

Supplementary Figure 1. Amino acid sequence alignment of domain 15 from different species shows the conservation of critical residues. All species show conservation of the cysteine (yellow) residue position as well as three out of the four essential carbohydrate-binding residues (red). The proposed linkage sensing Tyr residue is shown boxed in red. The newly identified critical Arg residue is shaded in cyan. (H.sapiens, NP_000867.2; P.troglodytes, XP_003311618.2; M.mulatta, XP_002804004.1; C.lupus, NP_001116074.1; B.taurus, NP_776777.1; M.musculus, NP_034645.2; R.norvegicus, NP_036888.1; G.gallus, NP_990301.1; D.rerio, NP_001034716.1)

Supplementary Figure 1

B. taurus	VKPQEVQVMNGTITNPANGRSFSLGDIYFKRFSASGDVRTNG-DRIYIEIQLSSITGSSSPACSGASICQRKANDQHF SRKVGTSNQTRY
H. sapiens	VKPQEVQVMNGTITNPINGKSFSLGDIYFKLFRASGDMRTNG-DNYLYEIQLSSITSSRN PACSGANICQVKPNDQHF SRKVGTS DKTKY
P. troglodytes	VKPQEVQVMNGTITNPINGKSFSLGDIYFKLFRASGDMRTNG-DNYLYEIQLSSITSSRN PACSGANICQVKPNDQHF SRKVGTS DKTKY
M. mulatta	VKPQEVQVMNGTITNPINGKSFSLGDIYFKLFRASGDMRTNG-DNYLYEIQLSSITSSRN PACSGANICQVKPDDQHF SRKVGTS DKTKY
C. lupus	VKPQEVQVMNGTITNPINGKSFSLGDIYFKLFSASGDMRTNG-DKYLEIQLSSITSSRN PACSGANICQVKPNDQHF SRKVGTS DKTKY
M. musculus	VRPQEVTMVNGTLTNPVTGKSFSLGEIYFKLFSASGDMRTNG-DNYLYEIQLSSITSSYPACAGANICQVKPNDQHF SRKVGTS DMTKY
R. novegicus	VRPQEVNMVNGTLTNPVTGKSFSLGEIYFKLFSASGDMRSNG-DNYLYEIQLSSISSSN PACSGANICQVKPNDQHF SRKVGTS DMTKY
G. gallus	VKPQEVVNGTIVNPATGKNFSLGDVYKLYMASGDI RTNG-DQYVVEIQLSGITNSSFP ECSEANICQVKTSERRF-RKIGWAKKAKY
D. rerio	VKQEEVEMVNGTIKVPKTGATFSLGALYYRLHNATGDIRANG-DRIYIYHIQLSGITDSSISMCLGANICQVKIN-DSYRRKIGSSSKAKY
X. tropicalis	SIPKPAEMKNGILSLD-DGVNVNLTDIYFKSYNATGDIRSNGKDSYVVEIQLSGKADSRVQECKDASVCQIKLNGD-FKRPGVSVRNVKY

B. taurus	YVQDGDLDVVF TSSSKCGKDKTKSVSSTIFFHCDPLVKDGIPF FSHETADCOYLF SWHTSAVCP LG----AGFDEE IAGDDAQ-E
H. sapiens	YLQDGDLDVVF ASSSKCGKDKTKSVSSTIFFHCDPLVEDGIPF FSHETADCOYLF SWYTSAVCP LG----VGF DSENPGDDGQ-M
P. troglodytes	YLQDGDLDVVF ASSSKCGKDKTKSVSSTIFFHCDPLVEDGIPF FSHETADCOYLF SWYTSAVCP LG----VGF DSENPGDDGQ-M
M. mulatta	YLQDGDLDVVF ASSSKCGKDKTKSVSSTIFFHCDPLVEDGIPF FSHETADCOYLF SWYTSAVCP LG----VGF DNE NP GDDEQ-V
C. lupus	YIQDGDLDVVF ASSSKCGKDKTKSVSSTIFFHCDPLVKDGIPF FSHETADCOYLF SWYTSAVCP LG----VDLGD NAGEDTQ-E
M. musculus	YVQDGDLDVVF TSSSKCGKDKTKSVSSTIFFHCDPLVKDGIPF FSHETADCOYLF SWYTSAVCP LG----VDFEDESAGP----E
R. novegicus	YVQDGDLDVVF TSSSTCGKDKTKSVSSTIFFHCDPLVKDGVPF FSHETADCOYLF SWYTSAVCP LG----VDFDDENAV P----E
G. gallus	YVEDDDL DVIFSSDSRCGDKSKFVSSS IFFHCSPHVQEGIPF FLHETADCOYLF TWYTSAVCP LISTIAPGIHGGQSDQEAQ-V
D. rerio	YIKGGNLDLV PSESVCGRDKTKTVSSAILFHC SPTAGEGIPF FLETTDCOYLF VVHTSTVCEFISS--SSIDSTDGGE----E
X. tropicalis	YINDDDLDAVFTSDSQCGKDKSKNATATILFYCSQIVGEGRPF FPHETTDCOYLF TWYTSAVCP LVPNGNP GSEPNYQGLSGRSQ