

Supplemental Table S4

Table S4. TWOW-1 Binding of Site-Directed Mutations												
A	B	C	D	E	F	G	H	I	J	K	L	M
mys allele	βPS AA Change	β3 AA	Domain	Relative	WT			Relative	Relative	Relative		
				TWOW-1	vs	No Mn/Mn	No Mn/Mn	No Mn/Mn	PS2 Integrin			
				Binding			Mut				Level	
				Median	S.E.	Z score	p=	Z score	Median	S.E.	Median	S.E.
<b>βPS Long Range disulfide mutant</b>												
	CC(46&505)AA	C13 &C435	PSI	2.18	0.19	11.9	0.000	9.88	2.49	0.21	0.87	0.03
<b>βPS SyMBS Mutants</b>												
	D231>A	D158	SyMBS	-0.07	0.09	-13.4	0.000	-19.21	-1.33	2.67	0.31	0.08
	N283>A	N215	SyMBS	0.08	0.04	-11.7	0.000	-5.80	0.43	0.16	0.28	0.07
<b>βPS ADMIDAS Mutants</b>												
b67	D200N	D127	ADMIDAS	2.15	0.11	11.6	0.000	1.5	1.39	0.04	0.25	0.06
	D200K	D127	ADMIDAS	2.86	0.18	19.6	0.000	5.01	1.85	0.05	0.34	0.05
	D200A	D127	ADMIDAS	1.47	0.16	3.9	0.004	3.02	1.59	0.17	0.37	0.07
	D200S	D127	ADMIDAS	1.23	0.09	1.2	0.214	-1.59	0.99	0.02	0.32	0.02
	D199A*	D126	ADMIDAS	1.55	0.16	4.8	0.002	-1.89	0.95	0.05	0.23	0.03
	D199S*	D126	ADMIDAS	1.65	0.18	5.9	0.000	-0.6	1.07	0.11	0.20	0.05
<b>βPS Deadbolt Mutants</b>												
	delQ758-H762	delD672-K676	β-TD	3.96	1.31	31.8	0.000	5.69	1.94	0.17	0.11	0.02
	R717A	R633A	β-TD	1.28	0.04	1.8	0.275	-2.67	0.84	0.04	0.45	0.11
	delQ758-H762+R717A	delD672-K676+R633A	β-TD	4.2	0.5	34.8	0.000	14.07	2.38	0.19	0.14	0.02
<b>βPS Transmembrane (TM) and Cytoplasmic (Cyto) Mutants</b>												
b1*	G792D	G708	TM	1.44	0.07	3.5	0.001	-0.9	1.08	0.04	0.50	0.06
b70*	S836T, P841T	S752,I757	Cyto	1.02	0.14	-1.1	0.390	0.3	1.24	0.11	0.61	0.23
	D807R**	D723	Cyto	1.28	0.07	1.8	0.375	-0.37	1.09	0.09	0.49	0.09
G1	T825>	T741>	Cyto	0.96	0.12	-1.9	0.503	1.46	1.39	0.07	0.68	0.10
	Trunc	T741>	Cyto	0.96	0.07	-1.9	0.212	-1.10	1.05	0.07	0.44	0.06
<b>αPS2 Cytoplasmic Mutants</b>												
	CGFFNR>CGFFNA**		Cyto	1.24	0.04	1.3	0.178	0.84	1.20	0.05	0.93	0.03
	CGFFNR>CGFANA		Cyto	3.24	0.06	23.8	0.000	12.48	2.83	0.31	0.77	0.09
	CGFFNR>VGFNFR*		Cyto	0.51	0.04	-6.8	0.000	-4.01	0.77	0.05	0.42	0.07

Table S4. TWOW-1 binding of site-directed mutations. Columns and shading is the same as in Table S2. As in Table S2 shading in Column A is according to TWOW-1 binding ability (Column G); red, z scores less than -10; dark pink, z scores between -5 and -10; no fill, z scores between -2.9 and 2.9; light green, z scores between 3 and 5; blue, z scores greater than 10. \* multiple independent cell lines were tested. \*\* cell lines with and without the myc-tag were tested and gave similar results that were combined.