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Applied Spectral Imaging

Revolutionizing Cytogenetics with AI Karyotyping

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BECAUSE EVERY DIAGNOSIS COUNTS

A three-decade legacy of innovation in **brightfield and fluorescent** imaging, delivering cutting-edge **diagnostic solutions** to **Pathology and Cytogenetic** laboratories worldwide.

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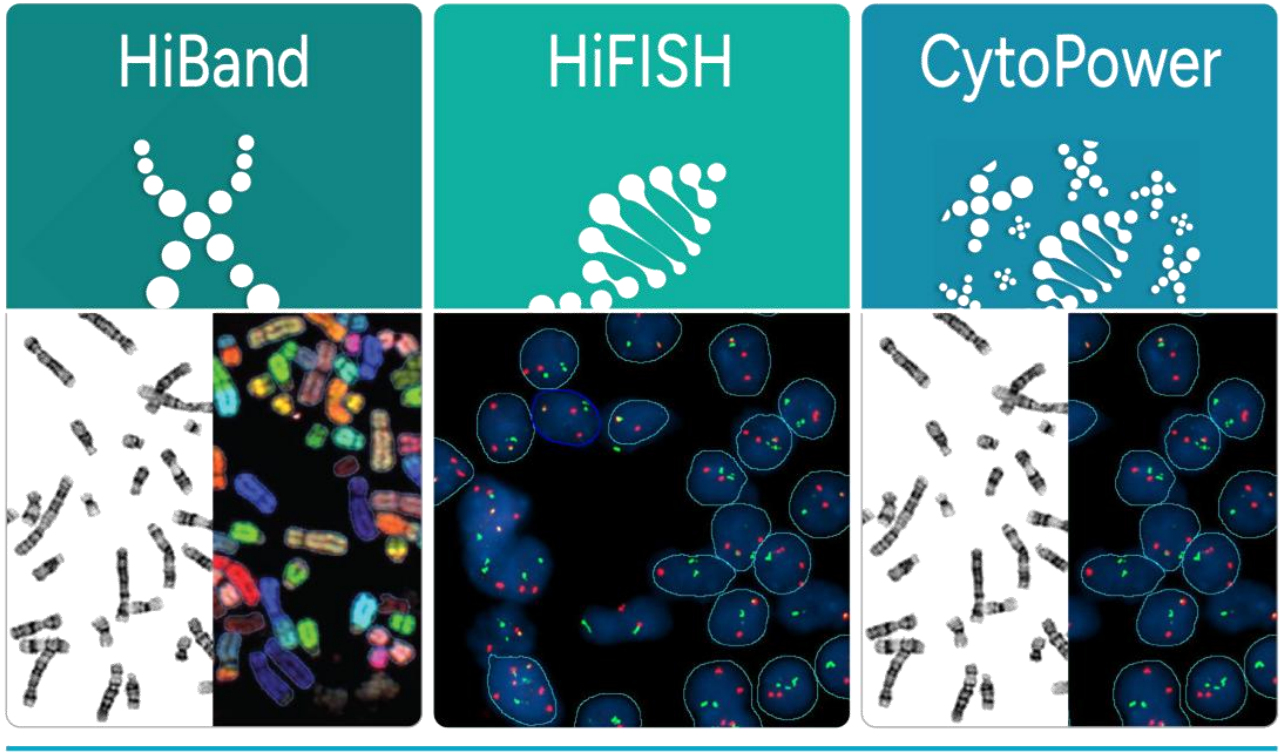
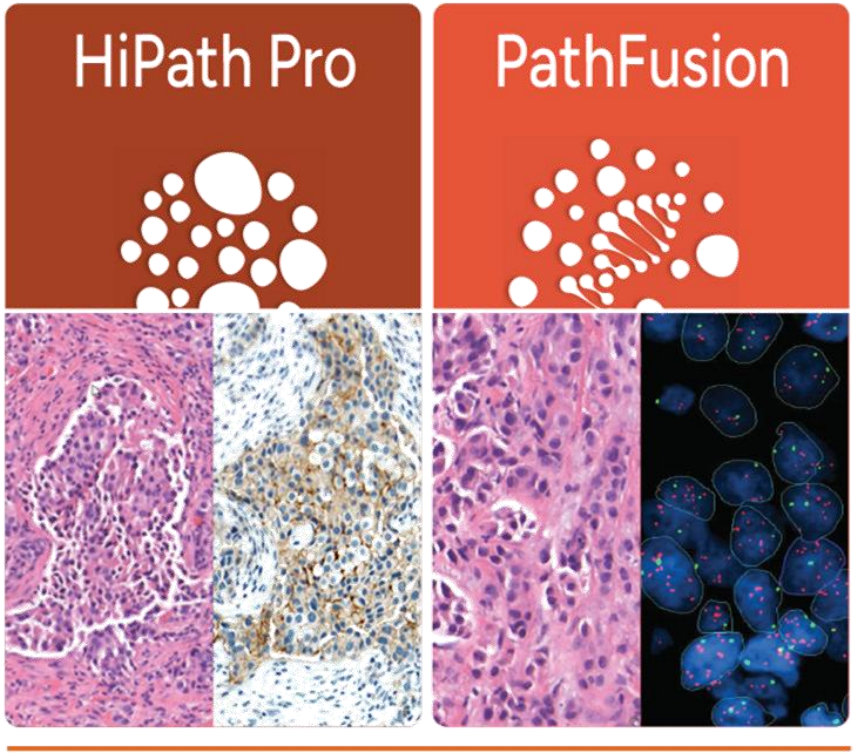
Product Families

ASI CYTOGENETICS



ASI PATHOLOGY



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ASI’s unique advantages with AI Karyotyping

ASI’s AI Karyotyping is **seamlessly embedded in the 100X scanning processes**, enabling **automated metaphase detection**, classification, and karyotype generation - all in real time

Powerful AI Segmentation
& Precise Karyogram Placement

User-Friendly Workflow
Intuitive interface, ideal for both experts and new users

50% Faster Turnaround
Integrated AI scanning halves case processing time

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Abstracts

1. **New artificial intelligence-based computer-aided chromosome analysis and karyotyping: A pilot evaluation**
   Taghiyev A, Best J, Rosenblum L, Greer K, Olson R, Diaz D, Glickman Y, Kasom M, Steele C
   Genetics in Medicine Open 2024, 2(1):101575 P671
   Poster can be found HERE

2. **Improved karyotyping efficiency with artificial intelligence: A multicenter evaluation of peripheral blood karyogram**
   Burnside R, Phelan K, Best J, Taghiyev A, Spudich L, Leftwich A, Cooke S, Olson R, Kasom M, Glickman Y, Steele C, Rosenblum L
   Genetics in Medicine Open 2025, 3(2):103053 P684
   Poster can be found HERE

3. **Multicenter evaluation of a new AI-based karyotyping software on bone marrow specimens**
   Burnside R, Best J, Spudich L, Leftwich A, Ospino M, Olson R, Adams H, Greer K, Holmes J, Prongay C, Merant L, Glickman Y, Kasom M, Steel C, Taghiyev A, Rosenblum L
   Genetics in Medicine Open 2025, 3(1):101918
   Presentation can be found HERE

4. **Enhancing interoperability to enable broader adoption of artificial intelligence in chromosome analysis and karyotyping: A pilot evaluation**
   Steele C, Alli A, Aly A, Nieves G, Soliman G, Rozkov L, Frenkel O, Zindany E, Rourke D, Glickman Y
   Genetics in Medicine Open 2025, 3(2):103033 P664
   Poster can be found HERE

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Q&A Karyotyping

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Q

What is ASI's Philosophy on AI Integration?

A

The term **AI** may reflect both traditional algorithms as well as **DNN based** (Deep Neural Network) algorithms. In the last versions, ASI has already integrated multiple DNN based algorithms into its products. Our algorithms incorporate both DNN and traditional methods in combination, to ensure optimal results.

The results of the AI are offered to the user as an aid and are never used to make autonomous clinical decisions or to provide diagnostic recommendations.

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Q

What does AI do?

A

AI (Deep Neural Network) keeps evolving, and with each version, ASI enhances its accuracy and capabilities to support cytogeneticists in achieving the best analysis.
In the current version, AI manages key tasks like:

- Removing nuclei and debris (even those touching chromosomes)
- Segmenting chromosomes, including overlapping clusters
- Performing karyotyping
- Correctly orienting chromosomes
- And more advanced refinements

Users have full control - choose AI for both segmentation and karyotyping or just one, depending on your needs. This flexibility can be a major advantage in certain cases.

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Q

Does AI detect metaphases?

A

Yes, the algorithm for identifying metaphases during the 10x scan can be considered AI-based, though it is not currently a DNN-based algorithm

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Q

What type of stain is used?

A

Typically, Giemsa stain is used for G-banding, which is the most common staining method in cytogenetics. Our MetScan and BandView software, however, are flexible and support a wide range of staining protocols.
The AI-based Karyotyping module has been specifically trained for G-banding and Q-banding, ensuring high accuracy and reliability with these stains.

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Q

What is the validity and accuracy of AI karyotyping?

A

The accuracy of **AI Karyotyping** depends on multiple factors, including the quality of metaphases, background cleanliness (e.g., residual cytoplasm), and overall slide preparation.
In our internal validation studies, the AI achieved:

- **Over 90% accuracy** in full chromosome placement (segmentation + classification) without any user intervention.
- **Over 99% accuracy** in chromosome placement for blood samples, following segmentation correction.
- **Over 96% accuracy** in chromosome placement for bone marrow samples, following segmentation correction.

These results demonstrate robust and clinically reliable performance across diverse sample types.

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Q

What is the Aided Karyotype workflow, and how is it different from traditional non-AI workflow?

A

The workflow stays mostly the same, with one major upgrade: The system now generates karyotypes for all captured cells. This makes it easier for techs to finalize karyotyping, even in labs that combine counting chromosomes and analyzing over the metaphases in their case analysis.

Users still have full control - if they choose to mark a karyotype as “Analyzed” or “Counted,” it won’t appear in CDM or related tools.

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Q

Does the AI detect the types of abnormalities (e.g. microdeletion, translocation etc?)

A

In the current version of our **AI-based Karyotyping** platform, the system does not automatically detect or report specific chromosomal abnormalities such as microdeletions or translocations. However, the AI provides highly accurate metaphase detection, segmentation, and karyogram organization, which significantly aids cytogeneticists in identifying such abnormalities manually.
That said, the development roadmap includes the integration of advanced abnormality recognition features. These will enable the system to assist in the detection and flagging of structural and numerical anomalies, including translocations and microdeletions, in future releases.

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Q

How does AI distinguish a mosaic from a normal karyotype and an abnormal one?

A

In the current version, the AI has been trained primarily on **normal chromosomes**, enabling it to reliably classify standard metaphases. It can detect and classify **polyploidy** and common abnormalities such as **trisomy**.
In mosaic cases, the **normal metaphases** will be classified accordingly, while **abnormal metaphases** will be analyzed chromosome by chromosome. The AI will attempt to classify each chromosome based on its morphology. However, **highly abnormal chromosomes** may be misclassified or left unclassified, depending on the extent of the abnormality.
As always, the AI results are intended as a **decision-support tool**. Final interpretation remains the responsibility of the cytogeneticist, as the software does **not provide autonomous diagnostic recommendations**.

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Q

Does the AI still depend on the resolution of the prepared chromosomes?

A

Yes, to some extent. While the AI is highly robust and supports analysis across **short, medium, long, and very long chromosomes** and varying banding resolutions, its **accuracy is influenced by the quality of the chromosome preparation** - including band clarity, contrast, and background cleanliness.
That said, the current model has been trained to handle a wide range of chromosome sizes and resolutions, maintaining strong performance even with variable slide quality.

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Q

Does AI karyotyping slow down scanning?

A

AI karyotyping runs in parallel with the capture process. While the system scans the second cell, AI is already analyzing the first. This ensures total scanning time stays quite the same. Depending on the nature of the metaphase and few capture parameters, some delay may be seen.

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Q

Does AI learn while scanning or karyotyping?

A

No, AI doesn’t learn during scanning.
The learning process happened during development, before release. We trained it using data from multiple labs and conducted rigorous validation to ensure the most accurate and reliable results.

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Q

In the system's automation, the code is set to scan 20 metaphases. How do you ensure only high-resolution metaphases are selected on a non-homogeneous slide?

A

The system uses a **scoring algorithm** based on predefined criteria - such as chromosome length, spread quality, and background clarity - to **prioritize higher-quality metaphases**. These scoring parameters can be configured, allowing the most well-spread and high-resolution metaphases to be ranked at the top and selected first.

That said, **human selection is still slightly more accurate**, which is why the system is typically set to capture more cells than strictly needed. This gives the cytogeneticist flexibility to choose the best metaphases during review.

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Q

Can we do Scanning and Analysis at the same time?

A

Yes. One of the key advantages of our AI-powered platform is that the analysis runs in parallel to the scanning process. As demonstrated during the session, the AI begins processing metaphases immediately as they are captured, allowing cells to be ready for review even before the full scan is complete. Additionally, analysis and review can be performed on any of the connected review stations across the network while scanning is in progress. However, please note that in the current version, if scanning with AI is enabled, the BandView application cannot be opened on the scanning station itself during the scan.

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Q

Can we do karyotyping while the system is scanning?

A

Yes, the ASI system is designed to allow parallel workflows. Thanks to real-time AI processing, metaphases are segmented, classified, and prepared for review as they are captured, meaning users can begin karyotyping immediately - even while scanning is still ongoing.
Karyotyping can be performed on any of the connected review stations across the network. However, please note that in the current version, karyotyping applications like BandView cannot be opened on the scanning station itself during an active AI scanning session.
This setup ensures optimal efficiency, allowing users to begin analysis without waiting for the full scan to complete.

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Q

If I manually review and re-karyotype the AI-assisted karyotypes, will the AI record and learn from the adjustments I make?

A

No. The AI model does not learn or adapt based on user interactions. Training was conducted exclusively during the development phase to ensure optimal accuracy, consistency, and robustness. This approach guarantees standardized results across all users and labs, avoiding unintended variability from individual edits.

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Q

Can we leave the scanner to scan 99 slides overnight with the tray loader?

A

The system is designed for high-throughput operation, and scanning 99 slides overnight with the tray loader is fully supported and expected. This is precisely the kind of workload the scanner was engineered to handle. Running unattended overnight scans will not harm the software or hardware, provided the system is properly maintained and environmental conditions are stable. Routine use of the tray loader for batch scanning is part of normal operation and does not reduce system lifespan.

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Q

Why do some cells in CDM show "None" instead of "Aided Karyotype" after scanning?

A

AI-based karyotyping is applied only when **35-50 objects** are detected in a metaphase. If the system identifies fewer or more, it keeps the segmentation but **does not proceed with karyotyping**, leaving the status as "None."
For oncology samples, labs can adjust these limits to accommodate polyploid cell populations.

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Q

Is this (AI) compatible with florescence slides and spectral karyology?

A

No. The current AI Karyotyping module is not compatible with fluorescence-based slides or spectral karyotyping (SKY). It has been specifically trained for brightfield G-banding and Q-banding preparations. Support for fluorescent or spectral imaging is not included in this version.

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Q

Can different types of slides (G-banded and FISH) be mixed on the stage and scanned simultaneously?

A

Yes. The ASI platform fully supports mixed slide types on the same scanning tray. G-banded and FISH slides can be loaded together and scanned in a single session. The system identifies the test type based on predefined case settings and automatically launches the appropriate application (e.g., BandView or FISHView) for each slide.

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Q

Can the AI be turned off for cases used for new technologist training?

A

Yes, absolutely. Our software is designed to be flexible. You can choose to disable AI functionalities - such as metaphase segmentation, classification, or AI-based Karyotyping - on a case-by-case basis. This is particularly useful for training new technologists who need to go through the manual workflow. The system allows full control, enabling users to switch between AI-assisted and manual modes as needed.

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Q

Can the AI be improved by images from a specific lab ?

A

Yes. While the current AI model is fixed and does not learn during routine use, **labs can contribute karyotype images** to ASI for use in training future models. These contributions help us enhance performance across a broader range of sample qualities and preparation styles.

Submitted images may be incorporated into future AI versions - pending review, annotation, and validation by our development team. This collaborative approach helps ensure the AI continues to evolve and reflect real-world laboratory diversity.

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Q

In case of abnormal bone marrow karyotyping, to what percent does the software pick the abnormality correctly?

A

In the current version, the software does **not autonomously detect or report chromosomal abnormalities**. While the AI performs highly accurate chromosome segmentation and classification - including on bone marrow samples - it does **not yet interpret clinical abnormalities** such as translocations, deletions, or marker chromosomes. However, the detection and automated interpretation of such abnormalities is part of ASI's roadmap and is being actively developed as we continue to enhance our AI capabilities.

The AI's role is to assist cytogeneticists by providing well-organized, high-quality karyograms. Final interpretation and identification of abnormalities remain the responsibility of the user.

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Q

If I prefer manual scanning and capturing, does the AI perform efficient automated chromosome segmentation in highly overlapped metaphases? And does the proofreading step add significant burden compared to manual segmentation?

A

Even when scanning and capturing are done manually, the AI can perform automated chromosome segmentation, including in highly overlapped metaphases. The AI applies advanced algorithms designed to separate touching or partially overlapping chromosomes with a high degree of accuracy.

While heavily overlapped metaphases may still require user proofreading, the AI significantly reduces the time and effort compared to fully manual segmentation. In most cases, the proofreading step is minimal, and users only need to correct a few elements rather than segment from scratch - resulting in a more efficient workflow overall.

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Q

Can the system differentiate subtle chromosomal abnormalities like cryptic translocations or complex rearrangements that are challenging under traditional G-banding?

A

Not at this time. The current AI model is not designed to detect or interpret subtle structural abnormalities such as cryptic translocations or complex rearrangements. These types of anomalies often fall below the resolution of standard G-banding and require complementary molecular cytogenetic techniques - such as FISH, array CGH, or next-generation sequencing - for accurate identification.

While the AI provides highly accurate metaphase detection, segmentation, and karyotype assembly, final interpretation of structural abnormalities remains the responsibility of the cytogeneticist.

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Q

What are the current limitations of this system? And how do you think we can overcome them?

A

While ASI's system delivers highly accurate chromosome segmentation and karyotype assembly, it does not yet autonomously detect or interpret clinical chromosomal abnormalities such as translocations, deletions, or marker chromosomes. Additionally, certain staining types - like R-band - are not currently supported, as they require dedicated AI training. To overcome these limitations, ASI is continuously improving its AI by training models on data from more diverse sources, including a broader range of sample types and cytogenetic abnormalities. Expanding our training datasets and collaborating with labs working on complex or uncommon cases is a key part of our strategy. These efforts are aimed at enabling future versions of the software to automatically detect and flag clinically relevant abnormalities.

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Q

Is it possible to capture additional metaphases retrospectively, if more images are required?

A

Yes, absolutely. The system allows retrospective capture of additional metaphases at any time, even after the initial scan is completed. Whether you're reviewing a case and need more metaphases for validation or reporting, you can simply return to the slide and continue scanning or capturing manually or automatically - depending on your workflow preferences.
This flexibility ensures that cytogeneticists can fully meet clinical or reporting requirements without needing to restart the entire process.

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Q

Isn't there a risk that the AI will select only standard karyotypes and overlook pathology?

A

This is a valid concern - and one we've addressed carefully in the design of the AI. The AI does not filter out abnormal metaphases, nor does it aim to identify only “standard” karyotypes. Instead, it uses objective criteria - such as chromosome spread, overlap, and clarity - to rank metaphases based on image quality, not content. As such, both normal and abnormal metaphases are included in the scan, provided they meet the quality thresholds. Importantly, the final review and selection remain under the cytogeneticist’s control, ensuring that no potential pathology is missed.
The AI is a decision-support tool - not a diagnostic filter - and is designed to assist, not replace, expert human judgment.

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Q

Is AI available in the ASI HiBand manual systems?

A

Yes. The AI capabilities are fully integrated into ASI's HiBand systems, including those operated manually. Regardless of whether the system is fully automated or manual, the AI-driven features - such as metaphase detection, segmentation, and karyotype generation - are available.

Additionally, with each new software release, our User Manual is updated to reflect the latest AI functionalities and workflow enhancements, ensuring users are always equipped with up-to-date guidance.

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Q

Where does the Mitotic Index function?

A

The Mitotic Index is automatically calculated during the 10x prescan of the slide and is displayed directly within the scanning application. This provides immediate feedback on the density of mitotic cells, allowing users to assess slide quality and determine whether to proceed with high-magnification scanning.

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Q

What happens if one of the chromosomes is missing from the captured image in a very low mitotic index case where no other metaphases are available?

A

In such cases, the AI will still perform segmentation and classification based on the available chromosomes within the captured metaphase. If a chromosome is missing or not visible, the resulting karyogram will reflect that absence.
This scenario highlights the importance of expert review, particularly in low mitotic index cases. The cytogeneticist must determine whether the missing chromosome is due to technical artifact, poor spread, or represents a true abnormality - and report accordingly.

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Q

Will AI karyotyping also work on fluorescent samples such as Q-band and/or fluorescent R-bands ?

A

Yes. Our AI Karyotyping has been **trained and validated for Q-band samples**, and it delivers excellent results with this fluorescent staining method.

At this time, R-band samples are not yet supported, as our AI has not been trained on this specific staining type. However, support for additional fluorescent banding methods, including R-band, is under consideration for future development.

Importantly, ASI is open and willing to collaborate on projects involving R-band. If your lab or research group is working with this method and would like to partner with us, we would be happy to explore opportunities to jointly advance AI development in this area.

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Q

Can the Software do Sister Chromatid Exchange (SCE) staining?

A

Yes, the software can detect and capture metaphases on slides stained for Sister Chromatid Exchange (SCE). However, it is important to note that our AI Karyotyping module was not specifically trained on SCE-stained samples. As a result, while scanning and manual analysis are fully supported, AI-based karyotyping should not be relied upon for automated interpretation of SCE preparations at this time.

We continue to evaluate specialized staining techniques like SCE for future AI training and development.

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Q

Is the AI workflow applicable to metaphase images acquired on scanner from other vendors?

A

Yes. It was trained and validated to also work on metaphase images captured on the **Leica CytoVision** scanner.

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Q

Can ASI software work with Leica's Cytoinsight GSL automated microscope?

A

While ASI software does not natively control Leica's CytoInsight GSI microscope for scanning, we can convert images acquired on the Leica system into ASI's platform using our **ScanLink** software module. This allows laboratories to import metaphase images from Leica's CytoVision station into the ASI environment for **AI-based Karyotyping** and advanced analysis.

This workflow provides a valuable bridge for labs using Leica hardware but seeking to benefit from ASI's robust AI segmentation, classification, and karyotype assembly tools.

However, it's important to note that ASI is **not currently compatible with Leica's new 12 MP camera**. We are continuously reviewing hardware integrations based on demand and feasibility and will consider future compatibility based on market needs and technical evaluations.

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Q

Can the AI detect hypertetraploidies?

A

Yes, the AI is capable of detecting and classifying hypertetraploid metaphases. It does not filter based on ploidy, so metaphases with elevated chromosome counts - such as hypertetraploidies - are captured, segmented, and karyotyped just like any other metaphase.

While the AI may not automatically label the metaphase as “hypertetraploid,” it will accurately classify and arrange all visible chromosomes, enabling the cytogeneticist to clearly recognize the abnormal ploidy level during review.

As always, final interpretation and diagnostic decisions remain with the user.

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Q

What is the Cytogenetic Perspective using AI for Fragile X since it requires molecular techniques?

A

From a cytogenetic standpoint, **Fragile X syndrome is not typically diagnosed through karyotyping**, as it involves detecting CGG trinucleotide repeat expansions in the FMR1 gene - something that requires **molecular techniques such as PCR or Southern blotting**.
AI-based karyotyping, including ASI's HiBand system, is not designed for diagnosing Fragile X syndrome. This condition falls outside the scope of conventional cytogenetic analysis and must be addressed through dedicated molecular diagnostics.

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Q

Does ASI's Metaphase scanner support a fully automated walkaway solution?

A

Naturally, ASI's default offering is a fully automated, walkaway solution—designed to streamline the entire workflow.
It includes 10x prescan, automatic oil dispersion on smears, intelligent cell selection, and high-magnification image capture. In parallel, AI-based Karyotyping is performed during acquisition, significantly accelerating case turnaround and minimizing manual intervention.

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Q

Can you download and save metaphase images?

A

Yes. All metaphase images are automatically saved in the system's database in both **JPEG** and high-quality **16-bit TIFF formats**. Users can access these saved images at any time, and simply just right-click on any image within the Scanning or BandView applications to export it as needed.

This ensures you have full access to **high-resolution** images for documentation, presentations, or further analysis outside the ASI system.

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Q

Are the karyotype images available in high-definition, suitable for printing or publication purposes?

A

Yes. All karyotype and metaphase images are saved in high-definition **16-bit TIFF format** at their original spatial resolution. This provides more than sufficient quality for printing, presentations, and scientific publications.

Each metaphase image can reach up to **5 megapixels** (at 2 bytes per pixel), depending on its size - ensuring exceptional clarity and detail for professional use.

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Q

Do the ideograms and band resolution adhere to the latest ISCN guidelines?

A

Yes. The software fully complies with the latest **ISCN** (International System for Human Cytogenomic Nomenclature) guidelines. It supports all standard banding resolutions, including **300, 400, 550, 700**, and **850 bands**, ensuring accurate and standardized karyotype representation.

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Q

With ISO scheduled to incorporate AI requirements into its standards, is GenASIs compliant with these new mandates?

A

ASI's **GenASIs** software does not use AI in its released **IVD applications** (e.g., BandView, FISHView …). AI is used by R&D, for developing optimized models for throughput improvement of BandView applications. Once the model is finalized it is integrated into the **GenASIs** application software

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Q

What´s the class of your software according to IVDR and how far are you with the process of certification according to IVDR?

A

ASI IVD System's software applications are classified pursuant IVDR as follows:

- BandView and FISHView – Class A
- ScanView and HiPath IHC – Class C

Class A devices already comply with the applicable IVDR requirements.

Class C devices are classified self-declared (IVDD) legacy devices till 2028. Conformance with IVDR requirements will require Notified Body (NB) certification.

The current status of the certification process:

- ASI's QMS complies with IVDR requirements, as of beginning 2023, and the Technical Documentation (TD) for all devices is maintained.
- An IVDR certification agreement with NB (BSI) was signed, by the end of 2024: ASI is planning to submit the TD by the end of 2025 and IVDR audit (stage 2) is planned, beginning 2026.

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Q

Will this replace my job?

A

No, your role stays the same - just easier.
The workflow may adjust to fit your lab’s needs.
Since segmentation and karyotyping are automated, your focus shifts to refining results.
You'll review, make final corrections, and apply your expertise to detect abnormalities.

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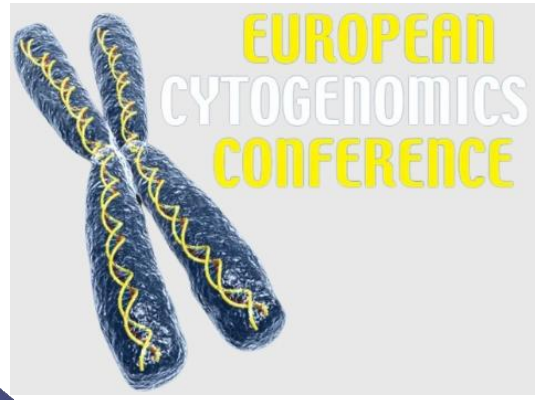

ECA
June 29 - July 1
Leuven, Belgium

sales@spectral-imaging.com
www.spectral-imaging.com

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