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'Cytology-on-a-Chip' Based Sensors for Monitoring of Potentially Malignant Oral Lesions

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DISCLOSURES

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Abstract

Despite significant advances in surgical procedures and treatment, long-term prognosis for patients with oral cancer remains poor, with survival rates among the lowest of major cancers. Better methods are desperately needed to identify potential malignancies early when treatments are more effective.

Objective—To develop robust classification models from cytology-on-a-chip measurements that mirror diagnostic performance of gold standard approach involving tissue biopsy.

Materials and Methods—Measurements were recorded from 714 prospectively recruited patients with suspicious lesions across 6 diagnostic categories (each confirmed by tissue biopsy - histopathology) using a powerful new ‘cytology-on-a-chip’ approach capable of executing high content analysis at a single cell level. Over 200 cellular features related to biomarker expression, nuclear parameters and cellular morphology were recorded per cell. By cataloging an average of 2,000 cells per patient, these efforts resulted in nearly 13 million indexed objects.

Results—Binary “low-risk”/“high-risk” models yielded AUC values of 0.88 and 0.84 for training and validation models, respectively, with an accompanying difference in sensitivity + specificity of 6.2%. In terms of accuracy, this model accurately predicted the correct diagnosis approximately 70% of the time, compared to the 69% initial agreement rate of the pool of expert pathologists. Key parameters identified in these models included cell circularity, Ki67 and EGFR expression, nuclear-cytoplasmic ratio, nuclear area, and cell area.

Conclusions—This chip-based approach yields objective data that can be leveraged for diagnosis and management of patients with PMOL as well as uncovering new molecular-level insights behind cytological differences across the OED spectrum.

Keywords

Cytology; Oral cancer; Oral epithelial dysplasia; Microfluidic; High content analysis; Machine Learning; Random Forest; LASSO

Introduction

It is estimated that 1–2% of adults in the United States present with a worrisome white or red patch or other potentially malignant oral lesion (PMOL) during a routine oral examination [1]. However, the vast majority of these lesions are benign, and only 1–2% will undergo progression into oral squamous cell carcinoma (OSCC) [2,3]. Oral healthcare providers are often the first line of defense in the early detection of oral cancer and are faced with the challenge of recognizing PMOL and deciding which patients to refer for tissue biopsy. This often difficult decision is becoming increasingly burdensome, confounded by the desire to reduce unwarranted biopsies and patient discomfort with the changing landscape of litigation directed at dentists for failing to refer patients [4]. To make matters worse, in PMOL, the histopathological diagnosis of oral epithelial dysplasia (OED) is not necessarily predictive of future malignant transformation, creating a demand for more sophisticated early risk assessment tools [5].

Though decades of studies aimed at developing non-invasive, adjunctive aids for monitoring oral lesions have not garnered widespread adoption [6], a new era of rapid, quantitative, and automated tools are beginning to pave the way towards data-driven clinical decision making. Recent advances in a diverse consortium of fields from automated sample processing to statistical machine learning, microfluidic-based single-cell analysis [7–9], and high content analysis/screening [10–14] have fueled a renewed interest in quantitative oral cytology. While offering strong potential for enhanced clinical insight relative to early disease detection, the “-omics” data derived from these new capabilities has a tendency to yield putative clinical models that do not perform as well in later validation studies. A recent review of 28 studies involving molecular classifiers by Castaldi et al. (2010) [15] found that the majority selected cross-validation practices that overestimated model performance [by ~17% (median) in terms of specificity].

To address these challenges, our team of bioengineers, oral medicine clinicians, oral and maxillofacial pathologists, and cancer biologists, designed and executed a prospective, international clinical study with the ultimate goal of equipping dental practitioners with simple, automated, quantitative risk assessment tools to assist in making difficult biopsy referral decisions. Here we describe this single-cell cytology-on-a-chip approach in the context of developing a multi-parameter image-based clinical decision tool.

The general method for collection and processing of cells within a microfluidic structure was demonstrated previously in the context of a small pilot study involving 52 patients using the single biomarker, EGFR, in order to differentiate between normal mucosa and OSCC [16]. The pilot yielded preliminary logistic regression models with sensitivity and specificity of 97% and 93% respectively, alongside area under the receiver operating characteristic (ROC) curve (AUC) equal to 0.94. These promising results paved the way for this more comprehensive follow-up with a Phase 2/3 clinical characterization-association study.

Many previous quantitative cytology studies have confirmed that measureable differences exist between the extreme phenotypes of normal mucosa/benign lesions and malignant lesions [17–19] such as the increased proportion of small, highly circular cells that resemble

more primitive stem cells. Though these differences can be surmised by visual examination by experts and non-experts alike, they miss the more subtle spectrum of changes seen in PMOL representing the different grades of OED described by histopathologists [20]. An attempt to leverage the subtle measureable differences among OED cytology samples in order to develop objective classification models for PMOL has not existed until now.

Materials and Methods

Study Population

This study was approved by the Institutional Review Boards of all participating institutions. Informed consent was obtained for all participants in the trial after the possible consequences of the procedures were explained. The study design and clinical protocol for this study have been reported previously in detail [21]. Briefly, lesion samples from a total of 714 patients were measured, of which 85 were previously diagnosed malignant cases. The slight enrichment of the malignant cases allowed for a more substantial model development process with more equivalent class sizes. All other patients were prospectively recruited based on their exhibiting PMOL for which scalpel biopsy was a necessary part of the standard clinical practice. Histopathological assessment of biopsy specimens was used to place lesions in one of six categories of oral epithelial dysplasia (OED). These comprised 348 benign, 49 mild dysplasia, 18 moderate dysplasia, 12 severe dysplasia, 2 carcinoma in situ (CIS), and 135 malignant lesions in addition to 150 healthy controls. To obtain greater confidence in the gold-standard pathological diagnoses, which have been notoriously unreliable [22,23], a 3-stage adjudication and consensus review process was performed which achieved 100% consensus agreement from an initial 69.9% agreement rate between any two pathologists across all patient biopsy specimens [21].

A summary of the major variables analyzed is provided in the Supplementary Methods and Supplementary Tables 1–3. The molecular biomarkers EGFR, αvβ6, CD147, β-catenin, MCM2, and Ki67 were selected based on their capacity, through prior immunohistochemistry studies, to distinguish stages of disease progression towards OSCC for patients with PMOL. Due to the flexible design of this chip-based approach, future studies may easily adapt these protocols as new prognostic molecular markers are identified.

Cytology-on-a-chip Sample Processing

Specific details for cytology-on-a-chip sample processing can be found in the Supplementary Methods and are adapted from the indirect-immunoassay protocol described in Weigum, et. al. (2010) [16]. In summary, sample processing comprised the following steps: 1) the microfluidic device was primed with PBS at a flow rate of 735μL/min for 2 minutes, 2) a cell suspension in 20% glycerol/0.1% PBSA was delivered at 1.5mL/min for 2 minutes whereby single cells were captured on an embedded nanoporous membrane, 3) cells were washed with PBS at 1mL/min for 2.5min, 4) a primary antibody solution was delivered through a 0.2μm PVDF syringe filter at 250μL/min for 2.5min, 5) a wash step similar to step 3 was performed, 6) a secondary antibody solution was delivered under the same conditions as step 4, 7) a final wash step was performed, and 8) fluorescence images were automatically captured.

Data Processing

Unlike most biomarker classification models that are developed with a single measure for each biomarker per patient, this study cataloged an average of 2,000 cells per patient, resulting in nearly 13 million indexed objects, each with over 200 unique measurements to digitize biomarker expression profiles, and cytoplasm and nuclear morphology. To reduce the magnitude of this database to a computationally appropriate size, statistical measures were used to represent the magnitude and distribution of cellular features for individual patients. These included: mean, median, variance, standard deviation, coefficient of variation (CV), skewness, kurtosis, $10^{th}/25^{th}/75^{th}/90^{th}$-percentiles, and z-scores of 0.5, 2.0, and 3.0 referring to the proportion of cells with biomarker values greater than 0.5/2.0/3.0 standard deviations from the mean. A more detailed description of the complete set of variables used in this study can be found in Supplementary Tables 1, 2, and 3. In order to develop predictive models, the data was split into optimization, training, and testing sets with 250, 311, and 153 patients, respectively.

Results

We have previously reported on the ability to isolate and interrogate single-cells within microfluidic structures for immunophenotyping [24–26], bacterial spore detection [27], and oral exfoliative cytology [28,16,29]. In addition to cell capture, the microfluidic device also serves as a delivery system for efficient transport of fluorescently-labeled antibodies and wash buffer. This cytology-on-a-chip methodology permits concurrent analysis of molecular biomarker expression and cellular/nuclear morphology using over 200 fluorescence intensity and shape parameters for each identified cell extracted from multi-spectral fluorescence images (Fig. 1, Panel II and Supplementary Figure 1). The time to complete this chip-based image analysis is approximately 20 minutes following sample preparation vs. about 1–3 days to complete a typical gold standard pathology exam.

Model Development

The completion of this clinical trial resulted in the formation of several different classification models used to correlate the biomarker signatures of individual patients to a pre-defined disease category. These categories were derived by dichotomizing the clinical spectrum of diagnoses at several cut-points (Fig. 2a) according to the 2005 WHO 5-point histopathological grading system of OED [20] and the binary “low/high”-risk grading system of OED proposed by Kujan et al [30].

Statistical machine learning techniques that minimize effect size inflation and selection bias were used to develop classification models, namely Random Forests using “out of bag” validation and the L1-regularized logistic regression (LASSO) methodology. In addition, different subsets of parameters were evaluated consisting of biomarkers (molecular + morphometric), clinical lesion characteristics, and demographic risk factors (Supplementary Tables 1, 2). The goal of this approach was to obtain a sparse model to prevent data over-fitting and yield generalizable models with high stability. The classification models were fit to 2/3 of the data (training dataset) while blinded to the remaining 1/3 of the data (test

dataset). Importantly, assays were completed in a blind fashion for all samples in the validation phase.

In addition to creating classification models, random forests can be used to automatically probe variable importance in high dimensional datasets. Variable importance, quantified by the Gini-index decrease, can be interpreted as the relative ability of a specific parameter to discriminate between “case” and “non-case” for the diagnostic split in question, and is therefore an estimate of the informative value of a parameter. These results are summarized as a heatmap (Fig. 2b, c and Supplementary Figure 2).

The key information here obtained reveals that molecular biomarkers are better suited for distinguishing benign lesions from earlier stage dysplastic + malignant lesions than for the higher diagnostic splits (cumulative normalized Gini-index ranges: 0.204 – 0.810 (2|3), 0.137 – 0.554 (3|4), 0.139 – 0.540 (H|L), 0.111 – 0.432 (4|5)). Conversely, the morphometric parameters cell area, cell circularity, and NC ratio along with the proliferation biomarker Ki67 demonstrate high importance across all 4 dichotomous splits.

To confirm the stability of the cytology dataset as it relates to model development, Gini-indices across 5 percentile summary measures (Fig. 2c) are compared to box plots of key variables (Fig. 2d). Variable importance is consistent with the observed biomarker trends for patients in different diagnostic categories. This key finding supports the development of stable models that translate the underlying biological phenomena into measures of variable importance.

LASSO Automated Variable Selection

The use of LASSO methodology helps prevent over-fitting a model by iteratively shrinking parameter effect sizes. The popularity of this method stems from its ability to automatically select the most influential variables and eliminate redundant model parameters that can be a major factor in high-dimensional data sets. A variable association visualization for the LASSO methodology is presented as a chord diagram (Fig. 3) where the chord width corresponds to the relative contribution of each parameter to model performance across the 4 diagnostic splits, in terms of its standardized odds-ratio.

Key parameters identified by the LASSO methodology include proliferation biomarker Ki67, cell area, cell circularity, nuclear area, and NC-ratio. Consistent with the random forest variable importance analysis, the odds-ratios from molecular biomarkers are found to play a more significant role in differentiating benign lesions from dysplastic + malignant lesions than in models at other diagnostic splits (combined odds-ratios of 9.558 (2|3), 3.337 (3|4), 4.087 (H|L), 3.253 (4|5)). Of the molecular biomarkers, Ki67 provides the most discriminatory information with odds-ratios of 1.162 (median, log-scale), 1.354 (10^{th} percentile, log-scale), 1.184 (10^{th} percentile, log-scale), and 1.307 (10^{th} percentile, log-scale) ((2|3), (3|4), (H|L), (4|5)). Several parameters demonstrate consistent model effects across all 4 diagnostic splits including cell area (average odds-ratios of 0.835, 0.935, 0.969, 0.904), nuclear area (1.111, 1.023, 1.116, 1.028), and lesion size (1.139, 1.072, 1.124, 1.183), ((2|3), (3|4), (H|L), (4|5)). Furthermore, LASSO results indicated that each of the

four diagnostic targets requires a unique combination of variables to achieve its highest performance.

Cellular Phenotype Identified by Morphometric Parameters

These key indicators for detecting dysplastic or malignant changes can also be leveraged along with the cytology image database created in this study to identify unique cellular phenotypes. In addition to routinely identified cell phenotypes such as binucleated cells and cells with micronuclei, 4 additional “categories” are created to describe unique cell sub-populations. These categories are defined based on significant differences across the key parameters corresponding to smoothness of cytoplasmic borders, cell circularity, cell area, nuclear area, NC-ratio, DAPI intensity, and Phalloidin intensity. The distribution of these custom phenotype labels for 300 randomized cells across 4 different patient diagnostic groups is compared (Fig. 4). Significantly higher proportions of cells that fit definitions for type B, C, D, and F in patients with OSCC are identified, referring to cells with higher than average circularity, higher NC-ratio, smaller overall cytoplasm area, enlarged nuclei, and those described as polynucleated. Morphometry-based phenotype identification also enables white blood cell (WBC) enumeration in cytology samples, an indicator with potential diagnostic utility that will be discussed in future publications. The ability to translate quantitative cytology metrics into visualizable cellular features has the potential to assist cytopathologists in discovering novel feature sets based on objective information.

Model Performance

A single primary diagnostic model and numerous secondary models are selected by the study team through a rigorous process involving participation of three independent statisticians. This blinding process allows for this trial to complete both model development and model validation. The latter is accomplished in a fully blinded manner with the oversight of a contract research organization (Rho Inc., Chapel Hill, NC) using external data that is not employed for model development. A summary of the performance values obtained for the LASSO and random forest classification models is provided (Table 1).

The study team selected the LASSO logistic regression model trained with the molecular biomarker and lesion characteristic datasets for differentiating “Low-risk” and “High-risk” lesions as the primary classification model in this study based on its superior performance of the LASSO model in the development stage (based on averaged high sensitivity, specificity, and AUC). These efforts yield AUC values of 0.88 and 0.84 for the training and validation models, respectively.

Across the training and validation datasets, the LASSO models that includes lesion characteristics outperforms those trained on biomarkers alone by boosting specificity an average of 6.56% (SD = 3.77%) (Sens: avg = −0.05%, SD = 4.31%; AUC: avg = 2.69%, SD = 1.28%). Interestingly, the addition of lesion characteristics did not appear to affect random forest models significantly (Sens: avg = −1.78%, SD = 2.19%; Spec: 3.34%, SD = 4.22%).

On average, validation performance for random forests displays a 2.58% drop in sensitivity (SD= 3.50%) and an increase of 3.01% for specificity (SD=2.31%), compared to a 5.88% sensitivity drop for LASSO (SD = 5.07%) and a corresponding increase of 3.79% in

specificity (SD = 2.96%). Additionally, LASSO model AUCs decreases an average of 4.0% (SD = 2.41%) across the different diagnostic splits between the validation and training datasets.

Parameters with significant information in discriminating between “Low-risk” and “High-risk” lesions selected by the primary LASSO model includes cell circularity (90^{th} percentile), nuclear Ki67 intensity (10^{th} percentile and coefficient of variation (cv)), cell-surface EGFR intensity (standard deviation), NC-ratio (median), nuclear area (skewness and cv), cell area (25^{th} percentile), and the lesion characteristics lichen planus and lesion size (long axis). Box plots illustrating the stable, monotonic trends of these variables across different diagnostic categories can be found in Supplementary Figure 3.

Discussion

In developing a chip-based approach to obtain a quantitative risk assessment for monitoring PMOL, this study sought to address three main questions: 1) Can a high content analysis (HCA) workflow be applied to primary patient cells? 2) How does model performance and composition change as a function of the diagnostic split position? 3) Can quantitative cytology tests produce diagnostic accuracy that rivals the gold standard pathology tests? Each of these key knowledge gaps is discussed below.

Can HCA be applied to primary patient cells?

Though HCA has been predominantly driven by screening applications involving cell lines grown in multi-well plates and advances in high-throughput laboratory automation, this study exemplifies how HCA can be applied to primary, patient-derived samples for personalized cellular scoring. This cytology-on-a-chip approach is unique in its ability to analyze hundreds of morphometric and biomarker expression parameters automatically across an entire cytology sample agnostic to clinical judgment or clinical history. In some instances, parameters that contributed to model performance and stability, such as NC-ratio, nuclear area, and Ki67 expression, confirmed previous reports of their roles in cyto- and histo-pathological grading [16],[17],[18],[31],[32].

This study also identifies biomarkers that present new insights into how the quantification of cell and nuclear morphometry can provide rich data streams that track with the different grades of OED. In the primary LASSO model, two nuclear area measures (skewness and cv) are identified as important variables in discriminating between “low-risk” and “high-risk” lesions. As summary measures of the distribution of nuclear area, both provide insight into the level of ansionucleosis (variation in size and shape of nuclei [33]) for each patient sample, which is a prominent feature of dysplasia and malignancy [34],[33], but not often quantified.

Cell circularity, a measure of the “roundness” of the cytoplasmic membrane, is frequently identified in several models to be a highly performing parameter. An increase in cell circularity may be attributed to the decrease in the amount of cytoplasm and reduction in the degree of cellular cohesion which have both been reported to occur with increased dysplasia grade [32]. The dominant summary statistic for cell circularity in these models is its 90^{th}

percentile measure, unlike the range of summary measures for cell area and NC-ratio, indicating cell circularity is skewed towards a fraction of cells with circularity measures in the upper 10% of the entire cell sample (Fig. 4 - cell types “B” and “C”).

How does model performance change with diagnostic classification?

One consistent finding from this study is that, at the higher end of the clinical spectrum (moderate-severe dysplasia cut-off), LASSO models (validation sens/spec/AUC = 85.7%/80.0%/0.883) and random forest models (validation sens/spec = 78.8%/68.3%) outperform models distinguishing low-grade lesions in terms of sensitivity, specificity, and AUC (Table 1). Longitudinal studies would be necessary to validate the malignant potential of these identified lesions. Histopathological grading has been shown to behave similarly [21], where higher accuracy and inter-observer agreement have been reported for high grade dysplastic or malignant lesions than for low grade dysplastic lesions, where considerable overlap from inflammatory and reactive changes can confound grading systems [35]. However, longitudinal studies are necessary to validate the malignant potential of these identified lesions.

Can quantitative cytology rival gold standard diagnostic accuracy?

Though some drop in performance is expected between training and validation, similar values for these measures can indicate low risk of model over-fitting and greater generalizability. When comparing model performance between training and validation datasets across all 4 diagnostic splits in this study, random forest models displayed the greatest stability, with a mean difference of 2.58% for sensitivity (SD: 3.50%) and 3.01% for specificity (SD: 2.31%). The LASSO models demonstrated fair stability with a mean difference of 5.88% for sensitivity (SD: 5.07%) and 3.79% for specificity (SD: 2.96%). Indeed, robust classification models are developed that accurately mirrored the performance of histopathological assessment by expert pathologists. In terms of accuracy, the “low/high-risk” model accurately predicted correct diagnoses approximately 70% of the time, compared to the 69% initial agreement rate of the pool of expert pathologists. Furthermore, the level of agreement between model development and model validation far exceeds typical studies as reported by Castaldi et al. (2010) [15]. Furthermore, the design of the model development process presented here championed an additional level of rigor to ensure future generalizability and the absence of human bias which included oversight from a contract research organization, three layers of blinding to the true classification of patient lesions, two sets of independent biostatisticians, and utilization of statistical methods that performed automatic feature selection.

In addition to the objective information that can be obtained with quantitative cytology, the ‘cytology-on-a-chip’ technique presented here is amenable to complete process automation due to its foundations in microfluidic reagent handling, image acquisition, and computational algorithms. Future portable analyzers, similar to those being developed in the McDevitt lab [37], will have the potential to bring sophisticated tools for monitoring PMOL in patients with suspicious lesions to regions with limited access to expert pathologist review.

Conclusions

We have demonstrated the utility of a new cytology-on-chip framework for extracting high-content, single-cell data composed of cellular and nuclear morphometric and molecular biomarker expression measurements that has the potential to serve as an adjunctive aid in assessing suspicious oral lesions. This new clinical decision tool has been developed and validated in the context of a major clinical study and has resulted in a rich database that has been exploited to develop new routines that provide insights into cytology characteristics associated with PMOL. These efforts demonstrate robust clinical performance and stable parameters for LASSO models with sensitivity and specificity values of ~85% and 70% in the model development phase and similar values (within 7%) in the validation phase.

Additionally, superior model performance is found to be associated with heterogeneous data sources. Models trained on data from biomarker expression, morphometric features, clinical impressions, and patient risk factors achieves superior performance compared to models trained on restricted data. This essential finding has implications for future diagnostic applications and adjunctive aid development by emphasizing the need to integrate several different sources of information into a successful risk assessment rather than relying on the expression of a single biomarker or feature.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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Abbreviations

PMOL	Potentially Malignant Oral Lesion(s)
OED	Oral Epithelial Dysplasia
OSCC	Oral Squamous Cell Carcinoma
HCA	High Content Analysis

AUC Area Under the (receiver-operator characteristic) Curve

NC ratio Nuclear-Cytoplasmic area Ratio

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Highlights

- Cytology-on-chip approach permits rapid molecular and morphometric analysis
- Stable, robust predictive models created from single-cell data
- Prognostic cytology features identified including cell circularity, Ki67 expression
- Unique combination of parameters required for different diagnostic splits

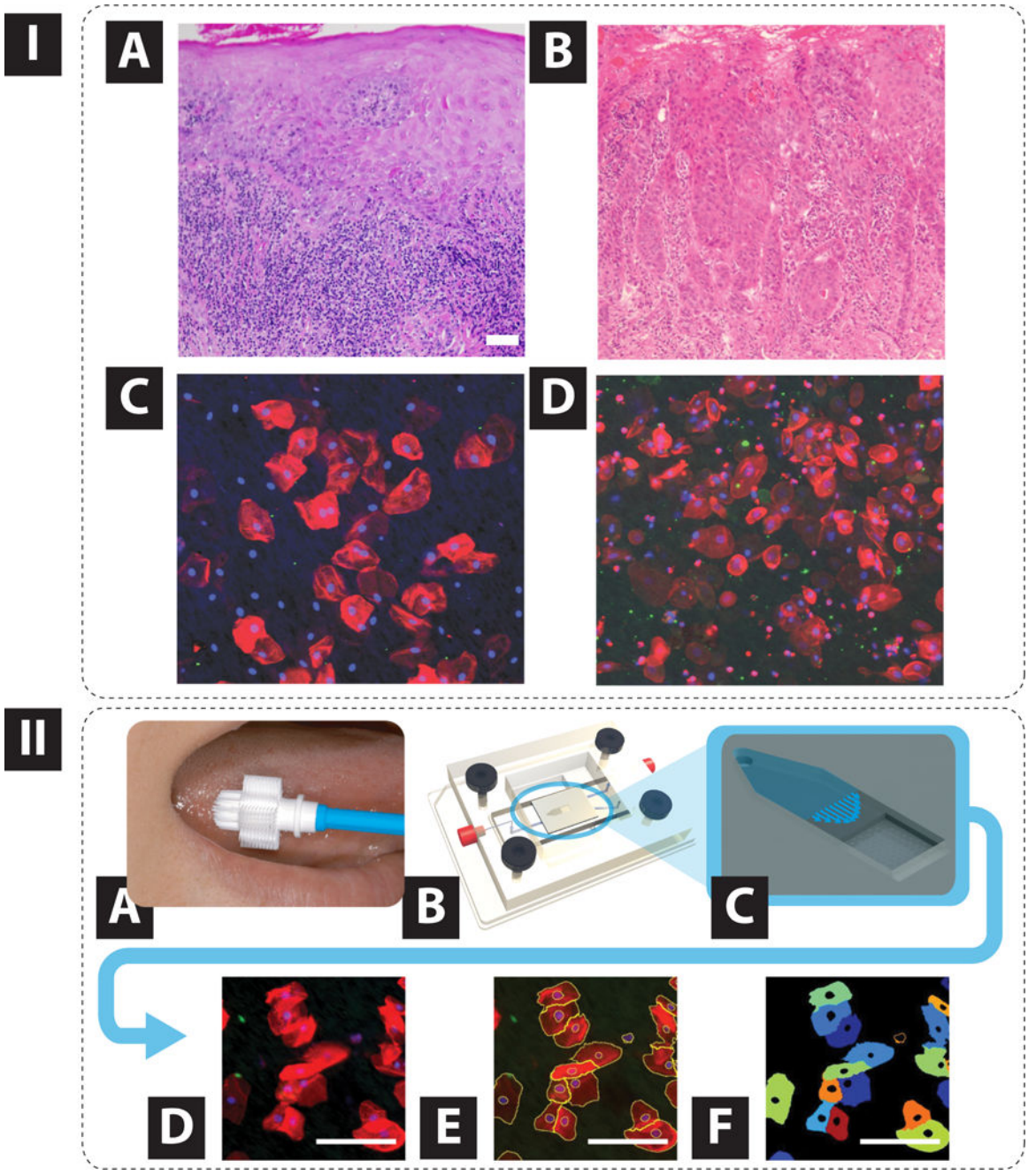

Figure 1. Diagram of cytology-on-a-chip processing and sample images

Panel I.) Representative histopathological (H&E staining) images (A–B) and immunofluorescence-cytology images (C–D) for 4 different patients. (A, C) are derived from Benign (Fig. 1.I.A = lichen planus diagnosis) and (B, D) from OSCC diagnoses as confirmed from independent agreement between two reviewing pathologists. Scale bars for A, B, C, and D = 100 μm. Panel II.) Diagram of "cytology-on-chip" sample processing in which a brush cytology sample is collected (A), processed in a suspension, and delivered through the microfluidic platform (B) to a cell-capture, nano-porous membrane (C). Multi-

spectral fluorescence images are recorded (D) and analyzed with automated software to identify single cells (E) and extract these regions for measurement (F).

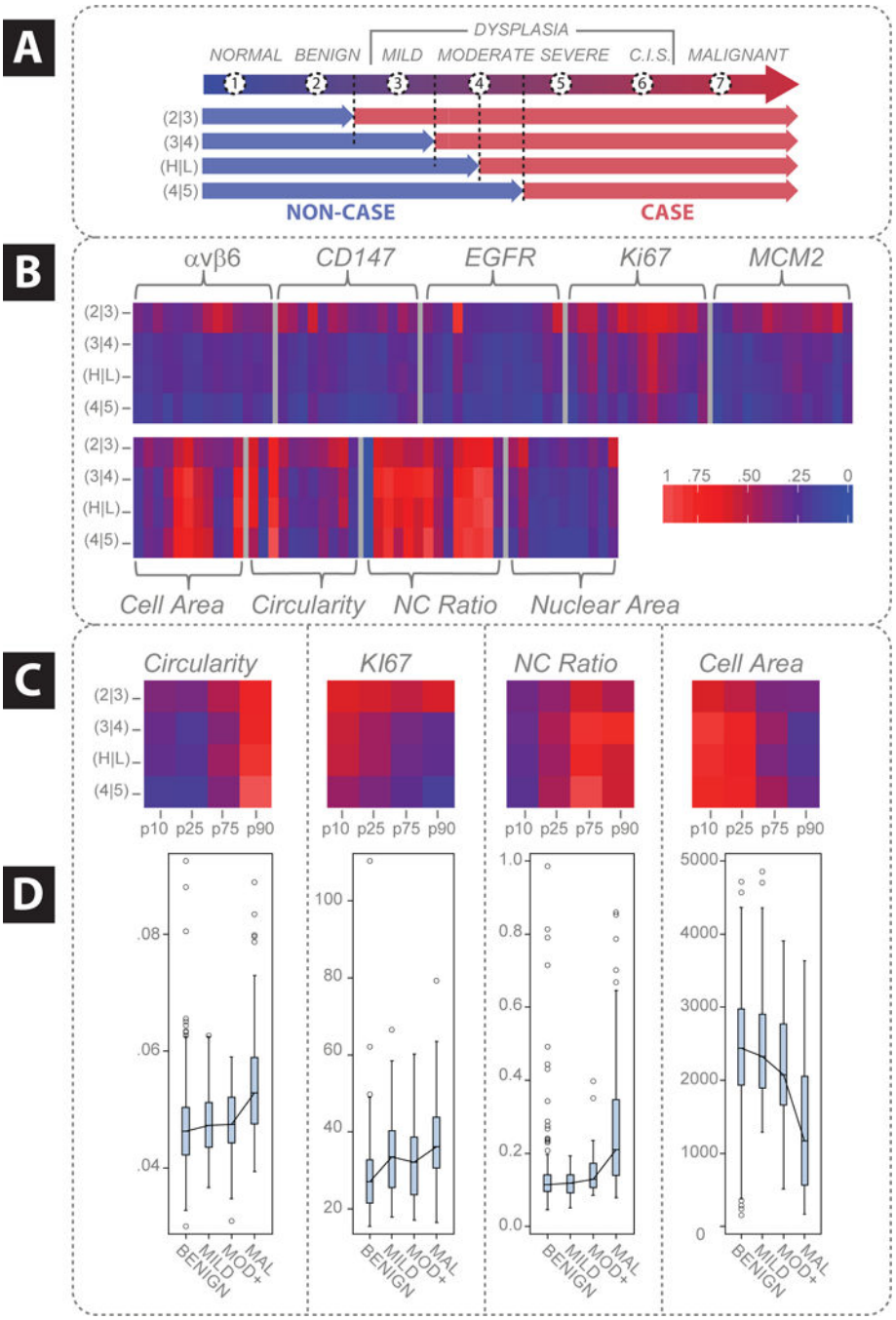

Figure 2. Variable importance from Random Forest models

A) Visual representation of diagnostic spectrum and the 4 diagnostic splits used in this trial to dichotomize diagnoses into either “Case” or “Non-case”. B) Univariate heat map of Gini values resulting from Random Forest modeling to demonstrate variable importance across all 4 diagnostic splits (y axis). Gini values from each model were scaled between 0 and 1 to generalize relative variable importance across all models. A value of 1 implies the variable is better able to discriminate between “case” and “non-case” than a variable with a value closer to 0. Groups of parameters are labeled by their corresponding marker; single boxes represent

specific summary measures (see Supplementary Figure 2 for more detailed labeling). Heatmaps should not be interpreted as “expression”, but rather as the information content associated with each parameter in its ability to differentiate between “case” and “non-case”. C) Parameter subset from (B) to focus on summary percentile measurements (p10, p25, p50, p75, p90 = 10^{th}, 25^{th}, 50^{th}, 75^{th}, 90^{th} percentile values). D) Box-and-whisker plots showing the distribution of median values for Circularity (unit-less value between 0 and 1), Ki67 (units = arbitrary fluorescence units (afu), nuclear-to-cytoplasmic (NC) ratio (unit-less ratio), and Cell Area (units = px^2), respectively. The box bottom and top represent the 25^{th} and 75^{th} percentiles, respectively. Median values are connected between boxes, and whiskers down/up to 1.5 interquartile range. (Ben = “benign”, Mild = “mild dysplasia”, Mod+ = “moderate/severe/CIS dysplasia”, Mal = “malignant”).

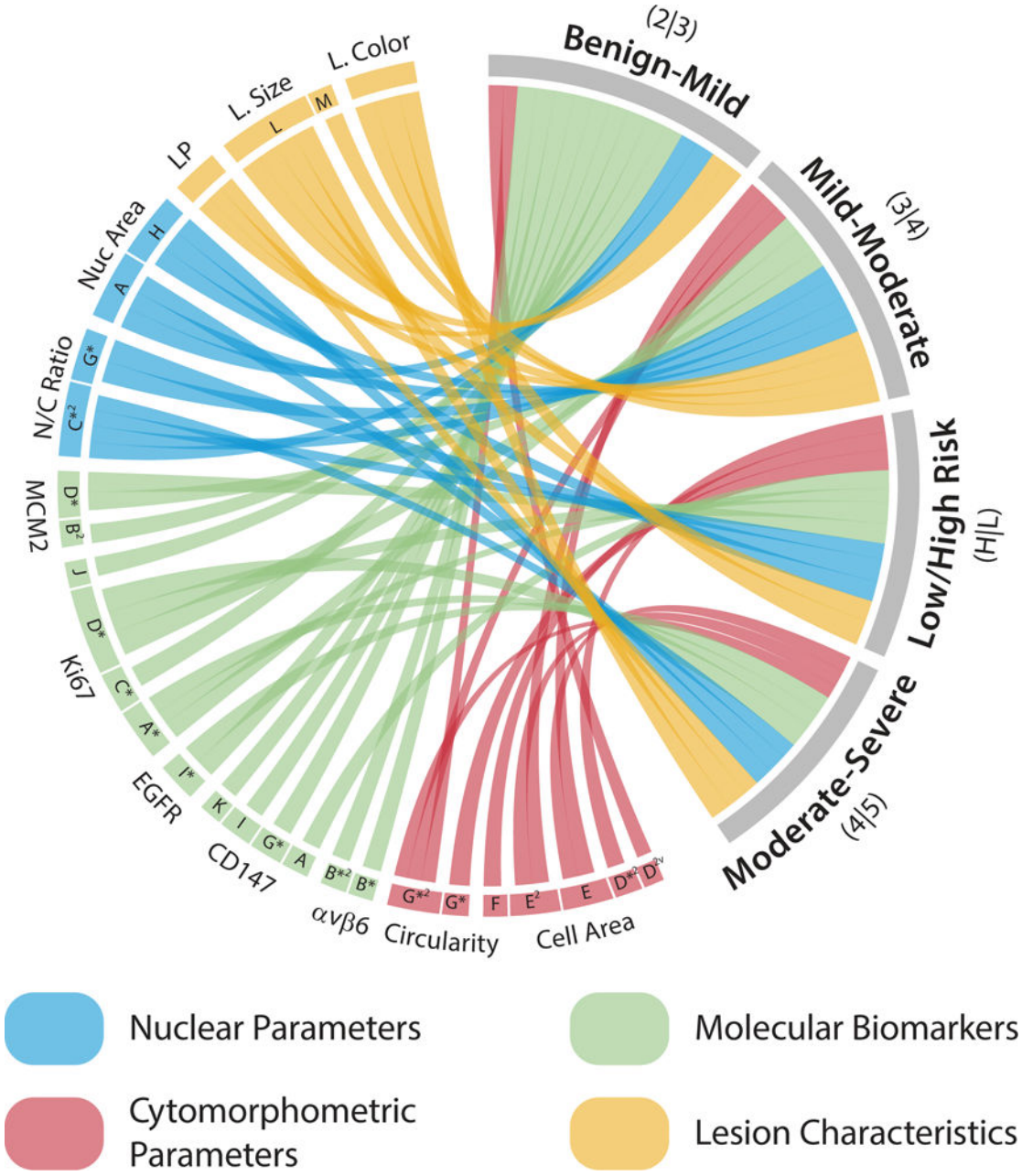

Figure 3. Chord Diagram of LASSO model parameter odds-ratios

Chord width refers to the relative contribution of a particular variable, based on standardized odds-ratios, calculated by exponentiating individual parameter coefficients from the logistic regression models. Odds-ratios of single parameters represent the odds that a model will predict the "Case" diagnosis for an increase of one standard deviation for the standardized (unit-less) parameter while holding all other parameters constant. Model splits are identified on the right side and their corresponding variables on the left side. Parameters are further color-coordinated by categorical grouping: Lesion characteristics (L. Size = Lesion Size, L. Color = Lesion Color, LP = presence of the clinical features of lichen planus), Nuclear parameters (NC = NC-ratio, Nuc Area = nuclear area), Biomarkers (αvβ6, CD147, EGFR,

Ki67, MCM2), and Cytomorphometric parameters (circularity, cell area). Summary statistic measures include A: coefficient of variation, B: variance, C: median, D: 10^{th} percentile, E: 25^{th} percentile, F: 75^{th} percentile, G: 90^{th} percentile, H: skewness, I: standard deviation, J: >0.5 Z-Score, K: >2.0 Z-Score, L: short-axis, M: long-axis, *: Log-scale, ^{2}:squared

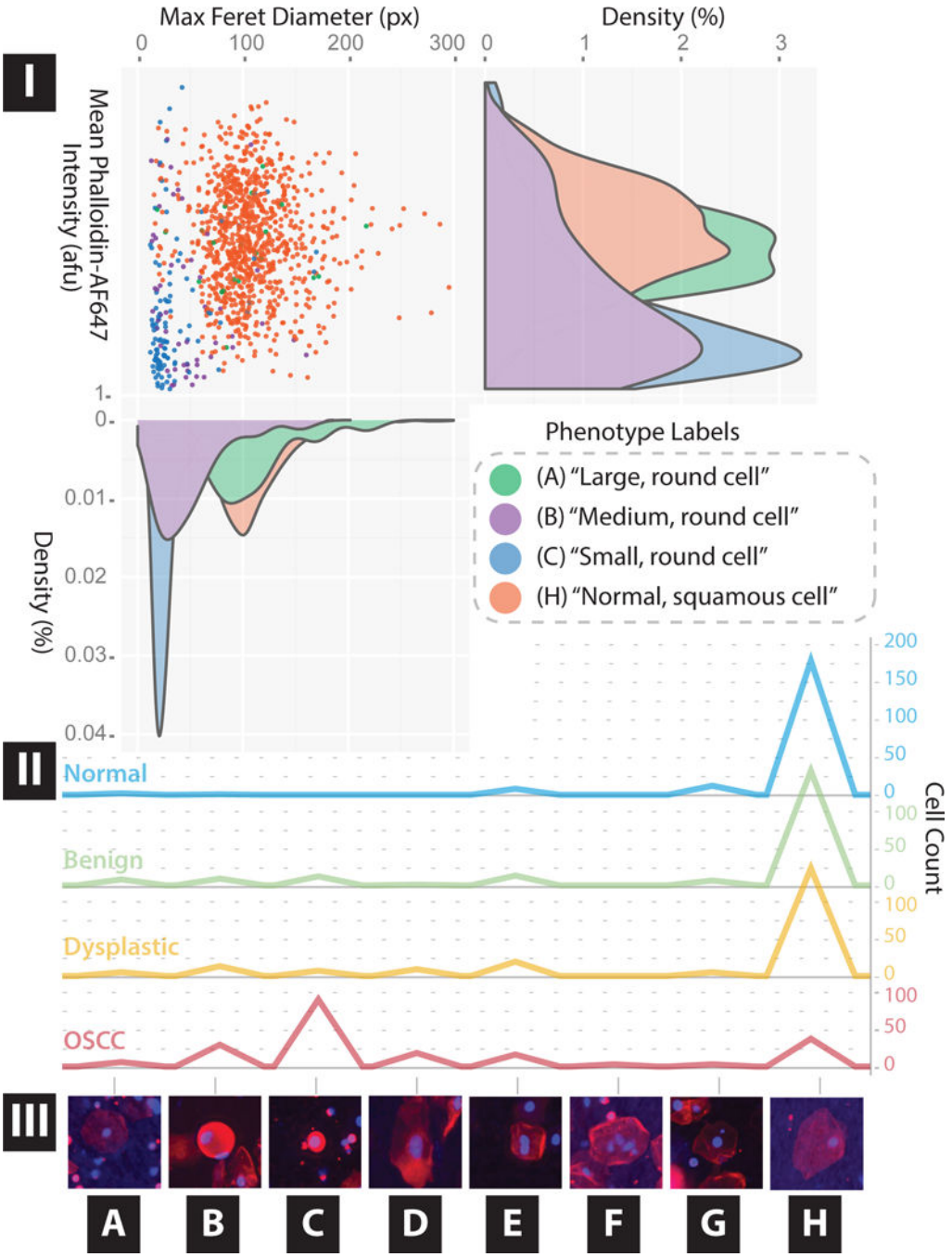

Figure 4. Cellular Phenotype Identified by Morphometric Parameters

Panel I) Scatterplot and density histograms for two morphometric parameters (Maximum Feret diameter and mean Phalloidin intensity) used to distinguish sub-populations of cells. Panel II) Bar plot of cell counts for each of the phenotypes identified by Panel III for 300 randomly selected cells from patients with final adjudicated diagnoses in categories "Normal", "Benign", "Dysplastic" (including mild, moderate, severe dysplasia and CIS), and "OSCC". These plots are visualized as a continuous line where peaks refer to the number of cells identified in each case in order to illustrate a "phenotype fingerprint" of the

disease categories. Panel III) Representative images of unique cellular phenotypes identified by significant differences in key morphometric parameters. Each thumbnail is cropped to the same dimensions of 120 μm ×120 μm. Phenotypic categories included A) Cells with smooth cytoplasmic border and high circularity, but low NC-ratio, B) Cells with high circularity, high NC-ratio, and medium cytoplasm area, C) Cells with high circularity, high N-C ratio, and small cytoplasm area, D) large cells with enlarged nuclei, E) Binucleated cells, F) Polynucleated cells, G) Cells with micronuclei, and H) Normal appearing squamous cells.

Table 1

Final model performance values for LASSO and random forest models. (“LC = parameter set with of lesion characteristics; Sens = sensitivity, Spec = specificity, AUC = area under ROC curve).

			Training			Validation		
	Dichotomous split	**Parameters**	**Sens %**	**Spec %**	**AUC**	**Sens%**	**Spec%**	**AUC**
Lasso	Low | | High	Biomarkers Only	90.8	58.7	0.871	85.0	59.2	0.802
		Biomarkers + LC	90.7	64.5	0.884	78.6	70.4	0.836
	Benign | | Mild	Biomarkers Only	90.1	45.0	0.814	92.7	53.1	0.800
		Biomarkers + LC	89.9	52.0	0.844	89.1	55.1	0.846
	Mild | | Moderate	Biomarkers Only	89.7	60.1	0.869	82.9	60.5	0.809
		Biomarkers + LC	89.6	67.2	0.880	82.9	72.3	0.839
	Moderate | | Severe	Biomarkers Only	89.4	72.6	0.903	77.1	73.6	0.846
		Biomarkers + LC	90.8	73.8	0.917	85.7	80.0	0.883
Random Forest	Low | | High	Biomarkers Only	89.5	51.1	–	86.8	53.0	–
		Biomarkers + LC	89.3	51.3	–	86.8	51.3	–
	Benign | | Mild	Biomarkers Only	91.0	42.0	–	90.9	50.0	–
		Biomarkers + LC	89.0	48.0	–	90.9	52.0	–
	Mild | | Moderate	Biomarkers Only	89.7	49.4	–	87.2	51.8	–
		Biomarkers + LC	87.0	50.4	–	87.2	52.6	–
	Moderate | | Severe	Biomarkers Only	90.9	56.3	–	84.9	59.2	–
		Biomarkers + LC	87.7	65.6	–	78.8	68.3	–