Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 09:32:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084282.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_SRR3084282 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084282.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 09:32:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084282.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,729,219
Mapped reads	2,442,813 / 89.51%
Unmapped reads	286,406 / 10.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,230 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	85,998 / 3.15%
Duplication rate	2.85%
Clipped reads	1,249,188 / 45.77%

2.2. ACGT Content

Number/percentage of A's	43,875,201 / 27.4%
Number/percentage of C's	30,706,918 / 19.18%
Number/percentage of T's	49,083,793 / 30.65%
Number/percentage of G's	36,268,043 / 22.65%
Number/percentage of N's	203,865 / 0.13%
GC Percentage	41.82%

2.3. Coverage

Mean	0.0517

Standard Deviation	0.3603

2.4. Mapping Quality

Mean Mapping Quality	44.79

2.5. Mismatches and indels

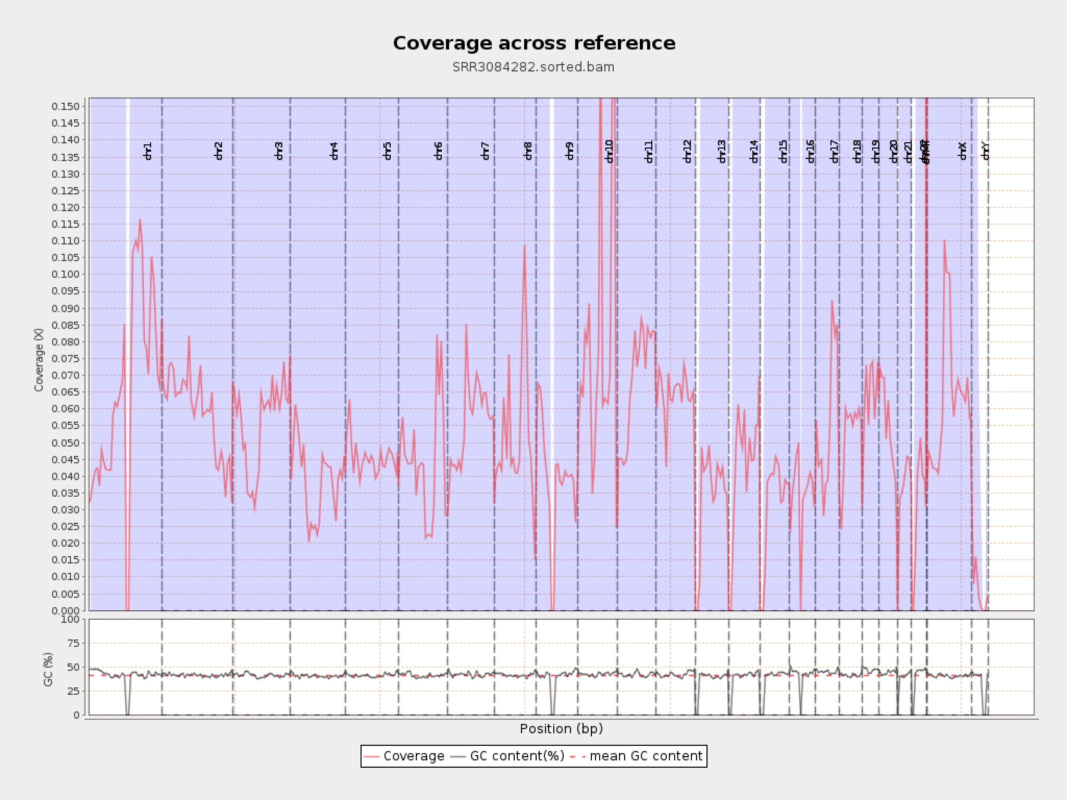
General error rate	1.06%
Mismatches	1,670,175
Insertions	12,413
Mapped reads with at least one insertion	0.5%
Deletions	34,514
Mapped reads with at least one deletion	1.4%
Homopolymer indels	46.03%

2.6. Chromosome stats

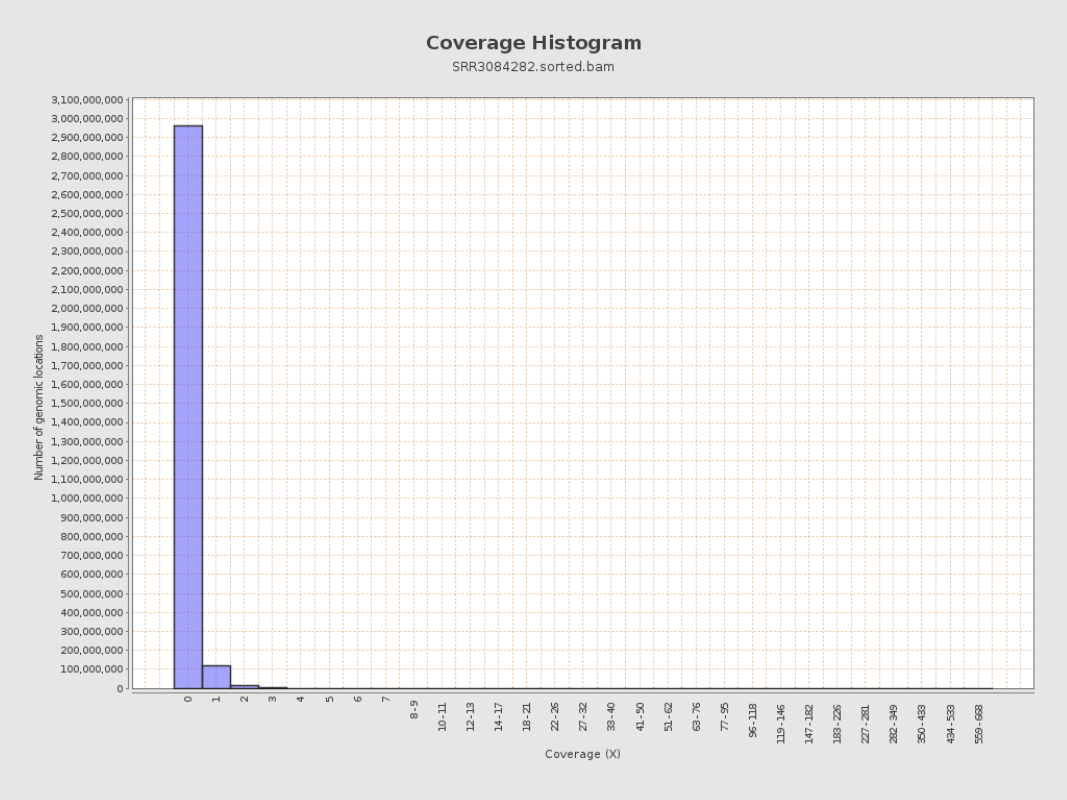
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16214701	0.0651	0.587
chr2	243199373	14475848	0.0595	0.4326
chr3	198022430	11054577	0.0558	0.2754
chr4	191154276	7427201	0.0389	0.2339
chr5	180915260	8224191	0.0455	0.2409
chr6	171115067	7555050	0.0442	0.2707
chr7	159138663	9035274	0.0568	0.5084

chr8	146364022	7673692	0.0524	0.3377
chr9	141213431	5540667	0.0392	0.2818
chr10	135534747	11258162	0.0831	0.535
chr11	135006516	9135207	0.0677	0.3903
chr12	133851895	8585546	0.0641	0.2883
chr13	115169878	3866148	0.0336	0.2076
chr14	107349540	4551231	0.0424	0.2381
chr15	102531392	3230574	0.0315	0.2094
chr16	90354753	3139902	0.0348	0.237
chr17	81195210	4573084	0.0563	0.2948
chr18	78077248	4030040	0.0516	0.4705
chr19	59128983	3820373	0.0646	0.437
chr20	63025520	3467213	0.055	0.2709
chr21	48129895	1715684	0.0356	0.225
chr22	51304566	1498307	0.0292	0.1918
chrMT	16571	37463	2.2608	1.9268
chrX	155270560	9726898	0.0626	0.3167
chrY	59373566	356409	0.006	0.1156

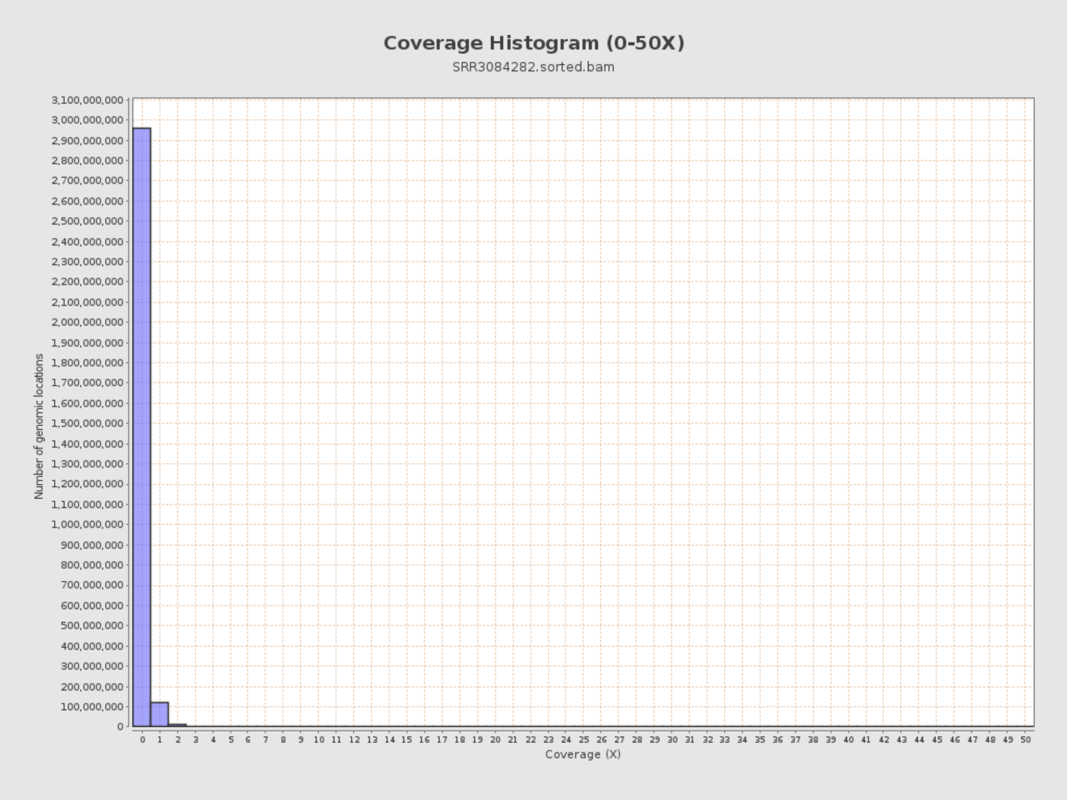
3. Results : Coverage across reference



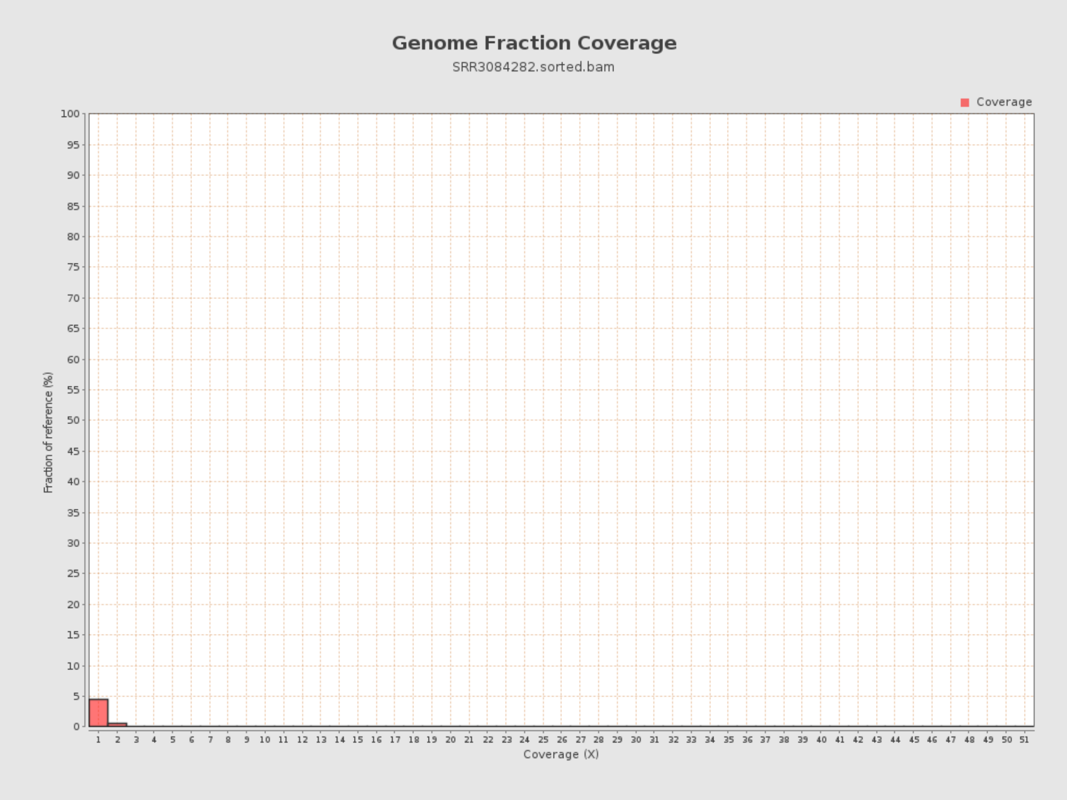
4. Results : Coverage Histogram



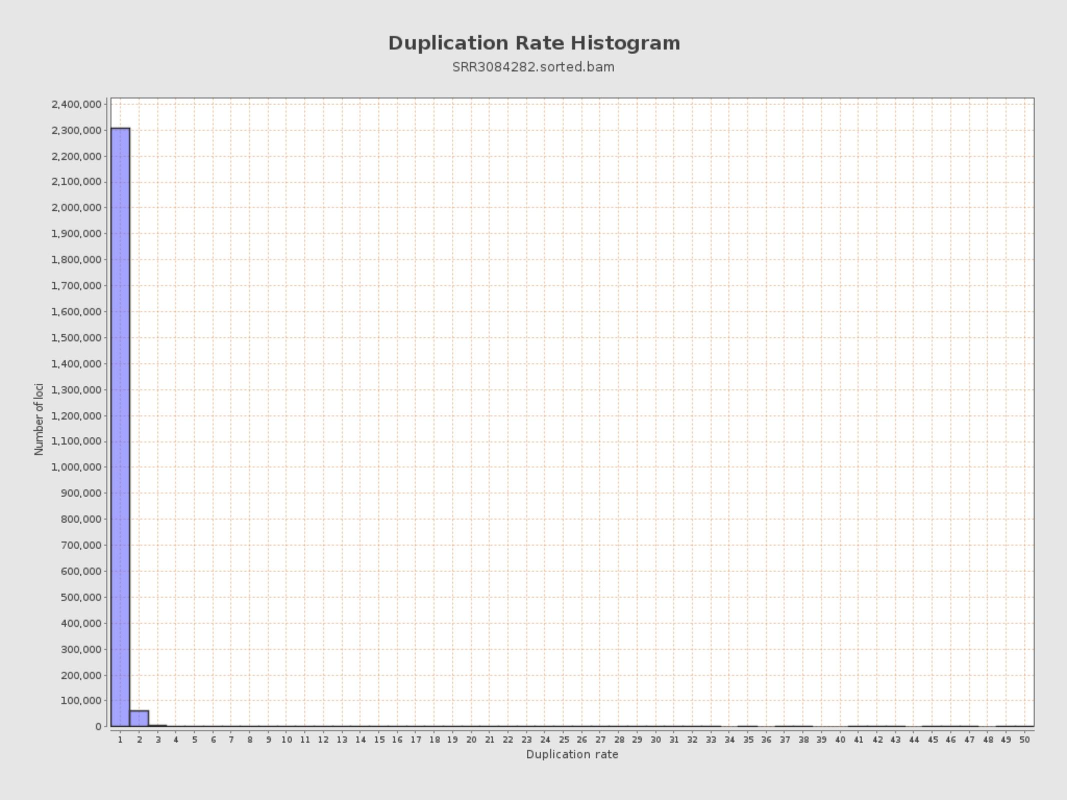
5. Results : Coverage Histogram (0-50X)



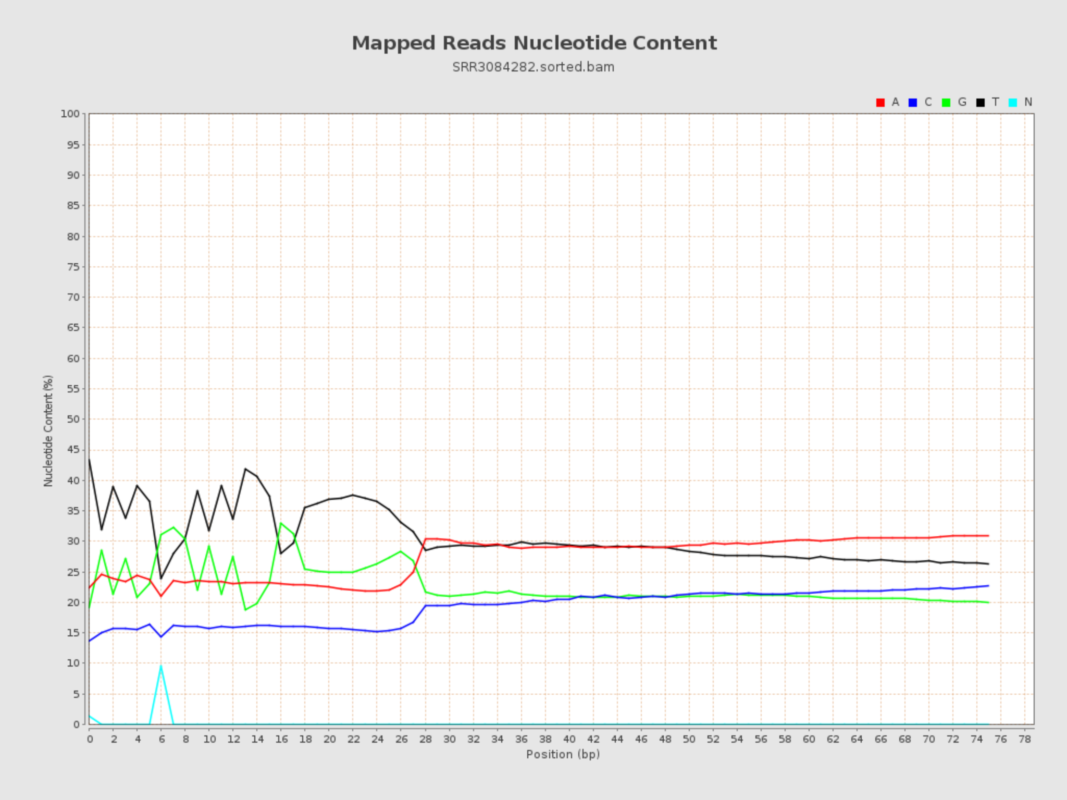
6. Results : Genome Fraction Coverage



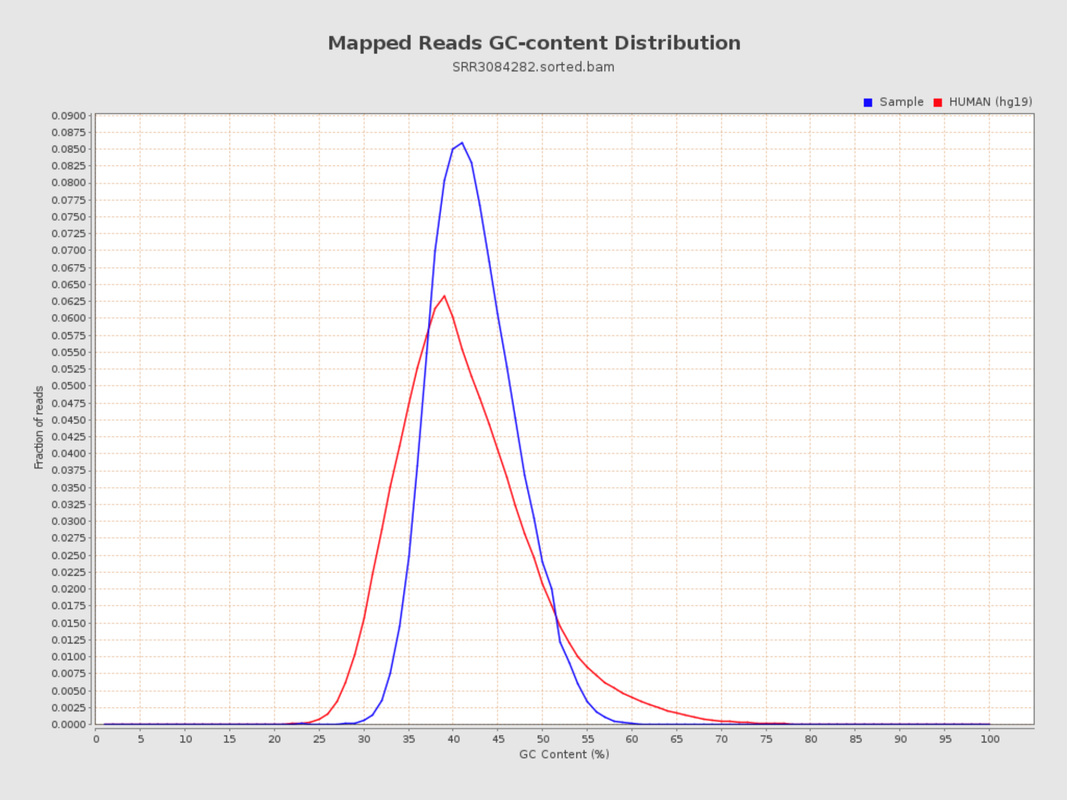
7. Results : Duplication Rate Histogram



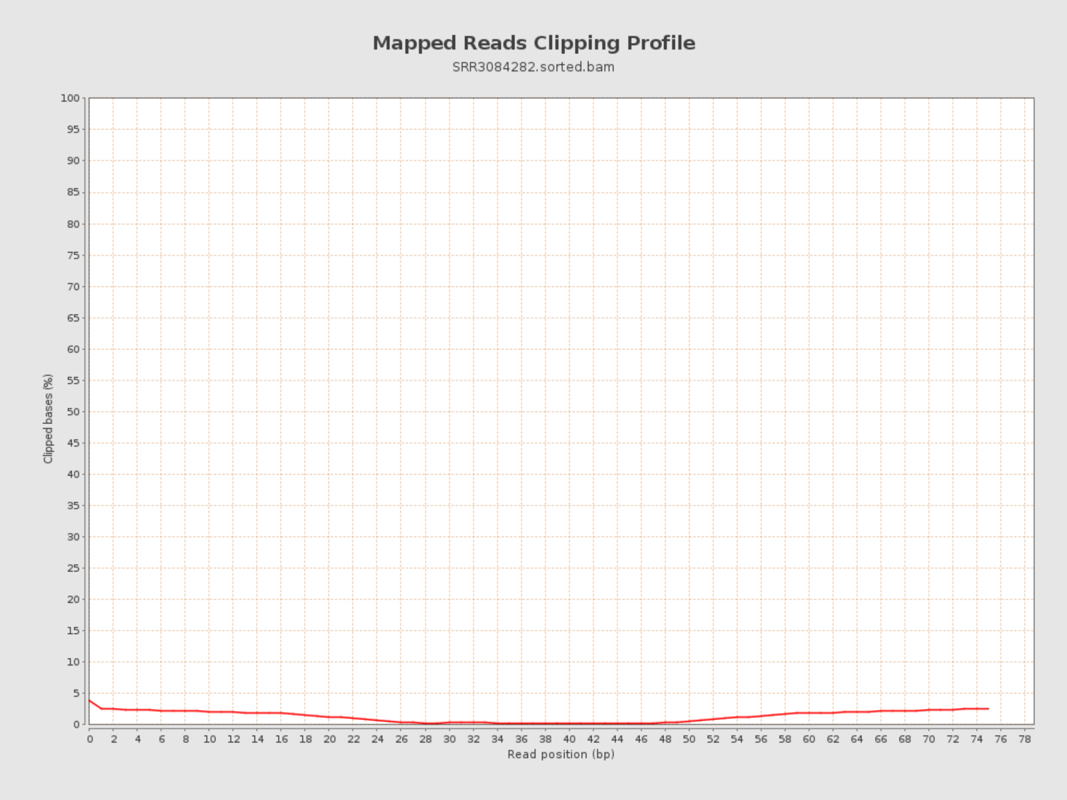
8. Results : Mapped Reads Nucleotide Content



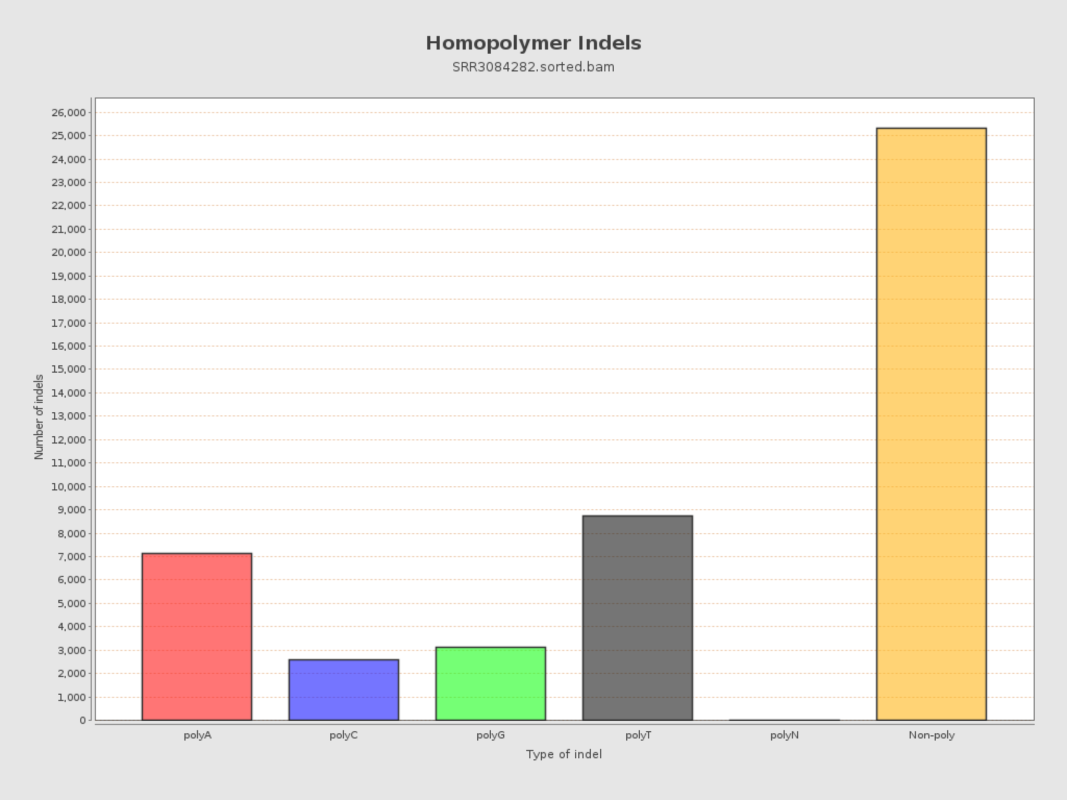
9. Results : Mapped Reads GC-content Distribution



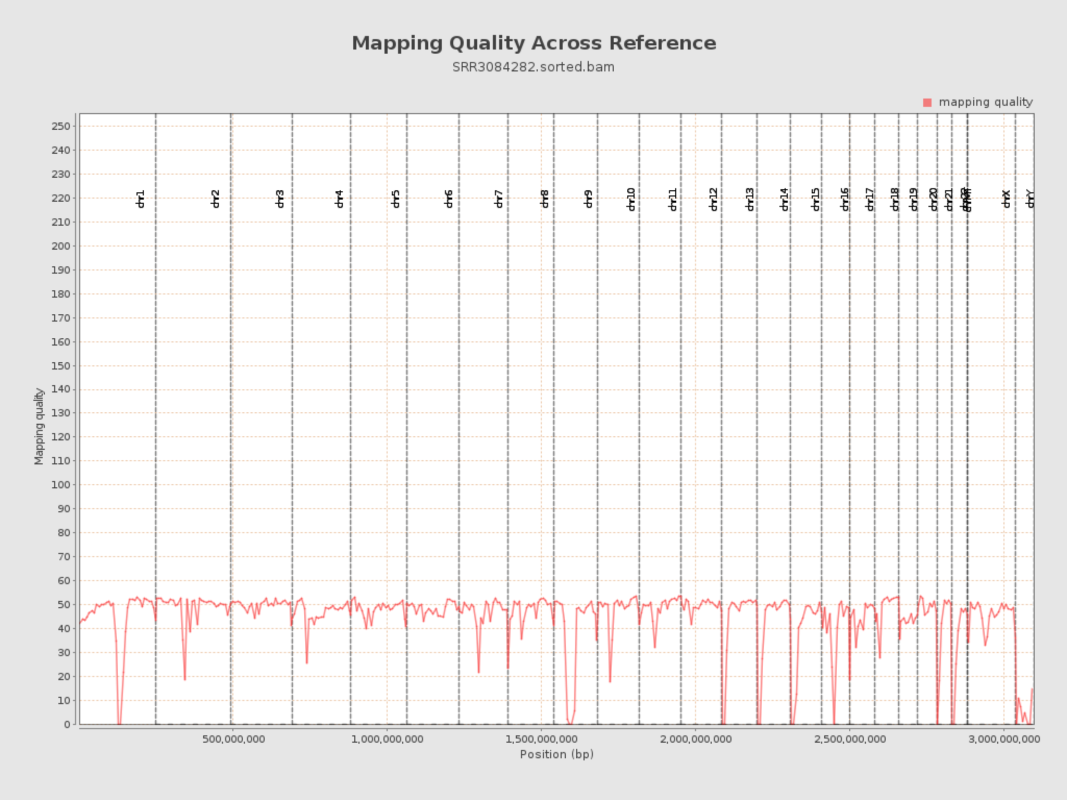
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram