

Supplementary Figure 1 | Structure and lentiviral co-transduction of E-HDF 2 **monolayers.** (a,b) Representative images of Vimentin⁺ E-HDFs in isotropic (a) or anisotropic 3 (b) monolayers. (c,d) Strong, ubiquitous co-expression of eGFP (left) and mCherry (right) in 4 isotropic (c) and anisotropic (d) E-HDF monolayers co-transduced with pRRL-CMV-NavSheP 5 D60N-P2A-Kir2.1-T2A-eGFP and pRRL-CMV-Cx43-P2A-mCherry lentiviruses. (e) Mixed 6 culture of HDFs transduced with pRRL-CMV-NavSheP D60N-P2A-Kir2.1-T2A-eGFP and 7 HDFs transduced with pRRL-CMV-Cx43-P2A-mCherry virus shown as a control to demonstrate 8 9 no cross-talk between read and green channels. Scale bars, 100 µm.

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NaChBa NavShe NavRos NavBp NavSi NavSi NavSi NavAb NavAb NavAb NavAb NavAb NavAb NavAb NavAb NavAb NavAb NavAb	Inc	110 107 98 105 111 95 102 98 108 96 97 113 116 99
NachBa NavSho NavRos NavBp NavSi NavSi NavAb NavAb NavAb NavAb NavAb NavAb NavAb NavAb NavAb NavAb NavAb NavAb	NC VLRILRVLRVLRAISVVPSLRRLVDALVMTIPALGNILILMSIFFYIFAVIGTMLFQHVS PEYFGNLQLSLLTLFQVVTLESWASGVMRPIFAEVPWSWLYFVSFVLIGTFIIFNLFIGV YLRSLRVLRVLRVLRVLSVASLLGSLPGLASIATVLLLIYYVFAVIATKIFGDAF PEWFGTIADSFYTLFQIMTLESWSMGISRPVMEVYPYAWVFFVPFILVATFTMLNLFIAI VLRALRILRVLRVISVAPSLRRVVEGFVTALPGMGSVFVLMAIIFYIGSVISTKLFAASF PQWFGSLPQSGYTLFQIMTLESWSMGIVRPVMEVYPFAWMFFIPFIMMTTFAVVNLLVGL VLRALRILRVLRVISVAPSLRRVVEGFVTALPGMGSVFVLMAIIFYIGSVISTKLFAASF PQWFGSLPQSGYTLFQIMTLESWSMGIVRPVMEVYPFAWMFFIPFIMMTTFAVVNLLVGL VLRALRILRVLRVISVAPSLRRVVEGFTALPGMGSVFVLMAIIFYIGSVISTKLFAASF PQWFGSLGVSUSVEFVLFQVTLESWASGIFRPIFAESGWSWLYFVSFIVIATFIMINLTVGE VVLRALRILRVLRVISVAPSLRRVVEGFTALPGMGSVFLLMTIIFYIGAVIATKLFAASF PDWFGDLGLSAVTLFQUTLESWSMGIVRPVMEVYPYAWVFVFVFIVTFIVGTFVFNLVGFF VVLRALRILRVLRVLSVAPRLRRVVEGFTALPGMGSVFLLMTIIFYIGAVIATKLFAASF PDWFGDLGSLSAVTLFQUTLESWSMGIVRPVMEVYPYAWVFVFVFIVTFIVGTFVFNLVGG VVLRALRILRVLRVLSVAPRLRRVVEGFTALPGMGSVFLLMGVIFYTFSVMATKLFGAGF PDWFGSLGKSAVSLFQVMTLESWSMGIVRPVMEVYPYAWVFFVPFILVTTFAVNLLVGL VLRALRILRVLRVLSVAPRLRRVVEGFTALPGMGSVFLLMGVIFYTFSVMATKLFGAGF PDWFGSLGKSAVSLFQUMTLESWSMGIVRPVMEVYPAWVFFVPFILVTTFAVNLLVGL VLRALRILRVLRVLLSVYTRRRVVEGFTALPGMGSVFLLMGVIFYTFSVMATKLFGAGF PDWFGSLGASYSLFQUMTLESWSMGIVRPVMEVYPAWVFFVPFILVTFVPFILVTFAVNLLVGL VLRALRILRVLRLLSVVFRKRRMVVEGFTALPGMGSVFLLMGVIFYTFSVMATKLFGAFPEWFGSLGASYSLFQUMTLESWSMGIVRPVMEVYPAWVFFVPFILVTFVVFILVMLVVGL ILSSLRILRVLRLLSVVFRKRRVVEGFTALPGMGSVFLLMGVIFYTFSVMATKLFGAFPEWFGSLGASYSLFQUMTLESWSMGIVRPVMEVYPAWVFFVFILVFFVFILVTFAVNLVVGL ILSSLRILRVLRLLSVVFRKRRVVEGFTALPGGNSVFLLMATTFFYTAMATUFGFFFEWFGSLGSSYSLFQUMTLESWSMGIVRPVMEVYPAWVFFVFILVFFVFILVSFTUVSFULVAI	230 227 218 225 231 215 222 218 228 228 216 217 233 236 218
NaChBa NavShe NavRos NavBp NavSil NavSu NavAb NavAb NavAb NavAs NavAs NavAs	IVNIVEKAELTDNEEDGEADGLKQEISALRKDVAELKSLLKQSK	

Supplementary Figure 2 | Homology of different BacNa_v orthologs. Residues E43 and D60 14 are indicated by green and red arrows respectively. The main regions labeled are: S1-S6 15 transmembrane helices, S4/S5 linker, P1 and P2 pore helices, and selectivity filter (SF). The 16 BacNa_v orthologs listed have been previously characterized either structurally or functionally: 17 NaChBac (Bacillus halodurans), NavSheP (Shewanella putrefaciens), NavRosD (Roseobacter 18 denitrificans), NavBacL (Bacillus licheniformis), NavBp (Bacillus pseudofirmus), NavSilP 19 (Silicibacter pomerovi), Na_vSulP (Sulfitobacter pontiacus), Na_vPz 20 (Paracoccus 21 zeaxanthinifaciens), NavAb1 (Alcanivorax borkumensis), NavAb (Arcobacter butzleri), NavMs (Magnetococcus marinus), NavCt (Caldalkalibacillus thermarum), NavAe (Alkalilimnicola 22 23 *ehrlichii*), and Na_vRh (*Rickettsiales sp.*)



Supplementary Figure 3 | **Electrophysiological properties of Na_vSheP mutants.** (**a**,**b**) Midpoints (V_{1/2}) of activation (**a**) and inactivation (**b**) curves of Na_vSheP mutants exhibit different depolarization shifts relative to the V_{1/2} of the wild-type (WT) channel. (**c**,**d**) Time constants of activation (τ_m , **c**) and inactivation (τ_h , **d**) measured at +20mV. Color-coding into groups is based on the characteristics of the respective amino acid side chains at residue 60. Recordings were performed at 25^oC (n = 4-10). Supplementary Table 1 shows a complete list of all activation and



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Supplementary Figure 4 | Computational modeling of E-HDF electrophysiology. (a) 37 Representative whole-cell voltage clamp recording of Na_vSheP D60A current in E-HDFs and the 38 corresponding computational traces. (b) Representative whole-cell voltage clamp recording of I_K 39 current in E-HDFs and the corresponding computational traces. (c,d) AP characteristics of E-40 41 HDFs expressing different BacNa_v mutants or Na_v1.5, obtained by computational modeling: APD_{80} (c) and AP threshold (d). For modeling BacNa_v currents, parameters derived from 42 voltage-clamp measurements at 25° C were scaled for the temperature of 37° C. Highly 43 hyperpolarized inactivation of WT and D60E channels prevented AP initiation. 44 45





47 Supplementary Figure 5 | Use of FACS to tune electrophysiological properties of E-Fibs. (a) 48 E-HDFs generated by co-transduction with Na_vSheP D60N-P2A-eGFP-Kir2.1 and Cx43-P2A-49 mCherry were sorted into three groups based on the level of eGFP expression (low, medium, 50 high). (b) Optical mapping of eGFP-sorted E-HDFs showed longer APD₈₀ associated with higher 51 eGFP intensity (n = 6-10). (c-d) When E-HDFs were sorted into three groups based on mCherry 52 expression level (low, medium, high, c), APD₈₀ was comparable among the groups (d, n = 5).

⁴P<0.01; [^]P<0.05 vs low eGFP group in **b**. Error bars indicate s.e.m; statistical significance was determined by one-way ANOVA, followed by Tukey's *post hoc* test to calculate P values.

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Supplementary Figure 6 | Computational studies of BacNa_v and Kir2.1 effects on E-HDF 59 electrical properties. (a-c) Maximum AP upstroke velocity (a), conduction velocity (b), and 60 threshold current required to elicit AP (c) in E-HDFs expressing varying levels (low, medium, 61 and high) of both Na_vSheP D60N and Kir2.1 (model 1) or the low level of Kir2.1 and varying 62 levels of only Na_vSheP D60N (model 2). Experimental data for AP upstroke and CV shown in 63 Fig. 3e,h are included for comparison. (d-f) Simulated effects of varying BacNa_v and Kir2.1 64 conductance values (G_{Na} and G_{K1}) on threshold current (**d**), AP upstroke (**e**), and CV (**f**). Solid 65 66 circles denote low (L), medium (M), or high (H) groups using either model 1 (M1, black circles) or model 2 (M2, white circles) shown in panels a-c. (g) Effects of varying intercellular 67 resistivity, R_i (shown relative to nominal R_i value used in panels **b** and **f**), on CV ratios between 68 69 the groups. Error bars indicate s.e.m.

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Supplementary Figure 7 | Stability of engineered cell phenotypes during long-term 73 74 expansion. (a) Growth curve of E-HDFs transduced with Na_vSheP D60N-Kir2.1 lentivirus following initial expansion and FACS. Cells senesced at passage eight. (b-d) Resting membrane 75 potential (b), maximum AP upstroke velocity (c), and APD₈₀ (d) of E-HDFs at various passages 76 throughout expansion assessed by patch clamp recordings (n = 8-10). (e-g) Optical mapping 77 78 studies in monolayers of monoclonal E-HEK293 cells expressing Na_vSheP D60A, Kir2.1, and Cx43, showing stable APD₈₀ (e), CV (f), and maximum capture rate (MCR, g) during 22 79 80 passages (n = 6-8). Properties beyond passage 22 were not examined and were presumed to remain stable. (**h**,**i**) Dependence of APD₈₀ (**h**) and CV (**i**) on pacing rate in monolayers made 81 from passage 22 E-HEK293 cells (n = 6). AP conduction at each pacing rate was mapped after 82 30s of pacing. All data were obtained at 37°C. Error bars indicate s.e.m; statistical significance 83 was determined by one-way ANOVA. 84

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Supplementary Figure 8 | Induction of excitability in various types of unexcitable human
 cells. Each human cell type (shown in different columns) was transduced with Na_vSheP D60N-

91 P2A-eGFP-K_{ir}2.1 lentivirus, expanded, and analyzed by voltage and current clamp recordings.

- 92 Engineered human astrocytes (E-HAs) were labeled for Glial fibrillary Acidic Protein (GFAP),
- 93 while engineered human dermal fibroblasts (E-HDFs), human ventricular fibroblast (E-HVFs),
- and human embryonic kidney 293 cells (E-HEK293s) were labeled for vimentin. Scale bars:
- $20\mu m$ (immunostaining images), 100ms and 2 nA (I_{Na} and I_K recordings), 25ms and 20mV (AP
- 96 recordings).
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Supplementary Figure 9 | Use of E-HDFs to improve impaired cardiomyocyte conduction. 99 (a) A zig-zag pattern of neonatal rat cardiomyocytes (CMs) used to simulate fast longitudinal 100 and slow transverse AP conduction characteristic of cardiac tissue with interstitial fibrosis. Cells 101 were stained with α -sarcomeric actin (red). (b,c) Representative fast longitudinal conduction (b) 102 and slow transverse conduction (c) in CM monoculture. (d,e) Slow unaltered transverse 103 conduction in CM + wt HDF co-culture (d) and CM + Na_vShePD60A+Kir2.1 HDF co-culture 104 (e). (f,g) Moderately and significantly improved transverse conduction in CM + Cx43 HDF (f) 105 106 and CM + E-HDF (g) co-cultures, respectively. In b-g: Scale bars, 1 mm. Pulse signs indicate positions of line stimulation. Circles denote recording sites. 107

Supplementary Figure 10 | Enhancement of cardiac AP conduction by BacNav expression. 110 (a) Schematic depicting exogenous expression of BacNa_v in cardiomyocytes (CMs) to augment 111 conduction. (b,c) Representative isochrone maps of AP conduction in electrically stimulated 112 isotropic monolayers of control neonatal rat CMs (b) and CMs transduced with Na_vSheP D60A 113 lentivirus (c). (d,e) CM monolayers transduced with Na_vSheP D60A lentivirus (CM + D60A) 114 show increased CV (d) and unaltered APD₈₀ (e) compared to control CM monolayers (n = 5). 115 *P<0.001 vs control CM. Pulse signs indicate location of stimulating electrode. Circles denote 116 504 recording sites. Error bars indicate s.e.m; statistical significance was determined by an 117 unpaired Student's t-test to calculate P value. 118

122 Supplementary Figure 11 | Consequences of ischemia on AP duration and firing in CM 123 monolayers with regional ischemia. (a) With time of ischemia, AP duration gradually decreases in the ischemic region of monolayers made of either control cardiomyocytes (CM) or 124 cardiomyocytes transduced with NavSheP D60A (CM + D60A) (n = 6). (b) Representative 125 optical AP traces in the non-ischemic (peripheral) and ischemic (central) regions of the 126 127 monolayer before (0 min) and during ischemia (6 min). (c) With time of ischemia, number of actively conducting recording sites within ischemic region is progressively reduced (n = 6). Error 128 bars indicate s.e.m. 129

	Activation			Inactivation		
Channel	V _{1/2} (mV)	Slope factor (mV)	Time constant (ms)	V _{1/2} (mV)	Slope factor (mV)	Time constant (ms)
SheP WT	-36.7	8.1	1.6	-139.5	8.9	31.7
D60E	-39.6	7.4	2.0	-132.9	9.5	27.8
D60A	-7.6	7.1	3	-76.1	9	42.4
D60I	-9.5	6.8	19.2	-80.6	7.8	54
D60L	0.9	7.3	6.2	-81.9	10.1	57.3
D60V	14.2	8.2	4	-84.6	10.4	70.5
D60C	-6.5	7.3	7	-91.7	9.2	46.3
D60M	-8.1	7.6	6.2	-87.1	8.6	44.5
D60N	-9.3	6.2	4.2	-80.8	9.8	38.6
D60Q	0.5	7.7	5.2	-75.8	8.5	38.2
D60S	-5.5	7	2.4	-84.6	8.6	34.9
D60T	-1.8	6.8	6.2	-83.6	8.2	34.3
D60F	30.4	8.9	28.8	-55.4	8.6	193
D60W	8.9	11	11.4	-81.2	9.7	104.5
D60Y	1	8.7	16.5	-77.5	8.9	61.9
D60G	-1.5	6.6	7.5	-84.2	9.4	54.6
D60P	11.3	7.5	4	-71.4	10.5	51.6
D60H	4.3	6.9	9.3	-69	8	43.6
D60K	8.3	7.5	7.7	-63.4	7.5	44.3
D60R	8.4	6.4	4.8	-52.8	7.2	56.4
E43A	0.3	8.2	3.5	-57.7	13.2	53.1
E43L	2.9	8.2	2.4	-87.3	7.5	92
E43V	10	8.3	4	-106.4	10.5	40.2
E43N	0	8.2	2.6	-61.3	15.8	58.2
E43Q	25.1	9.2	2.5	-44.1	15.5	82.9
E43S	5.5	10	4.5	-58.7	14	23.6
E43T	-2.5	7.6	2.7	-68.8	4.5	51.8
E43H	16.7	11.3	4.4	-69.9	14.6	53.9
E43K	12.8	10.5	3	-50.3	11.2	24.1
RosD G217A	-16.6	10.5	17.5	-78.2	9.8	260.2

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Supplementary Table 1 | Biophysical properties of $BacNa_v$ mutants. Activation and inactivation time constants were measured at +20mV clamp potential. Recordings were performed at 25^oC. Data shown are mean values (n = 4-10).

137	E43X	Primers	D60X	Primers
138 139 140 141 142 143 144	E43A	5'-ggctggctgaggtcgccatacctaactgc-3' 5'-gcagttaggtatggcgacctcagccagcc-3'	D60A	5'-aaatacactcagtagcaacttagcaagactcatcaacaaagtacc-3' 5'-ggtactttgttgatgagtcttgctaagttgctactgagtgtattt-3'
	E43C	5'-catcaggctggctgaggtgcacatacctaactgcaccgc-3° 5'-gcggtgcagttaggtatgtgcacctcagccagcctgatg-3	D60C	5'-cacaaatacactcagtagcaacttacaaagactcatcaacaaagtaccgtat-3' 5'-atacggtactttgttgatgagtctttgtaagttgctactgagtgtatttgtg-3'
	E43D	5'-ctggctgaggtatccatacctaactgcaccgcg-3' 5'-cgcggtgcagttaggtatggatacctcagccag-3'	D60E	5'-gtactttgttgatgagtcttgagaagttgctactgagtgtatttg-3' 5'-caaatacactcagtagcaacttctcaagactcatcaacaaagtac-3'
	E43F	5'-catcaggctggctgaggtgaacatacctaactgcaccgc-3' 5'-gcggtgcagttaggtatgttcacctcagccagcctgatg-3'	D60F	5'-cacaaatacactcagtagcaacttaaaaagactcatcaacaaagtaccgtat-3' 5'-atacggtactttgttgatgagtctttttaagttgctactggagtatttgtg-3'
145	E43G	5'-ggctggctgaggtccccatacctaactgc-3' 5'-gcagttaggtatggggacctcagccagcc-3'	D60G	5'-aaatacactcagtagcaacttaccaagactcatcaacaaagtacc-3' 5'-ggtactttgttgatgagtcttggtaagttgctactgagtgtattt-3'
	E43H	5'-tcaggctgggtgggtatgcatacctaactgcacc-3' 5'-ggtgcagttaggtatgcatacctcagccagcctga-3'	D60H	5'-atacactcagtagcaacttatgaagactcatcaacaaagtacc-3' 5'-ggtactttgttgatgagtcttcataagttgctactgagtgtat-3'
	E43I	5'-catcaggctggctgaggttatcatacctaactgcaccgc-3' 5'-gcggtgcagttaggtatgataacctcagccagcctgatg-3'	D60I	5'-cacaaatacactcagtagcaacttaataagactcatcaacaaagtaccgtat-3° 5'-atacggtactttgttgatgagtcttattaagttgctactgagtgtatttgtg-3'
	E43K	5'-ggctggctgaggtcttcatacctaactgcac-3' 5'-gtgcagttaggtatgaagacctcagccagcc-3'	D60K	5'-cactcagtagcaacttcttaagactcatcaacaaagtaccgtattgcgc-3' 5'-gcgcaatacggtactttgttgatgagtcttaagaagttgctactgagtg-3'
	E43L	5'-catcaggctggctgaggttaacatacctaactgcaccgc-3' 5'-gcggtgcagttaggtatgttaacctcagccagcctgatg-3'	D60L	5'-cactcagtagcaactttaaaagactcatcaacaaagtaccgtattgcgc-3' 5'-gcgcaatacggtactttgttgatgagtcttttaaagttgctactgagtg-3'
	E43M	5'-caggctggctgaggtcatcatacctaactgcacc-3' 5'-ggtgcagttaggtatgatgacctcagccagcctg-3'	D60M	5'-cactcagtagcaacttcataagactcatcaacaaagtaccgtattgcgc-3' 5'-gcgcaatacggtactttgttgatgagtcttatgaagttgctactgagtg-3'
	E43N	5'-atcaggctggctgaggtattcatacctaactgcaccg-3' 5'-cggtgcagttaggtatgaatacctcagccagcctgat-3'	D60N	5'-aatacactcagtagcaacttattaagactcatcaacaaagtaccg-3' 5'-cggtactttgttgatgagtcttaataagttgctactgagtgtatt-3'
	E43P	5'-caggctggctgaggtcggcatacctaactgcacc-3' 5'-ggtgcagttaggtatgccgacctcagccagcctg-3'	D60P	5'-caaatacactcagtagcaacttaggaagactcatcaacaaagtaccgt-3' 5'-acggtactttgttgatgagtcttcctaagttgctactgagtgtatttg-3'
	E43Q	5'-ggctggctgaggtctgcatacctaactgcac-3' 5'-gtgcagttaggtatgcagacctcagccagcc-3'	D60Q	5'-actcagtagcaacttctgaagactcatcaacaaagtaccgtattgc-3' 5'-gcaatacggtactttgttgatgagtcttcagaagttgctactgagt-3'
	E43R	5'-caggctggctgaggtcctcatacctaactgcacc-3' 5'-ggtgcagttaggtatgaggacctcagccagcctg-3'	D60R	5'-caaatacactcagtagcaacttacgaagactcatcaacaaagtaccgt-3' 5'-acggtactttgttgatgagtcttcgtaagttgctactgagtgtatttg-3'
	E43S	5'-caggctggctgaggtcgacatacctaactgcacc-3* 5'-ggtgcagttaggtatgtcgacctcagccagcctg-3'	D60S	5'-cacaaatacactcagtagcaacttactaagactcatcaacaaagtaccgtat-3° 5'-atacggtactttgttgatgagtcttagtaagttgctactgagtgtatttgtg-3'
	E43T	5'-caggctggctgaggtcgtcatacctaactgcacc-3* 5'-ggtgcagttaggtatgacgacctcagccagcctg-3'	D60T	5'-cacaaatacactcagtagcaacttagtaagactcatcaacaaagtaccgtat-3' 5'-atacggtactttgttgatgagtcttactaagttgctactgagtgtatttgtg-3'
	E43V	5'-ggctggctgaggtcaccatacctaactgc-3' 5'-gcagttaggtatggtgacctcagccagcc-3'	D60V	5'-ggtactttgttgatgagtcttgttaagttgctactgagtgtattt-3' 5'-aaatacactcagtagcaacttaacaagactcatcaacaaagtacc-3'
	E43W	5'-caggctggctgaggtccacatacctaactgcacc-3' 5'-ggtgcagttaggtatgtggacctcagccagcctg-3'	D60W	5'-cactcagtagcaacttccaaagactcatcaacaaagtaccgtattgcgc-3' 5'-gcgcaatacggtactttgttgatgagtctttggaagttgctactgagtg-3'
	E43Y	5'-atcaggctggctgaggtatacatacctaactgcaccg-3' 5'-cggtgcagttaggtatgtatacctcagccagcctgat-3'	D60Y	5'-aatacactcagtagcaacttataaagactcatcaacaaagtaccg-3' 5'-cggtacttigtigatgagtctttataagtigctactgagtgtatt-3'

Supplementary Table 2 | List of mutagenesis primers used to create Na_vSheP E43X and D60X libraries (designed by QuikChange® Primer Design Program).

Tome concentrations	
Intracellular Na+ concentration	10.7 mM
Extracellular Na+ concentration	135.3 mM
Intracellular K+ concentration	120 mM
Extracellular K+ concentration	5.4 mM
Membrane properties	
Total membrane surface area (A)	2134 µm ²
Total membrane capacitance (C_m)	22 pF
$BacNa_v$ maximum conductance (\overline{G}_{Na})	81.51 nS
$K_{ir}^{2.1}$ maximum total conductance (\overline{G}_{K1})	87.93 nS
Resting membrane potential (V_{rest})	-80.1 mV
Sodium Nernst potential (E_{Na}) at $37^{0}C$	67.8 mV
Potassium Nernst potential (E_{K}) at $37^{0}C$	-82.8 mV
Core-conductor model parameters	
Time step (Δt)	0.0025 ms
Space step (Δx)	24 µm
Cable radius	10.0 µm
Cable length	0.72 cm
Specific membrane capacitance (c_m)	$1.031 \ \mu F/cm^2$
Intracellular resistivity (R _i)	1.48 kΩ.cm

Ionic concentrations

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Supplementary Table 3 | Computational modeling parameters. Cell membrane properties (A, 147 C_m , \overline{G}_{Na} , \overline{G}_{K1} , V_{rest} , E_{Na} , and E_K) used in the model were mean experimental values derived from 148 whole-cell voltage-clamp recordings in a monoclonal HEK293 line expressing Kir2.1, Cx43, and 149 Na_vSheP D60A. Extracellular Na⁺ and K⁺ concentrations used in the model were the same as 150 used in the bath solution during patch clamp and optical mapping experiments. Intracellular Na⁺ 151 and K⁺ concentrations in the model were derived using Nernst equation, extracellular Na⁺ and K⁺ 152 concentrations and E_{Na} and E_K, respectively. Specific membrane capacitance (c_m) used in the 153 model was obtained by dividing mean cell membrane capacitance (C_m) with mean estimated cell 154 155 membrane surface area (A). Intracellular resistivity (R_i) was adjusted to exactly simulate the mean conduction velocity (21.04 cm/s) recorded by optical mapping in confluent isotropic 156 monolayers of the above-mentioned monoclonal HEK293 line expressing Kir2.1, Cx43, and 157 Na_vSheP D60A. 158