Category 1 Agents and Toxins

HHS & Overlap	USDA Veterinary Services (VS)
Select Agents and Toxins	Select Agents and Toxins
☐ Abrin	☐ African horse sickness virus
☐ Bacillus cereus Biovar anthracis	☐ African swine fever virus
☐ Bacillus anthracis – Overlap	\square Avian influenza virus [this is included here as a veterinary select
☐ Bacillus anthracis Pasteur strain – Overlap	agent in 9 CFR 121.3. Low pathogenicity strains are excluded.]
☐ Botulinum neurotoxins	☐ Classical swine fever virus
☐ Brucella abortus – Overlap	☐ Foot-and-mouth disease virus
☐ Brucella melitensis – Overlap	☐ Goat pox virus
☐ Brucella suis – Overlap	☐ Lumpy skin disease virus
☐ Burkholderia mallei - Overlap	☐ Mycoplasma capricolum
☐ Burkholderia pseudomallei – Overlap	☐ Mycoplasma mycoides
☐ Clostridium botulinum and neurotoxin-producing species of	☐ Newcastle disease virus
Clostridia	☐ Peste des petits ruminants virus
☐ Conotoxins (Short, paralytic alpha conotoxins containing the	☐ Rinderpest virus
following amino acid sequence X1CCX2PACGX3X4X5X6CX7)	☐ Sheep pox virus
☐ Coxiella burnetii	☐ Swine vesicular disease virus
☐ Crimean-Congo hemorrhagic fever virus	☐ Bacillus anthracis Pasteur strain
☐ Diacetoxyscirpenol	USDA Plant Protection and Quarantine (PPQ)
☐ Eastern equine encephalitis virus	Select Agents and Toxins
☐ Ebola virus	☐ Coniothyrium glycines
☐ Francisella tularensis	☐ Peronosclerospora philippinensis (Peronosclerospora sacchari)
☐ Hendra virus – Overlap	☐ Ralstonia solanacearum
☐ Lassa fever virus	☐ Rathayibacter toxicus
☐ Lujo virus ☐ Marburg virus	☐ Sclerophthora rayssiae
☐ Mpox virus Clade I	☐ Synchytrium endobioticum
☐ 1918-1919 H1N1 including reconstructed replication	☐ Xanthomonas oryzae
competent forms of the 1918 pandemic influenza virus	Other Risk Group 4 Pathogens
containing any portion of the coding regions of all eight gene	(non BSAT)
segments (Reconstructed 1918 Influenza virus)	☐ Tick-borne encephalitis virus complex including Absetterov, Central
☐ Nipah virus – Overlap	European encephalitis, Hanzalova, Hypr, and Kumlinge
☐ Ricin	☐ Herpesvirus simiae (herpes B or monkey B virus)
☐ Rickettsia prowazekii	☐ Hemorrhagic fever agents and viruses as yet undefined
☐ Rift Valley fever virus – Overlap	Other Risk Group 3 Pathogens
☐ Severe acute respiratory coronavirus (SARS-CoV)	(non BSAT)
☐ SARS-CoV/SARS-CoV-2 chimeric viruses resulting from any	☐ Bartonella
deliberate manipulation of SARS-CoV-2 to incorporate nucleic	☐ Brucella
acids coding for SARS-CoV virulence factors	☐ Orientia tsutsugamushi
☐ Saxitoxin	\square Pasteurella multocida type B -"buffalo" and other virulent strains
☐ Chapare virus	☐ Rickettsia akari, R. australis, R. canada, R. conorii, R. rickettsii, R,
☐ Guanarito virus	siberica, R. typhi (R. mooseri)
☐ Junín virus	☐ Chikungunya virus except the vaccine strain 181/25
☐ Machupo virus	☐ Semliki Forest virus
☐ Sabía virus	☐ St. Louis encephalitis virus
☐ Staphylococcal enterotoxins (subtypes A, B, C, D, E)	☐ Flexal virus
☐ T-2 toxin	☐ Lymphocytic choriomeningitis virus (LCM) (neurotropic strains)
☐ Tetrodotoxin	☐ Hantaviruses, including Hantaan virus
☐ Tick-borne encephalitis complex virus: Far Eastern subtype	☐ Middle East respiratory syndrome coronavirus (MERS-CoV)
☐ Tick-borne encephalitis complex virus: Siberian subtype	☐ Severe acute respiratory coronavirus 2 (SARS-CoV-2)
☐ Kyasanur Forest disease virus	☐ Japanese encephalitis virus except strain SA 14-14-2
☐ Omsk hemorrhagic fever virus	☐ West Nile virus
☐ Variola major virus (Smallpox virus)	☐ Yellow fever virus
☐ Variola minor virus (Alastrim)	☐ Human influenza A virus H2N2 (1957-1968)
☐ Venezuelan equine encephalitis virus – Overlap	Highly pathogenic avian influenza A virus H5Nx strains within the
☐ Yersinia pestis	Goose/Guangdong/96-like H5 lineage (e.g., H5N1, H5N6 etc.) Transmissible spongiform encephalopathy (TSE) agents (e.g.,
	Creutzfeldt-Jacob disease and kuru agents)
OTHER	
☐ Any attenuated pathogen or vaccine strain that is currently excluded from the Select Agent Regulations that exhibits the recovery of virulence at or near the wild type	
<u> </u>	te manipulation of clade II to incorporate nucleic acids coding for clade I
☐ Mpox virus clade I/II chimeric viruses resulting from any deliberate manipulation of clade II to incorporate nucleic acids coding for clade I virulence factors	