Supplementary Table 1. Amino acid positions and mutations identified from the screen.

amino acid positions identified from residue map stage	wild-type sequence	target mutation stage	target checking stage		
3	Y	-	-		
18	T	-	-		
19	N	-	-		
47	G	-	-		
60	A	-	-		
62	F	-	-		
71	A	S	S		
74	T	-	-		
75	W	-	-		
77	S	-	-		
84	I	LV	LV		
88	A	LSTV	not found		
90	E	ADFNPQT	ADNPQ		
91	M	FILST	F L		
93	K	-	-		
94	V	LT	L		
95	I	-	-		
98	F	AMRV	M V		
99	F	AEMRTV	AERTV		
100	F	not found	-		
102	F	GLNPST	LNPST		
103	K	AGHIPRTW	G P T W		
111	A	CGHLS	CGLS		
112	T	DGNPRSW	GNS		
114	Н	A G V	G V		
115	R	P S	P S		
117	Q	LPY	LPY		
123	E	A	A		
132	L	ACG	С		
133	I	CLP	not found		
134	Н	K R	K R		
136	S	-	-		
151	G	-	_		
173	V	-	-		
181	G	-	_		
185	G	-	_		
187	N	not found	-		

188	T	LV	L
202	T	ALRS	not found
205	K	AEPQRSTV	A V
206	G	not found	-
210	Q	LV	LV
214	G	-	-
246	T	-	-
250	T	I Q	I Q
251	I	-	-
269	V	-	-
272	Н	-	-
273	E	-	-

In order to prioritize residues to screen, we selected amino acid positions from the residue map stage with the highest improvement (A88, E90, M91, F98, F99, F102, K103, T112, H114, R115, Q117, H134, N187, T188, T202, K205, G206, Q210, T250; normalized mean > 1.5 from **Supp. Fig. 1b**) as well as those that were near the 1.5-fold changed residues (A71, I84, V94, F100, A111, E123, L132) to screen for target mutations. '-' indicates that the amino acid position has not been selected according to this criteria. 'not found' indicates amino acid positions that have been screened but mutations with statistically significant improvement have not been identified.

Supplementary Table 2. Layout of site-saturation libraries screened in the residue map stage.

Empty									
	Water								
Wild-type	Library 1	Library 2	Library 3		Library 11				
Wild-type	Library 1	Library 2	Library 3	<u> </u>	Library 11				
Wild-type	Library 1	Library 2	Library 3		Library 11				
Wild-type	Library 1	Library 2	Library 3		Library 11				
Water									
Empty									

Supplementary Table 3. Layout of mutants screened in the target mutation stage.

	Water								
	Wild- type	Mutant 1	Mutant 2		Mutant 6	Mutant 7	Mutant 8		
	Mutant 8	Mutant 7	Mutant 6		Mutant 2	Mutant 1	Wild- type		
Water	Wild- type	Mutant 9	Mutant 10		Mutant 14	Mutant 15	Mutant 16	Water	Empty
	Mutant 16	Mutant 15	Mutant 14		Mutant 10	Mutant 9	Wild- type		
	Wild- type	Mutant 17	Mutant 18		Mutant 22	Mutant 23	Mutant 24		
	Mutant 24	Mutant 23	Mutant 22		Mutant 18	Mutant 17	Wild- type		

Supplementary Table 4. Layout of mutants screened in the target checking stage.

	Water								
	Wild-type	Mutant 1	Mutant 2		Mutant 6	Mutant 7	Mutant 8		
	Mutant 8	Mutant 7	Mutant 6		Mutant 2	Mutant 1	Wild-type	-	
Water	Wild-type	Mutant 1	Mutant 2		Mutant 6	Mutant 7	Mutant 8	Water	Empty
vv ater	Mutant 8	Mutant 7	Mutant 6		Mutant 2	Mutant 1	Wild-type	vv ater	Empty
		_							
	Empty								
		=							

Supplementary Table 5. Composition of intracellular and extracellular solutions used to assess the ion selectivity of channelrhodopsins.

Solution	[Na] (mM)	[K] (mM)	[Ca] (mM)	[H] (mM)	рН	Other (mM)
Intracellular	0	140	0	5.10E-05	7.40	5 EGTA, 2 MgCl ₂ , 10 HEPES
145 mM NaCl	145	5	1	5.10E-05	7.40	10 HEPES, 5 glucose, 2 MgCl ₂
145 mM KCl	0	145	1	5.10E-05	7.40	10 HEPES, 5 glucose, 2 MgCl ₂
90 mM CaCl ₂	0	5	90	5.10E-05	7.40	10 HEPES, 5 glucose, 2 MgCl ₂
135 mM NMDG	5	5	1	5.10E-04	6.40	135 NMDG, 10 HEPES, 5 glucose, 2 MgCl ₂