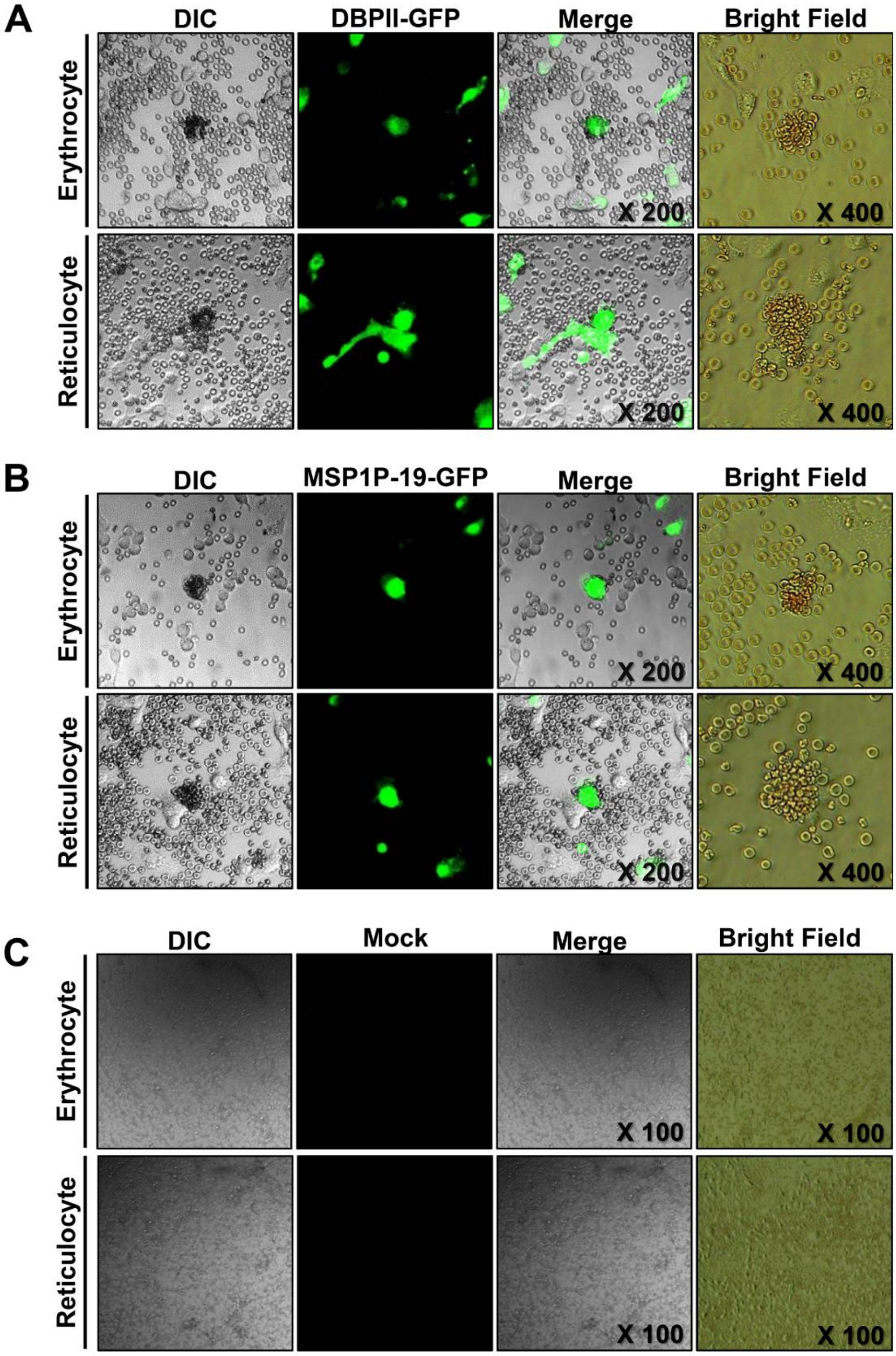

Fig. S1. Binding of PvDBPII and PvMSP1P-19 fragment expressed on COS-7 cells to reticulocyte and erythrocyte. (A) PvDBPII and (B) PvMSP1P-19 transfection efficiency was calculated by counting green fluorescence (GFP) positive cells using confocal microscopy and bright filed shows typical rosette formation under the light microscopy. The erythrocyte fraction (reticulocyte count > 0.5%) and reticulocyte fraction (reticulocyte count >80%) were used for control study. (C) Mock control used for non-specific binding confirmation for erythrocyte and reticulocyte fraction on 100x magnifier.

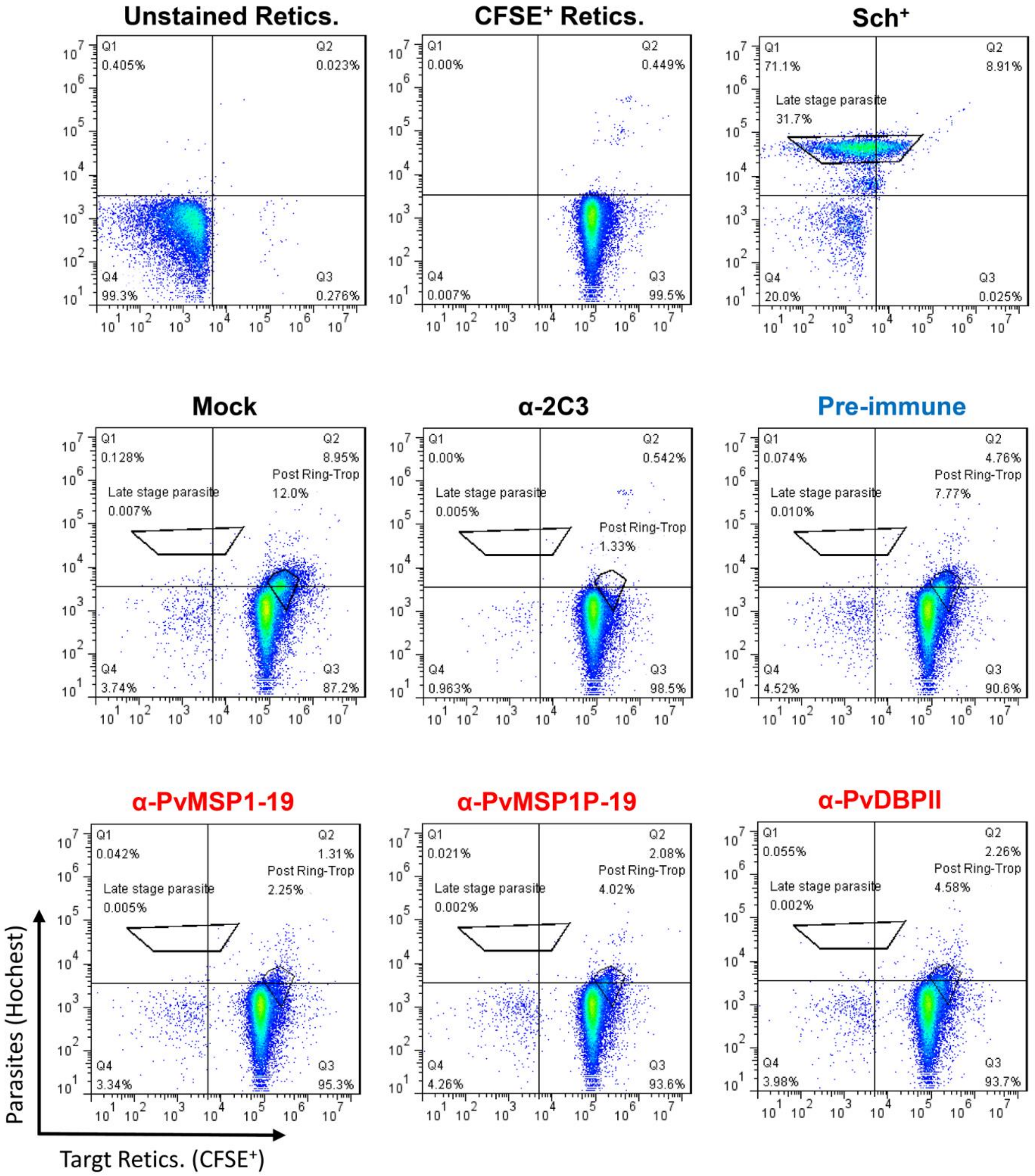

Fig. S2. The gating strategy of *P. vivax* invasion inhibition assay. Before invasion parasitemia shown late stage parasites gate in schizont enrichment panel (Sch+) and after post-invasion parasite shown post ring-trop. gate.

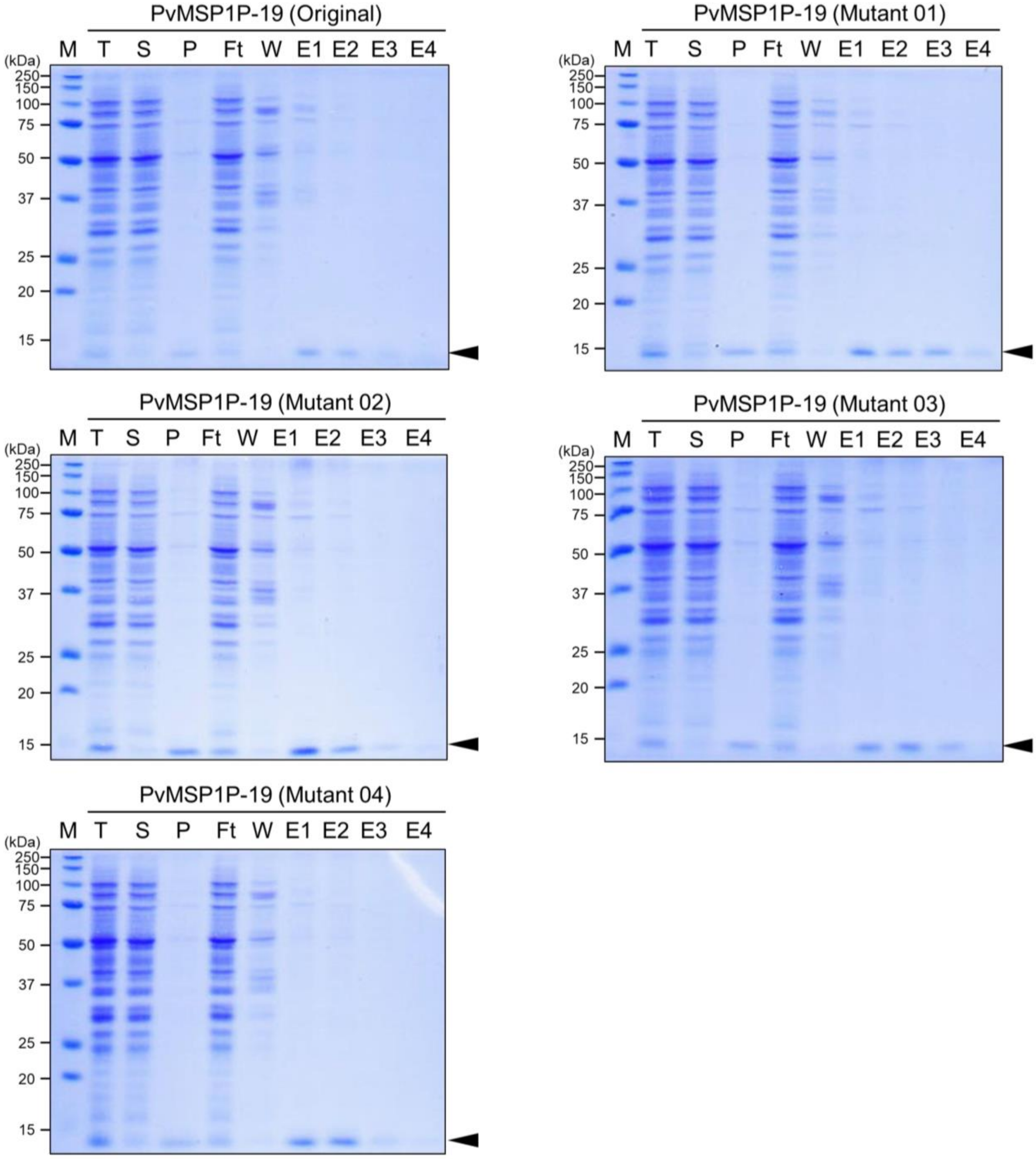

Fig. S3. PvMSP1P-19 and mutant protein expression. Recombinant protein expressed by WGCF and purified by Ni-NTA. The arrowhead indicates the specific bands for the purified PvMSP1P-19 and recombinant mutant proteins. T, total translation mix; S, supernatant; P, pellet; Ft, flow-through; W, wash fraction; E, elution.

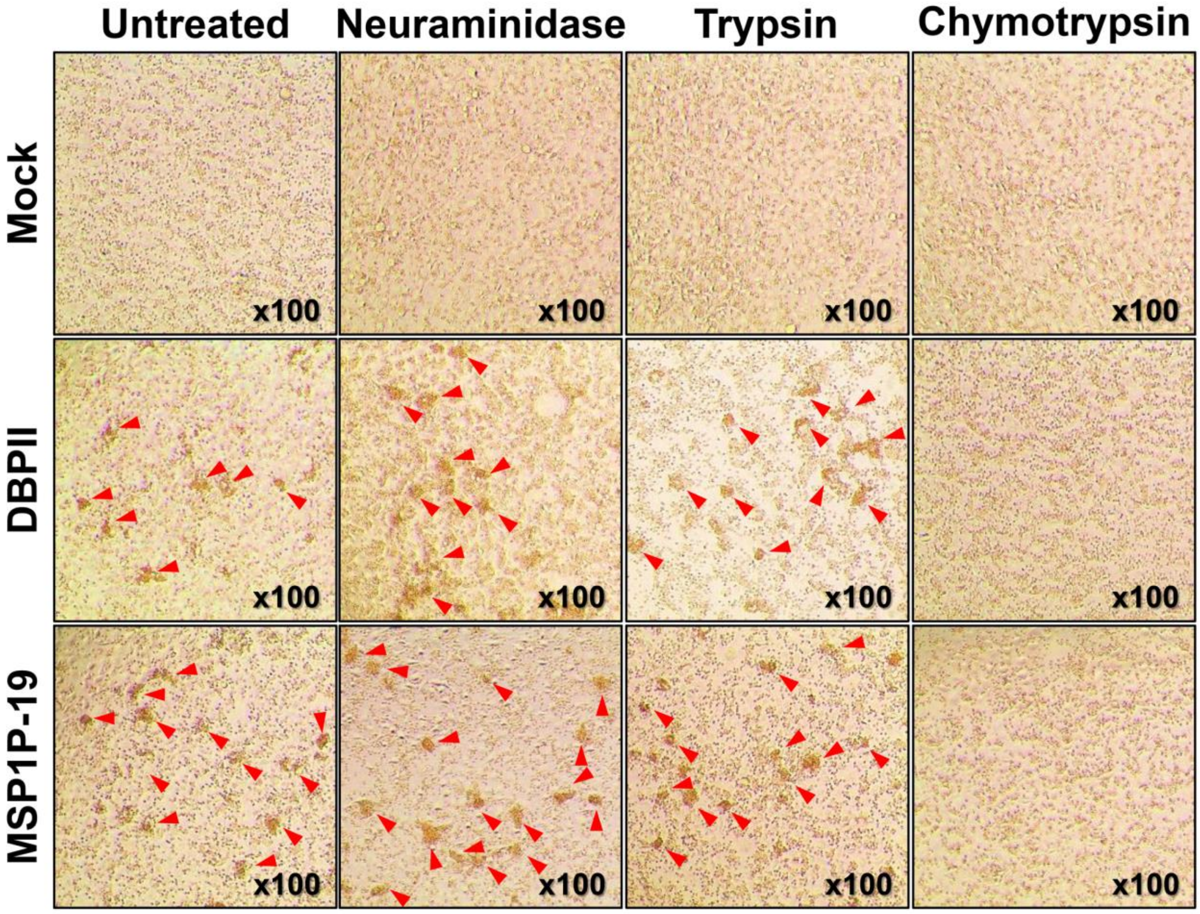

Fig. S4. PvMSP1P-19 and PvDBPII enzyme-treated reticulocyte specificity. The rosette formation shows on PvMSP1P-19 and PvDBPII expressed COS-7 cells with neuraminidase, trypsin treatment reticulocyte. Mock control and chymotrypsin treatment reticulocyte was not found rosette formation. The red arrow head indicates rosette formation under the light microscopy on 100x magnifier.

Table S1. PvMSP1P-19 peptide information

Peptide Name	Peptide Sequence	Peptide position	Length (aa.)
A1746	AAADRVEKNCRNRKCPLN	1746-1763	18
C1755	CRNRKCPLNSFCFIQTIN	1755-1722	18
S1764	SFCFIQTINEECLCLLNY	1764-1781	18
E1773	EECLCLLNYSMVGEKCIL	1773-1790	18
S1782	SMVGEKCILNEQNSCAVK	1782-1799	18
N1791	NEQNSCAVKNGGCDLKAT	1791-1808	18
N1800	NGGCDLKATCELKKNRVN	1800-1817	18
C1809	CELKKNRVNCICPKGTKP	1809-1826	18
C1818	CICPKGTKPMHEGVVCSF	1818-1835	18

aa., amino acid

Table S2. Primer sequences for recombinant PvMSP1P protein expression

Fragment code	**Forward primer (5'→3')**	**Reverse primer (5'→3')**	**Position (aa.)**	**Length (aa.)**	**MW (kDa)**	**pI**	**Features/ Structures**
PvMSP1p-19 (O)	GACCGTGTGGAAAAGAACTGC	GCTGCACACGACCCCCTC	1,749-1,834	86	9.6	8.1	EGF-like domain
PvMSP1p-19 (M1)	AAGCGTGTGaAgAAGAACTGC	GCTGCACACGACCCCCTC	1,749-1,834	86	9.6	8.1	EGF-like mutant 01
PvMSP1p-19 (M2)	GACCGTGTGGAAAAGAACTGC	GCTGCACACGACCCCCTC	1,749-1,834	86	9.6	8.1	EGF-like mutant 02
PvMSP1p-19 (M3)	GACCGTGTGGAAAAGAACTGC	GCTGCACACGACCCCCTC	1,749-1,834	86	9.7	8.1	EGF-like mutant 03
PvMSP1p-19 (M4)	GACCGTGTGaAAAAGAACTGC	GCTGCACACGACCCCCTC	1,749-1,834	86	9.5	8.1	EGF-like mutant 04

aa., amino acid; MW, molecular weight; kDa, kilodalton; pI, isoelectric point.