Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 01:41:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080552.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_SRR3080552 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080552.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 01:41:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080552.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,750,971
Mapped reads	2,267,046 / 82.41%
Unmapped reads	483,925 / 17.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,460 / 0.71%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	118,988 / 4.33%
Duplication rate	4.64%
Clipped reads	990,948 / 36.02%

2.2. ACGT Content

Number/percentage of A's	42,015,217 / 27.65%
Number/percentage of C's	27,263,325 / 17.94%
Number/percentage of T's	49,427,355 / 32.53%
Number/percentage of G's	33,128,433 / 21.8%
Number/percentage of N's	127,350 / 0.08%
GC Percentage	39.74%

2.3. Coverage

Mean	0.0491

Standard Deviation	0.3228

2.4. Mapping Quality

Mean Mapping Quality	47.69

2.5. Mismatches and indels

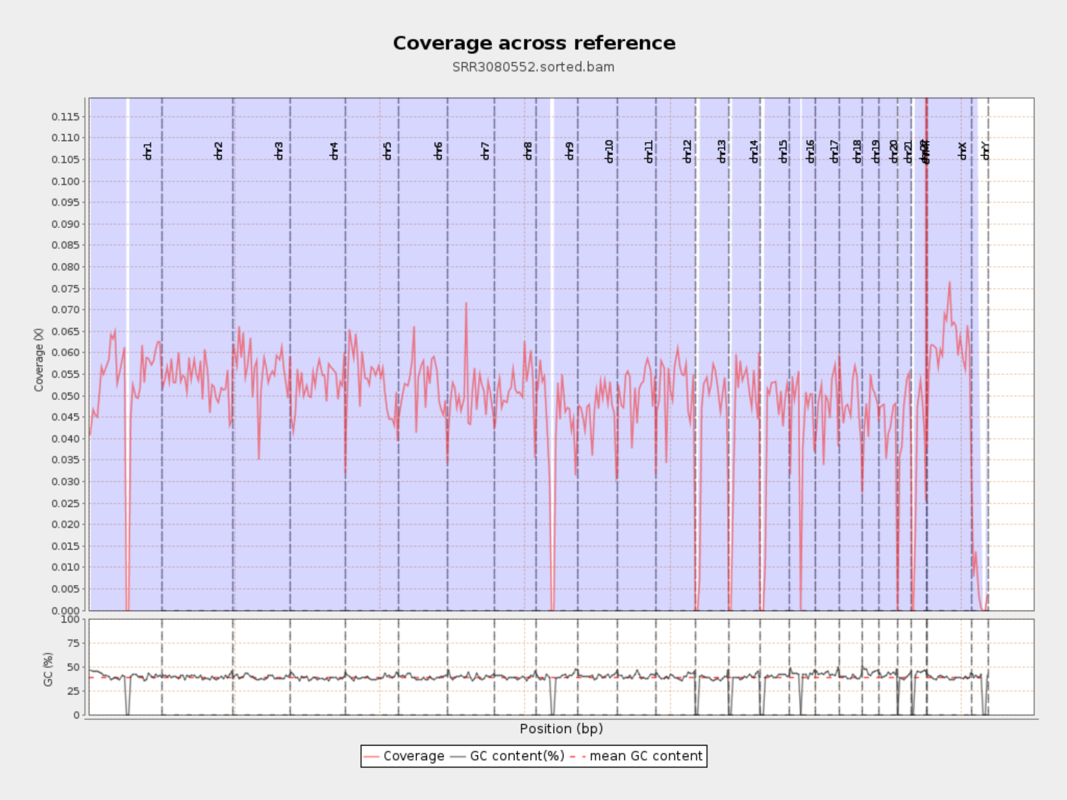
General error rate	0.91%
Mismatches	1,355,446
Insertions	12,341
Mapped reads with at least one insertion	0.54%
Deletions	35,530
Mapped reads with at least one deletion	1.55%
Homopolymer indels	49.62%

2.6. Chromosome stats

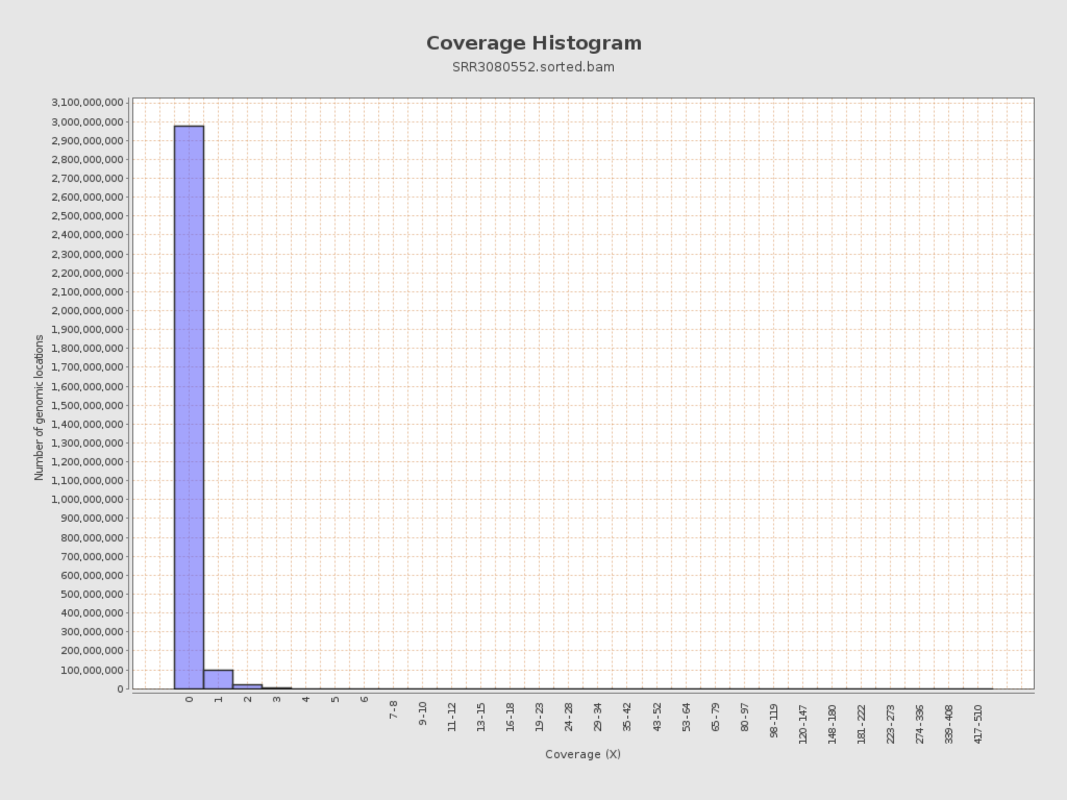
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12915162	0.0518	0.4458
chr2	243199373	12979511	0.0534	0.3283
chr3	198022430	11146491	0.0563	0.2866
chr4	191154276	10089461	0.0528	0.2807
chr5	180915260	9692240	0.0536	0.2798
chr6	171115067	8969193	0.0524	0.3195
chr7	159138663	8032412	0.0505	0.4901

chr8	146364022	7550987	0.0516	0.4104
chr9	141213431	5871201	0.0416	0.2745
chr10	135534747	6379496	0.0471	0.2881
chr11	135006516	6900017	0.0511	0.2881
chr12	133851895	6927278	0.0518	0.2737
chr13	115169878	4926642	0.0428	0.2506
chr14	107349540	4746105	0.0442	0.2595
chr15	102531392	4122281	0.0402	0.2411
chr16	90354753	3928539	0.0435	0.2629
chr17	81195210	3867452	0.0476	0.2718
chr18	78077248	3850271	0.0493	0.3871
chr19	59128983	2772687	0.0469	0.356
chr20	63025520	2742146	0.0435	0.255
chr21	48129895	1978824	0.0411	0.25
chr22	51304566	1657745	0.0323	0.2161
chrMT	16571	78455	4.7345	4.5479
chrX	155270560	9576109	0.0617	0.3114
chrY	59373566	319333	0.0054	0.1038

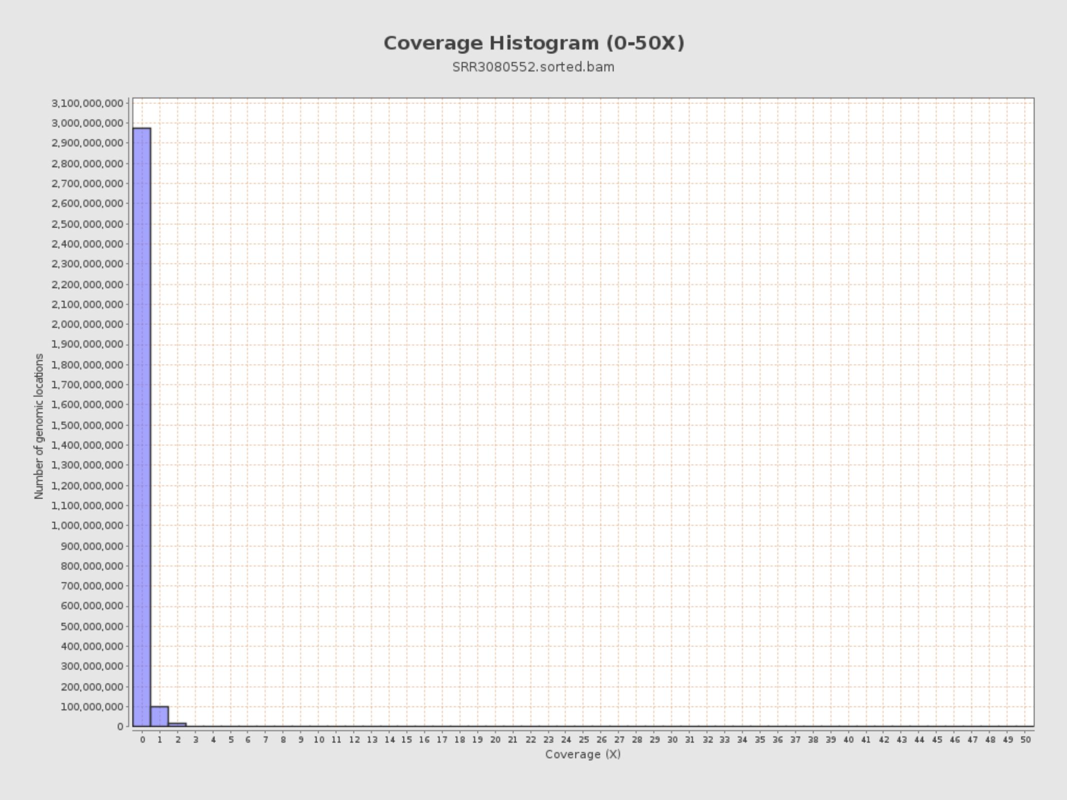
3. Results : Coverage across reference



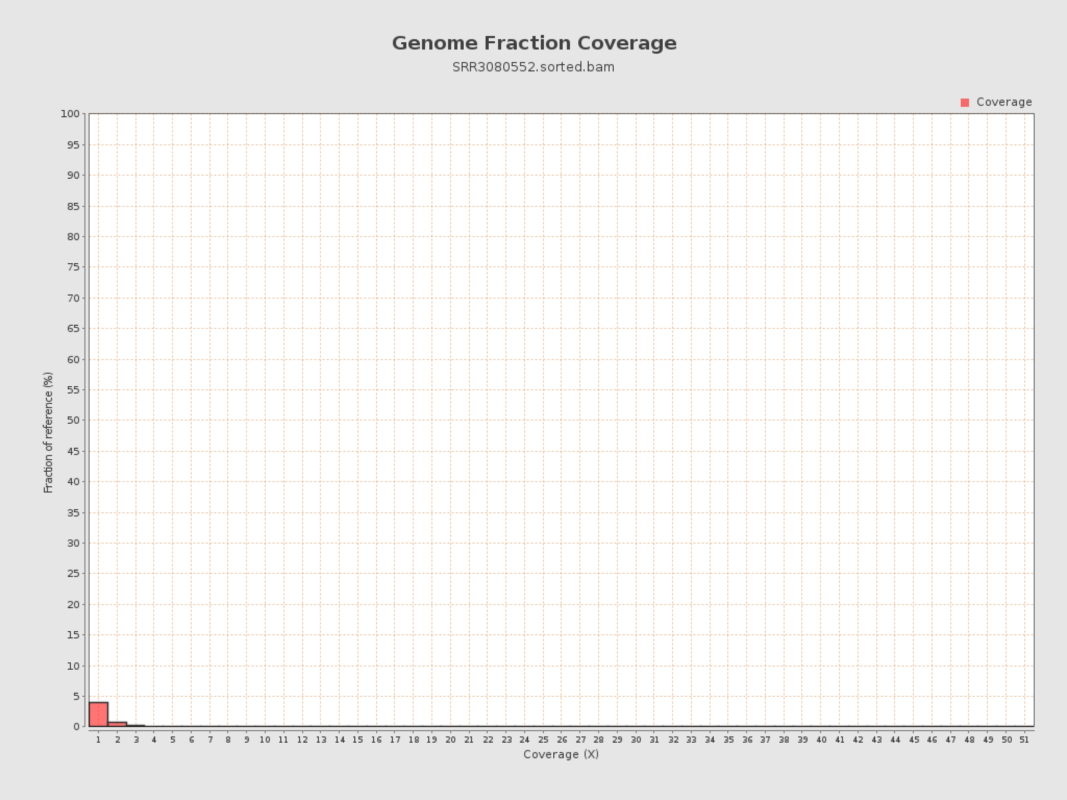
4. Results : Coverage Histogram



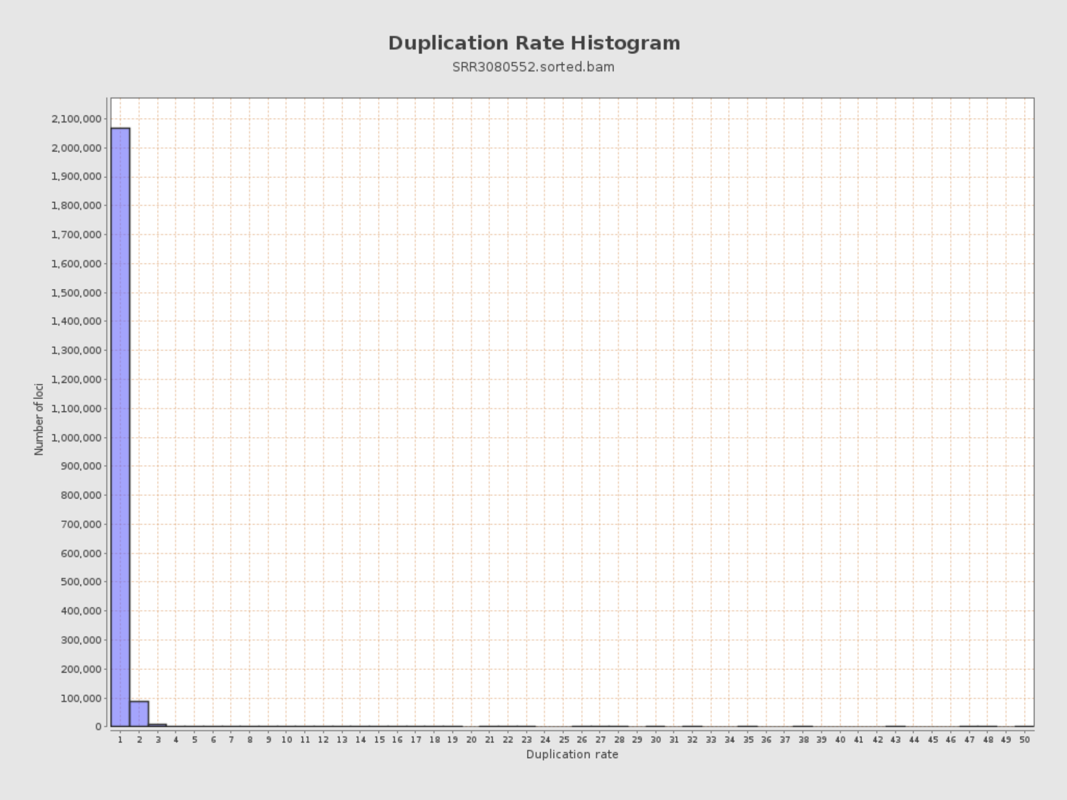
5. Results : Coverage Histogram (0-50X)



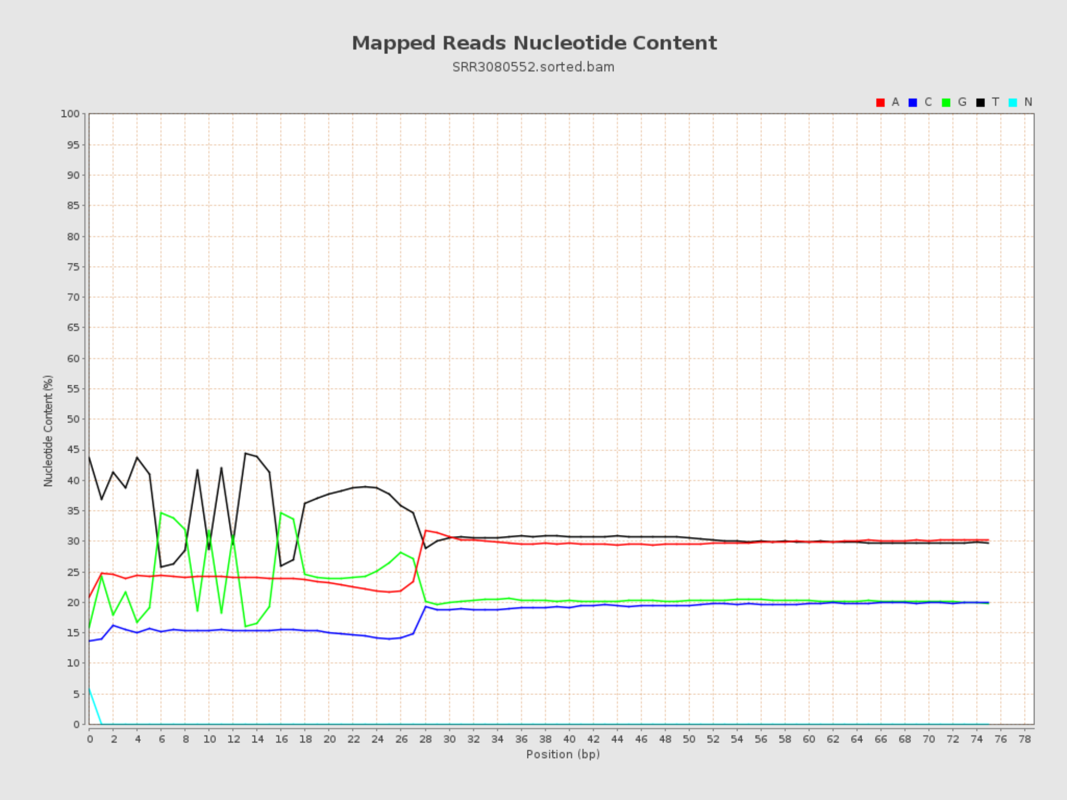
6. Results : Genome Fraction Coverage



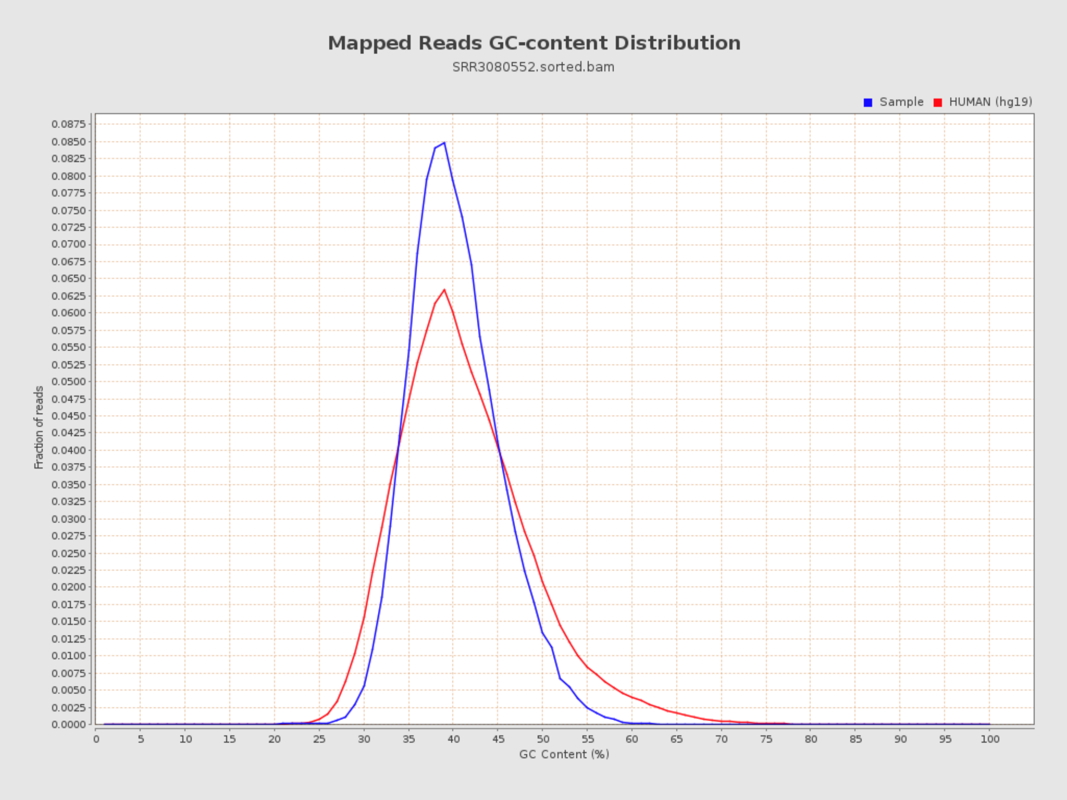
7. Results : Duplication Rate Histogram



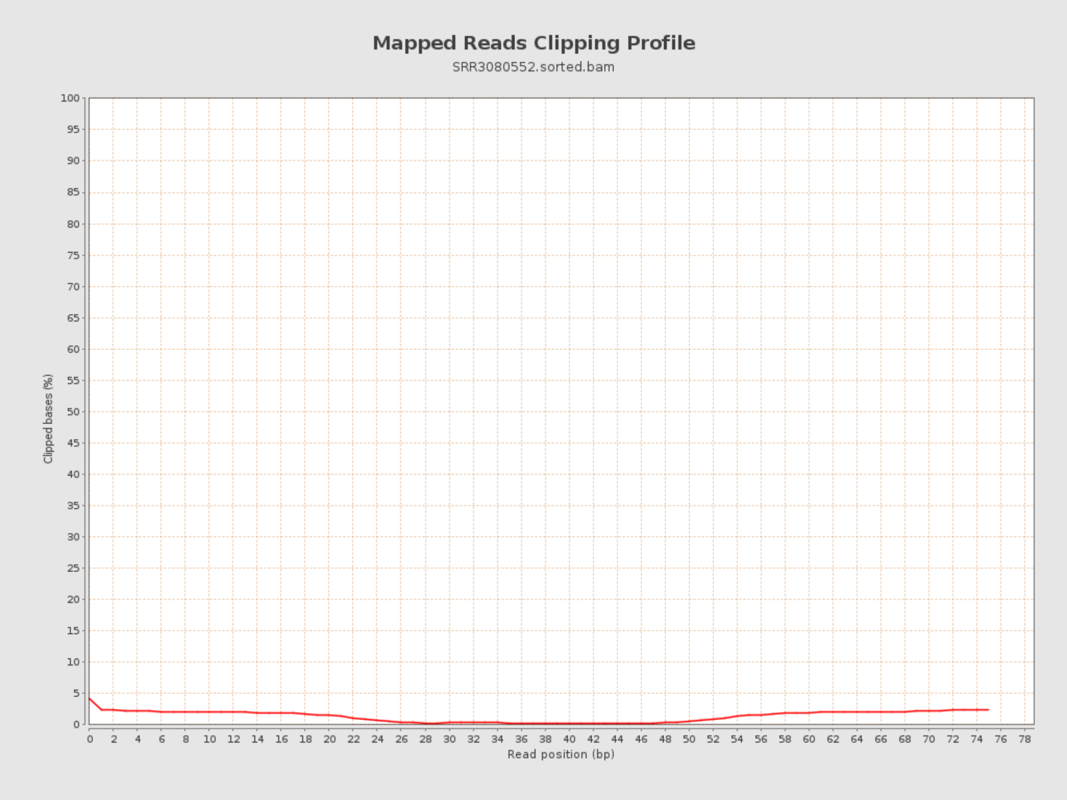
8. Results : Mapped Reads Nucleotide Content



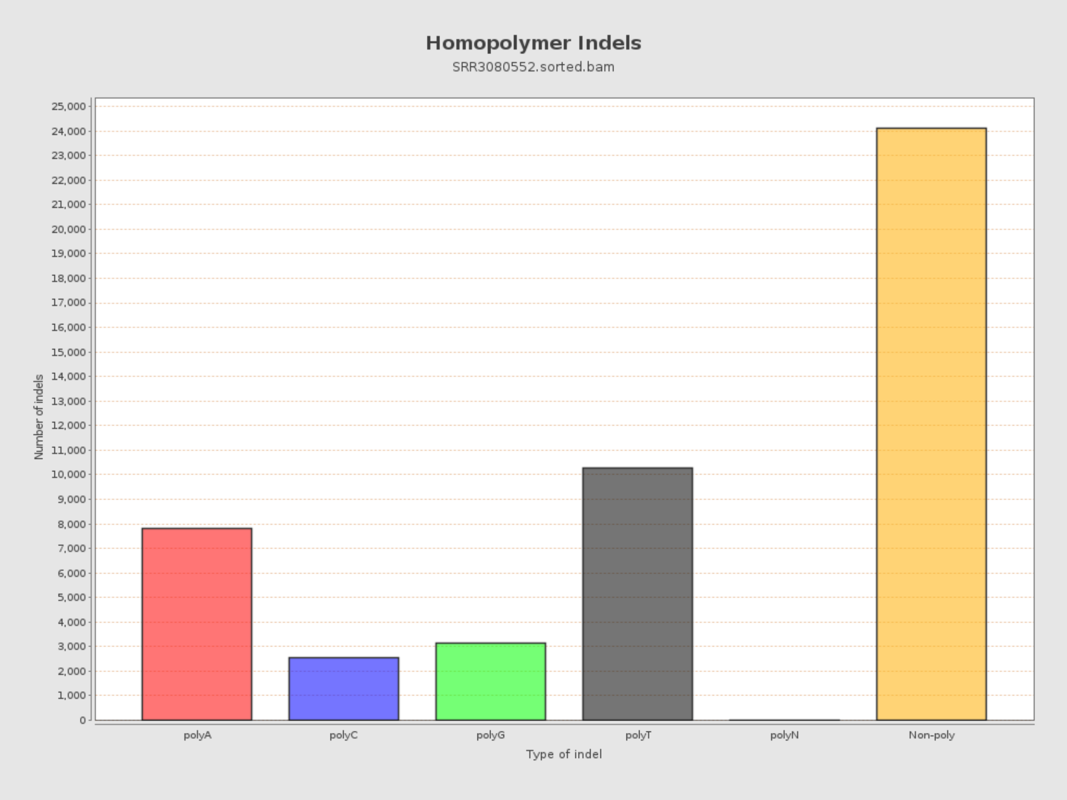
9. Results : Mapped Reads GC-content Distribution



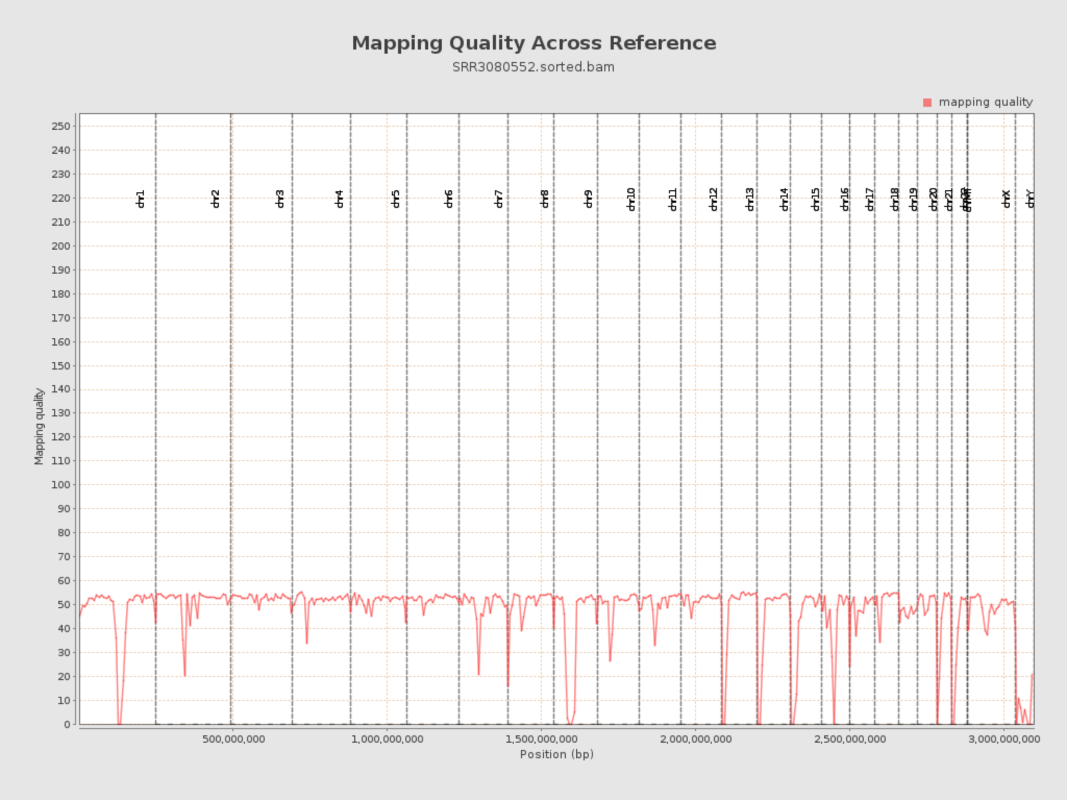
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram