

Metagenomics for Pathogen Genomics

2025 AMD Mountain Region
Bioinformatics Conference

Dr. Kelly F. Oakeson

What is Metagenomics?

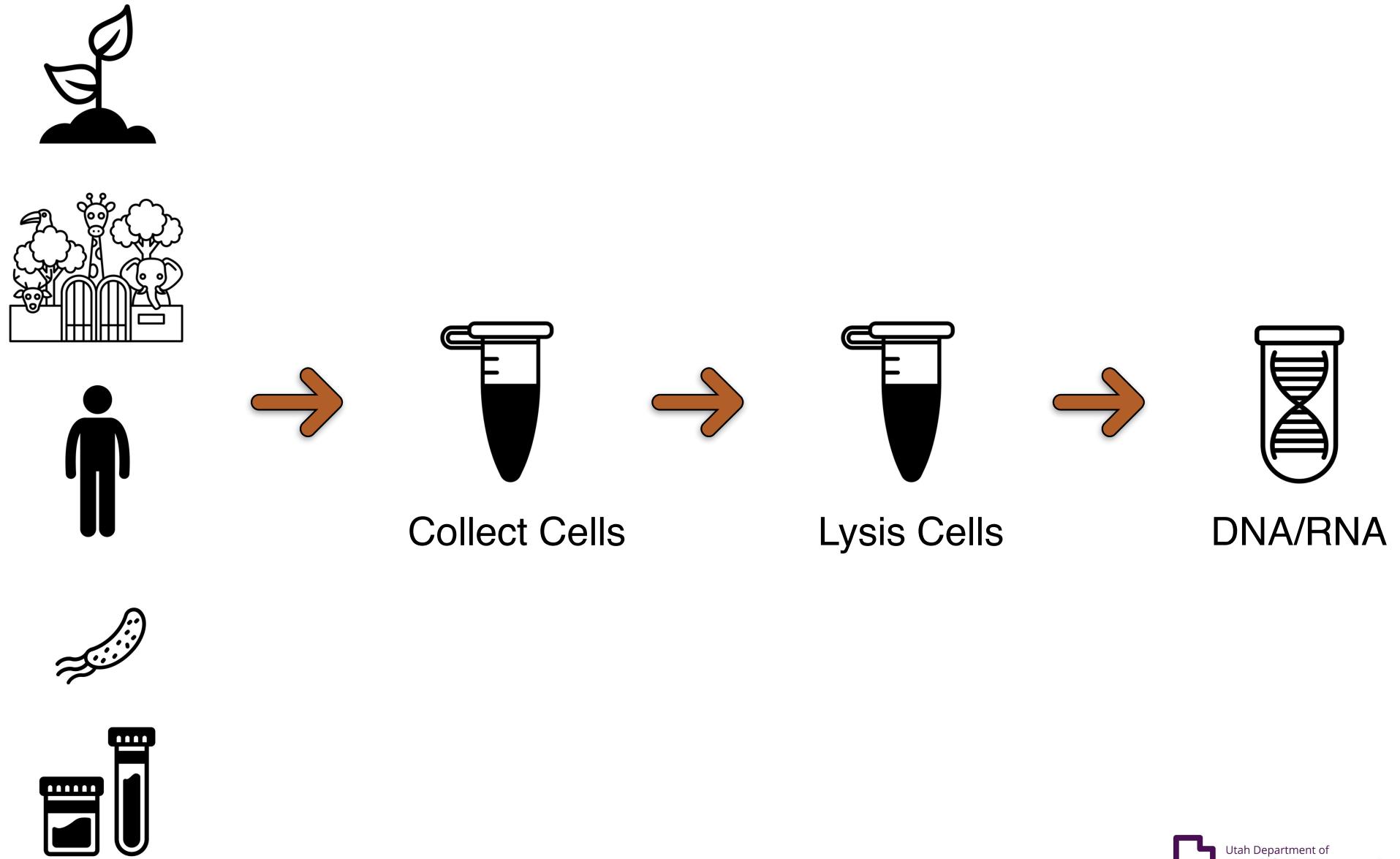


What is Metagenomics?

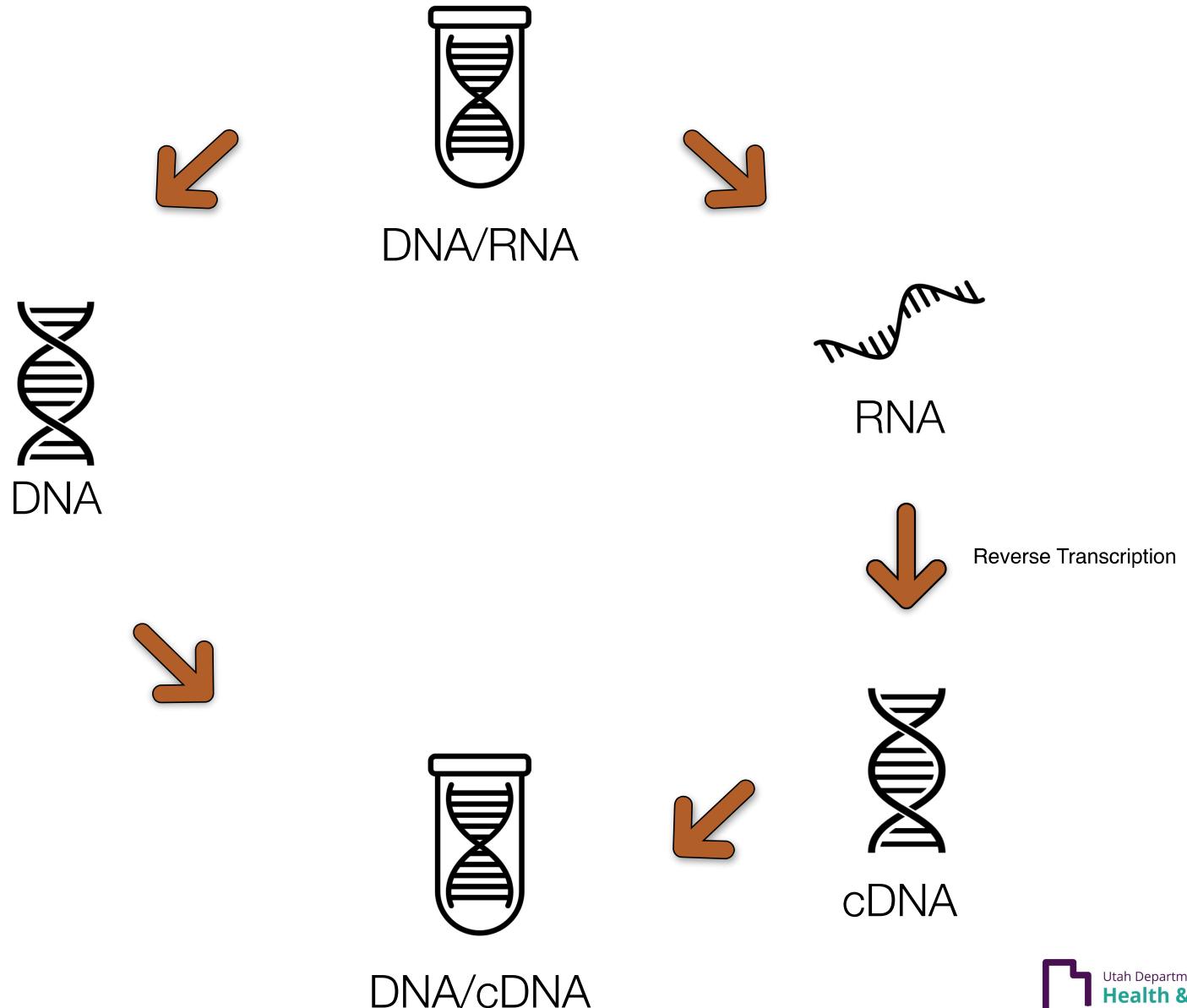


Metagenomics is the study of genetic material recovered directly from environmental or clinical samples, eliminating the need to isolate and culture individual species before sequencing them. This approach enables the analysis of entire microbial communities, providing insights into their composition, diversity, and functional potential.

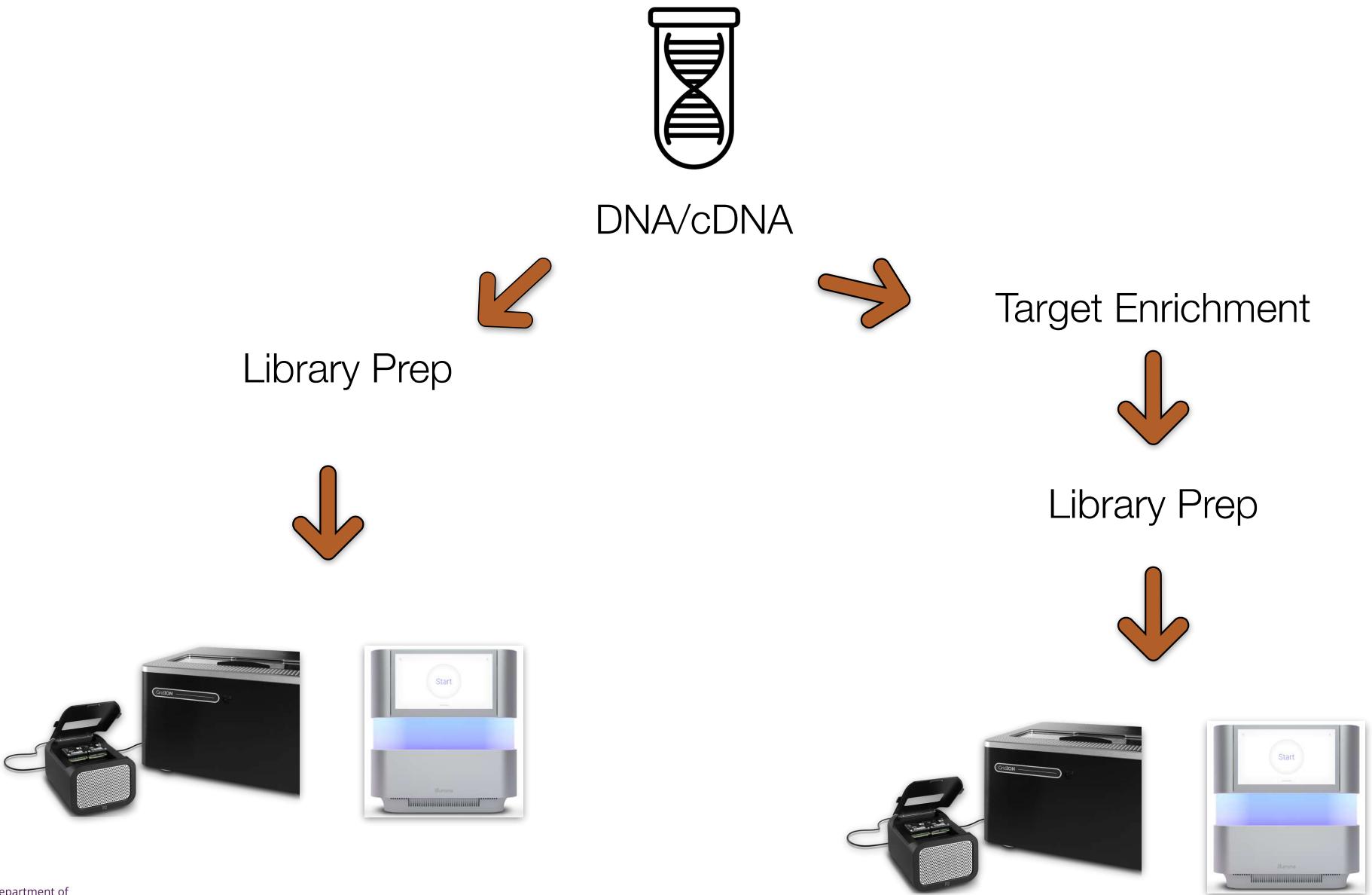
What is Metagenomics?



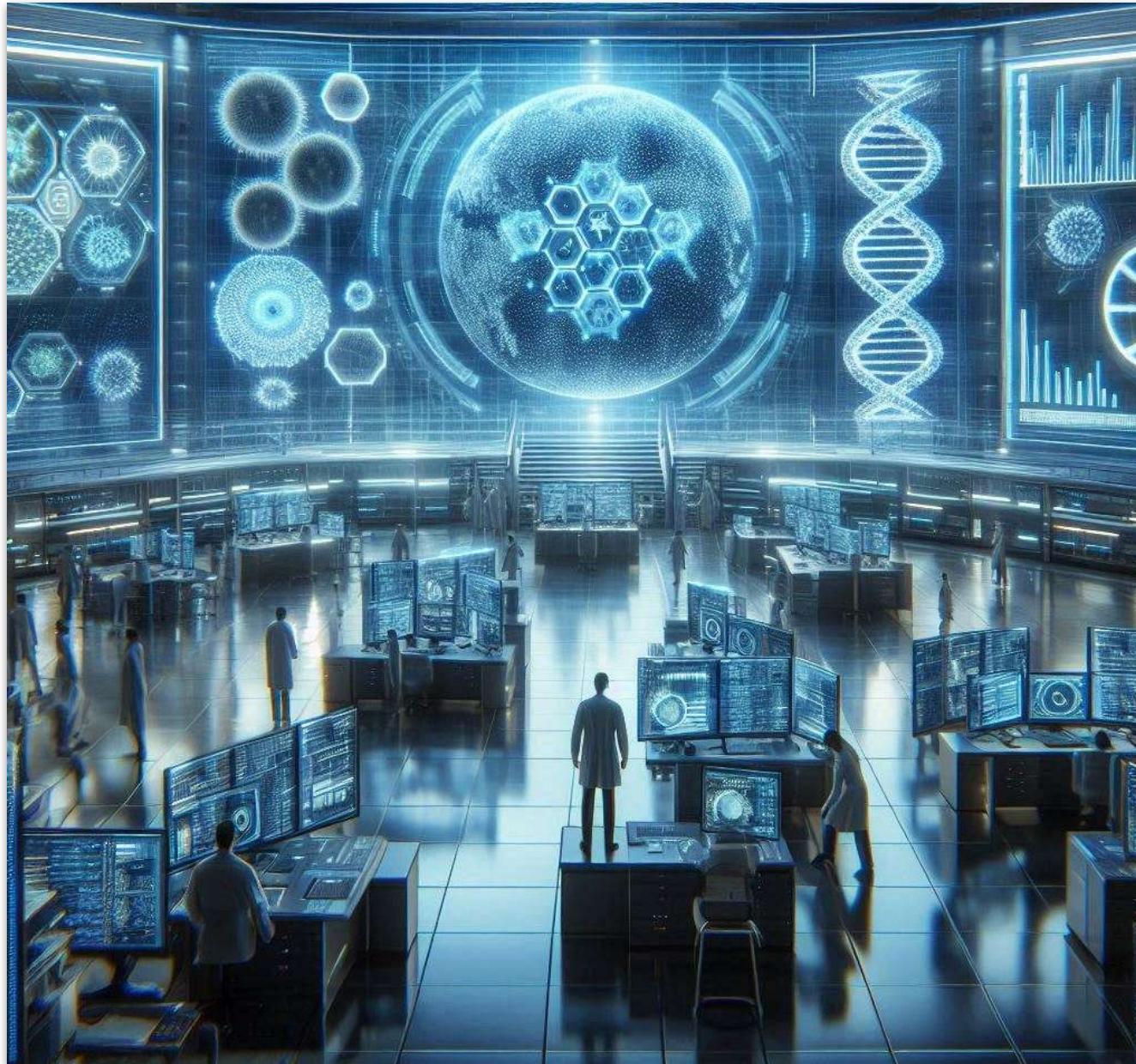
What is Metagenomics?



What is Metagenomics?



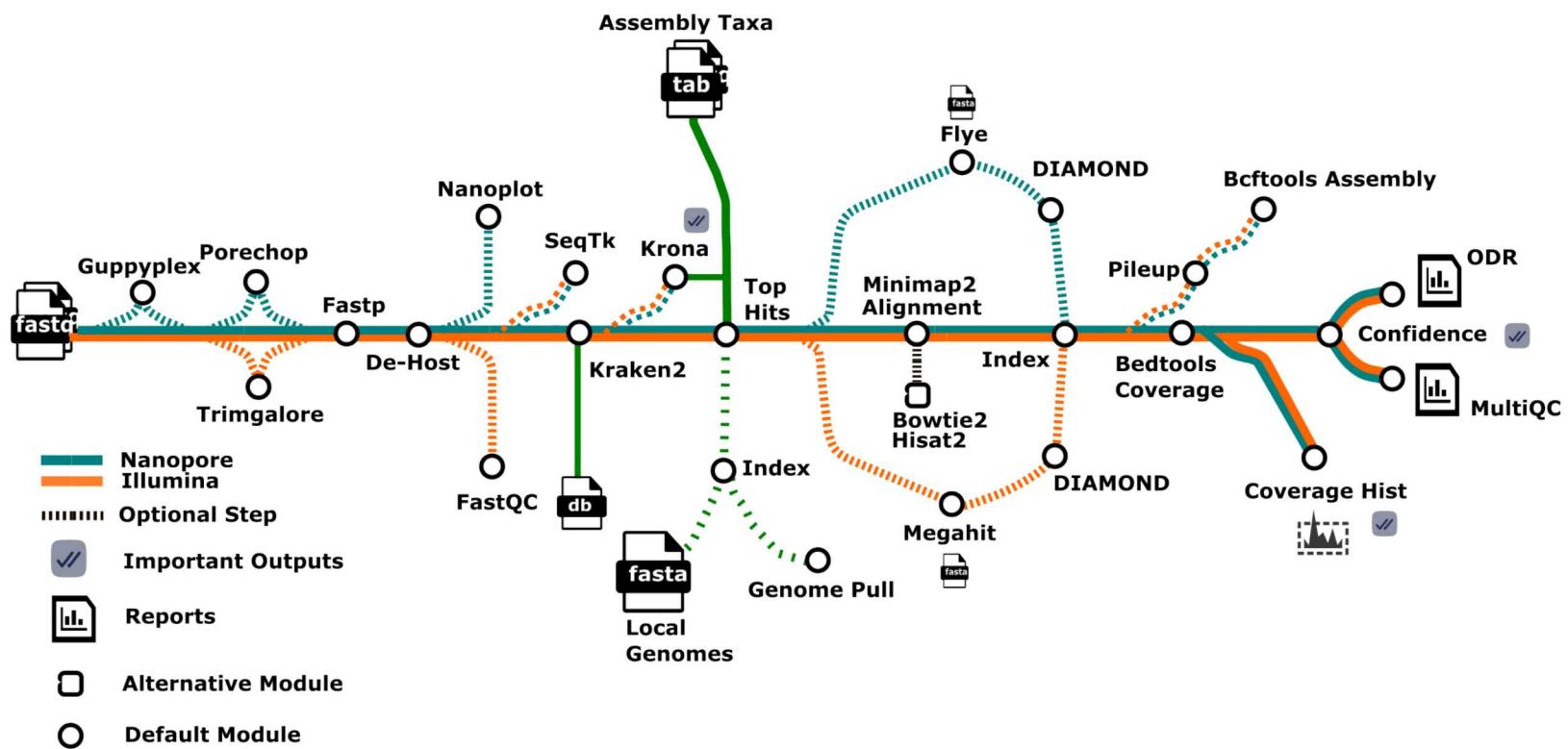
Threat Agnostic Sentinel Surveillance (TASS)



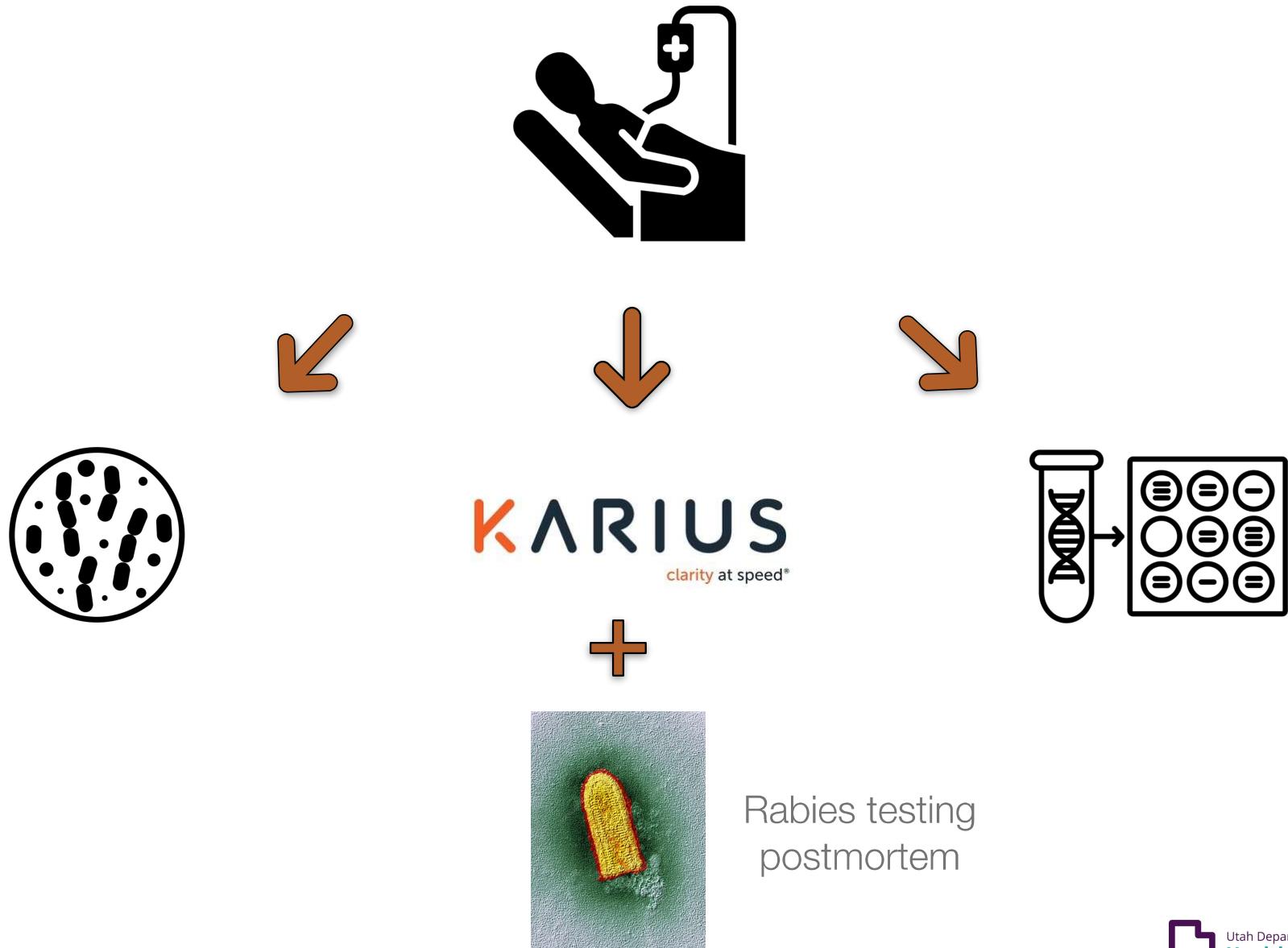
Threat Agnostic Sentinel Surveillance (TASS)

TaxTriage

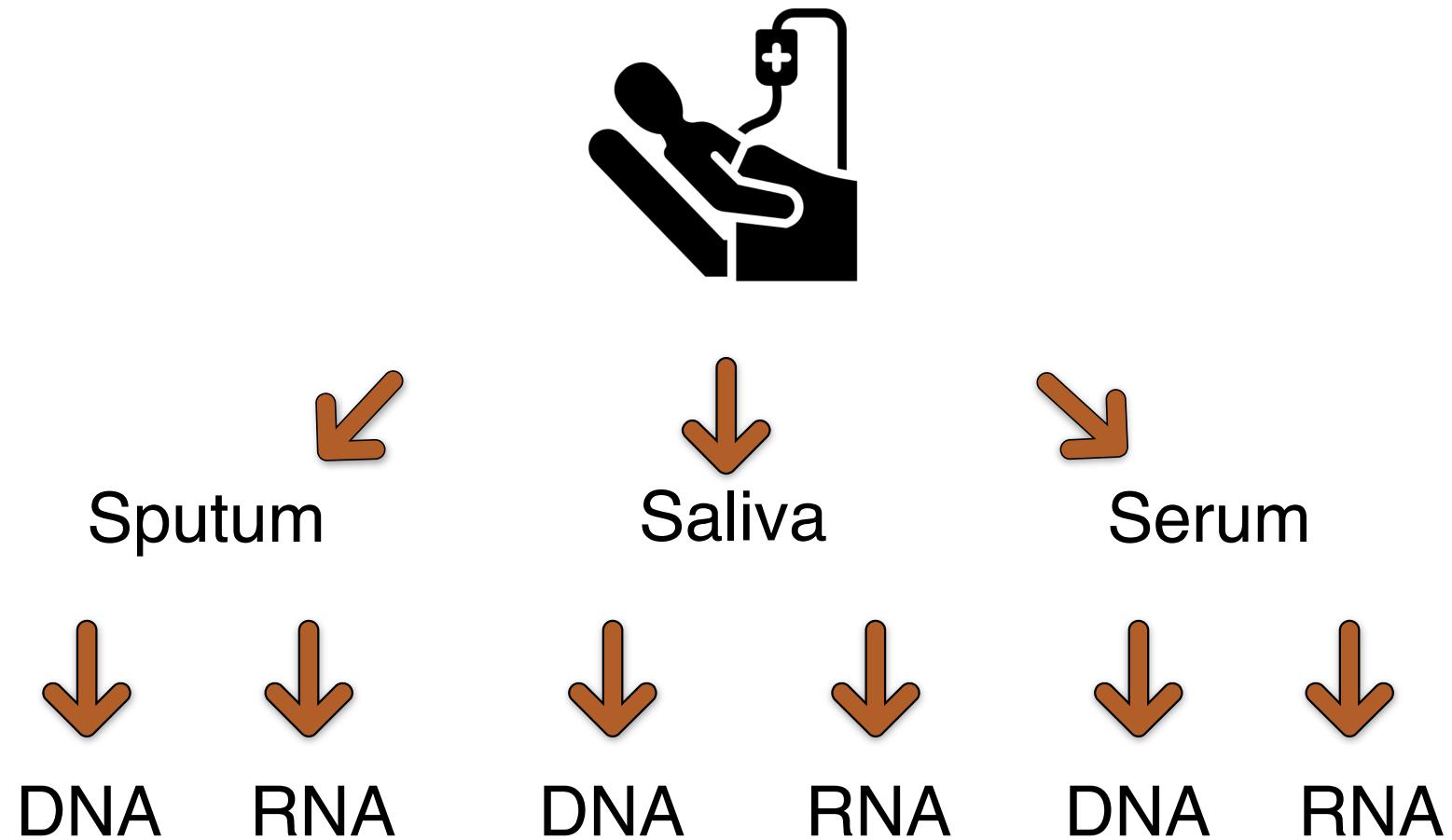
<https://github.com/jhuapl-bio/taxtriage>



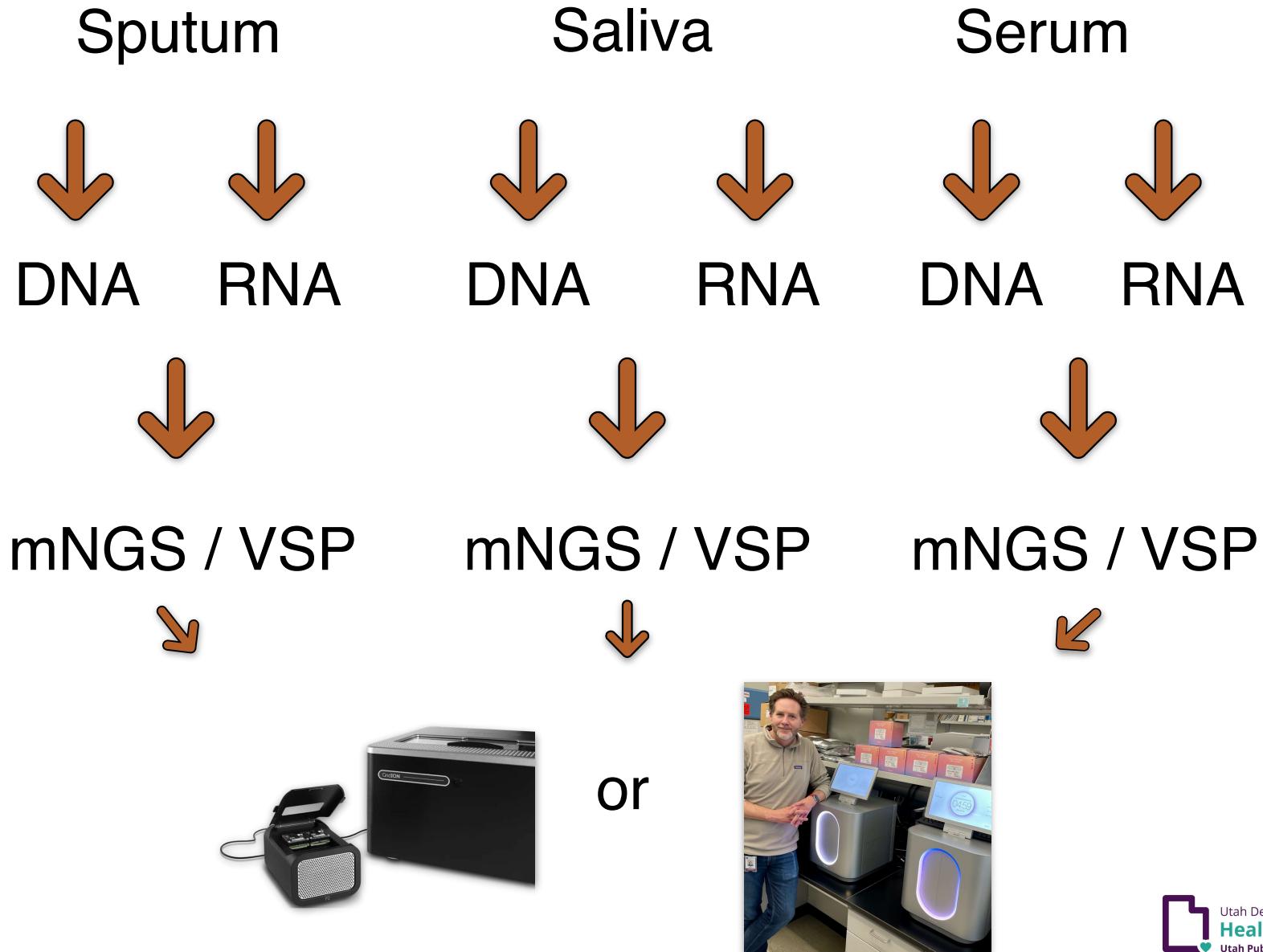
Threat Agnostic Sentinel Surveillance (TASS)



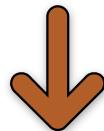
Threat Agnostic Sentinel Surveillance (TASS)



Threat Agnostic Sentinel Surveillance (TASS)



Threat Agnostic Sentinel Surveillance (TASS)



TaxTriage



Index	Specimen ID	Sample ID	Detected Organism	Microbial Category	Sample Type	% Reads	Coverage	Mean Depth	Mean BaseQ	Mean MapQ	Taxonomic ID #	Infected?	NB# Present	# Reads Aligned	Pathogenic SubCategory	K2 Reads
1	20170308_CP_PMA_50_L001	Human adenovirus intestinal K113	real	real	real	0.5	0.54	0.0	29.48	29.26	146122	real	100	204	Pathogenic Substrain	761.2
2	20170308_Saliva_PMA_50_L001	Noctiluca scintillans	real	real	real	0.0	0.0	0.0	37.44	37.21	146122	real	100	16	Pathogenic Substrain	805.0
3	20170308_Saliva_PMA_50_L001	Human adenovirus intestinal K113	real	real	real	0.2	0.54	0.0	27.44	27.26	146122	real	100	124	Pathogenic Substrain	2708.2
4	20170308_Saliva_PMA_50_L001	Human adenovirus intestinal K113	real	real	real	0.0	0.0	0.0	37.44	37.26	146122	real	100	124	Pathogenic Substrain	1320.2
5	20170308_Saliva_PMA_50_L001	Prevotella oralis	real	real	real	0.0	0.01	0.0	37.07	37.16	28139	real	100	2438	Commercial Listing	0.0
6	20170308_Saliva_PMA_50_L001	Staphylococcus enterica	real	real	real	0.3	0.50	0.0	12.54	13.44	1262	real	100	8719	Commercial Listing	0.0
7	20170308_Saliva_PMA_50_L001	Staphylococcus aureus	real	real	real	0.2	0.49	0.0	12.54	13.44	1262	real	100	8719	Commercial Listing	0.0
8	20170308_CPF_PMA_50_L001	Pseudomonas aeruginosa	real	real	real	2.6	0.01	0.0	39.18	37.26	329	real	100	4244	Commercial Listing	0.0
9	20170308_Saliva_PMA_50_L001	Methylophilus sediminis	real	real	real	0.4	0.49	0.0	27.74	28.24	2122	real	100	10499	Commercial Listing	0.0
10	20170308_Saliva_PMA_50_L001	Leptothrix sp.	real	real	real	0.0	0.01	0.0	37.48	38.87	10379	real	100	49	Pathogenic Substrain	2.0
11	20170308_Saliva_PMA_50_L001	Influenza A virus A/H3N2/OS/2009/US/2	real	real	real	0.0	0.01	0.0	37.48	38.87	10379	real	100	49	Pathogenic Substrain	30.0
12	20170308_Saliva_PMA_50_L001	Influenza A virus A/H3N2/OS/2009/US/2	real	real	real	0.0	0.01	0.0	14.18	13.48	335341	real	100	2367	Pathogenic Substrain	104.8
13	20170308_Saliva_PMA_50_L001	Staphylococcus aureus	real	real	real	0.0	0.01	0.0	37.48	38.87	10379	real	100	49	Pathogenic Substrain	0.0
14	20170308_Saliva_PMA_50_L001	Staphylococcus enterica	real	real	real	0.0	0.01	0.0	37.48	38.87	10379	real	100	49	Pathogenic Substrain	0.0
15	20170308_Saliva_PMA_50_L001	Staphylococcus phage phiSpha	real	real	real	0.0	0.01	0.0	37.48	38.87	1730208	real	100	204	Commercial Listing	650.0
16	20170308_Saliva_PMA_50_L001	Yersinia enterocolitica	real	real	real	0.0	0.01	0.0	37.48	38.87	1730208	real	100	194	Commercial Listing	0.0
17	20170308_Saliva_PMA_50_L001	Yersinia enterocolitica O:12b:K:R	real	real	real	0.0	0.01	0.0	28.28	28.40	1722988	real	100	1373	Commercial Listing	0.0
18	20170308_Saliva_PMA_50_L001	Streptococcus agalactiae	real	real	real	0.0	0.01	0.0	37.48	38.36	1322	real	100	654	Commercial Listing	0.0
19	20170308_Saliva_PMA_50_L001	Corynebacterium diphtheriae	real	real	real	0.1	0.01	0.0	37.48	38.87	1730208	real	100	102	Commercial Listing	0.0
20	20170308_Saliva_PMA_50_L001	Corynebacterium ulcerans	real	real	real	0.1	0.01	0.0	37.48	38.87	1730208	real	100	29	Commercial Listing	100.0
21	20170308_Saliva_PMA_50_L001	Culticoccus aviculae	real	real	real	0.1	0.01	0.0	37.48	38.36	1754493	real	100	234	Pathogenic Substrain	0.0
22	20170308_Saliva_PMA_50_L001	Shewanella viridis	real	real	real	0.0	0.01	0.0	12.50	12.59	159912	real	100	5172	Pathogenic Substrains	4740.0
23	20170308_Saliva_PMA_50_L001	Leptothrix sp.	real	real	real	0.0	0.01	0.0	37.48	38.87	10379	real	100	174	Pathogenic Substrain	0.0
24	20170308_Saliva_PMA_50_L001	Pseudomonas aeruginosa	real	real	real	0.0	0.01	0.0	37.48	38.87	10379	real	100	870	Pathogenic Substrain	0.0
25	20170308_Saliva_PMA_50_L001	Legionella neopneumophila	real	real	real	0.0	0.01	0.0	37.48	38.87	10379	real	100	294	Commercial Listing	0.0
26	20170308_Saliva_PMA_50_L001	Acinetobacter baumannii	real	real	real	0.0	0.01	0.0	37.48	38.87	1724453	real	100	124	Commercial Listing	0.0
27	20170308_Saliva_PMA_50_L001	Acinetobacter baumannii	real	real	real	0.0	0.01	0.0	37.48	38.76	10379	real	100	50	Commercial Listing	0.0
28	20170308_Saliva_PMA_50_L001	Staphylococcus parvulus	real	real	real	0.0	0.01	0.0	37.48	38.87	49612	real	100	8	Pathogenic Substrain	0.0
29	20170308_Saliva_PMA_50_L001	Staphylococcus hominis	real	real	real	0.0	0.01	0.0	37.48	38.87	49612	real	100	50	Pathogenic Substrain	0.0
30	20170308_Saliva_PMA_50_L001	Torulopsis garrigae	real	real	real	0.0	0.01	0.0	37.48	38.87	74793	real	100	30	Pathogenic Substrain	0.0
31	20170308_Saliva_PMA_50_L001	Leptothrix mirei ATCC 4327	real	real	real	0.0	0.01	0.0	25.11	25.46	1262	real	100	428	Commercial Listing	0.0
32	20170308_Saliva_PMA_50_L001	Lactococcus mirei ATCC 4327	real	real	real	0.1	0.01	0.0	37.48	38.87	10379	real	100	10060	Pathogenic Substrains	0.0
33	20170308_Saliva_PMA_50_L001	Lactococcus mirei ATCC 4327	real	real	real	0.0	0.01	0.0	37.48	38.87	532984	real	100	894	Pathogenic Substrains	0.0

Sample	Microorganism Name	Class Type	Coverage	Average Nucleotide Identity (%)	# Aligned Read Count	Consensus Genome Reference Accession	Consensus Genome Reference Description	
1	20170308_CPF_PMA_50_L001	Human adenovirus A (PhV-A)	real	0.0002%	100	481223	MSV00012	MSV00012, 2010_04 Human adenovirus A genome
2	20170308_CPF_PMA_50_L001	Human adenovirus B (PhV-B)	real	0.0002%	100	481224	MSV00013	MSV00013, 2010_04 Human adenovirus B genome
3	20170308_CPF_PMA_50_L001	Human adenovirus C (PhV-C)	real	0.0002%	100	481225	MSV00014	MSV00014, 2010_04 Human adenovirus C genome
4	20170308_CPF_PMA_50_L001	Human adenovirus D (PhV-D)	real	0.0002%	100	481226	MSV00015	MSV00015, 2010_04 Human adenovirus D genome
5	20170308_CPF_PMA_50_L001	Human adenovirus E (PhV-E)	real	0.0002%	100	481227	MSV00016	MSV00016, 2010_04 Human adenovirus E genome
6	20170308_CPF_PMA_50_L001	Human adenovirus F (PhV-F)	real	0.0002%	100	481228	MSV00017	MSV00017, 2010_04 Human adenovirus F genome
7	20170308_CPF_PMA_50_L001	Human adenovirus G (PhV-G)	real	0.0002%	100	481229	MSV00018	MSV00018, 2010_04 Human adenovirus G genome
8	20170308_CPF_PMA_50_L001	Human adenovirus H (PhV-H)	real	0.0002%	100	481230	MSV00019	MSV00019, 2010_04 Human adenovirus H genome
9	20170308_CPF_PMA_50_L001	Human adenovirus I (PhV-I)	real	0.0002%	100	481231	MSV00020	MSV00020, 2010_04 Human adenovirus I genome
10	20170308_CPF_PMA_50_L001	Human adenovirus J (PhV-J)	real	0.0002%	100	481232	MSV00021	MSV00021, 2010_04 Human adenovirus J genome
11	20170308_CPF_PMA_50_L001	Human adenovirus K (PhV-K)	real	0.0002%	100	481233	MSV00022	MSV00022, 2010_04 Human adenovirus K genome
12	20170308_CPF_PMA_50_L001	Human adenovirus L (PhV-L)	real	0.0002%	100	481234	MSV00023	MSV00023, 2010_04 Human adenovirus L genome
13	20170308_CPF_PMA_50_L001	Human adenovirus M (PhV-M)	real	0.0002%	100	481235	MSV00024	MSV00024, 2010_04 Human adenovirus M genome
14	20170308_CPF_PMA_50_L001	Human adenovirus N (PhV-N)	real	0.0002%	100	481236	MSV00025	MSV00025, 2010_04 Human adenovirus N genome
15	20170308_CPF_PMA_50_L001	Human adenovirus O (PhV-O)	real	0.0002%	100	481237	MSV00026	MSV00026, 2010_04 Human adenovirus O genome
16	20170308_CPF_PMA_50_L001	Human adenovirus P (PhV-P)	real	0.0002%	100	481238	MSV00027	MSV00027, 2010_04 Human adenovirus P genome
17	20170308_CPF_PMA_50_L001	Human adenovirus Q (PhV-Q)	real	0.0002%	100	481239	MSV00028	MSV00028, 2010_04 Human adenovirus Q genome
18	20170308_CPF_PMA_50_L001	Human adenovirus R (PhV-R)	real	0.0002%	100	481240	MSV00029	MSV00029, 2010_04 Human adenovirus R genome
19	20170308_CPF_PMA_50_L001	Human adenovirus S (PhV-S)	real	0.0002%	100	481241	MSV00030	MSV00030, 2010_04 Human adenovirus S genome
20	20170308_CPF_PMA_50_L001	Human adenovirus T (PhV-T)	real	0.0002%	100	481242	MSV00031	MSV00031, 2010_04 Human adenovirus T genome
21	20170308_CPF_PMA_50_L001	Human adenovirus U (PhV-U)	real	0.0002%	100	481243	MSV00032	MSV00032, 2010_04 Human adenovirus U genome
22	20170308_CPF_PMA_50_L001	Human adenovirus V (PhV-V)	real	0.0002%	100	481244	MSV00033	MSV00033, 2010_04 Human adenovirus V genome
23	20170308_CPF_PMA_50_L001	Human adenovirus W (PhV-W)	real	0.0002%	100	481245	MSV00034	MSV00034, 2010_04 Human adenovirus W genome
24	20170308_CPF_PMA_50_L001	Human adenovirus X (PhV-X)	real	0.0002%	100	481246	MSV00035	MSV00035, 2010_04 Human adenovirus X genome
25	20170308_CPF_PMA_50_L001	Human adenovirus Y (PhV-Y)	real	0.0002%	100	481247	MSV00036	MSV00036, 2010_04 Human adenovirus Y genome
26	20170308_CPF_PMA_50_L001	Human adenovirus Z (PhV-Z)	real	0.0002%	100	481248	MSV00037	MSV00037, 2010_04 Human adenovirus Z genome
27	20170308_CPF_PMA_50_L001	Leptothrix sp.	real	0.0002%	100	481249	MSV00038	MSV00038, 2010_04 Leptothrix sp. genome
28	20170308_CPF_PMA_50_L001	Leptothrix mirei ATCC 4327	real	0.0002%	100	481250	MSV00039	MSV00039, 2010_04 Leptothrix mirei ATCC 4327 genome
29	20170308_CPF_PMA_50_L001	Leptothrix mirei ATCC 4327	real	0.0002%	100	481251	MSV00040	MSV00040, 2010_04 Leptothrix mirei ATCC 4327 genome
30	20170308_CPF_PMA_50_L001	Leptothrix mirei ATCC 4327	real	0.0002%	100	481252	MSV00041	MSV00041, 2010_04 Leptothrix mirei ATCC 4327 genome
31	20170308_CPF_PMA_50_L001	Leptothrix mirei ATCC 4327	real	0.0002%	100	481253	MSV00042	MSV00042, 2010_04 Leptothrix mirei ATCC 4327 genome
32	20170308_CPF_PMA_50_L001	Leptothrix mirei ATCC 4327	real	0.0002%	100	481254	MSV00043	MSV00043, 2010_04 Leptothrix mirei ATCC 4327 genome
33	20170308_CPF_PMA_50_L001	Leptothrix mirei ATCC 4327	real	0.0002%	100	481255	MSV00044	MSV00044, 2010_04 Leptothrix mirei ATCC 4327 genome
34	20170308_CPF_PMA_50_L001	Leptothrix mirei ATCC 4327	real	0.0002%	100	481256	MSV00045	MSV00045, 2010_04 Leptothrix mirei ATCC 4327 genome
35	20170308_CPF_PMA_50_L001	Leptothrix mirei ATCC 4327	real	0.0002%	100	481257	MSV00046	MSV00046, 2010_04 Leptothrix mirei ATCC 4327 genome
36	20170308_CPF_PMA_50_L001	Leptothrix mirei ATCC 4327	real	0.0002%	100	481258	MSV00047	MSV00047, 2010_04 Leptothrix mirei ATCC 4327 genome
37	20170308_CPF_PMA_50_L001	Leptothrix mirei ATCC 4327	real	0.0002%	100	481259	MSV00048	MSV00048, 2010_04 Leptothrix mirei ATCC 4327 genome
38	20170308_CPF_PMA_50_L001							

Threat Agnostic Sentinel Surveillance (TASS)

Sample	Microorganism Name	Class Type	Coverage	Average Nucleotide Identity (ANI)	# Aligned Read Count	Consensus Genome
2072389_CSF_DNA	Human immunodeficiency virus 1 (HIV-1)	viral	3.85439%	100%	80	MK116212.1
2072389_CSF_DNA	Hepatitis E virus (HEV)	viral	1.1715%	93.0233%	63	MN646695.1
2072389_CSF_DNA	Influenza A virus	viral	0.788177%	100%	43	; ; MW940804; ; MW888219; ; ;
2072389_CSF_DNA	Influenza A virus (H3N2)	viral	0.767358%	100%	43	; ; MW940804; ; MW888219; ; ;
2072389_CSF_DNA	Influenza A virus (H3N2; human-like)	viral	0.767358%	100%	43	; ; MW940804; ; MW888219; ; ;
2072389_CSF_DNA	Rabies virus (RABV)	viral	0.567234%	98.5294%	31	OQ603637.1
2072389_CSF_DNA	West Nile virus (WNV)	viral	0.4152%	100%	21	LR743424.1
2072389_CSF_DNA	Influenza A virus (H5N1)	viral	0.323577%	100%	11	; ; OR105065; ; ; ;
2072389_CSF_DNA	Herpes simplex virus 2 (HSV2)	viral	0.0282065%	97.6744%	88	MT364888.1
2072389_CSF_DNA	Herpes simplex virus 1 (HSV1)	viral	0.0260153%	94.8718%	11	GCA_027937755.1
2072389_CSF_RNA	Hepatitis E virus (HEV)	viral	1.1715%	93.0233%	2	MN646695.1
2072389_CSF_RNA	Influenza A virus	viral	0.788177%	100%	36	; ; MW940804; ; MW888219; ; ;
2072389_CSF_RNA	Influenza A virus (H3N2)	viral	0.767358%	100%	36	; ; MW940804; ; MW888219; ; ;
2072389_CSF_RNA	Influenza A virus (H3N2; human-like)	viral	0.767358%	100%	36	; ; MW940804; ; MW888219; ; ;
2072389_CSF_RNA	West Nile virus (WNV)	viral	0.4152%	100%	173	LR743424.1
2072389_CSF_RNA	Herpes simplex virus 2 (HSV2)	viral	0.0242707%	100%	16	MT364888.1
2072392_Serum_DNA	Human immunodeficiency virus 1 (HIV-1)	viral	4.1863%	99.2327%	138	MK116212.1
2072392_Serum_DNA	Torque teno virus (TTV)	viral	2.46114%	100%	14	MN767852.1
2072392_Serum_DNA	Hepatitis E virus (HEV)	viral	1.1715%	93.0233%	125	MN646695.1
2072392_Serum_DNA	Influenza A virus	viral	0.788177%	100%	119	; ; MW940804; ; MW888219; ; ;
2072392_Serum_DNA	Influenza A virus (H3N2)	viral	0.767358%	100%	119	; ; MW940804; ; MW888219; ; ;



Threat Agnostic Sentinel Surveillance (TASS)

Table1

Sample	Microorganism Name	Class Type	% Coverage	% Average Nucleotide Identity (ANI)	# Aligned Read Count	Consensus Genome
2072393_Saliva_RNA	Influenza A virus	viral	0.856385%	99.115%	233400	; ; MW940804; ; MW888219; ;
2072393_Saliva_RNA	Influenza A virus (H3N2)	viral	0.833764%	99.115%	233400	; ; MW940804; ; MW888219; ;
2072393_Saliva_RNA	Influenza A virus (H3N2; human-like)	viral	0.833764%	99.115%	233400	; ; MW940804; ; MW888219; ;
2072393_Saliva_RNA	West Nile virus (WNV)	viral	0.568643%	93.6508%	126731	LR743424.1
2072392_Serum_RNA	West Nile virus (WNV)	viral	0.505461%	89.2857%	116773	LR743424.1
2072392_Serum_RNA	Influenza A virus	viral	6.72307%	97.0787%	102487	; ; MW940804; OP512110; MW888219; ;
2072392_Serum_RNA	Influenza A virus (H3N2; human-like)	viral	6.61967%	97.4215%	102487	; ; MW940804; OP512110; MW888219; ;
2072393_Saliva_RNA	Rabies virus (RABV)	viral	0.600601%	97.2222%	31252	OQ603637.1
2072392_Serum_RNA	Rabies virus (RABV)	viral	0.575576%	98.5507%	25652	OQ603637.1
2072393_Saliva_RNA	Hepatitis E virus (HEV)	viral	1.23961%	92.3077%	20555	MN646695.1
2072392_Serum_RNA	Hepatitis E virus (HEV)	viral	1.22599%	92.2222%	12917	MN646695.1
2072392_Serum_RNA	Influenza A virus (H3N2)	viral	5.8242407%	95.82279%	3953	KY926316; KY925131; KY925533; KY9262
2072392_Serum_RNA	Herpes simplex virus 2 (HSV2)	viral	0.0314864%	97.9167%	3365	MT364888.1
2072393_Saliva_RNA	Herpes simplex virus 2 (HSV2)	viral	0.0341102%	92.3077%	1175	MT364888.1
2072393_Saliva_RNA	Human immunodeficiency virus 1 (HIV-1)	viral	3.3833%	100%	386	MK116212.1
2072392_Serum_RNA	Influenza A virus (H5N1)	viral	0.951187%	94.5736%	213	; ; OR105065; ; GU066390; ;
2072392_Serum_RNA	Influenza A virus (H3N2; swine-like)	viral	1.99634%	92.7481%	190	; ; ; ON850319; OR637636; ; KR701372
2072389_CSF_RNA	West Nile virus (WNV)	viral	0.4152%	100%	173	LR743424.1
2072393_Saliva_RNA	Influenza A virus (H5N1)	viral	0.323577%	100%	141	; ; OR105065; ; ; ;
2072392_Serum_DNA	Human immunodeficiency virus 1 (HIV-1)	viral	4.1863%	99.2327%	138	MK116212.1
2072392_Serum_DNA	Hepatitis E virus (HEV)	viral	1.1715%	93.0233%	125	MN646695.1



Threat Agnostic Sentinel Surveillance (TASS)

multicq v1.27

Confidence Metrics
Kraken
fastp
Filtered Reads
Insert Sizes
Sequence Quality
GC Content
N content
FastQC
Sequence Counts
Sequence Quality Histograms
Per Sequence Quality Scores
Per Base Sequence Content
Per Sequence GC Content
Per Base N Content
Sequence Length Distribution
Sequence Duplication Levels
Overrepresented sequences by sample
Top overrepresented sequences
Adapter Content
Status Checks
Samtools
Coverage: global stats
Coverage: stats per region
Metadata
Software Versions

A modular tool to aggregate results from bioinformatics analyses across many samples into a single report.

This report has been generated by the nf-core/taxtriage analysis pipeline. For information about how to interpret these results, please see the documentation.

Report generated on 2025-03-17, 16:54 UTC based on data in: /fusion/s3/utah-phl-team/scratch/5jApRaEfV28KDK/9b/79273a4f3f684e9717df68d49b0e8f

+ Summarize report don't show again

Welcome! Not sure where to start? Watch a tutorial video (6:06)

Confidence Metrics

Confidence values for all organisms.

Index	Specimen ID	Detected Organism	TASS Score	Microbial Category	Sample Type	% Reads	Coverage	Mean Depth	Mean BaseQ	Mean MapQ	Taxonomic ID #	IsAnnotated	HHS Percentile	# Reads Aligned	Pathogenic Subsp/Strains	K2 Reads
0	2072389_CSF_DNA_S1_L001	Human endogenous retrovirus K113	1.0	Unknown	csf	0.0	0.54	0.00	37.58	37.29	166122	No	100.00	268		781.0
1	2072392_Serum_DNA_S3_L001	Legionella nagasakiensis*	1.0	Unknown	serum	0.0	0.57	0.00	37.61	36.19	166122	No	100.00	496		1377.0
2	2072393_Saliva_DNA_S2_L001	Nocardia blackiae*	1.0	Unknown	oral	0.0	0.32	0.00	37.64	37.01	166122	No	100.00	180		605.0
3	2072393_Saliva_RNA_S5_L001	Human endogenous retrovirus K113	0.9	Unknown	oral	0.0	0.54	0.00	37.65	37.65	166122	No	100.00	1258		2788.0
4	2072392_Serum_RNA_S6_L001	Human endogenous retrovirus K113	0.9	Unknown	serum	0.0	0.38	0.00	37.59	38.70	166122	No	100.00	1068		1552.0
5	2072393_Saliva_RNA_S5_L001	Prevotella denti	0.6	Commensal	oral	0.0	0.01	0.00	37.57	39.19	28129	Yes	100.00	3836	Commensal Listing	0.0
6	2072393_Saliva_RNA_S5_L001	Staphylococcus epidermidis	0.5	Commensal	oral	0.3	0.30	0.00	12.54	13.44	1282	Yes	100.00	89768	Commensal Listing	0.0
7	2072393_Saliva_DNA_S2_L001	Aeromonas sanarelli*	0.5	Commensal	oral	0.5	0.14	0.00	12.49	13.57	1282	Yes	100.00	15271	Commensal Listing	0.0
8	2072389_CSF_RNA_S4_L001	Paraclostridium dentum*	0.4	Opportunistic	csf	2.8	0.01	0.00	35.19	37.29	329	Yes	100.00	4244		0.0
9	2072393_Saliva_RNA_S5_L001	Metamycoplasma salivarium	0.4	Commensal	oral	0.6	0.03	0.00	37.74	32.54	2124	Yes	100.00	158969	Commensal Listing	0.0
10	2072392_Serum_RNA_S6_L001	Legionella nagasakiensis*	0.4	Opportunistic	serum	0.0	0.01	0.00	35.28	37.01	329	Yes	100.00	3679		0.0
11	2072393_Saliva_DNA_S2_L001	human gammaherpesvirus 4	0.3	Primary	oral	0.0	0.01	0.00	37.48	39.57	10376	Yes	100.00	63		32.0
12	2072392_Serum_RNA_S6_L001	Influenza A virus (A/New York/392/2004[H3N2])	0.3	Primary	serum	0.0	0.04	0.00	14.16	12.48	335341	Yes	100.00	3397		9184.0
13	2072393_Saliva_RNA_S5_L001	Prevotella verorallis	0.3	Commensal	oral	0.0	0.01	0.00	25.12	24.29	28137	Yes	100.00	2973	Commensal Listing	0.0
14	2072393_Saliva_RNA_S5_L001	Staphylococcus warneri	0.3	Commensal	oral	0.0	0.00	0.00	37.63	35.52	1292	Yes	100.00	884	Commensal Listing	0.0
15	2072393_Saliva_RNA_S5_L001	Staphylococcus phage SPbeta-like	0.3	Unknown	oral	0.0	0.01	0.00	37.68	35.29	1732063	No	100.00	226		659.0
16	2072393_Saliva_DNA_S2_L001	Legionella nagasakiensis*	0.2	Commensal	oral	0.0	0.00	0.00	18.54	20.62	1292	Yes	100.00	128	Commensal Listing	0.0
17	2072393_Saliva_RNA_S5_L001	Hoylella nanceiensis DSM 19126 = JCM 15639	0.2	Unknown	oral	0.0	0.00	0.00	28.26	28.46	1122988	No	100.00	1373		0.0
18	2072393_Saliva_RNA_S5_L001	Streptococcus anginosus	0.2	Commensal	oral	0.0	0.00	0.00	37.59	36.94	1328	Yes	100.00	638	Commensal Listing	0.0
19	2072393_Saliva_DNA_S2_L001	Cupriavidus metallidurans*	0.2	Commensal	oral	0.0	0.00	0.00	37.71	38.66	28129	Yes	100.00	182	Commensal Listing	0.0
20	2072393_Saliva_DNA_S2_L001	Corynebacterium pilbarensense	0.2	Unknown	oral	0.0	0.01	0.00	37.07	41.87	1732063	No	100.00	30		145.0
21	2072389_CSF_RNA_S4_L001	Cutibacterium acnes subsp. acnes	0.2	Unknown	csf	0.1	0.00	0.00	37.63	36.06	1734925	No	100.00	238		0.0
22	2072392_Serum_RNA_S6_L001	Shamonda virus	0.2	Unknown	serum	0.0	0.01	0.00	12.50	8.29	159150	No	100.00	3172		47421.0
23	2072393_Saliva_RNA_S5_L001	Shamonda virus	0.2	Unknown	oral	0.0	0.01	0.00	12.53	8.54	159150	No	100.00	3718		80028.0
24	2072393_Saliva_RNA_S5_L001	Paraclostridium dentum*	0.2	Opportunistic	oral	0.0	0.00	0.00	37.50	39.85	1283	Yes	100.00	870		0.0
25	2072393_Saliva_RNA_S5_L001	Legionella nagasakiensis*	0.2	Commensal	oral	0.0	0.00	0.00	37.59	35.36	29466	Yes	100.00	286	Commensal Listing	0.0
26	2072389_CSF_DNA_S1_L001	Cutibacterium acnes subsp. acnes	0.2	Unknown	csf	0.0	0.00	0.00	37.71	37.75	1734925	No	100.00	104		0.0
27	2072393_Saliva_DNA_S2_L001	Aeromonas sanarelli*	0.2	Commensal	oral	0.0	0.00	0.00	37.50	37.56	2124	Yes	100.00	59	Commensal Listing	0.0
28	2072393_Saliva_DNA_S2_L001	Staphylococcus pasteurii	0.2	Opportunistic	oral	0.0	0.00	0.00	37.41	39.00	45972	Yes	100.00	8		0.0
29	2072393_Saliva_RNA_S5_L001	Staphylococcus pasteurii	0.2	Opportunistic	oral	0.0	0.00	0.00	37.37	29.52	45972	Yes	100.00	90		0.0
30	2072393_Saliva_RNA_S5_L001	Tannerella serpentisiformis*	0.1	Unknown	oral	0.0	0.00	0.00	25.28	20.25	74703	No	100.00	30		0.0
31	2072393_Saliva_RNA_S5_L001	Staphylococcus hominis	0.1	Commensal	oral	0.0	0.00	0.00	25.11	21.98	1290	Yes	100.00	409	Commensal Listing	0.0
32	2072392_Serum_RNA_S6_L001	[Propionibacterium] nannntense SK182B-JCVI*	0.1	Unknown	serum	0.1	0.00	0.00	37.25	30.71	67082	No	100.00	15101		10806.0
33	2072393_Saliva_RNA_S5_L001	Lancefieldella rRNA ATCC 49626	0.1	Unknown	oral	0.0	0.00	0.00	20.97	17.57	553184	No	100.00	894		0.0

Threat Agnostic Sentinel Surveillance (TASS)

Specimen ID	Detected Organism	TASS Score	Microbial Category	% Reads	Coverage	Mean MapQ	Taxonomic ID #	# Reads Aligned
2072389_CSF_DNA_S1_L001	Human endogenous retrovirus K113	1.0	Unknown	0.0	0.54	37.29	166122	268
2072392_Serum_DNA_S3_L001	Legionella nagasakensis*	1.0	Unknown	0.0	0.57	36.19	166122	496
2072393_Saliva_DNA_S2_L001	Nocardia blacklockiae*	1.0	Unknown	0.0	0.32	37.01	166122	180
2072393_Saliva_RNA_S5_L001	Human endogenous retrovirus K113	0.9	Unknown	0.0	0.54	37.65	166122	1258
2072392_Serum_RNA_S6_L001	Human endogenous retrovirus K113	0.9	Unknown	0.0	0.38	38.70	166122	1068
2072393_Saliva_RNA_S5_L001	Prevotella denticola	0.6	Commensal	0.0	0.01	39.19	28129	3836
2072393_Saliva_RNA_S5_L001	Staphylococcus epidermidis	0.5	Commensal	0.3	0.30	13.44	1282	89768
2072393_Saliva_DNA_S2_L001	Aeromonas sanarellii*	0.5	Commensal	0.5	0.14	13.57	1282	15271
2072389_CSF_RNA_S4_L001	Paraclostridium dentum*	0.4	Opportunistic	2.8	0.01	37.29	329	4244
2072393_Saliva_RNA_S5_L001	Metamycoplasma salivarium	0.4	Commensal	0.6	0.03	32.54	2124	158969
2072392_Serum_RNA_S6_L001	Legionella nagasakensis*	0.4	Opportunistic	0.0	0.01	37.01	329	3679
2072393_Saliva_DNA_S2_L001	human gammaherpesvirus 4	0.3	Primary	0.0	0.01	39.57	10376	63
2072392_Serum_RNA_S6_L001	Influenza A virus (A/New York/392/2004(H3N2))	0.3	Primary	0.0	0.04	12.48	335341	3397
2072393_Saliva_RNA_S5_L001	Prevotella veroralis	0.3	Commensal	0.0	0.01	24.29	28137	2973
2072393_Saliva_RNA_S5_L001	Staphylococcus warneri	0.3	Commensal	0.0	0.00	35.52	1292	884
2072393_Saliva_RNA_S5_L001	Staphylococcus phage SPbeta-like	0.3	Unknown	0.0	0.01	35.29	1732063	226
2072393_Saliva_DNA_S2_L001	Legionella nagasakensis*	0.2	Commensal	0.0	0.00	20.62	1292	128
2072393_Saliva_RNA_S5_L001	Hoylella nanceiensis DSM 19126 = JCM 15639	0.2	Unknown	0.0	0.00	28.46	1122988	1373
2072393_Saliva_RNA_S5_L001	Streptococcus anginosus	0.2	Commensal	0.0	0.00	36.94	1328	638
2072393_Saliva_DNA_S2_L001	Cupriavidus metallidurans*	0.2	Commensal	0.0	0.00	38.66	28129	182
2072393_Saliva_DNA_S2_L001	Corynebacterium pilbarens*	0.2	Unknown	0.0	0.01	41.87	1732063	30
2072389_CSF_RNA_S4_L001	Cutibacterium acnes subsp. acnes	0.2	Unknown	0.1	0.00	36.06	1734925	238
2072392_Serum_RNA_S6_L001	Shamonda virus	0.2	Unknown	0.0	0.01	8.29	159150	3172

Threat Agnostic Sentinel Surveillance (TASS)

Specimen ID	Detected Organism	TASS Score	Microbial Category	% Reads	Coverage	Mean MapQ	Taxonomic ID #	# Reads Aligned	Pathogenic Subsp/Strains	K2
2072393_Saliva_RNA_S5_L001	Plasmodium vivax	0.1	Primary	7.5	0.00	1.21	5855	1953476		0.0
2072393_Saliva_RNA_S5_L001	Paraclostridium dentum*	0.1	Potential	5.6	0.00	1.39	2662455	1446613	SKVG24 (36.7%)	0.0
2072392_Serum_RNA_S6_L001	Legionella nagasakiensis*	0.1	Potential	5.2	0.00	1.66	2662455	1196880		0.0
2072392_Serum_RNA_S6_L001	Plasmodium vivax	0.1	Primary	5.2	0.00	1.48	5855	1164270		0.0
2072392_Serum_RNA_S6_L001	Paraclostridium dentum*	0.1	Primary	0.7	0.00	3.63	508771	166325		0.0
2072393_Saliva_RNA_S5_L001	Metamycoplasma salivarium	0.4	Commensal	0.6	0.03	32.54	2124	158969	Commensal Listing	0.0
2072393_Saliva_RNA_S5_L001	Aeromonas sanarellii*	0.1	Primary	0.5	0.00	3.53	508771	129249		0.0
2072393_Saliva_RNA_S5_L001	Nocardia blacklockiae*	0.1	Potential	0.4	0.00	3.49	480036	116340	N-17 (3.0%)	0.0
2072393_Saliva_RNA_S5_L001	Staphylococcus epidermidis	0.5	Commensal	0.3	0.30	13.44	1282	89768	Commensal Listing	0.0
2072392_Serum_RNA_S6_L001	Nocardia blacklockiae*	0.1	Potential	0.4	0.00	2.58	480036	87167		0.0
2072392_Serum_DNA_S3_L001	Toxoplasma gondii ME49	0.1	Primary	0.4	0.00	2.62	508771	25643		0.0
2072392_Serum_RNA_S6_L001	Plasmodium knowlesi strain H	0.1	Primary	0.1	0.00	2.28	5851	17512		0.0
2072393_Saliva_DNA_S2_L001	Aeromonas sanarellii*	0.5	Commensal	0.5	0.14	13.57	1282	15271	Commensal Listing	0.0
2072392_Serum_RNA_S6_L001	[Propionibacterium] namnetense SK182B-JCVI*	0.1	Unknown	0.1	0.00	30.71	67082	15101		108
2072389_CSF_DNA_S1_L001	Toxoplasma gondii ME49	0.1	Primary	0.4	0.00	2.15	508771	12883		0.0
2072393_Saliva_DNA_S2_L001	Toxoplasma gondii ME49	0.1	Primary	0.4	0.00	1.93	508771	10229		0.0
2072393_Saliva_RNA_S5_L001	Plasmodium knowlesi strain H	0.1	Primary	0.0	0.00	2.63	5851	7503		0.0
2072393_Saliva_RNA_S5_L001	BeAn 58058 virus	0.1	Unknown	0.0	0.00	30.04	67082	5879		180
2072389_CSF_RNA_S4_L001	Paraclostridium dentum*	0.4	Opportunistic	2.8	0.01	37.29	329	4244		0.0
2072393_Saliva_RNA_S5_L001	Prevotella denticola	0.6	Commensal	0.0	0.01	39.19	28129	3836	Commensal Listing	0.0
2072393_Saliva_RNA_S5_L001	Shamonda virus	0.2	Unknown	0.0	0.01	8.54	159150	3718		800
2072392_Serum_RNA_S6_L001	Legionella nagasakiensis*	0.4	Opportunistic	0.0	0.01	37.01	329	3679		0.0
2072392_Serum_RNA_S6_L001	Influenza A virus (A/New York/392/2004(H3N2))	0.3	Primary	0.0	0.04	12.48	335341	3397		918
2072392_Serum_RNA_S6_L001	Shamonda virus	0.2	Unknown	0.0	0.01	8.29	159150	3172		474
2072393_Saliva_RNA_S5_L001	Prevotella veroralis	0.3	Commensal	0.0	0.01	24.29	28137	2973	Commensal Listing	0.0
2072393_Saliva_RNA_S5_L001	Staphylococcus borealis	0.1	Commensal	0.0	0.00	5.03	2742203	2375	Commensal Listing	0.0
2072392_Serum_DNA_S3_L001	Plasmodium vivax	0.1	Primary	0.0	0.00	0.40	5855	2232		0.0
2072393_Saliva_RNA_S5_L001	Choristoneura fumiferana granulovirus	0.1	Unknown	0.0	0.00	32.08	56947	2054		521

PCR vs. Sequencing



VS



PCR vs. Sequencing



PCR vs. Sequencing

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Dashboard

View workflows Run and install analysis pipelines.

Track analyses View current and previous runs.

Latest updates



EPI2ME 24.08-01 Release
With the ever-growing popularity of EPI2ME workflows, we present a consolidated maintenance release of a selection of our workflows.
Published: 14 August 2024



Unexpected results, so now what?
Essentials of a Bioinformatician's toolkit.
Published: 1 July 2024



IGV for EPI2ME workflows
IGV integration for EPI2ME workflows.
Published: 9 June 2024

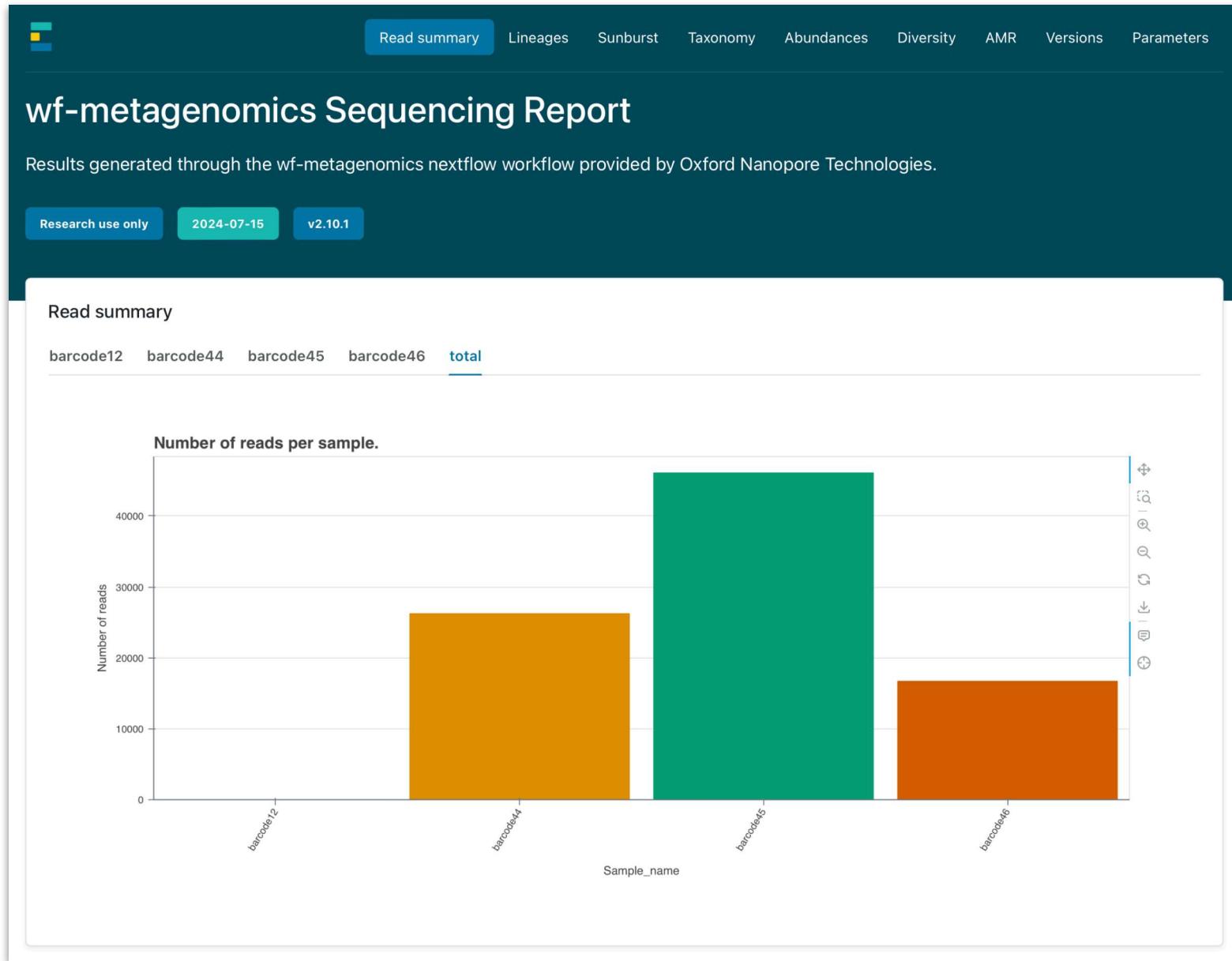


EPI2ME 24.06-01 Release
With all the excitement of London Calling we skipped our previous release window, so this one is a cracker!
Published: 4 June 2024

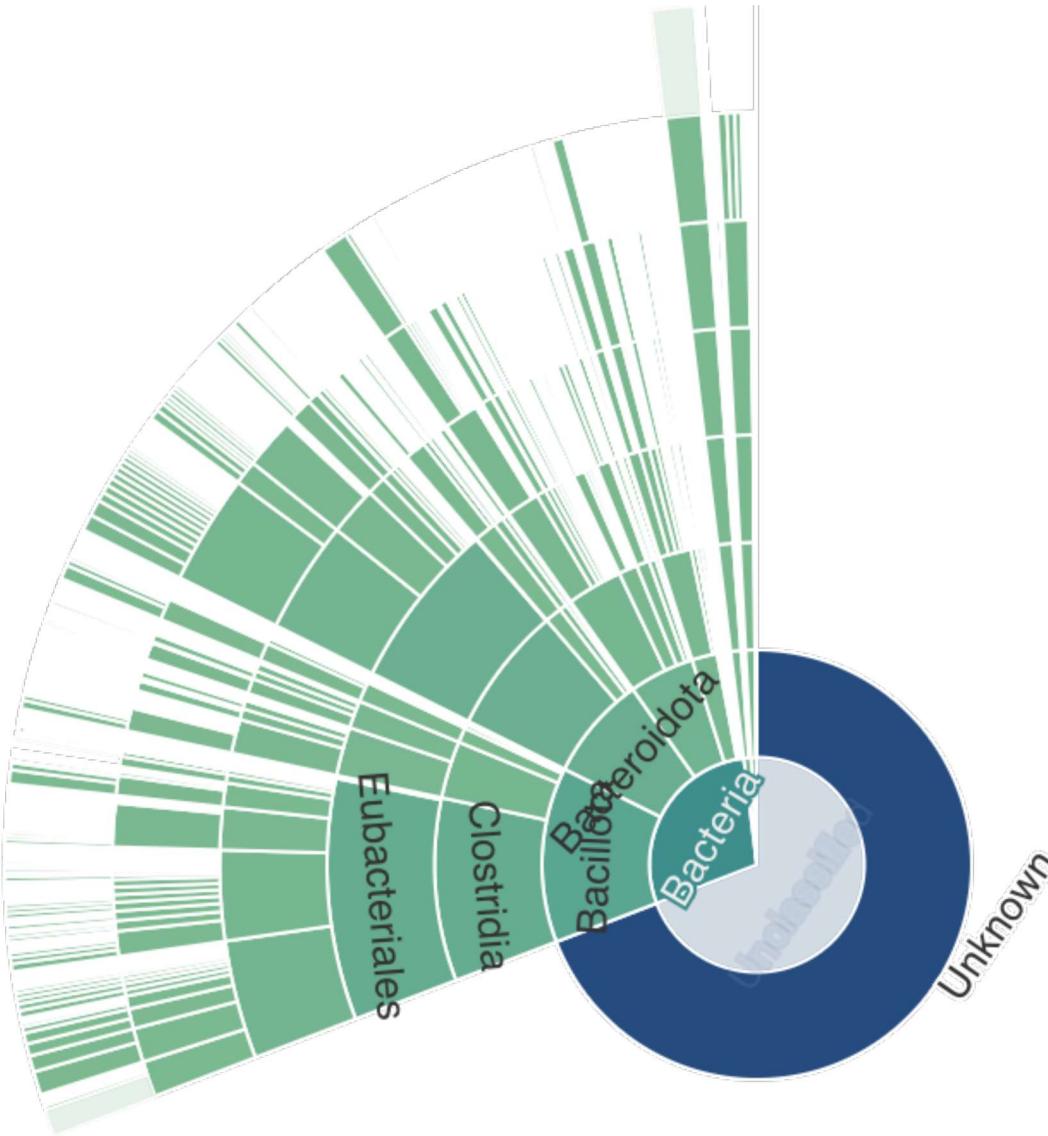
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<input type="checkbox"/> amazing_nightingale	wf-metagenomics	15 Jul 2024	Stopped With Error
<input type="checkbox"/> vigorous_goldwasser	wf-metagenomics	15 Jul 2024	Stopped By User

Health & Human Services
Utah Public Health Laboratory

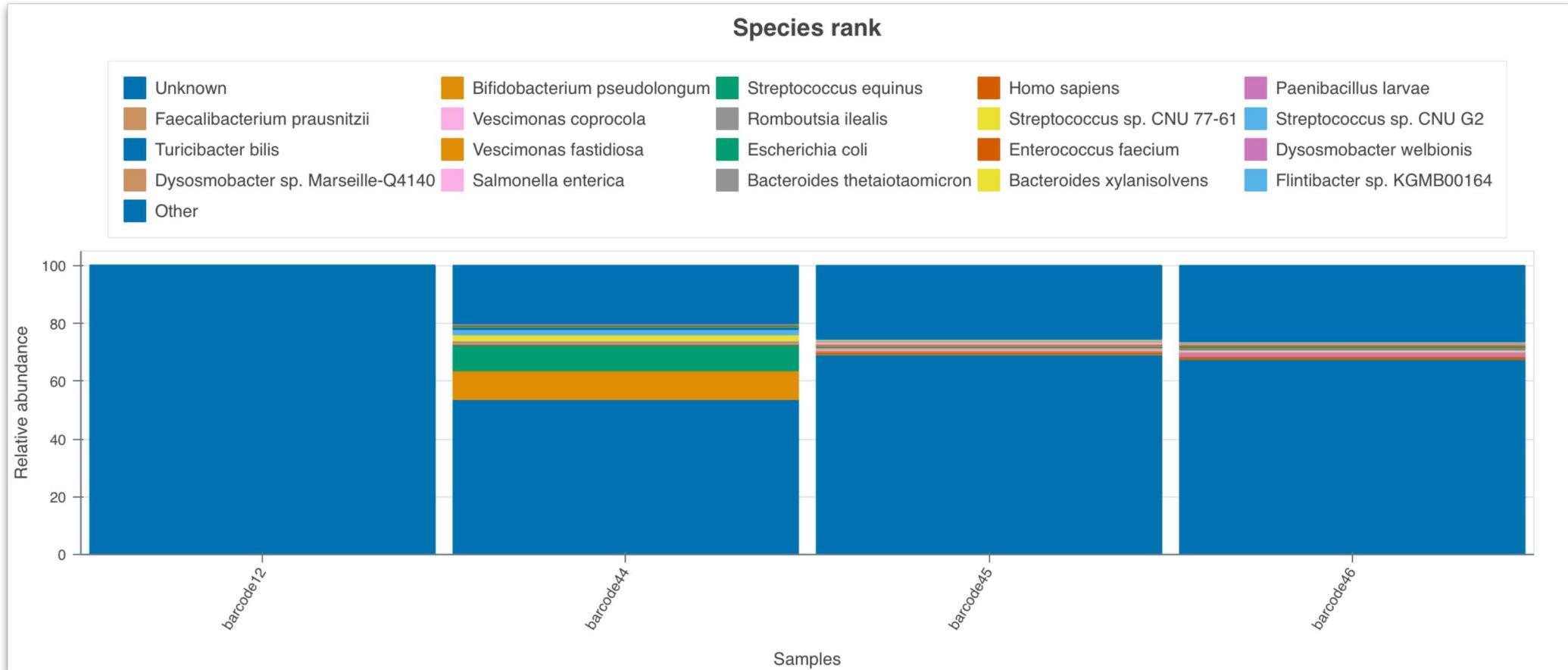
PCR vs. Sequencing



PCR vs. Sequencing



PCR vs. Sequencing



PCR vs. Sequencing

Read summary													
		Lineages		Sunburst		Taxonomy		Abundances		Diversity	AMR	Versions	Parameters
species		barcode12	barcode44	barcode45	barcode46	total	superkingdom	kingdom	phylum		class		
Unknown	1	13881	31235	54764	99881	Unclassified	Unknown	Unknown	Unknown		Unknown		
Paenibacillus larvae	0	0	0	868	868	Bacteria	Bacteria_none	Bacillota	Bacilli				
Homo sapiens	0	97	348	777	1222	Eukaryota	Metazoa	Chordata	Mammalia				
Vescimonas coprocola	0	29	228	474	731	Bacteria	Bacteria_none	Bacillota	Clostridia				
Faecalibacterium prausnitzii	0	56	249	431	736	Bacteria	Bacteria_none	Bacillota	Clostridia				
Vescimonas fastidiosa	0	18	156	309	483	Bacteria	Bacteria_none	Bacillota	Clostridia				
Romboutsia ilealis	0	196	135	306	637	Bacteria	Bacteria_none	Bacillota	Clostridia				
Bacteroides sp. PHL 2737	0	0	0	294	294	Bacteria	Bacteria_none	Bacteroidota	Bacteroidia				
Escherichia coli	0	118	49	291	458	Bacteria	Bacteria_none	Pseudomonadota	Gammaproteobact				
Enterococcus faecium	0	81	38	290	409	Bacteria	Bacteria_none	Bacillota	Bacilli				
Dysosmabacter welbionis	0	28	106	237	371	Bacteria	Bacteria_none	Bacillota	Clostridia				
Dysosmabacter sp. Marseille-Q4140	0	25	119	221	365	Bacteria	Bacteria_none	Bacillota	Clostridia				
Phocaeicola denonci	0	13	97	179	289	Bacteria	Bacteria_none	Bacteroidota	Bacteroidia				

Questions? Comments? Discussion?

SEQUENCING

