

Table S1. Effect of different gene knock-outs on YO-PRO-1 dye uptake by electroporated cells. The data for tested genes are presented in the alphabetical order. The average values of the mean or median YP fluorescence per cell are express in % to the parallel control (data not shown). The differences from the parallel control are expressed by t-values; the value over 3.0 corresponds to $p < 0.05$ using Dunnet's test for the comparison of multiple groups with control. See text for more details.

gene name	MEDIAN				MEAN			
	Average, %	s.e., %	t-value	SSMD	Average, %	s.e., %	t-value	SSMD
ANO6	104.8	1.8	1.87	0.66	101.1	7.05	0.09	0.03
ASIC1	112.9	7.75	1.64	0.8	167.2	43.05	1.55	0.77
ASIC2	102.1	12.98	0.16	0.09	92.5	10.89	-0.55	-0.22
ASIC3	114	3.17	3.75	1.6	116.6	9.24	1.64	0.77
ASIC4	99.3	9.75	-0.07	-0.03	97	8.22	-0.26	-0.09
ASIC5	107.7	7.24	1.05	0.51	136.5	37.9	0.96	0.47
ATP12A	107.9	2.28	2.62	1	123.8	18.22	1.27	0.68
ATP13A1	103.5	6.3	0.5	0.23	96.2	7.52	-0.34	-0.12
ATP13A2	107.6	5.45	1.31	0.65	133.4	21.06	1.56	0.85
ATP13A4	95.8	4.74	-0.85	-0.39	103	1.37	0.72	0.22
ATP13A5	102.8	2.13	1.13	0.46	119.4	9.15	1.86	0.77
ATP1A1	102.3	6.59	0.34	0.18	103.4	8.41	0.36	0.17
ATP1A2	105.8	8.06	0.71	0.35	116.5	16.17	0.98	0.45
ATP1A3	78	8.48	-2.57	-1.26	78.3	10.85	-1.82	-0.79
ATP1A4	92.9	4.57	-1.48	-0.67	104.5	10.63	0.39	0.18
ATP2A1	105.7	7.62	0.74	0.37	101.6	3.91	0.23	0.07
ATP2A2	101.5	0.97	0.68	0.21	105.3	5.24	0.8	0.33
ATP2A3	102.8	14.57	0.19	0.1	88.9	6.16	-1.09	-0.37
ATP2B1	91.4	1.66	-4.58	-1.92	85.3	1.02	-2.12	-0.62
ATP2B2	98.5	4.14	-0.36	-0.17	101	7.69	0.1	0.04
ATP2C1	105.7	6.09	0.93	0.45	93.1	5.85	-0.83	-0.29
ATP2C2	109.9	2.05	3.93	1.2	134.1	3.6	5.9	1.64
ATP4A	115.5	4.8	3.09	1.05	132	8.65	3.28	1.05
ATP5B	92.1	5.17	-1.5	-0.82	89.1	13.57	-0.73	-0.35
ATP6V1A	96.6	1.38	-2.11	-0.85	103.2	5	0.38	0.13
ATP6V1B2	106	2.71	1.79	0.73	125.6	1.65	5.74	1.75
ATP7A	95.7	2.02	-1.96	-0.86	104.5	13.17	0.3	0.13
ATP7B	110.8	6.29	1.64	0.84	131.9	17.24	1.8	0.96
BEST1	109.5	0.9	4.42	1.38	112.9	9.83	1.21	0.64
BEST2	103.3	4.5	0.72	0.34	90.2	4.12	-1.35	-0.44
BEST3	104.1	14.89	0.27	0.15	133.6	17.56	1.74	0.81

BEST4		105.2	3.45	1.31	0.53		113.5	17.41	0.72	0.32
CACHD1		103.7	3.58	0.98	0.44		118.6	6.07	2.38	0.89
CACNA1A		112.4	3.79	2.9	1.31		136.5	6.32	4.83	2.02
CACNA1B		101.4	3.93	0.33	0.15		96.4	19.52	-0.18	-0.1
CACNA1C		106.9	5.17	1.23	0.55		112.5	16.11	0.72	0.32
CACNA1D		102.8	1	1.21	0.38		110.1	6.14	1.12	0.39
CACNA1E		99.8	2.43	-0.09	-0.04		112.5	17.22	0.68	0.3
CACNA1G		113.8	3.46	3.67	1.21		137.1	8.13	3.99	1.27
CACNA1H		105.6	11.61	0.46	0.25		103.2	16.73	0.17	0.08
CACNA1I		102.9	5.24	0.52	0.23		102.2	9.66	0.19	0.07
CACNA1S		100.6	2.63	0.19	0.07		119.6	8.64	1.8	0.68
CACNA2D4		101.6	8.82	0.18	0.09		87.2	4.86	-1.66	-0.56
CACNB1		115.8	3.32	4.09	1.77		132.8	18.9	1.7	0.92
CACNB2		85.4	14.84	-0.98	-0.49		69.2	9.88	-2.67	-1.08
CACNB3		103.5	6.63	0.52	0.25		96.7	6.72	-0.37	-0.14
CACNB4		106	4.7	1.18	0.57		111.4	14.96	0.73	0.39
CACNG2		94.3	2.76	-1.97	-0.91		83.1	13.52	-1.12	-0.47
CACNG3		97.7	4.65	-0.49	-0.23		88.8	7.52	-1.17	-0.44
CACNG4		112.8	1.66	5	1.74		120.1	5.55	2.89	1.16
CACNG5		109.7	3.73	2.3	1.04		118.6	1.87	4.1	1.27
CACNG7		104.5	1.94	1.64	0.6		131.2	23.04	1.33	0.74
CATSPER2		102.6	2.15	1.04	0.43		107.1	12.88	0.51	0.23
CATSPER3		103.7	3.28	1.01	0.47		99.8	4.62	-0.03	-0.01
CHRNA1		98.8	3.12	-0.36	-0.15		110	8.48	1.07	0.46
CHRNA10		105.3	2.55	1.78	0.59		126.4	8.26	2.81	0.93
CHRNA2		107.6	4.6	1.53	0.73		124.3	17.77	1.33	0.72
CHRNA3		103.9	10.65	0.35	0.18		107.5	7.37	0.68	0.24
CHRNA4		93.5	3.68	-1.71	-0.8		81.8	5.25	-2.3	-0.79
CHRNA5		95.8	5.59	-0.72	-0.34		95.3	9.3	-0.46	-0.2
CHRNA6		110.3	5.14	1.86	0.83		126.3	10.49	2.12	0.85
CHRNA7		111.3	4	2.54	1.17		115.5	14.58	1.02	0.53
CHRNA9		110.4	1.14	4.61	1.48		111.7	7.77	1.33	0.6
CHRNA10		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA11		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA12		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA13		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA14		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA15		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA16		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA17		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA18		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA19		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA20		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA21		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA22		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA23		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA24		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA25		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA26		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA27		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA28		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA29		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA30		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA31		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA32		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA33		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA34		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA35		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA36		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA37		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA38		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA39		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA40		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA41		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA42		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA43		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA44		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA45		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA46		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA47		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA48		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA49		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA50		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA51		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA52		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA53		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA54		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA55		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA56		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA57		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA58		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA59		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA60		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA61		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA62		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA63		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA64		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA65		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA66		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA67		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA68		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA69		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA70		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA71		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA72		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA73		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA74		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA75		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA76		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA77		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA78		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA79		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA80		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA81		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA82		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA83		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA84		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA85		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA86		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA87		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA88		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA89		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA90		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA91		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA92		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA93		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA94		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA95		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA96		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA97		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA98		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA99		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA100		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA101		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA102		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA103		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA104		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA105		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA106		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA107		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA108		110.3	2.3	3.4	1.3		124.2	20.22	1.17	0.64
CHRNA109										

CLCN3		108.1	8.98	0.9	0.44		97.5	12.2	-0.18	-0.08
CLCN4		107.5	5.03	1.42	0.48		127	18.9	1.39	0.48
CLCN6		100.5	3.06	0.14	0.06		99.9	9.79	-0.01	0
CLCNKA		100.7	5.16	0.13	0.06		79.9	11.42	-1.56	-0.66
CLCNKB		128	29.62	0.94	0.53		122.9	15.02	1.34	0.6
CLIC1		100.1	4.02	0.02	0.01		86.4	8.64	-1.29	-0.5
CLIC2		102	3.7	0.49	0.24		117.1	14.86	1.11	0.58
CLIC3		102.9	3.21	0.8	0.37		109.4	14.05	0.64	0.33
CLIC4		99.2	3.46	-0.2	-0.1		116.6	9.95	1.54	0.74
CLIC5		99.1	4.12	-0.2	-0.1		113.8	9.52	1.33	0.63
CLIC6		102.6	2.48	0.66	0.23		95.4	1.5	-0.56	-0.16
CNGA1		96.2	1	-2.86	-1.05		103.2	22.13	0.14	0.06
CNGA2		95.1	6.21	-0.77	-0.41		78.7	16.4	-1.26	-0.67
CNGA3		103.9	4.08	0.87	0.42		128.1	11.57	2.25	1.09
CNGA4		105.1	5.79	0.86	0.42		87.9	2.72	-1.85	-0.57
CNGB1		102.7	6.02	0.45	0.22		93.8	11.2	-0.49	-0.2
CNGB3		112.8	5.78	2.1	1.07		104	4.33	0.69	0.26
FXYP1		111.4	3.68	2.76	1.25		120.6	6.07	2.87	1.22
FXYP3		116.7	0.28	8.81	2.57		130.5	15.69	1.89	1.18
FXYP3		108	5.03	1.52	0.52		114.1	7.02	1.69	0.53
FXYP4		106.3	5.96	1.03	0.5		88.9	6.3	-1.29	-0.46
FXYP6		104.1	6.52	0.6	0.32		110.4	3.9	1.71	0.59
FXYP7		116.2	3.1	4.46	1.92		91.9	14.9	-0.53	-0.28
GABRA1		93.8	11.31	-0.54	-0.27		94.7	21.83	-0.23	-0.11
GABRA2		105.2	5.03	0.98	0.48		117.1	18.43	0.91	0.49
GABRA3		112.5	4.16	2.8	1.38		133.4	6.05	4.56	1.88
GABRA4		105.2	3.93	1.18	0.49		118.4	10.8	1.45	0.59
GABRA5		94.4	3.18	-1.69	-0.79		85.1	4.64	-1.79	-0.58
GABRA6		103.7	5.2	0.66	0.29		123.6	6.07	2.63	0.91
GABRB1		105.9	3.96	1.32	0.55		106.4	14.04	0.41	0.18
GABRB2		102.9	5.79	0.48	0.26		124.9	6.51	3.22	1.36
GABRB3		102.8	1.93	0.98	0.34		110	10.82	0.79	0.32
GABRD		99.9	3.35	-0.02	-0.01		111.5	12.42	0.82	0.34
GABRE		100.4	4.65	0.09	0.04		86.7	4.17	-1.83	-0.6
GABRG1		106.8	1.78	2.87	1.09		132.4	14.36	2.17	1.13
GABRG2		105	5.05	0.98	0.47		96.5	5.25	-0.44	-0.15
GABRG3		95.8	2.68	-1.49	-0.69		96.1	6.5	-0.42	-0.15
GABRP		93.1	0.3	-4.36	-1.27		81.4	16.9	-1.07	-0.57
GABRQ		101.1	6.98	0.15	0.08		92.8	7.05	-0.78	-0.29
GABRR1		95	6.47	-0.76	-0.4		90.9	9.24	-0.9	-0.42
GABRR2		104.2	6.23	0.65	0.34		104.8	8.81	0.48	0.22

GABRR3		101.8	3.09	0.56	0.25		113	7.77	1.42	0.57
GLRA1		107.2	2.33	2.58	1.08		110.8	1.37	2.56	0.77
GLRA2		107.9	5.07	1.52	0.72		125.9	6.1	3.31	1.24
GLRA3		105.7	5.64	0.99	0.48		100.5	7.8	0.05	0.02
GLRB		99.1	3	-0.26	-0.12		105.1	8.42	0.53	0.21
GRIA1		96.4	2.31	-1.43	-0.62		93.3	9.12	-0.61	-0.24
GRIA2		114.2	2.66	4.37	1.78		133.1	17.92	1.8	0.98
GRIA3		96.2	5.16	-0.71	-0.37		103.2	2.29	0.69	0.22
GRIA4		93.9	17.32	-0.35	-0.2		93.8	27.59	-0.22	-0.12
GRID1		116	0.41	8.31	2.44		105	5.98	0.71	0.3
GRID2		106	2.82	1.71	0.66		114.6	14.32	0.93	0.4
GRIK1		102.6	2.34	0.84	0.31		112.5	9.94	1.04	0.41
GRIK2		109.3	4.78	1.8	0.79		117	1.56	2.5	0.73
GRIK3		113.4	4.74	2.63	1.28		136.3	14.68	2.39	1.27
GRIK4		104.4	9.88	0.44	0.24		99.8	4.98	-0.02	-0.01
GRIK5		113	1.95	5.19	2.03		137.9	16.38	2.24	1.19
GRIN1		107.8	3.9	1.84	0.89		106.8	19.94	0.33	0.18
GRIN2A		108.4	2.86	2.59	1.25		127.4	3.77	4.88	1.78
GRIN2B		97.4	5.3	-0.46	-0.21		93.4	9.93	-0.55	-0.22
GRIN2C		107.2	4.48	1.46	0.63		122.1	6.03	2.47	0.85
GRIN2D		103.5	11.07	0.31	0.17		122.9	15.1	1.45	0.75
GRIN3A		120.6	25.25	0.82	0.47		108.1	8.34	0.84	0.37
GRIN3B		102.1	8.81	0.23	0.13		112.3	9.04	1.21	0.55
HCN1		102	3.72	0.49	0.23		103.9	22.59	0.17	0.09
HCN2		102	13.62	0.14	0.08		104	15.78	0.23	0.1
HCN3		94.9	4.16	-1.15	-0.51		109.8	18.14	0.54	0.26
HCN4		106.5	9.5	0.68	0.37		109.6	7.81	1.06	0.46
HTR3A		92.4	4.55	-1.57	-0.71		105.9	10.78	0.53	0.25
HTR3B		96.8	3.19	-0.89	-0.38		112.6	9.77	1.24	0.58
HTR3C		93.7	2.36	-2.2	-0.86		93.1	8.93	-0.74	-0.34
HTR3D		109.1	4.83	1.83	0.86		125.1	14.15	1.67	0.76
HTR3E		91.2	6.58	-1.29	-0.61		93.1	6.25	-1.01	-0.44
ITPR1		105.1	1.1	2.64	0.88		103.4	8.8	0.35	0.16
ITPR2		104.7	3.34	1.28	0.6		118.4	13.6	1.3	0.67
ITPR3		112.5	2.43	4.08	1.62		128.2	7.33	3.41	1.54
KCNA1		113.4	4.1	2.97	1.39		99.8	22.44	-0.01	-0.01
KCNA10		75.4	17.81	-1.37	-0.67		77.2	18.24	-1.17	-0.53
KCNA2		104.3	3.13	1.08	0.4		103.5	9.89	0.29	0.11
KCNA4		93.3	10.13	-0.64	-0.3		86.1	14.23	-0.88	-0.38
KCNA5		107.4	11.05	0.65	0.34		113.9	15.93	0.78	0.35
KCNA6		106.1	6.79	0.87	0.46		122.1	2.91	4.01	1.3

KCNA7		120	19.3	1.03	0.57		115.7	26.13	0.57	0.29
KCNAB1		111.3	5.88	1.82	0.93		134.5	20.65	1.64	0.9
KCNAB2		112	6.1	1.87	0.96		123.8	15.8	1.47	0.78
KCNAB3		99.7	6.5	-0.04	-0.02		100	9.06	0	0
KCNB1		111	7.48	1.42	0.76		109.3	8.55	0.99	0.47
KCNB2		111.9	3.36	3.2	1.49		123.3	3.46	4.31	1.49
KCNC1		108.8	4.53	1.84	0.92		112	13.98	0.83	0.43
KCNC2		93.1	6.73	-1	-0.53		120.5	4.57	3.13	1.14
KCNC4		100.6	3.29	0.16	0.07		100	9.59	0	0
KCND1		110.2	2.13	3.85	1.55		141.6	8.48	4.4	2.02
KCND2		103.2	2.74	1.02	0.44		125.3	15.47	1.58	0.83
KCND3		90.8	10.7	-0.84	-0.4		101.8	14.31	0.11	0.05
KCNE1		125.4	36.08	0.7	0.41		128.3	29.88	0.94	0.52
KCNE1L		126.9	26.39	1.02	0.58		132.6	17.22	1.83	0.96
KCNE2		95.6	1.87	-1.81	-0.67		94.7	5.71	-0.76	-0.29
KCNE3		103	3.69	0.78	0.37		84.3	9.28	-1.36	-0.52
KCNF1		91.8	2.11	-3.09	-1.17		105.9	11.45	0.5	0.24
KCNG1		97.9	2.76	-0.65	-0.27		102.6	6.91	0.35	0.15
KCNG2		111.3	8.17	1.36	0.74		130.7	7.26	3.55	1.49
KCNG3		95.4	4.12	-1.03	-0.46		94	9.68	-0.59	-0.28
KCNG4		105	2.38	1.75	0.73		119.6	6.35	2.58	1.08
KCNH1		95	3.23	-1.51	-0.71		86.6	16.1	-0.76	-0.33
KCNH2		105.4	13.91	0.38	0.2		101.2	5.46	0.12	0.04
KCNH3		121.4	4.21	4.64	2.19		111.1	5.17	1.73	0.7
KCNH4		96.8	4.37	-0.69	-0.31		85	11.32	-1.29	-0.61
KCNH5		97.6	1.67	-1.28	-0.54		114.5	19.7	0.7	0.32
KCNH6		122.8	8.51	2.62	1.42		151.8	30.12	1.71	0.96
KCNH7		101	2.85	0.32	0.14		117.9	11.22	1.46	0.64
KCNH8		95.4	2.99	-1.43	-0.63		111.7	14.1	0.78	0.36
KCNJ1		86.3	10.8	-1.27	-0.63		87	14.88	-0.79	-0.34
KCNJ10		108.5	2.37	2.82	1.11		111.2	5.12	1.75	0.7
KCNJ11		108.9	5.36	1.56	0.78		79.5	38.71	-0.53	-0.3
KCNJ13		94.6	3.96	-1.26	-0.56		76.7	7.88	-2.79	-1.26
KCNJ14		118.1	0.89	8.71	2.71		137.2	25.39	1.45	0.81
KCNJ15		103.9	6.89	0.56	0.27		115.6	6.54	1.72	0.61
KCNJ16		92.2	9.31	-0.81	-0.38		79.3	12.56	-1.44	-0.6
KCNJ2		102.6	3.48	0.69	0.3		95.8	3.77	-0.57	-0.18
KCNJ3		102.5	3.83	0.62	0.28		87.4	7.06	-1.34	-0.49
KCNJ4		103.6	4.9	0.7	0.32		97.9	18.32	-0.11	-0.05
KCNJ5		103.4	5.11	0.65	0.3		92.7	11.64	-0.56	-0.23
KCNJ6		96.9	3.62	-0.71	-0.28		103.1	13.48	0.21	0.09

KCNJ8		113.1	3.58	3.44	1.55		134.5	18.06	1.84	0.86
KCNJ9		100.3	10.02	0.03	0.01		101.6	20.78	0.08	0.04
KCNK1		102.2	8.78	0.25	0.12		114	14.25	0.93	0.42
KCNK10		108.3	9.48	0.87	0.43		117.9	30	0.59	0.29
KCNK12		105.8	6.48	0.87	0.46		117.2	5.79	2.31	0.9
KCNK13		104.8	10.63	0.43	0.23		94.9	13.88	-0.32	-0.14
KCNK15		102.6	6.46	0.39	0.19		109.8	5.15	1.37	0.49
KCNK16		100.4	8.2	0.04	0.02		93.4	13.78	-0.43	-0.19
KCNK17		78.4	17.72	-1.21	-0.59		77.5	26.02	-0.84	-0.39
KCNK18		99.3	6.17	-0.11	-0.05		110.8	9.07	0.95	0.36
KCNK2		95.3	2.96	-1.53	-0.71		96.7	9.03	-0.29	-0.11
KCNK4		121.9	18.69	1.17	0.58		113	21.36	0.58	0.27
KCNK5		90.5	8.2	-1.1	-0.51		88.4	13.54	-0.77	-0.32
KCNK6		131.2	28.92	1.08	0.62		137.7	14.28	2.51	1.28
KCNK7		104.1	4.58	0.84	0.42		103.3	17.46	0.19	0.1
KCNK9		96.8	2.35	-1.15	-0.46		98	5.95	-0.23	-0.08
KCNMA1		97.4	3.88	-0.62	-0.27		91.3	10.6	-0.8	-0.38
KCNMB1		96.6	2.35	-1.2	-0.47		101.4	7.78	0.17	0.08
KCNMB2		84.5	12.95	-1.17	-0.56		46.2	23.33	-2.29	-1.12
KCNMB3		88.2	5.44	-2.09	-0.97		88.2	6.79	-1.61	-0.71
KCNMB4		101.5	5.47	0.27	0.13		108.9	9.66	0.77	0.3
KCNN1		102.5	3.29	0.71	0.32		117.7	10.11	1.58	0.67
KCNN2		96.7	6.25	-0.48	-0.21		95.1	5.06	-0.83	-0.33
KCNN3		94.5	3.26	-1.53	-0.65		98.6	12.23	-0.11	-0.05
KCNN4		103.5	9.67	0.36	0.17		118.2	29.36	0.62	0.35
KCNQ1		102.5	3.39	0.69	0.3		98.5	5.1	-0.18	-0.06
KCNQ2		98.1	2.7	-0.51	-0.18		95.5	8.21	-0.51	-0.23
KCNQ3		93.5	5.79	-1.03	-0.45		97.9	12.17	-0.15	-0.06
KCNQ4		95.6	23.96	-0.18	-0.11		102.1	35.16	0.06	0.03
KCNQ5		101.3	7.16	0.18	0.09		101.7	3.33	0.29	0.1
KCNT1		112.8	6.17	2.04	0.98		111.4	11.44	0.91	0.4
KCNT2		96.3	4.99	-0.72	-0.34		106.7	6.45	0.82	0.31
KCNV1		114.5	8.98	1.6	0.79		131.8	16.75	1.82	0.84
KCNV2		99	4.04	-0.2	-0.08		88	8.17	-1.13	-0.42
KCTD17		107.4	5.72	1.26	0.68		146.2	29.97	1.52	0.85
KCTD2		72.7	18.29	-1.49	-0.85		82.8	9.45	-1.63	-0.75
KCTD3		100.9	6.55	0.14	0.07		114.6	21.49	0.66	0.32
KCTD5		124.8	19.46	1.27	0.88		174.5	3.35	12.94	4.41
LENG9		104.1	3.27	1.1	0.45		107.3	7.29	0.57	0.18
MCOLN1		106.4	6.43	0.97	0.47		131.8	30.55	1.03	0.5
MCOLN2		94.3	7.93	-0.68	-0.31		91.6	16.43	-0.5	-0.24

MCOLN3		105.2	5.64	0.9	0.43		129.6	21.89	1.32	0.63
NALCN		97.6	9.74	-0.23	-0.11		85.4	12.29	-1.15	-0.55
NUPL2		98.6	4.27	-0.28	-0.11		108.4	9.31	0.72	0.28
P2RX1		87.5	7.72	-1.54	-0.71		89.4	14.17	-0.68	-0.29
P2RX2		102.1	8.46	0.25	0.12		80.9	12.43	-1.37	-0.58
P2RX3		95	4.45	-0.96	-0.39		88.4	10.23	-1.09	-0.51
P2RX4		87.3	9.02	-1.34	-0.62		95.9	9.91	-0.4	-0.18
P2RX6		95.8	7.49	-0.53	-0.24		87.4	7.31	-1.59	-0.7
P2RX7		105.9	8.5	0.66	0.31		91.9	10.32	-0.66	-0.26
PKD2		111.9	4.02	2.71	1.17		117.1	6.66	1.38	0.44
PKD2L1		103.9	3.98	0.93	0.42		98.6	6.32	-0.16	-0.06
PKD2L2		98.1	2.13	-0.78	-0.34		109.5	2.09	1.78	0.54
PKDREJ		112.9	2.12	4.64	1.71		110.1	9.64	0.7	0.24
RYR1		106.2	7.48	0.81	0.39		111.8	12.22	0.86	0.36
RYR2		101	2.51	0.32	0.13		98.8	11.21	-0.1	-0.05
RYR3		105.8	5.25	1.07	0.5		106.9	4.84	0.87	0.29
SCN10A		104.9	2.83	1.6	0.7		124.6	11.62	1.95	0.85
SCN11A		93.7	3.58	-1.61	-0.7		102.2	5.79	0.34	0.14
SCN1A		100.5	6.9	0.07	0.03		98.1	7.88	-0.22	-0.1
SCN1B		99.9	4.43	-0.02	-0.01		127	15.13	1.7	0.78
SCN2A		113.2	7.82	1.59	0.8		103.8	2.79	0.93	0.33
SCN2B		99.5	4.41	-0.11	-0.05		95.4	11.77	-0.35	-0.14
SCN3A		102.4	4.26	0.54	0.25		119.7	14.39	1.3	0.59
SCN3B		112.9	4.38	2.82	1.31		127.9	12.79	2.03	0.9
SCN4A		97	4.66	-0.61	-0.28		115.5	9.51	1.57	0.73
SCN4B		117.2	6.97	2.42	1.17		138	16.32	2.23	1.03
SCN5A		85.9	6.1	-2.23	-1.05		95.1	13.27	-0.36	-0.17
SCN7A		89.8	11.93	-0.83	-0.4		65.2	20.76	-1.66	-0.81
SCN8A		91.3	1.78	-2.66	-0.86		94.5	1.61	-1.59	-0.5
SCN9A		114.2	3.92	3.29	1.41		121.7	4.84	1.87	0.58
SCNN1A		91.7	7.42	-1.04	-0.47		79.7	8.52	-2.24	-1.01
SCNN1B		111.6	10.89	1.06	0.52		136.6	27.97	1.29	0.63
SCNN1D		105.5	7.9	0.68	0.33		137.5	29.76	1.24	0.61
SCNN1G		96.2	0.63	-2.18	-0.66		108.9	23.43	0.38	0.21
SHKBP1		98.7	2.63	-0.46	-0.2		103.6	6.56	0.44	0.17
SHROOM1		93.3	7.15	-0.88	-0.4		78.2	9.08	-1.92	-0.73
SHROOM2		110.9	7.04	1.52	0.73		156.7	50.85	1.11	0.55
SHROOM4		122.6	5.49	3.9	1.98		120.3	9	1.47	0.51
SLC9C1		92.8	3.19	-2.12	-0.94		106.1	10.49	0.52	0.22
TAS1R1		102.4	7.3	0.32	0.14		97.7	7.58	-0.22	-0.08
TAS1R3		98.4	7.3	-0.2	-0.09		93.8	5.1	-0.73	-0.24

TMC1		107.7	9.15	0.8	0.4		98	4.28	-0.21	-0.07
TMC2		111.6	4.24	2.52	1.1		114.2	9.38	1.01	0.35
TMC3		92.3	6.86	-1.06	-0.47		87.6	8.6	-1.13	-0.42
TMC4		104.6	11.03	0.41	0.19		114.3	12.64	0.99	0.41
TMC5		99.6	7.86	-0.04	-0.02		89	3.38	-2.43	-0.88
TMC6		108.7	5.67	1.48	0.7		111.1	9.14	1	0.39
TMC7		84.3	18.23	-0.86	-0.43		91	28.2	-0.31	-0.15
TMC8		104.8	2.49	1.57	0.6		111.8	8.05	0.89	0.3
TMEM235		90.3	4.23	-1.94	-0.81		77.4	12.58	-1.75	-0.94
TPCN1		90.8	5.4	-1.64	-0.76		68.7	31.83	-0.98	-0.48
TPCN2		98.5	4.67	-0.3	-0.13		110.5	11.23	0.88	0.4
TRPA1		99.1	6.22	-0.13	-0.06		126.5	12.21	2.06	0.94
TRPC1		90.3	4.46	-2.06	-0.94		96.4	15.75	-0.22	-0.11
TRPC3		94.3	4.85	-1.12	-0.52		99.6	23.04	-0.02	-0.01
TRPC4		96	5.17	-0.68	-0.28		99.6	4.43	-0.07	-0.03
TRPC5		98.5	1.77	-0.79	-0.34		101.3	8.1	0.13	0.05
TRPC6		99.6	2.21	-0.17	-0.08		93.3	6.23	-0.73	-0.25
TRPC7		95.9	1.28	-1.34	-0.41		85.8	4.29	-2.69	-1.04
TRPM1		106.5	11.44	0.55	0.29		103.7	10.21	0.28	0.11
TRPM2		94	6.48	-0.85	-0.37		87.2	4.38	-2.41	-0.94
TRPM3		93.6	6.16	-0.94	-0.41		90.4	9.1	-1	-0.46
TRPM4		118	17.87	1.01	0.5		128.1	14.86	1.74	0.76
TRPM5		99.5	4.58	-0.1	-0.05		110	22.04	0.43	0.2
TRPM6		96.1	7.05	-0.51	-0.23		92.2	9.84	-0.76	-0.35
TRPM7		107.8	11.42	0.66	0.35		105.8	15.31	0.33	0.15
TRPM8		102.4	2.73	0.81	0.35		124	7.64	2.64	1.05
TRPV1		105.9	3.07	1.8	0.8		118.7	11.63	1.48	0.65
TRPV2		121.5	14.35	1.49	0.74		114.9	15.79	0.88	0.39
TRPV3		97.3	4.15	-0.65	-0.31		96.8	4.24	-0.4	-0.13
TRPV4		114.6	13.19	1.1	0.54		102.7	11.13	0.21	0.09
TRPV5		103.3	3.68	0.85	0.39		121.9	7.7	2.39	0.95
TRPV6		96.4	3.77	-0.92	-0.44		96.5	8.59	-0.32	-0.12
TTYH1		97.7	6.63	-0.33	-0.16		98.2	4.9	-0.29	-0.11
TTYH2		118.5	7.68	2.38	1.16		153.1	39.68	1.33	0.65
TTYH3		65.1	15.07	-2.3	-1.14		76.6	19.43	-1.18	-0.57
VDAC1		105.8	12.68	0.44	0.24		87.9	32.5	-0.36	-0.19
VDAC2		109.7	8.74	1.05	0.53		99.7	4.3	-0.03	-0.01
VDAC3		111.5	2.63	3.58	1.4		117.5	8.99	1.27	0.43