

Supplemental Data

Response network analysis of differential gene expression in human epithelial lung cells during avian influenza infections

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1 RSV and Mock Response

1.1 RSV Response Microarray Statistics

Slides	RSV							
	0h 1	8h 1	0h 1	24h 1	0h 2	8h 2	0h 2	24h 2
Total Number of Features	45015		45015		45015		45015	
Number of Found Features*	41067		40892		40443		40498	
# of Features with Significant Signal [†]	31150	33165	31635	34148	31664	31379	31931	33463
# of Non-Uniformity Outliers	89	73	71	48	25	52	15	18
# of Population Outliers	264	249	204	176	213	202	246	222
# Saturated Features: SpikeIns	0	0	0	0	0	0	0	0
# Saturated Features: Non-Ctrl	0	2	0	3	0	2	0	0
Absolute Average Log-Ratio: SpikeIns	0.41		0.43		0.44		0.43	
Standard Dev. Log-Ratio: SpikeIns	0.02		0.02		0.02		0.01	
Average S/N: SpikeIns	27.95		26.91		29.27		37.66	
Absolute Average Log-Ratio: Non-Ctrl	0.16		0.15		0.13		0.09	
Standard Dev. Log-Ratio: Non-Ctrl	0.04		0.04		0.03		0.03	
Average S/N: Non-Ctrl	10.25		7.59		8.24		6.45	

*Ratio of (feature signal)/(local BG signal) > 1.5×(local BG noise); and spot $\emptyset$ ≥ 0.03×(nominal spot $\emptyset$)

[†]according to the Agilent estimation of background error model

1.2 Mock Response Microarray Statistics

Slides	Mock							
	0h 1	8h 1	0h 1	24h 1	0h 2	8h 2	0h 2	24h 2
Total Number of Features	45015		45015		45015		45015	
Number of Found Features*	40822		41070		40378		40530	
# of Features with Significant Signal [†]	30394	30527	31639	32975	31163	32211	31601	33428
# of Non-Uniformity Outliers	11	40	15	30	15	12	26	48
# of Population Outliers	183	161	137	126	117	112	182	216
# Saturated Features: SpikeIns	0	0	0	0	0	0	0	0
# Saturated Features: Non-Ctrl	0	3	0	1	0	2	0	2
Absolute Average Log-Ratio: SpikeIns	0.43		0.44		0.45		0.44	
Standard Dev. Log-Ratio: SpikeIns	0.01		0.01		0.01		0.01	
Average S/N: SpikeIns	44.57		41.48		45.13		37.91	
Absolute Average Log-Ratio: Non-Ctrl	0.03		0.22		0.03		0.08	
Standard Dev. Log-Ratio: Non-Ctrl	0.04		0.03		0.03		0.03	
Average S/N: Non-Ctrl	2.89		16.79		2.45		6.07	

*Ratio of (feature signal)/(local BG signal) > 1.5×(local BG noise); and spot $\emptyset$ ≥ 0.03×(nominal spot $\emptyset$)

[†]according to the Agilent estimation of background error model

1.3 RSV Scatter plots

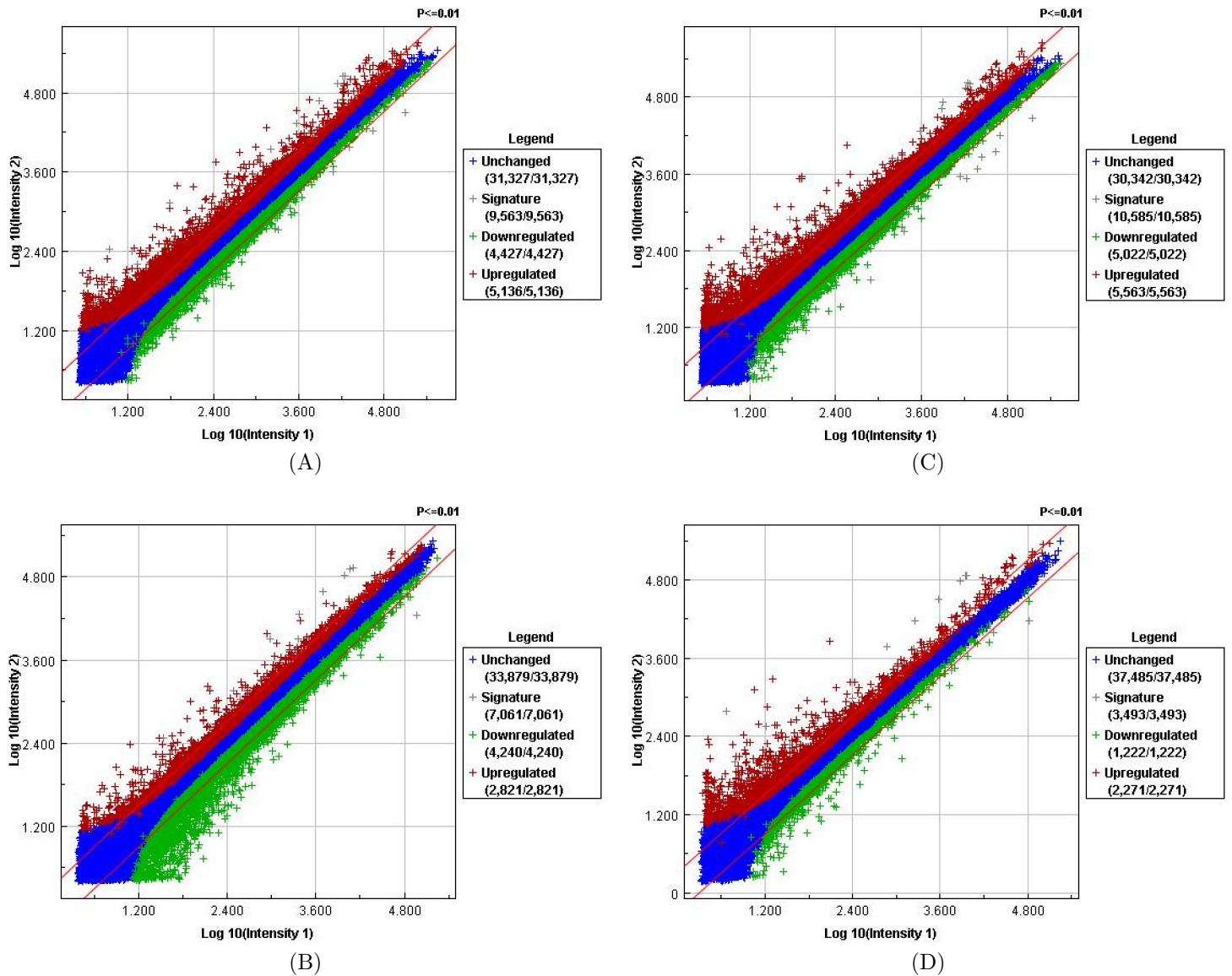


Figure 1: RSV scatter plots of signal intensities (C.f. Microarray service report by Miltenyi Biotec). The signal intensities of each feature represented by a dot is shown in double logarithmic scale. X-axis: Cy3-log signal intensity; y-axis: Cy5-log signal intensity. Red diagonal lines define the areas of 2-fold differential signal intensities. Blue cross: unchanged genes. Red cross: significantly upregulated genes (p-value < 0.01). Green cross: significantly downregulated genes (p-value < 0.01). Grey cross in legend: summary of significantly up- and downregulated signatures. (A) 0h RSV₁ versus RSV₁ at 8h; (B) 0h RSV₂ versus 8h RSV₂; (C) 0h RSV₁ versus 24h RSV₁; (D) 0h RSV₂ versus 24h RSV₂.

1.4 Mock Scatter plots

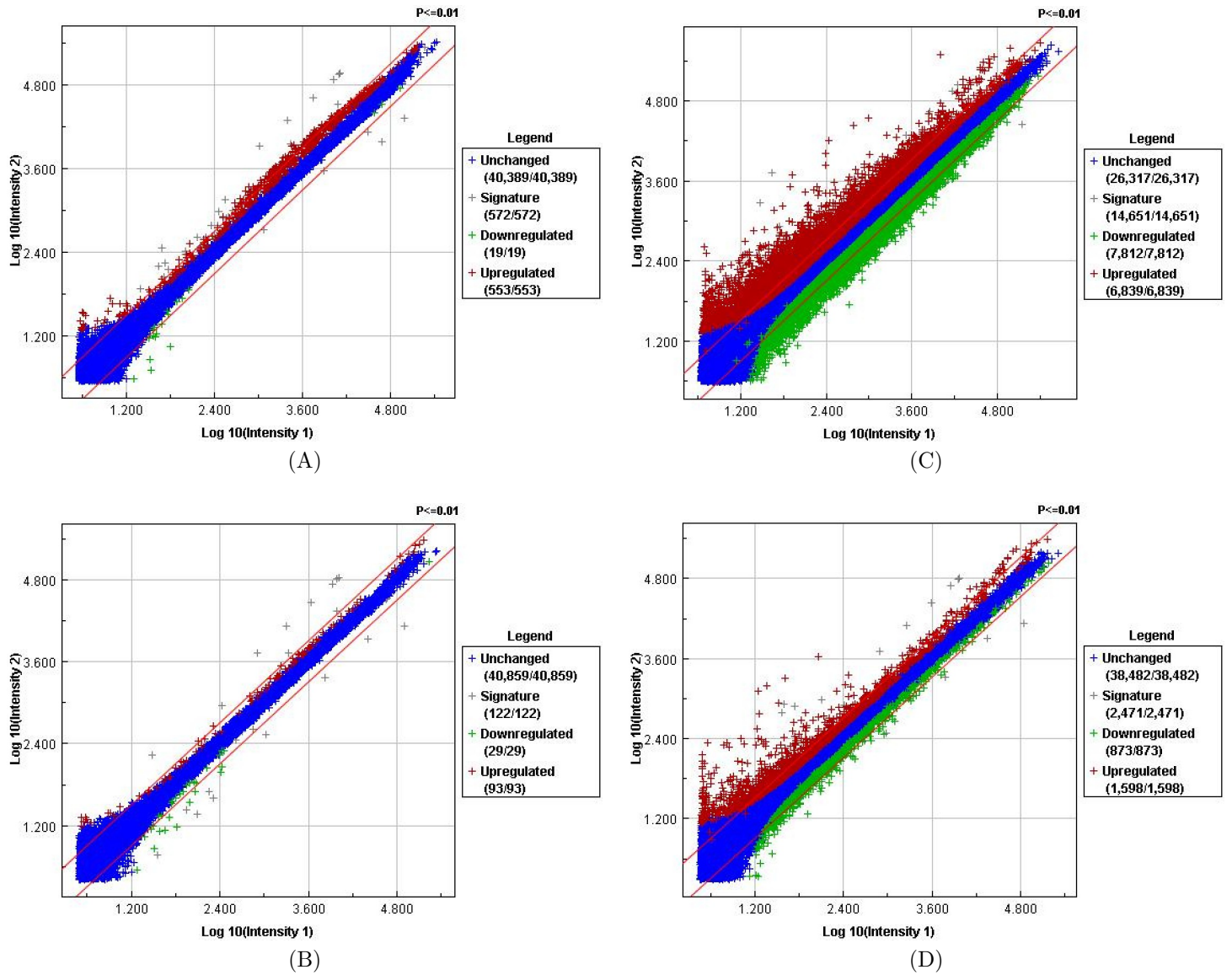


Figure 2: Mock infection scatter plots of signal intensities (C.f. Microarray service report by Miltenyi Biotec - see Figure caption of Figure 1). (A) 0h Mock₁ versus 8h Mock₁; (B) 0h Mock₂ versus 8h Mock₂; (C) 0h Mock₁ versus 24h Mock₁; (D) 0h Mock₂ versus 24h Mock₂.

2 H5N1 Response

2.1 H5N1 Response Microarray Statistics

Slides	H5N1											
	0h 1	8h 1	0h 2	8h 2	0h 3	8h 3	0h 1	24h 1	0h 2	24h 2	0h 2	24h 2
Total Number of Features	45015		45015		45015		45015		45015		45015	
Number of Found Features*	41840		41582		42301		42891		41392		41616	
# of Features with Significant Signal [†]	38807	38610	37303	37488	37765	40976	39725	42466	38007	38908	37901	36276
# of Non-Uniformity Outliers	4	35	6	37	13	31	8	20	20	134	61	121
# of Population Outliers	49	56	62	42	70	43	77	55	53	78	30	39
# Saturated Features: SpikeIns	0	0	0	0	0	0	0	0	0	0	0	0
# Saturated Features: Non-Ctrl	0	1	0	1	0	1	0	1	0	1	0	2
Absolute Average Log-Ratio: SpikeIns	0.47		0.50		0.47		0.46		0.47		0.47	
Standard Dev. Log-Ratio: SpikeIns	0.01		0.01		0.01		0.02		0.01		0.01	
Average S/N: SpikeIns	54.49		47.40		37.44		40.77		43.47		45.89	
Absolute Average Log-Ratio: Non-Ctrl	0.11		0.10		0.11		0.12		0.14		0.13	
Standard Dev. Log-Ratio: Non-Ctrl	0.03		0.03		0.03		0.02		0.03		0.03	
Average S/N: Non-Ctrl	9.49		9.17		8.48		10.51		12.55		10.99	

*Ratio of (feature signal)/(local BG signal) > 1.5×(local BG noise); and spot $\emptyset \geq 0.03 \times (\text{nominal spot}\emptyset)$

[†]according to the Agilent estimation of background error model

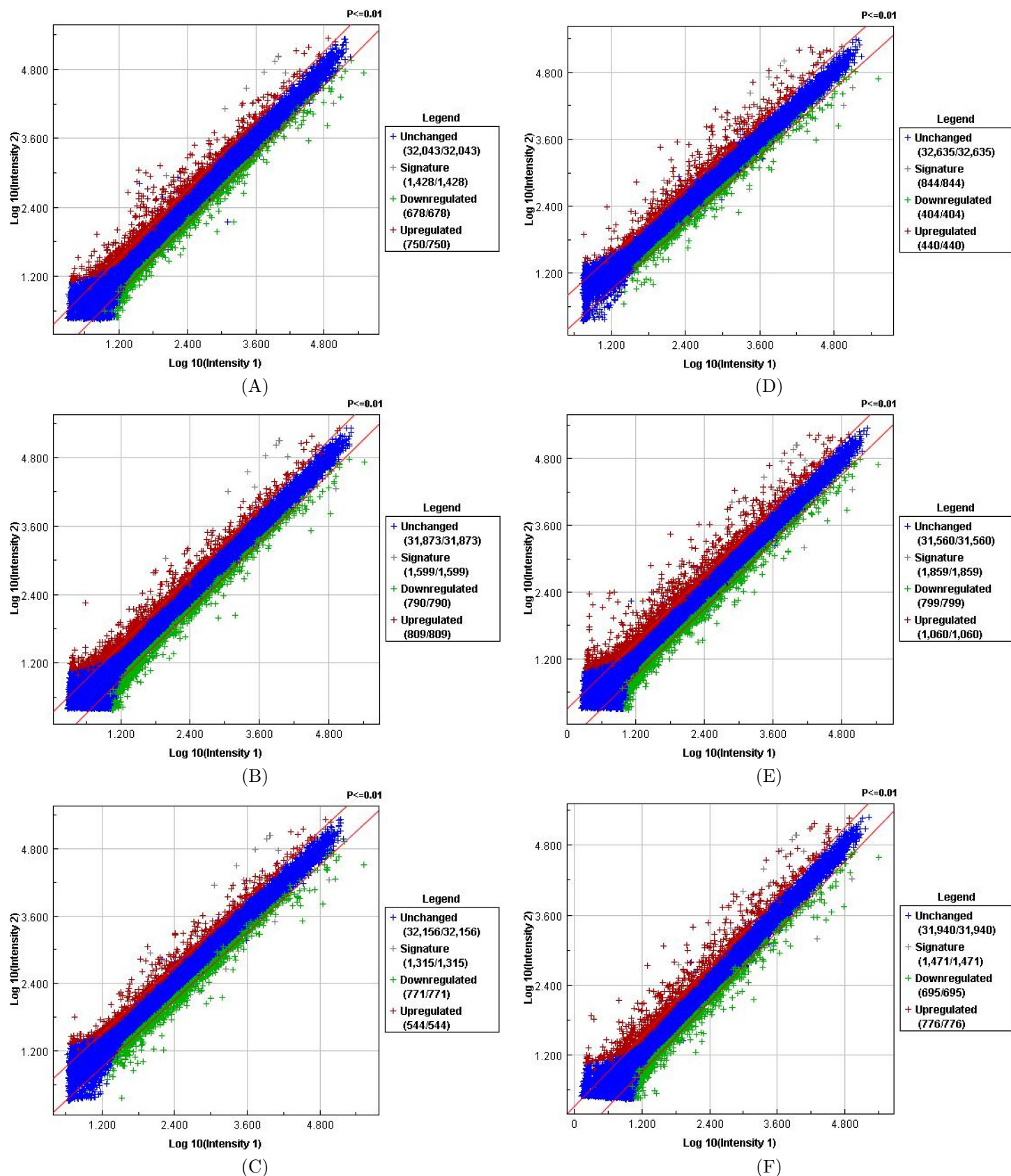


Figure 3: H5N1 scatter plots of signal intensities (C.f. Microarray service report by Miltenyi Biotec - see Figure caption of Figure 1). (A) 0h H5N1₁ versus 8h H5N1₁; (B) 0h H5N1₂ versus 8h H5N1₂; (C) 0h H5N1₃ versus 8h H5N1₃; (D) 0h H5N1₁ versus 24h H5N1₁; (E) 0h H5N1₂ versus 24h H5N1₂; (F) 0h H5N1₁ versus 24h H5N1₁.