

PATIENT REPORT

Patient: **Type of Specimen:** FFPE Tumor Tissue
Sex: **Specimen ID/Block ID:**
DOB: **Ordering Clinician:**
Medical Record/Patient #: **Client:**
Date of Collection: **Additional Recipient:**
Tissue Received:
Date Reported:

ASSAY DESCRIPTION

DecisionDx[®]-Melanoma molecular test for cutaneous melanoma is a proprietary gene expression assay that uses RT-PCR to determine the expression of a panel of 31 genes (3 control) in primary tumor tissue. The **DecisionDx-Melanoma** classification is calculated from the gene expression results and then compared to a training set of patients with known outcomes.¹

RESULTS

DecisionDx-Melanoma Class = 1

Sub-class: 1A

Probability Score:

Class 1A molecular signature is associated with a low risk of recurrence within 5 years. Class 1A result falls within probability score range of 0.00 to ≤ 0.41

The data in this report is derived from clinical studies involving patient populations with specific clinical features as noted in section titled Clinical Experience. These results have not been validated in patients with clinical features different from those described. The probability score is a linear value between 0 and 1. Sub-classification is also shown (A or B) based on the proximity of the probability score to the crossover point between Class 1 and Class 2 (0.5)

CLINICAL EXPERIENCE ^{1,2,3,4}

This test was developed using a training set of 164 samples and validated in 514 Stage I-III patient samples. This data was collected and verified under IRB approved multi-center studies to establish and validate the predictive accuracy of **DecisionDx-Melanoma** in primary cutaneous melanoma. Outcomes were collected and the ability of the molecular signature to predict metastasis was evaluated.

STAGE I AND II CLINICAL INFORMATION ^{1,3,4}

Approximately 70% of the patients in the clinical validation studies were clinically and/or pathologically node-negative (i.e. AJCC Stage I and II). The risk of recurrence for low risk Class 1 and high risk Class 2 molecular signatures for Stage I and II patients is shown below.

Molecular Signature Result		Recurrence-free Survival at 5 Years (Stage I and II)	Distant Metastasis-free Survival (Stage I and II)
Class 1	1A	92%	96%
	1B	90%	90%
Class 2	2A	77%	80%
	2B	48%	65%

n=356 Stage I and II patients (most recent censor: Oct. 2015); Log-rank (Mantel-Cox) test; p<0.0001

****See page 2 of this report for data pertaining to Stage III disease in this reported population****

ADDITIONAL STAGE I AND II CLINICAL INFORMATION ^{1,3,4}

Time to first recurrence in Stage I and II, Class 2 patients (n=55)

Variable	Time to first recurrence (years)	Time to distant recurrence (years)
25 th percentile	0.8	0.7
Median	1.6	1.6
75 th percentile	2.3	2.3

The performance characteristics reported in the multi-center clinical validation studies^{1,2} and the multi-center performance study³ have been shown to be consistent in two independent, prospective clinical studies^{5,6}.

STAGE III CLINICAL EXPERIENCE ^{1,2,4}

Approximately 30% of patients in the clinical validation studies were AJCC Stage III. The distant metastasis-free survival and melanoma-specific survival for low risk Class 1 and high risk Class 2 molecular signatures for Stage III patients are shown below

Sub-classification (A/B) is not applied in the Stage III population

Molecular Signature Result	Distant Metastasis-Free Survival at 5 Years (Stage III)	Melanoma-Specific Survival at 5 Years (Stage III)
Class 1	73%	93%
Class 2	46%	68%

n=158 Stage III patients (most recent censor: Oct. 2015); Log-rank (Mantel-Cox) test; p=0.002 for DMFS; p=0.009 for MSS

Time to first recurrence in Stage III, Class 2 patients (n=72)

Variable	Time to first recurrence (years)	Time to distant recurrence (years)
25 th percentile	0.4	0.7
Median	0.8	1.0
75 th percentile	1.5	1.8

ABOUT THE TEST

DecisionDx-Melanoma cutaneous melanoma assay uses RT-PCR to determine the expression of a panel of 31 genes (3 control) in the supplied tumor tissue. The twenty-eight discriminating genes are: BAP1 (two gene loci), MGP, SPP1, CXCL14, CLCA2, S100A8, BTG1, SAP130, ARG1, KRT6B, GJA1, ID2, EIF1B, S100A9, CRABP2, KRT14, ROBO1, RBM23, TACSTD2, DSC1, SPRR1B, TRIM29, AQP3, TYRP1, PPL, LTA4H and CST6. The three control genes are: FXR1, YKT6 and HNRNPL. The predicted classification is reported as Class 1 for low risk, and Class 2 for high risk of metastasis.

The DecisionDx-Melanoma 31 gene assay is an independent predictor of metastatic risk in multivariate analyses including Breslow's thickness, ulceration, mitotic rate, age, sentinel lymph node status and AJCC stage.

REFERENCE LIST

- Gerami P, et al. Development of a prognostic genetic signature to predict the metastatic risk associated with cutaneous melanoma. Clin Cancer Res 2015; 21(1):175-83.
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- Zager J, et al. Performance of a 31-gene expression profile in a previously unreported cohort of 334 cutaneous melanoma patients. ASCO 2016 (meeting abstract)
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- Hsueh E, et al. Prospective validation of gene expression profiling in primary cutaneous melanoma. ASCO 2016 (meeting abstract)
- Greenhaw B, et al. Estimation of prognosis in invasive melanoma using a gene expression profile test. Amer Coll Mohs Surg, 2016 (meeting abstract).

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