Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 02:56:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083664.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_SRR3083664 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083664.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 02:56:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083664.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,347,441
Mapped reads	1,926,007 / 82.05%
Unmapped reads	421,434 / 17.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,110 / 0.56%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	58,849 / 2.51%
Duplication rate	2.41%
Clipped reads	1,324,183 / 56.41%

2.2. ACGT Content

Number/percentage of A's	35,053,862 / 30%
Number/percentage of C's	22,660,630 / 19.39%
Number/percentage of T's	34,320,936 / 29.37%
Number/percentage of G's	24,796,706 / 21.22%
Number/percentage of N's	14,920 / 0.01%
GC Percentage	40.61%

2.3. Coverage

Mean	0.0378

Standard Deviation	0.3679

2.4. Mapping Quality

Mean Mapping Quality	45.04

2.5. Mismatches and indels

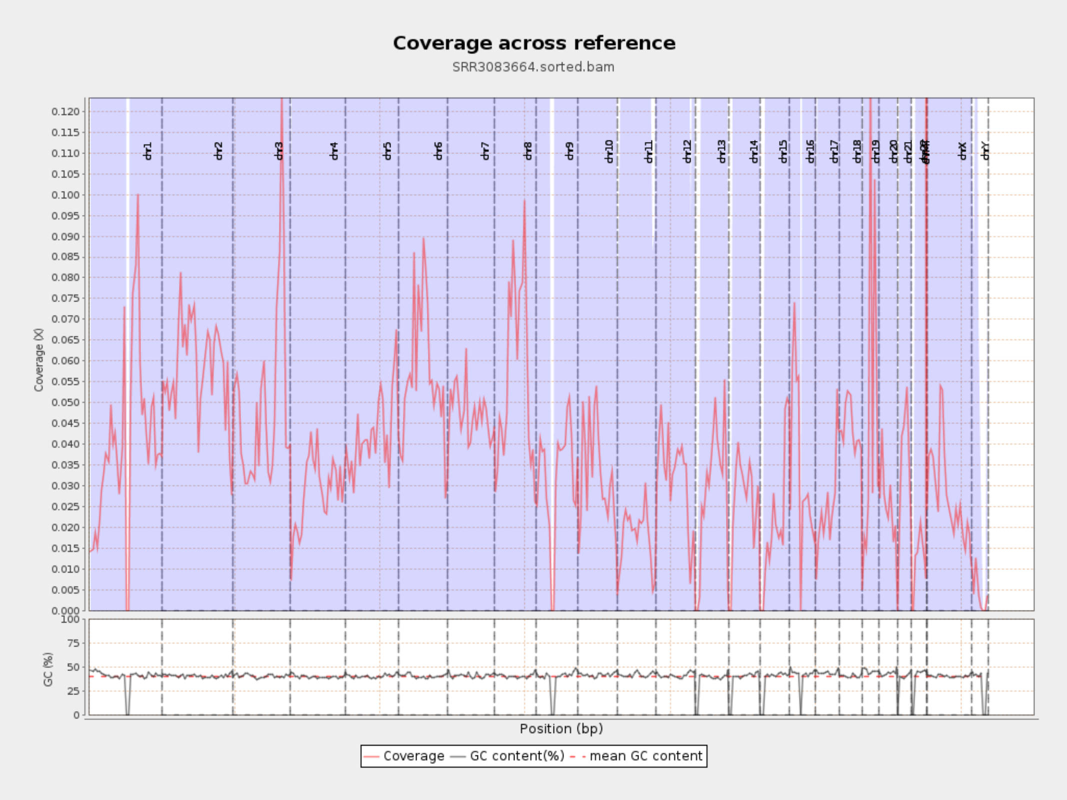
General error rate	0.86%
Mismatches	991,489
Insertions	7,834
Mapped reads with at least one insertion	0.4%
Deletions	23,395
Mapped reads with at least one deletion	1.2%
Homopolymer indels	46.44%

2.6. Chromosome stats

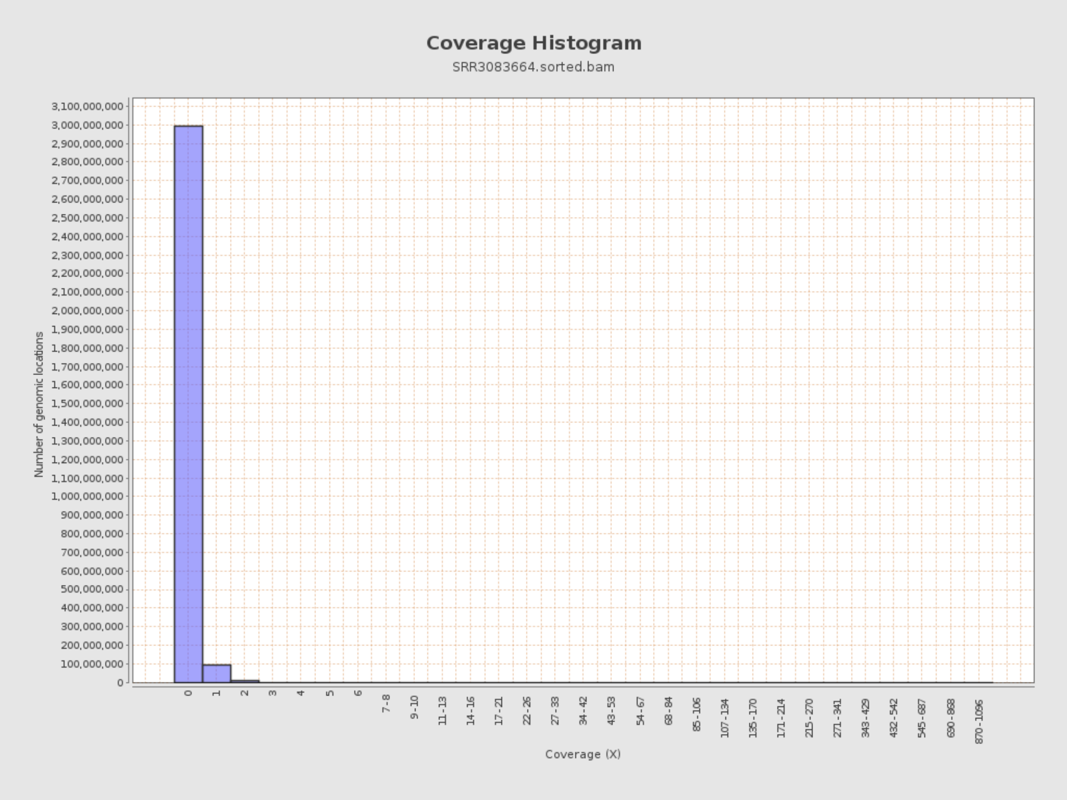
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10003477	0.0401	0.9227
chr2	243199373	14253016	0.0586	0.3165
chr3	198022430	9726293	0.0491	0.2454
chr4	191154276	5496684	0.0288	0.1885
chr5	180915260	7750249	0.0428	0.2274
chr6	171115067	9732139	0.0569	0.3063
chr7	159138663	7579215	0.0476	0.3904

chr8	146364022	8346096	0.057	0.4045
chr9	141213431	4543659	0.0322	0.2301
chr10	135534747	4506934	0.0333	0.3107
chr11	135006516	2388207	0.0177	0.1713
chr12	133851895	4328502	0.0323	0.1983
chr13	115169878	3402565	0.0295	0.1868
chr14	107349540	2778258	0.0259	0.1771
chr15	102531392	2125445	0.0207	0.1581
chr16	90354753	3108142	0.0344	0.217
chr17	81195210	2034657	0.0251	0.1802
chr18	78077248	3440058	0.0441	0.4073
chr19	59128983	2836886	0.048	0.564
chr20	63025520	1616070	0.0256	0.1804
chr21	48129895	1638059	0.034	0.2043
chr22	51304566	607490	0.0118	0.1177
chrMT	16571	34749	2.097	1.7277
chrX	155270560	4374797	0.0282	0.1931
chrY	59373566	232353	0.0039	0.0869

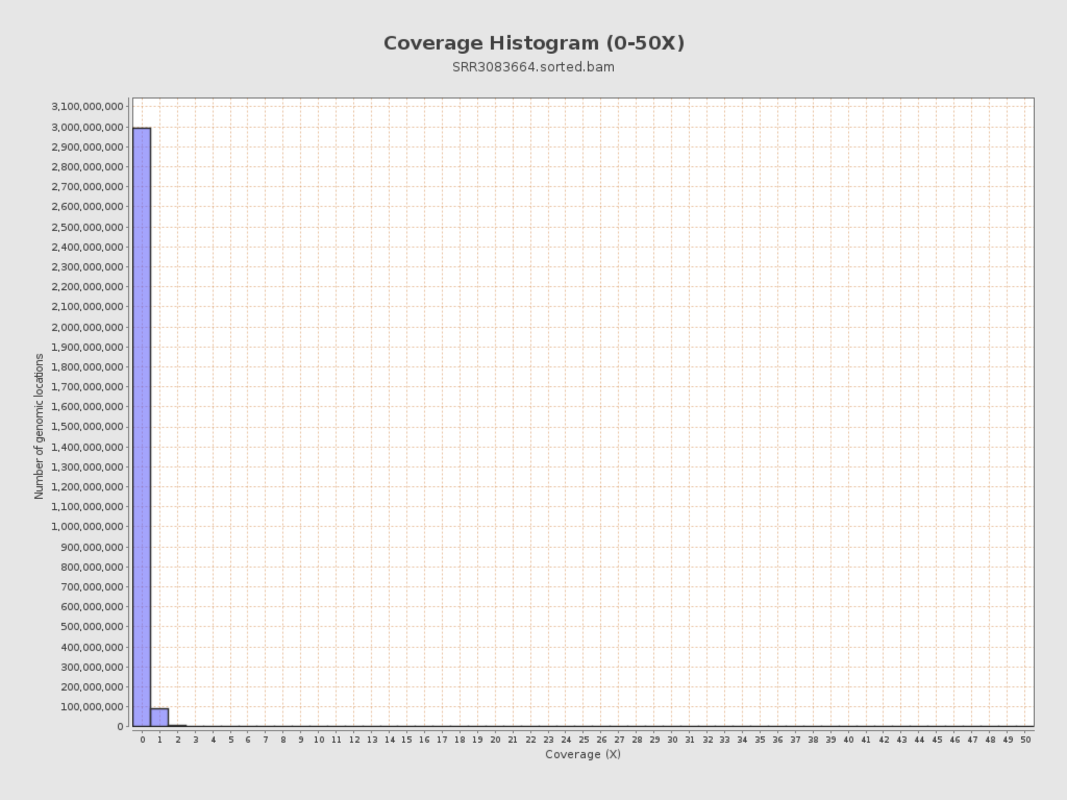
3. Results : Coverage across reference



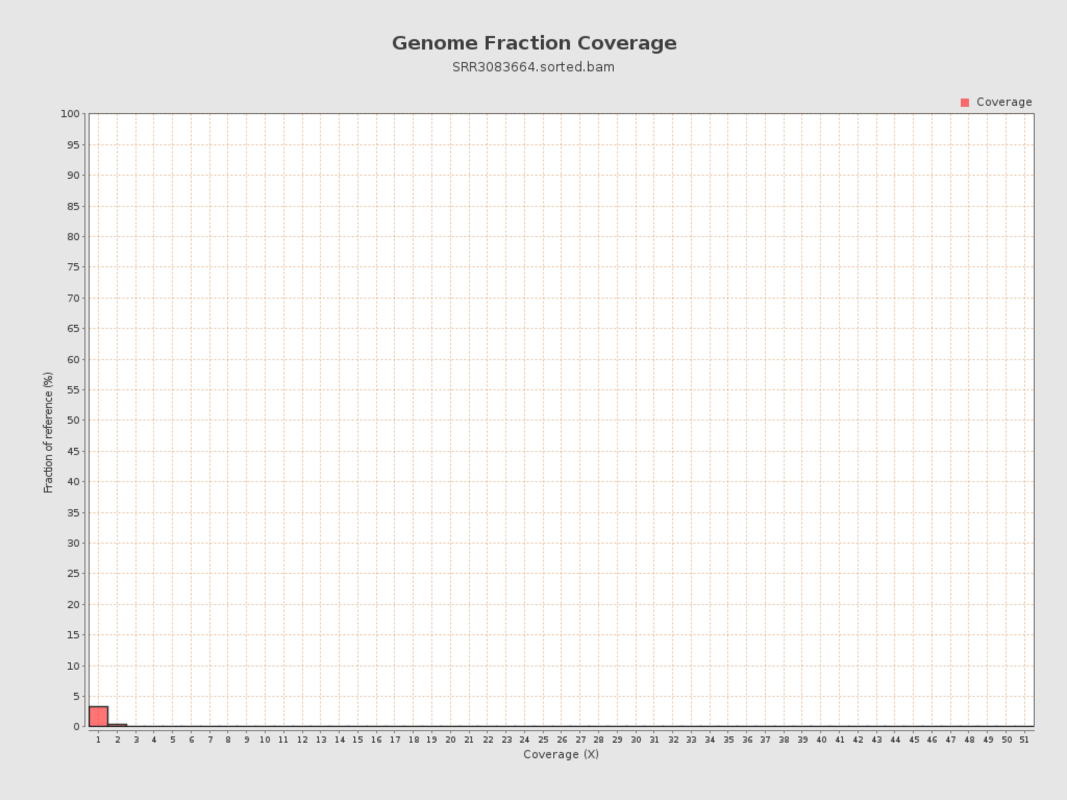
4. Results : Coverage Histogram



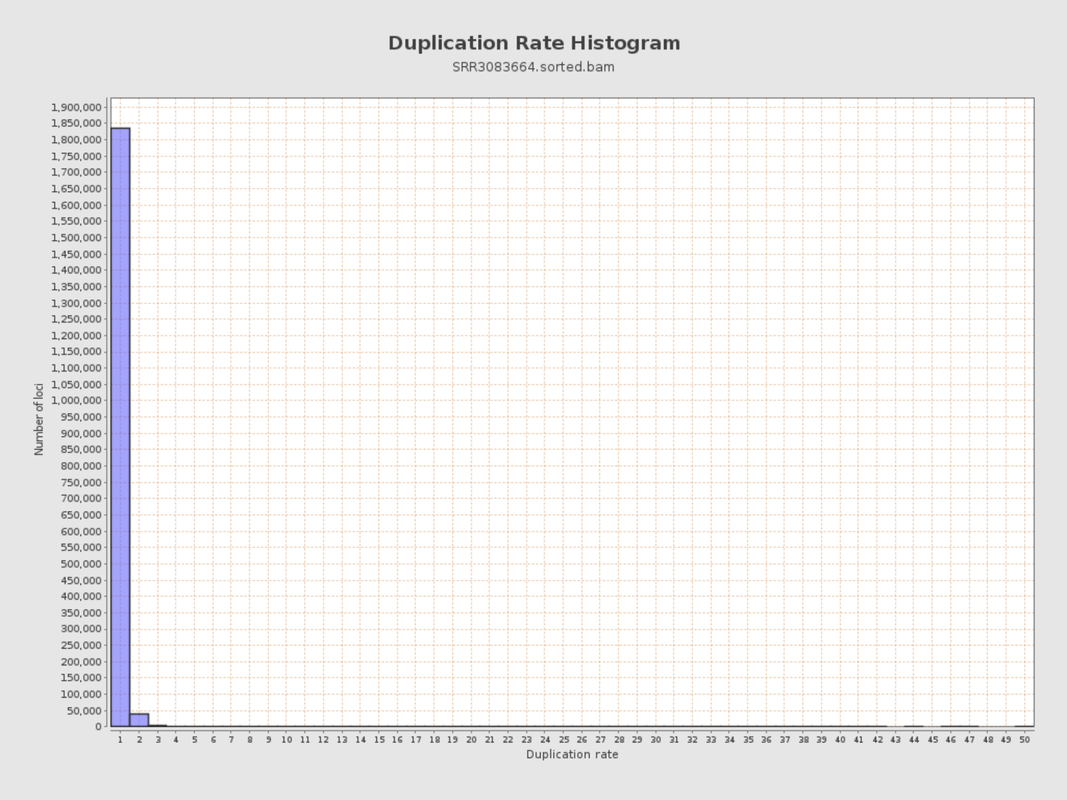
5. Results : Coverage Histogram (0-50X)



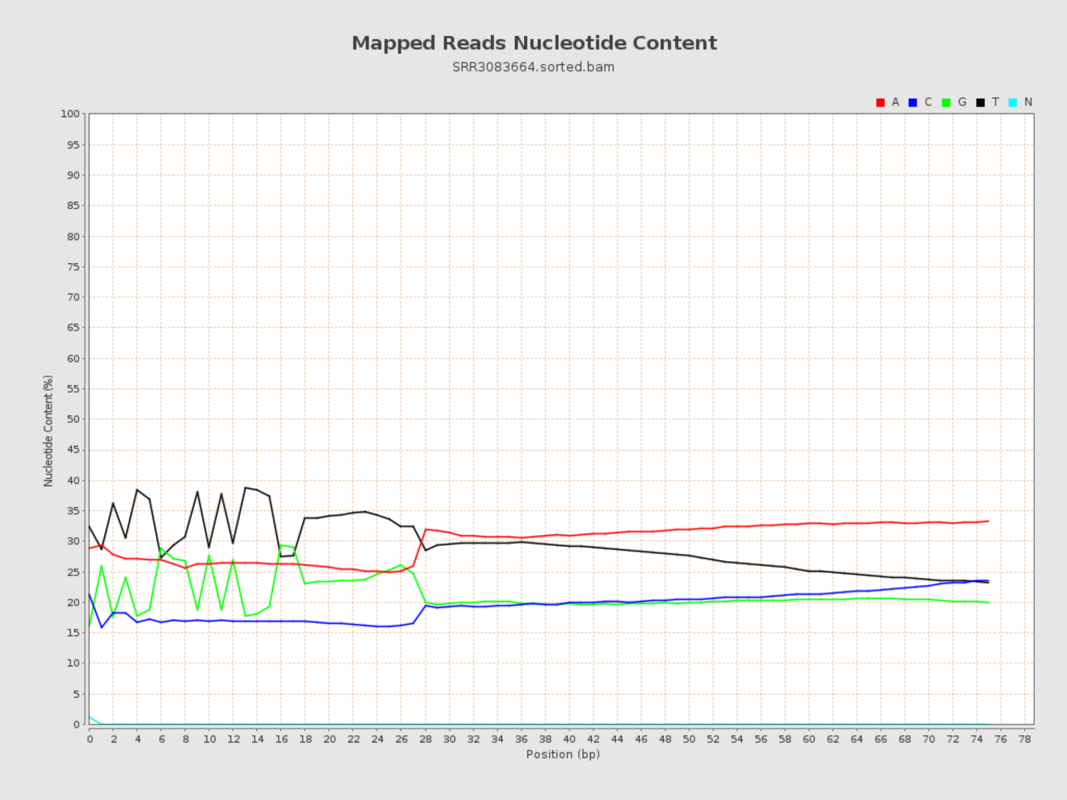
6. Results : Genome Fraction Coverage



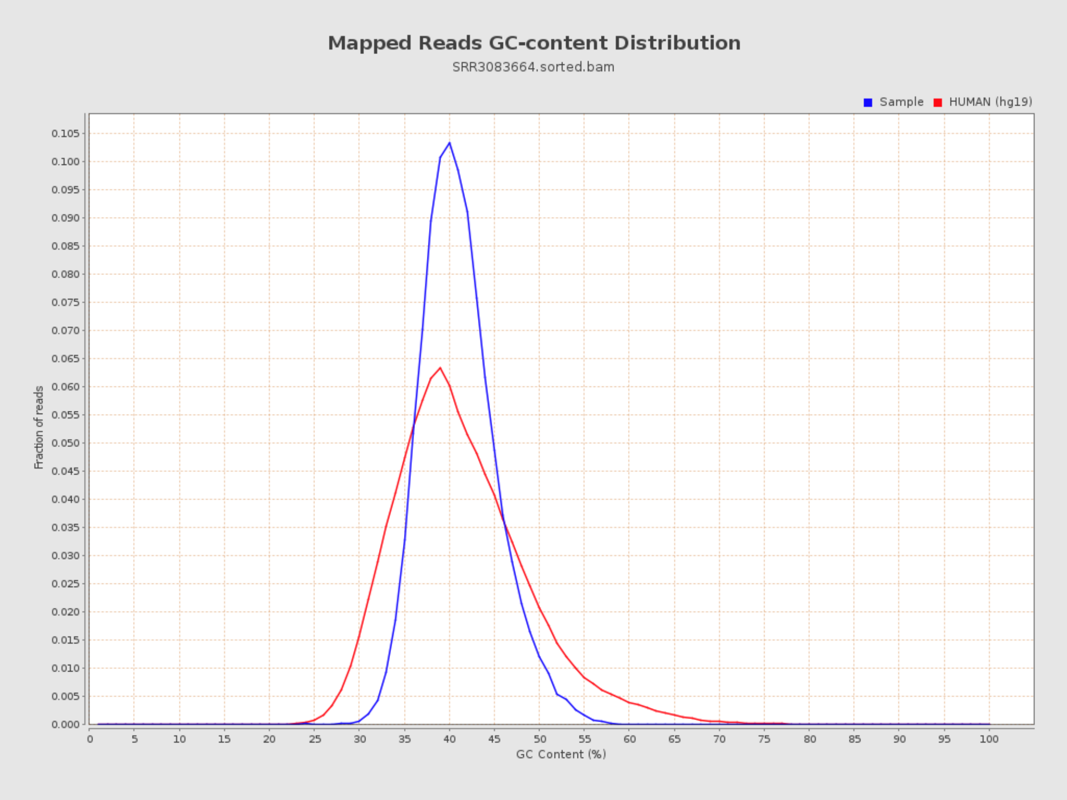
7. Results : Duplication Rate Histogram



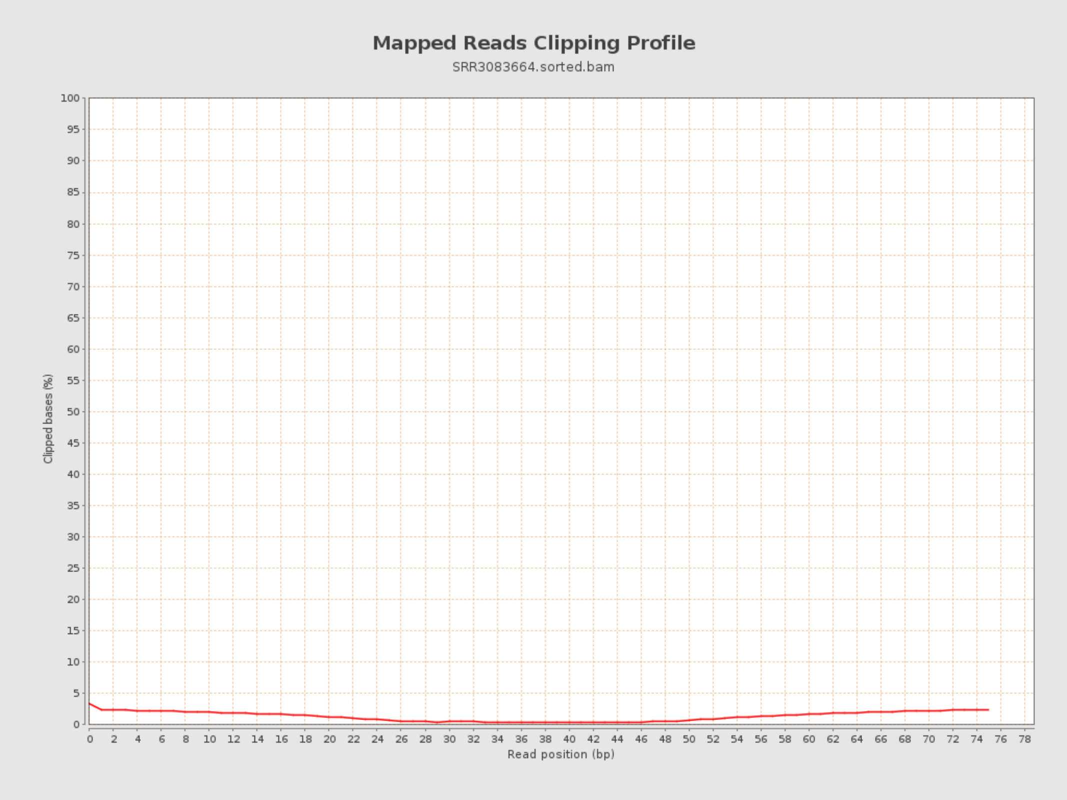
8. Results : Mapped Reads Nucleotide Content



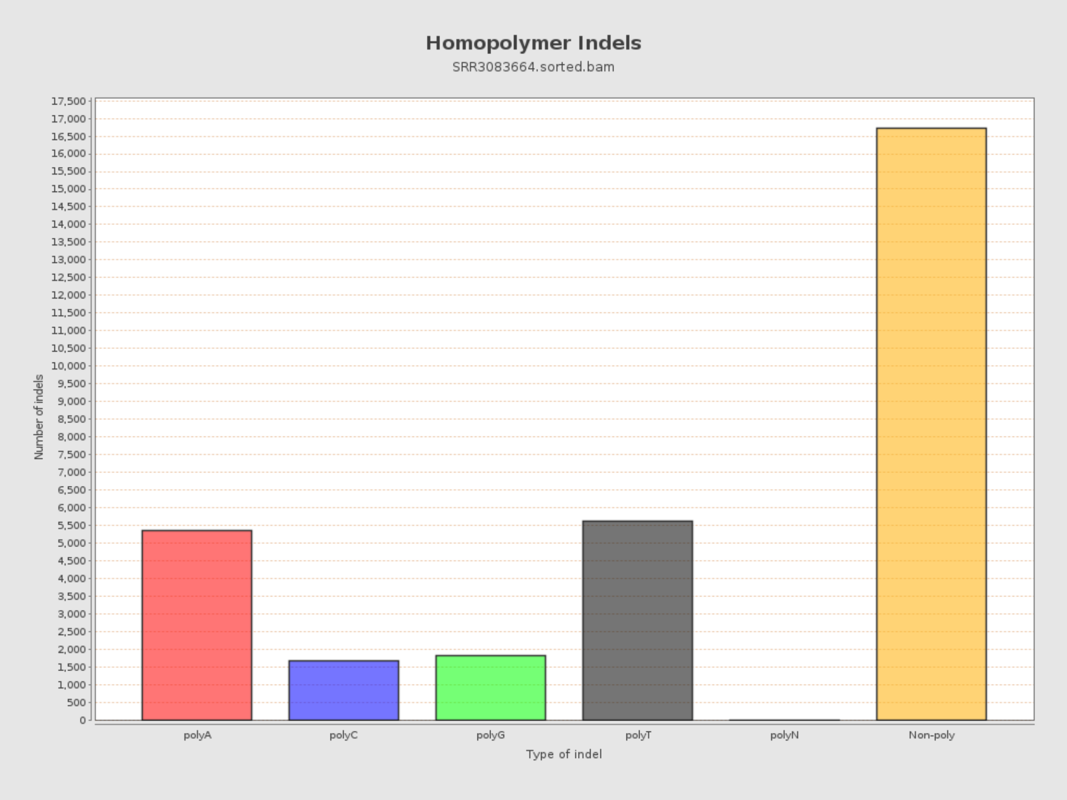
9. Results : Mapped Reads GC-content Distribution



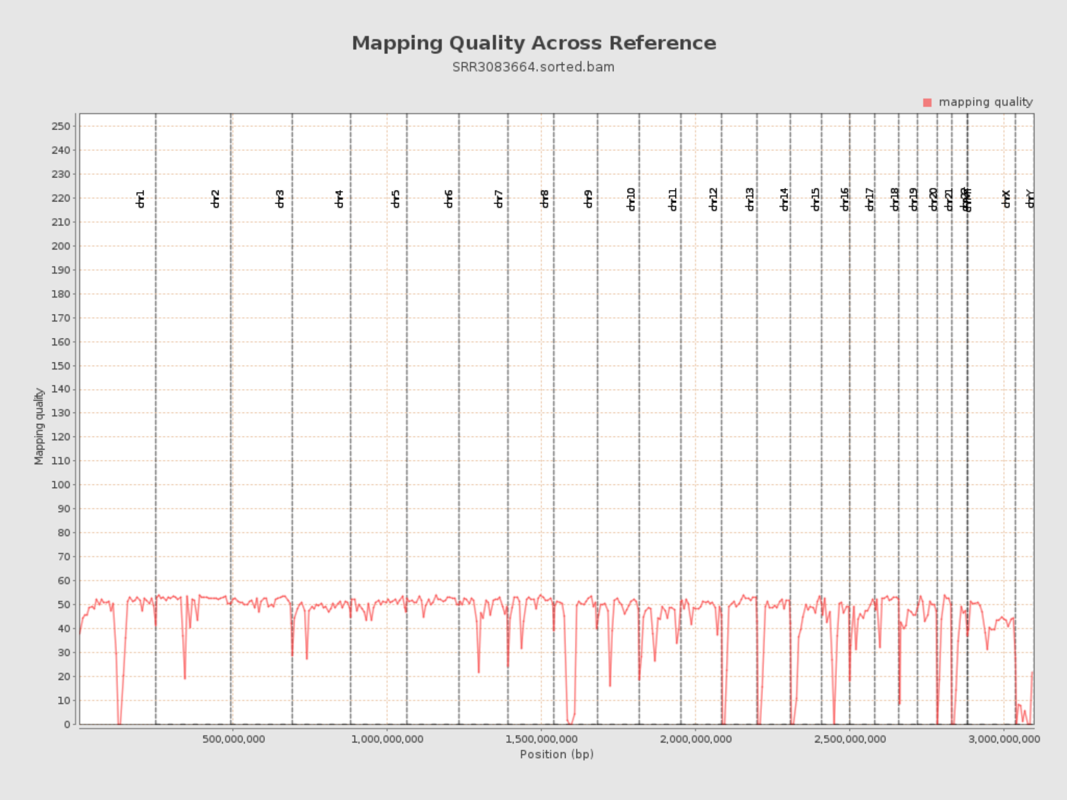
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram