

## ON-LINE APPENDIX: DETAILS OF TEXTURE ANALYSIS

We measured 41 features from each segmented tissue volume using in-house-developed Matlab texture-analysis software.<sup>1,2</sup> The 41 features included 12 histogram features, 5 GLCM features, 11 GLRL features, 4 GLGM features, and 9 Laws features. The extraneous math behind each texture feature in detail is described as follows.

### Histogram Features

The histogram features included mean, median, SD, entropy, second SD, range, geometric mean, harmonic mean, interquartile range, fourth moment, SD in a 5-pixel neighborhood (SD 5), and SD in a 9-pixel neighborhood (SD 9). SD 5 and SD 9 are SDs calculated on the basis of a pixel and its surrounding 4 and 8 pixels, thus creating a 5- and 9-pixel neighborhood, respectively. Histogram features are spatially invariant and are not affected by relationships with neighboring pixels.<sup>3</sup>

### Gray-Level Co-Occurrence Matrix Features

The GLCM features, in contrast to histogram features, are spatially dependent and are influenced by relationships with surrounding pixels. The GLCM is square and symmetric with rows and columns from 0 to  $N_g$ , where  $N_g$  represents the number of gray tones in the image. This notation allows the GLCM element in row  $i$  and column  $j$  to represent the number of times a given gray tone of value  $i$  is horizontally adjacent to gray tone  $j$  in the original quantized image. Herein, GLCMs were calculated using only directly adjacent pixels for simplicity. Horizontal, 45°, vertical, and 135° directions were averaged to eliminate any directional dependence. We tested the following GLCM features proposed by Haralick et al.<sup>4</sup>:

- 1) Contrast =  $\sum_{i,j} |i - j|^2 p(i, j)$
- 2) Correlation =  $\sum_{i,j} \frac{(i - \mu_i)(j - \mu_j) p(i, j)}{\sigma_i \sigma_j}$
- 3) Angular Second Moment =  $\sum_{i,j} p(i, j)^2$
- 4) Homogeneity =  $\sum_{i,j} \frac{p(i, j)}{1 + |i - j|}$
- 5) Entropy =  $\sum_{i,j} \ln(p(i, j)) p(i, j)$

where  $p(i, j)$  represents the  $(i, j)$  value of the GLCM.

### Gray-Level Run-Length Features

The GLRL matrix provides additional insights into a spatial dependence and was created on the basis of the published work of Tang.<sup>5</sup> Similar to the GLCM, the GLRL matrix is quantized to  $N_g$  gray tones to simplify texture extraction and to yield a more robust technique. The row index  $i$  of the GLRL matrix represents the gray tone of value  $i$ . In contrast, the column index  $j$  is the run-length, which is defined as a number of adjacent and equal-value pixels in a given direction. The value of each element in the GLRL matrix represents the number of pixel line segments (run) with run-length  $j$  and gray tone  $i$ . The same directions considered in

GLCM were averaged for the GLRL matrix. The features explored included equations using SRE, LRE, GLN, RLN, RP, LGRE, HGRE, SRLGE, short-run high gray-level emphasis (SRHGE), long-run low gray-level emphasis (LRLGE), and LRHGE, defined as follows:

- 6) SRE =  $\frac{1}{n_r} \sum_{i,j} \frac{p(i, j)}{j^2}$
- 7) LRE =  $\frac{1}{n_r} \sum_{i,j} p(i, j) j^2$
- 8) GLN =  $\frac{1}{n_r} \sum_i \left( \sum_j p(i, j) \right)^2$
- 9) RLN =  $\frac{1}{n_r} \sum_j \left( \sum_i p(i, j) \right)^2$
- 10) RP =  $\frac{n_r}{n_p}$
- 11) LGRE =  $\frac{1}{n_r} \sum_{i,j} \frac{p(i, j)}{i^2}$
- 12) HGRE =  $\frac{1}{n_r} \sum_{i,j} p(i, j) i^2$
- 13) SRLGE =  $\frac{1}{n_r} \sum_{i,j} \frac{p(i, j)}{i^2 j^2}$
- 14) SRHGE =  $\frac{1}{n_r} \sum_{i,j} \frac{p(i, j) i^2}{j^2}$
- 15) LRLGE =  $\frac{1}{n_r} \sum_{i,j} \frac{p(i, j) j^2}{i^2}$
- 16) LRHGE =  $\sum_{i,j} p(i, j) i^2 j^2$

where  $p(i, j)$  represents the  $(i, j)$  value of the GLRL matrix,  $n_r$  is the total number of runs, and  $n_p$  is the total number of pixels. The images were requantized in the texture analysis program using a standard of 30 gray levels. No smoothing filter was applied to the images in the texture-analysis program. The images were normalized by the mean and SD to minimize discrimination by the overall gray-level variation, which is unrelated to local image texture.

### Gray-Level Gradient Matrix Features

The GLGM was used to provide the histogram of the absolute gradient values in the ROI. As a preprocessing step, the gradient of each pixel within the ROI was computed using a  $3 \times 3$  neighborhood. The GLGM features mathematically summarize the gradient values of the pixels in the ROI and include mean, variance, skewness, and kurtosis.

### Laws Features

The Laws features are based on unidimensional vectors described by Kenneth Laws.<sup>6</sup> Vectors described by Laws included

level, spot, edge, ripple, wave, undulation, and oscillation. The vectors level, edge, ripple, and spot were used for our analysis. Two 5-pixel vectors are convolved to create 2D filter masks, and certain symmetric pairs were combined to form the final 9 filter masks L1–L9,<sup>7</sup> which were applied across an image.

## REFERENCES

1. Buch K, Fujita A, Li B et al. **Using texture analysis to determine human papillomavirus status of oropharyngeal squamous cell carcinomas on CT.** *AJNR Am J Neuroradiol* 2015;36:1343–48 CrossRef Medline
2. Yu H, Buch K, Li B et al. **Utility of texture analysis for quantifying hepatic fibrosis on proton density MR imaging.** *J Magn Reson Imaging* 2015;42:1259–65 CrossRef Medline
3. Castellano G, Bonilha L, Li LM et al. **Texture analysis of medical images.** *Clin Radiol* 2004;59:1061–69 CrossRef Medline
4. Haralick RM, Shanmugam K. **Textural features for image classification.** *IEEE Transactions on Systems, Man, and Cybernetics* 1973:610–21 CrossRef Medline
5. Tang X. **Texture information in run-length matrices.** *IEEE Trans Image Process* 1998;7:1602–09 CrossRef Medline
6. Laws KI. *Textured Image Segmentation* [dissertation and thesis]. Los Angeles: University of Southern California; 1980
7. Li B, Jara H, Yu H et al. **Enhanced Laws textures: a potential MR imaging surrogate marker of hepatic fibrosis in a murine model.** *Magn Reson Imaging* 2017;37:33–40 CrossRef Medline

**On-line Table 1: [<sup>18</sup>F] FDG-PET/CT characteristics and texture parameters differentiating lymph node characterization in patients with HIV infection (group 1 vs 2)**

Texture Parameter	Benign Nodes (n = 9)		Malignant Nodes (n = 13)		P Value <sup>a</sup>	AUC <sup>b</sup> (GLIMMROC)
	Mean	SD	Mean	SD		
<b>Node characteristics</b>						
Size (cm)	1.400	0.300	1.892	0.690	.024 <sup>c</sup>	0.752
Volume (cm <sup>3</sup> )	0.547	0.363	2.535	2.218	.007 <sup>c</sup>	0.889
SUVmax	5.111	1.610	8.562	3.886	.042 <sup>c</sup>	0.803
<b>Histogram</b>						
Mean	624.4	74.6	735.3	75.2	.017 <sup>c</sup>	0.872
Median	774.0	217.9	1013.1	71.2	.018 <sup>c</sup>	0.872
SD	506.4	13.4	495.0	18.3	.165	0.735
Entropy	6.012	0.048	5.894	0.231	.164	0.726
Second SD	93.76	28.70	59.85	19.19	.017 <sup>c</sup>	0.872
Range	273.7	82.9	175.4	54.5	.017 <sup>c</sup>	0.863
Geometric mean	199.6	44.7	272.8	63.8	.032 <sup>c</sup>	0.829
Harmonic mean	22.18	3.65	26.79	4.76	.076	0.769
IQR	1060.7	22.4	988.9	188.8	.296	0.718
Fourth moment	8.32E+10	5.65E+09	8.84E+10	6.11E+09	.152	0.769
SD 5	81.9	29.4	16.8	19.2	.018 <sup>c</sup>	0.872
SD 9	99.7	49.3	19.5	17.3	.017 <sup>c</sup>	0.889
<b>GLCM</b>						
Entropy	0.728	0.079	0.673	0.159	.409	0.598
Contrast	113.1	20.2	84.1	16.9	.009 <sup>c</sup>	0.889
Correlation	0.573	0.026	0.569	0.012	.713	0.641
Energy	0.036	0.019	0.081	0.047	.025 <sup>c</sup>	0.812
Homogeneity	0.451	0.065	0.542	0.069	.020 <sup>c</sup>	0.821
<b>GLRL</b>						
SRE	0.177	0.007	0.157	0.009	<.001 <sup>c</sup>	0.966 <sup>d</sup>
LRE	0.197	0.010	0.173	0.012	.001 <sup>c</sup>	0.957
GLN	0.183	0.009	0.160	0.011	.001 <sup>c</sup>	0.949
RLN	0.196	0.010	0.173	0.012	.002 <sup>c</sup>	0.932
RP	353.0	11.2	364.5	11.0	.033 <sup>c</sup>	0.769
LGRE	345.5	13.0	362.1	11.9	.013 <sup>c</sup>	0.821
HGRE	345.7	11.0	361.1	10.9	.008 <sup>c</sup>	0.795
SRLGE	346.6	13.3	361.8	12.3	.021 <sup>c</sup>	0.778
SRHGE	233.7	53.0	318.9	97.1	.148	0.812
LRLGE	295.2	63.2	398.3	99.8	.063	0.838
LRHGE	224.6	51.8	300.0	68.7	.035 <sup>c</sup>	0.863
<b>Laws features</b>						
L1	1,147,168.4	304,127.9	932,846.3	323,413.5	.240	0.705
L2	388,225.1	181,690.3	261,871.2	121,634.4	.127	0.718
L3	86,706.2	39,484.9	64,844.4	29,506.6	.267	0.692
L4	360,755.3	119,837.4	271,851.5	115,764.8	.189	0.718
L5	131,888.8	59,529.3	87,225.0	40,960.5	.124	0.731
L6	73,453.5	30,964.3	57,877.2	26,256.9	.333	0.641
L7	56,206.3	24,679.3	440,57.0	20,439.3	.334	0.654
L8	88,611.4	36,512.6	75,856.4	35,468.9	.499	0.615
L9	153,050.3	71,083.8	119,186.0	51,125.5	.314	0.667
<b>GLGM</b>						
MGR	3.768	1.830	5.310	4.040	DNC	0.598
VGR	11,832.0	5859.3	16,712.0	12,777.3	DNC	0.598
Skewness	39.2	10.9	36.2	11.7	.888	0.504
Kurtosis	1757.0	971.6	1539.7	943.6	.965	0.504

**Note:**—MGR indicates mean gradients; VGR, variance of gradients; SRHGE, short-run high gray-level emphasis; LRLGE, long-run low gray-level emphasis; DNC, did not converge.

<sup>a</sup> Indicates a significant difference by the mixed linear regression model (Proc MIXED) to adjust the variance-covariance matrix among multiple values recorded for each patient ( $P < .05$ ).

<sup>b</sup> Using the generalized linear mixed model (GLIMMROC).

<sup>c</sup> Significant.

<sup>d</sup> The highest AUC among 41 texture features.

**On-line Table 2: [<sup>18</sup>F] FDG-PET/CT characteristics and texture parameters differentiating lymph node characterization in patients with head and neck squamous cell carcinoma without HIV infection (group 3 vs 4)**

Texture Parameter	Benign Nodes (n = 39)		Malignant Nodes (n = 22)		P Value <sup>a</sup>	AUC <sup>b</sup> (GLIMMROC)
	Mean	SD	Mean	SD		
Node characteristics						
Size (cm)	1.439	0.048	1.687	0.831	.079	0.643
Volume (cm <sup>3</sup> )	1.122	0.147	3.468	4.718	.001 <sup>c</sup>	0.702
SUVmax	3.228	0.315	6.438	4.811	.007 <sup>c</sup>	0.731
Histogram						
Mean	670.6	68.4	751.8	137.3	.022 <sup>c</sup>	0.705
Median	889.8	150.6	966.2	136.0	.110	0.674
SD	508.5	14.9	491.8	35.9	.051	0.684
Entropy	6.016	0.083	5.877	0.281	.093	0.669
Second SD	81.23	20.00	64.29	30.34	.067	0.710
Range	236.8	57.7	186.8	87.5	.063	0.704
Geometric mean	225.9	50.6	297.6	124.5	.020 <sup>c</sup>	0.704
Harmonic mean	24.12	4.21	29.57	9.42	.020 <sup>c</sup>	0.713
IQR	1064.3	63.9	865.0	360.2	.022 <sup>c</sup>	0.723
Fourth moment	8.71E+10	5.74E+09	9.41E+10	1.00E+10	.018 <sup>c</sup>	0.719
SD 5	70.3	18.4	56.3	27.1	.093	0.702
SD 9	76.0	26.4	56.4	30.1	.050	0.719
GLCM						
Entropy	0.720	0.089	0.654	0.211	.327	0.662
Contrast	102.5	18.2	81.8	28.3	.015 <sup>c</sup>	0.754
Correlation	0.571	0.023	0.585	0.054	.249	0.660
Energy	0.041	0.022	0.072	0.055	.034 <sup>c</sup>	0.712
Homogeneity	0.475	0.056	0.541	0.104	.029 <sup>c</sup>	0.735
GLRL						
SRE	0.164	0.011	0.154	0.019	.036 <sup>c</sup>	0.695
LRE	0.182	0.013	0.171	0.023	.058	0.690
GLN	0.169	0.013	0.160	0.020	.085	0.678
RLN	0.183	0.014	0.170	0.023	.034 <sup>c</sup>	0.698
RP	361.1	13.2	361.6	17.7	.897	0.593
LGRE	357.0	13.6	358.3	19.1	.762	0.596
HGRE	357.4	12.6	357.0	16.6	.911	0.604
SRLGE	356.6	14.2	358.4	19.5	.689	0.600
SRHGE	254.2	77.2	367.0	193.6	.016 <sup>c</sup>	0.739
LRLGE	322.6	91.4	469.8	231.9	.006 <sup>c</sup>	0.759
LRHGE	246.2	60.5	352.7	168.8	.003 <sup>c</sup>	0.760 <sup>d</sup>
Laws features						
L1	1,130,272.9	280,670.9	876,676.6	413,942.2	.024 <sup>c</sup>	0.722
L2	371,685.0	154,845.3	261,999.9	163,324.6	.028 <sup>c</sup>	0.721
L3	84,684.4	28,548.0	63,767.4	37,769.9	.042 <sup>c</sup>	0.692
L4	362,238.8	127,726.5	271,857.8	147,205.1	.034 <sup>c</sup>	0.712
L5	110,368.1	39,585.5	81,654.7	56,071.2	.047 <sup>c</sup>	0.695
L6	74,901.6	26,669.0	53,389.7	35,140.2	.028 <sup>c</sup>	0.713
L7	56,163.6	19,300.0	41,735.0	26,088.3	.040 <sup>c</sup>	0.697
L8	99,735.3	44,247.6	68,408.7	45,045.0	.029 <sup>c</sup>	0.717
L9	156,786.6	51,085.0	118,283.7	63,350.0	.033 <sup>c</sup>	0.704
GLGM						
MGR	5.114	5.517	7.193	10.405	.313	0.594
VGR	15,957.8	17,126.3	22,013.3	318,54.8	.315	0.590
Skewness	42.0	16.1	42.0	16.9	.978	0.594
Kurtosis	2167.3	1381.5	2196.1	1385.7	.991	0.597

**Note:**—MGR indicates mean gradients; VGR, variance of gradients; SRHGE, short-run high gray-level emphasis; LRLGE, long-run low gray-level emphasis.

<sup>a</sup> Indicates a significant difference by the mixed linear regression model (Proc MIXED) to adjust the variance-covariance matrix among multiple values recorded for each patient ( $P < .05$ ).

<sup>b</sup> Using the generalized linear mixed model (GLIMMROC).

<sup>c</sup> Significant.

<sup>d</sup> The highest AUC among 41 texture features.

**On-line Table 3: [<sup>18</sup>F] FDG-PET/CT characteristics and texture parameters of benign lymph nodes differentiating HIV statuses (group 1 vs 3)**

Parameter	HIV-Positive (n = 9)		HIV-Negative (n = 39)		P Value <sup>a</sup>	AUC <sup>b</sup> (GLIMMROC)
	Mean	SD	Mean	SD		
Node characteristics						
Size (cm)	1.400	0.300	1.439	0.297	.781	0.556
Volume (cm <sup>3</sup> )	0.547	0.363	1.122	0.921	.137	0.761
SUVmax	5.111	1.610	3.228	1.966	.111	0.872
Histogram						
Mean	624.4	74.6	670.6	68.4	.226	0.670
Median	774.0	217.9	889.8	150.6	.231	0.655
SD	506.4	13.4	508.5	14.9	.816	0.541
Entropy	6.012	0.048	6.016	0.083	.897	0.581
Second SD	93.76	28.70	81.23	20.00	.314	0.598
Range	273.7	82.9	236.8	57.7	.295	0.615
Geometric mean	199.6	44.7	225.9	50.6	.323	0.644
Harmonic mean	22.18	3.65	24.12	4.21	.341	0.627
IQR	1060.7	22.4	1064.3	63.9	.894	0.670
Fourth moment	8.32E+10	5.65E+09	8.71E+10	5.74E+09	.108	0.685
SD 5	81.9	29.4	70.3	18.4	.334	0.587
SD 9	99.7	49.3	76.0	26.4	.168	0.604
GLCM						
Entropy	0.728	0.079	0.720	0.089	.588	0.524
Contrast	113.1	20.2	102.5	18.2	.338	0.647
Correlation	0.573	0.026	0.571	0.023	.717	0.530
Energy	0.036	0.019	0.041	0.022	.633	0.553
Homogeneity	0.451	0.065	0.475	0.056	.454	0.587
GLRL						
SRE	0.177	0.007	0.164	0.011	.017 <sup>d</sup>	0.826 <sup>c</sup>
LRE	0.197	0.010	0.182	0.013	.027 <sup>d</sup>	0.818
GLN	0.183	0.009	0.169	0.013	.021 <sup>d</sup>	0.818
RLN	0.196	0.010	0.183	0.014	.061	0.772
RP	353.0	11.2	361.1	13.2	.119	0.678
LGRE	345.5	13.0	357.0	13.6	.044 <sup>d</sup>	0.715
HGRE	345.7	11.0	357.4	12.6	.012 <sup>d</sup>	0.749
SRLGE	346.6	13.3	356.6	14.2	.088	0.678
SRHGE	233.7	53.0	254.2	77.2	.728	0.576
LRLGE	295.2	63.2	322.6	91.4	.585	0.590
LRHGE	224.6	51.8	246.2	60.5	.506	0.618
Laws features						
L1	1,147,168.4	304,127.9	1,130,272.9	280,670.9	.983	0.517
L2	388,225.1	181,690.3	371,685.0	154,845.3	.891	0.505
L3	86,706.2	39,484.9	84,684.4	28,548.0	.906	0.524
L4	360,755.3	119,837.4	362,238.8	127,726.5	.922	0.529
L5	131,888.8	59,529.3	110,368.1	39,585.5	.310	0.605
L6	73,453.5	30,964.3	74,901.6	26,669.0	.897	0.524
L7	56,206.3	24,679.3	56,163.6	19,300.0	.992	0.510
L8	88,611.4	36,512.6	99,735.3	44,247.6	.597	0.567
L9	153,050.3	71,083.8	156,786.6	51,085.0	.879	0.562
GLGM						
MGR	3.768	1.830	5.114	5.517	.486	0.533
VGR	11,832.0	5859.3	15,957.8	17,126.3	.490	0.516
Skewness	39.2	10.9	42.0	16.1	.688	0.547
Kurtosis	1757.0	971.6	2167.3	1381.5	.467	0.550

**Note:**—MGR indicates mean gradients; VGR, variance of gradients; SRHGE, short-run high gray-level emphasis; LRLGE, long-run low gray-level emphasis.

<sup>a</sup> Indicates a significant difference by the mixed linear regression model (Proc MIXED) to adjust the variance-covariance matrix among multiple values recorded for each patient ( $P < .05$ ).

<sup>b</sup> Using the generalized linear mixed model (GLIMMROC).

<sup>c</sup> The highest AUC among 41 texture features.

<sup>d</sup> Significant.

**On-line Table 4: [<sup>18</sup>F] FDG-PET/CT characteristics and texture parameters of malignant lymph nodes differentiating between HIV statuses (group 2 vs 4)**

Parameter	HIV-Positive (n = 13)		HIV-Negative (n = 22)		P Value <sup>a</sup>	AUC <sup>b</sup> (GLIMMROC)
	Mean	SD	Mean	SD		
Node characteristics						
Size (cm)	1.892	0.690	1.687	0.831	.186	0.601
Volume (cm <sup>3</sup> )	2.535	2.218	3.468	4.718	.409	0.549
SUVmax	8.562	3.886	6.438	4.811	.192	0.673
Histogram						
Mean	735.3	75.2	751.8	137.3	.876	0.594
Median	1013.1	71.2	966.2	136.0	.288	0.566
SD	495.0	18.3	491.8	35.9	.927	0.598
Entropy	5.894	0.231	5.877	0.281	.947	0.615
Second SD	59.85	19.19	64.29	30.34	.503	0.577
Range	175.4	54.5	186.8	87.5	.521	0.580
Geometric mean	272.8	63.8	297.6	124.5	.706	0.591
Harmonic mean	26.79	4.76	29.57	9.42	.510	0.598
IQR	988.9	188.8	865.0	360.2	.459	0.615
Fourth moment	8.84E+10	6.11E+09	9.41E+10	1.00E+10	.200	0.692
SD 5	16.8	19.2	56.3	27.1	.371	0.584
SD 9	19.5	17.3	56.4	30.1	.321	0.591
GLCM						
Entropy	0.673	0.159	0.654	0.211	.886	0.601
Contrast	84.1	16.9	81.8	28.3	.945	0.587
Correlation	0.569	0.012	0.585	0.054	.468	0.661
Energy	0.081	0.047	0.072	0.055	.619	0.633
Homogeneity	0.542	0.069	0.541	0.104	.776	0.594
GLRL						
SRE	0.157	0.009	0.154	0.019	.833	0.610
LRE	0.173	0.012	0.171	0.023	.976	0.610
GLN	0.160	0.011	0.160	0.020	.942	0.608
RLN	0.173	0.012	0.170	0.023	.918	0.608
RP	364.5	11.0	361.6	17.7	.594	0.584
LGRE	362.1	11.9	358.3	19.1	.445	0.622
HGRE	361.1	10.9	357.0	16.6	.444	0.622
SRLGE	361.8	12.3	358.4	19.5	.519	0.619
SRHGE	318.9	97.1	367.0	193.6	.453	0.563
LRLGE	398.3	99.8	469.8	231.9	.379	0.615
LRHGE	300.0	68.7	352.7	168.8	.338	0.626
Laws features						
L1	932,846.3	323,413.5	876,676.6	41,3942.2	.868	0.601
L2	26,1871.2	121,634.4	261,999.9	163,324.6	.853	0.577
L3	64,844.4	29,506.6	63,767.4	37,769.9	.896	0.563
L4	271,851.5	115,764.8	271,857.8	147,205.1	.859	0.577
L5	87,225.0	40,960.5	81,654.7	56,071.2	.987	0.545
L6	57,877.2	26,256.9	53,389.7	35140.2	.917	0.577
L7	44,057.0	20,439.3	41,735.0	26,088.3	.993	0.573
L8	75,856.4	35,468.9	68,408.7	45,045.0	.872	0.580
L9	119,186.0	51,125.5	118,283.7	63,350.0	.856	0.577
GLGM						
MGR	5.310	4.040	7.193	10.405	DNC	0.633
VGR	16,712.0	12,777.3	22,013.3	31,854.8	.469	0.633
Skewness	36.2	11.7	42.0	16.9	.597	0.517
Kurtosis	1539.7	943.6	2196.1	1385.7	.515	0.552

**Note:**—MGR indicates mean gradients; VGR, variance of gradients; SRHGE, short-run high gray-level emphasis; LRLGE, long-run low gray-level emphasis; DNC, did not converge.

<sup>a</sup> Indicates a significant difference by the mixed linear regression model (Proc MIXED) to adjust the variance-covariance matrix among multiple values recorded for each patient ( $P < .05$ ).

<sup>b</sup> Using the generalized linear mixed model (GLIMMROC).

**On-line Table 5: P value and AUC results of the subanalysis of selected texture features without and with exclusion of obvious necrotic parts to differentiate benign versus malignant lymph nodes in patients with HIV (group 1 vs 2)**

Texture Parameter	Without Exclusion of Obvious Necrotic Components		With Exclusion of Obvious Necrotic Components	
	P Value <sup>a</sup>	AUC <sup>b</sup> (GLIMMROC)	P Value <sup>a</sup>	AUC <sup>b</sup> (GLIMMROC)
Histogram				
Mean	.017 <sup>c</sup>	0.872	.037 <sup>c</sup>	0.846
Median	.018 <sup>c</sup>	0.872	.058	0.829
2D SD	.017 <sup>c</sup>	0.872	.041 <sup>c</sup>	0.829
Range	.017 <sup>c</sup>	0.863	.037 <sup>c</sup>	0.829
Geometric mean	.032 <sup>c</sup>	0.829	.042 <sup>c</sup>	0.838
SD 5	.018 <sup>c</sup>	0.872	.043 <sup>c</sup>	0.821
SD 9	.017 <sup>c</sup>	0.889	.034 <sup>c</sup>	0.855
GLCM				
Contrast	.009 <sup>c</sup>	0.889	.031 <sup>c</sup>	0.846
Energy	.025 <sup>c</sup>	0.812	.045 <sup>c</sup>	0.795
Homogeneity	.020 <sup>c</sup>	0.821	.036 <sup>c</sup>	0.821
GLRL				
SRE	<.001 <sup>c</sup>	0.966 <sup>d</sup>	.011 <sup>c</sup>	0.872
LRE	.001 <sup>c</sup>	0.957	.021 <sup>c</sup>	0.889 <sup>d</sup>
GLN	.001 <sup>c</sup>	0.949	.020 <sup>c</sup>	0.872
RLN	.002 <sup>c</sup>	0.932	.026 <sup>c</sup>	0.889 <sup>d</sup>
RP	.033 <sup>c</sup>	0.769	.065	0.752
LGRE	.013 <sup>c</sup>	0.821	.048 <sup>c</sup>	0.778
HGRE	.008 <sup>c</sup>	0.795	.023 <sup>c</sup>	0.769
SRLGE	.021 <sup>c</sup>	0.778	.062	0.752
LRHGE	.035 <sup>c</sup>	0.863	.079	0.812

<sup>a</sup>Indicates a significant difference by the mixed linear regression model (Proc MIXED) to adjust the variance-covariance matrix among multiple values recorded for each patient ( $P < .05$ ).

<sup>b</sup>Using the generalized linear mixed model (GLIMMROC).

<sup>c</sup>Significant.

<sup>d</sup>The highest AUC among 41 texture features.

**On-line Table 6: P value and AUC results of the subanalysis of selected texture features without and with exclusion of obvious necrotic parts to differentiate benign versus malignant lymph nodes in patients without HIV (group 3 vs 4)**

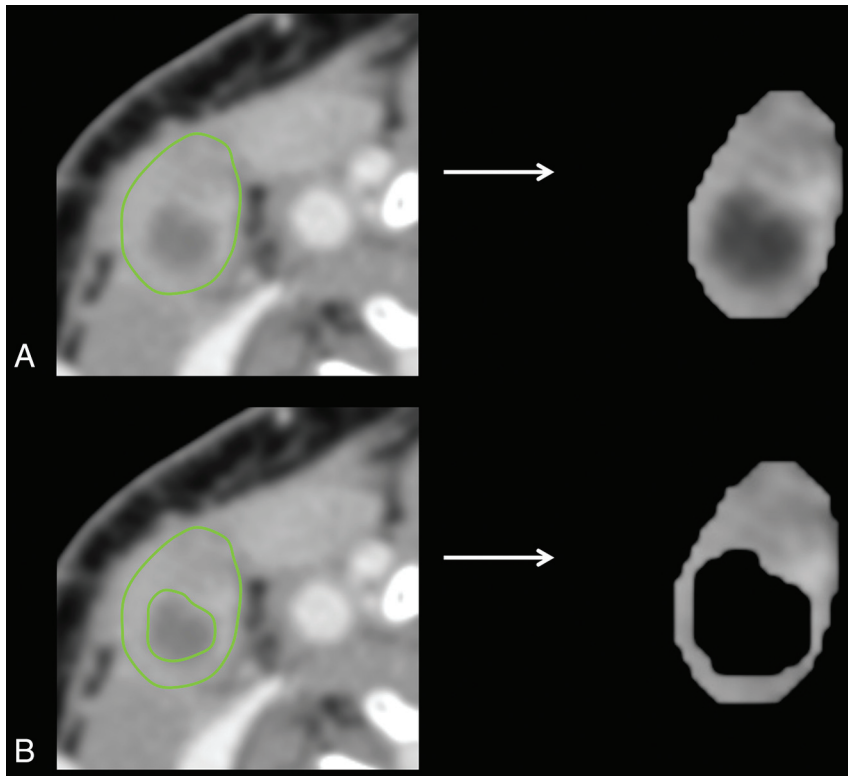
Texture Parameter	Without Exclusion of Obvious Necrotic Components		With Exclusion of Obvious Necrotic Components	
	P Value <sup>a</sup>	AUC <sup>b</sup> (GLIMMROC)	P Value <sup>a</sup>	AUC <sup>b</sup> (GLIMMROC)
Histogram				
Mean	.022 <sup>c</sup>	0.705	.059	0.672
Geometric mean	.020 <sup>c</sup>	0.704	.043 <sup>c</sup>	0.667
Harmonic mean	.020 <sup>c</sup>	0.713	.035 <sup>c</sup>	0.678
IQR	.022 <sup>c</sup>	0.723	DNC	0.682
Fourth moment	.018 <sup>c</sup>	0.719	.032 <sup>c</sup>	0.698
GLCM				
Contrast	.015 <sup>c</sup>	0.754	.047 <sup>c</sup>	0.720
Energy	.034 <sup>c</sup>	0.712	.037 <sup>c</sup>	0.679
Homogeneity	.029 <sup>c</sup>	0.735	.075	0.702
GLRL				
SRE	.036 <sup>c</sup>	0.695	.160	0.702
RLN	.034 <sup>c</sup>	0.698	.113	0.667
SRHGE	.016 <sup>c</sup>	0.739	.010 <sup>c</sup>	0.710
LRLGE	.006 <sup>c</sup>	0.759 <sup>d</sup>	.003 <sup>c</sup>	0.728 <sup>d</sup>
LRHGE	.003 <sup>c</sup>	0.760	<.001 <sup>c</sup>	0.726
Laws features				
L1	.024 <sup>c</sup>	0.722	.097	0.671
L2	.028 <sup>c</sup>	0.721	.110	0.677
L3	.042 <sup>c</sup>	0.692	.143	0.648
L4	.034 <sup>c</sup>	0.712	.137	0.666
L5	.047 <sup>c</sup>	0.695	.145	0.639
L6	.028 <sup>c</sup>	0.713	.112	0.660
L7	.040 <sup>c</sup>	0.697	.143	0.644
L8	.029 <sup>c</sup>	0.717	.124	0.670
L9	.033 <sup>c</sup>	0.704	.112	0.658

<sup>a</sup> Indicates a significant difference by the mixed linear regression model (Proc MIXED) to adjust the variance-covariance matrix among multiple values recorded for each patient ( $P < .05$ ).

<sup>b</sup> Using the generalized linear mixed model (GLIMMROC).

<sup>c</sup> Significant.





**ON-LINE FIGURE.** Workflow for image segmentation. Whole segmentation of lymph nodes was performed for each slice for primary analysis (A). For subanalysis in the inclusion or exclusion of necrosis parts of selected texture parameters differentiating among lymph node characterizations. Obvious necrotic or cystic areas within the lymph node were manually excluded (B).