SUPPLEMENTARY MATERIAL

SUPPLEMENTARY TABLE S1. Information on nucleic acid-positive samples and corresponding virus strain nomenclature.

Virus strains	GISAID Accession No.	Sample source	Sample type
A/Fujian/01/2024(H5N6)	EPI_ISL_19132453	Case A	Bronchoalveolar lavage fluid
A/Fujian/02/2024(H5N6)	EPI_ISL_19145644	Case B	Oropharyngeal
A/Environment/Fujian/02-Env01/2024(H5N6)	/	Shed Y	Poultry drinking water
A/Environment/Fujian/02-Env02/2024(H5N6)	/	Shed Z	Poultry drinking water
A/Environment/Fujian/02-Env03/2024(H5N6)	/	Shed Z	Poultry drinking water
A/Environment/Fujian/02-Env04/2024(H5N6)	/	LPM	Poultry drinking water
A/Environment/Fujian/02-Env05/2024(H5N6)	/	LPM	Poultry drinking water
A/Environment/Fujian/02-Env06/2024(H5N6)	/	LPM	Poultry drinking water
A/Environment/Fujian/02-Env07/2024(H5N6)	/	LPM	Poultry drinking water
A/Environment/Fujian/02-Env08/2024(H5N6)	/	LPM	Cutting board swab

Note: Shed Y was located approximately 50 meters from Case B's residence, with Shed Z situated adjacent to Shed Y. LPM refers to live poultry markets in Case B's vicinity.

SUPPLEMENTARY TABLE S2. Similarity analysis of viral genome segments using BLAST.

Virus	Segment and length (bp)	Strain with the highest similarity (accession ID, percent identity)	
		NCBI database	GISAID database
FJ01	PB2:2250	A/Guangdong/lgf/2021(H5N6) (OL519558.1, 98.68%)	A/Guangdong/lgf/2021 (H5N6) (EPI2255274, 98.68%)
FJ01	PB1:2239	A/duck/Guangxi/293D21/2017(H1N2) (MH667662.1, 96.44%)	A/duck/Hunan/S40199/2021(H5N6) (H5N6) (EPI1997200, 98.42%)
FJ01	PA: 2131	A/Guangdong/1/2021(H5N6) (OK284448.1, 99.02%)	A/Neogale vison/ China/FD/NV/SD/L4/2021 (H5N6) (EPI3351954, 99.07%)
FJ01	HA: 1725	A/Rattus norvegicus/China/FS21/2021 (H5N6) (OQ291577.1, 97.24%)	A/Rattus norvegicus/China/FS21/2021 (H5N6) (EPI2394816, 97.24%)
FJ01	NP: 1551	A/Guangdong/1/2021(H5N6) (OK284449.1, 99.04%)	A/Guangdong/1/2021 (H5N6) (EPI2200687, 99.04%)
FJ01	NA: 1398	A/Guangdong/1/2021(H5N6) (OK284452.1, 98.04%)	A/Guangdong/1/2021 (H5N6) (EPI2200690, 98.04%)
FJ01	MP: 1021	A/Guangdong/1/2021(H5N6) (OK284450.1, 99.42%)	A/Bar-headed Goose/Tibet/XZQ17-1/2021 (H5N8) (EPI1949225, 99.42%)
FJ01	NS: 872	A/Guangdong/1/2021(H5N6) (OK284453.1,97.98%)	A/Guangdong/1/2021 (H5N6) (EPI2200691, 97.98%)
FJ02	PB2: 2247	A/Guangdong/lgf/2021(H5N6) (OL519558.1, 98.55%)	A/Guangdong/lgf/2021 (H5N6) (EPI2255274, 98.55%)
FJ02	PB1: 2239	A/duck/Guangxi/293D21/2017(H1N2) (MH667662.1, 96.44%)	A/duck/Hunan/S40199/2021(H5N6) (EPI1997200, 98.42%)
FJ02	PA: 2133	A/Guangdong/1/2021(H5N6) (OK284448.1, 99.12%)	A/Neogale vison/China/FD/NV/SD/L4/2021 (H5N6) (EPI3351954, 99.16%)
FJ02	HA: 1725	A/Rattus norvegicus/China/FS21/2021(H5N6) (OQ291577.1, 97.24%)	A/Rattus norvegicus/China/FS21/2021 (H5N6) (EPI2394816, 97.24%)
FJ02	NP: 1552	A/Guangdong/1/2021(H5N6) (OK284449.1, 99.11%)	A/Guangdong/1/2021 (H5N6) (EPI2200687, 99.11%)
FJ02	NA: 1400	A/Guangdong/1/2021(H5N6) (OK284452.1, 98.18%)	A/Guangdong/1/2021 (H5N6) (EPI2200690, 98.18%)
FJ02	MP: 1021	A/Guangdong/1/2021(H5N6) (OK284450.1, 99.42%)	A/Bar-headed Goose/Tibet/XZQ17-1/2021 (H5N8) (EPI1949225, 99.42%)
FJ02	NS: 872	A/Guangdong/1/2021(H5N6 (OK284453.1, 97.98%)	A/Guangdong/1/2021 (H5N6) (EPI2200691, 97.98%)

Abbreviation: BLAST=basic local alignment search tool; NCBI=national center for biotechnology information (USA); GISAID=global initiative on sharing all influenza data.

SUPPLEMENTARY FIGURE S1. Phylogenetic analysis of H5 virus HA genes using the maximum likelihood method.

Note: The phylogenetic tree encompasses major H5 clades (indicated at terminal nodes) and is rooted in the reference strain A/Goose/Guangdong/1/1996 (H5N1). The tree was constructed using 1,000 bootstrap replicates, with values shown above branches. Viral strains from this study are denoted by red spots (case A), red triangles (case B), and black triangles (environmental isolates).

Abbreviation: HA=hemagglutinin.