SPIROMICS Protocol for Multicenter Quantitative CT to Phenotype the Lungs

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ONLINE DATA SUPPLEMENT

On line supplement

Procedural Verification Software : PVS

The study coordinator logs a subject into the PVS system and enters the study ID, scan date, and BMI. PVS then selects [one of] the site's approved CT scanner(s) and provides an appropriate scan protocol including the selected scanner, mA or mAs (based on BMI), kV, pitch, rotation speed, kernel, slice thickness, and spacing. Most importantly, if the subject is on a return visit, the system will find the subject's previous scanner and scan parameters; and these parameters, including the DFOV, will be used for the follow-up scan, critical for high quality longitudinal QCT results. In SPIROMICS, the baseline and follow-up (visit 1 and visit 2) scans are one year apart.

PVS parameters are displayed in the user interface and can be printed for hand-off to the radiology technologist. The radiology technologist or coordinator fills out the form and the technologist carries out an initial visual quality check of the scan quality, which includes assessment of positioning and whether a breath hold was achieved and maintained at the specified lung volume. Once the scan is completed the coordinator enters the information into PVS from the printed form. The scan technologist is identified for monitoring purposes. The coordinator must also select their own name as overseeing the visit. At this stage the scan is complete. Incorrect entries trigger a PVS alert as the coordinator is typing by highlighting the issue in red (supplemental **Figure 2b-S**). The coordinator, upon alert, either fixes the issue. If the issue cannot be fixed, the radiology center will designate the scan as a protocol exception classified as either a deviation or quality control (QC) error. Deviations refer to scanning errors associated with improper application of the imaging protocol leading to either an under or over radiation exposure relative to that prescribed by the MOP. QC errors are related to quality of the image data, unrelated to radiation dose. Examples of deviations include incorrect mA or mAs for a given BMI, wrong kV, pitch, rotation speed, or the scan covered more or less than the specified z-axis coverage. Example QC issues include motion artifacts, metal artifacts (rhinestone buttons, bras, etc.), and reconstructing the images with the wrong kernel, slice thickness or slice spacing. Radiation issues are flagged as deviations and reported to the Radiology Center. Reports are sent via PVS to the site same day or next working day

depending upon time of transmission. After PVS reporting is complete, CT image data are transmitted via DISPATCH, discussed below.

DICOM Selection Parser and Transfer Check software: DISPATCH

DISPATCH runs on the transferring site's local computer and uses a web-based application transfer images. The software directly links to the Radiology Center scan database, taking into account the trial protocol, including the number of visits, the type and timing of data collection and the subject identification number. In addition, DISPATCH will de-identify data according to the 18 HIPAA criteria to assure HIPAA compliance upon upload. This will allow all subject identifiers to be automatically removed prior to sending the data to the Radiology Center without removing other required important scan information. DISPATCH allows the user to ensure data was acquired according to the specific CT study protocol and checks for errors prior to data transmission. If scanning was not carried out appropriately, the site is notified immediately at the time of data transfer. This offers two advantages: 1) if the scan was reconstructed incorrectly (wrong kernel or incorrect DFOV) the data can be re-reconstructed if the raw projection data remains on the CT scanner's hard drives; 2) if there are other errors the site can learn from the mistake and avoid propagation to the next subjects CT study.

Table 1-S:
CT-derived Metrics along with their variable names and the lung volume from which they derived. Researchers interested in using SPIROMICS data should read the information in the "Obtaining SPIROMICS data" tab on the study web site at https://www2.cscc.unc.edu/spiromics/.

SPIROMICS CT Density Variables Description	Variable Name	CT Lung Volume
Both lungs: Percentage of low attenuation area below and including -950 Hounsfield units	both_percent_below_950	CT TLC
Both lungs: Percentage of low attenuation area below and including -910 Hounsfield units	both_percent_below_910	CT TLC
Left lower lobe: Percentage of low attenuation area below and including -950 Hounsfield units	left-lower_percent_below_950	CT TLC
Left lower lobe: Percentage of low attenuation area below and including -910 Hounsfield units	left-lower_percent_below_910	CT TLC
Left upper lobe: Percentage of low attenuation area below and including -950 Hounsfield units	left-upper_percent_below_950	CT TLC
Left upper lobe: Percentage of low attenuation area below and including -910 Hounsfield units	left-upper_percent_below_910	CT TLC
Right lower lobe: Percentage of low attenuation area below and including -950 Hounsfield units	right-lower_percent_below_950	CT TLC
Right lower lobe: Percentage of low attenuation area below and including -910 Hounsfield units	right-lower_percent_below_910	CT TLC
Right middle lobe: Percentage of low attenuation area below and including -950 Hounsfield units	right-middle_percent_below_950	CT TLC
Right middle lobe: Percentage of low attenuation area below and including -910 Hounsfield units	right-middle_percent_below_910	CT TLC
Right upper lobe: Percentage of low attenuation area below and including -950 Hounsfield units	right-upper_percent_below_950	CT TLC
Right upper lobe: Percentage of low attenuation area below and including -910 Hounsfield units	right-upper_percent_below_910	CT TLC
Both lungs: Percentage of low attenuation area below and -856 Hounsfield units	both_percent_below_856	CT RV
Left lower third: Percentage of low attenuation area below and -856 Hounsfield units	thirds-left-lower_percent_below_856	CT RV
Left middle third: Percentage of low attenuation area below and -856 Hounsfield units	thirds-left-middle_percent_below_856	CT RV
Left upper third: Percentage of low attenuation area below and -856 Hounsfield units	thirds-left-upper_percent_below_856	CT RV
Right lower third: Percentage of low attenuation area below and -856 Hounsfield units	thirds-right-lower_percent_below_856	CT RV
Right middle third: Percentage of low attenuation	thirds-right-	CT RV

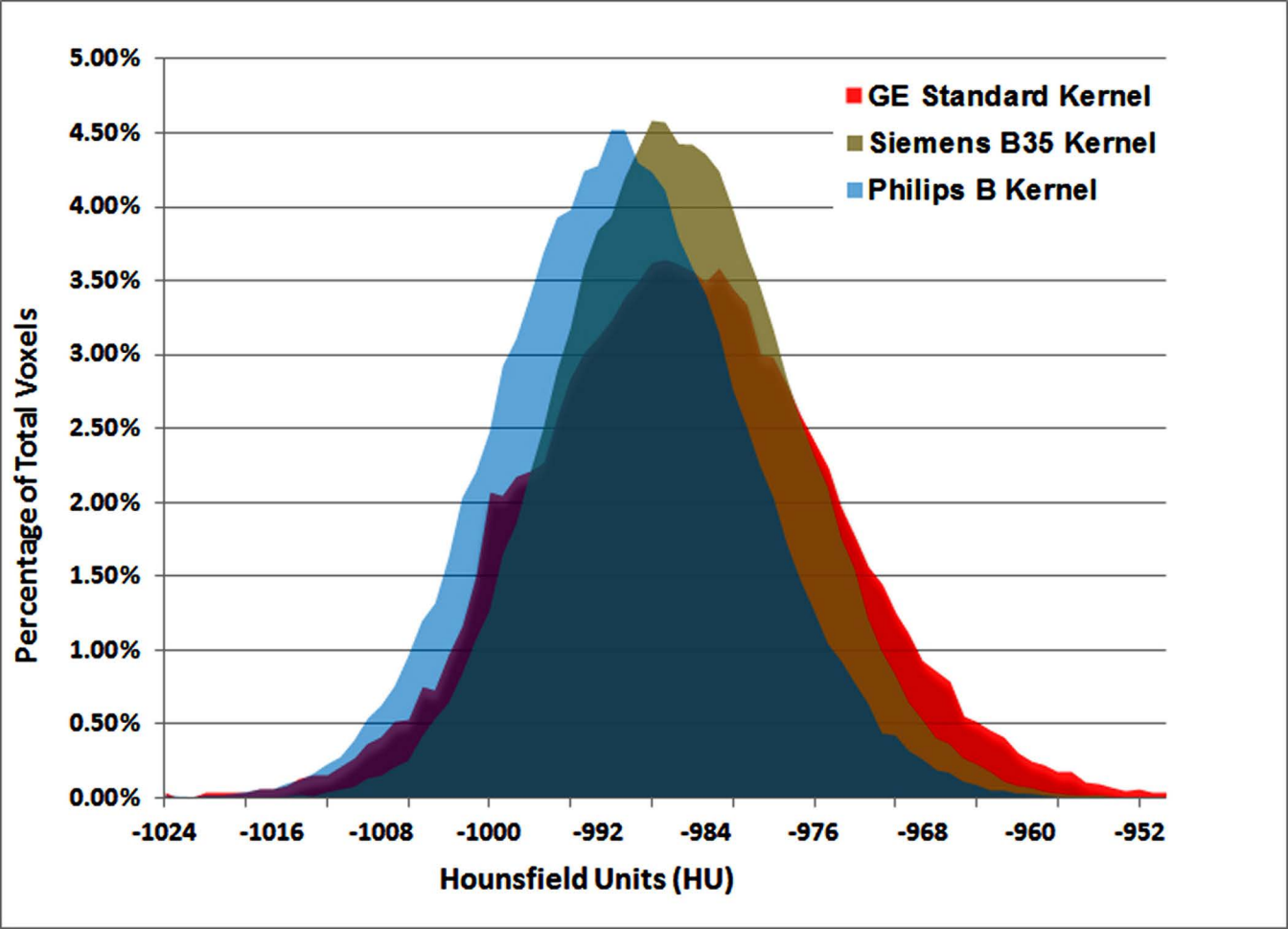
area below and -856 Hounsfield units	middle_percent_below_856	
Right upper third: Percentage of low attenuation area below and -856 Hounsfield units	thirds-right-upper_percent_below_856	CT RV
Left lower third: Percentage of low attenuation area below and -910 Hounsfield units	thirds-left-lower_percent_below_910	CT TLC
Left middle third: Percentage of low attenuation area below and -910 Hounsfield units	thirds-left-middle_percent_below_910	CT TLC
Left upper third: Percentage of low attenuation area below and -910 Hounsfield units	thirds-left-upper_percent_below_910	CT TLC
Right lower third: Percentage of low attenuation area below and -910 Hounsfield units	thirds-right-lower_percent_below_910	CT TLC
Right middle third: Percentage of low attenuation area below and -910 Hounsfield units	thirds-right-middle_percent_below_910	CT TLC
Right upper third: Percentage of low attenuation area below and -910 Hounsfield units	thirds-right-upper_percent_below_910	CT TLC
Left lower third: Percentage of low attenuation area below and -950 Hounsfield units	thirds-left-lower_percent_below_950	CT TLC
Left middle third: Percentage of low attenuation area below and -950 Hounsfield units	thirds-left-middle_percent_below_950	CT TLC
Left upper third: Percentage of low attenuation area below and -950 Hounsfield units	thirds-left-upper_percent_below_950	CT TLC
Right lower third: Percentage of low attenuation area below and -950 Hounsfield units	thirds-right-lower_percent_below_950	CT TLC
Right middle third: Percentage of low attenuation area below and -950 Hounsfield units	thirds-right-middle_percent_below_950	CT TLC
Right upper third: Percentage of low attenuation area below and -950 Hounsfield units	thirds-right-upper_percent_below_950	CT TLC
Left Lung %<-950: Apex divided by Base	l_apex_base_pctbe950_ratio	CT TLC
Left Lung %<-910: Apex divided by Base	l_apex_base_pctbe910_ratio	CT TLC
Right Lung %<-950: Apex divided by Base	r_apex_base_pctbe950_ratio	CT TLC
Right Lung %<-910: Apex divided by Base	r_apex_base_pctbe910_ratio	CT TLC
SPIROMICS CT Airway Variables Description	**Variable name**	**CT Lung Volume**
Pi10 value for airways with an inner perimeter <= 20mm on LB1 path and subtree	pi10_lb1_path_and_subtree_leq20	CT TLC
Pi10 value for airways with an inner perimeter <= 20mm on LB10 path and subtree	pi10_lb10_path_and_subtree_leq20	CT TLC
Pi10 value for airways with an inner perimeter <= 20mm on LB4 path and subtree	pi10_lb4_path_and_subtree_leq20	CT TLC
Pi10 value for airways with an inner perimeter <= 20mm on RB1 path and subtree	pi10_rb1_path_and_subtree_leq20	CT TLC
Pi10 value for airways with an inner perimeter <=	pi10_rb10_path_and_subtree_le	CT TLC

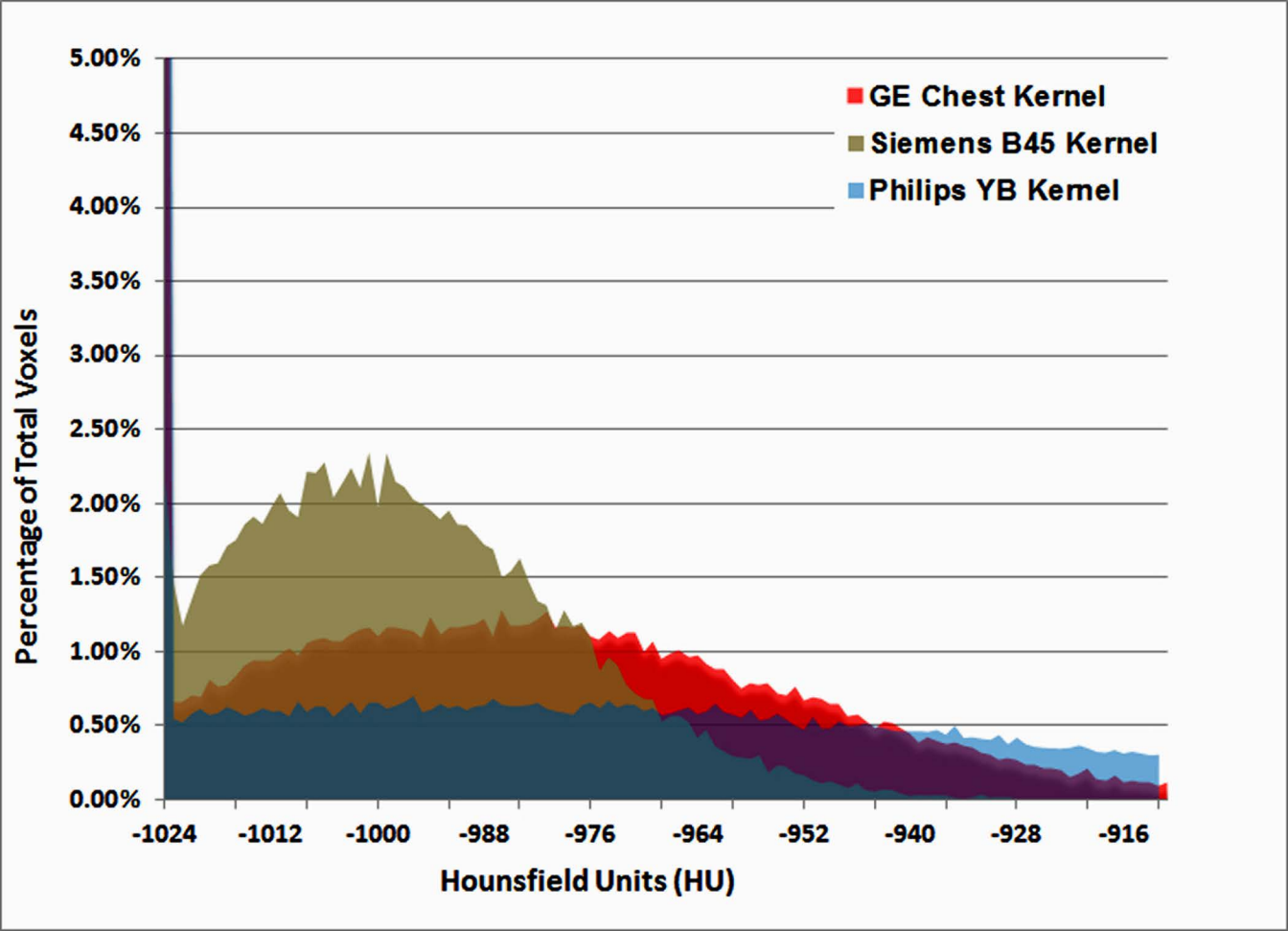
20mm on RB10 path and subtree	q20	
Pi10 value for airways with an inner perimeter <= 20mm on RB4 path and subtree	pi10_rb4_path_and_subtree_leq 20	CT TLC
Pi10 value for airways with an inner perimeter <= 20mm on whole airway tree	pi10_whole_tree_leq20	CT TLC
Pi10 value for airways with an inner perimeter <= 20mm on right airway tree	pi10_right_lung_leq20	CT TLC
Pi10 value for airways with an inner perimeter <= 20mm on left airway tree	pi10_left_lung_leq20	CT TLC
The thickest pi10_leq20 of the 5 standardized paths (eliminating segments with inner perimeter > than 20mm)	RB1_chld_avgavgwalthick50	CT TLC
The average pi10_leq20 of the 5 standardized paths (eliminating segments with inner perimeter > than 20mm)	RB10_chld_avgavgwalthick50	CT TLC
FOR 5 SEGMENTALS AND TWO GENERATIONS BEYOND:		
Wall thickness (At every centerline voxel position the wall thickness at every half-degree, for total of 720 measurements. These average values are averaged along the middle 1/3 of the airway segment to obtain the Average Average Wall Thickness.)	avgavgwallthickness	CT TLC
Wall thickness for middle 50% of segments (At every centerline voxel position the wall thickness at every half-degree, for total of 720 measurements. These average values are averaged along the middle 1/3 of the airway segment to obtain the Average Average Wall Thickness.)	avgwallthickness_50	CT TLC
Average of the avgwallthickness_50 for two children of Rb1	RB1_child_avgavgwallthickness_ 50	CT TLC
Average of the avgwallthickness_50 for two children of Rb10	RB10_child_avgavgwallthicknes s_50	CT TLC
Wall area (avgouterarea - avginnerarea)	avgwallarea	CT TLC
Wall area % ((avgouterarea - avginnerarea)/avgouterarea)	avgwallarea_percent	CT TLC
Length of segmental airway (Measured between parent-branchpoint and child-branchpoint. The center line length represents the true path length, i.e. it follows the curvature of the segment.)	centerlinelength	CT TLC
Branch angle (Angle between a segment and its parent segment)	angle	CT TLC
Lumen area	avginnerarea	CT TLC

Average diameter (At every centerline voxel position along the middle 1/3 of the airway segment the inner equivalent circle diameter is determined. These measurements are then averaged into Average Inner Equivalent Circle Diameter.)	avginnerequivalentcirclediameter	CT TLC
Tapering ratio (comparing lumen area or diameter at 30% and 70% distances along a segment)	taper_ratio	CT TLC
Average taper ratio of the two children of Rb1	Rb1_chld_taper_avgratio	CT TLC
Average taper ratio of the two children of Rb10	Rb10_chld_taper_avgratio	CT TLC
SPRIOMICS LAC (alpha) Variable Description	**Variable Name**	**CT Lung Volume**
Both lungs: Slope at -910	both_slope_below_910	CT TLC
Both lungs: Total intercept at -910	both_intercept_below_910	CT TLC
Both lungs: Total R-squared at -910	both_r_squared_below_910	CT TLC
Left lung: Slope at -910	left_slope_below_910	CT TLC
Left lung: Total intercept at -910	left_intercept_below_910	CT TLC
Left lung: Total R-squared at -910	left_r_squared_below_910	CT TLC
Left lower lobe: Total intercept at -910	left-lower_slope_below_910	CT TLC
Left lower lobe: Total R-squared at -910	left-lower_intercept_below_910	CT TLC
Left lower lobe: Slope at -910	left-lower_r_squared_below_910	CT TLC
Left upper lobe: Total intercept at -910	left-upper_slope_below_910	CT TLC
Left upper lobe: Total R-squared at -910	left-upper_intercept_below_910	CT TLC
Left upper lobe: Slope at -910	left-upper_r_squared_below_910	CT TLC
Right lung: Slope at -910	right_slope_below_910	CT TLC
Right lung: Total intercept at -910	right_intercept_below_910	CT TLC
Right lung: Total R-squared at -910	right_r_squared_below_910	CT TLC
Right lower lobe: Total intercept at -910	right-lower_slope_below_910	CT TLC
Right lower lobe: Total R-squared at -910	right-lower_intercept_below_910	CT TLC
Right lower lobe: Slope at -910	right-lower_r_squared_below_910	CT TLC
Right middle lobe: Total intercept at -910	right-middle_slope_below_910	CT TLC
Right middle lobe: Total R-squared at -910	right-middle_intercept_below_910	CT TLC
Right middle lobe: Slope at -910	right-middle_r_squared_below_910	CT TLC
Right upper lobe: Total intercept at -910	right-upper_slope_below_910	CT TLC
Right upper lobe: Total R-squared at -910	right-upper_intercept_below_910	CT TLC

Right upper lobe: Slope at -910	right-upper_r_squared_below_910	CT TLC
Both lungs: Slope at -950	both_slope_below_950	CT TLC
Both lungs: Total intercept at -950	both_intercept_below_950	CT TLC
Both lungs: Total R-squared at -950	both_r_squared_below_950	CT TLC
Left lung: Slope at -950	left_slope_below_950	CT TLC
Left lung: Total intercept at -950	left_intercept_below_950	CT TLC
Left lung: Total R-squared at -950	left_r_squared_below_950	CT TLC
Left lower lobe: Total intercept at -950	left-lower_slope_below_950	CT TLC
Left lower lobe: Total R-squared at -950	left-lower_intercept_below_950	CT TLC
Left lower lobe: Slope at -950	left-lower_r_squared_below_950	CT TLC
Left upper lobe: Total intercept at -950	left-upper_slope_below_950	CT TLC
Left upper lobe: Total R-squared at -950	left-upper_intercept_below_950	CT TLC
Left upper lobe: Slope at -950	left-upper_r_squared_below_950	CT TLC
Right lung: Slope at -950	right_slope_below_950	CT TLC
Right lung: Total intercept at -950	right_intercept_below_950	CT TLC
Right lung: Total R-squared at -950	right_r_squared_below_950	CT TLC
Right lower lobe: Total intercept at -950	right-lower_slope_below_950	CT TLC
Right lower lobe: Total R-squared at -950	right-lower_intercept_below_950	CT TLC
Right lower lobe: Slope at -950	right-lower_r_squared_below_950	CT TLC
Right middle lobe: Total intercept at -950	right-middle_slope_below_950	CT TLC
Right middle lobe: Total R-squared at -950	right-middle_intercept_below_950	CT TLC
Right middle lobe: Slope at -950	right-middle_r_squared_below_950	CT TLC
Right upper lobe: Total intercept at -950	right-upper_slope_below_950	CT TLC
Right upper lobe: Total R-squared at -950	right-upper_intercept_below_950	CT TLC
Right upper lobe: Slope at -950	right-upper_r_squared_below_950	CT TLC
Alpha (LAC) Apex minus Base with holes defined at -910_right lung	lac_r_apex_base_slp_910dif	CT TLC
Alpha (LAC) Apex minus Base with holes defined at -910_left lung	lac_l_apex_base_slp_910dif	CT TLC
Alpha (LAC) Apex minus Base with holes defined at -950_right lung	lac_r_apex_base_slp_950dif	CT TLC
Alpha (LAC) Apex minus Base with holes defined at -950_left lung	lac_l_apex_base_slp_950dif	CT TLC

SPIROMICE CORE/PEEL (2cm) Variable Descriptions	Variable Name	CT Lung Volume
Both lungs: vessel volume	B_vessel_vx	CT TLC
Both lungs: vessel percent	B_vessel_percent	CT TLC
Both lungs: core vessel volume	BC_vessel_vx	CT TLC
Both lungs: core vessel percent	BC_vessel_percent	CT TLC
Both lungs: core percentage of low attenuation area below and including -950 Hounsfield units	BC_%be_950	CT TLC
Both lungs: core percentage of low attenuation area below and including -910 Hounsfield units	BC_%be_910	CT TLC
Both lungs: peel vessel volume	BP_vessel_vx	CT TLC
Both lungs: peel vessel percent	BP_vessel_percent	CT TLC
Both lungs: peel percentage of low attenuation area below and including -950 Hounsfield units	BP_%be_950	CT TLC
Both lungs: peel percentage of low attenuation area below and including -910 Hounsfield units	BP_%be_910	CT TLC
Right lung: core vessel volume	RC_vessel_vx	CT TLC
Right lung: core vessel percent	RC_vessel_percent	CT TLC
Right lung: core percentage of low attenuation area below and including -950 Hounsfield units	RC_%be_950	CT TLC
Right lung: core percentage of low attenuation area below and including -910 Hounsfield units	RC_%be_910	CT TLC
Right lung: peel vessel volume	RP_vessel_vx	CT TLC
Right lung: peel vessel percent	RP_vessel_percent	CT TLC
Right lung: peel percentage of low attenuation area below and including -950 Hounsfield units	RP_%be_950	CT TLC
Right lung: peel percentage of low attenuation area below and including -910 Hounsfield units	RP_%be_910	CT TLC
Left lung: core vessel volume	LC_vessel_vx	CT TLC
Left lung: core vessel percent	LC_vessel_percent	CT TLC
Left lung: core percentage of low attenuation area below and including -950 Hounsfield units	LC_%be_950	CT TLC
Left lung: core percentage of low attenuation area below and including -910 Hounsfield units	LC_%be_910	CT TLC
Left lung: peel vessel volume	LP_vessel_vx	CT TLC
Left lung: peel vessel percent	LP_vessel_percent	CT TLC
Left lung: peel percentage of low attenuation area below and including -950 Hounsfield units	LP_%be_950	CT TLC
Left lung: peel percentage of low attenuation area below and including -910 Hounsfield units	LP_%be_910	CT TLC


GE Standard Kernel
Siemens B35 Kernel
Philips B Kernel
5.00%
4.50%
4.00%
3.50%
3.00%
2.50%
2.00%
1.50%
1.00%
0.50%
0.00%
Percentage of Total Voxels
-1024
-1016
-1008
-1000
-992
-984
-976
-968
-960
-952
Hounsfield Units (HU)


GE Chest Kernel
Siemens B45 Kernel
Philips YB Kernel
5.00%
4.50%
4.00%
3.50%
3.00%
2.50%
2.00%
1.50%
1.00%
0.50%
0.00%
Percentage of Total Voxels
-1024
-1012
-1000
-988
-976
-964
-952
-940
-928
-916
Hounsfield Units (HU)

SPIROMICS
@I-CLIC

Procedural Verification Software

Pending Scan

Logout Jered Sieren

- Register a Scan
- In Process
- Pending
- Reviewed
- Need Attention
- Deviations
- Quality Control Errors
- Contact List
- My Account

Tools and Reports
- Download PVS Report

Data Center Operations
- Update Scan Status
- List Users
- List Technologists
- Add a Site
- Add a User
- Add a Technologist

Site ID: UMich

User ID: sierenje

SPIROMICS ID: MU

Visit Number: 1

CT Acquisition Date: 2013-07-09 * (format: yyyy-mm-dd)

Subject BMI: 36.4

Please select the scanner that was used for this study

Scanner Doses (Needed for this Study)

	Size	Manufacturer	Model	SFOV	Inspiratory mA	Expiratory mA
◉	LARGE	GE MEDICAL SYSTEMS	DISCOVERY CT750 HD	LARGE	270	145

CT Image Acquisition *

Verified	Scan	SFOV	mA	kV	DFOV	CT Dose Index (CTDI) (mGy)
☑	INSPIRATION	LARGE	270	120	37	10.54
☑	EXPIRATION	LARGE	145	120	37	5.63

CT Image Quality *

Adequate Inspiratory Scan?	◉ Yes	○ No
Motion Artifact?	○ Yes	◉ No
Inclusion of All Parts of Lungs?	◉ Yes	○ No
Adequate Expiratory Scan?	◉ Yes	○ No

Pitch: 0.984 *

Slice Separation: 0.5 *

Scans Archived?	◉ Yes	○ No
Scans De-identified?	◉ Yes	○ No
Scans Transmitted via DISPATCH?	◉ Yes	○ No

Imaging Technologist: Ricky Higa *

Comments:

Admin Notes: (visible only by Administrator)

Contact Radiology Center: I-CLIC Information

Update Scan | Reset This Form | Print This Form

SPIROMICS
@I-CLIC

Procedural Verification Software

Pending Scan

Logout Jered Sieren

Register a Scan
In Process
Pending
Reviewed
Need Attention
Deviations
Quality Control Errors
Contact List
My Account

Tools and Reports
Download PVS Report

Data Center Operations
Update Scan Status
List Users
List Technologists
Add a Site
Add a User
Add a Technologist

Site ID: UMich
User ID: sierenje
SPIROMICS ID: MU
Visit Number: 1
CT Acquisition Date: 2013-07-09 * (format: yyyy-mm-dd)
Subject BMI: 36.4

Please select the scanner that was used for this study

Scanner Doses (Needed for this Study)

	Size	Manufacturer	Model	SFOV	Inspiratory mA	Expiratory mA
◉	LARGE	GE MEDICAL SYSTEMS	DISCOVERY CT750 HD	LARGE	270	145

CT Image Acquisition *

Verified	Scan	SFOV	mA	kV	DFOV	CT Dose Index (CTDI) (mGy)
☑	INSPIRATION	LARGE	270	120	34	10.54
☑	EXPIRATION	LARGE	145	120	37	5.63

CT Image Quality *

Adequate Inspiratory Scan?	◉ Yes	○ No
Motion Artifact?	○ Yes	◉ No
Inclusion of All Parts of Lungs?	◉ Yes	○ No
Adequate Expiratory Scan?	◉ Yes	○ No

Pitch: 0.984 *
Slice Separation: 0.5 *

Scans Archived?	◉ Yes	○ No
Scans De-identified?	◉ Yes	○ No
Scans Transmitted via DISPATCH?	◉ Yes	○ No

Imaging Technologist: Ricky Higa *

Comments:

Form Errors: • Inspiration DFOV and expiration DFOV values do not match.

Admin Notes: (visible only by Administrator)

Contact Radiology Center: I-CLIC Information

Project Setup

Current Working Directory:

patch training set\PIT01_PHANTOM,PIT01_PHANTOM | Browse

Current Project:

COPDGene | Validate

DISPATCH™

Project Validation

- Root
  - PIT01 PHANTOM
    - 4011
      - ☑
      - ☑ EXPIRATION

Upload Checked | Start Over

Attribute	Dicom Value	Expected Value(s)	Error Message
AcquisitionDate	20090706		
AcquisitionTime	073800		
Columns	512	512	
GantryDetectorTilt	0.0	0.0	
ImageType	ORIGINAL PRIMARY AXIAL		
InstitutionName	UPMC Health System Presby		
KVP	120	120	
Manufacturer	GE MEDICAL SYSTEMS	GE MEDICAL SYSTEMS,PHILI...	
PatientID	PIT01 PHANTOM		
PatientName	PIT01 PHANTOM		
PatientPosition	HFS	HFS,FFS	
PixelSpacing			
ProtocolName	5.46 GENETIC EPIDEMIOLOG...		
ReconstructionDiameter	365.0	Range(350.0 ,375.0)	
Rows	512	512	
SoftwareVersion	07MW18.4		
StationName	ct1x		
StudyDate	20090706		
StudyTime	073151		
SliceSpacing	0.5	0.5	
ExposureTime	500.0	500.0	
FilterType	BODY FILTER	BODY FILTER	
ManufacturerModelName	LIGHTSPEED VCT	LIGHTSPEED VCT,LIGHTSPEE...	
Pitch-GE-range			
SliceThickness	0.625	0.625	

INFO: There are 131 files in this series.
INFO: The manufacturer is GE MEDICAL S
INFO: The model is LIGHTSPEED VCT.