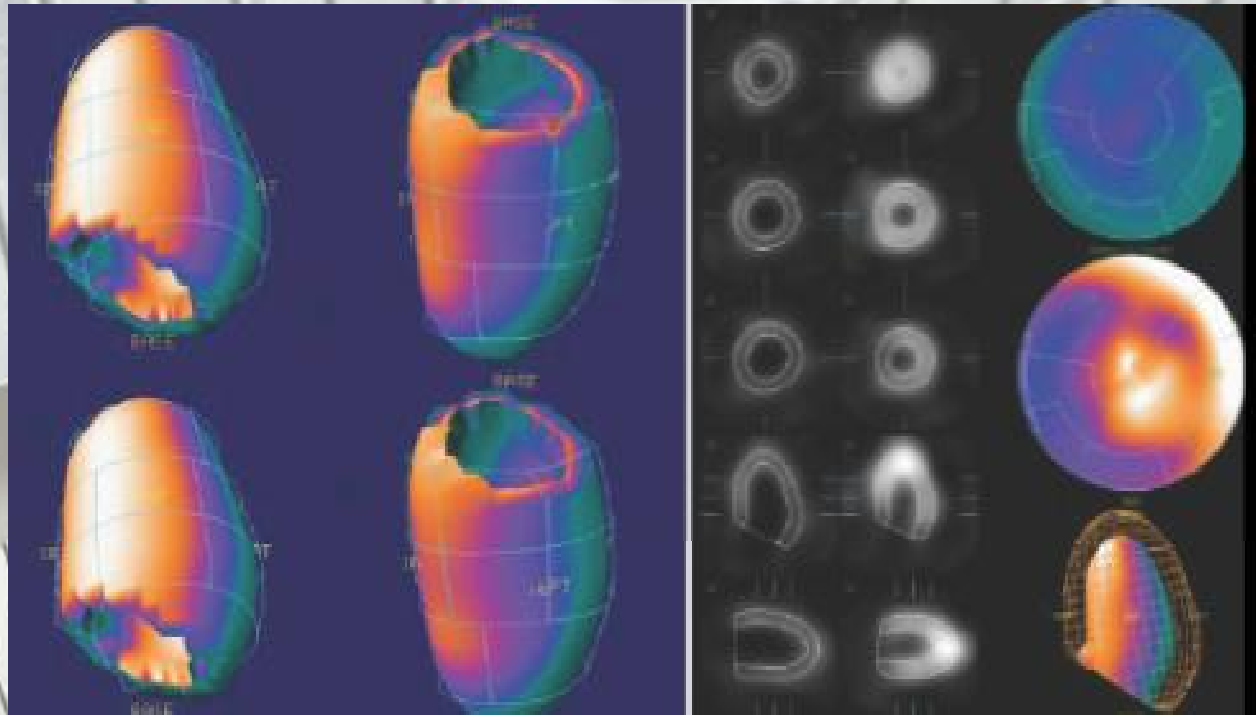


# Cardiac Training

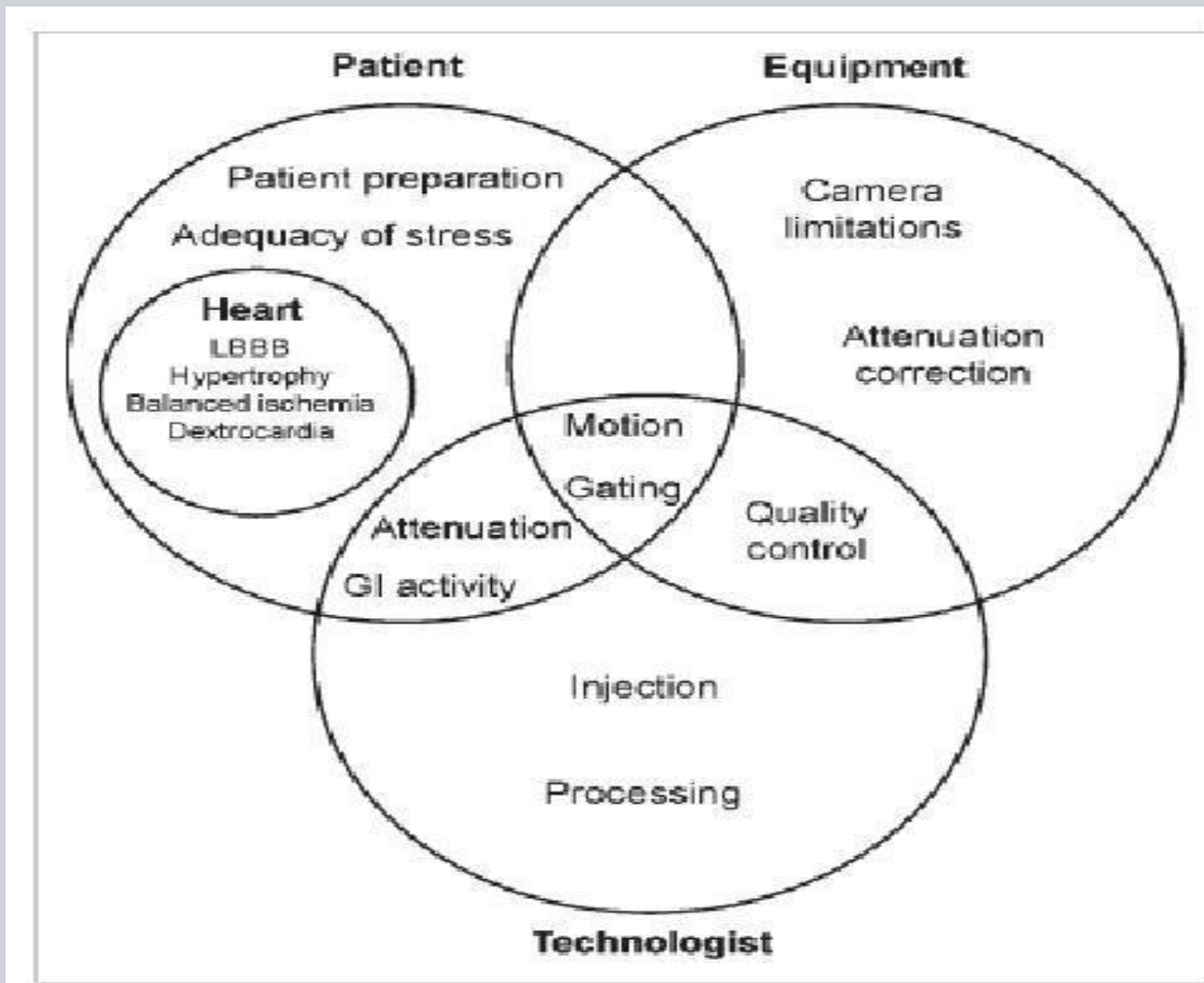


Jane Yang  
MI Application Specialist

## Summary

- Tips for Cardiac Training
- Quantification Analysis

# Important checks



# Camera, Radiopharmaceutical, Patient

- **Good new 90°MHR!!**
- **Well preparation of the radiopharmaceutical**
- **Proper center and positioning of the patient**
- **ECG must be checked properly before starting the scan. R Waves must be positiv !!! Check polarity for correctness on the PPM. Electrodes must be set correct please refer to the manuals.**
- **Make sure that the beats are centered and remain proper and correct inside the beat window for duration of the study.**

# Cardiac Creep

- **Verification:** Journal of Nuclear Medicine Technology 2006; 34:215-219

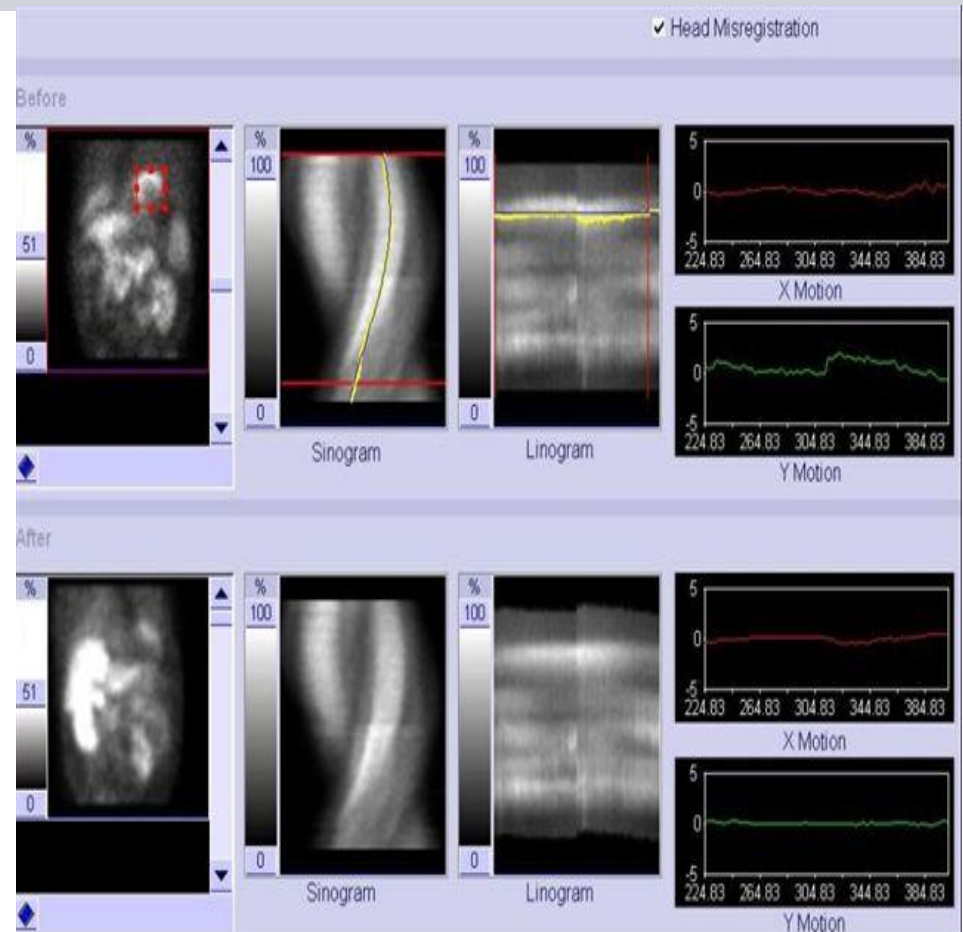
▪ **Cardiac creep is characterized by a gradual upward shift of the heart due to increased diaphragmatic excursion.**

## **Solution:**

- **A vertical change in position of the heart is usually noticed between the last frame of the first detector and the first frame of the second detector.**
- **Although these 2 datasets are theoretically accepted as consecutive images, there is actually an interval between them during which repositioning of the heart occurs. This phenomenon is characterized as "cardiac creep". It can be avoided most of the time by allowing the patient to rest on the camera bed (or chair) for approximately 3 to 5 minutes prior to imaging.**

# Check for Cardiac Creep

- This is observed on the linogram
- Enable Head Misregistration during Motion Correction.
- This will allow each detector to be corrected separately which can compensate for the motion during the scan.



# Avoid Truncation Artefacts!!!

The detectors run definitely out of the field of interest.

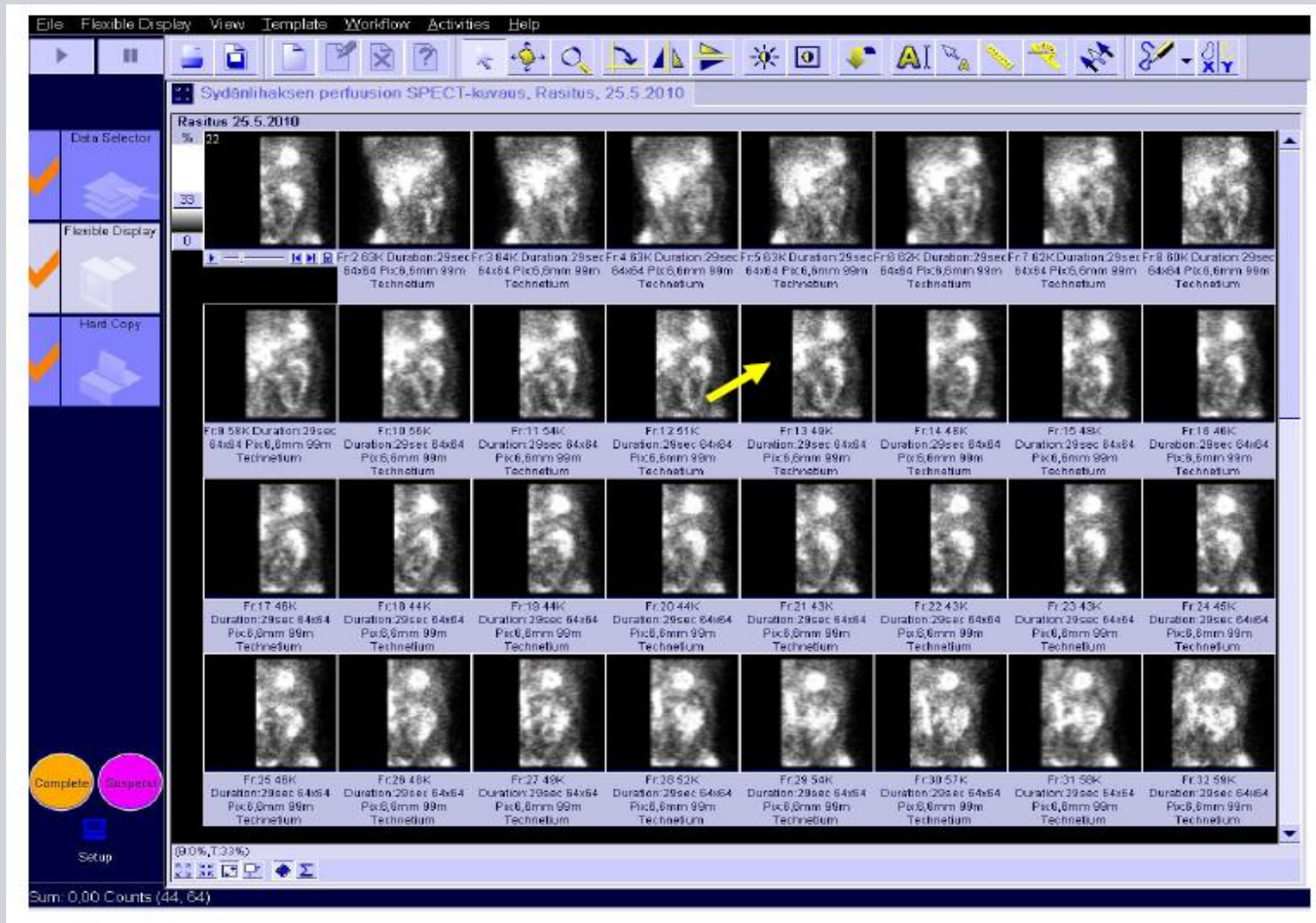
>typical cause is something obstructing a light rail such as a sheet or piece of clothing that is hanging over the

>The one detector runs out slowly due to the Autocontour.





# Avoid a cut of the Apex





## Summary

- Tips for Cardiac Training
- Quantification Analysis

## Corridor 4DM Getting Started



Getting Started  
with  
Corridor4DM v6.0

## Supported Databases

### Getting Started with 4DM v6.0

#### Supported Datasets

- Matrix Sizes
  - 64x64
  - 128x128
  - 256x256
- Time Bins
  - 8 Frames
  - 16 Frames
  - 32 Frames
  - Planar Gated ONLY

## Supported Databases

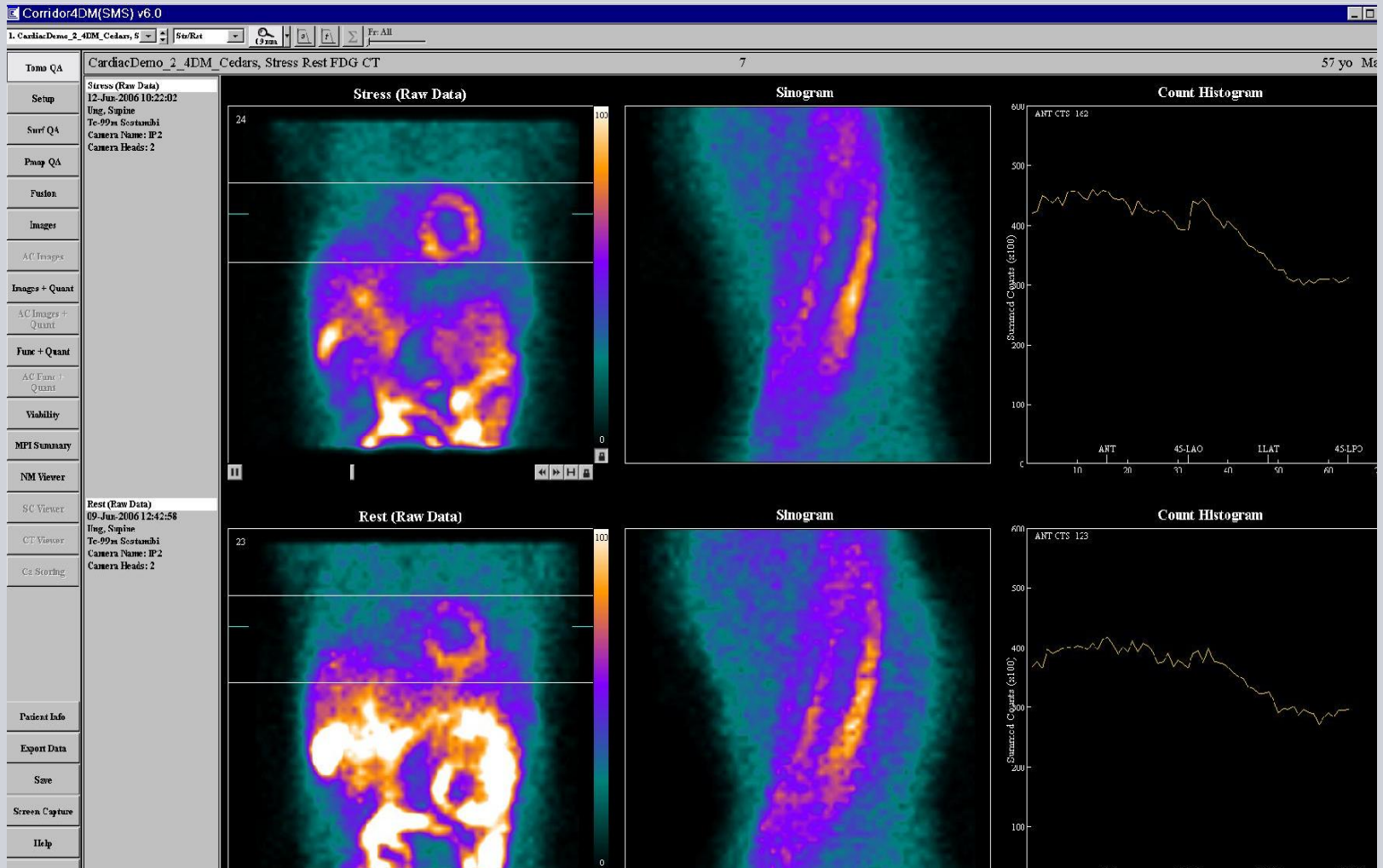
### Corridor4DM v6.0 Supported Datasets

- Cardiac SPECT and Gated SPECT datasets (Recon, Tomo, and Gated Tomo)
- Cardiac Gated Blood Pool SPECT datasets (SPECT MUGA)
- NM Planar Gated datasets (Planar MUGA)
- NM Static datasets
- NM Dynamic datasets (First Pass ERNA)
- Cardiac PET and Gated PET datasets
- PET Recon Dynamic or List mode datasets
- Uncorrected and Attenuation Corrected
- Raw Projection datasets for display (NM)
- DICOM Secondary Screen Capture (8 or 24 bit)
- DICOM Multi-Frame Secondary Screen Capture (8 or 24 bit)
- CT datasets (Volumetric or Recon datasets only)
- Extracted Coronary Vessels from Siemens Circulation, Philips Brilliance, and GE Advance workstations
- Siemens transformation matrix datasets

*Note: Vertical and horizontal long-axis datasets are automatically generated from the short axis dataset via Corridor4DM*

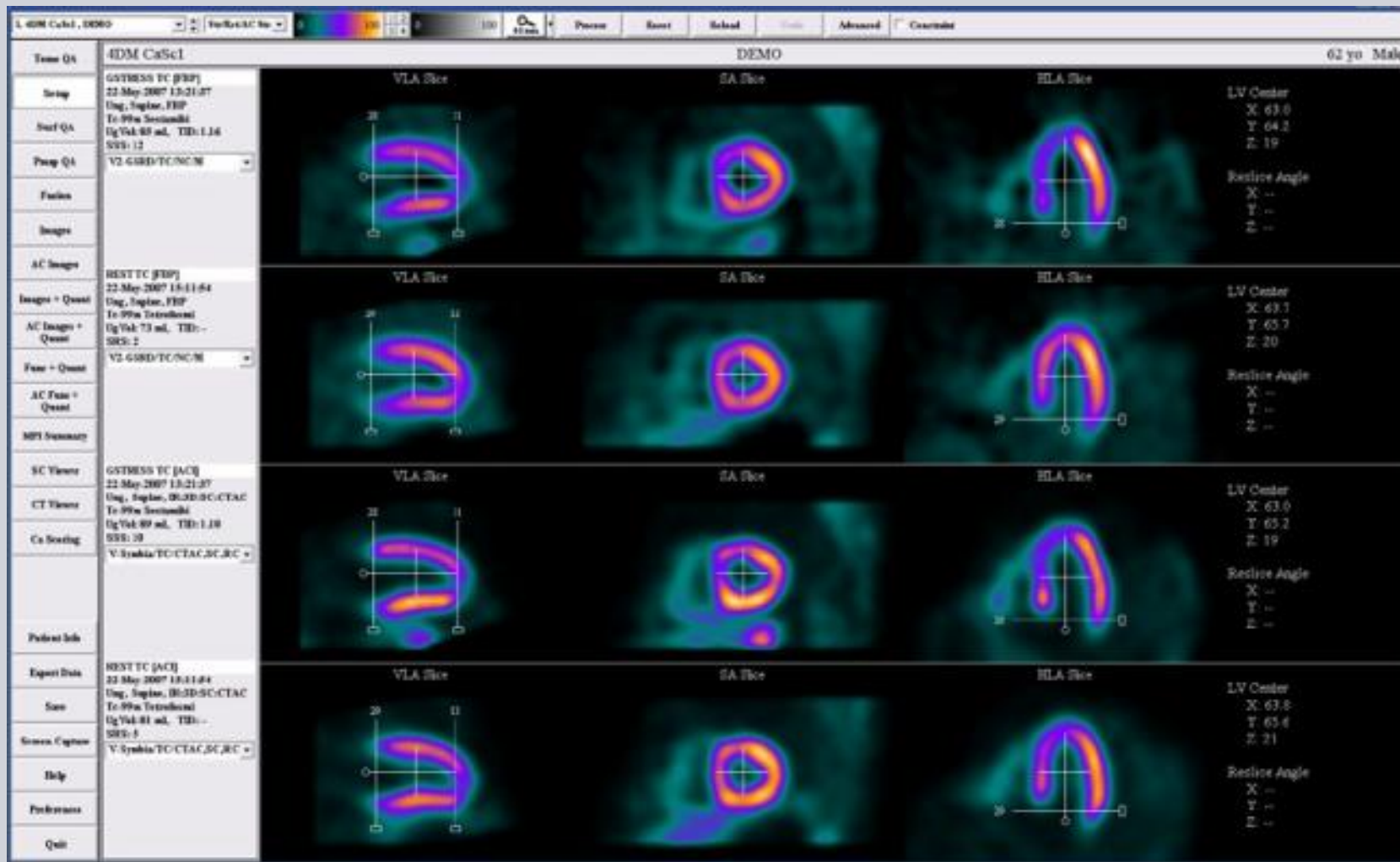
*Note: All in yellow denote new data support for v6.0*

# Tomo QA Page

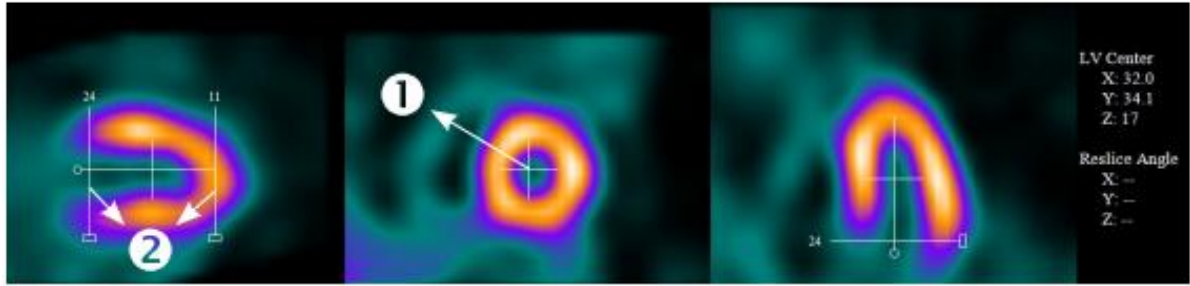




# Set up Page



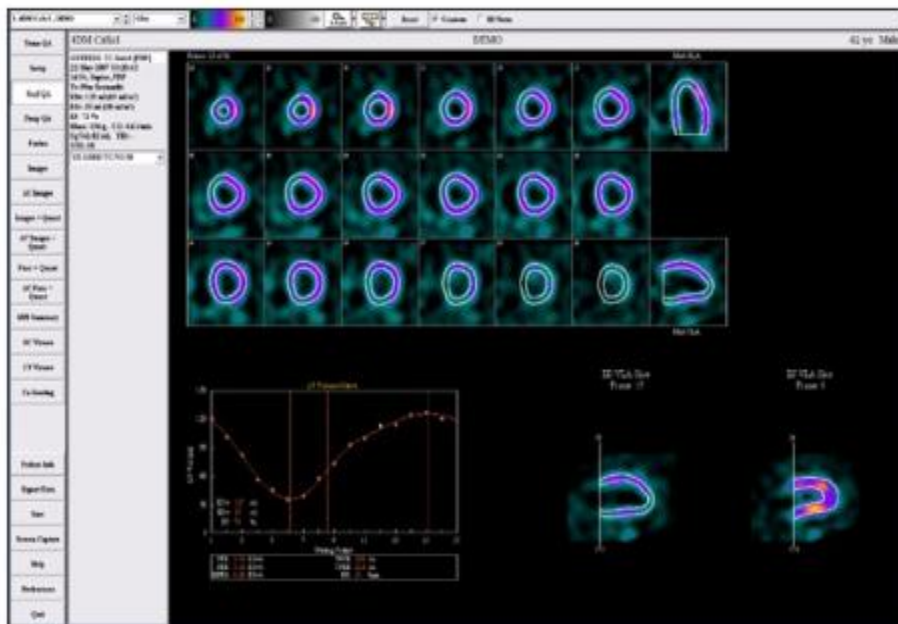
## Set up limitation

<b>1</b>	Proper positioning of the LV center aligns the crosshairs in the center of the ventricle.	 <p>The figure consists of three cardiac PET scan slices. The leftmost slice shows a cross-section of the heart with a crosshair centered on the ventricle and two vertical lines indicating the apical and basal limits. A circled '2' is at the bottom. The middle slice shows a similar view with a circled '1' and an arrow pointing to the crosshair. The rightmost slice shows a different view with a crosshair and a circled '2' at the bottom. On the far right, there is a text box with the following data: LV Center X: 32.0 Y: 34.1 Z: 17 Reslice Angle X: - Y: - Z: -</p>
<b>2</b>	Proper positioning of the apical and basal limits are at the center of the apical myocardium and the mitral valve plane.	

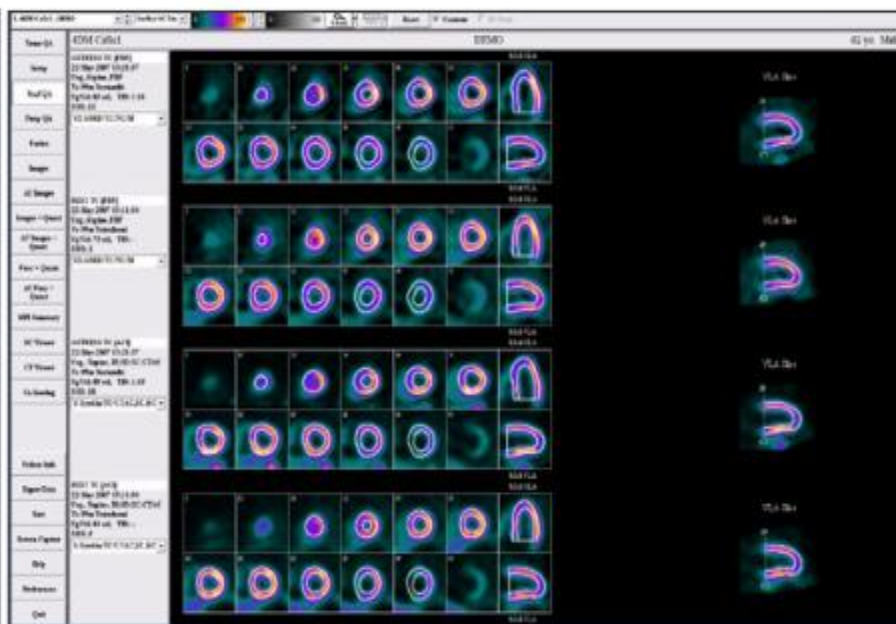
*Figure 4.6: Examples of proper positioning on the Setup screen*



# Surf QA Page

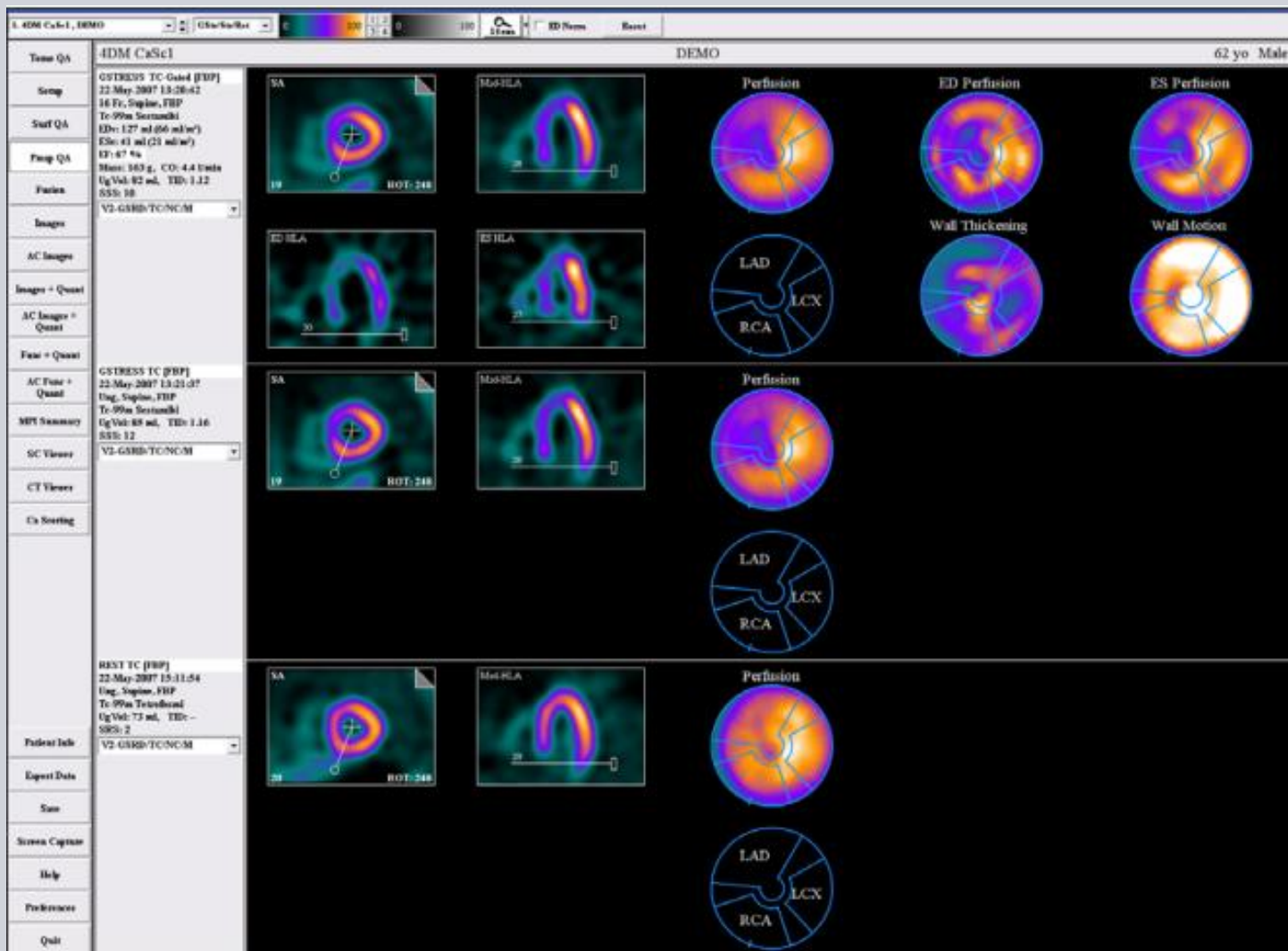


*Figure 4.8: The Surf QA screen with Contours applied to assess the LV surface generation on the gated dataset*

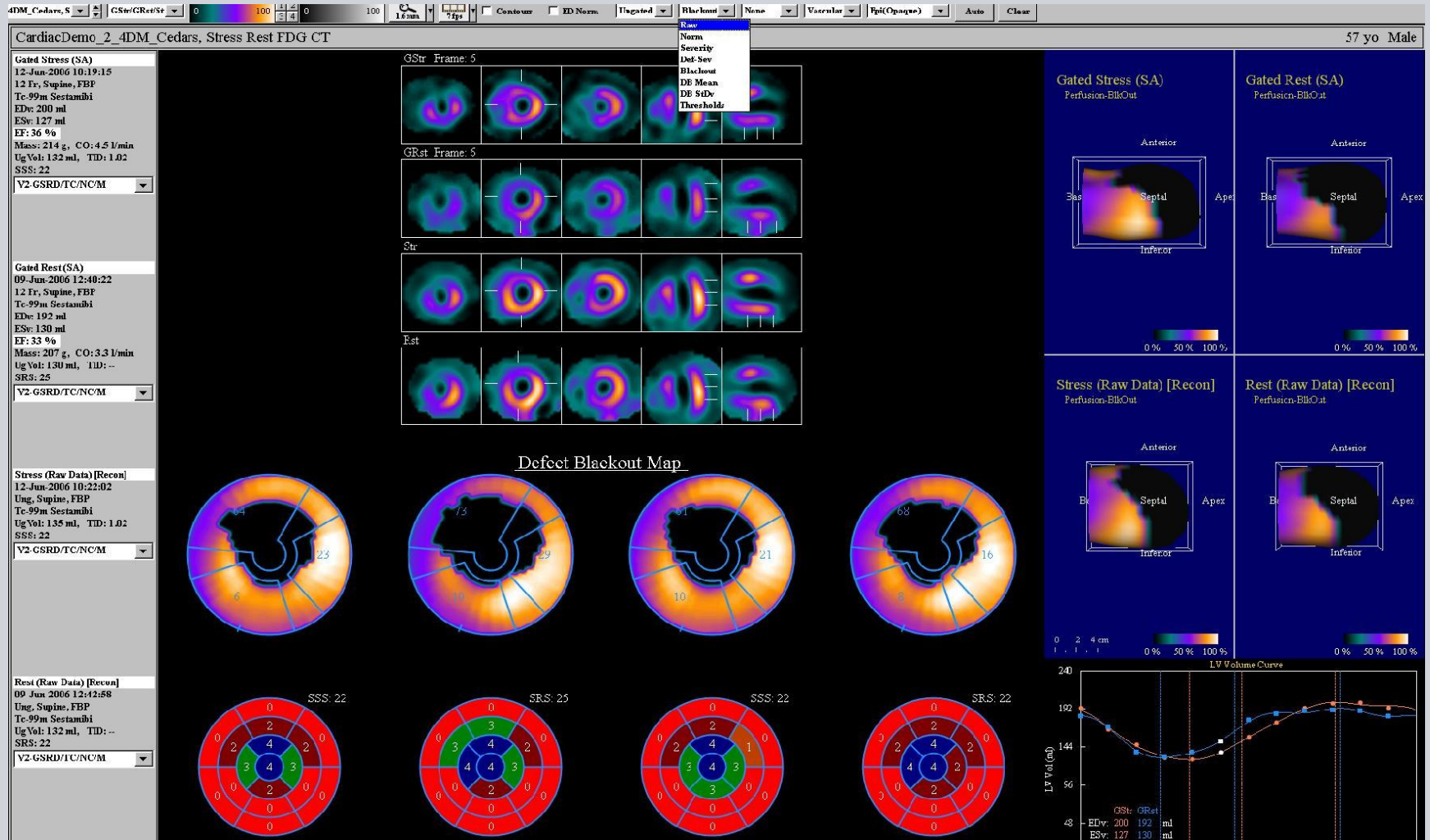


*Figure 4.9: The the Surf QA screen with the Str/Rst/AC Str/AC Rst option selected from the Dataset Selector drop-down menu*

# Pmap QA Page



# MPI Summary page



## P't information

Stress-Gated | Stress Prima

15 May 2007 12:01:38

8 Fr, Supine, IR:3D

Tc-99m Tetrofosmi

EDv: 141 ml

ESv: 49 ml

EF: 65 %

Mass: 161 g, CO: 5.5 l/min

Ug Vol: 93 ml, TID: 0.86

SSS: 16

V-Flash3D/NC/M

- TID :Transient Ischemic Dilation
- Cardiac Output

## TID Normal Range

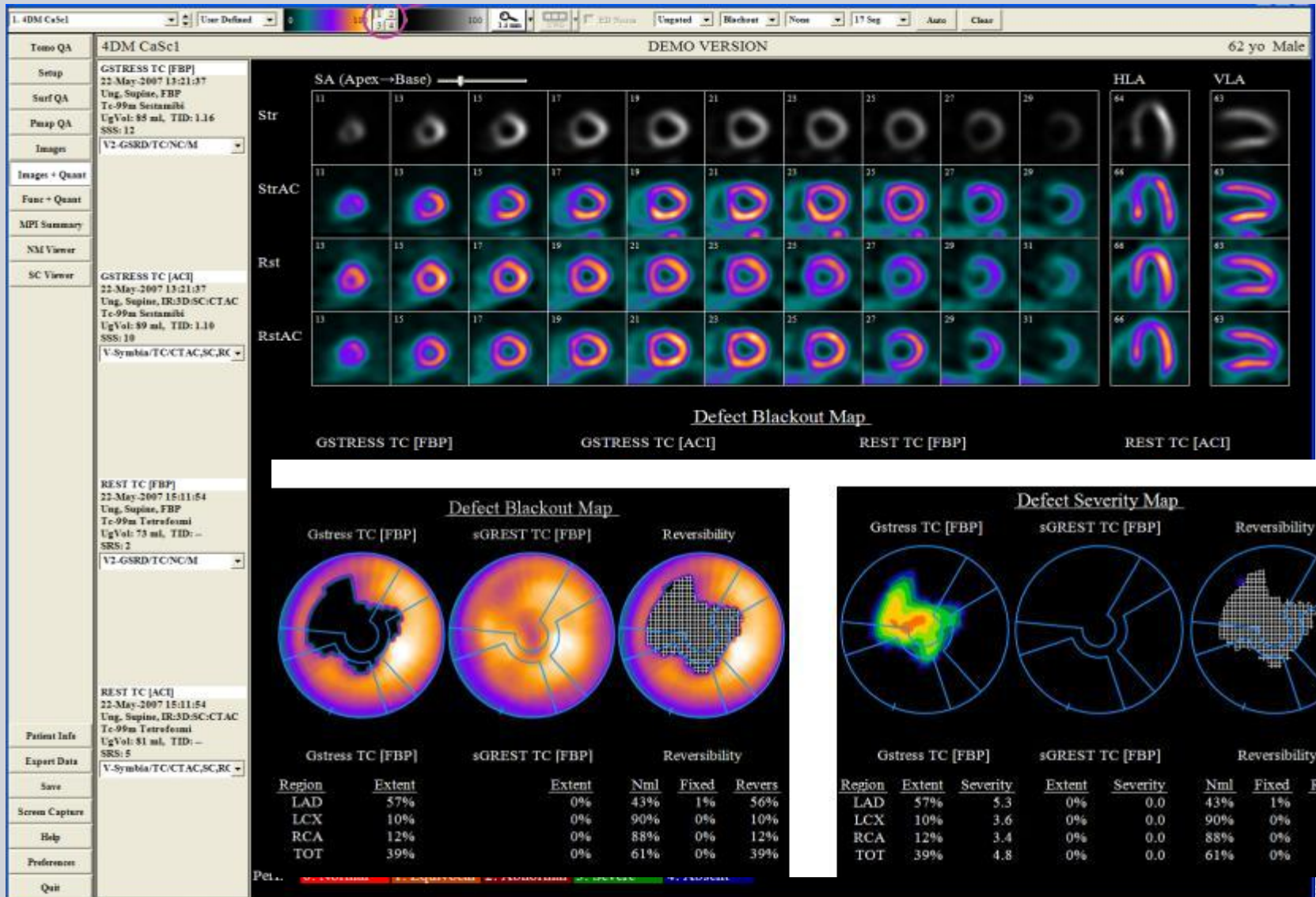
### Results – Dual Isotope

- NC mean normal ratios:
  - Composite = Males =  $1.00 \pm 0.09$  Females =  $1.01 \pm 0.12$
  - $1.01 \pm 0.11$
  - **Threshold = 1.23 \***
- AC mean normal ratios:
  - Males =  $1.02 \pm 0.09$  Females =  $1.03 \pm 0.11$
  - Composite =  $1.02 \pm 0.09$
  - **Threshold = 1.20**

\* Normal Threshold defined as composite + 2 standard deviations

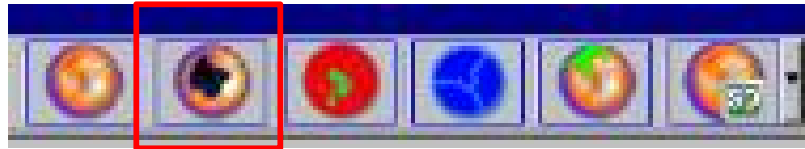


# Image + Quant Page



erved.

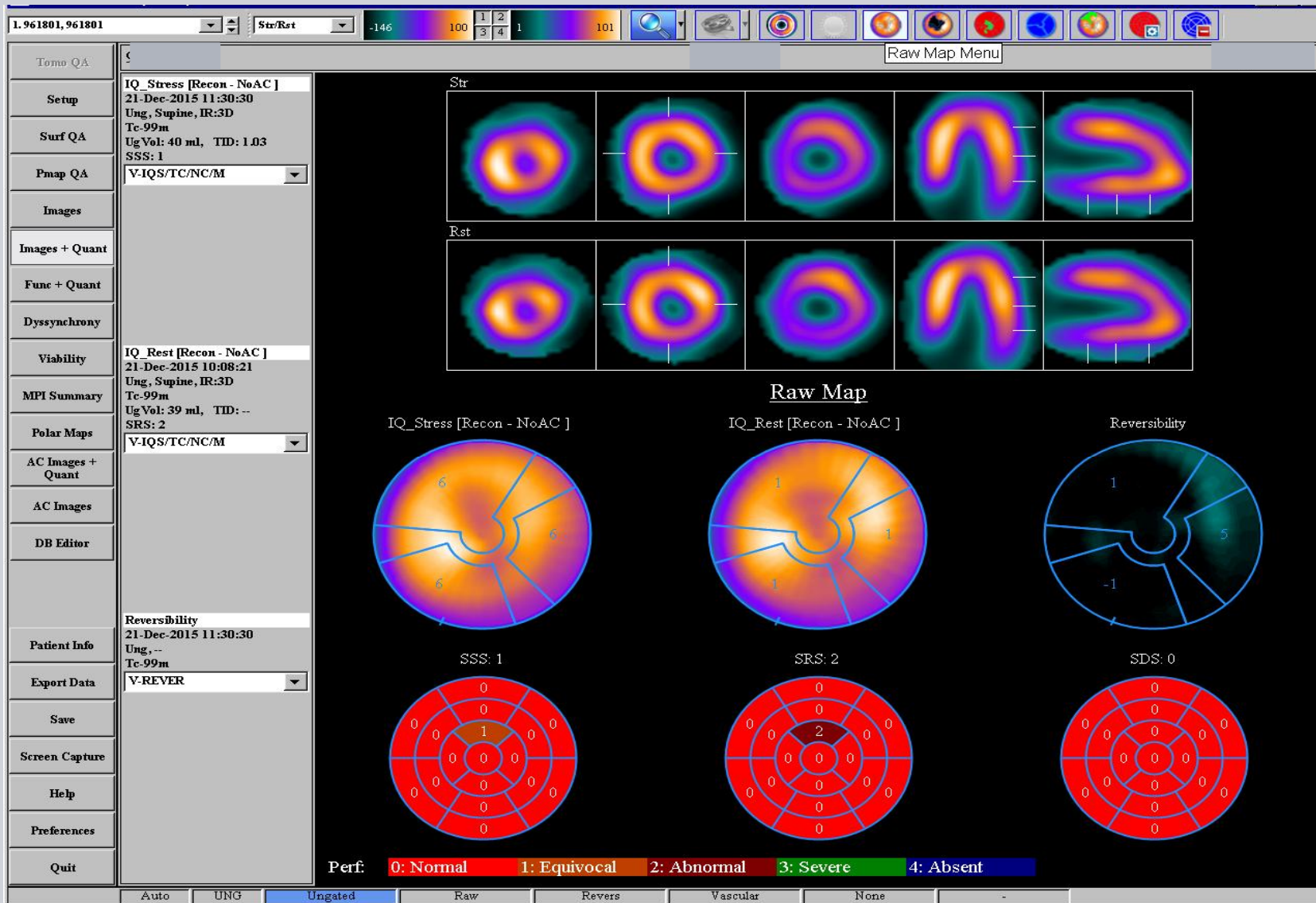
## Quant Map menu



- **Quant Map:** This drop-down menu controls the information displayed in the Quantification (Quant) panel. The available options are:
  - **Raw:** Displays the values reconstructed from image voxel values.
  - **Norm:** For Perfusion maps, displays values normalized such that regional maximum is 100.
  - **Severity:** Displays pixels in units of StDv from the normal mean.
  - **Def-Sev:** Displays all defect pixels that fall below the defect threshold in units of StDv below the normal mean.
  - **Blackout:** Displays all defect pixels that fall below the defect threshold with a zero value.
  - **DB Mean:** Displays normal database mean map for applied Normals database.
  - **DB StDv:** Displays normal database StDv map for applied Normals database.
  - **Thresholds:** Displays the number of standard deviations used to define the defect threshold.

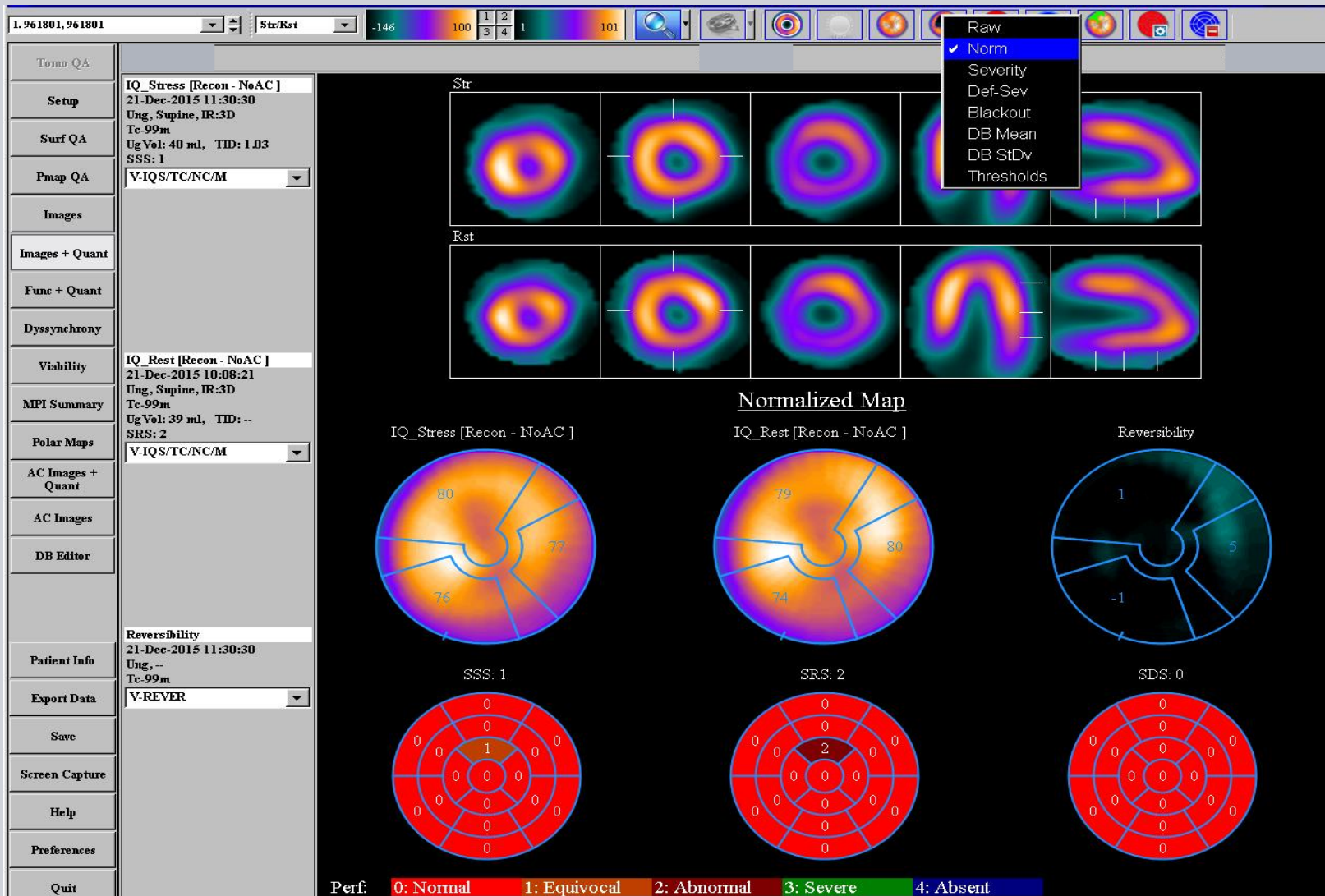


# Raw : Display the values reconstructed from image voxel value

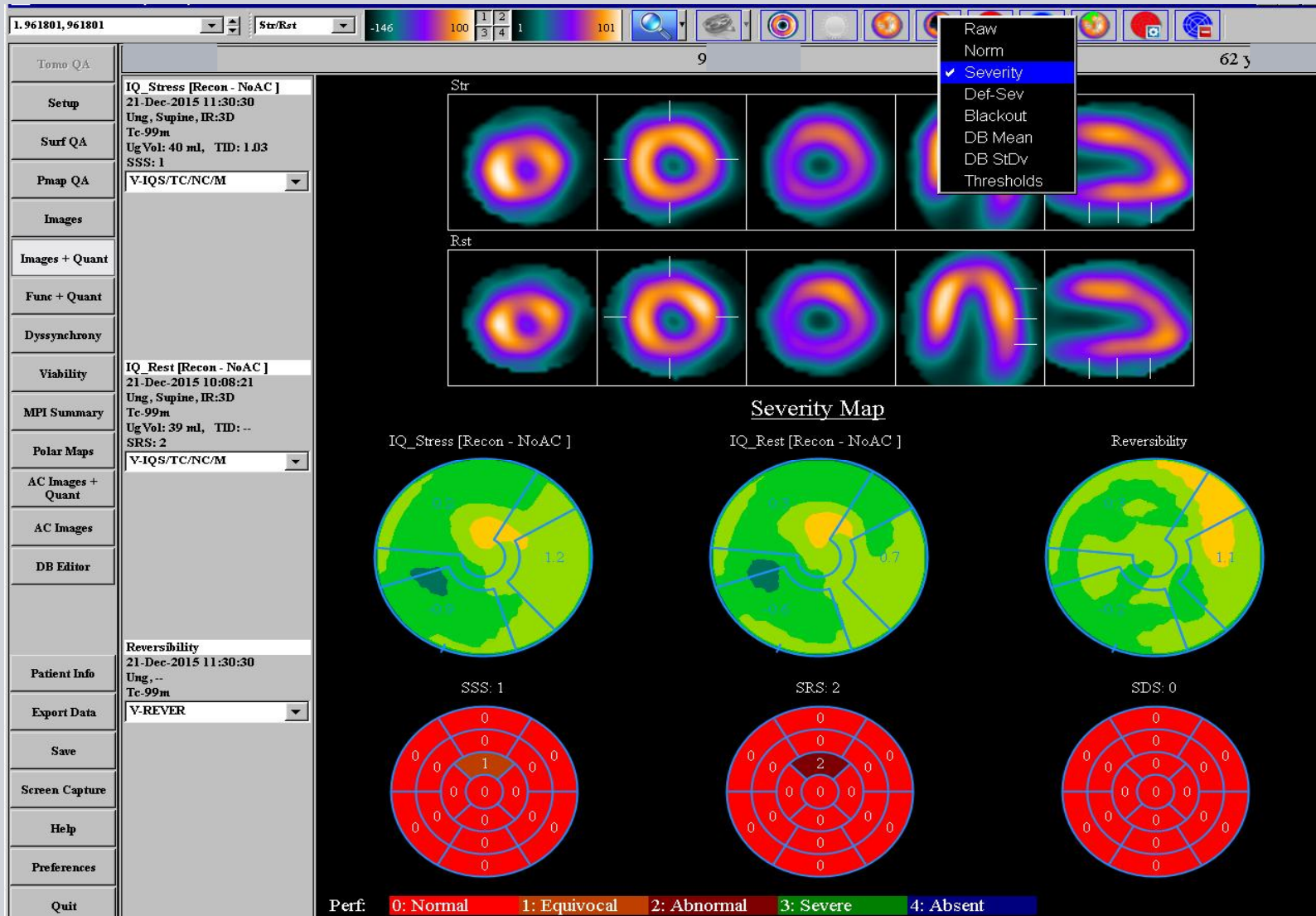


served.

# Norm: For Perfusion map , Displays values normalized such that regional maximum is 100



# Severity: Displays pixels in units of StDv from the normal mean

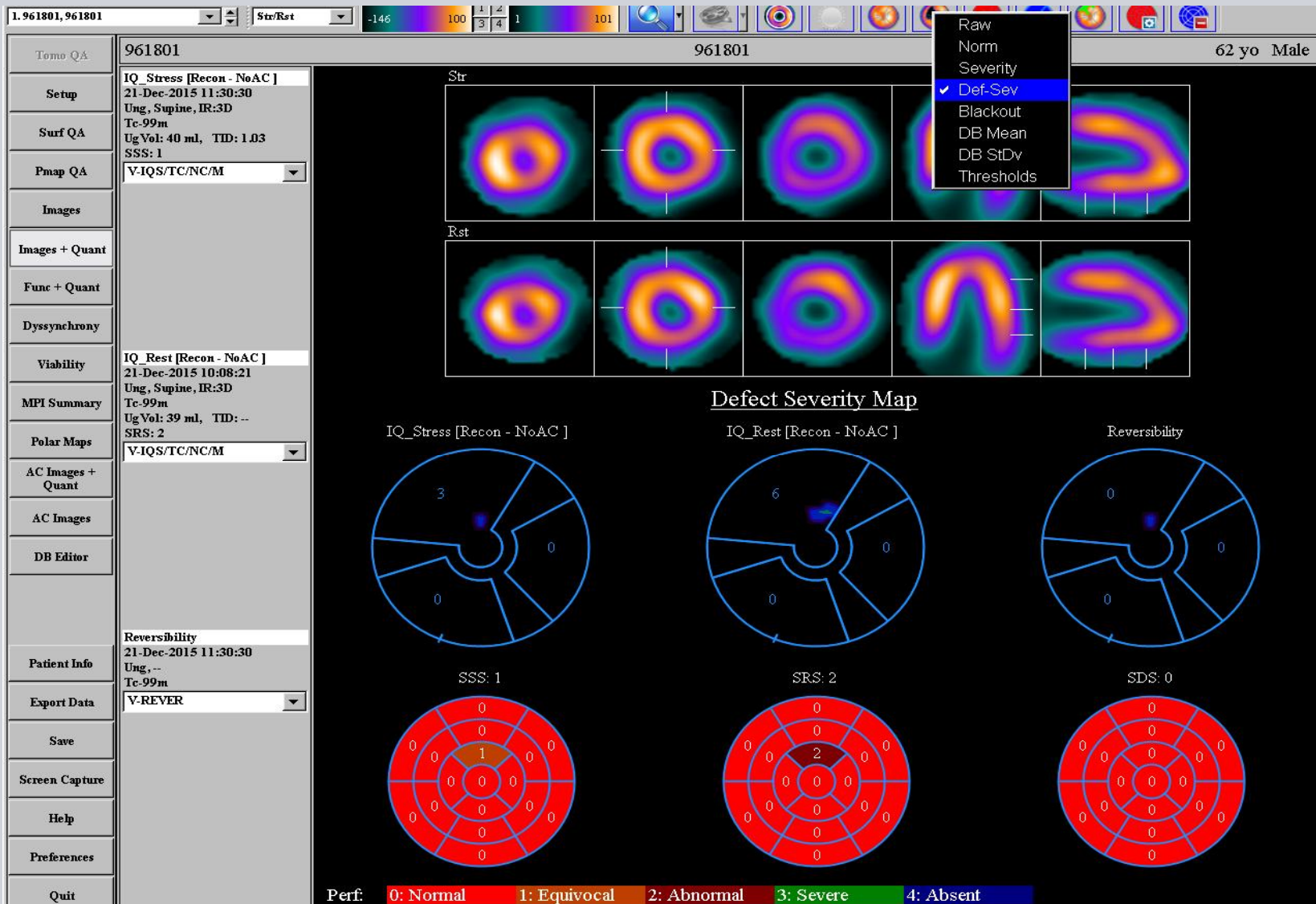


s reserved.



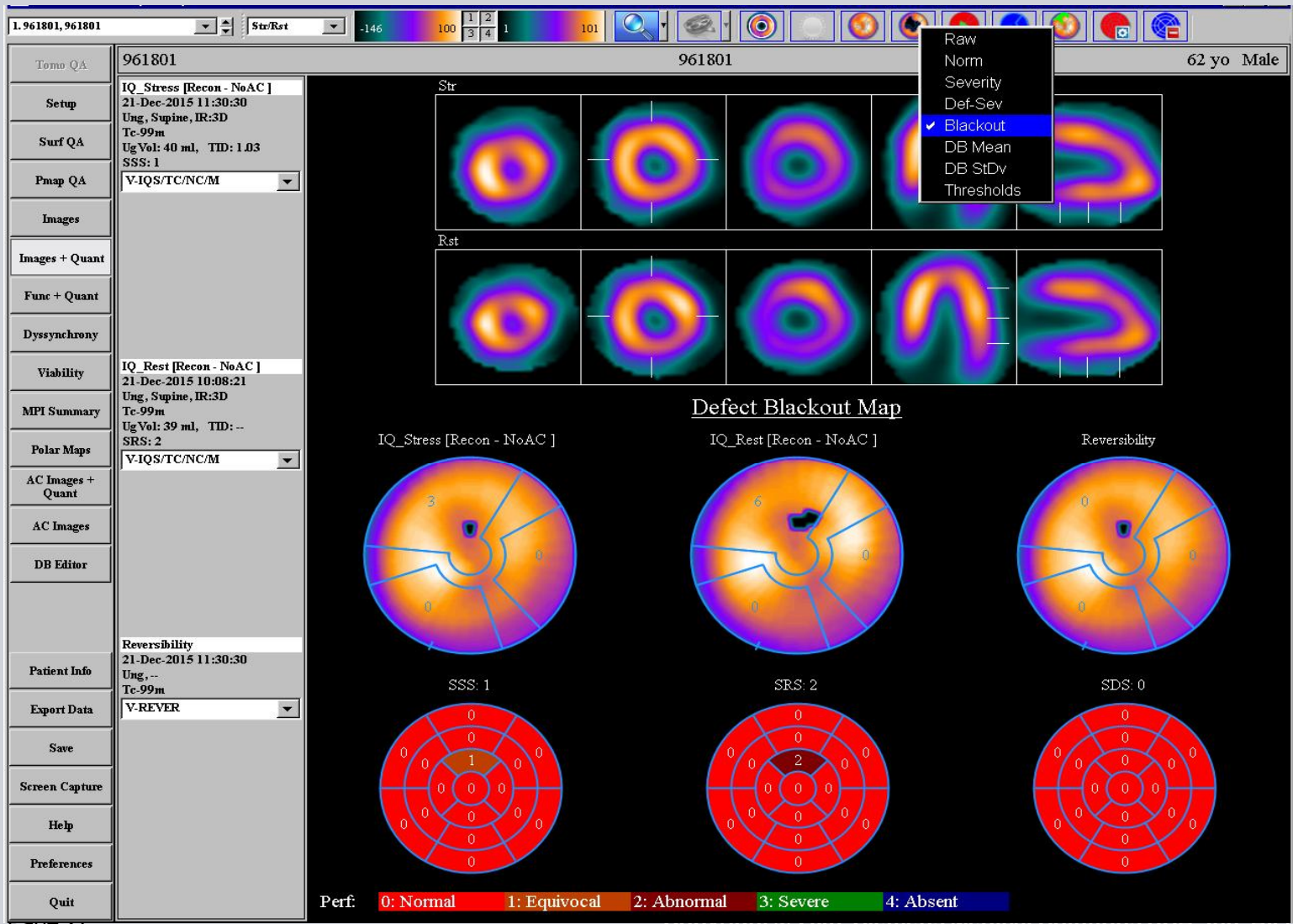
# Def-Sev:

Displays all defect pixels that fall below the defect threshold in units of StDv below the normal mean

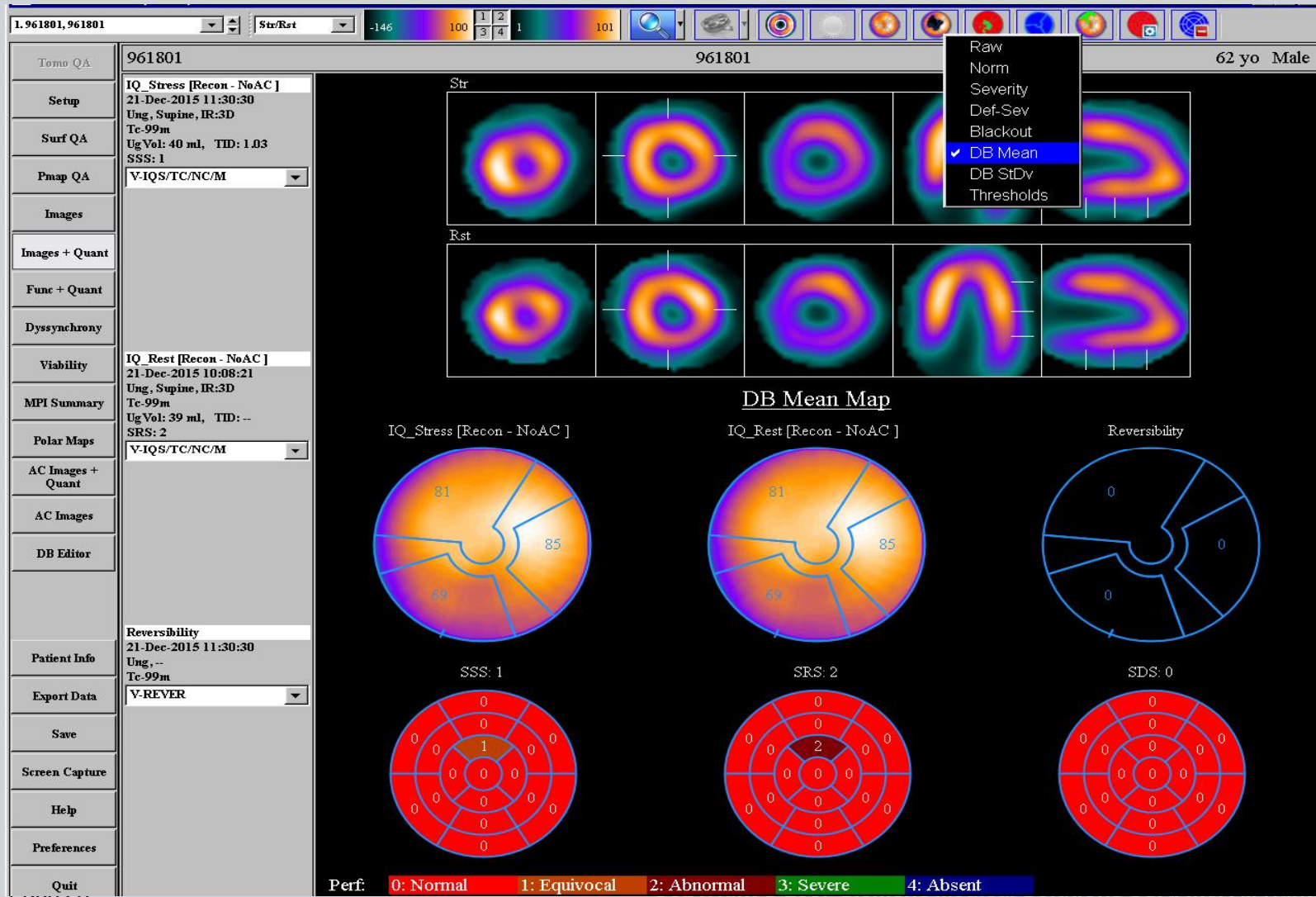


# Blackout:

Displays all defect pixels that fall below the defect threshold with a zero value



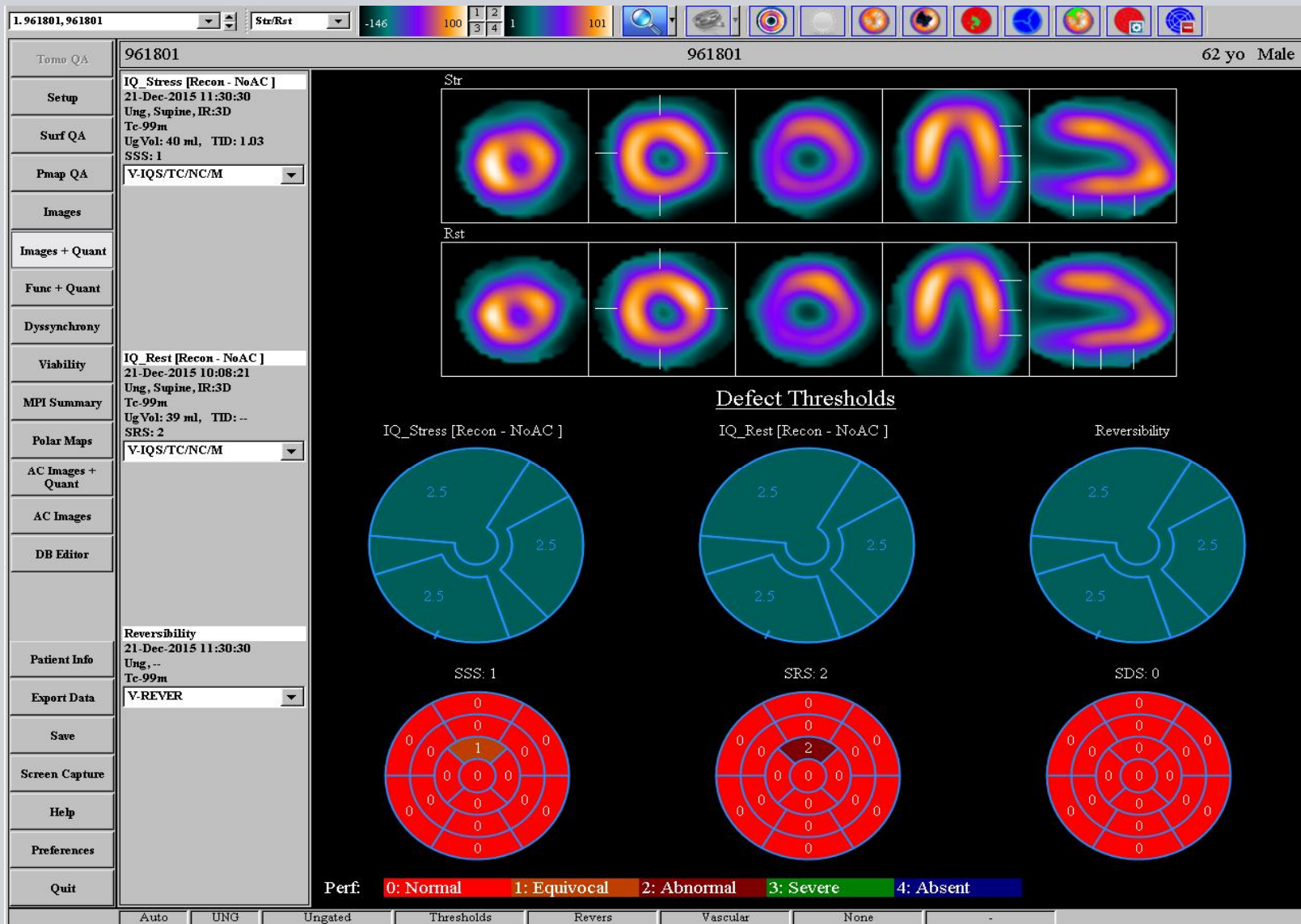
# DB Mean : Displays normal database mean map for applied Normals database



reserved.



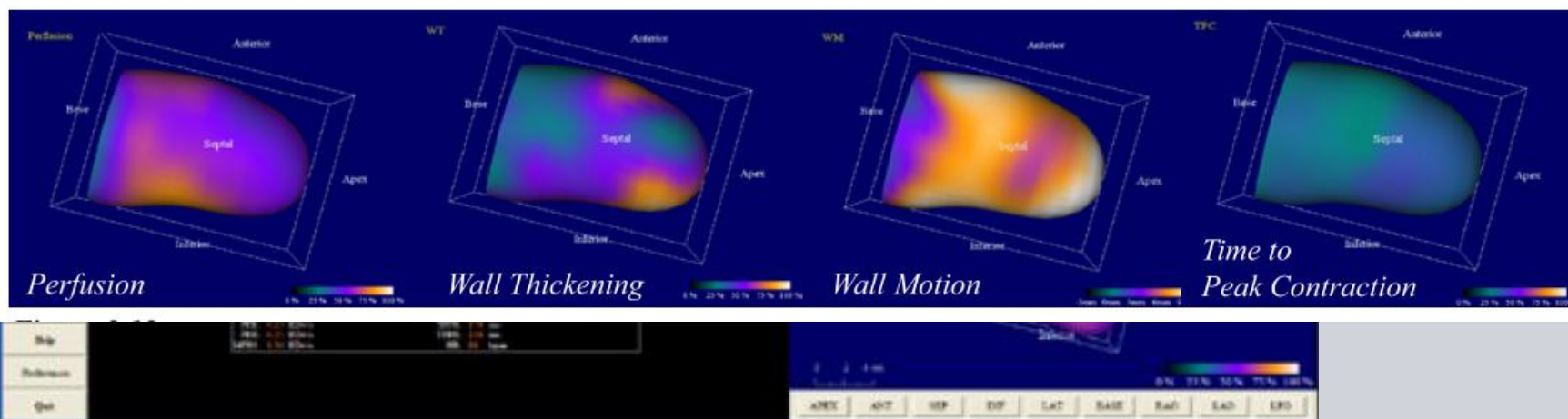
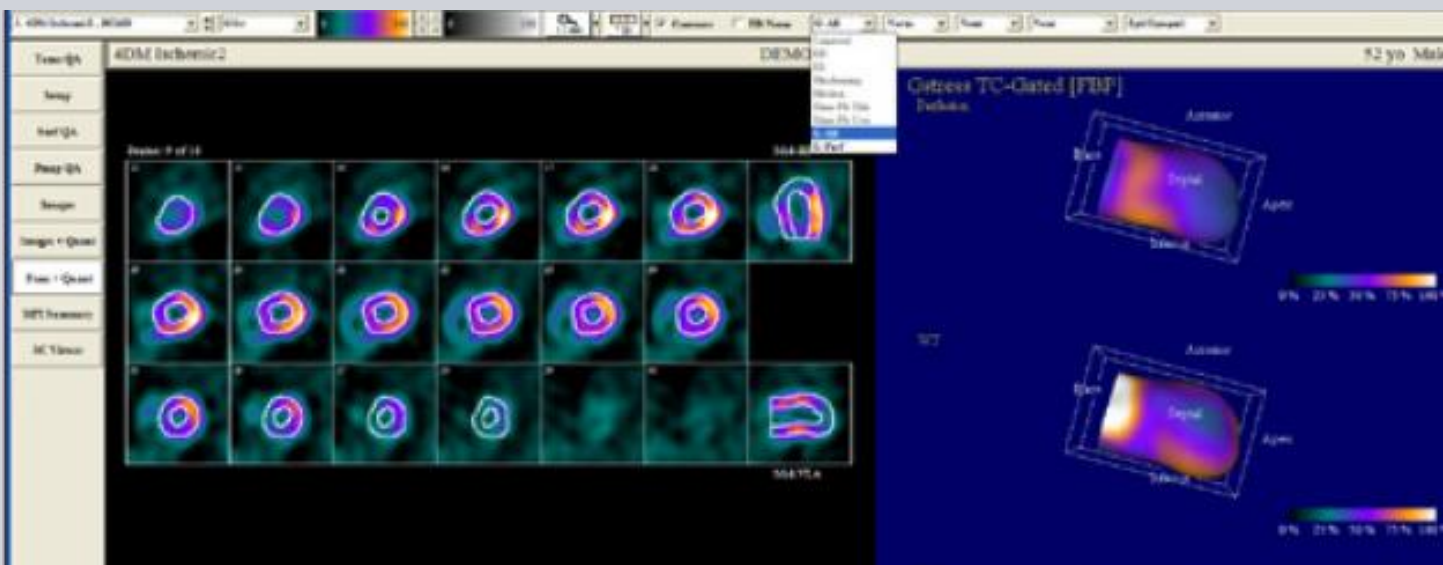
# Thresholds: Displays the number of standard deviations used to define the defect threshold



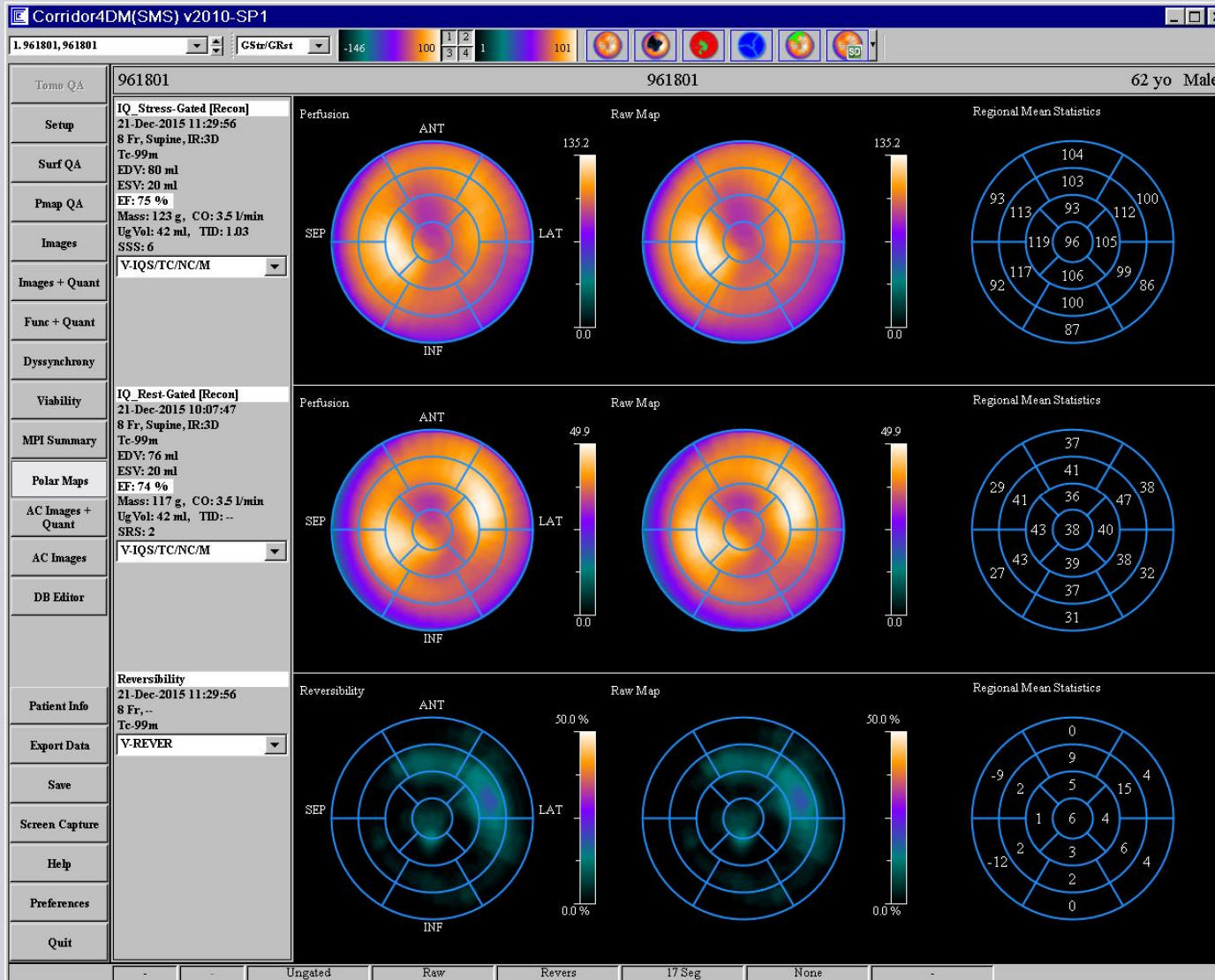
reserved.



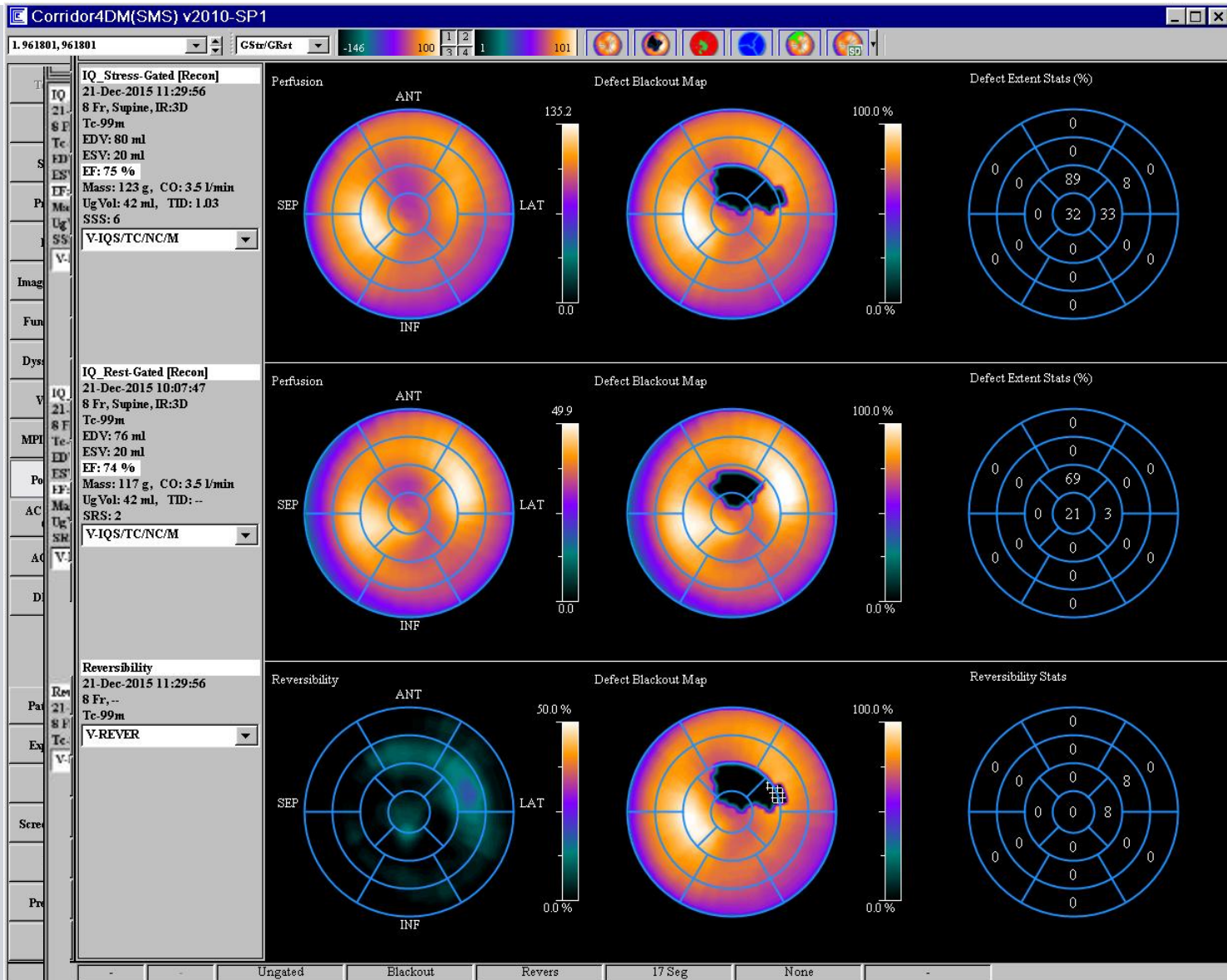
# Func+Quant Page



# Polar map Page

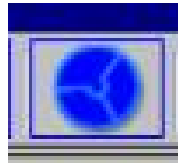


# Polar map Page



c. All rights reserved.

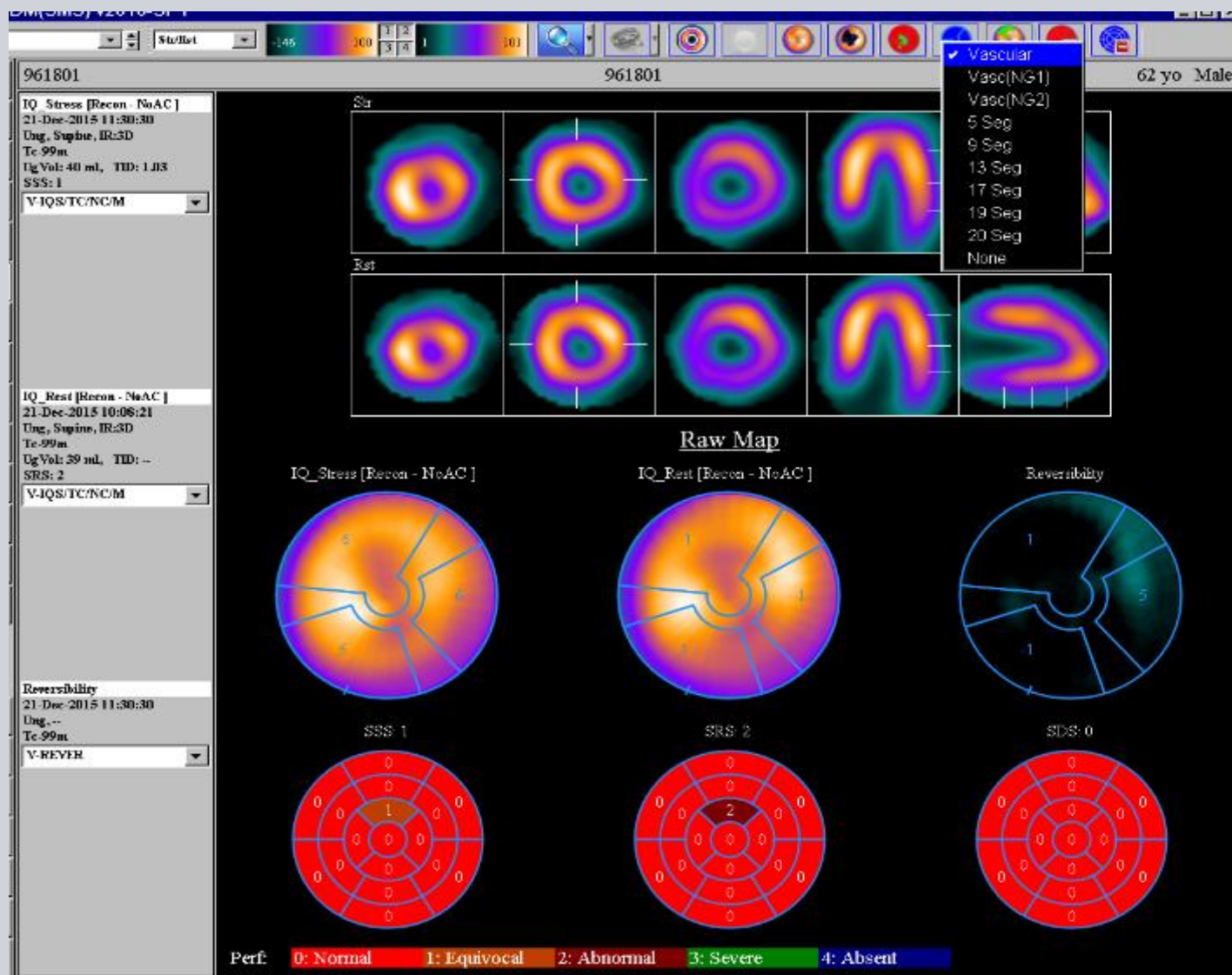
## Segmental Menu



- **Segmental Overlay:** This drop-down menu changes the overlay used to calculate regional statistics for the polar map in the DB-Comparison panel. The available options are:
  - **Vascular:** LAD, LCx, and RCA vascular territories (4DM default).
  - **Vasc(NG1):** **Vascular** overlay with no gaps between territories.
  - **Vasc(NG2):** A second variation of the **Vascular** overlay with no gaps between territories.
  - **5 Seg:** Overlay of the four Myocardial Walls (ANT, LAT, INF, SEP) and the apical segment.
  - **9 Seg**
  - **13 Seg**
  - **17 Seg**
  - **19 Seg**
  - **20 Seg**
  - **Bar Plot:** Available on the **Polar Maps** screen only
  - **Circ Plot:** Available on the **Polar Maps** screen only
  - **None:** No overlay or statistics are displayed

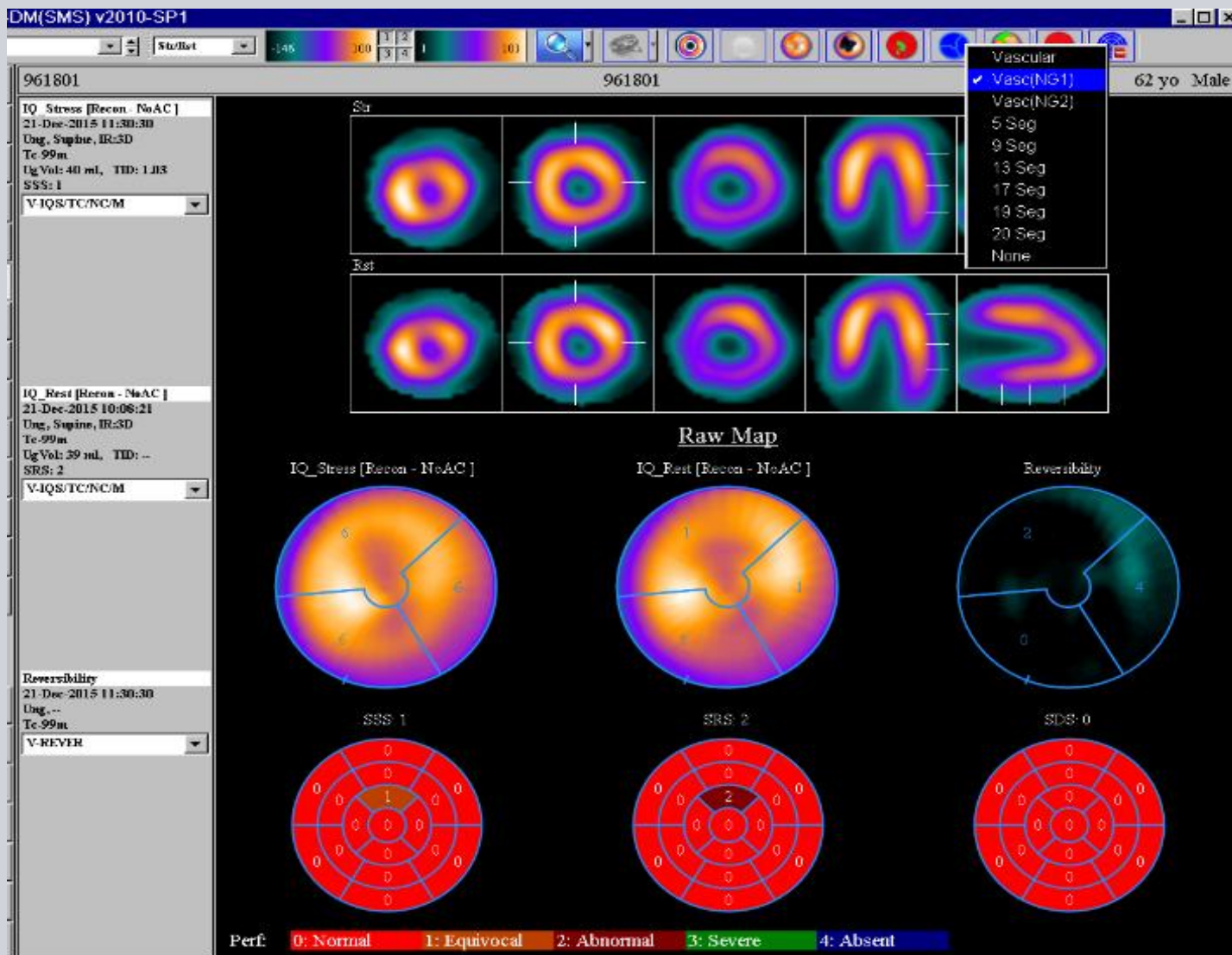


# Segmental

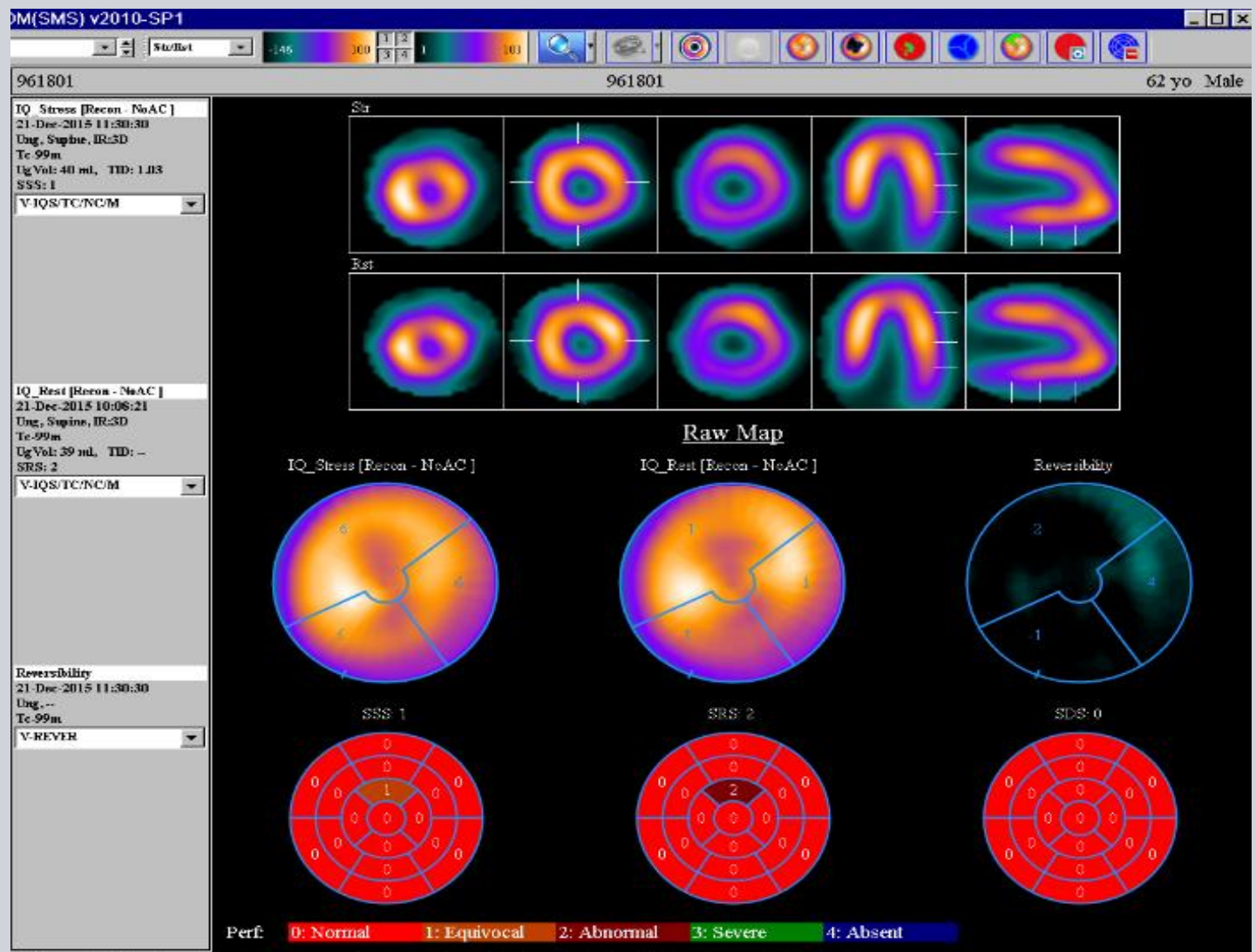


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# Vascular(NG1)

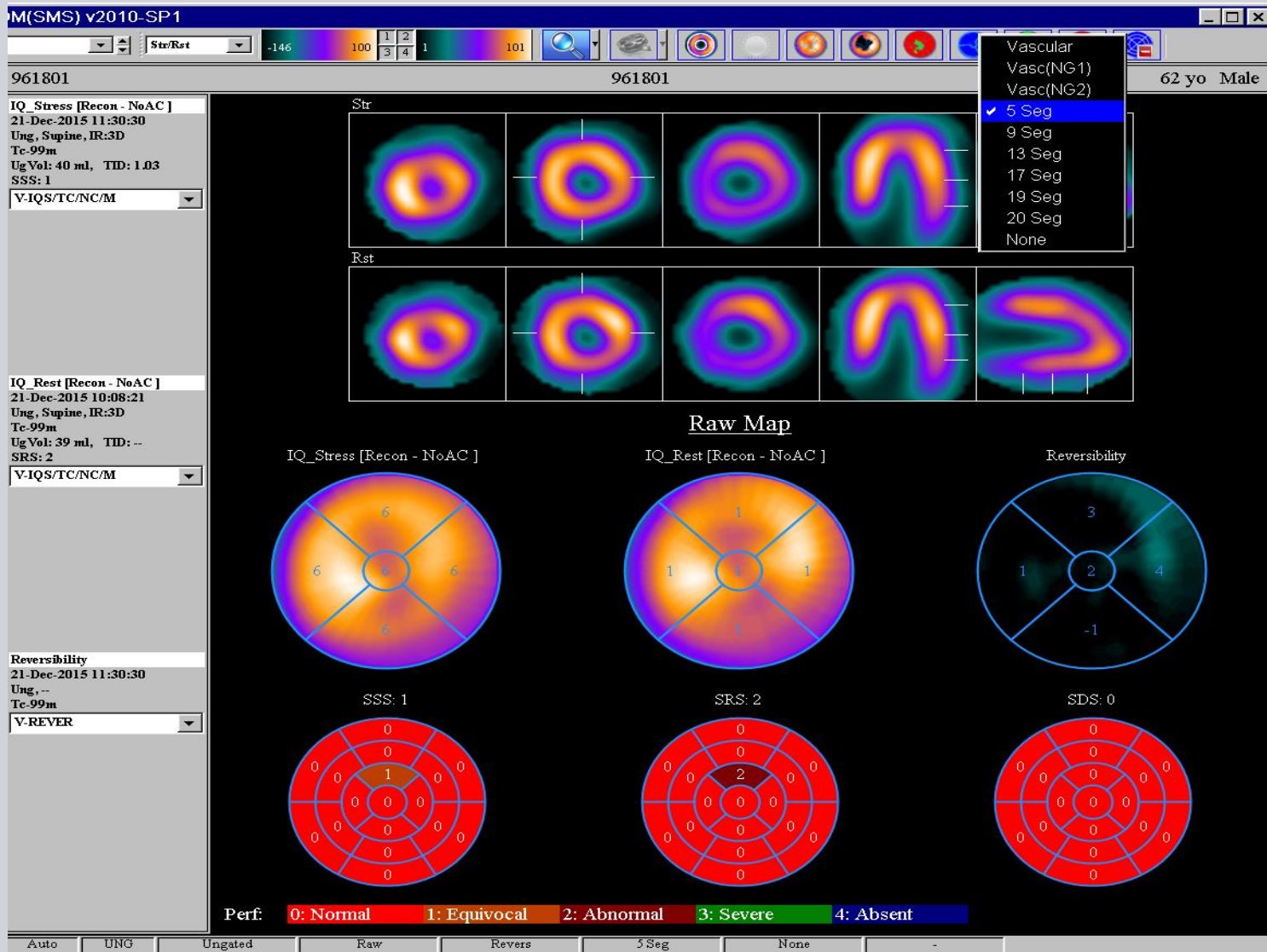


# Vascular(NG2)

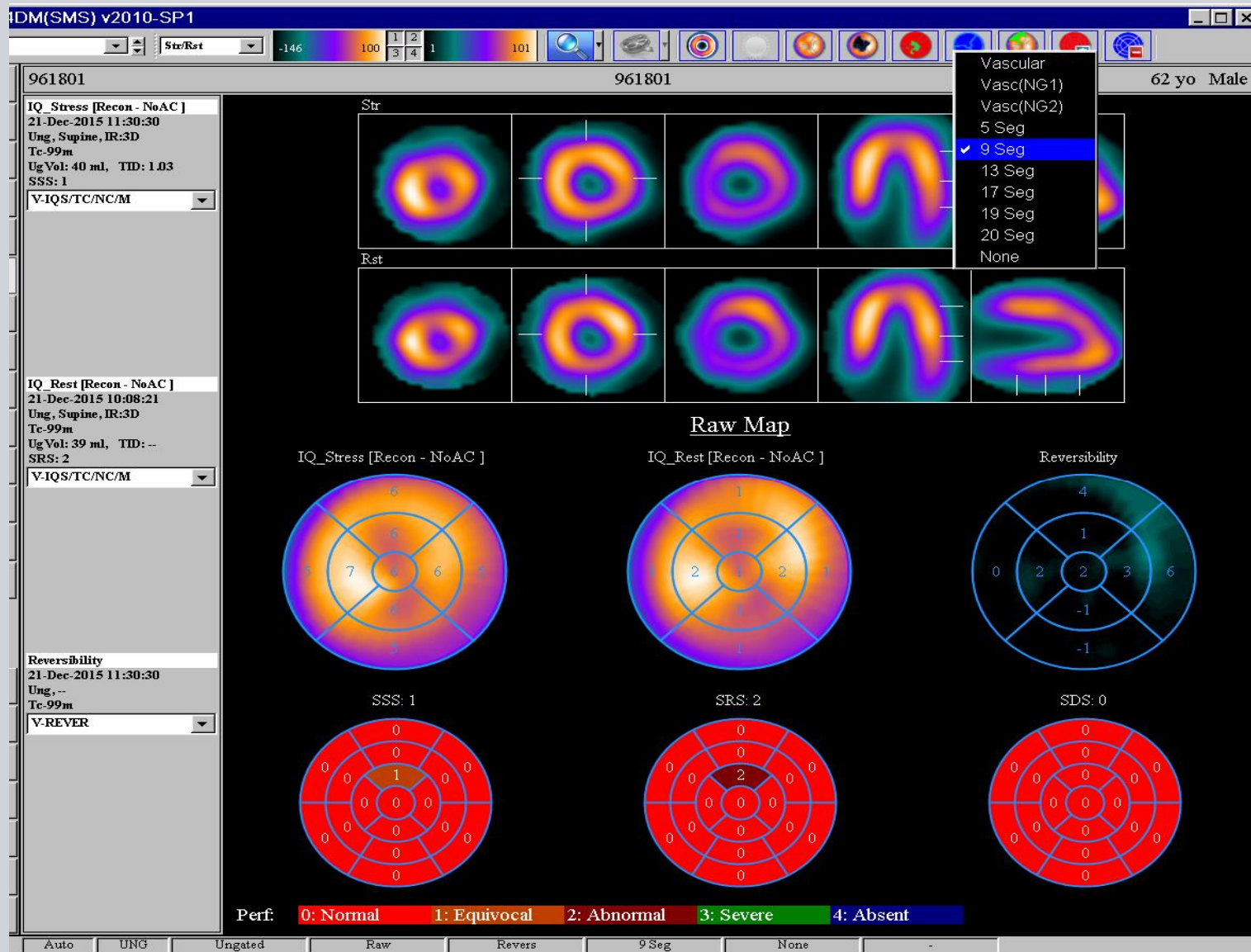




# 5 Seg

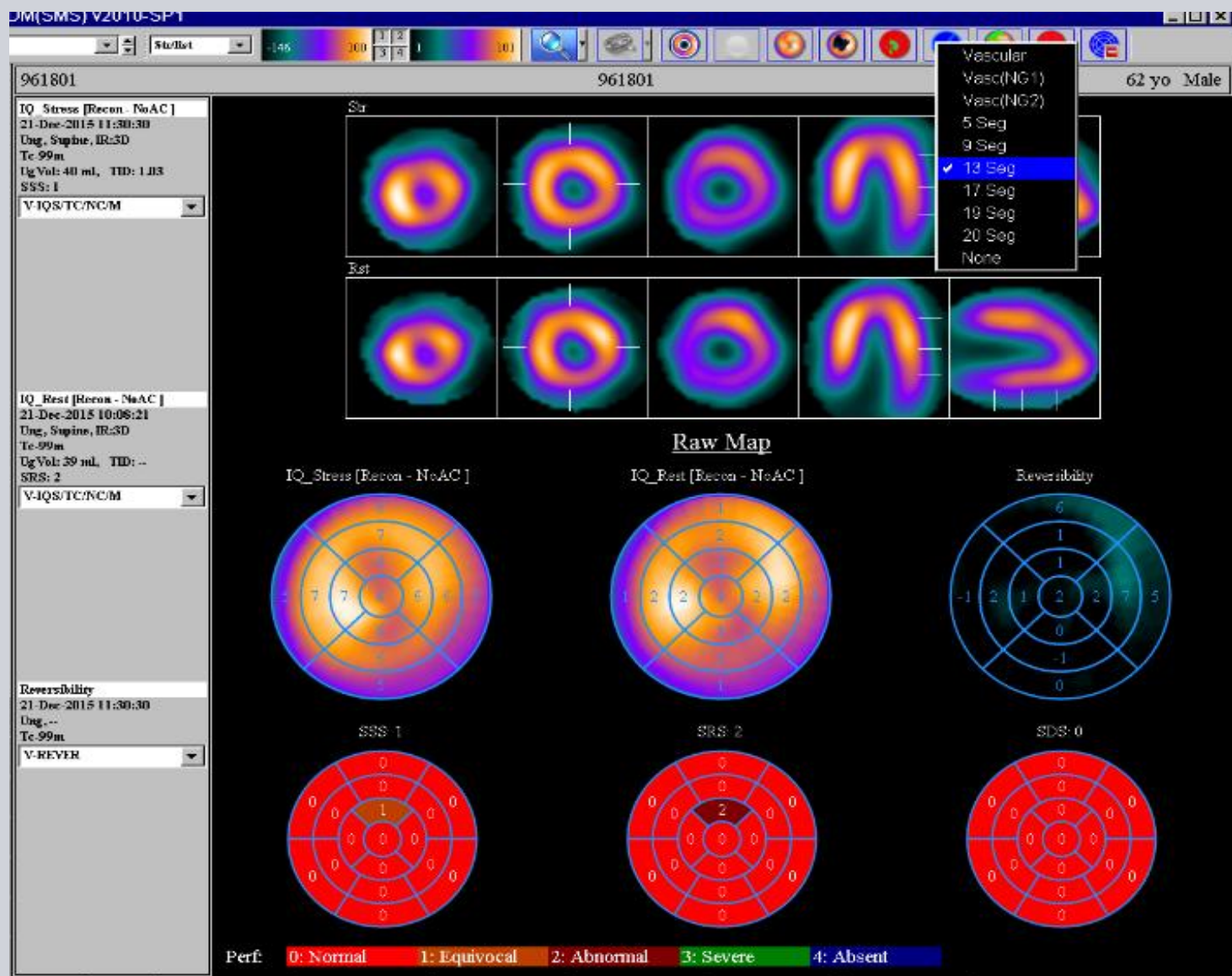


# 9 Seg



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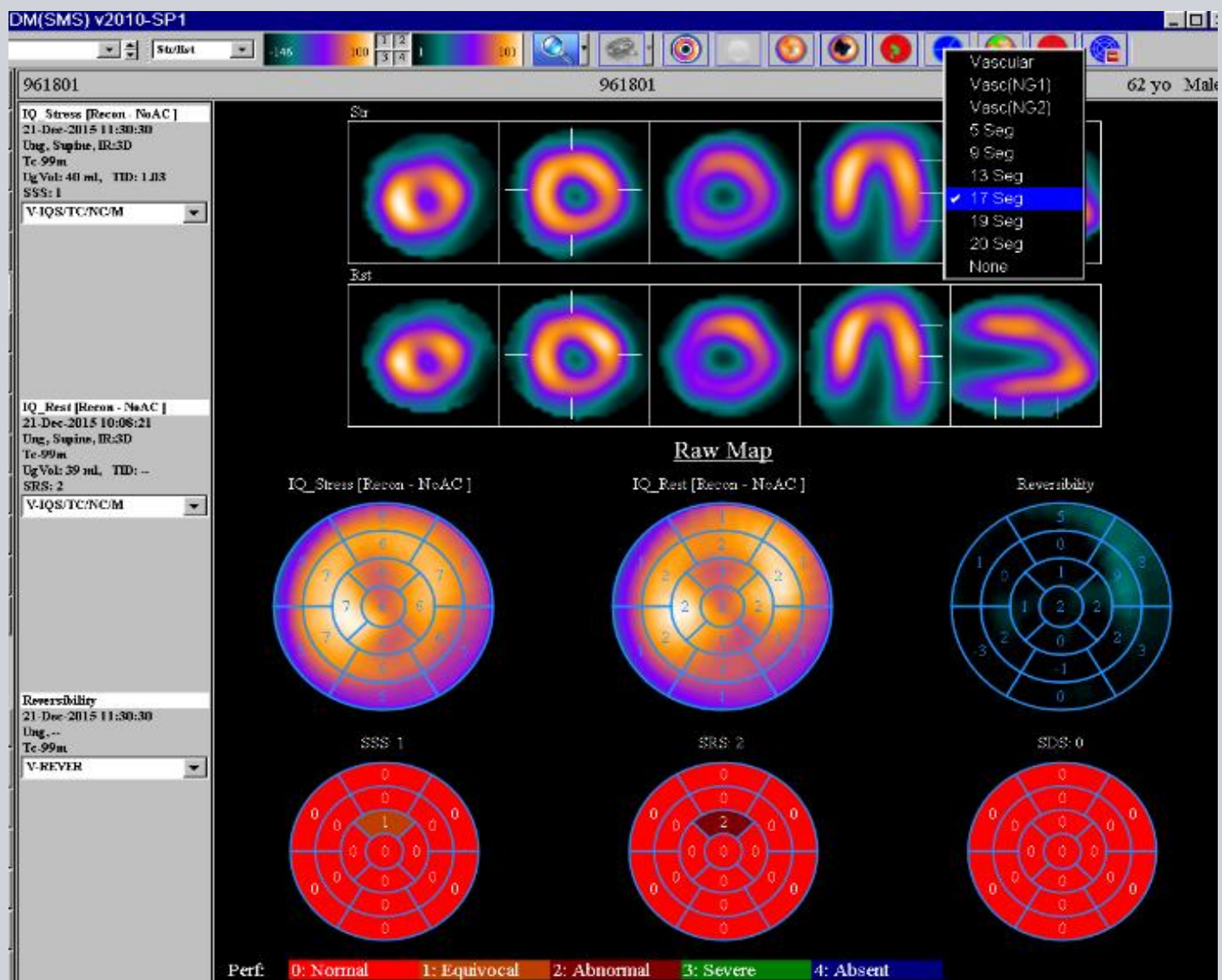
# 13 Seg



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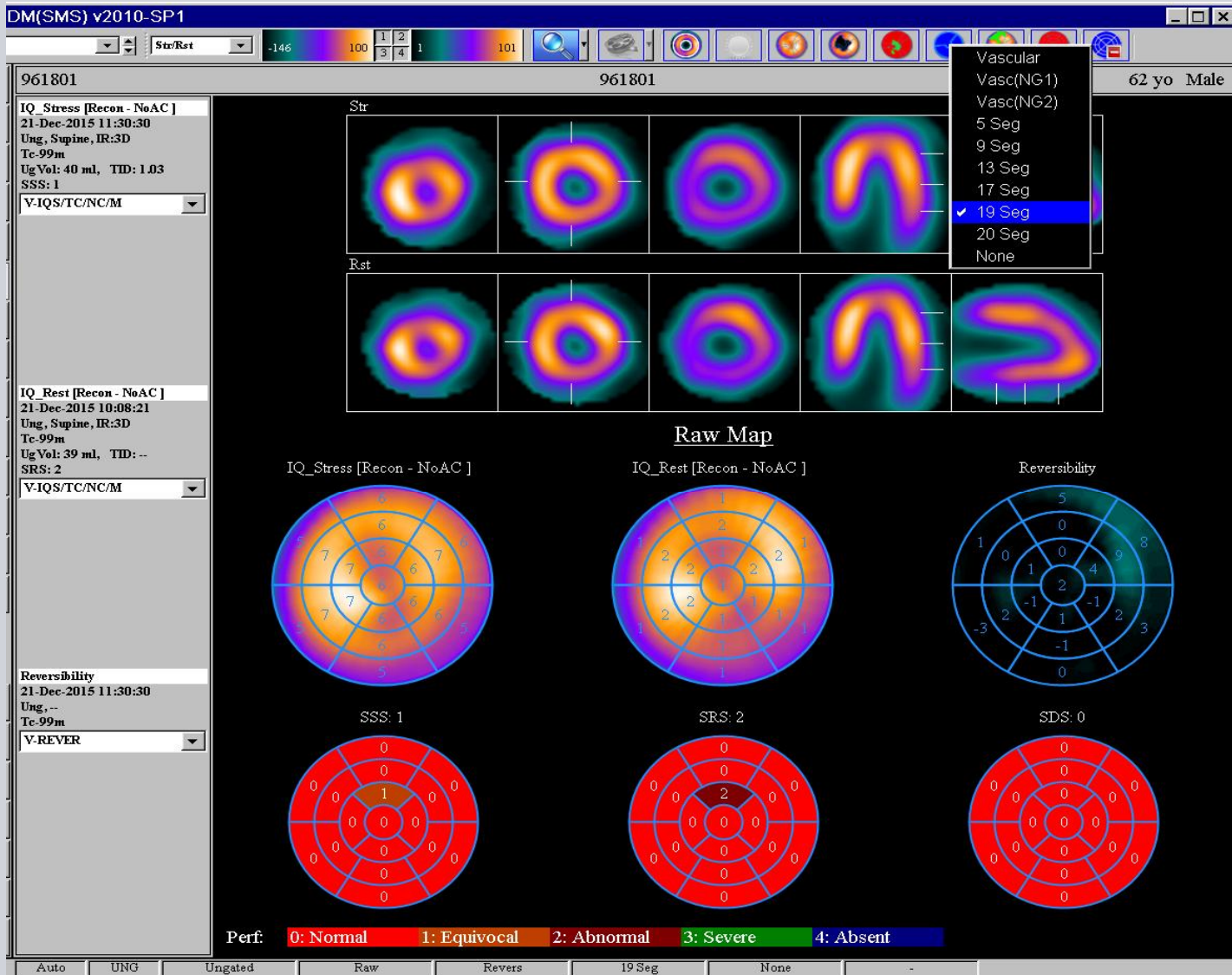


# 17 Seg



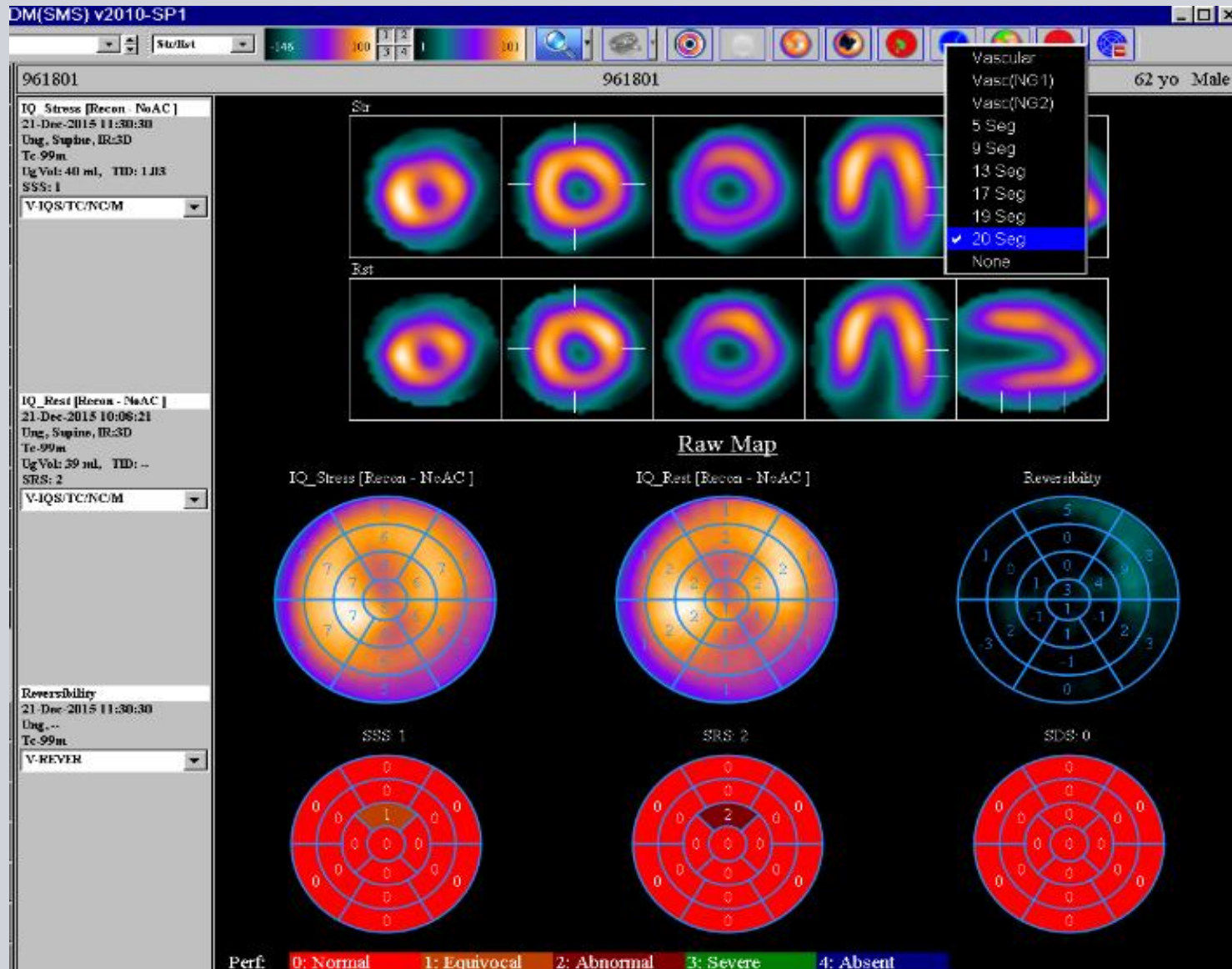
Inc. All rights reserved.

# 19 Seg

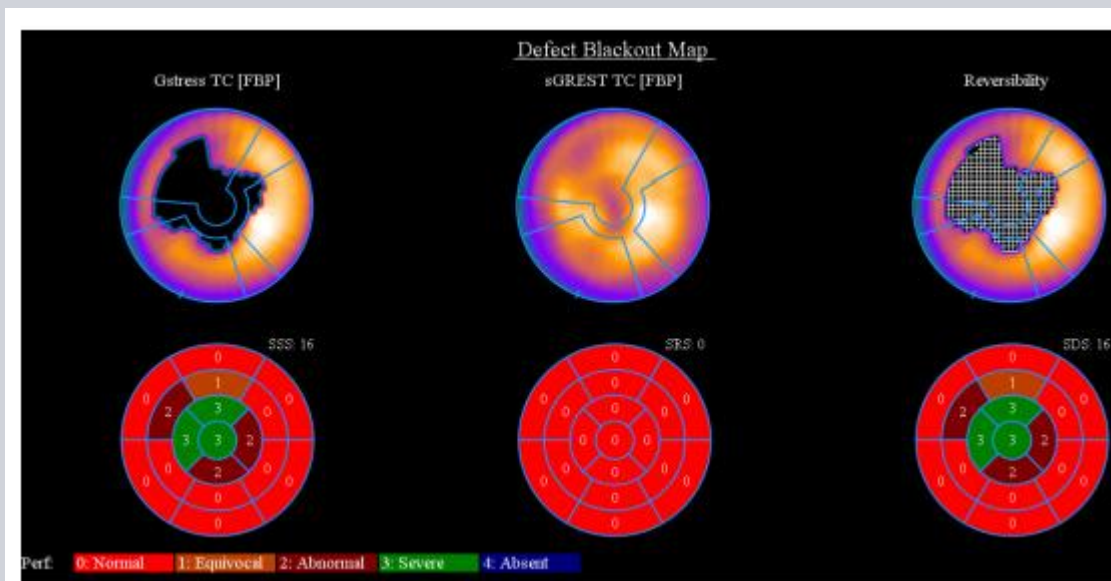




# 20 Seg



# Scores



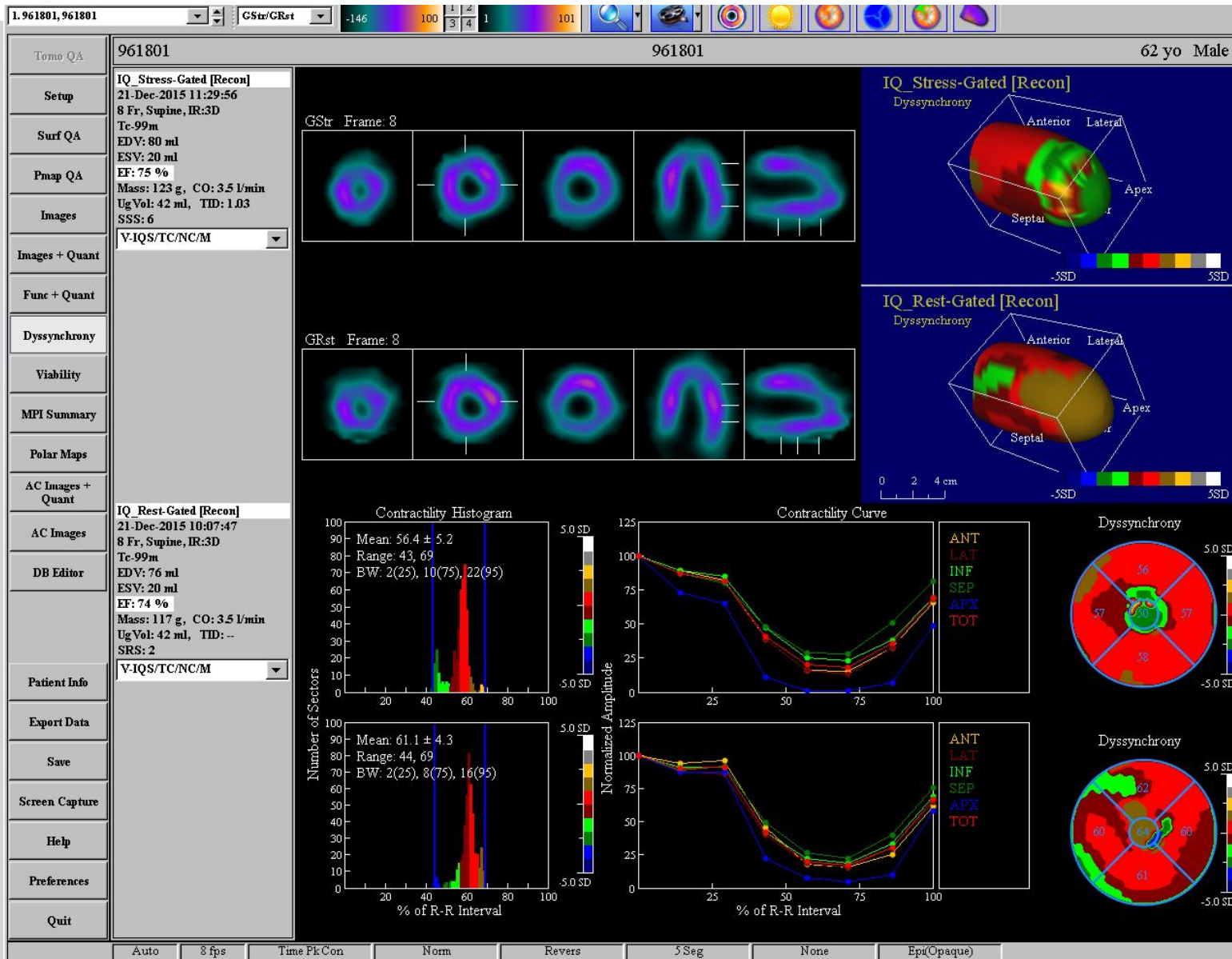
Score	Perfusion	Thickening	Motion
0	Normal	Normal	Normal
1	Equivocal defect	Equivocal	Equivocal
2	Abnormal	Abnormal	Hypokinetic
3	Severe defect	None	Akinetic
4	Absent Uptake		Dyskinetic

## LV Function Normal Range

**Table A.2. Normal LV Function Values for 8 Frame SPECT Studies**

	4D-MSPECT		
	Male	Female	
<b>EF</b>	59±6	68±6	
<b>EDv</b>	123±30	80±19	
<b>EDv/BSA</b>	61±15	46±10	
<b>ESv</b>	51±20	26±9	
<b>ESv/BSA</b>	26±10	15±5	
<b>Mass</b>	155±21	122±16	
<b>Mass/BSA</b>	78±10	70±8	

# Dyssynchrony Page



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# Databases

**Corridor4DM Preferences (Default Configuration)**

User: Utility

User Specific Settings:

- Screen Layout
- Colorbars
- Image Display
- Dataset Matching Strings
- Algorithms
- Normal Databases**
- Polar Map Defects Thresholds
- Segmental Scoring Thresholds

Global Settings:

- Clean Up Schedule

IN VIA Database Directory: C:\soft\inspect\bases\  
 Site Database Directory: C:\soft\inspect\local\

Database Filename	Protocol	Radlpharmaceutical	Gender	Gating	Corrections	Recon Arc	Status
V-C-Clear/TC/AC3D/F	Any	Tc-99m	F	N	IR:3D:AC	180 deg	Active
V-C-Clear/TC/AC3D/M	Any	Tc-99m	M	N	IR:3D:AC	180 deg	Active
V-CCAM/TC/NC/F	Any	Tc-99m	F	Y	FBP	180 deg	Active
V-CCAM/TC/NC/M	Any	Tc-99m	M	Y	FBP	180 deg	Active
V-CCAM/TL/NC/F	Any	Tl-201 Chloride	F	N	FBP	180 deg	Active
V-CCAM/TL/NC/M	Any	Tl-201 Chloride	M	N	FBP	180 deg	Active
V-DIFF12	DIFF12	Any	A	Y	Any	180 deg	Active
V-DIFF21	DIFF21	Any	A	Y	Any	180 deg	Active
V-FDG Viability	FDG Viability	Any	A	Y	Any	180 deg	Active
V-FDG U75,10	Any	F-18 FDG	B	Y	Any	180 deg	Active
V-Flash3D/NC/F	Any	Tc-99m	F	N	IR:3D	180 deg	Active
V-Flash3D/NC/M	Any	Tc-99m	M	N	IR:3D	180 deg	Active
V-PSRD/TC/AC	Any	Tc-99m	B	N	IR:AC	180 deg	Active
V-PSRD/TL/AC	Any	Tl-201 Chloride	B	N	IR:AC	180 deg	Active
V-RBB2/F/CTAC	Any	Rb-82	F	N	SC:CTAC	180 deg	Active
V-RBB2/M/CTAC	Any	Rb-82	M	N	SC:CTAC	180 deg	Active
V-REVER	Reversibility	Any	A	Y	Any	180 deg	Active
V-SRD/TL/NC/F	Any	Tl-201 Chloride	F	N	FBP	180 deg	Active
V-SRD/TL/NC/M	Any	Tl-201 Chloride	M	N	FBP	180 deg	Active
V-Symbia/TC/CTAC,SC,RC	Any	Tc-99m	B	N	IR:3D;SC:CT...	180 deg	Active
V2-GSRD/TC/NC/F	Any	Tc-99m	F	Y	FBP	180 deg	Active
V2-GSRD/TC/NC/M	Any	Tc-99m	M	Y	FBP	180 deg	Active

Buttons: Cancel, Save

Footer: Inlt DB List, Make Active, Make Inactive, Select All, Select None

Taskbar: Start, CapGM - MI Apps, Cardiac 2 16 Fr..., Corridor4DM{..., 6:12 AM



## Tc\_NAC Database

Database Name	Description	Protocol Support
V2-GSRD/TC/NC/F	<p>Database for Tc-99m Sestamibi or Tetrofosmin specific to uncorrected (NC) female patients.</p> <p>Reconstruction algorithm is specific to filtered backprojection (FBP).</p> <p>This database has perfusion and functional information; thus, it can be used for gated and ungated studies.</p>	<ul style="list-style-type: none"> <li>• Stress study in a dual isotope protocol.</li> <li>• Stress or rest studies in a 2-day Tc-99m labeled radiotracer protocol.</li> <li>• Stress or rest study in a 1-day rest/stress Tc-99m labeled radiotracer protocol.</li> <li>• Stress or rest study in a 1-day stress/rest Tc-99m labeled radiotracer protocol.</li> </ul> <p style="text-align: center;"><b>WARNING</b></p> <p style="text-align: center;">This database should only be used for uncorrected <b>FEMALE</b> studies reconstructed with FBP from data acquired from RAO-to-LPO.</p>
V2-GSRD/TC/NC/M	<p>Database for Tc-99m Sestamibi or Tetrofosmin tracers specific to uncorrected (NC) male patients.</p> <p>Reconstruction algorithm is specific to filtered backprojection (FBP).</p> <p>This database has perfusion and functional information; thus, it can be used for gated and ungated studies.</p>	<ul style="list-style-type: none"> <li>• Stress study in a dual isotope protocol.</li> <li>• Stress or rest studies in a 2-day Tc-99m labeled radiotracer protocol.</li> <li>• Stress or rest study in a 1-day rest/stress Tc-99m labeled radiotracer protocol.</li> <li>• Stress or rest study in a 1-day stress/rest Tc-99m labeled radiotracer protocol.</li> </ul> <p style="text-align: center;"><b>WARNING</b></p> <p style="text-align: center;">This database should only be used for uncorrected <b>MALE</b> studies reconstructed with FBP from data acquired from RAO-to-LPO.</p>

## TL\_NAC database

<p>V-SRD/TL/NC/F</p>	<p>TI-201 database specific to uncorrected (NC) female patients.</p> <p>Reconstruction algorithm is specific to filtered backprojection (FBP).</p> <p>This database can only be used for analysis of the perfusion data.</p>	<ul style="list-style-type: none"> <li>• Rest study in a dual isotope protocol.</li> <li>• Stress, rest, delay or redistribution study in a TI-201 only protocol.</li> </ul> <p style="text-align: center;"><b>WARNING</b></p> <p style="text-align: center;">This database should only be used for uncorrected <b>FEMALE</b> studies reconstructed with FBP from data acquired from RAO-to-LPO.</p>
<p>V-SRD/TL/NC/M</p>	<p>TI-201 database specific to uncorrected (NC) male patients.</p> <p>Reconstruction algorithm is specific to filtered backprojection (FBP).</p> <p>This database can only be used for analysis of the perfusion data.</p>	<ul style="list-style-type: none"> <li>• Rest study in a dual isotope protocol.</li> <li>• Stress, rest, delay or redistribution study in a TI-201 only protocol.</li> </ul> <p style="text-align: center;"><b>WARNING</b></p> <p style="text-align: center;">This database should only be used for uncorrected <b>MALE</b> studies reconstructed with FBP from data acquired from RAO-to-LPO.</p>

## AC Database

<p>V-PSRD/TC/AC</p>	<p>Database for Tc-99m Sestamibi or Tetrofosmin specific to Siemens PROFILE attenuation corrected (AC) studies.</p> <p>AC Reconstruction algorithm is specific to the Iter-W algorithm.</p> <p>This database can only be used for analysis of the perfusion data.</p>	<ul style="list-style-type: none"> <li>• Stress study in a dual isotope protocol.</li> <li>• Stress or rest studies in a 2-day Tc-99m labeled radiotracer protocol.</li> <li>• Stress or rest study in a 1-day rest/stress Tc-99m labeled radiotracer protocol.</li> <li>• Stress or rest study in a 1-day stress/rest Tc-99m labeled radiotracer protocol.</li> </ul> <p style="text-align: center;"><b>WARNING</b></p> <p style="text-align: center;">In addition to the above, this database should only be used for <b>PROFILE</b> attenuation corrected images reconstructed with the Iter-W algorithm.</p>
<p>V-PSRD/TL/AC</p>	<p>Tl-201 database specific to Siemens PROFILE attenuation corrected (AC) studies.</p> <p>AC Reconstruction algorithm is specific to the Iter-W algorithm.</p> <p>This database can only be used for analysis of the perfusion data.</p>	<ul style="list-style-type: none"> <li>• Rest study in a dual isotope protocol.</li> <li>• Stress, rest, delay or redistribution study in a Tl-201 only protocol.</li> </ul> <p style="text-align: center;"><b>WARNING</b></p> <p style="text-align: center;">In addition to the above, this database should only be used for <b>PROFILE</b> attenuation corrected images reconstructed with the Iter-W algorithm.</p>
<p>V-Symbia/TC/ CTAC,SC,RC</p>	<p>Database for Tc-99m Sestamibi or Tetrofosmin tracers specific to Siemens Symbia CT based Attenuation+Scatter+Flash3D corrected studies.</p> <p>This database can only be used for analysis of the perfusion data.</p>	<ul style="list-style-type: none"> <li>• Stress study in a dual isotope protocol.</li> <li>• Stress or rest studies in a 2-day Tc-99m labeled radiotracer protocol.</li> <li>• Stress or rest study in a 1-day rest/stress Tc-99m labeled radiotracer protocol.</li> <li>• Stress or rest study in a 1-day stress/rest Tc-99m labeled radiotracer protocol.</li> </ul> <p style="text-align: center;"><b>WARNING</b></p> <p style="text-align: center;">In addition to the above, this database should only be used for Symbia studies which have reconstructed incorporating CTAC, scatter, and Flash3D corrections.</p>

# View Normal database

4DM Ischemic2 DEMO 52 yo Male

Database: V2-GSRD/TC/NC/M Map: Ungated Perfusion

1

Mean Map Data			Stdv Map Data		
ANT-P	73.9 ± 8.1	(50.8-88.7)	ANT-P	6.4 ± 0.6	(3.7-7.7)
LAT-P	81.5 ± 8.8	(61.9-94.2)	LAT-P	5.9 ± 0.6	(4.6-7)
INF-P	62.6 ± 8.7	(42.2-78.5)	INF-P	5.8 ± 0.7	(4.5-7.4)
SEP-P	62.8 ± 15.1	(37.4-81.6)	SEP-P	7.5 ± 0.9	(5.8-8.9)
ANT-D	83.3 ± 2.9	(78.1-88.2)	ANT-D	6.5 ± 0.3	(5.7-7.3)
LAT-D	92.1 ± 4.3	(85.2-99.8)	LAT-D	5.9 ± 1.1	(3.6-7.2)
INF-D	78.0 ± 3.1	(72.7-85.3)	INF-D	6.6 ± 0.9	(5.4-8.3)
SEP-D	87.0 ± 3.0	(79.8-92.5)	SEP-D	6.5 ± 0.4	(5.7-7.2)
APX	81.4 ± 2.3	(76.8-84.8)	APX	6.9 ± 1.0	(3.4-9.9)
Total	77.9 ± 12.5	(57.4-99.8)	Total	6.5 ± 1.0	(3.6-9.9)

2

3

4

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Map (1) - H15H1059



- End ~

- *Thanks for your Attention*