# Sequencing of Plasma cfDNA from Patients with Locally Advanced Bladder Cancer for Surveillance and Therapeutic Efficacy Monitoring

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# Introduction

- Studies on different cancer types have shown that circulating tumor DNA (ctDNA) levels can be efficiently used to monitor treatment response to neoadjuvant therapy and/or detect disease recurrence earlier than clinical and radiological detection.<sup>1-3</sup>
- In bladder cancer, mutations in plasma have been previously used to monitor response during treatment and identify early signs of metastatic disease.4-5
- Recently, longitudinal ctDNA detection in patients with non-small cell lung cancer was described<sup>6</sup> and a personalized circulating tumor DNA (ctDNA) deteciton assay was developed and made available for research use only (Signatera™ RUO).

## Objective

• The aim of the study was to use patient-specific mutations identified in the primary tumor to detect metastatic relapse, evaluate prognosis, and monitor treatment response in ctDNA from longitudinally-collected plasma samples.

# Methods

# Clinical Protocol

- Patients diagnosed with locally advanced muscle-invasive bladder cancer (MIBC) and scheduled for chemotherapy were prospectively recruited between 2013 and 2017.
- All patients were treated with neoadjuvant or first line chemotherapy before cystectomy (CX) and had up to 2 years follow-up (**Figure 1A**).
- Plasma samples were longitudinally collected pre- and post-systemic therapy and at scheduled control visits after CX.

#### Figure 1. Schematic of Clinical Sample Collection



# Molecular Protocol (Signatera RUO)

- Patient-specific somatic mutations were identified by whole exome sequencing (WES) of tumor and matched normal samples.
- Personalized multiplex-PCR assays were used to detect patient-specific tumor DNA in plasma using cfDNA from longitudinally-collected plasma samples.
- For each patient, sequencing of 16 tumor-specific targets was performed and data were analayzed in a clinically-blinded fashion for the presence of ctDNA.
- Samples were considered ctDNA positive if and only if at least two positive patient-specific targets were called and met the qualifying confidence score threshold.
- Cinical results (radiographic imaging and treatment response) were unblinded and compared directly to the Signatera plasma call results.

## Results

• A total of 50 patients were included in the study (**Table 1**).

Table 1. Patient Characteristics and Demographics (N=50)						
Age (years),ª mean (range)	65.5 (43-77)					
Gender, n (%)		Tumor stage at CX, <sup>b</sup> n (%)				
Females Male	9 (18) 41 (82)	T0/Cis/Ta/T1 T2/T3/T4a	36 (72) 12 (24)			
Tumor stage at TUR-B, n (%)		Metastasis, <sup>c</sup> n (%)				
T1/T2 T4a/b	43 (86) 7 (14)	Local relapse (pelvis, rectum, urethra) Distant metastases (bone, lung, liver, skin)	6 (12) 6 (12)			
N stage before treatment, n (%)		Clinical follow-up, days (range)				
NO N1/N2	43 (86) 7 (14)	Disease free (CX; n=38) Clinical relapse (CX; n=10) Progression (CX unsuccessful; n=2)	434 (119-778) 347 (65-973) 280 (105-455)			
"At sampling; "n=48; "n=12. CX, cystectomy.						

# Plasma Sequencing QC

• In-line sequencing QC was performed across 5 HiSeq PE 2x50 runs; average per target depth-of-reads and background error rates are shown in **Figure 2**.

#### Figure 2. Plasma Sequencing QC



# Early Detection of Relapse

• Clinical relapse after CX was diagnosed for ten patients and ctDNA has been identified in plasma in nine of these patients with a median of 128 days prior to clinical relapse (**Table 2**). For one patient, the last control sample at 4 months post CX has not been analyzed yet.

Table 2. Molecular Versus Clinical Relapse (n=9)							
Diagnosis stage	CX stage	ctDNA detection lead time (days)	Clinical relapse after CX (days)	Location of metastasis			
T2, N0	T2, N0	0	973	bone			
T2, N0	TO, NO	265	624	local (urethra)			
T4a, N0	T4a, N0	0	119	local (pelvis)			
T2, N0	T3, N0	152	298	LN, lung, bone, local (pelvis)			
T2, N0	T2, N3	128	241	Liver, bone			
T2, N0	T4a, N0	96	379	local (pelvis)			
T2, N0	T1, N3	245	309	local			
T4b, N0	T3, N0	186	324	local (rectum)			
T4b, N0	T4a, N2	50	65	liver			
	<b>Diagnosis stage</b> T2, N0 T2, N0 T2, N0 T4a, N0 T2, N0 T2, N0 T2, N0 T2, N0 T2, N0 T2, N0 T4b, N0 T4b, N0 T4b, N0	Diagnosis stage CX stage   T2, N0 T2, N0   T2, N0 T0, N0   T4a, N0 T4a, N0   T2, N0 T3, N0   T2, N0 T2, N3   T2, N0 T4a, N0   T2, N0 T3, N0   T2, N0 T4a, N0   T2, N0 T1, N3   T2, N0 T1, N3   T4b, N0 T3, N0   T4b, N0 T4a, N2	Diagnosis stage CX stage ctDNA detection lead time (days)   T2, N0 T2, N0 0   T2, N0 T0, N0 265   T4a, N0 T4a, N0 0   T2, N0 T3, N0 152   T2, N0 T2, N3 128   T2, N0 T4a, N0 96   T2, N0 T1, N3 245   T4b, N0 T4a, N2 50	Diagnosis stageCX stagectDNA detection lead time (days)Clinical relapse after CX (days)T2, N0T2, N00973T2, N0T0, N0265624T4a, N0T4a, N00119T2, N0T3, N0152298T2, N0T2, N3128241T2, N0T4a, N096379T2, N0T1, N3245309T4b, N0T3, N0186324T4b, N0T4a, N25065			



Figure 3. Early Relapse Detection

- Figure 3 depicts 6 patients that had early relapse detection.
- ctDNA was detected at VAFs as low as 0.02% at the time of molecular recurrence, which had a lead time of up to 265 days prior to clinical recurrence (Figures 3D, 3E and 3F).

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# Prediction of Outcome

#### Figure 4. Relapse-Free Survival and ctDNA Status at Diagnosis and Post Cystectomy





# Treatment Response

Table 3. Prediction of Treatment Response following Chemotherapy						
Patient no.	Diagnosis stage	ctDNA VAF levels (%)	CX stage	ctDNA VAF levels (%)		
10 <sup>a</sup>	T4a	3.6	T2, N0	0.02		
11	T2	0.1	TO, NO	ND		
12 <sup>b,c</sup>	T1	ND	T4a, N0	0.05		
13	T2	0.1	TO, NO	ND		
14	T2	1.2	CIS, NO	ND		
15 <sup>a</sup>	T1	0.3	T2, N0	ND		
<sup>a</sup> Received first line chemotherapy before CX <sup>b</sup> Inderwent TLIR-P before TLIR-R. T1 tumor from Urethral pars prostatical <sup>b</sup> Treatment response defined by advancment from inoperable to operable state after chemo-						

herapy (despite clinical upstaging) VAF, variant allele frequency; CX, cystectomy; ND, not detected.

• In most patients, response to chemotherapy corresponded to a decrease in ctDNA VAFs (**Table 3**).

#### Figure 5. Neoadjuvant Treatment Response



• Figure 5 depicts two patients in which the treatment response was observed using ctDNA; ctDNA detected initially at diagnosis declined with neoadjuvant treatment and remained undetected after CX.

## Conclusions

- These data demonstrate that ctDNA analyses (e.g., via Signatera) can help inform on treatment response and identify disease recurrences up to 265 days earlier than radiographic imaging.
- Survival analyses identified significantly lower relapse free survival for patients with ctDNA at diagnosis or after CX.
- Ultimately, ctDNA analysis could be incorporated into routine follow-up for early detection of relapse and consequently potentially earlier initiation of alternate treatment such as immunotherapy.
- The benefit in overall survival gained by ctDNA relapse detection should be assessed in randomized clinical trials.

# References

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American Association for Cancer Research Annual Meeting 2018; Chicago, IL April 14–18, 2018







