Table S5, related to Figure 2. Characteristics of clients of SRα, Wrb, and hSnd2 with TMH.

	TMDs	Type	ΔGapp	Sequence	1st TMH	Size	%	N-glyco
SRα								
ABCC4	multi		5.118	LVLGIFTLIEESAKVIQPIFL	93-113	1325	7.8	+
ANO10	multi		1.133	IALYFGFLEYFTFALIPMAVI	208-228	660	32.7	
ASPH	1	II	-1.493	FFTWFMVIALLGVWTSVAVVW	54-74	758	8.4	+
ATL2	1	HP	-0.074	TLFAVMFAMYIISGLTGFIGL	477-497	583	83.5	+
ATP2B1	multi		4.019	FLQLVWEALQDVTLIILEIAA	98-118	1220	8.9	
ATP13A1	multi		1.928	VLPFAGLLYPAWLGAAAAGCW	67-87	1204	6.4	+
B3GALTL	1	II	-0.935	WWLLAPPALLALLTCSLAFGL	7-27	498	3.4	+
BST2	1	II	-5.685	KLLLGIGILVLLIIVILGVPLIIFTIKA	21-48	180	17.2	+
CAV1	1	HP	-0.726	ALFGIPMALIWGIYFAILSFL	105-125	178	64.4	
CEPT1	multi		-0.476	LITIIGLSINICTTILLVFYC	87-107	416	23.3	+
DEGS1	multi		-0.478	PNLIWIIIMMVLTQLGAFYIV	41-61	323	15.8	
ERGIC2	multi		1.141	GTVSLIAFTTMALLTIMEFSV	34-54	377	11.7	
ERLIN2	1	II	1.947	LGAVVAVASSFFCASLFSAVH	4-24	339	4.1	+
IKBIP	1		0.469	CLSLLSLGTCLGLAWFV	46-62	377	14.9	+
ITPR3	multi		0.138	LWGSISFNLAVFINIIIAFFY	2203-2223	2671	82.9	+
LNPEP	1	II	-2.599	MVVCAFVIVVAVSVIMVIYLL	111-131	1025	11.8	
PDE3A	multi		-0.598	LSSALCAGSLSFLLALLVRLV	61-81	1141	6.2	
PEX3	1		3.594	CIFLGTVLGGVYILGKYGQKK	16-36	373	7	
REEP3	multi	HP	0.697	MVSWMISRAVVLVFGMLYPAY	1-21	255	4.3	
SLC16A3	multi		-0.663	GGWGWAVLFGCFVITGFSYAF	18-38	465	6	
SLC35B2	multi		3.884	WWAVVVLAAFPSLGAGGETPE	5-25	432	3.5	
SPTLC1	1		1.444	ALYEAPAYHLILEGILILWII	16-36	513	5.1	
SUN1	1	II	-1.860	ICKFLVLLIPLFLLLAGLSL	316-335	785	41.5	
TMEM41B	multi		-1.951	MSLLILVSIFLSAAFVMFLVY	52-72	291	21.3	
TMEM209	multi		1.532	VVLAWGLLNVSMAGMIYTEMT	28-48	561	6.8	+
TMTC3	multi		1.675	ITLIVGVVTACYWNSLFCGFV	9-29	914	1.8	+
TOR1AIP2	1		-0.371	FWSYGPVILVVLVVAVVASSV	215-235	470	47.9	+
TVP23B	multi		1.886	PVASFFHLFFRVSAIIVYLL	34-53	205	21.5	
YIPF5	multi		0.365	TDLAGPMVFCLAFGATLLLAG	125-145	257	52.5	
ZMPSTE24	multi		1.532	IFGAVLLFSWTVYLWETFLAQ	19-39	475	6.1	
Wrb								
EXT2	1	II	-1.428	YITLFSIVLLGLIATGMFQFW	26-46	718	5	
FAR1	1	TA	-0.255	IRYGFNTILVILIWRIF	466-483	515	92.4	
GOLGA5	1	TA	-2.261	VFVIIYMALLHLWVMIVLLTYTP	699-719	731	97	
ITPR3	multi		0.138	LWGSISFNLAVFINIIIAFFY	2203-2223	2671	82.9	
LBR	multi		-2.378	VPGVFLIMFGLPVFLFLLLLM	212-232	615	36.1	
MARCH1	multi		0.107	IFCSVTFHVIAITCVVWSLYV	155-175	545	30.3	
MFSD7	multi		0.335	WVFLLAISLLNCSNATLWLSF	30-50	559	7.2	
MFSD10	multi		-1.459	VVFLGLLLDLLAFTLLLPLLP	27-47	455	8.1	
NEU1	1		-1.467	LGFWGGCRVWVFAAIFLLLSLAA	20-41	415	7.2	+
PTDSS1	multi		0.972	FFYRPHTITLLSFTIVSLMYF	36-56	473	9.7	
REEP3	multi	HP	0.697	MVSWMISRAVVLVFGMLYPAY	1-21	255	4.3	
SGPP1	multi		2.661	FCFGTELGNELFYILFFPFWI	132-152	441	32.2	
SPCS2	multi		1.255	ICTISCFFAIVALIWDYMHPF	87-107	226	82.9	
UBE2J2	1	TA	-1.019	GLLGGALANLFVIVGFAAFAYTW	227-247	259	91.5	
hSnd2								
MYO9A	1		1.571	IYTYVGSILIVINPFKFLPIY	175-195	2548	7.3	
PTDSS2	multi		-0.192	AHTLTVLFILTCTLGYVTLLE	63-83	487	15	+
PTGIS	1		-3.435	MAWAALLGLLAALLLLLLS	1-20	500	2.2	
SLC4A2	multi		-0.458	CLAAVIFIYFAALSPAITFGGLLG	708-731	1241	57.9	+
SLC7A2	multi		2.693	DLIALGVGSTLGAGVYVLAGEV	38-59	658	7.3	+
TMEM41B	multi		-1.951	MSLLILVSIFLSAAFVMFLVY	52-72	291	21.3	
TRPM7	multi		1.975	NSWYKVILSILVPPAILLLEY	756-776	1865	41.1	
VAMP4	1	TA	-3.47	IKAIMALVAAILLLVIIILIV	116-136	141	89.4	
VAMP8	1	TA	-4.429	MVLICVIVFIIILFIVLFAT	76-96	100	86	

1st TMH, most N-terminal transmembrane domain; TMD, number of transmembrane domains (including TMH); 1, single spanning; multi, multispanning; Type, membrane protein type; HP, hairpin; TA, tail anchor; ΔGapp, apparent delta G of TMH; Sequence, primary structure of TMH; amino acid residues of TMH; Size, number of amino acid residues of client; %, distribution of TMH in client (i.e. position of central amino acid residue of TMH in % of client); N-glyco, N-glycosylation.