

TUMOR RNA EXPRESSION PROFILE

RESEARCH USE ONLY

The information provided in this analysis has not been clinically validated and should not be used for clinical decision-making.

CLINICAL INFORMATION

Specimen Type: Biopsy
 Patient Age: 66
 PSA at Biopsy: 6.2
 Gleason Score: 3+3
 Pathologic features: N/A
 Biochemical Recurrence: No

RUO GRID INFORMATION

GRID ID: DPX000
 GRID profile Date: 9/26/2106
 Ordering Physician: Dr. John Smith
 Clinic/Hospital: Hospital Name
 Clinic/Hospital Address:
 Street Address, City, State Zip

SAMPLE

GENOMIC PROFILE SUMMARY*

Molecular subtype signatures (P.2)

- Neuroendocrine/small cell
- Adenocarcinoma
- Luminal
- Basal
- ERG
- ETS
- SPINK1
- TripleNeg

PREDICTIVE (P.3) 0 PERCENTILE RANK (%)** 100



PROGNOSTIC (P.4)



TUMOR GRADE/STAGE (P.5)



MOLECULAR PATHWAYS (P.5)



SELECT RNA MARKERS - TOP OUTLIERS (P.6)

RNA marker	PCA3	PERCENTILE RANK
RNA marker most over-expressed:	PCA3	98%
RNA marker most under-expressed:	SRD5A1	1%

*RNA signatures and genes listed above are intended as a summary of the RNA profile, for which more detail is provided in the following pages. "Average of x signatures" is the average of the percentile ranks of the individual signatures.

**Percentile Rank indicates the percentage of tumor RNA profiles in the GRID (n=2,829) with lower scores than for this profile.

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The GRID Tumor RNA Expression Profile contains 36 genomic signatures that provide insights into the molecular subtype, proliferation, androgen receptor signaling activity, androgen deprivation therapy (ADT) and radiation response, chemotherapy sensitivity as well as additional predictors of tumor grade, stage and metastasis risk.

18 Prognostic Signatures

Prognostic		Risk of metastasis		PERCENTILE RANK (%)	
		0	36	100	LOW METASTASIS RISK
SIGNATURE	INSTITUTION NAME	TUMOR SCORE	PERCENTILE RANK (%)	METASTATIC RISK	
Wu 2013	Massachusetts General Hospital	0.19	17%	LOWER	
Bismar 2006	Dana Farber Cancer Institute	0.36	59%	LOWER	
Penney 2011	Dana Farber Cancer Institute	0.13	23%	LOWER	
Agell 2012	Hospital del Mar-Mar Health Park	0.19	14%	LOWER	
Ramaswamy 2003	Dana Farber	0.53	81%	AVERAGE	
Varambally 2005	University of Michigan	0.22	24%	LOWER	
Bibikova 2007	UC San Diego	0.28	45%	LOWER	
Talantov 2010	Garvin Institute	0.09	13%	LOWER	
Nakagawa 2008	Mayo Clinic	0.12	4%	LOWER	
Stephenson 2005	Memorial Sloan Kettering Cancer Center	0.05	0%	LOWER	
Lapointe 2004	Johns Hopkins	0.19	35%	LOWER	
Yu 2007	University of Michigan	0.16	28%	LOWER	
Long 2011	Emory	0.34	36%	LOWER	
Long 2014	Emory	-0.36	12%	LOWER	
Singh 2002	Dana Farber Cancer Institute	0.34	24%	LOWER	
Klein 2014	Cleveland Clinic	0.22	52%	LOWER	
Cuzick 2011	King's College	0.48	68%	AVERAGE	
Larkin 2012	Queen Alexandria Hospital	0.30	44%	LOWER	

SIGNATURE	TUMOR SCORE	PERCENTILE RANK (%)	PREDICTED RESPONSE	ENDPOINT DESCRIPTION
ADT RESPONSE SIGNATURE				
ADT Response (Karnes2016)	0.06	42%	AVERAGE ADT RESPONSE	Response to adjuvant androgen deprivation therapy
RADIATION RESPONSE SIGNATURE				
RT Response (Zhao2016)	-1.41	7%	LOWER RT RESPONSE	Response to postoperative radiation
DRUG RESPONSE SIGNATURES				
Docetaxel (Lehrer2016)	-0.19	19%	AVERAGE SENSITIVITY	Sensitivity to docetaxel*
Dasatanib (Lehrer2016)	0.09	69%	AVERAGE SENSITIVITY	Sensitivity to dasatinib*

Predictive signatures for ADT, Radiation and Chemotherapy

6 BIOLOGICAL PATHWAYS; 36 MOLECULAR MARKERS

The expression levels of 36 genes are provided with their percentile rank against the normal distribution across our patient population (2,829).



Immuno-Oncology

B7-H3
PD1
PDL1

PDL2
CTLA4
IDO1



Proliferation / Growth Factors

Ki67
TOP2A
ERBB3

C-MET
HER2/NEU
EGFR



Androgen Signaling

PCA3
PSA (KLK3)
NKX3-1

SRD5A1
KLK2
AR



Small cell / neuroendocrine

pRB1
CCND1
AURKA

AURKA
NEAT1
MYCN



Invasion / Angiogenesis

SChLAP1
SPARCL1
HIF-1a

GSTP1
EZH2
VEGFR2



DNA Repair

ATM
ATR
RAD21

PRKDX
NBN
PARP1