

Supplementary Data

Impact of ChAdOx1 or DNA prime vaccination on magnitude, breadth, and focus of MVA boosted immunogen-specific T cell responses

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Table S1. Overlapping peptide pools design

HIV	Protein (% in HTI)	Gag (45%)							Pol (44%)							Vif		Nef				
	Subunit	p17		p24				p2p7p1p6	PRT		RT			INT		Vif		Nef				
Pool	ID	1C	1D	1E	1F	1G	1H	1I	1J	1K	1L	2A	2B	2C	2D	2E	2F	2G				
HTI	Fragment	1		2	3	4		5	6	7	8		9	10		11	12	13	14	15	16	
	Length (AA)	78		14	11	60		14	15	27	55		17	55		34	34	17	26	19	13	
	AA position in HXB2R protein		17-50	51-94	162-170 193-203		223-245	246-282	296-308 350-363	426-452		101-121	122-155	189-205 365-372		373-419	464-496	925-958	981-996	26-50	166-183	57-68
	OLP ID	First	5	16	27	35	43	51	61	69	78	86	96	107	117	127	132	140	146			
	Last	15	26	34	42	50	60	68	77	85	95	106	116	126	131	139	145	147				

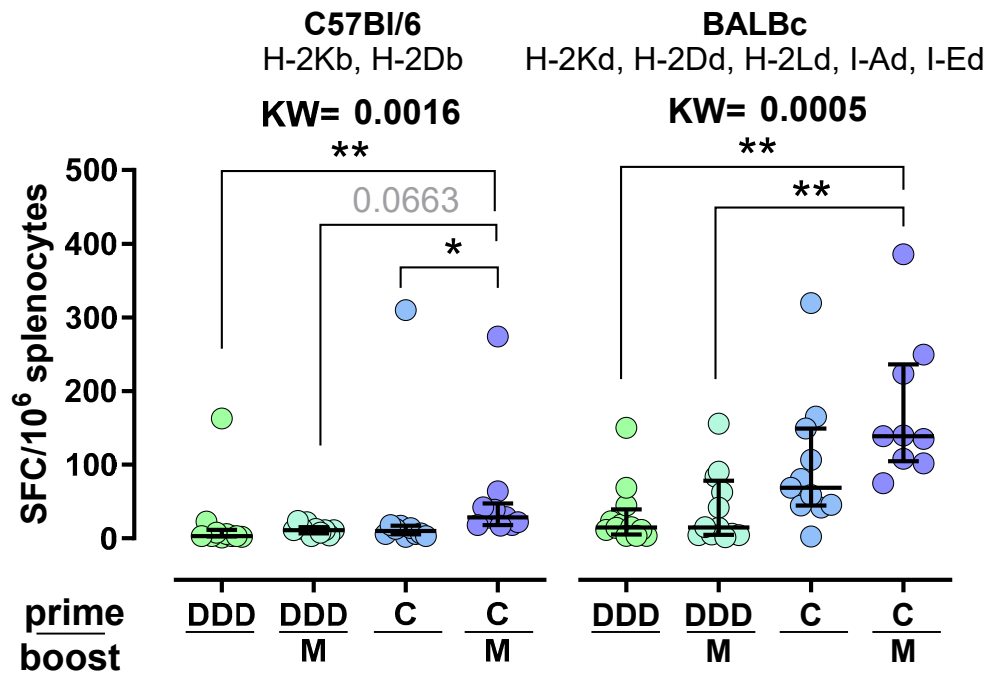


Figure S1. Mean INF γ SFC/10⁶ spleen cells background. Unstimulated negative control triplicates in C57BL/6 and BALBc mice vaccinated with four different prime-boost regimens (DDD, DDDM, C, and CM) are shown. Statistically significant differences ($p < 0.05$) between treatments were tested with the Kruskal-Wallis test with Dunn's correction for multiple comparisons. Significant adjusted Dunn's p values are shown as * $p < 0.05$ by, ** $p < 0.01$ by, *** $p < 0.001$, and **** $p < 0.0001$, trends ($p < 0.1$) are indicated by grey numbers.

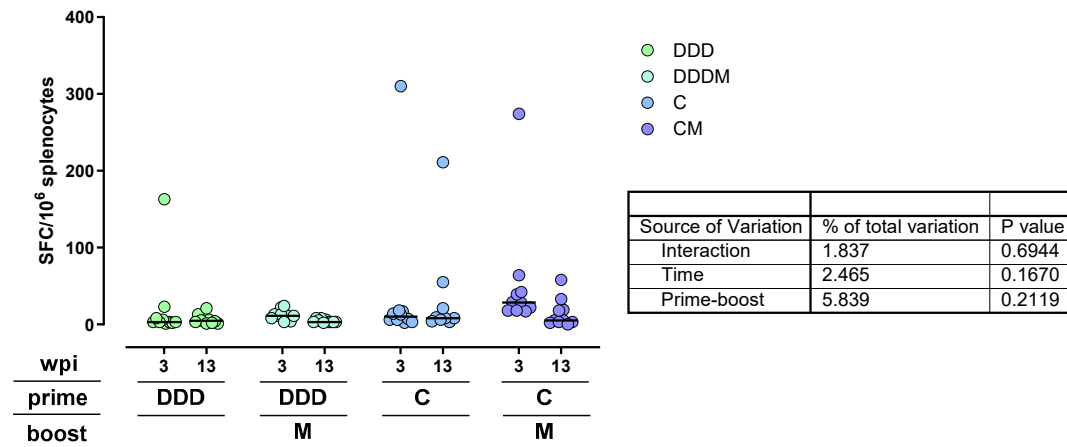


Figure S2. Mean INF γ SFC/106 spleen cells background. Unstimulated negative control triplicates in C57BL/6 mice vaccinated with four prime-boost regimens (DDD, DDDM, C, and CM) are shown 3- and 13-weeks post-immunization (wpi). Statistically significant differences ($p < 0.05$) between treatments were tested with a 2-way ANOVA with Tukey's correction for multiple comparisons. Significant adjusted Tukey's p values are shown as * $p < 0.05$ by, ** < 0.01 by, *** < 0.001 , and **** < 0.0001 .