

Supplementary Figure S5. Multiple sequence alignment of all TLP proteins. Four levels of conservation are shown. F-box and Tubby domains are marked with grey and black solid lines above sequences, respectively. Blue arrows show the BdTLP protein variants identified in parental lines, orange triangles show the amino acids required for plasma membrane tethering [REFs 11, 12]

[illegible]

CsTLp12	SYEGAKAFS	SRSG	WFGNHR	C	STCLVGE	KYS	RI	E	CCPVLKGTAVD	WCD	G	271
AtTLp7	HNKANPSN	GRAN	WFAHQ	C	WAGN	GH	W	W	ACPSFFPSSSS	AGLSSDCKP	CDVTKIM	276
BdTLp10	SYDGANKLY	SRSG	WFAHQ	C	WAGN	GH	W	W	CCPVGCAASD		S	272
CsTLp10	SYDGANKPSR	SRSG	WFAHQ	C	WAGN	GH	W	W	CCPVGCTASD		L	270
SbTLp10	SYDGANKPSR	SRSG	WFAHQ	C	WAGN	GH	W	W	CCPVGCTNSC		L	270
SbTLp11	SYDGAKASS	TRSL	WFGNHR	C	WAGN	GH	W	W	ECPSVGETWEN	S	L	249
CsTLp11	SYDGAKTSS	TRSG	WFGSTH	C	WAGN	GH	W	W	ECPSGETWEN	S	L	249
SbTLp9	SYDGAKASS	SRSG	WFGNHR	C	WAGN	GH	W	W	ECPSGETWEN	S	L	249
BdTLp9	SYDGAKASS	SRSG	WFGNHR	C	WAGN	GH	W	W	ECPSGETWEN	S	L	249
CsTLp9	SYDGAKASS	SRSG	WFGNHR	C	WAGN	GH	W	W	ECPSGETWEN	S	L	249
AtTLp9	CTGAAG	MCKE	SENFI	C	WAGN	GH	W	W	ECPSGETWEN	C	L	253
AtTLp11	LF-STGAAY	LFKE	SINPAF	A	WAGN	GH	W	W	LTITMIVESPVVASTSISFS	SRSG	PVFRSHSKD	276
SbTLp7	CTGAAYVSK	GFSAH	MLGAQ	A	WAGN	GH	W	W	LTITMIVESPVVASTSISFS	SRSG	PVFRSHSKD	276
AtTLp3	TNPGQVTS	TRSG	LLSLQ	A	WAGN	GH	W	W	LTITMIVESPVVASTSISFS	SRSG	PVFRSHSKD	276
BdTLp7	SHSGAVVSK			A	WAGN	GH	W	W	LTITMIVESPVVASTSISFS	SRSG	PVFRSHSKD	276
CsTLp7	SYAGCVISK	CGSA	VIGENR	A	WAGN	GH	W	W	LTITMIVESPVVASTSISFS	SRSG	PVFRSHSKD	276
BdTLp14	SYGAVVSK	SRSA	VIGENR	A	WAGN	GH	W	W	LTITMIVESPVVASTSISFS	SRSG	PVFRSHSKD	276
CsTLp14	SYGAVVSK	SRSA	VIGENR	A	WAGN	GH	W	W	LTITMIVESPVVASTSISFS	SRSG	PVFRSHSKD	276
SbTLp14	SYGAVVSK	SRSA	VIGENR	A	WAGN	GH	W	W	LTITMIVESPVVASTSISFS	SRSG	PVFRSHSKD	276
SbTLp6	SYNATSPVT	AGTNK	WYKGR	A	WAGN	GH	W	W	LTITMIVESPVVASTSISFS	SRSG	PVFRSHSKD	276
BdTLp6	SYNSTSVEN	SGKPC	WYKGR	A	WAGN	GH	W	W	LTITMIVESPVVASTSISFS	SRSG	PVFRSHSKD	276
CsTLp6	SYNATSDSC	SGKTC	WYKGR	A	WAGN	GH	W	W	LTITMIVESPVVASTSISFS	SRSG	PVFRSHSKD	276
SbTLp4	SCNT	SC	PGKTS	A	WAGN	GH	W	W	LTITMIVESPVVASTSISFS	SRSG	PVFRSHSKD	276
BdTLp4	SCNIPSVSC	PGKTS	WYKGR	A	WAGN	GH	W	W	LTITMIVESPVVASTSISFS	SRSG	PVFRSHSKD	276
CsTLp4	SCNTANVSQ	SGKTC	WYKGR	A	WAGN	GH	W	W	LTITMIVESPVVASTSISFS	SRSG	PVFRSHSKD	276
AtTLp5	AYNSQILS	PVFNK	WYKGR	A	WAGN	GH	W	W	LTITMIVESPVVASTSISFS	SRSG	PVFRSHSKD	276
BdTLp2	SHNAGSLLS	CERG	WYKGR	A	WAGN	GH	W	W	LTITMIVESPVVASTSISFS	SRSG	PVFRSHSKD	276
BdTLp2	SYNAGSLVS	CGRA	WYKGR	A	WAGN	GH	W	W	LTITMIVESPVVASTSISFS	SRSG	PVFRSHSKD	276
CsTLp2	SYNAGSLMS	CGMG	WYKGR	A	WAGN	GH	W	W	LTITMIVESPVVASTSISFS	SRSG	PVFRSHSKD	276
SbTLp3	SYNAGKLCA	CEBAP	WYKGR	A	WAGN	GH	W	W	LTITMIVESPVVASTSISFS	SRSG	PVFRSHSKD	276
BdTLp3	SYNAGKLCS	CERA	WYKGR	A	WAGN	GH	W	W	LTITMIVESPVVASTSISFS	SRSG	PVFRSHSKD	276
CsTLp3	SYNARTLCS	CERT	WYKGR	A	WAGN	GH	W	W	LTITMIVESPVVASTSISFS	SRSG	PVFRSHSKD	276
AtTLp1	AYNSNIARAV	PGVGL	WYKGR	A	WAGN	GH	W	W	LTITMIVESPVVASTSISFS	SRSG	PVFRSHSKD	276
AtTLp10	SPNTSSALIT	TRTSR	WYKGR	A	WAGN	GH	W	W	LTITMIVESPVVASTSISFS	SRSG	PVFRSHSKD	276
SbTLp1	SYNGAVVPP	AGTNS	WYKGR	A	WAGN	GH	W	W	LTITMIVESPVVASTSISFS	SRSG	PVFRSHSKD	276
BdTLp1	SHDGAVVPP	VGRSS	WYKGR	A	WAGN	GH	W	W	LTITMIVESPVVASTSISFS	SRSG	PVFRSHSKD	276
CsTLp1	SYNGAVVPP	VGRSS	WYKGR	A	WAGN	GH	W	W	LTITMIVESPVVASTSISFS	SRSG	PVFRSHSKD	276
BdTLp5	SYNGAVVPP	VGRSS	WYKGR	A	WAGN							

OsTLP12 : ---KRLSNSIPSSVILNNAPRWHECLOCWLNFRGR---MVASVKNFQLIIVPEFG-----EPS---DKNVILQFGKIGDIPTMDYRPLSAFCAFAICLSSITKLACE : 368
 AtTLP7 : ---KKPNKDGSSLTILNNAPRWHECLOCWLNFRGR---TVASVKNFQLIVTVDQS-----QPSGKGDEETVILQFGKVGDIPTMDYRPLSAFCAFAICLSSITKLACE : 379
 BdTLP10 : ---KEKFGSTSSSLNNAPRWHECLOCWLNFRGR---TVASVKNFQLIVPAGTS-----NFWGVGDEETVILQFGKIEDIPTMDYRPLSAFCAFAICLSSITKLACE : 375
 OsTLP10 : ---KKLI-STSSPILANNAPRWHECLOCWLNFRGR---TVASVKNFQLIVPAGTS-----DPWGIADENIVILQFGKIEDIPTMDYRPLSAFCAFAICLSSITKLACE : 372
 SbTLP10 : ---KEKT-PSSSSILNNAPRWHECLOCWLNFRGR---TVASVKNFQLIVTAGSG-----GFWGVGDEETVILQFGKIEDIPTMDYRPLSAFCAFAICLSSITKLACE : 372
 SbTLP11 : ---KVMSFRQGTILNNAPRWHECLOCWLNFRGR---TVASVKNFQLIVTTDTS-----HPDSVDD-ABVILQFGKVGDIPTMDYRPLSAFCAFAICLSSITKLACE : 351
 OsTLP11 : ---KTKSLRCTGTVLNNAPRWHECLOCWLNFRGR---TVASVKNFQLIVTADPS-----HPDSVGDEETVILQFGKVGDSIPTMDYRPLSAFCAFAICLSSITKLACE : 352
 SbTLP9 : ---KTKFRRPLGTVLNNAPRWHECLOCWLNFRGR---TVASVKNFQLIVAADPS-----DPTSSVDDIVILQFGKVGDIPTMDYRPLSAFCAFAICLSSITKLACE : 360
 BdTLP9 : ---KSKFKPMGTIVLNNAPRWHECLOCWLNFRGR---TVASVKNFQLIVAADPN-----DPTGSRDEETVILQFGKVGDIPTMDYRPLSAFCAFAICLSSITKLACE : 360
 OsTLP9 : ---KTKFKRPTGTVLNNAPRWHECLOCWLNFRGR---TVASVKNFQLIVAADPN-----DPASSKDEETVILQFGKVGDIPTMDYRPLSAFCAFAICLSSITKLACE : 356
 AtTLP9 : ASCSDSGNNLGDPEVILNNAPRWHECLOCWLNFRGR---TVASVKNFQLIVSD-CE-----AGQTSERVILQFGKVGDIPTMDYRPLSAFCAFAICLSSITKLACE : 380
 AtTLP11 : ---SSHKETIVLNNAPRWHECLOCWLNFRGR---TVASVKNFQLIVAGASCGSGTGM-----SPERQSERVILQFGKVGDIPTMDYRPLSAFCAFAICLSSITKLACE : 389
 SbTLP7 : SGVC--LATCNEARKVILNNAPRWHECLOCWLNFRGR---TVASVKNFQLIVSGESDL-----NNQGGDDVILQFGKVGDIPTMDYRPLSAFCAFAICLSSITKLACE : 399
 AtTLP3 : LPSGSPSSAACREGVILNNAPRWHECLOCWLNFRGR---TVASVKNFQLIVAPENG------AGFENEDVILQFGKVGDIPTMDYRPLSAFCAFAICLSSITKLACE : 407
 BdTLP7 : STTC--LSTCEESVILNNAPRWHECLOCWLNFRGR---TVASVKNFQLIVPDESAP-----TNHLEDATVILQFGKIGDIPTMDYRPLSAFCAFAICLSSITKLACE : 382
 OsTLP7 : STAS--LITCNGSHVILNNAPRWHECLOCWLNFRGR---TVASVKNFQLIVSDENF-----TNCEHDDVILQFGKVGDIPTMDYRPLSAFCAFAICLSSITKLACE : 406
 BdTLP14 : TASQ--LPTCMEERVILNNAPRWHECLOCWLNFRGR---TVASVKNFQLIVSDNGP-----ANCEHDRVILQFGKIGDIPTMDYRPLSAFCAFAICLSSITKLACE : 404
 OsTLP14 : ATSC--LSTCEESVILNNAPRWHECLOCWLNFRGR---TVASVKNFQLIVSDNGP-----TNCEQDQVILQFGKIGDIPTMDYRPLSAFCAFAICLSSITKLACE : 403
 SbTLP14 : STSC--SS--RSDRVILNNAPRWHECLOCWLNFRGR---TVASVKNFQLIVSDNGP-----GNCDNNRVILQFGKIGDIPTMDYRPLSAFCAFAICLSSITKLACE : 399
 SbTLP6 : ALSNADDEESTDTIVLNNAPRWHECLOCWLNFRGR---TVASVKNFQLIVAVNTQPAVGAPTPSQAAPLPAP-----APGPPPLDQGVILQFGKVGDIPTMDYRPLSAFCAFAICLSSITKLACE : 456
 BdTLP6 : SLS--DEDQCKDVILNNAPRWHECLOCWLNFRGR---TVASVKNFQLIVAA-ALPAAGALTPPHF-----AE-----PAPPPPPPHENDVILQFGKVGDIPTMDYRPLSAFCAFAICLSSITKLACE : 445
 OsTLP6 : VLS--DDEECKETVILNNAPRWHECLOCWLNFRGR---TVASVKNFQLIVAT-CPAAGAPT--PS-----Q-----PVPPPPPHENDVILQFGKVGDIPTMDYRPLSAFCAFAICLSSITKLACE : 440
 SbTLP4 : ALG--DNDECKDRVILNNAPRWHECLOCWLNFRGR---TVASVKNFQLIVAT-CPAAGAPT--LS-----SC-----ATPVPPPHENDVILQFGKVGDIPTMDYRPLSAFCAFAICLSSITKLACE : 437
 BdTLP4 : TLG--DNNESEKRVILNNAPRWHECLOCWLNFRGR---TVASVKNFQLIVAT-CPAAGAPT--PS-----Q-----PAPTPPSEHNDVILQFGKVGDIPTMDYRPLSAFCAFAICLSSITKLACE : 439
 OsTLP4 : ALG--DSESEKRVILNNAPRWHECLOCWLNFRGR---TVASVKNFQLIVAT-CPAAGAPT--PS-----Q-----PAPPPPPPHNDVILQFGKVGDIPTMDYRPLSAFCAFAICLSSITKLACE : 445
 AtTLP5 : --TRPKEEGKVRVILNNAPRWHECLOCWLNFRGR---TVASVKNFQLIVSAATVQCPGSGSDGALATRPDSLSPQ-----QP-----EQSNHDRVILQFGKVGDIPTMDYRPLSAFCAFAICLSSITKLACE : 429
 SbTLP2 : ---SGCAKERVILNNAPRWHECLOCWLNFRGR---TVASVKNFQLIVAPCLDSESSQ-----CACCQACQPSNSSSVLDHDRVILQFGKVGDIPTMDYRPLSAFCAFAICLSSITKLACE : 448
 BdTLP2 : ---D--GEAKEVILNNAPRWHECLOCWLNFRGR---TVASVKNFQLIVSALQPSVASSES-----SQPPCCQCTQPSSSSSSTSDHDRVILQFGKVGDIPTMDYRPLSAFCAFAICLSSITKLACE : 447
 OsTLP2 : ---DDIPEAKERVILNNAPRWHECLOCWLNFRGR---TVASVKNFQLIVAASSSS--CL-----ECQCCQCCQCNHASSSSASDHGVILQFGKVGDIPTMDYRPLSAFCAFAICLSSITKLACE : 451
 SbTLP3 : ---GSDDSEKERVILNNAPRWHECLOCWLNFRGR---TVASVKNFQLIVSSVQCPAPVGVSSAPPLAVTPPTCTQCPQASGPSSASSSHVHDRVILQFGKVGDIPTMDYRPLSAFCAFAICLSSITKLACE : 453
 BdTLP3 : ---DGDAAADKETVILNNAPRWHECLOCWLNFRGR---TVASVKNFQLIVGAPLPAFVASSEFSGCPAPA-----CQPAQCPQPSSSSSSSSHDTVILQFGKVGDIPTMDYRPLSAFCAFAICLSSITKLACE : 455
 OsTLP3 : ---CEQDGDVNVKERVILNNAPRWHECLOCWLNFRGR---TVASVKNFQLIVAAPQPSGGAASEPSCAGCAACQCTQCPQPSSSSSSSSHDTVILQFGKVGDIPTMDYRPLSAFCAFAICLSSITKLACE : 462
 AtTLP1 : ---VVLEEGKERNPPVILNNAPRWHECLOCWLNFRGR---TVASVKNFQLIVANGCPQCPQCPQ-----PQCPPLT--QPQPSGGCTGDPDRVILQFGKVGDIPTMDYRPLSAFCAFAICLSSITKLACE : 455
 AtTLP10 : ---CDDNEEASFRVILNNAPRWHECLOCWLNFRGR---TVASVKNFQLIVARCPQCPQGTGA-----A-AAPTS--APA-----HPEQDQVILQFGKVGDIPTMDYRPLSAFCAFAICLSSITKLACE : 445
 SbTLP1 : ---IAGDEEGCNKERVILNNAPRWHECLOCWLNFRGR---TVASVKNFQLIVAPSPAPAPAPAR-----A-PTPS--QPV-----PQCDQVILQFGKVGDIPTMDYRPLSAFCAFAICLSSITKLACE : 450
 BdTLP1 : ---INSDEEGCNKERVILNNAPRWHECLOCWLNFRGR---TVASVKNFQLIVAPLQPPAGA-----PT-PS--QPA-----PPEQDQVILQFGKVGDIPTMDYRPLSAFCAFAICLSSITKLACE : 445
 OsTLP1 : ---INGDEEGCNKERVILNNAPRWHECLOCWLNFRGR---TVASVKNFQLIVAPAQPPAGA-----PT-PS--QPA-----PPEQDQVILQFGKVGDIPTMDYRPLSAFCAFAICLSSITKLACE : 445
 BdTLP5 : ---VDGDDGEVVDKRVILNNAPRWHECLOCWLNFRGR---TVASVKNFQLIVASNPFPAGA-----PT-PS--QPG-----PVDPDQVILQFGKVGDIPTMDYRPLSAFCAFAICLSSITKLACE : 448
 OsTLP5 : ---MGGDNGEIKERVILNNAPRWHECLOCWLNFRGR---TVASVKNFQLIVAPSPPPAGA-----PT-PS--QPG-----PADPEKIVILQFGKVGDIPTMDYRPLSAFCAFAICLSSITKLACE : 448
 SbTLP5 : RLDNDEESETKERVILNNAPRWHECLOCWLNFRGR---TVASVKNFQLIVATTPPPAGA-----PT-PS--QPA-----PSPDPQVILQFGKVGDIPTMDYRPLSAFCAFAICLSSITKLACE : 480
 AtTLP6 : ---GGESVIEKIVILNNAPRWHECLOCWLNFRGR---TVASVKNFQLIVAAAAEA-----GRNMNIFEEQDQVILQFGKIGDIPTMDYRPLSAFCAFAICLSSITKLACE : 413
 AtTLP2 : ---SPSLRDCQVILNNAPRWHECLOCWLNFRGR---TVASVKNFQLIVAEI-----DASLDAPPEEHERVILQFGKIGDIPTMDYRPLSAFCAFAICLSSITKLACE : 394
 SbTLP8 : ---LSGLALACANETVILNNAPRWHECLOCWLNFRGR---TVASVKNFQLIVSV-----DPSLNPAAECQVILQFGKIGDIPTMDYRPLSAFCAFAICLSSITKLACE : 433
 BdTLP8 : ---LSGC--ICTSEAPVILNNAPRWHECLOCWLNFRGR---TVASVKNFQLIVSV-----DPSLGVPAACEQVILQFGKIGDIPTMDYRPLSAFCAFAICLSSITKLACE : 428
 OsTLP8 : ---LSGP--VCTNEVPVILNNAPRWHECLOCWLNFRGR---TVASVKNFQLIVSV-----DPSLGPAAECQVILQFGKIGDIPTMDYRPLSAFCAFAICLSSITKLACE : 428
 AtTLP8 : ---PLDWLENKEIKVILNNAPRWHECLOCWLNFRGR---TVASVKNFQLIVTET-----PRGTILQGRVILQFGKIGDIPTMDYRPLSAFCAFAICLSSITKLACE : 397
 OsTLP13 : ---PKDQEKKIKADQCS--SPPNNMTKRPVILNNAPRWHECLOCWLNFRGR---TVASVKNFQLIVTET-----GRGTILQGRVILQFGKIGDIPTMDYRPLSAFCAFAICLSSITKLACE : 419
 BdTLP13 : ---PKDWEKASRADQCS--SPPNNMTKRPVILNNAPRWHECLOCWLNFRGR---TVASVKNFQLIVTET-----GRGTILQGRVILQFGKIGDIPTMDYRPLSAFCAFAICLSSITKLACE : 394
 SbTLP13 : ---PKDQEKKASRADQCS--SPPNNMTKRPVILNNAPRWHECLOCWLNFRGR---TVASVKNFQLIVTET-----GRGTILQGRVILQFGKIGDIPTMDYRPLSAFCAFAICLSSITKLACE : 424