Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 17:05:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084845.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_SRR3084845 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084845.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 17:05:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084845.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,935,829
Mapped reads	2,598,355 / 88.5%
Unmapped reads	337,474 / 11.5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,262 / 0.76%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	143,865 / 4.9%
Duplication rate	4.43%
Clipped reads	891,607 / 30.37%

2.2. ACGT Content

Number/percentage of A's	52,345,969 / 29.11%
Number/percentage of C's	32,951,826 / 18.33%
Number/percentage of T's	57,814,886 / 32.15%
Number/percentage of G's	36,667,811 / 20.39%
Number/percentage of N's	28,349 / 0.02%
GC Percentage	38.72%

2.3. Coverage

Mean	0.0581

Standard Deviation	0.5293

2.4. Mapping Quality

Mean Mapping Quality	48.09

2.5. Mismatches and indels

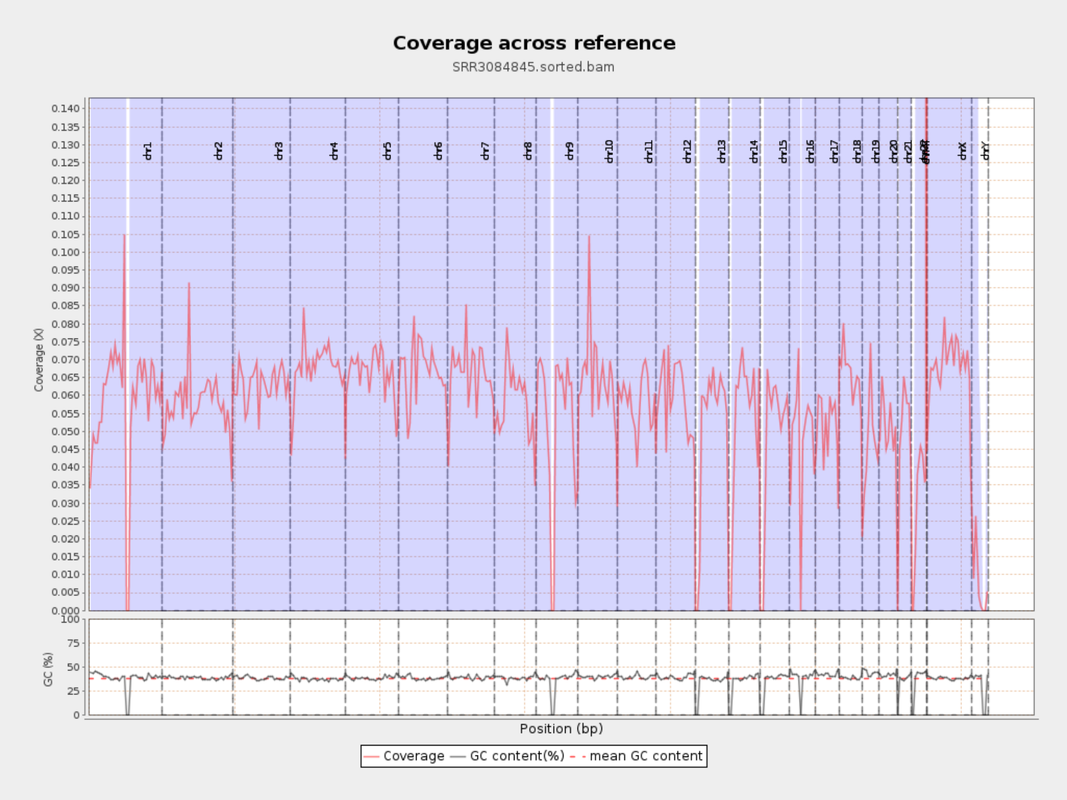
General error rate	0.86%
Mismatches	1,519,823
Insertions	15,143
Mapped reads with at least one insertion	0.58%
Deletions	39,917
Mapped reads with at least one deletion	1.52%
Homopolymer indels	47.73%

2.6. Chromosome stats

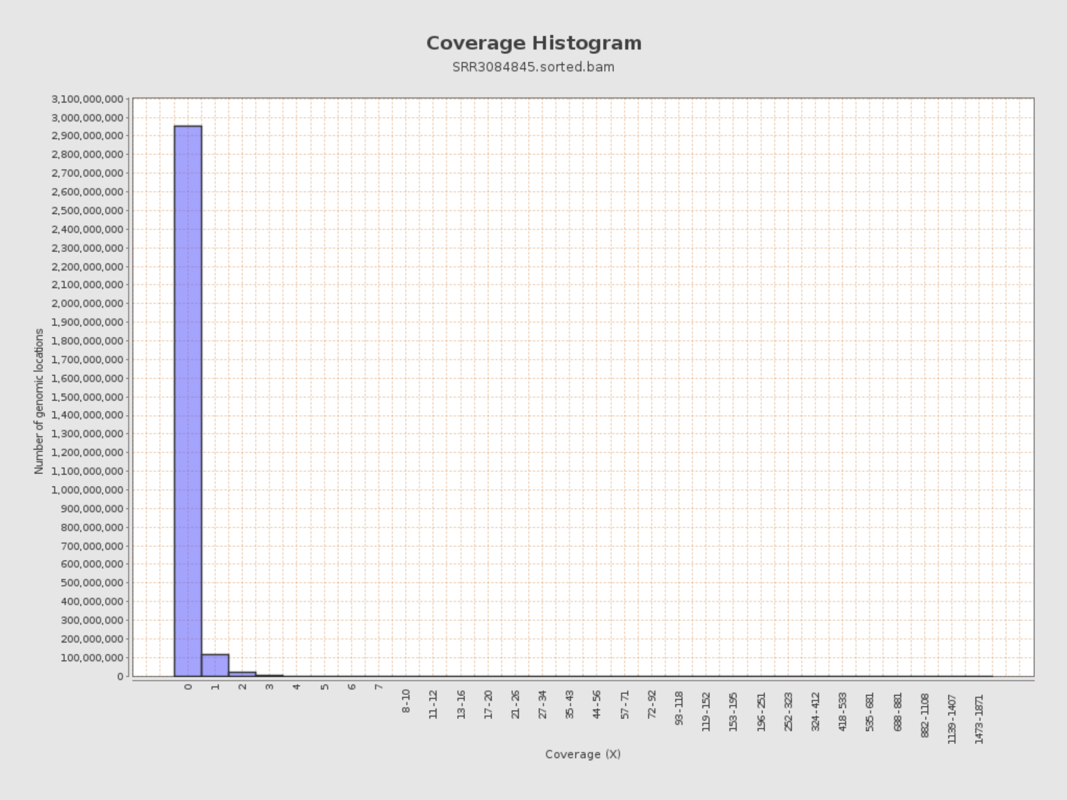
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14636744	0.0587	0.9674
chr2	243199373	14121999	0.0581	0.4626
chr3	198022430	12561973	0.0634	0.3056
chr4	191154276	12972001	0.0679	0.3447
chr5	180915260	11991838	0.0663	0.313
chr6	171115067	11438479	0.0668	0.33
chr7	159138663	10602734	0.0666	0.4367

chr8	146364022	8462905	0.0578	1.2166
chr9	141213431	7510277	0.0532	0.4451
chr10	135534747	8914320	0.0658	0.4961
chr11	135006516	7828610	0.058	0.3591
chr12	133851895	7968687	0.0595	0.3016
chr13	115169878	5810270	0.0504	0.271
chr14	107349540	5476458	0.051	0.3029
chr15	102531392	4917034	0.048	0.2636
chr16	90354753	4367039	0.0483	0.3031
chr17	81195210	4130039	0.0509	0.3156
chr18	78077248	5173202	0.0663	0.8973
chr19	59128983	2782598	0.0471	0.6726
chr20	63025520	3214312	0.051	0.2935
chr21	48129895	2340845	0.0486	0.2939
chr22	51304566	1460042	0.0285	0.2005
chrMT	16571	133702	8.0684	4.9439
chrX	155270560	10615246	0.0684	0.3513
chrY	59373566	449179	0.0076	0.2049

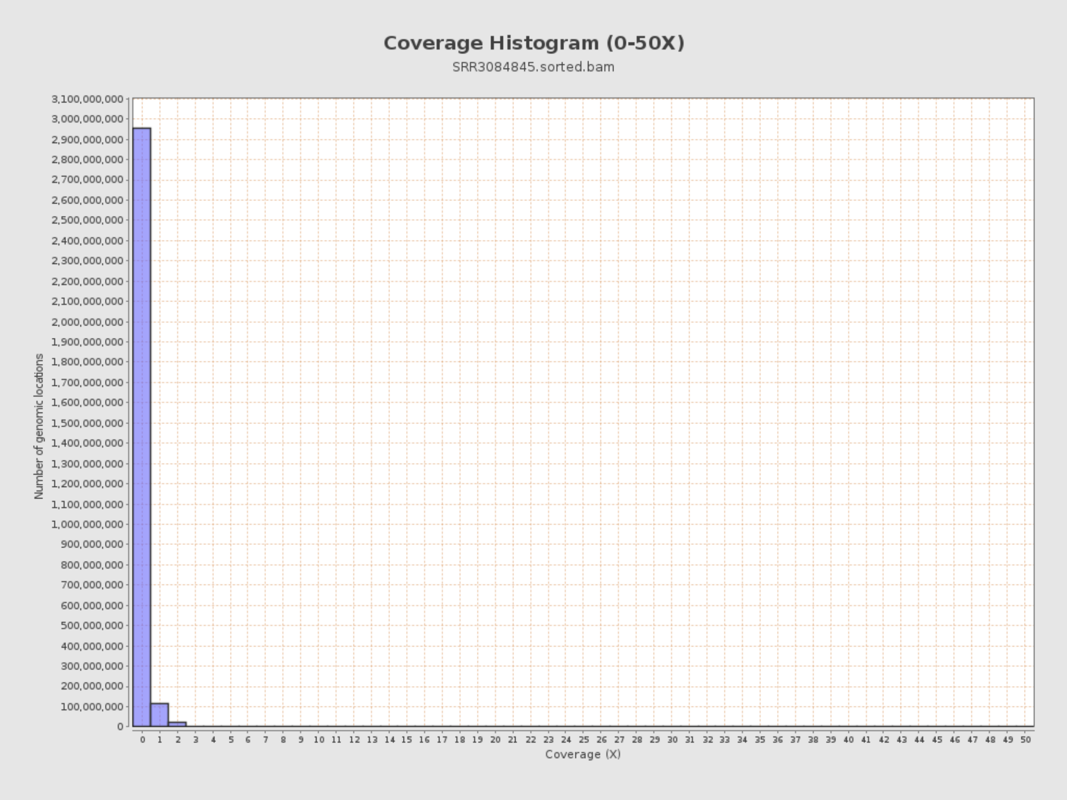
3. Results : Coverage across reference



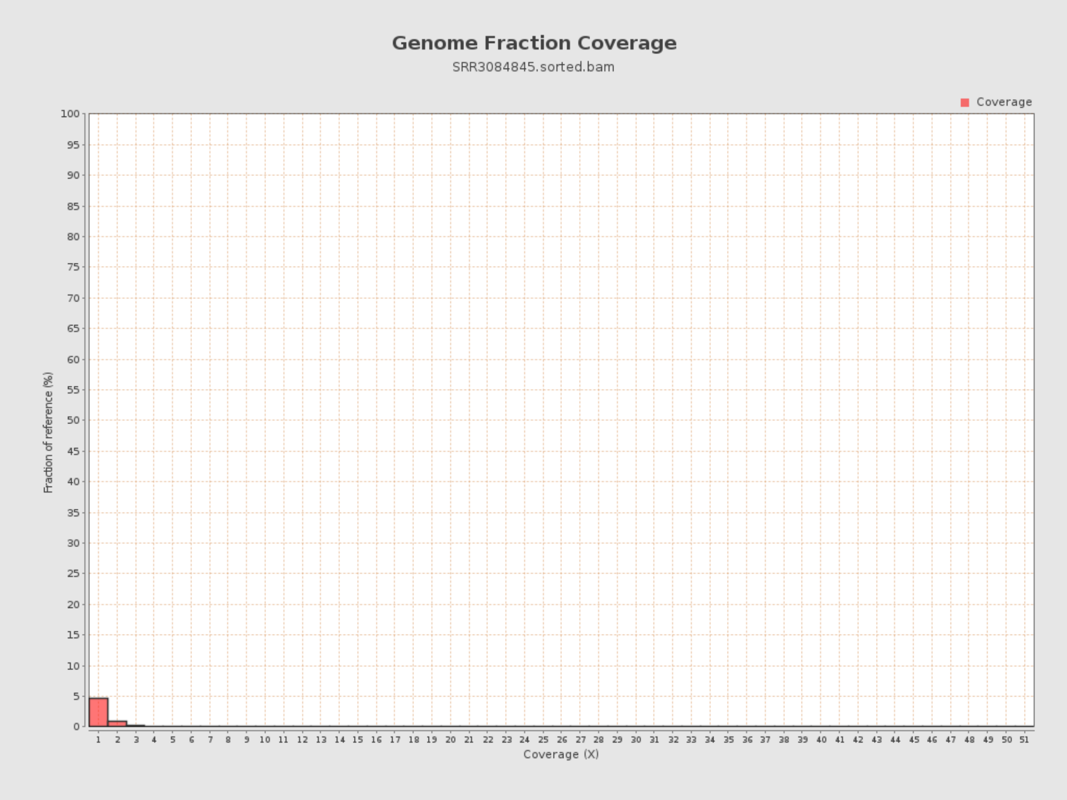
4. Results : Coverage Histogram



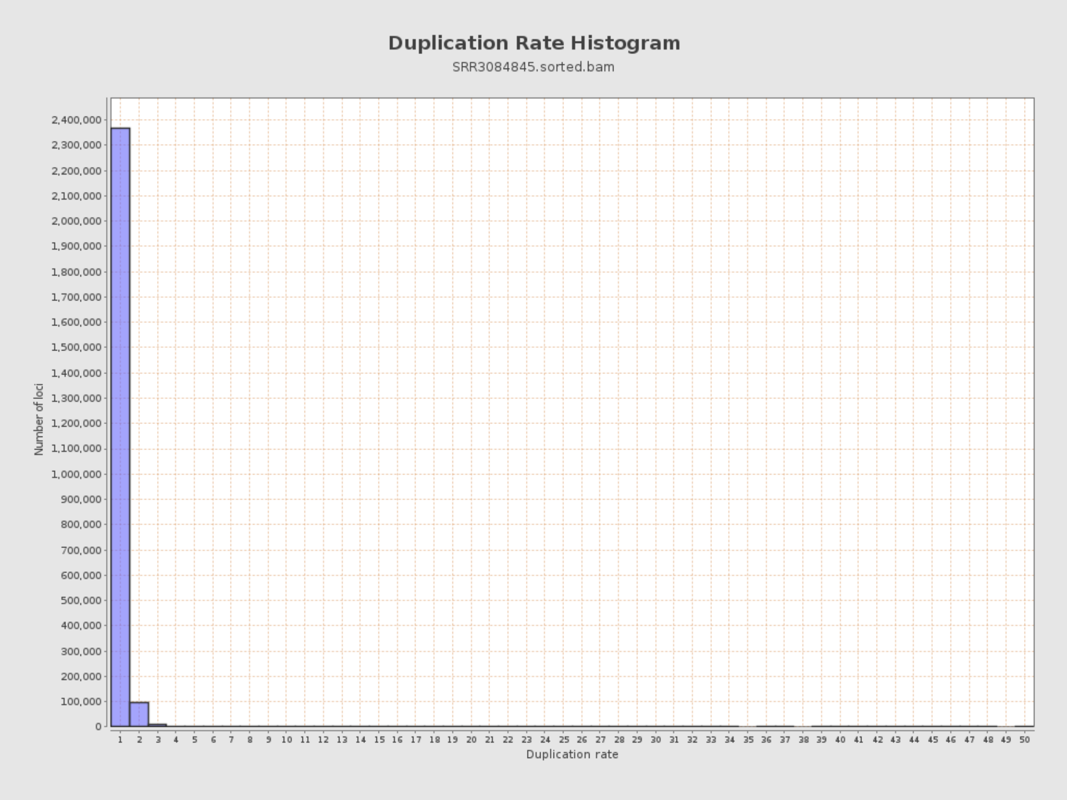
5. Results : Coverage Histogram (0-50X)



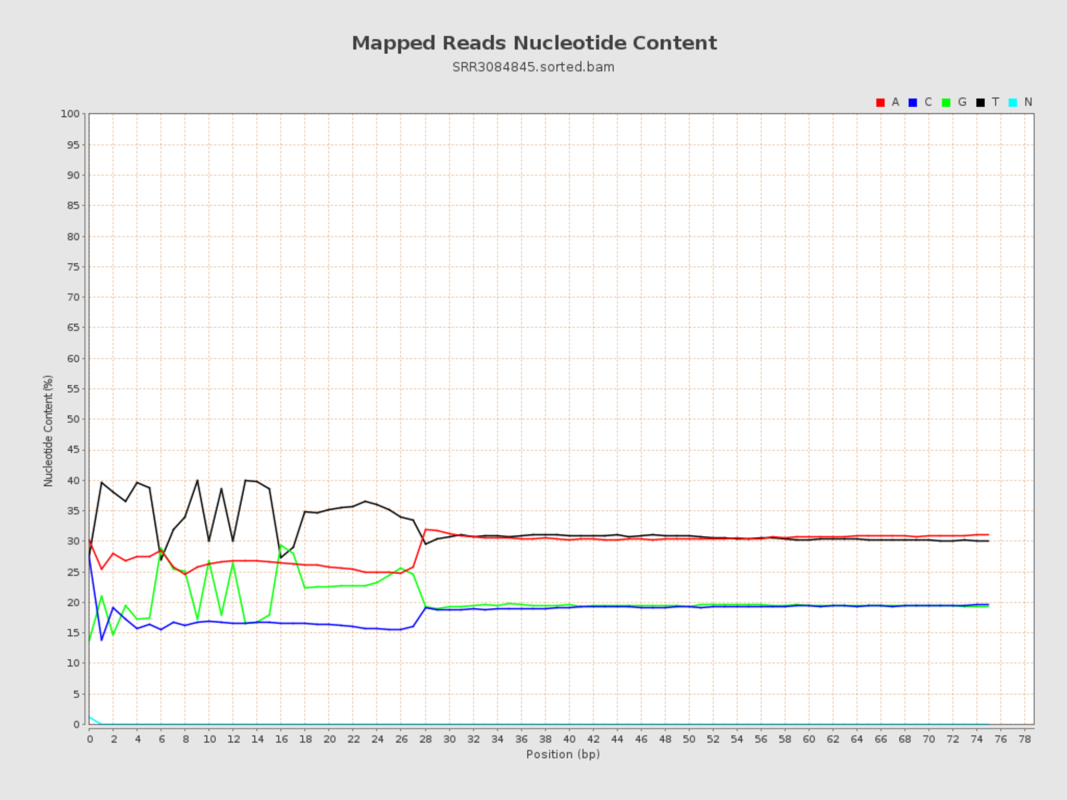
6. Results : Genome Fraction Coverage



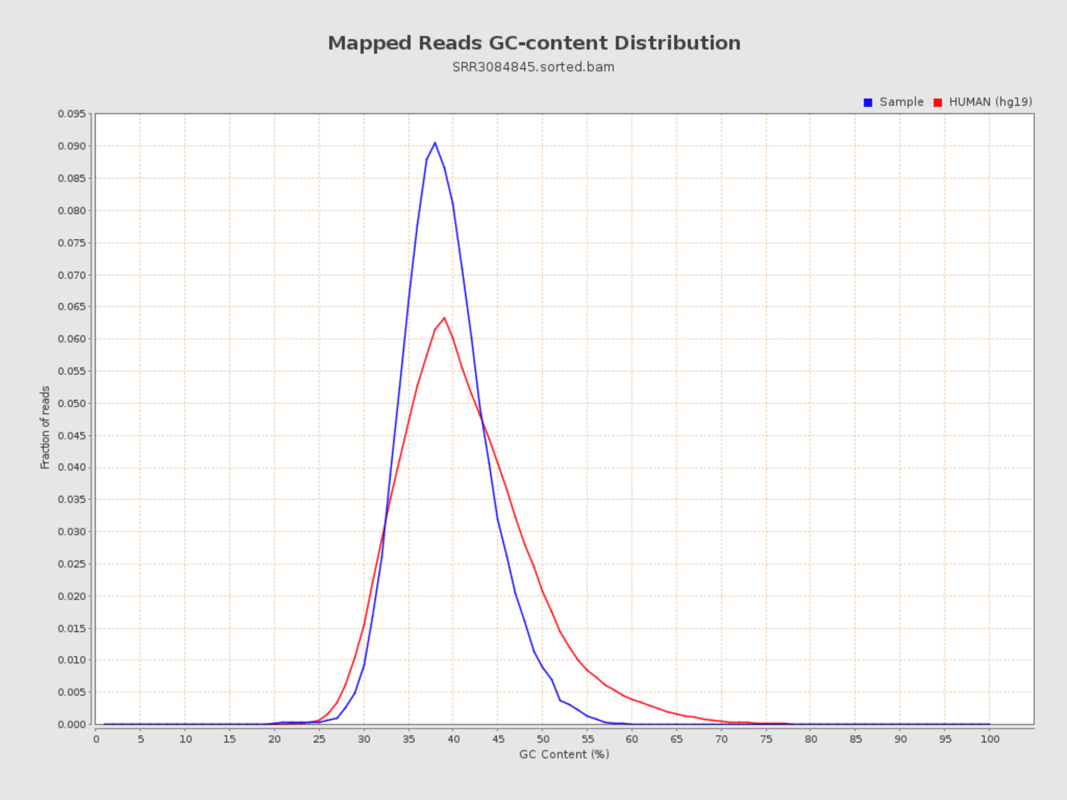
7. Results : Duplication Rate Histogram



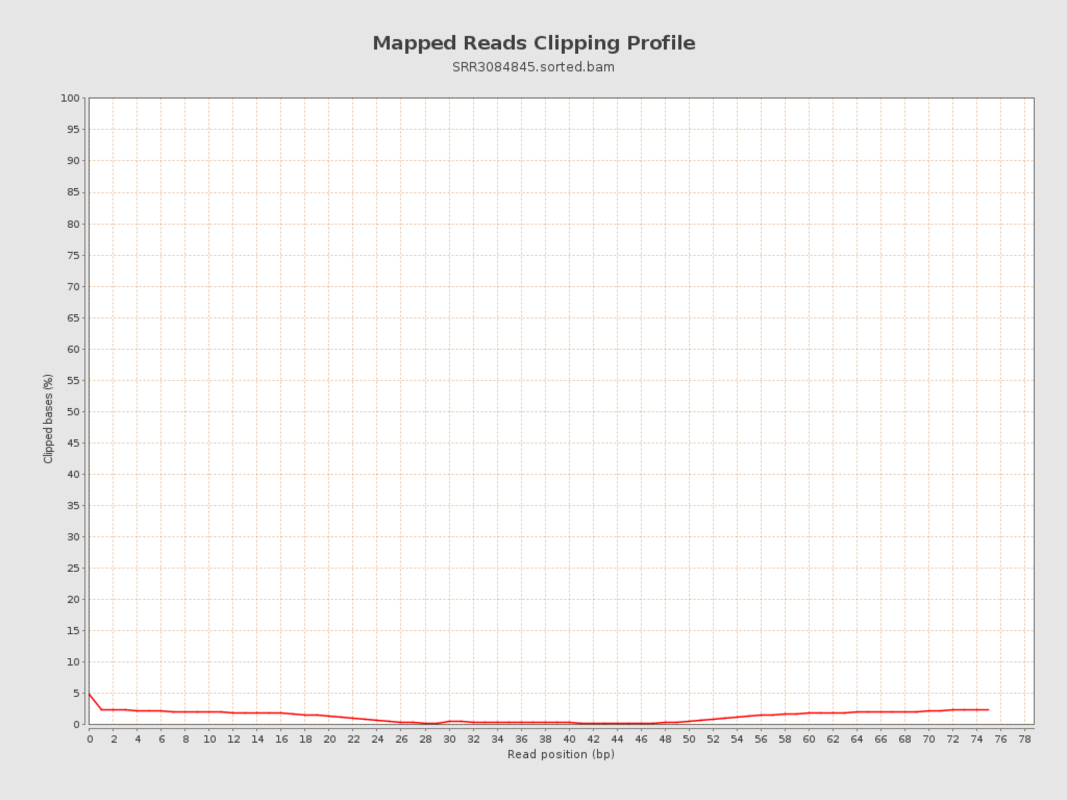
8. Results : Mapped Reads Nucleotide Content



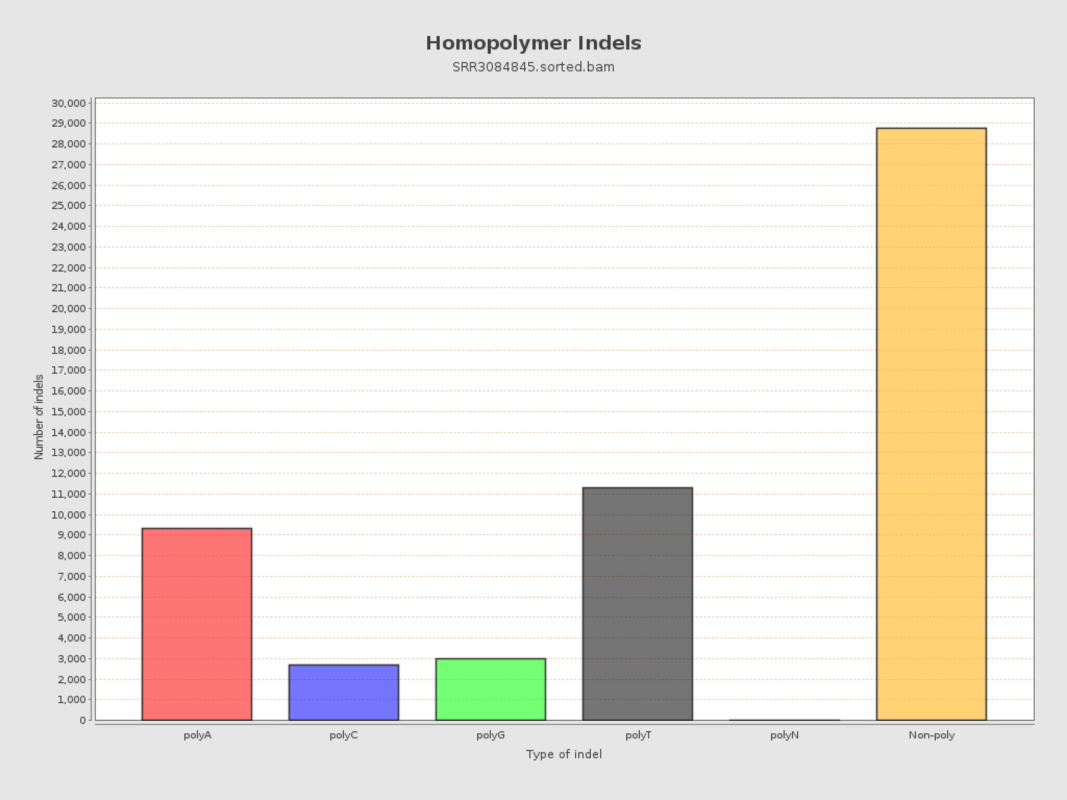
9. Results : Mapped Reads GC-content Distribution



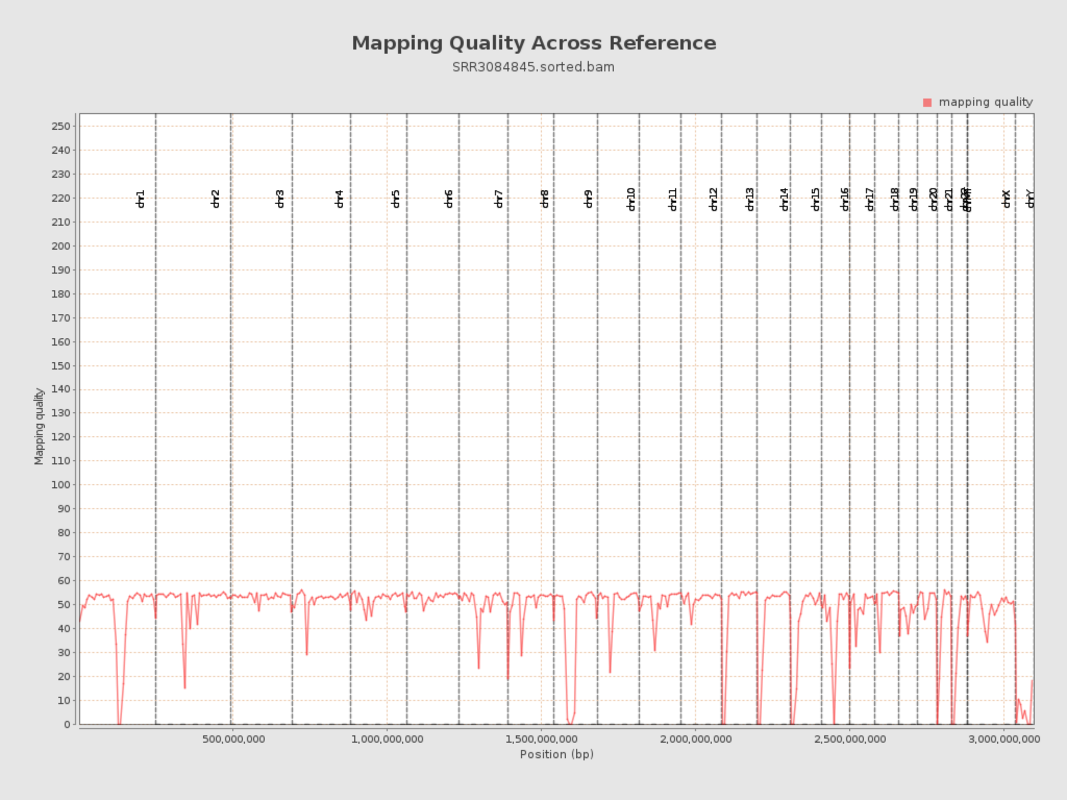
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram