Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 18:32:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084865.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_SRR3084865 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084865.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 18:32:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084865.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,051,527
Mapped reads	1,857,220 / 90.53%
Unmapped reads	194,307 / 9.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,665 / 1.01%
Read min/max/mean length	30 / 76 / 76.35
Duplicated reads (estimated)	83,372 / 4.06%
Duplication rate	3.9%
Clipped reads	812,639 / 39.61%

2.2. ACGT Content

Number/percentage of A's	33,901,429 / 27.26%
Number/percentage of C's	23,456,330 / 18.86%
Number/percentage of T's	38,865,003 / 31.25%
Number/percentage of G's	28,141,084 / 22.62%
Number/percentage of N's	17,224 / 0.01%
GC Percentage	41.48%

2.3. Coverage

Mean	0.0402

Standard Deviation	0.2808

2.4. Mapping Quality

Mean Mapping Quality	45.52

2.5. Mismatches and indels

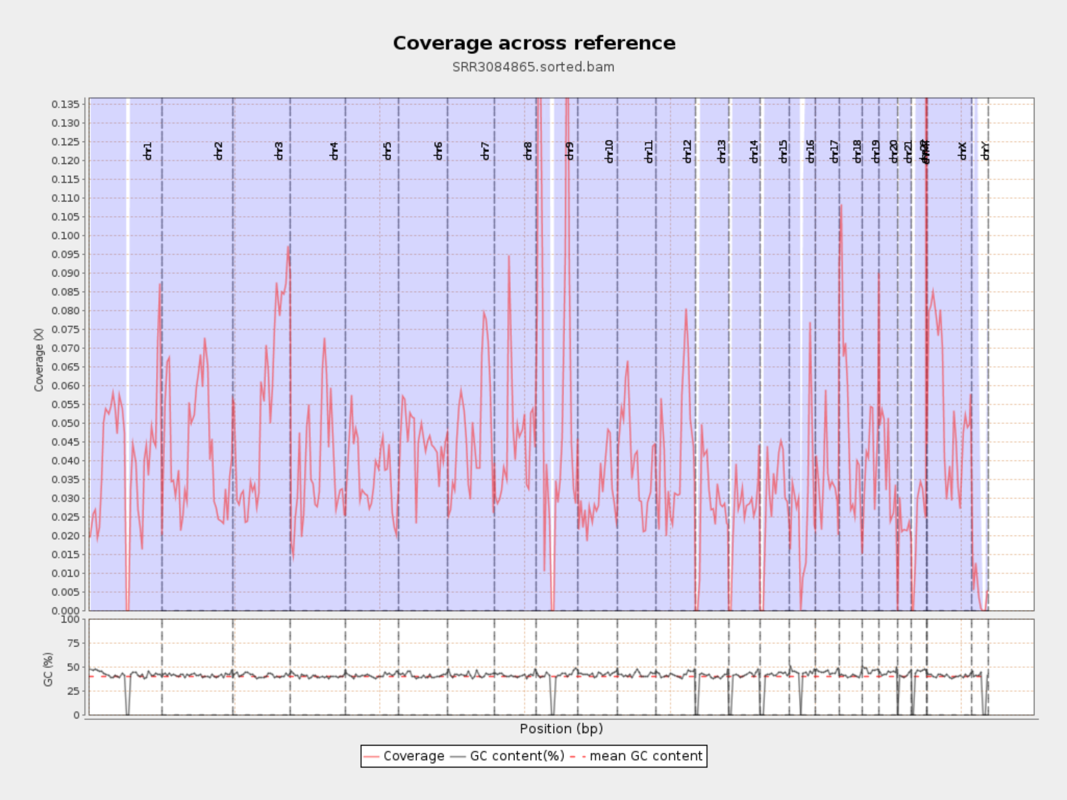
General error rate	0.78%
Mismatches	950,601
Insertions	9,718
Mapped reads with at least one insertion	0.52%
Deletions	28,523
Mapped reads with at least one deletion	1.52%
Homopolymer indels	48.27%

2.6. Chromosome stats

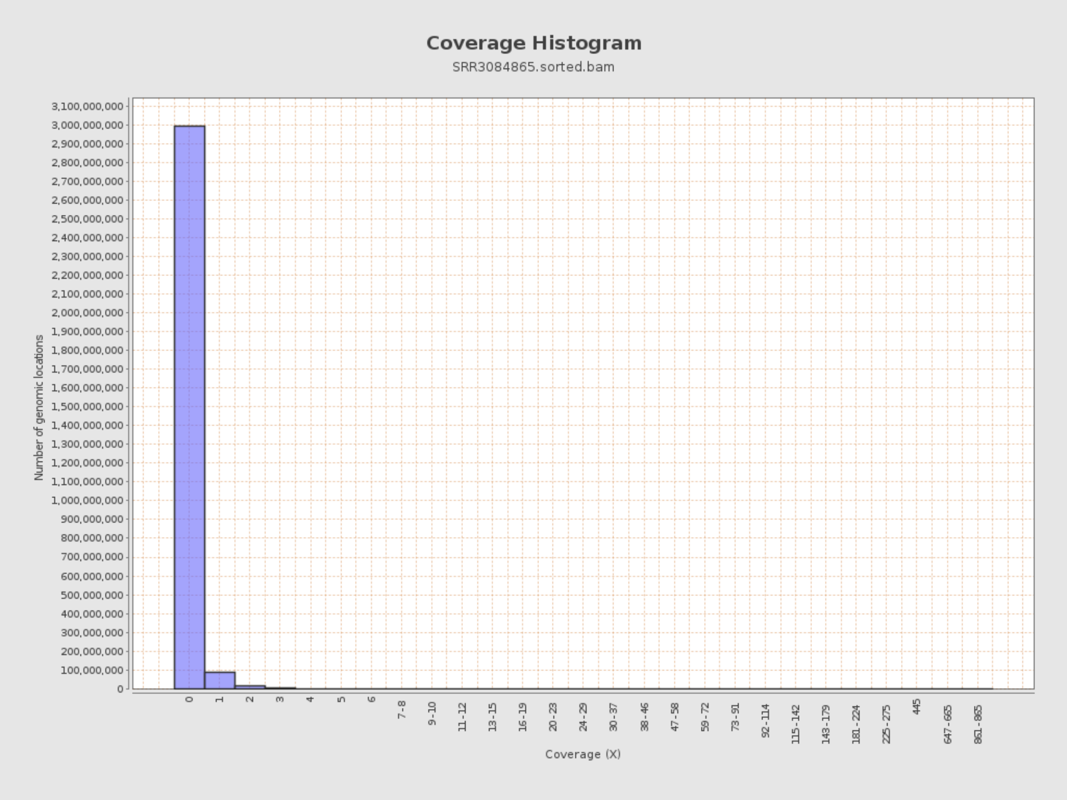
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9904449	0.0397	0.3308
chr2	243199373	10356094	0.0426	0.4505
chr3	198022430	10661429	0.0538	0.2713
chr4	191154276	7201506	0.0377	0.2282
chr5	180915260	6608314	0.0365	0.2239
chr6	171115067	7673979	0.0448	0.2636
chr7	159138663	7595325	0.0477	0.2862

chr8	146364022	6634471	0.0453	0.2886
chr9	141213431	8457289	0.0599	0.3308
chr10	135534747	4110889	0.0303	0.2101
chr11	135006516	5488331	0.0407	0.2682
chr12	133851895	5623152	0.042	0.2417
chr13	115169878	3076980	0.0267	0.1911
chr14	107349540	2714601	0.0253	0.1925
chr15	102531392	2988193	0.0291	0.2067
chr16	90354753	2599887	0.0288	0.2046
chr17	81195210	2838921	0.035	0.2268
chr18	78077248	4040126	0.0517	0.4071
chr19	59128983	2533377	0.0428	0.2833
chr20	63025520	2435539	0.0386	0.2312
chr21	48129895	1003944	0.0209	0.1737
chr22	51304566	1096499	0.0214	0.1689
chrMT	16571	24611	1.4852	1.5659
chrX	155270560	8469120	0.0545	0.2799
chrY	59373566	290725	0.0049	0.1088

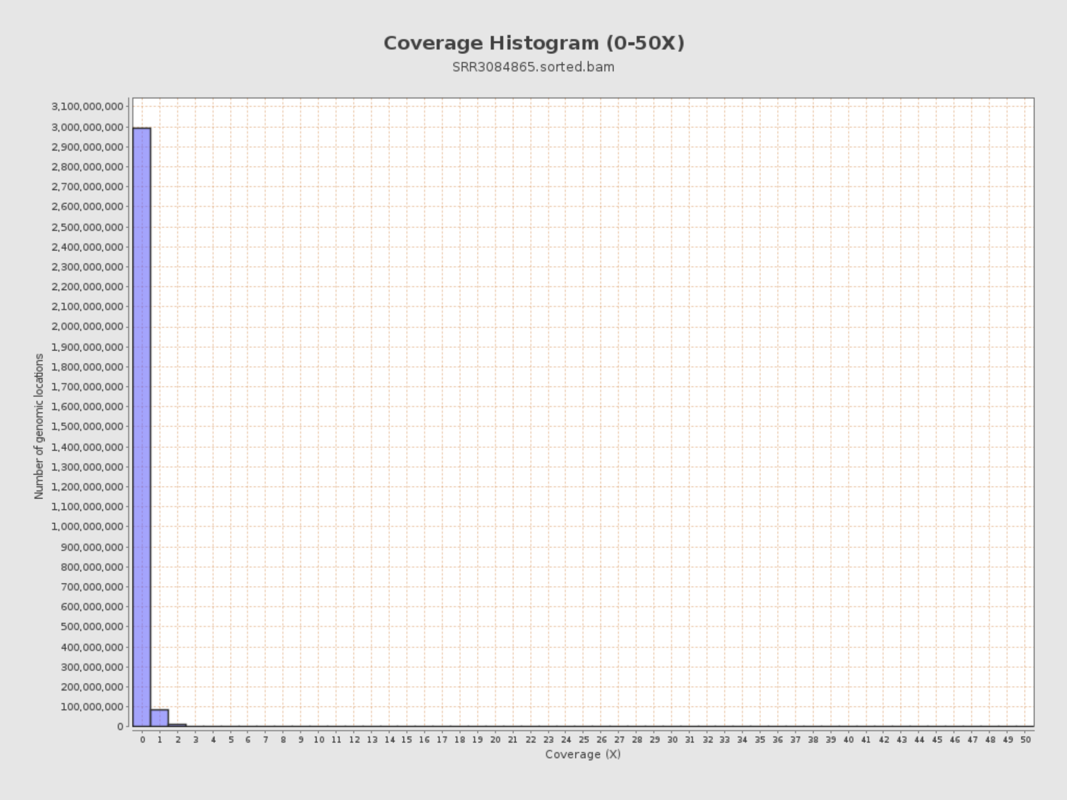
3. Results : Coverage across reference



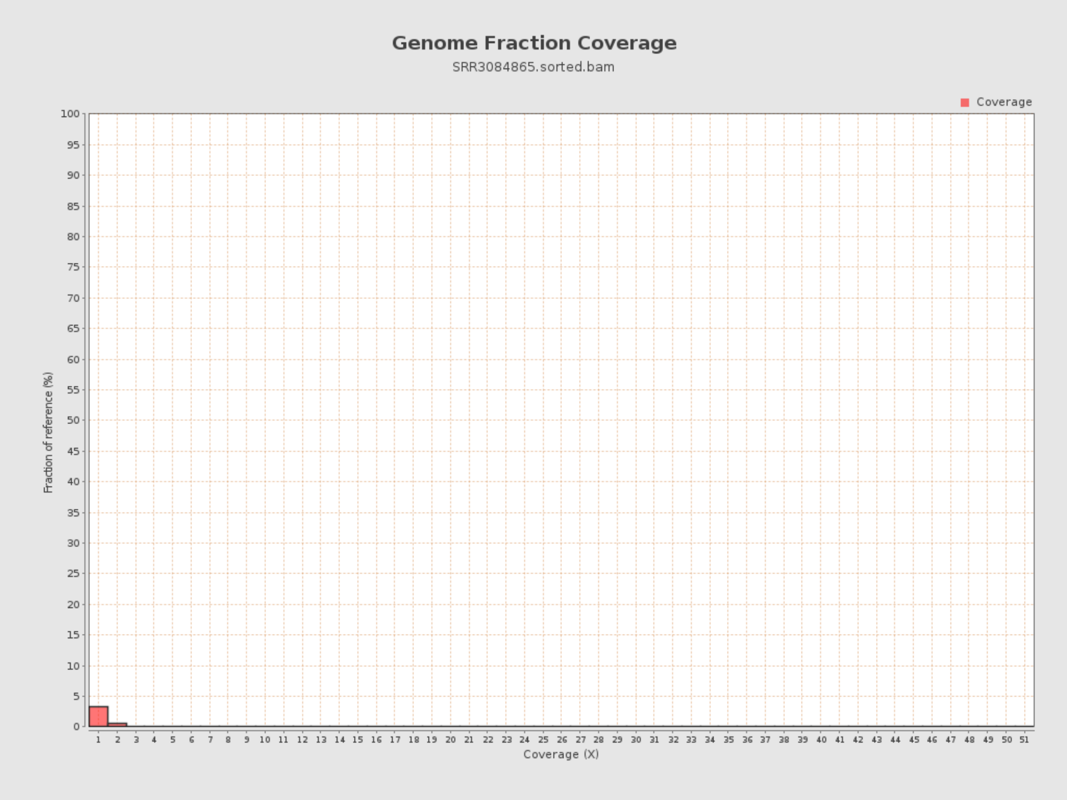
4. Results : Coverage Histogram



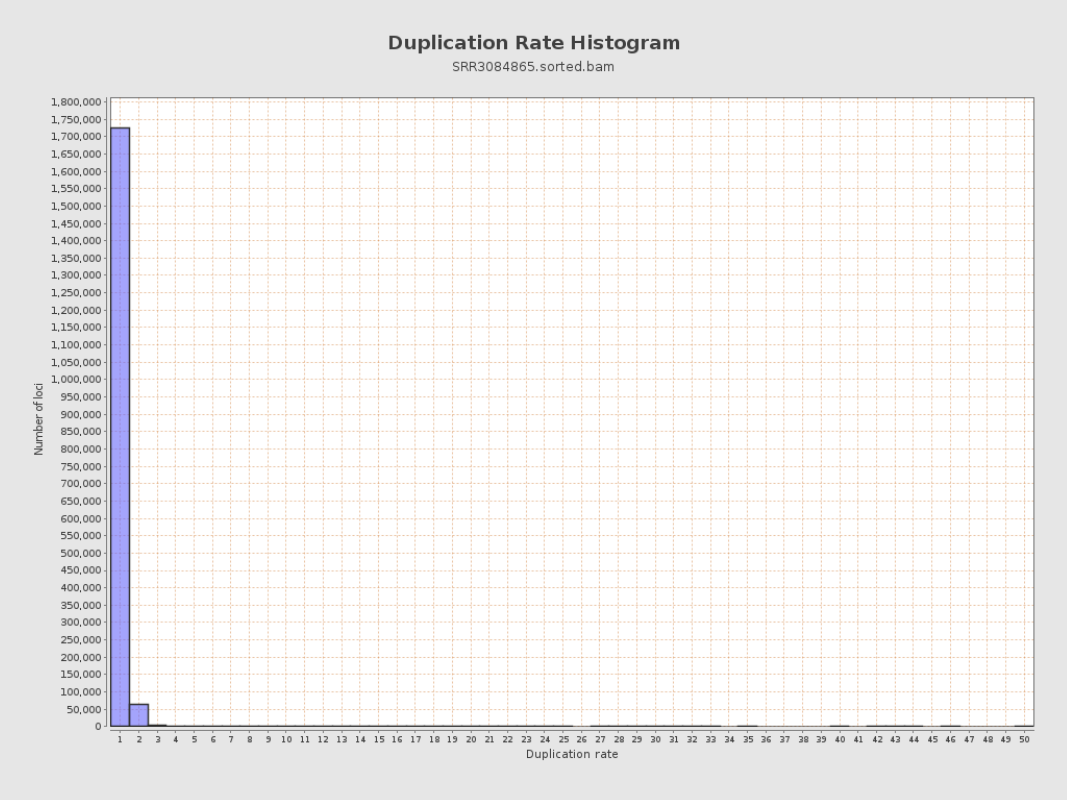
5. Results : Coverage Histogram (0-50X)



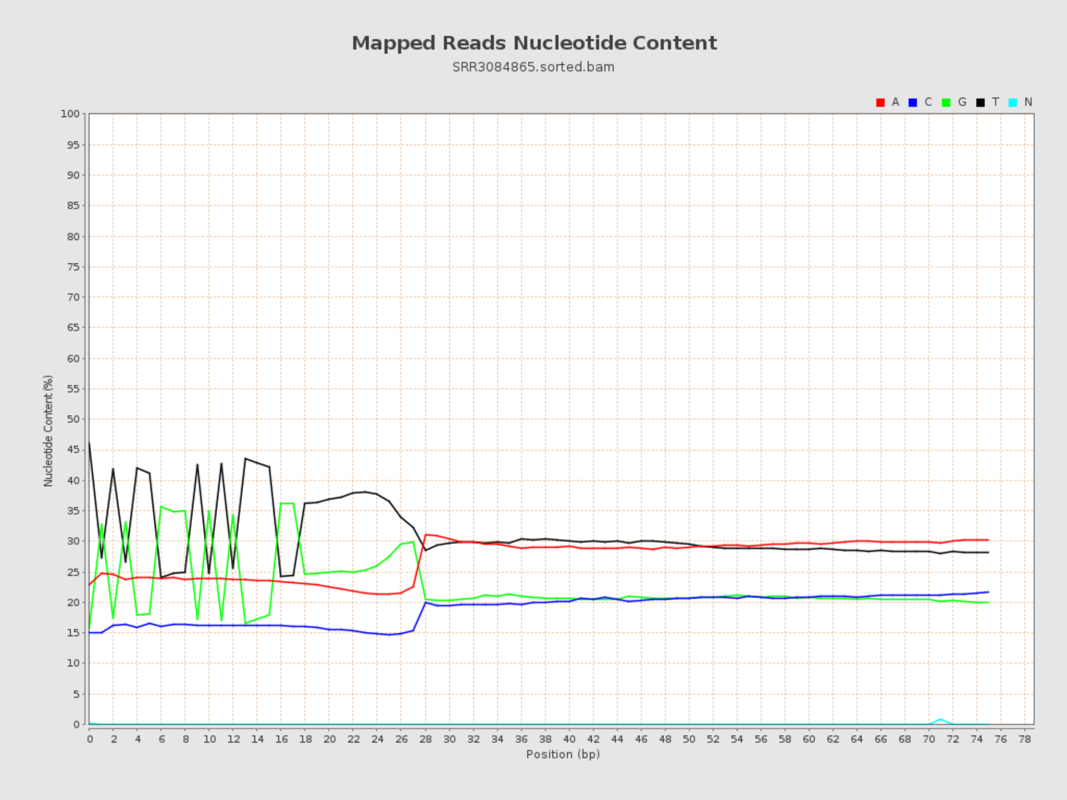
6. Results : Genome Fraction Coverage



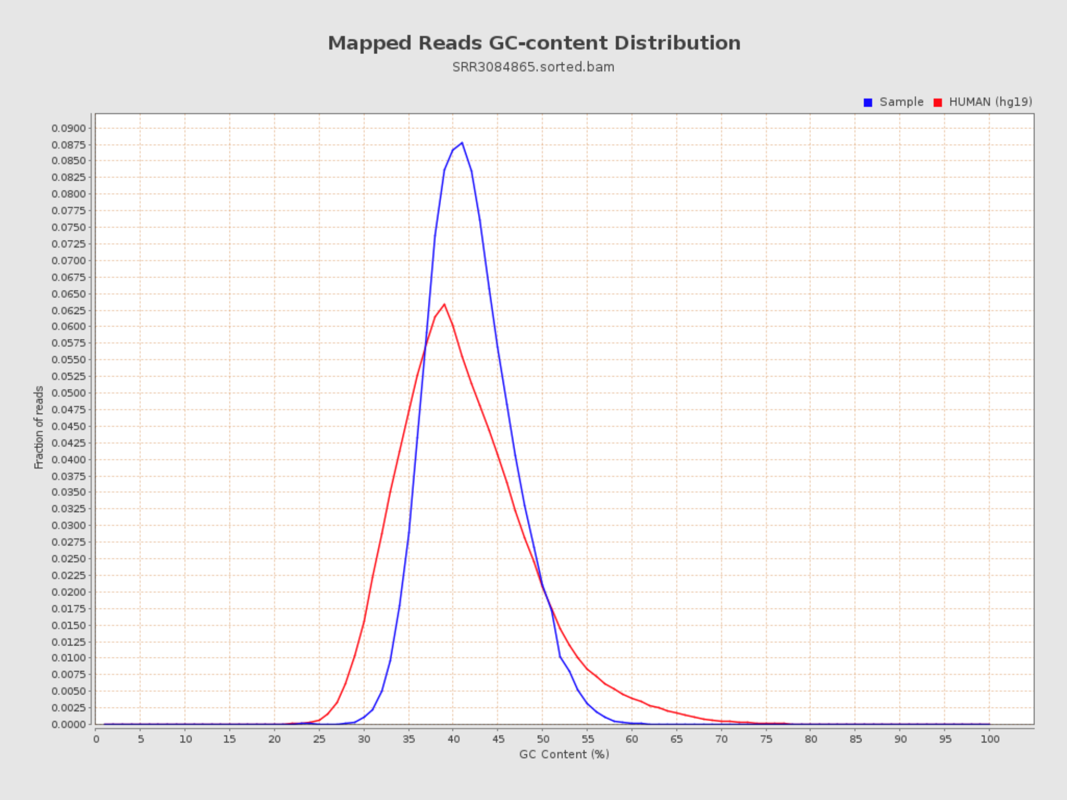
7. Results : Duplication Rate Histogram



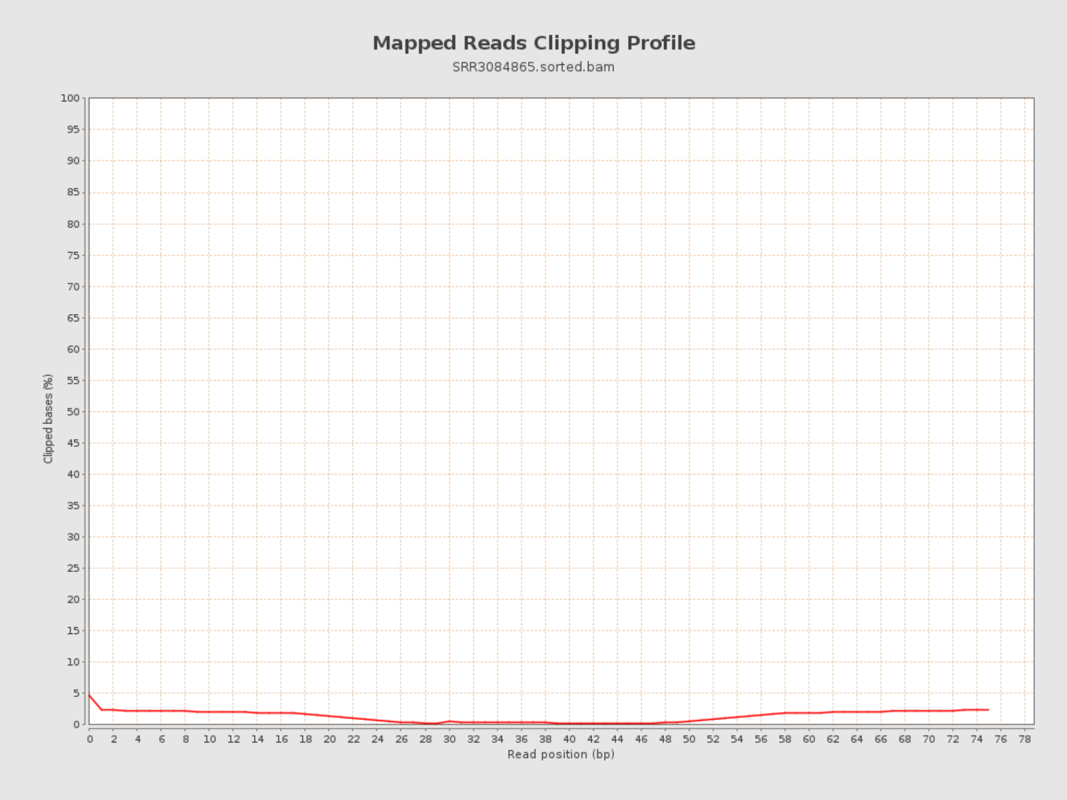
8. Results : Mapped Reads Nucleotide Content



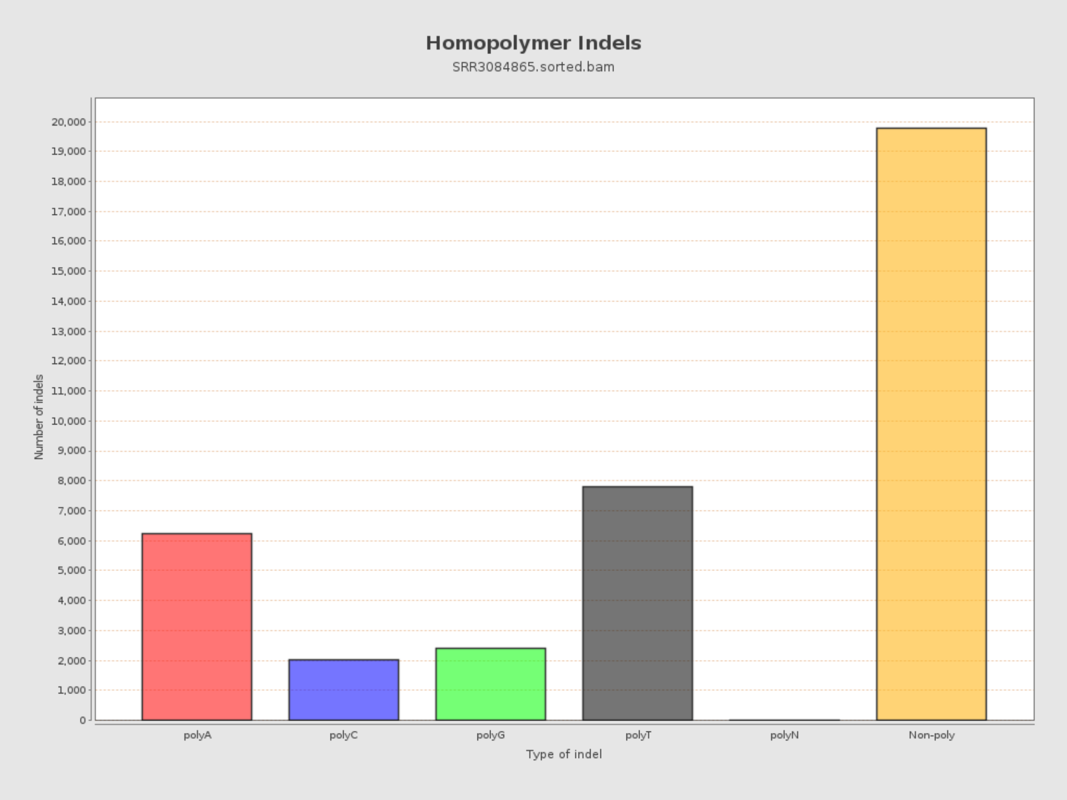
9. Results : Mapped Reads GC-content Distribution



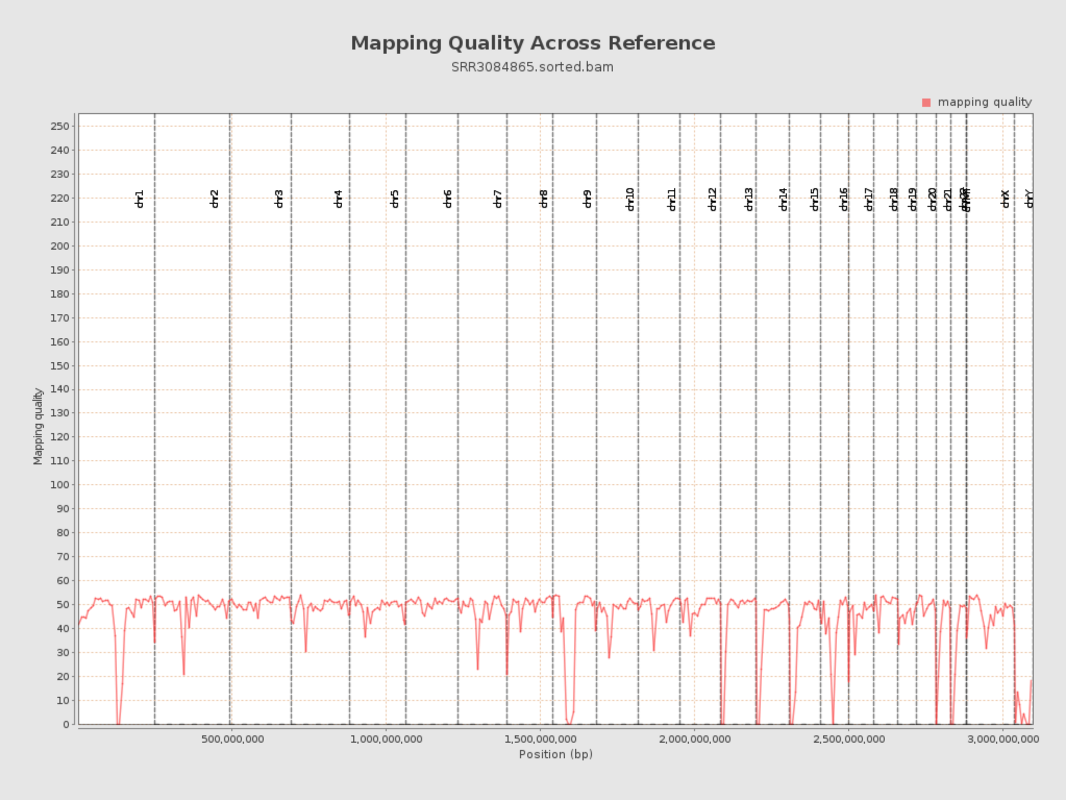
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram