Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 12:16:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084411.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_SRR3084411 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084411.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 12:16:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084411.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,195,485
Mapped reads	2,022,632 / 92.13%
Unmapped reads	172,853 / 7.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,246 / 0.69%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	65,937 / 3%
Duplication rate	2.69%
Clipped reads	866,431 / 39.46%

2.2. ACGT Content

Number/percentage of A's	38,776,732 / 28.41%
Number/percentage of C's	25,842,082 / 18.94%
Number/percentage of T's	42,508,668 / 31.15%
Number/percentage of G's	29,164,651 / 21.37%
Number/percentage of N's	179,657 / 0.13%
GC Percentage	40.31%

2.3. Coverage

Mean	0.0441

Standard Deviation	0.316

2.4. Mapping Quality

Mean Mapping Quality	46.08

2.5. Mismatches and indels

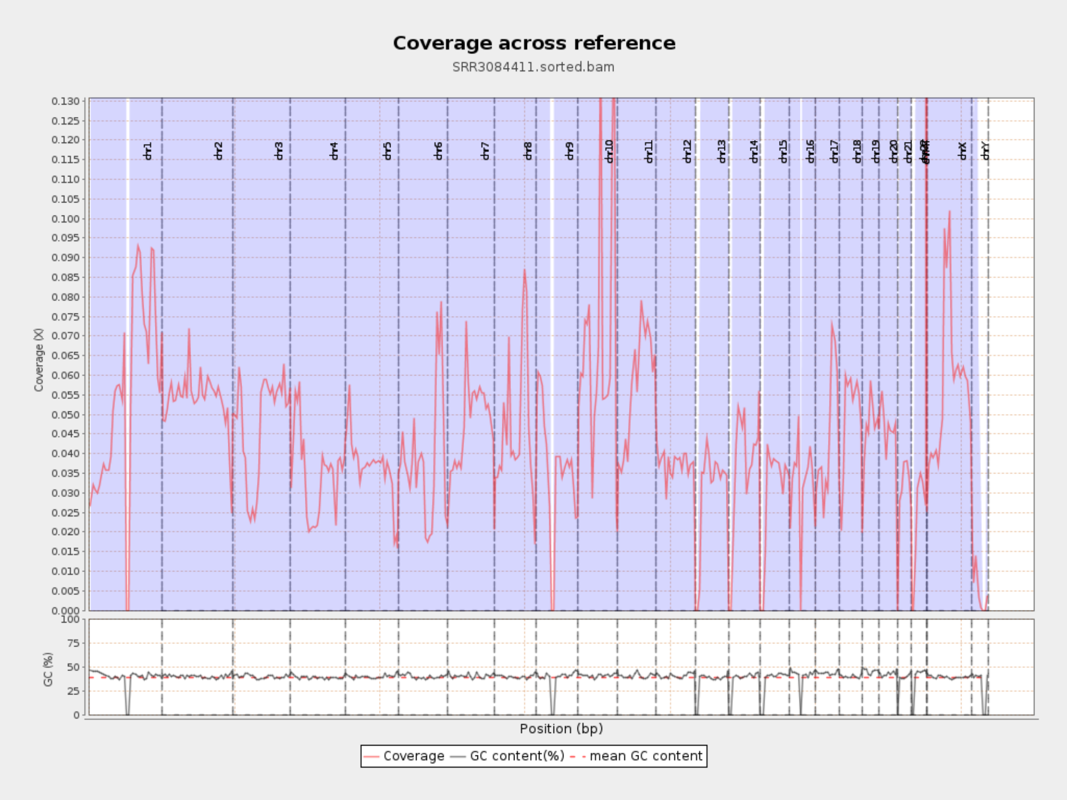
General error rate	1.01%
Mismatches	1,360,839
Insertions	9,694
Mapped reads with at least one insertion	0.47%
Deletions	27,847
Mapped reads with at least one deletion	1.36%
Homopolymer indels	46.8%

2.6. Chromosome stats

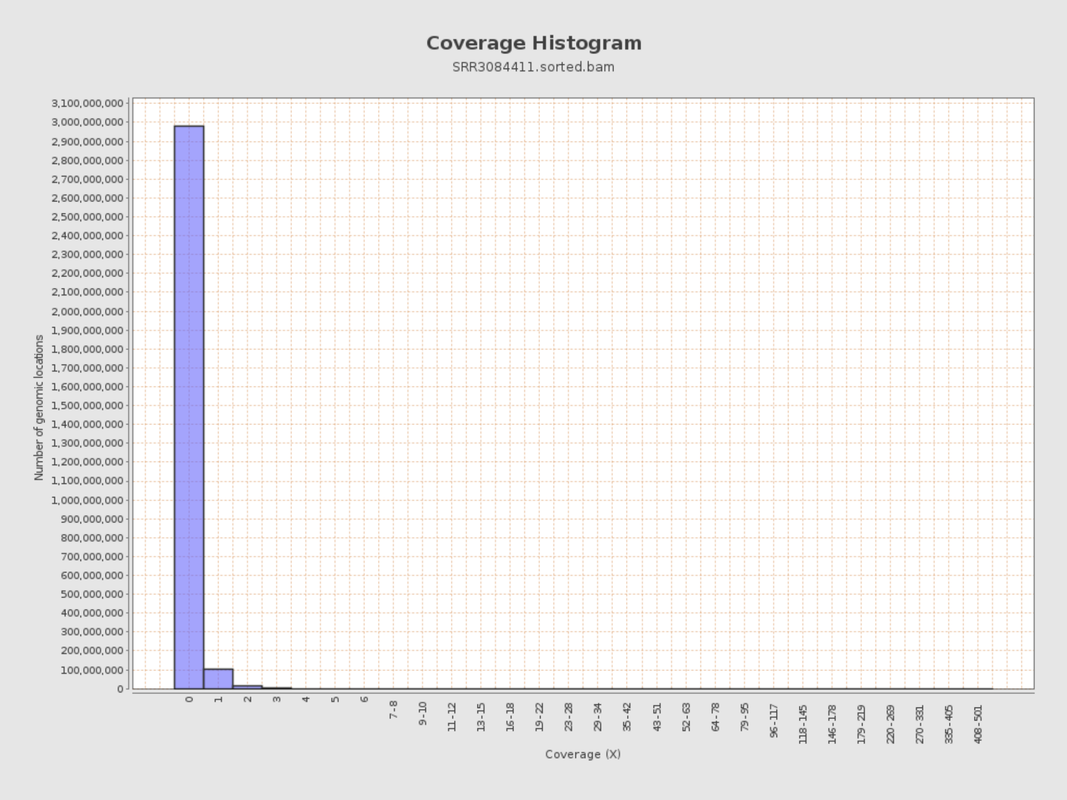
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13684010	0.0549	0.5194
chr2	243199373	13157002	0.0541	0.3529
chr3	198022430	9459051	0.0478	0.2484
chr4	191154276	6696842	0.035	0.2183
chr5	180915260	6645043	0.0367	0.2154
chr6	171115067	6638322	0.0388	0.2466
chr7	159138663	7681233	0.0483	0.4228

chr8	146364022	6792207	0.0464	0.3464
chr9	141213431	5122482	0.0363	0.2633
chr10	135534747	9690775	0.0715	0.4512
chr11	135006516	7691197	0.057	0.3215
chr12	133851895	4986288	0.0373	0.219
chr13	115169878	3436428	0.0298	0.194
chr14	107349540	3854774	0.0359	0.2196
chr15	102531392	3077345	0.03	0.1972
chr16	90354753	2938413	0.0325	0.2205
chr17	81195210	3604281	0.0444	0.2554
chr18	78077248	3864744	0.0495	0.4264
chr19	59128983	2768980	0.0468	0.3656
chr20	63025520	2919553	0.0463	0.2448
chr21	48129895	1433405	0.0298	0.2057
chr22	51304566	1149757	0.0224	0.1655
chrMT	16571	37411	2.2576	2.0912
chrX	155270560	8888587	0.0572	0.2989
chrY	59373566	301452	0.0051	0.1048

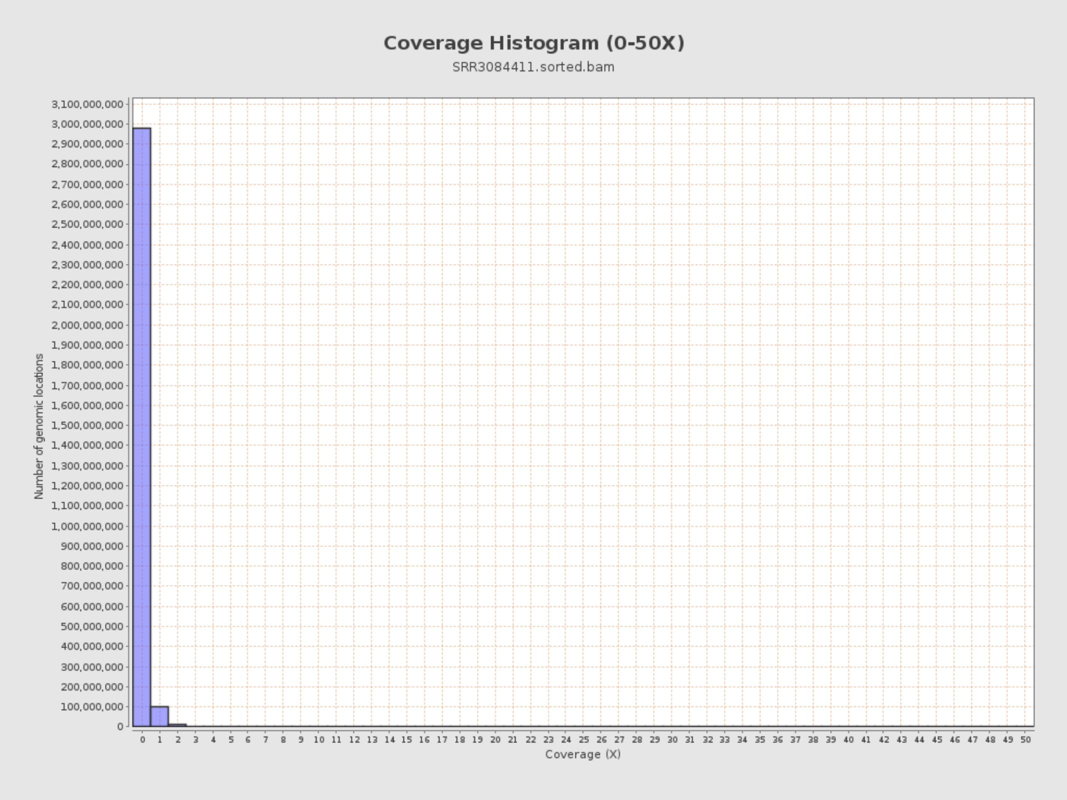
3. Results : Coverage across reference



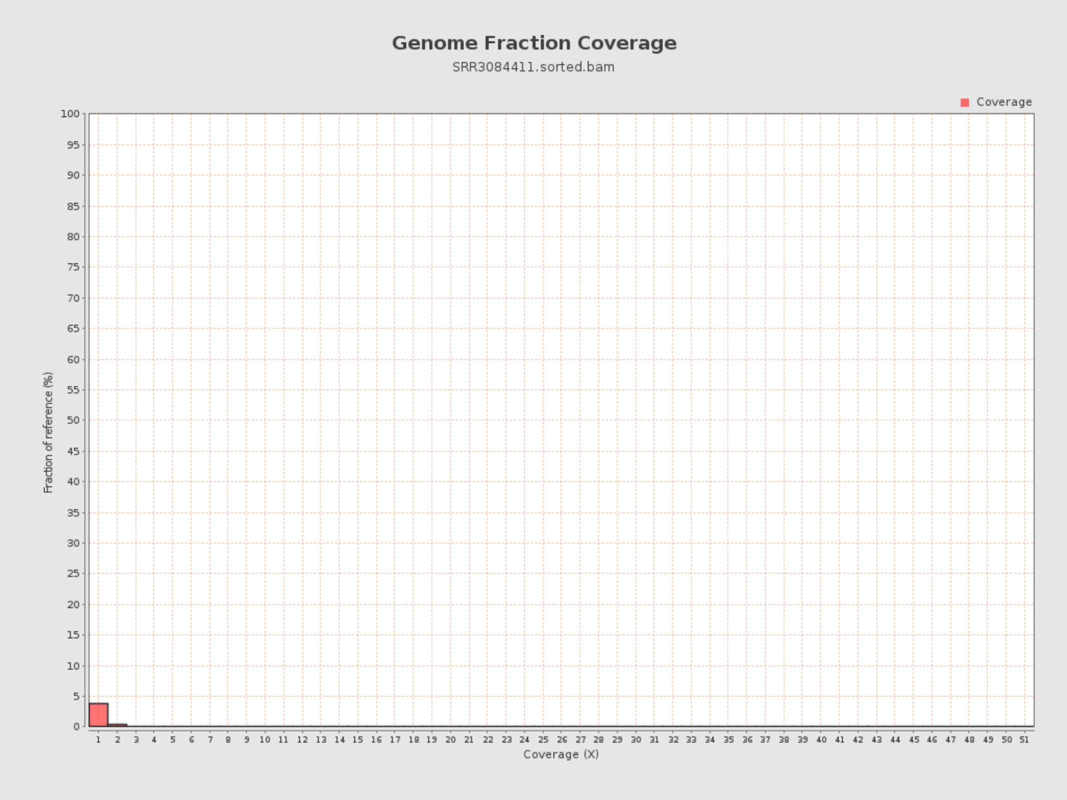
4. Results : Coverage Histogram



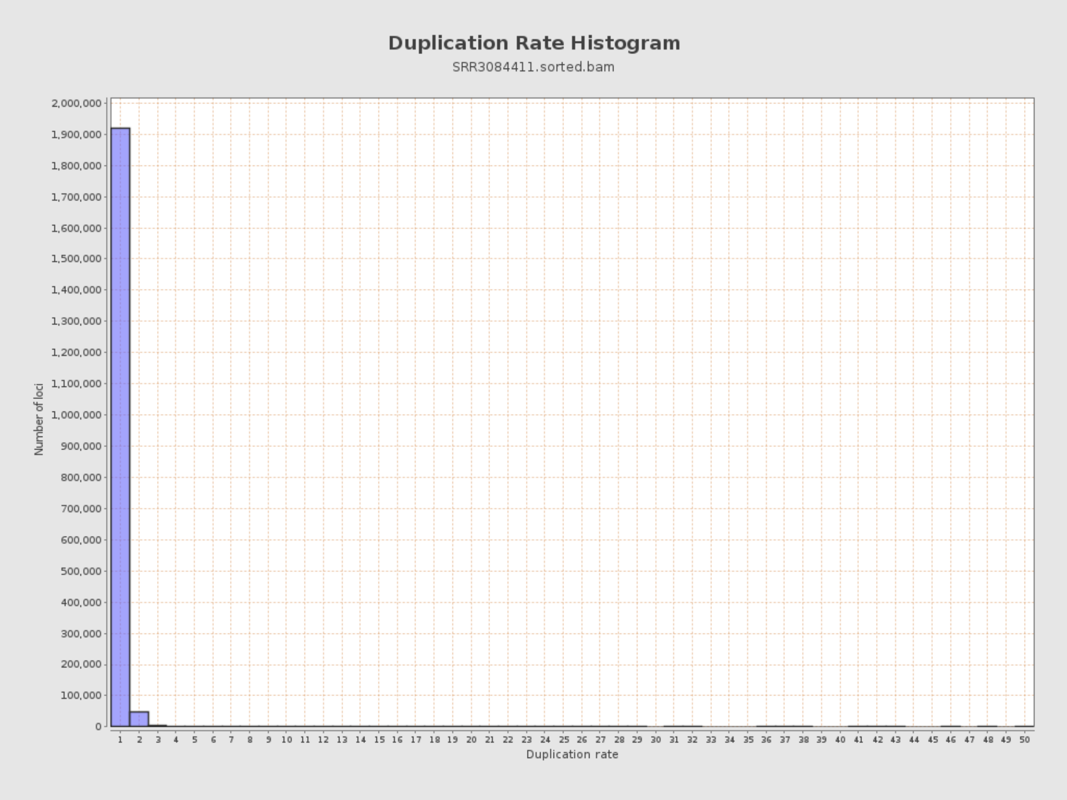
5. Results : Coverage Histogram (0-50X)



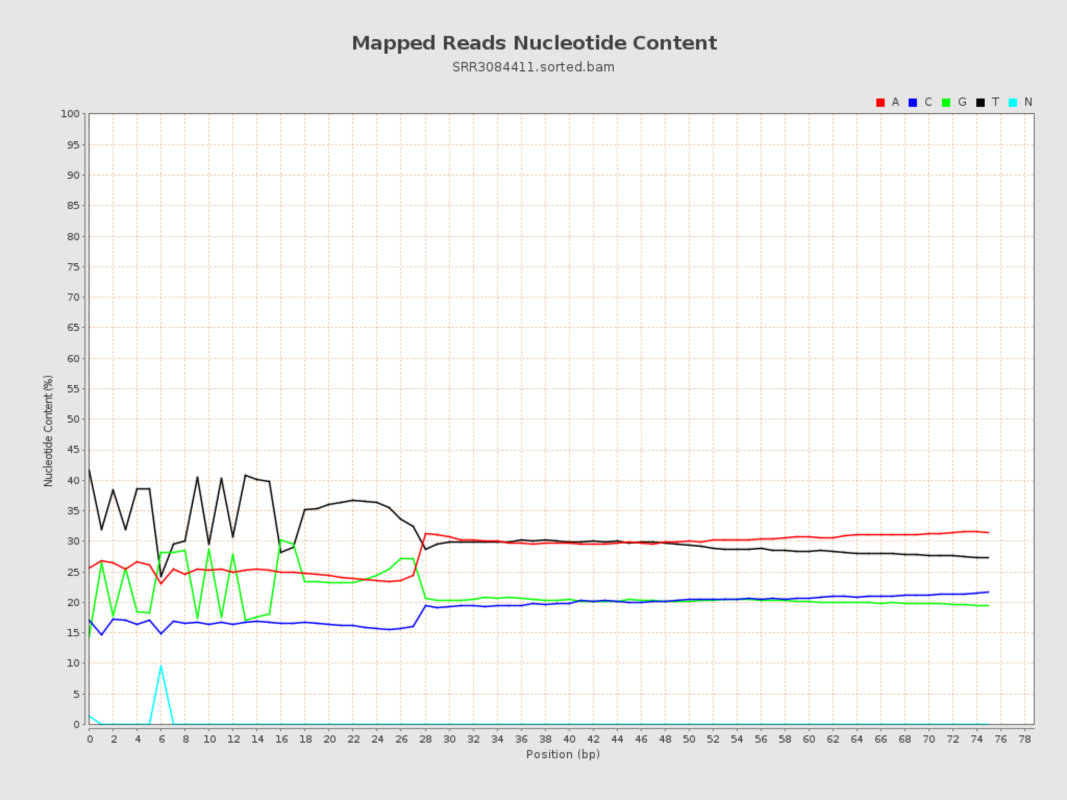
6. Results : Genome Fraction Coverage



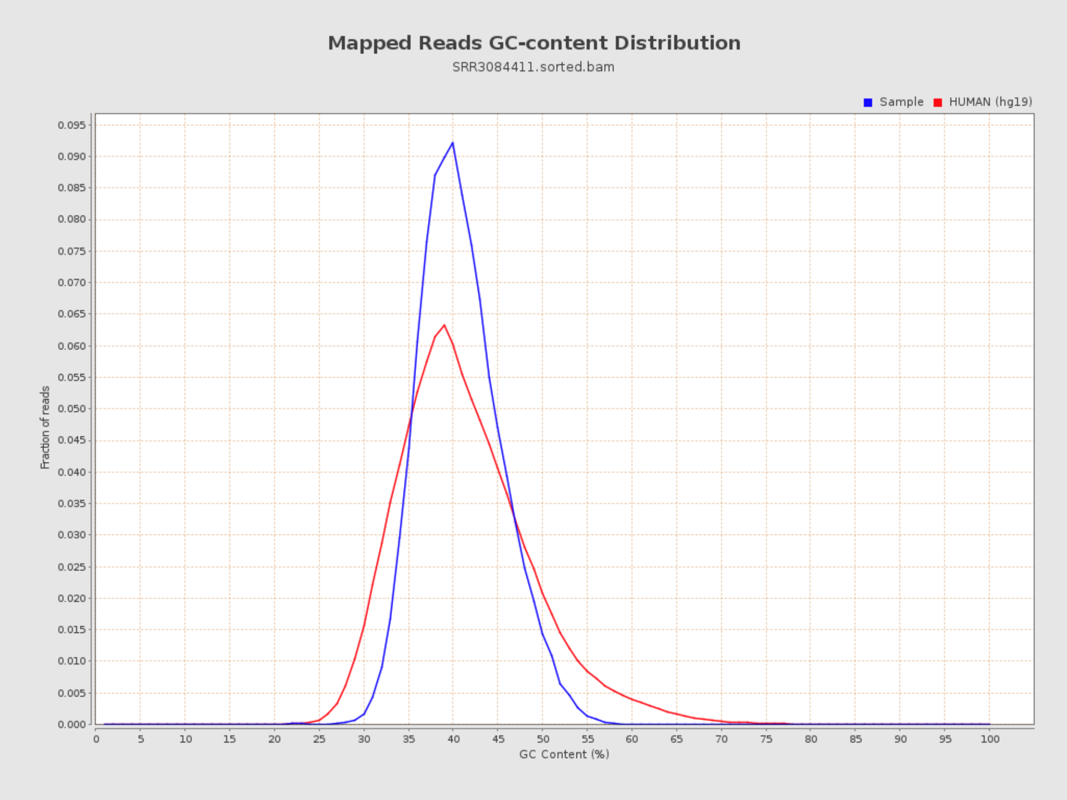
7. Results : Duplication Rate Histogram



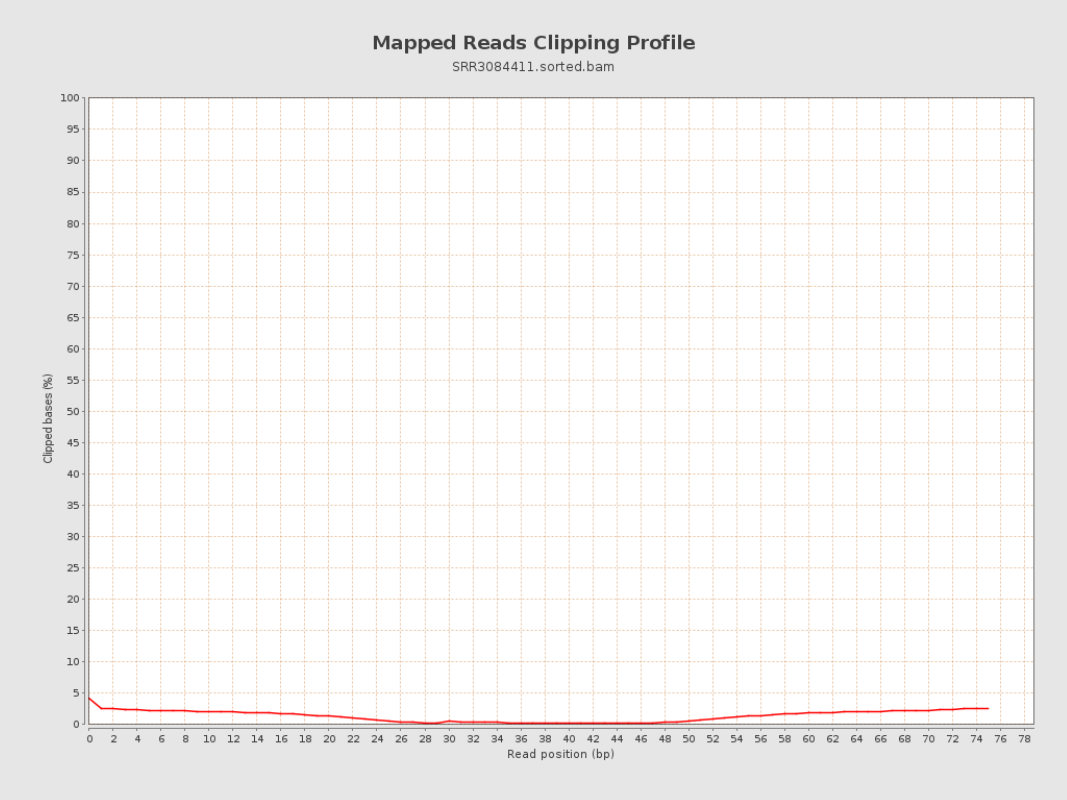
8. Results : Mapped Reads Nucleotide Content



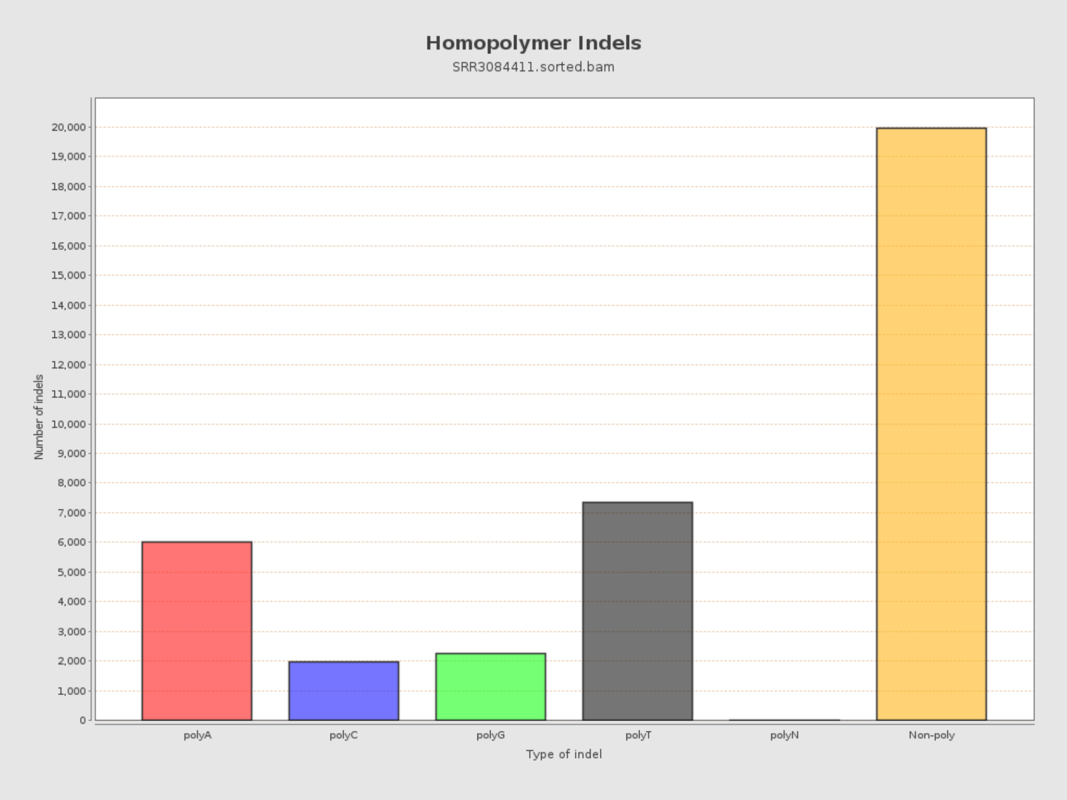
9. Results : Mapped Reads GC-content Distribution



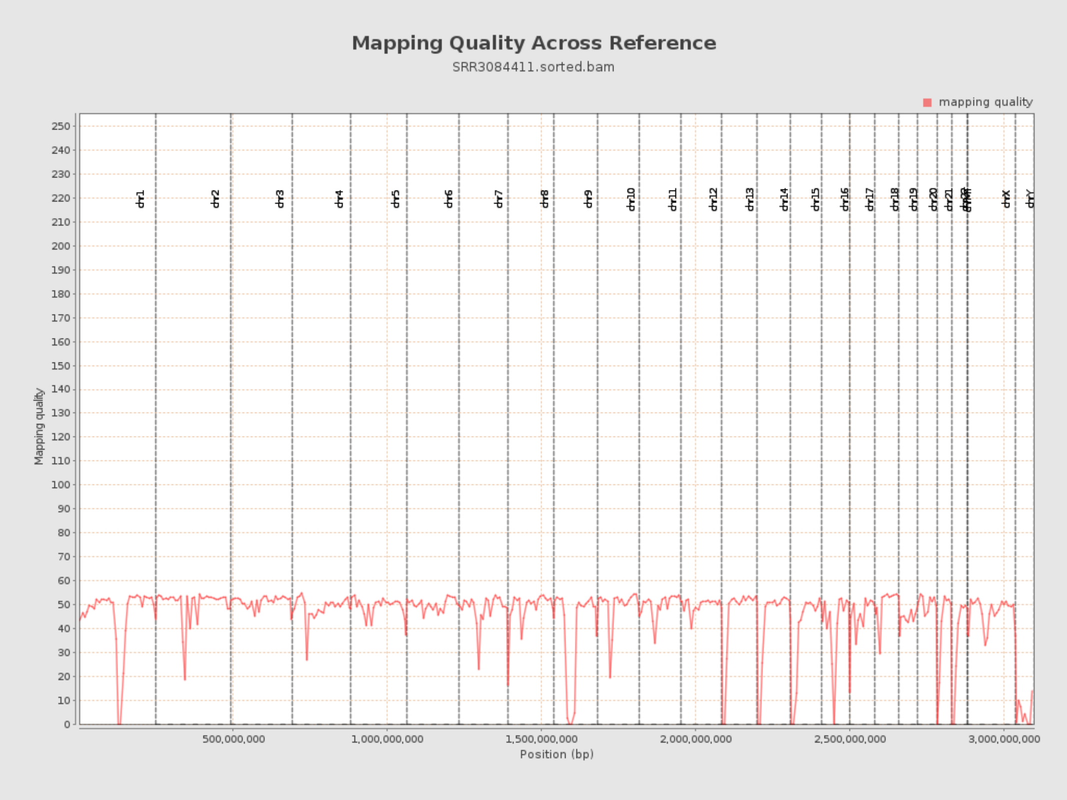
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram