Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 16:12:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082678.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_SRR3082678 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082678.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 16:12:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082678.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,090,034
Mapped reads	2,857,810 / 92.48%
Unmapped reads	232,224 / 7.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,018 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	119,411 / 3.86%
Duplication rate	3.16%
Clipped reads	1,380,749 / 44.68%

2.2. ACGT Content

Number/percentage of A's	51,548,697 / 27.31%
Number/percentage of C's	32,343,638 / 17.14%
Number/percentage of T's	62,983,817 / 33.37%
Number/percentage of G's	41,826,471 / 22.16%
Number/percentage of N's	49,610 / 0.03%
GC Percentage	39.29%

2.3. Coverage

Mean	0.061

Standard Deviation	0.4771

2.4. Mapping Quality

Mean Mapping Quality	46.76

2.5. Mismatches and indels

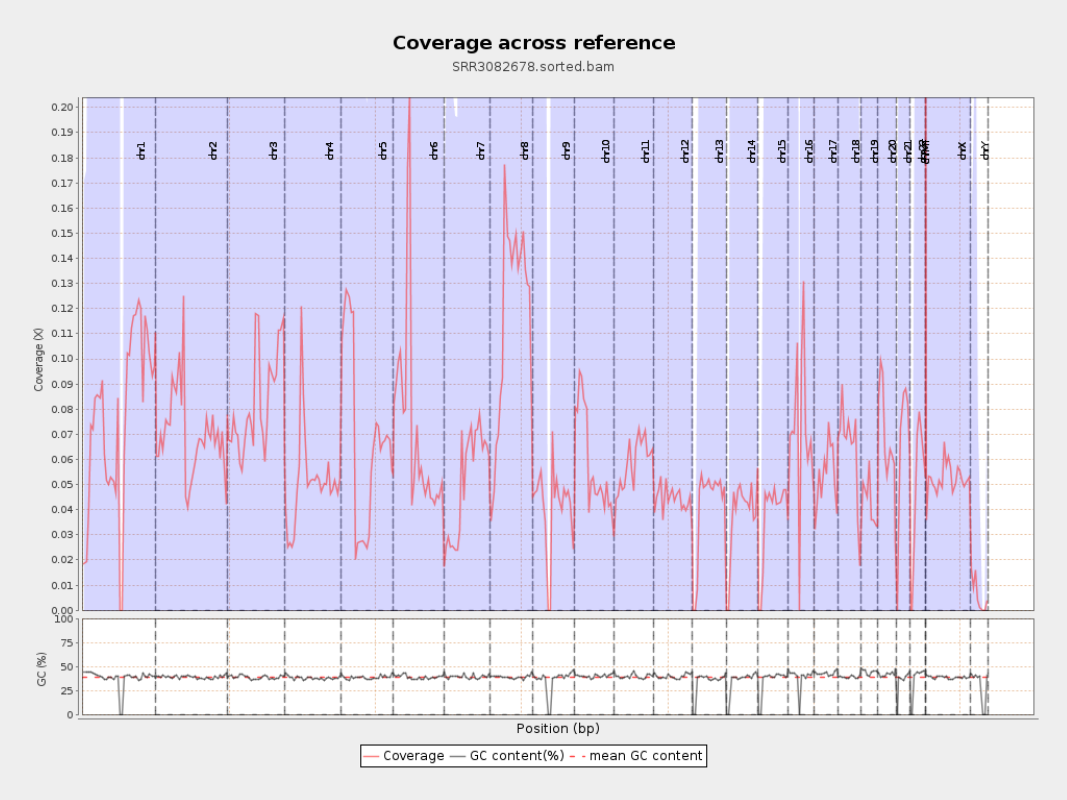
General error rate	0.91%
Mismatches	1,697,167
Insertions	16,849
Mapped reads with at least one insertion	0.58%
Deletions	44,695
Mapped reads with at least one deletion	1.55%
Homopolymer indels	48.97%

2.6. Chromosome stats

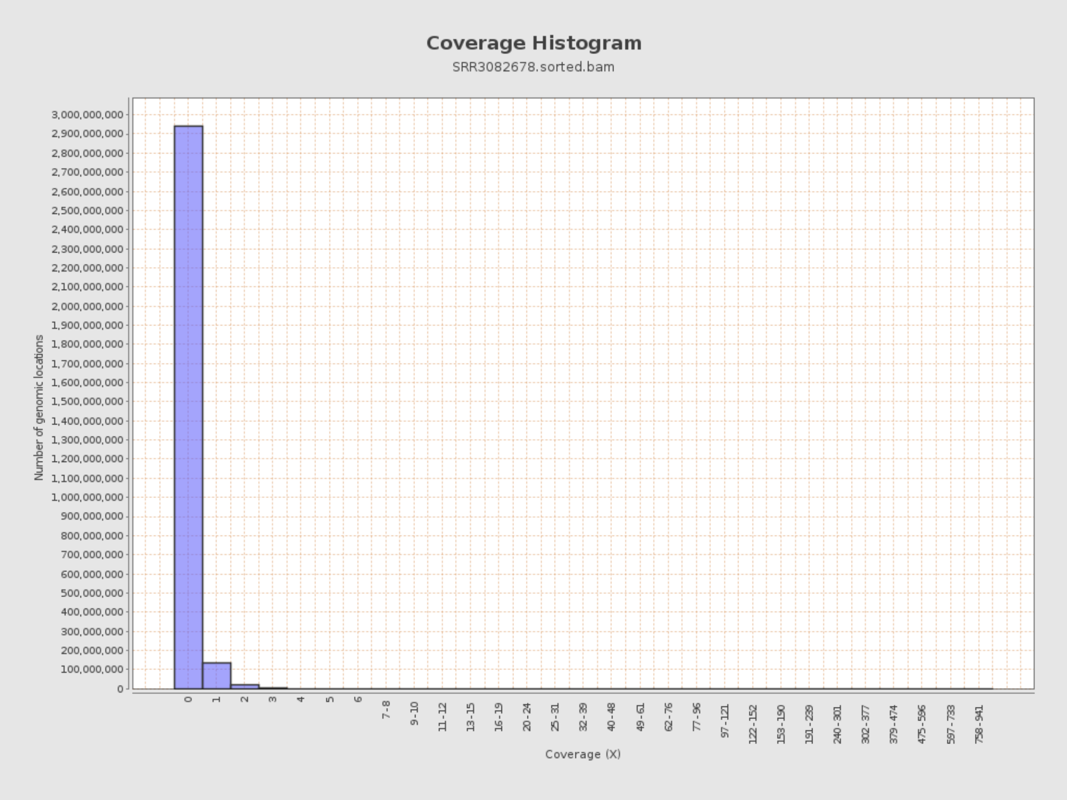
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18986677	0.0762	0.7247
chr2	243199373	17055879	0.0701	0.6608
chr3	198022430	16253673	0.0821	0.3344
chr4	191154276	9849668	0.0515	0.2717
chr5	180915260	12219606	0.0675	0.3057
chr6	171115067	12413516	0.0725	0.5835
chr7	159138663	8157417	0.0513	0.5327

chr8	146364022	16997887	0.1161	0.5817
chr9	141213431	5818037	0.0412	0.5214
chr10	135534747	7983691	0.0589	0.3873
chr11	135006516	7863475	0.0582	0.4032
chr12	133851895	5928861	0.0443	0.2517
chr13	115169878	4718596	0.041	0.2303
chr14	107349540	4030332	0.0375	0.2778
chr15	102531392	3741115	0.0365	0.2178
chr16	90354753	6369357	0.0705	0.3452
chr17	81195210	4374240	0.0539	0.339
chr18	78077248	5120889	0.0656	1.0206
chr19	59128983	2551495	0.0432	0.5432
chr20	63025520	4386044	0.0696	0.3176
chr21	48129895	3067581	0.0637	0.306
chr22	51304566	2476044	0.0483	0.2523
chrMT	16571	4773	0.288	0.6331
chrX	155270560	8110750	0.0522	0.3404
chrY	59373566	344428	0.0058	0.1243

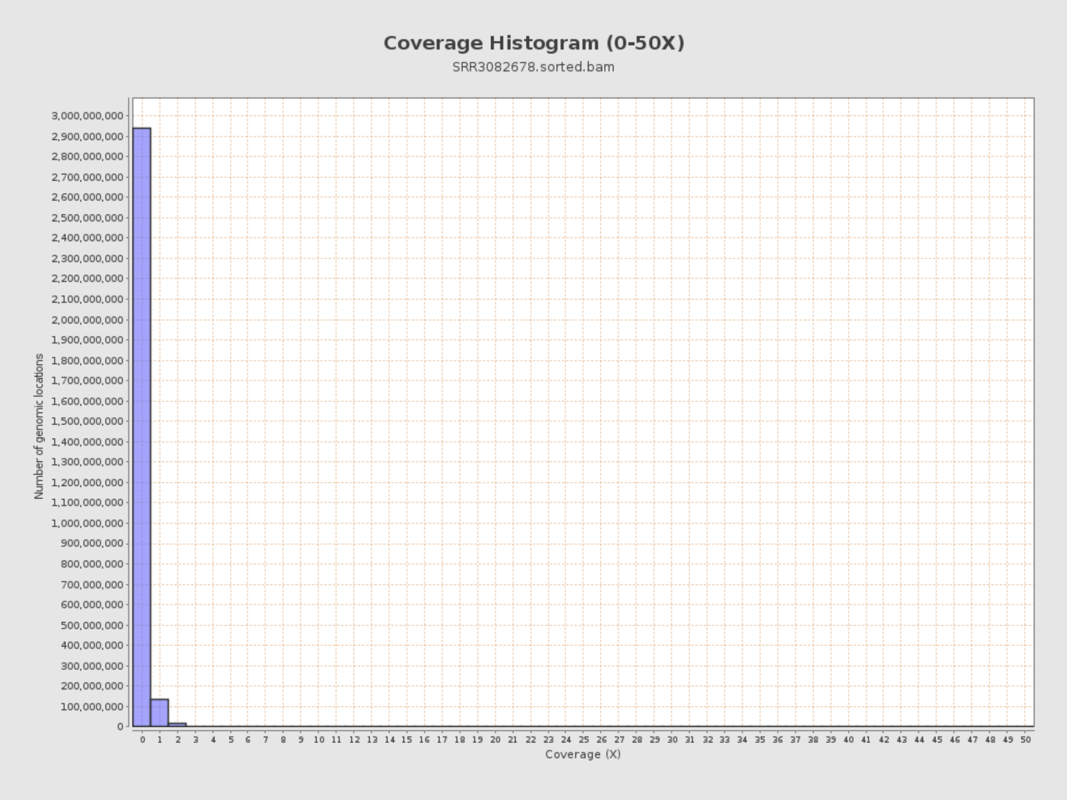
3. Results : Coverage across reference



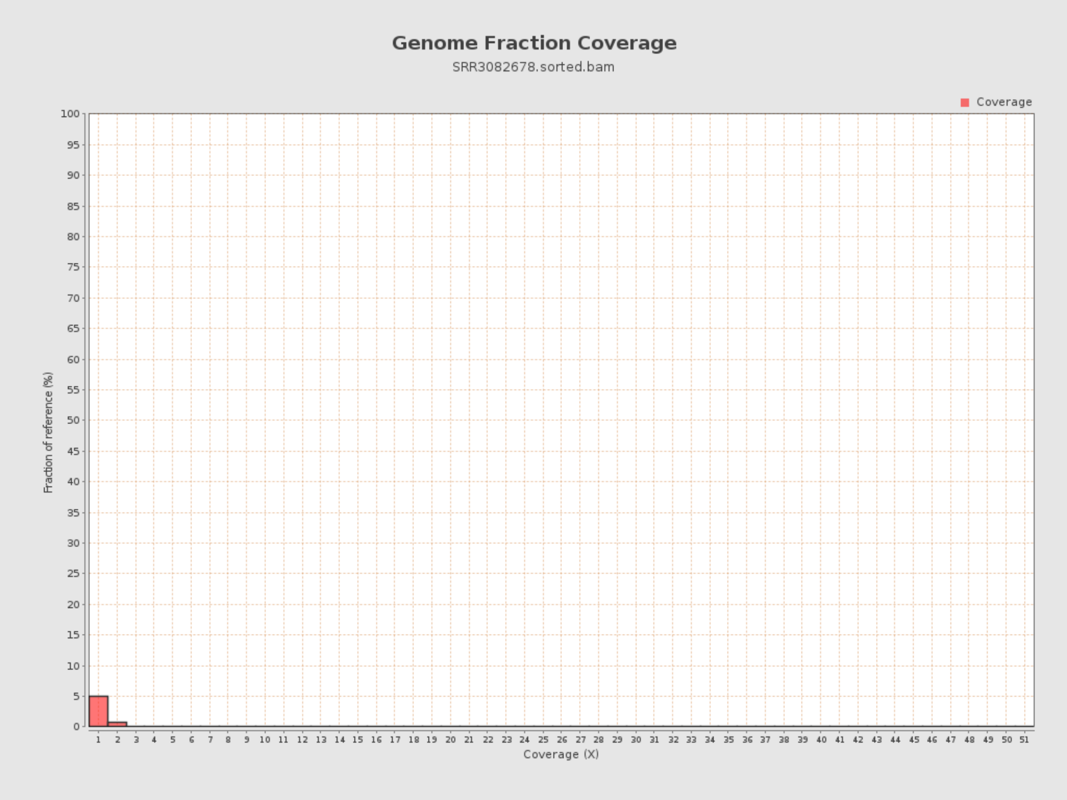
4. Results : Coverage Histogram



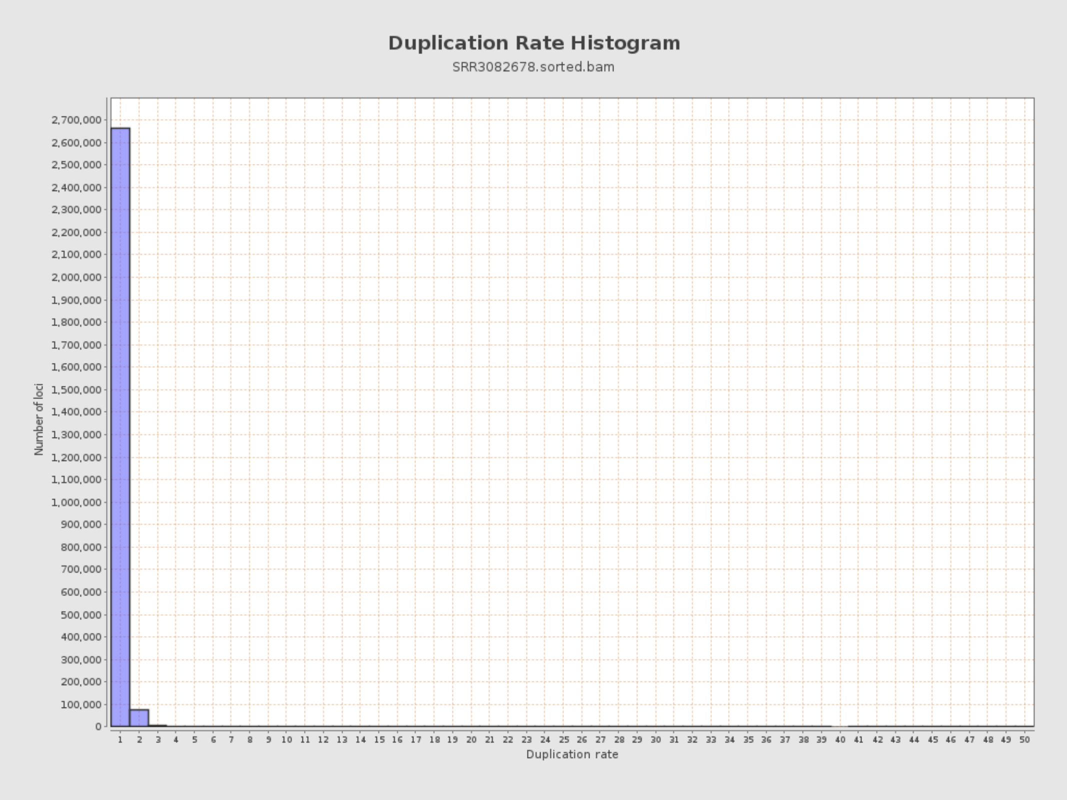
5. Results : Coverage Histogram (0-50X)



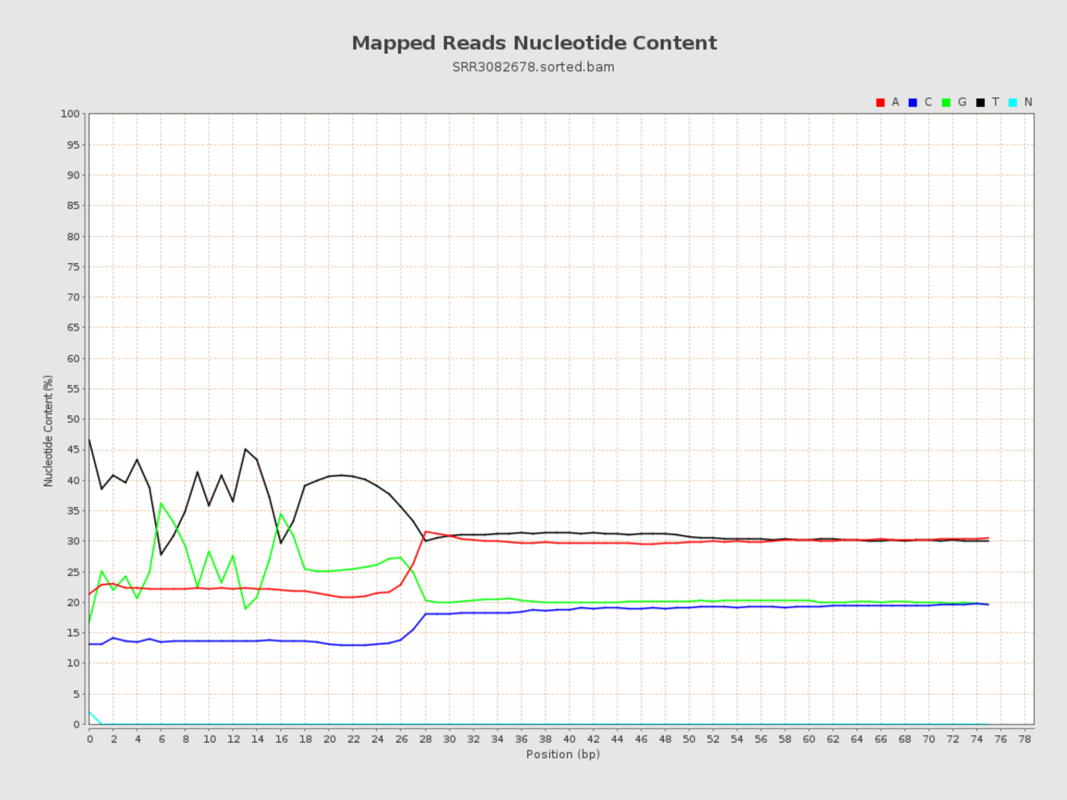
6. Results : Genome Fraction Coverage



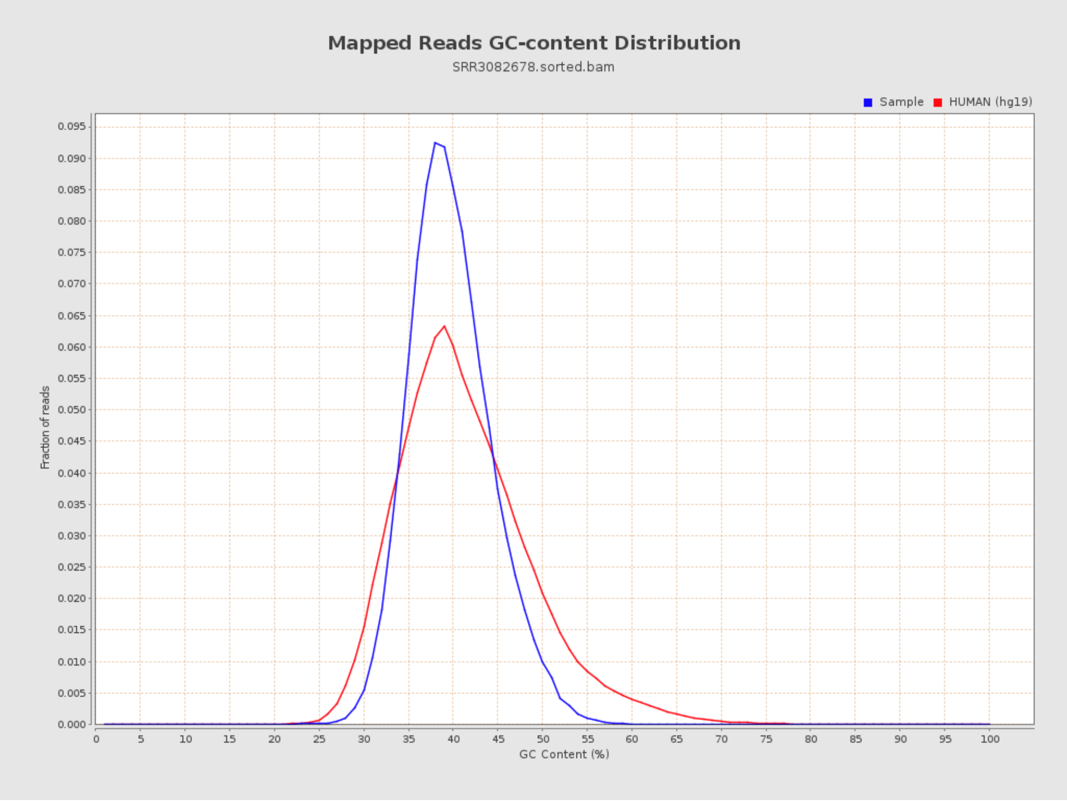
7. Results : Duplication Rate Histogram



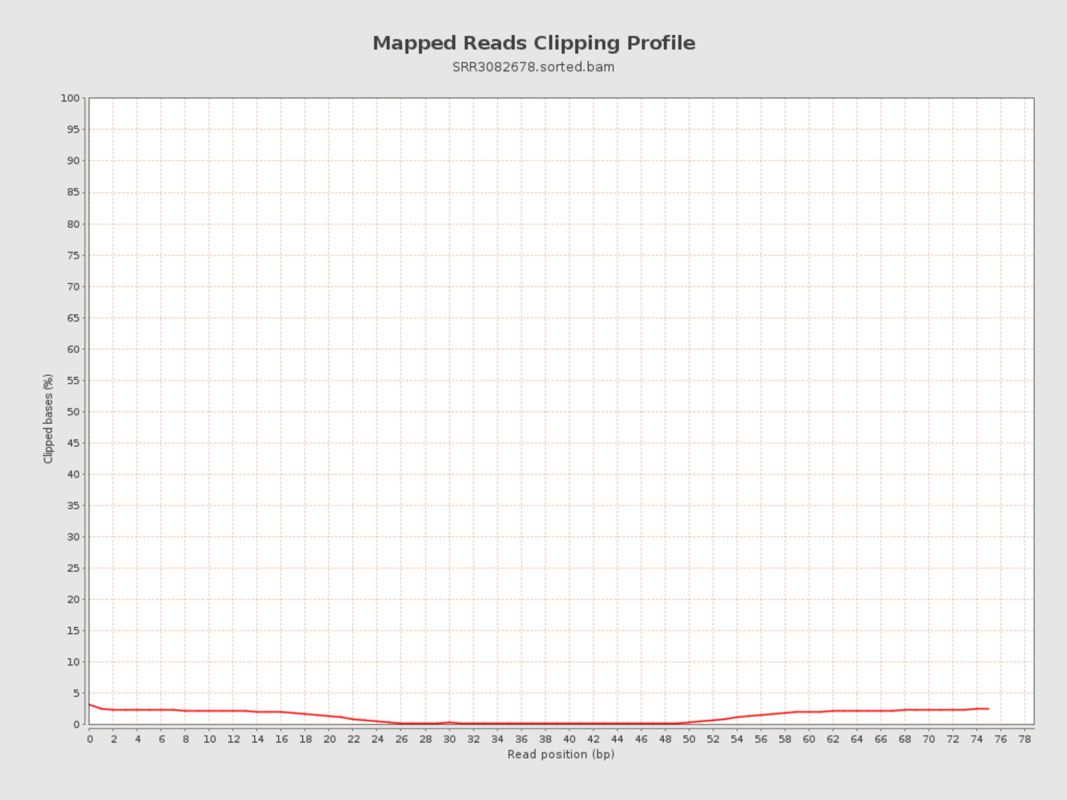
8. Results : Mapped Reads Nucleotide Content



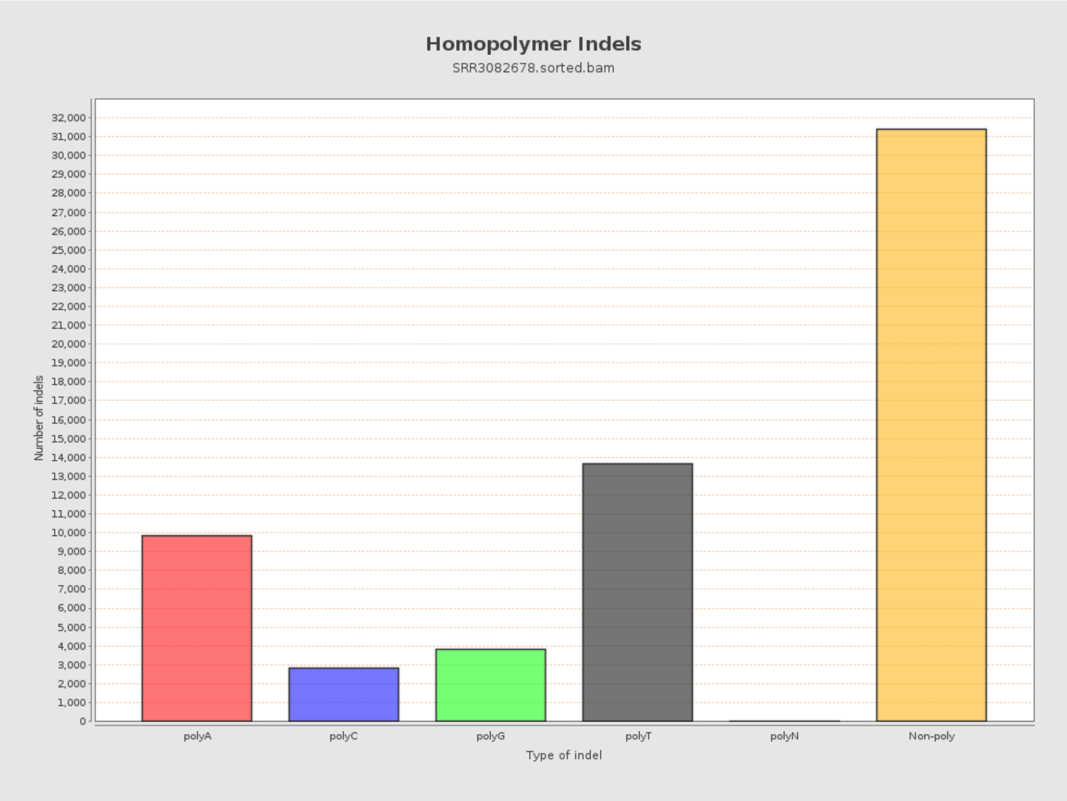
9. Results : Mapped Reads GC-content Distribution



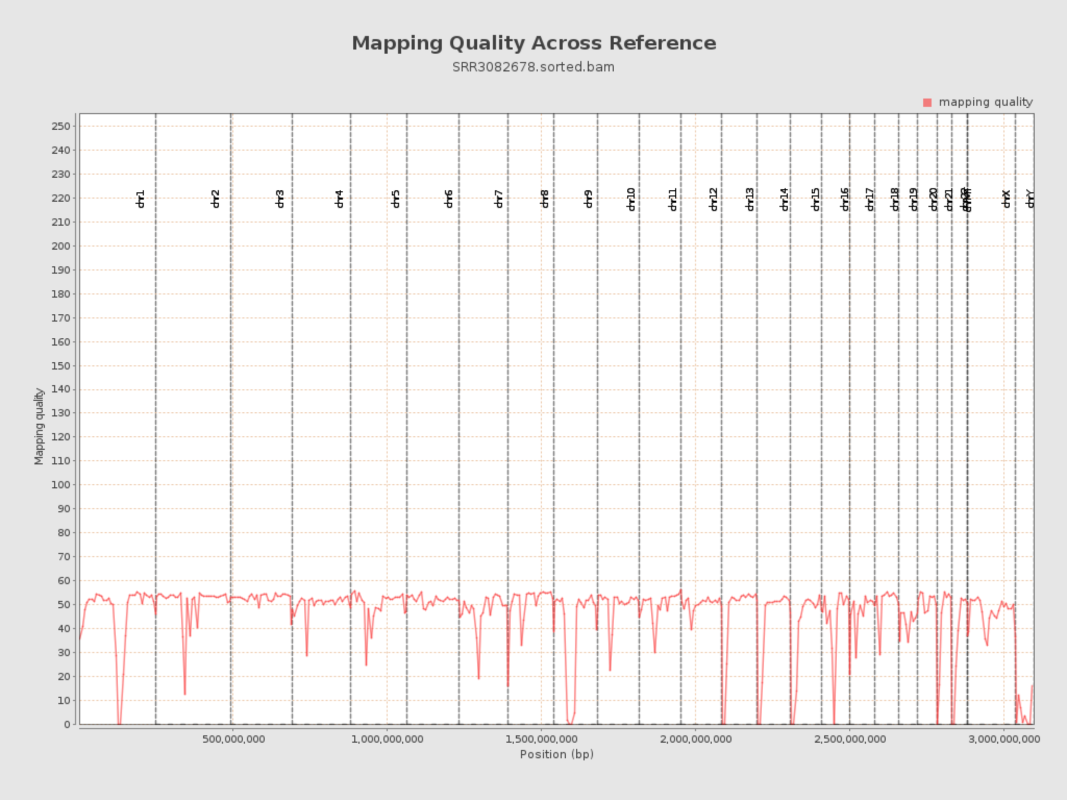
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram