Table S6, related to Figure 2. Characteristics of clients of Wrb plus hSnd2 and PEX3 with TMH.

	TMDs	Type	ΔGapp	Sequence	TMH	Size	%	N-glyco
hSnd2+Wrb								
AGPAT5	multi		1.565	LLPSVVLLGTAPTYVLAWGVW	15-35	364	6.9	
ATG9A	multi		-0.147	IFELMQFLFVVAFTTFLVSCV	67-87	839	9.2	+
ATP2C1	multi		4.913	LWKKYISQFKNPLIMLLLASA	71-91	919	8.8	
ATP12A	multi		3.561	EIVKFLKQMVGGFSILLWVGA	102-123	1093	10.3	
BCAP29	multi		-0.863	AVATFLYAEIGLILIFCLPFI	7-27	241	7.1	
C4orf3	1	TA	-2.704	SYWLDLWLFILFDVVVFLFVYFL	45-65	65	84.6	
CXCR4	multi		-0.37	IFLPTIYSIIFLTGIVGNGLVILVM	39-63	352	13.9	+
EMD	1	TA	-2.850	VPLWGQLLLFLVFVIVLFFIY	223-243	254	91.7	
GDPD4	multi		0.185	WVTFLGTGYWFFWSIFILSLA	18-38	520	5.4	+
JPH1	1	TA	-1.838	IMIVLVMLLNIGLAILFVHFL	640-660	661	98.3	
LEMD2	multi		-3.464	LLLWASLGLLLVFLGILWVKM	213-233	503	44.3	
MBOAT7	multi		2.483	LVVLLISIPIGFLFKKAGPGL	9-29	472	4	+
MXRA7	1		2.128	LLAALPALATALALLLAWLLV	7-27	170	10	
PLD3	1	II	-1.979	VLLVLILAVVGFGALMTQLFL	39-59	490	10	+
POMK	1	II	-0.095	VGLLLIMALMNTLLYLCLDHFFI	21-43	350	8.9	+
PRAF2	multi		0.209	LYYQTNYLLCFGIGLALAGYV	42-62	178	29.2	
RHBDD2	multi		2.164	WCLCPEVPSATFFTALLSLLV	11-31	364	5.8	
REEP5	multi	HP	-1.133	SFIALGVIGLVALYLVFGYGA	35-55	189	23.8	
SEC62	multi		-1.555	FVMGLILVIAVIAATLFPLWP	197-217	399	51.9	
SLC9A6	multi		3.829	LWLLLAVGVFDWAGASDGGGG	28-48	679	5.6	+
SLC16A7	multi		-0.035	GGWGWIVVGAAFISIGFSYAF	16-36	478	5.4	
SLC39A7	multi		0.193	WVAVGLLTWATLGLLVAGLGG	10-30	469	4.3	
SOAT1	multi		-2.080	IYHMFIALLILFILSTLVV	141-159	550	27.5	
STEAP4	multi		-0.321	LFPMWRFPFYLSAVLCVFLFF	196-216	459	44.9	
STX2	1	TA	-2.654	WIIIAVSVVLVAIIALIIGLSVGK	265-288	288	95.5	
STX3	1	TA	-4.337	LIIIIVLVVVLLGILALIIGLSV	264-284	289	94.8	
STX17	multi		-2.116	LAALPVAGALIGGMVGGPIGL	229-249	302	79.1	
TMEM33	multi		0.388	LFTVYCSALFVLPLLGLHEAA	32-52	247	17	+
TMEM38B	multi		0.584	SWFTAMLHCFGGGILSCLLLA	50-70	291	20.6	
TMEM181	multi		-2.195	HFVLVFVVFFICFGLTIFVGI	153-173	475	34.4	
PEX3								
ABCD3	multi		1.380	GYLVLIAVMLVSRTYCDVWMI	84-104	659	14.3	+
ACBD5	1		-0.121	GVLTFAIIWPFIAQWLVYLYY	497-517	525	96.6	
AIFM2	1		2.886	VESGALHVVIVGGGFGGIAAA	7-27	373	4.6	
ATL1	1	HP	-0.573	TLFVVIFITYVIAGVTGFIGL	450-470	558	82.4	
CCDC136	1	TA	-2.371	IFSLPLVGLVVISALLWCWWA	1130-1150	1154	98.8	
COLEC12	1	II	-2.162	FSIILLYILCALLTITVAILG	38-58	742	6.5	+
CYBRD1	multi		-2.348	LLGSALLVGFLSVIFALVWVL	12-32	286	7.7	+
DHRS7B	1	II	-0.36	FITSTAILPLLFGCLGVFGLF	18-38	325	8.6	
ENPP1	1	II	-0.985	VLSLVLSVCVLTTILGCIFGL	77-97	925	9.4	+
ERMP1	multi		2.156	AGTGLSEVRAALGLALYLIAL	64-84	904	8.2	+
FAR1	1	TA	-0.668	IRYGFNTILVILIWRIFI	466-483	515	92.4	
MAN1A1	1	II	-2.612	FVLLLVFSAFITLCFGAIFFL	42-62	653	8	+
PEX13	1		0.039	AATSAKSWPIFLFFAVILGGPYLIW	227-251	403	58.8	
PXMP2	multi		3.630	LYPVLTKAATSGILSALGNFL	31-51	195	21	
RTN3	multi	HP	-2.436	LIMLLSLAAFSVISVVSYLILALL	864-887	1032	84.7	
SGCD	1	II	-3.808	FFVLLLMILILVNLAMTIWIL	37-57	256	18.4	
STX6	1	TA	-5.096	WCAIAILFAVLLVVLILFLVL	235-255	255	96.1	+
TMEM192	multi		-1.154	TVIIVNLLWFIHLVFVVLAFL	47-67	271	21	
TMEM237	multi		1.917	MIGLFSHGFLAGCAVWNIVVI	227-247	408	58.1	
TMUB2	multi		-2.382	VMVVAGVVVLILALVLAWLST	36-56	321	14.3	
TOR1AIP1	1		0.705	WLLPLIAALASGSFWFF	339-355	583	59.9	
VAMP3	1	TA	-4.236	MWAIGITVLVIFIIIIVWVV	78-98	100	88	

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.