Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 03:03:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083670.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_SRR3083670 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083670.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 03:03:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083670.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,500,742
Mapped reads	2,632,012 / 75.18%
Unmapped reads	868,730 / 24.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,662 / 0.59%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	124,953 / 3.57%
Duplication rate	3.99%
Clipped reads	1,947,988 / 55.65%

2.2. ACGT Content

Number/percentage of A's	44,979,720 / 29.23%
Number/percentage of C's	31,573,946 / 20.52%
Number/percentage of T's	43,927,651 / 28.54%
Number/percentage of G's	33,404,118 / 21.7%
Number/percentage of N's	19,366 / 0.01%
GC Percentage	42.22%

2.3. Coverage

Mean	0.0497

Standard Deviation	0.3984

2.4. Mapping Quality

Mean Mapping Quality	44

2.5. Mismatches and indels

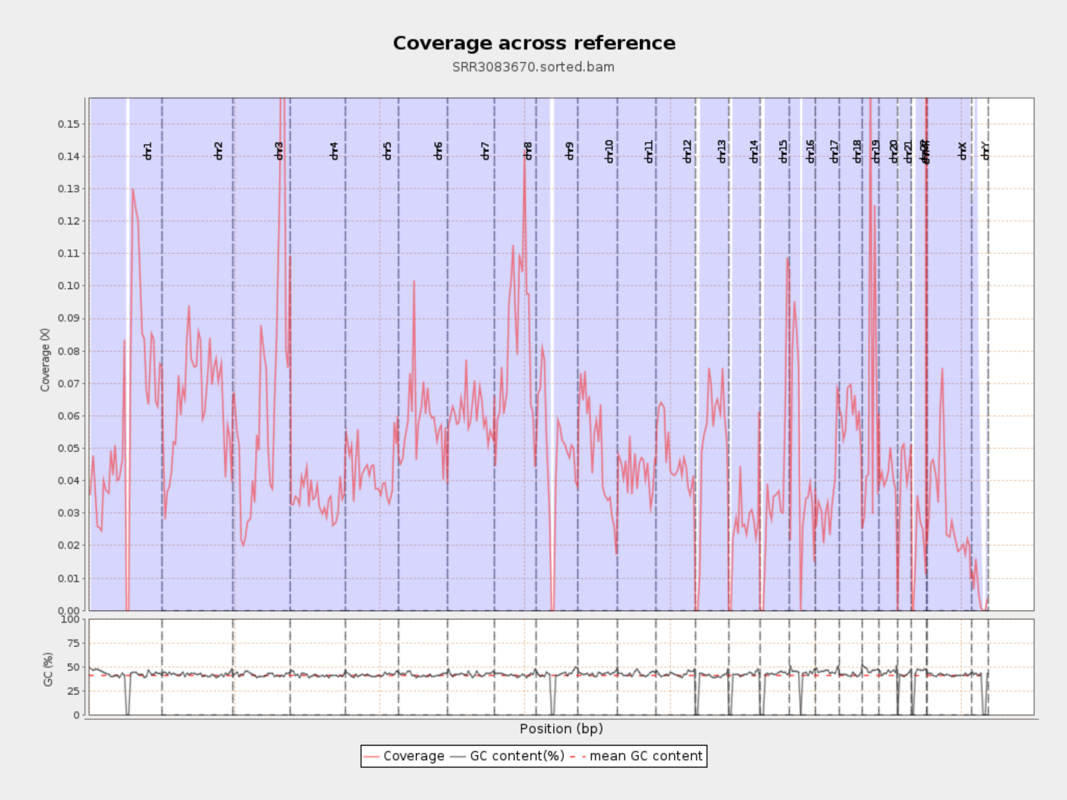
General error rate	0.82%
Mismatches	1,252,880
Insertions	9,847
Mapped reads with at least one insertion	0.37%
Deletions	28,225
Mapped reads with at least one deletion	1.06%
Homopolymer indels	45.1%

2.6. Chromosome stats

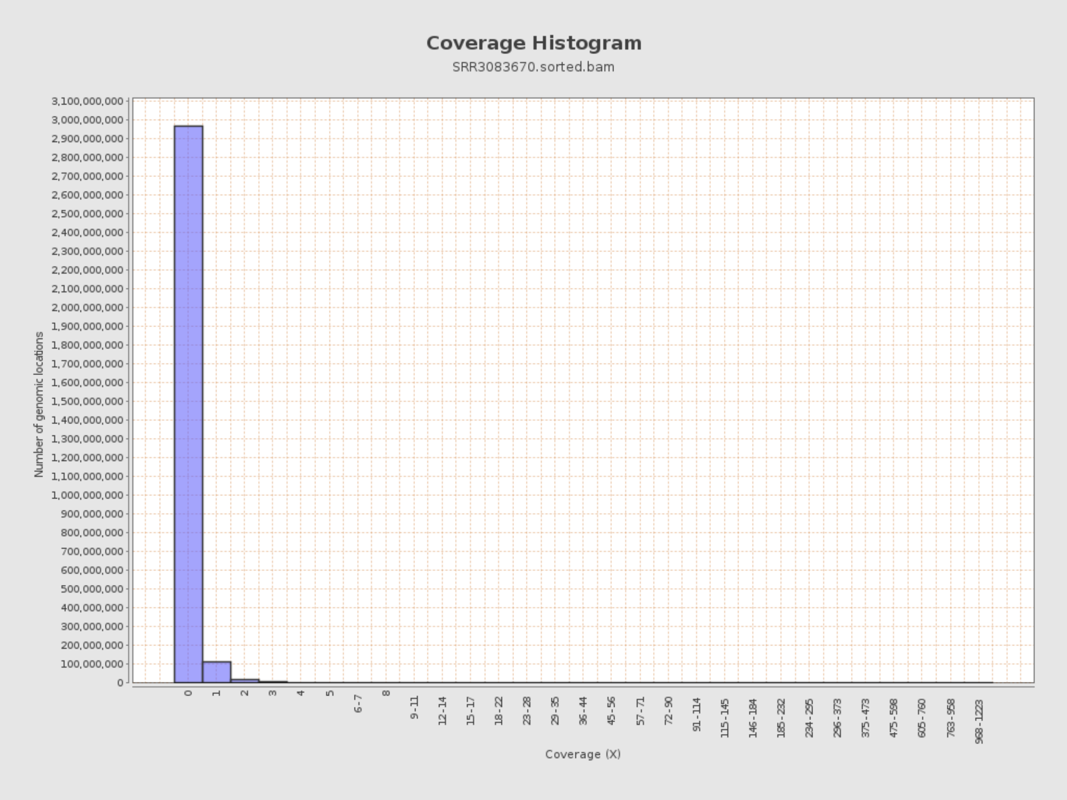
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14753334	0.0592	0.9164
chr2	243199373	15587495	0.0641	0.3715
chr3	198022430	13146166	0.0664	0.3029
chr4	191154276	6572103	0.0344	0.2254
chr5	180915260	7833291	0.0433	0.2415
chr6	171115067	10030059	0.0586	0.338
chr7	159138663	9675513	0.0608	0.4626

chr8	146364022	12106200	0.0827	0.4665
chr9	141213431	6842391	0.0485	0.2927
chr10	135534747	6744926	0.0498	0.3397
chr11	135006516	5764033	0.0427	0.2602
chr12	133851895	6315119	0.0472	0.2516
chr13	115169878	5866329	0.0509	0.2599
chr14	107349540	2641178	0.0246	0.184
chr15	102531392	3805014	0.0371	0.2252
chr16	90354753	4154175	0.046	0.2572
chr17	81195210	2907094	0.0358	0.2272
chr18	78077248	4711282	0.0603	0.4223
chr19	59128983	3840443	0.065	0.6088
chr20	63025520	2560237	0.0406	0.2389
chr21	48129895	1914814	0.0398	0.2355
chr22	51304566	942132	0.0184	0.1536
chrMT	16571	23664	1.428	1.4096
chrX	155270560	4904970	0.0316	0.2234
chrY	59373566	306792	0.0052	0.1039

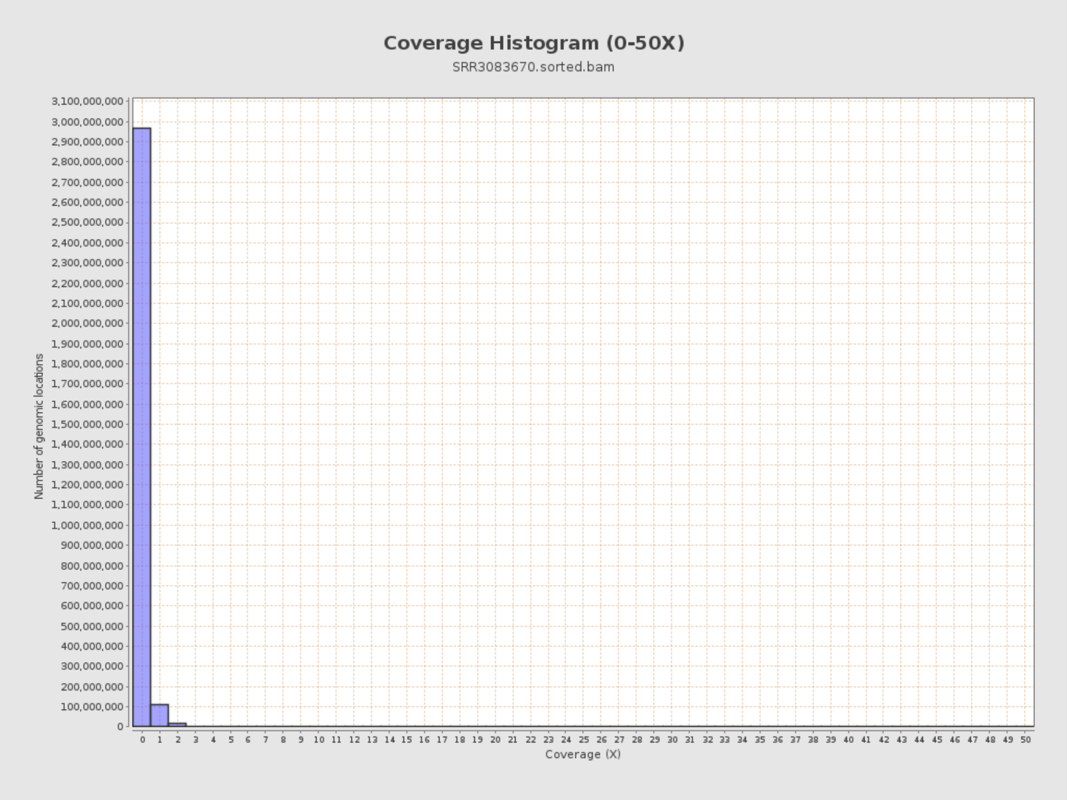
3. Results : Coverage across reference



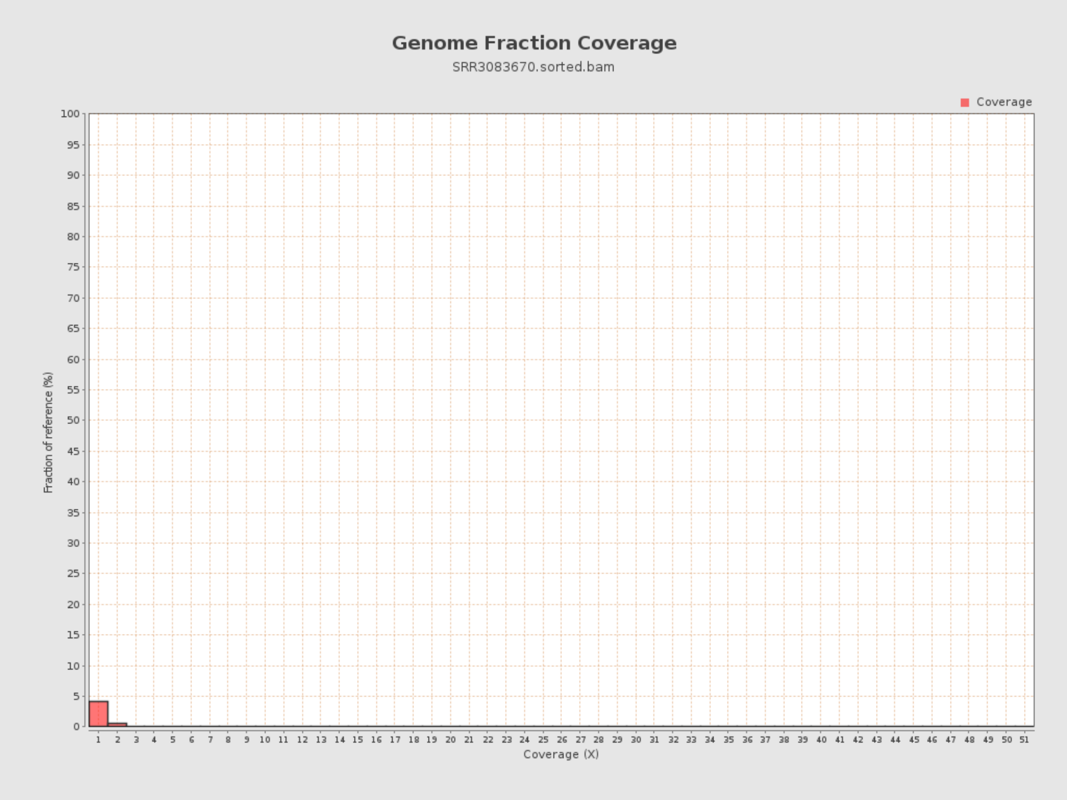
4. Results : Coverage Histogram



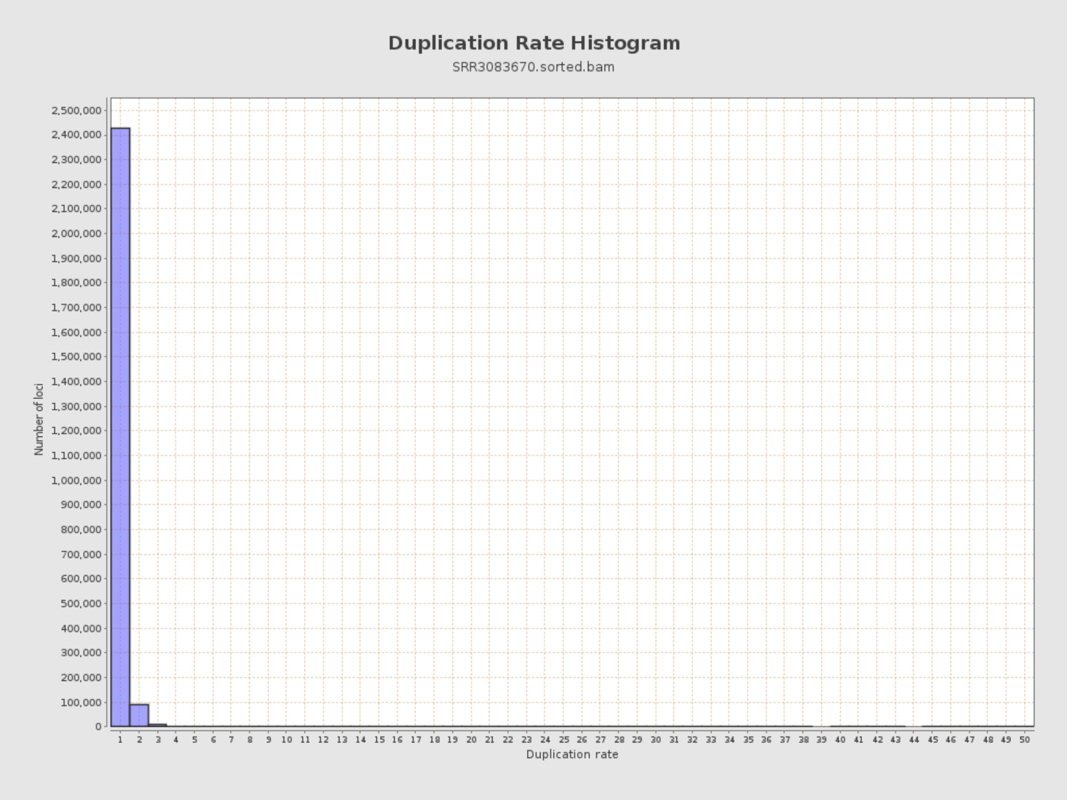
5. Results : Coverage Histogram (0-50X)



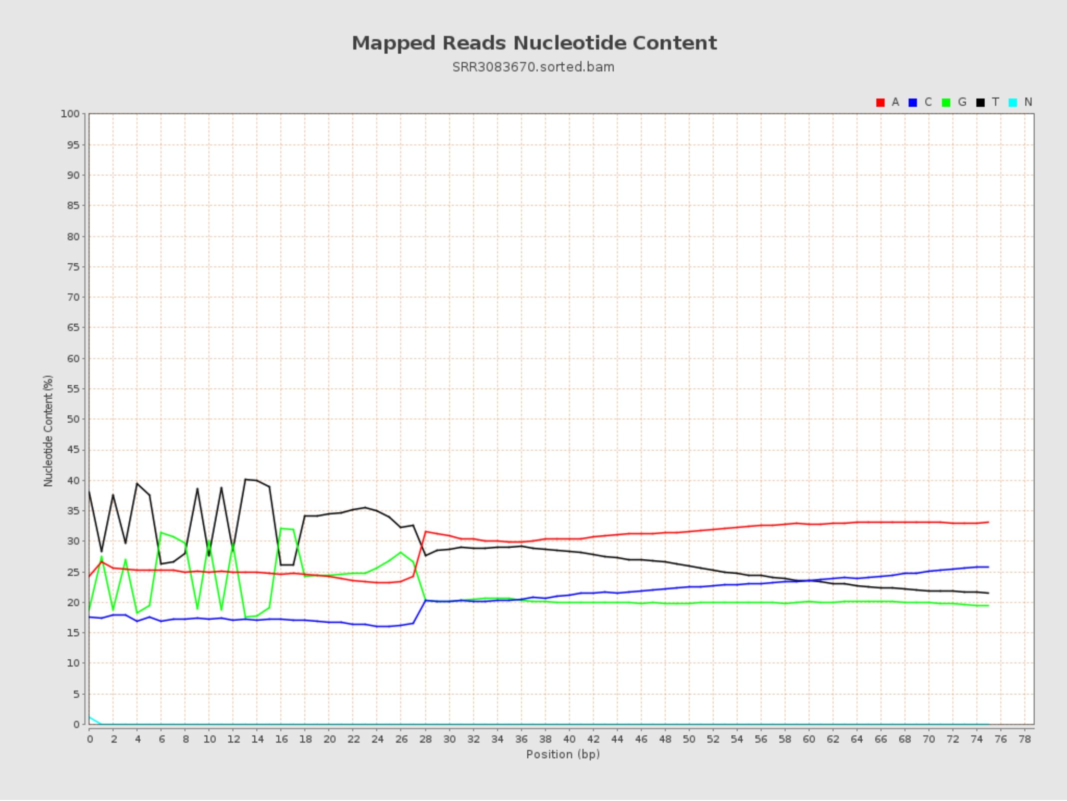
6. Results : Genome Fraction Coverage



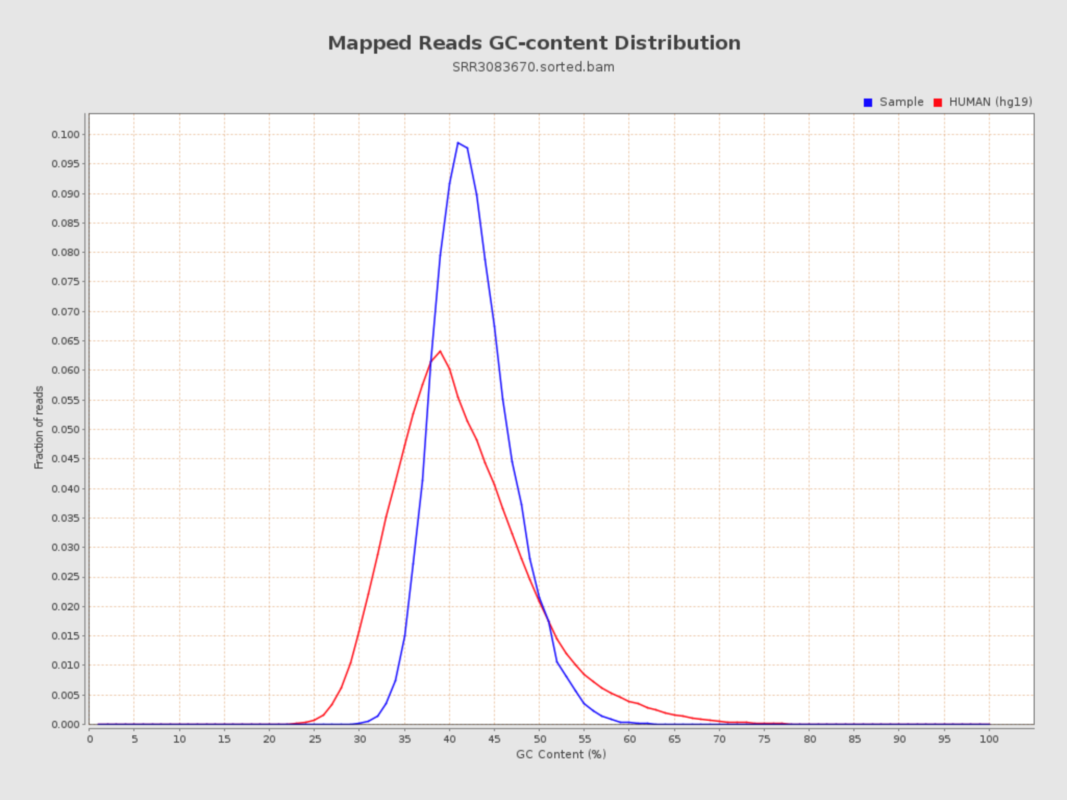
7. Results : Duplication Rate Histogram



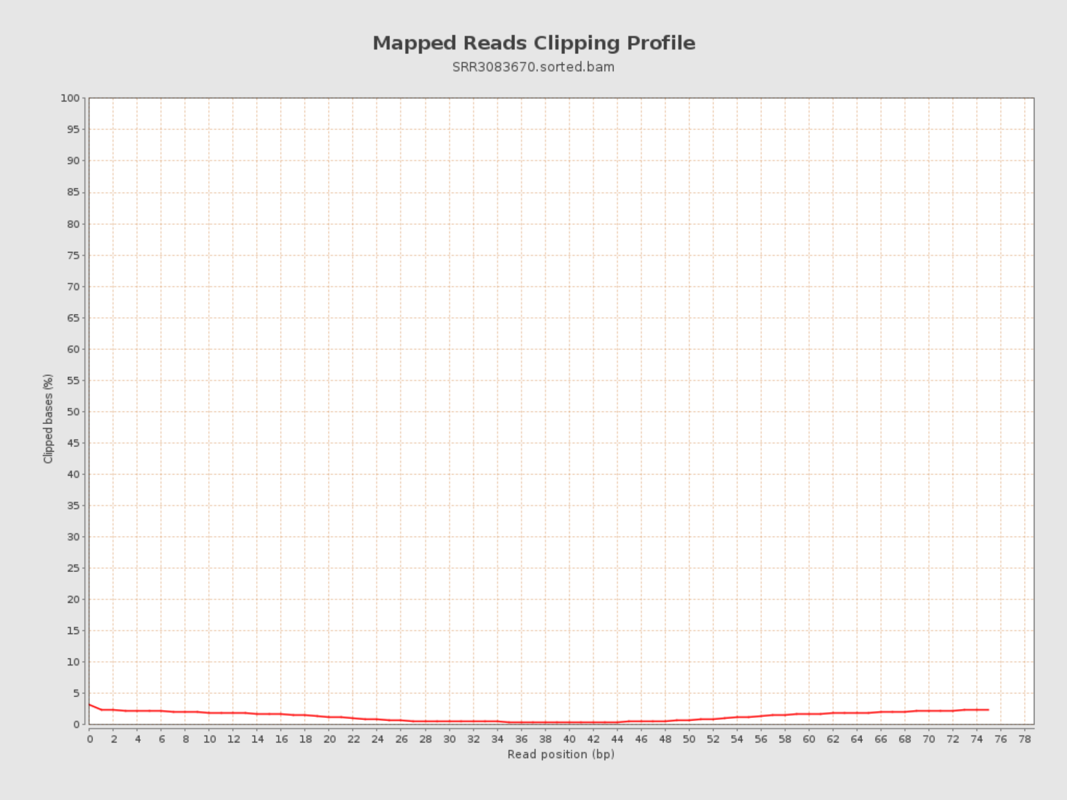
8. Results : Mapped Reads Nucleotide Content



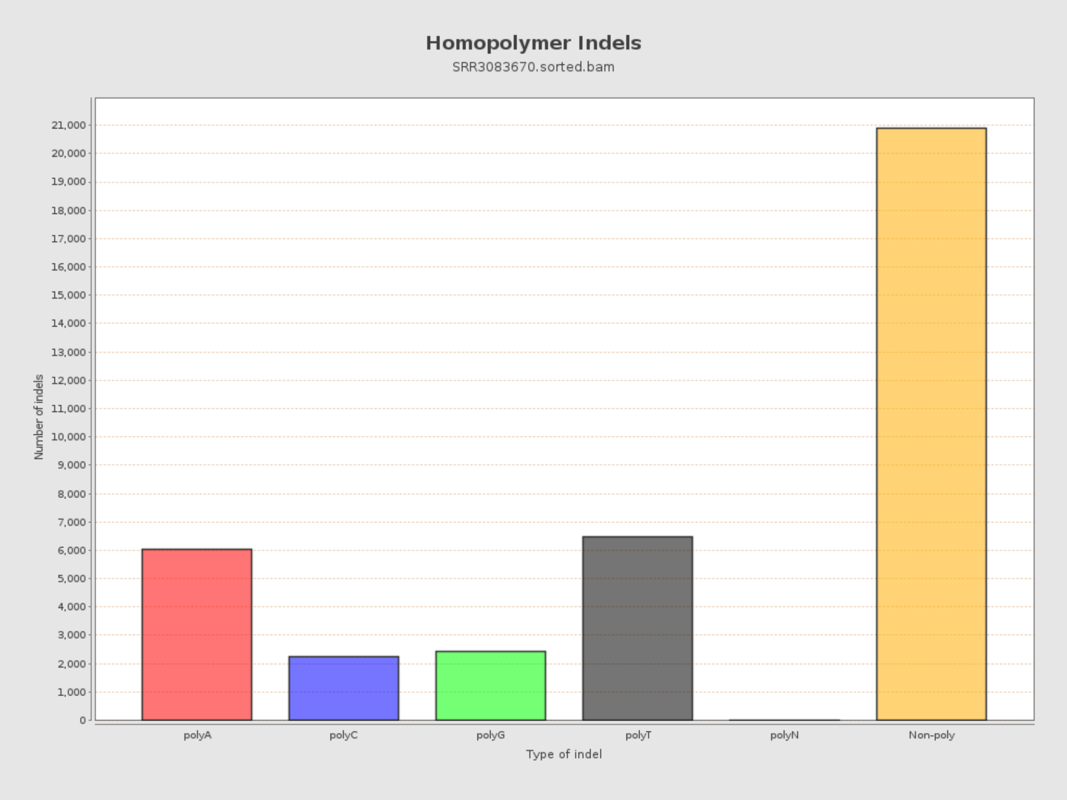
9. Results : Mapped Reads GC-content Distribution



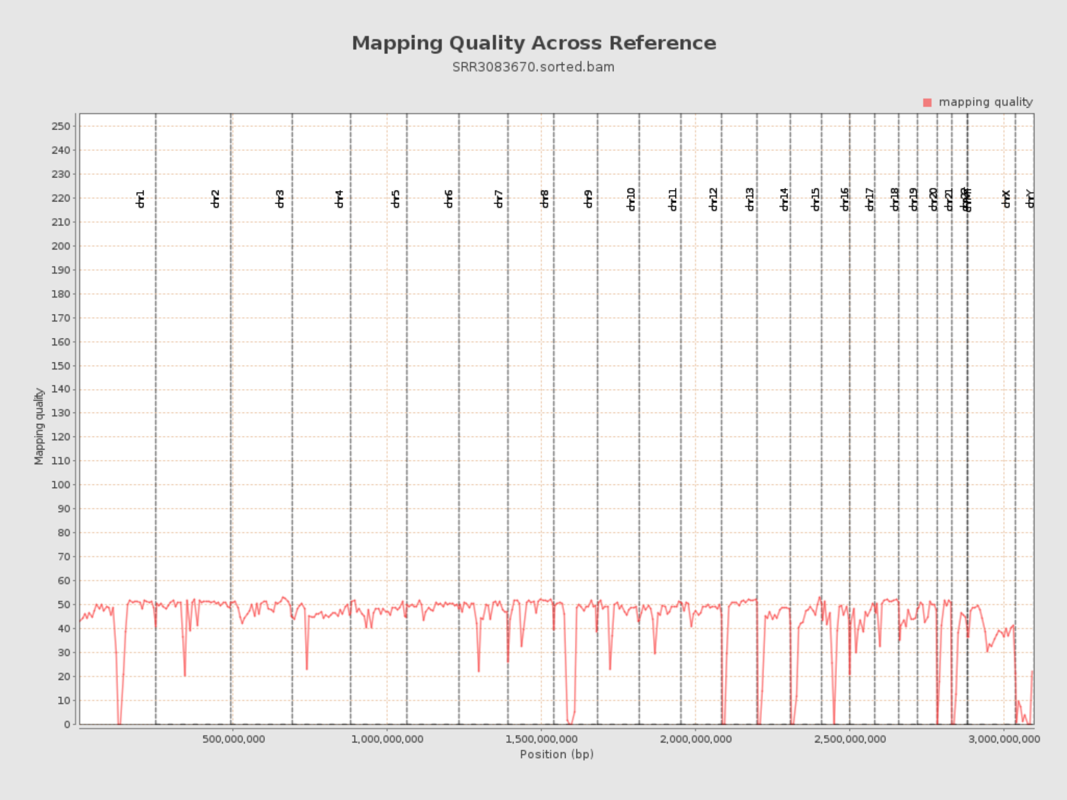
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram