

FIGURE 1. FUP MSP-1 p42 amino acid sequence

AISVTMDNIL	SGFENEYDVI	YLKPLAGVYR	SLKKQIEKNI	FTFNLNLNDI	LNSRLKKRKY	60
FLDVLES DLM	QFKHISSNEY	IIEDSFKLLN	SEQNTLLKS	YKYIKESVEN	DIKFAQEGIS	120
YYE KVLAKYK	DDLESIKKVI	KEEKEKFPSS	PPTTPPSPAK	TDEQKKESKF	LPFLTNIETL	180
YNNLVNKIDD	YLINLKAKIN	DCNVEKDEAH	VKITKLSDLK	AIDDKIDLFK	NHNDFEAIKK	240
LINDDTKKDM	LGKLLSTGLV	QNFPNTIISK	LIEGKFQDML	NISQHQC	VKK QCPENSGCFR	300
HLDEREECKC	LLNYKQEGDK	CVENPNPTCN	ENNGGCDADA	KCTEEDSGSN	GKKITCECTK	360
PDSYPLFDGI	FCS					373

FIGURE 2. Alignment of the MSP-1 p42 amino acid sequences from the three *P. falciparum* strains FUP, 3D7, and FVO.

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      10      20      30      40      50
  ---+-----+-----+-----+-----+
1 AIS-VTMDNILSGFENEYDVIYLKPLAGVYRSLKKQIEKNIFTFNLNLDILNSRLKKRK FUP_P42
1 +++-+++++ 3D7_P42
1 +VTPSVI+++++KI++++E+L+++++L+++VM+++V+VK+++++N++E FVO_P42

      60      70      80      90     100     110
  +-----+-----+-----+-----+-----+
60 YFLDVLES DLMQFKHISSNEYIIEDSFKLLNSEQKNTLLKSYKYIKESVENDIKFAQEGI FUP_P42
60 ++++++ 3D7_P42
61 N+KN+++++IPYKDLT+SN+VVK+PY+F++K+KRDKF+S++N+++DSIDT++N++NDVL FVO_P42

     120     130     140     150     160     170
  +-----+-----+-----+-----+-----+
120 SYYEKVLAKYKDDLESIKKVIKEEKEKFPSSPPTTPPSPAKTDEQKESKFLPFLTNIET FUP_P42
120 ++++++ 3D7_P42
121 G++KILSE+++S++D++++Y+N-----+K+GENE+Y++++N++++ FVO_P42

     180     190     200     210     220     230
  +-----+-----+-----+-----+-----+
180 LYNNLVNKKIDDYLINLKAKINDCNVEKDEAHVKITKLSDLKAIDDKIDLFKNHNDFDAIK FUP_P42
180 ++++++E+++ 3D7_P42
161 ++KTVND+++LFV+H+E++VLNYTY++SNVE+++KELNY++TIQ++LAD++KN+N+VG+A FVO_P42

     240     250     260     270     280     290
  +-----+-----+-----+-----+-----+
240 KLINDDTKKDMLGKLLSTGLV-QNFPNTIISKLIEGKFQDMLNISQHQCVKKQCPENSGC FUP_P42
240 ++++++ 3D7_P42
221 D+ST+YNHNNL+TKF++++M+FENLAKTVL+N+LD+NL+G+++++Q++++ FVO_P42

     300     310     320     330     340     350
  +-----+-----+-----+-----+-----+
299 FRHLDEREECKCLLNYKQEGDKCVENPNPTCNENNGGCDAKCTEEDSGSNGKKITCEC FUP_P42
299 ++++++T++++++SR+++++ 3D7_P42
281 ++++++ FVO_P42

     360     370
  +-----+-----+
359 TKPDSYPLFDGIFCS FUP_P42
359 ++++++ 3D7_P42
341 ++++++ FVO_P42

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FIGURE 3. Alignment of the amino acid sequences from the three N-terminally truncated subunits of Construct A, Construct B, and Construct C relative to the FUP MSP-1 p42 sequence.

	10	20	30	40	50	60	
	-----+	-----+	-----+	-----+	-----+	-----+	
1	AISVTMDNILSGFENEYDVIY <u>LKPLAGVYRS</u> LKKQIEKNIFTFNLNLNDILNSRLKKRKY						FUP_p42
	70	80	90	100	110	120	
	-----+	-----+	-----+	-----+	-----+	-----+	
61	FLDVLESDLMQFKHISSNEYIIEDSFKLLNSEQKNTLLKSYKYIKESVENDIKFAQEGIS						FUP_p42
	130	140	150	160	170	180	
	-----+	-----+	-----+	-----+	-----+	-----+	
121	YYEKVLAKYKDDLESIKKVIKEEKEKFPSSPPTTPPSPAKTDEQKKESKFLPFLTNIETL						FUP_p42
	190	200	210	220	230	240	
	-----+	-----+	-----+	-----+	-----+	-----+	
181	YNNLVNKIDDYLINLKAKINDCNVEKDE <u>AHVKITKLSDLKAID</u> DKIDLFKNHNDFDAIKK						FUP_p42
1	garsgggggt <u>AHVKITKLSDLKAID</u> DKIDLFKNHNDFDAIKK						Construct A
1	gars <u>LKPLAGVYRS</u> LKKQgggggt <u>AHVKITKLSDLKAID</u> DKIDLFKNHNDFDAIKK						Construct B
	250	260	270	280	290	300	
	-----+	-----+	-----+	-----+	-----+	-----+	
241	LINDDTKKDMLGKLLSTGLVQNFNPNTIISKLI <u>EGKFQDMLNISQHQCVKKQCPENSGCFR</u>						FUP_p42
42	LINDDTKKDMLGKLLSTGLVQNFNPNTIISKLI <u>EGKFQDMLNISQHQCVKKQCPENSGCFR</u>						Construct A
59	LINDDTKKDMLGKLLSTGLVQNFNPNTIISKLI <u>EGKFQDMLNISQHQCVKKQCPENSGCFR</u>						Construct B
1	garsgggggtMLGKLLSTGLVQNFNPNTIISKLI <u>EGKFQDMLNISQHQCVKKQCPENSGCFR</u>						Construct C
	310	320	330	340	350	360	
	-----+	-----+	-----+	-----+	-----+	-----+	
301	HLDEREECKLLNYKQEGDKCVENPNPTCNENNGGCDADAKCTEEDSGSNGKKITCECTK						FUP_p42
102	HLDEREECKLLNYKQEGDKCVENPNPTCNENNGGCDADATCTEEDSGSSRKKITCECTK						Construct A
119	HLDEREECKLLNYKQEGDKCVENPNPTCNENNGGCDADATCTEEDSGSSRKKITCECTK						Construct B
61	HLDEREECKLLNYKQEGDKCVENPNPTCNENNGGCDADAKCTEEDSGSNGKKITCECTK						Construct C
	370						
	-----+						
361	PDSYPLFDGIFCS						FUP_p42
162	PDSYPLFDGIFCS						Construct A
179	PDSYPLFDGIFCS						Construct B
121	PDSYPLFDGIFCS						Construct C

FIGURE 4. Alignment of the amino acid sequences from all MSP-1 C-terminal subunit protein Constructs relative to the FUP MSP-1 p33 sequence.

	10	20	30	40	50	60	
	-----+	-----+	-----+	-----+	-----+	-----+	
1	AISVTMDNILSGFENEYDVIY <u>LKPLAGVYRSLKKQ</u> IEKNIFTFNLNLNDILNSRLKKRKY						FUP_p42
	-----						Construct A
	-----LKPLAGVYRSLKKQ-----						Construct B
	-----						Construct C
	-----						Construct D
	-----						Construct E
	-----						Construct F
	-----						Construct G
	AISVTMDNILSGFENEYDVIYLKPLAGVYRSLKKQIEKNIFTFNLNLNDILNSRLKKRKY						Construct H
	AISVTMDNILSGFENEYDVI-----						Construct I
	AISVTMDNILSGFENEYDVIYLKPLAGVYRSLKKQIEKNI-----						Construct J
	-----						Construct K
	-----						Construct L
	-----						Construct M
	-----DNILS-----YLKPLAGVYRSLKKQI-----LNSRL-----						Construct N
	AISVTM-----GFENEYDVI-----EKNIFTFNLNLNDI-----KKRKY						Construct O
	-----						Construct P
	-----						Construct Q
	AISVTMDNILSGFENEYDVI-----						Construct R
	70	80	90	100	110	120	
	-----+	-----+	-----+	-----+	-----+	-----+	
61	FLDVLES						FUP_p42
	DLMQFKHISSNEYIIEDSFKLLNSEQKNTLLKSYKYIKESVENDIKFAQEGIS						Construct A
	-----						Construct B
	-----						Construct C
	-----						Construct D
	-----						Construct E
	-----KFAQEGIS						Construct F
	-----NTLLKSYKYIKESVENDIKFAQEGIS						Construct G
	FLDVLES						Construct H
	DLMQFKHISSNEYIIEDSFKLLNSEQKNTLLKSYKYIKESVENDIKFAQEGIS						Construct I
	-----						Construct J
	-----AQEGIS						Construct K
	-----ISSNEYIIEDSFKLLNSEQKNTL-----						Construct L
	-----						Construct M
	-----VLES						Construct N
	FLD-----MQFKHISSNEYIIEDSFKLLNSEQKNTLLKSYKYIKESVENDIKFAQEGIS						Construct O
	-----						Construct P
	-----						Construct Q
	-----ISSNEYIIEDSFKLLNSEQKNTL-----AQEGIS						Construct R

	130	140	150	160	170	180																																																					
121	Y	Y	E	K	V	L	A	K	Y	K	D	D	L	E	S	I	K	K	V	I	K	E	E	K	F	P	S	S	P	P	T	T	P	P	S	P	A	K	T	D	E	Q	K	K	E	S	K	F	L	P	F	L	T	N	I	E	T	L	FUP_p42
	-----																																Construct A																										
	-----																																Construct B																										
	-----																																Construct C																										
	-----KFLPFLTNIETL																																Construct D																										
	-----IKKVIKEEKEKFPSSPPTTPPSPAKTDEQKKESKFLPFLTNIETL																																Construct E																										
	Y	Y	E	K	V	L	A	K	Y	K	D	D	L	E	S	I	K	K	V	I	K	E	E	K	F	P	S	S	P	P	T	T	P	P	S	P	A	K	T	D	E	Q	K	K	E	S	K	F	L	P	F	L	T	N	I	E	T	L	Construct F
	Y	Y	E	K	V	L	A	K	Y	K	D	D	L	E	S	I	K	K	V	I	K	E	E	K	F	P	S	S	P	P	T	T	P	P	S	P	A	K	T	D	E	Q	K	K	E	S	K	F	L	P	F	L	T	N	I	E	T	L	Construct G
	Y	Y	E	K	V	L	A	K	Y	K	D	D	L	E	S	I	K	K	V	I	K	E	E	K	F	P	S	S	P	P	T	T	P	P	S	P	A	K	T	D	E	Q	K	K	E	S	K	F	L	P	F	L	T	N	I	E	T	L	Construct H
	-----																																Construct I																										
	-----																																Construct J																										
	Y	Y	E	K	V	L	A	K	Y	K	D	D	L	E	S	I	K	K	V	I	K	E	E	K	F	P	S	S	-----																		Construct K												
	-----																																Construct L																										
	-----																																Construct M																										
	-----KYKDDLESIKKV-----KFLPFLTNIETL																																Construct N																										
	Y	Y	E	K	V	L	A	-----VIKEEKEKFPSSPPTTPPSPAKTDEQKKES-----																		Construct O																																	
	-----																																Construct P																										
	-----																																Construct Q																										
	Y	Y	E	K	V	L	A	K	Y	K	D	D	L	E	S	I	K	K	V	I	K	E	E	K	F	P	S	S	-----																		Construct R												

	190	200	210	220	230	240																																																							
181	Y	N	N	L	V	N	K	I	D	D	Y	L	I	N	L	K	A	K	I	N	D	C	N	V	E	K	D	E	A	H	V	K	I	T	K	L	S	D	L	K	A	I	D	D	K	I	D	L	F	K	N	H	N	D	F	D	A	I	K	K	FUP_p42
	-----AHVKITKLSDLKAIDDKIDLFKNHNDFDAIKK																																Construct A																												
	-----AHVKITKLSDLKAIDDKIDLFKNHNDFDAIKK																																Construct B																												
	-----AHVKITKLSDLKAIDDKIDLFKNHNDFDAIKK																																Construct C																												
	Y	N	N	L	V	N	K	I	D	D	Y	L	I	N	L	K	A	K	I	N	D	C	N	V	E	K	D	E	A	H	V	K	I	T	K	L	S	D	L	K	A	I	D	D	K	I	D	L	F	K	N	H	N	D	F	D	A	I	K	K	Construct D
	Y	N	N	L	V	N	K	I	D	D	Y	L	I	N	L	K	A	K	I	N	D	C	N	V	E	K	D	E	A	H	V	K	I	T	K	L	S	D	L	K	A	I	D	D	K	I	D	L	F	K	N	H	N	D	F	D	A	I	K	K	Construct E
	Y	N	N	L	V	N	K	I	D	D	Y	L	I	N	L	K	A	K	I	N	D	C	N	V	E	K	D	E	A	H	V	K	I	T	K	L	S	D	L	K	A	I	D	D	K	I	D	L	F	K	N	H	N	D	F	D	A	I	K	K	Construct F
	Y	N	N	L	V	N	K	I	D	D	Y	L	I	N	L	K	A	K	I	N	D	C	N	V	E	K	D	E	A	H	V	K	I	T	K	L	S	D	L	K	A	I	D	D	K	I	D	L	F	K	N	H	N	D	F	D	A	I	K	K	Construct G
	Y	N	N	L	V	N	K	I	D	D	Y	L	I	N	L	K	A	K	I	N	D	C	N	V	E	K	D	E	A	H	V	K	I	T	K	L	S	D	L	K	A	I	D	D	K	I	D	L	F	K	N	H	N	D	F	D	A	I	K	K	Construct H
	-----VEKDEAHVKITKLSDLKAIDDKIDLFKNHNDFDAIKK																																Construct I																												
	-----VEKDEAHVKITKLSDLKAIDDKIDLFKNHNDFDAIKK																																Construct J																												
	-----VEKDEAHVKITKLSDLKAIDDKIDLFKNHNDFDAIKK																																Construct K																												
	-----VEKDEAHVKITKLSDLKAIDDKIDLFKNHNDFDAIKK																																Construct L																												
	--	N	L	V	N	K	I	D	D	Y	L	I	N	L	K	A	K	I	N	D	C	N	V	E	K	D	E	A	H	V	K	I	T	K	L	S	D	L	K	A	I	D	D	K	I	D	L	F	K	N	H	N	D	F	D	A	I	K	K	Construct M	
	-----																																Construct N																												
	Y	N	N	L	V	N	K	I	D	D	Y	L	I	N	L	K	A	K	I	N	D	C	N	V	E	K	D	E	A	H	V	K	I	T	K	L	S	D	L	K	A	I	D	D	K	I	D	L	F	K	N	H	N	D	F	D	A	I	K	K	Construct O
	-----VEKDEAHVKITKLSDLKAIDDKIDLFKNHNDFDAIKK																																Construct P																												
	--	N	L	V	N	K	I	D	D	Y	L	I	N	L	K	A	K	I	N	D	C	N	V	E	K	D	E	A	H	V	K	I	T	K	L	S	D	L	K	A	I	D	D	K	I	D	L	F	K	N	H	N	D	F	D	A	I	K	K	Construct Q	
	-----																																Construct R																												

	250	260	270	
	-----+-----+-----+-----			
241	LINDDTTKKDMLGKLLSTGLVQNF	PNTIISK	LIEGKFQDML	FUP_p42
	LINDDTTKKDMLGKLLSTGLVQNF	PNTIISK	LIEGKFQDML	Construct A
	LINDDTTKKDMLGKLLSTGLVQNF	PNTIISK	LIEGKFQDML	Construct B
	-----MLGKLLSTGLVQNF	PNTIISK	LIEGKFQDML	Construct C
	LINDDTTKKDMLGKLLSTGLVQNF	PNTIISK	LIEGKFQDML	Construct D
	LINDDTTKKDMLGKLLSTGLVQNF	PNTIISK	LIEGKFQDML	Construct E
	LINDDTTKKDMLGKLLSTGLVQNF	PNTIISK	LIEGKFQDML	Construct F
	LINDDTTKKDMLGKLLSTGLVQNF	PNTIISK	LIEGKFQDML	Construct G
	LINDDTTKKDMLG-----			Construct H
	LINDDTTKKDMLG-----			Construct I
	LINDDTTKKDMLG-----			Construct J
	LINDDTTKKDMLG-----			Construct K
	LINDDTTKKDMLG-----			Construct L
	-----			Construct M
	LINDDTTKKDMLG-----			Construct N
	LINDDTTKKDMLGKLLSTGLVQNF	PNTIISK	LIEGKFQDML	Construct O
	LINDDTTKKDMLG-----			Construct P
	LINDDTTKKDMLGKLLSTGLVQNF	PNTIISK	LIEGKFQDML	Construct Q
	-----			Construct R

Figure 5. Diagram of all MSP-1 C-terminal constructs – ordered by Name

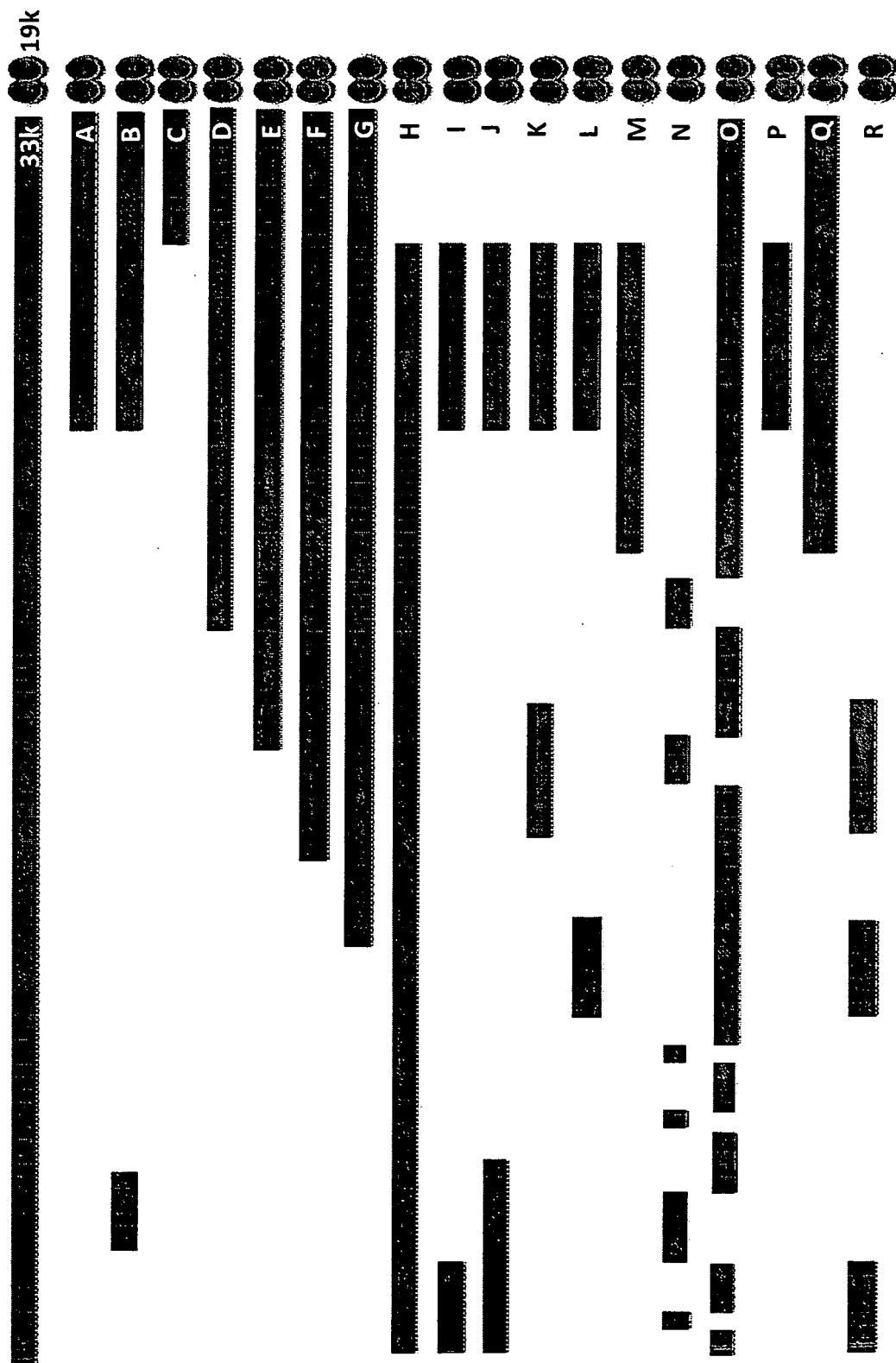


Figure 6. Diagram of all MSP-1 C-terminal constructs – ordered by Group

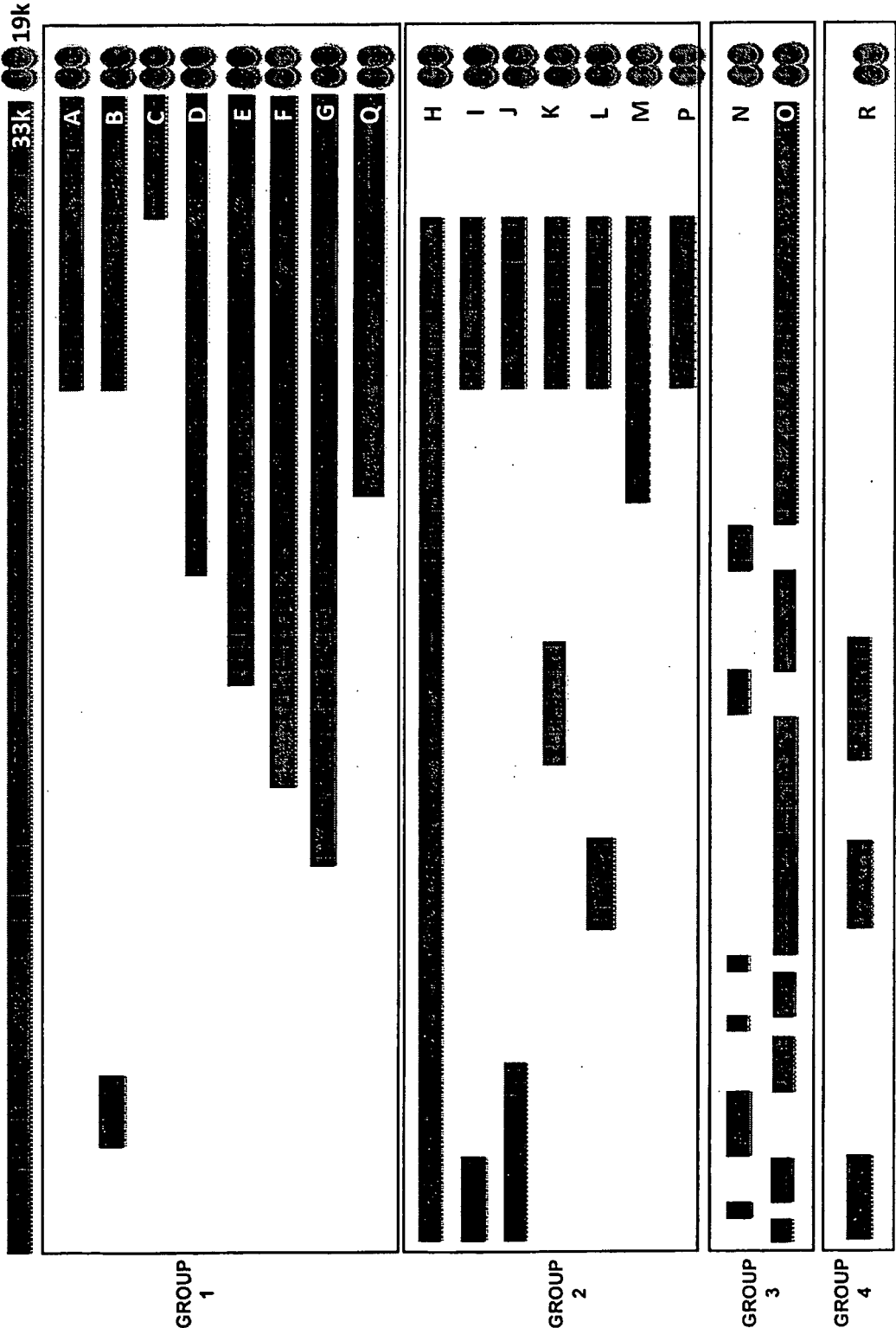


Figure 7. Mouse serum ELISA antibody titers for Group 1, 2 and 3 MSP-1 C-terminal constructs.

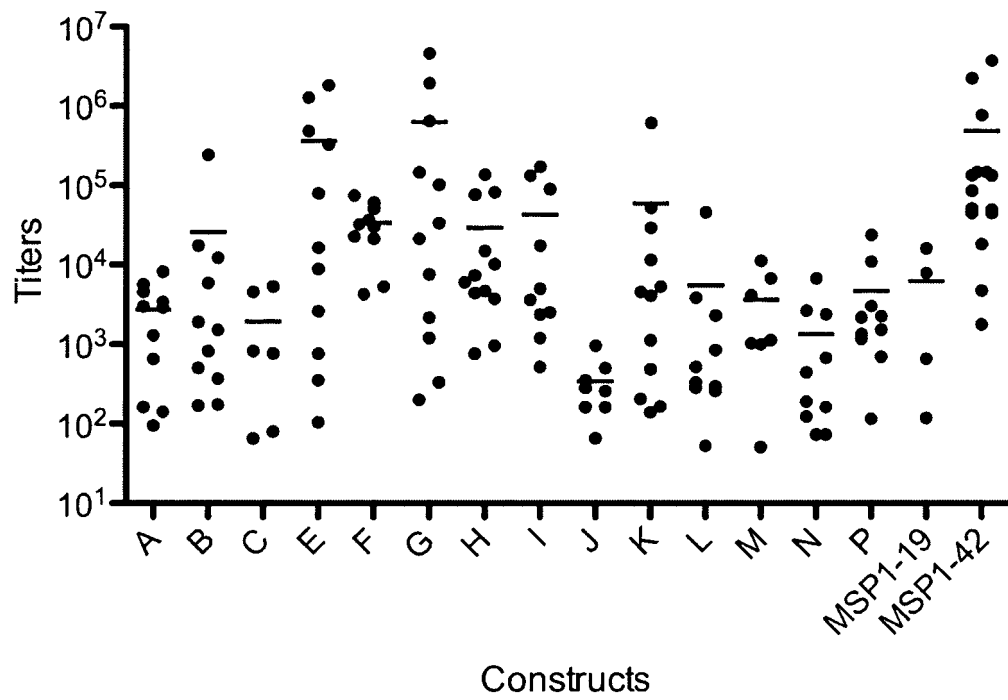


Figure 8. ELISPOT analysis of primed mouse splenocytes from Group 1, 2 and 3 MSP-1 C-terminal constructs.

