Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 20:22:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082934.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_SRR3082934 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082934.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 20:22:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082934.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,027,615
Mapped reads	1,790,399 / 88.3%
Unmapped reads	237,216 / 11.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,020 / 1.23%
Read min/max/mean length	30 / 76 / 76.43
Duplicated reads (estimated)	122,651 / 6.05%
Duplication rate	5.93%
Clipped reads	844,168 / 41.63%

2.2. ACGT Content

Number/percentage of A's	32,233,994 / 27.17%
Number/percentage of C's	22,197,470 / 18.71%
Number/percentage of T's	37,369,546 / 31.49%
Number/percentage of G's	26,849,541 / 22.63%
Number/percentage of N's	5,775 / 0%
GC Percentage	41.34%

2.3. Coverage

Mean	0.0383

Standard Deviation	0.2893

2.4. Mapping Quality

Mean Mapping Quality	45.19

2.5. Mismatches and indels

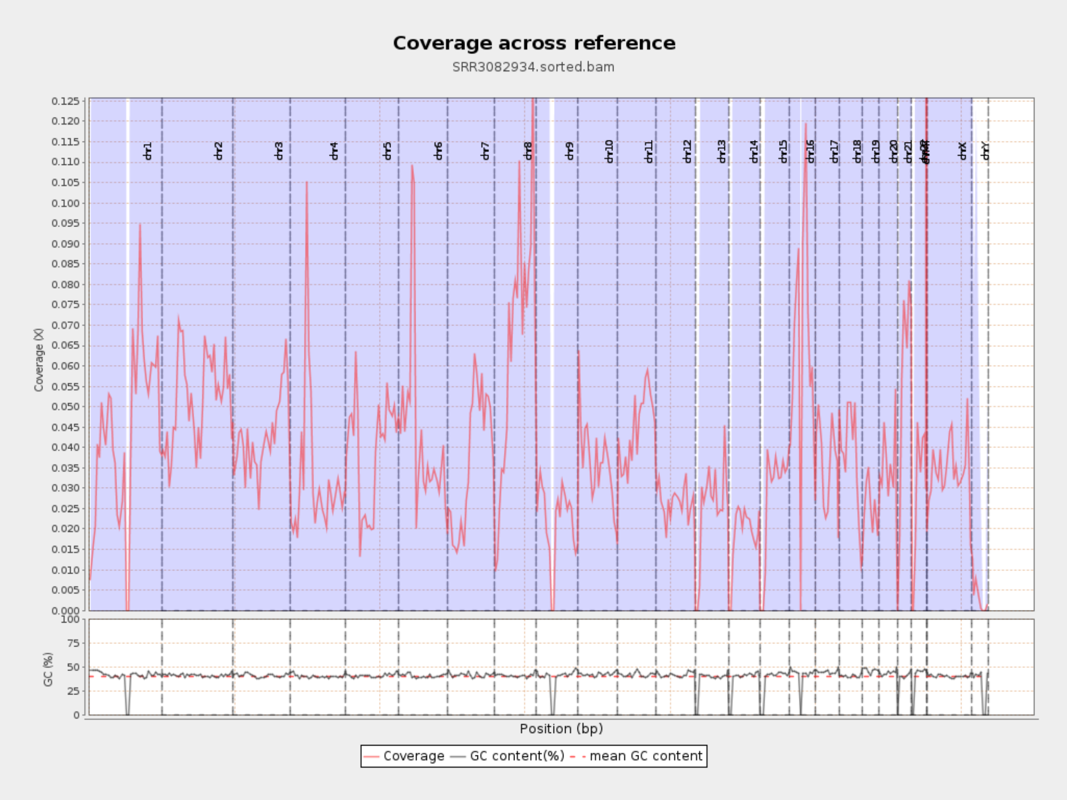
General error rate	0.74%
Mismatches	858,946
Insertions	8,962
Mapped reads with at least one insertion	0.5%
Deletions	26,862
Mapped reads with at least one deletion	1.49%
Homopolymer indels	47.78%

2.6. Chromosome stats

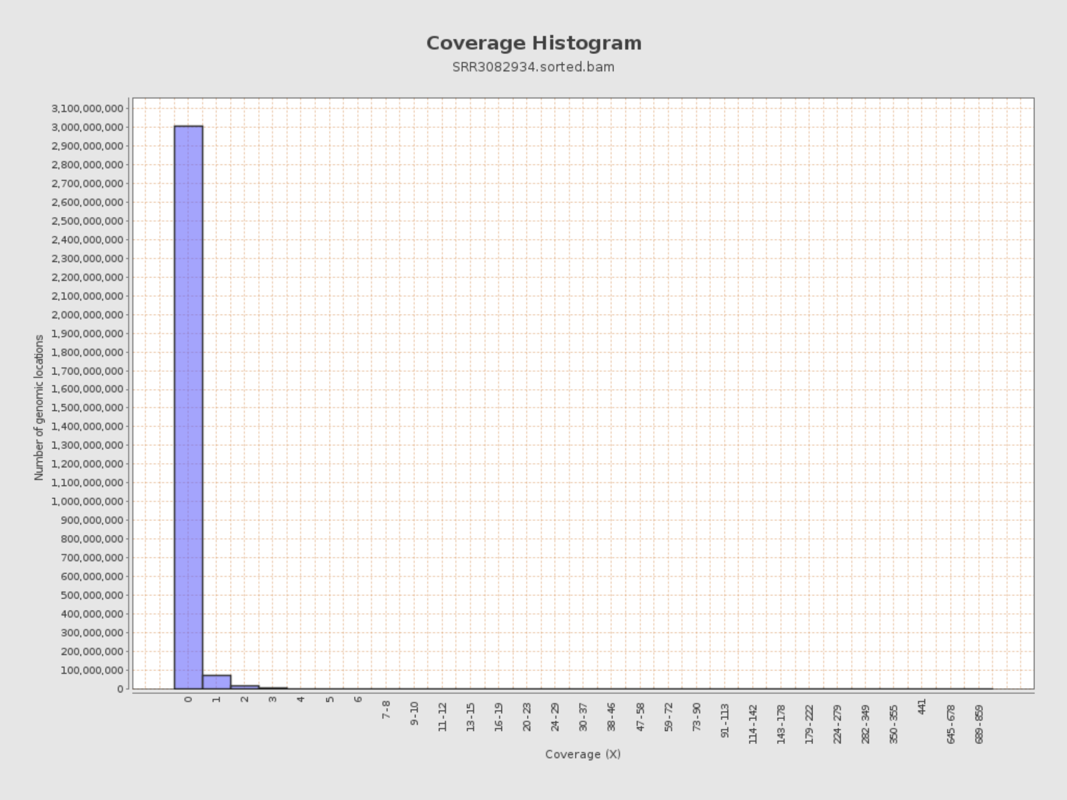
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10885030	0.0437	0.3897
chr2	243199373	12662389	0.0521	0.4527
chr3	198022430	8494454	0.0429	0.2605
chr4	191154276	6216917	0.0325	0.2343
chr5	180915260	7046746	0.039	0.2495
chr6	171115067	7399341	0.0432	0.2956
chr7	159138663	5892719	0.037	0.2552

chr8	146364022	9586924	0.0655	0.369
chr9	141213431	3125762	0.0221	0.2035
chr10	135534747	4988256	0.0368	0.2499
chr11	135006516	5966951	0.0442	0.2772
chr12	133851895	3557667	0.0266	0.2047
chr13	115169878	2887576	0.0251	0.2018
chr14	107349540	1948586	0.0182	0.1742
chr15	102531392	2876322	0.0281	0.2234
chr16	90354753	5832925	0.0646	0.3271
chr17	81195210	2906276	0.0358	0.246
chr18	78077248	2999027	0.0384	0.3333
chr19	59128983	1490004	0.0252	0.2738
chr20	63025520	2285454	0.0363	0.2445
chr21	48129895	2658769	0.0552	0.2999
chr22	51304566	1467589	0.0286	0.212
chrMT	16571	10060	0.6071	0.8773
chrX	155270560	5320032	0.0343	0.2382
chrY	59373566	194357	0.0033	0.0689

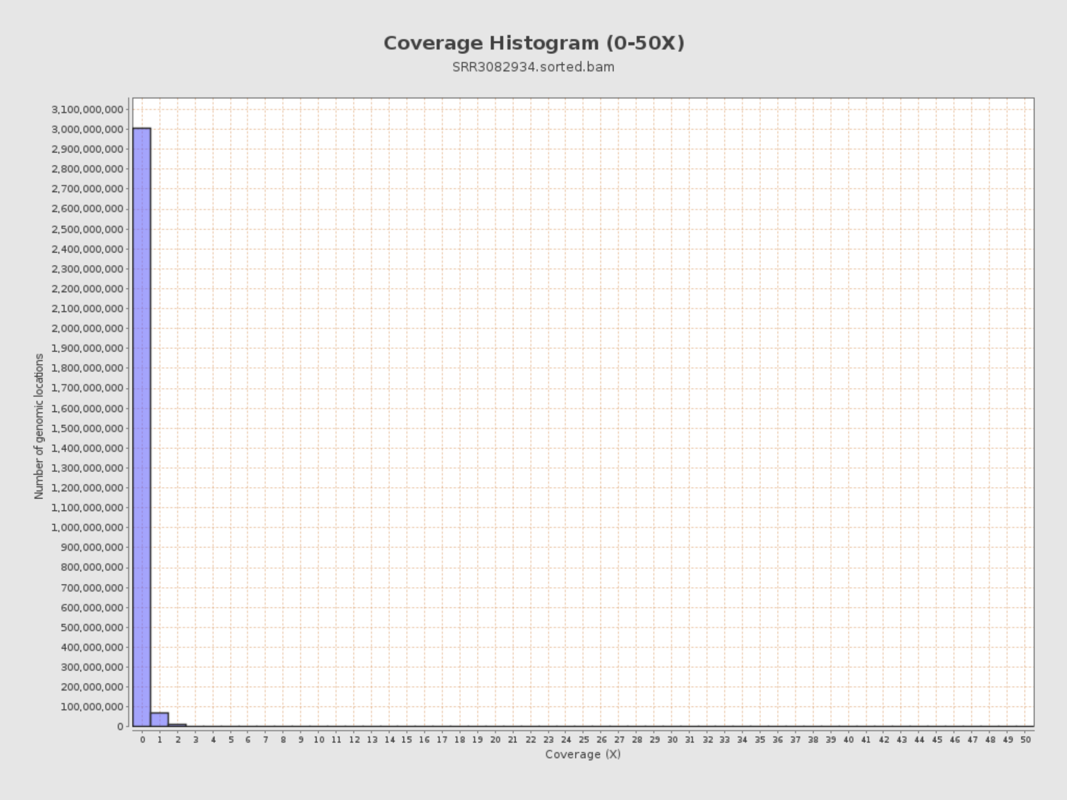
3. Results : Coverage across reference



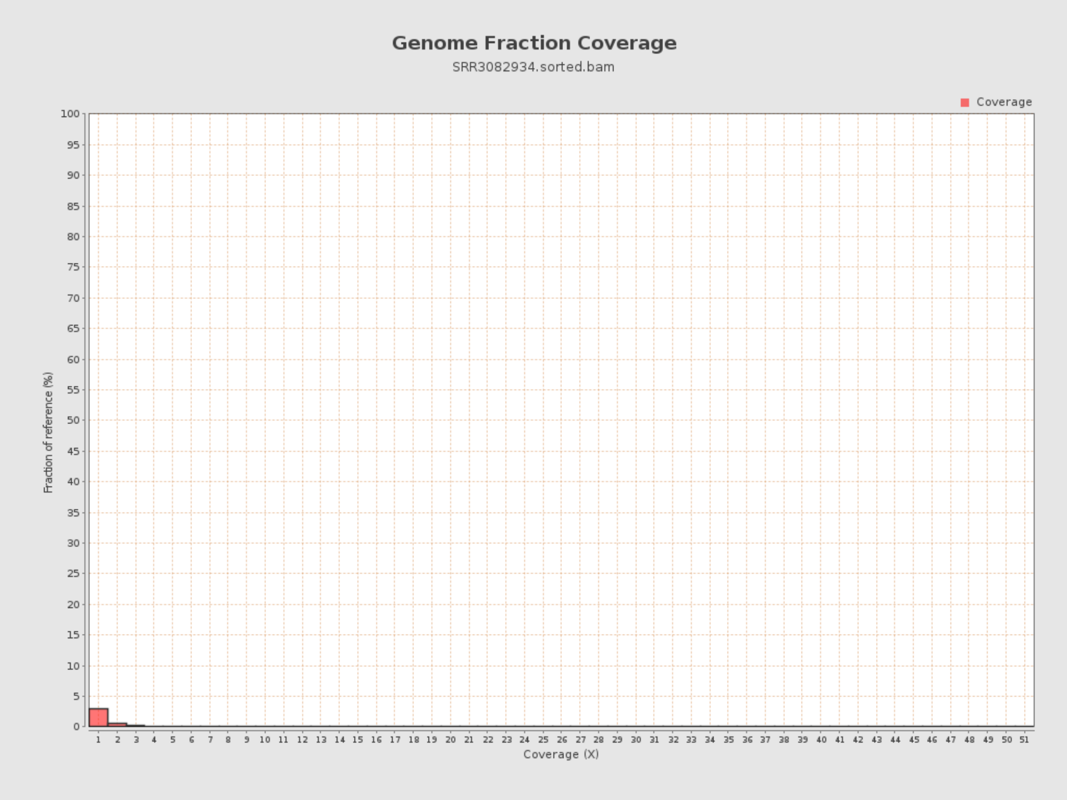
4. Results : Coverage Histogram



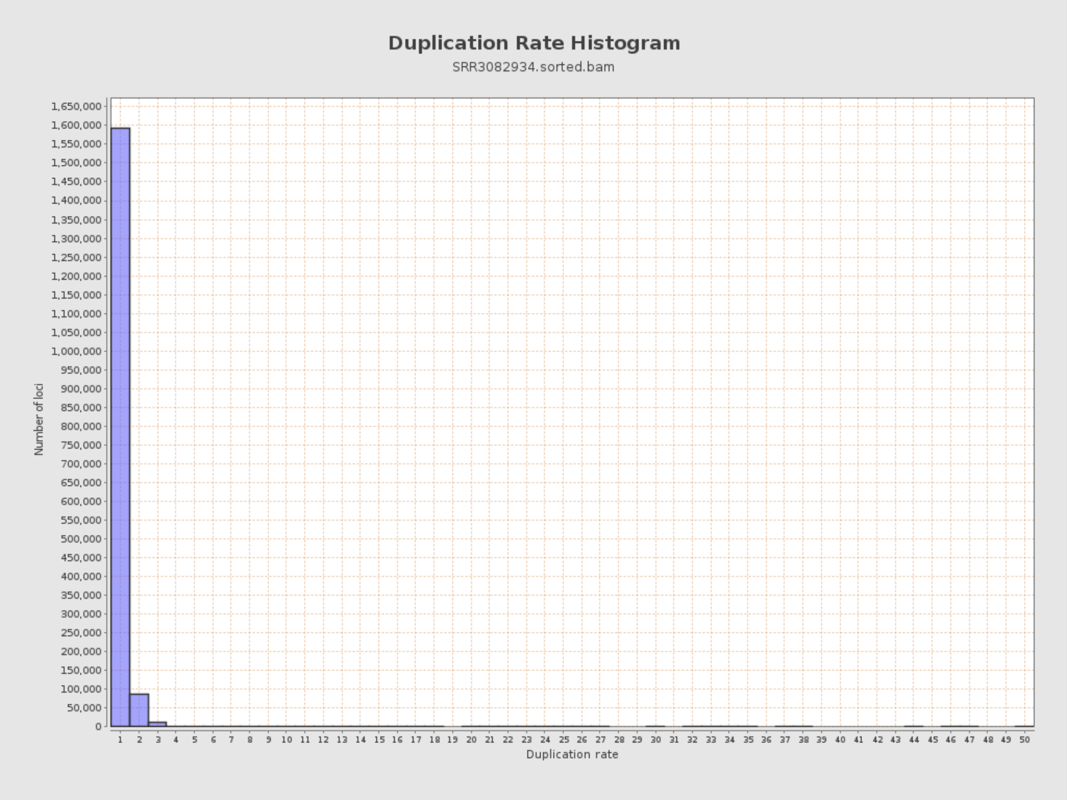
5. Results : Coverage Histogram (0-50X)



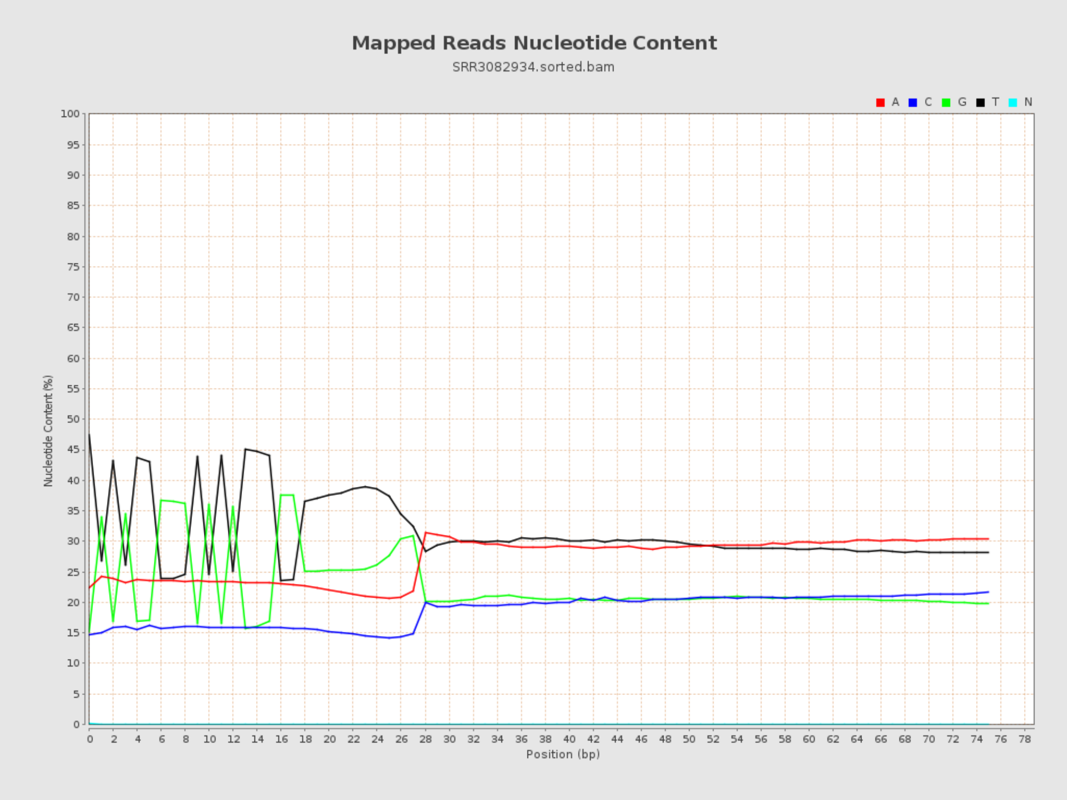
6. Results : Genome Fraction Coverage



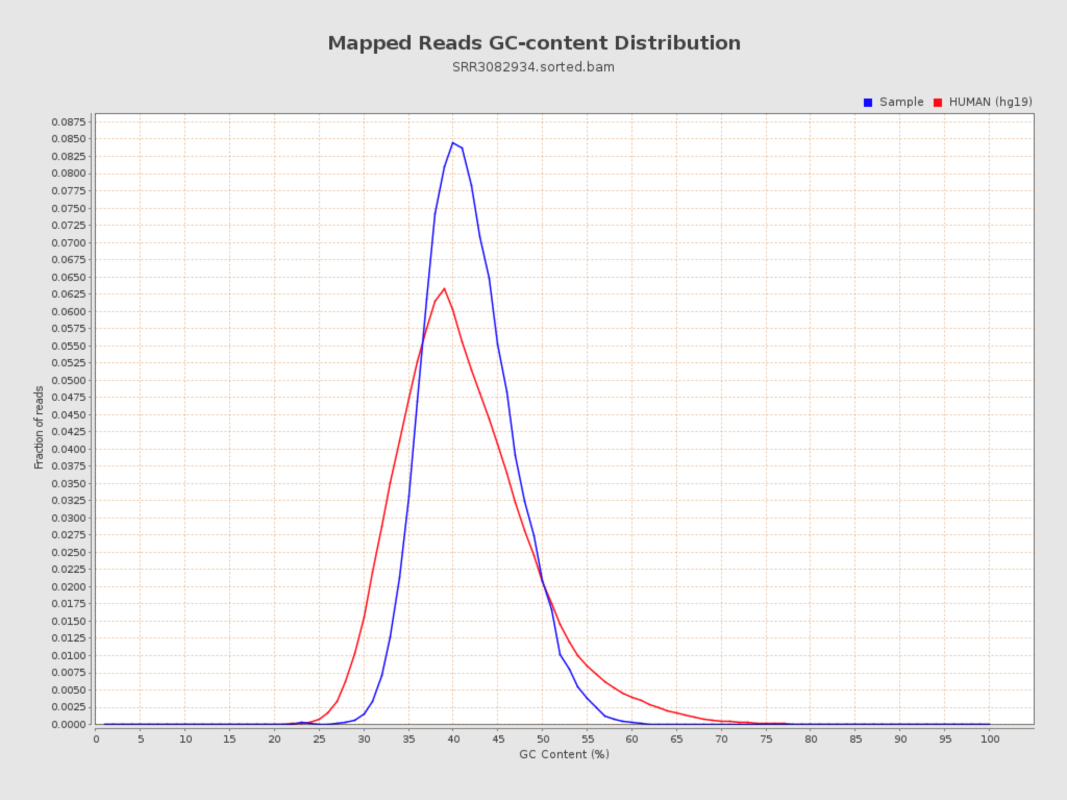
7. Results : Duplication Rate Histogram



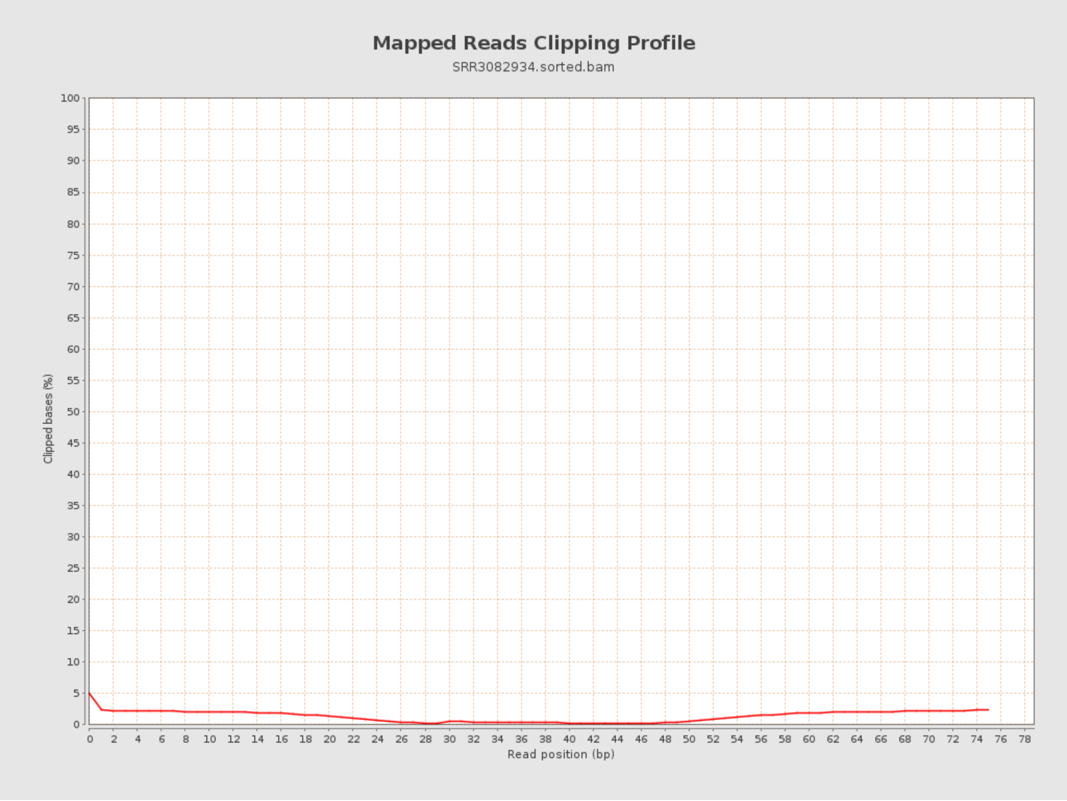
8. Results : Mapped Reads Nucleotide Content



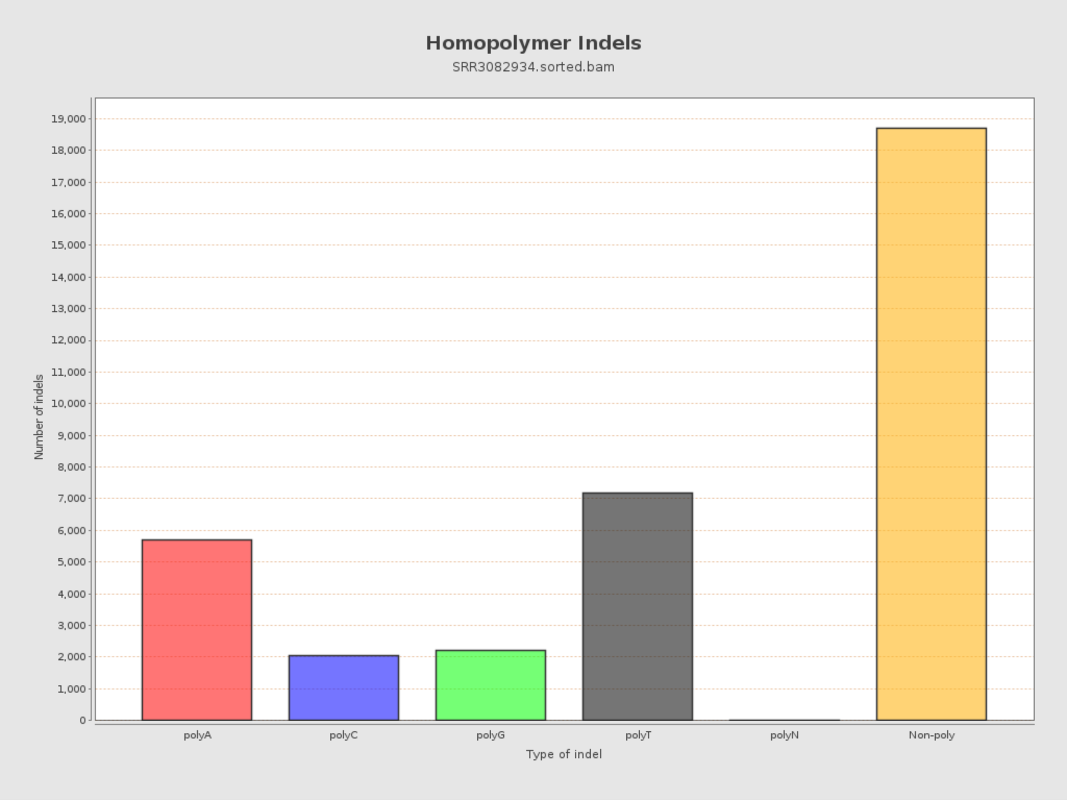
9. Results : Mapped Reads GC-content Distribution



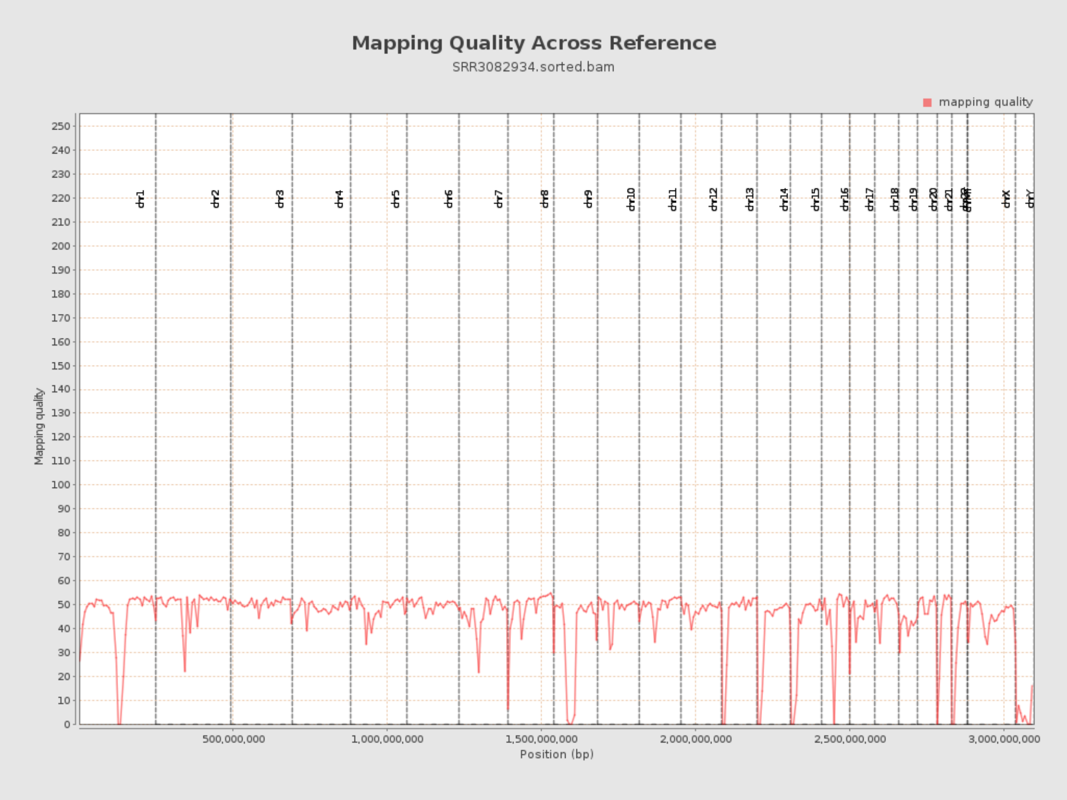
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram