NISTIR 7553

SlapSegII – Slap Fingerprint Segmentation Evaluation II

Testing Procedure and Results

Craig Watson
Patricia Flanagan
Brian Cochran

National Institute of Standards and Technology
U.S. Department of Commerce

NISTIR 7553

SlapSegII - Slap Fingerprint Segmentation Evaluation II

Testing Procedure and Results

Craig Watson
Patricia Flanagan
Brian Cochran
Information Technology Laboratory
Information Access Division

January 2009

U.S. Department of Commerce

National Institute of Standards and Technology
Patrick D. Gallagher, Deputy Director

Acknowledgements

The authors would like to thank the Federal Bureau of Investigation, Department of State and Department of Homeland Security for sponsoring this work. The authors would like to thank individuals and organizations identified in the report for their input/comments on the testing plan in preparation for this work. The authors would also like to thank all those involved with hand marking the ground truth data. It was a tedious and time consuming task.

*Disclaimer

Specific hardware and software products identified in this report were used in order to perform the evaluations described in this document. In no case does identification of any commercial product, trade name, or vendor, imply recommendation or endorsement by the National Institute of Standards and Technology, nor does it imply that the products and equipment identified are necessarily the best available for the purpose.

Contents

Summary

The SlapSegII evaluation is sponsored by the Federal Bureau of Investigation and Department of State. The evaluation is being performed to assess the current state-of-the-art in slap fingerprint segmentation. The evaluation uses operational data from both 2-inch and 3-inch platen live-scan devices. The 3-inch platen slap fingerprints are of particular interest because of their use in government systems transitioning from 2 finger identification to 10-print identification flats.

The most significant differences between SlapSegII and SlapSeg04 are the metrics used to determine successful segmentation and the availability of 3-inch slap fingerprint data. SlapSeg04 used fingerprint matching to determine if a segmentation algorithm was successful. SlapSegII uses hand marked segmentation boxes as a baseline for measuring a successful segmentation.

The results from SlapSegII are very encouraging. Many of the segmentation algorithms tested were able to successfully segment at least 3 fingers from a 2-inch or 3-inch four finger slap image for 96-99% of the slap images (both right and left hand). The 3-inch results combining both right and left hands showed that most algorithms were able to segment any 6 finger for more than 99% of the slap images. For 2inch by person, most algorithms were successful for 95-99% of the slap images.

The 3-inch thumb slaps proved more difficult to segment than the four finger slap images. This type of image is fairly new and presents a couple new issues not present in live-scan four finger slaps. First, there is no predictable anthropometric finger behavior to assist in segmentation as users generally place both fingers at the same vertical position on the platen. In four finger slaps the positioning of the four fingers can be used to improve segmentation. Second, some users tend to rotate the bottom of their thumbs outward when placing them on the platen and the general assumption has been that the 3-inch slap fingerprints are not rotated.

Not surprisingly, the inter-digital crease proved the most difficult edge to correctly detect. Even the better performing algorithms saw overall improvement if tolerances were relaxed or ignored around the crease.

Appendix A (3-inch) and Appendix B (2-inch) contain all the tables showing successful segmentation rates for individual finger positions, right and left hands, and various combinations of finger positions that would be of interest to operational systems. Appendix C shows segmentation statistics for each algorithm in the evaluation. Appendix D - Appendix G are plots of the segmentation box centers and sizes. Appendix H and Appendix I are plots (w/ confidence intervals) for the results from Appendix A and Appendix B.

Caveats

As with any biometrics evaluation, all factors of the testing procedure/evaluation should be considered when making policy, planning or operational decisions.

- The data used in this evaluation is both 2-inch and 3-inch slap image data captured on live-scan fingerprint readers. The data is considered operational. Data in other operational systems may not have the exact same characteristics depending on capture environment, user demographics, sensor type and capture policy.

- The success metric in SlapSegII uses strict limits on how much of the fingerprint ridge structure can be cropped during segmentation. This varies from previous work in SlapSeg04 which used fingerprint matching when determining successful segmentation.

- What affect will segmentation have on the matching performance of an AFIS system? The affect is AFIS dependant. Does the AFIS use pattern-class filtering? Over-cropping during segmentation could have a serious negative impact on pattern classification. Does the AFIS use all ten fingers for matching? The segmentation may not need to correctly segment all the fingers to successfully identify a person.

- What effect does over-cropping have on matcher performance? Some work was performed on this issue when determining the segmentation tolerances used in this study. More detailed work is already started based on the segmentation results from SlapSegII.

1. Introduction/Background

In 2004, NIST conducted a fingerprint slap segmentation study [1] to assess the state-of-the-art in fingerprint segmentation technology. Given the development of new technology it has become necessary to reassess the current state-of-the-art of segmentation algorithms. SlapSegII gives providers of this technology the opportunity to participate multiple times as their technology improves and compare their results to previous results on a fixed standard database. The SlapSegII evaluation strategy, data, and measure of successful segmentation are discussed in detail in this testing plan. By following the guidelines laid out in this document, participants can submit segmentation SDKs for evaluation by NIST as part of SlapSegII.

Fingerprint data is collected and maintained in the form of ten-print cards or Identification Flats (ID Flats). Traditional ten-print cards are comprised of the rolled impressions of the ten fingers as well as four slap impressions: the left slap (four fingers of the left hand), the right slap (the four fingers of the right hand) and the left and right thumb slaps. Slaps are taken by pressing the four fingers of one hand onto a scanner or fingerprint card simultaneously. The ten-print card slaps whether scanned inked cards or live-scan capture are also referred to in this document as 2-inch data which refers to the height of the capture area for the fingerprint slaps. ID Flats are ten-print fingerprint records which are constructed by capturing three discrete impressions: left four finger slap, right four finger slap, and both thumbs together. For this document the ID Flats are data that was captured on new live-scan devices that use a larger platen that is 3 inches in height so this data is referred to as 3-inch data.

Currently the Federal Bureau of Investigation (FBI) receives the majority of their fingerprint submissions electronically from live-scan devices, however, tens of millions of legacy fingerprint transactions are stored that were originally taken on paper cards and electronically converted. The Department of State (DOS) and Department of Homeland Security (DHS) US-VISIT program are migrating from 2 finger capture to 10 print ID Flats capture so the ability to evaluate and improve segmentation technology on this type of data will have a significant impact on those agencies.

The most significant differences between SlapSegII and SlapSeg04 are the metrics used to determine successful segmentation and the availability of 3-inch slap fingerprint data. SlapSeg04 used fingerprint matching to determine if a segmentation algorithm was successful. SlapSegII uses hand marked segmentation boxes as a baseline for measuring a successful segmentation. By conducting the evaluation using the ground truth dataset, NIST can better implement success measures to accurately determine the success of the segmenter independent of a successful match, thus providing a more accurate evaluation of the segmentation process and minimize the amount of human verification needed to check segmentation/matcher errors.

Sections 2 and 3 give a general overview of Slap fingerprint segmentation and pervious work performed. Section 4-6 are detailed descriptions of the SlapSegII evaluation procedures, data, and performance metrics. Section 7 and 8 are the major results from SlapSegII and description of future work planned. Appendix A - Appendix I are detailed result tables and plots from the SlapSegII evaluation.

2. Purpose of Slap Fingerprint Segmentation (SlapSeg)

Slap fingerprints are noted for the speed at which they can be collected and processed. However, a slap record is an image of multiple fingers. Fingerprint images must be matched against individual fingerprint images, not an image of a group of fingers. Thus, it is necessary to quickly and accurately separate, or segment, the grouped image of prints into individual fingerprint images which can be used for matching.

2.1. Definition

Slap segmentation is the process by which a single image containing four fingerprint images is divided into four images of the individual fingers or by finding the fingerprint segmentation positions and using them to separate the image into individual images at a later date. The term fingerprint segmentation positions refer to the expected positions of each of the four fingers and thumb of each hand relative to an adjacent finger of the hand. The fingerprint segmentation positions are defined in the ANSI/NIST-ITL 1-2007 data transmission standard (type-14 record) [3] for non-rotated segmentation boxes as the x-coordinate of the left and right edge and the y-coordinate of the top and bottom edge of the segmentation box. For rotated fingerprint images, segmentation positions are the x,y coordinates of the four corners of the rotated segmentation box. For this evaluation they will be in the following order: top-left corner, top-right, bottom-left, and bottom-right. Fingers are conventionally numbered as positions 1 and 6 (thumbs on the right and left hands, respectively), 2 and 7 (index fingers), 3 and 8 (middle fingers), 4 and 9 (ring fingers), and 5 and 10 (small fingers). Accurately labeling each finger is imperative for future matching efforts as well as the ability to correctly detect when fingers are not present in the image.

2.2. Issues

Slap segmentation can prove difficult due to a variety of scenarios. The most common challenge scenarios include fingerprints that are not clearly separated in an image, a fingerprint which appears as multiple images in a slap, background noise, the “halo” effect, and rotation. Many of these problems are the same as those that existed in the SlapSeg04 evaluation but the use of newer 3-inch platen capture devices can reduce problems such as finger spacing and rotation.

Slap segmentation can be adversely affected by fingers that are not clearly separated in an image (See Figure 1), which could be due to finger placement at

the time of capture. It is also possible that two neighboring fingerprints may have been over inked or too wet/oily at the time of capture, in which case a down sampling or an improper threshold may result in the fingerprints being detected as single component. However, the single component should not be split solely due to the large width of the detected component. The preferred method for splitting the component depends on the width of the component, the number of components detected, and the geometric relationship of the component to the other components.

Figure 1. Middle fingers touching in slap.

At the opposite end of the spectrum, an excessively dry or under inked finger or a fingerprint captured using uneven pressure may be detected as several components due to down sampling or improper thresholding. (See Figure 2). Whether to merge or delete these components depends on the relationship between each sub component and the rest of the components. Segmentation algorithms often use contrast equalization to enhance ridge detail and allow for better segmentation. Though this process can sometimes improve the matching quality of the segmented fingerprint, it sometimes has the opposite effect. However, SlapSegII will not judge the effect these changes have on fingerprint image quality in regards to matching as SlapSegII is focused on segmentation, not matching.

Figure 2. Low Contrast slap image.

Background noise such as extraneous print lines, printed letters, smudges, etc near the boundary of the slap print pose an additional challenge for segmentation. (See Figure 3.) "Noise", which may also be caused by dirt on the platen surface of the scanner, is most problematic in low contrast images.

Figure 3. "Noisy" slap image.

The "Halo" affect can make segmentation difficult as it introduces noise to the image. (See Figure 4.) The "Halo" affect is a moisture build up on platen surface of the scanner due to temperature variations (i.e. a warm hand being placed on a cool scanning surface).

Figure 4. Moisture/Condensation on the platen surface.

Image rotation poses an additional problem when a scanner with a two inch high scanning surface is used, as well as in some older paper data which has been scanned electronically. (See Figure 5.)

Figure 5. Slap rotation.

Amputated fingers could also pose a problem during the segmentation process. Livescan capture devices should correctly identify this problem during the enrollment process, however older devices may not have captured this information and electronically converted fingerprint cards may not have the proper flags for amputation. The segmentation software may incorrectly segment an image based on missing or amputated fingers.

Figure 6. Slap amputation.

Often the right and left little finger are not captured or only partially captured during the slap enrollment process. Vendors may fail to find these partial little fingers or have trouble processing transactions without little fingers. While this is actually a livescan capture issue versus a segmentation issue, the resulting image can pose challenges to the segmenter.

Figure 7. Partial little finger.

3. SlapSeg 2004

SlapSeg04 [1] was conducted to assess the accuracy of existing slap segmentation algorithms in segmenting slap fingerprint images into individual fingerprint images, using a variety of operational-quality slap fingerprints. The study was conducted by the National Institute of Standards and Technology (NIST) on behalf of the Department of Justice (DOJ) Justice Management Division (JMD), IDENT/IAFIS Integration Project, with the support of the US-

VISIT Program Office of the Department of Homeland Security (DHS) and the Federal Bureau of Investigation (FBI).

The study, which was conducted between October and December of 2004, used rolled images to match against the segmented slaps as the measure of segmentation success. This required manual checking to verify the results of each vendor as a low quality image may have segmented correctly without matching to the rolled image. The study examined records from about thirty thousand subjects from seven different operational datasets, none of which was 3-inch fingerprint data. SlapSeg04 incorporated several subtly different objectives including measurement of the accuracy of state-of-the-art slap segmentation software, assessment of the practicality of segmenting operational quality slap fingerprints, determination of the factors that cause slap segmentation and matching to fail, and assessment of the ability of segmentation algorithms to detect when segmentation was successful.

4. SlapSegII

SlapSegII is conducted by NIST in order to provide the ability to assess the current state-of-the-art in slap segmentation technology. SlapSegII gives vendors the opportunity to participate multiple times as their technology improves and compare their results to previous results on the same standard dataset. The use of hand marked ground truth segmentation boxes allows NIST to quickly analyze and report back results for each segmentation algorithm.

The study is sponsored by the FBI and DOS. The sponsors require the ability to test on large volumes of Sensitive But Unclassified (SBU) data. The FBI is accepting submissions consisting only of slap data, while DOS/DHS are currently migrating from 2 finger captures to ten finger captures for its US-VISIT program. The most efficient method for capturing ten fingers is slap images. Thus the sponsors will benefit from knowing what the current state of the art is in slap segmentation technology. Vendors will also benefit from the study as they will gain the knowledge of how their segmentation implementation will perform on a large dataset of operational quality law enforcement data. Thus, the study can prove extremely critical for improving segmentation technology.

4.1. Testing Strategy

NIST intends to use a measure of successful slap segmentation for SlapSegII that requires minimal manual verification of segmented slaps and does not rely on the ability to match segmented slap images. This success measure is based on comparing segmenter output with “ground truth” segmentation coordinates. In order to prove effective, it is imperative to have a controlled test location, submission process, and validation data, as well as a clear understanding of the input and expected output.

4.2. Test Location

All testing is conducted at the NIST laboratory in Gaithersburg, MD. The lab responds to needs for measurement methods, tools, data, and technology. NIST researchers collaborate with colleagues in industry, academic institutions, and other government agencies. The result is baseline research that advances the nation's technology infrastructure and is needed by U.S. industry to continually improve technology and services.

4.3. Who Should Participate

Makers of commercially available slap fingerprint segmentation software are invited to participate in the Slap Fingerprint Segmentation Evaluation II. In addition, companies, research organizations, or universities that have developed mature prototype or research slap fingerprint segmentation software are invited to participate. It is important to note that the segmentation software need not be "operational," nor a production system, nor commercially available. However, the software must, at a minimum, be a stable implementation capable of functioning as stated in for this document (sections 4.8 - 4.11). Additionally, anonymous participation is not permitted. The results of the evaluation are published with attribution to the participating organizations.

4.4. Submission Process

In order to simplify the submission process, NIST adheres to specific guidelines and processes for vendor submissions. NIST has written and maintains the control and scoring software. Vendors submit compiled command line executables that do not use any graphical user interface (GUI) and run on either Red Hat Enterprise Linux 5 or Windows Server 2003 operating systems*. Any data generated or obtained during the SlapSegII evaluations, as well as any documentation required by the Government from the participants, becomes the property of the Government. Participants do not possess a proprietary interest in the data and/or submitted documentation.

4.5. Application Process

In order to request participation in SlapSegII, potential participants must complete and submit the Application to Participate in SlapSegII which is available on the SlapSegII website fingerprint.nist.gov/SlapSegII. Incomplete forms are not accepted. When completing the application, the Responsible Party must be an individual with the authority to commit the organization to the terms in this document, and the Point of Contact must be an individual with detailed knowledge of the system to be considered for evaluation.

Participants may withdraw from the SlapSegII evaluations at any time before the software to be evaluated is received by NIST, without their participation and withdrawal being documented in SlapSegII evaluation results.

Upon receipt of the signed form by NIST, the organization is classified as a "Participant". (NIST must have received the form by the due date as posted on the SlapSegII website for inclusion in this initial evaluation report.) Registered participants then download the small Validation Dataset from the website.

4.6. Points of Contact

The SlapSegII Liaison is the government point of contact for SlapSegII. All correspondence should be directed to slapseg@nist.gov, which will be received by the SlapSegII Liaison and other SlapSegII personnel. Any correspondences may be posted on the FAQ (Frequently Asked Questions) area of the SlapSegII website at the discretion of the SlapSegII Liaison. The identity of those persons or organizations whose correspondences lead to FAQ postings will not be made public in the FAQ.

4.7. Validation Data

In order to minimize the variability introduced to testing by the physical differences in vendor hardware versus NIST hardware, NIST provides sample/validation data to the vendors prior to testing. This validation data is used to ensure that the software produces the same results on vendor computers and NIST computers. Thus ensuring the software being tested produces the required data format during testing.

4.7.1. Access to SlapSegII Validation Data

The SlapSegII validation data is supplied to Participants to assist in preparing for SlapSegII. The fingerprints in the SlapSegII validation data are representative of the SlapSegII test data only in format. Image quality, collection device, and other characteristics vary between the Validation and Test Datasets.

4.7.2. Validation and Submission Process

Prior to submission of their SDK the participant verifies that their software executes on the validation data and produces segmentation information in the required format. By utilizing validation data, NIST effectively minimizes the potential for errors due to hardware differences prior to testing.

After the participant has executed their software on the validation data, the output of the validation data is submitted to NIST along with the SDK. Software is sent by email (**file is encrypted using encryption key provided by NIST, procedures are posted on the SlapSegII website**) to slapseg@nist.gov, or on CD (recommend encrypting the files on the CD) to:

Slap Fingerprint Segmentation Evaluation II (SlapSegII) Liaison
National Institute of Standards and Technology
Information Access Division (894)
100 Bureau Drive, Stop 8940
Gaithersburg, MD 20899-8940

Upon receipt of the SDK and validation output, NIST attempts to reproduce the output by executing the SDK on the validation data using a NIST computer. In the event of disagreement in the output, if the software is found to be non-functional or non-compliant with section 4 of this document, or the validation dataset results cannot be replicated by NIST, participants will be notified with a detailed description of the problem(s) and given a reasonable opportunity to resubmit (as time allows) according to the discretion of the SlapSegII Liaison.

4.8. Application Inputs

SlapSegII investigates the accuracy of fingerprint image segmentation systems for use with multi-finger slap images. These slap images consist of both 2-inch slap data (fingerprint are rotated) and 3-inch slap data (no rotation). The 2-inch data contains left and right four finger slap images that are live-scan and rescanned ink. The 3-inch data contains left and right four finger slap images and both thumbs captured together. All 3-inch data is live-scan.

The submitted segmentation applications are assumed to run on Windows Server 2003 or Red Hat Linux Enterprise 5.0, on x86 platforms*. Other options must be approved by the Test Liaison. An application must have a command-line interface as specified in this document; no other user interface is permissible.

The segmentation application must be capable of taking as input an uncompressed raw slap image, and outputting the segmentation coordinates as specified in section 4.9.1.

4.8.1. Slap Image Files

The segmentation application must be capable of processing multi-finger slap images stored as raw pixel data files.

Syntactically correct samples are available on the website http://fingerprint.nist.gov/SlapSegII.

4.8.2. Resolution and Dimensions

All images for this test are 500 PPI resolution (horizontal and vertical, 19.7ppmm). The dimension of the 3-inch slap images are 1576 x 1572 pixels (80mm x79.9mm, 3.15in x 3.14in). The majority of the 2-inch slap images are 1600 x 950 pixels (81.3mm x 48.3mm, 3.2in x 1.9in) but can be as large as 1600 x 1000 pixels (81.3mm x 50.8mm, 3.2in x 2 in).

4.8.3. Raw File Format

Raw 8-bit grayscale image files are canonically encoded with black equal to 0, white equal to 255, etc.; stored left to right, top to bottom, with one 8-bit byte per pixel. The number of bytes in a file is exactly the image width * image height, as measured in pixels; there is no header.

4.8.4. Input Parameters

The following information is provided as parameters to the segmentation application:

Identifier [-i]

If this input is given the segmentation algorithm returns the software vendor's point of contact email address without performing any segmentation. This function is used to confirm that the correct segmentation algorithm is executed. Optionally, the vendor can provide version information after the email address.

Type [-t]

specifies the type of the fingerprint image: **2** (2-inch), **3** (3-inch).

Hand identifier[-h]

specifies **R** (right hand), **L** (left hand), or **T** (two thumb, 3-inch only) corresponding to the specified slap image.

Source [-s]

specifies the source of the fingerprint image: **L** (livescan), **P** (paper), or **U** (unspecified; could be livescan or paper).

The parameters (if present) are in the stated order. Parameters are separated by spaces or tabs.

4.9. Application Outputs

4.9.1. Segmentation Coordinates

The segmentation output for each input image is multiple lines of text which contain the segmentation box coordinates for each expected finger in the slap

image. The output coordinate format is based on the type-14 record from ANSI/NIST-ITL 1-2007 [3].

For 2-inch images the output is the x,y coordinates for all four corners of the segmentation box and the angle of rotation (theta) for the fingerprints in the image. The corner x,y coordinates are listed in the following order: top-left, top-right, bottom-left, and bottom-right. The rotation angle uses positive for clockwise rotation and negative for counter-clockwise rotation and is given in degrees of rotation. Zero degrees is at vertical. It is anticipated that the vertices form a rectangular segmentation box but it is not required in the way they are reported. For this evaluation the ground truth boxes are rotated rectangles, it is up to the reporting segmentation algorithm whether or not to report rectangular segmentation boxes for 2-inch slaps. Figure 8 shows a 2-inch slap image with segmentation boxes drawn.

Figure 8. 2-inch sample showing segmentation boxes, with vertices outside image limits..

All 3-inch input data is assumed to be vertical/non-rotated and the segmentation is the best fit vertical/non-rotated box for each finger in the slap image. The segmentation coordinates for the 3-inch slap are the x-position of the left side, x-position of the right side, y-position of the top, and y-position of the bottom of the segmentation box. All x,y positions are from the top-left corner (0,0) of the slap image.Figure 9 shows a 3-inch slap image with segmentation boxes drawn.

Figure 9. 3-inch slap image showing segmentation boxes.

The finger positions are the position codes defined in Table 12 of ANSI/NIST-ITL 1-2007 [3]:

01 Right thumb
02 Right index
03 Right middle
04 Right ring
05 Right little
06 Left thumb
07 Left index
08 Left middle
09 Left ring
10 Left little

The output is written to a file with the same name as the input file but changing the extension from .raw to .sgm. For example if the input file is `image.raw` the output file is `image.sgm`. The output file is written in the same directory path as the input file. Examples for each image type are:

2-inch Right Hand:

02,x_{tl},y_{tl},x_{tr},y_{tr},x_{bl},y_{bl},x_{br},y_{br}
03,x_{tl},y_{tl},x_{tr},y_{tr},x_{bl},y_{bl},x_{br},y_{br}
04,x_{tl},y_{tl},x_{tr},y_{tr},x_{bl},y_{bl},x_{br},y_{br}
05,x_{tl},y_{tl},x_{tr},y_{tr},x_{bl},y_{bl},x_{br},y_{br}
Theta

2-inch Left Hand:

07,x_{tl},y_{tl},x_{tr},y_{tr},x_{bl},y_{bl},x_{br},y_{br}
08,x_{tl},y_{tl},x_{tr},y_{tr},x_{bl},y_{bl},x_{br},y_{br}
09,x_{tl},y_{tl},x_{tr},y_{tr},x_{bl},y_{bl},x_{br},y_{br}
10,x_{tl},y_{tl},x_{tr},y_{tr},x_{bl},y_{bl},x_{br},y_{br}
theta

3-inch Right Hand:

02,x_{left},x_{right},y_{top},y_{bottom}
03,x_{left},x_{right},y_{top},y_{bottom}
04,x_{left},x_{right},y_{top},y_{bottom}
05,x_{left},x_{right},y_{top},y_{bottom}

3-inch Left Hand:

07,x_{left},x_{right},y_{top},y_{bottom}
08,x_{left},x_{right},y_{top},y_{bottom}
09,x_{left},x_{right},y_{top},y_{bottom}
10,x_{left},x_{right},y_{top},y_{bottom}

3-inch Two Thumb:

01,x_{left},x_{right},y_{top},y_{bottom}
06,x_{left},x_{right},y_{top},y_{bottom}

If the segmentation algorithm can't detect/segment one or more of the fingers it must output a -1 after the finger number. For example:

02,x_{left},x_{right},y_{top},y_{bottom}
03,-1
04,x_{left},x_{right},y_{top},y_{bottom}
05,x_{left},x_{right},y_{top},y_{bottom}

4.9.2. Error Codes and Handling

The segmentation application shall exit with a return code of zero on success. The participant must provide documentation of all (non-zero) error or warning codes (see section 4.10).

The application should include error/exception handling so that in the case of a crash, the return code is still provided to the calling shell.

We request that the following return codes are used:

Return code	Explanation
0	Success
1	Unable to read input file
2	Unable to open input file
10	0 fingers could be segmented
11	Only 1 finger could be segmented
12	Only 2 fingers could be segmented, for 4 finger slap image
13	Only 3 fingers could be segmented, for 4 finger slap image
20 – 63	Application-specific fatal errors (explained in documentation)
64 – 127	Application-specific non-fatal warnings (explained in documentation)

All errors, warnings and informational messages are limited to output displayed via standard output or standard error. No GUI-type dialog windows are permitted.

4.10. Software and Documentation

4.10.1. Application type and platform

The application provided will be command-line driven, and capable of being run in non-interactive "batch mode." No graphical user interface (GUI) is permitted.

Test participants will provide NIST with binaries only (i.e. no source code) for their segmentation application. Testing of segmentation systems is performed on commercial, off-the-shelf PCs. Applications running on Red Hat Enterprise Linux 5 or Microsoft Windows Server 2003 are preferred*; other operating systems must be approved by the Test Liaison.

4.10.2. Installation

Segmentation software must install and run easily to be evaluated. The application shall be immediately executable without use of an installation program. Please contact the Test Liaison if an installation program is absolutely necessary. The application shall be executable on any number of machines without requiring additional machine-specific license control procedures or activation.

It is preferred that the application is packaged as a single executable file. If external libraries (such as DLLs) are necessary, they must work from the application directory, and not require installation in another location.

4.10.3. External Communication

The segmentation software running on NIST hosts shall not write any data to external resources (e.g. server, file, network connections, or other process) other than those explicitly allowed in this document.

4.10.4. Documentation

Complete documentation of application usage shall be provided, and shall detail any additional functionality or behavior beyond what is specified in this document. The documentation must define all error and warning codes.

4.10.5. Speed

Software that runs excessively slow can't be evaluated. On average, segmentation software should take less than five (5) seconds to segment a slap image (using a 2.8 GHZ Pentium Xeon processor). Due to resource limitations, software that takes longer than that may not be evaluated. Processing speed is noted but will not be a primary evaluation criterion.

4.11. Validation Data Results

Participants must test their software using the SlapSegII validation data, and email these results to the Test Liaison for validation before sending software to NIST for evaluation

4.12. SlapSegII Calendar (Initial Evaluation)

Date	
5/8/2008	Announcement/Request for Comments
5/23/2008	End Comment Period
6/3/2008	Release Final Test Plan Start Accepting Applications
6/12/2008	Validation Data Available
6/27/2008	Last Day for Applications
8/7/2008	Validation Data Results Submission Deadline
8/13/2008	Software Submission Deadline
January 2009	Results Report Issued

5. Evaluation Data

In an operational environment, slap segmentation is required for ten-print cards and identification flats. Ten-print cards are synonymous with 2-inch data. Identification flats are synonymous with 3-inch data. Ten print cards contain right and left four finger slap images and plain impressions of each thumb in their own box. Identification flats contain right and left four finger slap images and a two finger slap that captures both thumbs in the same image.

The segmentation process varies for 2-inch data and 3-inch data, due to the size of the image and number of components within the image. Because of the differences in the segmentation process, the SlapSegII test evaluates segmentation of both 2-inch data and 3-inch data as separate tests. Vendors are given the option to participate in only the 2-inch test, only the 3-inch test, or both.

The 2-inch dataset is a random selection of law enforcement quality data with 19,680 right slap images and 22,577 left slap images. There are 12,492 with both right and left slap images from the same person. The data is mainly of live-scan images with some scanned ink images. There is rotation in the images.

The 3-inch segmentation evaluation uses randomly selected slap images from the Department of State identification flats. The 3-inch dataset contains 24,968 right hand slaps, 24,964 left hand slaps, and 24,422 thumb slaps. There are 24,377 cases that have all three slap images from the same person. The data contains only live-scan images. The fingerprints are assumed vertical with no rotation so there is no rotation of the segmentation boxes.

5.1. Dataset Ground Truth

The ground truth data is based on the NIST fingerprint segmentation algorithm (NFSEG.)[2] Humans examine every slap image starting with the NFSEG segmentation boxes and hand correct all errors producing the ground truth segmentation coordinates. The three main errors the examiners looked for were excess white space between a segmentation box edge and the fingerprint, a box side touching fingerprint ridges, and the bottom side correctly placed at the first crease. Figure 10 shows an example of ground truth segmentation boxes.

The ground truth boxes are placed to capture only the part of the finger above the first joint (ie. the finger tip). The left, right, and top sides of the segmentation boxes are placed so that a small amount of white space exists between the segmentation box and the edges of the fingerprint. Ground truth information is included with validation data allowing users to see what is considered a “small amount of white space.” If two fingers are touching, the box sides are placed along the point of contact.

The bottom side of the segmentation box is placed in the middle of the first joint/crease of the finger. If there is not a well defined white space at the crease,

the box is still placed in the middle of the crease cutting through any ridge information that existed. If there is a slight slant in the fingerprint, (see 2nd print in Figure 10) the bottom side is placed to include the lowest part of the crease inside the segmentation box. Ground truth segmentation boxes do not extend past the edges of the slap image for 3-inch slap images, but corners can be outside the edge of the image for 2-inch data depending on rotation angle.

After initial testing results were computed some ground truth data was reviewed as determined by statistical analysis to detect human errors. This included cases where all or almost all vendors miss the segmentation.

Figure 10. Sample Ground Truth Boxes.

5.2. Access to SlapSegII Test Data

The SlapSegII Test datasets are protected under the Privacy Act (5 U.S.C. 552a), and are treated as Controlled Unclassified Information (CUI) and/or Law Enforcement Sensitive. SlapSegII participants do not have access to SlapSegII test data, before, during, or after the test.

6. SlapSegII Successful Segmentation Metric

6.1. 3-inch Data

The measure of a successful segmentation for the 3-inch dataset is a comparison of the segmentation algorithm's output to hand marked ground truth coordinates determining if they are within an acceptable tolerance. The tolerances allowed are based on matching tests done with segmented slap image probes matched against a rolled gallery. A sample of segmented slap image data was selected from a dataset that also had rolled mates. Matching tests determined which tolerances around the hand-marked ground truth segmentation boxes had a minimal effect on matching results. The matchers used for this testing were matchers evaluated in the Proprietary Fingerprint Template evaluation (PFT)* http://fingerprint.nist.gov/PFT/index.html.

The baseline matching results were computed by matching the hand-marked ground truth segmented fingerprint images against the rolled fingerprint images. A matcher score threshold was chosen based on the baseline results and was fixed throughout the rest of the comparisons.

Next each ground truth segmentation box was adjusted by various amounts and resulting segmentation images were matched against their rolled mates. These results were compared with the baseline results to determine how varying the edges of the ground truth segmentation box affect the number of False Rejects (FR) and False Accepts (FA) during matching.

Figure 11 shows the averages for the various matching results and different segmentation tolerances across all the fingers from both hands. The first row in the table ("Ground Truth") shows the number of false rejects and false accepts for the hand marked ground truth segmentation boxes. The "change from ground truth" columns show the difference between the number of FRs & FAs for a given tolerance adjustment and the ground truth value from the first row. The average number of mates (genuine) in the dataset was 9,300 and the average number of non-mates (imposters) was 36,713. The average size of the segmented images over the entire dataset was 270 pixels x 436 pixels.

The "All sides" rows show results for varying all four sides at the same time at the given tolerance. These two rows show there is improvement in matcher performance when the size of the segmentation boxes increase beyond the size of the ground truth results. This allows the upper tolerance for the left, right, top and bottom to be set at +64 pixels. Since the crease is a difficult area to detect and the better matchers crop the input image during enrollment, the bottom tolerance allows +128 pixels over the ground truth bottom edge.

The last 8 rows of the table show the effects of varying the left, right, top and bottom individually by -32 and -64 pixels. These results indicate a significantly larger error rate for both FR and FA using a -64 pixel change to the left or right sides. The top and bottom are tolerant to a change of -64 pixels.

Variation	Average # False Reject	Change from Ground Truth	Average # False Accept	Change from Ground Truth
Ground Truth	77		24	
All Sides +32	68	-9	20	-4
All Sides +64	62	-15	18	-6
Left -32	86	9	34	10
Left -64	97	20	64	40
Right -32	87	10	37	13
Right -64	103	26	64	40
Top -32	78	1	25	1
Top -64	81	4	33	9
Bottom -32	80	3	27	3
Bottom -64	88	11	32	8

Figure 11. Matching results (number of FRs and FAs) for different segmentation box tolerances.

The 3-inch successful segmentation is then computed for each finger in the slap image as follows (gt = ground truth):

$$d_{left} = left_{gt} - left$$

$$d_{right} = right - right_{gt}$$

$$d_{top} = top_{gt} - top$$

$$d_{bottom} = bottom - bottom_{gt}$$

Successful segmentation of each finger is based on the following criteria:

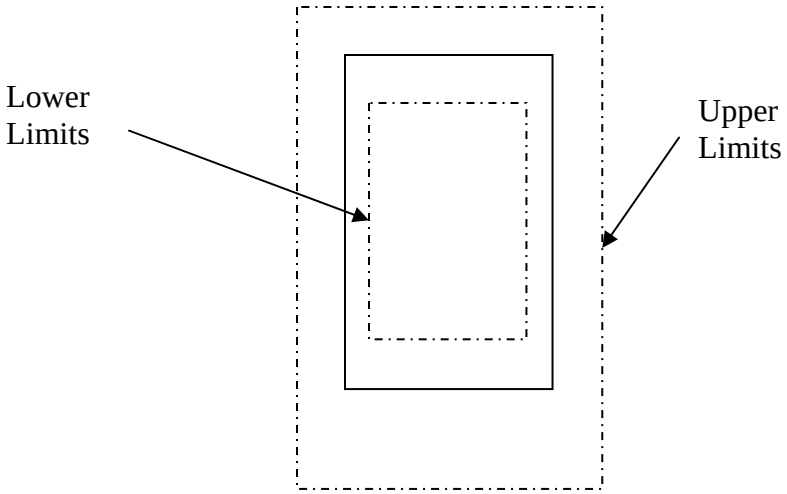
$$-32 <= d_{left} <= 64$$

$$-32 <= d_{right} <= 64$$

$$-64 <= d_{top} <= 64$$

$$-64 <= d_{bottom} <= 128$$

The image and table in Figure 12 show the segmentation tolerances for the left/right/top/bottom edges. The solid line box is the size of the “average” image at 270 x 436 pixels which at 500 dpi is 0.54 inches x 0.87 inches. All the boxes are adjusted by a factor of two for better viewing.



Side	Segmentation Tolerances	
	Lower Limit (pixels)	Upper Limit (pixels)
Left/Right	-32	+64
Top	-64	+64
Bottom	-64	+128

Figure 12. 3-inch Segmentation box tolerances.

To further validate the choice of these segmentation box tolerances the NIST segmenter used in SlapSeg 04 was run on the data sample used to make Figure 11 and scored against the hand marked ground truth coordinates using the tolerances previously discussed and shown in Figure 12. In SlapSeg04 the NIST segmenter was able to correctly segment 3 or more "matchable" fingers an average of 94.2% for slaps across the seven datasets used in that study [1]. Using this new metric for 3-inch data, the same segmenter can segment 3 or more fingers for 96.0% of the slap images. The reported results in section 7 use the tolerances shown in Figure 12 as the desired level of performance.

6.2. 2-inch Data

The measure of a successful segmentation for the 2-inch dataset is also a comparison of the segmentation algorithm's output to hand marked ground truth coordinates determining if they are within an acceptable tolerance. The difference from the 3-inch slaps is the need to account for rotation in the segmentation boxes. Again, the segmentation tolerances were based on matching tests performed with segmented slap images matched to a rolled gallery. Tolerance values were selected so that segmentation would not

significantly impact a fingerprint matcher's performance when matching the segmented fingerprint.

After trying several different methods of comparing segmentation output to ground truth for rotated data. An accurate and efficient method was developed to compare the four vertices (x_{tl},y_{tl},x_{tr},y_{tr},x_{bl},y_{bl},x_{br},y_{br}) of the segmentation box to the ground truth vertices and determine if the segmentation vertices are within tolerances similar to those used with 3-inch data. The variations between the reported segmentation vertices and the ground truth are computed relative to the ground truth rotation angle as shown in Figure 14 and Figure 15 (picture on the left). The rotation angle reported by the segmentation algorithm is not used directly to determine successful segmentation but it is still being reported to assist in any error checking as needed.

The acceptable distance tolerances for the vertices are set based on the matching done for the 3-inch slap data as described in the previous section 6.1. Additional matching was performed to determine the allowable rotation variance.

Figure 13 shows the averages for the various matching results at different rotation variations across all the fingers for both hands. The first row in the table ("Ground Truth") shows the number of false rejects and false accepts for the hand marked ground truth segmentation boxes. The "change from ground truth" columns show the difference between the number of FR & FA for a given rotation change (+/-5^o through +/- 20^o) and the ground truth rotation value. The average number of mates in the dataset was 9,300 and the average number of non-mates was 36,713. The average size of the segmented images over the entire dataset was 270 pixels x 436 pixels.

The number of false rejects increased as the rotation angle was increasingly varied from the ground truth angle. It is interesting that the number of false accepts did not increase in a similar fashion. There is no definitive increase in the number of false rejects that defines a clear tolerance point. The conservative point is to allow +/- 5^o from the ground truth angle. This coupled with the distance tolerances provides significant variation from ground truth boxes while still minimizing impact on the matcher. The chosen tolerance limits will also help preserve the ridge structure of the fingerprint for forensic purposes.

Variation	Average # False Reject	Change from Ground Truth	Average # False Accept	Change from Ground Truth
Ground Truth	77		24	
Rotate 5^o	80	3	31	7
Rotate -5^o	79	2	28	4
Rotate 10^o	82	5	30	6
Rotate -10^o	82	5	29	5
Rotate 15^o	84	7	30	6
Rotate -15^o	84	7	29	5
Rotate 20^o	85	8	30	6
Rotate -20^o	87	10	29	5

Figure 13. Matching results (number of FRs and FAs) for different segmentation box rotation tolerances.

For 2-inch data the reported segmentation vertices are compared to the ground truth vertices relative to the ground truth angle (varied by $+/-5^o$). If the reported segmentation vertices are within tolerance at any of the three angles $\{-5^o, 0^o, +5^o\}$ then they are accepted as a successful segmentation. This could mean that the top-left corner is within tolerance at $theta_{gt}+5^o$ and the bottom-right corner is within tolerance at $theta_{gt}-5^o$ and the segmentation box is still considered good.

The differences between the four vertices returned by the segmentation algorithm ($x_{tl},y_{tl},x_{tr},y_{tr},x_{bl},y_{bl},x_{br},y_{br}$) and the ground truth (gt) vertices are computed for each fingerprint in the slap image as follows (Figure 14 is a drawing of the parameter placement for the top-left corner):

$$dx1_{tl} = x_{tl} - x_{tlgt}$$
$$dx1_{tr} = x_{trgt} - x_{tr}$$
$$dx1_{bl} = x_{bl} - x_{blgt}$$
$$dx1_{br} = x_{brgt} - x_{br}$$
$$dy1_{tl} = y_{tl} - y_{tlgt}$$
$$dy1_{tr} = y_{tr} - y_{trgt}$$
$$dy1_{bl} = y_{blgt} - y_{bl}$$
$$dy1_{br} = y_{brgt} - y_{br}$$

$$d_{tl} = \text{sqrt}(((dx1_{tl})**2) + ((dy1_{tl})**2))$$
$$d_{tr} = \text{sqrt}(((dx1_{tr})**2) + ((dy1_{tr})**2))$$
$$d_{bl} = \text{sqrt}(((dx1_{bl})**2) + ((dy1_{bl})**2))$$
$$d_{br} = \text{sqrt}(((dx1_{br})**2) + ((dy1_{br})**2))$$

$$\text{theta1}_{tl} = \tan^{-1}(dy1_{tl}/dx1_{tl})$$
$$\text{theta1}_{tr} = \tan^{-1}(dy1_{tr}/dx1_{tr})$$
$$\text{theta1}_{bl} = \tan^{-1}(dy1_{bl}/dx1_{bl})$$
$$\text{theta1}_{br} = \tan^{-1}(dy1_{br}/dx1_{br})$$

$$\text{theta}_{tl} = \text{theta1}_{tl} + \text{theta}_{gt}$$
$$\text{theta}_{tr} = \text{theta1}_{tr} - \text{theta}_{gt}$$
$$\text{theta}_{bl} = \text{theta1}_{bl} - \text{theta}_{gt}$$
$$\text{theta}_{br} = \text{theta1}_{br} + \text{theta}_{gt}$$

$$dx_{tl} = \text{int}(d_{tl} * \cos(\text{theta}_{tl}) + 0.5)$$
$$dy_{tl} = \text{int}(d_{tl} * \sin(\text{theta}_{tl}) + 0.5)$$
$$dx_{tr} = \text{int}(d_{tr} * \cos(\text{theta}_{tr}) + 0.5)$$
$$dy_{tr} = \text{int}(d_{tr} * \sin(\text{theta}_{tr}) + 0.5)$$
$$dx_{bl} = \text{int}(d_{bl} * \cos(\text{theta}_{bl}) + 0.5)$$
$$dy_{bl} = \text{int}(d_{bl} * \sin(\text{theta}_{bl}) + 0.5)$$
$$dx_{br} = \text{int}(d_{br} * \cos(\text{theta}_{br}) + 0.5)$$
$$dy_{br} = \text{int}(d_{br} * \sin(\text{theta}_{br}) + 0.5)$$

These computations are repeated for theta_{gt}-5^{o} and theta_{gt}+5^{o} and successful segmentation is based on the difference values for any of the three angles theta_{gt}, theta_{gt}-5^{o} or theta_{gt}+5^{o} meeting the following criteria:

$$-32 <= \{dx_{tl}, dx_{tr}\} <= 64$$
$$-32 <= \{dx_{bl}, dx_{br}\} <= 64$$
$$-64 <= \{dy_{tl}, dy_{tr}\} <= 64$$
$$-64 <= \{dy_{bl}, dy_{br}\} <= 128$$

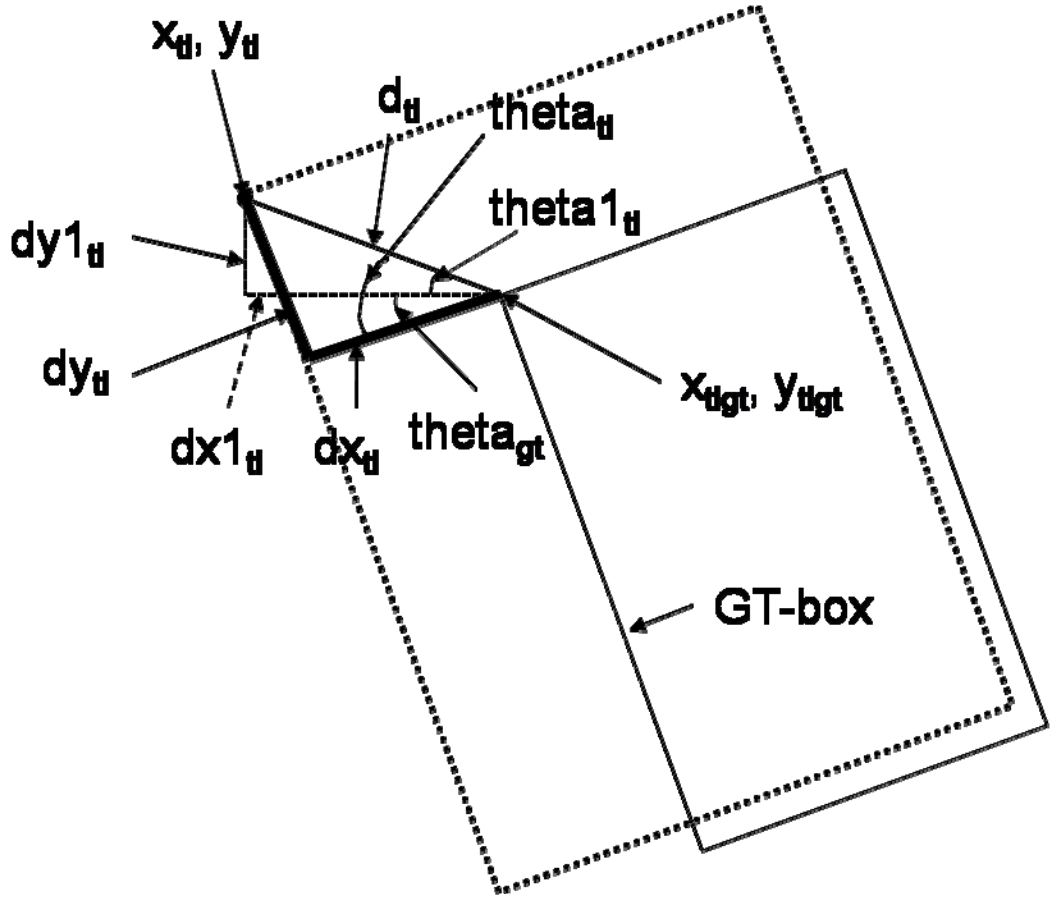
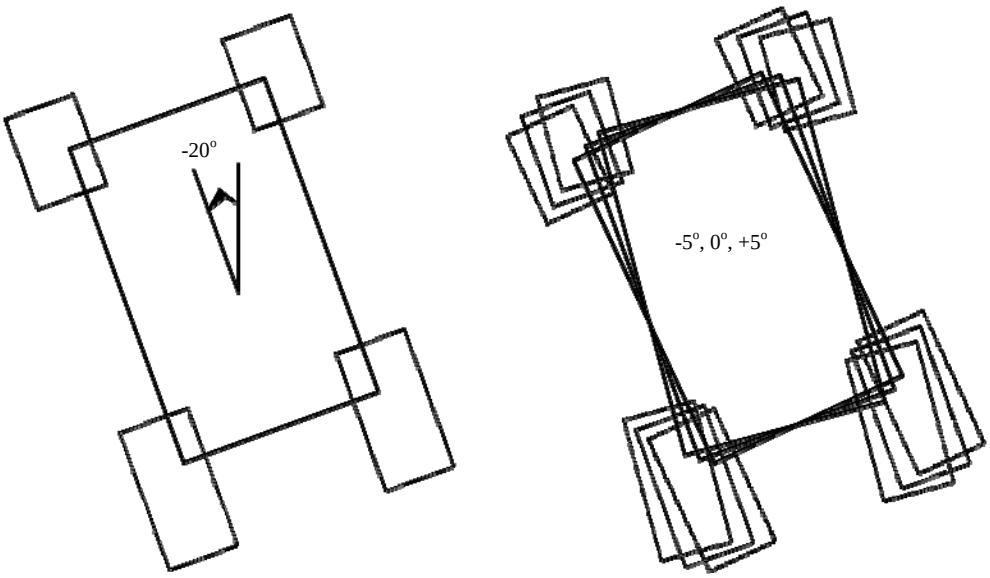


Figure 14. Shows the parameter placement (top-left corner) when computing the success measure for 2-inch segmentation boxes (this drawing is not to scale it is just intended to assist in understanding the formulas in section 6.2).

The images and table in Figure 15 show the segmentation tolerances allowed for 2-inch slap data. The solid line box is the size of the "average" image at 270 x 436 pixels which at 500 dpi is 0.54 inches x 0.87 inches and shown at a rotation angle of -20^o (image on the left). All the boxes are adjusted by a factor of two for better viewing. The "acceptable tolerance" box for each corner point is shown by the dotted line also rotated relative to the ground truth angle of rotation (-20^o for this example). The image on the right in Figure 15 shows the distance tolerances at +/-5^o from the ground truth angle of -20^o. Again, for successful segmentation all four vertices must be within tolerance at any of the three angular positions.



Side	Segmentation Tolerances	
	Lower Limit (pixels)	Upper Limit (pixels)
X-limits (dx)	-32	+64
Top Y-Limits (dy)	-64	+64
Bottom Y-Limits (dy)	-64	+128
Rotation	-5 degrees	+5 degrees

Figure 15. 2-inch segmentation tolerances.

To further validate the choice of these segmentation box tolerances the NIST segmenter that was used in SlapSeg 04 was run on the data sample used to make Figure 13 and scored against the hand marked ground truth coordinates using the tolerances previously discussed and shown in Figure 15. In SlapSeg04 the NIST segmenter was able to correctly segment 3 or more "matchable" fingers an average of 94.2% for slaps across the seven datasets used in that study [1]. Using this new metric for 2-inch data, the same segmenter can segment 3 more fingers for 93.7% of the slap images. The 2-inch results reported in section 7 use the tolerances shown in Figure 15 as the desired level of performance.

7. Results

A summary of some key results are given in this section but all the tables and plots generated while analyzing the slap segmentation results are included in appendices at the end of the document. The appendices are:

Appendix A. Result tables for 3-inch slap images.
Appendix B. Result tables for 2-inch slap images.
Appendix C. Detailed segmentation statistics.
Appendix D. Plots of 3-inch segmentation box centers.
Appendix E. Plots of 3-inch segmentation box widths and heights.
Appendix F. Plots of 2-inch segmentation box centers.
Appendix G. Plots of 2-inch segmentation box widths and heights.
Appendix H. Confidence intervals for 3-inch segmentation results.
Appendix I. Confidence intervals for 2-inch segmentation results.

The sample size for the 2-inch dataset is 19,680 right and 22,577 left slap images. There are 12,492 cases that have both the left and right hand from the same person. The sample size for the 3-inch dataset is 24,968 right, 24,964 left and 24,422 thumb slap images. There are 24,377 cases that have all three slap images from the same person.

Correct segmentation for SlapSegII means that the segmentation coordinates returned by the algorithm are both within the tolerance limits specified in section 6 and that the correct fingerprint position is reported in the output file as described in section 4.9.1.

The results from SlapSegII show there are many segmentation algorithms capable of segmenting fingerprints successfully while preserving the majority of the fingerprint ridge structure. Table 1 shows the successful segmentation rates for 3-inch data for both right and left hands. The columns show percentages for correctly segmenting all 5 finger positions, any 4, any 3, all the way to none. The majority of algorithms are able to correctly segment any 4 fingers for 95-99% of the slaps. This is a very encouraging result. Table 2 shows the same type of results but only using the right and left four finger slaps (no thumbs) and again a majority of algorithms correctly segment any 3 fingers for 96-99% of the slap images. Table 3 shows the results by person with columns for correctly segmenting all 10 fingers all the way to none. Most algorithms were able to correctly segment any 6 fingers for 99% of the cases. Figure 16 and Figure 17 are plots of the right hand results from Table 1 and similar plots for the other results are available in Appendix H.

A second set of results are listed for segmentation algorithm A (A+32) where original segmentation points are adjusted by adding 32 to all the values returned. This was done after analyzing the statistics tables shown in Appendix C. The table showed a significant # of errors below the minimum threshold and a

tendency for the algorithm to crop into the fingerprint image which was confirmed by visual inspection on a sample of the test data. This +32 adjustment significantly increased the performance of the algorithm which is clearly shown in the (A+32) results.

Algorithm J had significant problems with the fingerprint crease, specifically "overshooting" the crease. If the maximum limit on the crease is ignored, as shown in the "JBmx" row and in the "B" and "C" tables in Appendix A, there is a significant jump in performance for this algorithm.

	Right Hand						Left Hand					
	All 5	Any 4	Any 3	Any 2	Any 1	None	All 5	Any 4	Any 3	Any 2	Any 1	None
A	6.70	27.32	54.86	79.08	93.95	6.05	15.78	44.59	69.50	86.92	96.70	3.30
A+32	54.00	83.44	93.44	97.16	99.45	0.55	62.37	87.22	94.37	97.32	99.49	0.51
B	93.76	99.45	99.84	99.96	100.00	0.00	94.37	99.46	99.83	99.94	100.00	0.00
C	94.28	99.62	99.93	99.97	100.00	0.00	94.71	99.59	99.93	99.97	100.00	0.00
D	72.53	95.16	98.55	99.40	99.95	0.05	72.13	95.17	98.80	99.75	99.97	0.03
E	82.91	95.41	98.33	99.35	99.98	0.02	79.67	94.17	97.97	99.24	99.92	0.08
F	86.98	96.98	98.59	99.37	99.96	0.04	85.57	96.21	98.53	99.32	99.95	0.05
G	87.65	98.94	99.77	99.92	100.00	0.00	85.39	98.70	99.80	99.95	99.99	0.01
H	69.73	96.02	99.12	99.73	99.94	0.06	73.99	96.15	99.00	99.60	99.93	0.07
I	81.80	96.80	99.15	99.73	99.93	0.07	78.15	96.87	99.13	99.70	99.94	0.06
J	10.47	25.88	45.17	72.01	94.91	5.09	10.05	25.33	43.67	69.48	93.61	6.39
JBmx	64.91	90.22	96.90	98.81	99.79	0.21	63.22	88.76	95.24	97.04	99.61	0.39

Table 1. 3-inch segmentation results for right and left hands including thumbs.

	Right Hand					Left Hand				
	All 4	Any 3	Any 2	Any 1	None	All 4	Any 3	Any 2	Any 1	None
A	15.83	43.58	71.95	90.80	9.20	28.03	58.14	80.04	93.33	6.67
A+32	66.57	88.17	95.19	97.92	2.08	73.60	90.21	95.38	97.79	2.21
B	95.58	99.55	99.84	99.96	0.04	95.99	99.56	99.85	99.94	0.06
C	97.34	99.80	99.96	99.98	0.02	97.15	99.76	99.94	99.97	0.03
D	85.13	96.53	98.82	99.47	0.53	85.22	96.62	99.10	99.82	0.18
E	86.58	96.18	98.53	99.49	0.51	84.84	95.33	98.35	99.40	0.60
F	90.63	97.30	98.69	99.41	0.59	89.33	96.77	98.65	99.36	0.64
G	94.89	99.32	99.85	99.96	0.04	94.08	99.15	99.86	99.97	0.03
H	90.21	98.40	99.57	99.82	0.18	88.36	98.12	99.40	99.70	0.30
I	88.77	97.79	99.34	99.78	0.22	90.02	98.00	99.33	99.79	0.21
J	13.27	28.76	48.75	78.34	21.66	12.45	28.29	47.19	75.95	24.05
JBmx	74.72	92.78	97.71	99.18	0.82	72.68	91.26	95.87	97.32	2.68

Table 2. 3-inch segmentation results for right and left hands excluding thumbs.

A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan

Person	All 10	Any 9	Any 8	Any 7	Any 6	Any 5	Any 4	Any 3	Any 2	Any 1	None
A	1.80	8.20	20.86	37.93	56.65	73.22	85.82	93.53	97.80	99.58	0.42
A+32	39.50	65.52	82.08	90.30	95.07	97.56	98.93	99.51	99.85	99.95	0.05
B	89.32	98.04	99.49	99.84	99.95	99.98	99.99	100.00	100.00	100.00	0.00
C	90.21	98.30	99.66	99.89	99.96	99.99	100.00	100.00	100.00	100.00	0.00
D	58.02	82.00	94.47	97.96	99.29	99.76	99.92	99.98	100.00	100.00	0.00
E	70.14	87.37	94.17	97.23	98.93	99.47	99.76	99.92	99.99	100.00	0.00
F	76.52	91.69	96.19	98.17	99.43	99.73	99.83	99.93	100.00	100.00	0.00
G	78.09	93.50	99.02	99.68	99.89	99.95	99.98	100.00	100.00	100.00	0.00
H	59.90	81.10	95.20	98.22	99.35	99.68	99.89	99.93	99.97	99.99	0.01
I	66.65	89.93	96.74	98.78	99.50	99.78	99.89	99.95	99.98	100.00	0.00
J	3.95	10.33	18.61	28.02	38.72	51.25	66.21	81.58	93.69	98.22	1.78
JBmx	47.20	73.00	87.20	93.21	96.71	98.36	99.28	99.68	99.89	99.96	0.04

Table 3. 3-inch segmentation results for all ten fingers.

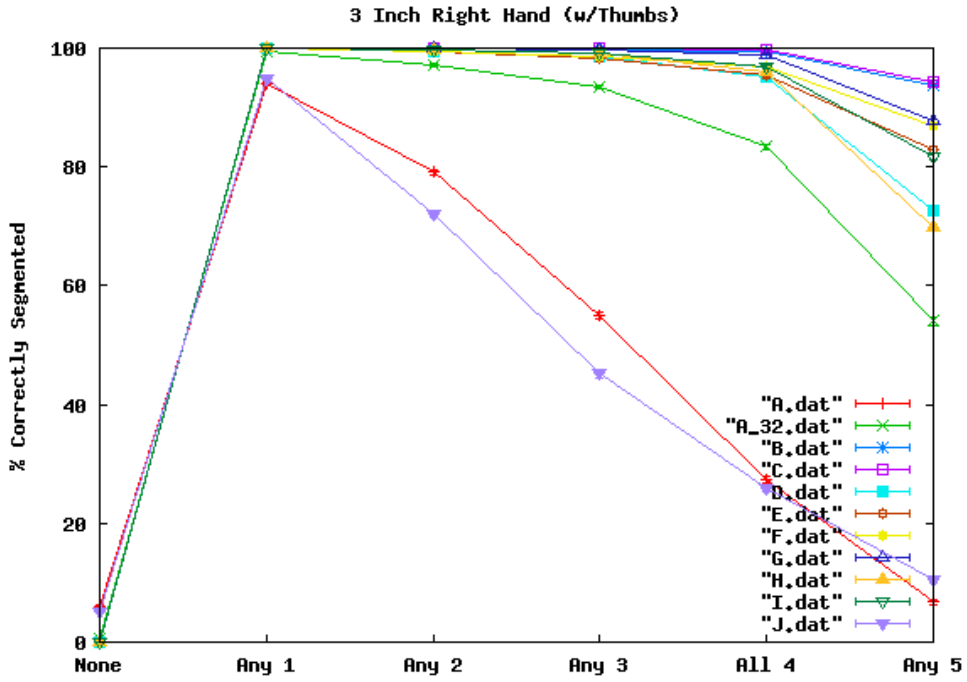


Figure 16. 3-inch segmentation results for right hand including thumbs.

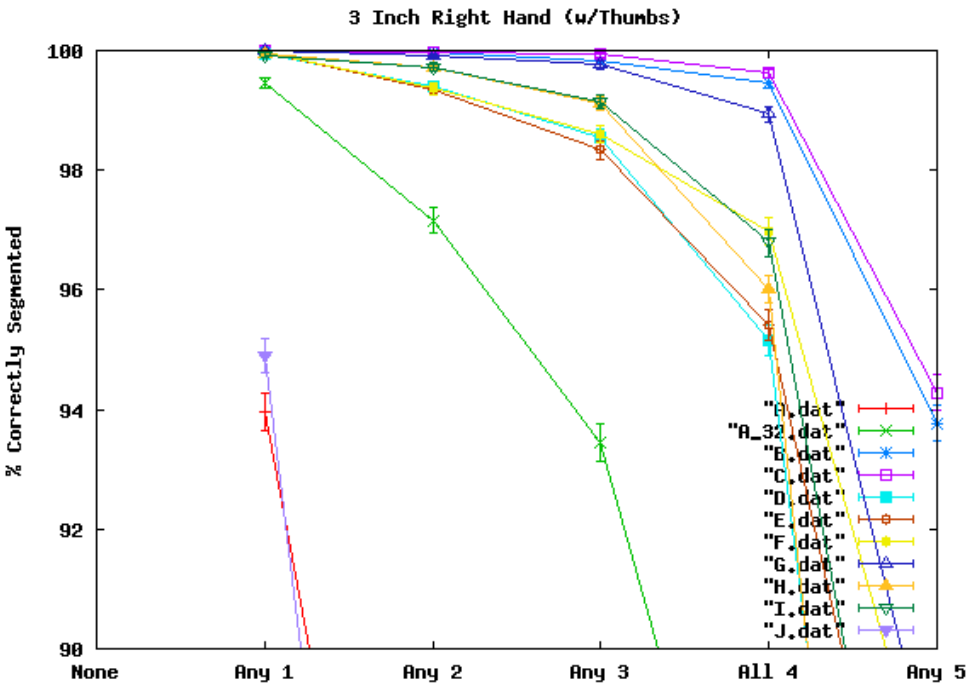


Figure 17. Same results as Figure 16 with scale 90-100% correct.

Appendix A shows all the results for 3-inch data by individual finger position and various finger combinations. A major result for the 3-inch data is that the thumbs cause the most problems for the segmentation algorithms as shown in Table 4. This is most likely a result of the “two thumb” slap image being the newest type of slap image. Most certainly algorithms will be able to adjust for this newer image type and improve overall accuracy in the not too distant future. Issues that exist with these “two thumb” slaps are the lack of “finger position geometry” and a higher frequency of users rotating their thumbs outward. As the thumbs are put on the platen together the tips are generally at the same vertical position, unlike the four finger slaps where the fingers are spread at “logical” positions in the image which can be used to improve confidence/accuracy in segmentation. There is also a problem with users rotating the bottom of their thumbs outward during image capture.

	Finger Position									
	RT	RI	RM	RR	RL	LT	LI	LM	LR	LL
A	39.79	68.76	61.73	47.38	44.26	53.85	56.58	64.50	67.84	70.71
A+32	79.46	93.36	87.30	84.10	83.28	83.32	91.62	87.92	87.95	89.95
B	97.99	99.22	98.79	98.31	98.69	98.11	99.08	98.88	98.62	98.92
C	96.68	99.58	99.31	98.88	99.35	97.27	99.55	99.14	98.95	99.29
D	85.31	96.20	94.92	93.99	95.16	84.74	96.05	95.00	94.98	95.05
E	94.77	95.41	94.67	94.86	96.27	92.56	95.18	93.73	94.35	95.16
F	95.55	96.10	96.25	96.53	97.44	95.09	95.97	95.49	96.19	96.84
G	92.19	99.02	98.62	98.13	98.31	90.68	98.51	98.17	98.29	98.17
H	76.35	98.22	97.38	97.11	95.48	82.85	97.62	97.11	97.07	94.01
I	91.66	97.55	96.82	96.21	95.16	86.40	97.89	96.89	96.50	96.12
J	78.36	38.18	39.15	36.60	56.15	77.08	33.12	38.83	38.80	54.32

Table 4. 3-inch segmentation results by finger position.

Table 5 shows the right and left hand results for the 2-inch slap images. Again, there are columns for correctly segmenting all 4, any 3, any 2, any 1 and none of the finger positions. These results are also very positive as most segmentation algorithms were able to segment any 3 of the finger positions around 96-99% correct for both the right and left hands. Performance is off slightly for getting all 4 finger positions ranging from 83-94% correct segmentations. Ignoring the crease pushes the numbers up to 86-96% correct segmentation. Table 6 shows results by person with columns for “All 8” down to “None.” Most algorithms were able to correctly segment “Any 6” fingers for 95-99% of the cases.

	Right Hand					Left Hand				
	All 4	Any 3	Any 2	Any 1	None	All 4	Any 3	Any 2	Any 1	None
A	18.63	40.34	60.00	78.02	21.98	19.30	41.46	59.98	77.37	22.63
A+32	64.09	86.20	94.41	97.74	2.26	66.06	86.35	94.13	97.77	2.23
B	91.05	97.70	98.88	99.46	0.54	90.31	97.54	98.80	99.43	0.57
C	94.01	98.76	99.45	99.73	0.27	94.67	99.01	99.57	99.81	0.19
E	92.98	99.31	99.80	99.95	0.05	91.71	98.80	99.70	99.88	0.12
F	93.12	99.36	99.79	99.92	0.08	93.34	99.18	99.80	99.89	0.11
G	89.62	97.48	98.99	99.57	0.43	90.03	96.94	98.58	99.27	0.73
H	83.12	96.85	99.09	99.59	0.41	83.78	96.16	98.52	99.16	0.84
I	89.19	97.03	98.48	99.15	0.85	88.58	96.92	98.53	99.24	0.76
J	24.96	49.96	71.08	87.31	12.69	21.76	46.95	69.50	87.81	12.19
JBmx	56.44	76.14	84.77	90.90	9.10	64.24	79.60	86.79	91.65	8.35

Table 5. 2-inch segmentation results for right and left hands.

	Person								
	All 8	Any 7	Any 6	Any 5	Any 4	Any 3	Any 2	Any 1	None
A	4.86	13.54	25.01	39.39	57.06	73.05	84.81	93.94	6.06
A+32	43.79	68.15	81.47	89.33	95.18	97.93	99.25	99.76	0.24
B	83.43	94.89	97.35	98.53	99.67	99.91	99.96	99.98	0.02
C	89.57	97.36	98.82	99.47	99.92	99.98	99.98	99.99	0.01
E	85.12	96.81	99.15	99.74	99.94	100.00	100.00	100.00	0.00
F	87.30	97.97	99.48	99.80	99.98	100.00	100.00	100.00	0.00
G	81.56	93.47	96.85	98.31	99.44	99.73	99.88	99.94	0.06
H	70.97	90.67	96.15	97.93	98.98	99.46	99.62	99.77	0.23
I	79.50	92.98	96.39	98.00	99.58	99.84	99.90	99.94	0.06
J	8.60	22.37	37.59	52.58	68.04	80.35	91.07	96.37	3.63
JBmx	41.98	61.33	72.27	80.23	89.66	93.76	96.37	97.84	2.16

Table 6. 2-inch segmentation results for all eight fingers.

Appendix B shows 2-inch data results for individual and combinations of finger positions. A little unexpected is how well the algorithms are able to correctly segment the “little” finger positions.

The scatter plots in Appendix D - Appendix G are useful visual aids for comparing the segmentation algorithm’s detected fingerprint locations and size. The locations and sizes are included for the ground truth allowing visual comparisons. As a good example, the 3-inch thumb plots for algorithm H are shown in Figure 18 and clearly show that some right thumbs are being marked as left thumbs.

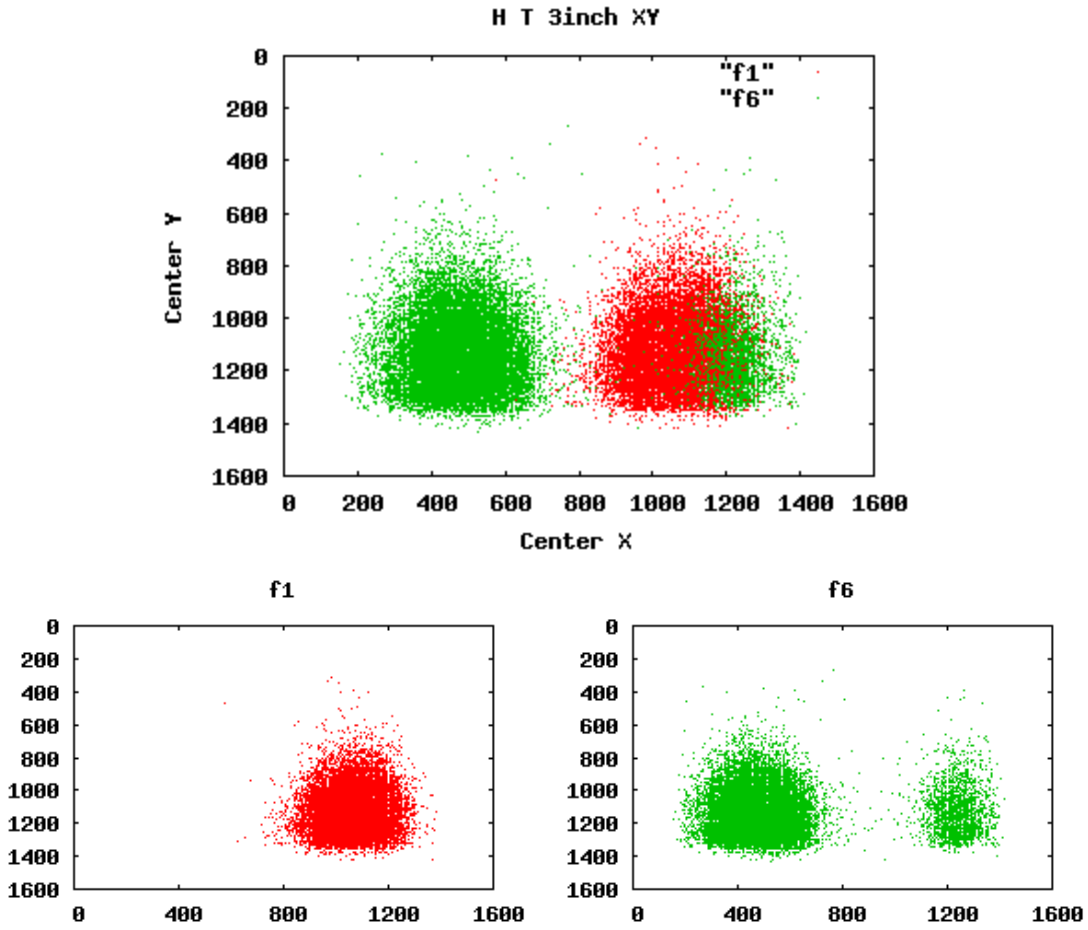


Figure 18. Scatter plot of algorithm H's segmentation center (x,y) position for 3-inch "two-thumb" slaps.

8. Future Work

Future work that has already started is evaluating the effects segmentation has on matching for the 2-inch slap dataset. Specifically, what affect does cropping of the segmented slap have on fingerprint matching performance? This particular dataset has rolled mates that can be used for matching. This is an extension of the matching work that was performed in section 6 when determining the segmentation tolerances used in the current performance metrics. Now the matching results of the ground truth segmentation boxes can be compared to the matching results of each segmentation algorithm and see how much, if any, difference occurs. These results will help study the impact of the segmentation process on the matching performance of an AFIS.

Other analysis might look at the success of segmentation on low quality slap images, images with "ghost" images present, or the affect of segmentation on fingerprint pattern classification.

9. References

1. Slap Fingerprint Segmentation Evaluation 2004 (SlapSeg04). NISTIR 7209. http://fingerprint.nist.gov/SlapSeg04

2. NIST Biometric Image Software, http://biometrics.nist.gov/nigos

3. "American National Standard for Information Systems – Data Format for the Interchange of Fingerprint, Facial, & Other Biometric Information – Part 1," ANSI/NIST-ITL 1-2007, NIST Special Publication 500-271, May 2007. http://fingerprint.nist.gov/standard/index.html

Appendix A. Result tables for 3-inch slap images.

This appendix shows successful segmentation rates for the 3-inch slap images by finger position, hand, and various combinations of fingers that may be of interest to different fingerprint matching applications.

The first table shows successful segmentation percentages for each finger position.

The second table combines the right and left hand for each finger position and shows results for getting both the right and left finger, either or none.

The third table looks at the results by right and left hand. Columns show segmentation rates for correctly segmenting all 5 finger positions, any 4, any 3, down to none.

The fourth table is similar to the third table but only uses the four finger slaps, no thumbs.

The fifth table is shows results for all ten fingers by combining right and left hands.

The last three tables show results for finger position combinations of thumb/index, thumb/index/middle and index/middle/ring.

All eight tables are then repeated (B) for the case where the maximum limited of the bottom (+128) is ignored and then repeated (C) again ignoring the bottom (crease) completely. This was done because previous work had shown the crease is usually the most difficult edge for the segmentation algorithm to detect and in general this how much the crease detection affects the success rate of the segmentation algorithm. The results in these tables show algorithm J definitely had difficulty detecting the crease and many other algorithms show significant increases in successfully segmenting “All 5” finger positions on a hand when the crease is ignored. Again, this is not a surprise as detecting the correct crease is a known difficulty for segmentation algorithms.

Most of the increase in segmentation performance comes from ignoring the maximum limit (+128) which will probably have less effect on matching but requires keeping/processing more of the slap fingerprint. This larger fingerprint area could have a detrimental effect on processing speeds for large scale systems, with no gain in system accuracy.

L/R -32/+64, T -64/+64, B -64/+128

Finger Position

	RT	RI	RM	RR	RL	LT	LI	LM	LR	LL
A	39.79	68.76	61.73	47.38	44.26	53.85	56.58	64.50	67.84	70.71
A+32	79.46	93.36	87.30	84.10	83.28	83.32	91.62	87.92	87.95	89.95
B	97.99	99.22	98.79	98.31	98.69	98.11	99.08	98.88	98.62	98.92
C	96.68	99.58	99.31	98.88	99.35	97.27	99.55	99.14	98.95	99.29
D	85.31	96.20	94.92	93.99	95.16	84.74	96.05	95.00	94.98	95.05
E	94.77	95.41	94.67	94.86	96.27	92.56	95.18	93.73	94.35	95.16
F	95.55	96.10	96.25	96.53	97.44	95.09	95.97	95.49	96.19	96.84
G	92.19	99.02	98.62	98.13	98.31	90.68	98.51	98.17	98.29	98.17
H	76.35	98.22	97.38	97.11	95.48	82.85	97.62	97.11	97.07	94.01
I	91.66	97.55	96.82	96.21	95.16	86.40	97.89	96.89	96.50	96.12
J	78.36	38.18	39.15	36.60	56.15	77.08	33.12	38.83	38.80	54.32

	Thumb			Index			Middle			Ring			Little		
	Both	Either	None	Both	Either	None	Both	Either	None	Both	Either	None	Both	Either	None
A	27.21	66.42	33.58	39.87	85.47	14.53	41.33	84.90	15.10	33.74	81.48	18.52	32.51	82.46	17.54
A+32	72.54	90.24	9.76	86.20	98.79	1.21	78.16	97.05	2.95	75.26	96.78	3.22	76.04	97.19	2.81
B	96.48	99.63	0.37	98.33	99.96	0.04	97.76	99.90	0.10	97.08	99.85	0.15	97.69	99.92	0.08
C	94.63	99.32	0.68	99.14	99.99	0.01	98.52	99.93	0.07	97.97	99.86	0.14	98.67	99.97	0.03
D	78.01	92.04	7.96	92.70	99.54	0.46	90.91	99.01	0.99	89.94	99.04	0.96	90.85	99.36	0.64
E	89.42	97.91	2.09	91.34	99.24	0.76	89.65	98.74	1.26	90.50	98.71	1.29	92.15	99.28	0.72
F	91.74	98.90	1.10	92.62	99.46	0.54	92.32	99.42	0.58	93.24	99.48	0.52	94.63	99.65	0.35
G	86.71	96.16	3.84	97.60	99.94	0.06	96.94	99.84	0.16	96.58	99.84	0.16	96.57	99.91	0.09
H	71.80	87.40	12.60	96.02	99.81	0.19	94.92	99.57	0.43	94.63	99.55	0.45	90.20	99.29	0.71
I	80.95	97.10	2.90	95.64	99.79	0.21	94.09	99.61	0.39	93.30	99.41	0.59	91.89	99.39	0.61
J	67.69	87.75	12.25	21.47	49.82	50.18	25.85	52.12	47.88	23.99	51.41	48.59	36.62	73.85	26.15

	Right Hand (w/Thumbs)						Left Hand (w/Thumbs)					
	All 5	Any 4	Any 3	Any 2	Any 1	None	All 5	Any 4	Any 3	Any 2	Any 1	None
A	6.70	27.32	54.86	79.08	93.95	6.05	15.78	44.59	69.50	86.92	96.70	3.30
A+32	54.00	83.44	93.44	97.16	99.45	0.55	62.37	87.22	94.37	97.32	99.49	0.51
B	93.76	99.45	99.84	99.96	100.00	0.00	94.37	99.46	99.83	99.94	100.00	0.00
C	94.28	99.62	99.93	99.97	100.00	0.00	94.71	99.59	99.93	99.97	100.00	0.00
D	72.53	95.16	98.55	99.40	99.95	0.05	72.13	95.17	98.80	99.75	99.97	0.03
E	82.91	95.41	98.33	99.35	99.98	0.02	79.67	94.17	97.97	99.24	99.92	0.08
F	86.98	96.98	98.59	99.37	99.96	0.04	85.57	96.21	98.53	99.32	99.95	0.05
G	87.65	98.94	99.77	99.92	100.00	0.00	85.39	98.70	99.80	99.95	99.99	0.01
H	69.73	96.02	99.12	99.73	99.94	0.06	73.99	96.15	99.00	99.60	99.93	0.07
I	81.80	96.80	99.15	99.73	99.93	0.07	78.15	96.87	99.13	99.70	99.94	0.06
J	10.47	25.88	45.17	72.01	94.91	5.09	10.05	25.33	43.67	69.48	93.61	6.39

	Right Hand					Left Hand				
	All 4	Any 3	Any 2	Any 1	None	All 4	Any 3	Any 2	Any 1	None
A	15.83	43.58	71.95	90.80	9.20	28.03	58.14	80.04	93.33	6.67
A+32	66.57	88.17	95.19	97.92	2.08	73.60	90.21	95.38	97.79	2.21
B	95.58	99.55	99.84	99.96	0.04	95.99	99.56	99.85	99.94	0.06
C	97.34	99.80	99.96	99.98	0.02	97.15	99.76	99.94	99.97	0.03
D	85.13	96.53	98.82	99.47	0.53	85.22	96.62	99.10	99.82	0.18
E	86.58	96.18	98.53	99.49	0.51	84.84	95.33	98.35	99.40	0.60
F	90.63	97.30	98.69	99.41	0.59	89.33	96.77	98.65	99.36	0.64
G	94.89	99.32	99.85	99.96	0.04	94.08	99.15	99.86	99.97	0.03
H	90.21	98.40	99.57	99.82	0.18	88.36	98.12	99.40	99.70	0.30
I	88.77	97.79	99.34	99.78	0.22	90.02	98.00	99.33	99.79	0.21
J	13.27	28.76	48.75	78.34	21.66	12.45	28.29	47.19	75.95	24.05

A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan

L/R -32/+64, T -64/+64, B -64/+128

Person

	All 10	Any 9	Any 8	Any 7	Any 6	Any 5	Any 4	Any 3	Any 2	Any 1	None
A	1.80	8.20	20.86	37.93	56.65	73.22	85.82	93.53	97.80	99.58	0.42
A+32	39.50	65.52	82.08	90.30	95.07	97.56	98.93	99.51	99.85	99.95	0.05
B	89.32	98.04	99.49	99.84	99.95	99.98	99.99	100.00	100.00	100.00	0.00
C	90.21	98.30	99.66	99.89	99.96	99.99	100.00	100.00	100.00	100.00	0.00
D	58.02	82.00	94.47	97.96	99.29	99.76	99.92	99.98	100.00	100.00	0.00
E	70.14	87.37	94.17	97.23	98.93	99.47	99.76	99.92	99.99	100.00	0.00
F	76.52	91.69	96.19	98.17	99.43	99.73	99.83	99.93	100.00	100.00	0.00
G	78.09	93.50	99.02	99.68	99.89	99.95	99.98	100.00	100.00	100.00	0.00
H	59.90	81.10	95.20	98.22	99.35	99.68	99.89	99.93	99.97	99.99	0.01
I	66.65	89.93	96.74	98.78	99.50	99.78	99.89	99.95	99.98	100.00	0.00
J	3.95	10.33	18.61	28.02	38.72	51.25	66.21	81.58	93.69	98.22	1.78

	Right Thumb/Index			Left Thumb/Index		
	Both	Either	None	Both	Either	None
A	28.02	80.53	19.47	31.20	79.23	20.77
A+32	74.61	98.21	1.79	76.70	98.24	1.76
B	97.25	99.97	0.03	97.24	99.95	0.05
C	96.32	99.95	0.05	96.88	99.94	0.06
D	82.00	99.51	0.49	81.34	99.45	0.55
E	90.66	99.52	0.48	88.44	99.29	0.71
F	91.91	99.75	0.25	91.39	99.67	0.33
G	91.32	99.89	0.11	89.33	99.86	0.14
H	75.28	99.29	0.71	81.14	99.33	0.67
I	89.56	99.65	0.35	84.71	99.57	0.43
J	30.02	86.51	13.49	26.03	84.17	15.83

	Right Thumb/Index/Middle				Left Thumb/Index/Middle			
	All 3	Any 2	Any 1	None	All 3	Any 2	Any 1	None
A	19.41	61.28	89.59	10.41	23.30	61.93	89.69	10.31
A+32	67.82	93.28	99.02	0.98	70.33	93.49	99.04	0.96
B	96.20	99.81	99.99	0.01	96.32	99.77	99.98	0.02
C	95.72	99.86	99.99	0.01	96.13	99.85	99.98	0.02
D	78.71	97.86	99.85	0.15	77.89	98.06	99.84	0.16
E	87.58	97.46	99.81	0.19	84.87	96.90	99.70	0.30
F	89.99	98.02	99.89	0.11	88.97	97.72	99.86	0.14
G	90.27	99.61	99.96	0.04	87.83	99.57	99.96	0.04
H	73.92	98.24	99.79	0.21	79.37	98.40	99.82	0.18
I	87.38	98.78	99.86	0.14	82.61	98.71	99.85	0.15
J	19.25	47.11	89.33	10.67	17.72	43.79	87.51	12.49

	Right Index/Middle/Ring				Left Index/Middle/Ring			
	All 3	Any 2	Any 1	None	All 3	Any 2	Any 1	None
A	27.47	62.64	87.76	12.24	33.73	66.94	88.25	11.75
A+32	75.36	92.32	97.08	2.92	78.19	92.47	96.83	3.17
B	96.70	99.67	99.94	0.06	96.96	99.72	99.90	0.10
C	97.95	99.86	99.96	0.04	97.84	99.83	99.97	0.03
D	88.59	97.44	99.08	0.92	88.82	97.76	99.44	0.56
E	89.10	96.90	98.93	1.07	87.94	96.44	98.88	1.12
F	92.35	97.66	98.88	1.12	91.33	97.37	98.95	1.05
G	96.37	99.50	99.92	0.08	95.60	99.43	99.93	0.07
H	93.99	99.00	99.72	0.28	93.31	98.84	99.66	0.34
I	92.53	98.47	99.57	0.43	93.11	98.58	99.59	0.41
J	18.18	36.08	59.67	40.33	17.38	35.49	57.87	42.13

A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan

(B) Crease Maximum Limit Ignored

Finger Position

	RT	RI	RM	RR	RL	LT	LI	LM	LR	LL
A	40.77	70.16	63.23	48.60	45.70	54.99	58.24	66.31	69.60	72.52
A+32	81.33	95.04	89.61	85.79	85.05	85.70	93.67	90.57	90.40	91.69
B	98.30	99.49	99.25	98.87	98.89	98.48	99.22	99.23	98.84	99.11
C	96.81	99.75	99.58	99.22	99.48	97.45	99.65	99.50	99.17	99.50
D	85.72	98.03	97.95	97.14	96.67	85.26	97.53	98.02	97.88	96.82
E	98.08	97.21	97.25	97.90	98.13	98.06	97.05	96.62	97.51	97.49
F	97.28	96.99	96.88	97.59	98.14	97.37	96.88	96.21	97.40	97.60
G	95.22	99.11	98.78	98.32	98.50	95.36	98.58	98.36	98.48	98.40
H	77.20	98.36	97.81	97.85	96.37	84.06	97.78	97.44	97.78	95.04
I	92.42	98.52	98.41	98.26	95.55	87.34	98.82	98.20	98.30	96.48
J	85.72	91.84	94.46	91.36	87.25	86.13	87.73	92.59	90.22	87.20

	Thumb			Index			Middle			Ring			Little		
	Both	Either	None	Both	Either	None	Both	Either	None	Both	Either	None	Both	Either	None
A	28.38	67.38	32.62	41.65	86.76	13.24	43.11	86.43	13.57	35.28	82.93	17.07	34.35	83.87	16.13
A+32	75.65	91.37	8.63	89.40	99.32	0.68	82.09	98.09	1.91	78.57	97.62	2.38	78.94	97.79	2.21
B	97.10	99.67	0.33	98.75	99.96	0.04	98.55	99.93	0.07	97.84	99.87	0.13	98.06	99.93	0.07
C	94.91	99.35	0.65	99.41	99.99	0.01	99.11	99.97	0.03	98.49	99.90	0.10	99.00	99.98	0.02
D	78.85	92.13	7.87	95.67	99.89	0.11	96.15	99.82	0.18	95.24	99.77	0.23	93.81	99.68	0.32
E	96.52	99.62	0.38	94.56	99.70	0.30	94.25	99.62	0.38	95.73	99.69	0.31	95.87	99.75	0.25
F	95.22	99.43	0.57	94.26	99.61	0.39	93.49	99.61	0.39	95.27	99.72	0.28	95.98	99.76	0.24
G	92.59	97.99	2.01	97.74	99.94	0.06	97.27	99.87	0.13	96.93	99.87	0.13	96.98	99.92	0.08
H	73.38	87.87	12.13	96.31	99.84	0.16	95.64	99.61	0.39	95.94	99.69	0.31	91.93	99.48	0.52
I	82.11	97.65	2.35	97.44	99.90	0.10	96.80	99.82	0.18	96.74	99.82	0.18	92.55	99.47	0.53
J	79.32	92.52	7.48	81.83	97.74	2.26	88.19	98.86	1.14	83.75	97.83	2.17	77.79	96.66	3.34

	Right Hand (w/Thumbs)						Left Hand (w/Thumbs)					
	All 5	Any 4	Any 3	Any 2	Any 1	None	All 5	Any 4	Any 3	Any 2	Any 1	None
A	7.33	29.19	56.87	80.52	94.56	5.44	17.00	46.90	71.83	88.62	97.32	2.68
A+32	57.90	86.20	95.04	98.03	99.64	0.36	67.11	90.31	96.41	98.48	99.73	0.27
B	95.36	99.62	99.86	99.96	100.00	0.00	95.55	99.54	99.85	99.95	100.00	0.00
C	95.26	99.67	99.94	99.97	100.00	0.00	95.67	99.69	99.93	99.97	100.00	0.00
D	79.80	97.37	98.94	99.45	99.95	0.05	78.90	97.53	99.30	99.82	99.98	0.02
E	92.23	97.90	98.96	99.51	99.98	0.02	90.93	97.47	98.85	99.50	99.99	0.01
F	91.14	97.65	98.74	99.38	99.98	0.02	90.06	97.29	98.75	99.38	99.99	0.01
G	91.07	99.15	99.78	99.93	100.00	0.00	90.40	99.01	99.83	99.95	99.99	0.01
H	71.87	96.80	99.24	99.74	99.94	0.06	76.57	96.89	99.12	99.61	99.93	0.07
I	85.61	98.26	99.54	99.81	99.94	0.06	81.64	98.17	99.56	99.82	99.95	0.05
J	64.91	90.22	96.90	98.81	99.79	0.21	63.22	88.76	95.24	97.04	99.61	0.39

	Right Hand					Left Hand				
	All 4	Any 3	Any 2	Any 1	None	All 4	Any 3	Any 2	Any 1	None
A	17.11	45.59	73.45	91.65	8.35	29.84	60.42	82.01	94.41	5.59
A+32	69.85	90.32	96.58	98.63	1.37	77.37	92.63	97.20	98.79	1.21
B	96.93	99.70	99.86	99.96	0.04	96.88	99.62	99.86	99.95	0.05
C	98.25	99.84	99.96	99.98	0.02	98.02	99.82	99.94	99.97	0.03
D	92.85	98.25	99.11	99.50	0.50	92.32	98.45	99.45	99.86	0.14
E	93.89	98.00	98.95	99.52	0.48	92.42	97.61	98.90	99.49	0.51
F	93.51	97.77	98.77	99.41	0.59	92.18	97.48	98.79	99.38	0.62
G	95.47	99.37	99.86	99.96	0.04	94.68	99.24	99.86	99.97	0.03
H	92.15	98.69	99.60	99.82	0.18	90.28	98.43	99.44	99.70	0.30
I	92.31	98.93	99.64	99.84	0.16	93.10	98.97	99.66	99.88	0.12
J	74.72	92.78	97.71	99.18	0.82	72.68	91.26	95.87	97.32	2.68

A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan

(B) Crease Maximum Limit Ignored

Person

	All 10	Any 9	Any 8	Any 7	Any 6	Any 5	Any 4	Any 3	Any 2	Any 1	None
A	2.07	9.16	22.57	40.56	59.65	75.80	87.62	94.67	98.34	99.70	0.30
A+32	44.53	70.65	86.17	93.16	96.69	98.55	99.42	99.76	99.93	99.99	0.01
B	91.81	98.50	99.57	99.88	99.95	99.98	99.99	100.00	100.00	100.00	0.00
C	91.97	98.58	99.72	99.90	99.96	99.99	100.00	100.00	100.00	100.00	0.00
D	68.43	87.39	96.96	98.82	99.63	99.86	99.96	99.99	100.00	100.00	0.00
E	84.88	94.84	97.49	98.81	99.66	99.81	99.89	99.94	100.00	100.00	0.00
F	83.23	94.28	97.12	98.56	99.61	99.78	99.86	99.94	100.00	100.00	0.00
G	84.42	95.89	99.25	99.73	99.89	99.95	99.98	100.00	100.00	100.00	0.00
H	63.40	82.87	96.00	98.47	99.45	99.73	99.89	99.93	99.98	99.99	0.01
I	71.85	93.30	98.29	99.36	99.73	99.89	99.94	99.97	99.99	100.00	0.00
J	47.20	73.00	87.20	93.21	96.71	98.36	99.28	99.68	99.89	99.96	0.04

	Right Thumb/Index			Left Thumb/Index		
	Both	Either	None	Both	Either	None
A	29.22	81.72	18.28	32.67	80.56	19.44
A+32	77.74	98.63	1.37	80.55	98.82	1.18
B	97.82	99.97	0.03	97.75	99.95	0.05
C	96.61	99.95	0.05	97.16	99.94	0.06
D	84.06	99.68	0.32	83.16	99.63	0.37
E	95.36	99.93	0.07	95.20	99.91	0.09
F	94.38	99.89	0.11	94.38	99.88	0.12
G	94.42	99.91	0.09	94.04	99.90	0.10
H	76.22	99.34	0.66	82.43	99.41	0.59
I	91.18	99.75	0.25	86.42	99.75	0.25
J	79.19	98.37	1.63	75.71	98.14	1.86

	Right Thumb/Index/Middle				Left Thumb/Index/Middle			
	All 3	Any 2	Any 1	None	All 3	Any 2	Any 1	None
A	20.47	63.16	90.53	9.47	24.75	64.00	90.79	9.21
A+32	71.59	95.04	99.35	0.65	74.87	95.65	99.43	0.57
B	97.19	99.86	99.99	0.01	97.14	99.82	99.98	0.02
C	96.27	99.88	99.99	0.01	96.73	99.88	99.98	0.02
D	83.15	98.66	99.89	0.11	81.99	98.92	99.91	0.09
E	94.08	98.50	99.95	0.05	93.46	98.31	99.96	0.04
F	92.96	98.26	99.93	0.07	92.38	98.14	99.94	0.06
G	93.47	99.67	99.96	0.04	92.67	99.66	99.97	0.03
H	75.09	98.47	99.80	0.20	80.92	98.54	99.82	0.18
I	90.16	99.29	99.91	0.09	85.21	99.27	99.89	0.11
J	76.13	96.39	99.50	0.50	72.74	94.36	99.35	0.65

	Right Index/Middle/Ring				Left Index/Middle/Ring			
	All 3	Any 2	Any 1	None	All 3	Any 2	Any 1	None
A	29.01	64.25	88.73	11.27	35.64	68.95	89.57	10.43
A+32	78.31	94.11	98.03	1.97	81.87	94.69	98.09	1.91
B	97.88	99.77	99.95	0.05	97.64	99.75	99.91	0.09
C	98.70	99.89	99.96	0.04	98.47	99.87	99.97	0.03
D	95.20	98.68	99.24	0.76	94.79	99.00	99.64	0.36
E	95.02	98.23	99.12	0.88	94.05	97.99	99.15	0.85
F	94.57	97.98	98.91	1.09	93.64	97.85	99.01	0.99
G	96.76	99.52	99.93	0.07	96.00	99.48	99.93	0.07
H	95.16	99.12	99.73	0.27	94.40	98.95	99.66	0.34
I	96.13	99.33	99.74	0.26	96.20	99.33	99.79	0.21
J	82.53	96.14	99.00	1.01	79.43	94.18	96.93	3.07

A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan

(C) Crease Ignored

Finger Position

	RT	RI	RM	RR	RL	LT	LI	LM	LR	LL
A	54.69	85.39	77.50	64.25	60.79	70.44	70.60	77.27	84.21	81.96
A+32	92.07	97.94	97.10	95.97	93.48	92.81	96.40	95.86	95.57	92.99
B	99.43	99.60	99.60	99.57	99.23	99.36	99.38	99.63	99.64	99.31
C	99.13	99.86	99.91	99.86	99.66	99.20	99.77	99.84	99.86	99.63
D	94.19	98.11	98.26	97.48	96.76	93.09	97.63	98.41	98.23	96.90
E	99.09	97.30	97.63	98.29	98.16	98.85	97.14	97.03	97.90	97.54
F	99.03	97.12	97.38	98.01	98.22	98.71	97.03	96.76	97.73	97.69
G	97.39	99.52	99.64	99.11	98.79	97.19	98.96	99.54	99.52	98.77
H	79.40	98.96	98.86	98.84	96.78	86.52	98.38	98.89	99.09	95.61
I	94.07	98.68	99.33	98.84	95.66	88.75	99.02	99.40	99.06	96.61
J	93.75	92.78	95.37	92.04	88.17	94.85	88.39	93.63	90.98	88.77

	Thumb			Index			Middle			Ring			Little		
	Both	Either	None	Both	Either	None	Both	Either	None	Both	Either	None	Both	Either	None
A	43.85	81.28	18.72	60.64	95.36	4.64	60.48	94.28	5.72	54.82	93.64	6.36	50.90	91.84	8.16
A+32	89.26	95.62	4.38	94.59	99.75	0.25	93.33	99.64	0.36	91.98	99.57	0.43	87.82	98.65	1.35
B	98.94	99.86	0.14	99.02	99.97	0.03	99.25	99.99	0.01	99.24	99.98	0.02	98.57	99.97	0.03
C	98.54	99.79	0.21	99.63	0.00	0.00	99.75	0.00	0.00	99.73	99.99	0.01	99.30	99.99	0.01
D	90.34	96.94	3.06	95.84	99.90	0.10	96.80	99.86	0.14	95.91	99.80	0.20	93.94	99.72	0.28
E	98.16	99.78	0.22	94.72	99.71	0.29	94.96	99.70	0.30	96.41	99.77	0.23	95.95	99.75	0.25
F	98.05	99.69	0.31	94.51	99.64	0.36	94.45	99.68	0.32	95.98	99.76	0.24	96.15	99.77	0.23
G	96.17	98.41	1.59	98.49	99.99	0.01	99.19	99.99	0.01	98.65	99.97	0.03	97.60	99.96	0.04
H	77.00	88.92	11.08	97.43	99.91	0.09	97.85	99.89	0.11	98.03	99.91	0.09	92.80	99.59	0.41
I	84.26	98.56	1.44	97.79	99.91	0.09	98.77	99.96	0.04	97.97	99.93	0.07	92.78	99.48	0.52
J	90.27	98.33	1.67	83.21	97.96	2.04	89.81	99.19	0.81	84.99	98.03	1.97	79.90	97.03	2.97

	Right Hand (w/Thumbs)						Left Hand (w/Thumbs)					
	All 5	Any 4	Any 3	Any 2	Any 1	None	All 5	Any 4	Any 3	Any 2	Any 1	None
A	18.57	52.88	79.29	93.24	98.63	1.37	34.87	69.09	86.40	95.03	99.09	0.91
A+32	82.34	96.40	98.64	99.28	99.89	0.11	81.37	95.43	98.06	98.90	99.87	0.13
B	97.79	99.80	99.88	99.97	100.00	0.00	97.75	99.76	99.87	99.95	100.00	0.00
C	98.54	99.93	99.98	99.99	100.00	0.00	98.48	99.89	99.95	99.98	100.00	0.00
D	88.21	98.04	99.08	99.50	99.96	0.04	86.80	98.22	99.42	99.84	99.98	0.02
E	93.90	98.08	98.98	99.52	99.99	0.01	92.42	97.66	98.88	99.50	100.00	0.00
F	93.73	97.86	98.79	99.41	99.98	0.02	92.24	97.52	98.77	99.39	99.99	0.01
G	94.93	99.64	99.91	99.97	100.00	0.00	94.47	99.61	99.92	99.97	100.00	0.00
H	75.40	98.08	99.61	99.79	99.96	0.04	81.08	98.29	99.49	99.69	99.94	0.06
I	88.39	98.74	99.68	99.84	99.94	0.06	84.62	98.77	99.64	99.84	99.96	0.04
J	72.94	92.55	97.64	99.08	99.90	0.10	72.27	91.28	95.93	97.31	99.84	0.16

	Right Hand					Left Hand				
	All 4	Any 3	Any 2	Any 1	None	All 4	Any 3	Any 2	Any 1	None
A	33.67	67.99	88.75	97.24	2.76	48.25	77.74	90.82	97.11	2.89
A+32	88.73	97.35	98.90	99.39	0.61	86.97	96.29	98.27	98.99	1.01
B	98.29	99.81	99.88	99.97	0.03	98.32	99.76	99.87	99.95	0.05
C	99.34	99.95	99.98	99.99	0.01	99.20	99.91	99.94	99.97	0.03
D	93.52	98.36	99.13	99.50	0.50	93.07	98.59	99.47	99.86	0.14
E	94.65	98.09	98.96	99.52	0.48	93.22	97.72	98.90	99.49	0.51
F	94.51	97.88	98.78	99.41	0.59	93.17	97.58	98.80	99.38	0.62
G	97.37	99.72	99.93	99.98	0.02	97.10	99.67	99.92	99.99	0.01
H	94.51	99.26	99.70	99.83	0.17	93.28	99.18	99.60	99.72	0.28
I	93.72	99.18	99.72	99.86	0.14	95.05	99.31	99.70	99.89	0.11
J	77.08	93.56	97.92	99.25	0.75	75.45	92.18	96.13	97.42	2.58

A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan

(C) Crease Ignored

Person

	All 10	Any 9	Any 8	Any 7	Any 6	Any 5	Any 4	Any 3	Any 2	Any 1	None
A	8.51	27.02	49.71	69.84	83.92	92.37	96.98	99.01	99.77	99.96	0.04
A+32	71.45	87.95	95.18	97.43	98.94	99.54	99.83	99.92	99.97	99.99	0.01
B	95.89	99.31	99.71	99.91	99.98	99.99	100.00	100.00	100.00	100.00	0.00
C	97.29	99.61	99.90	99.95	99.98	100.00	100.00	100.00	100.00	100.00	0.00
D	79.41	93.08	97.93	99.07	99.73	99.90	99.97	99.99	100.00	100.00	0.00
E	87.58	95.47	97.66	98.87	99.71	99.82	99.89	99.95	100.00	100.00	0.00
F	87.31	95.14	97.37	98.62	99.66	99.79	99.87	99.94	100.00	100.00	0.00
G	91.27	97.61	99.69	99.92	99.97	99.99	100.00	100.00	100.00	100.00	0.00
H	69.09	85.90	97.71	99.23	99.70	99.86	99.94	99.95	99.99	100.00	0.00
I	76.06	95.33	98.88	99.56	99.78	99.91	99.95	99.97	99.99	100.00	0.00
J	57.06	80.75	90.54	94.70	97.57	98.85	99.51	99.81	99.94	100.00	0.00

	Right Thumb/Index			Left Thumb/Index		
	Both	Either	None	Both	Either	None
A	47.10	92.98	7.02	50.33	90.72	9.28
A+32	90.39	99.61	0.39	89.61	99.60	0.40
B	99.05	99.98	0.02	98.77	99.98	0.02
C	99.01	99.98	0.02	99.00	99.98	0.02
D	92.43	99.87	0.13	90.92	99.79	0.21
E	96.43	99.96	0.04	96.06	99.93	0.07
F	96.18	99.97	0.03	95.84	99.90	0.10
G	96.95	99.96	0.04	96.19	99.95	0.05
H	78.71	99.65	0.35	85.24	99.66	0.34
I	92.93	99.82	0.18	87.98	99.79	0.21
J	87.25	99.27	0.73	84.01	99.23	0.77

	Right Thumb/Index/Middle				Left Thumb/Index/Middle			
	All 3	Any 2	Any 1	None	All 3	Any 2	Any 1	None
A	37.90	82.55	97.13	2.87	42.17	79.85	96.29	3.71
A+32	88.70	98.59	99.82	0.18	87.13	98.13	99.81	0.19
B	98.72	99.92	100.00	0.00	98.51	99.89	99.99	0.01
C	98.95	99.96	100.00	0.00	98.87	99.95	99.99	0.01
D	91.65	98.96	99.95	0.05	89.93	99.26	99.94	0.06
E	95.48	98.57	99.97	0.03	94.65	98.39	99.98	0.02
F	95.21	98.34	99.98	0.02	94.29	98.25	99.95	0.05
G	96.69	99.87	99.99	0.01	95.82	99.88	99.99	0.01
H	78.14	99.20	99.89	0.11	84.65	99.24	99.91	0.09
I	92.64	99.52	99.93	0.07	87.69	99.57	99.91	0.09
J	84.33	97.78	99.78	0.22	81.50	95.64	99.73	0.27

	Right Index/Middle/Ring				Left Index/Middle/Ring			
	All 3	Any 2	Any 1	None	All 3	Any 2	Any 1	None
A	48.54	82.54	96.05	3.95	53.69	83.38	95.01	4.99
A+32	93.27	98.44	99.30	0.70	91.14	97.81	98.88	1.12
B	98.96	99.86	99.96	0.04	98.91	99.84	99.91	0.09
C	99.69	99.96	99.98	0.02	99.55	99.95	99.97	0.03
D	95.85	98.76	99.24	0.76	95.53	99.09	99.64	0.36
E	95.77	98.32	99.13	0.87	94.83	98.09	99.15	0.85
F	95.52	98.08	98.92	1.08	94.56	97.94	99.02	0.98
G	98.48	99.83	99.97	0.03	98.19	99.85	99.97	0.03
H	97.34	99.54	99.77	0.23	97.16	99.48	99.72	0.28
I	97.51	99.55	99.80	0.20	98.06	99.61	99.82	0.18
J	84.41	96.67	99.10	0.90	81.27	94.68	97.05	2.95

A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan

Appendix B. Result tables for 2-inch slap images.

This appendix shows successful segmentation rates for the 2-inch slap images by finger position, hand, and various combinations of fingers that may be of interest to different fingerprint matching applications.

The first table shows successful segmentation percentages for each finger position.

The second table combines the right and left hand for each finger position and shows results for getting both the right and left finger, either or none.

The third table looks at the results by right and left hand. Columns show segmentation rates for correctly segmenting all 5 finger positions, any 4, any 3, down to none.

The fourth table is shows results for all ten fingers by combining right and left hands.

The last two tables show results for finger position combinations of index/middle and index/middle/ring.

All seven tables are then repeated (B) for the case where the maximum limited of the bottom (which is the bottom left and right y-positions) is ignored and then repeated (C) again ignoring the bottom (crease) completely. This was done as previous work had shown the crease is usually the most difficult edge for the segmentation algorithm to detect. The results in these tables show algorithm J definitely had difficulty detecting the crease and many other algorithms show significant increases in successfully segmenting “All 5” finger positions on a hand when the crease is ignored. Again, this is not a surprise as detecting the correct crease is a known difficulty for segmentation algorithms.

L/R -32/+64, T -64/+64, B -64/+128, Angle -/+5°

Finger Position

	RI	RM	RR	RL	LI	LM	LR	LL
A	54.75	53.70	46.18	42.36	51.74	48.91	49.65	47.81
A+32	86.61	82.75	83.86	89.21	86.99	81.61	84.94	90.76
B	95.88	96.33	96.93	97.95	96.41	95.90	96.39	97.37
C	97.42	97.67	97.98	98.87	98.53	97.85	97.97	98.73
E	97.57	97.90	97.97	98.60	97.73	97.11	96.94	98.31
F	97.25	97.93	98.26	98.76	98.28	97.55	97.54	98.84
G	95.95	96.25	96.44	97.02	97.28	95.44	95.87	96.23
H	94.49	92.20	96.00	95.95	95.39	94.60	94.30	93.33
I	95.17	95.49	95.78	97.41	95.67	95.03	95.13	97.43
J	61.99	46.08	53.49	71.75	56.93	45.92	54.81	68.36

	Index			Middle			Ring			Little		
	Both	Either	None	Both	Either	None	Both	Either	None	Both	Either	None
A	29.39	75.24	24.76	27.31	74.70	25.30	24.29	71.52	28.48	20.96	68.24	31.76
A+32	74.59	97.06	2.94	68.04	94.33	5.67	71.26	95.35	4.65	76.87	97.35	2.65
B	92.94	99.70	0.30	92.73	99.53	0.47	94.02	99.63	0.37	95.36	99.82	0.18
C	96.06	99.89	0.11	95.47	99.81	0.19	96.44	99.86	0.14	97.67	99.89	0.11
E	95.16	99.75	0.25	94.95	99.70	0.30	95.12	99.73	0.27	96.57	99.77	0.23
F	95.77	99.87	0.13	95.48	99.84	0.16	96.15	99.87	0.13	97.57	99.98	0.02
G	93.42	99.72	0.28	91.97	99.30	0.70	92.82	99.42	0.58	93.00	99.52	0.48
H	89.88	99.09	0.91	87.90	98.54	1.46	91.11	98.88	1.12	89.34	98.82	1.18
I	91.08	99.49	0.51	90.80	99.28	0.72	91.41	99.49	0.51	94.78	99.79	0.21
J	39.23	77.89	22.11	26.83	64.91	35.09	35.48	72.65	27.35	51.39	88.57	11.43

	Right Hand					Left Hand				
	All 4	Any 3	Any 2	Any 1	None	All 4	Any 3	Any 2	Any 1	None
A	18.63	40.34	60.00	78.02	21.98	19.30	41.46	59.98	77.37	22.63
A+32	64.09	86.20	94.41	97.74	2.26	66.06	86.35	94.13	97.77	2.23
B	91.05	97.70	98.88	99.46	0.54	90.31	97.54	98.80	99.43	0.57
C	94.01	98.76	99.45	99.73	0.27	94.67	99.01	99.57	99.81	0.19
E	92.98	99.31	99.80	99.95	0.05	91.71	98.80	99.70	99.88	0.12
F	93.12	99.36	99.79	99.92	0.08	93.34	99.18	99.80	99.89	0.11
G	89.62	97.48	98.99	99.57	0.43	90.03	96.94	98.58	99.27	0.73
H	83.12	96.85	99.09	99.59	0.41	83.78	96.16	98.52	99.16	0.84
I	89.19	97.03	98.48	99.15	0.85	88.58	96.92	98.53	99.24	0.76
J	24.96	49.96	71.08	87.31	12.69	21.76	46.95	69.50	87.81	12.19

A = Aware || B/C = Cogent || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan

L/R -32/+64, T -64/+64, B -64/+128, Angle -/+5°

	Person								
	All 8	Any 7	Any 6	Any 5	Any 4	Any 3	Any 2	Any 1	None
A	4.86	13.54	25.01	39.39	57.06	73.05	84.81	93.94	6.06
A+32	43.79	68.15	81.47	89.33	95.18	97.93	99.25	99.76	0.24
B	83.43	94.89	97.35	98.53	99.67	99.91	99.96	99.98	0.02
C	89.57	97.36	98.82	99.47	99.92	99.98	99.98	99.99	0.01
E	85.12	96.81	99.15	99.74	99.94	100.00	100.00	100.00	0.00
F	87.30	97.97	99.48	99.80	99.98	100.00	100.00	100.00	0.00
G	81.56	93.47	96.85	98.31	99.44	99.73	99.88	99.94	0.06
H	70.97	90.67	96.15	97.93	98.98	99.46	99.62	99.77	0.23
I	79.50	92.98	96.39	98.00	99.58	99.84	99.90	99.94	0.06
J	8.60	22.37	37.59	52.58	68.04	80.35	91.07	96.37	3.63

	Right Index/Middle			Left Index/Middle		
	Both	Either	None	Both	Either	None
A	38.35	70.10	29.90	33.94	66.72	33.28
A+32	75.11	94.25	5.75	75.33	93.27	6.73
B	93.60	98.60	1.40	93.67	98.63	1.37
C	95.72	99.37	0.63	96.85	99.52	0.48
E	95.69	99.77	0.23	95.26	99.58	0.42
F	95.44	99.74	0.26	96.13	99.70	0.30
G	93.12	99.09	0.91	94.00	98.71	1.29
H	88.06	98.63	1.37	91.49	98.51	1.49
I	92.31	98.35	1.65	92.30	98.39	1.61
J	36.86	71.21	28.79	35.86	66.99	33.01

	Right Index/Middle/Ring				Left Index/Middle/Ring			
	All 3	Any 2	Any 1	None	All 3	Any 2	Any 1	None
A	26.61	53.01	75.01	24.99	25.65	51.29	73.37	26.63
A+32	67.96	88.91	96.35	3.65	69.56	88.41	95.57	4.43
B	92.05	97.98	99.11	0.89	91.72	97.89	99.09	0.91
C	94.53	98.95	99.58	0.42	95.48	99.18	99.68	0.32
E	94.11	99.45	99.88	0.12	92.92	99.07	99.80	0.20
F	94.09	99.49	99.87	0.13	94.17	99.33	99.86	0.14
G	91.15	98.08	99.42	0.58	91.83	97.64	99.12	0.88
H	85.57	97.73	99.39	0.61	87.94	97.37	98.98	1.02
I	90.14	97.53	98.76	1.24	89.52	97.39	98.91	1.09
J	28.86	54.84	77.86	22.14	28.80	53.16	75.70	24.30

(B) Ignore Crease

Finger Position

	RI	RM	RR	RL	LI	LM	LR	LL
A	70.63	69.35	65.19	55.36	63.80	57.49	60.08	53.38
A+32	92.78	89.90	92.47	95.52	92.42	87.29	91.12	94.11
B	96.52	96.87	97.67	98.41	97.26	97.15	97.63	97.79
C	97.71	98.02	98.49	99.08	98.84	98.67	98.94	98.95
E	98.52	98.61	98.84	99.43	99.09	98.77	98.62	99.27
F	98.20	98.62	98.90	99.37	98.98	98.87	98.69	99.29
G	96.90	97.27	97.44	97.55	97.98	96.84	97.31	96.94
H	95.77	93.00	97.21	97.20	96.47	95.90	96.27	95.49
I	96.57	96.98	97.23	97.85	96.98	97.24	97.44	97.79
J	78.59	69.47	78.31	81.87	81.98	76.71	80.52	83.07

	Index			Middle			Ring			Little		
	Both	Either	None	Both	Either	None	Both	Either	None	Both	Either	None
A	44.82	87.03	12.97	40.53	85.69	14.31	39.09	85.13	14.87	30.18	76.91	23.09
A+32	84.35	98.86	1.14	78.05	96.97	3.03	82.46	98.27	1.73	84.73	98.56	1.44
B	94.36	99.80	0.20	94.51	99.66	0.34	95.79	99.83	0.17	96.29	99.87	0.13
C	96.65	99.90	0.10	96.76	99.86	0.14	97.73	99.94	0.06	98.19	99.92	0.08
E	97.77	99.97	0.03	97.49	99.90	0.10	97.76	99.91	0.09	98.79	99.99	0.01
F	97.31	99.97	0.03	97.61	99.95	0.05	97.94	99.94	0.06	98.73	99.99	0.01
G	94.86	99.80	0.20	94.27	99.56	0.44	95.04	99.64	0.36	94.20	99.61	0.39
H	92.25	99.30	0.70	89.73	98.86	1.14	94.17	99.19	0.81	92.60	99.19	0.81
I	93.65	99.72	0.28	94.60	99.74	0.26	95.03	99.78	0.22	95.73	99.85	0.15
J	67.27	93.84	6.16	57.16	90.00	10.00	67.29	92.68	7.32	71.19	94.01	5.99

	Right Hand					Left Hand				
	All 4	Any 3	Any 2	Any 1	None	All 4	Any 3	Any 2	Any 1	None
A	35.86	59.96	76.16	88.54	11.46	28.15	51.64	69.31	85.66	14.34
A+32	80.71	93.44	97.49	99.02	0.98	78.14	91.73	96.45	98.62	1.38
B	93.14	97.93	98.94	99.47	0.53	93.56	97.96	98.88	99.43	0.57
C	95.22	98.88	99.47	99.73	0.27	96.67	99.29	99.62	99.82	0.18
E	96.04	99.58	99.82	99.95	0.05	96.47	99.57	99.82	99.90	0.10
F	95.78	99.57	99.81	99.92	0.08	96.55	99.55	99.84	99.90	0.10
G	92.48	98.00	99.10	99.58	0.42	93.32	97.66	98.77	99.32	0.68
H	86.68	97.63	99.24	99.63	0.37	88.91	97.22	98.76	99.24	0.76
I	93.18	97.62	98.64	99.20	0.80	93.58	97.84	98.75	99.29	0.71
J	56.44	76.14	84.77	90.90	9.10	64.24	79.60	86.79	91.65	8.35

(B) Ignore Crease

	Person								
	All 8	Any 7	Any 6	Any 5	Any 4	Any 3	Any 2	Any 1	None
A	11.38	25.78	41.47	58.12	74.98	86.43	93.49	97.73	2.27
A+32	61.66	80.57	89.35	94.22	97.77	99.09	99.67	99.92	0.08
B	88.38	95.77	97.64	98.66	99.77	99.94	99.98	99.98	0.02
C	92.60	97.93	98.99	99.53	99.93	99.98	99.98	100.00	0.00
E	93.12	98.99	99.62	99.88	99.98	100.00	100.00	100.00	0.00
F	92.93	98.99	99.69	99.86	99.98	100.00	100.00	100.00	0.00
G	86.77	95.03	97.41	98.58	99.59	99.77	99.90	99.94	0.06
H	78.31	93.33	97.13	98.38	99.14	99.54	99.68	99.78	0.22
I	87.66	95.30	97.27	98.33	99.79	99.88	99.92	99.94	0.06
J	41.98	61.33	72.27	80.23	89.66	93.76	96.37	97.84	2.16

	Right Index/Middle			Left Index/Middle		
	Both	Either	None	Both	Either	None
A	57.08	82.89	17.11	43.93	77.36	22.64
A+32	85.55	97.13	2.87	83.74	95.98	4.02
B	94.73	98.66	1.34	95.62	98.79	1.21
C	96.34	99.39	0.61	97.92	99.59	0.41
E	97.28	99.85	0.15	98.06	99.80	0.20
F	97.01	99.81	0.19	98.07	99.79	0.21
G	94.92	99.25	0.75	95.88	98.94	1.06
H	89.93	98.84	1.16	93.63	98.73	1.27
I	94.95	98.60	1.40	95.47	98.75	1.25
J	62.89	85.17	14.83	71.58	87.11	12.89

	Right Index/Middle/Ring				Left Index/Middle/Ring			
	All 3	Any 2	Any 1	None	All 3	Any 2	Any 1	None
A	47.22	71.25	86.70	13.30	35.68	62.46	83.24	16.76
A+32	82.26	94.53	98.36	1.64	80.45	92.96	97.43	2.57
B	93.78	98.14	99.14	0.86	94.66	98.23	99.15	0.85
C	95.59	99.03	99.60	0.40	97.32	99.40	99.73	0.27
E	96.43	99.65	99.89	0.11	96.96	99.64	99.88	0.12
F	96.20	99.65	99.88	0.12	97.03	99.63	99.89	0.11
G	93.64	98.49	99.49	0.51	94.69	98.24	99.21	0.79
H	88.28	98.23	99.46	0.54	91.47	98.03	99.13	0.87
I	93.90	98.01	98.88	1.13	94.36	98.25	99.05	0.95
J	58.91	79.03	88.44	11.56	67.31	82.40	89.50	10.50

Appendix C. Detailed segmentation statistics.

The tables is this appendix show distribution statistics, by finger position, for the segmentation algorithms tested as compared to the hand marked ground truth for 3-inch slap images. The differences between the segmentation algorithm and ground truth are sorted into bins based on the tolerances allowed for correct segmentation. Specifically, the left/right edges must be within -32/+64 pixels of the ground truth, top edge -64/+64 and bottom edge -64/+128. For each finger position there is a column for each of the four segmentation box edges (L, R, T and B).

The first row (“No Finger Found”) shows the counts for when a finger was not detected by the segmentation algorithm. The next four rows show statistics for segmentation edges that are within the specified minimum (MN) and maximum (MX) pixel tolerances compared to the ground truth, so these are considered good segmentations. Rows 1 (MN <= d < 0) and 3 (0 <= d <= MX) show the average value for all differences in that range and rows 3 and 5 show the total count occurring in that range.

Rows 6-9 also show average difference values and bin counts but for ranges MN-32 <= d < MN and MX < d <= MX+32, which are just outside the accepted tolerance ranges. Rows 10-13 tally everything greater than 32 pixels away from the accepted tolerance range, d < MN-32 and d > MX+32.

The last three rows show the total count for each bin, the overall average difference value and the standard deviation of all the difference values.

A

No Finger Found	R. Thumb 89				R. Index 121				R Middle 76				R. Ring 101				R. Little 638			
	L	R	T	B	L	R	T	B	L	R	T	B	L	R	T	B	L	R	T	B
MN <= d < 0	-11.51	-22.67	-18.73	-39.86	-13.91	-19.45	-24.28	-44.11	-13.44	-21.10	-24.59	-42.53	-10.87	-22.12	-24.91	-43.57	-11.08	-21.52	-25.01	-42.61
#	17025	13116	21205	13835	21015	21047	23131	19172	19954	18639	22768	17533	18472	15578	22580	16069	18688	14855	22335	15711
0 <= d <= MX	6.89	17.68	7.81	44.54	8.18	8.81	9.97	37.99	8.91	11.52	10.55	45.39	7.67	13.60	11.92	42.42	6.00	15.44	9.66	36.70
#	5859	543	1942	1821	3195	686	1501	636	4234	1069	1836	1761	6012	657	1912	1463	4943	547	1374	1115
MN-32 <= d < MN	-38.17	-40.47	-77.62	-76.81	-37.47	-37.47	-73.54	-73.72	-36.90	-38.41	-77.98	-74.94	-38.79	-39.80	-74.05	-75.30	-40.46	-39.94	-79.73	-76.00
#	333	9284	113	4530	532	2998	25	3766	518	4945	25	3022	150	8224	38	4017	206	8229	97	4439
MX < d <= MX+32	80.98	80.79	77.80	143.34	78.66	78.00	77.63	142.43	74.74	78.45	76.89	143.89	74.84	78.19	78.82	140.11	80.15	81.16	75.13	143.39
#	32	54	23	131	29	8	19	43	25	19	46	97	19	24	53	57	13	34	19	84
d < MN-32	-322.82	-375.06	-244.13	-316.03	-246.71	-334.77	-730.13	-229.76	-253.14	-375.12	-596.86	-166.86	-199.63	-385.92	-764.44	-166.12	-179.11	-842.34	-414.09	-346.09
#	623	998	162	3897	21	209	130	876	33	271	215	2018	43	456	134	2934	60	1247	218	3076
d > MX+32	498.17	228.12	656.17	228.17	232.55	313.20	354.11	381.85	373.69	336.04	191.88	381.68	500.08	317.00	226.24	417.18	858.83	239.20	627.75	319.92
#	550	427	977	208	176	20	162	475	204	25	78	537	272	29	251	428	1058	56	925	543
Total #	24422	24422	24422	24422	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968
Average	-3.80	-38.33	8.71	-81.22	-9.94	-23.18	-23.41	-44.57	-7.20	-26.54	-26.13	-40.45	-1.27	-33.15	-23.38	-49.72	28.56	-67.05	-2.45	-73.88
Std Dev	101.52	107.18	142.20	173.12	25.87	36.93	64.65	89.41	40.47	49.76	67.46	90.71	62.67	75.05	66.67	93.59	199.33	225.63	136.72	180.26

No Finger Found	L. Thumb 35				L. Index 210				L. Middle 125				L. Ring 180				L. Little 797			
	L	R	T	B	L	R	T	B	L	R	T	B	L	R	T	B	L	R	T	B
MN <= d < 0	-13.81	-21.15	-20.82	-37.44	-10.87	-21.17	-23.92	-44.39	-12.62	-20.08	-23.62	-41.19	-14.29	-18.56	-23.34	-42.94	-14.19	-18.37	-23.17	-41.07
#	18516	17439	21738	14492	18579	17324	23127	18849	18931	18557	22626	17823	19576	20539	22553	17431	19423	20569	22038	19496
0 <= d <= MX	10.01	12.63	8.68	46.43	7.42	13.14	9.97	44.71	9.67	10.83	10.65	45.67	10.08	9.24	10.45	50.26	10.07	7.66	7.57	45.64
#	3843	379	1482	2769	5897	497	1368	578	5340	1043	1849	2321	4294	1014	1812	2039	3660	549	1494	732
MN-32 <= d < MN	-39.15	-38.27	-77.90	-76.62	-37.75	-39.93	-76.25	-73.72	-36.24	-39.48	-74.52	-74.38	-36.91	-38.76	-79.65	-74.56	-37.10	-39.07	-81.54	-73.49
#	822	5377	102	3914	141	6592	28	3888	297	4885	42	2509	573	2848	26	3082	679	2591	106	2525
MX < d <= MX+32	78.47	78.78	78.40	141.88	74.42	80.25	77.13	143.39	76.73	77.90	78.89	143.29	77.17	82.33	80.17	143.77	78.82	82.80	77.45	143.89
#	73	29	25	168	18	28	12	54	41	15	35	133	62	3	53	93	193	10	11	119
d < MN-32	-414.71	-342.05	-308.29	-362.26	-277.95	-659.29	-665.22	-283.60	-303.80	-509.01	-546.62	-185.65	-302.54	-438.95	-659.31	-211.22	-298.58	-319.44	-403.33	-738.66
#	634	718	135	2848	74	452	151	973	183	288	299	1514	224	334	177	1669	286	959	229	1383
d > MX+32	240.43	471.85	630.53	285.71	924.08	314.15	358.18	357.72	633.35	305.10	208.81	398.44	417.20	293.07	241.25	375.72	187.62	321.35	664.44	296.07
#	534	480	940	231	255	71	278	622	172	176	113	664	235	226	343	650	723	286	1086	709
Total #	24422	24422	24422	24422	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964
Average	-15.49	-24.02	4.32	-67.80	2.12	-35.93	-21.70	-45.79	-5.67	-25.87	-26.23	-32.53	-8.92	-22.52	-21.60	-38.89	-7.95	-27.58	4.89	-70.00
Std Dev	87.47	101.21	137.39	169.03	102.33	121.09	70.77	103.68	64.66	78.35	73.88	102.18	54.69	69.34	70.02	104.89	50.12	74.66	152.59	203.03

B

	R. Thumb				R. Index				R Middle				R. Ring				R. Little			
No Finger Found	3				3				22				7				35			
	L	R	T	B	L	R	T	B	L	R	T	B	L	R	T	B	L	R	T	B
MN <= d < 0	-6.58	-7.54	-5.27	-17.34	-5.52	-6.42	-6.58	-12.57	-5.19	-6.36	-6.30	-18.40	-5.18	-7.80	-6.52	-19.45	-5.68	-7.27	-7.83	-15.24
#	73	300	3983	5260	1448	1280	12371	1102	1375	1595	11723	1534	629	2732	11201	1827	1912	5426	11084	2614
0 <= d <= MX	30.30	24.49	12.82	38.66	15.05	16.57	8.34	39.07	16.22	16.30	9.40	45.03	18.11	14.76	9.13	45.90	13.44	11.21	8.87	33.01
#	24273	24042	20384	18769	23489	23609	12557	23739	23554	23280	13211	23198	24292	22146	13722	22785	22964	19398	13825	22159
MN-32 <= d < MN	-55.00	-42.91	-81.36	-76.79	-40.14	-38.17	-80.83	-77.56	-34.00	-38.22	-91.00	-77.35	-37.00	-36.70	-85.83	-76.72	-42.50	-38.43	-74.00	-77.78
#	3	11	11	205	7	6	6	16	1	9	3	67	1	46	6	145	8	90	8	72
MX < d <= MX+32	70.09	77.09	76.25	139.80	#DIV/0!	71.27	78.50	138.84	75.25	71.02	80.50	137.46	76.50	80.20	88.50	139.60	76.04	69.50	66.67	139.61
#	32	29	4	60	0	48	6	60	4	48	9	98	8	5	2	122	35	4	3	36
d < MN-32	-382.40	-839.57	-504.04	-204.12	-255.37	-216.25	-680.78	-196.92	-334.00	-811.44	-504.14	-383.98	-430.57	-662.00	-465.71	-167.78	-236.50	-922.91	-389.00	-561.03
#	26	15	34	81	19	2	18	24	15	18	7	41	14	20	17	51	6	44	2	66
d > MX+32	468.43	661.46	893.92	601.22	137.20	374.24	297.60	710.61	515.95	396.33	298.73	311.17	446.13	368.47	192.80	367.53	836.47	154.83	625.93	219.62
#	15	25	6	47	5	23	10	27	19	18	15	30	24	19	20	38	43	6	46	21
Total #	24422	24422	24422	24422	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968
Average	30.06	24.25	9.34	26.15	13.66	15.79	0.56	37.45	15.22	14.61	2.07	40.78	17.70	11.94	1.91	40.92	13.40	5.41	2.54	26.38
Std Dev	23.01	39.69	29.10	53.06	12.47	16.60	24.75	38.37	19.57	27.49	17.14	39.39	20.79	32.49	18.77	38.77	41.08	52.97	31.13	47.21

	L. Thumb				L. Index				L. Middle				L. Ring				L. Little			
No Finger Found	26				0				9				14				19			
	L	R	T	B	L	R	T	B	L	R	T	B	L	R	T	B	L	R	T	B
MN <= d < 0	-8.12	-5.40	-5.09	-16.44	-4.97	-8.57	-6.67	-12.66	-4.78	-7.12	-6.56	-18.11	-4.87	-7.25	-6.32	-19.02	-7.67	-7.30	-8.24	-14.70
#	171	129	5548	5718	1165	2424	12213	1124	1494	1831	11640	1685	1908	1176	10772	2458	4396	2468	10624	3077
0 <= d <= MX	27.60	26.08	11.76	37.55	16.41	15.28	8.34	40.22	16.23	16.83	9.50	45.50	15.16	18.39	10.24	42.80	12.30	14.34	9.85	30.95
#	24121	24226	18818	18335	23721	22439	12708	23726	23410	23069	13285	23048	23006	23709	14141	22203	20505	22351	14277	21719
MN-32 <= d < MN	-48.67	-46.13	-69.25	-77.79	-49.50	-37.15	-79.94	-77.09	-36.75	-36.25	-74.14	-77.53	-43.00	-40.07	-74.00	-76.67	-40.50	-38.65	-85.20	-73.98
#	12	8	4	147	2	65	8	35	4	16	7	83	2	14	3	158	15	46	5	41
MX < d <= MX+32	73.71	74.75	#DIV/0!	143.34	72.41	66.00	81.50	140.82	73.75	70.30	78.00	141.13	72.20	69.56	72.75	138.83	82.36	74.37	#DIV/0!	140.43
#	77	4	0	65	44	2	2	28	16	10	5	63	5	25	4	48	11	49	0	35
d < MN-32	-444.04	-410.14	-391.29	-410.10	-890.50	-270.05	-550.20	-196.09	-665.50	-507.33	-340.93	-249.59	-416.58	-586.86	-536.54	-264.03	-247.04	-268.45	-501.31	-625.92
#	13	43	26	96	13	20	15	23	7	30	22	29	13	29	23	64	13	30	31	39
d > MX+32	306.38	650.79	842.35	312.57	312.05	1080.54	238.33	574.41	428.82	924.81	204.60	381.76	386.37	620.77	301.19	484.80	182.65	341.58	684.04	462.80
#	28	12	26	61	19	14	18	28	33	8	5	56	30	11	21	33	24	20	27	53
Total #	24422	24422	24422	24422	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964
Average	27.53	25.44	8.37	23.43	15.26	13.20	0.81	38.17	15.36	14.72	1.73	41.45	13.86	16.77	2.84	35.94	8.81	12.14	2.23	25.19
Std Dev	19.75	29.46	34.67	57.72	26.00	31.14	20.21	34.89	23.16	29.40	17.22	39.52	20.73	29.88	24.73	44.42	14.27	20.01	33.64	47.75

C

	R. Thumb				R. Index				R Middle				R. Ring				R. Little			
No Finger Found	5				3				5				7				19			
	L	R	T	B	L	R	T	B	L	R	T	B	L	R	T	B	L	R	T	B
MN <= d < 0	-6.29	-8.12	-9.53	-19.31	-6.30	-6.26	-8.07	-12.10	-5.05	-6.49	-8.18	-15.80	-4.56	-8.27	-7.41	-15.63	-5.39	-6.46	-9.17	-12.85
#	1555	2809	7521	12352	866	568	13852	1543	662	655	14584	2069	303	1409	13778	1834	713	2867	11784	1784
0 <= d <= MX	21.08	17.86	12.50	26.05	13.91	17.65	10.33	31.92	15.31	17.10	11.50	35.85	18.23	16.51	11.40	36.02	14.26	13.76	10.73	30.57
#	22825	21453	16825	11414	24081	24378	11096	23340	24294	24298	10372	22733	24647	23533	11176	22876	24234	22050	13145	23077
MN-32 <= d < MN	-55.00	-42.12	-78.34	-76.48	-44.00	-41.43	-68.00	-73.00	-36.00	-43.33	-74.33	-76.04	-35.50	-39.00	-77.80	-77.84	-42.43	-39.71	-70.80	-76.78
#	5	86	29	460	8	7	1	20	1	3	3	67	2	11	5	123	7	31	20	37
MX < d <= MX+32	78.75	74.33	66.00	142.04	70.50	77.33	77.25	139.77	74.25	76.25	#DIV/0!	139.81	77.20	77.00	78.00	140.88	75.67	80.19	74.00	141.92
#	4	21	1	23	2	3	4	32	4	4	0	52	5	4	2	73	3	8	1	19
d < MN-32	-373.85	-426.61	-421.94	-177.86	-285.44	-225.50	-584.40	-131.00	-437.00	-806.50	-280.50	-188.92	-590.40	-761.00	-411.50	-137.83	-412.13	-1489.31	-360.93	-439.52
#	26	31	40	140	9	1	15	8	6	1	7	19	5	3	6	41	4	8	7	22
d > MX+32	600.29	689.64	1063.50	706.88	160.00	473.50	#DIV/0!	634.82	555.50	508.43	333.75	270.29	429.17	518.00	358.50	306.24	932.07	428.13	555.41	270.22
#	7	22	6	33	2	11	0	25	1	7	2	28	6	8	1	21	7	4	11	29
Total #	24422	24422	24422	24422	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968
Average	19.08	14.75	5.16	1.04	13.10	17.29	-0.23	29.80	14.69	16.59	-0.06	31.58	17.94	15.17	0.92	31.92	13.88	10.98	1.41	27.26
Std Dev	22.51	39.78	30.96	52.46	10.38	13.88	20.99	32.45	11.93	13.80	13.94	28.75	14.38	17.77	14.12	29.73	20.83	37.11	20.30	31.12

	L. Thumb				L. Index				L. Middle				L. Ring				L. Little			
No Finger Found	23				0				0				7				16			
	L	R	T	B	L	R	T	B	L	R	T	B	L	R	T	B	L	R	T	B
MN <= d < 0	-7.18	-5.71	-8.83	-19.02	-4.70	-8.88	-8.04	-11.92	-4.06	-6.91	-8.43	-16.12	-4.33	-7.64	-7.14	-15.86	-8.42	-7.96	-9.59	-12.80
#	3399	562	8569	12199	435	1484	13617	1565	591	858	14364	2321	724	608	13279	2565	2621	968	11203	2135
0 <= d <= MX	16.97	22.09	12.35	25.74	16.17	17.25	10.33	31.64	15.52	18.60	11.33	35.15	15.37	19.87	12.57	32.68	13.78	17.86	11.36	28.81
#	20873	23798	15781	11695	24504	23440	11329	23330	24347	24080	10577	22454	24218	24327	11663	22148	22297	23950	13709	22704
MN-32 <= d < MN	-43.96	-44.31	-75.56	-77.19	-37.00	-36.46	-82.88	-75.96	-39.33	-40.25	-76.00	-76.63	#DIV/0!	-42.71	-70.00	-78.65	-39.00	-39.11	-69.82	-74.79
#	67	16	27	332	1	28	8	25	3	4	8	64	0	7	2	136	20	22	19	28
MX < d <= MX+32	74.79	82.00	67.00	141.84	71.50	#DIV/0!	#DIV/0!	140.86	77.14	70.17	80.50	139.02	69.13	74.40	76.00	139.73	81.44	79.00	65.00	143.16
#	39	3	1	31	10	0	0	14	7	6	2	64	8	5	1	51	9	2	1	35
d < MN-32	-268.90	-448.90	-384.94	-309.73	-961.04	#DIV/0!	-430.20	-125.29	-605.22	-395.50	-585.35	-113.70	-415.00	-701.22	-522.08	-197.12	-171.90	-370.42	-473.69	-562.39
#	24	34	24	132	12	0	10	7	9	6	13	20	5	9	12	42	5	12	18	23
d > MX+32	338.03	804.06	929.33	414.48	115.00	1234.79	#DIV/0!	517.24	385.29	848.80	#DIV/0!	431.52	602.11	496.94	365.29	502.73	197.00	307.40	557.14	409.56
#	20	9	20	33	2	12	0	23	7	10	0	41	9	8	7	22	12	10	14	39
Total #	24422	24422	24422	24422	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964
Average	13.52	21.05	5.19	0.84	15.36	16.22	0.10	29.26	14.95	17.95	-0.37	30.90	14.95	19.08	1.93	27.33	11.48	16.74	1.85	25.34
Std Dev	21.08	28.64	34.20	55.21	23.95	29.53	16.18	27.63	16.43	20.57	19.37	34.52	15.99	19.69	19.20	34.87	12.22	15.04	25.10	37.15

D

No Finger Found	R. Thumb 54				R. Index 225				R Middle 18				R. Ring 10				R. Little 338			
	L	R	T	B	L	R	T	B	L	R	T	B	L	R	T	B	L	R	T	B
MN <= d < 0	-10.86	-11.01	-12.47	-22.89	-9.54	-6.10	-15.37	-7.97	-10.55	-6.94	-16.12	-8.73	-7.90	-8.26	-15.81	-8.85	-9.19	-7.01	-14.90	-7.86
#	19487	17757	17661	10815	20731	11835	20445	7373	20924	15032	20228	7437	19328	15741	20167	6366	20942	10845	19001	4655
0 <= d <= MX	5.09	8.08	5.94	18.42	5.10	5.79	7.15	15.34	5.24	5.33	7.06	19.21	4.50	6.23	7.01	20.22	4.05	6.83	6.88	17.40
#	4234	5984	6015	10793	3879	12834	4214	16830	3744	9608	4514	16476	5401	8766	4516	17516	3471	13472	5410	19416
MN-32 <= d < MN	-38.94	-41.34	-78.32	-77.24	-39.24	-40.26	-76.63	-78.70	-36.83	-38.72	-76.88	-76.55	-37.96	-39.35	-73.80	-77.35	-38.68	-38.34	-72.66	-76.65
#	225	475	120	1482	84	34	15	20	62	60	20	63	25	265	20	86	77	166	45	17
MX < d <= MX+32	76.19	76.29	72.90	142.52	81.36	80.00	80.48	143.64	79.91	83.31	76.41	142.57	80.17	80.25	78.58	143.01	82.63	74.88	83.11	143.22
#	26	33	5	112	28	13	25	277	16	26	11	477	12	22	57	516	4	20	22	134
d < MN-32	-197.91	-413.62	-349.33	-204.39	-214.11	-541.14	-632.00	-798.28	-330.43	-334.91	-248.22	-337.10	-453.23	-340.72	-329.17	-182.13	-407.18	-1170.65	-415.78	-963.39
#	399	122	551	1037	9	226	20	239	14	192	185	35	15	147	35	154	17	443	25	451
d > MX+32	527.32	314.16	714.88	260.27	273.40	243.96	389.23	236.25	299.45	227.40	200.30	220.46	298.41	391.07	173.09	209.92	955.37	414.77	688.97	229.42
#	51	51	70	183	237	26	249	229	208	50	10	480	187	27	173	330	457	22	465	295
Total #	24422	24422	24422	24422	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968
Average	-10.19	-8.13	-13.76	-12.75	-4.65	-4.57	-7.97	4.05	-5.79	-4.25	-13.57	16.37	-3.18	-4.95	-10.65	16.27	9.95	-19.96	2.51	-1.91
Std Dev	39.38	47.47	71.37	81.85	29.81	53.68	48.42	89.98	31.45	35.65	26.89	46.99	32.29	36.70	24.70	44.67	141.62	170.71	100.86	144.07

No Finger Found	L. Thumb 35				L. Index 106				L. Middle 19				L. Ring 43				L. Little 435			
	L	R	T	B	L	R	T	B	L	R	T	B	L	R	T	B	L	R	T	B
MN <= d < 0	-12.54	-9.53	-13.94	-22.51	-9.53	-7.74	-15.59	-8.65	-10.71	-7.41	-16.10	-9.99	-11.08	-6.53	-15.82	-9.64	-9.54	-6.74	-15.19	-8.21
#	19570	16968	19165	11764	19697	11707	20004	7106	20337	12767	19814	7497	20102	9317	18620	7945	17591	8387	17189	5652
0 <= d <= MX	8.64	5.80	7.25	18.78	4.44	6.12	6.15	14.66	4.38	5.66	5.68	18.97	5.75	6.29	6.31	18.63	6.21	6.49	6.38	15.28
#	3589	6505	4697	10033	5075	12768	4743	17286	4418	11903	4998	16472	4666	15400	6099	16021	6896	15981	7200	18342
MN-32 <= d < MN	-40.70	-39.80	-77.82	-77.10	-40.56	-40.07	-75.65	-75.82	-39.36	-38.13	-76.00	-76.53	-38.73	-38.34	-78.63	-78.28	-40.32	-39.45	-72.33	-75.32
#	540	165	104	1441	32	315	17	19	36	125	25	70	66	88	8	91	74	109	56	11
MX < d <= MX+32	75.61	77.90	78.22	142.58	79.33	78.87	78.88	142.40	79.32	79.70	73.83	142.29	80.90	82.74	77.46	142.56	77.56	82.44	82.65	143.99
#	33	30	43	128	12	30	29	206	22	23	15	466	20	21	45	488	82	9	17	145
d < MN-32	-548.76	-276.42	-318.98	-190.05	-523.58	-1164.50	-399.56	-713.25	-318.44	-577.07	-288.91	-320.52	-322.53	-590.30	-369.87	-337.25	-316.48	-377.37	-334.62	-1133.87
#	651	171	337	920	13	116	39	128	81	46	94	54	30	64	41	125	21	437	26	465
d > MX+32	461.78	597.55	511.84	259.98	826.33	367.57	374.32	242.15	366.52	324.62	209.64	219.56	378.18	279.49	206.07	216.29	185.32	255.67	770.19	218.38
#	39	583	76	136	135	28	132	219	70	100	18	405	80	74	151	294	300	41	476	349
Total #	24422	24422	24422	24422	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964
Average	-23.47	7.08	-12.55	-12.64	-2.43	-5.91	-9.93	7.27	-7.94	-0.97	-12.61	14.83	-7.06	0.69	-9.50	12.25	-2.91	-4.44	5.61	-7.90
Std Dev	98.14	103.26	56.14	71.67	69.97	86.41	37.54	65.68	32.51	40.01	23.94	48.05	28.27	38.11	28.34	52.49	26.32	53.32	112.40	163.59

E

No Finger Found	R. Thumb 15				R. Index 63				R Middle 30				R. Ring 21				R. Little 77			
	L	R	T	B	L	R	T	B	L	R	T	B	L	R	T	B	L	R	T	B
MN <= d < 0	-4.31	-5.44	-10.48	-12.86	-4.55	-6.16	-10.12	-11.19	-2.68	-6.59	-10.35	-12.65	-3.15	-7.74	-10.54	-11.75	-4.44	-4.50	-10.61	-11.81
#	508	450	15905	6242	780	185	16537	691	819	222	15757	1157	356	658	15161	891	511	1062	14814	235
0 <= d <= MX	18.97	20.31	5.62	22.99	22.98	28.02	10.88	35.88	23.27	26.02	11.55	35.31	23.76	24.47	11.68	36.91	20.98	20.87	11.50	44.15
#	23883	23803	8441	17021	23813	24257	8296	23602	23702	24338	9130	22881	24371	23942	9728	23067	24192	23556	9913	23936
MN-32 <= d < MN	-45.00	-43.50	-78.42	-77.31	-44.88	-40.90	-74.94	-74.63	-49.00	-35.50	-74.80	-78.80	-48.50	-37.50	-67.00	-76.75	-46.36	-44.50	-72.46	-72.33
#	2	13	33	149	4	5	9	16	2	2	5	79	3	1	6	64	32	2	24	6
MX < d <= MX+32	69.83	74.25	#DIV/0!	143.76	73.70	75.24	68.33	144.71	74.30	75.72	75.17	143.30	76.04	75.82	85.00	144.32	74.16	75.06	77.50	142.17
#	3	110	0	349	274	399	3	160	347	281	9	268	156	262	3	368	81	166	1	113
d < MN-32	-435.97	-640.64	-291.91	-220.50	-302.92	-437.45	-771.69	-729.27	-444.00	-533.21	-506.05	-350.57	-195.18	-540.65	-784.56	-257.37	-87.11	-880.75	-410.97	-759.55
#	17	14	34	108	6	57	61	62	4	49	46	45	11	47	25	63	23	118	118	96
d > MX+32	589.17	390.59	788.17	219.11	176.73	160.23	373.44	285.56	296.27	142.57	186.45	235.08	417.15	153.87	221.18	223.98	790.09	136.00	596.32	270.89
#	9	32	9	553	91	65	62	437	94	76	21	538	71	58	45	515	129	64	98	582
Total #	24422	24422	24422	24422	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968
Average	18.38	20.15	-5.10	18.30	23.15	27.79	-4.07	37.68	24.08	25.54	-3.07	37.49	24.72	23.40	-2.24	39.58	24.42	16.18	-1.40	46.23
Std Dev	20.25	30.18	23.96	55.57	18.36	28.39	45.65	62.89	26.05	31.96	29.60	48.24	29.45	34.36	30.76	46.44	64.90	75.33	50.80	70.13

No Finger Found	L. Thumb 12				L. Index 58				L. Middle 18				L. Ring 21				L. Little 70			
	L	R	T	B	L	R	T	B	L	R	T	B	L	R	T	B	L	R	T	B
MN <= d < 0	-2.68	-6.59	-10.35	-12.65	-2.90	-8.46	-10.18	-9.90	-2.26	-7.06	-10.50	-12.84	-2.49	-8.27	-10.39	-10.55	-7.82	-8.77	-10.88	-11.40
#	819	222	15757	1157	568	648	16181	658	852	335	15211	1272	1022	235	14177	1241	2308	358	13711	369
0 <= d <= MX	23.27	26.02	11.55	35.31	23.66	27.73	11.41	35.57	22.63	28.57	11.63	34.00	22.06	29.10	12.34	33.94	20.66	27.20	11.99	41.04
#	23702	24338	9130	22881	23947	23825	8654	23586	23793	23968	9689	22675	23579	24373	10712	22663	22210	24293	11002	23590
MN-32 <= d < MN	-49.00	-35.50	-74.80	-78.80	-33.50	-36.36	-75.15	-81.36	-33.50	-42.83	-70.50	-76.76	#DIV/0!	-50.00	-80.83	-76.44	-36.83	-47.13	-71.70	-78.25
#	2	2	5	79	1	7	10	21	1	3	6	80	0	8	3	50	3	34	33	8
MX < d <= MX+32	74.30	75.72	75.17	143.30	74.98	74.33	73.67	143.00	75.67	74.78	73.94	144.03	74.85	73.59	82.67	144.28	74.75	74.67	#DIV/0!	143.50
#	347	281	9	268	339	382	6	162	234	540	9	311	272	270	3	408	260	150	0	122
d < MN-32	-444.00	-533.21	-506.05	-350.57	-481.10	-1280.12	-698.51	-701.03	-338.55	-795.10	-617.13	-295.81	-281.98	-547.52	-737.25	-271.04	-305.05	-320.05	-440.40	-834.96
#	4	49	46	45	5	53	57	55	21	20	39	36	22	22	36	70	33	78	137	85
d > MX+32	296.27	142.57	186.45	235.08	606.40	171.80	352.35	267.87	285.77	193.97	232.10	233.10	213.26	246.42	293.71	232.46	160.41	350.51	641.55	270.99
#	94	76	21	538	104	49	56	482	63	98	10	590	69	56	33	532	150	51	81	790
Total #	24968	24968	24968	24968	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964
Average	24.08	25.54	-3.07	37.49	26.07	24.99	-3.46	37.84	22.64	29.07	-2.74	36.86	21.89	29.19	-1.28	36.69	18.99	26.44	-1.12	45.02
Std Dev	26.05	31.96	29.60	48.24	52.47	64.86	40.41	57.95	26.72	34.21	31.29	49.18	21.25	26.26	34.78	50.79	22.68	29.49	53.26	75.34

F

	R. Thumb				R. Index				R Middle				R. Ring				R. Little			
No Finger Found	9				102				58				41				91			
	L	R	T	B	L	R	T	B	L	R	T	B	L	R	T	B	L	R	T	B
MN <= d < 0	-4.32	-5.55	-9.82	-15.60	-4.57	-6.29	-9.73	-10.64	-2.81	-6.30	-9.95	-11.92	-3.40	-7.35	-10.08	-11.92	-4.35	-4.67	-10.20	-12.00
#	367	263	13876	7318	770	192	15863	1124	797	221	15174	1949	282	719	14590	1543	451	1136	14268	688
0 <= d <= MX	20.67	22.66	7.57	23.63	23.04	28.28	11.20	31.31	23.41	26.21	11.81	29.54	23.96	24.53	11.97	31.60	21.18	20.71	11.73	35.77
#	24010	23949	10488	16163	23777	24196	8937	23392	23655	24297	9686	22595	24390	23843	10270	22930	24233	23507	10451	23829
MN-32 <= d < MN	-53.50	-49.00	-78.04	-77.25	-41.00	-44.17	-79.50	-74.62	#DIV/0!	-36.50	-71.70	-76.42	-51.50	-41.00	-70.83	-77.27	-49.12	-40.25	-76.11	-77.37
#	1	6	14	290	2	3	11	26	0	2	5	94	5	2	6	87	29	4	19	15
MX < d <= MX+32	72.64	73.58	75.75	143.56	74.70	75.84	74.64	142.71	74.85	75.05	74.23	140.83	74.18	76.16	75.72	143.59	73.67	74.82	65.50	142.90
#	14	154	6	181	291	417	7	145	371	286	15	108	182	277	9	186	87	130	1	53
d < MN-32	-692.11	-619.17	-377.64	-188.03	-255.63	-442.55	-723.63	-730.89	-360.50	-587.45	-364.11	-394.74	-261.08	-680.40	-591.28	-393.34	-154.03	-926.17	-416.39	-747.28
#	19	12	25	148	4	96	49	101	3	85	44	84	6	72	25	79	20	136	110	119
d > MX+32	435.68	514.20	592.65	235.70	191.60	142.38	358.45	350.90	331.27	129.29	194.66	266.05	482.54	148.55	245.63	265.53	821.56	156.59	585.22	318.55
#	11	38	13	322	124	64	101	180	142	77	44	138	103	55	68	143	148	55	119	264
Total #	24422	24422	24422	24422	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968
Average	19.96	23.11	-2.42	13.08	23.58	27.29	-2.16	29.18	25.04	24.71	-1.73	26.27	25.83	22.42	-0.88	29.37	25.42	14.97	-0.02	33.88
Std Dev	25.99	35.03	24.98	52.26	19.82	33.85	43.09	65.26	31.56	41.64	24.75	43.17	38.05	47.35	28.69	45.25	71.51	83.53	52.91	70.76

	L. Thumb				L. Index				L. Middle				L. Ring				L. Little			
No Finger Found	5				89				40				47				92			
	L	R	T	B	L	R	T	B	L	R	T	B	L	R	T	B	L	R	T	B
MN <= d < 0	-5.22	-3.99	-11.03	-15.99	-2.83	-8.63	-9.85	-9.90	-2.27	-7.26	-10.13	-11.96	-2.64	-7.61	-10.04	-11.26	-7.90	-8.74	-10.44	-11.16
#	380	167	15726	7299	509	666	15589	1183	797	339	14662	2285	989	237	13781	2272	2327	378	13367	1029
0 <= d <= MX	21.16	22.96	7.39	23.65	23.74	27.70	11.54	30.40	22.54	28.67	11.72	28.14	21.81	29.32	12.59	28.06	20.22	27.36	12.39	31.85
#	23757	24202	8637	16133	23984	23752	9224	23337	23814	23894	10212	22238	23588	24324	11080	22188	22244	24245	11323	23419
MN-32 <= d < MN	-46.07	-41.75	-77.88	-78.09	#DIV/0!	-39.38	-77.90	-78.12	-42.17	-46.50	-75.63	-77.57	#DIV/0!	-45.07	-74.25	-78.55	-43.25	-46.54	-70.35	-75.85
#	7	4	12	218	0	8	5	34	3	1	8	106	0	7	4	55	4	26	30	17
MX < d <= MX+32	74.87	77.37	71.63	143.46	74.30	74.48	72.79	141.93	75.26	74.40	83.27	141.87	75.25	73.96	82.75	142.33	74.98	74.85	68.83	141.55
#	229	23	16	226	323	403	7	132	233	574	13	119	273	288	4	190	199	155	3	51
d < MN-32	-459.63	-394.46	-383.80	-168.39	-813.75	-1322.07	-577.41	-737.39	-354.96	-927.09	-417.22	-352.88	-271.13	-665.54	-667.36	-426.76	-295.63	-324.52	-5121.60	-846.03
#	16	12	20	121	8	88	46	89	26	44	36	69	26	48	29	84	40	100	132	113
d > MX+32	188.48	840.64	565.05	225.24	734.78	279.22	359.31	318.11	415.31	204.98	215.11	275.20	308.08	258.39	276.55	271.75	164.60	346.78	643.60	317.92
#	33	14	11	425	140	47	93	189	91	112	33	147	88	60	66	175	150	60	109	335
Total #	24422	24422	24422	24422	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964
Average	21.15	23.08	-4.54	14.56	27.57	23.18	-1.61	28.38	23.27	28.33	-1.46	24.96	22.13	28.68	0.00	25.29	18.38	26.39	-24.32	30.09
Std Dev	19.85	25.08	22.28	50.34	68.31	85.63	37.63	60.31	36.43	48.27	24.98	41.41	26.72	37.25	32.80	49.00	23.01	32.36	3930.11	76.32

G

No Finger Found	R. Thumb 40				R. Index 14				R Middle 12				R. Ring 11				R. Little 26			
	L	R	T	B	L	R	T	B	L	R	T	B	L	R	T	B	L	R	T	B
MN <= d < 0	-7.07	-7.59	-11.52	-19.57	-6.54	-5.57	-15.80	-17.18	-7.26	-5.71	-15.88	-17.82	-5.33	-6.82	-15.73	-17.92	-6.43	-6.64	-16.85	-17.25
#	12096	12616	17457	14475	15629	7876	20638	11678	15179	9863	19934	8839	9667	11220	20074	10471	13164	11074	20111	14043
0 <= d <= MX	6.13	8.62	4.81	35.33	5.29	6.98	6.57	16.67	5.91	6.44	6.47	20.28	6.06	6.50	6.31	22.44	5.37	6.27	6.04	19.20
#	11914	11257	6741	8368	9269	17040	4293	13139	9749	15053	5001	15852	15268	13556	4854	14231	11722	13701	4736	10740
MN-32 <= d < MN	-39.94	-40.53	-79.98	-77.67	-38.57	-41.00	-73.93	-77.35	-38.13	-38.40	-73.92	-76.12	-39.33	-38.71	-73.09	-76.63	-40.49	-38.10	-74.89	-75.14
#	36	87	45	426	53	33	15	99	24	35	13	178	12	172	22	163	43	154	67	65
MX < d <= MX+32	70.50	76.53	77.65	144.35	#DIV/0!	#DIV/0!	#DIV/0!	143.93	#DIV/0!	72.50	#DIV/0!	140.11	69.50	86.00	#DIV/0!	140.62	80.00	82.14	#DIV/0!	144.17
#	2	66	23	328	0	0	0	15	0	2	0	27	2	1	0	34	1	7	0	18
d < MN-32	-280.06	-639.22	-353.47	-420.53	-287.55	-351.25	-527.42	-383.55	-340.50	-684.83	-303.96	-183.38	-436.90	-735.79	-304.93	-204.23	-279.41	-1081.20	-422.29	-577.61
#	36	350	48	325	11	8	13	20	7	9	13	49	5	12	7	49	17	20	34	31
d > MX+32	616.22	314.28	778.77	233.31	226.08	421.32	483.44	574.56	499.83	445.25	240.36	308.11	622.04	435.07	338.32	261.58	943.62	427.46	674.50	332.39
#	338	46	108	500	6	11	9	17	9	6	7	23	14	7	11	20	21	12	20	71
Total #	24422	24422	24422	24422	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968
Average	7.55	-8.45	-4.23	0.27	-2.28	3.02	-12.07	0.60	-2.06	1.44	-11.51	6.10	1.89	-0.03	-11.42	4.77	-0.33	-0.38	-12.66	-1.31
Std Dev	77.58	86.80	60.75	92.21	11.01	14.47	21.24	33.42	14.41	17.32	14.90	30.01	19.45	22.84	15.06	32.11	33.40	38.06	29.76	40.71

No Finger Found	L. Thumb 31				L. Index 12				L. Middle 13				L. Ring 8				L. Little 30			
	L	R	T	B	L	R	T	B	L	R	T	B	L	R	T	B	L	R	T	B
MN <= d < 0	-7.46	-6.74	-12.94	-19.02	-6.24	-7.30	-16.09	-17.25	-7.74	-6.68	-15.97	-18.38	-7.79	-6.20	-15.79	-18.70	-7.47	-7.19	-16.67	-18.21
#	13070	11703	18953	13174	13252	8533	20054	11636	15378	7484	19142	8999	14868	5185	18235	11293	13754	6722	18141	14167
0 <= d <= MX	9.84	6.64	4.41	34.18	6.23	6.92	5.92	16.41	5.72	7.61	5.52	18.89	6.10	8.54	6.01	18.76	6.35	7.71	5.62	17.32
#	10764	12306	5266	9423	11685	16194	4876	13200	9548	17396	5787	15605	10042	19700	6704	13349	11095	18077	6675	10555
MN-32 <= d < MN	-41.60	-43.49	-77.00	-76.29	-40.36	-39.04	-73.75	-75.35	-39.24	-36.69	-72.08	-76.34	-37.86	-37.73	-73.60	-78.38	-39.66	-40.30	-74.01	-75.18
#	62	49	74	324	14	226	20	85	17	65	12	246	36	60	10	207	58	119	72	87
MX < d <= MX+32	76.77	76.67	78.60	144.15	84.00	#DIV/0!	#DIV/0!	143.50	66.67	74.00	76.50	144.12	90.00	76.50	#DIV/0!	142.19	84.70	78.50	#DIV/0!	144.00
#	142	3	5	505	3	0	0	14	3	1	3	26	1	2	0	32	20	4	0	16
d < MN-32	-609.11	-447.46	-276.29	-367.31	-876.50	-697.81	-508.75	-297.53	-521.83	-874.41	-367.00	-197.61	-437.75	-576.33	-516.39	-178.47	-470.58	-273.77	-356.31	-626.18
#	317	53	61	232	2	8	8	18	6	11	14	52	10	6	9	60	6	33	48	42
d > MX+32	219.88	641.40	743.33	225.49	603.94	836.67	462.75	542.73	627.33	620.86	248.50	345.22	376.43	545.14	462.83	411.20	183.26	423.00	669.02	314.73
#	67	308	63	764	8	3	6	11	12	7	6	36	7	11	6	23	31	9	28	97
Total #	24422	24422	24422	24422	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964
Average	-6.61	7.16	-8.08	8.46	-0.29	1.52	-11.88	0.49	-2.42	3.00	-11.13	4.67	-2.31	5.46	-10.02	1.05	-1.20	3.26	-10.76	-3.01
Std Dev	74.74	79.28	47.54	84.45	16.92	20.36	17.62	29.21	19.51	24.83	16.08	32.69	14.57	18.00	18.17	33.89	14.53	17.79	31.60	44.17

H

No Finger Found	R. Thumb 4129				R. Index 44				R Middle 23				R. Ring 25				R. Little 331			
	L	R	T	B	L	R	T	B	L	R	T	B	L	R	T	B	L	R	T	B
MN <= d < 0	-6.85	-9.71	-12.28	-22.98	-4.32	-5.28	-8.59	-22.45	-5.53	-5.18	-8.65	-29.99	-4.04	-6.90	-8.03	-31.78	-4.24	-6.93	-7.79	-23.11
#	2677	5766	2924	1509	11959	1737	14338	539	13558	3947	13875	705	4492	6018	12800	458	2580	5981	6246	450
0 <= d <= MX	15.67	12.76	21.00	36.93	9.14	16.59	12.20	43.29	8.41	13.77	12.83	47.78	12.11	11.66	13.00	49.06	13.91	11.84	15.50	46.75
#	17541	13974	17049	17810	12839	23095	10479	24099	11222	20892	10986	23820	20372	18724	12056	23978	21861	18365	18218	23672
MN-32 <= d < MN	-42.24	-41.44	-77.29	-78.59	-39.21	-42.02	-75.93	-78.99	-38.01	-39.03	-74.56	-78.09	-39.18	-38.44	-75.95	-78.98	-42.50	-40.06	-79.29	-76.76
#	65	457	98	308	87	27	28	78	112	48	34	160	31	157	28	149	54	211	34	66
MX < d <= MX+32	#DIV/0!	74.10	67.95	142.04	77.67	75.75	73.25	136.17	#DIV/0!	82.00	77.17	142.19	88.00	#DIV/0!	77.75	142.42	78.00	76.38	69.30	142.12
#	0	10	11	141	6	4	4	24	0	2	9	85	2	0	4	104	1	34	10	65
d < MN-32	-137.11	-1397.95	-175.14	-1296.79	-294.76	-293.76	-420.48	-373.73	-327.85	-628.08	-300.00	-197.38	-322.09	-907.32	-317.70	-215.84	-136.71	-1341.71	-281.20	-858.37
#	18	4209	218	4498	61	50	23	185	53	24	38	142	45	25	64	133	58	362	128	376
d > MX+32	1034.46	259.67	881.06	224.07	201.25	377.99	436.97	426.63	429.13	346.15	193.27	339.56	683.87	342.44	351.63	267.85	1014.09	273.37	594.57	312.20
#	4121	6	4122	156	16	55	96	43	23	55	26	56	26	44	16	146	414	15	332	339
Total #	24422	24422	24422	24422	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968
Average	184.84	-236.60	160.06	-212.07	1.92	15.19	1.40	39.15	0.31	10.80	0.51	44.36	9.24	6.54	1.50	47.07	28.15	-12.47	15.75	35.39
Std Dev	384.70	537.44	332.79	540.17	18.88	25.52	35.75	53.59	22.88	28.98	20.81	36.49	29.18	36.47	25.34	39.84	140.50	169.68	76.32	125.24

No Finger Found	L. Thumb 251				L. Index 67				L. Middle 24				L. Ring 17				L. Little 494			
	L	R	T	B	L	R	T	B	L	R	T	B	L	R	T	B	L	R	T	B
MN <= d < 0	-9.27	-7.34	-12.43	-20.91	-2.95	-6.98	-8.37	-22.54	-4.78	-6.19	-8.89	-29.61	-4.56	-6.60	-7.82	-29.05	-5.84	-7.48	-8.23	-22.26
#	6436	2157	3651	2344	4611	5082	13715	489	8146	5734	13545	768	10527	1951	11817	491	10273	1280	5486	558
0 <= d <= MX	11.26	17.73	21.24	34.33	12.64	12.81	12.94	42.76	11.39	11.59	13.10	46.11	10.24	17.27	14.26	44.84	11.31	20.52	17.02	42.96
#	14954	19653	19455	20364	20175	19594	11045	24086	16669	19077	11294	23657	14286	22907	12996	23837	13922	22901	18643	23129
MN-32 <= d < MN	-42.64	-43.74	-77.33	-78.11	-40.95	-39.75	-75.02	-77.40	-37.91	-38.60	-77.24	-76.85	-37.41	-40.20	-75.39	-79.70	-40.47	-44.36	-78.59	-79.67
#	447	80	101	319	38	175	25	77	66	73	27	213	63	28	19	174	186	88	54	92
MX < d <= MX+32	76.71	#DIV/0!	79.08	143.48	86.50	87.50	77.06	140.94	77.58	81.00	84.13	140.74	83.50	94.00	#DIV/0!	143.77	77.85	78.83	64.83	144.19
#	42	0	401	235	1	2	9	25	6	2	8	54	9	1	0	100	124	3	3	68
d < MN-32	-849.22	-530.32	-223.72	-556.32	-103.32	-884.32	-255.77	-376.37	-422.00	-540.39	-319.73	-186.94	-292.47	-358.36	-316.60	-170.77	-156.46	-333.34	-293.13	-859.63
#	2348	277	132	919	31	110	37	234	14	66	63	187	17	65	116	172	56	606	288	571
d > MX+32	258.01	915.68	518.02	280.35	781.64	110.50	379.78	339.35	487.56	611.08	182.46	382.45	329.89	434.54	347.69	309.84	187.08	227.10	613.32	339.46
#	195	2255	682	241	108	1	133	53	63	12	27	85	62	12	16	190	403	86	490	546
Total #	24422	24422	24422	24422	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964
Average	-75.78	92.01	29.30	8.81	12.87	4.47	2.72	37.91	6.96	6.19	0.44	42.34	4.49	14.56	2.42	43.44	6.66	10.99	19.40	27.16
Std Dev	259.87	271.54	120.66	170.04	58.87	71.11	35.39	56.16	31.91	39.47	23.75	40.58	22.03	26.41	29.69	41.89	29.29	61.14	95.71	154.03

I

	R. Thumb				R. Index				R Middle				R. Ring				R. Little			
No Finger Found	27				127				12				18				50			
	L	R	T	B	L	R	T	B	L	R	T	B	L	R	T	B	L	R	T	B
MN <= d < 0	-9.79	-9.66	-16.49	-18.31	-8.48	-7.24	-12.63	-15.60	-6.47	-7.81	-12.35	-20.78	-7.23	-8.81	-13.32	-20.49	-10.01	-5.51	-15.66	-15.12
#	56	374	626	5931	381	345	259	1331	343	550	252	2088	122	1183	219	977	194	2095	145	976
0 <= d <= MX	37.35	32.14	28.94	27.65	18.23	20.67	23.04	27.67	17.22	18.74	23.13	31.84	20.05	18.63	23.69	33.97	20.45	16.66	35.22	31.33
#	24107	23572	22621	17538	24372	24368	24409	23102	24523	24302	24609	22167	24726	23549	24603	23184	23982	22333	23768	23004
MN-32 <= d < MN	-45.29	-44.95	-79.81	-78.07	-41.33	-44.20	-81.50	-76.88	-44.00	-40.33	-86.14	-79.16	-54.23	-37.36	-80.40	-81.94	-52.01	-42.87	-72.00	-73.07
#	21	57	27	319	3	10	4	26	6	6	7	159	13	22	5	95	146	15	1	15
MX < d <= MX+32	72.09	75.99	75.73	141.63	77.30	71.33	70.87	143.05	72.91	79.00	72.55	143.13	76.00	77.51	71.15	143.64	79.67	79.96	69.78	141.71
#	23	168	724	150	15	6	54	134	11	13	31	231	3	96	26	297	6	268	199	52
d < MN-32	-261.44	-393.20	-195.99	-524.44	-366.23	-350.05	-261.42	-670.17	-293.40	-359.36	-285.89	-245.10	-235.92	-678.32	-417.22	-270.95	-129.27	-645.86	-406.88	-679.02
#	96	85	53	367	53	184	12	246	59	29	14	129	72	33	81	97	522	122	793	72
d > MX+32	417.50	279.47	532.29	236.25	182.73	387.80	463.36	218.79	292.75	263.20	243.18	218.88	588.95	233.46	303.76	258.87	570.38	185.36	526.10	387.29
#	119	166	371	117	144	55	230	129	26	68	55	194	32	85	34	318	118	135	62	849
Total #	24422	24422	24422	24422	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968
Average	37.88	31.82	36.21	8.51	17.98	18.34	26.68	19.98	16.46	18.40	23.11	27.79	19.87	17.32	22.35	34.39	19.27	13.12	22.38	39.74
Std Dev	41.27	49.32	79.48	88.90	24.27	38.75	47.56	81.95	21.43	23.16	19.35	41.64	29.26	36.96	32.13	47.65	57.51	66.99	86.75	84.39

	L. Thumb				L. Index				L. Middle				L. Ring				L. Little			
No Finger Found	33				122				7				30				50			
	L	R	T	B	L	R	T	B	L	R	T	B	L	R	T	B	L	R	T	B
MN <= d < 0	-9.73	-8.45	-16.02	-17.89	-7.93	-9.23	-12.76	-14.78	-6.27	-8.00	-11.40	-20.68	-6.19	-9.48	-16.10	-18.33	-10.69	-10.69	-15.67	-14.38
#	270	93	557	5830	114	1093	249	1486	245	767	316	2316	315	356	131	1484	1645	444	165	1491
0 <= d <= MX	33.48	34.43	29.17	27.23	19.38	19.94	23.59	27.59	18.54	19.78	23.49	31.63	18.19	22.11	24.92	30.91	18.33	23.25	36.43	28.27
#	23479	24074	21527	17585	24641	23644	24501	22993	24601	24092	24566	21931	24439	24478	24700	22684	22807	23843	24014	22585
MN-32 <= d < MN	-47.64	-46.14	-75.67	-78.16	#DIV/0!	-43.23	-72.75	-80.28	-64.00	-46.21	-81.80	-78.47	-39.33	-48.47	-83.33	-79.97	-43.22	-50.10	-91.00	-74.26
#	36	14	12	300	0	13	8	36	1	14	5	206	3	17	3	115	16	152	1	19
MX < d <= MX+32	75.15	70.50	77.31	142.55	74.00	76.90	74.83	142.33	76.48	74.31	80.50	141.81	76.99	70.75	79.50	142.59	79.66	75.17	67.70	143.80
#	366	8	1570	209	7	10	12	118	29	16	8	189	80	4	5	256	254	18	46	44
d < MN-32	-185.72	-316.93	-274.12	-555.86	-319.48	-1170.40	-216.83	-690.67	-423.48	-449.59	-335.03	-216.36	-294.53	-363.18	-423.40	-289.46	-247.88	-134.17	-388.00	-803.35
#	63	123	34	373	49	151	9	201	27	50	32	138	19	90	84	127	73	424	683	68
d > MX+32	226.38	345.93	351.81	264.86	965.89	309.18	472.88	236.31	356.94	526.28	274.51	253.33	253.95	407.00	322.49	273.61	130.58	242.28	676.62	373.18
#	208	110	722	125	153	53	185	130	61	25	37	184	108	19	41	298	169	83	55	757
Total #	24422	24422	24422	24422	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964
Average	34.59	33.87	40.30	8.46	24.41	12.07	26.46	20.76	18.71	18.49	22.96	26.96	18.85	20.53	23.68	29.88	16.98	20.30	25.94	34.04
Std Dev	28.24	40.41	85.47	95.91	81.21	101.29	44.39	76.97	29.03	35.03	21.46	43.14	24.09	32.24	34.11	52.05	22.76	29.59	80.48	82.79

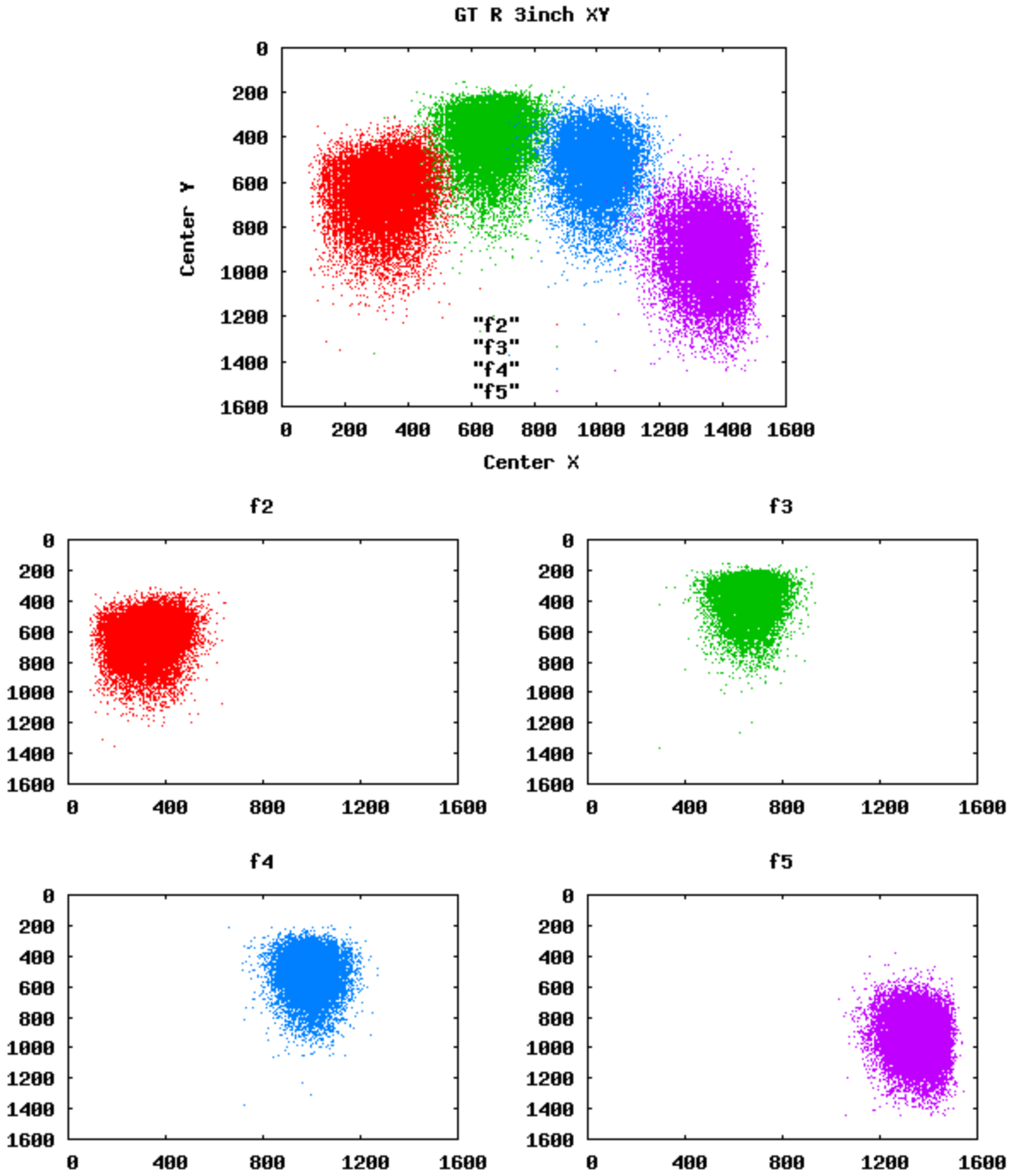
J

	R. Thumb				R. Index				R Middle				R. Ring				R. Little			
No Finger Found	75				3				13				57				760			
	L	R	T	B	L	R	T	B	L	R	T	B	L	R	T	B	L	R	T	B
MN <= d < 0	-13.04	-14.27	-19.34	-25.81	-13.03	-9.98	-24.86	-20.50	-12.88	-10.38	-23.98	-20.04	-10.51	-11.14	-23.77	-17.57	-11.78	-11.55	-23.80	-18.31
#	21888	19631	23619	10289	20800	19165	24008	6841	21255	19377	23838	4907	21321	16478	23816	4659	21536	16265	22798	11454
0 <= d <= MX	3.14	12.31	2.31	58.29	17.54	8.75	5.27	80.60	9.59	11.26	4.69	88.14	5.41	18.44	5.04	82.07	4.56	11.70	4.33	26.49
#	2043	3757	399	9787	3013	4717	651	2980	2962	4807	831	4974	2523	6953	779	4722	1431	6307	672	3139
MN-32 <= d < MN	-38.98	-40.48	-76.06	-71.01	-42.62	-44.48	-76.61	-77.05	-43.84	-40.43	-77.23	-78.60	-46.21	-41.42	-77.90	-79.67	-46.79	-40.65	-77.05	-76.32
#	360	735	178	2062	364	457	85	211	393	209	66	166	480	386	59	113	439	580	128	251
MX < d <= MX+32	#DIV/0!	76.38	#DIV/0!	142.73	79.42	79.12	87.00	144.90	76.00	79.27	79.07	144.21	79.13	77.56	87.31	144.49	79.43	79.25	73.00	146.32
#	0	84	0	1144	410	186	3	3535	31	213	7	4369	23	559	18	4187	7	411	3	782
d < MN-32	-199.55	-477.01	-160.51	-384.96	-130.09	-100.19	-603.05	-135.98	-252.30	-289.38	-572.61	-170.59	-148.29	-516.91	-567.07	-300.44	-103.05	-1146.37	-453.34	-874.29
#	70	181	142	381	100	185	120	104	205	92	222	108	415	190	188	152	550	1023	485	942
d > MX+32	827.30	211.07	892.57	186.95	124.78	341.16	205.33	206.88	281.99	293.32	218.63	208.81	425.64	187.78	179.43	208.50	1007.99	132.65	662.06	236.87
#	61	34	84	759	281	258	101	11297	122	270	4	10444	206	402	108	11135	1005	382	882	8400
Total #	24422	24422	24422	24422	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968	24968
Average	-10.51	-13.77	-17.09	12.98	-7.18	-3.45	-26.08	116.90	-11.11	-3.45	-27.98	124.94	-8.19	-2.03	-26.13	127.27	27.61	-49.15	-7.42	45.45
Std Dev	45.71	64.21	58.04	104.24	25.05	46.93	50.79	108.34	38.55	45.59	66.62	105.74	53.49	66.70	56.45	105.83	218.17	253.29	146.36	231.32

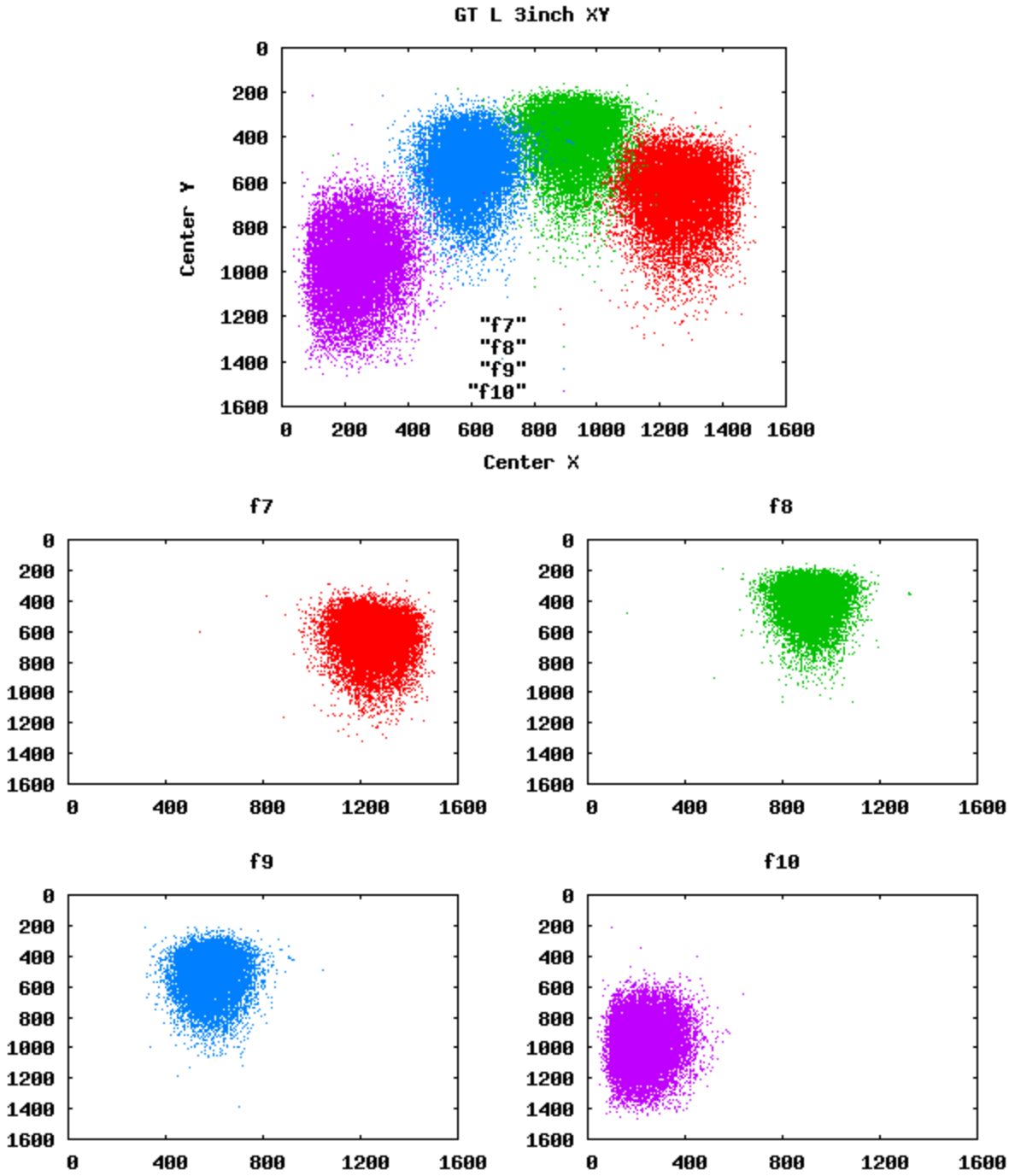
	L. Thumb				L. Index				L. Middle				L. Ring				L. Little			
No Finger Found	9				657				71				12				0			
	L	R	T	B	L	R	T	B	L	R	T	B	L	R	T	B	L	R	T	B
MN <= d < 0	-13.79	-12.93	-21.04	-27.17	-12.31	-10.13	-23.96	-20.31	-12.94	-9.47	-23.06	-20.44	-13.37	-8.38	-22.19	-20.14	-12.93	-8.97	-22.24	-20.57
#	19573	21510	23898	9142	19989	17032	23708	5656	19843	17622	23714	4468	17139	16697	23548	5099	18915	17322	23162	11537
0 <= d <= MX	16.30	3.13	2.48	59.71	12.11	11.96	2.41	86.17	13.38	6.98	3.16	89.03	22.05	4.10	8.84	86.59	16.65	3.54	1.77	34.88
#	4018	2453	257	10466	3109	5706	431	2926	3896	6127	482	5350	6101	6725	724	5246	4063	5641	452	2511
MN-32 <= d < MN	-40.25	-40.27	-77.98	-70.19	-46.89	-41.97	-75.70	-78.31	-41.52	-41.83	-74.27	-78.88	-40.43	-44.74	-76.71	-79.45	-43.01	-46.12	-76.12	-75.79
#	514	323	115	2212	508	643	60	135	162	354	44	185	112	554	28	156	307	646	161	407
MX < d <= MX+32	75.80	#DIV/0!	82.50	142.75	78.88	79.14	92.00	144.88	77.71	75.61	80.25	144.40	77.04	78.80	81.73	144.41	79.45	79.13	76.33	145.77
#	148	0	1	1379	233	501	2	3795	189	31	18	4596	605	15	121	4327	522	16	3	966
d < MN-32	-270.92	-225.14	-275.62	-237.00	-99.10	-1256.62	-580.19	-738.35	-332.49	-511.45	-344.19	-275.43	-325.08	-132.16	-584.25	-189.41	-297.45	-96.05	-447.64	-220.42
#	116	101	121	242	317	719	97	719	632	157	667	178	674	224	149	125	784	520	529	728
d > MX+32	178.33	784.73	772.67	205.21	924.43	129.03	379.73	205.78	320.12	348.77	173.03	215.71	144.39	360.06	149.23	205.65	127.93	374.00	452.73	234.77
#	53	35	30	981	808	363	666	11733	242	673	39	10187	333	749	394	10011	373	819	657	8815
Total #	24422	24422	24422	24422	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964	24964
Average	-9.66	-11.42	-21.34	23.01	20.10	-37.99	-15.01	102.55	-13.19	0.72	-30.84	127.48	-8.96	4.17	-21.50	120.14	-13.38	3.70	-18.66	74.88
Std Dev	32.87	37.90	40.25	87.40	180.79	221.32	78.93	179.46	70.20	81.42	65.47	112.13	62.14	69.71	57.99	101.54	59.04	74.45	103.77	137.21

Appendix D. Plots of 3-inch segmentation box centers.

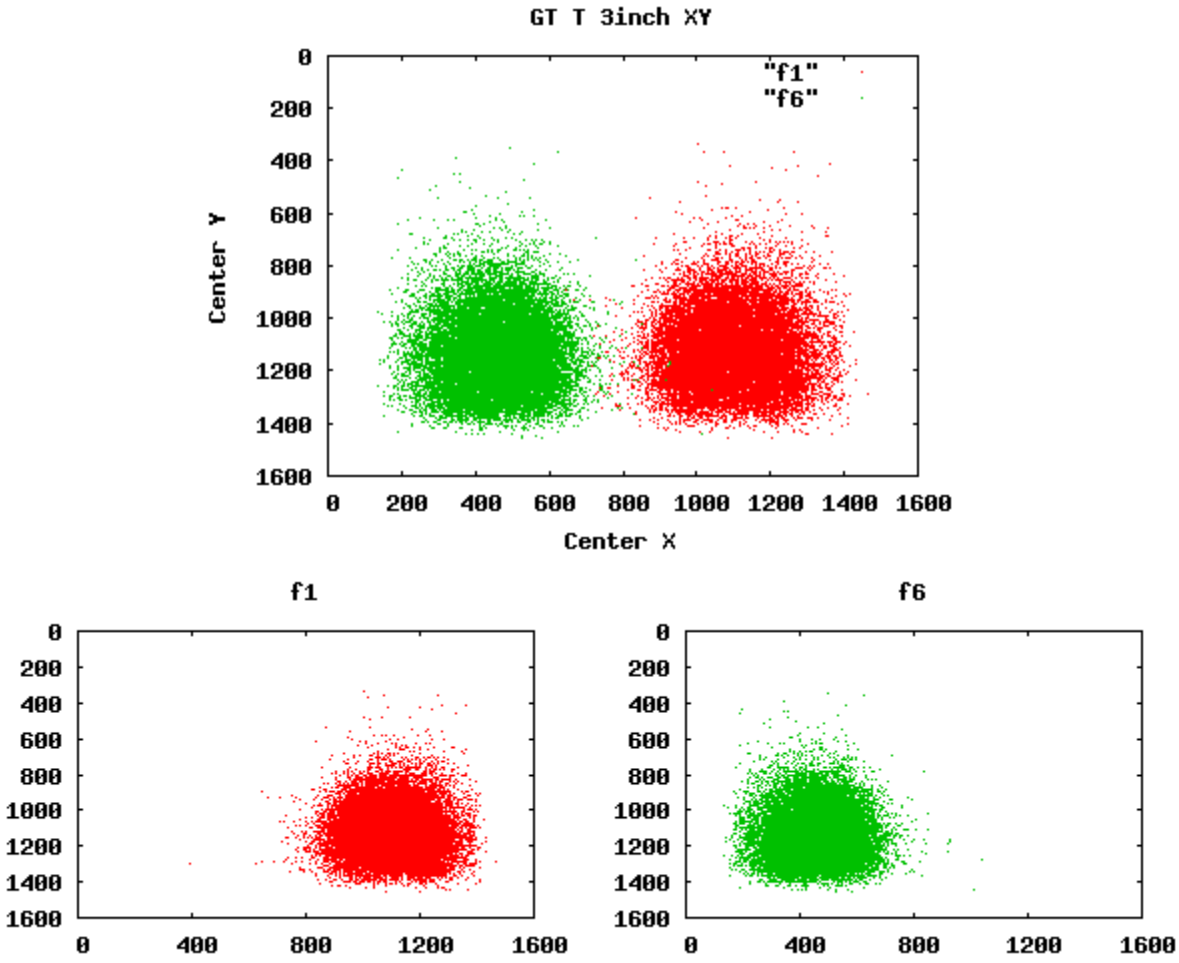
The plots in this appendix show the distribution of the segmentation box centers (x,y) for the 3-inch data. There is a combined plot for each slap image and then a smaller plot for each finger position. The individual finger plots are better for seeing the full “spread” of x,y positions detected. The plot for the ground truth (GT) is included as a baseline for comparison. The blank lines that appear in some of the plots are most likely caused by the segmentation algorithm doing some level of sampling of the input image. The reason the lines are not evenly distributed in some plots is an artifact of the sampling when scaling the images for displaying in the report.



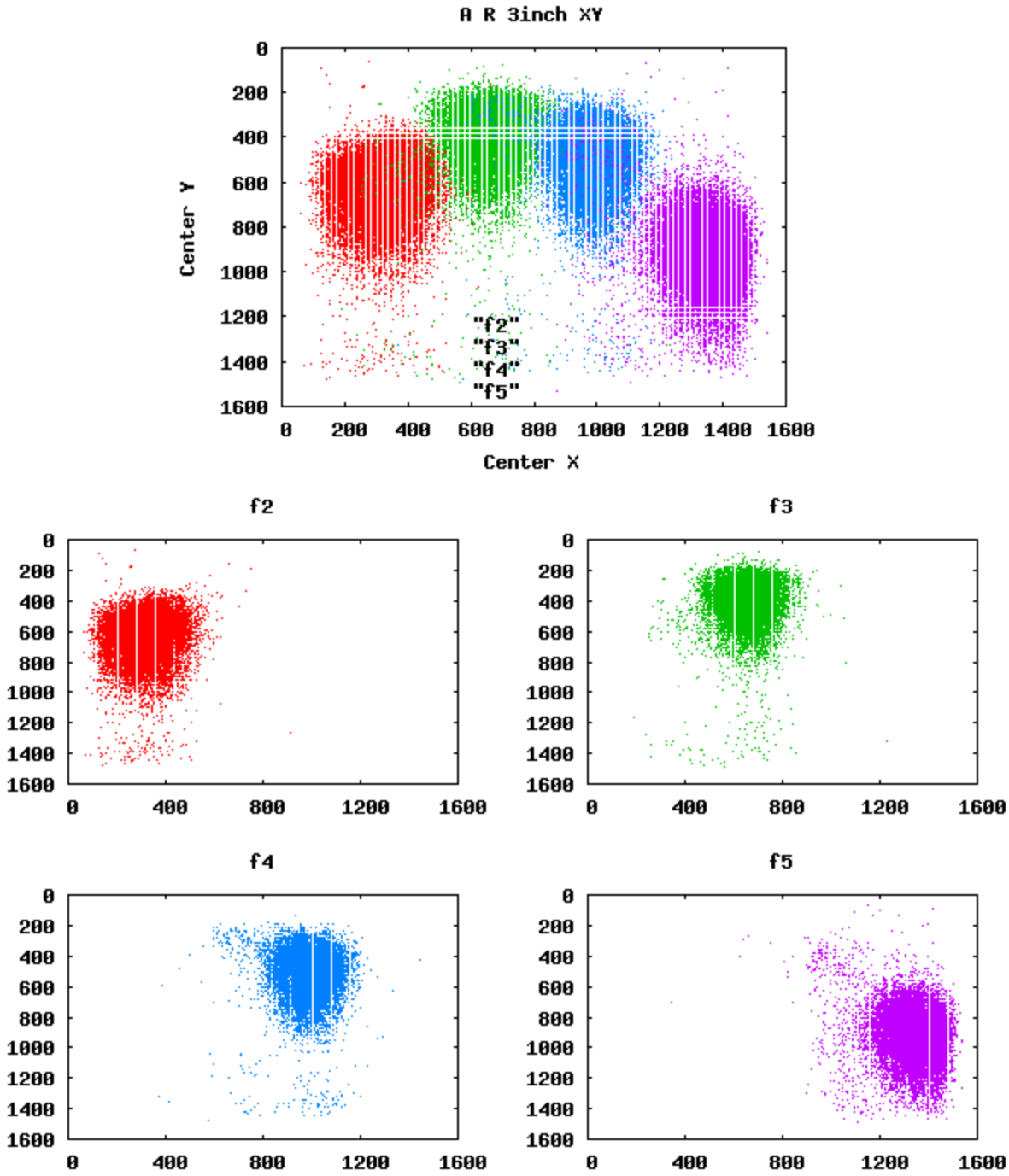
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



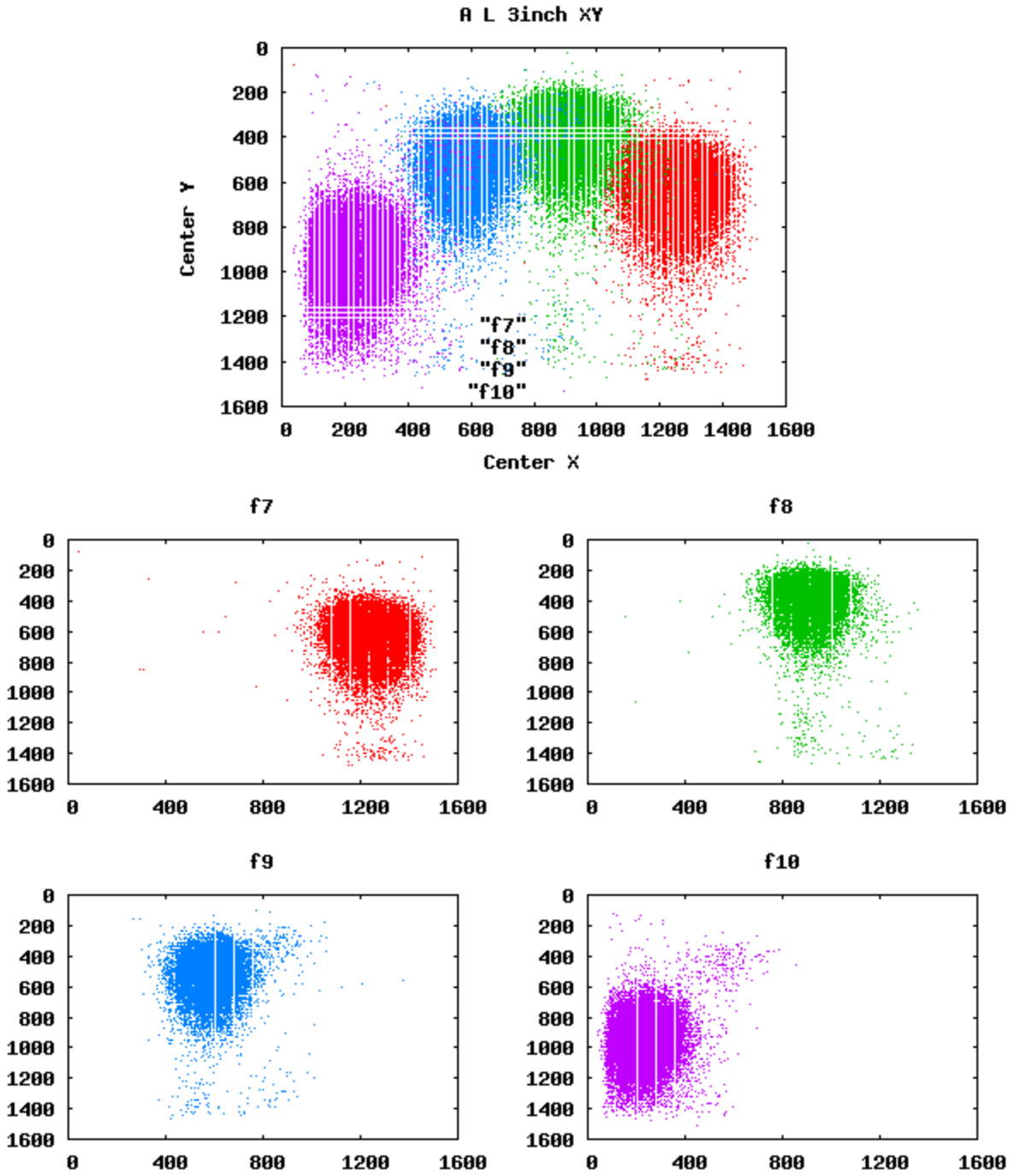
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



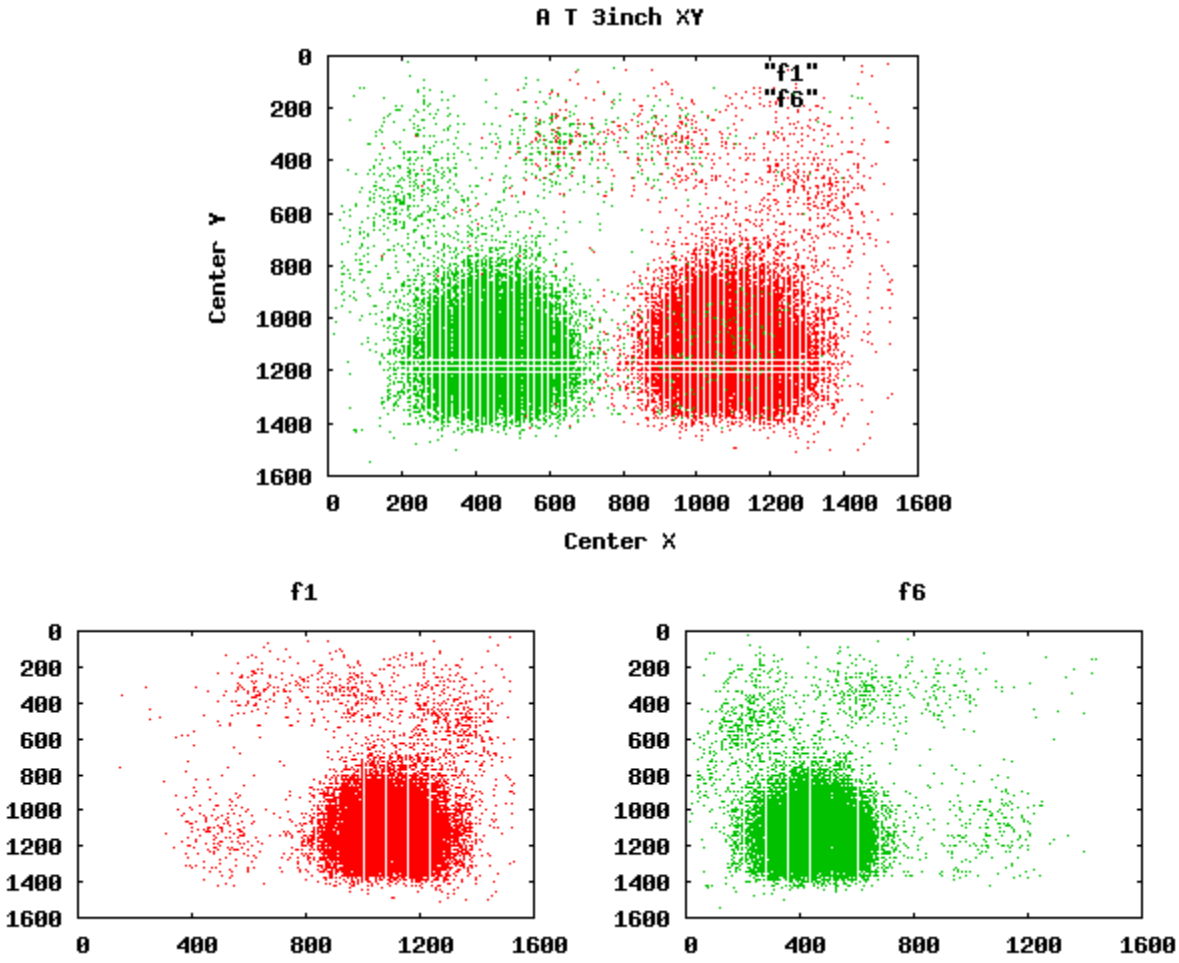
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



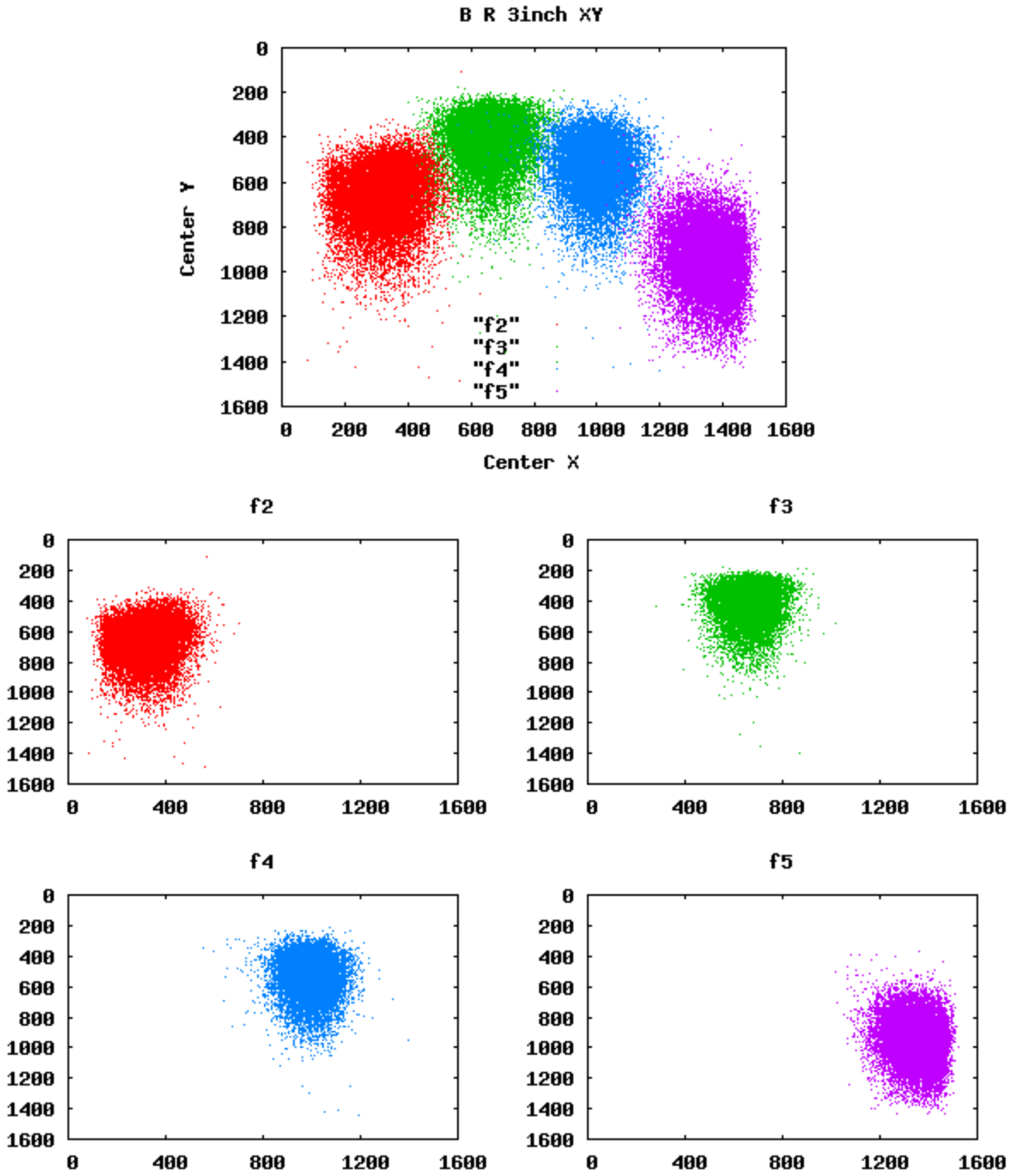
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



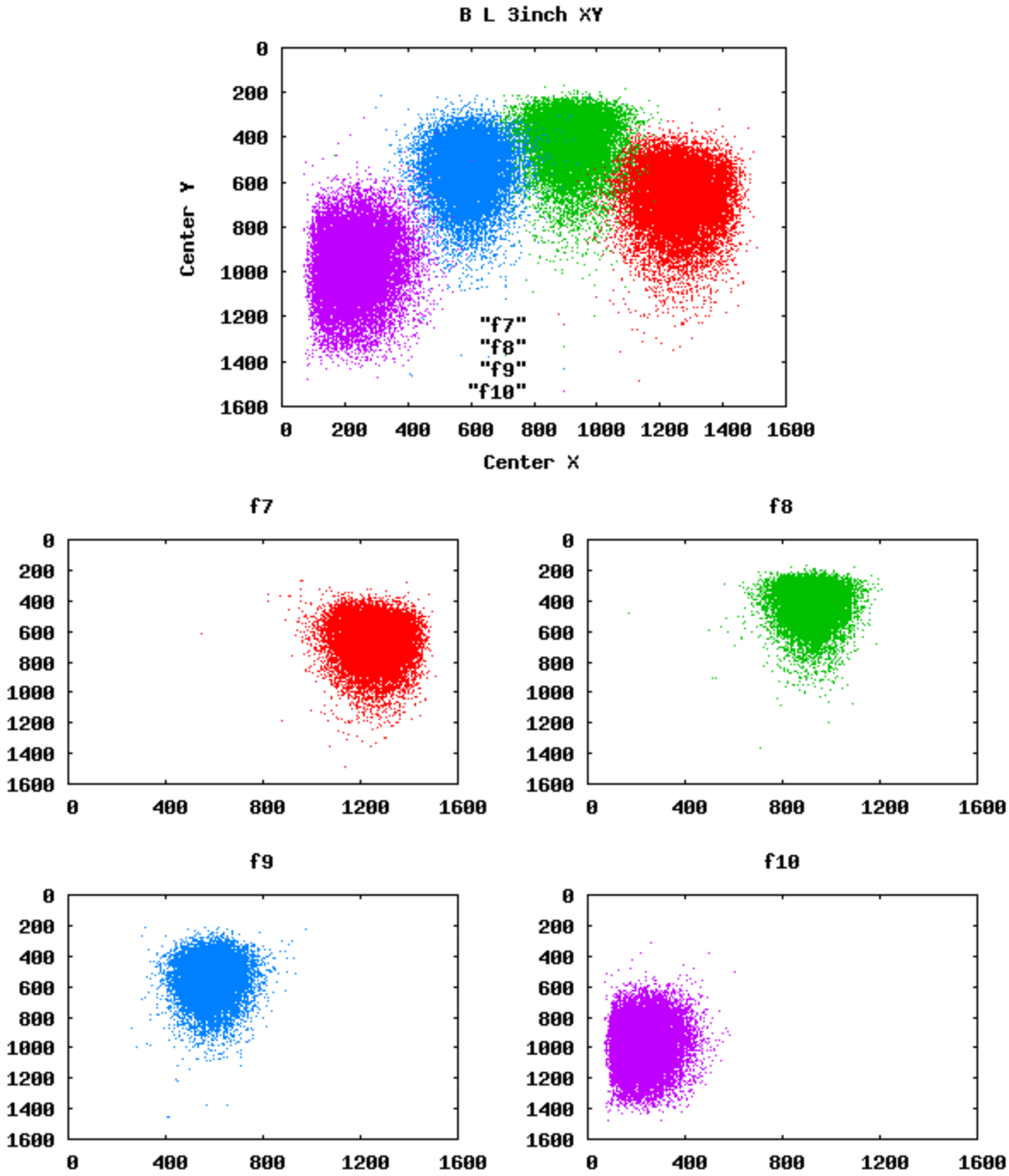
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



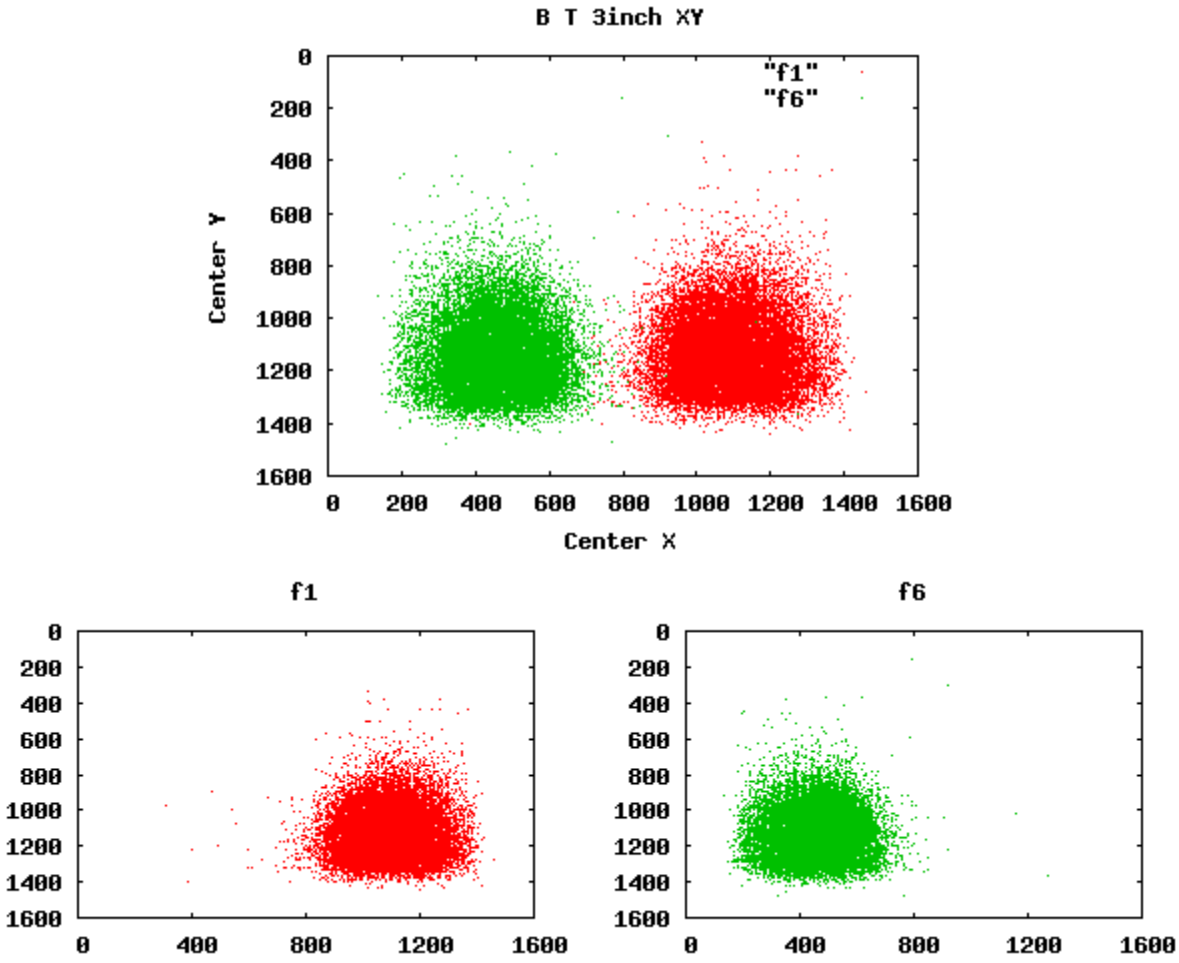
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



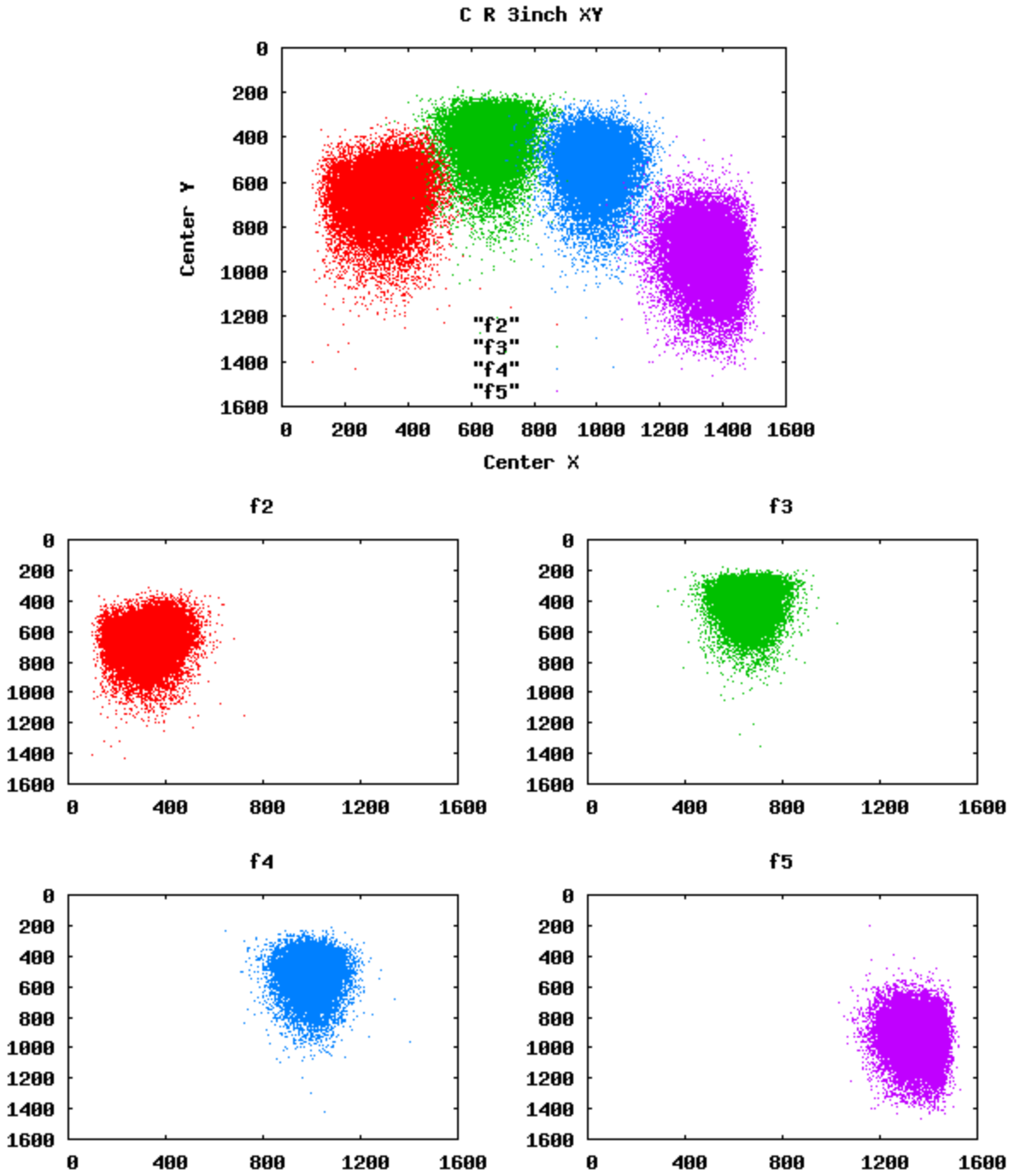
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



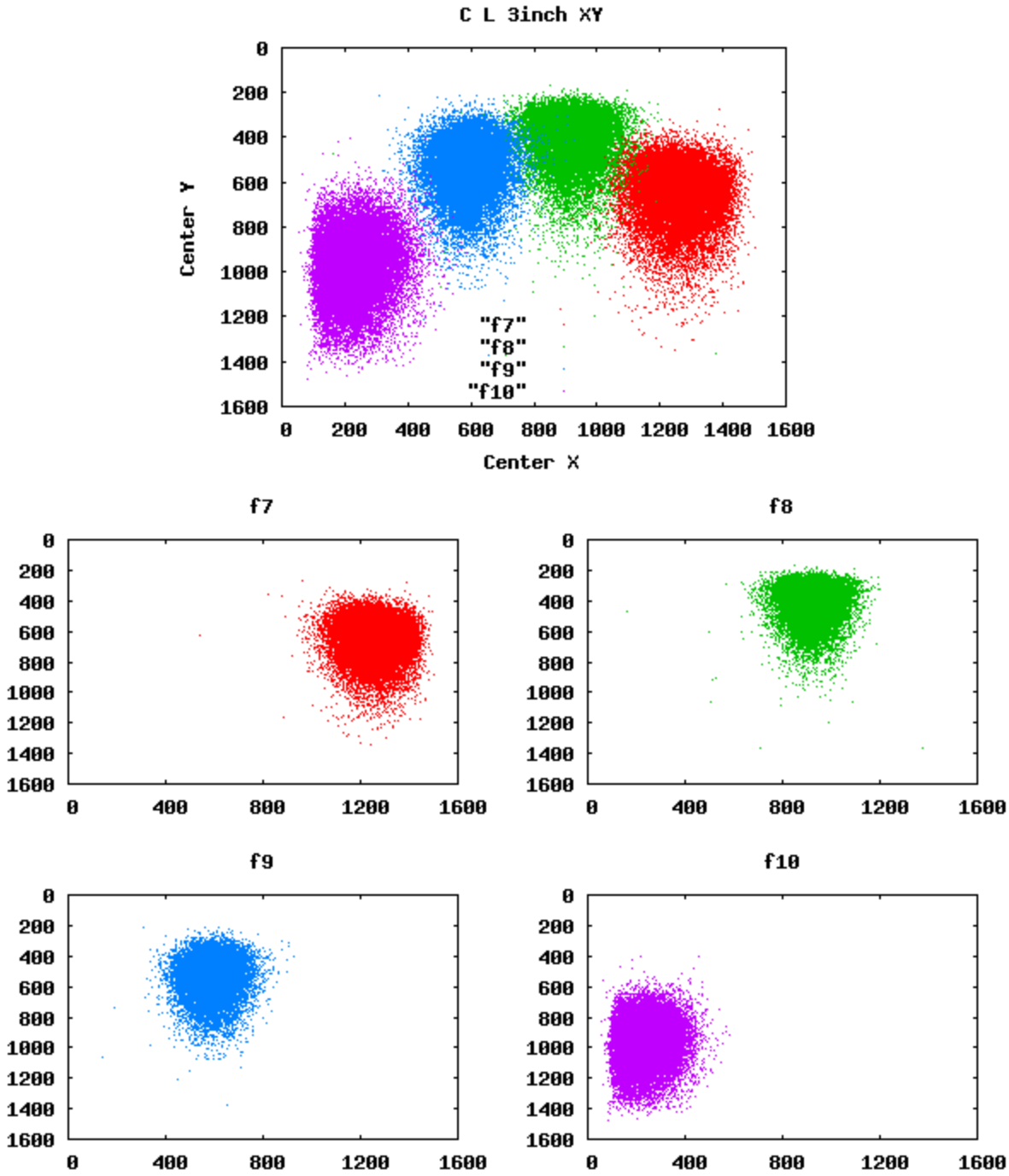
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



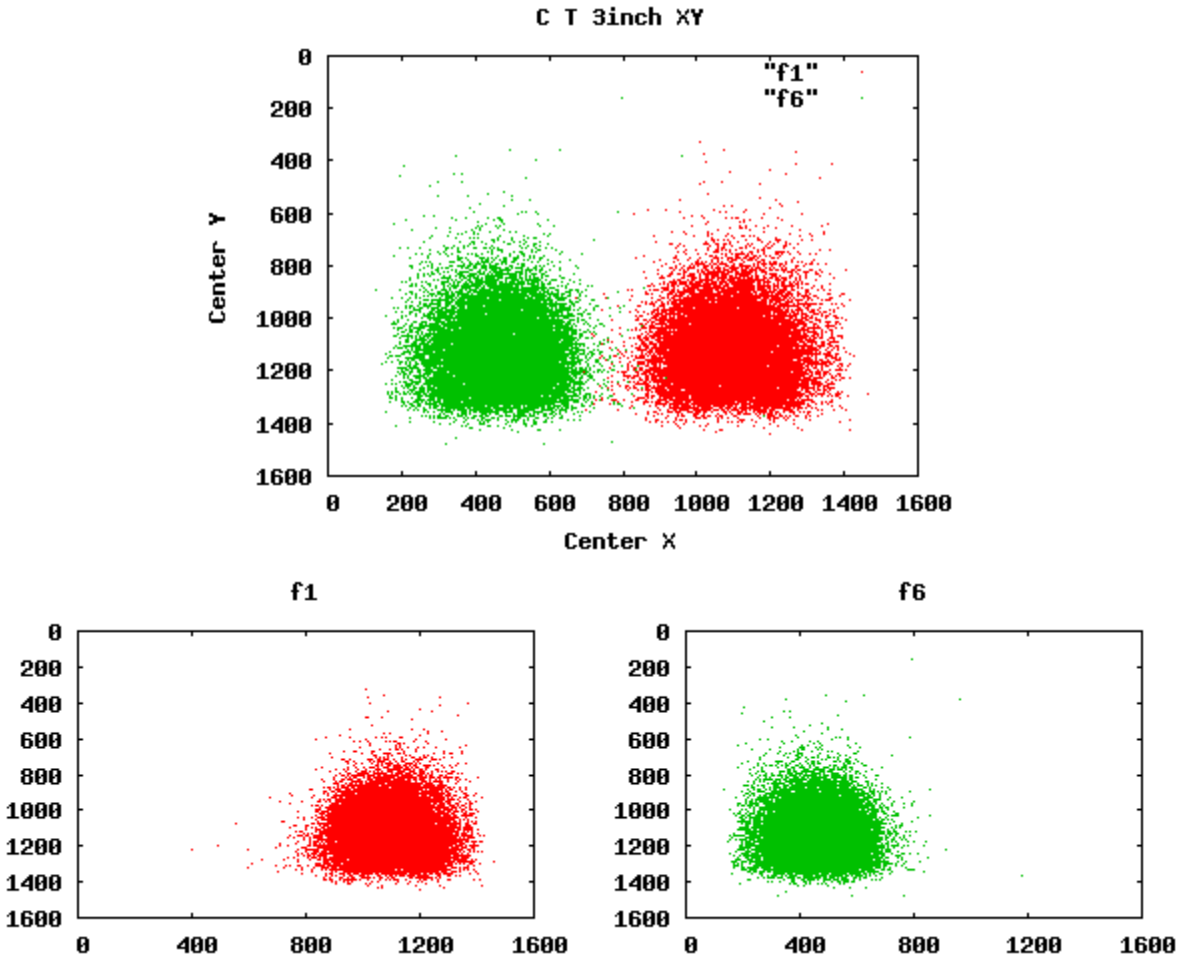
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



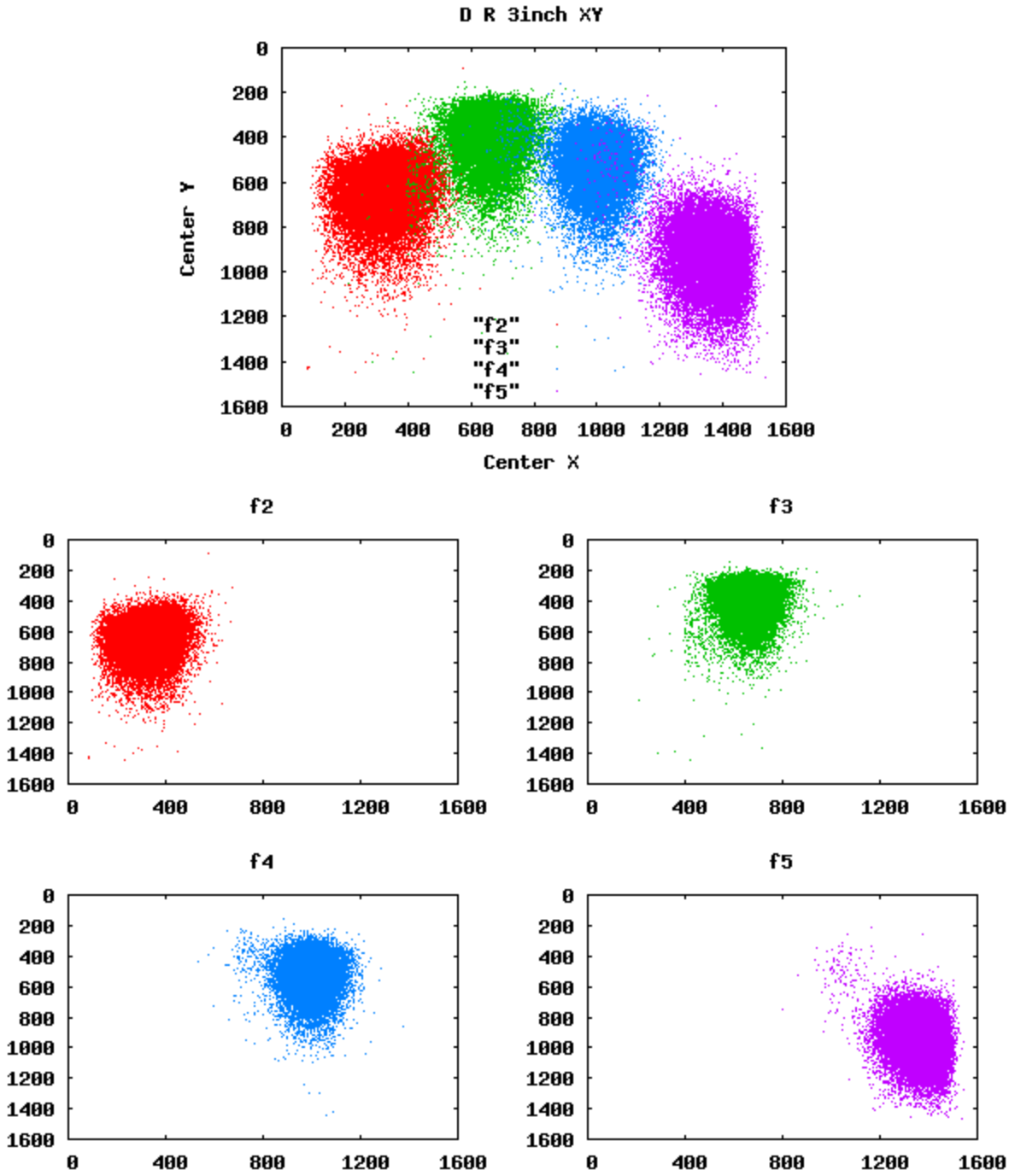
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



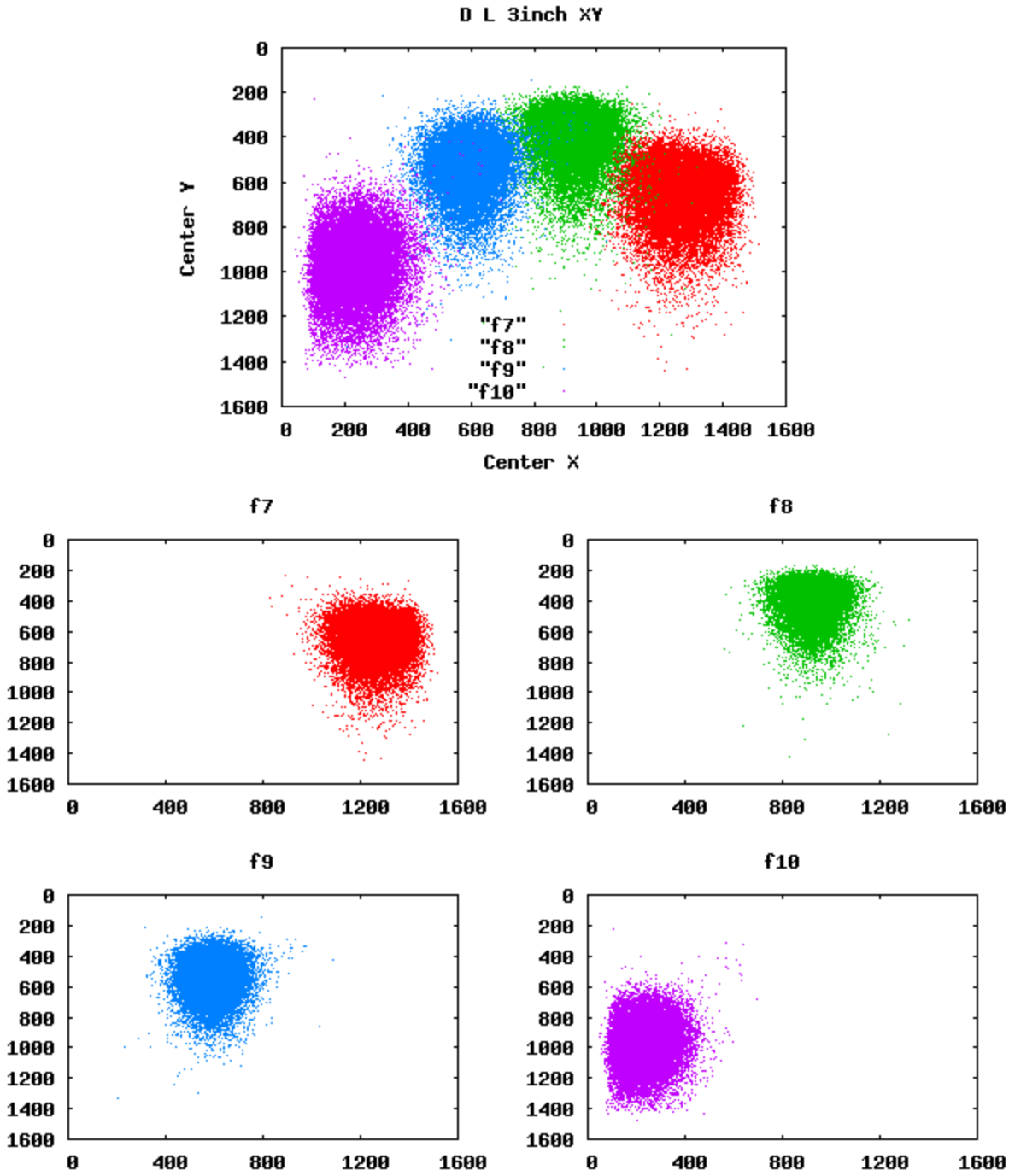
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



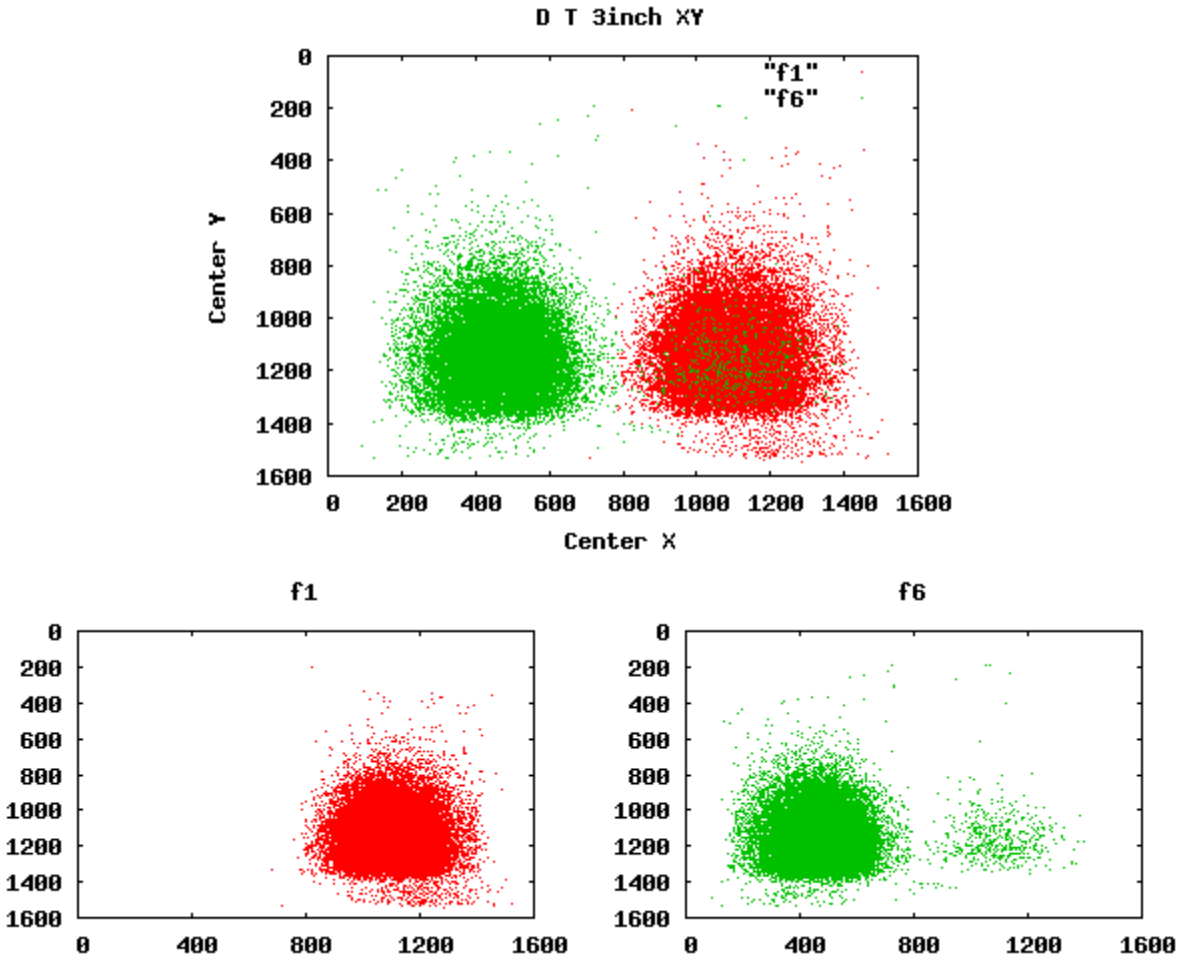
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



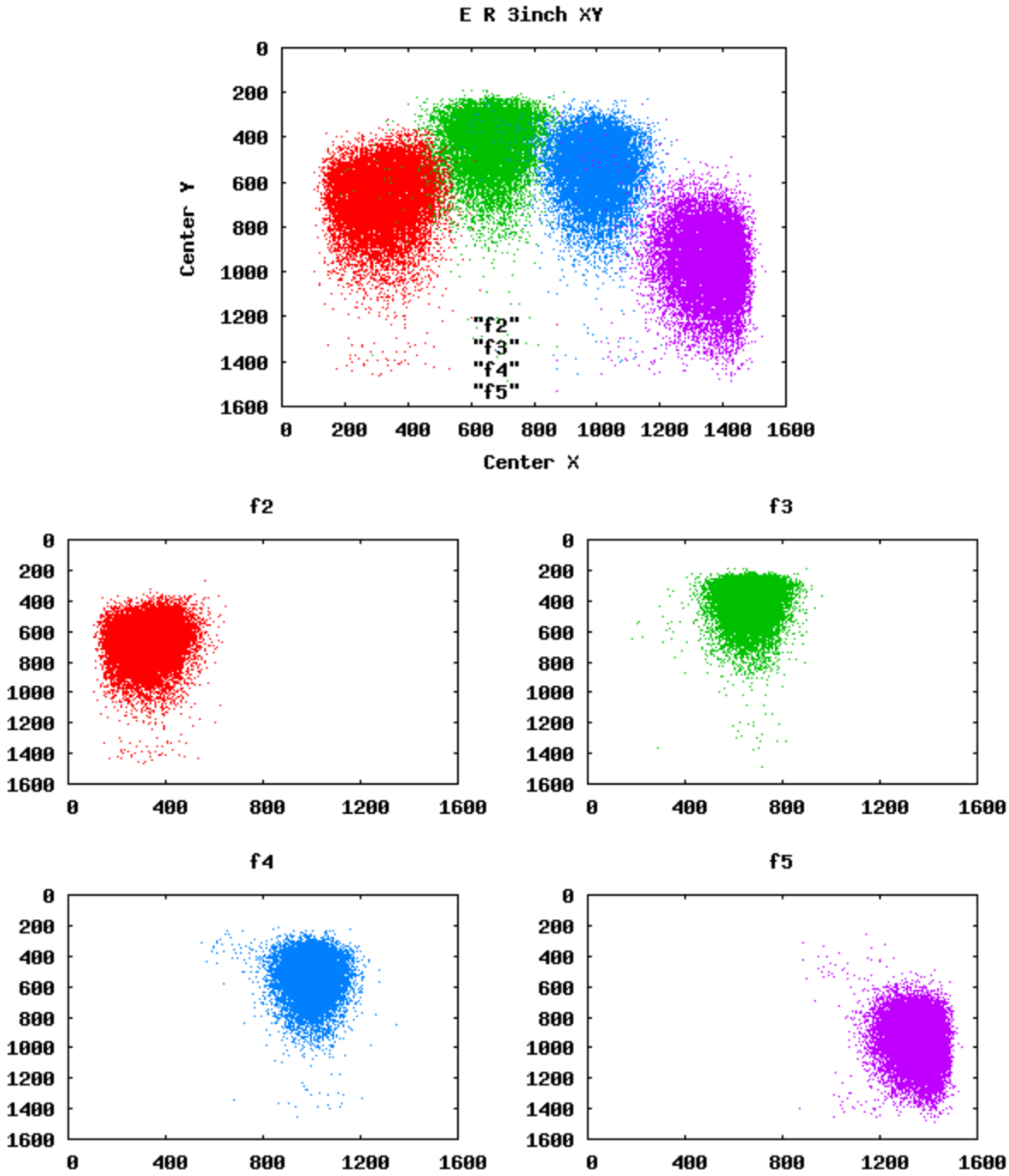
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



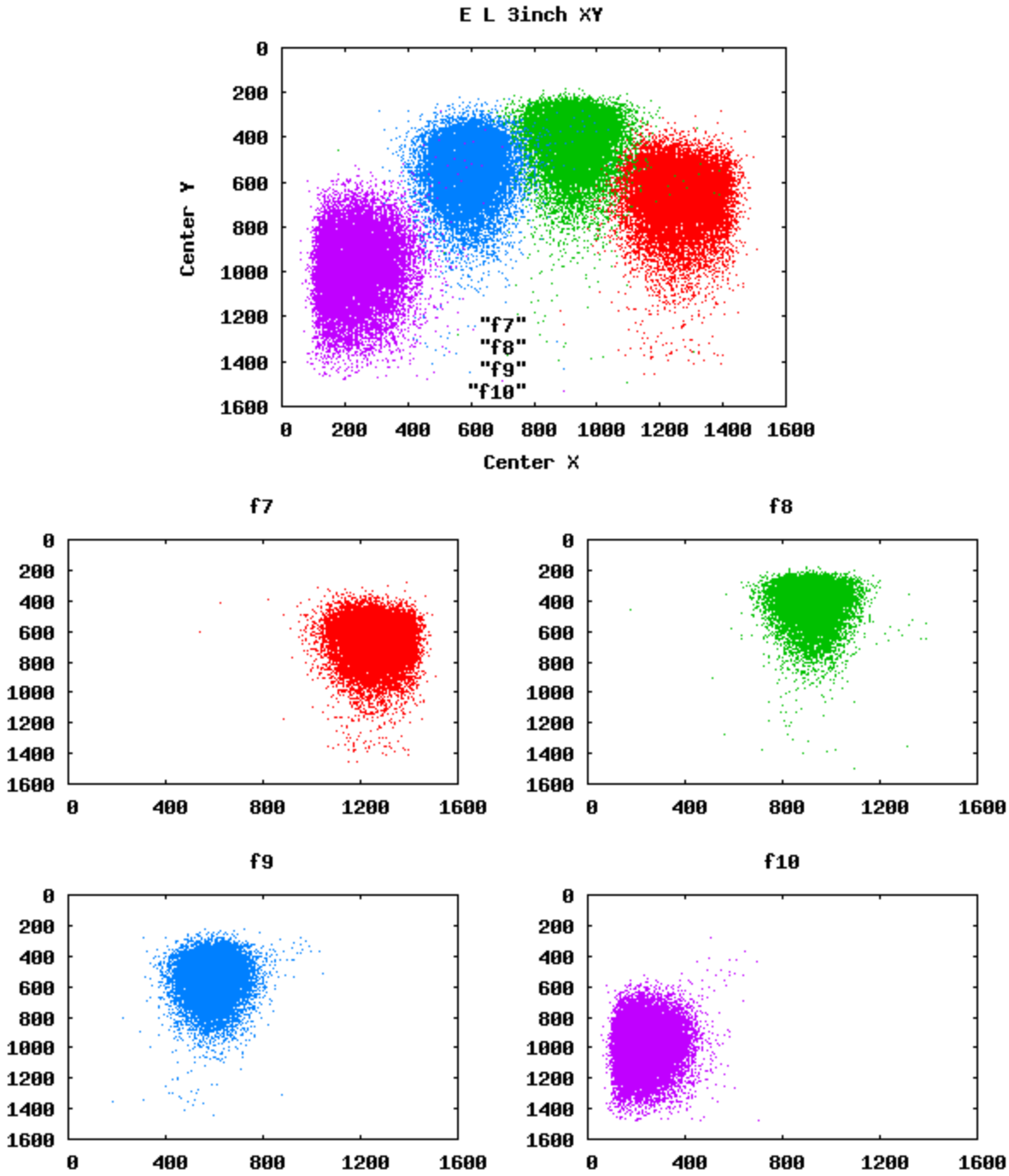
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



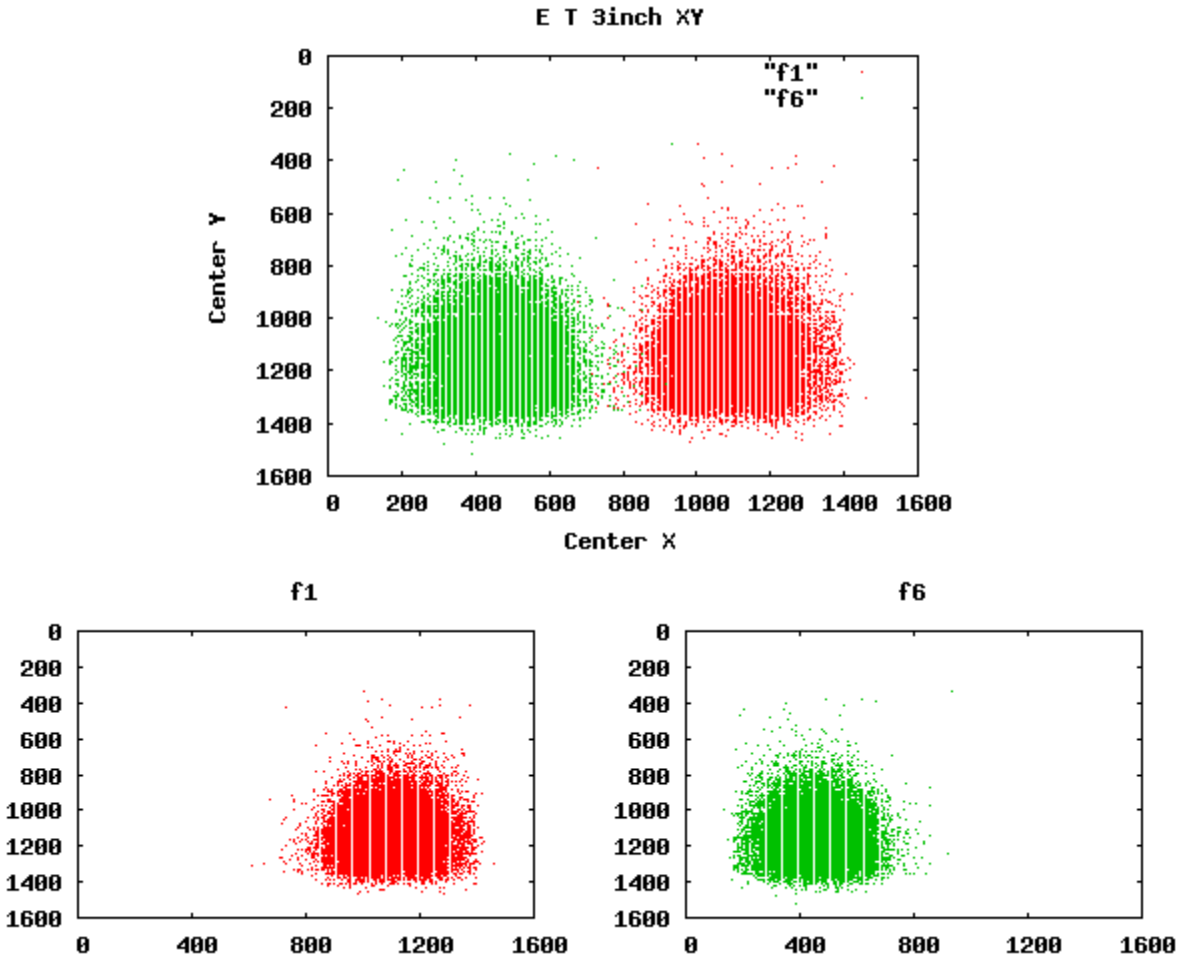
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



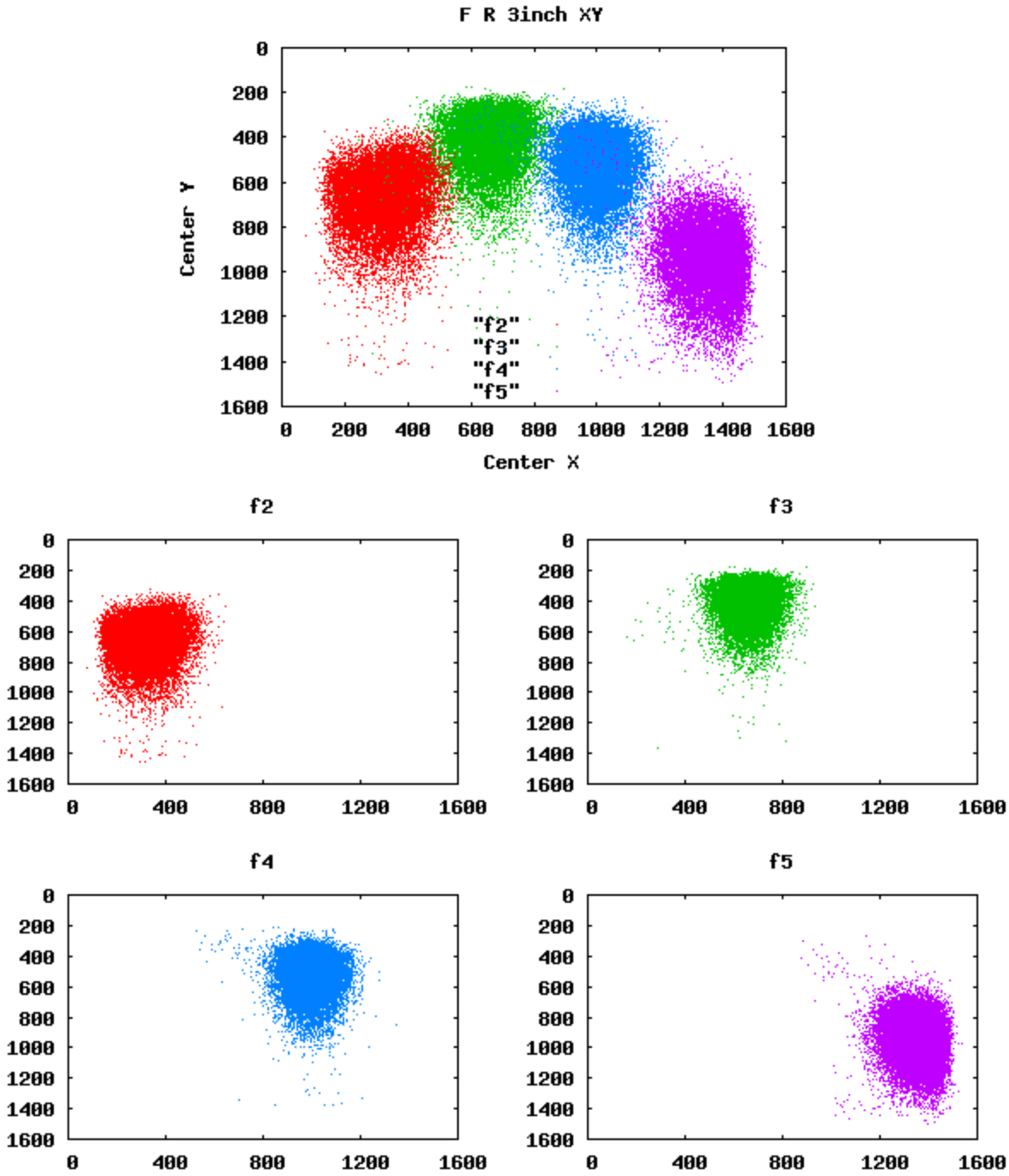
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



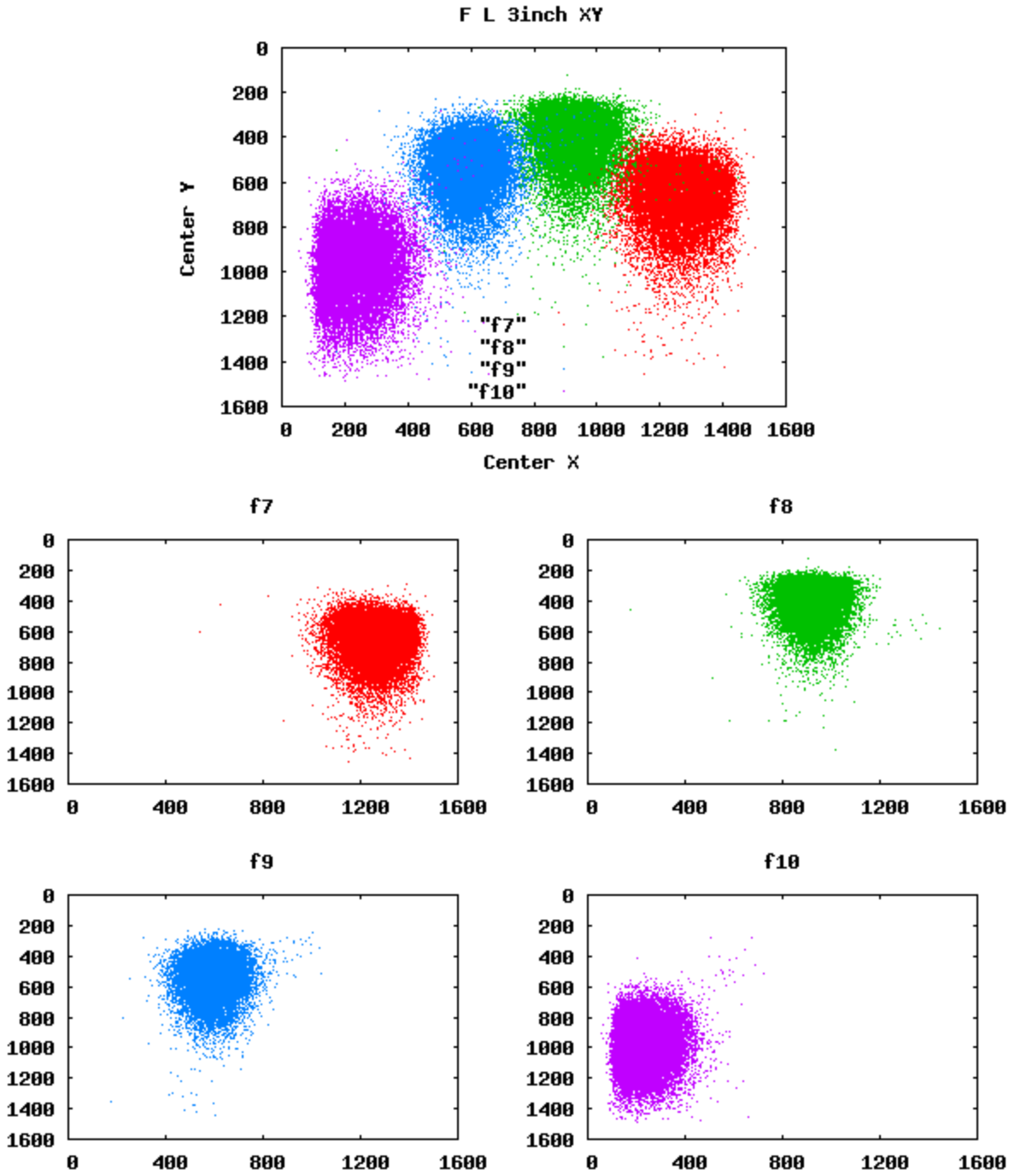
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



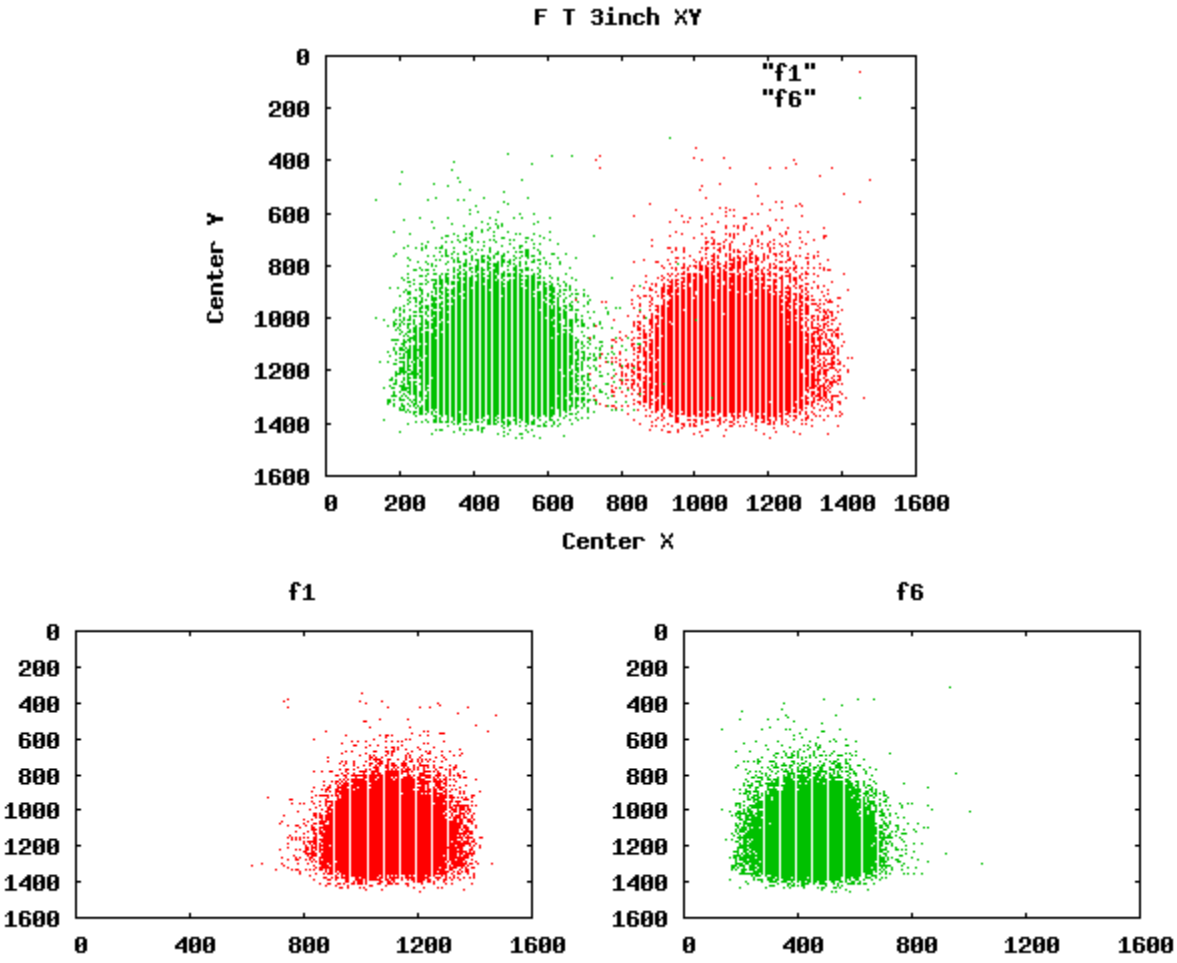
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



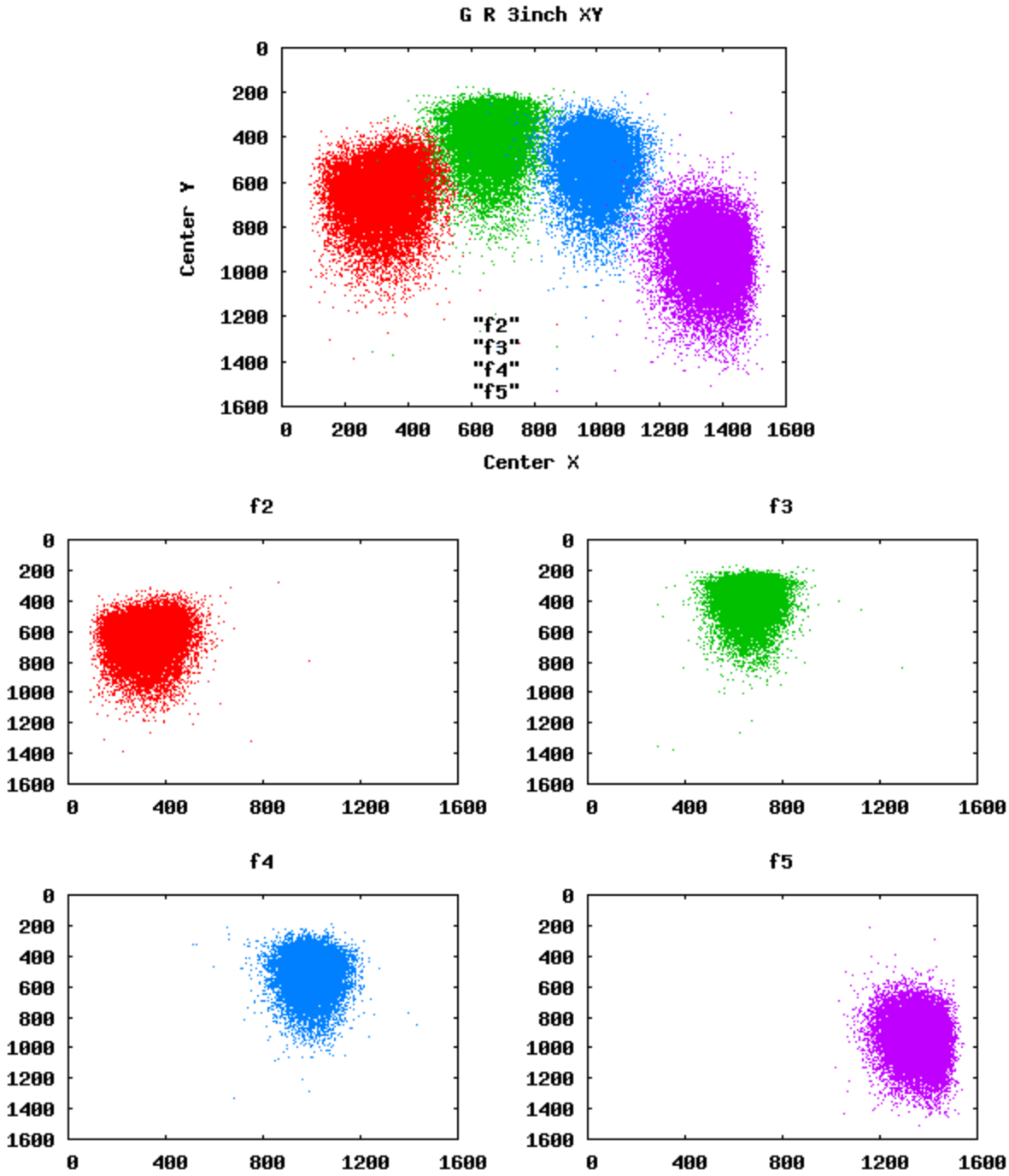
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



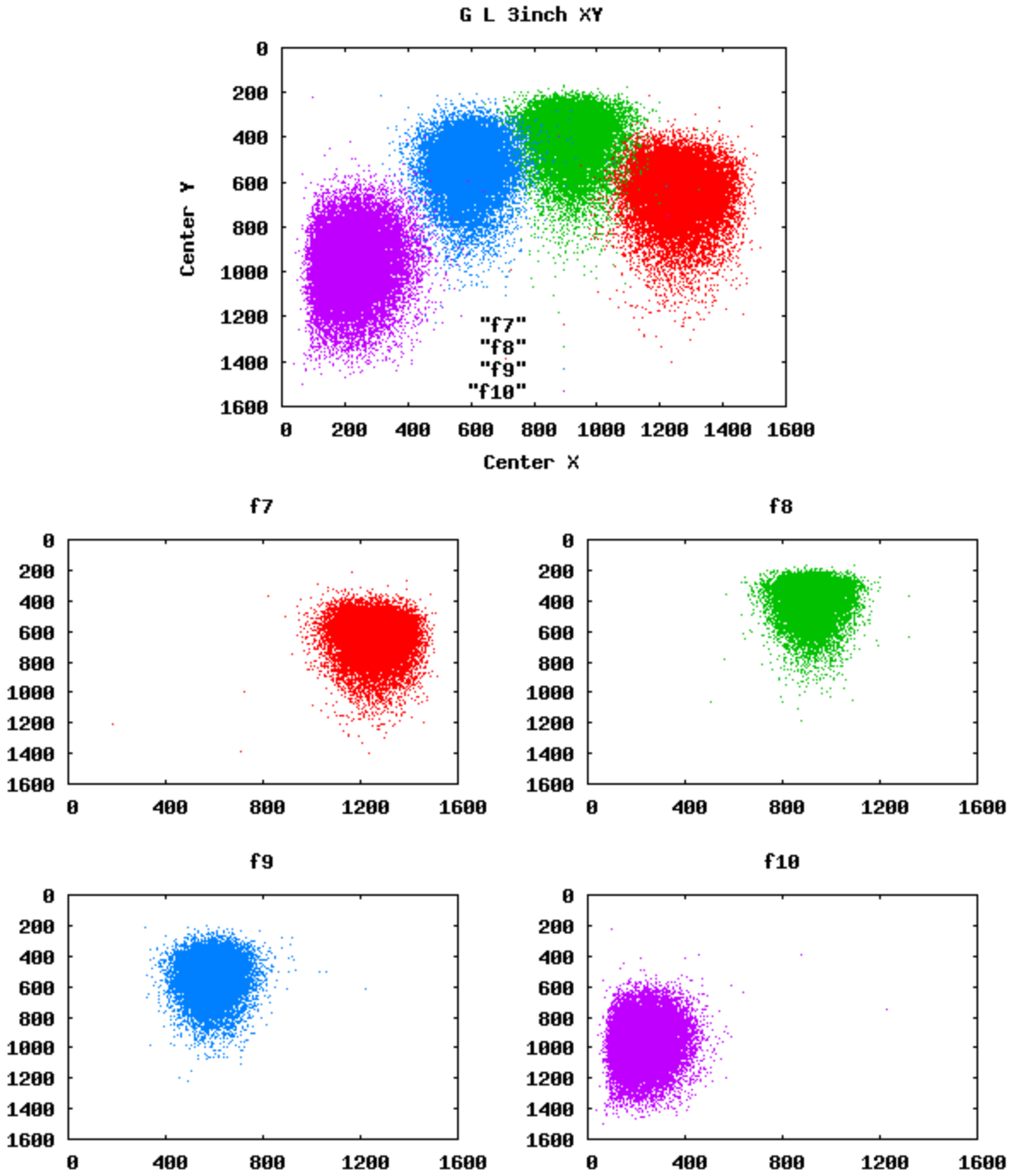
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



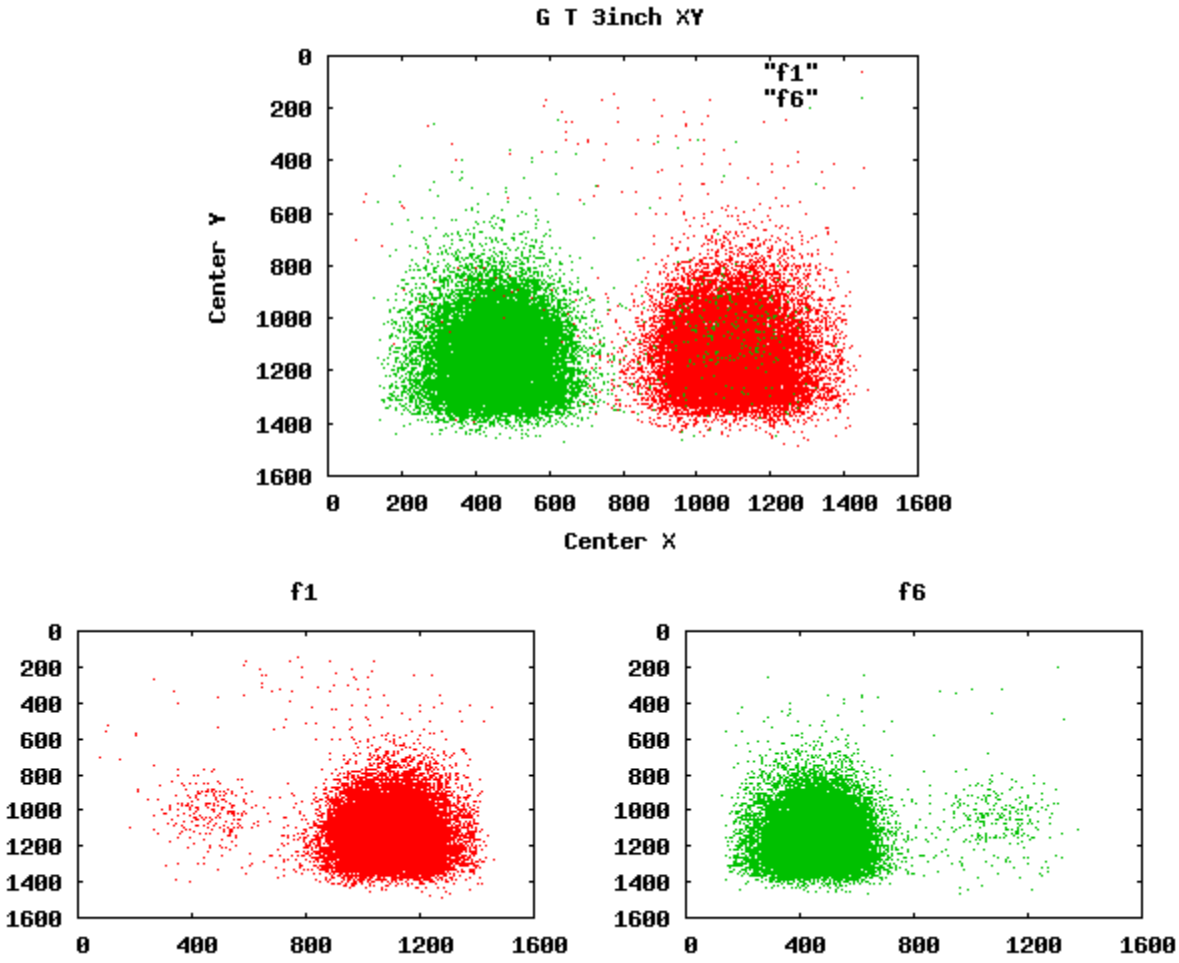
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



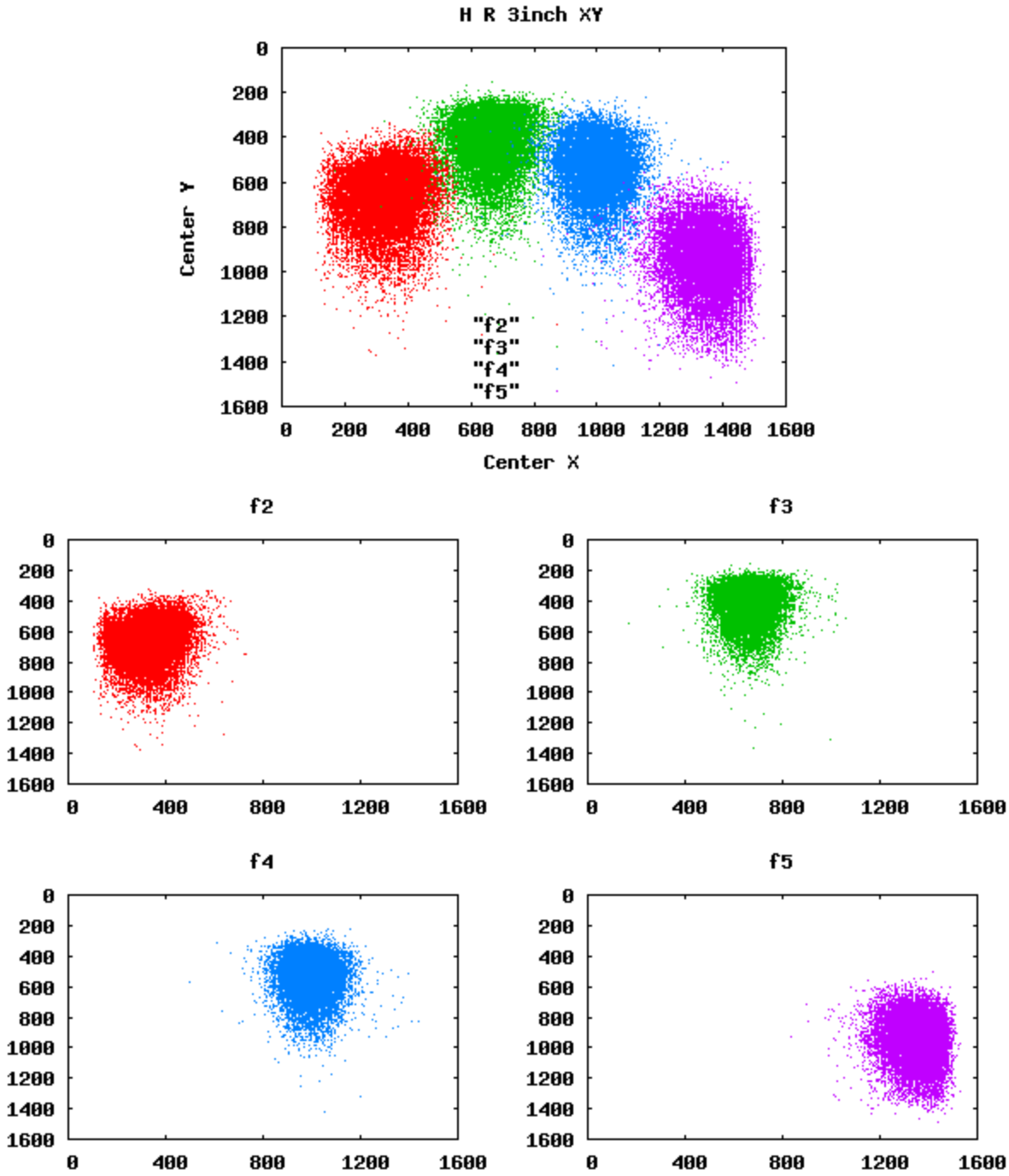
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



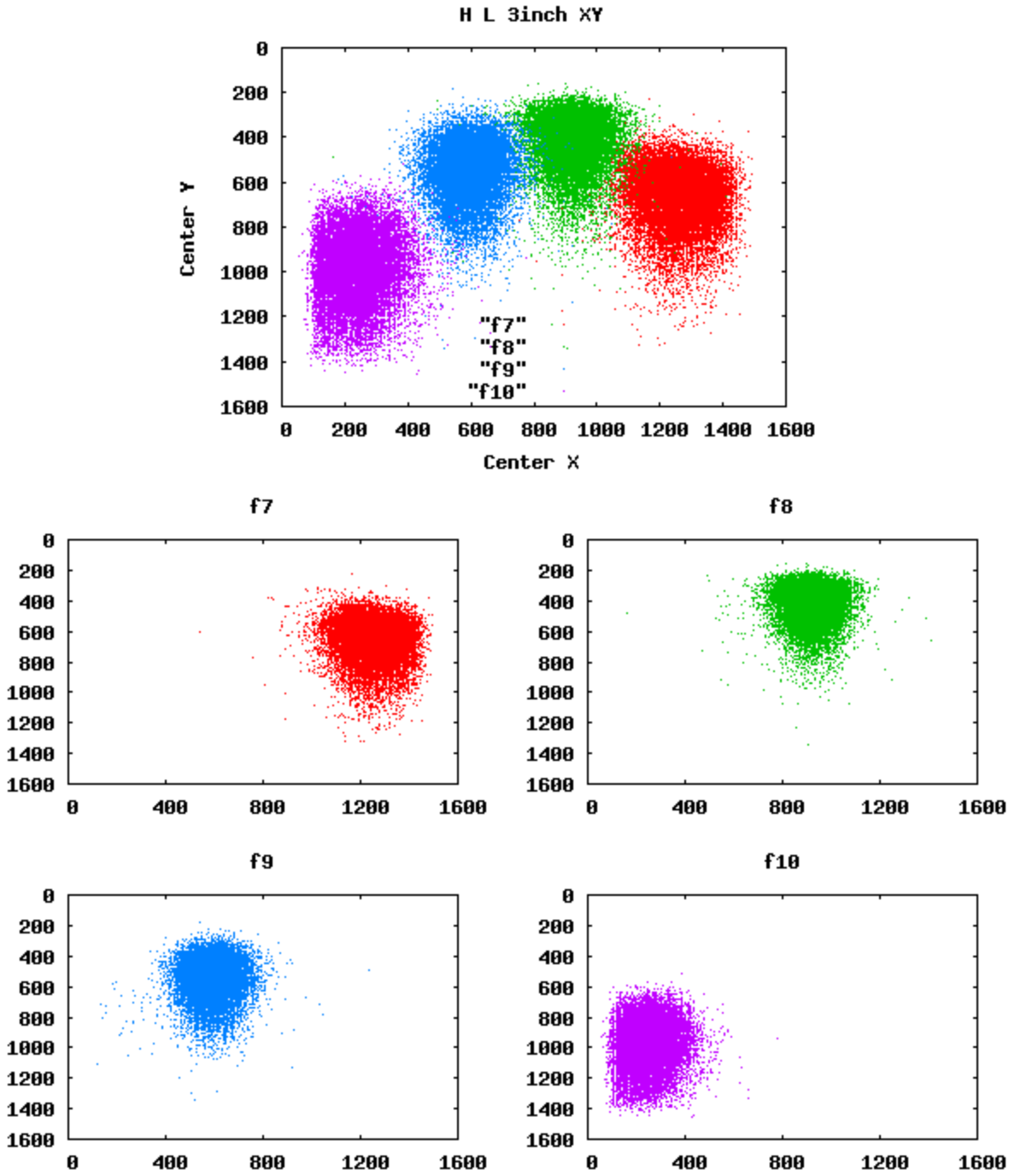
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



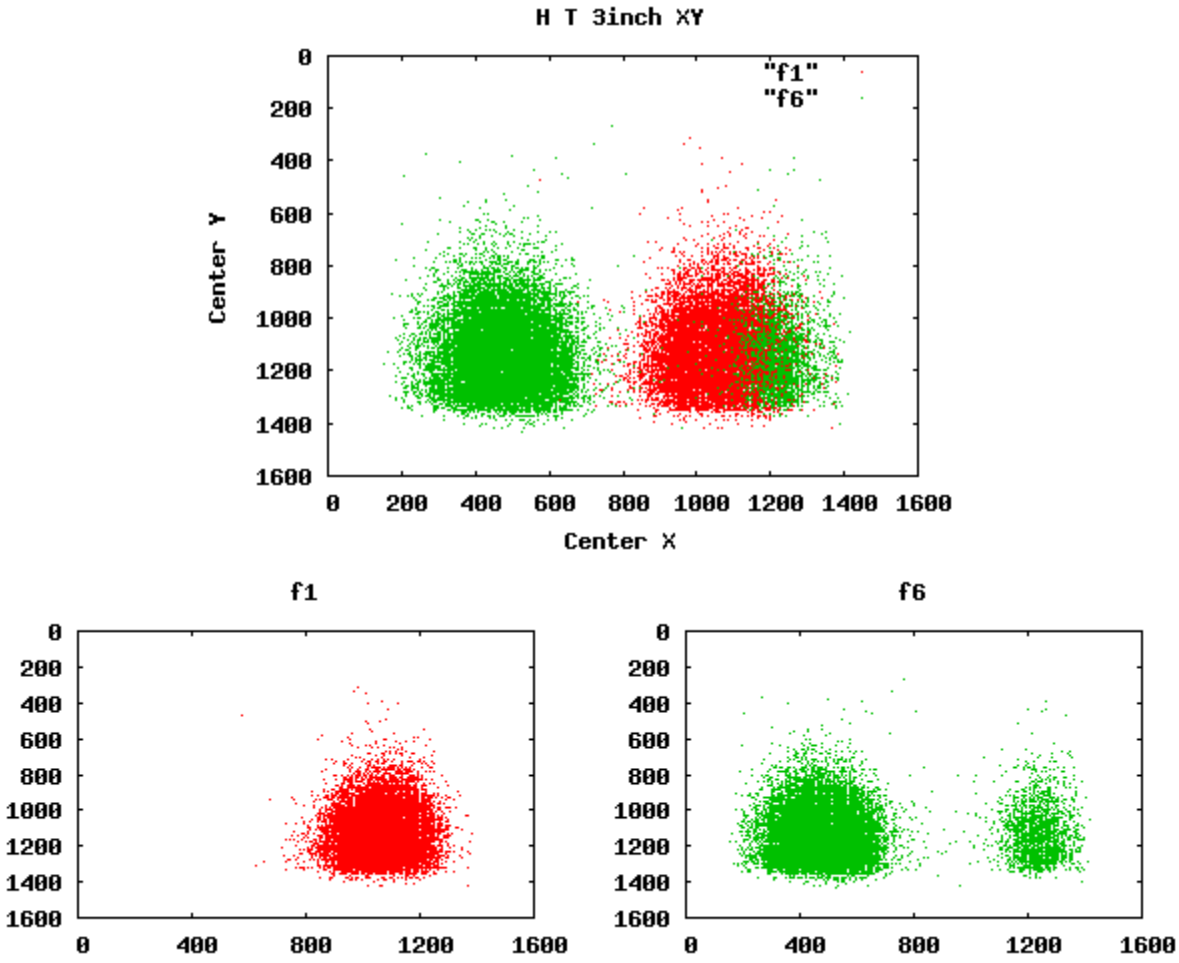
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



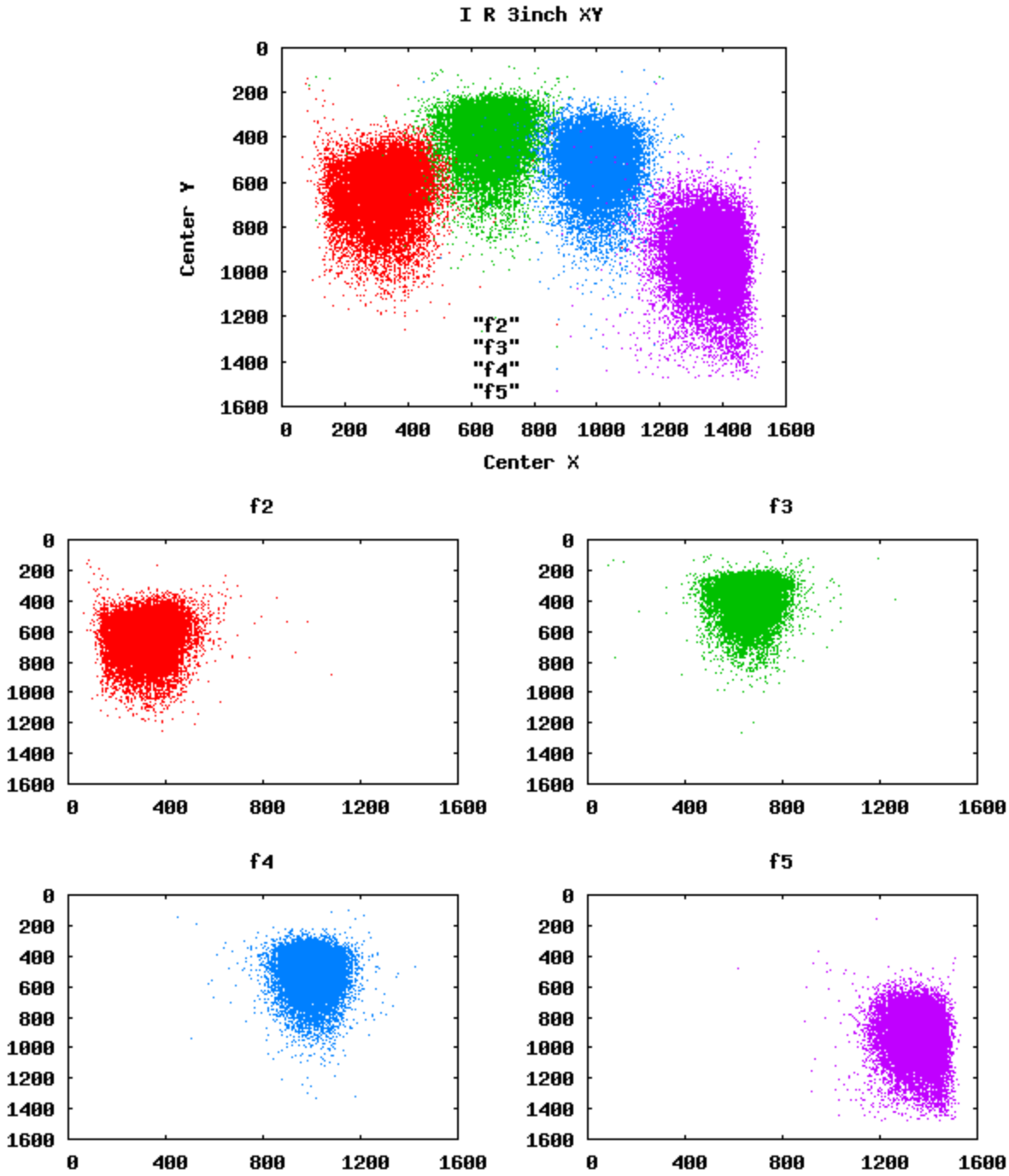
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



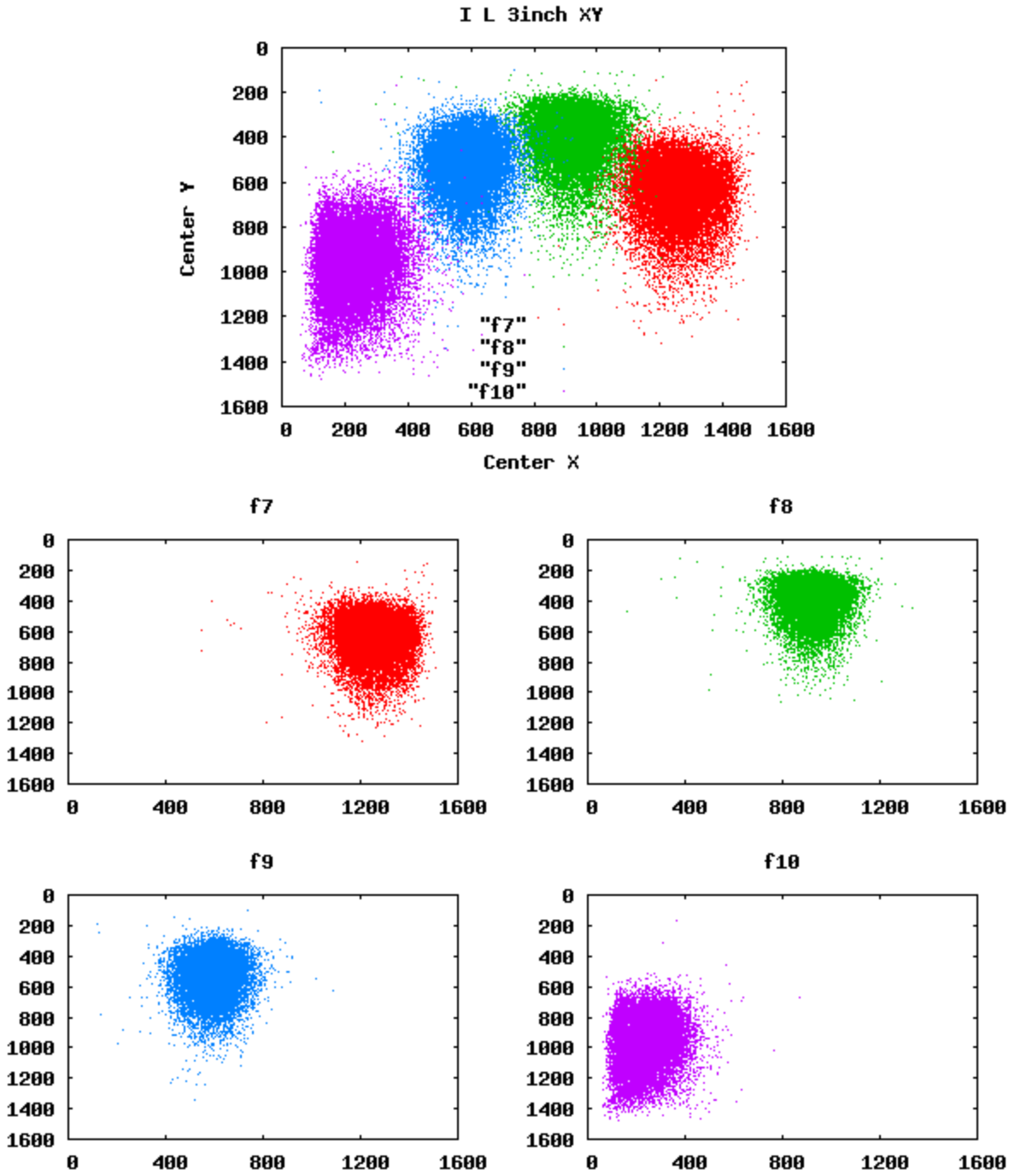
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



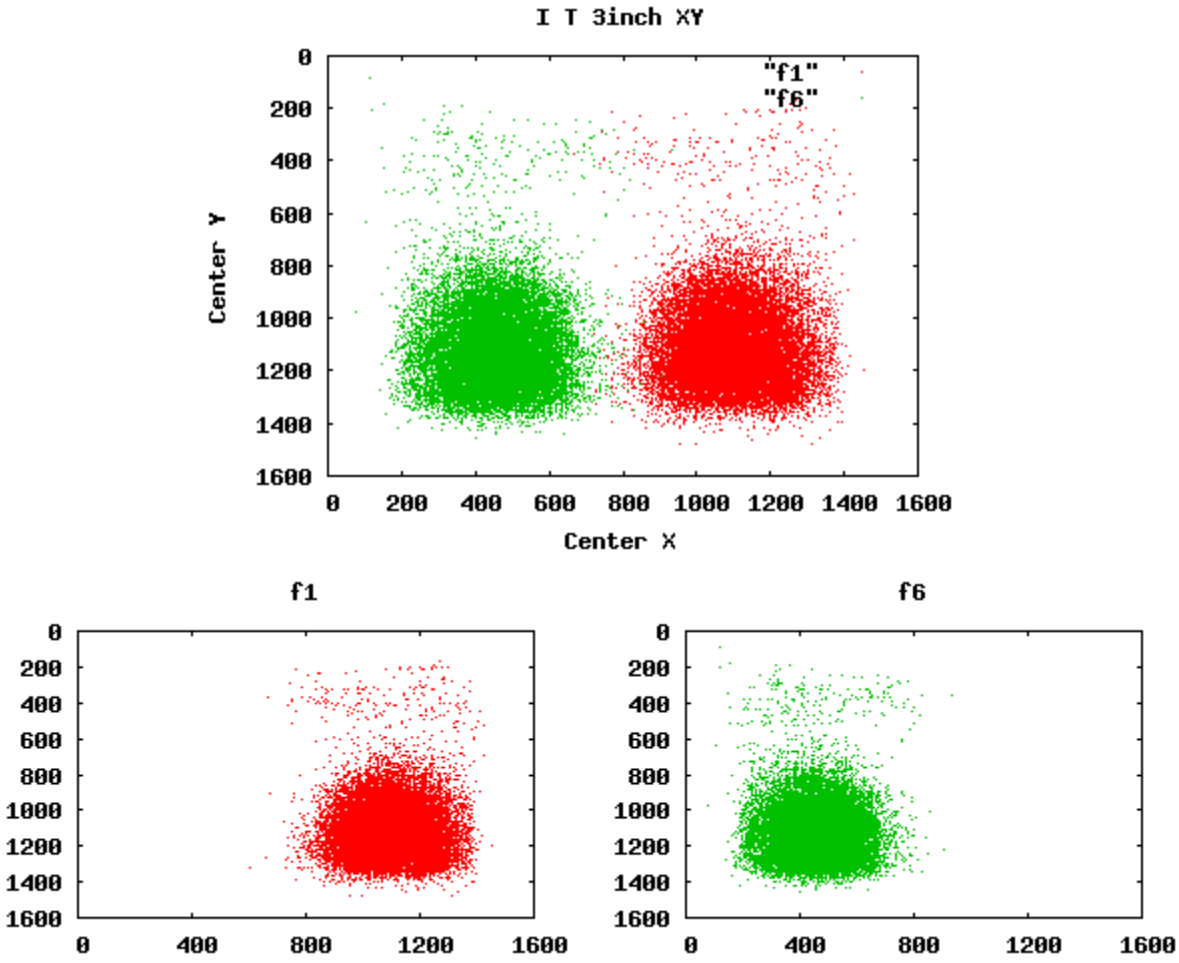
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



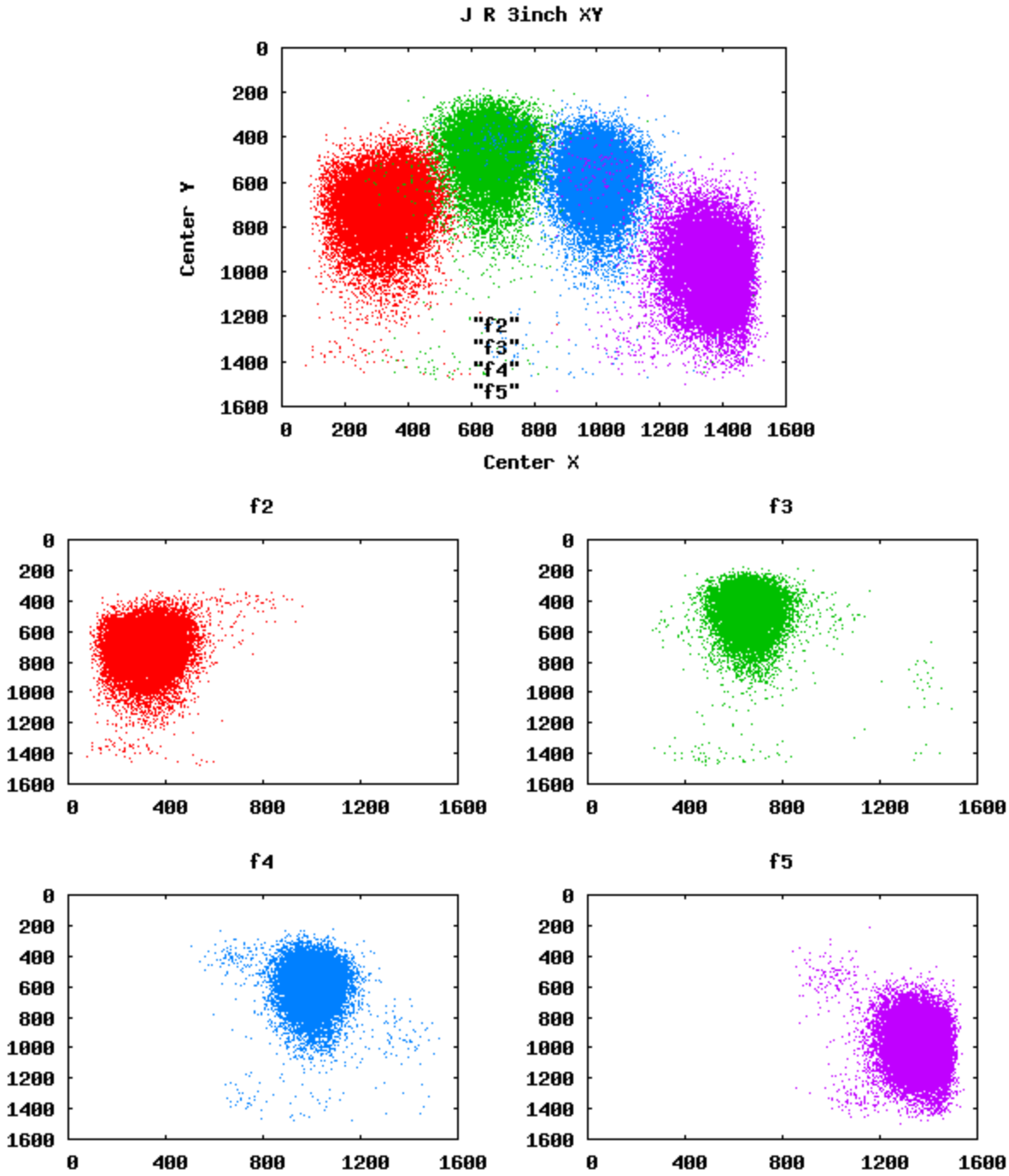
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



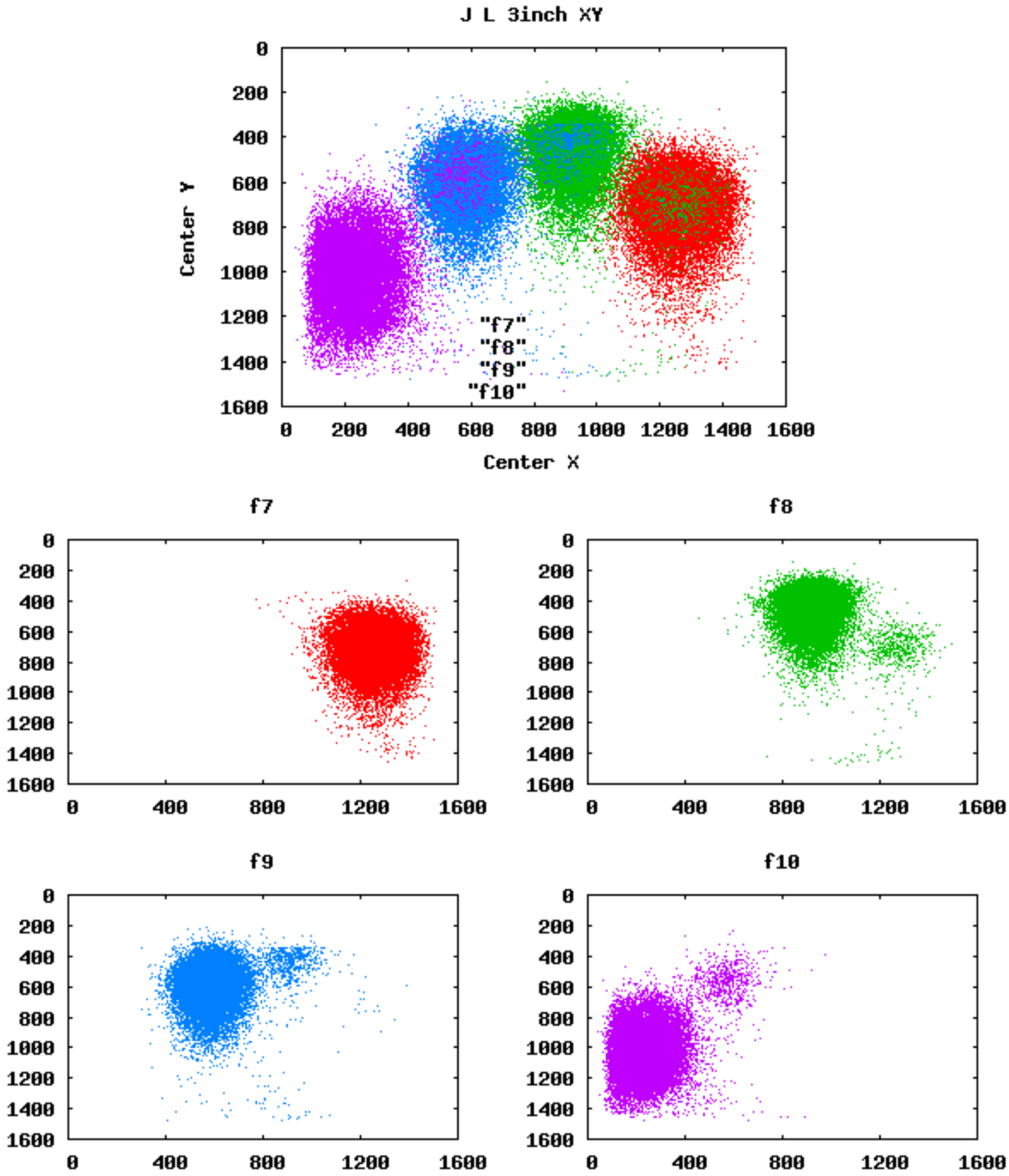
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



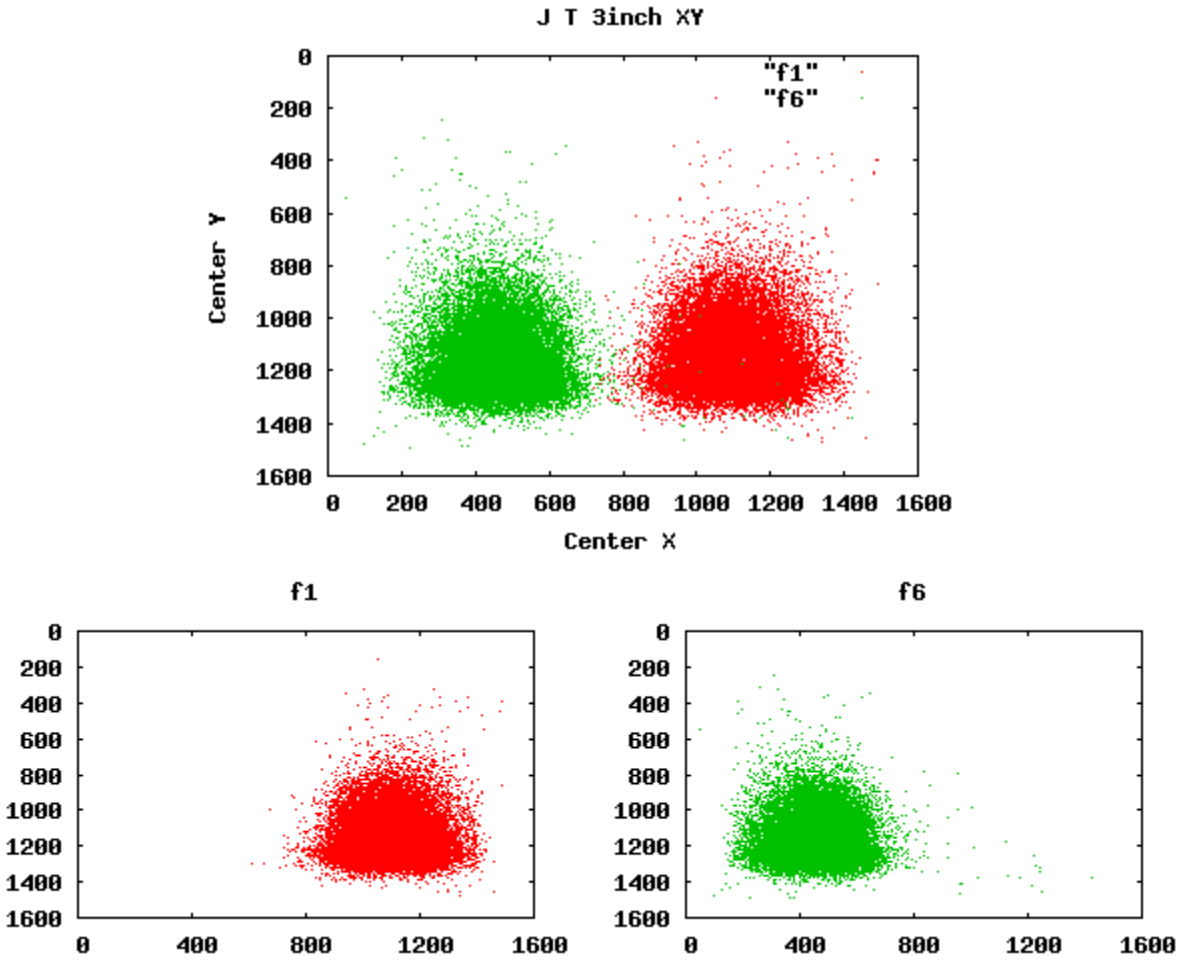
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



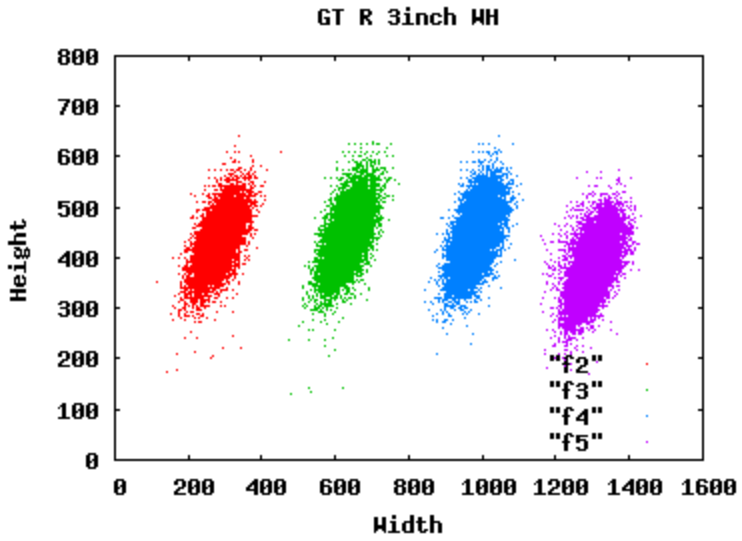
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan

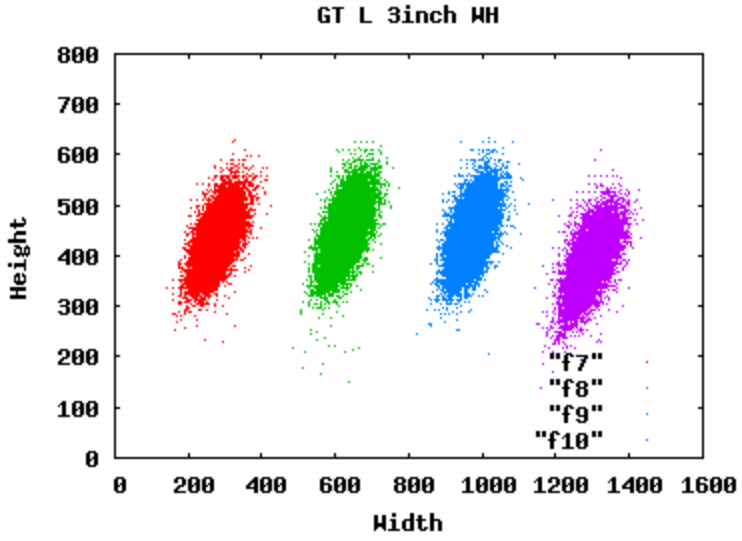


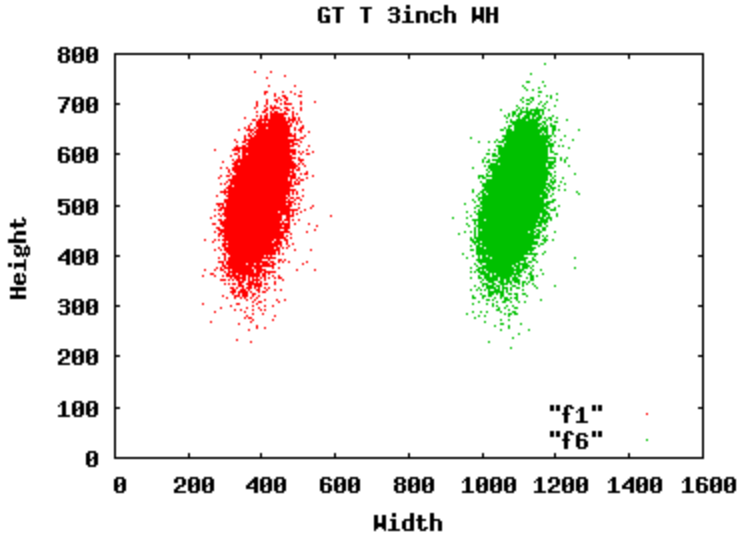
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan

Appendix E. Plots of 3-inch segmentation box widths and heights.

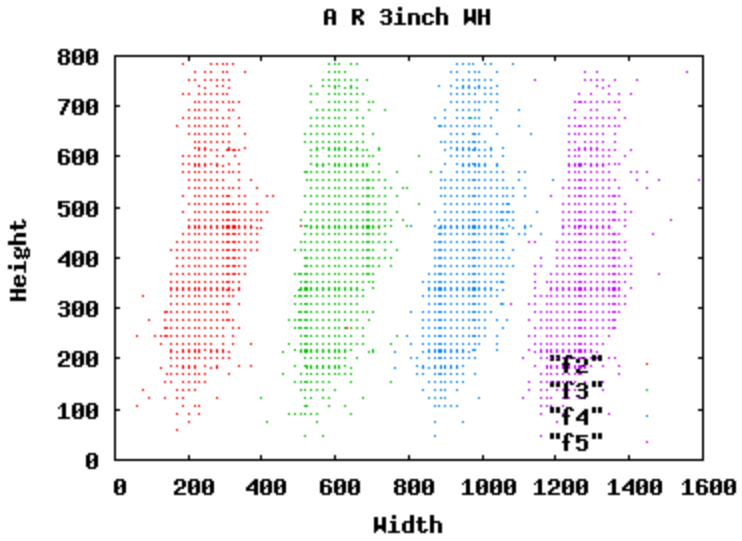
The plots in this appendix show the distribution of the segmentation box widths and heights for the 3-inch data. There is a combined plot for each slap image and then a smaller plot for each finger position. The individual finger plots are better for seeing the full "spread" of widths and heights detected. The widths are "spread out" on the plot by adding 350, 750 and 1050 to the 2nd, 3rd, and 4th widths plotted. The plot for the ground truth (GT) is included as a baseline for comparison. The blank lines that appear in some of the plots are most likely caused by the segmentation algorithm doing some level of sampling of the input image. The reason the lines are not evenly distributed in some plots is an artifact of the sampling when scaling the images for displaying in the report.

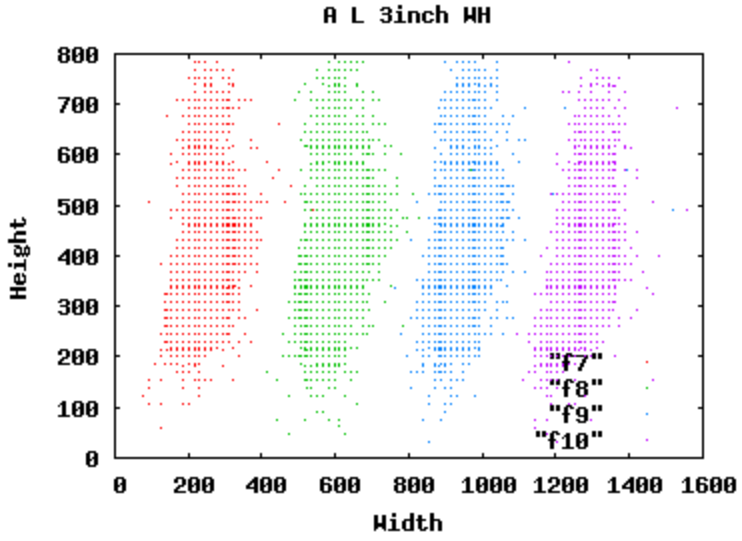


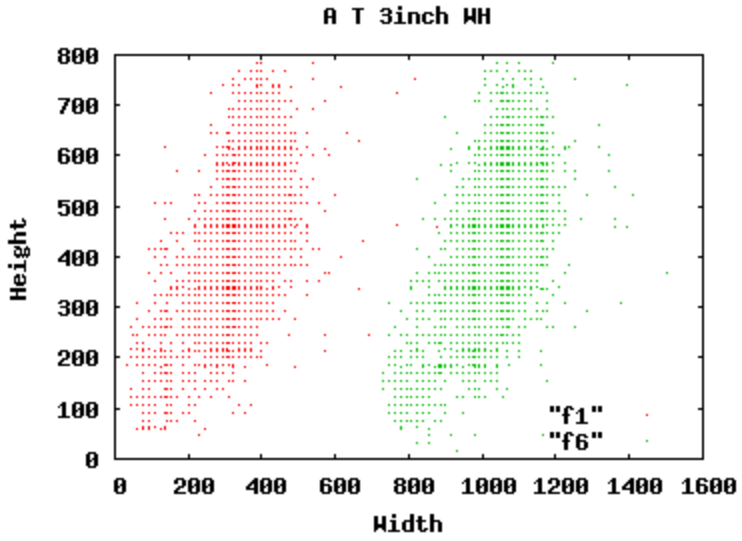




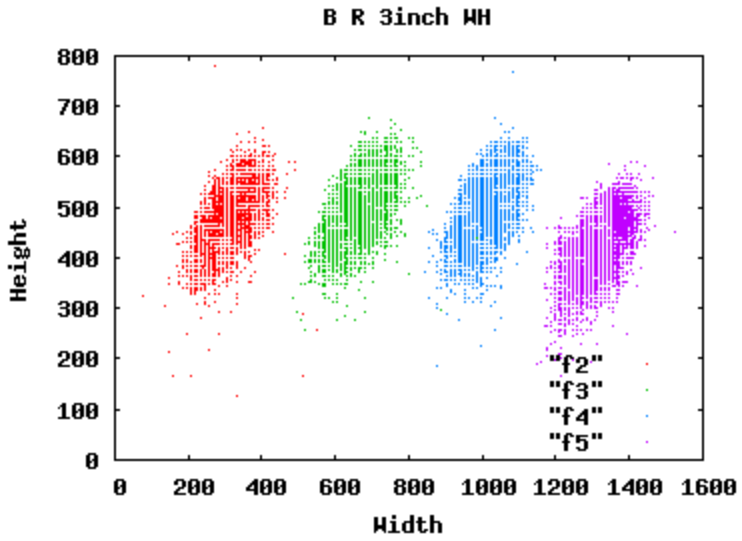
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan

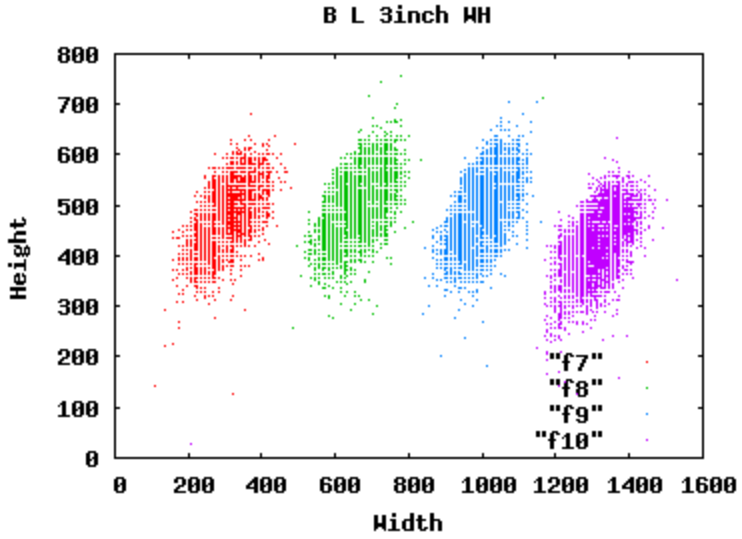


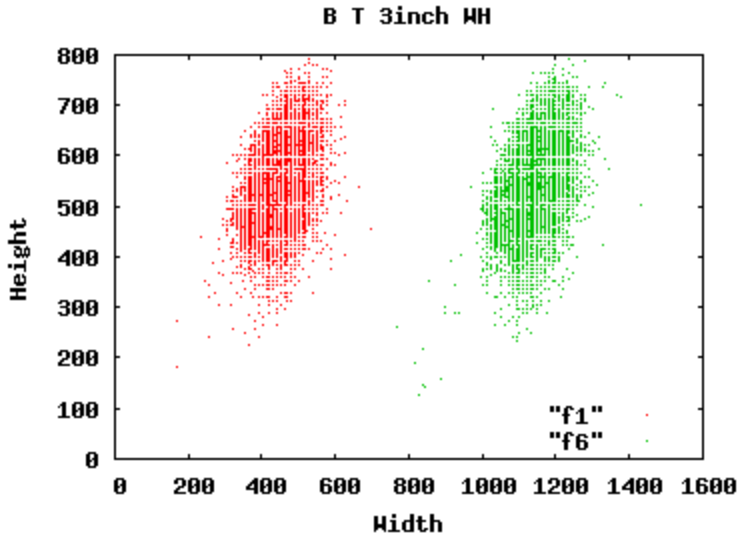




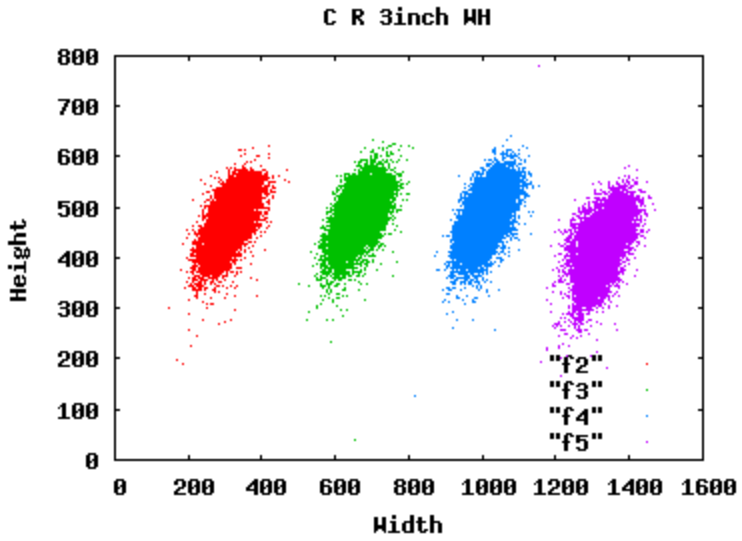
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan

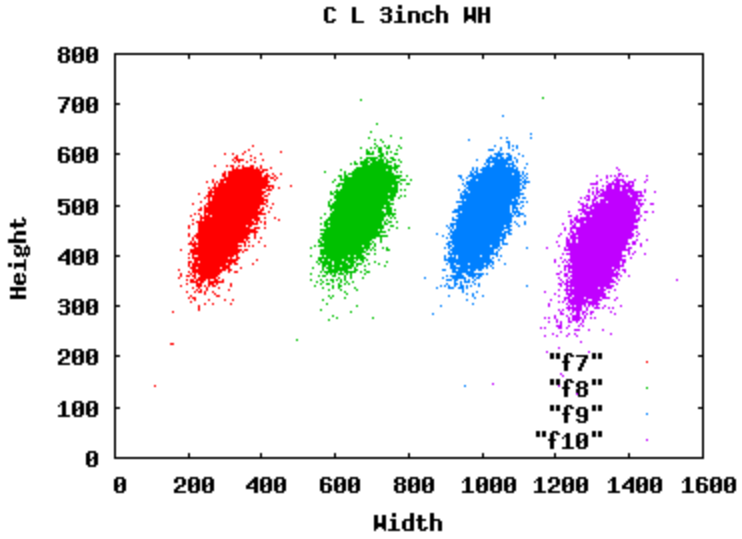


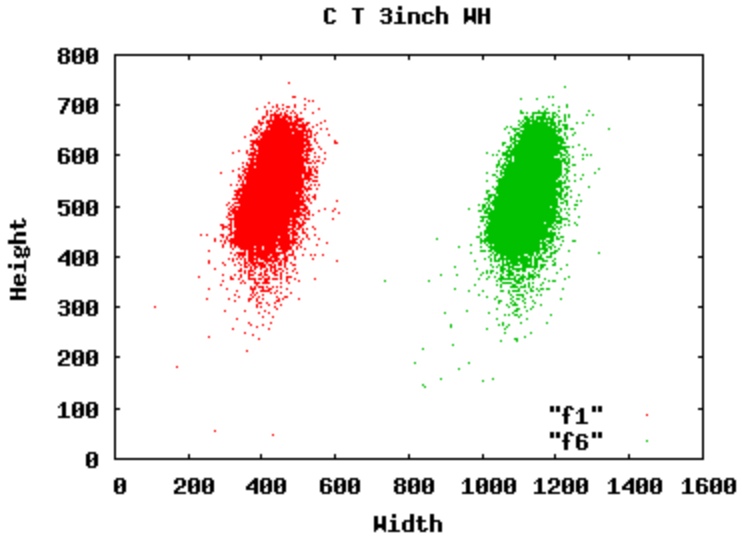




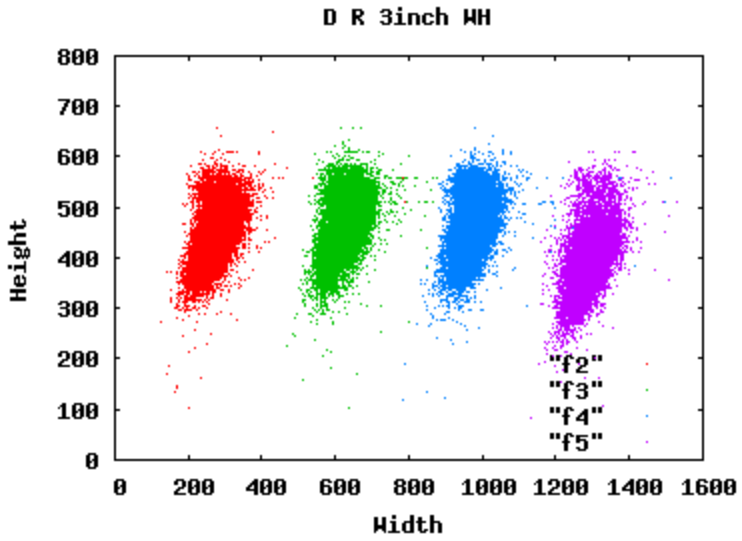
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan

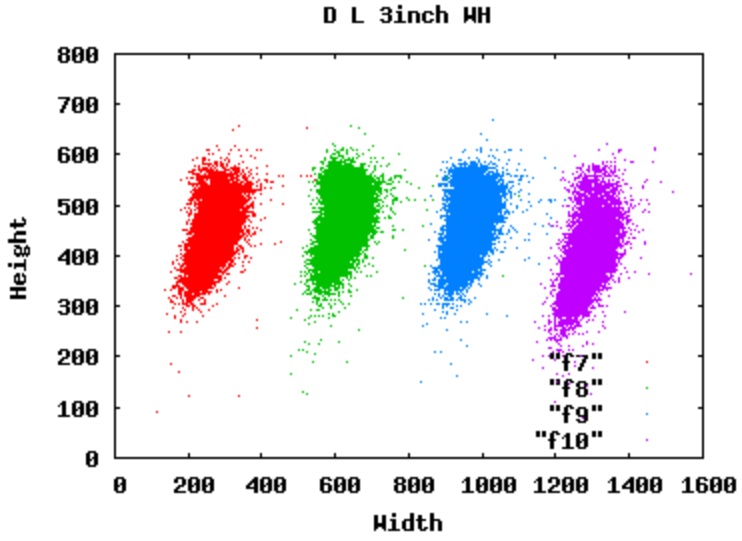


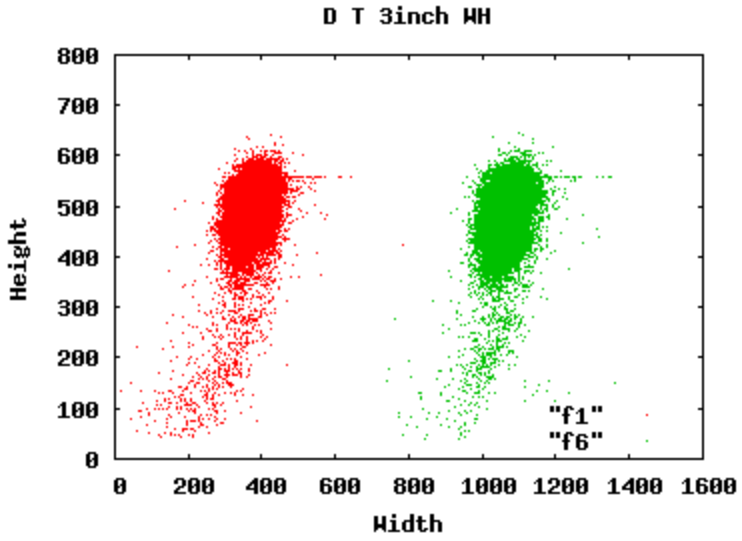




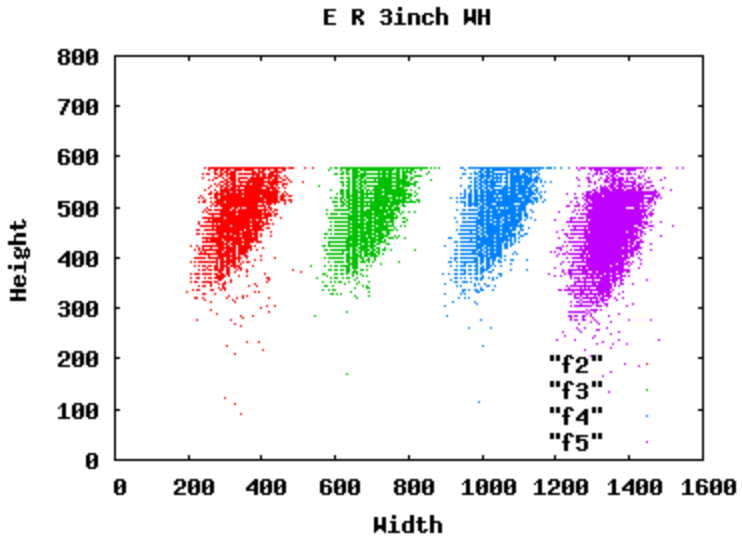
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan

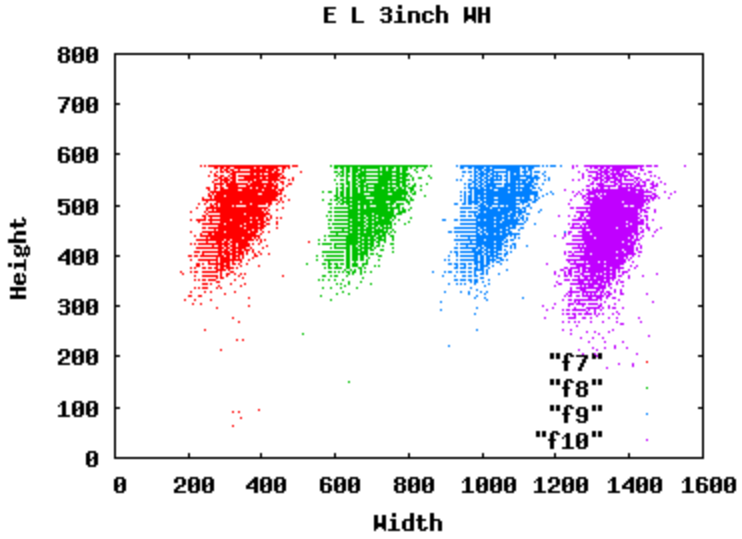


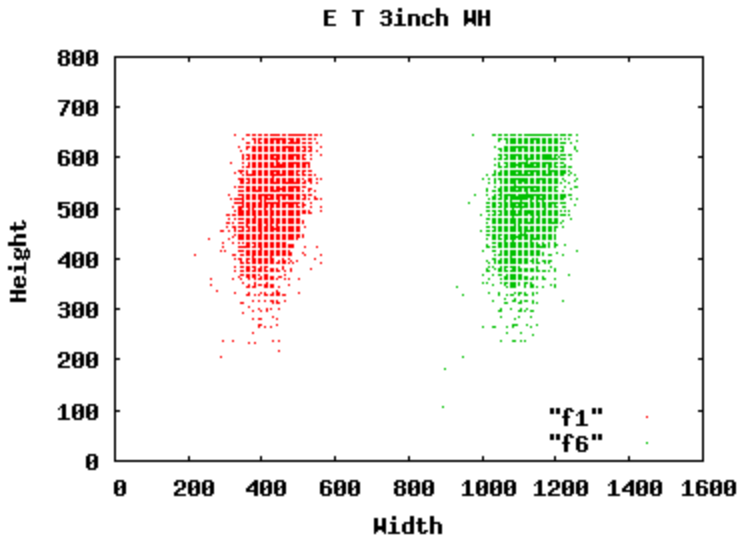




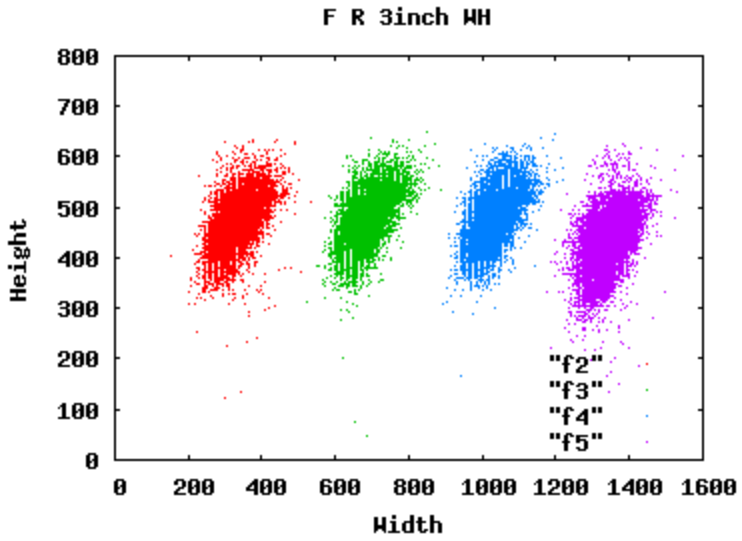
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan

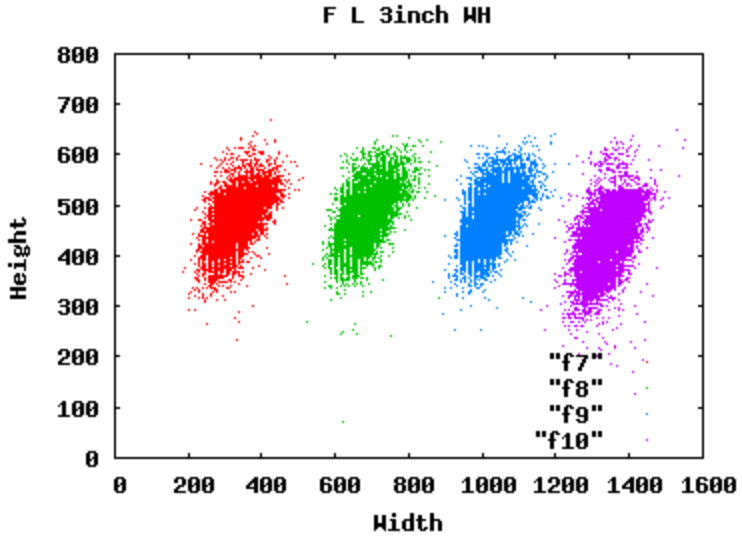


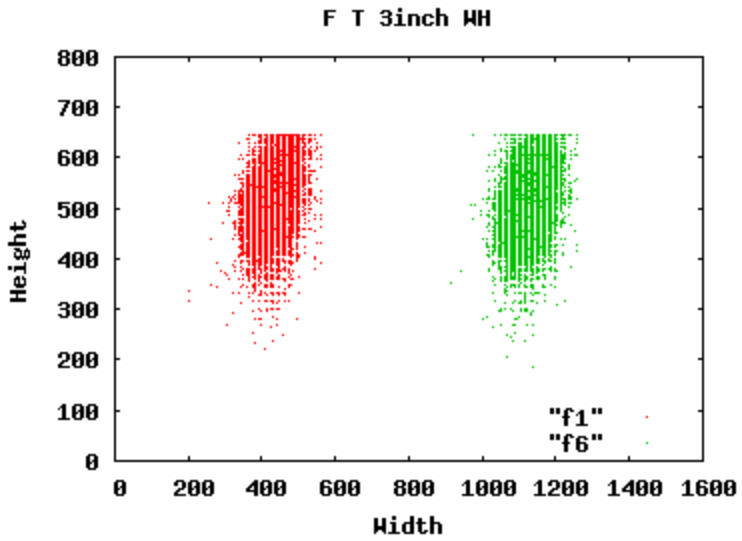




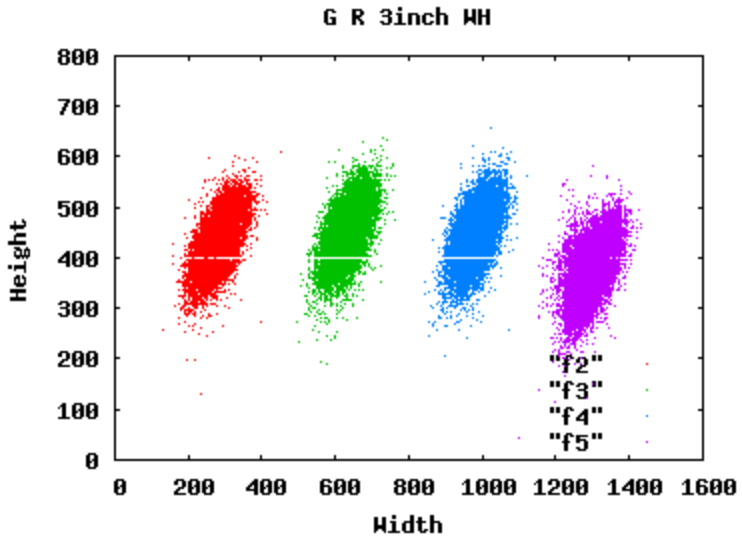
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan

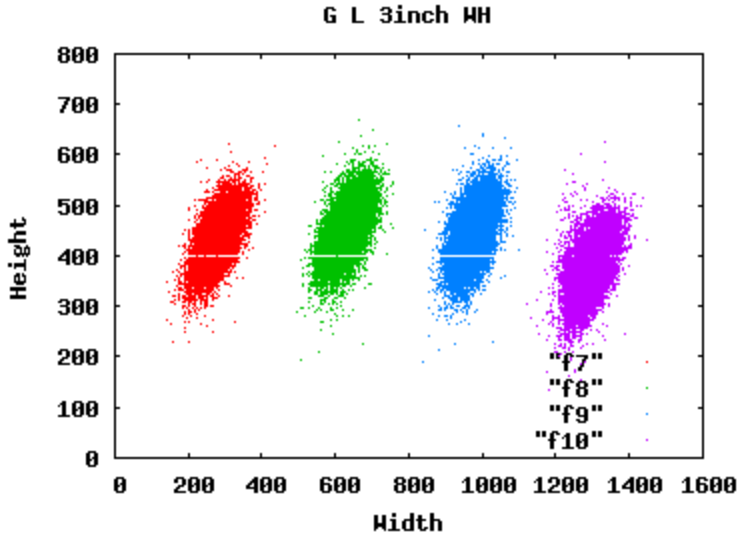


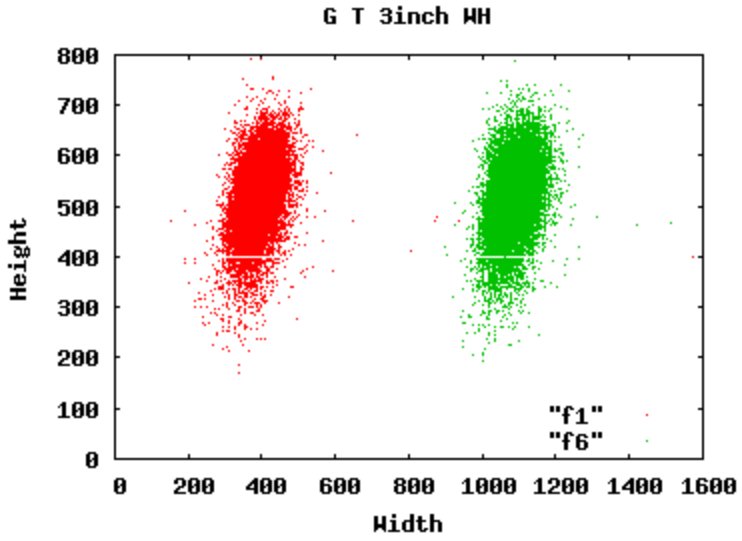




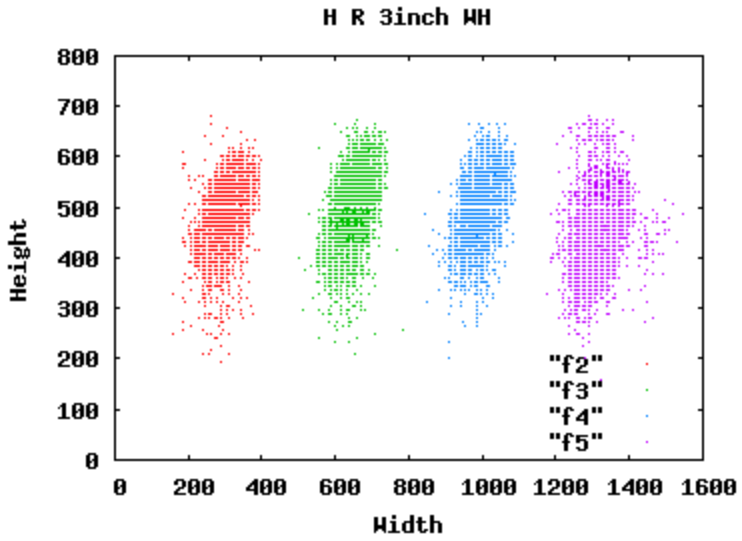
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan

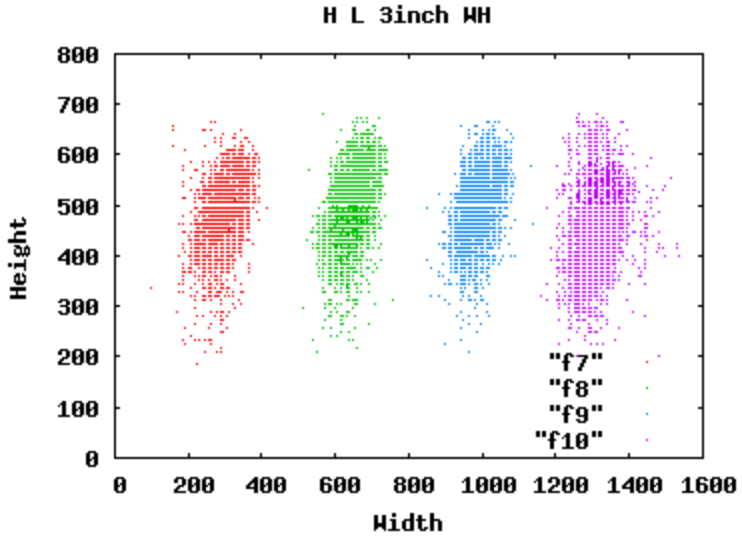


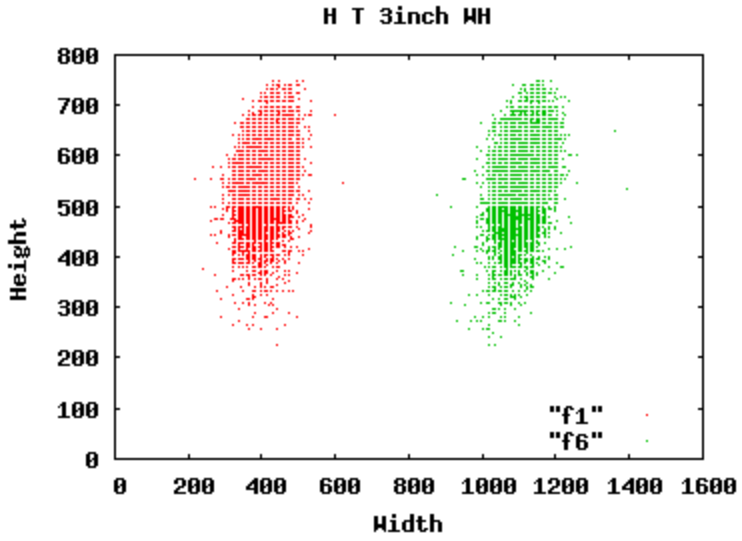




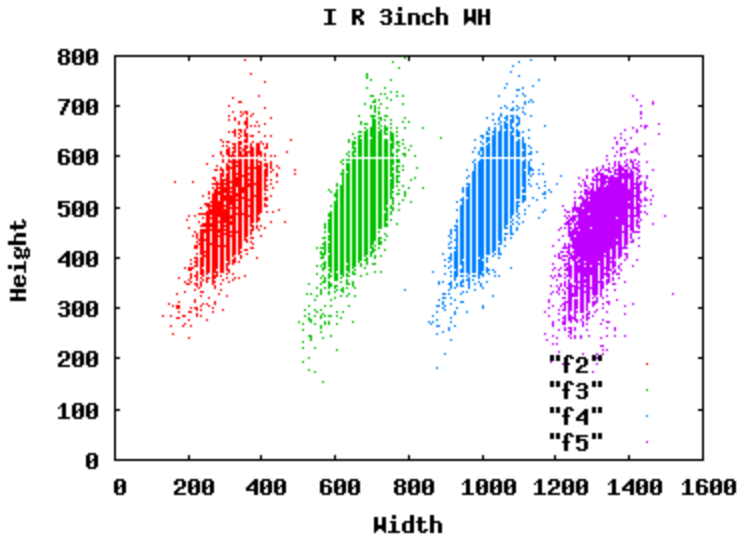
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan

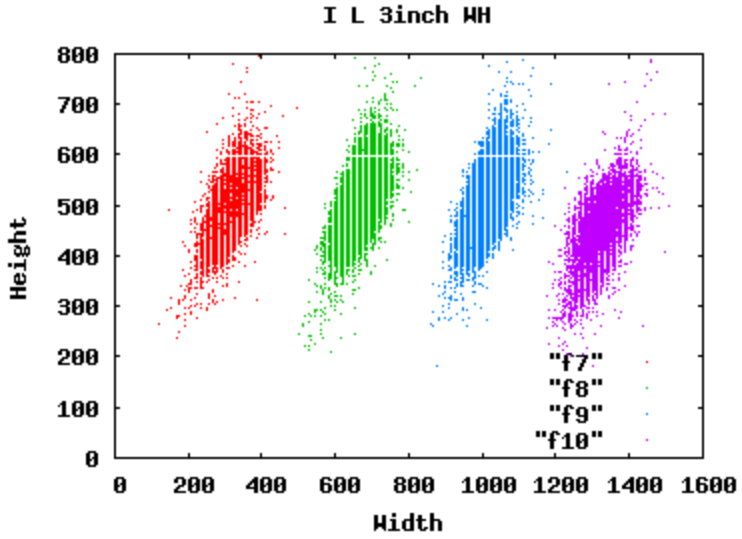


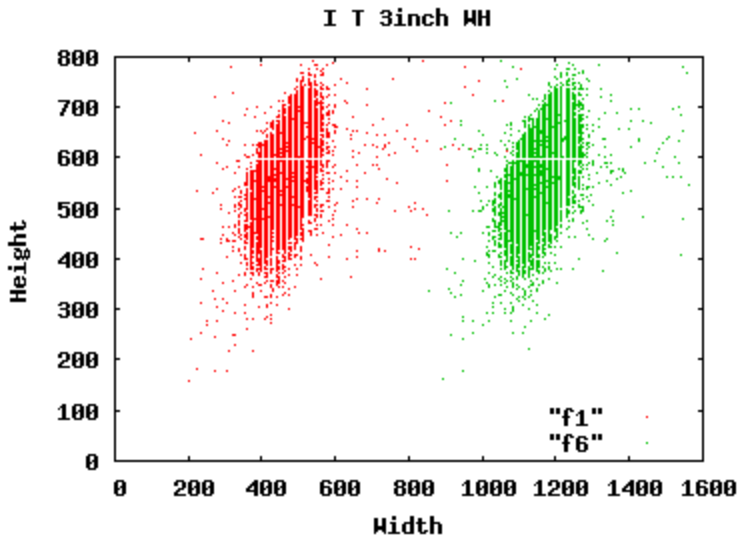




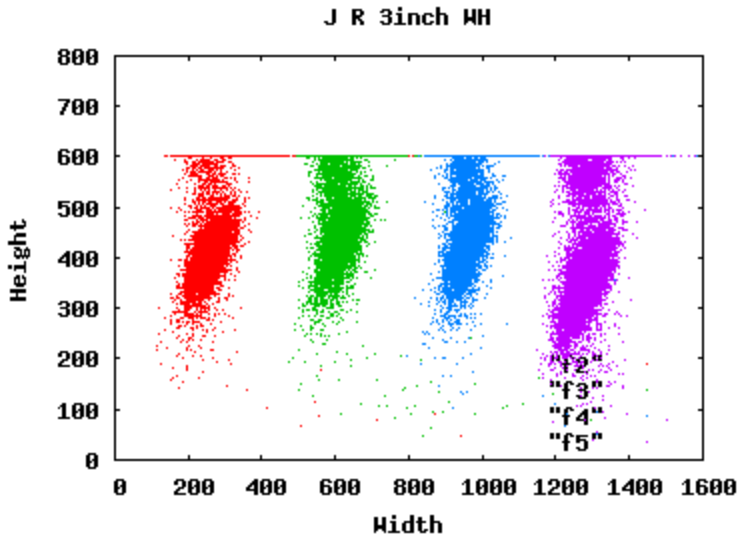
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan

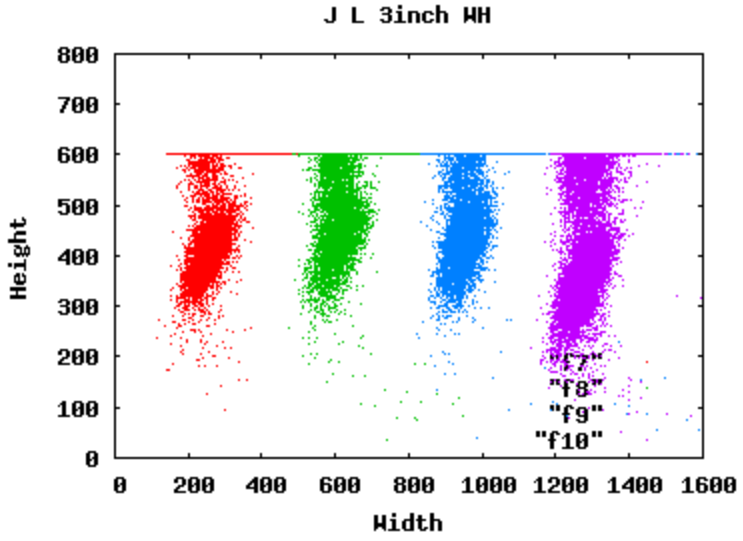


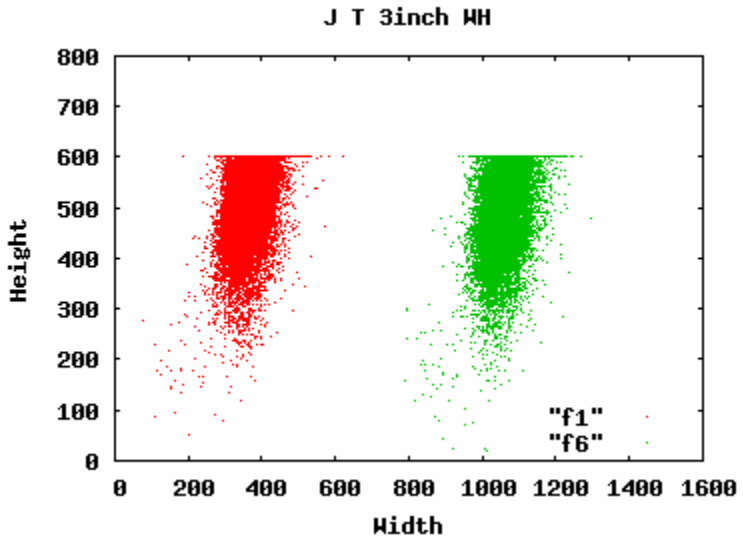




A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



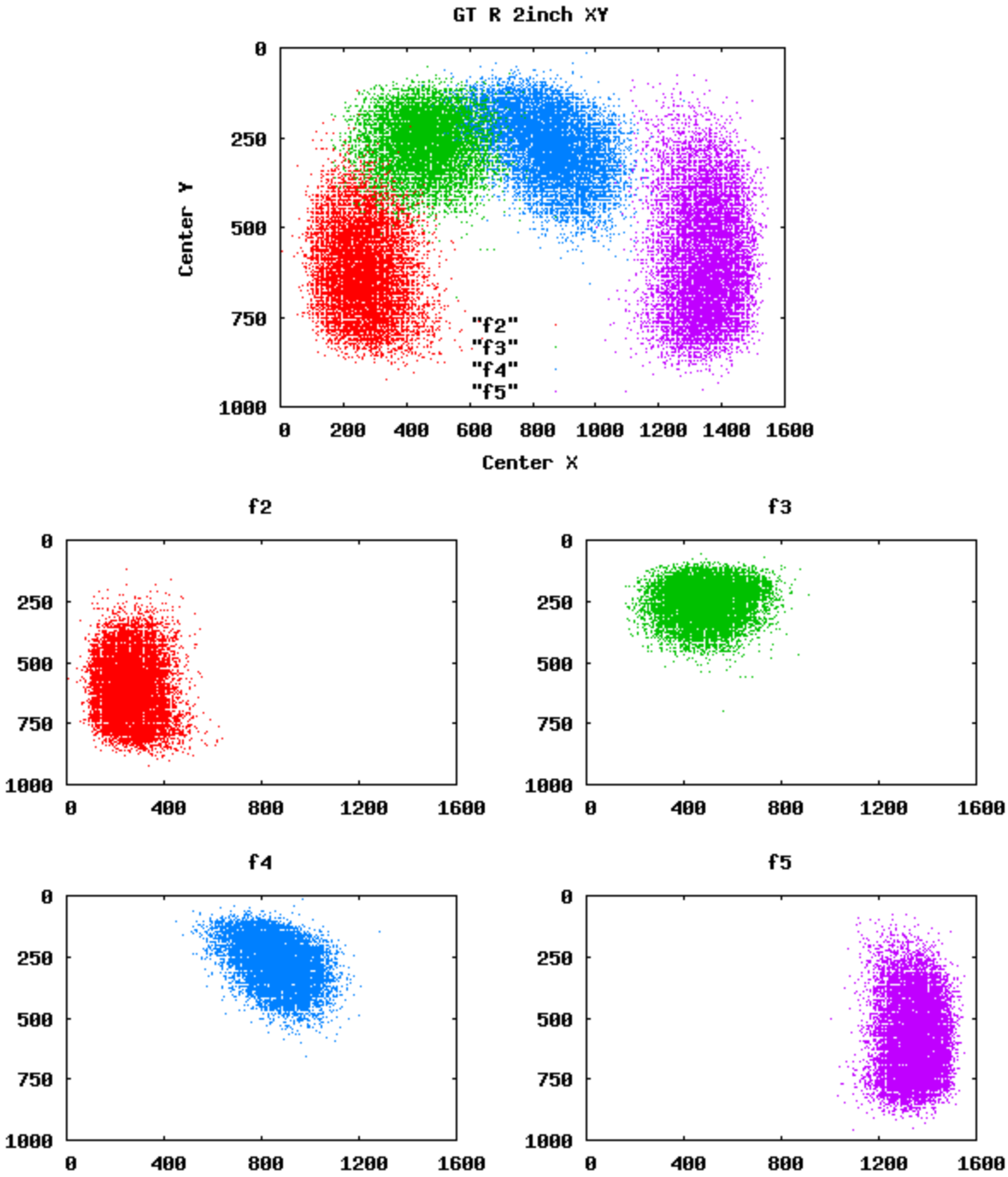




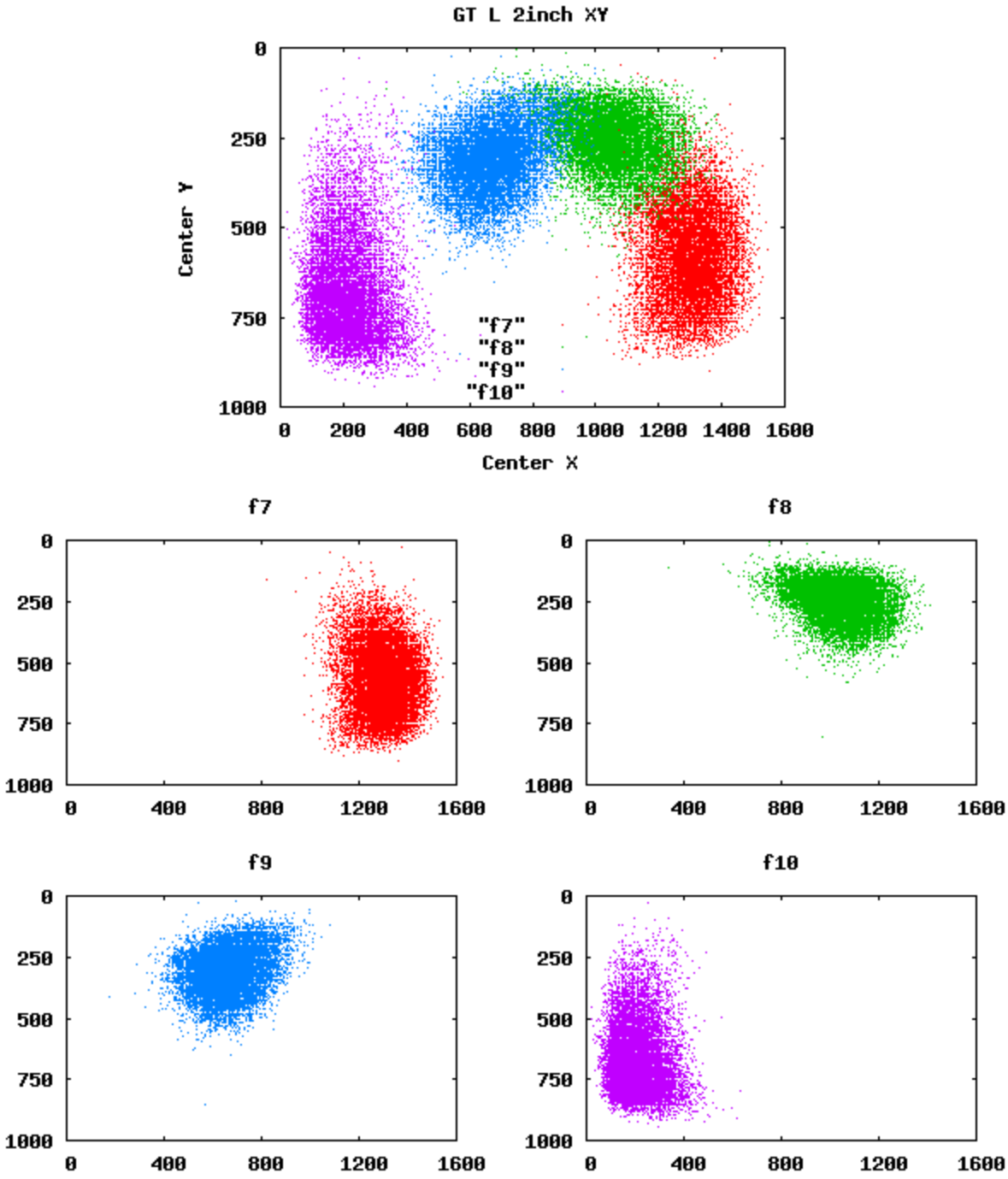
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan

Appendix F. Plots of 2-inch segmentation box centers.

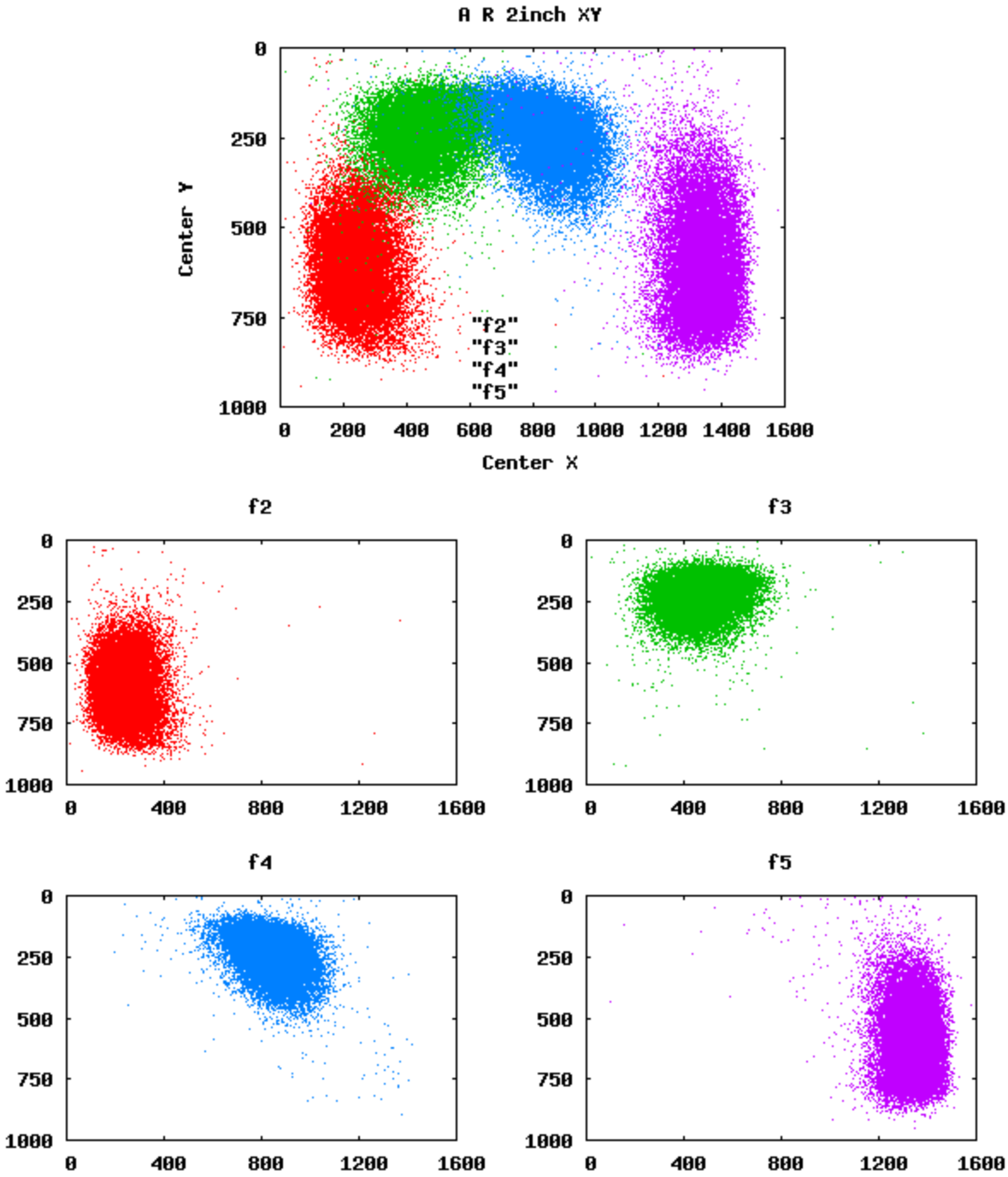
The plots in this appendix show the distribution of the segmentation box centers (x,y) for the 2-inch data. There is a combined plot for each slap image and then a smaller plot for each finger position. The individual finger plots are better for seeing the full “spread” of x,y positions detected. The plot for the ground truth (GT) is included as a baseline for comparison. The blank lines that appear in some of the plots are most likely caused by the segmentation algorithm doing some level of sampling of the input image. The reason the lines are not evenly distributed in some plots is an artifact of the sampling when scaling the images for displaying in the report.



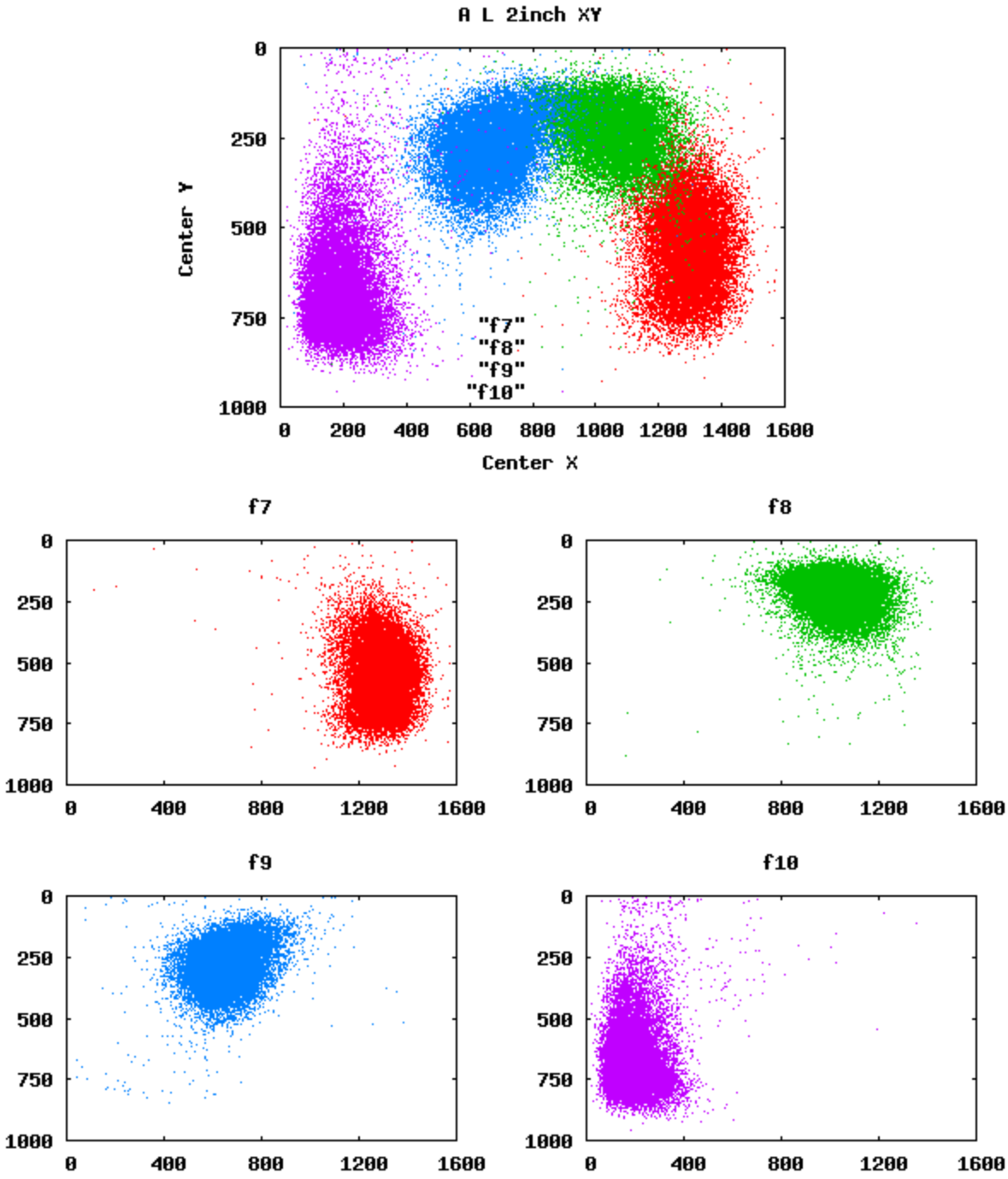
A = Aware || B/C = Cogent || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



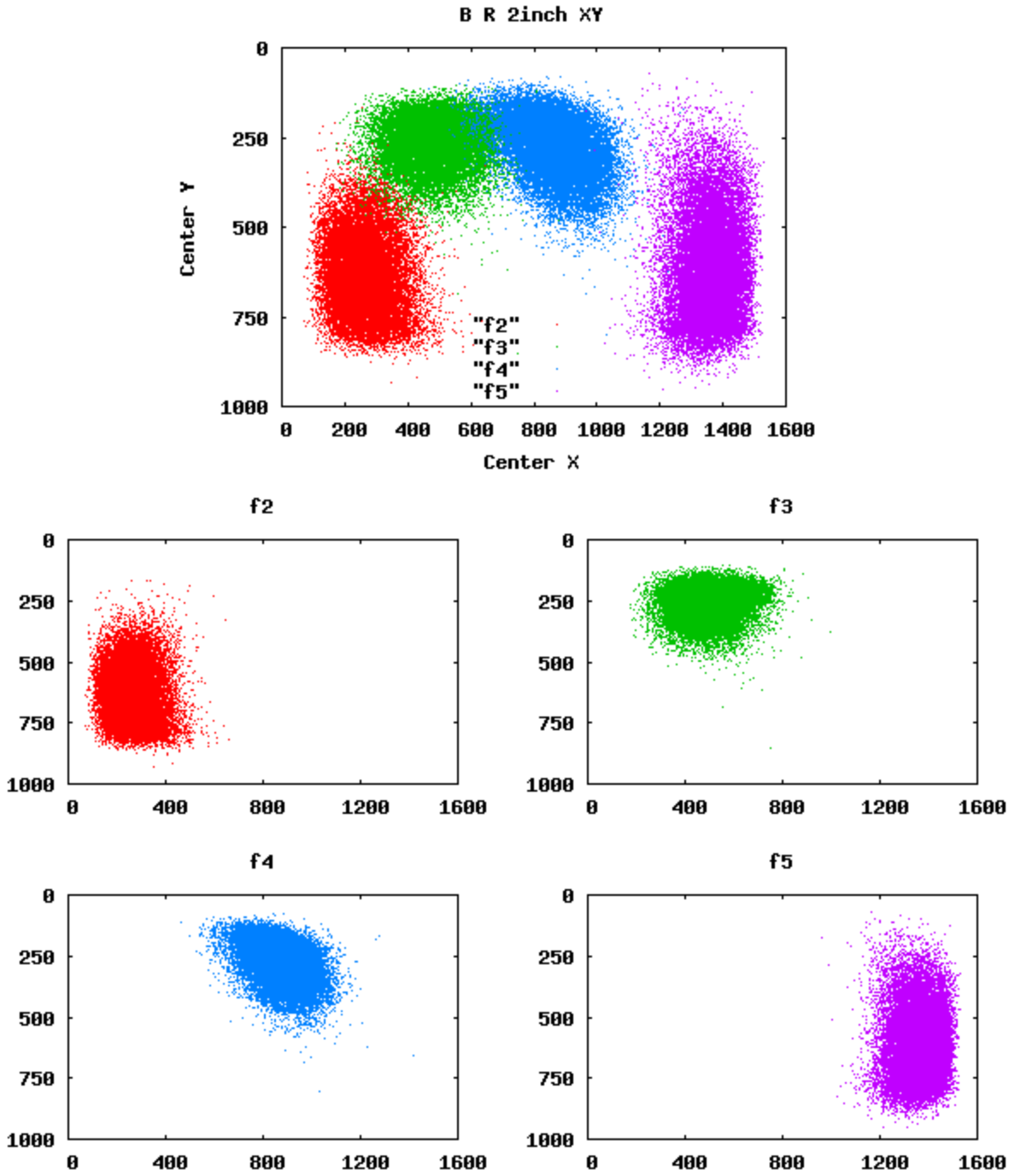
A = Aware || B/C = Cogent || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



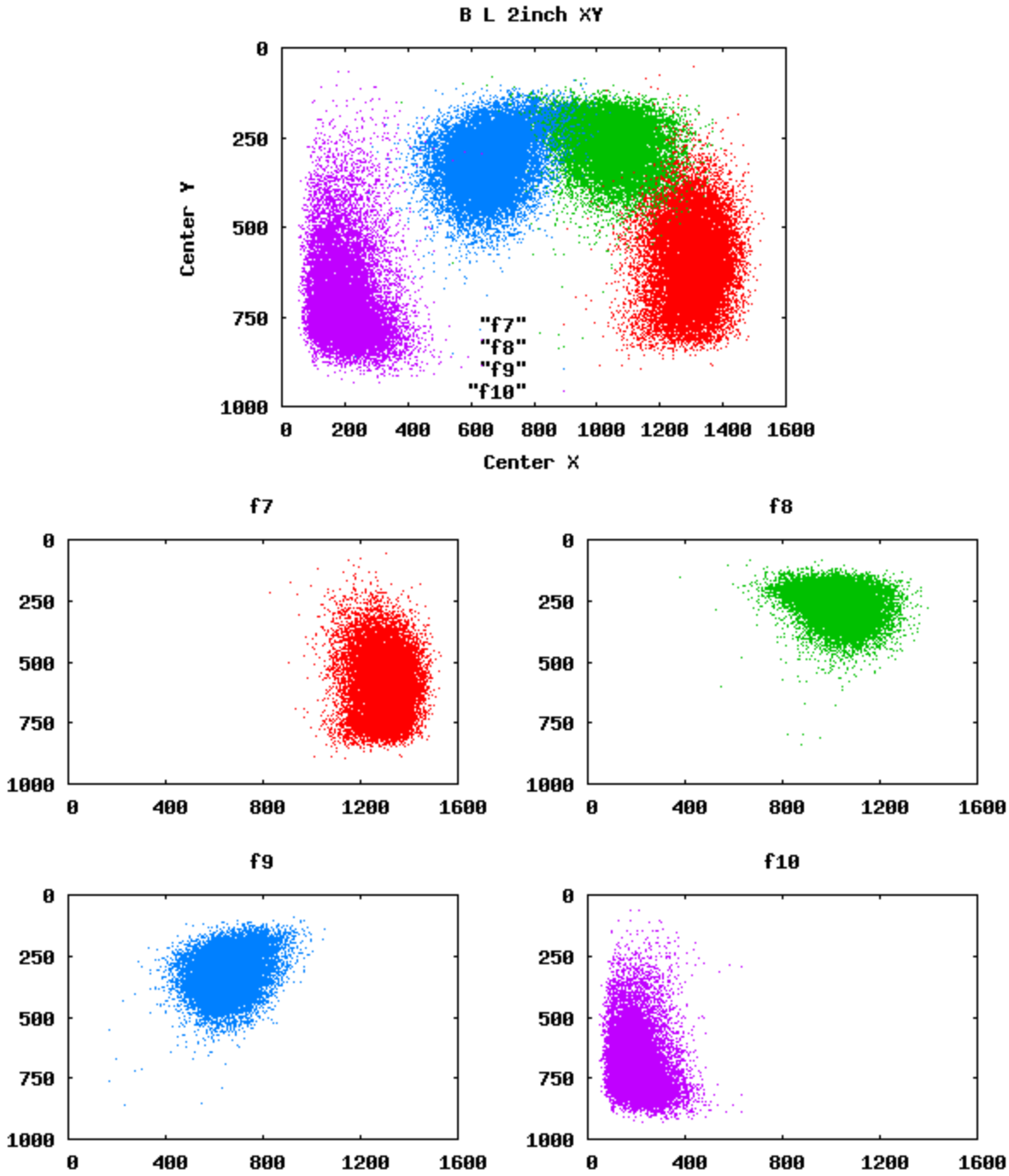
A = Aware || B/C = Cogent || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



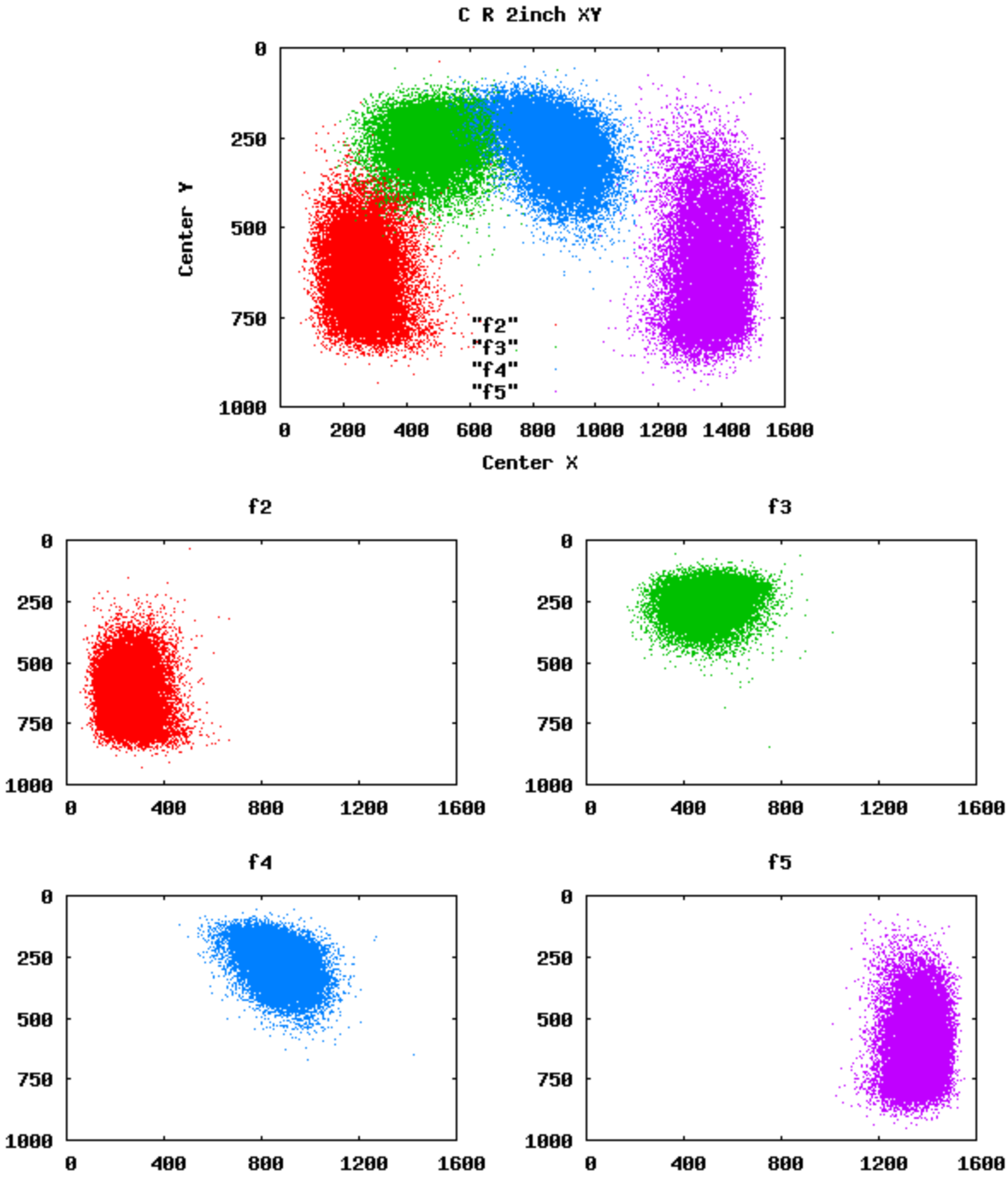
A = Aware || B/C = Cogent || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



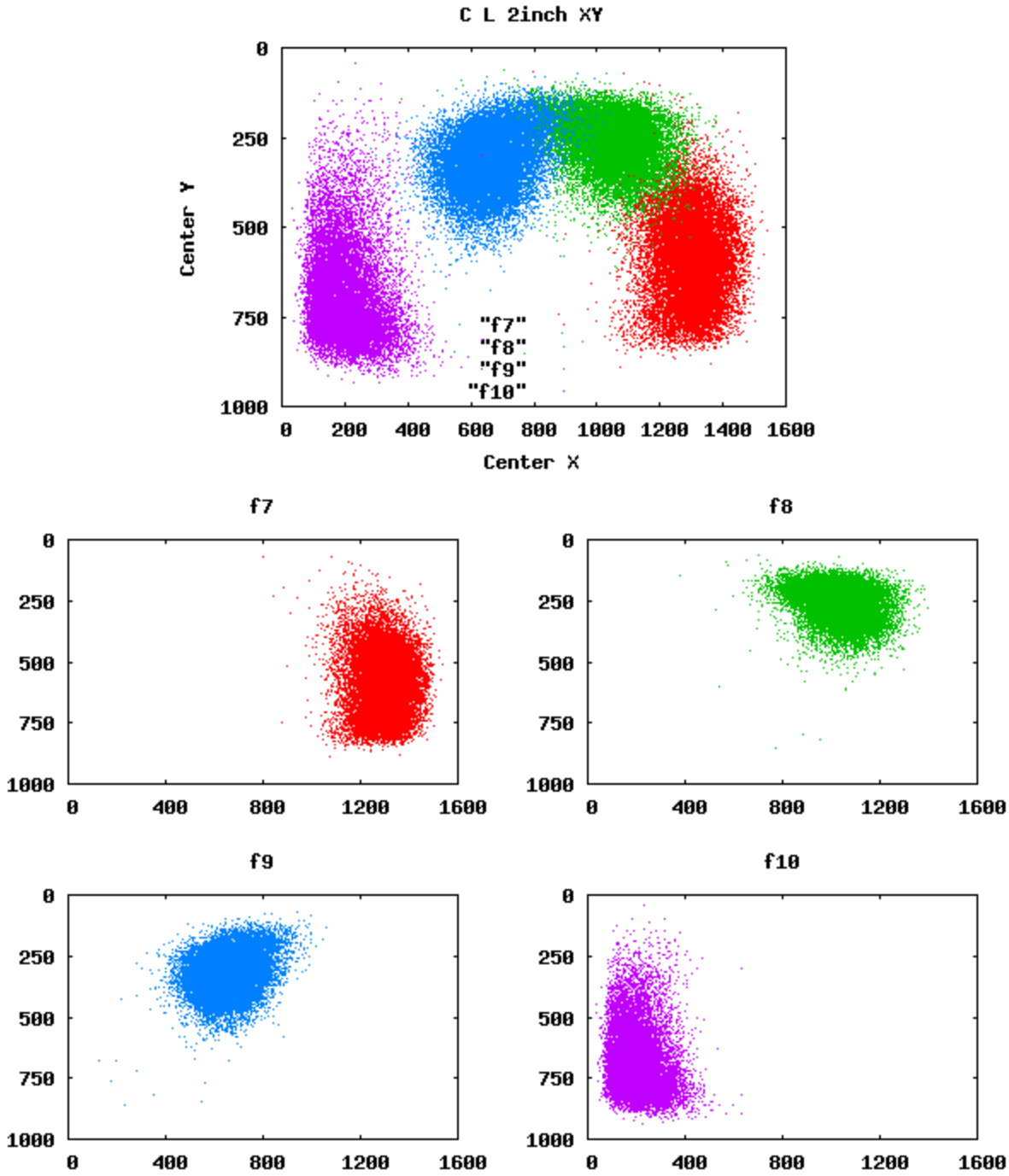
A = Aware || B/C = Cogent || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



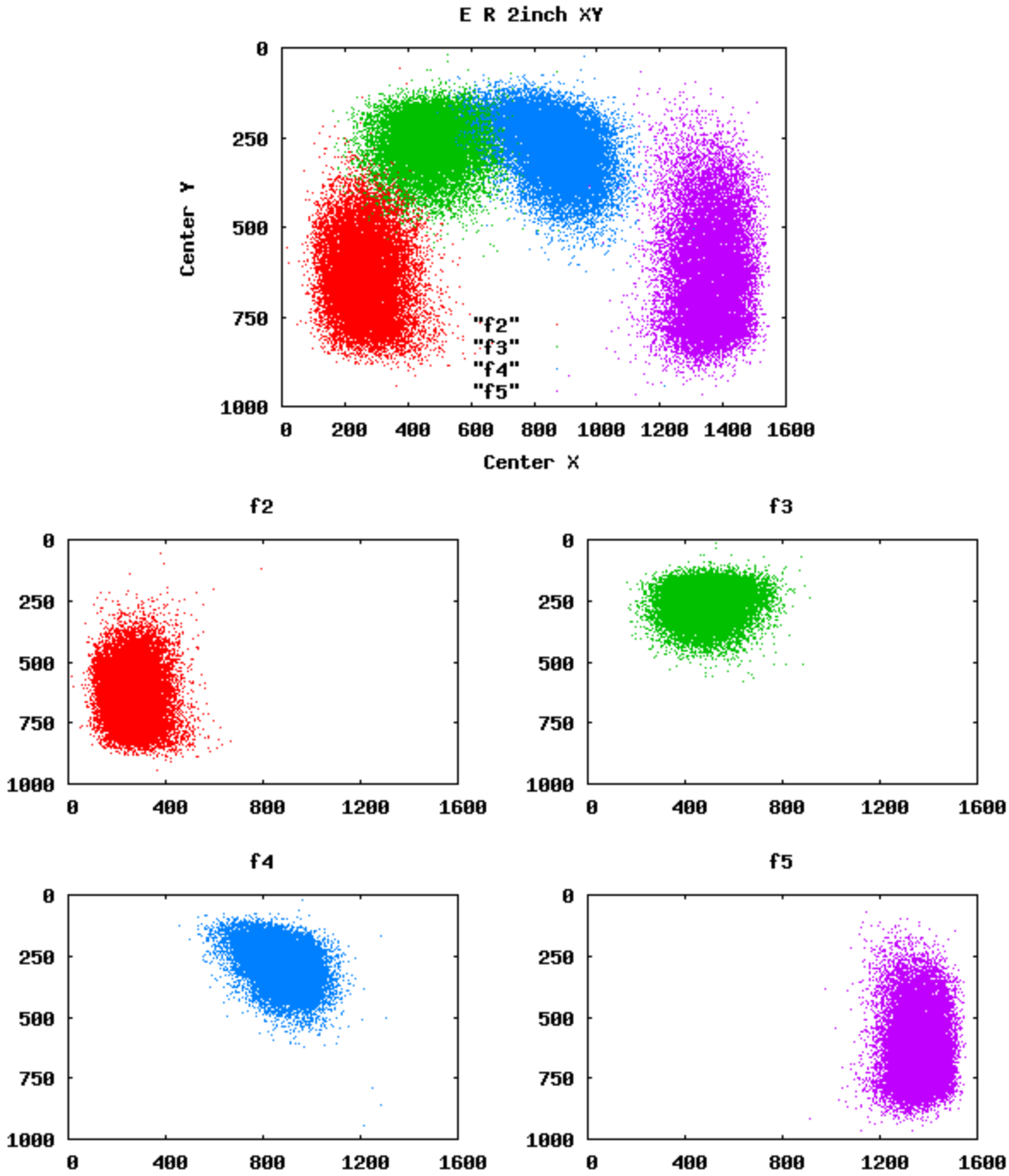
A = Aware || B/C = Cogent || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



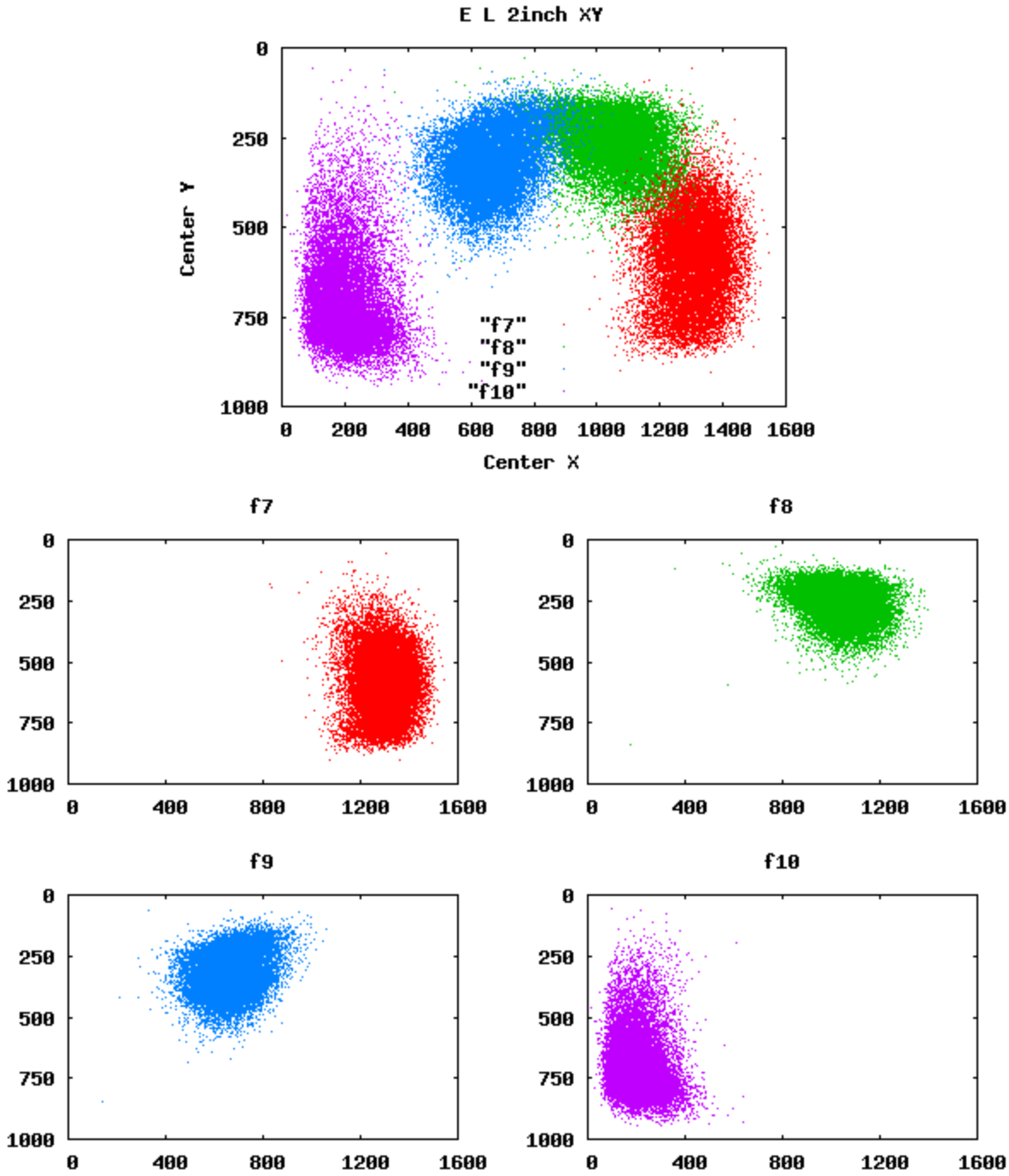
A = Aware || B/C = Cogent || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



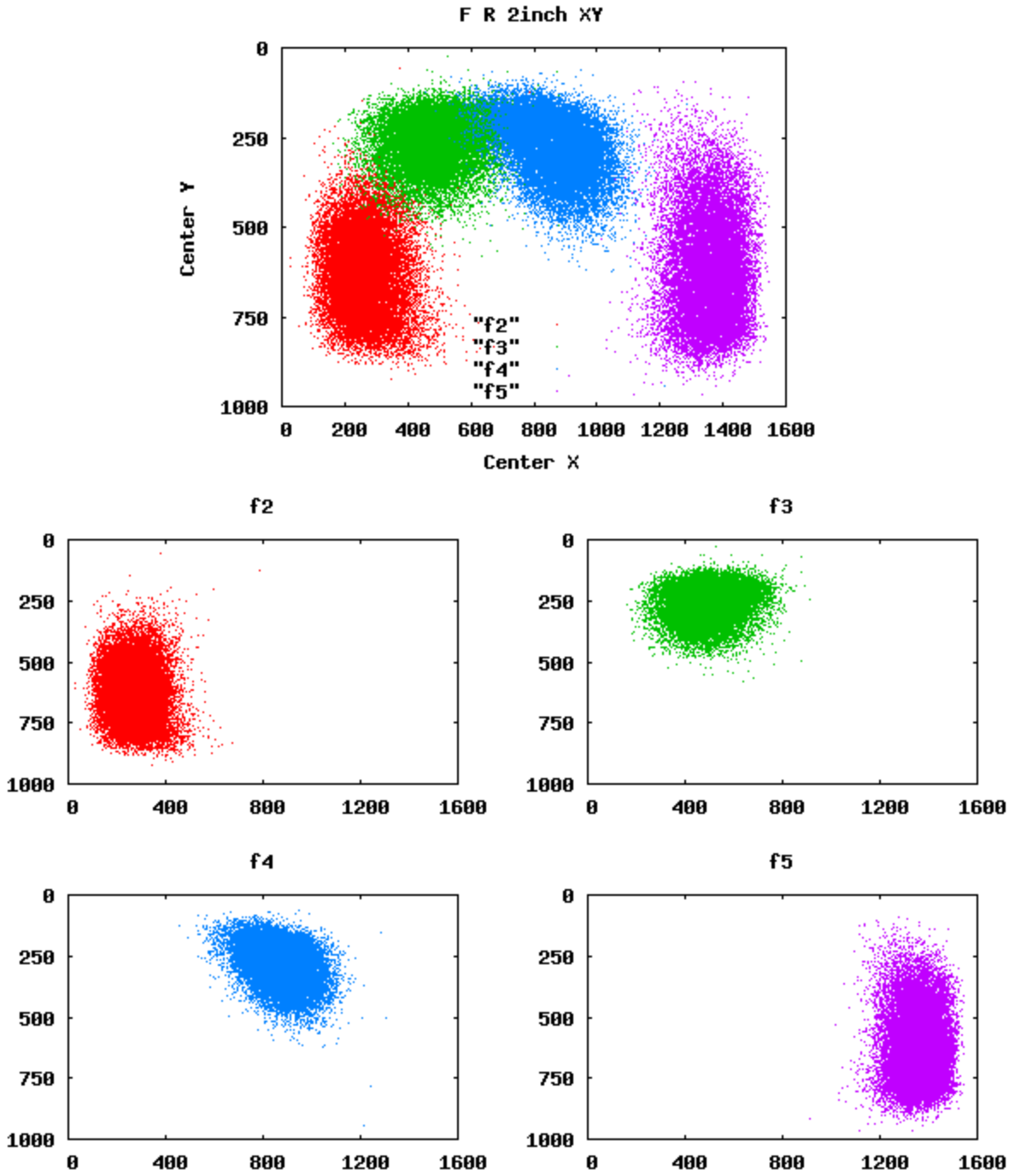
A = Aware || B/C = Cogent || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



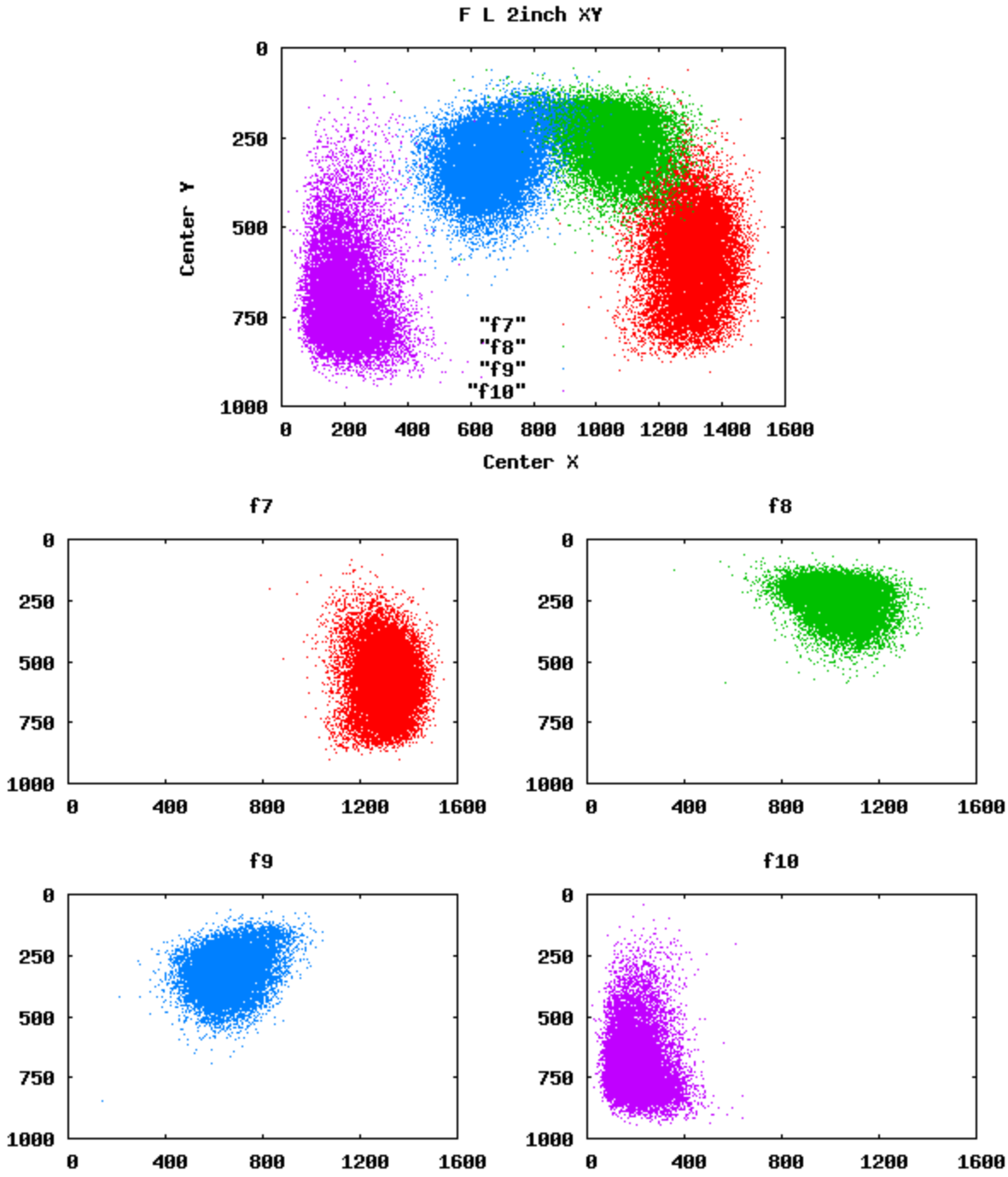
A = Aware || B/C = Cogent || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



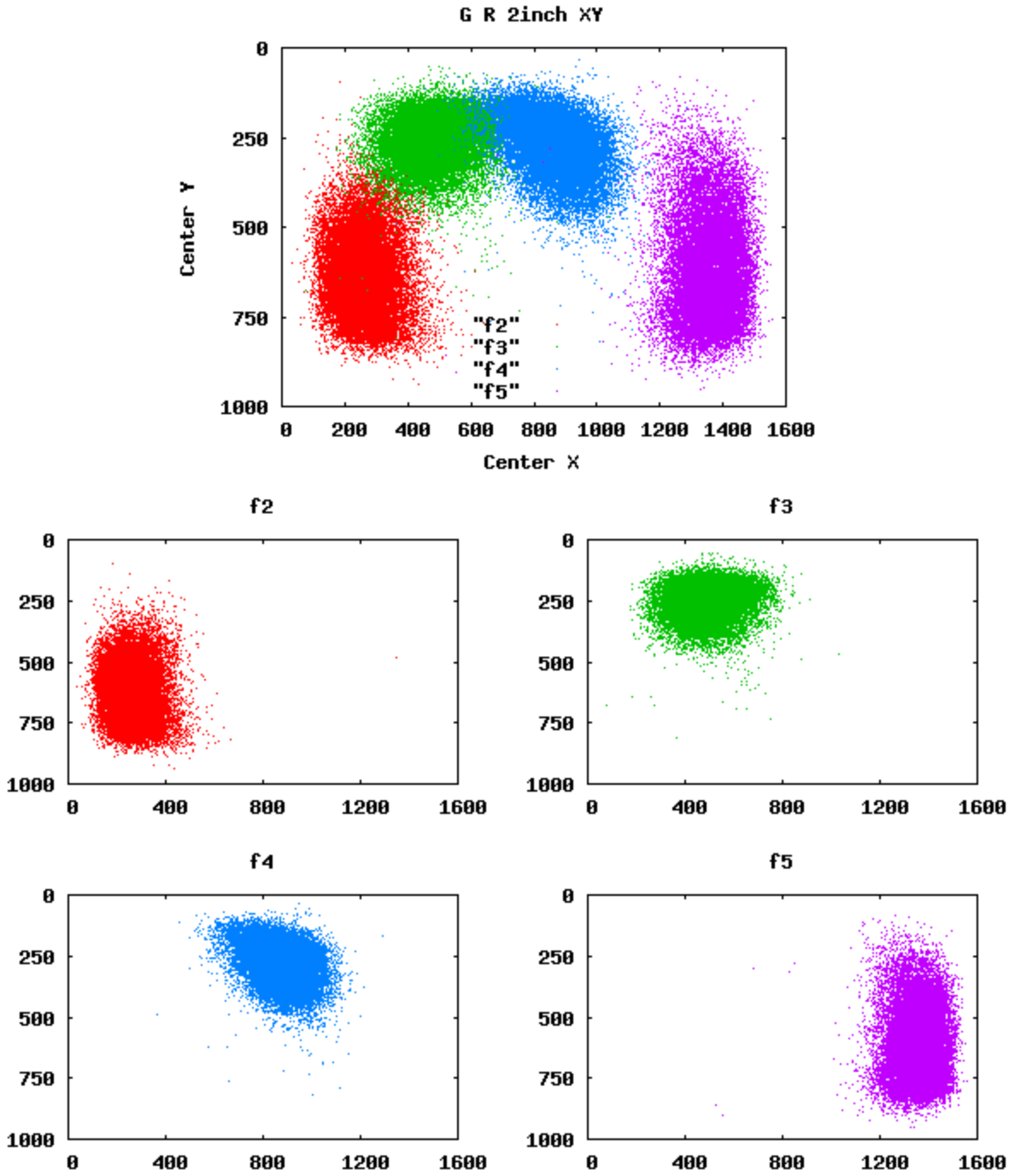
A = Aware || B/C = Cogent || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



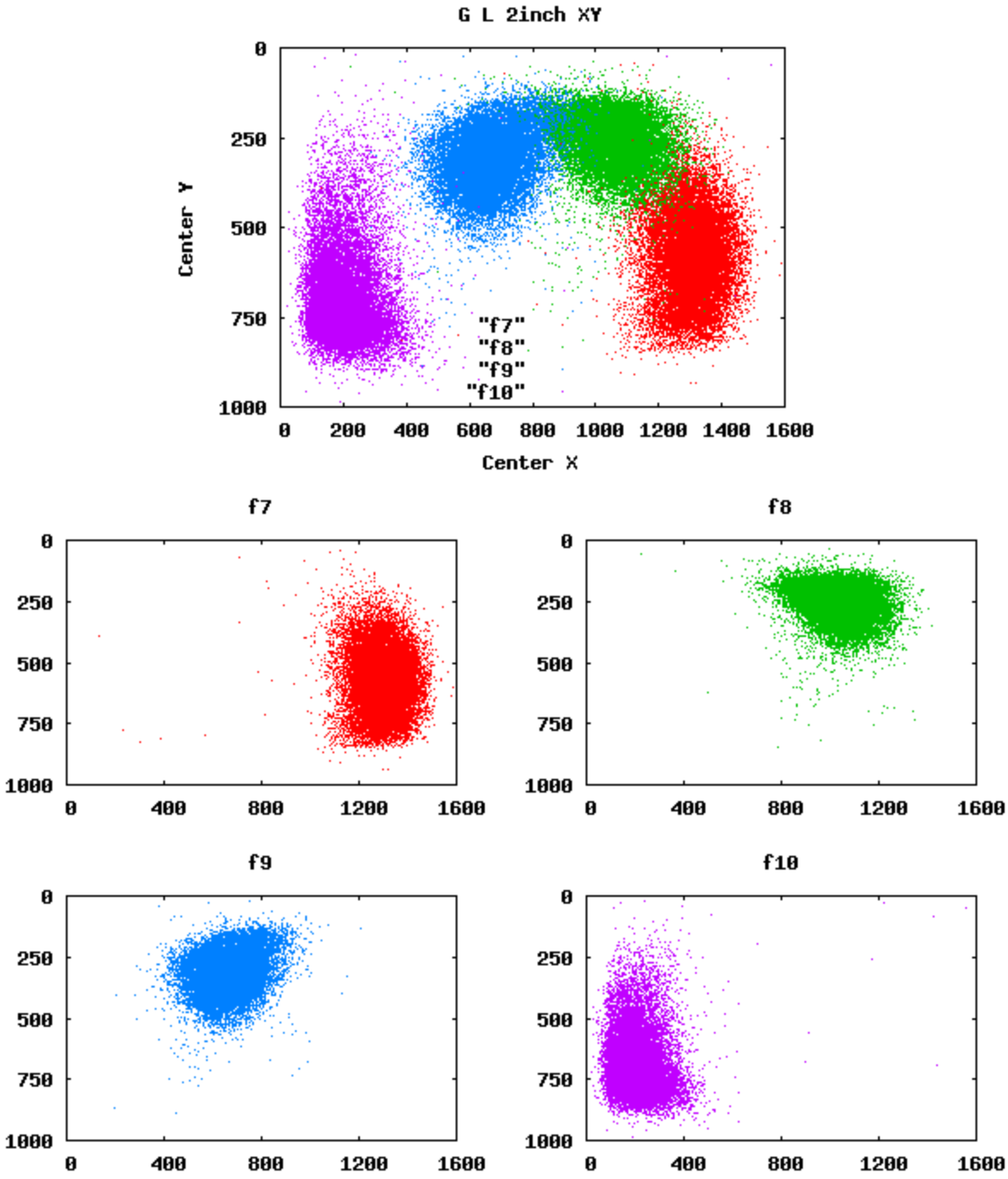
A = Aware || B/C = Cogent || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



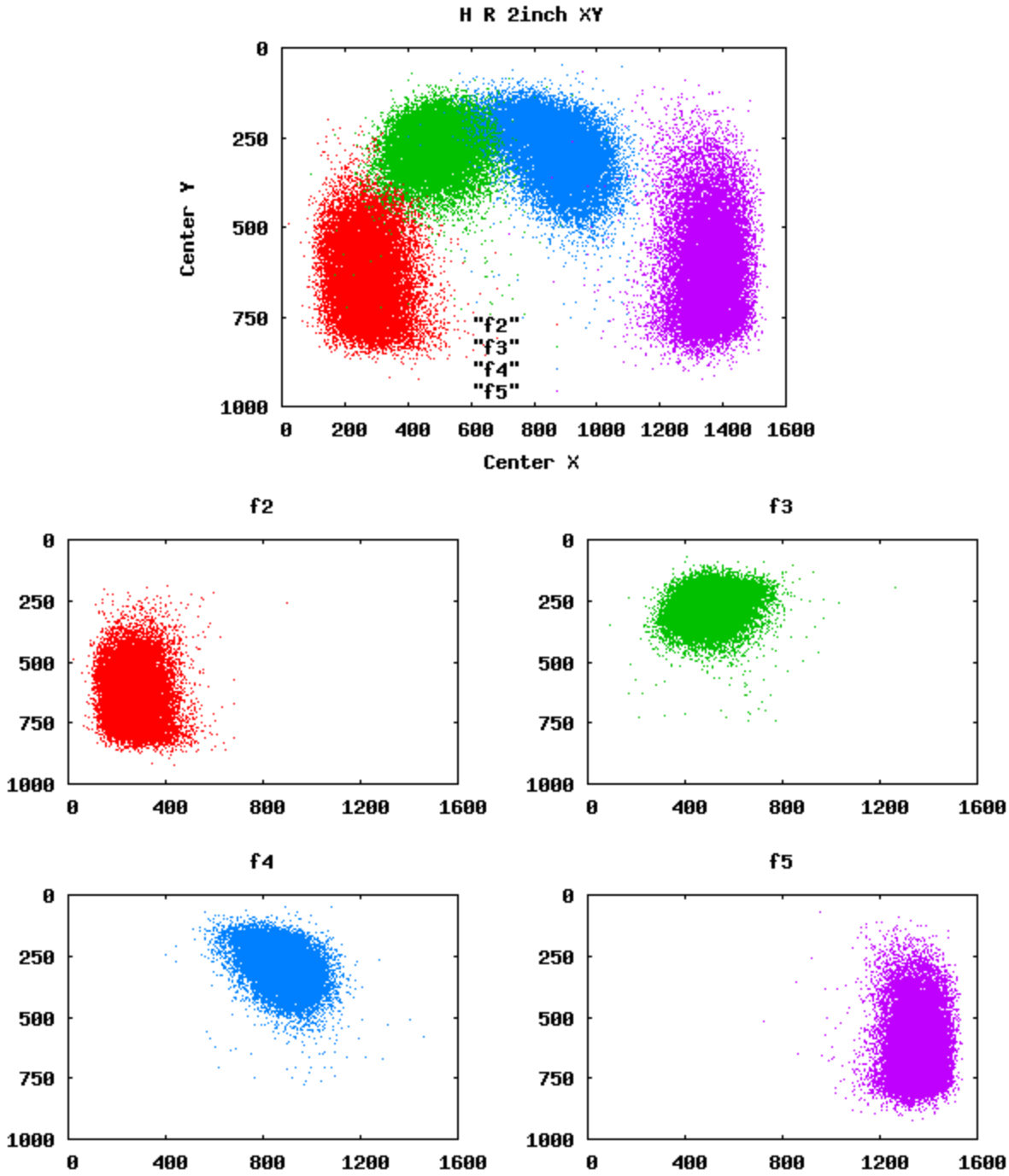
A = Aware || B/C = Cogent || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



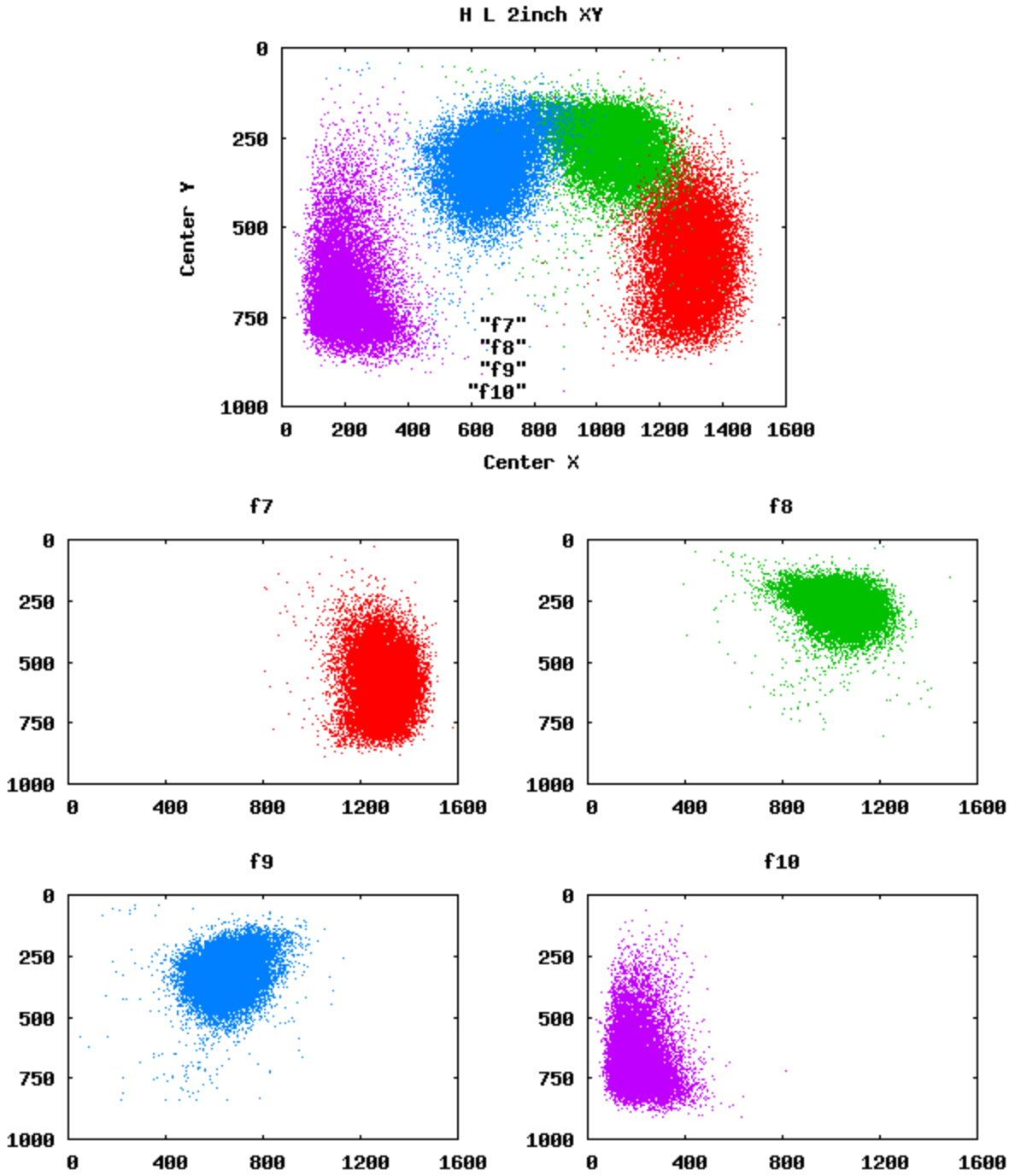
A = Aware || B/C = Cogent || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



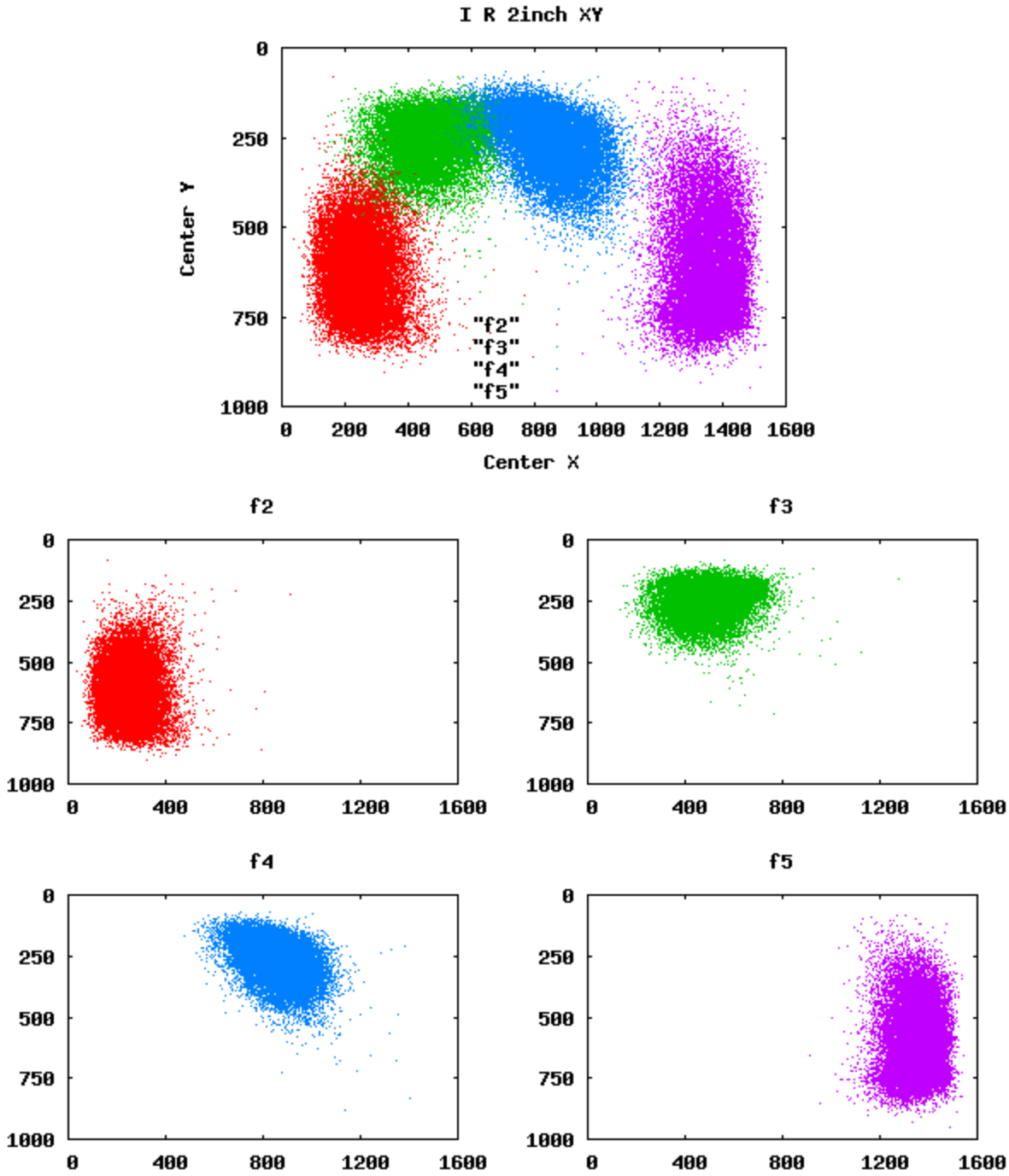
A = Aware || B/C = Cogent || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



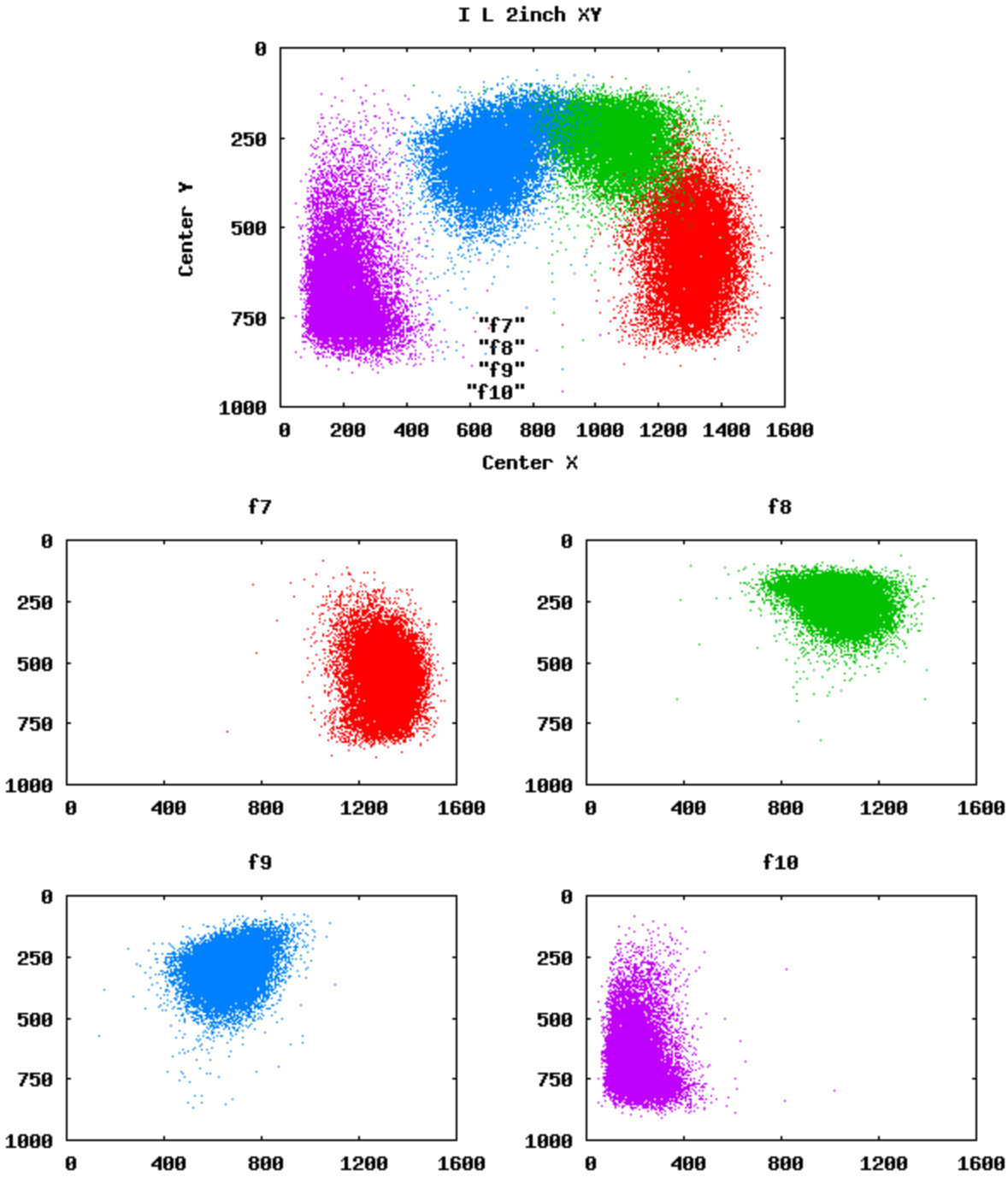
A = Aware || B/C = Cogent || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



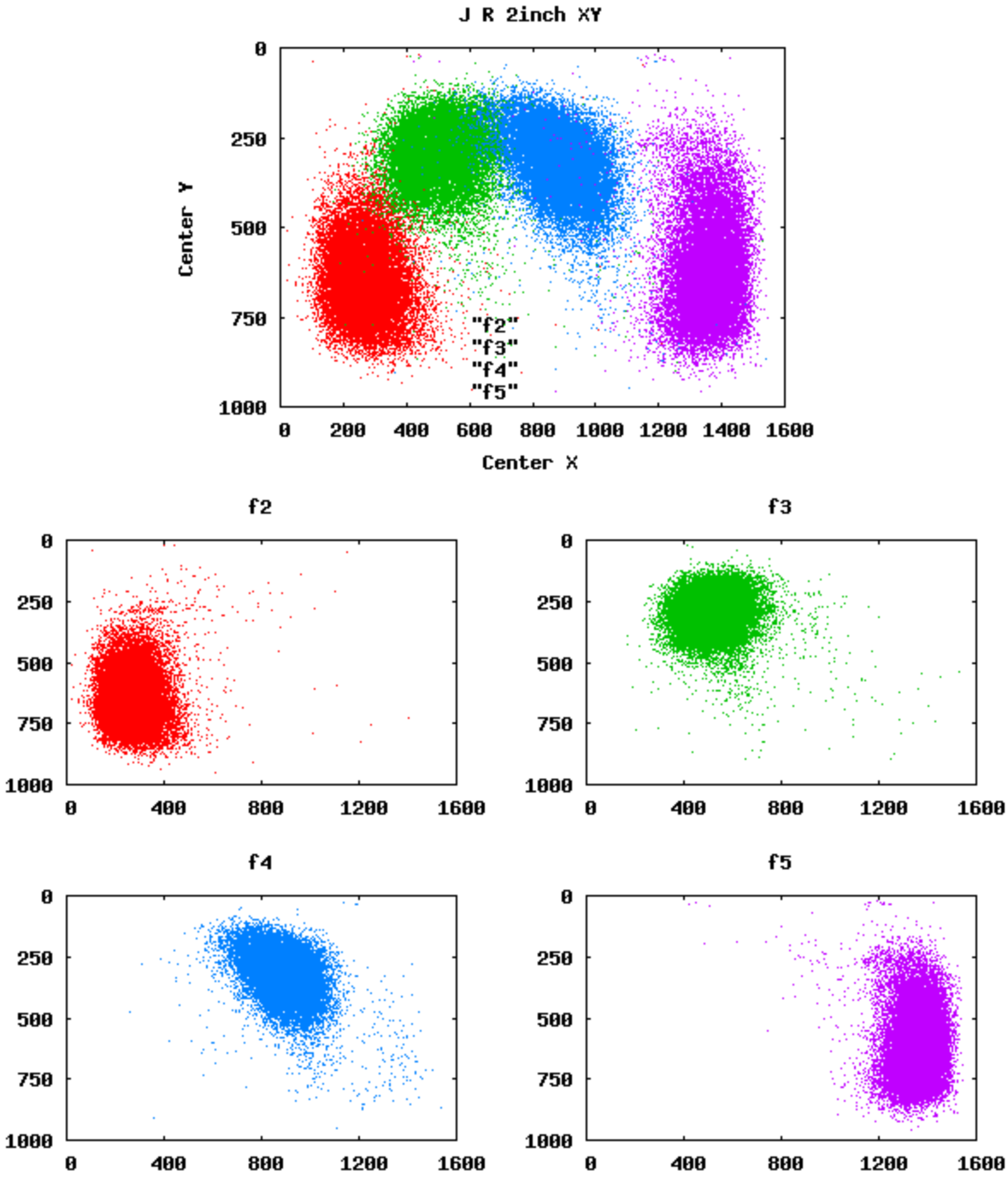
A = Aware || B/C = Cogent || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



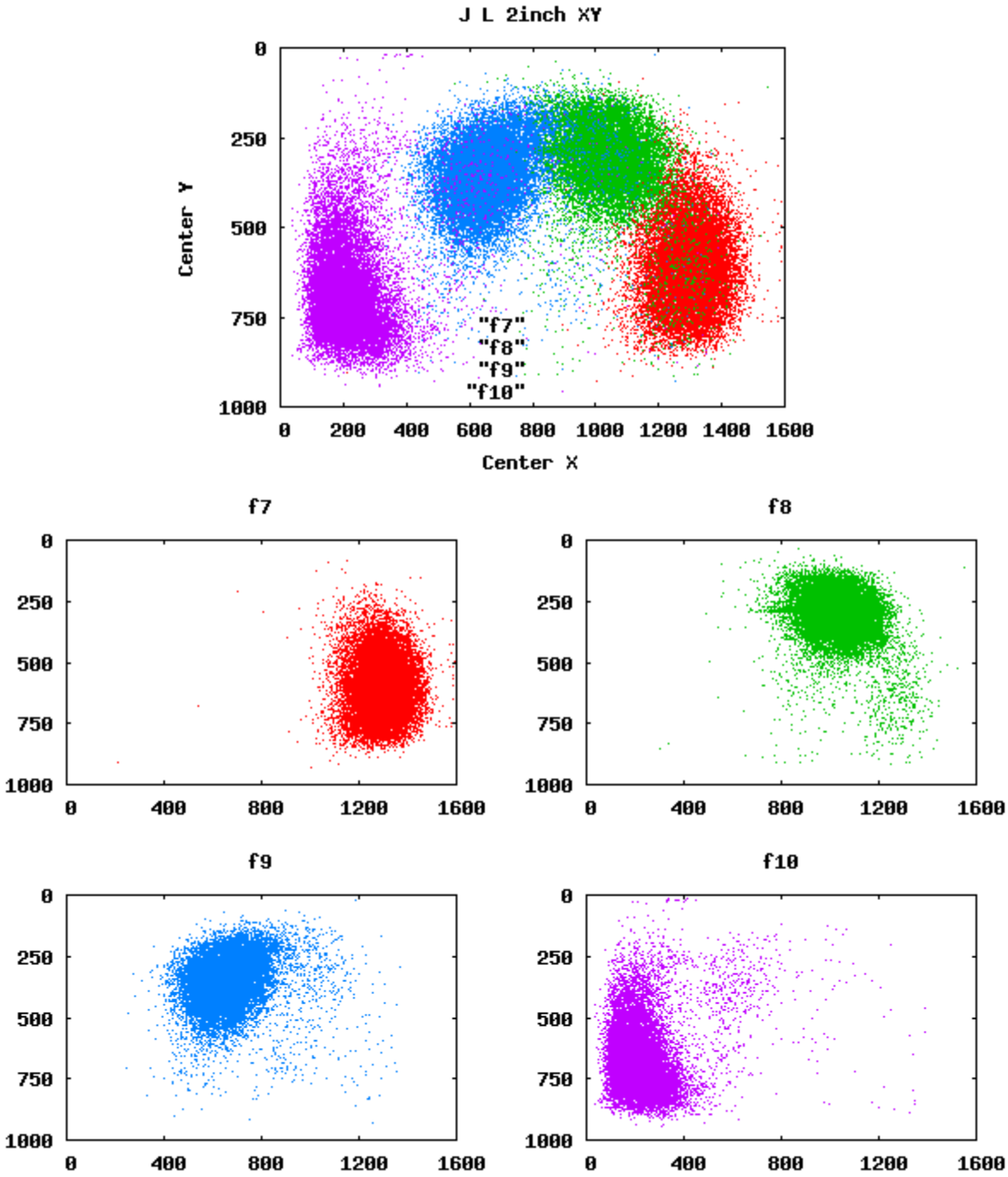
A = Aware || B/C = Cogent || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



A = Aware || B/C = Cogent || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



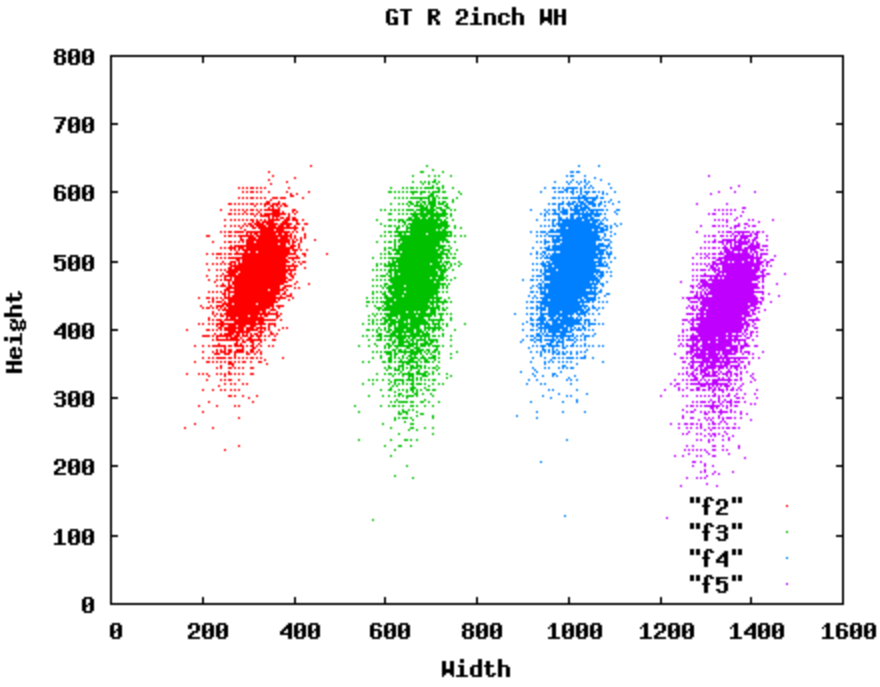
A = Aware || B/C = Cogent || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan

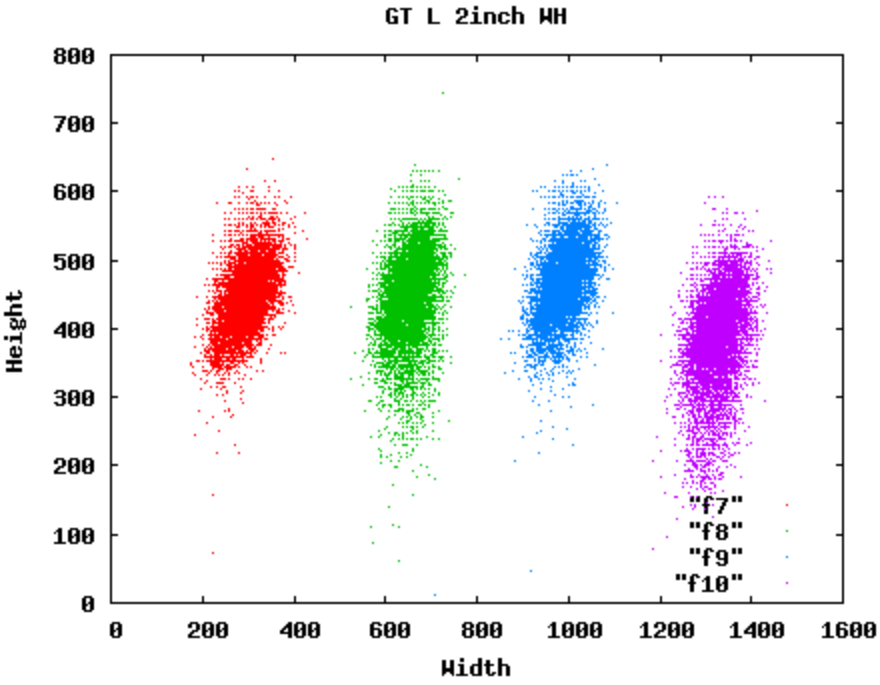


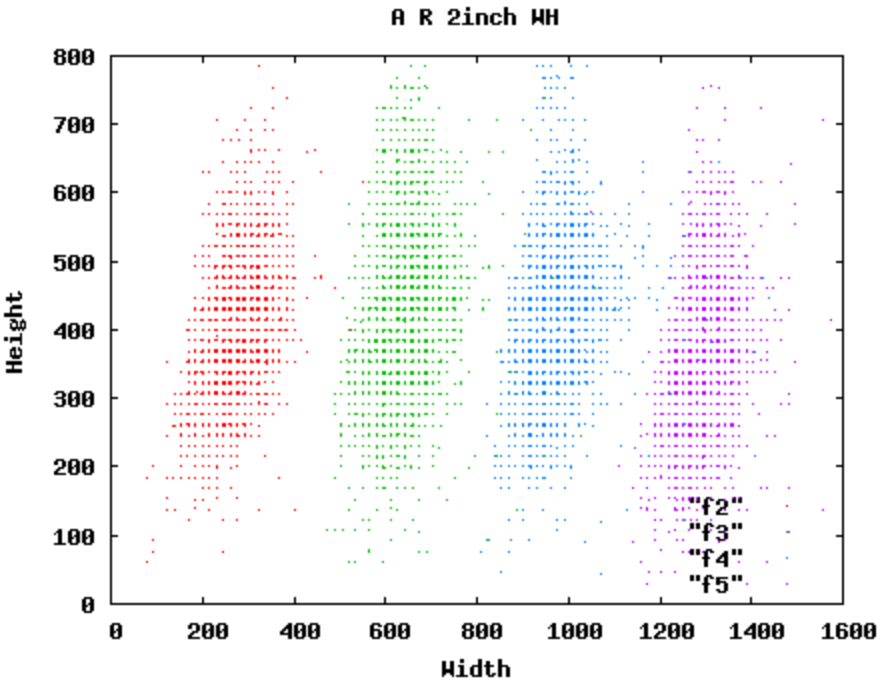
A = Aware || B/C = Cogent || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan

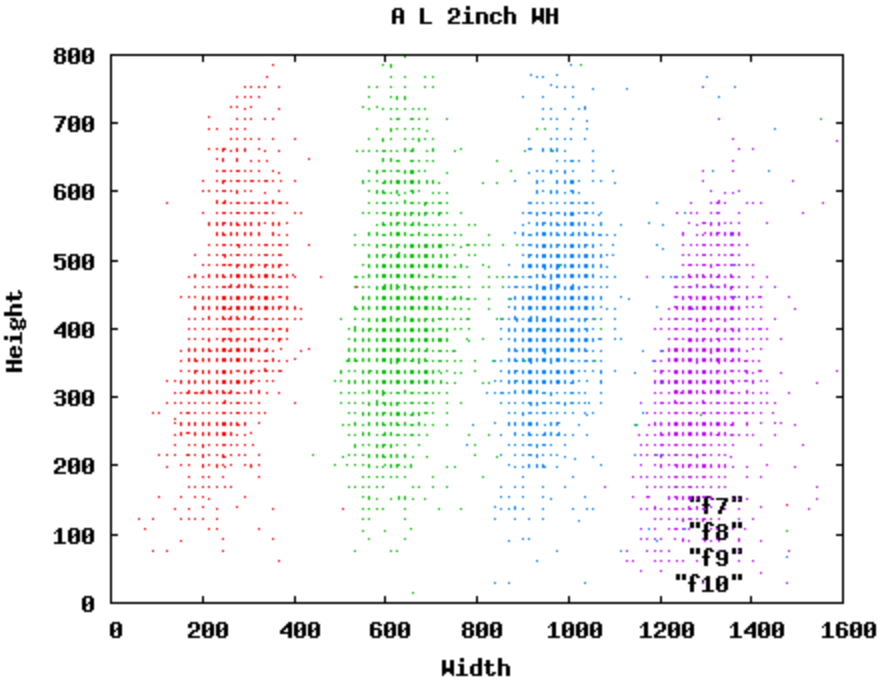
Appendix G. Plots of 2-inch segmentation box widths and heights.

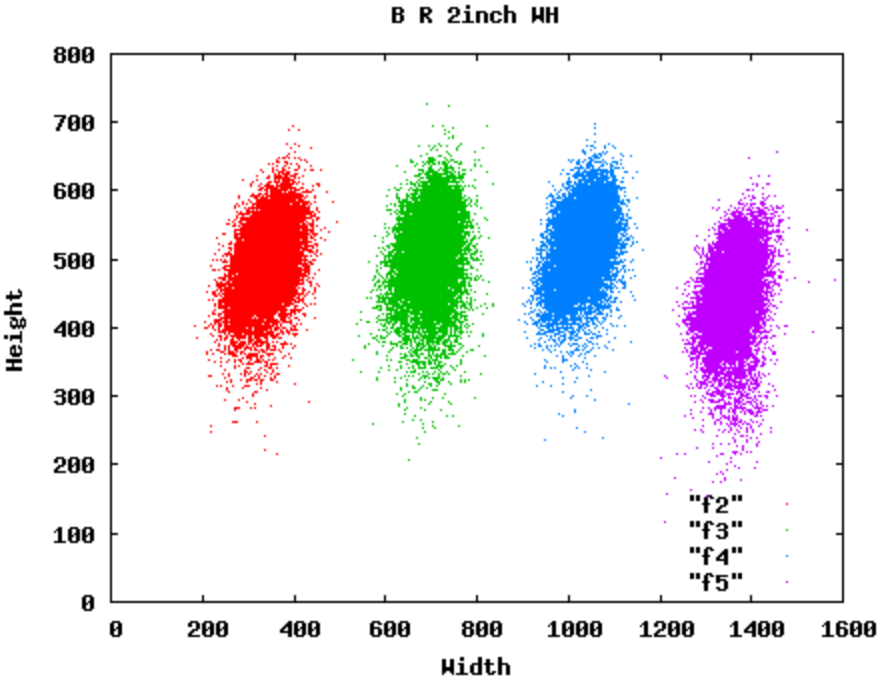
The plots in this appendix show the distribution of the segmentation box widths and heights for the 2-inch data. There is a combined plot for each slap image and then a smaller plot for each finger position. The individual finger plots are better for seeing the full "spread" of widths and heights detected. The widths are "spread out" on the plot by adding 350, 750 and 1050 to the 2nd, 3rd, and 4th widths plotted. The plot for the ground truth (GT) is included as a baseline for comparison. The blank lines that appear in some of the plots are most likely caused by the segmentation algorithm doing some level of sampling of the input image. The reason the lines are not evenly distributed in some plots is an artifact of the sampling when scaling the images for displaying in the report.

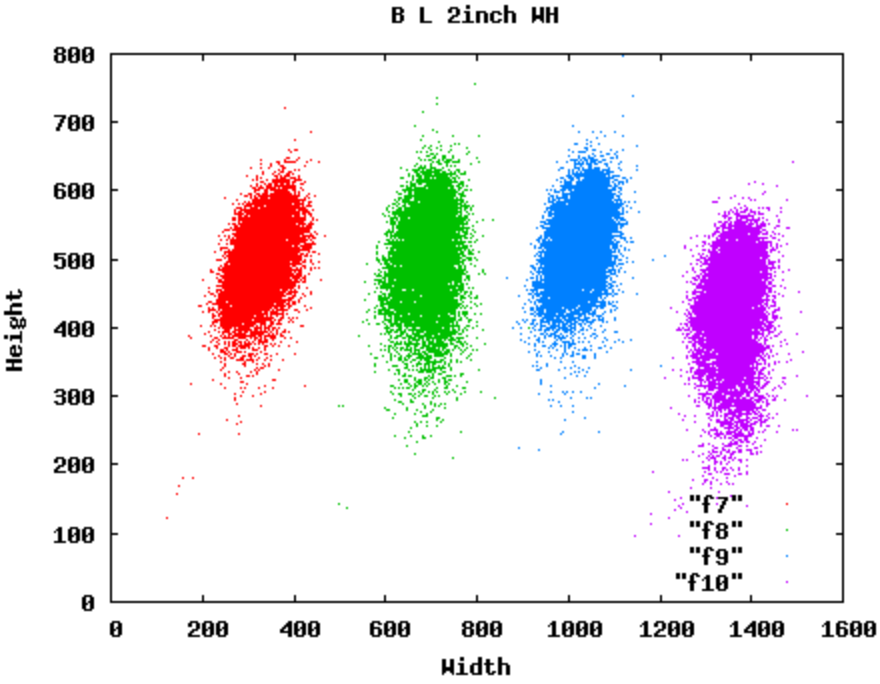

GT R 2inch WH
Height
Width
"f2"
"f3"
"f4"
"f5"

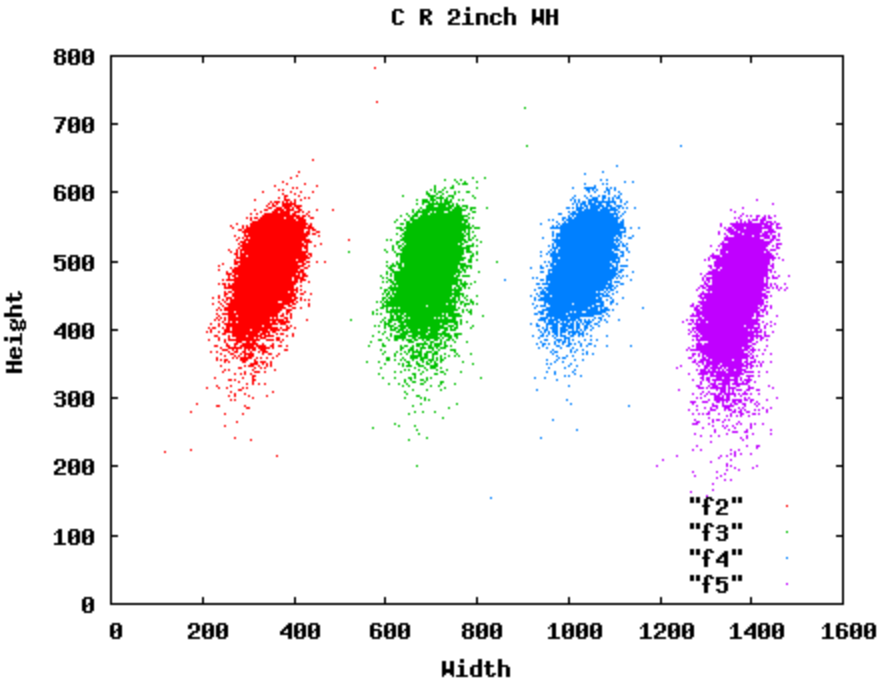

GT L 2inch WH
Height
Width
"f7"
"f8"
"f9"
"f10"

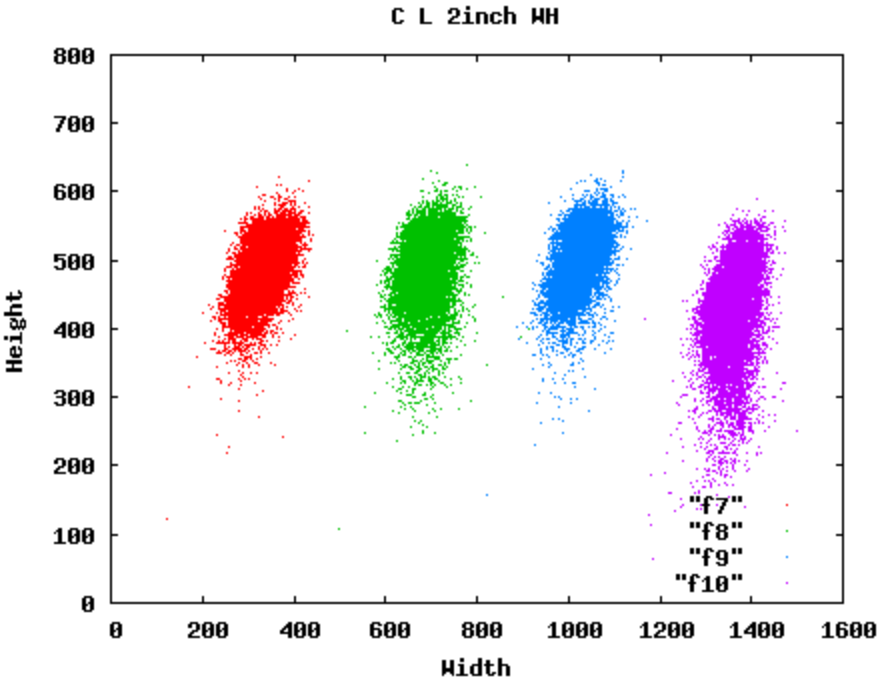

A R 2inch WH
Height
Width
0
100
200
300
400
500
600
700
800
0
200
400
600
800
1000
1200
1400
1600
"f2"
"f3"
"f4"
"f5"

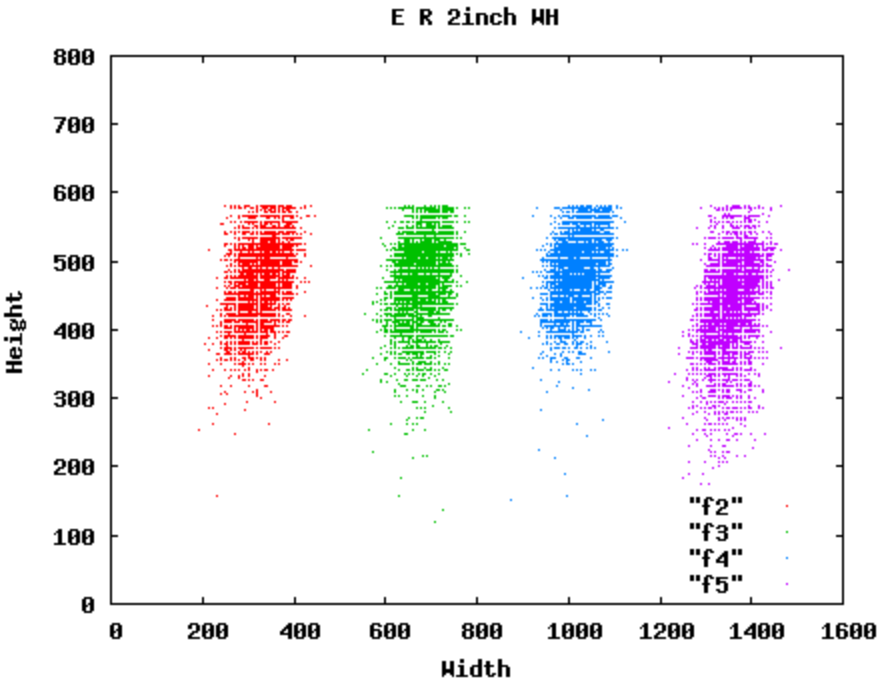

A L 2inch WH
Height
Width
0
100
200
300
400
500
600
700
800
0
200
400
600
800
1000
1200
1400
1600
"f7"
"f8"
"f9"
"f10"

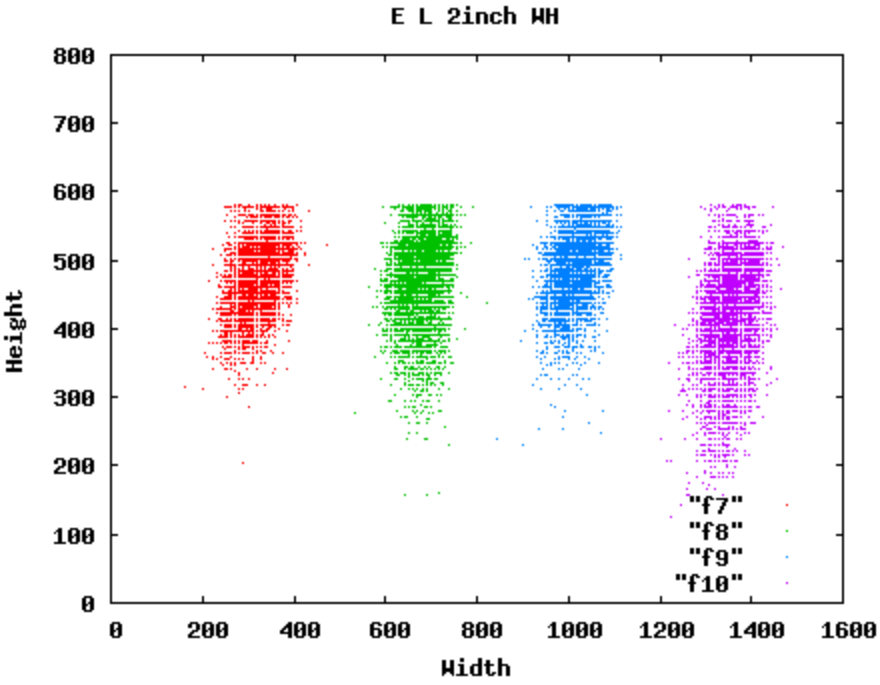

B R 2inch WH
Height
Width
"f2"
"f3"
"f4"
"f5"

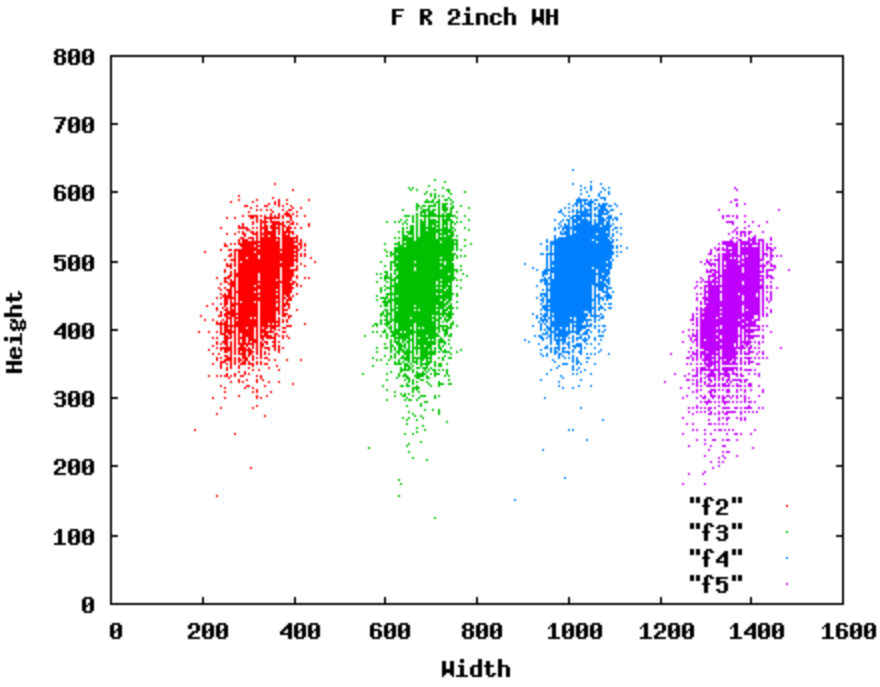

B L 2inch WH
Height
Width
"f7"
"f8"
"f9"
"f10"

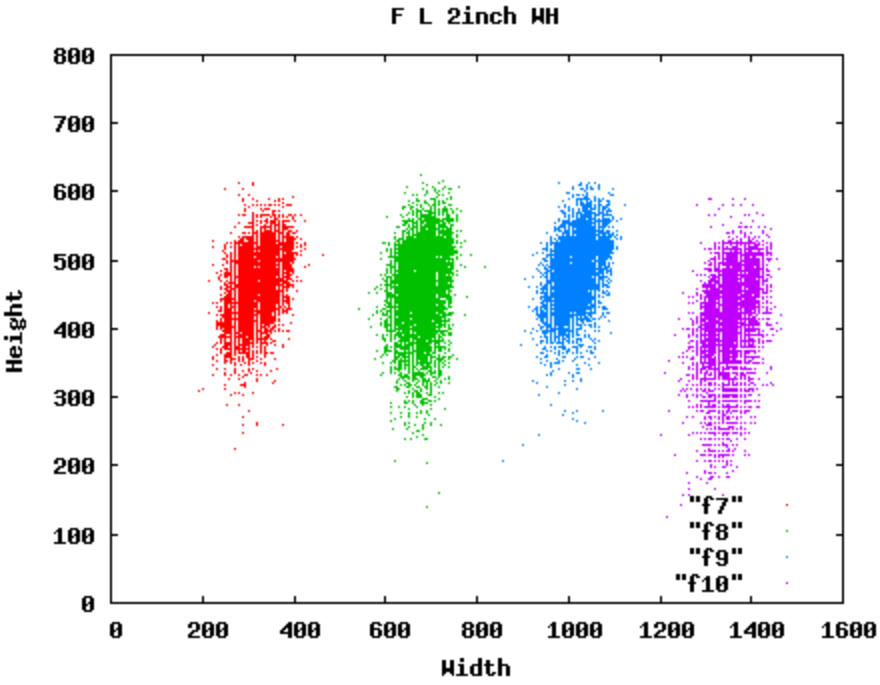

C R 2inch WH
Height
Width
"f2"
"f3"
"f4"
"f5"

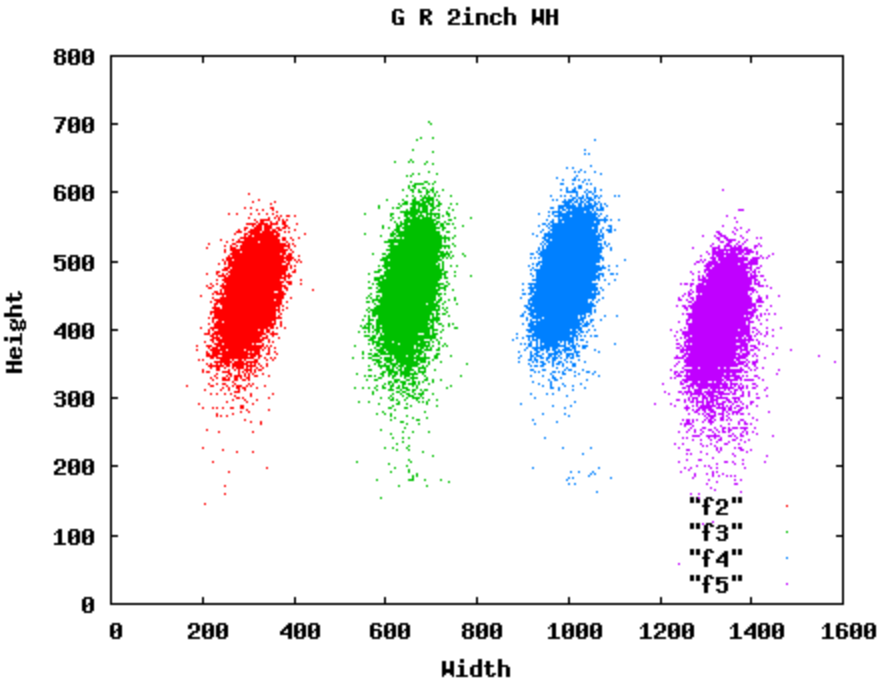

C L 2inch WH
Height
Width
"f7"
"f8"
"f9"
"f10"

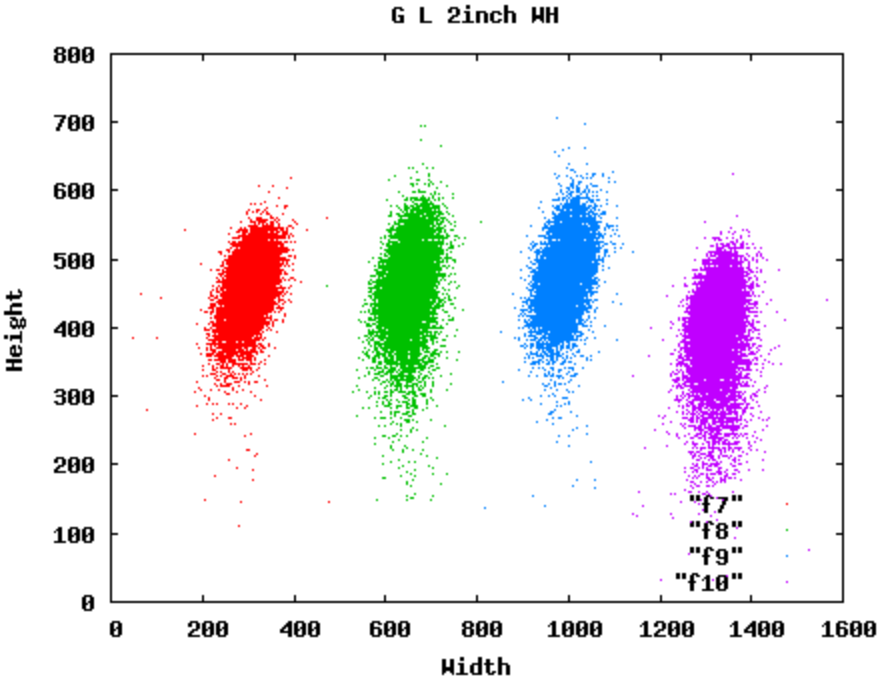

E R 2inch WH
Height
Width
"f2"
"f3"
"f4"
"f5"

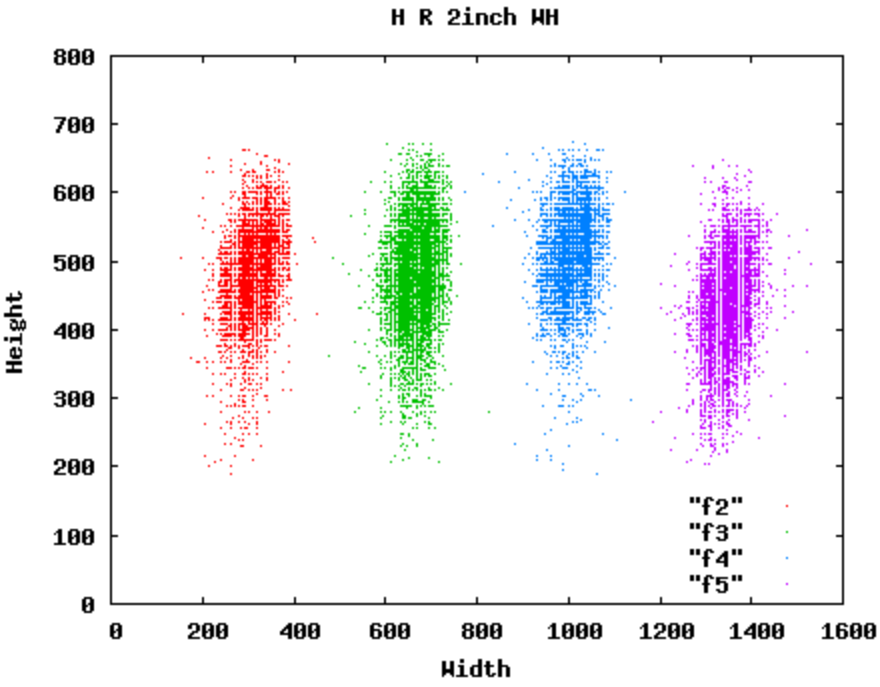

E L 2inch WH
Height
Width
"f7"
"f8"
"f9"
"f10"

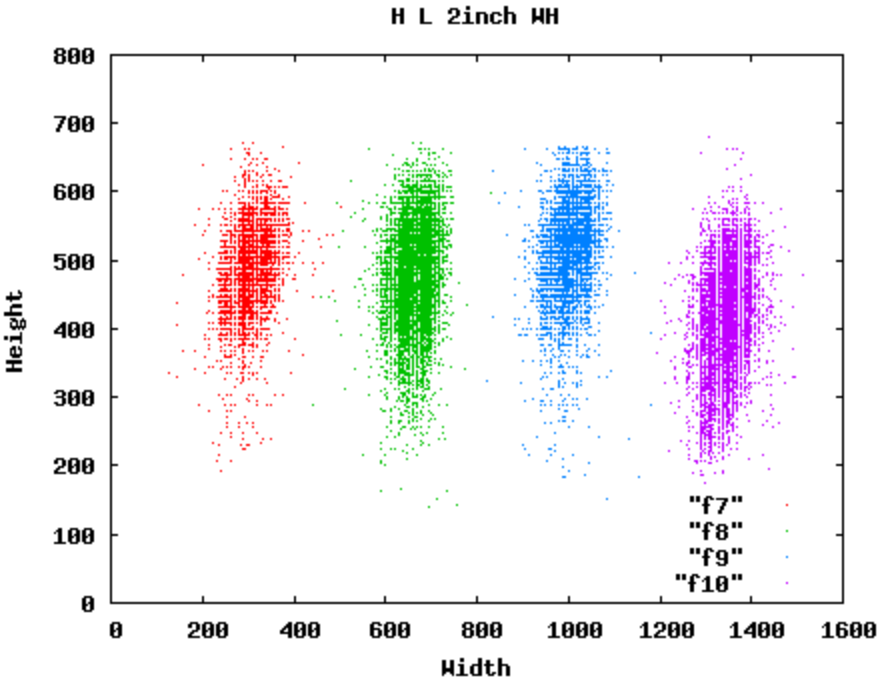

F R 2inch WH
Height
Width
"f2"
"f3"
"f4"
"f5"

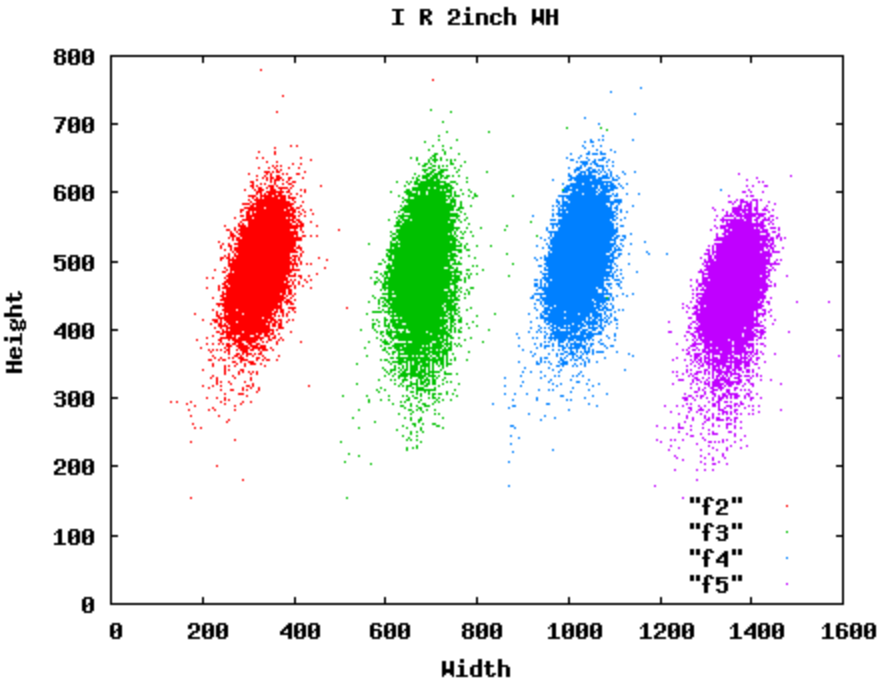

F L 2inch WH
Height
Width
"f7"
"f8"
"f9"
"f10"

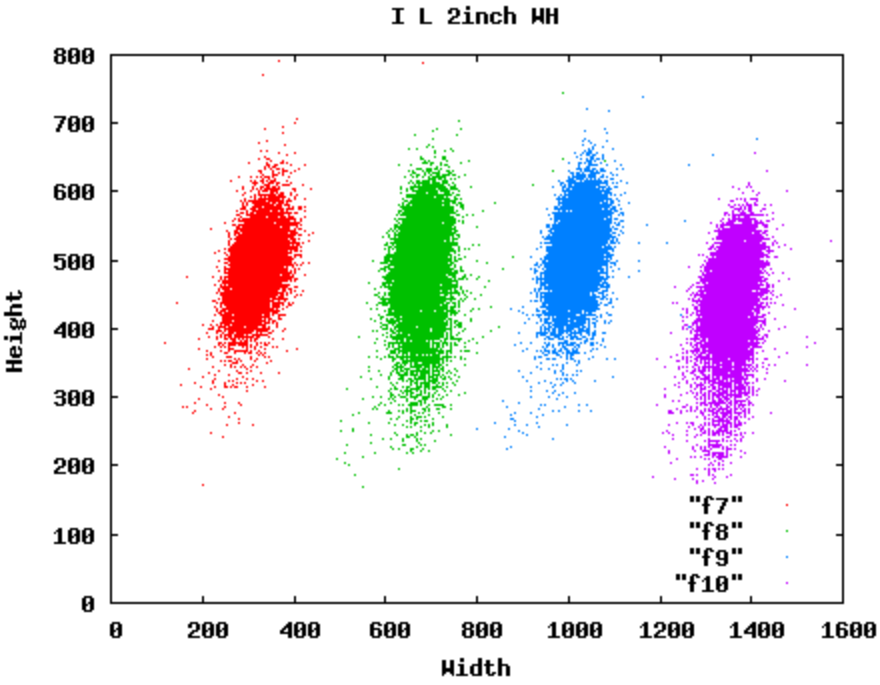

G R 2inch WH
Height
Width
"f2"
"f3"
"f4"
"f5"

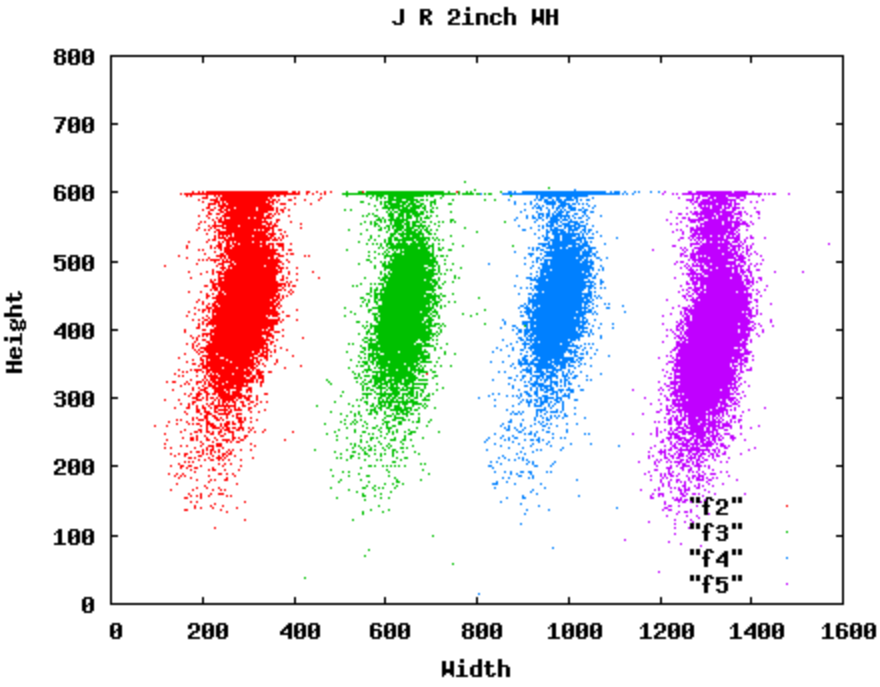

G L 2inch WH
Height
Width
"f7"
"f8"
"f9"
"f10"

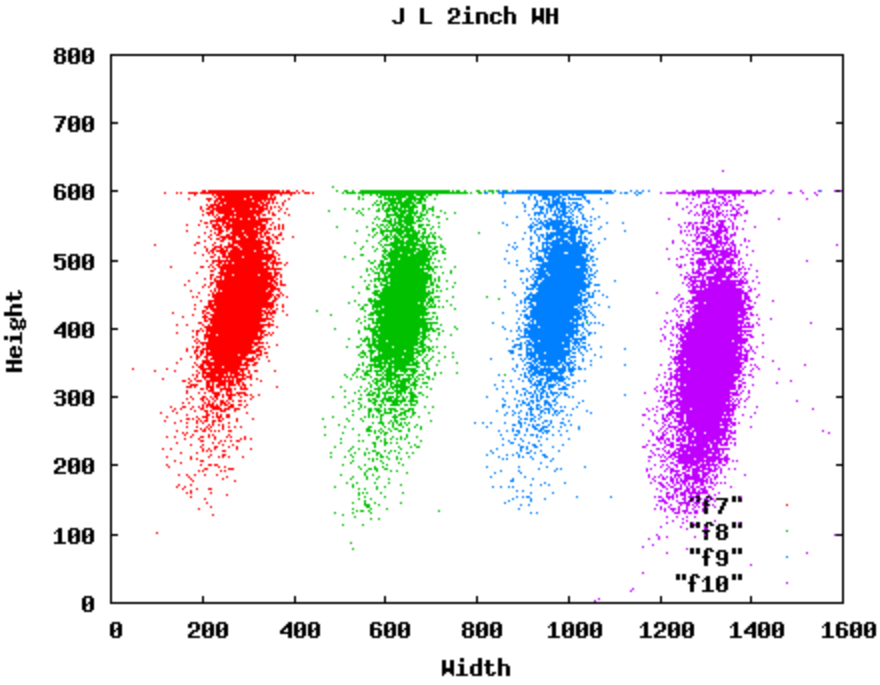

H R 2inch WH
Height
Width
0
100
200
300
400
500
600
700
800
0
200
400
600
800
1000
1200
1400
1600
"f2"
"f3"
"f4"
"f5"


H L 2inch WH
Height
Width
0
100
200
300
400
500
600
700
800
0
200
400
600
800
1000
1200
1400
1600
"f7"
"f8"
"f9"
"f10"


I R 2inch WH
Height
Width
"f2"
"f3"
"f4"
"f5"

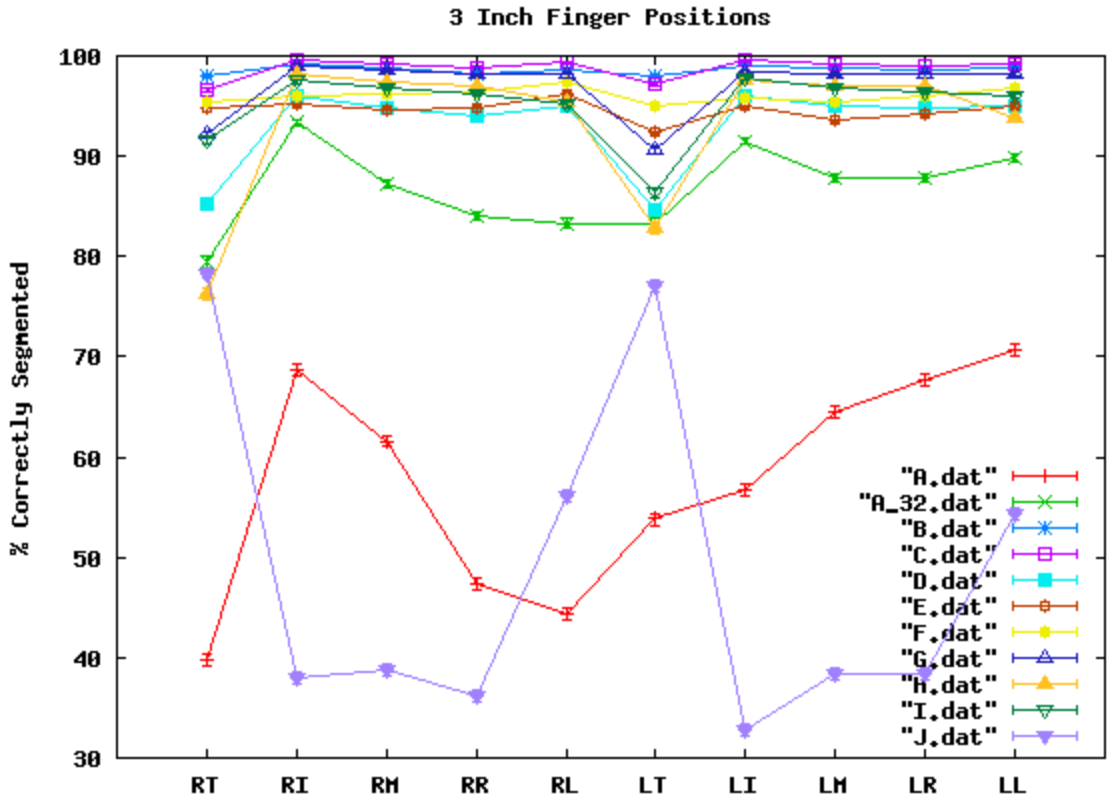

I L 2inch WH
Height
Width
"f7"
"f8"
"f9"
"f10"

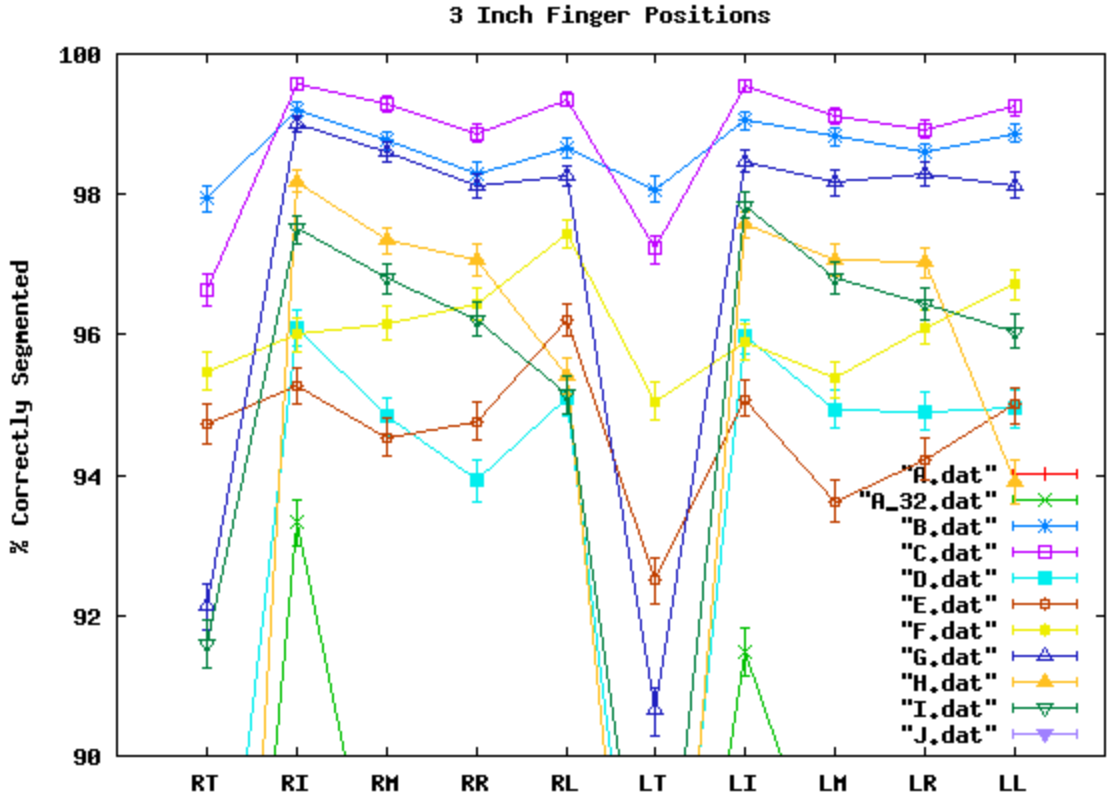

J R 2inch WH
Height
Width
"f2"
"f3"
"f4"
"f5"


J L 2inch WH
Height
Width
"f7"
"f8"
"f9"
"f10"

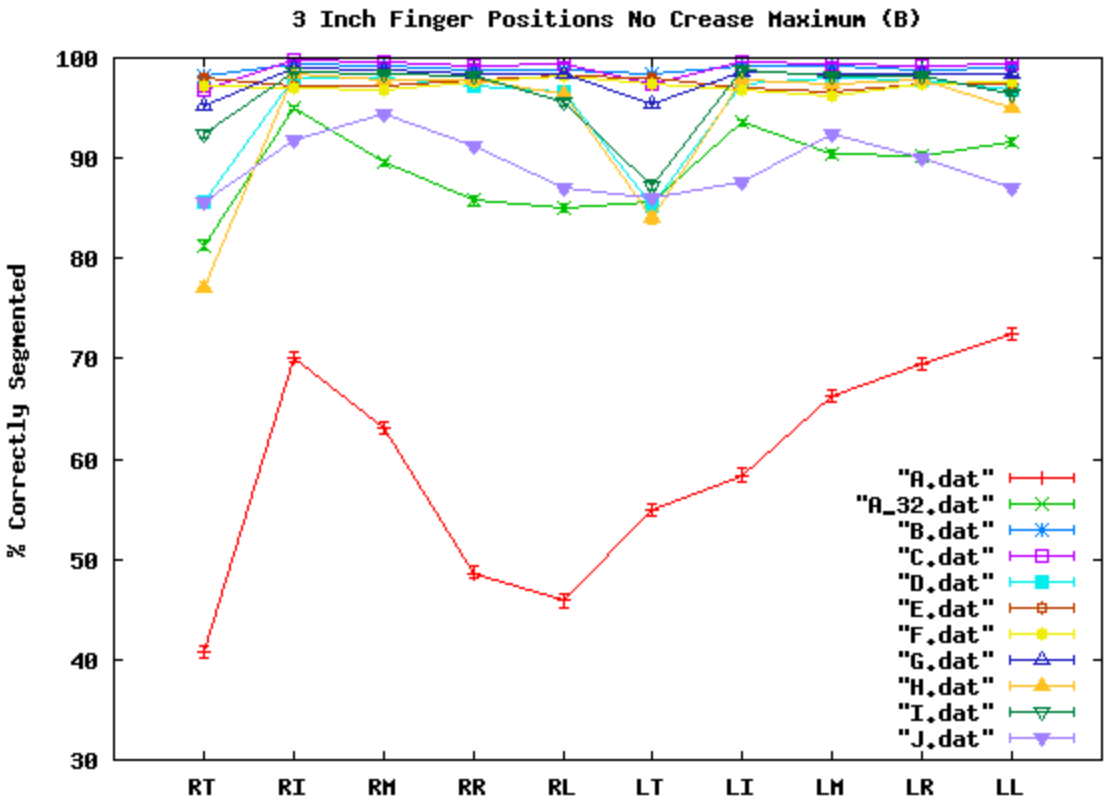
Appendix H. Confidence intervals for 3-inch segmentation results.

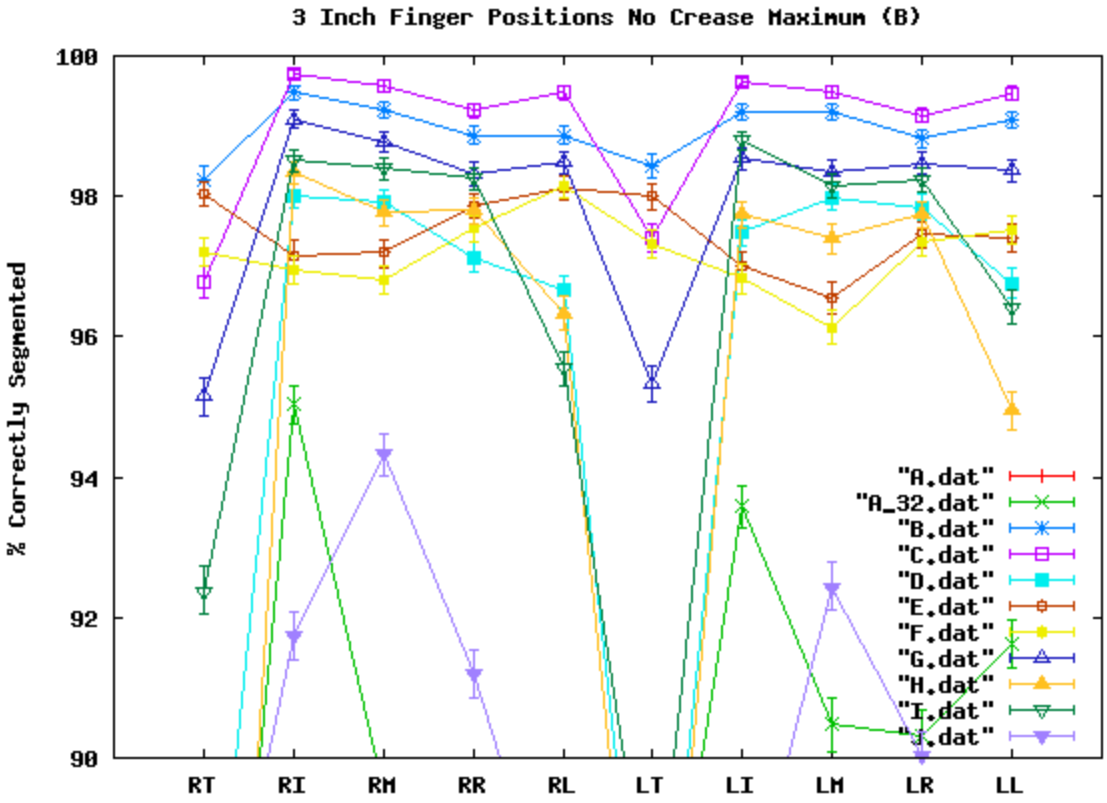
The plots in this appendix are an attempt to show 95% confidence intervals for the 3-inch segmentation results shown in tables in Appendix A for the finger positions and right/left hands. The confidence intervals were computed using the boot strap function in the R statistics package and a sampling of 1,000 iterations. The only issue is that the intervals were so small that they really don't show well in the plots. The plots are shown on two scales. The first shows the results for all the segmentation algorithms. The second shows only results in the range 90-100% correct segmentation. The "None" segmented is not included in the second plot just to make it easier to read.



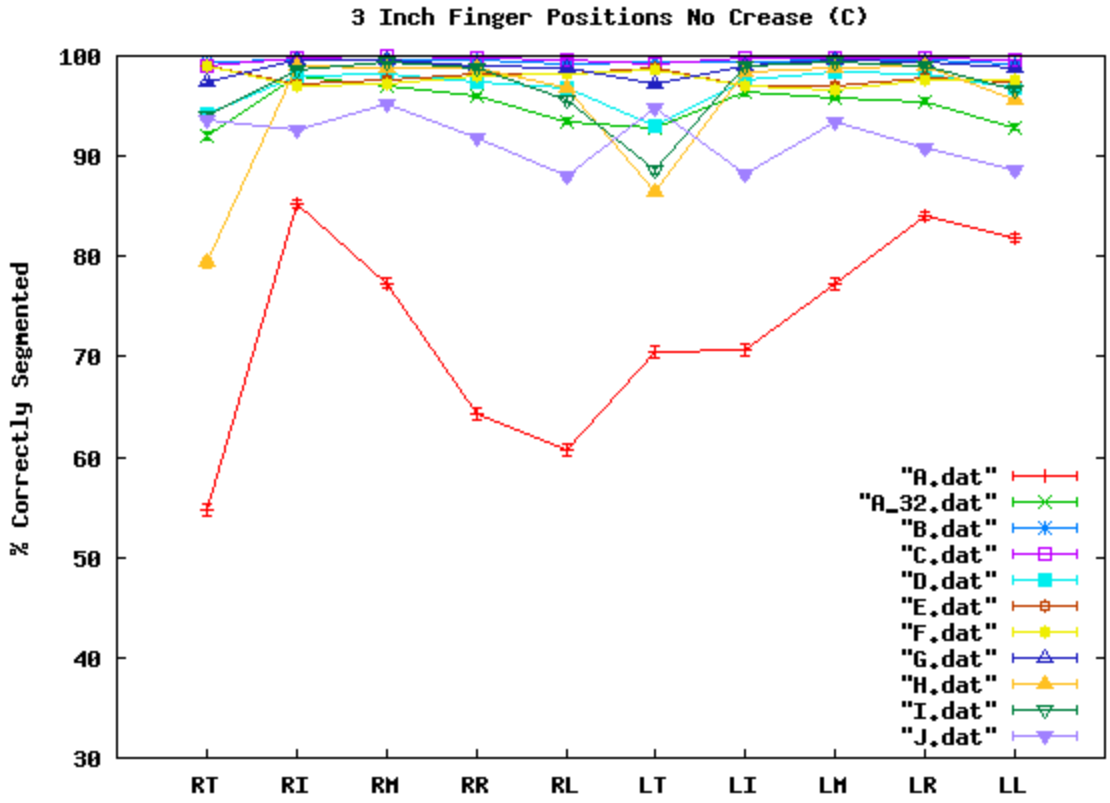


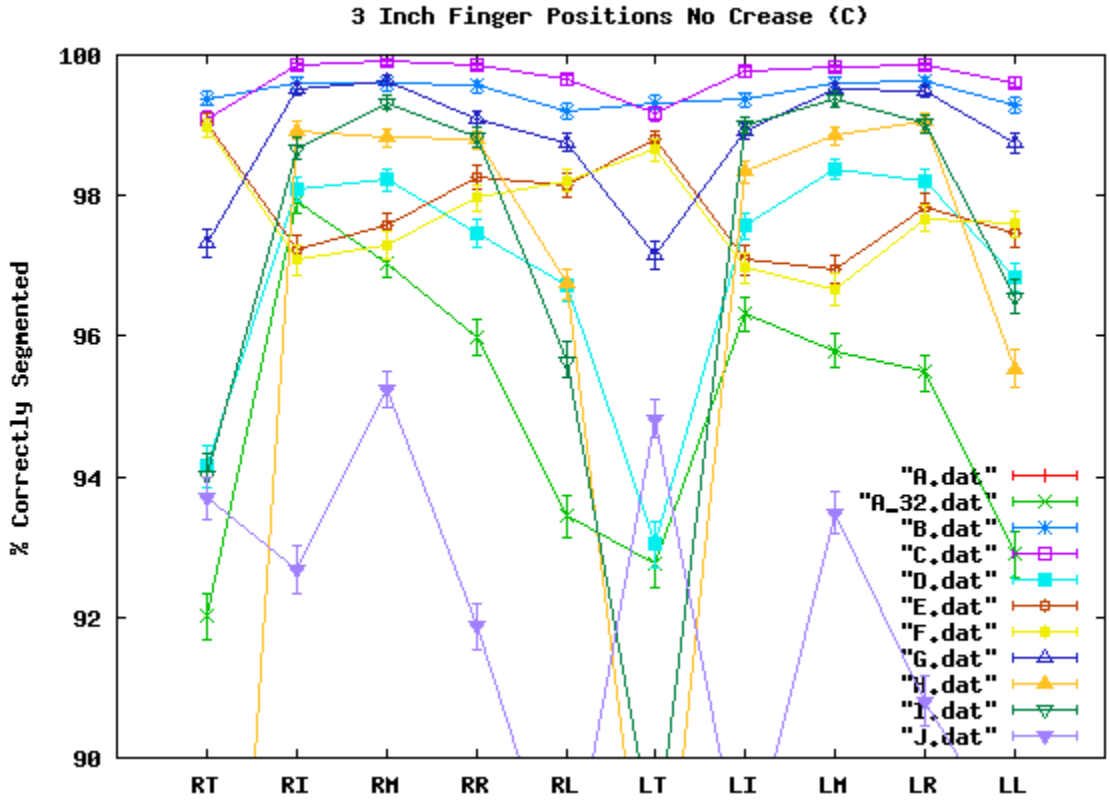
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



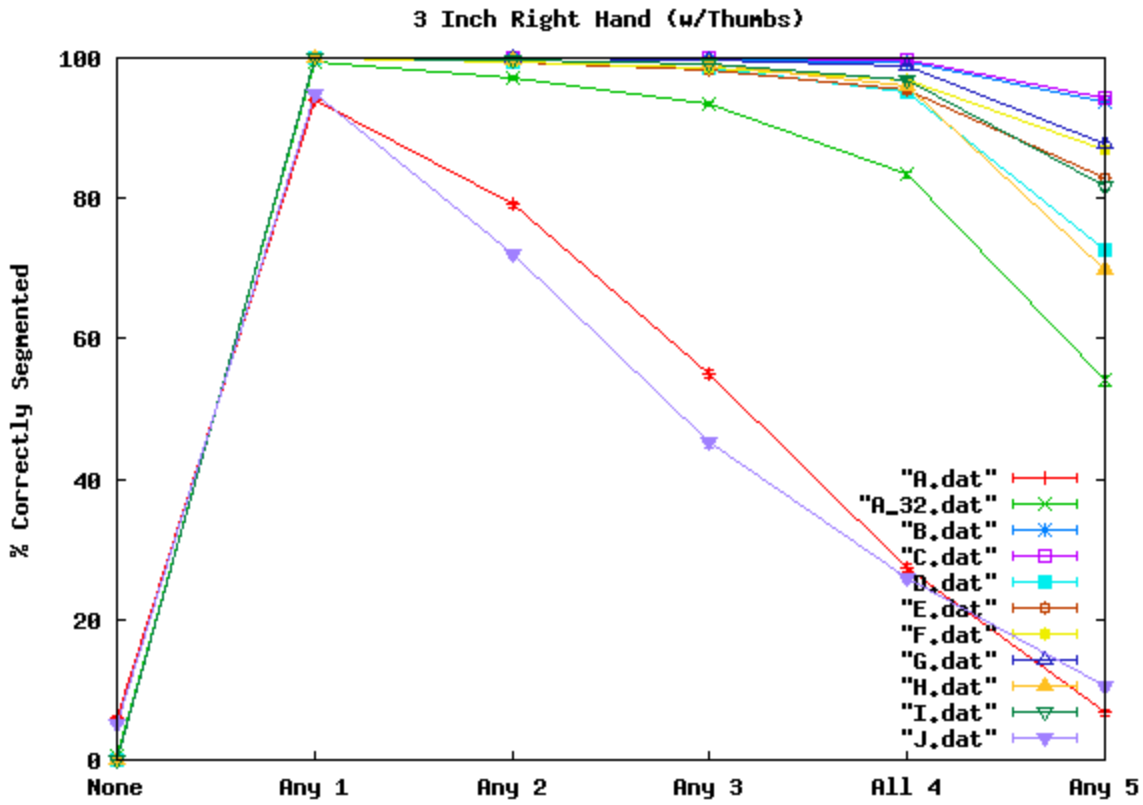


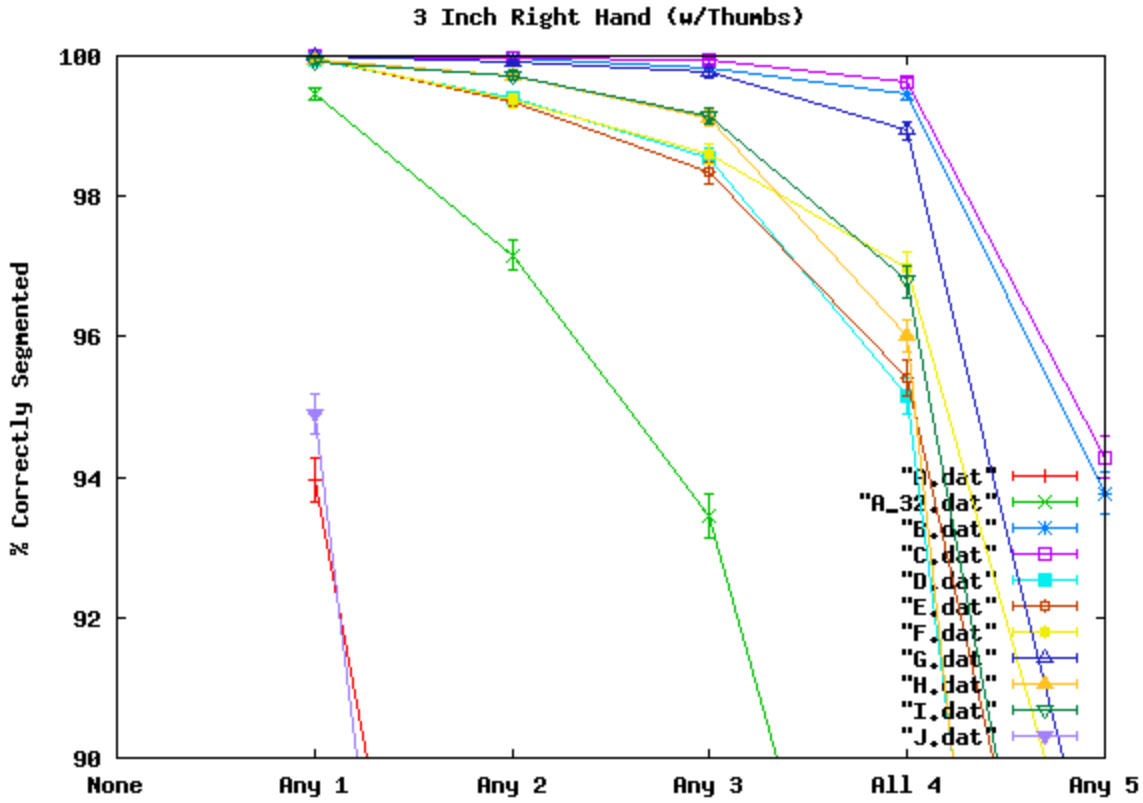
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



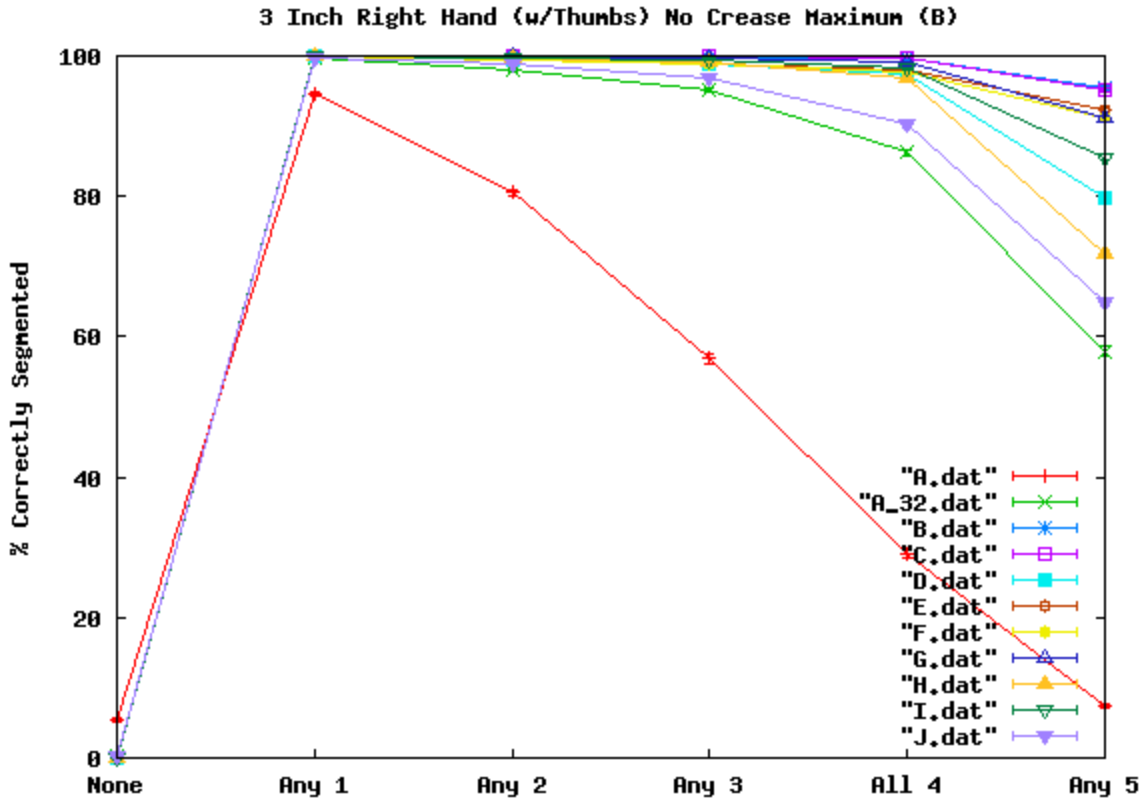


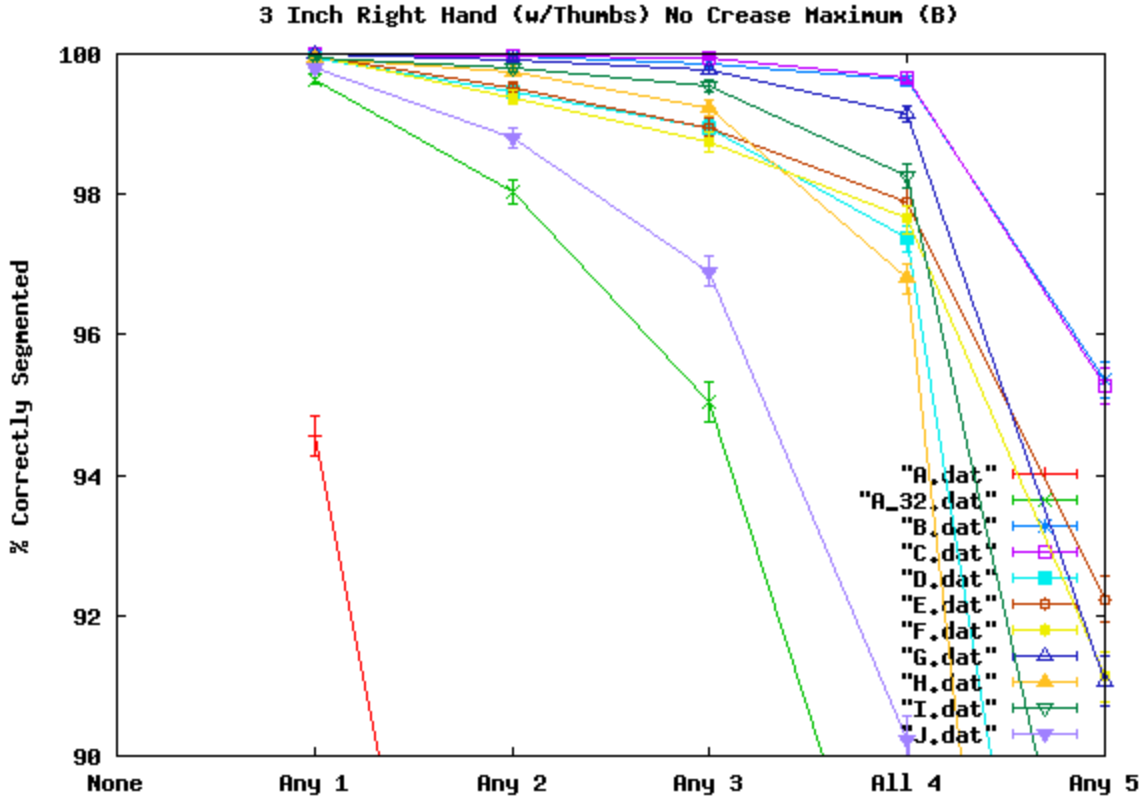
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



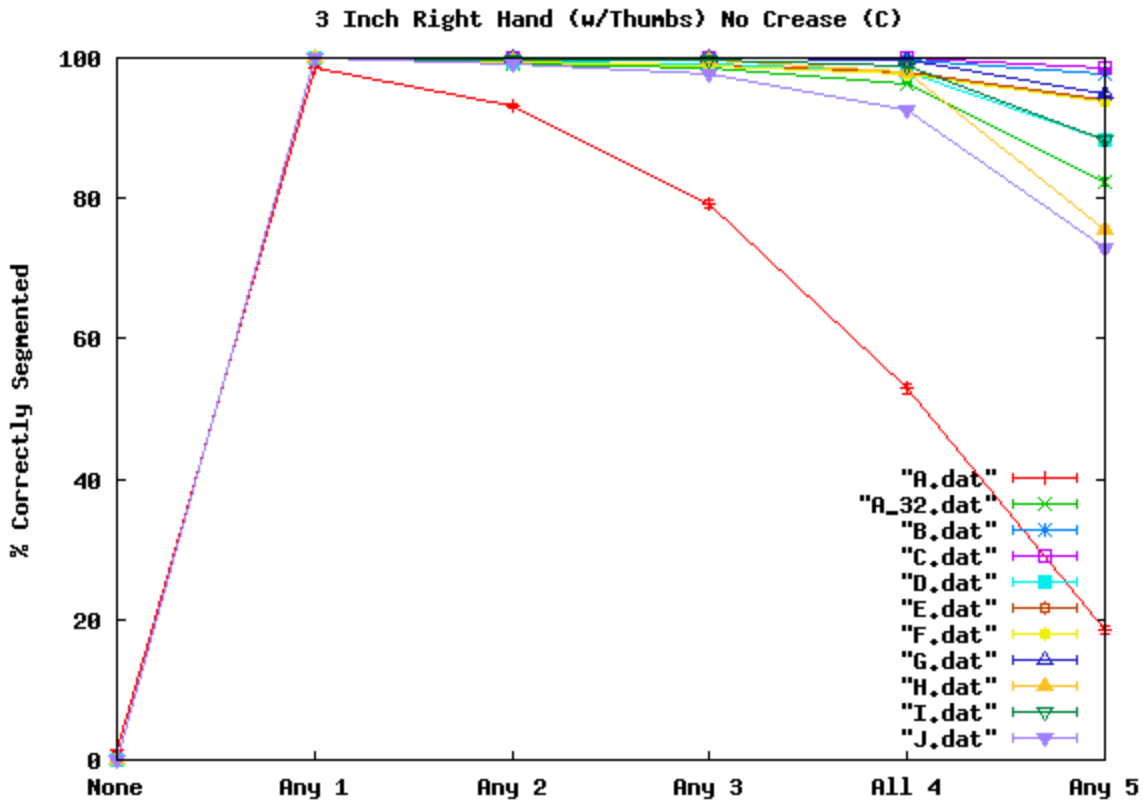


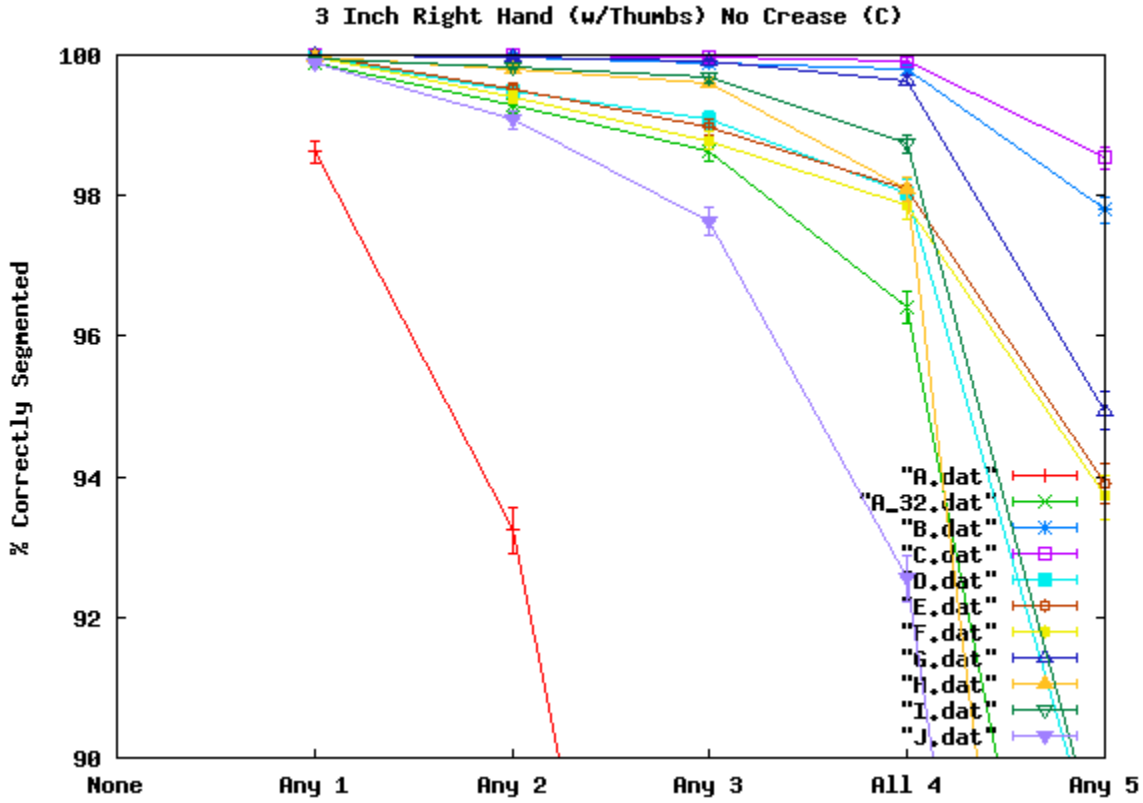
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



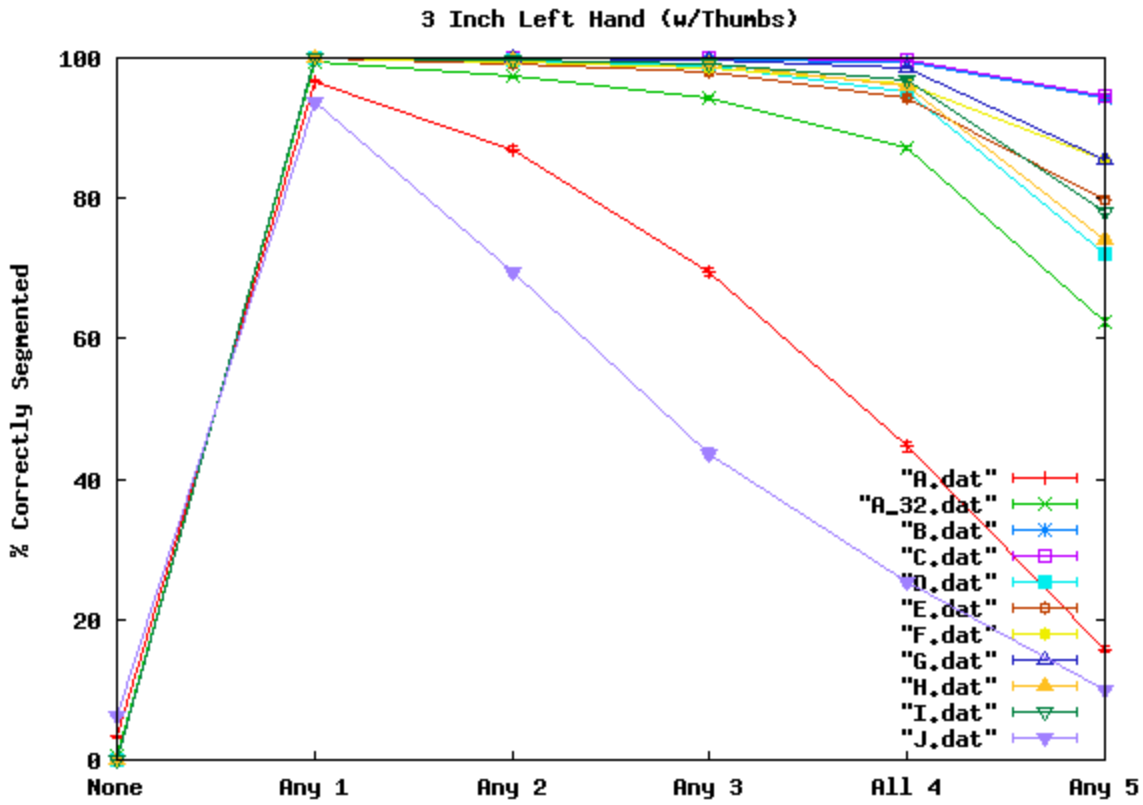


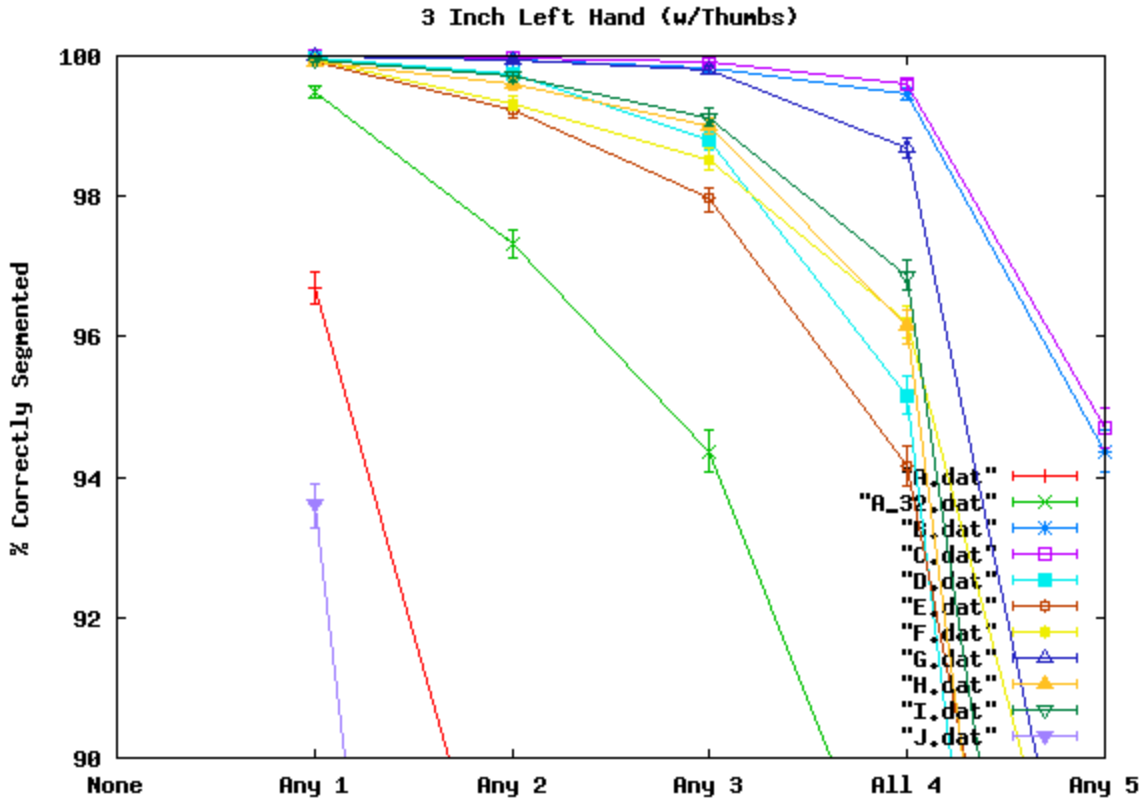
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



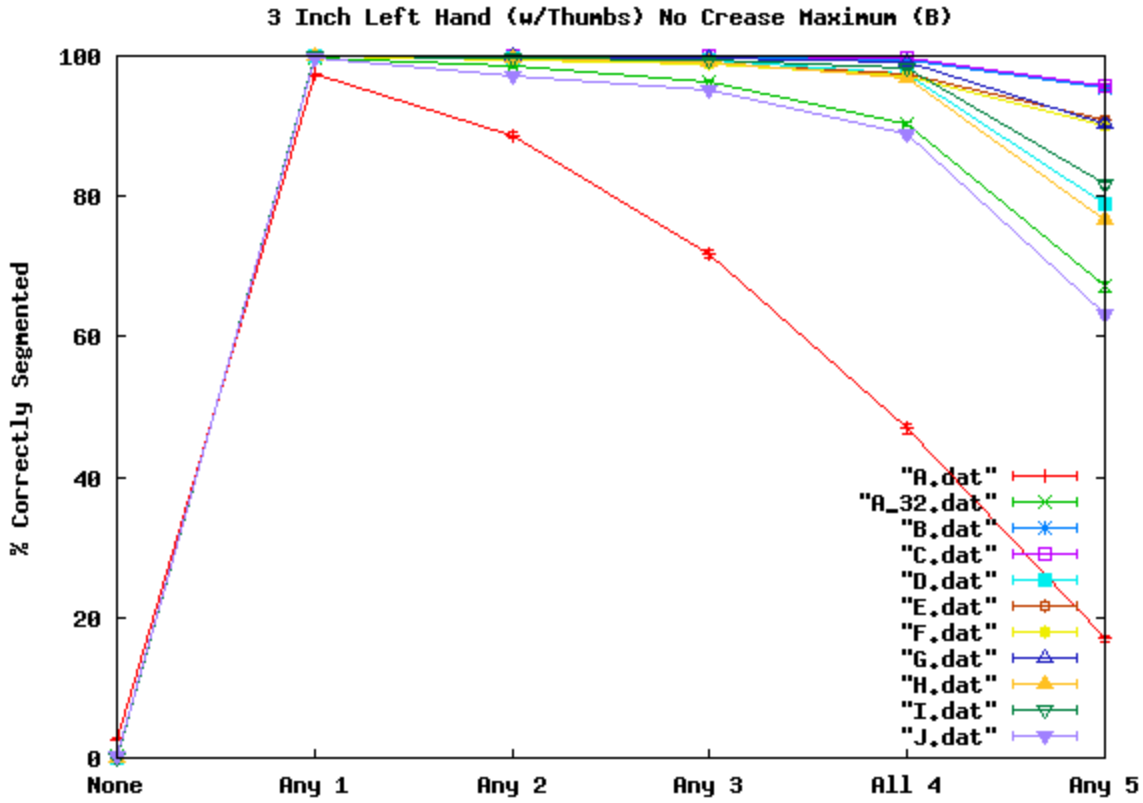


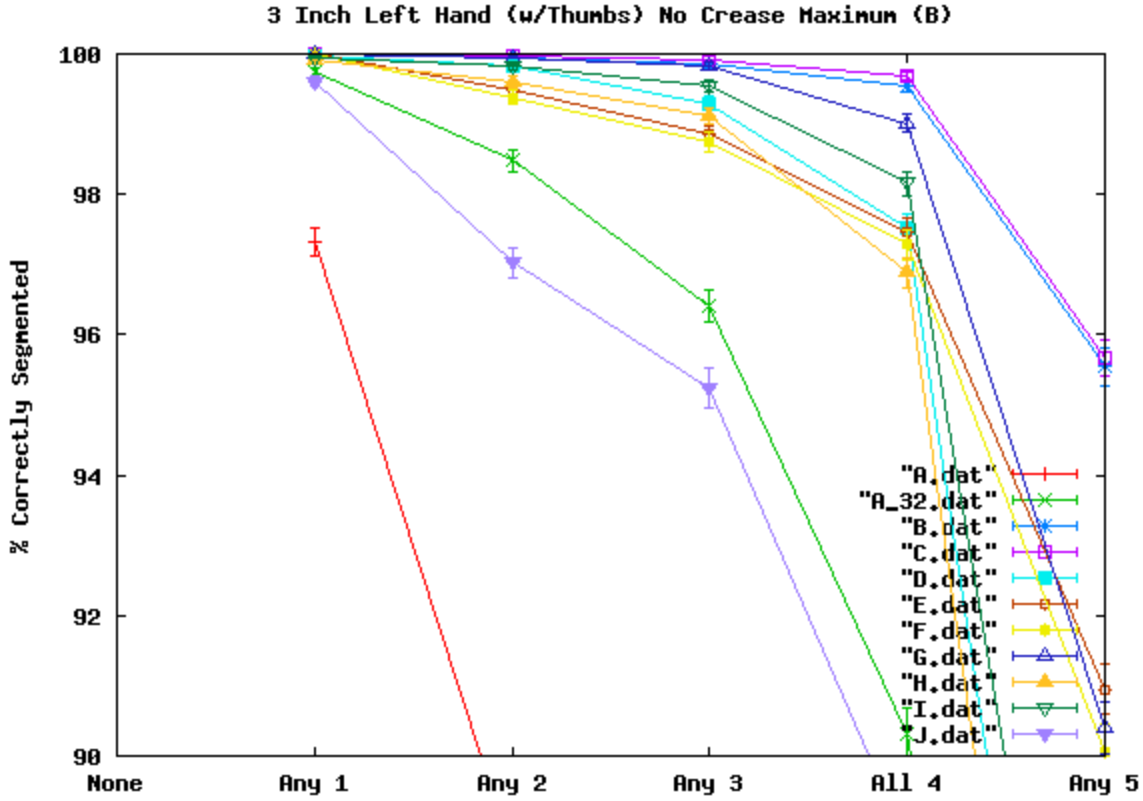
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



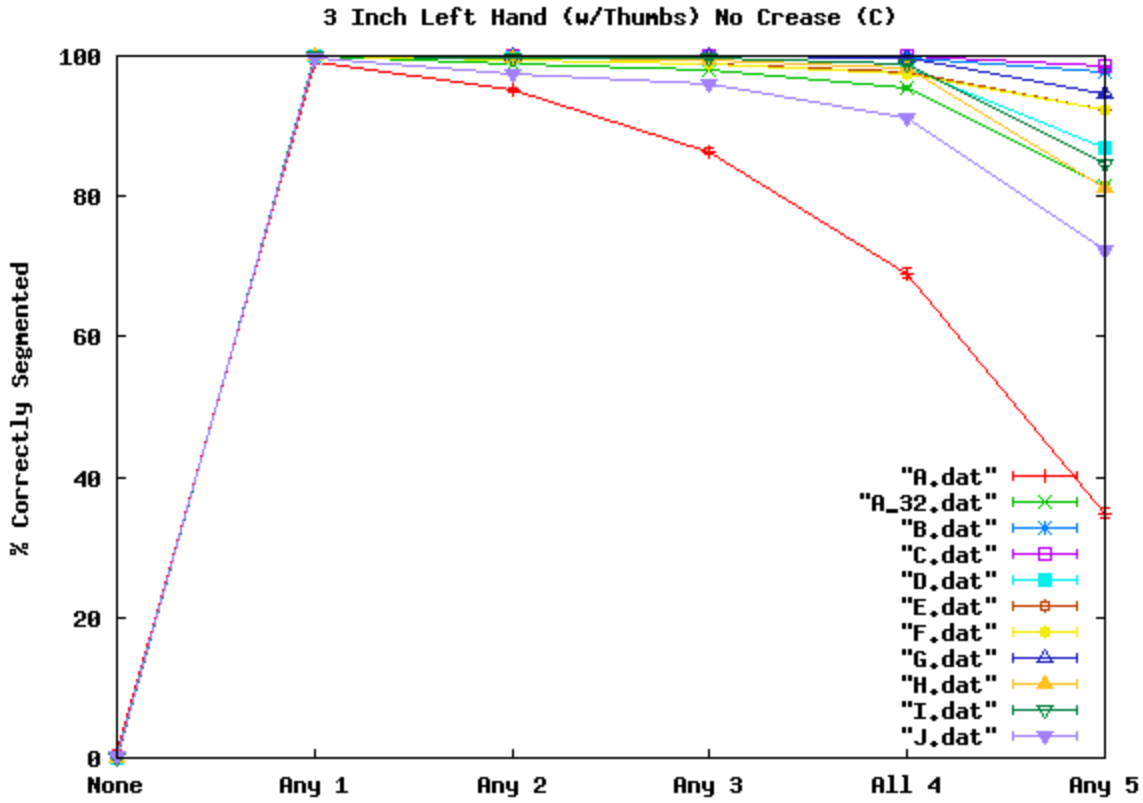


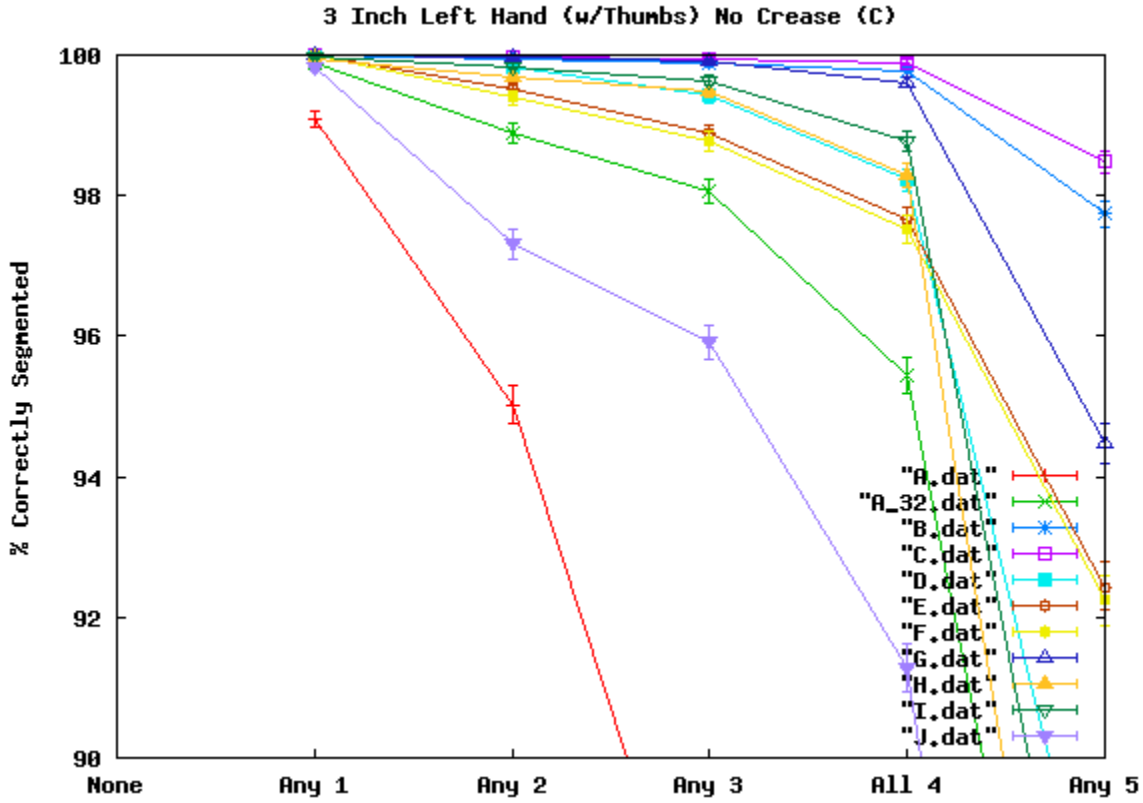
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



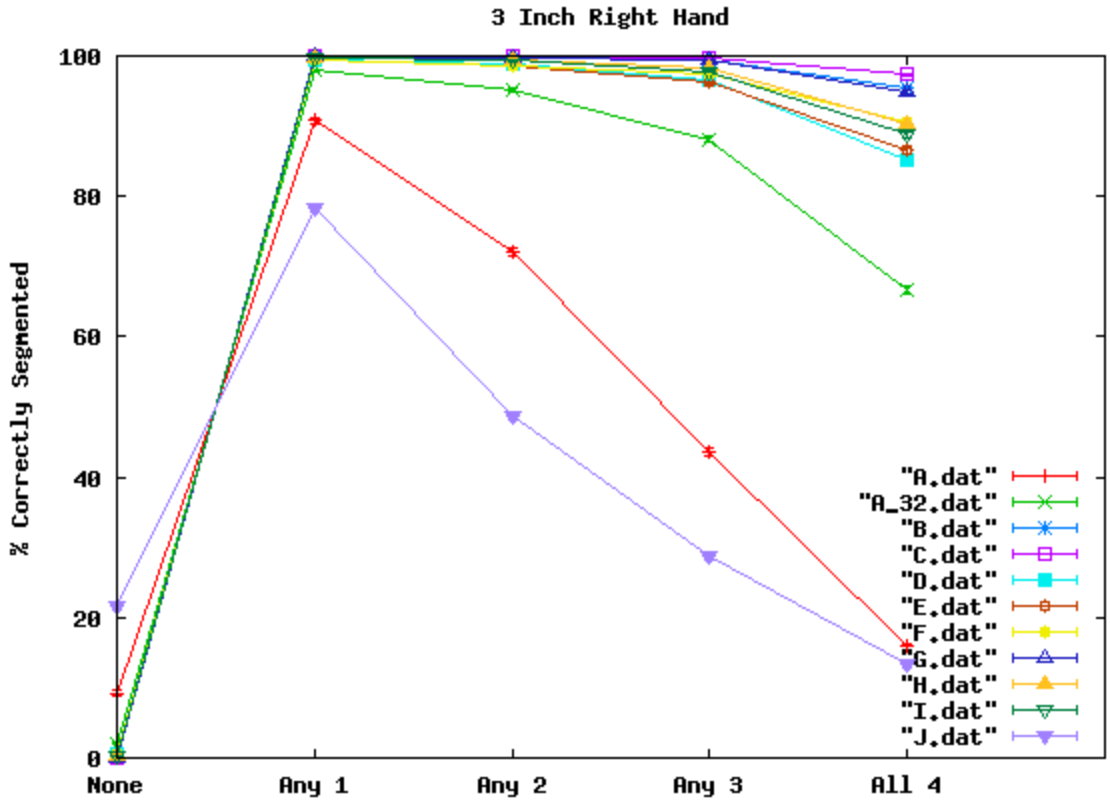


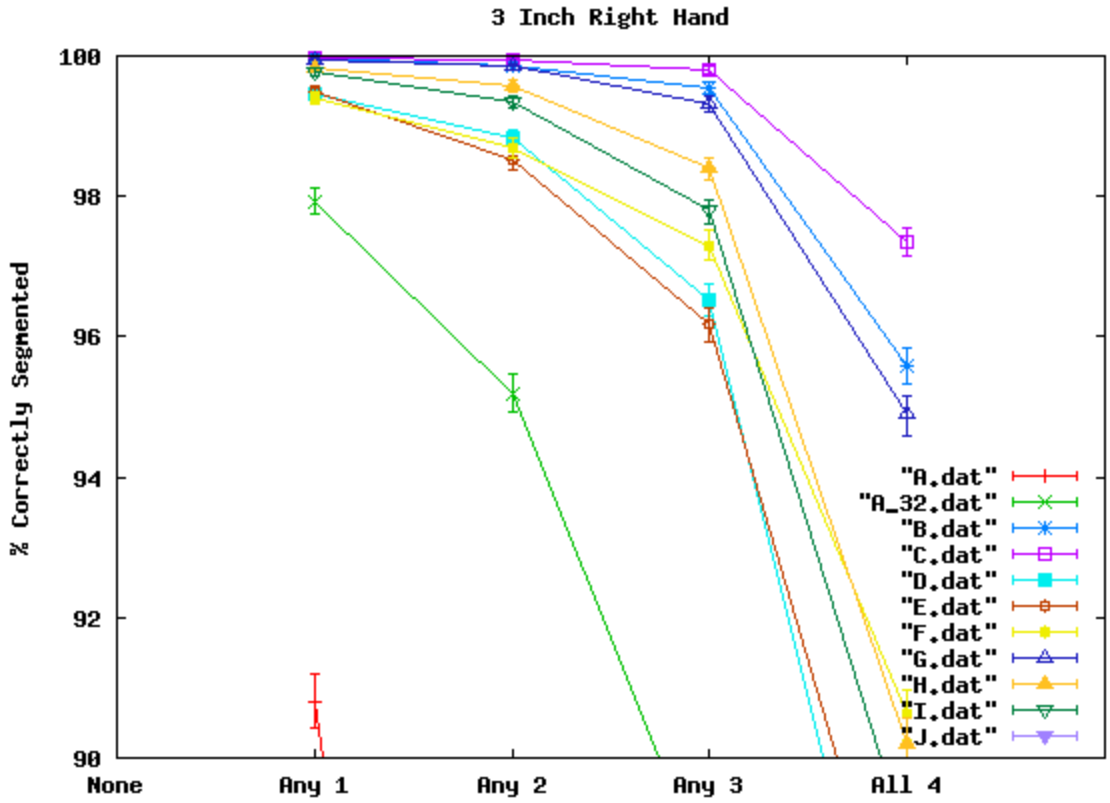
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



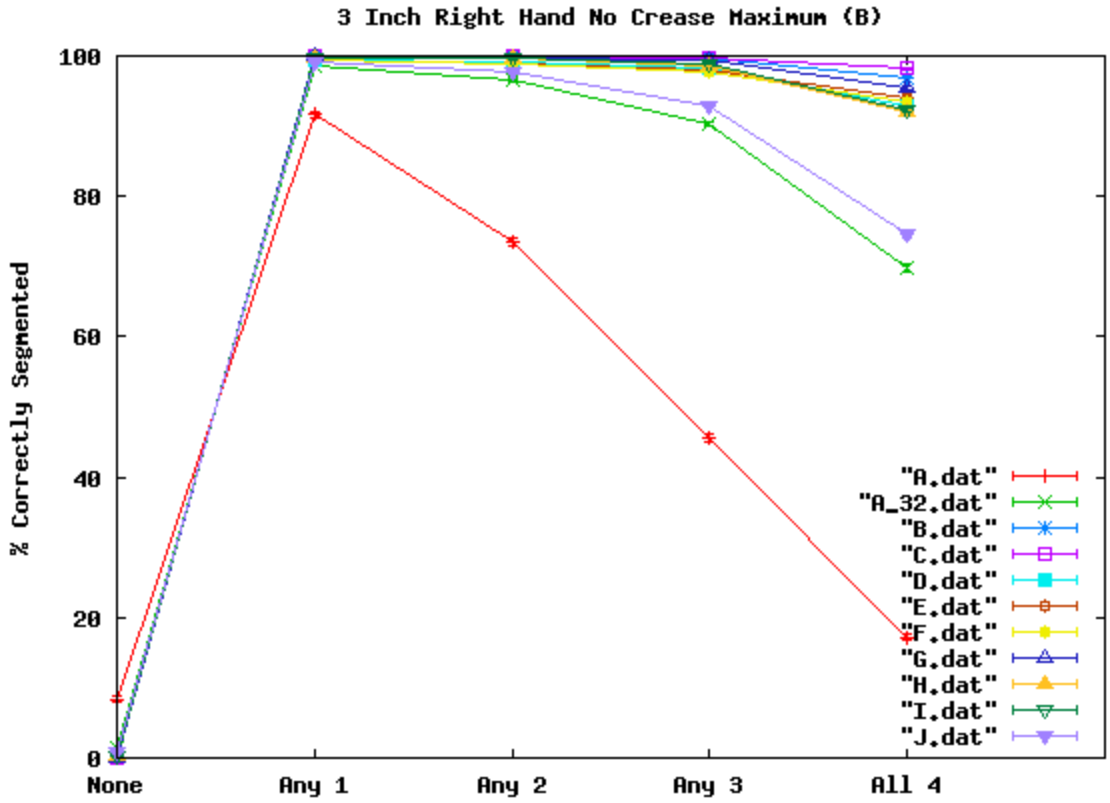


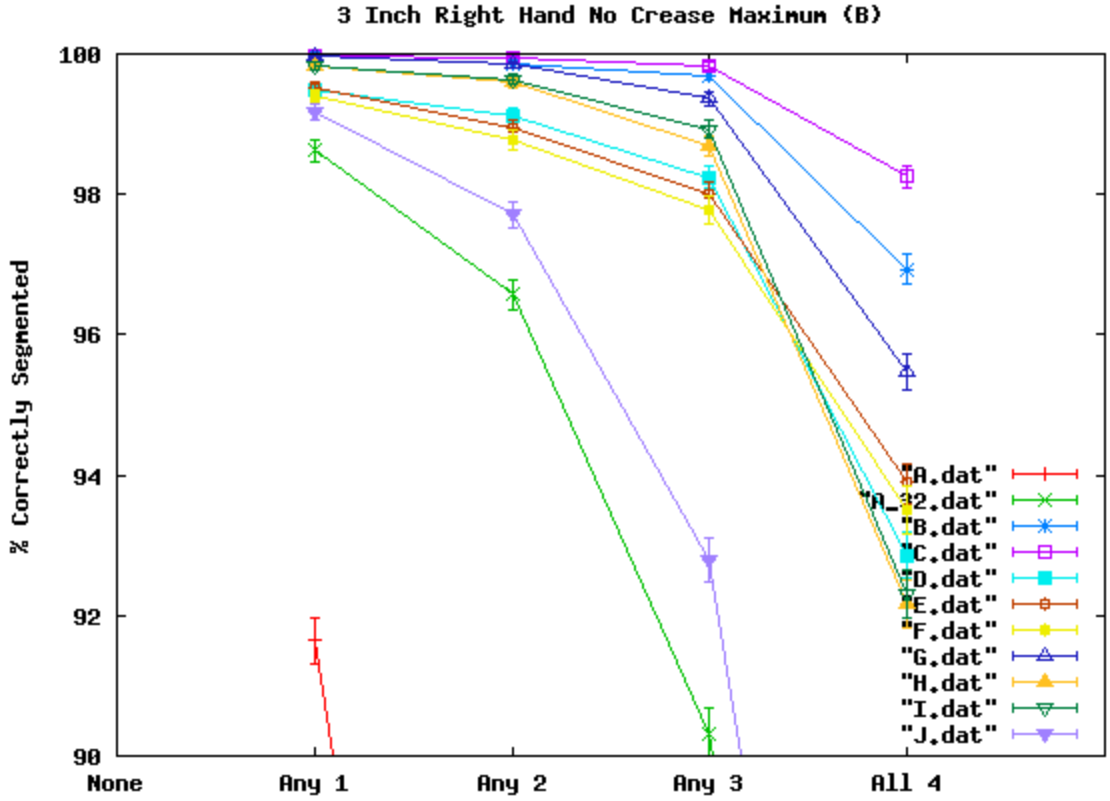
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



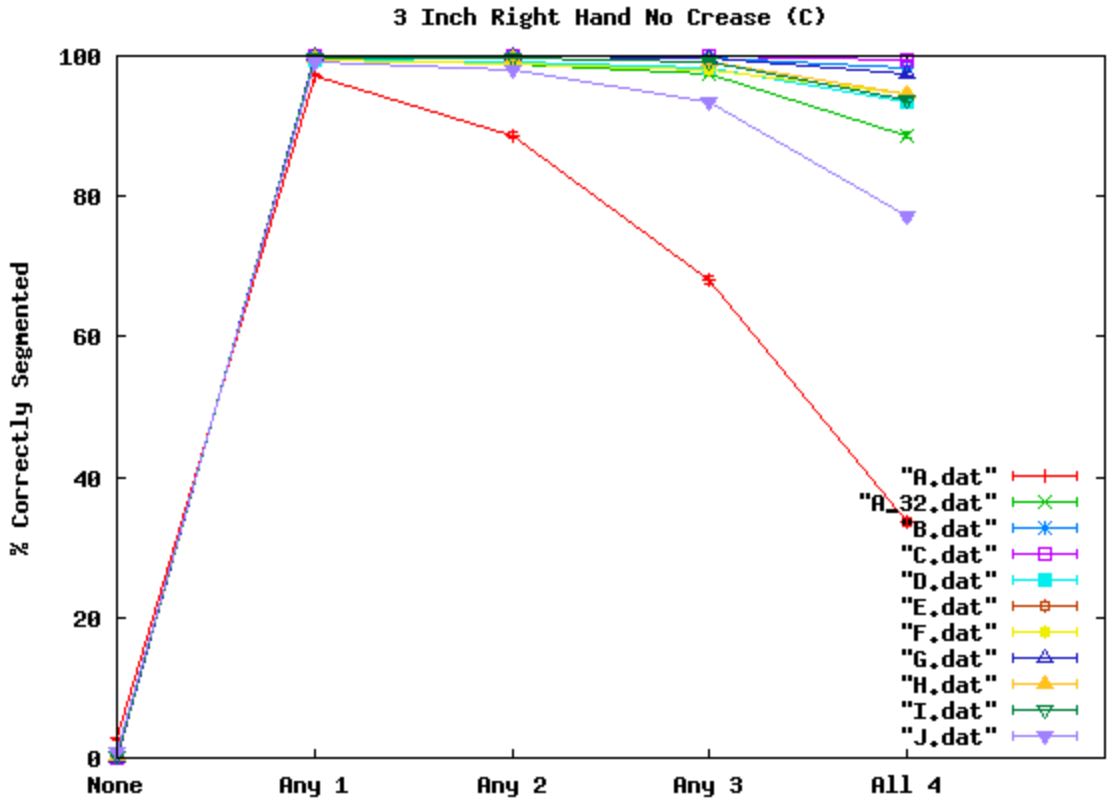


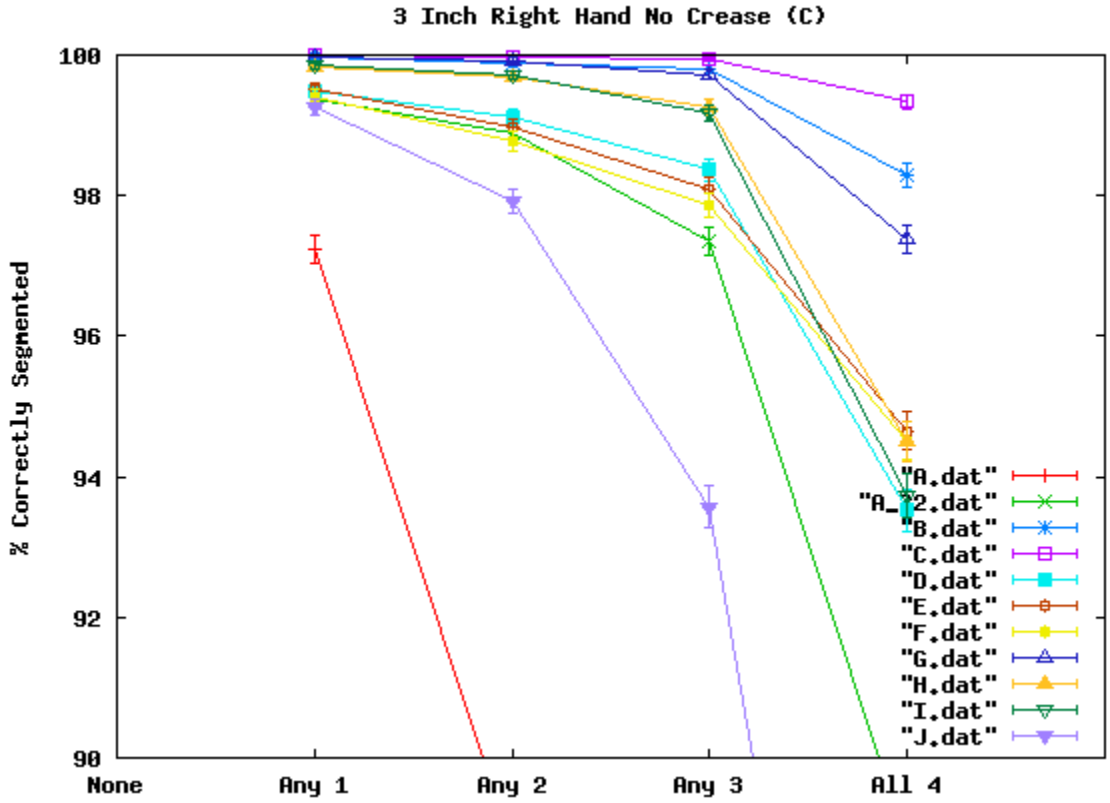
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



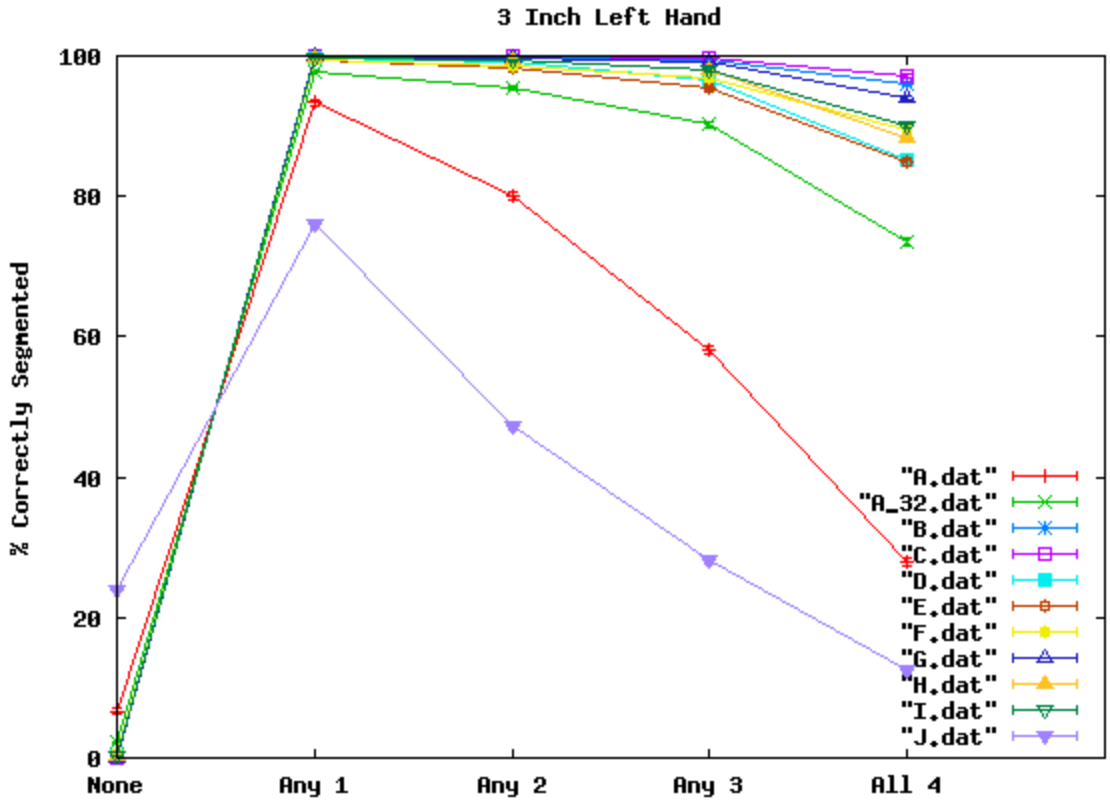


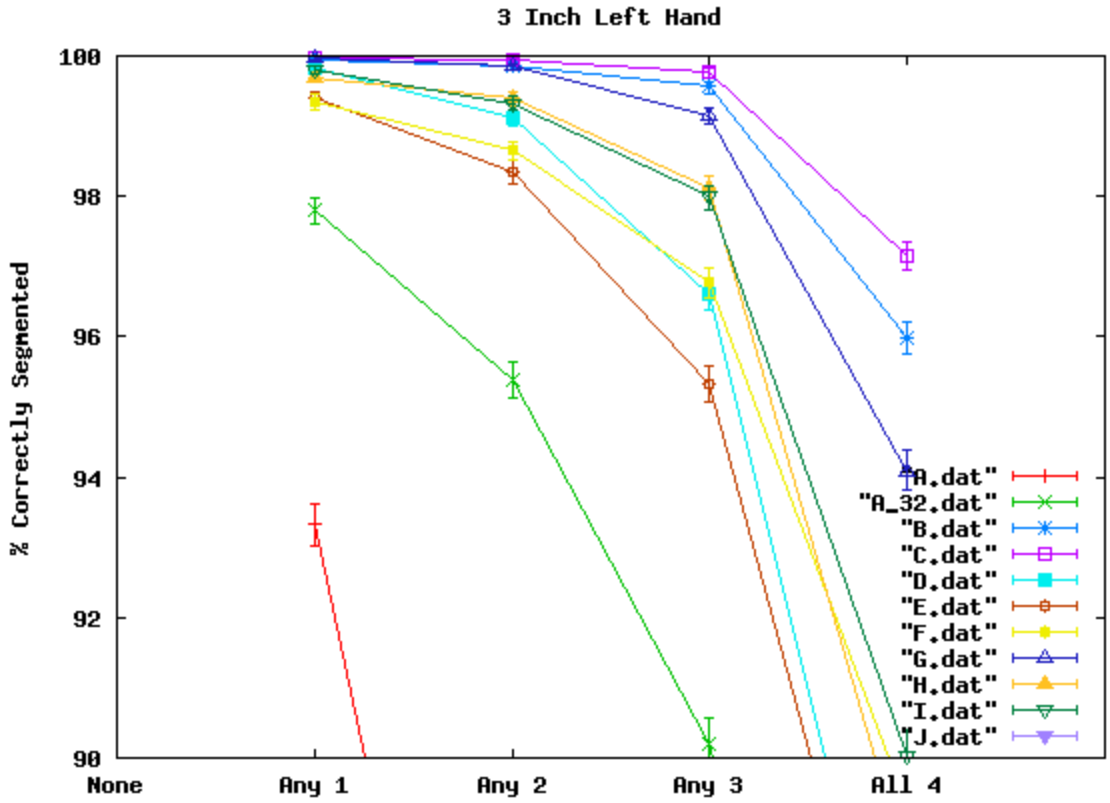
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



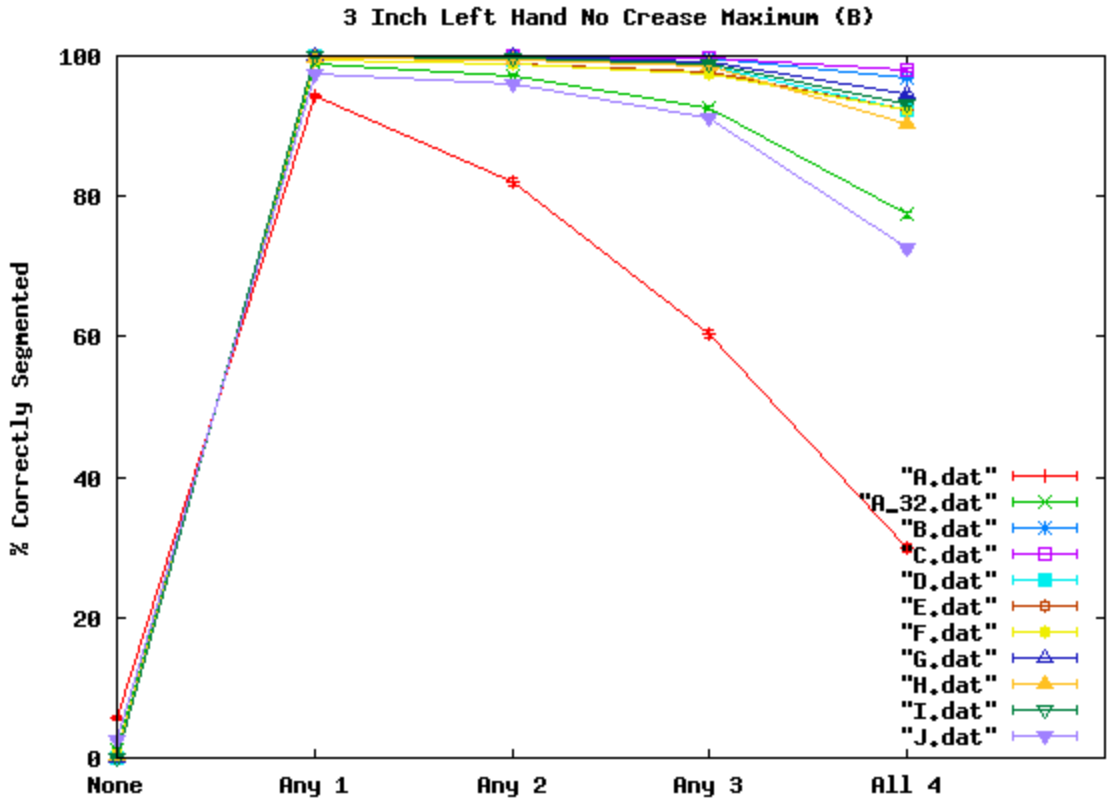


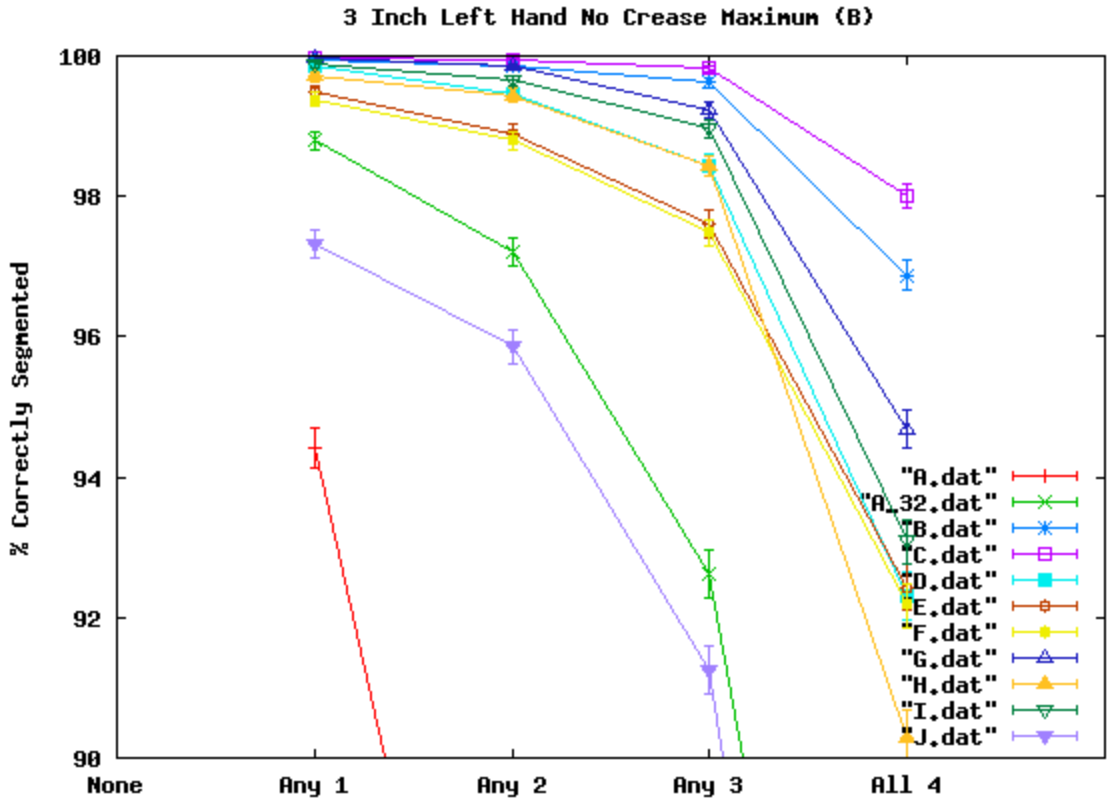
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



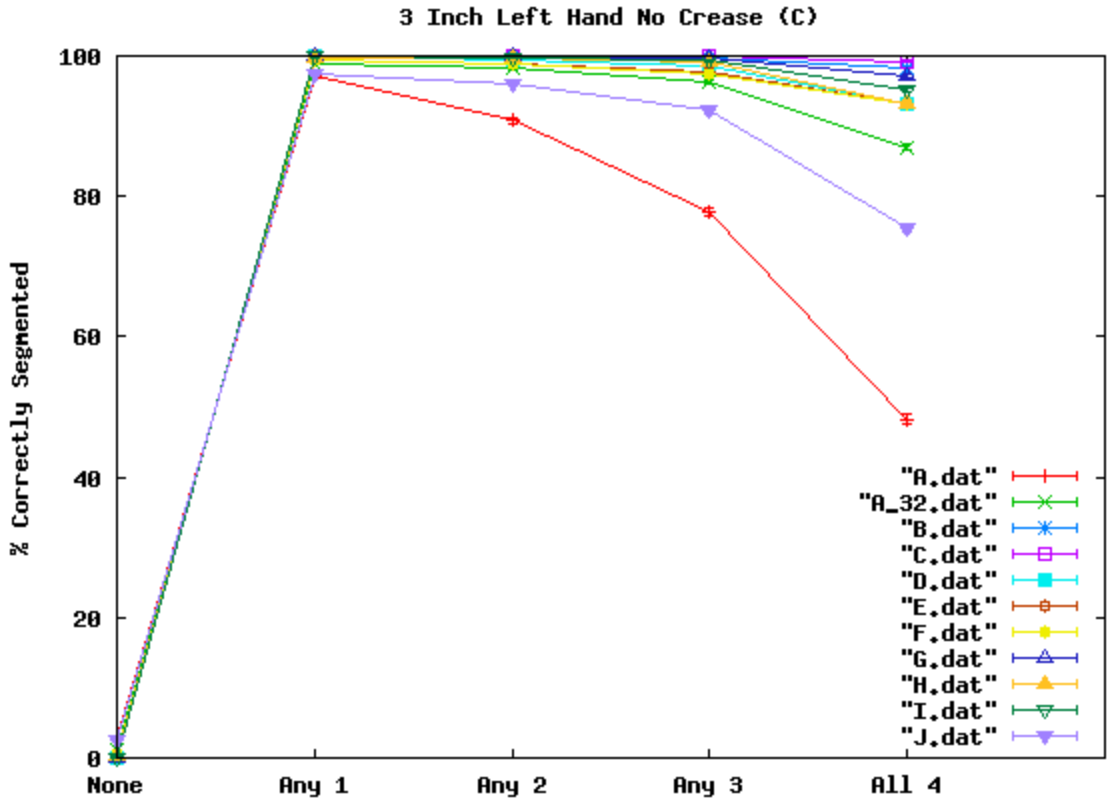


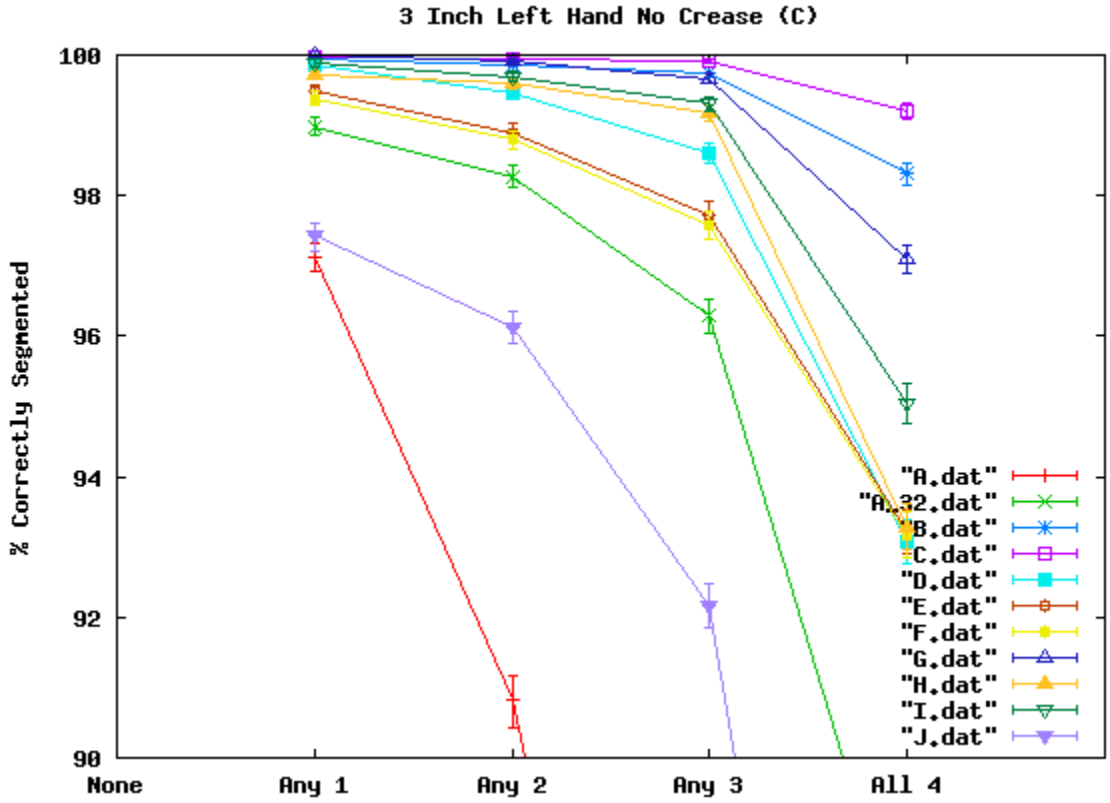
A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan





A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan

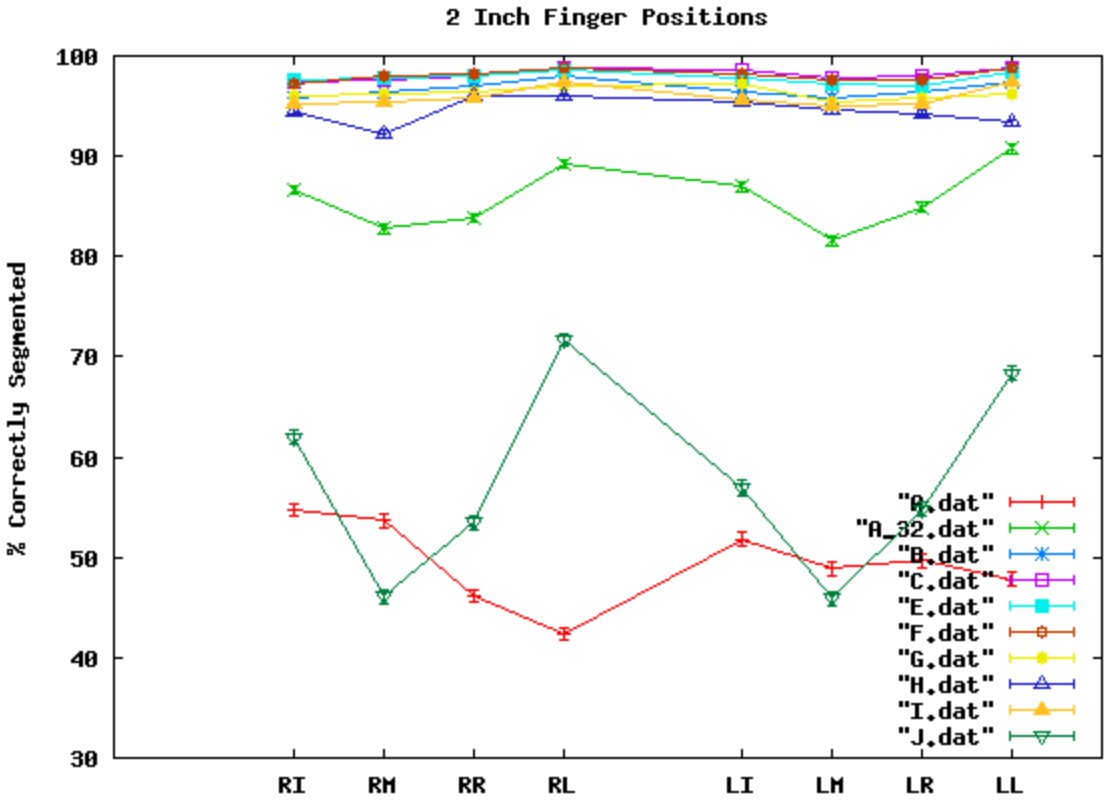


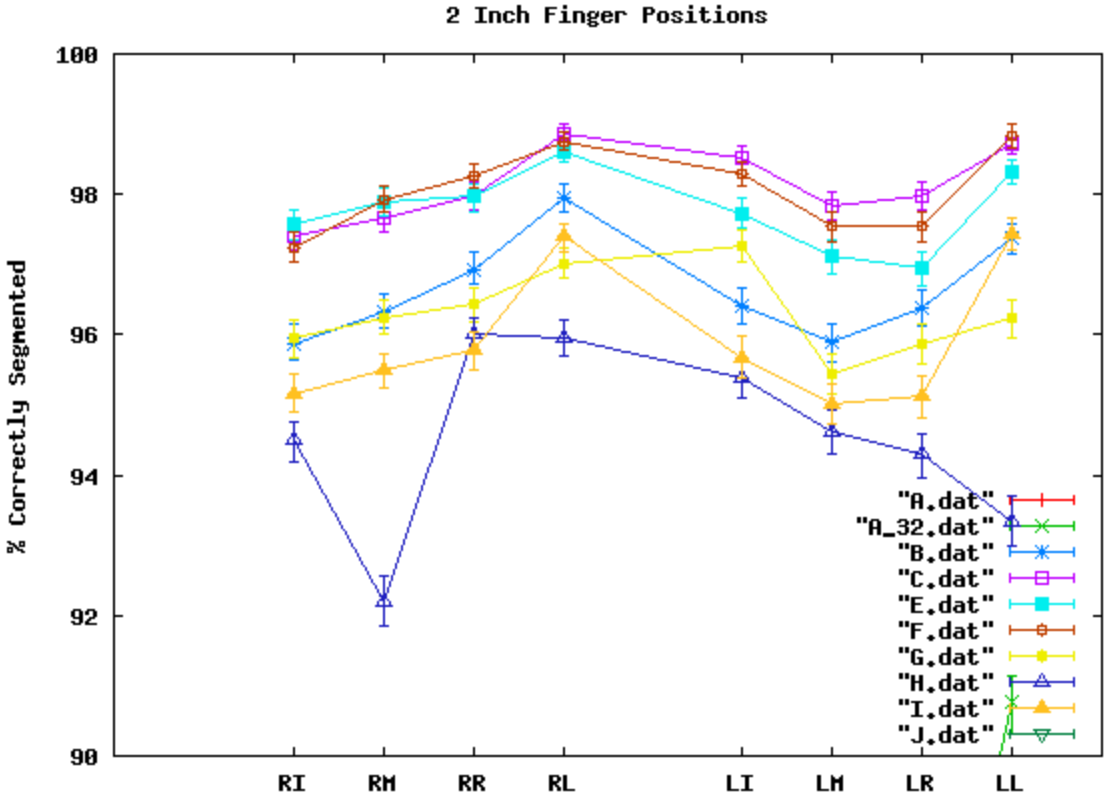


A = Aware || B/C = Cogent || D = Dermalog || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan

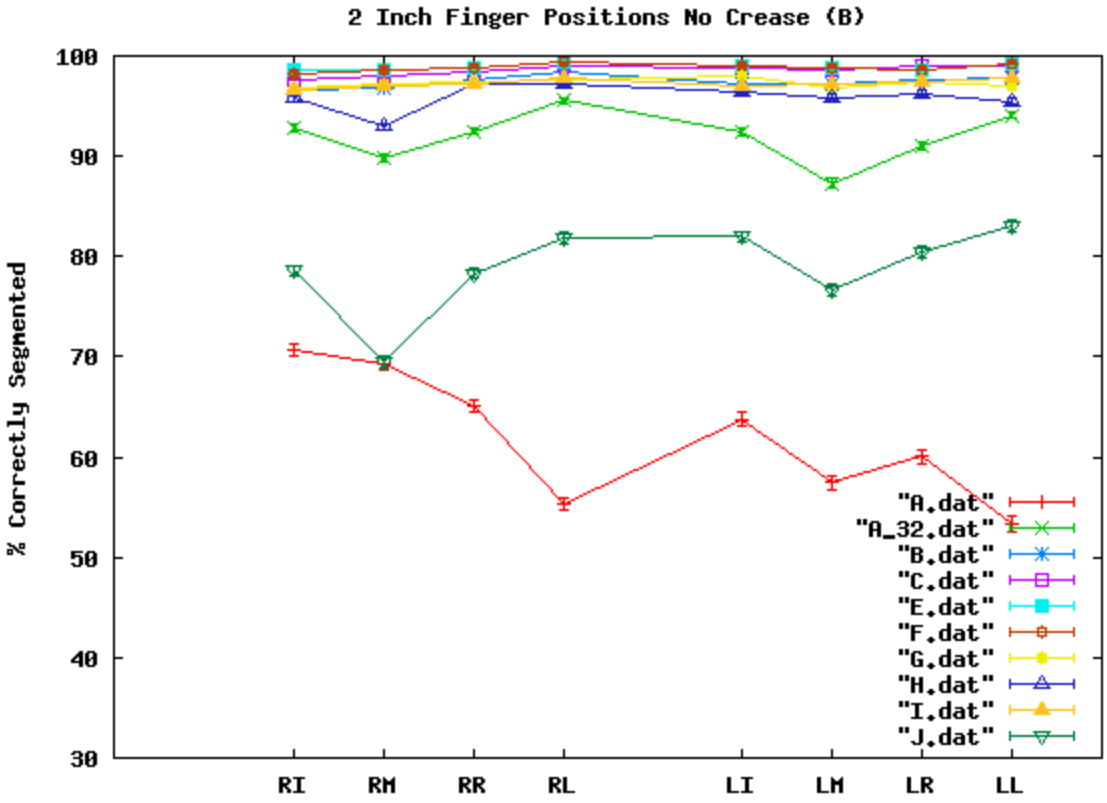
Appendix I. Confidence intervals for 2-inch segmentation results.

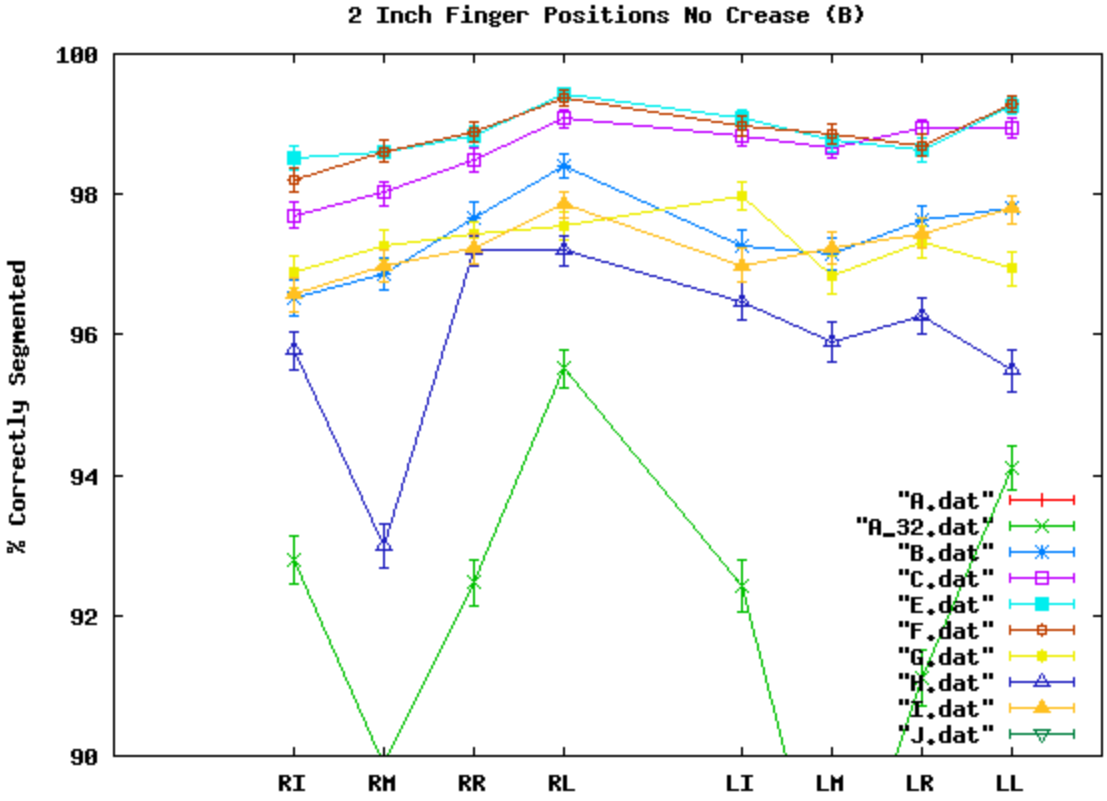
The plots in this appendix are an attempt to show 95% confidence intervals for the 2-inch segmentation results shown in tables in Appendix B for the finger positions and right/left hands. The confidence intervals were computed using the boot strap function in the R statistics package and a sampling of 1,000 iterations. The only issue is that the intervals were so small that they really don't show well in the plots. The plots are shown on two scales. The first shows the results for all the segmentation algorithms. The second shows only results in the range 90-100% correct segmentation. The "None" segmented is not included in the second plot just to make it easier to read.



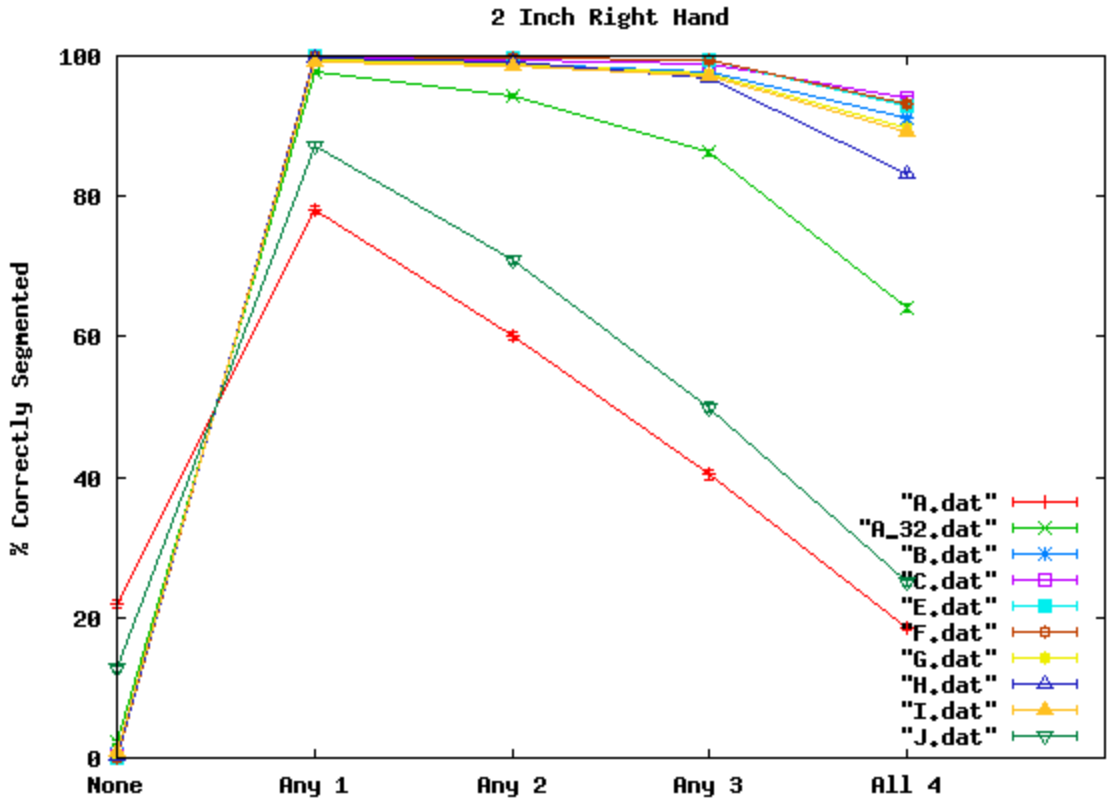


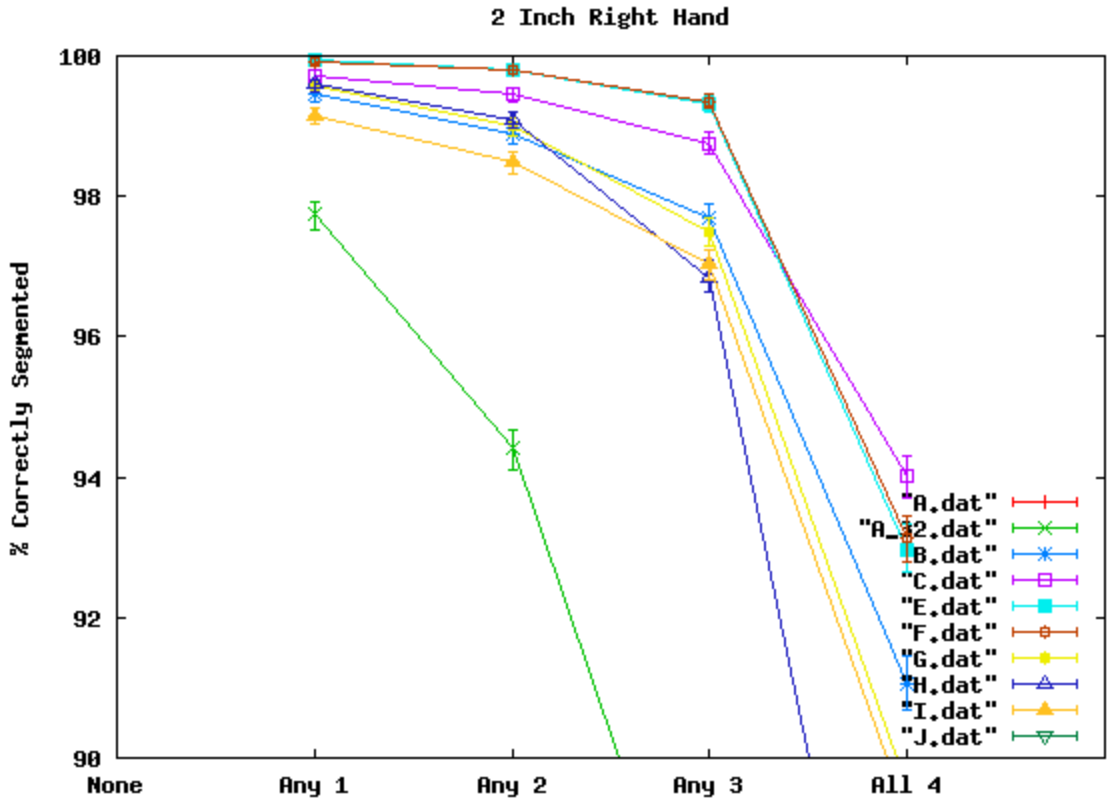
A = Aware || B/C = Cogent || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



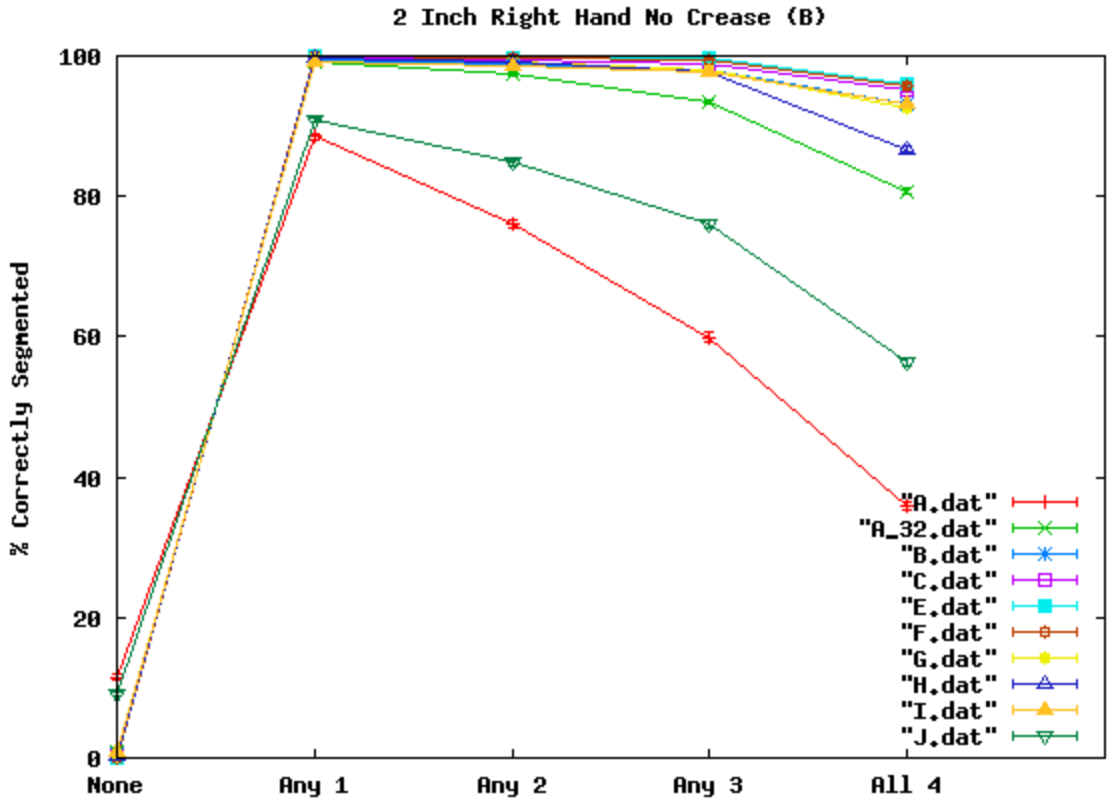


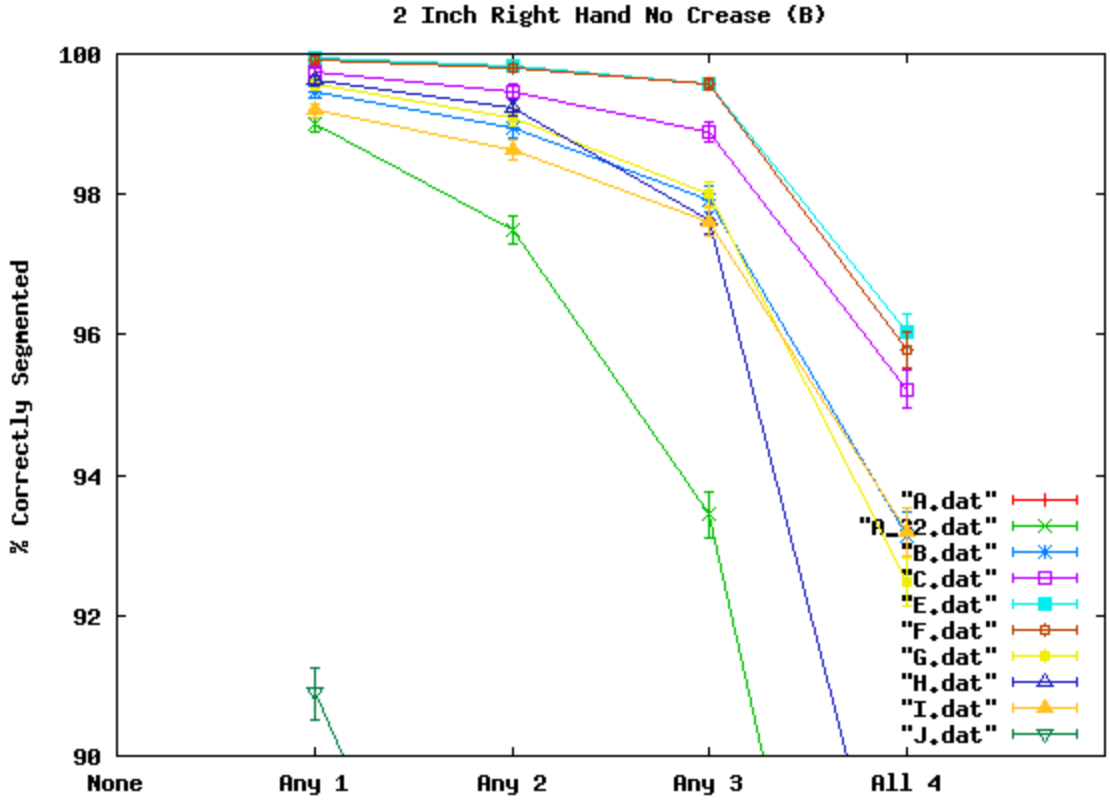
A = Aware || B/C = Cogent || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



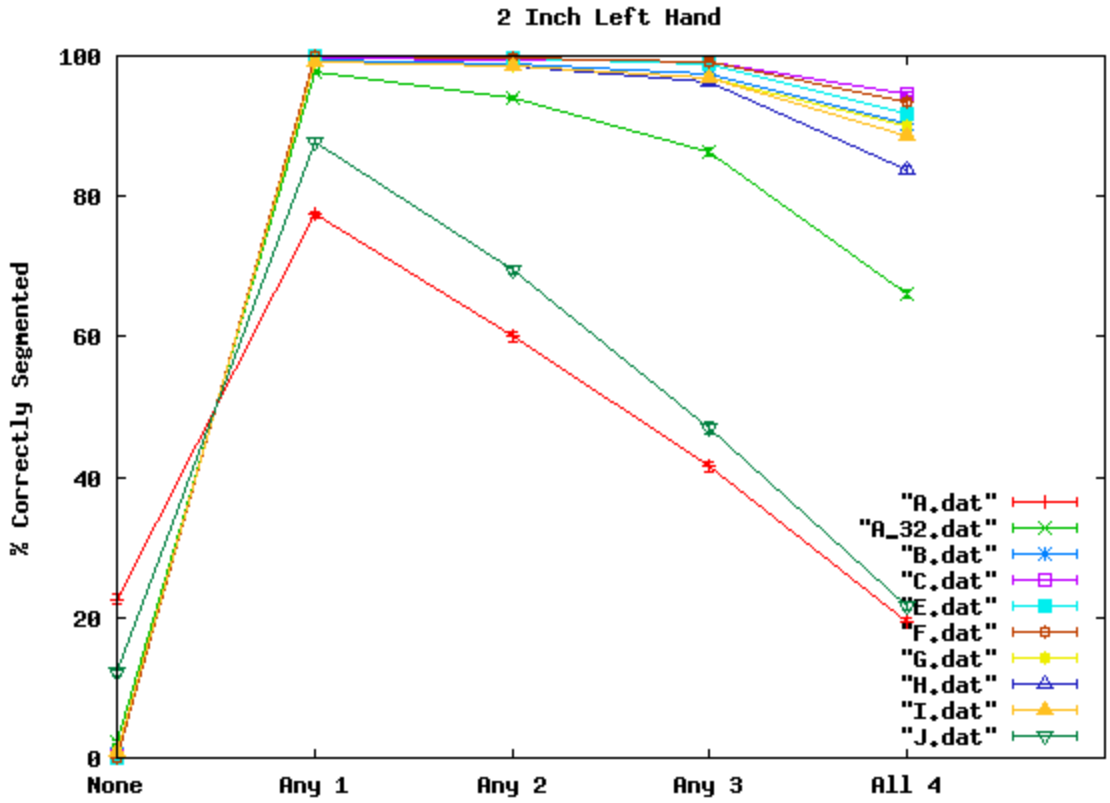


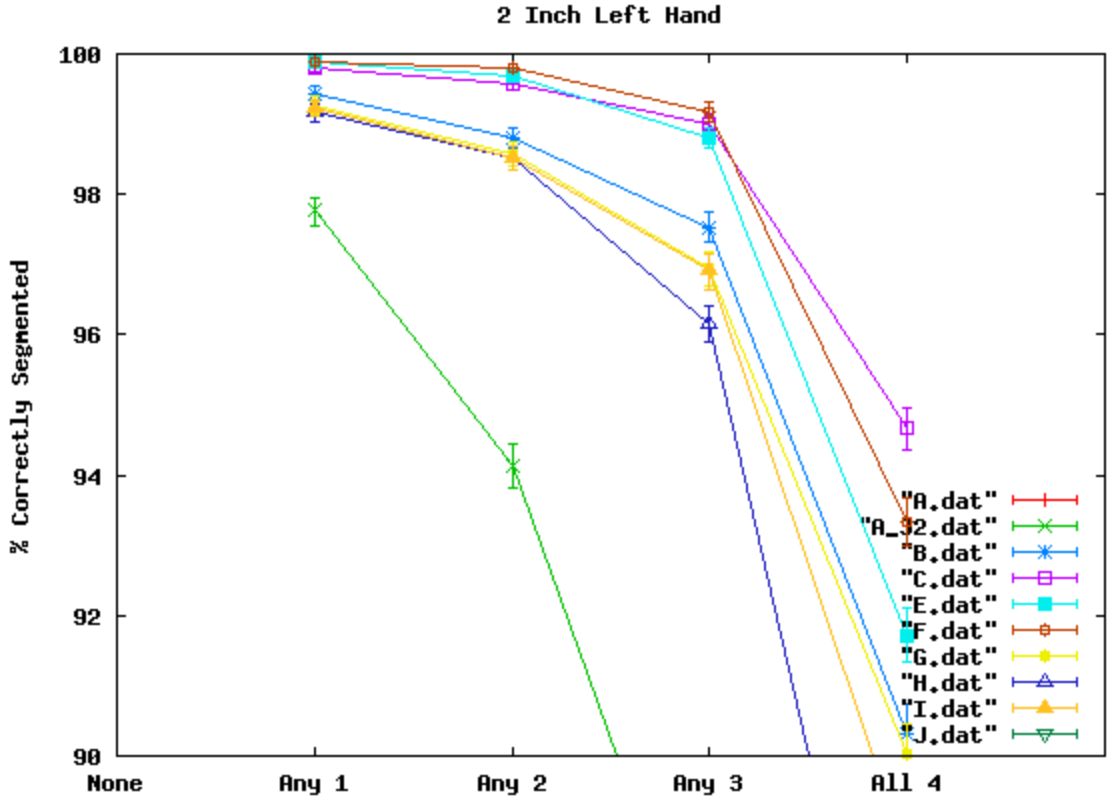
A = Aware || B/C = Cogent || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan



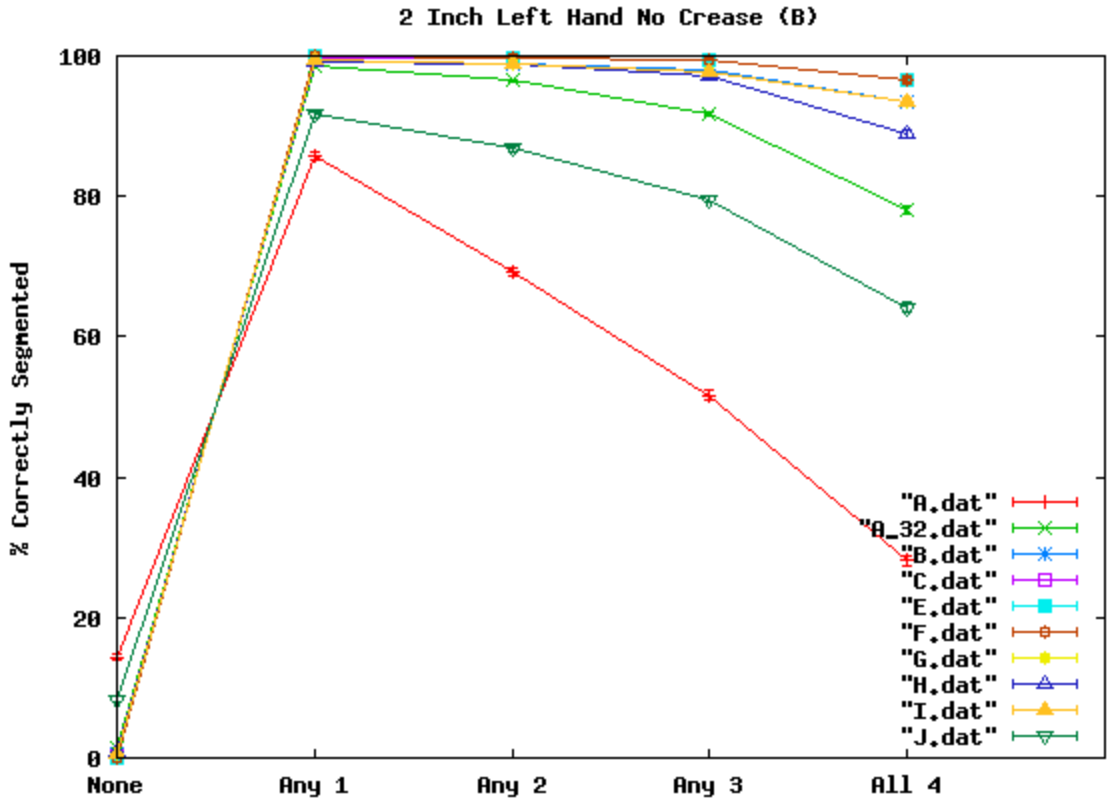


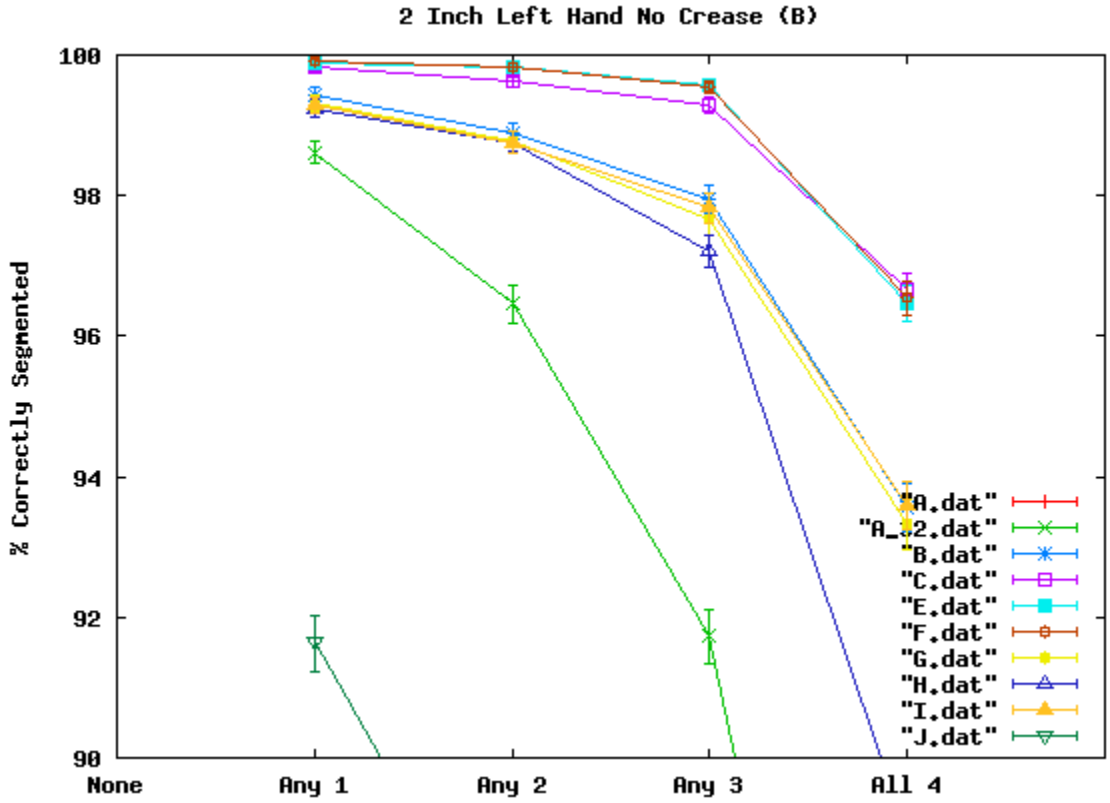
A = Aware || B/C = Cogent || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan





A = Aware || B/C = Cogent || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan





A = Aware || B/C = Cogent || E/F = NEC || G = Sagem Morpho || H/I = Sonda || J = Ultrascan