

Contamination Source Identification[®] CSI-Dx[®]

Taking on the Pandemic: Transforming Your Clinical Lab into a COVID-19 Ready Lab Using NGS + RT-qPCR

COVID-19 Data Challenges

COVID-19 response has demonstrated great advancements in

- Scientific knowledge at a molecular level
- Benefits of real-time epidemiology
- Positive use of mass communications

Reflecting on initial response:

- Initial testing response was built around government labs
- Subsequent responses were disjointed across suppliers and labs
- Assay platforms and reagent supplies were limiting testing

Challenges going forward:

- Testing capacity is still limiting
- Data is varied and imperfect
- Data is buried in siloed local systems





Next Generation Digital Platforms

Next generation digital platforms should be able to provide better integration of the science, laboratories, health systems and data management

- exchange for standardizing, adapting, and distributing testing methods
- interchangeable data model that make it possible to correlate different testing results with the epidemiological mapping
- modeling of virus movement and drift while integrating patient data vs outcomes would give us the opportunity to move into proactive response

Through our partnership with CSI, L7 has developed and qualified an integrated workflow for performing COVID-19 diagnostic testing







Contamination Source Identification®

CSI-Dx[™]

BACTERIA

There are approximately 39 trillion bacterial cells living amongst our 30 trillion human cells.

DIAGNOSE

verb: to identify the nature of an illness by examination of the symptoms.

a : unique in kind or quality b : unprecedented

DETECT

verb: to identify or perceive that which is hidden.

a : new and original b : revolutionary Diagnosis has always been at the heart of medicine.

At CSI, we are no longer diagnosing disease, we are detecting it.





VALIDATION of SARS-CoV-2 Detection





LIMIT OF DETECTION

"Spike-ins" of known counts of SARS-CoV-2 genome copies were spiked into pooled VTM of confirmed negative COVID-19 samples at increasing concentrations:

LOD of SARS-CoV-2: 10-32 Genome Copies per µL

ANALYTICAL & CLINICAL ACCURACY

Analytical validation compares 20 confirmed negative samples against 20 negative samples "spiked" with SARS-CoV-2 at 2x LOD:

Analytical Sensitivity: 100% Analytical Specificity: 100%

Clinical validation assess the CSI-Dx result against qPCR results of clinical specimines:

Clinical Sensitivity: 89% Clinical Specificity: 100%



CSI-DX Implementation Case Study Using L7 ESP Platform

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Contamination Source Identification® CSI-Dx®

CSI-DX process for COVID-19 detection using NGS and RT-qPCR

single platform to manage wet lab process, bio-informatics and lab operations







ESP CSI- Ordering and Accessioning Applet

Description: bulk ingest of accessions (done by clinics/hospital). Hospitals log into ESP and upload a CSV file with patients/sample info.

Advantage: Moved accessioning responsibility outside of the lab. Lab users just have to confirm that the information entered matches the received physical/faxed copy and that the sample is in good condition.

🕹 LIMS										Q system a	admin 👱
Worksheet: covid COVID Report										Archive	Save
< Prev COVID Re	eport - (0)	♦ Next > ♦	1 of 1 Protocols								₽
Aliquot	Patient Last Name	Patient First Name	Date of Birth	Gender	Physician Last Name	Physician First Name	Physician Phone	Physician Fax	File Link	Start	loD
ALIQ000001	Simpson	Homer	5/12/1989	Male	Riviera	Nicholas	400742742	400742742	Final Report	✓done区	suun col De
ALIQ000002	Parker	Peter	8/10/2001	Male	Stark	Tony	5031211212	5031211212	Final Report	✓done 🗹	rotoo
ALIQ000003	Everdeen	Katniss	3/12/1989	Female	Haymitch	Habernathy	4041211212	4041211212	Final Report	✓ done 🖸	4





COVID RT-qPCR branch

COVID-19 Chain







COVID RT-qPCR







COVID-19 RT-qPCR Bulk Results Ingest

Description: ingest results from RT-qPCR. Results for the 3 probes are mapped back to samples in ESP.

Advantage: No need to manually input data (i.e. reduced human error). Generated report can be printed and the heatmap can highlight contamination issues.

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Worksheet: CO' Rotor-Gene rt-qPC	VID_Testing_A	oril2020				Arch	ive Sav	e Save and	Contii	nue
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Aliquot		RP Well	File	Analysis Result	Ingest Notes	Start		Complete		lo O tails
24 Samples	5, 46, 47, 48	49, 50, 51, 52, 53, 54, 55, 56,	RotorGeneTestRun - test_run_r	r Pending analysis		✓ done 🗹				umn ol De
										Protoco





COVID RT-qPCR

Rotor-Gene Standard Report, 2020-04-03T16:23:40.573906

Expected Controls Results

Control Type	Name	2019 COV N1	2019 COV N2	RP	Expected CT Values
Extraction	HSC	-	-	+	<40 CT
Negative	NTC	-	-	-	None
Positive	nCoVPC	+	+	+	<40 CT

Controls Results

Control	Replicate 1	Replicate 2	Replicate 3
HSC	19	35	23
NTC	51	21	33
nCoVPC	236	532	162

Samples Results

Туре	Name	N1	N2	RP
	az9qz	39	21	14
	dc7ec	3	39	27
	ed1zx	12	12	35
	fv6rv	29	27	39
	gb5tb	7	19	40
	hn4yn	2	87	45
	ik6gh	45	12	35
	jm3um	43	56	23
	ol0nm	9	50	50
	ol7bn	5	74	23
	pl8ui	34	56	96
	pm9jk	12	43	67
	qa2qw	23	43	74
	rf2er	22	32	13
	sx8wx	35	40	16
	tg3df	78	5	33
	ub0op	7	40	40
	uj5ty	65	46	57
	vy9kl	5	20	20
	ws1as	34	32	57
	yh4cv	12	23	97

Explore RT-qPCR results directly in ESP with a table of Control and Sample measurements, as well as an interactive heatmap to highlight contamination Issues







COVID NGS branch









COVID Library Prep

Prev Biomek Lib Prep Ingest - (0)	Worksheet: COV	/ID-19 Test NGS - Lib	rary Prep				Arc	Q system	admin	e	Bulk ingest library prep details
4 Samples All Samples A01, A02, A03, A04 ¹ Upload a file Pending import Start Pipeline	< Prev Bion	nek Lib Prep Ingest - (0 Group) ¢ Ne	xt >	Protocols	Ingest Notes	Start		C	ails III	
	4 Samples	> All Samples	A01, A02, A03, A04	1 Upload a file	Pending import		Start Pipeline	<pre> Ø </pre>	olumns	^p rotocol Det	

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Worksheet: COV Library Prep	ID-19 Test NGS - Library Pre	D						Archive	Save
< Prev NEB	Kit Summary - (0)	🔶 Next >	2 of 2 Protocols NEB Kit F	Prep Submit to Next	Workflow				≣
Library	Primer Plate Index Well	PCR Plate Barcode	PCR Plate Sample Well	*I7 Index ID	I7 Index	15 Index ID	15 Index	NEBNext Ultra II RNA Library Prep Kit Lot Number	Col
LIB000001	A01	whj2794	A01	S762	TTACCGAC	S512	CGTATTCG	dbwk872	, in the summer of the second
LIB000002	A02	whj2794	A02	S729	AGTGACCT	S591	CTCCTAGA	dbwk872	, is the second
LIB000003	A03	whj2794	A03	S702	TCGGATTC	S523	TAGTTGCG	dbwk872	`
LIB000004	A04	whj2794	A04	S763	CAAGGTAC	S505	GAGATACG	dbwk872	
		WIJZ/ 04		3,03	CARGUIAC	5505	CACATACO	ubwko/2	

Select lot numbers





COVID Analysis

Submit bioinformatics scripts to be run remotely and ingest results from pipeline

LIMS					Q system	admin 👱
Worksheet: COVID COVID Analysis	-19 Test NGS - COVID	Analysis		Arc	hive Save Save and	l Continue
< Prev COVID F	RAPID-Dx - (0)	♦ Next >) \land 1 of 3 Protocols			≡
Library Pool	Group	*RunfolderName	*CSIdx Sample ID	Start	✓ Complete ≡	Col
4 Samples	> All Samples	TestRunRapidDx	e2n4bn-LIBPOOL000001, eff42c36-LIBPOOL000004, hs4k5k-LIBPOOL000002, sh36dk-LIBPOOL000003	Start Pipeline	×.	suun col De
						Proto

LIMS						Q	system adm	nin 🤇	3
Worksheet: COVIE COVID Analysis	D-19 T	est NGS - COVID Analysis			A	rchive Save	Save and Cor	ntinu	е
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Library Pool		Number of Raw Sequences	Number of Filtered Sequences	Number of ERCC Sequences	ERCC/Filtered Sequences Ratio	Number of H	uman Sequ	Col	etails
4 Samples		17882640, 20453714, 21934046, 26841438	16016823, 18421900, 19754993, 24117139	138582, 180170, 182306, 84802	102.247, 115.577, 132.289, 232.954	14729605, 16	932212, 1832	umns	
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CSI-DX Interpretation process

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Worksheet: COVID-19 COVID Analysis	9 Test NGS - COVID Analysis									Archive	S	ave
< Prev COVID And	alysis Results - (0)	♦ Next >	రు	3 of 3 Protocols								=
Library Pool	CSIdx Sample ID	*Sample Type		ERCC/Filtered Sequences Ratio	SARS-2 Count	*Result		*Next Step		✓ Complete =		Coli
LIBPOOL000001	e2n4bn-LIBPOOL000001	Sample	~	115.577	0	Not Detected	~	Report	~			
LIBPOOL000002	hs4k5k-LIBPOOL000002	Sample	~	102.247	0	Not Detected	~	Report	~			roto
LIBPOOL000003	sh36dk-LIBPOOL000003	Sample	~	132.289	72	+ 2019-nCOV	~	Report	~			4
LIBPOOL000004	eff42c36-LIBPOOL000004	Sample	~	232.954	43	+ 2019-nCOV	~	Report	~			
											_	





COVID Report Generation

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.7INFORMATICS

Generate physician ready reports with one click

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Worksheet: COVID-19 Tes COVID Report	t NGS - COVID Report			Archive	Save
< Prev COVID Report -	(3) ♦ Next >) 1 of 1 Protocols			≡
Property	LIBPOOL000001	LIBPOOL000002	LIBPOOL000003	LIBPOOL000004	Colr
Detection Method	NGS	NGS	NGS	NGS	suur col D
COVID-19 Results	Not Detected	Not Detected	+ 2019-nCOV	+ 2019-nCOV	rotoe
Report Result	Not Detected (Negative)	Not Detected (Negative)	Detected (Positive) [CRITICAL]	Detected (Positive) [CRITICAL]	<u>م</u>
Sample ID	e2n4bn	hs4k5k	sh36dk	eff42c36	
Collection Date	3/26/2020	3/26/2020	3/26/2020	3/26/2020	
Sample Type	Swab	Swab	Swab	Swab	
Patient Last Name	Pope	Leduc	Matthews	Targaryen	
Patient First Name	Olivia	Antoine	Taylor	Daenerys	
Date of Birth	12/23/1989	5/15/1985	12/23/1986	8/1/1983	
Gender	Female	Male	Unknown	Female	
Physician Last Name	Rosen	Rosen	Rosen	Rosen	
Physician First Name	David	David	David	David	
Physician Phone	5031211212	5031211212	5031211212	5031211212	
Physician Fax	5031211212	5031211212	5031211212	5031211212	
File Link	Final Report				
* File UUID	9d626a70-2353-4132-8868-1e48a94265f6				
Start	✓ done 🗹	Start Pipeline	Start Pipeline	Start Pipeline	
Complete					





SARS-CoV-2 Detection

Patient Information	Sample Information	Practice Information
Patient Name: Olivia Pope	Sample Type: Swab	Physician Name: David Rosen
DOB: 1989-12-23	Sample ID: e2n4bn	Phone: (503)121-1212
Sex: Female	Collection Date: 2020-03-26	Fax: (503)121-1212
Patient ID: e2n4bn	Samples Received: 2020-03-26	Report Completion Date: 2020-04-10

Test Description

The CSI-Dx^{**} test utilizes Next Generation Sequencing (NGS) technology and CSIØ's validated RAPID-Dx^{**} bioinformatic pipeline to directly detect pathogenic RNA from transcriptionally active bacteria, tungi, viruses, and protozoa. Sequencing of nucleic acids directly from clinical samples has allowed for the detection of a wide array of pathogens 12 and circumvents many of the limitations seen in previous methods of diagnostics such as culture or PCR3.9. The CSI-Dx^{***} test has been analytically validated to report the presence of pathogenic microbial and viral nucleic acid when present at levels above each microbe's established Limit of Detection (LOD). The results included within the report display qualitatively if the sample yielded normalized RNA sequence counts of Covid-19 above its LOD. It the sample yielded normalized RNA sequence counts below the LOD. It me RNA sequence counts above the analytically validated LCD, it is considered to be detected, whereas normalized RNA sequence counts below the LOD are considered to be not detected.

CSI DX Results			
Test	Result	Reference Interval	Notes
SARS-CoV-2	Detected (Positive) [CRITICAL]	None	

Disclame: (i) This test was developed and its performance characteristics determined by Contamination Source Identification® (ICLIA #800-2180522). This test has not been FDA deared or approved. The Pernsylvania Department of Health Bureau of Laboratories (BOL) independent review of his validation is perioding, and therefore all results in this report are considered presumptive and for research purposes only until the review is completed. This test is only authorized for the duration of time the declaration that circumstances exist justifying the authorization of the emergency use of in vitro diagnosic tests for detection of SAR8-CoV-2 virus and/or diagnosis of COVID-19 intection under section 564(1)(1) of the AL; 21 U.S.C. 380bbb-30(1)(1), unless the authorization is terminated or reviewed in sequences do cover. (ii) Negative results do not prectude 2019-nCoV infection and should not be used as the sole basis for teatment or other patient management desions. Optimum systement types and timing for pask viral levels during infections: caused by 2019-nCoV have not been determined. A taise negative results and y account if amplification inhibitors are present in the speciment or if inadequate numbers of organisms are present in the speciment (ii) Test performance can be affected because the equitaming the full clinical genetizme or if inadequate numbers of organisms are present in the speciment vorkers and clinical laboratories may not know the optimum types of samples nor the most ideal collection times to basis of viral RNA. Detection of Viral RNA point directate the presence or infections virus of that Covid 19 is the cusative agent for clinical symptoms. The performance or the stabilished for monitoring treatment and disease resolution of SARS-CoV-2. (iv) Contamination Source Identification, LLC assumes no lability for the misuse or misinterpretation o information outained through this report.

> Laboratory Director: Dr. Holmes Morton, M.D. R.T., Holmes Morton, M.D. Technical Supervisor: Dr. Regina Lamendella, M.D

CSI, 419 14th Street, Huntingdon, PA, 16652 For inquiries, the physician may contact: 717 - 413 - 1629 CLIA #39D-2180522 I PA Lab ID Number #37318

Final clinical report generation and electronic signatures

Physician Clinical Report Generation

Description: one-click final report generation.

Advantages: No need to look for different pieces of information across spreadsheets, LIMS, Analysis and Order forms nor input them into a PDF.

ESP generates Ready to fax PDF with e-signatures



COVID Report

Report elements are dynamic and depend on detection method (i.e. NGS or rt-qPCR), as well as test result.



NGS Negative/Positive

rt-qPCR Indeterminate







L7 ESP Platform Overview

ESP architecture allows users to define content





The process begins when ESP ingests a Sample Accessioning form is received from a clinical institution. As the samples move through the Sequencing workflow, ESP is gathering data from Illumina Sequencers, fluorimeters, a Biomek Liquid Handling Robot, and various bioinformatic pipelines. ESP enables the scientists to determine presence of a given pathogen in the patient's blood, and smoothly inform any physicians of the findings.

All of this data is kept inside ESP in a secure and query-able fashion.



