Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 21:22:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082958.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_SRR3082958 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082958.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 21:22:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082958.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,876,018
Mapped reads	4,210,798 / 86.36%
Unmapped reads	665,220 / 13.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,851 / 0.55%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	333,169 / 6.83%
Duplication rate	5.46%
Clipped reads	1,860,439 / 38.15%

2.2. ACGT Content

Number/percentage of A's	78,788,055 / 27.96%
Number/percentage of C's	49,240,847 / 17.48%
Number/percentage of T's	92,719,458 / 32.91%
Number/percentage of G's	60,950,499 / 21.63%
Number/percentage of N's	75,600 / 0.03%
GC Percentage	39.11%

2.3. Coverage

Mean	0.0911

Standard Deviation	0.6359

2.4. Mapping Quality

Mean Mapping Quality	46.84

2.5. Mismatches and indels

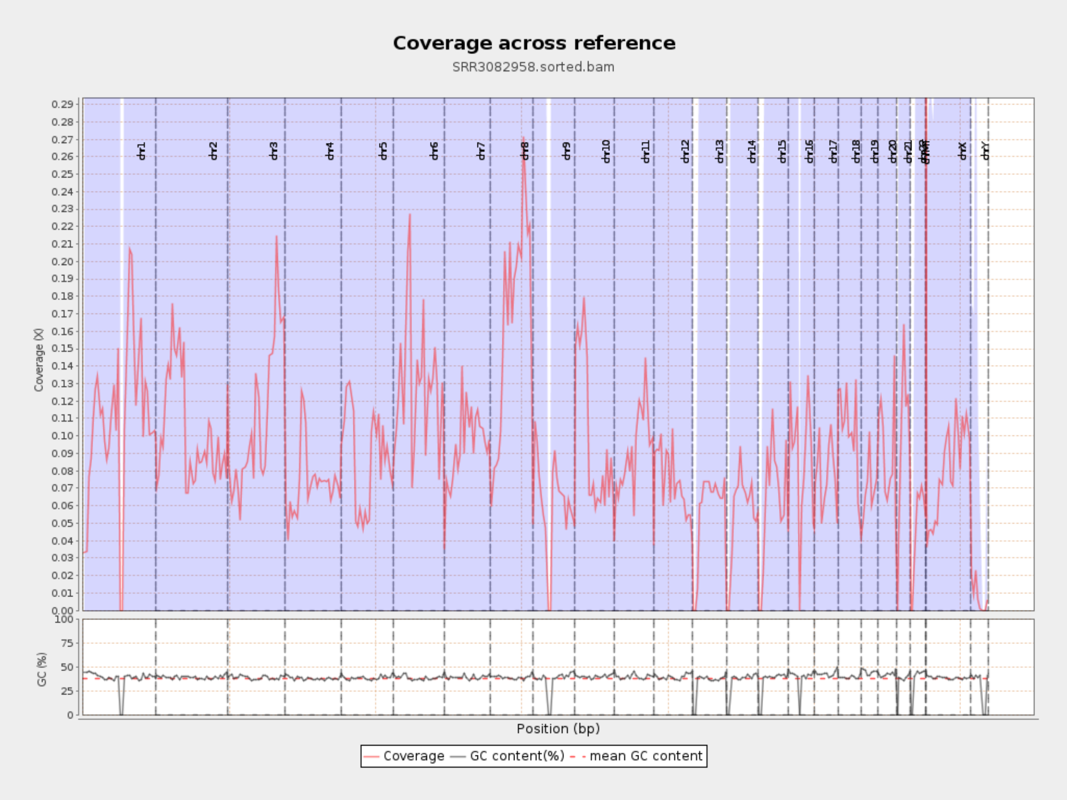
General error rate	0.96%
Mismatches	2,669,688
Insertions	25,229
Mapped reads with at least one insertion	0.59%
Deletions	66,928
Mapped reads with at least one deletion	1.57%
Homopolymer indels	48.76%

2.6. Chromosome stats

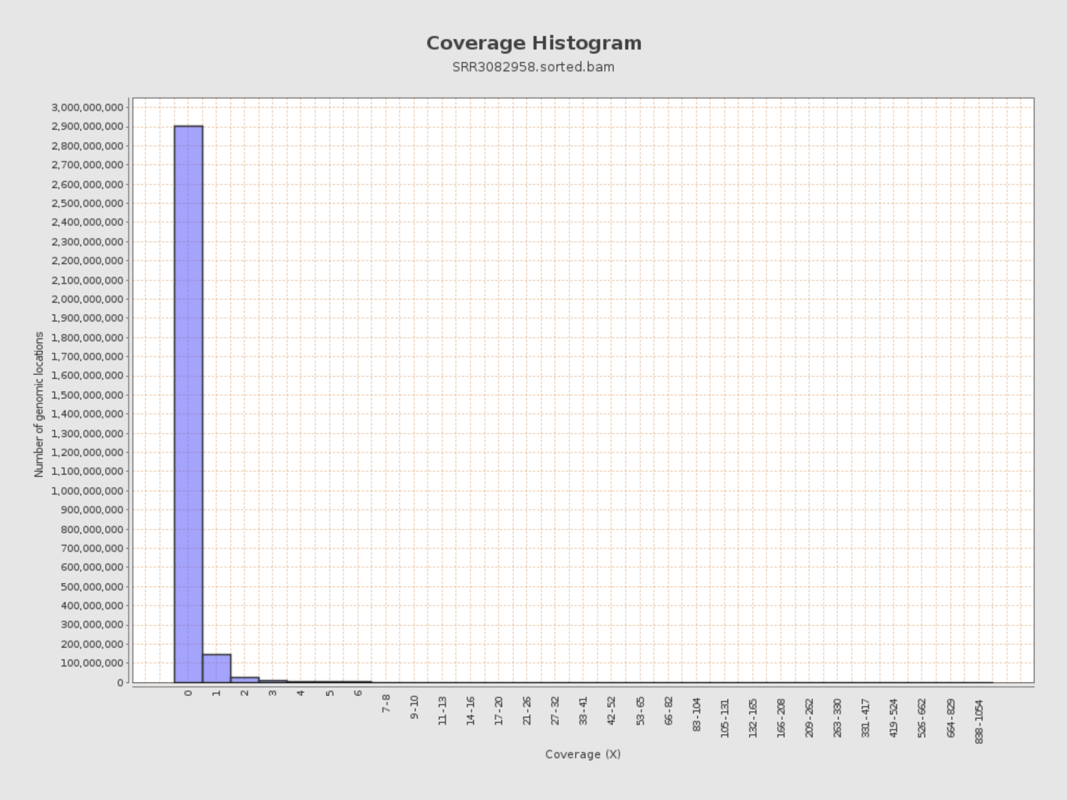
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	27468873	0.1102	1.0003
chr2	243199373	24920159	0.1025	0.753
chr3	198022430	21676629	0.1095	0.478
chr4	191154276	14079929	0.0737	0.3873
chr5	180915260	15806496	0.0874	0.4112
chr6	171115067	22499344	0.1315	0.7396
chr7	159138663	15140150	0.0951	0.8761

chr8	146364022	24502871	0.1674	0.9199
chr9	141213431	8740641	0.0619	0.5501
chr10	135534747	13525319	0.0998	0.6139
chr11	135006516	12396059	0.0918	0.5491
chr12	133851895	9995173	0.0747	0.4155
chr13	115169878	6540915	0.0568	0.3407
chr14	107349540	6064108	0.0565	0.3723
chr15	102531392	6410564	0.0625	0.371
chr16	90354753	7648170	0.0846	0.4441
chr17	81195210	6488941	0.0799	0.4939
chr18	78077248	8092897	0.1037	1.0716
chr19	59128983	4156566	0.0703	0.7323
chr20	63025520	5896514	0.0936	0.4599
chr21	48129895	4553552	0.0946	0.4276
chr22	51304566	2399497	0.0468	0.2824
chrMT	16571	11525	0.6955	1.1367
chrX	155270560	12408374	0.0799	0.45
chrY	59373566	458499	0.0077	0.1551

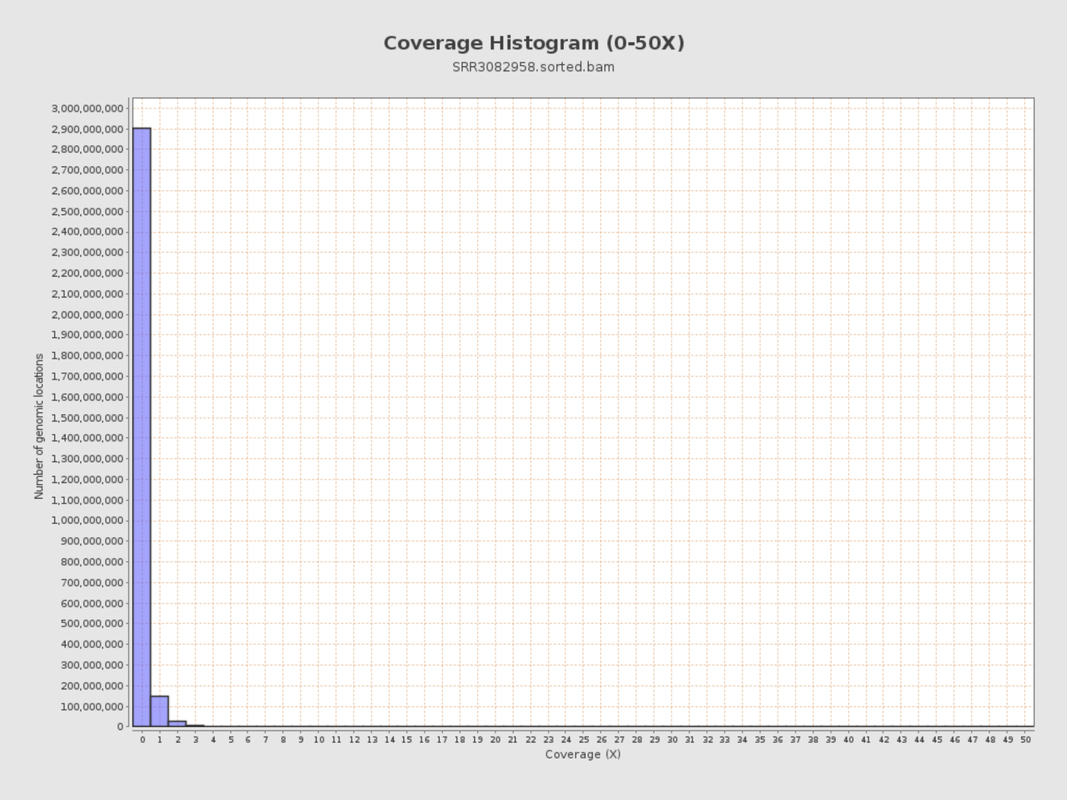
3. Results : Coverage across reference



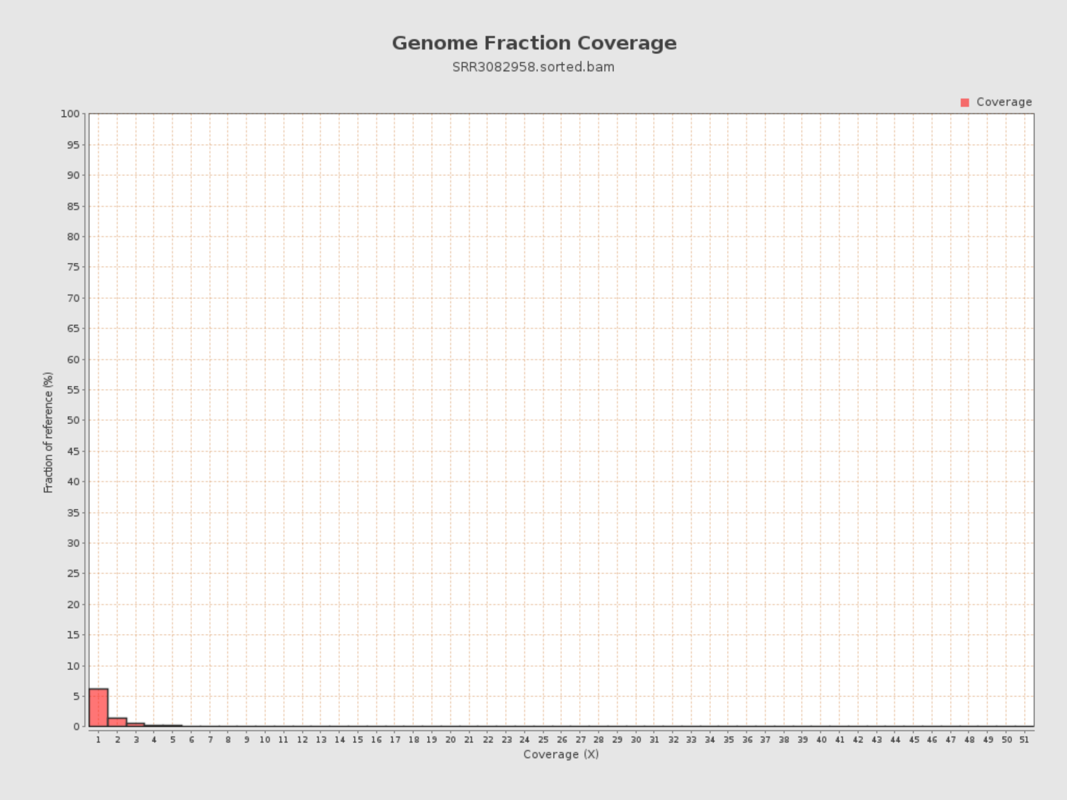
4. Results : Coverage Histogram



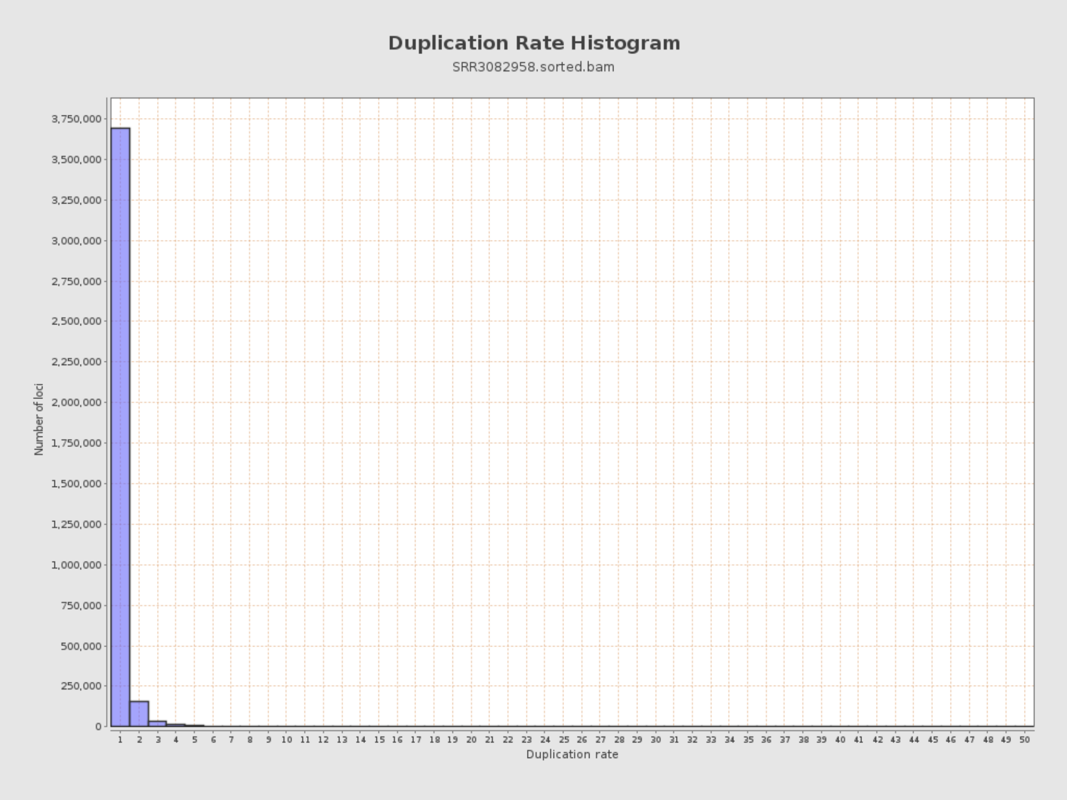
5. Results : Coverage Histogram (0-50X)



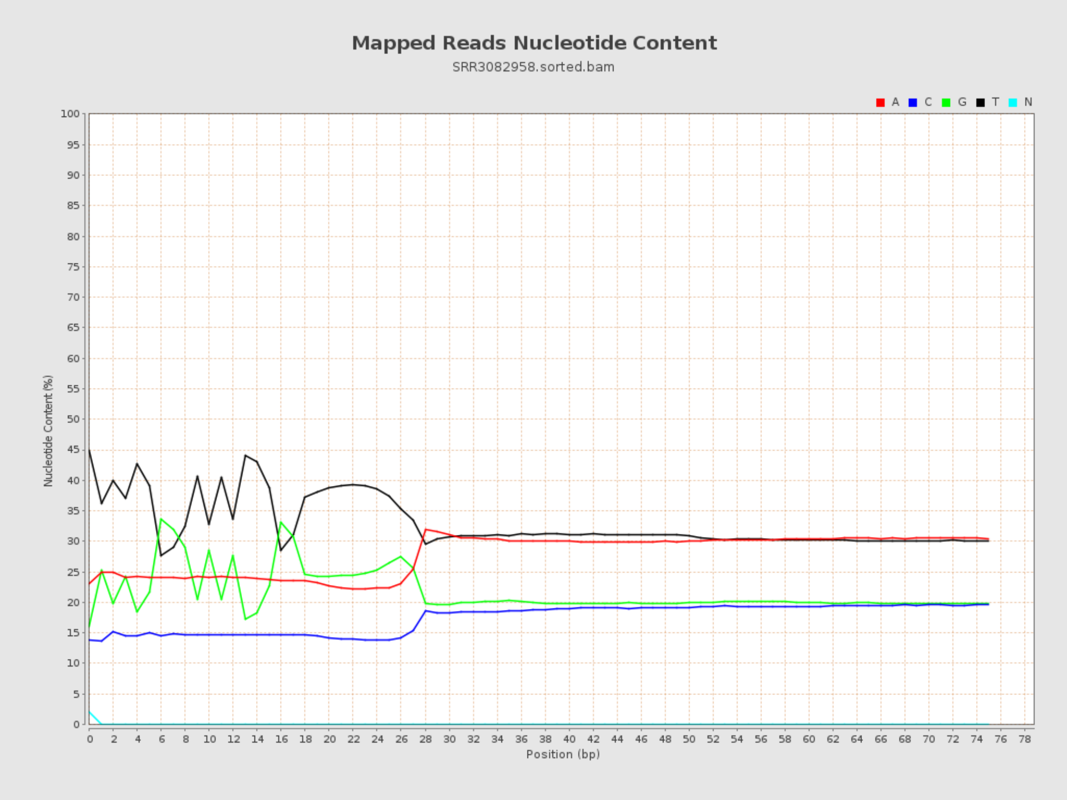
6. Results : Genome Fraction Coverage



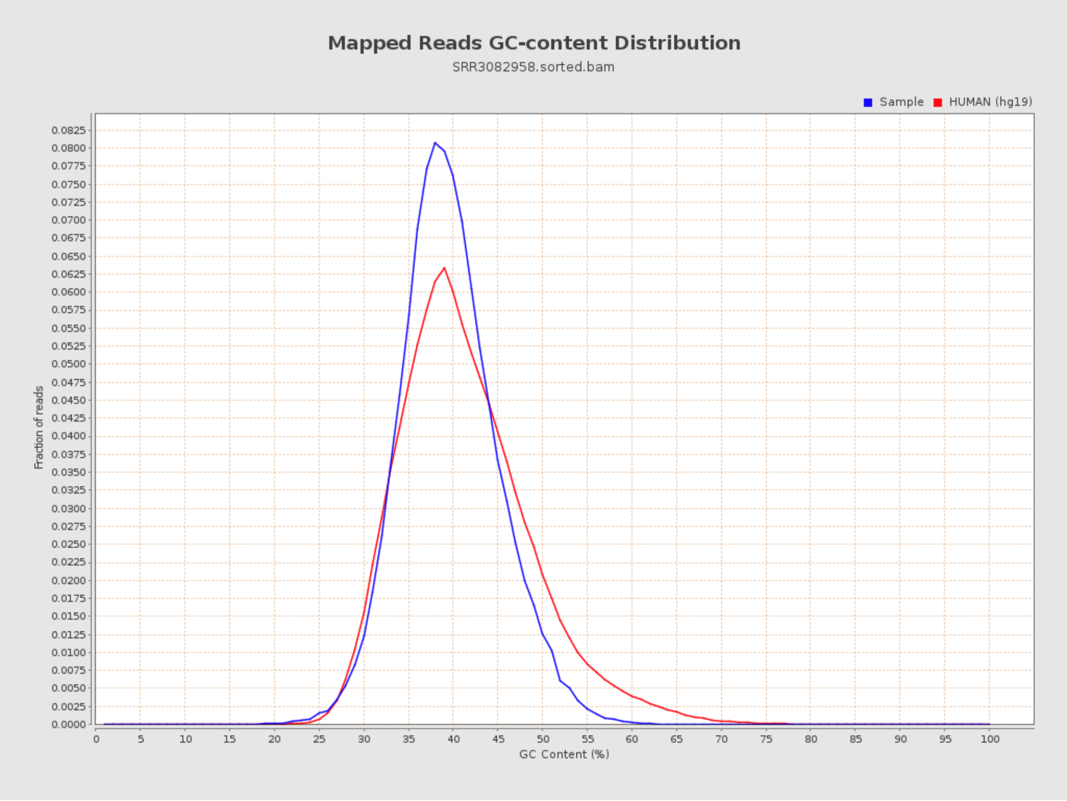
7. Results : Duplication Rate Histogram



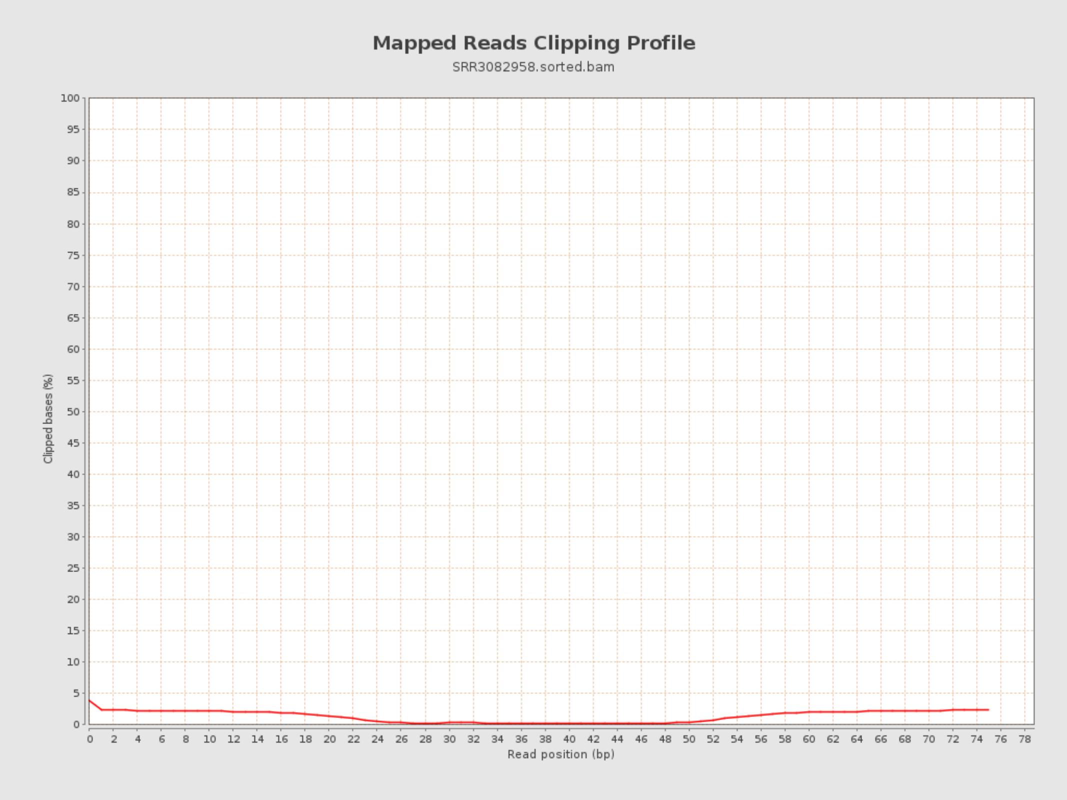
8. Results : Mapped Reads Nucleotide Content



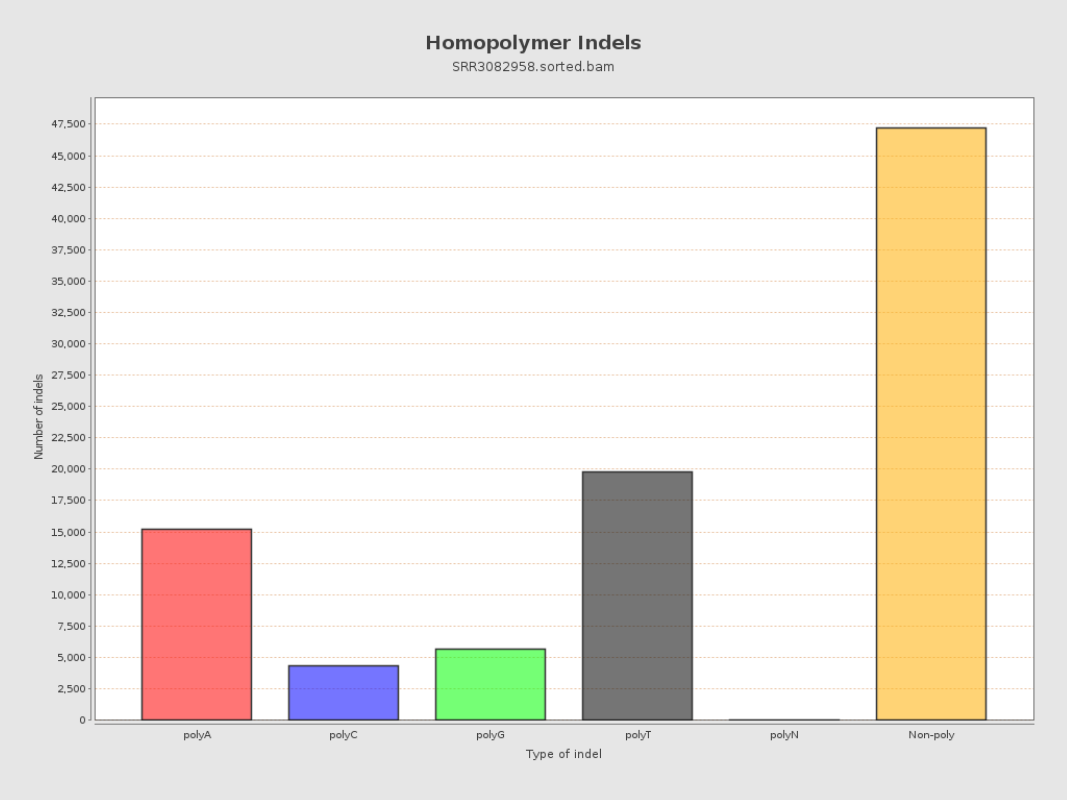
9. Results : Mapped Reads GC-content Distribution



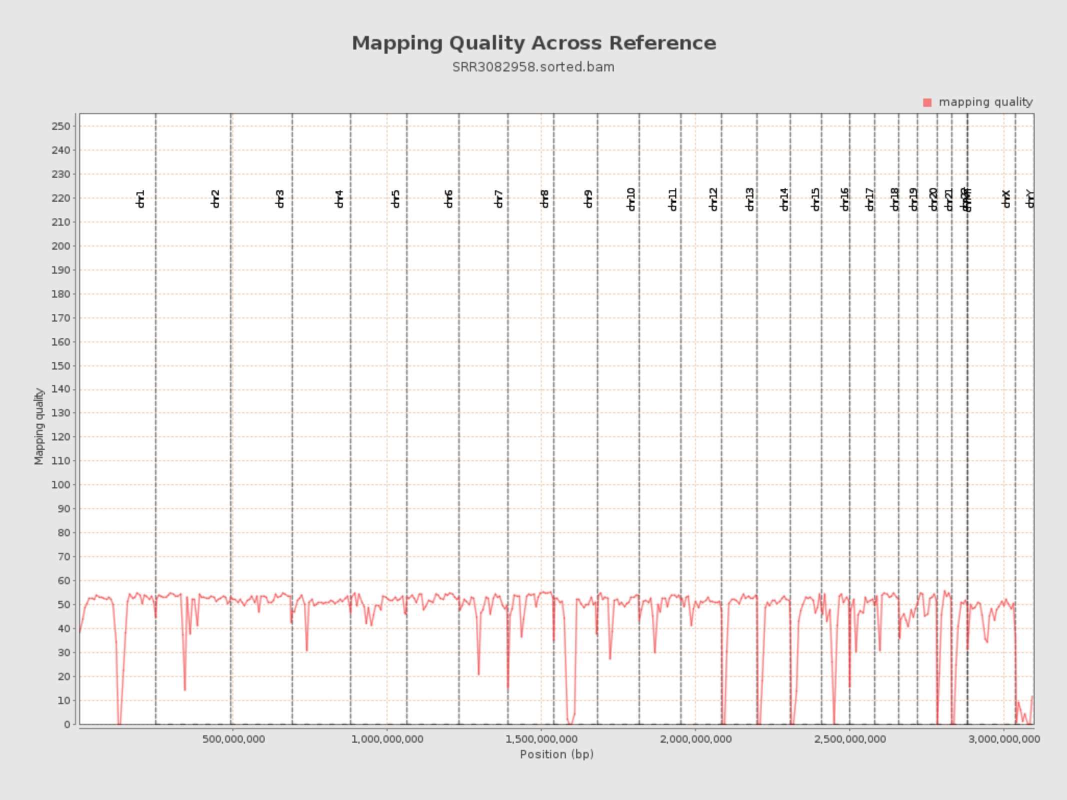
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram