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Early View

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# Computed tomography-based radiomics decodes prognostic and molecular differences in interstitial lung disease related to systemic sclerosis 

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Janssen-Cilag, had grant/research support from AbbVie, Protagen, Novartis Biomedical Research, received speaker fees from Boehringer-Ingelheim as well as congress support from Medtalk, Pfizer, Roche, Actelion, mepha, and MSD. In addition, B.M. has a patent mir-29 for the treatment of systemic sclerosis issued (US8247389, EP2331143).

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#### Abstract

Background: Radiomic features calculated from routine medical images show great potential for personalized medicine in cancer. Patients with systemic sclerosis (SSc), a rare, multi-organ autoimmune disorder, have a similarly poor prognosis due to interstitial lung disease (ILD).

Objectives: To explore computed tomography (CT)-based high-dimensional image analysis (radiomics) for disease characterisation, risk stratification, and relaying information on lung pathophysiology in SSc-ILD.

Methods: We investigated two independent, prospectively followed SSc-ILD cohorts (Zurich, derivation cohort, $n=90$; Oslo, validation cohort, $n=66$ ). For every subject, we defined 1'355 robust radiomic features from standard-of-care CT images. We performed unsupervised clustering to identify and characterize imaging-based patient clusters. A clinically applicable prognostic quantitative radiomic risk score (qRISSc) for progressionfree survival was derived from radiomic profiles using supervised analysis. The biological basis of qRISSc was assessed in a cross-species approach by correlation with lung proteomics, histological and gene expression data derived from mice with bleomycininduced lung fibrosis.


Results: Radiomic profiling identified two clinically and prognostically distinct SSc-ILD patient clusters. To evaluate the clinical applicability, we derived and externally validated a binary, quantitative radiomic risk score composed of 26 features, $q$ RISSc, that
accurately predicted progression-free survival and significantly improved upon clinical risk stratification parameters in multivariable Cox regression analyses in the pooled cohorts. A high qRISSc score, which identifies patients at risk for progression, was reverse translatable from human to experimental ILD and correlated with fibrotic pathway activation.

Conclusions: Radiomics-based risk stratification using routine CT images provides complementary phenotypic, clinical and prognostic information significantly impacting clinical decision-making in SSc-ILD.

Key Words: computed tomography, risk stratification, imaging biomarker, animal model, pathophysiology

Short Message. CT-based radiomics decodes phenotypic, prognostic and molecular differences in SSc-ILD and predicts progression-free survival with a significant impact on future clinical decision-making in SSc-ILD.

## Introduction

Despite the emergence of targeted therapies, interstitial lung disease (ILD), the leading cause of death in systemic sclerosis (SSc), remains a key challenge due to the high variability in patient-specific disease trajectories and progression rates [1]. This high interindividual variability warrants valid prognostic biomarkers for individual risk stratification and personalized management, which so far are lacking [2]. Traditionally, molecular data from tissue biopsies have been explored for precision medicine strategies. However, the invasiveness of tissue biopsies, the unsuitability for longitudinal assessments, the high risk of non-representative sampling due to spatial disease heterogeneity and the high costs associated with molecular profiling have mostly limited the clinical implementation. This applies even more to SSc-ILD, where lung biopsies are only exceptionally performed since they are not required for diagnosis [3]. Medical imaging, particularly high-resolution computed tomography (HRCT), is an integral part of the standard-of-care of SSc-ILD, as it allows both diagnosis and longitudinal monitoring of the entire lung pathology with high sensitivity [4-6].

Recently, high-dimensional image analysis, termed "radiomics", has opened novel avenues for imaging-based disease subtyping and outcome prediction [7-10]. Radiomic features are computationally retrieved, quantitative data derived from medical images, which describe the tissue in terms of its intensity, texture and advanced statistical properties [11]. Their unique and added value compared with visual or other quantitative imaging methodologies [12-14] lies in their ability to capture tissue phenotypes on different spatial scales ranging from the radiological/macroscopic to the molecular/microscopic level [8, 10, 15], which adds another dimension. Thereby, they
provide novel and complementary information compared to clinical reports, laboratory, and functional tests.

To address the high, unmet need for validated risk parameters, herein, we explored the potential of HRCT-based radiomics for disease characterization and outcome prediction in SSc-ILD.

## Methods

## Study Design and Datasets

We retrospectively investigated two independent prospectively followed cohorts of SScILD including 90 patients ( $76.7 \%$ female, median age 57.5 years) from the University Hospital Zurich (=derivation cohort) and 66 patients ( $75.8 \%$ female, median age 61.0 years) from the Oslo University Hospital (=validation cohort). All included patients met the following criteria: diagnosis of SSc according to the Very Early Diagnosis of Systemic Sclerosis (VEDOSS) [16] or the 2013 American College of Rheumatology//European League [17] against Rheumatism (ACR/EULAR) classification criteria [18], presence of ILD on HRCT, and availability of an HRCT scan fulfilling the predefined quality criteria (ref. Supplementary Methods). A summary of the patient's demographics and clinical characteristics at baseline for both study cohorts is given in Table 1.

A third dataset derived from an experimental cohort of 30 mice with bleomycin-induced lung fibrosis, a widely acknowledged preclinical model for ILD [19], was used for correlation studies with biological features, including proteomic, histological, and gene
expression data. For every subject, we defined and extracted 1'386 radiomic features (Supplementary File 1) from semi-automated segmented HRCT images, including 17 intensity, 137 texture, and 1'232 wavelet features using our in-house developed radiomics software Z-Rad. A detailed description of the study workflow is available in Fig.1. The local ethics committees approved the study (approval numbers: pre-BASEC-EK-839 (KEK-no.-2016-01515), KEK-ZH-no. 2010-158/5, BASEC-no. 2018-02165, BASEC-no. 2018-01873) and written informed consent was obtained from every patient.

## Statistical Analyses

Robustness of radiomic features against semi-automated lung delineation was assessed by intra- and inter-reader intraclass correlation (ICC) analysis, and unstable features (ICC $<0.75$ ) were excluded from further analyses, resulting in a final set of 1,355 robust radiomic features (Supplementary Fig.1). Unsupervised $k$-Means clustering was performed to identify homogeneous imaging-based patient clusters without a priori assumptions in the derivation cohort (Zurich; $n=90$ ). Next, a quantitative composite radiomic risk score (qRISSc) for progression-free survival (PFS) was built to evaluate the clinical applicability. PFS was defined as the time from the date of the HRCT to the date of the first occurrence of ILD progression (=relative decline in FVC\% predicted $\geq 15 \%$ ). qRISSc, composed of 26 features, was derived by two-step feature selection, including univariable Cox regression and cross-validated LASSO penalised regression, and was further developed into a binary score with an optimal cut-off value of 0.21 . Associations with clinical characteristics and PFS among the obtained patient clusters and qRISScbased risk groups were assessed by Fisher's Exact and Mann-Whitney $U$ test, or
univariable Cox regression, respectively. Multivariable Cox regression analyses with Hazards ratio (HR) and 95\% confidence interval (CI) and C-index were applied to analyse the predictive ability of conventional clinical risk factors and qRISSc for progressive ILD in the pooled cohorts $(n=156)$. The C-index is equivalent to the area under the curve in ROC analysis and can be used in Cox regression analysis [20]. Spearman correlation analysis with histological, gene expression and whole-lung proteomics data obtained from mice with bleomycin-induced lung fibrosis and pathway enrichment analysis was performed to define the biological basis of qRISSc.

A detailed description of the methods is provided in the online data supplement.

## Results

## Radiomic profiling captures clinical and prognostic differences among SSc-ILD patients

In a first discovery approach, we explored the radiomic phenotypes of the 90 SSc-ILD patients from the Zurich cohort with unsupervised clustering and examined their associations with clinical characteristics and patient outcome among the obtained clusters. Clustering of the 1,355 robust radiomic features revealed two distinct and stable patient clusters based on their radiomic profiles (Jaccard coefficient for cluster 1: 0.90 and for cluster 2: 0.82 , wherein 1 indicates perfect stability; Fig.2a/b). The differences in clinical characteristics were substantial (Fig. 2 and Supplementary Tab.1) with patients from cluster 2 ( $n=31$ ) having a significantly more impaired lung function ( $p<0.001$, Fig.2c), worse performance in the 6-min walk test (Fig.2c), and a higher frequency of pulmonary hypertension ( $p=0.001$, Fig.2a/c) than patients of cluster 1 ( $n=59$ ). Cluster 2 was also
significantly enriched for honeycombing ( $p=0.009$ ) as a radiological sign of more severe fibrotic lung remodelling.

Most notably, radiomic clusters did not stratify patients according to classical definitions of ILD severity, including limited and extensive disease extent as defined by HRCT analysis (HRCT threshold $<20 \%$ or $\geq 20 \%$ ) or PFTs (FVC $\geq 70 \%$ or $<70 \%$ ) [21], respectively. However, significant associations with both disease classifiers were detected ( $p=0.002$ and $p<0.001$, respectively).

Furthermore, the clusters did not differ in common SSc clinical, demographic and serological characteristics, including age, sex, SSc disease duration, active immunomodulatory therapy, the extent of skin involvement, autoantibody profiles or CRP levels [18, 22] (Fig. 2a/c and Supplementary Tab.1).

We next assessed whether the patients of the two clusters also differed in their outcome by survival analysis with the Kaplan-Meier estimator. Consistent with their worse disease phenotype, patients of cluster 2 showed a higher probability of faster disease progression and a decrease in PFS defined by either the time to a relative decline of $\geq 15 \%$ in FVC\% predicted $(p=0.001, H R=3.52,95 \% \mathrm{Cl}=(1.66-7.45)$, Fig.2d) or the time to decline assessed by a recently proposed FVC-DLCO composite index [22] ( $p=0.005, \mathrm{HR}=2.73$, $95 \% \mathrm{Cl}=(1.36-5.50)$, Fig.2e). In addition, a marginal association with time to visual disease progression on HRCT $(p=0.102)$ and overall survival ( $p=0.104$ ) was detected, suggesting a higher risk for visual ILD progression and all-cause death for patients of cluster 2 (Fig.2f/g).

Collectively, this exploratory analysis demonstrated that HRCT-based radiomic profiling captured clinical and prognostic differences in SSc-ILD that were complementary to the information provided by routine clinical, functional, and imaging tests.

## A clinically applicable radiomic risk score predicts progression-free survival in SSc-ILD and improves upon existing stratification parameters

Having found that radiomic features identified prognostically distinct SSc-ILD patient clusters, we next assessed the clinical applicability of radiomics for outcome prediction. To that end, we derived a prognostic composite radiomic signature as recently proposed by Lu et al. [10] for risk stratification in ovarian cancer using the Zurich cohort as a derivation cohort. The resulting quantitative radiomic risk score for PFS, qRISSc, comprising 26 radiomic features ( $n=4$ intensity, $n=9$ texture and $n=13$ wavelet features, Supplementary Tab.2), accurately stratified patients according to their risk for future lung decline with an optimal cut-off value of 0.21 . In the derivation cohort (Zurich), high-risk patients had a higher probability of earlier lung function decline than low-risk patients (median PFS time $=48.0$ months vs 82.30 months; Fig.3a). Most importantly, the final, binary version of qRISSc for risk stratification was independently confirmed. In the external validation cohort from Oslo, qRISSc-identified high-risk patients were at significant risk for progression (HR=5.14;95\% $\mathrm{Cl}=14-23.20$ ) with a median PFS time of 41.7 months compared with 88 months in the low-risk group ( $p=0.03$ ) (Fig.3b).

Similarly to what was previously shown for the two distinct radiomic patient clusters, qRISSc-stratified high- and low-risk patient groups differed in their clinical characteristics (Fig.3c, Supplementary Tabs. 3/4). High-risk patients consistently presented with worse lung function parameters and showed an association with the presence of pulmonary
hypertension, the extent of fibrosis on HRCT, and specific visual ILD HRCT patterns including honeycombing, and traction bronchiectasis (Fig.3c).

Next, we evaluated whether qRISSc improved upon previously proposed clinical risk factors for SSc-ILD progression, including age, sex, baseline FVC and DLCO, disease extent on HRCT, radiological subtype, SSc subtype, auto-antibody status, and CRP [2330 ] in both univariable and multivariable Cox regression analysis.

The univariable analysis only revealed baseline DLCO apart from qRISSc to be significantly and consistently associated with PFS among the two study cohorts (Fig.4a), yet with significantly weaker hazard ratios ( $\mathrm{HR}=0.95-0.97$, $\mathrm{p}<0.05$ ) than $q$ RISSc (HR=4.07-5.14, $\mathrm{p}<0.05$, Supplementary Tab. 5).

In multivariable Cox regression analysis of the pooled cohorts, the integration of qRISSc into models composed of different combinations of the clinically pertinent risk factors for SSc-ILD progression significantly improved the power of outcome prediction as measured by the C-index (Fig.4b, Supplementary Fig.2b) compared to the models exclusively composed of the clinical risk factors (Supplementary Tab. 6-8). In addition, in multivariable analysis same as in univariate analysis, qRISSc remained the strongest (HR=3.07-4.23) and often the only significant predictor in the combined models (Fig.4c/Supplementary Fig.2a, Supplementary Tabs. 7/8).

Of note, in the pooled study cohorts, qRISSc revealed to be also associated with other clinically used definitions of ILD progression, including different thresholds of FVC decline (i.e. an absolute FVC decline of $\geq 10 \%$ or $\geq 15 \%$, or a relative FVC decline of $\geq 5 \%$ or $\geq 10 \%$, $p<0.05$, Supplementary Fig3b-e), the FVC-DLCO composite index ( $p<0.001$, Supplementary Fig.3af), visual ILD progression on HRCT ( $p=0.031$, Supplementary

Fig.3bg), and overall survival ( $p<0.001$, Supplementary Fig.3eh). No significant association of qRISSc was found with an absolute FVC decline of $5 \%$ ( $p=0.16$,

## Supplementary Fig.3a).

Furthermore, we compared the prognostic performance of qRISSc to a quantitative score only composed of less complex, first order densitometric (intensity) features that were used in the past to quantify disease extent and progression in SSc-ILD [31-34]. While the intensity score was prognostic for future lung function decline in the derivation cohort ( $p=0.004$ ), it was not significant in the external validation cohort ( $p=0.08$ ), thus showing that the consideration of more abstract radiomic features provides additional important prognostic information (Supplementary Fig.4).

The clinical applicability of qRISSc was further confirmed by demonstrating that radiomic features, including qRISSc features, did not separate patients according to different imaging sites and settings employed in Zurich vs Oslo (Supplementary Fig.5; Supplementary Tab.9) [35].

In summary, our newly derived binary radiomic risk score, qRISSc, accurately predicted progression-free survival and significantly improved upon conventional risk stratification tools in two independent cohorts of SSc-ILD.

## The quantitative radiomic risk score is associated with fibrotic pathway activation on a molecular level

The added and complementary value of radiomic profiling might ultimately arise from the integrated in-depth analysis of tissue heterogeneity covering the spatial spectrum from the radiological/macroscopic to the molecular/microscopic level covering pathologic
information of the whole organ [36]. Therefore, we next assessed the association of qRISSc with specific pathophysiological processes to define the biological underpinning for the stratification into high- and low-risk patients.

Since lung biopsies are only rarely performed in SSc-ILD [3] and consequently, imagingmatched human biosamples were not available, we used a cross-species correlation approach, employing the mouse model of bleomycin-induced lung fibrosis as a model system for SSc-ILD. For this model, we have recently confirmed that radiomic signatures largely translate between experimental ILD in bleomycin-treated mice and ILD in SSc patients [37].

We firstly compared qRISSc values obtained in mice and our two patients' cohorts to ensure that qRISSc reverse translates from patients to mice. We found a very similar score distribution between all three datasets confirming the suitability of this animal model as a preclinical "radiomic surrogate" for human ILD (Fig.5a).

We then performed pathway enrichment analysis for significantly qRISSc-correlated proteins ( 634 out of 5,311 identified proteins (11.94\%) with rho $\geq|0.3|, \mathrm{p}<0.05$ ) derived from whole-lung tissue proteomics to reveal associations of qRISSc with molecular pathways and processes related to ILD (Fig.5d). We observed that pathways related to fibrosis development, particularly pathways associated with ECM organization and formation, were most significantly associated with qRISSc (Fig.5f/g). Consistently, the enriched biological processes that significantly correlated with qRISSc were also linked mainly to pro-fibrotic remodelling processes underlying ILD, including processes related to protein polymerization and ECM assembly (Fig.5e).

Among the highly and significantly qRISSc-correlated proteins were multiple ECM proteins, such as collagen 5a1, (CO5A1, rho $=0.48$ ), collagen $7 \alpha 1$ (CO7A1, rho=0.55), collagen 12a1 (COCA1, rho $=0.46$ ), collagen $15 \alpha 1$ (COFA1, rho=0.48), collagen $18 \alpha 1$ (COIA1, rho=0.47), filamin-C (FLNC, rho=0.66), and elastin (ELN, rho=0.63) as well as proteins required for ECM assembly and crosslinking, including members of the lysyl oxidase family, such as LOXL1 (rho=0.56) and LOXL2 (rho=0.68), or peroxidasin (PXDN, rho=0.64). In addition, proteins involved in TGF- $\beta$ activation, including latent-transforming growth factor beta-binding protein 2 (LTBP2: rho=0.50) and integrin $\beta 6$ (ITB6, rho $=0.55$ ), were strongly correlated with qRISSc (Fig.5g).

To complement the proteomic analysis, we additionally performed whole-slide digital histopathological and gene expression analysis of established fibrotic and inflammatory markers [38-40] (Fig.5b/c). In line with the proteomic data, qRISSc was also significantly correlated with fibrotic markers on a histological level with a higher qRISSc value corresponding to a higher fibrosis score (Ashcroft score [41], rho=0.55), and increased expression of aSMA, a marker for activated fibroblasts (rho=0.38). Consistently, qRISSc also showed significant association with the expression of fibrotic genes, including collagen $1 \alpha 1$ (Col1a1, rho $=-0.62$ ), collagen $3 \alpha 1$ (Col3a1, rho $=-0.59$ ), and fibronectin 1 (Fn1, rho=-0.65), where a lower $\Delta \mathrm{Ct}$ value and thus negative correlation indicates higher gene expression. Most notably, neither on the histological nor on the gene level, qRISSc correlated with inflammatory markers, such as the number of CD45+ inflammatory cells in tissue sections, interleukin 6 (I/6), and monocyte chemoattractant protein 1 (Mcp1) mRNA expression (Fig.5b/c).

Collectively, this demonstrates that qRISSc specifically reflects the underlying fibrotic remodelling processes in experimental ILD and suggests that fibrotic and not inflammatory pathway activation may be dominant in individuals identified by a high qRISSc score.

## Discussion

Herein, we showed that radiomics performed on standard-of-care HRCT images provided complementary clinical, prognostic and pathophysiologic information with great potential for risk stratification and outcome prediction in SSc-ILD.

Radiomic profiles captured ILD-specific differences based on image intensity, texture, and wavelet transformation and contained prognostic information. Clinical applicability was demonstrated by the accurate prediction of PFS in the combined SSc-ILD cohorts using a newly derived quantitative, binary radiomic risk score for SSc-ILD that can be calculated from a patient's routine HRCT scan. The integration of qRISSc into models composed of previously suggested risk factors [22-30] significantly improved the predictive power measured by the C-index. In all analyses, qRISSc was the strongest (HR=3.07-4.23) and often the only significant predictor in the combined models, thereby underlining the added value of qRISSc.

In both independent study cohorts, "high risk-patients" identified by clustering or risk scoring (qRISSc) were characterized by a more severe ILD phenotype, more compromised lung function, presence of pulmonary hypertension and specific visual ILD HRCT patterns including honeycombing and traction bronchiectasis, all of which have been discussed as potential risk factors in SSc-ILD [2, 42]. The fact that we did not
observe correlations with other suggested clinical risk factors such as, e.g. diffuse cutaneous SSc subset, older age, male sex, anti-topoisomerase 1-positivity [25, 43] or CRP [22] underlines that radiomic features capture lung-specific information independent of demographic and clinicoserological characteristics.

The benefit of radiomics might arise from the integrative and in-depth information obtained on whole lung pathology, where tissue heterogeneity is reflected on different spatial levels. In radiomic terms, spatial tissue heterogeneity is best described by texture features, which identify different image patterns by describing voxel intensities and their spatial arrangement [44]. In our study, most qRISSc features (e.g. "coarseness", "cluster tendency", "sum of variance") belonged to the class of texture features or of wavelet transformations thereof. Investigating the added value of qRISSc compared to a radiomic score composed only of intensity features further showed that inclusion of such more complex features is crucial for prognostic performance. Our results are in line with previous studies, where texture features outperformed first order (intensity) features for prognostic purposes $[8,10,15,33$ ] and where texture features were found to stratify patients according to disease severity [45]. In contrast to deep learning-based models, which require large datasets and represent "black box" approaches without an underlying biological rationale [46], radiomic features were shown to not only correlate with morphological but also with molecular tissue characteristics. This in-depth information provided by radiomics adds a new dimension to previously developed quantitative image analysis [12-14].

The hypothesis that radiomic features reflect the underlying pathophysiology was supported in our study, where we used a cross-species approach integrating imaging with molecular data to define the biological basis of qRISSc. In experimental ILD, a high qRISSc score was closely linked to specific fibrotic remodelling processes yet did not correlate with inflammation as assessed on a multiscale molecular level. The fibrotic pathway activation tied in with the worse outcome of the high-risk group of SSc-ILD patients identified by qRISSc [47]. The ability of radiomic markers to reflect the entire lung pathology is particularly attractive in a complex multi-organ disease with high molecular heterogeneity such as SSc [48]. The fact that radiomic features, including qRISSc, were reverse translatable from humans to mice demonstrates that well-characterized and representative animal models could prove valuable to test defined hypotheses in radiomics research, particularly for studying links with pathophysiology in rare diseases with low numbers of patients and limited access to biosamples.

Our study has some limitations, which despite the high-quality registry data from two independent, prospectively followed SSc cohorts from academic expert sites [49], mainly arise from the relatively low numbers of patients with this orphan disease. Appropriately, we did not impute missing data since the lack of data could not be assumed random. Furthermore, due to the modest sample size of our derivation cohort, we lacked the power to assess variable importance (measured by LASSO coefficients) and therefore assigned equal importance to each feature following a maximum-likelihood approach to construct qRISSc. Notably, despite this fact, we could fit significant multivariable models with good prognostic power on the combined cohort dataset, demonstrating the clinical applicability
of our quantitative radiomic risk score (qRISSc) and the potential to support clinical decision-making by improving upon existing risk parameters. Future large-scale collaborative studies designed to consider analytical methodologies for high-dimensional data will allow us to determine feature importance, perform proper weighting of score features, and evaluate further the added predictive value of radiomic signatures. Other limitations arise from exclusively focusing the analysis on SSc-ILD, which is relatively mild and of different aetiology compared with many other forms of fibrosing ILDs. Since the severity of ILD of the SSc patients included in our study was well in line with recently published data from the EUSTAR cohort [23], we consider our approach to apply to other SSc-ILD cohorts. Whether it applies to more severe forms and different aetiologies of fibrosing ILD, such as idiopathic pulmonary fibrosis, has yet to be determined.

Concerns about the reproducibility of radiomic features arise from their dependency on image acquisition and reconstruction methodologies and the intra-/inter-observer variability during image segmentation [50, 51]. In our study, radiomic features, including qRISSc, proved to be very stable against semi-automated lung segmentation. In addition, no batch-effects concerning different CT scanner types, scan and reconstruction protocols across two inhomogeneous cohorts of patients from independent sites occurred. This emphasizes the translational potential of our results and is a strong argument for the future clinical application of radiomics. We can, however, not exclude that the adherence to pre-defined quality criteria of the HRCT scan settings to ensure comparability between the two cohorts may have led to a specific selection bias of patients.

In conclusion, this work highlights radiomic profiling as a non-invasive means to capture the SSc-ILD heterogeneity by decoding clinical and prognostic differences and relaying pathophysiologic information. We provide a clinically applicable quantitative risk score for predicting PFS in SSc-ILD, which improves upon conventional risk factors. Whether it also allows the prediction of treatment response will be the subject of future studies.

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## Data Availability and Sharing

All data (clinical, radiomic, and molecular) and code for reproduction of the main findings of this study will be made publicly available after publication.

## Tables

Table 1: Summary of the patients' demographics and clinical characteristics for the two patient cohorts included in this study. Continuous variables are described as median $\pm$ interquartile range, and categorical variables are presented as absolute counts with relative frequencies (percent). P-values of univariate comparisons of baseline characteristics between the two cohorts are shown. Fisher's exact test was used to compare categorical, and Mann-Whitney U to compare continuous variables, respectively. Abbreviations: UIP = usual interstitial pneumonia, NSIP = nonspecific interstitial pneumonia, DIP = diffuse interstitial pneumonia, PAPsys $=$ systolic pulmonary artery pressure, FVC = forced vital capacity, FEV1 = forced expiratory volume in 1 second, DLCO = diffusing capacity for carbon monoxide, $6-M W T=6$-min walk test, $C R P=C$-reactive protein

| Characteristics | Zurich cohort $(\mathrm{n}=90)$ | Oslo cohort $(\mathrm{n}=66)$ | P-value |
| :---: | :---: | :---: | :---: |
| Age (years) | $57.5 \pm 17.8$ | $61.0 \pm 18.8$ | 0.641 |
| Sex |  |  |  |
| Male | 21 (23.3\%) | 16 (24.2\%) | 1.000 |
| Female | 69 (76.7\%) | 50 (75.8\%) |  |
| SSc disease duration (years)* | $5.0 \pm 8.2$ | $5.3 \pm 9.2$ | 0.874 |
| SSc subset (LeRoy 1988) |  |  |  |
| Limited cutaneous SSc | 41 (45.6\%) | 37 (56.1\%) | 0.041 |
| Diffuse cutaneous SSc | 42 (46.7\%) | 29 (43.9\%) |  |
| No skin involvement | 7 (7.8\%) | 0 (0.0\%) |  |
| Skin involvement |  |  |  |
| Limited cutaneous | 31 (34.4\%) | 37 (56.1\%) | <0.001 |
| Diffuse cutaneous | 43 (47.8\%) | 29 (43.9\%) |  |
| No skin involvement | 9 (10.0\%) | 0 (0.0\%) |  |
| Only sclerodactyly | 7 (7.8\%) | 0 (0.0\%) |  |
| Autoantibodies |  |  |  |
| Anti-centromere positive | 13 (14.4\%) | 7 (10.6\%) | 1.000 |
| Anti-topoisomerase I positive | 41 (45.6\%) | 24 (36.4\%) | 0.614 |
| Anti-RNA polymerase III positive | 7 (7.8\%) | 8 (12.1\%) | 0.261 |
| Anti-PMScl positive | 18 (20.0\%) | 4 (6.1\%) | 0.032 |
| FVC (\% predicted) | $87.5 \pm 33.9$ | $85.0 \pm 36.0$ | 0.605 |
| FVC $\geq 70 \%$ predicted | 64 (71.1\%) | 44 (66.7\%) | 0.851 |
| FVC $<70 \%$ predicted | 24 (26.7\%) | 15 (22.7\%) |  |
| DLCO (\% predicted) | $66.5 \pm 29.4$ | $61.0 \pm 29.0$ | 0.078 |
| FEV1 (\% predicted) | $88.7 \pm 31.2$ | $77.0 \pm 26.5$ | 0.088 |
| Pulmonary hypertension ${ }^{\dagger}$ | 20 (22.2\%) | 6 (9.1\%) | 0.048 |
| PAPsys (mmHg) ${ }^{\ddagger}$ | $26.0 \pm 10.0$ | $21.0 \pm 20.0$ | 0.028 |
| CRP (mg/l) | $3.1 \pm 5.6$ | $3.6 \pm 8.0$ | 0.259 |
| 6 min walk distance (m) | $511.0 \pm 161.0$ | n/a | n/a |
| $\mathrm{SpO}_{2}$ before 6-MWT (\%) | $96.0 \pm 2.0$ | n/a | n/a |
| $\mathrm{SpO}_{2}$ after 6-MWT (\%) | $95.0 \pm 7.0$ | n/a | n/a |
| Borg scale (unit; range 0-10) | $3.0 \pm 2.0$ | n/a | n/a |

Extent of lung fibrosis on CT

| $<20 \%$ | $50(55.6 \%)$ | $30(45.5 \%)$ | 0.257 |
| :--- | :--- | :--- | :--- |
| $\geq 20 \%$ | $40(44.4 \%)$ | $36(54.5 \%)$ |  |
| Ground glass opacification | $45(50.0 \%)$ | $42(63.6 \%)$ | 0.104 |
| Reticular changes | $87(96.7 \%)$ | $51(77.3 \%)$ | $<0.001$ |
| Traction bronchiectasis | $50(55.6 \%)$ | $27(40.9 \%)$ | 0.077 |
| Honeycombing | $22(24.4 \%)$ | $16(24.2 \%)$ | 1.000 |
| Bullae | $3(3.3 \%)$ | $4(6.1 \%)$ | 0.457 |
| Radiological subtype |  |  |  |
| $\quad$ NSIP | $49(54.4 \%)$ | $34(51.5 \%)$ |  |
| $\quad$ UIP\# | $37(41.1 \%)$ | $27(40.9 \%)$ | 0.602 |
| DIP | $1(1.1 \%)$ | $0(0.0 \%)$ |  |
| $\quad$ Unclassifiable | $3(3.3 \%)$ | $5(7.6 \%)$ |  |
| Immunomodulatory therapy ${ }^{\S}$ | $51(56.7 \%)$ | $28(42.4 \%)$ | 0.105 |
| Smoking status | $55(61.1 \%)$ | $24(36.4 \%)$ |  |
| $\quad$ Never | $21(23.3 \%)$ | $25(37.9 \%)$ | 0.025 |
| Former | $12(13.3 \%)$ | $5(7.6 \%)$ |  |
| $\quad$ Current | $20(22.2 \%)$ | $22(33.3 \%)$ | $\mathbf{0 . 0 0 9}$ |
| Died during follow-ups§ | $27(30.0 \%)$ | $11(16.7 \%)$ | 0.113 |
| Relative FVC decline $\geq 15 \%$ during follow-up | $21(23.3 \%)$ | $18(27.3 \%)$ | 0.316 |
| Visual HRCT progression during follow-up |  |  |  |

*Disease duration of SSc was calculated as the difference between the date of baseline CT and the date of manifestation of the first non-Raynaud's symptom.
${ }^{\dagger}$ Pulmonary hypertension was assessed by echocardiography or right heart catheterisation.
$\ddagger$ PAPsys was determined by right heart catheterisation.
"UIP includes the radiological diagnosis of both, "definite" and "probable" UIP.
§Immunomodulatory therapy included prednisone, methotrexate, rituximab, cyclophosphamide, mycophenolate mofetil, hydroxychloroquine, tocilizumab, imatinib, azathioprine, adalimumab, leflunomide, cyclosporine.
\$sCause of death included SSc-ILD, PAH, viral pneumonia, pulmonary embolism, septic shock, brain haemorrhage, caecal cancer, pancreatic carcinoma, lung cancer.

Figure Legends


Figure 1: Study workflow. In this study, we applied radiomics to three different datasets, including two independent cohorts of SSc-ILD patients from 1) the University Hospital Zurich (derivation cohort) and 2) the Oslo University Hospital (validation cohort), and one experimental ILD cohort, composed of 30 bleomycin-treated mice for association studies with biological features (i.e. proteomic, histological, and gene expression data). Patients were retrospectively selected based on the fulfilment of early/mild SSc according to the Very Early Diagnosis of Systemic Sclerosis (VEDOSS) criteria [16] or established disease according to the 2013 American College of Rheumatology//European League against

Rheumatism (ACR/EULAR) classification criteria [18], presence of ILD on HRCT as determined by a senior radiologist, and pre-defined quality criteria for their HRCT images. For every subject, in total, 1,386 radiomic features were extracted from semi-automated segmented CT images, including 17 intensity, 137 texture, and 1,232 wavelet features using our in-house developed software Z-Rad. Filtering of robust radiomic features (ICC $\geq 0.75$ ), unsupervised clustering, and construction of the quantitative radiomic ILD risk score (qRISSc) for progression-free survival in SSc-ILD were performed in the Zurich cohort. Independent and external validation of the built qRISSc was performed using the Oslo cohort.


Figure 2: Unsupervised $k$-Means clustering of radiomic data from SSc-ILD patients.
(a) Heatmap summarizing the $k$-Means clustering results (Zurich cohort, $n=90$ ). Before clustering, radiomic features were $z$-scored. Associations between the two identified
radiomic patient clusters with categorical clinical parameters (above) and visual ILD patterns depicted on HRCT (below) are shown. (b) $k$-Means cluster plot indicating two stable clusters (Jaccard coefficient for cluster 1 (blue): 0.90 and for cluster 2 (yellow): 0.82, wherein 1 indicates perfect stability). (c, first row) Boxplots comparing lung function parameters between the two clusters, including FVC\% predicted, DLCO\% predicted and FEV1\% predicted. (c, second row) Boxplots showing the systolic pulmonary artery pressure (PAPsys) and CRP values and the 6-min walk distance (6-MWD) from the 6min walk test for both clusters. (c, third row) Boxplots indicating the Borg scale of perceived exertion (scale 0-10, $0=$ no exertion, 1 = very weak, 2 = weak, 3 = moderate, $5=$ strong, 7 = very strong, $10=$ extreme exertion $)$, and oxygen saturation $(\mathrm{SpO} 2)$ at the beginning and end of the test per patient cluster. (d) Kaplan Meier curves for progressionfree survival (PFS) defined as either the time to a relative FVC decline $\geq 15 \%$, or (e) the time to the FVC-DLCO composite index (FVC-DLCO composite index = relative decrease in FVC\% predicted of $\geq 15 \%$, or a relative decline in FVC\% predicted of $\geq 10 \%$ combined with DLCO\% predicted of $\geq 15 \%$ according to [22]), or (f) the time to visual ILD progression on HRCT. (g) Kaplan Meier plot for overall survival (OS) defined as the time to all-cause death. The Hazard ratios (HR) with $95 \%$ confidence intervals and $p$-value of the univariate Cox regression are shown.

Abbreviations: $\mathrm{SSc}=$ systemic sclerosis, $\mathrm{P}(\mathrm{A}) \mathrm{H}=$ pulmonary (arterial) hypertension, FVC = forced vital capacity, FEV1 = forced expiratory volume in 1 second, DLCO = diffusing capacity for carbon monoxide, $C R P=C$-reactive protein, $F=$ female, $M=$ male, $D I P=$ diffuse interstitial pneumonia, NSIP = nonspecific interstitial pneumonia, UIP = usual interstitial pneumonia, $G G O=$ ground glass opacification, $T B=$ traction bronchiectasis

exact test was used for comparison of categorical and Mann-Whitney $U$ test to compare numerical variables, respectively.


Figure 4: Prognostic performance of qRISSc compared to other risk factors for SSc-ILD progression. (a) Bar plot indicating the results of the univariable Cox regression analysis of qRISSc compared to previously proposed clinical risk factors of SSc-ILD progression. (b) Bar plot comparing the predictive power (C-index) of the multivariable models composed of the clinical risk factors of SSc-ILD progression alone (clinical models) versus models also incorporating qRISSc (combined models). Two-way ANOVA was used to compare model performances. Model 1: Age + Male Sex + Baseline FVC
(\% predicted) + Anti-Topoisomerase $1 \pm$ qRISSc, Model 2: Age + Male Sex + Baseline FVC (\% predicted) $\pm q$ RISSc, Model 3: Age + Male Sex + Baseline DLCO (\% predicted) + HRCT threshold $\geq 20 \% \pm q R I S S c$, Model 4: Age + Male Sex + Baseline FVC (\% predicted) + HRCT threshold $\geq 20 \%$ + UIP subtype $\pm$ qRISSc, Model 5: Age + Male Sex + Baseline FVC (\% predicted) + diffuse cutaneous involvement $\pm$ qRISSc, Model 6: Age + Male Sex + Baseline FVC (\% predicted) + CRP $\pm q R I S S c$. Models 1 and 4 (exclusively composed of clinical covariates) were overall not significant. (c) Bar plot summarising the FDR-corrected results of the multivariable Cox regression analysis incorporating qRISSc (combined models) versus multivariable models composed of clinical risk factors alone (clinical models). Bars represent hazard radios for each predictor in each model, whereas colours indicate the $p$-value of the predictors corrected for multiple testing using false discovery rate (FDR). Covariates for uni- and multivariable Cox regression were selected based on literature evidence [2] and expert opinion.


Figure 5: Correlation analysis of qRISSc with molecular data in experimental ILD.
(a) Score distribution across the three datasets, demonstrating a similar qRISSc distribution between mice of the bleomycin-induced lung fibrosis model ( $n=30$ ) and SScILD patients (Zurich, $n=75$; Oslo, $n=66$ ). (b) Representative histological images of bleomycin-treated mice with low and high qRISSc that were stained for the myofibroblast marker alpha-smooth muscle actin ( $\alpha$ SMA, upper panel), the pan-leukocyte marker CD45
(middle panel) and picrosirius red to visualize collagen fibres (PSR, collagen = red, lower panel). Sections of the entire right caudal lobe (scale bar $=1 \mathrm{~mm}$ ) with higher magnification views (100x magnification, scale bar $=100 \mu \mathrm{~m}$ ) are shown. (c) Correlation matrix for qRISSc with histological parameters (percentage of aSMA and CD45 positivity, and Ashcroft score), and messenger RNA (mRNA) expression of inflammatory (II6, Mcp1) and fibrotic (Col1a1, Col3a1, Fn1) genes. A lower $\Delta C t$ value and thus negative correlation indicates higher gene expression. The Spearman correlation coefficient rho is shown. Non-significant associations are depicted in white. (d) Volcano plot for qRISSc-correlated proteins. Proteins with rho $\geq|0.3|$ and $p<0.05$ are highlighted in red. (e) Bar plot of the top 10 (based on p-value) biological processes associated with qRISSc. (f) Bar plot of the top 10 (based on p-value) pathways associated with qRISSc. (g) Heatplot indicating the top enriched proteins per molecular pathway. For (e-g), the most important associations are highlighted in purple. For pathway analyses, only proteins with rho $\geq|0.3|$ and $p<$ 0.05 were considered.ss

## Data Supplement

## Supplementary Methods

## Patient Cohorts and Clinical Data

In this study, 90 patients (76.7\% female, median age 57.5 years) from the University Hospital Zurich's (derivation cohort) and 66 patients ( $75.8 \%$ female, median age 61.0 years) from the Oslo University Hospital's prospective SSc patient cohorts (external validation cohort) were included. Both centres are part of the EUSTAR (European Scleroderma Trial and Research) network [1]. Patients were retrospectively selected based on the following criteria:
(1) Fulfilment of diagnosis of early/mild SSc according to the Very Early Diagnosis of Systemic Sclerosis (VEDOSS) criteria [2] or established disease according to the 2013 American College of Rheumatology//European league against rheumatism (ACR/EULAR) classification criteria [3],
(2) Presence of ILD on HRCT as determined by a senior radiologist, and
(3) Availability of an HRCT scan with the following settings:
(a) Slice thickness between 0.6 and 3 mm ,
(b) One of the following lung kernels available (B60f, B70f, BI64d, LUNG),
(c) Filtered-back projection as reconstruction algorithm, and
(d) CT image acquired in full inspiration.

For each patient, demographic and clinical parameters, including age, sex, SSc disease duration and subset, the extent of skin involvement, autoantibody status, CRP levels, presence of pulmonary hypertension according to right heart catheterisation or echocardiography as judged by the local investigators, and pulmonary function test (PFT) parameters were retrieved from the local patients' records. The recorded PFT parameters (expressed as \% predicted values) included forced vital capacity (FVC), forced expiratory volume in 1 second (FEV1), and diffusing capacity for carbon monoxide (DLCO). Data from the 6 -minute walk test ( $6-\mathrm{MWT}$ ), including walk distance, oxygen saturation (\% $\mathrm{SpO}_{2}$ ) before and after the test, and Borg scale of perceived exertion (Borg CR-10) [4], were only available for the derivation cohort. Disease duration of SSc was calculated as the difference between the date of first available CT and the date of manifestation of the first non-Raynaud's symptom. The follow-up period was defined as the time interval between the baseline visit and the last available follow-up visit for every patient. The mean follow-up time for the derivation cohort was $66.1( \pm 30.1)$ months and $43.9( \pm 30.9)$ months for the external validation cohort. All outcome events occurring in this period were considered in this study. As outcomes for SSc-ILD, we selected progression-free survival, which was defined as the time from the date of the HRCT to the date of the first occurrence of ILD progression. The primary endpoint for progression-free survival was the progression of ILD defined as a relative decline in FVC\% predicted from baseline to follow-up of $\geq 15 \%$ based on the criteria recommended for idiopathic pulmonary fibrosis trials by the American Thoracic Society/European Respiratory Society and previous clinical trials in SSc-ILD [5-8]. As a secondary and exploratory endpoint, we used a recently proposed FVC-DLCO composite index, in which progression is defined as either
a relative decrease in FVC\% predicted of $\geq 15 \%$ or a relative decline in FVC\% predicted of $\geq 10 \%$ combined with $\mathrm{DLCO} \%$ predicted of $\geq 15 \%$ [ 9 ]. As further exploratory and nonlung function-based outcome measures for SSc-ILD, we selected 1) visual ILD progression on HRCT and 2) overall survival, which were defined as the time from the date of the HRCT to the date of the first occurrence of visual ILD progression on HRCT or all-cause death, respectively.

The vital status was determined based on the electronic patients' records.
The local ethics committees approved the study (approval numbers: pre-BASEC-EK-839 (KEK-no.-2016-01515), KEK-ZH-no. 2010-158/5, BASEC-no. 2018-02165, BASEC-no. 2018-01873) and written informed consent was obtained from every patient.

## Pulmonary Function Tests

In brief, spirometry, body plethysmography, and DLCO measurements were performed by trained technicians in the Department of Pneumology of the University Hospital Zurich and Oslo. Measures included, among others FVC, FEV1, TLC, VC, and DLCO. The PFTs were performed following established protocols [10-13]. Since the PFTs were performed as part of the routine diagnostics, the respective pulmonologist on call interpreted the results and provided a written report, including the measured values and their interpretation.

## HRCT Image Acquisition and Visual CT Analysis

The settings used for the acquisition of HRCT images are summarized in Supplementary Table 9. All HRCT images were assessed for the presence of characteristic visual
features of ILD, including ground glass opacification (GGO), reticular changes, traction bronchiectasis, emphysema, and honeycombing. In addition, the radiological subtype (usual interstitial pneumonia (UIP), nonspecific interstitial pneumonia (NSIP), or diffuse interstitial pneumonia (DIP)) was determined. UIP includes the radiological diagnosis of both, "definite" and "probable" UIP [14, 15]. The extent of lung fibrosis was determined visually by the clinical radiologists in charge of routine diagnostics. All sections from the lung apex to the hemidiaphragm were assessed. All CT scans from both cohorts were reevaluated by a long-standing expert on chest radiology (T.F.). The extent of lung fibrosis on HRCT, defined as the presence of reticular changes and/or honeycombing, was categorized as either $<20 \%$ or $\geq 20 \%$ in relation to the total lung volume. For visual analysis of ILD progression on HRCT, all available follow-up HRCT scans from every patient were extracted from the electronic patient's records. Due to the differences in the types of scanners and kernels used, ILD progression on HRCT was visually assessed by a senior radiologist and expert in chest radiology (T.F.). ILD progression was defined as an increase in ground-glass, reticulation or honeycombing including more than a second lobule or the transition of ground-glass into reticulation or honeycombing. All visual analyses were performed using a standard picture archiving and communication system workstation (Impax, Version 6.5.5.1033; Agfa-Gevaert, Mortsel, Belgium) and a high definition liquid crystal display monitor (BARCO; Medical Imaging Systems, Kortrijk, Belgium).

## CT Segmentation and Extraction of Radiomic Features

The left and right lung lobes of each patient were semi-automatically segmented by two readers (J.S., M.B.) using the "region grow" function (lower threshold -950 HU, upper threshold: - 300 HU ) of MIM software (version 6.9.2, MIM Software Inc., Cleveland, Ohio, United States). Manual corrections were applied when computationally defined tissue borders did not coincide with the actual lung borders. In addition, pulmonary hilar vessels and atelectatic lung areas were carefully excluded from the regions of interest.

Radiomic analysis was performed on merged structures of both lung lobes using the inhouse developed software Z-Rad based on Python programming language 2.7. For radiomics analysis, CT images were resized to isotropic voxels of 2.75 mm and discretized to a fixed bin size of 50 HU . In total, 1,386 radiomic features were calculated per lung (HU limits: -1000 HU to 200 HU ), corresponding to the following radiomic feature classes:
(1) Intensity or histogram features $(n=17)$,
(2) Texture features $(n=137)$ of the Gray Level Co-occurrence Matrix ( $n=52$; GLCM), the Neighborhood Gray Tone Difference Matrix ( $n=5$; NGTDM), the Gray Level Run Length Matrix $(n=32)$; GLRLM), the Gray Level Size Zone Matrix ( $n=16$; GLSZM), the Gray Level Distance Matrix ( $n=16$; GLDZM) and the Neighboring Gray Level Dependence Matrix ( $n=16$; NGLDM), and
(3) Wavelet features $(n=1,232)$.

The first class of radiomic features relates to the histogram or distribution of voxel intensities using first-order statistics (e.g. mean, standard deviation, skewness and kurtosis) and quantifies tissue intensity characteristics. The second category, including the texture features, describes the intra-tissue heterogeneity by calculating the statistical, spatial inter-relationship between neighbouring voxel intensities [16]. The third group of features, the wavelet features, calculates the intensity and texture features after wavelet decompositions of the original image using eight different coiflet filters (high-pass to lowpass filters), thereby focusing the features on different frequency ranges [17].

A list of all radiomic features is provided in Supplementary File 1. Radiomic feature definitions were based on the Imaging Biomarker Standardization Initiative report by Zwanenburg et al. [18].

## Assessment of Radiomic Feature Stability

Intraclass correlation (ICC) analysis was performed to assess the stability of radiomic features against intra- and inter-operator variability in the semi-automated segmentation process (Supplementary Figure 1). For inter-operator ICC analysis, three examiners (J.S., M.B., C.B.), and for intra-operator ICC analysis, one examiner (J.S.) twice, independently contoured 15 randomly selected SSc patients from the derivation (Zurich) cohort, and radiomic features were extracted from the multiple delineation structures. The ICC coefficient for every radiomic feature was quantified using two-way mixed effect models and applying the "consistency" method (ICC(3,1)) according to [19] using "irr" package of
R. Only features with good reproducibility defined as ICC $\geq 0.75$ [20] were considered in further analyses.

## Unsupervised Clustering

Unsupervised clustering was performed to identify groups of patients with similar radiomic feature patterns in the derivation cohort (Zurich; $\mathrm{n}=90$ ). After confirmation of data clusterability by visual assessment of cluster tendency (VAT) and calculation of the Hopkin's statistic $H$ (with $H>0.5$ indicating clusterability) [21], the $k$-Means clustering algorithm [22] was applied to the z-scored radiomic data. Only robust radiomic features $(I C C \geq 0.75)$ entered the cluster analyses. The optimal number of clusters was determined by varying the number of $k$-clusters between 2 and 10 and selecting the optimal $k$ concerning best visual separation and stability as determined by Jaccard bootstrapping ( $\mathrm{n}=1,000$ iterations).

## Building a Quantitative Radiomic Risk Score for SSc-ILD

The Zurich cohort was used as a derivation cohort to build and train the radiomic risk score for ILD progression (qRISSc). Patients with no follow-up and survival data available on the electronic patients' records were excluded from the analysis, resulting in a final dataset of 75 patients. For score building, we adapted a recently described approach by Lu et al. [23] for $z$-scored, radiomic features. Following Lu and colleagues, we selected radiomic features in two steps: 1) Cox regression and 2) penalized LASSO regression using "cox" family with 10 -fold cross-validation. In the first step, we applied univariate Cox regression per radiomic feature only considering features with FDR of $p<0.005$. Features
selected in step 1) underwent further reduction by LASSO. Only features with non-zero coefficients were retained, thereby removing strongly inter-correlated, redundant features. Since limited by the modest sample size of the derivation cohort, we did not perform weighting of score features according to the coefficients from LASSO regression and assigned the same importance to each feature by dividing each standardized feature by the total number of features $j$. The final radiomic score was constructed as follows: $q R I S S c=\sum_{i=1}^{j} \alpha_{i} f_{i}$ with $\alpha=\frac{1}{j}$ being the feature weight and $f$ being the values of $z$ transformed radiomic features.

After having selected features in steps 1) and 2) we searched for the significant cut-off value for Cox regression by applying the "cox" function from the "cutoff" package of $R$. Due to the modest sample size, we searched for two groups, i.e. "low" and "high" risk patients composed of at least $25 \%$ of subjects for the minority group. We selected the one that was significant after correction for multiple testing from the proposed pairs of cutoffs. Once a score was built, we fitted a univariate Cox regression model on the external validation cohort (Oslo). Kaplan-Meier plots were used to visualize the Cox regression results. As a reference model to qRISSc, we analogously build a radiomic score composed only of less complex, first-order densitometric (intensity) features, which have been previously explored for the quantification of disease extent and progression of SScILD [24-27].

Multivariable Cox regression analyses were applied to analyse the predictive ability of conventional risk factors and qRISSc for progressive ILD in the pooled cohorts ( $n=156$ ). Ten events per variable were required in the multivariable analyses, and the variables were selected based on literature evidence and expert opinion [28-30]. We reported the
concordance index (C-index) as the general assessment of the quality of the model, the p-value of the whole model, and the hazard ratio (HR) with $95 \%$ confidence intervals for the quantitative radiomic risk score. The C-index is equivalent to the area under the curve in ROC analysis and can also be used in Cox regression analysis [31].

## Association Analyses with Clinical Characteristics

Association analyses were performed to explore associations of identified patient groups (k-Means clusters and risk groups) with clinical parameters.

Fisher's exact test was used to compare categorical, and Mann-Whitney U for comparison of continuous clinical variables, respectively.

## Association Analyses with Biological Data

To reveal possible associations of the radiomic risk score with the underlying pathophysiology of ILD, correlation analysis with histological, proteomics and quantitative PCR data was performed. Since lung biopsies are only very rarely performed in SSc-ILD and thus matched patient tissue samples have not been available for molecular analyses, we conducted a cross-species correlation approach, using the mouse model of bleomycin-induced lung fibrosis as a model system for SSc-ILD. For this animal model, we have recently confirmed the transferability of radiomics signatures between mice and humans [32].

## Animal Model of Experimental ILD

We applied the well-established preclinical model of bleomycin-induced lung fibrosis to model human SSc-ILD as described previously [33, 34]. In brief, 30 female, 8 -week-old C57BL/6J-rj (Janvier Labs, Le Genest-Saint-Isle, France) were randomized and intratracheally instilled with 2 U/kg bleomycin sulfate (BLM, Baxter 15,000 I.U., pharmacy of the canton Zurich, Switzerland) to induce ILD. For molecular and histological analyses, mice were sacrificed with carbon dioxide and subsequently transcardially perfused with ice-cold phosphate-buffered saline (PBS) solution to remove residual blood. All animal experiments were approved by the cantonal veterinary office (approval number $\mathrm{ZH} 235-$ 2018) and performed in strict compliance with the Swiss law for animal protection.

## Proteomic Data

For proteomic analyses, frozen left lung lobes (blood-free) collected from PBS-perfused BLM-treated mice were homogenized in 8 M urea/100mM Tris ( pH 8.0 ) buffer supplemented with protease inhibitors using the FastPrep system (MP Biomedicals). After reduction and alkylation, and overnight protein precipitation with ice-cold acetone, 10 ug of the cleaned protein mixture were digested into peptides using a two-step digestion protocol (LysC for 2 h at $37^{\circ} \mathrm{C}$ followed by Trypsin at room temperature overnight) and then subjected to liquid-chromatography-based tandem mass spectrometric analysis (LCMS/MS). For LC-MS/MS, mouse samples were randomly allocated to the analysis by loading 800 ng onto a pre-column (C18 PepMap 100, $5 \mu \mathrm{~m}, 100 \mathrm{~A}, 300 \mu \mathrm{~m}$ i.d. x 5 mm length) at a flow rate of $50 \mu \mathrm{~L} / \mathrm{min}$ with solvent $\mathrm{C}(0.05 \%$ TFA in water/acetonitrile 98:2).

After loading, peptides were eluted in backflush mode onto a home packed analytical Nano-column (Reprosil Pur C18-AQ, $1.9 \mu \mathrm{~m}, 120 \mathrm{~A}, 0.075 \mathrm{~mm}$ i.d. $\times 500 \mathrm{~mm}$ length) using an acetonitrile gradient of $5 \%$ to $40 \%$ solvent B ( $0.1 \%$ Formic Acid in water/acetonitrile $4,9: 95$ ) in 180 min at a flow rate of $250 \mathrm{~nL} / \mathrm{min}$. The column effluent was directly coupled to a Fusion LUMOS mass spectrometer (Thermo Fisher, Bremen; Germany) via a nano-spray ESI source. Data acquisition was done in data-dependent mode with precursor ion scans recorded in the orbitrap with a resolution of $120^{\prime} 000$ (at $\mathrm{m} / \mathrm{z}=250$ ) parallel to top speed HCD fragment spectra of the most intense precursor ions in the Linear trap for a cycle time of 3 seconds. Mass spectrometry data were processed by MaxQuant software, and set parameters are available in Supplementary Table 10. MaxQuant experimental design was such that the two repeated injections were combined, and match between runs allowed between all samples.

## Histological and Immunohistochemical Data

Formalin-fixed paraffin-embedded lung sections ( $4 \mu \mathrm{~m}$ thick) from all BLM-treated mice were stained with Hematoxylin and Eosin (HE) for the examination of the overall tissue architecture, and the presence of cellular infiltrates and stained with Picrosirius Red (PSR) to visualize collagen deposition using standard protocols. Furthermore, specific immunohistochemical stainings for the pan-leukocyte marker CD45 and the myofibroblast marker alpha-smooth muscle actin (aSMA) were performed as described in [33, 34]. Whole slide images of histological and immunohistological stainings were obtained with the AxioScan.Z1 slide scanner (Zeiss, Feldbach, Switzerland) in bright-field mode using a Plan-Apochromat 20x/0.8 M27 objective. Stainings were automatically quantified on
whole slide images using the open-source Orbit Image Analysis software (License: GPLv3; Actelion Pharmaceuticals Ltd) as described in [35, 36]. Furthermore, for histopathological scoring of pulmonary fibrosis, the Ashcroft score [37] was applied on PSR stained lung sections by two experienced blinded examiners (J.S., M.B.) as previously described [38].

## Gene Expression Data

Total RNA was isolated from perfused cranial lobes of the right mouse lung with the RNeasy Tissue Mini Kit from Qiagen (Hombrechtikon, Switzerland), reverse-transcribed into complementary DNA, and messenger RNA (mRNA) expressions of inflammatory (II6, Mcp1) and fibrotic (Col1a1, Col3a1, Fn1) genes were analyzed by SYBR Green quantitative real-time PCR as described in [33]. mRNA expression was expressed as $\Delta \mathrm{Ct}$ values (Ct (gene-of-interest) - Ct (reference gene)) with 60S acidic ribosomal protein P0 ( $\mathrm{Rp} / \mathrm{p} 0$ ) as a reference gene, with a lower $\Delta \mathrm{Ct}$ indicating higher target gene expression. A list of primers used in this study is provided in Supplementary Table 11.

## Micro-CT imaging, Radiomics Analysis and Score Calculation in Mice

CT images were acquired in free-breathing mice with prospective respiratory gating on a state-of-the-art micro-CT scanner (Skyscan 1176; Bruker-microCT, Kontich, Belgium) under isoflurane anaesthesia at the following time points: day $0,7,14,21,28$, and 35 . The following scan parameters were used: tube voltage 50 kV , tube current $500 \mu \mathrm{~A}$, filter Al 0.5 mm , averaging (frames) 3, rotation step 0.7 degrees, sync with event $50 \mathrm{~ms}, \mathrm{X}$-ray tube rotation 360 degrees, resolution $35 \mu \mathrm{~m}$, and slice thickness $35 \mu \mathrm{~m}$. Images were reconstructed with NRecon reconstruction software (v.1.7.4.6; Bruker) using the built-in
filtered-back projection Feldkamp algorithm and applying misalignment compensation, ring artefact reduction, and a beam hardening correction of $10 \%$ to the images.

Analogous to the radiomics analysis in patients, mouse lungs were segmented, resized to isotropic voxels $(150 \mu \mathrm{~m})$ and discretized to a fixed bin size of 50 HU , and all 1,386 radiomic features were extracted (HU limits: -1000 HU to 200 HU ).

The Hounsfield units depend on the tube voltage, and the Hounsfield scale is normalized for 120 keV for patient diagnostics. Our microCT scanner allows a maximum tube voltage of 80 keV . Thus, the Hounsfield units can be transferred to a limited extent. We addressed this by post-processing the microCT scans to adjust the pixel values to match the human patient data. This has been done by plotting the intensity histograms of several mice and patients from the Zurich cohort with the subsequent estimation of optimal parameters for linear transformation based on visual assessment. Specifically, the intercept value has been changed from -1000 to -1024 , whereas the slope was changed from 1.0 to 0.6 . These parameters were applied to all microCT scans. The choice of 2.75 mm voxel size in patients was dictated by the voxel size in mice and the difference in lung size between mice and humans. Since the voxel size in mice was 0.15 mm and the total lung capacity in humans was estimated to be 6000x greater than in mice [39], a comparable voxel size in patients was set to 2.75 mm .

For calculating the quantitative radiomic ILD risk score, the respective radiomic features were z-transformed and summed up as for patients.

## Correlation Analysis and Pathway Enrichment Analysis

Spearman's rank correlation coefficient rho was calculated between the quantitative radiomic ILD risk score and the different biological features for correlation analysis with established inflammatory and fibrotic markers on the tissue level.

For pathway enrichment analyses, rho was calculated between qRISSc and the LFQ intensity value of every protein identified in at least $50 \%$ of mice in the proteomics analyses, and only proteins with $p<0.05$ and $r h o \geq|0.3|$ entered further analyses. The resulting list of proteins, and their coding genes, were used as input for the pathway analysis using the 'ClusterProfiler' package of Bioconductor. Protein names were converted to gene IDs using the UniProt mapping tool (https://www.uniprot.org/uploadlists/). We investigated pathway enrichment searching against "Reactome" and "GO Biological Process" databases and retained results after adjustment ( $p<0.05$ ).

## Statistical Analyses

All statistical analyses were conducted in R using the following packages: "ggplot2", "tidyverse", "ggsci", "corrplot", "readxl", "clusterSim", "dplyr", "readxl", "survival", "glmnet", "cutoff", "survminer", "cluster", "fpc", "factoextra", "clustvarsel", "clustertend". For all analyses, a p-value of $<0.05$ was considered statistically significant.

## Supplementary Figures



Supplementary Figure 1: Assessment of radiomic feature robustness against inter-and intraoperator variability in the semi-automated lung segmentation process. (a) Representative transversal HRCT image showing excellent agreement and overlap in the semi-automatically delineated lung structures of the three different examiners (examiner 1: green and magenta, examiner 2: yellow, examiner 3: cyan) for the intra- and inter-operator ICC analyses. This confirmed the reproducibility and validity of our lung segmentation protocol. (b) Boxplots showing the distribution of the ICC coefficient per radiomic feature category for inter-operator ICC analysis and (c) intra-operator ICC analysis. In (b, c), the bright red line indicates the threshold defined for the ICC analyses (ICC $=0.75$; corresponding to good reproducibility [20]). The pie charts summarize the respective percentage and total numbers of robust (ICC $\geq 0.75$ ) and non-robust (ICC $<0.75$ ) radiomic features.


Supplementary Figure 2. Prognostic performance of qRISSc compared to other SSc-ILD risk factors. (a) Bar plot indicating the results of the multivariable Cox regression analysis incorporating qRISSc (combined models) versus multivariable models composed of clinical risk factors alone (clinical model). Bars represent hazard radios for each predictor in each model, whereas colours indicate the nominal pvalue of the predictors. Covariates for Cox regression were selected based on literature evidence [29] and expert opinion. Due to missing data for the systolic pulmonary artery pressure (PAPsys, in mmHg ) and the oxygen saturation at the end of the 6 -min walk test ( $\mathrm{SpO}_{2}$ after 6 MWT , in percent) in the validation cohort from Oslo, we only fitted the multivariable models on the derivation cohort from Zurich. (b) Bar plot comparing the predictive power (C-index) of multivariable models composed of clinical risk factors of SScILD progression alone (clinical models) versus models also incorporating qRISSc (combined models). Twoway ANOVA was used to compare model performances.




Numbers at risk

$$
\begin{gathered}
\text { high } \\
\text { low }
\end{gathered}
$$



Supplementary Figure 3: Associations of qRISSc-stratified patient groups with different clinical
outcomes. Kaplan Meier curves for progression-free survival (PFS) defined as the time to (a) an absolute decline of FVC predicted $\geq 5 \%$, (b) a relative decline of FVC predicted $\geq 5 \%$, (c) an absolute decline of FVC predicted $\geq 10 \%$, (d) a relative decline of FVC predicted $\geq 10 \%$, (e) an absolute decline of FVC predicted $\geq$ $15 \%$, (f) the time to the FVC-DLCO composite index ( $=$ relative decrease in FVC\% predicted of $\geq 15 \%$ or a relative decline in FVC\% predicted of $\geq 10 \%$ combined with DLCO\% predicted of $\geq 15 \%$ according to [9]), or ( $\mathbf{g}$ ) the time to the visual ILD progression on HRCT. (h) Kaplan Meier curves for overall survival (OS) defined as the time to all-cause death. The Hazard ratios (HR) with $95 \%$ confidence intervals and $p$-value of the univariate Cox regression for the combined study cohorts are shown.


Supplementary Figure 4: Assessment of the prognostic potential of a quantitative radiomics score that is only composed of less complex, first-order intensity features. Kaplan Meier curves of the constructed intensity score for progression-free survival (PFS) defined as the time to relative FVC decline $\geq 15 \%$ in (a) the derivation cohort from Zurich and (b) in the external validation cohort from Oslo. The Hazard ratios (HR) with $95 \%$ confidence intervals and p-values of the univariate Cox regression are shown. The intensity score was statistically constructed analogously to qRISSc yet only taking first-order intensity features instead of all radiomic features into consideration.


Supplementary Figure 5: Impact of different CT image acquisition and reconstruction settings on radiomic feature values and qRISSc.
Multidimensional scaling of $z$-transformed radiomic profiles of all robust radiomic features (left panel) or only qRISSc features (right panel) combined for all SSc-ILD patients from the Zurich ( $n=90$ ) and Oslo cohort ( $n=66$ ) for (a) the different CT scanner types, (b) different lung reconstruction kernels, and (c) different slice thicknesses.

## Supplementary Tables

Supplementary Table 1: Associations of the identified patients' clusters based on their radiomic profile with clinical parameters for the Zurich cohort. Continuous variables are described as median $\pm$ interquartile range, and categorical variables are presented as absolute values with relative frequencies (percent). P-values of univariate comparisons of baseline characteristics between the two clusters are shown. Fisher's exact test was used to compare categorical, and Mann-Whitney U to compare continuous variables, respectively. Abbreviations: UIP $=$ usual interstitial pneumonia, NSIP $=$ nonspecific interstitial pneumonia, DIP $=$ diffuse interstitial pneumonia, PAPsys $=$ systolic pulmonary artery pressure, FVC $=$ forced vital capacity, FEV1 = forced expiratory volume in 1 second, DLCO = diffusing capacity for carbon monoxide, $6-\mathrm{MWT}=6$-min walk test, $\mathrm{CRP}=\mathrm{C}$-reactive protein

| Characteristics | $\begin{aligned} & \hline \text { Cluster } 1 \\ & (\mathrm{n}=59) \\ & \hline \end{aligned}$ | Cluster 2 $(\mathrm{n}=31)$ | P-value |
| :---: | :---: | :---: | :---: |
| Age (years) | $58.0 \pm 17.0$ | $57.0 \pm 16.9$ | 0.693 |
| Sex |  |  |  |
| Male | 14 (23.7\%) | 7 (22.6\%) | 1.000 |
| Female | 45 (76.3\%) | 24 (77.4\%) |  |
| SSc disease duration (years)* | $5.0 \pm 8.0$ | $4.3 \pm 8.3$ | 0.507 |
| SSc subset (LeRoy 1988) |  |  |  |
| Limited cutaneous SSc | 30 (50.8\%) | 11 (35.5\%) | 0.234 |
| Diffuse cutaneous SSc | 26 (44.1\%) | 16 (51.6\%) |  |
| No skin involvement | 3 (5.1\%) | 4 (12.9\%) |  |
| Skin involvement |  |  |  |
| Limited cutaneous | 20 (33.9\%) | 11 (35.5\%) | 0.224 |
| Diffuse cutaneous | 27 (45.8\%) | 16 (51.6\%) |  |
| No skin involvement | 5 (8.5\%) | 4 (12.9\%) |  |
| Only sclerodactyly | 7 (11.9\%) | 0 (0.0\%) |  |
| Autoantibodies |  |  |  |
| Anti-centromere positive | 10 (16.9\%) | 3 (9.7\%) | 0.530 |
| Anti-topoisomerase I positive | 28 (47.5\%) | 13 (41.9\%) | 0.661 |
| Anti-RNA polymerase III positive | 4 (6.8\%) | 3 (9.7\%) | 0.602 |
| Anti-PMScl positive | 14 (23.7\%) | 4 (12.9\%) | 0.496 |
| FVC (\% predicted) | $97.0 \pm 26.0$ | $65.5 \pm 22.2$ | <0.001 |
| FVC $\geq 70 \%$ predicted | 54 (91.5\%) | 10 (32.3\%) |  |
| FVC $<70 \%$ predicted | 4 (6.8\%) | 20 (64.5\%) |  |
| DLCO (\% predicted) | $75.0 \pm 24.0$ | $48.0 \pm 25.5$ | <0.001 |
| FEV1 (\% predicted) | $95.8 \pm 19.0$ | $65.5 \pm 25.5$ | <0.001 |
| Pulmonary hypertension ${ }^{+}$ | 7 (11.9\%) | 13 (41.9\%) | 0.001 |
| PAPsys (mmHg) ${ }^{\ddagger}$ | $25.0 \pm 7.0$ | $32.0 \pm 18.0$ | <0.001 |
| CRP (mg/l) | $2.4 \pm 5.6$ | $4.2 \pm 6.1$ | 0.071 |
| 6 min walk distance (m) | $543.5 \pm 109.2$ | $407.0 \pm 173.0$ | <0.001 |
| $\mathrm{SpO}_{2}$ before 6-MWT (\%) | $97.0 \pm 1.2$ | $96.0 \pm 3.0$ | 0.011 |
| $\mathrm{SpO}_{2}$ after 6-MWT (\%) | $96.0 \pm 3.0$ | $88.5 \pm 9.8$ | <0.001 |
| Borg scale (unit; range 0-10) | $2.0 \pm 2.0$ | $4.0 \pm 3.0$ | <0.001 |


| Extent of lung fibrosis on CT |  |  |  |
| :---: | :---: | :---: | :---: |
| <20\% | 40 (67.8\%) | 10 (32.3\%) | 0.002 |
| $\geq 20 \%$ | 19 (32.2\%) | 21 (67.7\%) |  |
| Ground glass opacification | 30 (50.8\%) | 15 (48.4\%) | 1.000 |
| Reticular changes | 58 (98.3\%) | 29 (93.5\%) | 0.272 |
| Traction bronchiectasis | 30 (50.8\%) | 20 (64.5\%) | 0.267 |
| Honeycombing | 9 (15.3\%) | 13 (41.9\%) | 0.009 |
| Bullae | 1 (1.7\%) | 2 (6.5\%) | 0.272 |
| Radiological subtype |  |  |  |
| NSIP | 33 (55.9\%) | 16 (51.6\%) | 0.662 |
| UIP\# | 24 (40.7\%) | 13 (41.9\%) |  |
| DIP | 0 (0.0\%) | 1 (3.2\%) |  |
| Unclassifiable | 2 (3.4\%) | 1 (3.2\%) |  |
| Immunomodulatory therapy ${ }^{\text {§ }}$ | 29 (49.2\%) | 22 (71.0\%) | 0.073 |
| Smoking status |  |  |  |
| Never | 35 (59.3\%) | 20 (64.5\%) | 0.868 |
| Former | 14 (23.7\%) | 7 (22.6\%) |  |
| Current | 9 (15.3\%) | 3 (9.7\%) |  |

*Disease duration of SSc was calculated as the difference between the date of baseline CT and the date of manifestation of the first non-Raynaud's symptom.
${ }^{\dagger}$ Pulmonary hypertension was assessed by echocardiography or right heart catheterisation.
$\ddagger$ PAPsys was determined by right heart catheterisation.
"UIP includes the radiological diagnosis of both, "definite" and "probable" UIP.
${ }^{\text {S }}$ Immunomodulatory therapy included prednisone, methotrexate, rituximab, cyclophosphamide, mycophenolate mofetil, hydroxychloroquine, tocilizumab, imatinib, azathioprine, adalimumab, leflunomid, cyclosporine.

Supplementary Table 2: Radiomic features used to construct the quantitative radiomic risk score for SSc-ILD (qRISSc). A complete list of all radiomics features, including standardized feature names is provided in Supplementary File 1. Abbreviations: GLCM = Gray Level Co-occurrence Matrix, NGTDM = Neighborhood Gray Tone Difference Matrix, GLRLM = Gray Level Run Length Matrix, GLDZM = Gray Level Distance Matrix and NGLDM = Neighboring Gray Level Dependence Matrix

| Feature ID | Feature Name | Feature <br> Class | Feature <br> Subclass | Wavelet <br> Filter | LASSO <br> Coeff. |
| :--- | :--- | :--- | :--- | :--- | :--- |
| V3 | COV | Intensity | Intensity | Unfiltered | 15.14 |
| V10 | iqr | Intensity | Intensity | Unfiltered | 14.41 |
| V12 | mad | Intensity | Intensity | Unfiltered | 17.86 |
| V13 | rmad | Intensity | Unfiltered | -42.79 |  |
| V26 | variance | Texture | GLCM | Unfiltered | -11.36 |
| V29 | sum_variance | Texture | GLCM | Unfiltered | 0.01 |
| V40 | autocorrelation | Texture | GLCM | Unfiltered | -5.41 |
| V41 | clust_tendency | Texture | GLCM | Unfiltered | 11.66 |
| V66 | M_autocorrelation | Texture | mGLCM | Unfiltered | -0.29 |
| V84 | len_sshge | Texture | GLRLM | Unfiltered | -9.68 |
| V86 | len_Ishge | Texture | GLRLM | Unfiltered | -19.25 |
| V102 | M_len_Ishge | Texture | mGLRLM | Unfiltered | -0.0024 |
| V146 | NGLDM_hgse | Texture | NGLDM | Unfiltered | 59.55 |
| V588 | GLDZM_sizeVar_n.3 | Wavelet | GLDZM | HLH | -0.3 |
| V641 | idiff_n.4 | Wavelet | GLCM | HLL | 1.84 |
| V665 | M_homogenity_n.4 | Wavelet | mGLCM | HLL | -2.79 |
| V686 | coarseness.4 | Wavelet | NGTDM | HLL | 0.96 |
| V687 | neighContrast.4 | Wavelet | NGTDM | HLL | 0.03 |
| V840 | coarseness.5 | Wavelet | NGTDM | LHH | -0.83 |
| V994 | coarseness.6 | Wavelet | NGTDM | LHL | 1.03 |
| V998 | strength6 | Wavelet | NGTDM | LHL | 1.26 |
| V1082 | skewness.7 | Wavelet | Intensity | LLH | 1.55 |
| V1235 | COV.8 | Wavelet | Intensity | LLL | 6.6 |
| V1236 | skewness.8 | Wavelet | Intensity | LLL | 8.6 |
| V1242 | iqr.8 | Wavelet | Intensity | LLL | 16.99 |
| V1302 | coarseness.8 | Wavelet | NGTDM | LLL | 0.38 |
|  |  |  |  |  |  |

Supplementary Table 3: Associations of the patients' risk groups based on qRISSc with clinical parameters for the derivation (Zurich) dataset. Continuous variables are described as median $\pm$ interquartile range, and categorical variables are presented as absolute values with relative frequencies (percent). P-values of univariate comparisons of baseline characteristics between the two risk groups are shown. Fisher's exact test was used to compare categorical, and Mann-Whitney U to compare continuous variables, respectively. Abbreviations: UIP = usual interstitial pneumonia, NSIP = nonspecific interstitial pneumonia, DIP = diffuse interstitial pneumonia, PAPsys = systolic pulmonary artery pressure, FVC = forced vital capacity, FEV1 = forced expiratory volume in 1 second, DLCO = diffusing capacity for carbon monoxide, $6-\mathrm{MWT}=6-\mathrm{min}$ walk test, $C R P=$ C-reactive protein

| Characteristics | Low risk $(n=54)$ | High risk $(n=21)$ | P-value |
| :---: | :---: | :---: | :---: |
| Age (years) | $56.5 \pm 16.8$ | $56.0 \pm 18.0$ | 0.939 |
| Sex |  |  |  |
| Male | 14 (25.9\%) | 5 (23.8\%) | 1.000 |
| Female | 40 (74.1\%) | 16 (76.2\%) |  |
| SSc disease duration (years)* | $4.3 \pm 6.6$ | $5.0 \pm 9.3$ | 0.915 |
| SSc subset (LeRoy 1988) |  |  |  |
| Limited cutaneous SSc | 27 (50.0\%) | 9 (42.9\%) | 0.797 |
| Diffuse cutaneous SSc | 23 (42.6\%) | 10 (47.6\%) |  |
| No skin involvement | 4 (7.4\%) | 2 (9.5\%) |  |
| Skin involvement |  |  |  |
| Limited cutaneous | 18 (33.3\%) | 9 (42.9\%) | 0.481 |
| Diffuse cutaneous | 24 (44.4\%) | 10 (47.6\%) |  |
| No skin involvement | 6 (11.1\%) | 2 (9.5\%) |  |
| Only sclerodactyly | 6 (11.1\%) | 0 (0.0\%) |  |
| Autoantibodies |  |  |  |
| Anti-Centromere positive | 12 (22.2\%) | 0 (0.0\%) | 0.016 |
| Anti-Topoisomerase I positive | 28 (51.9\%) | 9 (42.9\%) | 0.609 |
| Anti-RNA polymerase III positive | 3 (5.6\%) | 3 (14.3\%) | 0.343 |
| Anti-PMScl positive | 12 (22.2\%) | 4 (19.0\%) | 1.000 |
| FVC (\% predicted) | $97.4 \pm 28.5$ | $65.0 \pm 18.0$ | <0.001 |
| FVC $\geq 70 \%$ predicted | 48 (88.9\%) | 6 (28.6\%) |  |
| FVC $<70 \%$ predicted | 6 (11.1\%) | 15 (71.4\%) |  |
| DLCO (\% predicted) | $74.4 \pm 24.2$ | $51.0 \pm 25.0$ | <0.001 |
| FEV1 (\% predicted) | $95.8 \pm 21.0$ | $65.0 \pm 27.0$ | $<0.001$ |
| Pulmonary hypertension ${ }^{+}$ | 3 (5.6\%) | 10 (47.6\%) | <0.001 |
| PAPsys (mmHg) ${ }^{\ddagger}$ | $24.0 \pm 7.0$ | $31.0 \pm 12.5$ | <0.001 |
| CRP (mg/l) | $2.4 \pm 5.4$ | $6.1 \pm 6.8$ | 0.006 |
| 6 min walk distance (m) | $543.0 \pm 118.0$ | $421.0 \pm 126.5$ | <0.001 |
| $\mathrm{SpO}_{2}$ before 6MWT (\%) | $97.0 \pm 1.0$ | $96.0 \pm 3.2$ | 0.087 |
| $\mathrm{SpO}_{2}$ after 6MWT (\%) | $96.0 \pm 3.0$ | $85.5 \pm 5.2$ | <0.001 |
| Borg (unit; range 0-10) | $2.0 \pm 2.0$ | $5.5 \pm 3.2$ | <0.001 |
| Extent of lung fibrosis on CT |  |  |  |
| <20\% | 40 (74.1\%) | 5 (23.8\%) | <0.001 |


| $\geq 20 \%$ | $14(25.9 \%)$ | $16(76.2 \%)$ |  |
| :--- | :--- | :--- | :--- |
| Ground glass opacification | $25(46.3 \%)$ | $11(52.4 \%)$ | 0.797 |
| Reticular changes | $52(96.3 \%)$ | $20(95.2 \%)$ | 1.000 |
| Traction bronchiectasis | $21(38.9 \%)$ | $17(81.0 \%)$ | $\mathbf{0 . 0 0 2}$ |
| Honeycombing | $5(9.3 \%)$ | $11(52.4 \%)$ | $<0.001$ |
| Bullae | $2(3.7 \%)$ | $1(4.8 \%)$ | 1.000 |
| Radiological subtype |  |  |  |
| NSIP | $29(53.7 \%)$ | $12(57.1 \%)$ |  |
| UIP\# | $23(42.6 \%)$ | $8(38.1 \%)$ | 0.461 |
| DIP | $0(0.0 \%)$ | $1(4.8 \%)$ |  |
| Unclassifiable | $2(3.7 \%)$ | $0(0.0 \%)$ |  |
| Immunomodulatory therapy | $30(55.6 \%)$ | $14(66.7 \%)$ | 0.441 |
| Smoking status |  |  |  |
| Never | $35(64.8 \%)$ | $13(61.9 \%)$ |  |
| Former | $12(22.2 \%)$ | $5(23.8 \%)$ | 1.000 |
| Current | $7(13.0 \%)$ | $2(9.5 \%)$ |  |

*Disease duration of SSc was calculated as the difference between the date of baseline CT and the date of manifestation of the first non-Raynaud's symptom.
${ }^{\dagger}$ Pulmonary hypertension was assessed by echocardiography or right heart catheterisation.
$\ddagger$ PAP sys was determined by right heart catheterisation.
"UIP includes the radiological diagnosis of both, "definite" and "probable" UIP.
${ }^{\text {E }}$ Immunomodulatory therapy included prednisone, methotrexate, rituximab, cyclophosphamide, mycophenolate mofetil, hydroxychloroquine, tocilizumab, imatinib, azathioprine, adalimumab, leflunomid, cyclosporine.

Supplementary Table 4: Associations of the patients' risk groups based on qRISSc with clinical parameters for the external and independent validation (Oslo) cohort. Continuous variables are described as median $\pm$ interquartile range, and categorical variables are presented as absolute values with relative frequencies (percent). P-values of univariate comparisons of baseline characteristics between the two risk groups are shown. Fisher's exact test was used to compare categorical, and Mann-Whitney U to compare continuous variables, respectively. Abbreviations: UIP = usual interstitial pneumonia, NSIP = nonspecific interstitial pneumonia, DIP = diffuse interstitial pneumonia, PAPsys = systolic pulmonary artery pressure, FVC = forced vital capacity, FEV1 = forced expiratory volume in 1 second, DLCO = diffusing capacity for carbon monoxide, $6-M W T=6-$ min walk test, $C R P=C$-reactive protein

| Characteristics | Low risk $(\mathrm{n}=47)$ | High risk $(n=19)$ | $p$ value |
| :---: | :---: | :---: | :---: |
| Age (years) | $58.0 \pm 22.0$ | $64.0 \pm 19.0$ | 0.311 |
| Sex |  |  |  |
| Male | 12 (25.5\%) | 4 (21.1\%) | 1.000 |
| Female | 35 (74.5\%) | 15 (78.9\%) |  |
| SSc disease duration (years)* | $4.3 \pm 9.1$ | $6.1 \pm 9.1$ | 0.325 |
| SSc subset (LeRoy 1988) |  |  |  |
| Limited cutaneous SSc | 26 (55.3\%) | 11 (57.9\%) | 1.000 |
| Diffuse cutaneous SSc | 21 (44.7\%) | 8 (42.1\%) |  |
| No skin involvement | 0 (0.0\%) | 0 (0.0\%) |  |
| Skin involvement |  |  |  |
| Limited cutaneous | 26 (55.3\%) | 11 (57.9\%) | 1.000 |
| Diffuse cutaneous | 21 (44.7\%) | 8 (42.1\%) |  |
| No skin involvement | 0 (0.0\%) | 0 (0.0\%) |  |
| Only sclerodactyly | 0 (0.0\%) | 0 (0.0\%) |  |
| Autoantibodies |  |  |  |
| Anti-Centromere positive | 5 (10.6\%) | 2 (10.5\%) | 1.000 |
| Anti-Topoisomerase I positive | 17 (36.2\%) | 7 (36.8\%) | 1.000 |
| Anti-RNA polymerase III positive | 8 (17.0\%) | 0 (0.0\%) | 0.046 |
| Anti-PMScl positive | 3 (6.4\%) | 1 (5.3\%) | 1.000 |
| FVC (\% predicted) | $92.0 \pm 25.5$ | $60.0 \pm 20.0$ | <0.001 |
| FVC $\geq 70 \%$ predicted | 36 (76.6\%) | 8 (42.1\%) |  |
| FVC $<70 \%$ predicted | 6 (12.8\%) | 9 (47.4\%) |  |
| DLCO (\% predicted) | $66.0 \pm 17.5$ | $35.0 \pm 20.0$ | <0.001 |
| FEV1 (\% predicted) | $82.0 \pm 22.0$ | $64.0 \pm 18.0$ | <0.001 |
| Pulmonary hypertension ${ }^{+}$ | 1 (2.1\%) | 5 (26.3\%) | 0.008 |
| PAPsys (mmHg) ${ }^{\ddagger}$ | $15.0 \pm 10.0$ | $35.0 \pm 18.8$ | 0.054 |
| CRP (mg/l) | $2.9 \pm 5.7$ | $5.4 \pm 9.0$ | 0.121 |
| 6 min walk distance (m) | n/a | n/a | $\mathrm{n} / \mathrm{a}$ |
| $\mathrm{SpO}_{2}$ before 6MWT (\%) | n/a | n/a | n/a |
| $\mathrm{SpO}_{2}$ after 6MWT (\%) | n/a | n/a | n/a |
| Borg (unit; range 0-10)) | n/a | n/a | n/a |
| Extent of lung fibrosis on CT |  |  |  |
| <20\% | 30 (63.8\%) | 0 (0.0\%) | <0.001 |


| $\geq 20 \%$ | $17(36.2 \%)$ | $19(100.0 \%)$ |  |
| :--- | :--- | :--- | :--- |
| Ground glass opacification | $33(70.2 \%)$ | $9(47.4 \%)$ | 0.097 |
| Reticular changes | $34(72.3 \%)$ | $17(89.5 \%)$ | 0.198 |
| Traction bronchiectasis | $12(25.5 \%)$ | $15(78.9 \%)$ | $<0.001$ |
| Honeycombing | $6(12.8 \%)$ | $10(52.6 \%)$ | $\mathbf{0 . 0 0 1}$ |
| Bullae | $2(4.3 \%)$ | $2(10.5 \%)$ | 0.573 |
| Radiological subtype |  |  |  |
| NSIP | $27(57.4 \%)$ | $7(36.8 \%)$ |  |
| UIP\# | $16(34.0 \%)$ | $11(57.9 \%)$ | 0.175 |
| DIP | $0(0.0 \%)$ | $0(0.0 \%)$ |  |
| Unclassifiable | $4(8.5 \%)$ | $1(5.3 \%)$ |  |
| Immunomodulatory therapy ${ }^{\S}$ | $16(34.0 \%)$ | $12(63.2 \%)$ | 0.053 |
| Smoking status |  |  |  |
| $\quad$ Never | $16(34.0 \%)$ | $8(42.1 \%)$ |  |
| Former | $17(36.2 \%)$ | $8(42.1 \%)$ | 0.578 |
| Current | $5(10.6 \%)$ | $0(0.0 \%)$ |  |

*Disease duration of SSc was calculated as the difference between the date of baseline CT and the date of manifestation of the first non-Raynaud's symptom.
${ }^{\dagger}$ Pulmonary hypertension was assessed by echocardiography or right heart catheterisation.
$\ddagger$ PAP sys was determined by right heart catheterisation.
"UIP includes the radiological diagnosis of both, "definite" and "probable" UIP.
${ }^{\text {S }}$ Immunomodulatory therapy included prednisone, methotrexate, rituximab, cyclophosphamide, mycophenolate mofetil, hydroxychloroquine, tocilizumab, imatinib, azathioprine, adalimumab, leflunomid, cyclosporine.

Supplementary Table 5: Summary of the univariable Cox regression analysis for qRISSc and the previously proposed clinical risk factors for SSc-ILD progression. Covariates for univariable Cox regression were selected based on literature evidence [29] and expert opinion.

| Predictor | HR (95\% CI) | P-value | C-Index (SE), p-value |
| :---: | :---: | :---: | :---: |
| Zurich |  |  |  |
| Age | 1.03 (0.99, 1.06) | 0.17 | 0.59 (0.06), p=0.17 |
| Male Sex | 1.38 (0.60, 3.16) | 0.45 | 0.53 (0.05), p=0.46 |
| Anti-Topoisomerase 1 positive | 1.04 (0.49, 2.22) | 0.92 | 0.46 (0.05), p=0.92 |
| Baseline FVC (\% predicted) | 0.98 (0.96, 1.00) | 0.04 | 0.62 (0.07), p=0.04 |
| Baseline DLCO (\% predicted) | 0.98 (0.96, 1.00) | 0.02 | 0.69 (0.05), p=0.02 |
| HRCT Threshold ( $\geq 20 \%$ ) | 1.94 (0.90, 4.19) | 0.09 | 0.61 (0.05), p=0.10 |
| UIP Subtype* | 0.88 (0.40, 1.92) | 0.74 | 0.49 (0.05), p=0.74 |
| Diffuse cutaneous skin involvement | 1.81 (0.84, 3.89) | 0.13 | 0.56 (0.05), p=0.13 |
| CRP | 1.01 (0.99, 1.04) | 0.31 | 0.63 (0.06), p=0.35 |
| qRISSc (high) | 4.10 (1.87, 9.03) | <0.001 | 0.67 (0.05), p=0.001 |
| Oslo |  |  |  |
| Age | 1.02 (0.97, 1.07) | 0.45 | 0.61 (0.11), p=0.44 |
| Male Sex | 0.22 (0.03, 1.71) | 0.15 | 0.61 (0.04), p=0.08 |
| Anti-Topoisomerase 1 positive | 1.07 (0.25, 4.55) | 0.93 | 0.48 (0.10), p=0.93 |
| Baseline FVC (\% predicted) | 1.00 (0.97, 1.03) | 0.87 | 0.60 (0.12), p=0.87 |
| Baseline DLCO (\% predicted) | 0.95 (0.92, 0.99) | 0.01 | 0.85 (0.06), p=0.008 |
| HRCT Threshold ( $\geq 20 \%$ ) | 2.04 (0.52, 8.00) | 0.31 | 0.65 (0.06), p=0.29 |
| UIP Subtype* | 1.38 (0.42, 4.55) | 0.60 | 0.55 (0.09), p=0.60 |
| Diffuse cutaneous skin involvement | 0.69 (0.19, 2.59) | 0.58 | 0.48 (0.09), p=0.59 |
| CRP | 1.00 (0.94, 1.07) | 0.98 | 0.52 (0.10), p=0.98 |
| qRISSc (high) | 5.14 (1.14, 23.2) | 0.03 | 0.71 (0.07), p=0.04 |
| Combined Cohorts |  |  |  |
| Age | 1.02 (1.00, 1.05) | 0.11 | 0.59 (0.05), p=0.10 |
| Male Sex | 0.96 (0.46, 2.04) | 0.92 | 0.50 (0.04), p=0.92 |
| Anti-Topoisomerase 1 positive | 1.05 (0.54, 2.02) | 0.89 | 0.47 (0.05), p=0.89 |
| Baseline FVC (\% predicted) | 0.98 (0.97, 1.00) | 0.04 | 0.62 (0.06), p=0.04 |
| Baseline DLCO (\% predicted) | 0.97 (0.96, 0.99) | 0.001 | 0.72 (0.04), p=0.001 |
| HRCT Threshold ( $\geq 20 \%$ ) | 1.98 (1.04, 3.76) | 0.04 | 0.62 (0.04), p=0.04 |
| UIP Subtype* | 1.01 (0.53, 1.94) | 0.98 | 0.53 (0.05), p=0.98 |
| Diffuse cutaneous skin involvement | 1.67 (0.88, 3.17) | 0.12 | 0.54 (0.05), p=0.12 |
| CRP | 1.01 (0.99, 1.04) | 0.40 | 0.60 (0.05), p=0.43 |
| qRISSc (high) | 4.07 (2.07, 8.00) | $<0.001$ | 0.68 (0.04), $\mathbf{p}<0.001$ |

*UIP includes the radiological diagnosis of both, "definite" and "probable" UIP.

Supplementary Table 6: Summary of the multivariable Cox regression analysis of the clinical models composed of previously proposed risk factors for SSc-ILD progression. Covariates for multivariable Cox regression were selected based on literature evidence [29] and expert opinion.

| Predictor | HR (95\% CI) | P-value | FDR | $\begin{aligned} & \text { C-Index (SE), } \\ & \text { p-value } \\ & \hline \end{aligned}$ |
| :---: | :---: | :---: | :---: | :---: |
| Model 1 |  |  |  |  |
| Age | 1.03 (1.00, 1.06) | 0.09 | 0.18 | $\begin{gathered} 0.64(0.05) \\ p=0.16 \end{gathered}$ |
| Male Sex | 0.92 (0.42, 2.03) | 0.84 | 0.88 |  |
| Baseline FVC (\% predicted) | 0.98 (0.97, 1.00) | 0.04 | 0.15 |  |
| Anti-Topoisomerase 1 positive | 1.07 (0.55, 2.11) | 0.84 | 0.88 |  |
| Model 2 |  |  |  |  |
| Age | 1.03 (1.00, 1.06) | 0.06 | 0.15 | $\begin{gathered} 0.66(0.05) \\ \mathrm{p}=0.04 \end{gathered}$ |
| Male Sex | 0.85 (0.39, 1.86) | 0.69 | 0.83 |  |
| Baseline FVC (\% predicted) | 0.98 (0.96, 1.00) | 0.02 | 0.12 |  |
| Model 3 |  |  |  |  |
| Age | 1.03 (1.00, 1.06) | 0.09 | 0.18 | $\begin{gathered} 0.71(0.04) \\ \mathrm{p}=0.006 \end{gathered}$ |
| Male Sex | 0.98 (0.45, 2.11) | 0.96 | 0.96 |  |
| Baseline DLCO (\% predicted) | 0.97 (0.95, 0.99) | 0.003 | 0.06 |  |
| HRCT Threshold ( $\geq 20 \%$ ) | 1.08 (0.52, 2.25) | 0.84 | 0.88 |  |
| Model 4 |  |  |  |  |
| Age | 1.02 (0.99, 1.05) | 0.15 | 0.28 | $\begin{gathered} 0.66 \text { (0.05) } \\ p=0.12 \end{gathered}$ |
| Male Sex | 0.83 (0.38, 1.82) | 0.64 | 0.83 |  |
| Baseline FVC (\% predicted) | 0.98 (0.97, 1.00) | 0.06 | 0.15 |  |
| HRCT Threshold ( $\geq 20 \%$ ) | 1.40 (0.68, 2.90) | 0.36 | 0.62 |  |
| UIP Subtype* | 0.79 (0.39, 1.59) | 0.50 | 0.77 |  |
| Model 5 |  |  |  |  |
| Age | 1.04 (1.01, 1.07) | 0.02 | 0.12 | $\begin{gathered} 0.69(0.04) \\ \mathbf{p}=0.02 \end{gathered}$ |
| Male Sex | 0.78 (0.36, 1.73) | 0.54 | 0.77 |  |
| Baseline FVC (\% predicted) | 0.98 (0.97, 1.00) | 0.03 | 0.15 |  |
| Diffuse cutaneous skin involvement | 2.01 (1.00, 4.04) | 0.05 | 0.15 |  |
| Model 6 |  |  |  |  |
| Age | 1.03 (1.00, 1.06) | 0.06 | 0.15 | $\begin{gathered} 0.68(0.06) \\ \mathrm{p}=0.03 \end{gathered}$ |
| Male Sex | 0.77 (0.35, 1.72) | 0.53 | 0.77 |  |
| Baseline FVC (\% predicted) | 0.98 (0.96, 0.99) | 0.005 | 0.06 |  |
| CRP (mg/l) | 1.01 (0.98, 1.04) | 0.67 | 0.83 |  |

*UIP includes the radiological diagnosis of both, "definite" and "probable" UIP.

Supplementary Table 7: Summary of the multivariable Cox regression analysis of the combined models, i.e. incorporating qRISSc and the previously proposed clinical risk factors for SSc-ILD progression. Covariates for multivariable Cox regression were selected based on literature evidence [29] and expert opinion.

| Predictor | HR (95\% CI) | $p$-value | FDR | C-Index (SE), p-value |
| :---: | :---: | :---: | :---: | :---: |
| Model 1 |  |  |  |  |
| Age | 1.03 (1.00, 1.06) | 0.06 | 0.15 | $\begin{gathered} 0.71(0.05) \\ p=0.009 \end{gathered}$ |
| Male Sex | 1.03 (0.46, 2.30) | 0.95 | 0.95 |  |
| Baseline FVC (\% predicted) | 0.99 (0.97, 1.01) | 0.37 | 0.58 |  |
| Anti-Topoisomerase 1 positive | 1.29 (0.65, 2.56) | 0.46 | 0.70 |  |
| qRISSc (high) | 3.48 (1.60, 7.55) | 0.002 | 0.01 |  |
| Model 2 |  |  |  |  |
| Age | 1.03 (1.00, 1.06) | 0.06 | 0.15 | $\begin{gathered} 0.74 \text { (0.04), } \\ \mathrm{p}=0.001 \end{gathered}$ |
| Male Sex | 0.96 (0.43, 2.13) | 0.92 | 0.95 |  |
| Baseline FVC (\% predicted) | 0.99 (0.97, 1.01) | 0.30 | 0.56 |  |
| qRISSc (high) | 3.59 (1.72, 7.50) | 0.001 | 0.01 |  |
| Model 3 |  |  |  |  |
| Age | 1.03 (1.00, 1.07) | 0.04 | 0.15 | $\begin{aligned} & 0.77(0.04), \\ & \mathrm{p}=2.72 \mathrm{E}-04 \end{aligned}$ |
| Male Sex | 0.95 (0.43, 2.10) | 0.90 | 0.95 |  |
| Baseline DLCO (\% predicted) | 0.98 (0.96, 1.00) | 0.05 | 0.15 |  |
| HRCT Threshold ( $\geq 20 \%$ ) | 0.92 (0.44, 1.93) | 0.83 | 0.95 |  |
| qRISSc (high) | 3.42 (1.58, 7.41) | 0.002 | 0.01 |  |
| Model 4 |  |  |  |  |
| Age | 1.03 (0.99, 1.06) | 0.12 | 0.25 | $\begin{gathered} 0.72 \text { (0.05), } \\ \mathrm{p}=0.006 \end{gathered}$ |
| Male Sex | 0.96 (0.42, 2.19) | 0.92 | 0.95 |  |
| Baseline FVC (\% predicted) | 0.99 (0.97, 1.01) | 0.33 | 0.56 |  |
| HRCT Threshold ( $\geq 20 \%$ ) | 1.04 (0.48, 2.25) | 0.92 | 0.95 |  |
| UIP Subtype* | 0.96 (0.47, 1.98) | 0.91 | 0.95 |  |
| qRISSc (high) | 3.49 (1.60, 7.61) | 0.002 | 0.01 |  |
| Model 5 |  |  |  |  |
| Age | 1.04 (1.01, 1.07) | 0.01 | 0.05 | $\begin{gathered} 0.75(0.04) \\ \mathrm{p}<0.001 \end{gathered}$ |
| Male Sex | 0.91 (0.41, 2.03) | 0.81 | 0.95 |  |
| Baseline FVC (\% predicted) | 0.99 (0.98, 1.01) | 0.33 | 0.56 |  |
| Diffuse cutaneous skin involvement | 2.48 (1.23, 5.01) | 0.01 | 0.05 |  |
| qRISSc (high) | 4.23 (2.03, 8.83) | <0.001 | 0.001 |  |
| Model 6 |  |  |  |  |
| Age | 1.03 (1.00, 1.06) | 0.07 | 0.16 | $\begin{gathered} 0.72(0.05) \\ p=0.003 \end{gathered}$ |
| Male Sex | 0.89 (0.39, 1.99) | 0.77 | 0.95 |  |
| Baseline FVC (\% predicted) | 0.99 (0.97, 1.01) | 0.18 | 0.35 |  |
| CRP (mg/l) | 1.01 (0.98, 1.04) | 0.69 | 0.95 |  |
| qRISSc (high) | 3.07 (1.38, 6.85) | 0.006 | 0.03 |  |

[^0]Supplementary Table 8. Summary of the multivariable Cox regression analysis for the clinical and combined models, incorporating systolic pulmonary artery pressure or oxygen saturation at the end of the $6-\mathrm{min}$ walk test as previously proposed risk factors for SSc-ILD progression, respectively. Covariates for multivariable Cox regression were selected based on literature evidence [29] and expert opinion. Due to missing data for the systolic pulmonary artery pressure (PAPsys, in mmHg ) and the oxygen saturation at the end of the $6-\mathrm{min}$ walk test $\left(\mathrm{SpO}_{2}\right.$ after 6 MWT , in percent) in the validation cohort from Oslo, we only fitted the multivariable models on the derivation cohort from Zurich.

| Predictor | HR (95\% CI) | p -value | C-Index (SE), p-value |
| :---: | :---: | :---: | :---: |
| Clinical 1 |  |  |  |
| Age | 1.05 (1.00, 1.10) | 0.05 | $\begin{gathered} 0.72(0.05), \\ p=0.06 \end{gathered}$ |
| Male Sex | 1.70 (0.58, 5.01) | 0.33 |  |
| Baseline FVC (\% predicted.) | 0.98 (0.96, 1.01) | 0.15 |  |
| $\mathrm{SpO}_{2}$ after 6-MWT (\%) | 0.97 (0.91, 1.03) | 0.34 |  |
| Clinical 2 |  |  |  |
| Age | 1.03 (0.99, 1.08) | 0.13 | $\begin{gathered} 0.74(0.05), \\ \mathrm{p}=0.006 \end{gathered}$ |
| Male Sex | 1.43 (0.49, 4.16) | 0.51 |  |
| Baseline FVC (\% predicted) | 0.98 (0.96, 1.00) | 0.10 |  |
| HRCT Threshold ( $\geq 20 \%$ ) | 0.90 (0.37, 2.22) | 0.82 |  |
| PAPsys (mmHg)* | 1.05 (1.02, 1.08) | 0.003 |  |
| Combined 1 |  |  |  |
| Age | 1.05 (1.00, 1.10) | 0.04 | $\begin{gathered} 0.76(0.06) \\ \mathrm{p}=0.01 \end{gathered}$ |
| Male Sex | 1.47 (0.52, 4.18) | 0.47 |  |
| Baseline FVC (\% predicted) | 0.99 (0.96, 1.02) | 0.67 |  |
| $\mathrm{SpO}_{2}$ after 6-MWT (\%) | 1.00 (0.92, 1.10) | 0.96 |  |
| qRISSc (high) | 4.91 (1.19, 20.26) | 0.03 |  |
| Combined 2 |  |  |  |
| Age | 1.03 (0.99, 1.08) | 0.13 | $\begin{gathered} 0.79 \text { (0.05), } \\ \mathbf{p}=0.002 \end{gathered}$ |
| Male Sex | 1.38 (0.46, 4.15) | 0.56 |  |
| Baseline FVC (\% predicted) | 0.99 (0.97, 1.02) | 0.47 |  |
| HRCT Threshold ( $\geq 20 \%$ ) | 0.85 (0.35, 2.06) | 0.71 |  |
| PAPsys (mmHg)* | 1.04 (1.01, 1.08) | 0.008 |  |
| qRISSc (high) | 3.05 (1.13, 8.20) | 0.03 |  |

*PAPsys was determined by right heart catheterization

Supplementary Table 9: Summary of HRCT image acquisition parameters for the two study cohorts. For slice thickness and tube voltage, data are presented as median and range of minimal and maximal values.

| CT parameter | Discovery (Zurich) cohort <br> $(\mathrm{n}=90)$ | Validation (Oslo) cohort <br> $(\mathrm{n}=66)$ |
| :--- | :--- | :--- |
| Manufacturer* | Siemens | Siemens, GE Medical Systems |
| Acquisition Model | Inspiration (breath hold) | Inspiration (breath hold) |
| Slice thickness $(\mathrm{mm})$ | 1 (range $0.6-2)$ | 2.5 (range 2-3) |
| Reconstruction kernels | B60f, B70f, Bl64 | B60f, B70f, LUNG |
| Tube voltage (kVP) | 120 (range $80-150)$ | 120 |

*HRCT scanners included SOMATOM Definition AS, SOMATOM Definition Flash, SOMATOM Force, SOMATOM Sensation 64, SOMATOM Sensation 16, Biograph 64, LightSpeed Pro 16, LightSpeed VCT.

## Supplementary Table 10: Parameter settings for MaxQuant analysis.

| Parameter | Value |
| :--- | :--- |
| Version | 1.6 .6 .0 |
| Machine name | PROXMOX-W10 |
| PSM FDR | 0.01 |
| PSM FDR Crosslink | 0.01 |
| Protein FDR | 0.01 |
| Site FDR | 0.01 |
| Use Normalized Ratios For Occupancy | TRUE |
| Min. peptide Length | 7 |
| Min. score for unmodified peptides | 0 |
| Min. score for modified peptides | 40 |
| Min. delta score for unmodified peptides | 0 |
| Min. delta score for modified peptides | 6 |
| Min. unique peptides | 0 |
| Min. razor peptides | 2 |
| Min. peptides | 2 |
| Use only unmodified peptides and | FALSE |
| Peptides used for protein quantification | Razor |
| Discard unmodified counterpart peptides | TRUE |
| Label min. ratio count | 2 |
| Use delta score | FALSE |
| iBAQ | TRUE |
| iBAQ log fit | TRUE |
| Match between runs | TRUE |
| Matching time window [min] | 0.7 |
| Match ion mobility window [indices] | 0.05 |
| Alignment time window [min] | 20 |
| Alignment ion mobility window [indices] | 1 |
| Find dependent peptides | FALSE |
| Fasta file | MusMusculus_SP_2019_10.fasta |
| Decoy mode | revert |
| Include contaminants | TRUE |
| Fixed modification | Carbamidomethylation of Cys |
| Variable modifications | Oxidation on Met; Acetyl on protein N-term |
| Advanced ratios | FALSE |
| Second peptides | TRUE |
| Stabilize large LFQ ratios | TRUE |
| Separate LFQ in parameter groups | FALSE |
| Require MS/MS for LFQ comparisons |  |
| Calculate peak properties | TRUE |
| Adin search max. combinations | Write msScans site intensities |


| Write msmsScans table | FALSE |
| :---: | :---: |
| Write ms3Scans table | FALSE |
| Write allPeptides table | FALSE |
| Write mzRange table | FALSE |
| Write pasefMsmsScans table | FALSE |
| Write accumulatedPasefMsmsScans table | FALSE |
| Max. peptide mass [Da] | 5500 |
| Min. peptide length for unspecific search | 8 |
| Max. peptide length for unspecific search | 25 |
| Razor protein FDR | TRUE |
| Max mods in site table | 3 |
| Match unidentified features | FALSE |
| Evaluate variant peptides separately | TRUE |
| Variation mode | None |
| MS/MS tol. (FTMS) | 20 ppm |
| Top MS/MS peaks per Da interval. (FTMS) | 6 |
| Da interval. (FTMS) | 20 |
| MS/MS deisotoping (FTMS) | TRUE |
| MS/MS deisotoping tolerance (FTMS) | 7 |
| MS/MS deisotoping tolerance unit (FTMS) | ppm |
| MS/MS higher charges (FTMS) | TRUE |
| MS/MS water loss (FTMS) | TRUE |
| MS/MS ammonia loss (FTMS) | TRUE |
| MS/MS dependent losses (FTMS) | TRUE |
| MS/MS recalibration (FTMS) | FALSE |
| MS/MS tol. (ITMS) | 0.4 Da |
| Top MS/MS peaks per Da interval. (ITMS) | 12 |
| Da interval. (ITMS) | 100 |
| MS/MS deisotoping (ITMS) | FALSE |
| MS/MS deisotoping tolerance (ITMS) | 0.15 |
| MS/MS deisotoping tolerance unit (ITMS) | Da |
| MS/MS higher charges (ITMS) | TRUE |
| MS/MS water loss (ITMS) | TRUE |
| MS/MS ammonia loss (ITMS) | TRUE |
| MS/MS dependent losses (ITMS) | TRUE |
| MS/MS recalibration (ITMS) | FALSE |
| MS/MS deisotoping (Unknown) | FALSE |
| MS/MS deisotoping tolerance (Unknown) | 0.15 |
| MS/MS deisotoping tolerance unit (Unknown) | Da |
| MS/MS higher charges (Unknown) | TRUE |
| MS/MS water loss (Unknown) | TRUE |
| MS/MS ammonia loss (Unknown) | TRUE |
| MS/MS dependent losses (Unknown) | TRUE |
| MS/MS recalibration (Unknown) | FALSE |

Supplementary Table 11: Murine primer sequences used for qRT-PCR.

| Gene | Forward primer (5' - 3') | Reverse primer (5' - 3') |
| :---: | :---: | :---: |
| Collagen 1 alpha 1 (Col1a1) | GAT GAC GTG CAA TGC AAT GAA | CCC TCG ACT CCT ACA TCT TCT GA |
| Collagen 3 alpha 1 (Col3a1) | AGC TTT GTG CAA AGT GGA ACC | ATA GGA CTG ACC AAG GTG GC |
| Fibronectin 1 (Fn1) | ATG TGG ACC CCT CCT GAT AGT | GCC CAG TGA TTT CAG CAA AGG |
| Interleukin 6 (II6) | TGA TGG ATG CTA CCA AAC TGG | GGT ACT CCA GAA GAC CAG AG |
| Monocyte chemoattractant protein 1 (Mcp-1) | CCA CTC ACC TGC TGC TAC TCA T | TGG TGA TCC TCT TGT AGC TCT CC |
| 60S acidic ribosomal protein P0 (Rp/p0) | GCA GGT GTT TGA CAA CGG CAG | GAT GAT GGA GTG TGG CAC CGA |

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|  | Feature |  |  |
| :---: | :---: | :---: | :---: |
| Index | Number | full name | Standardization Name |
| 1 | V1 | Mean | mean |
| 2 | V2 | SD | standard deviation |
| 3 | V3 | COV | coefficient of variation |
| 4 | V4 | skewness | skewness |
| 5 | V5 | kurtosis | kurtosis |
| 6 | V6 | var | variance |
| 7 | V7 | median | median |
| 8 | V8 | percentile10 | percentile 10th |
| 9 | V9 | percentile90 | percentile 90th |
| 10 | V10 | iqr | interquartile range |
| 11 | V11 | Hrange | range |
| 12 | V12 | mad | mean absolut deviation |
| 13 | V13 | rmad | robust mean absolut deviation |
| 14 | V14 | H_energy | energy |
| 15 | V15 | H_entropy | entropy |
| 16 | V16 | rms | root mean square |
| 17 | V17 | H_uniformity | uniformity |
| 18 | V18 | energy | energy |
| 19 | V19 | entropy | entropy |
| 20 | V20 | contrast | contrast |
| 21 | V21 | correlation | correlation |
| 22 | V22 | homogenity | homogeneity |
| 23 | V23 | homogenity_n | homogeneity normalized |
| 24 | V24 | idiff | inverese difference |
| 25 | V25 | idiff_n | inverese difference normalized |
| 26 | V26 | variance | variance |
| 27 | V27 | sum_average | sum of average |
| 28 | V28 | sum_entropy | sum of entropy |
| 29 | V29 | sum_variance | sum of variance |
| 30 | V30 | diff_entropy | difference entropy |
| 31 | V31 | diff_variance | difference variance |
| 32 | V32 | IMC1 | information measures of correlation 1 |
| 33 | V33 | IMC2 | information measures of correlation 2 |
| 34 | V34 | MCC | maximal correlation coefficient |
| 35 | V35 | joint_max | joint maximum |
| 36 | V36 | joint_average | joint average |
| 37 | V37 | diff_average | difference average |
| 38 | V38 | dissimilarity | dissimilarity |
| 39 | V39 | inverse_variance | inverse variance |
| 40 | V40 | autocorrelation | autocorrelation |
| 41 | V41 | clust_tendency | cluster tendency |
| 42 | V42 | clust_shade | cluster shade |
| 43 | V43 | clust_prominence | cluster prominence |
| 44 | V44 | M_energy | energy |
| 45 | V45 | M_entropy | entropy |
| 46 | V46 | M_contrast | contrast |
| 47 | V47 | M_correlation | correlation |


| 48 | V48 | M_homogenity | homogeneity |
| :---: | :---: | :---: | :---: |
| 49 | V49 | M_homogenity_n | homogeneity normalized |
| 50 | V50 | M_idiff | inverese difference |
| 51 | V51 | M_idiff_n | inverese difference normalized |
| 52 | V52 | M_variance | variance |
| 53 | V53 | M_sum_average | sum of average |
| 54 | V54 | M_sum_entropy | sum of entropy |
| 55 | V55 | M_sum_variance | sum of variance |
| 56 | V56 | M_diff_entropy | difference entropy |
| 57 | V57 | M_diff_variance | difference variance |
| 58 | V58 | M_IMC1 | information measures of correlation 1 |
| 59 | V59 | M_IMC2 | information measures of correlation 2 |
| 60 | V60 | M_MCC | maximal correlation coefficient |
| 61 | V61 | M _joint_max | joint maximum |
| 62 | V62 | M_joint_average | joint average |
| 63 | V63 | M_diff_average | difference average |
| 64 | V64 | M_dissimilarity | dissimilarity |
| 65 | V65 | M_inverse_variance | inverse variance |
| 66 | V66 | M_autocorrelation | autocorrelation |
| 67 | V67 | M_clust_tendency | cluster tendency |
| 68 | V68 | M_clust_shade | cluster shade |
| 69 | V69 | M_clust_prominence | cluster prominence |
| 70 | V70 | coarseness | coarseness |
| 71 | V71 | neighContrast | contrast |
| 72 | V72 | busyness | busyness |
| 73 | V73 | complexity | complexity |
| 74 | V74 | strength | strength |
| 75 | V75 | len_intensityVar | grey level non-uniformity |
| 76 | V76 | len_intensityVar_n | grey level non-uniformity normalized |
| 77 | V77 | len_sizeVar | zone size non-uniformity |
| 78 | V78 | len_sizeVar_n | zone size non-uniformity normalized |
| 79 | V79 | len_sse | short runs emphasis |
| 80 | V80 | len_Ise | long runs emphasis |
| 81 | V81 | len_lgse | low grey level run emphasis |
| 82 | V82 | len_hgse | high grey level run emphasis |
| 83 | V83 | len_sslge | short run low grey level emphasis |
| 84 | V84 | len_sshge | short run high grey level emphasis |
| 85 | V85 | len_Islge | long run low grey level emphasis |
| 86 | V86 | len_Ishge | long run high grey level emphasis |
| 87 | V87 | len_rpc | run percentage |
| 88 | V88 | len_grey_lev_var | grey level variance |
| 89 | V89 | len_zone_size_var | run length variance |
| 90 | V90 | len_size_entropy | run entropy |
| 91 | V91 | M_len_intensityVar | grey level non-uniformity |
| 92 | V92 | M_len_intensityVar_n | grey level non-uniformity normalized |
| 93 | V93 | M_len_sizeVar | zone size non-uniformity |
| 94 | V94 | M_len_sizeVar_n | zone size non-uniformity normalized |
| 95 | V95 | M_len_sse | short runs emphasis |
| 96 | V96 | M_len_Ise | long runs emphasis |
| 97 | V97 | M_len_lgse | low grey level run emphasis |


| 98 | V98 | M_len_hgse | high grey level run emphasis |
| :---: | :---: | :---: | :---: |
| 99 | V99 | M_len_sslge | short run low grey level emphasis |
| 100 | V100 | M_len_sshge | short run high grey level emphasis |
| 101 | V101 | M_len_Islge | long run low grey level emphasis |
| 102 | V102 | M_len_Ishge | long run high grey level emphasis |
| 103 | V103 | M_len_rpc | run percentage |
| 104 | V104 | M_len_grey_lev_var | grey level variance |
| 105 | V105 | M_len_zone_size_var | run length variance |
| 106 | V106 | M_len_size_entropy | run entropy |
| 107 | V107 | intensityVar | grey level non-uniformity |
| 108 | V108 | intensityVar_n | grey level non-uniformity normalized |
| 109 | V109 | sizeVar | zone size non-uniformity |
| 110 | V110 | sizeVar_n | zone size non-uniformity normalized |
| 111 | V111 | sse | small zone emphasis |
| 112 | V112 | Ise | large zone emphasis |
| 113 | V113 | Igse | low grey level zone emphasis |
| 114 | V114 | hgse | high grey level zone emphasis |
| 115 | V115 | sslge | small zone low grey level emphasis |
| 116 | V116 | sshge | small zone high grey level emphasis |
| 117 | V117 | Islge | large zone low grey level emphasis |
| 118 | V118 | Ishge | large zone high grey level emphasis |
| 119 | V119 | rpc | zone percentage |
| 120 | V120 | grey_lev_var | grey level variance |
| 121 | V121 | zone_size_var | zone size variance |
| 122 | V122 | size_entropy | zone size entropy |
| 123 | V123 | GLDZM_intensityVar | grey level non-uniformity |
| 124 | V124 | GLDZM_intensityVar_n | grey level non-uniformity normalized |
| 125 | V125 | GLDZM_sizeVar | zone size non-uniformity |
| 126 | V126 | GLDZM_sizeVar_n | zone size non-uniformity normalized |
| 127 | V127 | GLDZM_sse | small distance emphasis |
| 128 | V128 | GLDZM_Ise | large distance emphasis |
| 129 | V129 | GLDZM_lgse | low grey level zone emphasis |
| 130 | V130 | GLDZM_hgse | high grey level zone emphasis |
| 131 | V131 | GLDZM_sslge | small distance low grey level emphasis |
| 132 | V132 | GLDZM_sshge | small distance high grey level emphasis |
| 133 | V133 | GLDZM_Islge | large distance low grey level emphasis |
| 134 | V134 | GLDZM_Ishge | large distance high grey level emphasis |
| 135 | V135 | GLDZM_rpc | zone percentage |
| 136 | V136 | GLDZM_grey_lev_var | grey level variance |
| 137 | V137 | GLDZM_zone_size_var | zone distance variance |
| 138 | V138 | GLDZM_size_entropy | zone distance entropy |
| 139 | V139 | NGLDM_intensityVar | grey level non-uniformity |
| 140 | V140 | NGLDM_intensityVar_n | grey level non-uniformity normalized |
| 141 | V141 | NGLDM_sizeVar | dependence count non-uniformity |
| 142 | V142 | NGLDM_sizeVar_n | dependence count non-uniformity normalized |
| 143 | V143 | NGLDM_sse | low dependence emphasis |
| 144 | V144 | NGLDM_Ise | high dependence emphasis |
| 145 | V145 | NGLDM_lgse | low grey level count emphasis |
| 146 | V146 | NGLDM_hgse | high grey level count emphasis |
| 147 | V147 | NGLDM_sslge | low dependence low grey level emphasis |


| 148 | V148 | NGLDM_sshge | low dependence high grey level emphasis |
| :---: | :---: | :---: | :---: |
| 149 | V149 | NGLDM_Islge | high dependence low grey level emphasis |
| 150 | V150 | NGLDM_Ishge | high dependence high grey level emphasis |
| 151 | V151 | NGLDM_grey_lev_var | grey level variance |
| 152 | V152 | NGLDM_zone_size_var | dependence count variance |
| 153 | V153 | NGLDM_size_entropy | dependence count entropy |
| 154 | V154 | NGLDM_energy | dependence count energy |
| 155 | V155 | Mean | mean |
| 156 | V156 | SD | standard deviation |
| 157 | V157 | COV | coefficient of variation |
| 158 | V158 | skewness | skewness |
| 159 | V159 | kurtosis | kurtosis |
| 160 | V160 | var | variance |
| 161 | V161 | median | median |
| 162 | V162 | percentile10 | percentile 10th |
| 163 | V163 | percentile90 | percentile 90th |
| 164 | V164 | iqr | interquartile range |
| 165 | V165 | Hrange | range |
| 166 | V166 | mad | mean absolut deviation |
| 167 | V167 | rmad | robust mean absolut deviation |
| 168 | V168 | H_energy | energy |
| 169 | V169 | H_entropy | entropy |
| 170 | V170 | rms | root mean square |
| 171 | V171 | H_uniformity | uniformity |
| 172 | V172 | energy | energy |
| 173 | V173 | entropy | entropy |
| 174 | V174 | contrast | contrast |
| 175 | V175 | correlation | correlation |
| 176 | V176 | homogenity | homogeneity |
| 177 | V177 | homogenity_n | homogeneity normalized |
| 178 | V178 | idiff | inverese difference |
| 179 | V179 | idiff_n | inverese difference normalized |
| 180 | V180 | variance | variance |
| 181 | V181 | sum_average | sum of average |
| 182 | V182 | sum_entropy | sum of entropy |
| 183 | V183 | sum_variance | sum of variance |
| 184 | V184 | diff_entropy | difference entropy |
| 185 | V185 | diff_variance | difference variance |
| 186 | V186 | IMC1 | information measures of correlation 1 |
| 187 | V187 | IMC2 | information measures of correlation 2 |
| 188 | V188 | MCC | maximal correlation coefficient |
| 189 | V189 | joint_max | joint maximum |
| 190 | V190 | joint_average | joint average |
| 191 | V191 | diff_average | difference average |
| 192 | V192 | dissimilarity | dissimilarity |
| 193 | V193 | inverse_variance | inverse variance |
| 194 | V194 | autocorrelation | autocorrelation |
| 195 | V195 | clust_tendency | cluster tendency |
| 196 | V196 | clust_shade | cluster shade |
| 197 | V197 | clust_prominence | cluster prominence |


| 198 | V198 | M_energy | energy |
| :---: | :---: | :---: | :---: |
| 199 | V199 | M_entropy | entropy |
| 200 | V200 | M_contrast | contrast |
| 201 | V201 | M_correlation | correlation |
| 202 | V202 | M_homogenity | homogeneity |
| 203 | V203 | M_homogenity_n | homogeneity normalized |
| 204 | V204 | M_idiff | inverese difference |
| 205 | V205 | M_idiff_n | inverese difference normalized |
| 206 | V206 | M_variance | variance |
| 207 | V207 | M_sum_average | sum of average |
| 208 | V208 | M_sum_entropy | sum of entropy |
| 209 | V209 | M_sum_variance | sum of variance |
| 210 | V210 | M_diff_entropy | difference entropy |
| 211 | V211 | M_diff_variance | difference variance |
| 212 | V212 | M_IMC1 | information measures of correlation 1 |
| 213 | V213 | M_IMC2 | information measures of correlation 2 |
| 214 | V214 | M_MCC | maximal correlation coefficient |
| 215 | V215 | M_joint_max | joint maximum |
| 216 | V216 | M_joint_average | joint average |
| 217 | V217 | M_diff_average | difference average |
| 218 | V218 | M_dissimilarity | dissimilarity |
| 219 | V219 | M_inverse_variance | inverse variance |
| 220 | V220 | M_autocorrelation | autocorrelation |
| 221 | V221 | M_clust_tendency | cluster tendency |
| 222 | V222 | M_clust_shade | cluster shade |
| 223 | V223 | M_clust_prominence | cluster prominence |
| 224 | V224 | coarseness | coarseness |
| 225 | V225 | neighContrast | contrast |
| 226 | V226 | busyness | busyness |
| 227 | V227 | complexity | complexity |
| 228 | V228 | strength | strength |
| 229 | V229 | len_intensityVar | grey level non-uniformity |
| 230 | V230 | len_intensityVar_n | grey level non-uniformity normalized |
| 231 | V231 | len_sizeVar | zone size non-uniformity |
| 232 | V232 | len_sizeVar_n | zone size non-uniformity normalized |
| 233 | V233 | len_sse | short runs emphasis |
| 234 | V234 | len_Ise | long runs emphasis |
| 235 | V235 | len_lgse | low grey level run emphasis |
| 236 | V236 | len_hgse | high grey level run emphasis |
| 237 | V237 | len_sslge | short run low grey level emphasis |
| 238 | V238 | len_sshge | short run high grey level emphasis |
| 239 | V239 | len_Islge | long run low grey level emphasis |
| 240 | V240 | len_Ishge | long run high grey level emphasis |
| 241 | V241 | len_rpc | run percentage |
| 242 | V242 | len_grey_lev_var | grey level variance |
| 243 | V243 | len_zone_size_var | run length variance |
| 244 | V244 | len_size_entropy | run entropy |
| 245 | V245 | M_len_intensityVar | grey level non-uniformity |
| 246 | V246 | M_len_intensityVar_n | grey level non-uniformity normalized |
| 247 | V247 | M_len_sizeVar | zone size non-uniformity |


| 248 | V248 | M_len_sizeVar_n | zone size non-uniformity normalized |
| :---: | :---: | :---: | :---: |
| 249 | V249 | M_len_sse | short runs emphasis |
| 250 | V250 | M_len_Ise | long runs emphasis |
| 251 | V251 | M_len_lgse | low grey level run emphasis |
| 252 | V252 | M_len_hgse | high grey level run emphasis |
| 253 | V253 | M_len_sslge | short run low grey level emphasis |
| 254 | V254 | M_len_sshge | short run high grey level emphasis |
| 255 | V255 | M_len_Islge | long run low grey level emphasis |
| 256 | V256 | M_len_Ishge | long run high grey level emphasis |
| 257 | V257 | M_len_rpc | run percentage |
| 258 | V258 | M_len_grey_lev_var | grey level variance |
| 259 | V259 | M_len_zone_size_var | run length variance |
| 260 | V260 | M_len_size_entropy | run entropy |
| 261 | V261 | intensityVar | grey level non-uniformity |
| 262 | V262 | intensityVar_n | grey level non-uniformity normalized |
| 263 | V263 | sizeVar | zone size non-uniformity |
| 264 | V264 | sizeVar_n | zone size non-uniformity normalized |
| 265 | V265 | sse | small zone emphasis |
| 266 | V266 | Ise | large zone emphasis |
| 267 | V267 | Igse | low grey level zone emphasis |
| 268 | V268 | hgse | high grey level zone emphasis |
| 269 | V269 | sslge | small zone low grey level emphasis |
| 270 | V270 | sshge | small zone high grey level emphasis |
| 271 | V271 | Islge | large zone low grey level emphasis |
| 272 | V272 | Ishge | large zone high grey level emphasis |
| 273 | V273 | rpc | zone percentage |
| 274 | V274 | grey_lev_var | grey level variance |
| 275 | V275 | zone_size_var | zone size variance |
| 276 | V276 | size_entropy | zone size entropy |
| 277 | V277 | GLDZM_intensityVar | grey level non-uniformity |
| 278 | V278 | GLDZM_intensityVar_n | grey level non-uniformity normalized |
| 279 | V279 | GLDZM_sizeVar | zone size non-uniformity |
| 280 | V280 | GLDZM_sizeVar_n | zone size non-uniformity normalized |
| 281 | V281 | GLDZM_sse | small distance emphasis |
| 282 | V282 | GLDZM_Ise | large distance emphasis |
| 283 | V283 | GLDZM_lgse | low grey level zone emphasis |
| 284 | V284 | GLDZM_hgse | high grey level zone emphasis |
| 285 | V285 | GLDZM_sslge | small distance low grey level emphasis |
| 286 | V286 | GLDZM_sshge | small distance high grey level emphasis |
| 287 | V287 | GLDZM_Islge | large distance low grey level emphasis |
| 288 | V288 | GLDZM_Ishge | large distance high grey level emphasis |
| 289 | V289 | GLDZM_rpc | zone percentage |
| 290 | V290 | GLDZM_grey_lev_var | grey level variance |
| 291 | V291 | GLDZM_zone_size_var | zone distance variance |
| 292 | V292 | GLDZM_size_entropy | zone distance entropy |
| 293 | V293 | NGLDM_intensityVar | grey level non-uniformity |
| 294 | V294 | NGLDM_intensityVar_n | grey level non-uniformity normalized |
| 295 | V295 | NGLDM_sizeVar | dependence count non-uniformity |
| 296 | V296 | NGLDM_sizeVar_n | dependence count non-uniformity normalized |
| 297 | V297 | NGLDM_sse | low dependence emphasis |


| 298 | V298 | NGLDM_Ise | high dependence emphasis |
| :---: | :---: | :---: | :---: |
| 299 | V299 | NGLDM_Igse | low grey level count emphasis |
| 300 | V300 | NGLDM_hgse | high grey level count emphasis |
| 301 | V301 | NGLDM_sslge | low dependence low grey level emphasis |
| 302 | V302 | NGLDM_sshge | low dependence high grey level emphasis |
| 303 | V303 | NGLDM_Islge | high dependence low grey level emphasis |
| 304 | V304 | NGLDM_Ishge | high dependence high grey level emphasis |
| 305 | V305 | NGLDM_grey_lev_var | grey level variance |
| 306 | V306 | NGLDM_zone_size_var | dependence count variance |
| 307 | V307 | NGLDM_size_entropy | dependence count entropy |
| 308 | V308 | NGLDM_energy | dependence count energy |
| 309 | V309 | Mean | mean |
| 310 | V310 | SD | standard deviation |
| 311 | V311 | COV | coefficient of variation |
| 312 | V312 | skewness | skewness |
| 313 | V313 | kurtosis | kurtosis |
| 314 | V314 | var | variance |
| 315 | V315 | median | median |
| 316 | V316 | percentile10 | percentile 10th |
| 317 | V317 | percentile90 | percentile 90th |
| 318 | V318 | iqr | interquartile range |
| 319 | V319 | Hrange | range |
| 320 | V320 | mad | mean absolut deviation |
| 321 | V321 | rmad | robust mean absolut deviation |
| 322 | V322 | H_energy | energy |
| 323 | V323 | H_entropy | entropy |
| 324 | V324 | rms | root mean square |
| 325 | V325 | H_uniformity | uniformity |
| 326 | V326 | energy | energy |
| 327 | V327 | entropy | entropy |
| 328 | V328 | contrast | contrast |
| 329 | V329 | correlation | correlation |
| 330 | V330 | homogenity | homogeneity |
| 331 | V331 | homogenity_n | homogeneity normalized |
| 332 | V332 | idiff | inverese difference |
| 333 | V333 | idiff_n | inverese difference normalized |
| 334 | V334 | variance | variance |
| 335 | V335 | sum_average | sum of average |
| 336 | V336 | sum_entropy | sum of entropy |
| 337 | V337 | sum_variance | sum of variance |
| 338 | V338 | diff_entropy | difference entropy |
| 339 | V339 | diff_variance | difference variance |
| 340 | V340 | IMC1 | information measures of correlation 1 |
| 341 | V341 | IMC2 | information measures of correlation 2 |
| 342 | V342 | MCC | maximal correlation coefficient |
| 343 | V343 | joint_max | joint maximum |
| 344 | V344 | joint_average | joint average |
| 345 | V345 | diff_average | difference average |
| 346 | V346 | dissimilarity | dissimilarity |
| 347 | V347 | inverse_variance | inverse variance |


| 348 | V348 | autocorrelation | autocorrelation |
| :---: | :---: | :---: | :---: |
| 349 | V349 | clust_tendency | cluster tendency |
| 350 | V350 | clust_shade | cluster shade |
| 351 | V351 | clust_prominence | cluster prominence |
| 352 | V352 | M_energy | energy |
| 353 | V353 | M_entropy | entropy |
| 354 | V354 | M_contrast | contrast |
| 355 | V355 | M_correlation | correlation |
| 356 | V356 | M_homogenity | homogeneity |
| 357 | V357 | M_homogenity_n | homogeneity normalized |
| 358 | V358 | M_idiff | inverese difference |
| 359 | V359 | M_idiff_n | inverese difference normalized |
| 360 | V360 | M_variance | variance |
| 361 | V361 | M_sum_average | sum of average |
| 362 | V362 | M_sum_entropy | sum of entropy |
| 363 | V363 | M_sum_variance | sum of variance |
| 364 | V364 | M_diff_entropy | difference entropy |
| 365 | V365 | M_diff_variance | difference variance |
| 366 | V366 | M_IMC1 | information measures of correlation 1 |
| 367 | V367 | M_IMC2 | information measures of correlation 2 |
| 368 | V368 | M_MCC | maximal correlation coefficient |
| 369 | V369 | M_joint_max | joint maximum |
| 370 | V370 | M_joint_average | joint average |
| 371 | V371 | M_diff_average | difference average |
| 372 | V372 | M_dissimilarity | dissimilarity |
| 373 | V373 | M_inverse_variance | inverse variance |
| 374 | V374 | M_autocorrelation | autocorrelation |
| 375 | V375 | M_clust_tendency | cluster tendency |
| 376 | V376 | M_clust_shade | cluster shade |
| 377 | V377 | M_clust_prominence | cluster prominence |
| 378 | V378 | coarseness | coarseness |
| 379 | V379 | neighContrast | contrast |
| 380 | V380 | busyness | busyness |
| 381 | V381 | complexity | complexity |
| 382 | V382 | strength | strength |
| 383 | V383 | len_intensityVar | grey level non-uniformity |
| 384 | V384 | len_intensityVar_n | grey level non-uniformity normalized |
| 385 | V385 | len_sizeVar | zone size non-uniformity |
| 386 | V386 | len_sizeVar_n | zone size non-uniformity normalized |
| 387 | V387 | len_sse | short runs emphasis |
| 388 | V388 | len_Ise | long runs emphasis |
| 389 | V389 | len_Igse | low grey level run emphasis |
| 390 | V390 | len_hgse | high grey level run emphasis |
| 391 | V391 | len_sslge | short run low grey level emphasis |
| 392 | V392 | len_sshge | short run high grey level emphasis |
| 393 | V393 | len_Islge | long run low grey level emphasis |
| 394 | V394 | len_Ishge | long run high grey level emphasis |
| 395 | V395 | len_rpc | run percentage |
| 396 | V396 | len_grey_lev_var | grey level variance |
| 397 | V397 | len_zone_size_var | run length variance |


| 398 | V398 | len_size_entropy | run entropy |
| :---: | :---: | :---: | :---: |
| 399 | V399 | M_len_intensityVar | grey level non-uniformity |
| 400 | V400 | M_len_intensityVar_n | grey level non-uniformity normalized |
| 401 | V401 | M_len_sizeVar | zone size non-uniformity |
| 402 | V402 | M_len_sizeVar_n | zone size non-uniformity normalized |
| 403 | V403 | M_len_sse | short runs emphasis |
| 404 | V404 | M_len_Ise | long runs emphasis |
| 405 | V405 | M_len_lgse | low grey level run emphasis |
| 406 | V406 | M_len_hgse | high grey level run emphasis |
| 407 | V407 | M_len_sslge | short run low grey level emphasis |
| 408 | V408 | M_len_sshge | short run high grey level emphasis |
| 409 | V409 | M_len_Islge | long run low grey level emphasis |
| 410 | V410 | M_len_Ishge | long run high grey level emphasis |
| 411 | V411 | M_len_rpc | run percentage |
| 412 | V412 | M_len_grey_lev_var | grey level variance |
| 413 | V413 | M_len_zone_size_var | run length variance |
| 414 | V414 | M_len_size_entropy | run entropy |
| 415 | V415 | intensityVar | grey level non-uniformity |
| 416 | V416 | intensityVar_n | grey level non-uniformity normalized |
| 417 | V417 | sizeVar | zone size non-uniformity |
| 418 | V418 | sizeVar_n | zone size non-uniformity normalized |
| 419 | V419 | sse | small zone emphasis |
| 420 | V420 | Ise | large zone emphasis |
| 421 | V421 | Igse | low grey level zone emphasis |
| 422 | V422 | hgse | high grey level zone emphasis |
| 423 | V423 | sslge | small zone low grey level emphasis |
| 424 | V424 | sshge | small zone high grey level emphasis |
| 425 | V425 | Islge | large zone low grey level emphasis |
| 426 | V426 | Ishge | large zone high grey level emphasis |
| 427 | V427 | rpc | zone percentage |
| 428 | V428 | grey_lev_var | grey level variance |
| 429 | V429 | zone_size_var | zone size variance |
| 430 | V430 | size_entropy | zone size entropy |
| 431 | V431 | GLDZM_intensityVar | grey level non-uniformity |
| 432 | V432 | GLDZM_intensityVar_n | grey level non-uniformity normalized |
| 433 | V433 | GLDZM_sizeVar | zone size non-uniformity |
| 434 | V434 | GLDZM_sizeVar_n | zone size non-uniformity normalized |
| 435 | V435 | GLDZM_sse | small distance emphasis |
| 436 | V436 | GLDZM_Ise | large distance emphasis |
| 437 | V437 | GLDZM_lgse | low grey level zone emphasis |
| 438 | V438 | GLDZM_hgse | high grey level zone emphasis |
| 439 | V439 | GLDZM_sslge | small distance low grey level emphasis |
| 440 | V440 | GLDZM_sshge | small distance high grey level emphasis |
| 441 | V441 | GLDZM_Islge | large distance low grey level emphasis |
| 442 | V442 | GLDZM_Ishge | large distance high grey level emphasis |
| 443 | V443 | GLDZM_rpc | zone percentage |
| 444 | V444 | GLDZM_grey_lev_var | grey level variance |
| 445 | V445 | GLDZM_zone_size_var | zone distance variance |
| 446 | V446 | GLDZM_size_entropy | zone distance entropy |
| 447 | V447 | NGLDM_intensityVar | grey level non-uniformity |


| 448 | V448 | NGLDM_intensityVar_n | grey level non-uniformity normalized |
| :---: | :---: | :---: | :---: |
| 449 | V449 | NGLDM_sizeVar | dependence count non-uniformity |
| 450 | V450 | NGLDM_sizeVar_n | dependence count non-uniformity normalized |
| 451 | V451 | NGLDM_sse | low dependence emphasis |
| 452 | V452 | NGLDM_Ise | high dependence emphasis |
| 453 | V453 | NGLDM_lgse | low grey level count emphasis |
| 454 | V454 | NGLDM_hgse | high grey level count emphasis |
| 455 | V455 | NGLDM_sslge | low dependence low grey level emphasis |
| 456 | V456 | NGLDM_sshge | low dependence high grey level emphasis |
| 457 | V457 | NGLDM_Islge | high dependence low grey level emphasis |
| 458 | V458 | NGLDM_Ishge | high dependence high grey level emphasis |
| 459 | V459 | NGLDM_grey_lev_var | grey level variance |
| 460 | V460 | NGLDM_zone_size_var | dependence count variance |
| 461 | V461 | NGLDM_size_entropy | dependence count entropy |
| 462 | V462 | NGLDM_energy | dependence count energy |
| 463 | V463 | Mean | mean |
| 464 | V464 | SD | standard deviation |
| 465 | V465 | COV | coefficient of variation |
| 466 | V466 | skewness | skewness |
| 467 | V467 | kurtosis | kurtosis |
| 468 | V468 | var | variance |
| 469 | V469 | median | median |
| 470 | V470 | percentile10 | percentile 10th |
| 471 | V471 | percentile90 | percentile 90th |
| 472 | V472 | iqr | interquartile range |
| 473 | V473 | Hrange | range |
| 474 | V474 | mad | mean absolut deviation |
| 475 | V475 | rmad | robust mean absolut deviation |
| 476 | V476 | H_energy | energy |
| 477 | V477 | H_entropy | entropy |
| 478 | V478 | rms | root mean square |
| 479 | V479 | H_uniformity | uniformity |
| 480 | V480 | energy | energy |
| 481 | V481 | entropy | entropy |
| 482 | V482 | contrast | contrast |
| 483 | V483 | correlation | correlation |
| 484 | V484 | homogenity | homogeneity |
| 485 | V485 | homogenity_n | homogeneity normalized |
| 486 | V486 | idiff | inverese difference |
| 487 | V487 | idiff_n | inverese difference normalized |
| 488 | V488 | variance | variance |
| 489 | V489 | sum_average | sum of average |
| 490 | V490 | sum_entropy | sum of entropy |
| 491 | V491 | sum_variance | sum of variance |
| 492 | V492 | diff_entropy | difference entropy |
| 493 | V493 | diff_variance | difference variance |
| 494 | V494 | IMC1 | information measures of correlation 1 |
| 495 | V495 | IMC2 | information measures of correlation 2 |
| 496 | V496 | MCC | maximal correlation coefficient |
| 497 | V497 | joint_max | joint maximum |


| 498 | V498 | joint_average | joint average |
| :---: | :---: | :---: | :---: |
| 499 | V499 | diff_average | difference average |
| 500 | V500 | dissimilarity | dissimilarity |
| 501 | V501 | inverse_variance | inverse variance |
| 502 | V502 | autocorrelation | autocorrelation |
| 503 | V503 | clust_tendency | cluster tendency |
| 504 | V504 | clust_shade | cluster shade |
| 505 | V505 | clust_prominence | cluster prominence |
| 506 | V506 | M_energy | energy |
| 507 | V507 | M_entropy | entropy |
| 508 | V508 | M_contrast | contrast |
| 509 | V509 | M_correlation | correlation |
| 510 | V510 | M_homogenity | homogeneity |
| 511 | V511 | M_homogenity_n | homogeneity normalized |
| 512 | V512 | M_idiff | inverese difference |
| 513 | V513 | M_idiff_n | inverese difference normalized |
| 514 | V514 | M_variance | variance |
| 515 | V515 | M_sum_average | sum of average |
| 516 | V516 | M_sum_entropy | sum of entropy |
| 517 | V517 | M_sum_variance | sum of variance |
| 518 | V518 | M_diff_entropy | difference entropy |
| 519 | V519 | M_diff_variance | difference variance |
| 520 | V520 | M_IMC1 | information measures of correlation 1 |
| 521 | V521 | M_IMC2 | information measures of correlation 2 |
| 522 | V522 | M_MCC | maximal correlation coefficient |
| 523 | V523 | M_joint_max | joint maximum |
| 524 | V524 | M_joint_average | joint average |
| 525 | V525 | M_diff_average | difference average |
| 526 | V526 | M_dissimilarity | dissimilarity |
| 527 | V527 | M_inverse_variance | inverse variance |
| 528 | V528 | M_autocorrelation | autocorrelation |
| 529 | V529 | M_clust_tendency | cluster tendency |
| 530 | V530 | M_clust_shade | cluster shade |
| 531 | V531 | M_clust_prominence | cluster prominence |
| 532 | V532 | coarseness | coarseness |
| 533 | V533 | neighContrast | contrast |
| 534 | V534 | busyness | busyness |
| 535 | V535 | complexity | complexity |
| 536 | V536 | strength | strength |
| 537 | V537 | len_intensityVar | grey level non-uniformity |
| 538 | V538 | len_intensityVar_n | grey level non-uniformity normalized |
| 539 | V539 | len_sizeVar | zone size non-uniformity |
| 540 | V540 | len_sizeVar_n | zone size non-uniformity normalized |
| 541 | V541 | len_sse | short runs emphasis |
| 542 | V542 | len_Ise | long runs emphasis |
| 543 | V543 | len_lgse | low grey level run emphasis |
| 544 | V544 | len_hgse | high grey level run emphasis |
| 545 | V545 | len_sslge | short run low grey level emphasis |
| 546 | V546 | len_sshge | short run high grey level emphasis |
| 547 | V547 | len_Islge | long run low grey level emphasis |


| 548 | V548 | len_Ishge | long run high grey level emphasis |
| :---: | :---: | :---: | :---: |
| 549 | V549 | len_rpc | run percentage |
| 550 | V550 | len_grey_lev_var | grey level variance |
| 551 | V551 | len_zone_size_var | run length variance |
| 552 | V552 | len_size_entropy | run entropy |
| 553 | V553 | M_len_intensityVar | grey level non-uniformity |
| 554 | V554 | M_len_intensityVar_n | grey level non-uniformity normalized |
| 555 | V555 | M_len_sizeVar | zone size non-uniformity |
| 556 | V556 | M_len_sizeVar_n | zone size non-uniformity normalized |
| 557 | V557 | M_len_sse | short runs emphasis |
| 558 | V558 | M_len_Ise | long runs emphasis |
| 559 | V559 | M_len_lgse | low grey level run emphasis |
| 560 | V560 | M_len_hgse | high grey level run emphasis |
| 561 | V561 | M_len_sslge | short run low grey level emphasis |
| 562 | V562 | M_len_sshge | short run high grey level emphasis |
| 563 | V563 | M_len_Islge | long run low grey level emphasis |
| 564 | V564 | M_len_Ishge | long run high grey level emphasis |
| 565 | V565 | M_len_rpc | run percentage |
| 566 | V566 | M_len_grey_lev_var | grey level variance |
| 567 | V567 | M_len_zone_size_var | run length variance |
| 568 | V568 | M_len_size_entropy | run entropy |
| 569 | V569 | intensityVar | grey level non-uniformity |
| 570 | V570 | intensityVar_n | grey level non-uniformity normalized |
| 571 | V571 | sizeVar | zone size non-uniformity |
| 572 | V572 | sizeVar_n | zone size non-uniformity normalized |
| 573 | V573 | sse | small zone emphasis |
| 574 | V574 | Ise | large zone emphasis |
| 575 | V575 | lgse | low grey level zone emphasis |
| 576 | V576 | hgse | high grey level zone emphasis |
| 577 | V577 | sslge | small zone low grey level emphasis |
| 578 | V578 | sshge | small zone high grey level emphasis |
| 579 | V579 | Islge | large zone low grey level emphasis |
| 580 | V580 | Ishge | large zone high grey level emphasis |
| 581 | V581 | rpc | zone percentage |
| 582 | V582 | grey_lev_var | grey level variance |
| 583 | V583 | zone_size_var | zone size variance |
| 584 | V584 | size_entropy | zone size entropy |
| 585 | V585 | GLDZM_intensityVar | grey level non-uniformity |
| 586 | V586 | GLDZM_intensityVar_n | grey level non-uniformity normalized |
| 587 | V587 | GLDZM_sizeVar | zone size non-uniformity |
| 588 | V588 | GLDZM_sizeVar_n | zone size non-uniformity normalized |
| 589 | V589 | GLDZM_sse | small distance emphasis |
| 590 | V590 | GLDZM_Ise | large distance emphasis |
| 591 | V591 | GLDZM_lgse | low grey level zone emphasis |
| 592 | V592 | GLDZM_hgse | high grey level zone emphasis |
| 593 | V593 | GLDZM_sslge | small distance low grey level emphasis |
| 594 | V594 | GLDZM_sshge | small distance high grey level emphasis |
| 595 | V595 | GLDZM_Islge | large distance low grey level emphasis |
| 596 | V596 | GLDZM_Ishge | large distance high grey level emphasis |
| 597 | V597 | GLDZM_rpc | zone percentage |


| 598 | V598 | GLDZM_grey_lev_var | grey level variance |
| :---: | :---: | :---: | :---: |
| 599 | V599 | GLDZM_zone_size_var | zone distance variance |
| 600 | V600 | GLDZM_size_entropy | zone distance entropy |
| 601 | V601 | NGLDM_intensityVar | grey level non-uniformity |
| 602 | V602 | NGLDM_intensityVar_n | grey level non-uniformity normalized |
| 603 | V603 | NGLDM_sizeVar | dependence count non-uniformity |
| 604 | V604 | NGLDM_sizeVar_n | dependence count non-uniformity normalized |
| 605 | V605 | NGLDM_sse | low dependence emphasis |
| 606 | V606 | NGLDM_Ise | high dependence emphasis |
| 607 | V607 | NGLDM_lgse | low grey level count emphasis |
| 608 | V608 | NGLDM_hgse | high grey level count emphasis |
| 609 | V609 | NGLDM_sslge | low dependence low grey level emphasis |
| 610 | V610 | NGLDM_sshge | low dependence high grey level emphasis |
| 611 | V611 | NGLDM_Islge | high dependence low grey level emphasis |
| 612 | V612 | NGLDM_Ishge | high dependence high grey level emphasis |
| 613 | V613 | NGLDM_grey_lev_var | grey level variance |
| 614 | V614 | NGLDM_zone_size_var | dependence count variance |
| 615 | V615 | NGLDM_size_entropy | dependence count entropy |
| 616 | V616 | NGLDM_energy | dependence count energy |
| 617 | V617 | Mean | mean |
| 618 | V618 | SD | standard deviation |
| 619 | V619 | COV | coefficient of variation |
| 620 | V620 | skewness | skewness |
| 621 | V621 | kurtosis | kurtosis |
| 622 | V622 | var | variance |
| 623 | V623 | median | median |
| 624 | V624 | percentile10 | percentile 10th |
| 625 | V625 | percentile90 | percentile 90th |
| 626 | V626 | iqr | interquartile range |
| 627 | V627 | Hrange | range |
| 628 | V628 | mad | mean absolut deviation |
| 629 | V629 | rmad | robust mean absolut deviation |
| 630 | V630 | H_energy | energy |
| 631 | V631 | H_entropy | entropy |
| 632 | V632 | rms | root mean square |
| 633 | V633 | H_uniformity | uniformity |
| 634 | V634 | energy | energy |
| 635 | V635 | entropy | entropy |
| 636 | V636 | contrast | contrast |
| 637 | V637 | correlation | correlation |
| 638 | V638 | homogenity | homogeneity |
| 639 | V639 | homogenity_n | homogeneity normalized |
| 640 | V640 | idiff | inverese difference |
| 641 | V641 | idiff_n | inverese difference normalized |
| 642 | V642 | variance | variance |
| 643 | V643 | sum_average | sum of average |
| 644 | V644 | sum_entropy | sum of entropy |
| 645 | V645 | sum_variance | sum of variance |
| 646 | V646 | diff_entropy | difference entropy |
| 647 | V647 | diff_variance | difference variance |


| 648 | V648 | IMC1 | information measures of correlation 1 |
| :---: | :---: | :---: | :---: |
| 649 | V649 | IMC2 | information measures of correlation 2 |
| 650 | V650 | MCC | maximal correlation coefficient |
| 651 | V651 | joint_max | joint maximum |
| 652 | V652 | joint_average | joint average |
| 653 | V653 | diff_average | difference average |
| 654 | V654 | dissimilarity | dissimilarity |
| 655 | V655 | inverse_variance | inverse variance |
| 656 | V656 | autocorrelation | autocorrelation |
| 657 | V657 | clust_tendency | cluster tendency |
| 658 | V658 | clust_shade | cluster shade |
| 659 | V659 | clust_prominence | cluster prominence |
| 660 | V660 | M_energy | energy |
| 661 | V661 | M_entropy | entropy |
| 662 | V662 | M_contrast | contrast |
| 663 | V663 | M_correlation | correlation |
| 664 | V664 | M_homogenity | homogeneity |
| 665 | V665 | M_homogenity_n | homogeneity normalized |
| 666 | V666 | M_idiff | inverese difference |
| 667 | V667 | M_idiff_n | inverese difference normalized |
| 668 | V668 | M_variance | variance |
| 669 | V669 | M_sum_average | sum of average |
| 670 | V670 | M_sum_entropy | sum of entropy |
| 671 | V671 | M_sum_variance | sum of variance |
| 672 | V672 | M_diff_entropy | difference entropy |
| 673 | V673 | M_diff_variance | difference variance |
| 674 | V674 | M_IMC1 | information measures of correlation 1 |
| 675 | V675 | M_IMC2 | information measures of correlation 2 |
| 676 | V676 | M_MCC | maximal correlation coefficient |
| 677 | V677 | M_joint_max | joint maximum |
| 678 | V678 | M _oint_average | joint average |
| 679 | V679 | M_diff_average | difference average |
| 680 | V680 | M_dissimilarity | dissimilarity |
| 681 | V681 | M_inverse_variance | inverse variance |
| 682 | V682 | M_autocorrelation | autocorrelation |
| 683 | V683 | M_clust_tendency | cluster tendency |
| 684 | V684 | M_clust_shade | cluster shade |
| 685 | V685 | M_clust_prominence | cluster prominence |
| 686 | V686 | coarseness | coarseness |
| 687 | V687 | neighContrast | contrast |
| 688 | V688 | busyness | busyness |
| 689 | V689 | complexity | complexity |
| 690 | V690 | strength | strength |
| 691 | V691 | len_intensityVar | grey level non-uniformity |
| 692 | V692 | len_intensityVar_n | grey level non-uniformity normalized |
| 693 | V693 | len_sizeVar | zone size non-uniformity |
| 694 | V694 | len_sizeVar_n | zone size non-uniformity normalized |
| 695 | V695 | len_sse | short runs emphasis |
| 696 | V696 | len_Ise | long runs emphasis |
| 697 | V697 | len_lgse | low grey level run emphasis |


| 698 | V698 | len_hgse | high grey level run emphasis |
| :---: | :---: | :---: | :---: |
| 699 | V699 | len_sslge | short run low grey level emphasis |
| 700 | V700 | len_sshge | short run high grey level emphasis |
| 701 | V701 | len_Islge | long run low grey level emphasis |
| 702 | V702 | len_Ishge | long run high grey level emphasis |
| 703 | V703 | len_rpc | run percentage |
| 704 | V704 | len_grey_lev_var | grey level variance |
| 705 | V705 | len_zone_size_var | run length variance |
| 706 | V706 | len_size_entropy | run entropy |
| 707 | V707 | M_len_intensityVar | grey level non-uniformity |
| 708 | V708 | M_len_intensityVar_n | grey level non-uniformity normalized |
| 709 | V709 | M_len_sizeVar | zone size non-uniformity |
| 710 | V710 | M_len_sizeVar_n | zone size non-uniformity normalized |
| 711 | V711 | M_len_sse | short runs emphasis |
| 712 | V712 | M_len_Ise | long runs emphasis |
| 713 | V713 | M_len_lgse | low grey level run emphasis |
| 714 | V714 | M_len_hgse | high grey level run emphasis |
| 715 | V715 | M_len_sslge | short run low grey level emphasis |
| 716 | V716 | M_len_sshge | short run high grey level emphasis |
| 717 | V717 | M_len_Islge | long run low grey level emphasis |
| 718 | V718 | M_len_Ishge | long run high grey level emphasis |
| 719 | V719 | M_len_rpc | run percentage |
| 720 | V720 | M_len_grey_lev_var | grey level variance |
| 721 | V721 | M_len_zone_size_var | run length variance |
| 722 | V722 | M_len_size_entropy | run entropy |
| 723 | V723 | intensityVar | grey level non-uniformity |
| 724 | V724 | intensityVar_n | grey level non-uniformity normalized |
| 725 | V725 | sizeVar | zone size non-uniformity |
| 726 | V726 | sizeVar_n | zone size non-uniformity normalized |
| 727 | V727 | sse | small zone emphasis |
| 728 | V728 | Ise | large zone emphasis |
| 729 | V729 | Igse | low grey level zone emphasis |
| 730 | V730 | hgse | high grey level zone emphasis |
| 731 | V731 | sslge | small zone low grey level emphasis |
| 732 | V732 | sshge | small zone high grey level emphasis |
| 733 | V733 | Islge | large zone low grey level emphasis |
| 734 | V734 | Ishge | large zone high grey level emphasis |
| 735 | V735 | rpc | zone percentage |
| 736 | V736 | grey_lev_var | grey level variance |
| 737 | V737 | zone_size_var | zone size variance |
| 738 | V738 | size_entropy | zone size entropy |
| 739 | V739 | GLDZM_intensityVar | grey level non-uniformity |
| 740 | V740 | GLDZM_intensityVar_n | grey level non-uniformity normalized |
| 741 | V741 | GLDZM_sizeVar | zone size non-uniformity |
| 742 | V742 | GLDZM_sizeVar_n | zone size non-uniformity normalized |
| 743 | V743 | GLDZM_sse | small distance emphasis |
| 744 | V744 | GLDZM_Ise | large distance emphasis |
| 745 | V745 | GLDZM_lgse | low grey level zone emphasis |
| 746 | V746 | GLDZM_hgse | high grey level zone emphasis |
| 747 | V747 | GLDZM_sslge | small distance low grey level emphasis |


| 748 | V748 | GLDZM_sshge | small distance high grey level emphasis |
| :---: | :---: | :---: | :---: |
| 749 | V749 | GLDZM_Islge | large distance low grey level emphasis |
| 750 | V750 | GLDZM_Ishge | large distance high grey level emphasis |
| 751 | V751 | GLDZM_rpc | zone percentage |
| 752 | V752 | GLDZM_grey_lev_var | grey level variance |
| 753 | V753 | GLDZM_zone_size_var | zone distance variance |
| 754 | V754 | GLDZM_size_entropy | zone distance entropy |
| 755 | V755 | NGLDM_intensityVar | grey level non-uniformity |
| 756 | V756 | NGLDM_intensityVar_n | grey level non-uniformity normalized |
| 757 | V757 | NGLDM_sizeVar | dependence count non-uniformity |
| 758 | V758 | NGLDM_sizeVar_n | dependence count non-uniformity normalized |
| 759 | V759 | NGLDM_sse | low dependence emphasis |
| 760 | V760 | NGLDM_Ise | high dependence emphasis |
| 761 | V761 | NGLDM_lgse | low grey level count emphasis |
| 762 | V762 | NGLDM_hgse | high grey level count emphasis |
| 763 | V763 | NGLDM_sslge | low dependence low grey level emphasis |
| 764 | V764 | NGLDM_sshge | low dependence high grey level emphasis |
| 765 | V765 | NGLDM_Islge | high dependence low grey level emphasis |
| 766 | V766 | NGLDM_Ishge | high dependence high grey level emphasis |
| 767 | V767 | NGLDM_grey_lev_var | grey level variance |
| 768 | V768 | NGLDM_zone_size_var | dependence count variance |
| 769 | V769 | NGLDM_size_entropy | dependence count entropy |
| 770 | V770 | NGLDM_energy | dependence count energy |
| 771 | V771 | Mean | mean |
| 772 | V772 | SD | standard deviation |
| 773 | V773 | COV | coefficient of variation |
| 774 | V774 | skewness | skewness |
| 775 | V775 | kurtosis | kurtosis |
| 776 | V776 | var | variance |
| 777 | V777 | median | median |
| 778 | V778 | percentile10 | percentile 10th |
| 779 | V779 | percentile90 | percentile 90th |
| 780 | V780 | iqr | interquartile range |
| 781 | V781 | Hrange | range |
| 782 | V782 | mad | mean absolut deviation |
| 783 | V783 | rmad | robust mean absolut deviation |
| 784 | V784 | H_energy | energy |
| 785 | V785 | H_entropy | entropy |
| 786 | V786 | rms | root mean square |
| 787 | V787 | H_uniformity | uniformity |
| 788 | V788 | energy | energy |
| 789 | V789 | entropy | entropy |
| 790 | V790 | contrast | contrast |
| 791 | V791 | correlation | correlation |
| 792 | V792 | homogenity | homogeneity |
| 793 | V793 | homogenity_n | homogeneity normalized |
| 794 | V794 | idiff | inverese difference |
| 795 | V795 | idiff_n | inverese difference normalized |
| 796 | V796 | variance | variance |
| 797 | V797 | sum_average | sum of average |


| 798 | V798 | sum_entropy | sum of entropy |
| :---: | :---: | :---: | :---: |
| 799 | V799 | sum_variance | sum of variance |
| 800 | V800 | diff_entropy | difference entropy |
| 801 | V801 | diff_variance | difference variance |
| 802 | V802 | IMC1 | information measures of correlation 1 |
| 803 | V803 | IMC2 | information measures of correlation 2 |
| 804 | V804 | MCC | maximal correlation coefficient |
| 805 | V805 | joint_max | joint maximum |
| 806 | V806 | joint_average | joint average |
| 807 | V807 | diff_average | difference average |
| 808 | V808 | dissimilarity | dissimilarity |
| 809 | V809 | inverse_variance | inverse variance |
| 810 | V810 | autocorrelation | autocorrelation |
| 811 | V811 | clust_tendency | cluster tendency |
| 812 | V812 | clust_shade | cluster shade |
| 813 | V813 | clust_prominence | cluster prominence |
| 814 | V814 | M_energy | energy |
| 815 | V815 | M_entropy | entropy |
| 816 | V816 | M_contrast | contrast |
| 817 | V817 | M_correlation | correlation |
| 818 | V818 | M_homogenity | homogeneity |
| 819 | V819 | M_homogenity_n | homogeneity normalized |
| 820 | V820 | M_idiff | inverese difference |
| 821 | V821 | M_idiff_n | inverese difference normalized |
| 822 | V822 | M_variance | variance |
| 823 | V823 | M_sum_average | sum of average |
| 824 | V824 | M_sum_entropy | sum of entropy |
| 825 | V825 | M_sum_variance | sum of variance |
| 826 | V826 | M_diff_entropy | difference entropy |
| 827 | V827 | M_diff_variance | difference variance |
| 828 | V828 | M_IMC1 | information measures of correlation 1 |
| 829 | V829 | M_IMC2 | information measures of correlation 2 |
| 830 | V830 | M_MCC | maximal correlation coefficient |
| 831 | V831 | M_joint_max | joint maximum |
| 832 | V832 | M_joint_average | joint average |
| 833 | V833 | M_diff_average | difference average |
| 834 | V834 | M_dissimilarity | dissimilarity |
| 835 | V835 | M_inverse_variance | inverse variance |
| 836 | V836 | M_autocorrelation | autocorrelation |
| 837 | V837 | M_clust_tendency | cluster tendency |
| 838 | V838 | M_clust_shade | cluster shade |
| 839 | V839 | M_clust_prominence | cluster prominence |
| 840 | V840 | coarseness | coarseness |
| 841 | V841 | neighContrast | contrast |
| 842 | V842 | busyness | busyness |
| 843 | V843 | complexity | complexity |
| 844 | V844 | strength | strength |
| 845 | V845 | len_intensityVar | grey level non-uniformity |
| 846 | V846 | len_intensityVar_n | grey level non-uniformity normalized |
| 847 | V847 | len_sizeVar | zone size non-uniformity |


| 848 | V848 | len_sizeVar_n | zone size non-uniformity normalized |
| :---: | :---: | :---: | :---: |
| 849 | V849 | len_sse | short runs emphasis |
| 850 | V850 | len_Ise | long runs emphasis |
| 851 | V851 | len_lgse | low grey level run emphasis |
| 852 | V852 | len_hgse | high grey level run emphasis |
| 853 | V853 | len_sslge | short run low grey level emphasis |
| 854 | V854 | len_sshge | short run high grey level emphasis |
| 855 | V855 | len_Islge | long run low grey level emphasis |
| 856 | V856 | len_Ishge | long run high grey level emphasis |
| 857 | V857 | len_rpc | run percentage |
| 858 | V858 | len_grey_lev_var | grey level variance |
| 859 | V859 | len_zone_size_var | run length variance |
| 860 | V860 | len_size_entropy | run entropy |
| 861 | V861 | M_len_intensityVar | grey level non-uniformity |
| 862 | V862 | M_len_intensityVar_n | grey level non-uniformity normalized |
| 863 | V863 | M_len_sizeVar | zone size non-uniformity |
| 864 | V864 | M_len_sizeVar_n | zone size non-uniformity normalized |
| 865 | V865 | M_len_sse | short runs emphasis |
| 866 | V866 | M_len_Ise | long runs emphasis |
| 867 | V867 | M_len_lgse | low grey level run emphasis |
| 868 | V868 | M_len_hgse | high grey level run emphasis |
| 869 | V869 | M_len_sslge | short run low grey level emphasis |
| 870 | V870 | M_len_sshge | short run high grey level emphasis |
| 871 | V871 | M_len_Islge | long run low grey level emphasis |
| 872 | V872 | M_len_Ishge | long run high grey level emphasis |
| 873 | V873 | M_len_rpc | run percentage |
| 874 | V874 | M_len_grey_lev_var | grey level variance |
| 875 | V875 | M_len_zone_size_var | run length variance |
| 876 | V876 | M_len_size_entropy | run entropy |
| 877 | V877 | intensityVar | grey level non-uniformity |
| 878 | V878 | intensityVar_n | grey level non-uniformity normalized |
| 879 | V879 | sizeVar | zone size non-uniformity |
| 880 | V880 | sizeVar_n | zone size non-uniformity normalized |
| 881 | V881 | sse | small zone emphasis |
| 882 | V882 | Ise | large zone emphasis |
| 883 | V883 | Igse | low grey level zone emphasis |
| 884 | V884 | hgse | high grey level zone emphasis |
| 885 | V885 | sslge | small zone low grey level emphasis |
| 886 | V886 | sshge | small zone high grey level emphasis |
| 887 | V887 | Islge | large zone low grey level emphasis |
| 888 | V888 | Ishge | large zone high grey level emphasis |
| 889 | V889 | rpc | zone percentage |
| 890 | V890 | grey_lev_var | grey level variance |
| 891 | V891 | zone_size_var | zone size variance |
| 892 | V892 | size_entropy | zone size entropy |
| 893 | V893 | GLDZM_intensityVar | grey level non-uniformity |
| 894 | V894 | GLDZM_intensityVar_n | grey level non-uniformity normalized |
| 895 | V895 | GLDZM_sizeVar | zone size non-uniformity |
| 896 | V896 | GLDZM_sizeVar_n | zone size non-uniformity normalized |
| 897 | V897 | GLDZM_sse | small distance emphasis |


| 898 | V898 | GLDZM_Ise | large distance emphasis |
| :---: | :---: | :---: | :---: |
| 899 | V899 | GLDZM_lgse | low grey level zone emphasis |
| 900 | V900 | GLDZM_hgse | high grey level zone emphasis |
| 901 | V901 | GLDZM_sslge | small distance low grey level emphasis |
| 902 | V902 | GLDZM_sshge | small distance high grey level emphasis |
| 903 | V903 | GLDZM_Islge | large distance low grey level emphasis |
| 904 | V904 | GLDZM_Ishge | large distance high grey level emphasis |
| 905 | V905 | GLDZM_rpc | zone percentage |
| 906 | V906 | GLDZM_grey_lev_var | grey level variance |
| 907 | V907 | GLDZM_zone_size_var | zone distance variance |
| 908 | V908 | GLDZM_size_entropy | zone distance entropy |
| 909 | V909 | NGLDM_intensityVar | grey level non-uniformity |
| 910 | V910 | NGLDM_intensityVar_n | grey level non-uniformity normalized |
| 911 | V911 | NGLDM_sizeVar | dependence count non-uniformity |
| 912 | V912 | NGLDM_sizeVar_n | dependence count non-uniformity normalized |
| 913 | V913 | NGLDM_sse | low dependence emphasis |
| 914 | V914 | NGLDM_Ise | high dependence emphasis |
| 915 | V915 | NGLDM_lgse | low grey level count emphasis |
| 916 | V916 | NGLDM_hgse | high grey level count emphasis |
| 917 | V917 | NGLDM_sslge | low dependence low grey level emphasis |
| 918 | V918 | NGLDM_sshge | low dependence high grey level emphasis |
| 919 | V919 | NGLDM_Islge | high dependence low grey level emphasis |
| 920 | V920 | NGLDM_Ishge | high dependence high grey level emphasis |
| 921 | V921 | NGLDM_grey_lev_var | grey level variance |
| 922 | V922 | NGLDM_zone_size_var | dependence count variance |
| 923 | V923 | NGLDM_size_entropy | dependence count entropy |
| 924 | V924 | NGLDM_energy | dependence count energy |
| 925 | V925 | Mean | mean |
| 926 | V926 | SD | standard deviation |
| 927 | V927 | COV | coefficient of variation |
| 928 | V928 | skewness | skewness |
| 929 | V929 | kurtosis | kurtosis |
| 930 | V930 | var | variance |
| 931 | V931 | median | median |
| 932 | V932 | percentile10 | percentile 10th |
| 933 | V933 | percentile90 | percentile 90th |
| 934 | V934 | iqr | interquartile range |
| 935 | V935 | Hrange | range |
| 936 | V936 | mad | mean absolut deviation |
| 937 | V937 | rmad | robust mean absolut deviation |
| 938 | V938 | H_energy | energy |
| 939 | V939 | H_entropy | entropy |
| 940 | V940 | rms | root mean square |
| 941 | V941 | H_uniformity | uniformity |
| 942 | V942 | energy | energy |
| 943 | V943 | entropy | entropy |
| 944 | V944 | contrast | contrast |
| 945 | V945 | correlation | correlation |
| 946 | V946 | homogenity | homogeneity |
| 947 | V947 | homogenity_n | homogeneity normalized |


| 948 | V948 | idiff | inverese difference |
| :---: | :---: | :---: | :---: |
| 949 | V949 | idiff_n | inverese difference normalized |
| 950 | V950 | variance | variance |
| 951 | V951 | sum_average | sum of average |
| 952 | V952 | sum_entropy | sum of entropy |
| 953 | V953 | sum_variance | sum of variance |
| 954 | V954 | diff_entropy | difference entropy |
| 955 | V955 | diff_variance | difference variance |
| 956 | V956 | IMC1 | information measures of correlation 1 |
| 957 | V957 | IMC2 | information measures of correlation 2 |
| 958 | V958 | MCC | maximal correlation coefficient |
| 959 | V959 | joint_max | joint maximum |
| 960 | V960 | joint_average | joint average |
| 961 | V961 | diff_average | difference average |
| 962 | V962 | dissimilarity | dissimilarity |
| 963 | V963 | inverse_variance | inverse variance |
| 964 | V964 | autocorrelation | autocorrelation |
| 965 | V965 | clust_tendency | cluster tendency |
| 966 | V966 | clust_shade | cluster shade |
| 967 | V967 | clust_prominence | cluster prominence |
| 968 | V968 | M_energy | energy |
| 969 | V969 | M_entropy | entropy |
| 970 | V970 | M_contrast | contrast |
| 971 | V971 | M_correlation | correlation |
| 972 | V972 | M_homogenity | homogeneity |
| 973 | V973 | M_homogenity_n | homogeneity normalized |
| 974 | V974 | M_idiff | inverese difference |
| 975 | V975 | M_idiff_n | inverese difference normalized |
| 976 | V976 | M_variance | variance |
| 977 | V977 | M_sum_average | sum of average |
| 978 | V978 | M_sum_entropy | sum of entropy |
| 979 | V979 | M_sum_variance | sum of variance |
| 980 | V980 | M_diff_entropy | difference entropy |
| 981 | V981 | M_diff_variance | difference variance |
| 982 | V982 | M_IMC1 | information measures of correlation 1 |
| 983 | V983 | M_IMC2 | information measures of correlation 2 |
| 984 | V984 | M_MCC | maximal correlation coefficient |
| 985 | V985 | M_joint_max | joint maximum |
| 986 | V986 | M -joint_average | joint average |
| 987 | V987 | M_diff_average | difference average |
| 988 | V988 | M_dissimilarity | dissimilarity |
| 989 | V989 | M_inverse_variance | inverse variance |
| 990 | V990 | M_autocorrelation | autocorrelation |
| 991 | V991 | M_clust_tendency | cluster tendency |
| 992 | V992 | M_clust_shade | cluster shade |
| 993 | V993 | M_clust_prominence | cluster prominence |
| 994 | V994 | coarseness | coarseness |
| 995 | V995 | neighContrast | contrast |
| 996 | V996 | busyness | busyness |
| 997 | V997 | complexity | complexity |


| 998 | V998 | strength | strength |
| :---: | :---: | :---: | :---: |
| 999 | V999 | len_intensityVar | grey level non-uniformity |
| 1000 | V1000 | len_intensityVar_n | grey level non-uniformity normalized |
| 1001 | V1001 | len_sizeVar | zone size non-uniformity |
| 1002 | V1002 | len_sizeVar_n | zone size non-uniformity normalized |
| 1003 | V1003 | len_sse | short runs emphasis |
| 1004 | V1004 | len_Ise | long runs emphasis |
| 1005 | V1005 | len_lgse | low grey level run emphasis |
| 1006 | V1006 | len_hgse | high grey level run emphasis |
| 1007 | V1007 | len_sslge | short run low grey level emphasis |
| 1008 | V1008 | len_sshge | short run high grey level emphasis |
| 1009 | V1009 | len_Islge | long run low grey level emphasis |
| 1010 | V1010 | len_lshge | long run high grey level emphasis |
| 1011 | V1011 | len_rpo | run percentage |
| 1012 | V1012 | len_grey_lev_var | grey level variance |
| 1013 | V1013 | len_zone_size_var | run length variance |
| 1014 | V1014 | len_size_entropy | run entropy |
| 1015 | V1015 | M_len_intensityVar | grey level non-uniformity |
| 1016 | V1016 | M_len_intensityVar_n | grey level non-uniformity normalized |
| 1017 | V1017 | M_len_sizeVar | zone size non-uniformity |
| 1018 | V1018 | M_len_sizeVar_n | zone size non-uniformity normalized |
| 1019 | V1019 | M_len_sse | short runs emphasis |
| 1020 | V1020 | M_len_Ise | long runs emphasis |
| 1021 | V1021 | M_len_lgse | low grey level run emphasis |
| 1022 | V1022 | M_len_hgse | high grey level run emphasis |
| 1023 | V1023 | M_len_sslge | short run low grey level emphasis |
| 1024 | V1024 | M_len_sshge | short run high grey level emphasis |
| 1025 | V1025 | M_len_Islge | long run low grey level emphasis |
| 1026 | V1026 | M_len_Ishge | long run high grey level emphasis |
| 1027 | V1027 | M_len_rpc | run percentage |
| 1028 | V1028 | M_len_grey_lev_var | grey level variance |
| 1029 | V1029 | M_len_zone_size_var | run length variance |
| 1030 | V1030 | M_len_size_entropy | run entropy |
| 1031 | V1031 | intensityVar | grey level non-uniformity |
| 1032 | V1032 | intensityVar_n | grey level non-uniformity normalized |
| 1033 | V1033 | sizeVar | zone size non-uniformity |
| 1034 | V1034 | sizeVar_n | zone size non-uniformity normalized |
| 1035 | V1035 | sse | small zone emphasis |
| 1036 | V1036 | Ise | large zone emphasis |
| 1037 | V1037 | Igse | low grey level zone emphasis |
| 1038 | V1038 | hgse | high grey level zone emphasis |
| 1039 | V1039 | sslge | small zone low grey level emphasis |
| 1040 | V1040 | sshge | small zone high grey level emphasis |
| 1041 | V1041 | Islge | large zone low grey level emphasis |
| 1042 | V1042 | Ishge | large zone high grey level emphasis |
| 1043 | V1043 | rpc | zone percentage |
| 1044 | V1044 | grey_lev_var | grey level variance |
| 1045 | V1045 | zone_size_var | zone size variance |
| 1046 | V1046 | size_entropy | zone size entropy |
| 1047 | V1047 | GLDZM_intensityVar | grey level non-uniformity |


| 1048 | V1048 | GLDZM_intensityVar_n | grey level non-uniformity normalized |
| :---: | :---: | :---: | :---: |
| 1049 | V1049 | GLDZM_sizeVar | zone size non-uniformity |
| 1050 | V1050 | GLDZM_sizeVar_n | zone size non-uniformity normalized |
| 1051 | V1051 | GLDZM_sse | small distance emphasis |
| 1052 | V1052 | GLDZM_Ise | large distance emphasis |
| 1053 | V1053 | GLDZM_lgse | low grey level zone emphasis |
| 1054 | V1054 | GLDZM_hgse | high grey level zone emphasis |
| 1055 | V1055 | GLDZM_sslge | small distance low grey level emphasis |
| 1056 | V1056 | GLDZM_sshge | small distance high grey level emphasis |
| 1057 | V1057 | GLDZM_Islge | large distance low grey level emphasis |
| 1058 | V1058 | GLDZM_Ishge | large distance high grey level emphasis |
| 1059 | V1059 | GLDZM_rpc | zone percentage |
| 1060 | V1060 | GLDZM_grey_lev_var | grey level variance |
| 1061 | V1061 | GLDZM_zone_size_var | zone distance variance |
| 1062 | V1062 | GLDZM_size_entropy | zone distance entropy |
| 1063 | V1063 | NGLDM_intensityVar | grey level non-uniformity |
| 1064 | V1064 | NGLDM_intensityVar_n | grey level non-uniformity normalized |
| 1065 | V1065 | NGLDM_sizeVar | dependence count non-uniformity |
| 1066 | V1066 | NGLDM_sizeVar_n | dependence count non-uniformity normalized |
| 1067 | V1067 | NGLDM_sse | low dependence emphasis |
| 1068 | V1068 | NGLDM_Ise | high dependence emphasis |
| 1069 | V1069 | NGLDM_lgse | low grey level count emphasis |
| 1070 | V1070 | NGLDM_hgse | high grey level count emphasis |
| 1071 | V1071 | NGLDM_sslge | low dependence low grey level emphasis |
| 1072 | V1072 | NGLDM_sshge | low dependence high grey level emphasis |
| 1073 | V1073 | NGLDM_Islge | high dependence low grey level emphasis |
| 1074 | V1074 | NGLDM_Ishge | high dependence high grey level emphasis |
| 1075 | V1075 | NGLDM_grey_lev_var | grey level variance |
| 1076 | V1076 | NGLDM_zone_size_var | dependence count variance |
| 1077 | V1077 | NGLDM_size_entropy | dependence count entropy |
| 1078 | V1078 | NGLDM_energy | dependence count energy |
| 1079 | V1079 | Mean | mean |
| 1080 | V1080 | SD | standard deviation |
| 1081 | V1081 | COV | coefficient of variation |
| 1082 | V1082 | skewness | skewness |
| 1083 | V1083 | kurtosis | kurtosis |
| 1084 | V1084 | var | variance |
| 1085 | V1085 | median | median |
| 1086 | V1086 | percentile10 | percentile 10th |
| 1087 | V1087 | percentile90 | percentile 90th |
| 1088 | V1088 | iqr | interquartile range |
| 1089 | V1089 | Hrange | range |
| 1090 | V1090 | mad | mean absolut deviation |
| 1091 | V1091 | rmad | robust mean absolut deviation |
| 1092 | V1092 | H_energy | energy |
| 1093 | V1093 | H_entropy | entropy |
| 1094 | V1094 | rms | root mean square |
| 1095 | V1095 | H_uniformity | uniformity |
| 1096 | V1096 | energy | energy |
| 1097 | V1097 | entropy | entropy |


| 1098 | V1098 | contrast | contrast |
| :---: | :---: | :---: | :---: |
| 1099 | V1099 | correlation | correlation |
| 1100 | V1100 | homogenity | homogeneity |
| 1101 | V1101 | homogenity_n | homogeneity normalized |
| 1102 | V1102 | idiff | inverese difference |
| 1103 | V1103 | idiff_n | inverese difference normalized |
| 1104 | V1104 | variance | variance |
| 1105 | V1105 | sum_average | sum of average |
| 1106 | V1106 | sum_entropy | sum of entropy |
| 1107 | V1107 | sum_variance | sum of variance |
| 1108 | V1108 | diff_entropy | difference entropy |
| 1109 | V1109 | diff_variance | difference variance |
| 1110 | V1110 | IMC1 | information measures of correlation 1 |
| 1111 | V1111 | IMC2 | information measures of correlation 2 |
| 1112 | V1112 | MCC | maximal correlation coefficient |
| 1113 | V1113 | joint_max | joint maximum |
| 1114 | V1114 | joint_average | joint average |
| 1115 | V1115 | diff_average | difference average |
| 1116 | V1116 | dissimilarity | dissimilarity |
| 1117 | V1117 | inverse_variance | inverse variance |
| 1118 | V1118 | autocorrelation | autocorrelation |
| 1119 | V1119 | clust_tendency | cluster tendency |
| 1120 | V1120 | clust_shade | cluster shade |
| 1121 | V1121 | clust_prominence | cluster prominence |
| 1122 | V1122 | M_energy | energy |
| 1123 | V1123 | M_entropy | entropy |
| 1124 | V1124 | M_contrast | contrast |
| 1125 | V1125 | M_correlation | correlation |
| 1126 | V1126 | M_homogenity | homogeneity |
| 1127 | V1127 | M_homogenity_n | homogeneity normalized |
| 1128 | V1128 | M_idiff | inverese difference |
| 1129 | V1129 | M_idiff_n | inverese difference normalized |
| 1130 | V1130 | M_variance | variance |
| 1131 | V1131 | M_sum_average | sum of average |
| 1132 | V1132 | M_sum_entropy | sum of entropy |
| 1133 | V1133 | M_sum_variance | sum of variance |
| 1134 | V1134 | M_diff_entropy | difference entropy |
| 1135 | V1135 | M_diff_variance | difference variance |
| 1136 | V1136 | M_IMC1 | information measures of correlation 1 |
| 1137 | V1137 | M_IMC2 | information measures of correlation 2 |
| 1138 | V1138 | M_MCC | maximal correlation coefficient |
| 1139 | V1139 | M_joint_max | joint maximum |
| 1140 | V1140 | M_joint_average | joint average |
| 1141 | V1141 | M_diff_average | difference average |
| 1142 | V1142 | M_dissimilarity | dissimilarity |
| 1143 | V1143 | M_inverse_variance | inverse variance |
| 1144 | V1144 | M_autocorrelation | autocorrelation |
| 1145 | V1145 | M_clust_tendency | cluster tendency |
| 1146 | V1146 | M_clust_shade | cluster shade |
| 1147 | V1147 | M_clust_prominence | cluster prominence |


| 1148 | V1148 | coarseness | coarseness |
| :---: | :---: | :---: | :---: |
| 1149 | V1149 | neighContrast | contrast |
| 1150 | V1150 | busyness | busyness |
| 1151 | V1151 | complexity | complexity |
| 1152 | V1152 | strength | strength |
| 1153 | V1153 | len_intensityVar | grey level non-uniformity |
| 1154 | V1154 | len_intensityVar_n | grey level non-uniformity normalized |
| 1155 | V1155 | len_sizeVar | zone size non-uniformity |
| 1156 | V1156 | len_sizeVar_n | zone size non-uniformity normalized |
| 1157 | V1157 | len_sse | short runs emphasis |
| 1158 | V1158 | len_Ise | long runs emphasis |
| 1159 | V1159 | len_lgse | low grey level run emphasis |
| 1160 | V1160 | len_hgse | high grey level run emphasis |
| 1161 | V1161 | len_sslge | short run low grey level emphasis |
| 1162 | V1162 | len_sshge | short run high grey level emphasis |
| 1163 | V1163 | len_Islge | long run low grey level emphasis |
| 1164 | V1164 | len_Ishge | long run high grey level emphasis |
| 1165 | V1165 | len_rpc | run percentage |
| 1166 | V1166 | len_grey_lev_var | grey level variance |
| 1167 | V1167 | len_zone_size_var | run length variance |
| 1168 | V1168 | len_size_entropy | run entropy |
| 1169 | V1169 | M_len_intensityVar | grey level non-uniformity |
| 1170 | V1170 | M_len_intensityVar_n | grey level non-uniformity normalized |
| 1171 | V1171 | M_len_sizeVar | zone size non-uniformity |
| 1172 | V1172 | M_len_sizeVar_n | zone size non-uniformity normalized |
| 1173 | V1173 | M_len_sse | short runs emphasis |
| 1174 | V1174 | M_len_Ise | long runs emphasis |
| 1175 | V1175 | M_len_lgse | low grey level run emphasis |
| 1176 | V1176 | M_len_hgse | high grey level run emphasis |
| 1177 | V1177 | M_len_sslge | short run low grey level emphasis |
| 1178 | V1178 | M_len_sshge | short run high grey level emphasis |
| 1179 | V1179 | M_len_Islge | long run low grey level emphasis |
| 1180 | V1180 | M_len_Ishge | long run high grey level emphasis |
| 1181 | V1181 | M_len_rpc | run percentage |
| 1182 | V1182 | M_len_grey_lev_var | grey level variance |
| 1183 | V1183 | M_len_zone_size_var | run length variance |
| 1184 | V1184 | M_len_size_entropy | run entropy |
| 1185 | V1185 | intensityVar | grey level non-uniformity |
| 1186 | V1186 | intensityVar_n | grey level non-uniformity normalized |
| 1187 | V1187 | sizeVar | zone size non-uniformity |
| 1188 | V1188 | sizeVar_n | zone size non-uniformity normalized |
| 1189 | V1189 | sse | small zone emphasis |
| 1190 | V1190 | Ise | large zone emphasis |
| 1191 | V1191 | Igse | low grey level zone emphasis |
| 1192 | V1192 | hgse | high grey level zone emphasis |
| 1193 | V1193 | sslge | small zone low grey level emphasis |
| 1194 | V1194 | sshge | small zone high grey level emphasis |
| 1195 | V1195 | Islge | large zone low grey level emphasis |
| 1196 | V1196 | Ishge | large zone high grey level emphasis |
| 1197 | V1197 | rpc | zone percentage |


| 1198 | V1198 | grey_lev_var | grey level variance |
| :---: | :---: | :---: | :---: |
| 1199 | V1199 | zone_size_var | zone size variance |
| 1200 | V1200 | size_entropy | zone size entropy |
| 1201 | V1201 | GLDZM_intensityVar | grey level non-uniformity |
| 1202 | V1202 | GLDZM_intensityVar_n | grey level non-uniformity normalized |
| 1203 | V1203 | GLDZM_sizeVar | zone size non-uniformity |
| 1204 | V1204 | GLDZM_sizeVar_n | zone size non-uniformity normalized |
| 1205 | V1205 | GLDZM_sse | small distance emphasis |
| 1206 | V1206 | GLDZM_Ise | large distance emphasis |
| 1207 | V1207 | GLDZM_lgse | low grey level zone emphasis |
| 1208 | V1208 | GLDZM_hgse | high grey level zone emphasis |
| 1209 | V1209 | GLDZM_sslge | small distance low grey level emphasis |
| 1210 | V1210 | GLDZM_sshge | small distance high grey level emphasis |
| 1211 | V1211 | GLDZM_Islge | large distance low grey level emphasis |
| 1212 | V1212 | GLDZM_Ishge | large distance high grey level emphasis |
| 1213 | V1213 | GLDZM_rpc | zone percentage |
| 1214 | V1214 | GLDZM_grey_lev_var | grey level variance |
| 1215 | V1215 | GLDZM_zone_size_var | zone distance variance |
| 1216 | V1216 | GLDZM_size_entropy | zone distance entropy |
| 1217 | V1217 | NGLDM_intensityVar | grey level non-uniformity |
| 1218 | V1218 | NGLDM_intensityVar_n | grey level non-uniformity normalized |
| 1219 | V1219 | NGLDM_sizeVar | dependence count non-uniformity |
| 1220 | V1220 | NGLDM_sizeVar_n | dependence count non-uniformity normalized |
| 1221 | V1221 | NGLDM_sse | low dependence emphasis |
| 1222 | V1222 | NGLDM_Ise | high dependence emphasis |
| 1223 | V1223 | NGLDM_lgse | low grey level count emphasis |
| 1224 | V1224 | NGLDM_hgse | high grey level count emphasis |
| 1225 | V1225 | NGLDM_sslge | low dependence low grey level emphasis |
| 1226 | V1226 | NGLDM_sshge | low dependence high grey level emphasis |
| 1227 | V1227 | NGLDM_Islge | high dependence low grey level emphasis |
| 1228 | V1228 | NGLDM_Ishge | high dependence high grey level emphasis |
| 1229 | V1229 | NGLDM_grey_lev_var | grey level variance |
| 1230 | V1230 | NGLDM_zone_size_var | dependence count variance |
| 1231 | V1231 | NGLDM_size_entropy | dependence count entropy |
| 1232 | V1232 | NGLDM_energy | dependence count energy |
| 1233 | V1233 | Mean | mean |
| 1234 | V1234 | SD | standard deviation |
| 1235 | V1235 | COV | coefficient of variation |
| 1236 | V1236 | skewness | skewness |
| 1237 | V1237 | kurtosis | kurtosis |
| 1238 | V1238 | var | variance |
| 1239 | V1239 | median | median |
| 1240 | V1240 | percentile10 | percentile 10th |
| 1241 | V1241 | percentile90 | percentile 90th |
| 1242 | V1242 | iqr | interquartile range |
| 1243 | V1243 | Hrange | range |
| 1244 | V1244 | mad | mean absolut deviation |
| 1245 | V1245 | rmad | robust mean absolut deviation |
| 1246 | V1246 | H_energy | energy |
| 1247 | V1247 | H_entropy | entropy |


| 1248 | V1248 | rms |
| :--- | :--- | :--- |
| 1249 | V1249 | H_uniformity |
| 1250 | V1250 | energy |
| 1251 | V1251 | entropy |
| 1252 | V1252 | contrast |
| 1253 | V1253 | correlation |
| 1254 | V1254 | homorgy |
| 1255 | V1255 | homogenity |
| 1256 | V1256 | idiff |


| 1298 | V1298 | M_autocorrelation | autocorrelation |
| :---: | :---: | :---: | :---: |
| 1299 | V1299 | M_clust_tendency | cluster tendency |
| 1300 | V1300 | M_clust_shade | cluster shade |
| 1301 | V1301 | M_clust_prominence | cluster prominence |
| 1302 | V1302 | coarseness | coarseness |
| 1303 | V1303 | neighContrast | contrast |
| 1304 | V1304 | busyness | busyness |
| 1305 | V1305 | complexity | complexity |
| 1306 | V1306 | strength | strength |
| 1307 | V1307 | len_intensityVar | grey level non-uniformity |
| 1308 | V1308 | len_intensityVar_n | grey level non-uniformity normalized |
| 1309 | V1309 | len_sizeVar | zone size non-uniformity |
| 1310 | V1310 | len_sizeVar_n | zone size non-uniformity normalized |
| 1311 | V1311 | len_sse | short runs emphasis |
| 1312 | V1312 | len_Ise | long runs emphasis |
| 1313 | V1313 | len_lgse | low grey level run emphasis |
| 1314 | V1314 | len_hgse | high grey level run emphasis |
| 1315 | V1315 | len_sslge | short run low grey level emphasis |
| 1316 | V1316 | len_sshge | short run high grey level emphasis |
| 1317 | V1317 | len_Islge | long run low grey level emphasis |
| 1318 | V1318 | len_lshge | long run high grey level emphasis |
| 1319 | V1319 | len_rpo | run percentage |
| 1320 | V1320 | len_grey_lev_var | grey level variance |
| 1321 | V1321 | len_zone_size_var | run length variance |
| 1322 | V1322 | len_size_entropy | run entropy |
| 1323 | V1323 | M_len_intensityVar | grey level non-uniformity |
| 1324 | V1324 | M_len_intensityVar_n | grey level non-uniformity normalized |
| 1325 | V1325 | M_len_sizeVar | zone size non-uniformity |
| 1326 | V1326 | M_len_sizeVar_n | zone size non-uniformity normalized |
| 1327 | V1327 | M_len_sse | short runs emphasis |
| 1328 | V1328 | M_len_Ise | long runs emphasis |
| 1329 | V1329 | M_len_lgse | low grey level run emphasis |
| 1330 | V1330 | M_len_hgse | high grey level run emphasis |
| 1331 | V1331 | M_len_sslge | short run low grey level emphasis |
| 1332 | V1332 | M_len_sshge | short run high grey level emphasis |
| 1333 | V1333 | M_len_Islge | long run low grey level emphasis |
| 1334 | V1334 | M_len_Ishge | long run high grey level emphasis |
| 1335 | V1335 | M_len_rpc | run percentage |
| 1336 | V1336 | M_len_grey_lev_var | grey level variance |
| 1337 | V1337 | M_len_zone_size_var | run length variance |
| 1338 | V1338 | M_len_size_entropy | run entropy |
| 1339 | V1339 | intensityVar | grey level non-uniformity |
| 1340 | V1340 | intensityVar_n | grey level non-uniformity normalized |
| 1341 | V1341 | sizeVar | zone size non-uniformity |
| 1342 | V1342 | sizeVar_n | zone size non-uniformity normalized |
| 1343 | V1343 | sse | small zone emphasis |
| 1344 | V1344 | Ise | large zone emphasis |
| 1345 | V1345 | Igse | low grey level zone emphasis |
| 1346 | V1346 | hgse | high grey level zone emphasis |
| 1347 | V1347 | sslge | small zone low grey level emphasis |


| 1348 | V1348 | sshge | small zone high grey level emphasis |
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| 1349 | V1349 | Islge | large zone low grey level emphasis |
| 1350 | V1350 | Ishge | large zone high grey level emphasis |
| 1351 | V1351 | rpc | zone percentage |
| 1352 | V1352 | grey_lev_var | grey level variance |
| 1353 | V1353 | zone_size_var | zone size variance |
| 1354 | V1354 | size_entropy | zone size entropy |
| 1355 | V1355 | GLDZM_intensityVar | grey level non-uniformity |
| 1356 | V1356 | GLDZM_intensityVar_n | grey level non-uniformity normalized |
| 1357 | V1357 | GLDZM_sizeVar | zone size non-uniformity |
| 1358 | V1358 | GLDZM_sizeVar_n | zone size non-uniformity normalized |
| 1359 | V1359 | GLDZM_sse | small distance emphasis |
| 1360 | V1360 | GLDZM_Ise | large distance emphasis |
| 1361 | V1361 | GLDZM_Igse | low grey level zone emphasis |
| 1362 | V1362 | GLDZM_hgse | high grey level zone emphasis |
| 1363 | V1363 | GLDZM_sslge | small distance low grey level emphasis |
| 1364 | V1364 | GLDZM_sshge | small distance high grey level emphasis |
| 1365 | V1365 | GLDZM_Islge | large distance low grey level emphasis |
| 1366 | V1366 | GLDZM_Ishge | large distance high grey level emphasis |
| 1367 | V1367 | GLDZM_rpc | zone percentage |
| 1368 | V1368 | GLDZM_grey_lev_var | grey level variance |
| 1369 | V1369 | GLDZM_zone_size_var | zone distance variance |
| 1370 | V1370 | GLDZM_size_entropy | zone distance entropy |
| 1371 | V1371 | NGLDM_intensityVar | grey level non-uniformity |
| 1372 | V1372 | NGLDM_intensityVar_n | grey level non-uniformity normalized |
| 1373 | V1373 | NGLDM_sizeVar | dependence count non-uniformity |
| 1374 | V1374 | NGLDM_sizeVar_n | dependence count non-uniformity normalized |
| 1375 | V1375 | NGLDM_sse | low dependence emphasis |
| 1376 | V1376 | NGLDM_Ise | high dependence emphasis |
| 1377 | V1377 | NGLDM_lgse | low grey level count emphasis |
| 1378 | V1378 | NGLDM_hgse | high grey level count emphasis |
| 1379 | V1379 | NGLDM_sslge | low dependence low grey level emphasis |
| 1380 | V1380 | NGLDM_sshge | low dependence high grey level emphasis |
| 1381 | V1381 | NGLDM_Islge | high dependence low grey level emphasis |
| 1382 | V1382 | NGLDM_Ishge | high dependence high grey level emphasis |
| 1383 | V1383 | NGLDM_grey_lev_var | grey level variance |
| 1384 | V1384 | NGLDM_zone_size_var | dependence count variance |
| 1385 | V1385 | NGLDM_size_entropy | dependence count entropy |
| 1386 | V1386 | NGLDM_energy | dependence count energy |
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[^0]:    *UIP includes the radiological diagnosis of both, "definite" and "probable" UIP.

