Combining Multiple Magnetic Resonance Imaging Sequences Provides Independent Reproducible Radiomics Features

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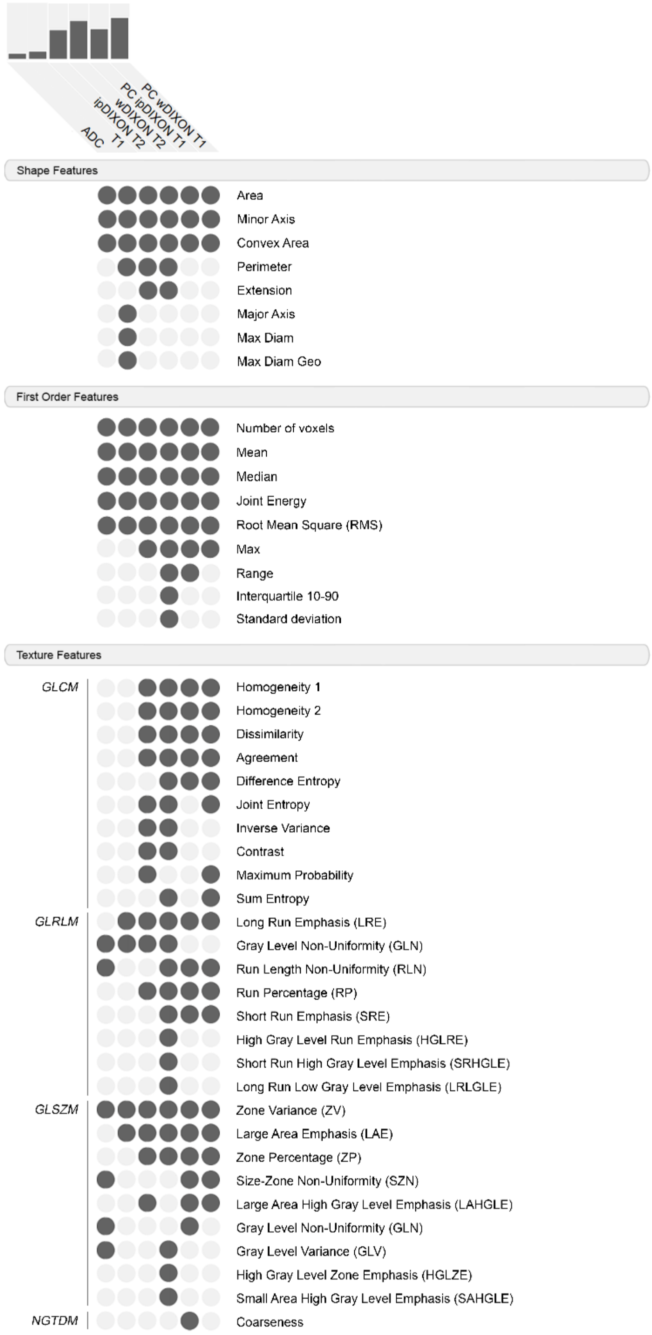
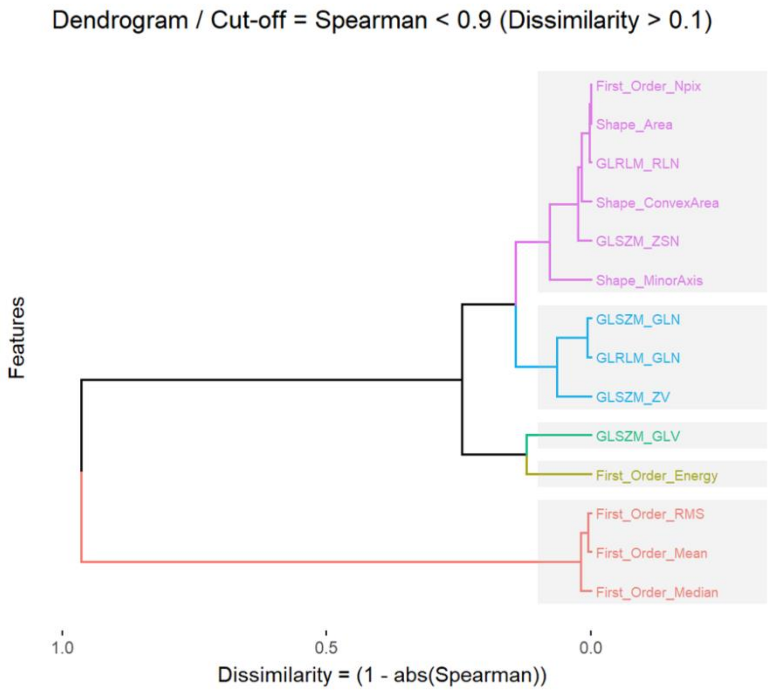
Supplementary Figures

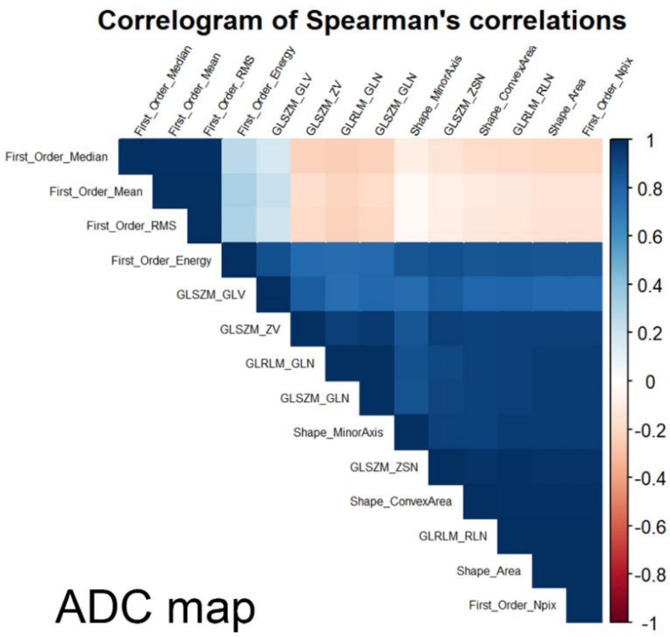


		ADC	T1	ipDIXON T2	wDIXON T2	PC ipDIXON T1	PC wDIXON T1
Shape Features							
	Area	●	●	●	●	●	●
	Minor Axis	●	●	●	●	●	●
	Convex Area	●	●	●	●	●	●
	Perimeter		●	●	●		
	Extension			●	●		
	Major Axis		●				
	Max Diam		●				
	Max Diam Geo		●				
First Order Features							
	Number of voxels	●	●	●	●	●	●
	Mean	●	●	●	●	●	●
	Median	●	●	●	●	●	●
	Joint Energy	●	●	●	●	●	●
	Root Mean Square (RMS)	●	●	●	●	●	●
	Max			●	●	●	●
	Range				●	●	
	Interquartile 10-90				●		
	Standard deviation				●		
Texture Features							
GLCM	Homogeneity 1			●	●	●	●
	Homogeneity 2			●	●	●	●
	Dissimilarity			●	●	●	●
	Agreement			●	●	●	●
	Difference Entropy				●	●	●
	Joint Entropy			●	●		●
	Inverse Variance			●	●		
	Contrast			●	●		
	Maximum Probability			●			●
	Sum Entropy				●		●
GLRLM	Long Run Emphasis (LRE)		●	●	●	●	●
	Gray Level Non-Uniformity (GLN)	●	●	●	●		
	Run Length Non-Uniformity (RLN)	●			●	●	●
	Run Percentage (RP)			●	●	●	●
	Short Run Emphasis (SRE)				●	●	●
	High Gray Level Run Emphasis (HGLRE)				●		
	Short Run High Gray Level Emphasis (SRHGLE)				●		
	Long Run Low Gray Level Emphasis (LRLGLE)				●		
GLSZM	Zone Variance (ZV)	●	●	●	●	●	●
	Large Area Emphasis (LAE)		●	●	●	●	●
	Zone Percentage (ZP)			●	●	●	●
	Size-Zone Non-Uniformity (SZN)	●				●	●
	Large Area High Gray Level Emphasis (LAHGLE)			●		●	●
	Gray Level Non-Uniformity (GLN)	●				●	
	Gray Level Variance (GLV)	●			●		
	High Gray Level Zone Emphasis (HGLZE)				●		
	Small Area High Gray Level Emphasis (SAHGLE)				●		
NGTDM	Coarseness					●	

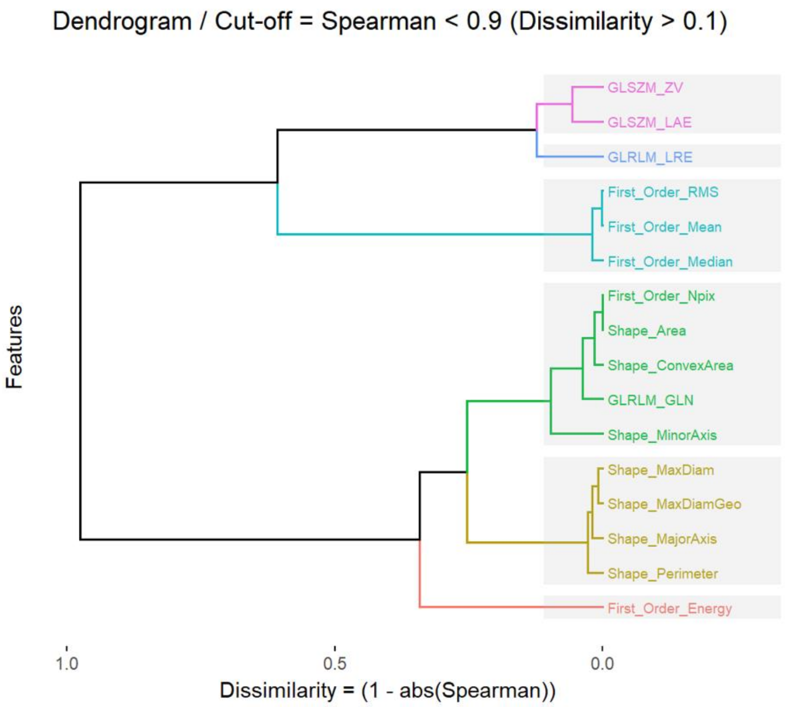
Supplementary Figure 1. Details of reproducible features extracted after the step one. Each MR sequence is displayed in a column. Each row displays a distinct feature. Features issued from the same categories (shape, first-order or texture) are grouped. A black point indicates a reproducible feature. Apparent Diffusion Coefficient map (ADC); Post-contrast in-phase DIXON T1 (PC ipDIXON T1); Post-contrast water DIXON T1 (PC wDIXON T1);

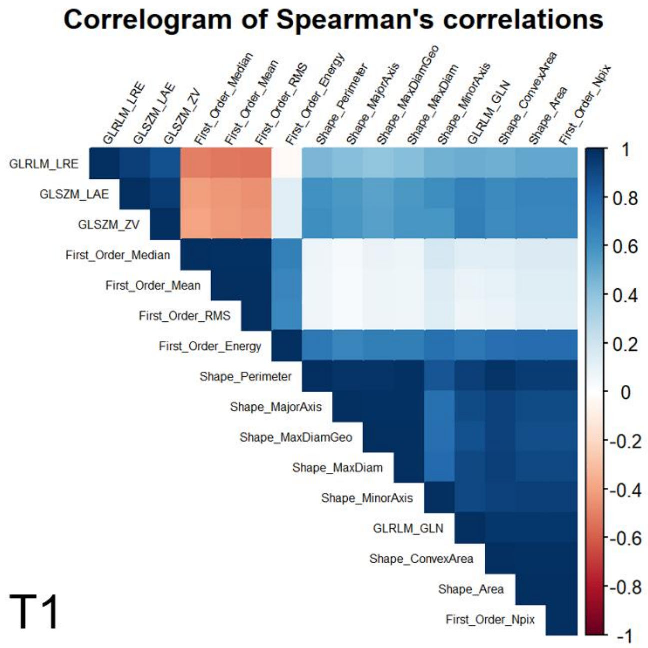
In-phase DIXON T2 (ipDIXON T2); Water DIXON T2 (wDIXON T2); grey-level co-occurrence (GLCM), grey-level run-length (GLRLM), grey-level size-zone (GLSZM), neighborhood grey-tone difference (NGTDM).

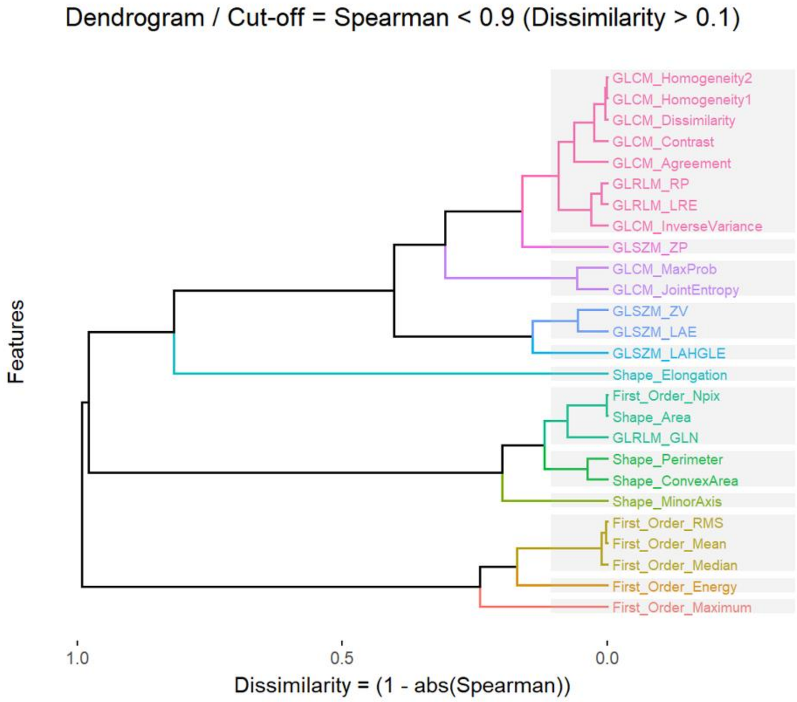

Dendrogram / Cut-off = Spearman < 0.9 (Dissimilarity > 0.1)
Features
First_Order_Npix
Shape_Area
GLRLM_RLN
Shape_ConvexArea
GLSZM_ZSN
Shape_MinorAxis
GLSZM_GLN
GLRLM_GLN
GLSZM_ZV
GLSZM_GLV
First_Order_Energy
First_Order_RMS
First_Order_Mean
First_Order_Median
1.0
0.5
0.0
Dissimilarity = (1 - abs(Spearman))

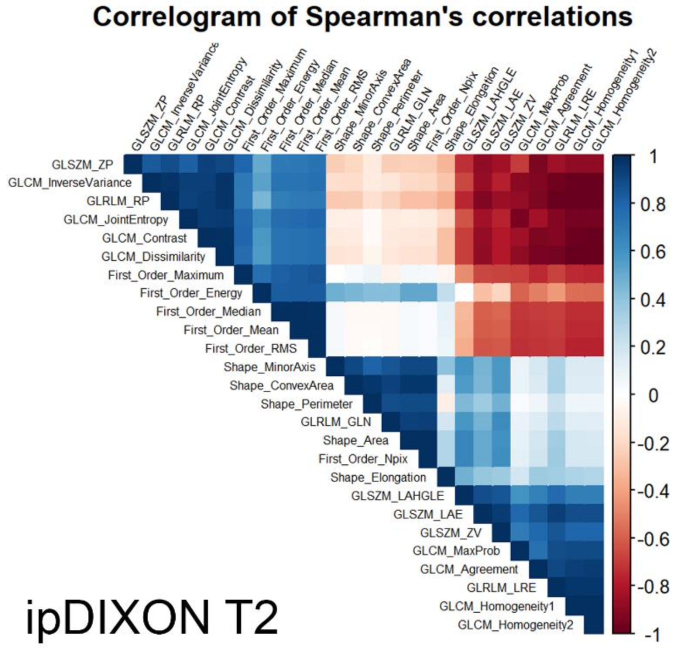

Correlogram of Spearman's correlations
First_Order_Median
First_Order_Mean
First_Order_RMS
First_Order_Energy
GLSZM_GLV
GLSZM_ZV
GLRLM_GLN
GLSZM_GLN
Shape_MinorAxis
GLSZM_ZSN
Shape_ConvexArea
GLRLM_RLN
Shape_Area
First_Order_Npix
1
0.8
0.6
0.4
0.2
0
-0.2
-0.4
-0.6
-0.8
-1

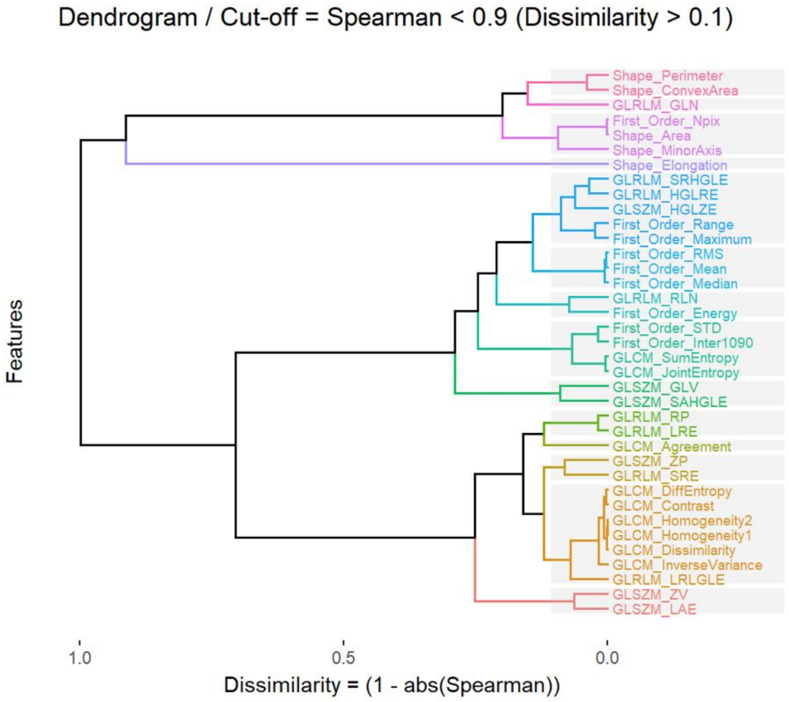
ADC map

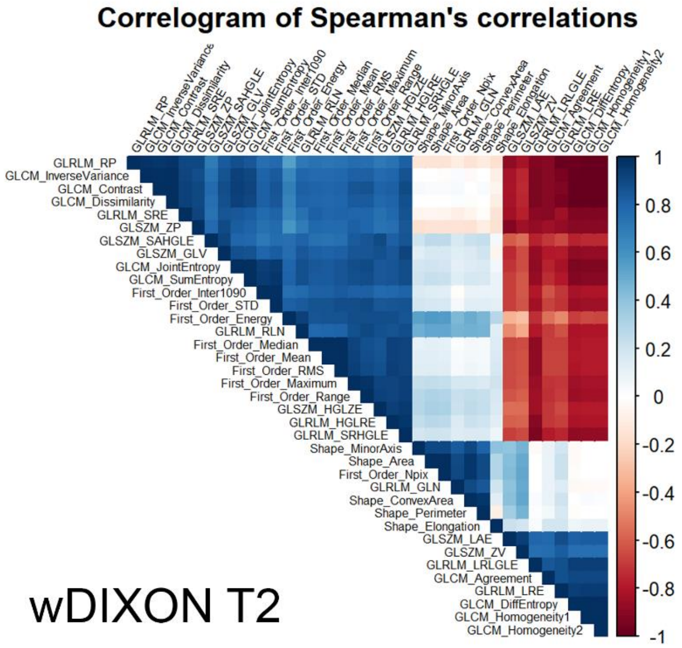

Dendrogram / Cut-off = Spearman < 0.9 (Dissimilarity > 0.1)
Features
GLSZM_ZV
GLSZM_LAE
GLRLM_LRE
First_Order_RMS
First_Order_Mean
First_Order_Median
First_Order_Npix
Shape_Area
Shape_ConvexArea
GLRLM_GLN
Shape_MinorAxis
Shape_MaxDiam
Shape_MaxDiamGeo
Shape_MajorAxis
Shape_Perimeter
First_Order_Energy
1.0
0.5
0.0
Dissimilarity = (1 - abs(Spearman))

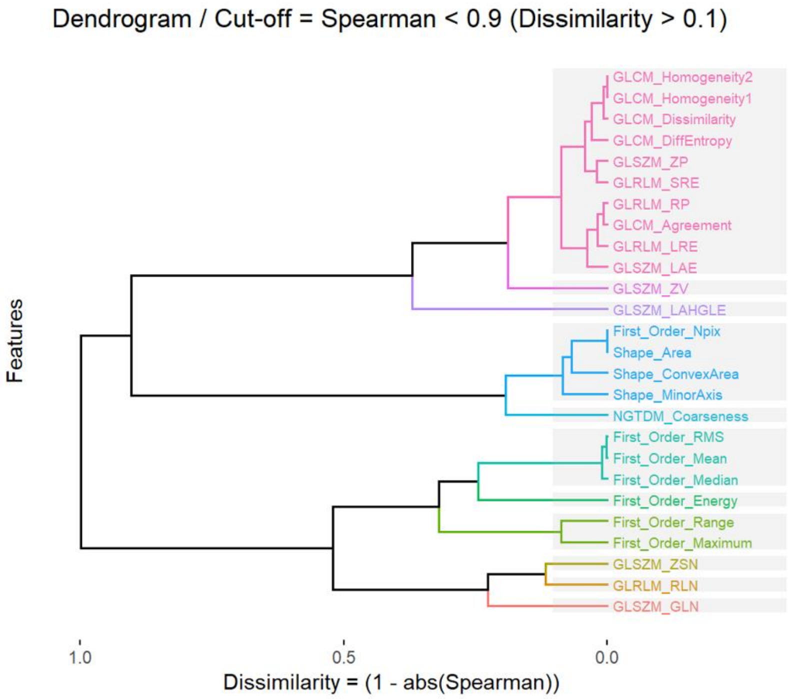

Correlogram of Spearman's correlations
GLRLM_LRE
GLSZM_LAE
GLSZM_ZV
First_Order_Median
First_Order_Mean
First_Order_RMS
First_Order_Energy
Shape_Perimeter
Shape_MajorAxis
Shape_MaxDiamGeo
Shape_MaxDiam
Shape_MinorAxis
GLRLM_GLN
Shape_ConvexArea
Shape_Area
First_Order_Npix
1
0.8
0.6
0.4
0.2
0
-0.2
-0.4
-0.6
-0.8
-1
T1

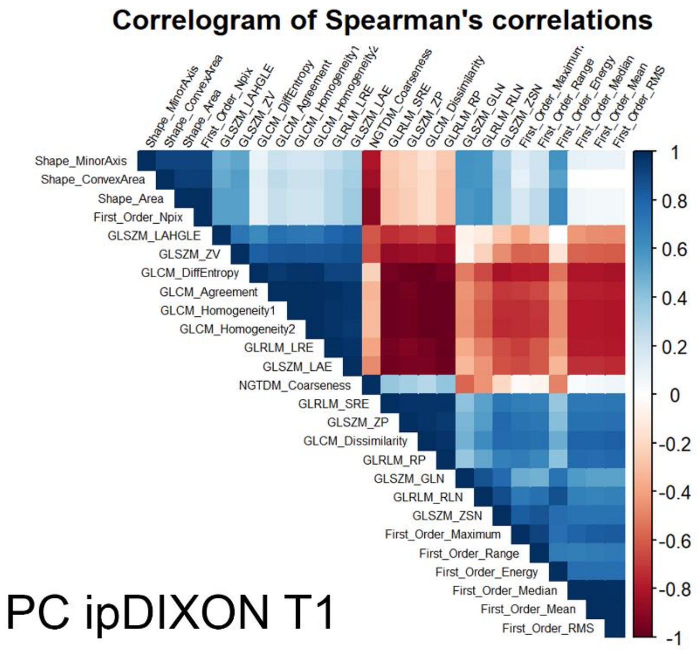

Dendrogram / Cut-off = Spearman < 0.9 (Dissimilarity > 0.1)
Features
GLCM_Homogeneity2
GLCM_Homogeneity1
GLCM_Dissimilarity
GLCM_Contrast
GLCM_Agreement
GLRLM_RP
GLRLM_LRE
GLCM_InverseVariance
GLSZM_ZP
GLCM_MaxProb
GLCM_JointEntropy
GLSZM_ZV
GLSZM_LAE
GLSZM_LAHGLE
Shape_Elongation
First_Order_Npix
Shape_Area
GLRLM_GLN
Shape_Perimeter
Shape_ConvexArea
Shape_MinorAxis
First_Order_RMS
First_Order_Mean
First_Order_Median
First_Order_Energy
First_Order_Maximum
1.0
0.5
0.0
Dissimilarity = (1 - abs(Spearman))


Correlogram of Spearman's correlations
GLSZM_ZP
GLCM_InverseVariance
GLRLM_RP
GLCM_JointEntropy
GLCM_Contrast
GLCM_Dissimilarity
First_Order_Maximum
First_Order_Energy
First_Order_Median
First_Order_Mean
First_Order_RMS
Shape_MinorAxis
Shape_ConvexArea
Shape_Perimeter
GLRLM_GLN
Shape_Area
First_Order_Npix
Shape_Elongation
GLSZM_LAHGLE
GLSZM_LAE
GLSZM_ZV
GLCM_MaxProb
GLCM_Agreement
GLRLM_LRE
GLCM_Homogeneity1
GLCM_Homogeneity2
1
0.8
0.6
0.4
0.2
0
-0.2
-0.4
-0.6
-0.8
-1
ipDIXON T2

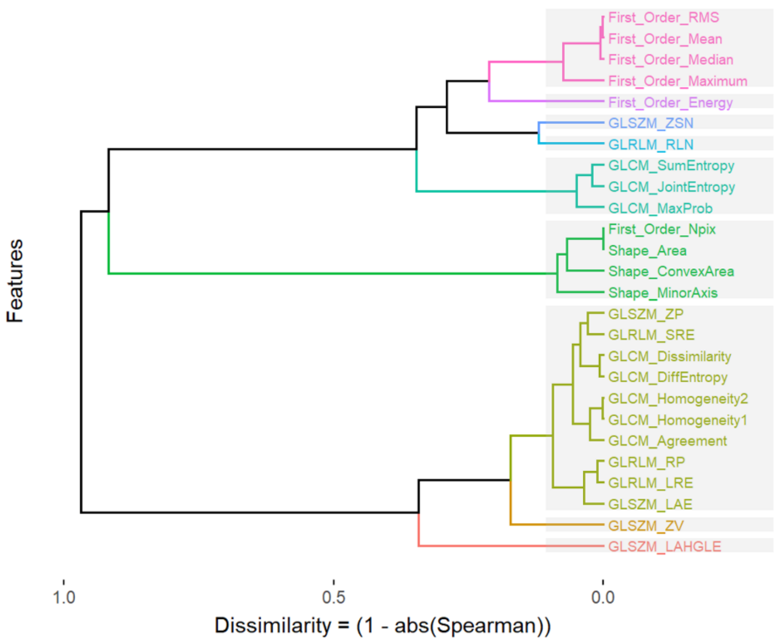

Dendrogram / Cut-off = Spearman < 0.9 (Dissimilarity > 0.1)
Features
Shape_Perimeter
Shape_ConvexArea
GLRLM_GLN
First_Order_Npix
Shape_Area
Shape_MinorAxis
Shape_Elongation
GLRLM_SRHGLE
GLRLM_HGLRE
GLSZM_HGLZE
First_Order_Range
First_Order_Maximum
First_Order_RMS
First_Order_Mean
First_Order_Median
GLRLM_RLN
First_Order_Energy
First_Order_STD
First_Order_Inter1090
GLCM_SumEntropy
GLCM_JointEntropy
GLSZM_GLV
GLSZM_SAHGLE
GLRLM_RP
GLRLM_LRE
GLCM_Agreement
GLSZM_ZP
GLRLM_SRE
GLCM_DiffEntropy
GLCM_Contrast
GLCM_Homogeneity2
GLCM_Homogeneity1
GLCM_Dissimilarity
GLCM_InverseVariance
GLRLM_LRLGLE
GLSZM_ZV
GLSZM_LAE
1.0
0.5
0.0
Dissimilarity = (1 - abs(Spearman))


Correlogram of Spearman's correlations
GLRLM_RP
GLCM_InverseVariance
GLCM_Contrast
GLCM_Dissimilarity
GLRLM_SRE
GLSZM_ZP
GLSZM_SAHGLE
GLSZM_GLV
GLCM_JointEntropy
GLCM_SumEntropy
First_Order_Inter1090
First_Order_STD
First_Order_Energy
GLRLM_RLN
First_Order_Median
First_Order_Mean
First_Order_RMS
First_Order_Maximum
First_Order_Range
GLSZM_HGLZE
GLRLM_HGLRE
GLRLM_SRHGLE
Shape_MinorAxis
Shape_Area
First_Order_Npix
GLRLM_GLN
Shape_ConvexArea
Shape_Perimeter
Shape_Elongation
GLSZM_LAE
GLSZM_ZV
GLRLM_LRLGLE
GLCM_Agreement
GLRLM_LRE
GLCM_DiffEntropy
GLCM_Homogeneity1
GLCM_Homogeneity2
1
0.8
0.6
0.4
0.2
0
-0.2
-0.4
-0.6
-0.8
-1
wDIXON T2

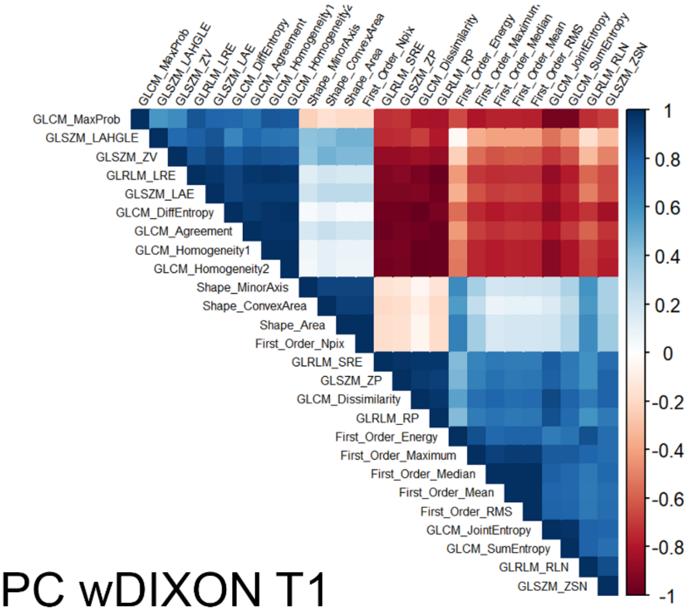

Dendrogram / Cut-off = Spearman < 0.9 (Dissimilarity > 0.1)
Features
GLCM_Homogeneity2
GLCM_Homogeneity1
GLCM_Dissimilarity
GLCM_DiffEntropy
GLSZM_ZP
GLRLM_SRE
GLRLM_RP
GLCM_Agreement
GLRLM_LRE
GLSZM_LAE
GLSZM_ZV
GLSZM_LAHGLE
First_Order_Npix
Shape_Area
Shape_ConvexArea
Shape_MinorAxis
NGTDM_Coarseness
First_Order_RMS
First_Order_Mean
First_Order_Median
First_Order_Energy
First_Order_Range
First_Order_Maximum
GLSZM_ZSN
GLRLM_RLN
GLSZM_GLN
1.0
0.5
0.0
Dissimilarity = (1 - abs(Spearman))


Correlogram of Spearman's correlations
Shape_MinorAxis
Shape_ConvexArea
Shape_Area
First_Order_Npix
GLSZM_LAHGLE
GLSZM_ZV
GLCM_DiffEntropy
GLCM_Agreement
GLCM_Homogeneity1
GLCM_Homogeneity2
GLRLM_LRE
GLSZM_LAE
NGTDM_Coarseness
GLRLM_SRE
GLSZM_ZP
GLCM_Dissimilarity
GLRLM_RP
GLSZM_GLN
GLRLM_RLN
GLSZM_ZSN
First_Order_Maximum
First_Order_Range
First_Order_Energy
First_Order_Median
First_Order_Mean
First_Order_RMS
1
0.8
0.6
0.4
0.2
0
-0.2
-0.4
-0.6
-0.8
-1
PC ipDIXON T1

Dendrogram / Cut-off = Spearman < 0.9 (Dissimilarity > 0.1)



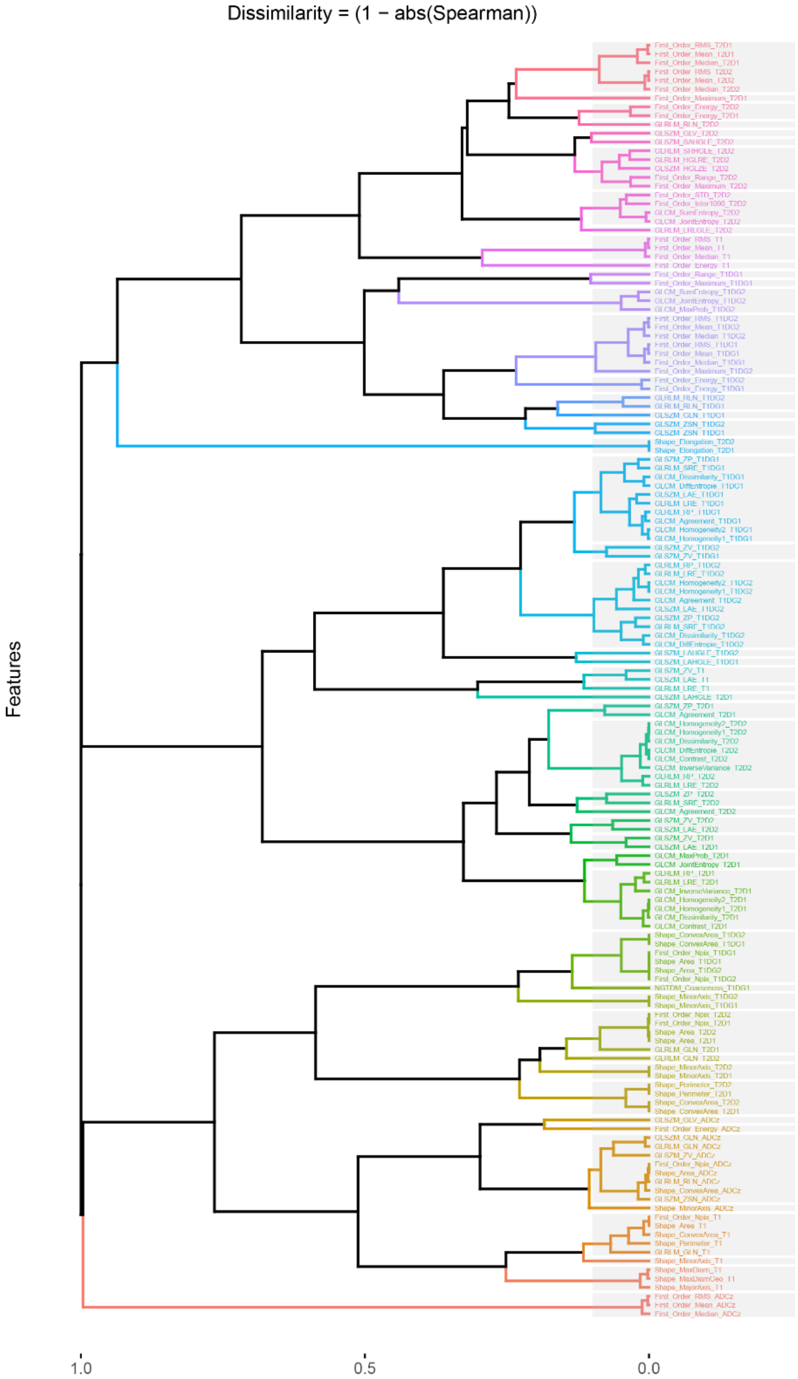
Correlogram of Spearman's correlations



PC wDIXON T1

Supplementary Figure 2. Dendrograms and Spearman's Correlation Matrices showing the reproducible features and clusters for each MR sequence with the threshold values ICC 0.8 / CCC 0.9. On the dendrograms, the features are displayed in the y-axis, and the dissimilarity in the x-axis (low dissimilarity on the right and high dissimilarity on the left of the axis). Two features or clusters of features are grouped by a branch according to their dissimilarity. All features with a dissimilarity < 0.1 indicating a high redundancy share the same colors and are grouped in the same grey box. All clusters with a dissimilarity ≥ 0.1 are considered independent. On the correlograms, the features are displayed in both x-axis and y-axis. Similarities between features compared two-by-two are color-coded in blue for a positive Spearman's correlation and in red for a negative correlation. The intensity of the correlation is represented by the intensity of the color, with higher correlations coded with darker colors and low correlations with lighter colors.

ADC map (a), T1-WI (b), ipDIXON T2-WI (c), wDIXON T2-WI (d), ipDIXON T1-WI (e), wDIXON T1-WI (f). Grey-level co-occurrence (GLCM), grey-level run-length (GLRLM), grey-level size-zone (GLSZM), neighborhood grey-tone difference.



Supplementary Figure 3. Dendrogram showing the reproducible features and clusters of multiple sequences pooled together with the threshold values ICC 0.8 / CCC 0.9. The features are displayed in the y-axis and the dissimilarity in the x-axis (low dissimilarity on the right and high dissimilarity on the left of the axis). Two features or clusters of features are grouped by a branch according to their dissimilarity. All features with a dissimilarity < 0.1 indicating a high redundancy share the same colors and are grouped in the same grey box. All clusters with a dissimilarity ≥ 0.1 are considered independent. Gray-level co-occurrence (GLCM), gray-level run-length (GLRLM), gray-level size-zone (GLSZM), neighborhood grey-tone difference (NGTDM).