

Supporting information for : Structural Modifications Controlling Membrane Raft Partitioning and Curvature in Human and Viral Proteins

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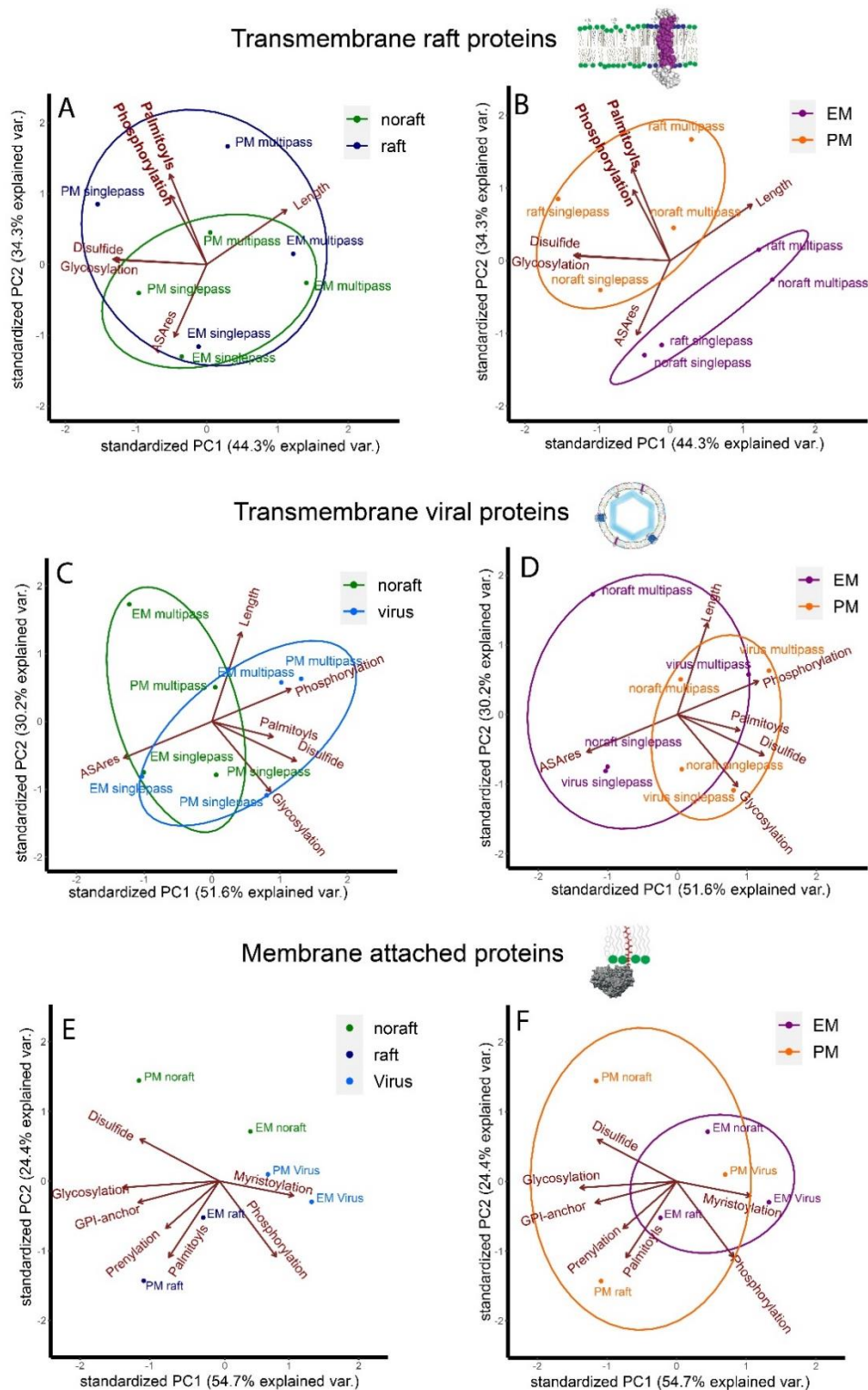


Figure S1 Principal component analysis on the fraction of modified proteins in transmembrane (A,B,C,D) and attached membrane proteins (E,F), in raft versus non-raft (A,B) and virus versus non-raft (C,D) proteins. After PCA, proteins are colored upon protein type in the left column (green=non-raft, dark blue=raft and light blue=viral) or cellular localization in the right column (orange=plasma membrane and purple=endomembranes).

Param1	Param2	Pcoef	pvalue	Significance
Fpalmitoyl	MVS	-0.96	0.0004879	1
Fphosphoryl	MVS	-0.58	0.1682139	0
Fglycosyl	MVS	-0.51	0.2448335	0
Fdisulfide	MVS	-0.86	0.0140998	1
Length	MVS	-0.11	0.8094234	0
ASares	MVS	0.28	0.543704	0
Fphosphoryl	Fpalmitoyl	0.54	0.2111766	0
Fglycosyl	Fpalmitoyl	0.67	0.1016425	0
Fdisulfide	Fpalmitoyl	0.83	0.0207802	1
Length	Fpalmitoyl	-0.09	0.8484208	0
ASares	Fpalmitoyl	-0.26	0.5660989	0
Fglycosyl	Fphosphoryl	0.1	0.8257213	0
Fdisulfide	Fphosphoryl	0.13	0.777667	0
Length	Fphosphoryl	-0.16	0.7250033	0
ASares	Fphosphoryl	-0.47	0.2925557	0
Fdisulfide	Fglycosyl	0.51	0.2437955	0
Length	Fglycosyl	-0.13	0.7833978	0
ASares	Fglycosyl	0.24	0.5979512	0
Length	Fdisulfide	0.17	0.7086394	0
ASares	Fdisulfide	0.06	0.900748	0
ASares	Length	0.18	0.7015171	0

Table S1 Correlation matrix of viral protein modifications corresponding to figure 6A in manuscript