Table S1: Results of fitting HXMS curves for peptides from p66 to eq 2.

Sequence	residue number	n-total	n-bonded	n-slow	k-slow	n-medium	k- medium	n-fast	k-fast
MEKEGKISKIGPENPYNTPVF[¤]	41-61	17	14	-	-	-	-	-	-
WEVQLGIPHPAGLKKKKSVTVL[¤]	88-109	19	10	-	-	-	-	-	-
DVGDAY[¤]	110-115	5	3	-	-	-	-	-	-
SVPLDEDF	117-124	6	4	4	2.20×10^{-5}	1	4.43×10^{-3}	1	2.24×10^{-1}
FRKYTAFTIPSINNETPGIRYQY[¤]	124-146	21	12	-	-	-	-	-	-
NVLPQGWKGSPAIF	147-160	11	7	7	2.06×10^{-5}	2	5.16×10^{-4}	2	6.76×10^{-2}
YMDDL[¥]	183-187	4	2	-	-	-	-	-	-
LYVGSD[¥]	187-192	5	4	-	-	-	-	-	-
LEIGQHRTKIEELRQHL	193-209	16	13	11	9.67×10^{-7}	2	5.64×10^{-4}	3	8.09×10^{-2}
LRWGLTTPDKKHQKEPPFLWMG	210-231	18	11	5	5.60×10^{-5}	5	8.58×10^{-3}	8	9.22
YELHPDKWTVQPIVL[¤]	232-246	13	7	-	-	-	-	-	-
PEKDSWTVND[¤]	247-256	8	4	-	-	-	-	-	-

IQKLVGKLNWASQIYPGIKVRQLCKL	257-282	24	20	13	8.77×10^{-5}	6	1.79×10^{-3}	5	1.06×10^{-1}
LRGTKALTEVIPLTEEAE	283-300	16	9	3	5.35×10^{-6}	6	1.93×10^{-3}	7	4.28×10^{-1}
LELAENREILKEPVHGVYYDPSKDLIAE	301-328	25	20	10	2.64×10^{-5}	7	6.86×10^{-4}	8	2.37×10^{-1}
IQKQGQGQWTYQ[¤]	329-340	11	8	-	-	-	-	-	-
IYQEPFKNLKTGKYARMRGAHTNDVKQLTE[¤]	341-370	28	14	-	-	-	-	-	-
AVQKITTES[¥]	371-379	8	8	-	-	-	-	-	-
IVIWGKTPKFKLPIQKETWETW	380-401	19	15	12	9.74×10^{-6}	3	1.65×10^{-3}	4	1.08×10^{-1}
VNTPPLVKL[¤]	417-425	6	2	-	-	-	-	-	-
WYQLEKEPIVGAET[¤]	426-439	12	2	-	-	-	-	-	-
LTNTTNQKTEL[¤]	469-479	10	6	-	-	-	-	-	-
EVNIVTDSQ[¥]	492-500	8	6	-	-	-	-	-	-
YALGIIQAQPDKSESEL[¤]	501-517	15	12	-	-	-	-	-	-
VNQIIEQLIKKEKVYL	518-533	15	13	0	-	6	2.77×10^{-3}	9	7.39
AWVPAHKGIGGNEQVDKLVSAGIRKIL[¤]	534-560	22	11	-	-	-	-	-	-

[¤] Peptide could be fit to eq 2 but the k-slow was indeterminate. [¥] Peptide could not be fit well to eq 2 due to the peptide rapidly taking up deuterium at early time points

and leveling off.

Table S2: Results of fitting HXMS curves for peptides from p51 to eq 2.

Sequence	residue number	n-total	n-bonded	n-slow	k-slow	n-medium	k-medium	N-fast	k-fast
MEKEGKISKIGPENPYNTPVF	41-61	17	13	11	9.51×10^{-6}	3	1.59×10^{-3}	3	1.88×10^{-1}
WEVQLGIPHPAGLKKKKSVTVL	88-109	19	10	8	5.02×10^{-5}	4	7.15×10^{-3}	7	2.86×10^{-1}
DVGDAY	110-115	5	5	3	9.97×10^{-5}	1	1.41×10^{-3}	1	1.87×10^{-2}
SVPLDEDF¤	117-124	6	3	-	-	-	-	-	-
FRKYTAFTIPSINNETPGIRYQY	124-146	21	16	13	8.31×10^{-6}	3	6.07×10^{-3}	5	3.59×10^{-1}
NVLPQGWKGSPAIF¤	147-160	11	8	-	-	-	-	-	-
YMDDL¤	183-187	4	2	-	-	-	-	-	-
LYVGSD¥	187-192	5	4	-	-	-	-	-	-
LEIGQHRTKIEELRQHL	193-209	16	11	12	1.53×10^{-5}	2	6.99×10^{-3}	2	3.49×10^{-1}
LRWGLTTPDKKHQKEPPFLWMG	210-231	18	5	4	5.05×10^{-5}	3	3.26×10^{-2}	11	2.69×10^{1}
YELHPDKWTVQPIVL	232-246	13	3	1	5.59×10^{-3}	3	4.50×10^{-2}	7	9.20

PEKDSWTVND	247-256	8	5	4	5.27×10^{-5}	2	7.66×10^{-3}	2	4.54×10^{-1}
IQKLVGKLNWASQIYPGIKVRQLCKL	257-282	24	18	7	8.52×10^{-5}	12	1.84×10^{-3}	5	6.01×10^{-2}
LRGTKALTEVIPLTEEAE	283-300	16	8	5	7.80×10^{-5}	4	5.06×10^{-3}	7	4.59×10^{-1}
LELAENREILKEPVHGVYYDPSKDLIAE	301-328	25	17	11	5.60×10^{-5}	6	1.64×10^{-3}	8	1.92×10^{-1}
IQKQGQGQWTYQ	329-340	11	9	6	3.21×10^{-5}	2	1.63×10^{-2}	3	5.63×10^{-1}
IYQEPFKNLKTGKYARMRGAHTNDVKQLTE	341-370	28	19	14	6.32×10^{-5}	8	1.51×10^{-2}	6	3.18×10^{-1}
AVQKITTES[¥]	371-379	8	8	-	-	-	-	-	-
IVIWGKTPKFKLPIQKETWETW	380-401	19	16	13	3.12×10^{-5}	2	5.44×10^{-3}	4	9.05×10^{-2}
VNTPPLVKL	417-425	6	3	1	1.36×10^{-4}	0	-	5	1.36×10^{1}
WYQLEKEPIVGAETF[¤]	426-440	13	1	-	-	-	-	-	-

[¤] Peptide could be fit to eq 2 but the k-slow was indeterminate. [¥] Peptide could not be fit well to eq 2 due to the peptide rapidly taking up deuterium at early time points and leveling off.

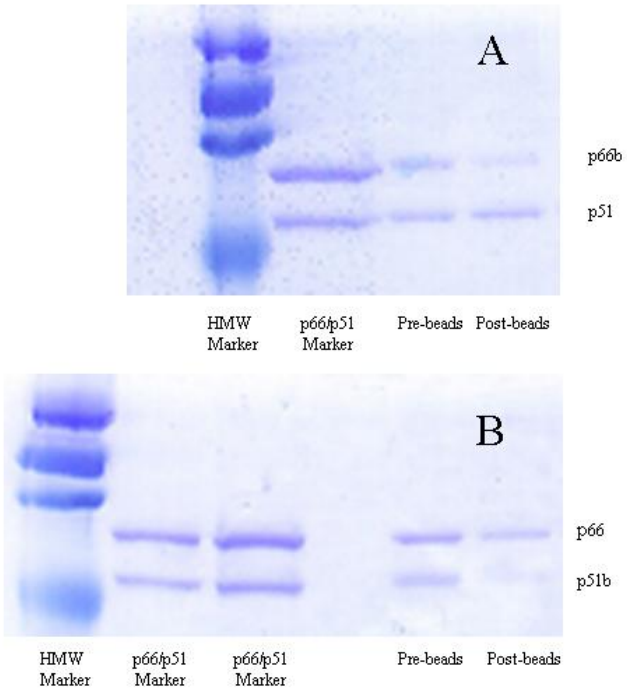

FIGURE S1. Separation of biotin labeled subunit of p66/p51 shown by SDS-PAGE. The labeled subunit was removed using NeutraAvidin beads as described in Experimental Procedures. Gel was scanned using an HP Scanjet and quantitated with UScanIt 5.3 (Silk Scientific, Orem, UT). A small amount of the biotinylated subunit is present after the separation. (A) Separation of labeled p66 from unlabeled p51. The relative intensities of the p66b:p51 bands pre-separation are 55:45, consistent with the mass ratio of 66481/53229 for the His-tagged subunits. The relative intensities of the p66b:p51 bands post separation are 20:80. After correction for mass, the molar ratio of p66b:p51 is 16:84. (B) Separation of labeled p51 from unlabeled p66. The relative intensities of the p66:p51b bands pre-separation are 56:44. The relative intensities of the p66:p51b bands post separation are 88:12. After correction for mass, the molar ratio of p66:p51b is 85:15.