Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 18:56:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082898.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_SRR3082898 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082898.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 18:56:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082898.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,227,534
Mapped reads	2,700,826 / 83.68%
Unmapped reads	526,708 / 16.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,874 / 0.55%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	143,631 / 4.45%
Duplication rate	4.31%
Clipped reads	1,162,315 / 36.01%

2.2. ACGT Content

Number/percentage of A's	50,307,396 / 27.75%
Number/percentage of C's	32,793,171 / 18.09%
Number/percentage of T's	59,187,480 / 32.65%
Number/percentage of G's	39,007,289 / 21.51%
Number/percentage of N's	9,783 / 0.01%
GC Percentage	39.6%

2.3. Coverage

Mean	0.0586

Standard Deviation	0.4635

2.4. Mapping Quality

Mean Mapping Quality	46.74

2.5. Mismatches and indels

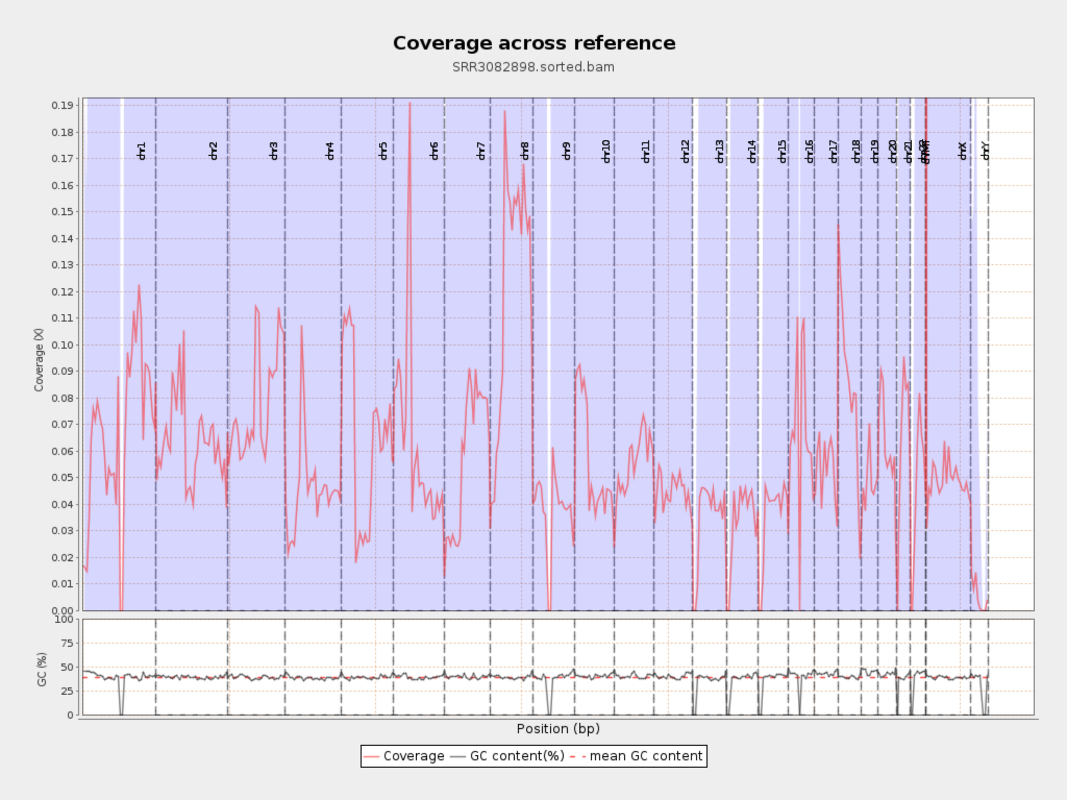
General error rate	0.9%
Mismatches	1,603,517
Insertions	14,514
Mapped reads with at least one insertion	0.53%
Deletions	39,817
Mapped reads with at least one deletion	1.46%
Homopolymer indels	48.12%

2.6. Chromosome stats

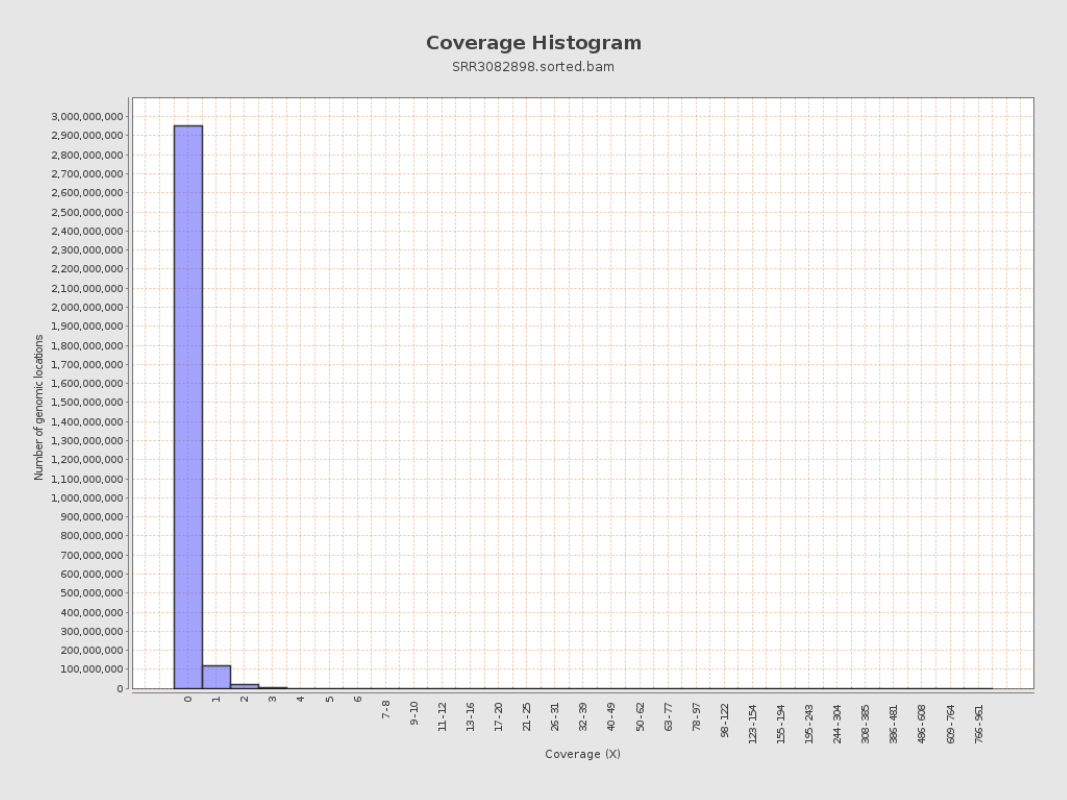
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16739067	0.0672	0.8969
chr2	243199373	15463858	0.0636	0.5968
chr3	198022430	15226767	0.0769	0.329
chr4	191154276	8855282	0.0463	0.2638
chr5	180915260	11673711	0.0645	0.3042
chr6	171115067	11029605	0.0645	0.4811
chr7	159138663	9236116	0.058	0.4045

chr8	146364022	17962362	0.1227	0.618
chr9	141213431	5314171	0.0376	0.4139
chr10	135534747	7703686	0.0568	0.3755
chr11	135006516	7560600	0.056	0.3744
chr12	133851895	5977832	0.0447	0.2568
chr13	115169878	4013848	0.0349	0.222
chr14	107349540	3607502	0.0336	0.2329
chr15	102531392	3573232	0.0349	0.2207
chr16	90354753	5914681	0.0655	0.3389
chr17	81195210	4378162	0.0539	0.3503
chr18	78077248	6792830	0.087	0.7725
chr19	59128983	2871839	0.0486	0.565
chr20	63025520	4044274	0.0642	0.3068
chr21	48129895	3014359	0.0626	0.3046
chr22	51304566	2367263	0.0461	0.2513
chrMT	16571	143369	8.6518	5.7502
chrX	155270560	7597348	0.0489	0.3
chrY	59373566	311307	0.0052	0.1113

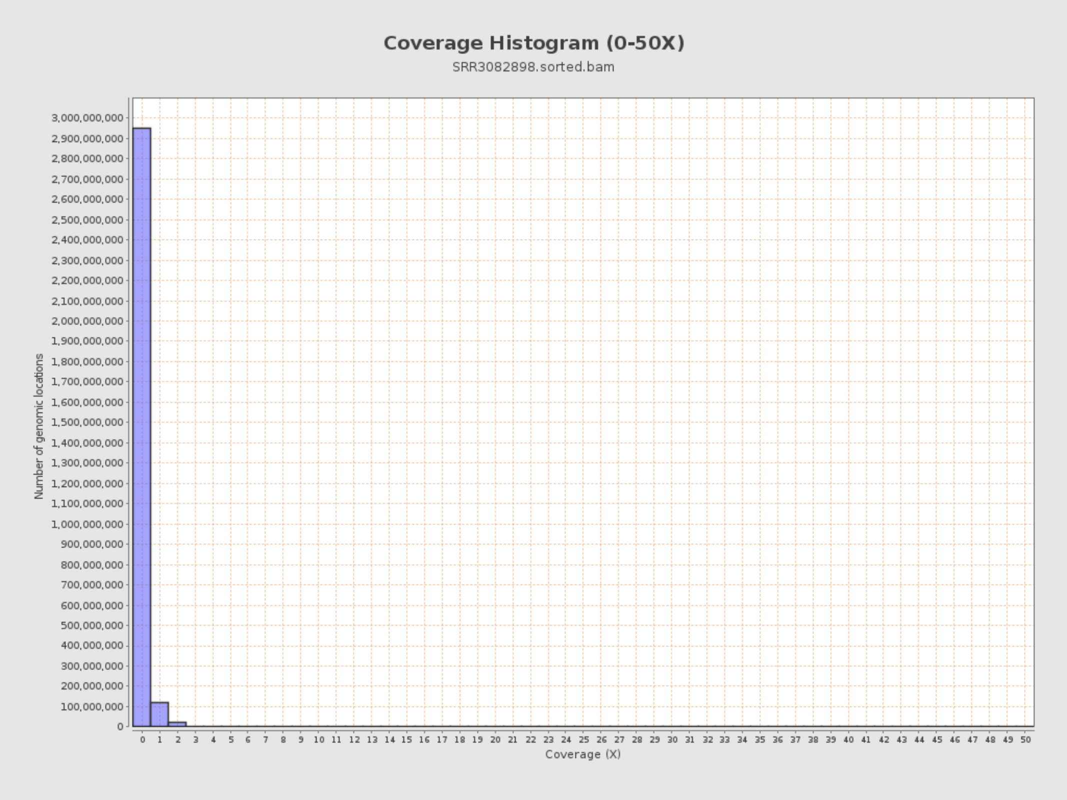
3. Results : Coverage across reference



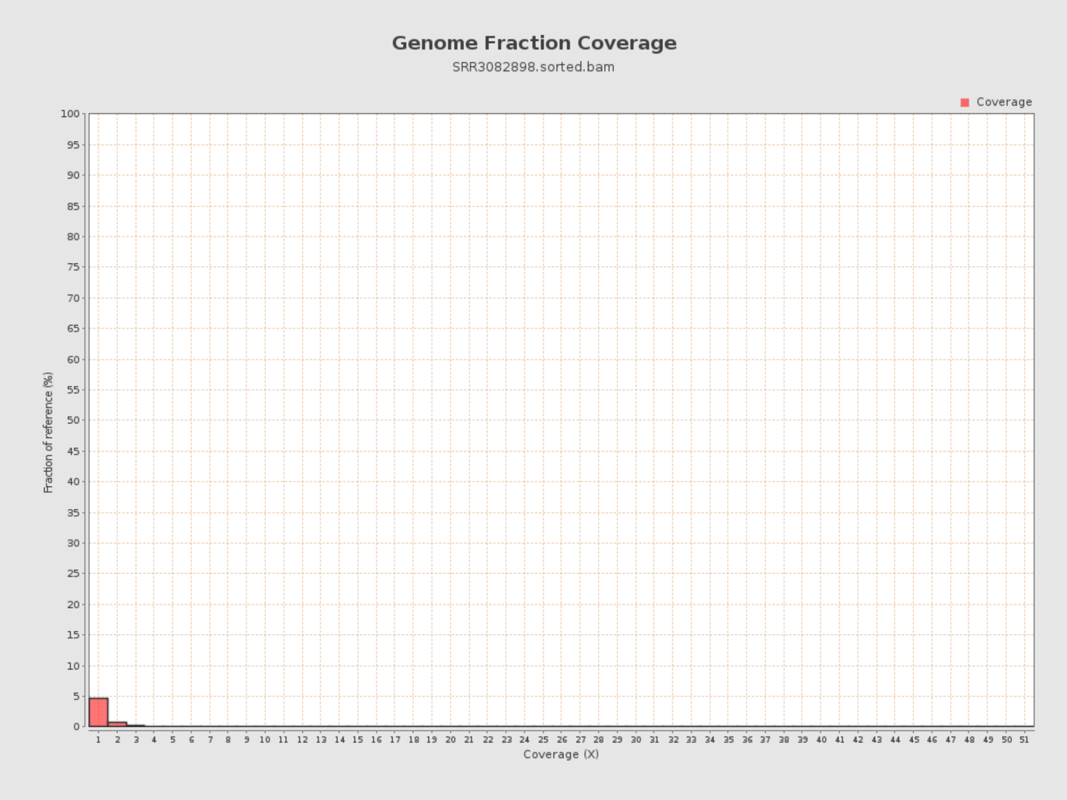
4. Results : Coverage Histogram



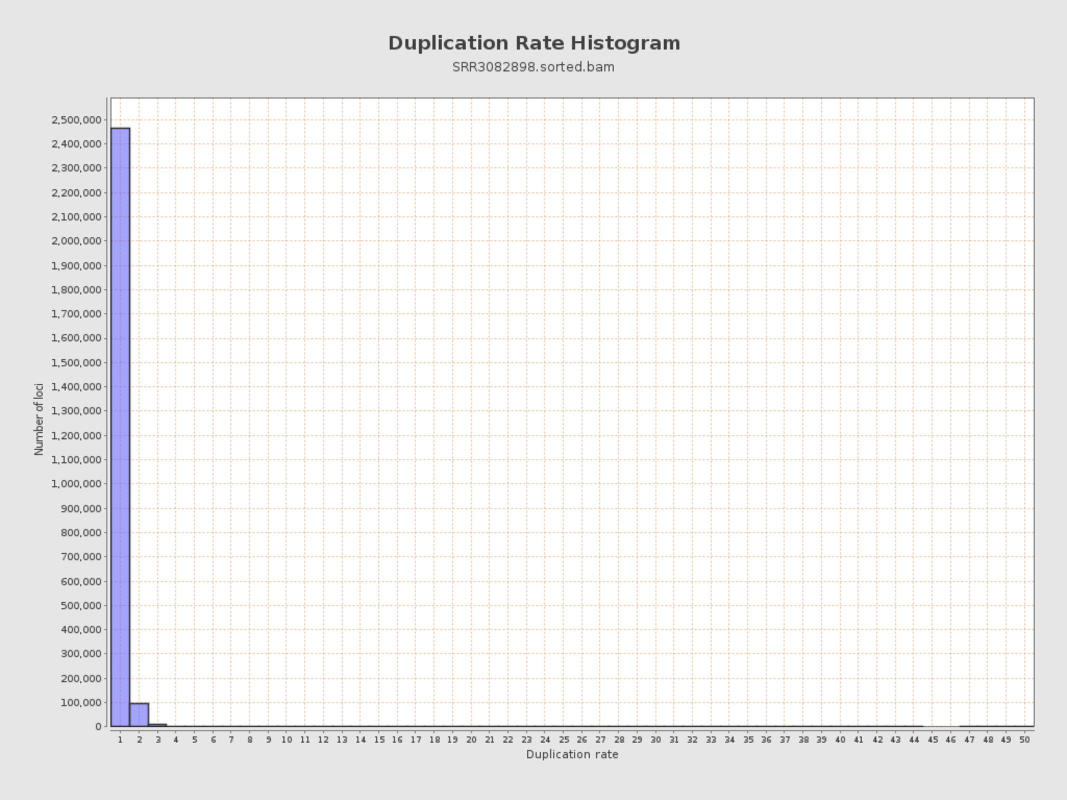
5. Results : Coverage Histogram (0-50X)



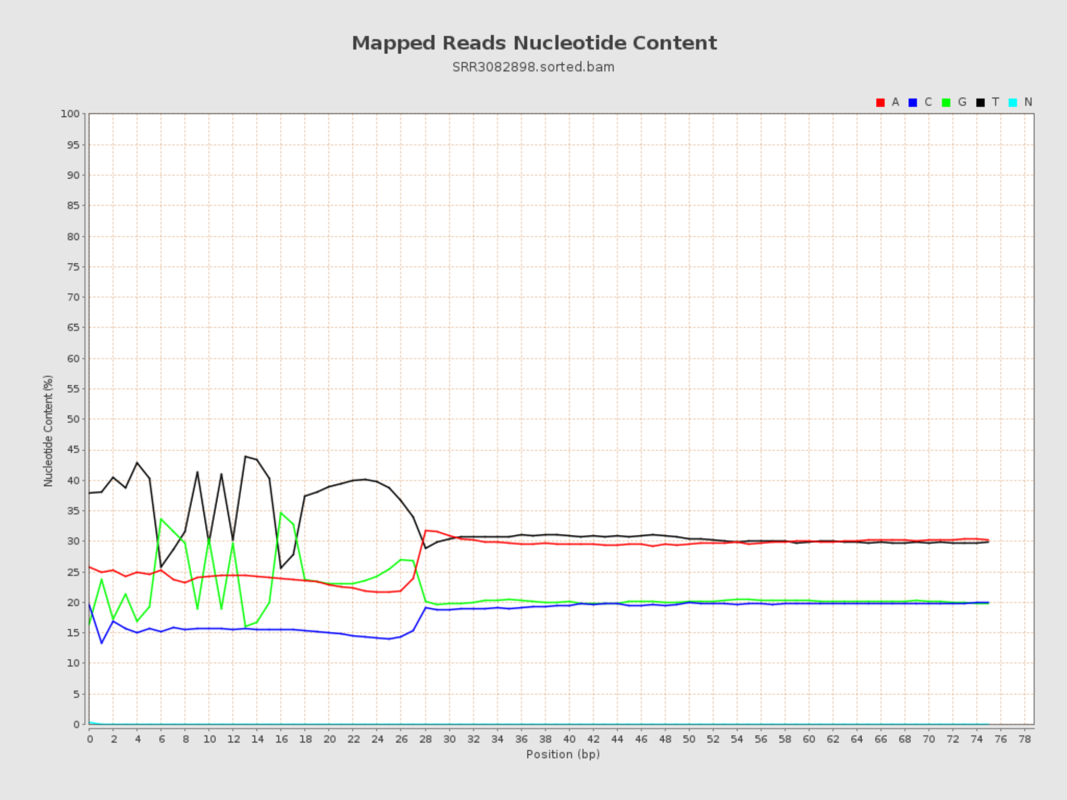
6. Results : Genome Fraction Coverage



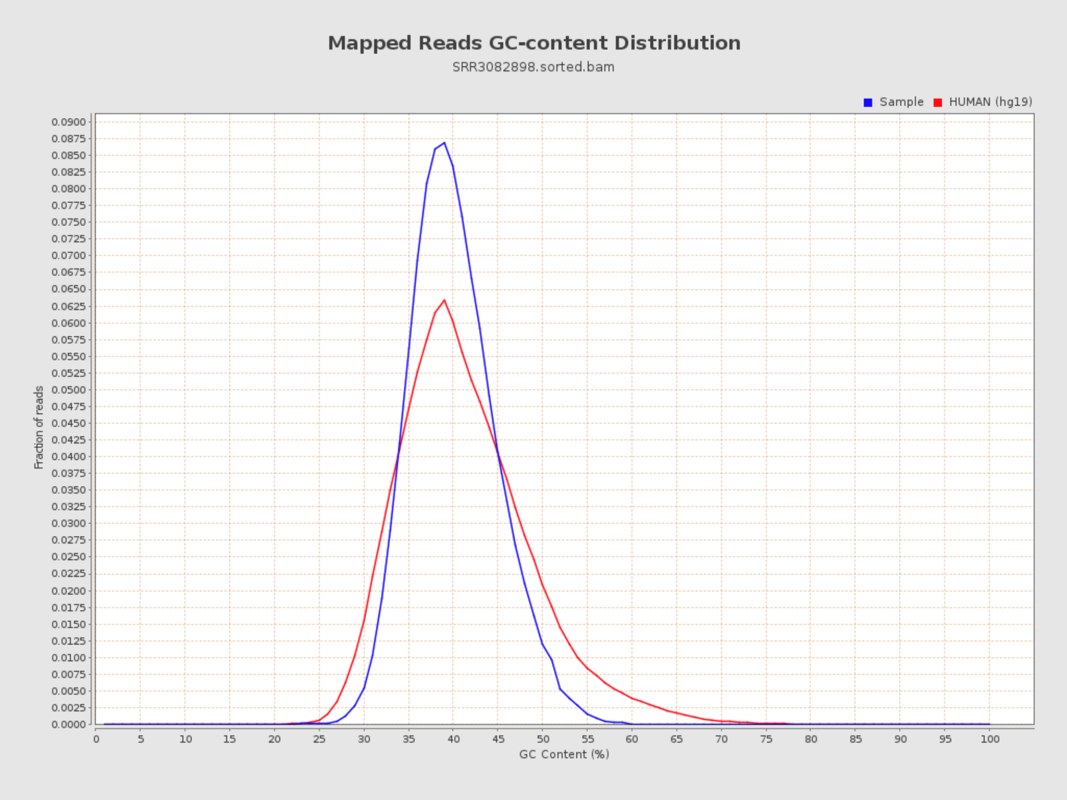
7. Results : Duplication Rate Histogram



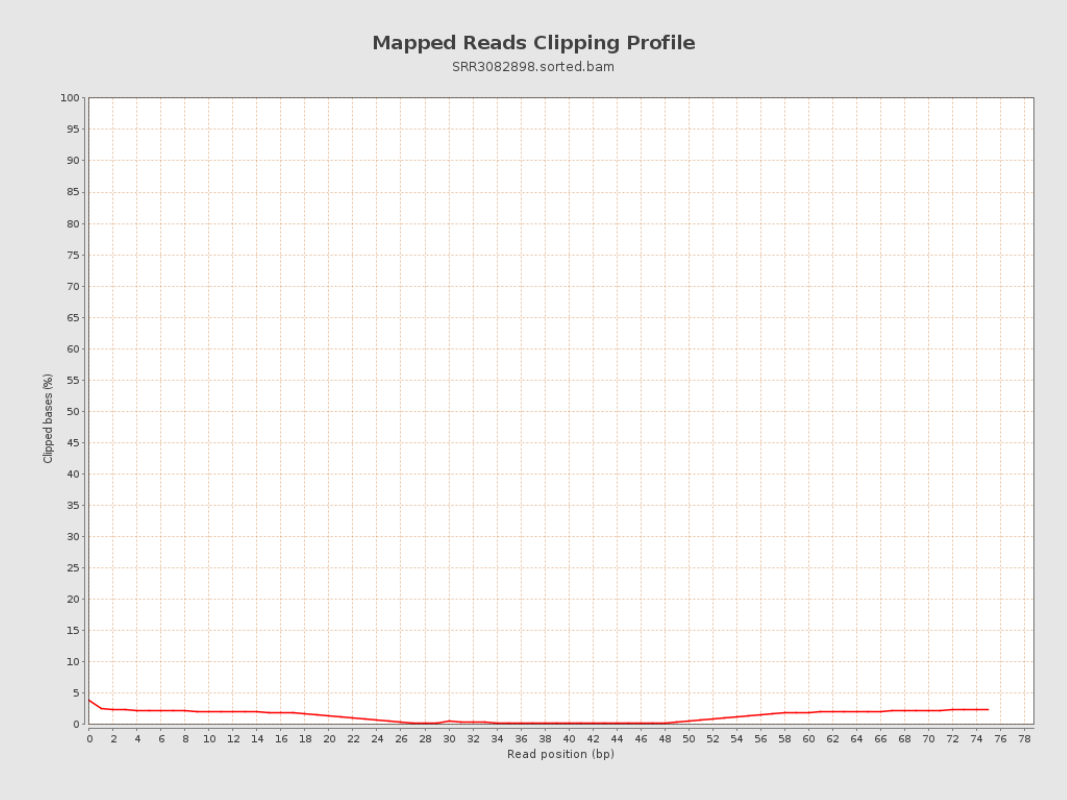
8. Results : Mapped Reads Nucleotide Content



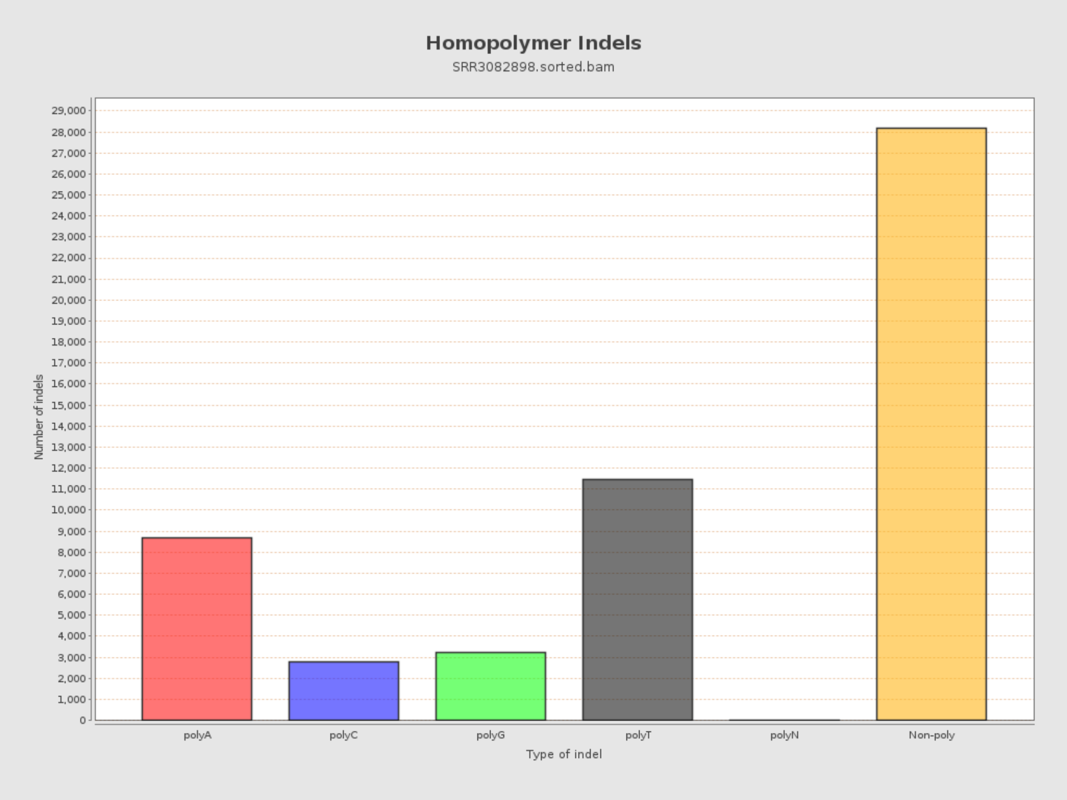
9. Results : Mapped Reads GC-content Distribution



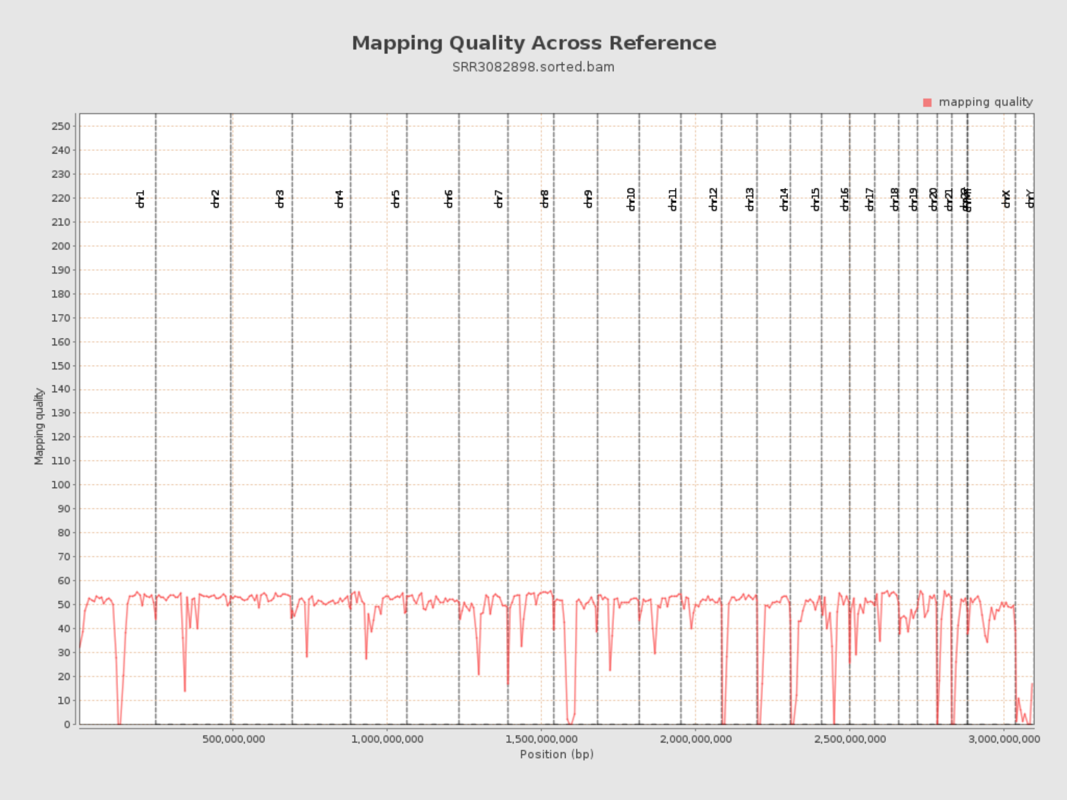
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram