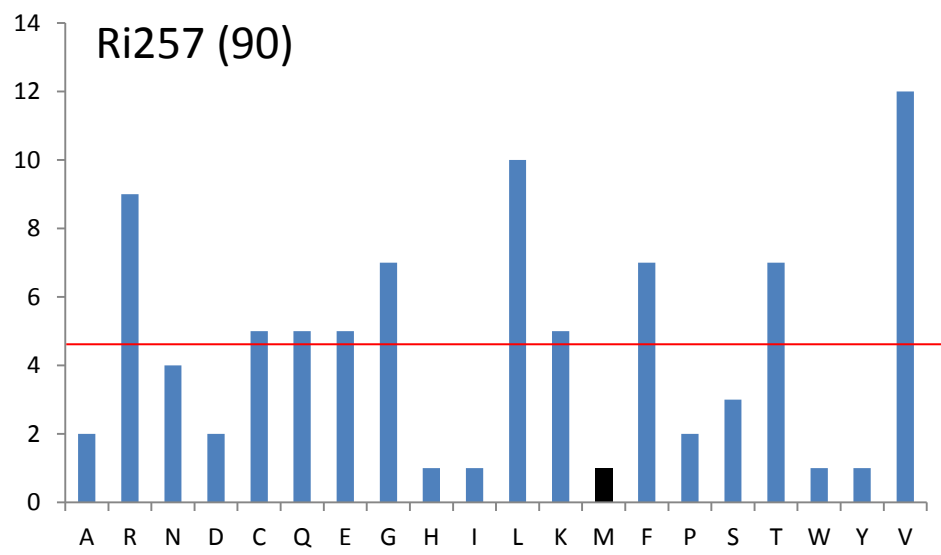
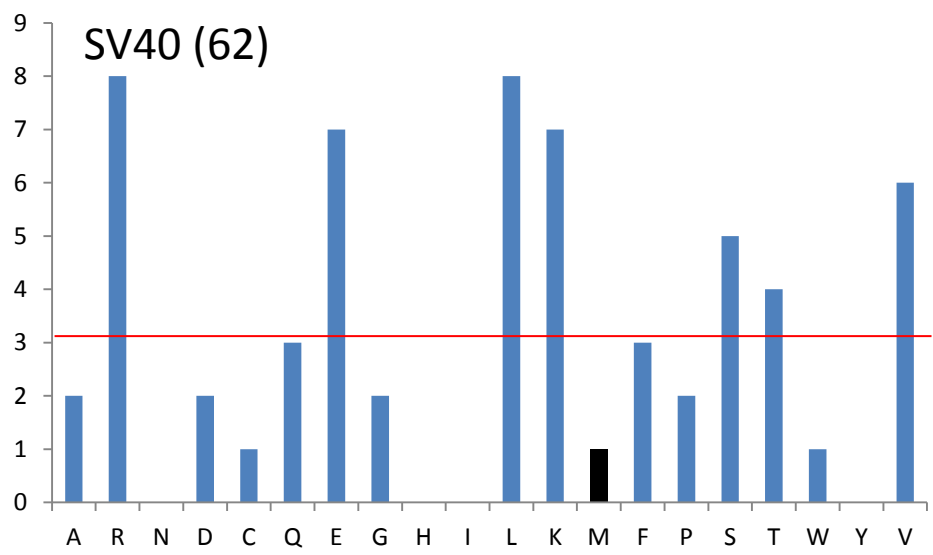
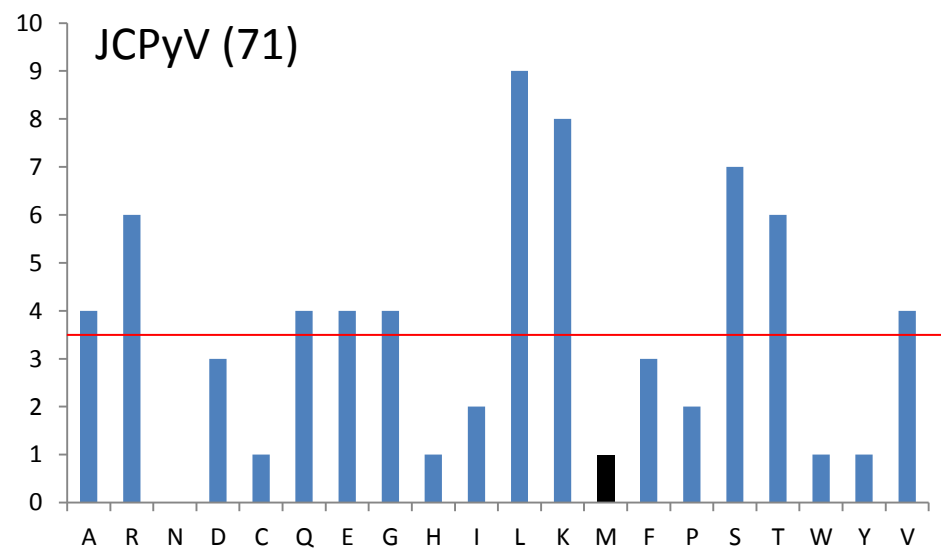
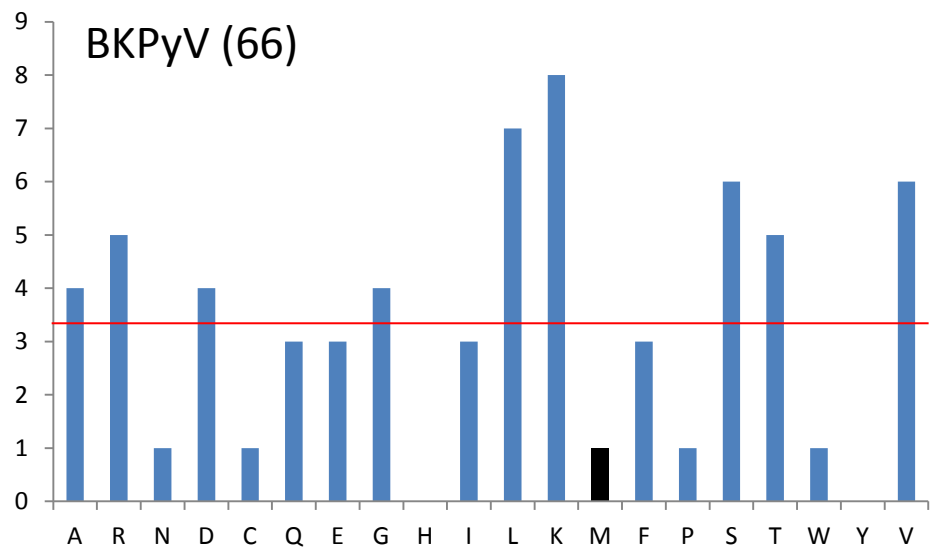


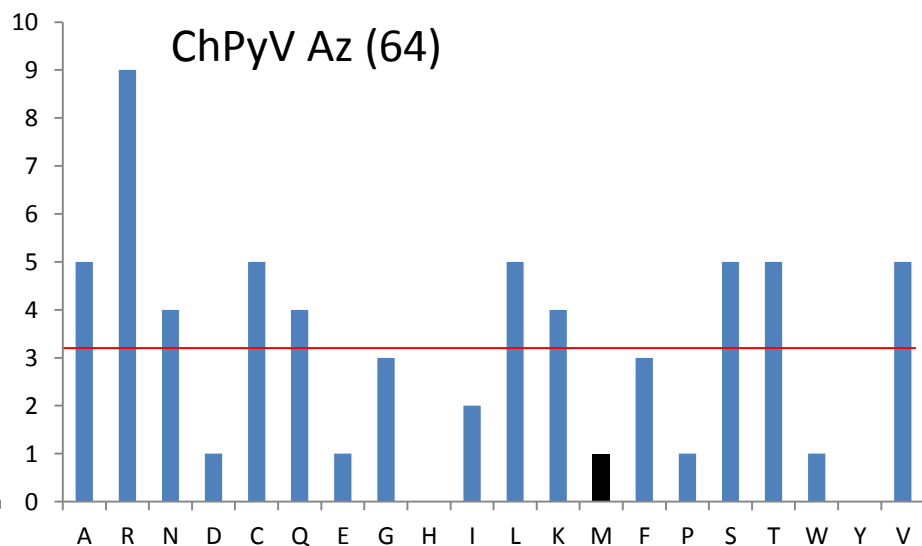
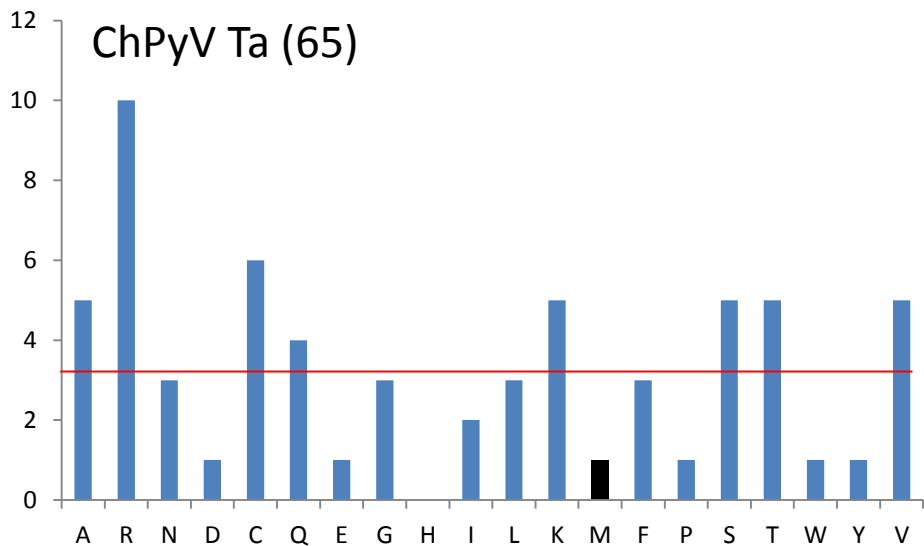
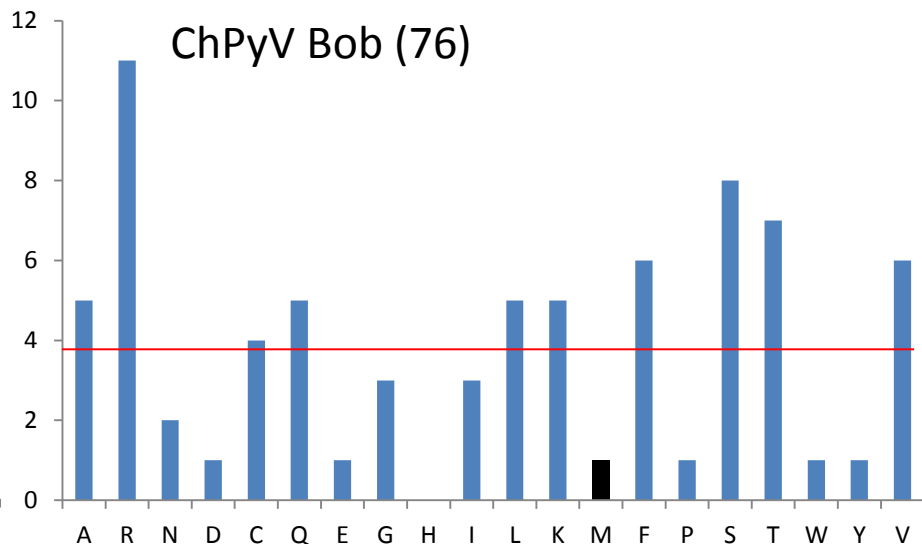
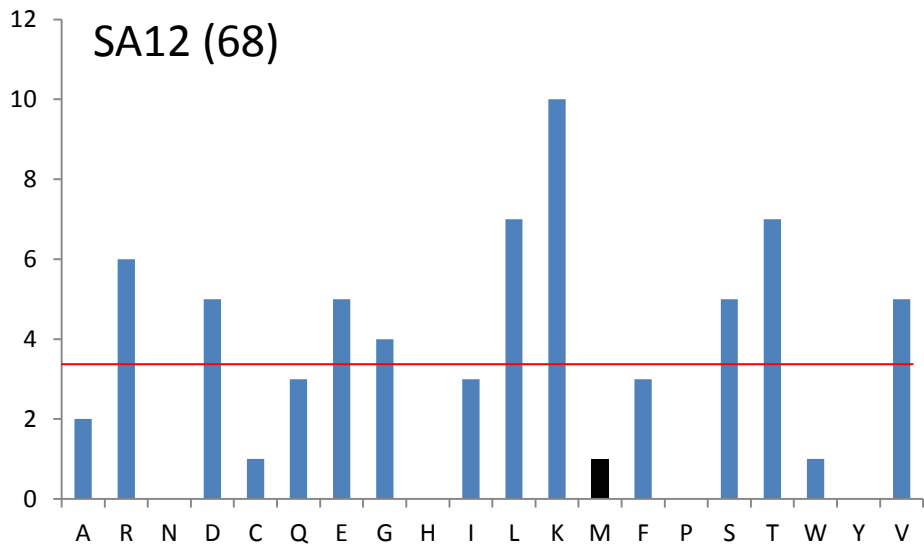
**Figure S1.** Prevalence of amino acids in agnoproteins from polyomaviruses. The number of each residue is represented by a blue bar, except for methionine which is shown in a black bar. The red line represents the theoretical expected frequency of a residue. E.g. BKPyV agnoprotein is 66 amino acids long. Therefore each amino acid is expected on average to occur  $66:20=3.3$  times.

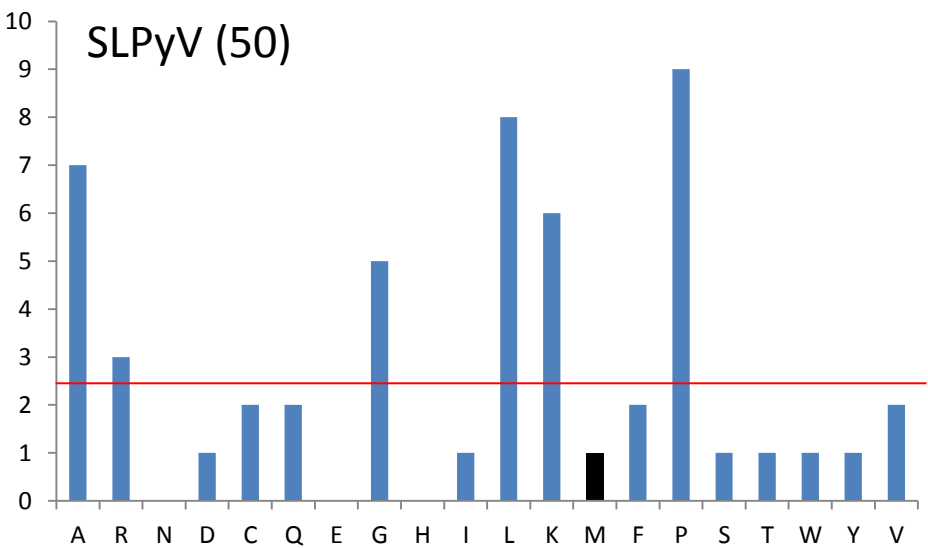
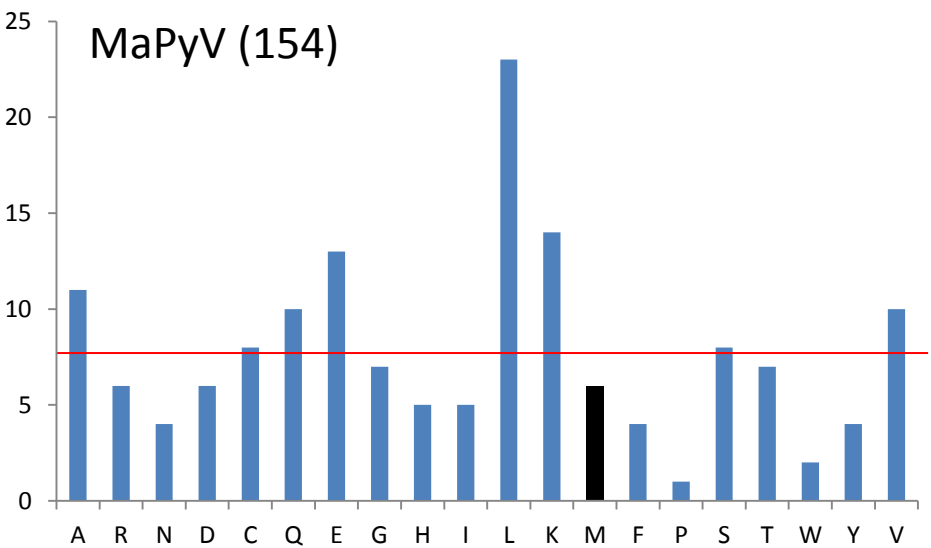
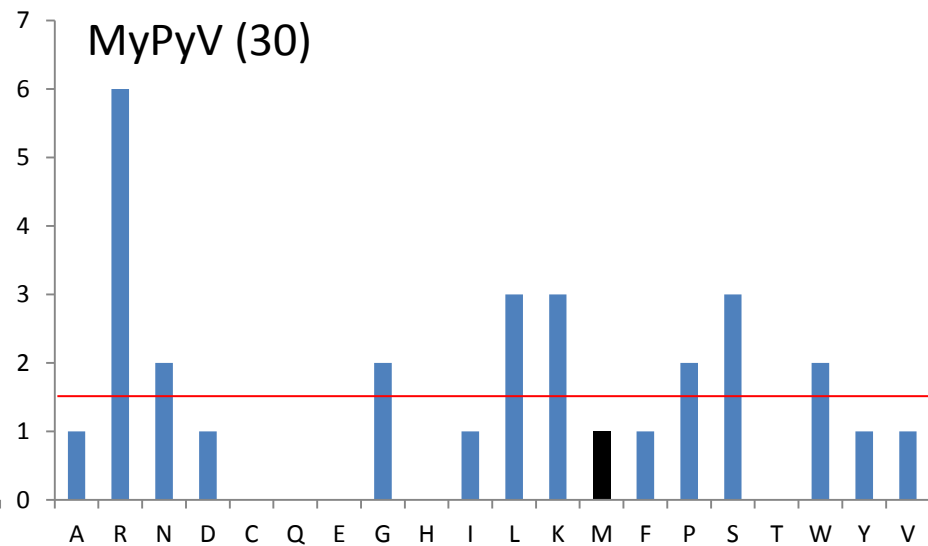
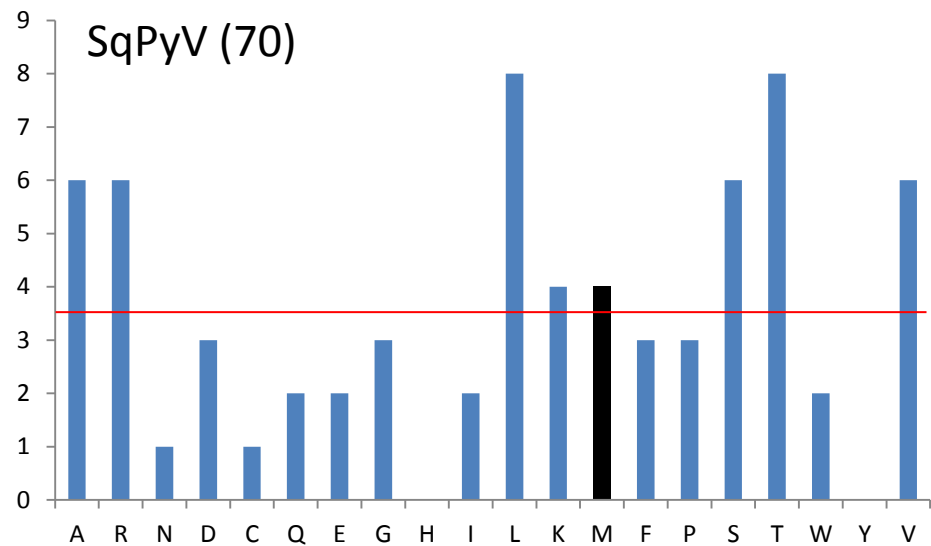
**Figure S2.** Kyte-Doolittle hydropathy plot of agnoproteins from polyomaviruses. The algorithm program <http://gcat.davidson.edu/DGPB/kd/kyte-doolittle.htm> was used.

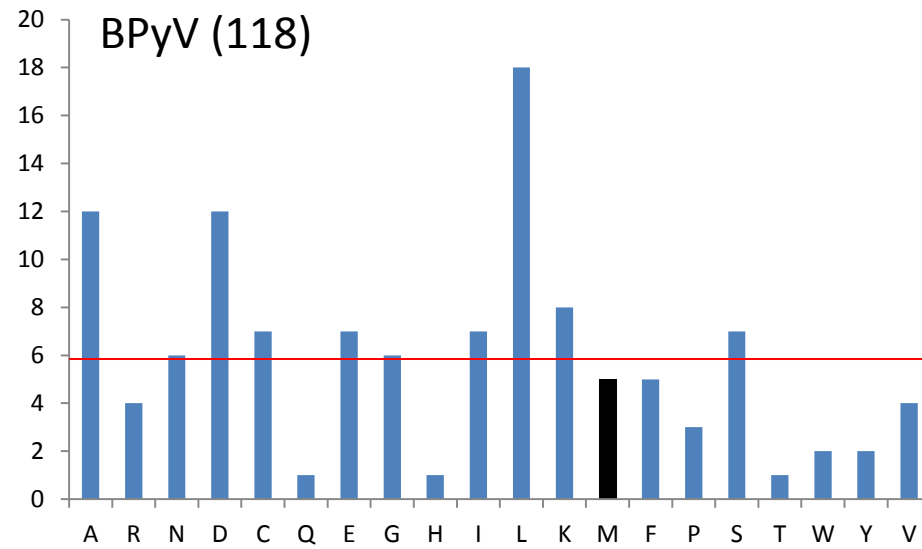
Table S1. Mutations in agnoprotein of PyV isolates. The one-letter amino acid code was used. Reported mutations are based on sequences deposited in the GenBank. Del= deletion.

<b>BKPyV</b>	<b>JCPyV</b>	<b>SV40</b>
R8L, R8Q	L3F, L3del	S21T
Q9H	Q5L	Q26L, Q26R
QASV9-12del	S7L	L28F, L28I
K13R	A10V	K49del
V14I, V14L	S11F	K51G, K51R
G15S	V12M	E54Q
K23R	K13T	K59N
F29L	V14G, V14L	
E38K	K23R	
F39L	L29F, L29I	
E43K	F31I	
EDS43-45del	L32W	
V46I, V46L	L33V	
D47H	D38E, D38G, D38N	
N50I	C40F	
S52G	CTGEDS40-45del	
ALP55-57del	T41E, T41I	
K60R	GE42-43del	
V63I	GEDSVD42-47del	
	E43G, E43K, E43Q	
	EDSV43-46del	
	EDSVD43-47del	
	D44A, D44G	
	S45R	
	V46E	
	D47G, D47H, D47N, D47V	
	Q52K	
	R53K	
	H54N, H54P	
	S55C, S55I, S55R, S55T	
	G56A, G56R	
	LTEQTYSS57-63del	
	E59Q	
	T61K, T61R	
	S63R	
	L65S	
	P68S	
	A70T	
	T71S	









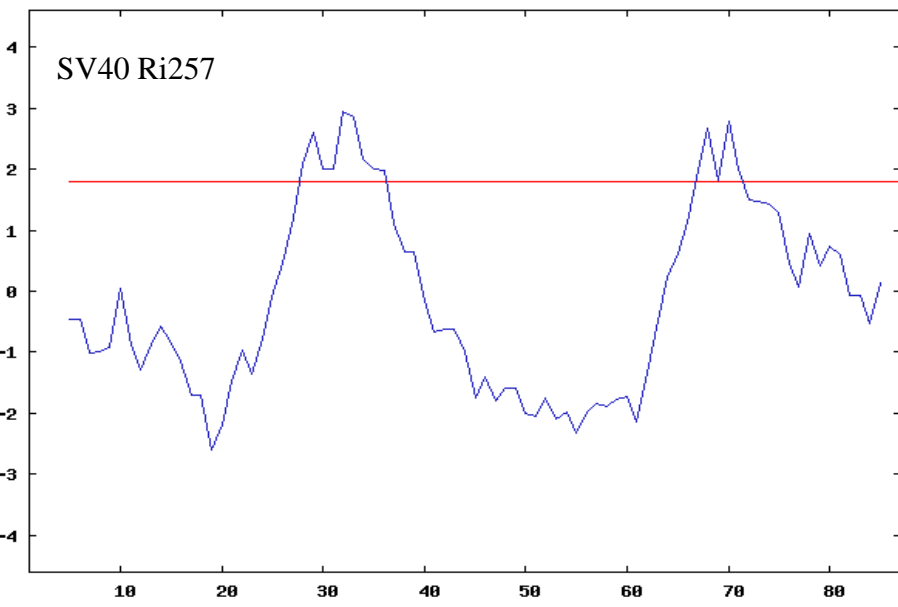
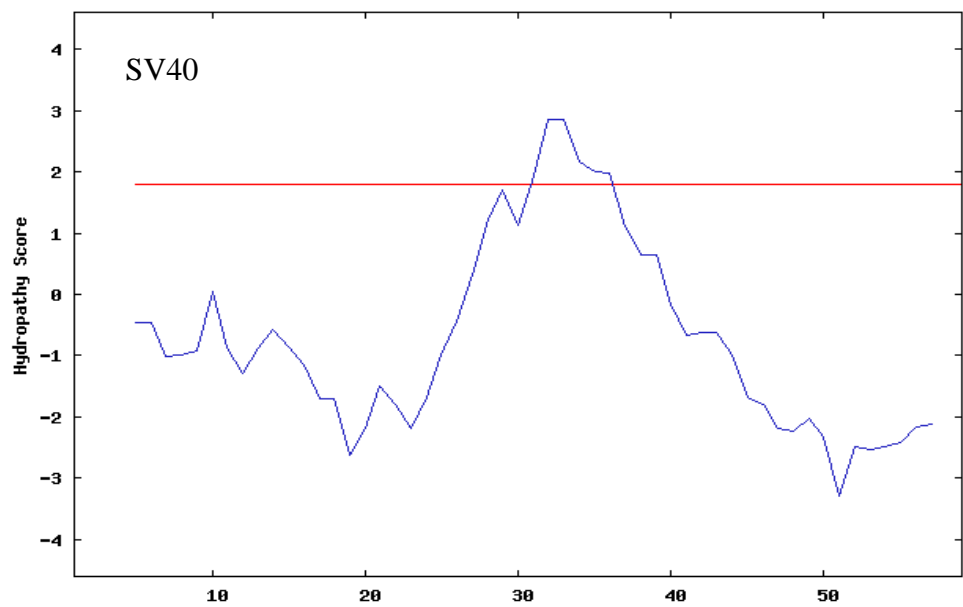
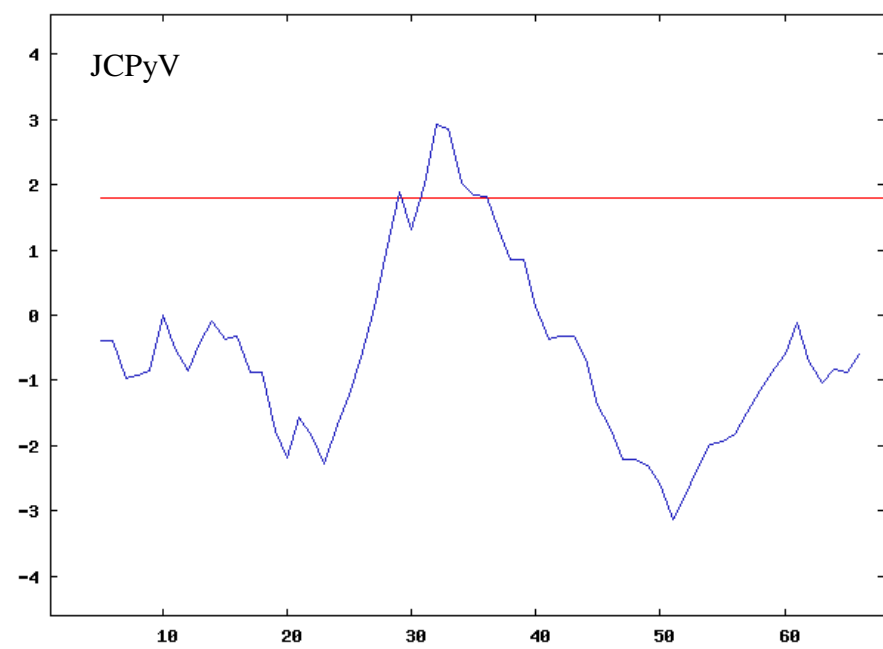
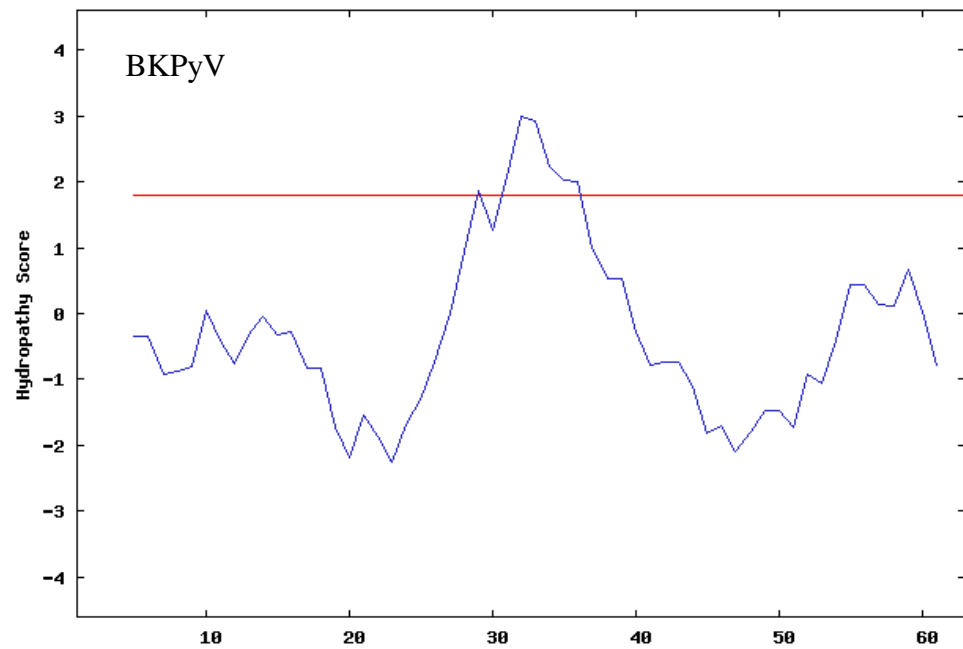


Figure S1

