

# Organism Discovery Report

This report was generated using TaxTriage **Local Build** on **2026-01-22 15:36** and is derived from an in development spreadsheet of human-host pathogens.

Samples with confidence score below **0.4** were filtered out.

★ denotes high consequence pathogens

Specimen ID (Type)	Detected Organism	# Reads Aligned	TASS Score	Taxonomic ID #	Pathogenic Subsp/Strains	Coverage	HHS Percentile	K2 Reads
Miseq_Run_A (nasal)	★ Monkeypox virus	1278 (1.09% - 1.09%)	0.99	10244	Zaire-96-l-16 (1.1%)	0.81	100.0	654
Miseq_Run_A (nasal)	★ Listeria monocytogenes EGD-e°	9649 (8.25% - 8.22%)	0.98	169963		0.59	100.0	4891
ONT_Run_A (stool)	★ Listeria monocytogenes EGD-e	201 (3.66% - 6.70%)	0.96	169963	EGD-e (3.7%)	0.3	100.0	199
Miseq_Run_A (nasal)	★ Severe acute respiratory syndrome coronavirus 2°	100 (0.09%)	0.96	2697049		0.64	100.0	50
ONT_Run_A (stool)	★ Salmonella enterica subsp. enterica serovar Typhimurium str. LT2°	103 (1.87% - 3.43%)	0.91	99287		0.09	100.0	84
ONT_Run_A (stool)	★ Salmonella enterica subsp. enterica serovar Typhimurium°	99 (1.86% - 3.30%)	0.91	90371		0.08	100.0	84
ONT_Run_A (stool)	★ Salmonella enterica subsp. enterica serovar Typhi str. Ty2°	32 (0.58% - 1.07%)	0.89	209261		0.05	100.0	0
ONT_Run_A (stool)	★ Listeria monocytogenes serotype 4b str. F2365°	14 (0.25% - 0.46%)	0.70	265669		0.02	100.0	0

Specimen ID (Type)	Detected Organism	# Reads Aligned	TASS Score	Taxonomic ID #	Pathogenic Subsp/Strains	Coverage	HHS Percentile	K2 Reads
ONT_Run_A (stool)	★ <i>Salmonella enterica</i> subsp. <i>enterica</i> °	105 (1.91% - 3.50%)	0.68	59201		0.09	100.0	126
Miseq_Run_A (nasal)	★ <i>Escherichia coli</i> O157:H7°	17666 (15.11% - 15.06%)	0.59	83334		0.55	100.0	27390
Miseq_Run_A (nasal)	★ <i>Listeria monocytogenes</i> serotype 4b str. F2365°	101 (0.09%)	0.48	265669		0.01	100.0	0
ONT_Run_A (stool)	★ <i>Escherichia coli</i> O157:H7	80 (1.45% - 2.66%)	0.45	83334	7.1_Anguil (1.5%)	0.09	100.0	60
Miseq_Run_A (nasal)	<i>Pseudomonas aeruginosa</i> PAO1°	33763 (28.89% - 28.77%)	0.99	208964		0.75	100.0	0
Miseq_Run_A (nasal)	Human respiratory syncytial virus A°	201 (0.17%)	0.98	208893		0.97	100.0	51
Miseq_Run_A (nasal)	<i>Pseudomonas aeruginosa</i> PA1°	7765 (6.64% - 6.61%)	0.95	1279007		0.23	100.0	20812
Miseq_Run_A (nasal)	human respiratory syncytial virus B	50 (0.04%)	0.95	11250		0.58	100.0	76
ONT_Run_A (stool)	<i>Pseudomonas aeruginosa</i> PAO1°	8 (0.14% - 0.26%)	0.75	208964		0.02	100.0	0
ONT_Run_A (stool)	<i>Pseudomonas aeruginosa</i> PA1°	7 (0.12% - 0.23%)	0.73	1279007		0.02	100.0	8
Miseq_Run_A (nasal)	<i>Neisseria gonorrhoeae</i> °	7123 (6.09% - 6.07%)	0.63	485		0.59	100.0	7200

See the `report/all.organisms.report.txt` file for a full list of everything identified

Organisms marked with \* are putative and have relatively lower references listing their annotations as a pathogen in the given sample types. Classifications of pathogens are described as:

- This is an unannotated organism or commensal organism for the given site.
- Primary Pathogen annotated in sample type(s) listed.
- Primary Pathogen annotated in sample type(s) other than your listed one.
- Opportunistic Pathogen
- Potential Pathogen

- Primary: Exposure to the agent generally results in a diseased state in both immunocompromised and immunocompetent individuals.
  - Opportunistic: Exposure to the agent causes a diseased state under certain conditions, including immunocompromised status, wound infections, and nosocomial infections.
  - Commensal: Organisms typically found in the human microbiota.
  - Potential: Organisms that have been associated with disease states but are not extensively studied.
  - °: Indicates a pathogenic subspecies/serotype/strain/etc with the same name as the species listed, just different taxids.
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- Specimen ID (Type): The unique identifier for the sample, including the type of specimen (e.g., blood, tissue).
  - Detected Organism: The organism detected in the sample, which could be a bacterium, virus, fungus, or parasite.
  - Microbial Category: The classification of the organism, indicating whether it is primary, opportunistic, commensal, or potential.
  - # Reads Aligned: The number of reads from the sequencing data that align to the organism's genome, indicating its presence. (%) refers to all alignments (more than 1 alignment per read can take place) for that species across the entire sample. The format is (total % of aligned reads in sample).
  - TASS Score: A metric between 0 and 1 that reflects the confidence of the organism's detection, with 1 being the highest confidence.
  - Taxonomic ID #: The taxid for the organism according to NCBI Taxonomy, which provides a unique identifier for each species. The parenthesis (if present) is the group it belongs to, usually the genus.
  - Pathogenic Subsp/Strains: Indicates specific pathogenic subspecies, serotypes, or strains, if detected in the sample. (%) indicates the percent of all aligned reads belonging to that strain.
  - K2 Reads: The number of reads classified by Kraken2, a tool for taxonomic classification of sequencing data. HHS Percentile: What percentile the abundance falls under relative to the given sample type based on HHS NCBI taxonomy classification information
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Please visit our [DOCUMENTATION PAGE](#) for more information on how confidence is calculated.

The following information highlights the description for the color combinations for each organism class in the annotated table(s)

Please see the relevant Discovery Analysis txt file for low confidence annotations that were not present in the pdf

Read amounts are represented as the **total number of aligned reads** of sufficient mapping quality (**% aligned for all reads in sample**)

## Commensals

These were identified & were listed as a commensal directly

Specimen ID (Type)	Detected Organism	# Reads Aligned	TASS Score	Taxonomic ID #	Coverage	HHS Percentile	K2 Reads
ONT_Run_A (stool)	Staphylococcus aureus subsp. aureus NCTC 8325°	907 (16.55% - 30.23%)	0.98	93061	0.58	100.0	901
Miseq_Run_A (nasal)	Escherichia coli str. K-12 substr. MG1655°	15465 (13.23% - 13.18%)	0.98	511145	0.6	100.0	0
Miseq_Run_A (nasal)	Staphylococcus aureus subsp. aureus NCTC 8325°	8915 (7.62% - 7.59%)	0.98	93061	0.57	100.0	4687
ONT_Run_A (stool)	Staphylococcus aureus RF122°	638 (11.64% - 21.26%)	0.97	273036	0.43	100.0	0
ONT_Run_A (stool)	Bacillus subtilis subsp. subtilis str. 168°	873 (15.93% - 29.10%)	0.97	224308	0.43	100.0	873
ONT_Run_A (stool)	Bacillus subtilis BSn5°	727 (13.26% - 24.23%)	0.97	936156	0.37	100.0	0
ONT_Run_A (stool)	Bacillus subtilis subsp. subtilis°	868 (15.83% - 28.93%)	0.97	135461	0.43	100.0	873
Miseq_Run_A (nasal)	Bacillus subtilis subsp. subtilis str. 168°	6475 (5.54% - 5.51%)	0.96	224308	0.34	100.0	7000
Miseq_Run_A (nasal)	Bacillus subtilis subsp. subtilis°	6456 (5.52%)	0.96	135461	0.34	100.0	7000
ONT_Run_A (stool)	Escherichia coli str. K-12 substr. MG1655°	134 (2.44% - 4.46%)	0.94	511145	0.17	100.0	0
ONT_Run_A (stool)	Enterococcus faecalis EnGen0336°	90 (1.64% - 3.00%)	0.93	1169293	0.16	100.0	0

Specimen ID (Type)	Detected Organism	# Reads Aligned	TASS Score	Taxonomic ID #	Coverage	HHS Percentile	K2 Reads
Miseq_Run_A (nasal)	Bacillus subtilis BSn5°	1043 (0.89% - 0.88%)	0.90	936156	0.06	100.0	0
Miseq_Run_A (nasal)	Staphylococcus aureus RF122°	427 (0.36%)	0.87	273036	0.04	100.0	0
ONT_Run_A (stool)	Saccharomyces cerevisiae S288C	243 (4.43% - 8.10%)	0.83	559292	0.1	100.0	4012

## Unannotated Organisms

The following table displays the unannotated organisms and their alignment statistics. Be aware that this is the exhaustive list of all organisms (species only) contained within the samples that had atleast one read aligned

Specimen ID (Type)	Detected Organism	# Reads Aligned	TASS Score	Coverage	HHS Percentile	K2 Reads
ONT_Run_A (stool)	Limosilactobacillus fermentum°	157 (2.86% - 5.23%)	0.95	0.27	100.0	198