

Automated Reading of Agar Plates using AI

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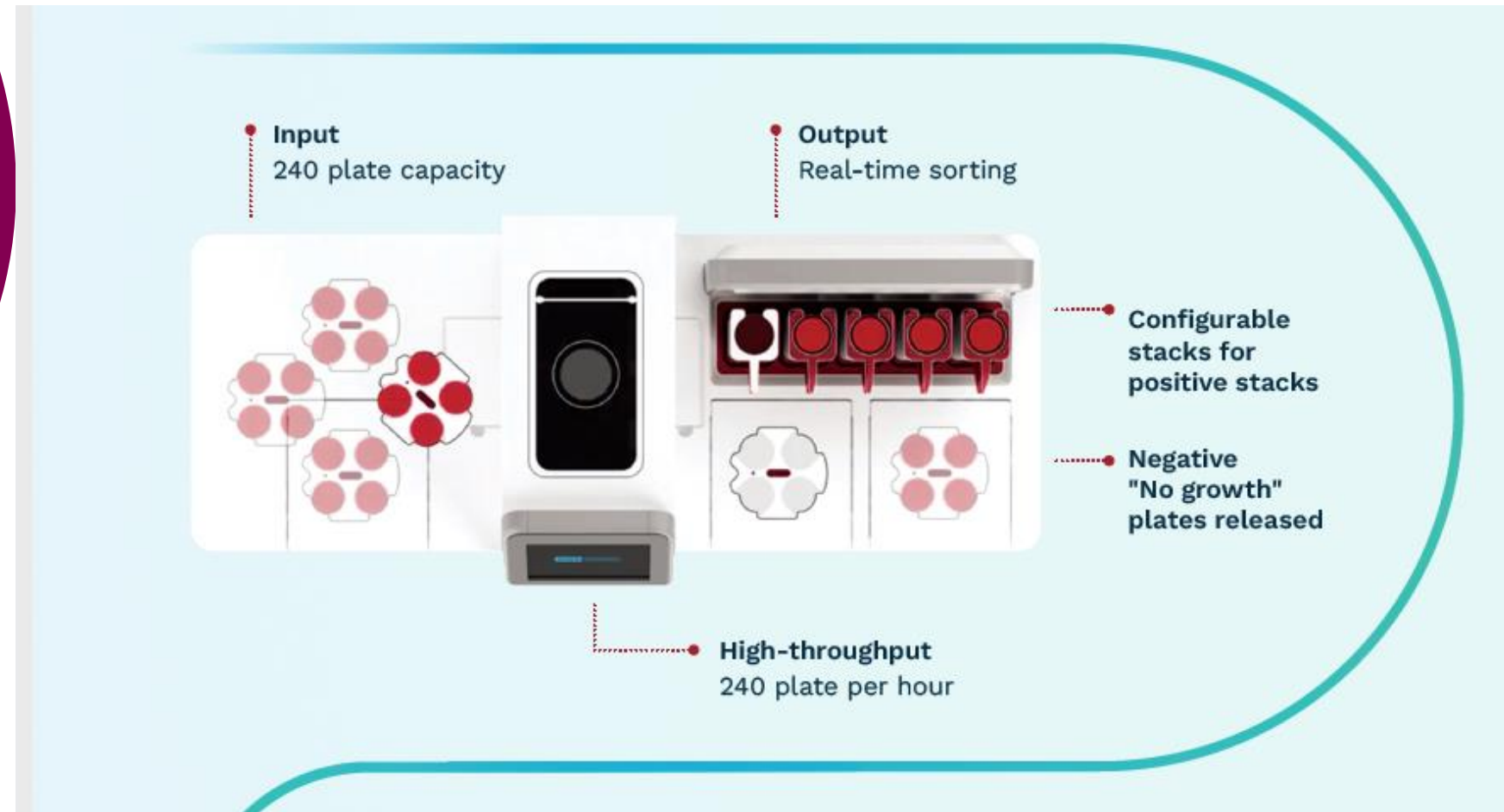


Introduction to APAS

APAS (Automated Plate Assessment System) Independence, by Clever Culture Systems (Adelaide, Australia), is an automated plate reader that uses a camera system and machine learning model to count and sort plates.



Topographical view





Why are AstraZeneca interested?

- Up to 30,000 EM agar plates are read manually and verified every month at large AZ sites
- Annual EM data from aseptic manufacturing facilities shows that >98% of plates are negative
- Occasionally humans make mistakes
- Resolves data integrity challenges





Benefits of this technology

- APAS processes ~200-240 plates/hour and sorts them into categories
- Only plates with growth or processing errors are second checked- vastly reducing technician time
- Data automatically transferred to LIMS system – manual transcription and chance of error removed
- Current process plates destroyed on day of reading – All images stored in APAS for 45 days
- Not media supplier restricted and different incubation practices can be accommodated



Benefits of using AI for this purpose

Imaging Plate Reader Challenges

- Colony variability
- Agar Supplier differences
- Plate labelling
- Rim colonies
- Condensation
- Plate issues and sampling faults

AI solution

- Machine learning trained by microbiologists allows all this variability to be managed
- Use AI and machine learning to improve the classifier



Data needed to develop the Machine Learning

Data Collection

- >8000 plates read by the reader.
- Duplicate read in normal way.
- Images analysed and algorithm developed

Colony variability

- Fungal isolates
- Coloured isolates
- Multi coloured isolates
- Swarming colonies
- Bacillus species

Plate variability

- Different media suppliers.
- Different labelling
- Different bar-coding methods

Count variability

- Inherent variability in manual counting



Pilot Primary Validation Study (ongoing)

Developed validation strategy to assess performance of APAS PharmaQC aligned with compendial requirements as outlined in USP<1223> and Ph.Eur 5.1. Testing protocols include detection of colonies deposited on the perimeter of plates and ability of APAS to detect a single colony only.

- Linearity
- Precision
- Specificity
- Accuracy
- Robustness
- Ruggedness
- Operational range
- Limit of Detection
- Limit of Quantification
- Repeatability



Ruggedness and Precision

Table 3. Ruggedness and Precision for Day 3

| Org Day 3 | Growth level CFU per plate | Replicate | APAS1 | | APAS2 | | APAS3 | | All APAS | |
|----------------------|----------------------------|-----------|-------|------|-------|------|-------|------|----------|------|
| | | | Mean | %CV | Mean | %CV | Mean | %CV | Mean | %CV |
| <i>E. coli</i> | 10-100 CFU | 1 | 48.7 | 4.3 | 51.8 | 5.7 | 48.3 | 6.2 | 49.6 | 6.2 |
| | | 2 | 43.9 | 6.5 | 46.1 | 8.1 | 45.3 | 6.5 | 45.1 | 7.2 |
| | | 3 | 66.7 | 3.6 | 63.5 | 5.5 | 74.7 | 8.4 | 68.3 | 9.4 |
| | | 4 | 64.1 | 4.8 | 67.2 | 3.4 | 69.9 | 3.7 | 67 | 5.3 |
| | | 5 | 68.9 | 5.2 | 68.3 | 6.3 | 73.2 | 6.1 | 70.2 | 6.5 |
| <i>S. aureus</i> | 10-100 CFU | 1 | 81.7 | 2.3 | 81.2 | 2.4 | 80.5 | 1.7 | 81.1 | 2.2 |
| | | 2 | 80.7 | 1.3 | 81.1 | 1.4 | 80.7 | 1.4 | 80.8 | 1.3 |
| | | 3 | 69.2 | 2.1 | 69.6 | 1.3 | 69.8 | 2.1 | 69.5 | 1.9 |
| | | 4 | 81.8 | 1.2 | 82.2 | 1.1 | 81.9 | 1.7 | 82 | 1.4 |
| | | 5 | 97.1 | 1.5 | 96.1 | 1.7 | 95.7 | 1.5 | 96.3 | 1.6 |
| <i>P. aeruginosa</i> | 10-100 CFU | 1 | 80.7 | 4.1 | 71.1 | 5.1 | 71.8 | 5.3 | 74.5 | 7.6 |
| | | 2 | 65 | 6 | 58 | 13.2 | 64 | 7.9 | 62.3 | 10.3 |
| | | 3 | 86.7 | 6.8 | 81.6 | 5.5 | 84.4 | 10.6 | 84.2 | 8.2 |
| | | 4 | 81.9 | 9.3 | 78.9 | 8.5 | 74.5 | 8.4 | 78.4 | 9.4 |
| | | 5 | 89 | 5.4 | 82.9 | 5.7 | 80 | 6.2 | 84 | 7.2 |
| <i>B. spizizenii</i> | 10-100 CFU | 1 | 27.5 | 14.7 | 24.3 | 12.8 | 30.6 | 19.4 | 27.5 | 18.6 |
| | | 2 | 19.3 | 14.7 | 16.5 | 8.8 | 17.1 | 9.3 | 17.7 | 13.3 |
| | | 3 | 52.3 | 12 | 60.3 | 11.4 | 45.1 | 17.1 | 52.6 | 17.7 |
| | | 4 | 34.9 | 7 | 35.1 | 8.6 | 37.6 | 7.7 | 35.9 | 8.3 |
| | | 5 | 45.7 | 13.2 | 36.5 | 24.5 | 44.3 | 17.9 | 42.2 | 20.4 |

This test measures the consistency of the APAS result within the same instrument and across multiple instruments

- 5 replicates for each organism
- 5 results readings taken at 3 different rotations per instrument
- Performed at Day 3 and Day 5 (not shown)
- Results compared across 3 APAS instruments
- Mean result and coefficient of variation (CV) calculated for each plate
- Results within CV range of compendial expectation (combined Ph.Eur and USP)

All APAS PharmaQC values are within the combined compendial limits (bar one ruggedness CV for *B.spizizenii* on Day 5)



Linearity and Accuracy

Table 5. Summary data for Linearity and Accuracy

| Organism | 1-10 | | | | 1-50 | | | | 1 - 100 | | | | Overall | | | |
|------------------------|-------|----------------|-------|-----------|-------|----------------|-------|-----------|---------|----------------|-------|-----------|---------|----------------|-------|-----------|
| | Cases | r ² | Slope | Intercept | Cases | r ² | Slope | Intercept | Cases | r ² | Slope | Intercept | Cases | r ² | Slope | Intercept |
| <i>A. brasiliensis</i> | 9 | 0.3971 | 1.19 | 1.44 | 17 | 0.7891 | 0.41 | 3.11 | 26 | 0.5116 | 0.22 | 5.85 | 36 | 0.4626 | 0.16 | 6.59 |
| <i>B. spizizenii</i> | 6 | 0.3405 | 0.67 | 5.59 | 10 | 0.9291 | 1.4 | 2.25 | 17 | 0.7601 | 0.79 | 11.83 | 36 | 0.7639 | 0.64 | 17.78 |
| <i>C. albicans</i> | 8 | 1 | 1 | 0 | 24 | 0.9898 | 1.03 | -0.43 | 32 | 0.984 | 0.99 | 0.3 | 36 | 0.9861 | 0.99 | 0.23 |
| <i>M. luteus</i> | 3 | 1 | 1.17 | -0.17 | 12 | 0.9879 | 0.9 | 1.42 | 20 | 0.8997 | 1.04 | -1.69 | 36 | 0.9416 | 0.91 | 4.42 |
| <i>S. aureus</i> | 6 | 0.8276 | 1 | 0.17 | 8 | 0.9932 | 0.98 | 0.2 | 18 | 0.9922 | 0.94 | 0.53 | 36 | 0.9877 | 0.83 | 4.44 |
| <i>S. epidermidis</i> | 3 | 1 | 1 | 0 | 18 | 0.9816 | 0.9 | 1.42 | 24 | 0.9698 | 0.84 | 2.67 | 36 | 0.9644 | 0.85 | 1.99 |
| <i>M. osloensis</i> | 8 | 0.2196 | 1.15 | 2.09 | 16 | 0.9522 | 0.98 | 2.59 | 22 | 0.9834 | 0.97 | 2.66 | 36 | 0.9962 | 0.96 | 2.62 |

This tests APAS ability to detect and count colonies over a range of counts. Counts were compared to that made by a trained microbiologist.

- A high level of agreement was observed for all bacterial organisms in the 1-50 range (r² values of 0.92-0.99)
- Intercepts were close to zero and slopes close to 1, indicating a high level of accuracy
- Counting difficulties observed with *A. brasiliensis* and *B. spizizenii* especially at the higher counts. This is due to colony morphology and overlapping colonies.



Proposed Secondary Validation Study

A two-stage approach:

1. Establish expected performance

- The number of positive plates chosen to deliver the confidence intervals from the statistical table below assuming a 1.5% positivity rate.
- Positive plates would be 'contrived' by exposing plates in general labs and interspersed with large enough number of negative plates to keep the humans 'reading' in representative manner.
- Statistically driven study; number of plates likely to be in the region of 3-5k by the use of 'contrived' plates.

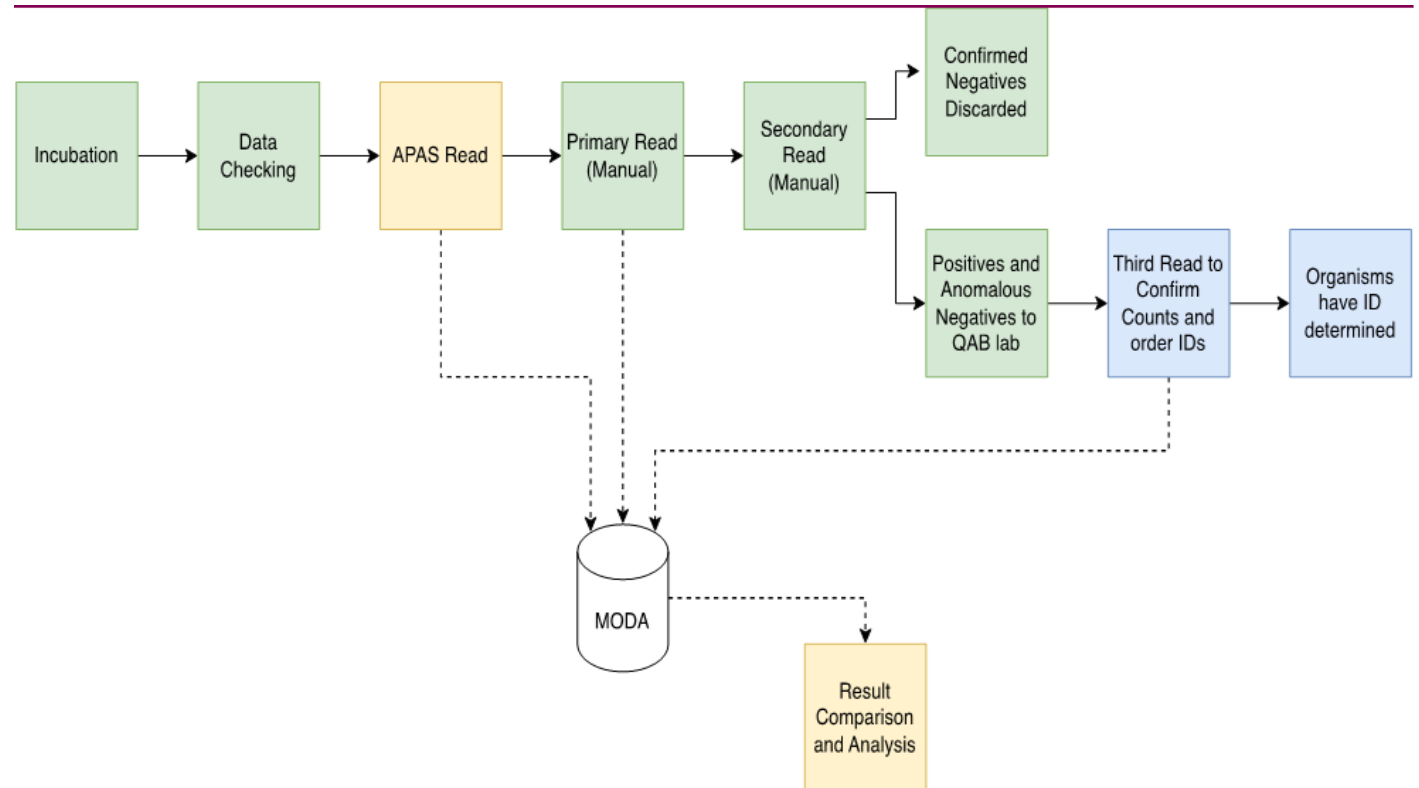
| PPA Target | Lower 95% Confidence Interval Target | True APAS PPA | Required Positive Plates | Approximate Total Plates (Rounded up to nearest 1000) |
|------------|--------------------------------------|---------------|--------------------------|---|
| 98.0% | 96.0% | 99.0% | 310 | 21, 000 |
| 98.0% | 96.0% | 99.5% | 150 | 10, 000 |
| 98.5% | 97.0% | 99.5% | 250 | 17, 000 |
| 99.0% | 98.0% | 99.5% | 510 | 34, 000 |



Proposed Secondary Validation Study

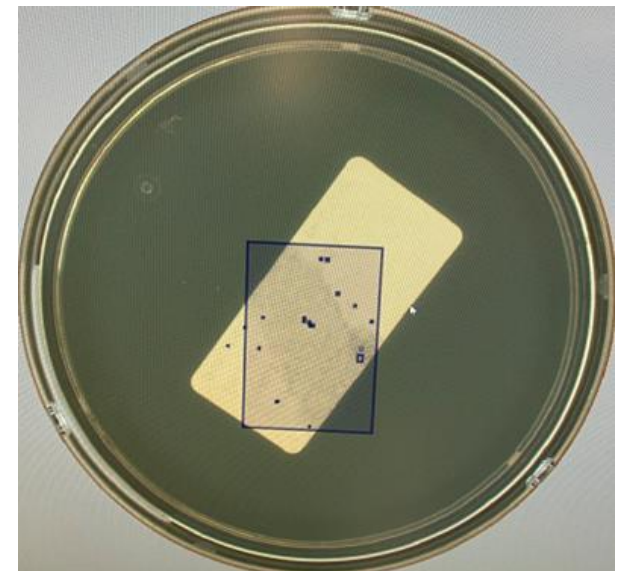
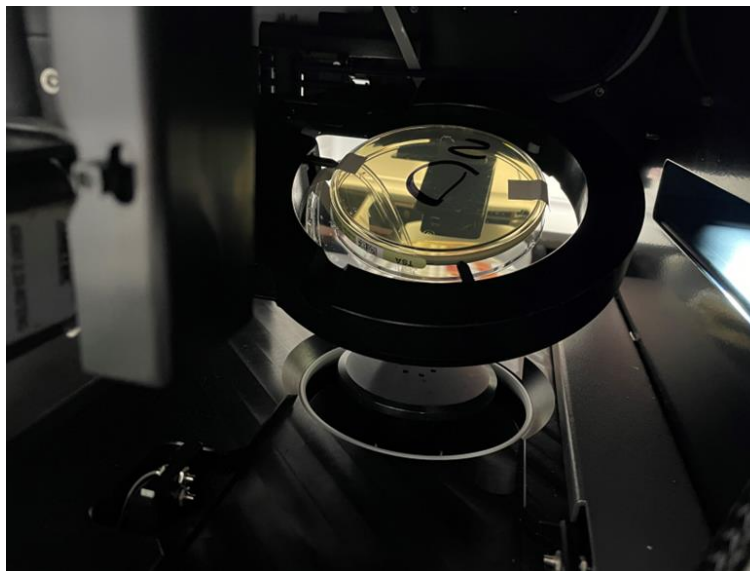
2. Establish in-use performance

- APAS instrument used as primary reader for real EM plates.
- ALL plates checked by humans and results corrected where necessary
- Rate of corrections tracked and used to form acceptance criteria for AZ validation



Key Learning Points

- Current practices using tape caused mechanical issues
- Data suggests that there is a 0% false negative rate and a 15.8% false positive
- Tape also caused false positives. Excluding tape from the results, false positive rate = 7.3% *Latest data 5.9%*



Key Learning Points

- Simple solution to utilise clip and bags used at other AZ sites introduced via change control.



Key Learning Points

- Pilot primary validation study has shown difficulties in counting accurately at higher end of the count range especially with some organisms.
- However, this is also seen in humans, where differences of 20-40 colonies have been observed.
- IS THIS IMPORTANT?
- APAS would sort these plates as requiring human review.

Update : Latest software is much improved in this aspect, however in the real world all positive plates are flagged for review.



Figure 3. Example of *B. spizizenii* growth demonstrating variable morphology, size, and confluence

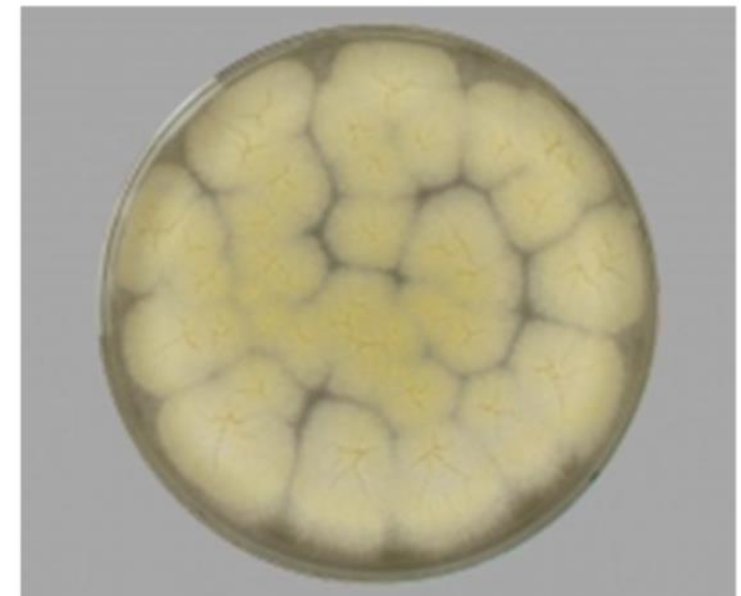
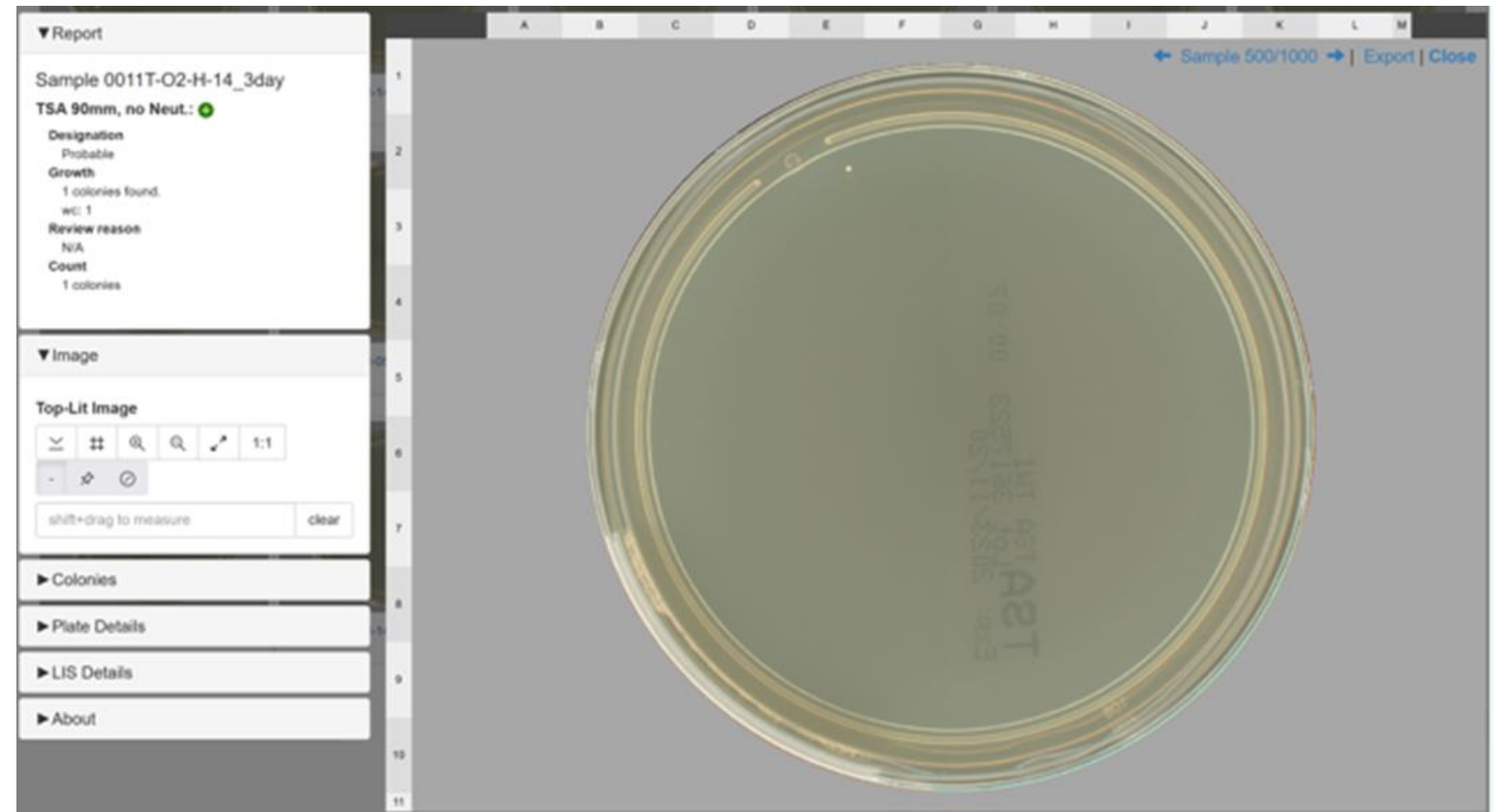
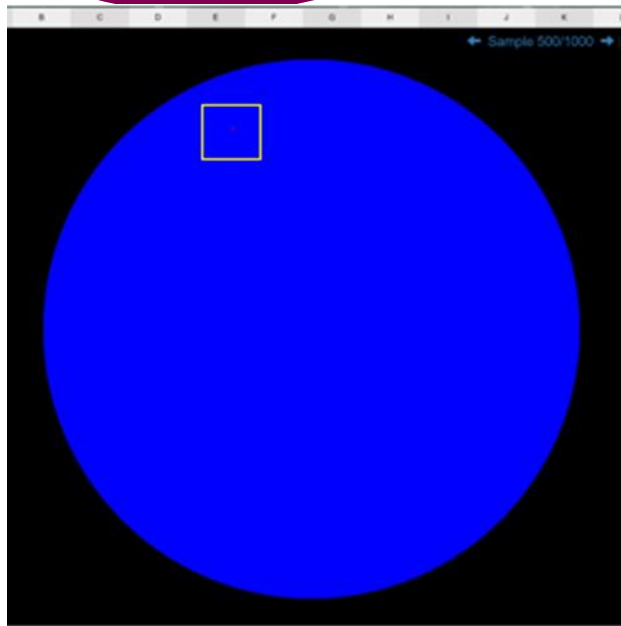


Figure 4. Example of *A. brasiliensis* growth changes over time demonstrating counting challenges



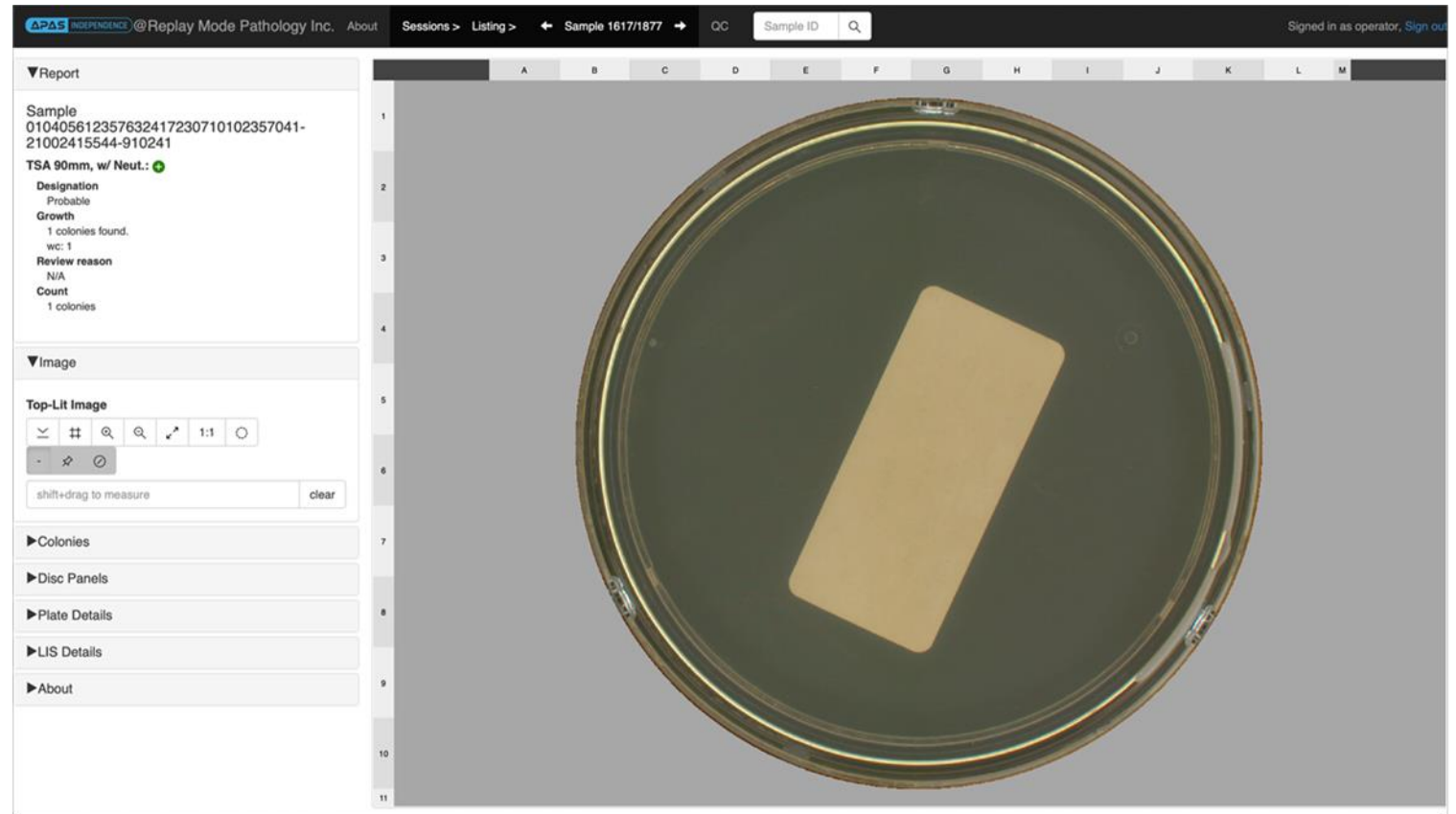
Key Learning Points

- APAS primary function is to sort 'Growth' from 'No Growth'
- Remember, over 98% of plates are zero cfu (AZ facility)
- The difference between 0 and 1 is massive in Grade A, the difference between 15 and 19 is negligible.
- Single colony detection the most important factor.



Key Learning Points

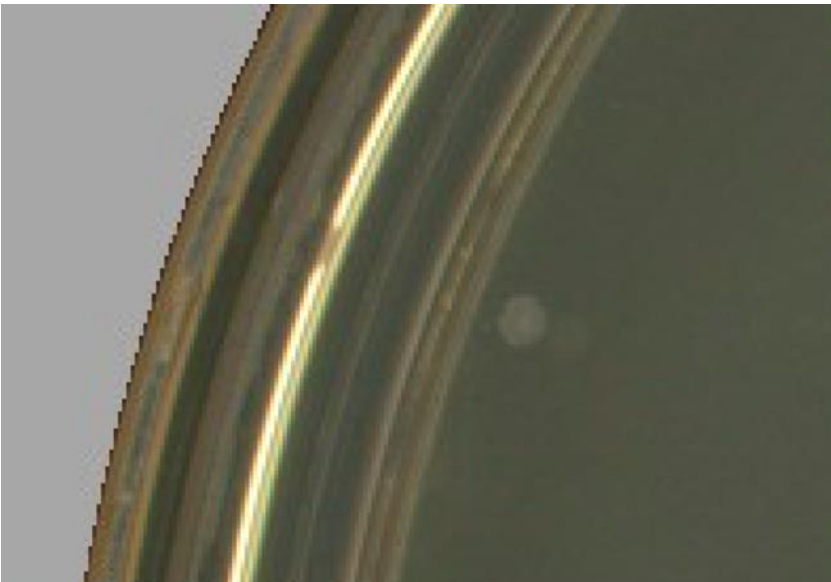
- Value of APAS proven during data collection
- Single colony missed by humans, detected by APAS
- Most important acceptance criteria are that it never misses a positive plate, and doesn't give too many false positives



The screenshot displays the APAS software interface. The top navigation bar includes the APAS logo, the user's name (@Replay Mode Pathology Inc.), and session information (Sample 1617/1877). The main content area is divided into a left sidebar and a main image area. The sidebar contains a 'Report' section with the following details:

- Sample: 010405612357632417230710102357041-21002415544-910241
- TSA 90mm, w/ Neut. (+)
- Designation: Probable
- Growth: 1 colonies found, wc: 1
- Review reason: N/A
- Count: 1 colonies

Below the report is an 'Image' section with a 'Top-Lit Image' view. The image shows a petri dish with a single colony visible. The interface includes a toolbar with zoom, pan, and measurement tools, and a list of expandable sections: Colonies, Disc Panels, Plate Details, LIS Details, and About.



▼ Report

Sample 0017T-31-09

TSA 90mm, no Neut.: +

Designation

Probable

Growth

2 colonies found.

Review reason

N/A

Count

2 colonies

▼ Image

Top-Lit Image



drag to move image

clear

▼ Colonies

wc

▶ Plate Details

▶ LIS Details

▶ About



▼ Report

Sample 0017T-31-09

TSA 90mm, no Neut.: +

Designation

Probable

Growth

2 colonies found.

Review reason

N/A

Count

2 colonies

▼ Image

Top-Lit Image



drag to move image

clear

▼ Colonies

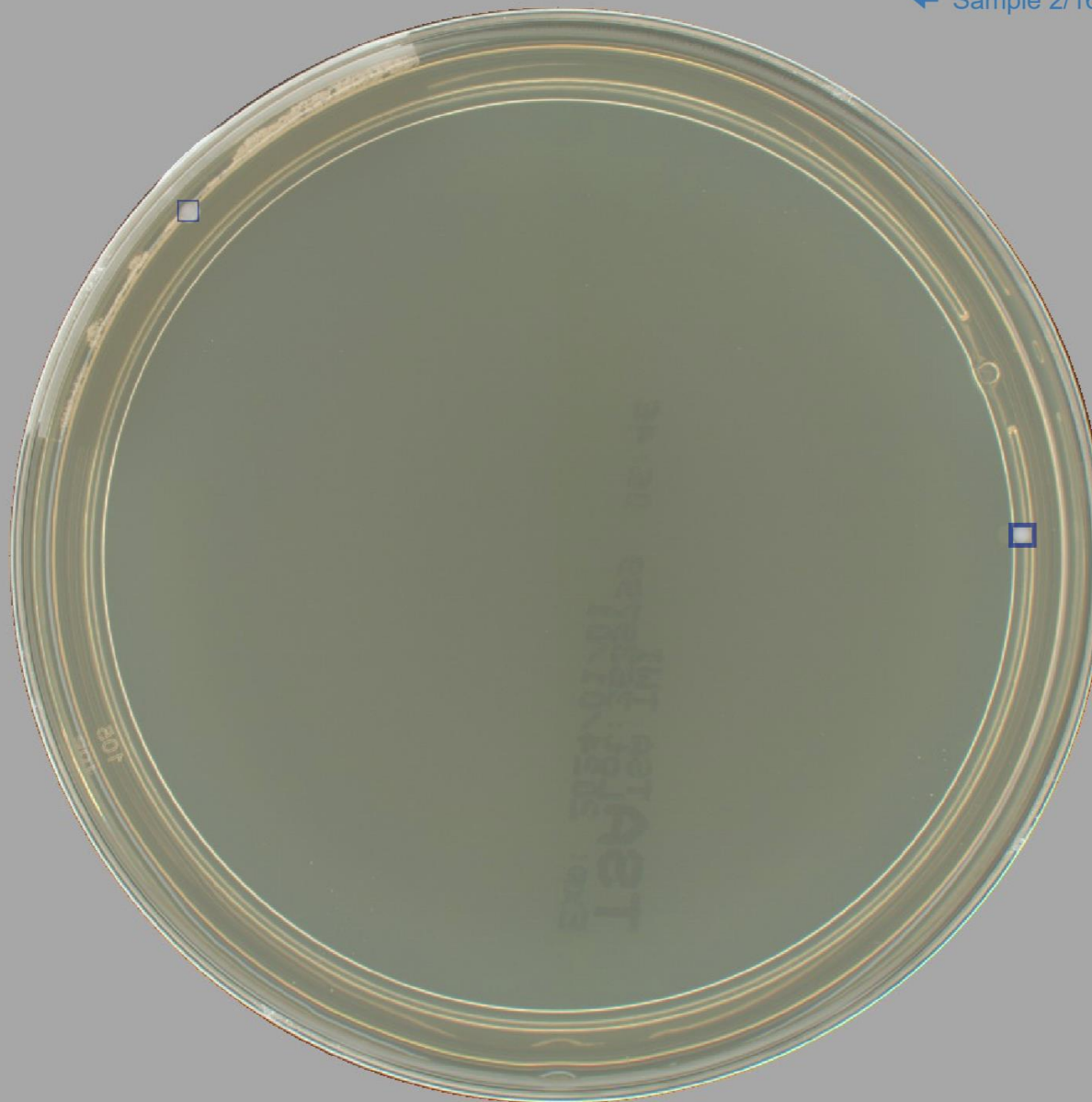
wc

► Plate Details

► LIS Details

► About

- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8
- 9
- 10
- 11



▼ Report

Sample 0011T-E1-H-04

TSA 90mm, no Neut.: 🔍

Designation

Review

Growth

5 colonies found, 4 bacterial, 1 mould.

Review reason

Mould colonies present

Count

5 colonies

▼ Image

Top-Lit Image



drag to move image clear

▼ Colonies

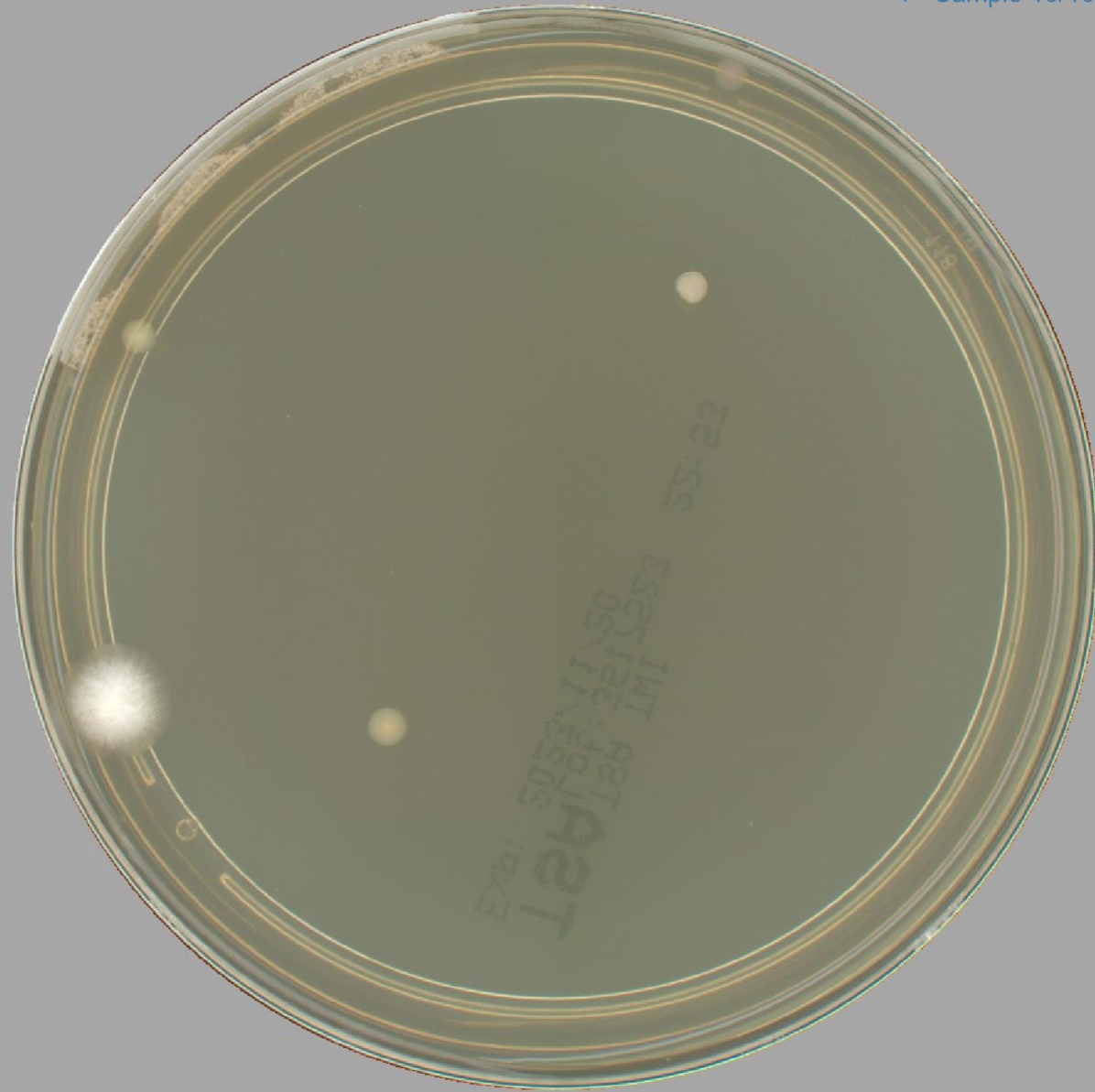
■ wc

■ yc

■ FF

■ PR

1
2
3
4
5
6
7
8
9
10
11



▼ Report

Sample 0011T-E1-H-04

TSA 90mm, no Neut.: 🔍

Designation

Review

Growth

5 colonies found, 4 bacterial, 1 mould.

Review reason

Mould colonies present

Count

5 colonies

▼ Image

Top-Lit Image



drag to move image

clear

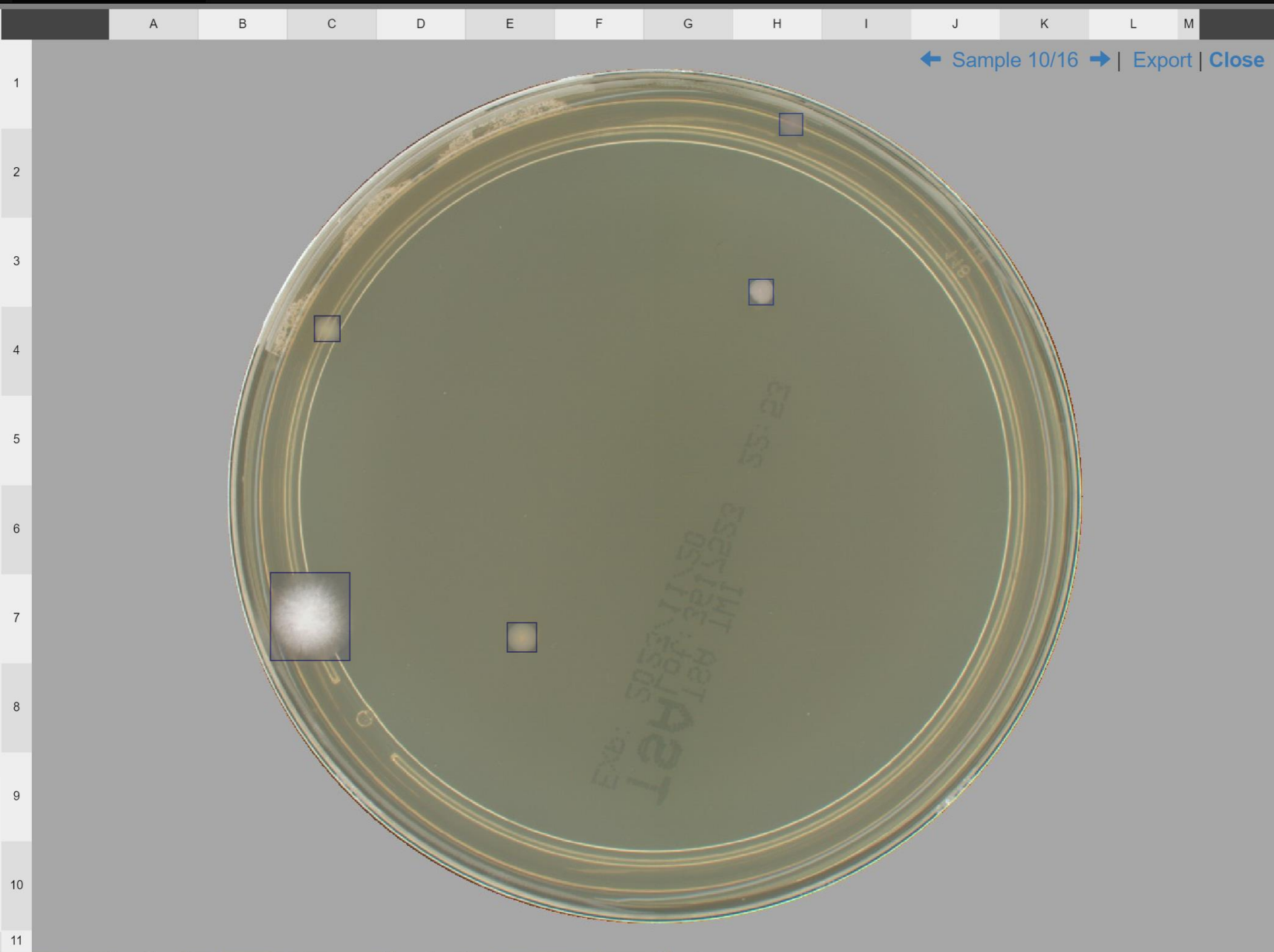
▼ Colonies

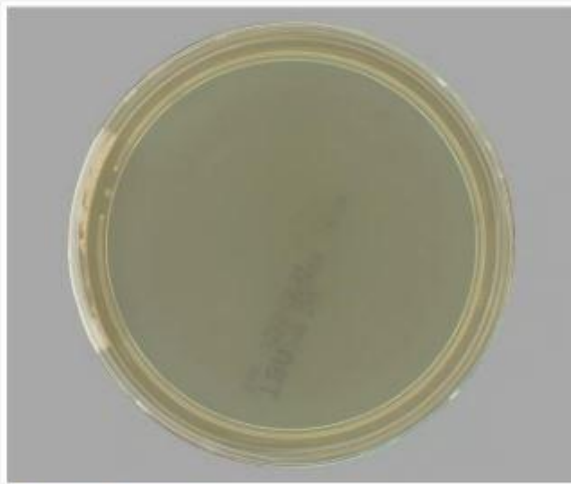
WC

YC

FF

PR





0012-SA-33-0.5-1
0 colonies found.



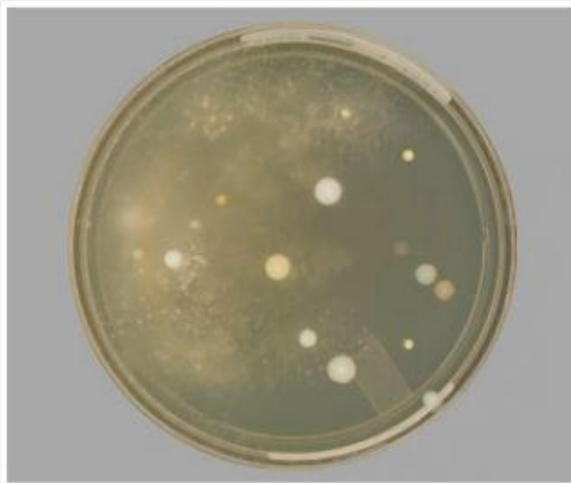
0017T-31-09
2 colonies found.



0006BN-A1-U4-2
50 colonies found, 38 bacterial, 12 mould.



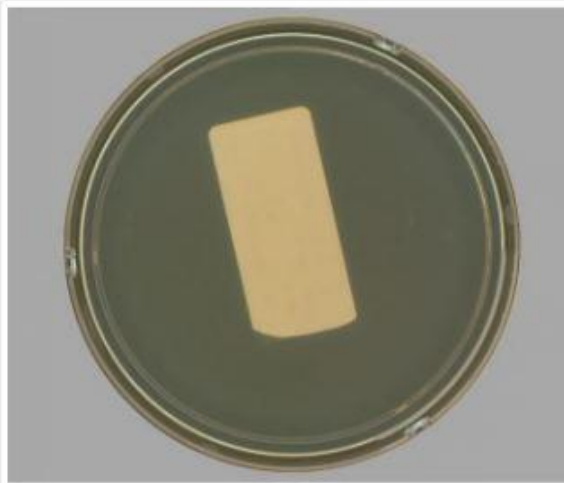
0006BN-A1-U2-1
30 colonies found, 28 bacterial, 2 mould.



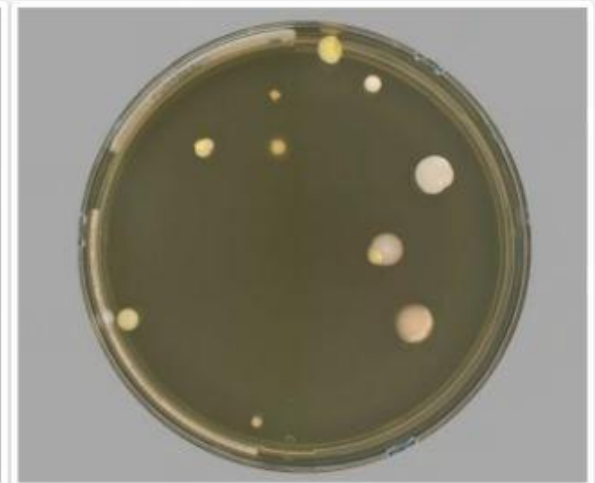
0006TN-D-U4-1
239 colonies found, 214 bacterial, 25 mould.



21003134863-910313
0 colonies found.



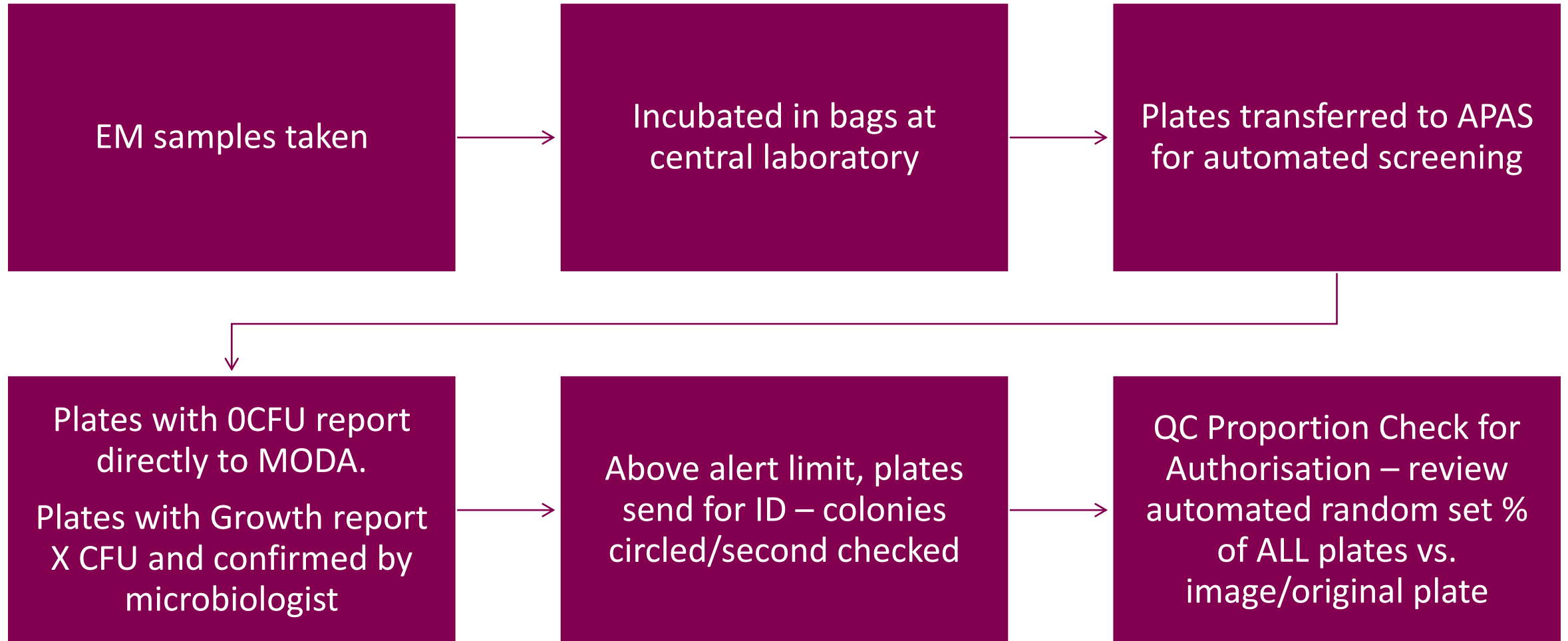
21005290102-910529
0 colonies found.



0006BN-D-U3-2
11 colonies found.



Envisaged Future State



Key Points for Regulatory Opinion

- Image Storage
 - Manual process plates are discarded, and the raw data is the count.
 - Other plate readers approved for use have no image storage capability.
 - Sustainability and software speed challenges with storing 30,000 a month.
 - Proposal is to store validation images.
 - In process images until authorisation of results in MODA.
- Guidance on the need to second check the negative plates.
- Once the model is “locked” and no longer learning. Follow normal laboratory change control GMP processes.
 - Software updates could either be compared against the original validation images or a set of plates with counts prepared and read before software update and then immediately after and results compared.
 - Are there specific expectations for validation for the AI algorithm even though it will be locked down?



Key Points for Regulatory Opinion

- Once validated, and because there is a secure audit trail and traceable data transfer from APAS to MODA, there will be enough evidence to minimise any requirement or expectation for second checks and /or verification of negative counts?
- What is the specific minimum expectation to define equivalent or better since there is some subjectivity in counting by humans?

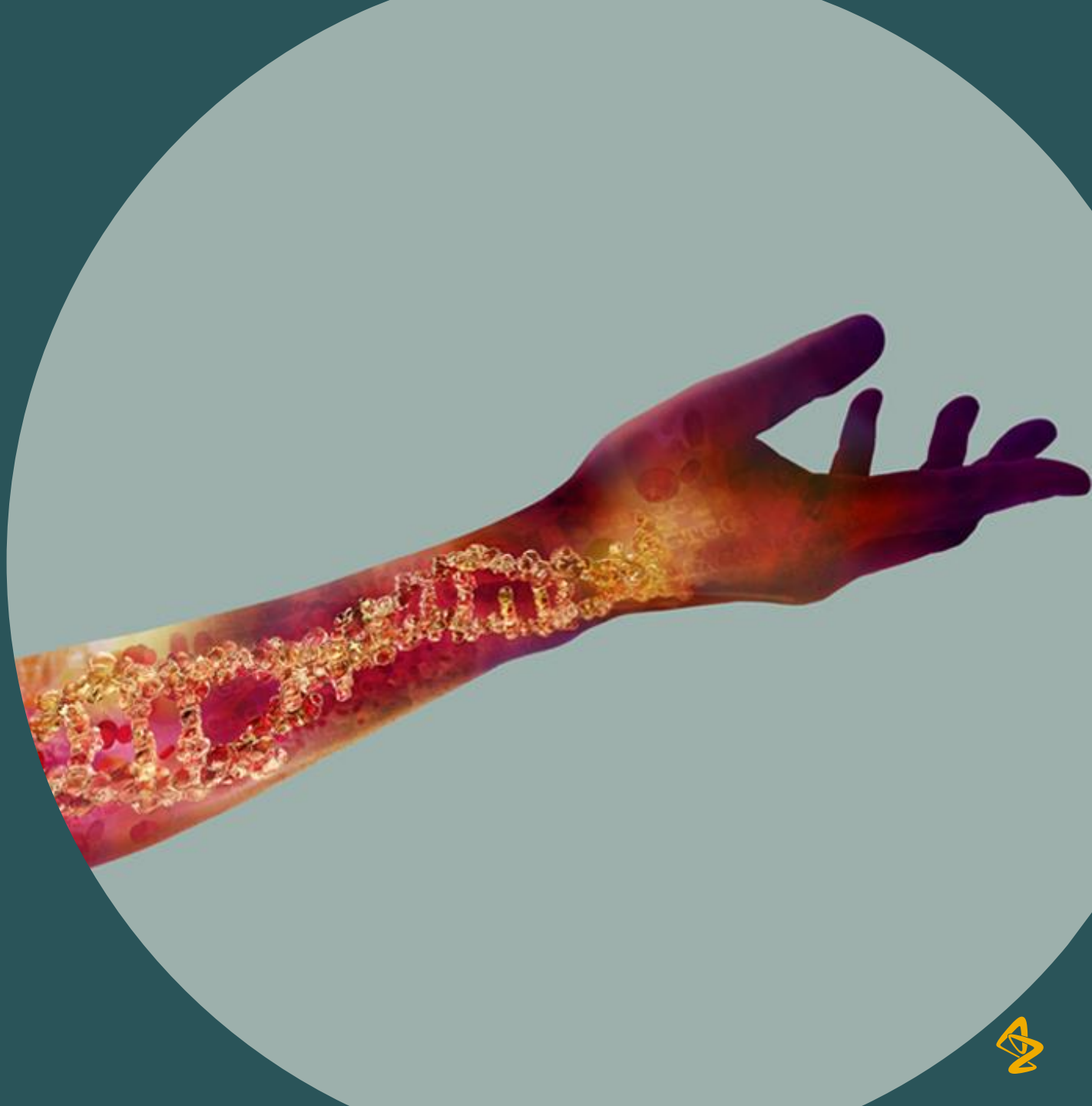


Potential Risks and future considerations

- Acceptance by regulators?
 - Considerations for image retention
 - Flawless interface with MODA
 - Requirement to expand to 55mm contact plates
 - Number of false positives needs to be acceptable
 - On-going Performance Monitoring of APAS
 - Consideration for number of 'checks' – percentage of negatives reviewed?
 - 'Reading' ability of humans needs to be retained
-
- We see all these as important but solvable and the benefits far exceed the risks.



Questions & Discussion



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