

DecisionDx®-SCC predicts biological risk of metastasis for SCC patients with one or more risk factors to inform risk-appropriate management.

# TEST RESULT AND RESULT DESCRIPTION

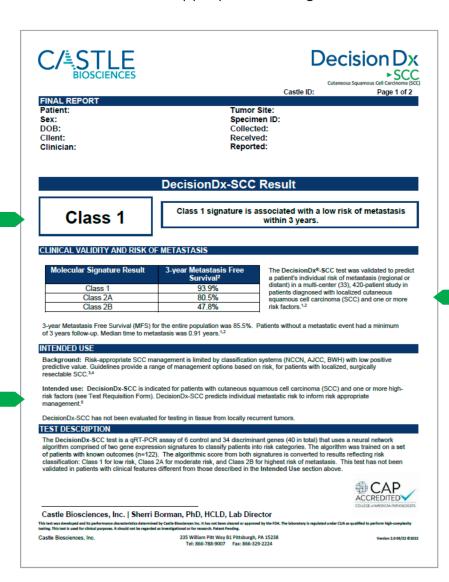
The test result for DecisionDx-SCC is reported as a classification of the gene expression profile result. Results are reported as:

- Class 1: Low risk <7% risk of metastasis
- Class 2A: Moderate risk 20% risk of metastasis
- Class 2B: High risk ≥50% risk of metastasis

## **INTENDED USE**

Informs risk appropriate management by predicting individual metastatic risk.

- Indicated for use in patients SCC and one or more highrisk factors.
- Results should be interpreted in the context of all other clinical and histopathological findings.



# VALIDATION AND SUPPORTING DATA

DecisionDx-SCC is validated to predict metastatic risk for SCC patients with one or more risk factors.

- Independently validated in a prospectively designed study of 420 SCC patients with 3year outcomes.
- DecisionDx-SCC is the strongest predictor in univariate and multivariate analyses.
- Test result adds significant information for SCC management.

## **TEST RESULT AND RISK FACTORS**

Metastatic risk is reported two ways: independently and segmented by number of traditional risk factors.

- Incorporation of traditional risk factors with DecisionDx-SCC results provides superior patient classification compared to traditional risk factors alone.
- Number of risk factors (1 or ≥2) further stratifies patient metastatic risk of patients in the independent validation study.

## **ADDITIONAL INFORMATION**

- DecisionDx-SCC is a gene expression profile test consisting of 40 genes (34 discriminant and 6 control).
- RT-PCR technology is used to measure gene expression levels of the discriminant genes which are normalized to the control genes.



# Decision Dx

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The table below presents overall rate of metastasis for patients with primary SCC compared to the subgroup that has 1 high-risk factor as well as  $\geq$ 2 high-risk factors from the 420 patient clinical validation cohort.\* A Class 1 result reduced the metastatic rate from 8.2% to 4.0% in patients with 1 high-risk factor. A Class 2B result more than doubled the metastasis rate to ≥50% in both groups. 12

\*Of 63 overall metastases, 60 occurred within 3 years. The remaining 3 occurred greater than 3 years following diagnosis

Result	Overall		1 Factor		≥2 Factors	
	n	Metastasis Rate	n	Metastasis Rate	n	Metastasis Rate
Overall Cohort	420	15.0%	171	8.2%	249	19.7%
				<u>'</u>		<u>'</u>
Class 1	212	6.6%	101	4.0%	111	9.0%
Class 2A	185	20.0%	65	10.8%	120	25.0%
Class 2B	23	52.2%	5	60.0%	18	50.0%

Risk factors included in the above table; location and size (areas H, M or any ≥2 cm), immunosuppression, any PNI, tumors with invasion (beyond subcutaneous fat, depth ≥2mm, or Clark level IV/V), poorly differentiated tumor histology, aggressive histolo subtypes<sup>(3,6)</sup> and lymphovascular invasion.

### COMPARISON WITH CLINICOPATHOLOGIC RISK FACTORS

Risk Factor	Hazard Ratio	p value
Class 1	1.00	-
DecisionDx-SCC Class 2A	3.22	<0.001
Class 2B	11.61	<0.001
Poor differentiation	3.93	<0.001
Perineural invasion	3.28	<0.001
Deep invasion**	3.11	<0.001
Tumor diameter (per cm)	1.15	<0.001
Immunosuppression	1.46	ns

\*\*Deep invasion; beyond subcutaneous fat, depth >6 mm or Clark level V

with a specific high-risk feature as hazard ratios. Hazard ratio represents the likelihood of a metastatic event in the group with the risk factor compared to the group without the risk factor (e.g. a Class 2B patient has a risk of metastasis that is 11.6 times greater than a Class 1 patient).

Multivariate analysis demonstrated independence of Class 2A and Class 2B molecular results (HR 2.33 and 6.86, respectively). Poor differentiation (HR 2.29) and deep invasion\*\*(HR 2.05) were also statistically significant.

#### ADDITIONAL INFORMATION ABOUT THE TEST

The proprietary DecisionDx-SCC test is an empirically derived multi-analyte algorithmic assay (e.q. MAAA). The 34 discriminating genes are: ACSBG1, ALOX12, APOBEC3G, ATP6V0E2, BBC3, BHLHB9, CEP76, DUXAP9, GTPBP2, HDDC3, ID2, LCE2B, LIME1, LOC100287896, LOC101927502, MMP10, MRC1, MSANTD4, NFASC, NFIC, PDPN, P13, PLS3, RCHY1, RNF135, RPP38, RUNX3, SLC1A3, SPP1, TAF8L, TFAP2B, ZNF48, ZNF496 and ZNF839. Six control genes consist of BAG6, FXR1, KMT2C, KMT2D, MDM2, MDM4.

All data shown in this report were collected and verified under an IRB approved multi-center study to establish and validate the test's prognostic accuracy in primary cutaneous squamous cell carcinoma. 1,2

### REFERENCE LIST

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  6. Connolly S, Baker D, Roenigk R, et al. J. Am Acad Dermatol 2012; 67 (4):531-550.

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# **COMPARISON WITH** TRADITIONAL RISK **FACTORS**

Multivariate analysis shows DecisionDx-SCC provides the strongest independent prognostic information.

- Class 2A risk is similar to the strongest established prognostic risk factors (deep invasion, poor differentiation, perineural invasion).
- Class 2B is the strongest predictor of metastatic risk (11.6x greater risk than Class 1 patient) in univariate analysis.
- Class 2B is a 3x stronger predictor of risk than the strongest traditional prognostic risk factors (deep invasion, poor differentiation, or perineural invasion).

