

**Table S5. Vaccine versus Native peptides.**

#	Sequence	Pool	#	Sequence	Pool
31	VFGKGIIIENSKTTF	V	112	VFGKGIIIENS <b>N</b> TTF	N
32	IIIENSKTTFLTPVA	V	113	IIIENS <b>N</b> TTFLTPVA	N
33	SKTTFLTPVATGNQY	V	114	<b>S</b> NTTFLTPVATGNQY	N
56	FRPAKDISFQ <b>N</b> LVYL	V	115	FRPAKDISFQ <b>N</b> YTYL	N
57	DISFQ <b>N</b> LVYLSKNVV	V	116	DISFQ <b>N</b> YTYLSKNVV	N
58	<b>N</b> LVYLSKNVVVDNWEK	V	117	<b>N</b> YTYLSKNVVVDNWEK	N
73	EKIKEGFKN <b>K</b> NREMI	V	118	EKIKEGFKN <b>N</b> ASMI	N
74	GFKN <b>K</b> NREMIKSAFL	V	119	GFKN <b>N</b> ASMIKSAFL	N
75	<b>N</b> REMIKSAFLPTGAF	V	120	<b>N</b> ASMIKSAFLPTGAF	N
83	IFNVKPTCLIN <b>D</b> KNY	V	121	IFNVKPTCLIN <b>S</b> SY	N
84	PTCLIN <b>D</b> KNYIATTA	V	122	PTCLIN <b>S</b> SYIATTA	N
85	<b>N</b> DKNYIATTALSHPI	V	123	<b>N</b> SSYIATTALSHPI	N
98	DSLKCPCDPEM <b>V</b> SQS	V	124	DSLKCPCDPEM <b>S</b> NS	N
99	PCDPEM <b>V</b> SQSTCRFF	V	125	PCDPEM <b>S</b> NSTCRFF	N
100	M <b>V</b> SQSTCRFFVCKCV	V	126	M <b>S</b> NSTCRFFVCKCV	N
32	IIIENSKTTFLTPVA	V	194	IIIENS <b>N</b> TTFLKPVA	N
147	SKTTFLTPVATGN <b>Q</b> D	V	195	<b>S</b> NTTFLKPVATGN <b>Q</b> D	N
148	LTPVATGN <b>Q</b> DLKDGG	V	196	LKPVATGN <b>Q</b> DLKDGG	N
167	FRPAKD <b>K</b> L <b>F</b> EN <b>V</b> YL	V	197	FRPAKD <b>K</b> L <b>F</b> EN <b>Y</b> TYL	N
168	DKL <b>F</b> EN <b>V</b> YLSKNVV	V	198	DKL <b>F</b> EN <b>Y</b> TYLSKNVV	N
169	<b>N</b> LVYLSKNVVVDN <b>W</b> EE	V	199	<b>N</b> YTYLSKNVVVDN <b>W</b> EE	N

15mer peptide sequences are shown, and pools indicated: V = sequence found in vaccine insert ( $n = 21$ ); N = sequence found in native parasite ( $n = 21$ ). Amino acids that were substituted to prevent potential N-linked glycosylation are highlighted in bold.

