Supplementary tables

Subjects (N = 68)	All SYS AE (n = 43)	
	Probable	**Possible**
Subjects (%)	14 (32.6)	29 (67.4)
Age (in years)		
Median (range)	30 21 – 40	29 23 - 50
Gender Male (%)	9 (64.3)	16 (55.2)
Ethnicity n (%)		
Chinese	10 (71.4)	22 (75.9)
Malay	2 (14.3)	2 (6.9)
Indian	0 (0)	3 (10.3)
Others^{A}	2 (14.3)	2 (6.9)
BMI kg/m^2		
Mean (±SD)	22.1 (±2.8)	22.0 (±3.0)

Supplementary Table 1. Demographics of subjects with possible and probable systemic AEs. Age, gender, ethnicity and BMI of the subjects that have completed the trial and analyzed for AEs attributed to YFLAV (*N* = 68). Those with systemic AEs are further subdivided by probable, or possible relatedness to YFLAV.

Gene-set name	NES	NOM p-value	FDR q-value
Toll receptor cascade	1.7540	0.0084	0.2287
NOD1 2 signaling pathway	1.7501	0.0119	0.2108
Innate immune system	1.7489	0.0040	0.1891
Interferon signaling	1.7243	0.0084	0.2206 f
Thrombin signaling through proteinase activated receptor PARS	1.7060	0.0096	0.2433
Signaling by ILS	1.6905	0.0281	0.2389
TRAF6 mediated IRF7 activation	1.6881	0.0103	0.2266
Actiated TAK1 mediates p38 MAPK activation	1.6860	0.0041	0.2160
TRAF6 mediated inducation of NFkB and MAP kinases upon TLR7 8 or 9 activation	1.6744	0.0124	0.2283
ADP signaling through P2RY12	1.6720	0.0057	0.2184
Circadian repression of expression by Rev ErbA	1.6680	0.0142	0.2131
G beta γ signaling through PLC β	1.6594	0.0091	0.2173
Prostacyclin signaling through prostacyclin receptor	1.6385	0.0112	0.2478
Signaling by hippo	1.6098	0.0115	0.24830

Supplementary Table 2. GSEA findings of systemic AEs following YF vaccination. Summary of up-regulated gene-sets from venous blood microarray data in subjects with delayed AEs (n = 18) compared to subjects without AEs (n = 8), at day 1versus day 0 post-vaccination. Gene-sets with FDR q < 0.25, ranked based on normalized enrichment scores (NES). Nominal (NOM) p-values of the gene sets are shown.