

## INTRODUCTION

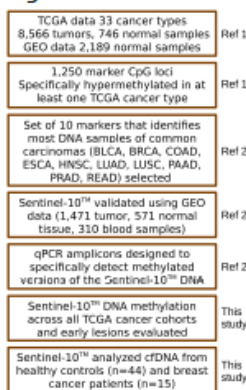
Multi-cancer early detection (MCEd) test that can identify cancer from a liquid biopsy, and can be used across various cancer types is an unmet clinical need. Tumors shed DNA into body fluids and therefore DNA methylation analysis of cell-free DNA from blood can be used for minimally invasive cancer tests. Sentinel-10™ liquid biopsy is based on a novel set of 10 biomarker loci (Fig 1, Ref 1, 2) hypermethylated in 10 common carcinoma types (marked purple in Table 1). We previously demonstrated that Sentinel-10™ can detect lung and pancreatic cancers (Refs 2, 3). Here, we present a new bioinformatics analysis revealing the performance of Sentinel-10™ in additional cancer types and in a clinical blood cohort of patients with breast cancer.

## MATERIALS AND METHODS

DNA methylation data from Illumina microarray platforms from The Cancer Genome Atlas (TCGA) and Gene Expression Omnibus (GEO) were downloaded from respective databases, normalized and analyzed as previously described (Ref 1) in R environment ver 4.2.0. Sentinel-10™ DNA methylation of cancer samples was tested against three control cohorts. Control Blood cohort consists of 1388 samples from two GEO datasets (GSE40279, GSE87571). NT.TCGA cohort consist of all 746 non-tumor tissue samples from TCGA database. NT.GEO cohort consist of 796 normal tissue samples from 16 GEO datasets (GSE50192, GSE48472, GSE48684, GSE61278, GSE61258, GSE63704, GSE79100, GSE64509, GSE63315, GSE51954, GSE51954, GSE61259, GSE60655, GSE64490, GSE61257, GSE70977).

Sentinel-10™ liquid biopsy test was performed by DNA methylation specific qPCR described before (Ref 2) that analyzed cDNA extracted from plasma samples obtained from healthy controls and breast cancer cases. Cancer cohort consisted of 15 women diagnosed with breast cancer, 14 stage IV cases and 1 stage II case; median age 66 (range 42-85); 13 white and 2 hispanic/latino women.

**Fig 1**



**Fig 1** The workflow of the Sentinel-10™ evolution

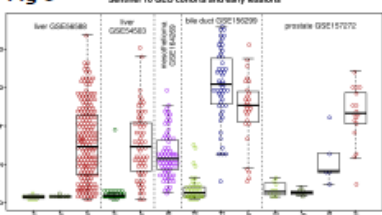
**Table 1**

TCGA Cancer Type Name	AUC Blood	AUC NT.TCGA	AUC NT.GEO
ACC	0.942	0.695	0.637
BLCA	0.999	0.882	0.995
BRCA	0.999	0.994	0.995
CESC	1.000	0.994	1.000
CHOL	0.998	0.977	0.987
COAD	1.000	0.993	0.999
DLBC	0.995	0.985	0.984
ESCA	1.000	0.991	0.999
GBM	0.996	0.957	0.985
HNSC	1.000	0.992	0.999
KICH	0.881	0.544	0.732
KIRC	0.984	0.893	0.952
KIPAN	0.943	0.682	0.941
LAML	0.964	0.807	0.904
LGCG	0.991	0.932	0.972
LHC	0.989	0.935	0.973
LIAD	0.999	0.984	0.998
LUSC	0.998	0.977	0.993
MESO	0.967	0.907	0.959
OV	0.871	0.567	0.740
PAAD	0.994	0.954	0.981
POPG	0.746	0.785	0.501
PRAD	0.998	0.978	0.992
READ	1.000	0.993	1.000
SARC	0.938	0.716	0.847
SKCM	0.958	0.796	0.893
STAD	1.000	0.993	0.999
UCEC	0.783	0.571	0.641
UCEC	0.909	0.548	0.755
THYM	0.829	0.625	0.620
UCEC	0.998	0.988	0.995
LUSC	0.999	0.978	0.995
LVM	0.736	0.827	0.530

**Table 1 - TCGA cancer cohorts:**

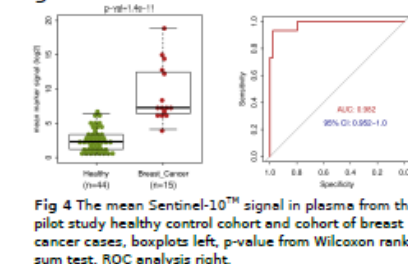
The last three columns show areas under the curve (AUC) for each cancer type, when DNA methylation from Sentinel-10™ loci is used to test respective cancer cohort and three independent control cohorts. The original 10 carcinoma types are marked purple and the additional 10 carcinoma types that have all three AUCs > 0.5 are marked blue.

**Fig 3**



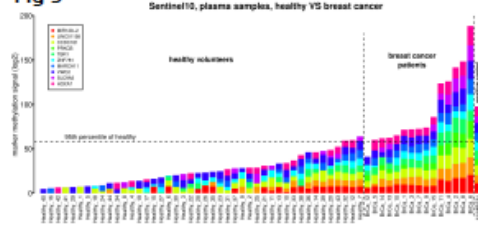
**Fig 3** Sentinel-10™ DNA methylation in independent data from GEO cohorts. Boxplots present cumulative DNA methylation of Sentinel-10™ loci in cohorts of cancer samples, normal samples, and early precancerous lesions from 5 GEO datasets.

**Fig 4**



**Fig 4** The mean Sentinel-10™ signal in plasma from the pilot study healthy control cohort and cohort of breast cancer cases, boxplots left, p-value from Wilcoxon rank sum test, ROC analysis right.

**Fig 5**



**Fig 5** The DNA methylation signals from individual Sentinel-10™ markers obtained from the pilot clinical study. Y-axis is in log2 scale.

## RESULTS

The bioinformatics analysis of all 33 TCGA cancer cohorts revealed that the Sentinel-10™ biomarker loci are predominantly hypermethylated in 10 additional cancer types (marked blue in Table 1). Therefore, the Sentinel-10™ MCEd test has the potential to detect 20 cancer types according to TCGA classification with high sensitivity and specificity (Fig 2, Table 1). These 20 TCGA cancer types account for 73.7% of new cancer cases and 80.5% of cancer deaths worldwide (Table 2).

Sentinel-10™ loci are also hypermethylated in independent hepatocellular carcinoma, mesothelioma, and cholangiocarcinoma cohorts from GEO (Fig 3). Furthermore, the Sentinel-10™ loci are hypermethylated early in cancer progression in bile duct and prostate early lesions (Fig 3) and in breast, colorectal, oesophageal, lung and pancreatic early lesions (Ref 4). Therefore Sentinel-10™ has potential to detect early cancer stages as soon as tumor DNA becomes present in blood or other body fluids.

The pilot clinical study (Figs 4 and 5), shows that the Sentinel-10™ liquid biopsy test can differentiate between blood from metastatic breast cancer cases and blood from cancer free controls with high sensitivity and specificity (AUC=0.982, 95% CI: 0.952-1.0).

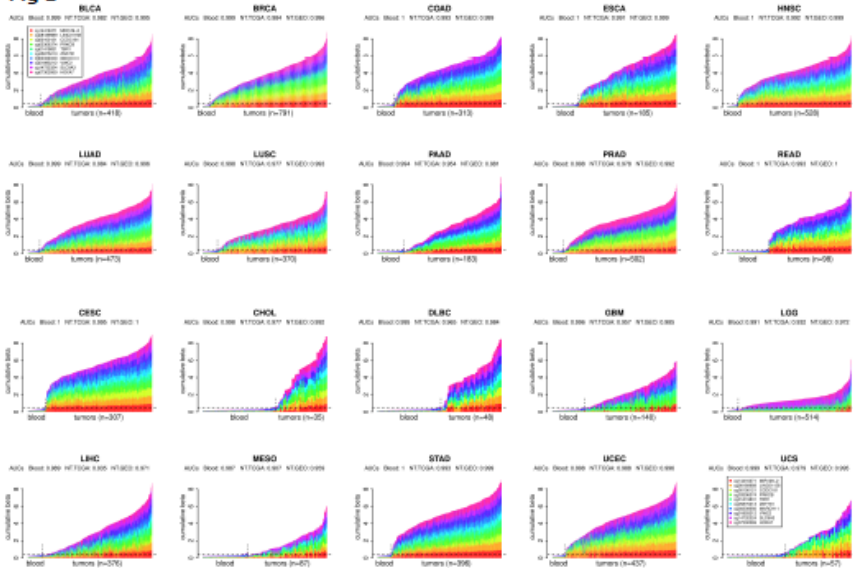
## CONCLUSIONS

- Sentinel-10™ has the potential to detect the majority of cancers.
- Sentinel-10™ can possibly detect early stages of cancers.
- The Sentinel-10™ liquid biopsy test detects breast cancer in blood samples.
- Sentinel-10™ represents an innovative MCEd test for cancer patients.

**Table 2**

Cancer Site	New Cases/New Deaths
Bladder	573,278 / 212,536
Brian, nervous system	308,102 / 251,329
Cervix uteri	604,127 / 341,831
Colon	1,148,515 / 576,858
Corpus uteri	417,367 / 97,370
Esophagus	604,100 / 544,076
Female breast	2,261,419 / 684,996
Gallbladder	115,949 / 84,695
Hodgkin lymphoma	83,087 / 23,376
Hypopharynx	84,294 / 38,599
Kaposi sarcoma	34,270 / 15,095
Kidney	431,296 / 179,369
Larynx	184,615 / 99,840
Leukemia	474,519 / 311,594
Lip, oral cavity	377,713 / 177,757
Liver	905,677 / 830,180
Lung	2,206,771 / 1,796,144
Melanoma of skin	324,635 / 57,043
Mesothelioma	30,870 / 26,278
Multiple myeloma	176,404 / 117,077
Nasopharynx	133,354 / 80,008
Non-Hodgkin lymphoma	544,852 / 259,793
Non-melanoma of skin	1,198,073 / 63,731
Oropharynx	98,412 / 48,143
Ovary	313,959 / 207,252
Pancreas	495,773 / 456,035
Penis	36,066 / 13,211
Prostate	1,414,259 / 375,304
Rectum	732,210 / 339,022
Salivary glands	53,583 / 22,778
Stomach	1,089,103 / 768,793
Testis	74,458 / 9,334
Thyroid	586,202 / 43,646
Vagina	17,808 / 7,995
Vulva	45,240 / 17,427
All sites	19,292,789 / 9,968,133
Sentinel10 sites	14,214,271 / 8,014,860
Sentinel10 percent of all	73.7 % / 80.5 %

**Fig 2**



**Fig 2** Sentinel-10™ DNA methylation in 20 TCGA cancer cohorts. First two rows represent cancers for which Sentinel-10™ was originally designed and the last two rows represent cancers where Sentinel-10™ would be also applicable based on the bioinformatics analysis. The plots represent DNA methylation of individual Sentinel-10™ loci in individual cancer samples. A representative sample of 50 control blood samples is shown for comparison. Horizontal dashed lines represent 95<sup>th</sup> percentile of cumulative DNA methylation of the entire control blood cohort (n=1388).

## REFERENCES

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2. Vrba L, Oshiro MM, Kim SS, et al. DNA methylation biomarkers discovered in silico detect cancer in liquid biopsies from non-small cell lung cancer patients. Epigenetics 2020;15:419-30.
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