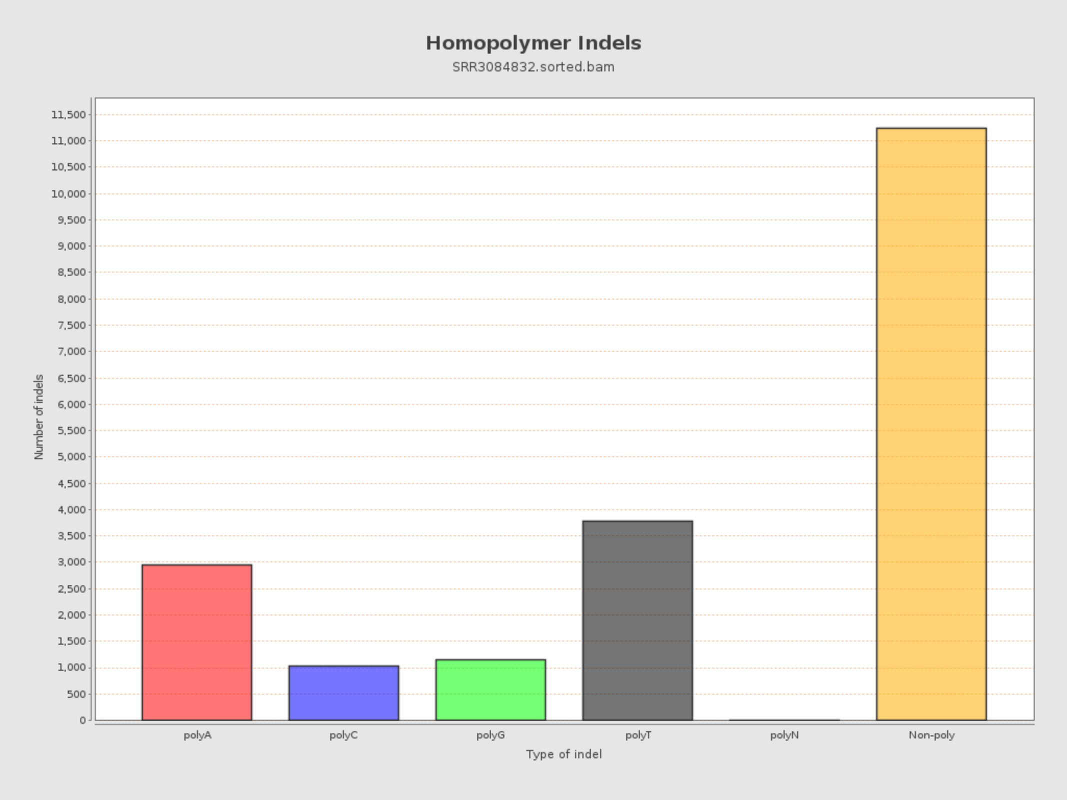
9. Results : Mapped Reads GC-content Distribution



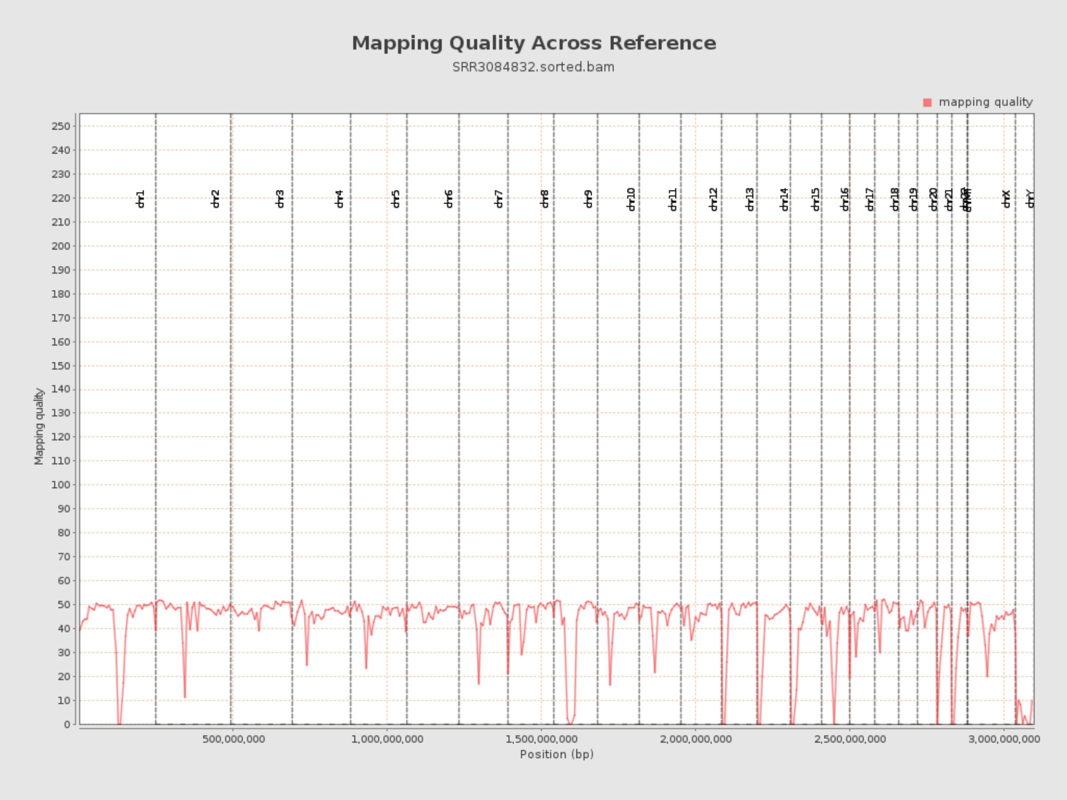
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram