

**TUMOR RNA EXPRESSION PROFILE**

**RESEARCH USE ONLY**

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

**CLINICAL INFORMATION**

Specimen Type: **Resection**  
Patient Age: **69**  
PSA at Biopsy: **9.4**  
Gleason Score: **3+4**  
Pathologic Features: **EPE**  
Biochemical Recurrence: **No**

**ORDER INFORMATION**

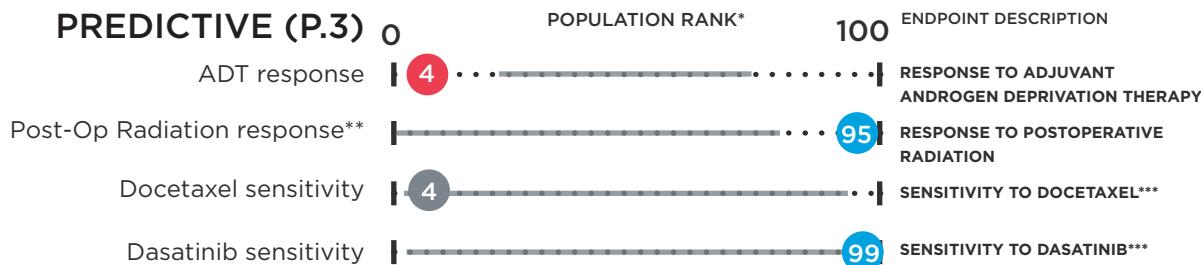
Patient Name: **First Last Name**  
Date of Birth: **MM/DD/YYYY**  
Decipher ID: **MC-001000**  
GRID profile Date: **MM/DD/2017**  
Ordering Physician: **Dr. First Last Name**  
Clinic/Hospital: **Practice Name**  
Clinic/Hospital Address: **Practice Address**  
**Street address, City, Zip, State, USA**

**GENOMIC PROFILE SUMMARY**

**Molecular subtype signatures (P.2)**

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

**PREDICTIVE (P.3)**



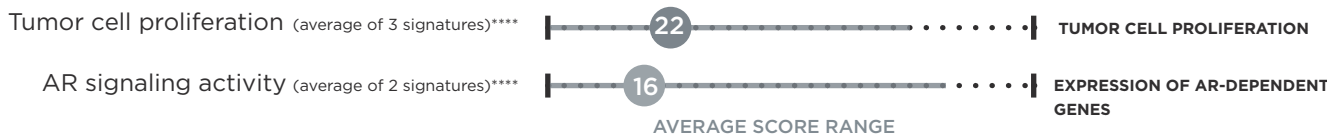
**PROGNOSTIC (P.4)**



**TUMOR GRADE/STAGE (P.5)**



**MOLECULAR PATHWAYS (P.5)**



**INDIVIDUAL RNA MARKERS - OUTLIERS (P.6)**

Over-expressed: N/A

Under-expressed: PCA3

\*Population Rank indicates the percentage of tumor RNA profiles in the GRID reference population (n=2,829) with lower scores than for this profile. If the tumor score for that signature or marker falls within the average distribution range (shown in grey line), then the result is colored grey (●). If the tumor score falls outside of the average distribution range, then it is colored either blue or red to indicate if the result is more favorable (●) or less favorable (●).

\*\*Model retrained and varies from published version.

\*\*\*Based on similarity to expression profiles of sensitive and insensitive *in vitro* cancer cell lines.

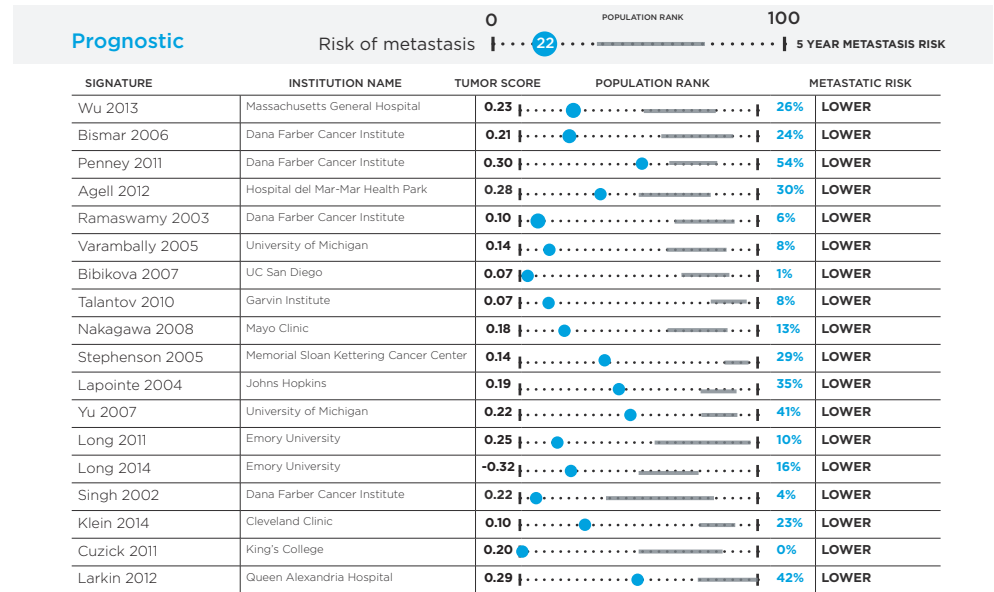
\*\*\*\*The listed RNA signatures and genes are intended as a summary of the RNA profile, for which more detail is provided in the following pages. "Average of x signatures" is the

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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



SIGNATURE	TUMOR SCORE	POPULATION RANK*	ENDPOINT DESCRIPTION
<b>ADT RESISTANCE SIGNATURE</b>			
ADT Response (Karnes2016)	-0.83	4%	Response to adjuvant androgen deprivation therapy
<b>POST-OP RADIATION RESPONSE SIGNATURE</b>			
Post-Op RT Response (Zhao2016)	0.42	95%	Response to postoperative radiation
<b>DRUG RESPONSE SIGNATURES</b>			
Docetaxel (Lehrer2016)	-0.34	4%	Sensitivity to docetaxel
Dasatinib (Lehrer2016)	0.40	99%	Sensitivity to dasatinib

## Predictive Signatures

ADT, Post-Op  
Radiation and  
Chemotherapy

## 6 BIOLOGICAL PATHWAYS - 36 MOLECULAR MARKERS

The expression levels of 36 genes are provided with their population rank against the normal distribution observed in our reference population (2,829 patients).

### IMMUNO-ONCOLOGY

PD1 PDL3/B7H3  
PDL1 CTLA4  
PDL2 IDO1

### PROLIFERATION / GROWTH FACTORS

Ki67 HER2/NEU  
TOP2A ERBB3  
EGFR c-MET

### ANDROGEN SIGNALING

AR PCA3  
KLK2 NKX3.1  
KLK3 SRD5A1

### SMALL CELL / NEUROENDOCRINE

pRB1 AURKA  
CCND1 NEAT1  
CHGA MYCN

### INVASION / ANGIOGENESIS

EZH2 SchLAPI  
GSTP1 SPARCL1  
HIF1A VEGFR2

### DNA REPAIR

ATM PRKDC  
ATR NBN  
RAD21 PARP1

FOR MORE INFORMATION, PLEASE VISIT [DECIPHERGRID.COM](http://DECIPHERGRID.COM) OR EMAIL [GRIDSUPPORT@GENOMEDX.COM](mailto:GRIDSUPPORT@GENOMEDX.COM)